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Oat SNP Marker Discovery and Mapping Based on 454 Pyrosequencing of Genome-Reduced *Avena magna* Murphy *et* Terrell

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A thesis submitted to the faculty of
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Master of Science

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ABSTRACT

Oat SNP Marker Discovery and Mapping Based on 454 Pyrosequencing of Genome-Reduced *Avena magna* Murphy *et* Terrell

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The size and complexity of the oat genomes (*Avena* L., $x = 7$) have made genetic studies, including the discovery of molecular markers, difficult. Recent attention to these species has resulted in the development of many DArT -based markers in the tetraploid *A. magna* Murphy et Terrill ($2n = 28$, CCDD genomes), along with numerous RFLP's, SSR's, DArT's, and EST-based SNPs in hexaploid *A. sativa* L. ($2n = 42$, AACCDD). Here we report the first SNP markers for tetraploid oat based on genome reduction and high-throughput pyrosequencing in two inbred lines of *A. magna*: A-169 (wild) and Ba 13-13 (domesticated). Initially, the genomes were reduced using restriction digests with *Eco*RI and *Bfa*I and sequenced to produce 706,426 reads for both genotypes that were subsequently assembled into 57,048 contigs with an average read length of 345 bp. Comparisons of the contigs between the two lines resulted in the detection of 31,304 *in silico* SNPs. High Resolution Melt (HRM) and KASPar assays were used to validate 1,108 of these *in silico* SNPs across a panel of diploid, tetraploid, and hexaploid oats. Of the assays, 119 were validated using HRM and 384 using KASPar genotyping in the Fluidigm EP1 system. Both sets of assays were then mapped on a population of 117 $F_{2:8}$ recombinant inbred lines (RILs) developed from the A-169 x Ba 13-13 cross. A map of the *A. magna* genome was then constructed. The markers and map provide a new set of genomic tools for tetraploid and hexaploid oat breeding and allow for tracking of genes controlling traits of economic importance and other interesting genes through the evolution of *Avena*.

Keywords: SNP, pyrosequencing, Bio-Rad, Fluidigm, *Avena*, oat, genetic map, genome reduction

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CHAPTER 1: SNP MARKER DEVELOPMENT VIA GENOME COMPLEXITY REDUCTION AND 454 PYROSEQUENCING

INTRODUCTION

Cultivated oat (*Avena sativa* L. and *A. byzantina* C. Koch, 2n = 6x = 42, AACCDD genomes) was the world's seventh most important cereal crop with 11.3 million harvested acres in 2008 (UN-FAO, faostat.fao.org). Although oat acreage worldwide has been declining over the past 100 years with the demise of the agrarian horse culture, the nutritional benefits of common oat are beginning to make oat a desired component of the human diet. In turn, the demand for high-quality commercial oat is increasing primarily due to its whole grain soluble fiber content. The ability of beta glucan to lower serum LDL cholesterol has been medically documented and led the Food and Drug Administration to allow the labeling of whole-oat products as heart healthy beginning in 1998 (Cervantes-Martinez 2001). Additionally, oat has a favorable fatty acid composition and higher and more complete protein composition than other cereals (Holland 2001). Oat is also used in some brands of dog and chicken feed (Magness 1973).

Avena magna ($2n = 4x = 28$, CCDD) is a weedy tetraploid species native to heavy clay soils in agricultural areas of northern Morocco. The species is of increasing interest to oat breeders due to its high protein content (up to 25% of the groat mass), large caryopses, and exceptional crown rust and powdery mildew resistance (Ladizinsky 1995; Ladizinsky 2000). This wild oat species has potential to improve hexaploid oat through gene transfer because it appears to be closely related to *A. insularis*, the tetraploid ancestor of hexaploid oat (Ladizinsky 1998; Jellen and Ladizinsky 2000). In order to facilitate genetic studies in *A. magna*, a recombinant inbred line (RIL) population derived from a cross between two *A. magna* genotypes, Ba 13-13 and A-169, was developed. The parental line Ba 13-13 is a phenotypically uniform, fertile, and cytogenetically stable oat derived from dual-backcross hybridization with hexaploid *A. sativa*, followed by repeated selfing, to transfer domestication syndrome genes (non-shattering, yellow lemma, glabrous, reduced awns) from *A. sativa* into *A. magna* (Ladizinsky 1995).

Recently, Oliver et al. (2011) reported the development of the first genetic map for *A. magna* using the A-169 x Ba 13-13 RIL population. Their map was based on EST-SNP and DArT markers. Since these new markers were derived either from cDNAs (EST-SNPs) or *PstI*-digested genomic sequence clones (DArTs), they are expected to be biased for coding regions, leaving gaps on the chromosomes of the genetic map. The development of genomic-based markers would serve to fill these gaps and extend the existing linkage groups.

Since *Avena* chromosomes – and therefore, the *Avena* genome – are massive (comparable in size to those of the Triticeae grasses), a stringent genome reduction- reduced complexity sequencing (GR-RSC) protocol might be useful to identify genomic SNPs for a fraction of the cost of alternative methods like whole-genome sequencing (Figure 1). Maughan et al. (2009) developed a genomic reduction approach based on restriction digest and restriction-site conservation to dramatically reduce the size and complexity of four *Amaranthus* genomes and produce the first SNP-based linkage map in this genus. Large genomes can theoretically be reduced by >90% using this restriction site conservation and biotin-streptavidin paramagnetic bead separation method. Multiplex identifier (MID)-barcodes were then attached to the target genomes. These barcodes allowed for pooling of the DNA samples followed by parallel, high-throughput DNA sequence analysis in matching genomic contigs from the four genotypes to identify single-base differences. Assays for these interparental SNPs were then designed without further genotyping.

Single-nucleotide polymorphisms were chosen as the marker of interest as they demonstrate lower mutation rates than tandem repeats (Xu et al. 2005). They are also the most frequent form of DNA sequence variation in eukaryotic genome sequences (Garg et al. 1999), allowing for dense genetic mapping. This type of high density, SNP-based linkage map affords the potential of identifying causal mutations (Rafalski 2002). Genome reduction and 454-pyrosequencing was used for SNP discovery on cattle (Van Tassell et al. 2008); however, due to pooled sampling of the restriction fragments, the individual alleles could not be assigned without further genotyping. Maize SNP discovery encountered similar problems (Barbazuk et al. 2007).

Putative SNPs generated from sequencing must be validated and translated into working PCR-based assays. A powerful technique called high resolution melting (HRM) was developed in 2003 and is capable of detecting polymorphisms, mutations, deletions, insertions or epigenetic differences in double-stranded DNA (Reed 2007). The method uses high data-density acquisition, and detects small sequence differences in PCR fragments, simply by direct melting and reannealing of the double helix. Melting curves can thus be used for mutation scanning, sequence matching, and mutliplex genotyping - analyses that traditionally required processing of PCR products by electrophoresis or other non-homogeneous means (Gundry 2003).

Here we report the use of GR-RSC to discover SNPs in our tetraploid oat mapping parents, eliminating the need for additional genotyping and providing novel genomic SNP markers to further populate the A-169 x Ba 13-13 linkage map. These genomic-based SNPs were further validated through polymorphism screening using a panel of tetraploid and hexaploid mapping-population parents. In addition, we compared the value of HRM versus KASPar/Fluidigm SNP assay platforms.

MATERIALS AND METHODS

Plant Materials

Deoxyribonucleic acid from *A. magna* lines Ba 13-13 and A-169 were used for genome reduction, sequencing, SNP identification and assay validation. Strain Ba 13-13 is a domesticated, tetraploid A. *magna* line originating in Israel that is morphologically similar to common hexaploid oat. The line originated from a cross between hexaploid *A. sativa* (cv. ‘Ogle’, ‘86-4189’, ‘86-4467’ or ‘86-5698’) and a wild tetraploid A. *magna* line, A-169. The pentaploid progeny from this cross were then backcrossed twice with a wild tetraploid parent, with selection in the offspring for individuals that were fertile, tetraploid, and carried the domestication traits (Ladizinsky 1995). An F_2 population was developed by crossing Ba 13-13 by A-169 at BYU (E. Jellen, personal communication). A single-seed descent approach was used to advance the population to the F_8 generation at BYU and USDA-ARS (Aberdeen, ID), resulting in 117 recombinant inbred lines (RILs). Ploidy levels were cytologically inspected at both the F_2 and F_8 stages. Plants were grown in a 22-30°C greenhouse with a 16 hour photoperiod.

DNA Extraction

Genomic DNA was extracted as described in Maughan et al. (2009). Approximately 4 cm of young leaf tissue from each sample was placed in individual 2 ml tubes and ground into powder by submerging the tubes in the liquid N_2 and emaceration using a plastic tube pestle. A cetyltrimethylammonium bromide (CTAB) extraction procedure was performed (Kidwell and Osborn 1992). In brief, 600 µl of extraction buffer [0.35 M sorbitol, 0.3 M TrisHCl pH 8.0, 5 mM EDTA pH 8.0, 2M NaCl, 2% CTAB, 5% (w/v) *N*-lauroylsarcosine, 2% (w/v) Polyvinylpyrrolidone (PVP40, K29-32), and 0.5 % (w/v) sodium metabisulfite] was added and mixed with the powder. The solution was incubated for 60 min at 65°C then mixed with 600 µl chloroform. After mixing, the solution was centrifuged at 10,000 *g* for 20 min and the aqueous phase was transferred to a new 2 mL tube. Chilled isopropanol (600 ul) was added to the aqueous layer and the solution was mixed by inversion to precipitate the DNA. The samples were centrifuged at 10,000 *g* for 30 min. and supernatant was discarded. The DNA pellet was rinsed twice with 70% ethanol, dried, and then suspended in 1xTE buffer and quantified using the NanoDrop ND 1000 Spectrophotometer (NanoDrop Technologies, Montchanin, DE, USA).

Genome Reduction

We reduced the genomes of Ba 13-13 and A-169 using the techniques of Maughan et al. (2009). Genomic DNA was subjected to a double digestion with four- and six-base specific restriction endonucleases *BfaI* and *EcoRI*, respectively. Double stranded adapters labeled with a 5′-biotin molecule were ligated to the 6-base recognition sites, while the four-base recognition sites were ligated to unlabeled adapters. Streptavidin paramagnetic beads were used to separate the four-base unlabeled fragments from the labeled six-base fragments. The MID barcodes were incorporated onto the remaining DNA fragments via complementary PCR primers. A PCR process allowed for the annealing of these barcodes into the remaining amplified DNA fragments. Parental genotypes Ba 13-13 and A-169 were labeled with their own unique 10-base MID sequence to allow for post-sequencing bioinformatic separation. Prepared samples were then pooled and electrophoresed to select for the 500-650 base pair fragments, which were excised from the gel.

454 Pyrosequencing, Assembly, and SNP Detection

The 454 pyrosequencing protocol was performed as described in Maughan et al. (2009). A single micro-bead sequencing run was performed as a service at the Brigham Young University DNA Sequencing Center (DNASC) using a Roche-454 GS FLX instrument and Titanium reagents (Roche, Branford, CT, USA). The DNA from lines Ba 13-13 and A-169 were uniquely labeled with separate MID barcodes. After sequencing, each parent was separated into respective MID- barcode pools bioinformatically using CLCBio Workbench (v. 3.5.1; Katrinebjerg, Aarhus N, Denmark). Contigs were assembled for each pool *de novo*. Roche Newbler assembler (v. 2.0.00; Branford, CT, USA) assembled these contigs following the parameters of minimum overlap length of 50 bp, with minimum overlap identity at 95%. Newbler's gsAssembler allowed for *de novo* assembly of reads into contigs for each parental line. A custom PerlScript (SNP_Finder 3.0; Maughan et al. 2009) created at Brigham Young University was used to identify SNPs between the parental reads within large contigs (>200 bp). Putative SNPs were identified based on the following criteria: 1) at least 10x read coverage; 2) MID-barcode alleles were 90% identical for each parent; and 3) 40% minimum allele frequency.

High Resolution Melt

Genotyping was performed by High Resolution Melt (HRM) analysis as described in Oliver et al. (2011), using a Bio-Rad C1000 thermal cycler with a CFX96 optics module. Bio-Rad's 1x SsoFast EvaGreen Supermix was mixed with 55 ng genomic DNA in each reaction. For each reaction 0.5 µM forward and reverse primers (Supplemental Table 1) were used in a 12.5 µl reaction volume. The thermocycling protocol used was as follows: 1) denaturation at 98°C for 2 min; 2) 46 cycles of 98°C for 2 sec and 55°C for 5 sec, 3) melt gradient from 65°C to 95°C, increasing in 0.2°C increments every 10 sec. Melt curves were analyzed using Bio-Rad Precision Melt Analysis Software Version 1.0.534.0511. The differences in relative fluorescence units as a function of melting temperatures allowed for differentiation of primary polymorphic alleles as well as insertions, deletions and null alleles.

False Discovery Validation

Thirteen primers (contig5030, contig5075, contig6122, contig6183, contig6404, contig6465, contig6923, contig7003,contig7325, contig7662, contig7937, contig8269, contig11641) were randomly chosen from the robust HRM reactions to validate SNPs via Sanger sequencing. These primers were used to PCR-amplify the genomic regions of Ba 13-13 and A-169. Qiagen HotStart Taq Master Mix (Qiagen, Valencia, California, USA) was used for the PCR amplification. The thermocycling conditions were as follows: 95°C for 15 min followed by 34 cycles of 94°C for 30 sec, 55°C for 1 min, and 72°C for 1 min. The final 10-min extension step was done at 72°C. PCR products were visualized using 1.2% agarose gel. The amplified PCR products were then extracted from the gel, and purified using a QIAquick PCR Purification Kit with QIAquick spin columns in a microcentrifuge (Qiagen, Valencia, CA, USA).

PCR-purified DNA was transformed into the pGEM®- T-Easy Vector system using JM109 competent cells, following the manufacturer’s protocol (Promega, Madison, WI, USA). The plasmid containing the DNA insert using the GenElute plasmid Miniprep Kit (Sigma, St.

Louis, MO, USA) followed by enzymatic cleavage. Plasmid DNA was then quantified using Nanodrop (ND 1000 Spectrophotometer, Nanodrop Technologies Inc., Montchanin, DE, USA) and 300-400 ng of it was amplified using Big Dye cycle sequencing and T3 forward (5'AATTAACCCTCACTAAAGGGA 3') and T7 reverse (5'TAATACGACTCACTATAGGG 3') primers. The sequencing reaction profile included 25 cycles of 96°C for 10 sec followed by 50°C for 6 sec, and 60°C for 4 min. Amplified PCR product was purified with Sephadex G-50 protocol (GE Healthcare) and sequenced with an ABI3730xl DNA Analyzer (Applied Biosystems, Foster City, California). Sequenced vectors were screened using the NCBI VecScreen. Sequences which were conserved with the genomic regions of grass families were included in the studies. Sequences were aligned using MEGA 4.1 software (Tamura et al. 2007).

RESULTS AND DISCUSSION

Genome reduction with methylation-sensitive and -insensitive enzymes allows the interrogation of areas of the chromosome neglected by EST-based markers. Maughan et al. (2009) reported that digestion with the *Bfa*I-*Eco*RI restriction enzyme cocktail produced a continuous smear with *Amaranthus* DNA following electrophoresis. Although the restriction-digested *A. magna* DNAs in our study likewise presented a continuous smear following electrophoresis, post GR-RSC in our case resulted in an unusually large fraction of sequences ranging from 200-400 bps - considerably smaller than the 500-650 bp fragments initially excised from the reduction gel. We attributed this disparity to sub-optimal 454 sequencing performance and/or inefficient size selection (Figure 2).

Table 1 presents the results of the GR-RCS procedure with *A. magna* DNA. Pyrosequencing returned a total of 706,426 reads. These were then assembled into 57,048 large contigs (> 300 bp), producing 27,200,520 total bases of sequence. Average read length was 345 bp with most reads greater than 40x quality. The average read depth per contig (Figure 3) was 16x. Barcodes MID1 (A-169) and MID2 (Ba 13-13) were removed prior to sequence assembly using Newbler's *de novo* assembler. As expected, reads from A-169 and Ba 13-13 were found in almost equal proportions, specifically 47% and 53%, respectively (Table 1).

Sequence classifications (gene ontology), as determined using BLAST2Go, are presented in Figure 4. The presence of a diverse distribution of sequences in terms of molecular function, biological process and cellular components indicates that the pool of GR-RSC treated *A. magna* DNAs included a wide range of transcribed sequences (Figure 4). As expected, SNP composition was predominantly in the form of C/T and A/G transitions (Figure 5).

SNP_Finder detected 31,304 total sequence variants, with most contigs containing only a single SNP and at an average 16X coverage at each SNP. SNP_Finder filtered these SNPs using strict parameters, resulting in 12,642 SNPs and 6,502 contigs containing true SNPs (Table 2). Of the 13 SNPs chosen for validation, only four verified the SNP-identified assembly from Newbler, while the remainder appeared to be amplified PCR products of orthologous and/or paralogous sequences—likely a result of the tetraploid nature of *A. magna*. This finding suggests that the relatedness of the two subgenomes may complicate the development of future SNP assays.

Conclusion

This paper emphasizes the development of rapid marker discovery in the oat genus *Avena* using the wild Moroccan tetraploid *A. magna* (Murphy 1968) as a source of new DNA sequence-based markers. Genetic marker discovery in tetraploid oat by single nucleotide polymorphisms (SNPs) should provide at least four major benefits for improvement of cultivated oat. First, it provides a new set of CCDD genome specific markers for application in cultivated hexaploid oat breeding assuming tetraploid markers are transferable to hexaploid oat. Second, it provides a basis for genetic map development in *A. magna*, and potentially also *A. murphyi* (Ladizinsky, 1995) and *A. insularis* Ladizinsky, all of which are potential genetic resources for exotic alleles to improve cultivated hexaploid oat. Third, the *A. magna*-derived SNPs may potentially be used to track the genetic heritage of genes controlling traits of economic importance and other chromosome segments of interest back through the evolutionary ancestors of oat. Lastly, these markers may be used to create a SNP panel that can be used to screen global diversity in all *Avena* species. Species-specific SNPs may be detected and analyzed for evolutionary patterns and divergences when *Avena* species of diverse genome composition are screened.

CHAPTER 2: SINGLE NUCLEOTIDE POLYMORHISM DEVELOPMENT AND GENETIC MAPPING IN TETRAPLOID *AVENA MAGNA*

INTRODUCTION

Common cultivated oat, *Avena sativa* L. and *A. byzantina* C. Koch, have attracted very little attention until recently, despite being the world's fifth of sixth most significant cereal crop. Current research and industry support have uncovered and promoted a series of unique health benefits from regular oat consumption. One of the most valuable findings was the ability of oat soluble fiber (beta-glucans) to lower serum LDL cholesterol (Braaten et al. 1994). Dietary protein from plant sources has also been shown to have profound health benefits (Nutall et al. 1984; Wang et al. 2008). The good quantity and quality of oat seed protein, combined with high oil content, anti-itch properties, antioxidants, and soluble fiber all make oat an attractive commodity for various industries including breakfast cereals, agronomy, and cosmetology (Eggum et al. 1989). While other cereal crops have comparable protein content, oats have been shown to have higher levels of the limiting amino acid lysine (Young and Pellett 1994). The health benefits from oat are attracting more attention and therefore increasing protein content is a valuable objective (Jones et al. 1948).

While common oat has a diploid chromosome number of $2n = 6x = 42$ (AACCDD genome composition), *A. magna* Murphy et Terrell (syn. *A. maroccana* Gdgr) has $2n = 4x = 28$ (CCDD genomes). The latter species inhabits disturbed field sites on heavy alluvial clays in northern Morocco. While seed protein percent in common oat ranges to near 17%, *A. magna* seed has been found to exceed 30% protein, making it a potentially valuable resource for improving common oat's protein content (Ladizinsky and Fainstein 1977). Besides high seed protein content, *A.*

magna carries other desirable qualities such as resistance to crown rust (*Puccinia coronata* f. sp. *avenae*) and powdery mildew (*Erysiphe graminis*; Ladizinsky 1995; Ohm and Shaner 1992).

Crosses between *A. magna* and *A. sativa* have been attempted for introgression purposes; however, hybrid progeny of such crosses are male-sterile pentaploids (Harlan et al. 1973; Ladizinsky 1995; Ladizinsky and Fainstein 1977; Thomas 1992). Pollination of these hybrids with either tetraploid or hexaploid pollen will rescue the sterility by converting it back to 4x or 6x, respectively, thus allowing traits of interest to be transferred in the process.

Ladizinsky (1995) took the novel approach of trying to transfer the 'domestication syndrome' traits from *A. sativa* to create a novel crop, *A. magna* subsp. *domestica*. He described the domestication syndrome in *A. magna* as being controlled by four loci: a partially dominant gene for large, geniculate awns (*A*); a dominant lemma color gene, with black being dominant to yellow (*Lc*); a dominant gene for pubescent versus glabrous lemma (*Lp*); and a dominant gene for non-shattering spikelets (basal articulation, *Ba*). One of the second-backcross *A. magna* lines having the domestication syndrome from *A. sativa* was named Ba 13-13 and was crossed with a wild *A. magna* line, A-169, to make an F_2 mapping population (Jellen 2000). Oliver et al. (2011) advanced these lines to the F_8 via single-seed descent to make a recombinant inbred line (RIL) mapping population and reported tight coupling linkage between the *A* (prominent awn) allele and a heterochromatic knob at the telomere of one of the C-genome chromosomes, with the *Lp* locus mapping to a different chromosome. This telomeric knob had previously been noted on apparently homologous chromosomes in *A. magna*, *A. sativa*, A. *insularis* Ladizinsky, and on chromosome 5C in the wild hexaploid *A. sterilis* L. (Jellen and Ladizinsky 2000; Jellen et al. 1993). Its segregation in the Ba 13-13 x A-169 progenies was also verified in the F_2 (Jellen 2000) and RIL populations (Oliver et al. 2011).

The creation of molecular genetic maps in cultivars and wild relatives of economically important allopolyploid crops like oat can provide powerful tools for marker-assisted selection (MAS), to evaluate breeding value of these genetic resources, and to resolve questions related to genome origins and evolution. Molecular markers that have been used for mapping in oat include sequence characterized amplified regions or SCARs (Chong et al. 2004; Orr and Molnar 2008); amplified fragment length polymorphisms or AFLPs (Jin et al. 2000; Yu and Wise 2000); restriction fragment length polymorphisms or RFLPs (O'Donoughue et al. 1995; Kremer et al. 2001); simple sequence repeats or SSRs (Li et al. 2002; Pal et al. 2002); diversity array technology or DArT markers (Tinker et al. 2009); and SNPs. (Groh et al. 2001).

The first genetic map created for tetraploid oat was an AFLP-based map in *A. barbata*, a weedy AABB-genome tetraploid (Gardner and Latta, 2006; Latta and Gardner 2009). Nineteen linkage groups were reported and 129 loci mapped. Oliver et al. (2011) reported the first complete linkage map of tetraploid oat in *A. magna*. This map was constructed of DArT markers, small numbers of SNPs and SSRs, domestication syndrome genes *A* and *Lp*, and the telomeric 5CL knob (Jellen 2000). The Oliver et al. (2011) map is potentially biased toward genic regions because it was based on DArT markers derived from cloned, *Pst*I-digested – and therefore, hypomethylated - oat genomic fragments.

Single-nucleotide polymorphisms are potentially the most abundant, and generally the most informative, genetic markers for linkage mapping – short of mapping by sequencing. The two main problems with SNP markers are the initial requirement of DNA sequence data – which can be very expensive to generate – to identify the SNPs, and design of precise assays that can discriminate among homologous, paralogous, and orthologous SNPs. Paralogous SNPs can be an obstacle in species with large, highly duplicated genomes, like *Avena*. Orthologous SNPs can be especially problematic in allopolyploid species like *A. magna* (4*x*) and *A. sativa* (6*x*). Highly sensitive SNP assay methods like high-resolution melt-curve analysis (HRM) have proven useful in the mapping of selected SNPs in hexaploid oat populations (Oliver et al. 2011). Although HRM is capable of detecting point mutations, deletions, insertions or epigenetic differences in double stranded DNA (Wittner et al. 2003), it can prove time-intensive and costly, In contrast, other SNP assaying chemistries like TaqMan (Applied Biosystems, Foster City, CA, USA), KASPar (KBiosciences, Hoddesdon, UK), and Golden Gate (Illumina, San Diego, CA, USA) can be run on high-throughput platforms like Illumina's BeadXpress Reader or the Fluidigm 96.96 EP1 instrument (Fluidigm, South San Francisco, CA, USA).

Here we report the development of 436 new *A. magna* genomic SNPs derived from genome-reduced restriction site conservation (GR-RSC) methodology. These SNPs allowed for the refinement of linkage groups in the Oliver et al. map (2011) by filling in gaps and extending linkage groups. We compared two alternative methodologies for detecting these genomic SNPs in an F_8 RIL-based mapping population: namely, high-resolution melting (HRM) analysis on a Bio-Rad instrument and KASPar assays detected on a Fluidigm 96.96 EP1 platform. This work provides a genetic foundation for further domestication of the tetraploid oat *A. magna* and for the transfer of economically useful genes from this species to common hexaploid oats.

MATERIALS AND METHODS

Plant Materials

A total of 117 *A.* RILs were previously developed by crossing *A. magna* subsp. *domestica* var. Ba 13-13 with wild A-169, then selfing the F_2 plants to the F_8 by single-seed descent to form the BAM population (Ladizinsky 1995; Oliver et al. 2011). Seed was provided by Dr. Eric Jackson (USDA-ARS, Aberdeen, ID, USA). Sixteen oat lines (Table 3) were selected for validation purposes while an additional 65 wild tetraploid lines and four hexaploid lines were selected to determine the level of diversity across the SNP loci (Table 4). These lines were provided by Dr. Rick Jellen at Brigham Young University and from the USDA-ARS germplasm bank at Aberdeen. All plants were grown in 4-inch square pots, in a greenhouse with an approximately 16-h photoperiod and a daytime temperature ranging from 22-30°C.

SNP Primer Development

A total of 1,208 previously identified GR-RSC SNPs were chosen for genotyping. RepeatMasker (v.3.2.9 Tritticae) database was used to eliminate sequences having significant homology to the *Triticum* cytoplasmic genomes. A primer design program, PrimerPicker (KBiosceinces 2009), processed the sequences using default parameters. Primers were then randomly selected and synthesized by Bioneer Inc. (Alameda, CA, USA).

HRM and KASPar Genotyping

Single-nucleotide polymorphism marker screening and genotyping was performed on two different platforms. Small-scale, HRM genotyping was performed using a Bio-Rad C1000 thermal cycler with a CFX96 optics module (Hercules, CA, USA) as previously described by Oliver et al. (2011), while large-scale genotyping of SNPs was performed using the Fluidigm (San Francisco, CA, USA) 96.96 Dynamic Array IFC's on the EP1 System. Protocols recommended by KBioscience and Fluidigm were followed.

In brief, Bio-Rad's 1x SsoFast EvaGreen Supermix was mixed with 55 ng genomic DNA in each reaction. In addition to the genomic DNA, 0.5 µM forward and reverse primers were used in a 12.5 µl reaction volume. The thermocycler protocol used was as follows: 1) denaturation at 98°C for 2 min; 2) 46 cycles of 98°C for 2 sec and 55°C for 5 sec; 3) melt gradient from 65°C to 95°C, increasing in 0.2°C increments every 10 sec. Melt curves were analyzed using Bio-Rad Precision Melt Analysis Software Version 1.0.534.0511. The differences in relative fluorescence units as a function of melting temperatures allowed for genotyping.

The KASPar (KBioscience Ltd., Hoddesdon, UK) assay was used to validate a portion of the identified SNPs. Assays were designed for SNPs where coverage was between 12-20X and SNP flanking sequences were at least 100 bp long. All assay primer sets were designed using PrimerPicker using default parameters.

The KASPar reactions produce fluorescence intensities at two unique wavelengths, each corresponding to the presence of a an alternate nucleotide at the SNP. Fluorescence intensities were measured with the Fluidigm EP1 reader and plotted two-dimensionally. Genotype calls based on EP1 measurements were made using the Fluidigm SNP Genotyping Analysis (Fluidigm 2011) program. All calls were manually checked for accuracy and ambiguous data points were left uncalled. The Fluidigm assay is based on KASPar genotyping chemistry, but using a nano-scale reaction volume. Each 96.96 Fluidigm chip accommodates 96 primer pairs x 96 genotypes, producing a total of 9,216 genotypic data points at a cost of ~$0.05/dpt. Genetic maps based on KASPar genotyping data were constructed in JMP Genomics v. 5.1 (SAS, Cary, NC, USA) using a regression mapping algorithm.

SNP Diversity Data Analysis

Alleles for each segregating RIL in the Bio-Rad assays were scored based on the melting curve profile of the mapping parents. Different alleles melt at different temperatures and the Bio-Rad software colors these as green or red. Missing data, or those RILs that did not amplify, were colored black. The alleles were exported into a spreadsheet where the colors were then converted into 0's and 1's for the biallelic data. A numerical value of 2 was assigned to designate missing data and were disregarded for mapping purposes. Fluidigm assays were scored and converted similarly, based on segregation of the parent's florescence. Both datasets were then converted into a binary matrix. Those reactions that had greater than 10% failure of RIL amplification were disregarded for both platforms.

Map Construction

Genotype calls for the 117 BAM RILs at each locus were determined automatically by the Fluidigm progarm and then verified via visual inspection upon comparison with the parental alleles. Using this information, preliminary mapping of linkage groups was performed in MapManager QTX v.1.1 (Rockefeller University, New York City, NY, USA). This framework map was constructed for consensus and reference using markers from the tetraploid map developed by Oliver et. al (2011). Further linkage analysis and map construction were performed using JMP Genomics v. 5.1. Multilocus ordering was determined using an algorithm based on the evolutionary optimization strategy (Mester et al. 2003; Mester et al. 2004), with maximum likelihood estimation to calculate pairwise recombination fractions (rf) for all marker pairs. Preliminary clustering and assignment of markers to a linkage group (LG) was evaluated at a rf = 0.05 threshold. Markers were then attached to the framework scaffold

Diversity Panel and Assay Validation

A panel of 16 oat lines representing various *Avena* genome combinations, including diploids and allopolyploids, was surveyed for SNP assay validation across the same 330 primers selected for the Bio-Rad analysis. Another 69 oat lines were selected for the tetraploid diversity analysis and assayed across the 768 primer sets selected for the Fluidigm EP1 analysis. The same platform protocols were used as described above. Each allele was scored as described above and converted to a binary matrix. The JMP Genomics v. 5.1 program was used to create a dendrogram via Neighbor-Joining analysis.

RESULTS AND DISCUSSION

SNP Assay Validation

A panel of 16 oat lines representing various *Avena* genome combinations, including diploids and allopolyploids, was surveyed for SNP assay validation across the same 330 primers selected for the Bio-Rad analysis. Another 69 oat lines were selected for the tetraploid diversity analysis and assayed across the 768 primer sets selected for the Fluidigm EP1 analysis. The same platform protocols were used as described above. Each allele was scored as described above and converted to a binary matrix. The JMP Genomics v. 5.1 program was used to create a dendrogram via Neighbor-Joining analysis.

For our purposes, any SNP with a >10% amplification failure rate was considered incomplete for mapping and discarded. The 65.3% and 58.6% attrition rates for HRM and KASPar markers, respectively, can possibly be attributed to a number of factors. In the case of the KASPar assays on the Fluidigm platform, DNA template concentrations may have been sub-optimal, given the very large size, and duplication, of the *A. magna* genome. Poor DNA quality might also be an issue and interfere with both assay types, as other researchers have noted that high-quality oat DNA is unusually difficult to purify owing to its high polysaccharide content (E. Jellen, personal communication). The failure of large portions of several reactions to separate from the origin was probably indicative of poor amplification.

Figure 6 demonstrates a robust Bio-Rad assay. RILs that contained the allele from the Ba

13-13 parent were designated green. Alleles from the A-169 parent were labeled red. The differences in melting temperatures between the two alleles are visualized by a shift or space in the melt curves. Similarly, Figure 7 shows strong segregation of alleles for a KASPar assay. Alleles from one parent fluoresced red, while alleles from the other parent fluoresced green. The SNP may be visualized by individual clustering of the RILs. Figure 8 displays the markers run on the two platforms and their BAM genetic map distributions. Whereas markers assayed via KASPar chemistry on the Fluidigm system were randomly distributed along the length of all 16 linkage groups, the HRM-assayed SNPs showed some clustering. This was particularly true on linkage groups 14 and 15. We cannot conceive of a rational explanation for this clustering effect with the HRM marker set.

Linkage Map Construction

Delineation of linkage groups, selection of framework markers, and resolution of marker order were performed using JMP Genomics mapping package, with algorithms based on marker order and incrementally-increasing recombination thresholds (Korol et al. 2009; Mester et al. 2004). Figure 9 illustrates a high degree of segregation distortion in the mapping data, with markers skewed toward the wild A-169 parent predominating on linkage groups 2, 4, 6, and 14. In contrast, linkage groups 5, 15, and 16 were heavily skewed toward markers from domesticated Ba 13-13. Linkage group 1 was unique in having only minor segregation distortion. Interestingly, linkage group 9, which harbors the telomeric knob in A-169 and several domestication syndrome genes originally contributed to Ba 13-13 by *A. sativa*, showed evidence of A-169 marker distortion at one end. Though the knob was not included as a marker for this map, cytological analysis of the F_8 BAM RILs verified a 41:59 skewed ratio in favor of lines homozygous for the knob (R. Jellen, personal communication). This region is likely represented by the three markers having >50% distortion toward A-169 at the “bottom” of the BA_09 column in Figure 9.

We expected 14 linkage groups for the 14 chromosomes in tetraploid oat. MapManager recovered 14 linkage groups (Figure 10). However, recombination analysis of each marker in JMPGenomics created 16 linkage groups (Figures 11 and 12). We believe increasing marker density would resolve the discrepancy between the two maps. The average distance of markers on the linkage groups was 12.1 cM, and ranged from 8.4 cM on linkage group 6 to just under 20 cM on linkage group 2. The largest gap on any linkage group was 35.8 cM on BAM 7 and the average across the linkage groups was 25.3 cM, suggesting the linkage groups were fairly sound (Table 5). In addition, the heat plot in Figure 12 detected a marker “island” at one end of linkage group 12 showing strong correlation with markers from linkage group 4 [red “lines” in the lower left (horizontal line) and upper right (vertical line) quadrants of the grid]. Whether this is indicative of synteny between these two linkage groups, the presence of a reciprocal translocation in these regions, or some other phenomenon remains to be seen.

An allotetraploid oat genome was recently resolved into 14 linkage groups for the first time with both C and D genome classes distinguished (Oliver et al. 2011). Figure 13 illustrates the importance of genomic-based markers to supplement existing maps created by EST-SNP and DArT markers. The red markers in Figure 13 clearly demonstrate how the GS-RSC SNPs from this study extended linkage groups and filled in “gaps”, especially in gene-poor regions of the chromosomes.

Avena Diversity Validation Panel

Thirty-two taxonomic entities have been distinguished among oats; however, there are discrepancies reported in the classification of some of the species (Jellen and Leggett 2006). Four basic genomes (A, B, C, and D) have been identified, with potentially a fifth genome (M) in *A. macrostachya*. Cytogenetic analysis, including C-banding, genomic and fluorescent in situ hybridization (GISH and FISH), provided the primary tools for identifying the individual chromosomes within the genus.

To further validate the accuracy of our results, we ran each of the 330 Bio-Rad assays across a selected diversity panel of 16 lines encompassing most known genome combinations and diversity within the genus *Avena* (Table 3). Melt curve analysis was scored based on differences in melting temperatures. Results were converted into binary matrix format and run through JMP Genomics v. 5.1 software to create a dendrogram (Figure 14). The resulting dendrogram formed four major clades. All six *A. magna* lines fell into the same clade, as expected. The diploid species formed two clades, with the CC genomes separating from the AA/DD genomes, which concurs with previous cytogenetic research (Jellen et al. 1994). The hexaploids, *A. insularis*, and *A. murphyi* constituted a fourth clade. The data confirmed what is most likely the correct relationship among the species. *Avena insularis* (4*x*, CCDD) is the progenitor of wild *A. sterilis* (6*x*, AACCDD), which in turn is the progenitor of domesticated *A.*

sativa (Jellen and Ladizinsky 2000; Zhou et al. 1999). The results further indicate that *A. murphyi* (AACC or CCDD) might either be a progenitor of *A. insularis*, or both tetraploids participated in the hybridization event that gave rise to *A. sterilis*. This latter scenario would have to invoke a partial restituion mechanism and stabilization of the amphidiploid nucleus with only two copies of the C genome.

Tetraploid Diversity Panel

A panel of tetraploids was created to determine genetic diversity based on the SNP markers interrogated. The diversity panel consisted of 65 wild tetraploid lines and four domesticated hexaploid lines (Table 4), representing seven oat species: *A. agadiriana* (AAAA or AABB); *A. barbata* (AABB); *A. magna* (CCDD); *A. murphyi* (AACC or CCDD); *A. sativa* (AACCDD); *A. sterilis* (AACCDD); and *A. vaviloviana* (AABB). A total of 318 SNP markers (636 alleles) were polymorphic on the Fluidigm EP1 platform. These polymorphisms created clear genotypic clusters for scoring.

A dendrogram created from biallelic scoring of these markers (Figure 15) produced six distinct clades. As expected, the majority of the *A. magna* accessions grouped together in two clades (red and green branch lines). Closely related in the adjoining clade was the *A. murphyi* group (blue branch lines). This supports the cytogenetic data that both species have at least one subgenome in common (the C). Interestingly, *A. vaviloviana* (AABB) grouped among *A. murphyi* accessions, suggesting they have an ancestral relationship or possibly share subgenomes (common variants of the A). The *A. agadiriana* (AAAA or AABB) accessions grouped together in a fourth clade (turquoise branch lines), along with several *A. murphyi* accessions, possibly indicating a molecular relationship between *A. murphyi* and *A. agadiriana*. As expected, the *A. sativa* (AACCDD) oat cultivars grouped together in their own clade (orange branch lines). However, PI 657271 (hexaploid *A. sterilis*) fell into the group with *A. agadiriana* and *A. murphyi* (turquoise). A sixth, small clade contained a mixture of species (purple branch lines). It should be noted that discrepancies in the clades may be the result of misclassification of USDA-ARS materials. Some of these misclassifications were confirmed by seed morphology analysis. Not only does the dendrogram further validate the accuracy of the KASPar/Fluidigm SNP assay method, but also it may potentially be used to extract species-specific SNPs, although polymorphisms arising from indel mutations would not be scorable using this marker platform – in contrast to the HRM method (Wittner et al. 2003).

The introduction of molecular markers has revolutionized genetics. Technology is enabling the study of species that were not previously viewed as economic priorities, being too remote, expensive or complex for consideration in plant breeding communities (Eathington et al. 2007). The array of polymorphisms and molecular techniques that are available is increasing, and the arrival of low-cost genomic sequencing is a source of an escalating set of available markers (Cullis 2002). As more genetic information becomes available, the application of molecular markers to other experimental methods will become simpler, allowing for novel genetic analysis that is currently impossible to undertake.

This study reports on the production and utilization of a toolbox of genomic sequence-based SNP markers and their application for genetic mapping and diversity analyses in an obscure secondary germplasm resource, *A. magna*. Although the GR-RSC technique has allowed for marker development in a species that could someday be commercialized into an important high-protein oat crop, its broader relevance is to potentially facilitate molecular genetic marker development in a wide range of minor crops and wild crop relatives (Maughan et al. 2009).

As cost and time requirements are decreased, scientists will view the functions of plants with incredible opportunity for innovative research. Unknown mutations will be identified, along with increased understanding of structure-function relationships (Bernardo 2008). Molecular markers can be used in either marker-assisted selection or marker assisted introgression. However, as sequencing supplies increased information, molecular properties may reduce the need for introgression, thereby removing the need for growing or rearing plants in order to measure phenotype.

Plant breeding programs can take advantage of this knowledge to increase crop yield, disease resistance, and a multitude of other qualities (Eathington et al. 2007). The understanding of the interaction between genes and environmental factors, including other organisms, also allows for discovering chromosomal conservation and evolution (Bernardo 2008). Such genetic variation, both within and outside specific plant species, augments transgenic possibilities, or the transfer of genes between species by molecular techniques (Gelvin 2003).

CHAPTER 3: LITERATURE REVIEW

INTRODUCTION

Here we emphasize the utility of rapid marker discovery in the oat genus *Avena* using the wild Moroccan tetraploid *A. magna* (Murphy, 1968) as a source of new DNA sequence-based markers. Genetic marker discovery in tetraploid oat by single nucleotide polymorphisms (SNPs) should provide at least four major benefits for improvement of cultivated oat. Firstly, it provides a new set of markers for application in cultivated hexaploid oat breeding. Secondly, it provides a basis for genetic map development in *A. magna*, and potentially also *A. murphyi* (Ladizinsky, 1995) and *A. insularis* Ladizinsky, all of which are potential genetic resources for exotic alleles to improve cultivated hexaploid oat. Thirdly, the *A. magna*-derived SNPs potentially allow for tracking the genetic heritage of genes controlling traits of economic importance and other chromosome segments of interest back through the evolutionary ancestors of oat. Finally, these markers also provide for creation of a SNP panel that can be used to screen global diversity in all *Avena* species. Consequently, species-specific SNPs may be detected and analyzed for evolutionary patterns and divergences when *Avena* species of diverse genome composition are screened.

Common cultivated oat (*Avena sativa* L. and *A. byzantina* C. Koch, 2n = 6x = 42, AACCDD genomes) was the world's seventh most important cereal crop, at 11.3 million harvested acres in 2008. (UN-FAO, faostat.fao.org). Although oat acreage worldwide has been declining over the past 100 years with the demise of the agrarian horse culture, the nutritional benefits of the common oat are beginning to make substantial contributions to the human diet. Therefore, the demand for high-quality commercial oats is increasing, due to the oat groat's elevated soluble fiber content. The ability of soluble beta glucan fibers to lower serum LDL cholesterol has been medically documented and led the Food and Drug Administration to approve whole-oat product labeling as a health benefit beginning in 1998 (Cervantes-Martinez, 2001). Additionally, these crops have higher protein and oil contents than the other cereal grains (Holland, 2001). While oats are suitable for human consumption as oatmeal and rolled oats, one of the most common uses is as livestock feed. Oats are also used in some brands of dog and chicken feed (Magness, 1973).

The species composition of the oat genus *Avena* has been extensively studied cytogenetically and taxonomically, the latest review being that of Jellen and Leggett (2006). Prior to C-banding homoeologous chromosome groups in oat were unable to be differentiated by physical identification (Rajhathy 1963, Thomas 1974). In the late 70's Yen and Filton (1977) reported the first differences in heterochromatin detected by Giemsa stained C-banding in diploids. In 1988, Fominaya et al. performed the same method on diploids and tetraploids. The C-genome chromosomes were found to have significantly darker staining heterochromatin than the A genome. Hutchinson and Postoyko (1986) and Jellen (1994) published similar results on hexaploid A. *sativa*. The seven C-genome chromosomes were easily distinguished from the others as a consequence of their darker staining. However, the A- and D- genome chromosomes were difficult to be separated from one another. Linares *et* al. (1992) later attempted to assign the A- and D-genome chromosomes in A. *byzantina* based on euchromatin staining intensity and prominence and location of telomeric and interstitial bands. The analysis by Jellen et al. (1993) on C-banding patterns in AA diploids, AABB tetraploids and AACC tetraploids indicated significant alterations to the A- and D-genomes which prompted further investigation to positively distinguish the two. In 1994, Jellen et al. provided the information necessary to differentiate the A- and D-genome using a powerful application of fluorescent microscopy known as fluorescent in situ hybridization (FISH). This technique allows for the detection of RNA or DNA sequences in a variety of cells, tissues and tumors. More specifically, FISH is a cytogenetic technique that is used to detect and localize a target nucleic acid sequence. FISH patterns combined with chromosome size and arm ratios identified by previous karyotyping analyses resulted in the development of a uniform nomenclature system to describe each chromosome in hexaploid oat. The A-genome comprises of the 8A, 11A, 13A, 15A, 16A, 17A, and 19A chromosomes. The C-genome comprises of the 1C, 2C, 3C, 4C, 5C, 6C, and 7C chromosomes. Finally, the D-genome contains the 9D, 10D, 12D, 14D, 18D, 20D, and 21D chromosomes. Correct and uniform identification facilitates the ability to perform further oat cytogenetic research. Homeologous relationships may be evaluated between the three genomes, subgenome origins may be determined, alien genes may be introduced, and genes and molecular markers may be correctly identified and anchored.

Avena magna (2n=4x=28) is a rather obscure, weedy tetraploid oat species native to heavy clay soils in agricultural areas of northern Morocco. It is of increasing interest to oat breeders due to its high protein content (up to 25% of the groat mass), large caryopses, and exceptional crown rust and powdery mildew resistance (Ladizinsky 1995; Ladizinsky 2000). This wild oat species has dramatic implications for genetic improvement of hexaploid oat because it is one of three possible ancestor-tetraploids of cultivated oat (Ladizinsky 1998; Jellen and Ladizinsky 2000). In order to facilitate genetic studies in *A. magna*, our lab made a recombinant inbred line (RIL) population derived from a cross between two *A. magna* genotypes: Ba 13-13 and A-169. Parent Ba 13-13 is a phenotypically uniform and cytogenetically stable line derived from dual-backcross hybridization with hexaploid *A. sativa*, followed by repeated selfing, to transfer Ladizinsky's domestication syndrome (non-shattering, yellow lemma, glabrous, reduced awns) into *A. magna* (Ladizinsky, 1995).

Since essentially nothing was previously known about the molecular nature of *A. magna*, we used a genomic complexity-reduction and pyrosequencing protocol for rapid marker discovery using Ba 13-13 and A-169. We followed a recently developed genomic reduction approach based on restriction-site conservation using unique multiplex identifier (MID)-barcodes (Maughan et al. 2009) to dramatically reduce the size of the two parental genomes in preparation for 454-pyrosequencing. The resulting sequence-based contigs were assembled and screened for Single Nucleotide Polymorphisms (SNPs). Putative SNPs are being validated by a low-throughput genotyping technique called High Resolution Melting (HRM), which is capable of detecting polymorphisms, mutations, deletions, insertions and epigenetic differences in double-stranded DNA (Reed, 2007). As these *A. magna*-based SNPs are validated, they are being mapped onto the tetraploid population and are also being screened for polymorphism using a panel of hexaploid mapping-population parents. Once validated, the panel of SNPs can be screened on other species for global diversity of all other genome combinations. Species-specific SNPs may be derived to facilitate gene transfer from wild species for breeding purposes and to clarify evolutionary relationships among subgenomes within *Avena*.

PLANT BREEDING

Plant breeding is a scientific art that has been practiced for thousands of years. Initially, selecting plants with desirable traits for propagation was standard for breeders. More complex molecular techniques have since evolved. Regardless of the breeding technique used, the goals of plant breeding programs remain largely unchanged. Improvements in disease and pest resistance, yield, quality and durability are among the qualities that are aggressively being explored (Eathington et al. 2007). Molecular techniques generate the fragments of DNA sequences that may represent variation in genomes. Genome variation between two lines within a species can be measured. These DNA fragments are called molecular markers (Tanksley 1983).

Gene mapping is produced as the chromosomal location or distance between markers is discovered. Genetic maps are created based on recombination frequencies. Partial exchange of homologous chromosomes during meiosis is referred to as recombination. The frequency of analysis may be determined by statistical analysis. Higher rates of recombination imply greater distances between molecular markers on the chromosome. Plant breeders may take advantage of these gene maps by using marker assisted selection. Marker assisted selection allows for the indirect selection of traits of interest based on the location of the molecular markers (Collard 2007). The goal of each molecular method is to generate dense, repeatable, accurate molecular marker maps. Sequencing methods are quickly emerging as the technique of choice for developing these maps, but its applications have yet to be fully realized (Rudd et al. 2005). As present limitations are diminished, and future applications and sequencing procedures are presented, the revolutionary effects of whole genome sequencing on plant breeding programs will be more fully recognized.

HISTORY OF MOLECULAR MAPPING

Gregor Mendel opened the door to modern genetics with his pea plant experiments in the mid-1800s. His discovery of patterned inheritable traits became the foundation of molecular mapping (Weiling 1991). In fact, until recently genetic linkage maps predominately contained markers for alleles with major phenotypic effects, or macromutations (Tanksley 1983). Many molecular techniques have emerged, contributing to denser, more accurate, rapid mapping. These methods include random fragment length polymorphisms (RFLPs; Tanksley et al. 1989), random amplified polymorphic DNAs (RAPDs; Martin et al. 1991), amplified fragment length polymorphisms (AFLPs; Blears et al. 1998), simple sequence repeats (SSRs; Oetting et al. 1995), diversity arrays technology (DArTs; Wenzl et al. 2004) and inter simple sequence repeats (ISSRs; Ratnaparkhe et al. 1998). Each of these marker systems has distinct disadvantages. Consequently, biotechnology has turned to sequencing to revolutionize molecular mapping.

Frederick Sanger successfully sequenced the phi X 174 bacteriophage genome in 1975 by enzymatic synthesis. His “shotgun” sequencing method commenced with utilizing random fragments of genomic DNA as primers to polymerase chain reaction (PCR) amplify the whole genome. The amplification products were overlapped and assembled based on overlapping contiguous transcripts, or contigs. Any gaps remaining between these contigs were resolved using custom primers (Sanger et al. 1977). Sequence segments, or reads, between 800-1000 nucleotides in length are capable. The method dramatically improved earlier DNA sequencing techniques developed by Allan Maxam and Walter Gilbert, as well as Sanger and Alan Coulson's own 'plus and minus' technique presented 2 years earlier (Sanger and Coulson 1975).Sanger’s method enabled unprecedented speed in sequencing projects, expanding the scope of realistic sequencing endeavors in all areas of biotechnology. Additionally, the use of radioisotopes and other toxic substances was limited, solidifying Sanger sequencing as the principle platform for nearly three decades (Sanger et al. 1977).

Perhaps the greatest accomplishment of the Sanger method was the complete sequencing of the human genome in 2000 (Waterston et al. 2002). This endeavor quickly drove the development of increasingly efficient automated procedures and process parallelization. New methods emerged to improve the speed, cost, throughput, and ability to process complex genomes for sequencing. This new wave of technology has become known as next-generation sequencing.

Next-generation sequencing was introduced by Pal Nyren and Mostafa Ronaghi in 1996 with their Pyrosequencing method (Nyren 2007). Unlike Sanger sequencing, which detects chain termination with dideoxynucleotides (Sanger et al. 1977), Pyrosequencing observes nucleotide incorporation by pyrophosphate release. Single strands of DNA act as templates while complementary strands are synthesized (Ronaghi et al. 1996). The DNA polymerase and chemiluminescent enzyme activity is monitored. Nucleotide solutions of A,C,G, and T are added and removed sequentially, producing light as the solutions complement the order of the unpaired template (Nyren 2007). The need for labeled primers, gel-electrophoresis and labeled nucleotides are thus eliminated. Despite the additional advantages of accuracy, flexibility, parallel processing, rapid analysis of large sample sizes and relatively simple automation, Pyrosequencing produces shorter DNA sequence read lengths of 300-500 nucleotides (Ronaghi et al. 1996). Consequently, genome assembly may prove more difficult, especially in the presence of repetitive DNA. The history of biotechnology has proven that limitations soon lead to improvements, with no exception here.

Pyrosequencing was first commercialized by Roche's 454 Life Sciences in 2005. Their GS20 sequencing machine and GS FLX series were the first next-generation sequencing methods on the market. As many as- 400-600 million base pairs are capable of being sequenced within hours (Wheeler 2008). Advances in speed, read lengths, higher accuracy, and lower cost allowed the first competitive alternative to Sanger sequencing

Despite the progress in genetic research by next-generation sequencing, the limitations in utilizing these methods remains historically unchanged. Cost, time, effectiveness, and reproducibility still remain the principle determining factors of any research-based method (Coombs 2008). New technology brings novel concerns as well. Whole genome sequence analyzers have generated unprecedented amounts of data in a short period of time. In addition to the storage of this massive quantity of data, there is a need for bioinformatics programs and computers capable of processing prodigious amounts of information (Rudd et al. 2005). These programs increase the cost and complexity of such methods because of the need to hire or train personnel to run these programs and interpret their output. Notwithstanding, genome sequencing has profoundly impacted plant breeding programs. Genetic markers and maps are being developed with unprecedented accuracy, speed and depth. The properties and functions of genomes are being discovered, as well as the ability to view the original transcriptome expression (Eathington et al. 2007).

EFFECTS OF MAPPING ON PLANT BREEDING

The introduction of molecular markers has revolutionized genetics. Technology is enabling the study of species that were not previously viewed as economic priorities, being too remote, expensive or complex for consideration in plant breeding communities (Eathington et al. 2007). The array of polymorphisms and molecular techniques that are available is increasing, and the arrival of genomic sequencing is a source of an escalating set of available markers (Cullis 2002). As more genetic information becomes available, the application of molecular markers to other experimental methods will become simpler, allowing for novel genetic analysis that is currently impossible to undertake.

As cost and time requirements are decreased, scientists will view the functions of plants with incredible opportunity for innovative research. Unknown mutations will be identified, along with increased understanding of structure-function relationships (Bernardo 2008). Not only will genes be sequenced, but the expression of genes will continue to be found. Epigenomic understanding will increase plant breeders’ knowledge of desirable traits. Molecular markers can be used in either marker-assisted selection or marker assisted introgression. However, as sequencing supplies increased information, molecular properties may reduce the need for introgression, thereby removing the need for growing or rearing plants in order to measure phenotype.

Characteristics that involve a large number of genes, or traits that are complicated to select due to genotype-environment interactions have been difficult to analyze. As sequencing allows for the direct monitoring of genotypes, the efficiency for selecting such traits is enhanced.

Plant breeding programs can take advantage of this knowledge to increase crop yield, disease resistance, and a multitude of other qualities that fall into this category (Eathington et al. 2007). The understanding of the interaction between genes and environmental factors, including other organisms, also allows for discovering chromosomal conservation and evolution (Bernardo 2008). Such genetic variation, both within and outside specific plant species, augments transgenic possibilities, or the transfer of genes between species by molecular techniques (Gelvin 2003). The transgenic properties alone, indicated by genomic sequencing of molecular markers, are invaluable to plant breeders.

REFERENCES

Barbazuk WB, Emrich S, Schnable PS (2007) SNP mining from maize 454 sequencing. Plant J 51: 910-918

Bernardo R (2008) Molecular markers and selection for complex traits in plants: Learning from the last 20 years. Crop Sci 48:1649-1664

Blears MJ, De Grandis SA, Lee H, Trevors JT (1998) Amplified fragment length polymorphism (AFLP): A review of the procedure and its applications. J Ind Microbiol Biotechnol 21:99-114

Braaten JT, Wood PJ, Scott FW, Riedel, KD, Poste LM, Collins MW (1991) Oat gum lowers glucose and insulin after an oral glucose load. Am J Clin Nutr 53:1425-1430

Cervantes-Martinez CT, Frey KJ, White PJ, Wesenberg DM, Holland JB (2004) Selection for better beta-glucan content in oat grain. Crop Sci 41:1085-1091

Chong J, Reimer E, Somers D, Aung T, Penner GA (2004) Two SCARs developed and associated with *Pc94.* Can J Plant Path 26:89-96

Collard BC, Mackill DJ (2007) Marker-assisted selection: an approach for precision plant breeding in the twenty-first century. Philos Trans R Soc Lond B Biol Sci 363:557–572

Coombs A (2008) The sequencing shakeup. Nat Biotechnol 26:1109–1112

Cullis CA (2002) The use of DNA polymorphisms in genetic mapping. Genet Eng P 24:179-189

Eathington SR, Crosbie TM, Edwards MD, Reiter RS, Bull JK (2007) Molecular markers in a commercial breeding program. Crop Sci 47:S154-S163

Eggum BO, Hansen I, Larsen T (1989) Protein quality and digestible energy of selected foods determined in balance trials with rats. Plant Foods Hum Nutr 39:13-21

Fominaya A, Vega C, Ferrer E (1988) C-banding and nucleolar activity of tetraploid *Avena* species. Genome 30:633-638

Gardner KM, Latta RG (2008) Heritable variation and genetic correlation of quantitative traits within and between ecotypes of *Avena barbata*. J Evol Biol 21:737–748.

Garg RR, Bally-Cuif L, Lee SE, Gong Z, Ni X, Hew CL, and Peng, C (1999) Cloning of zebrafish activin type IIB receptor (ActRIIB) cDNA and mRNA expression of ActRIIB in embryos and adult tissues. Mol. Cell Endocrinol 153: 169-181

Gelvin SB, (2003) *Agrobacterium*-mediated plant transformation: The biology behind the "gene-jockeying" tool. Microbiol Mol Biol Rev 67:16-37

Groh S, Kianian SF, Phillips RL, Rines HW, Stuthman DD,Wesenberg DM. (2001) Analysis of factors influencing milling yield and their association to other traits by QTL analysis in two hexaploid oat populations. Theor Appl Genet 103:9–18

Gundry CN, Vandersteen JG, Reed GH, Pryor RJ, Chen J, Wittwer CT (2003) Amplicon melting analysis with labeled primers: a closed-tube method for differentiating homozygotes and heterozygotes. Clin Chem 49: 396-406

Harlan JR, Price EG (1973) Comparative evolution of cereals. Evolution 27:311-32

Holland JB, Frey KJ, Hammond EG (2001) Correlated responses of fatty acid composition, grain quality and agronomic traits to nine cycles of recurrent selection for increased oil content in oat. Euphytica 122: 69-79

Hutchinson J, Postoyko J (1986) C-banding of Avena species of Avena species. In Genetic manipulation in plant breeding. Proc Int Symp Eucarpia. September 8-13, 1985, Berlin.

Jellen EN, Beard JL (2000) Geographical distribution of a chromosome 7C and 17 intergenomic translacation in cultivated oat. Crop Sci 40:256–26

Jellen EN, Gill BS, Cox TS (1994) Genomic in situ hybridization detects C-genome chromatin and intergenomic translocations in polyploidy oat species (Genus Avena). Genome 37:613-618

Jellen EN, Ladizinsky G (2000) Giemsa C-banding in *Avena insularis* Ladizinsky. Genet Resour Crop Evol 47:227-230

Jellen EN, Leggett JM (2006) Cytogenetic Manipulation in Oat Improvement. *Genetic Resources, Chromosome Engineering, and Crop Improvement: Cereals*, Volume 2. CRC Press, pp 200-211

Jin H, Domier LL, Shen X, Kolb FL (2000) Combined AFLP and RFLP mapping in two hexaploid oat recombinant inbred populations. Genome 43:94-101

Kremer CA, Lee M, Holland JB (2001) A restriction fragment length polymorphism based linkage map of a diploid Avena recombinant inbred line population. Genome 44:192–204

Ladizinsky G (1995) Domestication via hybridization of the wild tetraploid oats *Avena magna* and *A. murphyi.* Theor Appl Genet 9:639-646

Ladizinsky G (1998) A new species of *Avena* from Sicily, possibly the tetraploid progenitor of hexaploid oats. Genet Resour Crop Evol 45:263-269

Ladizinsky G, Fainstein R (1977) Introgression between the cultivated hexaploid oat *A. sativa* and the tetraploid wild A. magna and A. murphyi . Can J Genet Cytol 19:59–6

Latta RG, Gardner KM (2009) Natural selection on pleiotropic quantitative trait loci affecting a life-history trade-off in Avena barbata. Evolution 63:2153-2163

Li YC, Korol AB, Fahima T, Beiles A Nevo E.)2002) Microsatellites: genomic distribution, putative functions and mutational mechanisms: a review. Mol Eco 11:2453-2465

Linares C, Vega C, Ferrer E, Fominaya A (1992) Identification of C-banded chromosomes in meiosis and the analysis of nucleolar activity in *Avena byzantina*

C. Koch cv. `Kanota'. Theor Appl Genet 83:650-654

Magness JR, Markle GM, Compton CC (1971) Food and feed crops of the United States. Interregional Research Project IR-4, IR Bul. 1

Martin GB, Williams JG, Tanksley SD (1991) Rapid identification of markers linked to a *Pseudomonas* resistance gene in tomato by using random primers and near-isogenic lines. Proc Natl Acad Sci USA 88:2336-2340

Maughan PJ, Yourstone SM, Jellen EN, Udall JA (2009) SNP Discovery via genomic reduction, barcoding, and 454-pyrosequencing in Amaranth. Pl Genome 2:260-270

Mester D, Ronin Y, Nevo E, Korol A (2003), Efficient multipoint mapping: making use of dominant markers repulsion-phase. Theor. Appl. Genet. 107:1002–1112.

Mester D, Ronin Y , Nevo E. Korol A (2004) Fast and high precision algorithms for optimization in large scale genomic problems, *Comp. Biol. Chem.* 28**:**281–290

Mester D, Ronin, Y, Korostishevsk M, Pikus V, Glazman A, Korol A. (2005) Multilocus consensus genetic maps (MCGM): formulation, algorithms and results. Comp Biol Chem 30:12-20

Mukhopadhyay R (2009) DNA sequencers: the next generation. Anal Chem 10:1021-1027

Murphy HC, Sadanaga K, Zillinsky FJ, Terrell EE, Smith RT (1968) *Avena magna*: an important new tetraploid species of oats. Science 159:103-104

Nuttall FQ, Mooradian AD, Gannon MC, Billington C, Krezowski P (1984) Effect of protein ingestion on the glucose and insulin response to a standardized oral glucose load. Diabetes Care 7: 465-470

Nyrén P (2007) The history of pyrosequencing. Methods Mol Biol 373: 1–14

O’Donoughue LS, Kianian SF, Rayapati PJ, Penner GA, Sorrells ME, Tanksley SD, Phillips RL, Rines HW, Lee M, Fedak G, Molnar SJ, Hoffman D, Salas CA, Wu B, Autrique E, Van Deynze A (1995) A molecular linkage map of cultivated oat. Genome 38:368-380

Ohm HW, Patterson FL, Roberts JJ, Shaner GF (1974) Registration of Noble oats. Crop Sci 14:906

Oetting WS, Lee HK, Flanders DJ, Wiesner GL, Sellers TA, King RA (1995) Linkage analysis with multiplexed short tandem repeat polymorphisms using infrared fluorescence and M13 tailed primers. Genomics 30:450-458

Oliver RE, Jellen EN, Ladizinsky G, Korol AB, Kilian A, Beard JL, Dumlupinar Z, Wisniewski NH, Svedin E, Coon M, Redman RR, Maughan PJ, Obert DE, Jackson EW (2011) New Diversity Arrays Technology (DArT) markers for tetraploid oat (*Avena magna* Murphy et Terrell) provide the first complete oat linkage map and markers linked to domestication genes from hexaploid *A. sativa* L. BMC Genomics (in press)

Orr W, Molnar SJ (2008) Development of PCR-based SCAR and CAPS markers linked to b-glucan and protein QTL regions in oat. Genome 51: 421-425

Pal N, Sandhu JS, Domier LL, Kolb FL. (2002) Development and characterization of microsatellite and RFLP-derived PCR markers in oat. Crop Sci 42:912–918

Rafalski A (2002) Applications of single nucleotide polymorphisms in crop genetics. Curr Opin Plant Biol 5: 94–100

Rajhathy T, Dyc lt PL (1963) Chromosomal differentiation and speciation in diploid Avena .II. Caryotype of A. *pilosn*. Can J Gene Cytol 5: 175-179

Rajhathy T, Thomas H (1974). Cytogenetics of oats (Avena L.). Misc Publ No 2. Genet Soc Can (Ottowa)

Ratnaparkhe MB, Tekeoglu M, Muehlbauer FJ (1998) Inter-simple-sequence-repeat (ISSR) polymorphisms are useful for finding markers associated with disease gene clusters. Theor Appl Genet 97:515-519

Reed GH, Kent JO, Wittwer CT (2007) High-resolution DNA melting analysis for simple and efficient molecular diagnostics. Pharmacogenomics 8:597–608

Ronaghi M, Uhlen M, Nyren P (1996) Real-time DNA sequencing using detection of pyrophosphate release. Anal Biochem 242: 84

Rudd S, Schoof H, Mayer K (2005) Plant Markers - a database of predicted molecular markers from plants. Nucl Acids Res 33:D628-D632

Sanger F, Coulson AR (1975) A rapid method for determining sequences in DNA by primed synthesis with DNA polymerase. J Mol Biol 94:441–8

Sanger F, Nicklen S, Coulson AR (1977) DNA sequencing with chain-terminating inhibitors. Proc Natl Acad Sci USA 74:5463–5467

Schmid C, Bucher P (2007) ChIP-Seq Data reveal nucleosome architecture of human promoters. Cell 131:831-832

Tamura K, Dudley J, Nei M, Kumar S (2007) MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. Mol Biol Evol 24:1596-1599

Tanksley SD (1983) Molecular markers in plant breeding. Plant Mol Biol Rep 1:3-8

Tanksley SD, Young ND, Paterson AH, Bonierbale BW (1989) RFLP mapping in plant breeding: New tools for an old science. BioTechnol 7:257-264

Thiel T, Michalek W, Varshney RK, Graner A (2003) Exploiting EST databases for the development and characterization of gene-derived SSR-markers in barley (*Hordeum vulgare* L.). Theor Appl Genet 106:411-422

Thomas H (1992) Cytogenetics of *Avena*. In: Marshall HG, Sorrells ME (ed) Oat

Science and Technology, Monograph 33, Agronomy Series. Madison, WI: ASA and CSSA, pp 473-508

Tinker NA, Kilian A, Wight CP, Heller-Uszynska K, Wenzl P, Rines HW, Bjornstad A, Howarth CJ, Jannink JL, Anderson JM, Rossnagel BG, Stuthman DD, Sorrells ME, Jackson EW, Tuvesson S, Kolb FL, Olsson O, Federizzi LC, Carson ML, Ohm HH, Molnar SJ, Scoles GJ, Eckstein PE, Bonman JM, Ceplitis A, Langdon T (2009) New DArT markers for oat provide enhanced map coverage and global germplasm characterization. BMC Genom 10:39

Van Tassell CP, Smith TPL, Matukumalli LK, Taylor JF, Schnabel RD, Taylor Lawley C, Haudenschild CD, Moore SS, Warren WC, and Sonstegard TS (2008) SNP discovery and allele frequency estimation by deep sequencing of reduced representation libraries. Nature Methods 5:247–252

Wang X, Su B, Fujioka H, Zhu X (2008) Dynamin-like protein 1 reduction underlies mitochondrial morphology and distribution abnormalities in fibroblasts from sporadic Alzheimer's disease patients. Am J Pathol 173: 470-482

Waterston RH, Lander ES, Sulston JE (2002) On the sequencing of the human genome. Proc Natl Acad Sci USA 99:3712–6

Weiling F (1991) Historical study: Johann Gregor Mendel 1822-1884. Am J Med Genet 40: 1–25

Wenzl P, Carling J, Kudrna D, Jaccoud D, Huttner E, Kleinhofs A, Kilian A (2004) Diversity arrays technology (DArT) for whole-genome profiling of barley. Proc Natl Acad Sci USA 101:9915-9920

Wheeler DA (2008) The complete genome of an individual by massively parallel DNA sequencing. Nature 452:872–876

Wittner Ct, Reed G, Gundry CN, Vandersteen JG, Pryor RJ (2003) High-resolution genotyping by amplicons melting analysis using LCGreen. Clin Chem 49:853-860

Xu, Y, Padiath QS, Shapiro RE, Jones CR, Wu SC, Saigoh N, Saigoh K, Ptacek LJ, Fu YH (2005). Functional consequences of a CKIdelta mutation causing familial advanced sleep phase syndrome. Nature 434: 640—644

Yen ST, Filion WG (1977) Differential Giemsa staining in plants. V. Two types of constitutive heterochromatin in species of *Avena*. Can J Genet Cytol 19:739-743

Young VR, Pellett PL (1994). Plant-proteins in relation to human protein and amino-acid nutrition. Am J Clin Nutr 59**:**1203-1212.

Yu GX, Wise RP (2000) An anchored AFLP- and retrotransposon-based map of diploid Avena. Genome 43:736-49

Zhou X, Jellen EN, Murphy JP (1999) Progenitor germplasm of domesticated hexaploid oat. Crop Sci 39:1208-1214

TABLES

Table 1. Newbler Assembler results**.** All assembled contigs and unassembled singletons were compared to the NCBI non–redundant monocot database by BLASTx.

Total Number of Reads	706,426
Total Number of Bases	27,200,520
Number of Aligned Reads	1,177,520
Number of Aligned Bases	363,482,847
Number of Contigs	57,048
Number of Bases	31,911,706
Average read length per contig	345 bp
Average reads depth per contig	16x

Table 2. SNP markers identified by SNP Finder. Number of SNPs found and coverage. True SNP results are reported for strict parameters.

Total number of SNPs found	31,304
Average coverage	16x

True SNP Results for 10x, 40% MAF, 100% match within accession	
Total true species SNPs found	12642
Total contigs containing true SNPs	6502
Total true SNPs/assembly length	0.000268

Table 3. A list of 16 *Avena* diversity lines for SNP assay validation.

	VALIDATION PANEL		
	ID	***AVENA* SPECIES**	**GENOME DESIGNATION**
1	PI 657427	*damascena*	AdAd or DdDd
2	CN 23017	*canariensis*	AcAc or DcDc
3	PI 657352	*wiestii*	AsAs
4	PI 657576	*eriantha*	CdCd
5	PI 657337	*ventricosa*	CvCv
6	PI 657606	*murphyi*	AACC or CCDD
7	PI 657271	*sterilis*	AACCDD
8	PI 657514	*magna*	CCDD
9	PI 657613	*magna*	CCDD
10	PI 657620	*magna*	CCDD
11	Cc 7070	*magna*	CCDD
12	Cc 7071	*magna*	CCDD
13	Cc 7073	*magna*	CCDD
14	BYU 210	*insularis*	AACCDD
15	BYU 661	*sativa*	AACCDD
16	BYU 284	*sativa*	AACCDD

Table 4. The list of *Avena* genotypes used for the tetraploid-SNP diversity analysis.

Accession	**Species**	**Origin**	**Locality**
A-169	*magna*	Morocco	unknown
BA 13-13	*magna*	Israel	cultivated
GS7	*sativa*	Indiana	cultivated
Ogle	*sativa*	Illinois	cultivated
PI 412765	*vaviloviana*	Ethiopia	Shewa
PI 412767	*vaviloviana*	Ethiopia	Shewa
PI 412768	*vaviloviana*	Ethiopia	Shewa
PI 657271	*sterilis*	Morocco	Merchouch
PI 657274	*barbata*	Morocco	Merchouch
PI 657351	*barbata*	Morocco	Ain Aouda
PI 657355	*murphyi*	Morocco	Tangier
PI 657357	*murphyi*	Morocco	Tangier
PI 657358	*murphyi*	Morocco	Tangier
PI 657361	*murphyi*	Morocco	Tangier
PI 657364	*murphyi*	Morocco	Tangier
PI 657366	*murphyi*	Morocco	Tangier
PI 657367	*murphyi*	Morocco	Tangier
PI 657368	*murphyi*	Morocco	Tangier
PI 657370	*murphyi*	Morocco	Tangier
PI 657371	*murphyi*	Morocco	Tangier
PI 657372	*murphyi*	Morocco	Tangier
PI 657373	*murphyi*	Morocco	Tangier
PI 657374	*murphyi*	Morocco	Tangier
PI 657375	*murphyi*	Morocco	Tangier
PI 657379	*murphyi*	Morocco	Tangier
PI 657381	*murphyi*	Morocco	Tangier
PI 657394	*barbata*	Morocco	Larache
PI 657514	*magna*	Morocco	Maaziz
PI 657515	*magna*	Morocco	Maaziz
PI 657519	*magna*	Morocco	Had Brachoua
PI 657522	*magna*	Morocco	Rommani
PI 657528	*magna*	Morocco	Rommani
PI 657534	*magna*	Morocco	El Gara
PI 657535	*magna*	Morocco	El Gara
PI 657536	*magna*	Morocco	El Gara
PI 657538	*magna*	Morocco	El Gara
PI 657539	*magna*	Morocco	El Gara
PI 657541	*magna*	Morocco	Ben Slimane
PI 657544	*magna*	Morocco	Ben Slimane
PI 657546	*magna*	Morocco	Rommani
PI 657548	*magna*	Morocco	Rommani
PI 657551	*magna*	Morocco	Rommani
PI 657555	*magna*	Morocco	Had Moualine el Oued

PI 657557	*magna*	Morocco	Had Moualine el Oued
PI 657585	*agadiriana*	Morocco	Tifnit
PI 657590	*agadiriana*	Morocco	Tamri
PI 657591	*agadiriana*	Morocco	Tamri
PI 657592	*agadiriana*	Morocco	Tamri
PI 657594	*agadiriana*	Morocco	Tamri
PI 657595	*agadiriana*	Morocco	El Jadida
PI 657596	*agadiriana*	Morocco	El Jadida
PI 657598	*murphyi*	Morocco	Tangier
PI 657600	*murphyi*	Morocco	Tangier
PI 657601	*murphyi*	Morocco	Tangier
PI 657602	*murphyi*	Morocco	Tangier
PI 657604	*murphyi*	Morocco	Tangier
PI 657605	*murphyi*	Morocco	Tangier
PI 659373	*magna*	Morocco	Maaziz
PI 659376	*magna*	Morocco	Had Brachoua
PI 659378	*magna*	Morocco	Had Brachoua
PI 659380	*magna*	Morocco	Rommani
PI 659383	*magna*	Morocco	Rommani
PI 659385	*magna*	Morocco	Rommani
PI 659388	*magna*	Morocco	Maaziz
PI 659390	*magna*	Morocco	Maaziz
PI 659399	*magna*	Morocco	Rommani
PI 659406	*magna*	Morocco	Had Moualine el Oued
Provena	*sativa*	Idaho	cultivated
TAM-0301	*sativa*	Texas	cultivated

Table 5. Marker distribution and lengths of linkage groups in a genetic map constructed from a wild x cultivated *A. magna* RIL population. The map was constructed using JMP Genomics v.5.1.

Linkage Group	**Total no. markers**	**Total length (cM)**		**Largest gap (cM)**	**Ave. marker distance (cM)**
BAM 1	16	137.8		29.3	15.4
BAM 2	11	122.1		26.1	19.9
BAM 3	13	122.2		28.4	16.4
BAM 4	18	149.8		30.7	14.5
BAM 5	13	73.9		17.8	10.8
BAM 6	19	88.4		31.3	8.4
BAM 7	15	128		35.8	13.9
BAM 8	24	150		22.8	11.2
BAM 9	22	110.6		16.4	9.3
BAM 10	22	133.5		24.9	10.9
BAM 11	18	119.8		29	11.8
BAM 12	23	155.8		25.9	12.2
BAM 13	24	145.3		18.3	11
BAM 14	20	124.8		17.1	11.5
BAM 15	25	122.9		31.1	8.9
BAM 16	19	95.6		19.2	9.3
Total	302	1980.5	Ave	25.3	12.1

FIGURES

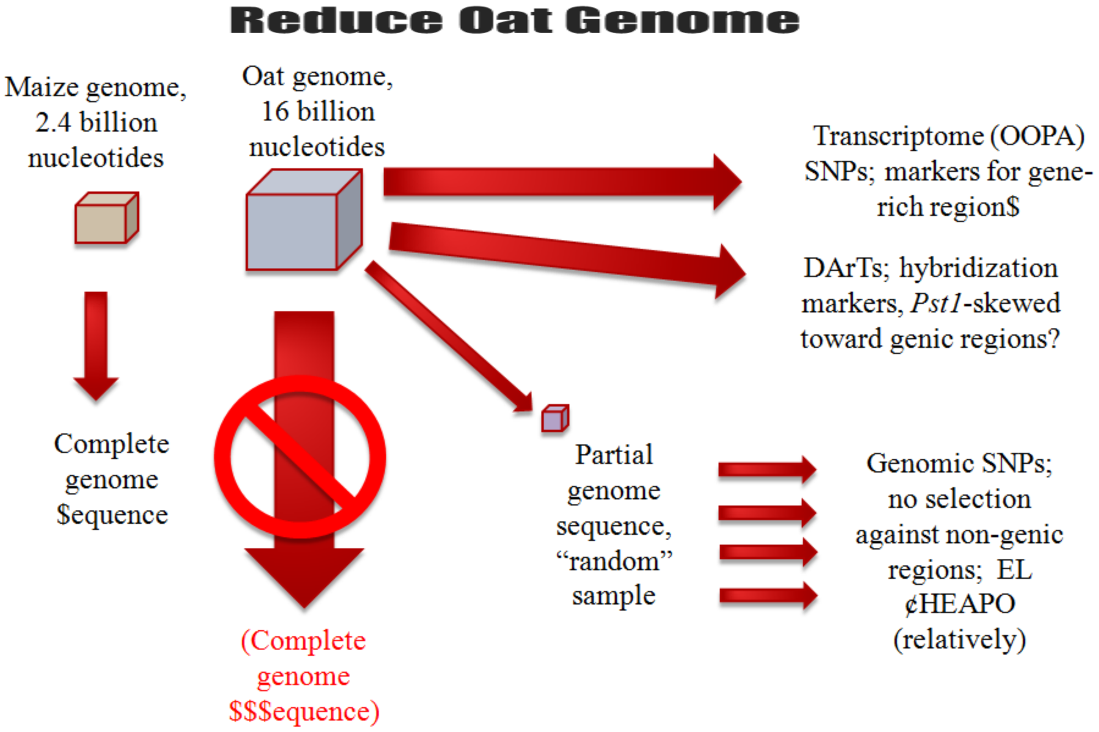
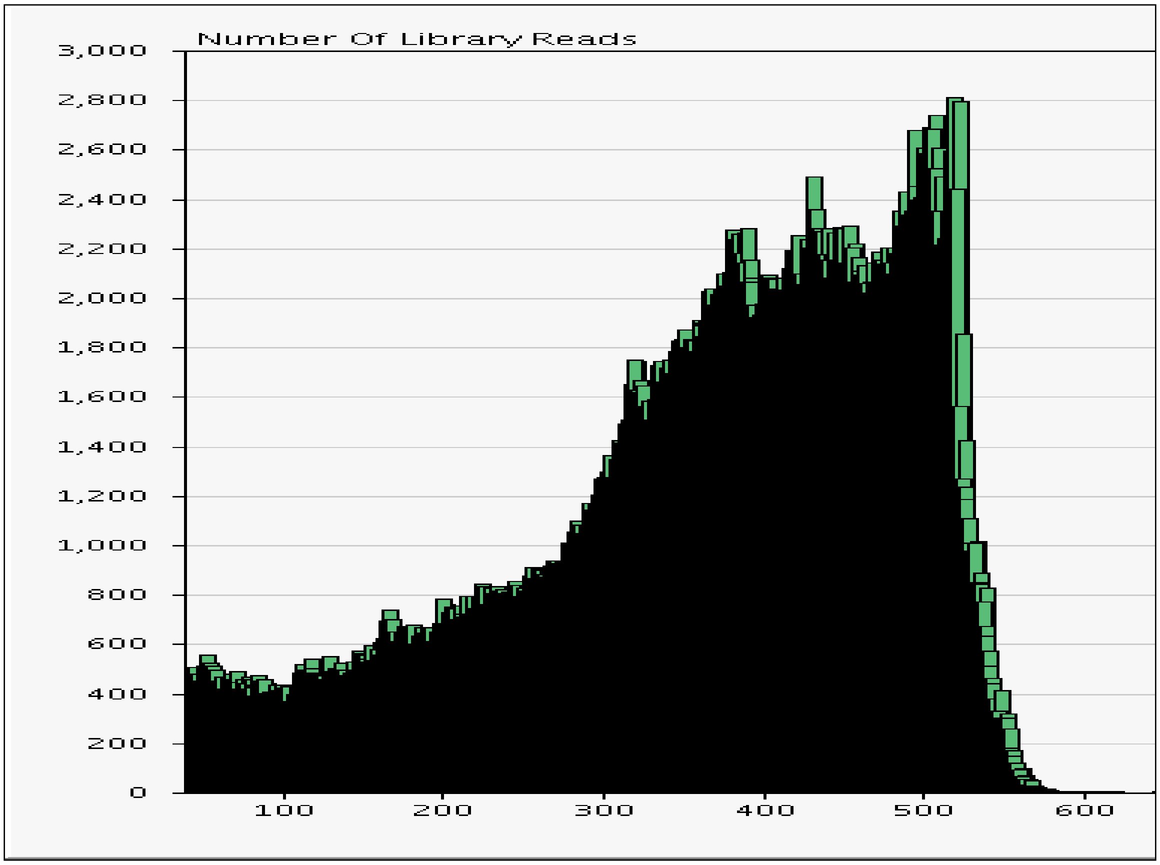


Figure 1. Alternative strategies for developing molecular genetic markers in oat. The cost of sequencing remains a concern, especially in large or complex genomes, or orphan crops. Transcriptome analysis and DArT arrays have been used to overcome cost and complexity obstacles. Genome reduction is a novel, relatively inexpensive method for generating genetic markers for such crops.

Figure 2. Frequency of pyrosequencing read lengths (in bp, x-axis) plotted against number of library reads.(y-axis).



Read Lengths (bp)

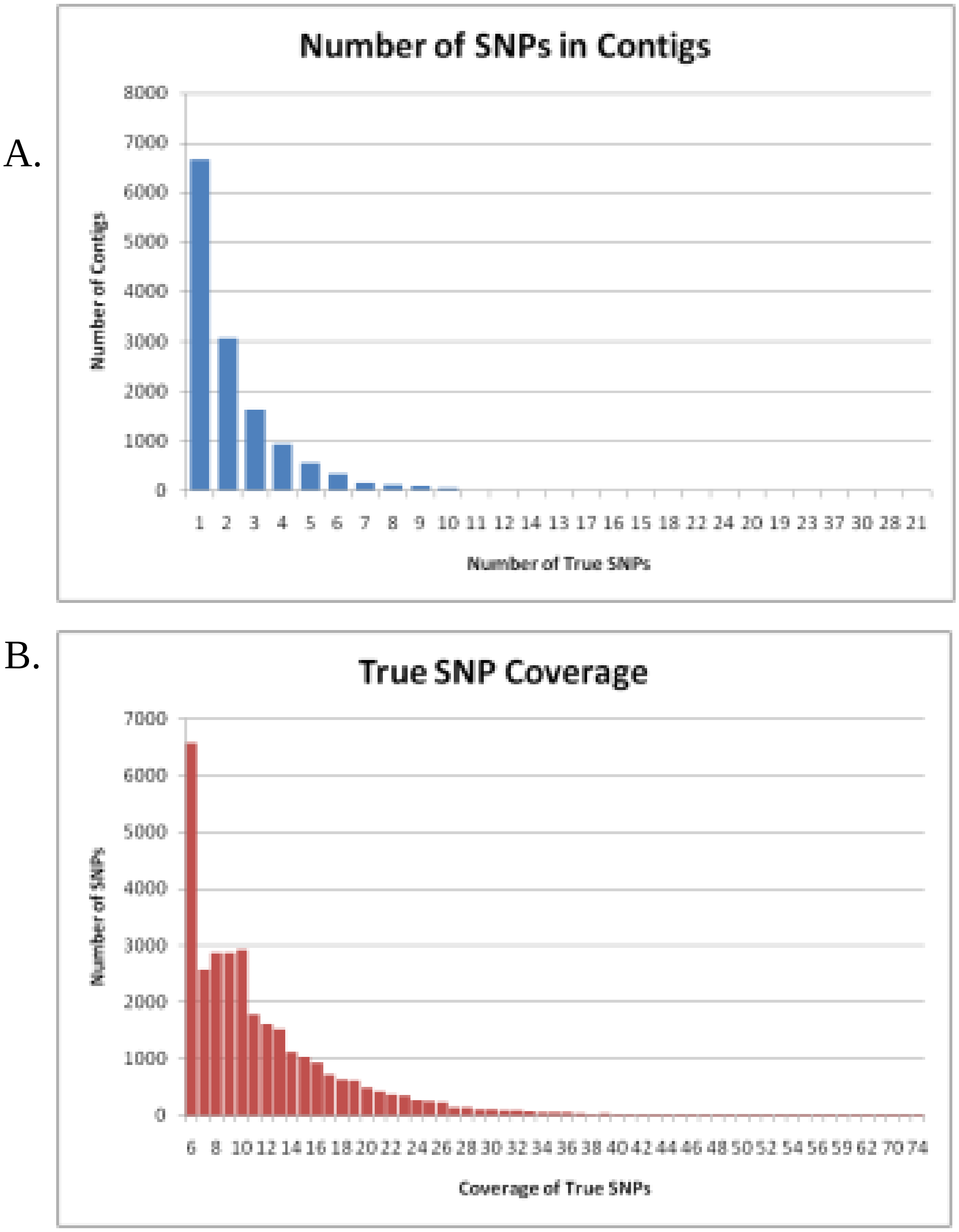
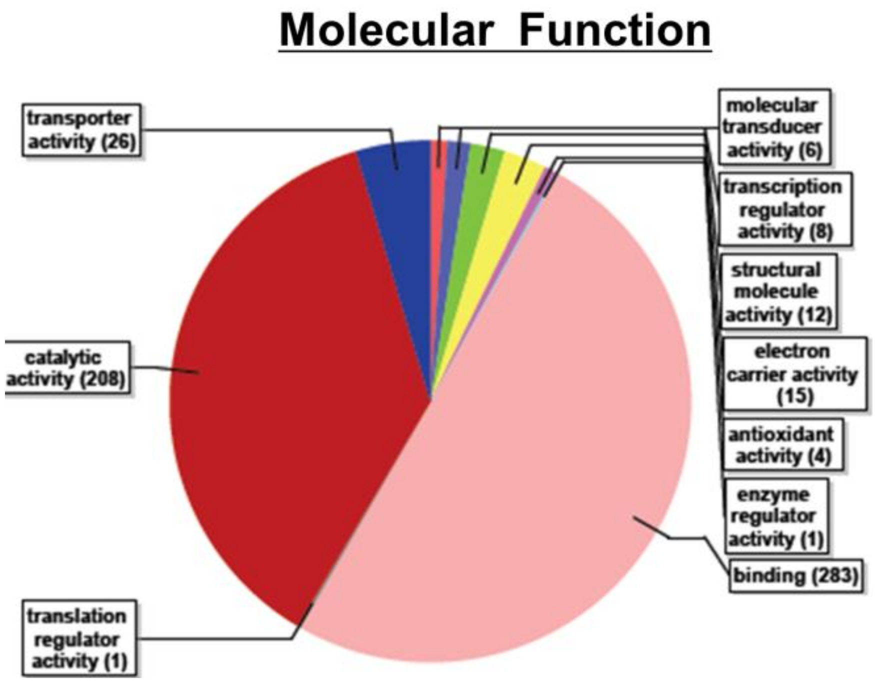
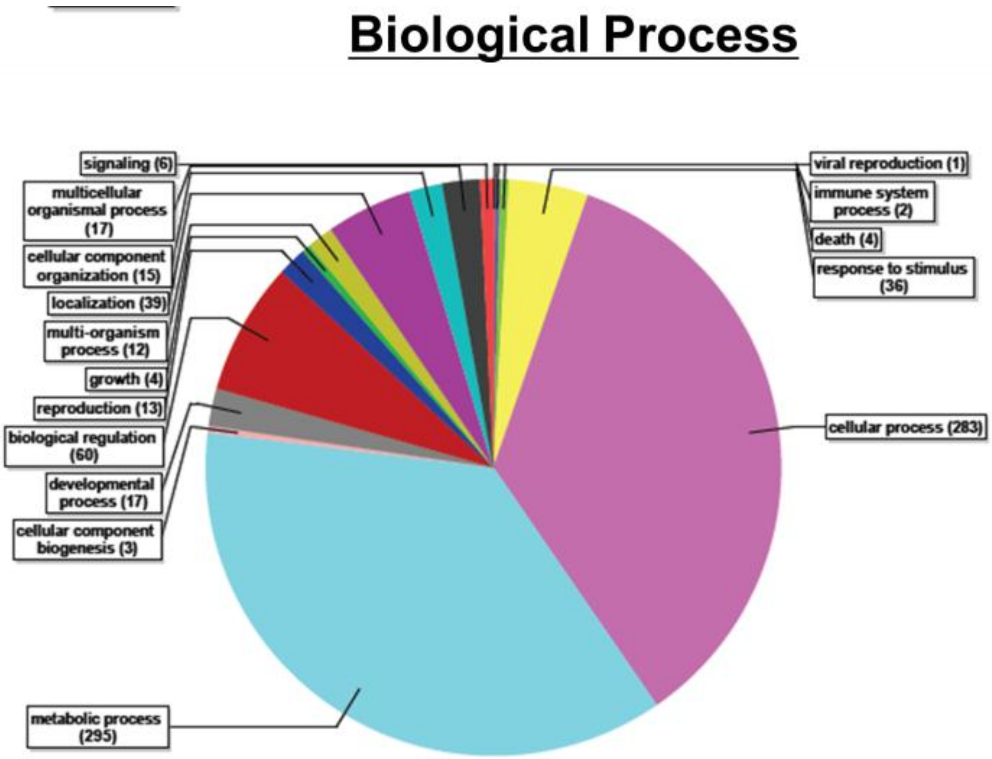


Figure 3. SNP detection and coverage results. 31,304 SNPs were identified. (A) Number of contigs sorted by SNP quantity. (B) Number of "true" SNPs with 6X coverage and above.

A.


Molecular Function
transporter activity (26)
catalytic activity (208)
translation regulator activity (1)
molecular transducer activity (6)
transcription regulator activity (8)
structural molecule activity (12)
electron carrier activity (15)
antioxidant activity (4)
enzyme regulator activity (1)
binding (283)

B.


Biological Process
signaling (6)
multicellular organismal process (17)
cellular component organization (15)
localization (39)
multi-organism process (12)
growth (4)
reproduction (13)
biological regulation (60)
developmental process (17)
cellular component biogenesis (3)
metabolic process (295)
viral reproduction (1)
immune system process (2)
death (4)
response to stimulus (36)
cellular process (283)

C.

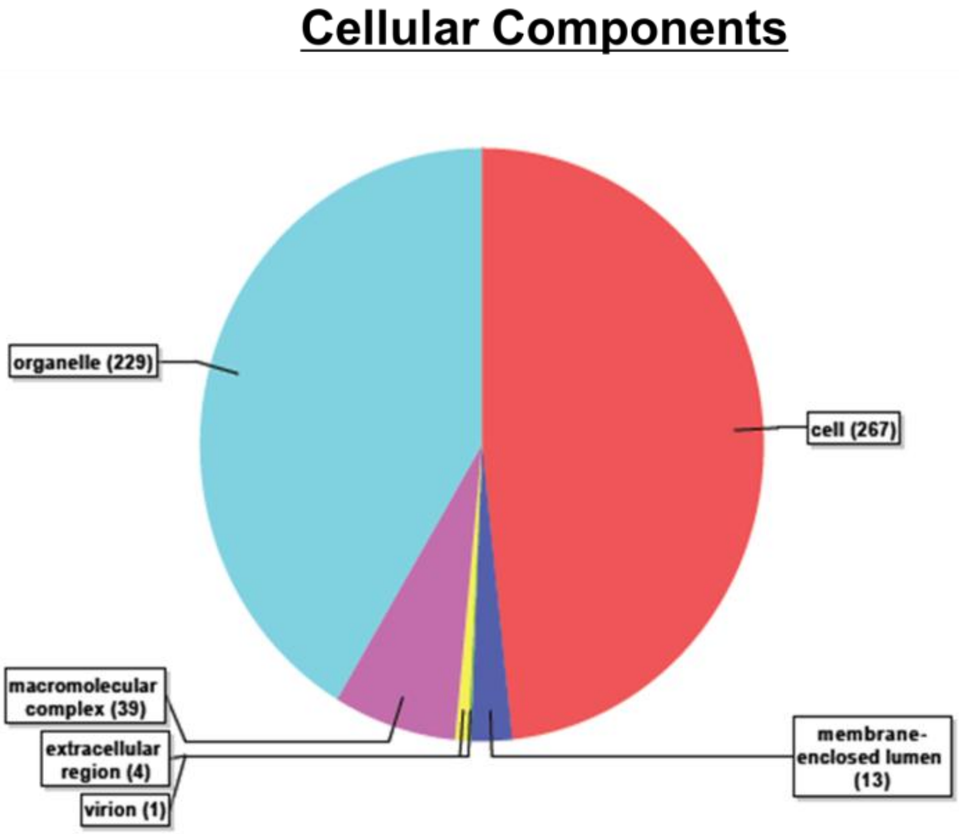


Figure 4. Putative gene ontology (GO) pie charts for the pool of GR-RSC DNAs from two *A. magna* lines, as determined by BLAST2Go, showing homology to genes for (A) molecular functions, (B) biological processes, and (C) cellular components.

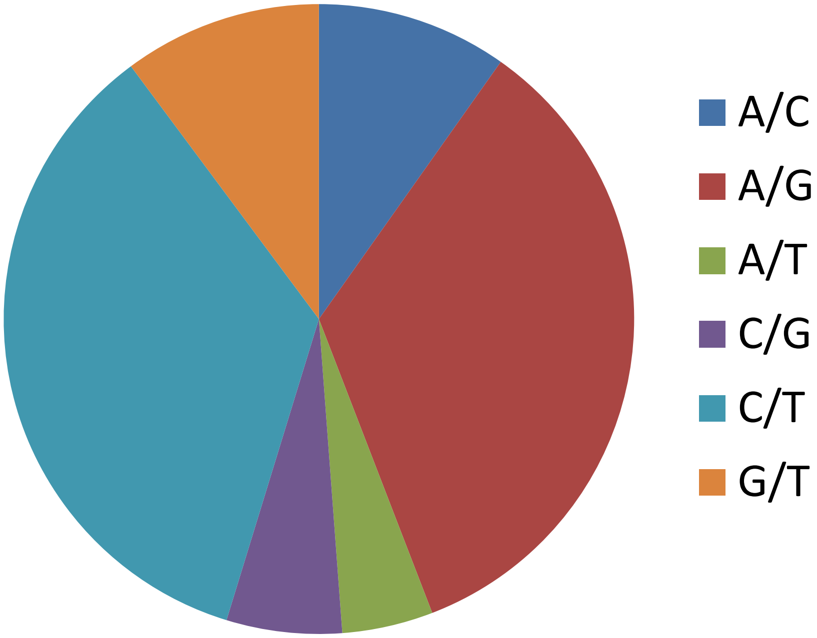


Figure 5. Pie chart depicting SNP classification results from the GR-RSC treated *A. magna* DNAs**.** As expected, C/T and A/G SNPs derived from pyrimidine/pyrimidine and purine/purine transition mutations were more prevalent than purine/pyrimidine transversions.

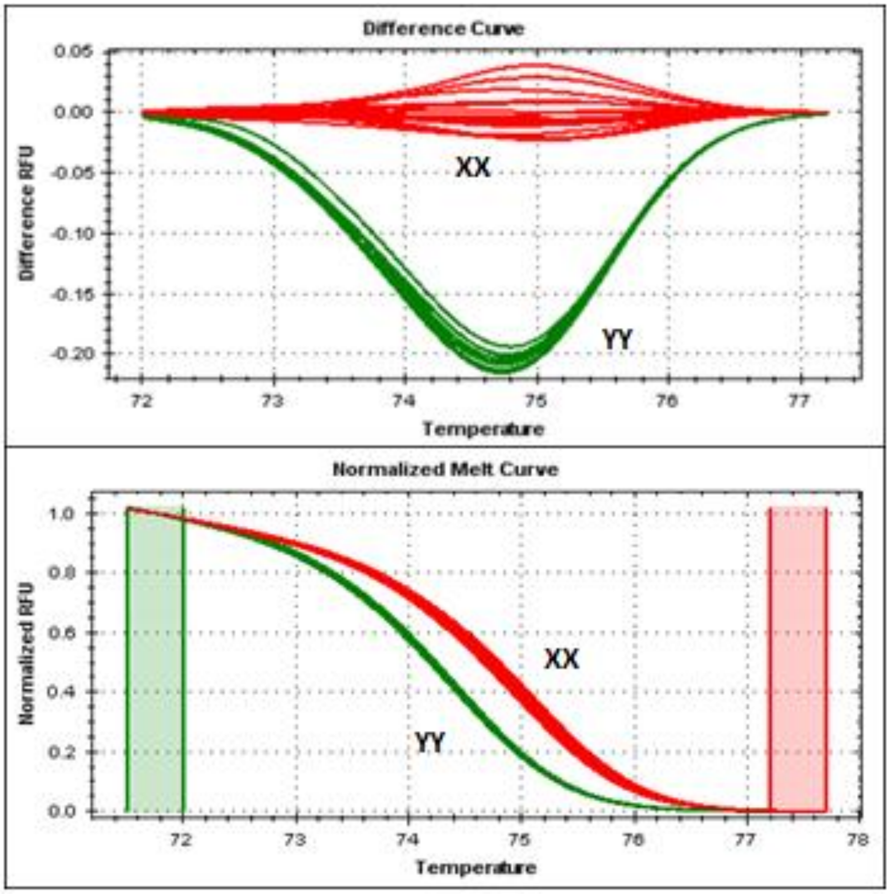


Figure 6. Bio-Rad Precision Melt analysis of contig5030 ran across a subset of the BAM RIL population. Differences in melting temperatures, indicated by red and green respectively, validate putative SNPs.

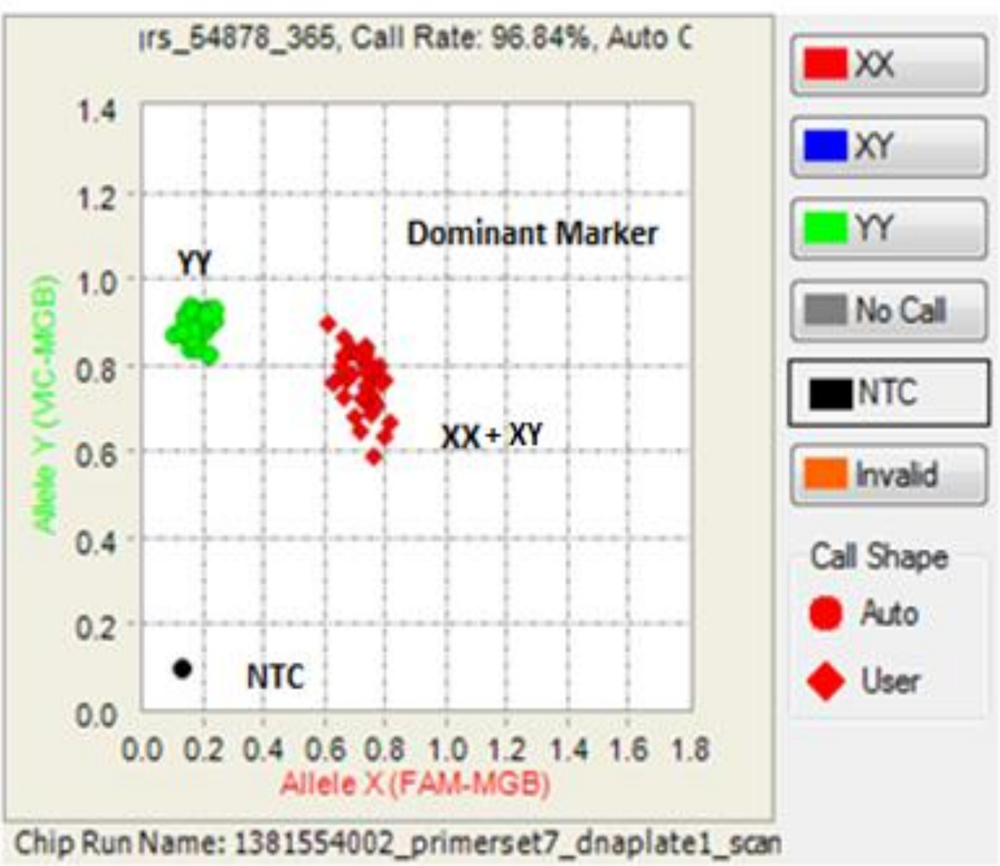


Figure 7. Fluidigm analysis. Example of SNP assays using the KASPar genotyping chemistry on Fluidigm access array on the F8 RIL mapping population. SNP loci grs_54878 demonstrates dominance. The no template control (NTC) is located at the origin of the Cartesian graph.

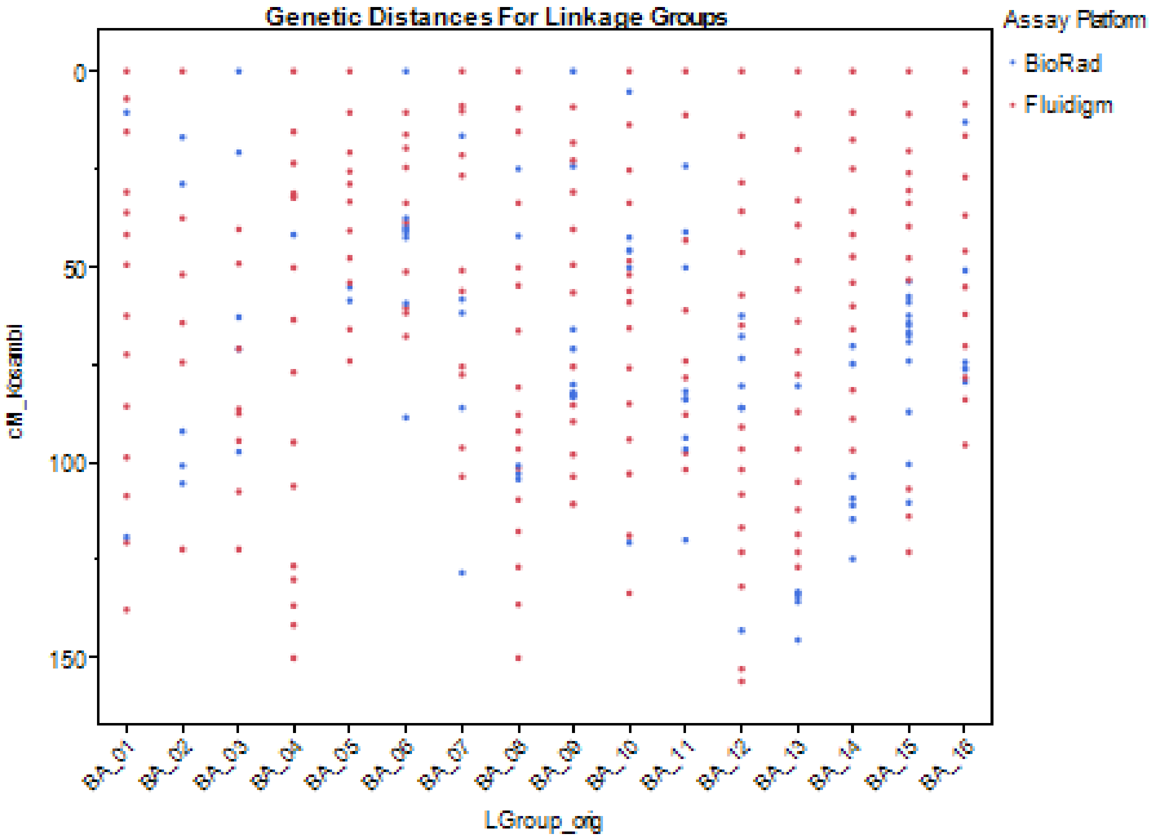


Figure 8. Marker groupings are demonstrated for both Fluidigm (red) and Bio-Rad (blue) genotyping platforms. While Bio-Rad appears to have minor clustering along a few linkage groups, the majority of the markers appear to have random distribution across all linkage groups, supporting the efficacy of both chemistries.

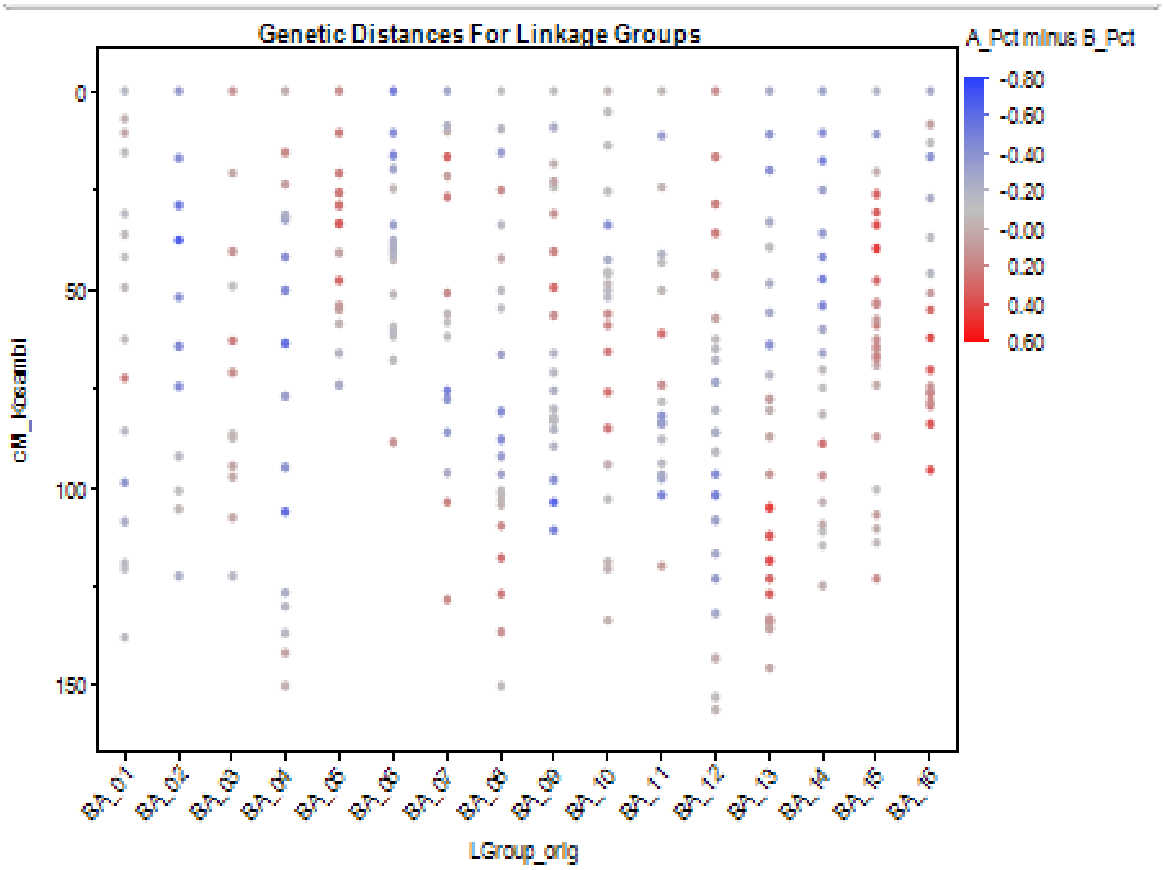
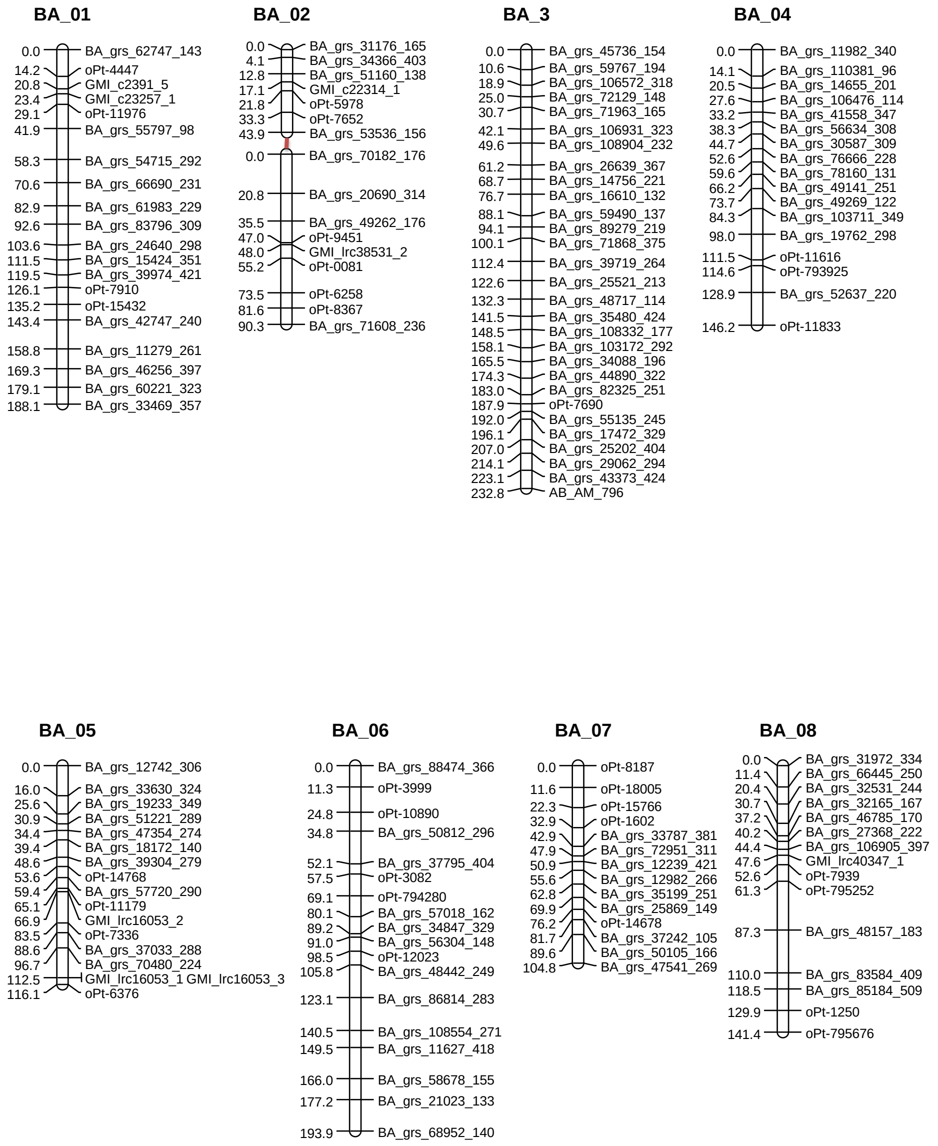


Figure 9. The genetic distances (cM) of markers on each linkage group is shown in addition to segregation distortion. The blue spectrum indicates predominance of the *A. magna* A-169 allele at a given locus, while red indicates the predominance of the Ba 13-13 mapping parent's allele at a given locus.


BA_01
0.0 BA_grs_62747_143
14.2 oPt-4447
20.8 GMI_c2391_5
23.4 GMI_c23257_1
29.1 oPt-11976
41.9 BA_grs_55797_98
58.3 BA_grs_54715_292
70.6 BA_grs_66690_231
82.9 BA_grs_61983_229
92.6 BA_grs_83796_309
103.6 BA_grs_24640_298
111.5 BA_grs_15424_351
119.5 BA_grs_39974_421
126.1 oPt-7910
135.2 oPt-15432
143.4 BA_grs_42747_240
158.8 BA_grs_11279_261
169.3 BA_grs_46256_397
179.1 BA_grs_60221_323
188.1 BA_grs_33469_357
BA_02
0.0 BA_grs_31176_165
4.1 BA_grs_34366_403
12.8 BA_grs_51160_138
17.1 GMI_c22314_1
21.8 oPt-5978
33.3 oPt-7652
43.9 BA_grs_53536_156
0.0 BA_grs_70182_176
20.8 BA_grs_20690_314
35.5 BA_grs_49262_176
47.0 oPt-9451
48.0 GMI_lrc38531_2
55.2 oPt-0081
73.5 oPt-6258
81.6 oPt-8367
90.3 BA_grs_71608_236
BA_3
0.0 BA_grs_45736_154
10.6 BA_grs_59767_194
18.9 BA_grs_106572_318
25.0 BA_grs_72129_148
30.7 BA_grs_71963_165
42.1 BA_grs_106931_323
49.6 BA_grs_108904_232
61.2 BA_grs_26639_367
68.7 BA_grs_14756_221
76.7 BA_grs_16610_132
88.1 BA_grs_59490_137
94.1 BA_grs_89279_219
100.1 BA_grs_71868_375
112.4 BA_grs_39719_264
122.6 BA_grs_25521_213
132.3 BA_grs_48717_114
141.5 BA_grs_35480_424
148.5 BA_grs_108332_177
158.1 BA_grs_103172_292
165.5 BA_grs_34088_196
174.3 BA_grs_44890_322
183.0 BA_grs_82325_251
187.9 oPt-7690
192.0 BA_grs_55135_245
196.1 BA_grs_17472_329
207.0 BA_grs_25202_404
214.1 BA_grs_29062_294
223.1 BA_grs_43373_424
232.8 AB_AM_796
BA_04
0.0 BA_grs_11982_340
14.1 BA_grs_110381_96
20.5 BA_grs_14655_201
27.6 BA_grs_106476_114
33.2 BA_grs_41558_347
38.3 BA_grs_56634_308
44.7 BA_grs_30587_309
52.6 BA_grs_76666_228
59.6 BA_grs_78160_131
66.2 BA_grs_49141_251
73.7 BA_grs_49269_122
84.3 BA_grs_103711_349
98.0 BA_grs_19762_298
111.5 oPt-11616
114.6 oPt-793925
128.9 BA_grs_52637_220
146.2 oPt-11833
BA_05
0.0 BA_grs_12742_306
16.0 BA_grs_33630_324
25.6 BA_grs_19233_349
30.9 BA_grs_51221_289
34.4 BA_grs_47354_274
39.4 BA_grs_18172_140
48.6 BA_grs_39304_279
53.6 oPt-14768
59.4 BA_grs_57720_290
65.1 oPt-11179
66.9 GMI_lrc16053_2
83.5 oPt-7336
88.6 BA_grs_37033_288
96.7 BA_grs_70480_224
112.5 GMI_lrc16053_1 GMI_lrc16053_3
116.1 oPt-6376
BA_06
0.0 BA_grs_88474_366
11.3 oPt-3999
24.8 oPt-10890
34.8 BA_grs_50812_296
52.1 BA_grs_37795_404
57.5 oPt-3082
69.1 oPt-794280
80.1 BA_grs_57018_162
89.2 BA_grs_34847_329
91.0 BA_grs_56304_148
98.5 oPt-12023
105.8 BA_grs_48442_249
123.1 BA_grs_86814_283
140.5 BA_grs_108554_271
149.5 BA_grs_11627_418
166.0 BA_grs_58678_155
177.2 BA_grs_21023_133
193.9 BA_grs_68952_140
BA_07
0.0 oPt-8187
11.6 oPt-18005
22.3 oPt-15766
32.9 oPt-1602
42.9 BA_grs_33787_381
47.9 BA_grs_72951_311
50.9 BA_grs_12239_421
55.6 BA_grs_12982_266
62.8 BA_grs_35199_251
69.9 BA_grs_25869_149
76.2 oPt-14678
81.7 BA_grs_37242_105
89.6 BA_grs_50105_166
104.8 BA_grs_47541_269
BA_08
0.0 BA_grs_31972_334
11.4 BA_grs_66445_250
20.4 BA_grs_32531_244
30.7 BA_grs_32165_167
37.2 BA_grs_46785_170
40.2 BA_grs_27368_222
44.4 BA_grs_106905_397
47.6 GMI_lrc40347_1
52.6 oPt-7939
61.3 oPt-795252
87.3 BA_grs_48157_183
110.0 BA_grs_83584_409
118.5 BA_grs_85184_509
129.9 oPt-1250
141.4 oPt-795676

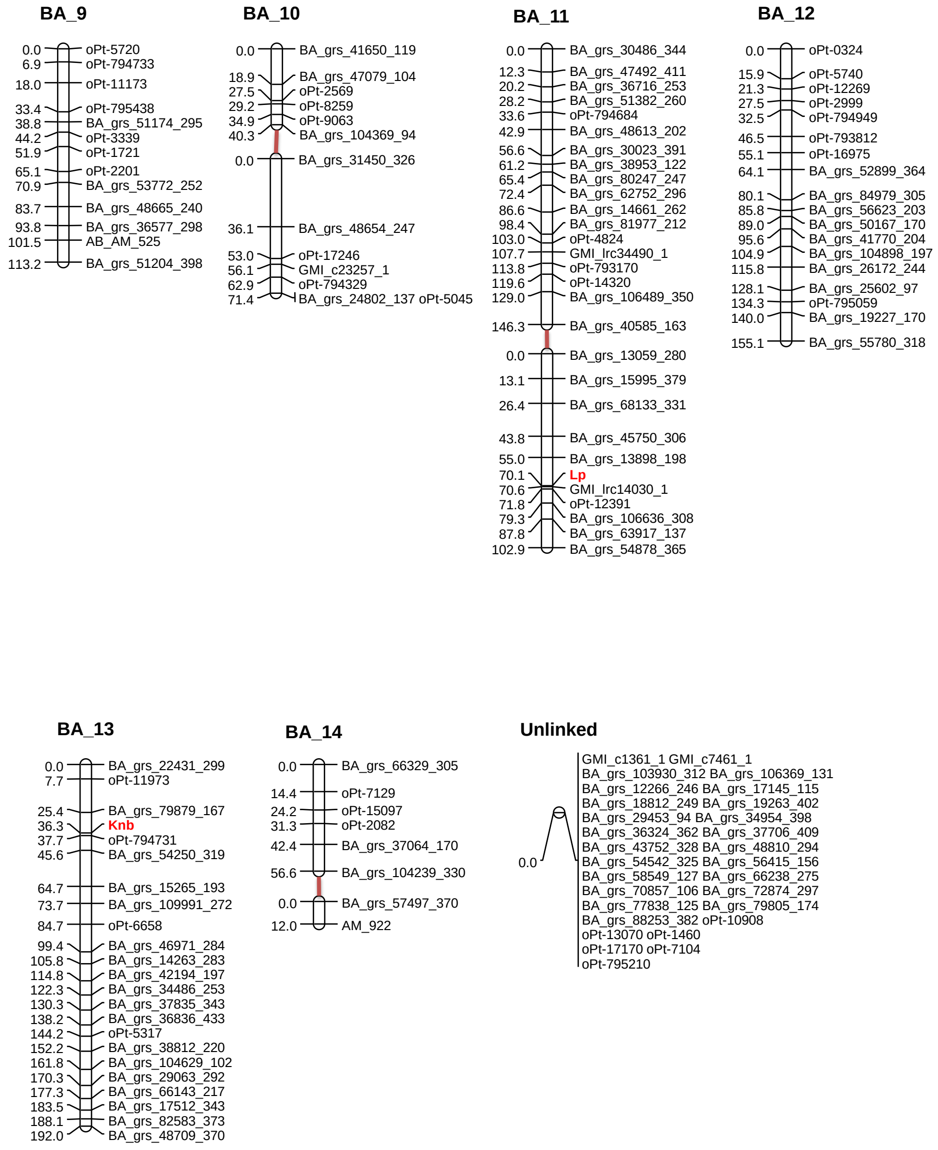
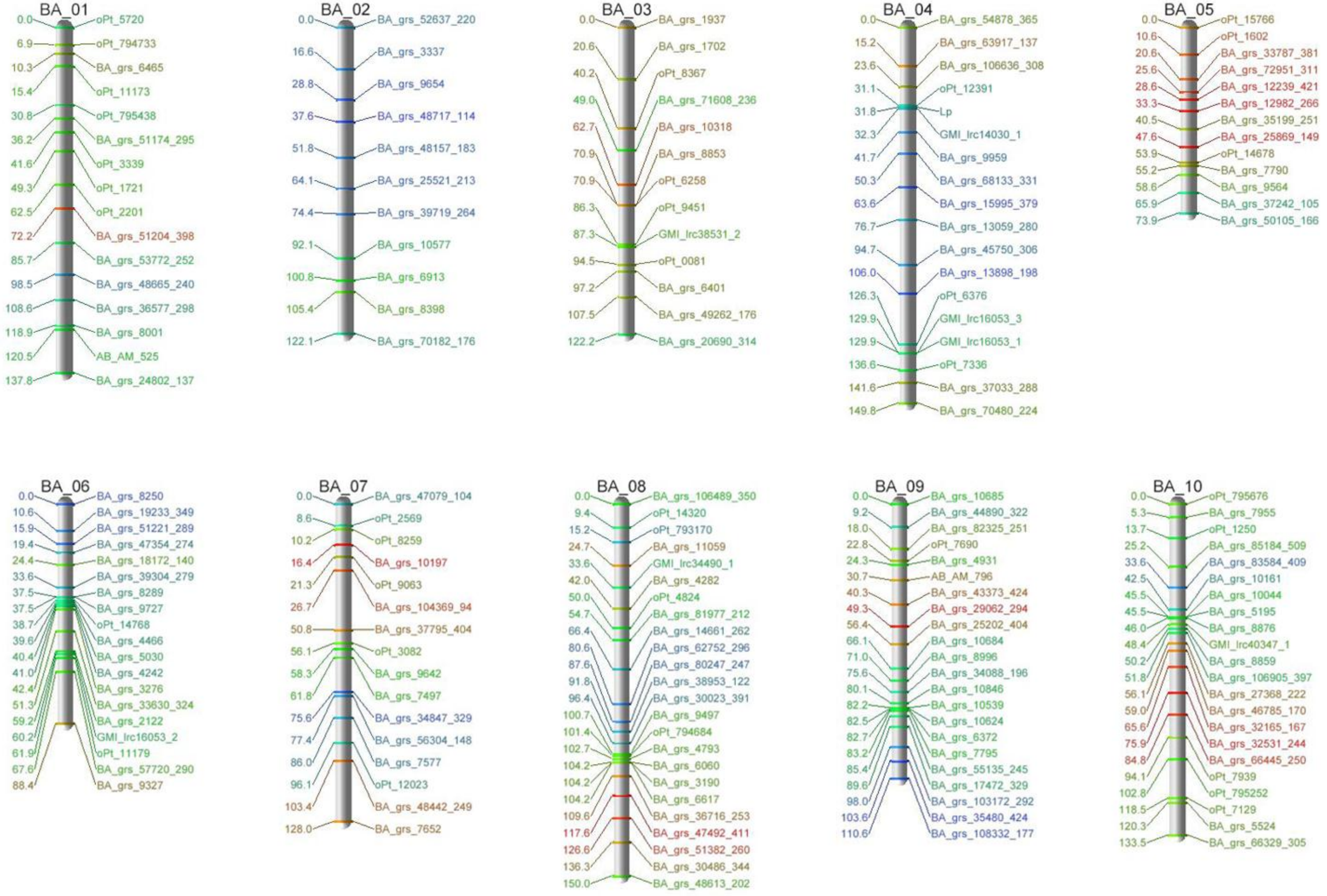


Figure 10. Genetic map of *A. magna* A-169 x Ba 13-13 RIL population, including GR-RSC SNP markers (BA_grs_XXX) generated from Fluidigm assays. Other markers are as follows: GMI_XXX, hexaploid EST-SNPs; oPt-XXX, DArTs; AB_AM_XXX, SSRs. Distance shown is in centiMorgans (cM) in Multipoint.


BA_01
0.0 oPt_5720
6.9 oPt_794733
10.3 BA_grs_6465
15.4 oPt_11173
30.8 oPt_795438
36.2 BA_grs_51174_295
41.6 oPt_3339
49.3 oPt_1721
62.5 oPt_2201
72.2 BA_grs_51204_398
85.7 BA_grs_53772_252
98.5 BA_grs_48665_240
108.6 BA_grs_36577_298
118.9 BA_grs_8001
120.5 AB_AM_525
137.8 BA_grs_24802_137
BA_02
0.0 BA_grs_52637_220
16.6 BA_grs_3337
28.8 BA_grs_9654
37.6 BA_grs_48717_114
51.8 BA_grs_48157_183
64.1 BA_grs_25521_213
74.4 BA_grs_39719_264
92.1 BA_grs_10577
100.8 BA_grs_6913
105.4 BA_grs_8398
122.1 BA_grs_70182_176
BA_03
0.0 BA_grs_1937
20.6 BA_grs_1702
40.2 oPt_8367
49.0 BA_grs_71608_236
62.7 BA_grs_10318
70.9 BA_grs_8853
70.9 oPt_6258
86.3 oPt_9451
87.3 GMI_lrc38531_2
94.5 oPt_0081
97.2 BA_grs_6401
107.5 BA_grs_49262_176
122.2 BA_grs_20690_314
BA_04
0.0 BA_grs_54878_365
15.2 BA_grs_63917_137
23.6 BA_grs_106636_308
31.1 oPt_12391
31.8 Lp
32.3 GMI_lrc14030_1
41.7 BA_grs_9959
50.3 BA_grs_68133_331
63.6 BA_grs_15995_379
76.7 BA_grs_13059_280
94.7 BA_grs_45750_306
106.0 BA_grs_13898_198
126.3 oPt_6376
129.9 GMI_lrc16053_3
129.9 GMI_lrc16053_1
136.6 oPt_7336
141.6 BA_grs_37033_288
149.8 BA_grs_70480_224
BA_05
0.0 oPt_15766
10.6 oPt_1602
20.6 BA_grs_33787_381
25.6 BA_grs_72951_311
28.6 BA_grs_12239_421
33.3 BA_grs_12982_266
40.5 BA_grs_35199_251
47.6 BA_grs_25869_149
53.9 oPt_14678
55.2 BA_grs_7790
58.6 BA_grs_9564
65.9 BA_grs_37242_105
73.9 BA_grs_50105_166
BA_06
0.0 BA_grs_8250
10.6 BA_grs_19233_349
15.9 BA_grs_51221_289
19.4 BA_grs_47354_274
24.4 BA_grs_18172_140
33.6 BA_grs_39304_279
37.5 BA_grs_8289
37.5 BA_grs_9727
38.7 oPt_14768
39.6 BA_grs_4466
40.4 BA_grs_5030
41.0 BA_grs_4242
42.4 BA_grs_3276
51.3 BA_grs_33630_324
59.2 BA_grs_2122
60.2 GMI_lrc16053_2
61.9 oPt_11179
67.6 BA_grs_57720_290
88.4 BA_grs_9327
BA_07
0.0 BA_grs_47079_104
8.6 oPt_2569
10.2 oPt_8259
16.4 BA_grs_10197
21.3 oPt_9063
26.7 BA_grs_104369_94
50.8 BA_grs_37795_404
56.1 oPt_3082
58.3 BA_grs_9642
61.8 BA_grs_7497
75.6 BA_grs_34847_329
77.4 BA_grs_56304_148
86.0 BA_grs_7577
96.1 oPt_12023
103.4 BA_grs_48442_249
128.0 BA_grs_7652
BA_08
0.0 BA_grs_106489_350
9.4 oPt_14320
15.2 oPt_793170
24.7 BA_grs_11059
33.6 GMI_lrc34490_1
42.0 BA_grs_4282
50.0 oPt_4824
54.7 BA_grs_81977_212
66.4 BA_grs_14661_262
80.6 BA_grs_62752_296
87.6 BA_grs_80247_247
91.8 BA_grs_38953_122
96.4 BA_grs_30023_391
100.7 BA_grs_9497
101.4 oPt_794684
102.7 BA_grs_4793
104.2 BA_grs_6060
104.2 BA_grs_3190
104.2 BA_grs_6617
109.6 BA_grs_36716_253
117.6 BA_grs_47492_411
126.6 BA_grs_51382_260
136.3 BA_grs_30486_344
150.0 BA_grs_48613_202
BA_09
0.0 BA_grs_10685
9.2 BA_grs_44890_322
18.0 BA_grs_82325_251
22.8 oPt_7690
24.3 BA_grs_4931
30.7 AB_AM_796
40.3 BA_grs_43373_424
49.3 BA_grs_29062_294
56.4 BA_grs_25202_404
66.1 BA_grs_10684
71.0 BA_grs_8996
75.6 BA_grs_34088_196
80.1 BA_grs_10846
82.2 BA_grs_10539
82.5 BA_grs_10624
82.7 BA_grs_6372
83.2 BA_grs_7795
85.4 BA_grs_55135_245
89.6 BA_grs_17472_329
98.0 BA_grs_103172_292
103.6 BA_grs_35480_424
110.6 BA_grs_108332_177
BA_10
0.0 oPt_795676
5.3 BA_grs_7955
13.7 oPt_1250
25.2 BA_grs_85184_509
33.6 BA_grs_83584_409
42.5 BA_grs_10161
45.5 BA_grs_10044
45.5 BA_grs_5195
46.0 BA_grs_8876
48.4 GMI_lrc40347_1
50.2 BA_grs_8859
51.8 BA_grs_106905_397
56.1 BA_grs_27368_222
59.0 BA_grs_46785_170
65.6 BA_grs_32165_167
75.9 BA_grs_32531_244
84.8 BA_grs_66445_250
94.1 oPt_7939
102.8 oPt_795252
118.5 oPt_7129
120.3 BA_grs_5524
133.5 BA_grs_66329_305

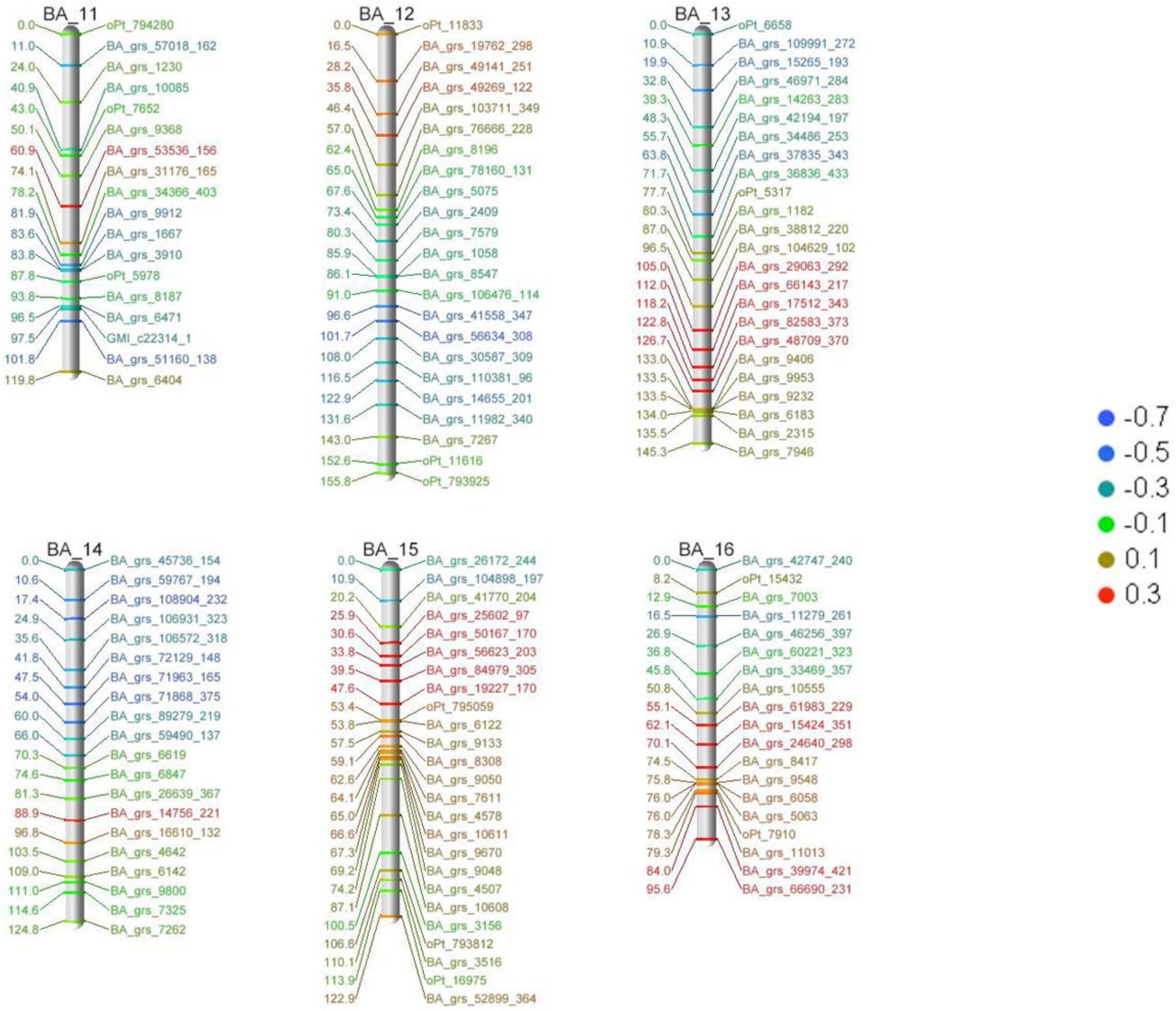


Figure 11. 302 markers were mapped across 16 linkage groups using JMP Genomics. Colors indicate magnitude of segregation distortion for individual markers

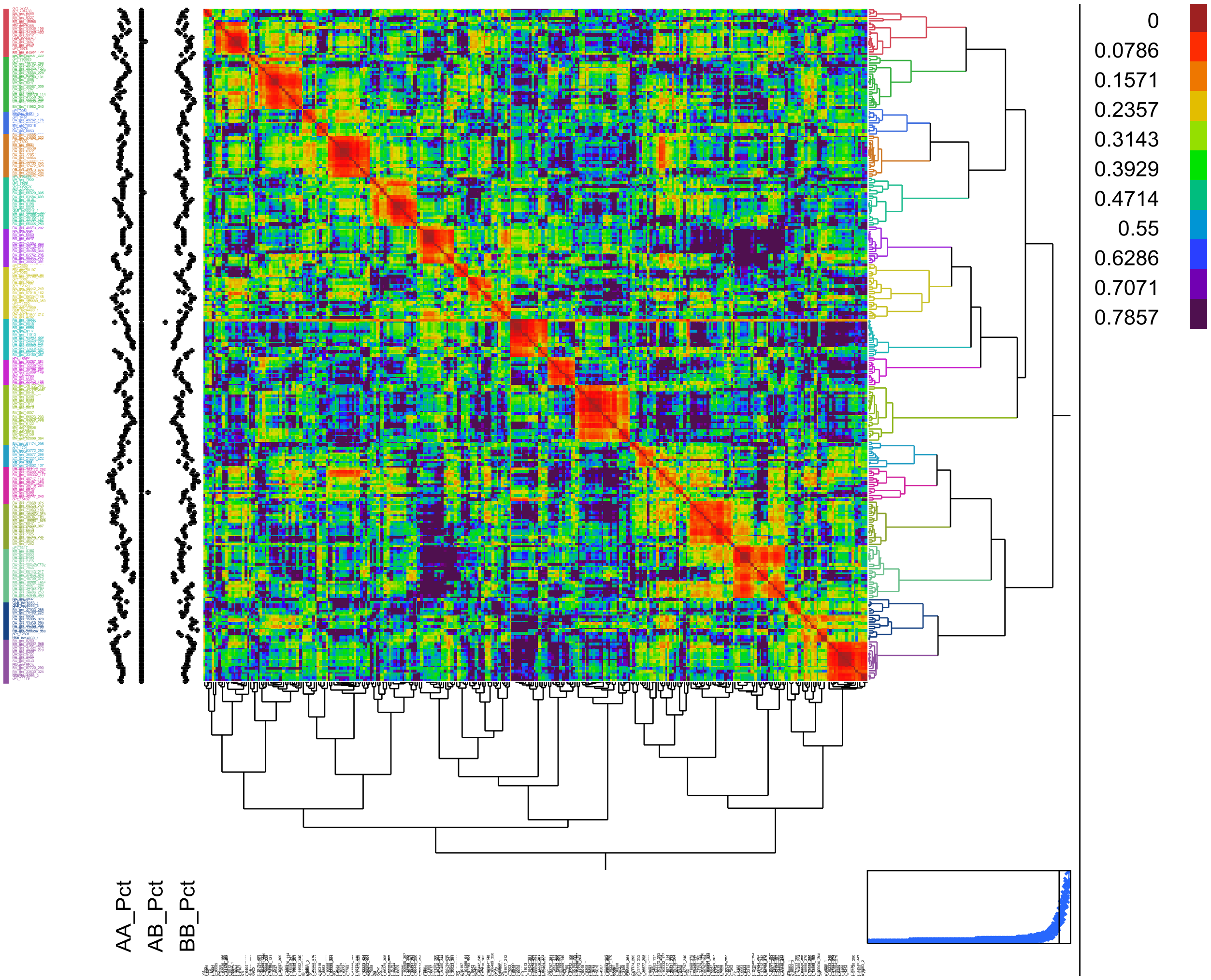


Figure 12. Heat Plot generated by JMP Genomics v. 5.1 (SAS, Cary, NC). Plot is based on marker-to-marker correlation coefficients. The key indicates decreasing levels of correlation between markers, i.e. dark red indicates 100% of the markers are shared between two RILs, dark purple indicates 21.43% shared markers.

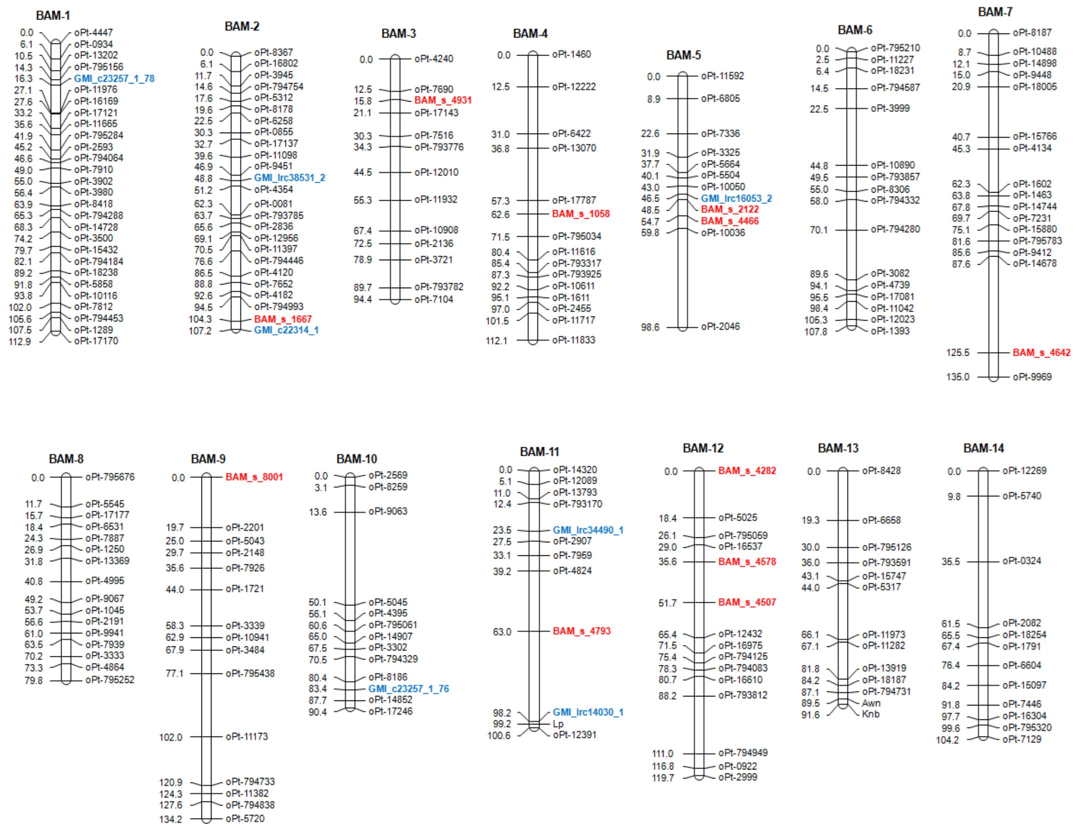


Figure 13. Linkage Groups. The SNP markers indicated in red are some of the genome complexity reduced SNPs added to linkage groups by Multipoint analysis. Their map locations demonstrate both linkage group extension and filling in “gaps” between EST based SNPS and Dart markers.

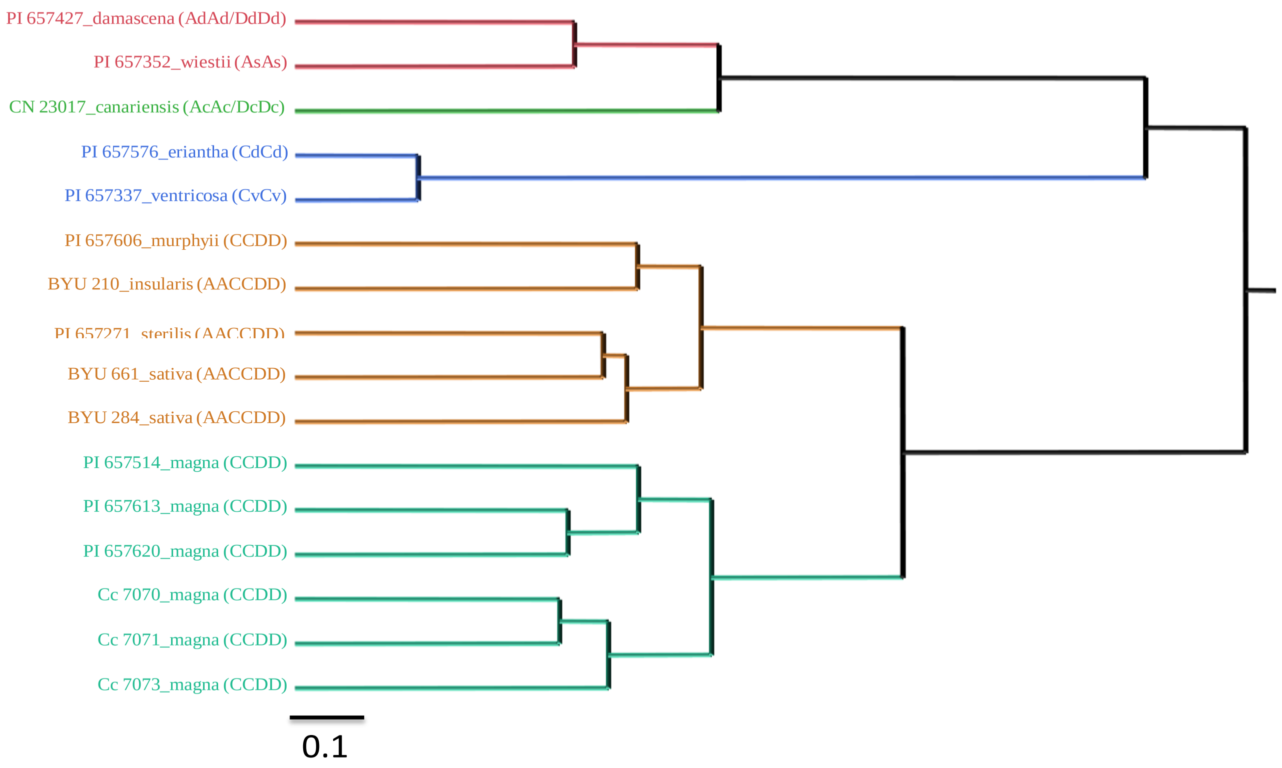
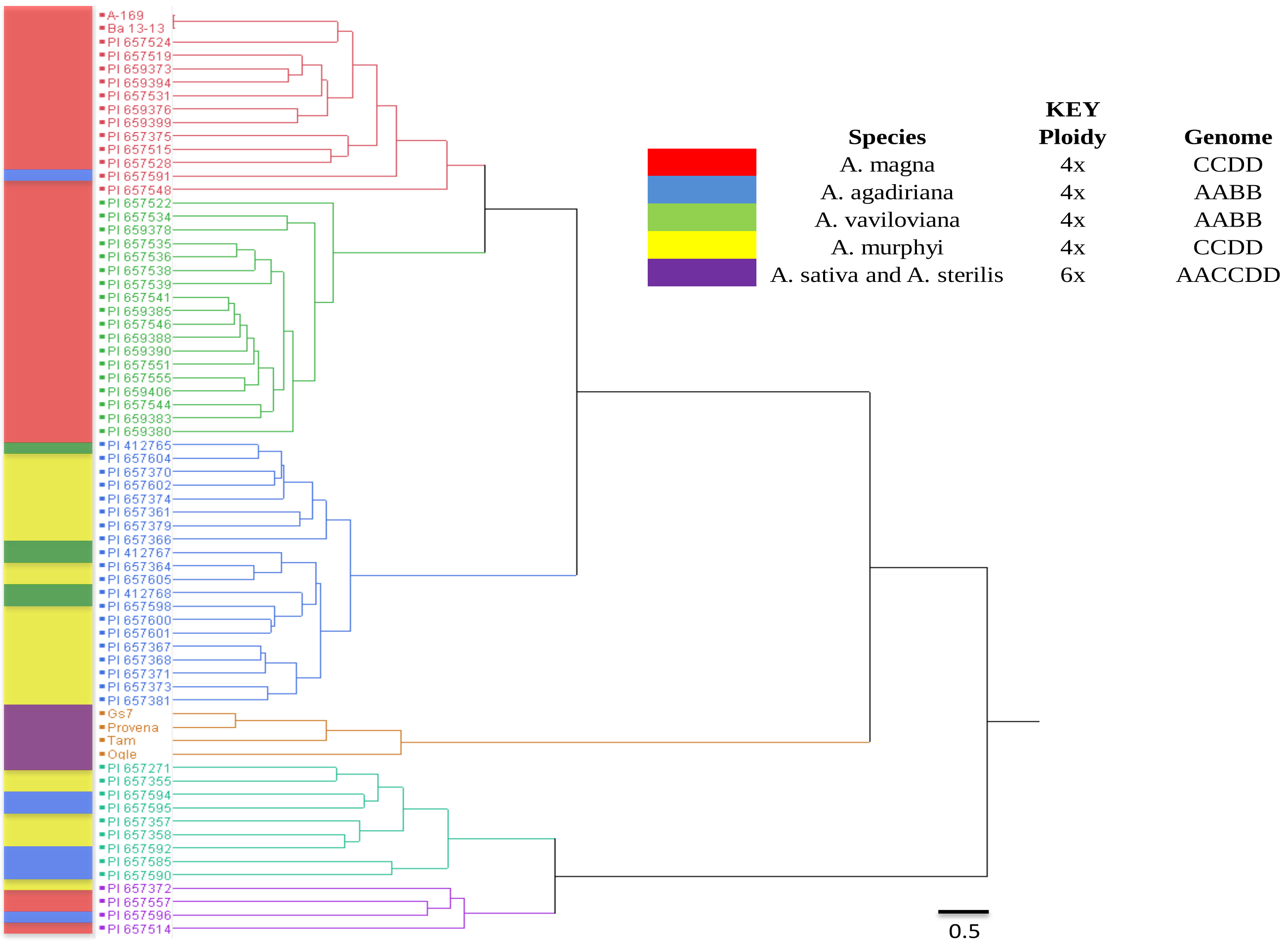


Figure 14. Sixteen Diversity Line Validation Panel Dendrogram generated from 330 primers run across diploid, tetraploid and hexaploid oat species having most known genome combinations. Bio-Rad’s HRM platform was utilized to validate panel.



KEY

	Species	**Ploidy**	**Genome**
🟥	A. magna	4x	CCDD
🟦	A. agadiriana	4x	AABB
🟩	A. vaviloviana	4x	AABB
🟨	A. murphyi	4x	CCDD
🟪	A. sativa and A. sterilis	6x	AACCDD

Figure 15. Tetraploid Diversity Dendrogram generated from 768 primers across a wide range of wild tetraploid *Avena* genotypes. Four hexaploid lines were also included as on out-group. Fluidigm EP1 platform was utilized to validate panel.

SUPPLEMENTAL DATA

Supplemental Table 1. List of 330 PCR primers used for High Resolution Melt analysis.

	Forward Primer	Allele 1	Allele 2	Reverse Primer
	contig00740_F, AAATCCCAAAAATGAAAGAGG	C	T	contig00740_R GATCCACTTCAATTGGGTAGATAAT
	contig00741_F, TTTGTACTATGTGTCATGTG	G	T	contig00741_R, TTCTCTTTCAGCAATTCCTTTTC
*	contig01058_F, CGTCTCCACCCTCTCTTC	C	T	contig01058_R, CCCTTTGAAGATGTCGT
*	contig02122_F, AGCAAGGCAGCCAACACT	C	T	contig02122_R, CATACGGACCTGAAAGC
	contig00813_F, CCCATTGGTGACTAAACTTGC	C	T	contig00813_R, CCAGAGCAGTGATGCGTCTA
	contig01530_F, GCTCAATCCGATGTGCAGAG	C	T	contig01530_R, AATGATTGGGAAAGTTGCTG
*	contig01667_F, TTGTGGGTTAACAATGG	G	A	contig01667_R, CCGTGTTGAATGCTAACGTC
	contig02239_F, AAGTTCCTCTCGATAAGATTGGTG	A	T	contig00239_R, GCAGATTAGGCAGAGGCAAG
	contig02735_F, TCGGGATTAGAAGGGCAA	T	C	contig02735_R, TGATCTTGTTTTATGTGGCGT
	contig03399_F, TGTCCCCTACCGACCAGT	A	G	contig03399_R, AATGACTTTGGCATTCACGTC
	contig03486_F, GACAACGTATCCGTCGAACC	A	G	contig03486_R, CTATTCTATTCCGCAGGCTTC
	contig03659_F, TCCGACGACAAATATGGTGA	T	C	contig03659_R, GAGTGGATGCGCAAAGTG
	contig04271_F, CTCGAATCTGAAGAAGATCGT	T	G	contig04721_R, TATTGATGCGTGTGCCTGA
*	contig04507_F, AATTCCGCCTGGATAGTAGC	T	C	contig04507_R, CGTTAAACTCTCAGTAACCCAGAA
	contig04646_F, TTCCCTCTGCATCAGTCCTAA	G	A	contig04646_R, CTTCCTTTCAATCCGCTCAT
	contig04737_F, CCTCGGGGTATCCTAAAACC	A	G	contig04737_R, AAAATTCCTGCTTCTCTACTTCG
	contig04846_F, TCGTTCACCACACCTTACGA	C	A	contig04846_R, TTGCATTGTCCGCTGGTA
	contig05114_F, TTGATGCAAAGGTAAGAGTTCA	C	T	contig05114_R, AACCTTGGCTTATGTTCTTTCC
	contig05335_F, GAGTACTGAAAGTTTAACGACCAAC	C	T	contig05335_R, TGGAGACGGGTCGATAACTA
	contig05451_F, CCGGGAGTGCATAAGTAGAT	G	A	contig05451_R, TGTTCGTGCGAGACAACG

	contig05553_F, GGCCGCAATGAGTTACAGAA	C	A	contig05553_R, CAAGGCCTGCGATTTGAT
	contig06414_F, ACCGAGGTGACCTTCAGAAC	A	G	contig06414_R, TGAAACTGCGAGTGTCCTTG
	contig06685_F, TGGTCCAAGTCAGAGCTGGT	G	T	contig06685_R, CTGCCTCGAATTGTGCTTG
	contig07523_F, TGGAACTGCAACTTGATGATGA	A	G	contig07523_R, AAGCCAATCCTTCTTTGGA
	contig07554_F, CCAGGAAAGGAACTCCATGA	G	T	contig07554_R,T TCTTCAAAGGTTGATTTTTATTCC
*	contig07611_FTGACCCTCCTCCCTTAGTTG	C	T	contig07611_R, AGCCACAATCCATGTGACATAC
	contig07686_F, CGTGGCATGCAAAGACATAG	C	T	contig07686_R, AGGTGTATTCGGTCGAGGTG
	contig07813_F, GGAAATGCAAAATTAAAGTAAACAA	G	T	contig07813_R, CTCCAAACCCTGCATTCATT
	contig07940_F, GTGCCGAGGAGGCTAAAGTT	A	G	contig07940_R, CTGGGTGGGGGTAGAAGG
*	contig08001_F, AACAACATGGGACAACAACG	C	T	contig08001_R, TCCACCGATTCTGAACGTCTA
*	contig05030_F, CGGACTGTTCCTTTGAGTCC	C	T	contig05030_R, TCCTCCCTATGGGAGTAGCC
	contig05049_F, AGGTCAGGTCATCATTGATCTCT	T	C	contig05049_R, TTCGCAAGTGTCTCGAAGTC
*	contig05063_F, GATCAAACCCTCGAAATGGA	C	T	contig05063_R, TGGCCAATAGTTGGTTTCAA
*	contig05075_F, CCGACACTTCACCAACTAAGTG	T	A	contig05075_R, CCTGACTCTCTACCGATGTAGGAC
	contig05084_F, AAATATGACCAAGCAGGGTATCA	C	A	contig05084_R, GTGTTGCCGCAATTTAATGA
	contig05100_F, CAAGGCATACAGTGCATCAAA	A	G	contig05100_R, TGCCCAAATCCAACTACTCA
	contig05146_F, GGAGTTGACCCTTTCCAAGA	G	A	contig05146_R, TGGAATCGCCCTACTTCTTC
	contig05169_F, TTTCTGACAAGGCACCAAA	A	T	contig05169_R, CTAAGAAAGGATTGGGTCCAC
	contig05185_F, CGATTGGAAAGAAGACTTACCG	A	G	contig05185_R, GCGCGGAGTTCACAGGT
*	contig05195_F, AAAGAACCGCGGTAAGGTG	A	G	contig05195_R, CCTCGTTAAATCCCATTGATTC
*	contig05264_F, AGAACGGGAAAGGCAAAGAT	C	G	contig05264_R, AGGGCGAGACGTGATCTACA
	contig05374_F, AACTTCCAAAGTATATGTAGGCAAA	A	T	contig05374_R, TGTGATCATTTGTGAGGACTAAA
*	contig05406_F, TGCGAGGTAATTGTGAATGG	G	A	contig05406_R, GTTGACGAGTGGAGGCTTG
	contig05435_F, GCCCTTAAATCGTTTATGCAG	T	C	contig05435_R, TGTTTAGAAGGCGTCTTTGG
*	contig05524_F, GTTTCGCAGGGAACAAACC	G	T	contig05524_R, CGTACCGCCAATTTGAGATTA
	contig05572_F, AAATCCCACGCCCATTCT	A	T	contig05572_R, GGGCAAGTTGATGTTTGTGA
	contig05573_F, GCTTGGAATCTCCGACTCAA	T	C	contig05573_R, ATGACCCACCGGAAGGA
	contig05594_F, AGGGCAGGCCTATACTGAGG	G	A	contig05594_R, ATCAGCGTCATGGTGGACTT
	contig05634_F, CATTTCGTCCACAACCATCC	C	T	contig05634_R, TCCCAAGATACTCCGCTGAC

	contig05650_F, CCTGCCGTGGAGTCGATA	G	T	contig05650_R, TGAACAAGGCTTGCCCTAAA
	contig05661_F, AACGGCTCAGTCTTGGCTTA	C	T	contig05661_R, AGTTGATGCAAAGGTAAGAGTTCA
	contig05664_F, CCCAAGATGGCATAAGAAGAA	C	A	contig05664_R, CTTCCCGATCCGCTACAA
	contig05715_F, GATGAAGGTCACAATAGAGGAGA	A	C	contig05715_R, ACCAACTCACCCATTCTTCTAA
	contig05772_F, TAGGCTATTGCCAGGCTCAG	G	A	contig05772_R, TTCATGACCCACTTCCTTGAC
	contig05805_F, ACTATCTTGATCGCCATCCTC	A	G	contig05805_R, GACGACTACGGTGCTACGAA
	contig05845_F, CTCTTTCCAAGTGGCGTTGT	C	T	contig05845_R, TCACACGACTTCGTCGACAC
	contig05851_F, TGTACTGTGGTGTTCGAGGAA	G	A	contig05851_R, TGGCATCTTGGGTTATTTCA
	contig05853_F, ACCGTTACCTGATTGGGTTG	A	G	contig05853_R, CAACACATGCCACAAAGCAT
	contig05916_F, GCGGACCTGCAATATTTCTAT	G	A	contig05916_R, TTGTTGATATAATATTCACGAAGTACTGTT
*	contig05961_F, AGTAGGATGGGTTGGGTCAT	G	C	contig05961_R, CATGGGCATACCAACATAATAAA
	contig05965_F, TTGGAAATATCTTCCCGAAACT	T	C	contig05965_R, GCCGCATAACGACCAACTAT
	contig05966_F, CGACATGGAAATGATGATCG	T	C	contig05966_R, GTTTGGGAGGAGAGCTTCG
	contig06020_F, TGGCAAAGTGTTCAATAGAGAAAG	G	C	contig06020_R, TCCGAATGCAAAGCTTGTTT
	contig06043_F, CAATAATGCCTAAAGGTCATGC	T	A	contig06043_R, TCAGAGTTTCTTTCACTAACCATAGG
*	contig06056_F, CCGAAACCGGTAGCTTCA	G	C	contig06056_R, GGTCGATCGATCTGCCTAAC
	contig06057_F, TAGGTACCAACGAGCCGAGT	G	C	contig06057_R, GGTCCTTCCCGAACCTTACT
*	contig06058_F, CGGTATCGCATCATCTAACTTT	T	C	contig06058_R, CCGCCCATGCTGTCT
*	contig06060_F, GGCGGTGGTTGTTATTGTTT	G	A	contig06060_R, TTGAGATATGACATAGAACCATTCAA
	contig06070_F, AGCCTGACAAGAATCTGACCA	G	T	contig06070_R, TGATGCACTTGTGGAAGAACA
	contig06113_F, TCGGATGGCTTGATACTTCA	G	A	contig06113_R, TAGCTGTTGCGTCGCTCTT
	contig06120_F, CTTGGCTCCTTTGAAATTACTGA	G	T	contig06120_R, TGGTCTCCTTAATTCCTACAGTTTG
*	contig06122_F, AGCTTCAGGGAAGTTGATGG	T	C	contig06122_R, GTGGCAAGAGTTGAACCAAA
*	contig06142_F, CCCATAGGTTCAACCGACAT	T	G	contig06142_R, CCGGGTGGATTTGTAATGAT
	contig06158_F, TGGTGTGGATACCGTTGTTT	G	A	contig06158_R, AAGGCCACGAGCATAAGGT
*	contig06183_F, AACTTGGGTACCGCGTTG	A	G	contig06183_R, CGGTTGACCCATAGTCAAGA
	contig06229_F, CCACTTGCTTAATTAGGGATGAA	T	C	contig06229_R, TGATGAACCCAAGTCAATTCC
	contig06239_F, GCAATCCCAGGATTACCATT	G	A	contig06239_R, TGTATGGTTTGTAATGGATGATGT
	contig06241_F, AGGTTCGTGCATCGTGTTC	A	G	contig06241_R, CGGATACCATGGTGCTCTAAA

	contig06279_F, CAGGGTGGACTCACCACCT	G	A	contig06279_R, GCCAGGGTGGCTCACA
	contig06323_F, TGCTTGCTTCGTTCTCGTATT	T	G	contig06323_R, TTCTTCTCAGAGATTGTCTTAATTTCA
	contig06329_F, GGAGAACCAAATAAAGACCCAAA	G	C	contig06329_R, TGTTTCTCTTAGTTATTCTTTCTTGGTG
	contig06330_F, GCAACCTCTTAGGCAAATCG	C	T	contig06330_R, AGGTGGGAATGGATTTGTGA
*	contig06372_F, GGACGCCTTCAAGAGGAAC	T	C	contig06372_R, AGCCTCCTCAGGGAGGTAAC
	contig06376_F, CAGCTACATGGTTGCAGGATT	T	A	contig06376_R, CATCCATTGGTGGGCTGTA
*	contig06401_F, AAACAATCAACCCTCCATCC	G	A	contig06401_R, TTGTTTGCATACCCAAAGGTT
*	contig06404_F, TGTCCATGGATTTGGTGACT	A	C	contig06404_R, TTTCGAAGGGAATTTAACCAA
	contig06427_F, CCAAACCGAAGCCTCGAC	G	C	contig06427_R, GGTGACGGTGAGCTTGGA
	contig06436_F, CAAGAATTATTGATCGTGTTATGGA	C	T	contig06436_R, TGTGTATAAAGAGCAAATGATCACC
*	contig06465_F, CCACGGCTTACTAAACCTGAA	C	A	contig06465_R, TGGTGTGCTTAGTCTTACTCATTG
*	contig06471_F, TGGAAACTCACATCGACGAA	T	C	contig06471_R, GATTGACCTTGAATTAATTGTCCTTT
	contig06526_F, CGTTTGTTCGTTGTCTTTATTACTTG	G	T	contig06526_R, CCCTGTGAATACTTAGCAAACGA
	contig06565_F, ATGGCAACCATCTCACCAAG	C	T	contig06565_R, GAACCCTCCTCCGACCATAC
	contig06583_F, TCTTGGTGTTTCTCCCTTGTTT	G	T	contig06583_R, CGATGATACCCTGCTTGGTC
	contig06605_F, TCGTATAGTTGCTGCGACATC	A	G	contig06605_R, TTCCGACCATATAGTTGGTTGTT
	contig06609_F, AGAGCTTTGACGAAGGCATC	A	G	contig06609_R, GACCAACTATACGGTGGGAATAA
	contig06610_F, CTATACGGCCGGACTAAGAAA	T	G	contig06610_R, AAATAATGAGAAGGGTCGACAA
*	contig06617_F, TTTGATCAGTATTCTAAATAGTGCAGTT	C	T	contig06617_R, ATCACCACAACATTGGACCT
	contig06619_F, CGGAAGCTTTAATAGGCCAAA	G	T	contig06619_R, ACCATCCACAAGGAACCACA
	contig06665_F, GAAGTTCCTCGGCCTCTACC	T	C	contig06665_R, CAGACAACGCAGCTGTGAAC
	contig06672_F, ACAACCAAGAAATCGCCAAA	C	A	contig06672_R, TGCTTAGGGCGAAGATGAAT
	contig06725_F, AAAGAAACCCGGTGCACAT	G	T	contig06725_R, GAAAGTCAAGGCCCTGGAAG
	contig06772_F, TCCGTACCTTCGACCCAATA	C	T	contig06772_R, CTTCTGCGCGGTGGTAAA
	contig06847_F, TCAGGATCATGGCAACCTAA	T	G	contig06847_R, CCAAGTTTGACATCTCCTCTACTTT
	contig06855_F, CTTCTGCTCCTCGTTGGAAT	C	T	contig06855_R, CACCACTGATGACCCACAAG
	contig06891_F, TGGGTATCCTCATAGCATGTCTC	C	A	contig06891_R, GCCATAGGTCATGCTACCAAC
	contig06897_F, TTGATTTCATCAAGACCCAAA	G	T	contig06897_R, TAGTAGCGGACGCCTTGTC
	contig06904_F, CAGACGGAGCGCTTGAA	T	C	contig06904_R, GTTCGATTAGGTCCGCTTTG

*	contig06913_F, CGGAGTTATGGAGAAGGTCGT	G	T	contig06913_R, TGGTCCTGCTACACGTTTGA
	contig06919_F, GTAGCACGTTGGGATGCAG	G	A	contig06919_R, TGGGATAGACCGGCACTCT
	contig06923_F, TCACTCTGTAGCGCGGAGTC	A	T	contig06923_R, CGTACCGCTTCGCGTTTA
	contig06926_F, ATTCCCGCCATATAGTTGGT	T	C	contig06926_R, CCATATAGATATCTTTGCCATCG
*	contig06948_F, GTCGTGCAAGCGCACATA	C	T	contig06948_R, TGAGTGGGCACGACGAA
	contig06997_F, CACCTAGCAGCACGTCGTT	G	A	contig06997_R, GACCTCCGGCTTCTTAATCC
*	contig07003_F, TCAGCTTAGGAGCCCTCTTG	C	T	contig07003_R, CACGTCCGCAACCTATGAT
	contig07005_F, TTTAGTTATGTGGTGCATTTCAAAG	C	T	contig07005_R, GCTCAAGTAGCATGCTGTCAGT
	contig07025_F, CCAGCAGCAGTTGTGGAAGT	T	C	contig07025_R, CGAACGGGAGACATCTTCAC
	contig07044_F, CTCGGTATATACGGCCTGGA	C	T	contig07044_R, CAAGAGTCCGTAGGCTACTCG
	contig07075_F, ACGTCTTTGCGGCATCTAAC	G	A	contig07075_R, CAGGAGCTTCTGCTTGTCG
	contig07112_F, TTTGTAACACCCTCGGATCG	C	T	contig07112_R, CTGGTGGGCACCTTTGAAT
	contig07179_F, TCTGTGAATACTTAGCAAACGGTA	C	T	contig07179_R, CCGTTTGTTCGTTACTTCTGTT
	contig07190_F, TTGGCTTATACCATCGTTCAACT	A	T	contig07190_R, AGGCAGGAGCATGTTATTGG
	contig07202_F, CCTGTTGATGCTCCCAAGAT	T	G	contig07202_R, GGGCGGAGGTTTGAGG
	contig07252_F, GGGCAAGTTGATGATTGTGAT	A	G	contig07252_R, AAGAATCCCACGCCCATTAT
*	contig07262_F, CCAACTATACGGCCGGAATTA	A	C	contig07262_R, TTTGGAGAAGGGTCGACAAC
*	contig07267_F, CTTTCGTGCGGGTGGA	T	C	contig07267_R, GATGGAGTCATGTTGTATATATCCATTT
	contig07312_F, CGTGCTTATATAGTTGACGCAAA	A	T	contig07312_R, TGGTTGTTCCTCTCAAGGAGTT
*	contig07325_F, TACGCCCGGCTTAGGAC	A	G	contig07325_R, TATTATGGGTCACCGGCTTT
	contig07394_F, GATCATGGGCGTAAGTGTATCA	C	T	contig07394_R, ACCACTTGCTCTTTCATTTGG
	contig07454_F, GCGTCACTATTCTATGTCATAATTCA	C	T	contig07454_R, CATAATTATCACCTCTCAAATACGAA
	contig07480_F, AATTCCGCTCGTATAGTTCTGG	T	C	contig07480_R, CCGCCGTATAGTTGTGAACC
*	contig07497_F, ATAGTCGGTGGCCTCTTCCT	G	A	contig07497_R, GGATGGACAATTCCATGACC
	contig07508_F, CCACGGTGTCGCCAAG	G	C	contig07508_R, CTTGTTCTTCAAGCAATCGAGAG
*	contig07577_F, TTGGTATATGCCTGATCTACAACAC	A	G	contig07577_R, GCCAGATTTAGCTCGGATTG
*	contig07579_F, TCGATTTCCATCGCCTCTAC	A	G	contig07579_R, GACTGCCTCAGCAAACTCG
	contig07599_F, TTGTTGGCGTGGTAGTTTC	A	G	contig07599_R, TGCTAACGCCAATTACGAC
	contig07612_F, TCGAGAGGTGGTGCACTTT	A	C	contig07612_R, TGGTCTGAGGGAATGCTTCT

	contig07623_F, TATGCAAGAAGCGTTCACCA	G	A	contig07623_R, CACCACTGTTGATTGCCAAC
	contig07634_F, CGCCTTTAAGTTAGGCATGA	A	G	contig07634_R, TTTCACTGTGGTTATACTTGCTCT
	contig07650_F, TCGAATCTGAAGAAGATTGTGTTG	C	T	contig07650_R, GGATTGTTGATGCGTGTGC
*	contig07652_F, GGAAGATGAAATCGAACTCACA	C	T	contig07652_R, AAAGTGAGCTAACGGCGTGT
	contig07662_F, TGGGCAGTCCGATAGAGA	C	T	contig07662_R, GGGTAGTATGGACTTTCTATCTCTACTAAT
	contig07671_F, TGAAGATGAAGATATTGATGTTATTCAA	G	A	contig07671_R, TGCAGGTCTCTGAATTTGGTC
	contig07692_F, CCCATCACAAATGAATCAACC	G	A	contig07692_R, ACGACGGAACAAGTTTGCAT
	contig07694_F, AACCAATGGCGTCCAATAAC	C	A	contig07694_R, TGTTTGACAGGATTTGAGATCG
	contig07698_F, TGATGGCTTAGCAACTGGAG	A	G	contig07698_R, TGTTTCTTCTTCCAGATCCTTG
	contig07717_F, CGATCAGAGACGTGGGAGAG	G	T	contig07717_R, AGTCTGACGGCCTCCCTATC
	contig07749_F, TCATCATATCAGGCATGGGTA	C	T	contig07749_R, TGGCTTTGGTATAGCCGAGT
	contig07754_F, ACCTCCTCTTGCTTGCTTCA	A	G	contig07754_R, GGTTGATTTGGCAATATGGAA
	contig07766_F, AAGCCGGAGCCATACGAT	C	T	contig07766_R, GTCCCAGGTATGGTCCTTCC
*	contig07790_F, GACGTCTACGCGGAGGAA	C	T	contig07790_R, ACCGCACCTCTCTCTCCTTC
*	contig07795_F, ACTTCCACTACGGCCTCCA	T	G	contig07795_R, CACGCGGTACACTTTGTCAG
	contig07849_F, ACTTCCACGCGGAACGTAT	C	A	contig07849_R, GCAATCCGCCAATATCCTC
	contig07850_F, TTTGGCGTGAGTCTTCAGG	C	T	contig07850_R, CAGAGAGATGGACCCAAAGC
	contig07896_F, TGATATTACTTCATTTGCCACTCG	A	G	contig07896_R, CAAACCCGCATAGAAACGAT
	contig07920_F, CCAAGACTTGCATGATATGGAG	C	A	contig07920_R, CCCACAAGCCAAATAACTTCA
	contig07937_F, AATTGATGGACAACGCTCTTC	G	A	contig07937_R, GGTGGGAGTTGTTGGTGTCT
*	contig07946_F, TGGTATCTGAACCAGGTTGG	A	G	contig07946_R, CCGGAACAGCATGTTGAA
*	contig07955_F, TCTTGCGAACATGTTATTTACAA	A	C	contig07955_R, AGCATAGTATTGTATTGCAGAGATTC
	contig07964_F, CCAGGAAATCCAAGGGTTCT	A	G	contig07964_R, CAAGTACTCCTCCCATGATCG
*	contig07998_F, CAAGATCGGTCTTCGGTCTG	A	G	contig07998_R, ACCGACAAGATCTCCACCAG
	contig08042_F, CAATTTGCAGCATTAGTTTACTCCT	G	T	contig08042_R, GGACCGAAATGAGGAGACCT
	contig08078_F, GCGTGAGCAGAACCTAATGA	G	A	contig08078_R, TTTCCGTGTCGCTCATTTC
	contig08099_F, TTTGTCCATACTTCATCTCATCAC	C	T	contig08099_R, TGCTAATGAAGATTGTGTGAAGTT
	contig08104_F, CGGAAGGGTAACCTTGCTAA	A	G	contig08104_R, TTCCTTTGCCCTTTGTCG
	contig08112_F, CGCCGGAACAGTTGTAGAAT	C	T	contig08112_R, GCATCACAAACATCAACTTGC

	contig08123_F, CGATCAGGTTCGGGATTAAC	C	T	contig08123_R, AGGAAGCCAACGATGAAGTC
*	contig08187_F, TCTTAAGCTTTCATCTTGCATTG	C	T	contig08187_R, CCATGGCGTTGCTAAGG
	contig08191_F, GAATCTGATTAGACATTTGGAGTGA	T	A	contig08191_R, TTTGAAATGATTAACTATATCCAAACC
*	contig08196_F, CTCCTGTTGAGCCGTGAAG	G	A	contig08196_R, TTTCTCGTCCGTCCTTGG
	contig08229_F, AGAAATTATAAGATCTATGGACCACTTT	A	G	contig08229_R, TGCATGTAATAATTAAGAGGGTGA
	contig08238_F, GGAAAGTTGTTGTCCCGAAA	G	A	contig08238_R, ACGCCTCTAAAGGACGTTCA
*	contig08250_F, CCACCCGGGACCACTT	C	T	contig08250_R, GCCACTGGTCAGTCTCTGGT
	contig08255_F, TGTGTATTGGGTGATTTGACTTT	G	A	contig08255_R, CTCATATCCAGTGGAATAAACACA
	contig08269_F, CCGGAGAGAGTCGGGATATAG	C	T	contig08269_R, TGTTTGCTTTGGAGCACTTG
*	contig08289_F, GTCCCGCTCACCGTCTT	C	T	contig08289_R, TCCTAAGAGCGGAAGTGACG
	contig08303_F, TCCCTCTCCTCTTCCTTTCC	A	G	contig08303_R, GTCGGAGCAGTGGGAGTG
*	contig08308_F, CTCCGGCCCGAGACC	C	T	contig08308_R, GAGGAAATTAGCCAATGCAAGA
	contig08310_F, TTCACCCATTACTACTCAGATTAAGTT	G	A	contig08310_R, CGAGTCGTAGAATGCATGTG
	contig08320_F, TGATGCTTTCTAAAGGATTACAGAA	G	C	contig08320_R, TCCAATTCTATATGTATTAGACTTCTTGC
	contig08335_F, CCAATAATGGCTTCCTCAAGA	T	A	contig08335_R, GACAGTGGTAGAGAAACTCAAAGG
	contig08350_F, ATTCCGGTCGTATGGTTGGT	G	T	contig08350_R, ATGGTTCCGGCCGTATAGTT
*	contig08398_F, CACTCTCTGTGCTGAGTATGGTAGA	A	G	contig08398_R, CAGACATGTAATCGCCCAAA
	contig08414_F, CTGAATGCTCAACACCCAAA	T	C	contig08414_R, TGTTGGTTGGTAGCCTCTAATTC
*	contig08417_F, CCGCCACATCACCTCATC	G	A	contig08417_R, TCGGGATGCATTCTCTAAGC
	contig08426_F, TCACAGACCGACATCACCAT	A	G	contig08426_R, CCGAGGGATCATTACCCTTT
	contig08456_F, TCGTTCGGGCTTCAACAC	T	C	contig08456_R, TGGTATTTAGTTGCTGGGTATATATAGGA
	contig08466_F, GAGGGTAGGACACGGAGGTT	C	T	contig08466_R, ATTGGAGTGCTGGCGAAAC
	contig08526_F, GTTCCTGGGTACGCGACT	C	T	contig08526_R, CCAGGGCACCGATCC
	contig08531_F, CTGCTTCCAGCTCCTTCGT	G	A	contig08531_R, CAGTCGCCGAGTGTGAGAC
	contig08542_F, AAGCTTGATGTCTACGCACTTC	G	A	contig08542_R, TGTTCTACAAACCTCTACACTTGGA
*	contig08547_F, TCCTCTCCCGTGCGTTT	A	T	contig08547_R, TTCGGTGTGAAGTCTTGTGG
	contig08552_F, CATGGGCAGGGTTATGGA	T	G	contig08552_R, ACGATTCAACATCCGAGTACG
	contig08566_F, CGGTACTGGCTCCGAGTCTA	T	G	contig08566_R, TATCCGGGAGCATAAATCCA
	contig08574_F, AACTCTGGGCCTTTGTTCCT	G	A	contig08574_R, CGCTTGACGCTTGAGTTCTT

	contig08577_F, CCTAAGAAGGACTGGCTCCAT	A	G	contig08577_R, TGTAATGGTTCAATTGGAGCTG
*	contig08585_F, ACATGTTGCGGATGCTCTT	G	A	contig08585_R, AGTAGCGTGATGCGGTAGTG
	contig08597_F, GACCCTCTCCGCCGTTAC	A	C	contig08597_R, TTCACGGAGCGAATTAATGG
	contig08614_F, CGAGGTTCCCATTCTGTAGG	A	G	contig08614_R, AAACCCTCGGTATTGATTCTTACT
	contig08631_F, CCCTCCGTCTTCTTCTTCTTG	T	C	contig08631_R, GTGTCCGACGATGATGCTC
	contig08636_F, AGGCTGGTATACAAGGACGTG	C	G	contig08636_R, CTCAAGTACAACCGCGATCA
*	contig08639_F, GTCGTTTATGTGTGCCAAGC	C	T	contig08639_R, CAGTTTGGTCGTCATTCTTCC
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	contig08685_F, TTCAGAGGTAGATGGGTGCAT	T	C	contig08685_R, TTGAGAATGGTCGTTCCTGA
	contig08692_F, AACCCGAAGAAGAACAAAGTT	G	A	contig08692_R, CCCTTCCACTAACACTTCTATGA
	contig08696_F, AAAGAAACCCGGAGCCATA	C	T	contig08696_R, TCCCAGGTATGGTCCTTCC
	contig08736_F, TGTAGGGTTTGCAGCATAGAAA	G	C	contig08736_R, ACCCGTTGCTTGTATCCAGT
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	contig08804_F, ATCATAGACCTACACTGTTCTTTACTTACT	G	A	contig08804_R, AGACCATGATAAGTGTGTTATTAGGA
	contig08844_F, GCAGATACAATTGGTAGGTAGTCG	A	G	contig08844_R, CAAGAAGTGAATGCAGATGTGA
*	contig08853_F, GAGTGGGCACCGGATAGTC	G	A	contig08853_R, CCAGTTCTGGGCCGACTT
	contig08855_F, GAAAGATCGAAGTTTAATTCCAGA	G	A	contig08855_R, CACTTTAAGTACTTCTTCAACTTCCA
*	contig08859_F, ATGGGTATTCTCGGACCGTA	A	G	contig08859_R, ACTATCGTTCGACCGCCTAC
*	contig08876_F, GCAGAGAATGAGGGTTTGAGA	C	T	contig08876_R, GCATTAGGAAGGCGAACAAA
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	contig08927_F, ATTTCCTCCGACCTCGTG	G	A	contig08927_R, ATCAAGCGGAGGATCTGG
*	contig08942_F, CCATTGCCATACACAACCAA	C	T	contig08942_R, GGACGACAACACACGAGAAG
	contig08966_F, TTGTTTCGACATCAACCCTTC	C	T	contig08966_R, TATTCCCGCCGTATAGTTGG
	contig08974_F, CGGCCCAGTGTCACTCC	A	G	contig08974_R, TCACGTTTAAAGAGTCACTGACCA
*	contig08996_F, ACCATGGCACATCTCAGGTC	C	T	contig08996_R, CTCGATCTCGGAAGTTGTGG
*	contig09048_F, CCGCTTGTGCTCGTTCAT	C	T	contig09048_R, ATCTCCCAAGCGAGTTCTCC
*	contig09050_F, AAGTGCACATCGATCTGTGG	C	T	contig09050_R, TGTCGGGCTGTGTCTATGAG
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*	contig09113_F, CCGAAACCATGGTGCTCTAA	A	G	contig09113_R, TCGTGCATCTATGTTCTCGTTC

	contig09133_F, TATTCCTCCAGCTCCACCTC	C	T	contig09133_R, TGAAGATTCCATCCTTTGCAC
	contig09134_F, GCAGTAGTAACAATTGCAGCAAAC	G	A	contig09134_R, ATTGTCTTGTCCATGCAACG
*	contig09232_F, GTCTTCAACTCGGCCAAGAG	T	C	contig09232_R, GACTGAAAGGTCAGGCTGGA
	contig09236_F, CGACCAACTATATGGCTGGAAT	C	T	contig09236_R, TTTGGAGAAGGGTCGACAAC
	contig09286_F, GGCTTATGAAACTTCCTCTCG	C	T	contig09286_R, TTTCGTTCTTATATTATTGATGCAAA
	contig09299_F, GCTTCGAAAGGTCTGACAGC	C	T	contig09299_R, TCAACTTCGCGAGTTCCTCT
*	contig09327_F, AAATTGATTGGAGACCCATGTC	G	A	contig09327_R, AGGACTTGCACACCTTCTCC
	contig09343_F, AACGTCGGTAATGCCCATAG	G	A	contig09343_R, TGTCTGATCAGCCGAAGAAA
	contig09347_F, CGACCAACTATACGGCAGGA	C	T	contig09347_R, GGACGGAAGGGATGATGTC
*	contig09368_F, GAATCCGTGCCAGATGAGT	A	T	contig09368_R, TAGTTGATGATCTGATGGAACG
	contig09380_F, GGAAGAACAACGGACAAGGA	C	G	contig09380_R, AAGACAAGGGCGATGCAG
*	contig09406_F, CAGTGCAGACGCATGGTTAT	T	C	contig09406_R, TTGCTTTGCATCGTCGTCT
	contig09410_F, TGAATAAGGAGGCAACTTAATAGCA	A	G	contig09410_R, TTTGTGGGTGGATGAAACCT
	contig09437_F, GATGGCATCAACCATAATTGG	T	C	contig09437_R, CCCAAACAAGATGGAGGAAA
*	contig09446_F, TCCTTTCTCTTCTCCATTCATCA	T	A	contig09446_R, TGCTCTCGAGGAACGTGATA
*	contig09497_F, CCTTGGTATTTACCCACCTTT	C	T	contig09497_R, ACCAACATGTAAAGACCGATTT
	contig09506_F, ACTTGTCAGCCATCTATAAAGTGA	T	C	contig09506_R, AGTGTAATGCCATATTCCGTCT
	contig09544_F, TGACTCATGGAGTCGTGTTG	T	G	contig09544_R, TCGTGCGGGTGGAAA
*	contig09548_F, ATGATTCCGGTGAGCACAA	T	C	contig09548_R, TAGCAGATGCGCCCAAA
	contig09553_F, TGGTTGCAGGATTACGACAA	G	T	contig09553_R, GCCAACATCAATGGGAGGTA
*	contig09564_F, CCGAATCGGAGAAAGAAATG	T	C	contig09564_R, TTAGGAGCGTAAATGGACAGG
	contig09570_F, CCCTTGTAGACCATACGTGGTT	G	A	contig09570_R, GAGGTCGGCCACACGTT
	contig09628_F, CTTGTCATATTTATACCCTCACCA	C	T	contig09628_R, GCTCTTGAATCATGATAAATAGGTAA
	contig09642_F, CAAGTTCAAGCCGGTGATG	A	C	contig09642_R, TGGTGTAAAGCTGCAGGAACT
	contig09654_F, AAGGAAGGCCCAAGAAACAT	C	T	contig09654_R, CAACACTAATACAATGTCGGTTCA
*	contig09670_F, TCTTCCTCCAACGAAACCAT	C	T	contig09670_R, GGTGTTAAATTAGAAGTTAAAGCTTTGTG
	contig09678_F, AGGGTTCGTCCCTTTGAACT	T	G	contig09678_R, TTCAGGTGACTCACGGAGACT
	contig09679_F, GTTCCCGCCGTATAGTTGC	T	C	contig09679_R, ATCCGGCCATATAGTTGTGC
	contig09713_F, ACCTCCTCTTGCTTGCTTTG	T	C	contig09713_R, GGTTGATTTGGCAATATGGAA

*	contig09727_F, AAACCAAATAGAGACCACTTCGAG	G	T	contig09727_R, GGTCAAACTATTCTTTGCCTCAA
*	contig09800_F, GTTAGTGCTGCGTCGCTTAG	A	G	contig09800_R, TACAAATCCAGACGGCACAC
	contig09806_F, GAAACCTCAAGGGATCTTCATC	A	G	contig09806_R, TGGAGGATCAGAGGAGAAACA
	contig09816_F, TGGAGAGACGGATTGGATCT	C	T	contig09816_R, TGTAGGCGAAGCTCTGCTG
*	contig09849_F, GGCTTCAAGGTCGATGAAAT	G	T	contig09849_R, ATGGCAAGCATCAAACATGA
	contig09873_F, GTAGCTTGGGAGAGACATTCG	A	G	contig09873_R, GGTCCCACAATACCCAGAAG
	contig09887_F, CCCAACCGGATAAGAAACAA	G	A	contig09887_R, TGATAGCCGGCCTGTCTTAC
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*	contig09912_F, CCCAACTATATGGGCGGAAT	C	T	contig09912_R, TGCGACATCAACACTTCCAT
	contig09928_F, GCTTCACCAGCCATCTTGAG	A	G	contig09928_R, TGAGGGCTTGATCGCTTAGT
	contig09941_F, TTTACTCCGGCGATCAATTC	A	G	contig09941_R, GGGAGGAGAGGGAGACGTT
	contig09945_F, TTGGACAAGAATTTGGTGTTTC	G	A	contig09945_R, GATTAGAGAGAGAGACAATGGCAGT
*	contig09953_F, TGAAAGTTTAGCACTAATAATAACATGAAA	G	A	contig09953_R, CGAATTGAAGAATTTGCCAGT
*	contig09959_F, CCCTTCGCCACTCTCTCTATC	A	G	contig09959_R, GCCCACTACGCACAGCA
	contig10021_F, GAACTTAGCATTCAAATTAGCAACA	C	A	contig10021_R, GGGTTTCATGATGTTGTTAGGA
*	contig10044_F, CTGGTGTGGTGTTTCCCTTC	G	A	contig10044_R, GTATTGATCGCCGGAGGTT
	contig10049_F, TCATAAATTCGTGGCATGGA	T	G	contig10049_R, GGTGCCTGAACCAATGAAAG
	contig10054_F, GGCCTCTTAGGCCATTTGT	C	T	contig10054_R, GTCACTGACCACAAACATCAAA
	contig10062_F, GCAACTCCTTTACTTGACGAGA	T	C	contig10062_R, GATACAAGAAATGAAATACTGGAATTAAA
	contig10066_F, GCGGAGAGGGAGAGGTTTA	G	T	contig10066_R, CGCTTGATTGCCATTGATT
*	contig10085_F, AAGGCTGGACACTGTGCTCT	G	A	contig10085_R, CGAAATTTCAGATGAGGTTGG
	contig10110_F, TGCTTGCAAATTATAGGATGG	C	T	contig10110_R, TGGGTATATATTTACAGGTGTTGAAA
*	contig10161_F, GTAGGCAGAGGTCGTTCTGG	T	C	contig10161_R, GAAGTGATGCATGACATTGAAAC
*	contig10197_F, CCACCTTTAAATGACCTCCA	A	G	contig10197_R, CCAAATCGTATACATAAATGGAGAA
*	contig10260_F, AGAAGTGCGTAGACATCAAGTCTTT	C	G	contig10260_R, AGCACTCACACCGGAGGAT
*	contig10318_F, TGCCACTGACTGGAACTGTC	T	G	contig10318_R, TTTGGTATGCGTGATCTACCTG
	contig10320_F, TGCATTAATGATTTCCTTGCAG	C	A	contig10320_R, AAGTAAGAATCAATACCGAGGGTTT
	contig10323_F, GTCCTTCTTTGGCGAGGTG	G	A	contig10323_R, TCCGAACTACTGGAGGATGC
	contig10327_F, TCATGGACACTGCATCTAACA	G	T	contig10327_R, CCAGTTGGATTATATCACTTCAAGA

	contig10364_F, GATTTGAGCAATATAAGGTCTTCG	C	G	contig10364_R, GAGGCAAATGCAAATAATGG
	contig10421_F, CTCCTTTGACCGCGTAGTTC	G	T	contig10421_R, AATCCTTTGGACGTGCTTTG
	contig10493_F, CAGTGGTATGCTGGGTCAC	C	T	contig10493_R, TCCAACCTACAGATCTTCCTAAA
	contig10509_F, ACGTCGTCGAGGTCGAAAT	A	C	contig10509_R, GCCTTCCGTCGTGGTGT
	contig10538_F, CATGATGGAATGATACACAATTTACA	C	T	contig10538_R, TTTCTTGTTCCTACACCTCAACC
*	contig10539_F, GGGTGGCACTACTCGACCTA	C	T	contig10539_R, TTGCATTTAATTGGCGTTCA
*	contig10555_F, GCGTCCATAACACATTCCAG	G	A	contig10555_R, CCCTTTGTGTTTGACAGGTTT
	contig10556_F, GGAGATAGGCCAGGGTTGA	A	T	contig10556_R, CCATTCAAATATTACACATGACTATGC
*	contig10577_F, TGGCTGTTTGGCCTTATTAAA	A	G	contig10577_R, TGATGGAGCATCTCAAGACAA
	contig10582_F, CAACAAACTCCAATAGTTGAAGCA	A	T	contig10582_R, AAACGCAAATGTTCCTCCAC
	contig10592_F, GCATATAAAGACCATCGGGATT	A	G	contig10592_R, ATGAGGCGTGACGTGGA
	contig10600_F, CGGCTACGTTACAGAGTCGAT	A	G	contig10600_R, TGACAAGGCCCAGAAGAGTT
*	contig10608_F, GGCTTGGTACTGCTACACTCC	T	C	contig10608_R, ATTCCAATACGGTGCCAATC
*	contig10611_F, AGGTTCCTGGTGCAACATTC	G	A	contig10611_R, CTCAATCACCACCTGAACGA
*	contig10624_F, ACAAGTTTAGGACACATCAAAGC	T	C	contig10624_R,TTTAGACCACAAGTATCTAATACAATATGA
	contig10626_F, TTAAGAACTCGGGTCCTTGGT	C	G	contig10626_R, GAGGCACGGATGGGTTAATA
	contig10635_F, TACCTTGAGCTTCGCCACA	A	G	contig10635_R, TTACAGGAAGCGAGGAAGGA
	contig10669_F, TTAGGTCTCACGGATTTGCAT	G	C	contig10669_R, GGCACAAGCAAGCAAATAAA
*	contig10684_F, TGCGCGTCGTCTTCAA	C	T	contig10684_R, ACGTACTGATCGGTTGTCGAT
*	contig10685_F, AAGATCCCAGTCACCAAAGAA	G	T	contig10685_R, ACGACAGCACAAATTTCCAT
	contig10729_F, GTGCATGACCTTTCGAGGTG	G	A	contig10729_R, TGCCATGAACGTGTGGAATA
	contig10730_F, TTGACGGGAGAGGTAGGAGA	T	C	contig10730_R, CAAGGCCCTATTGGAGGACT
	contig10736_F, TGTAGAGCTCGTTGGGAACC	C	A	contig10736_R, AAACCTTGGTTTCATAACTGAGGA
	contig10773_F, TGCATTCTTGTGCGATTACC	A	G	contig10773_R, CTCCGAAATGTTGTGTCCAA
*	contig10778_F, TGATGCATGCCATGGTAATA	C	T	contig10778_R, AAATAACTTGAACCTAATAATAAATGTCG
	contig10798_F, ATGCTCACCGATGCCTATTT	A	G	contig10798_R, CGCGAGTCTTTGGATAATGA
	contig10820_F, TGTTTGCAATACACAAAGAATCAA	C	T	contig10820_R, AAGAATGTTGATGGTATTCTTCCA
	contig10836_F, TGTGCCTCTGCATTATTTACC	C	T	contig10836_R, AATGCCGCATGTTTAATGTT
	contig10844_F, AGTTTAACCCTTACCTCATCGAC	G	A	contig10844_R, TGAGCATATTGCATGTTTCAA

*	contig10846_F, ATTAGCAGCGTCCTTGGAGA	T	C	contig10846_R, TTCCACCGATGTATGAATGC
	contig10863_F, GATGCTCCTGCAGTGCTAAG	T	C	contig10863_R,CCCACTGACTTTATTATTCTTGAAA
	contig10881_F, CGATGGAACCACAGAAACAT	T	C	contig10881_R, TTTCAAGGTGATTTGGATATTTG
	contig10884_F, TTCAATTAAGACATAATGCATCTCA	C	T	contig10884_R, ATTGTTAATACAATGTGATCAATGC
*	contig10914_F, CGGTGGAACCAACTATACGG	C	T	contig10914_R, ACTGAAGGCTTAACGACCAACT
	contig10925_F, CACATGAAGGTTCCGAAGGT	T	G	contig10925_R, GGAATCCGAAGTTGATGACG
	contig10937_F, TTTGCTATATTCTTCTCTTGTGATAAA	T	C	contig10937_R, CATCACGATCCGTATGAACTC
	contig10969_F, TTCCGACTTTCCTGGAACC	G	T	contig10969_R, GACTAACCTATTAACAAGATGCCACA
	contig11010_F, TGTCATCTTGATCACTTATTAATGTTT	T	A	contig11010_R, TCATTTCCAAGATCTCTCTAAGACT
	contig11012_F, CTTGCAGCTTGCTCTTCACA	T	C	contig11012_R, GAGACCTGATGGTGCTCGAC
*	contig11013_F, GGCTCGCGCTACAATTATG	T	C	contig11013_R, CGACCACTTGATTGTCATCC
	contig11017_F, AATGTAAGATGTTGGTAATTTACATTGG	C	G	contig11017_R, TCGCGCTCTCAGGTACATC
	contig11032_F, CCTTACTGGGCAATAATGGTTT	C	T	contig11032_R, TTGCCTTATGACTGCAAGGT
	contig11053_F, GGTACGTATAAGCGTCCCTGT	A	G	contig11053_R, GCGAGAGAGGTATGCATGAG
*	contig11059_F, TCTAAAGAACTTGCCGCTCA	A	G	contig11059_R, GGACATAGAAATAAGACACTATGCATTT
	contig11097_F, GACAAGCTTACGGCCAACTC	C	T	contig11097_R, GCCCTCTTCTCGGTTGTAGA
	contig11107_F, ATCAAGCACAACGGTCTGAA	T	C	contig11107_R, GTGGTACTGAAGTGGCTGGA
	contig11129_F, AGGGAAGACGTGATGGAATG	G	A	contig11129_R, CTTGGTCAAGTGCTGGGTCT
	contig11147_F, TGGCAATCAAAGTTTGGAATC	T	C	contig11147_R, TTTCCCTTCCATATATCCATGC

* Indicates robust primer sets used for genetic mapping

Allele 1 and 2 indicates the SNP being interrogated

Supplemental Table 2. List of 768 SNP primer pairs used in KASPar assays on the Fluidigm EP1 platform.

	Contig	Forward P:rimer 1	Forward Primer 2	Common Reverse Primer	A1	A 2
*	A1_BA_grs_79805_174	GAAGGTGACCAAGTTCATGCTGATCAAGCACCTGCTTCA	GAAGGTCGGAGTCAACGGATTGCTGATCAAGCACCTGCTTCG	CCTAACCTTGGTCGTAGACTCTTCTT	G	A
*	A1_BA_grs_106572_318	GAAGGTGACCAAGTTCATGCTCGCCGCTTCCTTCGGCAC	GAAGGTCGGAGTCAACGGATTCCGCCGCTTCCTTCGGCAT	TGGGCTATTTTGGCGGGTTTTGGAT	C	T
*	A1_BA_grs_13059_280	GAAGGTGACCAAGTTCATGCTCCAAGTGTCCTTCTCCACAATCG	GAAGGTCGGAGTCAACGGATTATCCAAGTGTCCTTCTCCACAATCA	AGGGTGAGAAGGTTCCGTTTCCAT	C	T
	A1_BA_grs_103150_240	GAAGGTGACCAAGTTCATGCTGTGGTTGTGGTGGTTGTTGTACTTTT	GAAGGTCGGAGTCAACGGATTGGTTGTGGTGGTTGTTGTACTTTC	TAGTTTTGATAAGAACAGCTCGGGATCAT	G	T
*	A1_BA_grs_46512_310	GAAGGTGACCAAGTTCATGCTATGGATCCTGCCTATGATTTCATTGT	GAAGGTCGGAGTCAACGGATTGGATCCTGCCTATGATTTCATTGC	TGCCATAGATGGCCCGGTTACTAT	A	G
*	A1_BA_grs_35017_353	GAAGGTGACCAAGTTCATGCTGCCACTCTCGACATGCTTGCAT	GAAGGTCGGAGTCAACGGATTCCACTCTCGACATGCTTGCAC	ACGATGGTGATCACAGGCACGG	C	A
*	A1_BA_grs_103711_349	GAAGGTGACCAAGTTCATGCTAAATAGATATCATTGTGAAAACAAATGTAGTAC	GAAGGTCGGAGTCAACGGATTAAATAGATATCATTGTGAAAACAAATGTAGTAG	CAGCATTTAATGTTGGTACACCTCTTGAA	G	C
	A1_BA_grs_18421_240	GAAGGTGACCAAGTTCATGCTACACTTCGGCTGACTTCTG	GAAGGTCGGAGTCAACGGATTGCTACACTTCGGCTGACTTCTA	CAAAGATTAGCAAAAAGGCACCAAGTCAT	C	T
*	A1_BA_grs_54715_292	GAAGGTGACCAAGTTCATGCTAAAGTGGAGCAATGGTTAGATGCG	GAAGGTCGGAGTCAACGGATTAAAAAGTGGAGCAATGGTTAGATGCA	CCGCCCCTCCTACTCCTCCTT	C	T
	A1_BA_grs_19061_246	GAAGGTGACCAAGTTCATGCTATTACAGCATGGTTCTGCTAATTCCAA	GAAGGTCGGAGTCAACGGATTACAGCATGGTTCTGCTAATTCCAG	CTTGAACCATTGTGTCATCTATGTTGTATA	G	A
*	A1_BA_grs_17145_115	GAAGGTGACCAAGTTCATGCTCATATATGTTCCCATACACTTGTATCTG	GAAGGTCGGAGTCAACGGATTCATATATGTTCCCATACACTTGTATCTC	CTACACCAAAGACTCTGGTCCTCTT	G	C
	A1_BA_grs_31757_316	GAAGGTGACCAAGTTCATGCTGCAAGCTCAAGAAAGCTGCCGA	GAAGGTCGGAGTCAACGGATTCAAGCTCAAGAAAGCTGCCGG	CCGGCGGCAGGTGACCCAA	G	A
	A1_BA_grs_106543_341	GAAGGTGACCAAGTTCATGCTGCAAATGTCGTGCCCGTTGAAGA	GAAGGTCGGAGTCAACGGATTCAAATGTCGTGCCCGTTGAAGC	GCTTCTTGGGACACTCATTGGAGTA	C	A
	A1_BA_grs_24955_237	GAAGGTGACCAAGTTCATGCTACATAGGTGGGTCTCGTGCTCT	GAAGGTCGGAGTCAACGGATTCATAGGTGGGTCTCGTGCTCC	GAACAGGGACGACATCGGAGGAA	G	A
*	A1_BA_grs_31450_326	GAAGGTGACCAAGTTCATGCTGATATCGATCACGATGTCGCCC	GAAGGTCGGAGTCAACGGATTAAGATATCGATCACGATGTCGCCT	ATGACTGACACCGTGACTGTGGAT	C	T
	A1_BA_grs_106517_325	GAAGGTGACCAAGTTCATGCTGTGAACATATCCTGCGGTTTAAGTCT	GAAGGTCGGAGTCAACGGATTGAACATATCCTGCGGTTTAAGTCC	CCGCTGCTGCCAATAAGTATTGTGTT	G	A
	A1_BA_grs_22344_361	GAAGGTGACCAAGTTCATGCTGAGCGGTATCGAAAAGCGGT	GAAGGTCGGAGTCAACGGATTGAGCGGTATCGAAAAGCGGC	CGCTTCAGTCATGAGCGGTACCAA	G	A
*	A1_BA_grs_16626_100	GAAGGTGACCAAGTTCATGCTCAATTTCTTTGAGCATTTAGTAGTCA	GAAGGTCGGAGTCAACGGATTCTCAATTTCTTTGAGCATTTAGTAGTCG	CAACCATGCTTTTACCACAACAGGGAA	G	A
	A1_BA_grs_20025_147	GAAGGTGACCAAGTTCATGCTAAGCAGTTCATCCTCGGACCCA	GAAGGTCGGAGTCAACGGATTGCAGTTCATCCTCGGACCCG	TGAAACCAACATTTTCAAGATTTGCAGCAT	G	A
	A1_BA_grs_33507_340	GAAGGTGACCAAGTTCATGCTGTATAATCATCATGGATATCGTCGC	GAAGGTCGGAGTCAACGGATTGTGTATAATCATCATGGATATCGTCGT	ACTGCGCTGACAGGTGGGCTTA	C	T
*	A1_BA_grs_47492_411	GAAGGTGACCAAGTTCATGCTGCGACGGCGGCGGACAG	GAAGGTCGGAGTCAACGGATTGGCGACGGCGGCGGACAA	GCCTCCACCCCCACCGTCTT	C	T
	A1_BA_grs_24908_398	GAAGGTGACCAAGTTCATGCTGCCGCGGCCCGTTCGAC	GAAGGTCGGAGTCAACGGATTCGCCGCGGCCCGTTCGAT	TTGGACGTAGCCGTCTATTGTGGTA	C	T
*	A1_BA_grs_44890_322	GAAGGTGACCAAGTTCATGCTGAAAACTTCATCAAGGTCCAGGCTT	GAAGGTCGGAGTCAACGGATTAAAACTTCATCAAGGTCCAGGCTC	CACGTTCCCCACATGTCAATCCATT	G	A
*	A1_BA_grs_68133_331	GAAGGTGACCAAGTTCATGCTCAAGAGAATAGAACAAAAGACCAGACTA	GAAGGTCGGAGTCAACGGATTAAGAGAATAGAACAAAAGACCAGACTG	ATCCTGACTTATGGCCGCAACCTAA	G	A
*	A1_BA_grs_106489_350	GAAGGTGACCAAGTTCATGCTCAAAGTTATGCTTCAAAATCTACGAAAGA	GAAGGTCGGAGTCAACGGATTCAAAGTTATGCTTCAAAATCTACGAAAGG	CAGTTTTATTGTTAGACTACTCTTTCATTT	G	A
	A1_BA_grs_22609_354	GAAGGTGACCAAGTTCATGCTCAAAGGACGACGCGCGGTCTA	GAAGGTCGGAGTCAACGGATTAAGGACGACGCGCGGTCTG	CGCGCCAGAGCGCCACACT	G	A
	A1_BA_grs_18947_212	GAAGGTGACCAAGTTCATGCTTCAATGCTTAGAAAAATTGTTTTGATGCC	GAAGGTCGGAGTCAACGGATTGTTCAATGCTTAGAAAAATTGTTTTGATGCA	ATGAAAGGAACTACTTATAGGGACTTGTAA	G	T
	A1_BA_grs_105025_249	GAAGGTGACCAAGTTCATGCTGTGGAAGAAACAAGAACAAGCCC	GAAGGTCGGAGTCAACGGATTGGTGGAAGAAACAAGAACAAGCCT	AATCCTTAGCTTCTTCCTTTGCCTTTCTT	C	T
*	A1_BA_grs_43752_328	GAAGGTGACCAAGTTCATGCTGGCAATGACCAAAGAAGAGCGG	GAAGGTCGGAGTCAACGGATTCGGCAATGACCAAAGAAGAGCGA	ACCACTCCCCTTGTGGGAGTCA	C	T
*	A1_BA_grs_14756_221	GAAGGTGACCAAGTTCATGCTGCCTCTGCCTAATCTATAACTCAC	GAAGGTCGGAGTCAACGGATTGCCTCTGCCTAATCTATAACTCAA	TGATCCGTTGGATTCTTTTACTTCAAGAAA	G	T
	A1_BA_grs_106894_242	GAAGGTGACCAAGTTCATGCTAGTTTGATGGCTCCCTGGCAAC	GAAGGTCGGAGTCAACGGATTATAGTTTGATGGCTCCCTGGCAAT	TACTGCGATACACCCCCCTATACTT	C	T

*	A1_BA_grs_58858_189	GAAGGTGACCAAGTTCATGCTGTGAATCTGAAGCAATGTCCACAACA	GAAGGTCGGAGTCAACGGATTGAATCTGAAGCAATGTCCACAACG	GTAGGTACAGAGGACCCCACCA	G	A
*	A1_BA_grs_22767_152	GAAGGTGACCAAGTTCATGCTGGGACAGATGTAGGAGGCCTT	GAAGGTCGGAGTCAACGGATTGGACAGATGTAGGAGGCCTC	AGGCTCCGTTGGACATCTCCTTAT	G	A
	A1_BA_grs_22792_208	GAAGGTGACCAAGTTCATGCTGATGTGCTCATCATACCTTCCTCT	GAAGGTCGGAGTCAACGGATTATGTGCTCATCATACCTTCCTCG	GTTGCTGACTGATGGCCCAAAATATAT	C	A
	A1_BA_grs_26306_310	GAAGGTGACCAAGTTCATGCTGAAAATACACCAGGACTAAAGTTCCTT	GAAGGTCGGAGTCAACGGATTAAAATACACCAGGACTAAAGTTCCTC	ATGCAAAGGCAGGAAATAAAGATGTTAGAT	G	A
*	A1_BA_grs_56001_322	GAAGGTGACCAAGTTCATGCTCAGCGGCTCGGAGTCCCTA	GAAGGTCGGAGTCAACGGATTAGCGGCTCGGAGTCCCTG	CTGGCGTGGGTGATACGAACGAT	G	A
*	A1_BA_grs_26172_244	GAAGGTGACCAAGTTCATGCTCAACCTTAAGGCTTTTGCCGACTT	GAAGGTCGGAGTCAACGGATTAACCTTAAGGCTTTTGCCGACTC	GGTGCATATCGTTGAATTTCGAGAGATA	G	A
*	A1_BA_grs_36324_362	GAAGGTGACCAAGTTCATGCTAAAATGAGTTTTGCGCGTCGCGT	GAAGGTCGGAGTCAACGGATTAAATGAGTTTTGCGCGTCGCGC	GCACTCAGTAAGAGTAACTCCAGCAA	G	A
*	A1_BA_grs_29455_185	GAAGGTGACCAAGTTCATGCTGACAAGCAACATGGACAAAGGCC	GAAGGTCGGAGTCAACGGATTATGACAAGCAACATGGACAAAGGCA	CGGGCAATGCACATACACCCTTTAA	G	T
*	A1_BA_grs_72951_311	GAAGGTGACCAAGTTCATGCTCGCCATGAACAAGTGGTTGATCC	GAAGGTCGGAGTCAACGGATTATCGCCATGAACAAGTGGTTGATCT	GATGCCATCTTCCATGATGCGGTT	C	T
*	A1_BA_grs_106369_131	GAAGGTGACCAAGTTCATGCTCAGCCCAACCAATCCCCAGG	GAAGGTCGGAGTCAACGGATTATCAGCCCAACCAATCCCCAGT	TTGGGATAGGGTCGGACGATTCATT	G	T
*	A1_BA_grs_26639_367	GAAGGTGACCAAGTTCATGCTGTAGTTCCTTTCATTATGTATTCACTTTGA	GAAGGTCGGAGTCAACGGATTAGTTCCTTTCATTATGTATTCACTTTGC	CCTTATTTCATGTTGGTCGAGTTGGTATT	C	A
	A1_BA_grs_78369_102	GAAGGTGACCAAGTTCATGCTGGCATTGTCCAACTCCTTCTGCT	GAAGGTCGGAGTCAACGGATTGCATTGTCCAACTCCTTCTGCC	GAACCAAGTGGACCACCTCAGCTT	G	A
	A1_BA_grs_49280_392	GAAGGTGACCAAGTTCATGCTCCTTGAATCCTCCTCCACTGGA	GAAGGTCGGAGTCAACGGATTCTTGAATCCTCCTCCACTGGC	GCATCAGTGATATCTGTAGATTTTTTGTAT	C	A
*	A1_BA_grs_17035_212	GAAGGTGACCAAGTTCATGCTCCATGCCGTCTATTGGCGTGG	GAAGGTCGGAGTCAACGGATTCCATGCCGTCTATTGGCGTGC	AATGATAATCAAGAAGTATGTACGCAGGTA	G	C
*	A1_BA_grs_24338_123	GAAGGTGACCAAGTTCATGCTGTGTTTCTCGAATAGATCTACGTGC	GAAGGTCGGAGTCAACGGATTGTGTTTCTCGAATAGATCTACGTGT	TCGGGTGATCCCTTGGGGAATTTTT	C	T
	A1_BA_grs_33636_363	GAAGGTGACCAAGTTCATGCTGGCCCGACAATTTGTCATATGTC	GAAGGTCGGAGTCAACGGATTGGGCCCGACAATTTGTCATATGTT	GCCGCGACCATGAGCCCCT	C	T
*	A1_BA_grs_70480_224	GAAGGTGACCAAGTTCATGCTGATCTACAGTCTGGAGAAGCAC	GAAGGTCGGAGTCAACGGATTCTGATCTACAGTCTGGAGAAGCAA	CAGGAGCAAAATGATATGTGACGTGAATT	C	G
	A1_BA_grs_48446_319	GAAGGTGACCAAGTTCATGCTCGTTGGCGATGTTCTGACCCG	GAAGGTCGGAGTCAACGGATTACGTTGGCGATGTTCTGACCCA	CAGCGTCCTACGCATCTAACGGTA	C	T
*	A1_BA_grs_51221_289	GAAGGTGACCAAGTTCATGCTCCTCAGCATAACGAGACAGCTG	GAAGGTCGGAGTCAACGGATTCCTCAGCATAACGAGACAGCTA	CAGGGGATATACAAGTGTCATGAAGTATA	C	T
	A1_BA_grs_76744_195	GAAGGTGACCAAGTTCATGCTCCCAGTGCCTCCTATTGCTCG	GAAGGTCGGAGTCAACGGATTCCCAGTGCCTCCTATTGCTCA	ATGCAAAGAATGTTCCACTGGAACCAATT	C	T
	A1_BA_grs_69395_181	GAAGGTGACCAAGTTCATGCTCAACATGGACTCAAACGTGTACTTC	GAAGGTCGGAGTCAACGGATTCCAACATGGACTCAAACGTGTACTTT	AGTGGACACCATAACAGAAGAAAGCAAAT	C	T
	A1_BA_grs_29797_358	GAAGGTGACCAAGTTCATGCTAATTCACTGATTATTCATTGATATGATTTCAC	GAAGGTCGGAGTCAACGGATTAATTCACTGATTATTCATTGATATGATTTCAT	GGTCCATGCTCCAAAAGTCATCAA	C	T
	A1_BA_grs_103027_340	GAAGGTGACCAAGTTCATGCTTCCTTCATTTTTGGGCTTCAGTCT	GAAGGTCGGAGTCAACGGATTCCTTCATTTTTGGGCTTCAGTCG	CCGTCCATCGAATATTCATGGAGGAA	C	A
	A1_BA_grs_34763_213	GAAGGTGACCAAGTTCATGCTGTTTCCACGATTTGGGATAGGTCA	GAAGGTCGGAGTCAACGGATTTCCACGATTTGGGATAGGTCG	TCCAGGATTTGCCCCGATAACCAA	G	A
*	A1_BA_grs_13744_133	GAAGGTGACCAAGTTCATGCTGTCGCCAACGTCAACAACTTCCT	GAAGGTCGGAGTCAACGGATTCGCCAACGTCAACAACTTCCC	TTGGAGTTGCTGGGGCTCCAGT	G	A
	A1_BA_grs_109415_206	GAAGGTGACCAAGTTCATGCTGCGACACCATGGGCTTCCGT	GAAGGTCGGAGTCAACGGATTCGACACCATGGGCTTCCGC	CCTACAGGTACTCGAGCTTGGTATA	G	A
	A1_BA_grs_16297_257	GAAGGTGACCAAGTTCATGCTCCTGCTACATCGAAGGAGTTGT	GAAGGTCGGAGTCAACGGATTCCTGCTACATCGAAGGAGTTGC	GCAACCGATCTTTCTGCAATTAAACCAAT	G	A
	A1_BA_grs_105050_157	GAAGGTGACCAAGTTCATGCTCATAGATCTGAGTATCAGTCATCCT	GAAGGTCGGAGTCAACGGATTCATAGATCTGAGTATCAGTCATCCC	GTATGGGTTAGGAGATCCGACTCAA	G	A
	A1_BA_grs_25863_171	GAAGGTGACCAAGTTCATGCTCATACAAGTGATTGCAAAGTGAATACATAA	GAAGGTCGGAGTCAACGGATTATACAAGTGATTGCAAAGTGAATACATAG	ATGTTTAGGCCTCTTACAAGTCCCTATAA	G	A
	A1_BA_grs_30162_304	GAAGGTGACCAAGTTCATGCTACTGGAGTAAAGTAAATATAAGATAGTATGAT	GAAGGTCGGAGTCAACGGATTCTGGAGTAAAGTAAATATAAGATAGTATGAC	CAAGTGCTTTGTATTTCCAAAAGAGGAAAA	G	A
*	A1_BA_grs_12266_246	GAAGGTGACCAAGTTCATGCTAATAGTTCGATGGTGTAGTGTTTTGTTTA	GAAGGTCGGAGTCAACGGATTAGTTCGATGGTGTAGTGTTTTGTTTG	GCATTCCTCGGATGACCACATCAAT	G	A
*	A1_BA_grs_12239_421	GAAGGTGACCAAGTTCATGCTAACATCCTTGACAAATATTCTGGCTATTT	GAAGGTCGGAGTCAACGGATTCATCCTTGACAAATATTCTGGCTATTG	CTACGTGTTGAGCCAATAATCATGGATAA	C	A
	A1_BA_grs_28156_127	GAAGGTGACCAAGTTCATGCTAAACATCCGCATGGAATGATGCCTA	GAAGGTCGGAGTCAACGGATTCATCCGCATGGAATGATGCCTG	GGGTTTTACCCTACTACAAATGTTTCAAAA	G	A
	A1_BA_grs_19668_156	GAAGGTGACCAAGTTCATGCTTATGGTCTTTCGTTTCAAGGTAG	GAAGGTCGGAGTCAACGGATTGCTTATGGTCTTTCGTTTCAAGGTAC	TACATAGTTGATGCAAAGGTGACGGTT	G	C
	A1_BA_grs_14608_294	GAAGGTGACCAAGTTCATGCTAATAAGGAGCAGAAGGTGCTGAAC	GAAGGTCGGAGTCAACGGATTAATAAGGAGCAGAAGGTGCTGAAG	AATCCATTTGCTAAGTATTCACAGGGATTT	G	C
*	A1_BA_grs_39974_421	GAAGGTGACCAAGTTCATGCTTTGCTCGCTGAGGCGAGAC	GAAGGTCGGAGTCAACGGATTCTTTGCTCGCTGAGGCGAGAA	GAAGTTGCCATCGAAGGAGAGGAT	G	T

*	A1_BA_grs_14015_350	GAAGGTGACCAAGTTCATGCTTTCTTTCAGGACTACTAAAGACTACG	GAAGGTCGGAGTCAACGGATTCTTTCTTTCAGGACTACTAAAGACTACA	TTTGGGTTAAGTTAGTAACTTACTAATTTT	C	T
	A1_BA_grs_109705_162	GAAGGTGACCAAGTTCATGCTTTATTGTGTTTTCACCCTTTTAAATTATTTCG	GAAGGTCGGAGTCAACGGATTTATTGTGTTTTCACCCTTTTAAATTATTTCA	CGACTCGGGGAGGTCGGCAA	C	T
*	A1_BA_grs_17079_189	GAAGGTGACCAAGTTCATGCTTGGCGTACTGCACAATACTTCG	GAAGGTCGGAGTCAACGGATTAGTTGGCGTACTGCACAATACTTCA	CTCCTGGATGTTTCGGTTGCGCTT	C	T
*	A1_BA_grs_106931_323	GAAGGTGACCAAGTTCATGCTTCAGGAGTTTGTATAATGGTGCGG	GAAGGTCGGAGTCAACGGATTTTCAGGAGTTTGTATAATGGTGCGT	GATGCAGTCAGTCGGTTCGTAAGAT	G	T
*	A1_BA_grs_36836_433	GAAGGTGACCAAGTTCATGCTGTCAATAGAGTGCCCCACAGAC	GAAGGTCGGAGTCAACGGATTGGTCAATAGAGTGCCCCACAGAT	ACGCTTCAGTTCTGTGGTGACCAT	C	T
	A1_BA_grs_13904_433	GAAGGTGACCAAGTTCATGCTGGAGTGGAGGCCAATGAAGAAAG	GAAGGTCGGAGTCAACGGATTGGAGTGGAGGCCAATGAAGAAAT	GCTGTTGCACCAAGCCCTTGCAT	G	T
*	A1_BA_grs_69245_242	GAAGGTGACCAAGTTCATGCTGCCGATTAATTACTCCCCTGCG	GAAGGTCGGAGTCAACGGATTGGCCGATTAATTACTCCCCTGCT	GTGAGGATTTTGTAACTGCCACGCA	G	T
	A1_BA_grs_30550_248	GAAGGTGACCAAGTTCATGCTGAACTCCCTGTCGGACCTCTC	GAAGGTCGGAGTCAACGGATTGAACTCCCTGTCGGACCTCTT	CCAGGCCCTAATGGCATTATCACAA	C	T
*	A1_BA_grs_33956_162	GAAGGTGACCAAGTTCATGCTCTCCAATGCTCAGATTCTCCAC	GAAGGTCGGAGTCAACGGATTCTCTCCAATGCTCAGATTCTCCAT	TTCGGTCATATCCGGAGTAATCTTGAAA	C	T
	A1_BA_grs_16159_326	GAAGGTGACCAAGTTCATGCTCGTCGAGTGGGCCTTCCG	GAAGGTCGGAGTCAACGGATTGTCGTCGAGTGGGCCTTCCA	TATACCCTACGGGTACCCGATGTTA	C	T
*	A1_BA_grs_25521_213	GAAGGTGACCAAGTTCATGCTCGGTGTGAGCTCGAGAACGG	GAAGGTCGGAGTCAACGGATTGCGGTGTGAGCTCGAGAACGT	CCATATTTCCCCCTCAAAACCCCAT	G	T
*	A1_BA_grs_41770_204	GAAGGTGACCAAGTTCATGCTCATCATGTTGCCTGTACTACTACG	GAAGGTCGGAGTCAACGGATTCCATCATGTTGCCTGTACTACTACA	TGGGAAATACTCTTGTGAATTGTTCGGTA	C	T
*	A1_BA_grs_43509_155	GAAGGTGACCAAGTTCATGCTCAGTGAGTAGTTGCAGAGTGACG	GAAGGTCGGAGTCAACGGATTACAGTGAGTAGTTGCAGAGTGACA	GAGTCTATTTTTCCTTCTGTTTTCGTACTT	C	T
	A1_BA_grs_25242_300	GAAGGTGACCAAGTTCATGCTCACAATGGTTCAGGTTTATTAAGTGC	GAAGGTCGGAGTCAACGGATTGTCACAATGGTTCAGGTTTATTAAGTGT	TTAGTGATTAAAGCTCTCACGAAACTTGAA	C	T
*	A1_BA_grs_20690_314	GAAGGTGACCAAGTTCATGCTATTGAATAATTCTTGTAAACAAAAATCACCAG	GAAGGTCGGAGTCAACGGATTCATTGAATAATTCTTGTAAACAAAAATCACCAA	CCATGTTTTCCCAACAAGACACCAATATT	C	T
	A1_BA_grs_107791_242	GAAGGTGACCAAGTTCATGCTATTATGTTGGAGATGGAACTGTCC	GAAGGTCGGAGTCAACGGATTACTATTATGTTGGAGATGGAACTGTCT	CCCGCATAATTCGTGTATAAAGAGCAAAT	C	T
	A1_BA_grs_38330_329	GAAGGTGACCAAGTTCATGCTATCGTGGTATCCACCGCTG	GAAGGTCGGAGTCAACGGATTGCTATCGTGGTATCCACCGCTA	CGACAAACGCGACGACAACCACAA	T	G
	A1_BA_grs_29915_265	GAAGGTGACCAAGTTCATGCTATATCTATACGGCTACAACTAATACGG	GAAGGTCGGAGTCAACGGATTCTATATCTATACGGCTACAACTAATACGA	GGTACAGAGGGTTTGATGACCAACTA	C	T
	A1_BA_grs_107247_238	GAAGGTGACCAAGTTCATGCTACGCTGACTCGATGCACTTTCG	GAAGGTCGGAGTCAACGGATTGACGCTGACTCGATGCACTTTCA	TCGCAGACTCGAGTGAAGACTCAT	C	T
	A1_BA_grs_16672_120	GAAGGTGACCAAGTTCATGCTAATTGAAGACTCTATCAGATAATCTTAAATAC	GAAGGTCGGAGTCAACGGATTGAATTGAAGACTCTATCAGATAATCTTAAATAT	TGAGTTCTTCTTCATCCCCTAAAAGCTTA	C	T
	A1_BA_grs_15840_171	GAAGGTGACCAAGTTCATGCTAAGGCGACGATGATCGACAGC	GAAGGTCGGAGTCAACGGATTGAAGGCGACGATGATCGACAGA	GGACCTTGGCCCGCACAGCAT	G	T
*	A1_BA_grs_37706_409	GAAGGTGACCAAGTTCATGCTGTGAGTCCAGGAGAGCACCGA	GAAGGTCGGAGTCAACGGATTGAGTCCAGGAGAGCACCGG	GCTGTGCGACTCGCCGGTGTA	G	A
	A1_BA_grs_72887_279	GAAGGTGACCAAGTTCATGCTGTCGTGGCAGAGCCGGACTT	GAAGGTCGGAGTCAACGGATTCGTGGCAGAGCCGGACTC	AAAGGCCCGTTTCTCTGCCACG	G	A
*	A1_BA_grs_33787_381	GAAGGTGACCAAGTTCATGCTGTCATGACTCCGATCTGAGCGT	GAAGGTCGGAGTCAACGGATTGTCATGACTCCGATCTGAGCGA	ACTTTCAGATCCGGAACCATAGGTTATAT	T	A
	A1_BA_grs_20427_213	GAAGGTGACCAAGTTCATGCTGTACGTGGTGAGCTGGTAGGTT	GAAGGTCGGAGTCAACGGATTACGTGGTGAGCTGGTAGGTG	AGCAGATGATTGTGCAAGCTGGCAT	C	A
	A1_BA_grs_21612_226	GAAGGTGACCAAGTTCATGCTGGGCGATACTTTGGTGTATGATGA	GAAGGTCGGAGTCAACGGATTGGCGATACTTTGGTGTATGATGG	ATGAGAACCGCAAGCTTCGCATGAT	G	A
	A1_BA_grs_46950_332	GAAGGTGACCAAGTTCATGCTGGAGGTTCTTGTCTTAGGCTACAT	GAAGGTCGGAGTCAACGGATTGAGGTTCTTGTCTTAGGCTACAC	CGACAGTAGGTGTATCAACATCCCAA	G	A
	A1_BA_grs_53297_269	GAAGGTGACCAAGTTCATGCTGATTGACCTGGCGAGTGATGGA	GAAGGTCGGAGTCAACGGATTGACCTGGCGAGTGATGGC	GATCCAAAAGGGTCGCACCTCCAA	C	A
	A1_BA_grs_42195_300	GAAGGTGACCAAGTTCATGCTGAGCATATCAATTCAGTTATCTTGGTGAT	GAAGGTCGGAGTCAACGGATTGCATATCAATTCAGTTATCTTGGTGAC	GTCCTTCTCCATAATCGAGAAGGCTT	G	A
*	A1_BA_grs_29391_265	GAAGGTGACCAAGTTCATGCTGACGAGGTCGGAGTCGCCA	GAAGGTCGGAGTCAACGGATTACGAGGTCGGAGTCGCCG	CGAGCAGCCAAGGAAATGAACATCAA	G	A
	A1_BA_grs_62899_192	GAAGGTGACCAAGTTCATGCTGAAAACAAGATGAAACAAGTTGAGAGCAA	GAAGGTCGGAGTCAACGGATTAAACAAGATGAAACAAGTTGAGAGCAG	CCCGAGTTGTGCTTCTCAAAGCTAT	G	A
	A1_BA_grs_105608_246	GAAGGTGACCAAGTTCATGCTCTCAATAAGATTGGTGTCTTGCTT	GAAGGTCGGAGTCAACGGATTCTCTCAATAAGATTGGTGTCTTGCTG	ATGTAGAGGCAAGAAATAAAGATGTTGGAT	C	A
	A1_BA_grs_62300_111	GAAGGTGACCAAGTTCATGCTCGTGGGGAAGGTACATAGTGCA	GAAGGTCGGAGTCAACGGATTGTGGGGAAGGTACATAGTGCG	GCAATGACGCCCCGTGGTTGAA	G	A
	A1_BA_grs_21506_179	GAAGGTGACCAAGTTCATGCTCGAAGTTCTCGGAGATCCTGCA	GAAGGTCGGAGTCAACGGATTGAAGTTCTCGGAGATCCTGCG	GGCCCGTGCGCATGAAGCTTT	G	A
*	A1_BA_grs_29453_94	GAAGGTGACCAAGTTCATGCTCCACCCTTGTTGATCATATCGTGT	GAAGGTCGGAGTCAACGGATTCACCCTTGTTGATCATATCGTGC	TTTATGATGCCAACTTGGGTGTAGGATTT	G	A
	A1_BA_grs_80443_334	GAAGGTGACCAAGTTCATGCTCAAACATATTTGCAAATAAACCATATGAAAGAT	GAAGGTCGGAGTCAACGGATTAAACATATTTGCAAATAAACCATATGAAAGAG	CTCTCGTATTGTTGTTGCACCAAACATTA	C	A

	A1_BA_grs_47639_143	GAAGGTGACCAAGTTCATGCTATCATGTAGTCGGCCACTTTGTTCT	GAAGGTCGGAGTCAACGGATTCATGTAGTCGGCCACTTTGTTCC	ACTTTTCTAAATGGGTCATGCGCCTTTAT	G	A
	A1_BA_grs_109256_130	GAAGGTGACCAAGTTCATGCTATCAATATGACTTGATGGTGCATGAGA	GAAGGTCGGAGTCAACGGATTCAATATGACTTGATGGTGCATGAGC	GAAGGACAAAACTTCCTCCTCACGAT	C	A
	A1_BA_grs_45658_314	GAAGGTGACCAAGTTCATGCTAGAAGAACAAGATCAGGCCAGCAT	GAAGGTCGGAGTCAACGGATTGAAGAACAAGATCAGGCCAGCAG	GCTGGTTGATCAGGTGACTTGATCTT	C	A
	A1_BA_grs_28367_110	GAAGGTGACCAAGTTCATGCTACATTATATAATTACCATTTTGCTCACTTAA	GAAGGTCGGAGTCAACGGATTACATTATATAATTACCATTTTGCTCACTTAC	CATTCATACACTCATATGTCGAACCTGTT	C	A
*	A1_BA_grs_48717_114	GAAGGTGACCAAGTTCATGCTACACACTTGTGGTGTGTGGCAAT	GAAGGTCGGAGTCAACGGATTCACACTTGTGGTGTGTGGCAAG	AATTCGCGTGTTTGGTTTAGCTATGTCAT	C	A
	A1_BA_grs_103902_301	GAAGGTGACCAAGTTCATGCTAATAGTCCTCGATGGAACCCCAT	GAAGGTCGGAGTCAACGGATTATAGTCCTCGATGGAACCCCAC	CTTGGAGTTCGTGTTGTATATATATCTGTT	G	A
	A1_BA_grs_46331_207	GAAGGTGACCAAGTTCATGCTAAACAGAGGGTGAAGCGAAATTCGT	GAAGGTCGGAGTCAACGGATTCAGAGGGTGAAGCGAAATTCGG	GAGAAAAACGCCTGTAATTAATAACTCCTT	C	A
	A1_BA_grs_50227_224	GAAGGTGACCAAGTTCATGCTTTGTTTCTTGCCTCTACATAATCTG	GAAGGTCGGAGTCAACGGATTCTTTGTTTCTTGCCTCTACATAATCTC	TAAGCAAAGACTGATCTGTTGGATCCTT	G	C
*	A1_BA_grs_104230_230	GAAGGTGACCAAGTTCATGCTAGATCGTCTTCAATGTCACTCTCC	GAAGGTCGGAGTCAACGGATTAGATCGTCTTCAATGTCACTCTCG	ACCGAGCTCAATGCAGGAGAATCTT	G	C
*	A1_BA_grs_61819_343	GAAGGTGACCAAGTTCATGCTTGTTGTCATGATGACGGTTGTG	GAAGGTCGGAGTCAACGGATTGCTTGTTGTCATGATGACGGTTGTA	CTGGATTCCACAAAACATGGGAAATACAA	C	T
	A1_BA_grs_32985_172	GAAGGTGACCAAGTTCATGCTGTTTTATTAGACAATTTGACAATAGTGTCTAC	GAAGGTCGGAGTCAACGGATTGTTTTATTAGACAATTTGACAATAGTGTCTAA	CACTTTATCAACAACTTCGCTACAACTTAA	G	T
	A1_BA_grs_27509_363	GAAGGTGACCAAGTTCATGCTGTTGCAGCCAAACACAAGTCCC	GAAGGTCGGAGTCAACGGATTGTTGCAGCCAAACACAAGTCCT	GTAGTGACCCTTGACTCCACATTCAA	C	T
	A1_BA_grs_39097_347	GAAGGTGACCAAGTTCATGCTGGTGGACTGAACCGAGAGATTC	GAAGGTCGGAGTCAACGGATTCGGTGGACTGAACCGAGAGATTT	GTTTAGAAAACTGAAACTACGTTGGAACTT	C	T
	A1_BA_grs_25707_394	GAAGGTGACCAAGTTCATGCTCTTCTCCAAACTTCAGTCAAATGG	GAAGGTCGGAGTCAACGGATTCTCTTCTCCAAACTTCAGTCAAATGA	CCATCAGCAAAGCTTCGAGTGGATA	C	T
*	A1_BA_grs_30609_104	GAAGGTGACCAAGTTCATGCTCTGCTCGTTTGGTCACACC	GAAGGTCGGAGTCAACGGATTCCTCTGCTCGTTTGGTCACACT	GCAAGGGCCGCTCGCGGTT	C	T
	A1_BA_grs_48287_118	GAAGGTGACCAAGTTCATGCTCCATATCACTACTATGAATTTTCAGCTC	GAAGGTCGGAGTCAACGGATTACCATATCACTACTATGAATTTTCAGCTT	CTGGTAATTGGGTATGTCAAAGTTAGCAA	C	T
*	A1_BA_grs_83584_409	GAAGGTGACCAAGTTCATGCTCAGCTGAATGGAAACGTCCAGG	GAAGGTCGGAGTCAACGGATTGCAGCTGAATGGAAACGTCCAGA	GGACTAGTCCCATGTAGCTTCTCTA	C	T
*	A1_BA_grs_13898_198	GAAGGTGACCAAGTTCATGCTAGCTGGACAGTCCGGTCCG	GAAGGTCGGAGTCAACGGATTAGCTGGACAGTCCGGTCCA	CACTACGTGGACACCACCTGGAA	C	T
	A1_BA_grs_63844_321	GAAGGTGACCAAGTTCATGCTACATGTTTCTGAGTGAAGTCACCG	GAAGGTCGGAGTCAACGGATTGACATGTTTCTGAGTGAAGTCACCA	CAAGAATGAAAGTATGATTTCATACGTGCA	C	T
*	A1_BA_grs_60221_323	GAAGGTGACCAAGTTCATGCTAAAACTCTTACTATCATGGTGTGGAAC	GAAGGTCGGAGTCAACGGATTAAAAAAACTCTTACTATCATGGTGTGGAAT	AAAGGCATTCTGATGAATACTAATGAGTTT	C	T
*	A1_BA_grs_43373_424	GAAGGTGACCAAGTTCATGCTTTTTCTTTTATCATGTCTTGTTTTACTGTGT	GAAGGTCGGAGTCAACGGATTTCTTTTATCATGTCTTGTTTTACTGTGC	GGAAATACAAAAAAAGGACCCAAGACACTT	G	A
	A1_BA_grs_32717_314	GAAGGTGACCAAGTTCATGCTTCCCCAATCACTTCATGTGCGTT	GAAGGTCGGAGTCAACGGATTCCCCAATCACTTCATGTGCGTC	TGTTATTGCGGTTGGCGGAGGTAT	G	A
*	A1_BA_grs_109991_272	GAAGGTGACCAAGTTCATGCTTCATCATGTAGAATTGAAGGATCTTCATA	GAAGGTCGGAGTCAACGGATTCATCATGTAGAATTGAAGGATCTTCATC	GGCAATACAATCCACATGACTTGGCTT	C	A
*	A1_BA_grs_21023_133	GAAGGTGACCAAGTTCATGCTGTTCCTTCTTCTTCTATCATTGCCAT	GAAGGTCGGAGTCAACGGATTGTTCCTTCTTCTTCTATCATTGCCAC	CGATCAAGAGGATGGGCTGCATAAT	G	A
	A1_BA_grs_51401_217	GAAGGTGACCAAGTTCATGCTGTCACCTCTAAATAACCACTGCGAT	GAAGGTCGGAGTCAACGGATTCACCTCTAAATAACCACTGCGAC	TTAATTGCGGTGGTTTGTATGGGTAACTA	G	A
*	A1_BA_grs_29063_292	GAAGGTGACCAAGTTCATGCTGTATTTTCGGGTTGAGACTTTGTGTA	GAAGGTCGGAGTCAACGGATTGTATTTTCGGGTTGAGACTTTGTGTG	GATGCATGTAGATAATGATGTACTCTACGT	G	A
	A1_BA_grs_18582_274	GAAGGTGACCAAGTTCATGCTGGCCTCACACATGTACAATTGTCA	GAAGGTCGGAGTCAACGGATTGCCTCACACATGTACAATTGTCG	GCTAACAGAGAAAGAACCATTCTCAGTTA	G	A
	A1_BA_grs_49868_258	GAAGGTGACCAAGTTCATGCTGGCCCTGGAAGAGGGTCCTA	GAAGGTCGGAGTCAACGGATTGCCCTGGAAGAGGGTCCTG	TCTCCCTCGGGAGCTTTTTCAGTTA	G	A
	A1_BA_grs_17361_296	GAAGGTGACCAAGTTCATGCTGGATTGGTGTTCTAAAAGTTCTTGAGT	GAAGGTCGGAGTCAACGGATTGGTGTTCTAAAAGTTCTTGAGC	CCAACTTAGCCACCCTTCAACACAT	G	A
	A1_BA_grs_55927_304	GAAGGTGACCAAGTTCATGCTGGATCGTTAGTCACTTCGCCGTA	GAAGGTCGGAGTCAACGGATTGATCGTTAGTCACTTCGCCGTC	GACGGTCAATGGTGCGATTCTTCTT	C	A
	A1_BA_grs_13365_171	GAAGGTGACCAAGTTCATGCTGCGATGGTTTTATATTCGCGACTCT	GAAGGTCGGAGTCAACGGATTCGATGGTTTTATATTCGCGACTCC	GGGTCAAAAGGAACAAGACCAAAATCTT	G	A
	A1_BA_grs_67743_294	GAAGGTGACCAAGTTCATGCTGCACGGGCCGGTGCAATTATT	GAAGGTCGGAGTCAACGGATTGCACGGGCCGGTGCAATTATG	ATGTTACCGTGTCGATGTCGGCATT	C	A
	A1_BA_grs_38821_285	GAAGGTGACCAAGTTCATGCTGAGGTAGTGTTCTTCACATAGAAGAAT	GAAGGTCGGAGTCAACGGATTAGGTAGTGTTCTTCACATAGAAGAAC	TTGCCGGCTTGGAGTCCTGCAA	G	A
	A1_BA_grs_104739_245	GAAGGTGACCAAGTTCATGCTGAGGAGGGTGAATGACGAAGTCA	GAAGGTCGGAGTCAACGGATTAGGAGGGTGAATGACGAAGTCG	GGAGAAGAAGGGCGCCGTCAAT	G	A
*	A1_BA_grs_16671_167	GAAGGTGACCAAGTTCATGCTGAGGACAGGTCAACCGCACCT	GAAGGTCGGAGTCAACGGATTGGACAGGTCAACCGCACCC	CACACCTTCCAATCGTTTGTATTTGGTT	G	A
*	A1_BA_grs_20038_136	GAAGGTGACCAAGTTCATGCTGAAGGGACCGTACCGTGCT	GAAGGTCGGAGTCAACGGATTGAAGGGACCGTACCGTGCG	TTACGACCATGTGTCCTGTGGCAAA	C	A

*	A1_BA_grs_83796_309	GAAGGTGACCAAGTTCATGCTGAAGAGATGAAAGGCCAGACTACAA	GAAGGTCGGAGTCAACGGATTAAGAGATGAAAGGCCAGACTACAG	CATCTGGATGATCCTGACTCACGAA	G	A
	A1_BA_grs_27756_174	GAAGGTGACCAAGTTCATGCTGAAAGAATCCAACGGTCAGTCTTGT	GAAGGTCGGAGTCAACGGATTAAAGAATCCAACGGTCAGTCTTGG	GGTTTAAAAGAACTCCTTGAGAGGAA	C	A
	A1_BA_grs_49498_297	GAAGGTGACCAAGTTCATGCTCTGCTTGTCCAAGTAGATTTGTGTTT	GAAGGTCGGAGTCAACGGATTCTGCTTGTCCAAGTAGATTTGTGTTC	CCTGTCACCTATAGCAGAAAAATACTCAA	G	A
	A1_BA_grs_15999_324	GAAGGTGACCAAGTTCATGCTCCTAAGCTTGATTGCGGACCGT	GAAGGTCGGAGTCAACGGATTCTAAGCTTGATTGCGGACCGC	GCTATTGGAGAGGTACCGAGTACAA	G	A
	A1_BA_grs_31313_342	GAAGGTGACCAAGTTCATGCTCCGTTTATCCAAGTACATTAGTGAGAAA	GAAGGTCGGAGTCAACGGATTCCGTTTATCCAAGTACATTAGTGAGAAT	GTCTTGTTAGTCCTTTCTATGAACTTCTTT	T	A
*	A1_BA_grs_18812_249	GAAGGTGACCAAGTTCATGCTCCCTGTTCTGGCGGTATTCGTT	GAAGGTCGGAGTCAACGGATTCCTGTTCTGGCGGTATTCGTC	ACGATGGAAACACGGGACCAAGTTA	G	A
	A1_BA_grs_109268_225	GAAGGTGACCAAGTTCATGCTCATAATCTACAACTCAAATTCTTGAAGTGA	GAAGGTCGGAGTCAACGGATTATAATCTACAACTCAAATTCTTGAAGTGG	GGAAAGACCATAAGCCGAGACTGAT	G	A
*	A1_BA_grs_39719_264	GAAGGTGACCAAGTTCATGCTCAACCAAGGCTTATCTAACCAAGCT	GAAGGTCGGAGTCAACGGATTCAACCAAGGCTTATCTAACCAAGCA	GTACAAGATGGATTAAGGCTAAGCCAT	T	A
	A1_BA_grs_54156_270	GAAGGTGACCAAGTTCATGCTATTAAAACTAATTAAATTACTGCAGTAACCACA	GAAGGTCGGAGTCAACGGATTAAAACTAATTAAATTACTGCAGTAACCACG	GTAGAATCATCTTATCAGAATAGATCCAA	G	A
*	A1_BA_grs_42747_240	GAAGGTGACCAAGTTCATGCTATACGTGTGAAATCAGAGGCGCT	GAAGGTCGGAGTCAACGGATTACGTGTGAAATCAGAGGCGCC	TACCATAACAAAAAAAAATCCTTGCAGTAT	G	A
*	A1_BA_grs_48442_249	GAAGGTGACCAAGTTCATGCTAGTTCTATGGAAGGATGTGGAGGT	GAAGGTCGGAGTCAACGGATTGTTCTATGGAAGGATGTGGAGGC	TAAACTCACGGGAGGAAACCAGATTT	G	A
*	A1_BA_grs_66238_275	GAAGGTGACCAAGTTCATGCTAGCATCCAGCTGAAAGGATACCTA	GAAGGTCGGAGTCAACGGATTGCATCCAGCTGAAAGGATACCTG	TGCTGAGAGGGAGAAGTTGTTCGAA	G	A
	A1_BA_grs_107263_216	GAAGGTGACCAAGTTCATGCTACTGCTCATGTCGGCAGACGA	GAAGGTCGGAGTCAACGGATTCTGCTCATGTCGGCAGACGG	CGACCCGGCAAGCGTCATAGAT	G	A
*	A1_BA_grs_37795_404	GAAGGTGACCAAGTTCATGCTACACTGGAATACATGTATTATTTCAACCA	GAAGGTCGGAGTCAACGGATTCACTGGAATACATGTATTATTTCAACCG	CTTGGAGATATGCCACTACAACTTCTTTA	G	A
	A1_BA_grs_86450_346	GAAGGTGACCAAGTTCATGCTAATAACGACAAGACAATCAAGCATGCT	GAAGGTCGGAGTCAACGGATTAACGACAAGACAATCAAGCATGCC	CTTGCCATGCTACATTATTGCCATGTAAA	G	A
	A1_BA_grs_55181_284	GAAGGTGACCAAGTTCATGCTAACCCTCTTTGGGTAATGATCCCT	GAAGGTCGGAGTCAACGGATTAACCCTCTTTGGGTAATGATCCCA	CCGAGATAGGCCAAGCTTGGCAA	T	A
*	A1_BA_grs_104898_197	GAAGGTGACCAAGTTCATGCTAACAAGATTGGTGTGTTGCTGGGA	GAAGGTCGGAGTCAACGGATTCAAGATTGGTGTGTTGCTGGGC	TTATGCAGAGGCAAGAAGTAAAGATGGTA	C	A
*	A1_BA_grs_21636_110	GAAGGTGACCAAGTTCATGCTGAACGAAATTTGGTCAAATTTTGAGTCG	GAAGGTCGGAGTCAACGGATTGAACGAAATTTGGTCAAATTTTGAGTCC	CTCTAACATCGCACCGCCTTCAAAT	G	C
*	A1_BA_grs_26396_267	GAAGGTGACCAAGTTCATGCTTGTTGAATTGTTTCGTTGATTTTGAATGC	GAAGGTCGGAGTCAACGGATTTTTGTTGAATTGTTTCGTTGATTTTGAATGT	AAAAAAGAGCAGAGGCGCTCGATGA	C	T
	A1_BA_grs_24713_153	GAAGGTGACCAAGTTCATGCTTGGGTAATACACTTAAGGAAACTTGC	GAAGGTCGGAGTCAACGGATTCTTGGGTAATACACTTAAGGAAACTTGT	CAGTTGTTGGGCCTCCCAAGTGTA	C	T
*	A1_BA_grs_55489_309	GAAGGTGACCAAGTTCATGCTGTTTTTCACTGTTTACCTATATGGTAACG	GAAGGTCGGAGTCAACGGATTGTTTTTCACTGTTTACCTATATGGTAACA	CACTGTATAAACTCCTGTTTGCTCTATCTT	C	T
	A1_BA_grs_68273_327	GAAGGTGACCAAGTTCATGCTGTCTCACGAATGCTATATCATCAATG	GAAGGTCGGAGTCAACGGATTAATGTCTCACGAATGCTATATCATCAATA	GGCAAGTTAATGATGCAAACTATGTACGAA	C	T
	A1_BA_grs_76755_240	GAAGGTGACCAAGTTCATGCTGTATTGTCACAAGAGCTTCCAAGTAC	GAAGGTCGGAGTCAACGGATTGTATTGTCACAAGAGCTTCCAAGTAA	TGAAAGAGCAAGTGGTCCTTATGTTTGTT	G	T
*	A1_BA_grs_52899_364	GAAGGTGACCAAGTTCATGCTGGTTTGGCATGGTTGCGACAG	GAAGGTCGGAGTCAACGGATTGGTTTGGCATGGTTGCGACAT	TATTCCTTGCACTGAGCAAGAACATGAT	G	T
	A1_BA_grs_23029_265	GAAGGTGACCAAGTTCATGCTGCCTCTGCCAGTACTGGACAG	GAAGGTCGGAGTCAACGGATTGCCTCTGCCAGTACTGGACAT	GCATCATCTCCCTCAAGGCCTAAT	G	T
*	A1_BA_grs_51174_295	GAAGGTGACCAAGTTCATGCTGCACTGTCAGTCACGTATTTGCC	GAAGGTCGGAGTCAACGGATTGCACTGTCAGTCACGTATTTGCT	ACCCGACACTTTGCCGAGTATCTAA	C	T
	A1_BA_grs_45013_235	GAAGGTGACCAAGTTCATGCTGAGCTTCATGATGAGTGTTGGTAC	GAAGGTCGGAGTCAACGGATTTGAGCTTCATGATGAGTGTTGGTAA	GGCCAAGGCCACCTTATATAAGAGTA	G	T
*	A1_BA_grs_104239_330	GAAGGTGACCAAGTTCATGCTGAACTCACATAAGAAGAATGGTGAGG	GAAGGTCGGAGTCAACGGATTAGAACTCACATAAGAAGAATGGTGAGA	GCTTTATTTATAAAGCAGGACGAAAGCCTA	C	T
*	A1_BA_grs_31972_334	GAAGGTGACCAAGTTCATGCTGAACTATTTCTCTAATTGTAGTACCAAATATG	GAAGGTCGGAGTCAACGGATTAGAACTATTTCTCTAATTGTAGTACCAAATATT	CGATTGGAATCGACGTCATGTTTAACTAA	G	T
	A1_BA_grs_42785_298	GAAGGTGACCAAGTTCATGCTCGTTATTGTTGAGGTTGAGGAGC	GAAGGTCGGAGTCAACGGATTGTCGTTATTGTTGAGGTTGAGGAGA	CCACCATAATGGGGACCAACAAGTT	G	T
	A1_BA_grs_33681_351	GAAGGTGACCAAGTTCATGCTCGAGCAATCCCTGACATCACC	GAAGGTCGGAGTCAACGGATTGCGAGCAATCCCTGACATCACT	GCAGAGAAGCTCAACGTGGTTGTAA	C	T
	A1_BA_grs_57629_198	GAAGGTGACCAAGTTCATGCTCCGTCTGCCGACATAAAGCAG	GAAGGTCGGAGTCAACGGATTGCCGTCTGCCGACATAAAGCAA	AGGTTACAGAGAGATATGCCGGCAA	C	T
	A1_BA_grs_30011_326	GAAGGTGACCAAGTTCATGCTCCCGTTGGCAGTTCTCTATGC	GAAGGTCGGAGTCAACGGATTCCCCGTTGGCAGTTCTCTATGA	CTACTCAACTTCAGTCATAAGTAAGCTCTT	G	T
	A1_BA_grs_11721_341	GAAGGTGACCAAGTTCATGCTCCAGATACAGTGGAAGCCCAC	GAAGGTCGGAGTCAACGGATTGTCCAGATACAGTGGAAGCCCAT	GTCCGTAGGCCACTCGAAGTCTT	C	T
*	A1_BA_grs_29686_290	GAAGGTGACCAAGTTCATGCTCACATCGCTGCACTCGCCG	GAAGGTCGGAGTCAACGGATTCTCACATCGCTGCACTCGCCA	AGTGGTGACCTTCTTGCTGCCG	C	T
*	A1_BA_grs_108332_177	GAAGGTGACCAAGTTCATGCTCACACTAAAGAGGTTCACAATCGG	GAAGGTCGGAGTCAACGGATTGACACACTAAAGAGGTTCACAATCGT	GTGTTGATGGCGAGCAAGATGATGAT	G	T

	A1_BA_grs_55725_301	GAAGGTGACCAAGTTCATGCTATAATCACATTATTATGAAAATAGTGTTTTCTG	GAAGGTCGGAGTCAACGGATTATAATCACATTATTATGAAAATAGTGTTTTCTA	TGCAAATCCAGTGTTGTCATCGCCT	C	T
	A1_BA_grs_14646_143	GAAGGTGACCAAGTTCATGCTAAGCCAAGACTAATCCGTTGGATTC	GAAGGTCGGAGTCAACGGATTATAAGCCAAGACTAATCCGTTGGATTA	TTCTTGCCTCTGCATAATCTACAACTCAA	G	T
	A1_BA_grs_15500_194	GAAGGTGACCAAGTTCATGCTAAATCTAATCTTGGAGATTGCGGGC	GAAGGTCGGAGTCAACGGATTAAAAATCTAATCTTGGAGATTGCGGGA	CGGAAGGCTTTAGCAACCAACGAT	G	T
	A1_BA_grs_15562_330	GAAGGTGACCAAGTTCATGCTTTTCATGAGTTCTTCTTCTTCTTTTCCTA	GAAGGTCGGAGTCAACGGATTCATGAGTTCTTCTTCTTCTTTTCCTG	ACCACCCCCAGAATTGAAGACTCTA	G	A
*	A1_BA_grs_47963_340	GAAGGTGACCAAGTTCATGCTTTGGGAAACCTGAGTGGCACA	GAAGGTCGGAGTCAACGGATTTGGGAAACCTGAGTGGCACC	CAAGTATCATTTCATGACTGAATGATCAAA	C	A
	A1_BA_grs_82362_346	GAAGGTGACCAAGTTCATGCTTGTCTATTGGATATTGATGCTTTGTTGAT	GAAGGTCGGAGTCAACGGATTGTCTATTGGATATTGATGCTTTGTTGAA	GGAAATTGTTCAAACTATTTTTTGTTGCAA	T	A
*	A1_BA_grs_17512_343	GAAGGTGACCAAGTTCATGCTTGGAAACAAGTATATCGAGGCACA	GAAGGTCGGAGTCAACGGATTGGAAACAAGTATATCGAGGCACG	GTATACCTTTTCACCAACTTTGTGTTCTTT	G	A
	A1_BA_grs_37686_300	GAAGGTGACCAAGTTCATGCTTCTCCTCCCTTCAAAGTTTCATCAT	GAAGGTCGGAGTCAACGGATTCTCCTCCCTTCAAAGTTTCATCAC	GTCGGCTGAAGGAAAGCTTACCAAT	G	A
	A1_BA_grs_53832_345	GAAGGTGACCAAGTTCATGCTTATAGTGATTTATACCAGGAGTAGGATTT	GAAGGTCGGAGTCAACGGATTAGTGATTTATACCAGGAGTAGGATTC	CGAGGTAACACATCTTACCCAGGTT	G	A
*	A1_BA_grs_17654_297	GAAGGTGACCAAGTTCATGCTTAACTGTAGTTACAAATTTTCATCCTCCA	GAAGGTCGGAGTCAACGGATTACTGTAGTTACAAATTTTCATCCTCCG	GCAAAACACAGTTGGTTACCCTACTTAAA	G	A
	A1_BA_grs_48743_286	GAAGGTGACCAAGTTCATGCTGTTTAGAGAGGTGGAGGAAGGCA	GAAGGTCGGAGTCAACGGATTTAGAGAGGTGGAGGAAGGCG	ACCTGGGTAAGCTGTGTTACCTCAT	G	A
	A1_BA_grs_19468_239	GAAGGTGACCAAGTTCATGCTGTACGGGAAACCTCTCGTCAGA	GAAGGTCGGAGTCAACGGATTACGGGAAACCTCTCGTCAGG	CCTTCCTTTCTGGCTTTAATGTACCAATT	G	A
	A1_BA_grs_46375_216	GAAGGTGACCAAGTTCATGCTGGGTCGGCTGTCCGAGT	GAAGGTCGGAGTCAACGGATTGGGTCGGCTGTCCGAGC	CTCACCCCGAAGAACCGAGCTA	G	A
*	A1_BA_grs_27368_222	GAAGGTGACCAAGTTCATGCTGGGACCACTTCAAAGGTCATGCA	GAAGGTCGGAGTCAACGGATTGGACCACTTCAAAGGTCATGCG	GGCGAGATTAAACCTCGACATCAATAATT	G	A
	A1_BA_grs_87512_320	GAAGGTGACCAAGTTCATGCTGGCAATGATGCGATCCTTTTTGTCAT	GAAGGTCGGAGTCAACGGATTGCAATGATGCGATCCTTTTTGTCAC	CGACCCTCGCCATACTTGCGAA	G	A
	A1_BA_grs_76379_100	GAAGGTGACCAAGTTCATGCTGGAATGGACTGGATGACTAAGCAA	GAAGGTCGGAGTCAACGGATTGAATGGACTGGATGACTAAGCAC	AGTGAGACAGTATGGTTTGCACAATCTAT	C	A
	A1_BA_grs_55883_168	GAAGGTGACCAAGTTCATGCTGCGAAATCATCACACGCTGCAGT	GAAGGTCGGAGTCAACGGATTCGAAATCATCACACGCTGCAGC	ACTACGAATGTGAGCGCTACACGTT	G	A
*	A1_BA_grs_106036_155	GAAGGTGACCAAGTTCATGCTGCCGAGCAGCTTCATCACGA	GAAGGTCGGAGTCAACGGATTGCCGAGCAGCTTCATCACGG	GCGGCCATGGCGCAGAGCT	G	A
	A1_BA_grs_106092_190	GAAGGTGACCAAGTTCATGCTGCCATTCATATATCCAATATGACAAGCAT	GAAGGTCGGAGTCAACGGATTCCATTCATATATCCAATATGACAAGCAC	CTTAAGGAATAGTCGATCCCATTTGTGAA	G	A
*	A1_BA_grs_49262_176	GAAGGTGACCAAGTTCATGCTGCCACCAATTTAGCCTGGCACA	GAAGGTCGGAGTCAACGGATTCCACCAATTTAGCCTGGCACG	ATGGAGGCCTCAGCAAATCTGTCTT	G	A
	A1_BA_grs_81051_272	GAAGGTGACCAAGTTCATGCTGCCAAGAAGATCTACAACAAGGCT	GAAGGTCGGAGTCAACGGATTCCAAGAAGATCTACAACAAGGCC	TCATGAGAGATTCAGGGGCGAGAA	G	A
	A1_BA_grs_50029_251	GAAGGTGACCAAGTTCATGCTGAAATCGGTACCACTTTCTGGCA	GAAGGTCGGAGTCAACGGATTGAAATCGGTACCACTTTCTGGCC	GGAGCAGGGAGGTGGTGAGATA	C	A
	A1_BA_grs_13399_237	GAAGGTGACCAAGTTCATGCTGAAAGAGCAATCAAAGCAAAATCTTTTTGA	GAAGGTCGGAGTCAACGGATTAAAGAGCAATCAAAGCAAAATCTTTTTGG	CTTTGGTTTGCGTCATCCTTTTTAGCTT	G	A
	A1_BA_grs_49013_332	GAAGGTGACCAAGTTCATGCTCGTGGCTCAGGATTTGTTTTTAAAAACAT	GAAGGTCGGAGTCAACGGATTGTGGCTCAGGATTTGTTTTTAAAAACAG	GGTGTGTATCAAAAGTTATGAATTTTGCAA	C	A
	A1_BA_grs_57545_273	GAAGGTGACCAAGTTCATGCTCGGTCAAGCTTTCCGACTTGCAT	GAAGGTCGGAGTCAACGGATTGGTCAAGCTTTCCGACTTGCAC	CTTCCAGTCCTCGATAAGCTTTGGAA	G	A
	A1_BA_grs_28284_295	GAAGGTGACCAAGTTCATGCTCCCAATGCACTTGGCCTCCA	GAAGGTCGGAGTCAACGGATTCCCAATGCACTTGGCCTCCG	ATCTGGAGTGTTATGGATCTTGATGAGAA	G	A
*	A1_BA_grs_20229_336	GAAGGTGACCAAGTTCATGCTCCATAACCATTATCAACACCAAGACAAT	GAAGGTCGGAGTCAACGGATTCATAACCATTATCAACACCAAGACAAG	AGTAGTTTAGGTATAATTTTTATCCCTCTT	C	A
	A1_BA_grs_108819_315	GAAGGTGACCAAGTTCATGCTCAGGCCATCCAAGGGTGTATCA	GAAGGTCGGAGTCAACGGATTAGGCCATCCAAGGGTGTATCG	AGGTGAACTCGCCCCTCTCCTT	G	A
	A1_BA_grs_41506_242	GAAGGTGACCAAGTTCATGCTCAAGTTGTCCACCTCTGAGCA	GAAGGTCGGAGTCAACGGATTCAAGTTGTCCACCTCTGAGCG	GAGCCTCGGGGCTCCACCAA	G	A
*	A1_BA_grs_33475_433	GAAGGTGACCAAGTTCATGCTCAAGTACATCCAGAATTTCACAATCATCA	GAAGGTCGGAGTCAACGGATTAGTACATCCAGAATTTCACAATCATCG	CACACTCGAAACCCCTTACGAGATT	G	A
	A1_BA_grs_77365_188	GAAGGTGACCAAGTTCATGCTCAACAAACATAAGGACCACTTGCTCT	GAAGGTCGGAGTCAACGGATTCAACAAACATAAGGACCACTTGCTCA	GGAAGCAAAAACAACCAGGGTGCAA	T	A
	A1_BA_grs_104834_200	GAAGGTGACCAAGTTCATGCTCAAATCACCTTGAAACGATATAGCATCT	GAAGGTCGGAGTCAACGGATTAAATCACCTTGAAACGATATAGCATCC	CTTCAGGGCTCTTAGCTCAATTTGCTT	G	A
	A1_BA_grs_26569_191	GAAGGTGACCAAGTTCATGCTATTCTTGAAGTAAAAGGATCCAACGGT	GAAGGTCGGAGTCAACGGATTCTTGAAGTAAAAGGATCCAACGGA	GTTTAAAAAGAACTCCTCGAGAGGAAGTT	T	A
	A1_BA_grs_87873_178	GAAGGTGACCAAGTTCATGCTAGATGCTCATTGTCTGCTTGCCTTA	GAAGGTCGGAGTCAACGGATTATGCTCATTGTCTGCTTGCCTTG	CCCCTTTGCACATGATATAGGAGCTA	G	A
	A1_BA_grs_38692_386	GAAGGTGACCAAGTTCATGCTAAAGCTCGAATTGATAATAAGAAGGAGA	GAAGGTCGGAGTCAACGGATTAAAGCTCGAATTGATAATAAGAAGGAGT	GGCCTCTTATTTAGTTTTGCAAAGTGGAA	T	A
	A1_BA_grs_22275_310	GAAGGTGACCAAGTTCATGCTAAAATTCTTGAAGTAAAAGGATCCAACGA	GAAGGTCGGAGTCAACGGATTAATTCTTGAAGTAAAAGGATCCAACGG	CAGATCGTGATGGTTTAAAAGAACTCCTT	G	A

*	A1_BA_grs_78315_333	GAAGGTGACCAAGTTCATGCTTTGAAAGCATAGGATTATATCATGTGTG	GAAGGTCGGAGTCAACGGATTTGAAAGCATAGGATTATATCATGTGTC	GCTCTATTTTCTGGATATCAACTGGCAAA	G	C
	A1_BA_grs_104383_178	GAAGGTGACCAAGTTCATGCTTCGTCCTTATGTTCATCATCAATGTG	GAAGGTCGGAGTCAACGGATTCGTCCTTATGTTCATCATCAATGTC	ATATTATGATGCTGATCAAGCACCTGCTT	G	C
*	A1_BA_grs_55797_98	GAAGGTGACCAAGTTCATGCTGTGTTTTGTTTTGTTTTGCTGGCAGC	GAAGGTCGGAGTCAACGGATTGTGTTTTGTTTTGTTTTGCTGGCAGG	CAGCACCACAGCCACCACACAA	G	C
	A1_BA_grs_64929_127	GAAGGTGACCAAGTTCATGCTGTCTTGCGATACTCATACCCCG	GAAGGTCGGAGTCAACGGATTGTCTTGCGATACTCATACCCCC	GTTCAGTATGTTGGATGCCATACACATAT	G	C
	A1_BA_grs_65123_174	GAAGGTGACCAAGTTCATGCTGAACACACATCCAATGACACTGG	GAAGGTCGGAGTCAACGGATTGAACACACATCCAATGACACTGC	ACCAGTGTCATTGCTTGTGTGTTCTTTT	G	C
	A1_BA_grs_24275_303	GAAGGTGACCAAGTTCATGCTATAAATTAATGAAGGGCTTTCCACTCC	GAAGGTCGGAGTCAACGGATTATAAATTAATGAAGGGCTTTCCACTCG	GACCTATGTTCGGAGAGGAACATGTA	G	C
*	A1_BA_grs_66143_217	GAAGGTGACCAAGTTCATGCTACGCTAAACTGGTGAAGCCTCG	GAAGGTCGGAGTCAACGGATTACGCTAAACTGGTGAAGCCTCC	AGCCCGCTTCCTGACTGACGAA	G	C
*	A1_BA_grs_69435_346	GAAGGTGACCAAGTTCATGCTTTTATCCCTTTTAAAGTAGTATATGCATTTTG	GAAGGTCGGAGTCAACGGATTTTATCCCTTTTAAAGTAGTATATGCATTTTA	TGGTGTACCAATCTGGACTACAGGT	G	A
	A1_BA_grs_28357_220	GAAGGTGACCAAGTTCATGCTTTGTCAACGAGGCGAGGTTGC	GAAGGTCGGAGTCAACGGATTGTTTGTCAACGAGGCGAGGTTGT	CGTCTAACCGTACCTTCCGTTTTCTT	C	T
*	A1_BA_grs_58549_127	GAAGGTGACCAAGTTCATGCTTGGTCAAGTATAGCTGAAGGCG	GAAGGTCGGAGTCAACGGATTGTTGGTCAAGTATAGCTGAAGGCA	GGAGTTTCTTGGCTAAACCACGGAA	C	T
	A1_BA_grs_25090_353	GAAGGTGACCAAGTTCATGCTTGCGGCGTCGAATCGG	GAAGGTCGGAGTCAACGGATTATAGCTTGCGGCGTCGAATCGA	CCAGTGGCCTTCCCACATGGTA	C	T
*	A1_BA_grs_73080_380	GAAGGTGACCAAGTTCATGCTTCTTGTTATCATGGTGATGGTTACTG	GAAGGTCGGAGTCAACGGATTCTTGTTATCATGGTGATGGTTACTA	GGTGAAGATAGTGGAGGTTCTGGAT	C	T
	A1_BA_grs_17541_108	GAAGGTGACCAAGTTCATGCTTAGAGGAGAAACAATAGCAAAAGTGG	GAAGGTCGGAGTCAACGGATTAAATTAGAGGAGAAACAATAGCAAAAGTGT	TTGGGGGGAGTTGATACGTCCAAAA	G	T
	A1_BA_grs_17488_98	GAAGGTGACCAAGTTCATGCTGTACGAAATAGGAGCCTCGCTTC	GAAGGTCGGAGTCAACGGATTGTACGAAATAGGAGCCTCGCTTT	TTTAGTTTCCTAACCGTGCAAAAGCACTT	C	T
	A1_BA_grs_54566_260	GAAGGTGACCAAGTTCATGCTGTACCAGTAGTTATCACTGCACG	GAAGGTCGGAGTCAACGGATTCGTACCAGTAGTTATCACTGCACA	TAAAGGTTATCATGAAGTCATGATTGCCAT	C	T
	A1_BA_grs_32763_100	GAAGGTGACCAAGTTCATGCTGGTGGGCATCTTTGAATCGTTTC	GAAGGTCGGAGTCAACGGATTCTGGTGGGCATCTTTGAATCGTTTA	TATGCATATTTTAGCGATTCCCGCCAAA	G	T
	A1_BA_grs_61439_255	GAAGGTGACCAAGTTCATGCTGGTCTCACGCCGGATCCAG	GAAGGTCGGAGTCAACGGATTGGGTCTCACGCCGGATCCAT	TCTTGGACGACATGATGGAGTGCAT	G	T
*	A1_BA_grs_33565_235	GAAGGTGACCAAGTTCATGCTGGTCGCCGGTGACGACAG	GAAGGTCGGAGTCAACGGATTGATGGTCGCCGGTGACGACAT	CGTGCATGCTGGGGTGGCCT	G	T
	A1_BA_grs_107959_119	GAAGGTGACCAAGTTCATGCTGGCAGCATCAAGCCGAGCTG	GAAGGTCGGAGTCAACGGATTGGCAGCATCAAGCCGAGCTA	AGCCTGGCAATCTCGTTGTCCTTA	C	T
	A1_BA_grs_17900_168	GAAGGTGACCAAGTTCATGCTGGAATTGAATTTAGTTCATCAAATAATTCCC	GAAGGTCGGAGTCAACGGATTAGGAATTGAATTTAGTTCATCAAATAATTCCT	GAAGACACCAATCTTATTGAGAGGAACTT	C	T
*	A1_BA_grs_20445_361	GAAGGTGACCAAGTTCATGCTGGAACAGGGAGGAGTCCACG	GAAGGTCGGAGTCAACGGATTGGGAACAGGGAGGAGTCCACA	GGCATTTCTTTCGTGGCTGGGAAT	C	T
*	A1_BA_grs_34954_398	GAAGGTGACCAAGTTCATGCTGATGATGTTCTCATTTGGAGAGTCG	GAAGGTCGGAGTCAACGGATTGATGATGTTCTCATTTGGAGAGTCA	CATATCCACCACATCTGCACCTACTA	C	T
	A1_BA_grs_71948_359	GAAGGTGACCAAGTTCATGCTGAGGATAGGGCAAAGGGCGC	GAAGGTCGGAGTCAACGGATTGAGGATAGGGCAAAGGGCGT	CGCTCTGCAGCCCAAGGATGAT	C	T
	A1_BA_grs_16376_362	GAAGGTGACCAAGTTCATGCTGAGCTTGACAACCTCATTGATTCG	GAAGGTCGGAGTCAACGGATTGTGAGCTTGACAACCTCATTGATTCA	CGGAGACCTGCACAACACAAACTAA	C	T
	A1_BA_grs_44192_96	GAAGGTGACCAAGTTCATGCTGACAACGATCCTTCGGCATACG	GAAGGTCGGAGTCAACGGATTCGACAACGATCCTTCGGCATACA	CATCTTGTTTGTCGATGTAGAAGTGGAT	C	T
	A1_BA_grs_106873_135	GAAGGTGACCAAGTTCATGCTGAATTATTTAATGAACTAAAGTCAATTCCTAC	GAAGGTCGGAGTCAACGGATTGGAATTATTTAATGAACTAAAGTCAATTCCTAA	GGGATGAAAAGTTCCTCCCACAACAA	G	T
*	A1_BA_grs_41558_347	GAAGGTGACCAAGTTCATGCTGAAGCCTTGACCATCAAACCACC	GAAGGTCGGAGTCAACGGATTGAAGCCTTGACCATCAAACCACA	CCAACTTGGTTCGTGAAGATTGGTCTT	G	T
*	A1_BA_grs_12742_306	GAAGGTGACCAAGTTCATGCTCTTAAGGAGTTCTTTTAAACCATCAC	GAAGGTCGGAGTCAACGGATTCCTCTTAAGGAGTTCTTTTAAACCATCAT	TCTTATATAGTGGATGCAAACATAAGAGTT	C	T
*	A1_BA_grs_89279_219	GAAGGTGACCAAGTTCATGCTCTCCGACATGGAATCTCTG	GAAGGTCGGAGTCAACGGATTGCTCTCCGACATGGAATCTCTA	CGAGGAACTCGTGGCCGACAA	C	T
	A1_BA_grs_18240_323	GAAGGTGACCAAGTTCATGCTCGTTTAAAGAAAGTACAAGAGAGTAGC	GAAGGTCGGAGTCAACGGATTGTCGTTTAAAGAAAGTACAAGAGAGTAGT	CCTATAGTTTCACGTTTCGTCAGTTACTT	C	T
	A1_BA_grs_31946_269	GAAGGTGACCAAGTTCATGCTCGTGCATCAGCCTATGCTTGAAC	GAAGGTCGGAGTCAACGGATTATCGTGCATCAGCCTATGCTTGAAA	GTATGTTCTGTGACTCAACTGCCCTT	G	T
	A1_BA_grs_15319_288	GAAGGTGACCAAGTTCATGCTCGTCGTTCGCCCCCATCG	GAAGGTCGGAGTCAACGGATTCTTCGTCGTTCGCCCCCATCA	GACGAGCAACTCTGGCGAGGAA	C	T
	A1_BA_grs_26253_268	GAAGGTGACCAAGTTCATGCTCCGAGGTAGGTGGAACTTCAG	GAAGGTCGGAGTCAACGGATTCTCCGAGGTAGGTGGAACTTCAA	TCGGGCTTCCTCCGAAGTCGTT	C	T
*	A1_BA_grs_21711_378	GAAGGTGACCAAGTTCATGCTCCAAGGCATATCCCATGATGGC	GAAGGTCGGAGTCAACGGATTAACCAAGGCATATCCCATGATGGT	TTAGTAGGGGGCGTTGTGAAGCTAT	C	T
*	A1_BA_grs_16610_132	GAAGGTGACCAAGTTCATGCTCACTAATAATAACAGGAAACTTATTTGTATCG	GAAGGTCGGAGTCAACGGATTCACTAATAATAACAGGAAACTTATTTGTATCA	GACTCTGCCAGATAATCTTAAATATAGATT	C	T
*	A1_BA_grs_37835_343	GAAGGTGACCAAGTTCATGCTCACCACTCATAGCAGTTCG	GAAGGTCGGAGTCAACGGATTGGCTCACCACTCATAGCAGTTCT	TTCTATCTACCAAGAAATCAAGGTAAGGTT	G	T

*	A1_BA_grs_62752_296	GAAGGTGACCAAGTTCATGCTCAAGGACAAAAATTATGGGCATGCTC	GAAGGTCGGAGTCAACGGATTACAAGGACAAAAATTATGGGCATGCTT	CGGTTCGTTCCTTCAAAAATCTTGTGTAT	C	T
*	A1_BA_grs_54542_325	GAAGGTGACCAAGTTCATGCTCAAGGAACTCATAAGTGAGCTCAG	GAAGGTCGGAGTCAACGGATTGCAAGGAACTCATAAGTGAGCTCAA	GCCAGGCTAACACTACTCGGCTA	C	T
	A1_BA_grs_52434_323	GAAGGTGACCAAGTTCATGCTCAAAATTTGACGCATTCCATCCTGTC	GAAGGTCGGAGTCAACGGATTCAAAATTTGACGCATTCCATCCTGTA	GAGAACATTTATCGGATGTTCAGCAACAA	G	T
*	A1_BA_grs_37064_170	GAAGGTGACCAAGTTCATGCTATGATGAATACTTCAATTTATATCATGGAATG	GAAGGTCGGAGTCAACGGATTATGATGAATACTTCAATTTATATCATGGAATA	CTTTATTTCCGTAATTCTAAATTCGACAAA	C	T
*	A1_BA_grs_43173_121	GAAGGTGACCAAGTTCATGCTATACTAAATAGTAGGTGAGCATGATTAAAG	GAAGGTCGGAGTCAACGGATTCATACTAAATAGTAGGTGAGCATGATTAAAT	TGGGTATCCCACCATTTAAATGTCATGTA	G	T
	A1_BA_grs_35479_123	GAAGGTGACCAAGTTCATGCTAGAGTGCGTCGGCGTCCTC	GAAGGTCGGAGTCAACGGATTGAGAGTGCGTCGGCGTCCTT	GCAAGCTACTCCGTCGAGTGGAT	C	T
*	A1_BA_grs_39532_207	GAAGGTGACCAAGTTCATGCTACTGACAAATGACGATAAGCAGTCG	GAAGGTCGGAGTCAACGGATTAAACTGACAAATGACGATAAGCAGTCA	GGCAAGGTGCTGCTCGATCGAA	C	T
	A1_BA_grs_25032_323	GAAGGTGACCAAGTTCATGCTACTCAAATTCTTGTAGTGAAATAATCCAAC	GAAGGTCGGAGTCAACGGATTCAACTCAAATTCTTGTAGTGAAATAATCCAAT	GGCTTATAAAAGAACTCCTTGAGAGGAAA	C	T
*	A1_BA_grs_66445_250	GAAGGTGACCAAGTTCATGCTACACCATGTGATTACTTAGTGTAGTTC	GAAGGTCGGAGTCAACGGATTATACACCATGTGATTACTTAGTGTAGTTT	GGTTTACTCAAGCAGAGTAATCTTCAGAT	C	T
	A1_BA_grs_25523_231	GAAGGTGACCAAGTTCATGCTAAGGACCATACCTGGGACCAC	GAAGGTCGGAGTCAACGGATTGAAGGACCATACCTGGGACCAT	CTTTGGGGTAAGTTGCGGACCATAT	C	T
*	A1_BA_grs_38210_262	GAAGGTGACCAAGTTCATGCTAAAGTCGAAGAAGGCCTCCG	GAAGGTCGGAGTCAACGGATTAAAGTCGAAGAAGGCCTCCA	GTGCCTCCACTTGCCATCGGTA	C	T
*	A1_BA_grs_103930_312	GAAGGTGACCAAGTTCATGCTTTAGATTATTATTTTTGCATTGTTGTGGTAGT	GAAGGTCGGAGTCAACGGATTAGATTATTATTTTTGCATTGTTGTGGTAGG	AAGGTGCGCGTGAACGCCGTAA	C	A
	A1_BA_grs_42341_263	GAAGGTGACCAAGTTCATGCTTGGCTTTGTCCCTCACCTCGA	GAAGGTCGGAGTCAACGGATTGGCTTTGTCCCTCACCTCGT	TTGAAGAGGCTGGCGAGTCGGT	T	A
	A1_BA_grs_44304_291	GAAGGTGACCAAGTTCATGCTTGCTTCCCTTCTGCCTTTTATGT	GAAGGTCGGAGTCAACGGATTGCTTCCCTTCTGCCTTTTATGC	CTCAGTCTGTAGTTGTTTTGCAGATACAT	G	A
	A1_BA_grs_105064_241	GAAGGTGACCAAGTTCATGCTTCTCGCTCTGGGTGATGTTA	GAAGGTCGGAGTCAACGGATTCTTCTCGCTCTGGGTGATGTTC	ATTGAGAAACAGGGCAATCAAAATAT	C	A
	A1_BA_grs_25522_236	GAAGGTGACCAAGTTCATGCTTCTCCATGGTCTACAGCCAGTT	GAAGGTCGGAGTCAACGGATTCTCCATGGTCTACAGCCAGTC	CCCATATTTAGTAAGTCTGAAGAGCCATT	G	A
	A1_BA_grs_63023_280	GAAGGTGACCAAGTTCATGCTTCCCCCTGATTTTTGCATTCATCAA	GAAGGTCGGAGTCAACGGATTCCCCCTGATTTTTGCATTCATCAC	GGATGACATGTATTCTGTAACATCCCAAT	C	A
	A1_BA_grs_41826_354	GAAGGTGACCAAGTTCATGCTTATTAGATGAACTAAGGTTAATTCCTCCA	GAAGGTCGGAGTCAACGGATTAGATGAACTAAGGTTAATTCCTCCC	TTCGAGGATGACAAGCTCCTCCAAA	C	A
*	A1_BA_grs_103172_292	GAAGGTGACCAAGTTCATGCTTATCGAGATAGTCGCAAAATACTGT	GAAGGTCGGAGTCAACGGATTATCGAGATAGTCGCAAAATACTGC	TAGCCCCAGATGTCGCGGTCTT	G	A
	A1_BA_grs_46030_403	GAAGGTGACCAAGTTCATGCTGTTTTTTATCTTAGTTAAGATACACTATTTGT	GAAGGTCGGAGTCAACGGATTGTTTTTTATCTTAGTTAAGATACACTATTTGC	ATGCATTTGATTGGACTATCAACCTTCTTT	G	A
	A1_BA_grs_44585_160	GAAGGTGACCAAGTTCATGCTGTGTTGTAATTCATATGCCACTAATCCA	GAAGGTCGGAGTCAACGGATTGTTGTAATTCATATGCCACTAATCCG	GCCCCAGGAACATGGGGAACTA	G	A
*	A1_BA_grs_31405_329	GAAGGTGACCAAGTTCATGCTGTGCAGAGGGGCTTAAGTAGGT	GAAGGTCGGAGTCAACGGATTGCAGAGGGGCTTAAGTAGGC	CGCGTCGCCGCTGCCGTT	G	A
	A1_BA_grs_40232_385	GAAGGTGACCAAGTTCATGCTGTGAGGGCGAGCTCCGACTT	GAAGGTCGGAGTCAACGGATTGAGGGCGAGCTCCGACTC	CGCAGAGCTGGGAAGTGACGAA	G	A
*	A1_BA_grs_108989_325	GAAGGTGACCAAGTTCATGCTGTCCTTCCAGTCGGACACCTTT	GAAGGTCGGAGTCAACGGATTCCTTCCAGTCGGACACCTTC	CTCATAAGCACGAGTTGGAGCGATA	G	A
*	A1_BA_grs_48810_294	GAAGGTGACCAAGTTCATGCTGTATCTGAGAGTTTAACGACCAACTATAA	GAAGGTCGGAGTCAACGGATTATCTGAGAGTTTAACGACCAACTATAC	GCCTATACGGGTCGCAACTATACAA	C	A
	A1_BA_grs_106419_97	GAAGGTGACCAAGTTCATGCTGGGCCACTTGCTCTGTTTGTTCA	GAAGGTCGGAGTCAACGGATTGGCCACTTGCTCTGTTTGTTCG	GCAAACAAAAACAAAGAGCAAGTAACAGAA	G	A
	A1_BA_grs_104109_202	GAAGGTGACCAAGTTCATGCTGGGCATCTGTCGGGCTGTCAT	GAAGGTCGGAGTCAACGGATTGGCATCTGTCGGGCTGTCAG	CGGCCATACCTCCAGTTCTTGTTA	C	A
	A1_BA_grs_30790_368	GAAGGTGACCAAGTTCATGCTGGATGGTTGATTCCCACAAACACTA	GAAGGTCGGAGTCAACGGATTGATGGTTGATTCCCACAAACACTG	CTTGTAGCACCGGACTTGATCAGAA	G	A
*	A1_BA_grs_85184_509	GAAGGTGACCAAGTTCATGCTGGAATTGATCGCGGCATTCACTT	GAAGGTCGGAGTCAACGGATTGGAATTGATCGCGGCATTCACTC	CTCTCTGCCGTTTTCTGCCTGTAAT	G	A
*	A1_BA_grs_109740_298	GAAGGTGACCAAGTTCATGCTGCGGGTCTCGACTTTTTGGCT	GAAGGTCGGAGTCAACGGATTGCGGGTCTCGACTTTTTGGCC	GACGAAGCGATGACTACAACAATGG	G	A
	A1_BA_grs_30146_331	GAAGGTGACCAAGTTCATGCTGCCGTAAAATATCAAGATCCTACATCTAA	GAAGGTCGGAGTCAACGGATTCCGTAAAATATCAAGATCCTACATCTAC	GCTACCTGTAACTTGTCCTTCTTAATGTA	C	A
	A1_BA_grs_79110_509	GAAGGTGACCAAGTTCATGCTGCCCGCTGAAACCCCATTCCA	GAAGGTCGGAGTCAACGGATTCCCGCTGAAACCCCATTCCC	CAGGATCAATCGGAATGTTCGCCAT	C	A
*	A1_BA_grs_55780_318	GAAGGTGACCAAGTTCATGCTGCACACAAAACATCGGAAAGGGAAA	GAAGGTCGGAGTCAACGGATTCACACAAAACATCGGAAAGGGAAG	GGATTTTTATGCTTTGTGTGTTGCAACAAA	G	A
	A1_BA_grs_107644_254	GAAGGTGACCAAGTTCATGCTGAGTCCCTCTTTTATCCTCCTTTGAT	GAAGGTCGGAGTCAACGGATTAGTCCCTCTTTTATCCTCCTTTGAC	CGGAATGCCCCCGTGACAGATT	G	A
	A1_BA_grs_47869_148	GAAGGTGACCAAGTTCATGCTGAGACCTTTCTTCTTCAGGCCGT	GAAGGTCGGAGTCAACGGATTAGACCTTTCTTCTTCAGGCCGC	CCAGCGGATGGTGGTGGATGAA	G	A
	A1_BA_grs_108107_265	GAAGGTGACCAAGTTCATGCTGACGGACATAGGGTGGTAGTGAT	GAAGGTCGGAGTCAACGGATTACGGACATAGGGTGGTAGTGAG	TTTCCAGAAGCAATCCCTCAGACCA	C	A

*	A1_BA_grs_22020_338	GAAGGTGACCAAGTTCATGCTGAAAATTCCACTCAAGATTAAAATTTTCATGTA	GAAGGTCGGAGTCAACGGATTAAAATTCCACTCAAGATTAAAATTTTCATGTG	CATTTGTAAGAAGGACTTTGTTATTTAGTA	G	A
*	A1_BA_grs_108511_161	GAAGGTGACCAAGTTCATGCTGAAAAGAATCCAAAGGATCAGTCTTGA	GAAGGTCGGAGTCAACGGATTAAAAGAATCCAAAGGATCAGTCTTGG	CTCTTGTTATAAATTTTGTTCCTATTTAGT	G	A
	A1_BA_grs_46464_325	GAAGGTGACCAAGTTCATGCTCTCCTACATACAACAAGAGACCGT	GAAGGTCGGAGTCAACGGATTCCTACATACAACAAGAGACCGG	GCTCAAGTGGAATGCTCAAGGCAAA	C	A
	A1_BA_grs_26548_143	GAAGGTGACCAAGTTCATGCTCGTTTACGAGAATTATTAAATGAATTAAGGTT	GAAGGTCGGAGTCAACGGATTCGTTTACGAGAATTATTAAATGAATTAAGGTC	CAACAAAGACTTCTTCTCTTTTAGAGGAAT	G	A
	A1_BA_grs_43072_300	GAAGGTGACCAAGTTCATGCTCGCCCCTGCGCACAACACTA	GAAGGTCGGAGTCAACGGATTGCCCCTGCGCACAACACTG	CGCAGGTCGGTGTCGCGCAT	G	A
*	A1_BA_grs_77838_125	GAAGGTGACCAAGTTCATGCTCCTAATTGCTGGTGATGATAATTTCTCA	GAAGGTCGGAGTCAACGGATTCTAATTGCTGGTGATGATAATTTCTCG	CCATATATAATGCAGAGGTCAGGGAAATA	G	A
	A1_BA_grs_71750_324	GAAGGTGACCAAGTTCATGCTCCGCAACCTGAGTCGAACCAT	GAAGGTCGGAGTCAACGGATTCCGCAACCTGAGTCGAACCAC	CGAATACAGAAGCAAAAGAAGAGACGAAA	G	A
	A1_BA_grs_48295_384	GAAGGTGACCAAGTTCATGCTCCGAGACCACCTTGGTGACCA	GAAGGTCGGAGTCAACGGATTCGAGACCACCTTGGTGACCG	GTGGTCCTCGGTGAAGGTGCAA	G	A
	A1_BA_grs_54151_274	GAAGGTGACCAAGTTCATGCTCCCTGCAAACTGTCCATGTGAGT	GAAGGTCGGAGTCAACGGATTCCTGCAAACTGTCCATGTGAGC	TCCTACTTCTTCAAGGGCCGTCAAT	G	A
*	A1_BA_grs_39304_279	GAAGGTGACCAAGTTCATGCTCCACGCGCAATAGTAAATAAAGT	GAAGGTCGGAGTCAACGGATTCTCCACGCGCAATAGTAAATAAAGC	CTAATGTAATGCATGCATGCAATGCTCAA	G	A
	A1_BA_grs_104526_322	GAAGGTGACCAAGTTCATGCTCCACACCACAAGCTTATTGATTACATT	GAAGGTCGGAGTCAACGGATTCACACCACAAGCTTATTGATTACATC	TCTTGCATGTGTGCAACTTTAACTGACA	G	A
	A1_BA_grs_56627_343	GAAGGTGACCAAGTTCATGCTCATTTTGACTGAGAGTAAAATTATGCATTTAAA	GAAGGTCGGAGTCAACGGATTCATTTTGACTGAGAGTAAAATTATGCATTTAAT	ATGAAACAATGATATGGTAACACTCGCATA	T	A
	A1_BA_grs_22311_214	GAAGGTGACCAAGTTCATGCTCACCAGGACTAAAGTTCCTCTCAA	GAAGGTCGGAGTCAACGGATTCACCAGGACTAAAGTTCCTCTCAT	GCAGTGTCGATGTTTGCCCAGCAA	T	A
	A1_BA_grs_18921_322	GAAGGTGACCAAGTTCATGCTCAATCATCAGCATCCAATGGCTCTTT	GAAGGTCGGAGTCAACGGATTAATCATCAGCATCCAATGGCTCTTC	GAACTTTCAGAACACCAATCCACCCAT	G	A
*	A1_BA_grs_32531_244	GAAGGTGACCAAGTTCATGCTCAATATATAGGGGAAACTCCACCAAATA	GAAGGTCGGAGTCAACGGATTAATATATAGGGGAAACTCCACCAAATC	GGAGAGACTCCACATAATTATGTGCATAA	C	A
*	A1_BA_grs_25202_404	GAAGGTGACCAAGTTCATGCTCAAGGGAGAAGAAGTCTATGTTGTTA	GAAGGTCGGAGTCAACGGATTCAAGGGAGAAGAAGTCTATGTTGTTG	GCACTTACCATTTGCTTATTCGGGGAT	G	A
*	A1_BA_grs_38572_283	GAAGGTGACCAAGTTCATGCTATTACCGAGATTATCCCTTCTCACATT	GAAGGTCGGAGTCAACGGATTACCGAGATTATCCCTTCTCACATA	TCGGGTTGTTCAGTCTGCTAATTTTGTTT	T	A
*	A1_BA_grs_108554_271	GAAGGTGACCAAGTTCATGCTATAGCAATGCTCCCCCTGACTA	GAAGGTCGGAGTCAACGGATTATAGCAATGCTCCCCCTGACTG	CCATCTACTACCTATCGTGCATGCTT	G	A
*	A1_BA_grs_38812_220	GAAGGTGACCAAGTTCATGCTATACGGCCATAATTTTAATTTCCGCCA	GAAGGTCGGAGTCAACGGATTACGGCCATAATTTTAATTTCCGCCG	CAATTTCTTTCCCAGGTACGGAGAGTT	G	A
	A1_BA_grs_28723_184	GAAGGTGACCAAGTTCATGCTATAATTTTGTCAAGTTCTCAAGGATCCTA	GAAGGTCGGAGTCAACGGATTAATTTTGTCAAGTTCTCAAGGATCCTG	TGAAAAGCAGCGAGGGAGATAGCAT	G	A
*	A1_BA_grs_110381_96	GAAGGTGACCAAGTTCATGCTAGTTTCTTATCTGCATTTCTACGGTGT	GAAGGTCGGAGTCAACGGATTGTTTCTTATCTGCATTTCTACGGTGC	GGAGAAATGAAGAAAAAGTC	G	A
*	A1_BA_grs_15007_124	GAAGGTGACCAAGTTCATGCTAGGTCCCACCTTTATCGAAGAACT	GAAGGTCGGAGTCAACGGATTAGGTCCCACCTTTATCGAAGAACA	CCTCGCAACAACTATAGGGGATCAA	T	A
	A1_BA_grs_70372_127	GAAGGTGACCAAGTTCATGCTAGGACGATGAGATATGTGAGGTCT	GAAGGTCGGAGTCAACGGATTGGACGATGAGATATGTGAGGTCC	GCCTGGAAAGCATTGCCGAAGATAT	G	A
	A1_BA_grs_75416_305	GAAGGTGACCAAGTTCATGCTAGCATCTGGATGATCCTGACTCAT	GAAGGTCGGAGTCAACGGATTGCATCTGGATGATCCTGACTCAC	CGAAAGGCCAGATTACAGGTATGGTT	G	A
	A1_BA_grs_65058_130	GAAGGTGACCAAGTTCATGCTAGCAACACCATCAGATGCATGCT	GAAGGTCGGAGTCAACGGATTGCAACACCATCAGATGCATGCG	GTTGGAGACATCCGCTAACTCTGTA	C	A
	A1_BA_grs_45261_178	GAAGGTGACCAAGTTCATGCTACTGCCACATGGCTATCGTAAAGAA	GAAGGTCGGAGTCAACGGATTGCCACATGGCTATCGTAAAGAG	GATGAGATTATTCGGCACTTATATTTTATT	G	A
	A1_BA_grs_32215_258	GAAGGTGACCAAGTTCATGCTACTCGCCAAGTCAACTTGGCGA	GAAGGTCGGAGTCAACGGATTCTCGCCAAGTCAACTTGGCGC	CACTGCGGTACTCAGTGGTGGAA	C	A
	A1_BA_grs_54474_354	GAAGGTGACCAAGTTCATGCTACTCAGGATGGGGAGGAGAGT	GAAGGTCGGAGTCAACGGATTCTCAGGATGGGGAGGAGAGC	TCTTCTTCTTTCCTGGAGCGGCAAT	G	A
*	A1_BA_grs_34366_403	GAAGGTGACCAAGTTCATGCTACGGATCCTCTGTTCTATCCCTTA	GAAGGTCGGAGTCAACGGATTCGGATCCTCTGTTCTATCCCTTG	CCTGATGGGTATGACATTAACCCCAT	G	A
*	A1_BA_grs_81977_212	GAAGGTGACCAAGTTCATGCTACATTTTTATCTCTTCTTATTCCAAATTGTCA	GAAGGTCGGAGTCAACGGATTCATTTTTATCTCTTCTTATTCCAAATTGTCC	CAGTGAGAGCAGCGTTTTTTAGATGTAAT	C	A
	A1_BA_grs_89672_241	GAAGGTGACCAAGTTCATGCTACAATACAAGATACTTGGAAGCTCTCA	GAAGGTCGGAGTCAACGGATTCAATACAAGATACTTGGAAGCTCTCG	ATGTTTTGTGTGCAACCATAATGCCACTA	G	A
	A1_BA_grs_70258_392	GAAGGTGACCAAGTTCATGCTAAGTGCATGGTGGATTGTGGAAGT	GAAGGTCGGAGTCAACGGATTGTGCATGGTGGATTGTGGAAGC	TTCATCTTGTGAGTGTATCCAGGTACAT	G	A
	A1_BA_grs_103686_196	GAAGGTGACCAAGTTCATGCTAAGGGTGAGCTAAGTTGGCTTGAT	GAAGGTCGGAGTCAACGGATTGGGTGAGCTAAGTTGGCTTGAC	TTGGTTTCGGACCGTGAAGCTGAAA	G	A
*	A1_BA_grs_107365_310	GAAGGTGACCAAGTTCATGCTAAGAATCAAAAGTCTAAGAGTAAAAGGTAATA	GAAGGTCGGAGTCAACGGATTGAATCAAAAGTCTAAGAGTAAAAGGTAATG	ATGACCGAAATTGTACGAGTACTCAAGTA	G	A
*	A1_BA_grs_57497_370	GAAGGTGACCAAGTTCATGCTAACCCCTGACCAAAGTTTATCACCA	GAAGGTCGGAGTCAACGGATTCCCCTGACCAAAGTTTATCACCG	GTCAATTAGCGCGGTCTGTGATGAA	G	A
*	A1_BA_grs_34495_308	GAAGGTGACCAAGTTCATGCTAAAATTTCCCAAGTCACTAAACTGGAAAA	GAAGGTCGGAGTCAACGGATTAATTTCCCAAGTCACTAAACTGGAAAG	TGGCCCACCAATAATTATCTCAATTCGTT	G	A

	A1_BA_grs_24003_202	GAAGGTGACCAAGTTCATGCTTATTTGGACAATAATGTTGAGCTACTTTG	GAAGGTCGGAGTCAACGGATTATTTGGACAATAATGTTGAGCTACTTTC	AGAAATACCGACTGGACAAGCATAGATTT	G	C
	A1_BA_grs_82447_112	GAAGGTGACCAAGTTCATGCTGGTGGATCCATATGTGCGTG	GAAGGTCGGAGTCAACGGATTCTGGTGGATCCATATGTGCGTC	ACATATGGATCCACCAGAGTTAATTGCTT	G	C
*	A1_BA_grs_60346_283	GAAGGTGACCAAGTTCATGCTGAAACCAGGATAACCATGGCTCC	GAAGGTCGGAGTCAACGGATTGAAACCAGGATAACCATGGCTCG	GCATCTAATGGCTCTTCAGACTTACTAAA	G	C
*	A1_BA_grs_72874_297	GAAGGTGACCAAGTTCATGCTACCGAAAACATCAGGCACCTGC	GAAGGTCGGAGTCAACGGATTACCGAAAACATCAGGCACCTGG	CTTTCCTTGATGATACTGGGATGGGAT	G	C
*	A1_BA_grs_11463_236	GAAGGTGACCAAGTTCATGCTAAGCCCGAGGAAGATGATCCTC	GAAGGTCGGAGTCAACGGATTAAGCCCGAGGAAGATGATCCTG	CTTCATCCCCTACCAAAATCTCCTCAT	G	C
*	A1_BA_grs_87637_89	GAAGGTGACCAAGTTCATGCTTTATTTCTCCAATAACTGTCAAGGCG	GAAGGTCGGAGTCAACGGATTCTTTTATTTCTCCAATAACTGTCAAGGCA	AACACATCATCAATGCTAAAGAACAGATAT	C	T
	A1_BA_grs_29681_335	GAAGGTGACCAAGTTCATGCTTTATGAAGAACTTCGCAACAACTTAC	GAAGGTCGGAGTCAACGGATTACTTTATGAAGAACTTCGCAACAACTTAA	ACAATTTAATAATAGTCTCTACCGGTTCAA	G	T
	A1_BA_grs_36345_222	GAAGGTGACCAAGTTCATGCTTACTACCTTAAATCCAAAAATTATCGTAATG	GAAGGTCGGAGTCAACGGATTGTTACTACCTTAAATCCAAAAATTATCGTAATA	GACAAGTACTCAGTAACGAATCTGGTAAT	C	T
	A1_BA_grs_16864_246	GAAGGTGACCAAGTTCATGCTTAAGCCAAACCGGTCGGTTGG	GAAGGTCGGAGTCAACGGATTGTTAAGCCAAACCGGTCGGTTGA	CTCTCGGTCAGAAGCAGTTGGTTT	C	T
	A1_BA_grs_110839_129	GAAGGTGACCAAGTTCATGCTGTTACCGCAAGGAGGAACATTGG	GAAGGTCGGAGTCAACGGATTATGTTACCGCAAGGAGGAACATTGT	ATTTGTCAAGCCAAGTCAAGTGGATTATAT	G	T
*	A1_BA_grs_30486_344	GAAGGTGACCAAGTTCATGCTGTGACATCTTGAAATAGTCGATGAGG	GAAGGTCGGAGTCAACGGATTAGTGACATCTTGAAATAGTCGATGAGA	GTCGCCAGTCCAGGGGAGCTT	C	T
	A1_BA_grs_27764_303	GAAGGTGACCAAGTTCATGCTGTCTACGCACTTCTATTCTTGTAGAC	GAAGGTCGGAGTCAACGGATTGTCTACGCACTTCTATTCTTGTAGAT	GCTACTGTTCTACAAACCTCTGCACTT	C	T
	A1_BA_grs_29207_269	GAAGGTGACCAAGTTCATGCTGGTTTTATATTCTTGAGTATTTTGCTGC	GAAGGTCGGAGTCAACGGATTGTGGTTTTATATTCTTGAGTATTTTGCTGA	GAGGCCTAAACATGCATCAAAACAAATTTT	G	T
*	A1_BA_grs_38319_99	GAAGGTGACCAAGTTCATGCTGGTTCTATCGTGTATGCATGAAGG	GAAGGTCGGAGTCAACGGATTAATGGTTCTATCGTGTATGCATGAAGA	TATCGCCCCAAGATTATCTGGCCTT	C	T
	A1_BA_grs_31368_179	GAAGGTGACCAAGTTCATGCTGGTGAAGCATACGCTTTGGTTCG	GAAGGTCGGAGTCAACGGATTGGTGAAGCATACGCTTTGGTTCA	AGGTTGGTTCCAATCGAGGGTGTT	C	T
	A1_BA_grs_71867_257	GAAGGTGACCAAGTTCATGCTGGGAGATGATGGCTCAATGCAC	GAAGGTCGGAGTCAACGGATTATAGGGAGATGATGGCTCAATGCAT	ACGAGCTCTACATCAACACTGCCAT	C	T
	A1_BA_grs_15779_266	GAAGGTGACCAAGTTCATGCTGGCTTCATAAAGTCCCCAGTCG	GAAGGTCGGAGTCAACGGATTAAAGGCTTCATAAAGTCCCCAGTCA	CTGCAGGGTATACCCATGTCAGTA	C	T
	A1_BA_grs_44822_218	GAAGGTGACCAAGTTCATGCTGGATGTTATCGACACACAGTATGATG	GAAGGTCGGAGTCAACGGATTGGATGTTATCGACACACAGTATGATA	GCGCTGGTCGCGCACCCTA	C	T
*	A1_BA_grs_33630_324	GAAGGTGACCAAGTTCATGCTGGAGCTCAGGTGATGGTCAGC	GAAGGTCGGAGTCAACGGATTGGAGCTCAGGTGATGGTCAGT	GTCGACTTCATCATTCACCCCCAT	C	T
	A1_BA_grs_11756_153	GAAGGTGACCAAGTTCATGCTGCAAGAGATCATCTACATCAACCAC	GAAGGTCGGAGTCAACGGATTGGCAAGAGATCATCTACATCAACCAT	ACATACCCTTGAAGACTGACAAAGCTTAA	C	T
	A1_BA_grs_43513_297	GAAGGTGACCAAGTTCATGCTGAGTCCCGAGGGCTACTGAC	GAAGGTCGGAGTCAACGGATTGGAGTCCCGAGGGCTACTGAT	CTTAGGGTAAATAATCATAGGGACCGATA	C	T
*	A1_BA_grs_71868_375	GAAGGTGACCAAGTTCATGCTGAGGGATAATGTTCCCACAAACAAAC	GAAGGTCGGAGTCAACGGATTAGAGGGATAATGTTCCCACAAACAAAT	ACTGATCATATTTGTCGTCCTTGACGAT	C	T
	A1_BA_grs_11718_249	GAAGGTGACCAAGTTCATGCTGAGGCAAGAAATAAAGATGTTAGATGC	GAAGGTCGGAGTCAACGGATTAGAGGCAAGAAATAAAGATGTTAGATGA	CCAGGACTAAAGTTCCTCTCAATAAGATT	G	T
	A1_BA_grs_22046_207	GAAGGTGACCAAGTTCATGCTGAGCTATGTGTTGAAGGGTGGC	GAAGGTCGGAGTCAACGGATTGAGCTATGTGTTGAAGGGTGGA	AATGTTGCAGATCTCGCAAATGTTGGTTT	G	T
	A1_BA_grs_105670_336	GAAGGTGACCAAGTTCATGCTGAGCCAGGAGAATGAGTCGCC	GAAGGTCGGAGTCAACGGATTGAGCCAGGAGAATGAGTCGCT	CCAACAGACCAGCGGATGGTC	C	T
*	A1_BA_grs_31301_210	GAAGGTGACCAAGTTCATGCTGAAGGAGTAATCAGAAATATCTATGTCTC	GAAGGTCGGAGTCAACGGATTGAAGGAGTAATCAGAAATATCTATGTCTT	GGAAATCTCGAGGCATATCAACAATATGAA	C	T
	A1_BA_grs_107213_257	GAAGGTGACCAAGTTCATGCTGAACCCGCTCGCCACCG	GAAGGTCGGAGTCAACGGATTGTGAACCCGCTCGCCACCA	GGCGGAGCGGCTTCGGCAA	C	T
*	A1_BA_grs_51382_260	GAAGGTGACCAAGTTCATGCTCCCTATTGAGGTTGGATACACG	GAAGGTCGGAGTCAACGGATTCTCCCTATTGAGGTTGGATACACT	GGTAGAACCGGATCCGAAGCGAA	G	T
	A1_BA_grs_13816_313	GAAGGTGACCAAGTTCATGCTCCCACCTTGCATATAATGAACTTGC	GAAGGTCGGAGTCAACGGATTCCCACCTTGCATATAATGAACTTGT	GAGTCTAATCAAGGGATCAAAGGAAAGAA	C	T
*	A1_BA_grs_45736_154	GAAGGTGACCAAGTTCATGCTCCACGCAATATGTCCACCTC	GAAGGTCGGAGTCAACGGATTCCTCCACGCAATATGTCCACCTT	ATAATTATTACGAAAAATGAGGGGTCGACA	C	T
*	A1_BA_grs_70857_106	GAAGGTGACCAAGTTCATGCTCATGGTGCGGACATCCTCCC	GAAGGTCGGAGTCAACGGATTATCATGGTGCGGACATCCTCCT	GTTTCATTGGGCCAGAGACAACTGAA	C	T
	A1_BA_grs_22268_229	GAAGGTGACCAAGTTCATGCTCAGTGAATGGTTAGAGGTTACGG	GAAGGTCGGAGTCAACGGATTCTCAGTGAATGGTTAGAGGTTACGA	CAGCTCGCCGCTCCTTCTGTTT	C	T
*	A1_BA_grs_18172_140	GAAGGTGACCAAGTTCATGCTCAGGTGTTTGGGGGCTTACTG	GAAGGTCGGAGTCAACGGATTGCAGGTGTTTGGGGGCTTACTA	ACCACCAAAAATAAAGACGTCCCATGTT	C	T
	A1_BA_grs_110873_224	GAAGGTGACCAAGTTCATGCTCACTTTCGCTGCAGCACGC	GAAGGTCGGAGTCAACGGATTACTCACTTTCGCTGCAGCACGT	GCGGATCTCAAGCTGTAACCACAA	C	T
	A1_BA_grs_47795_198	GAAGGTGACCAAGTTCATGCTCACCGAAGCAGTCCTCTACGG	GAAGGTCGGAGTCAACGGATTCACCGAAGCAGTCCTCTACGA	TTTGAAGCTGGCATCTTCGAGGCAT	C	T
*	A1_BA_grs_70422_294	GAAGGTGACCAAGTTCATGCTCACAACTGAATATTGAAGTTGTAGAAAAAC	GAAGGTCGGAGTCAACGGATTTCACAACTGAATATTGAAGTTGTAGAAAAAT	GCAATGCATCTGTCACGGATTGATTAAAT	C	T

	A1_BA_grs_43090_295	GAAGGTGACCAAGTTCATGCTCAAGTATTGTTAAATCAATTTTTTGAACCTCG	GAAGGTCGGAGTCAACGGATTCAAGTATTGTTAAATCAATTTTTTGAACCTCA	GTCTACCTTGATTCGGCTTTTTTGACTTA	C	T
*	A1_BA_grs_45750_306	GAAGGTGACCAAGTTCATGCTCAAGAGGAAGTCAAAGGAGAGGG	GAAGGTCGGAGTCAACGGATTCAAGAGGAAGTCAAAGGAGAGGA	CTTATATGGCTAAGTCTGGTGCCTGTA	C	T
*	A1_BA_grs_36187_311	GAAGGTGACCAAGTTCATGCTATTGCAATCAAGATAGTGCCCTTG	GAAGGTCGGAGTCAACGGATTCTATTGCAATCAAGATAGTGCCCTTA	GGGCTTTTCGAACATTTTAGGCATGTT	C	T
*	A1_BA_grs_42271_316	GAAGGTGACCAAGTTCATGCTATGGTGGGTGGAACGTCTATCG	GAAGGTCGGAGTCAACGGATTGATGGTGGGTGGAACGTCTATCA	GTGTAAGAGCCGGGTAGACTATCTT	C	T
	A1_BA_grs_17793_142	GAAGGTGACCAAGTTCATGCTATCTATTCTTTCATCTACAAGGAAATCG	GAAGGTCGGAGTCAACGGATTGTATCTATTCTTTCATCTACAAGGAAATCA	CAAATAGTTTTTCTGAATATGCTTGTGTTA	C	T
	A1_BA_grs_66231_310	GAAGGTGACCAAGTTCATGCTATCCTCATAGCATGTCTCCTATCC	GAAGGTCGGAGTCAACGGATTGTATCCTCATAGCATGTCTCCTATCT	CCAGTAGGCCATGGGCAATGCTA	C	T
	A1_BA_grs_18010_210	GAAGGTGACCAAGTTCATGCTATCACCGGGACTAAAAGTTCCTTTC	GAAGGTCGGAGTCAACGGATTAAATCACCGGGACTAAAAGTTCCTTTT	CAGTGTCCATGATTTCCCAGCAAGAT	C	T
	A1_BA_grs_39607_166	GAAGGTGACCAAGTTCATGCTATATTGCTATTGTTGCAAATCATATGACG	GAAGGTCGGAGTCAACGGATTCATATTGCTATTGTTGCAAATCATATGACT	GGTCACATGATTTTTACCGTGTATTCACAT	G	T
*	A1_BA_grs_29793_91	GAAGGTGACCAAGTTCATGCTATAAGAAGGAAACTATTTCACTGAAGTTTG	GAAGGTCGGAGTCAACGGATTATAATAAGAAGGAAACTATTTCACTGAAGTTTA	CTCTTCTTTAGTTTGGCGAAGGGGAA	C	T
*	A1_BA_grs_106476_114	GAAGGTGACCAAGTTCATGCTAGTAAAACACAATACTCGCAACAAGTC	GAAGGTCGGAGTCAACGGATTGAAGTAAAACACAATACTCGCAACAAGTA	GTGACCGTTACACCATGCAAAAAACTAATA	G	T
*	A1_BA_grs_50105_166	GAAGGTGACCAAGTTCATGCTAGGACCCACCTATGTCTGTAGG	GAAGGTCGGAGTCAACGGATTCAGGACCCACCTATGTCTGTAGA	CATGTTGAGTCCACATAGAAGTGCATATT	C	T
*	A1_BA_grs_40519_355	GAAGGTGACCAAGTTCATGCTAGCGGCTCGGCCAGAGAC	GAAGGTCGGAGTCAACGGATTGAGCGGCTCGGCCAGAGAT	CCTCCTTTGGCGATGGCAGCAA	C	T
	A1_BA_grs_56328_393	GAAGGTGACCAAGTTCATGCTACTGTGAGTATTGATTTTGTTACTGC	GAAGGTCGGAGTCAACGGATTCTACTGTGAGTATTGATTTTGTTACTGT	CAGTTATCCATATTGGAAACAAAGTAACAA	C	T
	A1_BA_grs_13164_197	GAAGGTGACCAAGTTCATGCTAATCACCAGGACTAAAGTTCCTCTC	GAAGGTCGGAGTCAACGGATTAAAATCACCAGGACTAAAGTTCCTCTT	GATACAATATCCATGTTTGCCCAGCAA	C	T
*	A1_BA_grs_24802_137	GAAGGTGACCAAGTTCATGCTAATAATTTGAACAACTTCATTTACTTCCCG	GAAGGTCGGAGTCAACGGATTAAAATAATTTGAACAACTTCATTTACTTCCCA	ATGTGTAACTCCAATTCGAAAATTTGAAAA	T	C
*	A1_BA_grs_11627_418	GAAGGTGACCAAGTTCATGCTAAGGTGAATCTATTGTGCACCACC	GAAGGTCGGAGTCAACGGATTGAAGGTGAATCTATTGTGCACCACT	CTTAAGGGTGAATCGGTGGATCCTT	C	T
	A1_BA_grs_23020_298	GAAGGTGACCAAGTTCATGCTAAGATCCCTCAATTCTTCATGATGTAG	GAAGGTCGGAGTCAACGGATTGAAGATCCCTCAATTCTTCATGATGTAT	ACTTGATCAATAGGTGTTTTGGAGAGCAT	G	T
	A1_BA_grs_25255_270	GAAGGTGACCAAGTTCATGCTAACTTACCCTTGAAGACTGAAAAG	GAAGGTCGGAGTCAACGGATTGCTAACTTACCCTTGAAGACTGAAAAA	CTTCATCATGACCTTGAGGTAGGCTT	C	T
*	A1_BA_grs_14263_283	GAAGGTGACCAAGTTCATGCTAACTATATATTACAAGTAAATTATAGGTTGCTC	GAAGGTCGGAGTCAACGGATTAACTATATATTACAAGTAAATTATAGGTTGCTA	GTTGTCAAAACTCTCGGTTGTTTCTCAAT	G	T
*	A1_BA_grs_84979_305	GAAGGTGACCAAGTTCATGCTAAATCAACGCCGCTGCAGCTG	GAAGGTCGGAGTCAACGGATTCAAATCAACGCCGCTGCAGCTA	GCAACCGCAGTCCACATAGTATTCAT	C	T
	A1_BA_grs_28099_287	GAAGGTGACCAAGTTCATGCTTTTTATCTAACACGGAAGATAATGAGTCA	GAAGGTCGGAGTCAACGGATTATCTAACACGGAAGATAATGAGTCG	GCGCCACGGGGTGGTGTGA	G	A
	A1_BA_grs_49516_365	GAAGGTGACCAAGTTCATGCTTTGGACCCAATATGTTTGGGGAA	GAAGGTCGGAGTCAACGGATTTGGACCCAATATGTTTGGGGAC	CCACTTCTTCAATATTGAGAGACAAGCAT	C	A
	A1_BA_grs_55748_286	GAAGGTGACCAAGTTCATGCTTGTTGTGGTTGCTGGTTGATCAGA	GAAGGTCGGAGTCAACGGATTGTTGTGGTTGCTGGTTGATCAGG	GAAGAACAAGATTAGGCCAGCAACATAAT	G	A
	A1_BA_grs_50960_123	GAAGGTGACCAAGTTCATGCTTGTTACTCCCTCCAATCCATATTACT	GAAGGTCGGAGTCAACGGATTGTTACTCCCTCCAATCCATATTACC	GGAACTACTTCCCTCCGATCCATAT	G	A
	A1_BA_grs_63693_289	GAAGGTGACCAAGTTCATGCTTGTGCTTATCAAAGTGATGCTTCCTA	GAAGGTCGGAGTCAACGGATTGTGCTTATCAAAGTGATGCTTCCTC	GCCACCATCTTGGAAAGCAAGATGAA	C	A
*	A1_BA_grs_70822_144	GAAGGTGACCAAGTTCATGCTTGGCCGGGAATCTGTTTGTCTTA	GAAGGTCGGAGTCAACGGATTGGCCGGGAATCTGTTTGTCTTG	GCTGTGGTCTCGTCTCGCTCTA	G	A
	A1_BA_grs_75304_237	GAAGGTGACCAAGTTCATGCTTGATGCTTTGTGTCTTGCCACAAAAT	GAAGGTCGGAGTCAACGGATTGATGCTTTGTGTCTTGCCACAAAAA	TCAAAATGGCACTATGGTTGCACACAAA	T	A
	A1_BA_grs_23792_245	GAAGGTGACCAAGTTCATGCTTCCTGGGCAAACATGGACACTA	GAAGGTCGGAGTCAACGGATTCCTGGGCAAACATGGACACTG	TTGCAGATTATGCAGAGGCAGGAAATAAA	G	A
	A1_BA_grs_73682_333	GAAGGTGACCAAGTTCATGCTTCATTCAAAGTAGGTAAGATGCTAAGAAT	GAAGGTCGGAGTCAACGGATTCATTCAAAGTAGGTAAGATGCTAAGAAG	CTTCCATGAACTTGGTACAATCTTTCATTA	C	A
*	A1_BA_grs_66690_231	GAAGGTGACCAAGTTCATGCTTCATGACACTAATCGGTGATGCGT	GAAGGTCGGAGTCAACGGATTCATGACACTAATCGGTGATGCGC	ACCTGGTCGTCCTGAAGCCGTT	G	A
*	A1_BA_grs_21436_323	GAAGGTGACCAAGTTCATGCTTATTTATTCCAGGCATTTGGGAGCAA	GAAGGTCGGAGTCAACGGATTTATTCCAGGCATTTGGGAGCAG	AATCGCTAAAATTGAAGTAGACCTTACCTT	G	A
	A1_BA_grs_39477_320	GAAGGTGACCAAGTTCATGCTTACTCTGTTAAGAGTTTAAACTTATGATGTTA	GAAGGTCGGAGTCAACGGATTCTCTGTTAAGAGTTTAAACTTATGATGTTG	GGAAGATCACAGTATGATTCGGTAACATT	G	A
	A1_BA_grs_38928_159	GAAGGTGACCAAGTTCATGCTGTGTTGCATTTGTTGATCTCTATGTGTA	GAAGGTCGGAGTCAACGGATTGTTGCATTTGTTGATCTCTATGTGTG	TACAATCCTCACAATCTACACGAAAGCAA	G	A
	A1_BA_grs_20941_153	GAAGGTGACCAAGTTCATGCTGTCCAGATATGGTGGAAGCCCAT	GAAGGTCGGAGTCAACGGATTCCAGATATGGTGGAAGCCCAC	CGTGGGCCACTCGAAGTCTTCAT	G	A
*	A1_BA_grs_20446_192	GAAGGTGACCAAGTTCATGCTGTATGCATAATGATAGTGTTTTGTTGTATGTT	GAAGGTCGGAGTCAACGGATTATGCATAATGATAGTGTTTTGTTGTATGTG	CACTCACTTGCTACTCCACAAACCTA	C	A
	A1_BA_grs_54317_241	GAAGGTGACCAAGTTCATGCTGGTTAAATCAGGCACGCACATCAAT	GAAGGTCGGAGTCAACGGATTGTTAAATCAGGCACGCACATCAAC	TGAATGAGTATATTTTCGACTGCTCTGTTT	G	A

	A1_BA_grs_74468_252	GAAGGTGACCAAGTTCATGCTGGTGTCATGAAGCACTTGGTGCA	GAAGGTCGGAGTCAACGGATTGTGTCATGAAGCACTTGGTGCG	ACGCTTCATGGAGACAATGGAAAACAATA	G	A
*	A1_BA_grs_35480_424	GAAGGTGACCAAGTTCATGCTGGGTTTAACATAACTGTTGTAGCTTCTA	GAAGGTCGGAGTCAACGGATTGGTTTAACATAACTGTTGTAGCTTCTG	TCAGCTACAAATTTAATTCGACAACTTCTA	G	A
*	A1_BA_grs_30859_114	GAAGGTGACCAAGTTCATGCTGGCTTTCTATGTCTTGTGTTCCTCT	GAAGGTCGGAGTCAACGGATTGCTTTCTATGTCTTGTGTTCCTCC	CTATGAAATTAAATTCAACCAACACACAAT	G	A
	A1_BA_grs_105257_144	GAAGGTGACCAAGTTCATGCTGGATCCGGAGTGGATTGCGCT	GAAGGTCGGAGTCAACGGATTGATCCGGAGTGGATTGCGCG	CTCGGTCCCTCATTCCAGGCAT	C	A
	A1_BA_grs_81326_338	GAAGGTGACCAAGTTCATGCTGGAGCGGTGATCTGTGGTCGT	GAAGGTCGGAGTCAACGGATTGAGCGGTGATCTGTGGTCGC	AGTCACTCTGTCCATGTCCCAGAT	G	A
	A1_BA_grs_105739_119	GAAGGTGACCAAGTTCATGCTGCAAGTGGCCACACTTGAGAGA	GAAGGTCGGAGTCAACGGATTCAAGTGGCCACACTTGAGAGC	TTGGTGTTCCGCGTGAACTTCACTT	C	A
*	A1_BA_grs_57018_162	GAAGGTGACCAAGTTCATGCTGATGGCTTGAAGAATCAGAGTGTCAT	GAAGGTCGGAGTCAACGGATTATGGCTTGAAGAATCAGAGTGTCAG	GTAAGATGCTTGAACTAAGTTTGTCGGTT	C	A
*	A1_BA_grs_44314_197	GAAGGTGACCAAGTTCATGCTGATAAAACACATAGTTCTCACACGAGTT	GAAGGTCGGAGTCAACGGATTATAAAACACATAGTTCTCACACGAGTC	TTGTGCCTGCGAGATACTATTTGCTATTT	G	A
	A1_BA_grs_89103_286	GAAGGTGACCAAGTTCATGCTGAGCATGTATTATCATGAGAGCTTCA	GAAGGTCGGAGTCAACGGATTGAGCATGTATTATCATGAGAGCTTCC	GTGGTCCTTATGTTTGTTGCAACAACTAT	C	A
	A1_BA_grs_103033_214	GAAGGTGACCAAGTTCATGCTGAGCAAATGGAAATTAGTGTAAAACCCA	GAAGGTCGGAGTCAACGGATTAGCAAATGGAAATTAGTGTAAAACCCG	CAGGAACGTTGTCCGTTGCGCTT	G	A
	A1_BA_grs_105652_255	GAAGGTGACCAAGTTCATGCTGAGAATCGTTCAGGAACATTGTCCA	GAAGGTCGGAGTCAACGGATTAGAATCGTTCAGGAACATTGTCCG	GGATTCAAACCCTGCATCAGAGTGTT	G	A
*	A1_BA_grs_44170_203	GAAGGTGACCAAGTTCATGCTGAATATAAGTTCTTATCGGTATGTTTTACCA	GAAGGTCGGAGTCAACGGATTGAATATAAGTTCTTATCGGTATGTTTTACCT	CTTCCAAGGTGAAACTTGCCCCTTT	T	A
*	A1_BA_grs_108904_232	GAAGGTGACCAAGTTCATGCTGAAGATGTCTGGTACCATGCCTT	GAAGGTCGGAGTCAACGGATTGAAGATGTCTGGTACCATGCCTG	CTTTTTCTATTCCATCACATACGTGTTCTT	C	A
	A1_BA_grs_52581_191	GAAGGTGACCAAGTTCATGCTGAAAGTACAAAACAGGTAAAGAAACCCT	GAAGGTCGGAGTCAACGGATTAAAGTACAAAACAGGTAAAGAAACCCC	TGAAAGGTATTATTAACCAGCATCTCAATT	G	A
*	A1_BA_grs_80598_119	GAAGGTGACCAAGTTCATGCTCTATGCAAGACAGGTCTGTCGT	GAAGGTCGGAGTCAACGGATTCTATGCAAGACAGGTCTGTCGC	GTGGTTCCTCCATCTACCCGACAA	G	A
*	A1_BA_grs_106905_397	GAAGGTGACCAAGTTCATGCTCGATTTTCCACTGTCAGAAATTGCCT	GAAGGTCGGAGTCAACGGATTTTCCACTGTCAGAAATTGCCC	TGAATAATATTTATTCGAAGCTCCTCCAAA	G	A
*	A1_BA_grs_17472_329	GAAGGTGACCAAGTTCATGCTCCGCTCATAGCAGTTCTGGCTA	GAAGGTCGGAGTCAACGGATTCGCTCATAGCAGTTCTGGCTG	AATTTTCCTTCTACTTAAGAATTTGAGGTA	G	A
*	A1_BA_grs_79879_167	GAAGGTGACCAAGTTCATGCTCCCGTTGAATCATGTCGACCATA	GAAGGTCGGAGTCAACGGATTCCCGTTGAATCATGTCGACCATG	GCTGTGTACCCATTGCGTGATATGAT	G	A
	A1_BA_grs_36216_169	GAAGGTGACCAAGTTCATGCTCCCCAAGAAATAAAAGTGTGAATCAAGA	GAAGGTCGGAGTCAACGGATTCCCAAGAAATAAAAGTGTGAATCAAGC	TTCCTTGAATATGCGCACTATCCACATA	C	A
*	A1_BA_grs_40585_163	GAAGGTGACCAAGTTCATGCTCCCAGCATAACAAAATACGGAAACAA	GAAGGTCGGAGTCAACGGATTCCCAGCATAACAAAATACGGAAACAG	GTAGCTTGTAACCTATATGCACATTCACAA	G	A
	A1_BA_grs_24451_323	GAAGGTGACCAAGTTCATGCTCCATCATGGACTAATGTGTAATGGTA	GAAGGTCGGAGTCAACGGATTCCATCATGGACTAATGTGTAATGGTC	CCATGCACTTTTGTGCGGGTGGAA	C	A
	A1_BA_grs_75715_300	GAAGGTGACCAAGTTCATGCTCCACAAAAATGTTGAACAATTTCTCTTTCT	GAAGGTCGGAGTCAACGGATTCACAAAAATGTTGAACAATTTCTCTTTCC	AATACATGCTCATAATGGCATTATGGTT	G	A
	A1_BA_grs_69833_156	GAAGGTGACCAAGTTCATGCTCATGTTGACGTCATCGTGGTCATT	GAAGGTCGGAGTCAACGGATTATGTTGACGTCATCGTGGTCATC	GACGCGACCGCCGAGGCAA	G	A
*	A1_BA_grs_104369_94	GAAGGTGACCAAGTTCATGCTCATCTACCGACATAAGCAACGGT	GAAGGTCGGAGTCAACGGATTCATCTACCGACATAAGCAACGGC	ACTATGGCAAAGGTTACAGAGAGACAT	G	A
	A1_BA_grs_22682_300	GAAGGTGACCAAGTTCATGCTCATCAGAGTGTTGAGAAGTGCAACA	GAAGGTCGGAGTCAACGGATTATCAGAGTGTTGAGAAGTGCAACG	ATCATTGATTCTTTCCTTTGTGAAGACAAT	G	A
*	A1_BA_grs_14647_345	GAAGGTGACCAAGTTCATGCTCATAGGCAAGACACCAATACACCTT	GAAGGTCGGAGTCAACGGATTATAGGCAAGACACCAATACACCTC	ATAAAGAAATTCCAATTGCTATAAACTCAA	G	A
*	A1_BA_grs_38953_122	GAAGGTGACCAAGTTCATGCTCATACAAGGAAGGGTGGATTTTGGAT	GAAGGTCGGAGTCAACGGATTATACAAGGAAGGGTGGATTTTGGAG	AGCTACTACTACTCCACTACCATACTA	C	A
*	A1_BA_grs_32165_167	GAAGGTGACCAAGTTCATGCTCAGTGAGAAGATCGGGCGT	GAAGGTCGGAGTCAACGGATTCTCAGTGAGAAGATCGGGCGA	GTGGATTGTGGATGCTCACCAAGTA	T	A
*	A1_BA_grs_68671_101	GAAGGTGACCAAGTTCATGCTCAGGCTCATCATCTTGCTCAGAT	GAAGGTCGGAGTCAACGGATTCAGGCTCATCATCTTGCTCAGAC	AGAAGATGATTCCGAGGAAGAAGATGATT	G	A
*	A1_BA_grs_39720_296	GAAGGTGACCAAGTTCATGCTCACTTATGTTAATAAGCAAGCTTTGTTCT	GAAGGTCGGAGTCAACGGATTCACTTATGTTAATAAGCAAGCTTTGTTCC	AAATCCAACAGATGAAGGTCACGAGAAA	G	A
*	A1_BA_grs_25869_149	GAAGGTGACCAAGTTCATGCTCACACACATAATTGAACAAGATATGAACA	GAAGGTCGGAGTCAACGGATTCACACACATAATTGAACAAGATATGAACG	CAGTTGTTCCACTTTTATGAATCATTTCTA	G	A
	A1_BA_grs_17346_249	GAAGGTGACCAAGTTCATGCTCAATGCTGCAAATCTTGCAAATGTTTGT	GAAGGTCGGAGTCAACGGATTAATGCTGCAAATCTTGCAAATGTTTGG	GGCTAAGTTGGCTTGATGTTTGGCT	C	A
*	A1_BA_grs_62582_348	GAAGGTGACCAAGTTCATGCTCAAGCTATTCATGTGGCTGGCAT	GAAGGTCGGAGTCAACGGATTCAAGCTATTCATGTGGCTGGCAG	GTCTAAAGCGTATGTCCGCAGTTCAA	C	A
	A1_BA_grs_43399_330	GAAGGTGACCAAGTTCATGCTCAAGAGAAGAAATGACTTCTGAAGTACA	GAAGGTCGGAGTCAACGGATTAAGAGAAGAAATGACTTCTGAAGTACC	GCTTCGAGGTTTCCTTTTGCCTCAT	C	A
*	A1_BA_grs_105572_134	GAAGGTGACCAAGTTCATGCTCAAGAACCTGCGGCCGAAGTTT	GAAGGTCGGAGTCAACGGATTAAGAACCTGCGGCCGAAGTTC	GCCCCGTCGCCACGTCACAT	G	A
*	A1_BA_grs_25782_310	GAAGGTGACCAAGTTCATGCTATTTTTCCTTCGTTCTATATAAACACACTTATT	GAAGGTCGGAGTCAACGGATTTCCTTCGTTCTATATAAACACACTTATG	GACGAGACTGGCATGCCGATATAAA	C	A

	A1_BA_grs_36615_245	GAAGGTGACCAAGTTCATGCTATTCCGAGAATATTCATTTTCTGACTTTCT	GAAGGTCGGAGTCAACGGATTCCGAGAATATTCATTTTCTGACTTTCC	CCACAGTGCCTGCTGCCTGTTT	G	A
	A1_BA_grs_21080_407	GAAGGTGACCAAGTTCATGCTATGTTACCGTTGGATTACCCAACGA	GAAGGTCGGAGTCAACGGATTGTTACCGTTGGATTACCCAACGG	GGACGAAGTTGGACCGTCAGCTT	G	A
*	A1_BA_grs_88253_382	GAAGGTGACCAAGTTCATGCTATGTGAAATAATTGTATCTAATATATGGGAT	GAAGGTCGGAGTCAACGGATTATGTGAAATAATTGTATCTAATATATGGGAG	CAAGTCCTCTATTGAGGATAATAGATAATA	C	A
	A1_BA_grs_49864_256	GAAGGTGACCAAGTTCATGCTATATTGATATGAAATTGAATTTCATGCACAACT	GAAGGTCGGAGTCAACGGATTGATATGAAATTGAATTTCATGCACAACG	GGCATGCTTGCTTTCTTTGATCCAATATA	C	A
	A1_BA_grs_109579_171	GAAGGTGACCAAGTTCATGCTATAAACATATTCAAACAACAGGCAAACACT	GAAGGTCGGAGTCAACGGATTAACATATTCAAACAACAGGCAAACACC	CAACCCTGATTAGTTGTTCAGAATGCAAA	G	A
*	A1_BA_grs_14655_201	GAAGGTGACCAAGTTCATGCTAGTATCCTCCTCCATATCAAGAGATTT	GAAGGTCGGAGTCAACGGATTGTATCCTCCTCCATATCAAGAGATTC	GAAAAGGCAAAAGGGAAGAAGGAATACAA	G	A
	A1_BA_grs_18911_393	GAAGGTGACCAAGTTCATGCTAGCCATTCTTGCCAAACCCGCT	GAAGGTCGGAGTCAACGGATTAGCCATTCTTGCCAAACCCGCA	CGAAATTGCCTGGTGGGCACCTT	T	A
*	A1_BA_grs_85179_325	GAAGGTGACCAAGTTCATGCTAGCAAGTGTGAACTTTCCTTTTGTGAT	GAAGGTCGGAGTCAACGGATTGCAAGTGTGAACTTTCCTTTTGTGAC	GATCTTCTATGGTCTCGAAGACCGTA	G	A
	A1_BA_grs_26464_348	GAAGGTGACCAAGTTCATGCTAGAGCCCATAGATGCAGATGATTGA	GAAGGTCGGAGTCAACGGATTAGCCCATAGATGCAGATGATTGG	CTTCCACTCCTGTCAACTTCCTAGAT	G	A
	A1_BA_grs_46873_246	GAAGGTGACCAAGTTCATGCTACTTTAGTTGGTCAAGGTAGAGCCT	GAAGGTCGGAGTCAACGGATTTAGTTGGTCAAGGTAGAGCCC	TTTTGTTCTGCGAATCTTCCAGTGCAA	G	A
	A1_BA_grs_56585_89	GAAGGTGACCAAGTTCATGCTACTTCATTAGAAACAACAATTTCAAGAACAATT	GAAGGTCGGAGTCAACGGATTCTTCATTAGAAACAACAATTTCAAGAACAATG	TCCATTATTAGGAGGATAAGGCCTATAATT	C	A
*	A1_BA_grs_34088_196	GAAGGTGACCAAGTTCATGCTACTGTCCCATCAGATAATGCCAGAA	GAAGGTCGGAGTCAACGGATTGTCCCATCAGATAATGCCAGAG	TTTATCTTTGAAACCAGTCGATCGAAACTT	G	A
*	A1_BA_grs_53536_156	GAAGGTGACCAAGTTCATGCTACTCGCTTGACCGCCCACAAAA	GAAGGTCGGAGTCAACGGATTACTCGCTTGACCGCCCACAAAT	AAAATTGAAAATGGGAAAGCTACGCTCGA	T	A
*	A1_BA_grs_61983_229	GAAGGTGACCAAGTTCATGCTACGATCCAATCTCCATTGACACCTT	GAAGGTCGGAGTCAACGGATTGATCCAATCTCCATTGACACCTC	GTTCTCCTCCGATGCTATGATGTCAA	G	A
	A1_BA_grs_62499_380	GAAGGTGACCAAGTTCATGCTACCATTGCATGTCTCTAATCCGGA	GAAGGTCGGAGTCAACGGATTCCATTGCATGTCTCTAATCCGGC	GCAGGCCATGGGCCGTGCTA	C	A
	A1_BA_grs_42338_149	GAAGGTGACCAAGTTCATGCTACCACCTTGACTGTGGCGAGT	GAAGGTCGGAGTCAACGGATTCCACCTTGACTGTGGCGAGC	GGAATTTTACTATGCCTTGTGTGGATGAA	G	A
	A1_BA_grs_42660_164	GAAGGTGACCAAGTTCATGCTAATTCTTGAAGTGAAAGAATCCAATGGATT	GAAGGTCGGAGTCAACGGATTCTTGAAGTGAAAGAATCCAATGGATC	GCTTAAAAGAACTCCTTGAGAGGAAAGAT	G	A
*	A1_BA_grs_33284_130	GAAGGTGACCAAGTTCATGCTAACTTCTCCAACGAATGATTTTGGT	GAAGGTCGGAGTCAACGGATTAACTTCTCCAACGAATGATTTTGGC	AGGAGTTCTGGCAGGAGGGATTAAA	G	A
*	A1_BA_grs_19227_170	GAAGGTGACCAAGTTCATGCTAAATTCTCTTGTGATGCAAATCCACGT	GAAGGTCGGAGTCAACGGATTCTCTTGTGATGCAAATCCACGC	CTTTGGATTTGCACCATAGGAAGTCAATT	G	A
*	A1_BA_grs_25042_402	GAAGGTGACCAAGTTCATGCTAAATCAGGTTGCAAAAGATAGATGGCA	GAAGGTCGGAGTCAACGGATTATCAGGTTGCAAAAGATAGATGGCG	AACAAAGTTTGCTGTTAACTTCAACAGCTT	G	A
	A1_BA_grs_50961_175	GAAGGTGACCAAGTTCATGCTAAACTCTCGCCCTCCATGCCTT	GAAGGTCGGAGTCAACGGATTCTCTCGCCCTCCATGCCTC	GTTGACGGCGTGTGCCCAGATT	G	A
	A1_BA_grs_29259_182	GAAGGTGACCAAGTTCATGCTAAAAAGGATAAGGAGAGGTAATTACTGAAT	GAAGGTCGGAGTCAACGGATTAAGGATAAGGAGAGGTAATTACTGAAG	AGATAACCCAACAGTTTCCTTGAGTCTT	C	A
	A1_BA_grs_33933_269	GAAGGTGACCAAGTTCATGCTTTTGCATCACTATTCTATATCATTATTTACTG	GAAGGTCGGAGTCAACGGATTTTGCATCACTATTCTATATCATTATTTACTC	CGGTCCATGCTCCAAAAGTCATCAA	G	C
	A1_BA_grs_57720_290	GAAGGTGACCAAGTTCATGCTTTTAGGGATGTTACCAACCAAAATGC	GAAGGTCGGAGTCAACGGATTTTAGGGATGTTACCAACCAAAATGG	TCCTTGATTGTCCTTTACCAACACCTAAT	G	C
	A1_BA_grs_33093_172	GAAGGTGACCAAGTTCATGCTTGACATTCGGCTCTTTTCAGCTTG	GAAGGTCGGAGTCAACGGATTGACATTCGGCTCTTTTCAGCTTC	CAAATCTTGCAAATGTTGGTTTCGAACC	G	C
	A1_BA_grs_72504_317	GAAGGTGACCAAGTTCATGCTGTGGTTACAGCTCAAGATCCAC	GAAGGTCGGAGTCAACGGATTGTGGTTACAGCTCAAGATCCAG	GATGGTGCTCCTACTCCTCCTCTT	G	C
	A1_BA_grs_94156_344	GAAGGTGACCAAGTTCATGCTGGAGAAAGTGAGTTGGTGGAGG	GAAGGTCGGAGTCAACGGATTGGAGAAAGTGAGTTGGTGGAGC	GAGATGGTGCCGAACCCGGTAA	G	C
*	A1_BA_grs_46371_201	GAAGGTGACCAAGTTCATGCTGACAATGTGATCAAATGCTAAAATTATACC	GAAGGTCGGAGTCAACGGATTGACAATGTGATCAAATGCTAAAATTATACG	GAGAAACTTATAAGGTAATCCCCAAGTGTT	G	C
	A1_BA_grs_45118_125	GAAGGTGACCAAGTTCATGCTCCTTTCGCCTATAAAATCCCTCTC	GAAGGTCGGAGTCAACGGATTCCTTTCGCCTATAAAATCCCTCTG	GCGCAGCGGAACTCTATCTGGAA	G	C
*	A1_BA_grs_11982_340	GAAGGTGACCAAGTTCATGCTCCGAAATCCTGGCTCCGTCG	GAAGGTCGGAGTCAACGGATTCCGAAATCCTGGCTCCGTCC	GACGGGGTCCCATGAGAACCAT	G	C
	A1_BA_grs_37297_209	GAAGGTGACCAAGTTCATGCTCAAGTCTCTCGTATTGTTGTTGCAAG	GAAGGTCGGAGTCAACGGATTCAAGTCTCTCGTATTGTTGTTGCAAC	GCCAACAACATGTTTGCAAACAAACCATA	G	C
	A1_BA_grs_18915_144	GAAGGTGACCAAGTTCATGCTATTAGACACCTTGATACTGATAGGAG	GAAGGTCGGAGTCAACGGATTATTAGACACCTTGATACTGATAGGAC	AGTTGGACTTCGTAGTTCATCATTGCTAA	G	C
*	A1_BA_grs_15265_193	GAAGGTGACCAAGTTCATGCTTTCCTTTGTGAATAGAATCGTTGAG	GAAGGTCGGAGTCAACGGATTCTTTCCTTTGTGAATAGAATCGTTGAT	CAAATCCCTGCATCAGAGTGTTGTGAA	G	T
*	A1_BA_grs_37033_288	GAAGGTGACCAAGTTCATGCTTTCAAGAATTTTCCCTCCCGCG	GAAGGTCGGAGTCAACGGATTAGTTTCAAGAATTTTCCCTCCCGCA	CTAACAGACACTCGGCAAAGATCCTT	C	T
	A1_BA_grs_20553_174	GAAGGTGACCAAGTTCATGCTTGGTATATACGGCCTGAATACG	GAAGGTCGGAGTCAACGGATTGCTTGGTATATACGGCCTGAATACA	AGTCTGTAGGTTACTCGAGTTCTTCATTT	C	T
	A1_BA_grs_14066_258	GAAGGTGACCAAGTTCATGCTTAGTCCTACAAAGGTCAGTACATTAG	GAAGGTCGGAGTCAACGGATTATTAGTCCTACAAAGGTCAGTACATTAA	GTCAAGTGCTTTTGCTTCATATAGTTGATT	C	T

	A1_BA_grs_50769_347	GAAGGTGACCAAGTTCATGCTGTTAGCTTGGCCTTGTCCTTG	GAAGGTCGGAGTCAACGGATTCTGTTAGCTTGGCCTTGTCCTTT	CCCAGTACTCACCAAATGGTGACAT	G	T
*	A1_BA_grs_52637_220	GAAGGTGACCAAGTTCATGCTGTCTTGTTCGGTTTCTGACGGC	GAAGGTCGGAGTCAACGGATTCGTCTTGTTCGGTTTCTGACGGT	CGTTTCCGATGCCATAAGGTGAACTT	C	T
	A1_BA_grs_84711_275	GAAGGTGACCAAGTTCATGCTGTATTTGTAAAGGGTCTAAACATGCATC	GAAGGTCGGAGTCAACGGATTGGTATTTGTAAAGGGTCTAAACATGCATA	TGTTATGTGAGCTTGCATGCTTGTTCAAT	G	T
*	A1_BA_grs_22431_299	GAAGGTGACCAAGTTCATGCTGTAAGGCTTCATCCAATCTATGGAC	GAAGGTCGGAGTCAACGGATTGGTAAGGCTTCATCCAATCTATGGAT	CCGTGGATCTGAAAAGAAAATAGATGGAA	C	T
*	A1_BA_grs_12982_266	GAAGGTGACCAAGTTCATGCTGGTCGATTAAGTTACCGACAAAACC	GAAGGTCGGAGTCAACGGATTAGGTCGATTAAGTTACCGACAAAACT	GAATAGTTGGTCATTAAACTCTCTGACAAT	C	T
*	A1_BA_grs_48613_202	GAAGGTGACCAAGTTCATGCTGGTCCTGCGACAGAACCGG	GAAGGTCGGAGTCAACGGATTGGGTCCTGCGACAGAACCGA	GCCGGAGTTGCTGCCGGTATTT	C	T
	A1_BA_grs_83392_186	GAAGGTGACCAAGTTCATGCTGGCTAAGTTGGCTTGACGTTCG	GAAGGTCGGAGTCAACGGATTGGCTAAGTTGGCTTGACGTTCA	CGGACCTAATGTTGCAAATCTTGCAAAT	C	T
*	A1_BA_grs_63917_137	GAAGGTGACCAAGTTCATGCTGGCAACAGACAACTCCAGGTTC	GAAGGTCGGAGTCAACGGATTATAGGCAACAGACAACTCCAGGTTA	GTACCGGATGAAGTTGATACAGATGTTAA	G	T
	A1_BA_grs_73155_260	GAAGGTGACCAAGTTCATGCTGCCTGCGCACTGCTCAC	GAAGGTCGGAGTCAACGGATTTCTGCCTGCGCACTGCTCAT	ACAGGTTCTCCTCCGATGATGTGAT	C	T
	A1_BA_grs_32821_383	GAAGGTGACCAAGTTCATGCTGCCATATTTTCAATTACATTGTTTTTATATTGC	GAAGGTCGGAGTCAACGGATTGCCATATTTTCAATTACATTGTTTTTATATTGT	CTTGTCCTACTTCCTGTGAAAAATGATTAT	C	T
*	A1_BA_grs_15995_379	GAAGGTGACCAAGTTCATGCTGCATGAGCACCATTGCACTTGAC	GAAGGTCGGAGTCAACGGATTATGCATGAGCACCATTGCACTTGAA	GGGAAAATCCCATTTAGGGTTTTGGATAA	G	T
	A1_BA_grs_62726_87	GAAGGTGACCAAGTTCATGCTGCATGAATGATATGCAAACTTTGAAATCG	GAAGGTCGGAGTCAACGGATTGCATGAATGATATGCAAACTTTGAAATCA	CACAGAAAAACCCCTTACCTATTAGTATTA	C	T
*	A1_BA_grs_88474_366	GAAGGTGACCAAGTTCATGCTGCAGTTGCTTGGTGTCG	GAAGGTCGGAGTCAACGGATTCTGCTGCAGTTGCTTGGTGTCA	GGCTTGTCTTTTTGAGAGATGGACATAT	C	G
	A1_BA_grs_13790_133	GAAGGTGACCAAGTTCATGCTGCACGCAAGTGCCTGGTGG	GAAGGTCGGAGTCAACGGATTCGCACGCAAGTGCCTGGTGA	GTGATTCCTGCCAAACCCGTATAGAA	C	T
*	A1_BA_grs_42194_197	GAAGGTGACCAAGTTCATGCTGCACAACCTTTGAGAGTACCAATAC	GAAGGTCGGAGTCAACGGATTGCACAACCTTTGAGAGTACCAATAA	GTTGAAGACATTAGTGGCATACATGTGAA	G	T
	A1_BA_grs_46915_291	GAAGGTGACCAAGTTCATGCTGCAAACTCTGCATTGTGGTAGCC	GAAGGTCGGAGTCAACGGATTGCAAACTCTGCATTGTGGTAGCT	GGTTGGCCGATTACCTACAAACCAT	C	T
	A1_BA_grs_15980_167	GAAGGTGACCAAGTTCATGCTGATGCAAATTAGGATAAGAGCCCTG	GAAGGTCGGAGTCAACGGATTAAGATGCAAATTAGGATAAGAGCCCTA	CTGGTCAGGGTTATGGATGCCATT	C	T
	A1_BA_grs_23617_280	GAAGGTGACCAAGTTCATGCTGATCTTTCTTTGTCAGGGTGCGC	GAAGGTCGGAGTCAACGGATTATGATCTTTCTTTGTCAGGGTGCGT	CATAGCCTCGGGGGTTACACCTA	C	T
*	A1_BA_grs_26909_108	GAAGGTGACCAAGTTCATGCTGATCCATGTTTCTTTTGTGTCGTGG	GAAGGTCGGAGTCAACGGATTCGATCCATGTTTCTTTTGTGTCGTGA	CCACAATCCAAAATATATATGGACCGCAA	C	T
*	A1_BA_grs_50812_296	GAAGGTGACCAAGTTCATGCTGAATCACTATAAGCTTCATATGATTTCATC	GAAGGTCGGAGTCAACGGATTGAATCACTATAAGCTTCATATGATTTCATT	CATGACTTAGAGGCTTCCACACCTT	C	T
	A1_BA_grs_84407_342	GAAGGTGACCAAGTTCATGCTCTTGCAAATGTTGGTTTCTGACCG	GAAGGTCGGAGTCAACGGATTATCTTGCAAATGTTGGTTTCTGACCA	GATTGTTGTTGTTGGCCATCTGAGCTA	C	T
	A1_BA_grs_50243_296	GAAGGTGACCAAGTTCATGCTCTTCTTCTTCCCTTGAGCGGC	GAAGGTCGGAGTCAACGGATTATCTTCTTCTTCCCTTGAGCGGT	CAGGTACGTCACGTCCCAGCT	C	T
	A1_BA_grs_15332_97	GAAGGTGACCAAGTTCATGCTCGGTTCTGGTGCTGGGCTC	GAAGGTCGGAGTCAACGGATTCCGGTTCTGGTGCTGGGCTA	GTGAAAAACATTTGAAAAGCATTCCTGAAA	G	T
	A1_BA_grs_14718_316	GAAGGTGACCAAGTTCATGCTCGCTGACACCCCGGTCCC	GAAGGTCGGAGTCAACGGATTCGCTGACACCCCGGTCCA	GTCAGCGTGCGAGGAAGACGAT	G	T
*	A1_BA_grs_71963_165	GAAGGTGACCAAGTTCATGCTCGATCCACTTTGGATCCTCACAC	GAAGGTCGGAGTCAACGGATTCGATCCACTTTGGATCCTCACAT	GGATTGACTTGGCATTGCTCAGTCAT	C	T
	A1_BA_grs_72187_397	GAAGGTGACCAAGTTCATGCTCGAACATGACGCAAGTCCATCG	GAAGGTCGGAGTCAACGGATTGCGAACATGACGCAAGTCCATCA	GTCATGCTCTTGTGCTTGAGTGGTT	C	T
*	A1_BA_grs_35199_251	GAAGGTGACCAAGTTCATGCTCGAAATGGCATACTGATTTTCCGC	GAAGGTCGGAGTCAACGGATTCCGAAATGGCATACTGATTTTCCGT	TCAGCCGGAGTGTCTGGCCTA	C	T
	A1_BA_grs_37563_221	GAAGGTGACCAAGTTCATGCTCGAAAATAACAAGTCTAAATTACAATGAC	GAAGGTCGGAGTCAACGGATTGCTCGAAAATAACAAGTCTAAATTACAATGAT	CCAAGTAGCGTTGGAGTCACCCTA	C	T
*	A1_BA_grs_26944_166	GAAGGTGACCAAGTTCATGCTCCTATAGGTCAAAAATGATTAATTCATACTTG	GAAGGTCGGAGTCAACGGATTCCTATAGGTCAAAAATGATTAATTCATACTTA	GGTCAAAGTTGATCATATGACTTAAATAAA	C	T
*	A1_BA_grs_70182_176	GAAGGTGACCAAGTTCATGCTCCCTTTGTTAGGTGCACTGAACG	GAAGGTCGGAGTCAACGGATTATCCCTTTGTTAGGTGCACTGAACA	CCACATCAGACTTTATGTATGTGACCAAA	C	T
	A1_BA_grs_28722_336	GAAGGTGACCAAGTTCATGCTCCCATTGTGTCGAATCAATAAATTGG	GAAGGTCGGAGTCAACGGATTCTCCCATTGTGTCGAATCAATAAATTGA	GAGTGTAGGGGATCGCAATAGTCTT	C	T
	A1_BA_grs_58333_313	GAAGGTGACCAAGTTCATGCTCCAGCCACAGCGGGAAGTAC	GAAGGTCGGAGTCAACGGATTCCAGCCACAGCGGGAAGTAT	GCGATCTTCATCGCCTTCTGTGAAT	C	T
	A1_BA_grs_46856_292	GAAGGTGACCAAGTTCATGCTCCACGTCTCTAAACACGCACTG	GAAGGTCGGAGTCAACGGATTCCCACGTCTCTAAACACGCACTA	GTGTCCACTGTCATGGTATTGTCGAT	C	T
*	A1_BA_grs_69683_186	GAAGGTGACCAAGTTCATGCTCATTCTAAGGCGAAGTATGTGGTTC	GAAGGTCGGAGTCAACGGATTCCATTCTAAGGCGAAGTATGTGGTTT	CAATCAGTTGTACAACCACGTCATGAA	C	T
*	A1_BA_grs_47344_307	GAAGGTGACCAAGTTCATGCTCATCCTCCATGACTTGAAGCTCC	GAAGGTCGGAGTCAACGGATTCATCCTCCATGACTTGAAGCTCT	ACGAGAAAAAGATGTGAGGTATCTGGAT	C	T
	A1_BA_grs_28088_290	GAAGGTGACCAAGTTCATGCTCACGTCTGCGGCCGAGGC	GAAGGTCGGAGTCAACGGATTCACGTCTGCGGCCGAGGT	GCGAACGGAGAAGATTCACTCAACAA	C	T

	A1_BA_grs_51857_292	GAAGGTGACCAAGTTCATGCTCACCCCCTGAAGACCAGTCG	GAAGGTCGGAGTCAACGGATTCCACCCCCTGAAGACCAGTCA	GCCTTATCAAATAAACAACTGCTTAAACTA	C	T
	A1_BA_grs_22166_320	GAAGGTGACCAAGTTCATGCTCAAATTCTTGAAGTAAAAGGATCCAACAG	GAAGGTCGGAGTCAACGGATTCAAATTCTTGAAGTAAAAGGATCCAACAT	GATGGTTTAAAAGAACTCCTTGAGAGAAAA	G	T
	A1_BA_grs_35383_265	GAAGGTGACCAAGTTCATGCTATGTGCATATTGATATGAAATTGAATTTCATG	GAAGGTCGGAGTCAACGGATTATGTGCATATTGATATGAAATTGAATTTCATA	TAGGGGAAACTCCACCAAATCCCAT	C	T
*	A1_BA_grs_54250_319	GAAGGTGACCAAGTTCATGCTATGCCCCTTGAAGATAGCGTGC	GAAGGTCGGAGTCAACGGATTAATGCCCCTTGAAGATAGCGTGT	CTACTTGTTCGAGAAAGTGAAGCATCATA	C	T
	A1_BA_grs_52730_329	GAAGGTGACCAAGTTCATGCTATCGTATAGTTATCGACCCATCTCC	GAAGGTCGGAGTCAACGGATTCATCGTATAGTTATCGACCCATCTCT	CGTATAGTTGGTCGTTAAACCTTCTGTA	C	T
	A1_BA_grs_84165_334	GAAGGTGACCAAGTTCATGCTATCCGTGGTGGGCCTCCTG	GAAGGTCGGAGTCAACGGATTCATCCGTGGTGGGCCTCCTA	GTCAGAGACATGTTTTTGAGAGGCTCA	C	T
	A1_BA_grs_23220_225	GAAGGTGACCAAGTTCATGCTATCCAACATCTTTATTTCTTGCCTCTG	GAAGGTCGGAGTCAACGGATTCATCCAACATCTTTATTTCTTGCCTCTA	GACTGATCCGTTGGATCCTTGTACTT	C	T
	A1_BA_grs_76545_306	GAAGGTGACCAAGTTCATGCTATATGATGCGGAAGCCGGACAG	GAAGGTCGGAGTCAACGGATTAATATGATGCGGAAGCCGGACAA	AGCAGCATCTCTGGCATGTTGCTTT	C	T
*	A1_BA_grs_67922_348	GAAGGTGACCAAGTTCATGCTATAGCCACCACAACTACATCAACG	GAAGGTCGGAGTCAACGGATTCATAGCCACCACAACTACATCAACA	CTTGATTAGTTTAGAAATATCCAACCTGTT	G	C
*	A1_BA_grs_68952_140	GAAGGTGACCAAGTTCATGCTAGTATTAAGAAGTCACTTACTGTAGCG	GAAGGTCGGAGTCAACGGATTGTAGTATTAAGAAGTCACTTACTGTAGCA	GGAGTCCTGGTCCGCGAGGAT	C	T
	A1_BA_grs_104864_280	GAAGGTGACCAAGTTCATGCTAGGGAAGCCTCTACGTCACTG	GAAGGTCGGAGTCAACGGATTGAGGGAAGCCTCTACGTCACTT	GGGATTCTTGGTGCGTGGAGGAA	G	T
*	A1_BA_grs_35833_439	GAAGGTGACCAAGTTCATGCTAGCCATTCCTCAAAACTGTTCTTGG	GAAGGTCGGAGTCAACGGATTGAGCCATTCCTCAAAACTGTTCTTGA	GATGAATTTTGGAGGCGAATTATTAGAGAA	C	T
	A1_BA_grs_74660_287	GAAGGTGACCAAGTTCATGCTAGATATAACAATGCTTCCCCTGACG	GAAGGTCGGAGTCAACGGATTGAGATATAACAATGCTTCCCCTGACA	TTACCTATTACCTGCTGTGCATGCTTTA	C	T
*	A1_BA_grs_77194_97	GAAGGTGACCAAGTTCATGCTAGAGGCTCATAGTATCACCCGG	GAAGGTCGGAGTCAACGGATTGAGAGGCTCATAGTATCACCCGA	TTCCTTTTACAGAAAGGGGTCAACTGTTA	C	T
	A1_BA_grs_15621_381	GAAGGTGACCAAGTTCATGCTACTTTATCGTTGGCCTCCACTTC	GAAGGTCGGAGTCAACGGATTGTACTTTATCGTTGGCCTCCACTTA	ATGCTGATGACTGGCTACAGACCAT	G	T
*	A1_BA_grs_48964_201	GAAGGTGACCAAGTTCATGCTACTTAAATAAAATTGGATATTAATAAATCCTCG	GAAGGTCGGAGTCAACGGATTACTTAAATAAAATTGGATATTAATAAATCCTCA	CTTTGGCCAAGCATTGGAAATAAAATATTT	C	T
*	A1_BA_grs_14661_262	GAAGGTGACCAAGTTCATGCTACTATATGCACTTTGTATGTGGTACTG	GAAGGTCGGAGTCAACGGATTCAACTATATGCACTTTGTATGTGGTACTA	GACATCCTTTTTAGGACAGAGGGAGTA	C	T
	A1_BA_grs_81202_340	GAAGGTGACCAAGTTCATGCTACGCCACCCAACGAGC	GAAGGTCGGAGTCAACGGATTGGCTACGCCACCCAACGAGA	CCCATTGGTCCTTCGAGTCTTGTAT	G	T
*	A1_BA_grs_60195_261	GAAGGTGACCAAGTTCATGCTAATGACCGTAGCAGCAAATACCG	GAAGGTCGGAGTCAACGGATTACAATGACCGTAGCAGCAAATACCA	CAGATTGGCTTCCACCAGCGTCAT	C	T
*	A1_BA_grs_51160_138	GAAGGTGACCAAGTTCATGCTAATGACCAAAGGAATTGACAGATTCAG	GAAGGTCGGAGTCAACGGATTAATAATGACCAAAGGAATTGACAGATTCAA	CTCTAAACTAAGTGGGATAAGTGAGGTTT	C	T
	A1_BA_grs_106084_135	GAAGGTGACCAAGTTCATGCTAATCCCCACCCTATAATTTGCAAGC	GAAGGTCGGAGTCAACGGATTAATCCCCACCCTATAATTTGCAAGA	GCACTTAATAAACCTGAACCATTGTGACTA	G	T
*	A1_BA_grs_33240_271	GAAGGTGACCAAGTTCATGCTAAGGAAACAAAATGAGATATACAGCGC	GAAGGTCGGAGTCAACGGATTCAAGGAAACAAAATGAGATATACAGCGT	CAACTACTTGAAGGACAAGATTGACAGAT	C	T
*	A1_BA_grs_50167_170	GAAGGTGACCAAGTTCATGCTAACAGATTAAGGAGGATAATATCCACC	GAAGGTCGGAGTCAACGGATTAATAACAGATTAAGGAGGATAATATCCACT	GTCATGTGTAATAGTTATTTTAAAACCCAA	C	T
*	A1_BA_grs_34847_329	GAAGGTGACCAAGTTCATGCTAAAATAGATGTCTCTGATTTATCAAAATTTGG	GAAGGTCGGAGTCAACGGATTAAAATAGATGTCTCTGATTTATCAAAATTTGA	CAAAGTTCTACTCCCTCCGTCTTCAA	C	T
*	A1_BA_grs_39190_179	GAAGGTGACCAAGTTCATGCTAAAACTAATTTGGGTTTTACCCACGC	GAAGGTCGGAGTCAACGGATTCTAAAACTAATTTGGGTTTTACCCACGA	ATCCACTAAGAAACGATGCCTATTTCCAA	G	T
	A1_BA_grs_40487_277	GAAGGTGACCAAGTTCATGCTTTTACTTCAAGAATTTGAGTTACAGATTATGT	GAAGGTCGGAGTCAACGGATTACTTCAAGAATTTGAGTTACAGATTATGC	TAAATTCCCTCTCAATAAGATTGGTGTCTT	G	A
*	A1_BA_grs_34486_253	GAAGGTGACCAAGTTCATGCTTTGATGTCAAAGCTTCCTGTTACTCT	GAAGGTCGGAGTCAACGGATTGATGTCAAAGCTTCCTGTTACTCC	CCATAGTCCACCCTCCAACATATGTA	G	A
	A1_BA_grs_51019_92	GAAGGTGACCAAGTTCATGCTTTCGTATGACTGAATGAGCACACA	GAAGGTCGGAGTCAACGGATTTCGTATGACTGAATGAGCACACG	GGCAATGGTTCATTCATTTTTTAGGACATA	G	A
*	A1_BA_grs_59490_137	GAAGGTGACCAAGTTCATGCTTTAGACGTGTGTGTCTCGTGCA	GAAGGTCGGAGTCAACGGATTAGACGTGTGTGTCTCGTGCG	ACATCCACGTGCAATTTCTTTTAGCATTAA	G	A
	A1_BA_grs_36058_254	GAAGGTGACCAAGTTCATGCTTTACCCTTTTCCATCCTGACTCA	GAAGGTCGGAGTCAACGGATTTACCCTTTTCCATCCTGACTCG	GACACTTCAAATAATTTGTTGACCCGGTA	G	A
	A1_BA_grs_80985_168	GAAGGTGACCAAGTTCATGCTTGTCTTTTCCTGCGATAGGCACAA	GAAGGTCGGAGTCAACGGATTGTCTTTTCCTGCGATAGGCACAG	CAACAACAACAACAACAATACTACCCCAA	G	A
*	A1_BA_grs_61430_134	GAAGGTGACCAAGTTCATGCTTGTCCACTCTAACTTGACCTTCTA	GAAGGTCGGAGTCAACGGATTGTCCACTCTAACTTGACCTTCTG	AGCCCCAAAGAATTTGAAGATGAAGTAAAA	G	A
	A1_BA_grs_104756_232	GAAGGTGACCAAGTTCATGCTTGTATTTCACTAATGATTATGTTACCTTCAAT	GAAGGTCGGAGTCAACGGATTGTATTTCACTAATGATTATGTTACCTTCAAC	CCCATACCAAGAGAAAATTATGAAACTATT	G	A
*	A1_BA_grs_14014_347	GAAGGTGACCAAGTTCATGCTTGATGTGTTTTATAAAGTAATTGCAATCTA	GAAGGTCGGAGTCAACGGATTCTTGATGTGTTTTATAAAGTAATTGCAATCTC	CACCACTCAAGTCGATAACCAATAATTCAT	C	A
	A1_BA_grs_38814_204	GAAGGTGACCAAGTTCATGCTTGACAGTATGCCGCCATGGTA	GAAGGTCGGAGTCAACGGATTGACAGTATGCCGCCATGGTG	CGACCTCGTCGCCGGGCAA	G	A
	A1_BA_grs_33610_229	GAAGGTGACCAAGTTCATGCTTCGCGATGATGACAACTTGCAGAA	GAAGGTCGGAGTCAACGGATTCGCGATGATGACAACTTGCAGAG	CATGTTGGTGGACTCAAAGGGCAAT	G	A

*	A1_BA_grs_56846_299	GAAGGTGACCAAGTTCATGCTTATTGTTTCCAAACCTCACCCATGTA	GAAGGTCGGAGTCAACGGATTGTTTCCAAACCTCACCCATGTC	GGTATGTCATGATGGAATGATGCACAATT	C	A
*	A1_BA_grs_15682_209	GAAGGTGACCAAGTTCATGCTTATGCTATTATAGATATGCATACACGATAAAT	GAAGGTCGGAGTCAACGGATTATGCTATTATAGATATGCATACACGATAAAA	AGATTTTATTGGCTTCTTATCTACCAATAT	T	A
	A1_BA_grs_58853_122	GAAGGTGACCAAGTTCATGCTGTTTCTTCCACTTTCATCTTACCCAAAT	GAAGGTCGGAGTCAACGGATTTCTTCCACTTTCATCTTACCCAAAG	ATCCTCCCTTTCTTCATGAAAAGCCAT	C	A
	A1_BA_grs_16845_418	GAAGGTGACCAAGTTCATGCTGTTTAGCAGGTTTGAGATCGACGTT	GAAGGTCGGAGTCAACGGATTTAGCAGGTTTGAGATCGACGTC	TAACTCTGCCCAAGCCAAGACGAAA	G	A
	A1_BA_grs_79173_335	GAAGGTGACCAAGTTCATGCTGTTGATCAAGACCCATCTCAAACCAT	GAAGGTCGGAGTCAACGGATTGATCAAGACCCATCTCAAACCAC	GAGACCACATAGTCAGTATCCT	G	A
	A1_BA_grs_27327_266	GAAGGTGACCAAGTTCATGCTGTTCTCTAAAGCTTTATCACCCTTCATTT	GAAGGTCGGAGTCAACGGATTCTCTAAAGCTTTATCACCCTTCATTC	GTATCTGGCGGAGTTCAAGAAGAAGTT	G	A
	A1_BA_grs_53408_169	GAAGGTGACCAAGTTCATGCTGTTCCGTACCCAATCGTCTGTTT	GAAGGTCGGAGTCAACGGATTGTTCCGTACCCAATCGTCTGTTC	AAGAGGATGGTTAATAATGGGTGGATGTA	G	A
*	A1_BA_grs_43203_300	GAAGGTGACCAAGTTCATGCTGTTATATGGAAAGTGGCCATGAAGAAA	GAAGGTCGGAGTCAACGGATTATATGGAAAGTGGCCATGAAGAAC	TACTATTCATCTGCCTGAGTTGGCTTAAA	C	A
	A1_BA_grs_79741_264	GAAGGTGACCAAGTTCATGCTGTGTTTCATGGAGAAGGTAAGGATGT	GAAGGTCGGAGTCAACGGATTGTTTCATGGAGAAGGTAAGGATGC	GCTTTGTTCATACAACATGTGATCCATCTT	G	A
	A1_BA_grs_24854_366	GAAGGTGACCAAGTTCATGCTGTGGTTCCAATTTTGCAACAGTGCAA	GAAGGTCGGAGTCAACGGATTGGTTCCAATTTTGCAACAGTGCAG	GACCCATTAAGAGATCCCAATAGTATCAT	G	A
	A1_BA_grs_22437_212	GAAGGTGACCAAGTTCATGCTGTGAGCTTGACAACCTCACTGATTT	GAAGGTCGGAGTCAACGGATTGAGCTTGACAACCTCACTGATTC	CAACACAAACTCAAGACTTTGCCCCAA	G	A
	A1_BA_grs_105522_310	GAAGGTGACCAAGTTCATGCTGTGAGATATGTACCTCAGATGA	GAAGGTCGGAGTCAACGGATTCTGTGAGATATGTACCTCAGATGC	AGTTGATACTCCCAGGCGGCAAATT	C	A
*	A1_BA_grs_30587_309	GAAGGTGACCAAGTTCATGCTGTCTCCAACCTCATAATCTTCCTGT	GAAGGTCGGAGTCAACGGATTCTCCAACCTCATAATCTTCCTGC	TATAGAGGGCCAGTGGCTGAGATAT	G	A
*	A1_BA_grs_36577_298	GAAGGTGACCAAGTTCATGCTGTCGATTGGGATAAGTTGTATCTGTA	GAAGGTCGGAGTCAACGGATTGTCGATTGGGATAAGTTGTATCTGTG	CAGCGAAACTTTATTATATCGAGGAGTGTT	G	A
*	A1_BA_grs_76666_228	GAAGGTGACCAAGTTCATGCTGTCATTAAACTATCAGTACCCAAGAAAAT	GAAGGTCGGAGTCAACGGATTGTCATTAAACTATCAGTACCCAAGAAAAG	CCGGTTGTATAGTTGTCATCGTATAGATA	C	A
*	A1_BA_grs_71608_236	GAAGGTGACCAAGTTCATGCTGTATTGGATGTAATATACTACATATATGATGTA	GAAGGTCGGAGTCAACGGATTATTGGATGTAATATACTACATATATGATGTG	TTCAGTAACCCCCCTCAGTGTATAATATA	G	A
*	A1_BA_grs_45226_173	GAAGGTGACCAAGTTCATGCTGTAACATCATTACACAATAGTCCACGATA	GAAGGTCGGAGTCAACGGATTAACATCATTACACAATAGTCCACGATG	GACTCATTGAGTCGTTGTTGTATATGTGTA	G	A
	A1_BA_grs_12489_263	GAAGGTGACCAAGTTCATGCTGGTTGCAGGACTACGGCAACA	GAAGGTCGGAGTCAACGGATTGGTTGCAGGACTACGGCAACG	CTTGAAGGCGACGTTGGGGCTA	G	A
	A1_BA_grs_108970_174	GAAGGTGACCAAGTTCATGCTGGGTTACCCCGAATCATCTCCA	GAAGGTCGGAGTCAACGGATTGGTTACCCCGAATCATCTCCG	CTTCACGCTACAAGCGCGGCAT	G	A
*	A1_BA_grs_36716_253	GAAGGTGACCAAGTTCATGCTGGGTGCTCCAAGTGCCTGGA	GAAGGTCGGAGTCAACGGATTGGTGCTCCAAGTGCCTGGC	CCCGCCGCCGCTGCAGATA	C	A
*	A1_BA_grs_62747_143	GAAGGTGACCAAGTTCATGCTGGGTGCACGAAAACGTTGCTCA	GAAGGTCGGAGTCAACGGATTGGTGCACGAAAACGTTGCTCC	GCACCATTGGAAAGAGGTGGAAGAT	C	A
	A1_BA_grs_18486_254	GAAGGTGACCAAGTTCATGCTGGGGACCCAACTTGACGGCT	GAAGGTCGGAGTCAACGGATTGGGACCCAACTTGACGGCC	GGTCCTTTTCGGCACGAATTCAACTT	G	A
	A1_BA_grs_29044_380	GAAGGTGACCAAGTTCATGCTGGGGAATTTTCCCAAGATTTATTGGAAT	GAAGGTCGGAGTCAACGGATTGGGAATTTTCCCAAGATTTATTGGAAG	GAAGAGCTTTTATTATTTCTTTTTGCCCAT	C	A
	A1_BA_grs_11886_318	GAAGGTGACCAAGTTCATGCTGGGCTTCCACCGTATCTGGAAT	GAAGGTCGGAGTCAACGGATTGGCTTCCACCGTATCTGGAAC	TGACATGGGTATACCCTGCAGGTA	G	A
	A1_BA_grs_38657_236	GAAGGTGACCAAGTTCATGCTGGGAGCCTCTATGTATTCAGGT	GAAGGTCGGAGTCAACGGATTGGGAGCCTCTATGTATTCAGGC	GTACTGACATGGGTATACCCTACAGAT	G	A
*	A1_BA_grs_24640_298	GAAGGTGACCAAGTTCATGCTGGCTTATATGGTGTAGAACATCCCT	GAAGGTCGGAGTCAACGGATTGCTTATATGGTGTAGAACATCCCC	CCGCACTATTAAGAGGGGTGATCTT	G	A
	A1_BA_grs_109496_109	GAAGGTGACCAAGTTCATGCTGGCTGGATGAGTTGGCTTGGAT	GAAGGTCGGAGTCAACGGATTGCTGGATGAGTTGGCTTGGAC	CGGACTCGATGTTGCAAATCTTGCAA	G	A
	A1_BA_grs_68552_274	GAAGGTGACCAAGTTCATGCTGGATTCTTTCACTTCAATAATTTGAGTTGT	GAAGGTCGGAGTCAACGGATTCTTTCACTTCAATAATTTGAGTTGC	ACATGGACACTGCATCCAACATCTTTATT	G	A
*	A1_BA_grs_56415_156	GAAGGTGACCAAGTTCATGCTGGATAGGGAATCACATTAGGGTTCA	GAAGGTCGGAGTCAACGGATTGATAGGGAATCACATTAGGGTTCG	AAGATCGACATCGACCAAGGCGAAT	G	A
*	A1_BA_grs_19233_349	GAAGGTGACCAAGTTCATGCTGGATAATACTAATAAGTTTCCTGTTATTATTAT	GAAGGTCGGAGTCAACGGATTGGATAATACTAATAAGTTTCCTGTTATTATTAG	GAGTTCTTCTTTTTCATACCCTGAAAGTTT	C	A
*	A1_BA_grs_46785_170	GAAGGTGACCAAGTTCATGCTGGACTAATACATACTTGTGATTACACCT	GAAGGTCGGAGTCAACGGATTGACTAATACATACTTGTGATTACACCG	CAAGGTAGTGTAGGATCTCAGAGTTTAAT	C	A
*	A1_BA_grs_37242_105	GAAGGTGACCAAGTTCATGCTGGAACATGAACTCATTTAAAGTTGGTCA	GAAGGTCGGAGTCAACGGATTGAACATGAACTCATTTAAAGTTGGTCG	GGAAGTTCTCTATTACTTCTTGCAATGGTT	G	A
	A1_BA_grs_24295_273	GAAGGTGACCAAGTTCATGCTGGAAAAATGGTAGTCACAGGCCA	GAAGGTCGGAGTCAACGGATTGGAAAAATGGTAGTCACAGGCCG	GGGCGGATAGTCCGCTCCTTA	G	A
	A1_BA_grs_27270_298	GAAGGTGACCAAGTTCATGCTGCGCTCAGTATTCCATTTGGTTTTTTT	GAAGGTCGGAGTCAACGGATTCGCTCAGTATTCCATTTGGTTTTTTC	CACTGTACGGTCCGATCGTACCAA	G	A
*	A1_BA_grs_33459_192	GAAGGTGACCAAGTTCATGCTGCCGACATGAGCAGCGGCT	GAAGGTCGGAGTCAACGGATTGCCGACATGAGCAGCGGCA	AAGAGATATGCTGGCAAGCCTGGTA	T	A
	A1_BA_grs_52311_297	GAAGGTGACCAAGTTCATGCTGCCCGAATGAGATGGGACAAAAAT	GAAGGTCGGAGTCAACGGATTCCCGAATGAGATGGGACAAAAAG	GAGCTGTTCGTTCTCTCATCTTGCAT	C	A

	A1_BA_grs_20008_266	GAAGGTGACCAAGTTCATGCTGCAGCCGAATGCCAAGAAGACA	GAAGGTCGGAGTCAACGGATTCAGCCGAATGCCAAGAAGACG	CAACTCCTCCGGACAGATCAGGTT	G	A
	A1_BA_grs_85228_186	GAAGGTGACCAAGTTCATGCTGCACCGGTAGAATGAAGAGGACA	GAAGGTCGGAGTCAACGGATTCACCGGTAGAATGAAGAGGACG	CAATATCTTGTTGATGGTCTCGTCAAGAA	G	A
	A1_BA_grs_90064_270	GAAGGTGACCAAGTTCATGCTGCACAGACATCACATAATAATAGT	GAAGGTCGGAGTCAACGGATTGCTGCACAGACATCACATAATAATAGA	TGTTTTGCCAGCTTGTACGCGTCAA	T	A
*	A1_BA_grs_30988_169	GAAGGTGACCAAGTTCATGCTGATTTTCGACTACGGCTGCAAGATT	GAAGGTCGGAGTCAACGGATTTTCGACTACGGCTGCAAGATA	GAGTCGTCGACTCGTCCAGAGA	T	A
	A1_BA_grs_18775_143	GAAGGTGACCAAGTTCATGCTGATTGTGAAGAGTGCTACTCTCCT	GAAGGTCGGAGTCAACGGATTGTGAAGAGTGCTACTCTCCC	CAAAATAGTAACACATGCAAGACTTAGCAA	G	A
*	A1_BA_grs_19762_298	GAAGGTGACCAAGTTCATGCTGAGAGAATATCTAACCCTATTCTGGT	GAAGGTCGGAGTCAACGGATTGAGAGAATATCTAACCCTATTCTGGC	GATACCAATGGATAAAATGCCAACCTAAAA	G	A
	A1_BA_grs_101314_162	GAAGGTGACCAAGTTCATGCTGACTTAGAATAGTCATAACATGGTGTGA	GAAGGTCGGAGTCAACGGATTACTTAGAATAGTCATAACATGGTGTGG	GGTATTCTCCTTTGATGCTTTATTTGGGTT	G	A
	A1_BA_grs_71126_320	GAAGGTGACCAAGTTCATGCTGACGTGATGTTTCCGGTCCTCA	GAAGGTCGGAGTCAACGGATTACGTGATGTTTCCGGTCCTCG	CTGAAACAATGAGCGAGCATATATACCAT	G	A
	A1_BA_grs_20193_254	GAAGGTGACCAAGTTCATGCTGACAACTACATGTACGAATACGCA	GAAGGTCGGAGTCAACGGATTGACAACTACATGTACGAATACGCG	AGGCAGGACTTCGTCGAGTCCT	G	A
	A1_BA_grs_46505_339	GAAGGTGACCAAGTTCATGCTGAATTGACCTTAGTTTATTGAGTAATTCCT	GAAGGTCGGAGTCAACGGATTAATTGACCTTAGTTTATTGAGTAATTCCC	ATAAAGATGTTAGATGCAGTGTCCATGATT	G	A
	A1_BA_grs_87628_362	GAAGGTGACCAAGTTCATGCTGAAACTAATAATAAAGCTTAACTACTAATGT	GAAGGTCGGAGTCAACGGATTGAAACTAATAATAAAGCTTAACTACTAATGC	GCCACATGAGAATAAGGCATTTAAACTAAT	G	A
*	A1_BA_grs_80247_247	GAAGGTGACCAAGTTCATGCTCTGATCCTTCTTGGCAGTGATGA	GAAGGTCGGAGTCAACGGATTCTGATCCTTCTTGGCAGTGATGG	ACAATGCCCCGCTCCTACCCAA	G	A
	A1_BA_grs_27940_398	GAAGGTGACCAAGTTCATGCTCTATCTGCAACTGGTTGGACATGA	GAAGGTCGGAGTCAACGGATTATCTGCAACTGGTTGGACATGC	CGCTTATACGTACCCTCCAAGTTCTT	C	A
*	A1_BA_grs_29062_294	GAAGGTGACCAAGTTCATGCTCGTTGTCCAATGGGTCGATTGAT	GAAGGTCGGAGTCAACGGATTCGTTGTCCAATGGGTCGATTGAG	GTAAGAGTTCACCACTGTATTGAAAAACAT	C	A
	A1_BA_grs_65827_243	GAAGGTGACCAAGTTCATGCTCGTTCTCGCCCGTGTTGATGAT	GAAGGTCGGAGTCAACGGATTGTTCTCGCCCGTGTTGATGAC	GCGGAAGCAATAGCTTCCTCAAACAT	G	A
	A1_BA_grs_14856_167	GAAGGTGACCAAGTTCATGCTCGTGGACTATTGTGTAATGATATTACTTT	GAAGGTCGGAGTCAACGGATTCGTGGACTATTGTGTAATGATATTACTTC	AGGCACTTGTGTGTGGGTGGAAAA	G	A
	A1_BA_grs_27884_186	GAAGGTGACCAAGTTCATGCTCGTCTGAGCACGCCGCCA	GAAGGTCGGAGTCAACGGATTCGTCTGAGCACGCCGCCG	ACGCGATTAAGATCCAACGGCTGTA	G	A
*	A1_BA_grs_48709_370	GAAGGTGACCAAGTTCATGCTCGTCTCGTGCCAACCCCCA	GAAGGTCGGAGTCAACGGATTGTCTCGTGCCAACCCCCG	ACGGTACCCCTTGTTCTTGCCATA	G	A
	A1_BA_grs_53073_187	GAAGGTGACCAAGTTCATGCTCGTCAGGTCGGTGGCGTGT	GAAGGTCGGAGTCAACGGATTGTCAGGTCGGTGGCGTGC	GCAGCGACCATAACATCACCTTGTA	G	A
	A1_BA_grs_62164_185	GAAGGTGACCAAGTTCATGCTCGTATTACTGATTAGGGTGTTCCCA	GAAGGTCGGAGTCAACGGATTGTATTACTGATTAGGGTGTTCCCG	CGCGAGGGATACAGCCACGATA	G	A
*	A1_BA_grs_46971_284	GAAGGTGACCAAGTTCATGCTCGGGTGACACCAGCACCAATT	GAAGGTCGGAGTCAACGGATTCGGGTGACACCAGCACCAATC	GCCACCATTTGGTATACCGCCGTT	G	A
*	A1_BA_grs_19263_402	GAAGGTGACCAAGTTCATGCTCGGCCGTATAGTTGGTTCCAGAT	GAAGGTCGGAGTCAACGGATTGGCCGTATAGTTGGTTCCAGAC	GGTAATCTAACTGACCCGAGATAGAAATA	G	A
*	A1_BA_grs_82325_251	GAAGGTGACCAAGTTCATGCTCGCGTGCAACGTCACCTTCTT	GAAGGTCGGAGTCAACGGATTCGCGTGCAACGTCACCTTCTC	CTTAGATGAAGGCAGAGCACGGTAT	G	A
	A1_BA_grs_56930_320	GAAGGTGACCAAGTTCATGCTCGCGCCCGTACCAGTGGTT	GAAGGTCGGAGTCAACGGATTGCGCCCGTACCAGTGGTC	GGAATTGGGAAGCAATTCCAAGGCAA	G	A
*	A1_BA_grs_13689_196	GAAGGTGACCAAGTTCATGCTCGCCGTCATCTACCAGCCCA	GAAGGTCGGAGTCAACGGATTCGCCGTCATCTACCAGCCCT	GTGAGGGTCGTTGGGGGGTTTA	T	A
	A1_BA_grs_59839_437	GAAGGTGACCAAGTTCATGCTCGCACCGCAGATGACTGGCT	GAAGGTCGGAGTCAACGGATTGCACCGCAGATGACTGGCC	TTGCGATTGGCAGCGAGTAGTAGAA	G	A
	A1_BA_grs_52013_239	GAAGGTGACCAAGTTCATGCTCGAGTGTCCAGTGGAATCGCAT	GAAGGTCGGAGTCAACGGATTGAGTGTCCAGTGGAATCGCAG	CTAAGTCATACACTCGAAAGGCTTCATAA	C	T
	A1_BA_grs_38605_241	GAAGGTGACCAAGTTCATGCTCCTCGTCCATATCACTTGATTCCTTA	GAAGGTCGGAGTCAACGGATTCTCGTCCATATCACTTGATTCCTTG	GTGGAAAGGGCAAAAGGGGAAGAAT	G	A
	A1_BA_grs_67060_298	GAAGGTGACCAAGTTCATGCTCCTCATCATGGGAGTCAGCAACA	GAAGGTCGGAGTCAACGGATTCTCATCATGGGAGTCAGCAACG	GGAGCCATCTCCATCGACTCCA	G	A
	A1_BA_grs_63261_245	GAAGGTGACCAAGTTCATGCTCCTAATCACTACATGTGTGACGTCA	GAAGGTCGGAGTCAACGGATTCTAATCACTACATGTGTGACGTCG	CGATATTGTCGCGATTGCTGCCATT	G	T
	A1_BA_grs_54171_335	GAAGGTGACCAAGTTCATGCTCCGGTGAAAAGAATCTGCACATCT	GAAGGTCGGAGTCAACGGATTCCGGTGAAAAGAATCTGCACATCA	AAGAGAGCCAGTGTGATGGGATCTT	T	A
	A1_BA_grs_53308_90	GAAGGTGACCAAGTTCATGCTCCCTACCGACAGGCCTTTGTA	GAAGGTCGGAGTCAACGGATTCCCTACCGACAGGCCTTTGTT	CGCACCGGTATACAACGAATCAGAT	T	A
	A1_BA_grs_75066_120	GAAGGTGACCAAGTTCATGCTCCCCTGGACTGGTACTATAGCTA	GAAGGTCGGAGTCAACGGATTCCCTGGACTGGTACTATAGCTG	CATATCCATCATCCACATGCACAGTATAT	G	A
*	A1_BA_grs_43059_259	GAAGGTGACCAAGTTCATGCTCCCCTACCAACGACTCGCCT	GAAGGTCGGAGTCAACGGATTCCCTACCAACGACTCGCCC	GGTGGCTGGAGAAGGAGGAAGTT	G	A
	A1_BA_grs_42311_200	GAAGGTGACCAAGTTCATGCTCCCAGCCACTCATACATGTTT	GAAGGTCGGAGTCAACGGATTCTCCCAGCCACTCATACATGTTC	TGGAGAAATGCAACTGATTTGAAGCGATT	G	A
*	A1_BA_grs_104629_102	GAAGGTGACCAAGTTCATGCTCCCAAGAAACCAAGAAAAGGAACTCT	GAAGGTCGGAGTCAACGGATTCCAAGAAACCAAGAAAAGGAACTCC	TTCATCTTCCACTGTTCATGCTTCCATAA	G	A

	A1_BA_grs_58830_200	GAAGGTGACCAAGTTCATGCTCCATGGCACAGATCTGGGACA	GAAGGTCGGAGTCAACGGATTCCATGGCACAGATCTGGGACG	GACTCAGGATGGGGAGGAGGA	G	A
	A1_BA_grs_73447_285	GAAGGTGACCAAGTTCATGCTCCATCTCCGCCTTCCCCTCA	GAAGGTCGGAGTCAACGGATTCATCTCCGCCTTCCCCTCG	GTCTGGACCTTACCTGACATCGATT	G	A
	A1_BA_grs_56980_100	GAAGGTGACCAAGTTCATGCTCATTATGAGAAGAAAATGAGTGCTGTCAT	GAAGGTCGGAGTCAACGGATTATGAGAAGAAAATGAGTGCTGTCAG	GTGCTCATCATAATTCATAAGTGTGCCAA	C	A
*	A1_BA_grs_46633_285	GAAGGTGACCAAGTTCATGCTCATTACAAGGATTTAGTAGGTAAATAACATATT	GAAGGTCGGAGTCAACGGATTACAAGGATTTAGTAGGTAAATAACATATG	TTTGTACATTGTCATTGATGATAGCATATA	C	A
	A1_BA_grs_21036_210	GAAGGTGACCAAGTTCATGCTCATGTCGTTAGAAACCAATACCTCT	GAAGGTCGGAGTCAACGGATTCATGTCGTTAGAAACCAATACCTCG	AGTTTCGTGAGGATCCTACAGCCAT	C	A
	A1_BA_grs_103043_193	GAAGGTGACCAAGTTCATGCTCATGCAAAAATAGATGAAATAACATAAGTATCA	GAAGGTCGGAGTCAACGGATTATGCAAAAATAGATGAAATAACATAAGTATCG	GGGAGGGGGTGATACGTCCATT	G	A
	A1_BA_grs_11338_127	GAAGGTGACCAAGTTCATGCTCACCACTAACAAGGATTCTTTCTGCA	GAAGGTCGGAGTCAACGGATTACCACTAACAAGGATTCTTTCTGCG	GCGATCATGGACATCAACCCTTGTT	G	A
	A1_BA_grs_35877_183	GAAGGTGACCAAGTTCATGCTATTTTTCTAATCTTCTTTTGTATCTTCTTCCA	GAAGGTCGGAGTCAACGGATTTTCTAATCTTCTTTTGTATCTTCTTCCG	GAATAGGGAGGGAAGGTGGGGTA	G	A
	A1_BA_grs_107962_149	GAAGGTGACCAAGTTCATGCTATTCGTTGTATACCGGTT	GAAGGTCGGAGTCAACGGATTCGTTGTATACCGGTG	CTACGGAAACAAACACCCCAAACAATATA	C	A
	A1_BA_grs_45108_445	GAAGGTGACCAAGTTCATGCTATTATCCCTCTTTCTACCTATTTTATATTTCT	GAAGGTCGGAGTCAACGGATTATCCCTCTTTCTACCTATTTTATATTTCC	GAGGTTCCAGGGAAGTATAAAGGAGTA	G	A
	A1_BA_grs_26197_264	GAAGGTGACCAAGTTCATGCTATTACTTCAGTAATGACCTCTCCTTATTA	GAAGGTCGGAGTCAACGGATTACTTCAGTAATGACCTCTCCTTATTC	TCTCATTAGAGGTCATTCTTGGCACAAA	C	A
	A1_BA_grs_19842_193	GAAGGTGACCAAGTTCATGCTATCGCCACCTGGTATAGGCGA	GAAGGTCGGAGTCAACGGATTCGCCACCTGGTATAGGCGG	TTTGAGGAAGTACACACGACCAAGTAATT	G	A
	A1_BA_grs_53256_289	GAAGGTGACCAAGTTCATGCTATCCGCTGTTGCGGTTGTCGTT	GAAGGTCGGAGTCAACGGATTCCGCTGTTGCGGTTGTCGTC	AGGACCGCGAAGAGGTCGACAT	G	A
*	A1_BA_grs_37642_255	GAAGGTGACCAAGTTCATGCTATCAATTCGACGAAAGTAGATCCTCAA	GAAGGTCGGAGTCAACGGATTCAATTCGACGAAAGTAGATCCTCAC	AGGATCCGATGGAAAGTTCTGATTCTTAT	C	A
	A1_BA_grs_52644_193	GAAGGTGACCAAGTTCATGCTATAGATTTCAATATAACTTGTCCATTAAAGGT	GAAGGTCGGAGTCAACGGATTATAGATTTCAATATAACTTGTCCATTAAAGGA	CCACCGGTGCCTCTGCATTAGTT	T	A
	A1_BA_grs_80127_217	GAAGGTGACCAAGTTCATGCTATACGAGGAGGCTCCACAAGGT	GAAGGTCGGAGTCAACGGATTATACGAGGAGGCTCCACAAGGA	AATATCGAGGGAGTGAGGATGCCAT	T	A
*	A1_BA_grs_86814_283	GAAGGTGACCAAGTTCATGCTAGTCTGGGACAATAAACATTGAACACA	GAAGGTCGGAGTCAACGGATTGTCTGGGACAATAAACATTGAACACG	CCAACTATCAGGTTGATGATGAAATCCTT	G	A
*	A1_BA_grs_59767_194	GAAGGTGACCAAGTTCATGCTAGGGAGAAGTTGTTCGAAGAGCA	GAAGGTCGGAGTCAACGGATTGGGAGAAGTTGTTCGAAGAGCG	GAGCAATGCAAAAATCCAGCCAAAAGAAT	G	A
*	A1_BA_grs_47079_104	GAAGGTGACCAAGTTCATGCTAGCAGCGAGGAAGAGCACCAA	GAAGGTCGGAGTCAACGGATTGCAGCGAGGAAGAGCACCAG	CTCGATGAGAGATAGAGGAGGACAA	G	A
*	A1_BA_grs_11530_300	GAAGGTGACCAAGTTCATGCTAGATTTATCTAAATTTTGACAAATCTAAGACAT	GAAGGTCGGAGTCAACGGATTAGATTTATCTAAATTTTGACAAATCTAAGACAA	CGACCGCTACTCGCTCTGTTTTAAA	T	A
*	A1_BA_grs_53772_252	GAAGGTGACCAAGTTCATGCTAGATCTCGAGCAAGATCGCTCTAT	GAAGGTCGGAGTCAACGGATTGATCTCGAGCAAGATCGCTCTAC	TACTGGCTTTTAACTATTGCACGATCGAT	G	A
	A1_BA_grs_44524_221	GAAGGTGACCAAGTTCATGCTAGAGTGGCAGATACATTGGTGTCAA	GAAGGTCGGAGTCAACGGATTAGTGGCAGATACATTGGTGTCAG	ACATTGCTCGGGTTCGCTAACTCAT	G	A
*	A1_BA_grs_33480_316	GAAGGTGACCAAGTTCATGCTAGAGCTGCCTATAATGATCCAGCTA	GAAGGTCGGAGTCAACGGATTAGCTGCCTATAATGATCCAGCTG	TAGGGGACTACATCAATTCAACTGCATTA	G	A
*	A1_BA_grs_41650_119	GAAGGTGACCAAGTTCATGCTAGACATTTACATGGTTGAAAGAAGTTTGA	GAAGGTCGGAGTCAACGGATTGACATTTACATGGTTGAAAGAAGTTTGC	GGAATAAGCAGTGCCTAAAGTAGCAAA	C	A
	A1_BA_grs_41971_299	GAAGGTGACCAAGTTCATGCTAGACATATTATCGCGTCGGGCAT	GAAGGTCGGAGTCAACGGATTGACATATTATCGCGTCGGGCAC	CAGCAACTCTAACAGCCAAACAAGGTA	G	A
*	A1_BA_grs_83083_209	GAAGGTGACCAAGTTCATGCTACTTTCCTAATTGGACCACCCCA	GAAGGTCGGAGTCAACGGATTCTTTCCTAATTGGACCACCCCG	TGGACTGTGTCTTGGAGCCCATTA	G	A
	A1_BA_grs_105440_108	GAAGGTGACCAAGTTCATGCTACTTGGACAAGCGGAGGAGT	GAAGGTCGGAGTCAACGGATTACTTGGACAAGCGGAGGAGC	TTTGCTGCTGAGATTTGGAGCATTTGAT	G	A
*	A1_BA_grs_51204_398	GAAGGTGACCAAGTTCATGCTACTGGTTGCAGACCACGGAGA	GAAGGTCGGAGTCAACGGATTCTGGTTGCAGACCACGGAGG	CCAAATAATGGGTGGCAAACAGTACTTT	G	A
	A1_BA_grs_89134_157	GAAGGTGACCAAGTTCATGCTACTGGTTCTGTCACAAAGATACAAATTAT	GAAGGTCGGAGTCAACGGATTACTGGTTCTGTCACAAAGATACAAATTAA	CATTACATTGTGCCACCCCATAGTTTAAA	T	A
*	A1_BA_grs_72129_148	GAAGGTGACCAAGTTCATGCTACTGGTTCCAACGGAACATTCTGTT	GAAGGTCGGAGTCAACGGATTGGTTCCAACGGAACATTCTGTG	CGGTACGCCGTATACTGACCCTT	C	A
	A1_BA_grs_87629_432	GAAGGTGACCAAGTTCATGCTACTGGAAGCCAATGAGAAGGTACTA	GAAGGTCGGAGTCAACGGATTGGAAGCCAATGAGAAGGTACTG	CAAGCTCTTGCATCTCCTACCAGAT	G	A
*	A1_BA_grs_31176_165	GAAGGTGACCAAGTTCATGCTACCCATCAGGGAGAATATCATTTTGT	GAAGGTCGGAGTCAACGGATTCCCATCAGGGAGAATATCATTTTGC	GTGATTAAAATCAACTCGGGTACCACATT	G	A
	A1_BA_grs_31932_150	GAAGGTGACCAAGTTCATGCTACCAATCCACCAATGCGAATGTCAT	GAAGGTCGGAGTCAACGGATTCAATCCACCAATGCGAATGTCAC	TCATCCAACACTTACGTTACGAAAGCAA	G	A
	A1_BA_grs_23681_127	GAAGGTGACCAAGTTCATGCTACATGGAGCACTAAAAGCATATTCGA	GAAGGTCGGAGTCAACGGATTCATGGAGCACTAAAAGCATATTCGG	CTTTTCGACTGCTGTCATTTTTTGGTTTTA	G	A
*	A1_BA_grs_47354_274	GAAGGTGACCAAGTTCATGCTACATGCATAGAAGTTTTTGATGCAATAGT	GAAGGTCGGAGTCAACGGATTCATGCATAGAAGTTTTTGATGCAATAGG	CCTCTTCAATTGACAAACAAGAATTAATAA	C	A
	A1_BA_grs_60258_411	GAAGGTGACCAAGTTCATGCTACATGAAGGACTTTTGCATAAGCCATT	GAAGGTCGGAGTCAACGGATTCATGAAGGACTTTTGCATAAGCCATC	CATTCTCTAATGGATGCTTTGGTATTTGTT	G	A

	A1_BA_grs_18518_151	GAAGGTGACCAAGTTCATGCTAATTTGAGTTGCAGATTACGTAGAGGA	GAAGGTCGGAGTCAACGGATTTGAGTTGCAGATTACGTAGAGGC	GGTAAATATGGACACTGCATCCAACAT	C	A
	A1_BA_grs_48751_262	GAAGGTGACCAAGTTCATGCTAATTAGTCCAAGTAAGGTTGGTACATTAT	GAAGGTCGGAGTCAACGGATTAGTCCAAGTAAGGTTGGTACATTAG	GACTTATCTTTTTTGGGTTGGATAAGTGTT	C	A
*	A1_BA_grs_12021_267	GAAGGTGACCAAGTTCATGCTAAGCTACGTGTACCCATTGCTGA	GAAGGTCGGAGTCAACGGATTAGCTACGTGTACCCATTGCTGG	GGATTACTAATGGACAGTATAAGAGTGGAA	G	A
	A1_BA_grs_47016_305	GAAGGTGACCAAGTTCATGCTAAGAAGGTCGGAGTATTTGTATGTCT	GAAGGTCGGAGTCAACGGATTAGAAGGTCGGAGTATTTGTATGTCC	GAGAAATCTCTCTGCCAAAGAAGAA	G	A
	A1_BA_grs_30528_368	GAAGGTGACCAAGTTCATGCTAAGAAGACGTGTAATGGATGCAGGA	GAAGGTCGGAGTCAACGGATTGAAGACGTGTAATGGATGCAGGC	CCTCGTCGCTCCCGTCGCTT	C	A
	A1_BA_grs_15019_243	GAAGGTGACCAAGTTCATGCTAACCTACGGACTCTCGATTGCTTA	GAAGGTCGGAGTCAACGGATTCCTACGGACTCTCGATTGCTTG	GGTTTATTAGGTTAGGGTTTTCCCCTTT	G	A
	A1_BA_grs_18673_214	GAAGGTGACCAAGTTCATGCTAAATTTCGGAAAATCCCAGTACTCA	GAAGGTCGGAGTCAACGGATTAAATTTCGGAAAATCCCAGTACTCG	TAGATGAGTGCATCTTGACATGGTGAA	G	A
*	A1_BA_grs_56304_148	GAAGGTGACCAAGTTCATGCTAAAGTTCTATACTATCACACCATATATTTTATT	GAAGGTCGGAGTCAACGGATTAAAGTTCTATACTATCACACCATATATTTTATG	TACATGAAATTTGTATGTGTAGGTTCACAT	C	A
	A1_BA_grs_53396_285	GAAGGTGACCAAGTTCATGCTAAAATAGGATTTACAATGGTGCAACTATCA	GAAGGTCGGAGTCAACGGATTATAGGATTTACAATGGTGCAACTATCC	TGTTGAAATGCCCTTATGCATTGCTTGAA	C	A
	A1_BA_grs_17433_232	GAAGGTGACCAAGTTCATGCTAAAACTTAGCGAAATACCTTGTTTTTGAT	GAAGGTCGGAGTCAACGGATTAAAACTTAGCGAAATACCTTGTTTTTGAC	CTGCTATATATATGTTGTTGTTGGTCGATA	G	A
*	A1_BA_grs_54878_365	GAAGGTGACCAAGTTCATGCTTTCTTAGCAAGGGAGAGGGC	GAAGGTCGGAGTCAACGGATTCTTTCTTAGCAAGGGAGAGGGG	GTCTGGCGAGTTTCCAGCGACAA	G	C
*	A1_BA_grs_48654_247	GAAGGTGACCAAGTTCATGCTTGCACTTCATTTAGATATATTATATCAAGTTG	GAAGGTCGGAGTCAACGGATTGCACTTCATTTAGATATATTATATCAAGTTC	CTCATCTATCACATGACAAACCTCAAGAA	G	C
*	A1_BA_grs_48954_165	GAAGGTGACCAAGTTCATGCTTGAATAAAGTTACTACATATTTGCAAAGATTC	GAAGGTCGGAGTCAACGGATTGAATAAAGTTACTACATATTTGCAAAGATTG	CGACTTCAACAATATTTTATGCAACTCCAA	G	C
*	A1_BA_grs_15424_351	GAAGGTGACCAAGTTCATGCTTAAGTACTTCTTCAACTATCATTTATTGATTC	GAAGGTCGGAGTCAACGGATTAAGTACTTCTTCAACTATCATTTATTGATTG	GAAGTATGTCTGGATGAATGATTGAAGTTT	G	C
*	A1_BA_grs_11279_261	GAAGGTGACCAAGTTCATGCTTAAATTTTGCTTTGATAGTTAGAAGGAAG	GAAGGTCGGAGTCAACGGATTCTTAAATTTTGCTTTGATAGTTAGAAGGAAC	AAGGCATTAGTCTCTTCCATTTGTGGAAA	G	C
*	A1_BA_grs_46326_352	GAAGGTGACCAAGTTCATGCTGTGCTACCACCCAAGTCACCC	GAAGGTCGGAGTCAACGGATTGTGCTACCACCCAAGTCACCG	ATGATGAAGCATCCGACTAAGACAAGAA	G	C
	A1_BA_grs_71922_213	GAAGGTGACCAAGTTCATGCTGGGCAAGGTCAGATAGCTCAC	GAAGGTCGGAGTCAACGGATTGGGCAAGGTCAGATAGCTCAG	GTTGCAATGGATGAAGGGAAGGAGAA	G	C
	A1_BA_grs_38932_277	GAAGGTGACCAAGTTCATGCTGGAACACTATGCTGCACCGAC	GAAGGTCGGAGTCAACGGATTGGAACACTATGCTGCACCGAG	CGTTTTTATTCTGTCCGCTCGGACA	G	C
*	A1_BA_grs_53534_342	GAAGGTGACCAAGTTCATGCTGCGAAAAATGTATCCACATTTTGCCG	GAAGGTCGGAGTCAACGGATTGCGAAAAATGTATCCACATTTTGCCC	CGAAGGGTAGAATTAGGATTTTGTGCATA	G	C
	A1_BA_grs_24133_220	GAAGGTGACCAAGTTCATGCTGCCGGAGAATTTCGCACCGG	GAAGGTCGGAGTCAACGGATTGCCGGAGAATTTCGCACCGC	GAAACGAGCGCGAGAAAATCTTGGAA	G	C
	A1_BA_grs_52701_211	GAAGGTGACCAAGTTCATGCTGCAACTTCTGTTATAGTTCCTGACTC	GAAGGTCGGAGTCAACGGATTGCAACTTCTGTTATAGTTCCTGACTG	GGTCTCCTTAAGTTCTTTCTCCTCCTT	G	C
	A1_BA_grs_43175_312	GAAGGTGACCAAGTTCATGCTGACCCTCAGCCGTTGGATTAC	GAAGGTCGGAGTCAACGGATTGACCCTCAGCCGTTGGATTAG	AATGCGAAGCGGTATGGGGCAATAT	G	C
*	A1_BA_grs_42447_129	GAAGGTGACCAAGTTCATGCTGAAATAGTTTCCTTCTGATTATCTACTC	GAAGGTCGGAGTCAACGGATTGAAATAGTTTCCTTCTGATTATCTACTG	GCCCTTATTCTTTTTAGATAGGTCCTTTTA	G	C
	A1_BA_grs_107582_142	GAAGGTGACCAAGTTCATGCTCGTCGGGAGAGTCAGGCAC	GAAGGTCGGAGTCAACGGATTCGTCGGGAGAGTCAGGCAG	GTGCAACTTTGTCTTTCAAGAGAATGTGTA	G	C
	A1_BA_grs_86796_211	GAAGGTGACCAAGTTCATGCTCCAAATTCAAGAAAAAAAGAAAGCACATAC	GAAGGTCGGAGTCAACGGATTCCAAATTCAAGAAAAAAAGAAAGCACATAG	CAAATGGGGATGGCCATTTGATTTAAGTT	G	C
*	A1_BA_grs_70743_208	GAAGGTGACCAAGTTCATGCTATGTCTTGTGACACTATACCACAGG	GAAGGTCGGAGTCAACGGATTATGTCTTGTGACACTATACCACAGC	TGACCAACGTCGGTAGGGAATGTT	G	C
	A1_BA_grs_16722_197	GAAGGTGACCAAGTTCATGCTAGTAAGGTTGTAGATCACCTGGAC	GAAGGTCGGAGTCAACGGATTAGTAAGGTTGTAGATCACCTGGAG	AAACTGGTCATGTCAACATTCTGTAACATA	G	C
*	A1_BA_grs_56623_203	GAAGGTGACCAAGTTCATGCTACTGAACATACTTTTCCTGTGAACAAG	GAAGGTCGGAGTCAACGGATTACTGAACATACTTTTCCTGTGAACAAC	GAGAAACAAAAAGGACAACGTGTATGCAA	G	C
	A1_BA_grs_33588_367	GAAGGTGACCAAGTTCATGCTTTTGATGAGACGGAGCCGCG	GAAGGTCGGAGTCAACGGATTCTTTTGATGAGACGGAGCCGCA	CCACTGGTATGGGCAGGTCCTA	C	T
*	A1_BA_grs_47541_269	GAAGGTGACCAAGTTCATGCTTTTATTTCCGTTACAACGCACGGG	GAAGGTCGGAGTCAACGGATTTTTATTTCCGTTACAACGCACGGA	ACCAAAGCGCATGGTGATGGACAAA	C	T
	A1_BA_grs_68625_250	GAAGGTGACCAAGTTCATGCTTTGTCCTTGAATGATCTCGTTCCG	GAAGGTCGGAGTCAACGGATTTTGTCCTTGAATGATCTCGTTCCA	GGTGCAACTCAATGGCAGATTGATATTT	C	T
	A1_BA_grs_48692_162	GAAGGTGACCAAGTTCATGCTTTGCTGCCAAAGAAGGCCACG	GAAGGTCGGAGTCAACGGATTTTGCTGCCAAAGAAGGCCACA	CGGAGGGGGTGATTTTTTCCACATA	C	T
	A1_BA_grs_35482_158	GAAGGTGACCAAGTTCATGCTTTGAGGATCTCGATGAAGAAGTCC	GAAGGTCGGAGTCAACGGATTATTTGAGGATCTCGATGAAGAAGTCT	GCTGTTCGGCACGCACATCGAT	C	T
	A1_BA_grs_78757_173	GAAGGTGACCAAGTTCATGCTTTCCAATCATCAAATCGTAACAAAGAAAC	GAAGGTCGGAGTCAACGGATTCATTTCCAATCATCAAATCGTAACAAAGAAAA	GTGGAAAAAAATTGGGGATAGTGTGGTTT	G	T
	A1_BA_grs_23049_342	GAAGGTGACCAAGTTCATGCTTGTCTTCATAAGAAGAGCCATAGAC	GAAGGTCGGAGTCAACGGATTCTTGTCTTCATAAGAAGAGCCATAGAT	TTGTTGTTAGGTTGAAGGCCAAAGATGAT	C	T
	A1_BA_grs_76099_302	GAAGGTGACCAAGTTCATGCTTGGGATCGACACTCCTATTTATCG	GAAGGTCGGAGTCAACGGATTTTGGGATCGACACTCCTATTTATCA	GATGACCCACAAGTATAGGGGTGTA	C	T

	A1_BA_grs_30365_191	GAAGGTGACCAAGTTCATGCTTGATGGTCTTGTCAATCCGG	GAAGGTCGGAGTCAACGGATTGCTTGATGGTCTTGTCAATCCGA	GGACCTGCAATACGGTCCGCAA	C	T
	A1_BA_grs_52811_326	GAAGGTGACCAAGTTCATGCTTGAAGTGGCATGACCATGTCATC	GAAGGTCGGAGTCAACGGATTGTTGAAGTGGCATGACCATGTCATT	GAATAAGTCAATCATCTGACTCCACCATA	C	T
	A1_BA_grs_32880_174	GAAGGTGACCAAGTTCATGCTTCTCCGAGGTGTAATGGACGC	GAAGGTCGGAGTCAACGGATTTCTCCGAGGTGTAATGGACGT	GACAAATCTCTTCATCCTTCCGAGAAAT	C	T
*	A1_BA_grs_78160_131	GAAGGTGACCAAGTTCATGCTTCCACACCTTTCGTATTAATAAGTTATAG	GAAGGTCGGAGTCAACGGATTCTTCCACACCTTTCGTATTAATAAGTTATAA	CTCAAATTAAGTGCTCGAACAGTAAAACTT	C	T
	A1_BA_grs_52683_312	GAAGGTGACCAAGTTCATGCTTCATCTTTGGTTCTCTTCCAGAC	GAAGGTCGGAGTCAACGGATTCTTCATCTTTGGTTCTCTTCCAGAT	GAAGGAAGAGGAAAGCATGCCAGAA	C	T
	A1_BA_grs_53746_224	GAAGGTGACCAAGTTCATGCTTCAAGTGAGAGATTGCCATGATTTG	GAAGGTCGGAGTCAACGGATTGTTCAAGTGAGAGATTGCCATGATTTT	ATTCTAATCCTGTAGGAGCTCCTTACAAT	G	T
	A1_BA_grs_35289_349	GAAGGTGACCAAGTTCATGCTTATTTGGAGGTGAGCTCACTCTG	GAAGGTCGGAGTCAACGGATTGTTATTTGGAGGTGAGCTCACTCTT	GATGTTCACTACAAGGCTCGTAGGA	G	T
*	A1_BA_grs_23902_337	GAAGGTGACCAAGTTCATGCTGTGGCCTCCCAAACATAACACG	GAAGGTCGGAGTCAACGGATTCGTGGCCTCCCAAACATAACACA	AATTCATTTGTCATCAATGTGTTGTTTGTT	C	T
	A1_BA_grs_11386_159	GAAGGTGACCAAGTTCATGCTGTGCTGGATTCTGTTGTTGTGAATC	GAAGGTCGGAGTCAACGGATTGTGCTGGATTCTGTTGTTGTGAATA	GTGAAAATTTGCAACATGGTTCAAAGGAAT	G	T
*	A1_BA_grs_47664_114	GAAGGTGACCAAGTTCATGCTGTGATAATCATTTGTCCATGATTTTTGGC	GAAGGTCGGAGTCAACGGATTGTGATAATCATTTGTCCATGATTTTTGGA	GTGCAAACCAACCATTGGAAAGAGAAATT	G	T
*	A1_BA_grs_47188_142	GAAGGTGACCAAGTTCATGCTGTCCGTATATCATGTTCTCGTCG	GAAGGTCGGAGTCAACGGATTAGGTCCGTATATCATGTTCTCGTCA	CAGCTCATAGTCCTCCGAAAACGAA	C	T
	A1_BA_grs_42224_318	GAAGGTGACCAAGTTCATGCTGTCACTCACACGGCCACGG	GAAGGTCGGAGTCAACGGATTGGTCACTCACACGGCCACGA	CTGCTGGCCAGTCGTGGCGAT	C	T
	A1_BA_grs_24550_366	GAAGGTGACCAAGTTCATGCTGTATCAAGGTGACAGTGAGCTCG	GAAGGTCGGAGTCAACGGATTGTATCAAGGTGACAGTGAGCTCA	AACAGACCAGCCGCCGTTGCTA	C	T
	A1_BA_grs_11448_330	GAAGGTGACCAAGTTCATGCTGTACACTAACCGGACATCACCC	GAAGGTCGGAGTCAACGGATTCGTACACTAACCGGACATCACCT	GACAGTCCGGTCCTGCTGGAAA	C	T
*	A1_BA_grs_78633_101	GAAGGTGACCAAGTTCATGCTGGTGCTGTCGTGAGGTCGAC	GAAGGTCGGAGTCAACGGATTGGTGCTGTCGTGAGGTCGAT	CAGCTTAATTCTAAGTTCTAATGCTGGCAT	C	T
	A1_BA_grs_32742_102	GAAGGTGACCAAGTTCATGCTGGTGCCTGACGATGACTCC	GAAGGTCGGAGTCAACGGATTCTGGTGCCTGACGATGACTCA	TCCGGGAGCTGTACTTCCGCAA	G	T
	A1_BA_grs_16269_315	GAAGGTGACCAAGTTCATGCTGGTCGACTACATACTCGACGG	GAAGGTCGGAGTCAACGGATTATGGTCGACTACATACTCGACGA	CCTCTGGGGTCTCAAGGTCCAT	C	T
*	A1_BA_grs_82583_373	GAAGGTGACCAAGTTCATGCTGGTCCACAATGAGCAAGTCCG	GAAGGTCGGAGTCAACGGATTGGGTCCACAATGAGCAAGTCCA	CCATCGTTGCTTCGTCATCTTCTGTT	C	T
	A1_BA_grs_27250_399	GAAGGTGACCAAGTTCATGCTGGTATCAGTTAACCACCTTAGGTG	GAAGGTCGGAGTCAACGGATTCGGTATCAGTTAACCACCTTAGGTT	CCGGGGACTCAAATTCGAGTTAGAT	G	T
	A1_BA_grs_59169_329	GAAGGTGACCAAGTTCATGCTGGGTTACCGGTATTCTTCGTCG	GAAGGTCGGAGTCAACGGATTGGGGTTACCGGTATTCTTCGTCA	CGTTCCCGTCCACCTCCGCAA	C	T
	A1_BA_grs_14011_86	GAAGGTGACCAAGTTCATGCTGGGGCGTTCGCCTAACTAAG	GAAGGTCGGAGTCAACGGATTAGGGGGCGTTCGCCTAACTAAA	CATACAAGTTAGACATGCATTTCCGACTT	C	T
	A1_BA_grs_32174_235	GAAGGTGACCAAGTTCATGCTGGGGCCTTTGGAAGCATTTCTTC	GAAGGTCGGAGTCAACGGATTGGGGCCTTTGGAAGCATTTCTTT	ATTGGATAGAGAAAATGGCACCACCAA	C	T
	A1_BA_grs_78039_332	GAAGGTGACCAAGTTCATGCTGGGGATATGAGTATCACGAGCG	GAAGGTCGGAGTCAACGGATTATGGGGATATGAGTATCACGAGCA	GTTGCAACAAACATAAGGACTACTTGCTT	C	T
	A1_BA_grs_12696_405	GAAGGTGACCAAGTTCATGCTGGCCTCCTCGCTAACC	GAAGGTCGGAGTCAACGGATTGCTGGCCTCCTCGCTAACT	TTGTAGCTACGTCGCCGACTGATT	C	T
	A1_BA_grs_27804_162	GAAGGTGACCAAGTTCATGCTGGCAAATATGGACACTGCATTCC	GAAGGTCGGAGTCAACGGATTGGGCAAATATGGACACTGCATTCA	TAAGCCAAGACTAATCCGTTGGATTCTTT	G	T
*	A1_BA_grs_48665_240	GAAGGTGACCAAGTTCATGCTGGATGTTACAAGTGGTCCTTAGG	GAAGGTCGGAGTCAACGGATTGGGATGTTACAAGTGGTCCTTAGA	CTAACCCCGTGCTGGTCTCCAA	C	T
	A1_BA_grs_40520_224	GAAGGTGACCAAGTTCATGCTGGACAAGTACGCCACCACCG	GAAGGTCGGAGTCAACGGATTGGACAAGTACGCCACCACCA	GGCATTGGTCGTCCACCACGAT	C	T
	A1_BA_grs_55573_159	GAAGGTGACCAAGTTCATGCTGGAAGAGTCACAGAAGCGTGAG	GAAGGTCGGAGTCAACGGATTGGAAGAGTCACAGAAGCGTGAT	TCCCTTTCGGCAGTGGAAGCAC	G	T
	A1_BA_grs_59466_289	GAAGGTGACCAAGTTCATGCTGCCTGACAATGACTTTTATGATGCG	GAAGGTCGGAGTCAACGGATTGGCCTGACAATGACTTTTATGATGCA	GGTAATAATTGTTTCATTGATCGATGCGTA	T	A
*	A1_BA_grs_58339_94	GAAGGTGACCAAGTTCATGCTGCCTCTGTCCGACACCGTAC	GAAGGTCGGAGTCAACGGATTGGCCTCTGTCCGACACCGTAT	ATAATAATGTTTAGATATAGGGAGGTGCAT	C	A
	A1_BA_grs_97232_198	GAAGGTGACCAAGTTCATGCTGCCGAGCAGGTTCGTCCAC	GAAGGTCGGAGTCAACGGATTGGCCGAGCAGGTTCGTCCAT	AAATCTGTGGGGCGTCACAGCAAT	C	T
*	A1_BA_grs_33469_357	GAAGGTGACCAAGTTCATGCTGCCCGAACCAAAGAAGTAGTCG	GAAGGTCGGAGTCAACGGATTGCCCGAACCAAAGAAGTAGTCA	GACTCTTCCTCCACTCCCTCCAA	C	T
	A1_BA_grs_46578_124	GAAGGTGACCAAGTTCATGCTGCCAGGCCATCAGATGATATCC	GAAGGTCGGAGTCAACGGATTGCCAGGCCATCAGATGATATCT	GCACCTCCGCGGTGACAAACAT	C	T
*	A1_BA_grs_48157_183	GAAGGTGACCAAGTTCATGCTGCAGCTGCTTGCCAGCGAC	GAAGGTCGGAGTCAACGGATTGGCAGCTGCTTGCCAGCGAT	CAGGCCCACATAACCTTTCGATGTT	C	T
	A1_BA_grs_71494_201	GAAGGTGACCAAGTTCATGCTGCACACAATACATCAGAAAGAGAAATTG	GAAGGTCGGAGTCAACGGATTGCACACAATACATCAGAAAGAGAAATTA	GTCTCGTTGCTATTGGTTATTGATGCTTT	C	T
	A1_BA_grs_12452_228	GAAGGTGACCAAGTTCATGCTGCACAAGGACCAGGAGGAGAC	GAAGGTCGGAGTCAACGGATTGCACAAGGACCAGGAGGAGAA	CGTGGGTTGAAGTAGTCGAACTTGTA	G	T

*	A1_BA_grs_68304_263	GAAGGTGACCAAGTTCATGCTGCAAGTCCATCCCTATCAGACC	GAAGGTCGGAGTCAACGGATTAGCAAGTCCATCCCTATCAGACA	AATGAAGGCCAACCTCCTGTCGAAA	G	T
	A1_BA_grs_42814_142	GAAGGTGACCAAGTTCATGCTGATTTTTCATTACCCTCACCTTGGC	GAAGGTCGGAGTCAACGGATTTTTCATTACCCTCACCTTGGA	TATTGTAATCACACATATGTAACCTATC	G	T
	A1_BA_grs_59471_274	GAAGGTGACCAAGTTCATGCTGATTGTAAGAAACTTGGGTACCGC	GAAGGTCGGAGTCAACGGATTCTGATTGTAAGAAACTTGGGTACCGT	TTTAGTGAATATCATTTTGCGGCCGGAAA	G	A
	A1_BA_grs_85766_116	GAAGGTGACCAAGTTCATGCTGATTGAGCAATAATATAACTATACACAACAAC	GAAGGTCGGAGTCAACGGATTGATTGAGCAATAATATAACTATACACAACAAT	GGTGTATCAGATAACAAAGAAACAGAGTTT	C	T
	A1_BA_grs_78962_114	GAAGGTGACCAAGTTCATGCTGATTATTAGTGCAAATAACAAAGGTACAG	GAAGGTCGGAGTCAACGGATTATGATTATTAGTGCAAATAACAAAGGTACAA	TACCACAGGTTCATCACTCAAATGCTTA	C	T
*	A1_BA_grs_25602_97	GAAGGTGACCAAGTTCATGCTGATGTAGATAAGAAGTTCAGTAGGAAC	GAAGGTCGGAGTCAACGGATTCAGATGTAGATAAGAAGTTCAGTAGGAAT	GACCATCAATCCCTCATGTACAATTTCTT	C	T
*	A1_BA_grs_106636_308	GAAGGTGACCAAGTTCATGCTGATGGGTCCAAGCTTATGTAAATGC	GAAGGTCGGAGTCAACGGATTAGATGGGTCCAAGCTTATGTAAATGT	CCATTGTTCGACCCTTCCAGGTATA	C	T
*	A1_BA_grs_56634_308	GAAGGTGACCAAGTTCATGCTGATGACCAAACGTTCTCGAGGG	GAAGGTCGGAGTCAACGGATTAAGATGACCAAACGTTCTCGAGGA	GTGCACCCACATAACACTTATAGAAACTA	C	T
	A1_BA_grs_24770_197	GAAGGTGACCAAGTTCATGCTGATCGTAATGTCTGGCATATTATCC	GAAGGTCGGAGTCAACGGATTCTGATCGTAATGTCTGGCATATTATCT	GATAGCATGCCAACTGAATTTGAAGCAAA	C	T
	A1_BA_grs_38476_404	GAAGGTGACCAAGTTCATGCTGAGTCTATAGAATCATGAGGTATCAC	GAAGGTCGGAGTCAACGGATTCGAGTCTATAGAATCATGAGGTATCAT	ATCATATTGCTGTCGTGGAGGCGAT	C	T
*	A1_BA_grs_49141_251	GAAGGTGACCAAGTTCATGCTGAATTTTGGCTTCGATCGTATAGTTG	GAAGGTCGGAGTCAACGGATTGGAATTTTGGCTTCGATCGTATAGTTA	GGTCGCTAAACTCTTAGATACTTTTGATTT	C	T
	A1_BA_grs_43235_276	GAAGGTGACCAAGTTCATGCTGAAGAATCATCTGCATGAAGAAAGAAATC	GAAGGTCGGAGTCAACGGATTGAAGAATCATCTGCATGAAGAAAGAAATA	GACTTCATGATAACCTTTGTATAACTCGTT	C	T
*	A1_BA_grs_30023_391	GAAGGTGACCAAGTTCATGCTGAACTGCCTTAAGAAGGAGATTGC	GAAGGTCGGAGTCAACGGATTATGAACTGCCTTAAGAAGGAGATTGT	CATTCTACTCGTCGGCAGCTTTCTT	C	T
	A1_BA_grs_49273_381	GAAGGTGACCAAGTTCATGCTCTGAGCCATATGAACAGGAG	GAAGGTCGGAGTCAACGGATTATGCTCTGAGCCATATGAACAGGAT	TCGCAAGGGTCTTCTTTCATTTAATTGTTT	G	T
	A1_BA_grs_54366_188	GAAGGTGACCAAGTTCATGCTCTAACAACTTGCAGGCACGATAAG	GAAGGTCGGAGTCAACGGATTTCTAACAACTTGCAGGCACGATAAA	CAAGGACTAAGATGTCCTCCTCGTT	C	T
	A1_BA_grs_16440_119	GAAGGTGACCAAGTTCATGCTCGTTGAGCCTGATCACGAC	GAAGGTCGGAGTCAACGGATTGCTCGTTGAGCCTGATCACGAT	CCGAACCCCCTACCATAATCAACAA	C	T
	A1_BA_grs_24346_208	GAAGGTGACCAAGTTCATGCTCGCGTTCAGTCGAGTCCCG	GAAGGTCGGAGTCAACGGATTCCGCGTTCAGTCGAGTCCCA	CGGCCCTACTCGTCAGTACGTA	C	T
	A1_BA_grs_50225_298	GAAGGTGACCAAGTTCATGCTCGATCGGTAGCAGGTGGGAC	GAAGGTCGGAGTCAACGGATTCGATCGGTAGCAGGTGGGAA	GCATGGGGCGTTTCCTCACCAT	A	G
*	A1_BA_grs_58678_155	GAAGGTGACCAAGTTCATGCTCGATACGGAGGGGGACTCG	GAAGGTCGGAGTCAACGGATTGCGATACGGAGGGGGACTCA	GTAACTATGCTCGGGATTTCTCGGTA	C	T
	A1_BA_grs_64219_182	GAAGGTGACCAAGTTCATGCTCGAATCTACGATTCGAGCAATTACTC	GAAGGTCGGAGTCAACGGATTCGAATCTACGATTCGAGCAATTACTT	AATTGACAGTAGTGCAGGACCTTAATCAT	C	T
	A1_BA_grs_28403_184	GAAGGTGACCAAGTTCATGCTCGAATAAAAATCATTCATAAAAGTGGAACAAC	GAAGGTCGGAGTCAACGGATTACGAATAAAAATCATTCATAAAAGTGGAACAAT	TCACACTTCGTGAGACGGTTATTCATAT	C	T
	A1_BA_grs_60745_305	GAAGGTGACCAAGTTCATGCTCCTACTCCTCCAGCTGCTGC	GAAGGTCGGAGTCAACGGATTGCCTACTCCTCCAGCTGCTGA	GTCCCCGTCCTCTTCCTCATCAT	G	T
	A1_BA_grs_11491_366	GAAGGTGACCAAGTTCATGCTCCGTCAATGGATTGATGACTTGTC	GAAGGTCGGAGTCAACGGATTCCCGTCAATGGATTGATGACTTGTT	GTGAATGCTTCTTGCATGTCCAACTAATT	C	T
*	A1_BA_grs_46256_397	GAAGGTGACCAAGTTCATGCTCCGGTGATGTCTTCGGCGATG	GAAGGTCGGAGTCAACGGATTCCGGTGATGTCTTCGGCGATA	GTAGCAAAATCAACAAAAGGTAGGTAGCAA	C	T
	A1_BA_grs_19849_241	GAAGGTGACCAAGTTCATGCTCCGAGTGTCCAGTGGAATCG	GAAGGTCGGAGTCAACGGATTCTCCGAGTGTCCAGTGGAATCA	TAAAATATGCTCAGTCACGCACTCGAA	C	T
	A1_BA_grs_27977_326	GAAGGTGACCAAGTTCATGCTCCCAAAATAAGGTGTTAGCAAAGGTC	GAAGGTCGGAGTCAACGGATTACCCAAAATAAGGTGTTAGCAAAGGTT	CTTGATGGAATTGAAGAAGATCATCAAGTT	C	T
	A1_BA_grs_77928_183	GAAGGTGACCAAGTTCATGCTCCAGAAGGATCTCAGTCAGGC	GAAGGTCGGAGTCAACGGATTGTCCAGAAGGATCTCAGTCAGGT	ACTCATTTGCATAATGCCCCATCTTCTT	C	T
	A1_BA_grs_81933_295	GAAGGTGACCAAGTTCATGCTCCAACCACTTCATGTGCACCG	GAAGGTCGGAGTCAACGGATTCCCAACCACTTCATGTGCACCA	GTTGTCACGATTGGCGGAGGTGTT	C	T
*	A1_BA_grs_33710_307	GAAGGTGACCAAGTTCATGCTCATGTCTCTATCATTGCTACTCCC	GAAGGTCGGAGTCAACGGATTGCATGTCTCTATCATTGCTACTCCA	TCTAGATTCGGATGTATGTAGACACGTTT	G	T
*	A1_BA_grs_29303_369	GAAGGTGACCAAGTTCATGCTCATGCATGGCACGCACATGTTG	GAAGGTCGGAGTCAACGGATTCATGCATGGCACGCACATGTTA	CCGATGGGAAACAACAAGCGGCA	C	T
	A1_BA_grs_58968_164	GAAGGTGACCAAGTTCATGCTCATCTCACGAAAGGTCAAGCATAC	GAAGGTCGGAGTCAACGGATTCCATCTCACGAAAGGTCAAGCATAT	TTCTTTAAGCAAGTGCTGGCTTATCCATT	C	T
	A1_BA_grs_53165_195	GAAGGTGACCAAGTTCATGCTCATCATAGCATGTAATTGCATTGCATTC	GAAGGTCGGAGTCAACGGATTATCATCATAGCATGTAATTGCATTGCATTT	CTTTTTATTCATGGCTCAAAATTGCACCAA	C	T
	A1_BA_grs_21211_197	GAAGGTGACCAAGTTCATGCTCATATTTTCTGGTGGCAACTGCTG	GAAGGTCGGAGTCAACGGATTGCATATTTTCTGGTGGCAACTGCTA	CCTCTACCCTTGAAGGGAGACGAT	T	G
	A1_BA_grs_39767_130	GAAGGTGACCAAGTTCATGCTCATATTTGAGGAGAGATGGCACG	GAAGGTCGGAGTCAACGGATTACCATATTTGAGGAGAGATGGCACA	CAACTTCTGGATTTTTTCCGTACTGCTAT	C	T
	A1_BA_grs_104918_246	GAAGGTGACCAAGTTCATGCTCATAAGACAGCTAACCTCAAGAGG	GAAGGTCGGAGTCAACGGATTGCATAAGACAGCTAACCTCAAGAGA	ATCTGCTGCCCTCAAGAATGCCTA	C	T
	A1_BA_grs_36952_124	GAAGGTGACCAAGTTCATGCTCAGTCACCCATACAGACCACTG	GAAGGTCGGAGTCAACGGATTGCAGTCACCCATACAGACCACTT	GGACTCCCTAAGCTAATTATGATATCCAT	G	T

	A1_BA_grs_25906_286	GAAGGTGACCAAGTTCATGCTCACTTCATGTGCGCCGTTATCC	GAAGGTCGGAGTCAACGGATTCCACTTCATGTGCGCCGTTATCA	GCGGAGGTGTCGCCTGCGT	G	T
	A1_BA_grs_65050_207	GAAGGTGACCAAGTTCATGCTCACTCGCCCATGAACTTTTGGG	GAAGGTCGGAGTCAACGGATTGCACTCGCCCATGAACTTTTGGA	GCCGTAGAGAAACAGTGTGTCGAAA	C	T
	A1_BA_grs_48971_177	GAAGGTGACCAAGTTCATGCTCACTACTTCTTTGTACTGTATTTGTTCG	GAAGGTCGGAGTCAACGGATTGCACTACTTCTTTGTACTGTATTTGTTCA	CGTCACATCTGGCTAATATGTCATAAGAT	C	T
	A1_BA_grs_48040_202	GAAGGTGACCAAGTTCATGCTCAATCCTGCATAAAAGGATTGGATAG	GAAGGTCGGAGTCAACGGATTAATTCAATCCTGCATAAAAGGATTGGATAA	GGGAAAGAATGAAATCTTTAGTGAGGAATT	C	T
	A1_BA_grs_11460_254	GAAGGTGACCAAGTTCATGCTCAAGTTTTCTGGAGAGATGACTTCG	GAAGGTCGGAGTCAACGGATTGCAAGTTTTCTGGAGAGATGACTTCA	GCAAATTGTTCAAGTGTTAAAGGATTTGAT	C	T
	A1_BA_grs_44566_218	GAAGGTGACCAAGTTCATGCTCAAGTAAGGTCGGTACATTAGCAC	GAAGGTCGGAGTCAACGGATTCCAAGTAAGGTCGGTACATTAGCAT	TGATTAATCTTCTTTGGTTGGATAAGTGTT	C	T
*	A1_BA_grs_55135_245	GAAGGTGACCAAGTTCATGCTCAAATTGACCGTATGGCCCTCAG	GAAGGTCGGAGTCAACGGATTCAAATTGACCGTATGGCCCTCAA	GGTAGACGGTTTTCTAATATTGCCAGAAT	C	T
	A1_BA_grs_55523_149	GAAGGTGACCAAGTTCATGCTCAAAGCATCAATATCCAATGGCAACG	GAAGGTCGGAGTCAACGGATTACAAAGCATCAATATCCAATGGCAACA	CCTGTGGTTTGCTTGCAAGCATGTT	C	T
	A1_BA_grs_34451_197	GAAGGTGACCAAGTTCATGCTATTTTAACAGAGGCAAAACATTAAACAC	GAAGGTCGGAGTCAACGGATTAACTATTTTAACAGAGGCAAAACATTAAACAT	TATCAATGGAATCAGGAGAGAGAATCATTT	C	T
*	A1_BA_grs_46767_204	GAAGGTGACCAAGTTCATGCTATTTGAGAATATGGAAATTAAGCCAAGAC	GAAGGTCGGAGTCAACGGATTCATTTGAGAATATGGAAATTAAGCCAAGAT	CTTACCTTAACACCAGTTGACAAAAGCTA	C	T
*	A1_BA_grs_66329_305	GAAGGTGACCAAGTTCATGCTATTGCCACGGTTGCTTTTTCATTGC	GAAGGTCGGAGTCAACGGATTATTGCCACGGTTGCTTTTTCATTGT	CTTATTGCCACGAAATGATGTTCATTGGAA	C	T
	A1_BA_grs_39022_147	GAAGGTGACCAAGTTCATGCTATTGAAGAACAAGACTATCTATTTAGTTGC	GAAGGTCGGAGTCAACGGATTAATATTGAAGAACAAGACTATCTATTTAGTTGT	GCAACTTAAATTGCAGGCATAAGTGAAGTA	C	T
	A1_BA_grs_49490_162	GAAGGTGACCAAGTTCATGCTATTCTCGCCCCTGCTCCGG	GAAGGTCGGAGTCAACGGATTCTCGCCCCTGCTCCGA	GGGCGCTGAGTGAGGGGAAAT	C	T
	A1_BA_grs_105835_262	GAAGGTGACCAAGTTCATGCTATTCCAATCATTCACTTAAATATAAAGTGAAC	GAAGGTCGGAGTCAACGGATTATTCCAATCATTCACTTAAATATAAAGTGAAT	TCCCAAGTTTTAGATTTATGATAGGTATAA	C	T
	A1_BA_grs_59440_334	GAAGGTGACCAAGTTCATGCTATGTTATACCATGCAATTGTGCATC	GAAGGTCGGAGTCAACGGATTGCTATGTTATACCATGCAATTGTGCATT	TATGCAACAAGACAAAACAAGGTATGCCA	C	T
	A1_BA_grs_106231_245	GAAGGTGACCAAGTTCATGCTATGTGAAATTGAATTTCATGCACAACTTAG	GAAGGTCGGAGTCAACGGATTGATGTGAAATTGAATTTCATGCACAACTTAA	GGCATGCTTGCTTTCTTTGATCCAATATA	C	T
*	A1_BA_grs_49269_122	GAAGGTGACCAAGTTCATGCTATGTAAAAGTGTTATGATATGGTTCTTGC	GAAGGTCGGAGTCAACGGATTCATATGTAAAAGTGTTATGATATGGTTCTTGT	TATATTATCACAGCCATCAATGAACAAGAT	C	T

* Indicates robust primer sets used for genetic mapping

Allele 1 and 2 indicates the SNP being interrogated