Report on Genotyping of Black Bass from Kentucky

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Executive Summary

- Two previously developed MassARRAY panels for assessing hybridization and genomic composition of Black Bass species were converted into a new GT-seq assay.
- Kentucky Department of Fish and Wildlife Resources sent 1,694 Black Bass samples to the Southeast Conservation Genetics Lab for genotyping.
- Genetic analyses were performed to test purity of Largemouth Bass versus Florida Bass and to test for hybridization among other Black Bass species.
- Results showed various levels of non-native Florida Bass introgression into native Largemouth Bass depending on sample collection location, but no apparent geographic pattern was seen in the data.
- No evidence of Alabama Bass introgression within sampled waterbodies was found.
- Results provide critical information for Black Bass management.
- The GT-seq assay is a new, cost-effective tool for Black Bass management that does not require specialized equipment.

Introduction

Genetics management of aquatic natural resources helps ensure that management goals are met (Shafer et al. 2015; Holderegger et al. 2019; Hohenlohe et al. 2021; Willi et al. 2022). For example, genetics management can be used to monitor introgression of invasive species into native species, thereby allowing managers to design mitigation efforts (Leroy et al. 2018; Gibson et al. 2019; Berrebi et al. 2022). Hatchery efforts can benefit from genetics management, whether for sportfish management, conservation, or both. When managers pursue captive propagation, broodstock can be checked for genetic background to ensure that the genetic background of produced fish match management objectives. Otherwise, hatchery produced fish may be counterproductive to management goals (Taylor et al. 2019). Genetic data is required to monitor for non-native introgression in native sportfish and ensure that hatchery produced fish have the desired genomic background.

Black Basses of the genus *Micropterus* (Perciformes: Centrarchidae) are economically important sportfish (Chen et al. 2003; Driscoll et al. 2012; Driscoll and Myers 2014). In recent years, genetic data have revealed that *Micropterus* is comprised of numerous closely related species, some of which are capable of hybridizing (Zhao et al. 2018; Thongda et al. 2020; Kim et al. 2022). For example, for many years, Florida Bass were considered a subspecies of Largemouth Bass, but recent systematics work has clarified *Micropterus* taxonomy and demonstrated that both entities are valid, separate species level (Kim et al. 2022). The accepted scientific names for Florida Bass is *Micropterus salmoides* (Lacepède, 1802) and for Largemouth Bass is *Micropterus nigricans* (Cuvier, 1828) (Page et al. 2023). To effectively manage *Micropterus* genetics, several genetic assays have been developed. Two assays are of particular interest to managers in Kentucky: 1) an assay that distinguishes between Florida Bass (*M. salmoides*) and Largemouth Bass (*M. nigricans*) (Zhao et al. 2018) and 2) an assay that tests for introgression of Alabama Bass (*M. henshalli*)and other species into native *Micropterus* (Thongda et al. 2020). These assays are comprised of single nucleotide polymorphisms (SNPs) that were determined to be diagnostic for each respective species. They were designed to work with a Sequenome MassARRAY genotyping system (Zhao et al. 2018; Thongda et al. 2020), which requires specialized equipment not available in most genetics labs or core facilities. Furthermore, the number of SNPs that can be included on a single MassARRAY run, or assay, is limited. In contrast, newer technologies such as GT-seq offer genotyping solutions that do not require specialized equipment aside from Illumina sequencers that are present in virtually every genetics core facility (Campbell et al. 2015). GT-seq also allows for including more loci on a single assay (Campbell et al. 2015), potentially offering cost savings compared to genotyping with other platforms.

To help fisheries managers in Kentucky more effectively manage their *Micropterus* populations, we converted two MassARRAY assays into a single GT-seq assay that consists for two panels that can be analyzed separately: one for examining purity of Largemouth Bass versus Florida Bass and a second for testing introgression among species. After designing the assay, we used it to genotype Black Bass from reservoirs across the state of Kentucky as well as hatchery broodfish. Our results provide a snapshot of the genetic background of Black Bass in Kentucky reservoirs and lay the foundation for future management and propagation of Black Bass in Kentucky.

Material and Methods

Sample Collection and DNA extraction

Black Bass were collected by the Kentucky Department of Fish and Wildlife Resources (KDFWR) between September 2022 and May 2023 (Table 1). For each sampled fish, a fin clip was taken and placed in ethanol. Fin clips were sent to the Southeast Conservation Genetics Lab in Auburn, Alabama, which is a joint U.S Fish and Wildlife Service and Auburn University genetics research lab. DNA was extracted from fin clips with either a 96-well format Qiagen DNeasy Blood & Tissue Kit or a 96-well format Omega Bio-Tek Mag-Bind Blood & Tissue DNA Kit. Most extractions were done with the Qiagen kit because it resulted in extractions with higher yields and larger genome fragments. In total, 1,694 samples were analyzed.

GT-seq panel design and genotyping

The MassARRAY primers for the 38 loci used in the Largemouth versus Florida Bass assay from Zhou et al. (2018) and for the 64 loci used for examining Black Bass introgression from Thongda et al. (2020) were downloaded from each publication's supplementary material. Each primer sequence had MassARRAY-specific nucleotides that we replaced with Illumina sequencer compatible adapter sequences (Tables 2, 3). The string of nucleotides targeting Black Bass genome regions were unchanged.

Forward and reverse modified primers for all target loci were pooled into a single tube at 0.252 µM concentration per primer. Initially, we followed the gt-seq protocol of Campbell et al. (2015), but initial runs resulted in a large proportion of primer dimers compared to target sequences. Therefore, we modified the protocol, which resulted in successful GT-seq library preps (see Appendix 1 for full protocol). To test whether the primer multiplex resulted in adequate sequencing coverage per locus, an initial batch of 92 samples from Paintsville Lake and 4 from Carr Creek Lake were multiplexed and sequenced on an Illumina MiSeq using a Micro flow cell with 2 x 150 bp chemistry. A second batch that

included the 1,598 remaining samples received from KDFWR was sequenced on an Illumina NovaSeq using an SP flow cell and 1 x 118 bp chemistry; for sequencing on the NovaSeq, the run included spiking a custom i5 index sequencing primer that was required because of differences in how i5 indexes are sequenced between the NovaSeq and MiSeq platforms.

Raw data were processed with fastp (Chen et al. 2018) using default parameters to remove adaptor sequences and low quality reads. Demultiplexing was done using the STACKS 2.62 program *process_radtags* (Rochette et al. 2019). Although *process_radtags* was designed for RADseq data, the program allows for 1 bp primer mismatch, which is not an option using standard GT-seq demultiplexing scripts. After demultiplexing, GT-seq loci were assembled with the script GTseq_Genotyper_v3.pl (available from https://github.com/GTseq/GTseq-Pipeline/). This script requires information on flanking regions of the target SNP for each locus and the two possible alleles that could be present at each locus. For loci in the introgression panel, this information was taken from the original publication (Thongda et al. 2020). For the Largemouth Bass versus Florida Bass panel, reference allele information was retrieved with blastn (Camacho et al. 2009) by comparing sequenced loci against reference transcriptomes from NCBI GenBank Transcriptome Shotgun Assembly database; this was required because information on which allele was indicative of Largemouth Bass versus Florida Bass was not provided in the original publication (Zhao et al. 2018).

The test GT-seq run performed on the MiSeq resulted in high sequencing success per sample. However, 8 of the original 38 loci used for the Largemouth versus Florida Bass assay failed to adequately sequence. This was likely a result of primer incompatibilities in the multiplex PCR reaction. However, 30 loci, if truly diagnostic as previously reported, should be suitable for making determinations on whether an individual is a "pure" Largemouth Bass, a "pure" Florida Bass, or an F1 hybrid.

Purity and introgression analyses

After assembly, genotypes for the Largemouth Bass versus Florida Bass assay loci were compiled into an excel spreadsheet with the script GTseq_GenoCompile_v3.pl (available from https://github.com/GTseq/GTseq-Pipeline/).

Following Thongda et al. (2020), the introgression analysis utilized a model-based approach to assign genomic admixture proportions to each individual. For this, we used the R (R Core Team 2022) package LEA (Frichot and François 2015) that assigns genomic background percentages of "pure" Black Bass species to each sampled individual. The analysis utilized reference genotypes for each Black Bass species from Thongda et al. (2020). The reference genotypes were combined with genotypes from

sampled individuals into a single dataset. Data were converted from the aforementioned excel spreadsheet to a PLINK (Chang et al. 2015) .ped file using GTseqTools v 0.1 (Mussmann 2023). ADMIXTURE coefficients were assigned to each individual using the sparse Non-Negative Matrix Factorization algorithm, implemented with the snmf function in LEA using K = 6 and alpha = 150 as parameters. We chose a K of 6 because we were testing for ADMIXTURE among the following *Micropterus* species or species complexes: Alabama Bass, Largemouth Bass, Smallmouth Bass (*M. dolomieu*), Shoal Bass (*M. cataractae*), Spotted Bass (*M. punctulatus*), and Coosa Bass (*M. coosae*). An alpha of 150 was used because it accurately grouped reference individuals together during a preliminary testing phase. For the introgression analysis, Largemouth Bass and Florida Bass are grouped together and all species within the Shoal Bass complex are grouped together (see Thongda et al. 2020 for more details). We ran the snmf function 300 times and cross-entropy criteria were calculated for each run. We reported the run with the lowest cross-entropy.

Results

        Assay design resulted in a GT-seq assay with a panel of 30 loci for assessing the purity of Largemouth Bass versus Florida Bass and a panel of 64 loci for assessing introgression among *Micropterus* species. Our analyses indicate that both panels are suitable for accomplishing objectives associated with genotyping Black Bass to assess genomic background for sportfish management.

        We examined purity of Largemouth Bass versus Florida Bass for 1,385 successfully sequenced putative Largemouth Bass samples (Table 4). We considered any individual that had greater than 95% Largemouth Bass reference alleles as "pure" Largemouth Bass; any individual with greater than 95% Florida Bass reference alleles were considered "pure" Florida Bass. An individual was considered an F1 hybrid of Florida and Largemouth Bass if greater than 90% of loci were heterozygous. Our inferences about purity assume that all genotyped loci are diagnostic of Largemouth versus Florida Bass, as stated in Zhao et al. (2018). However, our results seem to indicate that not all loci from the Zhao et al. (2018) panel are diagnostic, and managers could consider individuals with a lower percentage of putative Largemouth Bass alleles as "pure" Largemouth Bass (see Discussion for more details).

        Our analyses indicated that 485 of 1,380 individuals can be considered "pure" Largemouth Bass under a 95% threshold of having reference Largemouth Bass alleles. If the percentage is lowered to 90%, 931 individuals could be considered "pure" Largemouth Bass. No individuals were pure Florida Bass under either a 95% or 90% threshold. No individuals were F1 hybrids.

Even among individuals that were identified as pure Largemouth Bass, several loci of the Largemouth Bass versus Florida Bass assay were consistently heterozygous which suggests those loci may not be diagnostically useful for determining species. The percentage of sampled fish from each location that were identified as pure Largemouth Bass varied among lakes. Some lakes like Lake Beshear, Cave Run Lake, and Nolin River Lake had high percentages of pure Largemouth Bass, whereas others like Fishpond Lake and Greenbo Lake had no sampled fish that could be considered pure Largemouth Bass. No obvious geographical pattern was associated with lakes with relatively high percentages of Florida Bass alleles, but the four lakes with the highest percentage of FLB alleles were less than 200 acres in size. The locations with no pure Largemouth Bass are indicative of sites with recent Florida Bass introgression. We are unable to precisely determine the timing of hybridization events. However, in the absence of F1 hybrids, the introgression must have taken place more than one generation ago or is a result of introductions of introgressed Largemouth Bass or Florida Bass into those sites.

Genomic admixture analyses on all 1,678 successfully sequenced individuals indicated no genomic admixture among the vast majority of samples (Table 5). Genomic admixture, when present, was mostly between Largemouth Bass and Spotted Bass, but in four individuals, admixture was also seen between Smallmouth Bass and Largemouth Bass or between Smallmouth Bass and Spotted Bass. Two individuals from Martins Fork Lake were inferred to have only Coosa Bass ancestry. No sampled individual had any Alabama Bass ancestry.

Discussion

The GT-seq panel developed here will have broad utility for Black Bass management as it can be used to distinguish purity of Largemouth Bass versus Florida Bass and more broadly test for introgression among Black Bass species. Importantly, the GT-seq assay combines two different panels (i.e., the Florida versus Largemouth Bass panel of Zhao et al. 2018 and the Black Bass Introgression panel of Thongda et al. 2020) into a single assay. The result is a useful genetic management tool that is more cost-effective and has broader utility than previously developed tools. Our Black Bass GT-seq panel is also more accessible as it does not require specialized equipment like a Sequenome MassARRAY genotyping machine.

Our results indicate that the degree to which Largemouth Bass have hybridized with Florida Bass varies across locations in Kentucky. In some locations, Florida Bass hybridization may have never occurred, especially if some loci are not diagnostic, as previously reported (see below). In areas with

Florida Bass introgression, we found no evidence of F1 hybrids, indicating that introgression of Florida Bass alleles into native Largemouth Bass populations is more complicated than a recent hybridization event. That said, some locations have clearly experienced Florida Bass introgression more recently than others, with sites having higher amounts of Florida Bass alleles likely experiencing more recent and/or larger influxes of Florida Bass. In the absence of repeated introduction of Florida Bass, heterozygosity is expected to decrease over time as backcrossing with native species occur. Thus, sites with lower amounts of heterozygosity could have experienced Florida Bass introductions farther in the past than those sites with higher amounts of heterozygosity. That said, complex hybridization histories resulting from multiple introductions and recombination could obscure such a pattern and further complicate trying to determine relative timing on Florida Bass introductions from genomics data alone.

Hybridization of non-native Florida Bass with native Largemouth Bass, resulting in introgression of Florida Bass alleles, could cause outbreeding depression in native Largemouth Bass populations by disrupting native genomic composition (Waples 1991). Past research indicated that outbreeding depression can cause lower resistance to disease, and lower physiological performance in Largemouth Bass (Cooke et al. 2001; Goldberg et al. 2005). Research on other fish species has also found susceptibility to outbreeding depression (e.g., Huff et al. 2011). Although we are not aware of a study that explicitly tested for effects of outbreeding depression on native Largemouth Bass from Kentucky, introgression with Florida Bass unnaturally (i.e., via human-mediated actions) changes the genomic composition of a native species. The result is introgressed individuals with unknown, but likely reduced, fitness.

When we designed the Largemouth Bass versus Florida Bass component of our GT-seq assay, we assumed that included loci had diagnostic alleles for either Largemouth Bass or Florida Bass. This was based on the original publication the loci came from and on previous use of the loci in a MassARRAY SNP panel for genetics management of Largemouth Bass populations in the southeastern U.S (Zhao et al. 2018). However, multiple loci were heterozygous for individuals that would otherwise have been 100% pure Largemouth Bass. This genetic pattern could be the result of a complex history of hybridization and backcrosses with some alleles selectively maintaining heterozygosity after it was introduced during a past introgression event. Alternatively, a small number of loci may not have diagnostic alleles for Largemouth Bass versus Florida Bass, contrary to past reports (e.g., Zhao et al. 2018).

Upon examination of Zhao et al. 2018, it appears that all Largemouth Bass samples used to identify putatively diagnostic loci came from only two sites, one in Illinois and one in Minnesota, USA, but the methods of Zhao et al. 2018 are slightly unclear; it's possible the loci were only tested on

samples from a source lake in Illinois. Yet, Largemouth Bass have a much larger range (Kim et al. 2022), meaning that natural genetic variation within Largemouth Bass may have been overlooked when putatively determining alleles to be species specific. Thus, we think the most likely explanation for the often-heterozygous loci is that the loci are not diagnostic for Largemouth Bass. However, given that we cannot confidently reject either explanation without much greater geographic sampling, we decided to report all loci in the Largemouth Bass versus Florida Bass Panel. As discussed earlier, if these often-heterozygous loci are not diagnostic, then the percentage of pure Largemouth Bass in these samples would be higher than we reported. Managers and other interested parties should interpret results, specifically Table 4, with these issues in mind.

Results of the Black Bass introgression panel, which lumps Largemouth and Florida Bass together, indicated that the vast majority of the 1,678 sequenced samples had genomic backgrounds indicative of only one species, or species complex in the case of Shoal Bass or Largemouth and Florida Bass. Unlike in some other southeastern states, Alabama Bass do not appear to have invaded Kentucky. Nevertheless, non-native species can jump waterways suddenly and spread rapidly once established. Thus, there is still a non-zero risk to native Bass in Kentucky from Alabama Bass introgression. We think that continued monitoring is appropriate, especially in waterbodies that are most geographically proximate to locations that are known to harbor Alabama Bass.

Conclusions

The newly developed Black Bass GT-seq assay is a cost-effective tool for genetics management of Black Bass. We anticipate that the assay will be useful for sportfish management for years to come. The GT-seq assay demonstrated that Kentucky has waterbodies that both harbor a high percentage of pure Largemouth Bass and waterbodies that have seen Florida Bass introgression. In contrast, we observed no evidence of Alabama Bass introgression with native Kentucky species.

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Table 1: Sample Information for Sequenced Fish

Lake	Lab Code	Number of Samples	Bass Species^
Paintsville Lake	PVL	100	Largemouth
Minor Clark Hatchery	MCH	50	Largemouth
Carr Creek Lake	CRC	50	Largemouth
Fishpond Lake	FPL	50	Largemouth
Highsplint Lake	HSL	50	Largemouth
Yatesville Lake	YVL	50	Largemouth
Lake Barkley	BAR	50	Largemouth
Barren River Lake	BRL	50	Largemouth
Lake Cumberland	CBL	50	Largemouth
Cedar Creek Lake	CCL	50	Largemouth
Guist Creek Lake	GCL	50	Largemouth
Kentucky Lake	KEN	50	Largemouth
Kincaid Lake	KIN	50	Largemouth
Lake Malone	LMA	50	Largemouth
Laurel River Lake	LRL	50	Largemouth
Greenbo Lake	GBL	50	Largemouth
Green River Lake	GRL	50	Largemouth
Grayson Lake	GRY	50	Largemouth
Herrington Lake	HER	50	Largemouth
Jacobson Park Lake	JCP	50	Largemouth
Mill Creek Lake	MIL	50	Largemouth
Cave Run Lake	CRL	50	Largemouth
Lake Beshear	BES	50	Largemouth
Taylorsville Lake	TVL	50	Largemouth
Fishtrap Lake	FTL	50	Largemouth
Nolin River Lake	NRL	50	Largemouth
Rough River Lake	RRL	50	Largemouth
Lake Barkley	BAR	50	Spotted or Smallmouth
Lake Cumberland	CBL	50	Spotted or Smallmouth
Herrington Lake	HER	50	Spotted or Smallmouth
Kentucky Lake	KEN	44	Spotted or Smallmouth
Laurel River Lake	LRL	50	Spotted or Smallmouth
Martins Fork Lake	MF	50	Spotted or Smallmouth

^All samples were included in Black Bass species ID and genomic admixture analyses.
Only Largemouth Bass were tested for Florida Bass introgression

Table 2: List of 30-SNP multiplex primers for GT-Seq Panel to disntguish between Largemouth Bass and Florida Bass (5' to 3')

Locus ID	Forward GT-seq Primer	Reverse GT-seq Primer	Largemouth Bass Genotype	Florida Bass Genotype
Contig11272	CGACAGGTTCAGAGTTCTACAGTCCGACGATCAAGGAAGGCGATGTCTTCTG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTTTGAGCAGCAGATCAAGG	G	A
Contig12388	CGACAGGTTCAGAGTTCTACAGTCCGACGATCTTCTTCTTTCCAGCGACGTG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGCGGAGGACATGTTGTAAAC	A	T
Contig1240	CGACAGGTTCAGAGTTCTACAGTCCGACGATCAACGGTTTGGACTCAACAGG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTTTCAAATTGGAGTTGAGGG	G	A
Contig13020	CGACAGGTTCAGAGTTCTACAGTCCGACGATCAAGGAGTGATGTTTGATGGG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGGCTCAAAGTCAGAATCATC	T	C
Contig15950	CGACAGGTTCAGAGTTCTACAGTCCGACGATCAGAGAAGCTGCAGAGGAATC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTCTCTGTACAAAGTTGCGGG	G	A
Contig16665	CGACAGGTTCAGAGTTCTACAGTCCGACGATCGAACCACTGCCTTAGATTAC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGAGTGCATGCAAATCTGATG	C	A
Contig18101	CGACAGGTTCAGAGTTCTACAGTCCGACGATCAAAAGATGTCCTCTCCTGCG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCGGCCAGAAGAGAAAACCAC	A	C
Contig1826	CGACAGGTTCAGAGTTCTACAGTCCGACGATCTCAAAGAGAGCGAGAGGTAG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTCATGTTCACACTCTGCTC	A	T
Contig18667	CGACAGGTTCAGAGTTCTACAGTCCGACGATCGATCACCCTGTGGAAAACTG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACTGCAGAGAACTTCAGAGC	T	C
Contig19961	CGACAGGTTCAGAGTTCTACAGTCCGACGATCTGATGAACAACCCGTCTAGG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGAAAGAGTCCAGCAGCCAG	G	A
Contig20908	CGACAGGTTCAGAGTTCTACAGTCCGACGATCAGTATCACCCAAATCTGCCG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTGAGTGCGCTGAGACCAAAC	C	T
Contig21621	CGACAGGTTCAGAGTTCTACAGTCCGACGATCATAAGCGTGGATGACTCAGC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTGTAGGCCAATAGGATGGTG	T	C
Contig21676	CGACAGGTTCAGAGTTCTACAGTCCGACGATCGGGATTTGAAAATGAGCACAC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTAAGAGGTCCAGAGACTTTG	T	C
Contig21917	CGACAGGTTCAGAGTTCTACAGTCCGACGATCTCTTACAGATACAGAGCGCC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTTGTTGGGTGGATGGATTGG	A	G
Contig2242	CGACAGGTTCAGAGTTCTACAGTCCGACGATCGGATAGACATTGAGCACAGG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCCATCAGGCACGAGTACATC	G	A
Contig22709	CGACAGGTTCAGAGTTCTACAGTCCGACGATCAAAGGAGCCATCACCAGAAG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTGTCTGGGTTGTCCACTTTG	C	A
Contig22803	CGACAGGTTCAGAGTTCTACAGTCCGACGATCCAACACTGTTCCTCTTTCTC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTATCTGTCTGGCAGCCTCTTC	C	A
Contig23008	CGACAGGTTCAGAGTTCTACAGTCCGACGATCTTTCTCCACAGCCTCATAAG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTGGCAGTTCTAAATGGCATC	A	C
Contig2635	CGACAGGTTCAGAGTTCTACAGTCCGACGATCTACTGGACAAGACATGGTGG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTGGATTGACTGTCAGTGCTC	G	A
Contig28601	CGACAGGTTCAGAGTTCTACAGTCCGACGATCTTCTACTGTAAAGTTAGGC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTCCAATGGCCACTTAAGGAG	G	A
Contig31979	CGACAGGTTCAGAGTTCTACAGTCCGACGATCAATGAATGCACAGGCTTGTC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGGGCTAAGATGTATTCACAG	A	T
Contig3296	CGACAGGTTCAGAGTTCTACAGTCCGACGATCGTGAGTAAACAGGAAGACGG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTGTGTTGTGGTCTGCATAGC	C	A
Contig3379	CGACAGGTTCAGAGTTCTACAGTCCGACGATCCCAGCATTCTGTTGTTCACC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTGAGGCCTTCAAACACAGAG	G	C
Contig3616	CGACAGGTTCAGAGTTCTACAGTCCGACGATCTCCAGTCTTTGAACCCTGTC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCTGCTTTTAGCTGGTGTCTG	C	T
Contig4919	CGACAGGTTCAGAGTTCTACAGTCCGACGATCGTAGGCCAAGCGTTAAAGG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTACTTTTGTTAAGTGCCACC	G	T
Contig4936	CGACAGGTTCAGAGTTCTACAGTCCGACGATCTACTTCCCCGCCATTACCAC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACCGACCTGTGCCAAAAGC	A	G
Contig6127	CGACAGGTTCAGAGTTCTACAGTCCGACGATCATGTGAAAAGCATGTACTGG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCCAGGAATTGCCTTTGACTG	C	G
Contig6920	CGACAGGTTCAGAGTTCTACAGTCCGACGATCTCCCACCTTTCTTGAACTCC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGCATCAAGGTAGCAAAGGAG	T	C
Contig9758	CGACAGGTTCAGAGTTCTACAGTCCGACGATCTGTCTGCACAGCTGCTTCTC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGCCCCGCAGGAATTTAAAAG	T	G
Contig9870	CGACAGGTTCAGAGTTCTACAGTCCGACGATCCTTAGAATCTGTCCCTCCTG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTGGCGAATGATTTTGTGAGC	T	C

Table 3: Black Bass Introgression Primers

Locus ID	GT-seq Forward Primer	GT-seq Reverse Primer	SNP Alleles
MpRETP16597TP20237T	CGACAGGTTCAGAGTTCTACAGTCCGACGATCCTTACCTGCAGCTTTCAGAG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAACATACTGCAGCTGCAGGG	G/T
MpRETP17639A	CGACAGGTTCAGAGTTCTACAGTCCGACGATCAGTACTGTATGCGCAACCTG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGATGCTTCTGTGCTTATTCG	A/G
MpRETP29431T	CGACAGGTTCAGAGTTCTACAGTCCGACGATCCTCGCGTGAAACACACAAAC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGTTGGAGAAGACAGATGGG	C/T
MpRETP30468C	CGACAGGTTCAGAGTTCTACAGTCCGACGATCTTGTCTGCAGTTTCAGAGCG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACTTGACAATTTTCAGGCCC	C/G
MpRETP5605T	CGACAGGTTCAGAGTTCTACAGTCCGACGATCGCAGGTTTAAGCAAGTGCAG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTCATCCTGCCATGTTTCCTC	C/T
MpRETP8149T	CGACAGGTTCAGAGTTCTACAGTCCGACGATCAGCCTGAGATTGCCAAGATG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGGCTGAAGTCATTCTGGTC	C/T
MpRETP9363A	CGACAGGTTCAGAGTTCTACAGTCCGACGATCGCGTGACAATCAGGTCTTTT	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGCGTCTTATTTGTGGATGGG	A/T
MpSHTP18868C	CGACAGGTTCAGAGTTCTACAGTCCGACGATCAGTTCAACCTGCAGGCAAAG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGAGACCTGCTCCACTTTTTC	C/T
MpSMBTP16142A	CGACAGGTTCAGAGTTCTACAGTCCGACGATCTTTTCTTACTCTCCTTCTGC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTCAGCAGTGGGACCAAATTC	C/A
RETP10556A	CGACAGGTTCAGAGTTCTACAGTCCGACGATCGGCTGCTCACATAAACACAC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGCAGCACATGAAATCAACAC	G/A
RETP13743C	CGACAGGTTCAGAGTTCTACAGTCCGACGATCCAGCTAACTGGCTTTCTCTC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGAGCCTGCTCGTAACCTTG	C/G
RETP3097A	CGACAGGTTCAGAGTTCTACAGTCCGACGATCCTGGTTTCCCTGACAACATC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGTCAAACGCAGTCCGAGAG	G/A
RETP3652A	CGACAGGTTCAGAGTTCTACAGTCCGACGATCCGTACTCAACTCTACAGCTC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTTCATTCTGCAGGAAGCTC	T/A
RETP4454T	CGACAGGTTCAGAGTTCTACAGTCCGACGATCTGAAGCGTGGAGACAGAGTG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTTTGTGCTCTTGTTCTGGG	C/T
RETP4504A	CGACAGGTTCAGAGTTCTACAGTCCGACGATCAATCACAGCTGGTCATGCAC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACCACCAGTCATTGTTAGAG	C/A
RETP4592A	CGACAGGTTCAGAGTTCTACAGTCCGACGATCACACGCTCAGCCACGCACA	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTTTGATGTCCTGCTCCGCTC	C/A
RETP4714A	CGACAGGTTCAGAGTTCTACAGTCCGACGATCTCATCTGCTGCTTTGGCGTC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAAGAAGCAGATGCTGGAGAG	T/A
RETP4763G	CGACAGGTTCAGAGTTCTACAGTCCGACGATCACCCAGCCAATATGATCCAG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCAAAGTAGTGGTGCAGGTTG	A/G
RETP4967G	CGACAGGTTCAGAGTTCTACAGTCCGACGATCCCTGTTGCACACATAAACCC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAATGGACAACTGGGACTTGG	G/C
RETP5033T	CGACAGGTTCAGAGTTCTACAGTCCGACGATCTTACAAAATGTCTGCAGAGC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAAGGCCTAGTAACAGTCCAG	T/A
RETP5089T	CGACAGGTTCAGAGTTCTACAGTCCGACGATCTCTATCTGAGCCAGCGAGTC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTTGGAGAGCCAGCTGGTAG	G/T
RETP5103T	CGACAGGTTCAGAGTTCTACAGTCCGACGATCCAACTGTGTTCCTGCAGAGC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACACCGGGCATAGAGTAAAC	T/C
RETP5172C	CGACAGGTTCAGAGTTCTACAGTCCGACGATCCTGTGTGTATCTGTAATCTG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCTGGTTTTATAGCCGTGGTC	C/A
RETP5306A	CGACAGGTTCAGAGTTCTACAGTCCGACGATCGAAATTCGGCACTTGAGGAG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGCTTGAAGTTTGAGGGTCAC	A/T
RETP5317T	CGACAGGTTCAGAGTTCTACAGTCCGACGATCAGAGGCAACAACTGCTGAGG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACGTCCCTTTTTCCCACTTG	C/T
RETP5360T	CGACAGGTTCAGAGTTCTACAGTCCGACGATCTGCCTGTCAGCATGTTACTC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTAGGCACAGGTTAATGAAGC	C/T
RETP5475A	CGACAGGTTCAGAGTTCTACAGTCCGACGATCCGCAGTGGATGGTAATGTTC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTGTTGCGATGAAGCTTCAG	A/G
RETP7076G	CGACAGGTTCAGAGTTCTACAGTCCGACGATCACTGCAGATGGTGAGAAGGC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTGCAGAGAGAGCTGACATT	G/T
RETP7594T	CGACAGGTTCAGAGTTCTACAGTCCGACGATCAACATCTGTCTCTGCCGCTG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGCTTATCAGAGGGACACTTG	T/C

ShTP20328A	CGACAGGTTCAGAGTTCTACAGTCCGACGATCTGGCAAGCACAAACACCAAC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTTTCTACATCCTCTGGCTCG	A/G
ShTP6906C	CGACAGGTTCAGAGTTCTACAGTCCGACGATCAGCCTTTCATACTTTGGCCC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGCCTTCACTGCATTGATTTC	T/C
ShTP9651T	CGACAGGTTCAGAGTTCTACAGTCCGACGATCCCACAGAGGATGAGTGAGTG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTGACTCATGTGAAATGGTGG	C/T
ShTP9781T	CGACAGGTTCAGAGTTCTACAGTCCGACGATCTTAAGAGCCGCAGAGTTTCC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCAAACAGCAGCAGGAGGTC	T/C
SMRETP23527A	CGACAGGTTCAGAGTTCTACAGTCCGACGATCAAATAGCAGGAGGAAGGTTG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTACAGGTAACAGTGTGCCTC	G/A
SMRETP25045A	CGACAGGTTCAGAGTTCTACAGTCCGACGATCATGACCACTGCATAACCCAC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCTCTGTTCCACGGTCTTTTC	A/G
SMRETP6977C	CGACAGGTTCAGAGTTCTACAGTCCGACGATCCAGATGGAGACAGTTGCTTG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCTGTGCACTGTTCTGAAATG	C/A
SMShTP1235G	CGACAGGTTCAGAGTTCTACAGTCCGACGATCTAACTGTGCAGACACAGAGG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTGCCGGTATGCATACATCAG	G/A
SMShTP13277T	CGACAGGTTCAGAGTTCTACAGTCCGACGATCAGACGTAGATGAGCCCGTTG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACACAAGAACAGAGTCGTGG	T/C
SMShTP21440A	CGACAGGTTCAGAGTTCTACAGTCCGACGATCTCAATCATCACCACCCTGAC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCGGATTTTGTCTGCCTCTGC	A/G
SMShTP5127T	CGACAGGTTCAGAGTTCTACAGTCCGACGATCGCAGAGCTTGTTGGAAAACC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGAGTTGTAACCCAACTCTGC	T/A
SMShTP5873G	CGACAGGTTCAGAGTTCTACAGTCCGACGATCAGCTGCCTTTCTGTAAGTCC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACAGTCACAGGAGAAGGTC	G/A
SMShTP7448C	CGACAGGTTCAGAGTTCTACAGTCCGACGATCGATGGCTGCAGATTGAACAC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGATGTGTGTGAACGTGACC	C/A
SPMhRETP11109C	CGACAGGTTCAGAGTTCTACAGTCCGACGATCAGCAGCATCCTGAAGTCGTC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGTGTGTACTAGTACTCGGG	C/T
SPMhRETP1192T	CGACAGGTTCAGAGTTCTACAGTCCGACGATCCTGAACAGACTGCAGAACTC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACTTGTCGTGCTCTACACAG	A/T
SPMhRETP12009T	CGACAGGTTCAGAGTTCTACAGTCCGACGATCGAGTGAGCGTTGGAAACGAC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGGACTGCAGTACAACATGTG	A/T
SPMhRETP1486CG	CGACAGGTTCAGAGTTCTACAGTCCGACGATCTTACCCTCTCAATCTCGTGG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTATGTGGTTCCAGACAGAGTG	C/G
SPMhRETP15885T	CGACAGGTTCAGAGTTCTACAGTCCGACGATCCCTGCAGCTGTAAACAACAC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGCACATTTTCAGCACATTG	G/T
SPMhRETP18151G	CGACAGGTTCAGAGTTCTACAGTCCGACGATCGGACTGAGGGTGTCAACAAG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTGTCAGGCAGACTGACTTT	G/A
SPMhRETP18435T	CGACAGGTTCAGAGTTCTACAGTCCGACGATCAACATATCTGCAGGAGTCGG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAAAAGTTGCTGCCTGCTCTG	C/T
SPMhRETP18863TP20134T	CGACAGGTTCAGAGTTCTACAGTCCGACGATCCTTAATCCCTGCAGGCAAAC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCCATCAACAGCAGCACTATC	C/T
SPMhRETP21822TP22590A	CGACAGGTTCAGAGTTCTACAGTCCGACGATCAAGCTGTCAGTCACCTGGAG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGGTGAAGCTGGATCAGTGG	G/A
SPMhRETP24673A	CGACAGGTTCAGAGTTCTACAGTCCGACGATCCAGCGTTATCTCCTACTTTG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTATTACCTTGTCTGTTGTGTG	G/A
SPMhRETP26317T	CGACAGGTTCAGAGTTCTACAGTCCGACGATCGGGTATGTCTGTGGAAATGC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCGCCTTCCAGTTTTCTTGTC	C/T
SPMhRETP28164T	CGACAGGTTCAGAGTTCTACAGTCCGACGATCCAGCAGATTAATCCCTGAGC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTAACTGTGACCACCAGAAG	G/T
SPMhRETP2910G	CGACAGGTTCAGAGTTCTACAGTCCGACGATCGTCGCGTTTGGTGCAATTTG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTGCAGAGATCCACTCAGAGC	G/C
SPMhRETP3437TC	CGACAGGTTCAGAGTTCTACAGTCCGACGATCTTGAACTGCAGACTCACAGC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTACAGGCTTCATGATCAGGG	T/C
SPMhRETP4105A	CGACAGGTTCAGAGTTCTACAGTCCGACGATCCAGAGACAGCCAGTCAGAAC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTGTGCGAACAAACTGTTCGG	C/A
SPMhRETP6034TP13641T	CGACAGGTTCAGAGTTCTACAGTCCGACGATCCCTGCAGAGTTGTGAAGAAC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGCGTTTCAGAATTTCCTCC	C/T
SPMhRETP6389C	CGACAGGTTCAGAGTTCTACAGTCCGACGATCTGTAGATGTTGAGTCTGCCG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCATCAAAACGGCTTGCCGAC	C/T
SPMhRETP7161A	CGACAGGTTCAGAGTTCTACAGTCCGACGATCGCAGATGTGCTGCATTTTCC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGAGAGACAACTGCAGCAGAT	G/A
SPMhRETP7458TP15274C	CGACAGGTTCAGAGTTCTACAGTCCGACGATCTATCGCTCCGGTTTGATTGC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTGAATGAGGCTGCAGCTGAG	C/T

SPMhRETP8383G	CGACAGGTTCAGAGTTCTACAGTCCGACGATCACAATCTGCAGCACACAAGG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCAACAGGATCTGTCACAATG	G/C
SPMhRETP8469A	CGACAGGTTCAGAGTTCTACAGTCCGACGATCAAGAATGGCATGCACTCAGG	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCAGTGCCGGTGTGTTTTATG	G/A
SPMhRETP8660C	CGACAGGTTCAGAGTTCTACAGTCCGACGATCATGTGTGTTACTGCAGCACC	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCCCATCACAACTTTCACACC	T/C

Table 4: Results of Largemouth Bass versus Florida Bass Panel

Color Code:

>95% NB alleles ("pure NB")	>95% FL alleles ("pure FL")	>90% heterozygous alleles (F1 HYBRID)		Allele 1 is the NB Allele
485 individuals	0 Individuals	0 Individuals		Allele 2 is the FL Allele
				Allele 12 is the heterozygous Allele

Column headers: Sample, Contig11272, Contig12388, Contig1240, Contig13020, Contig15950, Contig16665, Contig18101, Contig1826, Contig18667, Contig19961, Contig20908, Contig21621, Contig21676, Contig21917, Contig2242, Contig22709, Contig22803, Contig23008, Contig2635, Contig28601, Contig31979, Contig3296, Contig3379, Contig3616, Contig4919, Contig4936, Contig6127, Contig6920, Contig9758, Contig9870, NB Markers, FL Markers, He Markers, NB%, FL%, Hetero%, Loci_genotyped

Sample	n₁	n₂	n₃	Value 1	Value 2	Prop	N
BRL_25.1	28	0	2	0.9667	0.0333	0.07	30
BRL_26.1	29	0	1	0.9833	0.0167	0.03	30
BRL_27.1	28	0	2	0.9667	0.0333	0.07	30
BRL_28.1	27	1	1	0.9483	0.0517	0.03	29
BRL_29.1	26	0	4	0.9333	0.0667	0.13	30
BRL_30.1	29	0	1	0.9833	0.0167	0.03	30
BRL_31.1	27	1	2	0.9333	0.0667	0.07	30
BRL_32.1	28	0	2	0.9667	0.0333	0.07	30
BRL_33.1	26	0	4	0.9333	0.0667	0.13	30
BRL_34.1	27	0	3	0.9500	0.0500	0.10	30
BRL_35.1	25	1	4	0.9000	0.1000	0.13	30
BRL_36.1	28	0	2	0.9667	0.0333	0.07	30
BRL_37.1	28	0	2	0.9667	0.0333	0.07	30
BRL_38.1	28	0	1	0.9828	0.0172	0.03	29
BRL_39.1	26	0	4	0.9333	0.0667	0.13	30
BRL_40.1	29	0	1	0.9833	0.0167	0.03	30
BRL_41.1	26	1	3	0.9167	0.0833	0.10	30
BRL_42.1	26	1	3	0.9167	0.0833	0.10	30
BRL_43.1	24	0	6	0.9000	0.1000	0.20	30
BRL_44.1	26	0	4	0.9333	0.0667	0.13	30
BRL_45.1	26	0	4	0.9333	0.0667	0.13	30
BRL_46.1	27	0	3	0.9500	0.0500	0.10	30
BRL_47.1	29	0	1	0.9833	0.0167	0.03	30
BRL_48.1	27	1	2	0.9333	0.0667	0.07	30
BRL_49.1	28	0	2	0.9667	0.0333	0.07	30
BRL_50.1	26	0	3	0.9483	0.0517	0.10	29
CBL_01.1	28	1	1	0.9655	0.0345	0.00	29
CBL_02.1	28	0	2	0.9667	0.0333	0.07	30
CBL_03.1	27	0	3	0.9500	0.0500	0.10	30
CBL_04.1	29	0	1	0.9833	0.0167	0.03	30
CBL_05.1	29	0	1	0.9833	0.0167	0.03	30
CBL_06.1	30	0	0	1.0000	0.0000	0.00	30
CBL_07.1	19	0	11	0.8167	0.1833	0.37	30
CBL_08.1	27	0	3	0.9500	0.0500	0.10	30
CBL_09.1	28	0	2	0.9667	0.0333	0.07	30
CBL_10.1	27	0	3	0.9500	0.0500	0.10	30
CBL_11.1	29	0	0	1.0000	0.0000	0.00	30
CBL_12.1	26	0	4	0.9333	0.0667	0.13	30
CBL_13.1	30	0	0	1.0000	0.0000	0.00	29
CBL_14.1	29	0	1	0.9833	0.0167	0.03	30
CBL_15.1	26	0	3	0.9483	0.0517	0.10	29
CBL_16.1	29	0	1	0.9833	0.0167	0.03	30
CBL_17.1	29	0	1	0.9833	0.0167	0.03	30
CBL_18.1	29	0	1	0.9833	0.0167	0.03	30
CBL_19.1	28	0	1	0.9828	0.0172	0.03	29
CBL_20.1	29	0	1	0.9833	0.0167	0.03	30
CBL_21.1	30	0	0	1.0000	0.0000	0.00	30
CBL_22.1	27	1	1	0.9483	0.0517	0.03	29
CBL_23.1	29	0	1	0.9833	0.0167	0.03	30
CBL_24.1	30	0	0	1.0000	0.0000	0.00	30
CBL_25.1	30	0	0	1.0000	0.0000	0.00	30
CBL_26.1	29	0	1	0.9833	0.0167	0.03	30
CBL_27.1	29	0	1	0.9833	0.0167	0.03	30
CBL_28.1	28	0	2	0.9667	0.0333	0.07	30
CBL_29.1	28	1	1	0.9500	0.0500	0.03	30
CBL_30.1	28	0	2	0.9667	0.0333	0.07	30
CBL_31.1	29	0	1	0.9833	0.0167	0.03	30
CBL_32.1	29	0	1	0.9833	0.0167	0.03	30
CBL_33.1	29	0	0	1.0000	0.0000	0.00	29
CBL_34.1	30	0	0	1.0000	0.0000	0.00	30
CBL_35.1	30	0	0	1.0000	0.0000	0.00	30
CBL_36.1	26	0	3	0.9483	0.0517	0.10	29
CBL_37.1	29	0	0	1.0000	0.0000	0.00	29
CBL_38.1	27	0	3	0.9500	0.0500	0.10	30
CBL_39.1	29	0	0	1.0000	0.0000	0.00	29
CBL_40.1	26	0	4	0.9333	0.0667	0.13	30
CBL_41.1	28	0	2	0.9667	0.0333	0.07	30
CBL_42.1	30	0	0	1.0000	0.0000	0.00	30
CBL_43.1	28	0	2	0.9667	0.0333	0.07	30
CBL_44.1	29	0	1	0.9833	0.0167	0.03	30
CBL_45.1	29	0	2	0.9655	0.0345	0.07	29
CBL_46.1	27	0	3	0.9500	0.0500	0.10	30
CBL_47.1	29	0	1	0.9833	0.0167	0.03	30
CBL_48.1	28	0	2	0.9667	0.0333	0.07	30
CBL_49.1	29	0	1	0.9833	0.0167	0.03	30
CBL_50.1	29	0	1	0.9833	0.0167	0.03	30
CCL_01.1	28	0	2	0.9667	0.0333	0.07	30
CCL_02.1	29	0	1	0.9833	0.0167	0.03	30
CCL_03.1	26	1	3	0.9167	0.0833	0.10	30
CCL_04.1	26	0	4	0.9333	0.0667	0.13	30
CCL_05.1	23	1	6	0.8667	0.1333	0.20	30
CCL_06.1	28	0	2	0.9667	0.0333	0.07	30
CCL_07.1	22	0	7	0.8667	0.1333	0.27	30
CCL_08.1	25	1	4	0.9000	0.1000	0.13	30
CCL_09.1	22	1	8	0.8621	0.1379	0.21	29
CCL_10.1	25	0	5	0.9167	0.0833	0.17	30
CCL_11.1	25	0	5	0.9167	0.0833	0.17	30
CCL_12.1	29	0	1	0.9833	0.0167	0.03	30
CCL_13.1	27	0	3	0.9500	0.0500	0.10	30
CCL_14.1	24	0	6	0.9000	0.1000	0.20	30
CCL_15.1	23	0	6	0.9107	0.0893	0.18	28
CCL_16.1	26	1	3	0.9167	0.0833	0.10	30
CCL_17.1	24	0	5	0.9333	0.0667	0.07	30
CCL_18.1	24	0	6	0.9000	0.1000	0.20	30
CCL_19.1	24	0	6	0.9333	0.0667	0.13	30
CCL_20.1	24	0	5	0.9138	0.0862	0.17	29
CCL_21.1	26	0	4	0.9333	0.0667	0.13	30
CCL_22.1	23	0	5	0.9167	0.0833	0.17	30
CCL_23.1	23	0	7	0.8833	0.1167	0.23	30
CCL_24.1	23	1	6	0.8966	0.1034	0.21	29
CCL_25.1	26	0	4	0.9333	0.0667	0.13	30
CCL_26.1	25	1	4	0.9000	0.1000	0.13	30
CCL_27.1	25	1	4	0.8864	0.1136	0.23	22
CCL_28.1	17	0	5	0.9167	0.0833	0.17	30
CCL_29.1	18	0	9	0.8036	0.1964	0.32	28
CCL_30.1	25	0	5	0.9167	0.0833	0.17	30
CCL_31.1	25	0	5	0.9167	0.0833	0.17	30
CCL_32.1	24	0	6	0.9000	0.1000	0.20	30
CCL_33.1	24	1	5	0.9310	0.0690	0.07	29
CCL_34.1	29	0	1	0.9833	0.0167	0.03	30
CCL_35.1	24	0	6	0.9000	0.1000	0.20	30
CCL_36.1	24	0	6	0.9000	0.1000	0.20	30
CCL_37.1	24	0	6	0.9000	0.1000	0.20	30
CCL_38.1	25	0	5	0.9167	0.0833	0.17	30
CCL_39.1	18	1	11	0.7833	0.2167	0.37	30
CCL_40.1	23	2	6	0.8333	0.1667	0.32	30
CCL_41.1	24	0	6	0.9333	0.0667	0.13	30
CCL_42.1	24	0	6	0.9000	0.1000	0.20	30
CCL_43.1	21	1	8	0.8621	0.1379	0.28	29
CCL_44.1	24	2	3	0.8793	0.1207	0.28	29
CCL_45.1	24	0	6	0.9000	0.1000	0.20	30
CCL_46.1	25	0	7	0.8793	0.1207	0.24	29
CCL_47.1	25	1	4	0.9000	0.1000	0.13	30
CCL_48.1	26	1	3	0.9167	0.0833	0.10	30
CCL_49.1	24	0	6	0.9000	0.1000	0.20	30
CCL_50.1	21	0	8	0.8621	0.1379	0.28	29
CRC_01.1	23	0	6	0.9259	0.0741	0.15	27
CRC_02.1	23	1	6	0.8667	0.1333	0.20	30
CRC_03.1	16	1	13	0.7500	0.2500	0.43	30

ID	n(11)	n(het)	n(12)	freq1	freq2	het	N
CRC_04.1	24	2	4	0.8667	0.1333	0.13	30
CRC_05.1		1	6	0.8621	0.1379	0.21	29
CRC_06.1	22	3	5	0.8167	0.1833	0.17	30
CRC_07.1	24	0	5	0.9138	0.0862	0.17	29
CRC_08.1	23	2	5	0.8500	0.1500	0.17	30
CRC_09.1	19	2	9	0.7833	0.2167	0.30	30
CRC_10.1	25	1	4	0.9000	0.1000	0.13	30
CRC_11.1	23	1	6	0.8667	0.1333	0.20	30
CRC_12.1	23	1	6	0.8667	0.1333	0.20	30
CRC_13.1	22	2	6	0.8333	0.1667	0.20	30
CRC_14.1	25	0	5	0.9167	0.0833	0.17	30
CRC_15.1	18	3	9	0.7500	0.2500	0.30	30
CRC_16.1	26	1	2	0.9310	0.0690	0.07	29
CRC_17.1	21	2	7	0.8167	0.1833	0.23	30
CRC_18.1	26	0	4	0.9333	0.0667	0.13	30
CRC_19.1	25	0	5	0.9000	0.1000	0.13	30
CRC_20.1	24	1	5	0.8833	0.1167	0.17	30
CRC_21.1	24	0	6	0.9000	0.1000	0.20	30
CRC_22.1	22	0	8	0.8667	0.1333	0.27	30
CRC_23.1	26	0	4	0.9333	0.0667	0.13	30
CRC_24.1	19	0	11	0.8167	0.1833	0.37	30
CRC_25.1	23	1	5	0.8793	0.1207	0.17	29
CRC_26.1	24	2	4	0.8667	0.1333	0.13	30
CRC_27.1	24	2	4	0.8667	0.1333	0.13	30
CRC_28.1	20	2	8	0.8000	0.2000	0.27	30
CRC_29.1	26	2	2	0.9000	0.1000	0.07	30
CRC_30.1	24	0	6	0.9000	0.1000	0.20	30
CRC_31.1	23	0	6	0.8966	0.1034	0.20	29
CRC_32.1	25	1	4	0.9000	0.1000	0.13	30
CRC_33.1	24	0	5	0.9138	0.0862	0.17	29
CRC_34.1	23	1	6	0.8667	0.1333	0.20	30
CRC_35.1	21	0	8	0.8621	0.1379	0.28	29
CRC_36.1	21	1	8	0.8333	0.1667	0.27	30
CRC_37.1	26	0	3	0.9483	0.0517	0.10	29
CRC_38.1	23	2	4	0.8621	0.1379	0.14	29
CRC_39.1	26	1	3	0.9167	0.0833	0.10	30
CRC_40.1	23	2	5	0.8500	0.1500	0.17	30
CRC_41.1	18	2	10	0.7931	0.2069	0.34	29
CRC_42.1	19	1	10	0.8000	0.2000	0.33	30
CRC_43.1	28	0	2	0.9667	0.0333	0.07	30
CRC_44.1	19	2	8	0.7931	0.2069	0.28	29
CRC_45.1	25	1	3	0.9138	0.0862	0.10	29
CRC_46.1	22	0	8	0.8667	0.1333	0.27	30
CRC_47.1	26	0	1	0.9815	0.0185	0.04	27
CRC_48.1	23	0	5	0.9107	0.0893	0.18	28
CRC_49.1	20	0	5	0.9000	0.1000	0.20	30
CRC_50.1	23	0	5	0.9107	0.0893	0.18	28
CRL_100.1	27	0	1	0.9821	0.0179	0.04	28
CRL_51.1	28	0	2	0.9667	0.0333	0.07	30
CRL_52.1	27	0	3	0.9500	0.0500	0.10	30
CRL_53.1	28	0	2	0.9667	0.0333	0.07	30
CRL_54.1	28	0	1	0.9500	0.0500	0.03	30
CRL_55.1	29	0	1	0.9833	0.0167	0.03	30
CRL_56.1	28	0	2	0.9667	0.0333	0.07	30
CRL_57.1	27	0	2	0.9655	0.0345	0.07	29
CRL_58.1	29	0	1	0.9833	0.0167	0.03	30
CRL_59.1	27	0	2	0.9655	0.0345	0.07	29
CRL_60.1	25	1	4	0.9000	0.1000	0.13	30
CRL_61.1	30	0	0	1.0000	0.0000	0.00	30
CRL_62.1	23	0	6	0.8966	0.1034	0.21	29
CRL_63.1	25	1	4	0.9000	0.1000	0.13	30
CRL_64.1	29	0	1	0.9833	0.0167	0.03	30
CRL_65.1	26	0	4	0.9333	0.0667	0.13	30
CRL_66.1	29	0	1	0.9833	0.0167	0.03	30
CRL_67.1	30	0	0	1.0000	0.0000	0.00	23
CRL_68.1	27	0	3	0.9500	0.0500	0.10	30
CRL_69.1	27	1	2	0.9333	0.0667	0.07	30
CRL_70.1	29	0	1	0.9833	0.0167	0.03	30
CRL_71.1	26	0	3	0.9483	0.0517	0.10	29
CRL_72.1	28	0	2	0.9667	0.0333	0.07	30
CRL_73.1	26	0	4	0.9333	0.0667	0.13	30
CRL_74.1	28	1	1	0.9655	0.0345	0.00	29
CRL_75.1	28	0	2	0.9667	0.0333	0.07	30
CRL_76.1	27	0	2	0.9821	0.0179	0.04	28
CRL_77.1	27	3	0	0.9500	0.0500	0.10	30
CRL_78.1	28	0	2	0.9500	0.0500	0.10	30
CRL_79.1	29	0	0	0.9833	0.0167	0.03	30
CRL_80.1	29	0	1	0.9833	0.0167	0.03	30
CRL_81.1	27	0	3	0.9500	0.0500	0.10	30
CRL_82.1	29	0	1	0.9833	0.0167	0.03	30
CRL_83.1	27	0	3	0.9500	0.0500	0.10	30
CRL_84.1	27	0	1	0.9828	0.0172	0.03	29
CRL_85.1	24	0	6	0.9000	0.1000	0.20	30
CRL_86.1	28	1	1	0.9500	0.0500	0.03	30
CRL_87.1	28	1	1	0.9500	0.0500	0.03	30
CRL_88.1	25	2	3	0.9583	0.0417	0.08	24
CRL_89.1	26	0	5	0.9167	0.0833	0.17	30
CRL_90.1	26	0	4	0.9333	0.0667	0.13	30
CRL_91.1	24	0	3	0.9444	0.0556	0.11	27
CRL_92.1	27	0	3	0.9500	0.0500	0.10	30
CRL_93.1	25	0	4	0.9483	0.0517	0.10	29
CRL_94.1	25	0	4	0.9310	0.0690	0.14	29
CRL_95.1	30	0	0	1.0000	0.0000	0.00	29
CRL_96.1	27	0	2	0.9655	0.0345	0.07	29
CRL_97.1	27	0	3	0.9500	0.0500	0.10	30
CRL_98.1	27	0	2	0.9655	0.0345	0.07	29
CRL_99.1	28	0	2	0.9667	0.0333	0.07	30
FPL_01.1	18	7	11	0.5833	0.4167	0.37	30
FPL_02.1	5	5	20	0.5000	0.5000	0.67	30
FPL_03.1	11	8	9	0.4833	0.5167	0.43	30
FPL_04.1	12	5	13	0.5667	0.4333	0.40	30
FPL_05.1	11	6	13	0.5833	0.4167	0.43	30
FPL_06.1	14	4	12	0.6667	0.3333	0.40	30
FPL_07.1	14	8	11	0.5500	0.4500	0.37	30
FPL_08.1	14	2	14	0.5500	0.4500	0.17	30
FPL_09.1	6	6	18	0.5000	0.5000	0.60	30
FPL_10.1	5	12	10	0.6071	0.3929	0.43	28
FPL_11.1	7	6	12	0.4828	0.5172	0.41	29
FPL_12.1	5	9	13	0.5000	0.5000	0.27	30
FPL_13.1	7	13	10	0.4000	0.6000	0.33	30
FPL_14.1	10	7	13	0.5500	0.4500	0.43	30
FPL_15.1	14	3	13	0.6333	0.3667	0.40	30
FPL_16.1	14	4	12	0.6333	0.3667	0.33	30
FPL_17.1	11	4	15	0.5690	0.4310	0.50	29
FPL_18.1	8	7	15	0.5167	0.4833	0.50	30
FPL_19.1	14	2	14	0.4667	0.5333	0.47	30
FPL_20.1	10	4	15	0.4833	0.5167	0.37	30
FPL_21.1	9	9	13	0.4833	0.5167	0.43	30
FPL_22.1	4	16	9	0.5862	0.4138	0.55	29
FPL_23.1	13	4	14	0.5000	0.5000	0.47	30
FPL_24.1	14	2	14	0.5000	0.5000	0.47	30
FPL_25.1	5	13	14	0.5833	0.4167	0.50	30
FPL_26.1	14	5	11	0.6000	0.4000	0.27	30
FPL_27.1	6	11	15	0.5345	0.4655	0.52	30
FPL_28.1	3	8	18	0.6833	0.3167	0.43	30
FPL_29.1	7	8	17	0.7000	0.3000	0.27	30
FPL_30.1	10	5	15	0.5833	0.4167	0.50	30
FPL_31.1	8	5	17	0.5500	0.4500	0.57	30
FPL_32.1	8	5	17	0.5500	0.4500	0.57	30

Genotype data matrix with per-locus summary statistics. The large central matrix contains allele codes (values 0, 11, 12, 22). The legible right-hand summary columns are transcribed below for each locus ID.

Locus	A	B	C	Freq1	Freq2	Ho	N
FPL_33.1	6	12	10	0.3929	0.6071	0.36	28
FPL_34.1	7	8	15	0.4833	0.5167	0.50	30
FPL_35.1	8	11	11	0.5500	0.4500	0.37	30
FPL_36.1	11	7	14	0.5667	0.4333	0.40	30
FPL_37.1	9	7	13	0.5333	0.4667	0.47	30
FPL_38.1	10	7	13	0.5500	0.4500	0.43	30
FPL_39.1	9	4	17	0.5833	0.4167	0.57	30
FPL_40.1	8	6	16	0.5333	0.4667	0.53	30
FPL_41.1	13	4	11	0.6607	0.3393	0.39	28
FPL_42.1	9	3	11	0.6304	0.3696	0.48	23
FPL_43.1	4	5	13	0.4773	0.5227	0.59	22
FPL_44.1	9	13	8	0.4333	0.5667	0.27	30
FPL_45.1	5	6	19	0.4833	0.5167	0.63	30
FPL_46.1	3	13	14	0.3333	0.6667	0.47	30
FPL_47.1	9	7	13	0.5345	0.4655	0.45	29
FPL_48.1	7	7	16	0.5000	0.5000	0.53	30
FPL_49.1	10	10	9	0.5000	0.5000	0.31	29
FPL_50.1	8	4	16	0.5714	0.4286	0.57	28
FTL_01.1	24	0	5	0.9138	0.0862	0.17	29
FTL_02.1	23	0	5	0.8966	0.1034	0.17	29
FTL_03.1	26	0	4	0.9333	0.0667	0.13	30
FTL_04.1	14	0	14	0.7308	0.2692	0.54	26
FTL_05.1	24	0	4	0.9286	0.0714	0.14	28
FTL_06.1	14	2	14	0.6786	0.3214	0.50	28
FTL_07.1	26	0	3	0.9483	0.0517	0.10	29
FTL_08.1	8	3	18	0.5862	0.4138	0.62	29
FTL_09.1	25	1	3	0.9138	0.0862	0.10	29
FTL_10.1	22	2	5	0.8448	0.1552	0.17	29
FTL_11.1	22	0	4	0.9231	0.0769	0.15	26
FTL_12.1	17	0	13	0.7833	0.2167	0.43	30
FTL_13.1	26	0	4	0.9333	0.0667	0.13	30
FTL_14.1	23	1	5	0.8793	0.1207	0.17	29
FTL_15.1	11	2	17	0.6500	0.3500	0.57	30
FTL_16.1	22	0	6	0.8929	0.1071	0.21	28
FTL_17.1	24	1	5	0.8833	0.1167	0.17	30
FTL_18.1	20	2	8	0.8000	0.2000	0.27	30
FTL_19.1	22	0	6	0.8929	0.1071	0.21	28
FTL_20.1	22	0	6	0.8929	0.1071	0.21	28
FTL_21.1	19	0	10	0.8276	0.1724	0.34	29
FTL_22.1	23	1	5	0.8793	0.1207	0.17	29
FTL_23.1	26	0	4	0.9333	0.0667	0.13	30
FTL_24.1	21	0	9	0.8500	0.1500	0.30	30
FTL_25.1	23	0	6	0.8966	0.1034	0.21	29
FTL_26.1	22	0	6	0.8929	0.1071	0.21	28
FTL_27.1	23	0	6	0.8966	0.1034	0.21	29
FTL_28.1	22	0	6	0.8793	0.1207	0.24	29
FTL_29.1	25	0	4	0.9310	0.0690	0.14	29
FTL_30.1	28	0	2	0.9667	0.0333	0.07	30
FTL_31.1	24	0	6	0.8750	0.1250	0.18	28
FTL_32.1	17	2	2	0.7586	0.2414	0.34	29
FTL_33.1	24	1	2	0.8966	0.1034	0.14	29
FTL_34.1	27	1	2	0.9333	0.0667	0.07	30
FTL_35.1	22	1	2	0.8500	0.1500	0.23	30
FTL_36.1	26	0	3	0.9483	0.0517	0.10	29
FTL_37.1	28	0	2	0.9667	0.0333	0.07	30
FTL_38.1	20	0	8	0.8571	0.1429	0.29	28
FTL_39.1	20	0	7	0.8833	0.1167	0.23	30
FTL_40.1	11	0	9	0.7750	0.2250	0.45	20
FTL_41.1	26	1	3	0.9167	0.0833	0.10	30
FTL_42.1	23	0	6	0.8966	0.1034	0.21	29
FTL_43.1	23	0	6	0.8667	0.1333	0.27	30
FTL_44.1	12	0	9	0.8393	0.1607	0.32	28
FTL_45.1	21	0	7	0.8750	0.1250	0.25	28
FTL_46.1	27	0	3	0.9500	0.0500	0.10	30
FTL_47.1	28	0	2	0.9667	0.0333	0.07	30
FTL_48.1	25	0	4	0.9310	0.0690	0.14	29
FTL_49.1	25	0	4	0.9138	0.0862	0.10	29
FTL_50.1	25	1	5	0.9107	0.0893	0.18	28
GBL_01.1	20	1	7	0.8167	0.1833	0.08	30
GBL_02.1	17	3	9	0.7414	0.2586	0.31	29
GBL_03.1	12	3	13	0.7414	0.2586	0.45	29
GBL_04.1	21	3	8	0.8000	0.2000	0.21	30
GBL_05.1	14	2	13	0.7069	0.2931	0.45	29
GBL_06.1	15	2	12	0.7241	0.2759	0.41	29
GBL_07.1	14	3	13	0.6833	0.3167	0.47	30
GBL_08.1	18	1	9	0.7833	0.2167	0.30	30
GBL_09.1	15	1	14	0.7333	0.2667	0.47	30
GBL_10.1	15	3	12	0.7000	0.3000	0.40	30
GBL_11.1	15	3	12	0.7333	0.2667	0.40	30
GBL_12.1	19	4	6	0.7586	0.2414	0.21	29
GBL_13.1	22	6	2	0.7667	0.2333	0.07	30
GBL_14.1	14	2	13	0.7069	0.2931	0.45	29
GBL_15.1	13	1	15	0.7069	0.2931	0.52	29
GBL_16.1	14	5	10	0.6552	0.3448	0.34	29
GBL_17.1	26	0	4	0.9333	0.0667	0.13	30
GBL_18.1	0	0	0	#DIV/0!	#DIV/0!	#DIV/0!	0
GBL_19.1	0	0	0	#DIV/0!	#DIV/0!	#DIV/0!	0
GBL_20.1	22	1	7	0.8500	0.1500	0.23	30
GBL_21.1	0	0	0	#DIV/0!	#DIV/0!	#DIV/0!	0
GBL_22.1	13	3	13	0.6724	0.3276	0.45	29
GBL_23.1	21	3	6	0.8000	0.2000	0.20	30
GBL_24.1	17	3	10	0.7333	0.2667	0.33	30
GBL_25.1	18	2	9	0.7759	0.2241	0.31	29
GBL_26.1	17	2	10	0.7586	0.2414	0.34	29
GBL_27.1	14	5	10	0.7167	0.2833	0.34	29
GBL_28.1	23	0	7	0.8833	0.1167	0.23	30
GBL_29.1	10	6	10	0.6207	0.3793	0.34	29
GBL_30.1	15	3	12	0.7000	0.3000	0.40	30
GBL_31.1	16	0	13	0.7759	0.2241	0.45	29
GBL_32.1	15	4	11	0.6833	0.3167	0.37	30
GBL_33.1	25	0	5	0.9167	0.0833	0.17	30
GBL_34.1	17	1	12	0.7667	0.2333	0.40	30
GBL_35.1	10	5	15	0.6667	0.3333	0.33	30
GBL_36.1	12	5	16	0.6667	0.3333	0.53	30
GBL_37.1	22	2	6	0.7931	0.2069	0.28	29
GBL_38.1	19	3	7	0.7833	0.2167	0.23	30
GBL_39.1	19	2	10	0.8000	0.2000	0.33	30
GBL_40.1	16	3	10	0.7167	0.2833	0.37	30
GBL_41.1	20	5	5	0.7500	0.2500	0.17	30
GBL_42.1	16	3	11	0.6833	0.3167	0.37	30
GBL_43.1	13	2	15	0.7667	0.2333	0.50	30
GBL_44.1	18	2	10	0.7667	0.2333	0.33	30
GBL_45.1	22	2	6	0.7931	0.2069	0.21	29
GBL_46.1	14	5	10	0.6552	0.3448	0.28	29
GBL_47.1	15	4	11	0.6833	0.3167	0.37	30
GBL_48.1	14	2	13	0.7586	0.2414	0.34	29
GBL_49.1	15	1	14	0.7333	0.2667	0.47	30
GBL_50.1	16	4	10	0.7000	0.3000	0.33	30
GCL_01.1	21	0	3	0.9375	0.0625	0.14	24
GCL_02.1	26	0	1	0.9815	0.0185	0.04	27
GCL_03.1	23	1	6	0.8667	0.1333	0.20	30
GCL_04.1	25	2	3	0.9000	0.1000	0.10	30
GCL_05.1	25	2	3	0.8333	0.1667	0.20	30
GCL_06.1	25	1	4	0.9000	0.1000	0.13	30
GCL_07.1	28	0	2	0.9667	0.0333	0.07	30
GCL_08.1	27	0	3	0.9500	0.0500	0.10	30
GCL_09.1	26	1	3	0.9167	0.0833	0.10	30
GCL_10.1	24	0	6	0.9000	0.1000	0.20	30
GCL_11.1	24	3	3	0.8500	0.1500	0.10	30

Sample	Hom common	Het	Hom rare	Freq 1	Freq 2	Ho	N
GCL_12.1	24	1	5	0.8833	0.1167	0.17	30
GCL_13.1	21	3	6	0.8000	0.2000	0.20	30
GCL_14.1	26	0	4	0.9333	0.0667	0.13	30
GCL_15.1	23	1	6	0.8667	0.1333	0.20	30
GCL_16.1	24	0	6	0.9000	0.1000	0.20	30
GCL_17.1	25	0	5	0.9167	0.0833	0.17	30
GCL_18.1	29	0	1	0.9833	0.0167	0.03	30
GCL_19.1	26	1	3	0.9167	0.0833	0.10	30
GCL_20.1	23	2	5	0.8500	0.1500	0.17	30
GCL_21.1	26	1	3	0.9167	0.0833	0.10	30
GCL_22.1	23	2	5	0.8500	0.1500	0.17	30
GCL_23.1	25	0	5	0.9167	0.0833	0.17	30
GCL_24.1	21	2	7	0.8167	0.1833	0.23	30
GCL_25.1	24	0	6	0.9000	0.1000	0.20	30
GCL_26.1	24	1	5	0.8833	0.1167	0.17	30
GCL_27.1	24	0	6	0.9000	0.1000	0.20	30
GCL_28.1	23	0	7	0.8833	0.1167	0.23	30
GCL_29.1	23	0	7	0.8833	0.1167	0.23	30
GCL_30.1	29	0	1	0.9833	0.0167	0.03	30
GCL_31.1	22	0	8	0.8667	0.1333	0.27	30
GCL_32.1	26	0	4	0.9333	0.0667	0.13	30
GCL_33.1	22	0	8	0.8667	0.1333	0.27	30
GCL_34.1	24	0	6	0.9000	0.1000	0.20	30
GCL_35.1	29	1	0	0.9667	0.0333	0.00	30
GCL_36.1	26	1	3	0.9167	0.0833	0.10	30
GCL_37.1	25	0	5	0.9167	0.0833	0.17	30
GCL_38.1	23	2	5	0.8500	0.1500	0.30	30
GCL_39.1	21	0	7	0.8833	0.1167	0.23	30
GCL_40.1	18	0	12	0.8000	0.2000	0.40	30
GCL_41.1	28	1	1	0.9500	0.0500	0.03	30
GCL_42.1	26	0	4	0.9333	0.0667	0.13	30
GCL_43.1	22	1	7	0.8500	0.1500	0.23	30
GCL_44.1	21	0	8	0.8621	0.1379	0.28	29
GCL_45.1	24	1	5	0.8833	0.1167	0.17	30
GCL_46.1	26	1	3	0.9167	0.0833	0.10	30
GCL_47.1	28	0	2	0.9667	0.0333	0.07	30
GCL_48.1	22	0	8	0.8667	0.1333	0.27	30
GCL_49.1	27	1	2	0.9333	0.0667	0.07	30
GCL_50.1	22	1	7	0.8500	0.1500	0.23	30
GRL_01.1	26	0	4	0.9333	0.0667	0.13	30
GRL_02.1	24	0	6	0.9000	0.1000	0.20	30
GRL_03.1	27	1	2	0.9333	0.0667	0.07	30
GRL_04.1	26	0	4	0.9333	0.0667	0.13	30
GRL_05.1	25	0	5	0.9167	0.0833	0.17	30
GRL_06.1	28	2	0	0.9667	0.0333	0.07	30
GRL_07.1	28	0	1	0.9828	0.0172	0.03	29
GRL_08.1	27	0	3	0.9500	0.0500	0.10	30
GRL_09.1	29	0	1	0.9833	0.0167	0.03	30
GRL_10.1	29	0	1	0.9833	0.0167	0.03	30
GRL_11.1	29	0	1	0.9833	0.0167	0.03	30
GRL_12.1	28	0	2	0.9667	0.0333	0.07	30
GRL_13.1	29	0	1	0.9833	0.0167	0.03	30
GRL_14.1	24	1	5	0.8833	0.1167	0.17	30
GRL_15.1	28	2	0	0.9667	0.0333	0.07	30
GRL_16.1	26	0	4	0.9333	0.0667	0.13	30
GRL_17.1	27	0	3	0.9500	0.0500	0.10	30
GRL_18.1	25	0	5	0.9167	0.0833	0.17	30
GRL_19.1	28	2	0	0.9667	0.0333	0.07	30
GRL_20.1	28	2	0	0.9667	0.0333	0.07	30
GRL_21.1	27	0	3	0.9500	0.0500	0.10	30
GRL_22.1	27	0	2	0.9655	0.0345	0.07	29
GRL_23.1	29	0	1	0.9833	0.0167	0.03	30
GRL_24.1	27	0	3	0.9500	0.0500	0.10	30
GRL_25.1	28	2	0	0.9667	0.0333	0.07	30
GRL_26.1	27	0	3	0.9500	0.0500	0.10	30
GRL_27.1	23	1	5	0.8793	0.1207	0.17	29
GRL_28.1	29	0	1	0.9667	0.0333	0.00	30
GRL_29.1	29	1	0	0.9833	0.0167	0.10	30
GRL_30.1	27	0	3	0.9500	0.0500	0.10	30
GRL_31.1	26	0	4	0.9333	0.0667	0.13	30
GRL_32.1	26	0	4	0.8966	0.1034	0.14	29
GRL_33.1	29	0	1	0.9833	0.0167	0.03	30
GRL_34.1	23	0	7	0.8833	0.1167	0.23	30
GRL_35.1	28	2	0	0.9667	0.0333	0.07	30
GRL_36.1	22	0	8	0.8667	0.1333	0.27	30
GRL_37.1	24	0	6	0.9138	0.0862	0.17	29
GRL_38.1	26	0	4	0.9333	0.0667	0.13	30
GRL_39.1	28	2	0	0.9667	0.0333	0.07	30
GRL_40.1	28	0	2	0.9333	0.0667	0.13	30
GRL_41.1	25	1	4	0.9138	0.0862	0.14	29
GRL_42.1	28	2	0	0.9667	0.0333	0.07	30
GRL_43.1	25	0	3	0.9464	0.0536	0.11	28
GRL_44.1	26	1	3	0.9138	0.0862	0.14	29
GRL_45.1	28	2	0	0.9667	0.0333	0.07	30
GRL_46.1	28	0	1	1.0000	0.0000	0.00	28
GRL_47.1	0	0	0	#DIV/0!	#DIV/0!	#DIV/0!	0
GRL_48.1	24	0	6	0.9000	0.1000	0.20	30
GRL_49.1	24	0	6	0.9000	0.1000	0.20	30
GRL_50.1	25	1	5	0.8833	0.1167	0.17	30
GRY_01.1	25	0	5	0.9167	0.0833	0.17	30
GRY_02.1	24	1	5	0.8833	0.1167	0.17	30
GRY_03.1	29	1	0	0.9833	0.0167	0.03	30
GRY_04.1	25	2	3	0.8833	0.1167	0.10	30
GRY_05.1	28	0	1	0.9828	0.0172	0.03	29
GRY_06.1	27	1	1	0.9483	0.0517	0.03	29
GRY_07.1	30	0	0	1.0000	0.0000	0.00	30
GRY_08.1	23	0	7	0.9600	0.0400	0.04	25
GRY_09.1	26	1	5	0.9464	0.0536	0.04	28
GRY_10.1	0	0	0	#DIV/0!	#DIV/0!	#DIV/0!	0
GRY_11.1	30	0	0	1.0000	0.0000	0.00	30
GRY_12.1	27	0	3	0.9500	0.0500	0.10	30
GRY_13.1	25	1	4	0.9000	0.1000	0.13	30
GRY_14.1	24	2	3	0.8793	0.1207	0.10	29
GRY_15.1	28	1	1	0.9500	0.0500	0.03	30
GRY_16.1	26	0	3	0.9483	0.0517	0.10	29
GRY_17.1	0	0	0	#DIV/0!	#DIV/0!	#DIV/0!	0
GRY_18.1	28	1	1	0.9500	0.0500	0.03	30
GRY_19.1	23	0	6	0.8966	0.1034	0.21	29
GRY_20.1	27	0	3	0.9500	0.0500	0.10	30
GRY_21.1	22	0	8	0.8667	0.1333	0.27	30
GRY_22.1	29	0	0	1.0000	0.0000	0.00	29
GRY_23.1	26	0	3	0.9483	0.0517	0.10	29
GRY_24.1	29	0	1	0.9833	0.0167	0.03	30
GRY_25.1	26	0	3	0.9483	0.0517	0.10	29
GRY_26.1	30	0	0	1.0000	0.0000	0.00	30
GRY_27.1	26	0	3	0.9483	0.0517	0.10	29
GRY_28.1	29	1	0	0.9833	0.0167	0.03	30
GRY_29.1	29	0	0	1.0000	0.0000	0.00	29
GRY_30.1	28	2	0	0.9667	0.0333	0.07	30
GRY_31.1	27	0	3	0.9500	0.0500	0.00	30
GRY_32.1	28	0	2	0.9667	0.0333	0.07	30
GRY_33.1	26	1	1	0.9310	0.0690	0.07	29
GRY_34.1	22	1	7	0.8500	0.1500	0.23	30
GRY_35.1	29	0	1	0.9833	0.0167	0.03	30
GRY_36.1	29	0	1	0.9833	0.0167	0.03	30
GRY_37.1	29	0	1	0.9833	0.0167	0.03	30
GRY_38.1	29	1	0	0.9667	0.0333	0.00	30
GRY_39.1	29	0	1	0.9833	0.0167	0.03	30
GRY_40.1	27	0	1	0.9821	0.0179	0.04	28

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GRY_41.1	25	0	5	0.9167	0.0833	0.17	30
GRY_42.1	27	1	2	0.9333	0.0667	0.07	30
GRY_43.1	26	0	4	0.9333	0.0667	0.13	30
GRY_44.1	26	0	3	0.9483	0.0517	0.10	29
GRY_45.1	25	0	3	0.9310	0.0690	0.14	29
GRY_46.1	28	0	1	0.9828	0.0172	0.03	29
GRY_47.1	24	0	6	0.9000	0.1000	0.20	30
GRY_48.1	26	1	3	0.9167	0.0833	0.10	30
GRY_49.1	25	1	4	0.9000	0.1000	0.13	30
GRY_50.1	25	0	5	0.9167	0.0833	0.10	30
HER_01.1	25	0	5	0.9167	0.0833	0.17	30
HER_02.1	9	3	18	0.6000	0.4000	0.60	30
HER_03.1	25	1	4	0.9000	0.1000	0.13	30
HER_04.1	27	0	3	0.9500	0.0500	0.10	30
HER_05.1	25	0	5	0.9167	0.0833	0.17	30
HER_06.1	26	1	3	0.9167	0.0833	0.10	30
HER_07.1	23	2	4	0.8621	0.1379	0.14	29
HER_08.1	26	1	3	0.9167	0.0833	0.10	30
HER_09.1	25	0	5	0.9167	0.0833	0.17	30
HER_10.1	28	1	1	0.9500	0.0500	0.03	30
HER_11.1	25	1	4	0.9000	0.1000	0.13	30
HER_12.1	24	0	6	0.9000	0.1000	0.20	30
HER_13.1	28	1	1	0.9500	0.0500	0.03	30
HER_14.1	26	1	3	0.9167	0.0833	0.10	30
HER_15.1	22	2	6	0.8333	0.1667	0.20	30
HER_16.1	23	1	5	0.8793	0.1207	0.17	29
HER_17.1	23	0	7	0.8833	0.1167	0.23	30
HER_18.1	26	0	4	0.9333	0.0667	0.13	30
HER_19.1	26	1	3	0.9167	0.0833	0.10	30
HER_20.1	28	0	2	0.9667	0.0333	0.07	30
HER_21.1	26	0	4	0.9333	0.0667	0.13	30
HER_22.1	25	0	5	0.9167	0.0833	0.17	30
HER_23.1	28	0	2	0.9667	0.0333	0.07	30
HER_24.1	27	0	3	0.9500	0.0500	0.10	30
HER_25.1	27	1	2	0.8333	0.1667	0.27	30
HER_26.1	25	0	5	0.9167	0.0833	0.17	30
HER_27.1	27	0	3	0.9500	0.0500	0.10	30
HER_28.1	27	0	3	0.9500	0.0500	0.10	30
HER_29.1	24	1	5	0.8833	0.1167	0.17	30
HER_30.1	25	0	5	0.9167	0.0833	0.17	30
HER_31.1	24	2	4	0.8667	0.1333	0.13	30
HER_32.1	26	0	4	0.9333	0.0667	0.13	30
HER_33.1	23	0	7	0.8833	0.1167	0.23	30
HER_34.1	25	0	5	0.9167	0.0833	0.17	30
HER_35.1	25	1	4	0.9000	0.1000	0.13	30
HER_36.1	23	1	6	0.8667	0.1333	0.20	30
HER_37.1	24	1	5	0.8833	0.1167	0.17	30
HER_38.1	0	0	0	#DIV/0!	#DIV/0!	#DIV/0!	0
HER_39.1	24	0	6	0.9000	0.1000	0.20	30
HER_40.1	25	2	3	0.8833	0.1167	0.10	30
HER_41.1	28	0	2	0.9667	0.0333	0.07	30
HER_42.1	25	1	4	0.9000	0.1000	0.13	30
HER_43.1	27	1	1	0.9167	0.0833	0.03	30
HER_44.1	19	1	10	0.8000	0.2000	0.33	30
HER_45.1	28	0	2	0.9667	0.0333	0.07	30
HER_46.1	25	1	4	0.9000	0.1000	0.13	30
HER_47.1	27	0	3	0.9500	0.0500	0.10	30
HER_48.1	30	0	0	1.0000	0.0000	0.00	30
HER_49.1	26	1	3	0.9167	0.0833	0.10	30
HER_50.1	28	0	2	0.9667	0.0333	0.07	30
HSL_01.1	6	10	14	0.4333	0.5667	0.47	30
HSL_02.1	3	10	17	0.3833	0.6167	0.57	30
HSL_03.1	8	14	8	0.4000	0.6000	0.27	30
HSL_04.1	5	14	11	0.3500	0.6500	0.37	30
HSL_05.1	9	11	10	0.4667	0.5333	0.33	30
HSL_06.1	6	16	8	0.3333	0.6667	0.27	30
HSL_07.1	4	15	11	0.3833	0.6167	0.50	30
HSL_08.1	6	13	15	0.3167	0.6833	0.50	30
HSL_09.1	6	17	7	0.3167	0.6833	0.23	30
HSL_10.1	4	16	12	0.2667	0.7333	0.40	30
HSL_11.1	5	16	9	0.4333	0.5667	0.53	30
HSL_12.1	6	18	6	0.3000	0.7000	0.20	30
HSL_13.1	9	15	6	0.4500	0.5500	0.50	30
HSL_14.1	5	15	10	0.3333	0.6667	0.33	30
HSL_15.1	7	18	5	0.3833	0.6167	0.23	30
HSL_16.1	6	15	11	0.4167	0.5833	0.43	30
HSL_17.1	5	12	13	0.3833	0.6167	0.43	30
HSL_18.1	8	14	12	0.3667	0.6333	0.47	30
HSL_19.1	4	15	10	0.3667	0.6333	0.50	30
HSL_20.1	4	12	13	0.3621	0.6379	0.45	29
HSL_21.1	8	17	5	0.3500	0.6500	0.17	30
HSL_22.1	5	14	14	0.3000	0.7000	0.47	30
HSL_23.1	6	11	12	0.4138	0.5862	0.41	29
HSL_24.1	6	16	8	0.4000	0.6000	0.40	30
HSL_25.1	1	9	20	0.3667	0.6333	0.67	30
HSL_26.1	10	14	6	0.3000	0.7000	0.33	30
HSL_27.1	5	15	10	0.4333	0.5667	0.50	30
HSL_28.1	10	14	6	0.3000	0.7000	0.20	30
HSL_29.1	2	14	14	0.3000	0.6667	0.47	30
HSL_30.1	5	15	10	0.3833	0.6167	0.33	30
HSL_31.1	10	13	6	0.4483	0.5517	0.21	29
HSL_32.1	12	15	3	0.3000	0.7000	0.40	30
HSL_33.1	8	9	13	0.4833	0.5167	0.43	30
HSL_34.1	3	15	12	0.3000	0.7000	0.40	30
HSL_35.1	6	14	10	0.3667	0.6333	0.33	30
HSL_36.1	6	14	10	0.4500	0.5500	0.50	30
HSL_37.1	4	14	14	0.4000	0.6000	0.47	30
HSL_38.1	3	16	11	0.2833	0.7167	0.53	30
HSL_39.1	11	8	11	0.5500	0.4500	0.37	30
HSL_40.1	2	17	11	0.2667	0.7333	0.33	30
HSL_41.1	6	15	9	0.4500	0.5500	0.50	30
HSL_42.1	3	8	19	0.4167	0.5833	0.63	30
HSL_43.1	7	11	12	0.4310	0.5690	0.38	29
HSL_44.1	7	15	8	0.3667	0.6333	0.50	30
HSL_45.1	6	15	11	0.4167	0.5833	0.43	30
HSL_46.1	6	14	10	0.4333	0.5667	0.60	30
HSL_47.1	3	14	13	0.3167	0.6833	0.43	30
HSL_48.1	2	17	11	0.2500	0.7500	0.37	30
HSL_49.1	4	11	15	0.3667	0.6333	0.53	30
HSL_50.1	3	11	16	0.4167	0.5833	0.43	30
JCP_01.1	28	1	1	0.9500	0.0500	0.03	30
JCP_02.1	30	0	0	1.0000	0.0000	0.00	30
JCP_03.1	28	0	1	0.9828	0.0172	0.03	29
JCP_04.1	27	0	3	0.9500	0.0500	0.10	30
JCP_05.1	24	0	6	0.9000	0.1000	0.20	30
JCP_06.1	23	1	3	0.8833	0.1167	0.10	30
JCP_07.1	25	0	5	0.9167	0.0833	0.17	30
JCP_08.1	25	0	3	0.9464	0.0536	0.11	28
JCP_09.1	27	0	3	0.9500	0.0500	0.10	30
JCP_10.1	27	0	3	0.9500	0.0500	0.10	30
JCP_11.1	27	0	3	0.9500	0.0500	0.10	30
JCP_12.1	25	0	5	0.9167	0.0833	0.17	30
JCP_13.1	27	0	3	0.9500	0.0500	0.10	30
JCP_14.1	27	0	3	0.9500	0.0500	0.10	30
JCP_15.1	29	1	1	0.9833	0.0167	0.03	30
JCP_16.1	28	1	1	0.9500	0.0500	0.03	30
JCP_17.1	29	1	1	0.9833	0.0167	0.03	30
JCP_18.1	26	1	3	0.9167	0.0833	0.10	30
JCP_19.1	28	0	2	0.9667	0.0333	0.07	30

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JCP_20.1	29	0	1	0.9833	0.0167	0.03	30
JCP_21.1	27	0	3	0.9500	0.0500	0.10	30
JCP_22.1	28	0	2	0.9667	0.0333	0.07	30
JCP_23.1	28	1	1	0.9500	0.0500	0.03	30
JCP_24.1	24	0	6	0.9000	0.1000	0.20	30
JCP_25.1	24	1	5	0.8833	0.1167	0.17	30
JCP_26.1	26	0	3	0.9483	0.0517	0.10	29
JCP_27.1	30	0	0	1.0000	0.0000	0.00	30
JCP_28.1	26	1	3	0.9167	0.0833	0.00	30
JCP_29.1	26	0	4	0.9333	0.0667	0.13	30
JCP_30.1	29	0	1	0.9833	0.0167	0.03	30
JCP_31.1	29	0	1	0.9833	0.0167	0.03	30
JCP_32.1	28	0	1	1.0000	0.0000	0.00	28
JCP_33.1	28	0	2	0.9667	0.0333	0.07	30
JCP_34.1	28	0	2	0.9667	0.0333	0.07	30
JCP_35.1	24	0	6	0.9000	0.1000	0.20	30
JCP_36.1	29	0	1	0.9833	0.0167	0.03	30
JCP_37.1	28	0	2	0.9667	0.0333	0.07	30
JCP_38.1	28	0	2	0.9667	0.0333	0.07	30
JCP_39.1	28	0	2	0.9667	0.0333	0.07	30
JCP_40.1	29	0	1	0.9833	0.0167	0.03	30
JCP_41.1	27	0	3	0.9500	0.0500	0.10	30
JCP_42.1	25	0	5	0.9167	0.0833	0.17	30
JCP_43.1	28	0	2	0.9667	0.0333	0.07	30
JCP_44.1	29	0	1	0.9833	0.0167	0.03	30
JCP_45.1	28	0	2	0.9667	0.0333	0.07	30
JCP_46.1	30	0	0	1.0000	0.0000	0.00	30
JCP_47.1	28	0	2	0.9667	0.0333	0.07	30
JCP_48.1	25	0	5	0.9167	0.0833	0.17	30
JCP_49.1	29	0	1	0.9833	0.0167	0.03	30
JCP_50.1	23	0	7	0.8833	0.1167	0.23	30
KEN_01.1	22	0	8	0.8667	0.1333	0.27	30
KEN_02.1	26	1	3	0.9167	0.0833	0.10	30
KEN_03.1	24	1	5	0.8833	0.1167	0.17	30
KEN_04.1	27	0	3	0.9500	0.0500	0.10	30
KEN_05.1	24	1	5	0.8833	0.1167	0.17	30
KEN_06.1	22	0	8	0.8667	0.1333	0.27	30
KEN_07.1	24	1	4	0.8966	0.1034	0.14	29
KEN_08.1	28	0	1	0.9667	0.0333	0.07	30
KEN_09.1	25	0	5	0.9167	0.0833	0.17	30
KEN_10.1	27	1	2	0.9333	0.0667	0.07	30
KEN_11.1	29	0	1	0.9833	0.0167	0.03	30
KEN_12.1	27	0	3	0.9500	0.0500	0.10	30
KEN_13.1	28	0	2	0.9667	0.0333	0.07	30
KEN_14.1	27	0	3	0.9500	0.0500	0.10	30
KEN_15.1	27	0	3	0.9500	0.0500	0.10	30
KEN_16.1	24	0	5	0.9138	0.0862	0.17	29
KEN_17.1	28	0	2	0.9667	0.0333	0.07	30
KEN_18.1	22	0	13	0.7833	0.2167	0.43	30
KEN_19.1	29	0	1	0.9833	0.0167	0.03	30
KEN_20.1	22	1	1	0.9783	0.0217	0.04	23
KEN_21.1	22	0	3	0.9483	0.0517	0.10	29
KEN_22.1	18	1	11	0.7833	0.2167	0.37	30
KEN_23.1	28	0	2	0.9667	0.0333	0.07	30
KEN_24.1	26	1	2	0.9310	0.0690	0.07	29
KEN_25.1	23	0	0	1.0000	0.0000	0.00	23
KEN_26.1	23	2	2	0.9000	0.1000	0.07	30
KEN_27.1	29	0	1	0.9833	0.0167	0.03	30
KEN_28.1	22	7	1	0.8500	0.1500	0.23	30
KEN_29.1	26	0	4	0.9333	0.0667	0.13	30
KEN_30.1	28	1	1	0.9500	0.0500	0.03	30
KEN_31.1	28	0	1	0.9828	0.0172	0.03	29
KEN_32.1	19	11	0	0.8167	0.1833	0.37	30
KEN_33.1	28	1	1	0.9828	0.0172	0.03	29
KEN_34.1	26	1	3	0.9167	0.0833	0.10	30
KEN_35.1	26	0	4	0.9333	0.0667	0.13	30
KEN_36.1	28	0	0	1.0000	0.0000	0.00	28
KEN_37.1	26	1	3	0.9167	0.0833	0.10	30
KEN_38.1	26	0	4	0.9333	0.0667	0.10	30
KEN_39.1	23	0	4	0.8966	0.1034	0.21	29
KEN_40.1	27	0	3	0.9500	0.0500	0.10	30
KEN_41.1	27	0	3	0.9500	0.0500	0.10	30
KEN_42.1	25	0	5	0.9167	0.0833	0.17	30
KEN_43.1	22	0	8	0.8667	0.1333	0.27	30
KEN_44.1	19	1	10	0.8000	0.2000	0.33	30
KEN_45.1	24	0	6	0.9333	0.0667	0.13	30
KEN_46.1	25	0	5	0.9167	0.0833	0.17	30
KEN_47.1	22	1	6	0.8621	0.1379	0.21	29
KEN_48.1	22	1	10	0.8276	0.1724	0.34	29
KEN_49.1	24	1	4	0.8833	0.1167	0.17	30
KEN_50.1	26	0	4	0.9333	0.0667	0.13	30
KIN_01.1	25	1	3	0.9138	0.0862	0.10	29
KIN_02.1	22	0	8	0.8667	0.1333	0.27	30
KIN_03.1	22	0	8	0.8833	0.1167	0.23	30
KIN_04.1	27	0	3	0.9500	0.0500	0.10	30
KIN_05.1	26	0	4	0.9333	0.0667	0.13	30
KIN_06.1	26	0	4	0.9333	0.0667	0.13	30
KIN_07.1	26	0	3	0.9483	0.0517	0.10	29
KIN_08.1	24	0	6	0.9000	0.1000	0.20	30
KIN_09.1	25	0	5	0.9167	0.0833	0.17	30
KIN_10.1	28	0	2	0.9667	0.0333	0.07	30
KIN_11.1	25	0	5	0.9167	0.0833	0.17	30
KIN_12.1	26	0	4	0.9333	0.0667	0.13	30
KIN_13.1	25	0	5	0.9167	0.0833	0.17	30
KIN_14.1	26	0	4	0.9333	0.0667	0.13	30
KIN_15.1	23	0	7	0.8833	0.1167	0.23	30
KIN_16.1	22	1	5	0.8793	0.1207	0.17	29
KIN_17.1	24	1	5	0.8833	0.1167	0.17	30
KIN_18.1	25	0	5	0.9167	0.0833	0.17	30
KIN_19.1	26	0	4	0.9333	0.0667	0.13	30
KIN_20.1	26	0	4	0.9333	0.0667	0.13	30
KIN_21.1	27	0	3	0.9500	0.0500	0.10	30
KIN_22.1	25	1	3	0.9138	0.0862	0.10	29
KIN_23.1	26	2	2	0.9000	0.1000	0.07	30
KIN_24.1	23	0	7	0.8500	0.1500	0.23	30
KIN_25.1	22	0	8	0.8500	0.1500	0.30	30
KIN_26.1	22	0	8	0.8667	0.1333	0.27	30
KIN_27.1	24	2	4	0.8667	0.1333	0.20	30
KIN_28.1	22	0	6	0.9000	0.1000	0.20	30
KIN_29.1	22	0	8	0.8667	0.1333	0.27	30
KIN_30.1	25	0	5	0.9333	0.0667	0.10	30
KIN_31.1	25	2	3	0.8833	0.1167	0.07	30
KIN_32.1	24	0	6	0.9000	0.1000	0.13	30
KIN_33.1	27	0	3	0.9500	0.0500	0.10	30
KIN_34.1	23	1	6	0.8667	0.1333	0.20	30
KIN_35.1	26	0	4	0.9333	0.0667	0.13	30
KIN_36.1	28	0	2	0.9667	0.0333	0.07	30
KIN_37.1	26	0	4	0.9333	0.0667	0.13	30
KIN_38.1	27	0	3	0.9500	0.0500	0.13	30
KIN_39.1	26	0	4	0.9333	0.0667	0.13	30
KIN_40.1	23	0	7	0.8500	0.1500	0.23	30
KIN_41.1	22	0	8	0.8667	0.1333	0.27	30
KIN_42.1	29	0	1	0.9833	0.0167	0.03	30
KIN_43.1	26	3	1	0.9167	0.0833	0.17	30
KIN_44.1	21	2	7	0.8167	0.1833	0.23	30
KIN_45.1	22	1	7	0.9138	0.0862	0.13	29
KIN_46.1	26	1	3	0.9167	0.0833	0.10	29
KIN_47.1	22	0	8	0.8667	0.1333	0.27	30
KIN_48.1							

Locus	n	Ho count	Het count	Freq1	Freq2	Value	N
KIN_49.1	23	2	5	0.8500	0.1500	0.17	30
KIN_50.1	26	0	4	0.9333	0.0667	0.13	30
LMA_01.1	25	1	4	0.9000	0.1000	0.13	30
LMA_02.1	26	1	2	0.9310	0.0690	0.07	29
LMA_03.1	25	1	4	0.9000	0.1000	0.13	30
LMA_04.1	26	0	4	0.9333	0.0667	0.13	30
LMA_05.1	23	2	5	0.8500	0.1500	0.17	30
LMA_06.1	23	2	5	0.8500	0.1500	0.17	30
LMA_07.1	25	1	4	0.9000	0.1000	0.13	30
LMA_08.1	22	1	3	0.9167	0.0833	0.10	30
LMA_09.1	28	0	2	0.9667	0.0333	0.07	30
LMA_10.1	26	0	3	0.9483	0.0517	0.10	29
LMA_11.1	26	1	3	0.9167	0.0833	0.10	30
LMA_12.1	29	0	1	0.9833	0.0167	0.03	30
LMA_13.1	27	0	2	0.9655	0.0345	0.07	29
LMA_14.1	27	0	3	0.9500	0.0500	0.10	30
LMA_15.1	25	0	5	0.9167	0.0833	0.17	30
LMA_16.1	26	0	4	0.9333	0.0667	0.13	30
LMA_17.1	28	1	1	0.9500	0.0500	0.03	30
LMA_18.1	26	0	4	0.9333	0.0667	0.13	30
LMA_19.1	17	0	0	1.0000	0.0000	0.00	17
LMA_20.1	27	0	4	0.9333	0.0667	0.13	30
LMA_21.1	27	0	3	0.9500	0.0500	0.10	30
LMA_22.1	27	1	2	0.9333	0.0667	0.07	30
LMA_23.1	24	0	0	1.0000	0.0000	0.00	24
LMA_24.1	28	0	4	0.9333	0.0667	0.13	30
LMA_25.1	29	0	1	0.9833	0.0167	0.03	30
LMA_26.1	22	0	8	0.8667	0.1333	0.27	30
LMA_27.1	26	0	4	0.9333	0.0667	0.13	30
LMA_28.1	27	0	3	0.9500	0.0500	0.10	30
LMA_29.1	27	0	3	0.9500	0.0500	0.10	30
LMA_30.1	23	1	6	0.8667	0.1333	0.20	30
LMA_31.1	29	0	1	0.9833	0.0167	0.03	30
LMA_32.1	28	0	2	0.9667	0.0333	0.07	30
LMA_33.1	25	1	4	0.9000	0.1000	0.13	30
LMA_34.1	26	1	3	0.9167	0.0833	0.10	30
LMA_35.1	25	0	4	0.9310	0.0690	0.14	29
LMA_36.1	29	0	1	0.9833	0.0167	0.03	30
LMA_37.1	25	0	5	0.9167	0.0833	0.17	30
LMA_38.1	28	0	2	0.9667	0.0333	0.07	30
LMA_39.1	18	0	2	0.9500	0.0500	0.10	20
LMA_40.1	27	0	3	0.9500	0.0500	0.10	30
LMA_41.1	26	1	3	0.9167	0.0833	0.10	30
LMA_42.1	28	0	2	0.9667	0.0333	0.07	30
LMA_43.1	26	1	4	0.9000	0.1000	0.13	30
LMA_44.1	26	0	4	0.9333	0.0667	0.13	30
LMA_45.1	26	0	4	0.9333	0.0667	0.13	30
LMA_46.1	27	1	2	0.9333	0.0667	0.07	30
LMA_47.1	26	0	4	0.9333	0.0667	0.13	30
LMA_48.1	28	0	2	0.9667	0.0333	0.07	30
LMA_49.1	26	0	4	0.9333	0.0667	0.13	30
LMA_50.1	29	0	1	0.9833	0.0167	0.03	30
LRL_01.1	23	1	6	0.8667	0.1333	0.20	30
LRL_02.1	27	0	3	0.9500	0.0500	0.10	30
LRL_03.1	26	0	4	0.9333	0.0667	0.13	30
LRL_04.1	28	1	1	0.9500	0.0500	0.03	30
LRL_05.1	28	0	2	0.9667	0.0333	0.07	30
LRL_06.1	28	0	2	0.9667	0.0333	0.07	30
LRL_07.1	28	0	2	0.9667	0.0333	0.07	30
LRL_08.1	27	1	2	0.9333	0.0667	0.07	30
LRL_09.1	21	0	9	0.8500	0.1500	0.30	30
LRL_10.1	27	0	3	0.9500	0.0500	0.10	30
LRL_11.1	26	1	3	0.9167	0.0833	0.10	30
LRL_12.1	29	0	1	0.9833	0.0167	0.03	30
LRL_13.1	29	0	1	0.9833	0.0167	0.03	30
LRL_14.1	26	0	4	0.9333	0.0667	0.13	30
LRL_15.1	27	0	3	0.9500	0.0500	0.10	30
LRL_16.1	26	0	4	0.9333	0.0667	0.13	30
LRL_17.1	21	3	6	0.8000	0.2000	0.20	30
LRL_18.1	23	0	7	0.8833	0.1167	0.23	30
LRL_19.1	28	0	2	0.9667	0.0333	0.07	30
LRL_20.1	25	1	4	0.9000	0.1000	0.13	30
LRL_21.1	24	0	6	0.9000	0.1000	0.20	30
LRL_22.1	26	0	3	0.9483	0.0517	0.10	29
LRL_23.1	28	0	2	0.9667	0.0333	0.07	30
LRL_24.1	23	1	6	0.8667	0.1333	0.20	30
LRL_25.1	29	0	1	0.9833	0.0167	0.03	30
LRL_26.1	30	0	0	1.0000	0.0000	0.00	30
LRL_27.1	17	1	12	0.7667	0.2333	0.40	30
LRL_28.1	28	0	2	0.9667	0.0333	0.07	30
LRL_29.1	30	0	0	1.0000	0.0000	0.00	30
LRL_30.1	26	0	3	0.9483	0.0517	0.10	29
LRL_31.1	28	0	1	0.9828	0.0172	0.03	29
LRL_32.1	24	0	6	0.9000	0.1000	0.20	30
LRL_33.1	24	1	5	0.8833	0.1167	0.17	30
LRL_34.1	24	1	5	0.8833	0.1167	0.17	30
LRL_35.1	26	0	4	0.9333	0.0667	0.13	30
LRL_36.1	26	0	4	0.9333	0.0667	0.13	30
LRL_37.1	27	1	2	0.9333	0.0667	0.07	30
LRL_38.1	28	0	2	0.9667	0.0333	0.07	30
LRL_39.1	27	0	3	0.9500	0.0500	0.10	30
LRL_40.1	26	0	4	0.9333	0.0667	0.13	30
LRL_41.1	27	0	3	0.9500	0.0500	0.10	30
LRL_42.1	25	3	3	0.8667	0.1333	0.07	30
LRL_43.1	24	2	4	0.8667	0.1333	0.13	30
LRL_44.1	21	0	2	0.9565	0.0435	0.09	23
LRL_45.1	29	0	1	0.9833	0.0167	0.03	30
LRL_46.1	27	0	2	0.9655	0.0345	0.07	29
LRL_47.1	18	1	11	0.7833	0.2167	0.37	30
LRL_48.1	27	0	3	0.9500	0.0500	0.10	30
LRL_49.1	25	0	5	0.9167	0.0833	0.17	30
LRL_50.1	5	12	12	0.3833	0.6167	0.43	30
MCH_100.1	28	0	2	0.9667	0.0333	0.07	30
MCH_51.1	21	3	6	0.8000	0.2000	0.20	30
MCH_52.1	23	2	5	0.8500	0.1500	0.17	30
MCH_53.1	23	0	7	0.8833	0.1167	0.23	30
MCH_54.1	26	0	4	0.9333	0.0667	0.13	30
MCH_55.1	25	0	5	0.9167	0.0833	0.17	30
MCH_56.1	24	0	6	0.9000	0.1000	0.20	30
MCH_57.1	21	0	9	0.8500	0.1500	0.30	30
MCH_58.1	28	0	2	0.9333	0.0667	0.07	30
MCH_59.1	16	4	10	0.7000	0.3000	0.33	30
MCH_60.1	1	25	4	0.5833	0.4167	0.83	30
MCH_61.1	25	1	4	0.9000	0.1000	0.13	30
MCH_62.1	24	0	5	0.9138	0.0862	0.17	29
MCH_63.1	27	1	0	0.9643	0.0357	0.00	28
MCH_64.1	24	0	6	0.9000	0.1000	0.20	30
MCH_65.1	24	0	6	0.9000	0.1000	0.20	30
MCH_66.1	26	0	4	0.9333	0.0667	0.13	30
MCH_67.1	25	0	5	0.9167	0.0833	0.17	30
MCH_68.1	24	1	5	0.8833	0.1167	0.17	30
MCH_69.1	23	0	7	0.8833	0.1167	0.23	30
MCH_70.1	26	1	3	0.8621	0.1379	0.21	30
MCH_71.1	24	0	5	0.8448	0.1552	0.24	29
MCH_72.1	25	0	5	0.9167	0.0833	0.17	30
MCH_73.1	27	0	3	0.9500	0.0500	0.10	30
MCH_74.1	25	3	4	0.9000	0.1000	0.13	30
MCH_75.1	20	0	10	0.8333	0.1667	0.33	30

Sample	N1	N2	N3	Prop1	Prop2	Dec	Total
MCH_77.1	19	1	10	0.8000	0.2000	0.33	30
MCH_78.1	13	0	17	0.7167	0.2833	0.57	30
MCH_79.1	25	0	5	0.9167	0.0833	0.17	30
MCH_80.1	9	3	18	0.6000	0.4000	0.60	30
MCH_81.1	23	0	7	0.8833	0.1167	0.23	30
MCH_82.1	22	0	8	0.8667	0.1333	0.27	30
MCH_83.1	26	0	4	0.9333	0.0667	0.13	30
MCH_84.1	21	0	9	0.8500	0.1500	0.30	30
MCH_85.1	29	0	1	0.9833	0.0167	0.03	30
MCH_86.1	28	0	2	0.9667	0.0333	0.07	30
MCH_87.1	10	3	17	0.6167	0.3833	0.57	30
MCH_88.1	20	1	8	0.8276	0.1724	0.28	29
MCH_89.1	26	0	4	0.9333	0.0667	0.13	30
MCH_90.1	12	0	14	0.7308	0.2692	0.54	26
MCH_91.1	25	0	4	0.9310	0.0690	0.14	29
MCH_92.1	24	0	6	0.9000	0.1000	0.20	30
MCH_93.1	22	1	7	0.8500	0.1500	0.23	30
MCH_94.1	22	0	7	0.8793	0.1207	0.24	29
MCH_95.1	27	0	2	0.9655	0.0345	0.07	29
MCH_96.1	28	0	2	0.9667	0.0333	0.07	30
MCH_97.1	27	0	3	0.9500	0.0500	0.10	30
MCH_98.1	23	0	7	0.8833	0.1167	0.23	30
MCH_99.1	26	0	4	0.9333	0.0667	0.13	30
MIL_01.1	29	0	1	0.9833	0.0167	0.03	30
MIL_02.1	11	9	9	0.5345	0.4655	0.31	29
MIL_03.1	16	2	12	0.7333	0.2667	0.40	30
MIL_04.1	18	2	10	0.7667	0.2333	0.33	30
MIL_05.1	23	1	6	0.8667	0.1333	0.20	30
MIL_06.1	8	12	10	0.4333	0.5667	0.33	30
MIL_07.1	22	1	6	0.8333	0.1667	0.20	30
MIL_08.1	14	1	15	0.7167	0.2833	0.50	30
MIL_09.1	26	1	3	0.9167	0.0833	0.10	30
MIL_10.1	23	2	5	0.8500	0.1500	0.17	30
MIL_11.1	27	0	3	0.9500	0.0500	0.10	30
MIL_12.1	7	10	13	0.4500	0.5500	0.43	30
MIL_13.1	18	2	10	0.7667	0.2333	0.33	30
MIL_14.1	16	1	13	0.7500	0.2500	0.43	30
MIL_15.1	22	0	8	0.8833	0.1167	0.27	30
MIL_16.1	13	1	15	0.7069	0.2931	0.52	29
MIL_17.1	28	0	2	0.9667	0.0333	0.07	30
MIL_18.1	27	0	2	0.9655	0.0345	0.07	29
MIL_19.1	17	1	12	0.7667	0.2333	0.40	30
MIL_20.1	20	0	10	0.8333	0.1667	0.33	30
MIL_21.1	26	0	4	0.9333	0.0667	0.13	30
MIL_22.1	27	0	3	0.9500	0.0500	0.10	30
MIL_23.1	18	2	10	0.7667	0.2333	0.33	30
MIL_24.1	26	0	3	0.9483	0.0517	0.10	29
MIL_25.1	20	0	10	0.8333	0.1667	0.33	30
MIL_26.1	30	0	0	1.0000	0.0000	0.00	30
MIL_27.1	8	3	19	0.5833	0.4167	0.63	30
MIL_28.1	18	1	11	0.7833	0.2167	0.37	30
MIL_29.1	23	1	6	0.8667	0.1333	0.20	30
MIL_30.1	19	1	10	0.8000	0.2000	0.33	30
MIL_31.1	27	0	3	0.9500	0.0500	0.10	30
MIL_32.1	20	0	10	0.8333	0.1667	0.33	30
MIL_33.1	8	11	11	0.4821	0.5179	0.39	28
MIL_34.1	12	4	17	0.5833	0.4167	0.57	30
MIL_35.1	27	0	2	0.9655	0.0345	0.07	29
MIL_36.1	10	2	18	0.6333	0.3667	0.60	30
MIL_37.1	15	1	14	0.7333	0.2667	0.47	30
MIL_38.1	26	1	3	0.9167	0.0833	0.10	30
MIL_39.1	13	4	13	0.6500	0.3500	0.43	30
MIL_40.1	12	2	16	0.6667	0.3333	0.53	30
MIL_41.1	7	10	13	0.4500	0.5500	0.43	30
MIL_42.1	28	0	2	0.9667	0.0333	0.07	30
MIL_43.1	28	0	2	0.9667	0.0333	0.07	30
MIL_44.1	24	1	5	0.8833	0.1167	0.17	30
MIL_45.1	12	2	16	0.7000	0.3000	0.53	30
MIL_46.1	16	2	12	0.7333	0.2667	0.40	30
MIL_47.1	28	0	2	0.9667	0.0333	0.07	30
MIL_48.1	13	2	15	0.6833	0.3167	0.50	30
MIL_49.1	13	0	16	0.7241	0.2759	0.55	29
MIL_50.1	20	0	9	0.8448	0.1552	0.31	29
NRL_02.1	27	0	3	0.9500	0.0500	0.10	30
NRL_06.1	30	0	0	1.0000	0.0000	0.00	30
NRL_08.1	28	1	0	0.9828	0.0172	0.03	29
NRL_100.1	28	0	1	0.9828	0.0172	0.03	29
NRL_104.1	28	0	2	0.9667	0.0333	0.07	30
NRL_106.1	30	0	0	1.0000	0.0000	0.00	30
NRL_108.1	0	0	0	#DIV/0!	#DIV/0!	#DIV/0!	0
NRL_112.1	29	0	0	1.0000	0.0000	0.00	29
NRL_114.1	28	0	2	0.9667	0.0333	0.07	30
NRL_120.1	28	0	2	0.9500	0.0500	0.07	30
NRL_122.1	24	1	1	0.9500	0.0500	0.07	30
NRL_124.1	29	0	1	0.9833	0.0167	0.03	30
NRL_125.1	28	0	2	0.9667	0.0333	0.07	30
NRL_126.1	30	0	0	1.0000	0.0000	0.00	30
NRL_130.1	30	0	0	1.0000	0.0000	0.00	30
NRL_132.1	29	0	1	0.9833	0.0167	0.03	30
NRL_138.1	28	0	2	0.9667	0.0333	0.07	30
NRL_144.1	30	0	0	1.0000	0.0000	0.00	30
NRL_145.1	27	0	3	0.9500	0.0500	0.10	30
NRL_16.1	29	0	1	0.9833	0.0167	0.03	30
NRL_17.1	29	0	0	0.9483	0.0517	0.03	29
NRL_21.1	28	0	2	0.9667	0.0333	0.00	30
NRL_23.1	23	1	1	0.9333	0.0667	0.07	30
NRL_24.1	27	1	1	0.9333	0.0667	0.07	30
NRL_26.1	28	0	2	0.9667	0.0333	0.07	30
NRL_28.1	28	0	2	0.9667	0.0333	0.07	30
NRL_35.1	29	0	0	0.9828	0.0172	0.03	29
NRL_36.1	30	0	0	1.0000	0.0000	0.00	30
NRL_38.1	29	0	1	0.9833	0.0167	0.03	30
NRL_41.1	27	0	3	0.9500	0.0500	0.10	30
NRL_42.1	26	1	2	0.9310	0.0690	0.07	29
NRL_48.1	27	0	3	0.9500	0.0500	0.10	30
NRL_50.1	26	0	3	0.9483	0.0517	0.10	29
NRL_55.1	29	0	1	0.9833	0.0167	0.03	30
NRL_57.1	28	0	2	0.9667	0.0333	0.07	30
NRL_58.1	29	0	1	0.9833	0.0167	0.03	30
NRL_60.1	29	0	0	1.0000	0.0000	0.00	29
NRL_64.1	29	0	1	0.9833	0.0167	0.03	30
NRL_69.1	27	0	2	0.9655	0.0345	0.07	29
NRL_73.1	29	0	1	0.9833	0.0167	0.03	30
NRL_74.1	29	0	1	0.9833	0.0167	0.03	30
NRL_75.1	29	0	1	0.9833	0.0167	0.03	30
NRL_80.1	29	0	0	0.9828	0.0172	0.03	29
NRL_82.1	29	0	1	0.9833	0.0167	0.03	30
NRL_87.1	26	0	3	0.9167	0.0833	0.10	30
NRL_90.1	28	0	1	0.9821	0.0179	0.04	28
NRL_94.1	29	0	2	0.9667	0.0333	0.07	30
NRL_97.1	29	0	1	0.9833	0.0167	0.03	30
NRL_98.1	29	0	1	0.9833	0.0167	0.03	30
NRL_99.1	29	0	1	0.9833	0.0167	0.03	30
PVL_100.1	29	1	1	0.9074	0.0926	0.11	27
PVL_101.1	23	0	4	0.9259	0.0741	0.15	27
PVL_102.1	24	0	4	0.9286	0.0714	0.14	28
PVL_103.1	26	0	2	0.9630	0.0370	0.07	27
PVL_104.1	25	0	3	0.9464	0.0536	0.11	28
PVL_105.1	24	1	3	0.9107	0.0893	0.11	28

Label	N	a	b	c	d	e	Total
PVL_106.1	28	0	0	1.0000	0.0000	0.00	28
PVL_107.1	25	0	3	0.9464	0.0536	0.11	28
PVL_108.1	22	1	4	0.8889	0.1111	0.15	27
PVL_109.1	26	0	1	0.9815	0.0185	0.04	27
PVL_110.1	0	1	0	#DIV/0!	#DIV/0!	#DIV/0!	0
PVL_111.1	25	0	3	0.9464	0.0536	0.11	28
PVL_112.1	24	0	5	0.9138	0.0862	0.17	29
PVL_113.1	24	0	2	0.9615	0.0385	0.08	26
PVL_114.1	24	1	4	0.8966	0.1034	0.14	29
PVL_115.1	25	0	3	0.9464	0.0536	0.11	28
PVL_116.1	26	0	1	0.9464	0.0536	0.04	28
PVL_117.1	22	0	4	0.9231	0.0769	0.15	26
PVL_118.1	18	2	8	0.7857	0.2143	0.29	28
PVL_119.1	27	0	1	0.9821	0.0179	0.04	28
PVL_120.1	27	0	2	0.9655	0.0345	0.07	29
PVL_121.1	25	0	3	0.9464	0.0536	0.11	28
PVL_122.1	24	0	4	0.9286	0.0714	0.14	28
PVL_123.1	25	0	2	0.9630	0.0370	0.07	27
PVL_124.1	25	0	2	0.9630	0.0370	0.07	27
PVL_125.1	24	1	3	0.9107	0.0893	0.11	28
PVL_126.1	25	0	3	0.9464	0.0536	0.11	28
PVL_127.1	26	0	2	0.9643	0.0357	0.07	28
PVL_128.1	22	0	2	0.8889	0.1111	0.22	27
PVL_129.1	21	1	6	0.9444	0.0556	0.04	27
PVL_130.1	26	1	2	0.9310	0.0690	0.07	29
PVL_131.1	0	0	0	#DIV/0!	#DIV/0!	#DIV/0!	0
PVL_132.1	24	1	4	0.8966	0.1034	0.14	29
PVL_133.1	25	0	2	0.9630	0.0370	0.07	27
PVL_134.1	24	0	2	0.9615	0.0385	0.08	26
PVL_135.1	25	0	2	0.9630	0.0370	0.07	27
PVL_136.1	24	0	3	0.9444	0.0556	0.11	28
PVL_137.1	21	0	7	0.8750	0.1250	0.25	28
PVL_138.1	25	0	3	0.9464	0.0536	0.11	28
PVL_139.1	23	0	3	0.9423	0.0577	0.12	26
PVL_140.1	26	0	2	0.9643	0.0357	0.07	28
PVL_141.1	20	0	7	0.8704	0.1296	0.26	27
PVL_142.1	18	2	8	0.7857	0.2143	0.29	28
PVL_143.1	24	0	3	0.9286	0.0714	0.14	28
PVL_144.1	24	0	5	0.9138	0.0862	0.17	29
PVL_145.1	25	0	3	0.9464	0.0536	0.11	28
PVL_146.1	26	0	3	0.9483	0.0517	0.10	29
PVL_147.1	24	0	3	0.9800	0.0200	0.04	25
PVL_148.1	26	0	0	1.0000	0.0000	0.00	26
PVL_149.1	22	0	4	0.9231	0.0769	0.15	26
PVL_150.1	26	0	2	0.9643	0.0357	0.07	28
PVL_26.1	28	0	0	1.0000	0.0000	0.00	28
PVL_31.1	24	0	3	0.9444	0.0556	0.11	27
PVL_41.1	26	1	1	0.9464	0.0536	0.04	28
PVL_51.1	26	1	3	0.9167	0.0833	0.10	30
PVL_52.1	26	2	1	0.9138	0.0862	0.10	29
PVL_53.1	27	0	3	0.9500	0.0500	0.10	30
PVL_54.1	28	0	2	0.9667	0.0333	0.07	30
PVL_55.1	28	1	1	0.9500	0.0500	0.03	30
PVL_56.1	26	1	3	0.9167	0.0833	0.10	30
PVL_57.1	23	0	7	0.8833	0.1167	0.23	30
PVL_58.1	28	0	2	0.9667	0.0333	0.07	30
PVL_59.1	28	0	2	0.9643	0.0357	0.07	28
PVL_60.1	20	0	7	0.8704	0.1296	0.26	27
PVL_61.1	23	0	4	0.9259	0.0741	0.15	27
PVL_62.1	24	0	2	0.9615	0.0385	0.08	26
PVL_63.1	23	1	3	0.9074	0.0926	0.11	27
PVL_64.1	25	0	2	0.9630	0.0370	0.07	27
PVL_65.1	21	0	7	0.8750	0.1250	0.25	28
PVL_66.1	28	0	1	0.9828	0.0172	0.03	29
PVL_67.1	22	0	5	0.8929	0.1071	0.21	28
PVL_68.1	23	0	5	0.9107	0.0893	0.18	28
PVL_69.1	25	0	3	0.9464	0.0536	0.11	28
PVL_70.1	20	1	7	0.8393	0.1607	0.25	28
PVL_71.1	23	0	7	0.9600	0.0400	0.08	25
PVL_72.1	26	0	2	0.9643	0.0357	0.07	28
PVL_73.1	23	0	4	0.9259	0.0741	0.15	27
PVL_74.1	23	0	3	0.9423	0.0577	0.12	26
PVL_75.1	20	0	5	0.8571	0.1429	0.29	28
PVL_76.1	21	1	5	0.8704	0.1296	0.19	27
PVL_77.1	24	0	5	0.9107	0.0893	0.18	28
PVL_80.1	25	0	3	0.9464	0.0536	0.11	28
PVL_81.1	23	0	5	0.9107	0.0893	0.18	28
PVL_82.1	23	0	4	0.9286	0.0714	0.14	28
PVL_83.1	24	0	4	0.9286	0.0714	0.14	28
PVL_84.1	27	0	1	0.9821	0.0179	0.04	28
PVL_86.1	22	0	4	0.9231	0.0769	0.15	26
PVL_87.1	24	0	4	0.9286	0.0714	0.14	28
PVL_88.1	24	0	3	0.9444	0.0556	0.11	28
PVL_89.1	26	0	3	0.9310	0.0690	0.14	29
PVL_90.1	22	2	4	0.8571	0.1429	0.14	28
PVL_91.1	26	0	1	0.9815	0.0185	0.04	27
PVL_92.1	24	0	3	0.9444	0.0556	0.11	27
PVL_93.1	26	0	2	0.9643	0.0357	0.07	28
PVL_94.1	26	0	1	0.9815	0.0185	0.04	27
PVL_95.1	28	0	2	0.9286	0.0714	0.14	28
PVL_96.1	28	0	0	1.0000	0.0000	0.00	28
PVL_97.1	25	0	3	0.9310	0.0690	0.14	29
PVL_98.1	25	0	3	0.9310	0.0690	0.14	29
PVL_99.1	27	0	2	0.9630	0.0370	0.07	30
RRL_01.1	25	1	4	0.8333	0.1667	0.33	30
RRL_09.1	25	1	4	0.9000	0.1000	0.13	30
RRL_10.1	26	1	3	0.9167	0.0833	0.10	30
RRL_101.1	22	1	7	0.8500	0.1500	0.23	30
RRL_105.1	20	1	9	0.8167	0.1833	0.30	30
RRL_106.1	24	1	5	0.8500	0.1500	0.30	30
RRL_108.1	25	0	4	0.9310	0.0690	0.14	29
RRL_112.1	21	1	7	0.8448	0.1552	0.24	29
RRL_118.1	26	1	3	0.8519	0.1481	0.27	30
RRL_120.1	12	0	11	0.7609	0.2391	0.48	23
RRL_121.1	26	0	4	0.9333	0.0667	0.13	30
RRL_124.1	24	1	5	0.7167	0.2833	0.27	30
RRL_125.1	23	3	4	0.8333	0.1667	0.13	30
RRL_128.1	21	0	6	0.8500	0.1500	0.30	30
RRL_13.1	24	0	6	0.9000	0.1000	0.20	30
RRL_130.1	24	0	6	0.9000	0.1000	0.20	30
RRL_133.1	18	0	11	0.7833	0.2167	0.37	30
RRL_137.1	18	4	7	0.8333	0.1667	0.23	30
RRL_138.1	24	0	5	0.9138	0.0862	0.17	29
RRL_139.1	19	4	7	0.7167	0.2833	0.27	30
RRL_142.1	24	0	5	0.9138	0.0862	0.17	29
RRL_16.1	19	0	10	0.7333	0.2667	0.33	30
RRL_19.1	23	0	6	0.8000	0.2000	0.40	30
RRL_25.1	24	1	5	0.9107	0.0893	0.18	30
RRL_32.1	26	0	4	0.9333	0.0667	0.13	30
RRL_37.1	21	1	8	0.8333	0.1667	0.17	30
RRL_39.1	21	0	9	0.8500	0.1500	0.30	30
RRL_40.1	19	1	10	0.8000	0.2000	0.33	30
RRL_42.1	19	0	11	0.8167	0.1833	0.37	30
RRL_43.1	23	0	7	0.8500	0.1500	0.17	30
RRL_44.1	21	0	9	0.9000	0.1000	0.30	30
RRL_45.1	19	0	11	0.8167	0.1833	0.37	30
RRL_46.1	24	1	5	0.8966	0.1034	0.21	29
RRL_48.1	22	3	5	0.8167	0.1833	0.17	30
RRL_52.1	22	1	7	0.8500	0.1500	0.23	30

Sample	n₁	n₂	n₃	Freq1	Freq2	Ratio	Total
RRL_54.1	24	1	5	0.8833	0.1167	0.17	30
RRL_59.1	26	2	2	0.9000	0.1000	0.07	30
RRL_60.1	21	1	8	0.8333	0.1667	0.27	30
RRL_61.1	24	0	6	0.9000	0.1000	0.20	30
RRL_65.1	23	0	7	0.8833	0.1167	0.23	30
RRL_66.1	22	0	8	0.8667	0.1333	0.27	30
RRL_70.1	23	2	5	0.8500	0.1500	0.17	30
RRL_75.1	21	0	8	0.8333	0.1667	0.27	30
RRL_80.1	24	0	5	0.9138	0.0862	0.17	29
RRL_82.1	27	0	3	0.9500	0.0500	0.10	30
RRL_88.1	26	0	3	0.9483	0.0517	0.10	29
RRL_93.1	19	2	8	0.7931	0.2069	0.28	29
RRL_95.1	19	3	8	0.7667	0.2333	0.27	30
RRL_97.1	22	0	5	0.9074	0.0926	0.19	27
RRL_99.1	26	1	6	0.8621	0.1379	0.21	29
TVL_01.1	25	0	5	0.9167	0.0833	0.17	30
TVL_05.1	28	1	1	0.9500	0.0500	0.03	30
TVL_06.1	26	0	4	0.9333	0.0667	0.13	30
TVL_07.1	25	1	3	0.9138	0.0862	0.10	29
TVL_11.1	22	1	7	0.8500	0.1500	0.23	30
TVL_12.1	25	1	3	0.9138	0.0862	0.10	29
TVL_14.1	23	1	6	0.8667	0.1333	0.20	30
TVL_15.1	21	0	9	0.8500	0.1500	0.30	30
TVL_16.1	22	2	6	0.8333	0.1667	0.20	30
TVL_17.1	20	0	10	0.8333	0.1667	0.33	30
TVL_18.1	26	1	3	0.9167	0.0833	0.10	30
TVL_19.1	27	0	2	0.9655	0.0345	0.07	29
TVL_21.1	27	2	1	0.9333	0.0667	0.07	30
TVL_23.1	27	0	3	0.9500	0.0500	0.10	30
TVL_27.1	27	0	3	0.9500	0.0500	0.10	30
TVL_29.1	28	0	2	0.9667	0.0333	0.07	30
TVL_31.1	20	0	10	0.8333	0.1667	0.33	30
TVL_37.1	27	0	3	0.9500	0.0500	0.10	30
TVL_38.1	26	1	3	0.9333	0.0667	0.13	30
TVL_39.1	23	1	6	0.8667	0.1333	0.20	30
TVL_40.1	27	0	3	0.9500	0.0500	0.10	30
TVL_41.1	24	0	6	0.9000	0.1000	0.20	30
TVL_42.1	21	0	8	0.8621	0.1379	0.28	29
TVL_43.1	24	0	6	0.9000	0.1000	0.20	30
TVL_45.1	24	0	6	0.9000	0.1000	0.20	30
TVL_47.1	28	0	2	0.9667	0.0333	0.07	30
TVL_48.1	24	1	5	0.8833	0.1167	0.17	30
TVL_53.1	22	1	6	0.8621	0.1379	0.21	29
TVL_54.1	27	1	2	0.9333	0.0667	0.07	30
TVL_55.1	28	0	2	0.9667	0.0333	0.07	30
TVL_57.1	26	1	3	0.9167	0.0833	0.10	30
TVL_58.1	28	0	2	0.9667	0.0333	0.07	30
TVL_61.1	27	1	2	0.9333	0.0667	0.07	30
TVL_62.1	28	0	2	0.9667	0.0333	0.07	30
TVL_63.1	25	1	4	0.9000	0.1000	0.13	30
TVL_71.1	27	0	3	0.9500	0.0500	0.10	30
TVL_73.1	24	0	6	0.9000	0.1000	0.20	30
TVL_74.1	27	0	3	0.9500	0.0500	0.10	30
TVL_77.1	27	0	2	0.9655	0.0345	0.07	29
TVL_78.1	20	0	1	0.9762	0.0238	0.05	21
TVL_79.1	25	0	5	0.9167	0.0833	0.17	30
TVL_80.1	19	1	10	0.8000	0.2000	0.33	30
TVL_82.1	22	2	6	0.8333	0.1667	0.20	30
TVL_85.1	27	0	3	0.9500	0.0500	0.10	30
TVL_87.1	27	0	3	0.9500	0.0500	0.10	30
TVL_90.1	25	1	4	0.9000	0.1000	0.13	30
TVL_92.1	26	0	4	0.9333	0.0667	0.13	30
TVL_95.1	26	0	4	0.9333	0.0667	0.13	30
TVL_97.1	26	0	4	0.9333	0.0667	0.13	30
TVL_99.1	26	1	3	0.9167	0.0833	0.10	30
YVL_01.1	23	1	6	0.8667	0.1333	0.20	30
YVL_02.1	27	0	3	0.9500	0.0500	0.10	30
YVL_03.1	28	0	2	1.0000	0.0000	0.00	30
YVL_04.1	26	0	2	0.9643	0.0357	0.07	28
YVL_53.1	24	1	7	0.8793	0.1207	0.24	29
YVL_06.1	21	0	7	0.8750	0.1250	0.25	28
YVL_07.1	21	1	7	0.8448	0.1552	0.24	29
YVL_08.1	0	0	0	#DIV/0!	#DIV/0!	#DIV/0!	0
YVL_09.1	26	0	3	0.9483	0.0517	0.10	29
YVL_10.1	24	1	5	0.8793	0.1207	0.17	29
YVL_11.1	23	0	5	0.9259	0.0741	0.15	27
YVL_12.1	28	0	2	0.9828	0.0172	0.03	30
YVL_13.1	27	0	2	0.9333	0.0667	0.07	30
YVL_14.1	29	1	1	0.9833	0.0517	0.03	30
YVL_15.1	25	1	3	0.9138	0.0862	0.10	29
YVL_16.1	26	0	3	0.9483	0.0517	0.10	29
YVL_17.1	27	0	3	0.9500	0.0500	0.10	30
YVL_18.1	23	1	5	0.8793	0.1207	0.17	29
YVL_19.1	26	0	2	0.9643	0.0357	0.07	28
YVL_20.1	26	0	3	0.9483	0.0517	0.10	29
YVL_21.1	26	0	3	0.9643	0.0357	0.07	28
YVL_22.1	25	1	2	0.9464	0.0536	0.07	28
YVL_23.1	0	0	0	#DIV/0!	#DIV/0!	#DIV/0!	0
YVL_54.1	15	0	0	1.0000	0.0000	0.00	15
YVL_25.1	26	0	3	0.9483	0.0517	0.10	28
YVL_26.1	25	1	4	0.8929	0.1071	0.14	28
YVL_27.1	25	0	5	0.9808	0.0192	0.04	26
YVL_28.1	24	0	5	0.9138	0.0862	0.17	29
YVL_29.1	28	0	3	0.9500	0.0500	0.03	30
YVL_30.1	29	0	3	0.9483	0.0517	0.10	29
YVL_31.1	23	0	7	0.8833	0.1167	0.23	30
YVL_32.1	28	0	2	0.9667	0.0333	0.07	30
YVL_33.1	23	0	4	0.8966	0.1034	0.21	29
YVL_34.1	0	0	0	#DIV/0!	#DIV/0!	#DIV/0!	0
YVL_35.1	26	0	4	0.9333	0.0667	0.13	30
YVL_36.1	25	0	4	0.9310	0.0690	0.14	29
YVL_37.1	26	0	3	0.9483	0.0517	0.10	29
YVL_38.1	26	0	4	0.9333	0.0667	0.13	30
YVL_39.1	20	0	1	0.9762	0.0238	0.05	21
YVL_40.1	24	0	4	0.8966	0.1034	0.14	29
YVL_41.1	0	0	0	#DIV/0!	#DIV/0!	#DIV/0!	0
YVL_42.1	24	0	6	0.9000	0.1000	0.20	30
YVL_43.1	26	0	4	0.9259	0.0741	0.15	27
YVL_44.1	26	0	4	0.9286	0.0714	0.14	28
YVL_45.1	26	0	4	0.9333	0.0667	0.13	30
YVL_46.1	20	0	6	0.8571	0.1429	0.29	28
YVL_47.1	23	0	8	0.8333	0.1667	0.27	30
YVL_48.1	26	0	4	0.9333	0.0667	0.13	30
YVL_49.1	26	0	4	0.9310	0.0690	0.07	29
YVL_50.1	23	0	7	0.8833	0.1167	0.23	30
Total	485	0	0				
	931.0000						

Table 5: Results of genetic admixture analyses. Values are the proportion of genomic background for each individual that matches reference genomic backgrounds

Samples	Alabama Bass	Coosa Bass	Largemouth Bass	Shoal Bass	Smallmouth Bass	Spotted Bass
BAR_10.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_11.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_1.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_12.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_13.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_14.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_15.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_16.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_17.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_18.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_19.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_20.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_2.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_22.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_24.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_25.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_26.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_27.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_28.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_29.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_30.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_31.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_3.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_32.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_33.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_34.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_35.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_36.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_37.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_38.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_39.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_40.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_41.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_42.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_43.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_44.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_45.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_46.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_47.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_48.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_49.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_50.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_51.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_5.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_52.1	0.000	0.000	0.889	0.000	0.110	0.000
BAR_53.1	0.000	0.000	0.390	0.000	0.000	0.610
BAR_54.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_55.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_56.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_57.1	0.000	0.000	0.275	0.000	0.000	0.725
BAR_58.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_59.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_60.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_61.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_6.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_62.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_63.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_64.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_65.1	0.000	0.000	0.310	0.000	0.000	0.690
BAR_66.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_67.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_68.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_69.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_70.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_71.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_7.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_72.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_73.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_74.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_75.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_76.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_77.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_78.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_79.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_80.1	0.000	0.000	0.000	0.000	0.000	1.000

BAR_81.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_8.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_82.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_83.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_84.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_85.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_86.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_87.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_88.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_89.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_90.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_91.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_9.1	0.000	0.000	1.000	0.000	0.000	0.000
BAR_92.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_93.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_94.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_95.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_96.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_97.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_98.1	0.000	0.000	0.000	0.000	0.000	1.000
BAR_99.1	0.000	0.000	0.000	0.000	0.000	1.000
BES_100.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_1.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_2.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_51.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_52.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_53.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_54.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_55.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_56.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_57.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_58.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_59.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_60.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_61.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_62.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_63.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_64.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_65.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_66.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_67.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_68.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_69.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_70.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_71.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_72.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_73.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_74.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_75.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_76.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_77.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_78.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_79.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_80.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_81.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_82.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_83.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_84.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_85.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_86.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_87.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_88.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_89.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_90.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_91.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_92.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_93.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_94.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_95.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_96.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_97.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_98.1	0.000	0.000	1.000	0.000	0.000	0.000
BES_99.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_10.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_11.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_1.1	0.000	0.000	1.000	0.000	0.000	0.000

BRL_12.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_13.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_14.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_15.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_16.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_17.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_18.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_19.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_20.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_21.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_2.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_22.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_23.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_24.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_25.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_26.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_27.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_28.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_29.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_30.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_31.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_3.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_32.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_33.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_34.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_35.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_36.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_37.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_38.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_39.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_40.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_41.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_4.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_42.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_43.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_44.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_45.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_46.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_47.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_48.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_49.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_50.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_5.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_6.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_7.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_8.1	0.000	0.000	1.000	0.000	0.000	0.000
BRL_9.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_100.1	0.000	0.000	0.000	0.000	0.000	1.000
CBL_10.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_11.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_1.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_12.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_13.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_14.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_15.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_16.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_17.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_18.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_19.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_20.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_21.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_2.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_22.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_23.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_24.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_25.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_26.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_27.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_28.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_29.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_30.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_31.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_3.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_32.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_33.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_34.1	0.000	0.000	1.000	0.000	0.000	0.000

CBL_35.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_36.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_37.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_38.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_39.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_40.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_41.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_4.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_42.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_43.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_44.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_45.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_46.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_47.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_48.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_49.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_50.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_51.1	0.000	0.000	0.000	0.000	1.000	0.000
CBL_5.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_52.1	0.000	0.000	0.000	0.000	1.000	0.000
CBL_53.1	0.000	0.000	0.000	0.000	1.000	0.000
CBL_54.1	0.000	0.000	0.000	0.000	1.000	0.000
CBL_55.1	0.000	0.000	0.000	0.000	1.000	0.000
CBL_56.1	0.000	0.000	0.000	0.000	1.000	0.000
CBL_57.1	0.000	0.000	0.000	0.000	1.000	0.000
CBL_58.1	0.000	0.000	0.000	0.000	1.000	0.000
CBL_59.1	0.000	0.000	0.000	0.000	1.000	0.000
CBL_60.1	0.000	0.000	0.000	0.000	1.000	0.000
CBL_61.1	0.000	0.000	0.000	0.000	1.000	0.000
CBL_6.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_62.1	0.000	0.000	0.000	0.000	1.000	0.000
CBL_63.1	0.000	0.000	0.000	0.000	1.000	0.000
CBL_64.1	0.000	0.000	0.000	0.000	1.000	0.000
CBL_65.1	0.000	0.000	0.000	0.000	1.000	0.000
CBL_66.1	0.000	0.000	0.000	0.000	1.000	0.000
CBL_67.1	0.000	0.000	0.000	0.000	1.000	0.000
CBL_68.1	0.000	0.000	0.000	0.000	1.000	0.000
CBL_69.1	0.000	0.000	0.000	0.000	1.000	0.000
CBL_70.1	0.000	0.000	0.000	0.000	1.000	0.000
CBL_71.1	0.000	0.000	0.000	0.000	1.000	0.000
CBL_7.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_72.1	0.000	0.000	0.000	0.000	1.000	0.000
CBL_73.1	0.000	0.000	0.000	0.000	1.000	0.000
CBL_74.1	0.000	0.000	0.000	0.000	1.000	0.000
CBL_75.1	0.000	0.000	0.000	0.000	1.000	0.000
CBL_76.1	0.000	0.000	0.000	0.000	0.000	1.000
CBL_77.1	0.000	0.000	0.000	0.000	0.000	1.000
CBL_78.1	0.000	0.000	0.000	0.000	0.000	1.000
CBL_79.1	0.000	0.000	0.000	0.000	0.000	1.000
CBL_80.1	0.000	0.000	0.000	0.000	0.000	1.000
CBL_81.1	0.000	0.000	0.000	0.000	0.000	1.000
CBL_8.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_82.1	0.000	0.000	0.000	0.000	0.000	1.000
CBL_83.1	0.000	0.000	0.000	0.000	0.000	1.000
CBL_84.1	0.000	0.000	0.000	0.000	0.000	1.000
CBL_85.1	0.000	0.000	0.000	0.000	0.000	1.000
CBL_86.1	0.000	0.000	0.000	0.000	0.000	1.000
CBL_87.1	0.000	0.000	0.000	0.000	0.000	1.000
CBL_88.1	0.000	0.000	0.000	0.000	0.000	1.000
CBL_89.1	0.000	0.000	0.000	0.000	0.000	1.000
CBL_90.1	0.000	0.000	0.000	0.000	0.000	1.000
CBL_91.1	0.000	0.000	0.000	0.000	0.000	1.000
CBL_9.1	0.000	0.000	1.000	0.000	0.000	0.000
CBL_92.1	0.000	0.000	0.000	0.000	0.000	1.000
CBL_93.1	0.000	0.000	0.000	0.000	0.000	1.000
CBL_94.1	0.000	0.000	0.000	0.000	0.000	1.000
CBL_95.1	0.000	0.000	0.000	0.000	0.000	1.000
CBL_96.1	0.000	0.000	0.000	0.000	0.000	1.000
CBL_97.1	0.000	0.000	0.000	0.000	0.000	1.000
CBL_98.1	0.000	0.000	0.000	0.000	0.000	1.000
CBL_99.1	0.000	0.000	0.000	0.000	0.000	1.000
CCL_10.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_11.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_1.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_12.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_13.1	0.000	0.000	1.000	0.000	0.000	0.000

CCL_14.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_15.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_16.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_17.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_18.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_19.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_20.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_21.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_2.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_22.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_23.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_24.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_25.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_26.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_27.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_28.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_29.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_30.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_31.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_3.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_32.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_33.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_34.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_35.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_36.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_37.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_38.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_39.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_40.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_41.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_4.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_42.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_43.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_44.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_45.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_46.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_47.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_48.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_49.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_50.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_5.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_6.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_7.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_8.1	0.000	0.000	1.000	0.000	0.000	0.000
CCL_9.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_10.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_11.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_1.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_12.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_13.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_14.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_15.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_16.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_17.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_18.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_19.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_20.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_21.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_2.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_22.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_23.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_24.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_25.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_26.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_27.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_28.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_29.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_30.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_31.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_3.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_32.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_33.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_34.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_35.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_36.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_37.1	0.000	0.000	1.000	0.000	0.000	0.000

CRC_38.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_39.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_40.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_41.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_4.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_42.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_43.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_44.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_45.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_46.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_47.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_48.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_49.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_50.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_5.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_6.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_7.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_8.1	0.000	0.000	1.000	0.000	0.000	0.000
CRC_9.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_100.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_51.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_52.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_53.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_54.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_55.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_56.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_57.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_58.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_59.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_60.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_61.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_62.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_63.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_64.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_65.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_66.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_67.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_68.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_69.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_70.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_71.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_72.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_73.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_74.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_75.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_76.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_77.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_78.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_79.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_80.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_81.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_82.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_83.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_84.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_85.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_86.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_87.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_88.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_89.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_90.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_91.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_92.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_93.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_94.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_95.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_96.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_97.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_98.1	0.000	0.000	1.000	0.000	0.000	0.000
CRL_99.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_10.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_11.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_1.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_12.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_13.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_14.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_15.1	0.000	0.000	1.000	0.000	0.000	0.000

FPL_16.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_17.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_18.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_19.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_20.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_21.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_2.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_22.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_23.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_24.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_25.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_26.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_27.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_28.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_29.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_30.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_31.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_3.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_32.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_33.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_34.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_35.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_36.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_37.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_38.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_39.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_40.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_41.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_4.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_42.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_43.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_44.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_45.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_46.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_47.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_48.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_49.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_50.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_5.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_6.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_7.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_8.1	0.000	0.000	1.000	0.000	0.000	0.000
FPL_9.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_10.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_11.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_1.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_12.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_13.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_14.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_15.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_16.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_17.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_18.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_19.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_20.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_21.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_2.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_22.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_23.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_24.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_25.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_26.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_27.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_28.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_29.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_30.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_31.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_3.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_32.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_33.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_34.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_35.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_36.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_37.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_38.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_39.1	0.000	0.000	1.000	0.000	0.000	0.000

FTL_40.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_41.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_4.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_42.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_43.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_44.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_45.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_46.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_47.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_48.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_49.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_50.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_5.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_6.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_7.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_8.1	0.000	0.000	1.000	0.000	0.000	0.000
FTL_9.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_10.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_11.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_1.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_12.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_13.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_14.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_15.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_16.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_17.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_20.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_2.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_22.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_23.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_24.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_25.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_26.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_27.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_28.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_29.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_30.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_31.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_3.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_32.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_33.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_34.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_35.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_36.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_37.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_38.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_39.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_40.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_41.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_4.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_42.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_43.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_44.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_45.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_46.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_47.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_48.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_49.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_50.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_5.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_6.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_7.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_8.1	0.000	0.000	1.000	0.000	0.000	0.000
GBL_9.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_10.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_11.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_1.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_12.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_13.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_14.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_15.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_16.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_17.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_18.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_19.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_20.1	0.000	0.000	1.000	0.000	0.000	0.000

GCL_21.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_2.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_22.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_23.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_24.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_25.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_26.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_27.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_28.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_29.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_30.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_31.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_3.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_32.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_33.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_34.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_35.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_36.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_37.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_38.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_39.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_40.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_41.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_4.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_42.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_43.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_44.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_45.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_46.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_47.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_48.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_49.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_50.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_5.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_6.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_7.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_8.1	0.000	0.000	1.000	0.000	0.000	0.000
GCL_9.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_10.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_11.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_1.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_12.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_13.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_14.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_15.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_16.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_17.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_18.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_19.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_20.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_21.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_2.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_22.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_23.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_24.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_25.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_26.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_27.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_28.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_29.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_30.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_31.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_3.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_32.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_33.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_34.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_35.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_36.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_37.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_38.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_39.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_40.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_41.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_4.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_42.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_43.1	0.000	0.000	1.000	0.000	0.000	0.000

GRL_44.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_45.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_46.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_48.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_49.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_50.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_5.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_6.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_7.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_8.1	0.000	0.000	1.000	0.000	0.000	0.000
GRL_9.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_11.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_1.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_12.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_13.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_14.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_15.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_16.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_18.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_19.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_20.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_21.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_2.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_22.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_23.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_24.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_25.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_26.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_27.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_28.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_29.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_30.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_31.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_3.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_32.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_33.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_34.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_35.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_36.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_37.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_38.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_39.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_40.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_41.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_4.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_42.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_43.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_44.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_45.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_46.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_47.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_48.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_49.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_50.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_5.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_6.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_7.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_8.1	0.000	0.000	1.000	0.000	0.000	0.000
GRY_9.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_100.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_10.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_11.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_1.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_12.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_13.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_14.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_15.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_16.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_17.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_18.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_19.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_20.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_21.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_2.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_22.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_23.1	0.000	0.000	1.000	0.000	0.000	0.000

HER_24.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_25.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_26.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_27.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_28.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_29.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_30.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_31.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_3.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_32.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_33.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_34.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_35.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_36.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_37.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_39.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_40.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_41.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_4.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_42.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_43.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_44.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_45.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_46.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_47.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_48.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_49.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_50.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_51.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_5.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_52.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_53.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_54.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_55.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_56.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_57.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_58.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_59.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_60.1	0.000	0.000	0.902	0.000	0.000	0.098
HER_61.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_6.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_62.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_63.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_64.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_65.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_66.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_67.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_68.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_69.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_70.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_71.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_7.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_72.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_73.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_74.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_75.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_76.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_77.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_78.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_79.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_80.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_81.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_8.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_82.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_83.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_84.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_85.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_86.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_87.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_88.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_89.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_90.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_91.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_9.1	0.000	0.000	1.000	0.000	0.000	0.000
HER_92.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_93.1	0.000	0.000	0.000	0.000	0.000	1.000

HER_94.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_95.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_96.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_97.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_98.1	0.000	0.000	0.000	0.000	0.000	1.000
HER_99.1	0.000	0.000	0.000	0.000	0.000	1.000
HSL_10.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_11.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_1.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_12.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_13.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_14.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_15.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_16.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_17.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_18.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_19.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_20.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_21.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_2.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_22.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_23.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_24.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_25.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_26.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_27.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_28.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_29.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_30.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_31.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_3.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_32.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_33.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_34.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_35.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_36.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_37.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_38.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_39.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_40.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_41.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_4.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_42.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_43.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_44.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_45.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_46.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_47.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_48.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_49.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_50.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_5.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_6.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_7.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_8.1	0.000	0.000	1.000	0.000	0.000	0.000
HSL_9.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_10.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_11.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_1.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_12.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_13.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_14.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_15.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_16.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_17.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_18.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_19.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_20.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_21.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_2.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_22.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_23.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_24.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_25.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_26.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_27.1	0.000	0.000	1.000	0.000	0.000	0.000

JCP_28.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_29.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_30.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_31.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_3.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_32.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_33.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_34.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_35.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_36.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_37.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_38.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_39.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_40.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_41.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_4.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_42.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_43.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_44.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_45.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_46.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_47.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_48.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_49.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_50.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_5.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_6.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_7.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_8.1	0.000	0.000	1.000	0.000	0.000	0.000
JCP_9.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_10.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_11.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_1.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_12.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_13.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_14.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_15.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_16.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_17.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_18.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_19.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_20.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_21.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_2.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_22.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_23.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_24.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_25.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_26.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_27.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_28.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_29.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_30.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_31.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_3.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_32.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_33.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_34.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_35.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_36.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_37.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_38.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_39.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_40.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_41.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_4.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_42.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_43.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_44.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_45.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_46.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_47.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_48.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_49.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_50.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_51.1	0.000	0.000	0.000	0.000	0.000	1.000

KEN_5.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_52.1	0.000	0.000	0.000	0.000	0.000	1.000
KEN_53.1	0.000	0.000	0.000	0.000	0.000	1.000
KEN_54.1	0.000	0.000	0.000	0.000	0.000	1.000
KEN_55.1	0.000	0.000	0.000	0.000	0.000	1.000
KEN_56.1	0.000	0.000	0.000	0.000	0.000	1.000
KEN_57.1	0.000	0.000	0.000	0.000	0.000	1.000
KEN_58.1	0.000	0.000	0.000	0.000	0.000	1.000
KEN_59.1	0.000	0.000	0.000	0.000	0.000	1.000
KEN_60.1	0.000	0.000	0.000	0.000	0.000	1.000
KEN_61.1	0.000	0.000	0.000	0.000	0.000	1.000
KEN_6.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_62.1	0.000	0.000	0.000	0.000	0.000	1.000
KEN_63.1	0.000	0.000	0.000	0.000	0.000	1.000
KEN_64.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_65.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_66.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_67.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_68.1	0.000	0.000	0.000	0.000	0.000	1.000
KEN_69.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_70.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_71.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_7.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_72.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_73.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_74.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_75.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_76.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_77.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_78.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_79.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_80.1	0.000	0.000	0.299	0.000	0.700	0.000
KEN_81.1	0.000	0.000	0.000	0.000	0.120	0.880
KEN_8.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_82.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_83.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_84.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_85.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_86.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_87.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_88.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_89.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_90.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_91.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_9.1	0.000	0.000	1.000	0.000	0.000	0.000
KEN_92.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_93.1	0.000	0.000	0.000	0.000	1.000	0.000
KEN_94.1	0.000	0.000	0.000	0.000	1.000	0.000
KIN_10.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_11.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_1.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_12.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_13.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_14.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_15.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_16.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_17.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_18.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_19.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_20.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_21.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_2.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_22.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_23.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_24.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_25.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_26.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_27.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_28.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_29.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_30.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_31.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_3.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_32.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_33.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_34.1	0.000	0.000	1.000	0.000	0.000	0.000

KIN_35.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_36.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_37.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_38.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_39.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_40.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_41.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_4.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_42.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_43.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_44.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_45.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_46.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_47.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_48.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_49.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_50.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_5.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_6.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_7.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_8.1	0.000	0.000	1.000	0.000	0.000	0.000
KIN_9.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_10.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_11.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_1.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_12.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_13.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_14.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_15.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_16.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_17.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_18.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_19.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_20.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_21.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_2.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_22.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_23.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_24.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_25.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_26.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_27.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_28.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_29.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_30.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_31.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_3.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_32.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_33.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_34.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_35.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_36.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_37.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_38.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_39.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_40.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_41.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_4.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_42.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_43.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_44.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_45.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_46.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_47.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_48.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_49.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_50.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_5.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_6.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_7.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_8.1	0.000	0.000	1.000	0.000	0.000	0.000
LMA_9.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_100.1	0.000	0.000	0.000	0.000	0.000	1.000
LRL_10.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_11.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_1.1	0.000	0.000	1.000	0.000	0.000	0.000

LRL_12.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_13.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_14.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_15.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_16.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_17.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_18.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_19.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_20.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_21.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_2.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_22.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_23.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_24.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_25.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_26.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_27.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_28.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_29.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_30.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_31.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_3.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_32.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_33.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_34.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_35.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_36.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_37.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_38.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_39.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_40.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_41.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_4.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_42.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_43.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_44.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_45.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_46.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_47.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_48.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_49.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_50.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_51.1	0.000	0.000	0.000	0.000	1.000	0.000
LRL_5.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_52.1	0.000	0.000	0.000	0.000	1.000	0.000
LRL_53.1	0.000	0.000	0.000	0.000	1.000	0.000
LRL_54.1	0.000	0.000	0.000	0.000	1.000	0.000
LRL_55.1	0.000	0.000	0.000	0.000	1.000	0.000
LRL_56.1	0.000	0.000	0.000	0.000	1.000	0.000
LRL_57.1	0.000	0.000	0.000	0.000	1.000	0.000
LRL_58.1	0.000	0.000	0.000	0.000	1.000	0.000
LRL_59.1	0.000	0.000	0.000	0.000	1.000	0.000
LRL_60.1	0.000	0.000	0.916	0.000	0.084	0.000
LRL_61.1	0.000	0.000	0.000	0.000	1.000	0.000
LRL_6.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_62.1	0.000	0.000	0.000	0.000	1.000	0.000
LRL_63.1	0.000	0.000	0.000	0.000	1.000	0.000
LRL_64.1	0.000	0.000	0.000	0.000	1.000	0.000
LRL_65.1	0.000	0.000	0.000	0.000	1.000	0.000
LRL_66.1	0.000	0.000	0.000	0.000	1.000	0.000
LRL_67.1	0.000	0.000	0.000	0.000	1.000	0.000
LRL_68.1	0.000	0.000	0.000	0.000	1.000	0.000
LRL_69.1	0.000	0.000	0.000	0.000	1.000	0.000
LRL_70.1	0.000	0.000	0.000	0.000	1.000	0.000
LRL_71.1	0.000	0.000	0.000	0.000	1.000	0.000
LRL_7.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_72.1	0.000	0.000	0.000	0.000	1.000	0.000
LRL_73.1	0.000	0.000	0.000	0.000	1.000	0.000
LRL_74.1	0.000	0.000	0.000	0.000	1.000	0.000
LRL_75.1	0.000	0.000	0.000	0.000	1.000	0.000
LRL_76.1	0.000	0.000	0.000	0.000	0.000	1.000
LRL_77.1	0.000	0.000	0.000	0.000	0.000	1.000
LRL_78.1	0.000	0.000	0.000	0.000	0.000	1.000
LRL_79.1	0.000	0.000	0.000	0.000	0.000	1.000
LRL_80.1	0.000	0.000	0.000	0.000	0.000	1.000
LRL_81.1	0.000	0.000	0.000	0.000	0.000	1.000

LRL_8.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_82.1	0.000	0.000	0.000	0.000	0.000	1.000
LRL_83.1	0.000	0.000	0.000	0.000	0.000	1.000
LRL_84.1	0.000	0.000	0.000	0.000	0.000	1.000
LRL_85.1	0.000	0.000	0.000	0.000	0.000	1.000
LRL_86.1	0.000	0.000	0.000	0.000	0.000	1.000
LRL_87.1	0.000	0.000	0.000	0.000	0.000	1.000
LRL_88.1	0.000	0.000	0.000	0.000	0.000	1.000
LRL_89.1	0.000	0.000	0.000	0.000	0.000	1.000
LRL_90.1	0.000	0.000	0.919	0.000	0.000	0.080
LRL_91.1	0.000	0.000	0.000	0.000	0.000	1.000
LRL_9.1	0.000	0.000	1.000	0.000	0.000	0.000
LRL_92.1	0.000	0.000	0.000	0.000	0.000	1.000
LRL_93.1	0.000	0.000	0.000	0.000	0.000	1.000
LRL_94.1	0.000	0.000	0.000	0.000	0.000	1.000
LRL_95.1	0.000	0.000	0.000	0.000	0.000	1.000
LRL_96.1	0.000	0.000	0.000	0.000	0.000	1.000
LRL_97.1	0.000	0.000	0.000	0.000	0.000	1.000
LRL_98.1	0.000	0.000	0.000	0.000	0.000	1.000
LRL_99.1	0.000	0.000	0.000	0.000	0.000	1.000
MCH_100.	0.000	0.000	1.000	0.000	0.000	0.000
MCH_1.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_2.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_51.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_52.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_53.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_54.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_55.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_56.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_57.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_58.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_59.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_60.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_61.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_62.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_63.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_64.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_65.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_66.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_67.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_68.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_69.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_70.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_71.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_72.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_73.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_74.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_75.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_76.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_77.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_78.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_79.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_80.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_81.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_82.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_83.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_84.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_85.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_86.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_87.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_88.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_89.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_90.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_91.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_92.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_93.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_94.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_95.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_96.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_97.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_98.1	0.000	0.000	1.000	0.000	0.000	0.000
MCH_99.1	0.000	0.000	1.000	0.000	0.000	0.000
MFL_10.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_11.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_1.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_12.1	0.000	0.000	0.000	0.000	0.000	1.000

MFL_13.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_14.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_15.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_16.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_17.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_18.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_19.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_20.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_21.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_2.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_22.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_23.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_24.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_25.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_26.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_27.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_28.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_29.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_30.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_31.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_3.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_32.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_33.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_34.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_35.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_36.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_37.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_38.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_39.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_40.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_41.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_4.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_42.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_43.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_44.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_45.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_46.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_47.1	0.000	0.000	0.000	0.000	1.000	0.000
MFL_48.1	0.000	1.000	0.000	0.000	0.000	0.000
MFL_49.1	0.000	1.000	0.000	0.000	0.000	0.000
MFL_50.1	0.000	0.000	0.000	0.000	1.000	0.000
MFL_5.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_6.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_7.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_8.1	0.000	0.000	0.000	0.000	0.000	1.000
MFL_9.1	0.000	0.000	0.000	0.000	0.000	1.000
MIL_10.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_11.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_1.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_12.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_13.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_14.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_15.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_16.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_17.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_18.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_19.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_20.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_21.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_2.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_22.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_23.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_24.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_25.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_26.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_27.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_28.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_29.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_30.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_31.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_3.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_32.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_33.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_34.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_35.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_36.1	0.000	0.000	1.000	0.000	0.000	0.000

MIL_37.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_38.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_39.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_40.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_41.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_4.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_42.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_43.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_44.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_45.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_46.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_47.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_48.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_49.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_50.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_5.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_6.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_7.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_8.1	0.000	0.000	1.000	0.000	0.000	0.000
MIL_9.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_100.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_104.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_106.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_112.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_114.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_120.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_122.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_124.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_125.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_126.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_130.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_132.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_138.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_144.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_145.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_16.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_17.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_21.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_2.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_23.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_24.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_26.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_28.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_35.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_36.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_38.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_41.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_42.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_48.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_50.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_55.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_57.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_58.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_60.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_6.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_64.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_69.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_73.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_74.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_75.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_80.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_8.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_82.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_87.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_90.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_94.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_97.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_98.1	0.000	0.000	1.000	0.000	0.000	0.000
NRL_99.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_100.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_101.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_102.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_103.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_104.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_105.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_106.1	0.000	0.000	1.000	0.000	0.000	0.000

PVL_107.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_108.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_109.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_111.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_112.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_113.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_114.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_115.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_116.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_117.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_118.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_119.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_120.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_121.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_122.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_123.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_124.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_125.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_126.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_127.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_128.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_129.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_130.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_132.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_133.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_134.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_135.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_136.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_137.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_138.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_139.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_140.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_141.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_142.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_143.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_144.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_145.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_146.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_147.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_148.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_149.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_150.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_26.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_31.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_41.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_51.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_52.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_53.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_54.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_55.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_56.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_57.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_58.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_59.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_60.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_61.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_62.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_63.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_64.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_65.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_66.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_67.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_68.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_69.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_70.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_71.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_72.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_73.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_74.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_75.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_76.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_77.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_80.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_81.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_82.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_83.1	0.000	0.000	1.000	0.000	0.000	0.000

PVL_84.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_86.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_87.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_88.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_89.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_90.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_91.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_92.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_93.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_94.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_95.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_96.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_97.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_98.1	0.000	0.000	1.000	0.000	0.000	0.000
PVL_99.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_101.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_10.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_105.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_106.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_108.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_112.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_118.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_1.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_120.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_121.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_124.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_125.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_128.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_130.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_13.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_133.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_137.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_138.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_139.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_142.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_16.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_19.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_25.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_32.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_37.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_39.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_40.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_42.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_43.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_44.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_45.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_46.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_48.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_52.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_54.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_59.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_60.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_61.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_65.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_66.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_70.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_75.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_80.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_82.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_88.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_9.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_93.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_95.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_97.1	0.000	0.000	1.000	0.000	0.000	0.000
RRL_99.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_11.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_1.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_12.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_14.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_15.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_16.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_17.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_18.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_19.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_21.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_23.1	0.000	0.000	1.000	0.000	0.000	0.000

TVL_27.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_29.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_31.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_37.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_38.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_39.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_40.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_41.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_42.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_43.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_45.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_47.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_48.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_5.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_53.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_54.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_55.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_57.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_58.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_61.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_6.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_62.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_63.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_71.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_7.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_73.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_74.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_77.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_78.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_79.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_80.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_82.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_85.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_87.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_90.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_92.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_95.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_97.1	0.000	0.000	1.000	0.000	0.000	0.000
TVL_99.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_1.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_2.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_10.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_11.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_12.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_13.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_14.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_15.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_16.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_17.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_18.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_19.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_20.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_21.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_22.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_54.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_25.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_26.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_27.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_28.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_29.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_30.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_31.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_3.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_32.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_33.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_35.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_36.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_37.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_38.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_39.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_40.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_4.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_42.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_43.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_44.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_45.1	0.000	0.000	1.000	0.000	0.000	0.000

YVL_46.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_47.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_48.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_49.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_50.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_53.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_6.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_7.1	0.000	0.000	1.000	0.000	0.000	0.000
YVL_9.1	0.000	0.000	1.000	0.000	0.000	0.000

Appendix 1

<table>
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<td>Conservation Genetics Program
Southeast Conservation Genetics Program</td>
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Standard Operating Procedure (SOP)
GTSeq

Materials:

Sequel Prep plates
Unlabeled Primers (Fwd and Rvs)
PCR Plus Master Mix (Qiagen)
Unlabeled barcode primers (i5-well position and i7-plate designation)
AMpure XP beads
Magnetic rack
Lo-Bind 2.0mL tubes
Lo-Bind 0.5mL tubes
Lo-Bind 1.7mL tubes
96-well plates
Filter Pipette tips all sizes
Reservoirs for chemicals
Project layout spreadsheet

Methods:

1. Open Project layout excel sheet. Fill in information on green tabs (GT and qPCR, print both pages).

PreAMP PCR

2. Make PreAmp PCR master mix
   a. Amount per sample
      i. Qiagen 2X PCR Plus MM   3.5μL
      ii. Primer mix (0.252μM)   0.5μL
      iii. ddH20   1.0μL
3. Label PCR plates: Plate Name, PreAmp, Date.
4. Add 5μL of PCR master mix to all wells of labeled plates.
5. Add 2μL of ExoSAP treated DNA.
6. Seal, vortex, and briefly centrifuge plate.

7. Place on thermal cycler and run program: GTSEQ30
    a. 95.0°-15:00
    b. 95.0°-00:30
    c. 57.0°-00:30 (5% ramp) ⎫— 30 cycles
    d. 72.0°-2:00
    e. 72.0°-00:30
    f. 4° hold
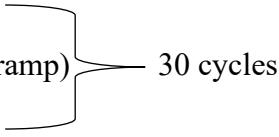
8. Take 3 uL from first or last two samples on plate for Qubit and gel

NOTE: Discard PreAmp-PCR plate after Barcoding step or if needed,

Dilute and Barcode

8. Dilute PreAmp-PCR (1:10) by adding 63µL nuclease-free H_2O directly to PreAmp-PCR.
9. Seal, vortex, and briefly centrifuge plate.
10. Make i7 working stock (10uM) if none is available (you will need a different i7 for each plate that is being sequenced):
    a. Nuclease-free H_2O 90µL
    b. i7 (100µM).   10µL
11. Label a new lo-bind centrifuge tube with i7 index number (one for each plate).
12. Make i7 master mix
    a. Amount per sample
        i. Qiagen 2X PCR Plus MM   5.0µL
        ii. 10uM Primers i7   1.0µL
13. Vortex and briefly spin down i7 master mix.
14. Label PCR plates: Plate Name, i7 index #, Date.
15. Add 6µL of i7 cocktail to all wells of labeled plates.
16. Add 3µL of diluted PreAmp-PCR product to all wells of barcode plate.
17. Thaw, mix gently, and briefly spin i5 barcode plate.
18. Add 1µL i5 barcode to each well. (Use 1 box of tips)
19. Seal, vortex, and briefly centrifuge plate.
20. Place on thermal cycler and run program: gtseq2
    a. 95.0°-15:00
    b. 95.0°-00:10
    c. 65.0°-00:30 ⎫— 10 cycles
    d. 72.0°-00:30
    e. 72.0°-5:00
    f. 4.0°-hold
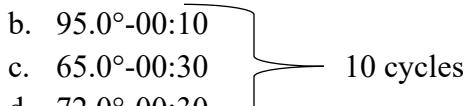
NOTE: If complete evaporation after cycling is observed, add 10µL nuclease-free H_2O to rehydrate.

Normalization

21. Label new SequelPrep Normalization plates: Plate Name, Seq, i7 index, Date
22. If you have a partial plate, aliquot liquids to wells that will have DNA only, for all steps below.
23. Binding Step
    a. Add 10μL of SequelPrep Normalization Binding Buffer to SequelPrep Normalization plate.
    b. Transfer ALL content of Barcoded DNA to SequelPrep Normalization plate. (Use new tips for each well.)
    c. Seal, vortex, and briefly centrifuge.
    d. Incubate plate at room temperature for minimum of 1 hour. Do not disturb plate.
24. Wash Step
    e. Aspirate all liquid from wells and <u>discard</u>. (Try not to scratch the bottom of wells. You do not have to change tips, you can use same tips for each column.)
    f. Dispense 50μL SequalPrep Normalization Wash Buffer.
    g. Using multichannel pipette (set to 55μL) and 1 set of tips, flush well by pipetting up and down twice and then completely aspirate the buffer from the wells and discard liquid.
    h. Invert and tap the plate on paper towels to remove any residual wash buffer from the wells. It is okay if a small amount of wash buffer (1-3μL) is present still.
25. Elution Step
    i. Add 20μL SequalPrep Normalization Elution Buffer to each well.
    j. Seal, vortex, and briefly centrifuge.
    k. Incubate at room temperature for 5 minutes. At this stage, plate can be stored overnight.

    NOTE: SequalPrep provides just enough wash buffer – do not take more than you need

Pooling and Size Select

26. Remove AMPure XP beads from fridge and allow to come to room temperature for 30 minutes.
27. Take all liquid from each well of a single normalized plate and combine into a strip tube.
28. Transfer all normalized DNA from strip tubes to two 2.0 mL lo-bind tubes and label: "NP" + the name of the plate. Vortex and spin down tubes. Store tubes at 4 °C or -20 °C for long term.
29. Remove long sequences with AMPure XP beads
    a. Vortex AMPure XP beads very well.
    b. Add 0.5X beads into each tube and mix well by pipetting. Avoid bubbles
    c. Incubate at room temperature for 5 minutes.

    d. Transfer tubes to magnetic stand and let sit for 4 minutes.

    e. Keeping tubes on magnetic stand, transfer supernatant to 2nd set of 2.0mL lo-bind tubes.

    f. Discard tubes with beads

30. Leave short sequences

    g. Again vortex AMPure XP beads.

    h. Add up to 1.0X (another 0.5X) AMPure XP beads, and mix well by pipetting.

    i. Incubate at room temperature for 5 minutes.

    j. Place on magnetic stand for 4 minutes.

    k. Keeping tubes on magnetic stand, remove and discard supernatant.

31. Wash step (keep tube on magnetic stand for entire wash)

    l. Mix FRESH 80% Ethanol:

        i. Amount per 8 plates

            1. 2450μL ethanol (200 proof)

            2. 1050μL nuclease-free H_2O.

    m. Add 500μL 80% Ethanol tubes containing beads, incubate, for 30 seconds.

    n. Remove and discard supernatant.

    o. Repeat wash (step o and p).

    p. Remove tubes from magnetic stand and wait 5 minutes to dry on bench top.

32. Ready for long term storage

    q. Label 0.5mL lo-bind tubes e.g. with plate name.

    r. Add 28μL EB to tubes containing beads and mix well by pipetting.

    s. Place on the magnetic stand for 2 minutes.

    t. Remove/transfer supernatant to newly labeled tube.