2013-03-13

Application of Genome Reduction, Next Generation Sequencing, and KASPar Genotyping in Development, Characterization, and Linkage Mapping of Single Nucleotide Polymorphisms in the Grain Amaranths and Quinoa

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Polymorphisms in the Grain Amaranths and Quinoa

Scott M. Smith

A thesis submitted to the faculty of
Brigham Young University
in partial fulfillment of the requirements for the degree of

Master of Science

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March 2013

ABSTRACT

Application of Genome Reduction, Next Generation Sequencing, and KASPar Genotyping
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Master of Science

The grain amaranths (*Amaranthus sp.*) and quinoa (*Chenopodium quinoa Willd.*) are important seed crops in South America. These crops have gained international attention in recent years for their nutritional quality and tolerance to abiotic stress. We report the identification and development of functional single nucleotide polymorphism (SNP) assays for both amaranth and quinoa. SNPs were identified using a genome reduction protocol and next generation sequencing. SNP assays are based on KASPar genotyping chemistry and were detected using the Fluidigm dynamic array platform. A diversity screen consisting of 41 amaranth accessions showed that the minor allele frequency (MAF) of the amaranth markers ranged from 0.05 to 0.5 with an average MAF of 0.27. A diversity screen of 113 quinoa accessions showed that the MAF of the quinoa markers ranged from 0.02 to 0.5 with an average MAF of 0.28. Linkage mapping in amaranth produced a linkage map consisting of 16 linkage groups, presumably corresponding to each of the 16 amaranth haploid chromosomes. This map spans 1288 cM with an average marker density of 3.1 cM per marker. Linkage mapping in quinoa resulted in a linkage map consisting of 29 linkage groups with 20 large linkage groups, spanning 1,404 cM with a marker density of 3.1 cM per SNP marker. The SNPs identified here represent important genomic tools needed for genetic dissection of agronomically important characteristics and advanced genetic analysis of agronomic traits in amaranth and quinoa. We also describe in detail the scalable and cost effective SNP genotyping method used in this research. This method is based on KBioscience's competitive allele specific PCR amplification of target sequences and endpoint fluorescence genotyping (KASPar™) using a FRET capable plate reader or Fluidigm's dynamic array high throughput platform.

ACKNOWLEDGEMENTS

First and foremost I would like to express my deep appreciation for my family, especially my wife, for her continual love and support throughout my education. I would also like to thank my graduate advisor and mentor, Dr. Maughan, for all his help and advice as well as for providing me with many opportunities that enriched my learning experience. Thanks to the rest of my committee, Dr. Jellen and Gongshe Hu for all their help and for Emir Islamovic who acted as a committee member even though he wasn't officially on my committee. Thanks to my fellow graduate peers who were all good sources of advice and friendship. Thanks to all the genetics faculty who have taught me so much in the classroom as well as in the lab.

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polymorphisms in the grain amaranths (Amaranthus sp.)

Introduction

The genus *Amaranthus* (Caryophyllales: Amaranthaceae) contains three domesticated

grain species, collectively referred to as the grain amaranths (*A. hypochondriacus* L., *A. cruentus*

L., and *A. caudatus* L.; Sauer 1976). These species, along with their putative progenitor species

(*A. hybridus* L., *A. quitensis* H.B.K., and *A. powellii* S. Wats.) are classified in what is termed the

A. hybridus complex and are considered paleo-allotetraploids ($2n=4x=32$; Greizerstein and

Poggio, 1994; Greizerstein and Poggio, 1995; Pal and Khoshoo, 1982). Amaranth was a major

domesticated food crop of the pre-Columbian New World civilizations, likely having been

domesticated multiple times over thousands of years ago (Mallory et al., 2008; Sauer, 1950). The

importance of the amaranths to these ancient civilizations cannot be overstated; indeed, the

Spaniards recorded that the Aztec emperor Moctezuma II required a tribute of approximately

200,000 bushels per year of amaranth, an amount nearly equal to the annual maize tribute (Sauer,

1950; Sauer, 1967; Sauer, 1993). At the time of the Spanish conquest, cultivation of the grain

amaranths was suppressed due to their deeply rooted use in indigenous religious practices

(Iturbide and Gispert, 1994; Sauer, 1976; Sauer, 1993). In the last few decades the grain

amaranths have begun to reclaim some of their importance, largely due to the potential

nutritional impact of their seed consumption on human health (Bressani et al., 1992; Tucker,

1986).

Amaranth grain is higher in fiber (8%) and fat (7 to 8%) than most cereals (Breene, 1991;

Pedersen et al., 1986). Crude grain protein content ranges from 12.5 to 22.5% on a dry matter

basis (Becker et al., 1981; Bressani et al., 1989; Bressani et al., 1987; Pedersen et al., 1986), and is relatively rich in the essential amino acid lysine normally limited in other cereal crops (0.73 to 0.84% of amaranth's total protein content; Bressani et al., 1987). Amaranth oil is also highly nutritious, containing a relatively high content of squalene (7-8%; Bressani et al., 1987) which has been shown to reduce cholesterol levels in humans (Berger et al., 2003; Martirosyan et al., 2007). The grain amaranths exhibit C_4 photosynthesis and grow rapidly under heat and drought-stress, as well as tolerate a variety of unfavorable abiotic conditions, including high salinity, acidity, or alkalinity, making them uniquely suited for subsistence agricultural. By implication, amaranth has the potential for significant impact on malnutrition (Emokaro et al., 2007). Genetic markers are essential tools for modern plant breeding research programs (Eathington et al., 2008). They are particularly important for germplasm conservation, core-collection characterization (Diwan et al., 1995; Tanksley and McCouch, 1997), and in breeding applications, such as marker-assisted selection (MAS). The first step toward the development of genetic markers for amaranth was the discovery and characterization of 179 microsatellite markers by Mallory et al. (2008). Unfortunately, only 37 of microsatellite markers segregated in their intraspecific *A. cruentus* F_2 mapping population resulting in a sparsely populated linkage map. A significant advance in the number of available markers occurred in 2009 when Maughan et al. reported the utilization of a novel genomic reduction strategy linked with next-generation sequencing to identify 27,658 putative single nucleotide polymorphisms (SNPs) among four diverse amaranth accessions. SNPs, defined as single base changes, are the most abundant type of DNA polymorphism found in eukaryotic genomes (Batley et al., 2003; Garg et al., 1999). Compared to microsatellites-based markers, SNPs exhibit a lower mutation rate and thus are less problematic in population genetic analyzes (Xu et al., 2005). SNPs have already been utilized in

a wide array of research areas, including association studies (Andrew et al., 2008), conservation genetics (Cramer et al., 2008), genetic diversity analysis (Kawuki et al., 2009), and are fast becoming the marker system of choice in marker-assisted plant breeding programs (Batley and Edwards, 2007).

The goals of this project were to i) develop the first large scale set of functional SNP assays for amaranth, ii) evaluate the informativeness (minor allele frequency) of the SNPs on a diversity panel consisting of the three grain amaranth species and their putative wild progenitor (*A. hybridus*), and iii) construct of the first complete genetic linkage map for the genus.

Materials and Methods

Plant Materials and DNA extraction.

The SNPs were used to genetically characterized a set of 41 diverse genotypes from the *A. hybridus* complex, including eleven *A. caudatus* accessions, ten *A. cruentus* accessions, ten *A. hypochondriacus* accessions, and ten *A. hybridus* accessions. Additionally, two accessions of *A. powellii*, and *A. retroflexus* L., and a single accession of *A. tuberculatus* (Moq.) Sauer were included in the diversity panel. These species were included to determine the utility of the SNP assays in these more distantly related, but important weedy relatives (Table 1). All seed samples were obtained from the USDA collection (USDA, Iowa State University, Ames, IA; Table 1). For linkage analysis, an interspecific F_2 population was developed from a cross of PI 481125 (maternal parent; *A. hypochondriacus*) and PI 642741 (*A. caudatus*). The F_2 population consisted of 134 plants produced by self-fertilizing a single F_1 plant. All plants were grown in greenhouses at Brigham Young University, Provo, UT in 12-cm pots using Sunshine Mix II (Sun Grow,

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Bellevue, WA) supplemented with Osmocote fertilizer (Scotts, Marysville, OH). Plants were

maintained at 18 °C under broad-spectrum halogen lamps with a 12-h photoperiod.

Total genomic DNA was extracted from 30mg of freeze-dried leaf tissue from a single plant for

each sample (diversity panel and F_2 population) according to procedures previously described

(Sambrook et al., 1989), with modifications described by Todd and Vodkin (Todd and Vodkin,

1996). Extracted DNA was quantified using a Nanodrop (ND 1000 Spectrophotometer,

NanoDrop Techonologies Inc., Montchanin, DE) and diluted to 20 ng μl^{-1} in 1/10 TE buffer

(10mM Tris, 1 mM EDTA, pH 8.0).

SNP Primer Design

A total of 480 putative SNPs were selected for genotyping from the 11,038 SNPs *in silico*

reported to be polymorphic between the parents of our mapping population (Maughan et al.,

2009). These 480 putative SNPs were selected based on several parameters, specifically that

they showed no significant homology to the RepeatMasker (v. 3.2.9 *Arabidopsis*) database or to

the *Arabidopsis* chloroplast (GenBank accession NC_000932) and mitochondrial (NC_001284)

genomes as determined by BLASTn (E-value $\geq$ 1e-05). These parameters were used to remove

putative SNPs that were potentially extranuclear in origin or matched repetitive DNA sequences.

The remaining sequences were then processed by the primer design software PrimerPicker

(KBiosciences Ldt., Hoddesdon, UK) using default design parameters and the first 480 SNPs

were selected for primers synthesis (Integrated DNA Technologies Inc., Iowa City, IA). Primer

sequence information for each of the functional KASPar™ SNP assays is provided in

Supplemental Table S1.

SNP Genotyping

The SNPs were genotyped by competitive allele-specific PCR KASPar™ chemistry (KBioscience Ldt., Hoddesdon, UK) using the Fluidigm (Fluidigm Corp., South San Francisco, CA) nanofluidic 96.96 dynamic array™ (Wang et al., 2009). For genotyping on the 96.96 dynamic array chip using the KASPar™ chemistry, a 5 µL sample mix, consisting of 2.25 µL genomic DNA (20 ng/µL), 2.5 µL of 2X KASP reagent Mix (KBioscience Ldt.) and 0.25 µL of 20X GT sample loading reagent (Fluidigm Corp., South San Francisco, CA) was prepared for each DNA sample. Similarly, a 4 µL 10X KASP Assay, containing 0.56 µL of the KASP assay primer mix (allele specific primers 12µM, common reverse primer 30 µM), 2 µL of 2X Assay Loading Reagent (Fluidigm Corp., South San Francisco, CA) and 1.44 µL DNase-free water was prepared for each SNP assay. The assay mix and sample mix were then loaded onto a 96.96 dynamic array chip, mixed and thermal cycled using an IFC Controller HX and FC1 thermal cycler (Fluidigm Corp., South San Francisco, CA) according to the manufacture's protocols. Thermal cycling consisted of an initial thermal mix cycle (70ºC – 30 min; 25ºC – 10 min) a hot-start Taq polymerase activation step (94ºC – 15 min) followed by a touchdown amplification protocol as follows: 10 cycles of 94ºC for 20 sec, 65ºC for 1 min (decreasing 0.8ºC per cycle), 26 cycles of 94ºC for 20 sec, 57ºC for 1 min; hold at 20ºC for 30 sec. End-point fluorescent images of the chip were acquired on an EP-1 imager (Fluidigm Corp., South San Francisco, CA) and the data analyzed with Fluidigm SNP genotyping Analysis Software®.

SNP Diversity Data Analysis

Alleles for each SNP were scored as present, absent, or missing (failed to amplify) and converted into a binary matrix to determine minor allele frequencies (MAF) for each SNP locus. The genetic distance among genotypes was calculated based on the matrices of allele frequencies

using Nei distance (Nei and Li, 1979). The clustering criterion used was neighbor joining and the resulting dendrogram was unrooted. Robustness of the topology of the cladogram was evaluated by bootstrap analysis (1000 replicates) of the data set.

Genetic Linkage Map Construction

Marker segregation was analyzed for conformity to Mendelian ratios expected in an F_2 population using a chi-squared test. Markers were initially grouped based on independence LOD scores ≥ 5.0 using the G2 statistic as calculated by JoinMap® 4 for recombination frequency (Van Ooijen, 2006). Markers within groups were then ordered using the regression mapping algorithms as described by Stam (1993), with the modification that the squares of the LODs are used as weights, in order to assign more weight to informative loci. Successive rounds of marker placement were utilized to add loci to the map. After the addition of each locus, a ripple test was applied to test for goodness-of-fit and assure the optimal map order.

Results and Discussion

SNP Assay Development

Maughan et al. (2009) previously reported the identification of 11,038 putative SNPs between the accessions PI 481125 and PI 642741 using a genomic reduction strategy based on restriction-site conservation and 454-pyrosequencing. Sequence information for all SNPs were deposited in dbSNP in GenBank under the handle MAUGHAN in batch number 2009A (GenBank: ss161123993 to ss161151650; build B131). From this sequence information, primer sets for 480 of the putative SNPs were designed for competitive allele-specific PCR based on the KASPar™ genotyping chemistry and screened using the Fluidigm 96.96 dynamic array chip. All 480 SNP markers were screened on the diversity panel and on an F_2 population derived from a

cross between PI 481125 and PI 642741 (Table 1). A total of 419 (87%) markers produced clearly separated genotypic clusters that could be easily scored with the automated Fluidigm SNP genotyping analysis software. The auto call software reported an average auto call rate of 94.3% across the diversity panel and F_2 population.

Diversity Panel

The diversity panel consisted of 46 samples, representing seven *Amaranthus* species. Limiting the analysis to just the grain amaranths (*A. caudatus*, *A. cruentus*, *A. hypochondricus*; *n*=31) and their putative wild ancestor (*A. hybridus*; *n*=10), a total of 414 (828 alleles) of the SNP markers were polymorphic, producing clearly separated genotypic clusters that could be scored with high confidence. Since SNPs are predominantly bi-allelic, the maximum MAF value of a SNP is 0.5 (which occurs when both alleles are present at equal frequencies in the test population). Across the full panel of grain amaranth and *A. hybridus* accessions, MAF values ranged from 0.05 to 0.5 with an average MAF-value of 0.27 per locus (Supplemental Table S1; Fig. 1). Considering a SNP with a MAF ≥ 0.3 to be highly polymorphic, 141 (34%) of the SNP loci were highly polymorphic (Table 2).

Within the *A. caudatus*, *A. cruentus*, *A. hypochondricus* and *A. hybridus* subgroups, a total of 136, 35, 186, and 263 SNP assays were polymorphic, respectively (Table 2). *A. hypochondricus* showed the highest total number of polymorphic SNP markers, while *A. cruentus* showed the lowest genetic diversity of the grain species with only 35 polymorphic markers. The reduced level of genetic diversity observed in *A. cruentus* is consistent with other observations using different types of genetic markers including, microsatellites, RFLP, isozyme, and AFLP (Chan and Sun, 1997; Mallory et al., 2008; Xu and Sun, 2001). Chan and Sun (1997) suggested that the decreased level of genetic diversity observed in *A. cruentus* might be a result

of a specialized domestication process where only a small subset of the original *A. hybridus* population was subjected to intense artificial selection to select for specific agronomic characteristics. Mallory et al. (2008) speculated that the limited and uniform cultivation range of *A. cruentus* might have further reduced the level of genetic diversity within the species. Conversely, *A. hybridus*, the putative wild progenitor species of the grain amaranths, showed the most genetic diversity of all the species included in the diversity panel. Indeed, *A. hybridus* showed a seven-fold increase in polymorphic loci when compared to *A. cruentus* and approximately twice as many polymorphic SNPs when compared to the other grain amaranths species (*A. caudatus* and *A. hypochondriacus*). The higher genetic diversity observed within *A. hybridus* is consistent with an expectation that a wild progenitor species should be genetically more diverse than a derived domesticated species, specifically as a result of genetic drift and selection (Hilu, 1995). Moreover, the observation that nearly 94% (388) of the grain amaranth sequence-based SNP assays worked with *A. hybridus* samples is notable in that it further confirms the close ancestral relationship between the grain amaranths and *A. hybridus*.

The grain amaranths are members of the genus *Amaranthus* (subfamily Amaranthoideae), which contains several other important plant species including several of the most damaging weedy species in the U.S. collectively referred to as the "pigweeds" (Basu et al., 2004; Wassom and Tranel, 2005). Various studies have already shown the utility of molecular markers for clarifying taxonomic relationships among the weedy species of the genus *Amaranthus* (Wassom and Tranel, 2005; Wetzel et al., 1999), yet taxonomic questions still exist and the need for additional, easy to use, genetic markers remains high. We evaluated the transferability/utility of these SNP assays on three distantly related weedy amaranth species, specifically *A. powellii* (Powell amaranth)*, A. retroflexus* (redroot pigweed) and *A. tuberculatus* var. *rudis* (common

waterhemp). Of the 414 SNP assays that were polymorphic in the grain amaranths and their putative ancestor (*A. hybridus*), 256 (62%) of the assays produced high confidence genotypic calls in both accessions of *A. powellii,* and *A. retroflexus,* whereas only 158 (38%) produced a high confidence genotypic call with the single *A. tuberculatus* accession included in the diversity panel (Supplemental Table S1). Between the two *A. powellii* accessions included in the diversity panel, 26 (10%) of the SNPs were polymorphic, while only three (1%) were polymorphic between the two *A. retroflexus* accessions. We note that the origins of the two accessions included in the analysis for both *A. powellii* and *A. retroflexus* accessions are geographically distinct (Table 1), suggesting that i) the *A. retroflexus* population is potentially much less diverse than the *A. powellii* population – an intriguing proposition considering that *A. retroflexus* is among the most widely distributed weeds in the world (Holm et al., 1997) or, perhaps more likely, ii) that the SNPs identified from the cultivated amaranths produce an inherent bias, such that species that are taxonomically closer (*A. powellii*) have a higher probability of sharing the genetic polymorphism (via an orthologous relationship).

Phylogenetic Analysis

Several hypotheses have been proposed for the evolutionary origins of the grain amaranths. The first hypothesis is based on geography and suggests that all three grain amaranths evolved independently, specifically *A. caudatus* from *A. quitensis* in South America; *A. cruentus* from *A. hybridus* in Central America; and *A. hypochondriacus* from *A. powellii* in Mexico (Sauer, 1967; Sauer, 1976). The second hypothesis, based on plant and seed morphology, suggests that *A. hybridus* gave rise to *A. cruentus*, which in turn hybridized with *A. powellii* and *A. quitensis* to give rise to *A. hypochondriacus* and *A. caudatus*, respectively (Sauer, 1967; Sauer, 1976). A third hypothesis, proposed more recently by Mallory et al. (2008)

suggested that *A. hybridus* is the progenitor species for all three domesticated species, but that each was derived from independent domestication events from genetically differentiated populations of *A. hybridus*. Our results support the designation of *A. hybridus* as the progenitor species of all three grain amaranth species. Indeed, neighbor-joining analysis reveals that *A. caudatus*, *A. cruentus* and *A. hypochondriacus* are monophyletic, while *A. hybridus* was polyphyletic with *A. hybridus* accessions in each of the three grain amaranth monophyletic clades (Fig. 2). We note that *A. powellii* (a previously suggested progenitor) formed a monophyletic group distinct from any of the grain amaranths. Obviously a larger investigation, including substantially more accessions of the grain amaranth progenitor species (*A. hybridus*, *A. powellii* and *A. quitensis*) is still needed to finely dissect the origins of the grain amaranths. However, we expect that taxonomic identification of these *Amaranthus* species may be ambiguous due to reciprocal gene flow via outcrossing in regions where the species are sympatric - a situation we have observed in Peruvian and Mesoamerican centers of origin of the crop species. The transferability, ease of use, and the highly polymorphic nature of the SNP assays reported here should facilitate such an investigation.

Linkage Map Construction

The parents of the mapping population were initially chosen based on the published research by Maughan et al. (2009) that showed that PI 481125 and PI 642741 were genetically diverse. PI 642741 has an easily identifiable dominant phenotypic marker (red stem color) that facilitated the identification of true hybrid F$_1$ plants. Both accessions are classified as *A. caudatus* accessions within the GRIN system (http://www.ars-grin.gov/npgs/), however our phylogenetic analysis clearly places PI 481125 within the *A. hypochondriacus* clade (Fig. 2). An independent genotypic analysis of a second plant sample of PI 481125 also grouped with the *A.*

hypochondriacus accessions, suggesting that PI 481125 was originally misclassified and should be reclassified as *A. hypochondriacus*. This reclassification also agrees well with the levels of genetic diversity identified by Maughan et al. (2009), where interspecific comparisons should be genetically more diverse than intraspecific comparisons. Based on these observations, our mapping population should be categorized as interspecific.

A total of 419 SNP loci were genotyped using the KASPar™ genotyping chemistry on a Fluidigm integrated fluidics chip (IFC). Included in the genotyping experiment were 134 F_2 individuals, the parental genotypes and a synthetic heterozygote (consisting of eqimolar quantities of DNA from the two parental samples). Of the 419 SNP assays, 411 (98%) produced genotypic clusters that could be easily scored. The remaining eight assays were lost due to issues associated with loading the IFC. Of these 411 assays, 373 (91%) produced three clearly separated clusters and were scored in a co-dominant fashion (1:2:1; Fig. 3), while the remaining 9% produced only two clearly separated clusters and were scored in a dominant fashion (3:1; Fig. 3). The dominant SNP assays are likely due to preferential amplification of one of the SNP allele-specific primers in the heterozygous samples (Walsh et al., 1992).

To validate the genotyping process, eight random SNPs were re-genotyped and compared across all 134 F_2 individuals. Thus a total of 1,072 data points, from two separate fluidic chips, were compared for genotyping accuracy. Twenty-five (2%) of the comparisons contained a missing value and thus could not be included in the comparative analysis. Of the remaining 1,047 comparisons, 1,021 (98%) were identical matches while 26 (2%) were mismatches, of which all were conflicts between homozygous to heterozygous calls.   Interestingly, 35% of the conflicts were accounted for by just three of the F_2 individuals – suggesting that the genotypic conflicts might be related to a DNA source and not specifically to the genotyping methodology *per se*.

Indeed, the 17 DNA samples with genotypic conflicts averaged 15X more missing data than samples without any observed genotype conflicts (*n*=117), supporting the conclusion that the genotyping conflicts were likely the result of problematic DNA samples. Consequently, the genotypic data for all 17 individuals were removed prior to linkage map construction. At a minimum LOD score of 5.0, pairwise linkage analysis grouped all 411 SNP markers into 16 linkage groups, presumably corresponding to each of the amaranth haploid chromosomes (2*n*=32; Fig. 4). The distribution of the markers within the linkage groups varied from 9 to 47 SNPs per linkage group. Regression mapping of the pairwise linkage groups successfully ordered all SNP markers within their respective linkage groups. The centiMorgan (cM) distance, corrected with the Kosambi mapping function, spanned by the SNP markers in the linkage groups ranged from a low of 23 to 144 cM. The total map consisted of 411 SNP loci and spanned 1288 cM. The largest interval between two linked markers was 27 cM on linkage group 12, while the average distance between all loci was 3.1 cM. Most intervals (93%) were less than 10 cM apart.

Of the 411 SNPs utilized for mapping, 22 (9.7%) showed significant segregation distortion (P<0.0001). Since the map is based on an interspecific mapping population (*A. caudatus* X *A. hypochondriacus*), segregation distortion was not unexpected. Indeed, segregation distortion in interspecific crosses has been reported to reach levels as high as 68.5% of the markers (Paterson et al., 1988). Skewed SNP markers mapped to a total of nine different clusters on seven linkage groups (Fig. 4). The presence of markers clusters skewed to a single parental genotype has been attributed to chromosomal regions containing possible gametophytic or zygotic viability factors (Lu et al., 2002; Zamir and Tadmor, 1986) and/or underlying genetic factors (i.e., QTL) conferring a selective advantage for the particular growing conditions used to

produce the mapping population. We note that significant morphological differences in seedling morphology, growth rate and seed production were observed among the F_2 plants. Flanking sequences for each of the 411 mapped SNPs were compared to the GenBank refseq_protein database using BLASTX. Twenty-four (5.8%) of query sequences returned significant (E<1e-10) homologies to the refseq_protein database and were mapped to 11 of the 16 linkage groups. The low homology to the refseq_protein database is consistent with the genome reduction methodology, which randomly samples the genome. Significant homologies to well annotated genes included: SPK1-guanylnucleotide exchange factor activity (NP_193367), ATMRP10-ATPase/transmembrane movement (NP_191829), WRKY20-transcription factor (NP_567752), SULTR3.4-sulfate transporter (NP_188220), RAP2.2-DNA binding/transcription factor (NP_566482), OVA1-methionine-tRNA ligase activity (NP_191100) and ATCUL2-ubiquitin protein ligase binding (NP_171797). Considering a refseq_protein database hit rate of 5.8%, we conclude that many of the 11,038 *in silico* SNP loci that were originally reported by Maughan et al. (2009) should be located in or very near (±150 bp) gene sequences, suggesting that a subsequent linkage map of amaranth could be based almost solely on genic-SNP sequences. Indeed, after removal of the SNPs with significant homologies to the *Arabidopsis* extranuclear genomes (8 SNP loci) and RepeatMasker database (272 SNP loci), a BLASTX analysis of the 11,038 *in silico* SNP loci identified 711 SNPs with significant sequence homologies (E<1e-10) to genic sequences in the refseq_protein database. The mapping population is being selfed (currently at $F_{2:5}$) and expanded to 200 individuals to form a recombinant inbred line population that should provide an immortalized mapping population for the amaranth community, as well as provide the first population readied for QTL analysis.

Conclusions

We report the first high-density, complete genetic linkage map of amaranth. The SNP markers and linkage map reported are essential steps towards the development of marker-assisted selection programs for recalcitrant traits of agronomic importance in amaranth. The SNP assays were developed on the KBioscience KASPar™ genotyping chemistry using a Fluidigm IFC Access array. The utilization of this chemistry combined with the nano-fluidic Fluidigm chip reduced the overall data point cost to $0.05 per data point – an important feature considering that the implementation of marker-assisted breeding strategies often requires the generation of thousands of data points per population (Eathington et al. 2008). Compared to other markers systems (e.g., AFLPs or SSRs), the SNP assays reported here are relatively inexpensive and easy to genotype. Indeed, a single 96.96 Fluidigm IFC is capable of producing 9,216 genotypic data points in a single run (~3 hours) with little technical expertise, and since each genotyping reaction is done on a nanoliter scale, the consumable reagent costs (i.e., Taq polymerase, primers) is only $0.001 data point (the remainder of the cost is the IFC). If a Fluidigm EP1 system is unavailable (a significant capital investment), the same KASPar™ SNP assays can be read on a standard FRET plate reader – an important consideration for laboratories in the Developing World, where amaranth is cultivated and where capital equipment may be limited. Worthy of note is the upfront cost of the allele specific and common reverse primers needed for each of the KASPar™ genotyping assays. At the current commercial minimum synthesis scale (25nM), each KASPar™ genotyping primer set cost approximately $11 to manufacture and is sufficient to run approximately six million Fluidigm IFC-based genotyping reactions.

The SNP markers reported here will be of particular value in ongoing efforts to characterize extensive amaranth germplasm collections and the development of core collections needed for

existing and emerging amaranth breeding programs in the Andes, Mexico, Asia, and sub-Saharan

Africa (Diwan et al., 1995; Tanksley and McCouch, 1997).

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Chapter 2: Single nucleotide polymorphisms identification, characterization and linkage mapping in Chenopodium quinoa

Introduction

Chenopodium, commonly known as the goosefoot genus, includes a wide array of species native to all inhabited continents. Most of these species are facultative autogamous annuals, having a base chromosome number of $x = 9$. (A subset of taxa previously classified in *Chenopodium*, but having a base chromosome number of $x = 8$, have more recently been reclassified in the genus *Dysphania*, as per Mosyakin & Clemants, 2002.) Many *Chenopodium* species are adapted to arid and/or saline environments and are notorious as invasive weed species, including *C. album* (lambsquarters) and *C. berlandieri* (pigweed). At least four species in the genus were domesticated anciently, either as vegetable or seed crops (McConnell, 1998). One of these, the autogamous Andean species *C. quinoa* (quinoa, $2n = 4x = 36$), has risen from a neglected subsistence crop of indigenous farmers to become an important export commodity of the Andean nations of Bolivia, Peru and Chile.

The prominence of quinoa in organic food markets has led to increasing attention by scientists to the crop's unique nutritional benefits, including an ideal amino acid balance in the seed, lack of gluten, and potentially novel abiotic stress tolerance mechanisms (Vacher, 1998; Maughan et al., 2009a; Morales et al., 2011). Heightened awareness of quinoa's role in food security issues in Andean South America, specifically as a major protein source for subsistence farmers and as a cash crop for marginal highland soils, has led to an increased interest in quinoa and the establishment of several new breeding programs in Andean South America. In addition to germplasm conservation, principal objectives of these programs include enhancing grain yield,

disease resistance, drought tolerance, heat tolerance during anthesis, and modifying saponin content (Ochoa et al., 1999). Breeders in these programs recognize that the development and use of molecular markers are critical to meeting these objectives (A. Gandarillas, personal comm.). Notable is the 2011 declaration of the Food and Agriculture Organization that 2013 is the official International Year of Quinoa with the main objective to, "promote the benefits, characteristics and potential use of quinoa in the fight against hunger and malnutrition, as a contribution to a global strategy on food security" (United Nations, 2011).

Genetic markers are essential tools for modern plant breeding research programs (Eathington et al., 2007). They are particularly important for germplasm conservation, core-collection characterization, and in breeding applications, such as marker-assisted selection (Ganal et al., 2009). In quinoa, Mason et al. (2005) developed the first set of 208 polymorphic simple-sequence repeat (SSR) markers, while Jarvis et al. (2008) reported the development of an additional 216 new SSR markers and a linkage genetic map consisting of 275 molecular markers, including 200 SSR markers. Unfortunately the map was incomplete as it consisted of 38 linkage groups (n=18) covering just over 900 cM.

Single nucleotide polymorphism (SNPs), defined as single-base changes, are quickly becoming the marker system of choice in plant breeding programs. SNPs are the most abundant type of sequence variation in eukaryotic genomes (Garg et al., 1999; Batley et al., 2003). They can be cost-effectively discovered and genotyped using several next-generation technologies, including bead arrays (Shen et al., 2005), nano-fluidic devices (Wang et al., 2009), and genotyping-by-sequencing (Miller et al., 2007; Maughan et al., 2010; Elshire et al., 2011). Indeed, SNPs have already been utilized in a wide array of research areas, ranging from genome

wide association studies (Aranzana et al., 2005; Huang et al., 2010; Poland et al., 2011), to dense linkage map development (Troggio et al., 2007; Close et al., 2009).

The goals of this project were to i) identify the first large scale set of SNPs for quinoa; ii) develop functional SNP assays for quinoa; iii) evaluate the informativeness (minor allele frequency) of the SNPs on a diversity panel consisting of accessions from the CIP international quinoa nursery, USDA germplasm collection, and the BYU *Cheonopodium* collection; and iv) construct the first SNP based genetic linkage map for quinoa.

Materials and Methods

Plant Materials and DNA extraction

Eight quinoa accessions were utilized in the initial genomic reduction experiment to identify SNPs (Table 3). The accessions represent the broad geographical distribution of quinoa (Andean, Valley and Coastal ecotypes) and include the parents of five quinoa mapping populations (designated as Pop1, Pop39, Pop40, PopM3 and PopGO; Table 4). Pop1 and Pop39 are the most advanced populations and were used for linkage map development. Both populations segregated for the presence of an easily identifiable dominant maker (stem color) that facilitated the identification of true hybrid F_1 plants and were selfed to $F_{2:8}$ recombinant inbred lines (RILs). The germplasm diversity panel included 113 quinoa accessions representing the USDA quinoa collection, CIP international quinoa nursery, and eight additional accessions representing several related *Chenopodium* taxa (i.e., *C. hircinum*, *C. berlandieri*, *C. watsonii*, and *C. ficifolium*). Accessions for the diversity panel from external sources were kindly provided by David Brenner (USDA, Iowa State University, Ames, IA), Angel Mujica (Universidad del Altiplano, Puno, Peru), Daniel Bertero (University of Buenos Aires, Argentina),

Eulogio de la Cruz (National Institute of Nuclear Research-ININ, Ocoyoacac, Mexico), and

Helena Storchova (Institute of Experimental Botany, Prague, Czech Republic). All plants were

greenhouse grown at 25 ^{o}C under broad-spectrum halogen lamps with a 12-h photoperiod in 15-

cm pots using Sunshine Mix II (Sun Grow, Bellevue, WA) supplemented with Osmocote

fertilizer (Scotts, Marysville, OH) at Brigham Young University, Provo, UT.

Total genomic DNA was extracted from 30 mg of freeze-dried leaf tissue from a single

plant (diversity panel and RIL populations) as previously described by Sambrook et al. (1989),

with modifications described by Todd and Vodkin (1996). Extracted DNA was quantified using

a Nanodrop (ND 1000 Spectrophotometer, NanoDrop Technologies Inc., Montchanin, DE) and

diluted to 150 ng μl^{-1} in DNAse-free water.

Genome Reduction

The genomic reduction protocol utilized was described in detail by Maughan et al.

(2009b). In brief, a total of 450 ng of total genomic DNA of each the eight DNA samples were

separately double-digested for 1 h at 37 ^{o}C with 3 U of the restriction enzymes *EcoR*I and *Bfa*I

(New England Biolabs, Beverly, MA) in 1X NEB4 restriction buffer. The resultant DNA

fragments were immediately ligated with 1.5 µM 5'-TEG biotinylated/3'-phosporylated *EcoR*I

adapters and 15 µM 3'-phosphorylated *Bfa*I adapters using 3 U of T$_4$ ligase (New England

Biolabs, Beverly, MA; Supplemental Table S2) at 16 ^{o}C for 3 hrs. DNA fragments smaller than

100 bp were excluded from the reactions via spin chromatography using Chroma Spin™-400

columns (ClonTech Laboratories, Mountain View, CA). Non-Biotin labeled DNA fragments

(*Bfa*I - *Bfa*I restriction fragments) were removed from the reaction using M-280 streptavidin

beads (Invitrogen, Carlsbad, CA) according to the manufacture's specifications. The remaining

*EcoR*I-*Bfa*I and *EcoR*I-*EcoR*I fragments, with the biotin label still attached, were resuspended in 100 µL of 10:1 TE buffer (10mM Tris, 1 mM EDTA, pH 8.0).

Eight primer pairs, designed to be complementary to the *EcoR*I and *Bfa*I adaptor sequences and to carry unique 5' 10-base MID barcode sequences, were synthesized by Integrated DNA Technologies (Iowa City, IA; Supplemental Table S2). A single MID-barcode primer pairs was used to amplify 1 µL of the streptavidin-cleaned DNA fragments for each of the eight quinoa SNP discovery samples. Amplification of each sample was performed in 50 µL PCR reactions using 1X Advantage HF 2 PCR Master Mix (ClonTech, Mountain View, CA) and 0.2 uM of the MIDX-*EcoR*I and MIDX-*Bfa*I primer pairs, with the following thermocycling profile: 95 $^{\circ}$C for 1 min followed by 22 cycles of 95 $^{\circ}$C for 15 s, 65 $^{\circ}$C for 30 s, 68 $^{\circ}$C for 2 min. DNA concentrations for each of the PCR reactions were determined fluorometrically using Quant-iT picogreen® dye (Invitrogen, Carlsbad, CA) and were used to construct a 5 µg pool with equimolar concentrations of each of the eight quinoa samples. The pooled sample was electrophoresized on a 1.5% Meaphor® agarose gel (Cambrex BioScience, East Rutherford, NJ) in 0.5X TAE at 40V for 8 hours and visualized with ethidium bromide staining. A gel slice representing DNA fragments ranging from ~500-650 bp, was removed and the DNA fragments extracted using a Qiaquick column (Qiagen, Germantown, MD) and sequenced using standard protocols for 454-pyrosequencing as a service at the Brigham Young University DNASC (Provo, UT) using a Roche-454 GS FLX instrument and Titanium reagents (Branford, CT) without DNA fragmentation.

SNP discovery

DNA reads from the454-pyrosequencing runs were bioinformatically trimmed and separated into unique MID-barcode pools representing the eight accessions used in the SNP

discovery experiment using the process-tagged sequences function in CLCBio Workbench (v. 4.0; Katrinebjerg, Aarhus N, Denmark). For SNP discovery, DNA sequence reads were *de novo* assembled using the Roche Newbler assembler (v. 2.3) with the minimum overlap length set to 50 bp, the minimum overlap identity set to 95%, and the minimum contig length set to ≥200 bp. Putative SNPs within contigs were identified from the exported .ace file using custom perl-scripts (Stajich et al., 2002; Maughan et al., 2009b) when: i) coverage depth at the SNP was ≥ 6; ii) the minor allele frequency (MAF) represented at least 20% of the reads; and iii) 100% of the alleles within a parental pool were identical. All SNPs, including 5' and 3' sequence information, have been deposited in dbSNP in GenBank. The SNPs are submitted under the handle MAUGHAN in batch number 2012A (GenBank: ss530859297 to ss530860195; build B138).

SNP assay development and genotyping

Putative SNP containing contigs that showed no significant homology to the RepeatMasker (v. 3.2.9 *Arabidopsis*) database or to the *Arabidopsis* chloroplast (GenBank accession NC_000932) or mitochondrial (NC_001284) genomes as determined by BLASTn analyzes (E-value ≥ 1e-05) were then processed by the primer design software PrimerPicker (KBiosciences Ldt., Hoddesdon, UK) using default design parameters. Primer sequence information for each of the functional KASPar™ SNP assays is provided in Supplemental Table S2. SNP genotyping was accomplished via competitive allele-specific PCR using KASPar™ genotyping chemistry (KBioscience Ldt., Hoddesdon, UK) with the Fluidigm (Fluidigm Corp., South San Francisco, CA) nanofluidic 96.96 dynamic array™ (Wang et al., 2009). For genotyping on the 96.96 dynamic array chip, a 5 µL sample mix, consisting of 2.25 µL genomic DNA (20 ng/µL), 2.5 µL of 2X KASP reagent Mix (KBioscience Ldt.) and 0.25 µL of 20X GT

sample loading reagent (Fluidigm Corp., South San Francisco, CA) was prepared for each DNA sample. Similarly, a 4 µL 10X KASP Assay, containing 0.56 µL of the KASP assay primer mix (allele specific primers 12µM, common reverse primer 30 µM), 2 µL of 2X Assay Loading Reagent (Fluidigm Corp., South San Francisco, CA) and 1.44 µL DNase-free water was prepared for each SNP assay. The assay mix and sample mix were then loaded onto a 96.96 dynamic array chip, mixed and thermal cycled using an IFC Controller HX and FC1 thermal cycler (Fluidigm Corp., South San Francisco, CA) according to the manufacture's protocols. Thermal cycling consisted of an initial thermal mix cycle (70ºC – 30 min; 25ºC – 10 min) a hot-start Taq polymerase activation step (94ºC – 15 min) followed by a touchdown amplification protocol as follows: 10 cycles of 94ºC for 20 sec, 65ºC for 1 min (decreasing 0.8ºC per cycle), 26 cycles of 94ºC for 20 sec, 57ºC for 1 min; hold at 20ºC for 30 sec. End-point fluorescent images of the chip were acquired on an EP-1 imager (Fluidigm Corp., South San Francisco, CA) and the data analyzed with Fluidigm SNP genotyping Analysis Software®.

SNP Diversity data analysis

A matrix of pairwise genetic distances was generated from this data using Nei's distance method (Nei et al., 1979). This distance matrix was used for the principal coordinate analysis, and to create the neighbor net visualization performed by the program Splitstree (Bryant et al., 2002). The population genetic software programs Structure v.2.2.3 (Pritchard et al., 2000) and Structure Harvester (Earl et al., 2012) were used to infer the number of distinct groups within our panel. Structure analysis was run five times, with 100,000 generations for each K (with K ranging from 1 to 7), with a burn-in period of 10,000.

Genetic linkage map construction

Marker segregation was analyzed for conformity to Mendelian ratios expected for an RIL population using a chi-squared test. Markers were initially grouped based on independence LOD scores ≥ 4.5 using the G2 statistic as calculated by JoinMap® 4 for recombination frequency (Van Ooijen, 2006). Markers within groups were then ordered using the regression mapping algorithms corrected with the Kosambi mapping function as described by Stam (1993), with the modification that the squares of the LODs were used as weights in order to assign more weight to informative loci. Successive rounds of marker placement were utilized to add loci to the map. After the addition of each locus, a ripple test was applied to test for goodness-of-fit and assure the optimal map order.

Results and Discussion

Genomic reduction and SNP discovery

The genomic reduction protocol utilized here is based on the conservation of restriction sites across individuals, followed by fragment selection and next-generation sequencing. MID-barcode tags are incorporated into the DNA fragments of the individual DNA samples, which are subsequently utilized to deconvolute the sequencing pool. Assembled fragments from the pool are then examined for SNP identification between accessions (see Maughan et al. 2009 for a figure detailing the genomic reduction protocol).

Stevens et al. (2006) estimated the genome size of quinoa to be 967 Mb. Assuming a 35% GC content, we calculated that the biotin-stepavidin bead selection of *Eco*RI (GAATTC) containing fragments should produce 330,397 fragments of which ~66,079 (~ 20%) are within the target size range (500-650bp). Thus the genomic reduction process should reduce the complexity of

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the DNA by nearly 52-fold, leaving approximately 19 MB of DNA for sequencing of each DNA

sample. A single 454-pyrosequencing run produces on average 1.3 million reads with an average

read length of ~400 bp or slightly more than 500 MB. Hence, we estimate that a single 454-

pyrosequencing run, with eight-pooled quinoa barcoded accessions would result in ~14X

coverage across the 19 MB of DNA of each pooled individual. Using 1.5 plates of 454-

pyrosequencing we obtained a total of 1,851,738 sequence reads producing a total of 518.3Mb of

sequence with an average read length of 284 bp. After removal of the MID-barcode and adapter

sequence, assembly of all reads using Newbler assembler created 22,911 large contigs (> 200bp;

13 Mb), with an average read length of 482 bp with 94% of the bases with quality scores above

40.

Since a major objective of this research was to identify SNPs specific to mapping

populations, sequence reads were sorted into eight MID-barcode pools corresponding to the eight

individuals utilized in genomic reduction experiment. A total of 1,717,000 (438Mb, 93%) were

unambiguously sorted into eight barcode pools. To enter a pool, an exact match to all 10 bases

on the MID-barcode was required. Although we attempted to mix the samples in equimolar

amounts prior to sequencing, the number of reads in each pool ranged from a high of 262,459

(15% of the total count) to a low of 183,495 (11%), a slight discrepancy likely due to difficulties

associated with fluorometric DNA quantification of the PCR samples prior to pooling.

After partitioning the reads into individual MID-barcode pools, the Newbler assembler

was used to remove the MID-barcode, adapter sequences and to create reference contigs specific

to each of the five mapping populations (see plant materials; Table 3). CLCBio Workbench

v.2.6.0 was then used to reference map parental reads for each population to the population

specific reference contigs created by Newbler for each population. The average reference contig

size across all five assemblies was 357 bp, with an average contig read depth of 18X and an average base coverage of 11X.

Population-specific SNPs were identified from each of the biparental assemblies using a minimum base cutoff coverage threshold ($\geq$6X) and a minor allele frequency threshold ($\geq$20%), further filtered based on a 100% within parent uniformity threshold (all reads derived from a single barcode were required to be genotypically identical). This parameter minimizes erroneous SNPs due to faulty assemblies (co-assembly of homoeologous regions) as well as SNPs that were heterozygous in the parental lines. Although quinoa displays disomic inheritance, it is an ancient allotetraploid (Ward, 2000), hence co-assembly of some homoeologous regions is possible even with the increased stringency assembly parameters (minimum length overlap = 50 bp and minimum overlap identity =95%). Therefore, at the minimum read depth of 6, two of the sequence reads (20%) would need to be called as the minor allele variant, of which, all would have to be derived from the same MID-barcode pool.

A total of 14,178 SNPs were identified across the five populations, ranging from a high of 3,615 SNPs in 1,888 contigs in Pop39 to a low of 2,092 SNPs in 995 contigs in PopM3 (Table 4), with an average of 2,836 SNPs observed in 1,462 contigs across all populations. The number of contigs that contained at least one SNP varied from a high of 1,128 (6%) in Pop39 to a low of 554 (3%) in PopM3. Over all populations, 5.1% of all contigs contained at least 1 SNP, with the largest class of contigs containing a single SNP (59%; Figure 5a). The average base coverage at a SNP across all populations was 7.8X (Figure 5b), whereas the average SNP density (SNP/bp) across the five populations was 1/2160 bp. The SNPs can also be described by their allele frequency within the sequencing pool. Here the minimum allele frequency threshold was set to 20%, meaning that at a minimum coverage of 6X, at least two reads from the same parental

source must have at least two separate but identical reads in the contig assembly (at the same coverage the opposing parental source would have four identical but separate sequence reads in the assembly). Over all populations, 28% of the SNPs fit within the 20-29% range, 37% within the 30-39% range, with the remaining 35% falling within the 40-50% range (Table 4). With regards to SNP type, transition mutations (A/G or C/T) were the most numerous, outnumbering transversions (A/T, C/A, G/C, G/T) by 1.6X margin, which is in accordance with the observation that transition SNPs are the most frequent SNP type reported in both plant and animal genomes and are thought to result from hypermutability effects of CpG dinucleotide sites and deamination of methylated cytosines (Zhang et al., 2004; Morton et al., 2006). Of the 14,178 SNPs identified, 94% (13,262) were unique to just one population, while the remaining 7% (916) were identified in at least one other population. The largest overlap of SNPs was between populations Pop1 and Pop39, where 331 SNPs were shared in common – we note that this was not unexpected as both populations share a common paternal parent (0654).

SNP assay development

Primer sets for 1,248 putative SNPs were designed for competitive allele-specific PCR based on the KASPar™ genotyping chemistry. The SNPs were selected from those that were putatively polymorphic in Pop1 and/or Pop39 with the intention that these populations would be used for linkage map development. All 1,248 SNPs were screened using the Fluidigm 96.96 dynamic array chip. A total of 511 (41%) SNPs produced clearly separated genotypic clusters that could be easily scored with the automated Fluidigm SNP genotyping analysis software (Figure 6). The percent conversion is significantly lower than that identified by Maughan et al. (2011) who reported a nearly 70% conversion rate for KASPar-based SNP assay development in *Amaranthus spp.*, diploid species, but only slightly higher than the 36% conversion rate reported

for tetraploid cotton (*Gossypium hirsutum*). Byers et al. (2012) speculated that the decrease in conversion rate for cotton was the result of increased complexity associated with polyploidy – a problem associated with the dual amplification of homoeologous (orthologs) loci using competitive allele-specific PCR (KASPar chemistry). While polyploidy is likely a major reason for SNP assay development failure, other factors, including paralogy, proximity of repeat elements, poor assemblies and/or sequencing errors may also contribute to assay design failure.

Diversity panel and phentic analysis

The diversity panel consisted of 113 accessions of *C. quinoa* and eight related *Chenopodium* taxa (Table 3). Of the 511 polymorphic SNP assays developed, 427 were successfully screened on the full diversity panel (SNP assays with greater than 20% missing data were removed from the analysis). Limiting the analysis to just the 113 quinoa accessions, a total of 854 alleles were identified with an average of 5.4% missing data per accessions for a total of 46,043 scored data points. Across the quinoa accessions, MAF ranged from 0.02 to 0.50 with an average MAF of 0.28 per SNP (Supplemental Table S3).   Considering a SNP with a MAF $\geq$ 0.35 as highly polymorphic and a SNP with MAF $\geq$ 0.10 as polymorphic, 198 (46%) of the SNP loci were highly polymorphic, while 385 (90%) were polymorphic (Table 4). We note that the maximum value for a bi-allelic SNP is 0.5 (both alleles present at equal frequency).

Phenetic analysis of the 113 quinoa accessions using Structure analysis clearly separated the accessions into two distinct subgroups according to Evanno delta K values (Earl et al., 2012), which are easily visualized using a Neighbor-Net tree (Bryant et al., 2002) or a principal coordinate analysis (Figure 7). The two groups agree well with previous morphological and microsatellite studies, which separated the quinoa accessions into two distinct groups: Chilean coastal and Andean ecotypes (Risi et al., 1989; Christensen et al., 2007). Six accessions were

placed intermediate to the coastal and Andean ecotypes, including E-DK-4, G205DK, 321079BB, CO1 (PI 596293) E1 (Ames 13228) and C11 (PI 614882) (Figure 7b). Since E-DK-4, G205DK, 321079BB, and CO1 are breeding lines, it is not surprising that they are positioned in an admixture position. E1 and C11 are the two accessions with the highest percentage of missing data (26% and 27%) and the lowest nodal bootstrap value (54%) in the dendrogram, thus their positioning is potentially artificial.

Quinoa is a member of a complex of interfertile New World species. Included in this complex are several weedy and domesticated species, including North American *C. berlandieri* and *C. berlandieri* subsp. *nuttaliae* and South American *C. hircinum*. Targeted DNA sequencing (E.N. Jellen and H. Storchova, personal communication) has revealed a close relationship between this complex and certain diploids, including North American *C. watsonii* and the Eurasia native *C. ficifolium,* which appears sporadically as a weed in eastern North America (Jellen et al., 2011). To assess the potential transferability and utility of the SNPs for germplasm characterization in these related species, we tested the functionality of the SNP assays across a *Chenopodium* species panel, including, two accessions *C. hircinum*, four accessions of *C. berlandieri (*subsp. *nuttaliae,* var. *macrocalycium,* var. *boscianum,* var. *zschackei*), and a single accession of both *C. watsonii* and *C. ficifolium* (Table 3). One-hundred and forty-four (34%) of the SNPs clearly amplified and separated all eight taxa into distinct genotypic clusters, while 318 (74%) were clearly genotyped in six of the eight taxa. Seventy-one (17%) failed to amplify in any of the related taxa. Perhaps not surprisingly, the most successful cross-species amplifications were in the two *C. hircinum* accessions, where 81% of the SNP assays were successful. Both *C. hircinum* accessions originate from the lowlands of Northwest Argentina, near the center of domestication of quinoa (near lake Titicaca, Bolivia), are allotetraploid and are

presumed potential progenitors of *C. quinoa* (Jellen et al., 2011). Indeed, quinoa and *C. hircinum* are difficult to separate systematically based solely on weedy versus domesticated characteristics due to a close crop-weed sympatric relationship where interspecific hybridization between the species is highly likely (Wilson, 1988). Between the two *C. hircinum* accessions, five SNP assays were polymorphic. Seventy-nine percent of the SNP assays amplified in the four *C. berlandieri* accessions. Like *C. hircinum*, the *C. berlandieri* complex is classified within subsect. Favosa, and North American *C. berlandieri* is considered the likely ancestor of the New World allotetraploid complex (Wilson, 1990; Wilson et al., 1993). Both *C. hircinum* and *C. berlandieri* are interfertile with quinoa and represent potentially important resources for quinoa germplasm enhancement. Perhaps not unexpectedly the two diploid species, *C. watsonii* and C. *ficifolium*, successfully amplified the fewest SNP assays, with Eurasian *C. ficifolium* successfully functioning with the fewest SNP assays (44%).

Inclusion of the eight related *Chenopodium* species within the phenetic analysis of the 113 quinoa accessions produced three clearly separated clusters (Figure 7a), representing the coastal and Andean quinoa ecotypes and a third cluster inclusive of the related *Chenopodium* species. The inability to clearly separate the related species into individual subgroups was not unexpected and is an example of marker ascertainment bias. We should expect *C. hircinum* and *C. berlandieri* to cluster separately and at a significant distance from each other; however, the quinoa-biased SNP assays (biased in that the SNP assays were developed to differentiate quinoa accessions, not *C. hircinum* or *C. berlandieri* accessions) are unlikely targeting polymorphic loci in the related *Chenopodium* species – suggesting that heterologous SNP assays should be used with caution in genus-level phylogenetic studies.

Genotyping validation

To validate the genotyping process, 13 random individuals from the diversity panel were re-genotyped and compared across all 511 SNP loci. From 5,341 paired data points, processed independently on separate fluidic chips, 5,341 (99.7%) were identical matches while 16 (0.30%) were mismatches.

Linkage map construction

Two mapping populations, Pop1 and Pop39, were used for linkage map construction. Since both populations were small (n=61 and n=67) but share a common paternal parent (0654) the data from both populations were combined to produce an integrated linkage map (n=128). All 511 SNP loci were genotyped across the entire integrated mapping population using the KASPar genotyping chemistry on a Fluidigm integrated fluidics chip (IFC). Of the 511 SNP assays, 469 (92%) produced genotypic clusters that could be easily scored, the remaining 42 assays were lost due to issues associate with loading the IFC or eliminated due to extreme segregation distortion (i.e., the SNP showed a pattern consistent with maternal extranuclear inheritance). Of the 469 assays, all produced clearly separated clusters that could be scored with confidence, with each homozygous cluster containing a parental DNA sample (KU-2, NL-6 or 0654; depending on the population) and were scored in a A:H:B fashion, where 0654 was always assigned the A genotype (Figure 6). Twenty-six (5.5%) SNPs showed segregation distortion (P<0.01). Since the map is based on crosses between two contrasting quinoa ecotypes (coastal versus Andean), segregation distortion was not unexpected. We note that the distortion was not nearly as high as has been seen in interspecific crosses, where segregation distortion was reported to reach levels as high as 68.5% (Paterson et al., 1988). Skewed markers mapped to a total of nine different linkage groups (Figure 8), although a majority (77%) mapped to just three

chromosomes on linkage groups 4, 7 and 15. Linkage group 15 contained the largest number of distorted markers (11), all skewed to the coastal parental ecotype. The presence of clusters of markers skewed to a single parental genotype is likely associated with chromosomal regions containing gametophytic/zygotic factors or selectable QTLs that likely conferred advantage during the development of the mapping populations (Zamir et al., 1986; Lu et al., 2002). For example, highland quinoas are commonly known to have sterile pollen at high temperatures (Jellen et al., 2011), so QTLs for heat tolerance from the coastal parent would likely be favored as a mapping population is advanced to homozygosity. Significant variation in seedling morphology, growth rates and seed production were observed among the RIL plants.

At a minimum LOD score of 4.5, pairwise linkage analysis grouped 451 (96%) SNP markers into 29 linkage groups. Twenty of the linkage groups were populated with ≥ 9 SNPs, while nine were small linkage groups consisting of five or fewer markers (Figure 8b). The distribution of the markers within the linkage groups varied from 44 to 2 SNPs per linkage group. The total map of 1,404 cM was spanned by the 451 SNP loci, with individual linkage groups ranging in size from 1 to 112 cM (Figure 8; Table S3). The largest interval between two linked markers was 22 cM, while the average distance between all loci was 3.3 cM. Most intervals (92%) were less than 10 cM apart. Compared to the two previous attempts at linkage map development in quinoa (Maughan et al., 2004; Jarvis et al., 2008), this map consists of nearly double the number of marker loci, spans a greater genetic distance and is significantly closer to the predicted total length the quinoa genetic map (1,700 cM; Maughan et al., 2004). Relative to the haploid number of chromosomes (*n*=18) in quinoa, the linkage groups identified in this study suggest that additional markers are still needed to coalesce linkage groups and provide complete coverage of the genome. To this end we are developing an additional set of EST-based SNPs and several

new and much larger RIL populations. These SNP assays and new RIL populations should provide the basis for the first replicated QTL studies in quinoa.

Conclusions

We report the identification of the first large scale set of putative SNP loci for quinoa as well as the development of >500 functional SNP assays for quinoa. To evaluate the informativeness and utility of the SNP assays, we screened a large diversity panel consisting of the 113 quinoa accessions from the CIP international quinoa nursery and USDA germplasm collection. Moreover we report the first genetic linkage map of quinoa based solely on SNP markers. The functional SNP assays were developed using KBioscience KASPar genotyping chemistry detected using a Fluidigm integrated fluidic chip (IFC). The combination of the KASPar chemistry with the nano-fluidic chip technology (9.7 nL reaction volume) not only significantly reduces the marker data point genotyping costs (~$0.05) but also significantly increase the speed of genotyping. Indeed a single Fluidigm 96.96 IFC is capable of producing 9,216 PCR reactions in a single run (~3 hours) with little technical expertise. If a Fluidigm system is unavailable, the KASPar SNP assays can be genotyped using a standard fluorescence resonance energy transfer plate reader – an important consideration considering that most quinoa breeding programs in S. America may have limited capital equipment resources. Compared to other marker systems (i.e., AFLP, SSRs), the SNP assays presented here are relatively inexpensive, easy to use and should greatly enhance future efforts to initiate marker assisted selection for recalcitrant agronomic traits in quinoa, including resistance to downy mildew (*Peronospora farinosa* f.sp. *chenopodii*), the most important disease of quinoa.

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Chapter 3: SNP Genotyping using KASPar Assays

1. Introduction

Single nucleotide polymorphisms (SNPs) are the most abundant type of polymorphism found in eukaryotic genomes (Dou et al., 2012). SNP markers can be used in a wide variety of applications, including association studies (Filiault and Maloof, 2012), conservation genetics (Ogden et al., 2012), genetic diversity analysis (Blair et al., 2012), and are fast becoming the marker system of choice in marker-assisted plant breeding programs (Foolad and Panthee, 2012). Many of these applications require large numbers of genotyped SNPs. KASPar chemistry provides a versatile method of genotyping that can be applied to small and large-scale projects. The utilization of the KASPar genotyping chemistry combined with the Fluidigm integrated nano-fluidic circuit (IFC) and EP1 endpoint fluorescence reader reduces a data point cost to $0.05 per data point which is significantly less expensive than traditional markers systems (e.g., AFLPs or SSRs) (Maughan et al., 2011). A single 96.96 Fluidigm IFC is capable of producing 9,216 genotypic data points in a single run (~4 hours) with little technical expertise and since each genotyping reaction is done on a nanoliter scale, the consumable reagent costs (i.e., Taq polymerase and primers) is only $0.001 per data point (the remainder of the cost is the IFC) (Maughan et al., 2011). If a Fluidigm EP1 endpoint fluorescence reader is unavailable (a significant capital investment), or for small-scale project, KASPar™ SNP assays can be read on a standard fluorescence resonance energy transfer (FRET) plate reader.

2. Materials

2.1. High throughput genotyping: KASPar amplification and genotyping using Fluidigm's Dynamic Array.

1. 2X KASPar reaction mix (contains Taq polymerase, reference dye ROX, secondary universal primers, 50mM MgCl, and DMSO) (KBioscience, PN KSB-1004-001) (*see* **Note 1**).

2. 1-50ng/µL Genomic DNA (*see* **Note 2**).

3. Competitive allele specific KASPar SNP primers (100 µM each) (*see* **Figure 9** & **Note 3**).

4. 2X Assay Loading Reagent. (Fluidigm, PN 85000736)

5. GT 20X Sample Loading Reagent. (Fluidigm, PN 85000741)

6. Nuclease free water.

7. Fluidigm chip (Dynamic Array integrated fluidic circuit (IFC); (*see* **Note 4**).

8. Fluidigm Control Line Fluid (comes with IFCs).

9. EP1 Reader (Fluidigm, PN EP1-EP1)

10. IFC Controller [HX] (Fluidigm, PN IFC-HX)

11. FC1 Cycler (Fluidigm, PN CYC-FC1)

12. Standard microfuge tubes (2.0 mL).

13. Standard 96-well polypropylene PCR plates.

14. Plate seals (Thermo Scientific, PN AB-0812).

15. Microplate plate sealer (Thermo Scientific, ALPS 50V, PN AB-1443)

2.2. Low throughput genotyping: PCR Plate (96 or 384-well) KASPar amplification and FRET reader.

    1. 2X KASPar reaction mix (contains Taq polymerase, reference dye ROX, secondary universal primers, 50mM MgCl, and DMSO) (KBioscience, PN KSB-1004-001)

    2. 1-50ng/µL Genomic DNA (*see* **Note 2**).

    3. SNP primers (100 µM each) *(see* **Note 3**).

    4. Nuclease free water.

    5. Standard 96- or 384-well Skirted PCR plate (*see* **Note 5**).

    6. Microfuge tubes (2.0 mL)

    7. Optical plate seal (Thermo Scientific, PN AB-0812).

    8. Thermal cycler (ABI 9700, Applied Biosystems, Foster City, CA.)

    9. FRET-capable plate reader (*see* **Note 6**)

    10. Microplate plate sealer (Thermo Scientific, ALPS 50V, PN AB-1443)

2.3. Specific Target Amplification (*see* **Note 7**)

    1. 2X Multiplex PCR Master Mix (Qiagen, PN 206143)

    2. 10X STA primers (100 µM) (*see* **Note 8**).

    3. TE buffer (10mM Tris, 1 mM EDTA, pH 8.0; autoclave).

    4. Nuclease free water

    5. 1-50ng/µL Genomic DNA (*see* **Note 2**)

6. Microfuge tubes (2.0 mL)

7. Standard polypropylene 96-well PCR plates.

8. Thermal cycler (ABI 9700, Applied Biosystems, Foster City, CA.)

3. Methods

   The KBiosciences KASParTM genotyping chemistry is designed on the concept of
competitive allele specific PCR (*see* **Figure 9**). In this protocol, genotype specific primers (one
for each of the SNP alleles) and fluorophore-labeled oligos are used in a competitive PCR
reaction to produce an allele specific fluorescent signal. Each allele specific primer has a SNP
specific base complementary to the target DNA template and one of the SNP alleles. Attached to
each SNP allele specific oligo is a unique 5' tail with sequence homology to universal secondary
oligos labeled with either a FAM or HEX fluorophore. Fluorescence from the secondary oligo is
initially suppressed by bound quencher molecules. During the first round of PCR, only the
correct allele specific primer binds and its 5' tail is incorporated into the PCR product. On the
second round of PCR, the reverse primer generates a sequence complementary to the 5' tail of
the allele specific sequence. This allows for the secondary fluorophore labeled oligo to bind and
become incorporated into the PCR product during the third round of PCR. Incorporation of the
fluorophore labeled oligo into the PCR product releases it from its quencher allowing it to
fluoresce. As PCR continues, generation of signal increases. After completion of PCR the
fluorescent signal can be read and a genotype determined (*see* **Figure 12**). If the starting
template DNA is of low quality or quantity, we highly recommend performing a specific target
amplification (STA) step (see 3.3. Specific Target Pre-Amplification) prior to KASPar

genotyping. STA reduces the complexity of the template DNA by targeting and pre-amplifying the SNP amplicons which may improve the results of the subsequent KASPar genotyping.

3.1. KASPar Genotyping via Fluidigm's Dynamic Array

1. Inject control line fluid into the top and bottom control line fluid reservoirs of the 96.96 chip (one syringe per reservoir) (*see* **Figure 10**).

2. Load chip into IFC Controller [HX] with the barcode facing out and "Prime" the IFC. Priming takes approximately 20 minutes.

3. Prepare working KASPar primer mix: In a 96-well PCR plate combine allele specific primer 1, allele specific primer 2, common reverse primer, and nuclease free water as follows (*see* **Note 9**):

Component	Volume (μL)	Final Concentration (μM)
Allele Specific Primer 1 (100 μM)	3	12
Allele Specific Primer 2 (100 μM)	3	12
Common Reverse Primer (100 μM)	7.5	30
Nuclease Free Water	11.5	
Total:	25 μL	

4. Prepare Pre-Assay cocktail: Combine 550 μL 2X Assay Loading Reagent and 396 μL nuclease free water into a PCR tube (pre-assay cocktail).

5. Distribute 8.6 μL of the pre-Assay cocktail into each well of a new 96-well plate containing 1.4 μL of individual working KASPar primer mix.

6. Prepare pre-sample cocktail: Combine 330μL of KASPar reagent, 33 μL of GT Sample Loading Reagent, and 22μL of nuclease free water into a new PCR tube (pre-sample cocktail)

7. Distribute 3.5 µL of the pre-sample cocktail into a new 96-well plate containing 2.5 µL of genomic DNA.

8. Seal sample and assay plates.

9. Mix samples and assays well by gently vortexing the sealed plates.

10. Pipette 4 µL of 10X assay mix into each assay inlet using an 8-channel pipette. Pipette by column the first 6 columns from prepared assay plate to chip assay inlets starting on the top left working right filling every other inlet in each of the 6 inlet columns. Pipette the remaining columns from the prepared assay plate (columns 7-12) just below the previously pipetted assays starting on the left working right. (*see* **Figure 11**).

11. Pipette 5 µL of samples into each sample inlet using an 8-channel pipette. Pipette by column the first 6 columns from prepared sample plate to chip sample inlets starting on the top left working right filling every other inlet in each of the 6 inlet columns. Pipette the remaining columns from the prepared sample plate (columns 7-12) just below the previously pipetted samples starting on the left working right. (*see* **Figure 11**).

12. Remove any bubbles in the sample and assay inlets (*see* **Note 10**).

13. Remove the blue plastic protector from the bottom of the IFC.

14. Place the chip in the FC1 Cycler with the barcode facing out and thermal cycle using the following touchdown conditions (*see* **Notes 11-12**):

Cycle Step	Temp	Time
1	70ºC	30 minutes
	25ºC	10 minutes
2	94ºC	15 minutes
3	94ºC	20 seconds
	65ºC	1 minute
4	94ºC	20 seconds
	64.2	1 minute
5	94ºC	20 seconds
	63.4	1 minute
6	94ºC	20 seconds
	62.6	1 minute
7	94ºC	20 seconds
	61.8	1 minute
8	94ºC	20 seconds
	61.0	1 minute
9	94ºC	20 seconds
	60.2	1 minute
10	94ºC	20 seconds
	59.4	1 minute
11	94ºC	20 seconds
	58.6	1 minute
12	94ºC	20 seconds
	57.8	1 minute
13	94ºC	20 seconds
	57.0	1 minute
14	Repeat Step 13 for an additional 25 cycles	
15	20ºC	30 seconds

15. Prepare to read the chip by turning on the EP1 Reader and opening the EP1 Data

    Collection software (*see* **Note 13**).

16. Remove the chip from the FC1 Cycler and place it in the EP1 Reader with the barcode

    facing out. Read the chip using EP1 Data Collection software's on screen directions.

17. Remove the chip from the EP1 Reader and place it back in the FC1 Cycler and cycle for

    an additional 5 cycles using the following conditions.

Cycle Step	Temp	Time
1	94ºC	20 seconds
	57.0	1 minute
2	Repeat Step 1 for an additional 4 cycles	
3	20ºC	30 seconds

18. Repeat steps 16 and 17 one more time to obtain reads for 36, 41, and 46 cycles (*see* **Note**

    14)

19. Use the Fluidigm SNP Genotyping Analysis software to analyze the genotyping results.

    Genotyping results are plotted by SNP assay on Cartesian graphs with each dot

    representing a single sample genotype. Samples with the same genotype should group

    together forming distinct genotype specific clusters (*see* **Figure 12**).

3.2. KASPar Genotyping via FRET-Capable Plate Reader

1. Prepare KASPar primer mix: In a 96-well PCR plate combine allele specific primer 1,

   allele specific primer 2, common reverse primer, and nuclease free water as described in

   the following table:

Component	Volume (μL)	Final Concentration (μM)
Allele Specific Primer 1 (100 μM)	3	12
Allele Specific Primer 2 (100 μM)	3	12
Common Reverse Primer (100 μM)	7.5	30
Nuclease Free Water	11.5	
Total:	25	

2. Prepare a DNA plate by pippeting 4μL of DNA into each well of a 96 or 384 well plate

   and dry down the DNA sample in a centrifugal evaporator (speed vac) or by leaving the

   sample uncovered for several hours at room temperature in a laminar flow hood. (*see* **Note**

   15)

3. Prepare individual KASPar primer master mixes for each SNP assay by combining the

   components in the following table into individually labeled microfuge tubes. The volumes

   in the following table are for 1 reaction (i.e., calculate the amount of primer master mix

   needed for number of DNA samples in your experiment plus overage). Dispense KASPar

   primer master mixes into each well of the prepared DNA plate (*see* **Note 16**).

Component	Volume (µL)
KASPar 2X reagent	4
KASPar primer mix	0.11
Nuclease free water*	4
Total:	8.11

*If you do not dry down your DNA samples, omit the Nuclease free water from the primer
master mix.

4. Seal the plate with an optically clear seal, vortex briefly and centrifuge the plate.

5. Thermal cycle the reaction using the touchdown conditions as shown in step 14 of 3.1.

6. Capture end-point fluorescence signal using a FRET-capable plate reader. Genotyping

   results can be plotted by SNP assay on Cartesian graphs with each dot representing a

   single sample genotype using KBiosciences Kluster Caller or other similar software

   packages (*see* **Figure 12**).

3.3. Specific Target Pre-Amplification

The specific target amplification (STA) is an optional step. STA reduces the complexity of the

template DNA by targeting and pre-amplifying the SNP amplicons. This step is most useful

when the starting template DNA is of low quality or quantity.

1. Prepare 10X STA Primer mix (final solution will contain 500 nM of each primer): In a

   single PCR tube, combine 2 µL of each forward primer and 2 µL of each reverse primer

and bring the final volume up to 400 µL by adding TE Buffer as described in the

following table:

Component	Volume (µL)(for 96 assays)
100 µM STA Forward (for all 96 assays)	2 each (192 total)
100 µM Common Reverse (for all 96 assays)	2 each (192 total)
TE Buffer	16
Total:	400

2. Prepare STA pre-mix: Combine Qiagen PCR Master Mix, primer mix from step 1, and

nuclease free water as described in the following table:

Component	Volume per sample (µL)	Volume for 96 samples plus overage (µL)
Qiagen 2X Multiplex PCR Master Mix	2.5	275.0
10X STA primer mix (500 nM each)	0.5	55.0
Nuclease free water	0.75	82.5
Total:	3.75	412.5

3. Combine STA pre-mix and genomic DNA into 96-well plate: Add 3.75 µL STA pre-mix

to each well followed by 1.25 µL genomic DNA to each well for a total reaction volume

of 5 µL.

4. Seal the 96-well plate and mix by vortexing.

5. Thermal cycle under the following conditions:

Cycle Step	Temp	Time
1	95ºC	15 minutes
2	95ºC	15 seconds
3	60ºC	4 minutes
4	Repeat Steps 3-4 for an additional 13 cycles	
5	Hold at 4ºC	

6. Dilute STA products 1:100 by adding 1 µL of STA product to 99 µL of TE. Use the diluted STA product in place of the genomic DNA template in the KASPar Genotyping reactions (both 3.1 and 3.2; above) with no change in reagent volumes.

4. Notes

1. The KASPar reaction mix sensitive to light and repeated freeze and thaw cycles. Improper storage will lead to poor genotyping results. We recommend thawing the KASPar reaction mix once and aliquoting out single use volumes into individual microcentrifuge tubes. Once aliquoted, wrap tubes in foil and store at -20ºC. KASPar reaction mix handled appropriately should produce quality results for up to 6 months.

2. Genomic DNA should be extracted using standard DNA extraction protocols that yield high quality DNA. If high quality DNA cannot be obtained or if concentrations are lower than desired the STA step may provide a more reliable results.

3. Competitive allele specific KASPar SNP primers consist of two allele specific forward primers and one common reverse primer. The allele specific forward primers include a 5' tail associated with either FAM or HEX fluorophore labeled oligos and also includes the polymorphic SNP base as the last (3') nucelotide. An example of general structure of the forward allele specific primers are shown below (*see* also **Figure 9**). The italicized 5' portion is the 5' tail corresponding to the sequence of the fluorophore labeled oligo, the underlined portion is the SNP assay specific sequence and the bolded 3' most nucleotide corresponds to the single nucleotide polymorphism.

Allele specific 1:   5'-

GAAGGTGACCAAGTTCATGCT<u>AAAGCTCATTATTCTTTCTAAAGAAATGATA</u>**G**

Allele specific 2:   5'-

GAAGGTCGGAGTCAACGGATTG<u>AAAGCTCATTATTCTTTCTAAAGAAATGATA</u>**A**

KASPar primers can be designed using any number of primer design software packages, including PrimerPicker (KBiosciences, 2009) and should be stored at -20ºC.

4. Fluidigm IFCs come in 96.96, 48.48, and 24.128 formats where the first number represents number of assays and the second number representing number of samples. The method described here is specific for the 96.96 format but can be adjusted to work with other IFC formats.

5. Ensure that the PCR plate is compatible with your plate reader.

6. Any FRET-capable plate reader can be used as long as it can read emission wavelengths of 520 (FAM), 556 (HEX), and 610 (ROX). We used a PHERAstar Plus (BMG LabTech GmbH, Ortenberg, Germany).

8. The STA primers consist of one forward primer and one reverse primer flanking each SNP. The reverse primer is identical to the reverse primer used in KASPar allele specific amplification. The forward primers are also identical to the allele specific primers but do not include the 5' tail or the polymorphic SNP base (*see* **Note 3**).

9. This protocol makes enough working KASPar primer mix to run approximately 17 96.96 chips (156,672 data points). Note that primers will autohydrolyze over time (likely accelerate by repeated freeze/thaw cycles) resulting in non-allele specific amplification

and poor data point clustering. Working KASPar primers should be stored at -20ºC in TE (10mM Tris, 1 mM EDTA, pH 7.5).

10. Bubbles left in inlets will prevent samples or assays from loading properly. To eliminate bubbles from inlets either use a clean bent pipette tip to gently pull bubble out or gently aspirate alcohol vapor over the inlet using a wash bottle (suction straw removed) containing a small amount of alcohol in the bottom. The alcohol fumes quickly break the surface tension of the bubbles eliminating them. Be careful not to over aspirate as the samples will evaporate.

11. Explanation of thermal cycling conditions:

Step 1: Thermal mixing step, which mixes the sample and assay of each reaction.

Step 2: Hot start

Step 3-12: Touchdown cycles - 0.8ºC degrees decrease each cycle.

Step 13-14: Amplification.

Step 15: Cool Down

12. Samples will amplify more quickly if using STA product as the starting DNA template. To prevent over-amplification, reduce the number of cycles in step 14 of the thermal cycling conditions to 17 additional cycles (*see* **Note 14**).

13. Before the chip can be read on the EP1 reader, it must be turned on to allow the camera to cool to the appropriate operating temperature (approx. 40 min).

14. Not all SNP assays will amplify at the same rate (i.e., some assays will provide better results with fewer or more cycles than the average). Obtaining three sets of data at 5 cycle

intervals allows for comparison and increases the probability of obtaining maximal separation of the genotype cluster.

15. Leaving the DNA hydrated is an alternative method. If using hydrated DNA, omit the nuclease free water from the primer master mix. We experience more consistent results with the dry down method, which we attribute to unequal evaporation of the DNA samples due to our use of a liquid handling robot for DNA distribution. We have also successfully scaled the reagents proportionally to create 4μL reactions which are successfully measured by the BMG PHERAstar Plus plate reader.

16. When designing your plate set up be sure to include positive controls, including homozygotes for allele 1 and allele 2 as well as a control heterozygous sample (a synthetic heterozygote can be made by mixing equal quantities of the homozygous samples). Negative controls, including a no template control (NTC; DNA free water is substitute for the DNA template), should also be included.

Arraying samples and assays by rows and columns with the last row or column for controls seems to be the most convenient for setting up. A sample set up may look like the following:

Genotyping of 11 samples with 8 SNP assays in a 96 well plate. Each row (minus the last row) will be filled with a single SNP assay (row A = SNP 1, row B = SNP 2, etc.). Each column will be filled with a single DNA sample (column 1 = Sample 1, column 2 = Sample 2, etc.). The last column will be used for controls. Multiple positive as well as multiple negative controls are included. For this example, prepare 8 KASPar primer specific master mixes. Each master mix should contain enough master mix for 14-16 samples (11 samples, 1 control, and 2-4 for overage). The table below depicts the plate set

up (first and second numbers in well positions represent SNP assay and Sample numbers, respectively)

		Sample 1	Sample 2	Sample 3	Sample 4	Sample 5	Sample 6	Sample 7	Sample 8	Sample 9	Sample 10	Sample 11	Controls
		1	2	3	4	5	6	7	8	9	10	11	12
SNP 1	A	1/1	1/2	1/3	1/4	1/5	1/6	1/7	1/8	1/9	1/10	1/11	1/A1
SNP 2	B	2/1	2/2	2/3	2/4	2/5	2/6	2/7	2/8	2/9	2/10	2/11	2/A1
SNP 3	C	3/1	3/2	3/3	3/4	3/5	3/6	3/7	3/8	3/9	3/10	3/11	3/A2
SNP 4	D	4/1	4/2	4/3	4/4	4/5	4/6	4/7	4/8	4/9	4/10	4/11	4/A2
SNP 5	E	5/1	5/2	5/3	5/4	5/5	5/6	5/7	5/8	5/9	5/10	5/11	5/Het
SNP 6	F	6/1	6/2	6/3	6/4	6/5	6/6	6/7	6/8	6/9	6/10	6/11	6/Het
SNP 7	G	7/1	7/2	7/3	7/4	7/5	7/6	7/7	7/8	7/9	7/10	7/11	7/NTC
SNP 8	H	8/1	8/2	8/3	8/4	8/5	8/6	8/7	8/8	8/9	8/10	8/11	8/NTC

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TABLES

Table 1. Amaranthus accessions used in the SNP diversity assay screens.
PI 481125 and PI 642741 are the parents of the mapping population.
[†]All Origin information is derived from the Germplasm Resources Information Network (http://www.ars-grin.gov/npgs/). Several accessions were collected in the Old World although they originate in the Americas according to Sauer (1967)
[‡]Reclassified here as *A. hypochondriacus* based on data reported herein.
[§]cv. 'Plainsman'.

	Name	Species	Geographical Location[†]
1	Ames 15170	*Amaranthus caudatus* L.	Nepal[†]
2	Ames 5127	*A. caudatus*	California, USA
3	PI 175039	*A. caudatus*	India[†]
4	PI 490440	*A. caudatus*	Peru
5	PI 490604	*A. caudatus*	Bolivia
6	PI 490609	*A. caudatus*	Ecuador
7	PI 553073	*A. caudatus*	New Jersey, USA
8	PI 568132	*A. caudatus*	Bolivia
9	PI 618622	*A. caudatus*	Unknown
10	PI 642741	*A. caudatus*	Bolivia
11	Ames 5310	*Amaranthus cruentus* L.	Mexico, Sonora
12	PI 477913	*A. cruentus*	Mexico
13	PI 477914	*A. cruentus*	Mexico
14	PI 482049	*A. cruentus*	Zimbabwe[†]
15	PI 566897	*A. cruentus*	India[†]
16	PI 604666	*A. cruentus*	Pennsylvania, USA
17	PI 606799	*A. cruentus*	Pennsylvania, USA
18	PI 618962	*A. cruentus*	Benin[†]
19	PI 628784	*A. cruentus*	Mexico, Puebla
20	PI 628793	*A. cruentus*	Zaire[†]
21	PI 481125[‡]	*Amaranthus hypochondriacus* L.	India[†]
22	PI 274279	*A. hypochondriacus*	India[†]
23	PI 337611	*A. hypochondriacus*	Uganda[†]
24	PI 477915	*A. hypochondriacus*	India[†]
25	PI 477916	*A. hypochondriacus*	Mexico
26	PI 511731	*A. hypochondriacus*	Mexico
27	PI 540446	*A. hypochondriacus*	Pakistan[†]
28	PI 558499[§]	*A. hypochondriacus*	Nebraska, USA
29	PI 568130	*A. hypochondriacus*	Iowa, USA
30	PI 619259	*A. hypochondriacus*	Nepal[†]

31	PI 633589	*A. hypochondriacus*	Mexico, Chihuahua
32	Ames 23369	*Amaranthus hybridus*	Brazil
33	Ames 23891	*A. hybridus*	Czech Republic
34	Ames 25132	*A. hybridus*	Nigeria
35	Ames 26852	*A. hybridus*	Portugal
36	PI 500249	*A. hybridus*	Zambia
37	PI 568179	*A. hybridus*	Iowa, USA
38	PI 603886	*A. hybridus*	Ohio, USA
39	PI 605351	*A. hybridus*	Greece
40	PI 632247	*A. hybridus*	North Carolina, USA
41	PI 636181	*A. hybridus*	Delaware, USA
42	PI 572261	*Amaranthus powellii subsp. Bouchonii*	Germany
43	PI 595317	*A. powellii subsp. Bouchonii*	California, USA
44	Ames 22592	*Amaranthus retroflexus*	Mongolia
45	PI 607447	*A. retroflexus*	Jamaica
46	PI 603873	*Amaranthus tuberculatus*	Nebraska, USA

Table 2. Summary analysis of Amaranthus SNP marker results.
Sample size, total number of polymorphic SNP loci, total alleles observed, minor allele frequency (MAF) range and average, and total highly polymorphic microsatellites are included. A total of 480 putative SNP markers were initially screened.
[†]Includes *A. hypochondriacus*, *A. cruentus*, *A. caudatus* and *A. hybridus* accessions.
[‡]Highly polymorphic SNP: MAF ≥ 0.3

	A. hypochondriacus	*A. cruentus*	*A. caudatus*	*A. hybridus*	*A. hybridus* complex[†]
Sample Size	11	10	10	10	41
Polymorphic SNPs	186	35	136	263	414
MAF Range	0.05 – 0.5	0.05 – 0.5	0.05 – 0.5	0.05 – 0.5	0.05 – 0.5
Average MAF	0.20	0.18	0.22	0.24	0.27
Highly polymorphic[‡]	41	7	43	84	141

Table 3. *Chenopodium* accessions included in the diversity panel.
Underscored accessions were used in the genomic reduction experiment for SNP discovery.
[†]*C. ficifolium* and *C. watsonii* are diploid species. All other species are allotetraploids.
[‡]Origin information is derived from the Germplasm Resources Information Network for all USDA accessions.
[§]PROINPA, The Foundation for the Promotion and Investigation of Andean Products, La Paz, Bolivia; CIP, Internal Potato Center; USDA-NPGS, Ames, IA, USA; IEB, Institute of Experimental Botany, Czech Republic; ININ, National Institute for Nuclear Investigation, Toluca, Mexico; UBA, University of Buenos Aires, Buenos Aires, Argentina; BYU, Brigham Young University, Provo, UT, USA.
[¶]Two different sources for KU-2 were included the genomic reduction (PROINPA and CIP).

Name	Species[†]	Coded Name	Passport Origin	Source[‡]
PI 614881	*C. quinoa*	A1	Argentina, Jujuy	USDA-NPGS
PI 614883	*C. quinoa*	A2	Argentina, Jujuy	USDA-NPGS
PI 614884	*C. quinoa*	A3	Argentina, Jujuy	USDA-NPGS
PI 587173	*C. quinoa*	A4	Argentina, Jujuy	USDA-NPGS
Jujuy	*C. quinoa*	A_Jujuy	Argentina, Jujuy	CIP-FAO
PI 614902	*C. quinoa*	B2	Bolivia, Oruro	USDA-NPGS
PI 614904	*C. quinoa*	B3	Bolivia, Oruro	USDA-NPGS
PI 614905	*C. quinoa*	B4	Bolivia, Oruro	USDA-NPGS
PI 614907	*C. quinoa*	B6	Bolivia, Oruro	USDA-NPGS
PI 614909	*C. quinoa*	B8	Bolivia, Oruro	USDA-NPGS
PI 614910	*C. quinoa*	B9	Bolivia, Oruro	USDA-NPGS
PI 614911	*C. quinoa*	B10	Bolivia, Oruro	USDA-NPGS
PI 614912	*C. quinoa*	B11	Bolivia, Oruro	USDA-NPGS
PI 614915	*C. quinoa*	B13	Bolivia, Oruro	USDA-NPGS
PI 614916	*C. quinoa*	B14	Bolivia, Oruro	USDA-NPGS
PI 614919	*C. quinoa*	B15	Bolivia, Oruro	USDA-NPGS
PI 614920	*C. quinoa*	B16	Bolivia, Oruro	USDA-NPGS
PI 614927	*C. quinoa*	B23	Bolivia, La Paz	USDA-NPGS
PI 614928	*C. quinoa*	B24	Bolivia, La Paz	USDA-NPGS
PI 614929	*C. quinoa*	B25	Bolivia, La Paz	USDA-NPGS
PI 614931	*C. quinoa*	B27	Bolivia, Oruro	USDA-NPGS
PI 614932	*C. quinoa*	B28	Bolivia, Oruro	USDA-NPGS
PI 614933	*C. quinoa*	B29	Bolivia, Oruro	USDA-NPGS
PI 614934	*C. quinoa*	B30	Bolivia, Oruro	USDA-NPGS
PI 614935	*C. quinoa*	B31	Bolivia, Oruro	USDA-NPGS
PI 614936	*C. quinoa*	B32	Bolivia, Oruro	USDA-NPGS
PI 614937	*C. quinoa*	B33	Bolivia, Oruro	USDA-NPGS
PI 614938	*C. quinoa*	B34	Bolivia, Oruro	USDA-NPGS
PI 478415	*C. quinoa*	B35	Bolivia, La Paz	USDA-NPGS
PI 478418	*C. quinoa*	B36	Bolivia, Potosi	USDA-NPGS
PI 478410	*C. quinoa*	B37	Bolivia, La Paz	USDA-NPGS
PI 478414	*C. quinoa*	B38	Bolivia, La Paz	USDA-NPGS
PI 614002	*C. quinoa*	B39	Bolivia, Cochabamba	USDA-NPGS
Ames 13215	*C. quinoa*	B40	Bolivia, La Paz	USDA-NPGS
PI 478408	*C. quinoa*	B41	Bolivia, La Paz	USDA-NPGS
Ames 13217	*C. quinoa*	B42	Bolivia, La Paz	USDA-NPGS
Ames 13218	*C. quinoa*	B43	Bolivia, La Paz	USDA-NPGS
Ames 13219	*C. quinoa*	B44	Bolivia, La Paz	USDA-NPGS
Embrapa	*C. quinoa*	BRZ_Embrapa	Brazil	CIP
Chucapaca	*C. quinoa*	B_Chucapaca	Bolivia	PROINPA

Jaccha Grano	*C. quinoa*	B_JacchaGrano	Bolivia	PROINPA
Kamiri	*C. quinoa*	B_Kamiri	Bolivia	CIP
L-26	*C. quinoa*	B_L-26	Bolivia	PROINPA
L-P	*C. quinoa*	B_LP	Bolivia	PROINPA
Maniquena	*C. quinoa*	B_Maniquena	Bolivia	PROINPA
Mocko	*C. quinoa*	B_Mocko	Bolivia	PROINPA
Pandela	*C. quinoa*	B_Pandela	Bolivia	PROINPA
Ratuqui	*C. quinoa*	B_Ratuqui	Bolivia	CIP
Real	*C. quinoa*	B_Real	Bolivia, Oruro	CIP
Sayana	*C. quinoa*	B_Sayana	Bolivia	CIP
Surumi	*C. quinoa*	B_Surumi	Bolivia	PROINPA
Ames 22153	*C. quinoa*	C1	Chile, Pichilemu	USDA-NPGS
Ames 22154	*C. quinoa*	C2	Chile, Cajon	USDA-NPGS
Ames 22155	*C. quinoa*	C3	Chile, Pichaman	USDA-NPGS
Ames 22156	*C. quinoa*	C4	Chile, Cajon	USDA-NPGS
Ames 22157	*C. quinoa*	C5	Chile, Lo Valdivia	USDA-NPGS
Ames 22158	*C. quinoa*	C6	Chile, Llico	USDA-NPGS
Ames 22159	*C. quinoa*	C7	Chile, Bucalemu	USDA-NPGS
Ames 22160	*C. quinoa*	C8	Chile, Iloca	USDA-NPGS
Ames 22161	*C. quinoa*	C9	Chile, Llico	USDA-NPGS
PI 614880	*C. quinoa*	C10	Chile, Los Lagos	USDA-NPGS
PI 614880	*C. quinoa*	C10b	Chile, Los Lagos	USDA-NPGS
PI 614882	*C. quinoa*	C11	Chile, La Araucania	USDA-NPGS
PI 614885	*C. quinoa*	C12	Chile, Bio-Bio	USDA-NPGS
PI 614886	*C. quinoa*	C13	Chile, Maule	USDA-NPGS
PI 614887	*C. quinoa*	C14	Chile, Bio-Bio	USDA-NPGS
PI 614888	*C. quinoa*	C15	Chile, Bio-Bio	USDA-NPGS
PI 614889	*C. quinoa*	C16	Chile, Bio-Bio	USDA-NPGS
PI 433232	*C. quinoa*	C17	Chile, Groben	USDA-NPGS
PI 584524	*C. quinoa*	C18	Chile, Chillan	USDA-NPGS
RU-2	*C. quinoa*	CENG_RU-2	England - Chilean origin	CIP
NL-6	*C. quinoa*	CHOL_NL6	Holland - Chilean origin	CIP
PI 596293	*C. quinoa*	CO1	US, Colorado	USDA-NPGS
Narino	*C. quinoa*	COL_Narino	Columbia	CIP
BaerI	*C. quinoa*	C_BaerI	Chile	CIP
G-205-95DK	*C. quinoa*	C_G20595DK	Denmark - Chilean origin	PROINPA
KU-2	*C. quinoa*	C_KU2	Chile	CIP
KU-2b¶	*C. quinoa*	C_KU2b	Chile	PROINPA
Ollague	*C. quinoa*	C_Ollague	Chile	CIP
Ames 13228	*C. quinoa*	E1	Equador, Otavalo	USDA-NPGS
ECU-420	*C. quinoa*	E_ECU420	Ecuador	CIP
Ingapirca	*C. quinoa*	E_Ingapirca	Ecuador	CIP
L-3204	*C. quinoa*	L-3204	Bolivia	PROINPA
NSL 86628	*C. quinoa*	MD1	US, Maryland	USDA-NPGS
PI 510532	*C. quinoa*	P1	Peru, Puno	USDA-NPGS
PI 510533	*C. quinoa*	P2	Peru, Puno	USDA-NPGS
PI 510536	*C. quinoa*	P3	Peru, Puno	USDA-NPGS
PI 510537	*C. quinoa*	P4	Peru, Puno	USDA-NPGS
PI 510543	*C. quinoa*	P5	Peru, Puno	USDA-NPGS
PI 510547	*C. quinoa*	P6	Peru, Puno	USDA-NPGS
PI 510551	*C. quinoa*	P8	Peru, Puno	USDA-NPGS

PI 596498	*C. quinoa*	P9	Peru, Cusco	USDA-NPGS
PI 510542	*C. quinoa*	P10	Peru, Puno	USDA-NPGS
PI 510540	*C. quinoa*	P11	Peru, Puno	USDA-NPGS
PI 510550	*C. quinoa*	P12	Peru, Puno	USDA-NPGS
PI 510545	*C. quinoa*	P13	Peru, Puno	USDA-NPGS
PI 510548	*C. quinoa*	P14	Peru, Puno	USDA-NPGS
Ames 26191	*C. quinoa*	P15	Peru, Puno	USDA-NPGS
PI 510546	*C. quinoa*	P16	Peru, Puno	USDA-NPGS
<u>0654</u>	*C. quinoa*	P_0654	Peru, Puno	PROINPA
03-21-072RM	*C. quinoa*	P_0321072RM	Peru, Puno	CIP
03-21-079BB	*C. quinoa*	P_0321079BB	Peru, Puno	CIP
CICA-17	*C. quinoa*	P_CICA17	Peru, Cusco	CIP
CICA-67	*C. quinoa*	P_CICA67	Peru	CIP
E-DK-4	*C. quinoa*	P_EDK4	Denmark - Peruvian origin	CIP
<u>G-205-95</u>	*C. quinoa*	P_G20595	Peruvian origin	CIP
Huariponcho	*C. quinoa*	P_Huariponcho	Peru, Puno	CIP
Illpa	*C. quinoa*	P_Illpa	Peru, Puno	CIP
Kancolla	*C. quinoa*	P_Kancolla	Peru, Puno	CIP
Salcedo	*C. quinoa*	P_Salcedo	Peru, Puno	CIP
NSL 86649	*C. quinoa*	SC1	US, South Carolina	USDA-NPGS
Ames 19047	*C. quinoa*	TX1	US, Texas	USDA-NPGS
NSL 92331	*C. quinoa*	WA1	US, Washington	USDA-NPGS
Ames 29207/ BYU 803	*C.berlandieri var. macrocalycium*	BYU 803/Ames 29207	Maine	USDA-NPGS
BYU 567	*C. berlandieri subsp. nuttaliae*	BYU 567	Mexico	ININ-Mexico
Ames 29307 BYU 802	*C. berlandieri var. boscianum*	BYU 802	Louisiana	USDA-NPGS
BYU 652	*C. berlandieri subsp. berlandieri var. zschackei*	BYU 652	Utah	BYU
BYU 943	*C.ficifolium*[†]	BYU 943	Czech Republic	IEB
BYU 1101	*C.hircinum*	BYU 1101	Argentina	UBA
BYU 1102	*C.hircinum*	BYU 1102	Argentina	UBA
BYU 839	*C.watsonii*[†]	BYU 839	New Mexico (2X)	BYU

Table 4. Summary information for SNPs identified for each of the Quinoa populations.
[†]Pop1 = KU-2 X 0654; Pop39 = NL-6 X 0654; Pop40 = NL-6 X Chucapaca; PopM3 = L-P X 0654; PopGO = G-205-95 X Ollague.
[‡]SNP were called if coverage at the base was ≥ 6X, the frequency of the minor allele was ≥20%, and 100% of the alleles called within a parental line were identical.
[§]Number of contigs with at least one SNP

Population[†]	SNPs[‡]	Unique contigs[‡]	SNP base coverage	Minor allele freq. range			SNP type (%)					
				20-29%	30-39%	40-49%	A/C	A/G	A/T	C/G	C/T	G/T
Pop1	2,885	1,514	7.8	817	1,072	996	10.2	30.6	12.2	4.5	31.3	11.2
Pop39	3,615	1,888	8.0	993	1,055	874	10.8	30.5	12.7	5.2	29.5	11.3
Pop40	2,918	1,551	8.0	767	1,102	1,049	10.9	31.0	11.5	5.7	30.4	10.5
PopM3	2,092	995	7.6	599	759	734	10.1	29.5	12.9	5.02	32.2	10.3
PopGO	2,668	1359	7.7	739	1,055	874	10.3	31.5	11.54	5.25	30.8	10.6
Average:	2,836	1461	7.8	783	1009	905	10.5	30.6	12.2	5.1	30.8	10.8

FIGURES
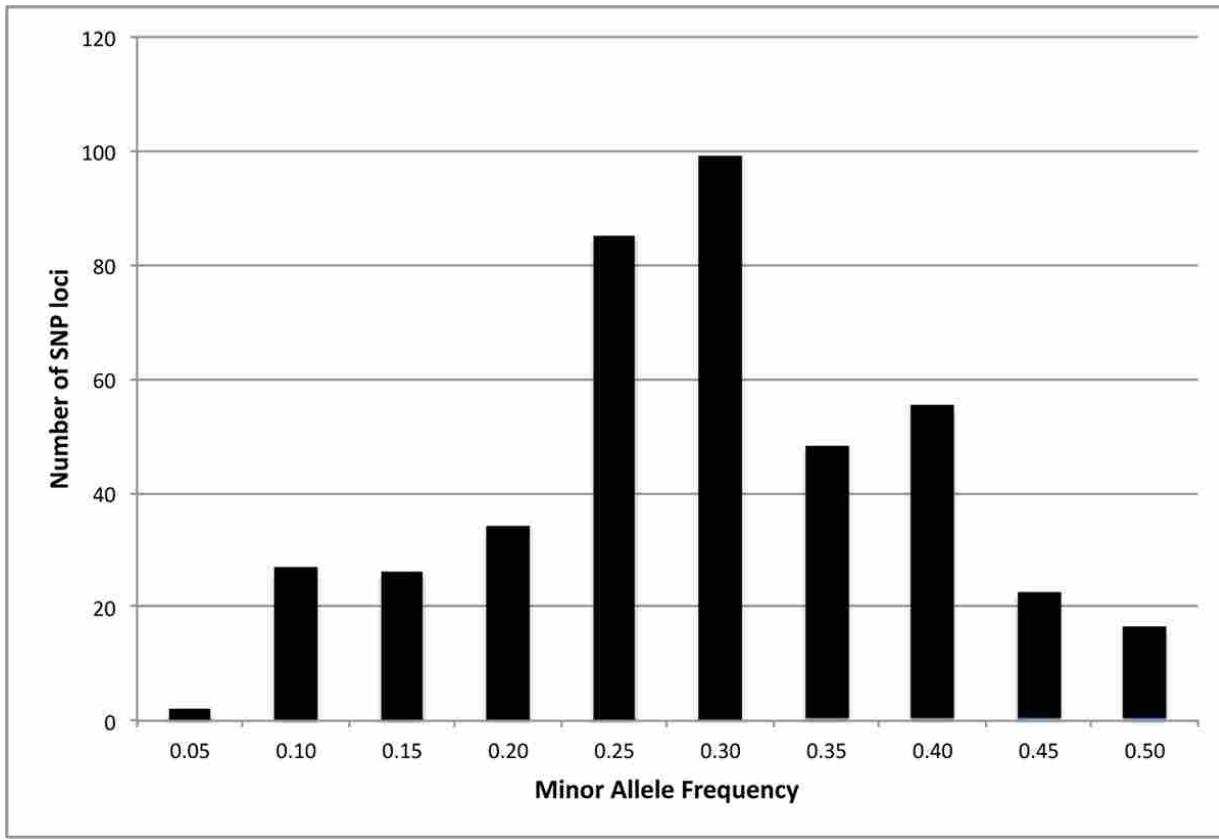
Figure 1. Minor allele frequency (MAF) distribution across 414 amaranth SNP loci.
Determined within the full panel of grain amaranth and *A. hybridus* accessions.
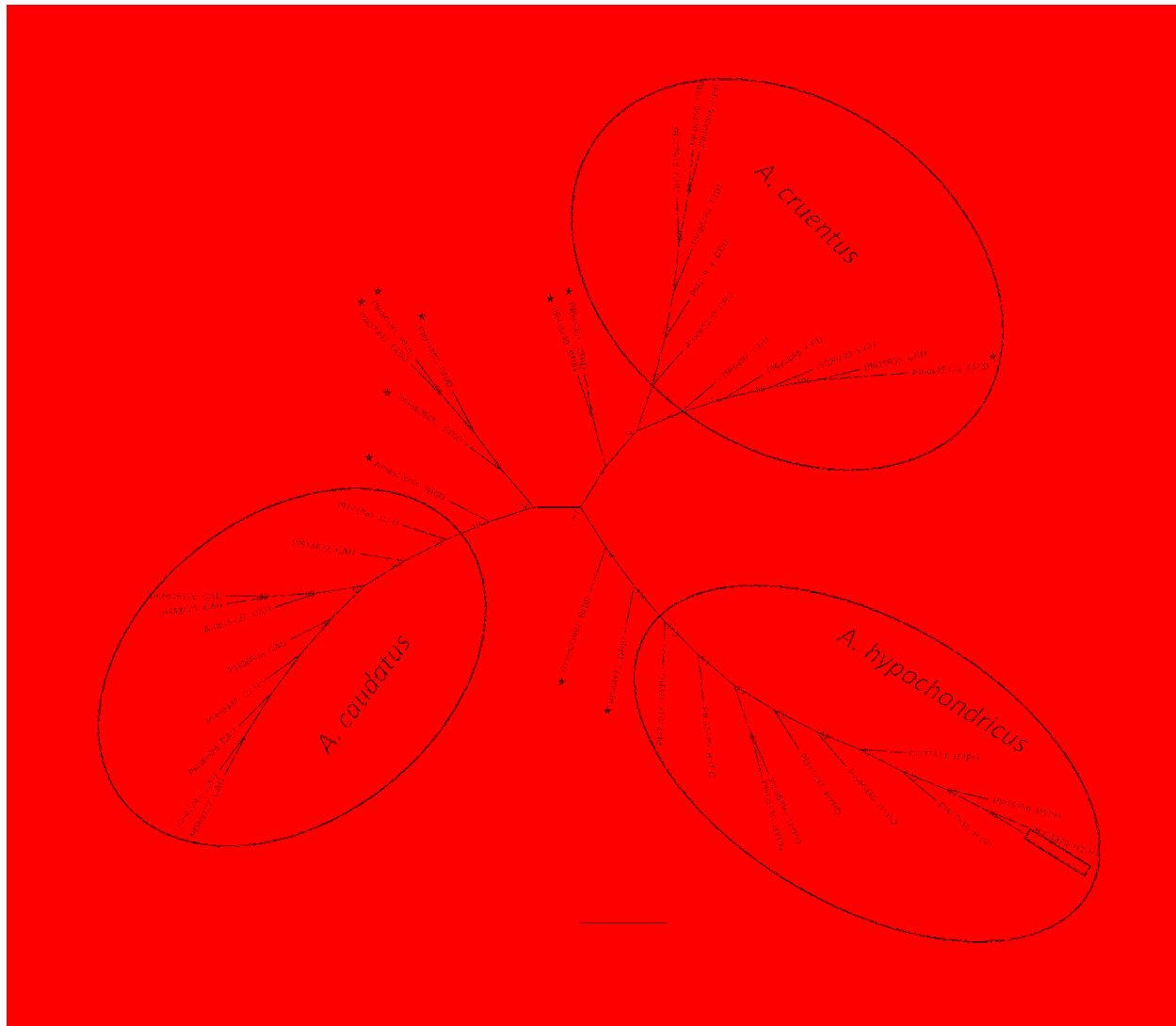
Figure 2.Amaranth unrooted neighbor joining tree.
Tree shows the genetic relationship among accessions of the *A. hybridus* complex (*A. caudatus*, *A. cruentus*, *A. hypochondriacus* and *A. hybridus*) genotypes based on SNP marker data. Bootstrap support values are given at each node. Individuals in the tree are identified by their abbreviated species. *A. hybridus* accessions are identified with stars (⋆). The boxed accession, PI 481125, was originally classified as *A. caudatus*.
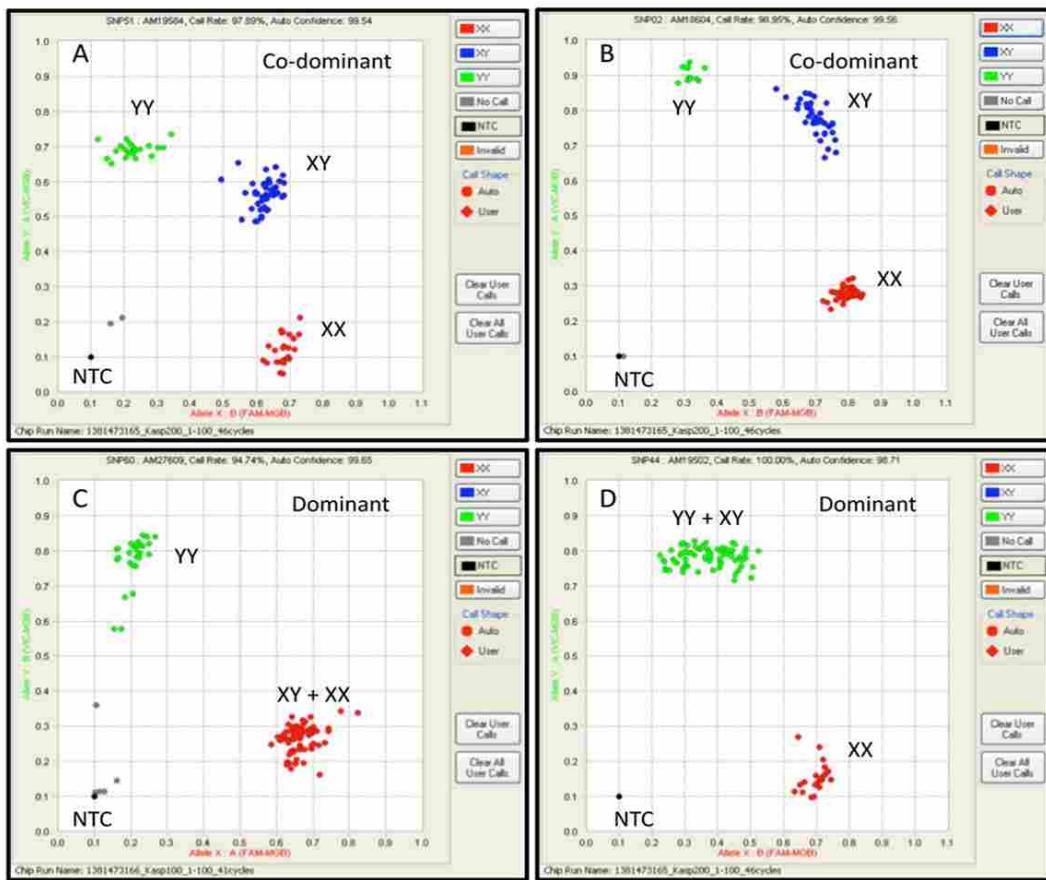
Figure 3. Example of Amaranthus SNP assays using the KASPar™ genotyping chemistry. Performed on the Fluidigm access array in the F_2 mapping population. Panels A and B show co-dominant SNP loci AM19584 and AM18604, while panels C and D show dominant SNP loci AM27609 and AM19502. No template controls (NTC) are identified at the origin of each Cartesian graph.
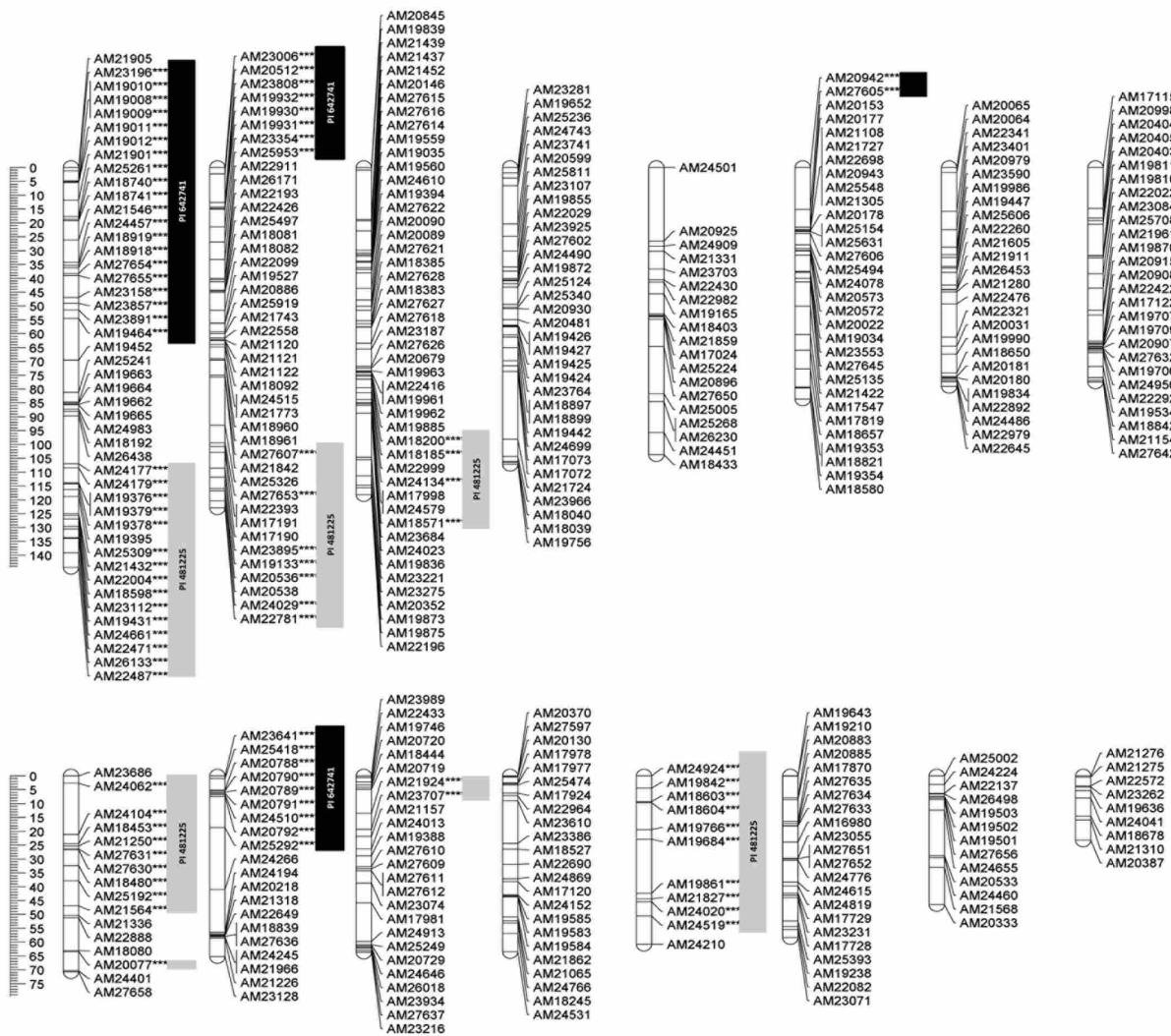
Figure 4. 16 group Amaranth linkage map.
Constructed from an interspecific *A. hypochondriacus* X *A. caudatus* F$_2$ population (2*n*=32). Distances are shown centiMorgans (cM) corrected with the Kosambi mapping function. SNP loci showing segregation distortion (*P*<0.001) to PI 642741 or PI 481125 are identified with blackened or shaded boxes, respectively.
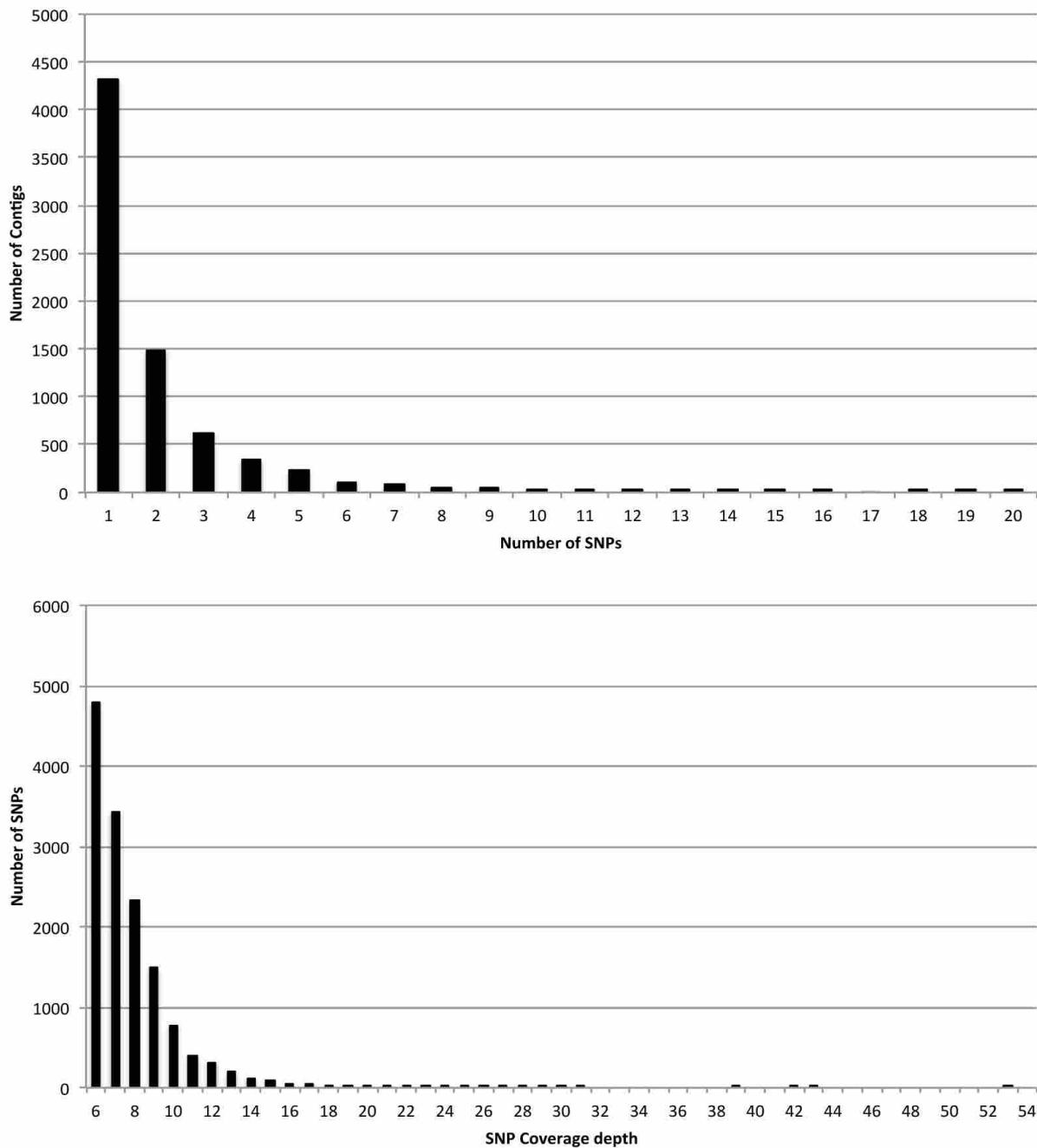
Figure 5. Distribution of SNPs and coverage depth in quinoa.
 A) The distribution of the number of SNPs by the number of contigs.   B) The distribution of coverage depth by the number of SNPs. The average depth of coverage at a SNP was 7.8X.
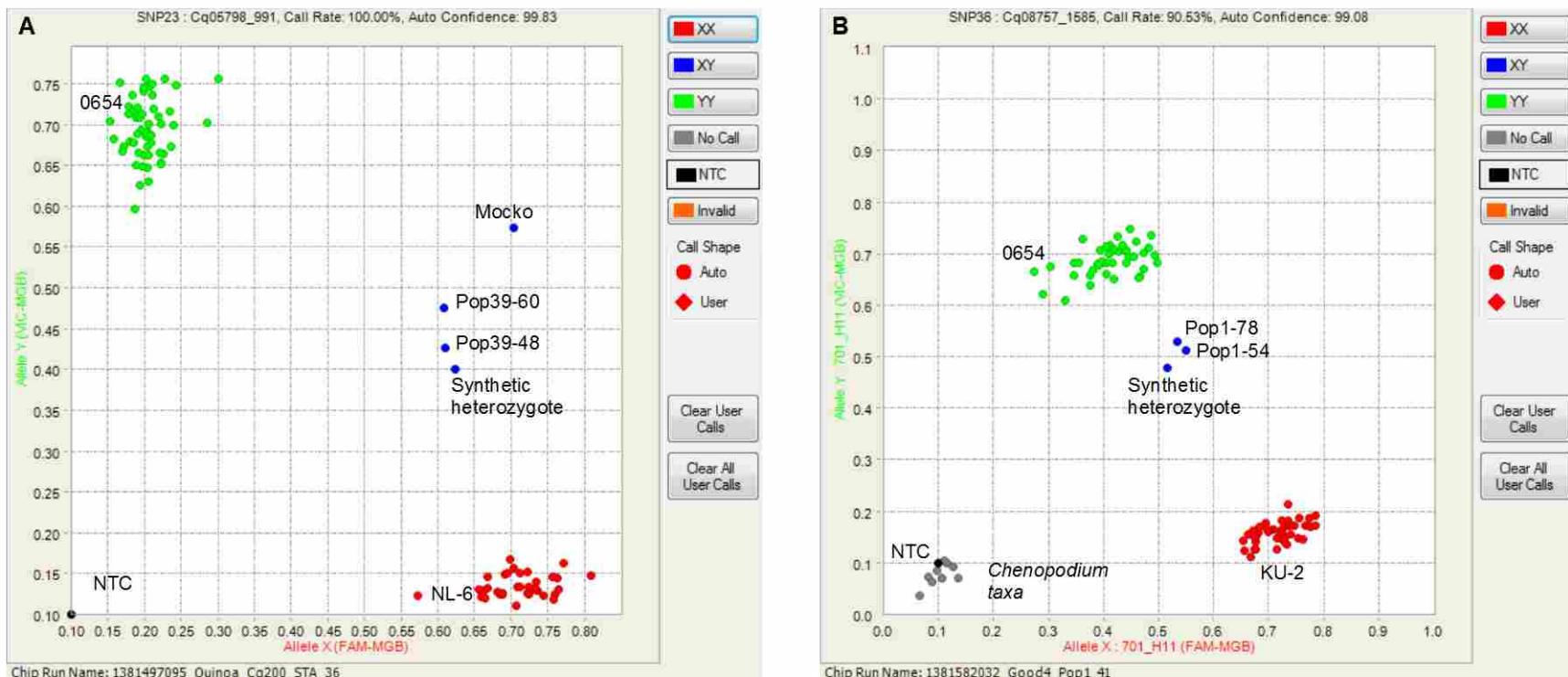
Figure 6. Example of quinoa SNP assays using the KASPar genotyping chemistry.
Performed on the Fluidigm access array platform. Panels A and B show SNP loci Cq05798_991 and Cq08757_1585, respectively. No template controls (NTC), synthetic heterozygous controls, and heterozygous samples are identified in each graph
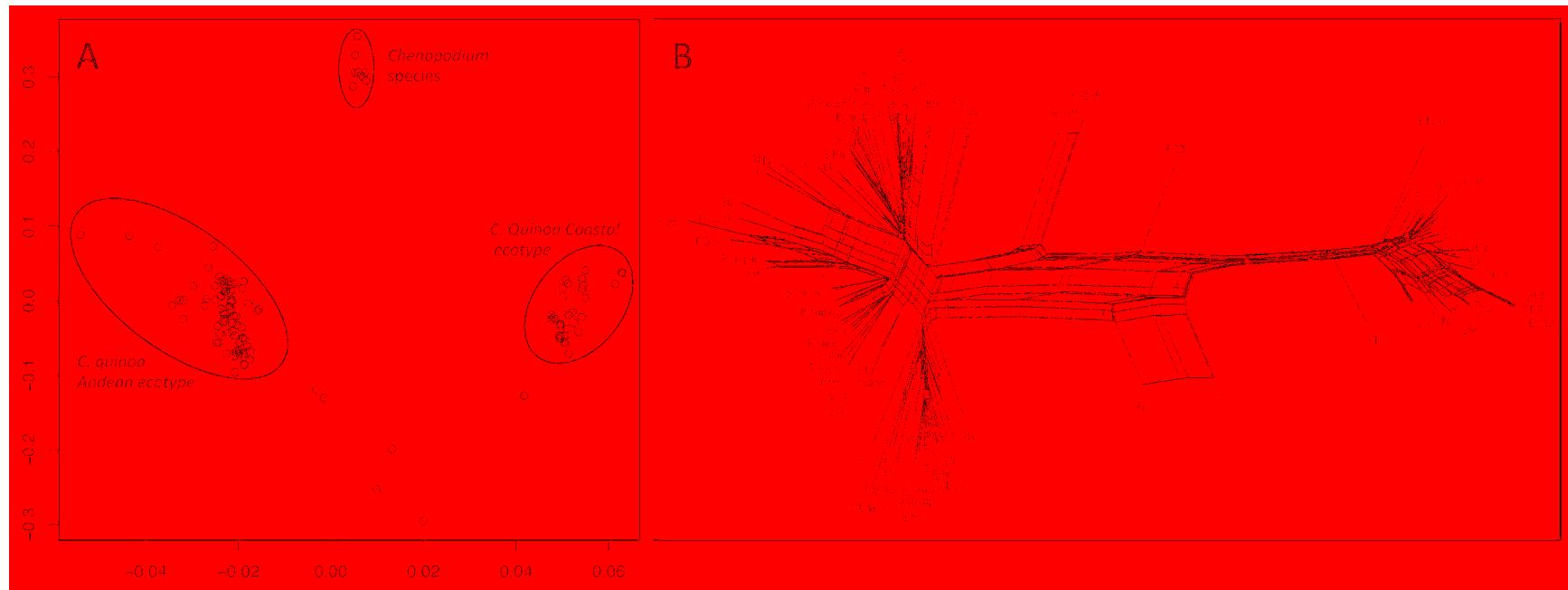
Figure 7. Quinoa principle coordinate and unrooted NeighborNet analysis.
A) Principle coordinate analysis of the entire *Chenopodium* diversity panel, including the eight related *Chenopodium taxa*. Principle coordinate 1 and 2 explain 72.3% and 7.3% of the total variance, repectively. B) Unrooted NeighborNet analysis using the 113 *C. quinoa* accessions. Accessions in the NeighborNet analysis are coded as given in Table 1.
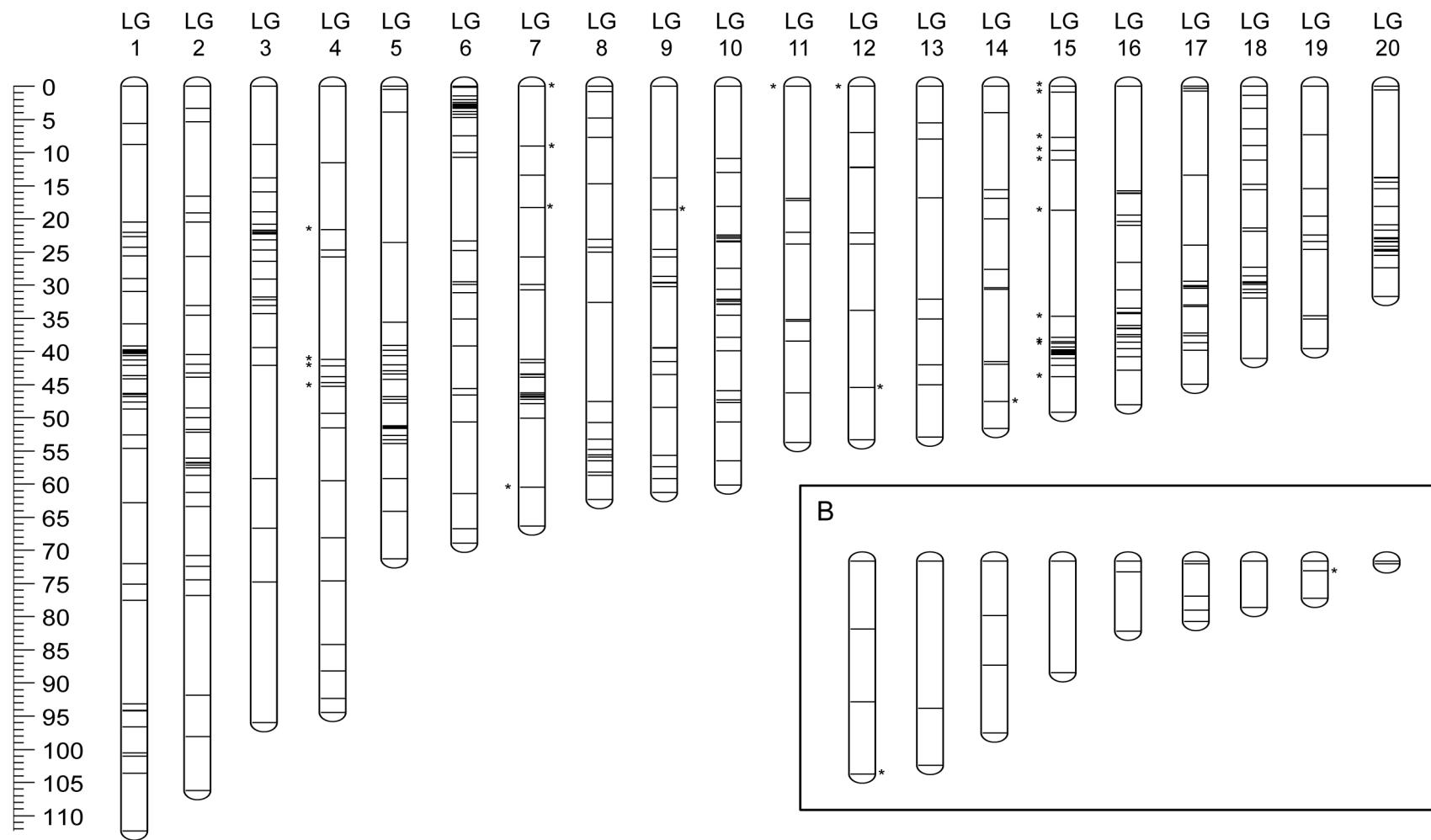
Figure 8. Integrated Quinoa linkage map.
constructed from a cross of KU-2 X 0654 and NL-6 X 0654. SNP loci showing segregation distortion (P<0.01) are identified with asterisks.
Asterisks to the left of the linkage group identify marker loci that are skewed towards the coastal parent (KU-2 or NL-6), while asterisks to the
right identify markers skewed towards the the 0654 paternal parental. Exact map positions for each SNP marker are provided in Supplemental
Table S2.

Components

DNA Template:
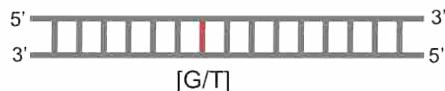
5' |||||||||||||||| 3'
3' |||||||||||||||| 5'

[G/T]

Primers:

5' ════════════ C 3'
5' ════════════ A 3'

Allele specific forwards

3' ────────── 5'

Common Reverse

KASPar Master Mix:

(F) Q   (H) Q

PCR: 1st Round

5' ||||||||||||||||||||| 3'
                    3' ═══════ 5'

5'
         ⟶ A
   |||||||| 3'
3' |||||||||||||||||| 5'
         T

5' ════════════ C 3'

PCR: 2nd Round

            A
5' ||||||||||||||||||||||||||| 3'
                    3' |||||| 5'
                    ⟵

PCR: 3rd Round

3' Q ═══════ 5'

5' (H) ═══════ ⟶ 3'
3' ═══════||||||||||||||| 5'
              T

Final Product

            A
5' (H) |||||||||||||||||||||||||| 3'
3' |||||||||||||||||||||||||| 5'
            T

70
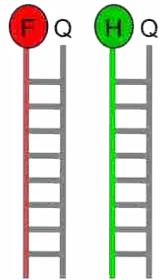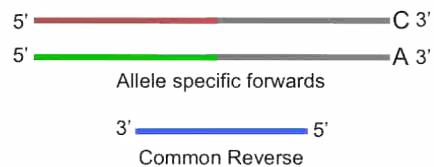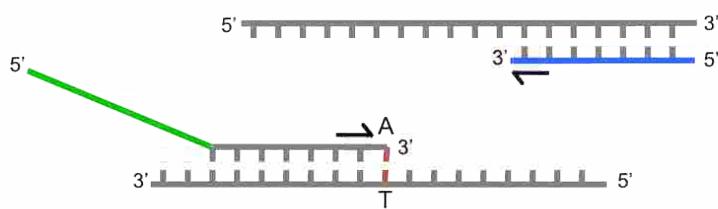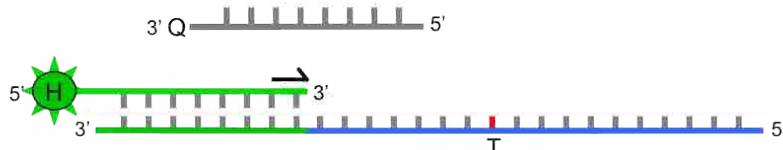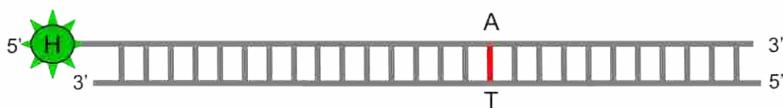
Figure 9. Diagram detailing the KASPar genotyping chemistry.
Components consist of: three user-designed primers (two allele specific forwards and one common reverse) unique to a single SNP, two universal secondary oligos with attached 5' fluorophore and bound quenchers (included in KASPar reagent), and DNA template. In the first rounds of PCR, only the common reverse and the allele specific primer that corresponds to the specific genotype of the DNA template hybridize and extend. In this first round of PCR, a 5' tail is incorporated into the PCR product. During the second cycle of PCR, the common reverse oligo binds the template made from the first round of PCR and extents producing a compliment to the allele specific 5' tail. In the third round of PCR, the secondary oligos with the attached fluorophore hybridize to the PCR produce releasing the fluorofore from its quencher and incorporating it into the final PCR product. As amplification continues additional fluorophores are released from their quenchers producing a strong allele specific signal.
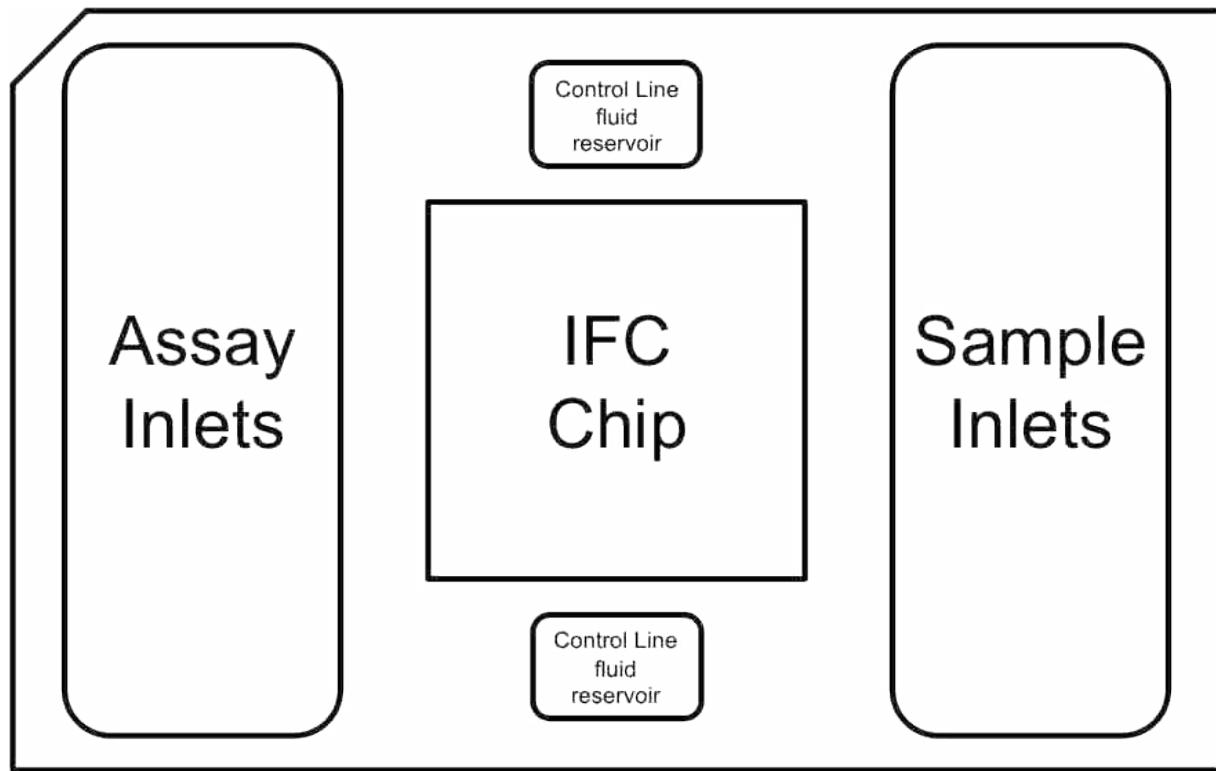
Figure 10. Diagram of a Fluidigm 96.96 chip layout.
Control line fluid is injected into each of the control line fluid reservoirs and primed using the IFC Controller (Control line fluid is pressurized causing it to enter the chip allowing control of various valves). Ninety-six assays and 96 samples are then loaded into their respective inlets (*see* **Figure 3**). Assays and samples are then forced into the IFC chip using the IFC controller.

Figure 11. Diagram of one set of IFC inlets (assay or sample) and how to load them.
Using an 8-channel pipette, pipette assays and samples into their appropriate inlets by column. A standard 8-channel pipette will pipette into every other inlet. Pipette column 1 of the prepared 96 well plate of assays into the first column (every other inlet as indicated by the blue highlighted inlets) then work right with columns 2, 3, 4, 5, and 6. Pipette column 7 of the prepared 96 well plate of assays into the first column of inlets (every other inlet as indicated by the purple highlighted inlets) just below those pipetted previously. Work your way right with columns 8, 9, 10, 11, and 12 until all inlets are filled. Repeat this pattern for prepared samples, pipetting them into the sample inlets.
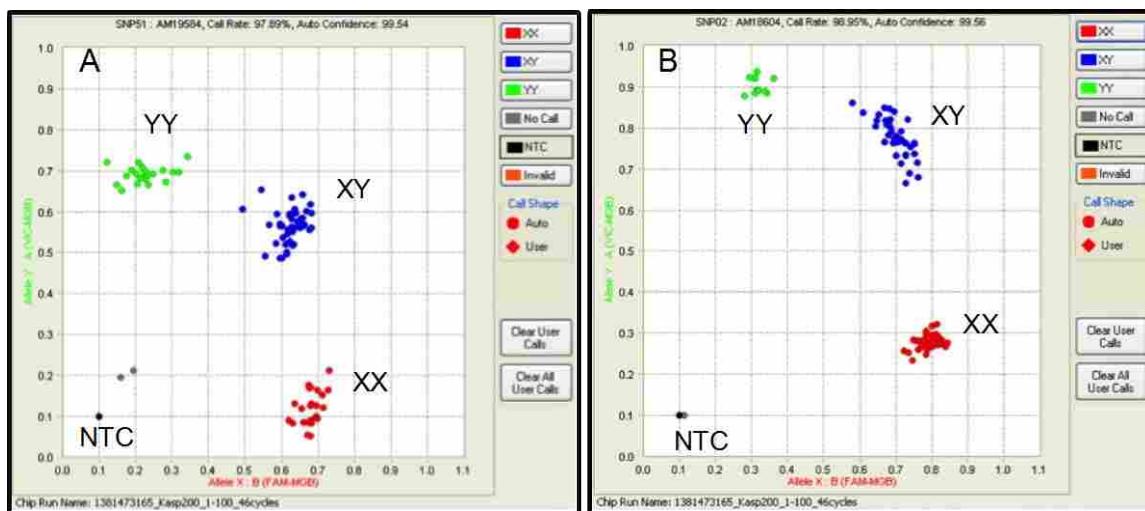
Figure 12. Example of SNP assays using KASPar genotyping on the Fluidigm access array. The image was obtained from Fluidigm's SNP Genotyping Analysis software and shows a Cartesian graph with three distinct genotypic cluster. Each dot represents one sample.

SUPPLEMENTAL TABLES

Supplemental Table S1. Amaranth SNP marker information.
Includes name, GenBank dbSNP accession ID, polymorphism type, KASPar™ primer sequences (A1, A2 and Common Reverse), minor allele frequency (MAF), and cross species amplification (CSA) for all 419 functional SNP assays tested.
[†]dbSNP in GenBank under the handle MAUGHAN in batch number 2009A, build B131.
[‡]KASPar™ primers: A1 are A2 primers are SNP allele specific. Bolded portions of the primers identify the sequence tags used in the KASPar™ secondary PCR reaction.
[§]MAF values presented were calculated based on the full panel of grain amaranth and *A. hybridus* accessions; NT = Not tested on the diversity panel
[¶]P=successful amplification in *A. powellii*; R= successful amplification in *A. retroflexus*; T=successful amplification in *A. tuberculatus*; '+'= polymorphism detected between the two accessions examined; NTD = Not tested in the diversity panel; NTP = Not tested in the F$_2$ population.

	Name	GenBank[†] SS#	SNP Type	A1 primer (5'→3')[‡]	A2 primer (5'→3')[‡]	Common Reverse (5'→3')[‡]	MAF[§]	CSA[¶]
1	AM16980	ss161140972	A/G	**GAAGGTGACCAAGTTCATGC**TATT ATAGCCAAGTCACTGGATTCCA	**GAAGGTCGGAGTCAACGGATT**AT AGCCAAGTCACTGGATTCCG	GGGACAAAGAAACCGGTTAGAGGTA	0.50	P+
2	AM17024	ss161141016	C/T	**GAAGGTGACCAAGTTCATGC**TGCA AAAAATACCCAAAAAGAACCGCC	**GAAGGTCGGAGTCAACGGATT**AG CAAAAATACCCAAAAAGAACCGCT	CCTTCTTCTTTCTAAAGCGCCTCCTT	0.19	P
3	AM17072	ss161141064	A/G	**GAAGGTGACCAAGTTCATGC**TATT ATTGGAATACTTGTTGTTTGCTTATC ATT	**GAAGGTCGGAGTCAACGGATT**AT TGGAATACTTGTTGTTTGCTTATCA TC	CTTATCCTCATGTCACCTGCACGTT	0.28	PR
4	AM17073	ss161141065	C/T	**GAAGGTGACCAAGTTCATGC**TGGC CTACATAATATACAATAGTGTAAAT AG	**GAAGGTCGGAGTCAACGGATT**GT GGCCTACATAATATACAATAGTGTA AATAA	TTTTTAATTACTCTGTGATGTATTGCTT TT	0.20	PRT
5	AM17115	ss161141107	C/T	**GAAGGTGACCAAGTTCATGC**TAAT TAAAGGGAGATTAAGAGAATAAATC TTG	**GAAGGTCGGAGTCAACGGATT**GT AATTAAAGGGAGATTAAGAGAATA AATCTTA	GACCATACCACAAAGCCTGCATCAA	0.34	PRT
6	AM17120	ss161141112	C/T	**GAAGGTGACCAAGTTCATGC**TACA TAATTTGTTCATTTTTTGTCCAAACC C	**GAAGGTCGGAGTCAACGGATT**AA CATAATTTGTTCATTTTTTGTCCAAA CCT	GGGATAACAAAAAGGAAGAGGAGAG ATTT	0.11	PR
7	AM17122	ss161141114	A/G	**GAAGGTGACCAAGTTCATGC**TACA AGGTTTATTAAGCAACAAGATTCCA A	**GAAGGTCGGAGTCAACGGATT**CA AGGTTTATTAAGCAACAAGATTCCA G	ACTGTTTTGAACTCTGAACTTGGGCTT A	0.46	
8	AM17190	ss161141182	C/T	**GAAGGTGACCAAGTTCATGC**TGAG CCAACCTGACGAATATTCCC	**GAAGGTCGGAGTCAACGGATT**AG AGCCAACCTGACGAATATTCCT	GTGTAGATGCAACACAGCTTCTCCTA	0.33	P+
9	AM17191	ss161141183	A/G	**GAAGGTGACCAAGTTCATGC**TGGA TAGAAGTGTAGATGCAACACAGT	**GAAGGTCGGAGTCAACGGATT**GA TAGAAGTGTAGATGCAACACAGC	AAGTAAAATAATTAGCGTCAGATAGG AGAA	0.26	PRT
10	AM17547	ss161141539	A/G	**GAAGGTGACCAAGTTCATGC**TTAG CTGTAATTCGAGTTTGCGTCATA	**GAAGGTCGGAGTCAACGGATT**AG CTGTAATTCGAGTTTGCGTCATG	CACCCGAAGTGAAGTCCACGAATTT	0.23	PRT
11	AM17728	ss161141720	A/G	**GAAGGTGACCAAGTTCATGC**TATC	**GAAGGTCGGAGTCAACGGATT**CA	GCTTGAGTATCAGTTGATCTTGACATA	0.30	PR

				ATTCCCATTACCATCATTTAGTATCAT	TTCCCATTACCATCATTTAGTATCAC	TTA		
12	AM17729	ss161141721	G/T	**GAAGGTGACCAAGTTCATGC**CTAAATGATGGTAATGGGAATGATTTATAG	**GAAGGTCGGAGTCAACGGATT**ATACTAAATGATGGTAATGGGAATGATTTATAT	CATGGGAATGACAAGGAACTTTTTATGAAA	0.26	PRT
13	AM17819	ss161141811	C/T	**GAAGGTGACCAAGTTCATGC**TGTTTAATGTCATAAAATCGCCGTCGG	**GAAGGTCGGAGTCAACGGATT**GTTTAATGTCATAAAATCGCCGTCGA	CATTTAAATTATCTTCCTTATGAAGATCAA	0.22	PRT
14	AM17870	ss161141862	A/G	**GAAGGTGACCAAGTTCATGC**TAATTATTGATTTTCGAATCAAGAAATGGAACA	**GAAGGTCGGAGTCAACGGATT**ATTGATTTTCGAATCAAGAAATGGAACG	CCTTCTTTGGATCCGAAAATCAACCATT	0.36	PRT
15	AM17924	ss161141916	C/G	**GAAGGTGACCAAGTTCATGC**TCAATTGTTCAACTGCACCAATTGATTAC	**GAAGGTCGGAGTCAACGGATT**CAATTGTTCAACTGCACCAATTGATTAG	TGTCGCTCTCCTGTTCTGGAGATTT	0.31	PR
16	AM17977	ss161141969	C/T	**GAAGGTGACCAAGTTCATGC**TTTGGTCTAATCAGGCTAAACATGC	**GAAGGTCGGAGTCAACGGATT**CTTTGGTCTAATCAGGCTAAACATGT	AAGGTACATCACATGGAAATTTTCTCGATT	0.36	P
17	AM17978	ss161141970	C/T	**GAAGGTGACCAAGTTCATGC**TACAAAATCTTGATTGAGAAATCAATCTCTG	**GAAGGTCGGAGTCAACGGATT**CACAAAATCTTGATTGAGAAATCAATCTCTA	CCATGTGATGTACCTTAGATAGTTGCATA	0.22	PR
18	AM17981	ss161141973	C/T	**GAAGGTGACCAAGTTCATGC**TGTATATTTTTTAGGTAGTGACATCTTATACG	**GAAGGTCGGAGTCAACGGATT**AAGTATATTTTTTAGGTAGTGACATCTTATACA	AACTTTATTTACAAGGGGTTGATGGATGAGA	0.35	PR
19	AM17998	ss161141990	C/T	**GAAGGTGACCAAGTTCATGC**TCCTAATTTTTACTCAATCTCAATTTACTCG	**GAAGGTCGGAGTCAACGGATT**TCCTAATTTTTACTCAATCTCAATTTACTCA	TCAACCAATCCCAACAAAAAGAAATAAAAA	0.23	PR
20	AM18039	ss161142031	A/G	**GAAGGTGACCAAGTTCATGC**TGAATTTGTTTCTATTACTAATATTTACTGTTA	**GAAGGTCGGAGTCAACGGATT**GAATTTGTTTCTATTACTAATATTTACTGTTG	CTACCATCCATTTCAATATATGTATTTGTA	0.35	P
21	AM18040	ss161142032	A/C	**GAAGGTGACCAAGTTCATGC**TATCTTTATTCTCTACCATCCATTTCAATATATT	**GAAGGTCGGAGTCAACGGATT**CTTTATTCTCTACCATCCATTTCAATATATG	ACTATATTCTTCCATTTCGTGAATTTGTTT	0.18	PR
22	AM18080	ss161142072	A/G	**GAAGGTGACCAAGTTCATGC**TATTATTCACGATAATTTTTCCTAATATAAACA	**GAAGGTCGGAGTCAACGGATT**ATTATTCACGATAATTTTTCCTAATATAAACG	CGGATTTTGTCGTGAATGAATAATCGCAA	0.14	PR
23	AM18081	ss161142073	G/T	**GAAGGTGACCAAGTTCATGC**TAATCGACGGCGTTATTAAACTCAC	**GAAGGTCGGAGTCAACGGATT**CTAATCGACGGCGTTATTAAACTCAA	CTTAATGCATTTTAGATATTTTATACATTA	0.15	P
24	AM18082	ss161142074	C/G	**GAAGGTGACCAAGTTCATGC**TCATAAAAATAACTTTTTGGGCATGATGCG	**GAAGGTCGGAGTCAACGGATT**CATAAAAATAACTTTTTGGGCATGATGCC	CGTCGATTAGCATGTGCACAACGAT	0.31	P
25	AM18092	ss161142084	A/G	**GAAGGTGACCAAGTTCATGC**TATAAACAGTACAATAATATTGTCTACAAAGCAT	**GAAGGTCGGAGTCAACGGATT**AACAGTACAATAATATTGTCTACAAAGCAC	CAAGTTGGATTCAGCCCAGACTTCTA	0.06	PR
26	AM18185	ss161142177	C/T	**GAAGGTGACCAAGTTCATGC**TTCACATCATGTAAGAATACATGTGTTTTC	**GAAGGTCGGAGTCAACGGATT**ATTCACATCATGTAAGAATACATGTGTTTTT	GCCATATACACGGCCGCAGTGAT	0.41	PRT
27	AM18192	ss161142184	G/T	**GAAGGTGACCAAGTTCATGC**TTTAGAACGTGAAACCAATCTGTGTTG	**GAAGGTCGGAGTCAACGGATT**ATTTAGAACGTGAAACCAATCTGTGTTT	GTTGATCGACAGATGATAAGGTCAGAAAT	0.29	
28	AM18200	ss161142192	A/G	**GAAGGTGACCAAGTTCATGC**TAAAACCCAATTGAAAAGATATGATTTTATGGAT	**GAAGGTCGGAGTCAACGGATT**ACCCAATTGAAAAGATATGATTTTATGGAC	CTTAAATGTAATCCCTTATTTCTCTCACTT	0.17	P

29	AM18245	ss161142237	A/G	**GAAGGTGACCAAGTTCATGC**TGTTAACAAAAAAACTTTCCTTTTGTCTACCAT	**GAAGGTCGGAGTCAACGGATT**AACAAAAAAACTTTCCTTTTGTCTACCAC	AACATTTTGTTTAATCCATGTGGTGACGTT	0.36	PR+
30	AM18383	ss161142375	A/G	**GAAGGTGACCAAGTTCATGC**TTTTTTAATTAGTTCATGAGTTGACTTTGTTGA	**GAAGGTCGGAGTCAACGGATT**TAATTAGTTCATGAGTTGACTTTGTTG	TACTTTTACCATTCAACTCATAATTCGGGA	0.37	PR
31	AM18385	ss161142377	C/T	**GAAGGTGACCAAGTTCATGC**TCACAATCATTTCAACATCTTTATGATCATG	**GAAGGTCGGAGTCAACGGATT**TCACAATCATTTCAACATCTTTATGATCATA	GAGCAAGAGTTATCTAAGTAAATCTAAGTT	0.28	P
32	AM18403	ss161142395	A/G	**GAAGGTGACCAAGTTCATGC**TCAAAGAATTAAGAAAAGAAGCTTGCAGGT	**GAAGGTCGGAGTCAACGGATT**AAGAATTAAGAAAAGAAGCTTGCAGGC	CAAAAGAACTTTTGGCCCTCAAAGTGAT	0.28	PT
33	AM18433	ss161142425	G/T	**GAAGGTGACCAAGTTCATGC**TAGACCCTGCGTTGTTGGGATTC	**GAAGGTCGGAGTCAACGGATT**AAAAGACCCTGCGTTGTTGGGATTA	GTCATTTTTCCATTTCATGACTAACGTCAA	0.19	PR
34	AM18444	ss161142436	A/G	**GAAGGTGACCAAGTTCATGC**TGGGAAATAGTAGAAGAGAGTGTATGTT	**GAAGGTCGGAGTCAACGGATT**GGAAATAGTAGAAGAGAGTGTATGTC	GATGGGTATATTTTCAGAGGATTCCAGAA	0.21	PR
35	AM18453	ss161142445	A/C	**GAAGGTGACCAAGTTCATGC**TGTCTTATACTTCCTCCATTTCTCGTTTT	**GAAGGTCGGAGTCAACGGATT**CTTATACTTCCTCCATTTCTCGTTTG	TATCTATTTTATCCTCGAATTGTATGTCAT	0.13	PR
36	AM18480	ss161142472	G/T	**GAAGGTGACCAAGTTCATGC**TCCAAATAAGCGCAGTACAACTCTTC	**GAAGGTCGGAGTCAACGGATT**CCAAATAAGCGCAGTACAACTCTTA	GGGACAGATGAAACATAATCGAGCGAA	0.15	PR
37	AM18527	ss161142519	A/G	**GAAGGTGACCAAGTTCATGC**TACCCGACAAAACTCAAACCTGACTA	**GAAGGTCGGAGTCAACGGATT**CCGACAAAACTCAAACCTGACTG	TATCGGGTTGGTCATATTTCGGGTTAATT	0.25	P
38	AM18571	ss161142563	C/T	**GAAGGTGACCAAGTTCATGC**TTGGTAGAAATGCCATGTGGTTTCG	**GAAGGTCGGAGTCAACGGATT**TGGTAGAAATGCCATGTGGTTTCA	AGCACCAAACAGCCTTCAAATTGAATCAT	0.38	PR
39	AM18580	ss161142572	C/T	**GAAGGTGACCAAGTTCATGC**TATTATTTGGCTTTTTGATAGAACCTTACC	**GAAGGTCGGAGTCAACGGATT**GTATTATTTGGCTTTTTGATAGAACCTTACT	TTCTAATGTAAGAGGCCTTACCCTTGTAA	0.20	PR
40	AM18598	ss161142590	C/T	**GAAGGTGACCAAGTTCATGC**TAGTATTTAAAGGAACAAATATACTCTATTACG	**GAAGGTCGGAGTCAACGGATT**AGTATTTAAAGGAACAAATATACTCTATTACA	GGTGGAATATTTAGCTTCGGTTGGGAA	0.37	PR
41	AM18603	ss161142595	C/G	**GAAGGTGACCAAGTTCATGC**TCCTGAAGAGTCATTCTGTATGGTATC	**GAAGGTCGGAGTCAACGGATT**CCTGAAGAGTCATTCTGTATGGTATG	GCTTTAGGATAAAACTCATCAAAATGGGTT	0.28	PRT
42	AM18604	ss161142596	A/G	**GAAGGTGACCAAGTTCATGC**TAAATCTTTATCATCAATACAGACCTCAATATT	**GAAGGTCGGAGTCAACGGATT**ATCTTTATCATCAATACAGACCTCAATATC	CCCATTTTGATGAGTTTTATCCTAAAGCTT	0.25	PR
43	AM18650	ss161142642	C/T	**GAAGGTGACCAAGTTCATGC**TGTGTTAAAATTACTCTATTCGCACTATGG	**GAAGGTCGGAGTCAACGGATT**AGTGTTAAAATTACTCTATTCGCACTATGA	CCAAGTCCAACAAATAATAGGACGATGAA	0.34	
44	AM18657	ss161142649	C/T	**GAAGGTGACCAAGTTCATGC**TCAAACAAAACCAGCCTCAATAAAACG	**GAAGGTCGGAGTCAACGGATT**CCAAACAAAACCAGCCTCAATAAAACA	GCTTTACTTGTTATTTTTTGCAACATGAAT	0.11	PRT
45	AM18678	ss161142670	C/T	**GAAGGTGACCAAGTTCATGC**TTATTTAAGACTCGATTAAAACTACACCTG	**GAAGGTCGGAGTCAACGGATT**CATTATTTAAGACTCGATTAAAACTACACCTA	GGGCATAGAGGGAATAATATTTGGGTTTTA	0.17	PR
46	AM18740	ss161142732	A/T	**GAAGGTGACCAAGTTCATGC**TATTCGATTAATTTCAACTGCAAACAAAGTAAAA	**GAAGGTCGGAGTCAACGGATT**CGATTAATTTCAACTGCAAACAAAGTAAAT	GATTGTGTTTAGTTTCTGATTTCGTTTATT	0.26	PRT
47	AM18741	ss161142733	C/T	**GAAGGTGACCAAGTTCATGC**TAAGGCGGCGAAAGAGGAAAGC	**GAAGGTCGGAGTCAACGGATT**GAAGGCGGCGAAAGAGGAAAGT	CGTCCAATATTAAATTTTCTCTCTCCTCTA	0.42	P+RT
48	AM18821	ss161142813	C/T	**GAAGGTGACCAAGTTCATGC**TTTTT	**GAAGGTCGGAGTCAACGGATT**GT	TTAAAAACTCAGAGCATAGCAAACGA	0.29	PR

				ACCCCTTAAATATTTACATCCAATCC	TTTACCCCCTTAAATATTTACATCCA ATCT	TGAA		
49	AM18839	ss161142831	C/G	**GAAGGTGACCAAGTTCATGC**TAAA ATTTTGGTGTTATTTGTTTAGATAAG TGTC	**GAAGGTCGGAGTCAACGGATT**AA AATTTTGGTGTTATTTGTTTAGATA AGTGTG	CTCTTTTTTTATTTATTCCAGGGGCAG TTA	0.29	PR
50	AM18842	ss161142834	A/T	**GAAGGTGACCAAGTTCATGC**TATA ATAGAAAATTGCCACGTCATAATCC TA	**GAAGGTCGGAGTCAACGGATT**AT AATAGAAAATTGCCACGTCATAATC CTT	GTATGTGTTGTCAAGCTATGTGCAAGA AA	0.26	PRT
51	AM18899	ss161142891	A/T	**GAAGGTGACCAAGTTCATGC**TGAC TTGATTGGTAATTAAAATTCATACTC TTAA	**GAAGGTCGGAGTCAACGGATT**GA CTTGATTGGTAATTAAAATTCATAC TCTTAT	CACATGTACTTAAACATAGCACATGC ACTA	0.29	PR
52	AM18918	ss161142910	C/T	**GAAGGTGACCAAGTTCATGC**TATA GAAGTAAATTTGATATGACAAATTA AAAAG	**GAAGGTCGGAGTCAACGGATT**AT AGAAGTAAATTTGATATGACAAATT AAAAAA	TCTCAATAACTCTTCTGCCCTACGAAA TT	0.28	P
53	AM18919	ss161142911	A/G	**GAAGGTGACCAAGTTCATGC**TAAA TTTGTTCTATTTATCTTTTTTAATTTG TCA	**GAAGGTCGGAGTCAACGGATT**AA ATTTGTTCTATTTATCTTTTTTAATT TGTCG	TTATGGTGTGTGGTAAAGTGAAAGA	0.27	PR
54	AM18960	ss161142952	A/T	**GAAGGTGACCAAGTTCATGC**TAAT TATGATTGGACACCATCAAGAAATA ATATA	**GAAGGTCGGAGTCAACGGATT**AA TTATGATTGGACACCATCAAGAAAT AATATT	CCAATGGGTAATGGGTGATAGAGTAT ATT	0.32	P
55	AM18961	ss161142953	A/C	**GAAGGTGACCAAGTTCATGC**TGAT GTTGGGTTTTATAGAGGAAATTTTGT TAT	**GAAGGTCGGAGTCAACGGATT**GT TGGGTTTTATAGAGGAAATTTTGTT AG	ACCCATTGGCTATTATTTTCATATTGA AAT	0.28	PT
56	AM19008	ss161143000	A/T	**GAAGGTGACCAAGTTCATGC**TGAG AAGTATAGGGCTGTCATCGTTA	**GAAGGTCGGAGTCAACGGATT**GA GAAGTATAGGGCTGTCATCGTTT	GTACTCCCTGCCTATGTCTAAGACAA	0.30	P+R
57	AM19009	ss161143001	C/T	**GAAGGTGACCAAGTTCATGC**TAAT AATGGGTAATTAATGAGTTAAGGGA C	**GAAGGTCGGAGTCAACGGATT**CT TAATAATGGGTAATTAATGAGTTAA GGGAT	CATCAGCAATTCTTCAAGCGAACCGA T	0.21	P+RT
58	AM19010	ss161143002	C/T	**GAAGGTGACCAAGTTCATGC**TGCG AACCGATTCTTGAGGGAAG	**GAAGGTCGGAGTCAACGGATT**AA GCGAACCGATTCTTGAGGGAAA	GGAGTACTCAACCTATAAGTCATGAC TTT	0.29	P+R
59	AM19011	ss161143003	C/T	**GAAGGTGACCAAGTTCATGC**TTTC TCGGAAGCTAACATGTCTCG	**GAAGGTCGGAGTCAACGGATT**CT TTCTCGGAAGCTAACATGTCTCA	GATTTGAACACTTAGTGCGCAAGATT GAA	0.31	P+R
60	AM19012	ss161143004	C/G	**GAAGGTGACCAAGTTCATGC**TCCA GTGGTATAAAAACCCGATCAAAG	**GAAGGTCGGAGTCAACGGATT**CC AGTGGTATAAAAACCCGATCAAAC	GAGACATGTTAGCTTCCGAGAAAGAA ATA	0.10	PR
61	AM19034	ss161143026	A/G	**GAAGGTGACCAAGTTCATGC**TGGA AGAAAGGCTGTCGACTTAACT	**GAAGGTCGGAGTCAACGGATT**GA AGAAAGGCTGTCGACTTAACC	GTAGCAAATTATGCAGCAAAGTACCC ATT	0.31	PRT
62	AM19035	ss161143027	A/T	**GAAGGTGACCAAGTTCATGC**TGGT CGATAGCTTTTGACTATTTAGCAT	**GAAGGTCGGAGTCAACGGATT**GG TCGATAGCTTTTGACTATTTAGCAA	GAACTGATGACAGAAAAGAGAACCCA TTA	0.24	PT
63	AM19133	ss161143125	A/G	**GAAGGTGACCAAGTTCATGC**TATA CTATAATTCGCAAATAATTCTTTATC AACT	**GAAGGTCGGAGTCAACGGATT**AT ACTATAATTCGCAAATAATTCTTTA TCAACC	GGTGTGGGAAATAACACTATTCTCACT AA	0.15	PR
64	AM19165	ss161143157	A/G	**GAAGGTGACCAAGTTCATGC**TAAA AATGCATTTAGACACACTTATATATG AGAT	**GAAGGTCGGAGTCAACGGATT**AA TGCATTTAGACACACTTATATATGA GAC	CCACACAAGTAGAGACCTCGCTTTT	0.30	P
65	AM19210	ss161143202	A/C	**GAAGGTGACCAAGTTCATGC**TAAT TTGGATTTGGATCAAATTCCACCATT T	**GAAGGTCGGAGTCAACGGATT**GG ATTTGGATCAAATTCCACCATTG	AATGACAAGGTTTGGGTAGTCATTCTC AA	0.29	PRT
66	AM19238	ss161143230	C/T	**GAAGGTGACCAAGTTCATGC**TCAT GGTTCTTTATATAGGAGTAAGGG	**GAAGGTCGGAGTCAACGGATT**AA TCATGGTTCTTTATATAGGAGTAAG GA	TCGGCTTTCCAAACAATCTCTTGCTTA TA	0.23	PR

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67	AM19353	ss161143345	A/C	**GAAGGTGACCAAGTTCATGC**TAAACGTTCCTGGGATGGAGAGTTT	**GAAGGTCGGAGTCAACGGATT**ACGTTCCTGGGATGGAGAGTTG	GATTACTAATCCGCGAATTTCTGTGGAAA	0.10	PR
68	AM19354	ss161143346	A/G	**GAAGGTGACCAAGTTCATGC**TCCATAACAATTTTCAATAGTTAATATTGCATCA	**GAAGGTCGGAGTCAACGGATT**CATAACAATTTTCAATAGTTAATATTGCATCG	CAGGACAAACAAAATGTTCTTTTTACTGAT	0.21	PRT
69	AM19376	ss161143368	C/G	**GAAGGTGACCAAGTTCATGC**TCGTCACATTCCCTCACTCAC	**GAAGGTCGGAGTCAACGGATT**CTCGTCACATTCCCTCACTCAG	CAATCCAATATCCACCTCAAAAACAAGGT	0.36	PT
70	AM19378	ss161143370	G/T	**GAAGGTGACCAAGTTCATGC**TCATCATCATCATCAATCCAATATCCC	**GAAGGTCGGAGTCAACGGATT**ATATCATCATCATCATCAATCCAATATCCA	GTACAGGTATGGATTGCTCGTCACAT	0.33	PRT
71	AM19379	ss161143371	C/G	**GAAGGTGACCAAGTTCATGC**TAGATAACGGTCAAATTGGATCACTTC	**GAAGGTCGGAGTCAACGGATT**AGATAACGGTCAAATTGGATCACTTG	ATGAATATTCTTCTTCACAATTGAGCTCAA	0.21	PR
72	AM19388	ss161143380	A/T	**GAAGGTGACCAAGTTCATGC**TGTTACTAAAACTCTTAACTTCACATGACTAT	**GAAGGTCGGAGTCAACGGATT**GTTACTAAAACTCTTAACTTCACATGACTAA	GATAGAATCTCACTTTCTTATCTTATCTTA	0.21	P
73	AM19394	ss161143386	A/T	**GAAGGTGACCAAGTTCATGC**TGGTACAGTTACAAGTTAAGTGTGTTCAA	**GAAGGTCGGAGTCAACGGATT**GGTACAGTTACAAGTTAAGTGTGTTCAT	GCACTTCTTCCGGAAAATCTTAAAACTCTT	0.25	PR
74	AM19395	ss161143387	G/T	**GAAGGTGACCAAGTTCATGC**TAGTGCTAAGTATGTGTTCACAGAGG	**GAAGGTCGGAGTCAACGGATT**AAGTGCTAAGTATGTGTTCACAGAGT	CAACATGTTCTTTCTGGGGACATATGTTT	0.44	RT
75	AM19424	ss161143416	C/T	**GAAGGTGACCAAGTTCATGC**TAGTCCCTTTAGCATATCAAACTCTTC	**GAAGGTCGGAGTCAACGGATT**TTAGTCCCTTTAGCATATCAAACTCTTT	ATAGATCAACCTGAACTCTTGAAGGCAA	0.40	P+R
76	AM19425	ss161143417	G/T	**GAAGGTGACCAAGTTCATGC**TCCTCTTTGGAATCAGGCTTCGG	**GAAGGTCGGAGTCAACGGATT**AAACCTCTTTGGAATCAGGCTTCGT	GAGAAATATCTACAAGCAAACAAACGTCCA	0.39	PRT
77	AM19426	ss161143418	A/T	**GAAGGTGACCAAGTTCATGC**TAAAGTTTAATGGGTTGGGCCTGAGT	**GAAGGTCGGAGTCAACGGATT**AAAGTTTAATGGGTTGGGCCTGAGA	GATTGATTTTACAGCTGGTCTCCTAAGAA	0.43	P+RT
78	AM19427	ss161143419	A/C	**GAAGGTGACCAAGTTCATGC**TATCCACTTATTAAATACTTAATGTCTACTCAA	**GAAGGTCGGAGTCAACGGATT**CCACTTATTAAATACTTAATGTCTACTCAC	AGTATATTGTAAGGAGGCATTAAGGATAAT	0.36	PR
79	AM19431	ss161143423	C/T	**GAAGGTGACCAAGTTCATGC**TGGCTAATAAGTTAATATCATGTTATGGGG	**GAAGGTCGGAGTCAACGGATT**GGCTAATAAGTTAATATCATGTTATGGGA	TAAGCTTTGAACTCCAACAAGATTGCGTA	0.38	PT
80	AM19442	ss161143434	A/C	**GAAGGTGACCAAGTTCATGC**TATTTCTGCTCAGAAAGCAACGCCTT	**GAAGGTCGGAGTCAACGGATT**CTGCTCAGAAAGCAACGCCTG	GTTTGTCTTTGTGGTTGTTCATTAGTGTTT	0.23	P
81	AM19447	ss161143439	A/C	**GAAGGTGACCAAGTTCATGC**TCCTATTACCACTAATTAGTATTGTTACCA	**GAAGGTCGGAGTCAACGGATT**CCTATTACCACTAATTAGTATTGTTACCC	GCTTGCGAAGCTGTACATGAACCAA	0.24	P+R
82	AM19452	ss161143444	G/T	**GAAGGTGACCAAGTTCATGC**TCGCATTTTACGTGCCGATTAACAC	**GAAGGTCGGAGTCAACGGATT**CCGCATTTTACGTGCCGATTAACAA	ATGATAGTAAGGTAACGTCGAACCATGAA	0.09	PRT
83	AM19464	ss161143456	A/G	**GAAGGTGACCAAGTTCATGC**TGAAATATAAAACAATATCTCACTTGATTTGAAT	**GAAGGTCGGAGTCAACGGATT**GAAATATAAAACAATATCTCACTTGATTTGAAC	CTGAAATTCACCCAAAGACCTGAATGAA	0.25	PR
84	AM19501	ss161143493	A/G	**GAAGGTGACCAAGTTCATGC**TAGATTCCAGACACATATCATAACTTCTTT	**GAAGGTCGGAGTCAACGGATT**CCAGACACATATCATAACTTCTTC	GTAAATCAACAAGTGAATGCTCTTCCTCAT	0.33	PRT
85	AM19502	ss161143494	C/T	**GAAGGTGACCAAGTTCATGC**TGCAAGCAGATTCCAGACACG	**GAAGGTCGGAGTCAACGGATT**ACTGCAAGCAGATTCCAGACACA	CTCATAGGACGAATCGTTTTGCCGAA	0.35	P
86	AM19503	ss161143495	C/T	**GAAGGTGACCAAGTTCATGC**TCATCATGCAACATACGCACCTAC	**GAAGGTCGGAGTCAACGGATT**AGCATCATGCAACATACGCACCTAT	GAAGAAGTGCATATGCTCTCCCCAT	0.08	
87	AM19527	ss161143519	C/G	**GAAGGTGACCAAGTTCATGC**TGAT	**GAAGGTCGGAGTCAACGGATT**GA	CTTTAGGTTTCTCTTCATGTCCTTCACT	0.26	PR

				GAGAAGTATAAGTAGGAGACATC	TGAGAAGTATAAGTAGGAGACATG	T		
88	AM19534	ss161143526	A/G	**GAAGGTGACCAAGTTCATGC**TCAATTCCCATGGGAATTTCACCAGTT	**GAAGGTCGGAGTCAACGGATT**AATTCCCATGGGAATTTCACCAGTC	GAGGTCACTTGATCTGTCTTTTAATCAATT	0.36	PRT
89	AM19559	ss161143551	C/T	**GAAGGTGACCAAGTTCATGC**TTTGTTGAACAGAAACAATGGACCAAC	**GAAGGTCGGAGTCAACGGATT**GTTTTGTTGAACAGAAACAATGGACCAAT	GCAGATTATTGTAGAAAAGAGATGGGTATT	0.38	PRT
90	AM19560	ss161143552	A/G	**GAAGGTGACCAAGTTCATGC**TAATCTGCATAATCATGTTCTAATTCATAAAAA	**GAAGGTCGGAGTCAACGGATT**AATCTGCATAATCATGTTCTAATTCATAAAAG	CCTTATTTGAAAGGCTTAAAGAAGCCGAA	0.22	PRT
91	AM19583	ss161143575	A/T	**GAAGGTGACCAAGTTCATGC**TACAAGTTAATCACCGTATGAACAAACAATA	**GAAGGTCGGAGTCAACGGATT**ACAAGTTAATCACCGTATGAACAAACAATT	GCTTTGCTATTCCTTATAGGTTGAAGGAA	0.37	PRT
92	AM19584	ss161143576	A/G	**GAAGGTGACCAAGTTCATGC**TCGTCTTTTCAGCTAATCAAGGGTGT	**GAAGGTCGGAGTCAACGGATT**GTCTTTTCAGCTAATCAAGGGTGC	CTTCAACCTATAAGGAATAGCAAAGCGAT	0.44	P+R
93	AM19585	ss161143577	A/G	**GAAGGTGACCAAGTTCATGC**TACCCTTGATTAGCTGAAAAGACGCA	**GAAGGTCGGAGTCAACGGATT**CCTTGATTAGCTGAAAAGACGCG	ATCGAGACATTTGCAGGCTTAAAATTAGAA	0.37	PR
94	AM19636	ss161143628	A/G	**GAAGGTGACCAAGTTCATGC**TGCCTTTGCGTAGGGCCGAAA	**GAAGGTCGGAGTCAACGGATT**GCCTTTGCGTAGGGCCGAAG	GCACAAGGTGCACCAAGGCTCTA	0.21	PR
95	AM19643	ss161143635	G/T	**GAAGGTGACCAAGTTCATGC**TCATTAGTTCCTAATCACTACATCAATCC	**GAAGGTCGGAGTCAACGGATT**CATTAGTTCCTAATCACTACATCAATCA	CACCTTTCTAGAACAATATGTTGGTACCTA	0.45	
96	AM19652	ss161143644	C/G	**GAAGGTGACCAAGTTCATGC**TATCTAAGTTGGGATTTGAAGAGTCC	**GAAGGTCGGAGTCAACGGATT**ATCTAAGTTGGGATTTGAAGAGTCG	CTTTTGTTAGTGCATCACTAACATGGATAA	0.12	R
97	AM19662	ss161143654	C/T	**GAAGGTGACCAAGTTCATGC**TCCGTTGACATTAGGGATGCTTGG	**GAAGGTCGGAGTCAACGGATT**ACCGTTGACATTAGGGATGCTTGA	GGATAATAACTAACAAGAAAAGAAAGGAAA	0.48	PR
98	AM19663	ss161143655	C/G	**GAAGGTGACCAAGTTCATGC**TGACTTTGATATAGCAAGTTACGATGAG	**GAAGGTCGGAGTCAACGGATT**GACTTTGATATAGCAAGTTACGATGAC	GGATAATAACTAACAAGAAAAGAAAGGAAA	0.50	PR
99	AM19684	ss161143676	C/T	**GAAGGTGACCAAGTTCATGC**TTCAATACGTGATAACTCAATGG	**GAAGGTCGGAGTCAACGGATT**GATGCTTCAATACGTGATAACTCAATGA	AGAAACAAAATCCAAAGGGCATTAGGGAA	0.29	PR
100	AM19706	ss161143698	A/T	**GAAGGTGACCAAGTTCATGC**TCTCAAATTCTTCAAAGAGTATGTAGTCAT	**GAAGGTCGGAGTCAACGGATT**CTCAAATTCTTCAAAGAGTATGTAGTCAA	TTTGGGCGGCTGACCGGGAAAA	0.41	PRT
101	AM19707	ss161143699	C/G	**GAAGGTGACCAAGTTCATGC**TCGACAAATGACTACATACTCTTTGAAC	**GAAGGTCGGAGTCAACGGATT**CGACAAATGACTACATACTCTTTGAAG	TACATACTCAAGCATCCTCATTTTCCCTT	0.49	P+R+T
102	AM19709	ss161143701	A/T	**GAAGGTGACCAAGTTCATGC**TAGCATATGGGTGACGTCACTGAA	**GAAGGTCGGAGTCAACGGATT**AGCATATGGGTGACGTCACTGAT	AGGCATTAGAAATCCAACGAAAATTTCCAA	0.22	P
103	AM19746	ss161143738	A/G	**GAAGGTGACCAAGTTCATGC**TGGTAGTAAACTCAAGATCACCAGGA	**GAAGGTCGGAGTCAACGGATT**GTAGTAAACTCAAGATCACCAGGG	TGTTGTGTCGTCACAAACGTCTTTGTTT	0.50	P+R
104	AM19756	ss161143748	G/T	**GAAGGTGACCAAGTTCATGC**TGAAGAAAGTATATTCCACTTGTAGTAGAC	**GAAGGTCGGAGTCAACGGATT**GAAGAAAGTATATTCCACTTGTAGTAGAA	GCTGAAAAAATAACCGAGAAGGCCCAA	0.26	PT
105	AM19766	ss161143758	A/G	**GAAGGTGACCAAGTTCATGC**TAGTGCAATTGTACCAGAAGAACCTTT	**GAAGGTCGGAGTCAACGGATT**GTGCAATTGTACCAGAAGAACCTTC	AAAGGGATTGAAATCCACATCTTCCTCTT	0.21	PR
106	AM19810	ss161143802	A/T	**GAAGGTGACCAAGTTCATGC**TGGGGCTGAACAGTTTCAAATATCAAT	**GAAGGTCGGAGTCAACGGATT**GGGGCTGAACAGTTTCAAATATCAAA	CTAAGTCCGTCCTTTGGAACACCAT	0.07	PR
107	AM19811	ss161143803	A/G	**GAAGGTGACCAAGTTCATGC**TTTTTTCCTTCACGAATCATTCATTTGGAT	**GAAGGTCGGAGTCAACGGATT**TCCTTCACGAATCATTCATTTGGAC	CGATGGAATATAGTCCTCATTCGCTTAT	0.35	P+R
108	AM19834	ss161143826	A/G	**GAAGGTGACCAAGTTCATGC**TACCTTTGATCGAGAAACGTAATCTCTT	**GAAGGTCGGAGTCAACGGATT**CCTTTGATCGAGAAACGTAATCTCTC	CTTATATTACGGATAGATGAGGAAGGGAT	0.30	PRT

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109	AM19836	ss161143828	A/G	**GAAGGTGACCAAGTTCATGC**TTATAGGGAGTGTTTTTGACAAAGTTATCT	**GAAGGTCGGAGTCAACGGATT**AGGGAGTGTTTTTGACAAAGTTATCC	GTGCATTAGTTGTCTCCATCTTCCTAATT	0.33	P+R
110	AM19839	ss161143831	C/T	**GAAGGTGACCAAGTTCATGC**TGCCAACATACTTCTGGAATCTTTATATC	**GAAGGTCGGAGTCAACGGATT**AGCCAACATACTTCTGGAATCTTTATATT	TGCTGGATATTATGCGAAATGCCTATGAT	0.27	PRT
111	AM19842	ss161143834	A/G	**GAAGGTGACCAAGTTCATGC**TGCTATCTGTACTTTCTGTGCCAT	**GAAGGTCGGAGTCAACGGATT**GCTATCTGTACTTTCTGTGCCAC	CTCTAAATCTATACACCAATACACGTGGA	0.31	PRT
112	AM19855	ss161143847	C/T	**GAAGGTGACCAAGTTCATGC**TCAAATAAACATATGCAGCTAAGAC	**GAAGGTCGGAGTCAACGGATT**GAGCTCAAATAAACATATGCAGCTAAGAT	GTTTCGAGTTCTCCCCAGTTGTCAA	0.43	PRT
113	AM19861	ss161143853	C/T	**GAAGGTGACCAAGTTCATGC**TAGTGGCGGGTAATGGTGAGC	**GAAGGTCGGAGTCAACGGATT**GTAGTGGCGGGTAATGGTGAGT	GGTCCACTAACTTCATAAAATAACAACTTA	0.37	PR
114	AM19870	ss161143862	A/G	**GAAGGTGACCAAGTTCATGC**TAACTTTTCTTATTACTTGAAAGACTTTGACTTT	**GAAGGTCGGAGTCAACGGATT**CTTTTCTTATTACTTGAAAGACTTTGACTTC	GATAGTCACTAAAGAAGGTCAAAGCTAAAT	0.15	P
115	AM19872	ss161143864	C/T	**GAAGGTGACCAAGTTCATGC**TAAATGATCGGAGGATTGATCAAATTCC	**GAAGGTCGGAGTCAACGGATT**ATAAATGATCGGAGGATTGATCAAATTCT	TAATTGATATGGAGACGATAGTTACTTCGA	0.28	P
116	AM19873	ss161143865	A/T	**GAAGGTGACCAAGTTCATGC**TCAATCTCATTTAGACATTTTAACTTTATTTTT	**GAAGGTCGGAGTCAACGGATT**CAAATCTCATTTAGACATTTTAACTTTATTTTA	AAAAGTTTTGGTTTTGTTTGTTTGAGAGAA	0.24	PR
117	AM19875	ss161143867	C/T	**GAAGGTGACCAAGTTCATGC**TCAATGAGATGAACAAAAAGAAAACAAGGC	**GAAGGTCGGAGTCAACGGATT**CAATGAGATGAACAAAAAGAAAACAAGGT	CCAGATAATTTCAGCTTTTATCGACCCTT	0.28	PRT
118	AM19885	ss161143877	A/T	**GAAGGTGACCAAGTTCATGC**TCAGATCGATATAACATATACTTGACGCA	**GAAGGTCGGAGTCAACGGATT**CAGATCGATATAACATATACTTGACGCT	CGTAAAAGGTACACTTTCCAAATATAAGAT	0.23	P
119	AM19930	ss161143922	A/C	**GAAGGTGACCAAGTTCATGC**TATAGGAGTATAATAGTTGAAATGATTATGATTA	**GAAGGTCGGAGTCAACGGATT**ATAGGAGTATAATAGTTGAAATGATTATGATTC	GAGGGAAATTGCATGTCACTCGGTT	0.26	PT
120	AM19931	ss161143923	A/G	**GAAGGTGACCAAGTTCATGC**TGATTCAGAATTAGTGTCAACCGAGTA	**GAAGGTCGGAGTCAACGGATT**CAGAATTAGTGTCAACCGAGTG	TTCTGCTTTTCTGACTGCTGAGTATTGTT	0.16	PRT
121	AM19932	ss161143924	C/G	**GAAGGTGACCAAGTTCATGC**TACTAAAATAAAAGTAATGTAGAATACTGTATAC	**GAAGGTCGGAGTCAACGGATT**ACTAAAATAAAAGTAATGTAGAATACTGTATAG	GCTGCTTTAGTTTGCAAGCATATAAGCTT	0.26	PRT
122	AM19961	ss161143953	A/G	**GAAGGTGACCAAGTTCATGC**TATGTTTGGAGGATTTGCTTAGGGTTT	**GAAGGTCGGAGTCAACGGATT**GTTTGGAGGATTTGCTTAGGGTTC	GTTAATTCCACATCCACCTCCTTTGAAA	0.12	PR
123	AM19962	ss161143954	G/T	**GAAGGTGACCAAGTTCATGC**TTTTACCACAATTGCGATCATTACAGC	**GAAGGTCGGAGTCAACGGATT**TTTACCACAATTGCGATCATTACAGA	CTGATAAATCTGAAGTAGTTGCCAACCAT	0.27	PR
124	AM19963	ss161143955	A/T	**GAAGGTGACCAAGTTCATGC**TGGAGTGATGTGGTTATTATATCGCCA	**GAAGGTCGGAGTCAACGGATT**GGAGTGATGTGGTTATTATATCGCCT	CTGTGCTATCAAGGGTATCTCGTGAT	0.13	PR
125	AM19990	ss161143982	A/T	**GAAGGTGACCAAGTTCATGC**TTTCACTATTTTTCTCTTTGCTACTATCTTATT	**GAAGGTCGGAGTCAACGGATT**TCACTATTTTTCTCTTTGCTACTATCTTATA	CCACGTCATTTGCCGTACTCTGTTT	0.30	P
126	AM20022	ss161144014	A/G	**GAAGGTGACCAAGTTCATGC**TCTTGACATATAAGACAACATCTTAAAATTGTT	**GAAGGTCGGAGTCAACGGATT**CTTGACATATAAGACAACATCTTAAAATTGTC	GAAAAGCATGTCTGGAGCAGTGTTGAA	0.12	PRT
127	AM20031	ss161144023	C/T	**GAAGGTGACCAAGTTCATGC**TCAAAACAACTTGTTGTGGAGATGGG	**GAAGGTCGGAGTCAACGGATT**AACAAAACAACTTGTTGTGGAGATGGA	ACTATGTTTCCTTTACAAATTCCCCTACAA	0.26	PR

128	AM20064	ss161144056	A/T	**GAAGGTGACCAAGTTCATGC**TCACATTCAAACTTTAAAAGCGTTCGCTA	**GAAGGTCGGAGTCAACGGATT**CACATTCAAACTTTAAAAGCGTTCGCTT	ATATGGCTTAGAGCCAATTGATCACCAA	0.25	PR
129	AM20065	ss161144057	A/G	**GAAGGTGACCAAGTTCATGC**TATAATGAATGGATATCTTGGTGATCAATTA	**GAAGGTCGGAGTCAACGGATT**ATAATGAATGGATATCTTGGTGATCAATTG	TGCAAGAGTATAGTTTATTGATATGGCTTA	0.26	PR
130	AM20077	ss161144069	C/G	**GAAGGTGACCAAGTTCATGC**TGTAACTATTGCTGTTTTCATGGC	**GAAGGTCGGAGTCAACGGATT**GCTGTAACTATTGCTGTTTTCATGGG	TGCATGAAAACGACGATGGATCAAGATA	0.19	PRT
131	AM20089	ss161144081	A/G	**GAAGGTGACCAAGTTCATGC**TATCAATTGAAGCCTAATTTTGAGATGTTGT	**GAAGGTCGGAGTCAACGGATT**CAATTGAAGCCTAATTTTGAGATGTTGC	ATTTGGTTCAAAAATGGACAACCCATTGAA	0.37	PRT
132	AM20090	ss161144082	A/G	**GAAGGTGACCAAGTTCATGC**TAAAGGATTGGAATATTATCAATTGAAGCCT	**GAAGGTCGGAGTCAACGGATT**GGAATATTATCAATTGAAGCCC	CATTGAAGAAGAATGAAACAACATCTCAAA	0.39	P+RT
133	AM20130	ss161144122	C/T	**GAAGGTGACCAAGTTCATGC**TAAAGGTTGAAAACTAATCAAATTTGGCC	**GAAGGTCGGAGTCAACGGATT**CTAAAGGTTGAAAACTAATCAAATTTGGCT	CAAAAATCTCACCCACCCCACCAAA	0.24	PR
134	AM20146	ss161144138	A/G	**GAAGGTGACCAAGTTCATGC**TATTGGTCGGAAAATTATCAATATGTCCTAT	**GAAGGTCGGAGTCAACGGATT**GGTCGGAAAATTATCAATATGTCCTAC	GCTTTGAGTAATTGCTTGATCAGAAAGTTA	0.25	
135	AM20153	ss161144145	A/G	**GAAGGTGACCAAGTTCATGC**TCTATAGTCTATACTACTCAAATCTTAATATCT	**GAAGGTCGGAGTCAACGGATT**CTATAGTCTATACTACTCAAATCTTAATATCC	ATCATAGAATCATAATGATACACCAGAGTT	0.04	PRT
136	AM20177	ss161144169	A/G	**GAAGGTGACCAAGTTCATGC**TAAATTTTCCAAAAGATAACTGGGGTGAAA	**GAAGGTCGGAGTCAACGGATT**TTCCAAAAGATAACTGGGGTGAAG	TAACCATTTATTTCTATGACCTACTTGTTT	0.31	PRT
137	AM20178	ss161144170	A/C	**GAAGGTGACCAAGTTCATGC**TATTCATCATTTTCTTTTCTATATTTTGGCAATT	**GAAGGTCGGAGTCAACGGATT**CATCATTTTCTTTTCTATATTTTGGCAATG	GTTTGTGAATGAGATTAAGAGAAAGAGAAT	0.28	PR
138	AM20180	ss161144172	A/G	**GAAGGTGACCAAGTTCATGC**TAACAAAGTTACTTTATCTTTCTCTTCTTCATT	**GAAGGTCGGAGTCAACGGATT**CAAAGTTACTTTATCTTTCTCTTCTTCATC	AAACATGTGGTCTTGCGTTTGAAATGGTT	0.41	PRT
139	AM20181	ss161144173	C/T	**GAAGGTGACCAAGTTCATGC**TCGCATGAAGTCTCCATCCACAG	**GAAGGTCGGAGTCAACGGATT**CGCATGAAGTCTCCATCCACAA	TCATGTTAAACTGAATTGTGATCAAGACTT	0.07	R
140	AM20333	ss161144325	A/C	**GAAGGTGACCAAGTTCATGC**TGGGTAATATCATTATTCTTCAATTTTCAGTT	**GAAGGTCGGAGTCAACGGATT**GGGTAATATCATTATTCTTCAATTTTCAGTG	CACGTACATCAGTACAGCTACACCTA	0.27	PRT
141	AM20352	ss161144344	C/T	**GAAGGTGACCAAGTTCATGC**TGTTGATCACCCATAACTCTTGGAAC	**GAAGGTCGGAGTCAACGGATT**GTTGATCACCCATAACTCTTGGAAT	CGATCTGGTCACAGGTCATATGGAT	0.27	PR
142	AM20370	ss161144362	A/G	**GAAGGTGACCAAGTTCATGC**TAATAATCCCACATGGGTTATAAAAAGTGA	**GAAGGTCGGAGTCAACGGATT**AATCCCACATGGGTTATAAAAAGTGG	GTCCCTTCCTATGTGGAGAAACTCAT	0.26	PRT
143	AM20403	ss161144395	C/T	**GAAGGTGACCAAGTTCATGC**TAGCAAATTTAACCTTTTAAATTGGTAATTAGG	**GAAGGTCGGAGTCAACGGATT**CAGCAAATTTAACCTTTTAAATTGGTAATTAGA	CCGATACTAAATAGTGTGAATGAGAATGAT	0.38	PRT
144	AM20404	ss161144396	A/C	**GAAGGTGACCAAGTTCATGC**TAATTCCCTAATATTTATAAATCAGTACCACAA	**GAAGGTCGGAGTCAACGGATT**CCCTAATATTTATAAATCAGTACCACAC	GTTGAAATTAAGGCTTTAGCAAATATTATA	0.35	PR
145	AM20405	ss161144397	A/G	**GAAGGTGACCAAGTTCATGC**TAAAGCCTTAATTTCAACAATATAAAGTC	**GAAGGTCGGAGTCAACGGATT**CTAAAGCCTTAATTTCAACAATATAAA	GAGAAAATTTAGAAAAATATTTGGCCACAT	0.08	PR

A

GTCG

#	AM	ss	SNP	Seq1	Seq2	Seq3	Value	Cat
				A	GTCG			
146	AM20481	ss161144473	C/G	**GAAGGTGACCAAGTTCATGC**TTTTTTTTGAAGTAAATAGGCATATAATAGTTC	**GAAGGTCGGAGTCAACGGATT**TTTTTTGAAGTAAATAGGCATATAATAGTTG	GTCCTACATGTTCTAAACACTCAACAACTT	0.38	
147	AM20512	ss161144504	C/T	**GAAGGTGACCAAGTTCATGC**TTGTTAAAGCTCTACAGTTCTTTGAGC	**GAAGGTCGGAGTCAACGGATT**GTTGTTAAAGCTCTACAGTTCTTTGAGT	GCAACTTCACATAAATAAGTGCACATGATT	0.18	PR
148	AM20533	ss161144525	C/T	**GAAGGTGACCAAGTTCATGC**TCGATAAAAGAAAAATATTTCTCCGCCTTC	**GAAGGTCGGAGTCAACGGATT**CGATAAAAGAAAAATATTTCTCCGCCTTT	CCAATCTTTAATGGGACTGACCCAGAT	0.39	PR
149	AM20536	ss161144528	A/G	**GAAGGTGACCAAGTTCATGC**TTAAAGTCTATAATTGTTTAAATTAGATCGTAT	**GAAGGTCGGAGTCAACGGATT**AAAGTCTATAATTGTTTAAATTAGATCGTAC	TGGCTTAATACTAAATAGCACTATCAATAT	0.23	P+RT
150	AM20572	ss161144564	A/G	**GAAGGTGACCAAGTTCATGC**TGATTGTAGTTGCGACATATTTGCATGAAT	**GAAGGTCGGAGTCAACGGATT**GTAGTTGCGACATATTTGCATGAAC	CCGGACCGGACCAAACCGATTT	0.26	P
151	AM20573	ss161144565	A/G	**GAAGGTGACCAAGTTCATGC**TATGAAGATAATTGAATTGCATTTAACAAGAGA	**GAAGGTCGGAGTCAACGGATT**GAAGATAATTGAATTGCATTTAACAAGAGG	CGCACTTTAGATACTTCTACAGAAAGTTAT	0.28	PR
152	AM20679	ss161144671	A/G	**GAAGGTGACCAAGTTCATGC**TAATGAATTTGAGAAGCTTGCAGACTCT	**GAAGGTCGGAGTCAACGGATT**GAATTTGAGAAGCTTGCAGACTCC	TGCAGCGCTTAATTTCTGGCACTGT	0.38	PRT
153	AM20719	ss161144711	C/T	**GAAGGTGACCAAGTTCATGC**TGTCTAAGTCTTAATCTCAGAAGATTGG	**GAAGGTCGGAGTCAACGGATT**AAAGTCTAAGTCTTAATCTCAGAAGATTGA	TGATTCATGTGAACGGTCATTGAAATTGAT	0.27	PRT
154	AM20720	ss161144712	A/G	**GAAGGTGACCAAGTTCATGC**TCAATCTTCTGAGATTAAGACTTAGACTTTA	**GAAGGTCGGAGTCAACGGATT**AATCTTCTGAGATTAAGACTTAGACTTG	TTTTCCTACTCTCCATGTCAAAGATATGTT	0.27	PRT
155	AM20729	ss161144721	A/G	**GAAGGTGACCAAGTTCATGC**TGAGATTCAATTTTAGTGACATTGAGCAAA	**GAAGGTCGGAGTCAACGGATT**GAGATTCAATTTTAGTGACATTGAGCAAG	GTTGCACTTGCAACTATATCTTCTCCAAT	0.26	PR
156	AM20788	ss161144780	G/T	**GAAGGTGACCAAGTTCATGC**TACTTCATGGTAAGTGGTGAAGTCC	**GAAGGTCGGAGTCAACGGATT**GTACTTCATGGTAAGTGGTGAAGTCA	CAAACTTTGTGTGTAGGGATTTTCGTATTA	0.35	PR
157	AM20789	ss161144781	C/G	**GAAGGTGACCAAGTTCATGC**TATTCTTTCTAACTAAAAAAACGGACTTCAC	**GAAGGTCGGAGTCAACGGATT**CTTTCTAACTAAAAAAACGGACTTCAG	ACCACGTAGTAAAAAGGGGTAAAGAGTA	0.34	P+R
158	AM20790	ss161144782	A/T	**GAAGGTGACCAAGTTCATGC**TGGACTTCACCACTTACCATGAAGTA	**GAAGGTCGGAGTCAACGGATT**GGACTTCACCACTTACCATGAAGTT	GAAAAAACTAATTGCAAAGACCACGTAGTA	0.43	PR
159	AM20845	ss161144837	C/T	**GAAGGTGACCAAGTTCATGC**TGTTTGATTTCTGAAATAATTGTTTACGCG	**GAAGGTCGGAGTCAACGGATT**CTGTTTGATTTCTGAAATAATTGTTTACGCA	GTTGTCCGCACAACAAATACTCTAACAAA	0.15	PRT
160	AM20883	ss161144875	C/G	**GAAGGTGACCAAGTTCATGC**TCCATGAATAGAATCTCACCATTG	**GAAGGTCGGAGTCAACGGATT**CCATGAGAATAGAATCTCACCATTC	AGACGATGCCTACTTGTCTTATGTGTTA	0.28	PRT
161	AM20885	ss161144877	C/T	**GAAGGTGACCAAGTTCATGC**TGTGCCAATGGTGAGATTCTATTCTC	**GAAGGTCGGAGTCAACGGATT**GTGCCAATGGTGAGATTCTATTCTT	GCACAACATTTTCGCACAGAAAATCGAAA	0.32	P+R
162	AM20886	ss161144878	C/T	**GAAGGTGACCAAGTTCATGC**TCCATCTAAAAATCAGGTTTGCTCTTTC	**GAAGGTCGGAGTCAACGGATT**CTCCATCTAAAAATCAGGTTTGCTCTTTT	CAAAAGTTGGGCACAACACAACAAACAA	0.20	T
163	AM20896	ss161144888	A/T	**GAAGGTGACCAAGTTCATGC**TACATTATCATCCTTTTGACTAATTTTAAATGAA	**GAAGGTCGGAGTCAACGGATT**ACATTATCATCCTTTTGACTAATTTTAAATGAT	TGTTATTATGCCTCTTAGTTTTGTACACAT	0.08	PR
164	AM20907	ss161144899	A/T	**GAAGGTGACCAAGTTCATGC**TAAT	**GAAGGTCGGAGTCAACGGATT**AA	CGGAACGACTTGCTCTGATACCTTT	0.21	PR

				CTTGATAGAAATTCATCACGTAACA GA	TCTTGATAGAAATTCATCACGTAAC AGT			
165	AM20908	ss161144900	C/G	**GAAGGTGACCAAGTTCATGC**TCAT GGGAATGTGGGAACAAGGC	**GAAGGTCGGAGTCAACGGATT**CA TGGGAATGTGGGAACAAGGG	TTGAGTAATTTTCCCCTCTAAGTGGGT AT	0.26	PR
166	AM20915	ss161144907	C/G	**GAAGGTGACCAAGTTCATGC**TTCA CTCGGCTGTTTGTTCTGTTAG	**GAAGGTCGGAGTCAACGGATT**CA CTCGGCTGTTTGTTCTGTTAC	AACTGATCGCGGATTGCAATCAATAC TA	0.20	PR
167	AM20925	ss161144917	C/T	**GAAGGTGACCAAGTTCATGC**TCGT CCAGGGGTTAAATCAACTCC	**GAAGGTCGGAGTCAACGGATT**CG TCCAGGGGTTAAATCAACTCT	AGAGGTATACGAAGAAAGGGAAGAA CTAT	0.21	PRT
168	AM20942	ss161144934	C/T	**GAAGGTGACCAAGTTCATGC**TGAG TGTCGGATGACGCGCAG	**GAAGGTCGGAGTCAACGGATT**AT GAGTGTCGGATGACGCGCAA	TAATGGCAGGCTTAATTGTACCAGCTA AT	0.13	
169	AM20943	ss161144935	A/G	**GAAGGTGACCAAGTTCATGC**TTTT AATAATAGAAGCTGCCAAACAAGTT TTT	**GAAGGTCGGAGTCAACGGATT**AA TAATAGAAGCTGCCAAACAAGTTTT C	CCGATCTTGTGGCTTTCAACGCTTA	0.25	P
170	AM20998	ss161144990	A/G	**GAAGGTGACCAAGTTCATGC**TACA AAAGATTAGTAAACTTAGCAAGTTG ATAT	**GAAGGTCGGAGTCAACGGATT**CA AAAGATTAGTAAACTTAGCAAGTT GATAC	CGCATCCTATGTGATGTTTTTGTCTTTT AT	0.38	PRT
171	AM21065	ss161145057	C/T	**GAAGGTGACCAAGTTCATGC**TCAT ATGAATTTGAATAAAAAACACTGTG CAG	**GAAGGTCGGAGTCAACGGATT**AC ATATGAATTTGAATAAAAAACACT GTGCAA	GGGTATGTTGTTATTTATGTTTTTATTG AT	0.26	PR
172	AM21108	ss161145100	A/T	**GAAGGTGACCAAGTTCATGC**TGTT TGAAGATCTTTTTACTTTCCTAAAAG GT	**GAAGGTCGGAGTCAACGGATT**GT TTGAAGATCTTTTTACTTTCCTAAA AGGA	ATGAAATTATGGCGCTCTACTTGCATG TT	0.46	
173	AM21120	ss161145112	C/T	**GAAGGTGACCAAGTTCATGC**TCCT CAAAATGATTTTATGAAAATCTACG ATC	**GAAGGTCGGAGTCAACGGATT**AC CTCAAAATGATTTTATGAAAATCTA CGATT	GGGAGATGTTTTGTACTTGATTTAGGC TT	0.37	PR
174	AM21121	ss161145113	C/T	**GAAGGTGACCAAGTTCATGC**TAAT AGACCTTTGGGCCTATCATCG	**GAAGGTCGGAGTCAACGGATT**GA ATAGACCTTTGGGCCTATCATCA	AAACATCTCCCGACTACACTTATTGAG AT	0.24	PR
175	AM21122	ss161145114	A/G	**GAAGGTGACCAAGTTCATGC**TGAT AGGCCCAAAGGTCTATTCACA	**GAAGGTCGGAGTCAACGGATT**AT AGGCCCAAAGGTCTATTCACG	GCAAGTTGATCAGTATAATTACCAAC CCAT	0.24	PR
176	AM21154	ss161145146	A/G	**GAAGGTGACCAAGTTCATGC**TAGG GAGAAAATTGTTGGTGGTGGA	**GAAGGTCGGAGTCAACGGATT**GG GAGAAAATTGTTGGTGGTGGG	CATGTAAATAGGCAAACAAATCTAAC AAAT	0.10	PRT
177	AM21157	ss161145149	C/T	**GAAGGTGACCAAGTTCATGC**TAAA ATGGATTATGAGACAAGATAACAAC C	**GAAGGTCGGAGTCAACGGATT**GA AAATGGATTATGAGACAAGATAAC AACT	TAATAGGCAAAGACATGATGAGAGAC TTAA	0.28	PRT
178	AM21226	ss161145218	A/C	**GAAGGTGACCAAGTTCATGC**TAAA CCTTTGATCAATCACAACAAAAAAT GA	**GAAGGTCGGAGTCAACGGATT**AA ACCTTTGATCAATCACAACAAAAA ATGC	GAACTTACTGCCTCCTTGTAGTCTGTA	0.23	PR
179	AM21250	ss161145242	A/G	**GAAGGTGACCAAGTTCATGC**TGTA AATATGATAGACTTTTATGTTAAAAT AAAA	**GAAGGTCGGAGTCAACGGATT**GT AAATATGATAGACTTTTATGTTAAA ATAAAG	TGTCCAATTTTGATTATTCGTCGCATA AAT	0.29	PR
180	AM21275	ss161145267	A/G	**GAAGGTGACCAAGTTCATGC**TGGG ATTACTTGGAATCAATGTAAAATTTT CA	**GAAGGTCGGAGTCAACGGATT**AC TTGGAATCAATGTAAAATTTTCG	GCTCTGGATTTATACTACTGTGGTTGA AT	0.24	PT
181	AM21276	ss161145268	C/T	**GAAGGTGACCAAGTTCATGC**TGGA TTTATACTACTGTGGTTGAATCAG	**GAAGGTCGGAGTCAACGGATT**CT GGATTTATACTACTGTGGTTGAATC AA	GGACAATAAACATGTACAAAGGGATT ACTT	0.08	P
182	AM21280	ss161145272	A/G	**GAAGGTGACCAAGTTCATGC**TATT GTCGAATATATCTTGAATAAGTCAT AAATT	**GAAGGTCGGAGTCAACGGATT**GT CGAATATATCTTGAATAAGTCATAA ATC	AAGAACTTGATATCAGGATCAAGGAG AGT	0.19	PRT
183	AM21305	ss161145297	C/G	**GAAGGTGACCAAGTTCATGC**TGTG	**GAAGGTCGGAGTCAACGGATT**GT	AGACTTCATTGAATTGACTGGTACAA	0.23	PRT

#	AM ID	ss ID	Allele	Forward primer	Reverse primer	Sequence	Value	Code
				AGAAATGTGTTTGTGGTGTGG	GAGAAATGTGTTTGTGGTGTGC	GTTA		
184	AM21310	ss161145302	A/T	**GAAGGTGACCAAGTTCATGC**TGGAAGAAGTTAATCGGAACTGATGGT	**GAAGGTCGGAGTCAACGGATT**GGAAGAAGTTAATCGGAACTGATGGA	CATCCTGTTCTACGGCATCTATGTATTAA	0.28	PRT
185	AM21318	ss161145310	G/T	**GAAGGTGACCAAGTTCATGC**TAAAAGAGGAAAATTGAGTCCCAAACG	**GAAGGTCGGAGTCAACGGATT**CAAAAGAGGAAAATTGAGTCCCAAACT	CATAAGCAAGTTCTCCAACCCTCCTT	0.28	R
186	AM21331	ss161145323	A/G	**GAAGGTGACCAAGTTCATGC**TATCATAGTCCTATACATCGCCTTCTTT	**GAAGGTCGGAGTCAACGGATT**CATAGTCCTATACATCGCCTTCTTC	GCGGTCCCGATAATGTCGTAAACAT	0.27	PRT
187	AM21336	ss161145328	C/G	**GAAGGTGACCAAGTTCATGC**TTGACTTTAAGTGACTTAAGGAATTTAAGG	**GAAGGTCGGAGTCAACGGATT**GACTTTAAGTGACTTAAGGAATTTAAGC	TAATTTCCTTCAATCTCCCGCTTATCCTT	0.39	PRT
188	AM21422	ss161145414	A/T	**GAAGGTGACCAAGTTCATGC**TAGTAAATATGATCATTTACAATGCCATTTTTCA	**GAAGGTCGGAGTCAACGGATT**AGTAAATATGATCATTTACAATGCCATTTTTCT	GACTTGATGGGTTTTATGCTTGTACTGTT	0.06	
189	AM21432	ss161145424	A/C	**GAAGGTGACCAAGTTCATGC**TGCATATACTCATTAAGCCATTTATTGTAATGT	**GAAGGTCGGAGTCAACGGATT**CATATACTCATTAAGCCATTTATTGTAATGG	GTTAAAAGTCGAAGAATCAAGGAGGGAT	0.24	PRT
190	AM21437	ss161145429	A/T	**GAAGGTGACCAAGTTCATGC**TTTTGCTGCAAAATTGAAAATCTACAACAA	**GAAGGTCGGAGTCAACGGATT**CTTTTGCTGCAAAATTGAAAATCTACAACAT	GCCTAAGATGATTAGTGACTAAGTAAGTAA	0.29	PRT
191	AM21439	ss161145431	A/G	**GAAGGTGACCAAGTTCATGC**TTAGTCACTAATCATCTTAGGCTATTGTTA	**GAAGGTCGGAGTCAACGGATT**GTCACTAATCATCTTAGGCTATTGTTG	TTAAAGAATGCTCCTCCCCCGCTTT	0.27	PRT
192	AM21452	ss161145444	G/T	**GAAGGTGACCAAGTTCATGC**TATCTGGACTTGGGGATGG	**GAAGGTCGGAGTCAACGGATT**GTGCTATCTGGACTTGGGGATGT	GCGAAGTAGTAATATTGTTTAAATGCGGAA	0.09	PR
193	AM21546	ss161145538	C/T	**GAAGGTGACCAAGTTCATGC**TTTCAAGGATATTCATGCTTTCAGTCG	**GAAGGTCGGAGTCAACGGATT**CATTTCAAGGATATTCATGCTTTCAGTCA	ACAGTAACGGGAGTGATGTGGTTATTATA	0.28	PR
194	AM21564	ss161145556	A/G	**GAAGGTGACCAAGTTCATGC**TCACAAAATGTCAAGTTACCTTTAATAGGT	**GAAGGTCGGAGTCAACGGATT**CACAAAATGTCAAGTTACCTTTAATAGGC	TTAGGCCTTTAGAGTGCTTAAACTTTTGAT	0.23	PR
195	AM21568	ss161145560	C/T	**GAAGGTGACCAAGTTCATGC**TAAATGTTGTGTACTTACGTTGTGTCG	**GAAGGTCGGAGTCAACGGATT**CAAATGTTGTGTACTTACGTTGTGTCA	TACCTTCTCCATACTCCTCGGTCAT	0.27	PRT
196	AM21605	ss161145597	A/T	**GAAGGTGACCAAGTTCATGC**TAAGATATCCATTCTTGTACTCACAATAA	**GAAGGTCGGAGTCAACGGATT**CTAAGATATCCATTCTTGTACTCACAATAT	TAAGTTTTTGAACTCTTGGTTTCACTCATA	0.30	P
197	AM21724	ss161145716	A/G	**GAAGGTGACCAAGTTCATGC**TCAGAGCAGTGCTCACACATGGAA	**GAAGGTCGGAGTCAACGGATT**AGAGCAGTGCTCACACATGGAG	TATACAAGAGAAGGTGAGGCACAATAGAA	0.40	P
198	AM21727	ss161145719	A/G	**GAAGGTGACCAAGTTCATGC**TTGATTGTCTGCTAAGCAAAATTTAAAGCT	**GAAGGTCGGAGTCAACGGATT**GTCTGCTAAGCAAAATTTAAAGCC	TGTTCAATTCTTGGCCTATCATCTCATATA	0.29	PRT
199	AM21743	ss161145735	A/G	**GAAGGTGACCAAGTTCATGC**TCCTTGTTTATGTCACTTATGATCAAGTCA	**GAAGGTCGGAGTCAACGGATT**CTTGTTTATGTCACTTATGATCAAGTCG	AAGAGAATTTGTACCAAAGCCGTGGAA	0.27	PRT
200	AM21773	ss161145765	A/G	**GAAGGTGACCAAGTTCATGC**TCAAATTTGGTTTCTAATATATTTTAAAGTGTT	**GAAGGTCGGAGTCAACGGATT**CAAATTTGGTTTCTAATATATTTTAAAGTGTC	GGCACGCACACTTCACGCGAAT	0.38	P
201	AM21827	ss161145819	C/T	**GAAGGTGACCAAGTTCATGC**TCGGGTCAAAGTTATTCGGATTTAAAC	**GAAGGTCGGAGTCAACGGATT**AATTCGGGTCAAAGTTATTCGGATTTAAAT	GGGTCGAATGGGTCATGTCAACTTT	0.33	P+R
202	AM21842	ss161145834	A/G	**GAAGGTGACCAAGTTCATGC**TGGCGCCTCGATGCGCTTCAT	**GAAGGTCGGAGTCAACGGATT**GCGCCTCGATGCGCTTCAC	CAAGGATAAGTTAATAACCAAACCCAACAA	0.37	P+RT

203	AM21859	ss161145851	A/T	**GAAGGTGACCAAGTTCATGC**TCCAATTCCCCATTTAACTAAATTTTACCAA	**GAAGGTCGGAGTCAACGGATT**CCAATTCCCCATTTAACTAAATTTTACCAT	AAAAGTACTCACTCTATTCGTCCTCAATTA	0.40	P
204	AM21862	ss161145854	A/G	**GAAGGTGACCAAGTTCATGC**TATGAATAAAATCTTACTTACCCAGTAATGTAA	**GAAGGTCGGAGTCAACGGATT**GAATAAAATCTTACTTACCCAGTAATGTAG	CTGATGCTGGTTTGAAAAAGTTAGATGAAT	0.07	PRT
205	AM21901	ss161145893	A/G	**GAAGGTGACCAAGTTCATGC**TGAGTATGTCCGGCCAGAATTGGA	**GAAGGTCGGAGTCAACGGATT**AGTATGTCCGGCCAGAATTGGG	GGGATGAGGTATACCGCTGGAAAAT	0.22	PR
206	AM21905	ss161145897	C/T	**GAAGGTGACCAAGTTCATGC**TGATTACTGAACTTGAAATCTTATTGAACATC	**GAAGGTCGGAGTCAACGGATT**ATGATTACTGAACTTGAAATCTTATTGAACATT	GCTTATTCATAAGGCAACAACAAACATCAT	0.23	P
207	AM21911	ss161145903	C/T	**GAAGGTGACCAAGTTCATGC**TGAACCTTCCCAGTTGGTAAGATC	**GAAGGTCGGAGTCAACGGATT**CTGAACCTTCCCAGTTGGTAAGATT	ACATGATCACAAGCATGATGCATCGTTT	0.23	PR
208	AM21924	ss161145916	C/T	**GAAGGTGACCAAGTTCATGC**TCAAATCTGAATTACCCCTCACTGAG	**GAAGGTCGGAGTCAACGGATT**CAAATCTGAATTACCCCTCACTGAA	CACATGCCCTTTTCATGCTTGGCAT	0.14	PRT
209	AM21961	ss161145953	A/C	**GAAGGTGACCAAGTTCATGC**TATCGTTTCTCATCTCCTGATCCTCT	**GAAGGTCGGAGTCAACGGATT**CGTTTCTCATCTCCTGATCCTCG	CGTCGCAGATAGACCTAAACCTGAA	0.12	PRT
210	AM21966	ss161145958	A/G	**GAAGGTGACCAAGTTCATGC**TATGAAATGTTAAATGGTGAACTATCTTGTTTT	**GAAGGTCGGAGTCAACGGATT**GAAATGTTAAATGGTGAACTATCTTGTTTC	GGAGCCAATTGCCAAGAGACATGAA	0.28	PRT
211	AM22004	ss161145996	A/G	**GAAGGTGACCAAGTTCATGC**TAGCTTAGAGCCAAGGCACAACAA	**GAAGGTCGGAGTCAACGGATT**GCTTAGAGCCAAGGCACAACAG	TCTTCTTCAGTCCAGAGCCTCCAAA	0.30	PRT
212	AM22022	ss161146014	A/T	**GAAGGTGACCAAGTTCATGC**TTGAGTAGAATTTAATTTCTATTAAACTGAATA	**GAAGGTCGGAGTCAACGGATT**GAGTAGAATTTAATTTCTATTAAACTGAATT	GCTGTGTGACCTGTGTCCTCTAAAT	0.26	P
213	AM22029	ss161146021	A/T	**GAAGGTGACCAAGTTCATGC**TGACACCTCCAAAGCGGTTAGGA	**GAAGGTCGGAGTCAACGGATT**GACACCTCCAAAGCGGTTAGGT	CATGCAGAACCTCCTCTGTGTGAAA	0.46	PRT
214	AM22082	ss161146074	A/C	**GAAGGTGACCAAGTTCATGC**TCCCATGGATAATGAGCGTTAACTTGA	**GAAGGTCGGAGTCAACGGATT**CCATGGATAATGAGCGTTAACTTGC	AGCGTTTTGGAAAAGAGTGAACCTCAT	0.08	PRT
215	AM22099	ss161146091	A/G	**GAAGGTGACCAAGTTCATGC**TACAAACTACTCCTGGATACTTTGAGAA	**GAAGGTCGGAGTCAACGGATT**CAAACTACTCCTGGATACTTTGAGAG	ATGACCCCGACACGCATCAATGATA	0.26	PR
216	AM22137	ss161146129	A/C	**GAAGGTGACCAAGTTCATGC**TGCATGCATACAAGCTTTAATTTGTCGAT	**GAAGGTCGGAGTCAACGGATT**CATGCATACAAGCTTTAATTTGTCGAG	CATTGCCCCACCCAATTGTTCCTTT	0.37	PR
217	AM22193	ss161146185	A/G	**GAAGGTGACCAAGTTCATGC**TCAAAGGGCATAACAGATTAGCTGAGA	**GAAGGTCGGAGTCAACGGATT**AAAGGGCATAACAGATTAGCTGAGG	GTCCAGCCAGCTGGCATAACAAATT	0.13	PR
218	AM22196	ss161146188	A/T	**GAAGGTGACCAAGTTCATGC**TGCATTTGATGTGTAAGGAGCTTCCT	**GAAGGTCGGAGTCAACGGATT**GCATTTGATGTGTAAGGAGCTTCCA	ATCCATAGCAATGACAGTTTCCATGAGAT	0.28	PR
219	AM22260	ss161146252	G/T	**GAAGGTGACCAAGTTCATGC**TAGAATAAGAGATTTAAAATAAGTCCAAGAATTG	**GAAGGTCGGAGTCAACGGATT**AGAATAAGAGATTTAAAATAAGTCCAAGAATTT	CAAAACCTCTTTTCTCTTACACTTCTTGAA	0.38	P+
220	AM22292	ss161146284	G/T	**GAAGGTGACCAAGTTCATGC**TAATTAAAACATAATTGAAGGATTTTATCTTAGC	**GAAGGTCGGAGTCAACGGATT**AATTAAAACATAATTGAAGGATTTTATCTTAGA	CCACTATTGCCACCCACAATTTAATACAA	0.26	PR
221	AM22321	ss161146313	A/G	**GAAGGTGACCAAGTTCATGC**TAAAGATTCTTGCTAAGGATGGTGTGAT	**GAAGGTCGGAGTCAACGGATT**AGATTCTTGCTAAGGATGGTGTGAC	ACATCAATTCTCAGTAGACCACATCAATAT	0.29	PT
222	AM22341	ss161146333	C/T	**GAAGGTGACCAAGTTCATGC**TATATGATTTGTTGACTAACCGTGGTTC	**GAAGGTCGGAGTCAACGGATT**CAATATGATTTGTTGACTAACCGTGGTTT	GCCTTTTCACTGTGACATGAAATAGCATA	0.13	PR
223	AM22393	ss161146385	C/T	**GAAGGTGACCAAGTTCATGC**TGTTTGACTAACCAACAAGACAAAAACC	**GAAGGTCGGAGTCAACGGATT**GTTTGACTAACCAACAAGACAAAAAC	CCACTCAACAAATACAAATAAAAGACTCTT	0.38	P

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No.	AM id	ss id	Allele	Sequence 1	Sequence 2	Sequence 3	Value	Type
224	AM22416	ss161146408	C/T	**GAAGGTGACCAAGTTCATGC**TTAGAGAGTTTATTTTGAAGTTATCATTAGATG	**GAAGGTCGGAGTCAACGGATT**AGAGAGTTTATTTTGAAGTTATCATTAGATA	CCTCTTGCTATACCTGTTGTTGTAACAAA	0.30	PRT
225	AM22422	ss161146414	C/T	**GAAGGTGACCAAGTTCATGC**TCGTAAAAGAATCATGTTGAGGTGATTAAC	**GAAGGTCGGAGTCAACGGATT**CGTAAAAGAATCATGTTGAGGTGATTAAT	AATGACACTGACTATCTGCAGTCTCTT	0.40	PR
226	AM22426	ss161146418	C/T	**GAAGGTGACCAAGTTCATGC**TATATTTAATTCAAGTGAAAATGTTGATTGCAC	**GAAGGTCGGAGTCAACGGATT**CATATTTAATTCAAGTGAAAATGTTGATTGCAT	TGCTCCCGACAAGAAAGATCTTAATCTTA	0.25	PT
227	AM22430	ss161146422	C/G	**GAAGGTGACCAAGTTCATGC**TGTTCCTTGTATTGAATACTTTATAATATGGG	**GAAGGTCGGAGTCAACGGATT**GTTCCTTGTATTGAATACTTTATAATATGGC	TGGTTTGTTACGTCAGGTGCTATATCATA	0.25	P+R
228	AM22433	ss161146425	A/T	**GAAGGTGACCAAGTTCATGC**TGGAAAAGAAGGTAAATTATTTCACCTAAATAAA	**GAAGGTCGGAGTCAACGGATT**GGAAAAGAAGGTAAATTATTTCACCTAAATAAT	CTTACAATATCAAGAGATGAGTGACCCTT	0.23	PR
229	AM22471	ss161146463	A/C	**GAAGGTGACCAAGTTCATGC**TCGGTGGTTTGAGTGTTAGAGAAAGA	**GAAGGTCGGAGTCAACGGATT**GGTGGTTTGAGTGTTAGAGAAAGC	CCACTTGATCCAGCCTACATTCCAT	0.18	PR
230	AM22476	ss161146468	A/G	**GAAGGTGACCAAGTTCATGC**TAAGTTATCAGAAAAGTGCTCAATTATTATGAT	**GAAGGTCGGAGTCAACGGATT**GTTATCAGAAAAGTGCTCAATTATTATGAC	CATTCGTGTCTGTATACAGCATGGCTT	0.39	P+R
231	AM22487	ss161146479	C/G	**GAAGGTGACCAAGTTCATGC**TATTAGCTTGAATGCTAAGGATATGGC	**GAAGGTCGGAGTCAACGGATT**ATTAGCTTGAATGCTAAGGATATGGG	GCTTTAGACACAAGAGAAATAAACTCCAAA	0.30	P+RT
232	AM22558	ss161146550	A/G	**GAAGGTGACCAAGTTCATGC**TATTTGTAAAGGGTAAAATTTGAAATAGTGCATA	**GAAGGTCGGAGTCAACGGATT**GTAAAGGGTAAAATTTGAAATAGTGCATG	GCACAAGGCCCCAAAATCAACAAAATTTT	0.23	PR
233	AM22572	ss161146564	A/G	**GAAGGTGACCAAGTTCATGC**TAAGCTTCTTAATCTTAACTATCTGTTAGAAATA	**GAAGGTCGGAGTCAACGGATT**GCTTCTTAATCTTAACTATCTGTTAGAAATG	CATCAGCCTGGATAGCATCAAGCAA	0.29	PR
234	AM22645	ss161146637	A/G	**GAAGGTGACCAAGTTCATGC**TCTTATATATTCATGAAAGATCGAATATGGAAT	**GAAGGTCGGAGTCAACGGATT**CTTATATATTCATGAAAGATCGAATATGGAAC	TGTTAGAGGCATGAAAAATATCCAAATCAA	0.24	P
235	AM22649	ss161146641	C/T	**GAAGGTGACCAAGTTCATGC**TCACTACAGTCTTTAGATATTATCGCG	**GAAGGTCGGAGTCAACGGATT**CCACTACAGTCTTTAGATATTATCGCA	CACAGTTTCCTCCACAGCAAGACAT	0.35	PRT
236	AM22690	ss161146682	C/G	**GAAGGTGACCAAGTTCATGC**TCGAAATTTTCAGCTTGCAGATAGAGG	**GAAGGTCGGAGTCAACGGATT**CGAAATTTTCAGCTTGCAGATAGAGC	TCCATGTTCTATTTTTTGGCTCTTTCTCTT	0.23	PRT
237	AM22698	ss161146690	A/G	**GAAGGTGACCAAGTTCATGC**TGTCAGAGAGTCCACCGACTCT	**GAAGGTCGGAGTCAACGGATT**GTCAGAGAGTCCACCGACTCC	GGTTCCATGAAAGATTGACATAATAAACAT	0.20	P
238	AM22781	ss161146773	A/G	**GAAGGTGACCAAGTTCATGC**TGGTACTAACTACAATTCAAAACATCTTAATAA	**GAAGGTCGGAGTCAACGGATT**GGTACTAACTACAATTCAAAACATCTTAATAG	CAGTACGACTATTCATAGGCCTTAACATA	0.29	PRT
239	AM22888	ss161146880	A/C	**GAAGGTGACCAAGTTCATGC**TCGAGCATTAATTTAAACATCTGACAGA	**GAAGGTCGGAGTCAACGGATT**CGAGCATTAATTTAAACATCTGACAGC	TGCTTTTGGCAAAGCTTCTGATTTGAGTA	0.17	PRT
240	AM22892	ss161146884	A/G	**GAAGGTGACCAAGTTCATGC**TCACCCTCGCTCTCTTCATGATGA	**GAAGGTCGGAGTCAACGGATT**ACCCTCGCTCTCTTCATGATGG	CAAACTTCTTCCCACCGCCATGAAT	0.33	PRT
241	AM22911	ss161146903	A/T	**GAAGGTGACCAAGTTCATGC**TAATCAAGTAGATTAAAAAGGGTTTTACTCTAA	**GAAGGTCGGAGTCAACGGATT**AATCAAGTAGATTAAAAAGGGTTTTACTCTAT	AGTAACATGTTGTTCCTTTTGCAGGTCTA	0.33	PR
242	AM22964	ss161146956	A/G	**GAAGGTGACCAAGTTCATGC**TGATAATCATTACTTACAGCTAACCTTCTT	**GAAGGTCGGAGTCAACGGATT**GATAATCATTACTTACAGCTAACCTTC	GAGTGGTAAGTGAGTGTGGAGCAT	0.28	P+RT

TC

243	AM22979	ss161146971	C/T	**GAAGGTGACCAAGTTCATGC**TATAGTGTTATAAATGTTTCATGACATCGG	**GAAGGTCGGAGTCAACGGATT**GTATAGTGTTATAAATGTTTCATGACATCGA	TTGCATGTGTGGGTCAGTTGCTGAT	0.28	P+R
244	AM22982	ss161146974	C/T	**GAAGGTGACCAAGTTCATGC**TAGAAGACATGAAGAGATTGATAACCAG	**GAAGGTCGGAGTCAACGGATT**ATAGAAGACATGAAGAGATTGATAACCAA	GACGTAAAATATCAAAGTACAATGTACAAA	0.20	PRT
245	AM22999	ss161146991	A/G	**GAAGGTGACCAAGTTCATGC**TGCATCGAAGATTGTTACATCGAGAGT	**GAAGGTCGGAGTCAACGGATT**CATCGAAGATTGTTACATCGAGAGC	CAATACCAAATTGATCCCAACCACTCTT	0.22	PR
246	AM23006	ss161146998	A/C	**GAAGGTGACCAAGTTCATGC**TACTAATAAGGTGACCCATATAGCTCT	**GAAGGTCGGAGTCAACGGATT**CTAATAAGGTGACCCATATAGCTCG	CGCTAATATTTGATATCAATGGGTCACTAA	0.45	PRT
247	AM23055	ss161147047	A/G	**GAAGGTGACCAAGTTCATGC**TACAATTACAGAGCATCCATATAATTCATATTTA	**GAAGGTCGGAGTCAACGGATT**CAATTACAGAGCATCCATATAATTCATATTTG	TTATTCATACGTGTATGGGATATTGGAGAA	0.23	PR
248	AM23071	ss161147063	A/T	**GAAGGTGACCAAGTTCATGC**TAAATTTCTTTTGACCAAAGATAACCCCAAT	**GAAGGTCGGAGTCAACGGATT**AAATTTCTTTTGACCAAAGATAACCCCAAA	TGAGAATATACGAAGTTTCTTTTCTGGTTA	0.23	PR
249	AM23074	ss161147066	A/G	**GAAGGTGACCAAGTTCATGC**TTAACCTTATGAATTGAACACTGTAGAGAT	**GAAGGTCGGAGTCAACGGATT**ACCTTATGAATTGAACACTGTAGAGAC	GCTTAAGTGCAGCCATGATTTCAGTAAAT	0.25	PRT
250	AM23084	ss161147076	A/G	**GAAGGTGACCAAGTTCATGC**TAATGGCGGAAAGGATCTCAATGGT	**GAAGGTCGGAGTCAACGGATT**GGCGGAAAGGATCTCAATGGC	TTCGACAACGATGACTGCCAGTCTT	0.28	PRT
251	AM23107	ss161147099	A/G	**GAAGGTGACCAAGTTCATGC**TATTTAACGTTTGTTCTTCGAAGTATATCTTAT	**GAAGGTCGGAGTCAACGGATT**AACGTTTGTTCTTCGAAGTATATCTTAC	TAGGTGTGTACCATCCTCACCACAT	0.43	PR
252	AM23112	ss161147104	C/G	**GAAGGTGACCAAGTTCATGC**TATCAAGGAAAAATTTACTTTAAAGCTATGTTAC	**GAAGGTCGGAGTCAACGGATT**ATCAAGGAAAAATTTACTTTAAAGCTATGTTAG	ACTCGAAGTGGAATACTTGGTTACGTATT	0.23	PR
253	AM23128	ss161147120	C/T	**GAAGGTGACCAAGTTCATGC**TCAATAGTGTAAGCGTTTGATATGACATTC	**GAAGGTCGGAGTCAACGGATT**ACAATAGTGTAAGCGTTTGATATGACATTT	AGGCCTCGTCTTTGTGGCCTAATAT	0.33	PT
254	AM23158	ss161147150	A/G	**GAAGGTGACCAAGTTCATGC**TCTCCCACGGATCATGTGCATAT	**GAAGGTCGGAGTCAACGGATT**CTCCCACGGATCATGTGCATAC	CCTGAAAAGTGTCCTAATCGTCAATGATA	0.28	PR
255	AM23187	ss161147179	A/T	**GAAGGTGACCAAGTTCATGC**TGTATGCTGTTTTATGTTGATGATGCTTAT	**GAAGGTCGGAGTCAACGGATT**GTATGCTGTTTTATGTTGATGATGCTTAA	CATTCAACAAACAATCCCCAACATCACAA	0.08	P
256	AM23196	ss161147188	C/T	**GAAGGTGACCAAGTTCATGC**TATATTCAGCAAATGATTCCTTCAATGATC	**GAAGGTCGGAGTCAACGGATT**CATATTCAGCAAATGATTCCTTCAATGATT	CACAACAGTGGCTTACTTTTTAATCAAGAT	0.31	PRT
257	AM23216	ss161147208	A/C	**GAAGGTGACCAAGTTCATGC**TAAACCTGACCTATTTAGTAAATTGGATCT	**GAAGGTCGGAGTCAACGGATT**ACCTGACCTATTTAGTAAATTGGATCG	CTGGTCTATATGTTGCATGTCGGGTT	0.33	P
258	AM23221	ss161147213	A/C	**GAAGGTGACCAAGTTCATGC**TATAACTTCAATATATGTTCTATTTCTTCTGAAA	**GAAGGTCGGAGTCAACGGATT**ATAACTTCAATATATGTTCTATTTCTTCTGAAC	CTCACTCTACTCTTACAAGCTCCATAATA	0.27	P
259	AM23231	ss161147223	G/T	**GAAGGTGACCAAGTTCATGC**TGTGTTAATTTGATGTTTGTTAGAATTGTTAATG	**GAAGGTCGGAGTCAACGGATT**GTGTTAATTTGATGTTTGTTAGAATTGTTAATT	CCCTGCATTCAAATCATCAACAAAAACATT	0.15	PRT
260	AM23262	ss161147254	G/T	**GAAGGTGACCAAGTTCATGC**TATAAAGGAAACCCCAAAAATTCATAATACC	**GAAGGTCGGAGTCAACGGATT**AATAAAGGAAACCCCAAAAATTCATAATACACA	ACGAAATCTTTTCCTGATAACAAAGATAAT	0.34	PR

261	AM23275	ss161147267	G/T	**GAAGGTGACCAAGTTCATGC**TTTAATGTCATATGCGGCATAATTTAATAG	**GAAGGTCGGAGTCAACGGATT**CTTTAATGTCATATGCGGCATAATTTAATAT	GACCTGGGCCATTTGTTTAAAAACCTTAT	0.29	PR
262	AM23281	ss161147273	C/G	**GAAGGTGACCAAGTTCATGC**TAGACGGTCTCTCAGGACACTTC	**GAAGGTCGGAGTCAACGGATT**AGACGGTCTCTCAGGACACTTG	GCCAATCAGATGGATAAAACAAGGGAAAT	0.25	PR
263	AM23354	ss161147346	A/G	**GAAGGTGACCAAGTTCATGC**TGTCCCCGGTGGGGAGAGAT	**GAAGGTCGGAGTCAACGGATT**CCCCGGTGGGGAGAGAC	CGATTAATTTGCTGCAGAAAACTACTTCTT	0.31	P
264	AM23386	ss161147378	C/T	**GAAGGTGACCAAGTTCATGC**TGCGCTCAATGTGCTTCACGCC	**GAAGGTCGGAGTCAACGGATT**GCGCTCAATGTGCTTCACGCT	ACGCAATCCAATAATGAGGCGCACT	0.22	PR
265	AM23401	ss161147393	A/G	**GAAGGTGACCAAGTTCATGC**TCAAGCACTGCAATAATGCCAGAGAA	**GAAGGTCGGAGTCAACGGATT**AAGCACTGCAATAATGCCAGAGAG	GTACTGAAGTGACTTTCTAAAATTGACAAT	0.24	P
266	AM23553	ss161147545	A/G	**GAAGGTGACCAAGTTCATGC**TAACAAGTGCTTACACTTCACAACACTT	**GAAGGTCGGAGTCAACGGATT**CAAGTGCTTACACTTCACAACACTC	GCATATTTGTAATCTTTAACGAGGCTCCTT	0.28	P
267	AM23590	ss161147582	A/G	**GAAGGTGACCAAGTTCATGC**TCAAAAATGAAATTTGCATTTGATTGAATACAT	**GAAGGTCGGAGTCAACGGATT**CAAAAATGAAATTTGCATTTGATTGAATACAC	CTTTCCATAAGCACTGGCTCAAATAACTT	0.24	PRT
268	AM23610	ss161147602	C/G	**GAAGGTGACCAAGTTCATGC**TAAAGAATAGGCAGCATCATGTGGTC	**GAAGGTCGGAGTCAACGGATT**AAAGAATAGGCAGCATCATGTGGTG	CATAGATGGTGCAGCTGGGATGATA	0.42	PT
269	AM23641	ss161147633	C/T	**GAAGGTGACCAAGTTCATGC**TCAAATTTCCAATTAACAACACAATATCAGAAC	**GAAGGTCGGAGTCAACGGATT**CAAATTTCCAATTAACAACACAATATCAGAAT	TCAAATAATGATCGGTCTTAATCTCATGTA	0.24	P
270	AM23684	ss161147676	A/G	**GAAGGTGACCAAGTTCATGC**TCATTCGATCAAGGTTTGCATTAAAGTAGT	**GAAGGTCGGAGTCAACGGATT**CGATCAAGGTTTGCATTAAAGTAGC	AGGAGCAAAGGCATGTAATCTTAATGCAT	0.05	PRT
271	AM23686	ss161147678	A/G	**GAAGGTGACCAAGTTCATGC**TGAGTGGTGCAAGGAAGATTACACTT	**GAAGGTCGGAGTCAACGGATT**AGTGGTGCAAGGAAGATTACACTC	AGCCTTGATCACATTTCTTGGTTTGTGTT	0.27	PR
272	AM23703	ss161147695	A/G	**GAAGGTGACCAAGTTCATGC**TTTATCTTGTTTGGGAAGTTCTAATTCTGT	**GAAGGTCGGAGTCAACGGATT**ATCTTGTTTGGGAAGTTCTAATTCTGC	CTTACTTCGGGTTAAGCCTGTGACAT	0.45	P+R
273	AM23707	ss161147699	C/G	**GAAGGTGACCAAGTTCATGC**TCCTCAGGAATTAGAGGCCAAGAG	**GAAGGTCGGAGTCAACGGATT**CCTCAGGAATTAGAGGCCAAGAC	CAGTGATGTTAGTGTTCAATGAACCATGAA	0.24	PRT
274	AM23741	ss161147733	A/G	**GAAGGTGACCAAGTTCATGC**TAATGCTTAAGGGATTGGGTTAATTTAAGA	**GAAGGTCGGAGTCAACGGATT**GCTTAAGGGATTGGGTTAATTTAAGG	GATAGGGAAGGGATGGGAAGGAAAT	0.03	PR
275	AM23764	ss161147756	C/T	**GAAGGTGACCAAGTTCATGC**TGATTTGTAGCTTGTGTGGATTGGC	**GAAGGTCGGAGTCAACGGATT**CGATTTGTAGCTTGTGTGGATTGGT	GGACCTGTAAATAGGAAAATGTCGAACAT	0.24	P
276	AM23808	ss161147800	C/T	**GAAGGTGACCAAGTTCATGC**TCATTGAGTTTACCACGCTGATAAGC	**GAAGGTCGGAGTCAACGGATT**ATCATTGAGTTTACCACGCTGATAAGT	GCAAAGCGGCTTTTGCAGGTGTCT	0.22	PR
277	AM23857	ss161147849	G/T	**GAAGGTGACCAAGTTCATGC**TAATTTTATTATCAGTGATAATTTGTCTTTGCTG	**GAAGGTCGGAGTCAACGGATT**AATTTTATTATCAGTGATAATTTGTCTTTGCTT	GTTGCTTTTGCAGAATCGAGCATAATGAT	0.08	PR
278	AM23891	ss161147883	A/T	**GAAGGTGACCAAGTTCATGC**TGACGCCTGCTGACCTGCATAAAA	**GAAGGTCGGAGTCAACGGATT**GATCGCCTGCTGACCTGCATAAT	TAGAGTCTCATTTTAGGCGAGTTACCAT	0.13	PR
279	AM23895	ss161147887	A/G	**GAAGGTGACCAAGTTCATGC**TGTCCTTACACGACTAAAAAACACCTTAT	**GAAGGTCGGAGTCAACGGATT**CCTTACACGACTAAAAAACACCTTAC	AATGGAGTATAGCATGTCAAGATCCAATAT	0.19	P
280	AM23925	ss161147917	A/T	**GAAGGTGACCAAGTTCATGC**TCAAAAACAAGCAACATTAACAGGGCTT	**GAAGGTCGGAGTCAACGGATT**CAAAAACAAGCAACATTAACAGGGCTA	GCACAGTTTGCTTGCTACTCCAGTT	0.14	PRT
281	AM23934	ss161147926	G/T	**GAAGGTGACCAAGTTCATGC**TCCTACACAAAGAACTCATATTCAAAATTATC	**GAAGGTCGGAGTCAACGGATT**ACCTACACAAAGAACTCATATTCAAAATTATA	CAATCCATGCACTTTAAACATCAAAGATTT	0.33	P

282	AM23966	ss161147958	A/T	**GAAGGTGACCAAGTTCATGC**TATTCGAAGTATAATAAATCAACTGCCTGTA	**GAAGGTCGGAGTCAACGGATT**CGAAGTATAATAAATCAACTGCCTGTT	GCTTCGTGTCAATTCTTAAATTATTTGGAT	0.21	PRT
283	AM23989	ss161147981	C/T	**GAAGGTGACCAAGTTCATGC**TACTTTCAACTTGTTTTAATATTTAAGCGG	**GAAGGTCGGAGTCAACGGATT**ATCTACTTTCAACTTGTTTTAATATTTAAGCGA	CTTTCTTATTGTAATAAACTTTTAGAGGTT	0.10	P
284	AM24013	ss161148005	C/T	**GAAGGTGACCAAGTTCATGC**TACATTATCAAAGTGGTCCTTTTTCCTC	**GAAGGTCGGAGTCAACGGATT**CACATTATCAAAGTGGTCCTTTTTCCTT	CCGTTGAATCTTAATCATACGTCCAAATTT	0.09	P
285	AM24020	ss161148012	A/T	**GAAGGTGACCAAGTTCATGC**TATTCGTCAGTCCATCTAAGCTAAAAGT	**GAAGGTCGGAGTCAACGGATT**CGTCAGTCCATCTAAGCTAAAAGA	CACATTTAGGGGATCTAATTGTAGTGATAT	0.38	PR
286	AM24023	ss161148015	A/T	**GAAGGTGACCAAGTTCATGC**TCCATCCTTGATGGAGCCGAATATT	**GAAGGTCGGAGTCAACGGATT**CCATCCTTGATGGAGCCGAATATA	TGCACATGAATTAACGAGTCATTTTACAAT	0.37	PRT
287	AM24029	ss161148021	A/G	**GAAGGTGACCAAGTTCATGC**TATAATTTTTTCAAACTGTAAGTACTGATTGCTA	**GAAGGTCGGAGTCAACGGATT**TTTTCAAACTGTAAGTACTGATTGCTG	GGTCGAACATGTTGAACATGCTCAGAA	0.37	P
288	AM24041	ss161148033	A/C	**GAAGGTGACCAAGTTCATGC**TCATTACAATAACCTTCACTAATGTGTCGA	**GAAGGTCGGAGTCAACGGATT**ACAATAACCTTCACTAATGTGTCGC	TCAAGATTGGAAACAAAGGTGTCTCGTA	0.44	
289	AM24062	ss161148054	A/G	**GAAGGTGACCAAGTTCATGC**TTCTGATCCGATCTTAGCTACCCAA	**GAAGGTCGGAGTCAACGGATT**CTGATCCGATCTTAGCTACCCAG	AAGCTGAAGTTGTCGAACACAGAAGTA	0.39	R
290	AM24078	ss161148070	A/G	**GAAGGTGACCAAGTTCATGC**TCATCGTTCTTTGCTGCAGCCCTT	**GAAGGTCGGAGTCAACGGATT**ATCGTTCTTTGCTGCAGCCCTC	TTTGCAGCATTTCCATCATCAAGGACTT	0.31	PRT
291	AM24104	ss161148096	A/G	**GAAGGTGACCAAGTTCATGC**TGGATATTACAAATTTGACTGTAGCAACAAAT	**GAAGGTCGGAGTCAACGGATT**GATATTACAAATTTGACTGTAGCAACAAC	CCCATGGATAGATCACAGTACCGAA	0.33	PR
292	AM24134	ss161148126	G/T	**GAAGGTGACCAAGTTCATGC**TGTAGCGCAAAAAGTGCGGTCAC	**GAAGGTCGGAGTCAACGGATT**AGTAGCGCAAAAAGTGCGGTCAA	AATCTCCTTATGCAGGGTGTTCAGTTTT	0.18	R
293	AM24152	ss161148144	A/G	**GAAGGTGACCAAGTTCATGC**TCCAATCCAGAGAAATTGCCAGCAAA	**GAAGGTCGGAGTCAACGGATT**CAATCCAGAGAAATTGCCAGCAAG	GTCGAGCTTTGAAATTTGCTCTCTGTT	0.30	PRT
294	AM24177	ss161148169	A/G	**GAAGGTGACCAAGTTCATGC**TTATGGTCGTTAAAAAATATACGAACCGAT	**GAAGGTCGGAGTCAACGGATT**GGTCGTTAAAAAATATACGAACCGAC	AAAGTTTAGCACCTCTTTGGTTGCTTCTT	0.36	PR
295	AM24179	ss161148171	C/T	**GAAGGTGACCAAGTTCATGC**TTTTATGGTCGTTAAAAAATATACGAACCG	**GAAGGTCGGAGTCAACGGATT**TTTTATGGTCGTTAAAAAATATACGAACCCA	AAAGTTTAGCACCTCTTTGGTTGCTTCTT	0.32	PR
296	AM24194	ss161148186	C/T	**GAAGGTGACCAAGTTCATGC**TATAATATAATAAGCTGGATCAAATGACCTG	**GAAGGTCGGAGTCAACGGATT**CATAATATAATAAGCTGGATCAAATGACCTA	ACCAATATTTTCCTTATGCCAATTGTTGTT	0.20	PRT
297	AM24210	ss161148202	C/T	**GAAGGTGACCAAGTTCATGC**TAATTCTATTTATATGAGTTCATTGAAGTCAAG	**GAAGGTCGGAGTCAACGGATT**CAATTCTATTTATATGAGTTCATTGAAGTCAAA	ACACCCAATGACTTAAATATACATCTCTAA	0.35	R
298	AM24224	ss161148216	A/G	**GAAGGTGACCAAGTTCATGC**TGGATGGGAACAAAGAAATGATGGCA	**GAAGGTCGGAGTCAACGGATT**GATGGGAACAAAGAAATGATGGCG	GGTTACATAACATGATGAGCATGAACCAA	0.23	PRT
299	AM24245	ss161148237	G/T	**GAAGGTGACCAAGTTCATGC**TCCTAACAGAATCATATGACTCTGTAG	**GAAGGTCGGAGTCAACGGATT**CCCTAACAGAATCATATGACTCTGTAT	CAACATTTAAAAATAATCCACAGCCCGAAA	0.29	PR
300	AM24266	ss161148258	C/G	**GAAGGTGACCAAGTTCATGC**TGCGGAGGAATTTGCTTGATTTCAC	**GAAGGTCGGAGTCAACGGATT**GCGGAGGAATTTGCTTGATTTCAG	GAACTCTTGATGGTTTTCAGGCACAAAAT	0.33	PRT
301	AM24401	ss161148393	C/G	**GAAGGTGACCAAGTTCATGC**TGAATATTTGAAGTAAAGTGAAGAGTCTGC	**GAAGGTCGGAGTCAACGGATT**GAATATTTGAAGTAAAGTGAAGAGTCTGG	GTATGTGTTTATTTTGGAGCATGCAACCTT	0.37	R
302	AM24451	ss161148443	C/G	**GAAGGTGACCAAGTTCATGC**TGAT	**GAAGGTCGGAGTCAACGGATT**GA	AATATAGATTCCTCTTCCCCCAATGGA	0.12	PRT

				CTTTGTCGACATCTTCGACAATG	TCTTTGTCGACATCTTCGACAATC	T		
303	AM24457	ss161148449	A/G	GAAGGTGACCAAGTTCATGCTTATACAGTGTGGCTTTGGAGGCA	GAAGGTCGGAGTCAACGGATTATACAGTGTGGCTTTGGAGGCG	TAAATTGAGAGCACAACGCAGTGTCAA	0.26	PRT
304	AM24460	ss161148452	A/G	GAAGGTGACCAAGTTCATGCTTAGATCAAGTCAGACACTGATTAACA	GAAGGTCGGAGTCAACGGATTAGATCAAGTCAGACACTGATTAACG	GATCTTGTTCTTTTTTCCTACCATAGTTAT	0.13	PRT
305	AM24486	ss161148478	A/T	GAAGGTGACCAAGTTCATGCTATTCATCTGAATCGGCGTTTGAGATAA	GAAGGTCGGAGTCAACGGATTCATCTGAATCGGCGTTTGAGATAT	CTGCCTTTATTGGTTAAGGTGATCACATA	0.10	PRT
306	AM24490	ss161148482	A/T	GAAGGTGACCAAGTTCATGCTGTGAGCGGATGACCCACATTACT	GAAGGTCGGAGTCAACGGATTGTGAGCGGATGACCCACATTACA	CATGTGAATGAAGTCGTGCGGCTAA	0.38	PR
307	AM24501	ss161148493	A/G	GAAGGTGACCAAGTTCATGCTCATCATCATCATACCCAGTGTATCCA	GAAGGTCGGAGTCAACGGATTATCATCATCATACCCAGTGTATCCG	TTCCCCAGACCCTGACCATAGATAT	0.24	PRT
308	AM24510	ss161148502	A/T	GAAGGTGACCAAGTTCATGCTTGATCAATAGTGGTGATCATTGTCTT	GAAGGTCGGAGTCAACGGATTCTTGATCAATAGTGGTGATCATTGTCTA	GAGCCTGCGTCATTTGAAAAACAAGATAT	0.09	PR
309	AM24515	ss161148507	A/T	GAAGGTGACCAAGTTCATGCTAAGCCTAATTTGCTGCAGGAATAGATA	GAAGGTCGGAGTCAACGGATTAAGCCTAATTTGCTGCAGGAATAGATT	TCAAAGAATGTTCTTCTGGGGTGTTTCTT	0.46	
310	AM24519	ss161148511	G/T	GAAGGTGACCAAGTTCATGCTCAAACAAGTTAAACTCATCGTCATGAG	GAAGGTCGGAGTCAACGGATTGCAAACAAGTTAAACTCATCGTCATGAT	GATAAGATATCTTCTGAGCAGACTGTGAT	0.10	PR
311	AM24531	ss161148523	C/T	GAAGGTGACCAAGTTCATGCTATACTTCTCCAAACATGAACTTGCTTC	GAAGGTCGGAGTCAACGGATTAAATACTTCTCCAAACATGAACTTGCTTT	GACTAAGTACAACGCATCAAAATCAAAGTT	0.32	P+RT
312	AM24579	ss161148571	A/T	GAAGGTGACCAAGTTCATGCTACATGCTTCTTGGTCAAATTATTGAAAATATA	GAAGGTCGGAGTCAACGGATTACATGCTTCTTGGTCAAATTATTGAAAATATT	CCTCTGTTTTAATCTGACGGAACCAAATT	0.37	PRT
313	AM24610	ss161148602	A/G	GAAGGTGACCAAGTTCATGCTAAAGTCATAAAGAAGGGAAATTTTAAGGAATA	GAAGGTCGGAGTCAACGGATTAGTCATAAAGAAGGGAAATTTTAAGGAATG	CTAATCTTTAAAGCCACCCAACTTATTCTA	0.26	PR
314	AM24615	ss161148607	A/G	GAAGGTGACCAAGTTCATGCTGGATATTTTCCCTTTCCACTGGAAGT	GAAGGTCGGAGTCAACGGATTGATATTTTCCCTTTCCACTGGAAGC	GAAATCGATCAAAAACACGAGCACGGA	0.31	P+RT
315	AM24646	ss161148638	A/G	GAAGGTGACCAAGTTCATGCTCAGTATATTTCGAGTTGATTCAATTATATCTTT	GAAGGTCGGAGTCAACGGATTAGTATATTTCGAGTTGATTCAATTATATCTTC	GGGATGCTTTCATCAATGATTGCTACTTT	0.34	P
316	AM24655	ss161148647	A/T	GAAGGTGACCAAGTTCATGCTGAATCTTCTCCAAATGAAAAGTTACTTCAAT	GAAGGTCGGAGTCAACGGATTGAATCTTCTCCAAATGAAAAGTTACTTCAAA	CAATTGTTAGGAACCCTTCAGGGGAT	0.26	PR
317	AM24661	ss161148653	C/T	GAAGGTGACCAAGTTCATGCTTGCACTTTGTGATTGTTTAACGATAAATC	GAAGGTCGGAGTCAACGGATTCTTGCACTTTGTGATTGTTTAACGATAAATT	GCCAAACATATGTTAGAGGCAACTTCAAT	0.22	PR
318	AM24699	ss161148691	A/T	GAAGGTGACCAAGTTCATGCTCAATAGGCGTCTTTTTATTTTTGGCTTTAT	GAAGGTCGGAGTCAACGGATTCAATAGGCGTCTTTTTATTTTTGGCTTTAA	TAATGTTCAAGTACTTGACTGCAGAGTCT	0.48	
319	AM24743	ss161148735	A/T	GAAGGTGACCAAGTTCATGCTCGCCATCATCATAAGTAGACACCT	GAAGGTCGGAGTCAACGGATTCGCCATCATCATAAGTAGACACCA	TGATACAAAACCTATGTATTACGGAACCAT	0.25	PRT
320	AM24766	ss161148758	A/G	GAAGGTGACCAAGTTCATGCTGAACTTAATTACAAGTTTTTTTAACCTCATACA	GAAGGTCGGAGTCAACGGATTAACTTAATTACAAGTTTTTTTAACCTCATACG	CGACCCTTTGTGCTTTACGAAAGAGAT	0.22	PRT
321	AM24776	ss161148768	C/T	GAAGGTGACCAAGTTCATGCTTGTATGAGTCTGAATAATAACAAAGTAGG	GAAGGTCGGAGTCAACGGATTCTTGTATGAGTCTGAATAATAACAAAGTAGA	CCCAAATCCTTATATTTGGCCACATCAAA	0.31	PR

322	AM24819	ss161148811	A/G	**GAAGGTGACCAAGTTCATGC**TGACAGGCATTAACCGTATTGACTCA	**GAAGGTCGGAGTCAACGGATT**ACAGGCATTAACCGTATTGACTCG	GGCTATTATTGTGGTAGAGGGAGCAA	0.40	PRT
323	AM24869	ss161148861	A/G	**GAAGGTGACCAAGTTCATGC**TGAGATTTGTTGTAATTATCTGTTTATTTGATGT	**GAAGGTCGGAGTCAACGGATT**AGATTTGTTGTAATTATCTGTTTATTTGATGC	GATAGCGTAACTACAAAACAATAGACAATA	0.26	PR
324	AM24909	ss161148901	G/T	**GAAGGTGACCAAGTTCATGC**TGACGGTTTAATAGACGGATCGGC	**GAAGGTCGGAGTCAACGGATT**AADACGGTTTAATAGACGGATCGGA	ACTCCCCTTCTTGAAATTCACTAAGACAA	0.26	PRT
325	AM24913	ss161148905	C/T	**GAAGGTGACCAAGTTCATGC**TCAAATCTTCCAAAGTCGTTGCAATTATAC	**GAAGGTCGGAGTCAACGGATT**CAAATCTTCCAAAGTCGTTGCAATTATAT	GATGTATTGGAGTCCTTTTGCATTGCATA	0.25	P
326	AM24924	ss161148916	C/T	**GAAGGTGACCAAGTTCATGC**TAACTTCGAGGAAATTCACTTCCTTTG	**GAAGGTCGGAGTCAACGGATT**AATAACTTCGAGGAAATTCACTTCCTTTA	GAACATCAGATGATGGCTATAATTGGAGAA	0.32	P+RT
327	AM24956	ss161148948	A/G	**GAAGGTGACCAAGTTCATGC**TCAAAAAATAATGGGTTCTGATTCAAGACAAT	**GAAGGTCGGAGTCAACGGATT**AAAAAATAATGGGTTCTGATTCAAGACAAC	TCGCCACCAAACATAACCAAATGACAAAT	0.21	P
328	AM24983	ss161148975	C/T	**GAAGGTGACCAAGTTCATGC**TGTTGGAGTAGTTCATTACGATAAGAG	**GAAGGTCGGAGTCAACGGATT**CGTTGGAGTAGTTCATTACGATAAGAA	GTTCAAATCTGGTTGGTGGATATGTTGAA	0.33	PR
329	AM25002	ss161148994	A/T	**GAAGGTGACCAAGTTCATGC**TACTCAATTTTGAACTTATAATCTTAATTCAATA	**GAAGGTCGGAGTCAACGGATT**ACTCAATTTTGAACTTATAATCTTAATTCAATT	CAATTAACTTAATGCGTTGCAGTAACTCAA	0.20	
330	AM25005	ss161148997	A/G	**GAAGGTGACCAAGTTCATGC**TATTGTGTAACAAATCAAAAAATTCAAATTCGA	**GAAGGTCGGAGTCAACGGATT**ATTGTGTAACAAATCAAAAAATTCAAATTCGG	GGTTTGAGCAGTCATAATCCTCAACTTTA	0.35	PR
331	AM25124	ss161149116	A/G	**GAAGGTGACCAAGTTCATGC**TAGTATGCTATGTCATAGGTGCCAATT	**GAAGGTCGGAGTCAACGGATT**GTATGCTATGTCATAGGTGCCAATC	CTCCACAACAAGATCTTTCCAAATTCGTT	0.26	PRT
332	AM25135	ss161149127	A/G	**GAAGGTGACCAAGTTCATGC**TCTTCTTTGATCTTGATTTATACCACCAT	**GAAGGTCGGAGTCAACGGATT**CTTCTTTGATCTTGATTTATACCACCAC	AAGAATTACGCTATCGTTGCTGGAACAAT	0.28	P+RT
333	AM25154	ss161149146	C/T	**GAAGGTGACCAAGTTCATGC**TGTCAGATTGGCACTCTTACCCG	**GAAGGTCGGAGTCAACGGATT**GTCAGATTGGCACTCTTACCCA	ATCTGGTCGAAGTAGCAGCCTGTT	0.10	PR
334	AM25192	ss161149184	A/G	**GAAGGTGACCAAGTTCATGC**TACAAGTTCATTAAGCAAAGACACAAACAT	**GAAGGTCGGAGTCAACGGATT**CAAGTTCATTAAGCAAAGACACAAACAAC	CCTGTTGTGCTGTGATGAAGAGACTT	0.25	PR
335	AM25224	ss161149216	A/G	**GAAGGTGACCAAGTTCATGC**TTATCTTGACCCTCAGTCCAAAATGTA	**GAAGGTCGGAGTCAACGGATT**ATCTTGACCCTCAGTCCAAAATGTG	TAGCATTTGGTCTTCGTGATGATGTCAAA	0.29	PRT
336	AM25236	ss161149228	A/G	**GAAGGTGACCAAGTTCATGC**TAGATATATCGAAACCCAATGAACCCT	**GAAGGTCGGAGTCAACGGATT**GATATATCGAAACCCAATGAACCCC	ACCAGCATAGCGACCCTTCAAAGTT	0.20	PRT
337	AM25241	ss161149233	C/G	**GAAGGTGACCAAGTTCATGC**TCATTTTGAATATCAAATGTGATCATATGGC	**GAAGGTCGGAGTCAACGGATT**CATTTTGAATATCAAATGTGATCATATGGG	CCTTTCTCTGACACACCAAAAATAAATCAA	0.50	
338	AM25249	ss161149241	A/G	**GAAGGTGACCAAGTTCATGC**TATAACAAAACTTGGACATGTACCATTATCT	**GAAGGTCGGAGTCAACGGATT**ACAAAACTTGGACATGTACCATTATCC	TTTGAAATGATGAACCCTATGTTACTTGGA	0.14	P
339	AM25261	ss161149253	A/G	**GAAGGTGACCAAGTTCATGC**TGTTGAAGCCAAAGATTCAGGTCGT	**GAAGGTCGGAGTCAACGGATT**GAAGCCAAAGATTCAGGTCGC	TCCTTCCTGACTGGCGTGCTCA	0.10	PRT
340	AM25268	ss161149260	A/G	**GAAGGTGACCAAGTTCATGC**TGATGATGAAGGAAAAGACTTATGTAGGAT	**GAAGGTCGGAGTCAACGGATT**GATGAAGGAAAAGACTTATGTAGGAC	AAAGGACTTATAATTAATGTTACGCTCCAT	0.26	PR
341	AM25292	ss161149284	A/G	**GAAGGTGACCAAGTTCATGC**TGGC	**GAAGGTCGGAGTCAACGGATT**GC	GAGAGACTTGCCATTTCCTACCCAT	0.26	PR

342	AM25309	ss161149301	A/G	TCTTAAAACAAGCCTCGACAAT **GAAGGTGACCAAGTTCATGC**TAAAACTATACTGAAAACTTACGCTATATAATTA	TCTTAAAACAAGCCTCGACAAC **GAAGGTCGGAGTCAACGGATT**AAAACTATACTGAAAACTTACGCTATATAATTG	CATGACTCTAAAAGGTTGTCATTGTAACAA	0.20	PR
343	AM25326	ss161149318	C/T	**GAAGGTGACCAAGTTCATGC**TGTAAATAGTCCCCATATGATATCTCG	**GAAGGTCGGAGTCAACGGATT**CTGTAAATAGTCCCCATATGATATCTCA	CACCTCAAGTACTCATGACAAATGTTCAA	0.26	PR
344	AM25340	ss161149332	A/T	**GAAGGTGACCAAGTTCATGC**TAGATTCGGGAACAACCTCAACCATT	**GAAGGTCGGAGTCAACGGATT**AGAATTCGGGAACAACCTCAACCATA	GTCATGGTCTTAAATTTACTTGGCGCAAA	0.24	PRT
345	AM25393	ss161149385	A/C	**GAAGGTGACCAAGTTCATGC**TATTTTTTGGTGATTACGAAAAAAGAGAAAAGT	**GAAGGTCGGAGTCAACGGATT**TTTGGTGATTACGAAAAAAGAGAAAAGG	GTGGTATTTTTTGGGCACGATACACATTA	0.29	P
346	AM25418	ss161149410	A/T	**GAAGGTGACCAAGTTCATGC**TGTGGGGTTTTTGTATCGTAAACTATCT	**GAAGGTCGGAGTCAACGGATT**GTGGGGTTTTTGTATCGTAAACTATCA	TCCTGGCTCATACGGATGCCTAAAA	0.10	PR
347	AM25474	ss161149466	C/T	**GAAGGTGACCAAGTTCATGC**TCATCCCAGAGAGGAGTGCTCC	**GAAGGTCGGAGTCAACGGATT**ACATCCCAGAGAGGAGTGCTCT	AGATCCTAACACCGTAGTGTCTTAACTAT	0.32	
348	AM25494	ss161149486	A/G	**GAAGGTGACCAAGTTCATGC**TGCGTATAAGCCAACTTGCTACCAA	**GAAGGTCGGAGTCAACGGATT**CGTATAAGCCAACTTGCTACCAG	TTCGCTTTAGGCTCTTAGGTTGGTTAAAT	0.18	PR
349	AM25497	ss161149489	A/G	**GAAGGTGACCAAGTTCATGC**TGTTAGTTTTGTAGAATCAAATGACAATGTCTT	**GAAGGTCGGAGTCAACGGATT**AGTTTTGTAGAATCAAATGACAATGTCTC	TCGACACTGATCTCCTCGGTAACAT	0.24	PRT
350	AM25548	ss161149540	C/T	**GAAGGTGACCAAGTTCATGC**TCAAATTTAGTTTATGTAAAATAACGATTCACG	**GAAGGTCGGAGTCAACGGATT**CAAATTTAGTTTATGTAAAATAACGATTCACA	GTAACCACGATCATCAATTTAAAAGTAGAA	0.46	P
351	AM25606	ss161149598	C/T	**GAAGGTGACCAAGTTCATGC**TAATATGATAATTTTGACCTTTGCAATGGAG	**GAAGGTCGGAGTCAACGGATT**AAAATATGATAATTTTGACCTTTGCAATGGAA	CATCCTCTGCACCAATAAGGCCAAA	0.24	PR
352	AM25631	ss161149623	G/T	**GAAGGTGACCAAGTTCATGC**TGTCGTTTAATGGAACCTTGATTACTC	**GAAGGTCGGAGTCAACGGATT**CGTCGTTTAATGGAACCTTGATTACTA	GGATAGTAAGATTGCATCAGGGATTGAAA	0.11	PRT
353	AM25708	ss161149700	C/T	**GAAGGTGACCAAGTTCATGC**TCGCTTCATGATGAGACGATCTC	**GAAGGTCGGAGTCAACGGATT**CTCGCTTCATGATGAGACGATCTT	GACACTTCATTTTTAGACCAAAAACGTATT	0.11	PR
354	AM25811	ss161149803	A/C	**GAAGGTGACCAAGTTCATGC**TAAAAGCCAAAACATTCATCAAAAAGAAACAA	**GAAGGTCGGAGTCAACGGATT**AAAGCCAAAACATTCATCAAAAAGAAACAC	TTGTCGGCAATTCTTCATTGTGTTTTAGAT	0.24	PRT
355	AM25919	ss161149911	A/G	**GAAGGTGACCAAGTTCATGC**TGTTATTGTTATGTATTCGAGGTGTAATTGT	**GAAGGTCGGAGTCAACGGATT**ATTGTTATGTATTCGAGGTGTAATTGC	CACAATATCTCTTTCAGCCATACCATCAA	0.25	PRT
356	AM25953	ss161149945	C/T	**GAAGGTGACCAAGTTCATGC**TTCATTTAAATTACAAAAATTACATTACATGCG	**GAAGGTCGGAGTCAACGGATT**CATTTAAATTACAAAAATTACATTACATGCA	ATGTGTATAAACACATCACAATACTCTCTA	0.38	
357	AM26018	ss161150010	C/G	**GAAGGTGACCAAGTTCATGC**TACGACTTACATTTAGTCGGAGGTG	**GAAGGTCGGAGTCAACGGATT**ACGACTTACATTTAGTCGGAGGTC	GAGTTAGGCCCTTATTAGCCACCAA	0.15	P
358	AM26133	ss161150125	A/C	**GAAGGTGACCAAGTTCATGC**TCAGGCAATGTGGCTGGTGATGAT	**GAAGGTCGGAGTCAACGGATT**AGGCAATGTGGCTGGTGATGAG	CTGCCTAAGTTTGCCTATCACACAGAT	0.36	PR
359	AM26171	ss161150163	C/T	**GAAGGTGACCAAGTTCATGC**TAGGCTTTCCAGCAACACTCGTG	**GAAGGTCGGAGTCAACGGATT**CAGGCTTTCCAGCAACACTCGTA	TGAGCATAGCTGACTAAATAACACTAACAA	0.38	PRT
360	AM26230	ss161150222	C/T	**GAAGGTGACCAAGTTCATGC**TTACATACCGAAATTGTTCAGAACCAC	**GAAGGTCGGAGTCAACGGATT**ATTACATACCGAAATTGTTCAGAACCAT	GAAGTTGAAGAGGAAGCTCAGGGAT	0.15	PRT
361	AM26438	ss161150430	C/T	**GAAGGTGACCAAGTTCATGC**TGAA	**GAAGGTCGGAGTCAACGGATT**GT	AACCTTCAATCTTCAACCATCTGCCAT	0.24	P

TAAATATTGAAGGTTGAACGTTGAAC | TGAATAAATATTGAAGGTTGAACGTTGAAT

#	AM	ss	SNP	Seq1	Seq2	Seq3	Val	Type
				TAAATATTGAAGGTTGAACGTTGAAC	TGAATAAATATTGAAGGTTGAACGTTGAAT			
362	AM26453	ss161150445	A/T	**GAAGGTGACCAAGTTCATGC**TAAAGTAGTAAATTTTGTAGGATTTTTGCTACT	**GAAGGTCGGAGTCAACGGATT**AAAGTAGTAAATTTTGTAGGATTTTTGCTACA	CAGTACAAAGCAACAAAAATCAATGAGGAA	0.19	PRT
363	AM26498	ss161150490	A/T	**GAAGGTGACCAAGTTCATGC**TGATTTGTTGCTGCTGGTTTGAGA	**GAAGGTCGGAGTCAACGGATT**CTGATTTGTTGCTGCTGGTTTGAGT	CAAACAACTCAGCAGAACCAGCACAA	0.24	PRT
364	AM27597	ss161151589	C/T	**GAAGGTGACCAAGTTCATGC**TTCCTGTTGTCCTTCAAGCCCC	**GAAGGTCGGAGTCAACGGATT**GTTCCTGTTGTCCTTCAAGCCCT	GCAAGTGCATGATAACATTGTGAAAGCTA	0.25	PRT
365	AM27602	ss161151594	A/G	**GAAGGTGACCAAGTTCATGC**TCCAGAATGGATCTGGTGGTCGT	**GAAGGTCGGAGTCAACGGATT**CAGAATGGATCTGGTGGTCGC	AGCTACTGGATACATTCTGACTTGTTGTT	0.08	PRT
366	AM27605	ss161151597	G/T	**GAAGGTGACCAAGTTCATGC**TAGAGTGTTTATAATGCAAATATTTGAGGTG	**GAAGGTCGGAGTCAACGGATT**GAAGAGTGTTTATAATGCAAATATTTGAGGTT	CGCTAACCTTGCATTAATGTGATGTTTCTA	0.29	PR
367	AM27606	ss161151598	C/G	**GAAGGTGACCAAGTTCATGC**TACTCTTTTGGCTATAACTTTTGATAGAAAC	**GAAGGTCGGAGTCAACGGATT**ACTCTTTTGGCTATAACTTTTGATAGAAAG	AGTTTAATTTCCAATACGCTAACCTTGCAT	0.10	PRT
368	AM27607	ss161151599	C/G	**GAAGGTGACCAAGTTCATGC**TTATAGGTGGTTGGACAACATGGC	**GAAGGTCGGAGTCAACGGATT**ATAGGTGGTTGGACAACATGGG	CCTACATACGTACCAAGTTGCATTTCTTA	0.26	PR+T
369	AM27609	ss161151601	A/G	**GAAGGTGACCAAGTTCATGC**TTGCTGACATTCACTATAAGTCCAACT	**GAAGGTCGGAGTCAACGGATT**GCTGACATTCACTATAAGTCCAACC	CATCTGGAGAAATGTTAAACTAATTTGCAT	0.17	PR
370	AM27610	ss161151602	A/T	**GAAGGTGACCAAGTTCATGC**TATTGTAGATATGTTAAATTTAGTTGGACTTATA	**GAAGGTCGGAGTCAACGGATT**GTAGATATGTTAAATTTAGTTGGACTTATT	GTATAAGCACCTTGTGTTTCTCCCATTAT	0.36	PR
371	AM27611	ss161151603	C/T	**GAAGGTGACCAAGTTCATGC**TAGGTTCTAAGATTATATTCACCAGCAG	**GAAGGTCGGAGTCAACGGATT**GAGGTTCTAAGATTATATTCACCAGCAA	CTTGTGTCTTTAGAGACCCTTC	0.36	PR
372	AM27612	ss161151604	C/T	**GAAGGTGACCAAGTTCATGC**TAATGATCGAACTATCAGCTCTGATAC	**GAAGGTCGGAGTCAACGGATT**AATTAATGATCGAACTATCAGCTCTGATAT	GTGCACCTCGTGTTTTTCCGATTCTT	0.21	PRT
373	AM27614	ss161151606	C/T	**GAAGGTGACCAAGTTCATGC**TCAAATTCAAAACTTAACAGTTGCCCG	**GAAGGTCGGAGTCAACGGATT**CCAAAATTCAAAACTTAACAGTTGCCCA	GTGAACAAGTAAATACCATGTGATCAAGTA	0.28	PRT
374	AM27615	ss161151607	C/G	**GAAGGTGACCAAGTTCATGC**TGAAAATTTATTCATAAGACAAACTACAAACAG	**GAAGGTCGGAGTCAACGGATT**GAAAATTTATTCATAAGACAAACTACAAACAC	TGCGCCTGTGAATCTGTGATGGTT	0.28	PRT
375	AM27616	ss161151608	A/G	**GAAGGTGACCAAGTTCATGC**TAACTTCCCTTAGAAAGAAATATCGTAT	**GAAGGTCGGAGTCAACGGATT**AACTTCCCTTAGAAAGAAATATCGTAC	GAGCCAAATGAGTTGGTGCAGAAGTT	0.39	PRT
376	AM27618	ss161151610	C/T	**GAAGGTGACCAAGTTCATGC**TGATTGTAAGGCTATCTATCAGCAACG	**GAAGGTCGGAGTCAACGGATT**AGATTGTAAGGCTATCTATCAGCAACA	GTAGGAATCTTTCTGCAAAGTAGTCTCTT	0.50	R
377	AM27621	ss161151613	G/T	**GAAGGTGACCAAGTTCATGC**TCAATTCTGTTGCTGATAGATAGCCTG	**GAAGGTCGGAGTCAACGGATT**ACAATTCTGTTGCTGATAGATAGCCTT	TTCTACAATGCTTCGAAGGAGGCGT	0.24	PRT
378	AM27622	ss161151614	C/T	**GAAGGTGACCAAGTTCATGC**TGATAGATAGCCTTACAATCTCAC	**GAAGGTCGGAGTCAACGGATT**GCTGATAGATAGCCTTACAATCTCAT	GGTTCCGATACAAAGACCTAAATACCAAA	0.44	
379	AM27626	ss161151618	A/C	**GAAGGTGACCAAGTTCATGC**TAGCACAATGTTACCTTCAATCTTGGAT	**GAAGGTCGGAGTCAACGGATT**GCACAATGTTACCTTCAATCTTGGAG	GTTCTTGCCCTTTGTCTCCATATTCTTT	0.41	PRT
380	AM27627	ss161151619	A/C	**GAAGGTGACCAAGTTCATGC**TAAGATTGAAGGTAACATTGTGCTGCA	**GAAGGTCGGAGTCAACGGATT**AGATTGAAGGTAACATTGTGCTGCC	GGACAACAACTCTTAGCAATGTAGAGAT	0.36	RT
381	AM27628	ss161151620	C/T	**GAAGGTGACCAAGTTCATGC**TGTAACATTGTGCTGCATTTAGCCTC	**GAAGGTCGGAGTCAACGGATT**GGTAACATTGTGCTGCATTTAGCCTT	GAAGGGGGACAACAACTCTTAGCAA	0.43	R
382	AM27630	ss161151622	C/T	**GAAGGTGACCAAGTTCATGC**TATA	**GAAGGTCGGAGTCAACGGATT**AA	GAAGGTCAAGGTCACCGTGTGAAAT	0.25	PRT

				TTTTAGGGAAATTTCATATGGCAACC	ATATATTTTAGGGAAATTTCATATGGCAACT		
383	AM27631	ss161151623	C/T	**GAAGGTGACCAAGTTCATGC**TCATATGAAATTTCCCTAAAATATATTTATGCG	**GAAGGTCGGAGTCAACGGATT**CCATATGAAATTTCCCTAAAATATATTTATGCA	GACTAATTCACTGGGAGTTGGGACAT	0.18	PR
384	AM27632	ss161151624	A/T	**GAAGGTGACCAAGTTCATGC**TACCCAATTTGAAACTTGCATCAAACGA	**GAAGGTCGGAGTCAACGGATT**ACCCAATTTGAAACTTGCATCAAACGT	CAATTAACGAATCGAATGGTCGGCCAA	0.37	PRT
385	AM27633	ss161151625	G/T	**GAAGGTGACCAAGTTCATGC**TGTTAAGGAGGGTAGTTACTCAGAAG	**GAAGGTCGGAGTCAACGGATT**GGTTAAGGAGGGTAGTTACTCAGAAT	CCACCCGTAACCGATCTAACCTAAA	0.18	PR
386	AM27634	ss161151626	C/T	**GAAGGTGACCAAGTTCATGC**TCCGGGTAACCTTTATTTAAGTTATTTAG	**GAAGGTCGGAGTCAACGGATT**GTCCGGGTAACCTTTATTTAAGTTATTTAA	GATCGGTTACGGGTGGCGTTATTAA	0.46	PR
387	AM27635	ss161151627	A/T	**GAAGGTGACCAAGTTCATGC**TGGAGGAATTTGCAACCTAATCTCGAT	**GAAGGTCGGAGTCAACGGATT**GGAGGAATTTGCAACCTAATCTCGAA	GATTTTGTAGAGAGAGTGAGTGGTGATTT	0.35	PR
388	AM27636	ss161151628	C/T	**GAAGGTGACCAAGTTCATGC**TACAAAACAATTATAATAAACTTCCCTTATCTTG	**GAAGGTCGGAGTCAACGGATT**ACAAAACAATTATAATAAACTTCCCTTATCTTA	GTGTTCTTACTTTGCATTAGTATTTGTGAT	0.30	P+R+T
389	AM27637	ss161151629	C/T	**GAAGGTGACCAAGTTCATGC**TGATTTTTCATCATCTGGGTATTTTGATAG	**GAAGGTCGGAGTCAACGGATT**AAATGATTTTTCATCATCTGGGTATTTTGATAA	GCAAATTAATTTGACTGTTTAACAGATAAA	0.20	PR
390	AM27642	ss161151634	A/G	**GAAGGTGACCAAGTTCATGC**TGTACACAAGTAATATATCAAATAGATGAATAA	**GAAGGTCGGAGTCAACGGATT**GTACACAAGTAATATATCAAATAGATGAATAG	CAAGCTAAGTAGCTGACACCAAAGCAT	0.42	
391	AM27645	ss161151637	A/G	**GAAGGTGACCAAGTTCATGC**TAAAGTATTAATTACATGAAAGGATTCGAAGAA	**GAAGGTCGGAGTCAACGGATT**AGTATTAATTACATGAAAGGATTCGAAGAG	CACAATATTCCTTTTGCAATTCCTCATCAT	0.26	PR
392	AM27650	ss161151642	A/T	**GAAGGTGACCAAGTTCATGC**TGAGCTTGGTTAATTTATAGATAAAATCGATGA	**GAAGGTCGGAGTCAACGGATT**GAGCTTGGTTAATTTATAGATAAAATCGATGT	CTTTGAAAATTATTCCATTGGAGGAGTTTT	0.20	P
393	AM27651	ss161151643	A/G	**GAAGGTGACCAAGTTCATGC**TTTCGTACGTTTCCGTGAGAGATTAAT	**GAAGGTCGGAGTCAACGGATT**CGTACGTTTCCGTGAGAGATTAAC	ATATGAACTGGACAATACTTGTGAATGTAT	0.13	PR
394	AM27652	ss161151644	A/G	**GAAGGTGACCAAGTTCATGC**TAACGTACGAAACATAACGCATGAAACA	**GAAGGTCGGAGTCAACGGATT**CGTACGAAACATAACGCATGAAACG	GCACAACTCGTGATTTAAAAAACTGACAAA	0.26	PR
395	AM27653	ss161151645	A/G	**GAAGGTGACCAAGTTCATGC**TGAAAAAAAGTGAAAAATTCTATTAGTATATTCA	**GAAGGTCGGAGTCAACGGATT**GAAAAAAAGTGAAAAATTCTATTAGTATATTCG	AATAGGACACTATTTTTAGTACGTT	0.39	PR
396	AM27654	ss161151646	C/G	**GAAGGTGACCAAGTTCATGC**TCCATAGTTGGCATCAACTTACTGC	**GAAGGTCGGAGTCAACGGATT**CCATAGTTGGCATCAACTTACTGG	CGTCTCCCATGAGACTTCCTGTAA	0.24	PT
397	AM27655	ss161151647	A/G	**GAAGGTGACCAAGTTCATGC**TATCAAAGTCCAACCCAAACAAAAATCAA	**GAAGGTCGGAGTCAACGGATT**CAAAGTCCAACCCAAACAAAAATCAG	GACGGTTGGTTTCCCAAGTAAAGGTT	0.33	
398	AM27656	ss161151648	A/C	**GAAGGTGACCAAGTTCATGC**TAACTTGATATTTATCCGATTTTATAATTGAAA	**GAAGGTCGGAGTCAACGGATT**AACTTGATATTTATCCGATTTTATAATTGAAC	CGATTTAAAATCGTCTTATGTATCCACATT	0.28	PR
399	AM27658	ss161151650	A/G	**GAAGGTGACCAAGTTCATGC**TATCATCTTTCTCATCGACAAAATAAACACA	**GAAGGTCGGAGTCAACGGATT**CATCTTTCTCATCGACAAAATAAACACG	GAGGTCTGTCGTGAGCTTCAAAGAA	0.33	PR
400	AM16690	ss161140682	A/C	**GAAGGTGACCAAGTTCATGC**TGTATTAGTATGATTAGACGTCTTGGTGTA	**GAAGGTCGGAGTCAACGGATT**AGTATGATTAGACGTCTTGGTGTC	CGAAATGCTAATACAACTAATAATACACAA	0.44	PR (NTP)
401	AM18129	ss161142121	A/T	**GAAGGTGACCAAGTTCATGC**TTTATTTGATACAATTTACTTACTTGATAC	**GAAGGTCGGAGTCAACGGATT**TATTTGATACAATTTACTTACTTGATA	TGAGACATCAAAGCCTATCATATCAAGAAA	0.32	PRT (NTP)

				AAT	CAAA			
402	AM19874	ss161143866	C/T	**GAAGGTGACCAAGTTCATGC**TCATTTTCTTATTTGGAAATGAATACCATCG	**GAAGGTCGGAGTCAACGGATT**ATCATTTTCTTATTTGGAAATGAATACCATCA	GGTTTTGTTTGTTTGAGAGAATAAATCAAA	0.22	(NTP)
403	AM20217	ss161144209	A/G	**GAAGGTGACCAAGTTCATGC**TGGATTTCTTCCGCTTGGACATCTTAT	**GAAGGTCGGAGTCAACGGATT**TCTTCCGCTTGGACATCTTAC	CGGATTTTTGTTGGCCCTCCTCTTT	0.37	PRT (NTP)
404	AM20931	ss161144923	A/G	**GAAGGTGACCAAGTTCATGC**TCGAAACCGAAACCGACCCACTA	**GAAGGTCGGAGTCAACGGATT**GAAACCGAAACCGACCCACTG	GGTCCAATCGAGTACGGGTTTGTAT	0.41	PRT (NTP)
405	AM22074	ss161146066	A/G	**GAAGGTGACCAAGTTCATGC**TTCCTGGAAGCCAAAATCTTCGACT	**GAAGGTCGGAGTCAACGGATT**CCTGGAAGCCAAAATCTTCGACC	CCAGAGAAGGGGGAGGTGGAA	0.10	PRT (NTP)
406	AM22693	ss161146685	A/C	**GAAGGTGACCAAGTTCATGC**TGATTATAATTATAACTGATTTTAACAGATTTTT	**GAAGGTCGGAGTCAACGGATT**ATAATTATAACTGATTTTAACAGATTTTG	AACAGTCGGGGAAGAGAGGGAAAAA	0.28	PRT (NTP)
407	AM25194	ss161149186	A/C	**GAAGGTGACCAAGTTCATGC**TTGAAATAATTAAGTCACTTTTGATCAAAACAA	**GAAGGTCGGAGTCAACGGATT**GAAATAATTAAGTCACTTTTGATCAAAACAC	GCCTAAGTTGTTCTAACTTTCTATAGCTTA	0.20	PR (NTP)
408	AM18897	ss161142889	C/T	**GAAGGTGACCAAGTTCATGC**TTATTCATGAAAGGATTCATAAATGATGGC	**GAAGGTCGGAGTCAACGGATT**AATTTATTCATGAAAGGATTCATAAATGATGGT	GTGGACACGCAAGCCGAACTAATTA	NT	NTD
409	AM19664	ss161143656	A/G	**GAAGGTGACCAAGTTCATGC**TAATAAGAATACCAGTGTTCCAGCTCT	**GAAGGTCGGAGTCAACGGATT**ATAAGAATACCAGTGTTCCAGCTCC	ACGGTGTCATCGTAACTTGCTATATCAAA	NT	NTD
410	AM19665	ss161143657	G/T	**GAAGGTGACCAAGTTCATGC**TCAGAGTCAGAGCTGGAACACG	**GAAGGTCGGAGTCAACGGATT**CCAGAGTCAGAGCTGGAACACT	CACCCAATGGATAGCGACAGTGAAT	NT	NTD
411	AM19986	ss161143978	A/G	**GAAGGTGACCAAGTTCATGC**TCAAAAGGCAATTGGGTGCACAAAGT	**GAAGGTCGGAGTCAACGGATT**AAAAGGCAATTGGGTGCACAAAGC	TATTGAGGGTCTCTTCTCCGGAGA	NT	NTD
412	AM20218	ss161144210	C/T	**GAAGGTGACCAAGTTCATGC**TAACCATGTTTGGTATAGCATCTCAG	**GAAGGTCGGAGTCAACGGATT**GTTAACCATGTTTGGTATAGCATCTCAA	AAGCGGAAGAAATCCAAAGTCTACCTTT	NT	NTD
413	AM20387	ss161144379	C/T	**GAAGGTGACCAAGTTCATGC**TGAAGAAATTCAAGATGATGATAGGGAG	**GAAGGTCGGAGTCAACGGATT**GAAGAAATTCAAGATGATGATAGGGAA	CATCATGGCAATACTTCCTGACAAGAAA	NT	NTD
414	AM20538	ss161144530	C/T	**GAAGGTGACCAAGTTCATGC**TGATACATCTTGGCAATTTAATACAAGTTC	**GAAGGTCGGAGTCAACGGATT**AATTGATACATCTTGGCAATTTAATACAAGTTT	CGAATTATGAATTGTATCAATCTTATGAAA	NT	NTD
415	AM20599	ss161144591	C/T	**GAAGGTGACCAAGTTCATGC**TGTAACATTACATAACAAACGCTTTCTAC	**GAAGGTCGGAGTCAACGGATT**CTGTAACATTACATAACAAACGCTTTCTAT	CTCACAATGGCTTTCAATCCATGATTTAAA	NT	NTD
416	AM20791	ss161144783	C/T	**GAAGGTGACCAAGTTCATGC**TACGTGAAACTTTAAAAGCCAATTTTTCTG	**GAAGGTCGGAGTCAACGGATT**CACCGTGAAACTTTAAAAGCCAATTTTTCTA	CGTGGTCTTTGCAATTAGTTTTTTCTGTTA	NT	NTD
417	AM20792	ss161144784	G/T	**GAAGGTGACCAAGTTCATGC**TGGCTTTTAAAGTTTCACGTGATAAATTTG	**GAAGGTCGGAGTCAACGGATT**AATTGGCTTTTAAAGTTTCACGTGATAAATTTT	TGCTTGGAAAAAAATAATTTATTGCTTGTT	NT	NTD
418	AM20930	ss161144922	C/G	**GAAGGTGACCAAGTTCATGC**TGGTTTGTATCGGGTCAATACCATAG	**GAAGGTCGGAGTCAACGGATT**GGTTTGTATCGGGTCAATACCATAC	CCCGATACCGTCTATACTAAAATGGATAT	NT	NTD
419	AM20979	ss161144971	A/G	**GAAGGTGACCAAGTTCATGC**TAAATATTTGAATGATGGGTTTCTTATATGTCAT	**GAAGGTCGGAGTCAACGGATT**ATTTGAATGATGGGTTTCTTATATGTCAC	GCATTTGGCAAGCCACATTTATCTGATT	NT	NTD

Supplemental Table S2. *Eco*RI and *Bfa*I adapter and primer sequences.
Each MID-barcode carries a unique barcode sequences (bolded).

Ligation Adapters	
*Eco*RI adapter1 (F)	5'/5BioTEG/-CTCGTAGACTGCGTACC
*Eco*RI adapter2 (R)	CATCTGACGCATGGTTAA-/5Phos/5'
*Bfa*I adapter1 (F)	5'-GACGATGAGTCCTGAG
*Bfa*I adapter2 (R)	ACTCAGGACTCAT-/5Phos/5'

MID-barcode primers pairs	Sequence (5'→3')	
	*Eco*RI	*Bfa*I
MID1	**ACGAGTGCGT**GACTGCGTACCAATTC	**ACGAGTGCGT**GATGAGTCCTGAGTA
MID2	**ACGCTCGACA**GACTGCGTACCAATTC	**ACGCTCGACA**GATGAGTCCTGAGTA
MID3	**AGACGCACTC**GACTGCGTACCAATTC	**AGACGCACTC**GATGAGTCCTGAGTA
MID4	**AGCACTGTAG**GACTGCGTACCAATTC	**AGCACTGTAG**GATGAGTCCTGAGTA
MID5	**ATCAGACACG**GACTGCGTACCAATTC	**ATCAGACACG**GATGAGTCCTGAGTAG
MID6	**ATATCGCGAG**GACTGCGTACCAATTC	**ATATCGCGAG**GATGAGTCCTGAGTAG
MID7	**CGTGTCTCTA**GACTGCGTACCAATTC	**CGTGTCTCTA**GATGAGTCCTGAGTAG
MID8	**CTCGCGTGTC**GACTGCGTACCAATTC	**CTCGCGTGTC**GATGAGTCCTGAGTAG

Supplemental Table S3. Quinoa SNP marker information.

Includes SNP marker name, GenBank dbSNP accession ID, polymorphism type, KASPar™ primer sequences (A1, A2 and Common Reverse), minor allele frequency (MAF), linkage group (LG; Figure 4) and position in centiMorgan for all 511 functional SNP assays tested sorted on linkage group and position.

[†]dbSNP in GenBank under the handle MAUGHAN in batch number 2012A, build B138.

[‡]KASPar™ primers: A1 are A2 primers are SNP allele specific. Note that the first 21 bases of the primers (bolded) are the sequence tags used in the KASPar™ secondary PCR reaction.

[§]Minor allele frequency (MAF) values presented were calculated based on the 113 *C. quinoa* accessions; NT = Not tested on the diversity panel.

[¶]Linkage Group; NM = Not Mapped.

SNP ID	GenBank SS #[†]	SNP type	A1 primer (5'→3')[‡]	A2 primer (5'→3')[‡]	Common reverse primer (5'→3')[‡]	MAF[§]	LG	Position (cM)
Cq07160_1275	530859972	G/T	**GAAGGTGACCAAGTTCATGCT**TAATGATCTTGTAATCAAATTCTACCAGC	**GAAGGTCGGAGTCAACGGATT**CATTAATGATCTTGTAATCAAATTCTACCAGA	CCAGGATCAATGTACAACGCACGTT	0.3	1	0.00
Cq08741_1131	530860128	G/T	**GAAGGTGACCAAGTTCATGCT**GTTATGATCGATAAATAACTTAGCTAACAG	**GAAGGTCGGAGTCAACGGATT**AAGTTATGATCGATAAATAACTTAGCTAACAT	CATTCTCCCAATATTTAATAAGGTAGGGAT	0.29	1	5.60
Cq04771_845	530859767	A/T	**GAAGGTGACCAAGTTCATGCT**AGATGTCAACTATTTTAGTTGATTGAAATCT	**GAAGGTCGGAGTCAACGGATT**AGATGTCAACTATTTTAGTTGATTGAAATCA	GAAGTGTACGAGATTCATTCCAAGTGATA	0.29	1	8.84
Cq07565_986	530860014	C/T	**GAAGGTGACCAAGTTCATGCT**TTGAACAATAAAATCAAACTTTATATTGACTG	**GAAGGTCGGAGTCAACGGATT**TGAACAATAAAATCAAACTTTATATTGACTA	GTATTCAATTGTCTTCTAAACATACACGAA	0.5	1	20.47
Cq07990_1447	530860062	A/T	**GAAGGTGACCAAGTTCATGCT**GAGGTGCATGTATATATGTACTTCAAGA	**GAAGGTCGGAGTCAACGGATT**GAGGTGCATGTATATATGTACTTCAAGT	ATCTCAACTCCATGCTCAACACATACAT	0.29	1	22.01
Cq05004_868	530859783	A/C	**GAAGGTGACCAAGTTCATGCT**CCCTGAAGCTATTTCTACCAATGCAT	**GAAGGTCGGAGTCAACGGATT**CCTGAAGCTATTTCTACCAATGCAG	GCCTCCTCACCCTATGCTGGTA	0.29	1	22.71
Cq01312	530859433	A/G	**GAAGGTGACCAAGTTCATGCT**TGGATTACTGATACACGGTCCACA	**GAAGGTCGGAGTCAACGGATT**ACTGATACACGGTCCACG	CAAAGTCTTGAGTATCGAATAACCAAGCTT	0.3	1	24.35
Cq07822_1014	530860049	A/C	**GAAGGTGACCAAGTTCATGCT**ATCTTTACCTCACCATCACAGTAACAT	**GAAGGTCGGAGTCAACGGATT**CTTTACCTCACCATCACAGTAACAG	GTTGCAAGTGTGGAGCGCTTAAGTT	0.27	1	25.62
Cq06292_1096	530859872	C/T	**GAAGGTGACCAAGTTCATGCT**GGAAAGTGGGTCATCAAGGGTC	**GAAGGTCGGAGTCAACGGATT**CGGAAAGTGGGTCATCAAGGGTT	TACAAGCTTATCTGCCATTTTTTTGGTTTT	0.01	1	29.02
Cq05564_663	530859820	C/T	**GAAGGTGACCAAGTTCATGCT**GTTTTGAAAAGTGAAATGATGACACGG	**GAAGGTCGGAGTCAACGGATT**GTTTTGAAAAGTGAAATGATGACACGA	GGACATTTCAAATACCATGTCCAACGTTA	0.21	1	31.04
Cq05440_657	530859813	A/G	**GAAGGTGACCAAGTTCATGCT**ATCATTTCCTTTAGAATATAGTAGTCAAATGTA	**GAAGGTCGGAGTCAACGGATT**CATTTCCTTTAGAATATAGTAGTCAAATGTG	AACTGTCGACTCTTGTATCTAAACAATGAA	0.25	1	35.82
Cq01610_260	530859457	A/T	**GAAGGTGACCAAGTTCATGCT**GAAATTATGTTCTATACTAAAGGAAATGCAAA	**GAAGGTCGGAGTCAACGGATT**GAAATTATGTTCTATACTAAAGGAAATGCAAT	TGGAGGTATTTTAACAACACATGTATTCAT	0.17	1	39.16

Cq10144_1722	530860172	A/G	**GAAGGTGACCAAGTTCATGCT**CGGGTGAACGCAGAAGGTTGTTT	**GAAGGTCGGAGTCAACGGATT**GGGTGAACGCAGAAGGTTGTTC	CTGGACTGGAAGCTTCGTCTTCTTT	NT	1	39.74
Cq06314_1104	530859879	C/T	**GAAGGTGACCAAGTTCATGCT**GTGACATTATATTTATAGTAATTGTCCCAG	**GAAGGTCGGAGTCAACGGATT**CTGTGACATTATATTTATAGTAATTGTCCCAA	CCCTCCACACACGGAATAAGAGATT	NT	1	39.87
Cq01459_296	530859440	A/C	**GAAGGTGACCAAGTTCATGCT**CGATTTTACCAATTATTTGTGAAATTATCAACA	**GAAGGTCGGAGTCAACGGATT**TTACCAATTATTTGTGAAATTATCAACC	CTATAGATTAGCCCCCCATTCCCAA	0.02	1	39.98
Cq01538	530859449	A/G	**GAAGGTGACCAAGTTCATGCT**CGGAAATTTTATGTAGAACTACTTTAAAGATAA	**GAAGGTCGGAGTCAACGGATT**GGAAATTTTATGTAGAACTACTTTAAAGATAG	GTAGTGTTACCCAAACGTTTCCAAACTTA	0.34	1	40.10
Cq00020_1	530859297	A/C	**GAAGGTGACCAAGTTCATGCT**AAAAAATAATGTATTATAATTTGGACTTTCT	**GAAGGTCGGAGTCAACGGATT**CTAAAAAATAATGTATTATAATTTGGACTTTCG	CGAATTAAAATTTGGTTATTTGGATCCGAT	0.31	1	40.12
Cq00528_99	530859352	C/T	**GAAGGTGACCAAGTTCATGCT**ATTGTTTTGAACATGGCCTTGAGGG	**GAAGGTCGGAGTCAACGGATT**AATTGTTTTGAACATGGCCTTGAGGA	GAAGGGTGACCCGAGTTTGGCTA	0.5	1	40.25
Cq01825_354	530859482	A/C	**GAAGGTGACCAAGTTCATGCT**CATACGGGAAACATCGATTGTGACAT	**GAAGGTCGGAGTCAACGGATT**ATACGGGAAACATCGATTGTGACAG	GGTCATCCTTTCATTCAGTCAAAGCTATA	0.39	1	40.25
Cq06203_738	530859863	C/T	**GAAGGTGACCAAGTTCATGCT**AGTTTGGAGAAAACTTACATAGATCGG	**GAAGGTCGGAGTCAACGGATT**AAGTTTGGAGAAAACTTACATAGATCGA	CGCTCAAATTTGTTGCAAATAAAAGCTCAT	NT	1	40.35
Cq01160_249	530859419	A/G	**GAAGGTGACCAAGTTCATGCT**CAATAGTTTTGCCTTACCACGGCA	**GAAGGTCGGAGTCAACGGATT**AATAGTTTTGCCTTACCACGGCG	GGCAGAAGCATTCCAGGTTATAGGTT	0.07	1	40.61
Cq04810_851	530859769	A/G	**GAAGGTGACCAAGTTCATGCT**ACCCCATTCGACGGCCCCA	**GAAGGTCGGAGTCAACGGATT**ACCCATTCGACGGCCCCG	CGAGGCTCTGGTCGCCGTGTT	0.4	1	41.35
Cq02091_392	530859510	A/T	**GAAGGTGACCAAGTTCATGCT**CAAATCTAATTGCATAGCATTAAATCAATCAAT	**GAAGGTCGGAGTCAACGGATT**CAAATCTAATTGCATAGCATTAAATCAATCAAA	AGGGGTAATTTATGATTGTTGATTTTCATT	0.29	1	42.07
Cq02559_492	530859563	G/T	**GAAGGTGACCAAGTTCATGCT**GTTATTGATTATGAACATATATGACATATAGAG	**GAAGGTCGGAGTCAACGGATT**GTTATTGATTATGAACATATATGACATATAGAT	CATAATGATCACAACATAGGTTCATAATAA	0.15	1	43.60
Cq08688_1577	530860125	C/T	**GAAGGTGACCAAGTTCATGCT**GAAGAGTCCATTCATGAGAGGGC	**GAAGGTCGGAGTCAACGGATT**ATGAAGAGTCCATTCATGAGAGGGA	AGCATCGTTGTAACCCTTCTTTGTCATTA	0.17	1	44.13
Cq05414_656	530859811	A/C	**GAAGGTGACCAAGTTCATGCT**AATTCAATATAAACAACACTTCATACATAATTA	**GAAGGTCGGAGTCAACGGATT**AATTCAATATAAACAACACTTCATACATAATTC	GTGTGTATATGTATATGGGCTTGATTGTAA	NT	1	46.33
Cq00418_77	530859341	A/T	**GAAGGTGACCAAGTTCATGCT**CCTAAGTACACGATCGCTCCAT	**GAAGGTCGGAGTCAACGGATT**CCTAAGTACACGATCGCTCCAA	CACAGTATTCTGCTAAGCGTCGCTA	NT	1	46.46
Cq01254_265	530859426	C/T	**GAAGGTGACCAAGTTCATGCT**GGGTCAGGAAGATGGAAGTTGG	**GAAGGTCGGAGTCAACGGATT**ATAGGGTCAGGAAGATGGAAGTTGA	GAAGAGCTAACCAAAGAAGAACTCTGATT	0.41	1	46.79
Cq04851_600	530859778	G/T	**GAAGGTGACCAAGTTCATGCT**GTGAATTATGGACAATAAATTAGTTGTCAG	**GAAGGTCGGAGTCAACGGATT**CAGTGAATTATGGACAATAAATTAGTTGTCAT	AGACATTTTTCACCCCCATTATCCAACTT	0.42	1	47.55
Cq05729_676	530859831	A/G	**GAAGGTGACCAAGTTCATGCT**GGTACACCTTTTATCATCTATTATTGACA	**GAAGGTCGGAGTCAACGGATT**GGTACACCTTTTATCATCTATTATTGACG	ACTAATCTGACATTCAGACAGCTGCATAT	0.31	1	48.66
Cq07631_1384	530860021	G/T	**GAAGGTGACCAAGTTCATGCT**CTCCTGCAGTTCCGAGCTAC	**GAAGGTCGGAGTCAACGGATT**CTCTCCTGCAGTTCCGAGCTAA	GCTTTGTCTTGGCCTTAGCGGATTT	0.45	1	52.61
Cq08105_1485	530860079	A/G	**GAAGGTGACCAAGTTCATGCT**GACCTATGATGCTACTTTTGATCATCTT	**GAAGGTCGGAGTCAACGGATT**ACCTATGATGCTACTTTTGATCATCTC	TAGTCCTCTCCTTCTGATAGGTTTGATTA	0.3	1	54.61

Cq08392_1541	530860100	A/G	**GAAGGTGACCAAGTTCATGCT**GCGGGGGACCTTGACATCGA	**GAAGGTCGGAGTCAACGGATT**CGGGGGACCTTGACATCGG	AAGTCAACGCCGGAATAATTTGGTCAAT	NT	1	62.77
Cq01616_261	530859459	A/G	**GAAGGTGACCAAGTTCATGCT**ATTGTCGAGTTCTGCATTAATTAGCTAAT	**GAAGGTCGGAGTCAACGGATT**GTCGAGTTCTGCATTAATTAGCTAAC	GCAACTACGAAAGTCACAAGTCTATGATA	0.34	1	72.00
Cq07496_1352	530860002	C/T	**GAAGGTGACCAAGTTCATGCT**AACAATAATAGAAGCCAATTAAGGATCTAC	**GAAGGTCGGAGTCAACGGATT**GTAACAATAATAGAAGCCAATTAAGGATCTAT	CTGCACTGCCCTTTTCAATTGCTGAA	NT	1	75.09
Cq01718_265	530859463	A/G	**GAAGGTGACCAAGTTCATGCT**ATTACTCTGTAGCTTAGATAACATAAATGTAT	**GAAGGTCGGAGTCAACGGATT**ACTCTGTAGCTTAGATAACATAAATGTAC	GTGGTTATAACTTATAATTTCTCTTCTTAT	0.06	1	77.47
Cq02386_351	530859540	A/G	**GAAGGTGACCAAGTTCATGCT**ACAGAACTGCGTCTTGCCAAACTT	**GAAGGTCGGAGTCAACGGATT**CAGAACTGCGTCTTGCCAAACTC	CACATCAGTGCTTGATTTTGCCGAGAA	0.37	1	93.10
Cq00607_126	530859361	A/G	**GAAGGTGACCAAGTTCATGCT**GGCGGTAACTTCGACTACATCGT	**GAAGGTCGGAGTCAACGGATT**GCGGTAACTTCGACTACATCGC	AATGAGCCGGAGTGAATCTCCCAAA	0.44	1	94.13
Cq02543_366	530859559	A/T	**GAAGGTGACCAAGTTCATGCT**GACAGAACAACCAAGCTAAGGTTATTA	**GAAGGTCGGAGTCAACGGATT**GACAGAACAACCAAGCTAAGGTTATTT	CCGTACCTTGCAACGTCCTTGATTA	0.19	1	94.18
Cq02090_391	530859508	C/T	**GAAGGTGACCAAGTTCATGCT**AAAGCTCATTATTCTTTCTAAAGAAATGATAG	**GAAGGTCGGAGTCAACGGATT**GAAAGCTCATTATTCTTTCTAAAGAAATGATAA	GGACAATTTCTGTCCAGAAACTATGCAAA	0.24	1	96.61
Cq00394_77	530859338	A/T	**GAAGGTGACCAAGTTCATGCT**TCAATTCAGTAAAAATATTTAAAAAAGGAAAA	**GAAGGTCGGAGTCAACGGATT**CAATTCAGTAAAAATATTTAAAAAAGGAAAT	GTTGCAATTTCAAAATTTAAATAGCTGCAA	NT	1	100.54
Cq09813_1679	530860162	A/C	**GAAGGTGACCAAGTTCATGCT**GTAGGCGATCAAAGAGAAATAGAAGA	**GAAGGTCGGAGTCAACGGATT**GTAGGCGATCAAAGAGAAATAGAAGC	CACCTGGTTTTTTCTGATTGCATCAAGTT	0.44	1	101.00
Cq02997	530859593	C/T	**GAAGGTGACCAAGTTCATGCT**ATGATAATATAAGATAGGATACCTGAAGTG	**GAAGGTCGGAGTCAACGGATT**AATGATAATATAAGATAGGATACCTGAAGTA	GAAGCCAGTTCATGGTGCTCTTGTT	0.39	1	103.56
Cq07632_994	530860023	G/T	**GAAGGTGACCAAGTTCATGCT**GCAACTACTCATGGTATCCATAGC	**GAAGGTCGGAGTCAACGGATT**TGCAACTACTCATGGTATCCATAGA	CTTCCCTTCCCCAACTATATATTTGAGAT	0.3	1	112.31
Cq01509_310	530859442	C/T	**GAAGGTGACCAAGTTCATGCT**GGATTATGTAAAAGATTTAATGTTACATACG	**GAAGGTCGGAGTCAACGGATT**CTGGATTATGTAAAAGATTTAATGTTACATACA	GGAGTAGTAAATTAGTACTCCTTAATACTA	NT	2	0.00
Cq04110	530859693	C/T	**GAAGGTGACCAAGTTCATGCT**AATTATTGACGATAAGCCAAATAAACTCG	**GAAGGTCGGAGTCAACGGATT**GAATTATTGACGATAAGCCAAATAAACTCA	GTCATACCAATTGCATCAAAGTTAGCCAA	0.06	2	3.26
Cq09225_1634	530860148	A/C	**GAAGGTGACCAAGTTCATGCT**GTGTATAAAGATTATTTGGGAATTGTTGGT	**GAAGGTCGGAGTCAACGGATT**GTATAAAGATTATTTGGGAATTGTTGGG	GTCAAGCAAGGACAACTCTTCGCAA	0.3	2	5.36
Cq06944_1247	530859953	G/T	**GAAGGTGACCAAGTTCATGCT**AGTTTATCTAATAAGCTAAAAACCTTAGTAG	**GAAGGTCGGAGTCAACGGATT**GTAGTTTATCTAATAAGCTAAAAACCTTAGTAT	CCCATGTTTACAGCAAATTACCATATCCAT	0.26	2	16.62
Cq07543_1366	530860009	A/T	**GAAGGTGACCAAGTTCATGCT**GGAAGGTATATGTGAATGTGGAAGGT	**GAAGGTCGGAGTCAACGGATT**GGAAGGTATATGTGAATGTGGAAGGA	GGGTTCATCTTATTCCCAAAAATTTCCATA	0.37	2	19.12
Cq06822_1226	530859933	G/T	**GAAGGTGACCAAGTTCATGCT**CAATCAAAGCATTATCTGATGAGTCTG	**GAAGGTCGGAGTCAACGGATT**GCAATCAAAGCATTATCTGATGAGTCTT	GTCATTCTTAAACGATGTTATCTTTGTCAA	0.49	2	20.52
Cq04222_751	530859709	C/T	**GAAGGTGACCAAGTTCATGCT**AGGAGAGAGAAAGAGGAGATACG	**GAAGGTCGGAGTCAACGGATT**GAGGGAGAGAGAAAGAGGAGATACA	CTTATTTCCCTACACTCTCCTCTGATTT	0.29	2	25.67

Cq04197_543	530859706	A/T	**GAAGGTGACCAAGTTCATGCT**GTAGCAAGTTCAGATTGGAATTTGTGA	**GAAGGTCGGAGTCAACGGATT**GTAGCAAGTTCAGATTGGAATTTGTGT	GGCAAACTCTCTTCGATACAACCTATTAT	0.11	2	33.12
Cq04415_792	530859737	C/T	**GAAGGTGACCAAGTTCATGCT**TAATTATGTGATTGCATGTTTAGTTACTTTAG	**GAAGGTCGGAGTCAACGGATT**AATTATGTGATTGCATGTTTAGTTACTTTAA	ACTACACGGAATGAAACTCGCCCAA	NT	2	34.49
Cq04519_805	530859743	A/G	**GAAGGTGACCAAGTTCATGCT**TATTGCAATATATATAACTACATCATTGCACA	**GAAGGTCGGAGTCAACGGATT**GCAATATATATAACTACATCATTGCACG	CCTTGTCTAAGATGGATAATATACACGGTA	0.34	2	40.48
Cq04579_819	530859751	G/T	**GAAGGTGACCAAGTTCATGCT**CAAAACTTCATGGACTCTTCGCAG	**GAAGGTCGGAGTCAACGGATT**CCAAAACTTCATGGACTCTTCGCAT	GATGTAACTCGTTCCCTTACAAGTGTATT	0.29	2	41.92
Cq07068_1264	530859963	A/T	**GAAGGTGACCAAGTTCATGCT**AGGAACCATAGAGAGCTCCTTCT	**GAAGGTCGGAGTCAACGGATT**AGGAACCATAGAGAGCTCCTTCA	ACCGGCGTCATTTTTGAGCCGTTTT	0.31	2	43.17
Cq04171_540	530859702	G/T	**GAAGGTGACCAAGTTCATGCT**GACCTGGTAACACAACAGCGAG	**GAAGGTCGGAGTCAACGGATT**AGACCTGGTAACACAACAGCGAT	GCAATGTCAAACCATTAAGTTCAACGTTAA	0.3	2	43.94
Cq08101_1476	530860076	G/T	**GAAGGTGACCAAGTTCATGCT**CATTGTGGTTGATTGGCTCAAGG	**GAAGGTCGGAGTCAACGGATT**CTCATTGTGGTTGATTGGCTCAAGT	AGTCACACAATGAGTCAAGAACACCAA	0.29	2	48.48
Cq00230_43	530859317	C/T	**GAAGGTGACCAAGTTCATGCT**AAGTGTGGAACTTAGCTTATAC	**GAAGGTCGGAGTCAACGGATT**CTGCTAAGTGTGGAACTTAGCTTATAT	CGACTGTTGTTGCTCTGGGAAACAT	0.36	2	50.02
Cq06322_773	530859882	A/G	**GAAGGTGACCAAGTTCATGCT**TGCCAAATCCGAGCTCAATTTGAAAT	**GAAGGTCGGAGTCAACGGATT**GCCAAATCCGAGCTCAATTTGAAAC	CCGTAAGAGGTTTTAGGGGTCACTT	0.29	2	51.84
Cq03054	530859597	A/T	**GAAGGTGACCAAGTTCATGCT**AAATGAAATCTTTGTATGTGGTTTTGAGAAAT	**GAAGGTCGGAGTCAACGGATT**AAATGAAATCTTTGTATGTGGTTTTGAGAAAA	GCTCATCAAGTAGCCATAATAATTAATAAT	0.09	2	52.18
Cq03683	530859656	A/G	**GAAGGTGACCAAGTTCATGCT**GGCTATTAAATACCAGCGGTACTCAA	**GAAGGTCGGAGTCAACGGATT**GCTATTAAATACCAGCGGTACTCAG	CTTTTGAGCAACAGCAGGCGGCAT	0.28	2	56.11
Cq02458_484	530859556	G/T	**GAAGGTGACCAAGTTCATGCT**CCTTCTCTTTCGAGTTTATAGC	**GAAGGTCGGAGTCAACGGATT**AAGCTCCTTCTCTTTCGAGTTTATAGA	CACACTTAAACTTATCGCCAAAATCAGGTT	0.28	2	56.69
Cq08435_1548	530860106	A/G	**GAAGGTGACCAAGTTCATGCT**TGATTTCTGTAACTAAAAGTGTTAATTTTCTA	**GAAGGTCGGAGTCAACGGATT**GATTTCTGTAACTAAAAGTGTTAATTTTCTG	CAATGCAGCACTTTGAGGATCACC	0.24	2	56.84
Cq05188_899	530859794	A/G	**GAAGGTGACCAAGTTCATGCT**AATTTGACCCATAAAGGCATTGTGCA	**GAAGGTCGGAGTCAACGGATT**TGACCCATAAAGGCATTGTGCG	AACCTTGGTCGGACAAGTTTGATTTCAAT	0.27	2	57.14
Cq04364_782	530859736	C/T	**GAAGGTGACCAAGTTCATGCT**CCGATCCTTTAACTAAAATCTCTGCC	**GAAGGTCGGAGTCAACGGATT**GCCGATCCTTTAACTAAAATCTCTGCT	CCCATTGCCTCGACGTGCTTGTT	NT	2	57.47
Cq07752_1405	530860039	A/G	**GAAGGTGACCAAGTTCATGCT**CAACAAACAAATCTGTCACAGAGACTTA	**GAAGGTCGGAGTCAACGGATT**AACAAACAAATCTGTCACAGAGACTTG	CAAGGGAATTGAAATGACTAACATCACCAT	0.38	2	58.69
Cq04324_768	530859725	C/G	**GAAGGTGACCAAGTTCATGCT**CACTTGGTGCAAATGCTTCTTGC	**GAAGGTCGGAGTCAACGGATT**CACTTGGTGCAAATGCTTCTTGG	GCCGGCAGAATGTTGAACCAATCTT	NT	2	61.32
Cq04549_810	530859748	A/C	**GAAGGTGACCAAGTTCATGCT**ATTTTGCTCTATTTATAGTATAAAGGGATCAT	**GAAGGTCGGAGTCAACGGATT**TGCTCTATTTATAGTATAAAGGGATCAG	GTGACACATGGCACTCCAACCCAT	0.04	2	63.42
Cq08986_1139	530860139	A/G	**GAAGGTGACCAAGTTCATGCT**CACCCTTAAAAATATCCGAGCATGTCCA	**GAAGGTCGGAGTCAACGGATT**ACCTTAAAAATATCCGAGCATGTCCG	TGATTTTGGTGTGAACAAATATATAGCCTT	0.19	2	70.83
Cq03552_650	530859646	A/T	**GAAGGTGACCAAGTTCATGCT**TCTCAATTTCTCACTACATAAACATTACAAAT	**GAAGGTCGGAGTCAACGGATT**CTCAATTTCTCACTACATAAACATTACAAAA	CTCTGACCAATTCATTTCATATGGTTCATT	0.24	2	72.40
Cq06605_1178	530859914	A/G	**GAAGGTGACCAAGTTCATGCT**CAGATGCTTCAATGTATGACTTGGCT	**GAAGGTCGGAGTCAACGGATT**AGATGCTTCAATGTATGACTTGGCC	ATACGCAGGCATTCTGGCGGGA	0.21	2	74.41
Cq03953	530859683	G/T	**GAAGGTGACCAAGTTCATGCT**AC	**GAAGGTCGGAGTCAACGGATT**CT	TGACCAATCCGTCCACAATAATAGCA	0.38	2	76.80

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				TAAGTGGGTCGAATTTAAGTACAAG	ACTAAGTGGGTCGAATTTAAGTACAAT	AA		
Cq03261_596	530859614	A/C	**GAAGGTGACCAAGTTCATGCT**ATTTAATTCTAAACCACAATTAAATGCAATGT	**GAAGGTCGGAGTCAACGGATT**ATTTAATTCTAAACCACAATTAAATGCAATGG	TGGAGTAATTAATTTTTCATGCAAAGATTA	0.29	2	91.81
Cq03291	530859619	A/G	**GAAGGTGACCAAGTTCATGCT**TCCAAAGTGGACTTATAAACGGACAA	**GAAGGTCGGAGTCAACGGATT**CCAAAGTGGACTTATAAACGGACAG	TTTCTGTCACACTGATTTAGTGACGGTTT	0.2	2	98.06
Cq05952_1020	530859847	A/G	**GAAGGTGACCAAGTTCATGCT**ATTTAATGCTTATATGTAGCCTTAAGGGT	**GAAGGTCGGAGTCAACGGATT**AATGCTTATATGTAGCCTTAAGGGC	CAACTATGAATTATATGGCATAATGCTATA	0.27	2	106.24
Cq04021_725	530859686	C/T	**GAAGGTGACCAAGTTCATGCT**TTGGAAGTTTTGAGAAGTTTTTCACATAG	**GAAGGTCGGAGTCAACGGATT**AAATTTGGAAGTTTTGAGAAGTTTTTCACATAA	CACCCACCTTACATCACCACTATCAA	0.2	3	0.00
Cq05728_969	530859829	A/T	**GAAGGTGACCAAGTTCATGCT**GGGCTTACTCATTAGGAGTAAGTCA	**GAAGGTCGGAGTCAACGGATT**GGGCTTACTCATTAGGAGTAAGTCT	CAACCTAAATGAGATAGAACAGTCCCAAA	0.28	3	8.77
Cq02024	530859496	C/T	**GAAGGTGACCAAGTTCATGCT**CAAGGGCGTCCCAATAATAAGTTG	**GAAGGTCGGAGTCAACGGATT**CCAAGGGCGTCCCAATAATAAGTTA	CAACAAGTTTCCAAGTGGTTGACATCAA	0.12	3	13.80
Cq10143_1719	530860171	A/C	**GAAGGTGACCAAGTTCATGCT**ATTACAACATGTGCAGGCGCTACAT	**GAAGGTCGGAGTCAACGGATT**ACAACATGTGCAGGCGCTACAG	TTATCTTTTGCCACGAGACATCATTTACTT	0.27	3	15.94
Cq07578_1375	530860018	A/G	**GAAGGTGACCAAGTTCATGCT**GCAACACATAATTCTAAAATATTTATGATCACT	**GAAGGTCGGAGTCAACGGATT**CAACACATAATTCTAAAATATTTATGATCACC	CCAGTTTAGGCTCCTTTTTGATCTTGTTA	0.23	3	18.90
Cq06387_1134	530859889	A/C	**GAAGGTGACCAAGTTCATGCT**GAAAGAAAAGAAAGACTGATCAGCTGT	**GAAGGTCGGAGTCAACGGATT**AAAGAAAAGAAAGACTGATCAGCTGG	CCGATCAGTGATTGCTATTGCTTTCTTT	0.39	3	20.79
Cq07782_1413	530860044	A/G	**GAAGGTGACCAAGTTCATGCT**TTGAAGTGGCCAAACATTGATTGCTA	**GAAGGTCGGAGTCAACGGATT**GAAGTGGCCAAACATTGATTGCTG	GACCTACCTCCATACGATGATAAACATAA	0.29	3	21.75
Cq08573_1565	530860119	C/T	**GAAGGTGACCAAGTTCATGCT**CAAGTGGAACATTCCCATACGTC	**GAAGGTCGGAGTCAACGGATT**CTCAAGTGGAACATTCCCATACGTT	GGTGAACCTGGCCCTGTTCCTT	0.08	3	21.84
Cq09275_1638	530860151	A/G	**GAAGGTGACCAAGTTCATGCT**AAACAAATCATTGATGTTTGCAATGACAGA	**GAAGGTCGGAGTCAACGGATT**CAAATCATTGATGTTTGCAATGACAGG	AGCTTGTCATTGCAAACATTAATTTGGGAT	0.42	3	22.03
Cq01317_231	530859434	A/G	**GAAGGTGACCAAGTTCATGCT**TTTAGCAATGCATGTATCAAGCATAATATT	**GAAGGTCGGAGTCAACGGATT**TAGCAATGCATGTATCAAGCATAATATC	TTAATATAATTGGGCAAGAATTATGAGTAA	0.35	3	22.19
Cq07416_1330	530859993	G/T	**GAAGGTGACCAAGTTCATGCT**CATATTTTTCATCATGCAACATGTTATTGTG	**GAAGGTCGGAGTCAACGGATT**CCATATTTTTCATCATGCAACATGTTATTGTT	AAAGCAATGTTATGGGGATGATAGGGAA	0.19	3	22.26
Cq03337_462	530859625	C/T	**GAAGGTGACCAAGTTCATGCT**CCTCTATTAAGTGAACGTTGAATATTATAAC	**GAAGGTCGGAGTCAACGGATT**AACCTCTATTAAGTGAACGTTGAATATTATAAT	AATCGCAAATCATTTAAATGACCTCGGTTA	0.31	3	23.20
Cq01528_313	530859445	A/G	**GAAGGTGACCAAGTTCATGCT**CATAAATTAAGGCTCTATAGTATCTAAGGTTT	**GAAGGTCGGAGTCAACGGATT**AAATTAAGGCTCTATAGTATCTAAGGTTC	GTTATGCTCAACTTGAATTTGTGCTCTGTT	NT	3	24.68
Cq08992_1619	530860141	G/T	**GAAGGTGACCAAGTTCATGCT**CCGTCAGATAGTGAACTGCACC	**GAAGGTCGGAGTCAACGGATT**ACCGTCAGATAGTGAACTGCACA	GACTGCCGTGCCACGACAGAAT	0.44	3	26.39
Cq03439_476	530859635	A/C	**GAAGGTGACCAAGTTCATGCT**AAAAGAGTTGTATGTTAGGTGTCTTTGATA	**GAAGGTCGGAGTCAACGGATT**AGAGTTGTATGTTAGGTGTCTTTGATC	AAAGAAACCAGTACTGCCACCTCCT	0.32	3	29.06
Cq07348_1320	530859988	A/C	**GAAGGTGACCAAGTTCATGCT**GT	**GAAGGTCGGAGTCAACGGATT**GT	GATGTTAATACCAAAAAATTAGGCAG	NT	3	31.79

			GTACACTTTTGGTTTGGGTCA	GTACACTTTTGGTTTGGGTCC	GACA			
Cq07348_1319	530859986	C/T	**GAAGGTGACCAAGTTCATGCT**GTACACAGATGAATTTCTAACATCGG	**GAAGGTCGGAGTCAACGGATT**GTGTACACAGATGAATTTCTAACATCGA	AACATAACCTTTCTCTGTCCCTCTCTT	0.3	3	32.22
Cq08102_1478	530860078	C/T	**GAAGGTGACCAAGTTCATGCT**AGTGCACGCACGATCTTCTCAG	**GAAGGTCGGAGTCAACGGATT**GAGTGCACGCACGATCTTCTCAA	CCAACACCATCCATACATGGTGGTT	0.39	3	33.12
Cq00362_72	530859333	G/T	**GAAGGTGACCAAGTTCATGCT**ACTTTGAAGATTGTATAGCTAATTAGTATTC	**GAAGGTCGGAGTCAACGGATT**GTACTTTGAAGATTGTATAGCTAATTAGTATTA	TTTTCCAATCTTCATTCAATAACCTACACA	0.46	3	34.29
Cq02891_400	530859584	A/T	**GAAGGTGACCAAGTTCATGCT**ATAGTTAGTTAGTTATAATCTCTTTAATT	**GAAGGTCGGAGTCAACGGATT**ATAGTTAGTTAGTTATAATCTCTTTAATA	GTGTTTTTTATCGAGTGGCCAATGAGAAT	0.44	3	39.43
Cq07233_1288	530859977	A/G	**GAAGGTGACCAAGTTCATGCT**TAGTGGCATGGTTTTGACACGTCA	**GAAGGTCGGAGTCAACGGATT**GTGGCATGGTTTTGACACGTCG	ACACATATTCAAGGCTTCAAGTCCCAT	0.24	3	42.15
Cq07172_1282	530859974	C/G	**GAAGGTGACCAAGTTCATGCT**GTTTACATTTTAGACGATTTTGTAAAGTTTTC	**GAAGGTCGGAGTCAACGGATT**GTTTACATTTTAGACGATTTTGTAAAGTTTTG	GTGTTAAAAGAGTCATAAAAAGACAGTGAT	0.3	3	59.25
Cq04675_586	530859759	A/T	**GAAGGTGACCAAGTTCATGCT**GTCCAAAGGTTCAAGGACTTGAAGT	**GAAGGTCGGAGTCAACGGATT**GTCCAAAGGTTCAAGGACTTGAAGA	CTTGGCTACTTTGTGTGTGTATTGCATAT	0.31	3	66.56
Cq01605	530859454	A/T	**GAAGGTGACCAAGTTCATGCT**CATATAAACGGCGTATCCATTACACTA	**GAAGGTCGGAGTCAACGGATT**CATATAAACGGCGTATCCATTACACTT	CTACTGCTTCGTGAGTAGTCTGGAT	0.48	3	74.84
Cq03485_642	530859637	A/T	**GAAGGTGACCAAGTTCATGCT**ATTATAAGTTAGTTTACGATAGGATTAGTGAAA	**GAAGGTCGGAGTCAACGGATT**ATAAGTTAGTTTACGATAGGATTAGTGAAT	AATCTACAAACCCAATTCAACTTCGCGAT	NT	3	96.00
Cq04358_778	530859732	C/T	**GAAGGTGACCAAGTTCATGCT**GCAGATTGAATGGCTGACTGGC	**GAAGGTCGGAGTCAACGGATT**TGCAGATTGAATGGCTGACTGGT	CCTTTTGGTCACAACAACCTCATGCAT	0.25	4	0.00
Cq08757_1585	530860132	C/T	**GAAGGTGACCAAGTTCATGCT**GAAATTAGCCTTCTCTGCATCTGG	**GAAGGTCGGAGTCAACGGATT**GAAATTAGCCTTCTCTGCATCTGA	ATGCGCTGGCTACTTTGATTCGGAA	0.31	4	11.50
Cq04283_548	530859716	C/T	**GAAGGTGACCAAGTTCATGCT**CGCATATTCAATCCGTTTCAACAC	**GAAGGTCGGAGTCAACGGATT**CGCATATTCAATCCGTTTCAACAT	TTTTGACAAGTTCTTCCCCCTAATCGAAT	0.2	4	21.56
Cq06516_802	530859905	C/G	**GAAGGTGACCAAGTTCATGCT**TATTTCAAACAATTACAGTAGTTATCTACTAC	**GAAGGTCGGAGTCAACGGATT**ATTTCAAACAATTACAGTAGTTATCTACTAG	ACCCACTTGTATAATTAACTGGTTTGACAA	0.29	4	24.65
Cq07662_1392	530860028	A/G	**GAAGGTGACCAAGTTCATGCT**GTTGAGATTCTTTACGTGTATGGTAGTA	**GAAGGTCGGAGTCAACGGATT**GAGATTCTTTACGTGTATGGTAGTG	TAATGCAATTGTTTTGGAAGAGCTTCACAT	0.16	4	25.85
Cq02319_443	530859535	A/C	**GAAGGTGACCAAGTTCATGCT**GAAATATGTTGTAACTCTTGTAAGCTTTGAAA	**GAAGGTCGGAGTCAACGGATT**AATATGTTGTAACTCTTGTAAGCTTTGAAC	ACTATAGTGGGTGTTTTTTTTGTTTATAAA	0.07	4	41.19
Cq03511_484	530859642	A/G	**GAAGGTGACCAAGTTCATGCT**ATTAAGGGGGTTTAGTAATCAAATATGCA	**GAAGGTCGGAGTCAACGGATT**AAGGGGGTTTAGTAATCAAATATGCG	TCTAAACTCGTTCTTTTGGGGATTGTGTT	0.11	4	42.25
Cq04631_580	530859755	A/C	**GAAGGTGACCAAGTTCATGCT**GTAGAATGAAAAGTTGATAAGAGGGGT	**GAAGGTCGGAGTCAACGGATT**AGAATGAAAAGTTGATAAGAGGGGG	ATGTAATTAGGCGGTTAAAGTAACTAACAT	NT	4	43.81
Cq07471_1344	530859999	C/T	**GAAGGTGACCAAGTTCATGCT**GTGTAGACCATCAAGTGATCTTCG	**GAAGGTCGGAGTCAACGGATT**GGTGTAGACCATCAAGTGATCTTCA	TTAAGAATGCGTTGGTAGGTACTCATGAT	0.19	4	44.68
Cq00249	530859319	A/G	**GAAGGTGACCAAGTTCATGCT**GAATACTTCCATAGATCGAATGGACTT	**GAAGGTCGGAGTCAACGGATT**AATACTTCCATAGATCGAATGGACTC	GCAAAATTTCTATTCACTCCATTTGCTATT	0.46	4	45.25
Cq05311_923	530859803	A/G	**GAAGGTGACCAAGTTCATGCT**GTGTTGTTATTTTTGTTTCATATGCTCA	**GAAGGTCGGAGTCAACGGATT**GTTGTTATTTTTGTTTCATATGCTCAAT	TAGAATCAACATCAACATAGGCTGACCAT	NT	4	49.28

			ATCT	CC				
Cq06843_1229	530859935	A/C	**GAAGGTGACCAAGTTCATGCT**CCCAGCAATGGTTCGGCAACTTT	**GAAGGTCGGAGTCAACGGATT**CCAGCAATGGTTCGGCAACTTG	GTAGGCGAGGGTCTTGAAATTGTTAATAA	0.3	4	51.51
Cq08630_1573	530860123	A/G	**GAAGGTGACCAAGTTCATGCT**CCACGTGTCGGGTGGTGAGT	**GAAGGTCGGAGTCAACGGATT**CACGTGTCGGGTGGTGAGC	AAGGGGACACGTGTCACCCCAA	NT	4	59.49
Cq04504_804	530859741	A/G	**GAAGGTGACCAAGTTCATGCT**CATTGTTGGATACTCGAATGGATTTACAA	**GAAGGTCGGAGTCAACGGATT**GTTGGATACTCGAATGGATTTACAG	CCATTCTTGTGGTTCTACTCCTTGCTT	NT	4	68.07
Cq03541	530859644	A/C	**GAAGGTGACCAAGTTCATGCT**AATGATTTAATCCTTCTAAATCATGTGAATCAA	**GAAGGTCGGAGTCAACGGATT**TAAATCCTTCTAAATCATGTGAATCAC	GTGTCATCTATTAAGAAACGGAGGAAGTA	0.42	4	74.58
Cq00360_70	530859331	C/T	**GAAGGTGACCAAGTTCATGCT**GTGGGGACCATGAGATGAGAG	**GAAGGTCGGAGTCAACGGATT**GGTGGGGACCATGAGATGAGAA	CGTACTCCATCCGTGTTTTAATAAGTGTT	NT	4	84.23
Cq02657	530859568	C/T	**GAAGGTGACCAAGTTCATGCT**AATCCATAAGGCAATCTTTGAACCAG	**GAAGGTCGGAGTCAACGGATT**CAAATCCATAAGGCAATCTTTGAACCAA	GGCATTTGAGCAGATAGACTTGGAGAA	0.33	4	88.25
Cq06585_1173	530859912	C/T	**GAAGGTGACCAAGTTCATGCT**AAATAATAGCGGCGGAGGAAGTAG	**GAAGGTCGGAGTCAACGGATT**CAAATAATAGCGGCGGAGGAAGTAA	TGGTGTCATTTTTCAGTAGACCTATCTTAA	0.34	4	92.35
Cq05696_673	530859827	A/T	**GAAGGTGACCAAGTTCATGCT**GTCAGCCATAGAAAAAAACTAACTAATTACA	**GAAGGTCGGAGTCAACGGATT**GTCAGCCATAGAAAAAAACTAACTAATTACT	GGTTTTGTTATGTGGGCTGTAGGGAA	0.28	4	94.41
Cq02650_498	530859566	A/T	**GAAGGTGACCAAGTTCATGCT**GAGCTCAGCATGACACCCTAATTA	**GAAGGTCGGAGTCAACGGATT**GAGCTCAGCATGACACCCTAATTT	ATTCACAAATCAACAAGCTTCCTAAATGTA	0.31	5	0.00
Cq07809_1416	530860048	A/G	**GAAGGTGACCAAGTTCATGCT**GGTACGATACAAGGGTCTTTTGGA	**GAAGGTCGGAGTCAACGGATT**GTACGATACAAGGGTCTTTTGGG	AGGAATTAAGGATTGCTGAATTGTCAACAA	0.31	5	0.55
Cq00782_143	530859377	C/T	**GAAGGTGACCAAGTTCATGCT**AATTCATAGCTCGTAATATTCATAAATAATCAC	**GAAGGTCGGAGTCAACGGATT**AATTCATAGCTCGTAATATTCATAAATAATCAT	CAATTAGTTCTGGGATTGTTCCAGGTATA	0.31	5	3.90
Cq02389_352	530859542	C/T	**GAAGGTGACCAAGTTCATGCT**ATTGGACCCACGGTTGTGACC	**GAAGGTCGGAGTCAACGGATT**ATTGGACCCACGGTTGTGACT	TGCATTTGCATTGCTTCCTAATCATAGTTT	0.12	5	23.62
Cq06229_1065	530859866	G/T	**GAAGGTGACCAAGTTCATGCT**AAAGAATTTAATGATTAAATTGGCTAACTAC	**GAAGGTCGGAGTCAACGGATT**CTAAAGAATTTAATGATTAAATTGGCTAACTAA	GGAACTCCCCAAAACATACAATCATTGTA	0.03	5	35.57
Cq10573_1259	530860187	A/C	**GAAGGTGACCAAGTTCATGCT**TTTTCACATGCAATTATTTTAGGAATCCATAA	**GAAGGTCGGAGTCAACGGATT**CACATGCAATTATTTTAGGAATCCATAC	TAAAATATAGTATATAAGCTAACCCCACAT	0.33	5	39.08
Cq06675_835	530859917	G/T	**GAAGGTGACCAAGTTCATGCT**CCCACACTTGAGCCCCACAG	**GAAGGTCGGAGTCAACGGATT**ATCCCACACTTGAGCCCCACAT	CTTCCCTTTGGAAACCTTCCATGCTT	0.29	5	39.78
Cq05777_989	530859836	A/G	**GAAGGTGACCAAGTTCATGCT**AACGGCCTTATAAAAGGGCGGAAA	**GAAGGTCGGAGTCAACGGATT**CGGCCTTATAAAAGGGCGGAAG	GTATCGCGGAGTGGGTACTCTAATT	0.48	5	40.61
Cq04841_853	530859774	C/T	**GAAGGTGACCAAGTTCATGCT**CGAAAATACCCTGAAGAGTATCACC	**GAAGGTCGGAGTCAACGGATT**GCGAAAATACCCTGAAGAGTATCACT	GCATAGCAAGAGCAAAGGATCGACAA	0.34	5	41.96
Cq04841_855	530859776	A/G	**GAAGGTGACCAAGTTCATGCT**ATAATGGTTATAAGCAGCAAAGGCACT	**GAAGGTCGGAGTCAACGGATT**AATGGTTATAAGCAGCAAAGGCACC	GGTGCCTTTGTTGTATTGTGAACCATTAT	NT	5	42.87
Cq00148_17	530859310	A/G	**GAAGGTGACCAAGTTCATGCT**AATATTACTCGTTAGAATTATTAATTCTTTCCA	**GAAGGTCGGAGTCAACGGATT**AATATTACTCGTTAGAATTATTAATTCTTTCCG	CCCAAGCAACCAACGAGCCGAA	0.41	5	43.36
Cq00971_207	530859401	A/G	**GAAGGTGACCAAGTTCATGCT**TACACCTCCGAACCTCCCGA	**GAAGGTCGGAGTCAACGGATT**ACACCTCCGAACCTCCCGG	CTTGGCTGCAGGATTCGAGTAGTAT	0.09	5	44.25
Cq00754	530859375	A/G	**GAAGGTGACCAAGTTCATGCT**AT	**GAAGGTCGGAGTCAACGGATT**GC	CCAACCATCTAAAGGTGGGACGTAA	0.44	5	46.84

			AGCAGTTTTAAAAACCAATCAGGCTATT	AGTTTTAAAAACCAATCAGGCTATC				
Cq06332_1120	530859884	A/G	**GAAGGTGACCAAGTTCATGCT**ATCTAAATGGAATTGTACATTTAACAATTGACA	**GAAGGTCGGAGTCAACGGATT**CTAAATGGAATTGTACATTTAACAATTGACG	GATCACCAAGCAAACTTTGATAT	0.32	5	47.20
Cq01871_361	530859485	C/T	**GAAGGTGACCAAGTTCATGCT**AGTTTTCTTAAACTTTTTATAAGGTAGAGATG	**GAAGGTCGGAGTCAACGGATT**GAGTTTTCTTAAACTTTTTATAAGGTAGAGATA	CCTGTTTTTTGACTAACCAAGTAGCCTAA	0.38	5	47.78
Cq00228_37	530859315	G/T	**GAAGGTGACCAAGTTCATGCT**AAGCTCTGATTTGTTCAAGAAGGGG	**GAAGGTCGGAGTCAACGGATT**CAAGCTCTGATTTGTTCAAGAAGGGT	TTTAGCCGGCCCCGAACACGAA	0.32	5	51.19
Cq03756_689	530859663	A/T	**GAAGGTGACCAAGTTCATGCT**CCCAGTTACCGCTGCCAATAACT	**GAAGGTCGGAGTCAACGGATT**CCCAGTTACCGCTGCCAATAACA	GTAATCATCATCTCTATGAAAGCTGAAGAA	0.36	5	51.43
Cq04632_825	530859757	A/G	**GAAGGTGACCAAGTTCATGCT**CACTATTTTCAGCATTCACAAGGTCA	**GAAGGTCGGAGTCAACGGATT**CACTATTTTCAGCATTCACAAGGTCG	AGAAACAAGATAAGGAAGTTGAACCTACTA	0.32	5	51.53
Cq04734_843	530859764	A/C	**GAAGGTGACCAAGTTCATGCT**CGAGCCGAAGAACTCCTAAAAATCA	**GAAGGTCGGAGTCAACGGATT**GAGCCGAAGAACTCCTAAAAATCC	AAGCTGTGTTGTCTCCAGCTGTGAT	0.41	5	51.59
Cq06480_1152	530859896	A/G	**GAAGGTGACCAAGTTCATGCT**AAGCTTCTCCCGCCCGGCT	**GAAGGTCGGAGTCAACGGATT**GCTTCTCCCGCCCGGCC	CAAGACCCAAAGAGGAAACCCAGAT	NT	5	51.64
Cq01809_352	530859480	A/G	**GAAGGTGACCAAGTTCATGCT**GAACCCCAATTCACCATTGACATCA	**GAAGGTCGGAGTCAACGGATT**AACCCCAATTCACCATTGACATCG	GGAACATGATATGGTTGCCAAAGATCTTA	NT	5	52.73
Cq01727_266	530859464	A/T	**GAAGGTGACCAAGTTCATGCT**TAGCAAAATTGCTCAAATGAAATATGGCA	**GAAGGTCGGAGTCAACGGATT**AGCAAAATTGCTCAAATGAAATATGGCT	CTTACAAAATCCTATTTTAGTAAGGCGGTT	NT	5	53.33
Cq06682_836	530859919	C/T	**GAAGGTGACCAAGTTCATGCT**AGAACACGTACGTACTATTGTGGG	**GAAGGTCGGAGTCAACGGATT**GTAGAACACGTACGTACTATTGTGGA	AATTGGCATTGTCACATATGCATATGCTTT	0.35	5	53.93
Cq01883_287	530859487	A/C	**GAAGGTGACCAAGTTCATGCT**TGAATGGTGTGTGTCACAAAATCACT	**GAAGGTCGGAGTCAACGGATT**GAATGGTGTGTGTCACAAAATCACG	GAAATGGTAAAGGCAAGCGGCTGAA	0.29	5	59.21
Cq05370_932	530859808	G/T	**GAAGGTGACCAAGTTCATGCT**GAGGATGGATCAACCCTCAAAGG	**GAAGGTCGGAGTCAACGGATT**GAGGATGGATCAACCCTCAAAGT	GGGGTTGCTTACTTTCCATCAAAATGAAGAT	NT	5	64.06
Cq06047_1034	530859854	C/T	**GAAGGTGACCAAGTTCATGCT**AATTGAAAATGGTTGATGGAAAATTG	**GAAGGTCGGAGTCAACGGATT**GTTGCTAATTGAAAATGGTTGATGGAAAATTA	CACATGCACAAATTCACCACAATTTCACTA	0.45	5	71.27
Cq05382_937	530859810	A/T	**GAAGGTGACCAAGTTCATGCT**AACAATCCAGATGCCTTGAATCAACA	**GAAGGTCGGAGTCAACGGATT**AACAATCCAGATGCCTTGAATCAACTT	GCATTAGCTTGTAGAGTGTAGACTCATTT	0.28	6	0.00
Cq02413_470	530859547	A/G	**GAAGGTGACCAAGTTCATGCT**ATGTCCTAAAGACACGAACGGCTT	**GAAGGTCGGAGTCAACGGATT**GTCCTAAAGACACGAACGGCTC	CTTTGTCTTGGGAAAACTTGTACCGAAAA	0.27	6	0.23
Cq02399	530859544	C/T	**GAAGGTGACCAAGTTCATGCT**GAGAAAATTAGCTAATCCCTAAGAAGTG	**GAAGGTCGGAGTCAACGGATT**ATGAGAAAATTAGCTAATCCCTAAGAAGTA	GCAATGGATGCTTAAGCTAAAGTAGGAAT	0.47	6	1.49
Cq01984_373	530859492	C/G	**GAAGGTGACCAAGTTCATGCT**CACAATTTCTTCTAACCTTGAGTTCTC	**GAAGGTCGGAGTCAACGGATT**CACAATTTCTTCTAACCTTGAGTTCTG	GTCTTCGATGGGTCAACCATCTTCAA	0.13	6	1.98
Cq06528_1162	530859907	A/T	**GAAGGTGACCAAGTTCATGCT**GTTACAAGCACAAAGTCAAAATTAGAACAAA	**GAAGGTCGGAGTCAACGGATT**GTTACAAGCACAAAGTCAAAATTAGAACAAT	GCCTTTGGTTTAAGTGATCAACCAACAAT	0.42	6	2.36
Cq04033_520	530859688	A/C	**GAAGGTGACCAAGTTCATGCT**ATGATCCATTTGGTGGCATTTATGGA	**GAAGGTCGGAGTCAACGGATT**GATCCATTTGGTGGCATTTATGGC	CATAACATAGAGAATTATCCAAAAGTAGAT	0.49	6	2.69
Cq00375	530859334	A/T	**GAAGGTGACCAAGTTCATGCT**AATATCTTAGTATATCTTATGAATGACCCAAAA	**GAAGGTCGGAGTCAACGGATT**AATATCTTAGTATATCTTATGAATGACCCAAAT	CGTTACTGATGGTGGCTTAAGCAGAA	0.13	6	2.81
Cq01140_233	530859412	A/G	**GAAGGTGACCAAGTTCATGCT**CA	**GAAGGTCGGAGTCAACGGATT**AA	TGCTTCAAAAACCCGAATTTTCTCGAA	0.13	6	2.93

			AATTTTCACCTTAATCTCTTACTTGTCATT	TTTTCACCTTAATCTCTTACTTGTCATC	AAA			
Cq00114_6	530859305	A/G	**GAAGGTGACCAAGTTCATGCT**AAACAAGTAACCCCTGACCAAAATCAA	**GAAGGTCGGAGTCAACGGATT**ACAAGTAACCCCTGACCAAAATCAG	TTTGGTCAAGGGGTTGCTA	0.29	6	2.94
Cq05770_980	530859834	A/C	**GAAGGTGACCAAGTTCATGCT**TACCCGGCTTAATTAATTGGATAAATTAAGATT	**GAAGGTCGGAGTCAACGGATT**CCGGCTTAATTAATTGGATAAATTAAGATG	AATATTTGAAGCTCCCACTAAATCAAGCAT	0.13	6	3.03
Cq07547_984	530860013	C/T	**GAAGGTGACCAAGTTCATGCT**GGAACAGCCAAAATTGGTTCCTG	**GAAGGTCGGAGTCAACGGATT**GGGAACAGCCAAAATTGGTTCCTA	GAATTTTCGATAATAATTGGCTAAACCCAA	0.13	6	3.14
Cq01932_289	530859489	C/T	**GAAGGTGACCAAGTTCATGCT**TTAGTAAGCGAACAGATGTCAG	**GAAGGTCGGAGTCAACGGATT**GCTTTAGTAAGCGAACAGATGTCAA	GCTGGTGTTTTGCGGGAAGCCAA	0.13	6	3.14
Cq06902_869	530859947	G/T	**GAAGGTGACCAAGTTCATGCT**GGAGTTCCCAACTCCTTCAACG	**GAAGGTCGGAGTCAACGGATT**GGGAGTTCCCAACTCCTTCAACT	GAAATATAAGAGGAGGATCGAGTAAGCAT	0.14	6	3.21
Cq05882_1002	530859843	C/G	**GAAGGTGACCAAGTTCATGCT**CAACCGGAGTCACTCGAACAC	**GAAGGTCGGAGTCAACGGATT**CAACCGGAGTCACTCGAACAG	CACCTCTCCGTTGAACCGGGT	0.28	6	3.29
Cq01730_339	530859470	C/T	**GAAGGTGACCAAGTTCATGCT**GAAGATGATCTACAGTCAAATTAACTTAAG	**GAAGGTCGGAGTCAACGGATT**ATGAAGATGATCTACAGTCAAATTAACTTAAA	CAGAAAACCCCAATAAACATAAATATAATT	0.42	6	3.77
Cq05603_951	530859822	A/G	**GAAGGTGACCAAGTTCATGCT**AGCTTTTGGTGATCCAAATAGTCGATA	**GAAGGTCGGAGTCAACGGATT**GCTTTTGGTGATCCAAATAGTCGATG	TGACATGATCACTGTCTGCCAAATTGAAA	0.14	6	4.20
Cq05931_1016	530859845	C/T	**GAAGGTGACCAAGTTCATGCT**ATTGTTGATGATTGGAAAGGGGTGG	**GAAGGTCGGAGTCAACGGATT**GTTGATGATTGGAAAGGGGTGA	CTTCGACCCTTCTTCTTTTTTTCTCAATAA	0.28	6	4.72
Cq03788	530859672	A/T	**GAAGGTGACCAAGTTCATGCT**CATTTGACTTCCGGTCAACATAATTGT	**GAAGGTCGGAGTCAACGGATT**CATTTGACTTCCGGTCAACATAATTGA	TACCCCGTACATGACCAGGATGTTA	0.47	6	7.51
Cq02952_557	530859589	A/C	**GAAGGTGACCAAGTTCATGCT**ATGGATTAAACTTCTGGTTCTCATTTTCA	**GAAGGTCGGAGTCAACGGATT**AAACTTCTGGTTCTCATTTTCC	CGCTATCTTAAAGTTTCGATAAGAGGATAA	0.28	6	10.03
Cq04541_573	530859746	A/G	**GAAGGTGACCAAGTTCATGCT**GATTATCTTTCTGGCTTCATTAAACCATTA	**GAAGGTCGGAGTCAACGGATT**ATCTTTCTGGCTTCATTAAACCATTG	AGAAATTGATGGGCACATTCAGAGAGTTT	0.25	6	10.70
Cq00617_127	530859362	C/T	**GAAGGTGACCAAGTTCATGCT**GCATTAAACCTCACAGTAGTCTTCG	**GAAGGTCGGAGTCAACGGATT**GGCATTAAACCTCACAGTAGTCTTCA	CGATCCATTATCTACAAGGGTCATAAGAA	0.29	6	23.26
Cq03209_587	530859605	A/T	**GAAGGTGACCAAGTTCATGCT**GAGTCTGGATGAATTGGGCATTGA	**GAAGGTCGGAGTCAACGGATT**GAGTCTGGATGAATTGGGCATTGT	CAGCTCATATCCTCCCTTTTCCTCAT	0.3	6	24.78
Cq00840_178	530859383	C/T	**GAAGGTGACCAAGTTCATGCT**CACACCATCAGGAACCTACTAAAC	**GAAGGTCGGAGTCAACGGATT**ATCACACCATCAGGAACCTACTAAAT	GGTACCAATAATATGGTGATTATAGTCAGT	0.49	6	29.53
Cq00104_5	530859303	C/T	**GAAGGTGACCAAGTTCATGCT**AAGGAGTATATCGGTATAACTAACATATAC	**GAAGGTCGGAGTCAACGGATT**AATAAGGAGTATATCGGTATAACTAACATATAT	CCATGCAAATGCAAAGTAAGTCGAACTTT	0.42	6	29.89
Cq06503_798	530859900	C/T	**GAAGGTGACCAAGTTCATGCT**GACCAAGTATCTCCTGACCGAAC	**GAAGGTCGGAGTCAACGGATT**ATGACCAAGTATCTCCTGACCGAAT	GGTTATTAGGGGATACTCGAGGACTT	0.38	6	31.12
Cq02440_481	530859554	A/G	**GAAGGTGACCAAGTTCATGCT**CCTCTGCTGGTATAGTTTTCTCTCTT	**GAAGGTCGGAGTCAACGGATT**CTCTGCTGGTATAGTTTTCTCTCTC	GCACAAAAGCTCAATGAAGCTAAGCTAAA	0.3	6	35.13
Cq08478_1105	530860112	C/T	**GAAGGTGACCAAGTTCATGCT**CTTTGTTTCCAAAAGATACTGAG	**GAAGGTCGGAGTCAACGGATT**ATTGCTCTTTGTTTCCAAAAGATACTGAA	GAGTAATGAAACCCTCTGCCATCCAA	0.3	6	39.25
Cq02258_430	530859526	C/G	**GAAGGTGACCAAGTTCATGCT**TTTGTCTTTTAAAGTTATTGATGGATTAATGC	**GAAGGTCGGAGTCAACGGATT**TTGTCTTTTAAAGTTATTGATGGATTAATGG	CTATCCATTAAGAGGACCCTCCCTT	0.36	6	45.60

Cq07904_1427	530860056	C/T	**GAAGGTGACCAAGTTCATGCTGG**CACTTATGTTTAGGTCATTCCTC	**GAAGGTCGGAGTCAACGGATT**GGCACTTATGTTTAGGTCATTCCTT	GAATCACATCTTGTCTTTATCGCGTGAAA	0.18	6	46.58
Cq10375_1753	530860176	A/G	**GAAGGTGACCAAGTTCATGCT**AAATATAGAGAATAAAGCAAAAATATACATATA	**GAAGGTCGGAGTCAACGGATT**AAATATAGAGAATAAAGCAAAAATATACATATG	CATTTAACCAGACACATATATTTGTTTCAT	0.04	6	50.57
Cq08755_1583	530860130	C/G	**GAAGGTGACCAAGTTCATGCT**GAAGAGCAGGGGCAGCTAATTG	**GAAGGTCGGAGTCAACGGATT**GAAGAGCAGGGGCAGCTAATTC	GTAAACTATAAAAGACTCAAGCTCATCCTA	NT	6	61.37
Cq07535_1362	530860006	C/T	**GAAGGTGACCAAGTTCATGCT**CAAATATAATAGGGCGATTCTATATGCC	**GAAGGTCGGAGTCAACGGATT**AACAATATAATAGGGCGATTCTATATGCT	GATTTTATTCTGACAAAGAGGGCGACTTT	0.38	6	66.71
Cq02123	530859515	C/T	**GAAGGTGACCAAGTTCATGCT**CTATCCAGCACTCTCGCAGTC	**GAAGGTCGGAGTCAACGGATT**CTCTATCCAGCACTCTCGCAGTT	GGTGAAAGGGTGAAGAAGGACGTAA	0.31	6	68.94
Cq01729_337	530859468	A/T	**GAAGGTGACCAAGTTCATGCT**GTTCACAATATTTTACATTTATGCCATGTT	**GAAGGTCGGAGTCAACGGATT**CTGTTCACAATATTTTACATTTATGCCATGTA	CCCATTGATCTTCTTGATCAATATAGCAAA	0.25	7	0.00
Cq02055_385	530859503	C/T	**GAAGGTGACCAAGTTCATGCT**GTGCAATTTACCTTATAATTTATTTTCTCCTG	**GAAGGTCGGAGTCAACGGATT**GTGCAATTTACCTTATAATTTATTTTCTCCTA	GATAGTAAAGTTGCATTGACAAACATGATA	0.11	7	9.04
Cq01729_335	530859466	C/T	**GAAGGTGACCAAGTTCATGCT**GTTGATCAATTTATTTTGTCAATCAATAGGG	**GAAGGTCGGAGTCAACGGATT**AAGTTGATCAATTTATTTTGTCAATCAATAGGA	GTCCCAGGTTTAATGAAGAAAAAGACTATA	0.31	7	13.43
Cq05277_913	530859797	C/T	**GAAGGTGACCAAGTTCATGCT**ATTTGCCTATTTGAGATCAATGTCATAAC	**GAAGGTCGGAGTCAACGGATT**ATTATTTGCCTATTTGAGATCAATGTCATAAT	GTCGATGAGTCTACTCCCAAGAGAA	0.2	7	18.32
Cq07623_1383	530860020	A/C	**GAAGGTGACCAAGTTCATGCT**TCAAAATAAACAAGCTCTATATCGCCAT	**GAAGGTCGGAGTCAACGGATT**CAAAATAAACAAGCTCTATATCGCCAG	CTTTGTTCTTGGTTTTTTTGCTTTTGCTTA	0.07	7	25.77
Cq02100_399	530859512	C/T	**GAAGGTGACCAAGTTCATGCT**TTGAGACAATATGATTCAATCACATCAC	**GAAGGTCGGAGTCAACGGATT**CTTTGAGACAATATGATTCAATCACATCAT	CTTGCAGATTCCGTGAAATAA	0.29	7	29.85
Cq03777_505	530859671	A/T	**GAAGGTGACCAAGTTCATGCT**CCATCCCTAAATAAAAGTCCCCGA	**GAAGGTCGGAGTCAACGGATT**CCATCCCTAAATAAAAGTCCCCGT	CTTCACCTTTAATCAACCAATCCCCAATA	0.17	7	30.70
Cq06686_1196	530859921	C/T	**GAAGGTGACCAAGTTCATGCT**GAGAATGGGATTCGGAATTAATGGAC	**GAAGGTCGGAGTCAACGGATT**GAGAATGGGATTCGGAATTAATGGAT	CCCACCCACTATCCAAACAAGGTAT	0.14	7	41.23
Cq08518_1554	530860114	A/G	**GAAGGTGACCAAGTTCATGCT**GCAGACACATCCCTAAGAAAGACAA	**GAAGGTCGGAGTCAACGGATT**CAGACACATCCCTAAGAAAGACAG	CCTAATTACAGTGCAACAAGAACCCTAAT	NT	7	41.67
Cq02860_537	530859580	A/G	**GAAGGTGACCAAGTTCATGCT**ATAGATATTTGAGAATTATAATACATGGCCTA	**GAAGGTCGGAGTCAACGGATT**AGATATTTGAGAATTATAATACATGGCCTG	TATCTGAATACATCTCCAATTGATACCATT	0.28	7	43.44
Cq00876_185	530859389	C/T	**GAAGGTGACCAAGTTCATGCT**TGTATGTGGTCCCAACATACAACG	**GAAGGTCGGAGTCAACGGATT**GTTGTATGTGGTCCCAACATACAACA	CCTCTTATTTTTTTTGGTACACTGCCGAT	NT	7	43.53
Cq03260_449	530859612	A/C	**GAAGGTGACCAAGTTCATGCT**TCAATATAATGTTTTTCATTGGTTGGATAGT	**GAAGGTCGGAGTCAACGGATT**CAATATAATGTTTTTCATTGGTTGGATAGG	GCTCCTCCCACTCACCCATCAA	0.17	7	43.94
Cq07647_1388	530860027	A/C	**GAAGGTGACCAAGTTCATGCT**CCTAAGTTTAGCACCCGGAGCTT	**GAAGGTCGGAGTCAACGGATT**CTAAGTTTAGCACCCGGAGCTG	CCATACATGTAGCCGGCCCTCTT	0.05	7	46.20
Cq00539_107	530859355	A/G	**GAAGGTGACCAAGTTCATGCT**CAAGTATCATGTTTGGCTTAAGAAGAAAT	**GAAGGTCGGAGTCAACGGATT**CAAGTATCATGTTTGGCTTAAGAAGAAAC	GGACTCATGGGAGAATGACAAAATTGATT	0.09	7	46.49
Cq00309_67	530859326	A/C	**GAAGGTGACCAAGTTCATGCT**AA	**GAAGGTCGGAGTCAACGGATT**AA	CAAGAGAACTAACAATACTCATGGTT	0.47	7	46.69

			GAGATTTAACAATCGTCATAAGTATATTAA	GAGATTTAACAATCGTCATAAGTATATTAC	GAAA			
Cq07860_1423	530860053	A/T	**GAAGGTGACCAAGTTCATGCT**CCCCATTTCTAAGCCAATGAAGCA	**GAAGGTCGGAGTCAACGGATT**CCCCATTTCTAAGCCAATGAAGCT	GAATAAGTATGCTGTAGCTCATAGTAGGAA	0.06	7	46.90
Cq00284	530859324	A/C	**GAAGGTGACCAAGTTCATGCT**CGGTAGTATAAATGTACGAATATAAATTGTTTT	**GAAGGTCGGAGTCAACGGATT**GGTAGTATAAATGTACGAATATAAATTGTTTG	TTGATGGTCGGATAATACGCCATTATCTA	0.48	7	46.94
Cq08444_1549	530860107	A/G	**GAAGGTGACCAAGTTCATGCT**GTGCGGTCTCAGTTATTTCCTTGA	**GAAGGTCGGAGTCAACGGATT**GCGGTCTCAGTTATTTCCTTGG	CCGACTGCTAAGACTTGGAGAACAA	NT	7	47.21
Cq07642_1387	530860025	C/T	**GAAGGTGACCAAGTTCATGCT**CATAATGAGTGTATACTTGTGACGG	**GAAGGTCGGAGTCAACGGATT**GTCATAATGAGTGTATACTTGTGACGA	GTTTAGAACTGTACCGGATCGACCTA	0.37	7	47.87
Cq01301	530859431	G/T	**GAAGGTGACCAAGTTCATGCT**TGTTACAAAAGGGGATTCAATTG	**GAAGGTCGGAGTCAACGGATT**GGCTTGTTACAAAAGGGGATTCAATTT	TACAGGGTATGAGGAAGCCTAATGTTTAT	0.17	7	50.07
Cq05101_881	530859790	C/T	**GAAGGTGACCAAGTTCATGCT**CACAAAAGTCTTTTGTCTTTTAATAGGAATG	**GAAGGTCGGAGTCAACGGATT**ACACAAAAGTCTTTTGTCTTTTAATAGGAATA	CACAGTCTCACTCCTGTTTACCTCAA	0.48	7	60.45
Cq10455_1761	530860180	A/G	**GAAGGTGACCAAGTTCATGCT**CCTGTACCATCGGACCAGGAT	**GAAGGTCGGAGTCAACGGATT**CCTGTACCATCGGACCAGGAC	GTTGACTTCATAGTCATCACCACATTCAT	NT	7	66.28
Cq07746_1404	530860037	C/T	**GAAGGTGACCAAGTTCATGCT**GTTTCAATGGTGGTGGTTTGCATAG	**GAAGGTCGGAGTCAACGGATT**GGTTTCAATGGTGGTGGTTTGCATAA	CTTTCAAAGGCATCAAGCCCACCTT	0.17	8	0.00
Cq02999_566	530859595	A/C	**GAAGGTGACCAAGTTCATGCT**CAAGAAAGACGGAATAATGTATTTCACAT	**GAAGGTCGGAGTCAACGGATT**CAAGAAAGACGGAATAATGTATTTCACAG	GTCTATACTTGCAAGTTTTCTGAGTGTGTA	0.32	8	0.77
Cq02983_564	530859591	A/G	**GAAGGTGACCAAGTTCATGCT**GGACTTCATTATATGTTCCTTTATTCATTATTT	**GAAGGTCGGAGTCAACGGATT**GACTTCATTATATGTTCCTTTATTCATTATTC	GAAACCCATGTGTCTTTGTACATGATACAA	0.15	8	4.76
Cq07710_1402	530860034	A/T	**GAAGGTGACCAAGTTCATGCT**TGTTTAGAAATGGGAGTCTCGCGT	**GAAGGTCGGAGTCAACGGATT**GTTTAGAAATGGGAGTCTCGCGA	GAGGGTTGGTAGATGAGAGAGAAAATAAA	0.48	8	7.69
Cq01153	530859415	C/T	**GAAGGTGACCAAGTTCATGCT**GTGTTAGGTGTGGAAGCATTTCTTC	**GAAGGTCGGAGTCAACGGATT**AGTGTTAGGTGTGGAAGCATTTCTTT	CGTTGTCGTGGAAGAAAAAGAGCTGTT	0.4	8	14.66
Cq02419_478	530859551	A/G	**GAAGGTGACCAAGTTCATGCT**CGCAGTCTCTGAAATCTTCACAGT	**GAAGGTCGGAGTCAACGGATT**GCAGTCTCTGAAATCTTCACAGC	GTGAAGCATGTTCGATGTCACTGTGTT	0.35	8	23.12
Cq04118_530	530859695	C/T	**GAAGGTGACCAAGTTCATGCT**CAAAAGAGGCACAAGGATATCTGG	**GAAGGTCGGAGTCAACGGATT**CAAAAGAGGCACAAGGATATCTGA	CCATAGAAGCATTTCGTAGAGGTCTAAAT	0.27	8	24.31
Cq01807_282	530859479	C/T	**GAAGGTGACCAAGTTCATGCT**AAGGGAGCCAAATCTCAGTAACAC	**GAAGGTCGGAGTCAACGGATT**AAGGGAGCCAAATCTCAGTAACAT	ATTTTTGTAGAGTTGAGTTGAGTTGGAGAT	0.49	8	24.98
Cq06309_1101	530859877	A/G	**GAAGGTGACCAAGTTCATGCT**ATCGTGCCAATAGGAAGGAGCAA	**GAAGGTCGGAGTCAACGGATT**CGTGCCAATAGGAAGGAGCAG	TAATTCACCAAGCATATGCCTTGCCAATT	0.47	8	32.57
Cq06007_1029	530859850	C/G	**GAAGGTGACCAAGTTCATGCT**GAAAATCTTGAATGACTATCTAAATTTATGG	**GAAGGTCGGAGTCAACGGATT**GAAAATCTTGAATGACTATCTAAATTTATGC	CTGGTATATATATATTTCCAATTTGACTTA	0.39	8	47.52
Cq04146_737	530859699	C/T	**GAAGGTGACCAAGTTCATGCT**CACTATTTAATTCTAAACCACAATTATATAGAG	**GAAGGTCGGAGTCAACGGATT**CACTATTTAATTCTAAACCACAATTATATAGAA	CCATGTTAAAACCATTTATTTATGGAGTAA	0.5	8	50.71
Cq01516_311	530859443	G/T	**GAAGGTGACCAAGTTCATGCT**CATTGTTGGCAAGCATACTCCAAAG	**GAAGGTCGGAGTCAACGGATT**CCATTGTTGGCAAGCATACTCCAAAT	TCTTAAAGGATTAGAGGTGGCACTCTT	0.34	8	53.17
Cq07028_1256	530859960	A/G	**GAAGGTGACCAAGTTCATGCT**CTCATGGATCTATCCAGCGCAA	**GAAGGTCGGAGTCAACGGATT**CTCATGGATCTATCCAGCGCAG	CTGCAAGGACATTATGGTCACAAATCATT	0.31	8	54.81
Cq01144_234	530859414	G/T	**GAAGGTGACCAAGTTCATGCT**CTCTATATTTATCGAGCTATCTTATCAA	**GAAGGTCGGAGTCAACGGATT**TTCTCTATATTTATCGAGCTATCTTATC	CTGGGTGATTGTATTAATTACTATCGAATT	0.29	8	55.58

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Cq00070_3	530859299	C/T	**GAAGGTGACCAAGTTCATGCT**TTTTATAGTAAAATTAACCCCGGCCC	**GAAGGTCGGAGTCAACGGATT**TTTTTATAGTAAAATTAACCCCGGCCT	GGTGTGATTAAATTTGACAAATCCCAATTA	0.32	8	55.89
Cq06120_730	530859859	C/T	**GAAGGTGACCAAGTTCATGCT**ACTACAATCATACTAACCAACATTATAACC	**GAAGGTCGGAGTCAACGGATT**CAACTACAATCATACTAACCAACATTATAACT	GTTAGTTTAGTTGATAAAAACCGTGTCTTT	0.31	8	56.46
Cq09636_1658	530860160	A/G	**GAAGGTGACCAAGTTCATGCT**CCCATCTGTGCAATGCAGAACCA	**GAAGGTCGGAGTCAACGGATT**CCATCTGTGCAATGCAGAACCG	GTTTGATACTTAGCTTATGTCTACTCAGTT	NT	8	58.16
Cq04220_750	530859708	G/T	**GAAGGTGACCAAGTTCATGCT**AGAGGCACAATCCTCCAGTCC	**GAAGGTCGGAGTCAACGGATT**CAGAGGCACAATCCTCCAGTCA	CACTGTGCGAAGTTCTCTGCCTTT	0.16	8	58.73
Cq03766	530859667	A/C	**GAAGGTGACCAAGTTCATGCT**AAGGAAAAGACGGGGTTGTGGAAAT	**GAAGGTCGGAGTCAACGGATT**GGAAAAGACGGGGTTGTGGAAAG	AACCCTTGCTTCTCCGCAACCAATT	0.3	8	62.27
Cq00356_66	530859329	C/T	**GAAGGTGACCAAGTTCATGCT**CCTGGTGCGAGGCACAACC	**GAAGGTCGGAGTCAACGGATT**GCCTGGTGCGAGGCACAACT	GGAAAAGAAAACACACACACCTAAAGAT	0.49	9	0.00
Cq00274_53	530859321	G/T	**GAAGGTGACCAAGTTCATGCT**CAAACTATTTCTTTCCACCCATGCTG	**GAAGGTCGGAGTCAACGGATT**CAAACTATTTCTTTCCACCCATGCTT	GATATCTTTCATAGCTCAATAGGGGAAAAT	0.37	9	13.77
Cq10656_1782	530860188	C/T	**GAAGGTGACCAAGTTCATGCT**CACGTTCAATTTAGGCACATATATTAAGG	**GAAGGTCGGAGTCAACGGATT**ACACGTTCAATTTAGGCACATATATTAAGA	CCTTGCATTAATTAGTATACCCCACTTGTT	0.25	9	18.61
Cq02231	530859522	A/G	**GAAGGTGACCAAGTTCATGCT**CGAATATAATTCTTGAGAACCTTGACATTA	**GAAGGTCGGAGTCAACGGATT**GAATATAATTCTTGAGAACCTTGACATTG	GCTTTGATGAATTGAAGATCGGACAACTT	0.21	9	24.64
Cq08242_1499	530860088	C/T	**GAAGGTGACCAAGTTCATGCT**CCTTTGCCCACCCTATGTAGC	**GAAGGTCGGAGTCAACGGATT**AATTCCTTTGCCCACCCTATGTAGT	CCACAACACAGAATGAGCATATGAAACAA	NT	9	25.79
Cq09993_1704	530860165	A/C	**GAAGGTGACCAAGTTCATGCT**AAATGTACAACATATAATCAAAGTAAACACAT	**GAAGGTCGGAGTCAACGGATT**AAATGTACAACATATAATCAAAGTAAACACAG	CTCTGTAGGAGTTACATGGTTTTACCTTA	0.21	9	28.65
Cq09010_1146	530860142	A/G	**GAAGGTGACCAAGTTCATGCT**GACTTCACATCAACCAAGGCTGT	**GAAGGTCGGAGTCAACGGATT**GACTTCACATCAACCAAGGCTGC	GTATATTAATTCGTTGTTCACATGGTTGTT	0.28	9	29.58
Cq00851_181	530859385	A/G	**GAAGGTGACCAAGTTCATGCT**GTACGAAAAAGTGAAAATGGAGAAATTGA	**GAAGGTCGGAGTCAACGGATT**GTACGAAAAAGTGAAAATGGAGAAATTGG	GACATTTTGAGCAATATCGTGCATGAGAT	0.26	9	29.72
Cq09993_1703	530860164	C/T	**GAAGGTGACCAAGTTCATGCT**AAGGTAAAACCATGTAACTCCTACAG	**GAAGGTCGGAGTCAACGGATT**GTAAGGTAAAACCATGTAACTCCTACAA	GGTTGATGCTATGTTTTTTATCCTTTATTT	0.28	9	30.18
Cq00541_106	530859357	C/T	**GAAGGTGACCAAGTTCATGCT**CCACTTCTTGTTCCATTACCAGTC	**GAAGGTCGGAGTCAACGGATT**CTCCACTTCTTGTTCCATTACCAGTT	TCTTTTGATGTCATTTATAGGCGGGGATA	0.25	9	39.41
Cq04469_800	530859739	A/C	**GAAGGTGACCAAGTTCATGCT**AGATTCATTTGAAAACTATGAATCTTGTTTAA	**GAAGGTCGGAGTCAACGGATT**AGATTCATTTGAAAACTATGAATCTTGTTTAC	CCTTTCTCCTAACTTGGAGAAGGGTT	0.28	9	39.52
Cq04356_774	530859730	C/T	**GAAGGTGACCAAGTTCATGCT**GAGTAAATTCAGTTATTTATCAACATTCATAC	**GAAGGTCGGAGTCAACGGATT**GAGTAAATTCAGTTATTTATCAACATTCATAT	GTTCTAATATTGTCTTTTGGGTGGACATTT	0.29	9	41.52
Cq02163_417	530859517	C/T	**GAAGGTGACCAAGTTCATGCT**AAAATGTATAGAGGCTGAGCCGG	**GAAGGTCGGAGTCAACGGATT**CAAAATGTATAGAGGCTGAGCCGA	GTCGGTAACCCAAACCTTGTGAAGAT	0.45	9	43.47
Cq03504_645	530859641	A/T	**GAAGGTGACCAAGTTCATGCT**CAGGATTTTGTTAAAATATACTTCCTCA	**GAAGGTCGGAGTCAACGGATT**CAGGATTTTGTTAAAATATACTTCCTCT	ATGACTACTGCAAAAGTTCAATTGTTGCAA	0.41	9	48.40
Cq05618_956	530859826	A/C	**GAAGGTGACCAAGTTCATGCT**CTCTCTATATCTCTGGCCTCAATTT	**GAAGGTCGGAGTCAACGGATT**CTCTCTATATCTCTGGCCTCAATTG	GCTCATAATCGGCTTCAATGGAGAATATA	0.5	9	55.69

Cq01075_194	530859405	C/G	**GAAGGTGACCAAGTTCATGCT**GTTGCCTGAACATTGGCGGTC	**GAAGGTCGGAGTCAACGGATT**GTTGCCTGAACATTGGCGGTG	CAGATTCATGCCTAATGTCTTCGTCTT	0.3	9	57.41
Cq08095_1467	530860072	C/T	**GAAGGTGACCAAGTTCATGCT**CTCCTATTGACTGCAAATCCAC	**GAAGGTCGGAGTCAACGGATT**CTCTCTCCTATTGACTGCAAATCCAT	AACAAGCATCAAACCAGGAGTTGGAATTA	NT	9	59.21
Cq02259_431	530859528	C/T	**GAAGGTGACCAAGTTCATGCT**ATGATTTATTATTTGCAATCTTGTACATATATG	**GAAGGTCGGAGTCAACGGATT**ATGATTTATTATTTGCAATCTTGTACATATATA	CAACAAATATAAAACGATACTCAAATCCAA	0.17	9	61.35
Cq00346_64	530859327	A/T	**GAAGGTGACCAAGTTCATGCT**GTGTAAAAACCTAAGCACCTAGTCTT	**GAAGGTCGGAGTCAACGGATT**GTGTAAAAACCTAAGCACCTAGTCTA	GGAAGGTTTTGGGCTTCCTAACCTA	0.05	10	0.00
Cq03197_434	530859604	A/C	**GAAGGTGACCAAGTTCATGCT**CCCGAGTGGTTTGAGGAGAAGA	**GAAGGTCGGAGTCAACGGATT**CCGAGTGGTTTGAGGAGAAGC	CAACCACCTTTGACCCGAAGCTATA	0.19	10	10.88
Cq08420_1547	530860102	C/T	**GAAGGTGACCAAGTTCATGCT**CACAACCACCAATTCACGCCTG	**GAAGGTCGGAGTCAACGGATT**AATCACAACCACCAATTCACGCCTA	TCTCTTAATCCTTTAAGTTGTTGCCTCATT	0.28	10	13.03
Cq05970_1024	530859849	A/G	**GAAGGTGACCAAGTTCATGCT**AATTTATTTATATGTTTACGTACACTAATA	**GAAGGTCGGAGTCAACGGATT**GCTAATTTATTTATATGTTTACGTACACTAATG	TTAAACTGCAACACATCGCTTCAGTCAAA	0.49	10	18.14
Cq04338_557	530859729	C/T	**GAAGGTGACCAAGTTCATGCT**ACTTAATGCAAACTTTTTGGCTCCTTC	**GAAGGTCGGAGTCAACGGATT**AAACTTAATGCAAACTTTTTGGCTCCTTT	CCCTCCATTTTTGCCAAAAAAATCTTCATT	0.27	10	22.39
Cq04523_807	530859744	G/T	**GAAGGTGACCAAGTTCATGCT**ATTTCTCTTCTTCTAATGAATAAGTCTCAC	**GAAGGTCGGAGTCAACGGATT**TCTCTTCTTCTAATGAATAAGTCTCAA	ATCAGCCTAAACTTAGCTGTTCACAAGTT	NT	10	22.70
Cq03713_678	530859660	A/G	**GAAGGTGACCAAGTTCATGCT**GGTGGTACCATCATAAGTACCTACT	**GAAGGTCGGAGTCAACGGATT**GTGGTACCATCATAAGTACCTACC	CGTCACAGCCGGTCAAGGTTAAAAT	0.23	10	22.87
Cq03432_475	530859634	A/G	**GAAGGTGACCAAGTTCATGCT**ATGTCCACTTGGGTATCCTGAGTA	**GAAGGTCGGAGTCAACGGATT**GTCCACTTGGGTATCCTGAGTG	CAATGGAGTGGGTAGTTGGAGTTGAA	0.27	10	23.34
Cq05089_879	530859788	G/T	**GAAGGTGACCAAGTTCATGCT**GGAAGCTAAGAGGAGTTACCTTTG	**GAAGGTCGGAGTCAACGGATT**GGGAAGCTAAGAGGAGTTACCTTTT	GTACAGGTGGGCTACACGACCAT	0.3	10	23.36
Cq03418_473	530859632	A/G	**GAAGGTGACCAAGTTCATGCT**CAAGTAACTCTTTAAACTACATTTACCCTAAT	**GAAGGTCGGAGTCAACGGATT**AGTAACTCTTTAAACTACATTTACCCTAAC	GGCTTATAAATGAAAGAATTAGGGCAAGAT	0.42	10	23.54
Cq02026	530859498	A/G	**GAAGGTGACCAAGTTCATGCT**TATCTCTGTACGATTTTTCACACTATAAA	**GAAGGTCGGAGTCAACGGATT**ATCTCTGTACGATTTTTCACACTATAAG	GCAACACTCAAAGGGTTAATTCCCATAAT	0.31	10	27.52
Cq07774_1006	530860042	C/T	**GAAGGTGACCAAGTTCATGCT**AAAGTTGGTATTATAACACCTTGGTATAC	**GAAGGTCGGAGTCAACGGATT**AAAGTTGGTATTATAACACCTTGGTATAT	CACCCAACTATGGGCAATAGCTCAA	0.16	10	30.60
Cq08239_1498	530860086	A/G	**GAAGGTGACCAAGTTCATGCT**CATCTTTCAGGCTCTTTAGATATCAAAGA	**GAAGGTCGGAGTCAACGGATT**CTTTCAGGCTCTTTAGATATCAAAGG	TCAGAAATTTGGTTGTTTCTTTCAGGGTTT	0.38	10	32.09
Cq02438_480	530859552	A/T	**GAAGGTGACCAAGTTCATGCT**CCCTCTTTATTCTTAGAAAACACTCGTA	**GAAGGTCGGAGTCAACGGATT**CCCTCTTTATTCTTAGAAAACACTCGTT	GTGATGGAAACTTAGTCACTTGTAACCTA	0.38	10	32.15
Cq02820_535	530859575	C/G	**GAAGGTGACCAAGTTCATGCT**CATATACATGTCAATATAATCATAAGAATTGC	**GAAGGTCGGAGTCAACGGATT**CATATACATGTCAATATAATCATAAGAATTGG	GGGGAAATTTTAGACTCAATTGAAATGCAT	0.32	10	32.39
Cq02917	530859588	A/G	**GAAGGTGACCAAGTTCATGCT**CGGCACCTTGGAAGCCACATATA	**GAAGGTCGGAGTCAACGGATT**GGCACCTTGGAAGCCACATATG	GCAAAATCGCCCAAAACACACCCTT	NT	10	32.76
Cq00425_85	530859345	C/T	**GAAGGTGACCAAGTTCATGCT**GCCGTTTCCCCGACAACGG	**GAAGGTCGGAGTCAACGGATT**AAGCCGTTTCCCCGACAACGA	GTAGTAACGACCTATTATCTACCGATCAA	NT	10	32.90

Cq06868_1235	530859940	A/C	**GAAGGTGACCAAGTTCATGCT**GTCTGTTCCATACACATCACAATGCA	**GAAGGTCGGAGTCAACGGATT**CTGTTCCATACACATCACAATGCC	GGACATAGAGATGTTTAGTCGACTACATA	NT	10	34.47
Cq07095_895	530859965	A/G	**GAAGGTGACCAAGTTCATGCT**GTTCAACATCCCTGATTCATGAGAGT	**GAAGGTCGGAGTCAACGGATT**CAACATCCCTGATTCATGAGAGC	GTTTGAAGATTAGAGTCGGAATTGAATCTT	NT	10	37.89
Cq05865_694	530859841	A/G	**GAAGGTGACCAAGTTCATGCT**AACAAATCTATCCAATCAAATCTAACGTGT	**GAAGGTCGGAGTCAACGGATT**CAAATCTATCCAATCAAATCTAACGTGC	CGAGTCACGTAGGCGACAAATAGAT	NT	10	39.91
Cq07798_1415	530860046	C/T	**GAAGGTGACCAAGTTCATGCT**TCACAAATCGAAGTCCTCATCATAAC	**GAAGGTCGGAGTCAACGGATT**TTCACAAATCGAAGTCCTCATCATAAT	GTTCTTGCCAAGTTGCCATGCATTGAA	0.25	10	45.89
Cq01059_221	530859403	C/T	**GAAGGTGACCAAGTTCATGCT**TGCTGCCTTGTTGAAACACTACAG	**GAAGGTCGGAGTCAACGGATT**TGCTGCCTTGTTGAAACACTACAA	GTGTAATTATAGCAGAATGAAACTGCACAA	0.09	10	47.31
Cq02067_387	530859505	A/G	**GAAGGTGACCAAGTTCATGCT**TTATTCATGTGGTTTAGAAGATTGCCAAT	**GAAGGTCGGAGTCAACGGATT**CATGTGGTTTAGAAGATTGCCAAC	GTGGAAGAAGAGATATTACAGGTGATTGAA	0.1	10	47.72
Cq02187	530859519	A/C	**GAAGGTGACCAAGTTCATGCT**ATGTTTACAAGGTTTACTCAAATTGTAAACAAA	**GAAGGTCGGAGTCAACGGATT**GTTTACAAGGTTTACTCAAATTGTAAACAAC	CGAAGTATCTTCCTAACCTTCTCTTCATT	0.4	10	50.55
Cq03316	530859623	A/T	**GAAGGTGACCAAGTTCATGCT**CAATGGCAATGCTAATGACCAGAAT	**GAAGGTCGGAGTCAACGGATT**CAATGGCAATGCTAATGACCAGAAA	CGCGTGCATGTTTCATATACCCTCAA	0.07	10	56.51
Cq02870_541	530859582	C/T	**GAAGGTGACCAAGTTCATGCT**GGGTGGCTTGAAAGAGACTCG	**GAAGGTCGGAGTCAACGGATT**AATGGGTGGCTTGAAAGAGACTCA	GTCTTGTGCATCAACTTAAACACTCCTAA	0.17	10	60.14
Cq11499_1871	530860195	A/C	**GAAGGTGACCAAGTTCATGCT**GCCATGTATTTGAAGGAAGAGGA	**GAAGGTCGGAGTCAACGGATT**GCCATGTATTTGAAGGAAGAGGC	CACGTTTCCATTATCCCTCCACCAA	NT	11	0.00
Cq07692_1398	530860032	A/G	**GAAGGTGACCAAGTTCATGCT**GGGAGAGGGAAGGAGAGCAGA	**GAAGGTCGGAGTCAACGGATT**GGGAGAGGGAAGGAGAGCAGG	CTTTGTTCCTCGTGTCTTCCTTAGATTAT	0.19	11	16.90
Cq06298_759	530859873	G/T	**GAAGGTGACCAAGTTCATGCT**GAGAGAATTAAGCTGTATTTTAGGGATTG	**GAAGGTCGGAGTCAACGGATT**AGAGAGAATTAAGCTGTATTTTAGGGATTT	ACCAAACTTTGCTTTGAAACA	0.31	11	17.23
Cq00829_177	530859382	C/T	**GAAGGTGACCAAGTTCATGCT**AAATGGAATTAAGAAATTAAAGGAAGAAAATTG	**GAAGGTCGGAGTCAACGGATT**AAATGGAATTAAGAAATTAAAGGAAGAAAATTA	TTATGTTTTTCCTTCCTCCAATTGCTCAAT	NT	11	21.97
Cq08765_1586	530860133	A/G	**GAAGGTGACCAAGTTCATGCT**CATAACACAATATCGAAGGCAGTAGA	**GAAGGTCGGAGTCAACGGATT**CATAACACAATATCGAAGGCAGTAGG	GCCCATGCAGAGGGGGATTTGAT	NT	11	23.78
Cq04257_546	530859713	C/T	**GAAGGTGACCAAGTTCATGCT**CAAAGGAAATTTGCAAAAGTCAATGGG	**GAAGGTCGGAGTCAACGGATT**ATCAAAGGAAATTTGCAAAAGTCAATGGA	GCCTTGAGATCATTAATTCGATCATAACTA	0.04	11	35.15
Cq01329	530859436	A/T	**GAAGGTGACCAAGTTCATGCT**CAACACTATAGAAAAGCAGCTATAAGTAAA	**GAAGGTCGGAGTCAACGGATT**CAACACTATAGAAAAGCAGCTATAAGTAAT	GGTGAGATATGGTGCGCCATGTAAA	0.3	11	35.42
Cq06989_878	530859956	C/T	**GAAGGTGACCAAGTTCATGCT**ATTTCGAATTAAATATTGATGTTGCAGCTC	**GAAGGTCGGAGTCAACGGATT**CATTTCGAATTAAATATTGATGTTGCAGCTT	GTCCATAAATTCAAAGCATATACTACGCAT	NT	11	38.36
Cq02410_357	530859545	C/T	**GAAGGTGACCAAGTTCATGCT**GGATTCTCAAGGCACATTCAC	**GAAGGTCGGAGTCAACGGATT**GCTGGATTCTCAAGGCACATTCAT	AGCATTGGCAAAACCGAGGGATCAA	0.34	11	38.43
Cq08289_1510	530860093	A/G	**GAAGGTGACCAAGTTCATGCT**GAAATTTTCAGTCACAGTACACCAA	**GAAGGTCGGAGTCAACGGATT**GAAATTTTCAGTCACAGTACACCAG	CAGAACAAAGCTAATCGAGGCGGTT	0.4	11	46.17
Cq06771_1211	530859926	A/G	**GAAGGTGACCAAGTTCATGCT**ACGCTCAAACCAATGGCCCTT	**GAAGGTCGGAGTCAACGGATT**ACGCTCAAACCAATGGCCCTC	CACACTTGGCAAGCGAAGACCGAA	0.16	11	53.74
Cq06082_722	530859856	C/T	**GAAGGTGACCAAGTTCATGCT**ACAAAGCCATGGAGAAACTCTCG	**GAAGGTCGGAGTCAACGGATT**AGACAAAGCCATGGAGAAACTCTCA	CTTACCAAGGATGACCGAGCGGTA	NT	12	0.00

Cq02314_441	530859533	A/G	**GAAGGTGACCAAGTTCATGCT**AACCTGGAGGGGATGGAAGCT	**GAAGGTCGGAGTCAACGGATT**CCTGGAGGGGATGGAAGCC	CTCTTTCCGGAATGGGTACTCTGTT	0.36	12	7.05
Cq05310_922	530859801	A/C	**GAAGGTGACCAAGTTCATGCT**GTTCTTGGAACTTTCATCATTAGTTCCT	**GAAGGTCGGAGTCAACGGATT**CTTGGAACTTTCATCATTAGTTCCG	TGGAACAGCTGGCTCGATCTTTGAT	0.17	12	12.25
Cq09271_1636	530860149	A/G	**GAAGGTGACCAAGTTCATGCT**CGCCTTCCTTTCTTGCCACAGTA	**GAAGGTCGGAGTCAACGGATT**GCCTTCCTTTCTTGCCACAGTG	AGACCAGAAAAATGGCATGAGAGTGTTAT	0.15	12	12.30
Cq03218_590	530859609	C/G	**GAAGGTGACCAAGTTCATGCT**ATGATTGTCATAAATAATTTGCACAAGTATTAG	**GAAGGTCGGAGTCAACGGATT**ATGATTGTCATAAATAATTTGCACAAGTATTAC	CAGTATTCTCATAGGTCGTTCCGGTA	0.36	12	22.15
Cq03218_589	530859607	A/T	**GAAGGTGACCAAGTTCATGCT**ACAAGTATTACTTTAGAACTATACCGGAT	**GAAGGTCGGAGTCAACGGATT**ACAAGTATTACTTTAGAACTATACCGGAA	CACTTGTTGGAAGGACACCATTCCTT	0.42	12	23.78
Cq08070_1462	530860069	A/G	**GAAGGTGACCAAGTTCATGCT**AAAAAATCTGAATCCTTCTATGAAAAATAAGCT	**GAAGGTCGGAGTCAACGGATT**AAATCTGAATCCTTCTATGAAAAATAAGCC	GCCATAGGTAAAAAGTTCTCCTTTCCTTT	0.43	12	33.76
Cq03720_680	530859662	C/G	**GAAGGTGACCAAGTTCATGCT**CCGTATGTGCCCCATTAATCATAC	**GAAGGTCGGAGTCAACGGATT**CCGTATGTGCCCCATTAATCATAG	CCGTAGAGAGCAGGCTACTGGAA	0.4	12	45.36
Cq09567_1656	530860158	C/T	**GAAGGTGACCAAGTTCATGCT**CTTTAACATGATATCGGAGCCAGC	**GAAGGTCGGAGTCAACGGATT**GTCTTTAACATGATATCGGAGCCAGT	TGGGCCCTCCTTATATACACCACTT	0.41	12	53.28
Cq04304_766	530859722	A/G	**GAAGGTGACCAAGTTCATGCT**GCATATATGTACTGAAATTTTGAAAGGTTTGA	**GAAGGTCGGAGTCAACGGATT**CATATATGTACTGAAATTTTGAAAGGTTTGG	GTATAGTGACCATTATTGCAGTGGCAA	0.12	13	0.00
Cq03672	530859653	A/T	**GAAGGTGACCAAGTTCATGCT**AATGTCAATGAGAGTTAAAATTTACAATGTACA	**GAAGGTCGGAGTCAACGGATT**AATGTCAATGAGAGTTAAAATTTACAATGTACT	CGTGAAAAATGCCCATAAAGTCGTTCTT	0.25	13	5.52
Cq03263	530859616	A/T	**GAAGGTGACCAAGTTCATGCT**GAAGATTGGCAATTTGCTTCCAGAAT	**GAAGGTCGGAGTCAACGGATT**GAAGATTGGCAATTTGCTTCCAGAAA	GAGAGGTACAAAGTTTGGTGTAGCGAA	0.32	13	8.00
Cq01607_330	530859456	C/T	**GAAGGTGACCAAGTTCATGCT**CAATGTACATAGAATCAAATTTGAGCAATTAG	**GAAGGTCGGAGTCAACGGATT**CAATGTACATAGAATCAAATTTGAGCAATTAA	TGGCCCATCTTAATTATATACTTATTCCAT	0.02	13	16.83
Cq00965	530859398	A/G	**GAAGGTGACCAAGTTCATGCT**TTCTTTGAAGAGGTGATATATAGAATATGTT	**GAAGGTCGGAGTCAACGGATT**CTTTGAAGAGGTGATATATAGAATATGTC	GCACCATTTCTTAGACCTATAACTCCAAA	0.49	13	32.07
Cq03600_654	530859648	C/T	**GAAGGTGACCAAGTTCATGCT**ACCGCTACCAGAGTTCCTAC	**GAAGGTCGGAGTCAACGGATT**CCTACCGCTACCAGAGTTCCTAT	TAAGAGTAGTTTTCATTCTCAGCCTCACT	0.37	13	35.10
Cq04713_841	530859762	A/G	**GAAGGTGACCAAGTTCATGCT**GATCTCTTATGCAAATAATGTAATTGATCAATA	**GAAGGTCGGAGTCAACGGATT**ATCTCTTATGCAAATAATGTAATTGATCAATG	CAGTACTAAAAGATCTTCTTGGTCTGTCAT	0.36	13	41.99
Cq01231_263	530859422	C/T	**GAAGGTGACCAAGTTCATGCT**GTGATTTCCCCAAACCAAGCGG	**GAAGGTCGGAGTCAACGGATT**GGTGATTTCCCCAAACCAAGCGA	ATAATATTGAAAGCTTACCCGCCTGCTT	0.4	13	44.96
Cq06024_716	530859852	A/T	**GAAGGTGACCAAGTTCATGCT**CGTAGTTTATGCCCCTGTTGTCTATT	**GAAGGTCGGAGTCAACGGATT**CGTAGTTTATGCCCCTGTTGTCTATA	TGCCTTAGGTATCATTATACCTTGGCTTT	0.17	13	52.92
Cq02712	530859572	A/T	**GAAGGTGACCAAGTTCATGCT**CTTGAAATATATCACGCAATCTATTCCAT	**GAAGGTCGGAGTCAACGGATT**CTTGAAATATATCACGCAATCTATTCCAA	CTTGCACACCATCATTGAACCCGAT	0.32	14	0.00
Cq00517	530859348	G/T	**GAAGGTGACCAAGTTCATGCT**ACCCGAATAATAGTGTTGGTGG	**GAAGGTCGGAGTCAACGGATT**CCTACCCGAATAATAGTGTTGGTGT	GTAAAAAAAAAAATTTCTTCTCTCCAGCCA	0.33	14	4.05
Cq05054_873	530859787	A/T	**GAAGGTGACCAAGTTCATGCT**CACAATTCTAAATTTCACCCCAAAAAAATTTAT	**GAAGGTCGGAGTCAACGGATT**CACAATTCTAAATTTCACCCCAAAAAAATTTAA	CCTCTTTATCTTCCATTTGCCCTCTTTAT	0.19	14	15.63

Cq10080_1218	530860169	A/G	**GAAGGTGACCAAGTTCATGCTCA**AAAGCTATACACCGATGCTAAGTTT	**GAAGGTCGGAGTCAACGGATT**AAAAGCTATACACCGATGCTAAGTTC	ATCATAACAGTACATCATCCGGGAAAGTT	0.13	14	16.95
Cq05264_908	530859795	C/T	**GAAGGTGACCAAGTTCATGCTCA**CTTTGTATATGTCTCCGACCATG	**GAAGGTCGGAGTCAACGGATT**ACACTTTGTATATGTCTCCGACCATA	CTTACCCCCTCTATAAAAAATGACGGAAA	0.28	14	20.04
Cq01536	530859447	C/T	**GAAGGTGACCAAGTTCATGCT**AGTTTTGAGGTGATTAGAGTCTCTTTG	**GAAGGTCGGAGTCAACGGATT**CAGTTTTGAGGTGATTAGAGTCTCTTTA	GTCTTTATTACTTCCCACTCTAATCACCTT	0.29	14	27.56
Cq01240_217	530859424	A/C	**GAAGGTGACCAAGTTCATGCT**AAAGCATCGTTCATTAATGAGCTTTTTATTTAA	**GAAGGTCGGAGTCAACGGATT**GCATCGTTCATTAATGAGCTTTTTATTTAC	CCAGAACTTGGAATGTAGATAACTTGAAAA	NT	14	30.38
Cq07754_1406	530860041	A/G	**GAAGGTGACCAAGTTCATGCT**ACTTTGAGGATGTCAAGGAAGCCA	**GAAGGTCGGAGTCAACGGATT**CTTTGAGGATGTCAAGGAAGCCG	CCACCAACTGGTCAACCTTTCTCTT	NT	14	30.61
Cq03236_595	530859611	C/T	**GAAGGTGACCAAGTTCATGCTCA**ATTCAATCAAATCAAGAAAAAAGAAAACCC	**GAAGGTCGGAGTCAACGGATT**CAATTCAATCAAATCAAGAAAAAAGAAAACCT	GGTGCTTATTTTCGACGAGACTTCAATT	0.28	14	41.53
Cq05024_869	530859785	C/T	**GAAGGTGACCAAGTTCATGCT**CCTAAGTCCCTAACTTAGATTCACC	**GAAGGTCGGAGTCAACGGATT**AACCTAAGTCCCTAACTTAGATTCACT	CTGAGTGTATGAGCATTCAGGGAGT	0.16	14	41.86
Cq00826	530859380	C/T	**GAAGGTGACCAAGTTCATGCT**CCAACTGTGCAATGCACAAACGG	**GAAGGTCGGAGTCAACGGATT**ACCAACTGTGCAATGCACAAACGA	CTACTCATGTTGGAGCAGAAGTAAAATTTT	0.15	14	47.51
Cq05483_945	530859815	A/T	**GAAGGTGACCAAGTTCATGCT**TACTACCTCAAAAAGGGGGGCTTT	**GAAGGTCGGAGTCAACGGATT**ACTACCTCAAAAAGGGGGCTTA	GCTGGAAAATCCACTTAAACAGTAATCTAA	0.28	14	51.60
Cq02359	530859538	A/T	**GAAGGTGACCAAGTTCATGCT**GATTGATTACTATTGTCTACAAATAATGGGTA	**GAAGGTCGGAGTCAACGGATT**GATTACTATTGTCTACAAATAATGGGTT	GCCATAGCCAAAGAAGAGTATAATTTCTCT	0.34	15	0.00
Cq06241_1073	530859868	A/C	**GAAGGTGACCAAGTTCATGCT**CCTATCAATAAAACGATCATAATGTCGATAT	**GAAGGTCGGAGTCAACGGATT**CTATCAATAAAACGATCATAATGTCGATAG	AGCAAAAAACAGATATTTTGTGTGTAGTCC	0.31	15	0.86
Cq07839_1421	530860051	C/T	**GAAGGTGACCAAGTTCATGCT**GCATGCTTATCAACTCATGGACTAC	**GAAGGTCGGAGTCAACGGATT**ATGCATGCTTATCAACTCATGGACTAT	ATACAGATACAGGACTCAGGTCTTTCAA	NT	15	7.70
Cq07440_1334	530859995	A/G	**GAAGGTGACCAAGTTCATGCTCA**AAGTTCTTCTATGCTCAACCTTTTCT	**GAAGGTCGGAGTCAACGGATT**AAAGTTCTTCTATGCTCAACCTTTTCC	GGGATGTGTTAGTTTGGCTAAAGGGTT	0.24	15	9.71
Cq05321_924	530859804	G/T	**GAAGGTGACCAAGTTCATGCT**CGGAATTAGTAGTGTTGTTTTGATAGAC	**GAAGGTCGGAGTCAACGGATT**CGGAATTAGTAGTGTTGTTTTGATAGA	TTAATTAGTTAAAGTCTCGGCCTCTCCA	0.45	15	11.09
Cq08115_1486	530860081	A/G	**GAAGGTGACCAAGTTCATGCT**TGCTGCATTACAAGCAGAGATGA	**GAAGGTCGGAGTCAACGGATT**GCTGCATTACAAGCAGAGATGG	CTTTTCTGGCACGTGATTATAAACATAAAA	0.32	15	18.70
Cq01747_343	530859471	C/T	**GAAGGTGACCAAGTTCATGCT**CCATGAATGACTCACTTTATGCTCC	**GAAGGTCGGAGTCAACGGATT**ACCATGAATGACTCACTTTATGCTCT	CACATTCATTTGTGAAGCCTCTCACTT	NT	15	34.71
Cq00565	530859359	A/G	**GAAGGTGACCAAGTTCATGCT**ATCTTACAGTTCTTGAAGAGACATTAAGTA	**GAAGGTCGGAGTCAACGGATT**CTTACAGTTCTTGAAGAGACATTAAGTG	CCTTCCTGACAAGTGTGAAAATTGTGTAT	0.34	15	37.86
Cq00095_4	530859301	A/T	**GAAGGTGACCAAGTTCATGCT**TTACTCTTTACAAAAAGTATTTACAATCTCCA	**GAAGGTCGGAGTCAACGGATT**TACTCTTTACAAAAAGTATTTACAATCTCCT	GGCGGTTATCCAGAATCTGGAATGTA	0.12	15	38.50
Cq04336_770	530859727	A/G	**GAAGGTGACCAAGTTCATGCT**AATGGAAGTCCGACGGTGGAATT	**GAAGGTCGGAGTCAACGGATT**ATGGAAGTCCGACGGTGGAATC	GTCAATGGATCGGCTACATTGTCGTT	0.33	15	38.84
Cq08188_1496	530860084	A/T	**GAAGGTGACCAAGTTCATGCT**GATTTCTATACGAGGTAACATGCTCTT	**GAAGGTCGGAGTCAACGGATT**TCTATACGAGGTAACATGCTCTA	GCGTACTCGTGGGTGCCTATGAT	0.35	15	39.33
Cq10567_1773	530860185	A/T	**GAAGGTGACCAAGTTCATGCT**CCTCTTTAGCTGCTTCCGAAGTA	**GAAGGTCGGAGTCAACGGATT**CCTCTTTAGCTGCTTCCGAAGTT	GGAGGAGTGTTTAGTTAGAAGAGTGATAA	0.28	15	39.71

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Cq05334_927	530859806	A/C	**GAAGGTGACCAAGTTCATGCT**AAGCTATCGTTCCATTGTGGTCAT	**GAAGGTCGGAGTCAACGGATT**AAGCTATCGTTCCATTGTGGTCAG	GATTCAAAACCTCAATTGCTATTCCTCAAT	0.14	15	39.78
Cq08431_1097	530860104	A/T	**GAAGGTGACCAAGTTCATGCT**GTAAAAACCATTGACTAAAACAATTCGATCT	**GAAGGTCGGAGTCAACGGATT**GTAAAAACCATTGACTAAAACAATTCGATCA	CACAGATTATTGTTCATGGGCCTGTTATT	0.12	15	39.79
Cq05513_659	530859817	C/T	**GAAGGTGACCAAGTTCATGCT**TCGTGTAATGTAGGGTTTAGGGTC	**GAAGGTCGGAGTCAACGGATT**GTTCGTGTAATGTAGGGTTTAGGGTT	CAGGGAAATTATCCAATCCCAAACCTAAA	0.08	15	39.96
Cq01567_320	530859450	A/G	**GAAGGTGACCAAGTTCATGCT**GGGAGTTGCCAATCTATTGTTGGAT	**GAAGGTCGGAGTCAACGGATT**GGAGTTGCCAATCTATTGTTGGAC	ATGATGCCGCATGGTGTTGATGCTT	0.37	15	40.14
Cq06561_1168	530859910	C/T	**GAAGGTGACCAAGTTCATGCT**CCATGGGGTATTATTGGCCG	**GAAGGTCGGAGTCAACGGATT**CTCCATGGGGTATTATTGGCCA	GTTGACAAACCAAGCATGTCGAGGTA	0.33	15	40.16
Cq05831_995	530859840	A/T	**GAAGGTGACCAAGTTCATGCT**CCCAATCGTGTAACCGAACCGT	**GAAGGTCGGAGTCAACGGATT**CCCAATCGTGTAACCGAACCGA	TCATTTAGTCCTTTGGATAAATTTGTCGTT	0.31	15	40.39
Cq06368_1128	530859887	G/T	**GAAGGTGACCAAGTTCATGCT**TGCAAAATTACTATTCACTCCATTGC	**GAAGGTCGGAGTCAACGGATT**CTTGCAAAATTACTATTCACTCCATTGA	CAAGATATGGTCTTGATACCCTGTTTGAA	NT	15	40.52
Cq01869_360	530859484	C/T	**GAAGGTGACCAAGTTCATGCT**AACTTAAATTGAGAATCTCCGAAGACC	**GAAGGTCGGAGTCAACGGATT**CAAACTTAAATTGAGAATCTCCGAAGACT	GGGACTTGTAAAGTTCTTTGAGTATTCTTT	0.45	15	41.00
Cq01758_270	530859473	G/T	**GAAGGTGACCAAGTTCATGCT**AAATCAAATAGCAAGATAAAGAGAAAAGATTAC	**GAAGGTCGGAGTCAACGGATT**AAATCAAATAGCAAGATAAAGAGAAAAGATTAA	ACCACTTTTTAGACTTTCAACTTCAATCAA	0.29	15	42.08
Cq00969_205	530859399	C/T	**GAAGGTGACCAAGTTCATGCT**ATCCTCCTACCAAAGAGTCCAATC	**GAAGGTCGGAGTCAACGGATT**GATCCTCCTACCAAAGAGTCCAATT	GTGTACCTGTCGACCAATGCTTCTT	0.43	15	43.82
Cq03299_609	530859621	C/T	**GAAGGTGACCAAGTTCATGCT**ATAGGCTTAAAATGTAATGTAAATTACTTTTG	**GAAGGTCGGAGTCAACGGATT**ATAGGCTTAAAATGTAATGTAAATTACTTTTA	GGACTTTTGGATGTCATGTTGGGGAT	NT	15	49.21
Cq00132_7	530859306	A/G	**GAAGGTGACCAAGTTCATGCT**CAATCTCAAATACACACCTCATCATAAATAA	**GAAGGTCGGAGTCAACGGATT**AATCTCAAATACACACCTCATCATAAATAG	CAGCAAGACAGCAACAGAGACACAA	0.35	16	0.00
Cq06351_1126	530859886	G/T	**GAAGGTGACCAAGTTCATGCT**ACTTACCCTACTACATTGTTAGTTGG	**GAAGGTCGGAGTCAACGGATT**CTACTTACCCTACTACATTGTTAGTTGT	GAGGATGGGTACTGGTGCCGAA	0.29	16	15.78
Cq02275_438	530859531	A/G	**GAAGGTGACCAAGTTCATGCT**GAAGTGGCAAAGTACAAACGTCTTATA	**GAAGGTCGGAGTCAACGGATT**AAGTGGCAAAGTACAAACGTCTTATG	CAGTACACCCCACATATAAACCCTCAT	0.49	16	16.08
Cq04362_779	530859734	C/T	**GAAGGTGACCAAGTTCATGCT**TTTTTGTTTTAGGGTGCTTTTAATGTTG	**GAAGGTCGGAGTCAACGGATT**AACTTTTTTGTTTTAGGGTGCTTTTAATGTTA	CCAGATTCAAAACAAACCCATTTCCCAAA	0.27	16	16.15
Cq00277	530859322	A/G	**GAAGGTGACCAAGTTCATGCT**ATTTACTTGCCTAAAACTTTGTGAAAATACAAA	**GAAGGTCGGAGTCAACGGATT**ACTTGCCTAAAACTTTGTGAAAATACAG	GTTTTTGTGTAACATACTCCCTCTTTTCTT	0.3	16	19.36
Cq01112_231	530859408	G/T	**GAAGGTGACCAAGTTCATGCT**CAATCATACTCACATCAGCACCTG	**GAAGGTCGGAGTCAACGGATT**CCAATCATACTCACATCAGCACCTT	CGAGGTCCGGAACCAAGGAGTT	0.35	16	20.38
Cq02214	530859521	C/T	**GAAGGTGACCAAGTTCATGCT**GTTCTTTGATGTTGATCACTTATTGACAG	**GAAGGTCGGAGTCAACGGATT**GTTCTTTGATGTTGATCACTTATTGACAA	CATCTCCTCCTCTACATCAAAGTACAAT	NT	16	21.02
Cq00187_22	530859312	A/G	**GAAGGTGACCAAGTTCATGCT**ATTGAATTTAGAGAAAACATCAATTTAAATACA	**GAAGGTCGGAGTCAACGGATT**GAATTTAGAGAAAACATCAATTTAAATACG	GATTTAAAGCACGTTTTCCTCATGTGGAA	0.31	16	26.59
Cq06162_1058	530859861	A/T	**GAAGGTGACCAAGTTCATGCT**TAT	**GAAGGTCGGAGTCAACGGATT**AT	AGTTATAGCTAACTAAGTTCT	0.4	16	30.67

			AACTGCTTAGCTTGTCAAGTTTGTA	AACTGCTTAGCTTGTCAAGTTTGTT				
Cq02851_398	530859579	A/T	**GAAGGTGACCAAGTTCATGCT**AGCGTTCATGGAATAATTGATCATCTTAAA	**GAAGGTCGGAGTCAACGGATT**AGCGTTCATGGAATAATTGATCATCTTAAT	ATGGAATTATGGGTTTCCTTTTCCAATTTA	0.31	16	33.52
Cq04152_744	530859701	A/C	**GAAGGTGACCAAGTTCATGCT**AGTGACATATATTCGTGTGTTTGATTAAATTT	**GAAGGTCGGAGTCAACGGATT**GTGACATATATTCGTGTGTTTGATTAAATTG	CGAGATACAACTTGATCTTGTACTTGTTTA	0.25	16	34.11
Cq07328_1308	530859984	A/G	**GAAGGTGACCAAGTTCATGCT**TAGGAGATATCCAAGGAGGGGAA	**GAAGGTCGGAGTCAACGGATT**AGGAGATATCCAAGGAGGGGAG	GTGAGGAAAAAAATTCAATTTCGGACGGTT	0.33	16	34.34
Cq02819_533	530859573	C/T	**GAAGGTGACCAAGTTCATGCT**ACAAGTTTGCAAAATAAAATAACAAGCATTTC	**GAAGGTCGGAGTCAACGGATT**GACAAGTTTGCAAAATAAAATAACAAGCATTTT	CTGAGTACCATGTTTCCCAAGGGTA	0.33	16	36.12
Cq01155	530859417	A/G	**GAAGGTGACCAAGTTCATGCT**AAGAAGAAGAGAGTGGGTACAACCT	**GAAGGTCGGAGTCAACGGATT**GAAGAAGAGAGTGGGTACAACCC	TGTCAAACAATCTGGTGTTCTCAAGCAAT	0.46	16	36.54
Cq06921_874	530859951	A/G	**GAAGGTGACCAAGTTCATGCT**ATAAGTGTAAATCTGGAAATCATGACAACT	**GAAGGTCGGAGTCAACGGATT**AGTGTAAATCTGGAAATCATGACAACC	TTGCTCCGCCAATTGACGATCTCTT	NT	16	36.58
Cq06645_1188	530859915	G/T	**GAAGGTGACCAAGTTCATGCT**AAATTGGCATAAATTTGACACTTAAGGC	**GAAGGTCGGAGTCAACGGATT**GTAAATTGGCATAAATTTGACACTTAAGGA	GGTATTATTGGACTACCATGAATAGGGAT	NT	16	36.58
Cq09162_1154	530860144	C/T	**GAAGGTGACCAAGTTCATGCT**ATGATATATCAATGCTTGAATAAGTCAAGC	**GAAGGTCGGAGTCAACGGATT**AAATGATATATCAATGCTTGAATAAGTCAAGT	ATGTACTCAACATCTCCTAAGTCTCTCAA	0.18	16	36.58
Cq09433_1647	530860156	C/T	**GAAGGTGACCAAGTTCATGCT**GAGAATACTGACCGTAGACTTGAG	**GAAGGTCGGAGTCAACGGATT**GGAGAATACTGACCGTAGACTTGAA	CCGTCCATTCTGGTCCTCAAATGAT	NT	16	36.58
Cq03289_603	530859618	G/T	**GAAGGTGACCAAGTTCATGCT**GAGAGAGATTTAAAAAGAAACACATTTGC	**GAAGGTCGGAGTCAACGGATT**AAGAGAGAAGATTTAAAAAGAAACACATTTGA	GCTGAATATCTGCTGACAACCACCAA	0.18	16	36.62
Cq02255	530859524	C/T	**GAAGGTGACCAAGTTCATGCT**TAGAAAGATAATAAGTGTAGAAATATTATGTC	**GAAGGTCGGAGTCAACGGATT**AGAAAGATAATAAGTGTAGAAATATTATGTT	CAAAAGCTAAACATCCAGTTCTTGTATCAA	0.34	16	37.48
Cq03178	530859602	C/T	**GAAGGTGACCAAGTTCATGCT**ATAACCTACCGTGTCACGGCG	**GAAGGTCGGAGTCAACGGATT**CATAACCTACCGTGTCACGGCA	GCAACAAGCAGTAGCGGAAAATTTAGAAA	0.32	16	37.82
Cq06508_1158	530859903	C/T	**GAAGGTGACCAAGTTCATGCT**ATGAGTTTGATCAACCTACTGGCC	**GAAGGTCGGAGTCAACGGATT**GATGAGTTTGATCAACCTACTGGCT	CGAGTAAGTATGCCAATGTGATTAGAATAT	NT	16	38.56
Cq08861_1590	530860137	C/T	**GAAGGTGACCAAGTTCATGCT**CGTACTCACTCTTGTTCTATGAGAC	**GAAGGTCGGAGTCAACGGATT**CGTACTCACTCTTGTTCTATGAGAT	CATATATTAAACCAACATAGTTGCGTGTGT	NT	16	39.59
Cq02908_545	530859586	C/T	**GAAGGTGACCAAGTTCATGCT**ACAAGCTCATACTTAAATTAACAAATGACG	**GAAGGTCGGAGTCAACGGATT**ATAACAAGCTCATACTTAAATTAACAAATGACA	CCATGTAAGGACAAAGACGGTCCAT	0.03	16	40.76
Cq08722_1578	530860127	A/C	**GAAGGTGACCAAGTTCATGCT**CCTGTCGTAGAGCTGTCGCT	**GAAGGTCGGAGTCAACGGATT**CCTGTCGTAGAGCTGTCGCG	TGTCGTTTTGCGACAGACTCTGTCA	0.45	16	42.77
Cq03866_707	530859678	A/T	**GAAGGTGACCAAGTTCATGCT**TGATTTTATTGAGAAATTTTGTTATGTGAGCT	**GAAGGTCGGAGTCAACGGATT**GATTTTATTGAGAAATTTTGTTATGTGAGCA	CAAAGAAACAAGCTCATAACTTAAGTTCAA	0.3	16	48.04
Cq08584_1113	530860121	A/G	**GAAGGTGACCAAGTTCATGCT**AGCTGTAGTAGTCATGTACACTTGTAT	**GAAGGTCGGAGTCAACGGATT**GCTGTAGTAGTCATGTACACTTGTAC	GTACTTCATATCTCATCAATTTCGATCCAA	0.2	17	0.00
Cq04319_554	530859723	A/T	**GAAGGTGACCAAGTTCATGCT**GATAGAATTGAGTATGCATGGATATTCATTTA	**GAAGGTCGGAGTCAACGGATT**GATAGAATTGAGTATGCATGGATATTCATTTT	TTCAGTAACATTAGCACCAGCAACCATAT	0.36	17	0.34

Cq08088_1466	530860071	G/T	**GAAGGTGACCAAGTTCATGCTGG**ATGCAAATCCTCATGAACATCAAC	**GAAGGTCGGAGTCAACGGATT**AGGATGCAAATCCTCATGAACATCAAA	CAAATGATTCCTTAGGTGTAACATGGCAA	NT	17	0.74
Cq02841_536	530859577	A/T	**GAAGGTGACCAAGTTCATGCTGG**GACATACTATCGAAAGCTGTTTTAT	**GAAGGTCGGAGTCAACGGATT**GGGACATACTATCGAAAGCTGTTTTAA	TCAATCATTATCTGAATTAAATCTTTAAAT	0.44	17	13.43
Cq07733_1403	530860035	C/T	**GAAGGTGACCAAGTTCATGCTGA**AGGTATTGAATCATTGATATTAGTTTTCC	**GAAGGTCGGAGTCAACGGATT**GAAGGTATTGAATCATTGATATTAGTTTTCT	GGAGCAGTAGTAATACTTCTTACAATCCTA	0.3	17	23.96
Cq07113_1273	530859970	C/T	**GAAGGTGACCAAGTTCATGCT**ATTTGATAGGTCTAAACTTTTTTTCCCAC	**GAAGGTCGGAGTCAACGGATT**CTATTTGATAGGTCTAAACTTTTTTTCCCAT	CTTCCATTCTTATTCATTCTGCAAACAAAT	0.33	17	29.37
Cq01651_264	530859461	C/T	**GAAGGTGACCAAGTTCATGCT**AACATGTGCATTGACAAGCGTGTTC	**GAAGGTCGGAGTCAACGGATT**AAACATGTGCATTGACAAGCGTGTTT	ACGTACTCCCTCTGTCCCAGTTTA	NT	17	30.10
Cq08463_1101	530860111	A/C	**GAAGGTGACCAAGTTCATGCT**GAATTTAATTGTATCCTTTTCAACCAATCCAT	**GAAGGTCGGAGTCAACGGATT**TAATTGTATCCTTTTCAACCAATCCAG	CATCGATTGTAAATAAGTTTGCAAGGAGAA	0.35	17	30.17
Cq00655_133	530859368	G/T	**GAAGGTGACCAAGTTCATGCT**AAACCTTTGGACCCTCCAAATGAG	**GAAGGTCGGAGTCAACGGATT**AAACCTTTGGACCCTCCAAATGAT	CAAACCGGATTTTATCTACGACCCAAT	NT	17	30.48
Cq00424_83	530859343	A/T	**GAAGGTGACCAAGTTCATGCT**ATGACAAAGAAATTATTTAAGAAATGGAAACAA	**GAAGGTCGGAGTCAACGGATT**ATGACAAAGAAATTATTTAAGAAATGGAAACAT	GAGATATCAATTGTCTCAGTTTCCTCAATT	0.15	17	33.05
Cq02013_294	530859494	A/G	**GAAGGTGACCAAGTTCATGCT**GATGACCTTGTCGCGATGAGATAA	**GAAGGTCGGAGTCAACGGATT**ATGACCTTGTCGCGATGAGATAG	CAGTATCTATCGCGAGAAGATGGCAT	0.22	17	33.18
Cq07368_1324	530859990	A/T	**GAAGGTGACCAAGTTCATGCT**ATTAACCTCTAAAAGACATGGAACTTTTAATTA	**GAAGGTCGGAGTCAACGGATT**AACCTCTAAAAGACATGGAACTTTTAATTT	AAATCTTAGTCCAGATTCGCTTACTAAATA	0.31	17	37.19
Cq06538_1165	530859908	G/T	**GAAGGTGACCAAGTTCATGCT**AGAAAATAATTATTTTGTGATCAAGCTTGTTG	**GAAGGTCGGAGTCAACGGATT**GAGAAAATAATTATTTTGTGATCAAGCTTGTTT	CTCTATAAATAGAGGTCATATTACCCCTTT	NT	17	37.62
Cq05556_661	530859819	C/T	**GAAGGTGACCAAGTTCATGCT**GTCTTAAAATGTTGGTTAGCAGGAAAAC	**GAAGGTCGGAGTCAACGGATT**AGTCTTAAAATGTTGGTTAGCAGGAAAAT	CATTCTTTCCATTTAAGAGAAGACCTCGAA	0.34	17	38.65
Cq00941_169	530859394	A/G	**GAAGGTGACCAAGTTCATGCT**GTGTTTTTGATGATTAATGAAAGTTGAAGGTT	**GAAGGTCGGAGTCAACGGATT**GTTTTTGATGATTAATGAAAGTTGAAGGTC	CGCCCCGTCAGCAAAGTGTTGTT	NT	17	39.81
Cq04233_752	530859711	C/T	**GAAGGTGACCAAGTTCATGCT**GTTCACCTATCATCTTTGATGTACTTG	**GAAGGTCGGAGTCAACGGATT**ATGTTCACCTATCATCTTTGATGTACTTA	CATGATTGATGGACCTTCGAAGTTCATTT	0.29	17	44.88
Cq03850	530859676	C/T	**GAAGGTGACCAAGTTCATGCT**CTCCTCTGTATCAATTAATTTTGTATAC	**GAAGGTCGGAGTCAACGGATT**ATACTCCTCTGTATCAATTAATTTTGTATAT	ATGATTGAACCGGCATCTTTCACAAGTAT	0.29	18	0.00
Cq04047	530859690	C/T	**GAAGGTGACCAAGTTCATGCT**GCCATGTTTGTAGTGGTAAGTGTAC	**GAAGGTCGGAGTCAACGGATT**GCCATGTTTGTAGTGGTAAGTGTAT	GTCATCATCTCACAATATAGACACACATTA	0.44	18	1.38
Cq03909_712	530859679	A/G	**GAAGGTGACCAAGTTCATGCT**TGACAGTAAGAGCGAAGATTACAAGA	**GAAGGTCGGAGTCAACGGATT**GACAGTAAGAGCGAAGATTACAAGG	CGCTTCAACAGATTTCCAATCCATATCAT	0.29	18	3.28
Cq00521_106	530859350	A/G	**GAAGGTGACCAAGTTCATGCT**CCAATACAATTATAATGCAAAACTCTAATTTAT	**GAAGGTCGGAGTCAACGGATT**CCAATACAATTATAATGCAAAACTCTAATTTAC	CTCTCAGCCTTAAATAATTAGTAATCACAT	0.07	18	6.43
Cq07475_1345	530860000	C/T	**GAAGGTGACCAAGTTCATGCT**ACATAGATATAAGTCATCAATTTGAATGCC	**GAAGGTCGGAGTCAACGGATT**ACATAGATATAAGTCATCAATTTGAATGCT	CTATAAGTGGTGACTGGTGAATGGAATTT	0.07	18	8.86

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Cq03094_576	530859598	G/T	**GAAGGTGACCAAGTTCATGCT**GACGACTTCCACAGTGCCTCG	**GAAGGTCGGAGTCAACGGATT**GACGACTTCCACAGTGCCTCT	AAGATAGCGAGGCAATGATACCTTCAAT	0.1	18	11.10
Cq03400_471	530859630	C/T	**GAAGGTGACCAAGTTCATGCT**GTTCCTGTAGCTTAGATATTTTAATTCCG	**GAAGGTCGGAGTCAACGGATT**AGTTCCTGTAGCTTAGATATTTTAATTCCA	GGGGGGGGGGGTGAATTGTAGAT	NT	18	14.82
Cq04297_551	530859720	C/T	**GAAGGTGACCAAGTTCATGCT**ACCCCTTTCACAAAATCCGGATC	**GAAGGTCGGAGTCAACGGATT**CTACCCCTTTCACAAAATCCGGATT	ACAGAACATAGCTGGATGTATGAAGGAA	NT	18	15.60
Cq00136_9	530859308	A/C	**GAAGGTGACCAAGTTCATGCT**AAGGTGTAGTTCAAGTCTAATATAAGGTAT	**GAAGGTCGGAGTCAACGGATT**GGTGTAGTTCAAGTCTAATATAAGGTAG	GCTTTCCTTAAATCAGGATGATTATCTATA	0.27	18	21.43
Cq07519_980	530860004	C/T	**GAAGGTGACCAAGTTCATGCT**GTTGTCAGCTTATAAAGAACTTTAGTCC	**GAAGGTCGGAGTCAACGGATT**AGTTGTCAGCTTATAAAGAACTTTAGTCT	AGCATATGTCCAATTTAGGAGAGCTGATT	0.31	18	21.88
Cq01275_266	530859427	A/G	**GAAGGTGACCAAGTTCATGCT**CCACTCTTGGTTGAATAAATTGTCGT	**GAAGGTCGGAGTCAACGGATT**CCACTCTTGGTTGAATAAATTGTCGC	CGTGGCAAAGTGAATAAATTATTGAGAGAA	NT	18	27.28
Cq04097_730	530859692	C/T	**GAAGGTGACCAAGTTCATGCT**CCATTTTGATTGTGTAGCTTGGCTC	**GAAGGTCGGAGTCAACGGATT**CCATTTTGATTGTGTAGCTTGGCTT	CCAATCACTTTTGGAAATAAACCATGATAA	NT	18	28.57
Cq06301_1098	530859875	A/G	**GAAGGTGACCAAGTTCATGCT**GTTCCATGATCTGTTCTAATATGTATCAATTA	**GAAGGTCGGAGTCAACGGATT**CCATGATCTGTTCTAATATGTATCAATTG	GATGAGTTTCTTGCATTTGTGAAGAAAGAA	0.29	18	29.47
Cq08281_1506	530860091	G/T	**GAAGGTGACCAAGTTCATGCT**AAGCAACGCTTTGCTAATTGCTCC	**GAAGGTCGGAGTCAACGGATT**GTAAGCAACGCTTTGCTAATTGCTCA	GTTGAGAGAGAATTAGATGCGACAATTTAT	NT	18	29.71
Cq06105_1043	530859857	C/T	**GAAGGTGACCAAGTTCATGCT**GGAATTACATTGCAAAAGTCATTATTCTTAC	**GAAGGTCGGAGTCAACGGATT**AGGAATTACATTGCAAAAGTCATTATTCTTAT	CGGGTTTGGTTTTGGGGAGACATTT	0.32	18	29.92
Cq01086_225	530859406	A/C	**GAAGGTGACCAAGTTCATGCT**CCCGTGATTTCTTTTCTTTTACATGATAAT	**GAAGGTCGGAGTCAACGGATT**CCGTGATTTCTTTTCTTTTACATGATAAG	CGACTTGGATCTCGTTGTCCACAAA	0.28	18	29.94
Cq01182_213	530859420	C/T	**GAAGGTGACCAAGTTCATGCT**TTGGCAGATTTACACATGAGTTTTATTAG	**GAAGGTCGGAGTCAACGGATT**GTTTGGCAGATTTACACATGAGTTTTATTAA	AACTTTCCTAATTTAAGCTTGCCAAGCTTT	0.3	18	29.94
Cq04693_587	530859760	C/G	**GAAGGTGACCAAGTTCATGCT**AGAATATGGAGATTATTCCATGGTGTC	**GAAGGTCGGAGTCAACGGATT**AGAATATGGAGATTATTCCATGGTGTG	CGGGTGAATGACATCCCTCTACTT	NT	18	30.59
Cq04745_591	530859765	C/T	**GAAGGTGACCAAGTTCATGCT**TCAAAAGCTAATAGAGTTGAGTTGTATAG	**GAAGGTCGGAGTCAACGGATT**CTTCAAAAGCTAATAGAGTTGAGTTGTATAA	TGGCAAAAGTATTGGACCCTTTTGCAAAA	0.25	18	31.12
Cq07309_1303	530859982	A/C	**GAAGGTGACCAAGTTCATGCT**CCATATAGGGAAGGATTTGACCATGT	**GAAGGTCGGAGTCAACGGATT**CATATAGGGAAGGATTTGACCATGG	CAGGTTAACAGCATCAGTGCCTCTT	NT	18	31.86
Cq04814_599	530859771	A/G	**GAAGGTGACCAAGTTCATGCT**GACCTGACATCAATCAAATTCCCCTA	**GAAGGTCGGAGTCAACGGATT**ACCTGACATCAATCAAATTCCCCTG	GTTCACAGATTAACCATCACAAGGGATAT	0.38	18	41.05
Cq01791_349	530859477	C/T	**GAAGGTGACCAAGTTCATGCT**GTAGCAAAAATCGGCAAGTCTTTCG	**GAAGGTCGGAGTCAACGGATT**AGTAGCAAAAATCGGCAAGTCTTTCA	GCTACTGGCTCGCAAACCACTAAAT	0.44	19	0.00
Cq02073_388	530859506	G/T	**GAAGGTGACCAAGTTCATGCT**AATATTTTCCCAATATTTCCTAACAATTACG	**GAAGGTCGGAGTCAACGGATT**CTAATATTTTCCCAATATTTCCTAACAATTACT	TTAGATCCACACCCTCCTTTTCATACTAT	0.29	19	7.33
Cq01769_275	530859475	A/G	**GAAGGTGACCAAGTTCATGCT**ACACTGGTGTTTAGCGCCAGGT	**GAAGGTCGGAGTCAACGGATT**CACTGGTGTTTAGCGCCAGGC	ACAAGACTATCGCCACATGCTGGAT	NT	19	15.38
Cq02042_383	530859501	A/C	**GAAGGTGACCAAGTTCATGCT**AAGGATGACATGCTACAATGCCTCA	**GAAGGTCGGAGTCAACGGATT**GGATGACATGCTACAATGCCTCC	CTCGTGGCTCGGCCATCTTTGTA	0.35	19	19.60
Cq03645_658	530859651	A/T	**GAAGGTGACCAAGTTCATGCT**TA	**GAAGGTCGGAGTCAACGGATT**AC	GGCGTTCATTCTCTTGCGGACTATT	NT	19	22.41

			CCTCCAGATGGTGACAAGCATT	CTCCAGATGGTGACAAGCATA				
Cq06399_782	530859891	G/T	**GAAGGTGACCAAGTTCATGCT**ACCCGATTTTGTGTATTCTTGACCC	**GAAGGTCGGAGTCAACGGATT**ACCCGATTTTGTGTATTCTTGACCA	AGTAGTAGGTTCGGGAGGGTCATT	NT	19	23.41
Cq02327_449	530859536	A/G	**GAAGGTGACCAAGTTCATGCT**GTGTACTTCGCTCTCACTCA	**GAAGGTCGGAGTCAACGGATT**CTGTGTACTTCGCTCTCACTCG	GGAGGTCTCTGTGCTTGCAAAACTT	0.37	19	24.56
Cq07111_1272	530859968	A/C	**GAAGGTGACCAAGTTCATGCT**GTTCAGTAATTAATCCCGAGAGTGCT	**GAAGGTCGGAGTCAACGGATT**CAGTAATTAATCCCGAGAGTGCG	CGATTGATAATTTCGGGCCATTTCTGATT	NT	19	34.56
Cq06847_858	530859937	A/C	**GAAGGTGACCAAGTTCATGCT**ATTTATCCGCCTCAAGCTCTCCTTT	**GAAGGTCGGAGTCAACGGATT**ATCCGCCTCAAGCTCTCCTTG	GGCTTAACCTCATTATCTAACCATTCTAAA	0.29	19	34.58
Cq00875_183	530859387	A/G	**GAAGGTGACCAAGTTCATGCT**GGTAGTTAATGAGCCTCAAGCTT	**GAAGGTCGGAGTCAACGGATT**GGTAGTTAATGAGCCTCAAGCTC	GGTAGGAAGAGCAGTGGGTGGTT	0.28	19	35.05
Cq06287_1095	530859870	A/G	**GAAGGTGACCAAGTTCATGCT**GATATTTTATTGTGTTCATAACCCCTTAAAGT	**GAAGGTCGGAGTCAACGGATT**ATTTTATTGTGTTCATAACCCCTTAAAGC	GAGCAAACTGATCCTCCGAGAACAA	0.31	19	39.63
Cq04832_852	530859772	C/T	**GAAGGTGACCAAGTTCATGCT**CATTTCATTTAATTCATTGCTAAGTTTATGTG	**GAAGGTCGGAGTCAACGGATT**CATTTCATTTAATTCATTGCTAAGTTTATGTA	ACAACAATATCATTAAGAGATCCAACCATT	NT	20	0.00
Cq01116	530859410	C/T	**GAAGGTGACCAAGTTCATGCT**GTTGAACCATCATATTATAAACATGTGAG	**GAAGGTCGGAGTCAACGGATT**GTTGAACCATCATATTATAAACATGTGAA	CGACTCCTCAAGCTTATAAGATGTGTTAT	0.22	20	0.63
Cq06890_1240	530859944	A/T	**GAAGGTGACCAAGTTCATGCT**GTGTTTAGTTTGGAAGGAATTGCAT	**GAAGGTCGGAGTCAACGGATT**CTGTGTTTAGTTTGGAAGGAATTGCAA	CAGAGTCTCAAGGTACTGCGAGAA	0.4	20	13.75
Cq07446_1335	530859997	A/C	**GAAGGTGACCAAGTTCATGCT**CGAGGGTGTCTTGTTTCTGGGT	**GAAGGTCGGAGTCAACGGATT**GAGGGTGTCTTGTTTCTGGGG	TCCCTAATCCCACCACCAGATCAAA	0.04	20	13.76
Cq07545_1368	530860011	A/C	**GAAGGTGACCAAGTTCATGCT**GAGGTAACATCTTCCCAACTCTACT	**GAAGGTCGGAGTCAACGGATT**AGGTAACATCTTCCCAACTCTACG	CCCAATCTCCATAAGGGTAACCGAT	0.18	20	14.53
Cq07999_1451	530860064	A/T	**GAAGGTGACCAAGTTCATGCT**GTTGGACCGTCTGGCTGACAA	**GAAGGTCGGAGTCAACGGATT**GTTGGACCGTCTGGCTGACAT	GGTTCTTGTTATTAGTCCCATTGGACTTA	NT	20	15.43
Cq08569_1564	530860118	C/G	**GAAGGTGACCAAGTTCATGCT**CCGAAACCATCCATATTTATCCTACG	**GAAGGTCGGAGTCAACGGATT**CCGAAACCATCCATATTTATCCTACC	GTTGTTGTTGTGGAGGTGGAGGATT	0.43	20	18.07
Cq09189_1630	530860146	C/T	**GAAGGTGACCAAGTTCATGCT**GAGTTGAAGCTGTACAACCAATCG	**GAAGGTCGGAGTCAACGGATT**GGAGTTGAAGCTGTACAACCAATCA	TTGGCTTTCCAACGCGATTTGAAGAAAA	NT	20	20.91
Cq07542_1363	530860007	G/T	**GAAGGTGACCAAGTTCATGCT**TTAAACGATACCTACGCTCAAGC	**GAAGGTCGGAGTCAACGGATT**CCTTTAAACGATACCTACGCTCAAGA	ACAAGGTTGTCCTTTTTTAGTTTGGAGAAA	0.46	20	21.66
Cq11413_1856	530860194	A/T	**GAAGGTGACCAAGTTCATGCT**CAGCCTTATTTAAATTCCATTAACAATGCAA	**GAAGGTCGGAGTCAACGGATT**CAGCCTTATTTAAATTCCATTAACAATGCAT	CAATTTAATTGAAGGCTGAAATTTCATTAA	NT	20	22.79
Cq00734_137	530859373	C/T	**GAAGGTGACCAAGTTCATGCT**TAGATGATCATCAAATCTTGTGGCTG	**GAAGGTCGGAGTCAACGGATT**GTTAGATGATCATCAAATCTTGTGGCTA	CGAGTGGAGGGGATGAGGATTAATT	NT	20	22.86
Cq04604_824	530859753	G/T	**GAAGGTGACCAAGTTCATGCT**GTAATGGAGAAATTCTTGAACGGAAG	**GAAGGTCGGAGTCAACGGATT**CTTGTAATGGAGAAATTCTTGAACGGAAT	CTTTGTATTTGTGCTCGTGTTGGTTTCTT	0.04	20	22.97
Cq00391_75	530859336	C/G	**GAAGGTGACCAAGTTCATGCT**AAGATGTGTGTTGGTTTGCTTGGC	**GAAGGTCGGAGTCAACGGATT**AAGATGTGTGTTGGTTTGCTTGGG	CTCCTCTATAAACTTCTAACTCATGACCAA	0.24	20	23.38
Cq05798_991	530859838	C/T	**GAAGGTGACCAAGTTCATGCT**TTCACTTCAAGGCCAATTGTCTCG	**GAAGGTCGGAGTCAACGGATT**TTCACTTCAAGGCCAATTGTCTCA	GGATTAAATTACCCAAGTTTTTAGATGCAA	0.28	20	23.55
Cq10745_1790	530860190	A/G	**GAAGGTGACCAAGTTCATGCT**AACATTCTTATTGCAGCGGTGCATTAT	**GAAGGTCGGAGTCAACGGATT**CATTCTTATTGCAGCGGTGCATTAC	GGAATGCAGCTGGAAAGCTTGGTTT	0.35	20	24.05
Cq04286	530859718	C/T	**GAAGGTGACCAAGTTCATGCT**TG	**GAAGGTCGGAGTCAACGGATT**GT	ACATGGCTTCAAAGCGTTATATGCAA	0.3	20	24.62

			ACTATTGGTTGTTGTTGCCTCG	TGACTATTGGTTGTTGTTGCCTCA	CAA			
Cq06451_1142	530859893	C/T	**GAAGGTGACCAAGTTCATGCT**ACTGTTTTTAAATCCGTCCTTATTCGG	**GAAGGTCGGAGTCAACGGATT**GACTGTTTTTAAATCCGTCCTTATTCGA	GGCTCCATTAAAGTGTCAGATAAGACTTA	0.1	20	24.72
Cq07878_1021	530860055	C/T	**GAAGGTGACCAAGTTCATGCT**AAATTTAGGGAAGGCGGATGTGC	**GAAGGTCGGAGTCAACGGATT**ACAAATTTAGGGAAGGCGGATGTGT	CAAGGACCATCTGAGGAAGATGGTT	0.28	20	24.90
Cq06484_792	530859898	A/C	**GAAGGTGACCAAGTTCATGCT**AAGGAAGGGTTAGGGAGATAACACA	**GAAGGTCGGAGTCAACGGATT**GGAAGGGTTAGGGAGATAACACC	GAGGTGTTCGATTGGCTTAGGGATA	NT	20	25.55
Cq00535_100	530859354	C/T	**GAAGGTGACCAAGTTCATGCT**ATTTCAAATGATAGAATTGTCCCAAACAG	**GAAGGTCGGAGTCAACGGATT**CATTTCAAATGATAGAATTGTCCCAAACAA	TATCCAAAAAGACCAAATGCATATTCTTAT	0.29	20	27.41
Cq03761_503	530859665	A/G	**GAAGGTGACCAAGTTCATGCT**AAATAAAATTTGAGGCATCAGGGCTCT	**GAAGGTCGGAGTCAACGGATT**ATAAAAATTTGAGGCATCAGGGCTCC	TTCGAGTAGCTTTTTTTACCTCTGCTGTA	0.08	20	31.73
Cq02030_382	530859499	G/T	**GAAGGTGACCAAGTTCATGCT**TGAAAAAATTTAGTGACATAGGGTATGC	**GAAGGTCGGAGTCAACGGATT**GTTGAAAAAATTTAGTGACATAGGGTATGA	TGAGTTAGGCTTCCTACAGTTGATGAATA	0.41	21	0.00
Cq07044_1262	530859961	A/G	**GAAGGTGACCAAGTTCATGCT**AGCATTTCTGCTCTGAAGCACACA	**GAAGGTCGGAGTCAACGGATT**GCATTTCTGCTCTGAAGCACACG	GATGCCTCATTCTAAGTAAAATTGGCACAA	0.37	21	10.16
Cq06730_1203	530859924	G/T	**GAAGGTGACCAAGTTCATGCT**GGTAGGGGTTTATATGAGGTGGC	**GAAGGTCGGAGTCAACGGATT**AGGTAGGGGTTTATATGAGGTGGA	CCAGATTATCCTAACCCAATTCAATCTGAA	0.29	21	21.19
Cq08452_1550	530860109	C/T	**GAAGGTGACCAAGTTCATGCT**TAAATGAGTTCAATCCTGTTCGCTC	**GAAGGTCGGAGTCAACGGATT**CTTAAATGAGTTCAATCCTGTTCGCTT	GAGCTAATCGGAAATATCTATCAACCGAT	0.06	21	32.09
Cq10473_1249	530860181	C/G	**GAAGGTGACCAAGTTCATGCT**AGAATTTTTGCTAAAAAAGTTTTATTTTTCTTG	**GAAGGTCGGAGTCAACGGATT**AGAATTTTTGCTAAAAAAGTTTTATTTTTCTTC	GACATGTATGAGTAATTAATCCGACAAATA	0.32	22	0.00
Cq06896_866	530859946	A/T	**GAAGGTGACCAAGTTCATGCT**CCGCCCAAAGCCAAGTATGCTTT	**GAAGGTCGGAGTCAACGGATT**CCGCCCAAAGCCAAGTATGCTTA	GACTGATTTCCAAAATGGTAAAACCTGTAT	0.39	22	22.20
Cq06788_1214	530859928	A/G	**GAAGGTGACCAAGTTCATGCT**TCACCAGGTCGTCGGCCA	**GAAGGTCGGAGTCAACGGATT**CACCAGGTCGTCGGCCG	CGACTAATCTCCGTTACAACTGCGAT	0.35	22	30.79
Cq00650	530859366	A/G	**GAAGGTGACCAAGTTCATGCT**CGTTTATTACACACTTTGAAATTGGTATTGTA	**GAAGGTCGGAGTCAACGGATT**GTTTATTACACACTTTGAAATTGGTATGTG	GTAAGTACAACCATGTTTCAAGTGAAGATA	0.26	23	0.00
Cq02262	530859529	G/T	**GAAGGTGACCAAGTTCATGCT**GGCTAATCATAGGGCCCAACC	**GAAGGTCGGAGTCAACGGATT**GGGCTAATCATAGGGCCCAACA	GAAAAACAAATCACAAGCAAGCTAAGCAAA	0.3	23	8.20
Cq08321_1514	530860097	A/G	**GAAGGTGACCAAGTTCATGCT**GTCTTTCCTCCGGATATTGCTCATT	**GAAGGTCGGAGTCAACGGATT**CTTCCTCCGGATATTGCTCATC	CCGCACTGACAGAACCACCAAATAA	0.29	23	15.71
Cq06457_790	530859894	G/T	**GAAGGTGACCAAGTTCATGCT**TTTTAAGAATATATGGTATGGTATTGGTCC	**GAAGGTCGGAGTCAACGGATT**CTTTTAAGAATATATGGTATGGTATTGGTCA	GTATGACCTTCATGGGGATACATGGTA	0.28	23	25.93
Cq04563_814	530859750	A/G	**GAAGGTGACCAAGTTCATGCT**GGGTTATTGACGAGACGTTTGGTA	**GAAGGTCGGAGTCAACGGATT**GGTTATTGACGAGACGTTTGGTG	GCCATCTTTCAAACACAAGTACACAACTA	0.38	24	0.00
Cq06851_1232	530859938	C/T	**GAAGGTGACCAAGTTCATGCT**GGAATCGACAACCAAGATGATAAGC	**GAAGGTCGGAGTCAACGGATT**GGAATCGACAACCAAGATGATAAGT	CAAGTTCAACCTTGCTTGTGTCAGCAA	0.47	24	16.82
Cq08098_1475	530860074	A/G	**GAAGGTGACCAAGTTCATGCT**GTATAAAAATCCATGATAACAGTATACGGAA	**GAAGGTCGGAGTCAACGGATT**ATAAAAATCCATGATAACAGTATACGGAG	TATTTTCGATGAAGAAAGAAGAAAGAGGAA	0.45	25	0.00
Cq01300	530859429	C/T	**GAAGGTGACCAAGTTCATGCT**GAACTCTTAACATATTGGCATACAATGC	**GAAGGTCGGAGTCAACGGATT**CGAACTCTTAACATATTGGCATACAATGT	GGATCTGAATCTTGGCGTTGGTCTT	0.3	25	1.57
Cq10399_1241	530860178	C/T	**GAAGGTGACCAAGTTCATGCT**AAGTGTAGTCTACATGTAGAAGTGTAG	**GAAGGTCGGAGTCAACGGATT**GAAGTGTAGTCTACATGTAGAAGTGTA	AAATAAAGGTCTTGTATACGACACCAACAT	0.29	25	10.62

				A				
Cq06805_1221	530859931	A/T	**GAAGGTGACCAAGTTCATGCT**ACCAGTCATGTCAATGAATATAAGATT	**GAAGGTCGGAGTCAACGGATT**CTACCAGTCATGTCAATGAATATAAGATA	TGCACTGCACCGTGTCTAACAACAT	0.42	26	0.00
Cq00881_189	530859391	A/G	**GAAGGTGACCAAGTTCATGCT**TAAAAACAAAAGATCAACACAATTGACAACAT	**GAAGGTCGGAGTCAACGGATT**AAAACAAAAGATCAACACAATTGACACAC	GCTTCCAATCTCTCACTGGTAAAATCTTT	0.43	26	0.37
Cq08253_1500	530860090	A/C	**GAAGGTGACCAAGTTCATGCT**AAATGATACAATGAATTGTTTAGTTGGA	**GAAGGTCGGAGTCAACGGATT**CTAAATGATACAATGAATTGTTTAGTTGGC	CGCACAACTCAATTATGGAACATCAACAT	0.06	26	5.31
Cq02114_402	530859514	C/T	**GAAGGTGACCAAGTTCATGCT**GCATCATATATTGCGTCGTATAAATTAC	**GAAGGTCGGAGTCAACGGATT**CTGCATCATATATTGCGTCGTATAAATTAT	CACATAAGGCTGTGGAAACTGATGATAAT	0.29	26	7.41
Cq00715_132	530859371	C/T	**GAAGGTGACCAAGTTCATGCT**AGTGTGTATTCTCCATAATTGTTGGG	**GAAGGTCGGAGTCAACGGATT**GAGTGTGTATTCTCCATAATTGTTGGA	GGTGTTGCGGGGCGGATACATA	0.48	26	9.06
Cq02418_474	530859549	C/T	**GAAGGTGACCAAGTTCATGCT**GAAAGACACCGACCAGACGGC	**GAAGGTCGGAGTCAACGGATT**GAAAGACACCGACCAGACGGT	CTCGGCCTCCATGTAAACGTACAAA	NT	27	0.00
Cq08059_1461	530860067	A/G	**GAAGGTGACCAAGTTCATGCT**GTTGTGAGAAAGTAACAAGACAATATTGTATA	**GAAGGTCGGAGTCAACGGATT**GTGAGAAAGTAACAAGACAATATTGTATG	GAGTTATGCTTAGCCACAACTAAGCTAAA	0.36	27	7.02
Cq07916_1431	530860060	C/G	**GAAGGTGACCAAGTTCATGCT**ATTTCAACTCCCCTAAGGACATGG	**GAAGGTCGGAGTCAACGGATT**TCAACTCCCCTAAGGACATGC	TATAATTATCAAATGACCATCTCAACCAAA	0.29	28	0.00
Cq10196_1733	530860174	A/T	**GAAGGTGACCAAGTTCATGCT**TCCTTTTTTTCCAGAGCATTACGTT	**GAAGGTCGGAGTCAACGGATT**CTTCCTTTTTTTCCAGAGCATTACGTA	ATGTTGAGAGCATCTGCAGTGATTATCAT	0.11	28	1.54
Cq07675_1396	530860030	A/G	**GAAGGTGACCAAGTTCATGCT**GATGGCTCTAAAATTTTCTTTGCTATATTATT	**GAAGGTCGGAGTCAACGGATT**GATGGCTCTAAAATTTTCTTTGCTATATTATC	CTGAGACCCAAAAAAAAGGATATTTGAGCAT	0.27	28	5.61
Cq04280	530859715	A/G	**GAAGGTGACCAAGTTCATGCT**CATGTCAATGAATGTAAGATTAATACAGTAT	**GAAGGTCGGAGTCAACGGATT**CATGTCAATGAATGTAAGATTAATACAGTAC	GTCTAACAACATGGAGTTGGAACATAGAA	0.26	29	0.00
Cq08302_1511	530860095	C/T	**GAAGGTGACCAAGTTCATGCT**ACATGTATGCATAAATCACACGTACG	**GAAGGTCGGAGTCAACGGATT**GACATGTATGCATAAATCACACGTACA	ATCCACTATACAATCAGCCTTCAGTGTT	0.25	29	0.42
Cq00210_33	530859314	A/C	**GAAGGTGACCAAGTTCATGCT**GGAAAGGAAGGGGTTTCTTTTGGTT	**GAAGGTCGGAGTCAACGGATT**GAAAGGAAGGGGTTTCTTTTGGTG	CTTCGAACCCTTTTGACCCAAAATTCAAA	NT	NM	NM
Cq00410_79	530859340	C/T	**GAAGGTGACCAAGTTCATGCT**CCCTAACACGTCGAAAAGACCG	**GAAGGTCGGAGTCAACGGATT**CCCTAACACGTCGAAAAGACCA	GAAGAGTATGTGCGTTCTTCATATGCTTA	0.32	NM	NM
Cq00504_90	530859347	C/T	**GAAGGTGACCAAGTTCATGCT**AAACATGATTGTGTTGATTGGTAAAACAC	**GAAGGTCGGAGTCAACGGATT**ATATAAACATGATTGTGTTGATTGGTAAAACAT	TCTCTTCTTCTCAACTGTTGTTGTTTCATT	0.18	NM	NM
Cq00628_129	530859364	C/T	**GAAGGTGACCAAGTTCATGCT**ATTCGGTATTTTCGCCTACTCTACC	**GAAGGTCGGAGTCAACGGATT**AAATTCGGTATTTTCGCCTACTCTACT	GGCTATTTAATTAGCGCGGATATTCTTAAT	0.3	NM	NM
Cq00699_147	530859369	A/C	**GAAGGTGACCAAGTTCATGCT**CAAAATAGCTTTTTCATTTTGGCTTAAAAGA	**GAAGGTCGGAGTCAACGGATT**CAAAATAGCTTTTTCATTTTGGCTTAAAAGC	GCCAAAAAATGTGTTTGGTAATTGGCCAT	0.04	NM	NM
Cq00787	530859378	A/G	**GAAGGTGACCAAGTTCATGCT**AACTAACCATGATTATTATAAGTACGATTAGT	**GAAGGTCGGAGTCAACGGATT**CTAACCATGATTATTATAAGTACGATTAGC	GATTATATAGAAGCTAAAACTATGCCGCTA	0.37	NM	NM
Cq00883_192	530859392	C/G	**GAAGGTGACCAAGTTCATGCT**CATTGTAGCTGAAGGTACATATCATG	**GAAGGTCGGAGTCAACGGATT**CATTGTAGCTGAAGGTACATATCATC	GTGATCCGGAAGGAGGTTACTATGAT	0.16	NM	NM
Cq00958	530859396	A/C	**GAAGGTGACCAAGTTCATGCT**CA	**GAAGGTCGGAGTCAACGGATT**CA	GGTTCCGATTCGATAGGAAGGGAAA	0.1	NM	NM

			TTCCCCCCACTTTCATACACA	TTCCCCCCACTTTCATACACC				
Cq01392_291	530859438	A/G	**GAAGGTGACCAAGTTCATGCT**ATATTTCTGAGCCTCAACCATCTGAA	**GAAGGTCGGAGTCAACGGATT**ATTTCTGAGCCTCAACCATCTGAG	ATATACTGTTAAAGGACCATCTCAACTAAA	0.13	NM	NM
Cq01584_326	530859452	A/T	**GAAGGTGACCAAGTTCATGCT**ACAGAGTCAAGTCACGAATGAGGAA	**GAAGGTCGGAGTCAACGGATT**ACAGAGTCAAGTCACGAATGAGGAT	CCTATTCAGATTGCTTTCTTTATCCACTAT	0.15	NM	NM
Cq01960_291	530859491	A/G	**GAAGGTGACCAAGTTCATGCT**GTCCTGACCTGTTTATTAAATAGGTCA	**GAAGGTCGGAGTCAACGGATT**CCTGACCTGTTTATTAAATAGGTCG	GGGCTGGAAAACAGGTCGGGTT	NT	NM	NM
Cq02510	530859558	C/T	**GAAGGTGACCAAGTTCATGCT**AGATGAAACAAGTACCTGATATCCTTC	**GAAGGTCGGAGTCAACGGATT**CAAGATGAAACAAGTACCTGATATCCTTT	GATTGAGAAGGCGAAACTCTGAAACTTT	0.08	NM	NM
Cq02558	530859561	G/T	**GAAGGTGACCAAGTTCATGCT**CCATTGTTGTAAGACCACATGAAAATC	**GAAGGTCGGAGTCAACGGATT**GTCCATTGTTGTAAGACCACATGAAAATA	AACGGAGTCCGTGAACGTTTTGGAT	0.47	NM	NM
Cq02644	530859565	C/T	**GAAGGTGACCAAGTTCATGCT**CCAAAACGAGGCATCACTACCC	**GAAGGTCGGAGTCAACGGATT**GCCAAAACGAGGCATCACTACCT	AAATTAACTTGCATACCCGGTATGCCTA	0.06	NM	NM
Cq02690_383	530859570	A/G	**GAAGGTGACCAAGTTCATGCT**TTTTCAACTCAATTCCATTTTAAAACTTAACA	**GAAGGTCGGAGTCAACGGATT**TTTCAACTCAATTCCATTTTAAAACTTAACG	GAAACAAGTGGTTGTTAAAAACATTGGGTA	0.18	NM	NM
Cq03134	530859600	C/T	**GAAGGTGACCAAGTTCATGCT**TTCCCTTTCACATGAGAGGTATGC	**GAAGGTCGGAGTCAACGGATT**AATTTCCCTTTCACATGAGAGGTATGT	CAGTAACGACGGGGATTGTTACAGAA	0.41	NM	NM
Cq03350_620	530859626	G/T	**GAAGGTGACCAAGTTCATGCT**GTCCCATCCATACGCGTCAATC	**GAAGGTCGGAGTCAACGGATT**GGTCCCATCCATACGCGTCAATA	GAGTCCAGATGCATCGCGCAGAA	0.22	NM	NM
Cq03384_629	530859628	A/T	**GAAGGTGACCAAGTTCATGCT**ATTGGAACGGGTAATTTTATATCTATATATGAA	**GAAGGTCGGAGTCAACGGATT**GGAACGGGTAATTTTATATCTATATATGAT	CAAGCAGCAACATACAAGCAATGAGTTAA	0.11	NM	NM
Cq03488	530859639	A/G	**GAAGGTGACCAAGTTCATGCT**TAGAGAACAGCAGAGGAGTATCATAT	**GAAGGTCGGAGTCAACGGATT**AGAGAACAGCAGAGGAGTATCATAC	GGCACCAACTATAGTGGTATGGATTTAAT	0.33	NM	NM
Cq03642_657	530859649	A/T	**GAAGGTGACCAAGTTCATGCT**CACAAGCCAAAACAAAAATTGCACTTTTAA	**GAAGGTCGGAGTCAACGGATT**CACAAGCCAAAACAAAAATTGCACTTTTAT	GTTTGGTGGATTTTGGTAGTACCGGTT	0.11	NM	NM
Cq03679_666	530859655	C/G	**GAAGGTGACCAAGTTCATGCT**GAAAAAGGATTTAACATTAAATGTATGTGGTG	**GAAGGTCGGAGTCAACGGATT**GAAAAAGGATTTAACATTAAATGTATGTGGTC	CACAATCCAACATTATAATCATTCAAGCAA	0.15	NM	NM
Cq03700_676	530859658	G/T	**GAAGGTGACCAAGTTCATGCT**CACTTCCTTGAAGTGCGTCTTCC	**GAAGGTCGGAGTCAACGGATT**CACTTCCTTGAAGTGCGTCTTCA	CGAAGAATAAAGGCCAGCTCCCAA	NT	NM	NM
Cq03767_691	530859669	A/G	**GAAGGTGACCAAGTTCATGCT**GCAAGAAAGCTACATTATTAGCTGATGT	**GAAGGTCGGAGTCAACGGATT**CAAGAAAGCTACATTATTAGCTGATGC	ATTTGGAGCCGCAGCCATGACAAAT	0.19	NM	NM
Cq03838_697	530859674	A/T	**GAAGGTGACCAAGTTCATGCT**AGCTTGTACTCCACCATAAATAACTATAT	**GAAGGTCGGAGTCAACGGATT**AGCTTGTACTCCACCATAAATAACTATAA	CTCTTATTCGAGGGAATCATGGATTTGTTA	0.29	NM	NM
Cq03949_717	530859681	A/G	**GAAGGTGACCAAGTTCATGCT**GTGAGGTTTGAAGCCTTACTGTA	**GAAGGTCGGAGTCAACGGATT**GTGAGGTTTGAAGCCTTACTGTG	CTTCCAAGTCCCATCAATATAATGACCTA	0.21	NM	NM
Cq03981_722	530859685	G/T	**GAAGGTGACCAAGTTCATGCT**ATGTGTGAGTCGAGACCCCAC	**GAAGGTCGGAGTCAACGGATT**CATGTGTGAGTCGAGACCCCAA	ACTGTAGAATAGGGCTGT	0.24	NM	NM
Cq04124	530859697	A/C	**GAAGGTGACCAAGTTCATGCT**GAGAGGTAGCATTCCCTTGCTAAA	**GAAGGTCGGAGTCAACGGATT**AGAGGTAGCATTCCCTTGCTAAC	AGGGATGATGGGAGCGTCGGTT	0.09	NM	NM
Cq04183_542	530859704	A/C	**GAAGGTGACCAAGTTCATGCT**CAAGACTGGGAATGTCCCCCTAA	**GAAGGTCGGAGTCAACGGATT**AAGACTGGGAATGTCCCCCTAC	TCGCTCTACGAGAGGCCTTGTATAT	0.42	NM	NM
Cq04926_859	530859781	G/T	**GAAGGTGACCAAGTTCATGCT**GT	**GAAGGTCGGAGTCAACGGATT**CG	GAAGCGTCAGAGAGTATAGAATTGTT	0.19	NM	NM

			CTCCTCCTTCCAGTTCCAC	TCTCCTCCTTCCAGTTCCAA	GTT			
Cq05119_886	530859792	C/T	**GAAGGTGACCAAGTTCATGCT**AGGACCGTAGGGTATGTGAAGG	**GAAGGTCGGAGTCAACGGATT**GAGGACCGTAGGGTATGTGAAGA	TTCCTGCCTTGATGATTGCCCACTT	0.07	NM	NM
Cq05301_920	530859799	A/G	**GAAGGTGACCAAGTTCATGCT**GATGAGGGAAGGGTGATGACAT	**GAAGGTCGGAGTCAACGGATT**GATGAGGGAAGGGTGATGACAC	CCTTCCCTTAATATGTTTTGGTGTCACAT	NT	NM	NM
Cq05610_954	530859824	A/T	**GAAGGTGACCAAGTTCATGCT**ACCTACTCTTTGACAATTATCACAAGTTA	**GAAGGTCGGAGTCAACGGATT**ACCTACTCTTTGACAATTATCACAAGTTT	GGTTTTTATTGGCCAAGTTTCTTTCGAGAT	0.24	NM	NM
Cq05743_978	530859833	A/G	**GAAGGTGACCAAGTTCATGCT**ATATATCGTTGGAAAGATATTTTCAAGCCT	**GAAGGTCGGAGTCAACGGATT**ATCGTTGGAAAGATATTTTCAAGCCC	ATTTATTTTGGTTCATAACATGGGTCCAAT	NT	NM	NM
Cq06206_1059	530859864	C/T	**GAAGGTGACCAAGTTCATGCT**ATTATTCAAACATACAATGTTAAATGGATTGTC	**GAAGGTCGGAGTCAACGGATT**ATTCAAACATACAATGTTAAATGGATTGTT	TTGACTCGATTGAGCTTACACCATCAAA	0.25	NM	NM
Cq06321_1117	530859880	C/T	**GAAGGTGACCAAGTTCATGCT**GTCTTGCTTTATACTTTCATACATAATTACC	**GAAGGTCGGAGTCAACGGATT**AGTCTTGCTTTATACTTTCATACATAATTACT	GGTAACGGTTTTGGGGGTTTCTTCTT	0.11	NM	NM
Cq06687_1197	530859922	A/G	**GAAGGTGACCAAGTTCATGCT**GATGTATGTGAATTGCCTTCCTTCAA	**GAAGGTCGGAGTCAACGGATT**GATGTATGTGAATTGCCTTCCTTCAG	GTTTACATAGGTTGTTCTGGTTGTGGAAA	0.19	NM	NM
Cq06800_1216	530859930	A/C	**GAAGGTGACCAAGTTCATGCT**ACATTATTAAAGCGTAATTGGTTTCGTGA	**GAAGGTCGGAGTCAACGGATT**CATTATTAAAGCGTAATTGGTTTCGTGC	CAACCAAAATAAGCATCACAATTAAACCAA	0.48	NM	NM
Cq06887_1239	530859942	A/T	**GAAGGTGACCAAGTTCATGCT**AAATCAGACTCATTGCCCTGGATTA	**GAAGGTCGGAGTCAACGGATT**AAATCAGACTCATTGCCCTGGATTT	CGGTATTACAATAAACTACAGTCCATACAT	0.17	NM	NM
Cq06914_1243	530859949	C/G	**GAAGGTGACCAAGTTCATGCT**AGGGATCTTGAACATCCATCACAC	**GAAGGTCGGAGTCAACGGATT**AGGGATCTTGAACATCCATCACAG	GTAAATAATAATCTGTTTTCGATAAGCTAA	0.05	NM	NM
Cq06987_1250	530859954	A/C	**GAAGGTGACCAAGTTCATGCT**CAGAACAGGCTATCAAACCTGGAAT	**GAAGGTCGGAGTCAACGGATT**AGAACAGGCTATCAAACCTGGAAG	GTAACATTAACGACAGATTTCCTCTACGAA	0.35	NM	NM
Cq07004_1251	530859958	A/G	**GAAGGTGACCAAGTTCATGCT**CGCGATGCGTGACGCCCAA	**GAAGGTCGGAGTCAACGGATT**GCGATGCGTGACGCCCAG	GTGAACCATCGAGTCTTTGAACGCAA	0.29	NM	NM
Cq07107_1271	530859967	A/G	**GAAGGTGACCAAGTTCATGCT**ATATCAAGCACACACTCAACATTCGT	**GAAGGTCGGAGTCAACGGATT**ATCAAGCACACACTCAACATTCGC	GGAATGAGTTTTTCTTATGTTGAGTGTGTA	0.14	NM	NM
Cq07224_1287	530859975	A/T	**GAAGGTGACCAAGTTCATGCT**AAACCTGCTCTTATGTGTACGAGCA	**GAAGGTCGGAGTCAACGGATT**AAACCTGCTCTTATGTGTACGAGCT	CAACAAATCTACAATAGCCTCCTTGTCTA	0.26	NM	NM
Cq07244_1289	530859979	A/G	**GAAGGTGACCAAGTTCATGCT**AATACAATTGCGAAGTTTTCAGAACTTT	**GAAGGTCGGAGTCAACGGATT**AATACAATTGCGAAGTTTTCAGAACTTC	TGGATCTGTATGGTTGATACATGATCGAA	0.14	NM	NM
Cq07295_1298	530859981	A/G	**GAAGGTGACCAAGTTCATGCT**GGGAATGGTTGTTTCCCCTTCAATAA	**GAAGGTCGGAGTCAACGGATT**GGAATGGTTGTTTCCCCTTCAATAG	GTTATAAAACCCCACCTCTTCTTCTCTTT	0.19	NM	NM
Cq07404_1329	530859991	A/G	**GAAGGTGACCAAGTTCATGCT**CATGAGCTGCATTGACTGATATTCCT	**GAAGGTCGGAGTCAACGGATT**ATGAGCTGCATTGACTGATATTCCC	CAGGTAGTGGAAAGAATTTCTTTGCAGA	0.2	NM	NM
Cq07568_1373	530860016	A/G	**GAAGGTGACCAAGTTCATGCT**GTTTGAGATAACATAGTGTTTGTTACGTAT	**GAAGGTCGGAGTCAACGGATT**TGAGATAACATAGTGTTTGTTACGTAC	TGACACATCCCATATCTTAAACTTTCATTT	0.07	NM	NM
Cq07911_1429	530860058	G/T	**GAAGGTGACCAAGTTCATGCT**AGGTGTCTGACATGTGTTGCCG	**GAAGGTCGGAGTCAACGGATT**AAGGTGTCTGACATGTGTTGCCT	CGTTGACCCTCGTTGACTAACATCTT	0.34	NM	NM
Cq08025_1457	530860065	A/G	**GAAGGTGACCAAGTTCATGCT**ATATAGAAAAACTACCAATGAATAATACAAAGT	**GAAGGTCGGAGTCAACGGATT**ATATAGAAAAACTACCAATGAATAATACAAAGC	CTATTCATTCCTTTTCCCTTGGTTGCTA	0.06	NM	NM
Cq08131_1490	530860083	A/G	**GAAGGTGACCAAGTTCATGCT**AT	**GAAGGTCGGAGTCAACGGATT**AT	CAAACAAGCATAAGAACAAATAAACA	0.46	NM	NM

				GTTTGCTTTAAAGGGATTTTAAAAT TCAATT	GTTTGCTTTAAAGGGATTTTAAAAT TCAATC	TGTT		
Cq08373_1537	530860098	C/G		**GAAGGTGACCAAGTTCATGCTCA** TAAGGGCCTATGACAATACTCG	**GAAGGTCGGAGTCAACGGATT**CA TAAGGGCCTATGACAATACTCC	CCTGCAGTGACATTCATAGTGATGGTT	0.48	NM	NM
Cq08561_1560	530860116	C/T		**GAAGGTGACCAAGTTCATGCTCA** AGACTGAAATGGGTTCTAAGTCAC	**GAAGGTCGGAGTCAACGGATT**CA AGACTGAAATGGGTTCTAAGTCAT	ATGAAGGGTCCCCTTCTGTTGGAAT	0.29	NM	NM
Cq08784_1587	530860135	A/G		**GAAGGTGACCAAGTTCATGCT**TG GTTGTGGTTGACAAGAACACGA	**GAAGGTCGGAGTCAACGGATT**GG TTGTGGTTGACAAGAACACGG	ATGCGGCAAATGATAGCATGATATCA GAT	0.15	NM	NM
Cq09347_1641	530860153	A/G		**GAAGGTGACCAAGTTCATGCT**CA ATCTGCAAATGATCCCGATGCT	**GAAGGTCGGAGTCAACGGATT**AA TCTGCAAATGATCCCGATGCC	GGTAAAACCTGTATGAAAAAGGGCAA CAA	0.34	NM	NM
Cq09408_1645	530860155	A/C		**GAAGGTGACCAAGTTCATGCT**GG AAAGTATTGCATTGTCAAGGTTGT	**GAAGGTCGGAGTCAACGGATT**GG AAAGTATTGCATTGTCAAGGTTGG	CATCCGGCATTGATTAGAAAATAAAA CATT	0.32	NM	NM
Cq10074_1712	530860167	C/T		**GAAGGTGACCAAGTTCATGCT**GG CAATTACACATCTATCAACATCAC	**GAAGGTCGGAGTCAACGGATT**CG GCAATTACACATCTATCAACATCAT	GGTAGTTTTTGTGTTAGGAAATGGGAC TT	0.04	NM	NM
Cq10502_1768	530860183	A/T		**GAAGGTGACCAAGTTCATGCT**GT CCGAAGCAAAAAGGAAGGCGT	**GAAGGTCGGAGTCAACGGATT**GT CCGAAGCAAAAAGGAAGGCGA	CGCCATACGATACGTCATTTGCAGTT	0.35	NM	NM
Cq11400_1851	530860192	A/T		**GAAGGTGACCAAGTTCATGCT**GT AACTTACCAGCTTATCTGGCAGTT	**GAAGGTCGGAGTCAACGGATT**GT AACTTACCAGCTTATCTGGCAGTA	CTCTCCATACGTTTGATAAGGAAACTG AA	0.1	NM	NM
Cq04926_858	530859779	A/T		**GAAGGTGACCAAGTTCATGCT**TCT CCTCTTTATCAATTGCTTAGCATTT	**GAAGGTCGGAGTCAACGGATT**CT CCTCTTTATCAATTGCTTAGCATTA	CCGTCAAATTCCGGAATTTAATCAATA CAA	0.19	NM	NM
Cq06504_1156	530859901	C/T		**GAAGGTGACCAAGTTCATGCT**CCT TTACGACACAAAACAAACAATGTA AC	**GAAGGTCGGAGTCAACGGATT**CC TTTACGACACAAAACAAACAATGT AAT	GGCCCTTTCCTATAATAGGGGATTATT AA	0.03	NM	NM