

## Phenotypic stability and genome wide association study of late blight resistance in potato genotypes adapted to the tropical highlands

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## Abstract

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Potato genotypes from a breeding population adapted to tropical highlands were analyzed for the stability of the late blight resistance and also for marker-phenotype association. We harmonized the historical evaluation data consisting of observations spanning six years from two field sites utilizing a resistance scale (sAUDPC) constructed by comparing the area under the disease progress curve (AUDPC) values of 172 genotypes with that of a susceptible control variety Yungay. In total, 70 potato genotypes had a coefficient of variability (CV) less than 0.5 and were considered stable across the environments tested. A principal component analysis (PCA) demonstrated that the ensemble of experiments form two distinct groups that reflect the stability of genotypes resistance to late blight. *Phytophthora infestans* isolates present in the experimental fields belong to the EC-1 clonal lineage and show variation in virulence beyond the concept of the avirulences determined by the conventionally used R1-R11 differential set. A Single Nucleotide Polymorphism (SNP) marker on chromosome 9 was associated with late blight resistance and linked to instability. Genotypes with either AACC or AAAC combinations for this SNP were highly resistant only in some environments, while the genotypes with AAAA combination had more moderate levels of resistance but were stable across environments.

## Introduction

Late blight caused by the oomycete *Phytophthora infestans* is one of the main constraints for potato production worldwide, causing yearly losses estimated at over € 10 billion (17). Host resistance would be the most effective way to control the disease, but efforts in this area have been hampered by the rapid evolution of *P. infestans* leading to new pathogen strains which overcome host resistance (10). Conventional theory suggests that the most extreme type of resistance is based on the gene-for-gene concept and is effective only against races of the pathogen that carry and express an avirulence (Avr) allele that is compatible with a major R gene in the host. Although R gene resistance provides an extreme resistance phenotype, it is vulnerable to changes in the pathogen population (9).

The late blight resistance phenotype in potato has commonly been classified into two categories: vertical and horizontal, where vertical resistance refers to R gene resistance described above (for recent discussion see (10)). As noted, vertical (R gene) resistance is generally expressed as complete with little or no disease symptoms, although vertical resistance may also have a partial phenotype. Nonetheless, vertical resistance is generally measured as present or absent. Horizontal resistance is, in theory, effective against all pathogen races and is expressed as a rate-reducing resistance phenotype. Horizontal resistance is generally assessed by a synoptic measure of disease progress over time, either by measuring the rate of disease increase or the area under the disease progress curve (AUDPC). Recently, an interval scale was proposed for converting synoptic resistance measures to more easily interpretable values between 0 and 9 (44). This scale has an interval structure (36), is anchored to a control cultivar to account for environmental effects and is thought to provide a robust comparison of genotypes' susceptibility to *P. infestans* among years and locations.

Theory for the genetic control of vertical resistance, defined by major R genes that recognize the corresponding Avr alleles of the pathogen, is broadly accepted and a number of genes like this from different *Solanum* species have been identified (40). On the other hand, different opinions exist regarding the genetic control of horizontal resistance (35). Horizontal resistance is assumed to be quantitatively inherited and is frequently referred to as quantitative resistance. The two resistance phenotypes may be very difficult to distinguish in the field (33), although some researchers have proposed that careful examination of the time of disease initiation and the rate of disease development can give insight into the type of resistance present (2).

In the 1980's, the International Potato Center (CIP) adopted a potato breeding strategy designed to avoid the incorporation of R genes into a population under improvement for horizontal resistance. The rationale for the exclusion of R genes from the population was to avoid the extreme resistance phenotype that would mask the expression of horizontal resistance in the recurrent selection program. The resulting population was known as "B3" and was derived from a wide range of late blight resistance sources (24). Late blight resistance evaluation was regularly carried out in highland tropical environments of Peru with high endemic disease pressure from the 'new' (sensu (34)) population of *P. infestans* (29).

Environmental conditions can influence the expression of quantitative resistance (39), and therefore genotype by environment (G x E) interaction is an important factor to consider when measuring potato late blight resistance (10,17,26,42). Furthermore, instability of R gene-based resistance is very sensitive to pathogen population dynamics. A G x E analysis that combines several genotypes evaluated in various environments enables the stability analysis of genotypes' performance and may help to select genotypes suitable for given environments. Recent immigrations and the rise of novel *P. infestans* clonal populations, as for example KE-1 in Africa (31), and super blight races such as 13\_A2 in China (26), highlight the importance of studying stability of resistance in relation to pathogen dynamics.

The objectives of the study were 1) to characterize the stability of the late blight resistance phenotype of elite tetraploid potato genotypes adapted to the tropical highlands by analyzing historical field data from experiments conducted over six years in two tropical highland locations where late blight is endemic, 2) to relate this stability or lack thereof to changes in the *P. infestans* populations present in the field, and 3) to identify marker-phenotype associations utilizing the SolCAP Infinium SNP platform.

## Materials and methods

### Resistance data

Historical data from replicated field trials of the late blight resistance evaluations of the tetraploid B3 population between years 2001-2006 were retrieved from the CIP corporate database. The evaluation sites were always the same two: Oxapampa (12°34'05" South 75°24'23" West) and Comas (11° 46' 0" South, 75° 5' 0" West). In the field each genotype was represented by an experimental unit consisting of ten plants planted in a plot of 3.00 m<sup>2</sup>. The order of genotypes was randomized and there were two biological replicates. Between 10 to 12 genotypes were planted together and surrounded by susceptible infector plants to assure uniform inoculum throughout the field. Disease severity had been recorded visually as percentage of foliage affected at 6-8 day intervals until the susceptible control had reached 100% infection. All trials included the same control genotypes: Yungay (moderately susceptible), Kory (resistant) and Amarilis (moderately resistant). The raw data were visualized using box plot to detect outliers. Genotypes with no replication, a high standard deviation (stdev/mean>0.33) for the AUDPC among replicates or that were absent from more than two experiments were not considered for the analysis. The total dataset contained 195 potato genotypes evaluated in each of the following nine field experiments: Oxapampa 2001, 2002, 2005 and 2006; Comas 2001, 2002, 2004, 2005, and 2006.

Resistance was evaluated using the susceptibility scale (44), which we here call the sAUDPC and which was based on the AUDPC. The AUDPC values were transformed to the susceptibility scale using the moderately susceptible control cultivar Yungay as a reference genotype, which had been assigned a scale value of 6 based on its performance relative to highly susceptible genotypes (unpublished data). The formula for transformation was:  $sAUDPCx = \left( \frac{AUDPCx}{AUDPC\ Yungay} \right) * 6$ ; where,  $sAUDPCx$  is the scale value of the genotype in question,  $AUDPCx$  is the AUDPC of the genotype in question and  $AUDPC\ Yungay$  is the AUDPC of the cultivar Yungay. The stability of resistance was estimated by calculating the coefficient of variation (CV) of the sAUDPC for each genotype across the nine field experiments based on the variance among experiment-level means and the overall mean.

Pairwise correlations for sAUDPC values between experiments were plotted with R Gclus package <http://cran.r-project.org/web/packages/gclus/gclus.pdf>. Principal component analysis (PCA) was run on sAUDPC values for all experiments with FactoMineR (20). Only the genotypes that had no missing data (in total 172) were used for the correlation analysis and PCA.

### *Phytophthora infestans* isolates

Isolates ( $n=230$ ) were collected between 1999 and 2006 from both evaluation sites. Leaflets containing a single lesion were incubated at 15 to 18°C in a sealed water-agar petri dish to promote sporulation. Isolates were recovered from the leaves using filter system as described previously (29). Isolates were characterized for mating-type, restriction fragment length polymorphism with probe RG-57 and mitochondrial DNA haplotype (mtDNA) as described previously (12,13,29).

### R gene differential sets in the field

A host differential set containing plants with 11 previously identified R genes from the Mexican species *S. demissum* was planted in each trial. The plant material was obtained from the Research Institute for Plant Protection, Wageningen, the Netherlands: R1 (CEBECO-43154-5; CIP 800986), R2 (CEBECO-44158-4; CIP 800987), R3 (CEBECO-4642-1; CIP 800988), R4 (CEBECO-4431-5; CIP 800989), R5 (Black 3053-18; CIP 800990), R6 (Black XD2-21; CIP 800991), R7 (Black 2182ef(7); CIP 800992), R8 (Black 2424a(5); CIP 800993), R9 (Black 2573; CIP 800994), R10 (Black 3618ad(1); CIP 800995), and R11 (Black 5008ab(6); CIP 800996). Tubers produced from in vitro plants of each differential were

planted in the same number of replications as each genotype in the experiments and were evaluated in the same way as the test genotypes.

### Genotypic data

In 2012 a subset of 103 of the potato genotypes were growing in the field and thus were available for DNA extraction. Genotyping was outsourced as a service to Michigan State University (MSU). SolCAP Potato Infinium SNP array (8) that contains 8303 SNPs distributed genome wide was used and the raw data of the 103 potato genotypes was processed together with genotypic data from the homozygous *S. tuberosum* Group *Phureja* DM1-3 516R44 (DM) clone previously subject to whole genome sequencing (43). Six diploid genotypes, and 2 additional tetraploid genotypes not part of the B3 population were included as controls for assessing SNP quality. Two diploid clones were genotyped three times and three tetraploid clones were genotyped twice. The normalized allele signal ratio (normalized X divided by the sum of normalized X and normalized Y) was calculated using Illumina GenomeStudio software (Illumina, Inc., San Diego, CA) and exported in csv format. A custom R script was used to call and filter the genotypes. Each SNP was run through the CodomMarker function of the fitTetra R package (41). Each sample was categorized into one of 5 possible tetraploid genotypes (AAAA, AAAB, AABB, ABBB, or BBBB). SNPs were then passed through filters testing for the following conditions: DM homozygosity (AA or BB); expected genotypes for diploids (AA, AB, BB); each replicated sample had the same genotype call; localization of the SNP to only one genome location (8); and less than 5 % of the genotype calls missing. 3192 SNPs passing these filters were included in the subsequent analysis. Because DM is a double monoploid the assumption was that the SNP should be homozygous in this genotype and therefore markers that were heterozygous in DM were excluded from the analysis. Furthermore, the analysis included only bi-allelic SNP.

### Population structure, association and LD

The SNP marker order on the physical map of potato was obtained by BLASTn analysis using the 101 bp long fragment flanking the SNP ([http://solcap.msu.edu/potato\\_infinium.shtml](http://solcap.msu.edu/potato_infinium.shtml)) as query against the *S. tuberosum* Group *Phureja* DM1-3 516R44 (CIP801092) Version 3 DM, Version 2.1.10 pseudomolecules (<http://potatogenomics.plantbiology.msu.edu/index.html>). The SNP tagged all 12 chromosomes with 163 to 299 markers per chromosome. In total, 243 markers were un-mapped.

The potato population structure was characterized by STRUCTURE software (30) on the basis of a subset of 120 SNP markers. Ten markers distributed along each of the 12 chromosomes were selected for this analysis and the data was handled as tetraploid. Three repetitive runs were made using a burnin time of 1,000,000 and 20,000 MCMC (Markov Chain Monte Carlo) repetitions. The allele frequencies were assumed to be correlated among populations and the structure was determined by assuming 1-10 subpopulations. The most probable number of populations was determined by plotting the natural logarithm (ln) likelihood against the number of subpopulations by Structure Harvester (7) and the examination of the Q matrices of each run. A kinship matrix was calculated using SPAGeDi (16) and for the association analysis the negative values were replaced by zero.

Marker phenotype associations were determined with TASSEL software (3). The markers were coded as diploids even though the initial marker identification was done at the tetraploid level. Therefore all three possible heterozygous genotypes (AAAB, AABB, and ABBB) for bi-allelic SNP were coded the same (AB). The entire marker-genotyped set of 103 potato genotypes was analyzed for sAUDPC in each experiment, although the dataset contained some missing data. The mixed linear model (MLM) took into account the population structure (Q matrix) and kinship (K matrix) and was run with the optimum level of compression. The variance components were estimated after each marker. The significance of the test was set to 0.05 and Bonferroni correction was applied to correct for multiple testing and against the identification of false positives. Minor allele frequency (>5%) was taken into account as a criterion for calling significant markers. The marker association was tested for PCA

coordinates of the first dimension (Dim 1) and the second dimension (Dim 2) as well as the coefficient of variation, but using only those 88 potato genotypes that had no missing phenotypic data.

The linkage disequilibrium (LD) coefficient ( $r^2$ ) was plotted against the physical marker order and the statistical parameters given by TASSEL were used to determine whether markers were in linkage disequilibrium with respect to one another. The significance level was set to  $p < 0.001$  and corrected for the number of markers analyzed for each chromosome. The physical distances between the markers vary on each chromosome as some adjacent markers may be found within the same gene, while others may be millions of base pairs apart. .

The Hardy-Weinberg equilibrium was calculated by SNP-HWE for R  
[http://www.sph.umich.edu/csg/abecasis/Exact/r\\_instruct.html](http://www.sph.umich.edu/csg/abecasis/Exact/r_instruct.html).

## Results

### Pathogen population

All isolates collected from potato fields from Comas ( $n=91$ ) and Oxapampa ( $n=139$ ) belonged to the clonal lineage EC-1 and were mating type A1. In all trials the differential plants with R1, R2, R3, R4, R6, R7, R10 and R11 became infected with late blight. The differential R5 was infected in four experiments (Comas2004, Comas2005, Oxa2001, Oxa2005), R8 in eight experiments (all but Oxa2005), and R9 in two experiments (Comas2001, Comas2002).

### Resistance

Most of the breeding materials included in this study had AUDPC values lower than the susceptible control genotype Yungay (supplementary table S1). However, pair-wise correlation analysis of the sAUDPC values indicated that the genotypes' relative levels of resistance varied considerably among experiments (supplementary figure S1, supplementary table S2) raising concerns about the stability of the resistance. Based on a bi-plot of sAUDPC CV and mean values (Fig 1) we identified a suitable cut-off level for stability at CV=0.5. Thus, 70 genotypes were considered stable and 102 unstable. Stability of genotypes was also evident by plotting sAUDPC values for locations (Fig 2). Stable genotypes generally had similar values across environments, except in Comas 2005. In contrast, unstable genotypes had more variability in mean sAUDPC values among locations, generally having higher values (more susceptible) in four locations: Comas2004, Oxa2001, Oxa2002 and Oxa2005., and also to a lesser extent in Oxa2006. The cultivar Yungay, that was used to calculate the sAUDPC and the relative CV, had a low CV (0.14) of the absolute AUDPC values (supplementary table S2).

Plotting locations on the first two dimensions of the PCA, which explained approximately 80% of the information in the dataset, produced a pattern that was generally consistent with the classification of locations described above (compare Figs 2 and 3). The PCA separated locations into two groups: group 1 consisted of the environments Oxa2001, Oxa2002 and Oxa2005 and group 2 contained the remaining locations (Fig 3). Thus, based on common association with Dimension 2 of the PCA, it appears that resistance in the unstable genotypes broke down in group 1 environments (Fig 4). This loss of resistance of unstable genotypes in group 1 locations did not appear to be related to the pathogen virulence pattern determined by the differential set. A common factor for the group 1 environments was that the R9 differential remained un-infected in all of them, but this is also the case for four out of six of the group 2 environments (Fig 3).

### Host population structure

Based on 120 SNP markers and 103 potato genotypes the most probable number of subpopulations in our dataset is three (supplementary fig S2), although there are genotypes with fairly mixed backgrounds (Fig 5). Population structure was linked to the marker c2\_56418 (see below) since the group of potato genotypes that are heterozygous for this marker (in total 56 genotypes) belong mostly to the subpopulations 3 (28 genotypes) and 2 (21 genotypes) (Fig 6).

### Marker-trait association

Two markers on chromosome 9 and one marker on chromosome 7 had significant association with the late blight resistance phenotype (Table 1). The marker c2\_56418 was significantly associated with sAUDPC in Comas2006, Oxa2006, and Comas2002 and with the second dimension of the PCA. This SNP is present in homozygous (AAAA) and heterozygous (AAAC or AACC) states. Potato genotypes with the heterozygous SNP genotype for c2\_56418 are more resistant in the group 2 environments (Oxa2006, Comas2001, Comas2002, Comas2004, Comas 2005 and Comas2006; see Fig 3.) and more susceptible in the group 1 environments (Fig 7.). Heterozygous genotypes also have much higher frequency of the founders 575049 (CEW-69-1) and BULK MEX in their pedigree (Table 2,



supplementary table S3). Furthermore, in Oxa2006, where the marker c2\_56418 explained 21% of the variation, there are 31 potato genotypes with the sAUDPC value 1 or less and 29 of those are heterozygous for the c2\_56418 SNP. Of those, all but three have the founders 575049 (CEW-69-1) and/or BULK MEX in their pedigree. Most potato genotypes that are heterozygous for this marker locus are unstable for the sAUDPC value (Fig 8).

The marker c2\_56418 is located toward the end of the long arm of chromosome 9 but has not been mapped to any gene in the reference potato genome assembly. The physical distance of c2\_56418 from its neighboring markers is 96 kb to the South (c1\_10509) and 538 kb to the North (c1\_14205), and neither of these two markers is in linkage disequilibrium (LD) with c2\_56418 (Fig 9). It is not surprising that the latter one is not in LD with the associated marker because of the large physical distance between them, which also contains a gap of unknown size in the potato genome sequence. As an example of the degree of LD nearby, three markers c2\_27699, c2\_27705 and c1\_8549 toward the end of the chromosome are in absolute LD and the physical distance between the first and last of these markers is 110 kb (Fig 9). Also marker c2\_27763 in *Sucrose Synthase* gene PGSC0003DMG400006672 that is associated with sAUDPC in one of the experiments (Comas2006) has been genetically mapped to chromosome 9(15) but is un-mapped in the genome assembly and therefore we cannot compare its physical location in relation to the marker c2\_56418.

Marker c1\_10011 is associated with the sAUDPC in Comas2002 and with the first dimension of principal component analysis (Table 1.). The SNP is in the gene PGSC0003DMG400006689, *Glucan endo-1,3-beta-glucosidase* in chromosome 7. However, this marker needs to be tested with a higher number of genotypes because there are too few individuals in one of the allele groups, making it difficult to draw meaningful conclusions of the SNP allele effect (Table 1).

Discussion

Increasing the level of late blight resistance in potato has been one of the main priorities of the International Potato Center (CIP) for decades. Early on, resistance provided by the *S. demissum* R genes was found to be ephemeral and therefore a strategy was formulated in the 1980's to avoid the incorporation of the major-effect R genes into potato populations bred for horizontal resistance (putatively resistant against all pathogen genotypes). In addition to the short-lived resistance, R genes tended to mask horizontal resistance and therefore made improvement for horizontal resistance impossible. To eliminate R genes, potential parents were test-crossed with a potato variety compatible with a putatively "simple" race (also known as race 0 and unable to infect a potato plant with any of the then-known R genes from *S. demissum*); if the resulting progeny had a hypersensitive reaction or no sporulation when inoculated with the simple race, the parent was not used for further crossing (24). Knowledge of both host and pathogen genetics has evolved since the B3 population was designed and additional R genes from other species than *S. demissum* have been identified (32). It now appears evident that this strategy to exclude the 11 known *S. demissum* R genes only eliminated some of the R genes in the B3 population.

The nine field experiments in our study formed two groups, but the grouping does not strictly follow the geographical location of the evaluation sites. While sites are situated in the Andes, they are geographically distant and are also in different agroecologies. In Comas, potato is commonly grown by local farmers, whereas in Oxapampa potato is only grown in home gardens, which could potentially have an impact on the source, quantity and genetic diversity of the inoculum. However, in both environments late blight epidemics are severe and *P. infestans* strains found from cultivated potato in both locations were of the EC-1 clonal lineage, which is consistent with previous reports from the Andean countries (6,29) .

In the specific virulence profiles of the isolates from the two locations, as determined by the differential set, avirulences corresponding to R5 and R9 were frequently present, sometimes together and sometimes separately. Previous reports document a similar trend, that the resistance of differentials R5, R8 and R9 is frequently not overcome (1,37). Our data indicated that pathogen population dynamics are likely driving resistance variability among experiments, but it was not clear that these interactions involve any of the *S. demissum* R genes. Furthermore, the instability in resistance reactions was also not associated with reactions of the *S. demissum* differentials. Thus, use of this differential set was not informative for explaining pathogen dynamics relevant to the potato genotypes we assessed. Rather than using the *S. demissum* R gene differential set, a more thorough analysis of the effector combinations and their expression in the isolates present in the study locations could have been more helpful. For the known effectors that act as avirulence determinants, this can be readily done (5,28) but when the R gene – Avr gene pair is unknown the analysis is not that straight forward.

The low CV of the absolute AUDPC values of cultivar Yungay enabled the use of this cultivar to calculate the relative CV using the sAUDPC as a measure of stability. The stability based on relative CV is consistent with the location plotting on the PCA bi-plot and with marker analyses. However, it is also important to take into account that stability does not necessarily equate to durability of resistance. We have measured stability of performance in small plots but this is not necessarily a guarantee of durability of resistance should a genotype be planted over much larger areas. Thus, for the genotypes presented here the durability of resistance remains to be tested.

Based on the pedigree, the resistance linked to the marker c2\_56418 could be attributed to the frequent occurrence of the founder clone 575049 (CEW-69-1), which is known as variety Montserrat from Mexico (4). This variety was reported to have stable resistance in Mexico over 5 years and also appears to contain major R genes of unknown kind (4). However, according to our results the resistance linked to this marker was not stable as the genotypes with the C allele in this locus remain resistant only in some of the experiments

The marker c2\_56418 locates towards the end of the long arm of chromosome 9, where we previously mapped a large effect QTL for late blight resistance originating from one of the resistant tetraploid genotypes of the B3 population (25). The physical location of the marker c2\_56418 is not in the *Rpi-vnt1* locus, but closer to the end of the chromosome. The LD decays relatively rapidly in this part of the chromosome suggesting that a larger collection of SNP would be beneficial for better coverage. According to the PGSC genome data and SolCAP SNP data the region with multiple copies of *Rpi-vnt1* like genes locates north of marker c1\_14205. The *Rpi-vnt1* region contains several SolCAP SNP markers, of which none were informative in our population perhaps indicating that the *Rpi-vnt1* like genes in the B3 genepool are more divergent from the *Rpi-vnt1* like genes found in *S. venturii* and *S. phureja*. Assuming that the increased resistance based on the average sAUDPC in Oxapampa is due to a single locus, the gene located between markers c1\_10590 and c1\_14205 could be a novel R gene. Recently the R8 gene from MaR8 was mapped in this genomic region by field inoculation with the *P. infestans* isolate IPO-C (race1, 2, 3, 4, 5, 6, 7, 10, 11) (21). We showed that in one of the experiments, Comas2005, the differential set genotype R8 was not infected, and thus the resistance seen in some of the B3 genotypes that year could be attributed to R8.

The reference potato genome sequence contains over 400 NBS-LRR type R genes and some of those are homologs of the LB resistance genes originally found in distinct *Solanum* species (22). The B3 potato genotypes from CIP, are also likely to contain multiple R genes, which may become functional depending on the effector composition of the pathogen population.

The central problem for measuring resistance in breeding populations is that a perfect system for screening using *P. infestans* isolates does not exist. The *P. infestans* genome contains hundreds of effector genes that may have a function in virulence (14). Most of the *P. infestans* isolates described

all over the world do show complex virulence patterns in terms of the 11 *S. demissum* R genes and no doubt also contain more effectors than are associated with the *S. demissum* R gene interactions. Therefore we can expect to encounter a mixture of virulence capacities in every isolate and a mixture of R genes in every potato accession, which makes it hard to identify unique gene-for-gene interactions. To further complicate the resistance screening, the phenotype conferred by a major resistance gene is not always clear in detached leaf assays or other controlled inoculations. Recently, it was shown that cultivar Sarpö Mira contains four R genes that confer qualitative resistance and an R gene that confers partial resistance, and the resistance phenotype is only detected in field conditions (32). Effectoromics is a promising new tool for R gene identification (40) that could facilitate the monitoring gene-for-gene phenotypes.

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Table 1. Significant (p<0.05) SNP associations for late blight resistance measured as sAUDPC and the first two principal componenet dimensions (Dim 1 and Dim 2) in the nine field experiments.

Chr <sup>a</sup>	SNP_ID <sup>b</sup>	genotypic class		deviation from HWE p<0.001 <sup>e</sup>	Significant experiment <sup>f</sup>	sAUDPC mean		PC <sup>g</sup>
		AA <sup>c</sup>	AB <sup>d</sup>			AA	AB	
7	c1_10011	15	87	*	Comas2002	2.3	0.9	Dim 1
					Comas2006	2	0.8	
9	c2_56418	58	45	ns	Oxa2006	2.9	1.3	Dim 2
					Comas2002	1.8	0.7	
	c2_27763 <sup>h</sup>	27	74	*	Comas2006	2.2	1	

a Potato chromosome

b SNP marker name

c number of potato genotypes with the homozygous allele composition

d number of potato genotypes with the heterozygous allele composition

e Asterisk indicates significant deviation and ns indicates no significant deviation from Hardy-Weinberg equilibrium at p<0.001.

f field experiment with significant marker-trait association

g principal component

h chromosome location from Hacket et al. 2013

Table 2. The frequency of potato clones that contain the two founders, 575049 and BULK MEX, in their pedigree grouped by snp\_c2\_56418 genotype

<b>snp_c2_56418 genotype</b>	<b>n</b>	<b>575049 (CEW-69-1)</b>	<b>BULK MEX</b>
AACC/AAAC	56	63%	59%
AAAA	45	33%	27%



**Figure legends:**

Fig 1. The mean and coefficient of variation (CV) of the sAUDPC values for 172 potato genotypes evaluated in nine field experiments. The CV of 0.5 was considered a cut-off value between stable and un-stable genotypes.

Fig 2. The pattern of the sAUDPC values of the stable and un-stable genotypes in each experiment. The experiments from left to right are: Comas2001, Comas2002, Comas2004, Comas2005, Comas2006, Oxa2001, Oxa2002, Oxa2005 and Oxa2006. The number of race specific (RS) resistance individuals was included in the graph showing the un-stable individuals.

Fig 3. Bi-plot of the first two dimensions of a principal component analysis showing the relationships among environments where resistance to potato late blight based on the sAUDPC was evaluated in 172 potato genotypes. The differential set plants R1-R11 that did not become infected during each experiment are shown after the name of the experiments. The experiments Oxa01, Oxa02 and Oxa05 formed group 1 and the rest of the experiments, group 2.

Fig 4. Bi-plot of first two dimensions of a principal component analysis based on sAUDPC values of 172 potato genotypes evaluated for late blight resistance in nine environments. The genotypes are identified based on stability; genotypes with an among-experiment coefficient of variation for sAUDPC of less than 0.5 were considered stable.

Fig 5. Structure plot of the assignment probabilities of the 103 potato genotypes. Each genotype is represented by a bar and the highest Q group membership defines sub-population (pop1, pop2, pop3) assignment. The plot is based on 120 SNPs and the highest probability run for K = 3.

Fig 6. Potato genotypes divided according to the snp\_c2\_56418 genotype and population structure assuming three sub populations.

Fig 7. SNP c2\_56418 allele effect on resistance measured as sAUDPC values (y-axis) showing the mean sAUDPC values of the potato genotypes with SNP genotype AAAA (n=45) versus AACC and AAAC (n=56) in each environment. The first six experiments form group 2 and the last three form group 1 in principal component analysis (PCA, see figure 3).

Fig 8. Bi-plot of first two dimensions of a principal component analysis based on sAUDPC values of only the potato genotypes that were SNP-genotyped and had no missing data. Potato genotypes are labeled according to the SNP c2\_56418 genotype (AAAA/AACC) and stability based on coefficient of variance (CV). Genotypes with an among-experiment coefficient of variation for sAUDPC of less than 0.5 were considered stable.

Fig 9. Heat plot showing the level of LD among 19 markers at the end of the long arm of chromosome 9. The physical location in the pseudomolecule 9 is indicated (see materials and methods) and the distance in base-pairs to the following marker is shown.

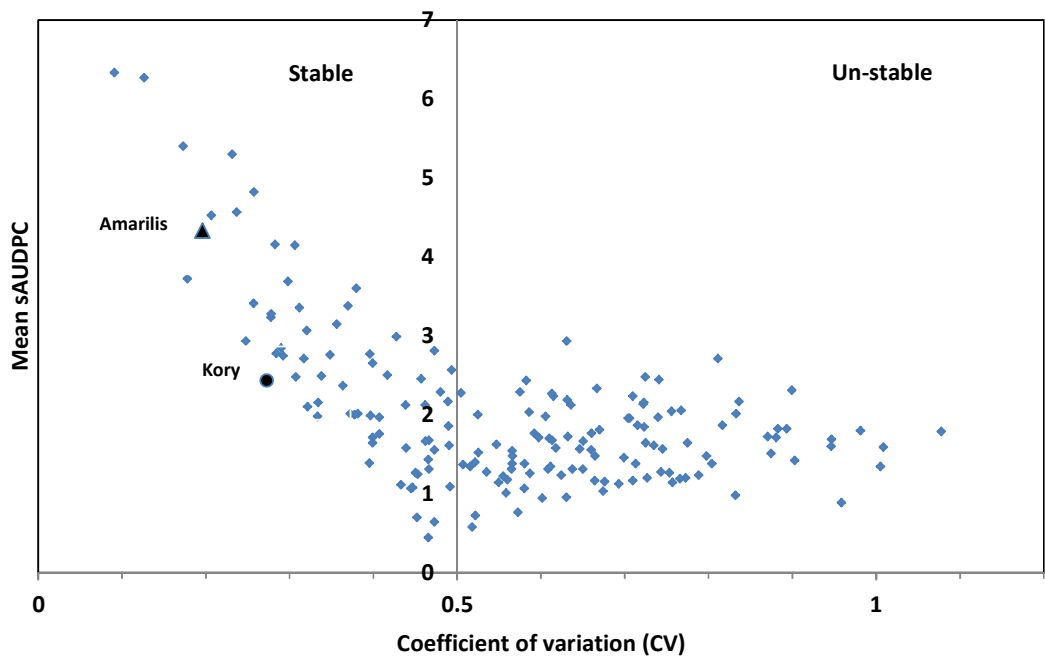
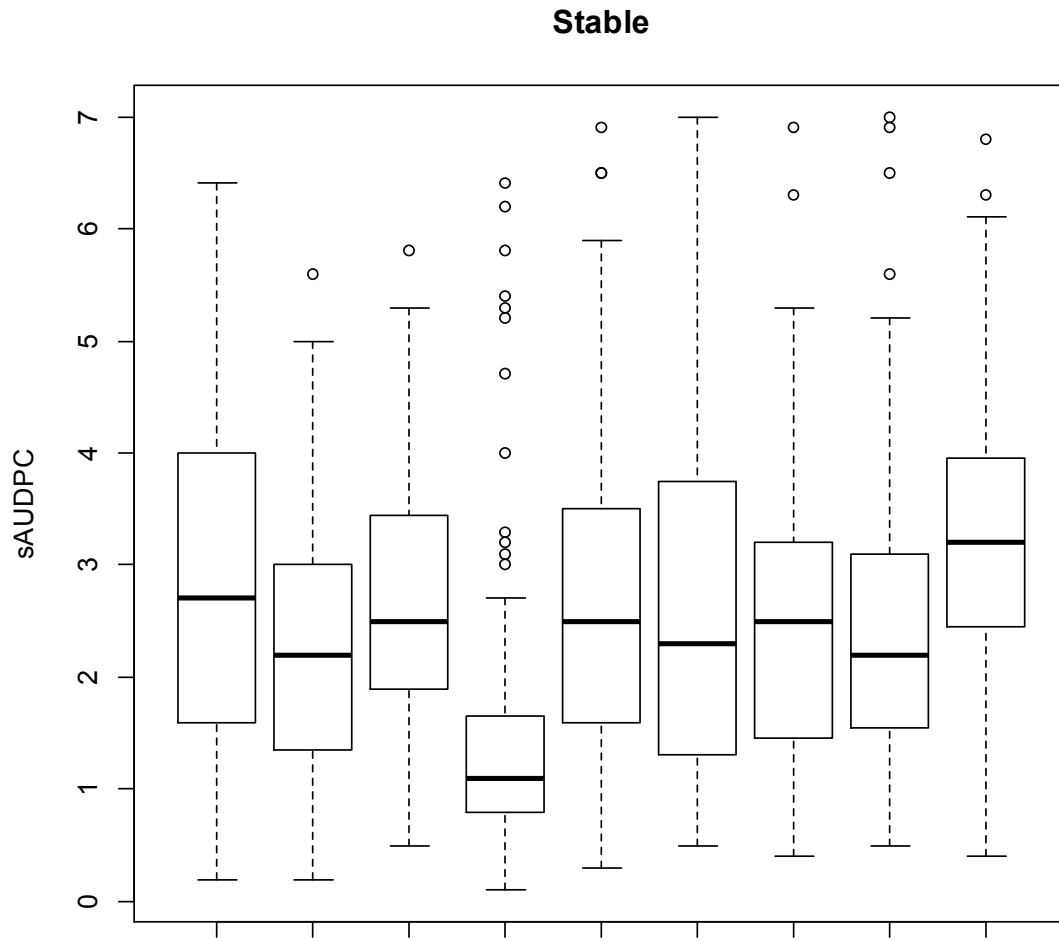


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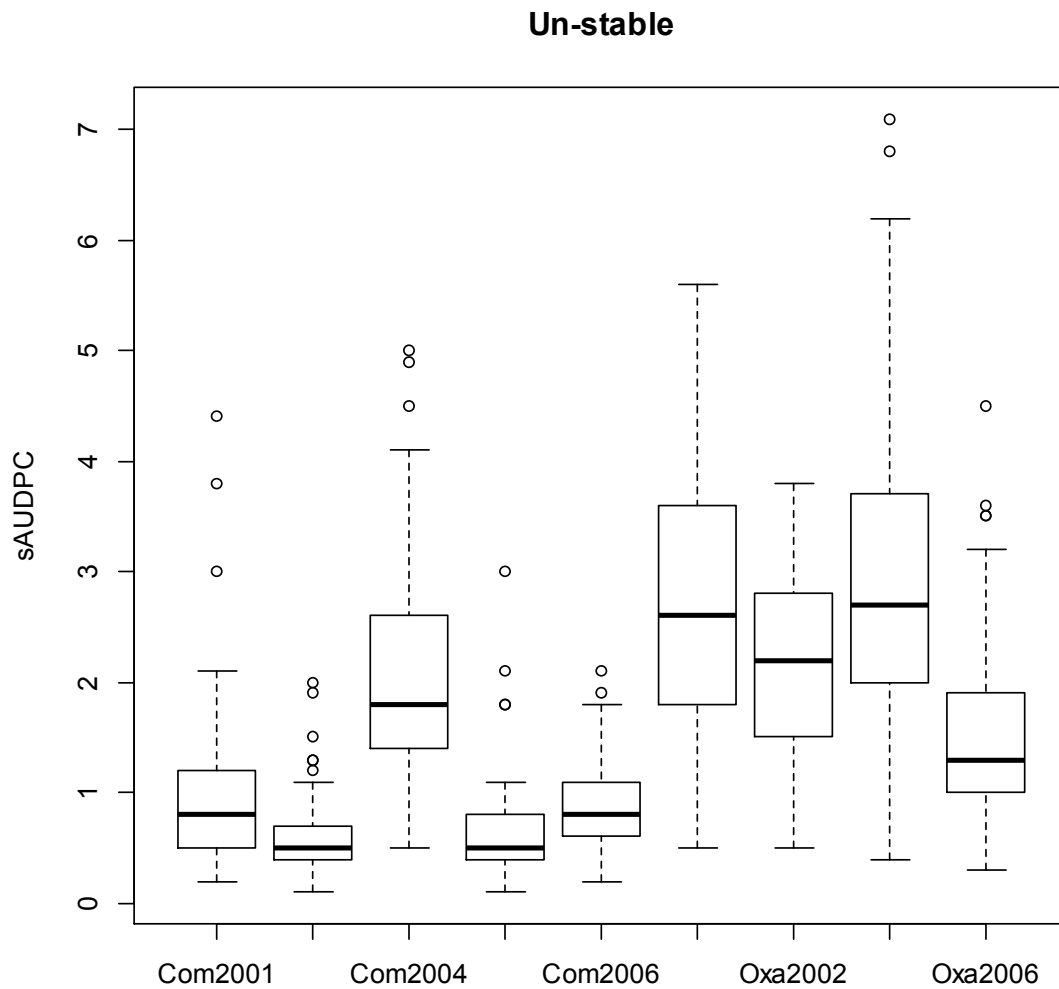


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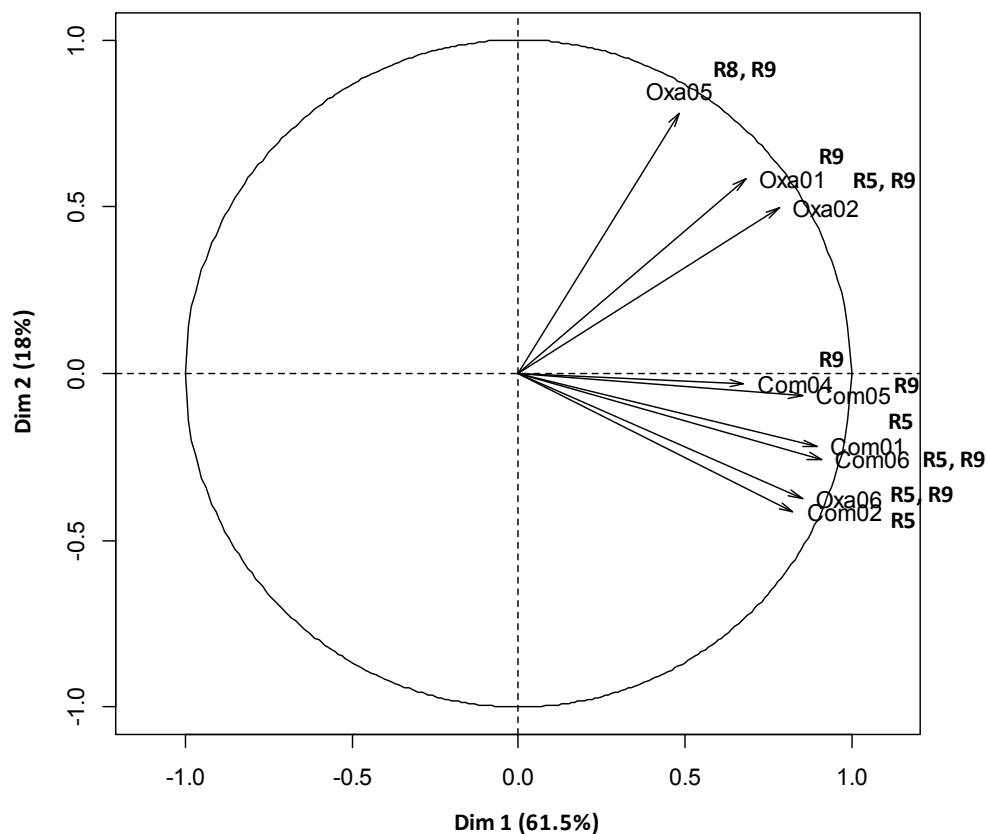


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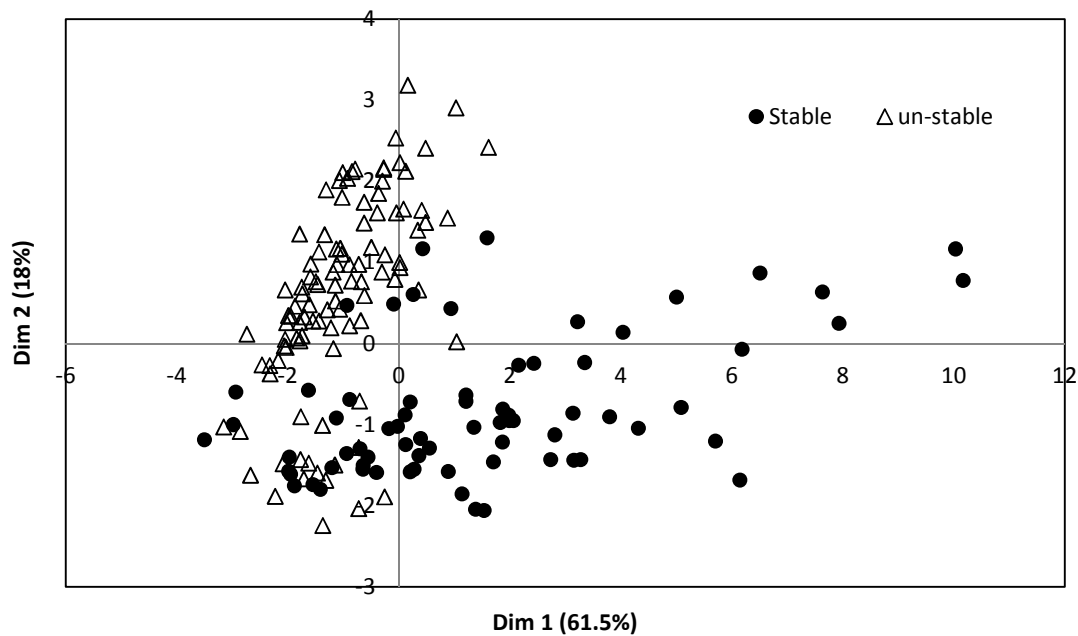


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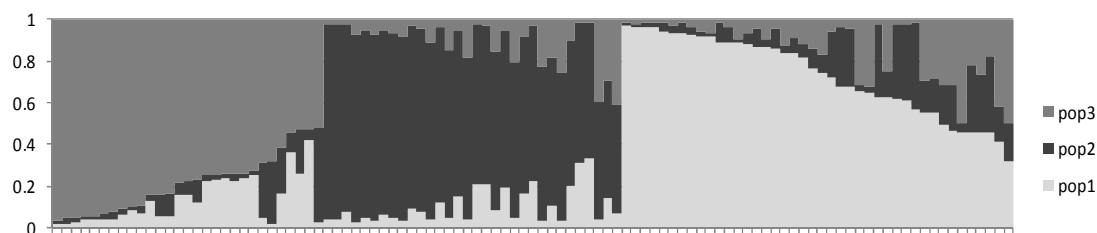


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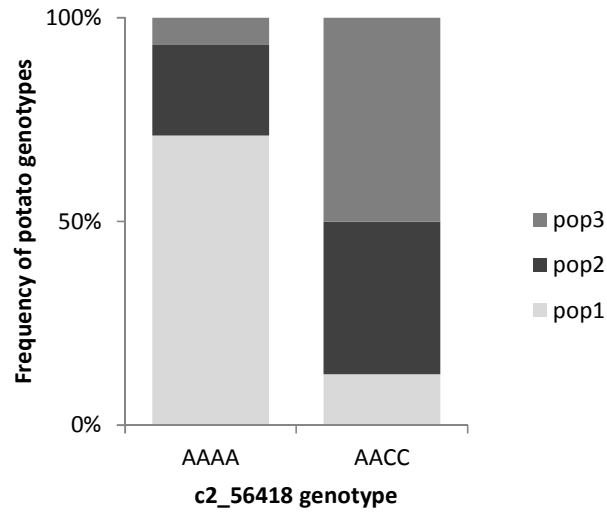


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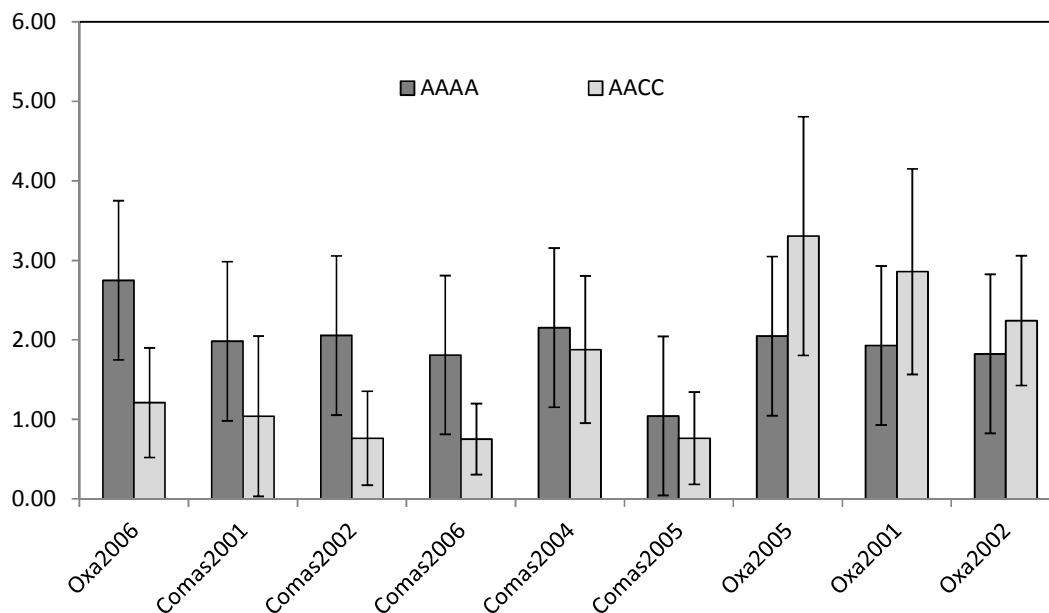


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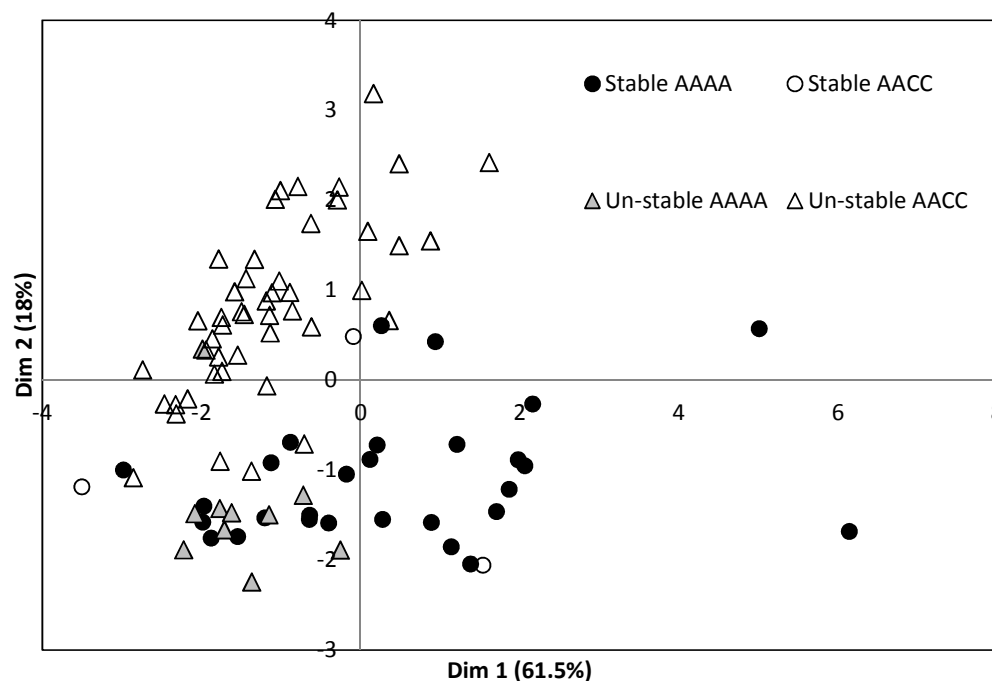


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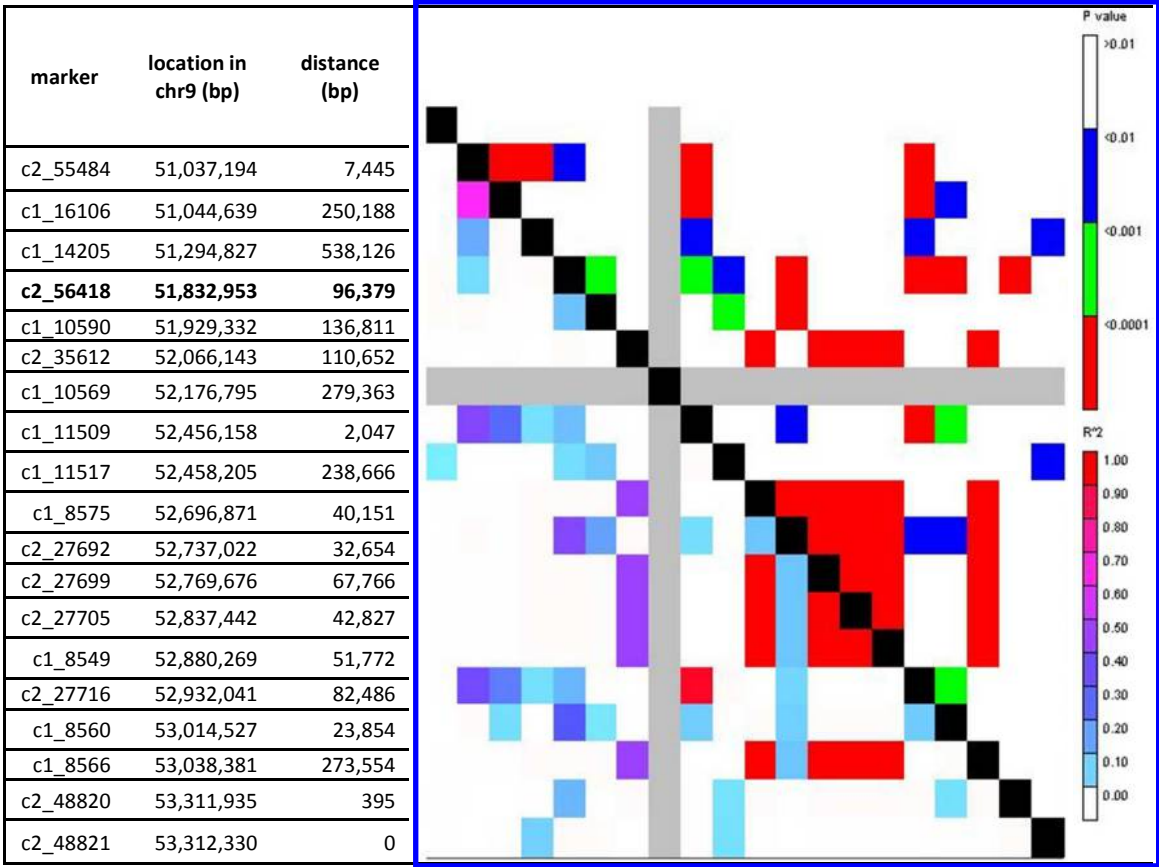


Fig 9. Heat plot showing the level of LD among 19 markers at the end of the long arm of chromosome 9. The physical location in the pseudomolecule 9 is indicated (see materials and methods) and the distance in base-pairs to the following marker is shown.

Supplementary table S1. AUDPC

potato genotype	Comas 2001	Comas 2002	Comas 2004	Comas 2005	Comas 2006	Oxa 2001	Oxa 2002	Oxa 2005	Oxa 2006
CIP377744.1	1010	1197	922	549	1027	1376	1373	859	1542
CIP384866.5	2167	1520	3088	1531	2286	1359	1531	1817	2571
CIP391002.6	1049	454	1337	158	994	490	499	748	1461
CIP391004.10	451	148	1419	263	460	1138	1103	NA	486
CIP391004.15	2639	1548	2659	1873	3071	2800	1873	2548	3036
CIP391004.18	479	274	1420	245	245	385	245	410	1324
CIP391004.4	2574	1495	2051	1698	1896	2678	2013	1503	2603
CIP391011.17	399	316	813	111	374	1435	875	2630	394
CIP391013.1	2615	1079	2080	1085	3139	2538	2371	2353	2720
CIP391046.14	2504	1824	2363	1750	2576	1628	1208	1820	2770
CIP391046.27	1508	1790	2459	333	1633	2205	1330	1233	2614
CIP391047.20	450	124	1003	210	229	884	823	1135	609
CIP391047.34	770	205	1576	NA	511	1147	858	NA	581
CIP391047.60	1109	263	1219	298	739	1785	NA	2148	1126
CIP391058.175	309	115	1669	105	226	1374	1295	1895	807
CIP391065.69	248	116	1675	53	368	1190	683	2798	404
CIP391065.81	213	249	956	210	334	1208	1033	1300	956
CIP391580.30	695	719	1629	193	984	928	875	893	1525
CIP391583.25	405	253	570	175	161	NA	1120	1713	524
CIP391585.167	134	209	829	123	238	788	1015	835	464
CIP391585.179	109	235	960	NA	238	1453	1365	1470	528
CIP391585.5	144	143	243	280	253	543	333	1350	271
CIP391586.109	2883	1988	2100	2030	596	NA	1663	2575	600
CIP391586.12	153	268	1873	210	NA	1785	1706	1135	2955
CIP391679.12	2829	2078	2620	2083	3683	2818	3080	3195	3158
CIP391679.7	2878	2320	2823	2030	3506	2958	2835	3143	3394
CIP391679.9	2590	1515	1639	1715	3493	2503	2188	2968	3036
CIP392617.54	75	689	696	70	189	376	219	NA	254
CIP392622.54	220	133	873	35	366	919	560	965	810
CIP392622.58	578	143	1669	263	776	1610	1050	1473	756
CIP392633.10	1775	1333	2011	455	2088	613	1470	1325	1809
CIP392633.2	2119	891	2201	368	1540	2013	1864	1273	1840
CIP392633.23	1018	756	1454	245	1516	735	1033	808	1606
CIP392633.54	1520	1131	1965	228	1590	525	1715	1343	1676
CIP392633.6	1838	1685	1665	368	2063	1391	1243	1433	2338
CIP392633.64	1565	1383	1804	140	1648	595	1243	1225	1649
CIP392634.49	76	124	1290	193	299	613	823	1190	358
CIP392634.52	330	183	599	175	330	910	718	1433	282
CIP392637.10	223	218	1491	53	333	1103	1033	1454	707
CIP392637.27	240	143	1916	595	596	884	893	1198	630
CIP392639.2	490	744	1168	315	916	508	525	958	1546
CIP392639.34	1436	914	1859	455	1528	1391	1120	1074	2103
CIP392639.53	921	1203	1846	158	661	893	630	985	1614
CIP392639.8	2719	1063	1951	1050	2659	2065	1418	1593	2585

CIP392640.18	150	108	1535	175	501	779	665	2410	850
CIP392640.9	240	98	1846	595	680	1365	1260	1383	1010
CIP392642.2	1720	1398	2114	508	1973	954	1575	1120	2159
CIP392650.12	189	244	1178	193	266	779	665	1085	530
CIP392650.49	135	195	697	333	528	901	840	1330	539
CIP392652.8	1824	668	1535	333	1065	1558	1488	2295	836
CIP392657.171	425	96	1108	105	113	1243	1033	1465	596
CIP392657.18	658	214	2408	193	498	1628	1488	3213	1050
CIP392657.8	1955	124	1936	70	395	1978	1680	1353	816
CIP393042.50	878	443	1125	158	926	394	368	350	953
CIP393072.55	1439	1279	1931	368	1254	1234	1365	988	1759
CIP393073.179	330	513	949	70	686	455	464	355	805
CIP393073.197	711	899	1865	175	642	385	980	985	1209
CIP393074.86	205	153	386	210	201	446	499	498	213
CIP393075.54	835	89	1000	350	635	525	954	445	1128
CIP393077.159	NA	1296	1177	NA	629	525	727	512	1099
CIP393077.51	1191	914	1979	350	1526	840	1330	868	1468
CIP393077.54	409	830	1488	123	583	446	665	395	949
CIP393079.24	271	174	593	35	317	490	665	854	558
CIP393079.4	205	259	984	70	372	621	683	843	445
CIP393083.2	374	461	1621	683	706	1925	1155	1725	633
CIP393084.31	525	819	1176	210	530	490	560	460	1008
CIP393085.5	955	53	714	245	541	1453	805	1084	674
CIP393111.3	453	160	NA	140	766	1523	551	910	1440
CIP393220.54	490	311	482	158	419	1295	770	1465	544
CIP393227.66	343	156	871	88	261	683	551	828	444
CIP393228.21	459	228	1919	175	415	893	823	1315	889
CIP393228.67	164	115	1351	88	212	875	543	400	352
CIP393242.50	1338	276	2144	88	940	560	359	559	1743
CIP393243.53	896	309	2688	193	534	376	289	293	1479
CIP393248.52	470	228	1108	210	609	1680	1348	2240	663
CIP393248.55	893	213	1603	187	653	1663	1304	2806	859
CIP393280.57	110	224	1360	35	708	1120	648	868	434
CIP393280.64	2379	1470	1393	414	1254	1190	691	610	1250
CIP393280.80	188	209	479	123	431	709	823	NA	254
CIP393280.82	238	124	1971	210	168	1094	805	1175	221
CIP393280.83	309	204	2163	210	409	1313	998	1595	1048
CIP393284.39	900	240	1183	280	839	1208	1295	2378	680
CIP393339.155	1228	271	1559	175	646	NA	1225	2603	1049
CIP393339.242	659	335	1124	99	399	1033	1120	1600	778
CIP393349.35	168	240	951	315	303	1006	1050	1843	730
CIP393349.55	274	285	1639	158	446	1505	1208	2140	1260
CIP393349.68	454	169	568	263	266	998	866	1255	473
CIP393360.64	93	181	1109	210	484	543	481	1290	543
CIP393371.157	1009	990	1630	251	1168	385	1006	711	1197
CIP393371.159	863	908	1429	NA	585	604	359	383	1285
CIP393371.164	718	406	1594	175	664	534	648	505	480

CIP393371.179	606	548	1149	123	484	368	280	368	631
CIP393371.58	75	191	269	44	139	219	228	299	331
CIP393382.44	2031	1058	1130	805	990	945	1243	1055	1851
CIP393385.39	574	276	2115	146	611	1558	1138	1474	1574
CIP393385.47	440	378	1735	152	717	1873	910	1575	1103
CIP393385.57	1726	649	1445	630	1556	1173	1085	1118	1993
CIP393438.96	645	293	1743	245	379	1418	1321	1985	1349
CIP393453.198	546	178	1780	245	458	1855	1225	1995	1455
CIP395007.213	626	264	768	105	560	753	674	1203	469
CIP395011.19	209	295	794	228	NA	949	779	635	404
CIP395011.2	264	223	871	158	634	1037	744	1153	625
CIP395013.211	1697	535	1361	298	871	1750	1575	3090	875
CIP395015.5	588	253	1142	333	740	1374	1365	2583	813
CIP395015.6	1063	558	1036	350	527	1120	1260	1430	823
CIP395016.255	263	231	655	105	383	852	1321	2378	353
CIP395017.14	634	295	1086	158	540	1956	1208	2020	562
CIP395017.227	155	216	758	123	468	945	836	1020	336
CIP395017.229	167	236	785	123	432	1324	1159	2200	640
CIP395017.242	389	223	715	193	125	933	1068	1428	604
CIP395037.107	159	396	626	105	459	280	499	460	1336
CIP395052.11	344	231	1026	158	334	1523	1173	2268	379
CIP395077.12	139	121	750	140	185	1597	1208	1263	809
CIP395084.9	1117	1624	1455	NA	1730	766	1304	NA	2284
CIP395096.2	1641	451	943	333	1702	976	1365	1860	892
CIP395096.3	256	226	896	333	340	897	1330	1460	636
CIP395096.7	458	531	931	280	1040	1772	1260	1165	810
CIP395097.4	531	353	762	140	749	1868	1278	1698	678
CIP395109.29	225	196	768	228	287	1531	1278	1200	876
CIP395109.34	248	311	489	368	309	853	980	970	382
CIP395109.4	150	424	532	280	1124	1046	1103	1170	515
CIP395109.7	1290	930	1016	525	2187	792	901	670	1578
CIP395111.13	658	250	889	140	443	1234	1295	1365	673
CIP395112.19	109	214	384	105	453	1689	875	1385	317
CIP395112.32	357	268	975	245	439	2380	1523	2593	653
CIP395112.36	361	373	768	210	375	2231	1531	1660	717
CIP395112.6	387	305	401	210	422	1251	1470	2383	559
CIP395112.9	600	298	1151	298	545	1947	1488	2008	515
CIP395114.5	490	226	916	210	495	2336	1435	2025	770
CIP395117.3	214	410	744	193	440	586	1216	853	2230
CIP395123.6	480	161	871	245	445	411	928	670	949
CIP395152.16	987	375	1171	368	718	1864	1260	1578	1046
CIP395169.17	141	209	610	140	250	1343	1138	1200	650
CIP395169.4	750	179	714	280	450	1208	1505	1673	611
CIP395179.21	943	1618	1036	368	1599	2174	1671	1023	1909
CIP396004.103	489	703	710	210	799	862	508	660	1594
CIP396004.225	633	643	785	280	500	1114	652	383	1758
CIP396004.263	915	1173	628	175	964	601	704	808	1363

CIP396004.301	337	440	619	123	458	315	280	233	1185
CIP396004.309	1811	1051	1131	998	1875	2047	1431	1428	2144
CIP396004.320	895	527	1072	525	964	1073	477	980	1625
CIP396004.337	1344	1114	1712	280	1768	513	831	1005	2036
CIP396008.104	416	676	786	228	NA	626	254	550	1531
CIP396009.207	1548	1169	1345	893	2249	2462	1855	1300	2293
CIP396009.225	813	796	1375	385	1589	1435	1015	1055	1927
CIP396009.239	1881	1007	1170	788	2640	1324	1470	1415	1964
CIP396009.240	1720	NA	1120	945	2046	1639	1571	1500	1955
CIP396009.258	1736	1481	1158	980	2096	2683	2122	1800	2734
CIP396010.217	207	206	1256	245	520	945	936	948	420
CIP396010.218	693	306	722	140	NA	583	1129	1288	444
CIP396012.266	394	230	636	123	327	799	713	1023	450
CIP396012.271	458	163	1225	228	333	1307	1374	1170	846
CIP396012.288	269	211	1023	210	213	1178	1601	1955	338
CIP396017.215	407	711	899	280	960	595	630	875	1573
CIP396018.241	434	624	666	NA	1009	467	508	NA	1722
CIP396023.109	194	139	774	158	164	1361	805	820	670
CIP396026.101	459	965	804	158	976	713	578	760	1588
CIP396026.103	83	224	383	315	330	525	324	238	189
CIP396027.111	779	NA	1224	420	1424	1103	1444	828	1938
CIP396027.205	896	999	598	333	1466	735	674	1765	1396
CIP396029.102	883	494	653	123	810	337	525	533	1399
CIP396029.205	1697	916	1458	438	1390	1741	1190	790	1865
CIP396029.250	556	294	1118	175	564	443	385	443	1593
CIP396030.105	165	334	733	140	379	223	254	235	780
CIP396031.108	431	434	784	298	778	1164	761	543	1279
CIP396031.118	2021	1390	1707	1313	2615	1598	1505	1265	1813
CIP396031.119	600	796	819	175	964	249	289	428	1371
CIP396033.102	299	505	765	280	794	477	175	365	978
CIP396034.103	415	349	768	350	380	748	254	318	1319
CIP396034.268	567	562	418	105	532	373	499	368	997
CIP396036.113	468	980	1395	263	985	718	998	798	1704
CIP396036.201	678	748	1135	NA	864	391	499	825	1571
CIP396037.215	774	658	514	245	480	367	350	548	1257
CIP396038.101	719	876	1258	280	1683	1098	814	778	1335
CIP396038.105	444	415	2635	333	961	1601	1199	948	1810
CIP396038.107	1408	860	1273	543	2003	1496	1243	1600	1774
CIP396039.103	401	259	1344	53	694	801	1068	1063	608
CIP396039.225	1339	966	591	420	1351	1146	626	545	1299
CIP396041.102	248	179	1310	158	480	1334	840	933	660
CIP396043.226	367	269	498	NA	289	782	624	NA	315
CIP396046.105	138	153	640	88	407	840	1251	1130	551
CIP396236.16	1665	501	1216	298	1673	618	1129	675	1939
CIP396236.20	536	432	634	123	536	490	442	563	1572
CIP396236.5	1939	1695	1725	350	1269	1797	1299	948	1968
CIP396240.2	272	163	1067	980	309	251	403	695	364



CIP396240.20	603	288	871	158	305	1820	1479	1730	810
CIP396240.23	392	207	NA	53	246	513	403	378	268
CIP396241.4	537	431	1669	210	944	1528	1155	1400	1247
CIP396244.12	232	425	1065	280	398	1149	648	1070	1070
CIP396244.17	278	237	750	175	594	1511	1186	1220	1365
CIP396247.15	432	114	1138	228	375	1902	1186	1165	1101
CIP396247.18	342	296	1048	298	668	875	1173	1283	688
CIP396256.4	231	216	1114	210	896	1464	1129	1110	1049
CIP396263.8	193	187	558	228	150	449	276	170	144
CIP396264.14	213	228	787	70	284	438	319	305	441
CIP720064	2687	2494	3203	1952	3213	2532	2680	2730	2996

Supplementary table S2.sAUDPC.

potato genotype	Comas 2001	Comas 2002	Comas 2004	Comas 2005	Comas 2006	Oxa 2001	Oxa 2002	Oxa 2005	Oxa 2006
CIP377744.1	2.30	2.90	1.70	1.70	1.90	3.30	3.10	1.90	3.10
CIP384866.5	4.80	3.70	5.80	4.70	4.30	3.20	3.40	4.00	5.10
CIP391002.6	2.30	1.10	2.50	0.50	1.90	1.20	1.10	1.60	2.90
CIP391004.10	1.00	0.40	2.70	0.80	0.90	2.70	2.50	NA	1.00
CIP391004.15	5.90	3.70	5.00	5.80	5.70	6.60	4.20	5.60	6.10
CIP391004.18	1.10	0.70	2.70	0.80	0.50	0.90	0.50	0.90	2.70
CIP391004.4	5.70	3.60	3.80	5.20	3.50	6.30	4.50	3.30	5.20
CIP391011.17	0.90	0.80	1.50	0.30	0.70	3.40	2.00	5.80	0.80
CIP391013.1	5.80	2.60	3.90	3.30	5.90	6.00	5.30	5.20	5.40
CIP391046.14	5.60	4.40	4.40	5.40	4.80	3.90	2.70	4.00	5.50
CIP391046.27	3.40	4.30	4.60	1.00	3.00	5.20	3.00	2.70	5.20
CIP391047.20	1.00	0.30	1.90	0.60	0.40	2.10	1.80	2.50	1.20
CIP391047.34	1.70	0.50	3.15	NA	0.83	2.80	2.15	NA	1.18
CIP391047.60	2.50	0.60	2.30	0.90	1.40	4.20	NA	4.70	2.30
CIP391058.175	0.70	0.30	3.10	0.30	0.40	3.30	2.90	4.20	1.60
CIP391065.69	0.60	0.30	3.10	0.20	0.70	2.80	1.50	6.10	0.80
CIP391065.81	0.50	0.60	1.80	0.60	0.60	2.90	2.30	2.90	1.90
CIP391580.30	1.60	1.70	3.10	0.60	1.80	2.20	2.00	2.00	3.10
CIP391583.25	0.90	0.60	1.10	0.50	0.30	NA	2.50	3.80	1.00
CIP391585.167	0.30	0.50	1.60	0.40	0.40	1.90	2.30	1.80	0.90
CIP391585.179	0.20	0.60	1.80	NA	0.40	3.40	3.10	3.20	1.10
CIP391585.5	0.30	0.30	0.50	0.90	0.50	1.30	0.70	3.00	0.50
CIP391586.109	6.40	4.80	3.90	6.20	1.10	NA	3.70	5.70	1.20
CIP391586.12	0.30	0.60	3.50	0.60	NA	4.20	3.80	2.50	5.90
CIP391679.12	6.30	5.00	4.90	6.40	6.90	6.70	6.90	7.00	6.30
CIP391679.7	6.40	5.60	5.30	6.20	6.50	7.00	6.30	6.90	6.80
CIP391679.9	5.80	3.60	3.10	5.30	6.50	5.90	4.90	6.50	6.10
CIP392617.54	0.20	1.70	1.30	0.20	0.40	0.90	0.50	NA	0.50
CIP392622.54	0.50	0.30	1.60	0.10	0.70	2.20	1.30	2.10	1.60
CIP392622.58	1.30	0.30	3.10	0.80	1.40	3.80	2.40	3.20	1.50
CIP392633.10	4.00	3.20	3.80	1.40	3.90	1.50	3.30	2.90	3.60
CIP392633.2	4.70	2.10	4.10	1.10	2.90	4.80	4.20	2.80	3.70
CIP392633.23	2.30	1.80	2.70	0.80	2.80	1.70	2.30	1.80	3.20
CIP392633.54	3.40	2.70	3.70	0.70	3.00	1.20	3.80	3.00	3.40
CIP392633.6	4.10	4.10	3.10	1.10	3.90	3.30	2.80	3.10	4.70
CIP392633.64	3.50	3.30	3.40	0.40	3.10	1.40	2.80	2.70	3.30
CIP392634.49	0.20	0.30	2.40	0.60	0.60	1.50	1.80	2.60	0.70
CIP392634.52	0.70	0.40	1.10	0.50	0.60	2.20	1.60	3.10	0.60
CIP392637.10	0.50	0.50	2.80	0.20	0.60	2.60	2.30	3.20	1.40
CIP392637.27	0.50	0.30	3.60	1.80	1.10	2.10	2.00	2.60	1.30
CIP392639.2	1.10	1.80	2.20	1.00	1.70	1.20	1.20	2.10	3.10
CIP392639.34	3.20	2.20	3.50	1.40	2.90	3.30	2.50	2.40	4.20
CIP392639.53	2.10	2.90	3.50	0.50	1.20	2.10	1.40	2.20	3.20
CIP392639.8	6.10	2.60	3.70	3.20	5.00	4.90	3.20	3.50	5.20

CIP392640.18	0.30	0.30	2.90	0.50	0.90	1.80	1.50	5.30	1.70
CIP392640.9	0.50	0.20	3.50	1.80	1.30	3.20	2.80	3.00	2.00
CIP392642.2	3.80	3.40	4.00	1.60	3.70	2.30	3.50	2.50	4.30
CIP392650.12	0.40	0.60	2.20	0.60	0.50	1.80	1.50	2.40	1.10
CIP392650.49	0.30	0.50	1.30	1.00	1.00	2.10	1.90	2.90	1.10
CIP392652.8	4.10	1.60	2.90	1.00	2.00	3.70	3.30	5.00	1.70
CIP392657.171	0.90	0.20	2.10	0.30	0.20	2.90	2.30	3.20	1.20
CIP392657.18	1.50	0.50	4.50	0.60	0.90	3.90	3.30	7.10	2.10
CIP392657.8	4.40	0.30	3.60	0.20	0.70	4.70	3.80	3.00	1.60
CIP393042.50	2.00	1.10	2.10	0.50	1.70	0.90	0.80	0.80	1.90
CIP393072.55	3.20	3.10	3.60	1.10	2.30	2.90	3.10	2.20	3.50
CIP393073.179	0.70	1.20	1.80	0.20	1.30	1.10	1.00	0.80	1.60
CIP393073.197	1.60	2.20	3.50	0.50	1.20	0.90	2.20	2.20	2.40
CIP393074.86	0.50	0.40	0.70	0.60	0.40	1.10	1.10	1.10	0.40
CIP393075.54	1.90	0.20	1.90	1.10	1.20	1.20	2.10	1.00	2.30
CIP393077.159	NA	3.15	2.30	NA	1.03	1.30	1.80	1.10	2.23
CIP393077.51	2.70	2.20	3.70	1.10	2.80	2.00	3.00	1.90	2.90
CIP393077.54	0.90	2.00	2.80	0.40	1.10	1.10	1.50	0.90	1.90
CIP393079.24	0.60	0.40	1.10	0.10	0.60	1.20	1.50	1.90	1.10
CIP393079.4	0.50	0.60	1.80	0.20	0.70	1.50	1.50	1.90	0.90
CIP393083.2	0.80	1.10	3.00	2.10	1.30	4.60	2.60	3.80	1.30
CIP393084.31	1.20	2.00	2.20	0.60	1.00	1.20	1.30	1.00	2.00
CIP393085.5	2.10	0.10	1.30	0.80	1.00	3.40	1.80	2.40	1.30
CIP393111.3	1.00	0.40	NA	0.40	1.40	3.60	1.20	2.00	2.90
CIP393220.54	1.10	0.70	0.90	0.50	0.80	3.10	1.70	3.20	1.10
CIP393227.66	0.80	0.40	1.60	0.30	0.50	1.60	1.20	1.80	0.90
CIP393228.21	1.00	0.50	3.60	0.50	0.80	2.10	1.80	2.90	1.80
CIP393228.67	0.40	0.30	2.50	0.30	0.40	2.10	1.20	0.90	0.70
CIP393242.50	3.00	0.70	4.00	0.30	1.80	1.30	0.80	1.20	3.50
CIP393243.53	2.00	0.70	5.00	0.60	1.00	0.90	0.60	0.60	3.00
CIP393248.52	1.00	0.50	2.10	0.60	1.10	4.00	3.00	4.90	1.30
CIP393248.55	2.00	0.50	3.00	0.60	1.20	3.90	2.90	6.20	1.70
CIP393280.57	0.20	0.50	2.50	0.10	1.30	2.70	1.40	1.90	0.90
CIP393280.64	5.30	3.50	2.60	1.30	2.30	2.80	1.50	1.30	2.50
CIP393280.80	0.40	0.50	0.90	0.40	0.80	1.70	1.80	NA	0.50
CIP393280.82	0.50	0.30	3.70	0.60	0.30	2.60	1.80	2.60	0.40
CIP393280.83	0.70	0.50	4.10	0.60	0.80	3.10	2.20	3.50	2.10
CIP393284.39	2.00	0.60	2.20	0.90	1.60	2.90	2.90	5.20	1.40
CIP393339.155	2.70	0.70	2.90	0.50	1.20	NA	2.70	5.70	2.10
CIP393339.242	1.50	0.80	2.10	0.30	0.70	2.40	2.50	3.50	1.60
CIP393349.35	0.40	0.60	1.80	1.00	0.60	2.40	2.40	4.10	1.50
CIP393349.55	0.60	0.70	3.10	0.50	0.80	3.60	2.70	4.70	2.50
CIP393349.68	1.00	0.40	1.10	0.80	0.50	2.40	1.90	2.80	0.90
CIP393360.64	0.20	0.40	2.10	0.60	0.90	1.30	1.10	2.80	1.10
CIP393371.157	2.30	2.40	3.10	0.80	2.20	0.90	2.30	1.60	2.40
CIP393371.159	1.90	2.20	2.70	NA	1.10	1.40	0.80	0.80	2.60
CIP393371.164	1.60	1.00	3.00	0.50	1.20	1.30	1.40	1.10	1.00

CIP393371.179	1.40	1.30	2.20	0.40	0.90	0.90	0.60	0.80	1.30
CIP393371.58	0.20	0.50	0.50	0.10	0.30	0.50	0.50	0.70	0.70
CIP393382.44	4.50	2.50	2.10	2.50	1.80	2.20	2.80	2.30	3.70
CIP393385.39	1.30	0.70	4.00	0.40	1.10	3.70	2.50	3.20	3.20
CIP393385.47	1.00	0.90	3.30	0.50	1.30	4.40	2.00	3.50	2.20
CIP393385.57	3.90	1.60	2.70	1.90	2.90	2.80	2.40	2.50	4.00
CIP393438.96	1.40	0.70	3.30	0.80	0.70	3.40	3.00	4.40	2.70
CIP393453.198	1.20	0.40	3.30	0.80	0.90	4.40	2.70	4.40	2.90
CIP395007.213	1.40	0.60	1.40	0.30	1.00	1.80	1.50	2.60	0.90
CIP395011.19	0.50	0.70	1.50	0.70	NA	2.20	1.70	1.40	0.80
CIP395011.2	0.60	0.50	1.60	0.50	1.20	2.50	1.70	2.50	1.30
CIP395013.211	3.80	1.30	2.60	0.90	1.60	4.10	3.50	6.80	1.80
CIP395015.5	1.30	0.60	2.10	1.00	1.40	3.30	3.10	5.70	1.60
CIP395015.6	2.40	1.30	1.90	1.10	1.00	2.70	2.80	3.10	1.60
CIP395016.255	0.60	0.60	1.20	0.30	0.70	2.00	3.00	5.20	0.70
CIP395017.14	1.40	0.70	2.00	0.50	1.00	4.60	2.70	4.40	1.10
CIP395017.227	0.30	0.50	1.40	0.40	0.90	2.20	1.90	2.20	0.70
CIP395017.229	0.40	0.60	1.50	0.40	0.80	3.10	2.60	4.80	1.30
CIP395017.242	0.90	0.50	1.30	0.60	0.20	2.20	2.40	3.10	1.20
CIP395037.107	0.40	1.00	1.20	0.30	0.90	0.70	1.10	1.00	2.70
CIP395052.11	0.80	0.60	1.90	0.50	0.60	3.60	2.60	5.00	0.80
CIP395077.12	0.30	0.30	1.40	0.40	0.30	3.80	2.70	2.80	1.60
CIP395084.9	2.58	3.10	2.75	NA	2.95	1.85	2.95	NA	4.60
CIP395096.2	3.70	1.10	1.80	1.00	3.20	2.30	3.10	4.10	1.80
CIP395096.3	0.60	0.50	1.70	1.00	0.60	2.10	3.00	3.20	1.30
CIP395096.7	1.00	1.30	1.70	0.90	1.90	4.20	2.80	2.60	1.60
CIP395097.4	1.20	0.80	1.40	0.40	1.40	4.40	2.90	3.70	1.40
CIP395109.29	0.50	0.50	1.40	0.70	0.50	3.60	2.90	2.60	1.80
CIP395109.34	0.60	0.70	0.90	1.10	0.60	2.00	2.20	2.10	0.80
CIP395109.4	0.30	1.00	1.00	0.90	2.10	2.50	2.50	2.60	1.00
CIP395109.7	2.90	2.20	1.90	1.60	4.10	1.90	2.00	1.50	3.20
CIP395111.13	1.50	0.60	1.70	0.40	0.80	2.90	2.90	3.00	1.30
CIP395112.19	0.20	0.50	0.70	0.30	0.80	4.00	2.00	3.00	0.60
CIP395112.32	0.80	0.60	1.80	0.80	0.80	5.60	3.40	5.70	1.30
CIP395112.36	0.80	0.90	1.40	0.60	0.70	5.30	3.40	3.60	1.40
CIP395112.6	0.90	0.70	0.80	0.60	0.80	3.00	3.30	5.20	1.10
CIP395112.9	1.30	0.70	2.20	0.90	1.00	4.60	3.30	4.40	1.00
CIP395114.5	1.10	0.50	1.70	0.60	0.90	5.50	3.20	4.50	1.50
CIP395117.3	0.50	1.00	1.40	0.60	0.80	1.40	2.70	1.90	4.50
CIP395123.6	1.10	0.40	1.60	0.80	0.80	1.00	2.10	1.50	1.90
CIP395152.16	2.20	0.90	2.20	1.10	1.30	4.40	2.80	3.50	2.10
CIP395169.17	0.30	0.50	1.10	0.40	0.50	3.20	2.50	2.60	1.30
CIP395169.4	1.70	0.40	1.30	0.90	0.80	2.90	3.40	3.70	1.20
CIP395179.21	2.10	3.90	1.90	1.10	3.00	5.20	3.70	2.20	3.80
CIP396004.103	1.10	1.70	1.30	0.60	1.50	2.00	1.10	1.50	3.20
CIP396004.225	1.40	1.50	1.50	0.90	0.90	2.60	1.50	0.80	3.50
CIP396004.263	2.00	2.80	1.20	0.50	1.80	1.40	1.60	1.80	2.70

CIP396004.301	0.80	1.10	1.20	0.40	0.90	0.70	0.60	0.50	2.40
CIP396004.309	4.00	2.50	2.10	3.10	3.50	4.90	3.20	3.10	4.30
CIP396004.320	2.00	1.30	2.00	1.60	1.80	2.50	1.10	2.20	3.30
CIP396004.337	3.00	2.70	3.20	0.90	3.30	1.20	1.90	2.20	4.10
CIP396008.104	0.90	1.60	1.50	0.70	NA	1.50	0.60	1.20	3.10
CIP396009.207	3.50	2.80	2.50	2.70	4.20	5.80	4.20	2.90	4.60
CIP396009.225	1.80	1.90	2.60	1.20	3.00	3.40	2.30	2.30	3.90
CIP396009.239	4.20	2.40	2.20	2.40	4.90	3.10	3.30	3.10	3.90
CIP396009.240	3.80	NA	2.10	2.90	3.80	3.90	3.50	3.30	3.90
CIP396009.258	3.90	3.60	2.20	3.00	3.90	6.40	4.80	4.00	5.50
CIP396010.217	0.50	0.50	2.40	0.80	1.00	2.20	2.10	2.10	0.80
CIP396010.218	1.50	0.70	1.40	0.40	NA	1.40	2.50	2.80	0.90
CIP396012.266	0.90	0.60	1.20	0.40	0.60	1.90	1.60	2.20	0.90
CIP396012.271	1.00	0.40	2.30	0.70	0.60	3.10	3.10	2.60	1.70
CIP396012.288	0.60	0.50	1.90	0.60	0.40	2.80	3.60	4.30	0.70
CIP396017.215	0.90	1.70	1.70	0.90	1.80	1.40	1.40	1.90	3.10
CIP396018.241	0.90	1.25	1.27	NA	1.75	1.10	1.23	NA	3.50
CIP396023.109	0.40	0.30	1.50	0.50	0.30	3.20	1.80	1.80	1.30
CIP396026.101	1.00	2.30	1.50	0.50	1.80	1.70	1.30	1.70	3.20
CIP396026.103	0.20	0.50	0.70	1.00	0.60	1.20	0.70	0.50	0.40
CIP396027.111	1.70	NA	2.30	1.30	2.70	2.60	3.20	1.80	3.90
CIP396027.205	2.00	2.40	1.10	1.00	2.70	1.70	1.50	3.90	2.80
CIP396029.102	2.00	1.20	1.20	0.40	1.50	0.80	1.20	1.20	2.80
CIP396029.205	3.80	2.20	2.70	1.30	2.60	4.10	2.70	1.70	3.70
CIP396029.250	1.20	0.70	2.10	0.50	1.10	1.10	0.90	1.00	3.20
CIP396030.105	0.40	0.80	1.40	0.40	0.70	0.50	0.60	0.50	1.60
CIP396031.108	1.00	1.00	1.50	0.90	1.50	2.80	1.70	1.20	2.60
CIP396031.118	4.50	3.30	3.20	4.00	4.90	3.80	3.40	2.80	3.60
CIP396031.119	1.30	1.90	1.50	0.50	1.80	0.60	0.60	0.90	2.70
CIP396033.102	0.70	1.20	1.40	0.90	1.50	1.10	0.40	0.80	2.00
CIP396034.103	0.90	0.80	1.40	1.10	0.70	1.80	0.60	0.70	2.60
CIP396034.268	1.30	1.40	0.80	0.30	1.00	0.90	1.10	0.80	2.00
CIP396036.113	1.00	2.40	2.60	0.80	1.80	1.70	2.20	1.80	3.40
CIP396036.201	1.50	1.80	2.10	NA	1.60	0.90	1.10	1.80	3.10
CIP396037.215	1.70	1.60	1.00	0.80	0.90	0.90	0.80	1.20	2.50
CIP396038.101	1.60	2.10	2.40	0.90	3.10	2.60	1.80	1.70	2.70
CIP396038.105	1.00	1.00	4.90	1.00	1.80	3.80	2.70	2.10	3.60
CIP396038.107	3.10	2.10	2.40	1.70	3.70	3.50	2.80	3.50	3.60
CIP396039.103	0.90	0.60	2.50	0.20	1.30	1.90	2.40	2.30	1.20
CIP396039.225	3.00	2.30	1.10	1.30	2.50	2.70	1.40	1.20	2.60
CIP396041.102	0.60	0.40	2.50	0.50	0.90	3.20	1.90	2.00	1.30
CIP396043.226	0.77	0.53	1.03	NA	0.50	1.77	1.37	NA	0.60
CIP396046.105	0.30	0.40	1.20	0.30	0.80	2.00	2.80	2.50	1.10
CIP396236.16	3.70	1.20	2.30	0.90	3.10	1.50	2.50	1.50	3.90
CIP396236.20	1.20	1.00	1.20	0.40	1.00	1.20	1.00	1.20	3.10
CIP396236.5	4.30	4.10	3.20	1.10	2.40	4.30	2.90	2.10	3.90
CIP396240.2	0.60	0.40	2.00	3.00	0.60	0.60	0.90	1.50	0.70

CIP396240.20	1.30	0.70	1.60	0.50	0.60	4.30	3.30	3.80	1.60
CIP396240.23	0.90	0.50	NA	0.20	0.50	1.20	0.90	0.80	0.50
CIP396241.4	1.20	1.00	3.10	0.60	1.80	3.60	2.60	3.10	2.50
CIP396244.12	0.50	1.00	2.00	0.90	0.70	2.70	1.40	2.40	2.10
CIP396244.17	0.60	0.60	1.40	0.50	1.10	3.60	2.70	2.70	2.70
CIP396247.15	1.00	0.30	2.10	0.70	0.70	4.50	2.70	2.60	2.20
CIP396247.18	0.80	0.70	2.00	0.90	1.20	2.10	2.60	2.80	1.40
CIP396256.4	0.50	0.50	2.10	0.60	1.70	3.50	2.50	2.40	2.10
CIP396263.8	0.40	0.40	1.00	0.70	0.30	1.10	0.60	0.40	0.30
CIP396264.14	0.50	0.50	1.50	0.20	0.50	1.00	0.70	0.70	0.90
CIP720064	6.00	6.00	6.00	6.00	6.00	6.00	6.00	6.00	6.00

Supplementary table S3a. Pedigree of parent 1.

genotype	parent1	grandparent 1-1	grandparent 1-2	great grandparent 1-1-1	great grandparent 1-1-2	great grandparent 1-2-1	great grandparent 1-2-2
395037.107	391004.4	387004.4	386206.4	381381.20	375333.1 (7XY.1)	380474.8	BK PRECOZ-84
391583.25	386209.15	380479.15	BK PRECOZ-84	676084 (INDIA-967)	LT XY BULK		
396009.258	391004.4	387004.4	386206.4	381381.20	375333.1 (7XY.1)	380474.8	BK PRECOZ-84
395112.32	391686.15	387303.1	383300.21 (C83.119)	378971.833	BULK MEX	377887.17 ((377887.17 x LT-7).21)	378017.2 (LT-7)
395112.36	391686.15	387303.1	383300.21 (C83.119)	378971.833	BULK MEX	377887.17 ((377887.17 x LT-7).21)	378017.2 (LT-7)
395017.14	393085.13	387348.20	390357.4	382181.27	C83.119	382138.4	385280.1 (XY.13)
392657.8	387341.1	382169.21	C83.119	380013.2	BULK MEX		
393083.2	387315.27	382121.5	C83.119	377803.11	BULK MEX		
395112.19	391686.15	387303.1	383300.21 (C83.119)	378971.833	BULK MEX	377887.17 ((377887.17 x LT-7).21)	378017.2 (LT-7)
393385.47	387231.7	382133.7	676008 (I-1039)	378971.928	BULK MEX	US 136.6	3345D(1) x 2288A(2)
395109.29	391589.26	387231.7	387334.5	382133.7	676008 (I-1034)	382155.2	383300.21 (C83.119)
395077.12	391586.109	387169.2	387170.9	322181.27	575049 (CEW-69-1)	382182.10	575049 (CEW-69-1)
396009.24	391004.4	387004.4	386206.4	381381.20	375333.1 (7XY.1)	380474.8	BK PRECOZ-84
395013.211	393085.5	387348.20	390357.4	382181.27	C83.119	382138.4	385280.1 (XY.13)
396009.225	391004.4	387004.4	386206.4	381381.20	375333.1 (7XY.1)	380474.8	BK PRECOZ-84
393248.55	387002.11	381378.22	375333.1 (7XY.1)	378971.833	PRECOZ BULK	N-558.43	OP
391046.14	386209.1	380479.15	BK PRECOZ-84	676084 (INDIA-967)	LT XY BULK		
393385.39	387231.7	382133.7	676008 (I-1039)	378971.928	BULK MEX	US 136.6	3345D(1) x 2288A(2)
396241.4	392634.52	387136.14	387170.9	382121.25	575049 (CEW-69-1)	382182.10	575049 (CEW-69-1)
395169.17	392652.8	387231.7	387170.9	382133.4	676008 (I-1039)	382182.10	575049 (CEW-69-1)
396023.109	391047.34	386209.10	387338.3	380479.15	BK PRECOZ-84	382160.30	383300.21 (C83.119)
393085.5	387348.20	382181.27	C83.119	378508.277	LB BULK		
395111.13	391686.5	387303.71	387205.8	381403.1	383300.21 (C83.119)	381397.16	676008 (I-1039)
391011.17	387041.12	381406.6	375333.1 (7XY.1)	378493.915	BULK	N-558.43	OP

391585.179	387132.2	382119.6	575049 (CEW-69-1)	378508.277	BULK MEX	(ALPHA x HOL32)	(USDA- 133.3) x (LEONA x PENN 3PD- 23)
392639.34	387143.22	382133.7	575049 (CEW-69-1)	378971.928	BULK MEX	(ALPHA x HOL32)	(USDA- 133.3) x (LEONA x PENN 3PD- 23)
396004.225	391002.6	386209.1	386206.4	380479.15	BK PRECOZ- 84	380474.8	BK PRECOZ- 84
395112.6	391686.15	387303.1	383300.21 (C83.119)	378971.833	BULK MEX	377887.17 ((377887.17 x LT-7).21)	378017.2 (LT- 7)
391058.175	387170.16	382182.10	575049 (CEW-69-1)	380112.3	PRECOZ BULK	(ALPHA x HOL32)	(USDA- 133.3) x (LEONA x PENN 3PD- 23)
393220.54	381400.22	378971.787	BULK MEX	INDIA-832	700111 (Paccosan)		
392657.171	387341.1	382169.21	C83.119	380013.2	BULK MEX		
396038.107	393077.54	387348.20	389746.2	382181.24	C83.119	381379.9	386614.16 (XY.16)
393280.64	387015.3	382171.26	375333.1 (7XY.1)	380086.3	BULK MEX	N-558.43	OP
393284.39	387015.12	382171.26	375333.1 (7XY.1)	380086.3	BULK MEX	N-558.43	OP
395015.6	393083.2	387315.27	390357.4	382121.25	C83.119	382138.4	385280.1 (XY.13)
391065.81	387348.20	382181.27	C83.119	378508.277	LB BULK		
391065.69	387348.20	382181.27	C83.119	378508.277	LB BULK		
393280.57	387015.3	382171.26	375333.1 (7XY.1)	380086.3	BULK MEX	N-558.43	OP
395011.19	393085.5	387348.20	390357.4	382181.27	C83.119	382138.4	385280.1 (XY.13)
391047.34	386209.10	380479.15	BK PRECOZ- 84	676084 (INDIA-967)	LT XY BULK		
396244.12	391580.30	387002.2	387214.9	381378.22	375333.1 (7XY.1)	381405.26	676008 (I- 1039)
392637.10	387143.22	382133.7	575049 (CEW-69-1)	378971.928	BULK MEX	(ALPHA x HOL32)	(USDA- 133.3) x (LEONA x PENN 3PD- 23)
393280.82	387015.3	382171.26	375333.1 (7XY.1)	380086.3	BULK MEX	N-558.43	OP
396256.4	391585.179	387132.2	387170.9	382119.6	575049 (CEW-69-1)	382182.10	575049 (CEW-69-1)
395017.227	393085.13	387348.20	390357.4	382181.27	C83.119	382138.4	385280.1 (XY.13)



393339.242	387164.4	382171.10	575049 (CEW-69-1)	380086.3	BULK MEX	(ALPHA x HOL32)	(USDA- 133.3) x (LEONA x PENN 3PD- 23)
396031.108	392633.64	387132.2	387334.5	382119.6	575049 (CEW-69-1)	382155.2	383300.21 (C83.119)
395011.2	393085.5	387348.20	390357.4	382181.27	C83.119	382138.4	385280.1 (XY.13)
393349.68	387170.6	382182.10	575049 (CEW-69-1)	380112.3	PRECOZ BULK	(ALPHA x HOL32)	(USDA- 133.3) x (LEONA x PENN 3PD- 23)
395096.2	393085.5	387348.20	390357.4	382181.27	C83.119	382138.4	385280.1 (XY.13)
395109.34	391589.26	387231.7	387334.5	382133.7	676008 (I- 1034)	382155.2	383300.21 (C83.119)
393382.44	387205.5	381397.16	676008 (I- 1039)	378504.721	BULK MEX	US 136.6	3345D(1) x 2288A(2)
391580.3	387002.2	381378.22	375333.1 (7XY.1)	378971.833	PRECOZ BULK	N-558.43	OP
392634.52	387136.14	382121.25	575049 (CEW-69-1)	378508.295	BULK MEX	(ALPHA x HOL32)	(USDA- 133.3) x (LEONA x PENN 3PD- 23)
393228.67	386209.10	380479.15	BK PRECOZ- 84	676084 (INDIA-967)	LT XY BULK		
395084.9	392633.6	387132.2	387334.5	382119.6	575049 (CEW-69-1)	382155.2	383300.21 (C83.119)
395109.7	391589.26	387231.7	387334.5	382133.7	676008 (I- 1034)	382155.2	383300.21 (C83.119)
396046.105	TXY.4						
396027.205	392633.23	387132.2	387334.5	382119.6	575049 (CEW-69-1)	382155.2	383300.21 (C83.119)
395096.3	393085.5	387348.20	390357.4	382181.27	C83.119	382138.4	385280.1 (XY.13)
392650.12	387181.7	381382.34	676008 (I- 1039)	378493.928	PRECOZ BULK	US 136.6	3345D(1) x 2288A(2)
396026.101	392633.4	387132.2	387334.5	382119.6	575049 (CEW-69-1)	382155.2	383300.21 (C83.119)
395117.3	392642.2	387164.4	387334.5	382171.10	575049 (CEW-69-1)	382155.2	383300.21 (C83.119)
396043.226	393401.55	387312.2	387170.9	382119.15	C83.119	382182.10	575049 (CEW-69-1)
393227.66	386209.10	380479.15	BK PRECOZ- 84	676084 (INDIA-967)	LT XY BULK		
396004.263	391002.6	386209.1	386206.4	380479.15	BK PRECOZ- 84	380474.8	BK PRECOZ- 84
396034.103	393042.50	387415.49	387415.6	380496.6 (P- 7)	800938 (AVRDC- 1287.19)	380406.6 (P- 7)	800938 (AVRDC- 1287.19)
393079.4	387004.13	381381.20	375333.1 (7XY.1)	378493.915	PRECOZ BULK	N-558.43	OP

396236.16	393072.55	387015.12	389746.2	382171.26	375333.1 (7XY.1)	381379.9	386614.16 (XY.16)
392633.64	387132.2	382119.6	575049 (CEW-69-1)	378508.277	BULK MEX	(ALPHA x HOL32)	(USDA- 133.3) x (LEONA x PENN 3PD- 23)
393371.159	387170.16	382182.10	575049 (CEW-69-1)	380112.3	PRECOZ BULK	(ALPHA x HOL32)	(USDA- 133.3) x (LEONA x PENN 3PD- 23)
396026.103	392633.4	387132.2	387334.5	382119.6	575049 (CEW-69-1)	382155.2	383300.21 (C83.119)
392634.49	387136.14	382121.25	575049 (CEW-69-1)	378508.295	BULK MEX	(ALPHA x HOL32)	(USDA- 133.3) x (LEONA x PENN 3PD- 23)
393242.5	387002.11	381378.22	375333.1 (7XY.1)	378971.833	PRECOZ BULK	N-558.43	OP
393371.164	387170.16	382182.10	575049 (CEW-69-1)	380112.3	PRECOZ BULK	(ALPHA x HOL32)	(USDA- 133.3) x (LEONA x PENN 3PD- 23)
392633.54	387132.2	382119.6	575049 (CEW-69-1)	378508.277	BULK MEX	(ALPHA x HOL32)	(USDA- 133.3) x (LEONA x PENN 3PD- 23)
393077.159	387348.20	382181.27	C83.119	378508.277	LB BULK		
393075.54	387315.27	382121.25	C83.119	378508.295	BULK MEX		
391585.5	387132.2	382119.6	575049 (CEW-69-1)	378508.277	BULK MEX	(ALPHA x HOL32)	(USDA- 133.3) x (LEONA x PENN 3PD- 23)
396008.104	391002.15	386209.1	386206.4	380479.15	BK PRECOZ- 84	380474.8	BK PRECOZ- 84
396018.241	391046.14	386209.1	387338.3	380479.15	BK PRECOZ- 84	382160.30	383300.21 (C83.119)
396004.337	391002.6	386209.1	386206.4	380479.15	BK PRECOZ- 84	380474.8	BK PRECOZ- 84
391002.6	386209.1	380479.15	BK PRECOZ- 84	676084 (INDIA-967)	LT XY BULK		
396236.2	393072.55	387015.12	389746.2	382171.26	375333.1 (7XY.1)	381379.9	386614.16 (XY.16)
393084.31	387326.27	382140.8	C83.119	377803.11	BULK MEX		
393079.24	387004.13	381381.20	375333.1 (7XY.1)	378493.915	PRECOZ BULK	N-558.43	OP
396033.102	392639.53	387143.22	387334.5	382133.7	575049 (CEW-69-1)	382155.2	383300.21 (C83.119)
393073.179	387015.13	382171.26	375333.1 (7XY.1)	380086.3	BULK MEX	N-558.43	OP
393077.54	387348.20	382181.27	C83.119	378508.277	LB BULK		

396029.25	392633.54	387132.2	387334.5	382119.6	575049 (CEW-69-1)	382155.2	383300.21 (C83.119)
393371.157	387170.16	382182.10	575049 (CEW-69-1)	380112.3	PRECOZ BULK	(ALPHA x HOL32)	(USDA- 133.3) x (LEONA x PENN 3PD- 23)
393073.197	387015.13	382171.26	375333.1 (7XY.1)	380086.3	BULK MEX	N-558.43	OP
396240.23	393371.58	387170.16	389746.2	382182.10	575049 (CEW-69-1)	381379.9	386614.16 (XY.16)
391004.18	387004.4	381381.20	375333.1 (7XY.1)	378493.915	PRECOZ BULK	N-558.43	OP
396264.14	393280.82	387015.3	386316.14 (XY.14)	382171.26	375333.1 (7XY.1)	379706.27 (LT-8)	378017.2 (LT- 7)
392617.54	387002.11	381378.22	375333.1 (7XY.1)	378971.833	PRECOZ BULK	N-558.43	OP
396036.201	393077.51	387348.20	389746.2	382181.27	C83.119	381379.9	386614.16 (XY.16)
396034.268	393042.50	387415.49	387415.6	380496.6 (P- 7)	800938 (AVRDC- 1287.19)	380406.6 (P- 7)	800938 (AVRDC- 1287.19)
396037.215	393077.54	387348.20	389746.2	382181.27	C83.119	381379.9	386614.16 (XY.16)
396004.301	391002.6	386209.1	386206.4	380479.15	BK PRECOZ- 84	380474.8	BK PRECOZ- 84
396240.2	393371.58	387170.16	389746.2	382182.10	575049 (CEW-69-1)	381379.9	386614.16 (XY.16)
393371.58	387170.16	382182.10	575049 (CEW-69-1)	380112.3	PRECOZ BULK	(ALPHA x HOL32)	(USDA- 133.3) x (LEONA x PENN 3PD- 23)
396031.119	392633.64	387132.2	387334.5	382119.6	575049 (CEW-69-1)	382155.2	383300.21 (C83.119)

Supplementary table S3b. Pedigree of parent 2.

genotype	parent2	grandparent 2-1	grandparent 2-2	great grandparent 2-1- 1	great grandparent 2-1- 2	great grandparent 2-2- 1	great grandparent 2-2- 2
395037.107	391679.12	381400.22	387205.8	378971.787	BULK MEX	381397.16	676008 (I-1039)
391583.25	387170.9	382182.10	575049 (CEW-69-1)	380112.3	PRECOZ BULK	(ALPHA x HOL32)	(USDA-133.3) x (LEONA x PENN 3PD-23)
396009.258	393280.58	387015.3	386316.14 (XY.14)	382171.26	375333.1 (7XY.1)	379706.27 (LT-8)	378017.2 (LT-7)
395112.32	393079.4	387004.13	390357.4	381381.20	375333.1 (7XY.1)	382138.4	385280.1 (XY.13)
395112.36	393079.4	387004.13	390357.4	381381.20	375333.1 (7XY.1)	382138.4	385280.1 (XY.13)
395017.14	392639.8	387143.22	387334.5	382133.7	575049 (CEW-69-1)	382155.2	383300.21 (C83.119)
392657.8	387170.9	382182.10	575049 (CEW-69-1)	380112.3	PRECOZ BULK	(ALPHA x HOL32)	(USDA-133.3) x (LEONA x PENN 3PD-23)
393083.2	390357.4	382138.4	385280.1 (XY.13)	374080.2	BULK MEX	379706.27 (LT-8)	575049 (CEW-69-1)
395112.19	393079.4	387004.13	390357.4	381381.20	375333.1 (7XY.1)	382138.4	385280.1 (XY.13)
393385.47	387170.9	382182.10	575049 (CEW-69-1)	380112.3	PRECOZ BULK	(ALPHA x HOL32)	(USDA-133.3) x (LEONA x PENN 3PD-23)
395109.29	393079.4	387004.13	390357.4	381381.20	375333.1 (7XY.1)	382138.4	385280.1 (XY.13)
395077.12	393053.6	387231.7	701241 (HUAGALINA)	382133.7	676008 (I-1039)		
396009.24	393280.58	387015.3	386316.14 (XY.14)	382171.26	375333.1 (7XY.1)	379706.27 (LT-8)	378017.2 (LT-7)
395013.211	391679.12	381400.22	387205.8	378971.787	BULK MEX	381397.16	676008 (I-1039)
396009.225	393280.58	387015.3	386316.14 (XY.14)	382171.26	375333.1 (7XY.1)	379706.27 (LT-8)	378017.2 (LT-7)
393248.55	386614.16 (XY.16)	Y84.007	800827 (ATLANTIC)			800823 (WAUSEON)	B-5141.6
391046.14	387338.3	382160.30	383300.21 (C83.119)	720044 (ROSITA)	BULK MEX	377887.17 ((377887.17 x LT- 7).21)	378017.2 (LT-7)
393385.39	387170.9	382182.10	575049 (CEW-69-1)	380112.3	PRECOZ BULK	(ALPHA x HOL32)	(USDA-133.3) x (LEONA x PENN 3PD-23)
396241.4	392626.9	387015.3	387334.5	382171.26	375333.1 (7XY.1)	382155.2	383300.21 (C83.119)
395169.17	391679.12	381400.22	387205.8	378971.787	BULK MEX	381397.16	676008 (I-1039)
396023.109	393280.57	387015.3	386316.14 (XY.14)	382171.26	375333.1 (7XY.1)	379706.27 (LT-8)	378017.2 (LT-7)
393085.5	390357.4	382138.4	385280.1 (XY.13)	374080.2	BULK MEX	379706.27 (LT-8)	575049 (CEW-69-1)
395111.13	393079.4	387004.13	39057.4	381381.20	375333.1 (7XY.1)	382138.4	385280.1 (XY.13)
391011.17	386206.4	380474.8	BK PRECOZ-84	374080.5	LT XY BULK		
391585.179	387170.9	382182.10	575049 (CEW-69-1)	380112.3	PRECOZ BULK	(ALPHA x HOL32)	(USDA-133.3) x (LEONA x PENN 3PD-23)
392639.34	387334.5	382155.2	383300.21 (C83.119)	CFJ-69.1	BULK MEX	377887.17 ((377887.17 x LT- 7).21)	378017.2 (LT-7)

396004.225	393382.64	387205.5	387338.3	381397.16	676008 (I-1039)	382160.30	383300.21 (C83.119)
395112.6	393079.4	387004.13	390357.4	381381.20	375333.1 (7XY.1)	382138.4	385280.1 (XY.13)
391058.175	387338.3	382160.30	383300.21 (C83.119)	720044 (ROSITA)	BULK MEX	377887.17 (((377887.17 x LT-7).21)	378017.2 (LT-7)
393220.54	387170.9	382182.10	575049 (CEW-69-1)	380112.3	PRECOZ BULK	(ALPHA x HOL32)	(USDA-133.3) x (LEONA x PENN 3PD-23)
392657.171	387170.9	382182.10	575049 (CEW-69-1)	380112.3	PRECOZ BULK	(ALPHA x HOL32)	(USDA-133.3) x (LEONA x PENN 3PD-23)
396038.107	393280.64	387015.3	386316.14 (XY.14)	382171.26	375333.1 (7XY.1)	379706.27 (LT-8)	378017.2 (LT-7)
393280.64	386316.14 (XY.16)	379706.27 (LT-8)	378017.2 (LT-7)	377257.1 (LT-1)	PVX + PVY BULK	ASC-77.055	?
393284.39	387170.9	382182.10	575049 (CEW-69-1)	380112.3	PRECOZ BULK	(ALPHA x HOL32)	(USDA-133.3) x (LEONA x PENN 3PD-23)
395015.6	391679.12	381400.22	387205.8	378971.787	BULK MEX	381397.16	676008 (I-1039)
391065.81	387338.3	382160.30	383300.21 (C83.119)	720044 (ROSITA)	BULK MEX	377887.17 (((377887.17 x LT-7).21)	378017.2 (LT-7)
391065.69	387338.3	382160.30	383300.21 (C83.119)	720044 (ROSITA)	BULK MEX	377887.17 (((377887.17 x LT-7).21)	378017.2 (LT-7)
393280.57	386316.14 (XY.16)	379706.27 (LT-8)	378017.2 (LT-7)	377257.1 (LT-1)	PVX + PVY BULK	ASC-77.055	?
395011.19	392639.8	387143.22	387334.5	382133.7	575049 (CEW-69-1)	382155.2	383300.21 (C83.119)
391047.34	387338.3	382160.30	383300.21 (C83.119)	720044 (ROSITA)	BULK MEX	377887.17 (((377887.17 x LT-7).21)	378017.2 (LT-7)
396244.12	392633.10	387132.2	387334.5	382119.6	575049 (CEW-69-1)	382155.2	383300.21 (C83.119)
392637.10	387170.9	382182.10	575049 (CEW-69-1)	380112.3	PRECOZ BULK	(ALPHA x HOL32)	(USDA-133.3) x (LEONA x PENN 3PD-23)
393280.82	386316.14 (XY.16)	379706.27 (LT-8)	378017.2 (LT-7)	377257.1 (LT-1)	PVX + PVY BULK	ASC-77.055	?
396256.4	392639.2	387143.22	387334.5	382133.7	575049 (CEW-69-1)	382155.2	383300.21 (C83.119)
395017.227	392639.8	387143.22	387334.5	382133.7	575049 (CEW-69-1)	382155.2	383300.21 (C83.119)
393339.242	SANI MILLA						
396031.108	393382.64	387205.5	387338.3	381397.16	676008 (I-1039)	382160.30	383300.21 (C83.119)
395011.2	392639.8	387143.22	387334.5	382133.7	575049 (CEW-69-1)	382155.2	383300.21 (C83.119)
393349.68	387338.3	382160.30	383300.21 (C83.119)	720044 (ROSITA)	BULK MEX	377887.17 (((377887.17 x LT-7).21)	378017.2 (LT-7)
395096.2	393053.6	387231.7	701241 (HUAGALINA)	382133.7	676008 (I-1039)		
395109.34	393079.4	387004.13	390357.4	381381.20	375333.1 (7XY.1)	382138.4	385280.1 (XY.13)
393382.44	387338.3	382160.30	383300.21 (C83.119)	720044 (ROSITA)	BULK MEX	377887.17 (((377887.17 x LT-7).21)	378017.2 (LT-7)

391580.3	387214.9	381405.26	676008 (I-1039)	378971.907	BULK	US 136.6	3345D(1) x 2288A(2)
392634.52	387170.9	382182.10	575049 (CEW-69-1)	380112.3	PRECOZ BULK	(ALPHA x HOL32)	(USDA-133.3) x (LEONA x PENN 3PD-23)
393228.67	387170.9	382182.10	575049 (CEW-69-1)	380112.3	PRECOZ BULK	(ALPHA x HOL32)	(USDA-133.3) x (LEONA x PENN 3PD-23)
395084.9	393053.6	387231.7	701241 (HUAGALINA)	382133.7	676008 (I-1039)		
395109.7	393079.4	387004.13	390357.4	381381.20	375333.1 (7XY.1)	382138.4	385280.1 (XY.13)
396046.105	393280.64	387015.3	386316.14 (XY.14)	382171.26	375333.1 (7XY.1)	379706.27 (LT-8)	378017.2 (LT-7)
396027.205	393382.64	387205.5	387338.3	381397.16	676008 (I-1039)	382160.30	383300.21 (C83.119)
395096.3	393053.6	387231.7	701241 (HUAGALINA)	382133.7	676008 (I-1039)		
392650.12	387170.9	382182.10	575049 (CEW-69-1)	380112.3	PRECOZ BULK	(ALPHA x HOL32)	(USDA-133.3) x (LEONA x PENN 3PD-23)
396026.101	393280.64	387015.3	386316.4 (XY.14)	382171.26	375333.1 (7XY.1)	379706.27 (LT-8)	378017.2 (LT-7)
395117.3	393079.4	387004.13	390357.4	381381.20	375333.1 (7XY.1)	382138.4	385280.1 (XY.13)
396043.226	393280.57	387015.3	386316.14 (XY.14)	382171.26	375333.1 (7XY.1)	379706.27 (LT-8)	378017.2 (LT-7)
393227.66	381400.22	378971.787	BULK MEX	INDIA-832	700111 (Paccosan)		
396004.263	393382.64	387205.5	387338.3	381397.16	676008 (I-1039)	382160.30	383300.21 (C83.119)
396034.103	393280.64	387015.3	386316.14 (XY.14)	382171.26	375333.1 (7XY.1)	379706.27 (LT-8)	378017.2 (LT-7)
393079.4	390357.4	382138.4	385280.1 (XY.13)	374080.2	BULK MEX	379706.27 (LT-8)	575049 (CEW-69-1)
396236.16	391679.7	381400.22	387205.8	378971.787	BULK MEX	381397.16	676008 (I-1039)
392633.64	387334.5	382155.2	383300.21 (C83.119)	CFJ-69.1	BULK MEX	377887.17 ((377887.17 x LT-7).21)	378017.2 (LT-7)
393371.159	389746.2	381379.9	386614.16 (XY.16)	378971.895	PRECOZ BULK	Y84.007	800827 (ATLANTIC)
396026.103	393280.64	387015.3	386316.4 (XY.14)	382171.26	375333.1 (7XY.1)	379706.27 (LT-8)	378017.2 (LT-7)
392634.49	387170.9	382182.10	575049 (CEW-69-1)	380112.3	PRECOZ BULK	(ALPHA x HOL32)	(USDA-133.3) x (LEONA x PENN 3PD-23)
393242.5	381400.22	378971.787	BULK MEX	INDIA-832	700111 (Paccosan)		
393371.164	389746.2	381379.9	386614.16 (XY.16)	378971.895	PRECOZ BULK	Y84.007	800827 (ATLANTIC)
392633.54	387334.5	382155.2	383300.21 (C83.119)	CFJ-69.1	BULK MEX	377887.17 ((377887.17 x LT-7).21)	378017.2 (LT-7)
393077.159	389746.2	381379.9	386614.16 (XY.16)	378971.895	PRECOZ BULK	Y84.007	800827 (ATLANTIC)
393075.54	389746.2	381379.9	386614.16 (XY.16)	378971.895	PRECOZ BULK	Y84.007	800827 (ATLANTIC)
391585.5	387170.9	382182.10	575049 (CEW-69-1)	380112.3	PRECOZ BULK	(ALPHA x HOL32)	(USDA-133.3) x (LEONA x PENN 3PD-23)

396008.104	393382.64	387205.5	387338.3	381397.16	676008 (I-1039)	382160.30	383300.21 (C83.119)
396018.241	393280.58	387015.3	386316.4 (XY.14)	382171.26	375333.1 (7XY.1)	379706.27 (LT-8)	378017.2 (LT-7)
396004.337	393382.64	387205.5	387338.3	381397.16	676008 (I-1039)	382160.30	383300.21 (C83.119)
391002.6	386206.4	380474.8	BK PRECOZ-84	374080.5	LT XY BULK		
396236.2	391679.7	381400.22	387205.8	378971.787	BULK MEX	381397.16	676008 (I-1039)
393084.31	390357.4	382138.4	385280.1 (XY.13)	374080.2	BULK MEX	379706.27 (LT-8)	575049 (CEW-69-1)
393079.24	390357.4	382138.4	385280.1 (XY.13)	374080.2	BULK MEX	379706.27 (LT-8)	575049 (CEW-69-1)
396033.102	393382.64	387205.5	387338.3	381397.16	676008 (I-1039)	382160.30	383300.21 (C83.119)
393073.179	389746.2	381379.9	386614.16 (XY.16)	378971.895	PRECOZ BULK	Y84.007	800827 (ATLANTIC)
393077.54	389746.2	381379.9	386614.16 (XY.16)	378971.895	PRECOZ BULK	Y84.007	800827 (ATLANTIC)
396029.25	393382.64	387205.5	387338.3	381397.16	676008 (I-1039)	382160.30	383300.21 (C83.119)
393371.157	389746.2	381379.9	386614.16 (XY.16)	378971.895	PRECOZ BULK	Y84.007	800827 (ATLANTIC)
393073.197	389746.2	381379.9	386614.16 (XY.16)	378971.895	PRECOZ BULK	Y84.007	800827 (ATLANTIC)
396240.23	391679.12	381400.22	387205.8	378971.787	BULK MEX	381397.16	676008 (I-1039)
391004.18	386206.4	380474.8	BK PRECOZ-84	374080.5	LT XY BULK		
396264.14	392639.2	387143.22	387334.5	382133.7	575049 (CEW-69-1)	382155.2	383300.21 (C83.119)
392617.54	387170.9	382182.10	575049 (CEW-69-1)	380112.3	PRECOZ BULK	(ALPHA x HOL32)	(USDA-133.3) x (LEONA x PENN 3PD-23)
396036.201	393382.64	387205.5	387338.3	381397.16	676008 (I-1039)	382160.30	383300.21 (C83.119)
396034.268	393280.64	387015.3	386316.14 (XY.14)	382171.26	375333.1 (7XY.1)	379706.27 (LT-8)	378017.2 (LT-7)
396037.215	393382.64	387205.5	387338.3	381397.16	676008 (I-1039)	382160.30	383300.21 (C83.119)
396004.301	393382.64	387205.5	387338.3	381397.16	676008 (I-1039)	382160.30	383300.21 (C83.119)
396240.2	391679.12	381400.22	387205.8	378971.787	BULK MEX	381397.16	676008 (I-1039)
393371.58	389746.2	381379.9	386614.16 (XY.16)	378971.895	PRECOZ BULK	Y84.007	800827 (ATLANTIC)
396031.119	393382.64	387205.5	387338.3	381397.16	676008 (I-1039)	382160.30	383300.21 (C83.119)