# OptiArch: Optimization of plant architecture in sunflower (*Helianthus annuus*) for yield increase

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**M.Sc. Yves Sprycha**

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## Gutachter

Prof. Dr. Renate Horn, Universität Rostock, Institut für Biowissenschaften

Prof. Dr. Wolfgang Link, Georg-August-Universität Göttingen, Institut für Nutzpflanzenwissenschaften

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| | |
|---|---|
| °C | Degree Celsius |
| µ | micro |
| A | Adenine |
| AA | Amino acid |
| ANOVA | Analysis of Variance |
| AOPD | agronomical optimal plant density |
| BLAST | Basic Local Alignment Search Tool |
| bp | Base pair |
| C | Cytosine |
| CaCl2 | Calcium chloride |
| cDNA | complementary DNA |
| Chr. | Chromosome |
| cm | Centimeter |
| cM | Centimorgan |
| CTAB | Cetyltrimethylammonium bromide |
| dATP | Desoxyadenosintriphosphate |
| ddH2O | double distilled water |
| DEPC | Diethyl pyrocarbonate |
| DNA | Deoxyribonucleic acid |
| dNTP | Desoxyribonukleosidtriphosphate |
| dt | decitonne |
| E. coli | Escherichia coli |
| et al. | et alii, et aliae, et alia |
| g | gram |
| G | Guanin |
| GFP | green fluorescent protein |
| h | hour |
| ha | Hektar |
| HRM | High Resolution Melting |
| IPR | iron content in polished rice |
| IPTG | Isopropyl-β-D-thiogalactopyranoside |
| IRD | Infrared Dyes |
| k | kilo |
| KASP | Kompetitive allele specific PCR |
| kb | Kilo base pair |
| kg | kilo gram |
| l | liter |
| m | Meter and milli |
| M | Molar |

| | |
|---|---|
| MgCl2 | Magnesiumchloride |
| min | Minute |
| n | nano |
| NCBI | National Center for Biotechnology Information |
| nt | nukleotide |
| ORF | Open reading frame |
| PCR | Polymerase Chain Reaction |
| Pet | petiole angle |
| PH | plant height |
| PL | panicle length and |
| RNA | ribonucleic acid |
| s | second |
| SDS | Sodium Dodecyl Sulfate |
| SNP | Single nucleotide polymorphism |
| SOC | Super Optimal broth with Catabolite repression |
| SPY | single plant yield |
| SSR | Simple Sequence Repeat |
| T | Thymine |
| TAC1 | Tiller angle control |
| TAE | Tris-Acetate-EDTA-Buffer |
| TBE | Tris-Borat-EDTA-Puffer |
| TE | Tris-EDTA |
| TP | tillering potential |
| U | Unit |
| U/min | Revolutions per minute |
| UPOV | Union Internationale pour la Protection des Obtentions Végétales |
| V | Volt |
| X-Gal | 5-Brom-4-chlor-3-indoxyl-β-D-galactopyranosid |
| YE | yield environment |
| YEB | Yeast Extract Broth |
| ZBR | zin in brown rice |
| ZPR | zinc in polished rice |
| α | alpha |
| Ω | Ohm |

# 1 Summary

The aim of this doctoral thesis was to optimize the plant architecture in the sunflower to a more compact, more efficient growth type. The focus was on leaf angle and plant height, on cultivation with higher plant density and on increasing the yield per hectare. The project consisted of two sub-projects - on the one hand the association studies on the genes of the plant architecture and on the other hand the field studies on the plant architecture. The sunflower association panel developed by the U.S. National Plant Germplasm System (NPGS) or accessible through the Plant Gene Resources of Canada (PGRC), exhibits significant phenotypic variation in leaf angle, plant height, branching, and branching angle. Since these clear differences in the plant architecture are present in the association panel, different gene variants should be found for the genes of the GA-signaling pathway as well as for the genes *HaTAC1* and *HaLAZY1*. Performance tests with different plant densities should show to what extent gene variants are identified that are relevant for breeding. The project offers the opportunity to investigate genes in the sunflower that have been shown to have a significant influence on plant architecture using a next-generation sequencing approach. First, seeds of the association panel were propagated and the panel was repeatedly phenotyped with a focus on the traits plant height and leaf angle (petiole angle and leaf sheath angle). In a second step, based on the phenotypes, accessions were selected for sequencing and crosses were performed to analyze inheritance. In addition, test hybrids were produced from the selected accessions, which are tested in yield trials for performance and the phenotypes mentioned.

The sunflower association panel could be evaluated at different locations with different climatic conditions. Based on correlation data between the locations in Germany (Bandow) and Spain (Guadalajara), 64 genotypes with specific growth types could be selected, which showed clear phenotypic differences in plant architecture. The selected genotypes could be assigned to the different growth types and then used for association studies. These growth types related to both the plant height and the formation of the petiole angle.

Fifty-three F1 hybrids were also scored and their plant architectural properties evaluated. These F1 hybrids were successfully used for performance tests with different plant densities. The performance tests were carried out at two locations with different climatic conditions in Germany and Romania. The results of the performance tests show some candidate sunflower hybrids that can provide increased yield by cultivating with increased plant density. Segregation analyses of the mode of inheritance of the traits plant height and petiole angle were carried out on five F2 populations. In two of these F2 populations, the hypothetical 1:3 phenotypic split for the trait plant height could be observed, indicating that this trait is under monogenic control. Comparing the F1 hybrids of the five crossbreeds studied with the parental individuals, it was found that the crossbred parents exhibited the observed

traits as previously assessed. The F1 hybrids showed their expected uniformity without the extreme phenotypes of either parent. It was found that the traits plant height and petiole angle are recessively inherited.

The genes of the GA signaling pathway and the branching angle were examined and the partial sequences of three genes were completed. Two homologues were identified for each of the genes *TAC1* and *LAZY1* in the sunflower. A candidate gene approach extended to 22 genes was used for further analyses. The 22 candidate genes of the 64 genotypes were sequenced using Amplicon Targeted Sequencing and a total of 306 SNPs and 111 InDels were identified. The SNP analyses enabled the identification of gene variants of the candidate genes.

The population structures of the small and the big association panels could be determined using SSR analyses. Association studies to identify phenotypically relevant SNPs were successfully performed with GLM analyses using TASSEL 5 and the Fischer's exact test. A total of 59 significantly associated SNPs were found in 11 candidate genes. Based on the significant SNPs, HRM markers were developed and tested within the small and big association panels and 25 ornamental sunflowers.

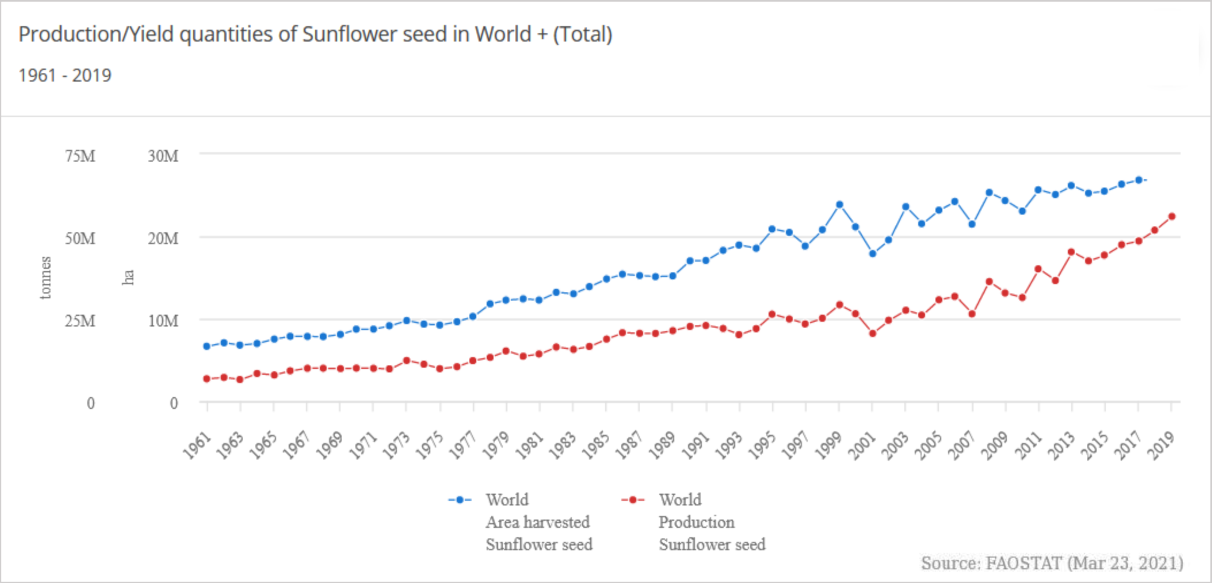
Although, the four HRM markers in the small association panel were convincing, they were not verified by the results of the extended analysis in the large panel. KASP analyses of the large association panel provided the molecular basis for a GLM analysis. The data from the KASP analysis of the large panel were combined with the existing data from the next-generation sequencing of the small association panel. The results of the GLM analysis showed associations of the 59 associated SNPs already identified with the petiole angle trait. A total of six SNPs in the three genes *HaGID1B*, *HaDELLA1* and *HaDELLA-Like2* were identified for this trait. Since the two SNPs GID071.16 and GID1071.24 in the HaGID1B gene were already identified as significantly associated with the formation of the petiole angle by analysis of the small association panel with TASSEL 5, they could be verified and thus be regarded as potential molecular markers for plant architecture.

# 2 Introduction

The sunflower (*Helianthus annuus* L.) is an annual plant classified into the family of *Asteraceae* and the genus *Helianthus*, which includes approx. 67 species worldwide (Schilling, 2006). The sunflower is characterised by a large, circular, composite inflorescence, long taproots, broad and roughly toothed, rough leaves. The flowers come in different sizes and colours, which can vary from cream to yellow to red in different varieties (Adeleke & Babalola, 2020). Compared to cereals, sunflowers grow optimal under high temperatures and drought conditions. The moisture retention due to the long, deep taproot system allows the plant to quickly recover from moisture loss and a survival under stressful conditions (Hussain *et al*., 2018). Due to this high drought tolerance and the ability to adapt to many different soils, the sunflower is grown in very many parts of the world (Vilvert *et al.,* 2018).

## 2.1 The economic importance of the sunflower

The economic relevance of the sunflower relates to different uses for food processing (Khurana & Singh, 2021) and in the ornamental plant sector (Jocić *et al*., 2015). Sunflower is used in the human diet, as oil and for medical purposes, but mostly it is used for oil production from seed, but it is also used as a protein crop for human consumption, as well as for feed (Jocić *et al*., 2015). In addition, sunflower oil comes in different fatty acid types such as high oleic (up to 90 %, C18:1) and conventional high-linoleic (C18:2) (Wittkop *et al.*, 2009). Sunflower is an important agricultural crop grown for its seeds worldwide. Globally, sunflower is the fourth largest source of vegetable oil next to soybean, palm and rapeseed and thus, the production of sunflower seed has increased over the years because of the increasing demand for its healthful oil (Khurana & Singh, 2021) (Fig. 1).



Source: FAOSTAT (Mar 23, 2021)

**Figure 1:** Summary of production/yield quantities of sunflower seeds in the world 1961 – 2019

## 2.2 Influence of the plant architecture on the yield

Feeding an ever-increasing global population poses a grand challenge in light of the declining availability of cropland under changing climate conditions. One of the best solutions to this problem is to continuously and sustainably improve crop productivity (Liang *et al*., 2021). Since the agriculturally usable area is constantly decreasing due to urbanization, soil erosion, salinization and many other factors, it is urgently necessary to significantly increase the yields per hectare. It is possible to achieve a significantly higher plant density through optimized plant architecture towards a more compact growth type and thus to achieve significantly higher yields (Hall *et al*., 2010, Dimitrijevic & Horn, 2018). The plant architecture plays an important role here, as it has a significant influence on various points such as the photosynthesis rate, lodging and plant density. Various features are taken into account, such as plant height and posture of the head, as well as branching and leaf angles. For example, breeding to a lower plant height for cereals has led to the “Green Revolution” (Peng *et al*., 1999). In sunflower, breeding for a more compact plant architecture could probably lead to increases in the yield per hectare that are comparable to those in cereals.

### 2.2.1 Increasing yield due to dwarfism

Sunflowers is prone to lodge due to large plant sizes and large heads, especially under heavy rainfalls and strong winds. Lodging resistance differs significantly between genotypes due to differences in plant height and root development (Polat *et al*., 2017). The reduced plant height is also a desirable feature in order to improve the efficiency of machine harvesting and to facilitate the application of pesticides against diseases and pests (Weiss, 2000; Koutroubas *et al*., 2014). In agriculture, semi-dwarf plants have several important advantages over their larger ancestral forms. In particular, shorter stems present less competition for limited resources, which improves yield in most environments (Pearce, 2021). Using the example of cereals, it becomes clear that semi-dwarf types can be of interest for breeding and the introduction of “*semi dwarf1*” (*sd1*) in rice and “*reduced height*” (*Rht1*) in wheat (Würschum *et al*., 2017) have led to an improved plant architecture and reduced lodging tendency (Khush, 2001). The reduced height turned out to be an agronomically important trait and led to a considerable increase in yield (Khush, 2001). A mutation in the *DWF2* gene was also found in oilseed rape as the basis for a reduced growth type. It is interesting that the mutation is not located in the DELLA domain of the gene, as in all other cases, but in the C-terminal GRAS domain. It also has a milder effect on the plant height than mutations in the DELLA domain (Muangprom *et al.,* 2005). In addition, genetic variants that limit the rate of cell elongation in the stem and result in a lower crop height mean that growers can take full advantage of fertilization and irrigation. Although many genes contribute to this, most of the semi-dwarf crops grown today carry one of a few variants that alter the level or activity of the plant hormone gibberellin (GA). Actively growing tissues contain high amounts of bioactive GA, which among other features promotes cell expansion (Pearce, 2021).

### 2.2.2 Impact of leaf and branching angles

The number of branches and their angles represent an important aspect of the plant architecture. In order to guarantee pollen production over a longer period of time, a recessively inherited branch was introduced into the restorer lines during the development of hybrid breeding programs in sunflower. In order to obtain unbranched F1 hybrids by crossing, it was ensured that the male sterile maternal lines did not show any branches (Nambeesan *et al*., 2015; Fick & Miller, 1997). The branching plays an important role in the adaptation of the plants to their surroundings. Variations in branching help to compete with their neighbors, as branching can also affect other developmental traits such as the duration of flowering time and reproductive success. So-called "domestication syndrome" describes the fact that many plants have less branching (i.e. increased apical dominance) compared to their wild ancestors (Nambeesan *et al*., 2015). In comparative genetic studies between cultivated and wild sunflowers, it was found that branching is influenced by numerous small effect sites that are distributed throughout the genome and thus represent a genetically complex trait (Burke *et al*., 2002). Crossings between wild sunflower and a highly improved oilseed cultivar showed, that domestication-related traits in sunflower are controlled by numerous QTL (Wills & Burke, 2007).

Leaf shape, including leaf length, leaf width, leaf angle, and leaf orientation value, are critical factors in determining a desirable plant architecture that greatly affect dense planting and yield (Zhong *et al.,* 2021). The expression of the petiole angles along the plant and the leaf position have an effect on light perception and the photosynthesis rate (Jones, 2014). In a recent study, the differences in the morphological and physiological properties of leaf deposition in two varieties of the ornamental plant *Hippeastrum rutilum* were analyzed. The aim of this study was to compare the differences between the two varieties with leaf deposits and upright leaves. The results of this study showed that lodging affects photosynthetic capacity in a negative way (Shi *et al.,* 2020).

The upright leaf position reduces the shading of the lower leaves and promotes better light distribution. This effect enables higher plant densities and thus higher yields (Tian *et al.,* 2011). The upright leaf position is an agronomically important feature and represents the driving force behind the increase in maize yields (Xin *et al.*, 2015). In the USA, a higher plant density due to a more compact growth type with upright leaf position is now standard in maize (Duvick & Cassman, 1999). In sunflower, higher plant densities have already led to increasing yields (Hall *et al.,* 2010).

## 2.3 Genetic background of the plant architecture

### 2.3.1 Genes of GA-signaling pathway

Plant growth regulators (PGRs) are organic compounds that control or modify one or more physiological features in plants. These synthetic compounds are widely used in plants, especially cereals, to reduce plant height. The best-known PGR group are the gibberellins. They influence many physiological functions in plants, but are essentially responsible for controlling cell elongation as well as shoot and stem growth (Polat *et al*., 2017; Spitzer *et al*., 2011). Mutants of the GA biosynthesis and the GA-signaling pathway have clear recognizable phenotypes and can be of great interest for breeding due to the reduced height. Examples of this are the introduction of *semi-dwarf1* (*sd1*) in rice and *reduced height1* (*Rht1*) in wheat, through which the lodging was reduced due to the lower plant height (Würschum *et al*., 2017).

In the GA signaling pathway, three main components are involved in signal transmission, the DELLA proteins, the GA receptor GID1 and SLY/GID2 as part of the SCF E3 ubiquitin ligase complex. The DELLA proteins belong to the family of the GRAS genes and are essentially localised transcription regulators, which repress the transmission of GA signals (Daviere & Achard, 2013). All DELLA repressors have an N-terminal DELLA regulatory domain containing the conserved amino acid sequence Asp-Glu-Leu-Leu-Ala (DELLA) and a C-terminal GRAS (for GAI, RGA, and SCARECROW) functional domain (Hauvermale *et al*., 2012). Alleles in which the eponymous DELLA motif in these proteins is disrupted result in constitutive repression of GA signaling and a dominantly inherited dwarf phenotype (Best *et al*., 2016). The GA signal is sensed by a soluble receptor protein, GA-INSENSITIVE DWARF1 (*GID1*). It was identified by map-based cloning of a GA-insensitive mutant in rice that carries a single copy of the gene (Ueguchi-Tanaka *et al.*, 2005). In barley a single homolog (*GSE1*) was defined using GA-insensitive *GID1* mutants and three homologs were identified in Arabidopsis (*GID1a, GID1b, GID1c*). Mutations in the GA receptor leads to phenotypes that are similar to those that result from severe GA biosynthetic mutations, but they cannot be saved by GA applications (Hauvermale *et al*., 2012). The SCF complex consists of three subunits: SKP1, Cullin and F-box protein (*SLY1*). It represents an E3 ubiquitin ligase and signals the 26 S proteasome, via ubiquitinylation of the protein, to degrade the bound substrate (Tao *et al.* 2017).

The sequence of the GA signaling pathway can be briefly described as follows (Fig. 2). When GA binds to its *GID1* receptor, the *GID1* receptor changes its conformation, allowing the GA/GID1 complex to bind to the DELLA protein. Then the SCF complex is able to bind to the DELLA protein. The F-box protein *SLY1* binds the substrate to be degraded with its C-terminus and marks it for the proteolytic degradation (Fig. 2).

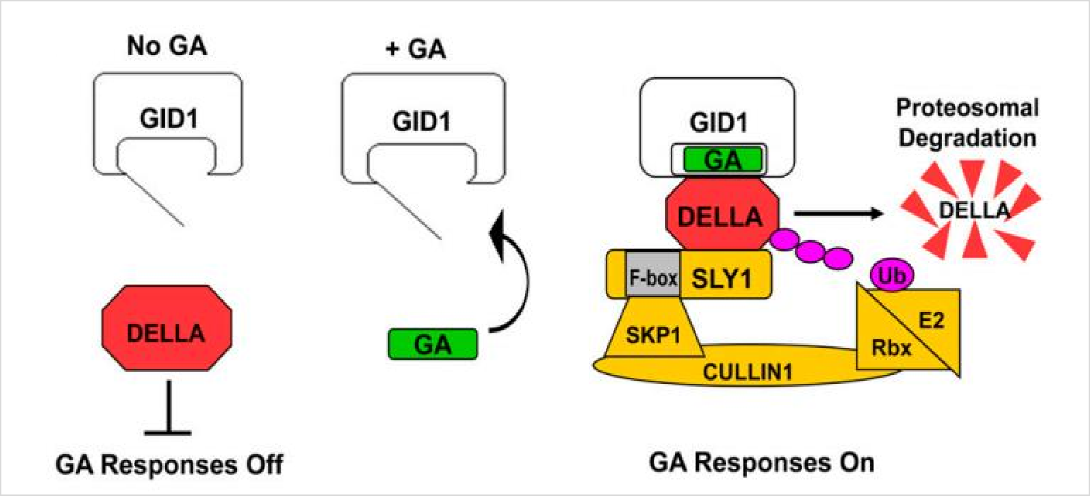


**Figure 2:** GA signaling model illustrating GA-dependent GID1-DELLA complex formation resulting in DELLA recognition and ubiquitinylation by the SCF/SLY1 E3. Polyubiquitinylation leads to DELLA proteolysis by the 26S proteasome, thereby lifting DELLA repression of GA responses (Hauvermale *et al*., 2012)

### 2.3.2 Role of the *TAC1* and *LAZY1* genes in plant architecture

The two genes *TAC1* (*TILLER ANGLE CONTROL 1*) and *LAZY1* belong to the genetic background of the leaf angle. This was initially described as grass-specific for rice and maize (Li *et al*., 2007; Yoshihara & Lino, 2007; Yu *et al.,* 2007). However, mutations in *LAZY1* lead to a widespread growth type as shown in Arabidopsis (Fig. 3). A mutation in *TAC1* leads to an upright, more compact growth type (Fig. 3).

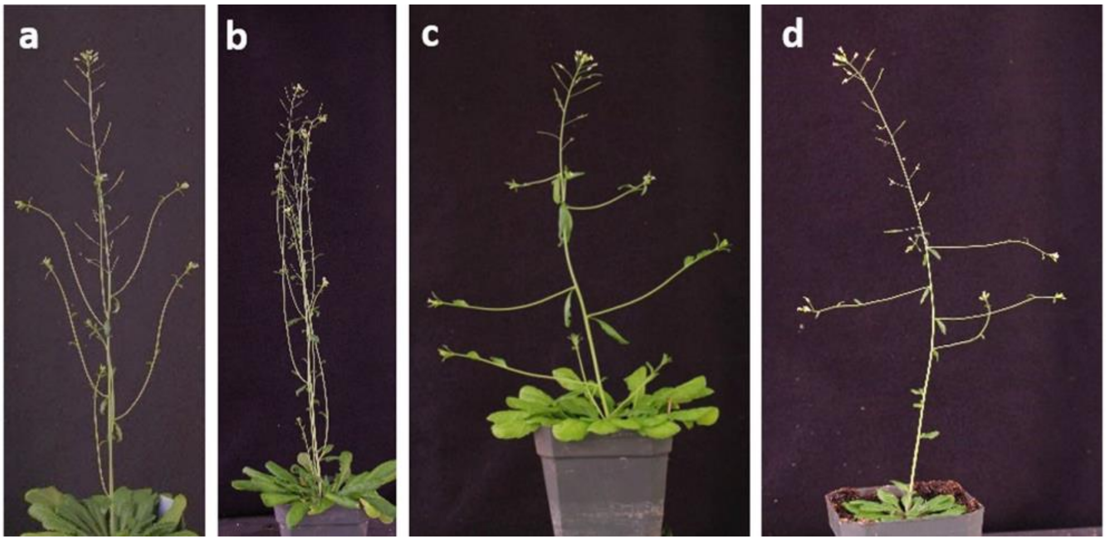


**Figure 3:** The *lazy1* branch phenotype is epistatic to *tac1*. **A)** Col, **B)** *tac1*, **C)** *lazy1*, **D)** *tac1;lazy1* (Hollender *et al*., 2020)

*TAC1* and *LAZY1* are members of a gene family that regulates lateral shoot orientation in plants, the IGT gene family (Dardick *et al*., 2013. They are important regulators of lateral organ orientation, that in both shoots and roots plays a key role in a plant's interaction with the environment and its ability to access resources such as light and water (Hollender *et al.*, 2020). While *TAC1* generally occurs as a single copy gene, many plant species have multiple *LAZY* genes, six of which were identified in *Arabidopsis* (Hollender *et al.*, 2020). The genes have four conserved amino acid regions or domains in common, with *LAZY* genes having an additional C-terminal domain. *LAZY1* is expressed during sensitivity to gravitropism and plays a negative role in polar auxin transport. The loss of function of *LAZY1* increases the polar auxin transport, which leads to a change in the endogenous IAA distribution in shoots. The reduced gravitropism causes a tiller-spread phenotype (He *et al*., 2017).

BLAST analyses have already shown that these grass-specific genes are ubiquitous in the plant kingdom and play an important role in the formation of branching and leaf angles in both angiosperms and gymnosperms (Dardick *et al.*, 2013). In the peach tree (*Prunus persica*) two different types of mutations were found in the *PpeTAC1* gene, which lead to the pillar growth types “Italian Pillar" and "New Jersey Pillar". The intermediate type "upright" was created through the intermediate inheritance. Varieties have been developed for both “pillar” and “upright” that lead to higher yields due to higher planting densities (Dardick *et al*., 2013).

The *LAZY1* gene is also important for oil plants. Genome-wide studies on branching in rapeseed (*Brassica napus*) showed that rapeseed has two *LAZY* orthologues (Liu *et al.,* 2016). A panel of 143 rapeseed accessions was analysed and showed significant variation of branching angles. The changes in the rapeseed branch angle alter plant architecture, allowing more efficient light capture as planting density increases (Liu *et al*., 2016).

## 2.4 Association studies in plant breeding

Since agro-morphological characteristics are extremely important for sunflower breeders when selecting high-performance genotypes, crops have so far been successfully improved by cross-pollination and screening for the associated heterosis effect in hybrid breeding. The precise use of hybrid power saves time and resources and can be improved through the use of new genetically based techniques such as association mapping. This method has proven very successful in developing rapid crop improvement based on molecular markers (Ibrar *et al.,* 2020). In recent years, it has been shown that association studies are very well suited as a method for identifying associations of markers with characteristics in various plants. The association methods initially concentrate on candidate gene strategies, which are based on prior knowledge of the pathways that control the traits to be considered. The development of new sequencing and high throughput genotyping technologies ultimately enabled significant advances in the genetic mapping of agronomic traits. Due to the increasing availability of markers, the candidate gene approach has become substituted by genome-wide association studies (GWAS) (Cadic *et al.,* 2013).

Investigating the sunflower gene pool, Mandel *et al.* (2011) selected an assortment of 433 cultivated accessions and 24 wild sunflower populations. All accessions were genotyped using 34 EST-SSRs for the population structure. These were taken from the larger set of SSR markers (Chapman *et al.*, 2008). The 34 markers were selected based on presumed neutrality and genetic position so that broad genomic coverage could be achieved with one marker on each arm of the 17 sunflower linkage groups. The results of the association analyses showed that the majority of the variety diversity stems from two genetic clusters of the wild sunflower population. In the end, a core set of 288 sunflower accessions captured almost 90 % of the alleles present in the full set of 433, while a core set of only 12 accessions was sufficient to capture nearly 50 % of the total allele diversity (Mandel *et al.,* 2011). The core set of the 288 sunflower accessions was used for association studies with regard to branching in the work of Nambeesan *et al.* (2015). This study enabled SNPs to be identified, which were in close proximity to potential candidate genes. It was also found that different genome regions play a role in the development of apical and basal branching (Nambeesan *et al.*, 2015).

Further association studies with various sunflower association panels were also successfully carried out with regard to the flowering date. Through the work of Darvishzade (2016) 248 loci and 67 alleles were detected. In total, 224 of these loci showed significant association with quantitative trait loci (QTL) controlling the investigated traits like flowering time or petiole length (Darvishzadeh, 2016). For association studies with *Sclerotinia sclerotiorum* resistance an association panel of 94 inbred sunflower lines was tested for sclerotinia head rot. Since no biological mechanisms or biochemical pathways were clearly identified for sclerotinia head rot, 43 candidate genes were selected. Association studies between the incidence of sclerotinia head rot and haplotype polymorphisms enabled the detection of a significant association between the candidate gene *HaRIC_B* and sclerotinia head rot incidence (Fusari *et al.*, 2012).

Studies with other crops such as rice or maize also showed that association studies can play an important role in plant breeding. The Rice Diversity Panel 1 (RDP1) was developed for genome-wide association studies (GWAS) to examine five rice subpopulations. It was examined for over 30 traits and genotyped with 700,000 SNPs. The aim was to identify GWAS-QTL from the RDP1-GWAS studies to identify underlying genes that may control certain yield component traits. The 256 recombinant inbred lines (RILs) were genotyped with 132 SSR markers and 70 QTLs were found. SNPs in the overlapping GWAS-QTL for RIL-QTL with high $R^2$ values could be assessed as potential DNA markers that are useful for breeding programs of the associated yield trait (Eizenga *et al.*, 2018).

Association studies recently led to new discoveries in maize as well. Using an F1 population, a genome-wide association study was carried out to identify candidate genes that influence plant height control (Zhang *et al.*, 2019). The population consisted of 300 maize hybrids in which 17,652 SNP markers were tested. The investigation identified nine significant SNP markers and two candidate genes for plant height. The identified candidate genes *Zm00001d018617* and *Zm00001d023659* encode for a gibberellin 2–oxidase 12 and the auxin response factor 2 respectively. They provide new insights into the genetic basis of plant height in maize (Zhang *et al.*, 2019). In another study on wheat (*Triticum aestivum*), 312 different pre-bred lines were examined for the genetic components of emergence percentage, head time, plant height, housing, thousand kernel weight and yield (Akram *et al*., 2020). In total, the study showed 200 significant and 61 highly significant associations. It was also found that chromosomes 1B and 2A carried yield-associated loci in two different seasons and that positive allele mining can increase yield by up to 8.20 % (Akram *et al.*, 2020).

## 2.5 The usefulness of molecular markers in plant breeding

For the development of a more targeted improvement of crops, marker-assisted selection (MAS) in plant breeding has proven to be very effective. The usefulness of this technique lies above all in the time savings and a greatly reduced effort in phenotyping, since it enables a more precise selection. The markers that are closely linked to the QTL that have an influence on the phenotype of the plant must be localized in the genome (Ibrar *et al.,* 2020). Thanks to the various molecular biological tools, the development of new varieties can now take place within a few years. While this process took up to 25 years, it is now possible to establish a new plant variety within 7-10 years (Darvishzadeh *et al.,* 2016). These tools include MAS, which requires the identification of closely linked markers (Darvishzadeh *et al.,* 2016).

Microsatellites or simple sequence repeat (SSR) markers are very often used for population structure analyses in association mapping studies, as they have been shown to generate more information than biallelic markers (Ibrar *et al.,* 2020). Microsatellites or SSR markers are one of the most reliable types of DNA markers because they are highly polymorphic and randomly distributed, and they are inherited co-dominantly according to Mendel's principles (Darvishzadeh *et al.,* 2016). They have been used as molecular markers for studies of genetic diversity in several agriculturally important crops (Darvishzadeh *et al.,* 2016). In addition, various molecular markers based on retrotransposons could be developed and used to characterize genetic resources in plants. The association mapping approach has also been applied to various plants that are of agricultural importance, such as maize, barley, tobacco and sunflower (Darvishzadeh *et al.,* 2016).

Various types of molecular markers are available for sunflowers, but microsatellites and SNPs are used the most. More than 2000 SSR markers could be developed from genomic and EST libraries in sunflower (Filippi *et al.,* 2015). In sunflower, various molecular markers form the basis for assessing genetic diversity and sunflower breeding has been facilitated by the use of markers. The development of specific molecular markers made it possible to identify desirable genes (Dimitrijevic & Horn, 2018).

The development of a large number of molecular markers was the driving force behind the progress in the breeding of sunflower hybrids (Dimitrijevic & Horn, 2018). A wide variety of markers were used in hybrid breeding with regard to disease resistance, quality traits, herbicide resistance and restoration of fertility (Horn *et al.,* 2019). The breeding of sunflower hybrids is based on the use of male-sterile sunflower lines (A-lines), maintainer lines (B-lines) for the maintenance of A-lines and fertility restorer lines (R-lines), which contain the restorer gene *Rf1*. Different markers were developed that are closely linked to the *Rf1* gene (Horn *et al*., 2019).

The examples listed show that the molecular approaches can be used to improve crop plants and thereby accelerate plant breeding. The classic approaches of plant breeding combined with the use of molecular markers can efficiently improve successful breeding of crops (Kumar *et al.,* 2020).

## 2.6 Objectives

The aim of the PhD thesis was to optimise the plant architecture of the sunflower towards a more compact, more efficient growth type. The focus was placed on the investigation of the petiole angles and the plant height. An increase in the yield per hectare should result from the possibility of growing sunflowers with a higher plant density. In order to achieve this, an optimised plant architecture should be obtained through the use of genetic diversity in a sunflower association panel.

The PhD thesis consists of two sub-projects. On the one hand from the association studies on the genes of plant architecture and on the other hand from the field studies on plant architecture. The association studies include the steps to supplement the partial gene sequences for 22 candidate genes, the division of the association panel into maintainer and restorer lines using molecular marker analyses and investigations of the plant architecture using the association panel. The aim was to develop SNP markers based on the sequence differences in the 22 candidate genes of 64 selected genotypes and to validate these markers for the plant architecture in the entire association panel.

The field studies included propagation and evaluation of the large association panel as well as 64 selected genotypes. Also, the creation of F1 test hybrids and the development of F2 population for heredity studies, as well as performance tests with different plant densities were carried out. The aim was to evaluate the new growth types in comparison to commercial sunflower hybrids with regard to yield and oil content.

# 3 Material and methods

## 3.1 Software, primers, ladders and database

For the experiments carried out, the used bioinformatics software (Tab. 1), primers (Suppl. Tab. A 1-3) as well as DNA ladders for gel electrophoretic separations and SSR analysis are shown in the following table and figure. As reference for the genomic sequences, the database HanXRQr2.0-SUNRISE (https://www.heliagene.org/HanXRQr2.0-SUNRISE/) was used (Badouin *et al.*, 2017), as well as the genome sequence of HA 412 (Kane *et al.,* 2011).

**Table 1:** Bioinformatics software

| PROGRAM | REFERENCE |
|---|---|
| Structure harvester | • Dent Earl, University of Calofornia, CA, USA |
| clumpp | • Rosenberg Lab, Stanford University, CA, USA |
| tassel version 5 | • Buckler Lab, Cornell University, NY, USA |
| Quantity One | • Bio-Rad Laboratories GmbH, München, Germany |
| smart protractor app | • Smart Tools Co., Daegu, Rep. of Korea |
| GraphPad Prism Version 8 | • GraphPad Software, San Diego, CA, USA |
| BioEdit Version 7.2.3 | • Ibis Biosciences, Carlsbad, CA, USA |
| structure Version 2.3.4 | • Pritchard Lab, Stanford University, CA, USA |
| Light cycler®96 sw 1.1 | • Roche Diagnostics GmbH, Mannheim, Germany |
| LI-COR e-Seq ™ software, version 3.1 | • LI-COR Biotechnology GmbH, Bad Homburg, Germany |
| R version 4.0.3 | • © The R Foundation, Vienna, Austria |

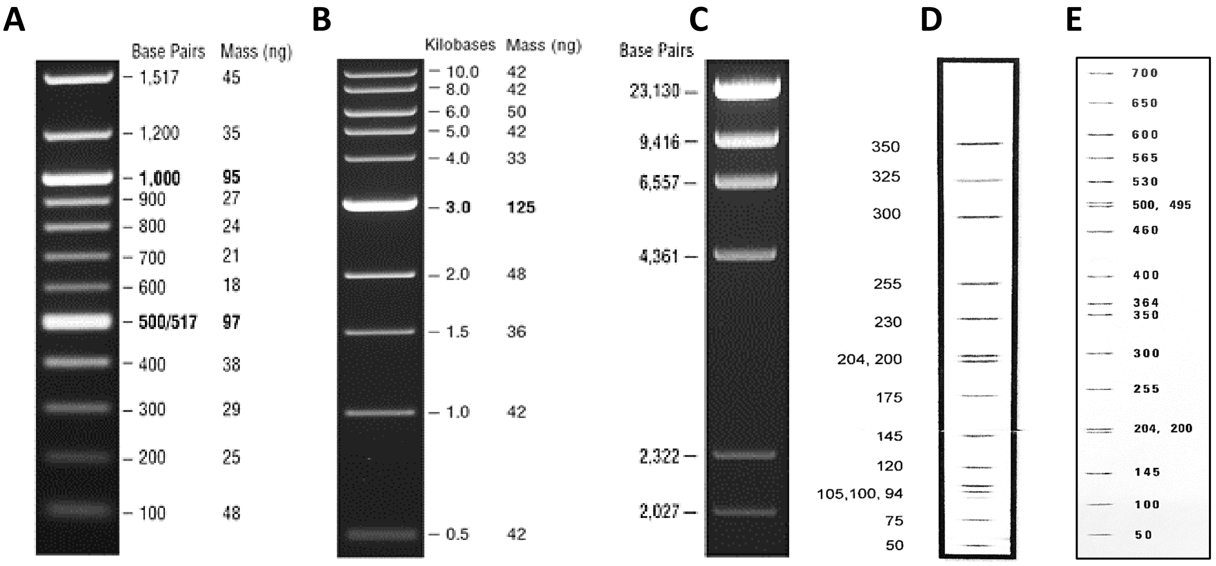


**Figure 4: Ladders for gel electrophoretic separation and IRDye sizing standard for SSR analysis. A)** 100 bp DNA ladder (https://www.neb.com/ products/n3231-100-bp-dna-ladder#Product%20Information); **B)** 1 kb DNA ladder (https://www.neb. com/products/n3232-1-kb-dna-ladder#Product%); **C)** λHindIII digest (https:// international.neb.com/ products/n3012- dna-hindiii-digest#Product%20Information); **D)** IRD 50-350 bp; **E)** IRD 50-700 bp

## 3.2 Plant material

The sunflower association panel was composed of sunflower accessions from USDA (United States Department of Agriculture), INRA (Institut National de la Recherche Agronomique) and GRIN-CA (Plant Gene Resources of Canada). In addition, different ornamental sunflower varieties were examined to obtain a greater variation in terms of plant height, branching and leaf angles.

### 3.2.1 Large association panel

From the original sunflower association panel of 557 accessions by the company STRUBE Research 444 accessions were used within this study. In addition, with four ornamental varieties these accessions were grown and evaluated in field trials in Bandow (MV, Germany) for a first evaluation in 2017 (Suppl. Tab. A 4). The association studies including SSR-, HRM-marker analyses were performed with a total of 448 accessions. KASP-marker analysis was performed using 445 of the 448 accessions.

### 3.2.2 Small association panel of 64 accessions

Based on the field data of the large association panel with 448 accessions in 2017, a successful selection of 64 genotypes with defined growth types could be made, which best represented the different growth types (Suppl. Tab. A 5). For this selection, the correlations of the different characteristics (petioles angle, height of growth) between the field data from Guadalajara, Spain and Bandow, Germany were compared. The $R^2$ (Coefficient of determination) is defined as a key figure for assessing the goodness of fit of a regression - for example, to assess how well measured values fit a model. The closer the coefficient of determination is to the value 1, the higher the "certainty" of the adjustment of the available data (Fahrmeir *et al.*, 2016). Lines of interest for further work were those, whose investigated features remained constant across the different climatic and environmental conditions. These selected genotypes were used to study the genetic diversity in the 22 candidate genes by targeted amplicon sequencing, as well as for SSR analysis and HRM analysis. In addition, 55 selected accessions were used to create test hybrids for performance tests (Suppl. Tab. A 8) and develop F2-populations for heredity studies of petiole angles and plant heights.

### 3.2.3 Ornamental sunflower varieties

To enlarge the number of semidwarf and dwarf sunflowers, the association panel was extended by 25 ornamental sunflower varieties bought from different producers as Benary (Erfurt, Thüringen, Germany), Swallowtail Garden Seeds (Santa Rosa, CA, USA), Nickys Nursery (Broadstairs, Kent, UK) and Premium Sunflowers (Lustadt, Rheinland-Pfalz, Germany) (Suppl. Tab. A 6).

## 3.3 Phenotyping of plant material

The phenotyping of the association panel was split into two parts. Part one represented a visual scoring of the plants, where branching type and plant heights were determined. The evaluations were performed according to the „Guidelines for the conduct of tests for distinctness, uniformity and stability – Sunflower (*Helianthus annuus* L.)“, published by UPOV (International union for the protection of new varieties of plants) in 2000.

The second part of phenotyping dealt with the measurement of plant height and leaf angle, split into leaf sheat angle and petiole angle. Only the petiole angles were reported within the PhD thesis. The evaluation was performed in stage E4. In this stage of development, the bud is clearly free from the leaves, its diameter varies from 5 to 8 cm, it remains horizontal and one part of the bracts is unfolded (UPOV, 2000).

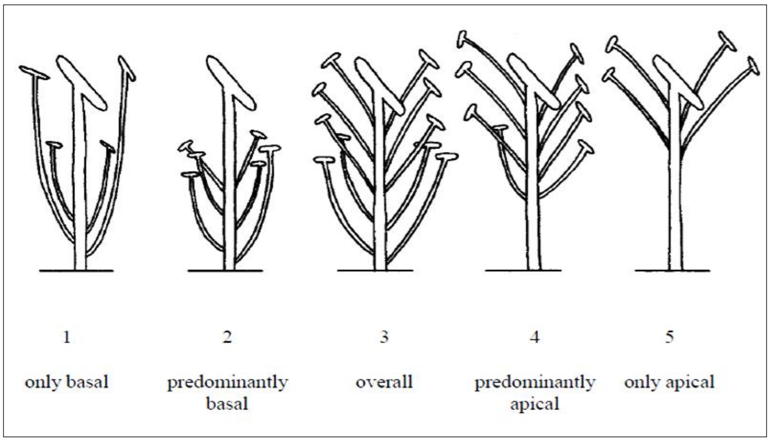


**Figure 5:** Plant type of branching. 1-5 scale to define branching type (UPOV, 2000)

In addition, the branching type of the different sunflower accessions was analysed. The scoring of the branching type and the type of branching were performed in development stage M0-M2, when all ray florets are wilted and the back of the head is still green or yellow. The different branching types were divided into five types from basal to apical (Fig. 5). The branching also had to be differentiated into three phenotypes like narrow branching, where the branches of the whole plant seem to be very close to the rest. In contrast to it, wide branching takes up a lot of space all around and in comparison to the „narrow“ and the „wide“, the „normal“ branching shows common space consumption. The flowering time is defined as the time, when 50 % of the sunflower accessions in the corresponding plot flower. To determine the time of flowering, the number of days between sowing and flowering were counted.

The second part of phenotyping included the measurement of the yield-related components like leaf angle (leaf sheath and petiole angle) and branching angle, as well as the measurement of the plant height. The measurement of the angles was carried out in development stage E4, using the „Smart Protractor“ and performed in the same three sections as the visual phenotyping. The petiole angle was measured as the angle between the stem and the highest point in the petiole (Fig. 6A). The leaf angle (Fig. 6A) was defined as the angle taken by the leaf sheath, but also the direction had to be recorded by adding a „minus“ or a „+“ sign, depending on the direction of the leaf whether it was down or up. The leaf sheat angle was not further evaluated within this work. The branching angle was the angle between stem and branch (Fig. 6B). To use the „Smart Protractor“ application with the smartphone, a wood stick (skewer) had to be added as an extension that facilitate both angle measurements. The plant height was measured in development stage M0, defined as the length of the central stem from the ground to the bottom of the flowering head (Fig. 6C).

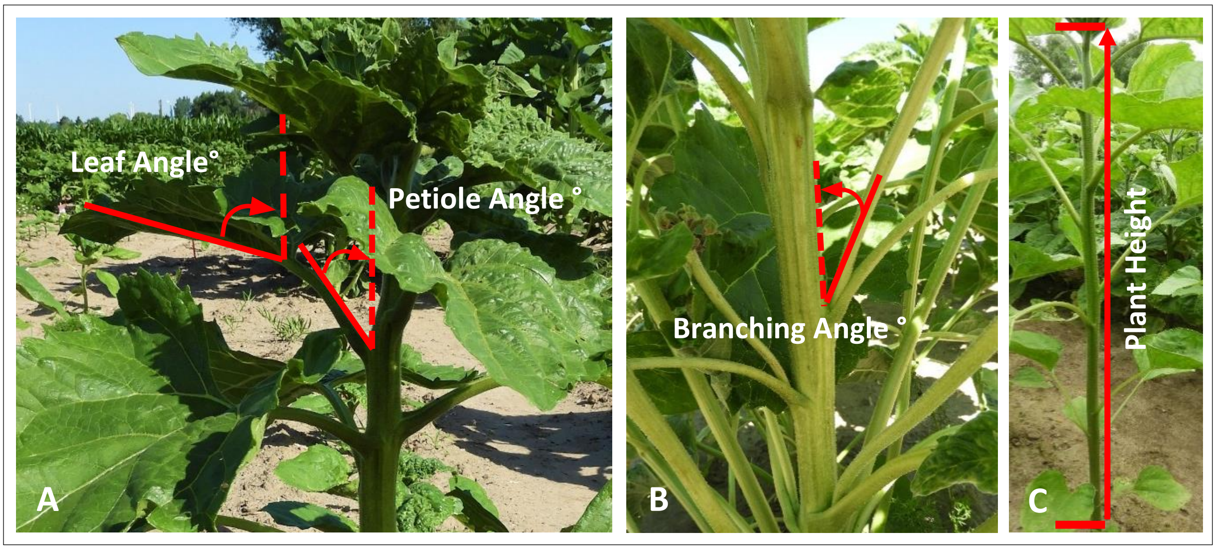


**Figure 6:** Measurement of angles and plant height. **A)** Detection of leaf angle and petiole angle; **B)** Recording of branching angle; **C)** Measurement of plant height

## 3.4 Field trials

### 3.4.1 Evaluation of the large association panel

In 2017, the large association panel consisted of 444 sunflower accessions and 4 commercial ornamental varieties (n = 448), which showed a great variation in terms of plant height, branching and leaf angles. The field trials for the association panel were carried out at two locations with different climatic conditions, in Germany, Bandow, M-V and in Spain, Guadalajara. In both locations the phenotyping of the plant material was performed as described. Three plants of each accession were evaluated with regard of the traits in 2017. From this panel, 64 genotypes with defined growth types were selected for following field trials in 2018 (three locations) and 2019 (Bandow, Germany). The third location in 2018 was Schlanstedt, which was only used as location in that year.

### 3.4.2 Evaluation of the small association panel

The field trials in 2018 were carried out at three locations with different climatic conditions. Two locations in Germany, Bandow, M-V and Schlanstedt, Saxony-Anhalt, and one location in Spain, Guadalajara. The panel of 64 selected sunflower accessions was analysed in three replications. In each block, three individuals per accession in Schlanstedt and Guadalajara, in Bandow six plants of each accession were evaluated.

### 3.4.3 Selection of accessions to perform test crosses

For the implementation of test crosses and following performance test, sunflower accessions were selected from the 64 selected genotypes, based on the field data of 2017 (Suppl. Tab. A 4). Two different groups of hybrids were tested. Group 1 consisted of 22 crosses of emasculated B line x R line and one LC-1093A (CMS) line x R line. Group 2 consisted of 31 crosses of LC-1093A (CMS) line x R line (Suppl. Tab. A 8).

### 3.4.4 Evaluation of F1- hybrids

In 2019, apart from the 64 genotypes 55 F1 hybrids produced by Strube Research and 21 ornamental sunflower accessions were rated in two repetitions, in a field trial in Germany, Bandow, M-V (Suppl. Tab. A 6, 7, 8). The phenotyping of the plant material was performed like described before for six plants of each accession.

### 3.4.5 Performance trials

Performance tests of only 53 F1 hybrids were carried out by the Hetterich company at the two locations in Mutzenroth, Bavaria, Germany and Sacalaz, Romania (Suppl. Tab. A 5), because two F1 hybrids had not enough seeds. Two groups of hybrids were tested. Group 1 was evaluated in just one replication at both locations in two plant densities (20 cm, 25 cm). Group 2 was examined in two replications at both locations in three plant densities (20 cm, 25 cm, 30 cm). For the performance tests, yield and oil content of the individual F1-hybrid combination in the various plant densities were determined. The seeds were planted in each plot (3 mx 8 m) in four rows with a row spacing of 75 cm. For comparison, five reference varieties in three plant densities were evaluated. The used reference varieties were ES Bella, ES Savana, ES Columbella, Sumatra and NK Delfi. Harvesting of the plots were performed in the following way to determine the yield at different plant densities:

- Harvesting the core plot (two rows in the middle)
- Number of heads harvested per core plot
- Number of heads per total plot

The raw data provide information on the number of total heads per plot and harvested heads, the yield per plot in kg, as well as the oil content per plot and the percentage of moisture. For the evaluations, the results for the yield were converted to dt/ha and mean values were formed for the measurements of the repetitions (Suppl. Tab. A 9, 10, 11).

### 3.4.6 Path analysis using R

The path analyses were performed using R version 4.0.3 with the package Iavaan (Rossel, 2012). The Iavaan ended normally after 123 iterations for the calculation for Germany and after 121 iterations for Romania. For the SemPath plots, that form a path diagram, the semPath (Epskamp, 2015) was used and the CorrPlots, which give information about the correlations of the various variables, were created using the R package GGally version 1.5.0 (by Barret Schloerke, 2020).

### 3.4.7 Segregation analyses in selected F2-populations

For analysing the test crosses, F2 populations of the five hybrids (Tab. 2) were produced in 2019, F1 generations and parental generations were included in the evaluation. The phenotyping of the plant material was performed as described before for six plants in each parental and F1 generation. In comparison, all plants of F2 populations were phenotyped. The field trials were performed in Germany, Bandow, M-V.

**Table 2:** Characteristics of test crossings

| FEMALE PARENT | M/R | PETIOLE ANGLE | GROWTH TYPE | | MALE PARENT | M/R | PETIOLE ANGLE | GROWTH TYPE |
|---|---|---|---|---|---|---|---|---|
| CM 104 | M | narrow | Semi-dwarf | | Commercial R-Line | R | normal | normal |
| ROMSUN V3355 | M | narrow | Semi-dwarf | **X** | Commercial R-Line | R | normal | normal |
| UGA-SAM1-185 | M | narrow | Semi-dwarf | | Commercial R-Line | R | normal | normal |
| NO. 2 | M | normal | normal | | UGA-SAM1-110 | M | narrow | Semi-dwarf |
| CMH 101 | R | narrow | normal | | ROMSUN V3355 | M | narrow | Semi-dwarf |

## 3.5 DNA isolation in sunflower

To complete the partial gene sequences of GA-signaling pathway and the genes *HaTAC1* and *HaLAZY1*, total genomic DNA of the sunflower accession HA 383 was extracted from fresh leaves by an optimized hexadecyltrimethylammoniumbromide (CTAB) method of Doyle (1991). The concentration and the quality of the extracted DNA were measured by a spectrophotometer, analysed on a 0.8 % agarose gel electrophoresis. The diluted DNA was stored at -20 °C. Also, the DNA of the large sunflower panel with 384 accessions and the DNA of the 25 ornamental sunflower accessions was extracted by this method.

The DNA extraction of the 64 selected genotypes for SSR analysis and HRM analysis was likewise carried out by the method described, however, the extraction buffer, developed by Gambino *et al.* (2008) containing PVP, which removed interfering substances such as polyphenols and polysaccharides, among other things was used to extract the DNA from sunflower leaves.

## 3.6 RNA isolation and synthesis of cDNA

To obtain the exon-intron structure of the genes of interest, RNA had to be isolated to perform cDNA synthesis. To extract RNA from fresh leaves of sunflower accession HA 383, the NucleoSpin®RNA Plant Kit (MACHEREY-NAGEL, Düren, Germany) was used. According to the user's manual, this kit allows fast and easy RNA isolation from a small amount of material (max. 100 mg) and delivers up to 70 µg total RNA. After isolation of total RNA, digestion of remaining traces of DNA was performed using kit included rDNA followed, based on manufacturers recommendation. Reverse transcription was carried out using RevertAidReverse-Transcriptase (Fisher Scientific GmbH, Schwerte, Germany) according to the manufacturer's instructions starting with 5 µg RNA.

### 3.6.1 Analysis of the 3'-region of *HaTAC1* gene using SMARTer® RACE 5'/3' Kit

A 3'RACE was performed to examine the 3' region of *HaTAC1* and to verify the exon-intron structure of the gene. In the SMARTer® RACE 5'/3' Kit (Clontech by TaKara Bio Inc., Kusatsu, Japan) a special property of MMLV is explored – the terminal transferase activity. Moloney Murine Leukemia Virus Reverse Transcriptase (M-MLV RT) is an RNA-dependent DNA polymerase that can be used in cDNA synthesis with long messenger RNA templates. During the elongation 3-5 nucleotides are added to the 3'-end of the generated cDNA strand, if 5'-end of template-RNA is achieved. During the RACE the sequence of the untranslated regions of cytoplasmic mRNA can be detected. Based on a short, known sequence of the coding region 3'-end can be analysed. For 3'-RACE the poly(A) tail of the mRNA is used as origin. The analysis of the 3'- region using the SMARTer® RACE 5'/3' Kit was performed according to the user's manual (Clontech by TaKara Bio Inc., Kusatsu, Japan) (Suppl. Tab. A 1).

## 3.7 Molecular methods for sequence analysis

In 2013, Ramos *et al.* analysed different commercial sunflower inbred lines with reduced height and showed, that the trait is controlled by semidominant allele *Rht1*. It completely cosegregated with a haplotype of *HaDELLA1* gene (Ramos *et al.,* 2013). Additionally, there were indications, that a second form of *HaDELLA* is present in sunflower (Blackman *et al.,* 2011). The GA receptor, GID1, was characterised in GA-insensitive mutants of rice (Ueguchi-Tanaka *et al*., 2005) and in *Arabidopsis thaliana* three different genes, encoding for GID1 were identified (*AtGID1a, AtGID1b*, *AtGID1c*) by Nakajima *et al.* (2006). The results, published by Blackman *et al.* (2011), showed a partial sequence with a high homology to *GID1b* of *A. thaliana* (At3g63010) and a BLASTN (Basic Local Alignment Search Tool) against sunflower genome showed three hits. So, it seemed like there is more than one *GID1* gene in sunflower. In 2011, Blackman *et al*., described a possible sequence of SLY1, as part of the SCF E3 Ubiquitin ligase in sunflower. Using the sunflower genome sequences of Loren Rieseberg

(Department of Botany and Biodiversity Research Centre, University of British Columbia, BC, Canada), it was possible to identify the genes of GA-signaling pathway during BLASTN.

The genome sequences of HA 412 (Kane *et al.,* 2011) and HanXRQ (Badouin *et al.,* 2017) served as reference. The genome sequences of HanXRQ were published in the heliagene.org database (https://www.heliagene.org/HanXRQr2.0-SUNRISE/). On the basis of this database, it was possible to complete the candidate genes from the genetic material of the HA 383 line faster and more effectively.

### 3.7.1 Gene cloning in sunflower

For completing of partial gene sequences, STS PCR (Suppl. Tab. A1) was performed using Phusion Polymerase (Fisher Scientific GmbH, Schwerte, Germany) including proof reading characteristics. The application was based on manufacturers recommendations using DNA concentration of 30 ng/µl. The PCR program consisted of a single denaturation (98 °C, 2:00 min), 25-30 cycles consisting of denaturation (98 °C, 0:30 min), primer annealing (55-60 °C, 0:30 min) and polymerisation (72 °C, 0:30 min per 1 kb) and the final elongation (72 °C, 5:00 min).

PCR reactions without the need for proof reading activity, like insert PCR test, were carried out with the FIREPol® DNA polymerase (Solis BioDyne OÜ, Tartu, Estonia) performed according to the manufacturer's instructions. The PCR program consisted of a one-off denaturation (94 °C, 2:00 min), followed by 25-30 cycles consisting of denaturation (94 °C, 0:30 min), primer annealing (55-60 °C, 0:30 min) and polymerisation (72 °C, 0:30 min per 500 bp) as well as a final elongation (72 °C, 5:00 min).

### 3.7.2 Cloning of the PCR products

The quantity and quality of the STS-PCR products or insert PCR tests were controlled on 2 % agarose gel (80 V for 30 min), for documentation the Gel Doc ™ EZ Gel Documentation System (Bio-Rad Laboratories GmbH, Munich, Germany) was used. The corresponding gel bands of the expected size were cut out and cleaned up described in manufacturer instructions using the peqGOLD Gel Extraction Kit (VWR Life Science Competence Center, Erlangen, Germany).

To allow subsequent ligation with T4 DNA ligase in the pGEM®-T Easy vector system (Promega GmbH, Mannheim, Germany) to the created blunt ends of the phusion polymerase, an adenine overhang had to be added. This A-tailing included a batch of 2.5 µl B buffer (0.8 M Tris-HCl, 0.2 M $(NH_4)$ $2SO_4$), 2.5 µl $MgCl_2$ (25 mM), 5.0 µl 1 mM dATP, 0.5 µl FIREPol® DNA polymerase (5 U / µl) and 14.5 µl gel eluate. The mixture was incubated at 72 °C. for 30 min. The ligation approach included, according to the manufacturer's instructions, 4 µl $H_2O$, 1 µl 10x ligase buffer, 1 µl vector, 1 µl T4 and 3 µl DNA fragment, which was incubated at 8 °C overnight.

For the transformation 50 µl of competent *E. coli* cells (DH5α stored at -80 °C) were incubated for 5 min on ice. The ligation mixture was added and incubated for 30 min on ice. It follows a heat shock for 90 sec at 42 °C. After incubation on ice for 5 min 600 µl SOC medium (2 % Tryptone, 0.5 % Yeast, 0.01 M NaCl, 2.5 mM KCl, 0.1 M $MgCl_2$, 0.02 M Glucose) were added and incubation for 60 min at 37 °C follows in a shaking incubator. The transformed cells were plated and grown on solid LB Ampicillin/IPTG/X-Gal medium (1 % Tryptone, 0.5 % Yeast, 1 % NaCl, 1.5 % Agar, 0.2 % Ampicillin, 0.005 % X-Gal, 0.0025 % IPTG) for 16 hours. Using the pGEM®-T Easy vector system a blue-white screening was possible. For separating, the white cells were picked with toothpicks and plated on a new solid LB Ampicillin/IPTG/X-Gal medium plate for 16 hours at 37 °C. The toothpicks were washed in 1.5 ml collection tubes containing 40 µl $ddH_2O$. The wash solution was used for an insert PCR test. Positive identified cells were verified by the use of vector-specific primers (T7/SP6) or gene-internal primers.

### 3.7.3 Minipreparation of plasmid DNA and sequence analysis

The positive verified cells were placed in liquid LB medium containing ampicillin and incubated for 16 h at 37 °C on a shaking incubator. Afterwards, the plasmid DNA was isolated using the Invisorb Spin Plasmid Mini TwoKit (Stratec Molecular, Berlin, Germany) according to the manufacturer's instructions. Final sequence analyses were carried out by GATC-BIOTECH / Eurofins Genomics GmbH (Ebersberg, Germany). There were 100 ng DNA in a volume of 5 µl used for Sanger sequencing (Sanger *et al*., 1977) and the evaluation of the sequence data was performed using the program BioEdit (Hall, 1999).

## 3.8 Targeted Amplicon Sequencing of 22 candidate genes

Leaf material from the 64 selected genotypes was sent to LGC Genomics GmbH (Berlin, Germany) on dry ice. The DNA was isolated there using an in-house protocol and used there for the next generation sequencing. The information of the 22 candidate genes was supplied in a bed format file to LGC Genomics (Suppl. Tab. A 24), who then derived the corresponding primers for the amplicon targeted sequencing. The sequencing was carried out with a 120-fold genome coverage. Final results of the SNP analysis were delivered by LGC. The information was sent as Excel table, containing information about all 22 genes, 2.000 bp upstream and 500 bp downstream, for the 64 genotypes like total SNPs per gene and region, i.e. how many SNPs or InDels, localised in 5’UTR, 3’UTR or coding sequence (cds). Afterwards, the results were used to identify significant SNPs using TASSEL v. 5 and Fischer Exact Test. Part of these SNPs were used for development of HRM markers and KASP assay analysis.

## 3.9 Determination of the population structure

### 3.9.1 SSR analyses

To carry out the association studies, SSR analyses for the 64 accessions panel were initially done. For this purpose, 34 SSR markers were used (Suppl. Tab. A 3), which were selected from previous publications (Chapman *et al.*, 2008; Tang *et al.*, 2002). These represent two markers per linkage group in order to achieve the most uniform possible genome-wide coverage (Suppl. Tab. A 3). The SSR PCR reactions were performed using the FIREPol® DNA polymerase (Solis BioDyne OÜ, Tartu, Estonia). The SSR PCR mix consisted of 0.3 µl dNTP's (10 mM), 1.5 µl 10x buffer B (0.8 M Tris-HCl, 0.2 M $(NH_4)$ $2SO_4$), 1.5 µl $MgCl_2$ (25 mM), 0.15 µl forward primer carrying a M13 tail (5 pmol/µl), 0.15 µl reverse primer (5 pmol/µl), 0.15 µl M13-IRD primer - fluorescent labelled primers IRD700 or IRD800 (biomers.net GmbH, Ulm, Germany), 8.7 µl $ddH_2O$, 0.05 µl FIREPol® DNA polymerase (5 U/µl) and 2.5 µl DNA (20 ng/µl). The SSRtail PCR program consisted of a denaturation (95 °C, 5:00 min), 36 cycles consisting of denaturation (95 °C, 0:20 min), primer annealing (55 °C, 0:20 min) and polymerisation (72 °C, 0:30 min) as well as a final elongation (72 °C, 4:00 min). To verify the markers associated with plant architectural features, the SSR analyses were extended to the large association panel. The evaluation was finished on a 7% polyacrylamide gel. DNA Analyzer 4300 (LI-COR Biotechnology GmbH, Bad Homburg, Germany) was used for visualizing the fluorescent labelled PCR products and evaluation with the LI-COR e-Seq ™ software, version 3.1 (LI-COR Biotechnology GmbH, Bad Homburg, Germany) followed.

### 3.9.2 Population analysis using STRUCTURE v. 2.3.4

The programs "STRUCTURE", "STRUCURE HARVESTER" and CLUMPP "were used to determine the population structure based on the SSR analyses. STRUCTURE V 2.3.4 was set to 50.000 for burn-in time, followed by 100.000 Markov Chain Monte Carlo (MCMC) iterations (Pritchard *et al.*, 2000). A total of 10 independent replicates were performed to determine the mean k value (Cadic *et al.,* 2013). To determine the most likely number of clusters, the DeltaK method of Evanno *et al.* (2005) was used.

## 3.10 Association studies using TASSEL v 5.0

The data from next generation sequencing of the 22 candidate genes by LGC Genomics and SSR analyses were used to identify SNPs significantly associated with traits of interest. Association studies for petiole angle and plant height were performed in TASSEL v. 5.0 (Bradbury *et al.*, 2007) using all SNPs MinAF ≥ 5%. Accessions were assigned to K population genetic clusters. The program TASSEL v. 5.0 was used to calculate the GLM (Generalized Linear Model) using three different data files like Hapmap file as an input for molecular data, Trait file and the CLUMPP K_outfile, containing information of population structure. The results were visualised in Manhattan plots. This was carried out separately for each individual year for the traits of plant height and petiole angle at the different locations. The significance levels were corrected using sequential Bonferroni correction (Mandel *et al*., 2013; Holm 1979), so significant threshold for all evaluations was p = 0.000164.

## 3.11 Identification of significant SNPs using Fischer Exact Test

As TASSEL using the Bonferroni correction was very stringent and the association panel of only 64 accessions was relatively small, the association studies were repeated forming groups (9 dwarfs vs. 55 all other plant height; 12 semi-dwarfs vs. 52 all other plant heights; 22 small petiole angles vs. 42 all other plant angles) and applying the Fischer Exact Test with a threshold p-value of less than 0.05. The calculations for the Fischer Exact Test were made based on the LGC next generation sequencing data and the phenotyping data of 2017 using the „Easy Fischer Exact Test Calculator“ (https://www.socscistatistics.com/tests/fisher/default2.aspx).

## 3.12 High Resolution Melting Analysis

The High Resolution Melting (HRM) is a method that allows the screening of unknown genetic variations, where the melting behavior of double stranded PCR products was analysed in terms of increasing temperatures (Chateigner-Boutin and Small, 2007). The main application for the HRM method is genotyping (LightCycler® 96 System, User Training Guide V2.0). For the HRM analysis the LightCycler ®96 System (Roche Diagnostics, Mannheim, Germany) and the device-specific software „LightCycler®96 SW 1.1“were used.

### 3.12.1 Development of HRM primers

For the SNP analyses using HRM markers short amplicons were needed (< 100 bp), because a single base variation affects the melting behavior of a small amplicon more than an amplicon of several hundred bp and short amplicons show the effects of SNPs most effective (LightCycler® 96 System, User Training Guide V2.0). An important factor is the type of base exchange. Exchanges of A>T or C>G are rather unsuitable, since the temperature level for the splitting of the double strands changes only very slightly, which means that these SNPs are difficult to detect. The following parameters had to be considered by HRM primer design: primers should have anealing temperature > 60 °C, primer length between 17-25 nt, sequence checked for the target gene using BLAST (http://www.ncbi.nlm.nih.gov/BLAST) should be unique, differences in temperature < 1 °C between forward and reverse primer (https://www.gene-quantification.de/LC480-Technical-Note-01-HRM.pdf). Primers were designed for the four genes, *HaDELLA1, HaDELLA2, HaDELLA-Like2* and *HaSNEEZY2*, with highly significant SNPs (Suppl. Tab. A 2).

### 3.12.2 HRM real time PCR and data analysis

The PCR mix was prepared according to the manufacturer's instructions (Roche Diagnostics, Mannheim, Germany) with 10 % extra volume to compensate pipetting losses. The target sequence was amplified in presence of a saturating fluorescent dye (ResoLight Dye). For the PCR mix the ingredients were used from the LightCycler® 480 High Resolution Melting Master (Roche Diagnostics, Mannheim, Germany), the concentration of $MgCl_2$ was optimised to 2.5 mM per sample. The PCR mix consisted of 5.0 µl 2x Master Mix, 1.0 µl forward primer (0.2 µM), 1.0 µl reverse primer (0.2 µM), 1.0 µl $MgCl_2$ (25 mM), 0.5 µl $H_2O$ (PCR grade) and 2.5 µl DNA (15 ng) for a total volume of 11 µl per sample. The HRM PCR program was the following: Preincubation (95 °C, 10:00 min), 3 Step Amplification 45 cycles (95 °C, 0:10 min; 60 °C, 0:15 min; 72 °C, 0:10 min), High Resolution Melting (95 °C, 1:00 min; 40 °C, 1:00 min; 65 °C, 1 sec; 97 °C, 1 sec). Subsequently, the device saved the run as „raw data" automatically. The raw data were finally analysed using the device-specific software „LightCycler®96 SW 1.1".

## 3.13 Kompetitive allele specific PCR (KASP)

Kompetitive allele specific PCR (KASP) is a proprietary technology of LGC Genomics that can distinguish alleles at variant loci (Steele *et al.,* 2018). It is a single-step genotyping technology that reveals alleles for SNP and InDel variants between parents and progeny using fluorescence resonance energy transfer (Cheon *et al*., 2020; Cheon *et al.,*2018; Semagn *et al*., 2014). This method has a scalability that makes it suitable for a wide range of experimental designs with a high number of samples (Cheon *et al*., 2018). To extend the SNP data of the next generation sequencing of candidate gene approach from the 64 selected genotypes, LGC Genomics was instructed to do KASP assay analyses for a total of 445 sunflower accessions, including the small association panel (n = 64), based on the SNP data analyses. The DNA (20 ng/µl) of the 445 sunflower accessions was send on dry ice to LGC Genomics and subsequently, the assay information was sent back as Excel table. Overall, the KASP assay included 84 SNP or InDel information for analysis (Suppl. Tab. A 27).

# 4 Results

## 4.1 Analysis of phenotyping of the large association panel

The field trials were sown and processed at two locations with different climatic conditions in Germany, Bandow, M-V and in Spain, Guadalajara over the years (2017-2019). There were no major problems with the quality of the plants at the different locations (Fig. 7). However, some of the failures in Germany were caused by heavy rainfall and wildlife damage. In Spain, the infestation with *Orobanche spp*. led to failures in some accessions.

**Figure 7:** Field trials in 2018. **A)** Germany, Bandow, bird's eye view; **B)** Germany, Bandow; **C)** Spain, Guadalajara

### 4.1.1 Classification according to plant height

Growth types of the association panel were identified for all accessions based on Schuster and Marquardt (2003). Dwarfs (≤ 65 cm), semi-dwarfs (66 - 107 cm) and normal growth type plants (≥ 107 cm) were assigned to all sunflower accessions (Fig. 8), so that apart from 373 normal-growing plants, 10 dwarfs and 65 semi-dwarfs were identified (Suppl. Tab. A 4).

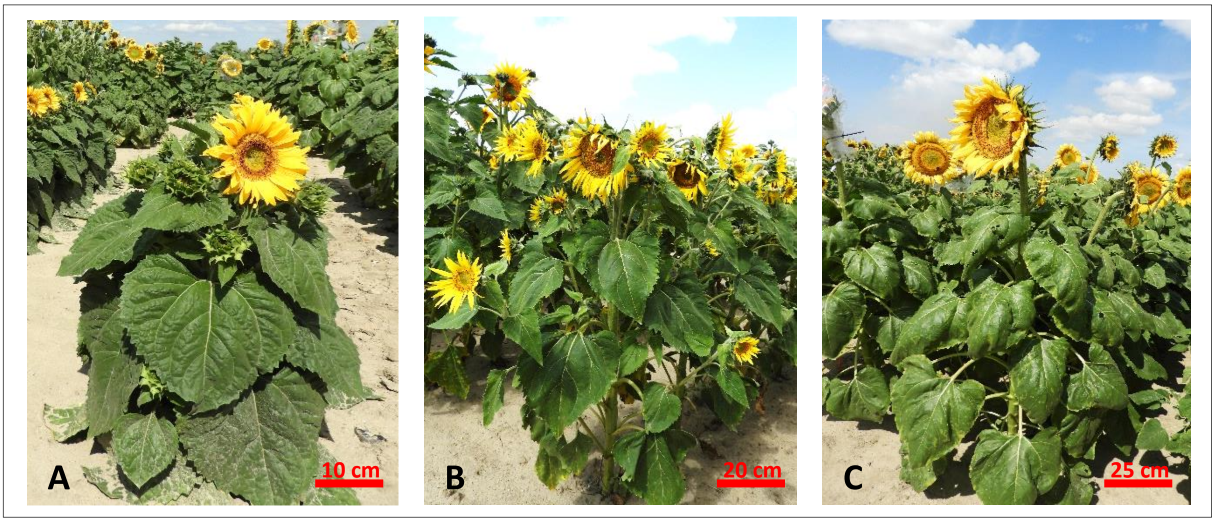


**Figure 8:** Different growth types of sunflower. **A)** Dwarf UGA-SAM1-118; **B)** Semi-dwarf UGA-SAM1-057; **C)** Normal growth type CMH 101

### 4.1.2 Classification according to petiole angle

The upper level showed values from 23 ° to 69 ° for the petiole angle, and values between 23 ° and 73 ° for the middle level. For the lower level, the values were between 25 ° -86 °. That results in all three types of petiole angles appearing in the association panel (Fig. 9). The evaluation of the petiole angles in the different levels showed a Gaussian normal distribution (Aitchison and Brown, 1957) (Suppl. Fig. A 1). The values for the upper level were used to classify the accessions with regard to the petiole angles. Petiole angles ≤ 40.0 ° were scored as narrow, values between 40.1° - 60.0 ° as normal and petiole angles larger than 60.0 ° as wide (Suppl. Fig. A3).

The large association panel consisted of 333 plants with normal petiole angles, 98 with narrow petiole angles and 17 with wide petiole angles regarding the upper plant level. When evaluating the leaf sheat angle, it should be noted that these showed no correlation to the petiole angle and must therefore be treated as an independent trait. Measured values for leaf sheat varied between -47 ° and 41 ° in the upper tier, between -55 ° and 38 ° on the middle level and values between -77 ° and 56 ° on the lower level.

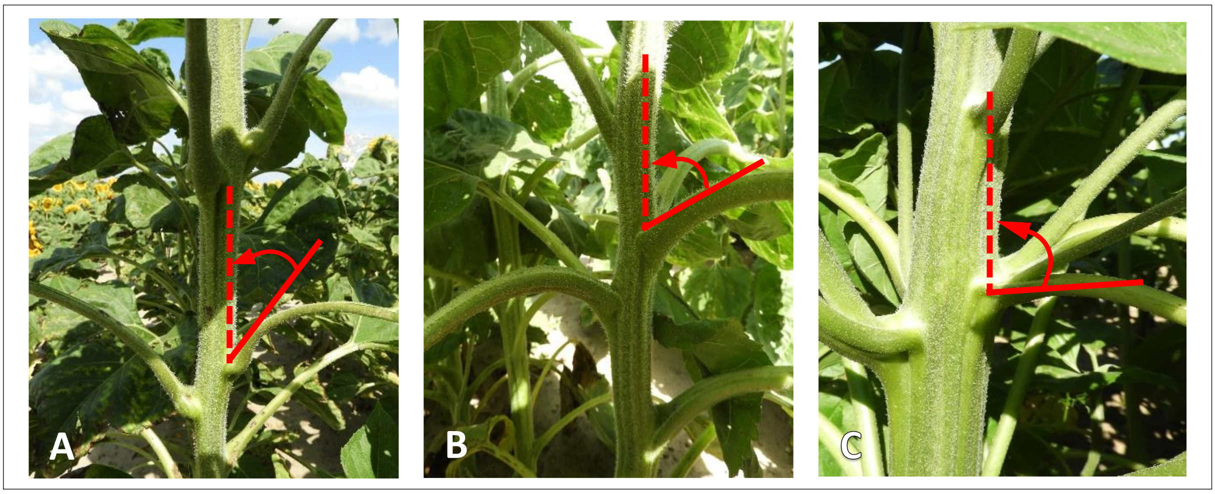


**Figure 9:** Different types of petiole angles in the upper tier. **A)** Narrow angle UGA-SAM1-183; **B)** Normal angle UGA-SAM1-273; **C)** Wide angle UGA-SAM1-276

### 4.1.3 Selection of 64 genotypes

Based on the field data of 2017 a successful selection of the 64 genotypes with defined growth types could be made. Investigated were the correlations of petiole angles and plant heights between Spain and Germany, whereby a step-by-step elimination of the accessions with low correlation values could take place until 64 genotypes were left. Finally, the 64 selected genotypes showed a correlation of petiole angles of $R^2 = 0.7991$ (Fig. 10 A) and for plant height of $R^2 = 0.7945$ (Fig. 10 B). Additionally, the 64 selected accessions were classified into different petiole angle types (Suppl. Fig. A 3) and growth types (Suppl. Fig. A 4). The small association panel showed 6 dwarfs, 12 semi-dwarfs and 46 normal growing plants. In relation to the petiole angle, 19 accessions with narrow angles, 41 with normal angles and 4 accessions with wide angles belong to the small association panel. Moreover, 38 accessions showed branches, of which 4 accessions only form apical branches, and 26 sunflower accessions showed no branches.

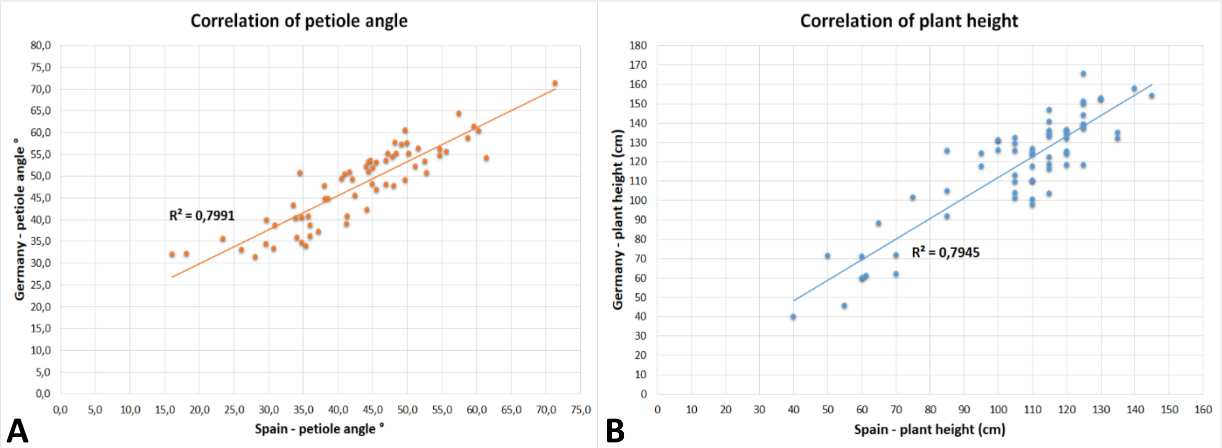


**Figure 10:** Correlating data of the 64 selected genotypes from Germany and Spain. **A)** Correlation of petiole angles in 2017; **B)** Correlation of plant heights in 2017

## 4.2 Analysis of phenotyping data of small association panel in different locations

### 4.2.1 Comparison of plant heights

The correlation values for the plant heights of the different accessions showed also good results in 2018, which confirmed the values of the previous year 2017 and thus the selection of 64 genotypes for further work. The characteristic of the plant height remained constant across the different climatic and environmental conditions, which resulted in the following correlation values of BAN/ES $R^2$ = 0.7457 (Fig. 11 A), BAN/SCHL $R^2$ = 0.7442 in 2018 (Fig. 11 B).

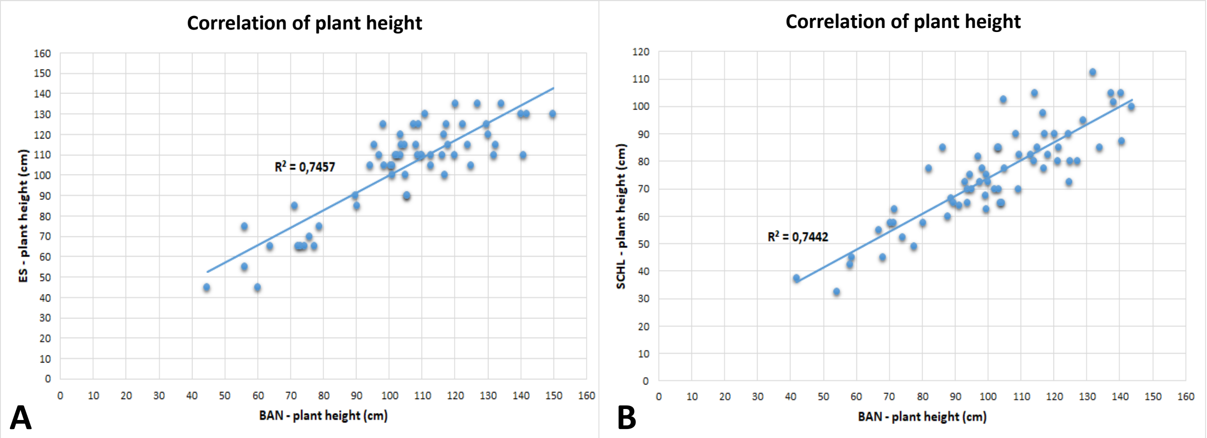


**Figure 11:** Correlating data of plant heights of the 64 selected genotypes. **A)** Correlation of data from Bandow (BAN) and Guadalajara (ES) in 2018; **B)** Correlation of data from Bandow and Schlanstedt (SCHL) in 2018

### 4.2.2 Comparison of petiole angles

The correlation values of the petiole angles indicated more variability in 2018 than in the previous year. In 2017, the correlation value between Spain and Germany was $R^2 = 0.7991$, which confirmed the selection of the 64 genotypes. The correlation value for 2018 was only $R^2 = 0.6078$ (Fig. 12 A). However, the additional correlation value in 2018 for the petiole angles of the data of Rostock and Schlansted was in the same range with a value of $R^2 = 0.6025$ (Fig. 12 B). This value also confirmed the selection of the 64 genotypes.

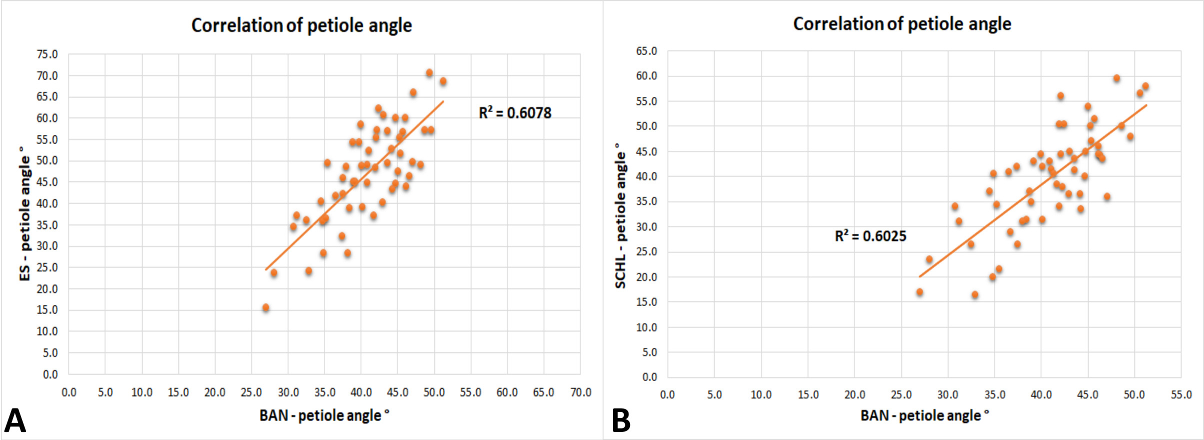


**Figure 12:** Correlation between petiole angles of the 64 selected genotypes in different locations in 2018. **A)** Correlation of data from Bandow (BAN) and Guadalajara (ES); **B)** Correlation of data from Bandow and Schlanstedt (SCHL)

## 4.3 Evaluation of the small association panel and F1 hybrids

The field trials for phenotyping in the third year were carried out in duplicate at the Bandow site in M-V. The field work took place between May and October 2019 (Fig. 13). All seeded accessions worked as planned and could be evaluated.

**Figure 13:** Different stages of field trial in Bandow, M-V in 2019. **A)** Sowing 08.05.2019; **B)** Flowering 27.07.2019; **C)** Harvest 10.10.2019

The rating of petiole angles showed measured values between 23 °-63 ° for the upper level, between 16 °-62 ° for the middle level and values between 42 °-78 ° for the lower level. To compare the repetitions of the Bandow location, the correlations of the petiole angles of the accessions were determined (Fig. 14 A). For the data of the two blocks, a very good correlation value of $R^2$ = 0.8972 was shown. This value reinforced the selection of 64 genotypes. In addition, the test hybrids also showed very stable, reproducible values (Fig 14 A). By measuring the plant height, the different growth types, identified in the two previous years, could be verified for all accessions. However, the measurements of plant heights showed values between 25 cm - 188 cm, whereas the test hybrids showed measured values between 107 cm – 166 cm (Fig. 14 B). Thus, all hybrids showed normal plant heights. All in all, the test hybrids exhibited the expected phenotypic homogeneity for plant height and petiole angle. The correlation between the two repetitions was also determined for this trait (Fig. 14 B). A very good correlation value of $R^2$ = 0.7901 was found for plant height, which included both, the 64 selected genotypes and the 53 test hybrids.

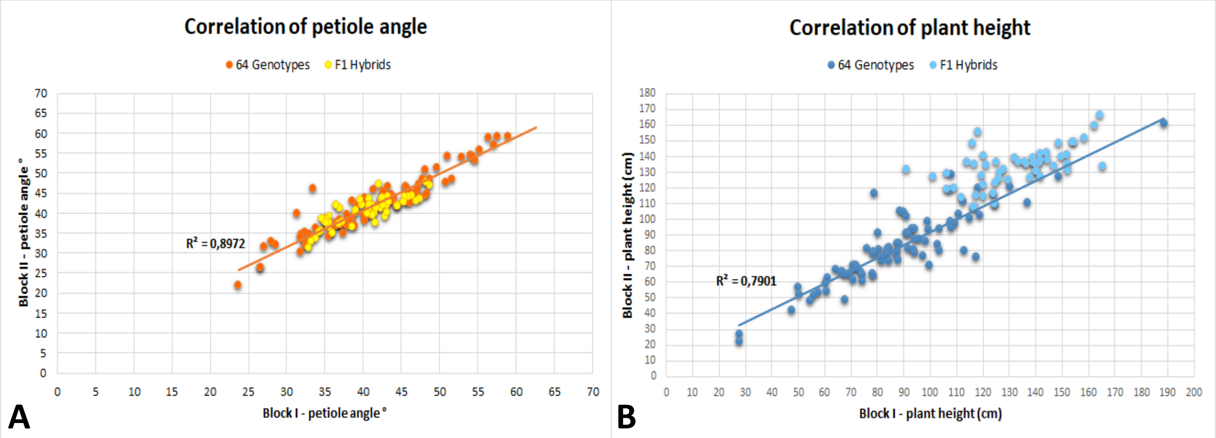


**Figure 14:** Correlation between the two replications of the 64 selected genotypes and the 53 F1 hybrids from Bandow, M-V in 2019. **A)** Correlation of petiole angles; **B)** Correlation of plant heights

## 4.4 Evaluation of performance tests

### 4.4.1 Yield and oil content

For the 22 cross combinations of the emasculated B-line x R-line for the Mutzenroth (DE) site with a plant density of 20 cm oil contents varied between 40.1 % - 49.2 % (Suppl. Fig.A 7 A), at 25 cm the oil content varied between 40.4 % and 48.5 % (Suppl. Fig. A 8 B). The situation was similar for the results from Sacalaz (RO). Here the oil content ranged between 41.0 % - 48.6 % for a plant density of 20 cm and between 41.7 % - 48.5 % for 25 cm. For the 30 cross combinations of the CMS line x R line, the overall oil content was slightly higher. With a plant density of 20 cm, oil contents between 43.3 % and 51.5 % could be determined for the Mutzenroth site (Suppl. Fig. A 8 A). At 25 cm the oil content was between 43.8 % - 51.8 % (Suppl. Fig. A 7 B) and at 30 cm the oil content varied between 43.4 % - 51.1

% (Suppl. Fig. A 8 C). Here, too, the values at the Sacalaz site were comparable with oil contents between 25.9 % - 48.7 % with a plant density of 20 cm. Furthermore, values between 43.7 % - 51.1 % at 25 cm and 40.9 % - 48.6 % oil content with a plant density of 30 cm were found (Suppl. Fig. A 8 C). The results for the oil contents at different plant densities were summarised in Fig. 15 for DE and in Fig. 16 for RO.

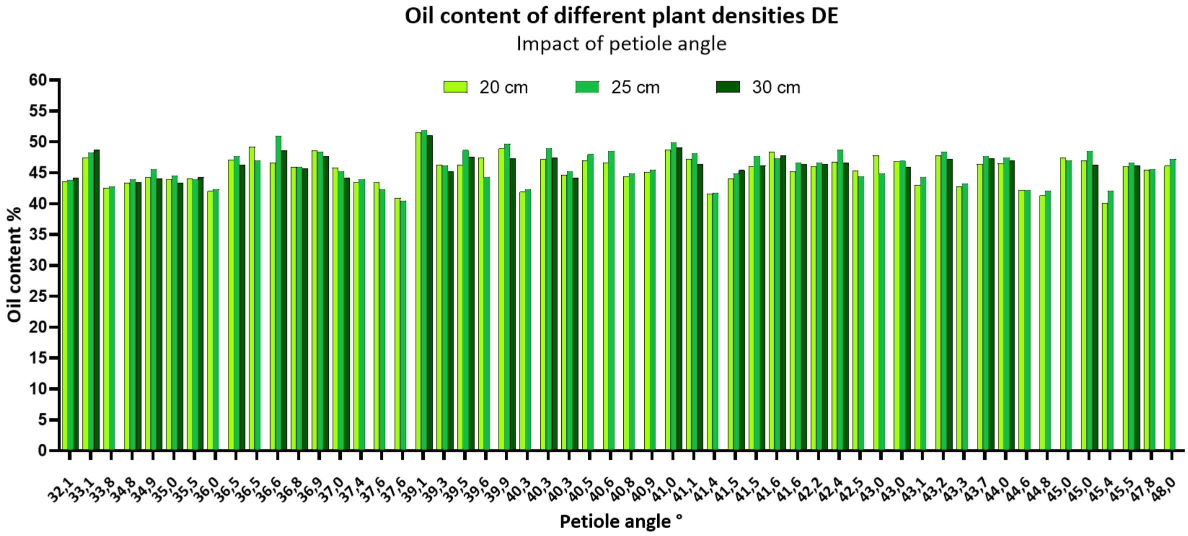


**Figure 15:** Oil contents of different plant densities DE, sorted by petiole angle from narrow (left) to wide (right)

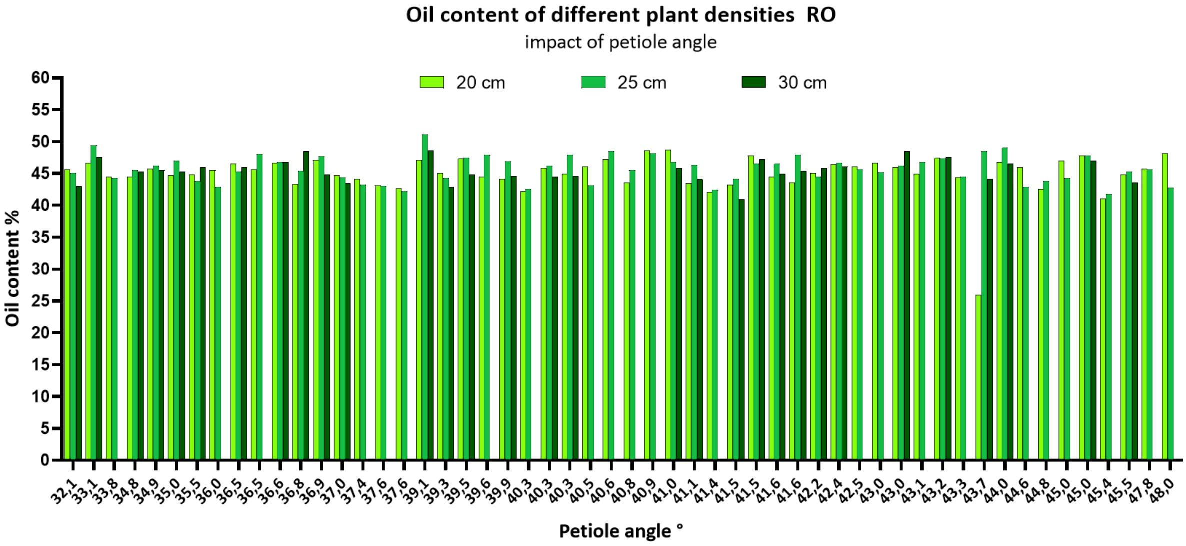


**Figure 16:** Oil contents of different plant densities RO, sorted by petiole angle from narrow (left) to wide (right)

The yields for a plant density of 20 cm at the Mutzenroth (DE) site ranged between 11.08 dt - 33.96 dt, the measured yields from the Sacalaz (RO) site were a little different. Here the yields varied between 17.67 dt – 31.92 dt (Suppl. Fig. A 8 A). For a plant density of 25 cm, yields between 16.33 dt – 35.75 dt could be achieved in Mutzenroth. Compared to the yields of Sacalaz of 14.58 dt – 38.50 dt, the results of Sacalaz were somewhat higher than at the Mutzenroth location (Suppl. Fig. A 8 B). If the results are considered for a plant density of 30 cm, it is noticeable that the yields of Mutzenroth are frequently higher with a range of 22.71 dt – 43.50 dt than the yields of Sacalaz with values between 14.17 dt – 28.33 dt (Suppl. Fig. A 8 C). The results for the yields at different plant densities are summarised in Fig. 17 for DE and in Fig. 18 for RO.

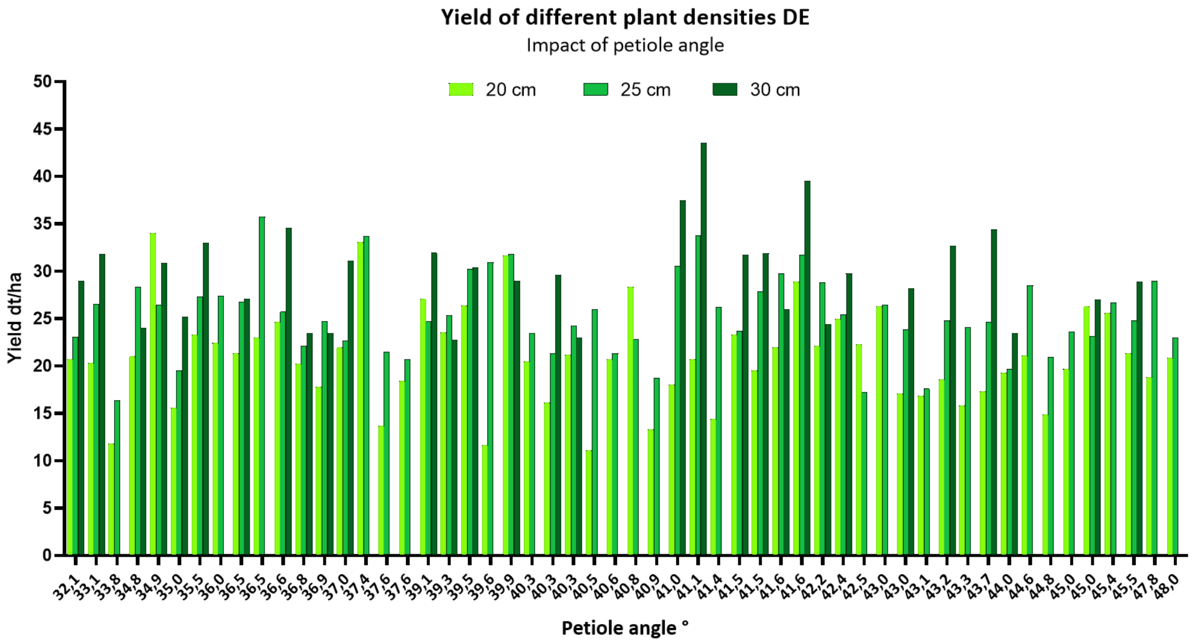


**Figure 17:** Yields obtained applying different plant densities in DE, sorted by petiole angle from narrow (left) to wide (right)

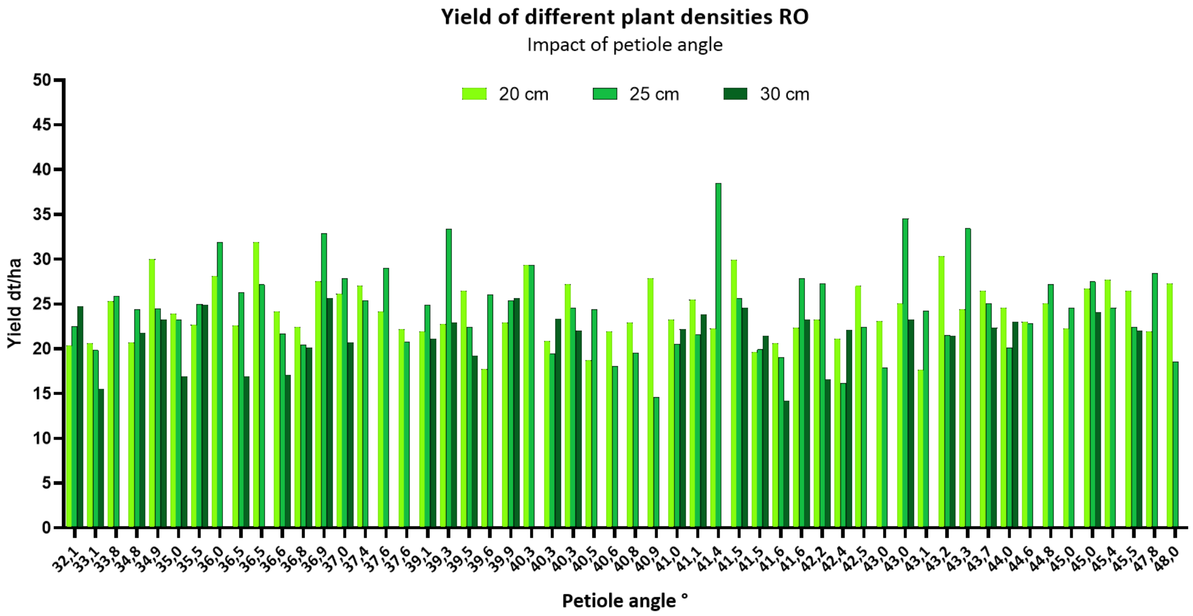


**Figure 18:** Yields obtained applying different plant densities in RO, sorted by petiole angle from narrow (left) to wide (right)

The analysis of the variance (ANOVA) of the values for oil content and yield at different plant densities at different locations showed different results (Tab. 3). While the null hypotheses can be accepted for the values of the oil content, the calculations for the yields showed significant differences, which means that the null hypothesis has to be rejected (Tab. 3). This could be due to the sample size being too small.

**Table 3:** Summarised results of AVANO (α = 0.05) for yield and oil content; SS = sum of squares, df = degree of freedom, MS = middle sum of squares

**YIELD DE**

| *CAUSE OF DISPERSION* | *SS* | *df* | *MS* | *F* | *P-Value* | *critical F-Value* |
|---|---|---|---|---|---|---|
| **DIFFERENCES BETWEEN GROUPS** | 1624.06256 | 2 | 812.0312799 | 8.7549041 | 0.00023995 | 3.048832572 |
| **WITHIN THE GROUPS** | 15860.52197 | 171 | 92.75159047 | | | |
| | | | | | | |
| **TOTAL** | 17484.58453 | 173 | | | | |
| **OIL CONTENT DE** | | | | | | |
| **DIFFERENCES BETWEEN GROUPS** | 16.51929438 | 2 | 8.259647188 | 1.62461297 | 0.20048092 | 3.057196806 |
| **WITHIN THE GROUPS** | 752.4424606 | 148 | 5.08407068 | | | |
| | | | | | | |
| **TOTAL** | 768.961755 | 150 | | | | |
| **YIELD RO** | | | | | | |
| **DIFFERENCES BETWEEN GROUPS** | 204.3718088 | 2 | 102.1859044 | 6.36954052 | 0.00222012 | 3.057196806 |
| **WITHIN THE GROUPS** | 2374.349264 | 148 | 16.04290043 | | | |
| | | | | | | |
| **TOTAL** | 2578.721072 | 150 | | | | |
| **OIL CONTENT RO** | | | | | | |
| **DIFFERENCES BETWEEN GROUPS** | 17.36833627 | 2 | 8.684168136 | 1.46912446 | 0.23346307 | 3.057196806 |
| **WITHIN THE GROUPS** | 874.8454717 | 148 | 5.911118052 | | | |
| | | | | | | |
| **TOTAL** | 892.2138079 | 150 | | | | |

However, when evaluating the yield data, the percentage of moisture present after drying must not be ignored. It is noticeable, that the moisture content of the data from Romania is relatively constant and lower than from Germany. Romania showed values between 3.4 % - 6.2 %, 5.2 % -7.0 % and 4.5 % - 5.8 % for the yields of the different plant densities (Suppl. Fig. A 7) and thus, fluctuations of less than 3 %. Compared with the data from Germany, moisture contents of 1.6 % - 17.4 %, 3.8 % - 15.8 % and 0.45 % - 13.7 % were observed (Suppl. Fig. A 7), so that the fluctuations was partly over 15 %.

From the data for the yield (dt/ha) and the oil content (%), the oil yield (l/ha) was calculated (Suppl. Tab. A 13) and the values of the different plant densities in the different locations could be compared. Figure 19 shows the dependence of oil yield to yield in all plant densities. Both locations showed increasing oil yield by increasing yield, but there were some differences in the results between the locations depending on plant density. For both locations, very good correlation values could be determined for all three plant densities. However, it should be noted that the $R^2$ value for the plant density of 20 cm at the site in Romania is lower than the others. With a value of $R^2 = 0.7726$, this differs somewhat from the other $R^2$ values. Germany showed the highest oil yields at plant density of 30 cm and the lowest oil yields at plant density of 20 cm, the distribution of the point clouds followed the plant densities. It must be noted, however, that the measured values go up to the highest ranges at a density of 25 cm (Fig. 19 A). Comparing the results from Romania it can be seen, that the highest oil yield occured at a plant density of 25 cm. It is noticeable, that the distribution of point clouds showed a different scatter depending on the plant densities (Fig. 19 B). The cloud with the lowest yields consists of the values measured at 30 cm, while the values for a plant density of 20 cm are average and the values measured at 25 cm have the highest range.

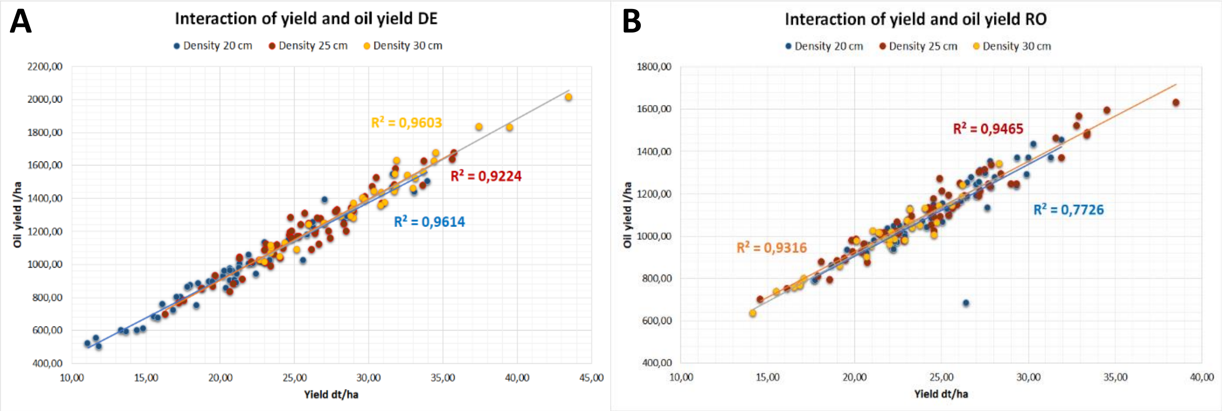


**Figure 19:** Scatter plots of the interaction of oil yield and yield in two locations at three different plant densities. **A)** Results from Mutzenroth (DE); **B)** Results from Sacalaz (RO)

The F1 hybrids with the highest oil yield/yield for the various plant densities are shown in Tab. 4 for the both locations. The reference variety ES Bella achieved a higher yield at a plant density of 20 cm than at 25 cm or 30 cm in Mutzenroth. Interestingly, four of the experimental hybrids showed a better performance under certain plant densities than the reference varieties.

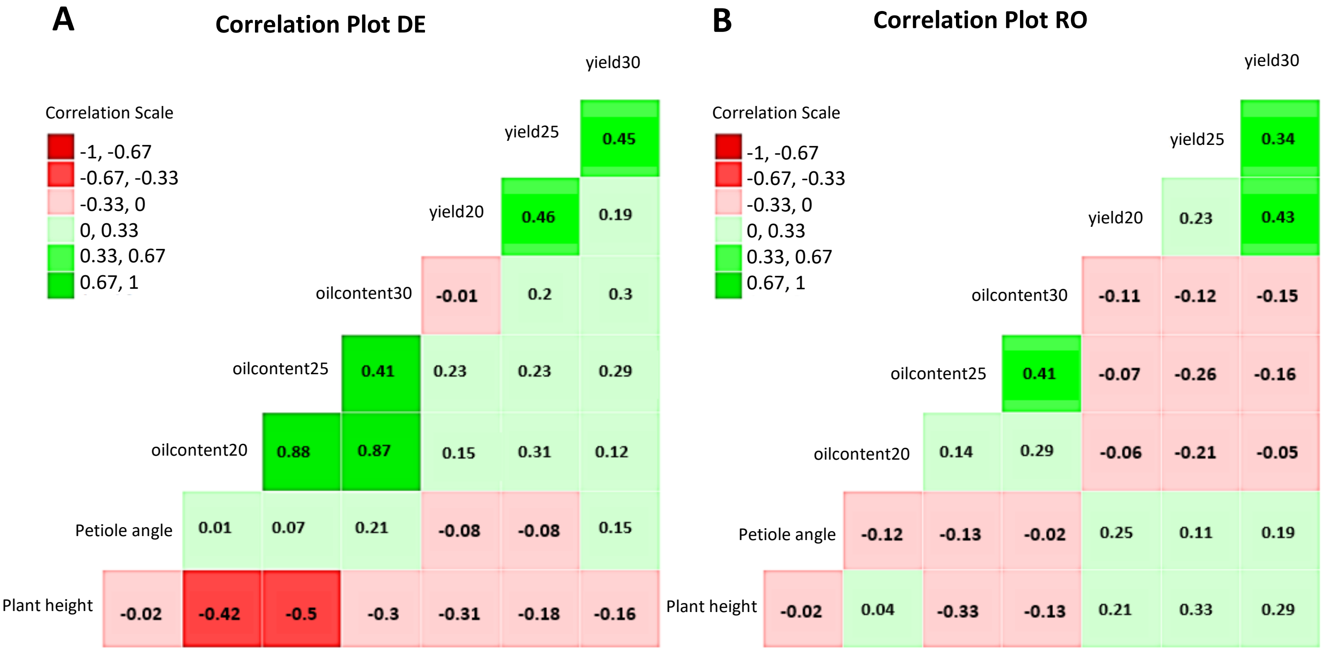
**Table 4:** Results of the highest oil yields in different plant densities in Germany and Romania in 2019

| LOCATION | DENSITY (CM) | F1 HYBRID | YIELD DT/HA | OIL CONTENT % | OIL YIELD L/HA |
|---|---|---|---|---|---|
| **DE** | 20 | ES Bella (reference) | 33.96 | 44.30 | 1504.35 |
| **DE** | 25 | LC-1093A x UGA-SAM1-041 | 35.75 | 46.90 | 1676.68 |
| **DE** | 30 | LC-1093A x UGA-SAM1-276 | 43.50 | 46.35 | 2016.23 |
| **RO** | 20 | LC-1093A x UGA-SAM1-041 | 31.92 | 45.60 | 1455.40 |
| **RO** | 25 | UGA-SAM1-082 x R-Line | 38.50 | 42.40 | 1632.40 |
| **RO** | 30 | ES Columbella (reference) | 28.33 | 47.35 | 1341.58 |

All three accessions (UGA-SAM1-041, UGA-SAM1-082 and UGA-SAM1-276), used for these F1-hybrids, showed a normal plant height. With regard to the petiole angle UGA-SAM1-082 showed a narrow petiole angle, whereas the other two accessions had normal petiole angles. The reference variety ES Bella showed a normal plant height and narrow petiole angle. For ES Columbella no values for plant height and petiole angles were available.

### 4.4.2 Evaluation of correlations using path analysis

Comparing all collected data the path analysis was performed to evaluate the types of relationships between the variables. The comparisons of the Romanian and German data showed clear differences in the correlations (Fig. 20). Positive correlations were observed between petiole angle and oil content for all plant densities in Germany, but only for plant density 25 cm in Romania. The results also showed positive correlation between petiole angle and yield for all plant densities (Fig. 20). In general, it means that the yields increased with the size of the petiole angle. Positive correlations were also shown for plant height and yield of all plant densities in Romania, i.e. the higher the plants were, the higher the yield was.



**A** **Correlation Plot DE**

Correlation Scale
🟥 -1, -0.67
🟥 -0.67, -0.33
🟥 -0.33, 0
🟩 0, 0.33
🟩 0.33, 0.67
🟩 0.67, 1

| | Petiole angle | oilcontent20 | oilcontent25 | oilcontent30 | yield20 | yield25 | yield30 |
|---|---|---|---|---|---|---|---|
| Plant height | -0.02 | -0.42 | -0.5 | -0.3 | -0.31 | -0.18 | -0.16 |
| Petiole angle | | 0.01 | 0.07 | 0.21 | -0.08 | -0.08 | 0.15 |
| oilcontent20 | | | 0.88 | 0.87 | 0.15 | 0.31 | 0.12 |
| oilcontent25 | | | | 0.41 | 0.23 | 0.23 | 0.29 |
| oilcontent30 | | | | | -0.01 | 0.2 | 0.3 |
| yield20 | | | | | | 0.46 | 0.19 |
| yield25 | | | | | | | 0.45 |

**B** **Correlation Plot RO**

Correlation Scale
🟥 -1, -0.67
🟥 -0.67, -0.33
🟥 -0.33, 0
🟩 0, 0.33
🟩 0.33, 0.67
🟩 0.67, 1

| | Petiole angle | oilcontent20 | oilcontent25 | oilcontent30 | yield20 | yield25 | yield30 |
|---|---|---|---|---|---|---|---|
| Plant height | -0.02 | 0.04 | -0.33 | -0.13 | 0.21 | 0.33 | 0.29 |
| Petiole angle | | -0.12 | -0.13 | -0.02 | 0.25 | 0.11 | 0.19 |
| oilcontent20 | | | 0.14 | 0.29 | -0.06 | -0.21 | -0.05 |
| oilcontent25 | | | | 0.41 | -0.07 | -0.26 | -0.16 |
| oilcontent30 | | | | | -0.11 | -0.12 | -0.15 |
| yield20 | | | | | | 0.23 | 0.43 |
| yield25 | | | | | | | 0.34 |

**Figure 20:** Correlation Plot of the relationships between the different variables; petiole angle, plant height, oil content of different plant densities, yield of different plant densities. **A)** Results from Mutzenroth (DE) in 2019; **B)** Results from Sacalaz (RO) in 2019

## 4.5 Evaluation of phenotyping data and segregation analysis of F2 populations

The field trials for the segregation analyses were successfully carried out between May and October 2020 (Fig. 21) and the F2 populations with the associated F1 generations and their parents were evaluated (Tab. 5). The six accessions of parental generation showed the expected values for the plant height and the petiole angles. The F1 hybrids demonstrated the expected uniformity with normal plant height, which indicated a recessive inheritance of the semi-dwarfism in these crosses. Two of the F1-hybrids showed normal petiole angles (> 40 °) and three showed narrow petiole angles (≤ 40 °).

**Figure 21:** Field trial for segregation analysis. **A)** Growth phase 22.07.2020; **B)** Flowering 24.08.2020; **C)** Harvest 13.10.2020

**Table 5:** Evaluation results of parents and F1 generations with regard to petiole angles (PET), flowering dates (FLO (D)) and plant heights (PH)

| PLANT MATERIAL | ° PET | ANGLE TYPE | FLO (D) | PH (CM) | GROWTH TYPE |
|---|---|---|---|---|---|
| CM 104 | 29.0 ± 7.3 | Narrow | 76 | 65 ± 2.6 | Semi-dwarf |
| ROMSUN V3355 | 29.8 ± 11.2 | Narrow | 68 | 72 ± 3.9 | Semi-dwarf |
| UGA-SAM1-185 | 39.9 ± 5.7 | Narrow | 74 | 104 ± 3.4 | Semi-dwarf |
| NO. 2 | 40.3 ± 6.8 | Normal | 71 | 137 ± 7.0 | Normal |
| CMH 101 | 28.9 ± 3.0 | Narrow | 76 | 134 ± 5.7 | Normal |
| UGA-SAM1-110 | 31.1 ± 3.2 | Narrow | 83 | 96 ± 9.1 | Semi-dwarf |
| F1 CM 104 X R-LINE | 40.0 ± 10.0 | Normal | 71 | 120 ± 7.7 | Normal |
| F1 ROMSUN V3355 X R-LINE | 38.6 ± 8.0 | Narrow | 65 | 121 ± 5.7 | Normal |
| F1 UGA-SAM1-185 X R-LINE | 43.5 ± 8.8 | Normal | 72 | 128 ± 3.9 | Normal |
| F1 NO. 2 X UGA-SAM1-110 | 38.4 ± 5.8 | Narrow | 71 | 133 ± 9.1 | Normal |
| F1 CMH 101 X ROMSUN V3355 | 36.2 ± 12.1 | Narrow | 86 | 128 ± 6.0 | Normal |

### 4.5.1 Evaluation of F2 populations

For the study of the inheritance of plant height and petiole angle F2-populations with a size of 40/80 individuals were planned. However, due to problems in this part of the field in 2020, the number of F2-individuals per cross combinations were considerably reduced. The data have to be regarded with extreme care, but might still give an indication with regard to the inheritance of the traits.

For the cross combination the CM 104 x R line, 54 individuals in the F2 population could be examined and compared, which was the largest of the five F2 populations. If the assessment data of the plant heights are considered, measured values between 60 cm - 123 cm were recorded in the F2 generation. This F2 population was composed of 21 plants with normal plant height (> 105 cm) and 33 plants with semi-dwarf phenotypes. If the measured values for the petiole angles are considered, angles between 31.0 ° - 64.0 ° were measured in the F2 individuals. Five plants had wide petiole angles and two had narrow angles, the majority of the population showed petiole angles in the normal range (Suppl. Fig. A 9).

The F2 population of the cross combination ROMSUN V3355 x R-Line comprised only 17 individuals. The data collected showed measurements between 38 cm - 98 cm for plant height (Suppl Fig. A 10). The population can be divided into 4 plants with dwarf phenotypes and 13 plants with semi-dwarf growth types. Eight plants showed narrow, predominantly apical branches. With regard to the readings of the petiole angles, values between 37.0 ° - 60.5 ° could be measured (Suppl. Fig. A 10). The measured values showed that the population had two plants with narrow angles, 13 with angles classified as normal and two plants with wide petiole angles.

The evaluation regarding the F2 population of the cross combination UGA-SAM1-185 x R-Line was done for 31 plants. The results for plant height showed measurements in a range of 81 cm – 178 cm (Suppl. Fig. A 10). Thus, the population consisted of seven plants with semi-dwarf growth type and 24 plants showing a normal growth type. In relation to the petiole angle, the F2 population showed values between 30.0 ° - 61.0 ° (Suppl. Fig. A 11). The distribution of measurements showed three plants with narrow angles, four plants with wide angles and 24 plants had as normal defined petiole angles.

For the evaluation of the F2 population of the cross combination No. 2 x UGA-SAM1-110 30 plants were available from the field trials. For this population, the measurement data for the plant height resulted in values of 112 cm – 161 cm, so that only normal growth type is present (Suppl. Fig. A 12) and no branches were formed. The data collected for petiole angles show measurements between 36.0° - 64.5° (Suppl. Fig. A 12). The population can be divided into 4 plants with narrow petiole angles, 25 plants with normal defined petiole angles and it is paradoxical to note, one plant with wide petiole angles.

For the F2 population of the cross combination CMH 101 x ROMSUN V3355 a population of 29 plants could be evaluated in described termsa . No branches were formed in the entire population. The results for plant height show measurements in a range of 104 cm – 159 cm (Suppl. Fig. A 13). Thus, the population consists of one plant with semi-dwarf growth type and 28 plants show the normal growth type. In relation to the petiole angle, the F2 population shows mainly wide petiole angles. Overall, values between 50.0 ° - 71.0 ° could be measured for the upper plant level. However, the population split into two groups, 13 plants with normal angles and 16 plants with wider values for petiole angles (Suppl. Fig. A 13).

### 4.5.2 Segregation analysis

Segregation analyses were performed for the five F2-populations regarding a monogamic, dominant-recessive inheritance for plant height ($\chi^2$ threshold 3.84) and a monogamic, intermediate inheritance for petiole angle ($\chi^2$ threshold 5.99) (Tab. 6).

**Table 6:** Summary of segregation analyses, α = 0,05, Plant height: D = dwarf, SD = semi-dwarf, N = normal, Petiole angle: NW = narrow, NL = normal, W = wide, # = Number of plants

| F2 HYBRID | # | PH (CM) | D | SD | N | X² | F | P | DIVISION |
|---|---|---|---|---|---|---|---|---|---|
| CM 104 X R-LINE | 54 | 65 - 123 | - | 33 | 21 | 5.56 | 1 | 0.01842213 | 3 : 1 |
| ROMSUN V3355 X R-LINE | 17 | 38 - 98 | 4 | 13 | - | 0.02 | 1 | 0.88863786 | 1 : 3 |
| UGA-SAM1-185 X R-LINE | 31 | 81 - 178 | - | 7 | 24 | 0.10 | 1 | 0.75573562 | 1 : 3 |
| NO. 2 X UGA-SAM1-110 | 30 | 112 - 161 | - | - | 30 | - | - | - | - |
| CMH 101 X ROMSUN V3355 | 29 | 104 - 159 | - | - | 29 | - | - | - | - |
| **F2 HYBRID** | **#** | **PETIOLE °** | **NW** | **NL** | **W** | **X²** | **F** | **p** | **DIVISION** |
| CM 104 X R-LINE | 54 | 31.0 - 64.0 | 2 | 47 | 5 | 29.96 | 2 | 0.00000031 | 1 : 2 : 1 |
| ROMSUN V3355 X R-LINE | 17 | 37.0 - 60.5 | 2 | 13 | 2 | 4.76 | 2 | 0.09233307 | 1 : 2 : 1 |
| UGA-SAM1-185 X R-LINE | 31 | 30.0 - 61.0 | 3 | 24 | 4 | 9.39 | 2 | 0.00915415 | 1 : 2 : 1 |
| NO. 2 X UGA-SAM1-110 | 30 | 36.0 - 64.5 | 4 | 25 | 1 | 7.54 | 1 | 0.00601954 | 1 : 2 : 1 |
| CMH 101 X ROMSUN V3355 | 29 | 50.0 - 70.0 | - | 13 | 16 | 6.08 | 1 | 0.01366852 | 1 : 3 |

## 4.6 Candidate gene approach for association studies

The candidate gene approach encompassed 18 genes of the GA-signaling pathway as well as four genes responsible for leaf angle and branching angle (Fig. 22).

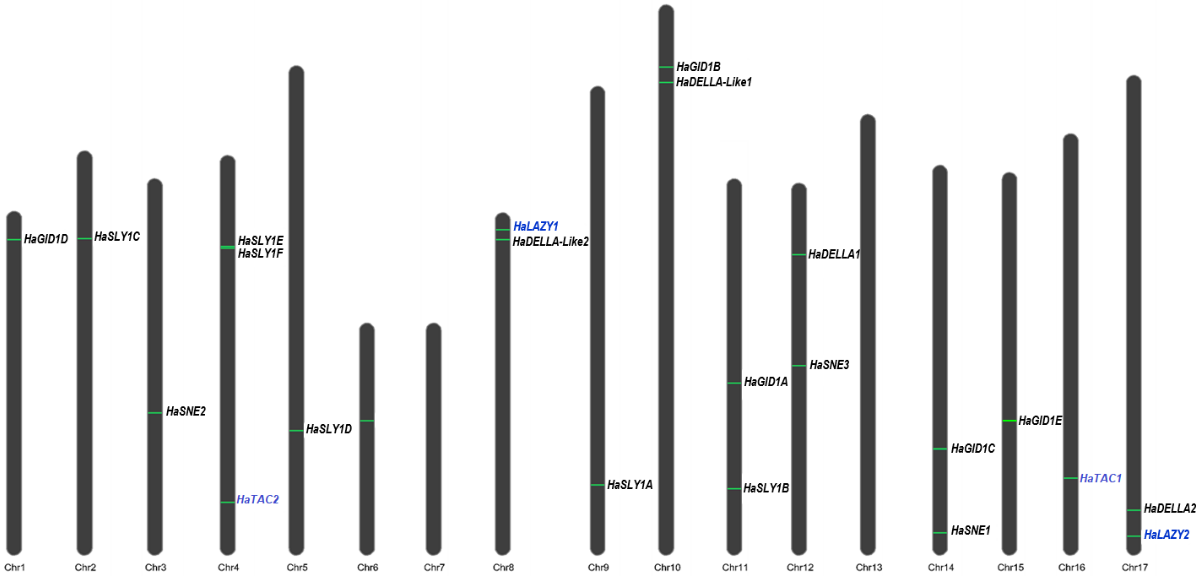


**Figure 22:** Positions of the examined 22 candidate genes on 14 of 17 chromosomes in the sunflower HanXRQ genome assembly v.1; labeled in black: genes of the GA signaling pathway; labeled in blue: genes responsible for leaf angle and branching angle

The detected genes of the GA-signaling pathway in sunflower consist of DELLA proteins (*HaDELLA1*, *HaDELLA2*, *HaDELLA-Like1*, *HaDELLA-Like2*), GA receptors (*HaGID1A-E*), SLEEPY family (*HaSLEEPY1A-F*) and SNEEZY family (*HaSNEEZY1-3*) (Suppl. Tab. A 24). Before publication of HanXRQ database, only partial sequences were known for genes *HaGID1C*, *HaGID1D*, *HaDELLA-Like2*, and *HaLAZY1*, which is why these had to be completed first. A sequence from HA 412 (Ha412NBC16S174.12) was already available for the *HaTAC1* gene, but it appeared to be incomplete because the normally highly conserved structure of five exons and four introns was not confirmed (Dardick *et al.*, 2013).

### 4.6.1 Partial genes of GA-signaling pathway

The gene sequences could be completed for the three genes *HaGID1C*, *HaGID1D* and *HaDELLA2* of the GA signaling pathway, which were only partially available before publication of HanXRQ database. By examining the cDNA, the exon-intron structure of the genes could be determined (Fig. 23). The annotation and expression of these genes was confirmed in the line HA 383. The gene *HaDELLA2* had a DNA sequence of 1.701 bp and showed no introns, as *HaDELLA-Like1* and *HaDELLA-Like2*. Only *HaDELLA1* had an annotated intron of 325 bp (Suppl. Fig. A 15).

For the gene *HaGID1C* a genomic length of 2.212 bp was determined. It showed a structure of three exons and two introns (Fig. 23). In contrast to *HaGID1C*, the cDNA analyses revealed that *HaGID1D* showed only one intron and a total length of 2.056 bp (Fig. 23). The obtained gene structures (*HaDELLA2, HaGID1C, HaGID1D),* were identical to the annotation of the HanXRQ reference genome v.1 (Badouin *et al.*, 2017).

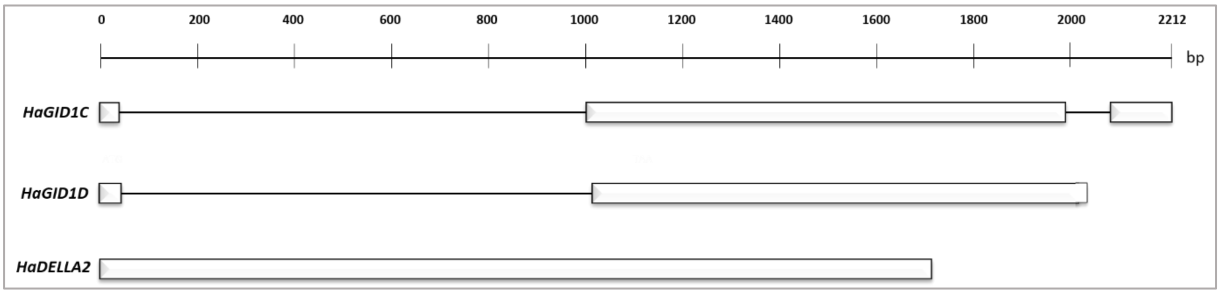


**Figure 23:** Genomic structures of the completed genes *HaDELLA2*, *HaGID1C* and *HaGID1D* of GA-signaling pathway

### 4.6.2 Partial genes *HaTAC1* and *HaLAZY1*

For the angular expression genes *HaTAC1* and *HaLAZY1* the genome sequences of HA 412 and HanXRQ were also used as reference. It was found that the complete gene sequence of *HaLAZY1* is present in

HanXRQ v.1 and has a size of 3.421 bp (HanXRQr2_Chr08g0320071). The gene shows an exon-intron structure of five exons and four introns (Fig. 24). The cDNA analyses confirmed the gene structure.

The known exon-intron-structure and the completeness of the existing gene sequence of *HaTAC1* from line HA 412 was checked in line HA 383. The sequencing of the amplificates resulted in a genomic sequence of 1.051 bp and also an exon-intron-structure with four exons and three introns based on the cDNA sequence (Fig. 24). Since the identified exon-intron structure of *HaTAC1* did not correspond to the exon-intron structure described for higher plants (Dardick *et al.,* 2013), 3'RACE was used to check whether another fifth exon was present. The investigation confirmed the already identified exon-intron structure with four exons and three introns for *HaTAC1*. A BLAST against the HanXRQ database showed that the sequence of HA 383 is the same as the sequence of HanXRQ for the *HaTAC1* gene (HanXRQChr16g0524641) on chromosome 16 and has also only four exons.

### 4.6.3 Identification of *HaTAC2* and *HaLAZY2*

A second BLAST of the sequence of HA 412 against the database showed a second *HaTAC* sequence (HanXRQChr04g0120361) on chromosome 4, which, however, only has three exons and not the exon-intron-structure with five exons described as conserved for higher plants. It is therefore assumed that the *TAC* genes of the sunflower might have a different exon-intron-structure than previously described. To decide whether the two *TAC1* genes are really full sequence *TAC1* genes despite the differing exon-intron structures, the sequences of *HaTAC1* and *HaTAC2* were compared with known sequences from different crops. It was found that the four conserved domains I-IV (Dardick *et al.,* 2013) were present in both *TAC* genes in the sunflower and that the characteristic IGT motif is also located in domain II in both gene sequences (Fig. 24). Thus, the two *TAC* genes, known in the sunflower as *HaTAC1* (HanXRQChr16g0524641) on chromosome 16 and *HaTAC2* (HanXRQChr04g0120361) on chromosome 4, could definitely be identified as *TAC* genes.

**Figure 24:** Multiple alignment of *TAC1-like* sequences in sunflower (HanXRQChr04g0120361; HanXRQChr16g0524641), apple (XP_008354051.1), pearapple (XP_009334382.1), peach (Dardick *et al.*, 2013) and jujube (XP_015869614.1). The conserved domains I-IV are indicated and numbered using roman numerals; IGT motif is marked in red

BLAST analyses also showed that a possible second *LAZY* (HanXRQChr17g0568921) gene is also present on chromosome 17 in sunflowers. When examining the amino acid sequence for the characteristic five domains, which have been described for the *LAZY1* gene (Dardick *et al.*, 2013), a total of four of the five conserved domains could be identified in *HaLAZY2* (Fig. 25). Despite the absence of domain II, in which the characteristic IGT motif of the gene family lies, this potential *HaLAZY2* gene was used for further analyses. Domain V, which contains the EAR motif, was also present in the potential second *LAZY* gene of the sunflower. Since this domain can give *LAZY* the ability to suppress auxin response genes (Yoshihara *et al.*, 2013; Dardick *et al.*, 2013), it appears to be an interesting candidate gene for plant architecture.

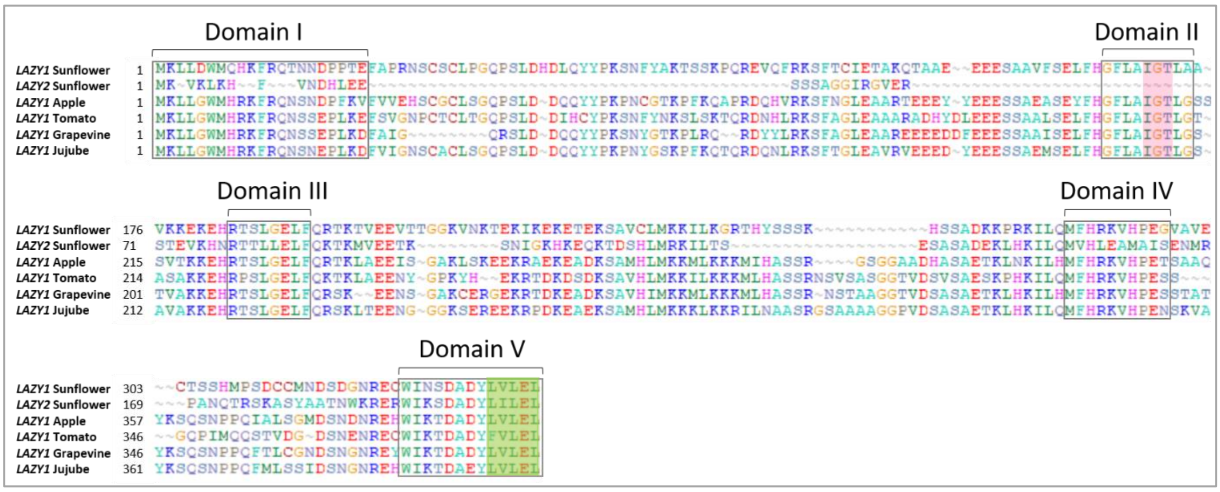


**Figure 25:** Multiple alignment of *LAZY1-like* sequences in sunflower (HanXRQChr08g0209951; HanXRQChr17g0568921), apple (XP_008389908.1), tomato (XP_004239242.1), grapevine (XP_010656172.1) and jujube (XP_015894302.1). The conserved domains I-V are indicated and numbers using roman numerals; IGT and EAR motif are marked in red and green, respectively.

The potential second *LAZY* gene *HaLAZY2* identified in this study was examined for the known conserved properties. It was found that, with a length of 204 amino acids, it was significantly shorter than the sequence of *HaLAZY1* (338 aa) and comparable sequences of apple (392 aa), tomato (380 aa), grapevine (381 aa) and jujube (396 aa). When examining the protein structure of *HaLAZY2*, it become obvious that this gene has only four and not five exons. A comparison with the amino acid sequence revealed gaps in the sequence of the first two conserved regions in domains I and II. While domain I was still partially present, domain II and thus the specific IGT motif were completely absent (Fig. 26). However, domains III-IV were complete as well as the EAR motif in domain V, which is important for the protein function. The potential second *LAZY* gene of the sunflower was included in the candidate gene approach and used for the association studies to identify SNPs significantly associated with traits of the plant architecture, even though missing domain II it might be non-functional. The gene structures of all *HaTAC* and *HaLAZY* genes are shown in Fig 26.

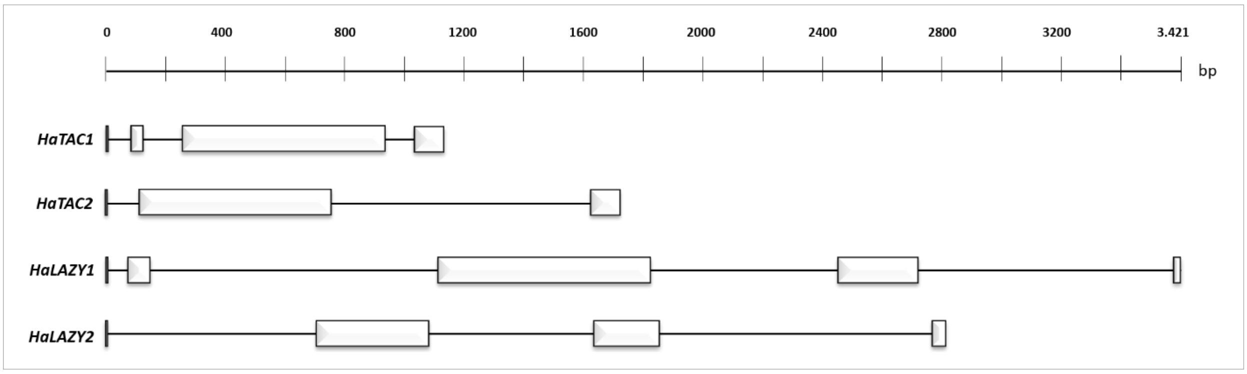


**Figure 26:** Genomic structures of the completed genes *HaTAC1*/*HaTAC2* and *HaLAZY1*/*HALAZY2* important for petiole angle

## 4.7 SNP detection based on targeted amplicon sequencing

The next generation sequencing results provided by LGC revealed gene variants for 20 of the 22 candidate genes examined (Tab. 7). The results showed that most of the SNPs were located in the cds of the genes. Most InDels, however, were located in the 5'-areas. A total of 306 SNPs and 111 InDels were found in the 22 candidate genes within the 64 selected genotypes (Tab. 7). It was also noticeable that the two genes *HaGID1A* and *HaSNE1* had no SNPs or InDels and were therefore highly conserved (Tab. 7).

**Table 7:** Summary of next generation sequencing, positioning of SNPs and InDels of the candidate gene approach; according to HanXRQ database v.1

| GENE | CHR | TOTAL (BP) | TOTAL SNPS | TOTAL INDELS | CDS (BP) | CDS SNPS | CDS INDELS | 5' SNPS | 5' INDELS | 3' SNPS | 3' INDELS |
|---|---|---|---|---|---|---|---|---|---|---|---|
| *HAGID1D* | chr01 | 4725 | 15 | 8 | 2032 | 11 | 2 | 0 | 3 | 4 | 3 |
| *HASLY1C* | chr02 | 3479 | 14 | 8 | 596 | 1 | 3 | 9 | 3 | 4 | 2 |
| *HASNE2* | chr03 | 3000 | 5 | 3 | 500 | 4 | 0 | 1 | 3 | 0 | 0 |
| *HASLY1E* | chr04 | 3078 | 5 | 4 | 578 | 1 | 0 | 2 | 4 | 2 | 0 |
| *HASLY1F* | chr04 | 3167 | 7 | 4 | 410 | 0 | 1 | 7 | 3 | 0 | 0 |
| *HATAC1* | chr04 | 4182 | 18 | 5 | 1065 | 7 | 1 | 9 | 4 | 2 | 0 |
| *HASLY1D* | chr05 | 3075 | 14 | 2 | 575 | 6 | 0 | 7 | 2 | 1 | 0 |
| *HADELLA-LIKE2* | chr08 | 5007 | 41 | 11 | 1518 | 20 | 3 | 20 | 6 | 1 | 2 |
| *HALAZY1* | chr08 | 5922 | 26 | 3 | 3095 | 18 | 1 | 6 | 2 | 2 | 0 |
| *HASLY1A* | chr09 | 3404 | 6 | 1 | 530 | 3 | 0 | 3 | 1 | 0 | 0 |
| *HADELLA-LIKE1* | chr10 | 4280 | 1 | 2 | 1709 | 0 | 0 | 1 | 1 | 0 | 1 |
| *HAGID1B* | chr10 | 6244 | 27 | 15 | 1907 | 15 | 2 | 7 | 6 | 5 | 7 |
| *HAGID1A* | chr11 | 5090 | 0 | 0 | 1620 | 0 | 0 | 0 | 0 | 0 | 0 |
| *HASLY1B* | chr11 | 4914 | 9 | 3 | 2331 | 3 | 2 | 4 | 1 | 2 | 0 |
| *HADELLA1* | chr12 | 5253 | 12 | 1 | 1995 | 12 | 0 | 0 | 1 | 0 | 0 |
| *HASNE3* | chr12 | 3018 | 10 | 4 | 518 | 3 | 0 | 6 | 4 | 1 | 0 |
| *HAGID1C* | chr14 | 5447 | 31 | 10 | 2213 | 18 | 4 | 11 | 4 | 2 | 2 |
| *HASNE1* | chr14 | 2970 | 0 | 0 | 470 | 0 | 0 | 0 | 0 | 0 | 0 |
| *HAGID1E* | chr15 | 5309 | 4 | 5 | 1936 | 4 | 0 | 0 | 4 | 0 | 1 |
| *HATAC2* | chr16 | 4584 | 3 | 5 | 1712 | 3 | 4 | 0 | 1 | 0 | 0 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| *HADELLA2* | chr17 | 4806 | 24 | 9 | 1700 | 14 | 1 | 9 | 6 | 1 | 2 |
| *HALAZY2* | chr17 | 5707 | 34 | 8 | 2810 | 17 | 3 | 10 | 4 | 7 | 1 |
| | **Σ** | **96661** | **306** | **111** | **31820** | **160** | **27** | **112** | **63** | **34** | **21** |

With regard to the genes of the GA signaling pathway, the DELLA genes *HaDELLA-Like2* and *HaDELLA2* (Fig. 27), as well as the GA receptors *HaGID1B* and *HaGID1C,* showed the most gene variants (Fig. 28). The four candidate genes selected for the development of the angles were also very variable. With the exception of *HaTAC2*, these genes showed a high number of SNPs in the examined area (Fig. 29) compared to the genes of the GA-signaling pathway.

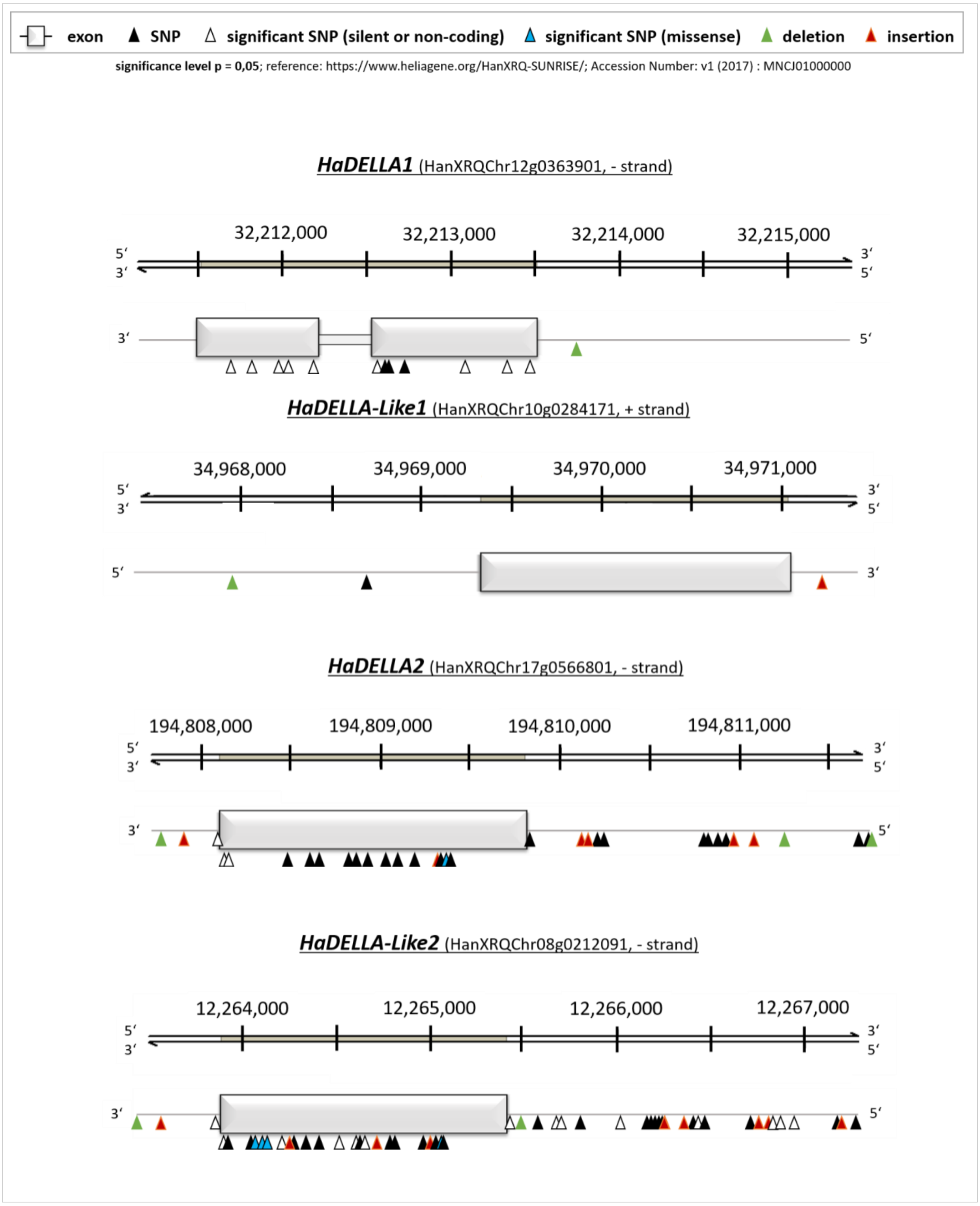


**Figure 27:** Positioning the mutations of the genes from DELLA family, + 2.000 bp upstream and 500 bp downstream. SNPs are presented as triangles in the colours black (not significantly associated), white (significantly associated silent or non-coding) and blue (significantly associated resulting in a missense mutation). Deletions (green) and insertions (red) are also shown in triangles

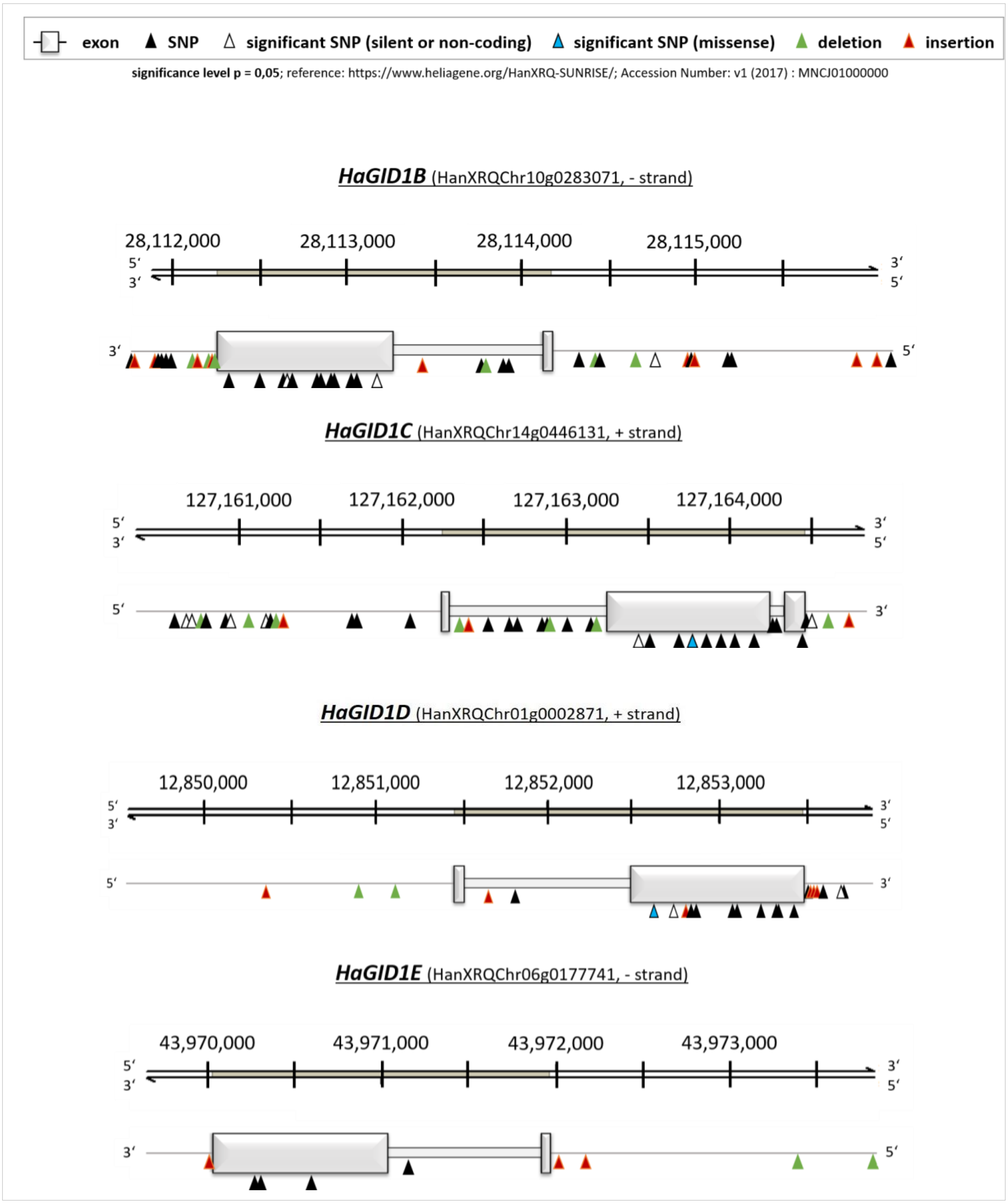


**Figure 28:** SNP positions of the genes of GA receptors, + 2.000 bp upstream and 500 bp downstream. SNPs are presented as triangles in the colours black (not significantly associated), white (significantly associated silent or non-coding) and blue (significantly associated resulting in a missense mutation). Deletions (green) and insertions (red) are also shown in triangles

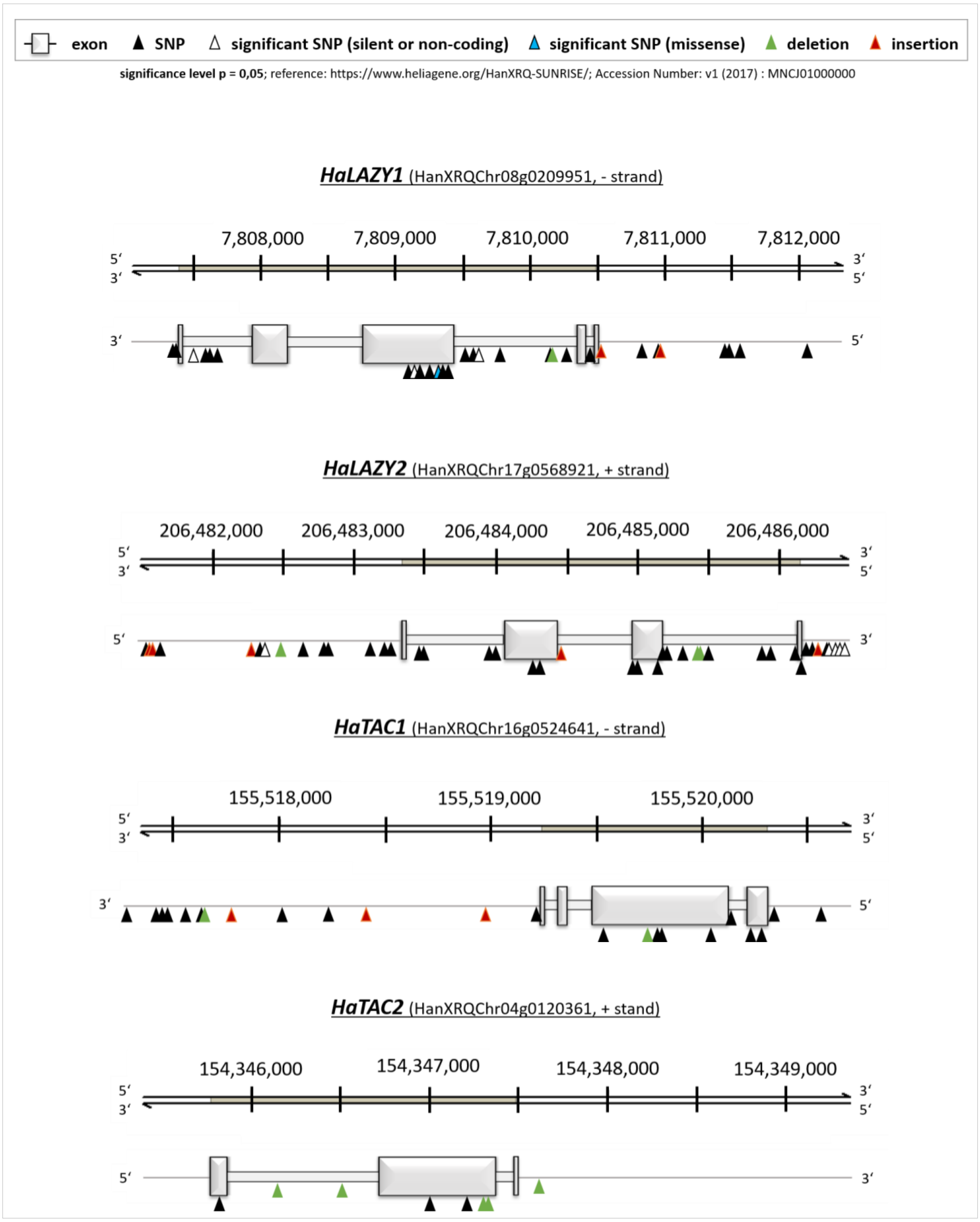


**Figure 29:** SNP positions of the genes *HaTAC1*/*HaTAC2* and *HaLAZY1*/*HaLAZY2*, + 2.000 bp upstream and 500 bp downstream. SNPs are presented as triangles in the colours black (not significantly associated), white (significantly associated silent or non-coding) and blue (significantly associated resulting in a missense mutation). Deletions (green) and insertions (red) are also shown in triangles

## 4.8 Detection of population structure of the association panel

### 4.8.1 Results of SSR analyses

The first step in investigating the population structure of the sunflower association panel was the performance of SSR analysis in the association panel. These analyses could be carried out successfully for all 34 SSR markers of the 17 linkage groups (Suppl. Tab. A 3) in the small and the large association panel. The results show both high and low polymorphic banding patterns of the SSR markers (Fig. 30). Overall, 11 markers were highly polymorphic and 23 markers showed a degree of lower polymorphics over all accessions. The band sizes varied from 125 - 430 bp across the 34 markers. On the basis of the electrophoresis results, the band sizes for all markers of all 64 genotypes could be recorded individually in a table, which was used as input file for the further work steps using STRUCTURE.

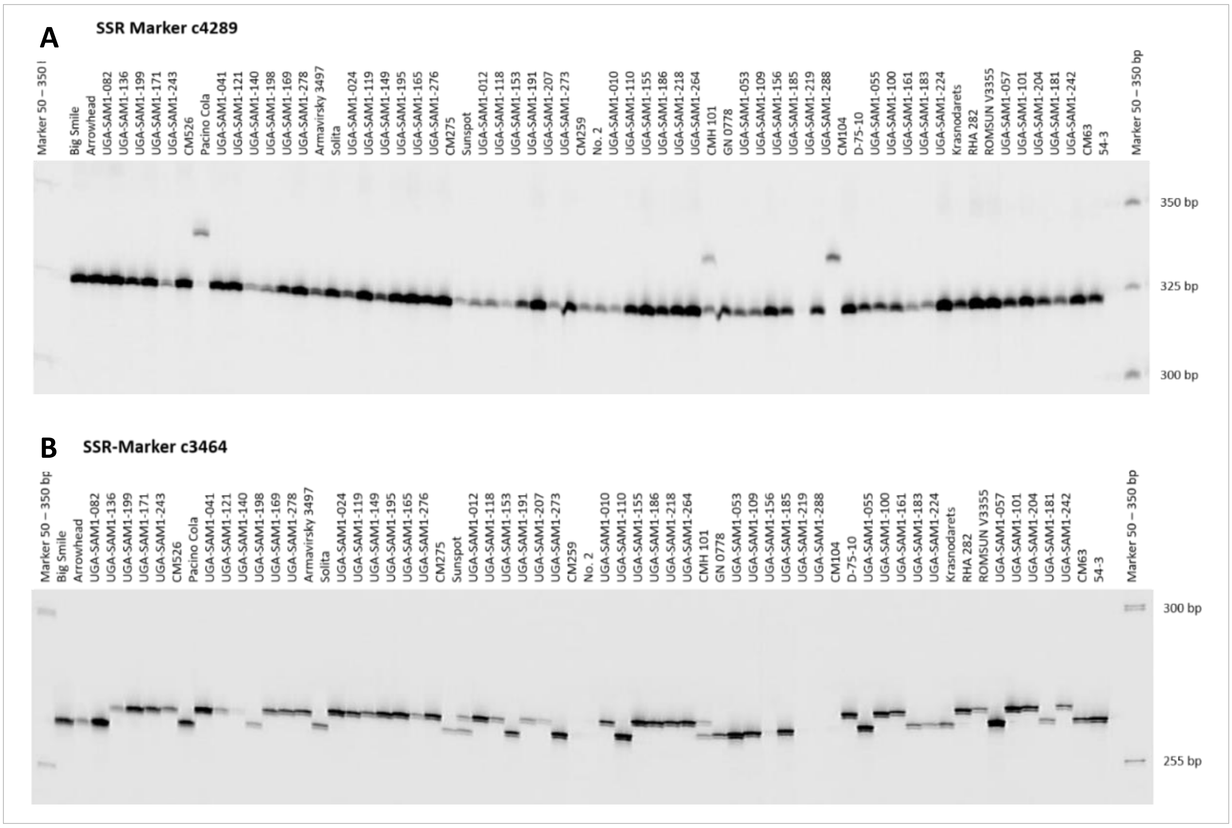


**Figure 30:** SSR marker linkage group 2 and 6 in the small association panel. **A)** Marker c4289 319-337 bp; **B)** Marker c3464 264-268 bp

### 4.8.2 Population structure of the small and the large association panel

The population structure was then determined using the "STRUCTURE" software. For this purpose, the population structure was calculated in 10-fold repetition based on the previously collected SSR data. There were 3 subpopulations identified within the selected small association panel of 64 accessions (Fig. 31). The large association panel of 384 sunflower accessions showed 2 subpopulations (Fig. 32).

The results of cluster analysis to determine the most likely number of clusters using the DeltaK method for the two association panels are shown in Suppl. Tab. A 15. The combination of the two panels (n = 448) resulted in a population with five subpopulations (Suppl. Fig. A 14).

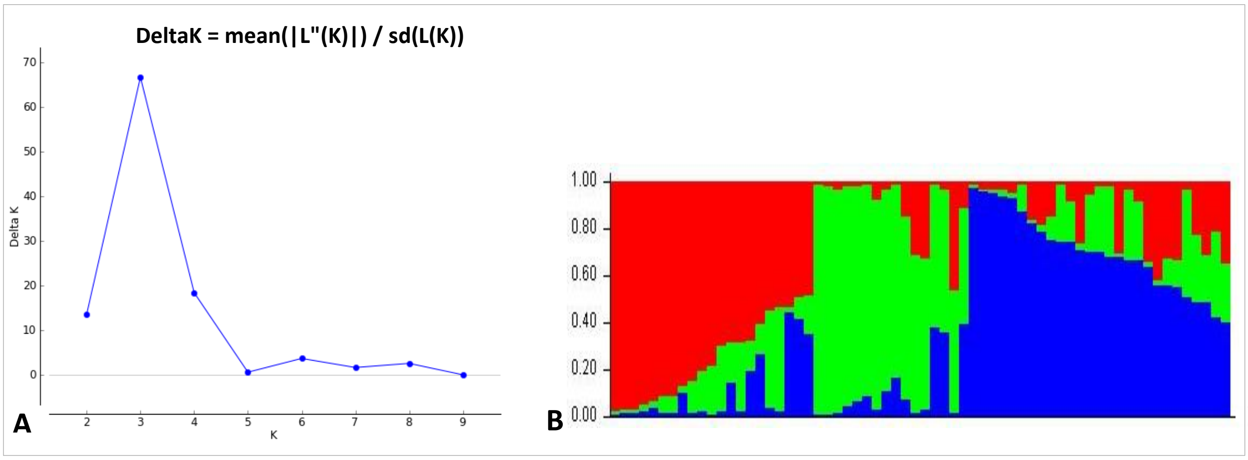


**Figure 31:** Data analysis with "STRUCTURE" in the small association panel (n = 64). **A)** Calculation of the population structure with 10 repetitions; **B)** Barplot, identification of 3 subpopulations within the selected association panel

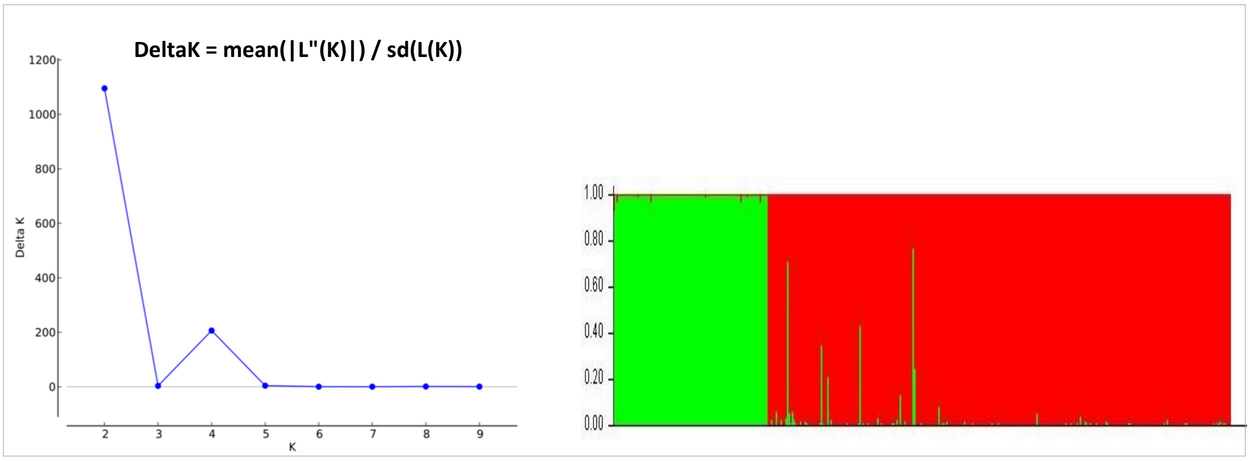


**Figure 32:** Data analysis with "STRUCTURE" in the large association panel (n = 384). **A)** Calculation of the population structure with 10 repetitions; **B)** Barplot, identification of 2 subpopulations within the large association panel

## 4.9 Identification of SNPs significantly associated with traits of plant architecture

### 4.9.1 Identification of SNPs using TASSEL

From the already existing sequencing data of the candidate genes of the 64 genotypes it is known that there are different gene variants of the genes examined. These gene variants differ mainly in the SNPs in the cds, which can influence the respective function of the gene. Based on these SNP data and the results of the population structure analysis, association studies using the Generalized Linear Model (GLM) could be carried out successfully. It was possible to identify significantly SNPs associated with the plant heights and the petiole angles (Fig. 33-35), which represent potential markers for the plant architecture. The analysis showed SNPs in the *HaDELLA-Like2* and *HaGID1B* genes (Tab. 8). The summary of all results of this analysis is shown in the Suppl. Tab. A 17.

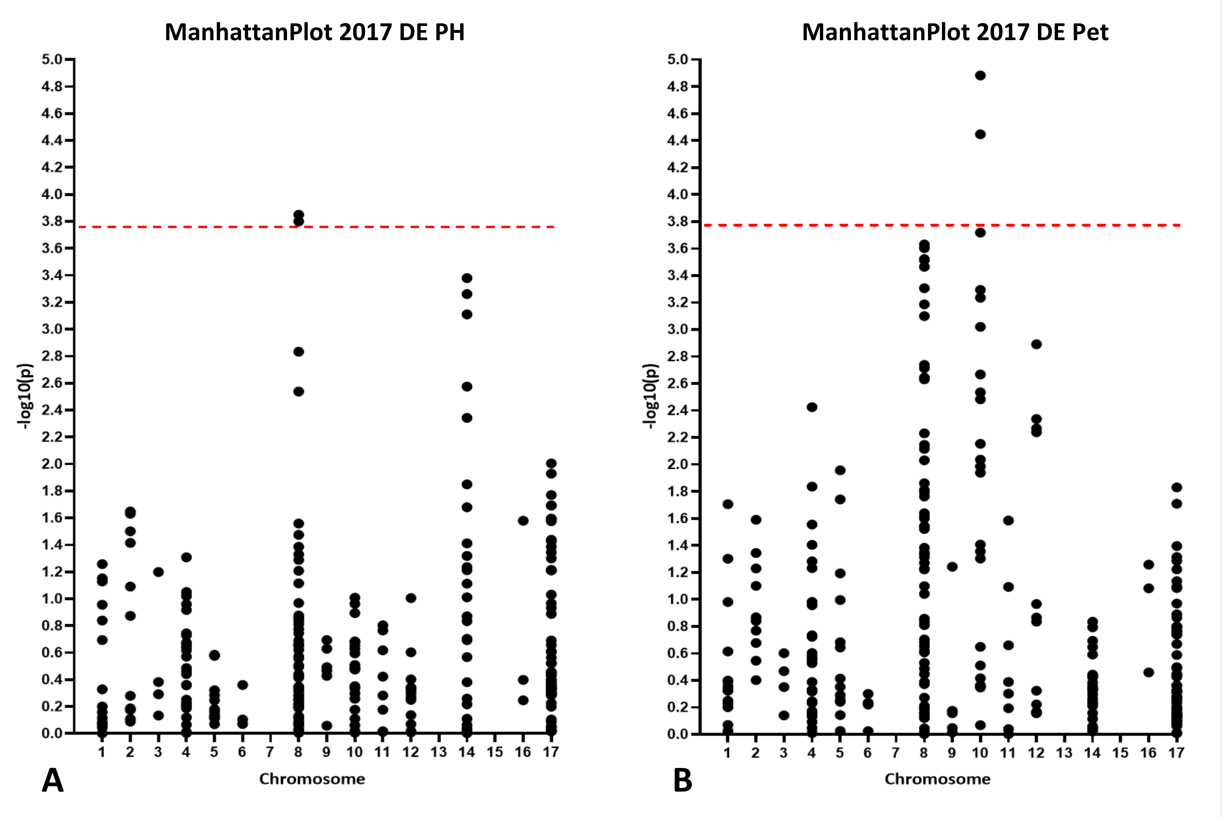


**Figure 33:** Results of GLM analysis for data of Germany in 2017 to identify significant SNPs. **A)** Significant associated SNPs for plant height; **B)** Significant associated SNPs for petiole angle; Limit p = 0,000164 (-log10 = 3,78515615)

**Table 8:** Significantly associated SNP markers for plant architecture identified using TASSEL in Germany in 2017 and 2019 and in Spain 2018

| TRAIT | GENE | SNP | CHR | POSITION | P-VALUE | YEAR |
|---|---|---|---|---|---|---|
| PLANT HEIGHT | *HaDELLA-Like2* | DEL091.30 | 8 | 8143660 | 1.4134E-04 | 2017 |
| PLANT HEIGHT | *HaDELLA-Like2* | DEL091.33 | 8 | 8143324 | 1.5819E-04 | 2017 |
| PETIOLE ANGLE | *HaGID1B* | GID071.16 | 10 | 21068624 | 1.3088E-05 | 2017 |
| PETIOLE ANGLE | *HaGID1B* | GID071.24 | 10 | 21068113 | 3.5770E-05 | 2017 |
| PETIOLE ANGLE | *HaDELLA-Like2* | DEL091.30 | 8 | 8143660 | 4.7469E-05 | 2019 |
| PETIOLE ANGLE | *HaDELLA-Like2* | DEL091.33 | 8 | 8143324 | 8.8209E-05 | 1019 |
| PETIOLE ANGLE | *HALAZY2* | LAZ921.16 | 17 | 206483470 | 6.5555E-05 | 2018 |
| PETIOLE ANGLE | *HALAZY2* | LAZ921.17 | 17 | 206483476 | 6.5555E-05 | 2018 |
| PETIOLE ANGLE | *HALAZY2* | LAZ921.19 | 17 | 206483990 | 9.7286E-05 | 1018 |

For the Spain, the corresponding SNPs missed the threshold (DEL091.30, p = 4,2657E-04; DEL091.33, p = 0,004237323; GID071.16, p = 0,013032815; GID071.24, p = 0,020934172). Five additional significantly with the petiole angle associated SNPs could be identified (Tab. 8) in Spain in 2018 (Fig. 34) and in Germany in 2019 (Fig. 35). GLM data analysis over all years did not served any significantly associated SNPs for plant height and petiole angle.

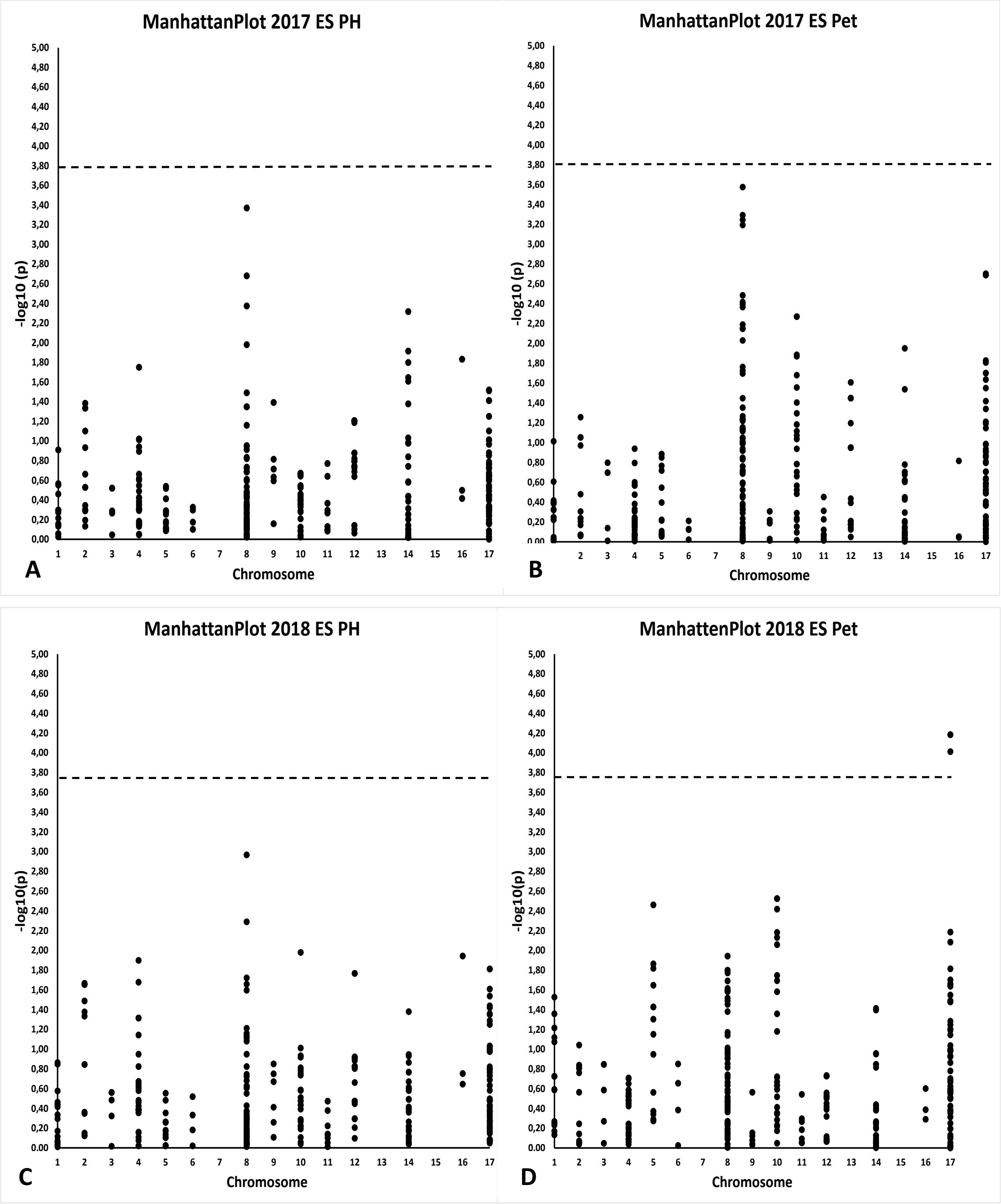


**Figure 34:** Results of GLM analysis for data of Spain in 2017 and 2018 to identify significant SNPs. A, C) SNPs associated with plant height; B, D) SNPs associated with petiole angle; Limit p = 0,000164 (-log10 = 3,78515615)

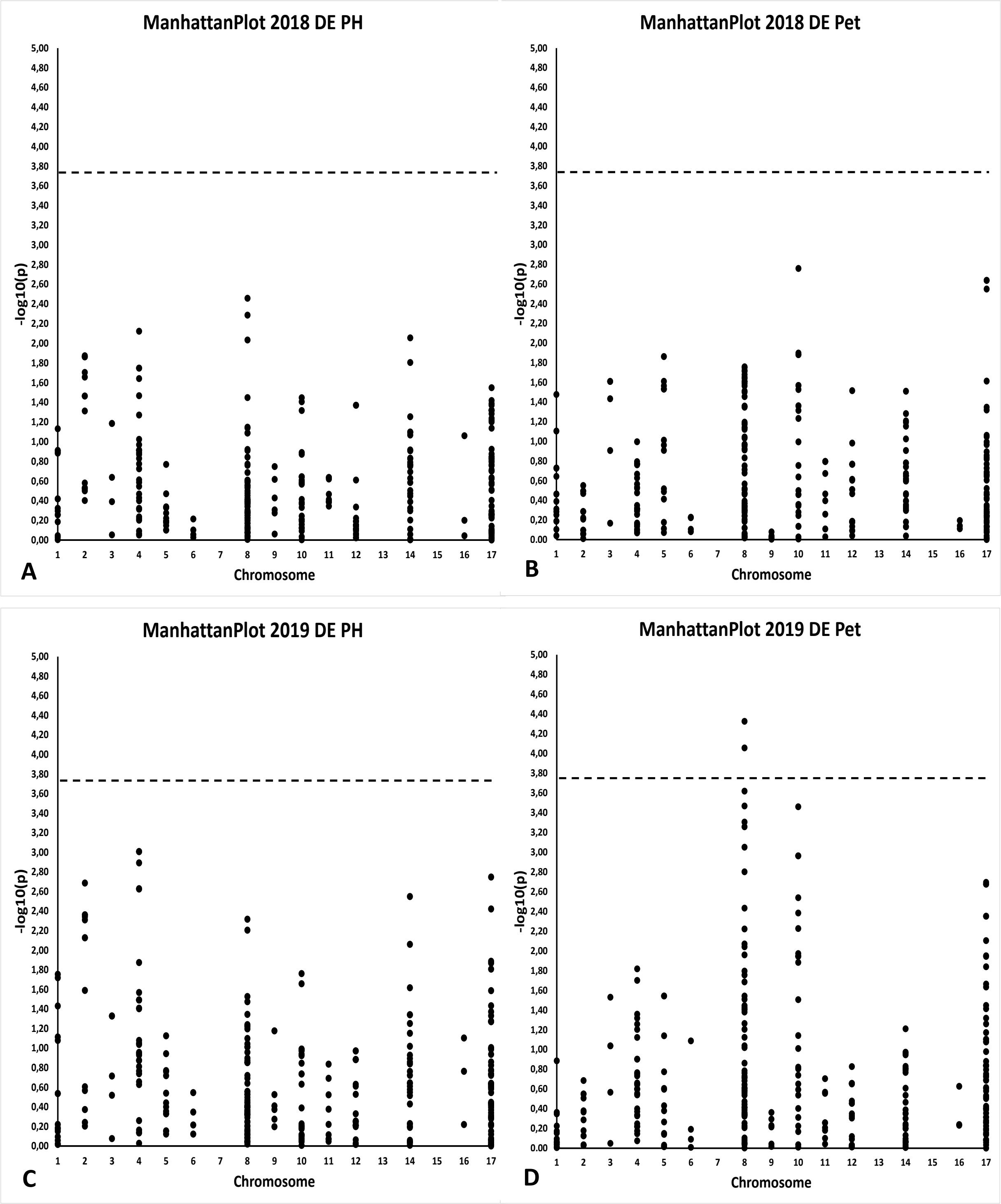


**Figure 35:** Results of GLM analysis for data of Germany in 2018 and 2019 to identify significant SNPs. A, C) SNPs associated with plant height; B, D) SNPs associated with petiole angle; Limit p = 0,000164 (-log10 = 3,78515615*)*

### 4.9.2 Identification of SNPs using the Fischer Exact Test

For a total of 22 candidate genes, seven significantly associated SNPs for different characteristics of the plant architecture were determined. Since the analysis with the TASSEL 5 program sets a very strict limit value through the Bonferroni correction (p = 0.000164) and the data set with 64 genotypes was relatively small, the association studies with the Fisher Exact Test were carried out on the basis of the existing sequencing data with a p -Value < 0.05. This recalculation made it possible to identify a total of 59 significantly associated SNPs in 11 different candidate genes (Tab. 9).

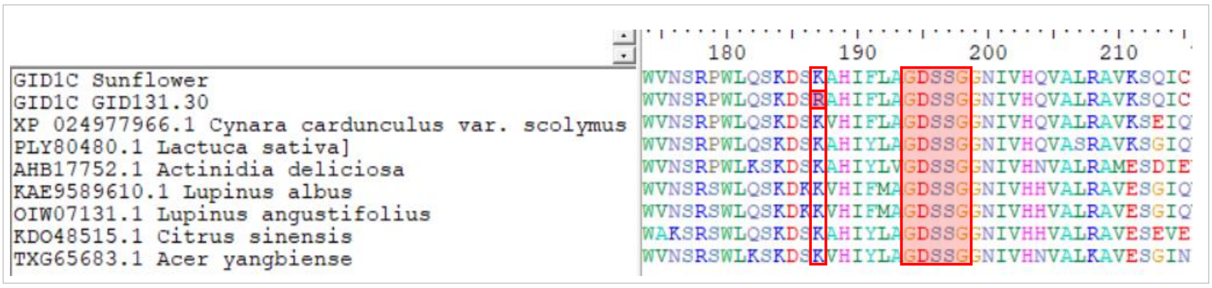
**Table 9:** Possible SNP markers for plant architecture identified in the small association panel using Fischer Exact Test. Narrow petiole angle ≤40 °, dwarf ≤65 cm, semi-dwarf 66 cm - 107 cm

| | **PETIOLE** | | **DWARF** | | **SEMI-DWARF** | |
|---|---|---|---|---|---|---|
| **GROUP** | **22 narrow** | **42 other** | **9 dwarfs** | **55 other** | **12 semi-dwarfs** | **52 other** |
| **GENE / SNP** | *HaDELLA-Like2* | 13 | *HaDELLA-Like2* | 4 | *HaDELLA-Like2* | 1 |
| | *HaDELLA2* | 3 | *HaDELLA2* | 1 | *HaGID1C* | 1 |
| | *HaDELLA1* | 9 | *HaGID1C* | 6 | *HaLAZY1* | 1 |
| | *HaGID1B* | 3 | *HaLAZY2* | 5 | *HaSLY1C* | 4 |
| | *HaGID1D* | 1 | *HaLAZY1* | 1 | *HaSLY1A* | 1 |
| | *HaLAZY1* | 1 | | | *HaSNE2* | 4 |
| **Σ** | **6** | **30** | **5** | **17** | **6** | **12** |

A total of 12 significantly associated SNPs could be identified for the “semi-dwarf” growth type, eight of which meet the criteria for an HRM marker (Tab. 10). The GID131.30 or SNE171.7 example shows that these are A/G or T/C exchanges. In the first case, this also results in an amino acid (AA) exchange. This AA exchange was found to be in close proximity to the conserved motif GDSSG (Fig. 36), which may have an impact on the interaction between GID1c and DELLA. HRM markers were developed and tested for these SNPs.

**Table 10**: Significantly associated SNPs for “semi-dwarf” growth type. bold: used for HRM marker development

| GENE | SNP | P-VALUE | ALLEL | AA CHANGE | POSITION | HRM SUITABLE |
|---|---|---|---|---|---|---|
| *HADELLA-LIKE2* | DEL091.16 | 0.04174 | T/C | A / A | 268 | yes |
| *HAGID1C* | **GID131.30** | 0.03452 | A/G | **K / R** | 186 | yes |
| *HALAZY1* | LAZ951.3 | 0.03274 | T/G | - | Intron | yes |
| *HASLY1C* | SLY061.3 | 0.02303 | A/T | - | 3' UTR | no |
| | SLY061.4 | 0.02303 | C/T | - | 3' UTR | yes |
| | SLY061.5 | 0.04261 | A/G | - | 3' UTR | yes |
| | SLY061.6 | 0.04486 | C/T | - | 3' UTR | yes |
| | SLY301.2 | 0.01697 | G/C | D / E | 44 | no |
| *HASLY1A* | SNE171.5 | 0.04174 | A/T | N / I | 8 | no |
| *HASNE2* | SNE171.6 | 0.04174 | G/C | P / P | 73 | no |
| | **SNE171.7** | 0.01878 | T/C | **L /L** | 92 | yes |
| | SNE171.8 | 0.00348 | C/T | G / G | 142 | yes |



```
                                                    180       190       200       210
GID1C Sunflower                                WVNSRPWLQSKDSKAHIFLAGDSSGGNIVHQVALRAVKSQIC
GID1C GID131.30                                WVNSRPWLQSKDSRAHIFLAGDSSGGNIVHQVALRAVKSQIC
XP 024977966.1 Cynara cardunculus var. scolymus WVNSRPWLQSKDSKVHIFLAGDSSGGNIVHQVALRAVKSEIQ
PLY80480.1 Lactuca sativa]                     WVNSRPWLQSKDSKAHIYLAGDSSGGNIVHQVASRAVKSGIQ
AHB17752.1 Actinidia deliciosa                 WVNSRPWLKSKDSKAHIYLVGDSSGGNIVHNVALRAMESDIE
KAE9589610.1 Lupinus albus                     WVNSRSWLQSKDKKVHIFMAGDSSGGNIVHHVALRAVESGIQ
OIW07131.1 Lupinus angustifolius               WVNSRSWLQSKDKKVHIFMAGDSSGGNIVHHVALRAVESGIQ
KDO48515.1 Citrus sinensis                     WAKSRSWLQSKDSKAHIYLAGDSSGGNIVHHVALRAVESEVE
TXG65683.1 Acer yangbiense                     WVNSRSWLKSKDSKVHIYLAGDSSGGNIVHNVALKAVESGIN
```

**Figure 36:** Comparison of the conserved GDSSG motif and surrounding region of sunflower (normal and semi-dwarf) with different plant species

For the “dwarf” growth type 17 significant SNPs were also identified in five genes (Tab. 11). The positions of most of these SNPs were located in the promoter regions of the candidate genes like *HaDELLA1-like2* and *HaGID1C* or in the 3'-UTR in *HaLAZY2*. Expression analyses would be of particular interest for investigations regarding the influence of these SNPs. For the HRM analyses, we concentrated on those SNPs that leads to amino acid exchanges and had a suitable base exchange. The SNPs DEL801.17 and LAZ951.11 were therefore used for marker development. In the first case, an amino acid exchange from isoleucine to valine occurred and in the second case from valine to alanine.

**Table 11:** Significantly associated SNPs for the “dwarf” growth type. Underlined: also identified as significantly associated with TASSEL 5, bold: HRM marker development

| GENE | SNP | P-VALUE | ALLEL | AA CHANGE | POSITION | HRM SUITABLE |
|---|---|---|---|---|---|---|
| *HADELLA-LIKE2* | DEL091.10 | 0.0179 | C/G | E / E | 399 | no |
| | <u>DEL091.30</u> | 0.04954 | G/C | - | Promoter | no |
| | DEL091.31 | 0.01786 | G/T | - | Promoter | yes |
| | <u>DEL091.33</u> | 0.01786 | A/C | - | Promoter | yes |
| *HADELLA2* | **DEL801.17** | 0.03971 | T/C | **I / V** | 147 | yes |
| *HAGID1C* | GID131.2 | 0.00747 | G/T | - | Promoter | yes |
| | GID131.3 | 0.01729 | C/T | - | Promoter | yes |
| | GID131.7 | 0.0075 | C/T | - | Promoter | yes |
| | GID131.9 | 0.0075 | A/G | - | Promoter | yes |
| | GID131.27 | 0.03638 | T/C | N / N | 75 | yes |
| | GID131.39 | 0.02674 | A/G | - | 3' UTR | yes |
| *HALAZY1* | **LAZ951.11** | 0.02498 | A/G | **V / A** | 61 | yes |
| *HALAZY2* | LAZ921.7 | 0.01729 | C/T | - | Promoter | yes |
| | LAZ921.41 | 0.03638 | A/G | - | 3' UTR | yes |
| | LAZ921.42 | 0.02151 | T/C | - | 3' UTR | yes |
| | LAZ921.43 | 0.04893 | T/C | - | 3' UTR | yes |
| | LAZ921.44 | 0.03971 | T/C | - | 3' UTR | yes |

The calculations for the trait “narrow petiole angle” resulted in a total of 30 significant SNPs in six different genes (Tab. 12). The two SNPs DEL091.8 and DEL091.9 in the *HaDELLA-Like2* gene and the SNP GID071.16 in the *HaGID1B* gene were selected for the development of HRM markers. These SNPs are well suited for the creation of HRM markers, as they represent base exchanges, which result in relatively large annealing temperature differences. In addition, the SNPs DEL091.8 and DEL091.9 cause amino acid exchanges. In case of DEL091.8, the C/T base exchange causes an amino acid exchange from valine to isoleucine. The A/C base exchange of the SNP DEL091.9 leads to an amino acid exchange from aspartic acid to glutamic acid. The SNP GID071.16 shows a base exchange of A/G, which, however, represents a silent mutation and does not cause an amino acid exchange (Tab. 12).

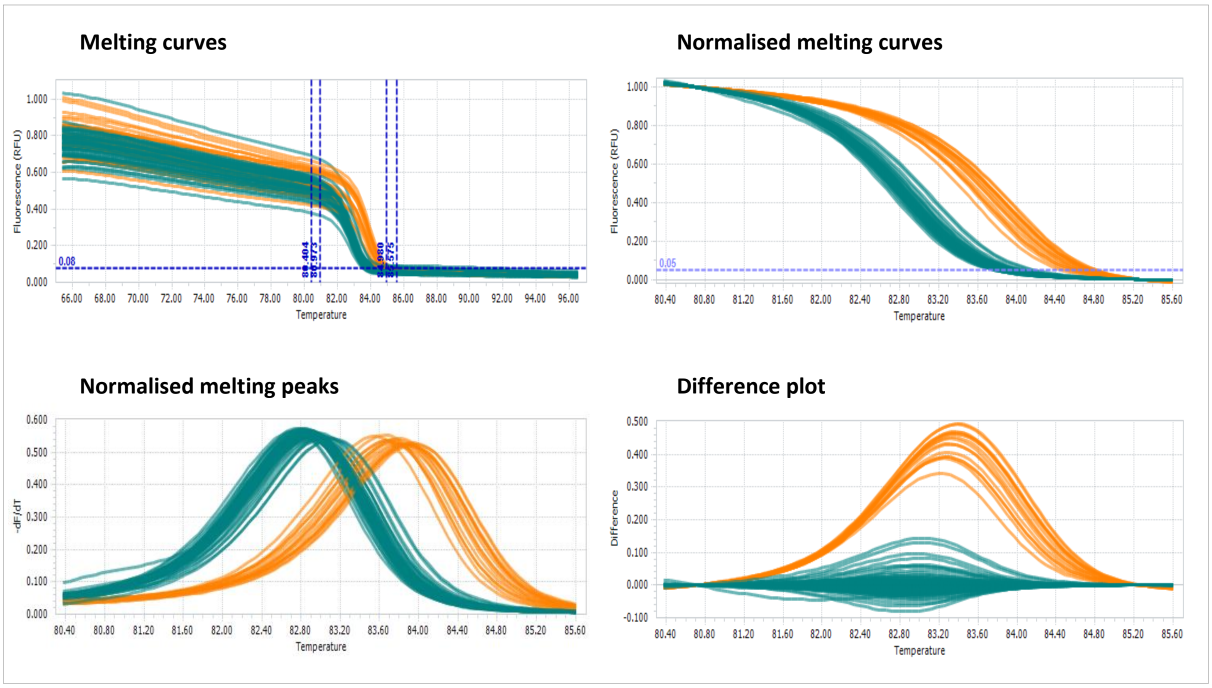
**Table 12:** Significantly associated SNPs for the characteristic "narrow petiole angle". underlined: also significant with TASSEL 5, bold: HRM marker development

| GENE | SNP | P-VALUE | ALLEL | AA CHANGE | POSITION | HRM SUITABLE |
|---|---|---|---|---|---|---|
| *HADELLA-LIKE2* | DEL091.3 | 0.01795 | T/A | E / D | 511 | no |
| | DEL091.4 | 0.00604 | A/C | G / G | 476 | yes |
| | DEL091.7 | 0.0035 | C/G | A / P | 447 | no |
| | **DEL091.8** | 0.0162 | C/T | **V / I** | 434 | yes |
| | **DEL091.9** | 0.037 | A/C | **D / E** | 425 | yes |
| | DEL091.15 | 0.01869 | T/C | S / S | 297 | yes |
| | DEL091.18 | 0.01002 | G/C | L / L | 256 | no |
| | DEL091.25 | 0.002967 | C/G | A / P | 117 | no |
| | DEL091.27 | 0.0135 | A/G | - | 3' UTR | yes |
| | DEL091.42 | 0.0351 | T/G | - | 3' UTR | yes |
| | DEL091.47 | 0.00604 | C/T | - | 3' UTR | yes |
| | DEL091.48 | 0.00604 | G/A | - | 3' UTR | yes |
| | DEL091.49 | 0.0162 | C/T | - | 3' UTR | yes |
| *HADELLA2* | DEL801.3 | 0.0246 | G/A | - | 3' UTR | yes |
| | DEL801.4 | 0.0162 | T/G | I / I | 558 | yes |
| | DEL801.5 | 0.0418 | A/G | R / R | 555 | yes |
| *HADELLA1* | DEL901.1 | 0.04486 | G/A | D / D | 499 | yes |
| | DEL901.2 | 0.04486 | A/G | A / A | 456 | yes |
| | DEL901.3 | 0.04486 | C/T | K / K | 404 | yes |
| | DEL901.4 | 0.04486 | A/G | H / H | 384 | yes |
| | DEL901.5 | 0.04486 | G/A | V / V | 334 | yes |
| | DEL901.6 | 0.04287 | G/A | L / L | 317 | yes |
| | DEL901.9 | 0.04486 | G/T | P / P | 262 | yes |
| | DEL901.10 | 0.04486 | C/G | P / P | 143 | no |
| | DEL901.11 | 0.04486 | G/A | D / D | 59 | yes |
| *HAGID1B* | **GID071.16** | 0.0027 | A/G | **L / L** | 216 | yes |
| | GID071.24 | 0.0329 | C/G | L / L | 45 | no |
| | GID071.34 | 0.01164 | G/A | - | Promoter | yes |
| *HAGID1D* | GID871.22 | 0.037 | T/C | - | 3' UTR | yes |
| *HALAZY1* | LAZ951.8 | 0.04538 | A/G | D / D | 121 | yes |

## 4.10 Results of HRM analyses

### 4.10.1 Dwarfism due to the DELPA mutation in *HaDELLA1*

In the case of sunflowers, a publication on the molecular causes of dwarfism has already been (Ramos *et al*., 2013), according to which a mutation in the *HaDELLA1* gene on linkage group 12 is responsible for this growth type. The mutation at position 143 in the DELLA domain of the gene represents a base exchange from T to C, which results in an AA exchange. This mutation turns the DELLA domain (Schwechheimer, 2008) into a no longer functional DELPA domain and thus leads to dwarfism in these sunflower lines (Ramos *et al*., 2013). Based on this SNP, it was possible to develop an HRM marker for the *HaDELLA1* gene (Suppl. Tab. A 2) and examine the dwarf and semi-dwarf accessions of the association panel for this mutation (Fig. 37). Ornamental sunflowers for which the presence (Pacino Cola) or absence (Big Smile) of the SNP is known were used as references for assigning the groups. The results of the HRM analysis clearly showed two curves. Group 1 (orange) included all accessions, which had the examined SNP in the *HaDELLA1* gene and consisted of the five accession Pacino cola, Sunspot, Solita, UGA-SAM1-118 and UGA-SAM1-119. Group 2 (green) shows the 27 accessions, which do not have the SNP. The group consisted of dwarfs and semi-dwarfs, whose dwarfism is therefore not based on the DELPA mutation, and some normal grown plants as reference (Suppl. Tab. A 26).



Melting curves

Normalised melting curves

Normalised melting peaks

Difference plot

**Figure 37:** HRM analyses of the T/C mutation in the DELLA domain in sunflowers. Group 1 (orange) Accessions with dwarfism based on the DELPA mutation; Group 2 (green) Accessions, whose dwarfism is not caused on the DELPA mutation.

The set of 25 ornamental sunflowers was also tested for the presence of the DELPA mutation (Fig. 38). It was found that six of the varieties examined were homozygous for the DELPA mutation and the two varieties Firecracker and Orange Hobbit were heterozygous for this mutation (Suppl. Tab. A 26).

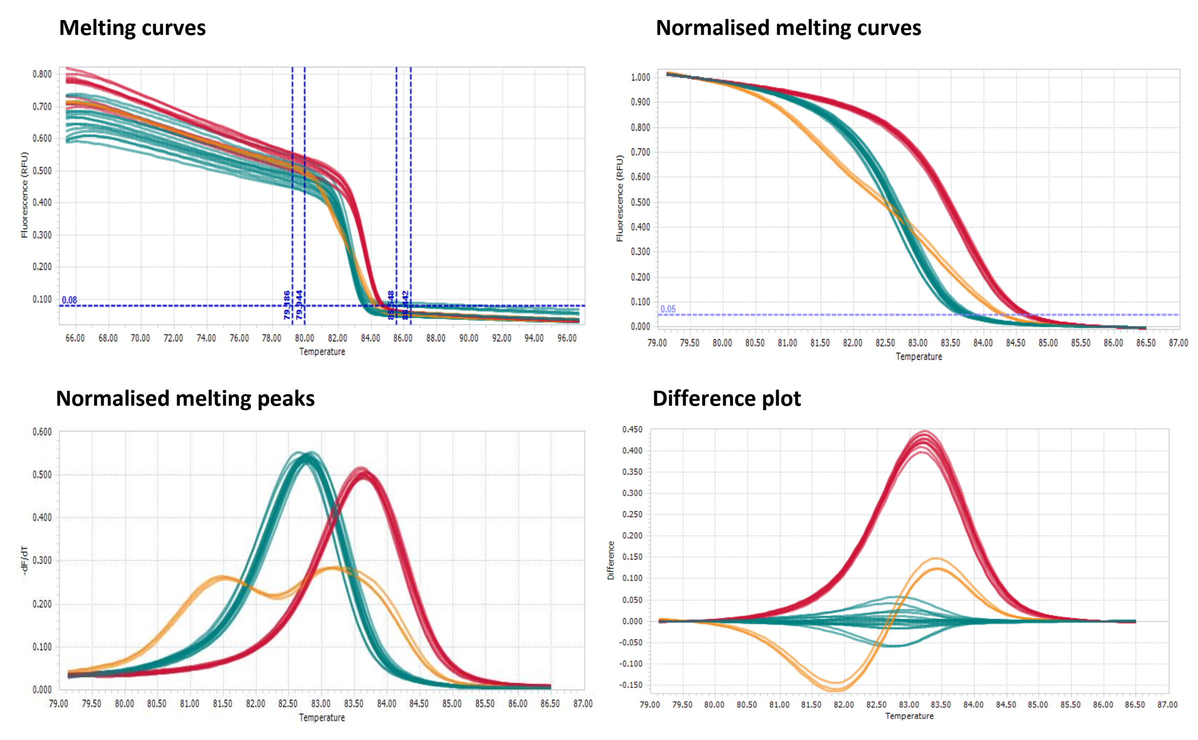
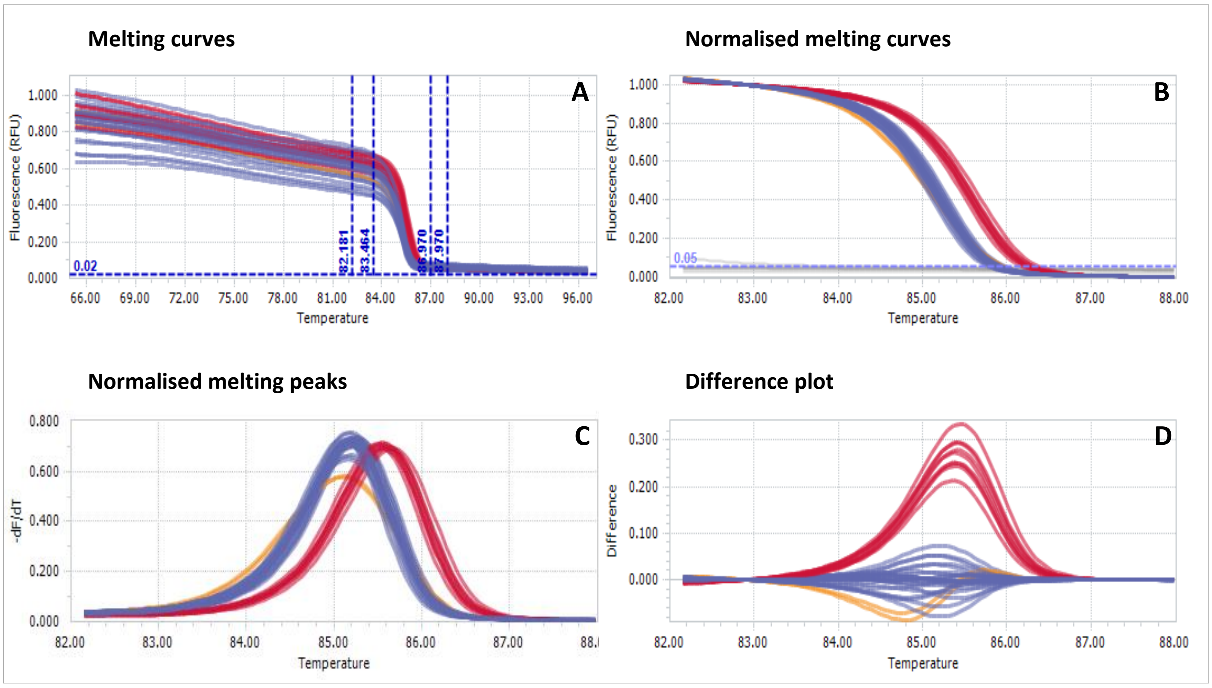


**Figure 38:** HRM analyses of the T/C mutation in the DELLA domain in ornamental sunflowers. Group 1 (red) Accessions, the dwarfism of which is due to the DELPA mutation; Group 2 (green) Accessions whose dwarfism is not based on the DELPA mutation; Group 3 (orange) Accessions that are heterozygous for the DELPA mutation.

In total, five accessions and eight ornamental sunflowers showed dwarfism due to the DELPA mutation. None of the semi-dwarfs or the accessions with normal growth showed the DELPA mutation. However, 22 accessions) and 17 ornamental sunflowers showed dwarfism, which resulted from a different mutation (Suppl. Tab. A 26).

### 4.10.2 HRM analyses of significant associated SNPs

For the seven identified significantly associated SNPs that met the conditions for an HRM analysis, HRM markers were developed and, in the first step, tested on a reference group of 12 accessions (Suppl. Tab. A 7). The results of the sequencing by LGC Genomics were used as the basis for the original calculations of the significance using the Fischer Exact Test. The HRM analysis made it possible to check the individual accessions again for the presence of the SNP to be examined, detecting the different groups (Fig. 39). After the developed markers were tested in all 64 genotypes of the small association panel, a few accessions of the respective reference group that were positive for the respective SNP were added, whereby the calculation of the p-value could be corrected and improved. The SNP SNE171.7 in the *HaSNEEZY2* gene results in a change of T/C, which represents a silent mutation. After screening the small association panel, the significance value improved from 0.01878 to 0.0035.


Melting curves

Normalised melting curves

Normalised melting peaks

Difference plot

**Figure 39:** Figure 30: HRM analysis for the SNP SNE171.7, significant for semi-dwarfs. Group 1 (blue) = accessions without SNP; Group2 (red) = accessions with SNP; Group 3 (orange) = heterozygous accessions.

The results showed three different groups for the SNP SNE171.7. The first group (blue) consists of eight accessions without this SNP. The second group (red) includes three accessions (UGA-SAM1-110, UGA-SAM1-273, GN 0778) whose dwarfism could be attributed to this SNP. Group three (orange) consists of a single accession No. 2, which appears to be heterozygous for the SNP SNE171.7, although this accession has a normal growth height.

The HRM marker for the SNP DEL801.17 in the *HaDELLA2* gene was developed and tested for the reference group of dwarf sunflowers. This SNP represents a T/C change at position 147, as a result of which an amino acid exchange of I>V takes place. Here, too, the p-value could be improved in the significance level after the 64 panel was analyzed (Tab. 13). Six accessions showed the SNP DEL801.17, two accessions (Big Smile, UGA-SAM1-119) were heterozygous for the SNP and four accessions, including the normal growth control accession No. 2, did not show the SNP (Fig. 40).

**Table 13:** Overview of the p-values of the four SNPs used for the HRM analyses; p-value I = based on sequencing data; p-value II = Corrected after SNP screening of the 64 genotypes using HRM

| SNP | P-VALUE I | P-VALUE II |
|---|---|---|
| **SNE171.7** | 0.01878 | 0.0035 |
| **DEL801.17** | 0.0397 | 0.0374 |
| **DEL091.8** | 0.0246 | 0.0162 |
| **DEL091.9** | 0.0068 | 0.0035 |

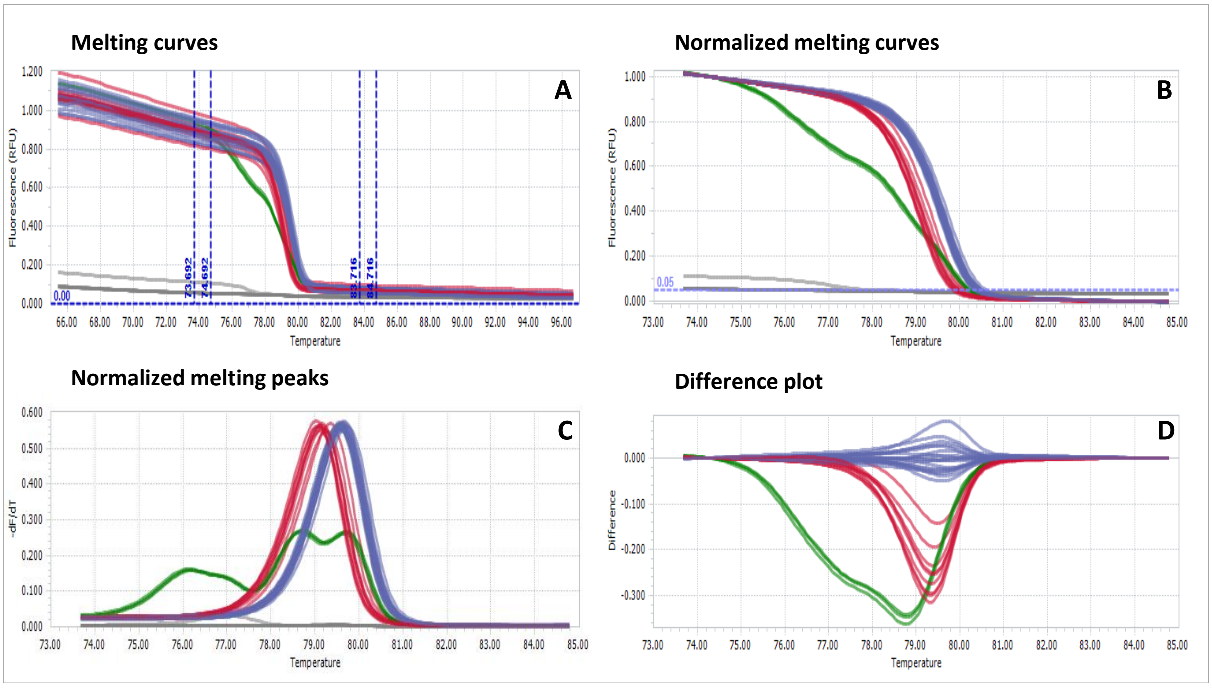


**Figure 40:** HRM analysis for the SNP DEL801.17, significantly associated with dwarfs. Group 1 (red) = accessions without SNP; Group2 (blue) = accessions with SNP; Group 3 (green) = heterozygous accessions.

HRM markers could also be developed and tested for the trait petiole angle by using significantly associated SNPs (Fig. 41, 42). The markers for the SNPs DEL091.8 and DEL091.9 were also selected for further work (Suppl. Tab. A 25), as these showed very good p values of 0.0246 and 0.0068 according to the HRM analysis in the small association panel. Both SNPs are present in the *HaDELLA-Like2* gene and represent a C/T and an A/C exchange. The C/T exchange of the SNP DEL091.8 at position 434 results in an amino acid exchange V>I, whereas the A/C exchange on Position 425 of the SNP DEL091.9 entails an amino acid exchange of D>E.

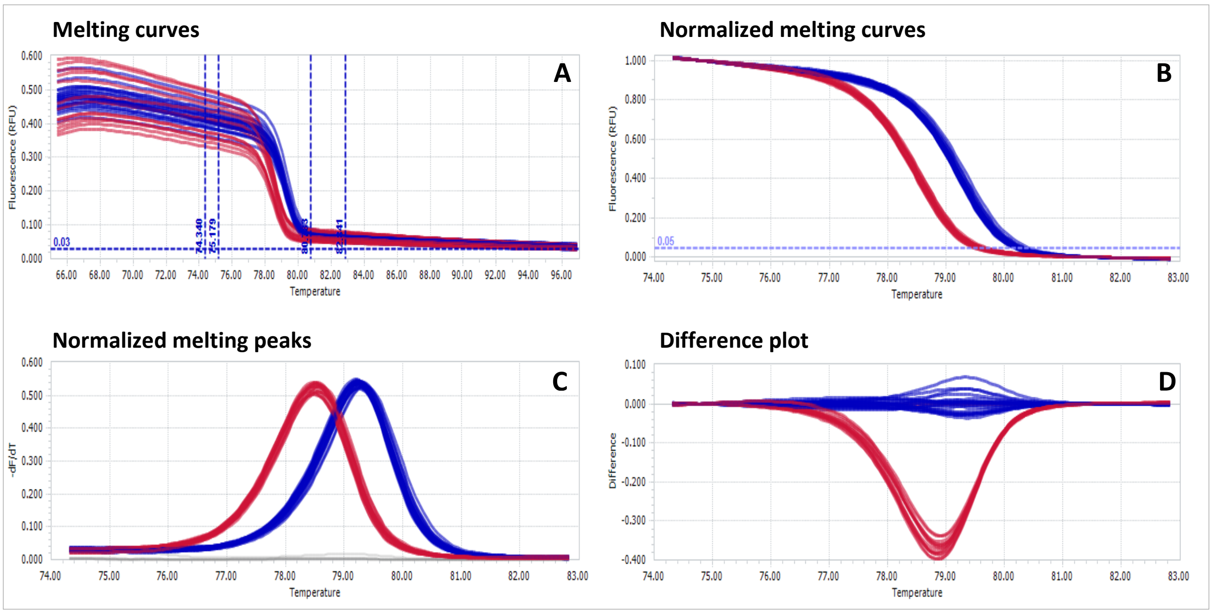


**Figure 41:** HRM analysis for the SNP DEL091.8, significantly associated with narrow petiole angles. Group 1 (blue) = accessions without SNP; Group2 (red) = accessions with SNP

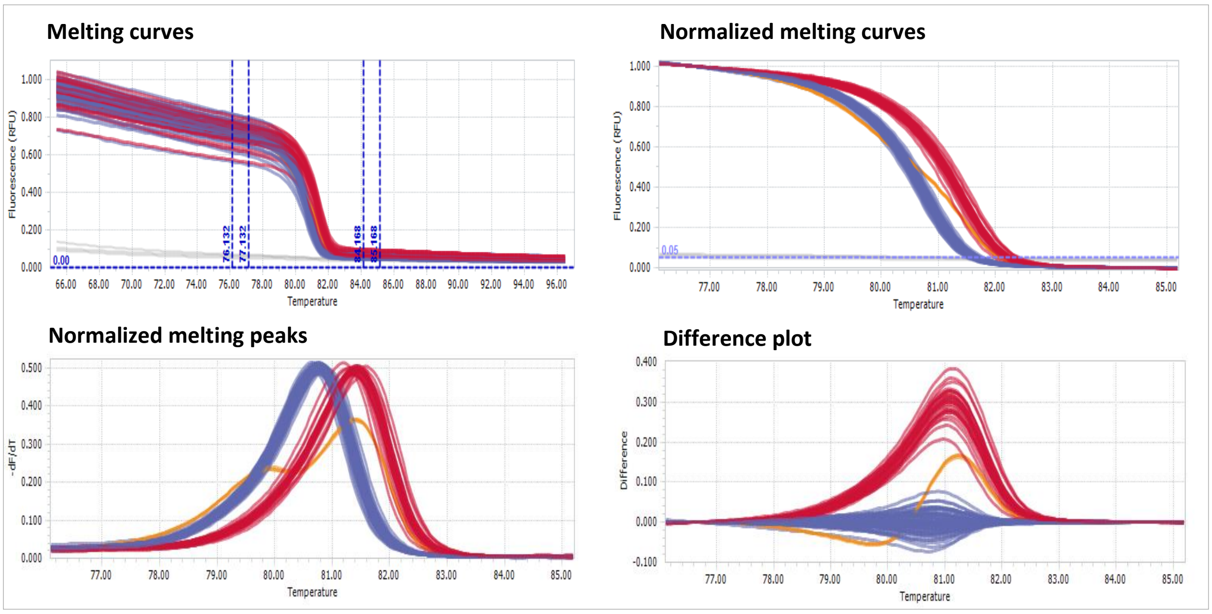


**Figure 42:** HRM analysis for the SNP DEL091.9, significantly associated with narrow petiole angles. Group 1 (blue) = accessions without SNP; Group2 (red) = accessions with SNP

The HRM analyses for the SNPs DEL091.8 and DEL091.9 were carried out with all narrow accessions of the small associations panel. A total of 20 accessions with narrow petiole angles and ten controls with normal petiole angles were examined. The results showed that the SNP DEL091.8 was present in ten accessions with narrow petiole angles. Twenty accessions did not show the SNP. A similar result was found for the SNP DEL091.9. Here, nine accessions with narrow petiole angles showed the SNP and one accession was heterozygous for the SNP DEL091.9. Twenty accessions lacked the SNP, ten of which were accessions with narrow petiole angles.

The analyses with the four confirmed HRM markers (SNE171.17, DEL801.17, DEL091.8 and DEL091.9) were extended to the large association panel and to the ornamental sunflower varieties (Suppl. Tab. A 25). The results of these analyses were summarised and the significance of the four examined SNPs was recalculated using the Fischer Exact Test (Tab. 14). The calculations showed that the investigated SNPs did not have a high level of significance and therefore seem unsuitable as markers for plant architecture.

**Table 14:** Calculation of significance of the four examined HRM markers using the Fischer Exact Test (p = 0.05)

| SNP | Semi-dwarfs | Others | p-value |
|---|---|---|---|
| **SNE171.7** | 38 | 435 | |
| with | 8 | 83 | 0.8315 |
| without | 30 | 352 | |
| **SNP** | **Dwarfs** | **Others** | **p-values** |
| **DEL801.17** | 20 | 453 | |
| with | 15 | 274 | 0.3455 |
| without | 5 | 179 | |

| SNP | Narrow Pet | Others | p-value |
|---|---|---|---|
| **DEL091.8** | 73 | 400 | |
| with | 22 | 121 | 1 |
| without | 51 | 279 | |
| **SNP** | **Narrow Pet** | **Others** | **p-value** |
| **DEL091.9** | 73 | 400 | |
| with | 22 | 121 | 1 |
| without | 51 | 279 | |

Furthermore, HRM primers were tested for the three SNPs GID131.30 (*HaGID1C*), GID071.16 (*HaGID1B*), DEL091.3 (*HaDELLA-Like2*) (Suppl. Fig. A 16-18). However, these turned out to be less suitable and were not used for further analyses.

## 4.11 Association studies based on KASP assay (LGC)

All SNPs, which had shown a significant association with traits of the plant architecture in the small association panel (Tab. 11-14), were analysed by KASP analysis in the large association panel (Suppl. Tab. A 27). For a total of 84 SNPs and InDels, 59 KASP assays could be developed successfully. Based on these data and the results of the population structure analysis for the summary of large and small association panels, association studies using the Generalized Linear Model (GLM) could be carried out successfully (Fig. 43). The results of the GLM analysis of the combined panel showed no significantly associated SNPs for “plant height”. However, six SNPs were identified for the trait “narrow petiole angle” that showed significant p-values after the analysis in the combined association panel (Tab. 15). Three of SNPs are located in the coding sequences of the genes *HaGID1B* and *HaDELLA1* but do not result in amino acid exchanges, thus, they represent silent mutations. Two of these SNPs, GID071.16 and DEL901.11, would be also suitable as HRM markers due to their base exchanges (A/G, G/A). The other three SNPs present in *HaDELLA-Like2* gene are located in the 3 'UTR and would be also suitable as HRM markers.

**Table 15:** Significantly associated SNPs for the “narrow petiole angle” identified with TASSEL 5 for data of KASP analysis in the combined association panel (n = 445), compared to data of Fischer Exact Test in the small association panel (n = 64)

| GENE | CHR | SNP | P (F.E. TEST) | P (KASP) | POSITION | ALLEL | AA CHANGE | POSITION |
|---|---|---|---|---|---|---|---|---|
| *HAGID1B* | 10 | GID071.16 | 0.0027 | 1.37E-05 | 21068624 | A/G | L/L | 216 |
| | | GID071.24 | 0.0329 | 9.22E-05 | 21068113 | C/G | L/L | 45 |
| *HADELLA1* | 12 | DEL901.11 | 0.04486 | 7.41E-04 | 25042890 | G/A | D/D | 59 |
| *HADELLA-LIKE2* | 8 | DEL091.27 | 0.0135 | 5.36E-05 | 8143914 | A/G | - | 3’ UTR |
| | | DEL091.48 | 0.00604 | 5.71E-05 | 8142473 | G/A | - | 3’ UTR |
| | | DEL091.47 | 0.00604 | 6.18E-05 | 8142506 | C/T | - | 3’ UTR |

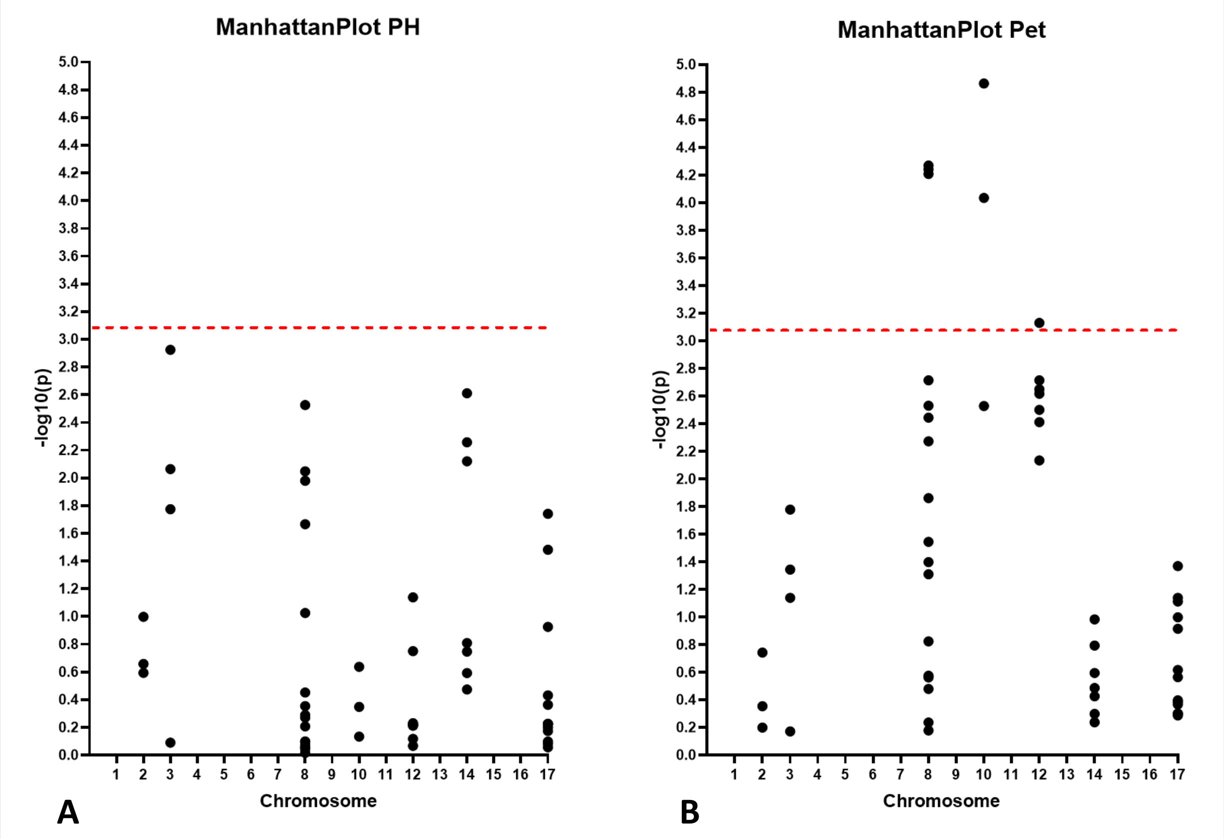


**Figure 43:** Results of GLM analysis for data of KASP analysis to detect significant SNPs in the combined association panel. A) Significantly associated SNPs for plant height; B) Significantly associated SNPs for petiole angle; Limit p = 0.000847 (-log10 = 3.07211659)

# 5 Discussion

## 5.1 Evaluation of at the plant architecture in field trials

In this doctoral study, an association panel of 448 sunflower accessions was used for the first broad phenotypic investigations regarding the plant architecture in 2017. Natural phenotypic variations in plant heights, branching and petiole angles were observed at two locations. The phenotyping at the different locations (Bandow, Germany, and Guadalajara, Spain) showed clear differences in the plant architecture between the genotypes of the association panel. The accessions proved to be phenotypically homogeneous. The selection of the 64 defined growth types was supported by the very good correlation values of the measurements of plant heights and petiole angles from Spain (Guadalajara) and the two locations in Germany (BAN, SCHL) in 2017 as well as in the following two years.

The measurements of plant heights over three environments showed high correlation values of $R^2 = 0.7457$ (BAN/ES) and $R^2 = 0.7442$ (BAN/SCHL) in 2018 as well as in 2019 with $R^2 = 0.7901$ (BAN/BAN). These results confirmed the selection of the 64 genotypes referred to as the small accession panel and ensured solid phenotypic data. For the small association panel, plant heights between 40 cm and 150 cm were measured, i.e. all growth types that Schuster and Marquardt (2003) described were included in the panel, but the classification of the height values had to be slightly adjusted to dwarfs (up to 65 cm), semi-dwarfs (66 cm – 107 cm) and normal (higher than 107 cm). This allowed better processing of the mean values that resulted from the measurements. Since the plant height has a strong influence on yield, plant density and lodging, it is considered to be one of the most important agronomic characteristics (Zhang *et al.,* 2019). In this study, the phenotypic data of the plant height at different locations showed a normal distribution (Suppl. Fig. A1, A2), suggesting that this trait represents a quantitative trait. It also indicated that plant height was mainly controlled by genetics (Zhang *et al.,* 2019). With regard to the plant heights of the 53 examined F1 hybrids, measured values ranged between 107 cm - 166 cm, which means that due to genetics and heterosis effects all test hybrids showed a normal growth type. The 22 F1-hybrids (sunflower accession x commercial R-Line) varied between 109 cm - 166 cm and the 31 F1-hybrids (LC1093A x sunflower accession) varied between 107 cm - 152 cm. With regard to the crosses of the accessions with reduced growth height, only normal growth heights could be determined. Crosses using the four dwarf accessions Big Smile, Sunspot, Pacino Cola and UGA-SAM1-118 showed plant heights between 112 cm - 128 cm. The F1-hybrids of eight semi-dwarf accessions crossed with the commercial R-Line or the LC1093A-CMS-Line showed values between 109 cm - 150 cm. It appeared that crosses with dwarfs/semi-dwarfs with the maternal line LC1093A resulted in a reduced height, but this was still in the lower range of normal sunflowers due to the heterosis effect.

The variability between the values of the upper level petiole angles in the different locations was somewhat higher. While the correlation value for the petiole angles between Rostock and Spain in 2017 was $R^2 = 0.7991$, the following year showed only values of $R^2 = 0.6078$ (BAN/ES) and $R^2 = 0.6025$ (BAN/SCHL). In total figures, this means that in 2017, petiole angles between 16° - 73° (ES) and 24° - 72° (BAN), and in the second year, petiole angles between 15° - 71° (ES), 14° - 59° (SCHL) and 24° - 52° (BAN) were measured at the different locations. Also, the examined F1 test-hybrids showed stable and reproducible values for the petiole angles. Values between 32° - 45° could be measured for the 31 F1-hybrids (LC1093A x sunflower accession) and values between 34° - 48° were measured for the 22 F1-hybrids (sunflower accession x commercial R-Line), which means, just only petiole angles classified as "narrow" or "normal" were found for the F1 hybrids. Although, parents like Sunspot or UGA-SAM1-010 with wide angles were used in the crosses, this trait did not seem to prevail over "narrow" or "normal". Since it is assumed that the second parent (commercial R-Line / LC1093A-CMS-Line) has a normal plant height and normal petiole angles, it seems that in the crosses involving the accessions Sunspot, Solita, UGA-SAM1-010 or UGA-SAM1-276 the narrow petiole angle is dominantly inherited.

However, the different correlation values may be due to the very different weather conditions at the locations or inaccuracies in manual measurement. The weather conditions in 2017 showed a very rainy summer for the locations in Germany. While the following summer of 2018 was very dry and hot. In contrast to the test fields in Spain, no automatic irrigation was installed in Germany, so the plants had to be watered manually every day. Since these dry conditions were also present during the germination and growth phase, the poor water supply could have had an impact on the plant height and the formation of the petiole angles, as a water deficit can affect plant development and growth (Robbins & Dinneny, 2018).

Not only the irrigation, but also the availability of nutrients at the different locations, could have affected the plant development. According to a recent study on winter wheat, yield and thus plant development in particular is regulated by the interaction of genotype × environment × management (G × E × M), whereby the agronomically optimal plant density (AOPD) depends on the yield environment (YE – low yield environment or high yield environment) (Bastos *et al.*, 2020). Therefore, the AOPD in sunflowers could change across the YE, with the plants having a greater need to reach the maximum yield at the low YE, which could impact the branching angles of the sunflower accessions. The winter wheat study showed that different yields were achieved under varying YEs. These were caused by the different tillering potential (TP) of the different genotypes. Compensation between heads per plant and grains per head took place among varying YEs. This could be explained by the fact that when the number of plants was below the carrying capacity of the available resources, the number of branches was increased to compensate for the deficit of plants for the AOPD (Bastos *et al.*, 2020). Other yield components such as kernel count and weight were modified with changes in plant density. Thus, increases in plant density typically increased heads and core count per unit area and decrease core weight and cores per head (Bastos *et al.*, 2020). The extent of these changes could also depend on the availability of resources at each YE for the performed sunflower field trials and thus have an impact on the growth height and the branching and petiole angle.

In sunflower, many successful association studies have been carried out in recent years and phenotypic and genotypic characteristics of different accessions have been investigated. New markers with significant associations to certain traits have been discovered (Dimitrijevic & Horn, 2018). A study was carried out on flowering time, in which the various approaches of mapping, coupling and association studies were combined. It was found, that a total of 11 regions in 10 linkage groups were found to be associated with flowering time (Cadic *et al.,* 2013). The association mapping carried out by Nambeesan *et al.* (2015) have shown that there is independent control of apical and basal branching (Nambeesan *et al.*, 2015). In 2020, Reinert and co-workers used the UGA-SAM population comprising 288 sunflower accessions (Mandel *et al.,* 2013; Nambeesan *et al.*, 2015) to investigate the phenotypic correlation between seed and floret traits (Reinert *et al.*, 2020). Association studies with well-considered and well-suited association panels have shown in recent years that this method is very suitable for investigations in sunflowers and that associations of markers with phenotypic characteristics can be identified. The advantages of association panels over working with biparental mapping populations are clear. Higher recombination rates allow for better resolution, different causes of a trait can be identified, and working with an association panel is less time-consuming as there is no need to establish a population (Dimitrijevic & Horn, 2018).

### 5.1.1 Association studies in different crops

The use of association panels with a high genetic diversity to study phenotypic traits is a widespread and successful method for many different plant species, which can be demonstrated by previous and current works. In 2016, Liu and co-workers published a study on the investigation and characterization of the branching angle in oilseed rape. In this study, a natural population of 143 rapeseed (*Brassica napus*) accessions was grown in three settings and examined for branching angle features to characterize their phenotypic patterns and genotypic variation. A significant phenotypic variation of the branch angles from 20 ° - 70 ° could be observed. Through association studies, several novel loci and candidate genes like e.g. *BnaA.Lazy1* and *BnaC.Lazy1* for the expression of the branching angles in rapeseed were discovered (Liu *et al.,* 2016). In maize (*Zea mays*), investigations of the plant height, involving a genome-wide association analysis (GWAS), were performed (Zhang *et al.*, 2019). Also in maize, the evaluation of adaptability and various yield traits such as thousand grain weight, yield, lodging and plant height were carried out using different association panels (Akram *et al*., 2020). A study in rice (*Oryza sativa*) by Eizenga *et al.* (2018) examined over 30 characteristics, which included both agronomic (flowering time, plant height, presence of awns) and panicle architecture, as well as seed and disease characteristics. The Rice Diversity Panel 1 (RDP1), which consists of 256 recombinant inbred lines, was used for this. It was found that a total of 11 regions across 10 linkage groups were associated with flowering time (Eizenga *et al.,* 2018). Interestingly, an association panel for peanut (*Arachis hypogaea*) was recently established (Zhang *et al*., 2018). The panel comprised 268 lines with extensive phenotypic and genetic variations, making it suitable for association analysis. Over three years, the most important agronomic and phenotypic characteristics such as leaf length, pod length and number of pods per plant, but also protein and oil content, were investigated. The association analysis revealed markers that are significantly associated with oil, protein, oleic acid and linoleic acid and identified alleles with positive and negative effects. These results showed that the association panel was suitable for further work (Zhang *et al.,* 2018). Recently, a study on the development of an association panel for chickpea (*Cicer arietinum*) to adapt legumes to European agro-ecosystems was reported (Rocchetti *et al.,* 2020). To create the panel, in a first step 1931 chickpea accessions were phenotypically assessed in a field trial. Based on the phenotypic data, an association panel of 480 genotypes could be assembled with the aim of analysing the genetic architecture of important adaptive and quality characteristics in order to accelerate breeding in chickpea. To develop an association panel for chickpea, genetic resources were mainly collected in Europe and the Mediterranean region (Rocchetti *et al.,* 2020).

However, working with association panels is not without problems. A major disadvantage is that rare alleles are difficult to associate with traits in association mapping. An example of this can be found in the work by Cadic *et al.* (2013). A major QTL for LG14 in sunflower, which had been previously identified by a mapping approach (Poormohammad Kiani *et al*., 2009), was not identified by the association study. In addition, if the structure of the panel is correlated with polymorphism at a locus, this can result in ‘‘false positive’’ association (Cadic *et al.*, 2013; Dimitrijevic & Horn, 2018). Nevertheless, the results of the studies described have shown the unlimited possibilities of using association panels in plant breeding. Above all, plant accessions can nowadays be molecularly characterizing on a large scale and thus allowing a targeted improvement of crop plants through adapted breeding programs.

## 5.2 Economic increase in yield through optimised plant architecture

Breeding for a more compact plant architecture could probably lead to increases in yield of sunflowers that are comparable to those obtained in cereals. The results of the performance tests done in Germany and Romania do not allow any general conclusion as to whether the yield can be increased with increasing plant density in all F1 test hybrids. Overall, it seems that the higher plant density only lead to an increase in the yield/oil content and thus to an increase in the oil yield with a few accessions (i.g. LC-1093A x UGA-SAM1-186, LC-1093A x UGA-SAM1-055, LC-1093A x UGA-SAM1-012 in RO; ES Bella, ES Columbella in DE (Suppl. Tab. A 9-11). However, sunflower breeding has a yet untapped potential, as it has been shown that greatly increased plant densities (higher than regarded as optimal – 5 plants/m$^2$) in sunflower can lead to increased yields (Lopéz Pereira *et al.*, 2004; Lopèz Pereira & Hall, 2012). When comparing the F1 hybrids and reference varieties in the different locations with different plant densities, it is noticeable that the reference variety ES Bella with narrow petiole angles and normal height had the highest yield with a plant density of 20 cm. This result could be observed both at the location in Germany and in Romania. Even though the yields of this reference variety were in the upper range, some of the experimental hybrids e.g. LC-1093A x UGA-SAM1-207 (20 cm), LC-1093A x UGA-SAM1-041 (25 cm), LC-1093A x UGA-SAM1-186 (30 cm) in Germany and LC-1093A x UGA-SAM1-041 (20 cm), LC-1093A x UGA-SAM1-136 (25 cm), UGA-SAM1-082 x R-Line (25 cm) in Romania performed better than the reference varieties.

There was a total of five hybrid combinations that showed the highest yield at lower plant density at both locations: LC-1093A x UGA-SAM1-218, LC-1093A x UGA-SAM1-198, LC-1093A x UGA-SAM1-121, LC-1093A x UGA-SAM1-100 and LC-1093A x Big Smile. The growth type of these F1 hybrids shows heights between 112 cm - 138 cm and narrow to lowest levels of normal petiole angles with values between 32°-42° (Suppl. Fig. A 5-6). The highest oil yield of the examined hybrids was achieved by F1 hybrid LC-1093A x UGA-SAM1-276 with 2016.23 l/ha with a plant density of 30 cm (Tab. 11). If the oil yields of these hybrids are considered for all plant densities at both locations, it can be seen that the values at the location in Romania are very constant over the different plant densities with 1107.44 l/ha (20 cm), 1001.24 l/ha (25 cm) and 1049.21 l/ha (30 cm). Compared to this, large differences between the individual plant densities were observed at the location in Germany, since oil yields of 975.47 l/ha (20 cm), 1625.06 l/ha (25 cm) and 2016.23 l/ha (30 cm) were determined. These differences can be due to various factors such as different irrigation, dry climate or insufficient fertilization.

The F1 hybrid LC-1093A x UGA-SAM1-041 seems to be particularly interesting because it was able to achieve the highest yield at both locations with one plant density each, which is also fairly constant (Tab. 10). With a plant density of 25 cm, this hybrid could achieve an oil yield of 1676.68 l/ha at the location in Germany. This value is relatively comparable to the one measured at the location in

Romania. With a plant density of 20 cm, this hybrid achieved an oil yield of 1455.40 l/ha, which is lower than the values for the normally used plant density. From the growth type F1 hybrid LC-1093A x UGA-SAM1-041 showed a normal plant height from 115 cm 130 cm and a narrow petiole angle with average of 37 ° in the upper level.

At the location in Romania, the hybrid UGA-SAM1-082 x R-Line showed the highest oil yield with a value of 1632.40 l/ha for the plant density of 25 cm. It is interesting that an enormous increase in yield was observed with changing the plant density from 20 cm to 25 cm. The raw data of these hybrids showed a yield of 0.22 $kg/m^2$ with a plant density of 20 cm in Romania, since 12 $m^2$ were harvested, the yield was 2.7 kg with 66 harvested plants. With a planting density of 25 cm, the yield was 4.6 kg with only 60 plants harvested. This could be an indication that this hybrid reacts very sensitive to changes in plant density. This was also supported by values measured in in Germany for this hybrid, since the yield increased from 1.7 kg (62 plants harvested) to 3.1 kg (54 plants harvested) with lowering the plant density by increasing the distance of the plants from 20 cm to 25 cm.

Correlation analyses of the performance test results have shown that there are different relationships between the individual variables. In general, it can be said that the yield increased with an increasing petiole angle. The height of the plants also had an impact on the yield. The analysis showed that the yield increased with a lower plant height.

Overall, the results of the performance tests showed very interesting values. It can be said, that sunflower hybrids with potential for cultivation with increased plant density for higher yield have been found. Even though narrower petiole angles make the handling of the sunflower plants on the field easier, the petiole angle on its own might not be the only reason for higher yields in the F1-hybrids that showed higher yields with higher plant densities. In the USA, however, a higher plant density is already standard in maize (Duvick & Cassman, 1999) and the fact that higher plant densities in sunflowers have already led to increasing yields (Hall *et al.*, 2010), shows interesting possibilities. In addition, the oil from the sunflower is superior to other vegetable oils due to the larger proportion of unsaturated fatty acids and the content of bioactive compounds like tocopherols and phytosterols (Debaeke & Izquierdo, 2021).

The study on winter wheat by Bastos *et. al*. (2020) showed that wheat plasticity and achievable yields do not depend on just one factor but are regulated by the interplay of genotype x environment x management and the agronomically optimal plant density depends on the yield environment (YE) (high YE, medium YE, low YE) (Bastos *et al.*, 2020). It is possible that in the case of sunflower, a combination of the various factors also has an impact on the yields that can be achieved and that the yield cannot be increased solely by a combination of increasing plant density and reducing the petiole angle. Generally, increasing plant density in winter wheat increases the number of heads and kernels per unit area and decreases the weight of kernels and kernels per head. However, the extent of these changes could depend on the availability of resources at each YE, so the variation of yield components at different YE should be investigated (Bastos *et al.*, 2020). The situation could be similar in sunflower, which means that the different YEs should also be taken into account here and the effects on the possible yield should be examined. A significant increase in yield could make sunflower more competitive again and bring in higher profits.

## 5.3 Segregation analyses to detect the mode of inheritance

Since there is little chance of finding superior recombinants in advanced generations, the F2 generation is critical to the success of a breeding program (Vankudoth *et al.*, 2021). Consequently, segregation analyses were carried out on five cross combinations in order to investigate the mode of inheritance and to detect the number of genes involved. For this purpose, the F2 populations, the F1 hybrids and their parental generations were evaluated and compared in terms of plant height and petiole angle. The F2 populations differed greatly in the number of seeds germinated. A total of 40 seeds were planted per population, except for the cross combination CM104 x R line, in which a total of 80 seeds were sown due to the large number of seeds present. Unfortunately, the seeds of the F2 populations showed a reduced ability to germinate, which could not be compensated even by growing plants in the greenhouse fill up losses in the field. As result, the five F2 populations showed individual numbers of 17 plants, 29 plants, 30 plants, 31 plants and 54 plants, respectively, which hampers the interpretation of the segregation analyses considerably (Tab. 9).

In summary, however, it can be said that the results of the $X^2$ test only showed a positive result for three segregation ratios in two populations. For the F2 population derived from UGA-SAM1-185 x R line, the expected segregation for one gene of 1:3 for the plant height was observed. The population consisted of 31 individuals: 7 semi-dwarfs and 24 with normal growth types. Looking at the parental generation, it became clear that this was a semi-dwarf x normal crossing, whereby the expected values for the F2 generation were met with an error probability of p = 0.75573562. The trait semi-dwarf in this cross combination seems to be recessively inherited by one gene.

The second population that showed the expected segregation results was the ROMSUN V3355 X R-line cross. This F2 population showed expected ratios for one gene, respectively, for both traits plant height and petiolar angle. For the plant height, this population segregated into 4 dwarfs and 13 half-dwarfs and thus a ratio of 1:3 was observed. The petioles, on the other hand, showed a segregation ratio of

1:2:1 with 2 narrow angles, 13 normal angles and 2 plants with wide petioles. The error probability of the two calculations was p = 0.09233307 and p = 0.88863786, respectively, and was therefore significant (α = 0.05). However, the population size of just 17 individuals could be critical as it may be too small.

Unfortunately, no significant segregation ratios could be observed in this thesis for the three other investigated F2 populations. It should be mentioned at this point, however, that the F2 populations of the cross combination No. 2 X UGA-SAM1-110 and CMH 101 X ROMSUN V3355 showed no obvious segregation at all for the trait plant height. All plants showed a normal growth type, although one parent had shown a semi-dwarf growth type (Tab. 8). The five F2 populations of the sunflower hybrid showed to some degree segregation for the two traits investigated. To further verify this, the segregation analyses would have to be repeated with larger populations in different locations and years. The results of the field studies showed that the six sunflower accessions used in the crosses with the R-line showed the expected traits of plant height and petiole angle in the form described before. Since no measurement data were available, it is assumed that the second parent, who was provided by Strube Research for three of the crosses described, had a normal growth type with normal petiole angles. The individuals of the F1 generation showed the expected uniformity with normal plant height and normal petiole angles (Tab. 8). Thus, in two cross combinations, the reduced plant height was inherited recessively, which would be difficult to use in hybrid breeding. The petiole angle showed an intermediate inheritance.

## 5.4 Genes of the GA-signaling pathway and branch angles

In this study, the genes of the GA-signaling pathway in sunflowers were examined. A total of 18 genes from four different gene families are involved in the sunflower GA-signaling pathway (Ewald *et al.,* 2016, Fig. 8). The gene sequences of the three genes *HaGID1C*, *HaGID1D* and *HaDELLA-Like2* were only partially known and could be completed during this work (Suppl. Fig. A 15). This set of genes, together with the four genes *HaTAC1*/*HaTAC2* and *HaLAZY1*/*HaLAZY2*, could then be used in a candidate gene approach for association studies using next generation sequencing (Targeted Amplicon Sequencing). Overall, this enabled the identification of gene variants in 20 of the 22 genes analysed. With the exception of the two genes, *HaGID1A* and *HaSNE1*, all investigated genes showed a large number of SNPs, insertions or deletions in the examined 64 genotypes of the small association panel in comparison to the reference genome of HanXRQ (Tab. 10). However, since the two genes mentioned do not have a single mutation, it is assumed that these are highly conserved in the sunflower genome. The number of mutations in the rest of the genes examined varied greatly (Tab. 10). It is important to note that the coding sequence as well as 2000 bp upstream and 500 bp downstream were analysed.

The gene, which showed the lowest number of mutations, was *HaDELLA-Like1* with only one SNP in the 5'-area and two InDels, a deletion in the 5'-area and an insertion in the 3'-area of the gene. In contrast, the *HaDELLA-Like2* gene represented the gene with the most detected mutations within the 64 genotypes. A total of 41 SNPs and 11 InDels could be determined here, with 20 SNPs and three insertions in the coding sequence, which could have effects on the structure and functionality of the genes. The comparison of the results for all genes showed that most of the SNPs are located in the coding region of the genes and most of the InDels in the 5'-region of the genes. If the observed SNPs in the coding sequences lead to missense or nonsense mutations, this will result in a change in the function of the individual genes and thus to a change in the GA-signaling pathway in the affected plants. These effects were only investigated more closely for the 59 SNPs significantly associated with features of the plant architecture.

### 5.4.1 Effects of the significant SNPs on the genes of the GA-signaling pathway

The phenotypes of the mutants of the GA-signaling pathway and GA biosynthesis play an important role in plant breeding, since GA is involved in many developmental processes - but especially in shoot growth (Kurepin & Pharis, 2014). The association studies in the small association panel (64 accessions) applying TASSEL 5.0 identified SNPs significantly associated with plant height or petiole angle, which represent potential markers for the plant architecture. SNPs represent single base changes with a common alternative of four possible nucleotides at the position, which occurs when a single nucleotide differs in a common sequence of different individuals (Vignal *et al.* 2002; Semagn *et al.*, 2014). From the data of the years 2017 - 2019 seven SNPs were found significantly associated with the petiole angle, for the plant height in total four significant SNPs were identified in the years 2017 and 2019. However, association studies using TASSEL 5.0 are very stringent because the Bonferroni correction is applied. Especially in a small association panel this might not detect all relevant SNPs. Therefore, association studies in the small association panel over all three years of field trials was repeated using the Fisher Exact Test ($p < 0.05$). This resulted in 59 significant SNPs in 11 candidate genes in the small association panel of 64 sunflower accessions, which were significantly associated with the plant height or the formation of the petiole angles. In total, 17 SNPs were identified for the dwarf phenotype, 12 SNPs for the semi-dwarf phenotype and 30 SNPs for the narrow petiole angles. Four of these SNPs corresponded to the SNPs previously identified by TASSEL 5 in the genes *HaDELLA-Like2* and *HaGID1B* (DEL091.30, DEL091.33, GID071.16, GID071.24). Of the 59 SNPs identified as significantly associated, only nine SNPs in six genes showed direct effects on the amino acid sequence by resulting in missense mutations (Suppl. Tab. A 16).

According to Miyata *et al.* (1979) the frequency of amino acid substitutions in relation to the randomly expected frequency decreases linearly with the increase in the physicochemical differences between amino acid pairs involved in the substitution. In several studies (Epstein, 1967; Grantham, 1974; Miyata *et al.,* 1979) the various properties such as size and polarity of the amino acids were evaluated. The resulting coefficient makes it possible to evaluate the strength of an amino acid substitution. A small coefficient indicates a conservative exchange, a large coefficient indicates a non-conservative exchange. However, 25 of the identified SNPs resulted in silent mutations. However, this can still be relevant if these SNPs are linked with deletions or insertions in the gene, because InDels were not included in the association studies and thereby would not be detected.

The SNP SNE171.5 in the *HaSNE2* gene can be assessed as a non-conservative amino acid exchange (Suppl. Tab. A 16), which could result in possible effects on protein function. In the case of this gene, additional deletions were observed in the 5'-UTR, which could have an influence on the gene expression. It is very noticeable that SNE171.5 was significantly associated with the semi-dwarf growth type, occured in the small association panel only in semi-dwarf sunflowers. These accessions are CM104, UGA-SAM1-100, UGA-SAM1-110, and UGA-SAM1-273. A closer look at the sequencing results showed that these four accessions each had all four SNPs identified as significant in the coding area, as well as two deletions in the 5'-UTR. The sequence of UGA-SAM-110 was also confirmed by Sanger sequencing (data not shown). Thus, the function of the F-box protein, for which the *HaSNEEZY2* gene codes, could be restricted and actually lead to semi-dwarf growth. Ariizumi *et al.* (2011) have already described that the *SLY1* homolog *SNEEZY* (*SNE*) can functionally replace the F-box protein *SLY1* in *Arabidopsis*. The mutants *sne-t2* and *sne-t3* initially showed no changed phenotype, but demonstrated an increased ABA sensitivity during seed germination (Ariizumi & Steber, 2011). A clearly recognizable reduction in the plant height could be observed in *Arabidopsis* double mutants, which showed an insertion mutation in the upstream region of the *SNEEZY* gene and in the gene sequence of *SLEEPY1*. These results thus indicate that *SNEEZY* normally acts as a redundant positive regulator of GA-signal transmission (Ariizumi & Steber, 2011). To assess this fact in the sunflower, further studies and gene expression analyses would have to be carried out. In sunflower, three *HaSNEEZY* genes and six *HaSLY1* genes were identified in the HanXRQ genome assembly (Ewald, 2016). Nothing is known about the interaction between the genes of these two gene families in sunflower.

Further studies showed that SNPs in other components of the GA-signaling pathway can also have an effect on the phenotype. Investigations of peach dwarf varieties showed that the interaction between the GID1c receptor and the DELLA1 protein was no longer possible due to a non-synonymous SNP in the *GID1c* sequence, which resulted in a GA-insensitive dwarf phenotype present in 30 peach varieties (Cheng *et al.*, 2019). This base exchange of C > T in the coding sequence of *GID1c* gene leads to a non-conservative amino acid exchange at position 191 and represents a change from serine to phenylalanine (S191F), which is located in the highly conserved motif GDSSG (Cheng *et al.*, 2019). In this doctoral study, the SNP GID131.30 identified in the *HaGID1C* gene is located in close proximity to the conserved motif and results in an amino acid exchange from lysine to arginine (K186R). An interaction between the GID1C receptor and the DELLA protein may also be influenced, needs to be investigated

The remaining significant SNPs were either silent mutations or were located in the 5‘- or 3‘-region of the genes, so there was no direct impact on the coding sequence of the genes, but there could be differences in the expression level. However, these were not investigated within this doctoral thesis. The four SNPs identified by TASSEL using data of the small association panel with 64 genotypes in Germany in 2017 (DEL091.30, DEL091.33 for petiole angle; GID071.16, GID071.24 for plant height) also represent only silent mutations. During the investigation of the significant associations, only the SNPs and not the InDels were analysed. It is therefore possible that the SNPs that cause a silent mutation have their meaning due to a link to another mutation (insertion/deletion) in the immediate vicinity or are so close to another gene within a QTL that is actually responsible for the investigated phenotype. This phenomenon is called linkage disequilibrium, the non-random association of alleles at different loci in a given population (Slatkin, 2008). On the other hand, recurring silent mutations have been described that can have an effect on phenotypes. It is assumed that the RNA-mediated regulation of gene expression might be changed by silent mutations (Lupino *et al.,* 2018).

There is a new study on rice (*Oryza sativa*), in which genotypes should be identified which have higher levels of nutrients such as zinc and iron (Babu *et al.,* 2020). Genome-wide association studies were carried out on 40 different genotypes. A total of 188 SNPs ($P < 0.01$) could be identified, which were associated with six traits (ZPR: zinc in polished rice; ZBR: zin in brown rice; IPR: iron content in polished rice; SPY: single plant yield; PL: panicle length and PH: plant height). The focus was on the characteristics ZPR and SPY. Two of the identified genes also showed silent mutations that had an influence on the trait. In *LOC_Os07g48050*, which codes for a peroxidase, an SNP was discovered, which represents an exchange of T > C. This silent mutation (TGT> TGC) explained 19% of the phenotypic variance. Another candidate gene *LOC_Os07g47950*, explained 23% of the phenotypic variance with the presence of three SNPs - G > A (GCG> ACG), a missense mutation that converts alanine to threonine; G > A (GCG> GCA), a silent mutation and C > T (CTC> TTC), a missense mutation that converts leucine to phenylalanine (Babu *et al.,* 2020). As the available studies show, it is quite possible that silent mutations in combination with other mutations or other factors can have an influence on certain plant characteristics. Accordingly, all SNPs identified as significant associated with plant height and petiole angle in this doctoral work should be further investigated to reveal the underlying mechanisms that influence plant architecture, independent of the fact that they might only lead to silent mutations. In Addition, the annotation of the genes should be verified by analysing the corresponding cDNA sequences.

## 5.5 Structure of *TAC1* and *LAZY1* genes and the effect of significant SNPs

The genes *TAC1* and *LAZY1* belong to the IGT family and can be characterized using four highly conserved domains (Hollender *et al.*, 2020). The *TAC1* homologous genes *HaTAC1* and *HaTAC2* investigated in this work have all four characteristic domains (Fig. 26). Domain II is of particular importance, as it represents the IGT motif that gives the gene family its name (Dardick *et al.,* 2013). Since the highly conserved domains were found in both *TAC1* homologs on chromosome 4 and chromosome 16, it can be assumed that there are at least two *TAC1* genes present in the sunflower genome. In rice, several *TAC* genes have been described that control the expression of the tiller angle in rice. However, these represent a number of genes belonging to different gene families, but they were all named *Tiller Angle Control (TAC)* because they showed an influence on the tiller angle. However, these additional *TAC* genes do not belong to the IGT family. Dong *et al*. (2016) identified *Tiller Angle Control 3* (*TAC3*), which encodes a conserved hypothetical protein and which is mainly expressed in the tiller base. Together with *D2* and *TAC1*, *TAC3* regulates the tiller angle in various rice varieties (Gao *et al.*, 2021). *Tiller Angle Control 4* (*TAC4*) has also recently been identified (Li *et al.,* 2020). This gene encodes a highly conserved core protein, which increases the indole acetic acid content and influences the auxin distribution and thus regulates the gravitropism of rice varieties. The loss of function of *TAC4* leads to a significant increase in the tiller angle (Li *et al.*, 2020). The occurrence of more than one *TAC* gene belonging to the IGT family seems to be an exception. In general, *TAC1* only occurs highly conserved as a single copy gene in all plant species investigated so far (Hollender *et al.,* 2020). A second *TAC* gene as in the sunflower is therefore a special feature.

In contrast to *TAC1*, *LAZY1* has an additional, fifth, highly conserved domain at the C-terminal end of the protein. This domain includes an ethylene-responsive amphiphilic repression (EAR) transcriptional repressor motif, which appears to be important for the protein function in many species (Dardick *et al*., 2013; Hollender *et al.,* 2020). It is also known that many species have multiple *LAZY* genes (Hollender *et al.,* 2020). It is therefore quite possible that several *LAZY* genes might be also present in the sunflower that could have an influence on the plant architecture.

Only the association studies in the small association panel using the Fisher Exact test ($p < 0.05$) detected significant associated SNPs for petiole angle and dwarfism in *HaLAZY1* and *HaLAZY2*. No significant associations could be found for the *HaTAC1* and *HaTAC2* genes. *HaLAZY1* showed three significantly associate SNPs, LAZ951.3, LAZ951.8 and LAZ951.11, of which only LAZ951.11 had a direct effect on the amino acid sequence and thus possibly an effect on the protein function (Suppl. Tab. A 16). This SNP, which is significant for dwarfism, represents an exchange from A > G, which causes an amino acid exchange from valine to alanine at position 61 (V61A). However, this exchange does not lie in any of the conserved domains and is only a conventional exchange, so the probability of this mutation having an effect on protein function is relatively low. LAZ951.8 was identified as significantly associated with the petiole angle. It is a silent mutation from A > G at position 121 of the amino acid sequence. The SNPs identified as significant in the *HaLAZY2* gene all related to the dwarf growth type. LAZ921.7 is located in the promoter region and thus could have an influence on the protein expression.

Although the biological function of *LAZY1* is still largely unknown, it is still clear that it is an important component of gravitropism. Loss of function of *LAZY1* results in an insensitivity to gravity and leads to asymmetrical and undirected plant growth, which is a major negative aspect for plant architecture (Yoshihara *et al.,* 2013). In addition, *LAZY1* influences the tiller angle by negatively regulating the polar auxin transport (Gao *et al.,* 2020). Since, the *HaLAZY2* gene found in the sunflower differs in several points from the known *LAZY1*, it is possible that the function has also changed or is modified as a result of the effects of the differences. *TAC1* and *LAZY1* have an opposite influence on the plant architecture and a pleiotropic mode of action (Hollender *et al.*, 2020), so that they influences several characteristics. This could also be the case for the newly identified *HaLAZY2*. However, further analyses should be carried out to support this thesis. Due to the significant associations observed, *HaLAZY2* seems to be a very promising candidate for plant architecture.

## 5.6 Molecular markers in sunflower

In recent years, many molecular markers, which were perceived to be of economic interest, have been developed to accelerate sunflower breeding (Dimitrijevic & Horn, 2018). Markers with economic interest in sunflower, including markers for resistance screening against pests and pathogens, have been improved (Rauf *et al.*, 2020). In this doctoral study, different molecular markers like SSR markers, SNP markers, KASP markers and HRM markers were used for different tasks and also newly developed and tested.

### 5.6.1 SSR markers for population structure

To study the population structures of the small and large association panels, 34 SSR markers were used (Suppl. Tab. A 3), which had been previously developed and published in various papers (Tang *et al.*, 2002; Chapman *et al.*, 2008; Mandel *et al.*, 2011). These 34 SSR markers were selected so that the most uniform possible genome coverage could be achieved with two markers per linkage group. The PCR products had fragment sizes between 125 bp and 430 bp and showed both slightly polymorphic to highly polymorphic banding patterns. The SSR analyses made it possible to identify the population structures of the small, the large and the combined association panel. As SSR markers are highly polymorphic, they are often used for population structure analysis in association mapping (Ibrar *et al.*, 2020). The small association panel consisted of three subpopulations (Fig. 31). It has not been conclusively clarified what these three subpopulations are, but they could represent restorers, maintainers and the F1 individuals of the ornamental sunflowers. Former investigations by Horn *et al.* (2019) indicate this. Here 59 of the 64 selected genotypes had been examined, excluding one inbred line and the four ornamental sunflower varieties, which were F1 hybrids. In this analysis, the population structure was divided into two subpopulations, restorers and maintainers.

This population structure could also be assumed for the association panel of 448 accessions, that was used for association studies including SSR-, HRM- and KASP-marker analyses. The investigations also revealed two subpopulations here, whereby it can be assumed that this could also be the two groups maintainer and restorer, since no ornamental sunflowers were included in this panel. However, when the data from the 448 genotypes panel and the 64 genotypes panel were combined and the population structure was calculated for this, five subpopulations were found instead of the three subpopulations actually expected in the 448 accessions examined (Suppl. Fig. A 14). In the association panel of the 448 accessions, the five groups most likely represent maintainers and restorers, either oil or non-oil types and open pollinated varieties.

### 5.6.2 HRM markers in sunflower

As genetic and genomic studies provide valuable insights into the inheritance and function of genes, new methods have constantly been developed to enable rapid and accurate analysis of genes. With the newly acquired knowledge about plant genes, crops can be improved (Simko, 2016, Dimitrijevic & Horn, 2018). Since the method of HRM analysis has proven very successful for high throughput genotyping, its use in plant research has increased significantly in recent years (Simko, 2016).

In this doctoral study it was possible to develop HRM markers based on SNPs for different characteristics of the plant architecture in sunflower. The first HRM marker was successfully derived from an SNP in the DELLA domain of the *HaDELLA1* gene, which causes dwarfism in sunflowers (Ramos *et al.,* 2013). With the help of this HRM marker it was possible to examine all dwarfs and semi-dwarfs of the small and large association panels as well as the ornamental sunflower varieties for the presence of the mutation and thus for one of the molecular causes for reduced plant height in sunflowers.

Although there are several possible causes for decreased plant height, gibberellins and brassinosteroids (BR) have been studied best. The genes, which were used in the Green Revolution to reduce plant heights in cereals, were involved in GA biosynthesis or the GA-signaling pathway. The semi-dwarf growth type *sd1* in rice is caused by coding a defective GA biosynthetic enzyme, which causes a lack of bioactive GA in the *sd1* mutant. The dwarf genes *Rht-B1b* and *Rht-D1b* were used in wheat. *Rht-B1b* and *Rht-D1b* encode mutated DELLA proteins, which constitutively block GA signal transmission (Silverstone *et al.*, 2001; Ramos *et al.*, 2013). Brassinosteroids are steroid hormones that regulate the development and growth of plants. According to Fujioka & Yokota, 2003) it is possible to change plant phenotypes by manipulating the expression of BR genes. For example, overexpression of the *DWF4* gene in Arabidopsis dramatically promotes vegetative growth and improves seed yields. However, mutants of the *DWF7* gene showed dwarfism due to a lack of BR (Fujioka & Yokota, 2003).

After the identification of the SNPs significantly associated with features of the plant architecture, these were checked for their nature, i.e. whether they meet the requirements for HRM markers (described in 3.13.1 Development of HRM primers). In total, HRM markers were developed for seven of the significantly associated SNPs and tested on a reference group of 12 genotypes. The markers were associated with the dwarf and semi-dwarf growth types as well as with narrow petiole angles. The test runs of the markers revealed the genotypes of some accessions for which sequencing data from LGC had previously been missing. The statistical evaluation of the significance of the examined SNPs could thus be corrected after a screen of the small association panel with its 64 accessions and improved the p-values for some SNPs. The HRM markers for the SNPs SNE171.7 in the *HaSNEEZY2* gene (semi-dwarf associated), DEL801.17 in *HaDELLA2* gene (dwarfism associated) and the two SNPs DEL091.8 and DEL091.9 in the *HaDELLA-Like2* gene (associated with narrow petiole angle) were selected on the basis of the corrected data to be verified in the association panel of 448 genotypes and the group consisting of 25 ornamental sunflower varieties. However, the calculation of the results from all available data ultimately showed relatively low significance values. However, it is possible that the reference groups for the respective traits in the total amount were too small to achieve a meaningful result. However, since the method of HRM analysis worked perfectly for all markers developed, the results can be regarded as a successful test run for the establishment of this method in the molecular investigation of sunflowers. Since HRM markers were initially developed for only seven of the 59 significantly associated SNPs and only four were used for further studies, there is still an enormous potential based on the data for the successful development of HRM markers for plant architecture in sunflowers.

It can be assumed that the use of the HRM method can have a considerable advantage for breeding sunflowers, as it is an efficient and inexpensive method for the analysis of SSRs and SNPs (Simko, 2016) and has already produced excellent results for many other crops. Investigations of various SNPs, InDels and SSRs have been successfully performed in several plant species such as almond (*Prunus dulcis*) (Wu *et al.*, 2008), grapevine (*Vitis berlandieri*, *Vitis riparia*, *Vitis vinifera*) (Mackay *et al*., 2008), olives (*Olea europaea*) (Muleo *et al*., 2009), black raspberry (*Rubus occidentalis* subgenus *Idaeobatus)* (Dosset *et al*., 2012) and in various *citrus* species such as grapefruit, orange, mandarin or lemon (Distefano *et al.*, 2012; Distefano *et al.*, 2013). The very latest studies have recently appeared on the creation of high-resolution linkage maps for the positions of important quantitative loci in onion (*Allium cepa*) (Cho *et al.,* 2021) and for the validation of variants in the genus *Eucalyptus* (Parveen *et al.*, 2020). It is also assumed that HRM analysis can be used for the analysis of markers in a wide range of applications in all species (Distefano *et al.*, 2012) and thus represents an excellent option for sunflower breeding. Since the method has not yet been established for sunflowers, the markers developed in this work represent the first, promising step in this direction.

### 5.6.3 Identification of significant associated SNPs using KASP markers

The p-values of the four examined SNPs (SNE171.7, DEL801.17, DEL091.8, DEL091.9) for characteristics of the plant architecture in the sunflower turned out to be not significant after the screening the 448 genotypes association panel using the HRM technology. The screening for all 59 SNPs identified as significantly associated in the small 64 genotypes association panel by the Fisher Exact test were commissioned to LGC using the KASP technology for 381 accessions of the large association panel. KASP is a fluorescence-based genotyping technology originally developed by KBioscience UK Limited (Semagn *et al.*, 2014). The mode of operation is based on an allele-specific oligo extension and fluorescence resonance energy transfer for signal generation (Kumpatla *et al.* 2012). In addition, this method is inexpensive and can be used in examinations that require a small number of markers (Semagn *et al.*, 2014).

Reviewing the results of the KASP assays, it became obvious that the genotyping of three accessions (UGA-SAM1-205, UGA-SAM1-231, Stepnyak) had failed completely. This could be due to internal errors during the implementation at LGC Genomics or to poor quality of the DNA sent. Overall, the results were available for 59 SNPs in 381 accessions. The failure rates of the individual analysed SNPs ranged between 1% and 56%. It should be mentioned that the failure rate for the SNP DEL801.17, which was significantly associated with dwarfism in the small panel ($p < 0.05$), was 56% and therefore could not be represented in the following GLM analysis. The evaluation of the results showed that there were no significantly associated SNPs for the characteristic plant height among the 59 examined SNPs (Fig. 43 A). However, a total of six SNPs (GID071.16, GID071.24, DEL091.11, DEL091.27, DEL091.48, DEL091.47) in three different genes (*HAGID1B, HADELLA1, HADELLA-Like2*) could be significantly associated with the characteristic of the narrow petiole angle (Fig. 43 B, Tab. 14). The SNPs in the *HaDELLA-Like2* gene are all located in the promoter region of the gene and could therefore have an influence on the expression. Interestingly, no significantly associated SNPs were identified in the genes *HaTAC1*, *HaTAC2*, *HaLAZY1* and *HaLAZY2*, which have actually been shown to control the formation of leaf and branch angles in many other plants (Yoshihara & Lino, 2007; Dardick *et al.*, 2013; Li *et al.*, 2017; Yoshihara & Spalding, 2017; Hollender *et al.*, 2020). The significantly with petiole angles associated SNPs in the genes *HaGID1B* and *HaDELLA1* both represent silent mutations and thus do not result in any change in the amino acid sequence.

The two SNPs GID071.16 and GID071.24 have already been identified as significantly associated with the expression of the petiole angle through the analysis of the small association panel over three years using TASSEL 5.0 (Tab. 11), which means that they can be considered verified. The basis on which the significant association of these SNPs with the expression of the petiole angle can be found should be investigated in further studies. Thus, these two SNPs could serve as markers for the plant architecture in sunflowers and can be applied in breeding programs to improve this crop.

Over the last few years, it has been shown that KASP markers can make a valuable contribution to improving breeding programs of various crops, as this method can reveal polymorphisms of SNP data that can be suitable for genetic analyses and molecular breeding (Cheon *et al.,* 2018). In rice (*Oryza japonica*), 506 SNP sites were converted into KASP markers and tested on 13 Japonica varieties. A total of 400 polymorphic KASP markers could be detected and a map with 205 KASP markers was constructed (Cheon *et al.*, 2018; Cheon *et al.,* 2020). Another study on indica rice breeding lines (generated 1.3 million KASP assay designs, which resulted in 92,500 potential functional markers (Steele *et al.,* 2018). For peanut (*Arachis hypogaea*), KASP markers could be developed to differentiate the genotypes of offsprings between high oleic peanuts and common peanuts (Zhao *et al.,* 2017). In apples (*Malus domestica*), the use of KASP markers showed that SNP-based genotyping with a small set of well-selected markers is just as efficient for the identification of apple varieties as the use of microsatellites (Winfield *et al.,* 2020). In a current study in coffee (*Coffea canephora*), KASP analyses and a set of 120 SNP markers allowed the examination of 400 coffee accessions for incorrect labelling. These investigations revealed incorrect labelling of the mother trees used in seed gardens and pollen contamination from unwanted paternal parents (Akpertey *et al.,* 2021).

Amazingly, the use of the KASP assays in sunflower breeding is not yet well established. However, a recent study showed that this method can also be useful for sunflowers. Various SNP markers were investigated, which were associated with resistance to downy mildew in sunflowers (Kösoğlu *et al*., 2021). The resistance genes $Pl_{arg}$, $Pl_{13}$ and $Pl_{8}$ were analysed in three crosses using KASP markers. The markers NSA002867 and NSA006138 were discriminatory for $Pl_{arg}$, the marker NSA000354 was discriminatory for *$Pl_{13}$*, and the markers NSA002220 and NSA002251 were discriminatory for *$Pl_8$*. Based on this study, the possibility of using a combination of SNP markers and KASP assays for marker assisted selection in sunflowers was shown (Kösoğlu *et al*., 2021). Since the use of KASP markers has already been successful in improving many crops, the potential of this method should also be used in sunflower breeding.

## 5.7 Known causes influencing the plant architecture

The plant architecture of crops has a major influence in agriculture, both for annual crops such as cereals or oil plants, and for perennial trees (Hill & Hollender, 2019). The crown architecture determines the productivity via the planting density and the efficiency of light absorption (Busov, 2018). The importance of plant architecture was demonstrated during the Green Revolution, when rice and wheat plants with short stems and upright ears were preferred in cultivation (Hedden, 2003). The advantage of these plants with modified architecture lies in the fact that they could be grown at a higher density, which increased the yields extremely. The dwarf traits, which had been introduced into plants, were based on mutations in genes that disrupt the action or production of gibberellins in plants (Hedden, 2003). In wheat, the *Rht* loci *Rht-B1* and *Rht-D1*, known as GA-insensitive, were used, which code for DELLA proteins. DELLA proteins act as growth repressors, which are broken down in the presence of gibberellin (Würschum *et al.,* 2017). GA insensitivity not only influences stem elongation, but also a number of other GA-dependent developmental processes such as root elongation, early seedling strength or coleoptile length (Botwright *et al.,* 2001; Bai *et al.,* 2013; Würschum *et al*., 2017).

Plant architecture can be influenced by mutations in certain genes as well as by various environmental factors. Some of these environmental factors are, for example, the availability of water or nutrients such nitrogen (N), phosphorus (P) and potassium (K). The availability of light at the respective location is also an important environmental factor for plants (Tian *et al*., 2014). These external environmental factors affecting the plant are perceived as different stimuli and are converted by the plant into hormone signals that can control growth and development in a wide variety of ways. Phytohormones that can have an impact on plant architecture are auxins, cytokinins, gibberellins, brassinosteroids or strigolactones, all with different effects on growth and development of the plant (Hill & Hollender, 2019). Strigolactones are important for branching, root growth, root hair extension and for budding out (Bennett & Leyser 2014). The mode of action of cytokinins extends over a wide spectrum and depends on the plant tissue. It includes the growth and branching of roots, vascular differentiation, shoot growth and seed development, but also the sprouting of buds as well as growth of flowers and leaf senescence (Teichmann and Muhr, 2015).

The TCPs (teosinte branched1/*Cycloidea*/proliferating cell factor) proteins are a group of plant-specific transcription factors that are involved in many processes such as embryonic development, flowering, leaf development and branching development (Madrigal *et al.*, 2017; Bresso *et al.*, 2018; He *et al.*, 2020). TPCs can be identified by the highly conserved TCP domain (He *et al.,* 2020). The TCP proteins can be divided into two subfamilies, class I and class II, which differ from class I by a deletion of four amino acids in the TCP domain (Li, 2015). Specific examples of how TCPs work can be found in Arabidopsis. The TCPs *branched1* (TCP18) and *branched2* (TCP12), which belong to the same subfamily, have a great influence on the control of branch growth (Wang *et al.,* 2019; He *et al.,* 2020), whereas TCP2–5, TCP10, TCP13, TCP17 and TCP24 are related to lateral organ organogenesis and control of leaf development (Efroni *et al.,* 2008; Koyama *et al.,* 2007; He *et al.,* 2020). Many genes of the TCP family have already been identified in a wide variety of plant species such as *Arabidopsis*, rice, tomato, euphrates-poplar (*Populus euphratic*a), wheat, potato and watermelon (He *et al.,* 2020).

So far, two mutations have been identified in sunflower, which reduce the plant height and thus influence the plant architecture. These mutations represent, on one hand, a deletion in the *ent-kaurenic acid oxidase1* (*HaKAO1*) gene sequence (Fambrini *et al.,* 2011) and, on the other hand, a point mutation in the *HaDELLA1* gene, which converts leucine to proline within the conserved DELLA domain of the gene (Ramos *et al.,* 2013). In a newer study, a spontaneously occurring, brachytic sunflower mutant within the sunflower inbred line TURF was identified (Mariotti *et al.,* 2018). The authors named the new dwarf mutant *lingering hope* (*linho*). Analyses of the genetic, morphology and physiology were carried out to find out the causes of its dwarfism and several other defects. The reduced plant height of the *linho* mutants was due to shortened internodes, the cells of which, however, were not smaller than those of the wild-type control. The mutant showed also a changed length/width ratio of the leaf blade, chlorosis and defects in the development of florescence. The brachytic trait was not associated with a specific hormone deficiency, but instead an increased level of several gibberellins was detected in the leaves. The study described *linho* as the first sunflower mutant with a change in the salicylic acid metabolism. It was assumed that the mutated phenotype is under monogenic control (Mariotti *et al.,* 2018).

As the results of the present studies show, there are many different factors that influence plant architecture. This fact shows once again the importance of further investigations and analyses of already recognized, but still undiscovered molecular and environmental influences on the architecture of plants.

## 5.8 Conclusions

In the present work the sunflower association panel could be evaluated at different locations with different climatic conditions. On the basis of correlation data between the locations in Germany (Bandow) and Spain (Guadalajara) it was possible to select 64 genotypes with specific growth types, which showed clear phenotypic differences in the plant architecture. The selected genotypes could be assigned to the different growth types regarding plant height and petiole angles and were used for association studies. Fifty-three F1 hybrids were also evaluated and their plant-architectural properties assessed. These F1 hybrids were successfully used for performance tests with different plant densities (20 cm, 25 cm, 30 cm). The performance tests were carried out at two locations with different climatic conditions in Germany and Romania. The results of the performance tests showed nine sunflower test hybrids at the location in Romania (LC-1093A x UGA-SAM1-186, LC-1093A x UGA-SAM1-055, LC-1093A x UGA-SAM1-012, LC-1093A x UGA-SAM1-276, LC-1093A x UGA-SAM1-195, LC-1093A x UGA-SAM1-196, LC-1093A x UGA-SAM1-024, LC-1093A x UGA-SAM1-119, LC-1093A x UGA-SAM1-101), that can deliver an increased yield by cultivation with an increased plant density (20 cm9. Eleven of the test hybrids performed equal or better than the reference varieties at the different locations with different plant densities (Suppl. Tab. A11).

Segregation analyses on the mode of inheritance of the characteristics plant height and petiole angle were carried out on five F2 populations. In two of these F2 populations, the hypothetical phenotypic segregation of 1:3 could be observed for the trait plant height, which suggests that this trait was under monogenic control and recessively inherited in these two cross combinations.

The genes of the GA-signaling pathway and the branching angle could be examined and partial sequences of three genes were successfully completed. For the genes *HaTAC1* and *HaLAZY1*, two additional homologs *HaTAC2* and *HaLAZY2* could be identified in the sunflower. A candidate gene approach expanded to 22 genes was used for further analyses. The 22 candidate genes from the 64 genotypes were sequenced using amplicon targeted sequencing and a total of 306 SNPs and 111 InDels were identified. The SNP analyses allowed the identification of gene variants for 20 of the 22 candidate genes. The two genes, *HaGID1A* and *HaSNE1*, proved to be highly conserved. Based on SSR analyses, the population structures of the small and large association panels could be determined. Association studies to identify phenotypically relevant SNPs were successfully carried out using GLM analyses with TASSEL 5.0 applying the Bonferroni correction and the Fisher Exact Test ($p < 0.05$). A total of 59 significantly associated SNPs were found in 11 candidate genes. Based on the significant SNPs, HRM markers were developed and tested within the small and large association panels as well as in 25 ornamental sunflowers. Although the four HRM markers in the small association panel were convincing, they could not be verified by the results in the large association panel. KASP analyses for the 59 SNPs in the large association panel provided the molecular basis for further GLM analysis. The data from the KASP analysis of the large panel were combined with the existing data from the next generation sequencing data of the small association panel. The results of the GLM analysis showed significant associations of six SNPs with petiole angles, which were located in the three genes *HaGID1B*, *HaDELLA1 and HaDELLA-Like2*. Since the two SNPs GID071.16 and GID071.24 in the *HaGID1B* gene had already been identified as being significantly associated with the formation of the petiole angle through the analysis of the small association panel applying TASSEL 5.0, they could be verified and thus represent potential molecular markers for the plant architecture.

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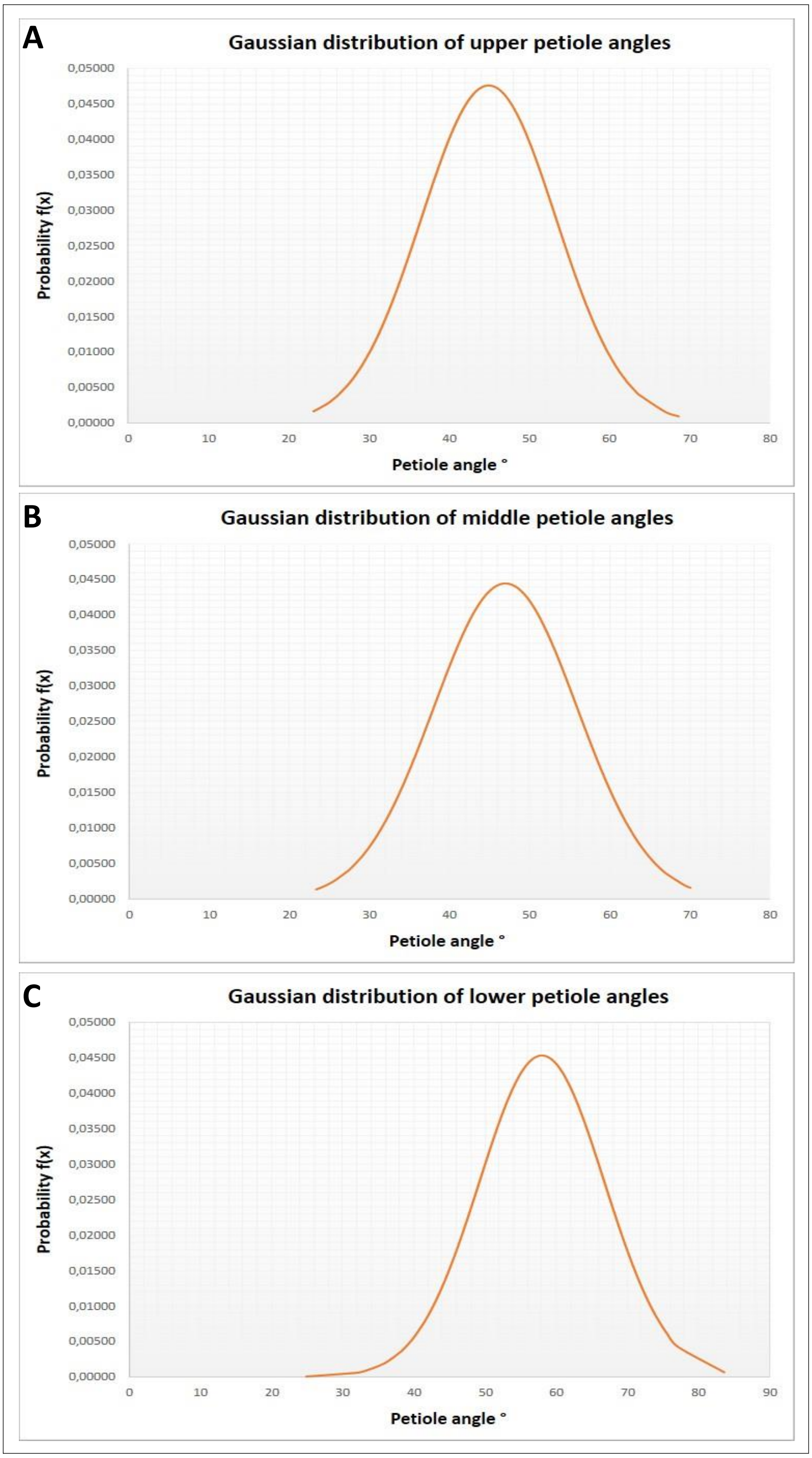
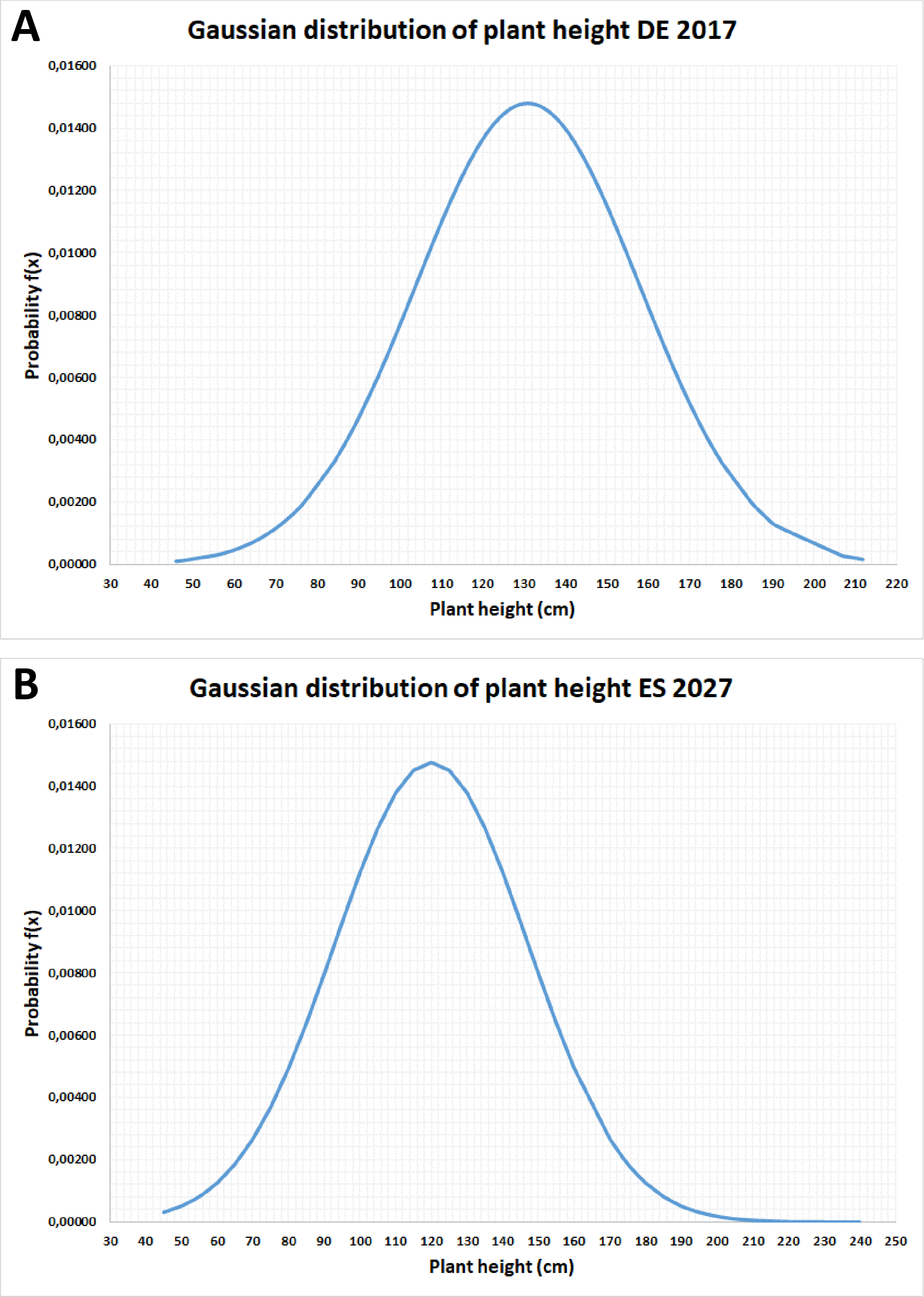
# Appendix

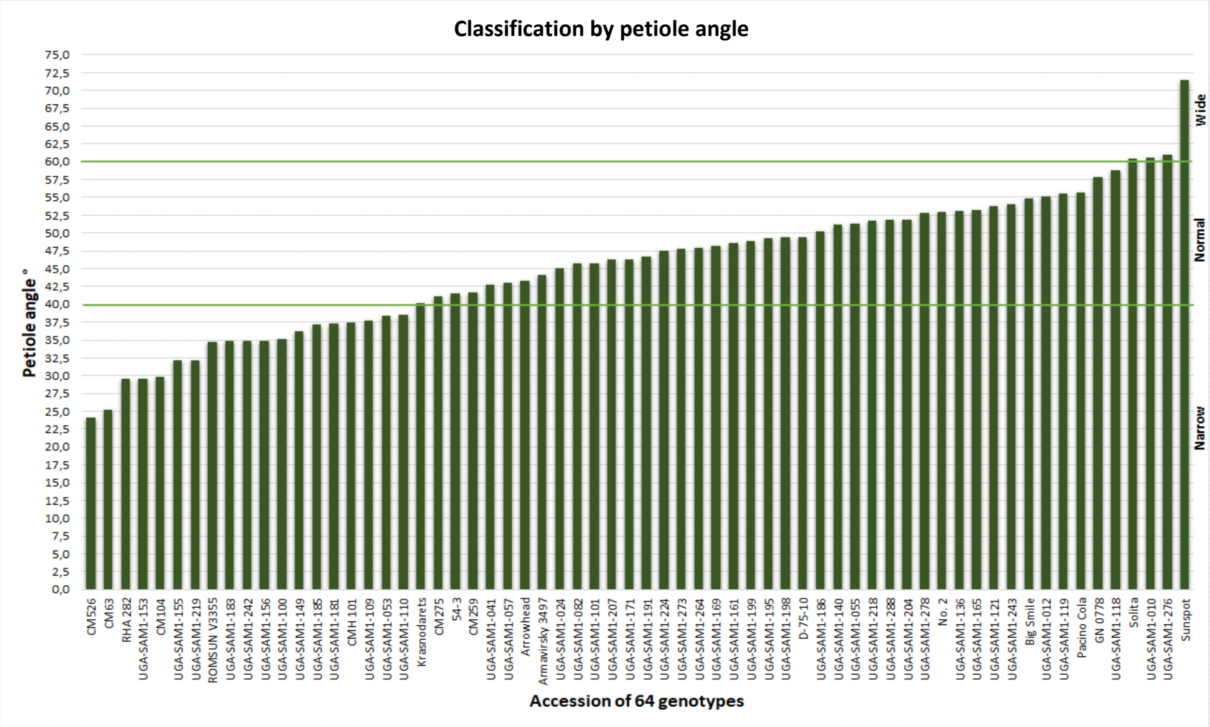
## Supplementary Figures



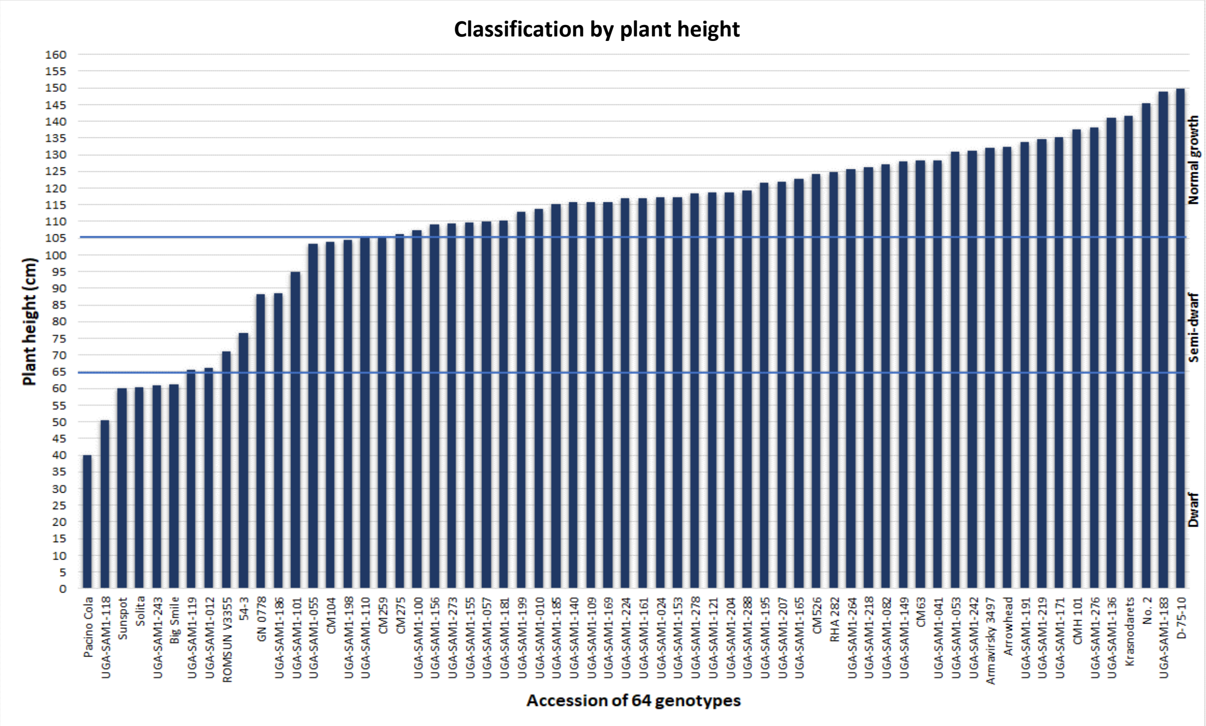
**Supplementary Figure A 1:** Normal Gaussian distribution of petiole angles of the small association panel in different plant levels of Germany in 2017. **A)** Upper level; **B)** Middle level; **C)** Lower level



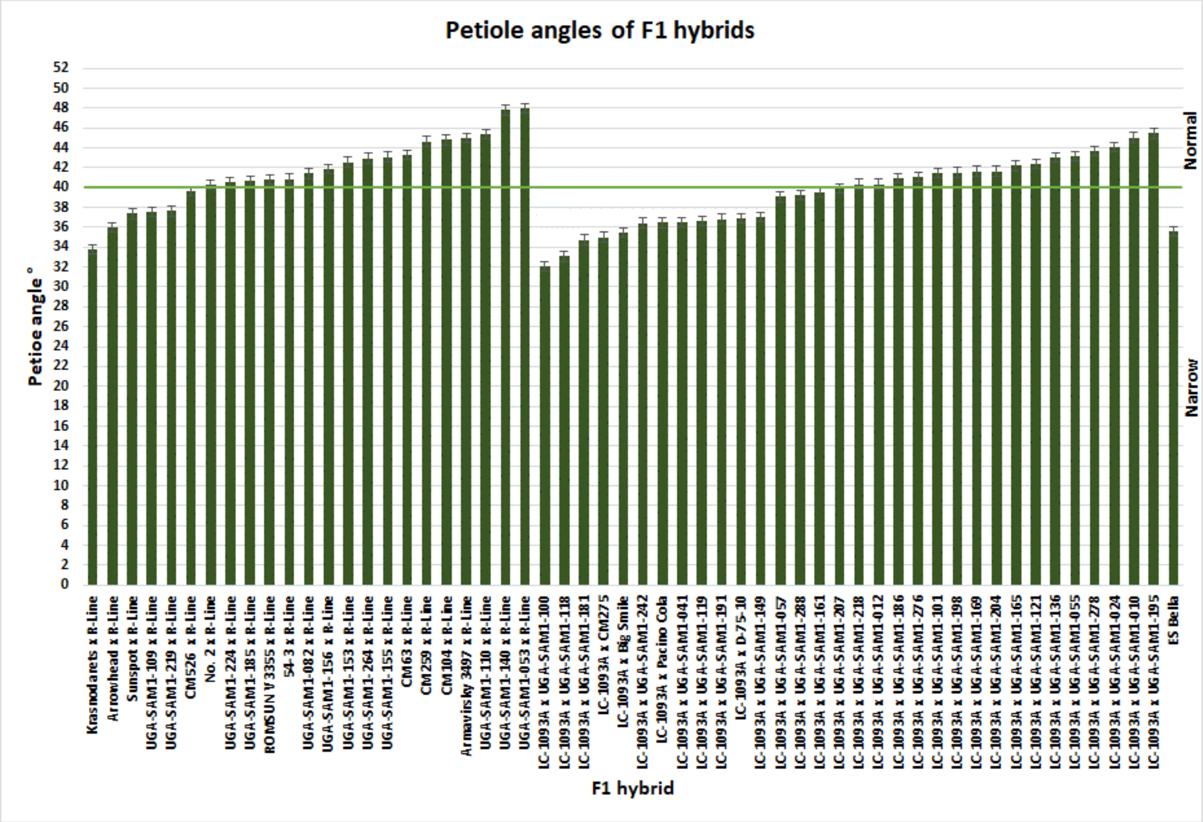
**Supplementary Figure A 2:** Normal Gaussian distribution of plant height of the small association panel in different locations in 2017 **A)** Germany (DE); **B)** Spain (ES)



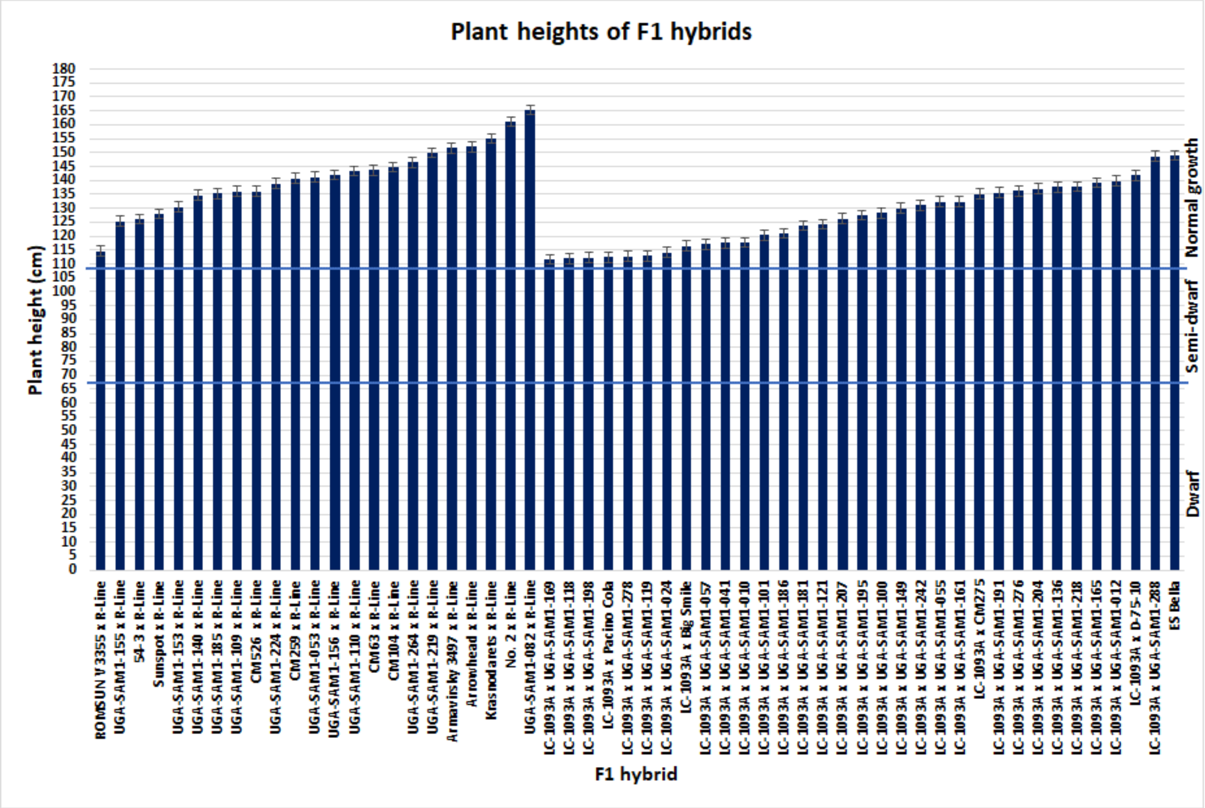
**Supplementary Figure A 3:** Classification of sunflowers in different petiole angle types based on data of 2017 in Germany. ≤ 40.0 °= narrow, 40.1 °- 60 ° = normal, ≥ 60.1 ° = wide



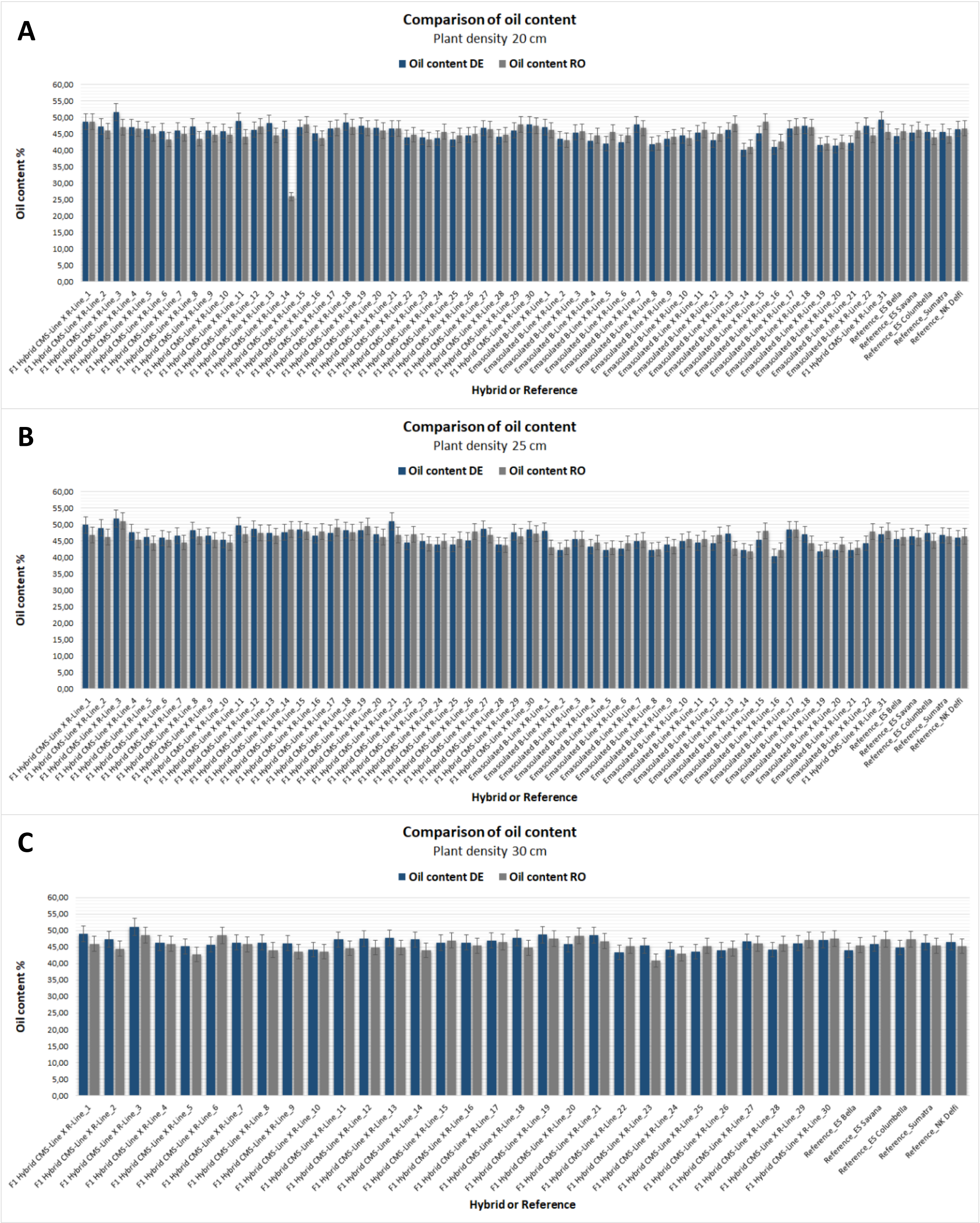
**Supplementary Figure A 4:** Classification of sunflowers in different plant height based on data of 2017 in Germany. ≤ 65 cm = dwarf, 66 cm – 105 cm = normal, ≥ 106 cm = normal



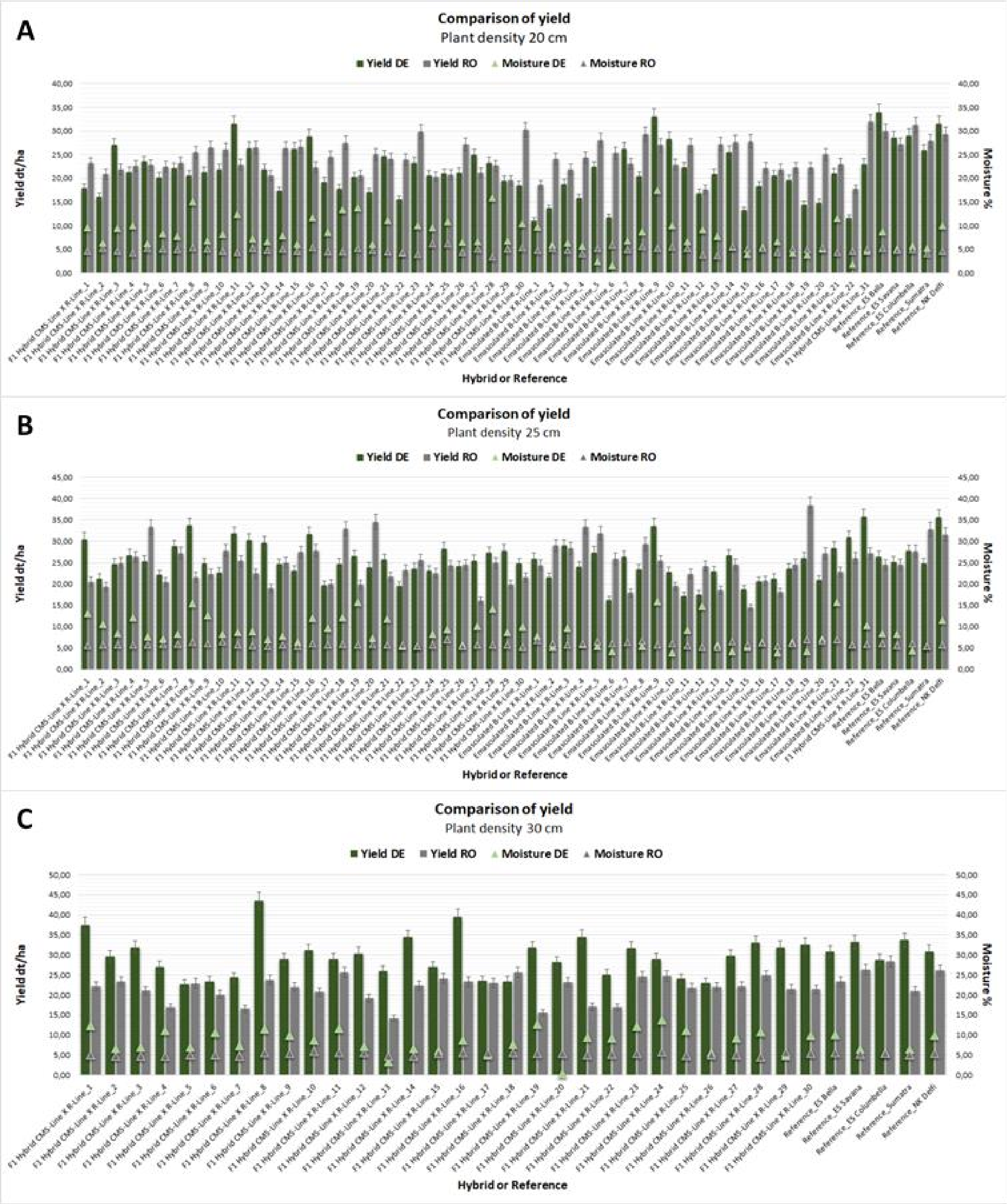
**Supplementary Figure A 5:** Mean values of petiole angles of the F1 hybrids and reference accession "ES Bella" sorted from narrow to wide based on data of 2019 in Germany. ≤ 40.0 °= narrow, 40.1 °- 60 ° = normal



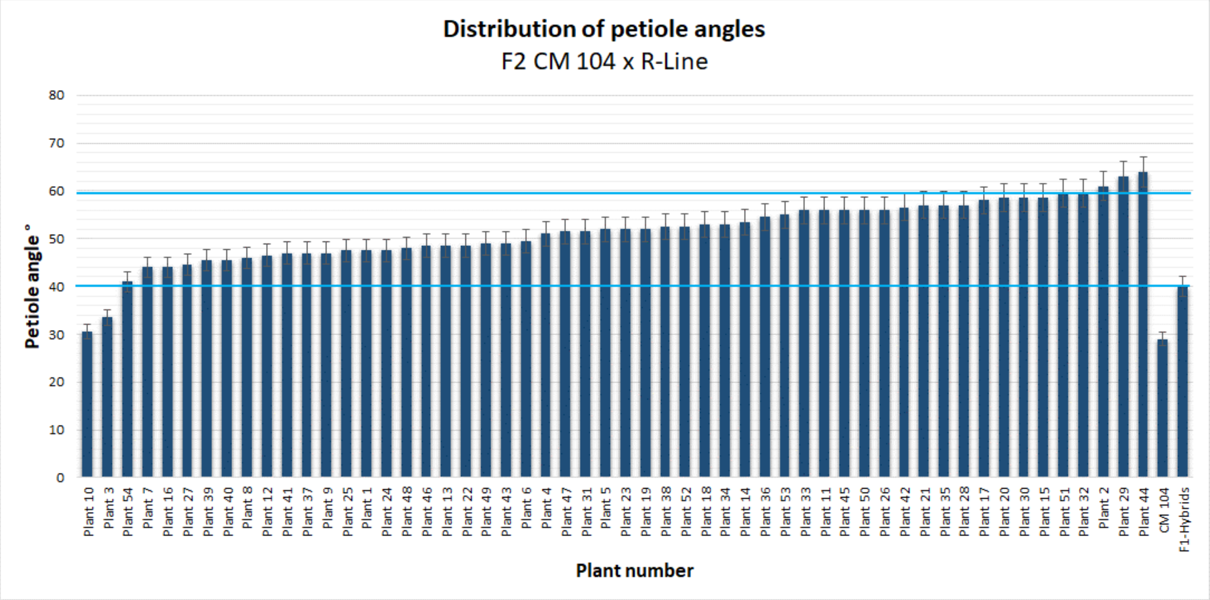
**Supplementary Figure A 6:** Mean values of plant heights of the F1 hybrids and reference accession "ES Bella" sorted from small to large based on data of 2019 in Germany. ≤ 65 cm = dwarf, 66 cm – 105 cm = normal, ≥ 106 cm = normal



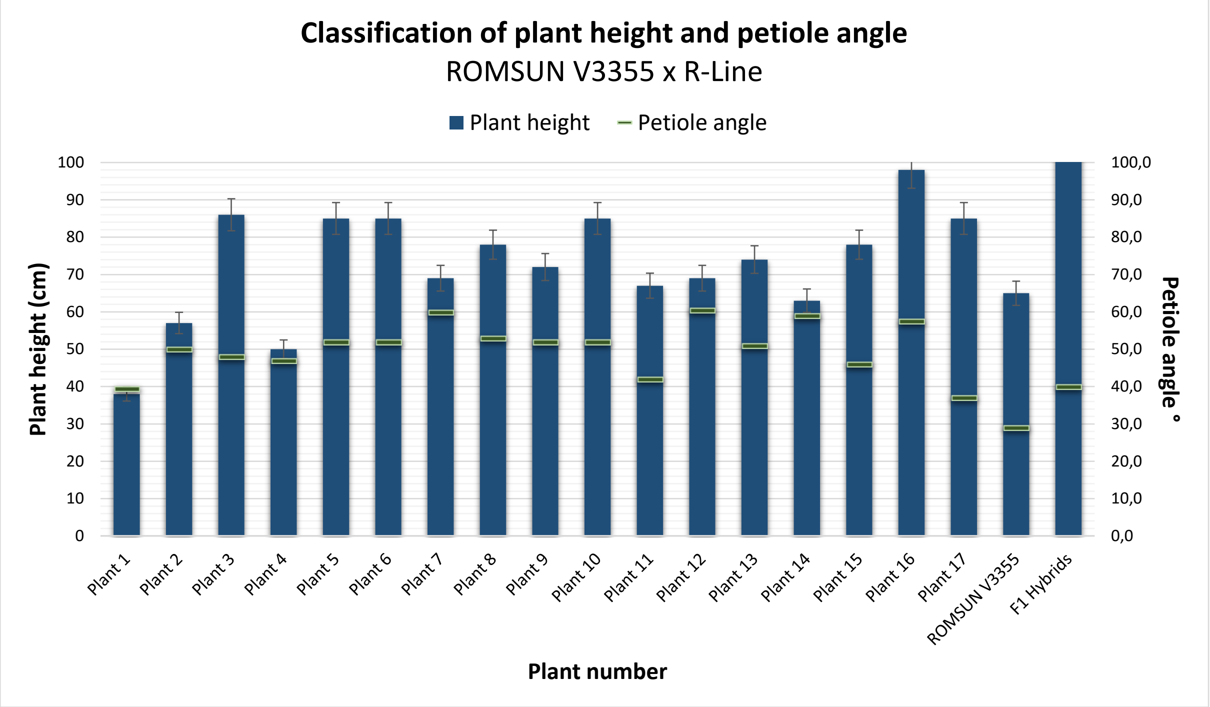
**Supplementary Figure A 7:** Comparing oil content of different plant densities in Germany (DE) and Romania (RO) in 2020. **A)** Plant density of 20 cm; **B)** Plant density of 25 cm; **C)** Plant density of 30 cm



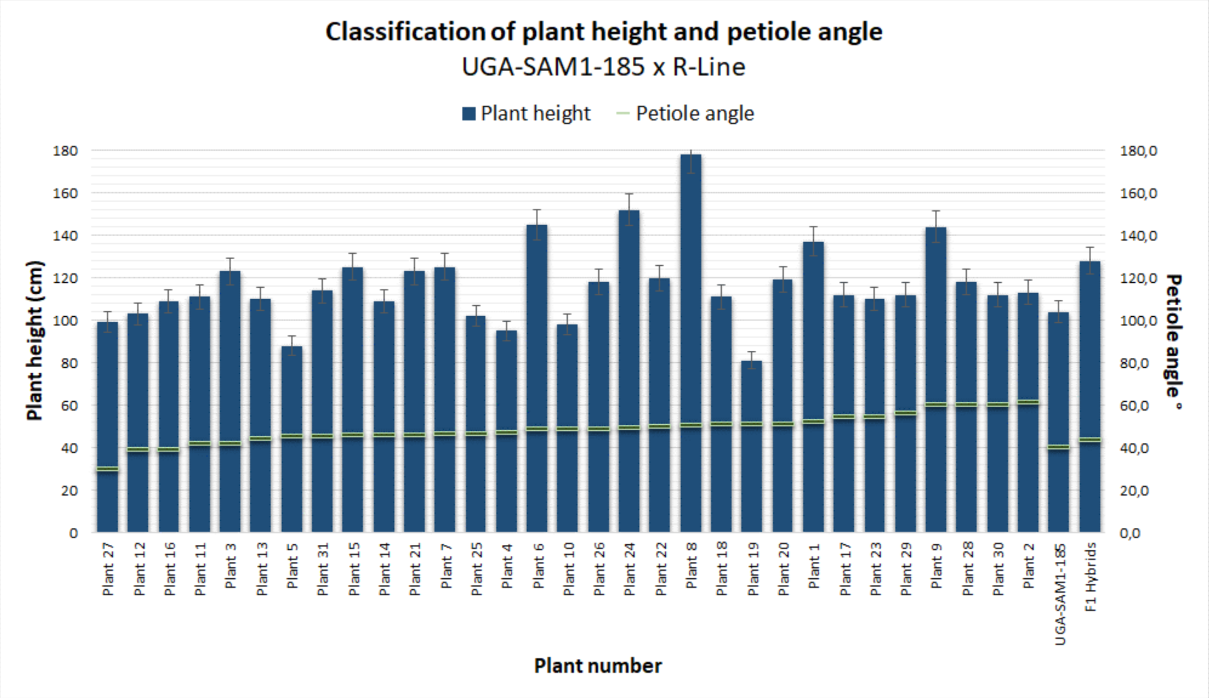
**Supplementary Figure A 8:** Comparing yield of different plant densities in Germany (DE) and Romania (RO) in 2020. **A)** Plant density of 20 cm; **B)** Plant density of 25 cm; **C)** plant density of 30 cm



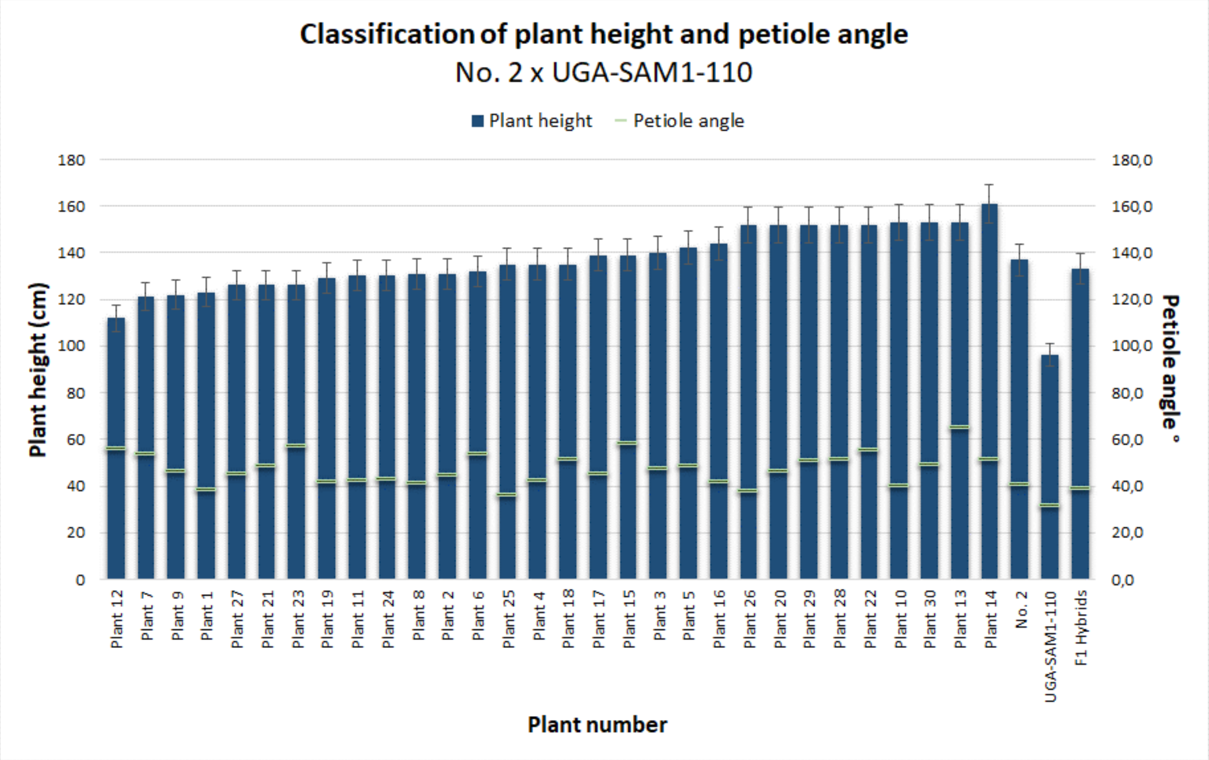
**Supplementary Figure A 9:** Distribution of petiole angles of F2 population, crossing CM 104 x R-Line (narrow angle x normal angle)



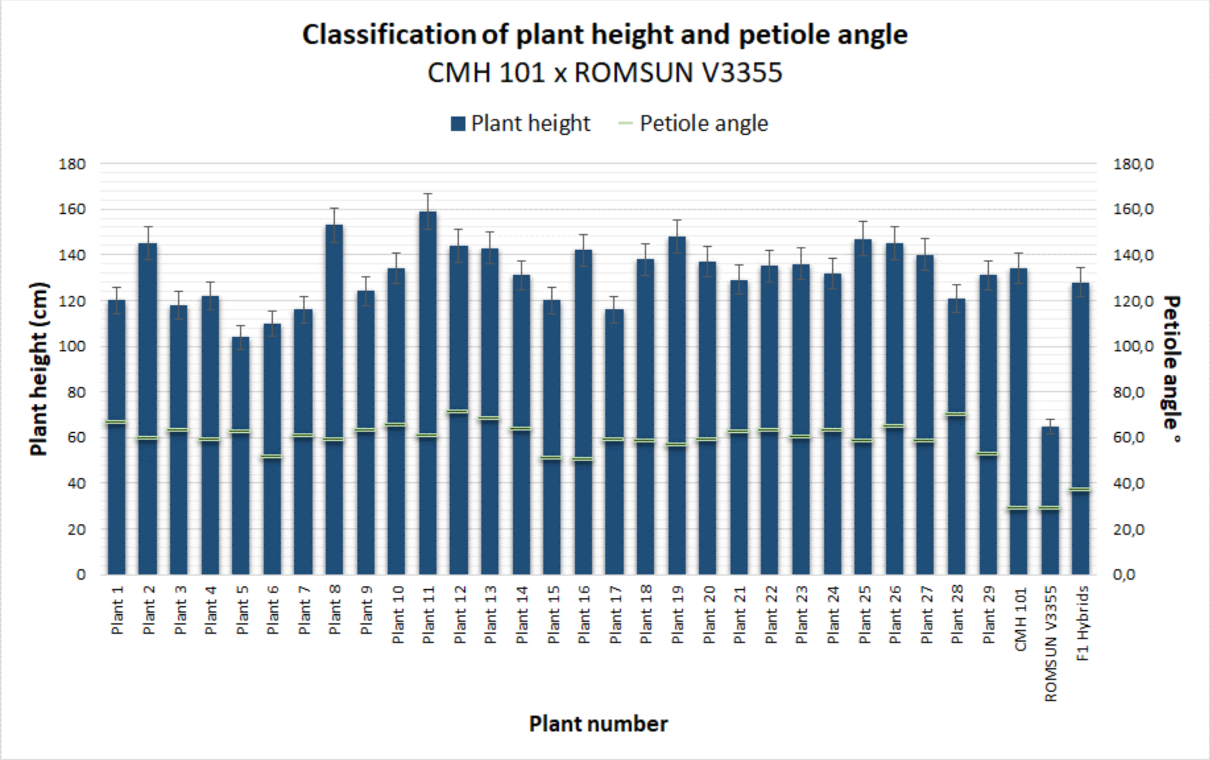
**Supplementary Figure A 10:** Evaluation of plant height and petiole angles of F2 population, crossing ROMSUN V3355 x R-Line



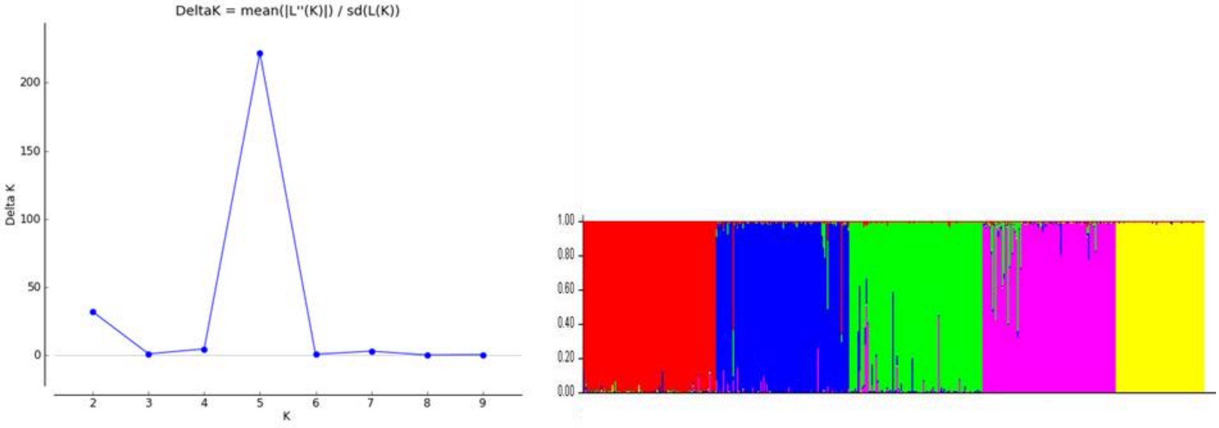
**Supplementary Figure A 11:** Distribution of plant height and petiole angles of F2 population, crossing UGA-SAM1-185 x R-Line, sorted by petiole angle values



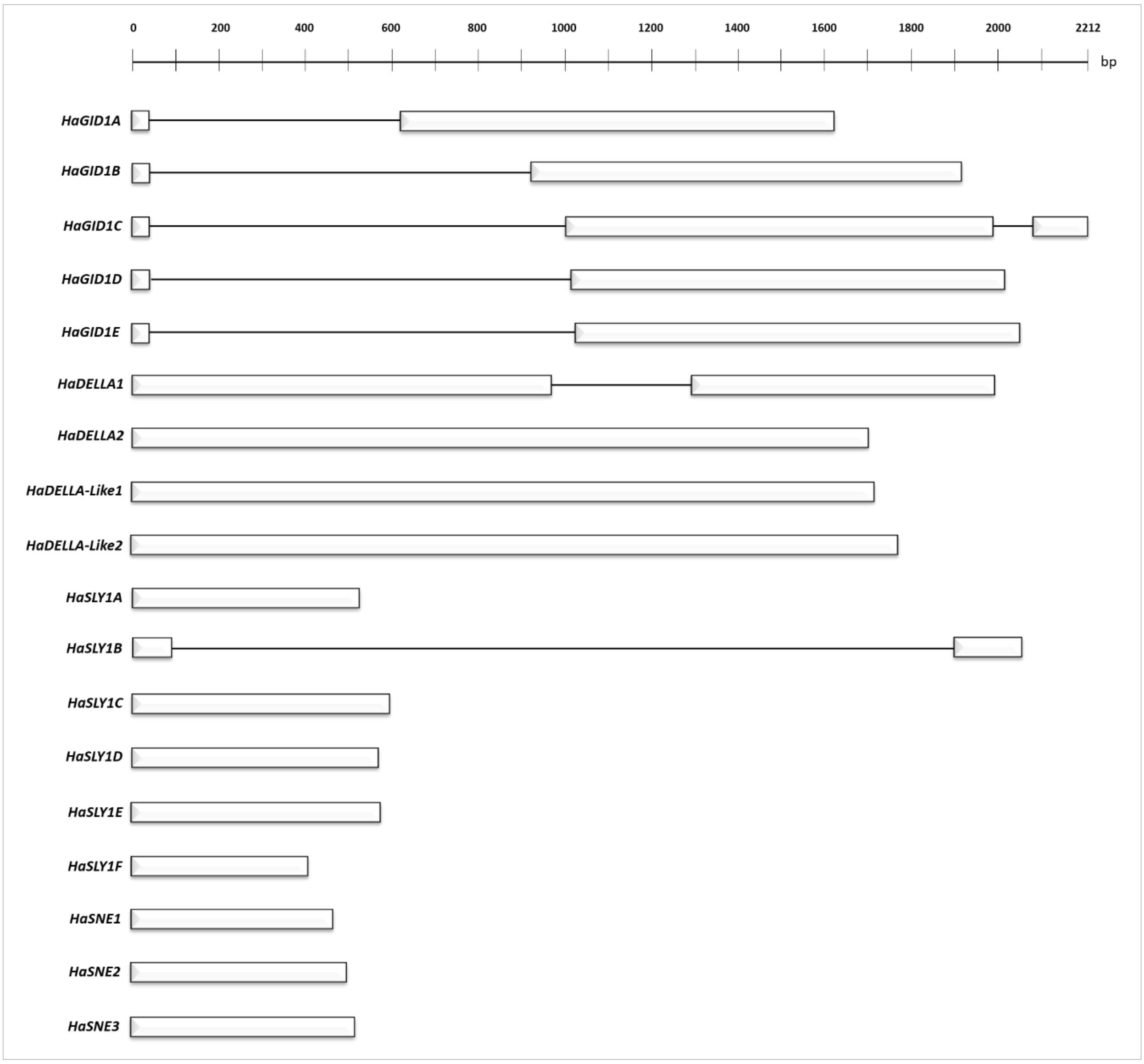
**Supplementary Figure A 12:** Distribution of plant height and petiole angles of F2 population, crossing No. 2 x UGA-SAM1-110, sorted by plant heights



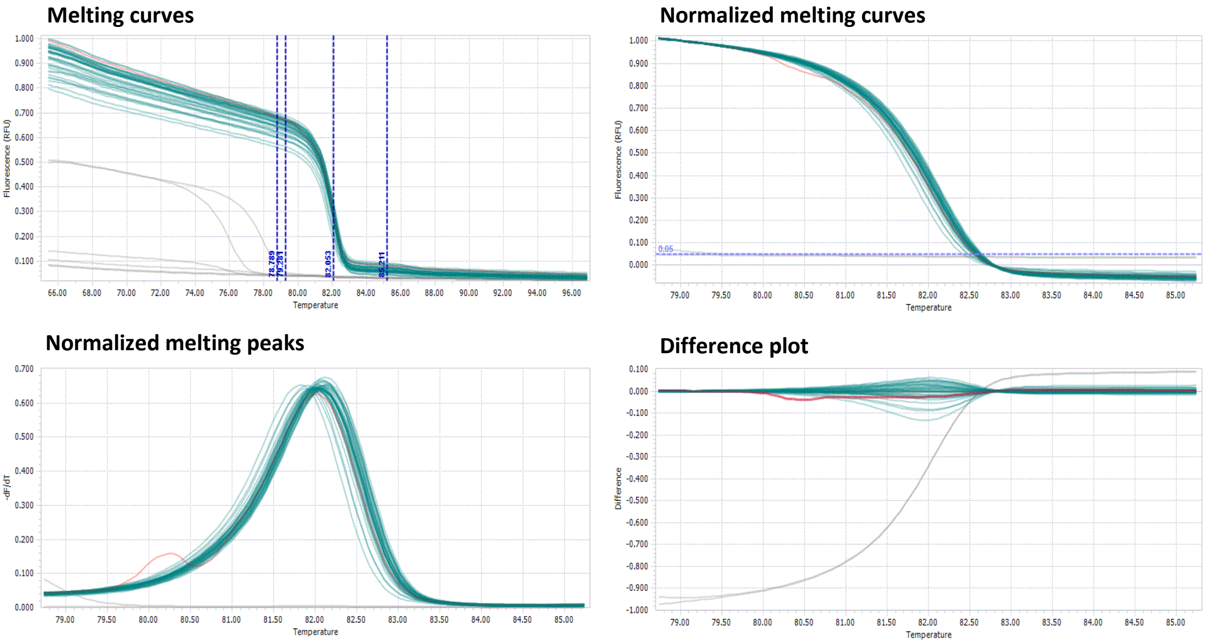
**Supplementary Figure A 13:** Evaluation of plant height and petiole angles of F2 population, crossing CMH 101 x ROMSUN V3355



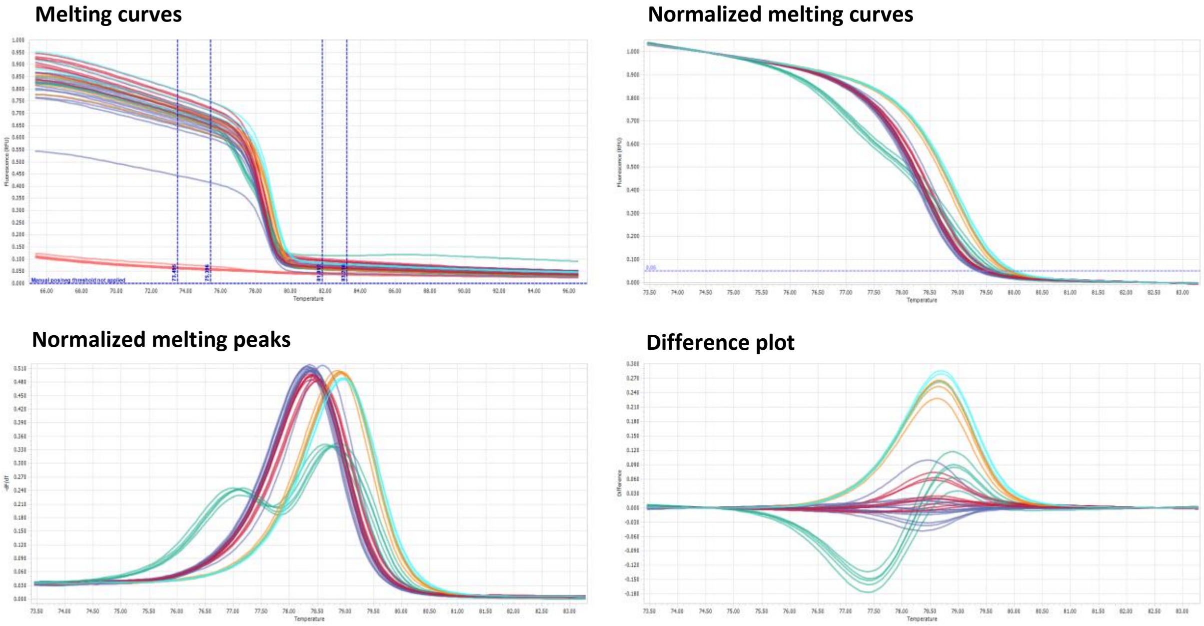
**Supplementary Figure A 14:** Calculation of population structure for combined association panel (n = 448), DeltaK = 5



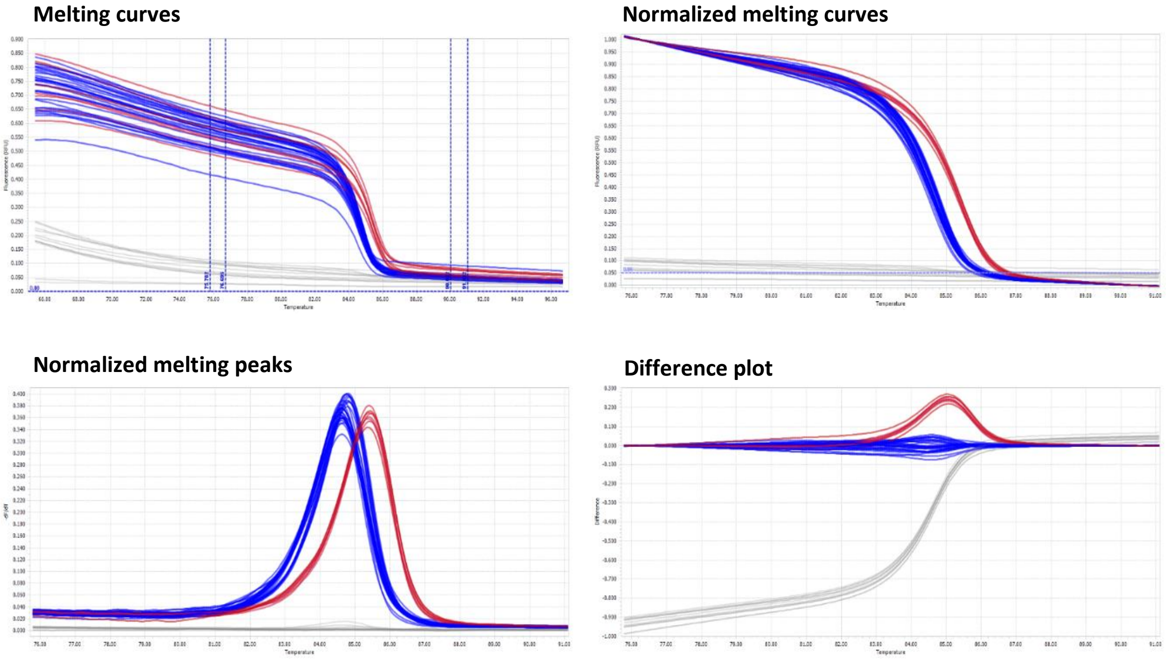
**Supplementary Figure A 15:** Genomic structures of the genes of GA-signaling pathway



**Supplementary Figure A 16: H**RM primer test for the SNP DEL091.3, significantly associated with narrow petiole angles.



**Supplementary Figure A 17:** HRM primer test for the SNP GID131.30, significantly associated with semi-dwarf growth type. Group 1 (blue + red) accessions without SNP; Group 2 (turquoise + orange) accessions with SNP; Group 3 (green) heterozygous accessions



Melting curves

Normalized melting curves

Normalized melting peaks

Difference plot

**Supplementary Figure A 18:** HRM primer test for the SNP GID131.30, significantly associated with narrow petiole angles. Group 1 (blue) accessions without SNP; Group 2 (red) accessions with SNP

# Supplementary Tables

**Supplementary Table A 1:** Primers for completion of partial candidate gene sequences

| PRIMER | SEQUENCE (5’-3’) | USAGE |
|---|---|---|
| SP6 | CGATTTAGGTGACACTATAG | • Insert PCR test<br>• Sequence analysis |
| T7 | TAATACGACTCACTATAGGG | • Insert PCR test<br>• Sequence analysis |
| SC 12733_8 5UTR S1 | CTCCACCAATTCTCACTCTTAACC | • PCR *HaDELLA2* |
| HADELLA2_REV1 | TCACCGAATTTTCCAAGC | • PCR *HaDELLA2* |
| SC 14532_11 5UTR S1 | CCACCTCCATTCACCAATCCTCAC | • PCR *HaDELA-Like2* |
| SC 14532_11 CDS A1 | TTTCAAGCGAGTCAAACACACCAC | • PCR *HaDELLA-Like2* |
| HAGID1C_CDS_FOR | ATGGCGGGAAGCGATCA | • PCR *HaGID1C* |
| HAGID1C_CDS_REV | TTAACAACAAAACACCAACTTCA | • PCR *HaGID1C* |
| HAGID1D_CDS_FOR | TCTCTGAAATACAAGGATTTCCC | • PCR *HaGID1D* |
| HAGID1D_CDS_REV | TCACAAAAACCAATCCCCCT | • PCR *HaGID1D* |
| HALAZY1_GEN_FOR | ATCTGACTACTCACTGATCTCTGC | • PCR *HaLAZY1* |
| HALAZY1_GEN_REV | CCAAATTCAACCAATCACAACC | • PCR *HaLAZY1* |
| HATAC1_GEN_FOR | ATGAAGGTATGCAATGGTTATTA | • PCR *HaTAC1* |
| HATAC1_GEN_REV | ATTCATGAGGTAGCATGCAC | • PCR *HaTAC1* |
| HATAC1_RACE_3`-END | GATTACGCCAAGCTTGATGATTCAGCTCAACCGATCAAGAA | • 3´RACE *HaTAC1* |
| HATAC1_RACE_3`-END2 | GATTACGCCAAGCTTGCACCGGATCCATTAAGAGTTTCTTG | • 3´RACE *HaTAC1* |

**Supplementary Table A 2:** Primers for HRM analysis

| PRIMER | SEQUENCE (5’-3’) | USAGE |
|---|---|---|
| HADELLA1_FOR_HRM | AACAAGACGCCGGAGATG | • DELPA mutation *HaDELLA1* |
| HADELLA1-REV_HRM | TGTCGGATGACTTGACTTTGT | • DELPA mutation *HaDELLA1* |
| SNE171.7_HRM_FOR-3 | TGGCGCTTGGTGGGTACC | • SNP SNE171.7 *HaSNEEZY2* |
| SNE171.7_HRM_REV-3 | TCCGTATCACCACCGTTGCTC | • SNP SNE171.7 *HaSNEEZY2* |
| DEL801.17_HRM_FOR | CGGCGAAGAAAGTTAAACCTAATTG | • SNP DEL801.17 *HaDELLA2* |
| DEL801.17_HRM_REV | ATGCTAGGGTTAGGGTTTGC | • SNP DEL801.17 *HaDELLA2* |
| DEL091.8_HRM_FOR | TTACGCGATGATGAAGTTGTG | • SNP DEL091.8 *HaDELA-Like2* |
| DEL091.8_HRM_REV | CGAGCCAACAACTGATGC | • SNP DEL091.8 *HaDELA-Like2* |
| DEL091.9_HRM_REV-1 | CCACAACTTCATCATCGCGT | • SNP DEL091.9 *HaDELA-Like2* |
| DEL091.9_HRM_FOR-2 | CGGGTTATTGCCGAGAGTTTAG | • SNP DEL091.9 *HaDELA-Like2* |

**Supplementary Table A 3:** Primers for SSR analysis (Tang *et al.* 2002; Chapman *et al*., 2008; Mandel *et al*., 2011)

| LG | LOCUS | PREVIOUS ALIAS | LENGTH (bp) | FORWARD (5’-3’) | REVERSE (5’-3’) |
|---|---|---|---|---|---|
| **1** | ORS728 | - | 364 | CTCCATAGCAACCACCTGAAA | CCAAACTCTGAATGATACTTGTGAC |
| **1** | ORS822 | - | 160 | CAATGCCATCTGTCATCAGCTAC | AAACAAACCTTTGGACGAAACTC |
| **2** | c4289 | HT0572 | 301 | CACGCCATATGAAAGCAACTCT | TCATGGATGTTCATCACCAGAC |
| **2** | E28P08 | HT0761 | 128 | GGTGGGTGTTTGATTTTGTGTG | TCTCCTCTCTCCCTTTGTCTGC |
| **3** | c0306 | HT0292 | 324 | ACTGTCAACACCTCCTTCGACT | GGCTTACACTTCTCTCCATCTCAA |
| **3** | E11N15 | HT0734 | 298 | GTTTCGCAGCTCTAGCATTGA | CCCCCTACAAGGCAACAAAATA |
| **4** | c1628 | HT0375 | 430 | GCTGAAACGGGTCAATAAAGTC | TGAAGAAATGCTTCCAATCTGA |
| **4** | ORS785 | - | 180 | CAAAATACCCAGGTCAAAGCA | CCTAGCTTATGGGACGTATGGA |
| **5** | ORS547 | - | 180 | TTGTCTTCATCTGCGTGTGA | TTGCTGTTGTTGATCGGTGT |
| **5** | c2443 | HT0440 | 247 | GAAGTTGGGAGGGTTGTTCAAG | CCTCCTGTTGGAACACCAAAT |
| **6** | c3464 | HT1034 | 250 | TGTGCAGCGACGACTATAAAGA | CGTCAAACACAAATACTCCAACAA |
| **6** | ORS1265 | - | 180 | GATGTTGATGTTGGTGAAGTTGC | CTCCGTCACCTTAAGCACTTGTA |
| **7** | c3258 | HT0520 | 198 | AATTAGAAGGCTATGGCACAACA | CCTTATGGCCACCACATTACAT |

| | | | | | |
|---|---|---|---|---|---|
| **7** | c3797 | HT0545 | 331 | CATTGAGGACGAGAAGCCAGT | GTTCCGTACCCTGTTTGAGCTT |
| **8** | ORS1161 | - | 236 | CAACTACGTCACGATACTCGCC | GGAGCTGAAGCTGAAGACAAATC |
| **8** | c3240 | HT0519 | 273 | TTTCGTGACCGAGAAAGGTAT | TGTGGCATACATAGAAATGATCTAA |
| **9** | c2104 | HT1014 | 171 | TGGTCCCAACACTACTGATAAGG | TCAAAGGGATTCGTGAAAGTAGTT |
| **9** | G16E04 | HT0834 | 383 | CTCAGGTGAACGGGATCCTTAT | CGGATTCGATTTCTTGCTTAGA |
| **10** | c1185 | HT0347 | 277 | GGGCTATGGTGCGAATGTAGG | GCCTGTCAAATGTCCTTGTTGAT |
| **10** | ORS878 | - | 214 | TGCAAGGTATCCATATTCCACAA | TATACGCACCGGAAAGAAAGTC |
| **11** | c2293 | HT0426 | 329 | AACCGTAAATGAAATCGGTGTG | GAGGGCAAAGTTGGGATACTCT |
| **11** | c5783 | - | 140 | GCCATCACAACATCAAATGG | AAGCTTGCACGTCCATACAC |
| **12** | F7O09 | HT0808 | 289 | TTATGGAATGGAGTGGGAGTTG | TTGTTGGTTGATGGGATCTTGT |
| **12** | ORS778 | - | 400 | CAACCAATCAATCCCACAAA | TGTTCACGCTTACACACATAATTG |
| **13** | ORS1030 | - | 430 | TGATGTAGTTAAGGAAGTTGTG | CGATCAATTTATATGACCGAATTACC |
| **13** | c1731 | HT0382 | 377 | GAAGTCTGCTTTGGTGTTGGTC | ATGGCTCTCTCATTTCCACTTG |
| **14** | B14H20 | HT0621 | 315 | GACCGAATAGGTTTCAACGATAA | TTGCCTCTGCTCTCCTCTTTC |
| **14** | c0737 | HT0319 | 274 | CAACTACCCATCACTGGCAAAT | ATCACCTCCAAACATCACAAGG |
| **15** | A11G17 | HT0586 | 312 | TGAACTCTTGTGTTGGCATCT | AAATGTGGATTTATGTATCTCAGTAA |
| **15** | c2518 | HT1024 | 257 | AAGCAGGTTGCATGAAGAGAAG | GTCGAAACGGGTCAGGTTGTAT |
| **16** | c2070 | - | 260 | GGGTAATGCAAAGTACTAAGATGTG | GCATCATCCAACAAACTAGAAGG |
| **16** | E10D18 | HT0723 | 325 | TCAAGCAATCAGACACCACATC | TGAACACAACCAAGAAATCCAA |
| **17** | c1779 | HT0998 | 383 | CATGTCCCGATCAAAGAGTTGT | CCATATCCTGGTTGTTGTGGAG |
| **17** | I8D12 | HT0941 | 125 | CTGAGTTTCGTGTACCATTTCTATTG | ACACCAATCAGTGGGTTTCATC |

**Supplementary Table A 4:** Field data of the large association panel of 2017 in Germany (Av. = average; PH = plant height; STABW.N = standard deviation)

| Origin | PI | Common name | Av. PH (cm), n = 3 | STABW. N | Petiole Angle (°) | | | | | | Av. petiole angle | STABW. N |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | pl 1 up R | pl 1 up L | pl 2 up R | pl 2 up L | pl 3 up R | pl 3 up L | | |
| **Benary** | | Big Smile | 61 | 5.2 | 43 | 40 | 43 | 44 | 42 | 42 | 42.3 | 1.2 |
| **Benary** | | Musicbox | 90 | 8.2 | 31 | 27 | 27 | 34 | 38 | 40 | 32.8 | 5.0 |
| **Benary** | | Pacino Cola | 56 | 4.2 | 31 | 47 | 44 | 24 | 14 | 29 | 31.5 | 11.3 |
| **Benary** | | Solita | 60 | 0.5 | 38 | 37 | 44 | 43 | 43 | 46 | 41.8 | 3.2 |
| **Benary** | | Sunspot | 69 | 5.7 | 34 | 32 | 27 | 29 | 35 | 29 | 31.0 | 2.9 |
| **Canada** | CN 36719 | 54-3 | 88 | 3.3 | 46 | 47 | 58 | 19 | 58 | 45 | 45.5 | 13.0 |
| **Canada** | CN 42283 | Armavirsky 3497 | 128 | 7.8 | 36 | 40 | 42 | 43 | 39 | 28 | 38.0 | 5.0 |
| **Canada** | CN 42282 | B-7422-1 | 121 | 6.2 | 61 | 46 | 49 | 58 | 51 | 45 | 51.7 | 5.9 |
| **Canada** | CN 42326 | C.14.2.3 | 153 | 6.0 | 33 | 38 | 48 | 45 | 51 | 50 | 44.2 | 6.6 |
| **Canada** | CN 35798 | Cakinskij 268 | 130 | 2.8 | 63 | 55 | 73 | 65 | 69 | 66 | 65.2 | 5.6 |
| **Canada** | CN 33963 | Cakinskij 269 | 150 | 2.2 | 58 | 46 | 49 | 47 | 44 | 42 | 47.7 | 5.1 |
| **Canada** | CN 32252 | CANP 3 | 107 | 4.8 | 50 | 53 | 43 | 75 | 41 | 46 | 51.3 | 11.3 |
| **Canada** | CN 42285 | Chernianka Reselect | 105 | 14.9 | 47 | 54 | 45 | 37 | 40 | 29 | 42.0 | 7.9 |
| **Canada** | CN 30587 | Ckalovskij Gigant | 186 | 4.5 | 24 | 31 | 62 | 46 | 39 | 40 | 40.3 | 12.0 |
| **Canada** | CN 32249 | Clairsol | 109 | 4.6 | 64 | 57 | 52 | 70 | 59 | 54 | 59.3 | 6.1 |
| **Canada** | CN 36523 | CM1 | 119 | 5.4 | 61 | 27 | 42 | 32 | 47 | 40 | 41.5 | 10.9 |
| **Canada** | CN 36529 | CM10 | 100 | 0.8 | 46 | 32 | 77 | 66 | 62 | 60 | 57.2 | 14.5 |
| **Canada** | CN 36594 | CM104 | 97 | 2.2 | 34 | 53 | 36 | 48 | 49 | 52 | 45.3 | 7.5 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Canada** | CN 36595 | CM105 | 67 | 3.7 | 44 | 40 | 25 | 24 | 41 | 45 | 36.5 | 8.7 |
| **Canada** | CN 36530 | CM11 | 86 | 2.9 | 52 | 44 | 50 | 56 | 41 | 42 | 47.5 | 5.5 |
| **Canada** | CN 36598 | CM110 | 103 | 1.2 | 53 | 65 | 58 | 52 | 61 | 64 | 58.8 | 5.0 |
| **Canada** | CN 36600 | CM118 | 148 | 2.6 | 55 | 52 | 57 | 68 | 53 | 71 | 59.3 | 7.4 |
| **Canada** | CN 36601 | CM119 | 156 | 2.2 | 38 | 47 | 30 | 43 | 26 | 30 | 35.7 | 7.6 |
| **Canada** | CN 36613 | CM140 | 149 | 2.6 | 29 | 52 | 60 | 58 | 50 | 55 | 50.7 | 10.3 |
| **Canada** | CN 36628 | CM188 | 154 | 1.4 | 43 | 57 | 59 | 50 | 48 | 53 | 51.7 | 5.4 |
| **Canada** | CN 36630 | CM196 | 108 | 4.1 | 44 | 45 | 63 | 40 | 39 | 59 | 48.3 | 9.3 |
| **Canada** | CN 36642 | CM227 | 87 | 6.8 | 43 | 48 | 55 | 43 | 55 | 50 | 49.0 | 4.9 |
| **Canada** | CN 36647 | CM248 | 116 | 1.2 | 42 | 55 | 48 | 50 | 49 | 48 | 48.7 | 3.8 |
| **Canada** | CN 36654 | CM259 | 98 | 4.1 | 35 | 43 | 34 | 36 | 38 | 33 | 36.5 | 3.3 |
| **Canada** | CN 36665 | CM275 | 114 | 5.9 | 48 | 59 | 58 | 50 | 61 | 42 | 53.0 | 6.8 |
| **Canada** | CN 36666 | CM276 | 141 | 7.3 | 43 | 30 | 35 | 36 | 45 | 41 | 38.3 | 5.2 |
| **Canada** | CN 36537 | CM28 | 116 | 0.5 | 60 | 63 | 46 | 56 | 71 | 58 | 59.0 | 7.5 |
| **Canada** | CN 36538 | CM29 | 102 | 2.5 | 33 | 38 | 41 | 30 | 40 | 31 | 35.5 | 4.3 |
| **Canada** | CN 36671 | CM291 | 136 | 7.4 | 41 | 51 | 58 | 55 | 47 | 44 | 49.3 | 6.0 |
| **Canada** | CN 36540 | CM31 | 108 | 4.2 | 54 | 56 | 44 | 42 | 46 | 40 | 47.0 | 6.0 |
| **Canada** | CN 36154 | CM338 X CM469DMR | 148 | 5.7 | 48 | 42 | 50 | 58 | 57 | 50 | 50.8 | 5.4 |
| **Canada** | CN 36681 | CM348 | 123 | 3.1 | 70 | 33 | 58 | 61 | 57 | 50 | 54.8 | 11.4 |
| **Canada** | CN 36683 | CM352 | 143 | 4.5 | 55 | 49 | 70 | 62 | 56 | 80 | 62.0 | 10.3 |
| **Canada** | CN 36155 | CM400 X CM469DMR | 173 | 5.9 | 52 | 59 | 53 | 50 | 47 | 44 | 50.8 | 4.7 |
| **Canada** | CN 36732 | CM447RF | 126 | 3.6 | 39 | 28 | 23 | 26 | 49 | 34 | 33.2 | 8.8 |
| **Canada** | CN 36553 | CM50 | 94 | 3.6 | 46 | 48 | 40 | 30 | 44 | 41 | 41.5 | 5.8 |
| **Canada** | CN 37369 | CM526 | 148 | 10.4 | 66 | 57 | 63 | 61 | 72 | 63 | 63.7 | 4.6 |
| **Canada** | CN 36734 | CM533RF | 151 | 9.9 | 31 | 47 | 44 | 49 | 44 | 38 | 42.2 | 6.0 |
| **Canada** | CN 36696 | CM561 | 151 | 6.6 | 54 | 47 | 53 | 44 | 63 | 55 | 52.7 | 6.1 |
| **Canada** | CN 36702 | CM568 | 136 | 1.4 | 45 | 44 | 67 | 54 | 54 | 46 | 51.7 | 8.0 |
| **Canada** | CN 45043 | CM604 | 110 | 4.0 | 56 | 40 | 40 | 46 | 40 | 41 | 43.8 | 5.8 |
| **Canada** | CN 45050 | CM611 | 95 | 7.0 | 36 | 40 | 38 | 40 | 54 | 46 | 42.3 | 6.0 |
| **Canada** | CN 36562 | CM63 | 143 | 5.3 | 36 | 57 | 69 | 52 | 61 | 54 | 54.8 | 10.1 |
| **Canada** | CN 36144 | CMH 101 | 146 | 7.9 | 54 | 59 | 66 | 68 | 60 | 59 | 61.0 | 4.7 |
| **Canada** | CN 42251 | CMS 2 CM 28 | 144 | 9.9 | 28 | 46 | 57 | 41 | 35 | 41 | 41.3 | 9.0 |
| **Canada** | CN 33282 | Commander | 152 | 3.3 | 47 | 58 | 56 | 48 | 56 | 57 | 53.7 | 4.4 |
| **Canada** | CN 32247 | Flambeau | 123 | 15.7 | 28 | 50 | 46 | 58 | 27 | 38 | 41.2 | 11.3 |
| **Canada** | CN 42255 | H1 | 159 | 6.6 | 31 | 26 | 23 | 33 | 26 | 37 | 29.3 | 4.8 |
| **Canada** | CN 35799 | Harkovskij 100 | 160 | 5.3 | 46 | 50 | 39 | 49 | 50 | 60 | 49.0 | 6.2 |
| **Canada** | CN 42276 | Hybrid 100. F2 | 152 | 6.9 | 27 | 37 | 28 | 27 | 19 | 34 | 28.7 | 5.7 |
| **Canada** | CN 42277 | Hybrid 150 | 148 | 1.6 | 46 | 52 | 49 | 38 | 41 | 48 | 45.7 | 4.8 |
| **Canada** | CN 36181 | IH-10 | 150 | 10.6 | 44 | 51 | 51 | 30 | 44 | 35 | 42.5 | 7.8 |
| **Canada** | CN 36180 | Iregi Kozepkorai Csikos | 114 | 3.3 | 41 | 55 | 59 | 38 | 47 | 38 | 46.3 | 8.2 |
| **Canada** | CN 33290 | Issanka | 147 | 9.2 | 48 | 32 | 55 | 61 | 48 | 50 | 49.0 | 8.9 |
| **Canada** | CN 33280 | Krasnodarets | 154 | 6.2 | 50 | 64 | 57 | 52 | 48 | 56 | 54.5 | 5.3 |
| **Canada** | CN 30594 | Kustanajskij 91 | 134 | 4.1 | 40 | 36 | 51 | 56 | 41 | 58 | 47.0 | 8.4 |
| **Canada** | CN 32246 | Marianne | 129 | 2.4 | 29 | 45 | 26 | 43 | 64 | 66 | 45.5 | 15.4 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Canada** | CN 43612 | MRS 30 | 152 | 3.4 | 62 | 60 | 70 | 63 | 48 | 49 | 58.7 | 7.8 |
| **Canada** | CN 37441 | NS-49 | 110 | 5.2 | 50 | 54 | 47 | 51 | 59 | 47 | 51.3 | 4.2 |
| **Canada** | CN 33283 | Outlook | 107 | 6.5 | 63 | 49 | 61 | 48 | 63 | 67 | 58.5 | 7.3 |
| **Canada** | CN 43751 | P266 | 134 | 3.8 | 44 | 32 | 49 | 53 | 42 | 36 | 42.7 | 7.2 |
| **Canada** | CN 43752 | P558 | 151 | 7.8 | 55 | 53 | 62 | 47 | 60 | 52 | 54.8 | 5.0 |
| **Canada** | CN 32626 | P-9 | 111 | 2.9 | 27 | 42 | 45 | 50 | 39 | 47 | 41.7 | 7.4 |
| **Canada** | CN 42228 | Pehuen | 131 | 6.8 | 38 | 47 | 55 | 38 | 55 | 46 | 46.5 | 6.9 |
| **Canada** | CN 42229 | PGR 15376 | 134 | 1.6 | 44 | 47 | 42 | 36 | 54 | 45 | 44.7 | 5.4 |
| **Canada** | CN 42244 | PGR 15391 | 137 | 4.3 | 58 | 59 | 55 | 56 | 61 | 60 | 58.2 | 2.1 |
| **Canada** | CN 31834 | PGR 3139 | 176 | 4.0 | 63 | 45 | 34 | 30 | 44 | 50 | 44.3 | 10.7 |
| **Canada** | CN 32627 | Podarok | 134 | 4.1 | 30 | 46 | 54 | 55 | 60 | 53 | 49.7 | 9.7 |
| **Canada** | CN 32250 | Remil | 126 | 5.7 | 47 | 46 | 50 | 57 | 45 | 40 | 47.5 | 5.2 |
| **Canada** | CN 42267 | RHA 282 | 131 | 6.6 | 57 | 67 | 63 | 67 | 73 | 30 | 59.5 | 14.0 |
| **Canada** | CN 29443 | Saliut | 170 | 2.5 | 58 | 57 | 56 | 55 | 64 | 63 | 58.8 | 3.4 |
| **Canada** | CN 35597 | Sunworth | 109 | 5.7 | 49 | 43 | 48 | 45 | 44 | 48 | 46.2 | 2.3 |
| **Canada** | CN 42243 | T66006-2-1-31-14-2-Nd1 | 120 | 7.4 | 48 | 62 | 40 | 44 | 44 | 50 | 48.0 | 7.0 |
| **Canada** | CN 39665 | Tombovskij Skorospenij | 132 | 12.2 | 43 | 52 | 45 | 32 | 58 | 53 | 47.2 | 8.4 |
| **Canada** | CN 42290 | VIR 110 | 133 | 4.6 | 28 | 44 | 53 | 36 | 48 | 51 | 43.3 | 8.8 |
| **Canada** | CN 42293 | VIR 113 | 125 | 4.5 | 36 | 54 | 52 | 46 | 34 | 43 | 44.2 | 7.4 |
| **Canada** | CN 42296 | VIR 117 | 149 | 3.8 | 50 | 39 | 40 | 45 | 59 | 38 | 45.2 | 7.4 |
| **Canada** | CN 30351 | VNIIMK 1646 | 129 | 17.3 | 43 | 40 | 52 | 45 | 63 | 42 | 47.5 | 7.9 |
| **Canada** | CN 42329 | W-177-8 | 152 | 8.2 | 34 | 35 | 39 | 33 | 35 | 56 | 38.7 | 8.0 |
| **USDA** | PI 650530 | 371-3 S | 116 | 8.3 | 42 | 39 | 49 | 44 | 46 | 40 | 43.3 | 3.4 |
| **USDA** | PI 650438 | Advance | 129 | 2.1 | 56 | 48 | 42 | 35 | 34 | 41 | 42.7 | 7.6 |
| **USDA** | PI 221441 | AFTAB-PARAST | 174 | 6.7 | 49 | 50 | 46 | 47 | 38 | 57 | 47.8 | 5.6 |
| **USDA** | PI 380576 | ARGE PEHUEN | 186 | 5.6 | 38 | 34 | 29 | 43 | 29 | 38 | 35.2 | 5.1 |
| **USDA** | PI 650649 | Arrowhead | 146 | 11.1 | 43 | 57 | 59 | 50 | 48 | 53 | 51.7 | 5.4 |
| **USDA** | PI 650415 | B-7422 | 132 | 15.2 | 52 | 44 | 41 | 46 | 42 | 38 | 43.8 | 4.4 |
| **USDA** | PI 617026 | BR1 | 136 | 9.6 | 56 | 46 | 43 | 52 | 60 | 65 | 53.7 | 7.6 |
| **USDA** | PI 480472 | CCA82-2 | 163 | 20.5 | 46 | 37 | 38 | 51 | 44 | 47 | 43.8 | 4.9 |
| **USDA** | PI 431542 | D-75-10 | 150 | 4.2 | 39 | 49 | 42 | 43 | 28 | 47 | 41.3 | 6.8 |
| **USDA** | PI 431538 | D-75-4 | 129 | 7.1 | 38 | 68 | 51 | 41 | 63 | 49 | 51.7 | 10.8 |
| **USDA** | PI 487194 | Egnazia | 151 | 8.5 | 30 | 36 | 30 | 33 | 33 | 46 | 34.7 | 5.5 |
| **USDA** | PI 287230 | ENISEJ | 139 | 4.5 | 43 | 48 | 57 | 47 | 47 | 49 | 48.5 | 4.2 |
| **USDA** | PI 432519 | GN 0778 | 102 | 3.3 | 45 | 41 | 52 | 49 | 48 | 33 | 44.7 | 6.2 |
| **USDA** | PI 175723 | GONONDU | 207 | 4.3 | 41 | 44 | 59 | 66 | 47 | 43 | 50.0 | 9.2 |
| **USDA** | PI 378894 | GUAYACAN INTA | 212 | 15.4 | 25 | 35 | 46 | 41 | 41 | 31 | 36.5 | 7.0 |
| **USDA** | PI 650472 | HS 61 | 160 | 10.3 | 66 | 63 | 54 | 48 | 55 | 59 | 57.5 | 6.0 |
| **USDA** | PI 650781 | Kosim | 187 | 3.4 | 45 | 59 | 56 | 47 | 46 | 52 | 50.8 | 5.3 |
| **USDA** | PI 496265 | Liao 2 | 185 | 2.9 | 59 | 50 | 35 | 49 | 30 | 39 | 43.7 | 9.9 |
| **USDA** | PI 331176 | MANFREDI INTA (3-WAY X)11 | 175 | 12.6 | 65 | 44 | 39 | 34 | 48 | 37 | 44.5 | 10.2 |
| **USDA** | PI 664198 | ND-NONOIL M2 | 117 | 8.2 | 48 | 47 | 46 | 40 | 52 | 41 | 45.7 | 4.1 |
| **USDA** | PI 221693 | No. 2 | 166 | 4.2 | 55 | 64 | 50 | 40 | 52 | 57 | 53.0 | 7.3 |
| **USDA** | PI 289626 | No. 5 | 124 | 6.8 | 42 | 59 | 46 | 54 | 49 | 54 | 50.7 | 5.6 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **USDA** | PI 251990 | No. K1879 | 157 | 6.4 | 48 | 46 | 65 | 52 | 58 | 55 | 54.0 | 6.4 |
| **USDA** | PI 431558 | NS-B-16-63/1 | 145 | 6.6 | 22 | 25 | 9 | 16 | 27 | 39 | 23.0 | 9.3 |
| **USDA** | PI 505839 | Odesskij 113 | 120 | 3.6 | 57 | 58 | 45 | 48 | 48 | 44 | 50.0 | 5.5 |
| **USDA** | PI 483077 | Pervenets | 130 | 6.3 | 44 | 55 | 46 | 52 | 51 | 53 | 50.2 | 3.9 |
| **USDA** | PI 213175 | PI 213175 | 160 | 2.8 | 46 | 49 | 33 | 39 | 48 | 42 | 42.8 | 5.6 |
| **USDA** | PI 596750 | Rf TUB-346 | 127 | 2.2 | 52 | 50 | 55 | 64 | 58 | 56 | 55.8 | 4.5 |
| **USDA** | PI 650497 | ROMSUN V3355 | 72 | 7.0 | 29 | 30 | 37 | 39 | 30 | 38 | 33.8 | 4.2 |
| **USDA** | PI 369360 | SENECA | 207 | 18.7 | 33 | 47 | 31 | 35 | 44 | 36 | 37.7 | 5.8 |
| **USDA** | PI 650731 | Stepnyak | 145 | 11.6 | 50 | 57 | 53 | 46 | 58 | 47 | 51.8 | 4.6 |
| **USDA** | PI 343798 | TCHERNIANKA SELECT W-17 | 149 | 6.3 | 29 | 48 | 70 | 60 | 58 | 77 | 57.0 | 15.5 |
| **USDA** | PI 664212 | UGA-SAM1-002 | 154 | 8.0 | 45 | 42 | 55 | 33 | 33 | 39 | 41.2 | 7.6 |
| **USDA** | PI 664232 | UGA-SAM1-003 | 112 | 4.1 | 38 | 42 | 30 | 39 | 38 | 50 | 39.5 | 5.9 |
| **USDA** | PI 509061 | UGA-SAM1-004 | 161 | 0.5 | 25 | 28 | 41 | 37 | 39 | 33 | 33.8 | 5.8 |
| **USDA** | PI 509062 | UGA-SAM1-005 | 150 | 5.7 | 49 | 51 | 51 | 54 | 49 | 43 | 49.5 | 3.4 |
| **USDA** | PI 560145 | UGA-SAM1-010 | 129 | 8.7 | 41 | 40 | 31 | 33 | 26 | 45 | 36.0 | 6.5 |
| **USDA** | PI 561921 | UGA-SAM1-012 | 65 | 2.1 | 56 | 54 | 66 | 57 | 67 | 58 | 59.7 | 5.0 |
| **USDA** | PI 578009 | UGA-SAM1-014 | 157 | 12.0 | 77 | 73 | 57 | 65 | 52 | 40 | 60.7 | 12.6 |
| **USDA** | PI 578010 | UGA-SAM1-015 | 123 | 1.2 | 57 | 52 | 64 | 51 | 52 | 51 | 54.5 | 4.7 |
| **USDA** | PI 578011 | UGA-SAM1-016 | 158 | 11.3 | 41 | 37 | 40 | 39 | 42 | 46 | 40.8 | 2.8 |
| **USDA** | PI 578873 | UGA-SAM1-018 | 145 | 12.2 | 44 | 61 | 46 | 50 | 48 | 56 | 50.8 | 5.9 |
| **USDA** | PI 597367 | UGA-SAM1-019 | 99 | 6.5 | 64 | 58 | 76 | 63 | 63 | 62 | 64.3 | 5.6 |
| **USDA** | PI 597373 | UGA-SAM1-022 | 124 | 0.9 | 24 | 53 | 38 | 43 | 38 | 28 | 37.3 | 9.5 |
| **USDA** | | UGA-SAM1-023 | 142 | 5.4 | 38 | 56 | 40 | 53 | 40 | 61 | 48.0 | 9.0 |
| **USDA** | PI 599758 | UGA-SAM1-024 | 128 | 4.6 | 34 | 34 | 24 | 45 | 39 | 38 | 35.7 | 6.4 |
| **USDA** | PI 599766 | UGA-SAM1-025 | 112 | 5.0 | 56 | 55 | 55 | 52 | 54 | 58 | 55.0 | 1.8 |
| **USDA** | PI 599775 | UGA-SAM1-026 | 128 | 2.8 | 36 | 32 | 38 | 40 | 40 | 45 | 38.5 | 4.0 |
| **USDA** | | UGA-SAM1-027 | 142 | 4.1 | 51 | 61 | 51 | 61 | 61 | 43 | 54.7 | 6.9 |
| **USDA** | PI 607921 | UGA-SAM1-031 | 110 | 3.5 | 45 | 47 | 48 | 48 | 57 | 45 | 48.3 | 4.1 |
| **USDA** | PI 607923 | UGA-SAM1-032 | 121 | 3.8 | 24 | 48 | 35 | 42 | 37 | 20 | 34.3 | 9.7 |
| **USDA** | PI 650575 | UGA-SAM1-035 | 103 | 1.9 | 45 | 49 | 40 | 8 | 48 | 47 | 39.5 | 14.4 |
| **USDA** | | UGA-SAM1-036 | 122 | 2.2 | 52 | 44 | 60 | 71 | 42 | 61 | 55.0 | 10.1 |
| **USDA** | PI 650582 | UGA-SAM1-037 | 134 | 8.1 | 30 | 43 | 37 | 33 | 43 | 21 | 34.5 | 7.7 |
| **USDA** | PI 650612 | UGA-SAM1-038 | 121 | 7.9 | 40 | 38 | 46 | 40 | 48 | 34 | 41.0 | 4.7 |
| **USDA** | PI 509060 | UGA-SAM1-039 | 164 | 3.7 | 46 | 37 | 20 | 17 | 31 | 24 | 29.2 | 10.1 |
| **USDA** | PI 534656 | UGA-SAM1-040 | 107 | 2.9 | 23 | 39 | 39 | 34 | 50 | 23 | 34.7 | 9.5 |
| **USDA** | PI 543746 | UGA-SAM1-041 | 138 | 1.9 | 37 | 50 | 48 | 35 | 51 | 48 | 44.8 | 6.4 |
| **USDA** | PI 599768 | UGA-SAM1-042 | 97 | 2.2 | 39 | 38 | 37 | 39 | 40 | 42 | 39.2 | 1.6 |
| **USDA** | PI 664233 | UGA-SAM1-045 | 143 | 9.2 | 42 | 39 | 54 | 60 | 31 | 53 | 46.5 | 10.0 |
| **USDA** | | UGA-SAM1-046 | 145 | 5.2 | 11 | 60 | 43 | 47 | 55 | 58 | 45.7 | 16.6 |
| **USDA** | PI 642771 | UGA-SAM1-047 | 176 | 5.0 | 28 | 17 | 36 | 43 | 50 | 35 | 34.8 | 10.5 |
| **USDA** | PI 642774 | UGA-SAM1-049 | 149 | 2.8 | 42 | 51 | 42 | 44 | 40 | 49 | 44.7 | 4.0 |
| **USDA** | PI 642775 | UGA-SAM1-050 | 119 | 1.2 | 71 | 54 | 58 | 64 | 47 | 57 | 58.5 | 7.5 |
| **USDA** | PI 340790 | UGA-SAM1-051 | 186 | 6.8 | 40 | 59 | 51 | 59 | 28 | 42 | 46.5 | 11.1 |
| **USDA** | | UGA-SAM1-052 | 103 | 2.5 | 61 | 54 | 58 | 59 | 64 | 59 | 59.2 | 3.0 |

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| **USDA** | PI 642777 | UGA-SAM1-053 | 146 | 0.8 | 38 | 63 | 53 | 51 | 47 | 44 | 49.3 | 7.8 |
| **USDA** | PI 655014 | UGA-SAM1-054 | 129 | 1.2 | 46 | 43 | 64 | 55 | 35 | 43 | 47.7 | 9.4 |
| **USDA** | | UGA-SAM1-055 | 101 | 3.3 | 49 | 55 | 60 | 55 | 50 | 59 | 54.7 | 4.1 |
| **USDA** | PI 664200 | UGA-SAM1-056 | 140 | 4.2 | 51 | 53 | 57 | 53 | 50 | 53 | 52.8 | 2.2 |
| **USDA** | PI 664216 | UGA-SAM1-057 | 110 | 2.4 | 58 | 50 | 40 | 37 | 44 | 33 | 43.7 | 8.3 |
| **USDA** | PI 664222 | UGA-SAM1-058 | 132 | 4.0 | 37 | 61 | 41 | 38 | 41 | 53 | 45.2 | 8.8 |
| **USDA** | PI 509059 | UGA-SAM1-059 | 138 | 4.3 | 41 | 44 | 46 | 45 | 46 | 47 | 44.8 | 2.0 |
| **USDA** | | UGA-SAM1-060 | 77 | 0.8 | 57 | 61 | 69 | 57 | 55 | 59 | 59.7 | 4.6 |
| **USDA** | PI 534650 | UGA-SAM1-061 | 142 | 7.3 | 29 | 44 | 26 | 38 | 36 | 32 | 34.2 | 6.0 |
| **USDA** | | UGA-SAM1-061 | 138 | 8.2 | 33 | 36 | 21 | 32 | 30 | 46 | 33.0 | 7.4 |
| **USDA** | | UGA-SAM1-062 | 143 | 6.7 | 30 | 26 | 36 | 31 | 39 | 41 | 33.8 | 5.3 |
| **USDA** | PI 549001 | UGA-SAM1-063 | 120 | 8.5 | 44 | 48 | 43 | 44 | 52 | 56 | 47.8 | 4.8 |
| **USDA** | PI 552931 | UGA-SAM1-065 | 112 | 0.5 | 44 | 51 | 50 | 48 | 38 | 41 | 45.3 | 4.7 |
| **USDA** | PI 552948 | UGA-SAM1-066 | 145 | 9.4 | 45 | 38 | 44 | 49 | 46 | 50 | 45.3 | 3.9 |
| **USDA** | | UGA-SAM1-067 | 59 | 1.7 | 59 | 57 | 60 | 56 | 59 | 61 | 58.7 | 1.7 |
| **USDA** | PI 599753 | UGA-SAM1-068 | 162 | 3.6 | 38 | 40 | 34 | 42 | 22 | 39 | 35.8 | 6.6 |
| **USDA** | PI 639165 | UGA-SAM1-069 | 136 | 3.6 | 38 | 49 | 35 | 42 | 40 | 38 | 40.3 | 4.4 |
| **USDA** | PI 599780 | UGA-SAM1-070 | 122 | 5.8 | 44 | 50 | 39 | 35 | 42 | 43 | 42.2 | 4.6 |
| **USDA** | PI 599781 | UGA-SAM1-071 | 141 | 6.8 | 30 | 51 | 46 | 54 | 39 | 31 | 41.8 | 9.3 |
| **USDA** | PI 599980 | UGA-SAM1-072 | 141 | 1.7 | 55 | 37 | 42 | 57 | 47 | 36 | 45.7 | 8.2 |
| **USDA** | PI 601368 | UGA-SAM1-073 | 119 | 2.9 | 52 | 39 | 47 | 42 | 41 | 56 | 46.2 | 6.1 |
| **USDA** | PI 650588 | UGA-SAM1-074 | 158 | 7.8 | 23 | 43 | 26 | 37 | 38 | 34 | 33.5 | 6.9 |
| **USDA** | | UGA-SAM1-076 | 146 | 6.6 | 58 | 70 | 38 | 51 | 43 | 51 | 51.8 | 10.3 |
| **USDA** | PI 664231 | UGA-SAM1-078 | 47 | 0.9 | 34 | 40 | 30 | 54 | 36 | 36 | 38.3 | 7.6 |
| **USDA** | PI 552933 | UGA-SAM1-080 | 133 | 10.8 | 64 | 48 | 65 | 58 | 62 | 62 | 59.8 | 5.7 |
| **USDA** | | UGA-SAM1-081 | 133 | 9.5 | 32 | 26 | 27 | 39 | 44 | 50 | 36.3 | 8.8 |
| **USDA** | PI 664193 | UGA-SAM1-082 | 135 | 4.9 | 47 | 44 | 54 | 58 | 44 | 42 | 48.2 | 5.8 |
| **USDA** | PI 664169 | UGA-SAM1-084 | 187 | 12.7 | 36 | 55 | 33 | 64 | 34 | 39 | 43.5 | 11.8 |
| **USDA** | PI 664175 | UGA-SAM1-086 | 189 | 1.2 | 44 | 54 | 46 | 43 | 38 | 57 | 47.0 | 6.5 |
| **USDA** | | UGA-SAM1-086 | 162 | 6.4 | 48 | 55 | 44 | 54 | 50 | 52 | 50.5 | 3.7 |
| **USDA** | PI 664177 | UGA-SAM1-087 | 164 | 6.6 | 24 | 29 | 38 | 44 | 47 | 41 | 37.2 | 8.2 |
| **USDA** | PI 664190 | UGA-SAM1-089 | 145 | 6.5 | 26 | 25 | 26 | 40 | 17 | 33 | 27.8 | 7.2 |
| **USDA** | | UGA-SAM1-090 | 131 | 5.0 | 28 | 26 | 17 | 21 | 38 | 46 | 29.3 | 9.9 |
| **USDA** | | UGA-SAM1-091 | 109 | 4.2 | 39 | 40 | 43 | 46 | 41 | 36 | 40.8 | 3.1 |
| **USDA** | | UGA-SAM1-092 | 140 | 5.6 | 44 | 58 | 59 | 61 | 45 | 50 | 52.8 | 6.8 |
| **USDA** | | UGA-SAM1-093 | 164 | 9.0 | 61 | 57 | 62 | 55 | 57 | 66 | 59.7 | 3.7 |
| **USDA** | | UGA-SAM1-095 | 115 | 3.3 | 37 | 43 | 47 | 43 | 54 | 46 | 45.0 | 5.1 |
| **USDA** | PI 655013 | UGA-SAM1-096 | 128 | 2.9 | 24 | 43 | 36 | 39 | 33 | 32 | 34.5 | 6.0 |
| **USDA** | PI 664199 | UGA-SAM1-097 | 108 | 6.7 | 35 | 42 | 37 | 48 | 35 | 49 | 41.0 | 5.8 |
| **USDA** | | UGA-SAM1-099 | 159 | 10.6 | 33 | 34 | 44 | 61 | 30 | 50 | 42.0 | 10.9 |
| **USDA** | PI 664204 | UGA-SAM1-100 | 104 | 4.0 | 32 | 39 | 31 | 45 | 37 | 34 | 36.3 | 4.7 |
| **USDA** | PI 664205 | UGA-SAM1-101 | 105 | 2.8 | 50 | 65 | 50 | 43 | 46 | 47 | 50.2 | 7.1 |
| **USDA** | PI 664206 | UGA-SAM1-102 | 154 | 6.3 | 40 | 55 | 54 | 46 | 44 | 40 | 46.5 | 6.0 |
| **USDA** | PI 664207 | UGA-SAM1-103 | 135 | 4.1 | 40 | 45 | 53 | 50 | 41 | 34 | 43.8 | 6.4 |
| **USDA** | PI 664211 | UGA-SAM1-104 | 128 | 6.3 | 48 | 30 | 46 | 44 | 44 | 48 | 43.3 | 6.2 |

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| **USDA** | | UGA-SAM1-105 | 142 | 13.1 | 36 | 35 | 35 | 42 | 34 | 33 | 35.8 | 2.9 |
| **USDA** | PI 664215 | UGA-SAM1-106 | 112 | 4.5 | 34 | 36 | 43 | 51 | 43 | 48 | 42.5 | 6.0 |
| **USDA** | PI 664218 | UGA-SAM1-107 | 146 | 7.5 | 50 | 57 | 28 | 43 | 42 | 43 | 43.8 | 8.8 |
| **USDA** | PI 664219 | UGA-SAM1-108 | 85 | 8.1 | 29 | 52 | 41 | 44 | 40 | 48 | 42.3 | 7.2 |
| **USDA** | PI 664221 | UGA-SAM1-109 | 136 | 3.7 | 45 | 51 | 47 | 46 | 64 | 55 | 51.3 | 6.6 |
| **USDA** | | UGA-SAM1-109 | 127 | 11.6 | 37 | 31 | 44 | 42 | 44 | 48 | 41.0 | 5.5 |
| **USDA** | PI 664227 | UGA-SAM1-110 | 101 | 7.4 | 40 | 44 | 39 | 49 | 40 | 49 | 43.5 | 4.2 |
| **USDA** | PI 664228 | UGA-SAM1-111 | 99 | 5.0 | 62 | 55 | 73 | 63 | 48 | 69 | 61.7 | 8.3 |
| **USDA** | PI 664229 | UGA-SAM1-112 | 136 | 5.0 | 45 | 52 | 44 | 23 | 43 | 47 | 42.3 | 9.1 |
| **USDA** | PI 509057 | UGA-SAM1-115 | 152 | 2.4 | 32 | 29 | 30 | 23 | 41 | 43 | 33.0 | 7.0 |
| **USDA** | PI 531074 | UGA-SAM1-118 | 64 | 4.8 | 43 | 48 | 46 | 46 | 42 | 50 | 45.8 | 2.7 |
| **USDA** | PI 531075 | UGA-SAM1-119 | 71 | 0.5 | 37 | 35 | 27 | 38 | 31 | 33 | 33.5 | 3.7 |
| **USDA** | PI 534649 | UGA-SAM1-120 | 112 | 2.6 | 46 | 37 | 32 | 44 | 30 | 35 | 37.3 | 5.9 |
| **USDA** | PI 534653 | UGA-SAM1-121 | 115 | 6.1 | 17 | 25 | 29 | 31 | 22 | 42 | 27.7 | 7.9 |
| **USDA** | PI 548997 | UGA-SAM1-123 | 150 | 11.4 | 46 | 49 | 40 | 44 | 52 | 43 | 45.7 | 3.9 |
| **USDA** | PI 548998 | UGA-SAM1-124 | 134 | 6.7 | 54 | 50 | 53 | 61 | 47 | 60 | 54.2 | 5.0 |
| **USDA** | PI 549003 | UGA-SAM1-125 | 160 | 4.8 | 68 | 59 | 60 | 61 | 66 | 59 | 62.2 | 3.5 |
| **USDA** | PI 549006 | UGA-SAM1-126 | 105 | 6.7 | 67 | 53 | 55 | 67 | 60 | 51 | 58.8 | 6.4 |
| **USDA** | PI 549009 | UGA-SAM1-127 | 127 | 5.6 | 63 | 42 | 52 | 64 | 57 | 50 | 54.7 | 7.7 |
| **USDA** | | UGA-SAM1-131 | 127 | 12.7 | 57 | 45 | 47 | 64 | 42 | 37 | 48.7 | 9.1 |
| **USDA** | PI 552937 | UGA-SAM1-132 | 99 | 2.9 | 60 | 55 | 53 | 52 | 56 | 59 | 55.8 | 2.9 |
| **USDA** | PI 552938 | UGA-SAM1-133 | 122 | 1.7 | 55 | 46 | 42 | 55 | 42 | 45 | 47.5 | 5.5 |
| **USDA** | PI 560141 | UGA-SAM1-136 | 150 | 2.6 | 25 | 38 | 33 | 43 | 25 | 38 | 33.7 | 6.8 |
| **USDA** | PI 552947 | UGA-SAM1-135 | 103 | 2.1 | 49 | 37 | 41 | 45 | 47 | 49 | 44.7 | 4.4 |
| **USDA** | PI 560142 | UGA-SAM1-137 | 170 | 10.3 | 39 | 41 | 35 | 38 | 28 | 37 | 36.3 | 4.1 |
| **USDA** | PI 578874 | UGA-SAM1-138 | 119 | 5.3 | 48 | 58 | 34 | 44 | 37 | 52 | 45.5 | 8.3 |
| **USDA** | PI 597365 | UGA-SAM1-140 | 110 | 4.5 | 45 | 30 | 48 | 40 | 23 | 43 | 38.2 | 8.8 |
| **USDA** | PI 597370 | UGA-SAM1-141 | 122 | 4.0 | 36 | 44 | 56 | 64 | 46 | 57 | 50.5 | 9.4 |
| **USDA** | | UGA-SAM1-142 | 112 | 6.8 | 32 | 29 | 33 | 37 | 37 | 38 | 34.3 | 3.2 |
| **USDA** | | UGA-SAM1-143 | 142 | 4.3 | 51 | 46 | 50 | 59 | 40 | 43 | 48.2 | 6.1 |
| **USDA** | | UGA-SAM1-145 | 138 | 2.5 | 53 | 72 | 43 | 57 | 66 | 61 | 58.7 | 9.3 |
| **USDA** | | UGA-SAM1-146 | 129 | 5.9 | 43 | 36 | 40 | 48 | 37 | 40 | 40.7 | 4.0 |
| **USDA** | PI 599978 | UGA-SAM1-147 | 162 | 2.9 | 64 | 51 | 51 | 69 | 61 | 62 | 59.7 | 6.6 |
| **USDA** | | UGA-SAM1-147 | 139 | 9.0 | 34 | 39 | 52 | 39 | 32 | 56 | 42.0 | 8.9 |
| **USDA** | PI 603987 | UGA-SAM1-148 | 114 | 5.9 | 51 | 63 | 52 | 55 | 60 | 57 | 56.3 | 4.2 |
| **USDA** | PI 607510 | UGA-SAM1-149 | 139 | 3.6 | 63 | 62 | 58 | 48 | 46 | 65 | 57.0 | 7.4 |
| **USDA** | | UGA-SAM1-149 | 129 | 4.5 | 58 | 38 | 44 | 53 | 49 | 39 | 46.8 | 7.2 |
| **USDA** | PI 617098 | UGA-SAM1-151 | 125 | 3.1 | 46 | 42 | 39 | 51 | 51 | 44 | 45.5 | 4.4 |
| **USDA** | | UGA-SAM1-151 | 126 | 7.4 | 42 | 39 | 42 | 39 | 50 | 46 | 43.0 | 3.9 |
| **USDA** | PI 632338 | UGA-SAM1-152 | 145 | 1.7 | 28 | 40 | 34 | 46 | 44 | 52 | 40.7 | 7.9 |
| **USDA** | PI 632342 | UGA-SAM1-153 | 123 | 3.9 | 74 | 57 | 74 | 65 | 60 | 70 | 66.7 | 6.6 |
| **USDA** | PI 633748 | UGA-SAM1-154 | 120 | 4.8 | 45 | 53 | 43 | 47 | 58 | 53 | 49.8 | 5.2 |
| **USDA** | PI 639169 | UGA-SAM1-155 | 123 | 1.2 | 69 | 46 | 53 | 56 | 51 | 44 | 53.2 | 8.2 |
| **USDA** | PI 650570 | UGA-SAM1-156 | 105 | 7.0 | 67 | 53 | 56 | 66 | 68 | 57 | 61.2 | 6.0 |
| **USDA** | PI 650599 | UGA-SAM1-158 | 137 | 1.7 | 26 | 42 | 12 | 42 | 25 | 45 | 32.0 | 11.9 |

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| **USDA** | | UGA-SAM1-160 | 115 | 7.4 | 59 | 50 | 57 | 61 | 40 | 46 | 52.2 | 7.5 |
| **USDA** | PI 597372 | UGA-SAM1-161 | 128 | 3.7 | 33 | 36 | 38 | 40 | 18 | 37 | 33.7 | 7.3 |
| **USDA** | PI 597376 | UGA-SAM1-162 | 130 | 6.3 | 52 | 47 | 36 | 53 | 45 | 34 | 44.5 | 7.3 |
| **USDA** | PI 597377 | UGA-SAM1-163 | 148 | 9.0 | 38 | 46 | 36 | 42 | 33 | 37 | 38.7 | 4.2 |
| **USDA** | PI 597378 | UGA-SAM1-164 | 155 | 9.0 | 54 | 62 | 39 | 51 | 47 | 43 | 49.3 | 7.5 |
| **USDA** | PI 599759 | UGA-SAM1-165 | 125 | 0.5 | 38 | 26 | 35 | 27 | 28 | 30 | 30.7 | 4.4 |
| **USDA** | PI 599763 | UGA-SAM1-166 | 119 | 2.1 | 44 | 41 | 27 | 26 | 36 | 35 | 34.8 | 6.6 |
| **USDA** | PI 599764 | UGA-SAM1-167 | 124 | 4.5 | 39 | 49 | 40 | 39 | 40 | 39 | 41.0 | 3.6 |
| **USDA** | PI 599765 | UGA-SAM1-168 | 128 | 1.2 | 30 | 44 | 22 | 43 | 47 | 38 | 37.3 | 8.7 |
| **USDA** | PI 599767 | UGA-SAM1-169 | 131 | 4.5 | 42 | 51 | 31 | 44 | 37 | 40 | 40.8 | 6.1 |
| **USDA** | PI 599769 | UGA-SAM1-170 | 191 | 12.1 | 53 | 51 | 40 | 34 | 25 | 36 | 39.8 | 9.7 |
| **USDA** | PI 599771 | UGA-SAM1-171 | 115 | 14.8 | 34 | 42 | 44 | 48 | 24 | 40 | 38.7 | 7.8 |
| **USDA** | PI 599772 | UGA-SAM1-172 | 122 | 4.9 | 50 | 55 | 47 | 49 | 53 | 62 | 52.7 | 4.9 |
| **USDA** | PI 599773 | UGA-SAM1-173 | 118 | 4.1 | 43 | 49 | 42 | 53 | 45 | 31 | 43.8 | 6.8 |
| **USDA** | PI 599774 | UGA-SAM1-174 | 109 | 1.6 | 27 | 62 | 35 | 37 | 46 | 58 | 44.2 | 12.5 |
| **USDA** | PI 599776 | UGA-SAM1-175 | 164 | 9.5 | 50 | 56 | 40 | 49 | 42 | 50 | 47.8 | 5.4 |
| **USDA** | PI 599778 | UGA-SAM1-176 | 140 | 9.2 | 51 | 38 | 45 | 39 | 58 | 59 | 48.3 | 8.4 |
| **USDA** | | UGA-SAM1-177 | 116 | 2.9 | 48 | 38 | 39 | 36 | 41 | 48 | 41.7 | 4.7 |
| **USDA** | PI 599786 | UGA-SAM1-179 | 178 | 0.0 | 45 | 62 | 23 | 47 | 56 | 53 | 47.7 | 12.4 |
| **USDA** | PI 599789 | UGA-SAM1-181 | 103 | 7.0 | 47 | 38 | 27 | 36 | 38 | 34 | 36.7 | 5.9 |
| **USDA** | PI 599979 | UGA-SAM1-183 | 158 | 0.8 | 32 | 33 | 39 | 38 | 30 | 37 | 34.8 | 3.3 |
| **USDA** | PI 599981 | UGA-SAM1-184 | 141 | 3.4 | 43 | 46 | 29 | 31 | 22 | 42 | 35.5 | 8.7 |
| **USDA** | PI 599984 | UGA-SAM1-185 | 126 | 1.2 | 64 | 73 | 64 | 57 | 52 | 41 | 58.5 | 10.2 |
| **USDA** | PI 600000 | UGA-SAM1-186 | 87 | 3.7 | 48 | 54 | 48 | 58 | 58 | 50 | 52.7 | 4.3 |
| **USDA** | PI 600723 | UGA-SAM1-187 | 123 | 11.9 | 35 | 42 | 34 | 47 | 40 | 48 | 41.0 | 5.4 |
| **USDA** | | UGA-SAM1-188 | 161 | 6.5 | 47 | 53 | 40 | 52 | 52 | 48 | 48.7 | 4.5 |
| **USDA** | | UGA-SAM1-189 | 175 | 15.8 | 39 | 47 | 44 | 21 | 38 | 41 | 38.3 | 8.3 |
| **USDA** | PI 603988 | UGA-SAM1-190 | 116 | 2.2 | 26 | 32 | 49 | 44 | 54 | 53 | 43.0 | 10.6 |
| **USDA** | PI 603989 | UGA-SAM1-191 | 133 | 0.5 | 41 | 45 | 40 | 55 | 23 | 38 | 40.3 | 9.5 |
| **USDA** | PI 603990 | UGA-SAM1-192 | 120 | 8.7 | 50 | 37 | 36 | 62 | 42 | 35 | 43.7 | 9.6 |
| **USDA** | | UGA-SAM1-193 | 111 | 3.9 | 24 | 53 | 41 | 26 | 37 | 43 | 37.3 | 10.0 |
| **USDA** | PI 607508 | UGA-SAM1-195 | 121 | 2.1 | 28 | 40 | 30 | 51 | 25 | 34 | 34.7 | 8.7 |
| **USDA** | | UGA-SAM1-195 | 149 | 10.3 | 34 | 30 | 31 | 41 | 44 | 31 | 35.2 | 5.4 |
| **USDA** | PI 607922 | UGA-SAM1-198 | 104 | 4.5 | 55 | 45 | 50 | 53 | 57 | 60 | 53.3 | 4.9 |
| **USDA** | PI 607925 | UGA-SAM1-199 | 125 | 2.9 | 44 | 44 | 53 | 41 | 34 | 37 | 42.2 | 6.0 |
| **USDA** | PI 607928 | UGA-SAM1-200 | 150 | 0.5 | 53 | 51 | 31 | 42 | 42 | 38 | 42.8 | 7.5 |
| **USDA** | | UGA-SAM1-200 | 150 | 1.2 | 48 | 46 | 42 | 38 | 36 | 35 | 40.8 | 4.9 |
| **USDA** | PI 607929 | UGA-SAM1-201 | 164 | 3.3 | 44 | 49 | 36 | 47 | 50 | 47 | 45.5 | 4.6 |
| **USDA** | | UGA-SAM1-201 | 124 | 6.7 | 37 | 50 | 27 | 42 | 42 | 30 | 38.0 | 7.8 |
| **USDA** | PI 617100 | UGA-SAM1-204 | 127 | 4.2 | 43 | 34 | 45 | 39 | 41 | 47 | 41.5 | 4.2 |
| **USDA** | PI 618725 | UGA-SAM1-205 | 138 | 5.4 | 35 | 34 | 43 | 32 | 37 | 38 | 36.5 | 3.5 |
| **USDA** | PI 618726 | UGA-SAM1-206 | 168 | 13.8 | 29 | 39 | 39 | 38 | 37 | 47 | 38.2 | 5.2 |
| **USDA** | PI 619204 | UGA-SAM1-207 | 124 | 0.8 | 39 | 42 | 43 | 32 | 46 | 41 | 40.5 | 4.3 |
| **USDA** | PI 619206 | UGA-SAM1-208 | 131 | 4.0 | 43 | 55 | 40 | 35 | 38 | 46 | 42.8 | 6.5 |
| **USDA** | | UGA-SAM1-209 | 148 | 3.7 | 44 | 45 | 46 | 65 | 46 | 43 | 48.2 | 7.6 |

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| **USDA** | PI 632340 | UGA-SAM1-210 | 164 | 7.0 | 30 | 26 | 37 | 42 | 26 | 27 | 31.3 | 6.1 |
| **USDA** | PI 632341 | UGA-SAM1-211 | 135 | 2.2 | 50 | 63 | 56 | 56 | 45 | 50 | 53.3 | 5.8 |
| **USDA** | PI 633744 | UGA-SAM1-212 | 104 | 7.8 | 51 | 57 | 38 | 49 | 37 | 58 | 48.3 | 8.3 |
| **USDA** | PI 633745 | UGA-SAM1-213 | 128 | 6.1 | 40 | 48 | 30 | 43 | 38 | 43 | 40.3 | 5.6 |
| **USDA** | PI 639162 | UGA-SAM1-214 | 125 | 3.7 | 47 | 56 | 31 | 44 | 36 | 29 | 40.5 | 9.5 |
| **USDA** | PI 639163 | UGA-SAM1-215 | 130 | 1.6 | 31 | 20 | 24 | 32 | 26 | 33 | 27.7 | 4.7 |
| **USDA** | PI 639164 | UGA-SAM1-216 | 159 | 2.4 | 60 | 59 | 72 | 62 | 33 | 65 | 58.5 | 12.2 |
| **USDA** | PI 639166 | UGA-SAM1-217 | 95 | 7.3 | 30 | 44 | 46 | 47 | 28 | 50 | 40.8 | 8.6 |
| **USDA** | PI 649793 | UGA-SAM1-218 | 129 | 2.4 | 48 | 44 | 28 | 39 | 31 | 43 | 38.8 | 7.2 |
| **USDA** | PI 650358 | UGA-SAM1-219 | 149 | 11.1 | 77 | 67 | 51 | 59 | 57 | 53 | 60.7 | 8.9 |
| **USDA** | PI 650361 | UGA-SAM1-220 | 128 | 5.2 | 67 | 51 | 55 | 41 | 64 | 52 | 55.0 | 8.6 |
| **USDA** | | UGA-SAM1-220 | 133 | 2.6 | 28 | 62 | 52 | 38 | 59 | 53 | 48.7 | 11.9 |
| **USDA** | PI 650571 | UGA-SAM1-221 | 117 | 7.8 | 53 | 42 | 48 | 48 | 36 | 52 | 46.5 | 5.9 |
| **USDA** | PI 650594 | UGA-SAM1-223 | 171 | 2.1 | 54 | 51 | 48 | 34 | 35 | 64 | 47.7 | 10.5 |
| **USDA** | PI 650597 | UGA-SAM1-224 | 121 | 1.7 | 44 | 42 | 50 | 42 | 45 | 47 | 45.0 | 2.8 |
| **USDA** | PI 650603 | UGA-SAM1-225 | 122 | 4.3 | 53 | 40 | 51 | 52 | 41 | 36 | 45.5 | 6.7 |
| **USDA** | | UGA-SAM1-227 | 168 | 3.4 | 15 | 35 | 19 | 39 | 16 | 35 | 26.5 | 10.0 |
| **USDA** | | UGA-SAM1-228 | 152 | 11.8 | 57 | 52 | 53 | 64 | 58 | 41 | 54.2 | 7.1 |
| **USDA** | PI 650842 | UGA-SAM1-229 | 139 | 6.8 | 60 | 50 | 64 | 60 | 52 | 59 | 57.5 | 4.9 |
| **USDA** | PI 664208 | UGA-SAM1-230 | 151 | 7.8 | 27 | 46 | 44 | 41 | 44 | 47 | 41.5 | 6.8 |
| **USDA** | PI 509051 | UGA-SAM1-231 | 148 | 4.6 | 31 | 43 | 49 | 51 | 41 | 36 | 41.8 | 6.9 |
| **USDA** | | UGA-SAM1-231 | 140 | 3.4 | 51 | 50 | 45 | 44 | 37 | 43 | 45.0 | 4.7 |
| **USDA** | PI 534654 | UGA-SAM1-232 | 84 | 2.6 | 30 | 27 | 39 | 27 | 32 | 40 | 32.5 | 5.3 |
| **USDA** | | UGA-SAM1-233 | 46 | 3.7 | 67 | 58 | 46 | 70 | 59 | 58 | 59.7 | 7.7 |
| **USDA** | PI 664202 | UGA-SAM1-237 | 145 | 6.1 | 37 | 39 | 42 | 49 | 39 | 28 | 39.0 | 6.2 |
| **USDA** | | UGA-SAM1-237 | 133 | 6.5 | 38 | 39 | 37 | 43 | 46 | 43 | 41.0 | 3.2 |
| **USDA** | PI 664214 | UGA-SAM1-238 | 124 | 6.2 | 42 | 45 | 40 | 38 | 35 | 24 | 37.3 | 6.7 |
| **USDA** | PI 664220 | UGA-SAM1-239 | 115 | 2.6 | 38 | 50 | 47 | 41 | 39 | 43 | 43.0 | 4.3 |
| **USDA** | | UGA-SAM1-240 | 130 | 3.3 | 45 | 44 | 49 | 48 | 40 | 51 | 46.2 | 3.6 |
| **USDA** | PI 509053 | UGA-SAM1-241 | 112 | 3.1 | 44 | 30 | 31 | 47 | 46 | 37 | 39.2 | 6.9 |
| **USDA** | | UGA-SAM1-241 | 102 | 3.3 | 50 | 38 | 38 | 34 | 47 | 49 | 42.7 | 6.2 |
| **USDA** | PI 509065 | UGA-SAM1-242 | 142 | 3.3 | 44 | 56 | 49 | 44 | 42 | 34 | 44.8 | 6.7 |
| **USDA** | PI 534652 | UGA-SAM1-243 | 61 | 0.0 | 66 | 50 | 65 | 37 | 46 | 70 | 55.7 | 12.1 |
| **USDA** | | UGA-SAM1-243 | 74 | 1.7 | 20 | 26 | 30 | 10 | 24 | 18 | 21.3 | 6.4 |
| **USDA** | PI 534658 | UGA-SAM1-244 | 142 | 2.1 | 29 | 37 | 41 | 37 | 39 | 43 | 37.7 | 4.4 |
| **USDA** | PI 549002 | UGA-SAM1-245 | 120 | 3.6 | 50 | 71 | 42 | 51 | 62 | 43 | 53.2 | 10.3 |
| **USDA** | PI 549014 | UGA-SAM1-246 | 126 | 4.1 | 47 | 49 | 55 | 39 | 34 | 30 | 42.3 | 8.7 |
| **USDA** | PI 552939 | UGA-SAM1-247 | 101 | 7.6 | 39 | 41 | 42 | 43 | 39 | 51 | 42.5 | 4.1 |
| **USDA** | | UGA-SAM1-248 | 94 | 1.7 | 26 | 34 | 50 | 37 | 36 | 47 | 38.3 | 8.1 |
| **USDA** | PI 599762 | UGA-SAM1-250 | 118 | 1.4 | 38 | 46 | 36 | 44 | 47 | 36 | 41.2 | 4.6 |
| **USDA** | | UGA-SAM1-251 | 111 | 6.2 | 31 | 44 | 39 | 52 | 42 | 51 | 43.2 | 7.2 |
| **USDA** | PI 618727 | UGA-SAM1-252 | 152 | 9.4 | 42 | 54 | 41 | 57 | 57 | 46 | 49.5 | 6.8 |
| **USDA** | | UGA-SAM1-253 | 125 | 2.4 | 46 | 41 | 44 | 40 | 54 | 55 | 46.7 | 5.9 |
| **USDA** | | UGA-SAM1-255 | 187 | 12.7 | 51 | 34 | 30 | 40 | 44 | 33 | 38.7 | 7.2 |
| **USDA** | | UGA-SAM1-256 | 165 | 4.8 | 45 | 63 | 50 | 43 | 45 | 54 | 50.0 | 6.9 |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **USDA** | PI 650353 | UGA-SAM1-257 | 178 | 1.7 | 45 | 46 | 44 | 46 | 35 | 31 | 41.2 | 5.9 |
| **USDA** | | UGA-SAM1-258 | 128 | 2.2 | 41 | 47 | 26 | 23 | 36 | 43 | 36.0 | 8.8 |
| **USDA** | | UGA-SAM1-259 | 127 | 5.7 | 41 | 43 | 40 | 52 | 31 | 53 | 43.3 | 7.5 |
| **USDA** | | UGA-SAM1-260 | 145 | 10.2 | 37 | 34 | 33 | 40 | 32 | 48 | 37.3 | 5.5 |
| **USDA** | | UGA-SAM1-262 | 130 | 7.3 | 38 | 33 | 49 | 32 | 46 | 48 | 41.0 | 7.0 |
| **USDA** | | UGA-SAM1-264 | 142 | 4.9 | 55 | 38 | 56 | 47 | 43 | 46 | 47.5 | 6.3 |
| **USDA** | | UGA-SAM1-270 | 97 | 8.2 | 45 | 32 | 51 | 38 | 45 | 57 | 44.7 | 8.1 |
| **USDA** | | UGA-SAM1-273 | 104 | 4.2 | 57 | 53 | 48 | 52 | 43 | 58 | 51.8 | 5.1 |
| **USDA** | | UGA-SAM1-274 | 107 | 9.9 | 32 | 47 | 50 | 31 | 38 | 25 | 37.2 | 8.9 |
| **USDA** | | UGA-SAM1-275 | 154 | 2.5 | 37 | 39 | 33 | 54 | 38 | 41 | 40.3 | 6.6 |
| **USDA** | | UGA-SAM1-276 | 159 | 6.5 | 32 | 21 | 27 | 32 | 20 | 26 | 26.3 | 4.7 |
| **USDA** | | UGA-SAM1-278 | 107 | 7.0 | 68 | 45 | 46 | 64 | 58 | 51 | 55.3 | 8.7 |
| **USDA** | | UGA-SAM1-279 | 137 | 3.6 | 26 | 28 | 42 | 37 | 38 | 44 | 35.8 | 6.7 |
| **USDA** | | UGA-SAM1-287 | 171 | 4.6 | 36 | 38 | 30 | 35 | 37 | 47 | 37.2 | 5.1 |
| **USDA** | | UGA-SAM1-288 | 134 | 11.1 | 56 | 57 | 40 | 46 | 31 | 53 | 47.2 | 9.3 |
| **USDA** | | UGA-SAM1-289 | 168 | 8.2 | 43 | 38 | 35 | 44 | 52 | 39 | 41.8 | 5.5 |
| **USDA** | PI 497247 | VIR 019 | 116 | 2.4 | 55 | 46 | 53 | 54 | 47 | 50 | 50.8 | 3.4 |
| **USDA** | PI 386230 | VIR 847 | 156 | 5.1 | 59 | 63 | 57 | 52 | 43 | 56 | 55.0 | 6.3 |
| **USDA** | PI 371936 | VOSHOD | 145 | 11.5 | 40 | 49 | 39 | 53 | 29 | 35 | 40.8 | 8.1 |
| **USDA** | PI 535894 | WIELKOPOLSKI | 169 | 4.3 | 29 | 31 | 60 | 66 | 44 | 61 | 48.5 | 14.7 |
| **USDA** | PI 650735 | Zaria | 155 | 6.3 | 53 | 61 | 58 | 63 | 39 | 50 | 54.0 | 8.0 |

**Supplementary Table A 5:** Small association panel of 64 sunflower accessions (M = maintainer; R = restorer, F1 = F1 hybrid; BR. Type = branching Type; FLO = flowering date) field data of Germany 2017

| ORIGIN | PI | COMMON NAME | MATERIAL | BR. TYPE | FLO (D) |
|---|---|---|---|---|---|
| CANADA | CN 36719 | 54-3 | M | 1 | 62 |
| CANADA | CN 42283 | Armavirsky 3497 | M | 0 | 64 |
| USDA | PI 650649 | Arrowhead | M | 0 | 62 |
| BENARY | | Big Smile | F1 | 0 | 62 |
| CANADA | CN 36594 | CM104 | M | 0 | 64 |
| CANADA | CN 36654 | CM259 | M | 2 | 70 |
| CANADA | CN 36665 | CM275 | M | 0 | 56 |
| CANADA | CN 37369 | CM526 | M | 0 | 66 |
| CANADA | CN 36562 | CM63 | M | 0 | 78 |
| CANADA | CN 36144 | CMH 101 | R | 0 | 64 |
| USDA | PI 431542 | D-75-10 | R | 3 | 68 |
| USDA | PI 432519 | GN 0778 | R | 0 | 72 |
| CANADA | CN 33280 | Krasnodarets | M | 0 | 62 |
| USDA | PI 221693 | No. 2 | M | 0 | 66 |
| BENARY | | Pacino Cola | F1 | 3 | 70 |
| CANADA | CN 42267 | RHA 282 | R | 0 | 68 |
| USDA | PI 650497 | ROMSUN V3355 | M | 0 | 58 |
| BENARY | | Solita | F1 | 3 | 74 |
| BENARY | | Sunspot | F1 | 0 | 70 |
| USDA | PI 560145 | UGA-SAM1-010 | R | 3 | 66 |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| USDA | PI 561921 | UGA-SAM1-012 | R | 3 | 50 |
| USDA | PI 599758 | UGA-SAM1-024 | R | 3 | 64 |
| USDA | PI 543746 | UGA-SAM1-041 | R | 3 | 70 |
| USDA | PI 642777 | UGA-SAM1-053 | M | 0 | 68 |
| USDA | PI 655015 | UGA-SAM1-055 | R | 3 | 68 |
| USDA | PI 664216 | UGA-SAM1-057 | R | 3 | 64 |
| USDA | PI 664193 | UGA-SAM1-082 | M | 0 | 68 |
| USDA | PI 664204 | UGA-SAM1-100 | R | 3 | 58 |
| USDA | PI 664205 | UGA-SAM1-101 | R | 3 | 62 |
| USDA | PI 664221 | UGA-SAM1-109 | M | 0 | 66 |
| USDA | PI 664227 | UGA-SAM1-110 | M | 0 | 68 |
| USDA | PI 531074 | UGA-SAM1-118 | R | 3 | 70 |
| USDA | PI 531075 | UGA-SAM1-119 | R | 3 | 74 |
| USDA | PI 534653 | UGA-SAM1-121 | R | 3 | 66 |
| USDA | PI 560141 | UGA-SAM1-136 | R | 3 | 68 |
| USDA | PI 597365 | UGA-SAM1-140 | M | 0 | 62 |
| USDA | PI 607510 | UGA-SAM1-149 | R | 3 | 70 |
| USDA | PI 632342 | UGA-SAM1-153 | M | 0 | 66 |
| USDA | PI 639169 | UGA-SAM1-155 | M | 0 | 68 |
| USDA | PI 650570 | UGA-SAM1-156 | M | 0 | 64 |
| USDA | PI 597372 | UGA-SAM1-161 | R | 3 | 68 |
| USDA | PI 599759 | UGA-SAM1-165 | R | 3 | 72 |
| USDA | PI 599767 | UGA-SAM1-169 | R | 3 | 68 |
| USDA | PI 599771 | UGA-SAM1-171 | M | 3 | 62 |
| USDA | PI 599789 | UGA-SAM1-181 | R | 3 | 66 |
| USDA | PI 599979 | UGA-SAM1-183 | R | 0 | 66 |
| USDA | PI 599984 | UGA-SAM1-185 | M | 0 | 59 |
| USDA | PI 600000 | UGA-SAM1-186 | R | 3 | 70 |
| USDA | PI 603989 | UGA-SAM1-191 | R | 3 | 72 |
| USDA | PI 607508 | UGA-SAM1-195 | R | 3 | 70 |
| USDA | PI 607922 | UGA-SAM1-198 | R | 3 | 66 |
| USDA | PI 607925 | UGA-SAM1-199 | M | 3 | 66 |
| USDA | PI 617100 | UGA-SAM1-204 | R | 3 | 70 |
| USDA | PI 619204 | UGA-SAM1-207 | R | 3 | 70 |
| USDA | PI 649793 | UGA-SAM1-218 | R | 3 | 70 |
| USDA | PI 650358 | UGA-SAM1-219 | M | 0 | 66 |
| USDA | PI 650597 | UGA-SAM1-224 | M | 0 | 68 |
| USDA | PI 509065 | UGA-SAM1-242 | R | 4 | 66 |
| USDA | PI 534652 | UGA-SAM1-243 | R | 0 | 66 |
| USDA |  | UGA-SAM1-264 | M | 0 | 66 |
| USDA |  | UGA-SAM1-273 | M | 0 | 72 |
| USDA |  | UGA-SAM1-276 | R | 3 | 70 |
| USDA |  | UGA-SAM1-278 | R | 3 | 62 |
| USDA |  | UGA-SAM1-288 | R | 3 | 66 |

**Supplementary Table A 6:** Ornamental sunflower varieties

| ORIGIN | NAME | GROWTH TYPE |
|---|---|---|
| SWALLOWTAIL GARDEN | Firecracker | semi-dwarf |
| SWALLOWTAIL GARDEN | Peach-Passion | semi-dwarf |
| SWALLOWTAIL GARDEN | Giganteus Organic | giant |
| SWALLOWTAIL GARDEN | Kong | giant |
| SWALLOWTAIL GARDEN | Mammoth Russian | giant |
| SWALLOWTAIL GARDEN | Little Tiger | dwarf |
| SWALLOWTAIL GARDEN | Little Becka | dwarf |
| SWALLOWTAIL GARDEN | Solar Flash | dwarf |
| NICKYS NURSERY | Sonja | Semi-dwarf |
| NICKYS NURSERY | Sunbright | semi-dwarf |
| NICKYS NURSERY | Suntastic | dwarf |
| NICKYS NURSERY | Buttercream | semi-dwarf |
| NICKYS NURSERY | Munchkin | semi-dwarf |
| NICKYS NURSERY | MS Mars | dwarf |
| PREMIUM SUNFLOWERS | F1 Vincent Choise Deep Orange | semi-dwarf |
| PREMIUM SUNFLOWERS | Jerusalem Dwarf Yellow | dwarf |
| PREMIUM SUNFLOWERS | F1 Choco Sun | dwarf |
| PREMIUM SUNFLOWERS | F1 Orange Hobbit | dwarf |
| PREMIUM SUNFLOWERS | F1 Merida Gold Kompakt | semi-dwarf |
| PREMIUM SUNFLOWERS | F1 Ikarus | semi-dwarf |
| PREMIUM SUNFLOWERS | Vanilleeis | semi-dwarf |
| BENARY | Solita | dwarf |
| BENARY | Big Smile | dwarf |
| BENARY | Pacino Cola | dwarf |
| BENARY | Sunspot | dwarf |

**Supplementary Table A 7:** Results of measurements of the field trials in Germany (Bandow) for the small association panel with 64 accessions and the ornamental sunflowers of the years 2017-2019. Accessions used for HRM marker tests marked with asterisk (*).

| | **2017 (N = 3)** | | **2018 (N = 6)** | | **2019 (N = 6)** | |
|---|---|---|---|---|---|---|
| **ACCESSION** | **Av. PH (cm)** | **Av. Pet. Angle °** | **Av. PH (cm)** | **Av. Pet. Angle °** | **Av. PH (cm)** | **Av. Pet. Angle °** |
| **UGA-SAM1-186** | 85 | 47 | 78 | 39 | 71 | 42 |
| **UGA-SAM1-100** | 105 | 34 | 91 | 35 | 86 | 36 |
| **UGA-SAM1-119** | 60 | 55 | 74 | 37 | 66 | 55 |
| **UGA-SAM1-273 *** | 115 | 44 | 89 | 39 | 78 | 37 |
| **UGA-SAM1-110** | 110 | 34 | 97 | 44 | 91 | 33 |
| **UGA-SAM1-219** | 125 | 31 | 138 | 46 | 111 | 30 |
| **UGA-SAM1-156** | 105 | 30 | 113 | 36 | 94 | 26 |
| **UGA-SAM1-288** | 120 | 53 | 90 | 44 | 83 | 41 |
| **CM259** | 126 | 36 | 88 | 45 | 71 | 44 |
| **UGA-SAM1-183 *** | 140 | 35 | 141 | 35 | 126 | 29 |
| **UGA-SAM1-082** | 120 | 42 | 115 | 33 | 107 | 37 |
| **UGA-SAM1-041 *** | 137 | 51 | 125 | 35 | 91 | 39 |
| **RHA 282** | 115 | 23 | 121 | 31 | 97 | 33 |

| | | | | | | |
|---|---|---|---|---|---|---|
| **UGA-SAM1-153** | 110 | 26 | 117 | 38 | 79 | 33 |
| **UGA-SAM1-198** | 105 | 46 | 82 | 42 | 67 | 46 |
| **UGA-SAM1-276** | 125 | 57 | 109 | 47 | 97 | 58 |
| **NO. 2 *** | 125 | 53 | 144 | 49 | 120 | 46 |
| **UGA-SAM1-185** | 105 | 34 | 121 | 35 | 92 | 39 |
| **ROMSUN V3355** | 70 | 35 | 70 | 42 | 70 | 34 |
| **UGA-SAM1-243** | 50 | 52 | 59 | 46 | 53 | 50 |
| **54-3** | 65 | 38 | 71 | 40 | 68 | 38 |
| **UGA-SAM1-055** | 105 | 47 | 100 | 49 | 79 | 49 |
| **GN 0778 *** | 75 | 61 | 80 | 47 | 58 | 57 |
| **D-75-10** | 145 | 50 | 129 | 42 | 98 | 40 |
| **ARMAVIRSKY 3497** | 125 | 43 | 124 | 44 | 97 | 33 |
| **UGA-SAM1-053** | 115 | 40 | 105 | 43 | 97 | 40 |
| **UGA-SAM1-012** | 70 | 50 | 72 | 51 | 67 | 54 |
| **UGA-SAM1-218** | 120 | 51 | 125 | 41 | 108 | 44 |
| **UGA-SAM1-149** | 115 | 36 | 102 | 37 | 79 | 36 |
| **CM526** | 115 | 16 | 127 | 27 | 101 | 23 |
| **KRASNODARETS** | 130 | 41 | 114 | 35 | 112 | 42 |
| **UGA-SAM1-118 *** | 55 | 59 | 54 | 45 | 56 | 54 |
| **UGA-SAM1-264 *** | 115 | 48 | 110 | 37 | 81 | 35 |
| **ARROWHEAD** | 125 | 44 | 132 | 31 | 96 | 43 |
| **UGA-SAM1-199** | 100 | 44 | 104 | 48 | 79 | 48 |
| **UGA-SAM1-204** | 105 | 48 | 103 | 42 | 87 | 44 |
| **UGA-SAM1-171** | 135 | 42 | 140 | 51 | 119 | 44 |
| **UGA-SAM1-057 *** | 110 | 38 | 99 | 37 | 84 | 36 |
| **UGA-SAM1-161** | 110 | 45 | 103 | 46 | 88 | 46 |
| **UGA-SAM1-181 *** | 110 | 37 | 104 | 45 | 91 | 37 |
| **CM275** | 95 | 48 | 103 | 37 | 94 | 40 |
| **UGA-SAM1-155 *** | 95 | 36 | 94 | 39 | 72 | 43 |
| **UGA-SAM1-101** | 85 | 41 | 94 | 40 | 82 | 43 |
| **CM104 *** | 110 | 28 | 86 | 28 | 82 | 27 |
| **UGA-SAM1-165** | 120 | 49 | 120 | 45 | 86 | 47 |
| **UGA-SAM1-242** | 125 | 31 | 117 | 40 | 103 | 34 |
| **CM63** | 120 | 18 | 114 | 33 | 86 | 30 |
| **UGA-SAM1-191** | 135 | 45 | 118 | 32 | 103 | 44 |
| **UGA-SAM1-169** | 100 | 44 | 98 | 41 | 86 | 44 |
| **UGA-SAM1-140** | 115 | 48 | 108 | 38 | 81 | 37 |
| **UGA-SAM1-278** | 110 | 50 | 97 | 49 | 85 | 46 |
| **UGA-SAM1-024** | 105 | 41 | 100 | 45 | 92 | 41 |
| **UGA-SAM1-121** | 115 | 50 | 100 | 50 | 92 | 48 |
| **UGA-SAM1-207** | 120 | 46 | 93 | 41 | 84 | 46 |
| **UGA-SAM1-195** | 125 | 45 | 105 | 47 | 97 | 44 |
| **UGA-SAM1-136** | 130 | 48 | 134 | 44 | 124 | 49 |
| **UGA-SAM1-224** | 115 | 47 | 95 | 42 | 87 | 40 |
| **CMH 101** | 125 | 36 | 138 | 38 | 119 | 37 |
| **UGA-SAM1-010 *** | 110 | 60 | 94 | 40 | 81 | 53 |
| **UGA-SAM1-109** | 100 | 35 | 117 | 35 | 99 | 37 |
| **BIG SMILE** | 61 | 55 | 42 | 46 | 51 | 54 |
| **PACINO COLA** | 40 | 56 | 67 | 56 | 70 | 58 |

| | | | | | | |
|---|---|---|---|---|---|---|
| **SOLITA** | 60 | 60 | 58 | 43 | 60 | 59 |
| **SUNSPOT** | 60 | 71 | 68 | 42 | 67 | 63 |
| **JERUSALEM DWARF YELLOW** | | - | 70 | 42 | 67 | 44 |
| **CHOCO SUN** | | - | 61 | 48 | 66 | 45 |
| **IKARUS** | | - | 110 | 39 | 94 | 32 |
| **MERIDA GOLD KOMPAKT** | | - | 62 | 45 | 54 | 51 |
| **PRADO GOLD** | | - | 81 | 44 | 71 | 42 |
| **ORANGE HOBBIT** | | - | 66 | 44 | 62 | 46 |
| **VINCENT CHOICE DEEP ORANGE** | | - | 120 | 38 | 113 | 37 |
| **FIRECRACKER** | | - | - | - | 71 | 39 |
| **PEACH-PASSION** | | - | - | - | 51 | 47 |
| **GIGANTEUS ORGANIC** | | - | - | - | 254 | 38 |
| **KONG** | | - | - | - | 290 | 42 |
| **MAMMOTH RUSSIAN** | | - | - | - | 175 | 38 |
| **LITTLE TIGER** | | - | - | - | 25 | 50 |
| **LITTLE BECKA** | | - | - | - | 45 | 43 |
| **SOLAR FLASH** | | - | - | - | 57 | 47 |
| **SONJA** | | - | - | - | 78 | 38 |
| **SUNBRIGHT** | | - | - | - | 117 | 31 |
| **SUNTASTIC** | | - | - | - | 27 | 53 |
| **BUTTERCREAM** | | - | - | - | 99 | 44 |
| **MUNCHKIN** | | - | - | - | 69 | 41 |

**Supplementary Table A 8:** Test hybrids for performance tests

| ORIGIN | HAR_SEEDID | HYBRID | FEMALE PARENT | MALE PARENT |
|---|---|---|---|---|
| STRUBE | B173Y_51603.S101 | Emasculated B-Line X R-Line_1 | UGA-SAM1-224 | R-Line (commercial pollinator) |
| STRUBE | B173Y_51791.S101 | Emasculated B-Line X R-Line_2 | UGA-SAM1-109 | R-Line (commercial pollinator) |
| STRUBE | B173Y_51413.S101 | Emasculated B-Line X R-Line_3 | UGA-SAM1-140 | R-Line (commercial pollinator) |
| STRUBE | B173Y_51890.S101 | Emasculated B-Line X R-Line_4 | CM63 | R-Line (commercial pollinator) |
| STRUBE | B173Y_51768.S101 | Emasculated B-Line X R-Line_5 | Arrowhead | R-Line (commercial pollinator) |
| STRUBE | B173Y_51857.S101 | Emasculated B-Line X R-Line_6 | Krasnodarets | R-Line (commercial pollinator) |
| STRUBE | B173Y_51667.S101 | Emasculated B-Line X R-Line_7 | UGA-SAM1-264 | R-Line (commercial pollinator) |
| STRUBE | B173Y_51716.S101 | Emasculated B-Line X R-Line_8 | No. 2 | R-Line (commercial pollinator) |
| STRUBE | - | Emasculated B-Line X R-Line_9 | Sunspot | R-Line (commercial pollinator) |
| STRUBE | B173Y_51102.S101 | Emasculated B-Line X R-Line_10 | ROMSUN V3355 | R-Line (commercial pollinator) |
| STRUBE | B173Y_51430.S101 | Emasculated B-Line X R-Line_11 | UGA-SAM1-153 | R-Line (commercial pollinator) |
| STRUBE | B173Y_51437.S101 | Emasculated B-Line X R-Line_12 | UGA-SAM1-155 | R-Line (commercial pollinator) |
| STRUBE | B173Y_51232.S101 | Emasculated B-Line X R-Line_13 | UGA-SAM1-053 | R-Line (commercial pollinator) |
| STRUBE | B173Y_51337.S101 | Emasculated B-Line X R-Line_14 | UGA-SAM1-110 | R-Line (commercial pollinator) |
| STRUBE | B173Y_52046.S101 | Emasculated B-Line X R-Line_15 | 54-3 | R-Line (commercial pollinator) |
| STRUBE | B173Y_51591.S101 | Emasculated B-Line X R-Line_16 | UGA-SAM1-219 | R-Line (commercial pollinator) |
| STRUBE | B173Y_51511.S101 | Emasculated B-Line X R-Line_17 | UGA-SAM1-185 | R-Line (commercial pollinator) |
| STRUBE | B173Y_51969.S101 | Emasculated B-Line X R-Line_18 | Armavirsky 3497 | R-Line (commercial pollinator) |
| STRUBE | B173Y_51292.S101 | Emasculated B-Line X R-Line_19 | UGA-SAM1-082 | R-Line (commercial pollinator) |
| STRUBE | B173Y_52031.S101 | Emasculated B-Line X R-Line_20 | CM104 | R-Line (commercial pollinator) |

|  |  |  |  |  |
|---|---|---|---|---|
| STRUBE | B173Y_51926.S101 | Emasculated B-Line X R-Line_21 | CM259 | R-Line (commercial pollinator) |
| STRUBE | B173Y_51952.S101 | Emasculated B-Line X R-Line_22 | CM526 | R-Line (commercial pollinator) |
| STRUBE | R173Y_51514.S101 | F1 Hybrid CMS-Line X R-Line_1 | LC-1093A (CMS) | UGA-SAM1-186 |
| STRUBE | R173Y_51588.S101 | F1 Hybrid CMS-Line X R-Line_2 | LC-1093A (CMS) | UGA-SAM1-218 |
| STRUBE | R173Y_51241.S101 | F1 Hybrid CMS-Line X R-Line_3 | LC-1093A (CMS) | UGA-SAM1-057 |
| STRUBE | - | F1 Hybrid CMS-Line X R-Line_4 | LC-1093A (CMS) | Pacino Cola |
| STRUBE | R173Y_51706.S101 | F1 Hybrid CMS-Line X R-Line_5 | LC-1093A (CMS) | UGA-SAM1-288 |
| STRUBE | R173Y_51525.S101 | F1 Hybrid CMS-Line X R-Line_6 | LC-1093A (CMS) | UGA-SAM1-191 |
| STRUBE | R173Y_51462.S101 | F1 Hybrid CMS-Line X R-Line_7 | LC-1093A (CMS) | UGA-SAM1-165 |
| STRUBE | R173Y_51688.S101 | F1 Hybrid CMS-Line X R-Line_8 | LC-1093A (CMS) | UGA-SAM1-276 |
| STRUBE | R173Y_51803.S101 | F1 Hybrid CMS-Line X R-Line_9 | LC-1093A (CMS) | UGA-SAM1-195 |
| STRUBE | R173Y_51798.S101 | F1 Hybrid CMS-Line X R-Line_10 | LC-1093A (CMS) | UGA-SAM1-149 |
| STRUBE | R173Y_51557.S101 | F1 Hybrid CMS-Line X R-Line_11 | LC-1093A (CMS) | UGA-SAM1-207 |
| STRUBE | R173Y_51450.S101 | F1 Hybrid CMS-Line X R-Line_12 | LC-1093A (CMS) | UGA-SAM1-161 |
| STRUBE | R173Y_51473.S101 | F1 Hybrid CMS-Line X R-Line_13 | LC-1093A (CMS) | UGA-SAM1-169 |
| STRUBE | R173Y_51696.S101 | F1 Hybrid CMS-Line X R-Line_14 | LC-1093A (CMS) | UGA-SAM1-278 |
| STRUBE | R173Y_51134.S101 | F1 Hybrid CMS-Line X R-Line_15 | LC-1093A (CMS) | UGA-SAM1-010 |
| STRUBE | R173Y_51549.S101 | F1 Hybrid CMS-Line X R-Line_16 | LC-1093A (CMS) | UGA-SAM1-204 |
| STRUBE | R173Y_51164.S101 | F1 Hybrid CMS-Line X R-Line_17 | LC-1093A (CMS) | UGA-SAM1-024 |
| STRUBE | R173Y_51046.S101 | F1 Hybrid CMS-Line X R-Line_18 | LC-1093A (CMS) | D-75-10 |
| STRUBE | R173Y_51355.S101 | F1 Hybrid CMS-Line X R-Line_19 | LC-1093A (CMS) | UGA-SAM1-118 |
| STRUBE | R173Y_51402.S101 | F1 Hybrid CMS-Line X R-Line_20 | LC-1093A (CMS) | UGA-SAM1-136 |
| STRUBE | R173Y_51358.S101 | F1 Hybrid CMS-Line X R-Line_21 | LC-1093A (CMS) | UGA-SAM1-119 |
| STRUBE | R173Y_51929.S101 | F1 Hybrid CMS-Line X R-Line_22 | LC-1093A (CMS) | CM275 |
| STRUBE | R173Y_51317.S101 | F1 Hybrid CMS-Line X R-Line_23 | LC-1093A (CMS) | UGA-SAM1-101 |
| STRUBE | R173Y_51314.S101 | F1 Hybrid CMS-Line X R-Line_24 | LC-1093A (CMS) | UGA-SAM1-100 |
| STRUBE | R173Y_51503.S101 | F1 Hybrid CMS-Line X R-Line_25 | LC-1093A (CMS) | UGA-SAM1-181 |
| STRUBE | R173Y_51137.S101 | F1 Hybrid CMS-Line X R-Line_26 | LC-1093A (CMS) | UGA-SAM1-012 |
| STRUBE | R173Y_51365.S101 | F1 Hybrid CMS-Line X R-Line_27 | LC-1093A (CMS) | UGA-SAM1-121 |
| STRUBE | - | F1 Hybrid CMS-Line X R-Line_28 | LC-1093A (CMS) | Big Smile |
| STRUBE | R173Y_51539.S101 | F1 Hybrid CMS-Line X R-Line_29 | LC-1093A (CMS) | UGA-SAM1-198 |
| STRUBE | R173Y_51775.S101 | F1 Hybrid CMS-Line X R-Line_30 | LC-1093A (CMS) | UGA-SAM1-055 |
| STRUBE | R173Y_51202.S101 | F1 Hybrid CMS-Line X R-Line_31 | LC-1093A (CMS) | UGA-SAM1-041 |

**Supplementary Table A 9:** Results of performance tests at plant density of 20 cm, DE (left), RO (right)

| HYBRID | YIELD DT/HA | MOIST. % | OIL CONT. % | YIELD DT/HA | MOIST. % | OIL CONT. % |
|---|---|---|---|---|---|---|
| F1 HYBRID CMS-LINE X R-LINE_1 | 18.00 | 9.60 | 48.65 | 23.21 | 4.70 | 48.70 |
| F1 HYBRID CMS-LINE X R-LINE_2 | 16.13 | 6.40 | 47.15 | 20.83 | 5.30 | 45.90 |
| F1 HYBRID CMS-LINE X R-LINE_3 | 27.04 | 9.45 | 51.50 | 21.92 | 4.65 | 47.05 |
| F1 HYBRID CMS-LINE X R-LINE_4 | 21.33 | 10.00 | 47.05 | 22.58 | 4.30 | 46.50 |
| F1 HYBRID CMS-LINE X R-LINE_5 | 23.50 | 6.25 | 46.30 | 22.79 | 5.20 | 44.95 |
| F1 HYBRID CMS-LINE X R-LINE_6 | 20.21 | 8.35 | 45.85 | 22.46 | 5.10 | 43.25 |
| F1 HYBRID CMS-LINE X R-LINE_7 | 22.13 | 7.75 | 46.00 | 23.29 | 5.00 | 44.95 |
| F1 HYBRID CMS-LINE X R-LINE_8 | 20.67 | 15.00 | 47.20 | 25.46 | 5.35 | 43.50 |
| F1 HYBRID CMS-LINE X R-LINE_9 | 21.29 | 6.75 | 46.00 | 26.50 | 5.15 | 44.80 |
| F1 HYBRID CMS-LINE X R-LINE_10 | 21.92 | 8.25 | 45.75 | 26.13 | 4.65 | 44.65 |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| F1 HYBRID CMS-LINE X R-LINE_11 | 31.63 | 12.35 | 48.90 | 22.92 | 4.40 | 44.10 |
| F1 HYBRID CMS-LINE X R-LINE_12 | 26.33 | 7.25 | 46.25 | 26.50 | 5.25 | 47.30 |
| F1 HYBRID CMS-LINE X R-LINE_13 | 21.92 | 6.60 | 48.25 | 20.63 | 4.75 | 44.45 |
| F1 HYBRID CMS-LINE X R-LINE_14 | 17.33 | 7.95 | 46.35 | 26.42 | 5.15 | 25.90 |
| F1 HYBRID CMS-LINE X R-LINE_15 | 26.25 | 6.10 | 46.90 | 26.71 | 4.70 | 47.80 |
| F1 HYBRID CMS-LINE X R-LINE_16 | 28.92 | 11.65 | 45.15 | 22.33 | 5.35 | 43.60 |
| F1 HYBRID CMS-LINE X R-LINE_17 | 19.25 | 8.55 | 46.50 | 24.54 | 4.55 | 46.75 |
| F1 HYBRID CMS-LINE X R-LINE_18 | 17.79 | 13.35 | 48.55 | 27.54 | 4.50 | 47.10 |
| F1 HYBRID CMS-LINE X R-LINE_19 | 20.29 | 13.85 | 47.40 | 20.63 | 5.25 | 46.70 |
| F1 HYBRID CMS-LINE X R-LINE_20 | 17.08 | 6.05 | 46.85 | 25.08 | 4.85 | 45.95 |
| F1 HYBRID CMS-LINE X R-LINE_21 | 24.63 | 11.20 | 46.55 | 24.17 | 4.50 | 46.55 |
| F1 HYBRID CMS-LINE X R-LINE_22 | 15.54 | 4.30 | 43.85 | 23.92 | 4.45 | 44.70 |
| F1 HYBRID CMS-LINE X R-LINE_23 | 23.33 | 10.00 | 43.95 | 29.92 | 4.00 | 43.20 |
| F1 HYBRID CMS-LINE X R-LINE_24 | 20.67 | 9.55 | 43.60 | 20.38 | 6.20 | 45.60 |
| F1 HYBRID CMS-LINE X R-LINE_25 | 20.96 | 10.85 | 43.30 | 20.71 | 6.25 | 44.45 |
| F1 HYBRID CMS-LINE X R-LINE_26 | 21.13 | 6.50 | 44.60 | 27.21 | 4.45 | 44.85 |
| F1 HYBRID CMS-LINE X R-LINE_27 | 24.92 | 6.70 | 46.70 | 21.13 | 5.10 | 46.40 |
| F1 HYBRID CMS-LINE X R-LINE_28 | 23.33 | 15.85 | 44.00 | 22.67 | 3.40 | 44.75 |
| F1 HYBRID CMS-LINE X R-LINE_29 | 19.50 | 6.85 | 46.00 | 19.58 | 5.05 | 47.75 |
| F1 HYBRID CMS-LINE X R-LINE_30 | 18.54 | 10.45 | 47.75 | 30.29 | 5.35 | 47.35 |
| EMASCULATED B-LINE X R-LINE_1 | 11.08 | 9.70 | 47.00 | 18.67 | 4.80 | 46.10 |
| EMASCULATED B-LINE X R-LINE_2 | 13.67 | 5.90 | 43.50 | 24.17 | 5.30 | 43.10 |
| EMASCULATED B-LINE X R-LINE_3 | 18.83 | 6.40 | 45.40 | 21.92 | 4.80 | 45.70 |
| EMASCULATED B-LINE X R-LINE_4 | 15.83 | 5.70 | 42.80 | 24.42 | 4.10 | 44.40 |
| EMASCULATED B-LINE X R-LINE_5 | 22.42 | 2.50 | 42.00 | 28.08 | 5.30 | 45.50 |
| EMASCULATED B-LINE X R-LINE_6 | 11.83 | 1.60 | 42.50 | 25.33 | 5.90 | 44.50 |
| EMASCULATED B-LINE X R-LINE_7 | 26.25 | 6.80 | 47.80 | 23.08 | 5.00 | 46.70 |
| EMASCULATED B-LINE X R-LINE_8 | 20.42 | 8.70 | 41.90 | 29.33 | 5.70 | 42.20 |
| EMASCULATED B-LINE X R-LINE_9 | 33.08 | 17.40 | 43.50 | 27.00 | 5.30 | 44.10 |
| EMASCULATED B-LINE X R-LINE_10 | 28.33 | 10.00 | 44.40 | 22.92 | 5.50 | 43.60 |
| EMASCULATED B-LINE X R-LINE_11 | 22.25 | 6.70 | 45.30 | 27.00 | 5.20 | 46.10 |
| EMASCULATED B-LINE X R-LINE_12 | 16.83 | 9.10 | 43.00 | 17.67 | 3.80 | 44.90 |
| EMASCULATED B-LINE X R-LINE_13 | 20.83 | 7.70 | 46.10 | 27.25 | 3.70 | 48.10 |
| EMASCULATED B-LINE X R-LINE_14 | 25.58 | 5.50 | 40.10 | 27.67 | 5.60 | 41.00 |
| EMASCULATED B-LINE X R-LINE_15 | 13.33 | 4.00 | 45.10 | 27.83 | 5.10 | 48.60 |
| EMASCULATED B-LINE X R-LINE_16 | 18.42 | 5.50 | 40.90 | 22.17 | 5.20 | 42.60 |
| EMASCULATED B-LINE X R-LINE_17 | 20.67 | 6.70 | 46.60 | 21.92 | 4.40 | 47.20 |
| EMASCULATED B-LINE X R-LINE_18 | 19.67 | 4.30 | 47.40 | 22.25 | 5.10 | 47.00 |
| EMASCULATED B-LINE X R-LINE_19 | 14.42 | 3.90 | 41.60 | 22.25 | 5.00 | 42.10 |
| EMASCULATED B-LINE X R-LINE_20 | 14.83 | 5.10 | 41.30 | 25.08 | 5.40 | 42.50 |
| EMASCULATED B-LINE X R-LINE_21 | 21.08 | 11.50 | 42.20 | 23.00 | 4.40 | 46.00 |
| EMASCULATED B-LINE X R-LINE_22 | 11.67 | 1.90 | 47.40 | 17.75 | 4.70 | 44.50 |
| F1 HYBRID CMS-LINE X R-LINE_31 | 23.00 | 4.70 | 49.20 | 31.92 | 5.10 | 45.60 |
| REFERENCE_ES BELLA | 33.96 | 8.80 | 44.30 | 30.00 | 5.20 | 45.65 |
| REFERENCE_ES SAVANA | 28.54 | 5.10 | 45.25 | 27.17 | 4.75 | 46.20 |
| REFERENCE_ES COLUMBELLA | 29.00 | 5.65 | 45.50 | 31.29 | 4.90 | 43.80 |
| REFERENCE_SUMATRA | 25.88 | 5.30 | 45.60 | 27.88 | 4.15 | 44.25 |
| REFERENCE_NK DELFI | 31.58 | 10.05 | 46.45 | 29.38 | 4.70 | 46.65 |

**Supplementary Table A 10:** Results of Performance tests at plant density of 25 cm, DE (left), RO (right)

| HYBRID | YIELD DT/HA | MOIST. % | OIL CONT. % | YIELD DT/HA | MOIST. % | OIL CONT. % |
|---|---|---|---|---|---|---|
| F1 HYBRID CMS-LINE X R-LINE_1 | 30.54 | 13.00 | 49.90 | 20.54 | 5.55 | 46.80 |
| F1 HYBRID CMS-LINE X R-LINE_2 | 21.33 | 10.50 | 48.95 | 19.42 | 5.65 | 46.15 |
| F1 HYBRID CMS-LINE X R-LINE_3 | 24.75 | 8.45 | 51.85 | 24.92 | 5.65 | 51.05 |
| F1 HYBRID CMS-LINE X R-LINE_4 | 26.79 | 12.20 | 47.65 | 26.33 | 5.75 | 45.25 |
| F1 HYBRID CMS-LINE X R-LINE_5 | 25.33 | 7.60 | 46.15 | 33.38 | 5.70 | 44.25 |
| F1 HYBRID CMS-LINE X R-LINE_6 | 22.13 | 7.10 | 45.85 | 20.42 | 5.85 | 45.35 |
| F1 HYBRID CMS-LINE X R-LINE_7 | 28.83 | 8.15 | 46.60 | 27.25 | 5.90 | 44.50 |
| F1 HYBRID CMS-LINE X R-LINE_8 | 33.75 | 15.45 | 48.15 | 21.63 | 6.40 | 46.30 |
| F1 HYBRID CMS-LINE X R-LINE_9 | 24.83 | 12.65 | 46.55 | 22.42 | 6.05 | 45.30 |
| F1 HYBRID CMS-LINE X R-LINE_10 | 22.67 | 8.25 | 45.25 | 27.83 | 6.55 | 44.40 |
| F1 HYBRID CMS-LINE X R-LINE_11 | 31.83 | 8.65 | 49.65 | 25.42 | 5.75 | 46.90 |
| F1 HYBRID CMS-LINE X R-LINE_12 | 30.25 | 8.80 | 48.65 | 22.46 | 5.50 | 47.45 |
| F1 HYBRID CMS-LINE X R-LINE_13 | 29.75 | 7.05 | 47.35 | 19.00 | 5.40 | 46.50 |
| F1 HYBRID CMS-LINE X R-LINE_14 | 24.67 | 7.70 | 47.70 | 25.04 | 5.75 | 48.45 |
| F1 HYBRID CMS-LINE X R-LINE_15 | 23.13 | 6.40 | 48.50 | 27.50 | 5.35 | 47.75 |
| F1 HYBRID CMS-LINE X R-LINE_16 | 31.75 | 11.90 | 46.65 | 27.88 | 6.10 | 47.90 |
| F1 HYBRID CMS-LINE X R-LINE_17 | 19.67 | 9.65 | 47.45 | 20.08 | 5.70 | 49.00 |
| F1 HYBRID CMS-LINE X R-LINE_18 | 24.71 | 12.15 | 48.30 | 32.92 | 5.85 | 47.65 |
| F1 HYBRID CMS-LINE X R-LINE_19 | 26.54 | 15.70 | 48.20 | 19.83 | 5.75 | 49.40 |
| F1 HYBRID CMS-LINE X R-LINE_20 | 23.83 | 7.30 | 46.90 | 34.54 | 5.85 | 46.15 |
| F1 HYBRID CMS-LINE X R-LINE_21 | 25.71 | 11.80 | 50.90 | 21.71 | 5.70 | 46.75 |
| F1 HYBRID CMS-LINE X R-LINE_22 | 19.54 | 5.35 | 44.45 | 23.29 | 5.75 | 47.00 |
| F1 HYBRID CMS-LINE X R-LINE_23 | 23.67 | 5.45 | 44.90 | 25.67 | 5.40 | 44.05 |
| F1 HYBRID CMS-LINE X R-LINE_24 | 23.08 | 8.25 | 43.80 | 22.54 | 5.80 | 44.95 |
| F1 HYBRID CMS-LINE X R-LINE_25 | 28.33 | 9.35 | 43.95 | 24.38 | 6.95 | 45.45 |
| F1 HYBRID CMS-LINE X R-LINE_26 | 24.25 | 5.75 | 45.20 | 24.54 | 5.45 | 47.90 |
| F1 HYBRID CMS-LINE X R-LINE_27 | 25.46 | 10.10 | 48.70 | 16.13 | 5.75 | 46.70 |
| F1 HYBRID CMS-LINE X R-LINE_28 | 27.33 | 14.20 | 43.95 | 24.96 | 5.80 | 43.75 |
| F1 HYBRID CMS-LINE X R-LINE_29 | 27.88 | 8.70 | 47.70 | 19.92 | 5.70 | 46.45 |
| F1 HYBRID CMS-LINE X R-LINE_30 | 24.83 | 9.90 | 48.40 | 21.50 | 5.30 | 47.25 |
| EMASCULATED B-LINE X R-LINE_1 | 26.00 | 7.80 | 48.00 | 24.42 | 6.80 | 43.10 |
| EMASCULATED B-LINE X R-LINE_2 | 21.50 | 5.30 | 42.30 | 29.00 | 6.00 | 43.00 |
| EMASCULATED B-LINE X R-LINE_3 | 29.00 | 9.60 | 45.60 | 28.42 | 5.80 | 45.60 |
| EMASCULATED B-LINE X R-LINE_4 | 24.08 | 5.90 | 43.20 | 33.42 | 6.00 | 44.50 |
| EMASCULATED B-LINE X R-LINE_5 | 27.42 | 5.40 | 42.30 | 31.92 | 6.50 | 42.90 |
| EMASCULATED B-LINE X R-LINE_6 | 16.33 | 4.20 | 42.70 | 25.92 | 6.10 | 44.30 |
| EMASCULATED B-LINE X R-LINE_7 | 26.42 | -1.40 | 44.90 | 17.92 | 6.30 | 45.20 |
| EMASCULATED B-LINE X R-LINE_8 | 23.42 | 5.40 | 42.30 | 29.33 | 6.60 | 42.50 |
| EMASCULATED B-LINE X R-LINE_9 | 33.67 | 15.80 | 43.90 | 25.42 | 5.80 | 43.20 |
| EMASCULATED B-LINE X R-LINE_10 | 22.83 | 3.80 | 44.90 | 19.50 | 6.00 | 45.50 |
| EMASCULATED B-LINE X R-LINE_11 | 17.25 | 9.20 | 44.40 | 22.42 | 5.60 | 45.60 |
| EMASCULATED B-LINE X R-LINE_12 | 17.58 | 14.70 | 44.30 | 24.25 | 5.20 | 46.80 |
| EMASCULATED B-LINE X R-LINE_13 | 23.00 | 5.80 | 47.20 | 18.58 | 5.30 | 42.70 |
| EMASCULATED B-LINE X R-LINE_14 | 26.67 | 4.20 | 42.10 | 24.58 | 6.50 | 41.70 |
| EMASCULATED B-LINE X R-LINE_15 | 18.75 | 5.20 | 45.40 | 14.58 | 5.80 | 48.10 |
| EMASCULATED B-LINE X R-LINE_16 | 20.67 | 6.30 | 40.40 | 20.75 | 6.20 | 42.20 |

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|---|---|---|---|---|---|---|
| EMASCULATED B-LINE X R-LINE_17 | 21.33 | 3.90 | 48.50 | 18.08 | 5.40 | 48.50 |
| EMASCULATED B-LINE X R-LINE_18 | 23.58 | 6.40 | 47.00 | 24.58 | 6.10 | 44.30 |
| EMASCULATED B-LINE X R-LINE_19 | 26.17 | 4.20 | 41.70 | 38.50 | 7.00 | 42.40 |
| EMASCULATED B-LINE X R-LINE_20 | 20.92 | 7.20 | 42.10 | 27.17 | 6.70 | 43.80 |
| EMASCULATED B-LINE X R-LINE_21 | 28.50 | 15.70 | 42.20 | 22.83 | 7.00 | 42.90 |
| EMASCULATED B-LINE X R-LINE_22 | 30.92 | 5.80 | 44.30 | 26.08 | 5.80 | 47.90 |
| F1 HYBRID CMS-LINE X R-LINE_31 | 35.75 | 10.20 | 46.90 | 27.17 | 5.90 | 48.00 |
| REFERENCE_ES BELLA | 26.46 | 8.40 | 45.55 | 24.50 | 6.10 | 46.15 |
| REFERENCE_ES SAVANA | 25.21 | 8.15 | 46.35 | 24.58 | 5.55 | 45.90 |
| REFERENCE_ES COLUMBELLA | 27.79 | 4.30 | 47.45 | 27.71 | 6.10 | 45.00 |
| REFERENCE_SUMATRA | 24.83 | 5.45 | 46.70 | 32.79 | 5.45 | 46.45 |
| REFERENCE_NK DELFI | 35.67 | 11.55 | 45.90 | 31.58 | 5.75 | 46.35 |

**Supplementary Table A 11:** Results of Performance tests at plant density of 30 cm, DE (left), RO (right)

| HYBRID | YIELD DT/HA | MOIST. % | OIL CONT. % | YIELD DT/HA | MOIST. % | OIL CONT. % |
|---|---|---|---|---|---|---|
| F1 HYBRID CMS-LINE X R-LINE_1 | 37.46 | 12.40 | 49.00 | 22.17 | 5.00 | 45.90 |
| F1 HYBRID CMS-LINE X R-LINE_2 | 29.63 | 6.70 | 47.40 | 23.33 | 4.70 | 44.50 |
| F1 HYBRID CMS-LINE X R-LINE_3 | 31.92 | 7.00 | 51.05 | 21.08 | 4.70 | 48.60 |
| F1 HYBRID CMS-LINE X R-LINE_4 | 27.04 | 11.20 | 46.20 | 16.92 | 4.80 | 45.95 |
| F1 HYBRID CMS-LINE X R-LINE_5 | 22.71 | 7.00 | 45.20 | 22.92 | 5.05 | 42.75 |
| F1 HYBRID CMS-LINE X R-LINE_6 | 23.42 | 10.55 | 45.70 | 20.13 | 5.10 | 48.50 |
| F1 HYBRID CMS-LINE X R-LINE_7 | 24.38 | 7.40 | 46.35 | 16.54 | 4.70 | 45.85 |
| F1 HYBRID CMS-LINE X R-LINE_8 | 43.50 | 11.55 | 46.35 | 23.79 | 5.55 | 44.10 |
| F1 HYBRID CMS-LINE X R-LINE_9 | 28.92 | 10.00 | 46.15 | 22.04 | 5.35 | 43.60 |
| F1 HYBRID CMS-LINE X R-LINE_10 | 31.08 | 8.75 | 44.20 | 20.71 | 5.85 | 43.50 |
| F1 HYBRID CMS-LINE X R-LINE_11 | 29.00 | 11.70 | 47.25 | 25.63 | 5.50 | 44.60 |
| F1 HYBRID CMS-LINE X R-LINE_12 | 30.38 | 7.10 | 47.55 | 19.17 | 5.50 | 44.80 |
| F1 HYBRID CMS-LINE X R-LINE_13 | 26.00 | 3.35 | 47.80 | 14.17 | 4.80 | 44.85 |
| F1 HYBRID CMS-LINE X R-LINE_14 | 34.42 | 6.70 | 47.25 | 22.33 | 4.70 | 44.05 |
| F1 HYBRID CMS-LINE X R-LINE_15 | 27.00 | 6.15 | 46.30 | 24.08 | 5.35 | 47.00 |
| F1 HYBRID CMS-LINE X R-LINE_16 | 39.50 | 8.65 | 46.35 | 23.29 | 5.55 | 45.40 |
| F1 HYBRID CMS-LINE X R-LINE_17 | 23.46 | 5.15 | 47.00 | 23.04 | 5.35 | 46.50 |
| F1 HYBRID CMS-LINE X R-LINE_18 | 23.42 | 7.60 | 47.70 | 25.63 | 5.60 | 44.75 |
| F1 HYBRID CMS-LINE X R-LINE_19 | 31.79 | 12.70 | 48.70 | 15.50 | 5.40 | 47.60 |
| F1 HYBRID CMS-LINE X R-LINE_20 | 28.17 | 0.45 | 45.85 | 23.21 | 5.45 | 48.45 |
| F1 HYBRID CMS-LINE X R-LINE_21 | 34.54 | 9.35 | 48.55 | 17.08 | 5.15 | 46.80 |
| F1 HYBRID CMS-LINE X R-LINE_22 | 25.17 | 9.15 | 43.35 | 16.88 | 5.30 | 45.30 |
| F1 HYBRID CMS-LINE X R-LINE_23 | 31.75 | 12.25 | 45.40 | 24.58 | 5.40 | 40.90 |
| F1 HYBRID CMS-LINE X R-LINE_24 | 29.00 | 13.70 | 44.20 | 24.75 | 5.80 | 43.00 |
| F1 HYBRID CMS-LINE X R-LINE_25 | 24.04 | 11.20 | 43.50 | 21.79 | 4.90 | 45.30 |
| F1 HYBRID CMS-LINE X R-LINE_26 | 23.00 | 5.55 | 44.10 | 22.04 | 5.10 | 44.55 |
| F1 HYBRID CMS-LINE X R-LINE_27 | 29.75 | 9.20 | 46.65 | 22.13 | 5.15 | 46.05 |
| F1 HYBRID CMS-LINE X R-LINE_28 | 33.00 | 10.80 | 44.25 | 24.88 | 4.50 | 45.95 |
| F1 HYBRID CMS-LINE X R-LINE_29 | 31.88 | 4.85 | 46.15 | 21.46 | 5.65 | 47.20 |
| F1 HYBRID CMS-LINE X R-LINE_30 | 32.63 | 9.85 | 47.20 | 21.38 | 5.35 | 47.55 |
| REFERENCE_ES BELLA | 30.83 | 10.05 | 44.05 | 23.29 | 5.50 | 45.50 |
| REFERENCE_ES SAVANA | 33.17 | 6.45 | 45.90 | 26.25 | 5.25 | 47.30 |

| | | | | | | |
|---|---|---|---|---|---|---|
| REFERENCE_ES COLUMBELLA | 28.79 | 5.50 | 44.85 | 28.33 | 5.45 | 47.35 |
| REFERENCE_SUMATRA | 33.71 | 6.50 | 46.35 | 20.96 | 5.10 | 45.40 |
| REFERENCE_NK DELFI | 30.88 | 9.90 | 46.50 | 26.21 | 5.45 | 45.25 |

**Supplementary Table A 12**: Comparison of the F1 Hybrids showing the highest yield, oil content and oil yield at various plant densities

| Loc | Density (cm) | F1 Hybrid | Pet ° | Yield dt/ha | Oil content % | Oil yield l/ha |
|---|---|---|---|---|---|---|
| DE | 20 | ES Bella (reference) | narrow | 33.96 | 44.30 | 1504.35 |
| DE | 25 | LC-1093A x UGA-SAM1-041 | narrow | 35.75 | 46.90 | 1676.68 |
| DE | 30 | LC-1093A x UGA-SAM1-276 | normal | 43.50 | 46.35 | 2016.23 |
| RO | 20 | LC-1093A x UGA-SAM1-041 | narrow | 31.92 | 45.60 | 1455.40 |
| RO | 25 | UGA-SAM1-082 x R-Line | normal | 38.50 | 42.40 | 1632.40 |
| RO | 30 | ES Columbella (reference) | - | 28.33 | 47.35 | 1341.58 |

**Supplementary Table A 13:** Oil yield (l/ha) at three different plant densities in Germany and Romania

| HYBRID | 20 CM DE | 25 CM DE | 30 CM DE | 20 CM RO | 25 CM RO | 30 CM RO |
|---|---|---|---|---|---|---|
| F1 HYBRID CMS-LINE X R-LINE_1 | 875.70 | 1524.03 | 1835.46 | 1130.25 | 961.35 | 1017.45 |
| F1 HYBRID CMS-LINE X R-LINE_2 | 760.29 | 1044.27 | 1404.23 | 956.25 | 896.08 | 1038.33 |
| F1 HYBRID CMS-LINE X R-LINE_3 | 1392.65 | 1283.29 | 1629.35 | 1031.18 | 1272.00 | 1024.65 |
| F1 HYBRID CMS-LINE X R-LINE_4 | 1003.73 | 1276.62 | 1249.33 | 1050.13 | 1191.58 | 777.32 |
| F1 HYBRID CMS-LINE X R-LINE_5 | 1088.05 | 1169.13 | 1026.42 | 1024.49 | 1476.84 | 979.69 |
| F1 HYBRID CMS-LINE X R-LINE_6 | 926.55 | 1014.43 | 1070.14 | 971.32 | 925.90 | 976.06 |
| F1 HYBRID CMS-LINE X R-LINE_7 | 1017.75 | 1343.63 | 1129.78 | 1046.96 | 1212.63 | 758.44 |
| F1 HYBRID CMS-LINE X R-LINE_8 | 975.47 | 1625.06 | 2016.23 | 1107.44 | 1001.24 | 1049.21 |
| F1 HYBRID CMS-LINE X R-LINE_9 | 979.42 | 1155.99 | 1334.50 | 1187.20 | 1015.48 | 961.02 |
| F1 HYBRID CMS-LINE X R-LINE_10 | 1002.69 | 1025.67 | 1373.88 | 1166.48 | 1235.80 | 900.81 |
| F1 HYBRID CMS-LINE X R-LINE_11 | 1546.46 | 1580.53 | 1370.25 | 1010.63 | 1192.04 | 1142.88 |
| F1 HYBRID CMS-LINE X R-LINE_12 | 1217.92 | 1471.66 | 1444.33 | 1253.45 | 1065.65 | 858.67 |
| F1 HYBRID CMS-LINE X R-LINE_13 | 1057.48 | 1408.66 | 1242.80 | 916.78 | 883.50 | 635.38 |
| F1 HYBRID CMS-LINE X R-LINE_14 | 803.40 | 1176.60 | 1626.19 | 684.19 | 1213.27 | 983.78 |
| F1 HYBRID CMS-LINE X R-LINE_15 | 1231.13 | 1121.56 | 1250.10 | 1276.66 | 1313.13 | 1131.92 |
| F1 HYBRID CMS-LINE X R-LINE_16 | 1305.59 | 1481.14 | 1830.83 | 973.73 | 1335.21 | 1057.44 |
| F1 HYBRID CMS-LINE X R-LINE_17 | 895.13 | 933.18 | 1102.54 | 1147.32 | 984.08 | 1071.44 |
| F1 HYBRID CMS-LINE X R-LINE_18 | 863.79 | 1193.41 | 1116.98 | 1297.21 | 1568.48 | 1146.72 |
| F1 HYBRID CMS-LINE X R-LINE_19 | 961.83 | 1279.31 | 1548.25 | 963.19 | 979.77 | 737.80 |
| F1 HYBRID CMS-LINE X R-LINE_20 | 800.35 | 1117.78 | 1291.44 | 1152.58 | 1594.10 | 1124.44 |
| F1 HYBRID CMS-LINE X R-LINE_21 | 1146.29 | 1308.55 | 1677.00 | 1124.96 | 1014.86 | 799.50 |
| F1 HYBRID CMS-LINE X R-LINE_22 | 681.50 | 868.63 | 1090.98 | 1069.08 | 1094.71 | 764.44 |
| F1 HYBRID CMS-LINE X R-LINE_23 | 1025.50 | 1062.63 | 1441.45 | 1292.40 | 1130.62 | 1005.46 |
| F1 HYBRID CMS-LINE X R-LINE_24 | 901.07 | 1011.05 | 1281.80 | 929.10 | 1013.25 | 1064.25 |
| F1 HYBRID CMS-LINE X R-LINE_25 | 907.50 | 1245.25 | 1045.81 | 920.49 | 1107.84 | 987.16 |
| F1 HYBRID CMS-LINE X R-LINE_26 | 942.18 | 1096.10 | 1014.30 | 1220.29 | 1175.55 | 981.96 |
| F1 HYBRID CMS-LINE X R-LINE_27 | 1163.61 | 1239.82 | 1387.84 | 980.20 | 753.04 | 1018.86 |
| F1 HYBRID CMS-LINE X R-LINE_28 | 1026.67 | 1201.30 | 1460.25 | 1014.33 | 1091.93 | 1143.01 |
| F1 HYBRID CMS-LINE X R-LINE_29 | 897.00 | 1329.64 | 1471.03 | 935.10 | 925.13 | 1012.83 |
| F1 HYBRID CMS-LINE X R-LINE_30 | 885.36 | 1201.93 | 1539.90 | 1434.31 | 1015.88 | 1016.38 |
| EMASCULATED B-LINE X R-LINE_1 | 520.92 | 1248.00 | - | 860.53 | 1052.36 | - |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| EMASCULATED B-LINE X R-LINE_2 | 594.50 | 909.45 | - | 1041.58 | 1247.00 | - |
| EMASCULATED B-LINE X R-LINE_3 | 855.03 | 1322.40 | - | 1001.59 | 1295.80 | - |
| EMASCULATED B-LINE X R-LINE_4 | 677.67 | 1040.40 | - | 1084.10 | 1487.04 | - |
| EMASCULATED B-LINE X R-LINE_5 | 941.50 | 1159.73 | - | 1277.79 | 1369.23 | - |
| EMASCULATED B-LINE X R-LINE_6 | 502.92 | 697.43 | - | 1127.33 | 1148.11 | - |
| EMASCULATED B-LINE X R-LINE_7 | 1254.75 | 1186.11 | - | 1077.99 | 809.83 | - |
| EMASCULATED B-LINE X R-LINE_8 | 855.46 | 990.53 | - | 1237.87 | 1246.67 | - |
| EMASCULATED B-LINE X R-LINE_9 | 1439.13 | 1477.97 | - | 1190.70 | 1098.00 | - |
| EMASCULATED B-LINE X R-LINE_10 | 1258.00 | 1025.22 | - | 999.17 | 887.25 | - |
| EMASCULATED B-LINE X R-LINE_11 | 1007.93 | 765.90 | - | 1244.70 | 1022.20 | - |
| EMASCULATED B-LINE X R-LINE_12 | 723.83 | 778.94 | - | 793.23 | 1134.90 | - |
| EMASCULATED B-LINE X R-LINE_13 | 960.42 | 1085.60 | - | 1310.73 | 793.51 | - |
| EMASCULATED B-LINE X R-LINE_14 | 1025.89 | 1122.67 | - | 1134.33 | 1025.13 | - |
| EMASCULATED B-LINE X R-LINE_15 | 601.33 | 851.25 | - | 1352.70 | 701.46 | - |
| EMASCULATED B-LINE X R-LINE_16 | 753.24 | 834.93 | - | 944.30 | 875.65 | - |
| EMASCULATED B-LINE X R-LINE_17 | 963.07 | 1034.67 | - | 1034.47 | 877.04 | - |
| EMASCULATED B-LINE X R-LINE_18 | 932.20 | 1108.42 | - | 1045.75 | 1089.04 | - |
| EMASCULATED B-LINE X R-LINE_19 | 599.73 | 1091.15 | - | 936.73 | 1632.40 | - |
| EMASCULATED B-LINE X R-LINE_20 | 612.62 | 880.59 | - | 1066.04 | 1189.90 | - |
| EMASCULATED B-LINE X R-LINE_21 | 889.72 | 1202.70 | - | 1058.00 | 979.55 | - |
| EMASCULATED B-LINE X R-LINE_22 | 553.00 | 1369.61 | - | 789.88 | 1249.39 | - |
| F1 HYBRID CMS-LINE X R-LINE_31 | 1131.60 | 1676.68 | - | 1455.40 | 1304.00 | - |
| REFERENCE_ES BELLA | 1504.35 | 1205.18 | 1358.21 | 1369.50 | 1130.68 | 1059.77 |
| REFERENCE_ES SAVANA | 1291.51 | 1168.41 | 1522.35 | 1255.10 | 1128.38 | 1241.63 |
| REFERENCE_ES COLUMBELLA | 1319.50 | 1318.71 | 1291.31 | 1370.58 | 1246.88 | 1341.58 |
| REFERENCE_SUMATRA | 1179.90 | 1159.72 | 1562.38 | 1233.47 | 1523.17 | 951.51 |
| REFERENCE_NK DELFI | 1467.05 | 1637.10 | 1435.69 | 1370.34 | 1463.89 | 1185.93 |

**Supplementary Table A 14:** Comparison of the oil yield of 11 F1-hybrids against oil yield of reference varieties

| LOC | PLANT DENSITY | REFERENCE VARIETY | OIL YIELD (L/HA) REF. | F1 HYBRID | OIL YIELD (L/HA) |
|---|---|---|---|---|---|
| **DE** | 20 cm | ES Bella | 1504.35 | LC-1093A x UGA-SAM1-207 | 1546.46 |
| **DE** | 25 cm | NK Delfi | 1637.10 | LC-1093A x UGA-SAM1-041 | 1676.68 |
| **DE** | 30 cm | Sumatra | 1562.38 | LC-1093A x UGA-SAM1-119 | 1677.00 |
|  |  |  |  | LC-1093A x UGA-SAM1-204 | 1830.83 |
|  |  |  |  | LC-1093A x UGA-SAM1-278 | 1626.19 |
|  |  |  |  | LC-1093A x UGA-SAM1-057 | 1629.35 |
|  |  |  |  | LC-1093A x UGA-SAM1-186 | 1835.46 |
| **RO** | 20 cm | ES Columbella | 1370.58 | LC-1093A x UGA-SAM1-041 | 1455.40 |
|  |  |  |  | LC-1093A x UGA-SAM1-055 | 1434.31 |
| **RO** | 25 cm | Sumatra | 1523.17 | LC-1093A x D-75-10 | 1568.48 |
|  |  |  |  | LC-1093A x UGA-SAM1-136 | 1594.10 |
|  |  |  |  | UGA-SAM1-082 x R-Line | 1632.40 |

**Supplementary Table A 15:** Results of the DeltaK method of Evanno *et al.* (2005) to determine most likely number of clusters

**RESULTS OF THE SMALL ASSOCIATION PANEL**

| K | Reps | Mean LnP(K) | Stdev LnP(K) | Ln'(K) | \|Ln''(K)\| | Delta K |
|---|---|---|---|---|---|---|
| **1** | 10 | -3110880000 | 0.799722 | — | — | — |
| **2** | 10 | -2871260000 | 3912146 | 239620000 | 53410000 | 13652352 |
| **3** | 10 | -2685050000 | 0.769199 | 186210000 | 51290000 | 66679778 |
| **4** | 10 | -2550130000 | 2219635 | 134920000 | 40950000 | 18448983 |
| **5** | 10 | -2456160000 | 10675018 | 93970000 | 7020000 | 0.657610 |
| **6** | 10 | -2369210000 | 2973756 | 86950000 | 11090000 | 3729291 |
| **7** | 10 | -2293350000 | 3017817 | 75860000 | 5140000 | 1703218 |
| **8** | 10 | -2222630000 | 3938711 | 70720000 | 10340000 | 2625224 |
| **9** | 10 | -2162250000 | 7320481 | 60380000 | 0.550000 | 0.075132 |
| **10** | 10 | -2102420000 | 7294260 | 59830000 | — | — |

**RESULTS OF THE LARGE ASSOCIATION PANEL**

| K | Reps | Mean LnP(K) | Stdev LnP(K) | Ln'(K) | \|Ln''(K)\| | Delta K |
|---|---|---|---|---|---|---|
| **1** | 10 | -23294260000 | 0.306232 | — | — | — |
| **2** | 10 | -21056680000 | 0.993087 | 2237580000 | 1087990000 | 1095563391 |
| **3** | 10 | -19907090000 | 65483576 | 1149590000 | 217580000 | 3322665 |
| **4** | 10 | -18975080000 | 3018020 | 932010000 | 622810000 | 206363778 |
| **5** | 10 | -18665880000 | 13373589 | 309200000 | 54300000 | 4060241 |
| **6** | 10 | -18410980000 | 68317897 | 254900000 | 23190000 | 0.339443 |
| **7** | 10 | -18179270000 | 70299124 | 231710000 | 18500000 | 0.263161 |
| **8** | 10 | -17966060000 | 104442597 | 213210000 | 105490000 | 1010029 |
| **9** | 10 | -17858340000 | 238756902 | 107720000 | 154230000 | 0.645971 |
| **10** | 10 | -17596390000 | 121878815 | 261950000 | — | — |

**RESULTS OF THE COMBINED ASSOCIATION PANEL**

| K | Reps | Mean LnP(K) | Stdev LnP(K) | Ln'(K) | \|Ln''(K)\| | Delta K |
|---|---|---|---|---|---|---|
| **1** | 10 | -29.923.750.000 | 0.287711 | — | — | — |
| **2** | 10 | -26.329.700.000 | 54.314.496 | 3.594.050.000 | 1.738.300.000 | 32.004.348 |
| **3** | 10 | -24.473.950.000 | 415.861.062 | 1.855.750.000 | 491.570.000 | 1.182.053 |
| **4** | 10 | -23.109.770.000 | 85.335.730 | 1.364.180.000 | 410.000.000 | 4.804.553 |
| **5** | 10 | -22.155.590.000 | 3.129.590 | 954.180.000 | 693.850.000 | 221.706.360 |
| **6** | 10 | -21.895.260.000 | 82.830.781 | 260.330.000 | 72.500.000 | 0.875278 |
| **7** | 10 | -21.562.430.000 | 52.475.477 | 332.830.000 | 166.050.000 | 3.164.335 |
| **8** | 10 | -21.395.650.000 | 130.700.712 | 166.780.000 | 43.710.000 | 0.334428 |
| **9** | 10 | -21.185.160.000 | 80.038.216 | 210.490.000 | 45.990.000 | 0.574601 |
| **10** | 10 | -20.928.680.000 | 50.909.414 | 256.480.000 | — | — |

**Supplementary Table A 16**: Significant SNPs with effect on aa sequences, including pair distance of Miyata et al. (1979)

| gene | SNP | trait | alleles | aa change | aa position | Pair distance |
|---|---|---|---|---|---|---|
| *HaSNE2* | SNE171.5 | Plant height | A/T | N/I | 8 | 3.37 |
| *HaDELLA2* | DEL801.17 | Plant height | T/C | I/V | 147 | 0.85 |
| *HaSLY1A* | SLY301.2 | Plant height | G/C | D/E | 44 | 0.90 |
| *HaGID1C* | GID131.30 | Plant height | A/G | K/R | 186 | 0.40 |
| *HaDELLA-Like2* | DEL091.7 | Petiole angle | C/G | A/P | 447 | 0.06 |
|  | DEL091.8 | Petiole angle | C/T | V/I | 434 | 0.85 |
|  | DEL091.9 | Petiole angle | A/C | D/E | 425 | 0.90 |
|  | DEL091.25 | Petiole angle | C/G | A/P | 117 | 0.06 |
| *HaLAZY1* | LAZ951.11 | Plant height | A/G | V/A | 61 | 1.85 |

**Supplementary Table A 17:** Summary of GLM results for data of the small association panel (64 genotypes) in Germany 2017, limit value p = 0.000164

| MARKER | CHR | TRAIT | POS | P | TRAIT | POS | P |
|---|---|---|---|---|---|---|---|
| **GID871.5** | 1 | PlantHT | 12851807 | 0.695102623 | PetAngle | 12851807 | 0.851608644 |
| **GID871.6** | 1 | PlantHT | 12852614 | 0.9962248 | PetAngle | 12852614 | 0.943066647 |
| **GID871.7** | 1 | PlantHT | 12852731 | 0.767098672 | PetAngle | 12852731 | 0.563244843 |
| **GID871.9** | 1 | PlantHT | 12852833 | 0.074331032 | PetAngle | 12852833 | 0.399131408 |
| **GID871.10** | 1 | PlantHT | 12852858 | 0.070534257 | PetAngle | 12852858 | 0.404638957 |
| **GID871.11** | 1 | PlantHT | 12853069 | 0.110631047 | PetAngle | 12853069 | 0.628264299 |
| **GID871.12** | 1 | PlantHT | 12853100 | 0.901568621 | PetAngle | 12853100 | 0.242907862 |
| **GID871.13** | 1 | PlantHT | 12853241 | 0.860396126 | PetAngle | 12853241 | 0.104449007 |
| **GID871.14** | 1 | PlantHT | 12853328 | 0.469949212 | PetAngle | 12853328 | 0.469026186 |
| **GID871.15** | 1 | PlantHT | 12853334 | 0.469949212 | PetAngle | 12853334 | 0.469026186 |
| **GID871.16** | 1 | PlantHT | 12853430 | 0.202347963 | PetAngle | 12853430 | 0.049877704 |
| **GID871.17** | 1 | PlantHT | 12853511 | 0.055247717 | PetAngle | 12853511 | 0.588422898 |
| **GID871.21** | 1 | PlantHT | 12853600 | 0.629836689 | PetAngle | 12853600 | 0.439471528 |
| **GID871.22** | 1 | PlantHT | 12853709 | 0.827580912 | PetAngle | 12853709 | 0.019662781 |
| **GID871.23** | 1 | PlantHT | 12853714 | 0.144988712 | PetAngle | 12853714 | 0.474732138 |
| **SLY061.3** | 2 | PlantHT | 39413612 | 0.081098702 | PetAngle | 39413612 | 0.209854752 |
| **SLY061.4** | 2 | PlantHT | 39413618 | 0.081098702 | PetAngle | 39413618 | 0.209854752 |
| **SLY061.5** | 2 | PlantHT | 39413737 | 0.038445166 | PetAngle | 39413737 | 0.170082719 |
| **SLY061.6** | 2 | PlantHT | 39413802 | 0.031568055 | PetAngle | 39413802 | 0.137034462 |
| **SLY061.7** | 2 | PlantHT | 39414098 | 0.667404526 | PetAngle | 39414098 | 0.396041805 |
| **SLY061.11** | 2 | PlantHT | 39415029 | 0.133798437 | PetAngle | 39415029 | 0.284435754 |
| **SLY061.14** | 2 | PlantHT | 39415287 | 0.022484016 | PetAngle | 39415287 | 0.144472096 |
| **SLY061.15** | 2 | PlantHT | 39415439 | 0.023373297 | PetAngle | 39415439 | 0.135421183 |
| **SLY061.16** | 2 | PlantHT | 39415448 | 0.023373297 | PetAngle | 39415448 | 0.135421183 |
| **SLY061.17** | 2 | PlantHT | 39415600 | 0.779383565 | PetAngle | 39415600 | 0.045282298 |
| **SLY061.19** | 2 | PlantHT | 39415765 | 0.817630907 | PetAngle | 39415765 | 0.058861084 |
| **SLY061.20** | 2 | PlantHT | 39415978 | 0.779383565 | PetAngle | 39415978 | 0.045282298 |
| **SLY061.21** | 2 | PlantHT | 39416235 | 0.651018461 | PetAngle | 39416235 | 0.025645513 |
| **SLY061.22** | 2 | PlantHT | 39416259 | 0.52516064 | PetAngle | 39416259 | 0.079242433 |
| **SNE171.1** | 3 | PlantHT | 104932867 | 0.510591309 | PetAngle | 104932867 | 0.721941916 |
| **SNE171.5** | 3 | PlantHT | 104934540 | 0.06324517 | PetAngle | 104934540 | 0.339804927 |
| **SNE171.6** | 3 | PlantHT | 104934736 | 0.06324517 | PetAngle | 104934736 | 0.339804927 |
| **SNE171.7** | 3 | PlantHT | 104934791 | 0.733984772 | PetAngle | 104934791 | 0.249989925 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **SNE171.8** | 3 | PlantHT | 104934943 | 0.414628227 | PetAngle | 104934943 | 0.445852374 |
| **SLY321.1** | 4 | PlantHT | 40919975 | 0.180702229 | PetAngle | 40919975 | 0.003759835 |
| **SLY321.2** | 4 | PlantHT | 40920036 | 0.120974373 | PetAngle | 40920036 | 0.014564579 |
| **SLY321.3** | 4 | PlantHT | 40920185 | 0.758439156 | PetAngle | 40920185 | 0.976952898 |
| **SLY321.6** | 4 | PlantHT | 40920969 | 0.560525958 | PetAngle | 40920969 | 0.052191844 |
| **SLY321.8** | 4 | PlantHT | 40921919 | 0.36240927 | PetAngle | 40921919 | 0.184408288 |
| **SLY351.2** | 4 | PlantHT | 41287638 | 0.211544094 | PetAngle | 41287638 | 0.104269319 |
| **SLY351.4** | 4 | PlantHT | 41287804 | 0.347553294 | PetAngle | 41287804 | 0.058515408 |
| **SLY351.6** | 4 | PlantHT | 41288086 | 0.219365208 | PetAngle | 41288086 | 0.027831544 |
| **SLY351.7** | 4 | PlantHT | 41288167 | 0.434363271 | PetAngle | 41288167 | 0.583857735 |
| **SLY351.8** | 4 | PlantHT | 41288598 | 0.219365208 | PetAngle | 41288598 | 0.027831544 |
| **SLY351.9** | 4 | PlantHT | 41288616 | 0.219365208 | PetAngle | 41288616 | 0.027831544 |
| **SLY351.11** | 4 | PlantHT | 41289089 | 0.228789301 | PetAngle | 41289089 | 0.039333979 |
| **TAC361.1** | 4 | PlantHT | 155517271 | 0.632654134 | PetAngle | 155517271 | 0.807937416 |
| **TAC361.2** | 4 | PlantHT | 155517418 | 0.088981118 | PetAngle | 155517418 | 0.706562528 |
| **TAC361.3** | 4 | PlantHT | 155517438 | 0.607549016 | PetAngle | 155517438 | 0.279501179 |
| **TAC361.4** | 4 | PlantHT | 155517453 | 0.088981118 | PetAngle | 155517453 | 0.706562528 |
| **TAC361.5** | 4 | PlantHT | 155517553 | 0.616442462 | PetAngle | 155517553 | 0.273064419 |
| **TAC361.6** | 4 | PlantHT | 155517627 | 0.327049197 | PetAngle | 155517627 | 0.903988806 |
| **TAC361.9** | 4 | PlantHT | 155518008 | 0.241331154 | PetAngle | 155518008 | 0.408258068 |
| **TAC361.10** | 4 | PlantHT | 155518227 | 0.09547696 | PetAngle | 155518227 | 0.48068091 |
| **TAC361.13** | 4 | PlantHT | 155519213 | 0.649001689 | PetAngle | 155519213 | 0.264926555 |
| **TAC361.14** | 4 | PlantHT | 155519529 | 0.595613566 | PetAngle | 155519529 | 0.733688446 |
| **TAC361.16** | 4 | PlantHT | 155519787 | 0.438535498 | PetAngle | 155519787 | 0.188944677 |
| **TAC361.17** | 4 | PlantHT | 155519800 | 0.971768749 | PetAngle | 155519800 | 0.466730304 |
| **TAC361.18** | 4 | PlantHT | 155520038 | 0.268943649 | PetAngle | 155520038 | 0.110285733 |
| **TAC361.19** | 4 | PlantHT | 155520121 | 0.109728545 | PetAngle | 155520121 | 0.671105846 |
| **TAC361.20** | 4 | PlantHT | 155520230 | 0.04923936 | PetAngle | 155520230 | 0.24951914 |
| **TAC361.21** | 4 | PlantHT | 155520277 | 0.858534472 | PetAngle | 155520277 | 0.56899675 |
| **TAC361.22** | 4 | PlantHT | 155520338 | 0.186251078 | PetAngle | 155520338 | 0.89641327 |
| **TAC361.23** | 4 | PlantHT | 155520558 | 0.990483337 | PetAngle | 155520558 | 0.296214165 |
| **SLY141.1** | 5 | PlantHT | 163484536 | 0.56736741 | PetAngle | 163484536 | 0.445028706 |
| **SLY141.2** | 5 | PlantHT | 163484898 | 0.658792527 | PetAngle | 163484898 | 0.941946926 |
| **SLY141.3** | 5 | PlantHT | 163484956 | 0.688751031 | PetAngle | 163484956 | 0.207139539 |
| **SLY141.4** | 5 | PlantHT | 163484969 | 0.520231795 | PetAngle | 163484969 | 0.512585005 |
| **SLY141.5** | 5 | PlantHT | 163485239 | 0.260120019 | PetAngle | 163485239 | 0.064119719 |
| **SLY141.6** | 5 | PlantHT | 163485248 | 0.264953032 | PetAngle | 163485248 | 0.011025061 |
| **SLY141.7** | 5 | PlantHT | 163485257 | 0.773059259 | PetAngle | 163485257 | 0.573683018 |
| **SLY141.8** | 5 | PlantHT | 163485366 | 0.516111514 | PetAngle | 163485366 | 0.100811168 |
| **SLY141.10** | 5 | PlantHT | 163485423 | 0.754219054 | PetAngle | 163485423 | 0.555829965 |
| **SLY141.11** | 5 | PlantHT | 163485618 | 0.730021818 | PetAngle | 163485618 | 0.018156228 |
| **SLY141.12** | 5 | PlantHT | 163485624 | 0.730021818 | PetAngle | 163485624 | 0.018156228 |
| **SLY141.13** | 5 | PlantHT | 163486432 | 0.688586085 | PetAngle | 163486432 | 0.385800082 |
| **SLY141.14** | 5 | PlantHT | 163486451 | 0.851638426 | PetAngle | 163486451 | 0.719819023 |
| **SLY141.15** | 5 | PlantHT | 163486868 | 0.476530163 | PetAngle | 163486868 | 0.226558898 |
| **GID741.2** | 6 | PlantHT | 43970283 | 0.787404165 | PetAngle | 43970283 | 0.944589448 |
| **GID741.3** | 6 | PlantHT | 43970298 | 0.436427273 | PetAngle | 43970298 | 0.600967576 |
| **GID741.4** | 6 | PlantHT | 43970589 | 0.781373437 | PetAngle | 43970589 | 0.58201865 |
| **GID741.5** | 6 | PlantHT | 43971149 | 0.850449304 | PetAngle | 43971149 | 0.500881721 |

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| **LAZ951.1** | 8 | PlantHT | 7807354 | 0.646972677 | PetAngle | 7807354 | 0.053578888 |
| **LAZ951.2** | 8 | PlantHT | 7807376 | 0.454458928 | PetAngle | 7807376 | 0.059852232 |
| **LAZ951.3** | 8 | PlantHT | 7807503 | 0.817869549 | PetAngle | 7807503 | 0.090855906 |
| **LAZ951.4** | 8 | PlantHT | 7807600 | 0.947267423 | PetAngle | 7807600 | 0.155101239 |
| **LAZ951.5** | 8 | PlantHT | 7807614 | 0.849314917 | PetAngle | 7807614 | 0.719137497 |
| **LAZ951.6** | 8 | PlantHT | 7807682 | 0.987102206 | PetAngle | 7807682 | 0.041363472 |
| **LAZ951.7** | 8 | PlantHT | 7809093 | 0.447998422 | PetAngle | 7809093 | 0.002337926 |
| **LAZ951.8** | 8 | PlantHT | 7809138 | 0.46757162 | PetAngle | 7809138 | 7.9515E-04 |
| **LAZ951.9** | 8 | PlantHT | 7809176 | 0.385053145 | PetAngle | 7809176 | 0.02437273 |
| **LAZ951.10** | 8 | PlantHT | 7809246 | 0.488415208 | PetAngle | 7809246 | 0.357225322 |
| **LAZ951.11** | 8 | PlantHT | 7809319 | 0.239691189 | PetAngle | 7809319 | 0.295141489 |
| **LAZ951.12** | 8 | PlantHT | 7809351 | 0.762137834 | PetAngle | 7809351 | 0.007650793 |
| **LAZ951.13** | 8 | PlantHT | 7809384 | 0.554141974 | PetAngle | 7809384 | 0.139014203 |
| **LAZ951.14** | 8 | PlantHT | 7809516 | 0.203892517 | PetAngle | 7809516 | 0.009306611 |
| **LAZ951.15** | 8 | PlantHT | 7809577 | 0.741721706 | PetAngle | 7809577 | 0.007151752 |
| **LAZ951.16** | 8 | PlantHT | 7809616 | 0.831535196 | PetAngle | 7809616 | 0.691035035 |
| **LAZ951.17** | 8 | PlantHT | 7809770 | 0.610306776 | PetAngle | 7809770 | 0.408853168 |
| **LAZ951.18** | 8 | PlantHT | 7810149 | 0.634674314 | PetAngle | 7810149 | 0.045006638 |
| **LAZ951.20** | 8 | PlantHT | 7810266 | 0.361769973 | PetAngle | 7810266 | 0.017257771 |
| **LAZ951.21** | 8 | PlantHT | 7810443 | 0.041119933 | PetAngle | 7810443 | 0.148813555 |
| **LAZ951.23** | 8 | PlantHT | 7810829 | 0.630459449 | PetAngle | 7810829 | 0.013744891 |
| **LAZ951.24** | 8 | PlantHT | 7810961 | 0.18005507 | PetAngle | 7810961 | 0.208164356 |
| **LAZ951.26** | 8 | PlantHT | 7811459 | 0.842536529 | PetAngle | 7811459 | 0.025034518 |
| **LAZ951.27** | 8 | PlantHT | 7811479 | 0.319708925 | PetAngle | 7811479 | 0.046184928 |
| **LAZ951.28** | 8 | PlantHT | 7811553 | 0.570180462 | PetAngle | 7811553 | 0.015435967 |
| **LAZ951.29** | 8 | PlantHT | 7812053 | 0.145428287 | PetAngle | 7812053 | 0.992440844 |
| **DEL091.3** | 8 | PlantHT | 12263870 | 0.770476013 | PetAngle | 12263870 | 0.001827709 |
| **DEL091.4** | 8 | PlantHT | 12263903 | 0.520765379 | PetAngle | 12263903 | 6.5109E-04 |
| **DEL091.5** | 8 | PlantHT | 12263912 | 0.154494438 | PetAngle | 12263912 | 0.650488497 |
| **DEL091.6** | 8 | PlantHT | 12264043 | 0.871404003 | PetAngle | 12264043 | 0.533851898 |
| **DEL091.7** | 8 | PlantHT | 12264064 | 0.046766906 | PetAngle | 12264064 | 3.0029E-04 |
| **DEL091.8** | 8 | PlantHT | 12264103 | 0.222433988 | PetAngle | 12264103 | 0.197637171 |
| **DEL091.9** | 8 | PlantHT | 12264128 | 0.311270004 | PetAngle | 12264128 | 0.241030891 |
| **DEL091.10** | 8 | PlantHT | 12264206 | 0.002896475 | PetAngle | 12264206 | 0.614243207 |
| **DEL091.12** | 8 | PlantHT | 12264269 | 0.526303528 | PetAngle | 12264269 | 0.730781955 |
| **DEL091.13** | 8 | PlantHT | 12264332 | 0.139175013 | PetAngle | 12264332 | 0.632556657 |
| **DEL091.14** | 8 | PlantHT | 12264404 | 0.840035642 | PetAngle | 12264404 | 0.030079195 |
| **DEL091.15** | 8 | PlantHT | 12264512 | 0.216808741 | PetAngle | 12264512 | 0.002268364 |
| **DEL091.16** | 8 | PlantHT | 12264599 | 0.926957225 | PetAngle | 12264599 | 0.961539373 |
| **DEL091.17** | 8 | PlantHT | 12264604 | 0.10736005 | PetAngle | 12264604 | 0.001931791 |
| **DEL091.18** | 8 | PlantHT | 12264635 | 0.027635999 | PetAngle | 12264635 | 2.4943E-04 |
| **DEL091.20** | 8 | PlantHT | 12264789 | 0.167623382 | PetAngle | 12264789 | 0.246959555 |
| **DEL091.21** | 8 | PlantHT | 12264795 | 0.358690601 | PetAngle | 12264795 | 0.059419252 |
| **DEL091.22** | 8 | PlantHT | 12264962 | 0.133364339 | PetAngle | 12264962 | 0.752625381 |
| **DEL091.24** | 8 | PlantHT | 12265025 | 0.062009842 | PetAngle | 12265025 | 0.048481251 |
| **DEL091.25** | 8 | PlantHT | 12265054 | 0.051454769 | PetAngle | 12265054 | 3.4245E-04 |
| **DEL091.26** | 8 | PlantHT | 12265056 | 0.373922674 | PetAngle | 12265056 | 0.755804094 |
| **DEL091.27** | 8 | PlantHT | 12265422 | 0.076818584 | PetAngle | 12265422 | 4.9340E-04 |
| **DEL091.29** | 8 | PlantHT | 12265567 | 0.14406402 | PetAngle | 12265567 | 0.697085004 |

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| **DEL091.30** | 8 | PlantHT | 12265676 | 1.4134E-04 | PetAngle | 12265676 | 0.048465552 |
| **DEL091.31** | 8 | PlantHT | 12265683 | 0.001466517 | PetAngle | 12265683 | 0.139703758 |
| **DEL091.32** | 8 | PlantHT | 12265802 | 0.03356726 | PetAngle | 12265802 | 0.07970724 |
| **DEL091.33** | 8 | PlantHT | 12266012 | 1.5819E-04 | PetAngle | 12266012 | 0.222381581 |
| **DEL091.34** | 8 | PlantHT | 12266161 | 0.556975116 | PetAngle | 12266161 | 0.326212816 |
| **DEL091.35** | 8 | PlantHT | 12266179 | 0.266956028 | PetAngle | 12266179 | 0.005868687 |
| **DEL091.36** | 8 | PlantHT | 12266186 | 0.359080087 | PetAngle | 12266186 | 0.029094182 |
| **DEL091.37** | 8 | PlantHT | 12266199 | 0.277373874 | PetAngle | 12266199 | 0.028659154 |
| **DEL091.38** | 8 | PlantHT | 12266211 | 0.555420864 | PetAngle | 12266211 | 0.652770101 |
| **DEL091.41** | 8 | PlantHT | 12266403 | 0.486362339 | PetAngle | 12266403 | 0.640709483 |
| **DEL091.42** | 8 | PlantHT | 12266417 | 0.59885309 | PetAngle | 12266417 | 0.016007883 |
| **DEL091.43** | 8 | PlantHT | 12266464 | 0.22034473 | PetAngle | 12266464 | 0.022962703 |
| **DEL091.47** | 8 | PlantHT | 12266830 | 0.240669727 | PetAngle | 12266830 | 2.3407E-04 |
| **DEL091.48** | 8 | PlantHT | 12266863 | 0.309721978 | PetAngle | 12266863 | 3.0610E-04 |
| **DEL091.49** | 8 | PlantHT | 12266939 | 0.313231293 | PetAngle | 12266939 | 0.424015427 |
| **DEL091.50** | 8 | PlantHT | 12267167 | 0.214623432 | PetAngle | 12267167 | 0.901899012 |
| **DEL091.52** | 8 | PlantHT | 12267267 | 0.214623432 | PetAngle | 12267267 | 0.901899012 |
| **SLY301.1** | 9 | PlantHT | 178666111 | 0.321528637 | PetAngle | 178666111 | 0.66884749 |
| **SLY301.2** | 9 | PlantHT | 178666159 | 0.340773995 | PetAngle | 178666159 | 0.967561955 |
| **SLY301.3** | 9 | PlantHT | 178666187 | 0.202412397 | PetAngle | 178666187 | 0.897551109 |
| **SLY301.4** | 9 | PlantHT | 178666431 | 0.875062234 | PetAngle | 178666431 | 0.696758128 |
| **SLY301.5** | 9 | PlantHT | 178666702 | 0.372752328 | PetAngle | 178666702 | 0.904389612 |
| **SLY301.7** | 9 | PlantHT | 178668175 | 0.234573914 | PetAngle | 178668175 | 0.057157396 |
| **GID071.1** | 10 | PlantHT | 28111762 | 0.985665294 | PetAngle | 28111762 | 0.044119276 |
| **GID071.4** | 10 | PlantHT | 28111944 | 0.109002484 | PetAngle | 28111944 | 0.039154945 |
| **GID071.5** | 10 | PlantHT | 28111956 | 0.12759091 | PetAngle | 28111956 | 0.049756415 |
| **GID071.7** | 10 | PlantHT | 28111995 | 0.445178293 | PetAngle | 28111995 | 0.383695934 |
| **GID071.13** | 10 | PlantHT | 28112319 | 0.309579139 | PetAngle | 28112319 | 0.01149674 |
| **GID071.14** | 10 | PlantHT | 28112493 | 0.208100424 | PetAngle | 28112493 | 0.009199054 |
| **GID071.15** | 10 | PlantHT | 28112634 | 0.867431853 | PetAngle | 28112634 | 0.002150453 |
| **GID071.16** | 10 | PlantHT | 28112657 | 0.334950682 | PetAngle | 28112657 | 1.3088E-05 |
| **GID071.17** | 10 | PlantHT | 28112679 | 0.208100424 | PetAngle | 28112679 | 0.009199054 |
| **GID071.18** | 10 | PlantHT | 28112826 | 0.253923811 | PetAngle | 28112826 | 0.854555339 |
| **GID071.19** | 10 | PlantHT | 28112847 | 0.463483956 | PetAngle | 28112847 | 0.449360313 |
| **GID071.20** | 10 | PlantHT | 28112916 | 0.235831744 | PetAngle | 28112916 | 0.010338629 |
| **GID071.21** | 10 | PlantHT | 28112919 | 0.331466366 | PetAngle | 28112919 | 0.308544085 |
| **GID071.22** | 10 | PlantHT | 28113024 | 0.776669022 | PetAngle | 28113024 | 1.9118E-04 |
| **GID071.23** | 10 | PlantHT | 28113051 | 0.504842668 | PetAngle | 28113051 | 5.0811E-04 |
| **GID071.24** | 10 | PlantHT | 28113168 | 0.666766408 | PetAngle | 28113168 | 3.5770E-05 |
| **GID071.26** | 10 | PlantHT | 28113769 | 0.551335255 | PetAngle | 28113769 | 0.4326615 |
| **GID071.28** | 10 | PlantHT | 28113897 | 0.460073177 | PetAngle | 28113897 | 9.5568E-04 |
| **GID071.29** | 10 | PlantHT | 28113914 | 0.95758372 | PetAngle | 28113914 | 0.865596751 |
| **GID071.30** | 10 | PlantHT | 28114325 | 0.330402097 | PetAngle | 28114325 | 0.002915038 |
| **GID071.34** | 10 | PlantHT | 28114759 | 0.098225282 | PetAngle | 28114759 | 0.003281814 |
| **GID071.36** | 10 | PlantHT | 28114977 | 0.504842668 | PetAngle | 28114977 | 5.0811E-04 |
| **GID071.38** | 10 | PlantHT | 28115179 | 0.987853867 | PetAngle | 28115179 | 5.8049E-04 |
| **GID071.39** | 10 | PlantHT | 28115187 | 0.207412307 | PetAngle | 28115187 | 0.007013195 |
| **GID071.42** | 10 | PlantHT | 28116112 | 0.318874941 | PetAngle | 28116112 | 0.224257013 |
| **DEL171.2** | 10 | PlantHT | 34968719 | 0.222684758 | PetAngle | 34968719 | 0.438970695 |

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| **SLY611.1** | 11 | PlantHT | 138990416 | 0.377664193 | PetAngle | 138990416 | 0.914230615 |
| **SLY611.2** | 11 | PlantHT | 138990539 | 0.521895516 | PetAngle | 138990539 | 0.498750246 |
| **SLY611.3** | 11 | PlantHT | 138990639 | 0.971807649 | PetAngle | 138990639 | 0.639871851 |
| **SLY611.4** | 11 | PlantHT | 138990798 | 0.971807649 | PetAngle | 138990798 | 0.639871851 |
| **SLY611.5** | 11 | PlantHT | 138991001 | 0.666225557 | PetAngle | 138991001 | 0.025983143 |
| **SLY611.8** | 11 | PlantHT | 138992806 | 0.171669983 | PetAngle | 138992806 | 0.996737688 |
| **SLY611.9** | 11 | PlantHT | 138993071 | 0.241232429 | PetAngle | 138993071 | 0.218430952 |
| **SLY611.10** | 11 | PlantHT | 138993192 | 0.157196056 | PetAngle | 138993192 | 0.080786452 |
| **SLY611.11** | 11 | PlantHT | 138993311 | 0.9611044 | PetAngle | 138993311 | 0.408719082 |
| **DEL901.1** | 12 | PlantHT | 32211683 | 0.24926222 | PetAngle | 32211683 | 0.00128471 |
| **DEL901.2** | 12 | PlantHT | 32211812 | 0.24926222 | PetAngle | 32211812 | 0.00128471 |
| **DEL901.3** | 12 | PlantHT | 32211968 | 0.479203014 | PetAngle | 32211968 | 0.00539651 |
| **DEL901.4** | 12 | PlantHT | 32212028 | 0.479203014 | PetAngle | 32212028 | 0.00539651 |
| **DEL901.5** | 12 | PlantHT | 32212178 | 0.50441282 | PetAngle | 32212178 | 0.005758114 |
| **DEL901.6** | 12 | PlantHT | 32212556 | 0.459954256 | PetAngle | 32212556 | 0.004595079 |
| **DEL901.7** | 12 | PlantHT | 32212608 | 0.098774969 | PetAngle | 32212608 | 0.692321713 |
| **DEL901.8** | 12 | PlantHT | 32212620 | 0.958794782 | PetAngle | 32212620 | 0.599437777 |
| **DEL901.9** | 12 | PlantHT | 32212719 | 0.24926222 | PetAngle | 32212719 | 0.00128471 |
| **DEL901.10** | 12 | PlantHT | 32213076 | 0.24926222 | PetAngle | 32213076 | 0.00128471 |
| **DEL901.11** | 12 | PlantHT | 32213328 | 0.535428726 | PetAngle | 32213328 | 0.005400208 |
| **DEL901.12** | 12 | PlantHT | 32213465 | 0.851405817 | PetAngle | 32213465 | 0.678583718 |
| **SNE981.1** | 12 | PlantHT | 81945604 | 0.396454742 | PetAngle | 81945604 | 0.14615784 |
| **SNE981.2** | 12 | PlantHT | 81945790 | 0.731077048 | PetAngle | 81945790 | 0.696371275 |
| **SNE981.5** | 12 | PlantHT | 81946423 | 0.454719382 | PetAngle | 81946423 | 0.136275112 |
| **SNE981.6** | 12 | PlantHT | 81946530 | 0.454719382 | PetAngle | 81946530 | 0.136275112 |
| **SNE981.8** | 12 | PlantHT | 81947032 | 0.396454742 | PetAngle | 81947032 | 0.14615784 |
| **SNE981.9** | 12 | PlantHT | 81947042 | 0.396454742 | PetAngle | 81947042 | 0.14615784 |
| **SNE981.11** | 12 | PlantHT | 81947454 | 0.562181061 | PetAngle | 81947454 | 0.108060443 |
| **SNE981.12** | 12 | PlantHT | 81947533 | 0.454719382 | PetAngle | 81947533 | 0.136275112 |
| **SNE981.13** | 12 | PlantHT | 81947575 | 0.454719382 | PetAngle | 81947575 | 0.136275112 |
| **SNE981.14** | 12 | PlantHT | 81948022 | 0.981563586 | PetAngle | 81948022 | 0.474821073 |
| **GID131.1** | 14 | PlantHT | 127160607 | 0.922886939 | PetAngle | 127160607 | 0.870805327 |
| **GID131.2** | 14 | PlantHT | 127160680 | 0.004541276 | PetAngle | 127160680 | 0.767471504 |
| **GID131.3** | 14 | PlantHT | 127160706 | 7.76E-04 | PetAngle | 127160706 | 0.468428364 |
| **GID131.5** | 14 | PlantHT | 127160797 | 0.967340835 | PetAngle | 127160797 | 0.471203166 |
| **GID131.6** | 14 | PlantHT | 127160916 | 0.20297223 | PetAngle | 127160916 | 0.367693448 |
| **GID131.7** | 14 | PlantHT | 127160942 | 0.004543672 | PetAngle | 127160942 | 0.376965701 |
| **GID131.9** | 14 | PlantHT | 127161170 | 0.00266021 | PetAngle | 127161170 | 0.441272568 |
| **GID131.10** | 14 | PlantHT | 127161183 | 0.992778827 | PetAngle | 127161183 | 0.462901815 |
| **GID131.13** | 14 | PlantHT | 127161687 | 0.146330329 | PetAngle | 127161687 | 0.160616791 |
| **GID131.14** | 14 | PlantHT | 127161715 | 0.776688384 | PetAngle | 127161715 | 0.25615581 |
| **GID131.15** | 14 | PlantHT | 127162040 | 0.551038601 | PetAngle | 127162040 | 0.202802122 |
| **GID131.18** | 14 | PlantHT | 127162519 | 0.048127744 | PetAngle | 127162519 | 0.543685587 |
| **GID131.19** | 14 | PlantHT | 127162646 | 0.862293513 | PetAngle | 127162646 | 0.615783043 |
| **GID131.20** | 14 | PlantHT | 127162694 | 0.992490028 | PetAngle | 127162694 | 0.360051026 |
| **GID131.21** | 14 | PlantHT | 127162874 | 0.061370897 | PetAngle | 127162874 | 0.950393862 |
| **GID131.22** | 14 | PlantHT | 127162881 | 0.07724648 | PetAngle | 127162881 | 0.901769443 |
| **GID131.24** | 14 | PlantHT | 127163001 | 0.014160316 | PetAngle | 127163001 | 0.911013864 |
| **GID131.25** | 14 | PlantHT | 127163141 | 0.020936667 | PetAngle | 127163141 | 0.613777196 |

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| **GID131.27** | 14 | PlantHT | 127163432 | 4.1766E-04 | PetAngle | 127163432 | 0.504694046 |
| **GID131.28** | 14 | PlantHT | 127163504 | 0.058167292 | PetAngle | 127163504 | 0.414409904 |
| **GID131.29** | 14 | PlantHT | 127163681 | 0.94311477 | PetAngle | 127163681 | 0.372228011 |
| **GID131.30** | 14 | PlantHT | 127163764 | 0.607281271 | PetAngle | 127163764 | 0.588441015 |
| **GID131.31** | 14 | PlantHT | 127163847 | 0.038836214 | PetAngle | 127163847 | 0.146188518 |
| **GID131.32** | 14 | PlantHT | 127163939 | 0.058167292 | PetAngle | 127163939 | 0.414409904 |
| **GID131.33** | 14 | PlantHT | 127164023 | 0.271009976 | PetAngle | 127164023 | 0.225084969 |
| **GID131.34** | 14 | PlantHT | 127164137 | 0.94311477 | PetAngle | 127164137 | 0.372228011 |
| **GID131.35** | 14 | PlantHT | 127164254 | 0.198321718 | PetAngle | 127164254 | 0.457741468 |
| **GID131.36** | 14 | PlantHT | 127164266 | 0.135121433 | PetAngle | 127164266 | 0.464699333 |
| **GID131.37** | 14 | PlantHT | 127164443 | 0.415271731 | PetAngle | 127164443 | 0.572290849 |
| **GID131.38** | 14 | PlantHT | 127164454 | 0.097585447 | PetAngle | 127164454 | 0.615055983 |
| **GID131.39** | 14 | PlantHT | 127164489 | 5.4757E-04 | PetAngle | 127164489 | 0.695356871 |
| **TAC641.1** | 16 | PlantHT | 154345819 | 0.399905019 | PetAngle | 154345819 | 0.055084745 |
| **TAC641.4** | 16 | PlantHT | 154346996 | 0.566858898 | PetAngle | 154346996 | 0.346809462 |
| **TAC641.5** | 16 | PlantHT | 154347203 | 0.026377941 | PetAngle | 154347203 | 0.082648741 |
| **DEL801.3** | 17 | PlantHT | 194808097 | 0.822988766 | PetAngle | 194808097 | 0.040213615 |
| **DEL801.4** | 17 | PlantHT | 194808128 | 0.48906537 | PetAngle | 194808128 | 0.051743388 |
| **DEL801.5** | 17 | PlantHT | 194808137 | 0.631802233 | PetAngle | 194808137 | 0.358720481 |
| **DEL801.6** | 17 | PlantHT | 194808477 | 0.513265809 | PetAngle | 194808477 | 0.480683358 |
| **DEL801.7** | 17 | PlantHT | 194808602 | 0.47170788 | PetAngle | 194808602 | 0.257798945 |
| **DEL801.8** | 17 | PlantHT | 194808652 | 0.503653139 | PetAngle | 194808652 | 0.171820722 |
| **DEL801.9** | 17 | PlantHT | 194808815 | 0.503653139 | PetAngle | 194808815 | 0.171820722 |
| **DEL801.10** | 17 | PlantHT | 194808854 | 0.129274766 | PetAngle | 194808854 | 0.374256451 |
| **DEL801.11** | 17 | PlantHT | 194808920 | 0.453648977 | PetAngle | 194808920 | 0.972537342 |
| **DEL801.12** | 17 | PlantHT | 194809025 | 0.020356124 | PetAngle | 194809025 | 0.16140553 |
| **DEL801.13** | 17 | PlantHT | 194809088 | 0.037407743 | PetAngle | 194809088 | 0.477858114 |
| **DEL801.14** | 17 | PlantHT | 194809186 | 0.363145546 | PetAngle | 194809186 | 0.128757842 |
| **DEL801.16** | 17 | PlantHT | 194809335 | 0.272605896 | PetAngle | 194809335 | 0.360359622 |
| **DEL801.17** | 17 | PlantHT | 194809363 | 0.117131523 | PetAngle | 194809363 | 0.486138426 |
| **DEL801.18** | 17 | PlantHT | 194809373 | 0.372190564 | PetAngle | 194809373 | 0.82587614 |
| **DEL801.19** | 17 | PlantHT | 194809815 | 0.503653139 | PetAngle | 194809815 | 0.171820722 |
| **DEL801.22** | 17 | PlantHT | 194810204 | 0.594669541 | PetAngle | 194810204 | 0.473020219 |
| **DEL801.23** | 17 | PlantHT | 194810236 | 0.78671355 | PetAngle | 194810236 | 0.019511317 |
| **DEL801.24** | 17 | PlantHT | 194810797 | 0.505317046 | PetAngle | 194810797 | 0.434557012 |
| **DEL801.25** | 17 | PlantHT | 194810815 | 0.050203437 | PetAngle | 194810815 | 0.435610077 |
| **DEL801.26** | 17 | PlantHT | 194810872 | 0.009907183 | PetAngle | 194810872 | 0.048527127 |
| **DEL801.27** | 17 | PlantHT | 194810919 | 0.220320531 | PetAngle | 194810919 | 0.777109084 |
| **DEL801.31** | 17 | PlantHT | 194811667 | 0.891932783 | PetAngle | 194811667 | 0.073208231 |
| **DEL801.32** | 17 | PlantHT | 194811721 | 0.397138114 | PetAngle | 194811721 | 0.838944341 |
| **LAZ921.1** | 17 | PlantHT | 206481522 | 0.962954889 | PetAngle | 206481522 | 0.059871747 |
| **LAZ921.2** | 17 | PlantHT | 206481523 | 0.934980217 | PetAngle | 206481523 | 0.014759009 |
| **LAZ921.5** | 17 | PlantHT | 206481620 | 0.466330871 | PetAngle | 206481620 | 0.082222361 |
| **LAZ921.7** | 17 | PlantHT | 206482328 | 0.016967273 | PetAngle | 206482328 | 0.728013573 |
| **LAZ921.8** | 17 | PlantHT | 206482347 | 0.045206416 | PetAngle | 206482347 | 0.567185346 |
| **LAZ921.10** | 17 | PlantHT | 206482628 | 0.036539621 | PetAngle | 206482628 | 0.640752115 |
| **LAZ921.11** | 17 | PlantHT | 206482782 | 0.10812607 | PetAngle | 206482782 | 0.979703279 |
| **LAZ921.12** | 17 | PlantHT | 206482792 | NaN | PetAngle | 206482792 | NaN |
| **LAZ921.13** | 17 | PlantHT | 206483103 | 0.245232684 | PetAngle | 206483103 | 0.473698909 |

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|---|---|---|---|---|---|---|---|
| **LAZ921.14** | 17 | PlantHT | 206483214 | 0.041105931 | PetAngle | 206483214 | 0.214137399 |
| **LAZ921.15** | 17 | PlantHT | 206483252 | 0.247429068 | PetAngle | 206483252 | 0.08056462 |
| **LAZ921.16** | 17 | PlantHT | 206483470 | 0.061500713 | PetAngle | 206483470 | 0.15866172 |
| **LAZ921.17** | 17 | PlantHT | 206483476 | 0.061500713 | PetAngle | 206483476 | 0.15866172 |
| **LAZ921.18** | 17 | PlantHT | 206483951 | 0.45111151 | PetAngle | 206483951 | 0.107146469 |
| **LAZ921.19** | 17 | PlantHT | 206483990 | 0.061045072 | PetAngle | 206483990 | 0.136218461 |
| **LAZ921.20** | 17 | PlantHT | 206484255 | 0.011776035 | PetAngle | 206484255 | 0.711240839 |
| **LAZ921.21** | 17 | PlantHT | 206484302 | 0.51984536 | PetAngle | 206484302 | 0.790856113 |
| **LAZ921.23** | 17 | PlantHT | 206484967 | 0.025471884 | PetAngle | 206484967 | 0.18174422 |
| **LAZ921.24** | 17 | PlantHT | 206484979 | 0.025471884 | PetAngle | 206484979 | 0.18174422 |
| **LAZ921.25** | 17 | PlantHT | 206485147 | 0.020274526 | PetAngle | 206485147 | 0.726459059 |
| **LAZ921.26** | 17 | PlantHT | 206485168 | 0.3521207 | PetAngle | 206485168 | 0.655429194 |
| **LAZ921.27** | 17 | PlantHT | 206485184 | 0.420297948 | PetAngle | 206485184 | 0.537822073 |
| **LAZ921.28** | 17 | PlantHT | 206485185 | 0.026549614 | PetAngle | 206485185 | 0.697319734 |
| **LAZ921.29** | 17 | PlantHT | 206485313 | 0.347833874 | PetAngle | 206485313 | 0.736908272 |
| **LAZ921.32** | 17 | PlantHT | 206485496 | 0.456314451 | PetAngle | 206485496 | 0.622652126 |
| **LAZ921.33** | 17 | PlantHT | 206485873 | 0.300801395 | PetAngle | 206485873 | 0.323626325 |
| **LAZ921.34** | 17 | PlantHT | 206485928 | 0.959453175 | PetAngle | 206485928 | 0.741631983 |
| **LAZ921.35** | 17 | PlantHT | 206485936 | 0.959453175 | PetAngle | 206485936 | 0.741631983 |
| **LAZ921.36** | 17 | PlantHT | 206486107 | 0.43666895 | PetAngle | 206486107 | 0.53239115 |
| **LAZ921.37** | 17 | PlantHT | 206486155 | 0.460920798 | PetAngle | 206486155 | 0.317465008 |
| **LAZ921.38** | 17 | PlantHT | 206486181 | 0.433746497 | PetAngle | 206486181 | 0.683372007 |
| **LAZ921.40** | 17 | PlantHT | 206486230 | 0.204254365 | PetAngle | 206486230 | 0.866277062 |
| **LAZ921.41** | 17 | PlantHT | 206486337 | 0.300549583 | PetAngle | 206486337 | 0.792821293 |
| **LAZ921.42** | 17 | PlantHT | 206486407 | 0.403523847 | PetAngle | 206486407 | 0.585622324 |
| **LAZ921.43** | 17 | PlantHT | 206486412 | 0.892041776 | PetAngle | 206486412 | 0.713484078 |
| **LAZ921.44** | 17 | PlantHT | 206486453 | 0.093220733 | PetAngle | 206486453 | 0.521732103 |

**Supplementary Table A 18:** Summary of GLM results for data of the small association panel (64 genotypes) in Germany 2018, limit value p = 0.000164

| MARKER | CHR | TRAIT | POS | P | TRAIT | POS | P |
|---|---|---|---|---|---|---|---|
| **GID871.10** | 1 | PlantHT | 12852858 | 0.12273327 | PetAngle | 12852858 | 0.56137677 |
| **GID871.11** | 1 | PlantHT | 12853069 | 0.12417213 | PetAngle | 12853069 | 0.18849428 |
| **GID871.12** | 1 | PlantHT | 12853100 | 0.93706196 | PetAngle | 12853100 | 0.48996975 |
| **GID871.13** | 1 | PlantHT | 12853241 | 0.99128583 | PetAngle | 12853241 | 0.07878546 |
| **GID871.14** | 1 | PlantHT | 12853328 | 0.55396155 | PetAngle | 12853328 | 0.65014401 |
| **GID871.15** | 1 | PlantHT | 12853334 | 0.55396155 | PetAngle | 12853334 | 0.65014401 |
| **GID871.16** | 1 | PlantHT | 12853430 | 0.50689149 | PetAngle | 12853430 | 0.03343464 |
| **GID871.17** | 1 | PlantHT | 12853511 | 0.0739616 | PetAngle | 12853511 | 0.22828653 |
| **GID871.21** | 1 | PlantHT | 12853600 | 0.38180958 | PetAngle | 12853600 | 0.34370832 |
| **GID871.22** | 1 | PlantHT | 12853709 | 0.47591789 | PetAngle | 12853709 | 0.78895653 |
| **GID871.23** | 1 | PlantHT | 12853714 | 0.13088772 | PetAngle | 12853714 | 0.1873274 |
| **GID871.5** | 1 | PlantHT | 12851807 | 0.6522853 | PetAngle | 12851807 | 0.34617103 |
| **GID871.6** | 1 | PlantHT | 12852614 | 0.38100131 | PetAngle | 12852614 | 0.40956138 |
| **GID871.7** | 1 | PlantHT | 12852731 | 0.90305962 | PetAngle | 12852731 | 0.91359662 |
| **GID871.9** | 1 | PlantHT | 12852833 | 0.12858048 | PetAngle | 12852833 | 0.52058033 |
| **SLY061.11** | 2 | PlantHT | 39415029 | 0.02207101 | PetAngle | 39415029 | 0.80403214 |

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|---|---|---|---|---|---|---|---|
| **SLY061.14** | 2 | PlantHT | 39415287 | 0.0133833 | PetAngle | 39415287 | 0.88354468 |
| **SLY061.15** | 2 | PlantHT | 39415439 | 0.01374541 | PetAngle | 39415439 | 0.8739986 |
| **SLY061.16** | 2 | PlantHT | 39415448 | 0.01374541 | PetAngle | 39415448 | 0.8739986 |
| **SLY061.17** | 2 | PlantHT | 39415600 | 0.29561204 | PetAngle | 39415600 | 0.51918966 |
| **SLY061.19** | 2 | PlantHT | 39415765 | 0.30507544 | PetAngle | 39415765 | 0.62079186 |
| **SLY061.20** | 2 | PlantHT | 39415978 | 0.29561204 | PetAngle | 39415978 | 0.51918966 |
| **SLY061.21** | 2 | PlantHT | 39416235 | 0.26329605 | PetAngle | 39416235 | 0.28215904 |
| **SLY061.22** | 2 | PlantHT | 39416259 | 0.39663751 | PetAngle | 39416259 | 0.34019837 |
| **SLY061.3** | 2 | PlantHT | 39413612 | 0.03440355 | PetAngle | 39413612 | 0.32131919 |
| **SLY061.4** | 2 | PlantHT | 39413618 | 0.03440355 | PetAngle | 39413618 | 0.32131919 |
| **SLY061.5** | 2 | PlantHT | 39413737 | 0.04875361 | PetAngle | 39413737 | 0.60067433 |
| **SLY061.6** | 2 | PlantHT | 39413802 | 0.01975473 | PetAngle | 39413802 | 0.80434978 |
| **SLY061.7** | 2 | PlantHT | 39414098 | 0.31642145 | PetAngle | 39414098 | 0.97829862 |
| **SNE171.1** | 3 | PlantHT | 104932867 | 0.88472454 | PetAngle | 104932867 | 0.68330894 |
| **SNE171.5** | 3 | PlantHT | 104934540 | 0.0653514 | PetAngle | 104934540 | 0.02464988 |
| **SNE171.6** | 3 | PlantHT | 104934736 | 0.0653514 | PetAngle | 104934736 | 0.02464988 |
| **SNE171.7** | 3 | PlantHT | 104934791 | 0.40728138 | PetAngle | 104934791 | 0.03701846 |
| **SNE171.8** | 3 | PlantHT | 104934943 | 0.23081387 | PetAngle | 104934943 | 0.12418079 |
| **SLY321.1** | 4 | PlantHT | 40919975 | 0.10734592 | PetAngle | 40919975 | 0.48608275 |
| **SLY321.2** | 4 | PlantHT | 40920036 | 0.03414081 | PetAngle | 40920036 | 0.29557487 |
| **SLY321.3** | 4 | PlantHT | 40920185 | 0.86513048 | PetAngle | 40920185 | 0.3003396 |
| **SLY321.6** | 4 | PlantHT | 40920969 | 0.62902163 | PetAngle | 40920969 | 0.17108917 |
| **SLY321.8** | 4 | PlantHT | 40921919 | 0.25868475 | PetAngle | 40921919 | 0.16142562 |
| **SLY351.11** | 4 | PlantHT | 41289089 | 0.13493417 | PetAngle | 41289089 | 0.17373426 |
| **SLY351.2** | 4 | PlantHT | 41287638 | 0.16826172 | PetAngle | 41287638 | 0.27308288 |
| **SLY351.4** | 4 | PlantHT | 41287804 | 0.37241405 | PetAngle | 41287804 | 0.1011266 |
| **SLY351.6** | 4 | PlantHT | 41288086 | 0.12212427 | PetAngle | 41288086 | 0.17018563 |
| **SLY351.7** | 4 | PlantHT | 41288167 | 0.58123239 | PetAngle | 41288167 | 0.33496199 |
| **SLY351.8** | 4 | PlantHT | 41288598 | 0.12212427 | PetAngle | 41288598 | 0.17018563 |
| **SLY351.9** | 4 | PlantHT | 41288616 | 0.12212427 | PetAngle | 41288616 | 0.17018563 |
| **TAC361.1** | 4 | PlantHT | 155517271 | 0.4752348 | PetAngle | 155517271 | 0.84606978 |
| **TAC361.10** | 4 | PlantHT | 155518227 | 0.00754033 | PetAngle | 155518227 | 0.68091924 |
| **TAC361.13** | 4 | PlantHT | 155519213 | 0.3401634 | PetAngle | 155519213 | 0.6970037 |
| **TAC361.14** | 4 | PlantHT | 155519529 | 0.48744433 | PetAngle | 155519529 | 0.55522111 |
| **TAC361.16** | 4 | PlantHT | 155519787 | 0.18877735 | PetAngle | 155519787 | 0.73383266 |
| **TAC361.17** | 4 | PlantHT | 155519800 | 0.81014799 | PetAngle | 155519800 | 0.50133231 |
| **TAC361.18** | 4 | PlantHT | 155520038 | 0.1296548 | PetAngle | 155520038 | 0.70572245 |
| **TAC361.19** | 4 | PlantHT | 155520121 | 0.02286647 | PetAngle | 155520121 | 0.45014758 |
| **TAC361.2** | 4 | PlantHT | 155517418 | 0.01790629 | PetAngle | 155517418 | 0.48527055 |
| **TAC361.20** | 4 | PlantHT | 155520230 | 0.14836924 | PetAngle | 155520230 | 0.49361341 |
| **TAC361.21** | 4 | PlantHT | 155520277 | 0.09482507 | PetAngle | 155520277 | 0.85623554 |
| **TAC361.22** | 4 | PlantHT | 155520338 | 0.05367201 | PetAngle | 155520338 | 0.21651077 |
| **TAC361.23** | 4 | PlantHT | 155520558 | 0.89107683 | PetAngle | 155520558 | 0.48619304 |
| **TAC361.3** | 4 | PlantHT | 155517438 | 0.24441791 | PetAngle | 155517438 | 0.51157024 |
| **TAC361.4** | 4 | PlantHT | 155517453 | 0.01790629 | PetAngle | 155517453 | 0.48527055 |
| **TAC361.5** | 4 | PlantHT | 155517553 | 0.28470154 | PetAngle | 155517553 | 0.23672278 |
| **TAC361.6** | 4 | PlantHT | 155517627 | 0.60627238 | PetAngle | 155517627 | 0.8087953 |
| **TAC361.9** | 4 | PlantHT | 155518008 | 0.39837066 | PetAngle | 155518008 | 0.78971974 |
| **SLY141.1** | 5 | PlantHT | 163484536 | 0.65020608 | PetAngle | 163484536 | 0.30464291 |

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|---|---|---|---|---|---|---|---|
| **SLY141.10** | 5 | PlantHT | 163485423 | 0.45996349 | PetAngle | 163485423 | 0.09758201 |
| **SLY141.11** | 5 | PlantHT | 163485618 | 0.79222422 | PetAngle | 163485618 | 0.02950272 |
| **SLY141.12** | 5 | PlantHT | 163485624 | 0.79222422 | PetAngle | 163485624 | 0.02950272 |
| **SLY141.13** | 5 | PlantHT | 163486432 | 0.46944498 | PetAngle | 163486432 | 0.10954451 |
| **SLY141.14** | 5 | PlantHT | 163486451 | 0.53309176 | PetAngle | 163486451 | 0.38846905 |
| **SLY141.15** | 5 | PlantHT | 163486868 | 0.64327391 | PetAngle | 163486868 | 0.66746694 |
| **SLY141.2** | 5 | PlantHT | 163484898 | 0.66642526 | PetAngle | 163484898 | 0.77379538 |
| **SLY141.3** | 5 | PlantHT | 163484956 | 0.60071837 | PetAngle | 163484956 | 0.85010187 |
| **SLY141.4** | 5 | PlantHT | 163484969 | 0.17048492 | PetAngle | 163484969 | 0.32607578 |
| **SLY141.5** | 5 | PlantHT | 163485239 | 0.6424105 | PetAngle | 163485239 | 0.02731834 |
| **SLY141.6** | 5 | PlantHT | 163485248 | 0.33899289 | PetAngle | 163485248 | 0.01375127 |
| **SLY141.7** | 5 | PlantHT | 163485257 | 0.46635549 | PetAngle | 163485257 | 0.12393345 |
| **SLY141.8** | 5 | PlantHT | 163485366 | 0.71250567 | PetAngle | 163485366 | 0.02460555 |
| **GID741.2** | 6 | PlantHT | 43970283 | 0.88153493 | PetAngle | 43970283 | 0.83276083 |
| **GID741.3** | 6 | PlantHT | 43970298 | 0.79143702 | PetAngle | 43970298 | 0.78615937 |
| **GID741.4** | 6 | PlantHT | 43970589 | 0.94096526 | PetAngle | 43970589 | 0.59323718 |
| **GID741.5** | 6 | PlantHT | 43971149 | 0.6114606 | PetAngle | 43971149 | 0.59915199 |
| **DEL091.10** | 8 | PlantHT | 12264206 | 0.37458115 | PetAngle | 12264206 | 0.50640467 |
| **DEL091.12** | 8 | PlantHT | 12264269 | 0.8583496 | PetAngle | 12264269 | 0.19441386 |
| **DEL091.13** | 8 | PlantHT | 12264332 | 0.27691259 | PetAngle | 12264332 | 0.34706411 |
| **DEL091.14** | 8 | PlantHT | 12264404 | 0.78931447 | PetAngle | 12264404 | 0.03514848 |
| **DEL091.15** | 8 | PlantHT | 12264512 | 0.51126748 | PetAngle | 12264512 | 0.02478212 |
| **DEL091.16** | 8 | PlantHT | 12264599 | 0.49794118 | PetAngle | 12264599 | 0.50477251 |
| **DEL091.17** | 8 | PlantHT | 12264604 | 0.74928933 | PetAngle | 12264604 | 0.07584925 |
| **DEL091.18** | 8 | PlantHT | 12264635 | 0.20604223 | PetAngle | 12264635 | 0.02592339 |
| **DEL091.20** | 8 | PlantHT | 12264789 | 0.4225331 | PetAngle | 12264789 | 0.87560987 |
| **DEL091.21** | 8 | PlantHT | 12264795 | 0.58904822 | PetAngle | 12264795 | 0.21050994 |
| **DEL091.22** | 8 | PlantHT | 12264962 | 0.07130112 | PetAngle | 12264962 | 0.90819609 |
| **DEL091.24** | 8 | PlantHT | 12265025 | 0.24663438 | PetAngle | 12265025 | 0.30295823 |
| **DEL091.25** | 8 | PlantHT | 12265054 | 0.24650846 | PetAngle | 12265054 | 0.01783899 |
| **DEL091.26** | 8 | PlantHT | 12265056 | 0.14349454 | PetAngle | 12265056 | 0.94200188 |
| **DEL091.27** | 8 | PlantHT | 12265422 | 0.53474693 | PetAngle | 12265422 | 0.01943672 |
| **DEL091.29** | 8 | PlantHT | 12265567 | 0.25160079 | PetAngle | 12265567 | 0.9411742 |
| **DEL091.3** | 8 | PlantHT | 12263870 | 0.67561236 | PetAngle | 12263870 | 0.06391749 |
| **DEL091.30** | 8 | PlantHT | 12265676 | 0.00517587 | PetAngle | 12265676 | 0.09052609 |
| **DEL091.31** | 8 | PlantHT | 12265683 | 0.00349135 | PetAngle | 12265683 | 0.14747233 |
| **DEL091.32** | 8 | PlantHT | 12265802 | 0.53556542 | PetAngle | 12265802 | 0.4059434 |
| **DEL091.33** | 8 | PlantHT | 12266012 | 0.03563235 | PetAngle | 12266012 | 0.27170313 |
| **DEL091.34** | 8 | PlantHT | 12266161 | 0.41022314 | PetAngle | 12266161 | 0.17779081 |
| **DEL091.35** | 8 | PlantHT | 12266179 | 0.83420841 | PetAngle | 12266179 | 0.03165493 |
| **DEL091.36** | 8 | PlantHT | 12266186 | 0.94381465 | PetAngle | 12266186 | 0.31300784 |
| **DEL091.37** | 8 | PlantHT | 12266199 | 0.83834688 | PetAngle | 12266199 | 0.11941597 |
| **DEL091.38** | 8 | PlantHT | 12266211 | 0.12338308 | PetAngle | 12266211 | 0.578656 |
| **DEL091.4** | 8 | PlantHT | 12263903 | 0.63956389 | PetAngle | 12263903 | 0.04434586 |
| **DEL091.41** | 8 | PlantHT | 12266403 | 0.4241163 | PetAngle | 12266403 | 0.6262831 |
| **DEL091.42** | 8 | PlantHT | 12266417 | 0.67568346 | PetAngle | 12266417 | 0.0223258 |
| **DEL091.43** | 8 | PlantHT | 12266464 | 0.74899245 | PetAngle | 12266464 | 0.02302403 |
| **DEL091.47** | 8 | PlantHT | 12266830 | 0.39029091 | PetAngle | 12266830 | 0.02466412 |
| **DEL091.48** | 8 | PlantHT | 12266863 | 0.45248678 | PetAngle | 12266863 | 0.02099472 |

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| **DEL091.49** | 8 | PlantHT | 12266939 | 0.25546428 | PetAngle | 12266939 | 0.53134344 |
| **DEL091.5** | 8 | PlantHT | 12263912 | 0.28001029 | PetAngle | 12263912 | 0.42701772 |
| **DEL091.50** | 8 | PlantHT | 12267167 | 0.08177096 | PetAngle | 12267167 | 0.76149432 |
| **DEL091.52** | 8 | PlantHT | 12267267 | 0.08177096 | PetAngle | 12267267 | 0.76149432 |
| **DEL091.6** | 8 | PlantHT | 12264043 | 0.83282736 | PetAngle | 12264043 | 0.3066759 |
| **DEL091.7** | 8 | PlantHT | 12264064 | 0.40659346 | PetAngle | 12264064 | 0.0273827 |
| **DEL091.8** | 8 | PlantHT | 12264103 | 0.35224455 | PetAngle | 12264103 | 0.12257788 |
| **DEL091.9** | 8 | PlantHT | 12264128 | 0.408772 | PetAngle | 12264128 | 0.07277863 |
| **LAZ951.1** | 8 | PlantHT | 7807354 | 0.9868603 | PetAngle | 7807354 | 0.45718298 |
| **LAZ951.10** | 8 | PlantHT | 7809246 | 0.0726784 | PetAngle | 7809246 | 0.65571024 |
| **LAZ951.11** | 8 | PlantHT | 7809319 | 0.33358566 | PetAngle | 7809319 | 0.48134931 |
| **LAZ951.12** | 8 | PlantHT | 7809351 | 0.45812556 | PetAngle | 7809351 | 0.10743699 |
| **LAZ951.13** | 8 | PlantHT | 7809384 | 0.8344743 | PetAngle | 7809384 | 0.9651168 |
| **LAZ951.14** | 8 | PlantHT | 7809516 | 0.11993725 | PetAngle | 7809516 | 0.04503989 |
| **LAZ951.15** | 8 | PlantHT | 7809577 | 0.52279282 | PetAngle | 7809577 | 0.093165 |
| **LAZ951.16** | 8 | PlantHT | 7809616 | 0.29478714 | PetAngle | 7809616 | 0.86430794 |
| **LAZ951.17** | 8 | PlantHT | 7809770 | 0.56146103 | PetAngle | 7809770 | 0.43102864 |
| **LAZ951.18** | 8 | PlantHT | 7810149 | 0.3900984 | PetAngle | 7810149 | 0.4533054 |
| **LAZ951.2** | 8 | PlantHT | 7807376 | 0.25963417 | PetAngle | 7807376 | 0.92472424 |
| **LAZ951.20** | 8 | PlantHT | 7810266 | 0.31690198 | PetAngle | 7810266 | 0.07285597 |
| **LAZ951.21** | 8 | PlantHT | 7810443 | 0.00927132 | PetAngle | 7810443 | 0.10793398 |
| **LAZ951.23** | 8 | PlantHT | 7810829 | 0.43450345 | PetAngle | 7810829 | 0.01747946 |
| **LAZ951.24** | 8 | PlantHT | 7810961 | 0.5987709 | PetAngle | 7810961 | 0.3404519 |
| **LAZ951.26** | 8 | PlantHT | 7811459 | 0.76684888 | PetAngle | 7811459 | 0.46813107 |
| **LAZ951.27** | 8 | PlantHT | 7811479 | 0.9050766 | PetAngle | 7811479 | 0.06751181 |
| **LAZ951.28** | 8 | PlantHT | 7811553 | 0.39195603 | PetAngle | 7811553 | 0.01903276 |
| **LAZ951.29** | 8 | PlantHT | 7812053 | 0.72117341 | PetAngle | 7812053 | 0.51710513 |
| **LAZ951.3** | 8 | PlantHT | 7807503 | 0.61867757 | PetAngle | 7807503 | 0.06567611 |
| **LAZ951.4** | 8 | PlantHT | 7807600 | 0.55839067 | PetAngle | 7807600 | 0.50034165 |
| **LAZ951.5** | 8 | PlantHT | 7807614 | 0.17418955 | PetAngle | 7807614 | 0.33745035 |
| **LAZ951.6** | 8 | PlantHT | 7807682 | 0.51741529 | PetAngle | 7807682 | 0.57246949 |
| **LAZ951.7** | 8 | PlantHT | 7809093 | 0.28759292 | PetAngle | 7809093 | 0.04394184 |
| **LAZ951.8** | 8 | PlantHT | 7809138 | 0.91516597 | PetAngle | 7809138 | 0.03087343 |
| **LAZ951.9** | 8 | PlantHT | 7809176 | 0.16886457 | PetAngle | 7809176 | 0.11172816 |
| **SLY301.1** | 9 | PlantHT | 178666111 | 0.17911484 | PetAngle | 178666111 | 0.93728198 |
| **SLY301.2** | 9 | PlantHT | 178666159 | 0.37355887 | PetAngle | 178666159 | 0.99158661 |
| **SLY301.3** | 9 | PlantHT | 178666187 | 0.24189918 | PetAngle | 178666187 | 0.98080583 |
| **SLY301.4** | 9 | PlantHT | 178666431 | 0.86899285 | PetAngle | 178666431 | 0.95534474 |
| **SLY301.5** | 9 | PlantHT | 178666702 | 0.49370571 | PetAngle | 178666702 | 0.91711079 |
| **SLY301.7** | 9 | PlantHT | 178668175 | 0.53157108 | PetAngle | 178668175 | 0.83718126 |
| **DEL171.2** | 10 | PlantHT | 34968719 | 0.13457554 | PetAngle | 34968719 | 0.94115652 |
| **GID071.1** | 10 | PlantHT | 28111762 | 0.03580499 | PetAngle | 28111762 | 0.23126748 |
| **GID071.13** | 10 | PlantHT | 28112319 | 0.64582941 | PetAngle | 28112319 | 0.10148534 |
| **GID071.14** | 10 | PlantHT | 28112493 | 0.22773016 | PetAngle | 28112493 | 0.44073452 |
| **GID071.15** | 10 | PlantHT | 28112634 | 0.41505189 | PetAngle | 28112634 | 0.01315662 |
| **GID071.16** | 10 | PlantHT | 28112657 | 0.42940541 | PetAngle | 28112657 | 0.00174849 |
| **GID071.17** | 10 | PlantHT | 28112679 | 0.22773016 | PetAngle | 28112679 | 0.44073452 |
| **GID071.18** | 10 | PlantHT | 28112826 | 0.76044601 | PetAngle | 28112826 | 0.98801305 |
| **GID071.19** | 10 | PlantHT | 28112847 | 0.46664042 | PetAngle | 28112847 | 0.52767457 |

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|---|---|---|---|---|---|---|---|
| **GID071.20** | 10 | PlantHT | 28112916 | 0.25664308 | PetAngle | 28112916 | 0.45402143 |
| **GID071.21** | 10 | PlantHT | 28112919 | 0.26458617 | PetAngle | 28112919 | 0.05867042 |
| **GID071.22** | 10 | PlantHT | 28113024 | 0.74922756 | PetAngle | 28113024 | 0.013159 |
| **GID071.23** | 10 | PlantHT | 28113051 | 0.62043148 | PetAngle | 28113051 | 0.02709948 |
| **GID071.24** | 10 | PlantHT | 28113168 | 0.92630922 | PetAngle | 28113168 | 0.01269948 |
| **GID071.26** | 10 | PlantHT | 28113769 | 0.27079939 | PetAngle | 28113769 | 0.34808112 |
| **GID071.28** | 10 | PlantHT | 28113897 | 0.81045752 | PetAngle | 28113897 | 0.34949097 |
| **GID071.29** | 10 | PlantHT | 28113914 | 0.99370931 | PetAngle | 28113914 | 0.57012559 |
| **GID071.30** | 10 | PlantHT | 28114325 | 0.69443119 | PetAngle | 28114325 | 0.17643663 |
| **GID071.34** | 10 | PlantHT | 28114759 | 0.12887845 | PetAngle | 28114759 | 0.04363858 |
| **GID071.36** | 10 | PlantHT | 28114977 | 0.62043148 | PetAngle | 28114977 | 0.02709948 |
| **GID071.38** | 10 | PlantHT | 28115179 | 0.57045758 | PetAngle | 28115179 | 0.0486415 |
| **GID071.39** | 10 | PlantHT | 28115187 | 0.22718989 | PetAngle | 28115187 | 0.31745973 |
| **GID071.4** | 10 | PlantHT | 28111944 | 0.03929897 | PetAngle | 28111944 | 0.73436975 |
| **GID071.42** | 10 | PlantHT | 28116112 | 0.38657809 | PetAngle | 28116112 | 0.04364991 |
| **GID071.5** | 10 | PlantHT | 28111956 | 0.04828451 | PetAngle | 28111956 | 0.73486849 |
| **GID071.7** | 10 | PlantHT | 28111995 | 0.24663441 | PetAngle | 28111995 | 0.02978278 |
| **SLY611.1** | 11 | PlantHT | 138990416 | 0.38785742 | PetAngle | 138990416 | 0.40278797 |
| **SLY611.10** | 11 | PlantHT | 138993192 | 0.45197091 | PetAngle | 138993192 | 0.55219388 |
| **SLY611.11** | 11 | PlantHT | 138993311 | 0.24005653 | PetAngle | 138993311 | 0.21304064 |
| **SLY611.2** | 11 | PlantHT | 138990539 | 0.40357097 | PetAngle | 138990539 | 0.34428827 |
| **SLY611.3** | 11 | PlantHT | 138990639 | 0.23137702 | PetAngle | 138990639 | 0.16056277 |
| **SLY611.4** | 11 | PlantHT | 138990798 | 0.23137702 | PetAngle | 138990798 | 0.16056277 |
| **SLY611.5** | 11 | PlantHT | 138991001 | 0.41110273 | PetAngle | 138991001 | 0.16106859 |
| **SLY611.8** | 11 | PlantHT | 138992806 | 0.34201791 | PetAngle | 138992806 | 0.78021542 |
| **SLY611.9** | 11 | PlantHT | 138993071 | 0.41082983 | PetAngle | 138993071 | 0.93941527 |
| **DEL901.1** | 12 | PlantHT | 32211683 | 0.77443097 | PetAngle | 32211683 | 0.17160644 |
| **DEL901.10** | 12 | PlantHT | 32213076 | 0.77443097 | PetAngle | 32213076 | 0.17160644 |
| **DEL901.11** | 12 | PlantHT | 32213328 | 0.94554527 | PetAngle | 32213328 | 0.34226531 |
| **DEL901.12** | 12 | PlantHT | 32213465 | 0.46266597 | PetAngle | 32213465 | 0.9148849 |
| **DEL901.2** | 12 | PlantHT | 32211812 | 0.77443097 | PetAngle | 32211812 | 0.17160644 |
| **DEL901.3** | 12 | PlantHT | 32211968 | 0.04262609 | PetAngle | 32211968 | 0.30997149 |
| **DEL901.4** | 12 | PlantHT | 32212028 | 0.04262609 | PetAngle | 32212028 | 0.30997149 |
| **DEL901.5** | 12 | PlantHT | 32212178 | 0.95187459 | PetAngle | 32212178 | 0.10453319 |
| **DEL901.6** | 12 | PlantHT | 32212556 | 0.60028363 | PetAngle | 32212556 | 0.24388835 |
| **DEL901.7** | 12 | PlantHT | 32212608 | 0.24549261 | PetAngle | 32212608 | 0.03060236 |
| **DEL901.8** | 12 | PlantHT | 32212620 | 0.88943614 | PetAngle | 32212620 | 0.24912271 |
| **DEL901.9** | 12 | PlantHT | 32212719 | 0.77443097 | PetAngle | 32212719 | 0.17160644 |
| **SNE981.1** | 12 | PlantHT | 81945604 | 0.64639075 | PetAngle | 81945604 | 0.66559892 |
| **SNE981.11** | 12 | PlantHT | 81947454 | 0.80481859 | PetAngle | 81947454 | 0.73581178 |
| **SNE981.12** | 12 | PlantHT | 81947533 | 0.70512038 | PetAngle | 81947533 | 0.65483845 |
| **SNE981.13** | 12 | PlantHT | 81947575 | 0.70512038 | PetAngle | 81947575 | 0.65483845 |
| **SNE981.14** | 12 | PlantHT | 81948022 | 0.72776599 | PetAngle | 81948022 | 0.81594739 |
| **SNE981.2** | 12 | PlantHT | 81945790 | 0.86049251 | PetAngle | 81945790 | 0.8084058 |
| **SNE981.5** | 12 | PlantHT | 81946423 | 0.70512038 | PetAngle | 81946423 | 0.65483845 |
| **SNE981.6** | 12 | PlantHT | 81946530 | 0.70512038 | PetAngle | 81946530 | 0.65483845 |
| **SNE981.8** | 12 | PlantHT | 81947032 | 0.64639075 | PetAngle | 81947032 | 0.66559892 |
| **SNE981.9** | 12 | PlantHT | 81947042 | 0.64639075 | PetAngle | 81947042 | 0.66559892 |
| **GID131.1** | 14 | PlantHT | 127160607 | 0.9828583 | PetAngle | 127160607 | 0.74260823 |

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|---|---|---|---|---|---|---|---|---|
| **GID131.10** | 14 | PlantHT | 127161183 | 0.47434942 | PetAngle | 127161183 | 0.18231584 |
| **GID131.13** | 14 | PlantHT | 127161687 | 0.17758279 | PetAngle | 127161687 | 0.47938838 |
| **GID131.14** | 14 | PlantHT | 127161715 | 0.50374436 | PetAngle | 127161715 | 0.34253184 |
| **GID131.15** | 14 | PlantHT | 127162040 | 0.4086577 | PetAngle | 127162040 | 0.2447258 |
| **GID131.18** | 14 | PlantHT | 127162519 | 0.08574595 | PetAngle | 127162519 | 0.16599166 |
| **GID131.19** | 14 | PlantHT | 127162646 | 0.77722312 | PetAngle | 127162646 | 0.40409691 |
| **GID131.2** | 14 | PlantHT | 127160680 | 0.20287965 | PetAngle | 127160680 | 0.06220398 |
| **GID131.20** | 14 | PlantHT | 127162694 | 0.87690002 | PetAngle | 127162694 | 0.35061588 |
| **GID131.21** | 14 | PlantHT | 127162874 | 0.14709192 | PetAngle | 127162874 | 0.73773052 |
| **GID131.22** | 14 | PlantHT | 127162881 | 0.14946151 | PetAngle | 127162881 | 0.45981414 |
| **GID131.24** | 14 | PlantHT | 127163001 | 0.16194289 | PetAngle | 127163001 | 0.07038043 |
| **GID131.25** | 14 | PlantHT | 127163141 | 0.26008085 | PetAngle | 127163141 | 0.40731756 |
| **GID131.27** | 14 | PlantHT | 127163432 | 0.01569486 | PetAngle | 127163432 | 0.21296002 |
| **GID131.28** | 14 | PlantHT | 127163504 | 0.0799191 | PetAngle | 127163504 | 0.22390152 |
| **GID131.29** | 14 | PlantHT | 127163681 | 0.99498617 | PetAngle | 127163681 | 0.25400964 |
| **GID131.3** | 14 | PlantHT | 127160706 | 0.17320544 | PetAngle | 127160706 | 0.1244528 |
| **GID131.30** | 14 | PlantHT | 127163764 | 0.62745266 | PetAngle | 127163764 | 0.22580272 |
| **GID131.31** | 14 | PlantHT | 127163847 | 0.12400383 | PetAngle | 127163847 | 0.66298942 |
| **GID131.32** | 14 | PlantHT | 127163939 | 0.0799191 | PetAngle | 127163939 | 0.22390152 |
| **GID131.33** | 14 | PlantHT | 127164023 | 0.31357913 | PetAngle | 127164023 | 0.09479125 |
| **GID131.34** | 14 | PlantHT | 127164137 | 0.99498617 | PetAngle | 127164137 | 0.25400964 |
| **GID131.35** | 14 | PlantHT | 127164254 | 0.33729929 | PetAngle | 127164254 | 0.50076007 |
| **GID131.36** | 14 | PlantHT | 127164266 | 0.23529037 | PetAngle | 127164266 | 0.50682302 |
| **GID131.37** | 14 | PlantHT | 127164443 | 0.35692813 | PetAngle | 127164443 | 0.92019451 |
| **GID131.38** | 14 | PlantHT | 127164454 | 0.17025834 | PetAngle | 127164454 | 0.24071518 |
| **GID131.39** | 14 | PlantHT | 127164489 | 0.0088032 | PetAngle | 127164489 | 0.05233442 |
| **GID131.5** | 14 | PlantHT | 127160797 | 0.97766125 | PetAngle | 127160797 | 0.44359062 |
| **GID131.6** | 14 | PlantHT | 127160916 | 0.12138501 | PetAngle | 127160916 | 0.16645764 |
| **GID131.7** | 14 | PlantHT | 127160942 | 0.08074478 | PetAngle | 127160942 | 0.03098528 |
| **GID131.9** | 14 | PlantHT | 127161170 | 0.05585934 | PetAngle | 127161170 | 0.06412054 |
| **TAC641.1** | 16 | PlantHT | 154345819 | 0.90367152 | PetAngle | 154345819 | 0.77575958 |
| **TAC641.4** | 16 | PlantHT | 154346996 | 0.63109303 | PetAngle | 154346996 | 0.72500873 |
| **TAC641.5** | 16 | PlantHT | 154347203 | 0.0870931 | PetAngle | 154347203 | 0.64006412 |
| **DEL801.10** | 17 | PlantHT | 194808854 | 0.23168415 | PetAngle | 194808854 | 0.65803227 |
| **DEL801.11** | 17 | PlantHT | 194808920 | 0.51644288 | PetAngle | 194808920 | 0.1705987 |
| **DEL801.12** | 17 | PlantHT | 194809025 | 0.04115463 | PetAngle | 194809025 | 0.81713977 |
| **DEL801.13** | 17 | PlantHT | 194809088 | 0.15663967 | PetAngle | 194809088 | 0.74139103 |
| **DEL801.14** | 17 | PlantHT | 194809186 | 0.2619497 | PetAngle | 194809186 | 0.10845661 |
| **DEL801.16** | 17 | PlantHT | 194809335 | 0.88161303 | PetAngle | 194809335 | 0.95782786 |
| **DEL801.17** | 17 | PlantHT | 194809363 | 0.9465914 | PetAngle | 194809363 | 0.3868278 |
| **DEL801.18** | 17 | PlantHT | 194809373 | 0.91139508 | PetAngle | 194809373 | 0.37848512 |
| **DEL801.19** | 17 | PlantHT | 194809815 | 0.54853074 | PetAngle | 194809815 | 0.34810927 |
| **DEL801.22** | 17 | PlantHT | 194810204 | 0.54337517 | PetAngle | 194810204 | 0.59747973 |
| **DEL801.23** | 17 | PlantHT | 194810236 | 0.96372543 | PetAngle | 194810236 | 0.1280886 |
| **DEL801.24** | 17 | PlantHT | 194810797 | 0.06295783 | PetAngle | 194810797 | 0.54412678 |
| **DEL801.25** | 17 | PlantHT | 194810815 | 0.16069775 | PetAngle | 194810815 | 0.7397699 |
| **DEL801.26** | 17 | PlantHT | 194810872 | 0.02826967 | PetAngle | 194810872 | 0.08998905 |
| **DEL801.27** | 17 | PlantHT | 194810919 | 0.50480834 | PetAngle | 194810919 | 0.21535051 |
| **DEL801.3** | 17 | PlantHT | 194808097 | 0.56033662 | PetAngle | 194808097 | 0.08713545 |

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|---|---|---|---|---|---|---|---|
| **DEL801.31** | 17 | PlantHT | 194811667 | 0.84590832 | PetAngle | 194811667 | 0.9171039 |
| **DEL801.32** | 17 | PlantHT | 194811721 | 0.56152407 | PetAngle | 194811721 | 0.73242861 |
| **DEL801.4** | 17 | PlantHT | 194808128 | 0.1438062 | PetAngle | 194808128 | 0.44941102 |
| **DEL801.5** | 17 | PlantHT | 194808137 | 0.13321927 | PetAngle | 194808137 | 0.30235437 |
| **DEL801.6** | 17 | PlantHT | 194808477 | 0.77823134 | PetAngle | 194808477 | 0.67398157 |
| **DEL801.7** | 17 | PlantHT | 194808602 | 0.83096937 | PetAngle | 194808602 | 0.53591621 |
| **DEL801.8** | 17 | PlantHT | 194808652 | 0.54853074 | PetAngle | 194808652 | 0.34810927 |
| **DEL801.9** | 17 | PlantHT | 194808815 | 0.54853074 | PetAngle | 194808815 | 0.34810927 |
| **LAZ921.1** | 17 | PlantHT | 206481522 | 0.53724619 | PetAngle | 206481522 | 0.97469266 |
| **LAZ921.10** | 17 | PlantHT | 206482628 | 0.19325809 | PetAngle | 206482628 | 0.24865659 |
| **LAZ921.11** | 17 | PlantHT | 206482782 | 0.17178278 | PetAngle | 206482782 | 0.22258818 |
| **LAZ921.12** | 17 | PlantHT | 206482792 | NaN | PetAngle | 206482792 | NaN |
| **LAZ921.13** | 17 | PlantHT | 206483103 | 0.23877576 | PetAngle | 206483103 | 0.22739473 |
| **LAZ921.14** | 17 | PlantHT | 206483214 | 0.03817426 | PetAngle | 206483214 | 0.04509025 |
| **LAZ921.15** | 17 | PlantHT | 206483252 | 0.1991886 | PetAngle | 206483252 | 0.2065169 |
| **LAZ921.16** | 17 | PlantHT | 206483470 | 0.04818212 | PetAngle | 206483470 | 0.00230833 |
| **LAZ921.17** | 17 | PlantHT | 206483476 | 0.04818212 | PetAngle | 206483476 | 0.00230833 |
| **LAZ921.18** | 17 | PlantHT | 206483951 | 0.14970237 | PetAngle | 206483951 | 0.18830806 |
| **LAZ921.19** | 17 | PlantHT | 206483990 | 0.04268058 | PetAngle | 206483990 | 0.00283372 |
| **LAZ921.2** | 17 | PlantHT | 206481523 | 0.57846202 | PetAngle | 206481523 | 0.52797425 |
| **LAZ921.20** | 17 | PlantHT | 206484255 | 0.07308455 | PetAngle | 206484255 | 0.13971646 |
| **LAZ921.21** | 17 | PlantHT | 206484302 | 0.4519329 | PetAngle | 206484302 | 0.74506183 |
| **LAZ921.23** | 17 | PlantHT | 206484967 | 0.04787377 | PetAngle | 206484967 | 0.51848591 |
| **LAZ921.24** | 17 | PlantHT | 206484979 | 0.04787377 | PetAngle | 206484979 | 0.51848591 |
| **LAZ921.25** | 17 | PlantHT | 206485147 | 0.05204761 | PetAngle | 206485147 | 0.1016775 |
| **LAZ921.26** | 17 | PlantHT | 206485168 | 0.8184767 | PetAngle | 206485168 | 0.49435366 |
| **LAZ921.27** | 17 | PlantHT | 206485184 | 0.72373002 | PetAngle | 206485184 | 0.79083487 |
| **LAZ921.28** | 17 | PlantHT | 206485185 | 0.06039464 | PetAngle | 206485185 | 0.22019874 |
| **LAZ921.29** | 17 | PlantHT | 206485313 | 0.39471264 | PetAngle | 206485313 | 0.57708272 |
| **LAZ921.32** | 17 | PlantHT | 206485496 | 0.5911066 | PetAngle | 206485496 | 0.72867275 |
| **LAZ921.33** | 17 | PlantHT | 206485873 | 0.30786231 | PetAngle | 206485873 | 0.20688001 |
| **LAZ921.34** | 17 | PlantHT | 206485928 | 0.79925462 | PetAngle | 206485928 | 0.84086357 |
| **LAZ921.35** | 17 | PlantHT | 206485936 | 0.79925462 | PetAngle | 206485936 | 0.84086357 |
| **LAZ921.36** | 17 | PlantHT | 206486107 | 0.17549447 | PetAngle | 206486107 | 0.56774842 |
| **LAZ921.37** | 17 | PlantHT | 206486155 | 0.14207 | PetAngle | 206486155 | 0.57538247 |
| **LAZ921.38** | 17 | PlantHT | 206486181 | 0.5978944 | PetAngle | 206486181 | 0.04809832 |
| **LAZ921.40** | 17 | PlantHT | 206486230 | 0.55554482 | PetAngle | 206486230 | 0.46622335 |
| **LAZ921.41** | 17 | PlantHT | 206486337 | 0.0579627 | PetAngle | 206486337 | 0.58082981 |
| **LAZ921.42** | 17 | PlantHT | 206486407 | 0.14933672 | PetAngle | 206486407 | 0.02443174 |
| **LAZ921.43** | 17 | PlantHT | 206486412 | 0.85722359 | PetAngle | 206486412 | 0.57502974 |
| **LAZ921.44** | 17 | PlantHT | 206486453 | 0.31287941 | PetAngle | 206486453 | 0.15178977 |
| **LAZ921.5** | 17 | PlantHT | 206481620 | 0.27142774 | PetAngle | 206481620 | 0.14637382 |
| **LAZ921.7** | 17 | PlantHT | 206482328 | 0.11940189 | PetAngle | 206482328 | 0.6391912 |
| **LAZ921.8** | 17 | PlantHT | 206482347 | 0.19923161 | PetAngle | 206482347 | 0.33439461 |

**Supplementary Table A 19:** Summary of GLM results for data of the small association panel (64 genotypes) in Germany 2019, limit value p = 0.000164

| MARKER | CHR | TRAIT | POS | P | TRAIT | POS | P |
|---|---|---|---|---|---|---|---|
| **GID871.10** | 1 | PlantHT | 12852858 | 0.01761388 | PetAngle | 12852858 | 0.92332411 |
| **GID871.11** | 1 | PlantHT | 12853069 | 0.08349147 | PetAngle | 12853069 | 0.80636601 |
| **GID871.12** | 1 | PlantHT | 12853100 | 0.70791348 | PetAngle | 12853100 | 0.70380398 |
| **GID871.13** | 1 | PlantHT | 12853241 | 0.96622384 | PetAngle | 12853241 | 0.43369184 |
| **GID871.14** | 1 | PlantHT | 12853328 | 0.29137191 | PetAngle | 12853328 | 0.98695363 |
| **GID871.15** | 1 | PlantHT | 12853334 | 0.29137191 | PetAngle | 12853334 | 0.98695363 |
| **GID871.16** | 1 | PlantHT | 12853430 | 0.60216562 | PetAngle | 12853430 | 0.45010145 |
| **GID871.17** | 1 | PlantHT | 12853511 | 0.03717723 | PetAngle | 12853511 | 0.97056512 |
| **GID871.21** | 1 | PlantHT | 12853600 | 0.80612013 | PetAngle | 12853600 | 0.8803155 |
| **GID871.22** | 1 | PlantHT | 12853709 | 0.66892063 | PetAngle | 12853709 | 0.1305817 |
| **GID871.23** | 1 | PlantHT | 12853714 | 0.0770077 | PetAngle | 12853714 | 0.673644 |
| **GID871.5** | 1 | PlantHT | 12851807 | 0.95179492 | PetAngle | 12851807 | 0.87619796 |
| **GID871.6** | 1 | PlantHT | 12852614 | 0.87903355 | PetAngle | 12852614 | 0.59680442 |
| **GID871.7** | 1 | PlantHT | 12852731 | 0.65359096 | PetAngle | 12852731 | 0.85753145 |
| **GID871.9** | 1 | PlantHT | 12852833 | 0.01912815 | PetAngle | 12852833 | 0.91202205 |
| **SLY061.11** | 2 | PlantHT | 39415029 | 0.02578113 | PetAngle | 39415029 | 0.43044363 |
| **SLY061.14** | 2 | PlantHT | 39415287 | 0.00490572 | PetAngle | 39415287 | 0.66420292 |
| **SLY061.15** | 2 | PlantHT | 39415439 | 0.00435021 | PetAngle | 39415439 | 0.75085018 |
| **SLY061.16** | 2 | PlantHT | 39415448 | 0.00435021 | PetAngle | 39415448 | 0.75085018 |
| **SLY061.17** | 2 | PlantHT | 39415600 | 0.57602596 | PetAngle | 39415600 | 0.28259251 |
| **SLY061.19** | 2 | PlantHT | 39415765 | 0.627338 | PetAngle | 39415765 | 0.31172932 |
| **SLY061.20** | 2 | PlantHT | 39415978 | 0.57602596 | PetAngle | 39415978 | 0.28259251 |
| **SLY061.21** | 2 | PlantHT | 39416235 | 0.42480547 | PetAngle | 39416235 | 0.20686741 |
| **SLY061.22** | 2 | PlantHT | 39416259 | 0.24827165 | PetAngle | 39416259 | 0.41812413 |
| **SLY061.3** | 2 | PlantHT | 39413612 | 0.00747225 | PetAngle | 39413612 | 0.92696217 |
| **SLY061.4** | 2 | PlantHT | 39413618 | 0.00747225 | PetAngle | 39413618 | 0.92696217 |
| **SLY061.5** | 2 | PlantHT | 39413737 | 0.0020608 | PetAngle | 39413737 | 0.9260428 |
| **SLY061.6** | 2 | PlantHT | 39413802 | 0.00455093 | PetAngle | 39413802 | 0.94012119 |
| **SLY061.7** | 2 | PlantHT | 39414098 | 0.27166836 | PetAngle | 39414098 | 0.51722863 |
| **SNE171.1** | 3 | PlantHT | 104932867 | 0.1931208 | PetAngle | 104932867 | 0.89415805 |
| **SNE171.5** | 3 | PlantHT | 104934540 | 0.04704704 | PetAngle | 104934540 | 0.09203303 |
| **SNE171.6** | 3 | PlantHT | 104934736 | 0.04704704 | PetAngle | 104934736 | 0.09203303 |
| **SNE171.7** | 3 | PlantHT | 104934791 | 0.84120893 | PetAngle | 104934791 | 0.02960996 |
| **SNE171.8** | 3 | PlantHT | 104934943 | 0.30360499 | PetAngle | 104934943 | 0.27210273 |
| **SLY321.1** | 4 | PlantHT | 40919975 | 0.18268861 | PetAngle | 40919975 | 0.17220618 |
| **SLY321.2** | 4 | PlantHT | 40920036 | 0.01336122 | PetAngle | 40920036 | 0.05543479 |
| **SLY321.3** | 4 | PlantHT | 40920185 | 0.94078484 | PetAngle | 40920185 | 0.84309839 |
| **SLY321.6** | 4 | PlantHT | 40920969 | 0.11080198 | PetAngle | 40920969 | 0.04818942 |
| **SLY321.8** | 4 | PlantHT | 40921919 | 0.2361946 | PetAngle | 40921919 | 0.39934261 |
| **SLY351.11** | 4 | PlantHT | 41289089 | 0.03962598 | PetAngle | 41289089 | 0.27949484 |
| **SLY351.2** | 4 | PlantHT | 41287638 | 0.02704779 | PetAngle | 41287638 | 0.28905835 |
| **SLY351.4** | 4 | PlantHT | 41287804 | 0.1335456 | PetAngle | 41287804 | 0.22734995 |
| **SLY351.6** | 4 | PlantHT | 41288086 | 0.03224284 | PetAngle | 41288086 | 0.25211501 |
| **SLY351.7** | 4 | PlantHT | 41288167 | 0.73683021 | PetAngle | 41288167 | 0.56656509 |
| **SLY351.8** | 4 | PlantHT | 41288598 | 0.03224284 | PetAngle | 41288598 | 0.25211501 |

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|---|---|---|---|---|---|---|---|
| **SLY351.9** | 4 | PlantHT | 41288616 | 0.03224284 | PetAngle | 41288616 | 0.25211501 |
| **TAC361.1** | 4 | PlantHT | 155517271 | 0.22091961 | PetAngle | 155517271 | 0.21888242 |
| **TAC361.10** | 4 | PlantHT | 155518227 | 0.00235035 | PetAngle | 155518227 | 0.01527368 |
| **TAC361.13** | 4 | PlantHT | 155519213 | 0.17178228 | PetAngle | 155519213 | 0.18561288 |
| **TAC361.14** | 4 | PlantHT | 155519529 | 0.72608272 | PetAngle | 155519529 | 0.71423275 |
| **TAC361.16** | 4 | PlantHT | 155519787 | 0.11775647 | PetAngle | 155519787 | 0.07555734 |
| **TAC361.17** | 4 | PlantHT | 155519800 | 0.55054042 | PetAngle | 155519800 | 0.47116573 |
| **TAC361.18** | 4 | PlantHT | 155520038 | 0.0891342 | PetAngle | 155520038 | 0.06283969 |
| **TAC361.19** | 4 | PlantHT | 155520121 | 0.00236966 | PetAngle | 155520121 | 0.17747784 |
| **TAC361.2** | 4 | PlantHT | 155517418 | 9.8237E-04 | PetAngle | 155517418 | 0.1255101 |
| **TAC361.20** | 4 | PlantHT | 155520230 | 0.13397845 | PetAngle | 155520230 | 0.04398148 |
| **TAC361.21** | 4 | PlantHT | 155520277 | 0.03912484 | PetAngle | 155520277 | 0.60125773 |
| **TAC361.22** | 4 | PlantHT | 155520338 | 0.0012812 | PetAngle | 155520338 | 0.22336252 |
| **TAC361.23** | 4 | PlantHT | 155520558 | 0.68753985 | PetAngle | 155520558 | 0.42601473 |
| **TAC361.3** | 4 | PlantHT | 155517438 | 0.11381316 | PetAngle | 155517438 | 0.60572976 |
| **TAC361.4** | 4 | PlantHT | 155517453 | 9.8237E-04 | PetAngle | 155517453 | 0.1255101 |
| **TAC361.5** | 4 | PlantHT | 155517553 | 0.15460184 | PetAngle | 155517553 | 0.67035883 |
| **TAC361.6** | 4 | PlantHT | 155517627 | 0.09187465 | PetAngle | 155517627 | 0.46010376 |
| **TAC361.9** | 4 | PlantHT | 155518008 | 0.0834622 | PetAngle | 155518008 | 0.01997709 |
| **SLY141.1** | 5 | PlantHT | 163484536 | 0.28942058 | PetAngle | 163484536 | 0.16848964 |
| **SLY141.10** | 5 | PlantHT | 163485423 | 0.70621139 | PetAngle | 163485423 | 0.72584783 |
| **SLY141.11** | 5 | PlantHT | 163485618 | 0.47001183 | PetAngle | 163485618 | 0.02876683 |
| **SLY141.12** | 5 | PlantHT | 163485624 | 0.47001183 | PetAngle | 163485624 | 0.02876683 |
| **SLY141.13** | 5 | PlantHT | 163486432 | 0.44195097 | PetAngle | 163486432 | 0.54296907 |
| **SLY141.14** | 5 | PlantHT | 163486451 | 0.36320505 | PetAngle | 163486451 | 0.97090191 |
| **SLY141.15** | 5 | PlantHT | 163486868 | 0.39919401 | PetAngle | 163486868 | 0.37201215 |
| **SLY141.2** | 5 | PlantHT | 163484898 | 0.75687318 | PetAngle | 163484898 | 0.95848512 |
| **SLY141.3** | 5 | PlantHT | 163484956 | 0.17003217 | PetAngle | 163484956 | 0.93389088 |
| **SLY141.4** | 5 | PlantHT | 163484969 | 0.11421679 | PetAngle | 163484969 | 0.41880535 |
| **SLY141.5** | 5 | PlantHT | 163485239 | 0.07505825 | PetAngle | 163485239 | 0.25365556 |
| **SLY141.6** | 5 | PlantHT | 163485248 | 0.17381768 | PetAngle | 163485248 | 0.07265743 |
| **SLY141.7** | 5 | PlantHT | 163485257 | 0.70075442 | PetAngle | 163485257 | 0.7099762 |
| **SLY141.8** | 5 | PlantHT | 163485366 | 0.19159015 | PetAngle | 163485366 | 0.24857837 |
| **GID741.2** | 6 | PlantHT | 43970283 | 0.75635718 | PetAngle | 43970283 | 0.81330826 |
| **GID741.3** | 6 | PlantHT | 43970298 | 0.28528966 | PetAngle | 43970298 | 0.98211536 |
| **GID741.4** | 6 | PlantHT | 43970589 | 0.45039714 | PetAngle | 43970589 | 0.64423568 |
| **GID741.5** | 6 | PlantHT | 43971149 | 0.60999508 | PetAngle | 43971149 | 0.08187425 |
| **DEL091.10** | 8 | PlantHT | 12264206 | 0.02971707 | PetAngle | 12264206 | 0.09604259 |
| **DEL091.12** | 8 | PlantHT | 12264269 | 0.95839178 | PetAngle | 12264269 | 0.47546271 |
| **DEL091.13** | 8 | PlantHT | 12264332 | 0.44698071 | PetAngle | 12264332 | 0.0207334 |
| **DEL091.14** | 8 | PlantHT | 12264404 | 0.76413166 | PetAngle | 12264404 | 0.20755918 |
| **DEL091.15** | 8 | PlantHT | 12264512 | 0.22874768 | PetAngle | 12264512 | 0.01764449 |
| **DEL091.16** | 8 | PlantHT | 12264599 | 0.8382803 | PetAngle | 12264599 | 0.91758762 |
| **DEL091.17** | 8 | PlantHT | 12264604 | 0.47832314 | PetAngle | 12264604 | 0.01608967 |
| **DEL091.18** | 8 | PlantHT | 12264635 | 0.09050116 | PetAngle | 12264635 | 4.97E-04 |
| **DEL091.20** | 8 | PlantHT | 12264789 | 0.47502536 | PetAngle | 12264789 | 0.38557557 |
| **DEL091.21** | 8 | PlantHT | 12264795 | 0.62099386 | PetAngle | 12264795 | 0.2759563 |
| **DEL091.22** | 8 | PlantHT | 12264962 | 0.05758911 | PetAngle | 12264962 | 0.4333442 |
| **DEL091.24** | 8 | PlantHT | 12265025 | 0.47316571 | PetAngle | 12265025 | 0.00601819 |

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| **DEL091.25** | 8 | PlantHT | 12265054 | 0.11048238 | PetAngle | 12265054 | 8.93E-04 |
| **DEL091.26** | 8 | PlantHT | 12265056 | 0.1904363 | PetAngle | 12265056 | 0.19432591 |
| **DEL091.27** | 8 | PlantHT | 12265422 | 0.29655531 | PetAngle | 12265422 | 0.0015879 |
| **DEL091.29** | 8 | PlantHT | 12265567 | 0.43503659 | PetAngle | 12265567 | 0.03597915 |
| **DEL091.3** | 8 | PlantHT | 12263870 | 0.46512781 | PetAngle | 12263870 | 0.19169619 |
| **DEL091.30** | 8 | PlantHT | 12265676 | 0.00482199 | PetAngle | 12265676 | 4.7469E-05 |
| **DEL091.31** | 8 | PlantHT | 12265683 | 0.03357294 | PetAngle | 12265683 | 2.4148E-04 |
| **DEL091.32** | 8 | PlantHT | 12265802 | 0.06061257 | PetAngle | 12265802 | 3.4140E-04 |
| **DEL091.33** | 8 | PlantHT | 12266012 | 0.14018666 | PetAngle | 12266012 | 8.8209E-05 |
| **DEL091.34** | 8 | PlantHT | 12266161 | 0.39912357 | PetAngle | 12266161 | 0.2659271 |
| **DEL091.35** | 8 | PlantHT | 12266179 | 0.73562777 | PetAngle | 12266179 | 0.03878646 |
| **DEL091.36** | 8 | PlantHT | 12266186 | 0.69755337 | PetAngle | 12266186 | 0.06260088 |
| **DEL091.37** | 8 | PlantHT | 12266199 | 0.56266207 | PetAngle | 12266199 | 0.05458392 |
| **DEL091.38** | 8 | PlantHT | 12266211 | 0.14093038 | PetAngle | 12266211 | 0.39167685 |
| **DEL091.4** | 8 | PlantHT | 12263903 | 0.29843071 | PetAngle | 12263903 | 0.04182172 |
| **DEL091.41** | 8 | PlantHT | 12266403 | 0.35496678 | PetAngle | 12266403 | 0.38771802 |
| **DEL091.42** | 8 | PlantHT | 12266417 | 0.81942882 | PetAngle | 12266417 | 0.03750327 |
| **DEL091.43** | 8 | PlantHT | 12266464 | 0.57071951 | PetAngle | 12266464 | 0.00912608 |
| **DEL091.47** | 8 | PlantHT | 12266830 | 0.1268415 | PetAngle | 12266830 | 0.00370378 |
| **DEL091.48** | 8 | PlantHT | 12266863 | 0.13974763 | PetAngle | 12266863 | 0.01101581 |
| **DEL091.49** | 8 | PlantHT | 12266939 | 0.28052125 | PetAngle | 12266939 | 0.24680583 |
| **DEL091.5** | 8 | PlantHT | 12263912 | 0.51223906 | PetAngle | 12263912 | 0.03961412 |
| **DEL091.50** | 8 | PlantHT | 12267167 | 0.09742253 | PetAngle | 12267167 | 0.4595894 |
| **DEL091.52** | 8 | PlantHT | 12267267 | 0.09742253 | PetAngle | 12267267 | 0.4595894 |
| **DEL091.6** | 8 | PlantHT | 12264043 | 0.31948539 | PetAngle | 12264043 | 0.82919749 |
| **DEL091.7** | 8 | PlantHT | 12264064 | 0.20337895 | PetAngle | 12264064 | 5.55E-04 |
| **DEL091.8** | 8 | PlantHT | 12264103 | 0.07985557 | PetAngle | 12264103 | 0.16485378 |
| **DEL091.9** | 8 | PlantHT | 12264128 | 0.34045448 | PetAngle | 12264128 | 0.13778764 |
| **LAZ951.1** | 8 | PlantHT | 7807354 | 0.7757358 | PetAngle | 7807354 | 0.86998862 |
| **LAZ951.10** | 8 | PlantHT | 7809246 | 0.38739229 | PetAngle | 7809246 | 0.55883232 |
| **LAZ951.11** | 8 | PlantHT | 7809319 | 0.70695969 | PetAngle | 7809319 | 0.46444529 |
| **LAZ951.12** | 8 | PlantHT | 7809351 | 0.81998782 | PetAngle | 7809351 | 0.33709625 |
| **LAZ951.13** | 8 | PlantHT | 7809384 | 0.36395232 | PetAngle | 7809384 | 0.24526112 |
| **LAZ951.14** | 8 | PlantHT | 7809516 | 0.04532829 | PetAngle | 7809516 | 0.0085296 |
| **LAZ951.15** | 8 | PlantHT | 7809577 | 0.75846505 | PetAngle | 7809577 | 0.36076586 |
| **LAZ951.16** | 8 | PlantHT | 7809616 | 0.88040255 | PetAngle | 7809616 | 0.8972524 |
| **LAZ951.17** | 8 | PlantHT | 7809770 | 0.40114628 | PetAngle | 7809770 | 0.26051085 |
| **LAZ951.18** | 8 | PlantHT | 7810149 | 0.90957467 | PetAngle | 7810149 | 0.59791447 |
| **LAZ951.2** | 8 | PlantHT | 7807376 | 0.27700769 | PetAngle | 7807376 | 0.18693786 |
| **LAZ951.20** | 8 | PlantHT | 7810266 | 0.39903447 | PetAngle | 7810266 | 0.07547333 |
| **LAZ951.21** | 8 | PlantHT | 7810443 | 0.06371246 | PetAngle | 7810443 | 0.62213304 |
| **LAZ951.23** | 8 | PlantHT | 7810829 | 0.90585406 | PetAngle | 7810829 | 0.22771633 |
| **LAZ951.24** | 8 | PlantHT | 7810961 | 0.42689043 | PetAngle | 7810961 | 0.4465096 |
| **LAZ951.26** | 8 | PlantHT | 7811459 | 0.38464887 | PetAngle | 7811459 | 0.41083664 |
| **LAZ951.27** | 8 | PlantHT | 7811479 | 0.45154928 | PetAngle | 7811479 | 0.17346055 |
| **LAZ951.28** | 8 | PlantHT | 7811553 | 0.90224602 | PetAngle | 7811553 | 0.25276094 |
| **LAZ951.29** | 8 | PlantHT | 7812053 | 0.00624072 | PetAngle | 7812053 | 0.78801932 |
| **LAZ951.3** | 8 | PlantHT | 7807503 | 0.40381397 | PetAngle | 7807503 | 0.2904732 |
| **LAZ951.4** | 8 | PlantHT | 7807600 | 0.6318014 | PetAngle | 7807600 | 0.99761753 |

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| **LAZ951.5** | 8 | PlantHT | 7807614 | 0.67621014 | PetAngle | 7807614 | 0.89677875 |
| **LAZ951.6** | 8 | PlantHT | 7807682 | 0.91745834 | PetAngle | 7807682 | 0.44296925 |
| **LAZ951.7** | 8 | PlantHT | 7809093 | 0.13440128 | PetAngle | 7809093 | 0.02872582 |
| **LAZ951.8** | 8 | PlantHT | 7809138 | 0.48691237 | PetAngle | 7809138 | 0.09168937 |
| **LAZ951.9** | 8 | PlantHT | 7809176 | 0.05897365 | PetAngle | 7809176 | 0.03106511 |
| **SLY301.1** | 9 | PlantHT | 178666111 | 0.29833305 | PetAngle | 178666111 | 0.61102 |
| **SLY301.2** | 9 | PlantHT | 178666159 | 0.38941512 | PetAngle | 178666159 | 0.91002398 |
| **SLY301.3** | 9 | PlantHT | 178666187 | 0.42429079 | PetAngle | 178666187 | 0.59032689 |
| **SLY301.4** | 9 | PlantHT | 178666431 | 0.63537363 | PetAngle | 178666431 | 0.96233036 |
| **SLY301.5** | 9 | PlantHT | 178666702 | 0.53306834 | PetAngle | 178666702 | 0.50753708 |
| **SLY301.7** | 9 | PlantHT | 178668175 | 0.0667033 | PetAngle | 178668175 | 0.43552837 |
| **DEL171.2** | 10 | PlantHT | 34968719 | 0.10704567 | PetAngle | 34968719 | 0.92385563 |
| **GID071.1** | 10 | PlantHT | 28111762 | 0.76613113 | PetAngle | 28111762 | 0.07234096 |
| **GID071.13** | 10 | PlantHT | 28112319 | 0.90407901 | PetAngle | 28112319 | 0.1827818 |
| **GID071.14** | 10 | PlantHT | 28112493 | 0.10242095 | PetAngle | 28112493 | 0.01138262 |
| **GID071.15** | 10 | PlantHT | 28112634 | 0.23423199 | PetAngle | 28112634 | 0.03133856 |
| **GID071.16** | 10 | PlantHT | 28112657 | 0.62056804 | PetAngle | 28112657 | 3.4806E-04 |
| **GID071.17** | 10 | PlantHT | 28112679 | 0.10242095 | PetAngle | 28112679 | 0.01138262 |
| **GID071.18** | 10 | PlantHT | 28112826 | 0.79200743 | PetAngle | 28112826 | 0.6804382 |
| **GID071.19** | 10 | PlantHT | 28112847 | 0.78521814 | PetAngle | 28112847 | 0.98020312 |
| **GID071.20** | 10 | PlantHT | 28112916 | 0.11518378 | PetAngle | 28112916 | 0.01312889 |
| **GID071.21** | 10 | PlantHT | 28112919 | 0.40881299 | PetAngle | 28112919 | 0.22384753 |
| **GID071.22** | 10 | PlantHT | 28113024 | 0.63076719 | PetAngle | 28113024 | 0.00415043 |
| **GID071.23** | 10 | PlantHT | 28113051 | 0.18383872 | PetAngle | 28113051 | 0.00109353 |
| **GID071.24** | 10 | PlantHT | 28113168 | 0.83235894 | PetAngle | 28113168 | 0.00290374 |
| **GID071.26** | 10 | PlantHT | 28113769 | 0.86630282 | PetAngle | 28113769 | 0.59776721 |
| **GID071.28** | 10 | PlantHT | 28113897 | 0.98736463 | PetAngle | 28113897 | 0.09783844 |
| **GID071.29** | 10 | PlantHT | 28113914 | 0.67019439 | PetAngle | 28113914 | 0.48931976 |
| **GID071.30** | 10 | PlantHT | 28114325 | 0.65151715 | PetAngle | 28114325 | 0.25528322 |
| **GID071.34** | 10 | PlantHT | 28114759 | 0.14299123 | PetAngle | 28114759 | 0.00596015 |
| **GID071.36** | 10 | PlantHT | 28114977 | 0.18383872 | PetAngle | 28114977 | 0.00109353 |
| **GID071.38** | 10 | PlantHT | 28115179 | 0.59459836 | PetAngle | 28115179 | 0.01068239 |
| **GID071.39** | 10 | PlantHT | 28115187 | 0.10483596 | PetAngle | 28115187 | 0.01141494 |
| **GID071.4** | 10 | PlantHT | 28111944 | 0.01734867 | PetAngle | 28111944 | 0.15132973 |
| **GID071.42** | 10 | PlantHT | 28116112 | 0.76595788 | PetAngle | 28116112 | 0.29076572 |
| **GID071.5** | 10 | PlantHT | 28111956 | 0.02202886 | PetAngle | 28111956 | 0.15758261 |
| **GID071.7** | 10 | PlantHT | 28111995 | 0.11938092 | PetAngle | 28111995 | 0.39684415 |
| **SLY611.1** | 11 | PlantHT | 138990416 | 0.14613889 | PetAngle | 138990416 | 0.79553387 |
| **SLY611.10** | 11 | PlantHT | 138993192 | 0.76830382 | PetAngle | 138993192 | 0.6224186 |
| **SLY611.11** | 11 | PlantHT | 138993311 | 0.89814019 | PetAngle | 138993311 | 0.6612026 |
| **SLY611.2** | 11 | PlantHT | 138990539 | 0.30003444 | PetAngle | 138990539 | 0.90848288 |
| **SLY611.3** | 11 | PlantHT | 138990639 | 0.84961397 | PetAngle | 138990639 | 0.55344646 |
| **SLY611.4** | 11 | PlantHT | 138990798 | 0.84961397 | PetAngle | 138990798 | 0.55344646 |
| **SLY611.5** | 11 | PlantHT | 138991001 | 0.42175326 | PetAngle | 138991001 | 0.27101447 |
| **SLY611.8** | 11 | PlantHT | 138992806 | 0.60228974 | PetAngle | 138992806 | 0.19757767 |
| **SLY611.9** | 11 | PlantHT | 138993071 | 0.20354199 | PetAngle | 138993071 | 0.27895951 |
| **DEL901.1** | 12 | PlantHT | 32211683 | 0.13103164 | PetAngle | 32211683 | 0.22087092 |
| **DEL901.10** | 12 | PlantHT | 32213076 | 0.13103164 | PetAngle | 32213076 | 0.22087092 |
| **DEL901.11** | 12 | PlantHT | 32213328 | 0.24514379 | PetAngle | 32213328 | 0.33321251 |

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| **DEL901.12** | 12 | PlantHT | 32213465 | 0.47015338 | PetAngle | 32213465 | 0.96317465 |
| **DEL901.2** | 12 | PlantHT | 32211812 | 0.13103164 | PetAngle | 32211812 | 0.22087092 |
| **DEL901.3** | 12 | PlantHT | 32211968 | 0.10684436 | PetAngle | 32211968 | 0.35226057 |
| **DEL901.4** | 12 | PlantHT | 32212028 | 0.10684436 | PetAngle | 32212028 | 0.35226057 |
| **DEL901.5** | 12 | PlantHT | 32212178 | 0.29737836 | PetAngle | 32212178 | 0.47215027 |
| **DEL901.6** | 12 | PlantHT | 32212556 | 0.63470919 | PetAngle | 32212556 | 0.22389546 |
| **DEL901.7** | 12 | PlantHT | 32212608 | 0.2346464 | PetAngle | 32212608 | 0.44830928 |
| **DEL901.8** | 12 | PlantHT | 32212620 | 0.94078136 | PetAngle | 32212620 | 0.14915251 |
| **DEL901.9** | 12 | PlantHT | 32212719 | 0.13103164 | PetAngle | 32212719 | 0.22087092 |
| **SNE981.1** | 12 | PlantHT | 81945604 | 0.55838999 | PetAngle | 81945604 | 0.93257548 |
| **SNE981.11** | 12 | PlantHT | 81947454 | 0.57513865 | PetAngle | 81947454 | 0.76204516 |
| **SNE981.12** | 12 | PlantHT | 81947533 | 0.61641994 | PetAngle | 81947533 | 0.97307041 |
| **SNE981.13** | 12 | PlantHT | 81947575 | 0.61641994 | PetAngle | 81947575 | 0.97307041 |
| **SNE981.14** | 12 | PlantHT | 81948022 | 0.86645867 | PetAngle | 81948022 | 0.8118047 |
| **SNE981.2** | 12 | PlantHT | 81945790 | 0.96675182 | PetAngle | 81945790 | 0.49692148 |
| **SNE981.5** | 12 | PlantHT | 81946423 | 0.61641994 | PetAngle | 81946423 | 0.97307041 |
| **SNE981.6** | 12 | PlantHT | 81946530 | 0.61641994 | PetAngle | 81946530 | 0.97307041 |
| **SNE981.8** | 12 | PlantHT | 81947032 | 0.55838999 | PetAngle | 81947032 | 0.93257548 |
| **SNE981.9** | 12 | PlantHT | 81947042 | 0.55838999 | PetAngle | 81947042 | 0.93257548 |
| **GID131.1** | 14 | PlantHT | 127160607 | 0.9077193 | PetAngle | 127160607 | 0.74148484 |
| **GID131.10** | 14 | PlantHT | 127161183 | 0.90851634 | PetAngle | 127161183 | 0.24701161 |
| **GID131.13** | 14 | PlantHT | 127161687 | 0.11809665 | PetAngle | 127161687 | 0.29122276 |
| **GID131.14** | 14 | PlantHT | 127161715 | 0.64660508 | PetAngle | 127161715 | 0.8687592 |
| **GID131.15** | 14 | PlantHT | 127162040 | 0.28290659 | PetAngle | 127162040 | 0.80560251 |
| **GID131.18** | 14 | PlantHT | 127162519 | 0.05612489 | PetAngle | 127162519 | 0.16217459 |
| **GID131.19** | 14 | PlantHT | 127162646 | 0.5919829 | PetAngle | 127162646 | 0.98864557 |
| **GID131.2** | 14 | PlantHT | 127160680 | 0.26529292 | PetAngle | 127160680 | 0.17096811 |
| **GID131.20** | 14 | PlantHT | 127162694 | 0.62931037 | PetAngle | 127162694 | 0.63435071 |
| **GID131.21** | 14 | PlantHT | 127162874 | 0.18966416 | PetAngle | 127162874 | 0.4089782 |
| **GID131.22** | 14 | PlantHT | 127162881 | 0.07062334 | PetAngle | 127162881 | 0.4443238 |
| **GID131.24** | 14 | PlantHT | 127163001 | 0.37262599 | PetAngle | 127163001 | 0.3430893 |
| **GID131.25** | 14 | PlantHT | 127163141 | 0.2293808 | PetAngle | 127163141 | 0.97609762 |
| **GID131.27** | 14 | PlantHT | 127163432 | 0.00282727 | PetAngle | 127163432 | 0.86924567 |
| **GID131.28** | 14 | PlantHT | 127163504 | 0.04560569 | PetAngle | 127163504 | 0.1559806 |
| **GID131.29** | 14 | PlantHT | 127163681 | 0.92444266 | PetAngle | 127163681 | 0.8619616 |
| **GID131.3** | 14 | PlantHT | 127160706 | 0.13867369 | PetAngle | 127160706 | 0.11358607 |
| **GID131.30** | 14 | PlantHT | 127163764 | 0.87674294 | PetAngle | 127163764 | 0.06178586 |
| **GID131.31** | 14 | PlantHT | 127163847 | 0.02422306 | PetAngle | 127163847 | 0.92922818 |
| **GID131.32** | 14 | PlantHT | 127163939 | 0.04560569 | PetAngle | 127163939 | 0.1559806 |
| **GID131.33** | 14 | PlantHT | 127164023 | 0.17330586 | PetAngle | 127164023 | 0.57054296 |
| **GID131.34** | 14 | PlantHT | 127164137 | 0.92444266 | PetAngle | 127164137 | 0.8619616 |
| **GID131.35** | 14 | PlantHT | 127164254 | 0.30568973 | PetAngle | 127164254 | 0.59111284 |
| **GID131.36** | 14 | PlantHT | 127164266 | 0.22668063 | PetAngle | 127164266 | 0.50015491 |
| **GID131.37** | 14 | PlantHT | 127164443 | 0.59464295 | PetAngle | 127164443 | 0.10958316 |
| **GID131.38** | 14 | PlantHT | 127164454 | 0.24596145 | PetAngle | 127164454 | 0.62982166 |
| **GID131.39** | 14 | PlantHT | 127164489 | 0.00872245 | PetAngle | 127164489 | 0.84894117 |
| **GID131.5** | 14 | PlantHT | 127160797 | 0.98405979 | PetAngle | 127160797 | 0.87829635 |
| **GID131.6** | 14 | PlantHT | 127160916 | 0.14536715 | PetAngle | 127160916 | 0.44776196 |
| **GID131.7** | 14 | PlantHT | 127160942 | 0.12790239 | PetAngle | 127160942 | 0.14828738 |

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| **GID131.9** | 14 | PlantHT | 127161170 | 0.09584585 | PetAngle | 127161170 | 0.10670768 |
| **TAC641.1** | 16 | PlantHT | 154345819 | 0.60449469 | PetAngle | 154345819 | 0.57674186 |
| **TAC641.4** | 16 | PlantHT | 154346996 | 0.1727489 | PetAngle | 154346996 | 0.23660467 |
| **TAC641.5** | 16 | PlantHT | 154347203 | 0.07900198 | PetAngle | 154347203 | 0.58735613 |
| **DEL801.10** | 17 | PlantHT | 194808854 | 0.10302829 | PetAngle | 194808854 | 0.59708156 |
| **DEL801.11** | 17 | PlantHT | 194808920 | 0.48520187 | PetAngle | 194808920 | 0.37661577 |
| **DEL801.12** | 17 | PlantHT | 194809025 | 0.00178779 | PetAngle | 194809025 | 0.82561307 |
| **DEL801.13** | 17 | PlantHT | 194809088 | 0.01562488 | PetAngle | 194809088 | 0.92882227 |
| **DEL801.14** | 17 | PlantHT | 194809186 | 0.14999466 | PetAngle | 194809186 | 0.08397212 |
| **DEL801.16** | 17 | PlantHT | 194809335 | 0.36427226 | PetAngle | 194809335 | 0.82141403 |
| **DEL801.17** | 17 | PlantHT | 194809363 | 0.38687052 | PetAngle | 194809363 | 0.16025807 |
| **DEL801.18** | 17 | PlantHT | 194809373 | 0.7065602 | PetAngle | 194809373 | 0.72968137 |
| **DEL801.19** | 17 | PlantHT | 194809815 | 0.2294995 | PetAngle | 194809815 | 0.14612707 |
| **DEL801.22** | 17 | PlantHT | 194810204 | 0.45804487 | PetAngle | 194810204 | 0.54607364 |
| **DEL801.23** | 17 | PlantHT | 194810236 | 0.92470125 | PetAngle | 194810236 | 0.4434751 |
| **DEL801.24** | 17 | PlantHT | 194810797 | 0.16767765 | PetAngle | 194810797 | 0.20580932 |
| **DEL801.25** | 17 | PlantHT | 194810815 | 0.0129753 | PetAngle | 194810815 | 0.72443738 |
| **DEL801.26** | 17 | PlantHT | 194810872 | 0.00379042 | PetAngle | 194810872 | 0.01126066 |
| **DEL801.27** | 17 | PlantHT | 194810919 | 0.26135219 | PetAngle | 194810919 | 0.8315776 |
| **DEL801.3** | 17 | PlantHT | 194808097 | 0.6197685 | PetAngle | 194808097 | 0.03581954 |
| **DEL801.31** | 17 | PlantHT | 194811667 | 0.97507381 | PetAngle | 194811667 | 0.52640534 |
| **DEL801.32** | 17 | PlantHT | 194811721 | 0.17086419 | PetAngle | 194811721 | 0.14463451 |
| **DEL801.4** | 17 | PlantHT | 194808128 | 0.59780811 | PetAngle | 194808128 | 0.08344362 |
| **DEL801.5** | 17 | PlantHT | 194808137 | 0.37729469 | PetAngle | 194808137 | 0.20441757 |
| **DEL801.6** | 17 | PlantHT | 194808477 | 0.23441498 | PetAngle | 194808477 | 0.01454879 |
| **DEL801.7** | 17 | PlantHT | 194808602 | 0.28517344 | PetAngle | 194808602 | 0.30434224 |
| **DEL801.8** | 17 | PlantHT | 194808652 | 0.2294995 | PetAngle | 194808652 | 0.14612707 |
| **DEL801.9** | 17 | PlantHT | 194808815 | 0.2294995 | PetAngle | 194808815 | 0.14612707 |
| **LAZ921.1** | 17 | PlantHT | 206481522 | 0.83650447 | PetAngle | 206481522 | 0.24331423 |
| **LAZ921.10** | 17 | PlantHT | 206482628 | 0.10069286 | PetAngle | 206482628 | 0.29436546 |
| **LAZ921.11** | 17 | PlantHT | 206482782 | 0.35815301 | PetAngle | 206482782 | 0.13213376 |
| **LAZ921.12** | 17 | PlantHT | 206482792 | NaN | PetAngle | 206482792 | NaN |
| **LAZ921.13** | 17 | PlantHT | 206483103 | 0.50538957 | PetAngle | 206483103 | 0.39192313 |
| **LAZ921.14** | 17 | PlantHT | 206483214 | 0.18470887 | PetAngle | 206483214 | 0.02173493 |
| **LAZ921.15** | 17 | PlantHT | 206483252 | 0.24733389 | PetAngle | 206483252 | 0.06751238 |
| **LAZ921.16** | 17 | PlantHT | 206483470 | 0.05363893 | PetAngle | 206483470 | 0.00212114 |
| **LAZ921.17** | 17 | PlantHT | 206483476 | 0.05363893 | PetAngle | 206483476 | 0.00212114 |
| **LAZ921.18** | 17 | PlantHT | 206483951 | 0.51102853 | PetAngle | 206483951 | 0.01141704 |
| **LAZ921.19** | 17 | PlantHT | 206483990 | 0.04673954 | PetAngle | 206483990 | 0.00202886 |
| **LAZ921.2** | 17 | PlantHT | 206481523 | 0.91748652 | PetAngle | 206481523 | 0.18915116 |
| **LAZ921.20** | 17 | PlantHT | 206484255 | 0.02591161 | PetAngle | 206484255 | 0.31494772 |
| **LAZ921.21** | 17 | PlantHT | 206484302 | 0.18999162 | PetAngle | 206484302 | 0.70165832 |
| **LAZ921.23** | 17 | PlantHT | 206484967 | 0.05326665 | PetAngle | 206484967 | 0.00447711 |
| **LAZ921.24** | 17 | PlantHT | 206484979 | 0.05326665 | PetAngle | 206484979 | 0.00447711 |
| **LAZ921.25** | 17 | PlantHT | 206485147 | 0.03693404 | PetAngle | 206485147 | 0.26372533 |
| **LAZ921.26** | 17 | PlantHT | 206485168 | 0.97753426 | PetAngle | 206485168 | 0.65605244 |
| **LAZ921.27** | 17 | PlantHT | 206485184 | 0.96895025 | PetAngle | 206485184 | 0.87348268 |
| **LAZ921.28** | 17 | PlantHT | 206485185 | 0.04249677 | PetAngle | 206485185 | 0.39723738 |
| **LAZ921.29** | 17 | PlantHT | 206485313 | 0.86571294 | PetAngle | 206485313 | 0.55357332 |

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|---|---|---|---|---|---|---|---|
| **LAZ921.32** | 17 | PlantHT | 206485496 | 0.40491515 | PetAngle | 206485496 | 0.18511466 |
| **LAZ921.33** | 17 | PlantHT | 206485873 | 0.25262059 | PetAngle | 206485873 | 0.40751037 |
| **LAZ921.34** | 17 | PlantHT | 206485928 | 0.87266907 | PetAngle | 206485928 | 0.48647272 |
| **LAZ921.35** | 17 | PlantHT | 206485936 | 0.87266907 | PetAngle | 206485936 | 0.48647272 |
| **LAZ921.36** | 17 | PlantHT | 206486107 | 0.76082057 | PetAngle | 206486107 | 0.17767208 |
| **LAZ921.37** | 17 | PlantHT | 206486155 | 0.42951277 | PetAngle | 206486155 | 0.03876465 |
| **LAZ921.38** | 17 | PlantHT | 206486181 | 0.23961883 | PetAngle | 206486181 | 0.07873505 |
| **LAZ921.40** | 17 | PlantHT | 206486230 | 0.36700985 | PetAngle | 206486230 | 0.10517396 |
| **LAZ921.41** | 17 | PlantHT | 206486337 | 0.18436375 | PetAngle | 206486337 | 0.63729235 |
| **LAZ921.42** | 17 | PlantHT | 206486407 | 0.138573 | PetAngle | 206486407 | 0.07923243 |
| **LAZ921.43** | 17 | PlantHT | 206486412 | 0.97060835 | PetAngle | 206486412 | 0.02333374 |
| **LAZ921.44** | 17 | PlantHT | 206486453 | 0.01355254 | PetAngle | 206486453 | 0.04826239 |
| **LAZ921.5** | 17 | PlantHT | 206481620 | 0.52791937 | PetAngle | 206481620 | 0.00788835 |
| **LAZ921.7** | 17 | PlantHT | 206482328 | 0.11611227 | PetAngle | 206482328 | 0.05523656 |
| **LAZ921.8** | 17 | PlantHT | 206482347 | 0.09877968 | PetAngle | 206482347 | 0.24914005 |

**Supplementary Table A 20:** Summary of GLM results for data of the small association panel (64 genotypes) in Spain 2017, limit value p = 0.000164

| MARKER | CHR | TRAIT | POS | P | TRAIT | POS | P |
|---|---|---|---|---|---|---|---|
| **GID871.10** | 1 | PlantHT | 12852858 | 0.27232834 | PetAngle | 12852858 | 0.41234823 |
| **GID871.11** | 1 | PlantHT | 12853069 | 0.53440974 | PetAngle | 12853069 | 0.40208686 |
| **GID871.12** | 1 | PlantHT | 12853100 | 0.94551049 | PetAngle | 12853100 | 0.97497009 |
| **GID871.13** | 1 | PlantHT | 12853241 | 0.69826762 | PetAngle | 12853241 | 0.93375687 |
| **GID871.14** | 1 | PlantHT | 12853328 | 0.50535295 | PetAngle | 12853328 | 0.5671621 |
| **GID871.15** | 1 | PlantHT | 12853334 | 0.50535295 | PetAngle | 12853334 | 0.5671621 |
| **GID871.16** | 1 | PlantHT | 12853430 | 0.1233567 | PetAngle | 12853430 | 0.9779555 |
| **GID871.17** | 1 | PlantHT | 12853511 | 0.34693664 | PetAngle | 12853511 | 0.40007405 |
| **GID871.21** | 1 | PlantHT | 12853600 | 0.87907688 | PetAngle | 12853600 | 0.24765911 |
| **GID871.22** | 1 | PlantHT | 12853709 | 0.71136876 | PetAngle | 12853709 | 0.0970657 |
| **GID871.23** | 1 | PlantHT | 12853714 | 0.61138287 | PetAngle | 12853714 | 0.47161259 |
| **GID871.5** | 1 | PlantHT | 12851807 | 0.51385718 | PetAngle | 12851807 | 0.59965299 |
| **GID871.6** | 1 | PlantHT | 12852614 | 0.88845636 | PetAngle | 12852614 | 0.47819266 |
| **GID871.7** | 1 | PlantHT | 12852731 | 0.73732311 | PetAngle | 12852731 | 0.89847288 |
| **GID871.9** | 1 | PlantHT | 12852833 | 0.28078612 | PetAngle | 12852833 | 0.38379058 |
| **SLY061.11** | 2 | PlantHT | 39415029 | 0.21783556 | PetAngle | 39415029 | 0.49543612 |
| **SLY061.14** | 2 | PlantHT | 39415287 | 0.0413728 | PetAngle | 39415287 | 0.67657796 |
| **SLY061.15** | 2 | PlantHT | 39415439 | 0.04639499 | PetAngle | 39415439 | 0.57976143 |
| **SLY061.16** | 2 | PlantHT | 39415448 | 0.04639499 | PetAngle | 39415448 | 0.57976143 |
| **SLY061.17** | 2 | PlantHT | 39415600 | 0.50136273 | PetAngle | 39415600 | 0.08864229 |
| **SLY061.19** | 2 | PlantHT | 39415765 | 0.51468818 | PetAngle | 39415765 | 0.10691361 |
| **SLY061.20** | 2 | PlantHT | 39415978 | 0.50136273 | PetAngle | 39415978 | 0.08864229 |
| **SLY061.21** | 2 | PlantHT | 39416235 | 0.45352985 | PetAngle | 39416235 | 0.05552694 |
| **SLY061.22** | 2 | PlantHT | 39416259 | 0.73713932 | PetAngle | 39416259 | 0.62229176 |
| **SLY061.3** | 2 | PlantHT | 39413612 | 0.29680071 | PetAngle | 39413612 | 0.85078686 |
| **SLY061.4** | 2 | PlantHT | 39413618 | 0.29680071 | PetAngle | 39413618 | 0.85078686 |
| **SLY061.5** | 2 | PlantHT | 39413737 | 0.11721526 | PetAngle | 39413737 | 0.87328461 |

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|---|---|---|---|---|---|---|---|
| **SLY061.6** | 2 | PlantHT | 39413802 | 0.07931551 | PetAngle | 39413802 | 0.86421917 |
| **SLY061.7** | 2 | PlantHT | 39414098 | 0.6409136 | PetAngle | 39414098 | 0.33208709 |
| **SNE171.1** | 3 | PlantHT | 104932867 | 0.5158995 | PetAngle | 104932867 | 0.97806949 |
| **SNE171.5** | 3 | PlantHT | 104934540 | 0.30261881 | PetAngle | 104934540 | 0.20098244 |
| **SNE171.6** | 3 | PlantHT | 104934736 | 0.30261881 | PetAngle | 104934736 | 0.20098244 |
| **SNE171.7** | 3 | PlantHT | 104934791 | 0.54298833 | PetAngle | 104934791 | 0.1598063 |
| **SNE171.8** | 3 | PlantHT | 104934943 | 0.90243097 | PetAngle | 104934943 | 0.72767493 |
| **SLY321.1** | 4 | PlantHT | 40919975 | 0.37682416 | PetAngle | 40919975 | 0.61438683 |
| **SLY321.2** | 4 | PlantHT | 40920036 | 0.28492046 | PetAngle | 40920036 | 0.3350215 |
| **SLY321.3** | 4 | PlantHT | 40920185 | 0.49507379 | PetAngle | 40920185 | 0.64656934 |
| **SLY321.6** | 4 | PlantHT | 40920969 | 0.45602486 | PetAngle | 40920969 | 0.8818809 |
| **SLY321.8** | 4 | PlantHT | 40921919 | 0.11502454 | PetAngle | 40921919 | 0.2511003 |
| **SLY351.11** | 4 | PlantHT | 41289089 | 0.49683977 | PetAngle | 41289089 | 0.87957609 |
| **SLY351.2** | 4 | PlantHT | 41287638 | 0.32454933 | PetAngle | 41287638 | 0.84210649 |
| **SLY351.4** | 4 | PlantHT | 41287804 | 0.65614741 | PetAngle | 41287804 | 0.66583799 |
| **SLY351.6** | 4 | PlantHT | 41288086 | 0.49215022 | PetAngle | 41288086 | 0.85304654 |
| **SLY351.7** | 4 | PlantHT | 41288167 | 0.24977142 | PetAngle | 41288167 | 0.92884523 |
| **SLY351.8** | 4 | PlantHT | 41288598 | 0.49215022 | PetAngle | 41288598 | 0.85304654 |
| **SLY351.9** | 4 | PlantHT | 41288616 | 0.49215022 | PetAngle | 41288616 | 0.85304654 |
| **TAC361.1** | 4 | PlantHT | 155517271 | 0.51109149 | PetAngle | 155517271 | 0.97405536 |
| **TAC361.10** | 4 | PlantHT | 155518227 | 0.09719986 | PetAngle | 155518227 | 0.16048342 |
| **TAC361.13** | 4 | PlantHT | 155519213 | 0.73879024 | PetAngle | 155519213 | 0.68628837 |
| **TAC361.14** | 4 | PlantHT | 155519529 | 0.66230074 | PetAngle | 155519529 | 0.76384072 |
| **TAC361.16** | 4 | PlantHT | 155519787 | 0.43652462 | PetAngle | 155519787 | 0.46873736 |
| **TAC361.17** | 4 | PlantHT | 155519800 | 0.90263092 | PetAngle | 155519800 | 0.56761654 |
| **TAC361.18** | 4 | PlantHT | 155520038 | 0.41155528 | PetAngle | 155520038 | 0.26698324 |
| **TAC361.19** | 4 | PlantHT | 155520121 | 0.12790672 | PetAngle | 155520121 | 0.71724658 |
| **TAC361.2** | 4 | PlantHT | 155517418 | 0.09578725 | PetAngle | 155517418 | 0.59159513 |
| **TAC361.20** | 4 | PlantHT | 155520230 | 0.01783821 | PetAngle | 155520230 | 0.27135716 |
| **TAC361.21** | 4 | PlantHT | 155520277 | 0.71087887 | PetAngle | 155520277 | 0.62354662 |
| **TAC361.22** | 4 | PlantHT | 155520338 | 0.21784098 | PetAngle | 155520338 | 0.49510463 |
| **TAC361.23** | 4 | PlantHT | 155520558 | 0.88984914 | PetAngle | 155520558 | 0.41591269 |
| **TAC361.3** | 4 | PlantHT | 155517438 | 0.70158441 | PetAngle | 155517438 | 0.81840783 |
| **TAC361.4** | 4 | PlantHT | 155517453 | 0.09578725 | PetAngle | 155517453 | 0.59159513 |
| **TAC361.5** | 4 | PlantHT | 155517553 | 0.69062138 | PetAngle | 155517553 | 0.7001377 |
| **TAC361.6** | 4 | PlantHT | 155517627 | 0.38116131 | PetAngle | 155517627 | 0.98370548 |
| **TAC361.9** | 4 | PlantHT | 155518008 | 0.24080413 | PetAngle | 155518008 | 0.11533753 |
| **SLY141.1** | 5 | PlantHT | 163484536 | 0.51271149 | PetAngle | 163484536 | 0.60084222 |
| **SLY141.10** | 5 | PlantHT | 163485423 | 0.75814304 | PetAngle | 163485423 | 0.84300643 |
| **SLY141.11** | 5 | PlantHT | 163485618 | 0.81797844 | PetAngle | 163485618 | 0.13079124 |
| **SLY141.12** | 5 | PlantHT | 163485624 | 0.81797844 | PetAngle | 163485624 | 0.13079124 |
| **SLY141.13** | 5 | PlantHT | 163486432 | 0.69028989 | PetAngle | 163486432 | 0.28477486 |
| **SLY141.14** | 5 | PlantHT | 163486451 | 0.79450773 | PetAngle | 163486451 | 0.86458218 |
| **SLY141.15** | 5 | PlantHT | 163486868 | 0.66258277 | PetAngle | 163486868 | 0.40225909 |
| **SLY141.2** | 5 | PlantHT | 163484898 | 0.5284896 | PetAngle | 163484898 | 0.78029683 |
| **SLY141.3** | 5 | PlantHT | 163484956 | 0.78910804 | PetAngle | 163484956 | 0.88529024 |
| **SLY141.4** | 5 | PlantHT | 163484969 | 0.38790825 | PetAngle | 163484969 | 0.61131086 |
| **SLY141.5** | 5 | PlantHT | 163485239 | 0.28970025 | PetAngle | 163485239 | 0.19163935 |
| **SLY141.6** | 5 | PlantHT | 163485248 | 0.30415852 | PetAngle | 163485248 | 0.14164832 |

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|---|---|---|---|---|---|---|---|
| **SLY141.7** | 5 | PlantHT | 163485257 | 0.77322303 | PetAngle | 163485257 | 0.82402155 |
| **SLY141.8** | 5 | PlantHT | 163485366 | 0.55781871 | PetAngle | 163485366 | 0.17186772 |
| **GID741.2** | 6 | PlantHT | 43970283 | 0.79444856 | PetAngle | 43970283 | 0.74440983 |
| **GID741.3** | 6 | PlantHT | 43970298 | 0.47333747 | PetAngle | 43970298 | 0.95252823 |
| **GID741.4** | 6 | PlantHT | 43970589 | 0.505873 | PetAngle | 43970589 | 0.7565828 |
| **GID741.5** | 6 | PlantHT | 43971149 | 0.67109665 | PetAngle | 43971149 | 0.61543085 |
| **DEL091.10** | 8 | PlantHT | 12264206 | 0.00209503 | PetAngle | 12264206 | 0.05779213 |
| **DEL091.12** | 8 | PlantHT | 12264269 | 0.33426046 | PetAngle | 12264269 | 0.97616818 |
| **DEL091.13** | 8 | PlantHT | 12264332 | 0.2054661 | PetAngle | 12264332 | 0.35674863 |
| **DEL091.14** | 8 | PlantHT | 12264404 | 0.88457004 | PetAngle | 12264404 | 0.04444055 |
| **DEL091.15** | 8 | PlantHT | 12264512 | 0.67098234 | PetAngle | 12264512 | 5.6871E-04 |
| **DEL091.16** | 8 | PlantHT | 12264599 | 0.59724489 | PetAngle | 12264599 | 0.41457543 |
| **DEL091.17** | 8 | PlantHT | 12264604 | 0.72732488 | PetAngle | 12264604 | 0.00431344 |
| **DEL091.18** | 8 | PlantHT | 12264635 | 0.24609078 | PetAngle | 12264635 | 2.6631E-04 |
| **DEL091.20** | 8 | PlantHT | 12264789 | 0.15140535 | PetAngle | 12264789 | 0.58468816 |
| **DEL091.21** | 8 | PlantHT | 12264795 | 0.36967419 | PetAngle | 12264795 | 0.07366514 |
| **DEL091.22** | 8 | PlantHT | 12264962 | 0.03239922 | PetAngle | 12264962 | 0.98291897 |
| **DEL091.24** | 8 | PlantHT | 12265025 | 0.20735229 | PetAngle | 12265025 | 0.10276103 |
| **DEL091.25** | 8 | PlantHT | 12265054 | 0.50044011 | PetAngle | 12265054 | 0.00647681 |
| **DEL091.26** | 8 | PlantHT | 12265056 | 0.14680097 | PetAngle | 12265056 | 0.83710895 |
| **DEL091.27** | 8 | PlantHT | 12265422 | 0.55589667 | PetAngle | 12265422 | 6.4242E-04 |
| **DEL091.29** | 8 | PlantHT | 12265567 | 0.18935095 | PetAngle | 12265567 | 0.0972363 |
| **DEL091.3** | 8 | PlantHT | 12263870 | 0.93891185 | PetAngle | 12263870 | 0.03578751 |
| **DEL091.30** | 8 | PlantHT | 12265676 | 4.2657E-04 | PetAngle | 12265676 | 0.00713262 |
| **DEL091.31** | 8 | PlantHT | 12265683 | 0.01050997 | PetAngle | 12265683 | 0.09099954 |
| **DEL091.32** | 8 | PlantHT | 12265802 | 0.06937082 | PetAngle | 12265802 | 5.1075E-04 |
| **DEL091.33** | 8 | PlantHT | 12266012 | 0.00423732 | PetAngle | 12266012 | 0.94927048 |
| **DEL091.34** | 8 | PlantHT | 12266161 | 0.25490638 | PetAngle | 12266161 | 0.94256848 |
| **DEL091.35** | 8 | PlantHT | 12266179 | 0.87107523 | PetAngle | 12266179 | 0.02018612 |
| **DEL091.36** | 8 | PlantHT | 12266186 | 0.80928481 | PetAngle | 12266186 | 0.07252772 |
| **DEL091.37** | 8 | PlantHT | 12266199 | 0.42245941 | PetAngle | 12266199 | 0.07020869 |
| **DEL091.38** | 8 | PlantHT | 12266211 | 0.32833466 | PetAngle | 12266211 | 0.71338566 |
| **DEL091.4** | 8 | PlantHT | 12263903 | 0.95391244 | PetAngle | 12263903 | 0.01885656 |
| **DEL091.41** | 8 | PlantHT | 12266403 | 0.74326731 | PetAngle | 12266403 | 0.2536901 |
| **DEL091.42** | 8 | PlantHT | 12266417 | 0.8775917 | PetAngle | 12266417 | 0.00708593 |
| **DEL091.43** | 8 | PlantHT | 12266464 | 0.46284697 | PetAngle | 12266464 | 0.01732173 |
| **DEL091.47** | 8 | PlantHT | 12266830 | 0.76423473 | PetAngle | 12266830 | 0.00402448 |
| **DEL091.48** | 8 | PlantHT | 12266863 | 0.8005356 | PetAngle | 12266863 | 0.00383445 |
| **DEL091.49** | 8 | PlantHT | 12266939 | 0.70345746 | PetAngle | 12266939 | 0.17362442 |
| **DEL091.5** | 8 | PlantHT | 12263912 | 0.2052836 | PetAngle | 12263912 | 0.3001425 |
| **DEL091.50** | 8 | PlantHT | 12267167 | 0.04491869 | PetAngle | 12267167 | 0.90249089 |
| **DEL091.52** | 8 | PlantHT | 12267267 | 0.04491869 | PetAngle | 12267267 | 0.90249089 |
| **DEL091.6** | 8 | PlantHT | 12264043 | 0.79302872 | PetAngle | 12264043 | 0.74012001 |
| **DEL091.7** | 8 | PlantHT | 12264064 | 0.38395957 | PetAngle | 12264064 | 0.00328604 |
| **DEL091.8** | 8 | PlantHT | 12264103 | 0.36463842 | PetAngle | 12264103 | 0.07604455 |
| **DEL091.9** | 8 | PlantHT | 12264128 | 0.53073083 | PetAngle | 12264128 | 0.19051305 |
| **LAZ951.1** | 8 | PlantHT | 7807354 | 0.66567987 | PetAngle | 7807354 | 0.43807019 |
| **LAZ951.10** | 8 | PlantHT | 7809246 | 0.18495198 | PetAngle | 7809246 | 0.86726342 |
| **LAZ951.11** | 8 | PlantHT | 7809319 | 0.35049823 | PetAngle | 7809319 | 0.47518875 |

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|---|---|---|---|---|---|---|---|
| **LAZ951.12** | 8 | PlantHT | 7809351 | 0.63708898 | PetAngle | 7809351 | 0.08941642 |
| **LAZ951.13** | 8 | PlantHT | 7809384 | 0.72060799 | PetAngle | 7809384 | 0.06045867 |
| **LAZ951.14** | 8 | PlantHT | 7809516 | 0.12236614 | PetAngle | 7809516 | 0.10049929 |
| **LAZ951.15** | 8 | PlantHT | 7809577 | 0.60863348 | PetAngle | 7809577 | 0.07204572 |
| **LAZ951.16** | 8 | PlantHT | 7809616 | 0.47113469 | PetAngle | 7809616 | 0.74477213 |
| **LAZ951.17** | 8 | PlantHT | 7809770 | 0.33191949 | PetAngle | 7809770 | 0.79719309 |
| **LAZ951.18** | 8 | PlantHT | 7810149 | 0.63449635 | PetAngle | 7810149 | 0.4707836 |
| **LAZ951.2** | 8 | PlantHT | 7807376 | 0.55493253 | PetAngle | 7807376 | 0.0543493 |
| **LAZ951.20** | 8 | PlantHT | 7810266 | 0.45903523 | PetAngle | 7810266 | 0.19781371 |
| **LAZ951.21** | 8 | PlantHT | 7810443 | 0.111791 | PetAngle | 7810443 | 0.6453714 |
| **LAZ951.23** | 8 | PlantHT | 7810829 | 0.7136191 | PetAngle | 7810829 | 0.12089275 |
| **LAZ951.24** | 8 | PlantHT | 7810961 | 0.44501016 | PetAngle | 7810961 | 0.51234486 |
| **LAZ951.26** | 8 | PlantHT | 7811459 | 0.77162595 | PetAngle | 7811459 | 0.147869 |
| **LAZ951.27** | 8 | PlantHT | 7811479 | 0.93947333 | PetAngle | 7811479 | 0.11557332 |
| **LAZ951.28** | 8 | PlantHT | 7811553 | 0.66998485 | PetAngle | 7811553 | 0.07666642 |
| **LAZ951.29** | 8 | PlantHT | 7812053 | 0.11378448 | PetAngle | 7812053 | 0.34208644 |
| **LAZ951.3** | 8 | PlantHT | 7807503 | 0.87579782 | PetAngle | 7807503 | 0.05890496 |
| **LAZ951.4** | 8 | PlantHT | 7807600 | 0.66570846 | PetAngle | 7807600 | 0.20542635 |
| **LAZ951.5** | 8 | PlantHT | 7807614 | 0.67052113 | PetAngle | 7807614 | 0.9477698 |
| **LAZ951.6** | 8 | PlantHT | 7807682 | 0.63933907 | PetAngle | 7807682 | 0.14243834 |
| **LAZ951.7** | 8 | PlantHT | 7809093 | 0.25320808 | PetAngle | 7809093 | 0.10194031 |
| **LAZ951.8** | 8 | PlantHT | 7809138 | 0.91394285 | PetAngle | 7809138 | 0.00934532 |
| **LAZ951.9** | 8 | PlantHT | 7809176 | 0.29409585 | PetAngle | 7809176 | 0.26186302 |
| **SLY301.1** | 9 | PlantHT | 178666111 | 0.19341466 | PetAngle | 178666111 | 0.49370867 |
| **SLY301.2** | 9 | PlantHT | 178666159 | 0.15354129 | PetAngle | 178666159 | 0.93634843 |
| **SLY301.3** | 9 | PlantHT | 178666187 | 0.04063767 | PetAngle | 178666187 | 0.60333399 |
| **SLY301.4** | 9 | PlantHT | 178666431 | 0.69660925 | PetAngle | 178666431 | 0.97133846 |
| **SLY301.5** | 9 | PlantHT | 178666702 | 0.23364727 | PetAngle | 178666702 | 0.65109049 |
| **SLY301.7** | 9 | PlantHT | 178668175 | 0.25477757 | PetAngle | 178668175 | 0.64717949 |
| **DEL171.2** | 10 | PlantHT | 34968719 | 0.37902616 | PetAngle | 34968719 | 0.70305393 |
| **GID071.1** | 10 | PlantHT | 28111762 | 0.61883192 | PetAngle | 28111762 | 0.05079939 |
| **GID071.13** | 10 | PlantHT | 28112319 | 0.95117802 | PetAngle | 28112319 | 0.51347844 |
| **GID071.14** | 10 | PlantHT | 28112493 | 0.40132402 | PetAngle | 28112493 | 0.16452352 |
| **GID071.15** | 10 | PlantHT | 28112634 | 0.22131808 | PetAngle | 28112634 | 0.06568727 |
| **GID071.16** | 10 | PlantHT | 28112657 | 0.83289404 | PetAngle | 28112657 | 0.01303282 |
| **GID071.17** | 10 | PlantHT | 28112679 | 0.40132402 | PetAngle | 28112679 | 0.16452352 |
| **GID071.18** | 10 | PlantHT | 28112826 | 0.29743324 | PetAngle | 28112826 | 0.9626973 |
| **GID071.19** | 10 | PlantHT | 28112847 | 0.51505954 | PetAngle | 28112847 | 0.80496587 |
| **GID071.20** | 10 | PlantHT | 28112916 | 0.44483568 | PetAngle | 28112916 | 0.11560109 |
| **GID071.21** | 10 | PlantHT | 28112919 | 0.52753402 | PetAngle | 28112919 | 0.21860598 |
| **GID071.22** | 10 | PlantHT | 28113024 | 0.40350292 | PetAngle | 28113024 | 0.02786535 |
| **GID071.23** | 10 | PlantHT | 28113051 | 0.28580992 | PetAngle | 28113051 | 0.00538273 |
| **GID071.24** | 10 | PlantHT | 28113168 | 0.46798632 | PetAngle | 28113168 | 0.02093417 |
| **GID071.26** | 10 | PlantHT | 28113769 | 0.81660325 | PetAngle | 28113769 | 0.3009677 |
| **GID071.28** | 10 | PlantHT | 28113897 | 0.29903156 | PetAngle | 28113897 | 0.03948619 |
| **GID071.29** | 10 | PlantHT | 28113914 | 0.91216907 | PetAngle | 28113914 | 0.19821616 |
| **GID071.30** | 10 | PlantHT | 28114325 | 0.21691659 | PetAngle | 28114325 | 0.27207634 |
| **GID071.34** | 10 | PlantHT | 28114759 | 0.40682667 | PetAngle | 28114759 | 0.01352069 |
| **GID071.36** | 10 | PlantHT | 28114977 | 0.28580992 | PetAngle | 28114977 | 0.00538273 |

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|---|---|---|---|---|---|---|---|
| **GID071.38** | 10 | PlantHT | 28115179 | 0.36104963 | PetAngle | 28115179 | 0.08490589 |
| **GID071.39** | 10 | PlantHT | 28115187 | 0.43493397 | PetAngle | 28115187 | 0.07690595 |
| **GID071.4** | 10 | PlantHT | 28111944 | 0.21267926 | PetAngle | 28111944 | 0.57985845 |
| **GID071.42** | 10 | PlantHT | 28116112 | 0.75396378 | PetAngle | 28116112 | 0.09207261 |
| **GID071.5** | 10 | PlantHT | 28111956 | 0.22807312 | PetAngle | 28111956 | 0.60231563 |
| **GID071.7** | 10 | PlantHT | 28111995 | 0.34740659 | PetAngle | 28111995 | 0.32858321 |
| **SLY611.1** | 11 | PlantHT | 138990416 | 0.54059396 | PetAngle | 138990416 | 0.89167006 |
| **SLY611.10** | 11 | PlantHT | 138993192 | 0.16986522 | PetAngle | 138993192 | 0.59502803 |
| **SLY611.11** | 11 | PlantHT | 138993311 | 0.82709399 | PetAngle | 138993311 | 0.75782375 |
| **SLY611.2** | 11 | PlantHT | 138990539 | 0.507486 | PetAngle | 138990539 | 0.94766419 |
| **SLY611.3** | 11 | PlantHT | 138990639 | 0.80110603 | PetAngle | 138990639 | 0.84734353 |
| **SLY611.4** | 11 | PlantHT | 138990798 | 0.80110603 | PetAngle | 138990798 | 0.84734353 |
| **SLY611.5** | 11 | PlantHT | 138991001 | 0.74329857 | PetAngle | 138991001 | 0.35380515 |
| **SLY611.8** | 11 | PlantHT | 138992806 | 0.22945699 | PetAngle | 138992806 | 0.48765218 |
| **SLY611.9** | 11 | PlantHT | 138993071 | 0.43086882 | PetAngle | 138993071 | 0.97085397 |
| **DEL901.1** | 12 | PlantHT | 32211683 | 0.06217032 | PetAngle | 32211683 | 0.03569196 |
| **DEL901.10** | 12 | PlantHT | 32213076 | 0.06217032 | PetAngle | 32213076 | 0.03569196 |
| **DEL901.11** | 12 | PlantHT | 32213328 | 0.18724527 | PetAngle | 32213328 | 0.11290285 |
| **DEL901.12** | 12 | PlantHT | 32213465 | 0.72325034 | PetAngle | 32213465 | 0.75193008 |
| **DEL901.2** | 12 | PlantHT | 32211812 | 0.06217032 | PetAngle | 32211812 | 0.03569196 |
| **DEL901.3** | 12 | PlantHT | 32211968 | 0.18046907 | PetAngle | 32211968 | 0.11292101 |
| **DEL901.4** | 12 | PlantHT | 32212028 | 0.18046907 | PetAngle | 32212028 | 0.11292101 |
| **DEL901.5** | 12 | PlantHT | 32212178 | 0.15104666 | PetAngle | 32212178 | 0.11223862 |
| **DEL901.6** | 12 | PlantHT | 32212556 | 0.23046419 | PetAngle | 32212556 | 0.02475562 |
| **DEL901.7** | 12 | PlantHT | 32212608 | 0.0651438 | PetAngle | 32212608 | 0.40514305 |
| **DEL901.8** | 12 | PlantHT | 32212620 | 0.86615683 | PetAngle | 32212620 | 0.06368065 |
| **DEL901.9** | 12 | PlantHT | 32212719 | 0.06217032 | PetAngle | 32212719 | 0.03569196 |
| **SNE981.1** | 12 | PlantHT | 81945604 | 0.1328661 | PetAngle | 81945604 | 0.62091077 |
| **SNE981.11** | 12 | PlantHT | 81947454 | 0.20569181 | PetAngle | 81947454 | 0.89464804 |
| **SNE981.12** | 12 | PlantHT | 81947533 | 0.16088203 | PetAngle | 81947533 | 0.66718887 |
| **SNE981.13** | 12 | PlantHT | 81947575 | 0.16088203 | PetAngle | 81947575 | 0.66718887 |
| **SNE981.14** | 12 | PlantHT | 81948022 | 0.72856233 | PetAngle | 81948022 | 0.71972561 |
| **SNE981.2** | 12 | PlantHT | 81945790 | 0.79377041 | PetAngle | 81945790 | 0.36792383 |
| **SNE981.5** | 12 | PlantHT | 81946423 | 0.16088203 | PetAngle | 81946423 | 0.66718887 |
| **SNE981.6** | 12 | PlantHT | 81946530 | 0.16088203 | PetAngle | 81946530 | 0.66718887 |
| **SNE981.8** | 12 | PlantHT | 81947032 | 0.1328661 | PetAngle | 81947032 | 0.62091077 |
| **SNE981.9** | 12 | PlantHT | 81947042 | 0.1328661 | PetAngle | 81947042 | 0.62091077 |
| **GID131.1** | 14 | PlantHT | 127160607 | 0.86596422 | PetAngle | 127160607 | 0.92033763 |
| **GID131.10** | 14 | PlantHT | 127161183 | 0.80473075 | PetAngle | 127161183 | 0.93003999 |
| **GID131.13** | 14 | PlantHT | 127161687 | 0.18147475 | PetAngle | 127161687 | 0.74070867 |
| **GID131.14** | 14 | PlantHT | 127161715 | 0.78947597 | PetAngle | 127161715 | 0.95336994 |
| **GID131.15** | 14 | PlantHT | 127162040 | 0.48694759 | PetAngle | 127162040 | 0.62009374 |
| **GID131.18** | 14 | PlantHT | 127162519 | 0.41109693 | PetAngle | 127162519 | 0.1667455 |
| **GID131.19** | 14 | PlantHT | 127162646 | 0.91160352 | PetAngle | 127162646 | 0.86260374 |
| **GID131.2** | 14 | PlantHT | 127160680 | 0.04200429 | PetAngle | 127160680 | 0.70572436 |
| **GID131.20** | 14 | PlantHT | 127162694 | 0.96150141 | PetAngle | 127162694 | 0.6410901 |
| **GID131.21** | 14 | PlantHT | 127162874 | 0.10555219 | PetAngle | 127162874 | 0.83423377 |
| **GID131.22** | 14 | PlantHT | 127162881 | 0.1041551 | PetAngle | 127162881 | 0.94580935 |
| **GID131.24** | 14 | PlantHT | 127163001 | 0.10492969 | PetAngle | 127163001 | 0.01123635 |

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|---|---|---|---|---|---|---|---|
| **GID131.25** | 14 | PlantHT | 127163141 | 0.09335266 | PetAngle | 127163141 | 0.79301577 |
| **GID131.27** | 14 | PlantHT | 127163432 | 0.01220022 | PetAngle | 127163432 | 0.37399224 |
| **GID131.28** | 14 | PlantHT | 127163504 | 0.36906124 | PetAngle | 127163504 | 0.19810959 |
| **GID131.29** | 14 | PlantHT | 127163681 | 0.959318 | PetAngle | 127163681 | 0.80315516 |
| **GID131.3** | 14 | PlantHT | 127160706 | 0.00483483 | PetAngle | 127160706 | 0.21027296 |
| **GID131.30** | 14 | PlantHT | 127163764 | 0.95543025 | PetAngle | 127163764 | 0.02903789 |
| **GID131.31** | 14 | PlantHT | 127163847 | 0.14499369 | PetAngle | 127163847 | 0.90545929 |
| **GID131.32** | 14 | PlantHT | 127163939 | 0.36906124 | PetAngle | 127163939 | 0.19810959 |
| **GID131.33** | 14 | PlantHT | 127164023 | 0.56233973 | PetAngle | 127164023 | 0.84590741 |
| **GID131.34** | 14 | PlantHT | 127164137 | 0.959318 | PetAngle | 127164137 | 0.80315516 |
| **GID131.35** | 14 | PlantHT | 127164254 | 0.55677802 | PetAngle | 127164254 | 0.36031927 |
| **GID131.36** | 14 | PlantHT | 127164266 | 0.36493411 | PetAngle | 127164266 | 0.35586435 |
| **GID131.37** | 14 | PlantHT | 127164443 | 0.62816879 | PetAngle | 127164443 | 0.24297323 |
| **GID131.38** | 14 | PlantHT | 127164454 | 0.25997685 | PetAngle | 127164454 | 0.23972279 |
| **GID131.39** | 14 | PlantHT | 127164489 | 0.02264904 | PetAngle | 127164489 | 0.24921771 |
| **GID131.5** | 14 | PlantHT | 127160797 | 0.7217796 | PetAngle | 127160797 | 0.97199514 |
| **GID131.6** | 14 | PlantHT | 127160916 | 0.26363054 | PetAngle | 127160916 | 0.50813194 |
| **GID131.7** | 14 | PlantHT | 127160942 | 0.024737 | PetAngle | 127160942 | 0.99240011 |
| **GID131.9** | 14 | PlantHT | 127161170 | 0.01595337 | PetAngle | 127161170 | 0.93977537 |
| **TAC641.1** | 16 | PlantHT | 154345819 | 0.38461995 | PetAngle | 154345819 | 0.88740941 |
| **TAC641.4** | 16 | PlantHT | 154346996 | 0.31799363 | PetAngle | 154346996 | 0.1531236 |
| **TAC641.5** | 16 | PlantHT | 154347203 | 0.01475877 | PetAngle | 154347203 | 0.9047476 |
| **DEL801.10** | 17 | PlantHT | 194808854 | 0.54772696 | PetAngle | 194808854 | 0.3940306 |
| **DEL801.11** | 17 | PlantHT | 194808920 | 0.36966086 | PetAngle | 194808920 | 0.15570219 |
| **DEL801.12** | 17 | PlantHT | 194809025 | 0.14037919 | PetAngle | 194809025 | 0.92184923 |
| **DEL801.13** | 17 | PlantHT | 194809088 | 0.21049724 | PetAngle | 194809088 | 0.60761867 |
| **DEL801.14** | 17 | PlantHT | 194809186 | 0.24135619 | PetAngle | 194809186 | 0.03828409 |
| **DEL801.16** | 17 | PlantHT | 194809335 | 0.28445456 | PetAngle | 194809335 | 0.68977191 |
| **DEL801.17** | 17 | PlantHT | 194809363 | 0.22869433 | PetAngle | 194809363 | 0.32466827 |
| **DEL801.18** | 17 | PlantHT | 194809373 | 0.69665538 | PetAngle | 194809373 | 0.67425708 |
| **DEL801.19** | 17 | PlantHT | 194809815 | 0.47560921 | PetAngle | 194809815 | 0.12349394 |
| **DEL801.22** | 17 | PlantHT | 194810204 | 0.46312224 | PetAngle | 194810204 | 0.55894625 |
| **DEL801.23** | 17 | PlantHT | 194810236 | 0.51235411 | PetAngle | 194810236 | 0.30188107 |
| **DEL801.24** | 17 | PlantHT | 194810797 | 0.67183428 | PetAngle | 194810797 | 0.75334777 |
| **DEL801.25** | 17 | PlantHT | 194810815 | 0.19101661 | PetAngle | 194810815 | 0.65849086 |
| **DEL801.26** | 17 | PlantHT | 194810872 | 0.10812707 | PetAngle | 194810872 | 0.07146483 |
| **DEL801.27** | 17 | PlantHT | 194810919 | 0.29886418 | PetAngle | 194810919 | 0.9222653 |
| **DEL801.3** | 17 | PlantHT | 194808097 | 0.87659153 | PetAngle | 194808097 | 0.02320953 |
| **DEL801.31** | 17 | PlantHT | 194811667 | 0.68726753 | PetAngle | 194811667 | 0.80249323 |
| **DEL801.32** | 17 | PlantHT | 194811721 | 0.35549433 | PetAngle | 194811721 | 0.11663951 |
| **DEL801.4** | 17 | PlantHT | 194808128 | 0.22701135 | PetAngle | 194808128 | 0.0616658 |
| **DEL801.5** | 17 | PlantHT | 194808137 | 0.40086028 | PetAngle | 194808137 | 0.16031424 |
| **DEL801.6** | 17 | PlantHT | 194808477 | 0.48257695 | PetAngle | 194808477 | 0.41715602 |
| **DEL801.7** | 17 | PlantHT | 194808602 | 0.48703679 | PetAngle | 194808602 | 0.23646985 |
| **DEL801.8** | 17 | PlantHT | 194808652 | 0.47560921 | PetAngle | 194808652 | 0.12349394 |
| **DEL801.9** | 17 | PlantHT | 194808815 | 0.47560921 | PetAngle | 194808815 | 0.12349394 |
| **LAZ921.1** | 17 | PlantHT | 206481522 | 0.68897496 | PetAngle | 206481522 | 0.13987529 |
| **LAZ921.10** | 17 | PlantHT | 206482628 | 0.16319284 | PetAngle | 206482628 | 0.43098413 |
| **LAZ921.11** | 17 | PlantHT | 206482782 | 0.17232673 | PetAngle | 206482782 | 0.73479455 |

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|---|---|---|---|---|---|---|---|
| **LAZ921.12** | 17 | PlantHT | 206482792 | NaN | PetAngle | 206482792 | NaN |
| **LAZ921.13** | 17 | PlantHT | 206483103 | 0.0987928 | PetAngle | 206483103 | 0.29872652 |
| **LAZ921.14** | 17 | PlantHT | 206483214 | 0.09733593 | PetAngle | 206483214 | 0.06442354 |
| **LAZ921.15** | 17 | PlantHT | 206483252 | 0.03034744 | PetAngle | 206483252 | 0.26007308 |
| **LAZ921.16** | 17 | PlantHT | 206483470 | 0.25044347 | PetAngle | 206483470 | 0.00205484 |
| **LAZ921.17** | 17 | PlantHT | 206483476 | 0.25044347 | PetAngle | 206483476 | 0.00205484 |
| **LAZ921.18** | 17 | PlantHT | 206483951 | 0.45618378 | PetAngle | 206483951 | 0.01488834 |
| **LAZ921.19** | 17 | PlantHT | 206483990 | 0.25321573 | PetAngle | 206483990 | 0.00198582 |
| **LAZ921.2** | 17 | PlantHT | 206481523 | 0.68960406 | PetAngle | 206481523 | 0.10332759 |
| **LAZ921.20** | 17 | PlantHT | 206484255 | 0.13202429 | PetAngle | 206484255 | 0.19619566 |
| **LAZ921.21** | 17 | PlantHT | 206484302 | 0.35393442 | PetAngle | 206484302 | 0.25975097 |
| **LAZ921.23** | 17 | PlantHT | 206484967 | 0.03890306 | PetAngle | 206484967 | 0.0199475 |
| **LAZ921.24** | 17 | PlantHT | 206484979 | 0.03890306 | PetAngle | 206484979 | 0.0199475 |
| **LAZ921.25** | 17 | PlantHT | 206485147 | 0.18537082 | PetAngle | 206485147 | 0.19739936 |
| **LAZ921.26** | 17 | PlantHT | 206485168 | 0.45990268 | PetAngle | 206485168 | 0.55760638 |
| **LAZ921.27** | 17 | PlantHT | 206485184 | 0.58569674 | PetAngle | 206485184 | 0.75057954 |
| **LAZ921.28** | 17 | PlantHT | 206485185 | 0.21772822 | PetAngle | 206485185 | 0.31762862 |
| **LAZ921.29** | 17 | PlantHT | 206485313 | 0.50508121 | PetAngle | 206485313 | 0.42135588 |
| **LAZ921.32** | 17 | PlantHT | 206485496 | 0.69807368 | PetAngle | 206485496 | 0.80723281 |
| **LAZ921.33** | 17 | PlantHT | 206485873 | 0.5210426 | PetAngle | 206485873 | 0.32437496 |
| **LAZ921.34** | 17 | PlantHT | 206485928 | 0.67667514 | PetAngle | 206485928 | 0.86369606 |
| **LAZ921.35** | 17 | PlantHT | 206485936 | 0.67667514 | PetAngle | 206485936 | 0.86369606 |
| **LAZ921.36** | 17 | PlantHT | 206486107 | 0.57585981 | PetAngle | 206486107 | 0.63554766 |
| **LAZ921.37** | 17 | PlantHT | 206486155 | 0.82130351 | PetAngle | 206486155 | 0.13390609 |
| **LAZ921.38** | 17 | PlantHT | 206486181 | 0.17253459 | PetAngle | 206486181 | 0.02824182 |
| **LAZ921.40** | 17 | PlantHT | 206486230 | 0.22618182 | PetAngle | 206486230 | 0.04585451 |
| **LAZ921.41** | 17 | PlantHT | 206486337 | 0.32025435 | PetAngle | 206486337 | 0.66854028 |
| **LAZ921.42** | 17 | PlantHT | 206486407 | 0.3861699 | PetAngle | 206486407 | 0.27716193 |
| **LAZ921.43** | 17 | PlantHT | 206486412 | 0.94204355 | PetAngle | 206486412 | 0.10482554 |
| **LAZ921.44** | 17 | PlantHT | 206486453 | 0.07917635 | PetAngle | 206486453 | 0.89555605 |
| **LAZ921.5** | 17 | PlantHT | 206481620 | 0.63263623 | PetAngle | 206481620 | 0.01562773 |
| **LAZ921.7** | 17 | PlantHT | 206482328 | 0.03088593 | PetAngle | 206482328 | 0.258107 |
| **LAZ921.8** | 17 | PlantHT | 206482347 | 0.05635445 | PetAngle | 206482347 | 0.2296761 |

**Supplementary Table A 21:** Summary of GLM results for data of the small association panel (64 genotypes) in Spain 2018, limit value p = 0.000164

| MARKER | CHR | TRAIT | POS | P | TRAIT | POS | P |
|---|---|---|---|---|---|---|---|
| **GID871.10** | 1 | PlantHT | 12852858 | 0.13704725 | PetAngle | 12852858 | 0.5636909 |
| **GID871.11** | 1 | PlantHT | 12853069 | 0.4624039 | PetAngle | 12853069 | 0.06092268 |
| **GID871.12** | 1 | PlantHT | 12853100 | 0.76804641 | PetAngle | 12853100 | 0.67707958 |
| **GID871.13** | 1 | PlantHT | 12853241 | 0.88680255 | PetAngle | 12853241 | 0.07627161 |
| **GID871.14** | 1 | PlantHT | 12853328 | 0.36467491 | PetAngle | 12853328 | 0.18811142 |
| **GID871.15** | 1 | PlantHT | 12853334 | 0.36467491 | PetAngle | 12853334 | 0.18811142 |
| **GID871.16** | 1 | PlantHT | 12853430 | 0.34495721 | PetAngle | 12853430 | 0.08439686 |
| **GID871.17** | 1 | PlantHT | 12853511 | 0.26530644 | PetAngle | 12853511 | 0.02977577 |
| **GID871.21** | 1 | PlantHT | 12853600 | 0.92151217 | PetAngle | 12853600 | 0.25563192 |
| **GID871.22** | 1 | PlantHT | 12853709 | 0.67522432 | PetAngle | 12853709 | 0.73714426 |
| **GID871.23** | 1 | PlantHT | 12853714 | 0.50707517 | PetAngle | 12853714 | 0.04383206 |

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|---|---|---|---|---|---|---|---|
| **GID871.5** | 1 | PlantHT | 12851807 | 0.38415855 | PetAngle | 12851807 | 0.25875723 |
| **GID871.6** | 1 | PlantHT | 12852614 | 0.97619306 | PetAngle | 12852614 | 0.18867299 |
| **GID871.7** | 1 | PlantHT | 12852731 | 0.84448157 | PetAngle | 12852731 | 0.5880507 |
| **GID871.9** | 1 | PlantHT | 12852833 | 0.14195406 | PetAngle | 12852833 | 0.53956588 |
| **SLY061.11** | 2 | PlantHT | 39415029 | 0.03259745 | PetAngle | 39415029 | 0.5703398 |
| **SLY061.14** | 2 | PlantHT | 39415287 | 0.02159123 | PetAngle | 39415287 | 0.91404373 |
| **SLY061.15** | 2 | PlantHT | 39415439 | 0.02222319 | PetAngle | 39415439 | 0.88149648 |
| **SLY061.16** | 2 | PlantHT | 39415448 | 0.02222319 | PetAngle | 39415448 | 0.88149648 |
| **SLY061.17** | 2 | PlantHT | 39415600 | 0.74567809 | PetAngle | 39415600 | 0.14561988 |
| **SLY061.19** | 2 | PlantHT | 39415765 | 0.75579852 | PetAngle | 39415765 | 0.17332291 |
| **SLY061.20** | 2 | PlantHT | 39415978 | 0.74567809 | PetAngle | 39415978 | 0.14561988 |
| **SLY061.21** | 2 | PlantHT | 39416235 | 0.70729041 | PetAngle | 39416235 | 0.09090478 |
| **SLY061.22** | 2 | PlantHT | 39416259 | 0.43510772 | PetAngle | 39416259 | 0.27342544 |
| **SLY061.3** | 2 | PlantHT | 39413612 | 0.1430655 | PetAngle | 39413612 | 0.15572983 |
| **SLY061.4** | 2 | PlantHT | 39413618 | 0.1430655 | PetAngle | 39413618 | 0.15572983 |
| **SLY061.5** | 2 | PlantHT | 39413737 | 0.04202629 | PetAngle | 39413737 | 0.72199472 |
| **SLY061.6** | 2 | PlantHT | 39413802 | 0.0464558 | PetAngle | 39413802 | 0.85034963 |
| **SLY061.7** | 2 | PlantHT | 39414098 | 0.44952354 | PetAngle | 39414098 | 0.90234475 |
| **SNE171.1** | 3 | PlantHT | 104932867 | 0.32794554 | PetAngle | 104932867 | 0.25982013 |
| **SNE171.5** | 3 | PlantHT | 104934540 | 0.27524678 | PetAngle | 104934540 | 0.14267675 |
| **SNE171.6** | 3 | PlantHT | 104934736 | 0.27524678 | PetAngle | 104934736 | 0.14267675 |
| **SNE171.7** | 3 | PlantHT | 104934791 | 0.96396834 | PetAngle | 104934791 | 0.89898924 |
| **SNE171.8** | 3 | PlantHT | 104934943 | 0.47559015 | PetAngle | 104934943 | 0.53727829 |
| **SLY321.1** | 4 | PlantHT | 40919975 | 0.43707031 | PetAngle | 40919975 | 0.61109522 |
| **SLY321.2** | 4 | PlantHT | 40920036 | 0.24809066 | PetAngle | 40920036 | 0.32495761 |
| **SLY321.3** | 4 | PlantHT | 40920185 | 0.84350727 | PetAngle | 40920185 | 0.62748589 |
| **SLY321.6** | 4 | PlantHT | 40920969 | 0.69311978 | PetAngle | 40920969 | 0.29159312 |
| **SLY321.8** | 4 | PlantHT | 40921919 | 0.02100912 | PetAngle | 40921919 | 0.27821533 |
| **SLY351.11** | 4 | PlantHT | 41289089 | 0.4143764 | PetAngle | 41289089 | 0.30317907 |
| **SLY351.2** | 4 | PlantHT | 41287638 | 0.40650269 | PetAngle | 41287638 | 0.25977483 |
| **SLY351.4** | 4 | PlantHT | 41287804 | 0.78036991 | PetAngle | 41287804 | 0.25909788 |
| **SLY351.6** | 4 | PlantHT | 41288086 | 0.40712842 | PetAngle | 41288086 | 0.29843513 |
| **SLY351.7** | 4 | PlantHT | 41288167 | 0.41417138 | PetAngle | 41288167 | 0.73110532 |
| **SLY351.8** | 4 | PlantHT | 41288598 | 0.40712842 | PetAngle | 41288598 | 0.29843513 |
| **SLY351.9** | 4 | PlantHT | 41288616 | 0.40712842 | PetAngle | 41288616 | 0.29843513 |
| **TAC361.1** | 4 | PlantHT | 155517271 | 0.33017957 | PetAngle | 155517271 | 0.71385441 |
| **TAC361.10** | 4 | PlantHT | 155518227 | 0.01264209 | PetAngle | 155518227 | 0.19943765 |
| **TAC361.13** | 4 | PlantHT | 155519213 | 0.44210277 | PetAngle | 155519213 | 0.64803308 |
| **TAC361.14** | 4 | PlantHT | 155519529 | 0.69999393 | PetAngle | 155519529 | 0.69338768 |
| **TAC361.16** | 4 | PlantHT | 155519787 | 0.23614292 | PetAngle | 155519787 | 0.57360491 |
| **TAC361.17** | 4 | PlantHT | 155519800 | 0.95261759 | PetAngle | 155519800 | 0.33547117 |
| **TAC361.18** | 4 | PlantHT | 155520038 | 0.22188789 | PetAngle | 155520038 | 0.57287012 |
| **TAC361.19** | 4 | PlantHT | 155520121 | 0.07210796 | PetAngle | 155520121 | 0.91746207 |
| **TAC361.2** | 4 | PlantHT | 155517418 | 0.04850389 | PetAngle | 155517418 | 0.81373003 |
| **TAC361.20** | 4 | PlantHT | 155520230 | 0.21247802 | PetAngle | 155520230 | 0.37691019 |
| **TAC361.21** | 4 | PlantHT | 155520277 | 0.34743188 | PetAngle | 155520277 | 0.35497097 |
| **TAC361.22** | 4 | PlantHT | 155520338 | 0.1502131 | PetAngle | 155520338 | 0.86870275 |
| **TAC361.23** | 4 | PlantHT | 155520558 | 0.95458919 | PetAngle | 155520558 | 0.32988255 |
| **TAC361.3** | 4 | PlantHT | 155517438 | 0.41619063 | PetAngle | 155517438 | 0.82230699 |

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| **TAC361.4** | 4 | PlantHT | 155517453 | 0.04850389 | PetAngle | 155517453 | 0.81373003 |
| **TAC361.5** | 4 | PlantHT | 155517553 | 0.37600631 | PetAngle | 155517553 | 0.75194684 |
| **TAC361.6** | 4 | PlantHT | 155517627 | 0.26397809 | PetAngle | 155517627 | 0.22376911 |
| **TAC361.9** | 4 | PlantHT | 155518008 | 0.11254301 | PetAngle | 155518008 | 0.19549816 |
| **SLY141.1** | 5 | PlantHT | 163484536 | 0.94420407 | PetAngle | 163484536 | 0.01521017 |
| **SLY141.10** | 5 | PlantHT | 163485423 | 0.54577847 | PetAngle | 163485423 | 0.45564366 |
| **SLY141.11** | 5 | PlantHT | 163485618 | 0.78917155 | PetAngle | 163485618 | 0.03741995 |
| **SLY141.12** | 5 | PlantHT | 163485624 | 0.78917155 | PetAngle | 163485624 | 0.03741995 |
| **SLY141.13** | 5 | PlantHT | 163486432 | 0.95512583 | PetAngle | 163486432 | 0.0136788 |
| **SLY141.14** | 5 | PlantHT | 163486451 | 0.73290734 | PetAngle | 163486451 | 0.07076603 |
| **SLY141.15** | 5 | PlantHT | 163486868 | 0.44386552 | PetAngle | 163486868 | 0.53278547 |
| **SLY141.2** | 5 | PlantHT | 163484898 | 0.5483281 | PetAngle | 163484898 | 0.42510949 |
| **SLY141.3** | 5 | PlantHT | 163484956 | - | PetAngle | 163484956 | 0.27359699 |
| **SLY141.4** | 5 | PlantHT | 163484969 | 0.67829124 | PetAngle | 163484969 | 0.11288104 |
| **SLY141.5** | 5 | PlantHT | 163485239 | 0.32982434 | PetAngle | 163485239 | 0.0034579 |
| **SLY141.6** | 5 | PlantHT | 163485248 | 0.27980744 | PetAngle | 163485248 | 0.04974596 |
| **SLY141.7** | 5 | PlantHT | 163485257 | 0.5526888 | PetAngle | 163485257 | 0.51254504 |
| **SLY141.8** | 5 | PlantHT | 163485366 | 0.66320087 | PetAngle | 163485366 | 0.02254622 |
| **GID741.2** | 6 | PlantHT | 43970283 | 0.46546894 | PetAngle | 43970283 | 0.41302225 |
| **GID741.3** | 6 | PlantHT | 43970298 | 0.30312246 | PetAngle | 43970298 | 0.22157446 |
| **GID741.4** | 6 | PlantHT | 43970589 | 0.9548412 | PetAngle | 43970589 | 0.94478902 |
| **GID741.5** | 6 | PlantHT | 43971149 | 0.65835619 | PetAngle | 43971149 | 0.14101608 |
| **DEL091.10** | 8 | PlantHT | 12264206 | 0.42489022 | PetAngle | 12264206 | 0.34485276 |
| **DEL091.12** | 8 | PlantHT | 12264269 | 0.42988534 | PetAngle | 12264269 | 0.14014571 |
| **DEL091.13** | 8 | PlantHT | 12264332 | 0.24515053 | PetAngle | 12264332 | 0.3667946 |
| **DEL091.14** | 8 | PlantHT | 12264404 | 0.23679732 | PetAngle | 12264404 | 0.07249769 |
| **DEL091.15** | 8 | PlantHT | 12264512 | 0.89893361 | PetAngle | 12264512 | 0.0324043 |
| **DEL091.16** | 8 | PlantHT | 12264599 | 0.7038452 | PetAngle | 12264599 | 0.23252647 |
| **DEL091.17** | 8 | PlantHT | 12264604 | 0.76884645 | PetAngle | 12264604 | 0.02554219 |
| **DEL091.18** | 8 | PlantHT | 12264635 | 0.72262316 | PetAngle | 12264635 | 0.0114356 |
| **DEL091.20** | 8 | PlantHT | 12264789 | 0.47857801 | PetAngle | 12264789 | 0.53691638 |
| **DEL091.21** | 8 | PlantHT | 12264795 | 0.67522731 | PetAngle | 12264795 | 0.36943201 |
| **DEL091.22** | 8 | PlantHT | 12264962 | 0.07338246 | PetAngle | 12264962 | 0.65392774 |
| **DEL091.24** | 8 | PlantHT | 12265025 | 0.20854008 | PetAngle | 12265025 | 0.12176354 |
| **DEL091.25** | 8 | PlantHT | 12265054 | 0.87874009 | PetAngle | 12265054 | 0.03521791 |
| **DEL091.26** | 8 | PlantHT | 12265056 | 0.15013773 | PetAngle | 12265056 | 0.70698679 |
| **DEL091.27** | 8 | PlantHT | 12265422 | 0.89131448 | PetAngle | 12265422 | 0.02509308 |
| **DEL091.29** | 8 | PlantHT | 12265567 | 0.2406033 | PetAngle | 12265567 | 0.5946842 |
| **DEL091.3** | 8 | PlantHT | 12263870 | 0.64379288 | PetAngle | 12263870 | 0.0203943 |
| **DEL091.30** | 8 | PlantHT | 12265676 | 0.00108072 | PetAngle | 12265676 | 0.33539859 |
| **DEL091.31** | 8 | PlantHT | 12265683 | 0.00514618 | PetAngle | 12265683 | 0.98963036 |
| **DEL091.32** | 8 | PlantHT | 12265802 | 0.17991993 | PetAngle | 12265802 | 0.01688136 |
| **DEL091.33** | 8 | PlantHT | 12266012 | 0.01903129 | PetAngle | 12266012 | 0.26032256 |
| **DEL091.34** | 8 | PlantHT | 12266161 | 0.37420527 | PetAngle | 12266161 | 0.56863532 |
| **DEL091.35** | 8 | PlantHT | 12266179 | 0.52659501 | PetAngle | 12266179 | 0.06747657 |
| **DEL091.36** | 8 | PlantHT | 12266186 | 0.7935634 | PetAngle | 12266186 | 0.30444281 |
| **DEL091.37** | 8 | PlantHT | 12266199 | 0.69096818 | PetAngle | 12266199 | 0.27428624 |
| **DEL091.38** | 8 | PlantHT | 12266211 | 0.24718559 | PetAngle | 12266211 | 0.81707975 |
| **DEL091.4** | 8 | PlantHT | 12263903 | 0.94289576 | PetAngle | 12263903 | 0.0261028 |

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| **DEL091.41** | 8 | PlantHT | 12266403 | 0.64020374 | PetAngle | 12266403 | 0.41753351 |
| **DEL091.42** | 8 | PlantHT | 12266417 | 0.68293519 | PetAngle | 12266417 | 0.03036774 |
| **DEL091.43** | 8 | PlantHT | 12266464 | 0.92333809 | PetAngle | 12266464 | 0.1077815 |
| **DEL091.47** | 8 | PlantHT | 12266830 | 0.97197914 | PetAngle | 12266830 | 0.02427174 |
| **DEL091.48** | 8 | PlantHT | 12266863 | - | PetAngle | 12266863 | 0.01592205 |
| **DEL091.49** | 8 | PlantHT | 12266939 | 0.50453671 | PetAngle | 12266939 | 0.25751167 |
| **DEL091.5** | 8 | PlantHT | 12263912 | 0.23713487 | PetAngle | 12263912 | 0.77425383 |
| **DEL091.50** | 8 | PlantHT | 12267167 | 0.07703974 | PetAngle | 12267167 | 0.64250164 |
| **DEL091.52** | 8 | PlantHT | 12267267 | 0.07703974 | PetAngle | 12267267 | 0.64250164 |
| **DEL091.6** | 8 | PlantHT | 12264043 | 0.91471979 | PetAngle | 12264043 | 0.91311298 |
| **DEL091.7** | 8 | PlantHT | 12264064 | 0.51940346 | PetAngle | 12264064 | 0.01587122 |
| **DEL091.8** | 8 | PlantHT | 12264103 | 0.43218738 | PetAngle | 12264103 | 0.55460757 |
| **DEL091.9** | 8 | PlantHT | 12264128 | 0.48954472 | PetAngle | 12264128 | 0.34005643 |
| **LAZ951.1** | 8 | PlantHT | 7807354 | 0.87990977 | PetAngle | 7807354 | 0.56963911 |
| **LAZ951.10** | 8 | PlantHT | 7809246 | 0.08320089 | PetAngle | 7809246 | 0.56958735 |
| **LAZ951.11** | 8 | PlantHT | 7809319 | 0.23720869 | PetAngle | 7809319 | 0.39975976 |
| **LAZ951.12** | 8 | PlantHT | 7809351 | 0.6252542 | PetAngle | 7809351 | 0.0416552 |
| **LAZ951.13** | 8 | PlantHT | 7809384 | 0.91020441 | PetAngle | 7809384 | 0.19515232 |
| **LAZ951.14** | 8 | PlantHT | 7809516 | 0.02203514 | PetAngle | 7809516 | 0.35850702 |
| **LAZ951.15** | 8 | PlantHT | 7809577 | 0.74445169 | PetAngle | 7809577 | 0.09725962 |
| **LAZ951.16** | 8 | PlantHT | 7809616 | 0.281609 | PetAngle | 7809616 | 0.37854746 |
| **LAZ951.17** | 8 | PlantHT | 7809770 | 0.18915283 | PetAngle | 7809770 | 0.72612537 |
| **LAZ951.18** | 8 | PlantHT | 7810149 | 0.45636489 | PetAngle | 7810149 | 0.12502053 |
| **LAZ951.2** | 8 | PlantHT | 7807376 | 0.49541594 | PetAngle | 7807376 | 0.18138777 |
| **LAZ951.20** | 8 | PlantHT | 7810266 | 0.11255682 | PetAngle | 7810266 | 0.68357929 |
| **LAZ951.21** | 8 | PlantHT | 7810443 | 0.02535731 | PetAngle | 7810443 | 0.02606578 |
| **LAZ951.23** | 8 | PlantHT | 7810829 | 0.87505515 | PetAngle | 7810829 | 0.31533466 |
| **LAZ951.24** | 8 | PlantHT | 7810961 | 0.71497187 | PetAngle | 7810961 | 0.18697831 |
| **LAZ951.26** | 8 | PlantHT | 7811459 | 0.89289083 | PetAngle | 7811459 | 0.21580283 |
| **LAZ951.27** | 8 | PlantHT | 7811479 | 0.83919083 | PetAngle | 7811479 | 0.11245456 |
| **LAZ951.28** | 8 | PlantHT | 7811553 | 0.86977099 | PetAngle | 7811553 | 0.33567155 |
| **LAZ951.29** | 8 | PlantHT | 7812053 | 0.52209877 | PetAngle | 7812053 | 0.72878231 |
| **LAZ951.3** | 8 | PlantHT | 7807503 | 0.8146498 | PetAngle | 7807503 | 0.10247246 |
| **LAZ951.4** | 8 | PlantHT | 7807600 | 0.57197387 | PetAngle | 7807600 | 0.34178872 |
| **LAZ951.5** | 8 | PlantHT | 7807614 | 0.59217935 | PetAngle | 7807614 | 0.78194132 |
| **LAZ951.6** | 8 | PlantHT | 7807682 | 0.55109189 | PetAngle | 7807682 | 0.15310294 |
| **LAZ951.7** | 8 | PlantHT | 7809093 | 0.06923813 | PetAngle | 7809093 | 0.43136622 |
| **LAZ951.8** | 8 | PlantHT | 7809138 | 0.77806968 | PetAngle | 7809138 | 0.02582074 |
| **LAZ951.9** | 8 | PlantHT | 7809176 | 0.06156996 | PetAngle | 7809176 | 0.5433613 |
| **SLY301.1** | 9 | PlantHT | 178666111 | 0.17791008 | PetAngle | 178666111 | 0.27315528 |
| **SLY301.2** | 9 | PlantHT | 178666159 | 0.38794884 | PetAngle | 178666159 | 0.93112885 |
| **SLY301.3** | 9 | PlantHT | 178666187 | 0.14140839 | PetAngle | 178666187 | 0.83784929 |
| **SLY301.4** | 9 | PlantHT | 178666431 | 0.78190701 | PetAngle | 178666431 | 0.9129474 |
| **SLY301.5** | 9 | PlantHT | 178666702 | 0.21362981 | PetAngle | 178666702 | 0.75774767 |
| **SLY301.7** | 9 | PlantHT | 178668175 | 0.55202528 | PetAngle | 178668175 | 0.70418318 |
| **DEL171.2** | 10 | PlantHT | 34968719 | 0.1544829 | PetAngle | 34968719 | 0.66985978 |
| **GID071.1** | 10 | PlantHT | 28111762 | 0.01049355 | PetAngle | 28111762 | 0.02625415 |
| **GID071.13** | 10 | PlantHT | 28112319 | 0.59651281 | PetAngle | 28112319 | 0.3879402 |
| **GID071.14** | 10 | PlantHT | 28112493 | 0.33499968 | PetAngle | 28112493 | 0.23295119 |

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| **GID071.15** | 10 | PlantHT | 28112634 | 0.40499236 | PetAngle | 28112634 | 0.00875337 |
| **GID071.16** | 10 | PlantHT | 28112657 | 0.51568894 | PetAngle | 28112657 | 0.00382626 |
| **GID071.17** | 10 | PlantHT | 28112679 | 0.33499968 | PetAngle | 28112679 | 0.23295119 |
| **GID071.18** | 10 | PlantHT | 28112826 | 0.61355978 | PetAngle | 28112826 | 0.89584497 |
| **GID071.19** | 10 | PlantHT | 28112847 | 0.91004301 | PetAngle | 28112847 | 0.45252934 |
| **GID071.20** | 10 | PlantHT | 28112916 | 0.36872146 | PetAngle | 28112916 | 0.25570719 |
| **GID071.21** | 10 | PlantHT | 28112919 | 0.16444224 | PetAngle | 28112919 | 0.19354921 |
| **GID071.22** | 10 | PlantHT | 28113024 | 0.64374697 | PetAngle | 28113024 | 0.00658871 |
| **GID071.23** | 10 | PlantHT | 28113051 | 0.26002408 | PetAngle | 28113051 | 0.00299232 |
| **GID071.24** | 10 | PlantHT | 28113168 | 0.78356492 | PetAngle | 28113168 | 0.00739849 |
| **GID071.26** | 10 | PlantHT | 28113769 | 0.26238446 | PetAngle | 28113769 | 0.51969891 |
| **GID071.28** | 10 | PlantHT | 28113897 | 0.54203486 | PetAngle | 28113897 | 0.01795116 |
| **GID071.29** | 10 | PlantHT | 28113914 | 0.52644524 | PetAngle | 28113914 | 0.44197792 |
| **GID071.30** | 10 | PlantHT | 28114325 | 0.87579012 | PetAngle | 28114325 | 0.04380447 |
| **GID071.34** | 10 | PlantHT | 28114759 | 0.09749173 | PetAngle | 28114759 | 0.06608238 |
| **GID071.36** | 10 | PlantHT | 28114977 | 0.26002408 | PetAngle | 28114977 | 0.00299232 |
| **GID071.38** | 10 | PlantHT | 28115179 | 0.36961123 | PetAngle | 28115179 | 0.02027712 |
| **GID071.39** | 10 | PlantHT | 28115187 | 0.30946383 | PetAngle | 28115187 | 0.21389811 |
| **GID071.4** | 10 | PlantHT | 28111944 | 0.11672593 | PetAngle | 28111944 | 0.58899308 |
| **GID071.42** | 10 | PlantHT | 28116112 | 0.18358577 | PetAngle | 28116112 | 0.19013187 |
| **GID071.5** | 10 | PlantHT | 28111956 | 0.12089118 | PetAngle | 28111956 | 0.602995 |
| **GID071.7** | 10 | PlantHT | 28111995 | 0.17567592 | PetAngle | 28111995 | 0.30344065 |
| **SLY611.1** | 11 | PlantHT | 138990416 | 0.59951525 | PetAngle | 138990416 | 0.65495982 |
| **SLY611.10** | 11 | PlantHT | 138993192 | 0.88754662 | PetAngle | 138993192 | 0.54080466 |
| **SLY611.11** | 11 | PlantHT | 138993311 | 0.79767639 | PetAngle | 138993311 | 0.87649901 |
| **SLY611.2** | 11 | PlantHT | 138990539 | 0.33660338 | PetAngle | 138990539 | 0.28698113 |
| **SLY611.3** | 11 | PlantHT | 138990639 | 0.72661099 | PetAngle | 138990639 | 0.8831252 |
| **SLY611.4** | 11 | PlantHT | 138990798 | 0.72661099 | PetAngle | 138990798 | 0.8831252 |
| **SLY611.5** | 11 | PlantHT | 138991001 | 0.74412908 | PetAngle | 138991001 | 0.80895791 |
| **SLY611.8** | 11 | PlantHT | 138992806 | 0.9742513 | PetAngle | 138992806 | 0.50661394 |
| **SLY611.9** | 11 | PlantHT | 138993071 | 0.41874287 | PetAngle | 138993071 | 0.88780802 |
| **DEL901.1** | 12 | PlantHT | 32211683 | 0.33636207 | PetAngle | 32211683 | 0.18677474 |
| **DEL901.10** | 12 | PlantHT | 32213076 | 0.33636207 | PetAngle | 32213076 | 0.18677474 |
| **DEL901.11** | 12 | PlantHT | 32213328 | 0.50565523 | PetAngle | 32213328 | 0.35551911 |
| **DEL901.12** | 12 | PlantHT | 32213465 | 0.13038162 | PetAngle | 32213465 | 0.27744801 |
| **DEL901.2** | 12 | PlantHT | 32211812 | 0.33636207 | PetAngle | 32211812 | 0.18677474 |
| **DEL901.3** | 12 | PlantHT | 32211968 | 0.01713504 | PetAngle | 32211968 | 0.30053173 |
| **DEL901.4** | 12 | PlantHT | 32212028 | 0.01713504 | PetAngle | 32212028 | 0.30053173 |
| **DEL901.5** | 12 | PlantHT | 32212178 | 0.62381621 | PetAngle | 32212178 | 0.40768895 |
| **DEL901.6** | 12 | PlantHT | 32212556 | 0.21796542 | PetAngle | 32212556 | 0.29537624 |
| **DEL901.7** | 12 | PlantHT | 32212608 | 0.11977145 | PetAngle | 32212608 | 0.3148558 |
| **DEL901.8** | 12 | PlantHT | 32212620 | 0.80125281 | PetAngle | 32212620 | 0.18499901 |
| **DEL901.9** | 12 | PlantHT | 32212719 | 0.33636207 | PetAngle | 32212719 | 0.18677474 |
| **SNE981.1** | 12 | PlantHT | 81945604 | 0.12324908 | PetAngle | 81945604 | 0.85997654 |
| **SNE981.11** | 12 | PlantHT | 81947454 | 0.15744394 | PetAngle | 81947454 | 0.76823294 |
| **SNE981.12** | 12 | PlantHT | 81947533 | 0.14953927 | PetAngle | 81947533 | 0.81753829 |
| **SNE981.13** | 12 | PlantHT | 81947575 | 0.14953927 | PetAngle | 81947575 | 0.81753829 |
| **SNE981.14** | 12 | PlantHT | 81948022 | 0.35727157 | PetAngle | 81948022 | 0.38164334 |
| **SNE981.2** | 12 | PlantHT | 81945790 | 0.50995264 | PetAngle | 81945790 | 0.47991741 |

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| **SNE981.5** | 12 | PlantHT | 81946423 | 0.14953927 | PetAngle | 81946423 | 0.81753829 |
| **SNE981.6** | 12 | PlantHT | 81946530 | 0.14953927 | PetAngle | 81946530 | 0.81753829 |
| **SNE981.8** | 12 | PlantHT | 81947032 | 0.12324908 | PetAngle | 81947032 | 0.85997654 |
| **SNE981.9** | 12 | PlantHT | 81947042 | 0.12324908 | PetAngle | 81947042 | 0.85997654 |
| **GID131.1** | 14 | PlantHT | 127160607 | 0.43683409 | PetAngle | 127160607 | 0.74879082 |
| **GID131.10** | 14 | PlantHT | 127161183 | 0.42080531 | PetAngle | 127161183 | 0.89470736 |
| **GID131.13** | 14 | PlantHT | 127161687 | 0.17190355 | PetAngle | 127161687 | 0.41471399 |
| **GID131.14** | 14 | PlantHT | 127161715 | 0.60633813 | PetAngle | 127161715 | 0.87352857 |
| **GID131.15** | 14 | PlantHT | 127162040 | 0.32192193 | PetAngle | 127162040 | 0.37328934 |
| **GID131.18** | 14 | PlantHT | 127162519 | 0.24420688 | PetAngle | 127162519 | 0.11169585 |
| **GID131.19** | 14 | PlantHT | 127162646 | 0.76495686 | PetAngle | 127162646 | 0.96149276 |
| **GID131.2** | 14 | PlantHT | 127160680 | 0.54494569 | PetAngle | 127160680 | 0.74730068 |
| **GID131.20** | 14 | PlantHT | 127162694 | 0.60473415 | PetAngle | 127162694 | 0.99520131 |
| **GID131.21** | 14 | PlantHT | 127162874 | 0.11357659 | PetAngle | 127162874 | 0.84084817 |
| **GID131.22** | 14 | PlantHT | 127162881 | 0.17097675 | PetAngle | 127162881 | 0.54125853 |
| **GID131.24** | 14 | PlantHT | 127163001 | 0.8177209 | PetAngle | 127163001 | 0.04016042 |
| **GID131.25** | 14 | PlantHT | 127163141 | 0.75957704 | PetAngle | 127163141 | 0.80289743 |
| **GID131.27** | 14 | PlantHT | 127163432 | 0.04173914 | PetAngle | 127163432 | 0.84906287 |
| **GID131.28** | 14 | PlantHT | 127163504 | 0.25084315 | PetAngle | 127163504 | 0.1427747 |
| **GID131.29** | 14 | PlantHT | 127163681 | 0.87875895 | PetAngle | 127163681 | 0.91158928 |
| **GID131.3** | 14 | PlantHT | 127160706 | 0.39670381 | PetAngle | 127160706 | 0.55423484 |
| **GID131.30** | 14 | PlantHT | 127163764 | 0.9142295 | PetAngle | 127163764 | 0.03863158 |
| **GID131.31** | 14 | PlantHT | 127163847 | 0.21386645 | PetAngle | 127163847 | 0.96286122 |
| **GID131.32** | 14 | PlantHT | 127163939 | 0.25084315 | PetAngle | 127163939 | 0.1427747 |
| **GID131.33** | 14 | PlantHT | 127164023 | 0.68020965 | PetAngle | 127164023 | 0.36461511 |
| **GID131.34** | 14 | PlantHT | 127164137 | 0.87875895 | PetAngle | 127164137 | 0.91158928 |
| **GID131.35** | 14 | PlantHT | 127164254 | 0.65311976 | PetAngle | 127164254 | 0.61857145 |
| **GID131.36** | 14 | PlantHT | 127164266 | 0.40179157 | PetAngle | 127164266 | 0.55716941 |
| **GID131.37** | 14 | PlantHT | 127164443 | 0.77967903 | PetAngle | 127164443 | 0.57445534 |
| **GID131.38** | 14 | PlantHT | 127164454 | 0.38621488 | PetAngle | 127164454 | 0.1120735 |
| **GID131.39** | 14 | PlantHT | 127164489 | 0.11740302 | PetAngle | 127164489 | 0.11069857 |
| **GID131.5** | 14 | PlantHT | 127160797 | 0.65729001 | PetAngle | 127160797 | 0.63439724 |
| **GID131.6** | 14 | PlantHT | 127160916 | 0.13664391 | PetAngle | 127160916 | 0.1528309 |
| **GID131.7** | 14 | PlantHT | 127160942 | 0.32442184 | PetAngle | 127160942 | 0.39349316 |
| **GID131.9** | 14 | PlantHT | 127161170 | 0.26337847 | PetAngle | 127161170 | 0.41421991 |
| **TAC641.1** | 16 | PlantHT | 154345819 | 0.22628943 | PetAngle | 154345819 | 0.51218091 |
| **TAC641.4** | 16 | PlantHT | 154346996 | 0.1765966 | PetAngle | 154346996 | 0.25037773 |
| **TAC641.5** | 16 | PlantHT | 154347203 | 0.011412 | PetAngle | 154347203 | 0.40999883 |
| **DEL801.10** | 17 | PlantHT | 194808854 | 0.37734449 | PetAngle | 194808854 | 0.48547337 |
| **DEL801.11** | 17 | PlantHT | 194808920 | 0.83358162 | PetAngle | 194808920 | 0.10487545 |
| **DEL801.12** | 17 | PlantHT | 194809025 | 0.03811392 | PetAngle | 194809025 | 0.88368042 |
| **DEL801.13** | 17 | PlantHT | 194809088 | 0.10507045 | PetAngle | 194809088 | 0.95304611 |
| **DEL801.14** | 17 | PlantHT | 194809186 | 0.1580985 | PetAngle | 194809186 | 0.01987161 |
| **DEL801.16** | 17 | PlantHT | 194809335 | 0.85726005 | PetAngle | 194809335 | 0.77434581 |
| **DEL801.17** | 17 | PlantHT | 194809363 | 0.59802804 | PetAngle | 194809363 | 0.37636658 |
| **DEL801.18** | 17 | PlantHT | 194809373 | 0.85142781 | PetAngle | 194809373 | 0.31704671 |
| **DEL801.19** | 17 | PlantHT | 194809815 | 0.33046819 | PetAngle | 194809815 | 0.11762116 |
| **DEL801.22** | 17 | PlantHT | 194810204 | 0.56075845 | PetAngle | 194810204 | 0.31474135 |
| **DEL801.23** | 17 | PlantHT | 194810236 | 0.83170573 | PetAngle | 194810236 | 0.20800703 |

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|---|---|---|---|---|---|---|---|
| **DEL801.24** | 17 | PlantHT | 194810797 | 0.0516016 | PetAngle | 194810797 | 0.56229482 |
| **DEL801.25** | 17 | PlantHT | 194810815 | 0.09361962 | PetAngle | 194810815 | 0.94676754 |
| **DEL801.26** | 17 | PlantHT | 194810872 | 0.1044949 | PetAngle | 194810872 | 0.02832001 |
| **DEL801.27** | 17 | PlantHT | 194810919 | 0.20428819 | PetAngle | 194810919 | 0.80060116 |
| **DEL801.3** | 17 | PlantHT | 194808097 | 0.71227654 | PetAngle | 194808097 | 0.07163278 |
| **DEL801.31** | 17 | PlantHT | 194811667 | 0.42592417 | PetAngle | 194811667 | 0.93525842 |
| **DEL801.32** | 17 | PlantHT | 194811721 | 0.26211453 | PetAngle | 194811721 | 0.2728133 |
| **DEL801.4** | 17 | PlantHT | 194808128 | 0.6853315 | PetAngle | 194808128 | 0.25370997 |
| **DEL801.5** | 17 | PlantHT | 194808137 | 0.66494264 | PetAngle | 194808137 | 0.21646528 |
| **DEL801.6** | 17 | PlantHT | 194808477 | 0.32126494 | PetAngle | 194808477 | 0.11920531 |
| **DEL801.7** | 17 | PlantHT | 194808602 | 0.33595342 | PetAngle | 194808602 | 0.10054109 |
| **DEL801.8** | 17 | PlantHT | 194808652 | 0.33046819 | PetAngle | 194808652 | 0.11762116 |
| **DEL801.9** | 17 | PlantHT | 194808815 | 0.33046819 | PetAngle | 194808815 | 0.11762116 |
| **LAZ921.1** | 17 | PlantHT | 206481522 | 0.83619079 | PetAngle | 206481522 | 0.1045932 |
| **LAZ921.10** | 17 | PlantHT | 206482628 | 0.41665508 | PetAngle | 206482628 | 0.0627174 |
| **LAZ921.11** | 17 | PlantHT | 206482782 | 0.04461649 | PetAngle | 206482782 | 0.13684554 |
| **LAZ921.12** | 17 | PlantHT | 206482792 | - | PetAngle | 206482792 | NaN |
| **LAZ921.13** | 17 | PlantHT | 206483103 | 0.09282907 | PetAngle | 206483103 | 0.27140573 |
| **LAZ921.14** | 17 | PlantHT | 206483214 | 0.02465111 | PetAngle | 206483214 | 0.05209434 |
| **LAZ921.15** | 17 | PlantHT | 206483252 | 0.53272738 | PetAngle | 206483252 | 0.28006746 |
| **LAZ921.16** | 17 | PlantHT | 206483470 | 0.09946767 | PetAngle | 206483470 | 6.5555E-05 |
| **LAZ921.17** | 17 | PlantHT | 206483476 | 0.09946767 | PetAngle | 206483476 | 6.5555E-05 |
| **LAZ921.18** | 17 | PlantHT | 206483951 | 0.31787944 | PetAngle | 206483951 | 0.03241614 |
| **LAZ921.19** | 17 | PlantHT | 206483990 | 0.09499644 | PetAngle | 206483990 | 9.7286E-05 |
| **LAZ921.2** | 17 | PlantHT | 206481523 | 0.49344324 | PetAngle | 206481523 | 0.10141624 |
| **LAZ921.20** | 17 | PlantHT | 206484255 | 0.05623318 | PetAngle | 206484255 | 0.02250004 |
| **LAZ921.21** | 17 | PlantHT | 206484302 | 0.819743 | PetAngle | 206484302 | 0.95961264 |
| **LAZ921.23** | 17 | PlantHT | 206484967 | 0.01544712 | PetAngle | 206484967 | 0.03320798 |
| **LAZ921.24** | 17 | PlantHT | 206484979 | 0.01544712 | PetAngle | 206484979 | 0.03320798 |
| **LAZ921.25** | 17 | PlantHT | 206485147 | 0.0364359 | PetAngle | 206485147 | 0.01538151 |
| **LAZ921.26** | 17 | PlantHT | 206485168 | 0.37076623 | PetAngle | 206485168 | 0.25976689 |
| **LAZ921.27** | 17 | PlantHT | 206485184 | 0.38866719 | PetAngle | 206485184 | 0.44054077 |
| **LAZ921.28** | 17 | PlantHT | 206485185 | 0.0438923 | PetAngle | 206485185 | 0.02305843 |
| **LAZ921.29** | 17 | PlantHT | 206485313 | 0.89546775 | PetAngle | 206485313 | 0.19791451 |
| **LAZ921.32** | 17 | PlantHT | 206485496 | 0.15878406 | PetAngle | 206485496 | 0.41223693 |
| **LAZ921.33** | 17 | PlantHT | 206485873 | 0.53026034 | PetAngle | 206485873 | 0.23805197 |
| **LAZ921.34** | 17 | PlantHT | 206485928 | 0.62662849 | PetAngle | 206485928 | 0.63931084 |
| **LAZ921.35** | 17 | PlantHT | 206485936 | 0.62662849 | PetAngle | 206485936 | 0.63931084 |
| **LAZ921.36** | 17 | PlantHT | 206486107 | 0.45462822 | PetAngle | 206486107 | 0.74028987 |
| **LAZ921.37** | 17 | PlantHT | 206486155 | 0.18601554 | PetAngle | 206486155 | 0.30713589 |
| **LAZ921.38** | 17 | PlantHT | 206486181 | 0.15092423 | PetAngle | 206486181 | 0.02171196 |
| **LAZ921.40** | 17 | PlantHT | 206486230 | 0.16346572 | PetAngle | 206486230 | 0.06433483 |
| **LAZ921.41** | 17 | PlantHT | 206486337 | 0.10587381 | PetAngle | 206486337 | 0.42603267 |
| **LAZ921.42** | 17 | PlantHT | 206486407 | 0.2338848 | PetAngle | 206486407 | 0.05689468 |
| **LAZ921.43** | 17 | PlantHT | 206486412 | 0.53544597 | PetAngle | 206486412 | 0.16601449 |
| **LAZ921.44** | 17 | PlantHT | 206486453 | 0.02910938 | PetAngle | 206486453 | 0.00826126 |
| **LAZ921.5** | 17 | PlantHT | 206481620 | 0.42718912 | PetAngle | 206481620 | 0.00653789 |
| **LAZ921.7** | 17 | PlantHT | 206482328 | 0.17280357 | PetAngle | 206482328 | 0.25646305 |
| **LAZ921.8** | 17 | PlantHT | 206482347 | 0.47518374 | PetAngle | 206482347 | 0.09193345 |

**Supplementary Table A 22:** Summary of GLM results for data of the small association panel (64 genotypes) in Spain 2019, limit value p = 0.000164

| MARKER | CHR | TRAIT | POS | P | TRAIT | POS | P |
|---|---|---|---|---|---|---|---|
| **GID871.10** | 1 | PlantHT | 12852858 | 0.01761388 | PetAngle | 12852858 | 0.92332411 |
| **GID871.11** | 1 | PlantHT | 12853069 | 0.08349147 | PetAngle | 12853069 | 0.80636601 |
| **GID871.12** | 1 | PlantHT | 12853100 | 0.70791348 | PetAngle | 12853100 | 0.70380398 |
| **GID871.13** | 1 | PlantHT | 12853241 | 0.96622384 | PetAngle | 12853241 | 0.43369184 |
| **GID871.14** | 1 | PlantHT | 12853328 | 0.29137191 | PetAngle | 12853328 | 0.98695363 |
| **GID871.15** | 1 | PlantHT | 12853334 | 0.29137191 | PetAngle | 12853334 | 0.98695363 |
| **GID871.16** | 1 | PlantHT | 12853430 | 0.60216562 | PetAngle | 12853430 | 0.45010145 |
| **GID871.17** | 1 | PlantHT | 12853511 | 0.03717723 | PetAngle | 12853511 | 0.97056512 |
| **GID871.21** | 1 | PlantHT | 12853600 | 0.80612013 | PetAngle | 12853600 | 0.8803155 |
| **GID871.22** | 1 | PlantHT | 12853709 | 0.66892063 | PetAngle | 12853709 | 0.1305817 |
| **GID871.23** | 1 | PlantHT | 12853714 | 0.0770077 | PetAngle | 12853714 | 0.673644 |
| **GID871.5** | 1 | PlantHT | 12851807 | 0.95179492 | PetAngle | 12851807 | 0.87619796 |
| **GID871.6** | 1 | PlantHT | 12852614 | 0.87903355 | PetAngle | 12852614 | 0.59680442 |
| **GID871.7** | 1 | PlantHT | 12852731 | 0.65359096 | PetAngle | 12852731 | 0.85753145 |
| **GID871.9** | 1 | PlantHT | 12852833 | 0.01912815 | PetAngle | 12852833 | 0.91202205 |
| **SLY061.11** | 2 | PlantHT | 39415029 | 0.02578113 | PetAngle | 39415029 | 0.43044363 |
| **SLY061.14** | 2 | PlantHT | 39415287 | 0.00490572 | PetAngle | 39415287 | 0.66420292 |
| **SLY061.15** | 2 | PlantHT | 39415439 | 0.00435021 | PetAngle | 39415439 | 0.75085018 |
| **SLY061.16** | 2 | PlantHT | 39415448 | 0.00435021 | PetAngle | 39415448 | 0.75085018 |
| **SLY061.17** | 2 | PlantHT | 39415600 | 0.57602596 | PetAngle | 39415600 | 0.28259251 |
| **SLY061.19** | 2 | PlantHT | 39415765 | 0.627338 | PetAngle | 39415765 | 0.31172932 |
| **SLY061.20** | 2 | PlantHT | 39415978 | 0.57602596 | PetAngle | 39415978 | 0.28259251 |
| **SLY061.21** | 2 | PlantHT | 39416235 | 0.42480547 | PetAngle | 39416235 | 0.20686741 |
| **SLY061.22** | 2 | PlantHT | 39416259 | 0.24827165 | PetAngle | 39416259 | 0.41812413 |
| **SLY061.3** | 2 | PlantHT | 39413612 | 0.00747225 | PetAngle | 39413612 | 0.92696217 |
| **SLY061.4** | 2 | PlantHT | 39413618 | 0.00747225 | PetAngle | 39413618 | 0.92696217 |
| **SLY061.5** | 2 | PlantHT | 39413737 | 0.0020608 | PetAngle | 39413737 | 0.9260428 |
| **SLY061.6** | 2 | PlantHT | 39413802 | 0.00455093 | PetAngle | 39413802 | 0.94012119 |
| **SLY061.7** | 2 | PlantHT | 39414098 | 0.27166836 | PetAngle | 39414098 | 0.51722863 |
| **SNE171.1** | 3 | PlantHT | 104932867 | 0.1931208 | PetAngle | 104932867 | 0.89415805 |
| **SNE171.5** | 3 | PlantHT | 104934540 | 0.04704704 | PetAngle | 104934540 | 0.09203303 |
| **SNE171.6** | 3 | PlantHT | 104934736 | 0.04704704 | PetAngle | 104934736 | 0.09203303 |
| **SNE171.7** | 3 | PlantHT | 104934791 | 0.84120893 | PetAngle | 104934791 | 0.02960996 |
| **SNE171.8** | 3 | PlantHT | 104934943 | 0.30360499 | PetAngle | 104934943 | 0.27210273 |
| **SLY321.1** | 4 | PlantHT | 40919975 | 0.18268861 | PetAngle | 40919975 | 0.17220618 |
| **SLY321.2** | 4 | PlantHT | 40920036 | 0.01336122 | PetAngle | 40920036 | 0.05543479 |
| **SLY321.3** | 4 | PlantHT | 40920185 | 0.94078484 | PetAngle | 40920185 | 0.84309839 |
| **SLY321.6** | 4 | PlantHT | 40920969 | 0.11080198 | PetAngle | 40920969 | 0.04818942 |
| **SLY321.8** | 4 | PlantHT | 40921919 | 0.2361946 | PetAngle | 40921919 | 0.39934261 |
| **SLY351.11** | 4 | PlantHT | 41289089 | 0.03962598 | PetAngle | 41289089 | 0.27949484 |
| **SLY351.2** | 4 | PlantHT | 41287638 | 0.02704779 | PetAngle | 41287638 | 0.28905835 |
| **SLY351.4** | 4 | PlantHT | 41287804 | 0.1335456 | PetAngle | 41287804 | 0.22734995 |
| **SLY351.6** | 4 | PlantHT | 41288086 | 0.03224284 | PetAngle | 41288086 | 0.25211501 |
| **SLY351.7** | 4 | PlantHT | 41288167 | 0.73683021 | PetAngle | 41288167 | 0.56656509 |
| **SLY351.8** | 4 | PlantHT | 41288598 | 0.03224284 | PetAngle | 41288598 | 0.25211501 |

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|---|---|---|---|---|---|---|---|
| **SLY351.9** | 4 | PlantHT | 41288616 | 0.03224284 | PetAngle | 41288616 | 0.25211501 |
| **TAC361.1** | 4 | PlantHT | 155517271 | 0.22091961 | PetAngle | 155517271 | 0.21888242 |
| **TAC361.10** | 4 | PlantHT | 155518227 | 0.00235035 | PetAngle | 155518227 | 0.01527368 |
| **TAC361.13** | 4 | PlantHT | 155519213 | 0.17178228 | PetAngle | 155519213 | 0.18561288 |
| **TAC361.14** | 4 | PlantHT | 155519529 | 0.72608272 | PetAngle | 155519529 | 0.71423275 |
| **TAC361.16** | 4 | PlantHT | 155519787 | 0.11775647 | PetAngle | 155519787 | 0.07555734 |
| **TAC361.17** | 4 | PlantHT | 155519800 | 0.55054042 | PetAngle | 155519800 | 0.47116573 |
| **TAC361.18** | 4 | PlantHT | 155520038 | 0.0891342 | PetAngle | 155520038 | 0.06283969 |
| **TAC361.19** | 4 | PlantHT | 155520121 | 0.00236966 | PetAngle | 155520121 | 0.17747784 |
| **TAC361.2** | 4 | PlantHT | 155517418 | 9.8237E-04 | PetAngle | 155517418 | 0.1255101 |
| **TAC361.20** | 4 | PlantHT | 155520230 | 0.13397845 | PetAngle | 155520230 | 0.04398148 |
| **TAC361.21** | 4 | PlantHT | 155520277 | 0.03912484 | PetAngle | 155520277 | 0.60125773 |
| **TAC361.22** | 4 | PlantHT | 155520338 | 0.0012812 | PetAngle | 155520338 | 0.22336252 |
| **TAC361.23** | 4 | PlantHT | 155520558 | 0.68753985 | PetAngle | 155520558 | 0.42601473 |
| **TAC361.3** | 4 | PlantHT | 155517438 | 0.11381316 | PetAngle | 155517438 | 0.60572976 |
| **TAC361.4** | 4 | PlantHT | 155517453 | 9.8237E-04 | PetAngle | 155517453 | 0.1255101 |
| **TAC361.5** | 4 | PlantHT | 155517553 | 0.15460184 | PetAngle | 155517553 | 0.67035883 |
| **TAC361.6** | 4 | PlantHT | 155517627 | 0.09187465 | PetAngle | 155517627 | 0.46010376 |
| **TAC361.9** | 4 | PlantHT | 155518008 | 0.0834622 | PetAngle | 155518008 | 0.01997709 |
| **SLY141.1** | 5 | PlantHT | 163484536 | 0.28942058 | PetAngle | 163484536 | 0.16848964 |
| **SLY141.10** | 5 | PlantHT | 163485423 | 0.70621139 | PetAngle | 163485423 | 0.72584783 |
| **SLY141.11** | 5 | PlantHT | 163485618 | 0.47001183 | PetAngle | 163485618 | 0.02876683 |
| **SLY141.12** | 5 | PlantHT | 163485624 | 0.47001183 | PetAngle | 163485624 | 0.02876683 |
| **SLY141.13** | 5 | PlantHT | 163486432 | 0.44195097 | PetAngle | 163486432 | 0.54296907 |
| **SLY141.14** | 5 | PlantHT | 163486451 | 0.36320505 | PetAngle | 163486451 | 0.97090191 |
| **SLY141.15** | 5 | PlantHT | 163486868 | 0.39919401 | PetAngle | 163486868 | 0.37201215 |
| **SLY141.2** | 5 | PlantHT | 163484898 | 0.75687318 | PetAngle | 163484898 | 0.95848512 |
| **SLY141.3** | 5 | PlantHT | 163484956 | 0.17003217 | PetAngle | 163484956 | 0.93389088 |
| **SLY141.4** | 5 | PlantHT | 163484969 | 0.11421679 | PetAngle | 163484969 | 0.41880535 |
| **SLY141.5** | 5 | PlantHT | 163485239 | 0.07505825 | PetAngle | 163485239 | 0.25365556 |
| **SLY141.6** | 5 | PlantHT | 163485248 | 0.17381768 | PetAngle | 163485248 | 0.07265743 |
| **SLY141.7** | 5 | PlantHT | 163485257 | 0.70075442 | PetAngle | 163485257 | 0.7099762 |
| **SLY141.8** | 5 | PlantHT | 163485366 | 0.19159015 | PetAngle | 163485366 | 0.24857837 |
| **GID741.2** | 6 | PlantHT | 43970283 | 0.75635718 | PetAngle | 43970283 | 0.81330826 |
| **GID741.3** | 6 | PlantHT | 43970298 | 0.28528966 | PetAngle | 43970298 | 0.98211536 |
| **GID741.4** | 6 | PlantHT | 43970589 | 0.45039714 | PetAngle | 43970589 | 0.64423568 |
| **GID741.5** | 6 | PlantHT | 43971149 | 0.60999508 | PetAngle | 43971149 | 0.08187425 |
| **DEL091.10** | 8 | PlantHT | 12264206 | 0.02971707 | PetAngle | 12264206 | 0.09604259 |
| **DEL091.12** | 8 | PlantHT | 12264269 | 0.95839178 | PetAngle | 12264269 | 0.47546271 |
| **DEL091.13** | 8 | PlantHT | 12264332 | 0.44698071 | PetAngle | 12264332 | 0.0207334 |
| **DEL091.14** | 8 | PlantHT | 12264404 | 0.76413166 | PetAngle | 12264404 | 0.20755918 |
| **DEL091.15** | 8 | PlantHT | 12264512 | 0.22874768 | PetAngle | 12264512 | 0.01764449 |
| **DEL091.16** | 8 | PlantHT | 12264599 | 0.8382803 | PetAngle | 12264599 | 0.91758762 |
| **DEL091.17** | 8 | PlantHT | 12264604 | 0.47832314 | PetAngle | 12264604 | 0.01608967 |
| **DEL091.18** | 8 | PlantHT | 12264635 | 0.09050116 | PetAngle | 12264635 | 0.00049676 |
| **DEL091.20** | 8 | PlantHT | 12264789 | 0.47502536 | PetAngle | 12264789 | 0.38557557 |
| **DEL091.21** | 8 | PlantHT | 12264795 | 0.62099386 | PetAngle | 12264795 | 0.2759563 |
| **DEL091.22** | 8 | PlantHT | 12264962 | 0.05758911 | PetAngle | 12264962 | 0.4333442 |
| **DEL091.24** | 8 | PlantHT | 12265025 | 0.47316571 | PetAngle | 12265025 | 0.00601819 |

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|---|---|---|---|---|---|---|---|
| **DEL091.25** | 8 | PlantHT | 12265054 | 0.11048238 | PetAngle | 12265054 | 0.00089348 |
| **DEL091.26** | 8 | PlantHT | 12265056 | 0.1904363 | PetAngle | 12265056 | 0.19432591 |
| **DEL091.27** | 8 | PlantHT | 12265422 | 0.29655531 | PetAngle | 12265422 | 0.0015879 |
| **DEL091.29** | 8 | PlantHT | 12265567 | 0.43503659 | PetAngle | 12265567 | 0.03597915 |
| **DEL091.3** | 8 | PlantHT | 12263870 | 0.46512781 | PetAngle | 12263870 | 0.19169619 |
| **DEL091.30** | 8 | PlantHT | 12265676 | 0.00482199 | PetAngle | 12265676 | 4.7469E-05 |
| **DEL091.31** | 8 | PlantHT | 12265683 | 0.03357294 | PetAngle | 12265683 | 0.00024148 |
| **DEL091.32** | 8 | PlantHT | 12265802 | 0.06061257 | PetAngle | 12265802 | 0.0003414 |
| **DEL091.33** | 8 | PlantHT | 12266012 | 0.14018666 | PetAngle | 12266012 | 8.8209E-05 |
| **DEL091.34** | 8 | PlantHT | 12266161 | 0.39912357 | PetAngle | 12266161 | 0.2659271 |
| **DEL091.35** | 8 | PlantHT | 12266179 | 0.73562777 | PetAngle | 12266179 | 0.03878646 |
| **DEL091.36** | 8 | PlantHT | 12266186 | 0.69755337 | PetAngle | 12266186 | 0.06260088 |
| **DEL091.37** | 8 | PlantHT | 12266199 | 0.56266207 | PetAngle | 12266199 | 0.05458392 |
| **DEL091.38** | 8 | PlantHT | 12266211 | 0.14093038 | PetAngle | 12266211 | 0.39167685 |
| **DEL091.4** | 8 | PlantHT | 12263903 | 0.29843071 | PetAngle | 12263903 | 0.04182172 |
| **DEL091.41** | 8 | PlantHT | 12266403 | 0.35496678 | PetAngle | 12266403 | 0.38771802 |
| **DEL091.42** | 8 | PlantHT | 12266417 | 0.81942882 | PetAngle | 12266417 | 0.03750327 |
| **DEL091.43** | 8 | PlantHT | 12266464 | 0.57071951 | PetAngle | 12266464 | 0.00912608 |
| **DEL091.47** | 8 | PlantHT | 12266830 | 0.1268415 | PetAngle | 12266830 | 0.00370378 |
| **DEL091.48** | 8 | PlantHT | 12266863 | 0.13974763 | PetAngle | 12266863 | 0.01101581 |
| **DEL091.49** | 8 | PlantHT | 12266939 | 0.28052125 | PetAngle | 12266939 | 0.24680583 |
| **DEL091.5** | 8 | PlantHT | 12263912 | 0.51223906 | PetAngle | 12263912 | 0.03961412 |
| **DEL091.50** | 8 | PlantHT | 12267167 | 0.09742253 | PetAngle | 12267167 | 0.4595894 |
| **DEL091.52** | 8 | PlantHT | 12267267 | 0.09742253 | PetAngle | 12267267 | 0.4595894 |
| **DEL091.6** | 8 | PlantHT | 12264043 | 0.31948539 | PetAngle | 12264043 | 0.82919749 |
| **DEL091.7** | 8 | PlantHT | 12264064 | 0.20337895 | PetAngle | 12264064 | 0.00055517 |
| **DEL091.8** | 8 | PlantHT | 12264103 | 0.07985557 | PetAngle | 12264103 | 0.16485378 |
| **DEL091.9** | 8 | PlantHT | 12264128 | 0.34045448 | PetAngle | 12264128 | 0.13778764 |
| **LAZ951.1** | 8 | PlantHT | 7807354 | 0.7757358 | PetAngle | 7807354 | 0.86998862 |
| **LAZ951.10** | 8 | PlantHT | 7809246 | 0.38739229 | PetAngle | 7809246 | 0.55883232 |
| **LAZ951.11** | 8 | PlantHT | 7809319 | 0.70695969 | PetAngle | 7809319 | 0.46444529 |
| **LAZ951.12** | 8 | PlantHT | 7809351 | 0.81998782 | PetAngle | 7809351 | 0.33709625 |
| **LAZ951.13** | 8 | PlantHT | 7809384 | 0.36395232 | PetAngle | 7809384 | 0.24526112 |
| **LAZ951.14** | 8 | PlantHT | 7809516 | 0.04532829 | PetAngle | 7809516 | 0.0085296 |
| **LAZ951.15** | 8 | PlantHT | 7809577 | 0.75846505 | PetAngle | 7809577 | 0.36076586 |
| **LAZ951.16** | 8 | PlantHT | 7809616 | 0.88040255 | PetAngle | 7809616 | 0.8972524 |
| **LAZ951.17** | 8 | PlantHT | 7809770 | 0.40114628 | PetAngle | 7809770 | 0.26051085 |
| **LAZ951.18** | 8 | PlantHT | 7810149 | 0.90957467 | PetAngle | 7810149 | 0.59791447 |
| **LAZ951.2** | 8 | PlantHT | 7807376 | 0.27700769 | PetAngle | 7807376 | 0.18693786 |
| **LAZ951.20** | 8 | PlantHT | 7810266 | 0.39903447 | PetAngle | 7810266 | 0.07547333 |
| **LAZ951.21** | 8 | PlantHT | 7810443 | 0.06371246 | PetAngle | 7810443 | 0.62213304 |
| **LAZ951.23** | 8 | PlantHT | 7810829 | 0.90585406 | PetAngle | 7810829 | 0.22771633 |
| **LAZ951.24** | 8 | PlantHT | 7810961 | 0.42689043 | PetAngle | 7810961 | 0.4465096 |
| **LAZ951.26** | 8 | PlantHT | 7811459 | 0.38464887 | PetAngle | 7811459 | 0.41083664 |
| **LAZ951.27** | 8 | PlantHT | 7811479 | 0.45154928 | PetAngle | 7811479 | 0.17346055 |
| **LAZ951.28** | 8 | PlantHT | 7811553 | 0.90224602 | PetAngle | 7811553 | 0.25276094 |
| **LAZ951.29** | 8 | PlantHT | 7812053 | 0.00624072 | PetAngle | 7812053 | 0.78801932 |
| **LAZ951.3** | 8 | PlantHT | 7807503 | 0.40381397 | PetAngle | 7807503 | 0.2904732 |
| **LAZ951.4** | 8 | PlantHT | 7807600 | 0.6318014 | PetAngle | 7807600 | 0.99761753 |

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| **LAZ951.5** | 8 | PlantHT | 7807614 | 0.67621014 | PetAngle | 7807614 | 0.89677875 |
| **LAZ951.6** | 8 | PlantHT | 7807682 | 0.91745834 | PetAngle | 7807682 | 0.44296925 |
| **LAZ951.7** | 8 | PlantHT | 7809093 | 0.13440128 | PetAngle | 7809093 | 0.02872582 |
| **LAZ951.8** | 8 | PlantHT | 7809138 | 0.48691237 | PetAngle | 7809138 | 0.09168937 |
| **LAZ951.9** | 8 | PlantHT | 7809176 | 0.05897365 | PetAngle | 7809176 | 0.03106511 |
| **SLY301.1** | 9 | PlantHT | 178666111 | 0.29833305 | PetAngle | 178666111 | 0.61102 |
| **SLY301.2** | 9 | PlantHT | 178666159 | 0.38941512 | PetAngle | 178666159 | 0.91002398 |
| **SLY301.3** | 9 | PlantHT | 178666187 | 0.42429079 | PetAngle | 178666187 | 0.59032689 |
| **SLY301.4** | 9 | PlantHT | 178666431 | 0.63537363 | PetAngle | 178666431 | 0.96233036 |
| **SLY301.5** | 9 | PlantHT | 178666702 | 0.53306834 | PetAngle | 178666702 | 0.50753708 |
| **SLY301.7** | 9 | PlantHT | 178668175 | 0.0667033 | PetAngle | 178668175 | 0.43552837 |
| **DEL171.2** | 10 | PlantHT | 34968719 | 0.10704567 | PetAngle | 34968719 | 0.92385563 |
| **GID071.1** | 10 | PlantHT | 28111762 | 0.76613113 | PetAngle | 28111762 | 0.07234096 |
| **GID071.13** | 10 | PlantHT | 28112319 | 0.90407901 | PetAngle | 28112319 | 0.1827818 |
| **GID071.14** | 10 | PlantHT | 28112493 | 0.10242095 | PetAngle | 28112493 | 0.01138262 |
| **GID071.15** | 10 | PlantHT | 28112634 | 0.23423199 | PetAngle | 28112634 | 0.03133856 |
| **GID071.16** | 10 | PlantHT | 28112657 | 0.62056804 | PetAngle | 28112657 | 0.00034806 |
| **GID071.17** | 10 | PlantHT | 28112679 | 0.10242095 | PetAngle | 28112679 | 0.01138262 |
| **GID071.18** | 10 | PlantHT | 28112826 | 0.79200743 | PetAngle | 28112826 | 0.6804382 |
| **GID071.19** | 10 | PlantHT | 28112847 | 0.78521814 | PetAngle | 28112847 | 0.98020312 |
| **GID071.20** | 10 | PlantHT | 28112916 | 0.11518378 | PetAngle | 28112916 | 0.01312889 |
| **GID071.21** | 10 | PlantHT | 28112919 | 0.40881299 | PetAngle | 28112919 | 0.22384753 |
| **GID071.22** | 10 | PlantHT | 28113024 | 0.63076719 | PetAngle | 28113024 | 0.00415043 |
| **GID071.23** | 10 | PlantHT | 28113051 | 0.18383872 | PetAngle | 28113051 | 0.00109353 |
| **GID071.24** | 10 | PlantHT | 28113168 | 0.83235894 | PetAngle | 28113168 | 0.00290374 |
| **GID071.26** | 10 | PlantHT | 28113769 | 0.86630282 | PetAngle | 28113769 | 0.59776721 |
| **GID071.28** | 10 | PlantHT | 28113897 | 0.98736463 | PetAngle | 28113897 | 0.09783844 |
| **GID071.29** | 10 | PlantHT | 28113914 | 0.67019439 | PetAngle | 28113914 | 0.48931976 |
| **GID071.30** | 10 | PlantHT | 28114325 | 0.65151715 | PetAngle | 28114325 | 0.25528322 |
| **GID071.34** | 10 | PlantHT | 28114759 | 0.14299123 | PetAngle | 28114759 | 0.00596015 |
| **GID071.36** | 10 | PlantHT | 28114977 | 0.18383872 | PetAngle | 28114977 | 0.00109353 |
| **GID071.38** | 10 | PlantHT | 28115179 | 0.59459836 | PetAngle | 28115179 | 0.01068239 |
| **GID071.39** | 10 | PlantHT | 28115187 | 0.10483596 | PetAngle | 28115187 | 0.01141494 |
| **GID071.4** | 10 | PlantHT | 28111944 | 0.01734867 | PetAngle | 28111944 | 0.15132973 |
| **GID071.42** | 10 | PlantHT | 28116112 | 0.76595788 | PetAngle | 28116112 | 0.29076572 |
| **GID071.5** | 10 | PlantHT | 28111956 | 0.02202886 | PetAngle | 28111956 | 0.15758261 |
| **GID071.7** | 10 | PlantHT | 28111995 | 0.11938092 | PetAngle | 28111995 | 0.39684415 |
| **SLY611.1** | 11 | PlantHT | 138990416 | 0.14613889 | PetAngle | 138990416 | 0.79553387 |
| **SLY611.10** | 11 | PlantHT | 138993192 | 0.76830382 | PetAngle | 138993192 | 0.6224186 |
| **SLY611.11** | 11 | PlantHT | 138993311 | 0.89814019 | PetAngle | 138993311 | 0.6612026 |
| **SLY611.2** | 11 | PlantHT | 138990539 | 0.30003444 | PetAngle | 138990539 | 0.90848288 |
| **SLY611.3** | 11 | PlantHT | 138990639 | 0.84961397 | PetAngle | 138990639 | 0.55344646 |
| **SLY611.4** | 11 | PlantHT | 138990798 | 0.84961397 | PetAngle | 138990798 | 0.55344646 |
| **SLY611.5** | 11 | PlantHT | 138991001 | 0.42175326 | PetAngle | 138991001 | 0.27101447 |
| **SLY611.8** | 11 | PlantHT | 138992806 | 0.60228974 | PetAngle | 138992806 | 0.19757767 |
| **SLY611.9** | 11 | PlantHT | 138993071 | 0.20354199 | PetAngle | 138993071 | 0.27895951 |
| **DEL901.1** | 12 | PlantHT | 32211683 | 0.13103164 | PetAngle | 32211683 | 0.22087092 |
| **DEL901.10** | 12 | PlantHT | 32213076 | 0.13103164 | PetAngle | 32213076 | 0.22087092 |
| **DEL901.11** | 12 | PlantHT | 32213328 | 0.24514379 | PetAngle | 32213328 | 0.33321251 |

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| **DEL901.12** | 12 | PlantHT | 32213465 | 0.47015338 | PetAngle | 32213465 | 0.96317465 |
| **DEL901.2** | 12 | PlantHT | 32211812 | 0.13103164 | PetAngle | 32211812 | 0.22087092 |
| **DEL901.3** | 12 | PlantHT | 32211968 | 0.10684436 | PetAngle | 32211968 | 0.35226057 |
| **DEL901.4** | 12 | PlantHT | 32212028 | 0.10684436 | PetAngle | 32212028 | 0.35226057 |
| **DEL901.5** | 12 | PlantHT | 32212178 | 0.29737836 | PetAngle | 32212178 | 0.47215027 |
| **DEL901.6** | 12 | PlantHT | 32212556 | 0.63470919 | PetAngle | 32212556 | 0.22389546 |
| **DEL901.7** | 12 | PlantHT | 32212608 | 0.2346464 | PetAngle | 32212608 | 0.44830928 |
| **DEL901.8** | 12 | PlantHT | 32212620 | 0.94078136 | PetAngle | 32212620 | 0.14915251 |
| **DEL901.9** | 12 | PlantHT | 32212719 | 0.13103164 | PetAngle | 32212719 | 0.22087092 |
| **SNE981.1** | 12 | PlantHT | 81945604 | 0.55838999 | PetAngle | 81945604 | 0.93257548 |
| **SNE981.11** | 12 | PlantHT | 81947454 | 0.57513865 | PetAngle | 81947454 | 0.76204516 |
| **SNE981.12** | 12 | PlantHT | 81947533 | 0.61641994 | PetAngle | 81947533 | 0.97307041 |
| **SNE981.13** | 12 | PlantHT | 81947575 | 0.61641994 | PetAngle | 81947575 | 0.97307041 |
| **SNE981.14** | 12 | PlantHT | 81948022 | 0.86645867 | PetAngle | 81948022 | 0.8118047 |
| **SNE981.2** | 12 | PlantHT | 81945790 | 0.96675182 | PetAngle | 81945790 | 0.49692148 |
| **SNE981.5** | 12 | PlantHT | 81946423 | 0.61641994 | PetAngle | 81946423 | 0.97307041 |
| **SNE981.6** | 12 | PlantHT | 81946530 | 0.61641994 | PetAngle | 81946530 | 0.97307041 |
| **SNE981.8** | 12 | PlantHT | 81947032 | 0.55838999 | PetAngle | 81947032 | 0.93257548 |
| **SNE981.9** | 12 | PlantHT | 81947042 | 0.55838999 | PetAngle | 81947042 | 0.93257548 |
| **GID131.1** | 14 | PlantHT | 127160607 | 0.9077193 | PetAngle | 127160607 | 0.74148484 |
| **GID131.10** | 14 | PlantHT | 127161183 | 0.90851634 | PetAngle | 127161183 | 0.24701161 |
| **GID131.13** | 14 | PlantHT | 127161687 | 0.11809665 | PetAngle | 127161687 | 0.29122276 |
| **GID131.14** | 14 | PlantHT | 127161715 | 0.64660508 | PetAngle | 127161715 | 0.8687592 |
| **GID131.15** | 14 | PlantHT | 127162040 | 0.28290659 | PetAngle | 127162040 | 0.80560251 |
| **GID131.18** | 14 | PlantHT | 127162519 | 0.05612489 | PetAngle | 127162519 | 0.16217459 |
| **GID131.19** | 14 | PlantHT | 127162646 | 0.5919829 | PetAngle | 127162646 | 0.98864557 |
| **GID131.2** | 14 | PlantHT | 127160680 | 0.26529292 | PetAngle | 127160680 | 0.17096811 |
| **GID131.20** | 14 | PlantHT | 127162694 | 0.62931037 | PetAngle | 127162694 | 0.63435071 |
| **GID131.21** | 14 | PlantHT | 127162874 | 0.18966416 | PetAngle | 127162874 | 0.4089782 |
| **GID131.22** | 14 | PlantHT | 127162881 | 0.07062334 | PetAngle | 127162881 | 0.4443238 |
| **GID131.24** | 14 | PlantHT | 127163001 | 0.37262599 | PetAngle | 127163001 | 0.3430893 |
| **GID131.25** | 14 | PlantHT | 127163141 | 0.2293808 | PetAngle | 127163141 | 0.97609762 |
| **GID131.27** | 14 | PlantHT | 127163432 | 0.00282727 | PetAngle | 127163432 | 0.86924567 |
| **GID131.28** | 14 | PlantHT | 127163504 | 0.04560569 | PetAngle | 127163504 | 0.1559806 |
| **GID131.29** | 14 | PlantHT | 127163681 | 0.92444266 | PetAngle | 127163681 | 0.8619616 |
| **GID131.3** | 14 | PlantHT | 127160706 | 0.13867369 | PetAngle | 127160706 | 0.11358607 |
| **GID131.30** | 14 | PlantHT | 127163764 | 0.87674294 | PetAngle | 127163764 | 0.06178586 |
| **GID131.31** | 14 | PlantHT | 127163847 | 0.02422306 | PetAngle | 127163847 | 0.92922818 |
| **GID131.32** | 14 | PlantHT | 127163939 | 0.04560569 | PetAngle | 127163939 | 0.1559806 |
| **GID131.33** | 14 | PlantHT | 127164023 | 0.17330586 | PetAngle | 127164023 | 0.57054296 |
| **GID131.34** | 14 | PlantHT | 127164137 | 0.92444266 | PetAngle | 127164137 | 0.8619616 |
| **GID131.35** | 14 | PlantHT | 127164254 | 0.30568973 | PetAngle | 127164254 | 0.59111284 |
| **GID131.36** | 14 | PlantHT | 127164266 | 0.22668063 | PetAngle | 127164266 | 0.50015491 |
| **GID131.37** | 14 | PlantHT | 127164443 | 0.59464295 | PetAngle | 127164443 | 0.10958316 |
| **GID131.38** | 14 | PlantHT | 127164454 | 0.24596145 | PetAngle | 127164454 | 0.62982166 |
| **GID131.39** | 14 | PlantHT | 127164489 | 0.00872245 | PetAngle | 127164489 | 0.84894117 |
| **GID131.5** | 14 | PlantHT | 127160797 | 0.98405979 | PetAngle | 127160797 | 0.87829635 |
| **GID131.6** | 14 | PlantHT | 127160916 | 0.14536715 | PetAngle | 127160916 | 0.44776196 |
| **GID131.7** | 14 | PlantHT | 127160942 | 0.12790239 | PetAngle | 127160942 | 0.14828738 |

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| **GID131.9** | 14 | PlantHT | 127161170 | 0.09584585 | PetAngle | 127161170 | 0.10670768 |
| **TAC641.1** | 16 | PlantHT | 154345819 | 0.60449469 | PetAngle | 154345819 | 0.57674186 |
| **TAC641.4** | 16 | PlantHT | 154346996 | 0.1727489 | PetAngle | 154346996 | 0.23660467 |
| **TAC641.5** | 16 | PlantHT | 154347203 | 0.07900198 | PetAngle | 154347203 | 0.58735613 |
| **DEL801.10** | 17 | PlantHT | 194808854 | 0.10302829 | PetAngle | 194808854 | 0.59708156 |
| **DEL801.11** | 17 | PlantHT | 194808920 | 0.48520187 | PetAngle | 194808920 | 0.37661577 |
| **DEL801.12** | 17 | PlantHT | 194809025 | 0.00178779 | PetAngle | 194809025 | 0.82561307 |
| **DEL801.13** | 17 | PlantHT | 194809088 | 0.01562488 | PetAngle | 194809088 | 0.92882227 |
| **DEL801.14** | 17 | PlantHT | 194809186 | 0.14999466 | PetAngle | 194809186 | 0.08397212 |
| **DEL801.16** | 17 | PlantHT | 194809335 | 0.36427226 | PetAngle | 194809335 | 0.82141403 |
| **DEL801.17** | 17 | PlantHT | 194809363 | 0.38687052 | PetAngle | 194809363 | 0.16025807 |
| **DEL801.18** | 17 | PlantHT | 194809373 | 0.7065602 | PetAngle | 194809373 | 0.72968137 |
| **DEL801.19** | 17 | PlantHT | 194809815 | 0.2294995 | PetAngle | 194809815 | 0.14612707 |
| **DEL801.22** | 17 | PlantHT | 194810204 | 0.45804487 | PetAngle | 194810204 | 0.54607364 |
| **DEL801.23** | 17 | PlantHT | 194810236 | 0.92470125 | PetAngle | 194810236 | 0.4434751 |
| **DEL801.24** | 17 | PlantHT | 194810797 | 0.16767765 | PetAngle | 194810797 | 0.20580932 |
| **DEL801.25** | 17 | PlantHT | 194810815 | 0.0129753 | PetAngle | 194810815 | 0.72443738 |
| **DEL801.26** | 17 | PlantHT | 194810872 | 0.00379042 | PetAngle | 194810872 | 0.01126066 |
| **DEL801.27** | 17 | PlantHT | 194810919 | 0.26135219 | PetAngle | 194810919 | 0.8315776 |
| **DEL801.3** | 17 | PlantHT | 194808097 | 0.6197685 | PetAngle | 194808097 | 0.03581954 |
| **DEL801.31** | 17 | PlantHT | 194811667 | 0.97507381 | PetAngle | 194811667 | 0.52640534 |
| **DEL801.32** | 17 | PlantHT | 194811721 | 0.17086419 | PetAngle | 194811721 | 0.14463451 |
| **DEL801.4** | 17 | PlantHT | 194808128 | 0.59780811 | PetAngle | 194808128 | 0.08344362 |
| **DEL801.5** | 17 | PlantHT | 194808137 | 0.37729469 | PetAngle | 194808137 | 0.20441757 |
| **DEL801.6** | 17 | PlantHT | 194808477 | 0.23441498 | PetAngle | 194808477 | 0.01454879 |
| **DEL801.7** | 17 | PlantHT | 194808602 | 0.28517344 | PetAngle | 194808602 | 0.30434224 |
| **DEL801.8** | 17 | PlantHT | 194808652 | 0.2294995 | PetAngle | 194808652 | 0.14612707 |
| **DEL801.9** | 17 | PlantHT | 194808815 | 0.2294995 | PetAngle | 194808815 | 0.14612707 |
| **LAZ921.1** | 17 | PlantHT | 206481522 | 0.83650447 | PetAngle | 206481522 | 0.24331423 |
| **LAZ921.10** | 17 | PlantHT | 206482628 | 0.10069286 | PetAngle | 206482628 | 0.29436546 |
| **LAZ921.11** | 17 | PlantHT | 206482782 | 0.35815301 | PetAngle | 206482782 | 0.13213376 |
| **LAZ921.12** | 17 | PlantHT | 206482792 | NaN | PetAngle | 206482792 | NaN |
| **LAZ921.13** | 17 | PlantHT | 206483103 | 0.50538957 | PetAngle | 206483103 | 0.39192313 |
| **LAZ921.14** | 17 | PlantHT | 206483214 | 0.18470887 | PetAngle | 206483214 | 0.02173493 |
| **LAZ921.15** | 17 | PlantHT | 206483252 | 0.24733389 | PetAngle | 206483252 | 0.06751238 |
| **LAZ921.16** | 17 | PlantHT | 206483470 | 0.05363893 | PetAngle | 206483470 | 0.00212114 |
| **LAZ921.17** | 17 | PlantHT | 206483476 | 0.05363893 | PetAngle | 206483476 | 0.00212114 |
| **LAZ921.18** | 17 | PlantHT | 206483951 | 0.51102853 | PetAngle | 206483951 | 0.01141704 |
| **LAZ921.19** | 17 | PlantHT | 206483990 | 0.04673954 | PetAngle | 206483990 | 0.00202886 |
| **LAZ921.2** | 17 | PlantHT | 206481523 | 0.91748652 | PetAngle | 206481523 | 0.18915116 |
| **LAZ921.20** | 17 | PlantHT | 206484255 | 0.02591161 | PetAngle | 206484255 | 0.31494772 |
| **LAZ921.21** | 17 | PlantHT | 206484302 | 0.18999162 | PetAngle | 206484302 | 0.70165832 |
| **LAZ921.23** | 17 | PlantHT | 206484967 | 0.05326665 | PetAngle | 206484967 | 0.00447711 |
| **LAZ921.24** | 17 | PlantHT | 206484979 | 0.05326665 | PetAngle | 206484979 | 0.00447711 |
| **LAZ921.25** | 17 | PlantHT | 206485147 | 0.03693404 | PetAngle | 206485147 | 0.26372533 |
| **LAZ921.26** | 17 | PlantHT | 206485168 | 0.97753426 | PetAngle | 206485168 | 0.65605244 |
| **LAZ921.27** | 17 | PlantHT | 206485184 | 0.96895025 | PetAngle | 206485184 | 0.87348268 |
| **LAZ921.28** | 17 | PlantHT | 206485185 | 0.04249677 | PetAngle | 206485185 | 0.39723738 |
| **LAZ921.29** | 17 | PlantHT | 206485313 | 0.86571294 | PetAngle | 206485313 | 0.55357332 |

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| **LAZ921.32** | 17 | PlantHT | 206485496 | 0.40491515 | PetAngle | 206485496 | 0.18511466 |
| **LAZ921.33** | 17 | PlantHT | 206485873 | 0.25262059 | PetAngle | 206485873 | 0.40751037 |
| **LAZ921.34** | 17 | PlantHT | 206485928 | 0.87266907 | PetAngle | 206485928 | 0.48647272 |
| **LAZ921.35** | 17 | PlantHT | 206485936 | 0.87266907 | PetAngle | 206485936 | 0.48647272 |
| **LAZ921.36** | 17 | PlantHT | 206486107 | 0.76082057 | PetAngle | 206486107 | 0.17767208 |
| **LAZ921.37** | 17 | PlantHT | 206486155 | 0.42951277 | PetAngle | 206486155 | 0.03876465 |
| **LAZ921.38** | 17 | PlantHT | 206486181 | 0.23961883 | PetAngle | 206486181 | 0.07873505 |
| **LAZ921.40** | 17 | PlantHT | 206486230 | 0.36700985 | PetAngle | 206486230 | 0.10517396 |
| **LAZ921.41** | 17 | PlantHT | 206486337 | 0.18436375 | PetAngle | 206486337 | 0.63729235 |
| **LAZ921.42** | 17 | PlantHT | 206486407 | 0.138573 | PetAngle | 206486407 | 0.07923243 |
| **LAZ921.43** | 17 | PlantHT | 206486412 | 0.97060835 | PetAngle | 206486412 | 0.02333374 |
| **LAZ921.44** | 17 | PlantHT | 206486453 | 0.01355254 | PetAngle | 206486453 | 0.04826239 |
| **LAZ921.5** | 17 | PlantHT | 206481620 | 0.52791937 | PetAngle | 206481620 | 0.00788835 |
| **LAZ921.7** | 17 | PlantHT | 206482328 | 0.11611227 | PetAngle | 206482328 | 0.05523656 |
| **LAZ921.8** | 17 | PlantHT | 206482347 | 0.09877968 | PetAngle | 206482347 | 0.24914005 |

**Supplementary Table A 23:** Candidate gene approach. Coding sequence + 2000 bp Promotor 5'-region + 500 bp Terminator 3'-region; Based on database HanXRQ-SUNRISE (https://www.heliagene.org/HanXRQ-SUNRISE/) (Badouin *et al.,* 2017)

| **CHR** | **CHR START** | **CHR END** | **GENE ID** | **GENE NAME** | **CDS START** | **CDS STOP** | **TOTAL BP** |
|---|---|---|---|---|---|---|---|
| CHR12 | 32215504 | 32211009 | HanXRQChr12g0363901 | *HaDELLA1* | 32213504 | 32211509 | 4495 |
| CHR17 | 194811801 | 194807601 | HanXRQChr17g0566801 | *HaDELLA2* | 194809801 | 194808101 | 4200 |
| CHR10 | 34967327 | 34971536 | HanXRQChr10g0284171 | *HaDELLA-Like1* | 34969327 | 34971036 | 4209 |
| CHR08 | 12267402 | 12263384 | HanXRQChr08g0212091 | *HaDELLA-Like2* | 12265402 | 12263884 | 4018 |
| CHR11 | 91712764 | 91708644 | HanXRQChr11g0338161 | *HaGID1A* | 91710764 | 91709144 | 4120 |
| CHR10 | 28116166 | 28111759 | HanXRQChr10g0283071 | *HaGID1B* | 28114166 | 28112259 | 4407 |
| CHR14 | 127160237 | 127164950 | HanXRQChr14g0446131 | *HaGID1C* | 127162237 | 127164450 | 4713 |
| CHR01 | 12849455 | 12853987 | HanXRQChr01g0002871 | *HaGID1D* | 12851455 | 12853487 | 4532 |
| CHR15 | 43973958 | 43969522 | HanXRQChr06g0177741 | *HaGID1E* | 43971958 | 43970022 | 4436 |
| CHR09 | 178668212 | 178665182 | HanXRQChr09g0267301 | *HaSLY1A* | 178666212 | 178665682 | 3030 |
| CHR11 | 138994951 | 138990120 | HanXRQChr11g0345611 | *HaSLY1B* | 138992951 | 138990620 | 4831 |
| CHR02 | 39416418 | 39413322 | HanXRQChr02g0038061 | *HaSLY1C* | 39414418 | 39413822 | 3096 |
| CHR05 | 163487336 | 163484261 | HanXRQChr05g0150141 | *HaSLY1D* | 163485336 | 163484761 | 3075 |
| CHR04 | 40922618 | 40919540 | HanXRQChr04g0103321 | *HaSLY1E* | 40920618 | 40920040 | 3078 |
| CHR04 | 41289285 | 41286375 | HanXRQChr04g0103351 | *HaSLY1F* | 41287285 | 41286875 | 2910 |
| CHR14 | 164734200 | 164731230 | HanXRQChr14g0458611 | *HaSNE1* | 164732200 | 164731730 | 2970 |
| CHR03 | 104932518 | 104935518 | HanXRQChr03g0075171 | *HaSNE2* | 104934518 | 104935018 | 3000 |
| CHR12 | 81945420 | 81948438 | HanXRQChr12g0373981 | *HaSNE3* | 81947420 | 81947938 | 3018 |
| CHR08 | 7812485 | 7806890 | HanXRQChr08g0209951 | *HaLAZY1* | 7810485 | 7807390 | 5595 |
| CHR17 | 206481333 | 206486643 | HanXRQChr17g0568921 | *HaLAZY2* | 206483333 | 206486143 | 5310 |
| CHR04 | 155517240 | 155520805 | HanXRQChr04g0120361 | *HaTAC1* | 155519240 | 155520305 | 3565 |
| CHR16 | 154349482 | 154345270 | HanXRQChr16g0524641 | *HaTAC2* | 154347482 | 154345770 | 4212 |

**Supplementary Table A 24:** Transfer of the candidate gene approach to the new assembly of HanXRQ v. 2. Coding sequence + 2000 bp Promotor 5'-region + 500 bp Terminator 3'-region; Based on database HanXRQr2.0-SUNRISE (https://www.heliagene.org/HanXRQr2.0-SUNRISE/) (Badouin *et al.*, 2017)

| **CHR** | **CHR START** | **CHR END** | **GENE ID** | **GENE NAME** | **CDS START** | **CDS STOP** | **TOTAL BP** |
|---|---|---|---|---|---|---|---|
| CHR12 | 25040460 | 25045713 | HanXRQr2_Chr12g0533641 | *HaDELLA1* | 25042460 | 25045213 | 5253 |
| CHR17 | 179879137 | 179883943 | HanXRQr2_Chr17g0826681 | *HaDELLA2* | 179881137 | 179883443 | 4806 |
| CHR10 | 176608436 | 176612716 | HanXRQr2_Chr10g0463411 | *HaDELLA-Like1* | 176610436 | 176612216 | 4280 |
| CHR08 | 8141718 | 8146725 | HanXRQr2_Chr08g0322811 | *HaDELLA-Like2* | 8143718 | 8146225 | 5007 |
| CHR11 | 120071228 | 120066138 | HanXRQr2_Chr11g0497661 | *HaGID1A* | 120066638 | 120069228 | 5090 |
| CHR10 | 21064628 | 21070872 | HanXRQr2_Chr10g0424901 | *HaGID1B* | 21066628 | 21070372 | 6244 |
| CHR14 | 128248592 | 128243145 | HanXRQr2_Chr14g0648601 | *HaGID1C* | 128243645 | 128246592 | 5447 |
| CHR01 | 5788149 | 5783424 | HanXRQr2_Chr01g0002451 | *HaGID1D* | 5783924 | 5786149 | 4725 |
| CHR15 | 4604430 | 4599121 | HanXRQr2_Chr15g0674031 | *HaGID1E* | 4599621 | 4602430 | 5309 |
| CHR09 | 164517405 | 164514001 | HanXRQr2_Chr09g0404141 | *HaSLY1A* | 164514501 | 164515405 | 3404 |
| CHR11 | 11470004 | 11465090 | HanXRQr2_Chr11g0472751 | *HaSLY1B* | 11465590 | 11468004 | 4914 |
| CHR02 | 33564131 | 33560652 | HanXRQr2_Chr02g0054421 | *HaSLY1C* | 33561152 | 33562131 | 3479 |
| CHR05 | 133022138 | 133019063 | HanXRQr2_Chr05g0220701 | *HaSLY1D* | 133019563 | 133020138 | 3075 |
| CHR04 | 34412008 | 34415086 | HanXRQr2_Chr04g0151561 | *HaSLY1E* | 34414008 | 34414586 | 3078 |
| CHR04 | 34046317 | 34049484 | HanXRQr2_Chr04g0151511 | *HaSLY1F* | 34048317 | 34048984 | 3167 |
| CHR14 | 165685154 | 165688124 | HanXRQr2_Chr14g0665461 | *HaSNE1* | 165687154 | 165687624 | 2970 |
| CHR03 | 121235389 | 121232389 | HanXRQr2_Chr03g0113211 | *HaSNE2* | 121232889 | 121233389 | 3000 |
| CHR12 | 68795236 | 68792218 | HanXRQr2_Chr12g0546651 | *HaSNE3* | 68792718 | 68793236 | 3018 |
| CHR08 | 3519871 | 3513949 | HanXRQr2_Chr08g0320071 | *HaLAZY1* | 3514449 | 3517871 | 5922 |
| CHR17 | 188286159 | 188291866 | HanXRQr2_Chr17g0828911 | *HaLAZY2* | 188288159 | 188291366 | 5707 |
| CHR04 | 187091940 | 187087758 | HanXRQr2_Chr04g0181821 | *HaTAC1* | 187088258 | 187089940 | 4182 |
| CHR16 | 178071281 | 178066697 | HanXRQr2_Chr16g0767041 | *HaTAC2* | 178067197 | 178069281 | 4584 |

**Supplementary Table A 25:** Summary of HRM analyses of markers for the traits plant height and petiole angle in the combined association panel (n = 448) extended by 17 ornamental sunflower accessions

| COMMON NAME | SNE171.7 (T/C) | DE801.17 (T/C) | DEL091.8 (C/T) | DEL091.9 (A/C) |
|---|---|---|---|---|
| 3100402 | TT | CC | CC | AA |
| 3100404 | TC | TC | CT | AC |
| 371-3 S | TT | TT | CC | AA |
| 43-48 VK-32 | TT | TT | CC | AA |
| 6 SC UG L6 | TT | CC | TT | CC |
| ADVANCE | CC | TT | CC | AA |
| AFTAB-PARAST | TC | TT | CT | AC |
| AGUAPEI | CC | TC | CC | AA |
| AMES 101 | TT | TT | CC | AA |
| AMES 21671 | TT | TC | CC | AA |
| AMES 2350 | CC | CC | CT | AA |
| ARGE PEHUEN | TT | TC | CC | AA |
| ARMAVIREC | TT | CC | CC | AA |
| ARMAVIRSKY | TT | CC | CC | AA |
| AYCICEGI | TT | TC | CT | AC |
| B4268 | TT | TT | TT | NN |
| B-7422 | TT | TT | CC | AA |
| BEKECSI "B" | CC | TC | CT | AC |
| BLACK SAYAR | TC | CC | CT | AC |
| BR1 | TT | TT | CC | AA |
| BR2 | TT | TT | CC | AA |
| BR4 | TT | TC | CC | AA |
| CAKINSKIJ 268 | CC | CC | CC | AA |

| | | | | |
|---|---|---|---|---|
| CAKINSKIJ 269 | TT | CC | TT | CC |
| CAKINSKIJ 321 | TT | CC | CT | AC |
| CCA82-2 | CC | TC | CT | AC |
| CHANG LING | CC | TC | CC | AA |
| CINZA 42 | TT | TC | CT | AC |
| CLAIRSOL | TT | CC | CC | AA |
| CM101 | TT | CC | CC | AA |
| CM105 | CC | TC | CC | AA |
| CM112 | TT | CC | CC | AA |
| CM119 | CC | CC | CC | AA |
| CM122 | TT | TC | CC | AA |
| CM126 | TT | CC | TT | CC |
| CM28 | TT | CC | TT | CC |
| CM29 | TT | CC | TT | CC |
| CM31 | TT | CC | CC | AA |
| CM338 X CM469DMR | TT | TT | TT | CC |
| CM400 X CM469DMR | TT | CC | CT | AC |
| CM50 | TT | CC | CC | CC |
| CM53 | TT | CC | CC | AA |
| CM59 | TT | CC | CC | AA |
| CM85 | TC | TC | CT | AC |
| CM86 | TT | TC | CC | AA |
| CO-PB 68 | TT | TC | CC | AA |
| CORONA | TT | TT | CC | AA |
| CSEHSZLOVAKIAI "B" | TT | TC | CC | AA |
| D-75-4 | TT | CC | CC | AA |
| DAMAYA | TT | TC | TT | CC |
| DARK STRIPE | CC | TC | CT | AC |
| EGNAZIA | TT | CC | CC | AA |
| ENISEJ | TT | TC | CC | AA |
| FRANCIA "E" | TT | CC | CT | AC |
| FUKSINKA 10 | TT | CC | CC | AA |
| GEORGIA | CC | TT | CC | AA |
| GIGANT 549 | TT | CC | CC | AA |
| GIZA | TC | CC | CT | AC |
| GN 0778 | TT | TT | CC | AA |
| GONONDU | TT | TC | CC | AA |
| GUAYACAN INTA | TT | TT | CC | AA |
| HARKOVSKIJ 100 | TT | TC | TT | CC |
| HATZOR AYALA | TT | CC | CC | AA |
| HAVASUPAI | TC | CC | CC | AA |
| HEMAS | TT | CC | CT | AC |
| HIDATSA #2 | CC | TC | TT | CC |
| HOPI | TT | TC | TT | CC |
| HS 61 | TT | TT | CT | AC |
| IMPIRA INTA | CC | TT | TT | CC |
| JB 4 | TC | TC | CC | AA |
| JDANOVSKY6432 ND 31%OIL | TC | TC | CT | AC |
| JUPITER | TC | TC | CT | AC |
| KARLIK | TT | TC | TT | CC |
| KENYA WHITE | TT | CC | CC | AA |
| KORTUS | TT | TC | CC | AA |
| KOSIM | TT | TT | TT | CC |
| KRZYNOWLOSKI MIEJSCOWY | TT | CC | CC | AA |
| KVUGLIK A-41 | TT | CC | CC | AA |
| L-2625-1(UKRAINE)-1 | TT | CC | CC | AA |
| LIAO 2 | TT | CC | TT | CC |
| LOVASZPATONAI | TT | TC | TT | CC |
| LUCIOLE | TT | CC | CT | AC |
| MANDAN #1 | TC | CC | CC | AA |
| MANFREDI INTA (3-WAY X)11 | TC | CC | CT | AC |
| MENNONITE | TT | TC | CT | AC |

| | | | | |
|---|---|---|---|---|
| ND-NONOIL B3 | CC | TC | CC | AA |
| ND-NONOIL M2 | TT | TT | CC | AA |
| NO. 2770 | TC | TC | CT | AC |
| NO. 3332 | TT | TT | CT | AC |
| NO. 5 | TC | CC | CT | AC |
| NO. 9588 | TT | CC | CT | AC |
| NO. K1879 | TC | TC | CT | AC |
| NOVOSADSKI BR. 4 | CC | TC | CT | AC |
| NS-B-16-63/1 | TT | TT | CC | AA |
| ODESSKIJ 113 | CC | TC | CC | AA |
| OLEISTY BOROVSKIJ | TT | TT | TT | CC |
| PEREDOVIK | TT | TC | CT | AC |
| PERVENETS | TT | TC | CC | AA |
| PI 263178 | TT | TC | CT | AC |
| PI 500688 | TT | TC | CT | AC |
| PROGRESS | TT | CC | CC | AA |
| RECORD | TT | CC | CT | AC |
| RELAX HYBRID GERMPLASM | CC | TT | CC | AA |
| RF TUB-346 | TT | TT | CC | AA |
| ROMSUN N-2-2004 | TT | CC | CC | AA |
| SAE-005 | CC | TC | CC | AA |
| SALIUT | CC | CC | CT | AC |
| SANNACE | CC | TT | CT | AC |
| SATURN | TT | TT | CC | AA |
| SENECA | TC | CC | CT | AC |
| SEPASOL | TT | CC | TT | CC |
| SKOROSPELYI | TT | TT | CC | AA |
| SMENA | TT | CC | CT | AA |
| SMENA | TT | CC | CC | AC |
| SPUTNIK | TT | TC | CC | AA |
| START | TT | CC | CC | AA |
| STEPNYAK | CC | TC | TT | CC |
| SUNDAK | TT | TC | TT | CC |
| SUNRISE | TT | CC | CC | AA |
| SZARATOVSZKIJ RANNI | TT | TC | CC | AA |
| TCHERNIANKA SELECT W-17 | TT | TC | CC | AA |
| UGA-SAM1-001 | TT | TT | TT | CC |
| UGA-SAM1-002 | TT | TT | TT | CC |
| UGA-SAM1-003 | TT | TT | TT | CC |
| UGA-SAM1-004 | CC | TT | CC | AA |
| UGA-SAM1-005 | CC | CC | CC | AA |
| UGA-SAM1-006 | TT | CC | TT | CC |
| UGA-SAM1-007 | TT | CC | TT | CC |
| UGA-SAM1-008 | TT | CC | TT | CC |
| UGA-SAM1-009 | TT | CC | CC | AA |
| UGA-SAM1-011 | TT | TT | CC | AA |
| UGA-SAM1-013 | TT | CC | CC | AA |
| UGA-SAM1-014 | TT | TT | CC | AA |
| UGA-SAM1-015 | CC | CC | CC | AA |
| UGA-SAM1-016 | TT | CC | CC | AA |
| UGA-SAM1-017 | TT | TT | CC | AA |
| UGA-SAM1-018 | TT | TC | TT | CC |
| UGA-SAM1-019 | TT | CC | CC | AA |
| UGA-SAM1-020 | TT | CC | TT | CC |
| UGA-SAM1-021 | TT | TC | TT | CC |
| UGA-SAM1-022 | CC | CC | CC | AA |
| UGA-SAM1-023 | TT | TT | CC | AA |
| UGA-SAM1-025 | CC | TT | CC | AA |
| UGA-SAM1-026 | TT | TT | CC | AA |
| UGA-SAM1-027 | TT | CC | CC | AA |
| UGA-SAM1-028 | CC | TT | TT | CC |
| UGA-SAM1-029 | TT | CC | CC | AA |

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|---|---|---|---|---|
| UGA-SAM1-030 | TT | TT | CC | AA |
| UGA-SAM1-031 | TT | CC | CC | AA |
| UGA-SAM1-032 | TT | CC | CC | AA |
| UGA-SAM1-033 | CC | CC | CC | AA |
| UGA-SAM1-034 | TT | CC | TT | CC |
| UGA-SAM1-035 | TT | TT | CC | AA |
| UGA-SAM1-036 | TT | TT | CC | AA |
| UGA-SAM1-037 | TT | TC | CC | AA |
| UGA-SAM1-038 | TT | TT | CC | AA |
| UGA-SAM1-039 | CC | TT | CC | AA |
| UGA-SAM1-040 | CC | TT | CC | AA |
| UGA-SAM1-042 | TT | TT | CC | AA |
| UGA-SAM1-043 | TT | TT | CC | AA |
| UGA-SAM1-044 | TT | CC | TT | CC |
| UGA-SAM1-045 | TT | CC | TT | CC |
| UGA-SAM1-046 | TT | TC | CC | AA |
| UGA-SAM1-047 | TT | TT | CC | AA |
| UGA-SAM1-048 | TT | CC | CC | AA |
| UGA-SAM1-049 | TT | TT | CC | AA |
| UGA-SAM1-050 | TT | TT | TT | CC |
| UGA-SAM1-051 | TT | CC | TT | CC |
| UGA-SAM1-052 | TT | CC | CC | AA |
| UGA-SAM1-054 | TT | TT | CC | AA |
| UGA-SAM1-056 | TT | CC | TT | CC |
| UGA-SAM1-058 | TT | TT | CC | AA |
| UGA-SAM1-059 | TT | TT | CC | AA |
| UGA-SAM1-060 | TT | CC | CC | AA |
| UGA-SAM1-061 | TT | TT | TT | CC |
| UGA-SAM1-062 | TT | CC | CC | AA |
| UGA-SAM1-063 | TT | TT | CC | AA |
| UGA-SAM1-064 | TT | TC | CC | AA |
| UGA-SAM1-065 | TT | TT | CC | AA |
| UGA-SAM1-066 | CC | TT | CC | AA |
| UGA-SAM1-067 | TT | CC | TT | CC |
| UGA-SAM1-068 | CC | TC | CC | AA |
| UGA-SAM1-069 | TT | TT | CC | AA |
| UGA-SAM1-070 | CC | CC | CC | AA |
| UGA-SAM1-071 | TT | TC | TT | CC |
| UGA-SAM1-072 | TT | TC | CC | AA |
| UGA-SAM1-073 | TT | TT | CC | AA |
| UGA-SAM1-074 | CC | CC | CC | AA |
| UGA-SAM1-075 | TC | CC | TT | CC |
| UGA-SAM1-076 | TT | CC | CC | AA |
| UGA-SAM1-077 | TT | CC | CC | AA |
| UGA-SAM1-078 | TT | CC | CC | AA |
| UGA-SAM1-079 | TT | TC | CC | AA |
| UGA-SAM1-080 | TT | TT | CC | AA |
| UGA-SAM1-081 | TT | CC | CC | AA |
| UGA-SAM1-083 | CC | CC | CC | AA |
| UGA-SAM1-084 | TT | TC | NN | CC |
| UGA-SAM1-086 | TT | CC | TT | CC |
| UGA-SAM1-087 | TT | CC | CC | AA |
| UGA-SAM1-088 | TT | TT | CC | AA |
| UGA-SAM1-089 | CC | CC | CC | AA |
| UGA-SAM1-090 | TT | CC | CC | AA |
| UGA-SAM1-091 | CC | CC | CC | AA |
| UGA-SAM1-092 | TT | TC | TT | CC |
| UGA-SAM1-093 | TT | TC | CC | AA |
| UGA-SAM1-094 | CC | CC | CC | AA |
| UGA-SAM1-095 | CC | CC | CC | AA |
| UGA-SAM1-096 | TT | CC | CC | AA |
| UGA-SAM1-097 | TT | CC | CC | AA |

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|---|---|---|---|---|
| UGA-SAM1-098 | TT | CC | TT | CC |
| UGA-SAM1-099 | TT | CC | TT | CC |
| UGA-SAM1-102 | CC | CC | TT | CC |
| UGA-SAM1-103 | CC | TC | CC | CC |
| UGA-SAM1-104 | TT | TT | CC | AA |
| UGA-SAM1-105 | TT | CC | TT | CC |
| UGA-SAM1-106 | CC | TC | CC | AA |
| UGA-SAM1-107 | TC | CC | CT | AC |
| UGA-SAM1-108 | TT | TC | CC | AA |
| UGA-SAM1-111 | TT | CC | CC | AA |
| UGA-SAM1-112 | CC | CC | CC | AA |
| UGA-SAM1-113 | TT | CC | TT | CC |
| UGA-SAM1-114 | CC | CC | TT | CC |
| UGA-SAM1-115 | TT | CC | CC | AA |
| UGA-SAM1-116 | CC | CC | CC | AA |
| UGA-SAM1-117 | TT | CC | CC | AA |
| UGA-SAM1-120 | TT | TC | CC | AA |
| UGA-SAM1-122 | TT | CC | CC | AA |
| UGA-SAM1-123 | TT | TC | CC | AA |
| UGA-SAM1-124 | TT | TT | NN | AA |
| UGA-SAM1-125 | TT | TC | CC | AA |
| UGA-SAM1-126 | TT | TC | CC | AA |
| UGA-SAM1-127 | TT | TC | CT | AC |
| UGA-SAM1-128 | TT | TC | CC | AA |
| UGA-SAM1-129 | TT | CC | CC | AA |
| UGA-SAM1-130 | TT | CC | CC | AA |
| UGA-SAM1-131 | TT | CC | CT | AC |
| UGA-SAM1-132 | TT | CC | CC | AA |
| UGA-SAM1-133 | TT | CC | TT | CC |
| UGA-SAM1-134 | CC | CC | CC | AA |
| UGA-SAM1-137 | TT | TT | CC | AA |
| UGA-SAM1-138 | TT | CC | TT | CC |
| UGA-SAM1-139 | TT | TT | TT | CC |
| UGA-SAM1-141 | TT | TT | CC | AA |
| UGA-SAM1-142 | CC | TT | CC | AA |
| UGA-SAM1-143 | TT | TC | CC | AA |
| UGA-SAM1-144 | TT | TT | CC | AA |
| UGA-SAM1-145 | TT | TT | CC | AA |
| UGA-SAM1-146 | TT | TC | CC | AA |
| UGA-SAM1-147 | TT | TT | CC | AA |
| UGA-SAM1-148 | TT | TT | CC | AA |
| UGA-SAM1-150 | TT | TT | CC | AA |
| UGA-SAM1-151 | TT | TC | CC | AA |
| UGA-SAM1-152 | TT | TT | CC | AA |
| UGA-SAM1-154 | CC | TT | TT | CC |
| UGA-SAM1-157 | TT | TT | CC | AA |
| UGA-SAM1-158 | TT | TT | CC | AA |
| UGA-SAM1-160 | TT | CC | CC | AA |
| UGA-SAM1-162 | TT | CC | CC | AA |
| UGA-SAM1-163 | TT | CC | CC | AA |
| UGA-SAM1-164 | TT | CC | CC | AA |
| UGA-SAM1-166 | TT | TT | TT | CC |
| UGA-SAM1-167 | TT | TC | CC | AA |
| UGA-SAM1-168 | TT | CC | CC | AA |
| UGA-SAM1-170 | TT | CC | CC | AA |
| UGA-SAM1-172 | TT | CC | CC | AA |
| UGA-SAM1-173 | TT | TT | CC | AA |
| UGA-SAM1-174 | TT | TT | CC | AA |
| UGA-SAM1-175 | TT | TT | CC | AA |
| UGA-SAM1-176 | TT | TT | CC | AA |
| UGA-SAM1-177 | CC | CC | NN | AA |
| UGA-SAM1-178 | CC | CC | TT | CC |

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|---|---|---|---|---|
| UGA-SAM1-179 | TT | TT | CC | AA |
| UGA-SAM1-180 | TT | CC | TT | CC |
| UGA-SAM1-182 | TT | CC | TT | CC |
| UGA-SAM1-184 | CC | CC | TT | CC |
| UGA-SAM1-187 | TT | CC | CC | AA |
| UGA-SAM1-188 | TT | CC | CC | AA |
| UGA-SAM1-189 | TT | CC | CC | AA |
| UGA-SAM1-190 | TT | TT | TT | CC |
| UGA-SAM1-192 | TT | TT | CC | AA |
| UGA-SAM1-193 | TT | TT | TT | CC |
| UGA-SAM1-194 | TT | TT | CC | AA |
| UGA-SAM1-196 | TT | CC | TT | CC |
| UGA-SAM1-197 | TT | TT | CC | AA |
| UGA-SAM1-200 | TT | TT | CC | AA |
| UGA-SAM1-201 | CC | CC | CC | AA |
| UGA-SAM1-202 | TT | CC | TT | CC |
| UGA-SAM1-203 | CC | TT | CC | AA |
| UGA-SAM1-205 | NN | TT | CC | AA |
| UGA-SAM1-206 | TT | TT | TT | CC |
| UGA-SAM1-208 | TT | TT | CC | AA |
| UGA-SAM1-209 | TT | TT | CC | AA |
| UGA-SAM1-210 | TT | TT | CC | AA |
| UGA-SAM1-211 | TT | CC | CC | AA |
| UGA-SAM1-212 | TT | TT | CC | AA |
| UGA-SAM1-213 | TT | TT | CC | AA |
| UGA-SAM1-214 | TT | TT | CC | AA |
| UGA-SAM1-215 | TT | CC | CC | AA |
| UGA-SAM1-216 | TT | TT | CC | AA |
| UGA-SAM1-217 | TT | CC | CC | AA |
| UGA-SAM1-220 | TT | CC | CC | AA |
| UGA-SAM1-221 | TT | CC | CC | AA |
| UGA-SAM1-223 | TT | TT | CC | AA |
| UGA-SAM1-225 | TT | TC | CC | AA |
| UGA-SAM1-226 | TT | CC | CC | AA |
| UGA-SAM1-227 | TT | TC | TT | CC |
| UGA-SAM1-228 | TT | TC | CC | AA |
| UGA-SAM1-229 | TT | CC | CC | AA |
| UGA-SAM1-230 | CC | CC | TT | CC |
| UGA-SAM1-231 | TT | TT | TT | CC |
| UGA-SAM1-232 | TT | TC | CT | AC |
| UGA-SAM1-233 | TT | CC | CC | AA |
| UGA-SAM1-234 | TT | TC | CC | AA |
| UGA-SAM1-235 | CC | TC | TT | CC |
| UGA-SAM1-236 | TT | TC | CC | AA |
| UGA-SAM1-237 | CC | CC | TT | CC |
| UGA-SAM1-238 | TT | TC | CC | AA |
| UGA-SAM1-239 | TT | CC | CC | AA |
| UGA-SAM1-240 | TC | CC | CC | AA |
| UGA-SAM1-241 | TT | TT | CC | AA |
| UGA-SAM1-244 | TT | CC | CC | AA |
| UGA-SAM1-245 | TT | CC | CC | AA |
| UGA-SAM1-246 | TT | CC | CC | AA |
| UGA-SAM1-247 | TT | TC | CC | AA |
| UGA-SAM1-248 | TT | TC | CC | AA |
| UGA-SAM1-249 | TT | TT | CC | AA |
| UGA-SAM1-250 | TT | CC | CC | AA |
| UGA-SAM1-251 | TT | TT | CC | AA |
| UGA-SAM1-252 | TT | TT | TT | CC |
| UGA-SAM1-253 | TT | CC | TT | CC |
| UGA-SAM1-254 | TC | TC | CC | AA |
| UGA-SAM1-255 | TT | CC | CC | AA |
| UGA-SAM1-256 | TC | TT | CC | AA |

| | | | | |
|---|---|---|---|---|
| UGA-SAM1-257 | TT | TT | CC | AA |
| UGA-SAM1-258 | TT | CC | CC | AA |
| UGA-SAM1-259 | TT | TC | TT | CC |
| UGA-SAM1-260 | TT | TT | CC | AA |
| UGA-SAM1-261 | TT | TT | CC | AA |
| UGA-SAM1-262 | TT | CC | TT | CC |
| UGA-SAM1-263 | TT | TT | CC | AA |
| UGA-SAM1-265 | TT | CC | CC | AA |
| UGA-SAM1-266 | TT | TT | CC | AA |
| UGA-SAM1-267 | TT | CC | CC | AA |
| UGA-SAM1-268 | TT | TT | CC | AA |
| UGA-SAM1-269 | TT | TC | CC | AA |
| UGA-SAM1-270 | TT | CC | CC | AA |
| UGA-SAM1-271 | TT | TT | CC | AA |
| UGA-SAM1-272 | TT | CC | TT | CC |
| UGA-SAM1-274 | TT | TT | CC | AA |
| UGA-SAM1-275 | TT | TT | TT | CC |
| UGA-SAM1-277 | TT | CC | TT | CC |
| UGA-SAM1-279 | TT | TT | CC | AA |
| UGA-SAM1-280 | TT | TT | CC | AA |
| UGA-SAM1-281 | TT | TT | CC | AA |
| UGA-SAM1-282 | TT | TT | TT | CC |
| UGA-SAM1-283 | TT | TT | TT | CC |
| UGA-SAM1-284 | TT | TT | CC | AA |
| UGA-SAM1-285 | TC | TC | TT | CC |
| UGA-SAM1-286 | TT | CC | TT | CC |
| UGA-SAM1-287 | TT | TT | TT | CC |
| UGA-SAM1-289 | TT | TT | CC | AA |
| USSR MAYAK '66 | TT | CC | CT | AC |
| USSR VNIIMK 8931 '66 | TT | TC | CC | AA |
| VALLEY | TT | TT | CC | AA |
| VIR 019 | TT | CC | TT | CC |
| VIR 107 | TT | TT | CC | AA |
| VIR 160 | TT | TT | CC | AA |
| VIR 847 | TT | TC | CC | AA |
| VK-12 | TT | CC | TT | CC |
| VK-47 | CC | TT | TT | CC |
| VNIIMK 1646 | TT | CC | CC | AA |
| VNIIMK 1646 4 MOTH RES | TT | CC | CC | AA |
| VNIIMK 6540 | TT | TC | CC | AA |
| VNIIMK 8883 | TT | CC | TT | CC |
| VOSHOD | TT | CC | CT | AC |
| W.Y. I/7 | TT | TC | CT | AC |
| W-31 | TT | TC | CT | AC |
| WIELKOPOLSKI | TT | TT | TT | CC |
| YAWNE | TT | TC | CC | AA |
| ZARIA | TT | TT | CC | AA |
| ZELANKA 368 | TT | CC | CC | AA |
| PI 213175 | CC | CC | TT | CC |
| PI 256334 | TT | TT | CC | AA |
| 54-3 | TT | TT | TT | CC |
| ARMAVIRSKY 3497 | TT | TT | CC | AA |
| ARROWHEAD | TT | TT | CC | AA |
| BIG SMILE | TC | CC | CC | AA |
| CM104 | CC | CC | CC | AA |
| CM259 | TT | TT | CC | AA |
| CM275 | TT | TT | CC | AA |
| CM526 | TT | TT | TT | CC |
| CM63 | TT | TT | CC | AA |
| CMH 101 | TT | TT | CC | AC |
| D-75-10 | TT | TT | CC | AA |
| GN 0778 | CC | TT | CC | AA |

| | | | | |
|---|---|---|---|---|
| KRASNODARETS | TT | TT | CC | AA |
| NO. 2 | TC | TC | CC | AA |
| PACINO COLA | TT | TC | CC | AA |
| RHA 282 | TT | CC | CC | AA |
| ROMSUN V3355 | TT | CC | CC | AA |
| SOLITA | TT | TC | CC | AA |
| SUNSPOT | TT | TT | CT | AC |
| UGA-SAM1-010 | TT | TT | CC | AA |
| UGA-SAM1-012 | TT | CC | CC | AA |
| UGA-SAM1-024 | TT | TT | CC | AA |
| UGA-SAM1-041 | TT | TT | CC | AA |
| UGA-SAM1-053 | TT | TT | TT | CC |
| UGA-SAM1-055 | TT | TC | CC | AA |
| UGA-SAM1-057 | TT | TT | CC | AA |
| UGA-SAM1-082 | TT | TT | TT | CC |
| UGA-SAM1-100 | CC | TT | TT | CC |
| UGA-SAM1-101 | TT | TT | TT | CC |
| UGA-SAM1-109 | TT | TT | CC | AA |
| UGA-SAM1-110 | CC | TT | CC | AA |
| UGA-SAM1-118 | TT | CC | CC | AA |
| UGA-SAM1-119 | TT | TC | CC | AA |
| UGA-SAM1-121 | TT | CC | CC | AA |
| UGA-SAM1-136 | TT | TT | CC | AA |
| UGA-SAM1-140 | TT | TT | TT | CC |
| UGA-SAM1-149 | TT | CC | TT | CC |
| UGA-SAM1-153 | TT | TT | CC | AA |
| UGA-SAM1-155 | TT | TT | CC | AA |
| UGA-SAM1-156 | TT | TT | CC | AA |
| UGA-SAM1-161 | TT | TT | CC | AA |
| UGA-SAM1-165 | TT | CC | CC | AA |
| UGA-SAM1-169 | TT | TT | CC | AA |
| UGA-SAM1-171 | TT | TT | CC | AA |
| UGA-SAM1-181 | TT | TT | CC | AA |
| UGA-SAM1-183 | TT | TT | CC | AA |
| UGA-SAM1-185 | TT | CC | TT | CC |
| UGA-SAM1-186 | TT | TT | CC | AA |
| UGA-SAM1-191 | TT | TT | CC | AA |
| UGA-SAM1-195 | TT | TT | CC | AA |
| UGA-SAM1-198 | TT | TT | CC | AA |
| UGA-SAM1-199 | TT | TT | CC | AA |
| UGA-SAM1-204 | TT | CC | CC | AA |
| UGA-SAM1-207 | TT | TT | CC | AA |
| UGA-SAM1-218 | TT | TT | CC | AA |
| UGA-SAM1-219 | TT | TT | TT | CC |
| UGA-SAM1-224 | TT | TT | CC | AA |
| UGA-SAM1-242 | TT | TT | CC | AA |
| UGA-SAM1-243 | TT | CC | CC | AA |
| UGA-SAM1-264 | TT | TT | CC | AA |
| UGA-SAM1-273 | CC | TT | CC | AA |
| UGA-SAM1-276 | TT | CC | CT | CC |
| UGA-SAM1-278 | TT | TT | CC | AA |
| UGA-SAM1-288 | TT | TT | CC | AA |
| FIRECRACKER | TC | TC | CT | AA |
| PEACH-PASSION | CC | TC | CC | AA |
| GIGANTEUS ORGANIC | TT | TC | CT | AC |
| KONG | TT | TC | CC | AA |
| MAMMOTH RUSSIAN | TT | TC | CC | AA |
| LITTLE TIGER | TT | TC | CC | AA |
| LITTLE BECKA | CC | TC | CC | AA |
| SOLAR FLASH | TT | TC | CC | AA |
| SUNTASTIC | TT | TC | CC | AA |
| BUTTERCREAM | NN | TT | CC | AA |

| | | | | |
|---|---|---|---|---|
| MUNCHKIN | TC | TC | CT | AA |
| JERUSALEM DWARF YELLOW | TT | TC | CC | AA |
| CHOCO SUN | TT | TC | CC | AA |
| ORANGE HOBBIT | TC | TC | CC | AA |
| MERIDA GOLD KOMPAKT | TT | TC | CC | AA |
| IKARUS | TT | TT | CC | AA |
| PRADO GOLD | NN | CC | NN | AA |

**Supplementary Table A 26:** Field data (2017 and 2019 in Germany) and marker analyses regarding accessions and ornamental sunflowers analysed for the DELPA-Mutation (n = 51)

| ACCESSION | YEAR DE | PH CM | AV. PET ° | STABW.N PET ° | DELPA | GEN. CONF. |
|---|---|---|---|---|---|---|
| **PACINO COLA** | 2017 | 56 | 39 | 11.3 | pos. control | CC |
| **UGA-SAM1-118** | 2017 | 64 | 45 | 2.7 | yes | CC |
| **UGA-SAM1-119** | 2017 | 71 | 33 | 3.7 | yes | CC |
| **SOLITA** | 2017 | 60 | 42 | 3.2 | yes | CC |
| **SUNSPOT** | 2017 | 69 | 31 | 2.9 | yes | CC |
| **MERIDA GOLD** | 2019 | 54 | 51 | 7.4 | yes | CC |
| **CHOCO SUN** | 2019 | 66 | 45 | 7.1 | yes | CC |
| **JERUSALEM DWARF YELLOW** | 2019 | 67 | 44 | 5.6 | yes | CC |
| **FIRECRACKER** | 2019 | 71 | 39 | 8.5 | yes | TC |
| **ORANGE HOBBIT** | 2019 | 62 | 46 | 5.8 | yes | TC |
| **BIG SMILE** | 2017 | 61 | 46 | 1.2 | neg. control | TT |
| **PRADO GOLD** | 2019 | 71 | 42 | 10.7 | no | TT |
| **IKARUS** | 2019 | 94 | 32 | 9.3 | no | TT |
| **LITTLE TIGER** | 2019 | 25 | 50 | 9.5 | no | TT |
| **LITTLE BECKA** | 2019 | 45 | 43 | 7.2 | no | TT |
| **SOLAR FLASH** | 2019 | 57 | 47 | 6.1 | no | TT |
| **VINCENT CHOICE DEEP ORANGE** | 2019 | 113 | 37 | 6.7 | no | TT |
| **PEACH PASSION** | 2019 | 51 | 47 | 9.3 | no | TT |
| **SUNBRIGHT** | 2019 | 117 | 31 | 6.7 | no | TT |
| **SUNTASTIC** | 2019 | 27 | 53 | 8.4 | no | TT |
| **BUTTERCREAM** | 2019 | 99 | 44 | 9.3 | no | TT |
| **MUNCHKIN** | 2019 | 69 | 41 | 7.7 | no | TT |
| **GIGANTEUS ORGANIC** | 2019 | 254 | 38 | 11.6 | no | TT |
| **KONG** | 2019 | 290 | 42 | 4.1 | no | TT |
| **MAMMOTH RUSSIAN** | 2019 | 175 | 38 | 10.6 | no | TT |
| **ROMSUN V3355** | 2017 | 72 | 34 | 4.2 | no | TT |
| **54-3** | 2017 | 88 | 45 | 13.0 | no | TT |
| **GN 0778** | 2017 | 102 | 45 | 6.2 | no | TT |
| **CM104** | 2017 | 97 | 31 | 7.5 | no | TT |
| **CM259** | 2017 | 98 | 36 | 3.3 | no | TT |
| **UGA-SAM1-052** | 2017 | 103 | 59 | 3.0 | no | TT |
| **UGA-SAM1-012** | 2017 | 62 | 60 | 5.0 | no | TT |
| **UGA-SAM1-060** | 2017 | 78 | 60 | 4.6 | no | TT |
| **UGA-SAM1-055** | 2017 | 101 | 55 | 4.1 | no | TT |
| **UGA-SAM1-067** | 2017 | 59 | 59 | 1.7 | no | TT |
| **UGA-SAM1-100** | 2017 | 104 | 36 | 4.7 | no | TT |
| **UGA-SAM1-101** | 2017 | 105 | 50 | 7.1 | no | TT |

| | | | | | | |
|---|---|---|---|---|---|---|
| **UGA-SAM1-110** | 2017 | 101 | 43 | 4.2 | no | TT |
| **UGA-SAM1-132** | 2017 | 99 | 56 | 2.9 | no | TT |
| **UGA-SAM1-135** | 2017 | 103 | 45 | 4.4 | no | TT |
| **UGA-SAM1-181** | 2017 | 103 | 37 | 5.9 | no | TT |
| **UGA-SAM1-186** | 2017 | 87 | 53 | 4.3 | no | TT |
| **UGA-SAM1-198** | 2017 | 104 | 53 | 4.9 | no | TT |
| **UGA-SAM1-233** | 2017 | 46 | 60 | 7.7 | no | TT |
| **UGA-SAM1-232** | 2017 | 84 | 32 | 5.3 | no | TT |
| **UGA-SAM1-243** | 2017 | 61 | 56 | 12.1 | no | TT |
| **UGA-SAM1-273** | 2017 | 104 | 51 | 5.1 | no | TT |
| **UGA-SAM1-278** | 2017 | 107 | 55 | 8.7 | no | TT |
| **UGA-SAM1-270** | 2017 | 97 | 45 | 8.1 | no | TT |
| **UGA-SAM1-183** | 2017 | 158 | 35 | 3.3 | no | TT |
| **NO. 2** | 2017 | 166 | 53 | 7.3 | no | TT |

**Supplementary Table A 27:** Summary of KASP analysis for 59 SNPs in the large association panel (n = 381)

| DNA \ ASSAY | DEL091.15 | DEL091.18 | DEL091.25 | DEL091.27 | DEL091.3 | DEL091.42 | DEL091.47 | DEL091.48 | DEL091.49 | DEL091.7 | DEL091.8 | DEL091.9 | DEL801.3 | DEL801.4 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **NUMBER ?** | 8 | 7 | 9 | 45 | 6 | 11 | 17 | 60 | 44 | 35 | 20 | 6 | 8 | 8 |
| **NUMBER G:G** | 47 | 58 | 295 | 0 | 0 | 0 | 235 | 0 | 285 | 150 | 242 | 82 | 0 | 0 |
| **NUMBER G:C** | 0 | 0 | 16 | 0 | 0 | 0 | 0 | 0 | 0 | 34 | 0 | 0 | 0 | 0 |
| **NUMBER G:T** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **NUMBER G:A** | 0 | 0 | 0 | 0 | 0 | 0 | 77 | 0 | 0 | 0 | 40 | 0 | 0 | 0 |
| **NUMBER C:C** | 0 | 301 | 60 | 185 | 0 | 47 | 0 | 320 | 0 | 161 | 0 | 0 | 254 | 79 |
| **NUMBER C:G** | 0 | 14 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **NUMBER C:T** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 38 | 0 |
| **NUMBER C:A** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **NUMBER A:G** | 5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **NUMBER A:C** | 0 | 0 | 0 | 0 | 0 | 3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 39 |
| **NUMBER A:A** | 319 | 0 | 0 | 0 | 285 | 319 | 51 | 0 | 52 | 0 | 78 | 0 | 0 | 253 |
| **NUMBER A:T** | 0 | 0 | 0 | 0 | 11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **NUMBER T:C** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **NUMBER T:T** | 0 | 0 | 0 | 150 | 77 | 0 | 0 | 0 | 0 | 0 | 0 | 249 | 79 | 0 |
| **NUMBER T:G** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 44 | 0 | 0 |
| **NUMBER T:A** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **DUPE** | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |
| **UNCALLABLE** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| **GESAMT** | 380 | 381 | 381 | 381 | 380 | 381 | 381 | 381 | 381 | 381 | 380 | 381 | 381 | 380 |

| **DNA \ ASSAY** | **DEL801.5** | **DEL901.10** | **DEL901.11** | **DEL901.2** | **DEL901.3** | **DEL901.4** | **DEL901.5** | **DEL901.6** | **DEL901.9** | **GID071.16** | **GID071.24** | **GID071.34** | **GID871.22** | **LAZ951.8** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **NUMBER ?** | 85 | 22 | 9 | 6 | 7 | 12 | 7 | 7 | 8 | 7 | 5 | 8 | 40 | 4 |
| **NUMBER G:G** | 0 | 328 | 0 | 0 | 335 | 0 | 0 | 0 | 0 | 0 | 301 | 0 | 143 | 3 |
| **NUMBER G:C** | 0 | 3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 13 | 0 | 0 | 0 |
| **NUMBER G:T** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **NUMBER G:A** | 0 | 0 | 0 | 0 | 8 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 121 |
| **NUMBER C:C** | 0 | 28 | 337 | 28 | 0 | 32 | 341 | 336 | 339 | 118 | 61 | 229 | 0 | 0 |
| **NUMBER C:G** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **NUMBER C:T** | 0 | 0 | 3 | 0 | 0 | 0 | 4 | 7 | 0 | 0 | 0 | 44 | 0 | 0 |
| **NUMBER C:A** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 5 | 0 | 0 | 0 | 0 | 0 |
| **NUMBER A:G** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 19 | 0 |
| **NUMBER A:C** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **NUMBER A:A** | 0 | 0 | 0 | 0 | 30 | 0 | 0 | 0 | 29 | 0 | 0 | 0 | 177 | 245 |
| **NUMBER A:T** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **NUMBER T:C** | 0 | 0 | 0 | 6 | 0 | 8 | 0 | 0 | 0 | 42 | 0 | 0 | 0 | 0 |
| **NUMBER T:T** | 295 | 0 | 32 | 339 | 0 | 328 | 29 | 31 | 0 | 213 | 0 | 99 | 0 | 0 |
| **NUMBER T:G** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **NUMBER T:A** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **DUPE** | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 1 | 1 |
| **UNCALLABLE** | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 7 |
| **GESAMT** | 381 | 381 | 381 | 379 | 381 | 381 | 381 | 381 | 381 | 381 | 381 | 381 | 380 | 381 |

| DNA \ ASSAY | DEL091.10 | DEL091.33 | DEL801.17 | DEL801.24 | GID131.2 | GID131.27 | GID131.3 | GID131.39 | GID131.7 | GID131.9 | LAZ921.41 | LAZ921.42 | LAZ921.43 | LAZ921.44 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **NUMBER ?** | 6 | 30 | 215 | 55 | 6 | 6 | 9 | 24 | 141 | 12 | 117 | 7 | 115 | 6 |
| **NUMBER G:G** | 320 | 151 | 0 | 0 | 0 | 78 | 307 | 0 | 66 | 0 | 0 | 0 | 0 | 0 |
| **NUMBER G:C** | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **NUMBER G:T** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **NUMBER G:A** | 0 | 0 | 0 | 0 | 0 | 0 | 30 | 0 | 0 | 0 | 186 | 0 | 0 | 0 |
| **NUMBER C:C** | 48 | 0 | 0 | 117 | 326 | 0 | 0 | 70 | 0 | 26 | 0 | 0 | 173 | 0 |
| **NUMBER C:G** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **NUMBER C:T** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 188 | 20 | 190 |
| **NUMBER C:A** | 0 | 0 | 0 | 0 | 24 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **NUMBER A:G** | 0 | 0 | 0 | 0 | 0 | 37 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **NUMBER A:C** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **NUMBER A:A** | 0 | 0 | 164 | 0 | 24 | 258 | 33 | 0 | 174 | 0 | 73 | 0 | 0 | 0 |
| **NUMBER A:T** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **NUMBER T:C** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 36 | 0 | 22 | 0 | 0 | 0 | 0 |
| **NUMBER T:T** | 0 | 199 | 0 | 207 | 0 | 0 | 0 | 250 | 0 | 320 | 0 | 183 | 71 | 183 |
| **NUMBER T:G** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **NUMBER T:A** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **DUPE** | 1 | 1 | 1 | 2 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 2 | 2 | 2 |
| **UNCALLABLE** | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 0 |
| **GESAMT** | 381 | 381 | 381 | 381 | 381 | 380 | 380 | 381 | 381 | 381 | 379 | 380 | 381 | 381 |

| DNA \ ASSAY | LAZ921.7 | LAZ951.11 | DEL091.16 | GID131.30 | LAZ951.3 | SLY061.3 | SLY061.5 | SLY061.6 | SNE171.5 | SNE171.7 | SNE171.8 | TAC271.2 | LAZ921.16 | LAZ921.17 | LAZ921.19 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| NUMBER ? | 81 | 11 | 8 | 14 | 9 | 9 | 18 | 12 | 9 | 8 | 9 | 14 | 8 | 40 | 47 |
| NUMBER G:G | 0 | 125 | 26 | 0 | 53 | 0 | 196 | 0 | 0 | 37 | 312 | 0 | 0 | 75 | 0 |
| NUMBER G:C | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| NUMBER G:T | 0 | 0 | 0 | 0 | 274 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| NUMBER G:A | 0 | 88 | 0 | 0 | 0 | 0 | 35 | 0 | 0 | 0 | 20 | 0 | 0 | 0 | 0 |
| NUMBER C:C | 300 | 0 | 0 | 19 | 0 | 0 | 0 | 127 | 0 | 0 | 0 | 0 | 61 | 0 | 259 |
| NUMBER C:G | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| NUMBER C:T | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 23 |
| NUMBER C:A | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| NUMBER A:G | 0 | 0 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 18 | 0 | 0 | 0 | 0 | 0 |
| NUMBER A:C | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| NUMBER A:A | 0 | 153 | 342 | 0 | 0 | 123 | 129 | 0 | 35 | 317 | 39 | 20 | 0 | 266 | 0 |
| NUMBER A:T | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| NUMBER T:C | 0 | 0 | 0 | 20 | 0 | 0 | 0 | 43 | 0 | 0 | 0 | 0 | 25 | 0 | 0 |
| NUMBER T:T | 0 | 0 | 0 | 328 | 45 | 204 | 0 | 198 | 318 | 0 | 0 | 343 | 286 | 0 | 51 |
| NUMBER T:G | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| NUMBER T:A | 0 | 0 | 0 | 0 | 0 | 43 | 0 | 0 | 19 | 0 | 0 | 4 | 0 | 0 | 0 |
| DUPE | 0 | 1 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| UNCALLABLE | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| GESAMT | 381 | 379 | 380 | 381 | 381 | 380 | 379 | 381 | 381 | 380 | 380 | 381 | 381 | 381 | 381 |

| DNA \ ASSAY | SNE171.3 | SNE171.1 |
|---|---|---|
| **NUMBER ?** | 39 | 46 |
| **NUMBER G:G** | 0 | 37 |
| **NUMBER G:C** | 0 | 0 |
| **NUMBER G:T** | 0 | 0 |
| **NUMBER G:A** | 0 | 5 |
| **NUMBER C:C** | 0 | 0 |
| **NUMBER C:G** | 0 | 0 |
| **NUMBER C:T** | 0 | 0 |
| **NUMBER C:A** | 0 | 0 |
| **NUMBER A:G** | 0 | 0 |
| **NUMBER A:C** | 0 | 0 |
| **NUMBER A:A** | 0 | 292 |
| **NUMBER A:T** | 0 | 0 |
| **NUMBER T:C** | 0 | 0 |
| **NUMBER T:T** | 0 | 0 |
| **NUMBER T:G** | 0 | 0 |
| **NUMBER T:A** | 0 | 0 |
| **DUPE** | 0 | 0 |
| **UNCALLABLE** | 0 | 0 |
| **GESAMT** | 39 | 380 |

**Supplementary Table A 28:** SNPs analysed by KASP-Assays through LGC. SNP positions are given according to the HanXRQ genome sequence assembly v.2

| SNP ID | SEQUENCE | POSITION |
|---|---|---|
| **DEL091.15** | TACTTCACCGAAGCACTAGCTTGCAGAATCTACAAACTAAACCCTAAATC[G/A]CCACACAATTCACCAATCCTTAATAACATTCTTCAATCGCATTTCTACGA | HanXRQChr08 8144824 |
| **DEL091.18** | CACACGCTGATGGCATGCGCCGAAGCCGTACAAAACGCCGATCAAAAGCT[G/C]GCCGAAACCCTAGTAAGCCGAGCCGGTATGTTAGCAGCTTCACAAGCCGG | HanXRQChr08 8144701 |
| **DEL091.25** | TTCAACCACCTCTCACCATCAATAATCCCTTCTCAAACGACATCGTTCAG[C/G]CTCAACCACCTGCTGCTGTTATAAACAATAATTCCTTCTTAAACGACGCC | HanXRQChr08 8144282 |
| **DEL091.27** | CCCTTTCCCGATCCCCAATCCCACCGCCCTTTCACACCCACCAATTTGAT[C/T]TCATTTCAATTTATTCCCTATGAAGCGTGAATACCCAAATCAGAATTACG | HanXRQChr08 8143914 |
| **DEL091.3** | GACTCGCTTGAGAGTGGTGTGTTTGACTCGCTTGAAAGTGGTGCGAGCGA[T/A]GAGGATAAGGCTATGTCGGAGGTGTATTTGGGGAAGCAGATTTGTAATGT | HanXRQChr08 8145466 |
| **DEL091.4** | ACTGAGTCGTTGCATTATTATTCGACGCTTTTCGACTCGCTTGAGAGTGG[G/T]GTGTTTGACTCGCTTGAAAGTGGTGCGAGCGAAGAGGATAAGGCTATGTC | HanXRQChr08 8145433 |
| **DEL091.42** | TTAAAGCTGGGTGTTGATCTTCTTTTATTTCCTTGATTGCAAATAAACTA[C/A]CCGGGGTGATTACCGACCTAAATTCTTGCTAATTGCTTAATTTTTTTTTT | HanXRQChr08 8142919 |
| **DEL091.47** | GCGAGTGATTCCCGTTTCGCGTGTCGGATGTTTGTTTGGTGCGTTTGGTT[A/G]CGTTAGTTAGTTAGAGCACTTTAAGTGTTTTAGCGAGGTATTAAGTGTTG | HanXRQChr08 8142506 |
| **DEL091.48** | AAGGGTGCCTTCGTATGAAGGTGCCTGTTTCGTGCGAGTGATTCCCGTTT[T/C]GCGTGTCGGATGTTTGTTTGGTGCGTTTGGTTGCGTTAGTTAGTTAGAGC | HanXRQChr08 8142473 |
| **DEL091.49** | GCAGCAAGTGGTGAATGAGGGACTGAGCTGGGTATTTATAGAAAGAGGAT[A/G]TTTGGTGTGAGCTGGGTTCTGTACGAAGGGTGCCTTCGTATGAAGGTGCC | HanXRQChr08 8142397 |
| **DEL091.7** | AAGTTGTGGCGGTTAATTCGGTGTTTGAGATGCATCAGTTGTTGGCTCGA[C/G]CGGGTTCGGTTGAGAAGGTGTTGACCGCGTTGAAAGTGTTAAATCCGGTT | HanXRQChr08 8145272 |
| **DEL091.8** | CGGATATTGAACCGGGGATGTTGGATTTACGCGATGATGAAGTTGTGGCG[A/G]TTAATTCGGTGTTTGAGATGCATCAGTTGTTGGCTCGAGCGGGTTCGGTT | HanXRQChr08 8145233 |
| **DEL091.9** | TCTCGGGTTATTGCCGAGAGTTTAGCGGATATTGAACCGGGGATGTTGGA[G/T]TTACGCGATGATGAAGTTGTGGCGGTTAATTCGGTGTTTGAGATGCATCA | HanXRQChr08 8145208 |
| **DEL801.3** | GGCATACTCGTCCGCTCATAACCACCTCGGCTTGGAAAATTCGGTGAACT[T/C]GGAAGAAACCAACTCGAGTATCGACTCGGTGGGTTCGGAGTCAAACCACC | HanXRQChr17 179883116 |
| **DEL801.4** | GTGGAAGAGGATGGGTGTTTGATGCTCGGGTGGCATACTCGTCCGCTCAT[C/A]ACCACCTCGGCTTGGAAAATTCGGTGAACTCGGAAGAAACCAACTCGAGT | HanXRQChr17 179883085 |
| **DEL801.5** | TACCGAGTGGTGGAAGAGGATGGGTGTTTGATGCTCGGGTGGCATACTCG[C/T]CCGCTCATAACCACCTCGGCTTGGAAAATTCGGTGAACTCGGAAGAAACC | HanXRQChr17 179883076 |
| **DEL901.1** | GACCGAGTTGAACGGCATGAGACGTTGGCTCAATGGAAGACTCGGTTTGA[T/C]TCGGCTGGGTTTCAACCGGTTCATCTCGGGTCAAACGCCTACAAGCAAGC | HanXRQChr12 25044535 |
| **DEL901.10** | ACGAGTACGTCCCCCGGAAGTGCCGGAGTAGATGACCTCCAAGCGATCCC[C/G]GGGGACGCTATTTATCCTCCAACAAAGAAACAAAAATCTTTATCGGAGGA | HanXRQChr12 25043142 |
| **DEL901.11** | GGAGATGACGAGCTGCTAGCAGTTCTCGGCTACAAAGTCAAGTCATCCGA[T/C]ATGGTTGACGTCGCGCAAAAGATCGAACACCTGGAGGGCGTTTTATCCAA | HanXRQChr12 25042890 |
| **DEL901.2** | CTTGAGAGCAGCGGCGGTGGTGGTTCGGTTGAAAGTGGTGGCGTTGCGGC[C/T]GCGAATAATCAGGATAAGATTATGTCTGAGGTGTATCTCGGGAAGCAGAT | HanXRQChr12 25044406 |
| **DEL901.3** | GCTCGGCCAGGGGCGGTGGAGAAGGTGTTGTCCGCGGTGAAGGAGATGAA[A/G]CCGGAGATTTTAACGGTGGTTGAGCAAGAAGCTAATCATAACGGACCGGT | HanXRQChr12 25044250 |
| **DEL901.4** | GAGTTACGAGAAGATGAAGTTGTTGCGGTGAACTCGGTGTTTGAAATGCA[C/T]GAGTTGTTGGCTCGGCCAGGGGCGGTGGAGAAGGTGTTGTCCGCGGTGAA | HanXRQChr12 25044190 |
| **DEL901.5** | ACGAGGTTAACATTTTCTGCAGGTGATAACACGGATCATTTGCAGGAAGT[T/C]GGATGGAAACTGGCGCAATTGGCGGATACGATTCATGTTGAGTTTCAATA | HanXRQChr12 25044040 |
| **DEL901.6** | CGTTGATGCAGGCGTTGGCTCTTCGCCCTGGCGGTCCTCCTACCTTTCGG[T/C]TAACCGGAATCGGCCCTCCCTCAGGTAATATTCGATATATTAGTTAGAGT | HanXRQChr12 25043662 |
| **DEL901.9** | GCTCCAGCCTTTCGAGATCTTCTTCAGATGCATTTTTATGAGACGTGCCC[A/C]TACCTTAAATTCGCTCATTTTACGGCGAATCAGGCGATATTAGAAGCTTT | HanXRQChr12 25043499 |
| **GID071.16** | ACATAGCCCACCACGTGGCGGTTCGGGCCGCTGAGTCGGGTGTGGAAGTG[C/T]TAGGGAACATATTGTTGCACCCATTGTTTGGGGGCGAAGAGCGAAAAGAA | HanXRQChr10 21068624 |
| **GID071.24** | TTAGCTTACAATATGCTCCGGCGACCGGACGGCACCTTCAACCGTGAACT[C/G]GCCGAGTTTCTTGACCGGAAAGTGGCCGCCAACACCGTTCCGGTGGACGG | HanXRQChr10 21068113 |
| **GID071.34** | AAAAAAAGAAATTATTAAACCATTTTAGTGTTAGGTGTTGTTTGTGTGTA[T/C]GTGGGTCCCACTTTCAAGCAGCATTTCGGCCGCCTGCTTTGTCGTCTCTC | HanXRQChr10 21066523 |

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|---|---|---|
| **GID871.22** | AAAAAATACTTATCTTACCCTCATTTTAACAATTTATAAATATCAGTTAT[G/A]TCTATTTTTCATGTTAATTTACTTCTAAGGTAAAAATATAGAGTTCATAG | HanXRQChr01 5783815 |
| **LAZ951.8** | TTAATGAGCTTCAGTTCATTCTCCATTGCTTCGGGTTCTAGGACCACCAT[A/G]TCGTTCTCAATGTAGGTGGCAAACGTCGGTGTTTTTGGTTCGTTAGTGAC | HanXRQChr08 3516485 |
| **DEL091.10** | AATAATATTGATTATTTACAAGAAGTTGGGTGTAACTTAGCTCAGTTAGC[C/G]GATACGATTCATGTCGAGTTTGAATACTCTCGGGTTATTGCCGAGAGTTT | HanXRQChr08 8145130 |
| **DEL091.30** | TGACACGATGTGGGTTAACTAGCGTTGCCTGACATCCCCACCCCATAAAC[G/C]CCCCCACTCCCCCAATAGCCTTATATCACAATTTCTCCCCATTTAAAAAA | HanXRQChr08 8143660 |
| **DEL091.31** | CCAACACTGACACGATGTGGGTTAACTAGCGTTGCCTGACATCCCCACCC[A/C]ATAAACCCCCCCACTCCCCCAATAGCCTTATATCACAATTTCTCCCCATT | HanXRQChr08 8143653 |
| **DEL091.33** | AGGCTTTGTGGCGGGGTAGGGTTCGGGTTTTCTTGGTATCCAAAGGGATT[G/T]TTTGGGTCGTATTCACGGTTAAAAGGATGCATTGTAGAGGATGTGGGTTA | HanXRQChr08 8143324 |
| **DEL801.17** | CGGCGAAGAAAGTTAAACCTAATTGCAGTTCTTCGTCTTCATCTTCAACC[G/A]TTACCGGTTCTGCAAACCCTAACCCTAGCATCCAGAACAACAACAGCAAC | HanXRQChr17 179881850 |
| **DEL801.24** | GTCAACAATGGTCAAATCAAATCCTAATTAGCAAAAAATCAGAGGCGTTC[C/T]AGTGTTTCCAGCCAAATTCAGGCCAGATTCTTGACCAAAACAGGTGAATT | HanXRQChr17 179880416 |
| **GID131.2** | TATGTGGCCCTGAAGAATGTAGCAGCTTTCATCCTTCATCTTGTTACGGC[A/C]TTGCTTGTACCGTAGTTTTTGAACACAAACAAGGAGGACTTCATTGATGC | HanXRQChr14 128247692 |
| **GID131.27** | ACCCCGCCTTCGGTCTCCGGTGCAGCCGGTCTGTAGATTCTAGATAGAAG[G/A]TTAGTTGACCGGTCAATCACAATATCGAAGGAGAATACCCCATCCACAGG | HanXRQChr14 128244940 |
| **GID131.3** | CAAGGTCCCAACGGTAGTTTCAGGAATATGTGGCCCTGAAGAATGTAGCA[A/G]CTTTCATCCTTCATCTTGTTACGGCCTTGCTTGTACCGTAGTTTTTGAAC | HanXRQChr14 128247666 |
| **GID131.39** | GCTACAGTCACAATATATGCTAAAAACCTTGAGGAATTTGGATCCAGAAG[C/T]TGGAAAGTCTGGATCTTGAGCTTGAGGATGAAACAGAGTTAACAACAAAA | HanXRQChr14 128243883 |
| **GID131.7** | GAGCGACAACAACTCTTGACCAGCGGTACGTTCGGCGCATAGACACGACT[A/G]GGCACCTACACCTTCTTAATCCACTGAGACCGTCCTTGTTAAAGTTTCAG | HanXRQChr14 128247430 |
| **GID131.9** | GGAACGTGTTTATCCATATCATTAAAGATATTAAAATTACGTTAAATTAA[C/T]GCCATATAAAAATTTATCCATTTCATTTGAAGTGCAAAATCAGTGGTTAT | HanXRQChr14 128247202 |
| **LAZ921.41** | GTCTGTTTTTTATTATATGGAACAGGACAAGATATGAATGAATTATCCTT[A/G]TATGCCTTACATAGATAGATAAAGCTATTGTGTCATATACTTAGTTTATA | HanXRQChr17 188291219 |
| **LAZ921.42** | TAAAGCTATTGTGTCATATACTTAGTTTATACAATGTGTGCGCTTTGTGC[T/C]ATCTTTGAAATGTAATTTGTATGGCTTGAAATGTTCATTTGGTAGTAAAC | HanXRQChr17 188291289 |
| **LAZ921.43** | CTATTGTGTCATATACTTAGTTTATACAATGTGTGCGCTTTGTGCTATCT[T/C]TGAAATGTAATTTGTATGGCTTGAAATGTTCATTTGGTAGTAAACTAATG | HanXRQChr17 188291294 |
| **LAZ921.44** | GTGCTATCTTTGAAATGTAATTTGTATGGCTTGAAATGTTCATTTGGTAG[T/C]AAACTAATGCAAGTTATTTGCGTTGTCTTAAAAATCTTATACAAAACAAA | HanXRQChr17 188291335 |
| **LAZ921.7** | CACTCATGCTCCGTTCCCTATTCTCGTTGTGCTTATATCACCACTACCAA[C/T]ATAACCGTTCAATTTGTTGGGCCATTGGACTGGGCTGGTTGGATCTCCAC | HanXRQChr17 188291213 |
| **LAZ951.11** | CTGCTGTTTGTTTTGCAGTCTCTATGCATGTGAATGATTTACGAAACTGC[A/G]CTTCTCGTTGCGGTTTGCTTGAAGTCTTTGCGTAAAAGTTCGATTTGGGA | HanXRQChr08 3516666 |
| **DEL091.16** | GCCGATCAAAAGCTCGCCGAAACCCTAGTAAGCCGAGCCGGTATGTTAGC[G/A]GCTTCACAAGCCGGCGCGATGCGAAAAGTGGCCTTATACTTCACCGAAGC | HanXRQChr08 8144737 |
| **GID131.30** | GATGTACTATGTTACCACCAGAGCTATCTCCAGCCAAGAAAATATGAGCT[C/T]TTGAGTCTTTACTCTGCAGCCACGGCCTTGAGTTGACCCATTCAAGGGCG | HanXRQChr14 128244608 |
| **LAZ951.3** | TAACATTGTTGTTGGTTGGAGTATTAACATATGGATGTTCATTCAATACA[T/G]AACTAGTTTTAGATAGAAAACTGCGAGAACCATATAAACACGTGTACCTA | HanXRQChr08 3514848 |
| **SLY061.3** | TCATACATAATGCCAACAATGAATACGACAAAACTCTCACCCACCTTCTC[A/T]TTTTCCCACCTGCCCTCTTTTCCCCCACAACAAGACAACCCCCAAATACC | HanXRQChr02 33561309 |
| **SLY061.4** | ATAATGCCAACAATGAATACGACAAAACTCTCACCCACCTTCTCATTTTC[C/T]CACCTGCCCTCTTTTCCCCCACAACAAGACAACCCCCAAATACCGCCGTT | HanXRQChr02 33561315 |
| **SLY061.5** | GAAGTTCGCCGGACTTAACATTCATCGCCACCGTCTAACCACCATCAACT[A/G]TTTCTTACTACAAAAGTTACAAACAATAATATAAAACCAAAAAATCAAAC | HanXRQChr02 33561434 |
| **SLY061.6** | AGTTACAAACAATAATATAAAACCAAAAAATCAAACAACTAATTCATCAT[C/T]TCTTTTCATTCATTGGAATTCATTTGTTACGGTTATTGTAACCCAACTTT | HanXRQChr02 33561499 |
| **SLY301.2** | TTCTCATCCAGCAGAACAGCAGTCGTCGTCTCCGGCGTGTCCGGTGAGTT[G/C]TCCGGCACCGGATCTGTTTCCGGAACCGGATCTGCGCGGATCTTCTTTTT | HanXRQChr09 164515192 |
| **SNE171.5** | GGTCGTTTATGGAAATGTTGTGTTTCTCTCTCTTGGTTTCTCTCTCTAGA[A/T]TATTGTTGTGTGTATGCAACATTGCTGCCTAAATGTTAAAATAGTGAAGT | HanXRQChr03 121233367 |
| **SNE171.6** | AACCTCCGGTACCCACCAAGCGCCAGCACCACCGACCGAACACCAACTGA[G/C]GGCGGCACAGACAACTGGCGGAAACATAAGTGTTCCCATAATGCATCGTT | HanXRQChr03 121233171 |
| **SNE171.7** | GTTGCTCCTCCTTTTCTTCAGCCGGCTCACCACCGGCCGAACACACATTA[G/A]ATACAACCTCCGGTACCCACCAAGCGCCAGCACCACCGACCGAACACCAA | HanXRQChr03 121233116 |

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|---|---|---|
| **SNE171.8** | AACCTTAACGACTTCGCCGCCGACTCACCACCACCAACCGCCCCACCGTC[A/G]CCCAACAACAACCGCTCATAATACTCCACACAAAACAACGACAACGACAA | HanXRQChr03 121232964 |
| **DELPA** | AAAGATGTGGGACGAATTCAATGAACAAGACGCCGGAGATGACGAGCTGC[T/C]AGCAGTTCTCGGCTACAAAGTCAAGTCATCCGACATGGTTGACGTCGCGC | HanXRQChr12 25042856 |
| **TAC271.2** | TTCTCTATTGTAAGTATAATTATTGTTGATCACCTTAAACATATGGTCAA[A/T]GATACACACTTGCACCTAGTTCATGTCCCGTGATAATTTTTAACACGTTT | HanXRQChr17 185043534 |
| **LAZ921.16** | GCTTCTTTAGGACTATGGTTATAGTCACCAACCCGGATTTGAGGTTGTTA[C/T]TCGTAGGGGTGCAAACGAGCCGAGCCGACTCGTTTAACATATGAAAGCTC | HanXRQChr17 188288352 |
| **LAZ921.17** | TTAGGACTATGGTTATAGTCACCAACCCGGATTTGAGGTTGTTACTCGTA[G/A]GGGTGCAAACGAGCCGAGCCGACTCGTTTAACATATGAAAGCTCGAGCTC | HanXRQChr17 188288358 |
| **LAZ921.19** | TTAGCTATTAAATATACTATAGGTTGAATATTGTATCAAATCTATTTATG[T/C]ATGTCTTAGGGTGGGCATCATCTAACAACCTAGTATGATTAACTTTTTGT | HanXRQChr17 188288872 |
| **SNE171.3** | CCCATCCACTCAAACCACCCTCATCTTACAAATACCCTCACTCACCTTCAC[CTCTCAGT/ATCT]CACATATCACAACTTCACTATTTTAACATTTAGGCAGCAATGTTGCATACA | HanXRQChr3 121233436 |
| **SNE171.4** | CCCATCCACTCAAACCACCCTCATCTTACAAATACCCTCACTCACCTTCACCTCTCAGTCACA[TATCACAACTTCA/TA]CTATTTTAACATTTAGGCAGCAATGTTGCATACACACAACAATAATCTAG | HanXRQChr3 121233424 |
| **SNE171.1** | AACAAAGAAATTGACTATTTTAGTTTTTTTCTATTTTACTATATCACAGAC[A/G]TAAAGTGAATTAAGTATTACAAAGTGTTTTTTGAACAGTTATCATCACTG | HanXRQChr3 121235040 |
| **LAZ951.19** | TATTAGCTCATTTCCTTATATATTAGTAGTTTAGTACTGTATTATCTAAGA[CTTATATAA/CTTATATTATATAA]GAGTTACATAATTTGAAATTGTTTTATAACTTGTAACTTGATGCTTTTAT | HanXRQChr08 3517527 |
| **SNE171.9** | CGGTGGGGCGGTTGGTGGTGGTGAGTCGGCGGCGAAGTCGTTAAGGTTTTT[A/G]TGTAAGACGGTGAACGTCTRAGTGTTKTAAGGTAGGGWWGAGCAAATGGT | HanXRQChr3 121232910 |
| **SNE171.10** | GTGAGTCGGCGGCGAAGTCGTTAAGGTTTTTRTGTAAGACGGTGAACGTCT[A/G]AGTGTTKTAAGGTAGGGWWGAGCAAATGGTATCYGGTATSRTATTAAACT | HanXRQChr3 121232890 |
| **SNE171.11** | GTGAGTCGGCGGCGAAGTCGTTAAGGTTTTTRTGTAAGACGGTGAACGTCT[AAGTGTTT/GAGTGTTG]TAAGGTAGGGWWGAGCAAATGGTATCYGGTATSRTATTAAACTGTATCGT | HanXRQChr3 121232883 |
| **GID071.35** | ATTATCATATGATGAAAAAAGTGAGTTATATGAATTTGTAGGATGATTAAA[GTG/GTTG]TGGATATTTCTTTCATCAAACTTACTTTAAAATATTATTCCCATTGTTAT | HanXRQChr10 21066328 |
| **GID071.37** | GATTAAAGTGTGGATATTTCTTTCATCAAACTTACTTTAAAATATTATTCC[CAT/CATTTCTAT]TGTTATGATTCGATTATGTACGATTGGTCTGGTTGAGTACTCTTCAATCG | HanXRQChr10 21066284 |
| **GID071.40** | GCAGAAATCCCCGCTCTCTTCAAGATGTCCCCCAAAACGTCTCTCAAATGG[CTA/CTAATTA]AACTCGTTTGATTTATACAGAAATAAAAAAAAATCATAAAGTTTAGTATG | HanXRQChr10 21065361 |
| **GID071.31** | CATTTCTGGGTGTTTCTGAAACAAGATGAGACACTTGTTATTGTCTGATGT[T/A]AAAAAAAAAGATGAGTGGGTTTGAAGGGGGTGTAGAGAGAGACTTCTAGA | HanXRQChr10 21066850 |
| **GID131.4** | CAGGGCCACATATTCCTGAAACTACCGTTGGGACCTTGACGCCAACTCTAA[AAACCA/AA]ACTAAGGAAAAACTTAAAACAGACACGATAGAAGATCATTGTTGTTGTGC | HanXRQchr14 128247602 |
| **GID131.8** | GCAAGACAAAACTAGTGACTCACATAAAAAGCATGATGGATTGGCTTATCC[CGGGAC/CGGAC]TTAAGGATGCCACACGGAGATCAAAAGATAACTTCGTGACATTAGCATCC | HanXRQchr14 128247312 |
| **GID131.11** | AATTTTAATATCTTTAATGATATGGATAAACACGTTCCACTTTTACAAGCA[ACG/AG]GTGTTCGAATCCTTAATTTTTGAAACAAAAAAATATCAAATCCATAAAAC | HanXRQchr14 128247138 |
| **GID131.12** | CCACTTTTACAAGCAACGGTGTTCGAATCCTTAATTTTTGAAACAAAAAAA[TAT/TGAT]CAAATCCATAAAACATGCATACCACAAGTATCATTCATGTAATTAACTCT | HanXRQchr14 128247102 |
| **GID131.23** | AGAAATCACGTTACGCATGCTGTGTGTTAAATGAAATGTAACAATGAAGTT[ATGTGAAGT/AT]TGTGAACTGGTTTAGGTTATGAATTAGGTTATTTAAGTTGTTATTTGTTC | HanXRQchr14 128245463 |
| **GID131.26** | GGTTACGAAATAGGTGATTGAAGTTGCTATTCGTTCGATTTTGACGGAAAC[ATTAGGGATTTAGCCTT/AT]TAGGGTTTATGTTCTGAAAATTTTCATTTGTTTTTGTGCGTAGAAAGTGG | HanXRQchr14 128245185 |
| **GID131.40** | GCATATGTGGTGTTGAGAACTCTATATTATGTGTATACGTGTTTTAAGACC[CATATATATATG/CATATATATG]TATATATATGTTTGGTAAGTGCCGAATTTACTCCCTTATCGTCATTTTAT | HanXRQchr14 128243756 |
| **GID131.41** | GCATTTTGGGTTTTAATAAGATATAAGATATGATTCTTACTTTTTTTGGTA[GCAC/TCAT]GTTGTTCCACTACTACCAGTAAATGGAACCTTGCATGTTTTCCCACTTGC | HanXRQchr14 128243638 |

**Supplementary Table A 29:** GLM data for the traits plant height (PlantHt) and petiole angle (PetAngle) of KASP marker analysis of the combined association panel (n = 445)

| TRAIT | MARKER | CHR | POS | MARKER_F | P | PERM_P | MARKER_RSQ | ADD_F | ADD_P | DOM_F | DOM_P | MARKER_DF | MARKER_MS | ERROR_DF | ERROR_MS | MODEL_DF | MODEL_MS | MINOR OBS |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **PLANTHT** | SNE171.5 | 3 | 104934540 | 6.99963 | 0.00119 | 1 | 0.05891 | 2.21461 | 0.13849 | 11.65139 | 7.9618E-4 | 2 | 9724.63822 | 176 | 1389.30698 | 7 | 12234.05798 | 70 |
| **PLANTHT** | GID131.39 | 14 | 127164489 | 3.86246 | 0.00245 | 1 | 0.08124 | 4.78838 | 0.00315 | 2.35815 | 0.09774 | 5 | 5052.71783 | 167 | 1308.15987 | 10 | 9252.23637 | 49 |
| **PLANTHT** | DEL091.16 | 8 | 12264599 | 4.18403 | 0.00298 | 1 | 0.07677 | 5.55893 | 0.00117 | 0.14569 | 0.70319 | 4 | 5871.1301 | 164 | 1403.22411 | 9 | 8418.9693 | 48 |
| **PLANTHT** | GID131.27 | 14 | 127163432 | 3.43497 | 0.00553 | 1 | 0.0717 | 4.24799 | 0.00632 | 2.13249 | 0.12166 | 5 | 4748.61884 | 172 | 1382.43511 | 10 | 9335.75987 | 48 |
| **PLANTHT** | GID131.3 | 14 | 127160706 | 3.27098 | 0.00757 | 1 | 0.06965 | 3.90483 | 0.00989 | 2.23692 | 0.10988 | 5 | 4560.36908 | 172 | 1394.19204 | 10 | 8757.52322 | 58 |
| **PLANTHT** | SNE171.7 | 3 | 104934791 | 3.51989 | 0.00864 | 1 | 0.0603 | 2.87189 | 0.03786 | 5.25328 | 0.02311 | 4 | 4933.75456 | 173 | 1401.67897 | 9 | 9422.57536 | 59 |
| **PLANTHT** | DEL091.9 | 8 | 12264128 | 3.49637 | 0.00896 | 1 | 0.05914 | 2.35973 | 0.0732 | 6.67666 | 0.01059 | 4 | 4932.45621 | 174 | 1410.73623 | 9 | 9791.62559 | 52 |
| **PLANTHT** | DEL091.7 | 8 | 12264064 | 4.69365 | 0.01048 | 1 | 0.04549 | 5.22745 | 0.02356 | 4.05866 | 0.04565 | 2 | 7171.05099 | 157 | 1527.8183 | 7 | 10774.54801 | 60 |
| **PLANTHT** | SNE171.8 | 3 | 104934943 | 3.10802 | 0.01679 | 1 | 0.05351 | 2.66745 | 0.04928 | 4.27975 | 0.04005 | 4 | 4379.3892 | 174 | 1409.06212 | 9 | 9134.01394 | 58 |
| **PLANTHT** | LAZ921.16 | 17 | 206483470 | 4.10339 | 0.01813 | 1 | 0.03612 | 0.00501 | 0.94367 | 8.20157 | 0.0047 | 2 | 5845.10443 | 175 | 1424.45648 | 7 | 10630.50514 | 34 |
| **PLANTHT** | DEL091.8 | 8 | 12264103 | 2.7209 | 0.02158 | 1 | 0.05921 | 2.71499 | 0.04643 | 2.65112 | 0.07351 | 5 | 3866.7309 | 169 | 1421.12383 | 10 | 8634.24008 | 52 |
| **PLANTHT** | LAZ921.19 | 17 | 206483990 | 3.48553 | 0.03295 | 1 | 0.03282 | 0.01995 | 0.88785 | 6.95038 | 0.0092 | 2 | 5106.48687 | 162 | 1465.05401 | 7 | 10549.92306 | 29 |
| **PLANTHT** | DEL901.11 | 12 | 32213328 | 2.06082 | 0.07262 | 1 | 0.04517 | 3.42806 | 0.01839 | 0.0652 | 0.9369 | 5 | 2949.0844 | 172 | 1431.02521 | 10 | 8031.59263 | 51 |
| **PLANTHT** | DEL091.33 | 8 | 12266012 | 2.17149 | 0.09432 | 1 | 0.04007 | 2.17149 | 0.09432 | NaN | NaN | 3 | 3561.68244 | 134 | 1640.20058 | 8 | 5856.26444 | 41 |
| **PLANTHT** | SLY061.6 | 2 | 39413802 | 2.33084 | 0.10028 | 1 | 0.02139 | 1.97364 | 0.16185 | 2.669 | 0.10415 | 2 | 3386.42709 | 172 | 1452.87659 | 7 | 9530.02912 | 56 |
| **PLANTHT** | LAZ921.7 | 17 | 206482328 | 2.17514 | 0.11854 | 1 | 0.03392 | 3.37998 | 0.06872 | 0.97119 | 0.32659 | 2 | 3889.01488 | 108 | 1787.93919 | 7 | 5169.02067 | 4 |
| **PLANTHT** | GID131.2 | 14 | 127160680 | 1.6868 | 0.15516 | 1 | 0.03011 | 2.2191 | 0.08764 | 0.12347 | 0.72573 | 4 | 2464.34851 | 173 | 1460.95654 | 9 | 8292.30899 | 59 |
| **PLANTHT** | DEL901.10 | 12 | 32213076 | 1.74586 | 0.17754 | 1 | 0.01549 | 1.15168 | 0.28467 | 2.33128 | 0.12861 | 2 | 2554.85426 | 174 | 1463.37598 | 7 | 10759.92269 | 53 |
| **PLANTHT** | GID131.9 | 14 | 127161170 | 1.59241 | 0.17923 | 1 | 0.03317 | 1.90294 | 0.13152 | 0.67319 | 0.41324 | 4 | 2294.62051 | 150 | 1440.97154 | 9 | 6733.24939 | 39 |
| **PLANTHT** | SLY061.5 | 2 | 39413737 | 1.5288 | 0.2198 | 1 | 0.01426 | 0.05897 | 0.80843 | 2.99794 | 0.08521 | 2 | 2261.54272 | 168 | 1479.2893 | 7 | 9796.60798 | 61 |
| **PLANTHT** | GID071.24 | 10 | 28113168 | 1.47977 | 0.23054 | 1 | 0.01338 | 0.56879 | 0.45175 | 2.38624 | 0.12422 | 2 | 2190.91231 | 174 | 1480.57943 | 7 | 9964.77751 | 39 |
| **PLANTHT** | SLY061.3 | 2 | 39413612 | 1.37828 | 0.25473 | 1 | 0.0125 | 1.39297 | 0.2395 | 1.36073 | 0.245 | 2 | 2023.49519 | 175 | 1468.13202 | 7 | 9538.61678 | 58 |
| **PLANTHT** | GID131.30 | 14 | 127163764 | 1.32542 | 0.25556 | 1 | 0.02926 | 1.14608 | 0.33203 | 1.58291 | 0.20835 | 5 | 1937.58523 | 172 | 1461.86132 | 10 | 7961.74699 | 56 |
| **PLANTHT** | GID131.7 | 14 | 127160942 | 1.14073 | 0.33609 | 1 | 0.02429 | 1.14073 | 0.33609 | NaN | NaN | 3 | 2054.64768 | 107 | 1801.16681 | 8 | 7627.23876 | 34 |
| **PLANTHT** | DEL091.27 | 8 | 12265422 | 1.09666 | 0.35295 | 1 | 0.01996 | 1.09666 | 0.35295 | NaN | NaN | 3 | 1466.43196 | 133 | 1337.17728 | 8 | 5314.20235 | 45 |
| **PLANTHT** | LAZ921.17 | 17 | 206483476 | 1.00082 | 0.36981 | 1 | 0.0096 | 0.03604 | 0.84967 | 1.9654 | 0.16283 | 2 | 1380.82706 | 164 | 1379.69232 | 7 | 8764.02902 | 44 |
| **PLANTHT** | DEL801.17 | 17 | 194809363 | 0.92537 | 0.43254 | 1 | 0.0241 | 1.33614 | 0.26866 | 0.13279 | 0.71653 | 3 | 1216.08449 | 79 | 1314.16056 | 7 | 6790.00402 | 28 |
| **PLANTHT** | DEL091.49 | 8 | 12266939 | 0.90161 | 0.44185 | 1 | 0.01307 | 0.90161 | 0.44185 | NaN | NaN | 3 | 1250.80335 | 159 | 1387.29795 | 7 | 9514.01324 | 54 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **PLANTHT** | GID071.16 | 10 | 28112657 | 0.92952 | 0.44815 | 1 | 0.01671 | 1.24042 | 0.29663 | 0.01781 | 0.894 | 4 | 1393.72222 | 173 | 1499.40476 | 9 | 8241.09323 | 46 |
| **PLANTHT** | DEL091.18 | 8 | 12264635 | 0.67024 | 0.51294 | 1 | 0.00646 | 1.0621 | 0.3042 | 0.28286 | 0.59553 | 2 | 998.28108 | 169 | 1489.44011 | 7 | 8166.16145 | 43 |
| **PLANTHT** | DEL091.25 | 8 | 12265054 | 0.62581 | 0.53603 | 1 | 0.0058 | 1.19887 | 0.27506 | 0.05924 | 0.80798 | 2 | 885.38186 | 173 | 1414.76844 | 7 | 8633.61798 | 43 |
| **PLANTHT** | DEL901.6 | 12 | 32212556 | 0.70882 | 0.58694 | 1 | 0.01293 | 0.95049 | 0.41756 | 3.9157E-4 | 0.98424 | 4 | 1075.30961 | 171 | 1517.04286 | 9 | 8149.98916 | 52 |
| **PLANTHT** | DEL801.4 | 17 | 194808128 | 0.74008 | 0.59444 | 1 | 0.0172 | 0.78042 | 0.50639 | 0.6839 | 0.50604 | 5 | 1134.72242 | 169 | 1533.24004 | 10 | 7074.9828 | 52 |
| **PLANTHT** | LAZ921.44 | 17 | 206486453 | 0.52113 | 0.59513 | 1 | 0.00728 | 0.46859 | 0.49489 | 0.57523 | 0.4496 | 2 | 953.70865 | 126 | 1830.09495 | 7 | 4462.79841 | 56 |
| **PLANTHT** | LAZ921.42 | 17 | 206486407 | 0.52087 | 0.59518 | 1 | 0.00632 | 0.78563 | 0.37697 | 0.26032 | 0.61072 | 2 | 918.06814 | 137 | 1762.57821 | 7 | 7019.86005 | 55 |
| **PLANTHT** | DEL901.3 | 12 | 32211968 | 0.7252 | 0.60539 | 1 | 0.01647 | 1.2099 | 0.30767 | 0.0185 | 0.98167 | 5 | 1078.58548 | 173 | 1487.29155 | 10 | 7008.14961 | 51 |
| **PLANTHT** | DEL901.4 | 12 | 32212028 | 0.7158 | 0.61237 | 1 | 0.01644 | 1.19429 | 0.31351 | 0.0184 | 0.98177 | 5 | 1074.7484 | 171 | 1501.45595 | 10 | 7003.45268 | 51 |
| **PLANTHT** | LAZ951.8 | 8 | 7809138 | 0.24773 | 0.61931 | 1 | 0.00114 | 0.24773 | 0.61931 | NaN | NaN | 1 | 368.07279 | 172 | 1485.7844 | 6 | 11290.5417 | 27 |
| **PLANTHT** | DEL801.5 | 17 | 194808137 | 0.5793 | 0.62952 | 1 | 0.00912 | 0.09035 | 0.91366 | 1.55651 | 0.21422 | 3 | 843.8116 | 143 | 1456.59634 | 8 | 8658.42922 | 52 |
| **PLANTHT** | DEL801.3 | 17 | 194808097 | 0.64049 | 0.6691 | 1 | 0.01469 | 0.7404 | 0.52931 | 0.49708 | 0.60918 | 5 | 975.43813 | 171 | 1522.96261 | 10 | 7151.05365 | 52 |
| **PLANTHT** | GID071.34 | 10 | 28114759 | 0.50219 | 0.73416 | 1 | 0.00929 | 0.64794 | 0.58526 | 0.07534 | 0.78404 | 4 | 752.28475 | 172 | 1498.00206 | 9 | 7354.81524 | 49 |
| **PLANTHT** | DEL901.2 | 12 | 32211812 | 0.46454 | 0.76169 | 1 | 0.00836 | 0.62208 | 0.60161 | 0.00249 | 0.96023 | 4 | 697.45374 | 175 | 1501.38654 | 9 | 7879.37227 | 52 |
| **PLANTHT** | DEL901.9 | 12 | 32212719 | 0.46285 | 0.76293 | 1 | 0.00836 | 0.61869 | 0.60378 | 0.00587 | 0.939 | 4 | 696.25151 | 174 | 1504.27073 | 9 | 7950.12572 | 52 |
| **PLANTHT** | DEL091.3 | 8 | 12263870 | 0.23072 | 0.7942 | 1 | 0.00208 | 0.19516 | 0.65919 | 0.2671 | 0.60594 | 2 | 347.06592 | 176 | 1504.24317 | 7 | 9843.01636 | 41 |
| **PLANTHT** | LAZ921.43 | 17 | 206486412 | 0.22798 | 0.79654 | 1 | 0.00346 | 0.02075 | 0.88575 | 0.43532 | 0.51086 | 2 | 386.88897 | 103 | 1697.03779 | 6 | 8116.68311 | 34 |
| **PLANTHT** | DEL091.47 | 8 | 12266830 | 0.46258 | 0.80368 | 1 | 0.01105 | 0.71386 | 0.54499 | 0.09712 | 0.9075 | 5 | 702.58947 | 167 | 1518.83798 | 10 | 6416.10462 | 36 |
| **PLANTHT** | SNE171.1 | 3 | 104932867 | 0.2077 | 0.81267 | 1 | 0.00209 | 0.11489 | 0.73509 | 0.30101 | 0.58402 | 2 | 298.88368 | 159 | 1439.02323 | 7 | 8250.02749 | 15 |
| **PLANTHT** | LAZ921.41 | 17 | 206486337 | 0.19327 | 0.82456 | 1 | 0.003 | 0.24443 | 0.62206 | 0.14411 | 0.70501 | 2 | 352.49461 | 104 | 1823.85619 | 6 | 7491.31253 | 39 |
| **PLANTHT** | LAZ951.3 | 8 | 7807503 | 0.16024 | 0.85209 | 1 | 0.00196 | 0.30422 | 0.58212 | 0.01837 | 0.89237 | 2 | 281.65147 | 141 | 1757.64544 | 7 | 5751.5253 | 46 |
| **PLANTHT** | DEL901.5 | 12 | 32212178 | 0.38681 | 0.85739 | 1 | 0.00873 | 0.64874 | 0.58474 | 0.00498 | 0.99503 | 5 | 578.5053 | 173 | 1495.58187 | 10 | 7240.82867 | 52 |
| **PLANTHT** | DEL801.24 | 17 | 194810797 | 0.30249 | 0.87596 | 1 | 0.00609 | 0.4 | 0.75319 | 0.01746 | 0.89504 | 4 | 433.0319 | 156 | 1431.57672 | 8 | 7628.22815 | 36 |
| **PLANTHT** | DEL091.10 | 8 | 12264206 | 0.1306 | 0.87768 | 1 | 0.00162 | 0.25723 | 0.61284 | 0.00581 | 0.93935 | 2 | 233.27493 | 137 | 1786.22985 | 7 | 6161.00896 | 27 |
| **PLANTHT** | DEL091.48 | 8 | 12266863 | 0.21968 | 0.88264 | 1 | 0.00313 | 0.32536 | 0.72272 | 0.0121 | 0.91253 | 3 | 333.90275 | 169 | 1519.95395 | 8 | 7951.72556 | 38 |
| **PLANTHT** | DEL091.15 | 8 | 12264512 | 0.26905 | 0.89756 | 1 | 0.0052 | 0.36025 | 0.78179 | 0.00189 | 0.96535 | 4 | 414.34692 | 167 | 1540.01387 | 9 | 6866.50479 | 40 |
| **PLANTHT** | DEL091.42 | 8 | 12266417 | 0.19701 | 0.96327 | 1 | 0.00499 | 0.32978 | 0.80382 | 0.00391 | 0.9961 | 5 | 309.15975 | 161 | 1569.22635 | 10 | 5712.77851 | 36 |
| **PETANGLE** | GID071.16 | 10 | 28112657 | 7.49503 | 1.37E-05 | 1 | 0.14711 | 8.61536 | 2.3065E-5 | 3.72874 | 0.05512 | 4 | 497.11259 | 173 | 66.32559 | 9 | 226.94006 | 46 |
| **PETANGLE** | DEL091.27 | 8 | 12265422 | 8.10348 | 5.36E-05 | 1 | 0.15434 | 8.10348 | 5.3607E-5 | NaN | NaN | 3 | 543.84549 | 133 | 67.11259 | 8 | 205.63433 | 45 |
| **PETANGLE** | DEL091.48 | 8 | 12266863 | 7.91241 | 5.71E-05 | 1 | 0.12221 | 9.32036 | 1.4426E-4 | 4.69171 | 0.03171 | 3 | 531.86545 | 169 | 67.21913 | 8 | 212.02671 | 38 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **PETANGLE** | DEL091.47 | 8 | 12266830 | 5.76385 | 6.18E-05 | 1 | 0.14636 | 6.59737 | 3.0487E-4 | 4.14522 | 0.0175 | 5 | 392.20609 | 167 | 68.04589 | 10 | 203.53472 | 36 |
| **PETANGLE** | GID071.24 | 10 | 28113168 | 9.80574 | 9.22E-05 | 1 | 0.10092 | 18.42694 | 2.9182E-5 | 1.16696 | 0.28152 | 2 | 669.85645 | 174 | 68.31269 | 7 | 198.44082 | 39 |
| **PETANGLE** | DEL901.11 | 12 | 32213328 | 4.47286 | 7.41E-04 | 1 | 0.1145 | 6.21208 | 4.9421E-4 | 1.78044 | 0.17166 | 5 | 311.53101 | 172 | 69.64919 | 10 | 162.39562 | 51 |
| **PETANGLE** | DEL091.15 | 8 | 12264512 | 4.44862 | 0.00193 | 1 | 0.09575 | 4.90599 | 0.00271 | 2.90924 | 0.08993 | 4 | 320.75292 | 167 | 72.10168 | 9 | 150.94318 | 40 |
| **PETANGLE** | DEL901.10 | 12 | 32213076 | 6.47759 | 0.00193 | 1 | 0.06888 | 12.15855 | 6.1785E-4 | 0.80985 | 0.36941 | 2 | 467.16463 | 174 | 72.12012 | 7 | 145.0684 | 53 |
| **PETANGLE** | DEL901.3 | 12 | 32211968 | 3.90064 | 0.00224 | 1 | 0.10082 | 5.03707 | 0.00226 | 2.10093 | 0.12545 | 5 | 274.30328 | 173 | 70.32259 | 10 | 143.82742 | 51 |
| **PETANGLE** | DEL901.4 | 12 | 32212028 | 3.86624 | 0.00241 | 1 | 0.10113 | 4.97955 | 0.00244 | 2.10118 | 0.12546 | 5 | 273.95379 | 171 | 70.85802 | 10 | 142.75418 | 51 |
| **PETANGLE** | DEL091.25 | 8 | 12265054 | 6.03207 | 0.00294 | 1 | 0.06478 | 11.27721 | 9.6391E-4 | 0.79989 | 0.37237 | 2 | 426.0121 | 173 | 70.62458 | 7 | 133.52993 | 43 |
| **PETANGLE** | GID071.34 | 10 | 28114759 | 4.17987 | 0.00296 | 1 | 0.08822 | 4.1642 | 0.00706 | 4.00954 | 0.04681 | 4 | 298.09739 | 172 | 71.31741 | 9 | 138.86005 | 49 |
| **PETANGLE** | DEL901.2 | 12 | 32211812 | 4.13849 | 0.00315 | 1 | 0.08601 | 4.5615 | 0.00419 | 2.73459 | 0.09999 | 4 | 292.66696 | 175 | 70.71837 | 9 | 137.27863 | 52 |
| **PETANGLE** | DEL901.9 | 12 | 32212719 | 4.13911 | 0.00315 | 1 | 0.08644 | 4.54625 | 0.00428 | 2.77906 | 0.0973 | 4 | 293.90591 | 174 | 71.00696 | 9 | 138.31402 | 52 |
| **PETANGLE** | DEL091.42 | 8 | 12266417 | 3.66921 | 0.00359 | 1 | 0.1016 | 4.93567 | 0.00263 | 1.70544 | 0.18496 | 5 | 253.90358 | 161 | 69.19839 | 10 | 135.39605 | 36 |
| **PETANGLE** | DEL901.6 | 12 | 32212556 | 4.01589 | 0.00387 | 1 | 0.08529 | 4.35052 | 0.00554 | 2.87008 | 0.09206 | 4 | 285.5678 | 171 | 71.10952 | 9 | 136.94493 | 52 |
| **PETANGLE** | DEL091.18 | 8 | 12264635 | 5.39935 | 0.00533 | 1 | 0.05979 | 10.78324 | 0.00124 | 0.07418 | 0.78568 | 2 | 396.05448 | 169 | 73.35231 | 7 | 121.71612 | 43 |
| **PETANGLE** | DEL901.5 | 12 | 32212178 | 3.28652 | 0.00734 | 1 | 0.08632 | 4.50044 | 0.00455 | 1.43228 | 0.24158 | 5 | 234.95278 | 173 | 71.4899 | 10 | 124.16774 | 52 |
| **PETANGLE** | LAZ951.8 | 8 | 7809138 | 6.19749 | 0.01374 | 1 | 0.03467 | 6.19749 | 0.01374 | NaN | NaN | 1 | 462.95397 | 172 | 74.70021 | 6 | 83.9534 | 27 |
| **PETANGLE** | SNE171.5 | 3 | 104934540 | 4.19262 | 0.01664 | 1 | 0.04529 | 8.04834 | 0.00509 | 0.36573 | 0.54612 | 2 | 306.24133 | 176 | 73.04298 | 7 | 95.43406 | 70 |
| **PETANGLE** | DEL091.3 | 8 | 12263870 | 3.63159 | 0.02848 | 1 | 0.03947 | 6.75461 | 0.01014 | 0.52664 | 0.46899 | 2 | 266.78257 | 176 | 73.46163 | 7 | 84.00813 | 41 |
| **PETANGLE** | DEL091.49 | 8 | 12266939 | 2.83736 | 0.03988 | 1 | 0.0505 | 2.83736 | 0.03988 | NaN | NaN | 3 | 215.53928 | 159 | 75.96471 | 7 | 103.72197 | 54 |
| **PETANGLE** | DEL801.3 | 17 | 194808097 | 2.35389 | 0.04263 | 1 | 0.06403 | 1.46433 | 0.22601 | 3.62166 | 0.02881 | 5 | 168.26178 | 171 | 71.48238 | 10 | 91.67989 | 52 |
| **PETANGLE** | SNE171.7 | 3 | 104934791 | 2.48733 | 0.04524 | 1 | 0.05412 | 3.33555 | 0.02075 | 1.5178E-4 | 0.99018 | 4 | 184.04958 | 173 | 73.9949 | 9 | 89.16661 | 59 |
| **PETANGLE** | DEL091.33 | 8 | 12266012 | 2.68958 | 0.0489 | 1 | 0.05417 | 2.68958 | 0.0489 | NaN | NaN | 3 | 181.11503 | 134 | 67.33957 | 8 | 125.76326 | 41 |
| **PETANGLE** | LAZ921.19 | 17 | 206483990 | 2.66835 | 0.07241 | 1 | 0.03172 | 0.67278 | 0.41328 | 4.64887 | 0.03255 | 2 | 208.69527 | 162 | 78.21121 | 7 | 70.04397 | 29 |
| **PETANGLE** | SNE171.8 | 3 | 104934943 | 2.18559 | 0.07254 | 1 | 0.04761 | 2.90445 | 0.03628 | 0.07508 | 0.78441 | 4 | 161.90597 | 174 | 74.07873 | 9 | 79.37574 | 58 |
| **PETANGLE** | DEL801.4 | 17 | 194808128 | 2.02834 | 0.07708 | 1 | 0.05635 | 1.4687 | 0.22485 | 2.82088 | 0.06236 | 5 | 148.12436 | 169 | 73.02749 | 10 | 80.20149 | 52 |
| **PETANGLE** | LAZ921.16 | 17 | 206483470 | 2.33089 | 0.10022 | 1 | 0.02582 | 0.48467 | 0.48724 | 4.16839 | 0.04269 | 2 | 175.60045 | 175 | 75.33629 | 7 | 59.96673 | 34 |
| **PETANGLE** | GID131.7 | 14 | 127160942 | 2.1053 | 0.10386 | 1 | 0.05538 | 2.1053 | 0.10386 | NaN | NaN | 3 | 163.91851 | 107 | 77.86 | 8 | 68.49756 | 34 |
| **PETANGLE** | DEL801.24 | 17 | 194810797 | 1.85361 | 0.12135 | 1 | 0.04526 | 1.42788 | 0.23672 | 3.0742 | 0.08151 | 4 | 145.38898 | 156 | 78.4356 | 8 | 76.59377 | 36 |
| **PETANGLE** | DEL091.8 | 8 | 12264103 | 1.64918 | 0.14964 | 1 | 0.04627 | 0.47066 | 0.70313 | 3.39717 | 0.03577 | 5 | 125.39127 | 169 | 76.03247 | 10 | 69.99063 | 52 |
| **PETANGLE** | GID131.27 | 14 | 127163432 | 1.60816 | 0.16033 | 1 | 0.04447 | 1.97459 | 0.11956 | 1.05658 | 0.34989 | 5 | 120.22151 | 172 | 74.75728 | 10 | 65.73975 | 48 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **PETANGLE** | SLY061.5 | 2 | 39413737 | 1.72994 | 0.18044 | 1 | 0.02008 | 0.00959 | 0.92211 | 3.45016 | 0.065 | 2 | 135.19986 | 168 | 78.15271 | 7 | 48.41198 | 61 |
| **PETANGLE** | LAZ921.7 | 17 | 206482328 | 1.44153 | 0.24108 | 1 | 0.02503 | 1.98316 | 0.1619 | 0.90168 | 0.34445 | 2 | 114.67542 | 108 | 79.5514 | 7 | 81.41383 | 4 |
| **PETANGLE** | GID131.9 | 14 | 127161170 | 1.35147 | 0.25361 | 1 | 0.03467 | 1.46625 | 0.22605 | 1.00695 | 0.31725 | 4 | 93.72931 | 150 | 69.35337 | 9 | 45.48827 | 39 |
| **PETANGLE** | DEL091.7 | 8 | 12264064 | 1.33703 | 0.2656 | 1 | 0.01667 | 2.53403 | 0.11341 | 0.15361 | 0.69564 | 2 | 96.31478 | 157 | 72.03623 | 7 | 34.84456 | 60 |
| **PETANGLE** | LAZ921.44 | 17 | 206486453 | 1.31655 | 0.27172 | 1 | 0.02026 | 0.31658 | 0.57466 | 2.31325 | 0.13078 | 2 | 94.57704 | 126 | 71.83711 | 7 | 40.55258 | 56 |
| **PETANGLE** | DEL091.9 | 8 | 12264128 | 1.29571 | 0.27359 | 1 | 0.02879 | 1.03276 | 0.37947 | 2.06568 | 0.15244 | 4 | 97.94938 | 174 | 75.59538 | 9 | 50.79783 | 52 |
| **PETANGLE** | GID131.3 | 14 | 127160706 | 1.17032 | 0.32574 | 1 | 0.03277 | 1.22414 | 0.30249 | 1.08776 | 0.33928 | 5 | 88.53033 | 172 | 75.64596 | 10 | 49.87748 | 58 |
| **PETANGLE** | DEL091.16 | 8 | 12264599 | 1.15914 | 0.33086 | 1 | 0.0273 | 0.74049 | 0.52933 | 2.39632 | 0.12355 | 4 | 90.28274 | 164 | 77.88746 | 9 | 50.26842 | 48 |
| **PETANGLE** | GID131.2 | 14 | 127160680 | 1.0686 | 0.37364 | 1 | 0.02401 | 1.01903 | 0.38562 | 1.21353 | 0.27216 | 4 | 81.09812 | 173 | 75.89228 | 9 | 42.27952 | 59 |
| **PETANGLE** | DEL801.5 | 17 | 194808137 | 0.98859 | 0.40008 | 1 | 0.01998 | 1.45989 | 0.23568 | 0.06494 | 0.79922 | 3 | 74.42732 | 143 | 75.28652 | 8 | 51.42457 | 52 |
| **PETANGLE** | LAZ921.42 | 17 | 206486407 | 0.89206 | 0.41218 | 1 | 0.01276 | 1.46022 | 0.22896 | 0.33098 | 0.56603 | 2 | 65.45879 | 137 | 73.37907 | 7 | 29.38798 | 55 |
| **PETANGLE** | DEL801.17 | 17 | 194809363 | 0.93328 | 0.42869 | 1 | 0.0322 | 1.03949 | 0.35836 | 0.72794 | 0.39613 | 3 | 67.24129 | 79 | 72.04822 | 7 | 81.92216 | 28 |
| **PETANGLE** | SLY061.6 | 2 | 39413802 | 0.82261 | 0.441 | 1 | 0.00944 | 0.30069 | 0.58416 | 1.34393 | 0.24795 | 2 | 63.09801 | 172 | 76.70452 | 7 | 24.146 | 56 |
| **PETANGLE** | LAZ921.17 | 17 | 206483476 | 0.69932 | 0.4984 | 1 | 0.00841 | 0.19557 | 0.6589 | 1.20283 | 0.27436 | 2 | 55.77522 | 164 | 79.75584 | 7 | 27.15143 | 44 |
| **PETANGLE** | LAZ921.43 | 17 | 206486412 | 0.69743 | 0.5002 | 1 | 0.01316 | 0.26518 | 0.60768 | 1.12935 | 0.2904 | 2 | 49.78135 | 103 | 71.3785 | 6 | 35.37974 | 34 |
| **PETANGLE** | GID131.39 | 14 | 127164489 | 0.87276 | 0.50071 | 1 | 0.02531 | 1.39705 | 0.24549 | 0.10844 | 0.89729 | 5 | 66.17733 | 167 | 75.82508 | 10 | 41.28291 | 49 |
| **PETANGLE** | LAZ921.41 | 17 | 206486337 | 0.66886 | 0.51448 | 1 | 0.01247 | 0.1485 | 0.70076 | 1.18895 | 0.27806 | 2 | 44.91197 | 104 | 67.14745 | 6 | 37.04183 | 39 |
| **PETANGLE** | GID131.30 | 14 | 127163764 | 0.76401 | 0.57693 | 1 | 0.02162 | 0.34128 | 0.7955 | 1.39578 | 0.25043 | 5 | 58.84787 | 172 | 77.02484 | 10 | 36.07216 | 56 |
| **PETANGLE** | LAZ951.3 | 8 | 7807503 | 0.54927 | 0.5786 | 1 | 0.00761 | 0.88885 | 0.34739 | 0.21461 | 0.64389 | 2 | 36.99363 | 141 | 67.35028 | 7 | 32.38159 | 46 |
| **PETANGLE** | SLY061.3 | 2 | 39413612 | 0.46179 | 0.63092 | 1 | 0.00522 | 0.43545 | 0.51019 | 0.48938 | 0.48513 | 2 | 35.52847 | 175 | 76.93711 | 7 | 19.94617 | 58 |
| **PETANGLE** | DEL091.10 | 8 | 12264206 | 0.41403 | 0.66181 | 1 | 0.0058 | 0.2168 | 0.64222 | 0.61187 | 0.43544 | 2 | 29.05411 | 137 | 70.17395 | 7 | 57.0941 | 27 |
| **PETANGLE** | SNE171.1 | 3 | 104932867 | 0.39931 | 0.67145 | 1 | 0.00497 | 0.2082 | 0.6488 | 0.59096 | 0.44319 | 2 | 31.25792 | 159 | 78.27916 | 7 | 17.74965 | 15 |

# Acknowledgements

“The world is thankless, many say. I haven't yet found them to be ungrateful when you know how to do something for them in the right way.“ - *Johann Wolfgang von Goethe*

here is probably no adequate way to express my gratitude to all those who have contributed, both big and small, to the successful completion of this thesis. However, I can try to put it into words.

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# Honour declaration

I hereby certify that I will complete the submitted doctoral thesis independently and without unauthorized outside help and only with the help that I gave in my doctoral thesis specified. All passages in the text that are published literally or analogously scriptures are taken, and all information based on oral information are identified as such. In the examinations I have carried out and mentioned in the doctoral thesis, I have the principles of the good scientific practice adhered to.

location, date

signature

# Curriculum vitae

## Personal Information

Yves Sprycha

Birth date: 02/04/1990 Berlin, Germany

## Education

| | |
|---|---|
| 02/2017 – 11/2020 | University of Rostock<br>Ph.D. student<br>Institute for Biological Sciences, Department of Plant Genetics |
| 10/2012 – 10/2014 | University of Rostock<br>Master of Science<br>Diversity and Evolution |
| 10/2009 – 09/2012 | University of Rostock<br>Bachelor of Science<br>Biological Sciences |
| 08/1996 – 07/2009 | Freie Waldorfschule Berlin Südost<br>High School Diploma |

## Experiences

| | |
|---|---|
| Since 11/2022 | Scientific Associate at Julius Kühn-Institut (JKI)<br>Federal Research Centre for Cultivated Plants |
| 06/2021 – 10/2022 | Coordinator for tissue donation<br>Transplantation Medicine Mecklenburg-West Pomerania |
| 02/2017 – 11/2020 | Scientific Associate at University of Rostock<br>Institute for Biological Sciences, Department of Plant Genetics |
| 12/2015 – 02/2017 | Project collaborator in the field of "Ornithology and Benthic Organisms and Habitats" at the Institute for Applied Ecosystem Research (IfAÖ) |
| 06/2015 – 09/2015 | Student assistant at the University of Rostock<br>Institute for Biological Sciences, Department of Plant Genetics |
| 01/2015 – 05/2015 | Student assistant at CENTOGENE Rostock<br>Department Primerdesign |
| 09/2014 – 11/2014 | Student assistant at the University of Rostock<br>Institute for Biological Sciences, Department of Plant Genetics |

**Publications**

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