Final report

Development and delivery of improved genomic prediction tools for sheep

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Abstract

The objectives of this project were to develop and deliver knowledge and tools to improve genomic prediction for significant economic traits in sheep, in particular for eating quality and reproduction traits. Genome wide association studies (GWAS) on imputed whole genome sequence genotypes were used to prioritize and validate sequence variants associated with genetic variation of economic traits using larger phenotypic and genotypic data sets for a larger number of economic traits compared to previous analysis in 2018. Informative SNPs were selected based on summary statistics of GWAS, pruned for linkage disequilibrium and minor allele frequency. We selected 3700 top SNPs selected across 17 traits, which showed between 0.04 and 0.16 improvement in accuracy of genomic prediction. We implemented the information from top SNPs in the Sheep Genetics single step evaluation in OVIS, and fine-tuned the weight (lambda) put on the genomic relationships. Accuracy improvements are less obvious in single step OVIS runs because of complexity of analysis and the difficulty to disentangle accuracy improvement from top SNPs and dependency on the information known prior to genotyping, including information from correlated traits. Results of this study will be directly useful in upgrading SNP chip content and also enhancing genomic prediction for industry which will bring accumulated genetic gain and financial benefit to the sheep industry.

Executive summary

Background

Genomic enhanced prediction of ASBVs was introduced in Australia in 2011, and has already had significant impact on achieving genetic gains, especially for eating quality. Further work in the Sheep CRC found that finding new predictive SNPs from analysing whole genome sequence information could increase the accuracy of genomic prediction and a set of predictive SNPs was added to the sheep genotyping arrays used by some genotyping service providers in Australia. The phenotypic and genotypic information that is entered in the Sheep Genetics database is continually growing and larger datasets should provide more accurate selection of predictive SNPs. Moreover, data on reproductive traits had been too limited for use in association studies but a new evaluation system to analyse reproductive component traits, with significant data on genotyped animals that have the new phenotypes is now available.

Application of genomic information such as predictive SNPs derived from next generation sequencing data would be useful in further enhancing the accuracy of genetic evaluation of economic traits in the sheep industry. This is useful, especially for economic traits which are difficult to collect phenotypes for breeding animals, such as carcase and eating quality traits, or for reproduction traits, which are only measured on females and after they have been selected for mating.

The main target audience of the research project is the Australian sheep seedstock industry, with representation from all commercial sheep breeds. The expected outcomes are improved genomic prediction accuracy of genetic merit and improved rates of genetic gain, especially for eating quality and reproduction traits, and this will benefit the entire lamb production industry and ultimately the consumers of lamb.

Objectives

The primary objective of the project was to update the set of informative SNPs, using more data and for a larger number of production and reproduction traits and using whole genome sequence data, in order to deliver improved genomic prediction accuracy to the Australian sheep industry. The updated set of informative genetic markers was used to evaluate whether the genomic prediction accuracy would be improved compared to the previous test performed in 2018. The project was successful and showed a consistent higher prediction accuracy based on an updated list of informative SNPs.

Methodology

In this project, advanced statistical genetic methods were used for the analysis of phenotypic data collected by breeders (mainly for reproduction traits) and collected from the resource flocks (mainly for eating quality traits). Phenotypic data was combined with imputed whole genome sequence genotypes of ~200,000 Australian sheep, to undertake association analysis to find and select predictive SNPs, and to validate increased genomic prediction accuracy from using these SNPs. Different models and methods on using selected SNPs in the Sheep Genetics single step genetic evaluation (OVIS) were explored and tested.

Phenotypic data was based on fixed and mixed linear model analysis, which was performed in *ASReml* program software. Genotype quality control, variant calling and genotype imputation to whole genome sequence data was performed in *R, Plink, GATK and Beagle 5*, respectively. To find chromosomal regions and informative SNPs, a genome wide association study (GWAS) was performed based on single trait analysis in *Gemma* program software and a multiple trait meta-analysis was developed using R and Python scripts. Selection of informative SNPs was based on a strategy using SNP p-values, conditional and joint analysis of significant SNPs, pruning of SNPs in high LD with each other and considering genetic SNPs minor allele frequencies.

Results/key findings

With the updated and larger data sets GWAS results showed a larger number of chromosomal regions with quantitative trait loci (QTL) for slaughter and eating quality traits, with numerous new significant chromosomal regions as well as confirmed significant genomic regions detected in previous analyses in 2018. Some chromosomal regions affected several carcase and eating quality traits. A meta-analysis on combined summary statistics of single trait GWAS results confirmed results of single trait GWAS but did not show new significant regions.

GWAS results in reproduction traits showed chromosomal regions affecting litter size. GDF9 was found to have a major effect on litter size due to a missense mutation in some maternal breeds. GWAS on tail-length showed one highly significant chromosomal region with a large effect.

We selected a set of 3,700 significant SNPs across seventeen production and reproduction traits. When including this set of informative markers to the full SNP panel, increased accuracy was observed in single trait genomic prediction (GBLUP) of between 0.04 and 0.16 (absolute value) in EQ traits compared to standard 50k genotypes. Higher prediction accuracy can be achieved by using statistical methods which allow putting more weight on informative SNPs in the analysis, e.g. by fitting them as an additional random effect with a separate genomic relationship matrix. The accuracy improvements were less pronounced in single-step OVIS runs because of complexity of analysis and the difficulty to disentangle accuracy improvement from top SNPs and dependency on the information known prior to genotyping, including information from correlated traits.

Benefits to industry

Adding a new set of predictive SNPs to genotyping arrays for Australian sheep is expected to enhance the genomic prediction accuracy of live traits, eating quality and reproduction traits and increase the accuracy of ASBV produced by the Sheep Genetics single step evaluation in OVIS. The increase would be most notably for younger animals without much information on these traits, allowing earlier selection for hard to measure traits such as eating quality and reproduction, and therefore improving rates of genetic gain for these traits. Tail length is related to fly-strike incidence in Australian sheep and selection on tail length would be very useful in controlling fly-strike incidence.

Future research and recommendations

Ongoing work is needed to find predictive genetic variants for quantitative traits and genetic defects, with more data becoming available at an increased rate. With increased uptake of genotyping, data from breeder flocks, commercial animals and abattoirs might become available and work needs to be done to combine such data, which maybe of variable quality. Further predictive SNPs and possibly causal variants affecting variation in economic traits need to be added to genotyping arrays such that genomic prediction accuracy will increase and start approaching the numbers as achieved in the dairy industry (~0.6 to 0.9). Imputed sequence data is used and its imputation accuracy would benefit from further genome sequencing of key animals. Ongoing work is also needed to implement these predictive SNPs in genetic evaluation, with expected large increases in the number of genotyped animals and increased variability in genotype array data and phenotypic data quality. It would be useful to develop evaluation methods where imputation of all animals to the same common set of SNP genotypes is not a requirement. For genetic defects a more systematic reporting of affected phenotypes is required.

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1. Background

In last two decades and along with developments in advanced genotyping technology such as next generation sequencing, genomic tools have revolutionized practical genetics and breeding. Worldwide, in animal and plant genetics there are massive investments in genomic and genetic technologies, including next generation sequencing, long read sequencing, functional genomics, gene editing technologies and genomic prediction methodologies, and globally breeding programs are rapidly changing through genomic selection. Australia's sheep and cattle industries have some specific challenges due to the low cost nature of most enterprises and quality and quantity of data in industry section but at the same time they have enormous opportunities to increase productivity and product quality.

This project was designed to follow up on the successful work of the Sheep CRC, where sequence information was analysed to deliver informative markers associated with quantitative trait loci. Since that work, larger phenotypic and genotypic data sets have become available and include more traits. New predictive SNPs could therefore be found, to be added to SNP arrays used by industry, and the genetic evaluation model should optimally exploit the information provided by significant markers by giving them more weight in the analysis.

In 2018, the Sheep CRC provided a list with 2000 predictive SNPs to Neogen to add to the existing 15k chip that was commercially used. Later in the year it became clear that Neogen was planning to design a new 50k ovine SNP chip and the number of SNPs to be added to an industry SNP array could be increased. Between November 2018 and February 2019, the CRC delivered a list with about 10,000 SNPs to Neogen, and these have been added to the newly design SNP array. The same list was provided to MLA who made it available to other genotyping service providers. The accuracy of imputing sequence information was reported by (Bolormaa et al. 2019) and the additional accuracy obtained from using predictive SNPs obtained by association analysis with imputed sequence data was published by Moghaddar et al. (2019). However, the added value of predictive SNPs information was not evaluated within the OVIS framework, OVIS being the single step genetic evaluation software used by Sheep Genetics, and neither had there been work done on how to best use this information in the evaluation model.

We consider it an ongoing activity to find SNPs that are highly predictive, as larger datasets can now be used to find better predictors, genotyping service providers will be interested in improving the marker content of their arrays. This final report will describe the activity that has been undertaken to follow up from this CRC work. The main objective was to make a new list with predictive SNPs, including predictive SNPs for reproduction traits, which had not been produced before. Another objective is to develop and evaluate methods on how to use information on predictive SNPs ("top-SNPs") in single step genetic evaluation, through implementation in the OVIS software used by Sheep Genetics.

Results of this project will be directly useful in enhancing the genomic prediction pipeline for slaughter and eating quality traits and reproduction traits. Limited data was available on genetic defects, but some strong genomic predictors of tail length maybe useful in decreasing fly strike incidence.

2. Objectives

The objectives of the project were:

- Develop knowledge, expertise and information for better defined and more targeted methods to detect predictive SNPs.
- Find more predictive SNP panels that are validated to enhance the accuracy of genomic prediction for most traits.
- Add optimised sets of selective SNPs to genotyping tools.
- Evaluate improved prediction validated for smaller breeds and for animals less strongly related to the reference flock.
- An adapted genetic evaluation pipeline to accommodate more genotyped animals and maximize the extra value of selected SNP panels.
- Increased accuracies of ASBVs for animals that are genotyped.
- Increased accuracy of genomic prediction in other commercial applications such as Flock Profiling, and similar applications where prediction of genetic merit can enhance outcomes of decision support tools (e.g. in ASKBILL, or in supply chains).
- Enhanced genomic prediction for genetic defects and inherited diseases.
- Enhanced opportunities for the Australian sheep industry to benefit from the developments in genotyping technology, to ensure that the industry has access to the best genotyping tools at lowest cost, and better-informed strategies to use them.

3. Methodology

3.1 Selection of informative SNPs

3.1.1 Phenotypes

Phenotypic data on slaughter and eating quality traits were extracted from the Sheep Genetics evaluation databases for Merinos, maternal, and terminal sire breeds. The slaughter and eating quality phenotypes originated from research data sets (Sheep CRC Information Nucleus Flock (INF) and the MLA Resource Flock (RF)), while most live weight and scan trait data came from industry flocks, with both sources including a mixture of purebred and crossbred population (admixed population). New data on reproduction traits came from breeder flocks, partly through co-investment with the MLA RF project. Table 1 to 5 show the traits and number of phenotypic and genotypic records for carcase/eating quality traits and reproduction traits. Figures

and **Error! Reference source not found.** show the breed composition of the animals with post weaning weight used in this study as an example of the breed content underlying these data sets, with the breed and population structure of the data illustrated as a plot of the first two principal components of the genomic relationship matrix.

The traits within the group of weight and eating quality traits were C-site carcase fat (CCFAT), carcase eye muscle depth (CEMD), carcase weight (CWT) dress percentage (DRESS), intra muscular fat (IMF), lean meat yield (LMY) post weaning scan fat (PCF), post weaning eye muscle depth (PEMD), post weaning weight (PWT), and shear force at 5 days old aging (SF5), pre-joining adult weight (AWT) and ewe's body condition score (BCS). Compared to the previous report we analysed four extra available slaughter and EQ traits which were CWT, DRESS, LMY and PCF. The traits evaluated within the group of reproduction traits were yearling and adult conception rate (YCON and CON); yearling and adult litter size (YLS and LS); yearling and adult ewe rearing ability (YERA and ERA) and maternal behaviour score (MBS).

Table 1: Final combined number of animals with phenotypes and animals with phenotypes and genotypes and it's percentage for slaughter and EQ traits

Trait	No of phenotypes 2021	No of phenotypes and genotypes	% of animals with phenotypes and genotypes
CCFAT	23,377	20,281	0.87
CEMD	22,489	20,393	0.91
CWT	22,929	20,831	0.91
DRESS	15,982	15,977	1.00
IMF	22,407	20,320	0.91
LMY	2,707	2,707	1.00
PCF	71,809	51,319	0.71
PEMD	71,886	51,597	0.72
PWT	135,022	92,586	0.69
SF5	22,062	20,474	0.93

Table 2: Number of reproduction records from research and industry in data from maternal breeds

Trait	No Animals	No Phenotypes	Research Data	Industry Data	No of Genotypes
YCON	42,250	42,250	1,445	40,805	5,217
CON	18,5673	138,035	1,571	184,101	6,907
YLS	64,526	64,526	555	63,971	3,617
LS	305,916	703,503	1,523	701,980	7,613
YERA	47,430	47,430	424	47,006	2,361
ERA	258,845	561,571	727	560,844	5,475
MBS	15,825	24,410	560	23,850	6,289

Table 3: Number of phenotypes and genotypes for on farm productivity traits in ewes from Maternal breeds

Trait	No of Phenotypes	No of Genotypes
AWT	64,440	6,289
BCS	24,931	4,731

Table 4. Number of reproduction data from combined research and industry data in Merinos

Trait	No of Animals	Total No of Phenotypes	Total No Of Genotypes	% Genotyped
YCON	3,737	3,738	305	8.16
CON	138,035	223,195	8,077	3.62
YLS	5,348	5,348	161	3.01
LS	295,748	547,807	8,850	1.62
ERA	174,588	288,321	7,292	2.53
MBS	5,150	6,382	1,049	20.37

Table 5. Number of phenotypes and genotypes for on farm productivity traits in ewes in the Merino data set

Trait	No of Animals	Total No of Phenotypes	Total No Of Genotypes	% Genotyped
AWT	28,992	43,238	6967	0.24
BCS	12,721	21,123	6551	0.51

Figure 1: breed composition of the animals with post weaning weight records

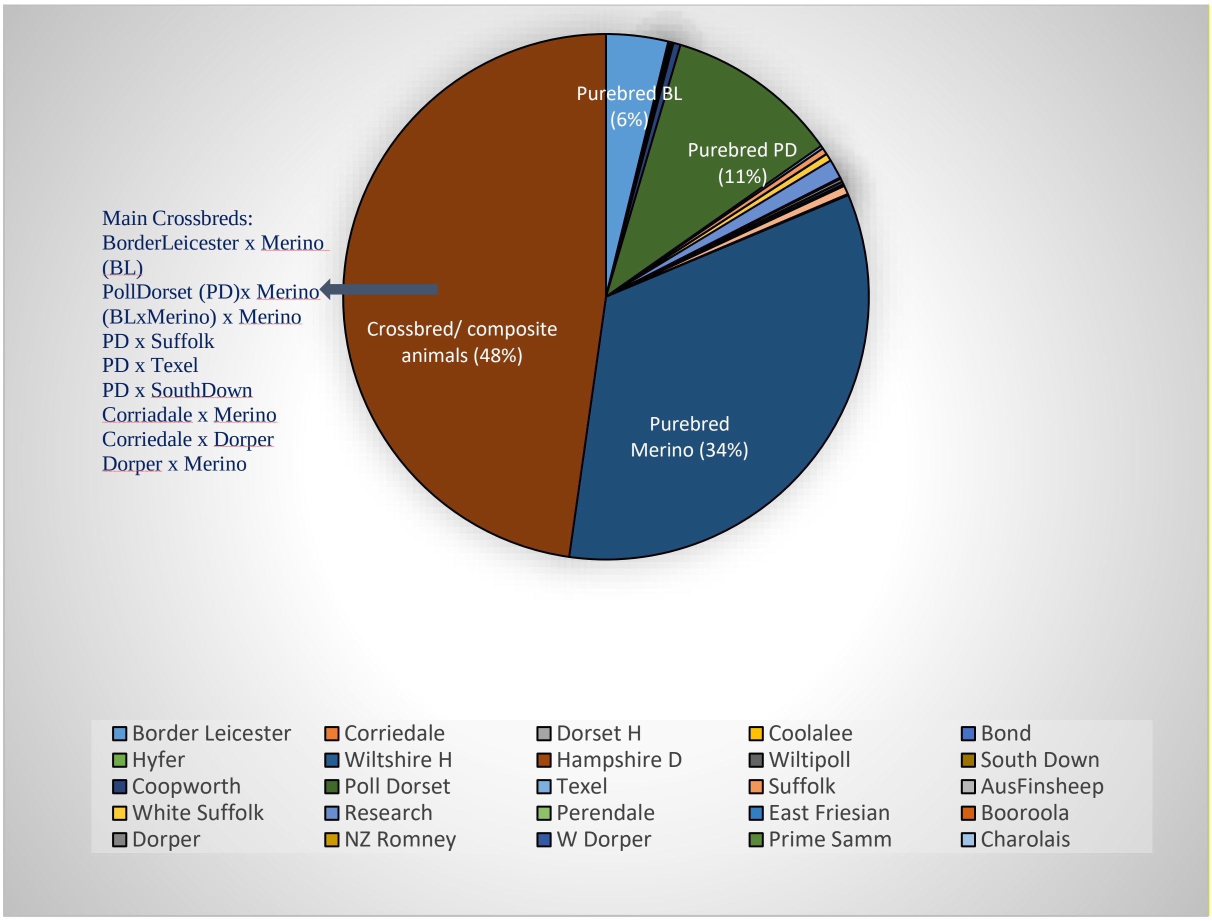
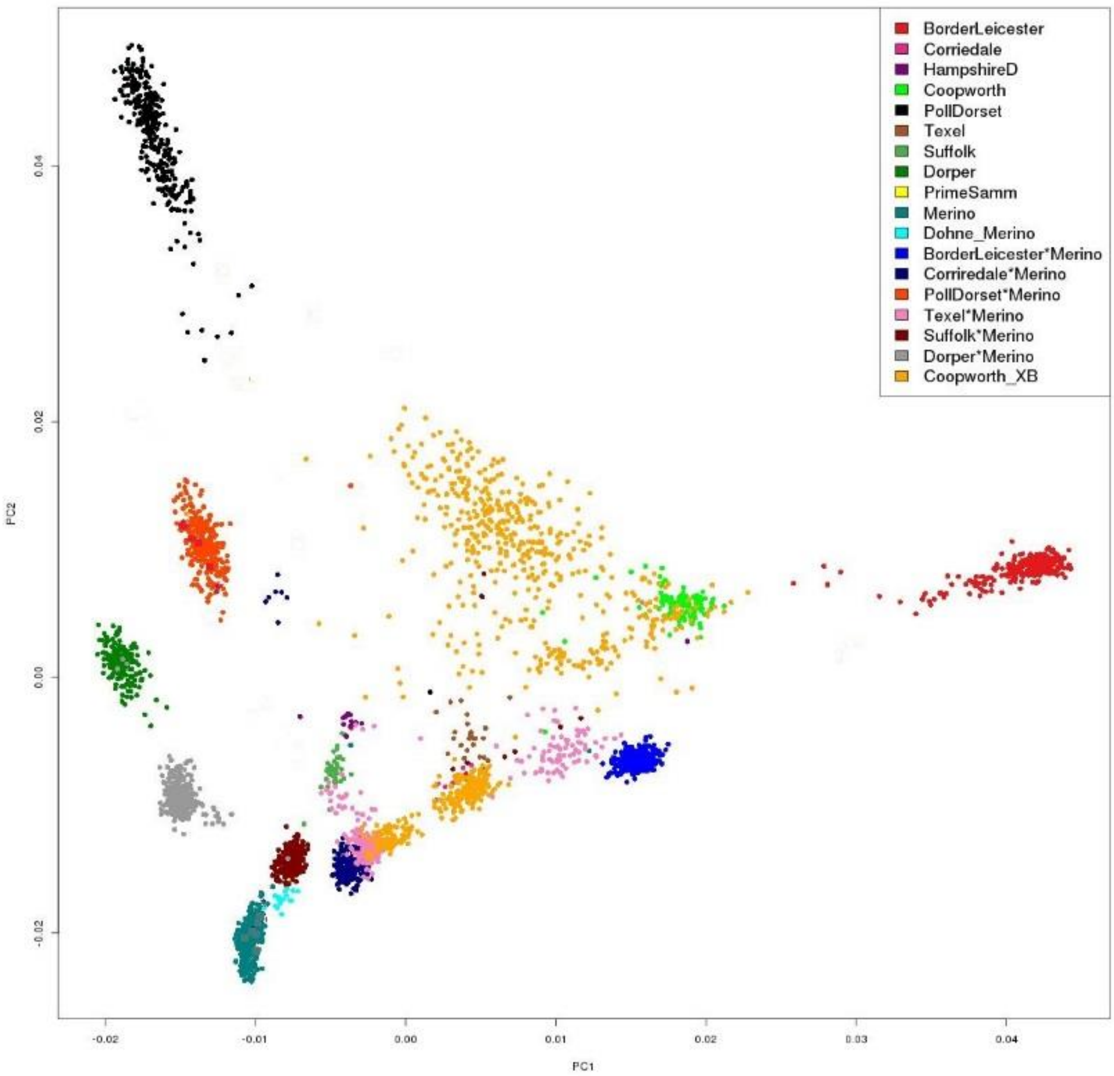


Figure 2: Population structure based on the first two principal components of genomic relationship matrix



Phenotypes for GWAS analysis of carcase traits were pre-corrected for non-additive genetic effect using information from the OVIS analyses for Merinos, maternal, and terminal breeds. Phenotypes were scaled pre-adjusted for various systematic effects as per standard procedures. After OVIS analyses were conducted, the corrected phenotypes for GWAS were derived as the estimated breeding value plus residual value. These corrected phenotypes are therefore free of other terms fitted in the OVIS model, including fixed contemporary group effects, and random genetic group, maternal, and sire by flock effects. These were derived separately for each of the three OVIS analyses, such that a simple fixed effect model with analysis source (three levels) could be fitted in the GWAS analyses.

By contrast for GWAS analysis of reproduction traits, raw phenotypes were first edited for any probable errors including outliers (more than 4 SD deviated from mean) and missing classification information. The phenotypic records were pre-corrected for environmental effects and non-direct genetic effects before being used in association study. Phenotype pre-correction was performed in a univariate BLUP analysis and separately within each data source, with sources being Merino, maternal and terminal, referring to the three analyses in Sheep Genetics. The fitting model used for pre-correction of phenotypes was as below:

$$\mathbf{y = Xb + ZQq + Zg + e}$$

where **y** is a vector of phenotypes; **b** is a vector of fixed effects; **q** is a vector with random breed effects, q ~ N(0, $\mathbf{I\sigma^2_q}$) where **Q** is a matrix with breed proportion of each animal according to genomic information, i.e. assigning animals to breeds, and $\boldsymbol{\sigma^2_q}$ is the variance explained by the breed proportion matrix; **g** ~ N(0, $\mathbf{G\sigma^2_g}$) contains random additive effects where **G** is the genomic relationship matrix (GRM) constructed with 50k SNP genotypes and $\boldsymbol{\sigma^2_g}$ is the variance explained by SNPs; **e** is the vector of random residual effects; **X** and **Z** are design matrices connecting phenotypes to fixed effects and to animals, respectively. The fixed effects consisted of contemporary groups (flock, year, sex and management group), birth and rearing type, age of dam, age at measurement and weight at measurement (for eating quality traits only). Genetic group effects derived from 50k common SNP genotypes and maternal effects (for slaughter traits only) were fitted as random effects. ASReml 4.0 used for phenotype pre-correction.

3.1.2 Genotypes

Genotyping of animals used in this research was based on numerous SNP marker density panels. To find a final set of genotypes across all the data, genotype imputation was used first to obtain a complete set of high density (HD) genotypes. Before imputation a genotype, quality control was performed on different sets of genotypes as below. Genotypes were retained if the GenCal (GC) score was greater than or equal to 0.6 , individual SNP genotypes call rates were greater than or equal to 90%, if the heterozygosity for a SNP deviated by less than 3 standard deviations from the average of population heterozygosity, if the SNP minor allele frequency was higher than 0.001, if SNPs were not located on chromosome X, or if the SNP genotype frequency did not deviate from the Hardy-Weinberg Equilibrium ($p < 1\times10E{-}10$). Imputation to 600K SNP density (HD) was based on reference set of 2,266 animals with observed HD genotypes, including sires and dams or progeny with a high genetic relationship to the rest of population as reference set. The final imputation step was performed to impute to sequence data based on a reference set of 726 multi-breed animals with observed whole genome sequence (WGS) genotypes. Among these, 376 animals had been sequenced by the Sheep-CRC (with on average 10x sequencing coverage), with samples representing the main sheep breeds in research flocks. These data were then combined with an additional set of 350 samples from European sheep breeds, which were available through the “Sheep Genomes DB” project. Prior to imputation, HD genotypes were pre-phased using Eagle 2.0 and then Minimac 3.0 was used for WGS imputation. Following imputation, imputed sequence variants with imputation quality statistic “r” (provided by the Minimac software) lower than 0.63 were discarded from the analysis. The final set consisted of 31,154,249 variants (including SNPs and InDels) for each animal.

3.1.3 Genome Wide Association Study (GWAS)

To find genomic regions in significant association with genetic variance of production traits, genome wide association analysis (GWAS) was performed on imputed sequence genomes. The association study was performed on single traits, followed by a multi-trait meta-analysis GWAS. All available data was used in the association studies.

3.1.3.1 Single trait GWAS

In single trait GWAS the following fitting model was used on pre-corrected phenotypes for environmental and non-direct genetic effect:

$$y = Xb + Zu + e.$$

In this equation **y** refers to the pre-corrected phenotypes, ***b*** refers to intercept and fixed effects in the model, with the fixed effects being data source (maternal, terminal, Merino genetic evaluation analyses) and individual SNP effect, **X** contains a column with ones for the intercept, a column of 1 to 3 for data source and a column of genotypes (dosage of the second allele) for the SNP, **u** refers to the polygenic term which was fitted according to a covariance structure proportional to the genomic relationship matrix (**G**) such that $Var(u) = \sigma_g^2 G$, and **e** is the random residual term. The genomic relationships matrix (**G**) was calculated based on the Yang et al. (2010) algorithm, and **X** and **Z** are incidence matrices relating effects to observations. The polygenic term was fitted to account for any population structure that maybe confounded with SNP genotypes, which could lead to false positive and or false negative results.

3.1.3.2 Multi-trait GWAS meta-analysis

A multi-trait GWAS meta-analysis (e.g. Bolormaa et al. 2021) were also tested on a group of 10 traits including traits listed in Table 1. Meta-analysis was based on an approximate chi-square statistic estimated as $t'V^{-1}t$. In this equation t is the signed t-value derived from single trait p-values and its standard deviation across all 10 traits, and V is the correlation matrix derived from signed t-values between traits.

3.1.4 Selection of informative SNPs

Selection of informative SNPs was based on the following procedure. In stage 1, SNPs with low p-value in each trait (i.e. highly significant) were selected from all significant regions based on performing GWAS on combined OVIS sources (Merino, maternals and terminal). The significance threshold for selection of SNPs were -log10 p value >= 5.5 for weight traits, EQ traits, BCS and Tail Length, and -log10 p value >= 5 for reproduction traits. In the stage 2, SNPs from significant regions based on performing GWAS on each OVIS source, and that were not significant in GWAS on combined data, were selected. Selected SNPs in stage 1 and 2 were then pruned for local LD. Different parameters were checked for pruning. The final pruning was based on: LD >=0 .80, Window Size = 5000, Sliding Window Size = 100 SNPs. Pruning was performed in *Plink 1.9* software. Furthermore, in each pairwise LD analysis, SNP with higher MAF retained in data. Conditional and joint analysis (CoJo) of single SNP GWAS provided a few additional significant SNPs for each significant chromosomal region. We added the results of CoJo to the final list of SNPs if SNPs were not already represented in the list. CoJo analysis was performed in *GCTA* program (Yang et al, 2011).

SNP selection from meta-analysis was based on a stronger threshold (-log 10 p-value >=6.5). After pruning for high LD according to above criteria, SNPs which were not available on single trait GWAS were added to the final list. However, given that meta-analysis did not show additional significant regions, and that some significant regions in single trait GWAS turned out to be not significant in the meta-analysis, we limited selection of SNP from meta-analysis to only highly significant SNPs.

After finding the aggregated list of top SNPs from single trait GWAS (on combined data and on each data source) and meta- analysis, the list of SNPs was sorted uniquely and SNPs with very low MAF were removed from the list. The MAF threshold for discarding the SNPs was 0.005. Specification of a low MAF threshold was intended to retain possible new mutations. However, on the other hand genetic variants with very low MAF may suffer from lower imputation accuracy.

3.1.5 Prediction accuracy using informative SNPs from single trait GBLUP analyses

Tests of prediction accuracy using updated informative SNPs were performed in two sets of data. First prediction accuracy was evaluated on sets of animals with available phenotypes and genotypes. A validation set was randomly selected across sire families, such that there were no common sires in prediction reference set and validation set. This design was chosen to keep the relationship between the prediction reference set and the validation low and is expected to lead to more conservative prediction of accuracy of genomic prediction, but relatively more benefit from selected SNPs.

Tests of prediction accuracy was done to evaluate the additional benefit of adding 3,700 top SNPs to the marker panel, with the final list compiled across 15 traits. Genomic predictions were obtained by GBLUP, with comparisons including the use of a GRM based on the current standard SNP panel, a GRM based on the standard SNP panel augmented with informative SNPs, or, alternatively, by fitting the selected SNPs as an additional random effect in the model, i.e. by fitting two GRMs in the model, one for standard SNPs and one for informative SNPs, respectively.

The second test of prediction accuracy was based on Sheep Genetics genetic evaluation pipeline and using larger set of data on animals with only phenotypes and animals with phenotypes and real or imputed genotypes in single step GBLUP as described in Section 3.2.1.

3.2 OVIS methodology to accommodate predictive SNP panels

The predictive SNPs developed by the Sheep CRC in 2018 were commercialized on the Neogen GGP Ovine 50K test in 2019, and in 2020 implemented in Sheep Genetics evaluations as part of an upgrade to a new “union” marker set to be used in single step evaluations using the OVIS software. Methodology to include predictive SNPs in OVIS was tested (Li et al. 2021), comparing adding predictive SNPs to a single G matrix with all other (randomly selected) SNPs with fitting separate G matrices for randomly selected and predictive SNPs. Results showed small accuracy improvements due to using predictive SNPs, but no benefit to fitting G matrices separately.

3.2.1 Validation of predictive SNPs in multi-trait single step OVIS evaluations

New predictive SNPs from GWAS analyses in 2021 were tested in the OVIS terminal sire evaluation using a forward cross-validation procedure. Data from the November LAMBPLAN analysis were extracted as well as three sets of SNPs for the animals in this analysis which had imputed sequence data. The first set of SNPs were the SNPs that were not part of either set of predictive SNPs, the 2018 Sheep CRC SNPs on the Neogen GGP panel, or the 2021 L.GEN.1815 predictive SNPs (n = 54,892). The second set of SNPs included all SNPs used in OVIS as of November 2021, including the 2018 Sheep CRC SNPs. The final set added the 2021 SNPs to the current OVIS panel.

These sets of SNPs were then used to generate breed-adjusted genomic relationship matrices (Gurman et al. 2019). For reporting purposes, we will refer to ‘A’ as a model that does not contain genomic data (pedigree only), “G_r” as the GRM constructed from only unselected SNPs, “G_rt1” as a GRM constructed from unselected SNPs and the 2018 Sheep CRC predictive SNPs, and “G_rt2” as the GRM constructed from previous SNPs and the 2021 predictive SNPs. Because

A forward cross-validation was then performed using phenotypes for animals born after 2018 removed from the analysis. Breeding values were then calculated using the remaining data. Single step genomic BLUP evaluations were performed using the AGBU linear model solver. The accuracy of SS-GBLUP EBVs from the different models was assessed by the correlation between EBVs and adjusted phenotypes for the genotyped animals removed from the analysis, and the dispersion (regression slope) was assessed from the regression of adjusted phenotype on EBV, with an expected value of 1 indicating absence of over- or under-prediction. Phenotypes were adjusted for contemporary groups in these comparisons.

The metrics based on EBVs from full and partial analyses were also derived, see Legarra and Reverter (2018). The first metric is

$$acc_{LR} = \sqrt{\frac{cov\left(\hat{\boldsymbol{u}}_p, \hat{\boldsymbol{u}}_w\right)}{\left(\overline{d\imath ag(\boldsymbol{K})} - \overline{\boldsymbol{K}}\right) \times \sigma_g^2}}$$

where $\hat{\boldsymbol{u}}_p$ as the EBVs from the partial analyses (data removed for the validation animals) for the validation animals, $\hat{\boldsymbol{u}}_w$ as the EBVs from the whole analyses (data retained for the validation animals) for the validation animals, $\boldsymbol{K}$ as the mean of the relationship matrix, H, for the validation animals, and $\sigma_{g,\infty}^2$ as the is the genetic variance at equilibrium in a population under selection, assumed for simplification to be σ_g^2. Dispersions was calculated as:

$$disp_{LR} = \frac{cov\left(\hat{\boldsymbol{u}}_p, \hat{\boldsymbol{u}}_w\right)}{var\left(\hat{\boldsymbol{u}}_p\right)}$$

and bias as:

$$bias_{LR} = \overline{\hat{\boldsymbol{u}}_p} - \overline{\hat{\boldsymbol{u}}_w}$$

The number of animals with a genotype and phenotype in the validation group for each trait is shown in Table 6. While we have presented here all traits for which the most recent set of SNPs have targeted, the number of animals with phenotype and genotype for AWT, LMY and to a lesser extent, DRESS. This means that while we cannot calculate standard errors in this form of cross validation analysis, the standard errors around the metrics for these traits would be large and therefore the metrics for these traits cannot be interpreted with the same level of confidence.

Table 6: Validation animals for each trait with a genotype and a phenotype.

	# validation animals with genotypes
PWT	2432
AWT	62
CWT	1152
PCF	2263
CCFAT	1147
IMF	1150
SF5	1086
PEMD	2266
CEMD	1148
DRESS	535
LMY	42

3.2.2 Optimal weighting of pedigree and genomic information in single step

When conducting SS-GBLUP analyses (Legarra et al. 2014), a single genetic effect is usually fitted as an H matrix, where a proportion of genomic information is blended with a portion of the pedigree information based on a parameter lambda (λ), written as $\lambda G + (1 - \lambda)A_{22}$, where G is the genomic relationship matrix and A_{22} is the numerator relationship matrix for genotyped animals. Alternatively, pedigree and genomic effects can be fitted separately, and the value of lambda implied through the variance components assumed for each effect. These two alternatives give equivalent (identical) breeding values. Fitting effects separately can be extended to fitting separate G matrixes for predictive SNPs, and this was the approach used in the study of Li et al. (2021) within L.GEN.1815. In order to parameterise the variances used, variance components for separate pedigree and genomic sources, including predictive SNPs, were estimated by Gurman et al. (2021), and implied in these estimates was information regarding the value of lambda for different traits.

McMillan and Swan (2017) used cross-validation to investigate the accuracy of genomic predictions for different lambda values for the Australian terminal sire sheep single-step evaluation. They concluded the value of 0.5 for lambda in routine industry evaluations was an appropriate parameter. However, the previous study was based on univariate SS-GBLUP analyses, and the assessment of lambda value for multi-variate SS-GBLUP analyses is unknown. Furthermore, these analyses were based on variance components estimated from pedigree-only models.

Based on the results of Gurman et al. (2021) in this project, there are indications that the value of lambda may be higher than 0.5 for carcase traits in terminal sire breeds. In this report, the accuracy and bias of genomic predictions across a range of lambda values were investigated based on cross-validation for a range of carcass and weight traits.

3.2.2.1 Phenotypic and pedigree data

Phenotypic data were included for six traits: intramuscular fat (IMF, %), shear force (SF5, Newtons), carcass eye muscle depth (CEMD, mm), C-site carcass fat (CCFAT, mm), carcass weight (CWT, kg), and post-weaning body weight (PWT, kg). A group of 9,688 animals, originating from terminal breed sires and with SNP genotypes and records for all six traits, was identified as the focus of this study for estimation of variance components and cross-validation. These animals originated from the Sheep CRC and MLA Reference Flock populations. Pre-adjusted phenotypes and contemporary group codes were extracted from the LAMBPLAN terminal sire evaluation, with data summarised in Table 6. Pre-adjustments resulting from LAMBPLAN terminal sire evaluation are for a combination of birth type, rearing type, age and dam age, depending on the trait. Pedigree information was extracted from the LAMBPLAN database and included 44,874 animals for REML analyses to estimate variance components (based on ancestors of animals with genotypes and phenotypes) and 1,985,749 for the cross-validation analyses using the full data set (based on the full LAMBPLAN terminal sire pedigree). A G matrix was constructed for the 9688 animals in REML analyses, with a second G was constructed for 29,434 animals with genotypes in SS-GBLUP analysis.

Table 7. Data summary for cross-validation (Ngeno: number of genotyped animals, Nobs: number of observations, Ncg: number of contemporary groups)

Trait	Unit	Ngeno	Nobs	Ncg	mean	Min	max	sd
imf	%	9688	9688	376	4.24	1.12	9.91	0.99
sf5	Newtons	9688	9688	376	34.88	10.89	166.26	15.22
cemd	mm	9688	9688	376	31.31	17.36	48	3.87
ccfat	mm	9688	9688	376	4.13	0.34	19.01	1.96
cwt	kg	9688	9688	376	21.89	10.41	35.54	2.95
pwt	kg	9688	9688	444	58.58	27.41	113.74	9.47

The cross-validation analysis was conducted based on the full LAMBPLAN terminal sire data set for these six traits (full data set). The number of records in the full data set is shown in

Table .

Table 8. Number of records for each trait and between trait pairs in the full data set used in SS-GBLUP analyses for cross-validation. These records were derived from the LAMPLAN terminal sire evaluation.

Trait	imf	sf5	cemd	ccfat	cwt	pwt
imf	14,832	14,591	14,656	14,568	14,832	12,362
sf5		14,840	14,672	14,585	14,840	12,270
cemd			16,753	16,522	16,753	13,357
ccfat				16,560	16,560	13,165
cwt					18,048	14,627
pwt						1,674,789

3.2.2.2 Models for estimation of variance components

Univariate “GREML” analyses were performed using MTG2 (Lee and van der Werf 2016). Variance components were estimated using the model:

$$y = X\beta + Zu + Zg + Zm + \epsilon$$

Where:

y is the vector of pre-adjusted phenotypes, which are obtained from the LAMBPLAN terminal sire analysis,

X is the design matrix for the fixed effects (contemporary groups),

β is the vector of contemporary group solutions,

Z is the design matrix for the random effects associated with breeding values for individual animals (animals with records by breeding values), which in this case is I.

u is the vector of random additive genetic effects with N$(0, G_w\sigma_a^2)$,

G_w is the weighted GRM $G_w = \lambda G + (1 - \lambda)A_{22}$

Q is the matrix of genetic group proportions, defined by the breed of origin from the pedigree,

g is the vector of random genetic group effects with N(0, $QQ'\sigma_g^2$),

M is the design matrix for the random maternal permanent environment effects,

m is a vector of random maternal effects only fitted for two weight traits (CWT and PWT) with N(0, $MM'\sigma_m^2$) and

ϵ is the vector of residuals effects with N(0, $I\sigma_e^2$).

For GREML, the value of λ was varied between 0 and 1 in steps of 0.05.

3.2.2.3 *Cross-validation design*

Procedures to integrate predictive markers with existing genotype panels in the calculation of breeding were investigated using a k-fold cross-validation (CV) approach. Five folds were randomly allocated, stratified by breed and sire families from the dataset in

Table . Hence, for each validation set, there were no members of the same sire family also used in the training set. These allocations where replicated five times (Table 9). Cross-validation for each fold in each replicate was then performed where phenotypes for animals belonging to the fold used for validation were removed from the analysis. Breeding values were then calculated using the remaining folds as a training set.

With regard to the breed level stratification, the majority of animals were of White Suffolk (323 sires, 3801 progeny) or Poll Dorset (319 sires, 4080 progeny) origin. Other breeds included Suffolk (40 sires, 499 progeny), White Dorper (35 sires, 309 progeny), Texel (31 sires, 413 progeny) and Dorper (29 sires, 235 progeny).

Table 9. Number of sires and progeny allocated to each cross-validation fold for 5 replicates

CV	**Replicate 1**		**Replicate 2**		**Replicate 3**		**Replicate 4**		**Replicate 5**	
fold	Nsire	Nprog	Nsire	Nprog	Nsire	Nprog	Nsire	Nprog	Nsire	Nprog
1	165	1997	165	2043	162	1823	164	1985	165	2036
2	165	1929	161	1679	166	1968	162	1893	165	1986
3	163	1807	164	1997	164	1997	166	1897	163	1927
4	162	2040	167	1861	164	2002	166	1880	166	1850
5	167	1915	165	2108	166	1898	164	2033	163	1889

3.2.2.4 Single step GBLUP models used in cross-validation

The SS-GBLUP model was used to estimate breeding values in the full data sets for the cross validation. The only difference between the model used for cross-validation and GREML was that the cross-validation model used a single step relationship matrix, H.

For the cross-validation analyses, a total of eleven lambda values were examined ranging from 0 to 0.9 in increments of 0.1 and also $\lambda = 0.99$ (to allow for inversion) were used to build G to estimate a series of variance components. SS-GBLUP analyses to estimate breeding values were performed using the AGBU linear model solver. The variance components used in this cross-validation data sets were based on those estimates from the GREML analyses. However, two scenarios were examined; 1) the variances for genetic groups were equal to additive genetic variances; 2) the variances for genetic groups were from the estimates directly from the GREML analyses.

3.2.2.5 Accuracy and bias for cross-validation

The average accuracy and bias across five replicates of the different models was assessed by two metrics: 1) the correlation coefficient between EBVs and adjusted phenotypes (adjusted for the fixed effect of contemporary groups) for the animals in the validation data set, scaled by the squared root of heritability (Acc1), and the bias was calculated as the regression slope of adjusted phenotype on EBVs (Bias1); 2) accuracy and bias metrics were also calculated using the LR method (Legarra and Reverter, 2018) as the correlation (Acc2) and regression slopes (Bias2) between the EBVs from the full analysis and the partial analysis for the animals in the validation data set.

3.3 Expected benefits of genomic information in LAMBPLAN analyses

Many sheep breeders are genotyping their sheep to obtain more accurate Australian sheep breeding values (ASBVs) earlier in life to make more informed breeding decisions. It is known that the accuracy of ASBVs will vary depending on a range of factors, including how related an animal is to the animals that are part of the reference, which is the animals with genotypes and phenotypes. In the analysis done by Sheep Genetics, it important to know how much genomic information contributes to the accuracy of the ASBV, and this is particularly of interest for animals from the numerically smaller breeds, as these have limited numbers of genotyped animals from which to predict.

The calculation of accuracies in the OVIS evaluation pipeline is approximated using methods which accumulate estimated progeny numbers (Graser and Tier 1997). In this method, the various sources of information that contribute to an accuracy (information from parents, progeny, correlated traits, siblings etc) are converted to the effective progeny numbers (EPN). This concept was extended to represent the effective progeny numbers (EPN) for genomic information (Li, Swan, and Tier 2017).

Using genomic EPN used in the calculation of breeding value accuracies in the OVIS evaluation pipeline, we can quantify the expected benefits of genomics for subsets of genotyped animals without phenotypic information and assess the impacts for different breeds in the maternal and terminal LAMBPLAN analyses.

Genomic EPN are routinely calculated for all genotyped animals and animals which receive inferred genomic information through single step as part of the LAMBPLAN analyses. These EPNs were retrieved from the results of the terminal and maternal analyses, along with the phenotypes used in these analyses. EPNs for animals without phenotypes were extracted because these are the animals that are expected to gain the most benefit from genomics in terms of accuracy. Further, animals with a phenotype will be gaining most of their accuracy from their own phenotype. These EPNs were then converted to accuracy values, by the formula of Graser and Tier (1997):

$$acc = \sqrt{\frac{EPN}{EPN + \lambda}}, \quad \lambda = \frac{4 - h^2}{h^2}$$

where EPN is the estimated progeny number obtained from the routine analyses, and h^2 is the heritability taken from the same analysis. This formula gives the accuracy from having a genotype for an animal with no other known information. These accuracies were then averaged across combinations of breed groups, trait groups and years of birth.

4. Results

4.1 Results of GWAS

GWAS on final data sets confirmed the highly significant genomic regions detected in previous analysis and also showed numerous new significant regions based on larger data sets. Results confirmed previous highly significant regions for CCFAT detected on chromosomes 1 and 6 as well as new significant regions on chromosomes 2, 3, 7 and 11. For CEMD, results confirmed a significant region on chromosome 11 and also showed new significant regions on chromosomes 6 and 18. For IMF results confirmed five significant regions on chromosomes 18, 10, 12, 16 and 6 that were reported previously, plus new highly significant regions on chromosomes 2 (two regions) 5 and 23. GWAS on other carcass traits showed five highly significant regions on chromosomes 6, 11, 16 , 3 and 5 for CWT, six significant regions for DRESS on chromosomes 6, 8,11, 14, 20 and 24 and two significant regions on chromosomes 6 and 11 for LMY. In PCF GWAS on updated data showed new highly significant regions on chromosome 2, 3, 7, 8, 9, 13, 18, 19, 21, 24, 25 and 26. In PEMD new significant region detected on chromosome 1, 2 (3 new regions), 7, 9, 12, 14, 15, 16, 19, 21 and 22. In PWT new significant region detected on chromosome 8, 13, 17 and 18. Manhattan plots for GWAS on the combined data set are reported with details in milestone reports. GWAS showed more highly significant SNPs and regions affecting the trait compared to previous runs on smaller data size in 2018-2019.

Table compares the number of SNPs after pruning (LD≥0.95, window size=5000, sliding window=100) and number of significant regions between two analyses.

Comparison of GWAS within sources showed chromosomal regions significant within breed sources. This is basically due to differences in genetic architecture of traits in different breeds from natural and artificial selection. In CCFAT chromosome 9 showed a highly significant region in maternal and Merinos breed sources but the region was not significant in terminals. CEMD showed significant regions on chromosome 14 and 18 in terminals, but these regions were not significant in maternals and in Merinos. CWT showed a highly significant region on chromosome 5 only in maternals. Dressing percentage showed a highly significant region on chromosome 9 only in maternals. IMF showed a significant region on chromosome 2 in maternals and terminals, while this region was not significant in Merinos. Appendix A shows the results of GWAS for carcass and eating quality traits, reproduction traits, ewe efficiency traits, and tail length.

For reproduction traits GWAS showed regions on several different chromosomes that significantly affected phenotypic differences. For litter size GWAS showed significant QTLs in maternal breeds in which one highly significant region on chromosome 5 (GDF9 region) was common between yearling litter size (YLS) and adult litter size (LS). No significant region was found in common for yearling conception rate (YCON) and adult conception rate (CON) in maternals or in Merinos.

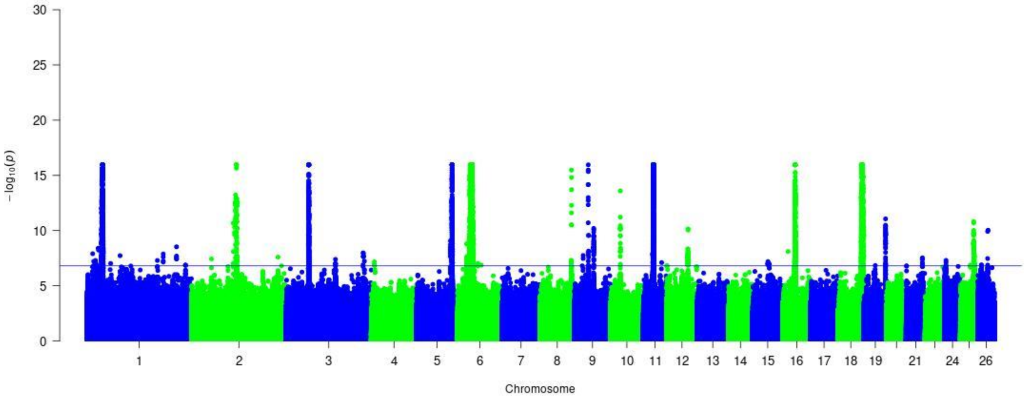
For tail length GWAS results indicated highly significant regions on chromosomes 11 and 19 which can be used in breeding program to decrease the tail length. Genomic analysis of other genetic defects including jaw abnormality (under shot and overshot) and Entropion (turned-in eye lids) indicated mostly a polygenic control of the phenotype.

Table 10. Number of significant SNPs (-Log P≥5.5) pruned for LD (LD≥0.95, window size=5000, sliding window=100) and number of highly significant region between 2018-19 data and 2021

	-Log P ≥ 5.5	-Log P ≥ 5.52	No of Significant Regions	No of Significant Regions
Trait	**2018-2019 data**	**2021 data**	**2018-2019 data**	**2021 Data**
CCFAT	654	1262	3	7
CEMD	52	94	5	8
CWT	NA*	817	NA	16
DRESS	NA	640	NA	8
IMF	529	1286	4	10
LMY	NA	329	NA	5
PCF	NA	1800	NA	26
PEMD	806	1122	8	25
PWT	1221	2439	14	26
SF5	528	1286	7	18

Results of multi-trait GWAS meta-analysis are shown in Figure 2. Comparison of results of single trait and meta-analysis confirmed single trait GWAS results but did not show additional significant regions for EQ traits. Furthermore, comparison of genetic correlations between traits based on signed t-values and pedigree information showed similar direction, but the strength of correlation coefficients were notably different. LMY which had the smallest number of phenotypes and genotypes in the meta-analysis showed the most different association in comparison to the genetic correlation. Consequently, selection of informative top SNPs which will be explained in next section was mainly based on single trait GWAS analysis on combined and on within source.

Figure 2: Multi-trait GWAS meta-analysis of eating quality traits



4.2 Selection of informative SNPs

Selection of informative SNPs in significant association with genetic variation of production and reproduction trait was based on GWAS results. GWAS performed on within the three Sheep Genetics evaluations (Merino, maternal, and terminal sire breeds) and also on the combined data set on the traits listed below from ~31 million imputed SNPs in the whole genome sequence. Results of the final GWAS on EQ traits are reported in previous section and results of GWAS on final reproduction traits, pre-joining adult weight (AWT) and body condition score (BCS) in breeding ewes, and tail-length were reported in previous milestone reports for this project.

Traits used in the selection of top SNPS:

Body weight traits: PWT, AWT, BCS

Eating quality traits: CCFAT, CEMD, CWT, DRESS, IMF, LMY, PCF, PEMD, SF5

Reproduction trait: YCON, CON, YLS, LS

Genetic defects: tail length

Following GWAS analysis, selection of informative SNPs was carried out as follows:

1. For each trait, all SNPs with lowest p-value (or highest –log10 p values) were selected across all the significant regions based on GWAS of combined data. We selected SNPs from all regions provided they passed the significance threshold. To avoid selection of SNPs from a few highly significant regions the significant threshold was -log10 p value >= 5.5 for weight traits, EQ traits, BCS and tail length, and -log10 p value >= 5 for reproduction traits. This would allow significant SNPs across the whole genome to be selected.
2. Next, we selected SNPs which were significant within each OVIS source (Merino, maternal, and terminal breeds) according to same threshold criteria described in 1. The results of GWAS within source were added to stage 1 for SNPs which had not been selected before.
3. SNPs selected in steps 1 and 2 were then pruned for local LD. Different parameters were checked for pruning. The final pruning was based on: LD>=0.80, Window Size=5000, Sliding Window Size=100 SNPs. Pruning was performed in Plink 1.9 software. Furthermore, in each pairwise LD analysis, SNP with higher MAF were retained.
4. To ensure important SNPs were not overlooked, we checked the final list of top SNPs with results of CoJo (conditional and joint analysis) for each trait, and added any SNPs not detected in steps 1 and 2. CoJo was performed using the GCTA program.
5. Selection of SNPs from meta-analysis was based on a stronger threshold (-log 10 p-value >=6.5). After pruning for high LD according to the above criteria, SNPs which were not available on single trait GWAS were added to the final list. However, given that meta-analysis did not show additional significant regions, and that some significant regions detected in single trait GWAS turned out to be not significant in meta-analysis, we limited selection of SNP from meta-analysis to very highly significant SNPs.
6. After compiling an aggregated list of informative SNPs from single trait GWAS and meta-analysis, the final list of SNPs was sorted uniquely and SNPs with very low MAF removed. The MAF threshold for discarding the SNPs was very low and less than 0.005. Considering low MAF threshold was mainly due to keeping probable new mutations in the data however, on the other hand genetic variants with very low MAF may suffer from lower imputation accuracy.

The complete list of selected SNPs per trait including the SNP name, minor allele frequency (MAF) and GWAS p-value are reported on Appendix C.

Table 11 shows the number of SNPs which are significant between traits in final list of selected SNPs. Common SNPs arise from genetic correlations between traits and chromosomal regions with pleiotropic effects.

Table 11. Number of significant SNPs between traits

Trait	CEMD	CWT	DRESS	IMF	LMY	PCF	PEMD	PWT	SF	AWT	BCS	YCON-CON	YLS-LS	Tail-L
CCFAT	0	134	81	8	55	2	41	83	3	0	0	0	0	1
CEMD		3	1	14	2	1	26	6	4	1	0	0	0	0
CWT			53	6	51	1	37	58	3	1	1	0	0	0
DRESS				6	42	0	30	6	2	0	0	0	0	0
IMF					10	0	49	4	88	0	0	0	0	0
LMY						0	41	62	3	0	0	0	2	0
PCF							3	2	0	0	0	0	0	0
PEMD								44	35	2	0	0	1	0
PWT									2	2	5	0	1	0
SF										0	0	0	0	0
AWT											0	0	0	0
BCS												0	0	0
YCON-CON													0	0
YLS-LS														0

4.3 Tests of accuracy of genomic predictions using informative SNPs

Prediction accuracies in EQ and reproduction traits using informative SNPS are shown in Figure 3 and respectively. Results showed between additional 0.04 to 0.16 absolute value of accuracy according to using the new set of informative SNPs. Results also showed higher prediction accuracy when informative SNPS are fitted as additional GRM.

In a second test, the prediction accuracy was evaluated using combined informative SNPs (3,700 SNPs) across traits. Prediction was based on GBLUP and the genomic relationship matrix was calculated according to standard 60k genotypes, 60k+ old selected SNPs (1G old), 60k+new selected SNPs (1G new), 60k+old selected SNPs (2G old), 60k+new selected SNPs fitted simultaneously (2G new). Results of this test are plotted in Figure 5, showing higher prediction accuracies (between 0.02 and 0.09 and on average 0.04) across Merino, maternal, and terminal breeds, and combined data based on the new set of informative SNPs, compared to accuracy obtained using previous set of informative markers. These results are also in line with GWAS results on larger data which showed more significant chromosomal regions and SNPs compared to GWAS on smaller data in the previous study in 2018.

Figure 3: Accuracy of genomic prediction as correlation between GBV and adjusted phenotype based on 60k and 60k plus informative SNPs per trait

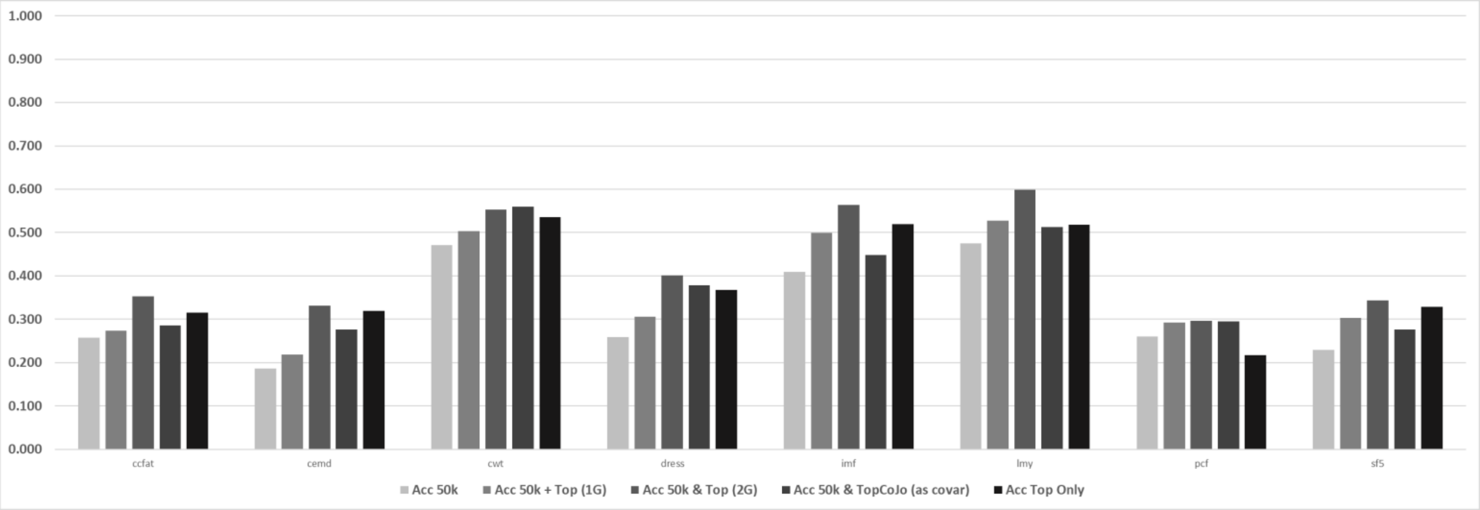


Figure 4: Test of genomic prediction using informative markers in reproduction traits based on 5-fold cross validate

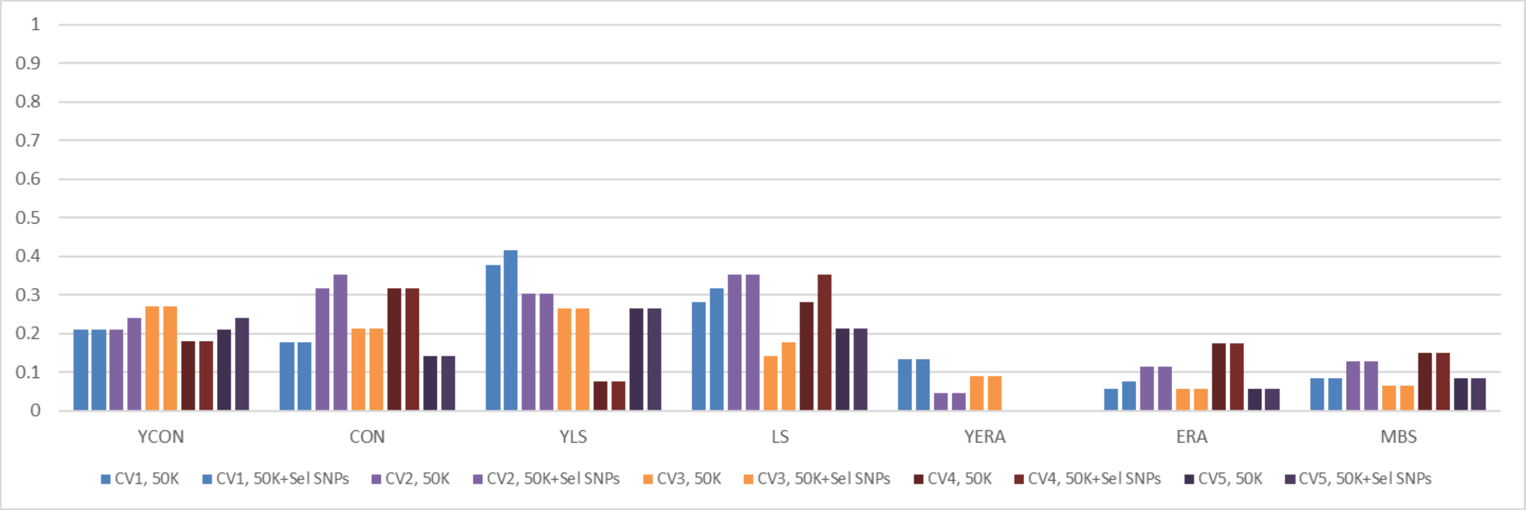
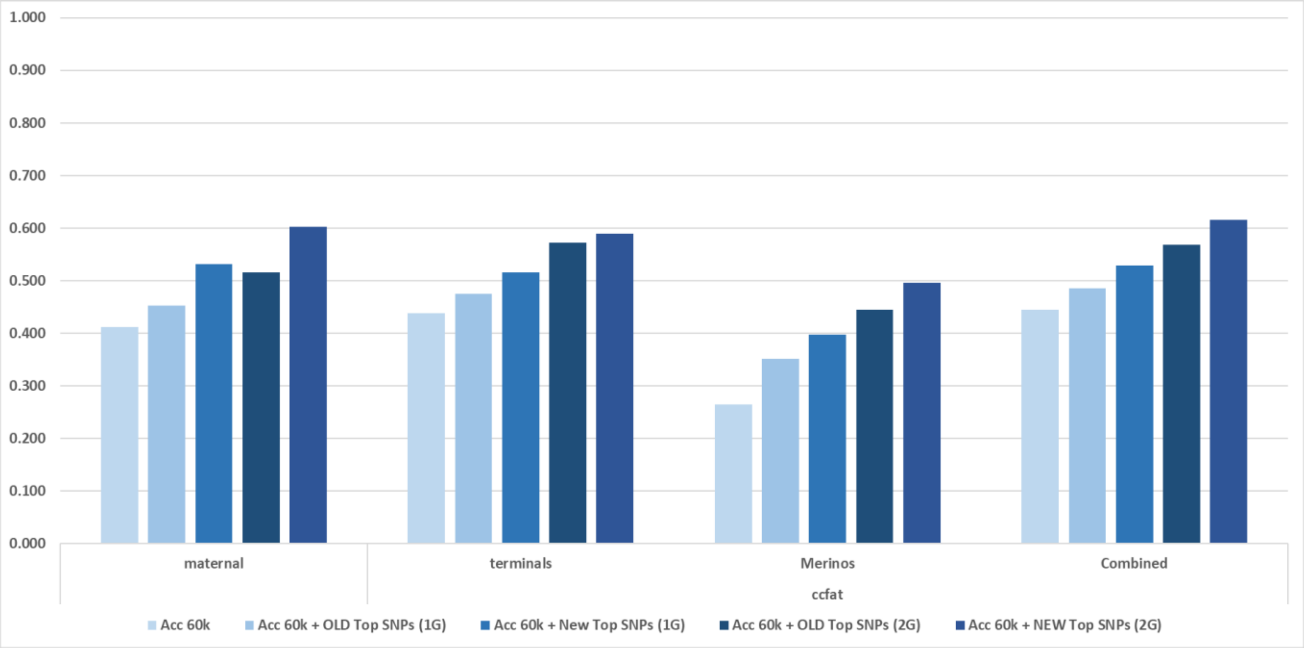


Figure 5: Comparison of accuracy of genomic prediction between using previous vs new set of informative SNPs for CCFAT in Merinos, maternal, and terminals breeds, and combined data (accuracies scaled by dividing by square root of h2).



4.4 OVIS methodology to accommodate predictive SNPs

4.4.1 Validation of predictive SNPs in multi-trait single step OVIS evaluations

Validation accuracies based on phenotypes and the LR method are presented in Table and

Table 4 respectively. Generally, these accuracies are higher than what would be theoretically expected within a population, being the EBV accuracy times the square root of the heritability. These accuracies are therefore likely inflated by differences between breed groups and cohorts. However, what really matters in these comparisons is the differences between the models used. The most notable increase in accuracies were observed between the pedigree only model (A) and the single step model containing only unselected SNPs (G_r). For some traits, a small increase can be seen with the introduction of the first set of predictive SNPs (G_r compared to G_rt1) and a further small increase can be seen adding in the new set of predictive SNPs (G_rt2), see CCFAT, SF5, CEMD, DRESS. Similar patterns were observed in the LR accuracies. Dispersions for the two methods in

Table 3 and 1 Legarra and Reverter (2018)

[2] A = Pedigree only model, G_r = single step with unselected SNP, G_rt1 = G_r with previous set of top SNPs added, G_rt2 = G_rt1 single step with new set of predictive SNPs added

Table 5 respectively generally did not deviate substantially from the expected value of 1, with little difference between analysis methods and G matrixes used.

While not as large as the accuracy gains observed from single trait GBLUP models shown in Section 4.3 (see Figure 3 and Figure 5 for example), the results confirm those findings, and show there is value in pursuing predictive SNPs. In addition, further research to explore alternative approaches to modelling predictive SNPs in the large scale genetic evaluation procedures remains a worthwhile area of research.

Table 12. Phenotypic accuracies for animals with genotypes in the validation group.

Model[1] **Trait**	A	G_r	G_rt1	G_rt2
PWT	0.966	1.047	1.045	1.043
AWT	0.471	0.735	0.743	0.713
CWT	0.258	0.499	0.499	0.503
PCF	0.401	0.466	0.459	0.462
CCFAT	0.287	0.285	0.290	0.319
IMF	0.587	0.626	0.623	0.632
SF5	0.398	0.506	0.510	0.531
PEMD	0.757	0.808	0.807	0.813
CEMD	0.669	0.652	0.655	0.673
DRESS	0.944	0.834	0.841	0.843
LMY	0.732	0.704	0.710	0.681

[1] A = Pedigree only model, G_r = single step with unselected SNP, G_rt1 = G_r with previous set of top SNPs added, G_rt2 = G_rt1 single step with new set of predictive SNPs added.

Table 13 Phenotypic dispersions (regression slopes) for animals with genotypes in the validation group.

Model[1] **Trait**	A	G_r	G_rt1	G_rt2
PWT	1.173	1.171	1.168	1.171
AWT	1.107	1.391	1.408	1.360
CWT	0.336	0.542	0.541	0.547
PCF	0.932	0.901	0.880	0.873
CCFAT	0.579	0.467	0.470	0.514
IMF	1.168	1.030	1.022	1.035
SF5	0.827	0.860	0.861	0.883
PEMD	0.926	0.944	0.941	0.942
CEMD	1.052	1.007	1.007	1.027
DRESS	1.109	0.961	0.964	0.961
LMY	1.693	1.296	1.281	1.225

[1] A = Pedigree only model, G_r = single step with unselected SNP, G_rt1 = G_r with previous set of top SNPs added, G_rt2 = G_rt1 single step with new set of predictive SNPs added

Table 14. LR accuracies[1] for animals with genotypes in the validation group.

Model[1] **Trait**	A	G_r	G_rt1	G_rt2
PWT	1.157	1.293	1.294	1.290
AWT	0.610	0.770	0.769	0.762
CWT	0.614	0.787	0.789	0.791
PCF	0.353	0.435	0.438	0.443
CCFAT	0.433	0.518	0.524	0.535
IMF	0.654	0.770	0.770	0.776
SF5	0.517	0.652	0.658	0.673
PEMD	0.878	0.933	0.933	0.941
CEMD	0.985	1.013	1.017	1.030
DRESS	0.843	0.858	0.862	0.868
LMY	0.667	0.765	0.776	0.764

[1] Legarra and Reverter (2018)

[2] A = Pedigree only model, G_r = single step with unselected SNP, G_rt1 = G_r with previous set of top SNPs added, G_rt2 = G_rt1 single step with new set of predictive SNPs added

Table 15. LR dispersion[1] for animals with genotypes in the validation group.

Model[1] **Trait**	A	G_r	G_rt1	G_rt2
PWT	0.845	0.857	0.856	0.858
AWT	1.112	1.136	1.135	1.124
CWT	0.671	0.705	0.705	0.711
PCF	0.912	0.938	0.929	0.924
CCFAT	0.764	0.701	0.702	0.721
IMF	1.107	1.001	0.996	1.007
SF5	0.801	0.823	0.826	0.839
PEMD	0.931	0.943	0.940	0.941
CEMD	1.034	1.035	1.033	1.038
DRESS	1.072	1.047	1.047	1.043
LMY	1.249	0.955	0.949	0.919

[1] Legarra and Reverter (2018)

[2] A = Pedigree only model, G_r = single step with unselected SNP, G_rt1 = G_r with previous set of top SNPs added, G_rt2 = G_rt1 single step with new set of predictive SNPs added

Table 16. LR bias for animals with genotypes in the validation group.

Model[1] **Trait**	A	G_r	G_rt1	G_rt2
PWT	-0.245	-0.173	-0.169	-0.159
AWT	0.259	0.085	0.107	0.079
CWT	-0.087	-0.042	-0.041	-0.035
PCF	0.008	0.001	0.001	0.001
CCFAT	0.081	0.049	0.048	0.046
IMF	0.007	-0.006	-0.008	-0.010
SF5	-0.061	0.130	0.128	0.135
PEMD	0.045	0.041	0.042	0.041
CEMD	-0.012	-0.004	-0.002	0.001
DRESS	-0.036	-0.058	-0.058	-0.056
LMY	0.219	0.216	0.218	0.229

[1] A = Pedigree only model, G_r = single step with unselected SNP, G_rt1 = G_r with previous set of top SNPs added, G_rt2 = G_rt1 single step with new set of predictive SNPs added

4.4.2 Optimal weighting of genomic and pedigree information in single step

4.4.2.1 Variance component estimates

The log-likelihood curves estimated for each value of λ examined are presented in Figure along with the heritability estimates. Heritability estimates ranged from 0.21 to 0.29 for most of the traits except for a high estimate for IMF (0.62). Of note here is the curve for the genetic variance, which for all traits sees a peak between lambda values of 0.2 and 0.3, with these values decreasing either side of this peak. The genetic variance estimated at $\lambda = 0$ was similar to that estimated at the lambda value where the maximum log-likelihood value was estimated. This finding is interesting and may suggest that the optimal lambda value based on log-likelihood could be set based on a pedigree only model, though this would require different lambdas by trait and does not take into account multi-trait models.

Estimates for all random effects are summarised in

Figure **6**. The ratio of maternal variance to total variance was similar for CWT (0.18) and PWT (0.20). Genetic group effects were strong for two weight traits, accounting for 2-3 times more variance relative to additive genetic variances. In contrast, genetic group effects were moderate for CCFAT (1.22) and low for all other meat quality traits. These estimates along with covariances estimated from bivariate analyses (results not shown) were used for SS-GBLUP cross-validation analyses. One interesting finding is that the maximum log-likelihood value was often estimated to occur at a value of lambda where the genetic variance was similar to that estimated from a pedigree-only model (see Figure).

4.4.2.2 Cross-validation results

Mean accuracy for different lambda values for all traits across folds and replicates from cross-validation are shown in Figure 7 for both the traditional correlation of partial EBVs and adjusted phenotypes scaled by the square root of the heritability, ‘acc1’ and the correlation of the partial and full EBVs ‘acc2’. In general, accuracies saw a slight decrease in between $\lambda = 0$ and 0.2 for the weight traits and then accuracies appeared to increase until $\lambda = 1$. For the carcase traits, this pattern was less pronounced and generally accuracies appeared to linearly increase as λ increased, although for ‘acc2’ there was a similar decrease in accuracies between $\lambda = 0$ and 0.2. For the model with Va=Vg, the maximum phenotypic accuracies were 0.580, 0.510, 0.504, 0.556, 0.775 and 0.822 for IMF, SF5, CEMD, CCFAT, CWT, PWT, respectively. For the model that used estimated genetic group variances, the maximum phenotype accuracies were 0.578, 0.509, 0.502, 0.556, 0.784 and 0.826. For the model with Va=Vg, the maximum EBV correlations were 0.728, 0.763, 0.783, 0.794, 0.9104 and 0.946 for IMF, SF5, CEMD, CCFAT, CWT, PWT, respectively. For the model that used estimated genetic group variances, the maximum phenotype accuracies were 0.726, 0.763, 0.781, 0.794, 0.914 and 0.946.

The regression coefficients (slope) of adjusted phenotype on EBV, ‘bias1’ and the slope of partial and whole EBVs ‘bias2’ for all values of λ are shown in **Error! Reference source not found.**. Note that the slope estimate is expected to be 1 if there is no bias for EBV to predict phenotypes. Meanwhile, slope > 1 indicates an under-estimate of phenotypes for EBV, and vice versa. Generally, biases were small, but were all less than 1. For the phenotype biases, ‘bias1’, were closest to one for λ values mostly less than 0.5 and around 0.3 and became slightly more biased either side. An exception was observed for CWT when Va=Vg where the optimal was observed at $\lambda = 0.99$, For the model that set Va = Vg, the least bias was observed for IMF at $\lambda = 0.3$ (0.978), SF5 at $\lambda = 0.2$ (0.951), CEMD at $\lambda = 0.5$ (0.905), CCFAT at $\lambda = 0.2$ (0.961), CWT at $\lambda = 0.99$ (0.962) and PWT at $\lambda = 0.1$ (0.905). When the estimated genetic group variances were used, the highest phenotype bias was observed for IMF at $\lambda = 0.2$ (0.989), SF5 at $\lambda = 0.2$ (0.972), CEMD at $\lambda = 0.4$ (0.929), CCFAT at $\lambda = 0.2$ (0.964), CWT at $\lambda = 0.99$ (0.934) and PWT at $\lambda = 0.1$ (0.904). For the EBV slopes and the model with Va=Vg, the least bias was observed for IMF at $\lambda = 0.2$ (0.979), SF5 at $\lambda = 0.99$ (0.987), CEMD at $\lambda = 0.99$ (0.950), CCFAT at $\lambda = 0.99$ (0.993), CWT at $\lambda = 0.99$ (0.993) and PWT at $\lambda = 0.99$ (0.969). For the model that used the estimated genetic group variances, the least bias was observed for IMF at $\lambda = 0.2$ (0.987), SF5 at $\lambda = 0.99$ (0.994), CEMD at $\lambda = 0.99$ (0.956), CCFAT at $\lambda = 0.99$ (0.992), CWT at $\lambda = 0.99$ (0.985) and PWT at $\lambda = 0.99$ (0.968). For all traits, the biases were smaller for the model that used estimated genetic groups, except in the case of CWT and approximately the same for PWT for the EBV biases.

Similar to the previous findings of McMillan and Swan (2017), accuracies were observed to increase as the value of lambda increased. However, in this study, the previous asymptotic nature of the accuracies for higher values of lambda was not observed and accuracies continued to increase. Furthermore, previously large levels of bias observed for some traits were largely eliminated.

One interesting finding of this study is the difference in optimal lambda values estimated by log-likelihood and by cross validation accuracies and biases. While the log-likelihood values suggest that a higher value of λ than the current 0.5 could be used, they are not 1, which is the value being suggested by the cross validation. This difference is of interest and warrants further investigation.

Figure 7: Log-likelihood values (logl) and heritability estimates (h2) for different lambda values ranging from 0.0 to 0.99 from univariate REML analyses for IMF, SF5, CEMD, CCFAT, CWT AND PWT

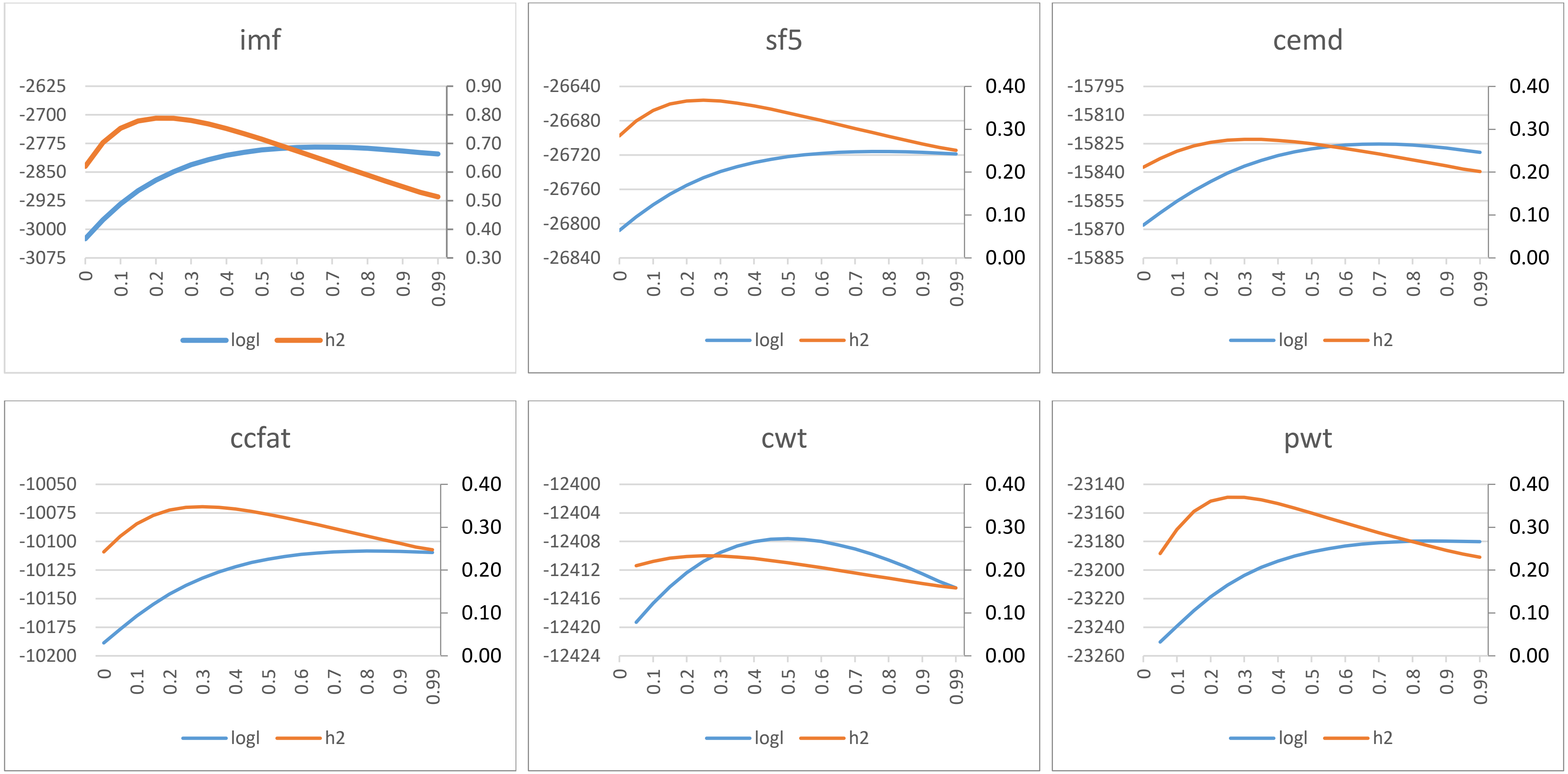


Figure 6: Variance components estimates (Ve: residual variance; Va: additive genetic variance; Vg: genetic group variance; Vm: maternal variance due to dam; Vp: phenotypic variance) for different lambda values ranging from 0.0 to 0.99 from univariate REML analyses

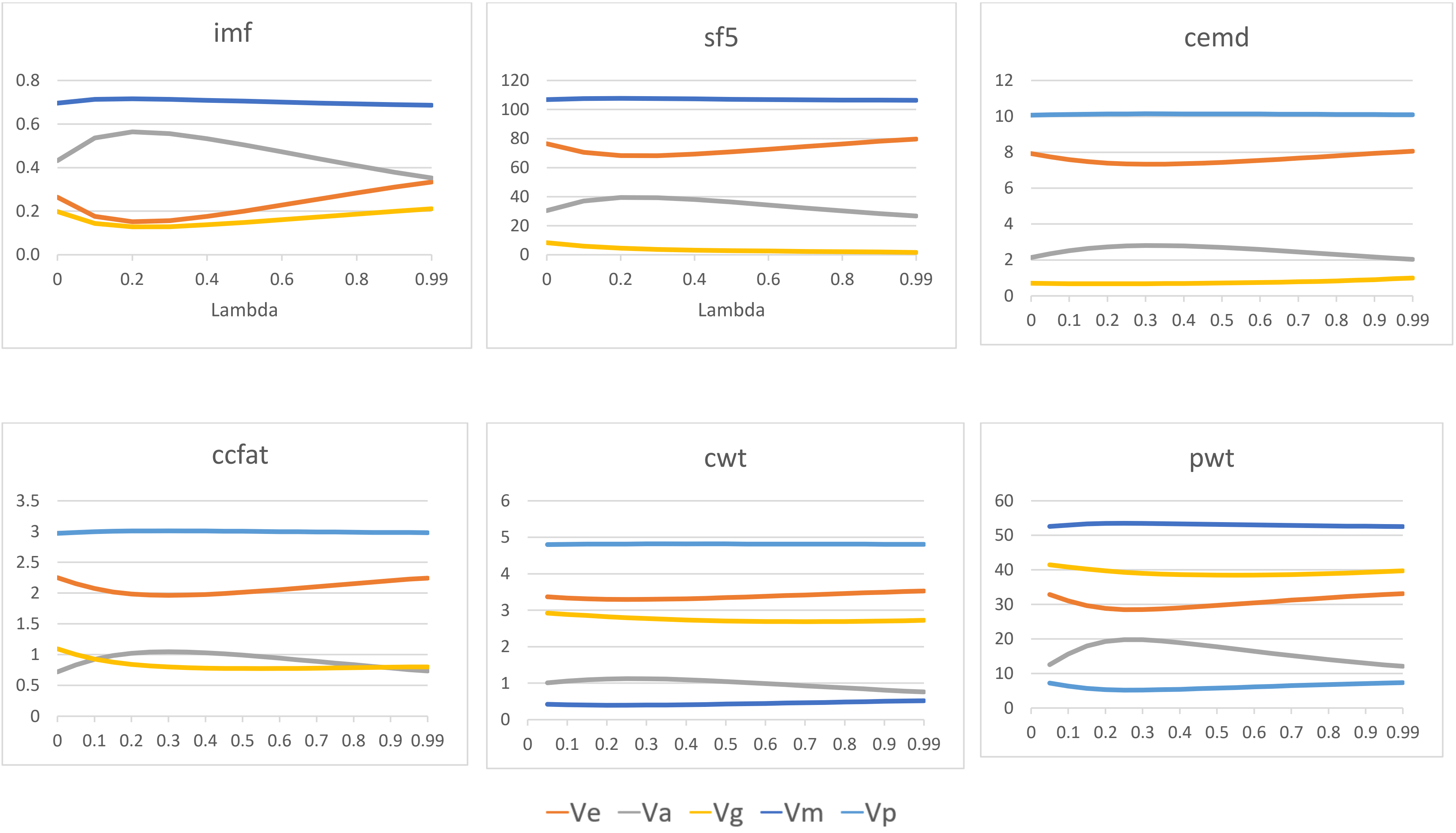


Figure 7: Correlation coefficient between EBVs and adjusted phenotypes (Acc1), the correlation coefficient between the EBVs from the full analysis and the partial analysis (Acc2) for both Vg = Va and Vg is /= Va for different lambda values ranging from 0.0 to 0.99 for IMF, SF5, CEMD, CCFAT, CWT AND PWT.

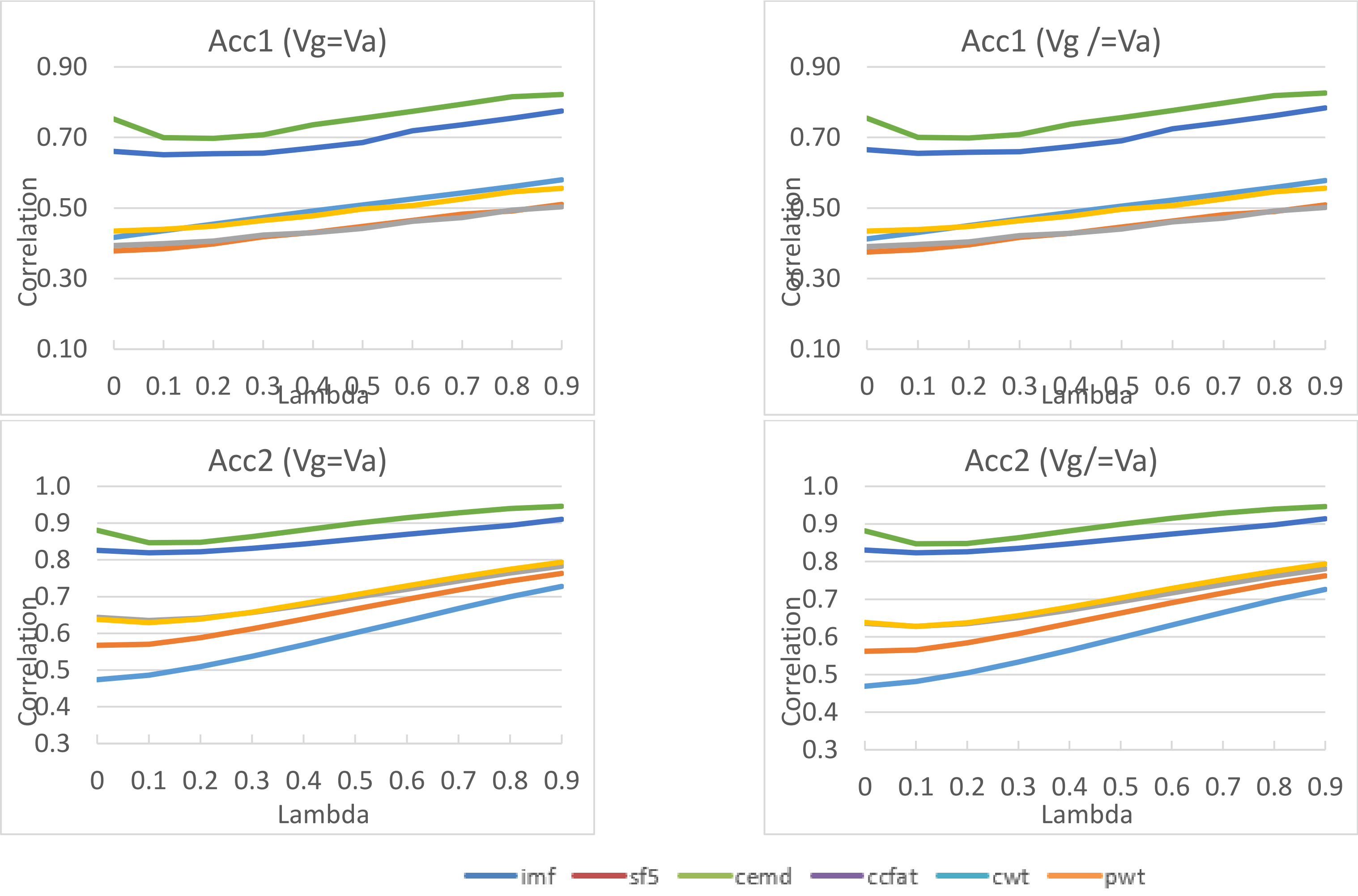
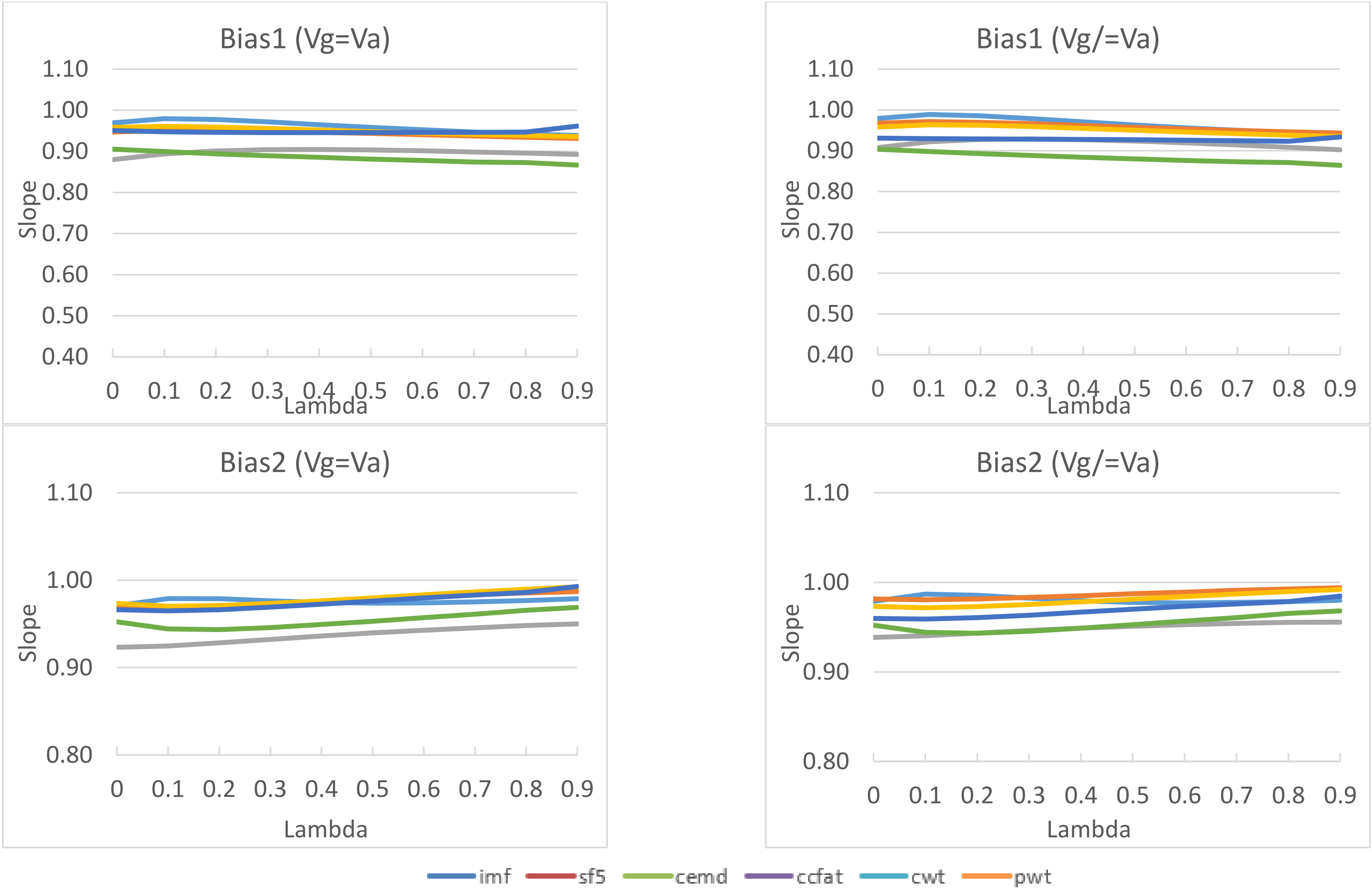


Figure 10: Regression slope between EBVs and adjusted phenotypes (Bias1), the regression slope between the EBVs from the full analysis and the partial analysis (Bias2) for both Vg = Va and Vg is /= Va for different lambda values ranging from 0.0 to 0.99 for IMF, SF5, CEMD, CCFAT, CWT AND PWT.



4.5 Expected benefits of genomic information from accuracies

The mean genomic accuracies for animals without phenotypes are presented by breed in Table **4**17. The breeds that have the largest mean averaged across all traits are Coopworths (0.341), followed by the Commercial Maternals (0.328) and the Border Leicester sheep (0.296). The breeds that had the smallest accuracies in the maternal run were the Poll Dorsets (0.215), followed by the Texels (0.221) and the White Suffolks (0.256), because these breeds have low representation in that analysis. These accuracies are split by trait group in

Figure **8**, where differences can be seen in the accuracies between the trait groups for various breeds. For example, Coopworths had higher body weight accuracies than carcase yield and eating quality accuracies. Accuracies were generally lower for wool traits and scrotal traits, and lowest for staple length and strength traits, for which there is very little reference population data.

Table 4. Mean genomic accuracies for maternal sheep without phenotypes

Breed	Mean	Std. Dev
Border Leicester (02)	0.296	0.0882
Corriedale (03)	0.288	0.0703
Coopworth (15)	0.341	0.0822
Poll Dorset (16)	0.215	0.0623
Texel (17)	0.221	0.0753
White Suffolk (23)	0.256	0.0891
Research (26)	0.288	0.0894
NZ Corriedale (83)	0.277	0.0695
Commercial Maternals (CM)	0.328	0.0787

Figure 8: Accuracy increases for maternal sheep without phenotypes split by trait groups

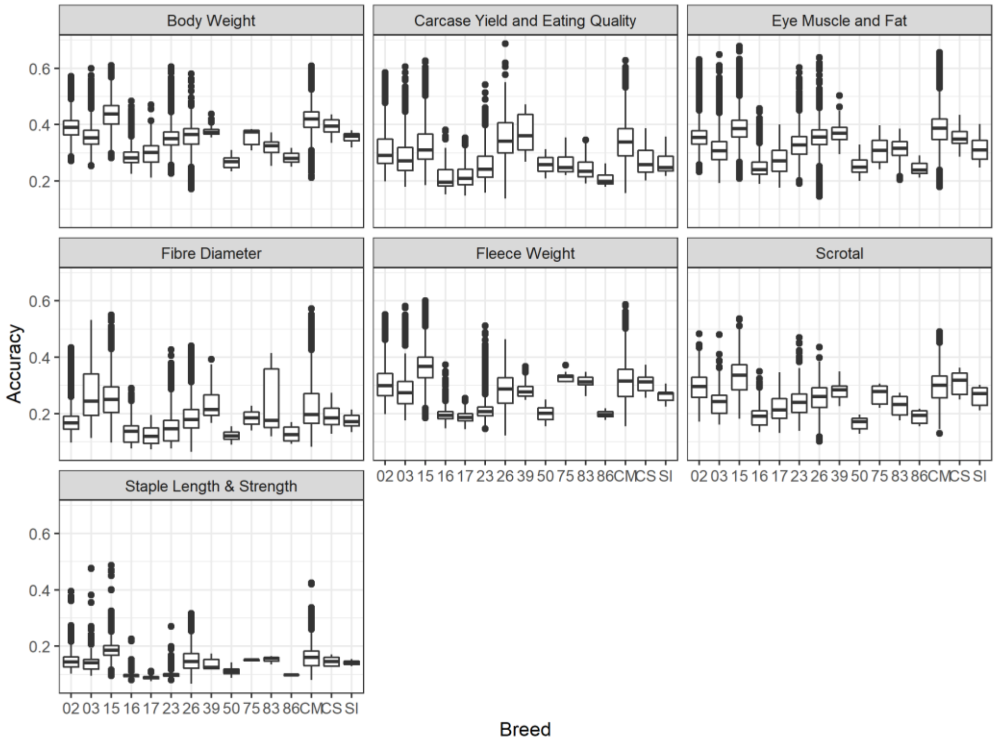
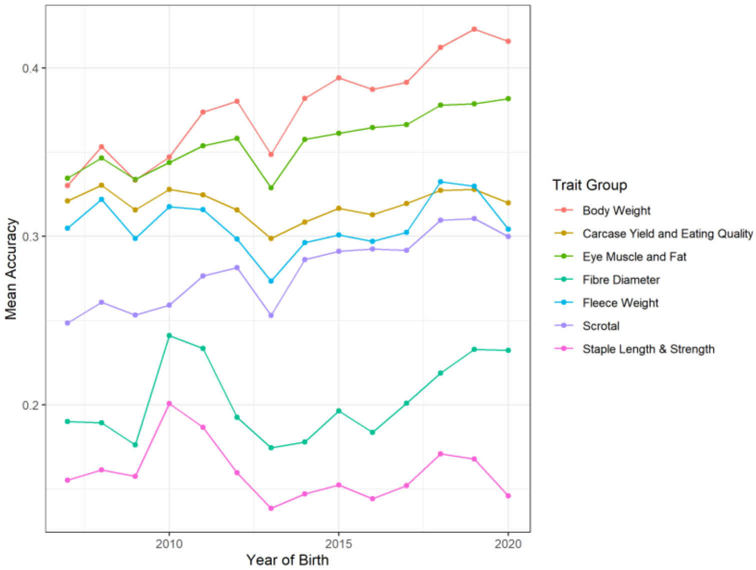


Fig. 12 summarises accuracies by year of birth and trait group. This plot shows that as the year of birth increases, the expected benefits from genomic information has increased, for body weight and eye muscle and fat traits. Fleece weight, carcase yield and eating quality traits stay roughly constant over time. These patterns reflect growth in genomic reference populations over time.

Figure 9: Mean accuracies for maternal sheep without phenotypes calculated within each year of birth and trait group. Years of birth have been restricted to animals born from 2007 onwards.



Mean accuracies from genomics for terminal sheep are presented in Table 18. The breeds that have the highest accuracies were Suffolk (0.295), the Australian and NZ Poll Dorsets (0.289 and 0.290, respectively) and the White Suffolk (0.284). The breeds that have the lowest accuracies were the Hampshire Down (0.203) and Southdown (0.205) breeds. In terms of trait groups (**Figure 10: Accuracy increases for terminal sheep without phenotypes split by trait groups**Figure 10), the fibre diameter, fleece weight and staple length and strength traits had the lowest benefit from genomics, which is expected as these traits are not routinely measured for terminal sire sheep. In terms of the accuracy changes over time (

Figure 114), accuracies for body weight have been increasing over time, while eye muscle and fat has stayed approximately static and carcase yield and eating quality traits have been decreasing.

Table 18. Mean accuracies across traits for terminal sheep without phenotypes

Breed	Mean	Std. Dev
Hampshire Down (11)	0.203	0.118
Southdown (14)	0.205	0.124
Coopworth (15)	0.239	0.122
Poll Dorset (16)	0.289	0.154
Texel (17)	0.227	0.134
Suffolk (19)	0.295	0.163
White Suffolk (23)	0.284	0.151
Research (26)	0.233	0.151
Dorper (40)	0.265	0.146
White Dorper (47)	0.248	0.132
NZ Poll Dorset (86)	0.290	0.151
Commercial Terminals (CT)	0.251	0.139

Figure 10: Accuracy increases for terminal sheep without phenotypes split by trait groups

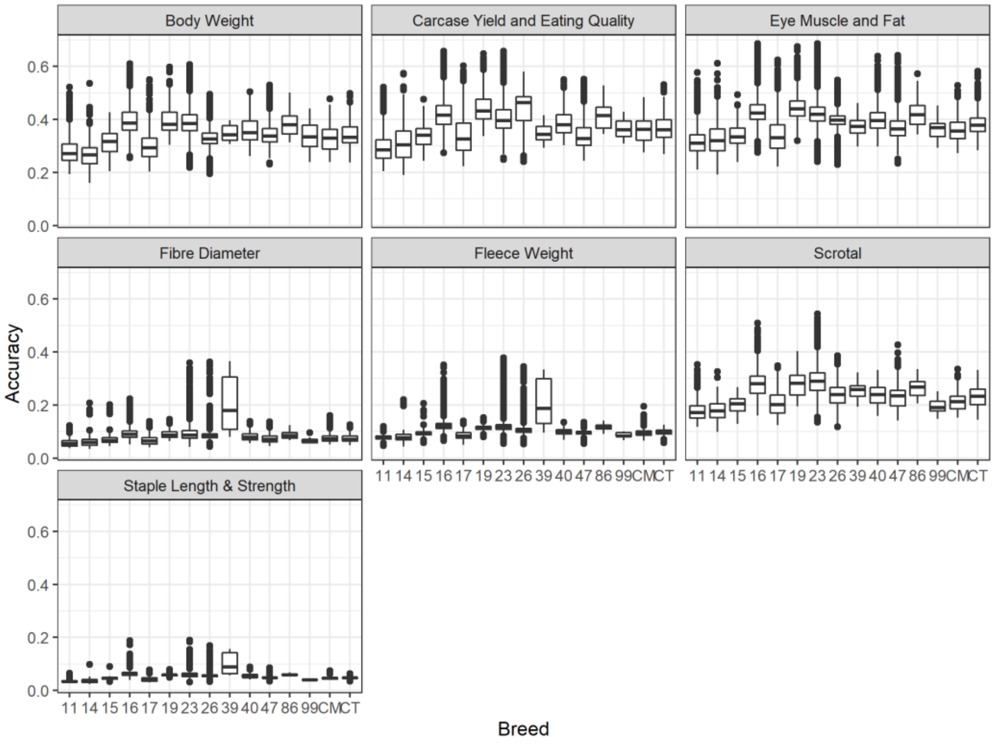
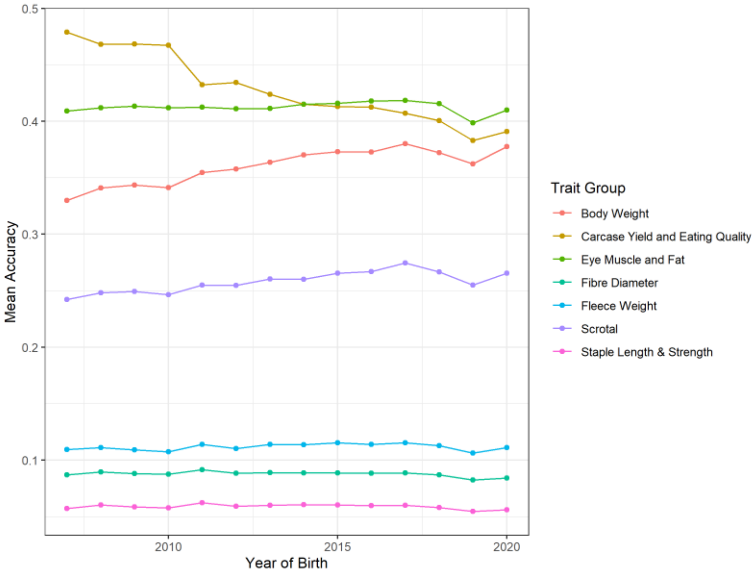


Figure 11: Mean accuracies for terminal sheep without phenotypes calculated within each year of birth and trait group. Years of birth have been restricted animals born during and after 2007.



For these comparisons in maternal and terminal breeds, we chose to examine only animals that did not have a phenotype. We note that for some well-recorded traits such as body weight the number of animals without a phenotype can be low. This means that in some cases the summary statistics may have more error for well-recorded traits.

In routine LAMBPLAN analyses, the lambda weighting parameter is used to blend genomic and pedigree information. Lambda is currently set to 0.5 in routine analyses, resulting in the amount of information arising from the genomics being reduced. Lambda has not been considered in the accuracies presented here, which means that the values presented here are best-case scenarios of the true accuracy increases that can be expected.

This study shows that the accuracy benefits from genomics are variable across different subsets of animals. Breeds with many animals with genotypes phenotypes will have the largest benefits from genomics. Breeds with fewer genotypes and phenotypes recorded will still benefit from genomics, but that benefit will be less than that observed in breeds with more phenotypes. The benefits from genomics also change over time, reinforcing the need for reference populations to be supported into the future.

4.6 SNPs to be added for genetic defects or monogenic traits.

4.6.1 Genetic Analysis of tail length in INF/RF research sheep data

Background and objectives

Tail docking at marking age at the second or third palpation tail joint, using knife, hot knife or rubber band, is a common management practice in Australian sheep. The main reason for this intervention is to prevent flystrike. However, tail docking may bring about some animal welfare discussion and selection for shorter tails could be an alternative. This study is looking at the genetic control of tail length and also genome wide association analysis to find significant chromosomal regions covering QTLs affecting tail length.

Methods

The objectives of the project were:

1. Genetic analysis of Tail length at birth and at marking in INF/RF research data, including:
    a. Investigation of significant environmental effects
    b. Evaluation of the variance components.
    c. Estimation of heritability.
2. Genomic analysis of Tail length in phenotyped and genotyped animals:
    a. Perform a GWAS using high density and whole genome sequence (WGS) data.
        i. Manhattan plot
        ii. Q-Q Plot
    b. Selection of the most significant SNPs to be considered in a SNP chip design

Summary of the data and heritability estimates

There were 6,231 tail length records in total, obtained from the INF and RF flocks Kirby and Katanning only. This decreased to 6,225 records after editing the raw data based on comments at recording (mainly broken tail). From 6173 there are 905 are at birth time and 5,210 records at marking time (10 to 44 days old). The rest (57 records) did not have an age at recording and was not used in analysis.

Statistical analysis

The significant fixed effects of the fitting model were: Year (2010, 2014. 2015, 2016, 2017), Flock (INF01, INF08), Gender (male, female),SireBreed (15 levels), DamBreed (Merino, research , crossbreds and commercial maternal), age at observation (birth or marking) and Birth Type (1,2,3 and 4). The random effect of the model were animal additive genetic effect (fitted through pedigree) and residual.

Table 19. Summary statistics and h2 for Tail Length records in INF data

	Min, Max, Average , SD (cm)	Phen-Var	Genetic-Var	h^2
All data (n=6225)	7, 38, 23.2, 3.85	8.58 (0.17)*	4.68 (0.45)	0.54 (0.05)
At birth (n= 906)	12, 29, 20.01, 2.68	6.60 (0.37)	4.16 (0.92)	0.63 (0.12)
At marking (n= 5319)	0.0 ,41 ,23.87, 3.75	9.47 (0.20)	4.47 (0.51)	0.47 (0.05)

*: The parameter estimates are followed by the standard error.

GWAS and selection of highly significant sequence variants

A GWAS was performed using imputed WGS data on sheep Tail Length (4,138 animals with both phenotypes and genotypes) and based on applying a linear mixed model fitting individual SNP plus a genomic relationship matrix (G) made out of 50k standard genotypes on Adjusted phenotypes

(Figure 10). Adjusted phenotypes was based on accounting for environmental effects and also genetic groups derived from genotypic information (GenoQ-Matrix).

Selection of highly significant SNPs was according to –Log 10 PValues (>=4.5), and then pairwise pruning for high LD>=0.80 and considering MAF >= 0.15. A Manhattan plot for Tail length is in Appendix 8.3.

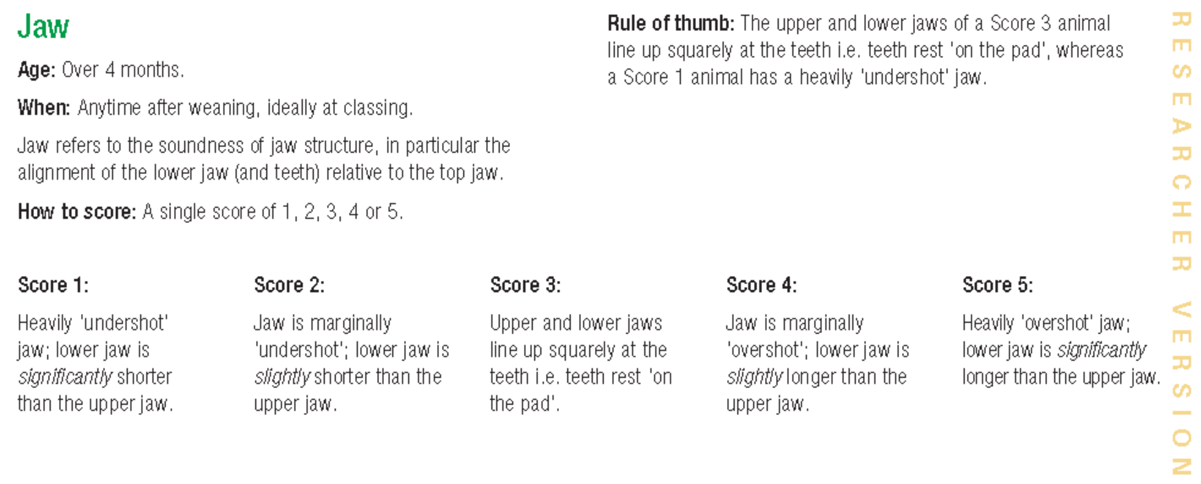
The conclusion is that Tail Length is a highly heritable trait with a heritability of around 40% and with some clear QTL regions. The top SNPs in the main QTL regions explain 25% of the genetic variation. Therefore, tail length can be selected for and there are some useful genetic markers that could be used to achieve relatively high accuracies of genomic prediction.

4.7 Genetic Analysis of Jaw abnormality (JAWR)

Background and objectives

Jaw abnormalities are present in many sheep breeds and are indicated as failure of the incisor teeth to properly meet the dental pad. A jaw is undershot if the incisor teeth extend forward past the dental pad; it is overshot if the teeth hit in back of the dental pad (this condition is known as parrot mouth). Figure 19 shows different degrees of severity of the jaw defect and also the scoring schedule for recording jaw abnormality. The objectives of this study was to find chromosomal regions and genetic variants in significant association with this defect.

Figure 22. Jaw score card



Jaw

Age: Over 4 months.

When: Anytime after weaning, ideally at classing.

Jaw refers to the soundness of jaw structure, in particular the alignment of the lower jaw (and teeth) relative to the top jaw.

How to score: A single score of 1, 2, 3, 4 or 5.

Rule of thumb: The upper and lower jaws of a Score 3 animal line up squarely at the teeth i.e. teeth rest 'on the pad', whereas a Score 1 animal has a heavily 'undershot' jaw.

Score 1: Heavily 'undershot' jaw; lower jaw is *significantly* shorter than the upper jaw.

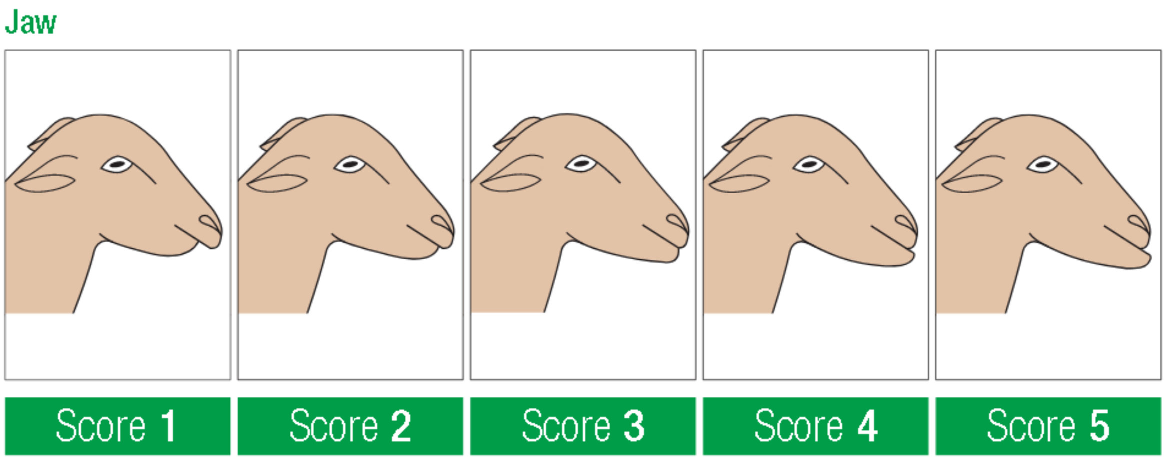
Score 2: Jaw is marginally 'undershot'; lower jaw is *slightly* shorter than the upper jaw.

Score 3: Upper and lower jaws line up squarely at the teeth i.e. teeth rest 'on the pad'.

Score 4: Jaw is marginally 'overshot'; lower jaw is *slightly* longer than the upper jaw.

Score 5: Heavily 'overshot' jaw; lower jaw is *significantly* longer than the upper jaw.

RESEARCHER VERSION



Methods

Data, phenotypes and genotypes

22,946 jaw score extracted from INF and RF research data base. A jaw score card is shown in Figure 22. These are termed JAWR scores, as opposed to JAW score that are available in the Sheep Genetics database, but scored on a different scale. Among these 22,946 animals with a JAWR phenotype we had genotypes records mostly typed with low or medium density genotype panel in which imputed to HD genotypes and then to sequence level. Tables 20 and 21 shows the distribution of the phenotypes by breed and breed of sire, respectively.

Table 20. Distribution of phenotypes for jaw by animal breed group.

	Breed Index (animals)							
JAWR Score	BLxM	MATxM	MxM	NA	TxBLxM	TxM	TxMAT	Total
1	2	22	17	35	1	11	11	99
2	4	224	318	62	3	95	159	865
3	128	3,614	5,767	7,221	223	2,439	2,493	21,885

4	NA	12	55	5	NA	8	6	86
5	NA	1	7	1	NA	NA	1	10
Total	134	3,873	6,164	7,324	227	2,553	2,670	22,945

Table 21. Distribution of phenotypes for jaw by sire breed group.

	Sire Breed						
JAWR	Follower	Maternal	Merino	NA	Syndicate	Terminal	Total
1	NA	21	16	42	NA	20	99
2	NA	221	311	82	2	249	865
3	3	3,551	5,498	7,948	14	4,871	21,885
4	NA	12	54	5	NA	15	86
5	NA	1	6	2	NA	1	10
Total	3	3,806	5,885	8,079	16	5,156	22,945

Repeated measurement was also studied, which showed in many cases the severity of jaw abnormality is decreasing in older ages.

Polygenic analysis of JAWR

Mixed model analysis using an animal model was based on 22,945 phenotypic records and the analysis involved a total of 51,187 animals linked to the data via pedigree. The model included fixed effects of flock (9 levels), drop (11 levels) and age-stage (6 levels). The estimated variance components were 0.0026, 0.0547 and 0.0573 for additive genetic, residual and phenotypic variance, giving an estimated heritability value of 0.045 with a standard error of 0.01.

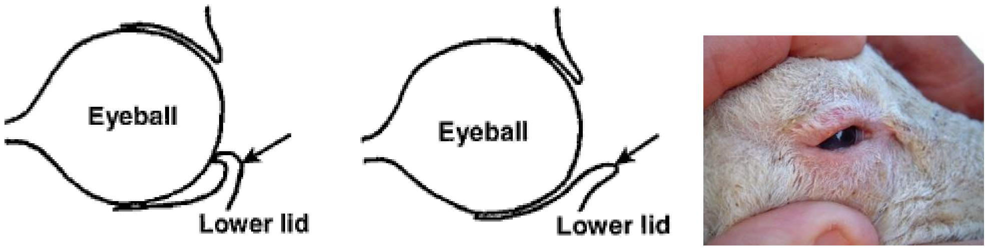
GWAS analysis

A Manhattan plot for FAWR is in Appendix 8.3. The conclusion is that JAWR is a lowly heritable trait and results do not show any significant chromosomal regions explaining phenotypic variation.

4.8 Genetic Analysis of Entropion (turned in eyelid) in sheep data.

Background and objectives

Entropion is a common congenital disorder in lambs and is characterised by the turning in of one or both lower eyelids. In-turned hairs rub on the cornea and cause severe irritation and can lead to blindness if not treated. Treatment is commonly done by unrolling the eyelid and/or surgically stapling it in correct alignment for a few weeks. The condition is seen in most sheep breeds, and is considered heritable although the nature of the inheritance is unknown. Figure 23 explains the Entropion and Ecyropion condition.



Entropion **Ectropion** **Entropion in a lamb**

Figure 23. Diagram of the Entropion condition

The objectives of this study were to perform a genetic analysis for this disorder and to find potential chromosomal regions and genetic variants in significant association with this defect.

Phenotypes

In total 5,405 phenotypes form one Coopworth flock were available for this analysis in which 375 and 195 animals had 50k genotypes and imputed sequence data available respectively. Scoring system was as below:

0 = normal eye lid's

1 = one eye has a turned-in lid

2 = two eyes have turned-in lids

Table 22 and 23 show the number of phenotypes recorded per year for all the data, data with 50k genotypes available and data with imputed sequence data available.

Table 22. Overall number of records across years.

Recording Year	**Entropion Score**			**Total**
	0	**1**	**2**	
2013	670	55	34	759
2014	583	44	45	672
2015	732	61	31	824
2016	765	82	56	903
2017	956	82	53	1091
2018	998	102	55	1155
Total	4704	**426**	**274**	5404

Table 23. Number of records across different years for animals with 50k genotypes.

Recording Year	**Entropion Score**			Total
	0	1	2	
2013	3	0	1	4
2014	167	12	12	191
2015	68	9	5	82
2016	69	14	15	98
Total	307	**35**	**33**	375

Table 24. Number of records across different years for animals with imputed sequence genotypes.

Recording Year	**Entropion Score**			Total
	1	3	5	
2013	3	0	1	4
2014	167	12	12	191
Total	170	**12**	**13**	195

Genetic analysis

A GREML performed on 50k genotyped animals to find the additive genetic variance component and heritability. Table 14 shows the variance components and the heritability associated with standard error.

Table 26. Variance components and Heritability estimate of Entropion based on GREML on 375 animals with phenotypes and genotypes.

Component	Value	SE
Ve	1.007	0.17
Va	0.499	0.20
h^2	0.331	0.12

Genome wide association study (GWAS):

GWAS performed based on linear mixed model and using phenotypes and 50k genotypes on 375 animals or phenotypes and genotypes on 195 animals with imputed sequence. GWAS results are reported Appendix 8.3. Results are promising and show some significant regions on chromosomes 1 and 11, particularly when based on sequence data. However, because of the small size of the data (25 affected animals) the power of analysis is not very high. We are continuing to increase the number of genotyped animals and to impute them to sequence level for further analysis.

5. Conclusion

5.1 Key findings

- A new set of informative SNPs and application tools were developed for economic traits in sheep including slaughter, eating quality, reproduction and tail length traits.
- Informative SNPs were validated and showed up to 0.15 absolute value enhancement in prediction accuracy for eating quality (EQ) traits.
- Selected informative SNPs were validated for minor breeds and for animals less strongly related to the reference flock and showed improvement in prediction accuracy (0.06 higher absolute value of prediction accuracy).
- Genetic evaluation pipelines were tested and adapted to accommodate informative SNPs which showed improvement in accuracy of ASBVs for slaughter and EQ traits.
- GWAS confirmed a larger number of chromosomal regions in significant association with carcass and eating quality traits. These regions were used to prioritise informative SNPs.
- Analysis of reproduction traits showed regions associated with higher litter size (in the GDF9 region, plus numerous novel significant regions which need further investigation).
- Analysis of tail length showed two highly significant regions controlling the trait. Information would be useful in genetically reducing tail length.

5.2 Benefits to industry

- A new set of prioritised SNPs (top SNPs) would be directly useful for upgrading the current Ovine SNP chip and would be useful for improving the national genetic evaluation pipeline for slaughter, eating quality, reproduction, ewe on-farm productivity and genetic control of tail length.
- The methodology developed and tools for inclusion of top SNPs such as fitting an additional genomic relationship matrix for informative SNPs may be useful in upgrading Sheep Genetics evaluations.
- The results of GWAS would be useful in further fine mapping of the significant chromosome regions.

6. Future research and recommendations

High quality phenotypes and genotypes are critical in successful practical research in animal genetics particularly for traits with lower heritability. As a result, larger volumes of high-quality phenotyping and genotyping for traits such as eating quality traits and reproduction traits are recommended.

Larger numbers of genome sequencing on key animals in each main research breed group (Merinos, maternal and terminal breeds) would be very useful to enhance the accuracy of genotype imputation, and hence financial support for whole genome sequencing plus upgrading the computing hardware and essential software development support are highly recommended.

Analysis of reproduction traits showed potential new significant regions which had not been reported in literature before. Further investigation based on more advanced genomic research is required in this field.

For genetic defects a larger phenotypic and advanced genotypic database is required. Cooperation with other research institutes on data sharing is also recommended. It should also be noted that the OMIA database (https://www.omia.org/home/) contains information about monogenic traits, including often information about the actual causal variants. OMIA contains 79 monogenic variants in sheep (Appendix 8.5).

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8. Appendix

8.1 Manhattan plots of carcase and eating quality traits

8.1.1 GWAS results of combined data set

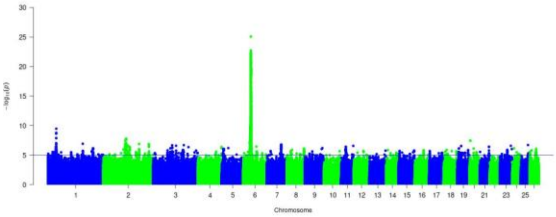


Figure 1. Carcase Fat (CCFAT)

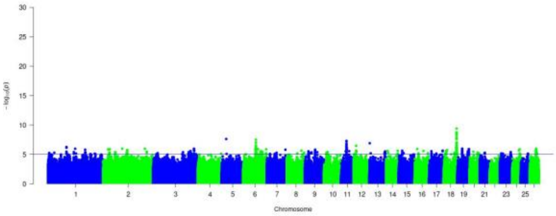


Figure 2. Carcase Eye Muscle Depth (CEMD)

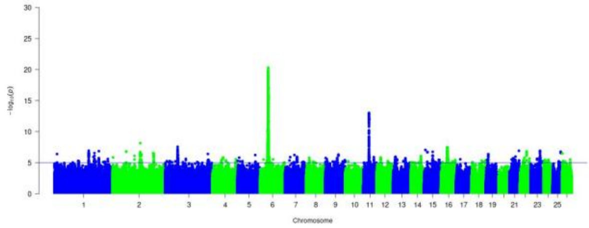


Figure 3. Carcase Weight(CWT)

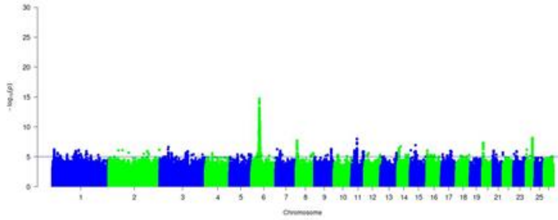


Figure 4. Dress percentage (DRESS)

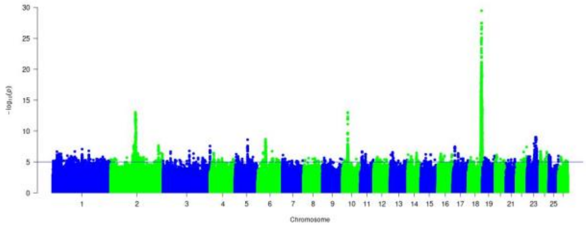


Figure 5. Intra Muscular Fat (IMF)

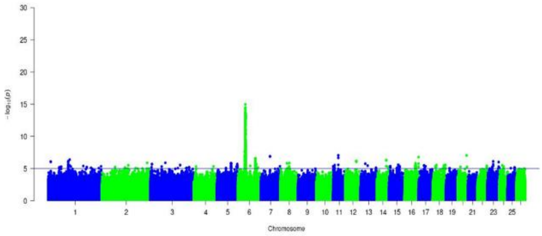


Figure 6. Lean Meat Yield (LMY)

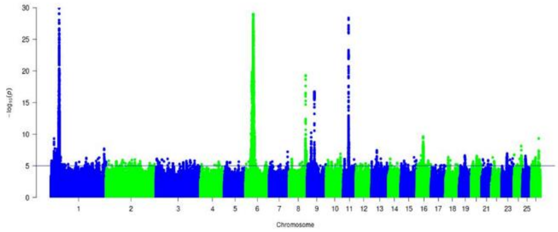


Figure 7. Post weaning Fat (PCF)

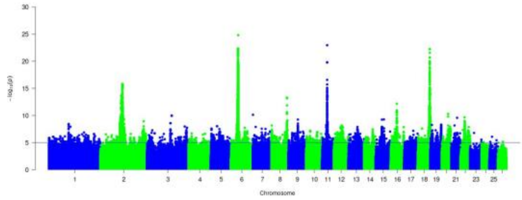


Figure 8. Post Weaning Eye Muscle Depth (PEMD)

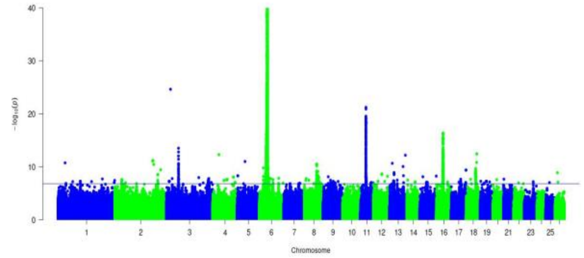


Figure 9. Post Weaning weight (PWT)

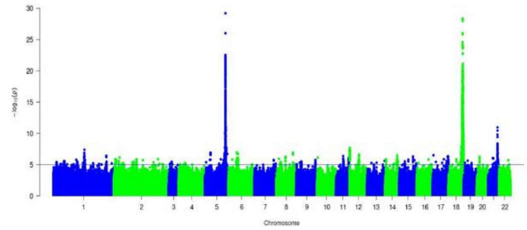


Figure 10. Shear Force Day 5 aging (GWAS) for SF5

8.1.2 GWAS results of maternal data set

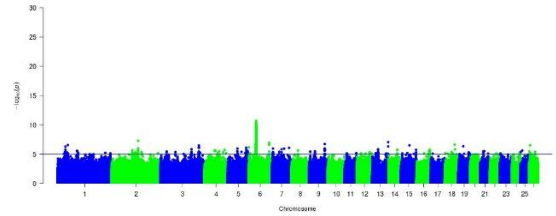


Fig 1. Carcase fat (CCFAT)

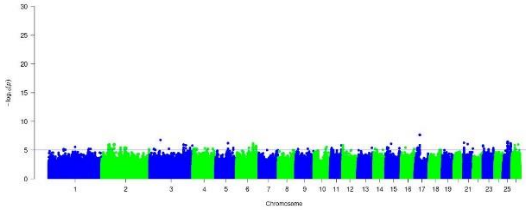


Fig 2. Carcase Eye Muscle Depth (CEMD)

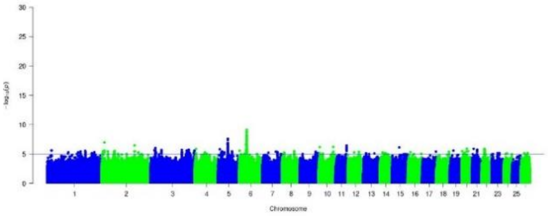


Fig 3. Carcase Weight (CWT)

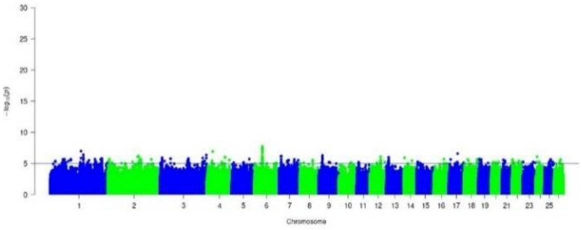


Fig 4. Dress Percentage (DRESS)

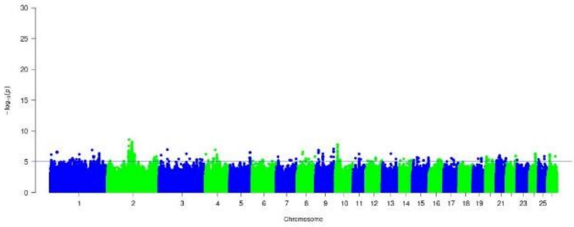


Fig 5. Intra Muscular Fat (IMF)

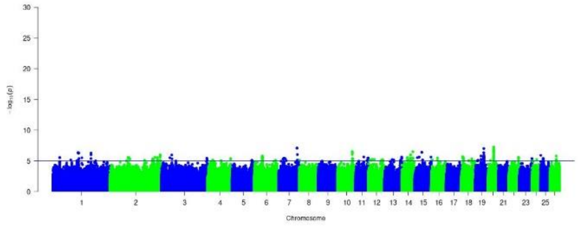


Fig 6. Lean Meat Yield (LMY)

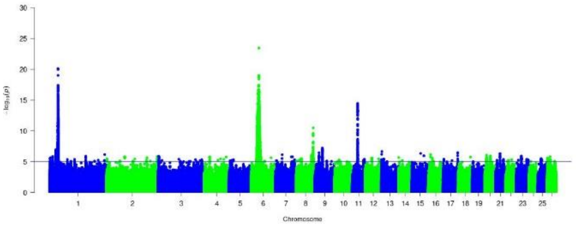


Fig 7. Post Weaning Fat PCF)

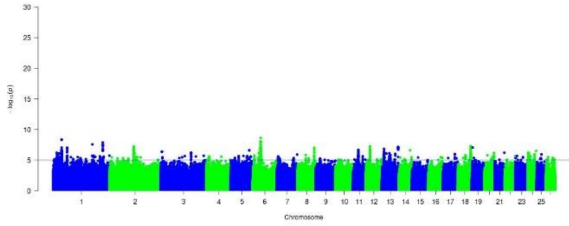


Fig 8. Post Weaning Eye Muscle Depth (PEMD)

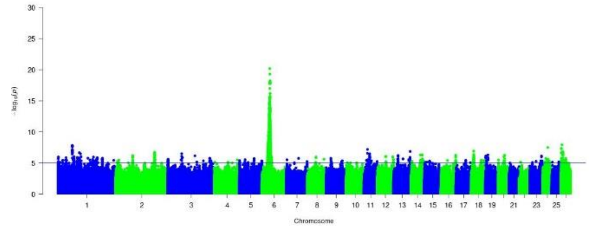


Fig 9. Post Weaning Weight (PWT)

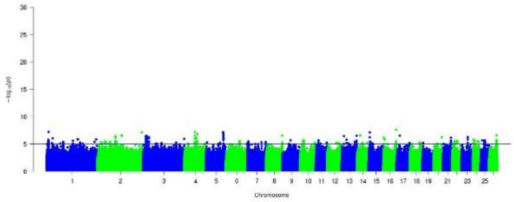


Fig 10. Shear Force Day 5 aging (SF5)

8.1.3 GWAS results of terminal data set

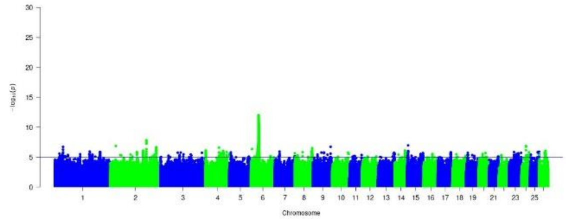


Fig 1. Carcase Fat (CCFAT)

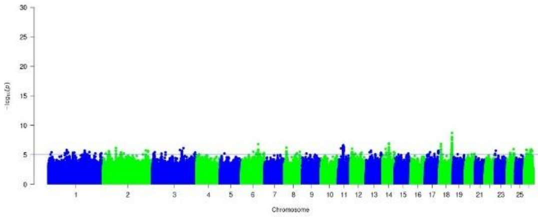


Fig 2. Carcase Eye Muscle Depth (CEMD) in terminals

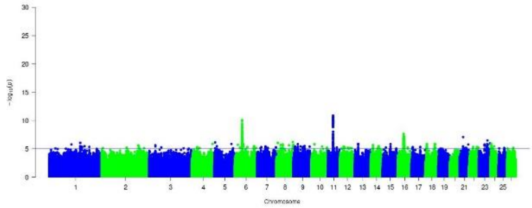


Fig 3. Carcase Weight (CWT)

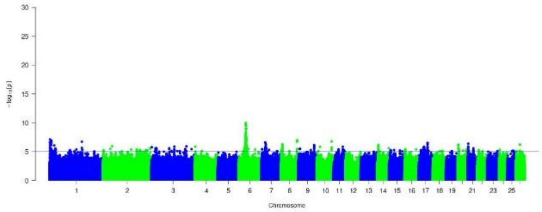


Fig 4. Dressing Percentage (DRESS)

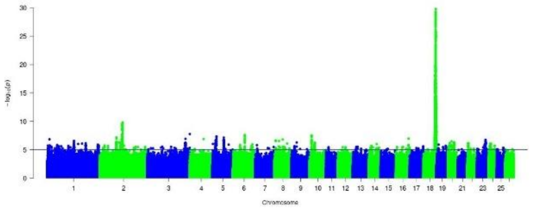


Fig 5. Intra muscular Fat (IMF)

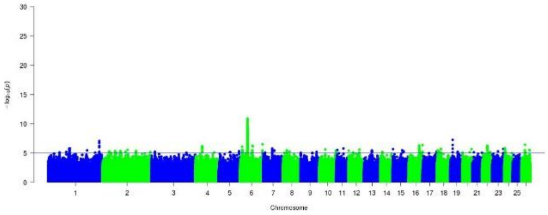


Fig 6. Lean Meat yield (LMY)

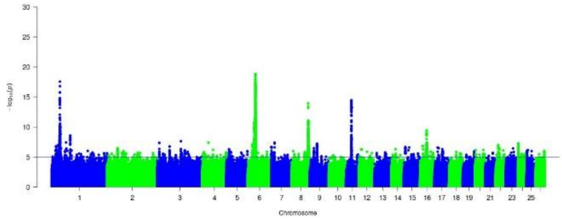


Fig 7. Post Weaning Fat (PCF)

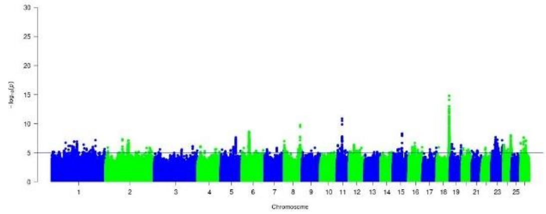


Fig 8. Post Weaning Eye Muscle Depth (PEMD)

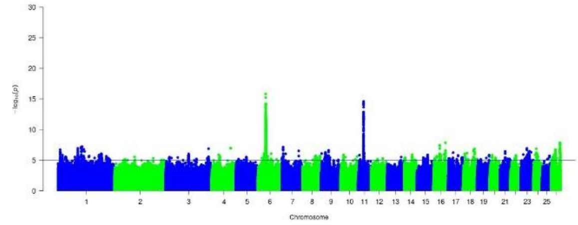


Fig 9. Post Weaning Weight (PWT0

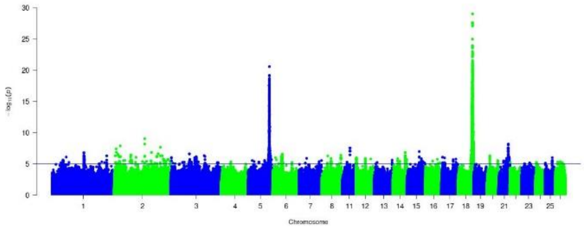


Fig 10. Shear Force at day 5 aging (SF5)

8.1.4 GWAS results of Merino data set

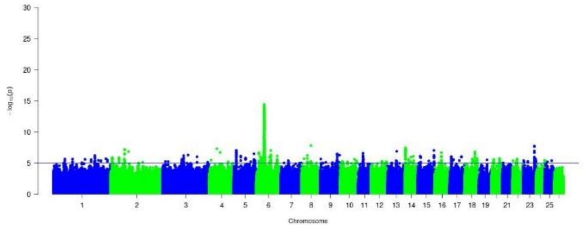


Fig 1. Carcase Fat (CCFAT)

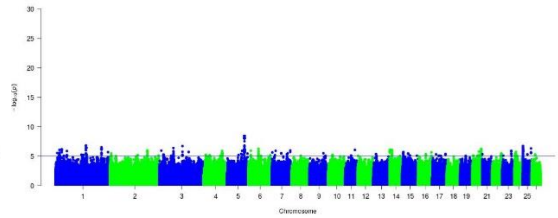


Fig 2. Carcase Eye Muscle Depth (CEMD)

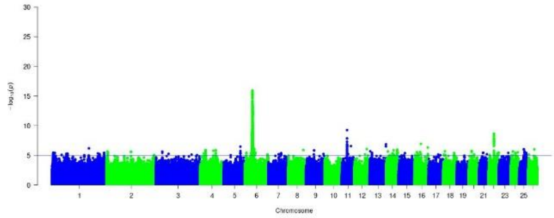


Fig 3. Carcase Weight (CWT)

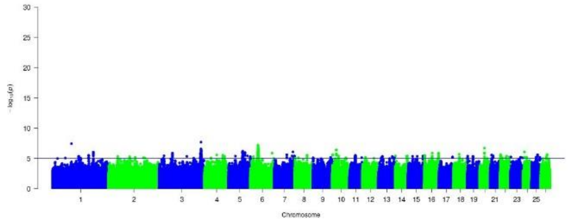


Fig 4. Dress Percentage (DRESS)

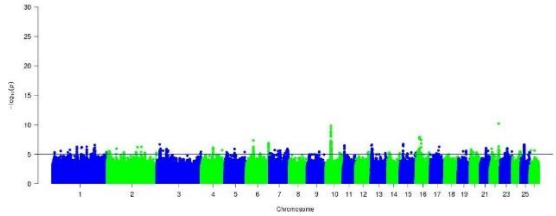


Fig 5. Intra Muscular Fat (IMF)

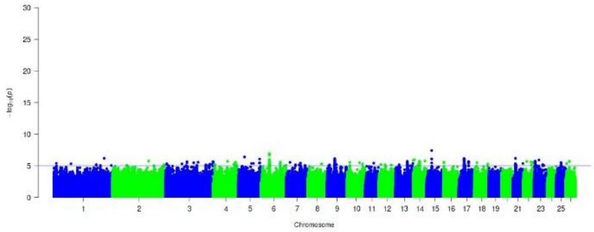


Fig 6. Lean Meat yield (LMY)

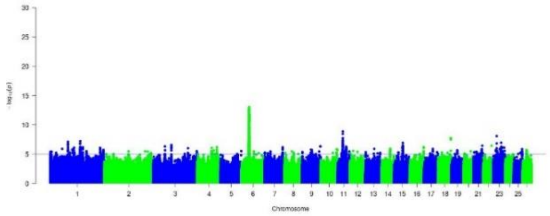


Fig 7. Post Weaning Fat (PCF)

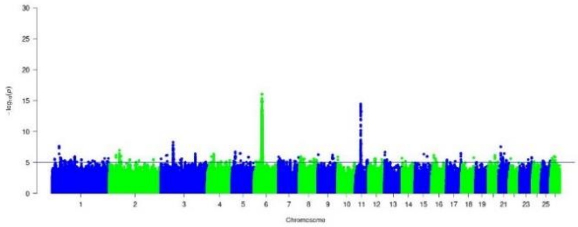


Fig 8. Post Weaning Eye Muscle Depth (PEMD)

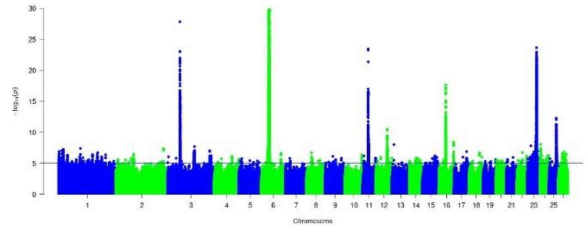


Fig 9. Post Weaning Weight (PWT)

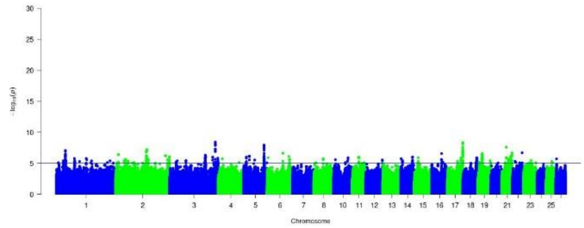


Fig 10. Shear Force at day 5 aging

8.2 Manhattan plot of reproduction and ewe on-farm productivity traits

8.2.1 GWAS results of maternal breeds

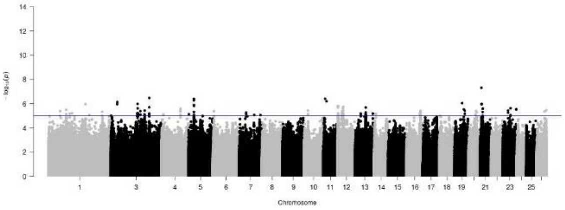


Figure 1. Yearling Conception (YCON).

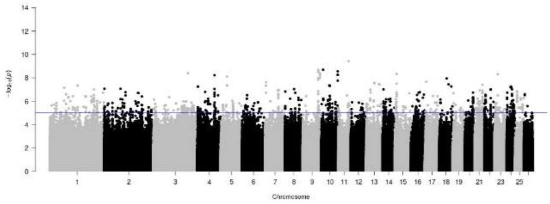


Figure 2. Adult Conception (CON)

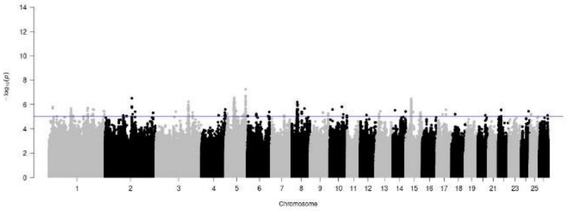


Figure 3. Yearling Litter Size (YLS)

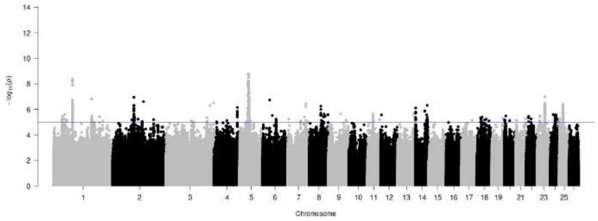


Figure 4. Adult Litter Size LS)

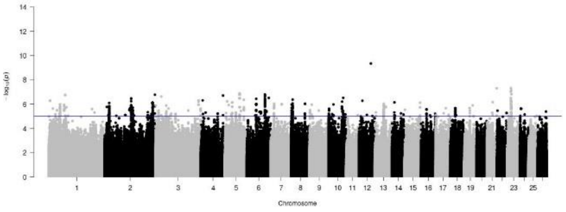


Figure 5. Yearling Rearing Ability .

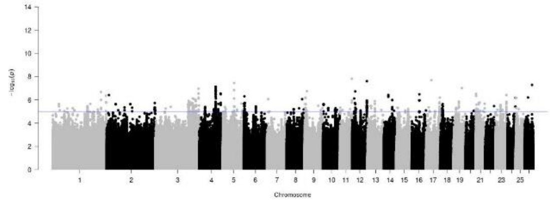
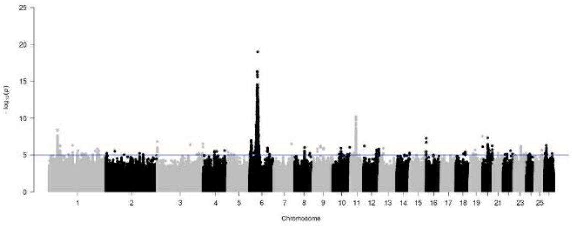


Figure 6.Adult Rearing Ability in maternals



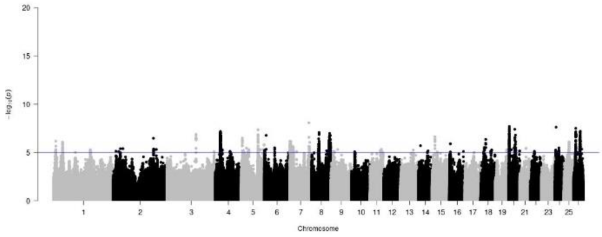


Figure 7. Ewes Adult Weight (AW).

Figure 8. Ewes Body Condition Score (BCS)

8.2.2 GWAS results for the Merino data set

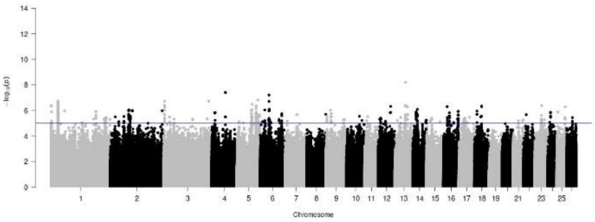


Figure 1. Yearling Conception (YCON)

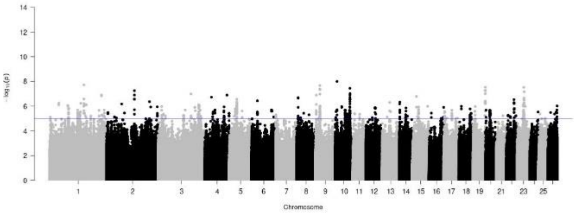


Figure 2. Adult Conception (CON)

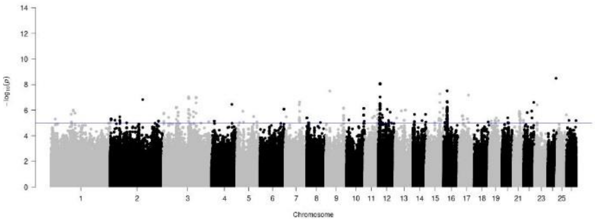


Figure 3. Yearling Litter Size (YLS)

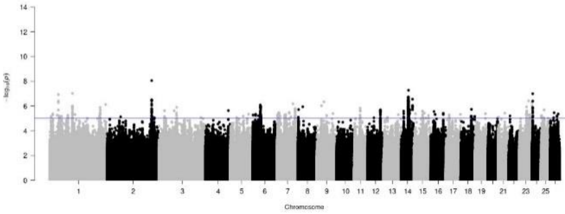


Figure 4. Adult Litter Size (LS)

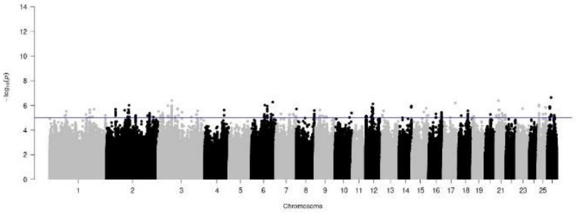


Figure 5. Ewes Rearing ability in Merinos.

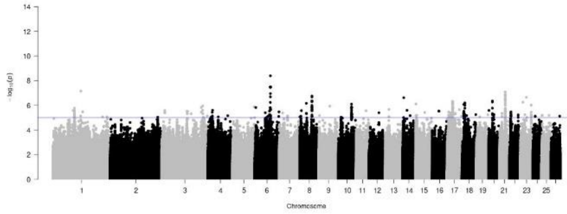


Figure 6. Maternal Behaviour Score in Merinos

8.3 GWAS results of genetic defects

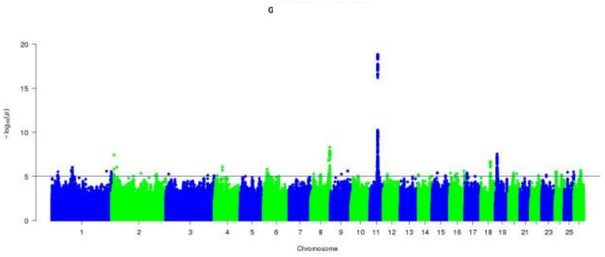


Figure 1. Tail length

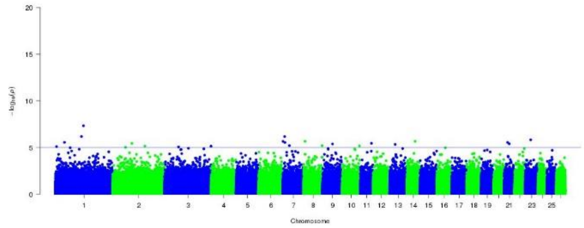


Figure 2. Jaw abnormality (undershot and overshot)

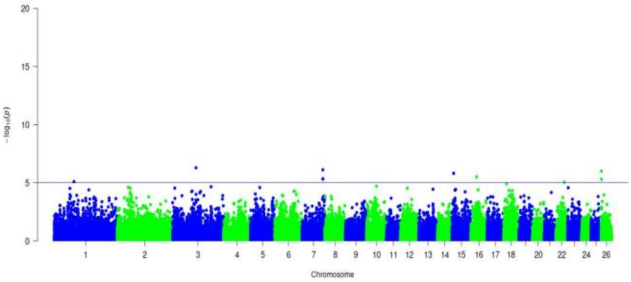


Figure 3. Entropion

8.4 List of top SNPs by trait

SNP names are indicated by chromosome number and base pair (nucleotide) position

MAF is minor allele frequency

p-value is significance level in GWAS

Appendix 8-2

8-2-1. Selected SNP for CCAFT

SNP	MAF	p-value	SNP	MAF	p-value	SNP	MAF	p-value
1:173062371	0.044	2.13E-06	3:86627992	0.007	7.22E-07	6:35498049	0.436	3.18E-10
1:173353586	0.027	2.17E-06	3:95579868	0.403	2.18E-07	6:35507850	0.332	3.02E-07
1:173353618	0.05	1.21E-07	4:117755789	0.35	4.40E-07	6:35516700	0.23	1.77E-08
1:173940885	0.02	1.93E-06	4:117755960	0.265	6.88E-07	6:35530719	0.24	1.11E-06
1:219056594	0.008	2.38E-06	4:91050237	0.008	2.56E-06	6:35535684	0.104	8.22E-10
1:224715699	0.114	7.06E-07	5:32725046	0.344	6.51E-07	6:35554926	0.461	2.78E-07
1:23094173	0.049	2.86E-06	5:9214024	0.03	9.49E-07	6:35606116	0.258	2.80E-06
1:33415963	0.372	3.11E-06	6:23767901	0.069	2.95E-06	6:35666809	0.021	2.49E-06
1:38655906	0.249	6.81E-07	6:31444398	0.323	2.28E-06	6:35695267	0.051	9.34E-07
1:38848575	0.117	1.59E-06	6:32634406	0.032	8.79E-09	6:35720400	0.297	2.81E-06
1:38995166	0.087	3.58E-07	6:32634462	0.022	1.40E-06	6:35743422	0.488	2.58E-08
1:40599007	0.128	2.74E-06	6:32635229	0.023	5.99E-08	6:35852208	0.107	1.01E-06
1:40634718	0.202	9.54E-08	6:32707254	0.096	9.05E-08	6:35867874	0.311	2.79E-06
1:40670198	0.08	1.69E-09	6:32711144	0.265	7.91E-08	6:35878794	0.25	3.55E-11
1:40684243	0.165	5.86E-07	6:32870332	0.298	9.25E-07	6:35913693	0.356	5.32E-08
1:40804742	0.206	2.83E-06	6:32912844	0.496	1.98E-06	6:35929864	0.24	3.05E-06
1:40848347	0.125	1.29E-08	6:32977319	0.044	1.56E-06	6:35936351	0.178	1.21E-06
1:40903761	0.119	3.38E-10	6:33003096	0.102	2.34E-06	6:35961654	0.258	1.14E-08
1:40945325	0.477	1.22E-06	6:33003623	0.152	2.53E-06	6:35963072	0.249	1.32E-11
1:41001723	0.336	1.93E-06	6:33071880	0.49	1.13E-06	6:35965698	0.403	4.45E-11
1:41021483	0.402	3.36E-07	6:33103102	0.054	1.14E-07	6:35966405	0.045	1.52E-07
1:41174047	0.137	1.11E-06	6:33206019	0.092	9.20E-07	6:35966879	0.052	8.72E-11
2:100922291	0.053	1.09E-06	6:33841448	0.448	1.71E-06	6:35991380	0.376	1.75E-07
2:109397462	0.035	8.22E-07	6:33858567	0.432	1.82E-08	6:36010136	0.209	3.14E-06
2:110028263	0.039	3.84E-08	6:33858848	0.212	1.78E-07	6:36019095	0.034	1.44E-06
2:116230968	0.035	1.52E-06	6:33928624	0.5	5.59E-08	6:36045974	0.225	4.84E-08
2:123492885	0.023	3.21E-07	6:33942276	0.313	7.38E-09	6:36057406	0.418	5.95E-07
2:132458429	0.01	1.29E-06	6:33950409	0.237	4.38E-07	6:36087980	0.403	2.60E-10
2:163977138	0.306	3.05E-06	6:34017160	0.155	2.84E-06	6:36091302	0.18	2.70E-06
2:179525769	0.005	9.85E-07	6:34041575	0.5	2.58E-08	6:36092348	0.467	1.90E-07
2:179848714	0.009	2.03E-06	6:34391905	0.302	1.07E-06	6:36099144	0.217	3.06E-06
2:228103010	0.144	3.50E-07	6:34442652	0.291	2.28E-06	6:36155169	0.202	1.91E-06
2:228161305	0.254	1.36E-07	6:35138403	0.177	2.71E-08	6:36155985	0.125	2.12E-08
2:228958101	0.379	2.34E-06	6:35141343	0.458	7.35E-07	6:36386041	0.481	2.40E-06
3:100532343	0.152	2.86E-06	6:35159511	0.119	1.19E-06	6:36397120	0.399	2.21E-11
3:115057787	0.105	2.61E-07	6:35181582	0.353	1.50E-06	6:36402740	0.135	2.33E-06
3:115570078	0.008	1.73E-06	6:35190895	0.29	7.87E-07	6:36405655	0.486	7.78E-08
3:149793255	0.18	1.36E-06	6:35192394	0.211	2.28E-06	6:36407873	0.349	2.23E-08
3:149835623	0.281	1.53E-06	6:35229033	0.493	2.25E-07	6:36416658	0.154	7.87E-14
3:149854479	0.327	2.06E-06	6:35229559	0.259	1.20E-07	6:36416848	0.263	3.18E-18
3:149865282	0.24	2.23E-06	6:35236143	0.31	2.04E-09	6:36418606	0.461	1.05E-07
3:153693336	0.375	2.08E-07	6:35236570	0.22	8.42E-07	6:36429324	0.307	2.56E-06
3:176979443	0.008	4.49E-07	6:35246276	0.161	1.05E-06	6:36453411	0.455	1.32E-08

3:215319972	0.017	1.70E-06	6:35429074	0.175	9.63E-09	6:36455904	0.386	2.50E-09
3:72710527	0.151	1.53E-06	6:35434302	0.093	5.52E-07	6:36456235	0.295	6.92E-07
3:86140654	0.005	2.87E-06	6:35495306	0.065	4.16E-07	6:36457365	0.131	2.35E-06

8-2-2. Selected SNP for CCAFT (continued)

SNP	MAF	p-value	SNP	MAF3	p-value	SNP5	MAF	p-value
6:36466037	0.306	1.45E-06	6:36832552	0.088	6.49E-07	6:36981300	0.437	2.69E-14
6:36469220	0.122	1.13E-10	6:36834137	0.062	4.52E-11	6:36982738	0.034	1.82E-06
6:36469985	0.44	4.43E-07	6:36835643	0.428	1.52E-09	6:36988013	0.189	2.88E-06
6:36471430	0.374	7.78E-13	6:36837272	0.053	9.13E-08	6:36988094	0.469	6.75E-07
6:36477126	0.205	2.12E-07	6:36840356	0.133	1.45E-17	6:36988131	0.496	3.75E-10
6:36519290	0.392	8.27E-09	6:36840440	0.253	8.40E-13	6:36988302	0.499	7.10E-15
6:36522684	0.038	7.97E-10	6:36851287	0.081	1.11E-12	6:36989257	0.349	3.78E-11
6:36523063	0.068	3.79E-12	6:36865990	0.019	2.50E-06	6:36989893	0.386	3.04E-17
6:36523313	0.185	3.97E-09	6:36866029	0.474	3.02E-11	6:36992853	0.447	2.22E-09
6:36535133	0.173	2.64E-07	6:36866583	0.321	2.20E-12	6:36996570	0.011	1.30E-06
6:36538270	0.02	1.08E-07	6:36866760	0.39	1.29E-08	6:36998406	0.093	8.94E-17
6:36544865	0.289	4.65E-07	6:36872846	0.409	3.36E-09	6:37002148	0.022	2.68E-07
6:36545291	0.358	2.13E-11	6:36879203	0.24	3.28E-15	6:37003049	0.349	3.19E-09
6:36569337	0.405	2.18E-10	6:36879227	0.105	2.23E-13	6:37003412	0.047	1.24E-06
6:36572558	0.063	1.05E-08	6:36879259	0.165	1.17E-06	6:37005285	0.051	5.72E-10
6:36572923	0.49	8.47E-09	6:36880062	0.3	2.51E-09	6:37006436	0.397	9.30E-13
6:36579402	0.016	5.90E-08	6:36887719	0.241	1.91E-12	6:37009450	0.238	4.65E-11
6:36585143	0.031	6.23E-09	6:36898164	0.056	9.74E-10	6:37010465	0.479	3.06E-18
6:36604289	0.03	1.28E-09	6:36898239	0.282	2.35E-06	6:37010551	0.31	9.22E-13
6:36609880	0.357	2.68E-06	6:36898348	0.186	8.17E-07	6:37011023	0.109	2.66E-13
6:36613173	0.042	2.82E-06	6:36904636	0.361	2.94E-12	6:37011044	0.318	2.12E-12
6:36615051	0.221	1.49E-11	6:36906978	0.025	3.82E-07	6:37011080	0.072	2.98E-11
6:36619961	0.067	7.52E-07	6:36909193	0.343	3.63E-11	6:37012192	0.166	2.17E-11
6:36620324	0.205	4.00E-07	6:36909980	0.497	2.67E-09	6:37012416	0.46	1.48E-08
6:36620355	0.488	1.32E-06	6:36910736	0.412	4.37E-09	6:37013810	0.452	2.17E-06
6:36622287	0.11	9.84E-12	6:36927951	0.478	9.46E-10	6:37014626	0.084	2.67E-14
6:36625256	0.076	1.03E-07	6:36928435	0.203	2.64E-08	6:37015772	0.163	4.10E-07
6:36625308	0.309	5.76E-07	6:36928519	0.149	3.03E-06	6:37018597	0.19	5.64E-07
6:36627488	0.071	3.00E-08	6:36934495	0.281	2.01E-06	6:37019549	0.101	3.56E-09
6:36642513	0.474	9.97E-08	6:36934675	0.326	8.74E-09	6:37022183	0.226	7.66E-09
6:36656453	0.057	3.49E-08	6:36940386	0.103	1.75E-12	6:37022629	0.118	2.06E-06
6:36658788	0.06	5.72E-07	6:36940694	0.294	8.13E-07	6:37023017	0.05	4.38E-07
6:36680718	0.188	3.01E-07	6:36941213	0.491	5.46E-08	6:37032632	0.073	7.27E-09
6:36700818	0.044	1.16E-07	6:36941395	0.329	3.10E-06	6:37033477	0.189	5.82E-08
6:36713038	0.079	9.33E-08	6:36941720	0.441	1.99E-09	6:37058703	0.052	2.47E-06
6:36760092	0.048	1.38E-07	6:36941838	0.029	2.25E-06	6:37063340	0.172	4.41E-08
6:36762815	0.052	2.71E-08	6:36950661	0.071	1.52E-08	6:37064430	0.035	1.52E-06
6:36783500	0.376	8.05E-07	6:36954786	0.457	1.75E-10	6:37069087	0.047	1.23E-08
6:36783699	0.417	1.07E-06	6:36960302	0.398	2.56E-06	6:37071173	0.128	6.56E-19
6:36786075	0.46	2.16E-09	6:36966043	0.346	2.28E-06	6:37072037	0.071	4.01E-14

6:36789954	0.423	1.36E-08	6:36972708	0.24	3.15E-10	6:37074303	0.183	1.35E-19
6:36795735	0.144	1.54E-06	6:36973028	0.312	8.91E-09	6:37074322	0.174	3.65E-08
6:36805368	0.496	1.13E-10	6:36973237	0.118	2.80E-11	6:37076032	0.061	1.09E-06
6:36813228	0.078	9.03E-08	6:36978506	0.386	6.53E-07	6:37084369	0.117	1.34E-14
6:36813951	0.483	2.12E-06	6:36978600	0.4	2.25E-14	6:37101989	0.111	2.73E-06
6:36825884	0.21	5.96E-09	6:36979766	0.417	6.06E-14	6:37102022	0.11	1.45E-15

8-2-2. Selected SNP for CCAFT (continued)

SNP	MAF	p-value	SNP	MAF	p-value	SNP	MAF	p-value
6:37105197	0.082	1.03E-06	6:37601754	0.049	7.38E-07	6:37830213	0.5	1.27E-06
6:37107425	0.086	1.74E-06	6:37604515	0.319	1.86E-06	6:37836920	0.3	1.29E-09
6:37109146	0.095	1.21E-12	6:37612530	0.068	3.23E-07	6:37837432	0.401	6.03E-07
6:37110007	0.037	3.11E-06	6:37625024	0.044	2.03E-06	6:37837603	0.497	3.04E-06
6:37131598	0.08	2.35E-11	6:37648267	0.045	3.23E-08	6:37842690	0.203	1.17E-09
6:37133484	0.32	9.19E-10	6:37648758	0.103	5.31E-18	6:37845320	0.453	4.45E-10
6:37137051	0.113	2.19E-13	6:37654053	0.07	3.73E-09	6:37859990	0.298	2.99E-06
6:37139057	0.23	4.74E-14	6:37656311	0.266	2.04E-07	6:37869535	0.057	1.09E-06
6:37142711	0.425	9.89E-09	6:37657622	0.031	1.81E-07	6:37879860	0.116	2.13E-09
6:37145137	0.428	1.05E-12	6:37665116	0.474	9.80E-09	6:37879989	0.082	1.74E-06
6:37149869	0.048	3.83E-08	6:37668421	0.16	1.55E-06	6:37883706	0.041	5.15E-07
6:37150615	0.039	3.92E-07	6:37669350	0.048	9.79E-07	6:37884729	0.091	4.72E-08
6:37152570	0.049	5.83E-07	6:37669807	0.045	2.02E-08	6:37903482	0.071	3.32E-08
6:37153282	0.073	9.70E-14	6:37669996	0.31	4.57E-09	6:37908123	0.098	1.09E-07
6:37161805	0.043	4.36E-09	6:37670760	0.216	4.33E-10	6:37923320	0.169	1.26E-07
6:37166642	0.492	2.99E-09	6:37674269	0.073	1.98E-10	6:37924023	0.08	3.89E-07
6:37172072	0.017	2.72E-06	6:37675450	0.44	2.68E-07	6:37927727	0.463	1.85E-06
6:37176390	0.326	3.97E-07	6:37676194	0.033	2.43E-08	6:37951389	0.038	2.43E-06
6:37176711	0.061	1.55E-07	6:37696908	0.318	2.12E-13	6:37951495	0.058	9.74E-08
6:37181370	0.49	3.31E-07	6:37697120	0.042	2.50E-08	6:37952935	0.057	2.99E-06
6:37204168	0.431	9.22E-08	6:37698503	0.422	5.30E-14	6:37953962	0.096	3.16E-10
6:37218091	0.5	3.12E-09	6:37705732	0.184	1.88E-07	6:37979645	0.294	1.68E-08
6:37226765	0.345	1.75E-07	6:37706793	0.08	1.95E-09	6:37979655	0.212	5.30E-10
6:37240986	0.062	2.78E-06	6:37707299	0.387	1.68E-10	6:37979773	0.046	1.16E-08
6:37251745	0.5	1.21E-07	6:37709304	0.023	1.66E-06	6:37980923	0.424	9.57E-08
6:37257975	0.424	5.22E-12	6:37710933	0.306	2.21E-09	6:37986032	0.197	1.07E-07
6:37277138	0.04	1.56E-07	6:37711273	0.048	1.04E-08	6:38000387	0.312	7.39E-08
6:37334908	0.201	7.89E-10	6:37713567	0.204	2.09E-10	6:38005410	0.332	2.28E-06
6:37353278	0.274	1.73E-07	6:37718589	0.279	7.31E-13	6:38005482	0.264	9.92E-10
6:37364653	0.039	1.15E-08	6:37719524	0.072	1.79E-09	6:38006817	0.259	1.55E-14
6:37372676	0.061	2.70E-13	6:37719901	0.106	8.28E-12	6:38006942	0.355	6.14E-11
6:37423973	0.053	1.04E-11	6:37721941	0.243	3.11E-12	6:38007578	0.468	2.27E-09
6:37459157	0.493	1.61E-07	6:37740727	0.068	8.27E-07	6:38008090	0.479	1.49E-09
6:37495708	0.045	7.07E-13	6:37741444	0.116	2.16E-09	6:38014752	0.283	2.65E-06
6:37500865	0.212	2.70E-12	6:37754328	0.079	2.92E-06	6:38034182	0.382	6.09E-07
6:37512442	0.06	4.19E-10	6:37763397	0.459	3.19E-10	6:38034949	0.351	5.82E-08

6:37514000	0.032	3.11E-06	6:37763537	0.245	2.98E-08	6:38043172	0.479	8.84E-08
6:37523721	0.412	1.19E-07	6:37763969	0.101	4.51E-09	6:38049083	0.262	3.15E-06
6:37534372	0.04	6.85E-10	6:37764030	0.019	8.61E-07	6:38055672	0.251	1.39E-10
6:37534465	0.414	1.13E-08	6:37766859	0.369	4.69E-07	6:38058502	0.241	1.19E-07
6:37538667	0.047	2.75E-06	6:37790065	0.043	1.46E-06	6:38063325	0.5	6.24E-07
6:37577411	0.293	1.27E-06	6:37794740	0.061	2.41E-10	6:38086736	0.362	1.99E-06
6:37578145	0.069	5.51E-07	6:37796547	0.079	1.70E-09	6:38089484	0.105	1.09E-07
6:37578424	0.3	1.58E-10	6:37811859	0.326	7.50E-10	6:38089953	0.434	1.06E-07
6:37581725	0.416	6.91E-11	6:37814517	0.433	1.89E-08	6:38093707	0.344	8.96E-08
6:37584836	0.224	1.38E-11	6:37817127	0.213	1.29E-09	6:38101093	0.279	1.08E-09

8-2-2. Selected SNP for CCAFT (continued)

SNP	MAF	p-value	SNP	MAF	p-value	SNP	MAF	p-value
6:38104879	0.045	4.10E-11	6:38411715	0.331	4.50E-11	8:19965180	0.215	2.04E-06
6:38109871	0.239	4.66E-07	6:38433540	0.128	4.29E-08	8:26255224	0.029	1.27E-06
6:38111955	0.422	8.01E-07	6:38434529	0.488	1.31E-06	8:86137042	0.087	2.51E-06
6:38113129	0.03	1.85E-06	6:38436558	0.212	3.03E-06	8:86139223	0.038	1.79E-06
6:38147798	0.268	1.06E-08	6:38439866	0.253	4.48E-11	9:36522980	0.032	2.42E-06
6:38152146	0.103	1.85E-06	6:38450801	0.03	3.17E-07	9:83665579	0.086	9.33E-07
6:38173320	0.206	5.86E-07	6:38451457	0.115	2.09E-13	9:87131819	0.292	6.62E-07
6:38218375	0.153	3.46E-09	6:38452446	0.5	6.03E-07	10:78927819	0.006	2.19E-06
6:38223695	0.33	1.46E-08	6:38454163	0.373	2.76E-09	11:22896586	0.135	4.18E-07
6:38225971	0.154	5.55E-11	6:38455268	0.08	3.86E-12	11:22899836	0.112	2.53E-06
6:38229683	0.25	4.16E-11	6:38457703	0.258	7.08E-08	11:22899939	0.22	2.10E-06
6:38233138	0.087	9.06E-08	6:38462659	0.112	5.77E-08	11:60048433	0.144	2.73E-07
6:38234207	0.076	2.68E-07	6:38465221	0.061	3.30E-11	12:49019375	0.322	2.96E-06
6:38234814	0.185	6.04E-15	6:38477168	0.089	3.65E-09	12:49023865	0.389	1.99E-06
6:38236712	0.074	2.56E-06	6:38489858	0.088	1.90E-06	13:80110242	0.015	1.76E-06
6:38237867	0.087	6.87E-08	6:38489985	0.469	7.04E-10	14:8428651	0.095	1.43E-06
6:38248380	0.059	1.40E-06	6:38495392	0.07	1.92E-06	15:4216043	0.005	2.00E-06
6:38251399	0.088	5.98E-10	6:38497995	0.478	1.29E-08	15:5377498	0.027	2.38E-06
6:38252358	0.362	5.88E-12	6:38499032	0.269	1.44E-06	15:77497240	0.441	2.57E-06
6:38252498	0.234	5.44E-08	6:38499078	0.421	5.92E-07	16:43897771	0.027	1.47E-06
6:38260171	0.075	2.98E-06	6:38508302	0.179	5.51E-08	16:43990081	0.155	2.29E-06
6:38283984	0.317	2.99E-06	6:38512827	0.48	2.76E-06	17:2844969	0.12	2.06E-06
6:38283997	0.073	4.05E-08	6:38522144	0.265	2.51E-06	18:15057455	0.006	1.33E-06
6:38284033	0.042	2.69E-06	6:38522481	0.267	4.61E-09	18:40253396	0.006	2.10E-06
6:38286593	0.487	1.31E-06	6:38525769	0.377	4.00E-07	18:64441554	0.065	2.27E-06
6:38294606	0.092	3.73E-08	6:38546202	0.058	3.04E-09	18:7761258	0.044	2.66E-06
6:38297721	0.317	3.75E-07	6:38580974	0.181	1.39E-07	19:18944061	0.273	2.98E-07
6:38303354	0.252	2.97E-08	6:38583317	0.453	3.54E-07	19:53552427	0.192	1.69E-06
6:38306553	0.071	1.10E-07	6:38589794	0.383	2.20E-06	19:53555015	0.259	1.39E-06
6:38307327	0.111	1.75E-06	6:38593800	0.45	1.37E-06	19:7182410	0.378	2.90E-06
6:38317540	0.072	1.76E-07	6:38608484	0.392	3.01E-07	19:7196660	0.408	7.71E-07
6:38322543	0.118	2.50E-09	6:38608684	0.272	1.82E-07	19:7872712	0.038	7.54E-07

6:38322803	0.462	7.69E-07	6:38745328	0.243	1.20E-06	20:20391580	0.011	7.80E-07
6:38329453	0.077	5.81E-09	6:38749598	0.14	1.24E-08	20:4006977	0.326	3.57E-08
6:38334283	0.149	2.05E-08	6:38753103	0.145	2.47E-08	21:1672241	0.017	2.91E-06
6:38334728	0.445	1.22E-07	6:38760428	0.162	7.08E-07	21:46229002	0.088	3.83E-07
6:38337106	0.366	3.07E-08	6:38764913	0.039	2.21E-07	23:36550427	0.129	1.29E-06
6:38337580	0.031	1.42E-06	6:39770909	0.146	7.99E-07	23:36892549	0.423	1.73E-06
6:38358787	0.322	4.30E-09	6:40255156	0.199	4.16E-07	23:54489937	0.112	2.67E-07
6:38359443	0.057	1.29E-07	6:40255289	0.114	2.16E-06	23:59350038	0.465	9.52E-07
6:38360947	0.491	2.01E-06	6:41146902	0.316	9.67E-07	24:8346142	0.033	7.36E-07
6:38372635	0.302	1.91E-06	6:64717751	0.147	3.71E-07	25:35997715	0.017	1.99E-07
6:38372993	0.066	2.18E-06	6:67993379	0.333	2.53E-06	26:1037389	0.308	2.55E-06
6:38395999	0.107	2.54E-08	7:18957241	0.482	2.03E-06	26:31053277	0.035	2.34E-06
6:38397081	0.085	4.45E-10	7:70536717	0.104	1.21E-06	26:8940970	0.209	1.60E-06
6:38402476	0.086	8.84E-10	7:72351881	0.007	2.04E-06			

8-2-3. Selected SNP for CEMD

SNP	MAF	p-value	SNP	MAF	p-value	SNP	MAF	p-value
1:128596950	0.397	8.16E-06	5:23750961	0.447	8.40E-06	10:17820558	0.387	5.57E-06
1:128596959	0.417	4.14E-06	6:113951115	0.180	9.47E-06	11:22226047	0.076	3.01E-06
1:135334381	0.232	1.11E-06	6:113951772	0.164	6.46E-06	11:25968500	0.203	6.82E-06
1:139770543	0.243	7.15E-06	6:113955316	0.153	1.37E-06	11:25971861	0.254	5.10E-06
1:185228968	0.088	1.61E-06	6:12121836	0.014	9.95E-06	11:25972725	0.230	5.12E-07
1:185913799	0.208	6.63E-06	6:60192628	0.210	6.11E-06	11:25972852	0.275	7.02E-06
1:211632717	0.016	9.23E-06	6:62529046	0.062	3.16E-08	11:25977352	0.276	4.13E-06
1:233381861	0.031	7.60E-06	6:62545759	0.029	9.89E-08	11:26384150	0.129	2.53E-06
1:236795890	0.126	9.24E-06	6:62552729	0.024	2.71E-06	11:26385750	0.166	2.86E-07
1:31134234	0.160	5.19E-06	6:62557307	0.028	7.00E-07	11:26388169	0.138	1.52E-07
1:5695149	0.073	5.74E-06	6:62571352	0.025	2.38E-06	11:26412639	0.287	8.65E-06
1:91846176	0.368	3.43E-06	6:62574148	0.022	7.02E-07	11:26431075	0.162	1.60E-06
1:91848440	0.322	6.78E-07	6:62576146	0.022	4.33E-06	11:26434709	0.311	5.05E-08
1:91972454	0.261	7.35E-06	6:62919949	0.457	1.84E-06	11:26445930	0.213	6.40E-08
2:116431168	0.043	4.89E-06	6:63137352	0.058	8.84E-06	11:26450446	0.318	2.55E-07
2:119220913	0.030	6.39E-06	6:63142239	0.245	8.39E-06	11:26818910	0.286	8.04E-06
2:120015963	0.252	9.84E-06	6:63144452	0.276	8.42E-06	11:26827137	0.298	2.15E-06
2:120097828	0.031	5.37E-06	6:64426870	0.127	4.01E-06	11:26836567	0.291	1.41E-06

2:207955549	0.012	1.09E-06	6:73497496	0.397	1.28E-06	11:26836898	0.273	7.51E-06
2:217462744	0.118	3.57E-06	6:85388627	0.036	8.36E-06	11:26841877	0.230	7.15E-07
2:24036472	0.036	1.45E-06	6:85389118	0.051	4.39E-06	11:26849356	0.238	3.33E-06
2:31111427	0.044	5.37E-06	6:87236293	0.399	8.22E-06	11:26851724	0.229	5.05E-06
2:32609618	0.041	1.36E-06	6:87236506	0.401	2.77E-06	11:39945015	0.117	2.86E-06
2:60262984	0.249	4.71E-06	6:94759801	0.125	4.77E-06	12:12499854	0.304	3.43E-07
2:60264287	0.355	9.86E-06	6:94791830	0.126	9.63E-06	12:12500490	0.419	2.51E-06
2:60316999	0.339	7.65E-06	6:96345311	0.006	9.09E-06	12:3167505	0.212	9.54E-06
2:94976302	0.495	1.08E-06	7:16211383	0.344	8.25E-06	13:1194680	0.024	1.26E-07
3:145334260	0.062	9.12E-06	7:16221745	0.453	9.79E-06	13:5953652	0.024	6.59E-06
3:150100534	0.199	4.25E-06	7:39392082	0.435	8.17E-06	13:76055593	0.019	9.97E-06
3:16415671	0.166	9.17E-06	7:47542036	0.499	8.81E-06	13:77402302	0.011	4.64E-06
3:176714311	0.010	6.94E-06	7:48794235	0.192	5.31E-06	13:77947359	0.043	3.16E-06
3:178992892	0.319	4.04E-06	7:93088327	0.432	1.63E-06	13:78764949	0.043	8.88E-06
3:187163559	0.316	7.00E-06	8:52319752	0.266	6.72E-06	13:78847138	0.412	5.76E-06
3:187167400	0.289	6.65E-06	8:72268134	0.078	2.33E-06	13:78848285	0.377	6.10E-06
3:187170576	0.279	5.21E-06	8:86378198	0.010	5.24E-06	14:11018381	0.017	4.72E-06
3:187735138	0.059	4.72E-06	9:17560740	0.187	3.17E-06	14:58430262	0.028	7.84E-06
3:191333743	0.026	7.26E-06	9:18956366	0.018	4.46E-06	14:58430296	0.020	2.49E-06
3:204544121	0.277	1.15E-06	9:18973034	0.017	5.87E-06	14:6339713	0.172	2.57E-06
3:204544557	0.184	8.00E-06	9:32644262	0.181	4.58E-06	15:17725159	0.021	3.74E-06
3:204713502	0.181	6.70E-06	9:50207991	0.072	4.81E-06	15:17740405	0.023	9.01E-06
3:205697560	0.251	2.49E-06	9:50692597	0.086	6.08E-06	15:24811496	0.249	6.09E-06
3:214960928	0.242	9.22E-06	9:50692683	0.065	2.02E-06	16:11985486	0.349	1.22E-06
3:23396379	0.059	6.19E-06	9:50740611	0.087	2.57E-06	16:18180350	0.062	6.76E-06
4:116023740	0.007	7.74E-06	9:61700089	0.023	4.33E-06	16:42995414	0.151	2.68E-06
5:22157306	0.056	2.44E-08	10:12283042	0.410	6.18E-06	16:65377353	0.011	6.23E-06

8-2-3. Selected SNP for CEMD (continued)

SNP	MAF	p-value	SNP	MAF	p-value
17:10949302	0.006	2.95E-06	18:64767861	0.047	1.86E-07
17:11694216	0.353	7.29E-06	18:64839427	0.056	1.61E-07
17:35510823	0.197	7.17E-06	18:64963696	0.033	1.59E-06

17:66804033	0.043	2.94E-06	18:64971969	0.041	6.63E-07
17:66998842	0.098	2.32E-06	18:65198142	0.041	9.08E-08
18:12528729	0.465	4.26E-06	18:65352641	0.039	1.33E-07
18:12528872	0.498	4.20E-06	18:65428716	0.094	6.64E-07
18:12528886	0.495	2.70E-06	18:65432112	0.073	7.01E-06
18:16986630	0.112	1.92E-06	18:65434501	0.080	5.73E-06
18:36996300	0.015	9.53E-06	18:65440359	0.096	1.71E-06
18:53514283	0.142	9.63E-06	18:65482025	0.045	3.55E-06
18:60562378	0.031	8.69E-06	18:65554262	0.216	3.83E-06
18:60562854	0.037	6.90E-06	18:8568143	0.005	6.75E-06
18:62673134	0.049	3.36E-06	19:23847950	0.062	3.56E-06
18:62736651	0.042	7.72E-06	19:23852910	0.058	1.11E-06
18:62904073	0.040	8.20E-06	19:23853336	0.070	2.24E-06
18:63271231	0.054	2.86E-06	19:24193959	0.043	9.48E-06
18:63375826	0.076	9.72E-06	19:52236393	0.311	6.13E-06
18:63393322	0.096	6.70E-07	19:52240476	0.303	6.25E-06
18:63921780	0.049	5.08E-06	19:57100446	0.404	7.16E-06
18:63931158	0.086	5.32E-06	19:57102703	0.399	8.57E-06
18:63966986	0.046	9.99E-06	19:57113784	0.413	7.02E-06
18:64100625	0.372	9.86E-06	19:57152385	0.460	6.71E-06
18:64122145	0.044	2.36E-07	19:57167474	0.417	3.26E-06
18:64140159	0.086	1.68E-06	19:57183963	0.446	1.34E-06
18:64196620	0.154	5.05E-06	19:57183989	0.413	3.98E-06
18:64430827	0.071	1.76E-09	20:19311317	0.036	3.55E-06
18:64433061	0.066	2.35E-09	20:40488671	0.183	6.18E-06
18:64437483	0.095	4.69E-06	20:47539609	0.194	6.92E-06
18:64468635	0.118	1.88E-07	21:24954938	0.008	5.43E-06
18:64477623	0.158	2.00E-07	21:25717570	0.026	8.00E-06
18:64478234	0.053	2.49E-08	23:13731725	0.086	8.60E-06
18:64530703	0.059	5.15E-09	23:15660842	0.027	7.76E-06
18:64542455	0.055	4.04E-10	23:54004672	0.075	7.23E-06
18:64547823	0.071	1.33E-08	23:54017743	0.076	9.21E-06
18:64567047	0.083	5.09E-07	23:6791202	0.369	6.73E-06
18:64577721	0.091	9.52E-06	25:35498133	0.075	7.37E-06
18:64600329	0.084	4.38E-06	26:30562441	0.186	6.74E-06
18:64633326	0.082	4.01E-06	26:30887097	0.128	8.62E-06
18:64633367	0.215	2.88E-07	26:30895366	0.143	1.80E-06
18:64681537	0.201	2.62E-06	26:30902013	0.152	1.09E-06
18:64684599	0.242	9.42E-06	26:31132752	0.428	2.36E-06
18:64685705	0.165	1.31E-06	26:31145452	0.441	6.45E-06
18:64697907	0.032	6.20E-06	26:34711412	0.007	5.91E-06
18:64743593	0.065	4.55E-06	26:36307964	0.007	8.05E-06

8-2-3. Selected SNP for CWT

SNP	MAF	p-value	SNP	MAF	p-value	SNP	MAF	p-value
1:11806031	0.062	4.12E-07	6:35243386	0.083	2.57E-06	6:36760092	0.048	2.66E-06
1:162265499	0.313	2.42E-07	6:35429074	0.175	3.96E-09	6:36781042	0.015	1.36E-06
1:162308518	0.364	1.26E-06	6:35456207	0.292	6.36E-07	6:36781466	0.017	3.46E-07
1:184833977	0.016	1.17E-06	6:35495306	0.066	1.84E-06	6:36783500	0.377	3.80E-08
1:189386912	0.19	3.02E-06	6:35498049	0.436	5.46E-08	6:36783648	0.396	1.76E-06
1:189389951	0.289	2.44E-06	6:35504886	0.224	2.84E-06	6:36787319	0.295	2.59E-08
1:210305433	0.062	1.41E-07	6:35534567	0.176	2.51E-06	6:36789954	0.423	2.45E-07
1:252799130	0.327	2.56E-06	6:35535684	0.105	3.03E-07	6:36799095	0.006	2.71E-06
2:103821339	0.065	3.05E-06	6:35732545	0.443	2.46E-07	6:36803405	0.498	2.52E-08
2:130967573	0.267	5.30E-07	6:35735599	0.11	3.12E-06	6:36804256	0.303	8.06E-10
2:130968512	0.197	7.24E-09	6:35739057	0.307	6.65E-07	6:36806632	0.021	6.66E-08
2:130968529	0.147	1.93E-07	6:35752300	0.333	1.93E-07	6:36808905	0.036	7.39E-08
2:130968555	0.344	2.86E-06	6:35867550	0.282	9.11E-08	6:36809459	0.495	2.12E-06
2:134908351	0.051	8.70E-07	6:35878794	0.25	1.97E-06	6:36813827	0.497	2.74E-06
2:136522755	0.386	5.33E-07	6:35913693	0.356	8.55E-07	6:36832552	0.089	1.70E-06
2:1903459	0.016	1.42E-06	6:35945072	0.176	4.30E-07	6:36834137	0.062	1.72E-06
2:191700350	0.02	3.01E-07	6:35963072	0.25	1.86E-11	6:36835643	0.429	5.11E-11
2:194766598	0.013	1.11E-06	6:35963930	0.366	4.60E-07	6:36840356	0.133	8.04E-13
2:194827947	0.044	4.26E-07	6:35965698	0.403	1.49E-06	6:36840440	0.254	2.97E-10
2:194833243	0.024	7.79E-07	6:35966103	0.336	8.25E-10	6:36851287	0.081	8.08E-09
2:195015098	0.014	1.58E-06	6:36038584	0.438	6.66E-08	6:36866583	0.322	5.28E-07
2:64376245	0.01	1.54E-07	6:36045974	0.226	1.17E-06	6:36866760	0.391	6.82E-08
3:202710636	0.065	3.98E-07	6:36059390	0.369	2.81E-08	6:36879227	0.107	1.40E-08
3:58729692	0.034	1.65E-06	6:36087980	0.403	2.84E-07	6:36880062	0.3	6.00E-13
3:58916180	0.04	1.35E-06	6:36090861	0.181	2.35E-07	6:36887719	0.241	1.02E-07
3:59040425	0.048	2.63E-06	6:36092652	0.453	8.01E-07	6:36898164	0.056	4.52E-08
3:59052481	0.069	6.30E-07	6:36155169	0.203	3.81E-07	6:36898348	0.187	2.88E-06
3:59118649	0.05	1.08E-06	6:36155985	0.125	1.28E-08	6:36902169	0.423	6.05E-07
3:59137010	0.042	9.77E-07	6:36381285	0.03	3.33E-07	6:36904636	0.36	4.10E-11
3:59381200	0.044	1.38E-07	6:36386878	0.051	1.50E-07	6:36909193	0.343	7.32E-07
3:59407478	0.046	2.13E-07	6:36397120	0.401	3.04E-09	6:36909980	0.499	2.93E-11
3:59645865	0.033	2.90E-06	6:36402740	0.135	4.46E-07	6:36910736	0.411	2.16E-09
3:59831043	0.056	2.28E-06	6:36403368	0.034	7.79E-08	6:36912577	0.225	2.00E-08
3:60686544	0.072	2.04E-06	6:36405622	0.023	8.30E-07	6:36924347	0.363	6.22E-07
3:98204126	0.054	2.45E-06	6:36405863	0.31	3.05E-06	6:36927951	0.478	9.13E-07
4:110989221	0.188	2.84E-06	6:36416658	0.155	3.69E-10	6:36934495	0.281	2.99E-06
4:50130211	0.216	2.52E-06	6:36416848	0.265	5.41E-12	6:36935847	0.375	4.14E-07
5:7659195	0.452	1.56E-06	6:36463998	0.339	2.52E-06	6:36940386	0.103	3.34E-09
5:83463368	0.046	5.99E-07	6:36469220	0.123	1.18E-07	6:36940694	0.295	1.28E-07
6:14956237	0.007	3.14E-06	6:36523063	0.068	2.47E-07	6:36941213	0.491	3.21E-09
6:34569016	0.427	1.09E-06	6:36569337	0.404	5.38E-09	6:36942436	0.46	2.20E-06
6:35138403	0.178	3.10E-08	6:36572923	0.489	1.35E-12	6:36954786	0.458	2.84E-08
6:35139680	0.29	8.46E-09	6:36591456	0.023	2.77E-06	6:36959953	0.259	2.48E-06
6:35192394	0.212	2.03E-07	6:36642513	0.474	9.83E-07	6:36960302	0.398	2.03E-08

6:35202513	0.434	6.95E-07	6:36713038	0.08	2.45E-06	6:36961104	0.499	6.59E-08

8-2-3. Selected SNP for CWT (continued)

SNP	MAF	p-value	SNP	MAF	p-value	SNP	MAF	p-value
6:36961588	0.39	1.50E-06	6:37098254	0.019	5.12E-08	6:37713567	0.204	1.33E-07
6:36965594	0.39	4.60E-07	6:37102022	0.111	2.20E-15	6:37718589	0.281	1.20E-09
6:36966509	0.059	9.42E-07	6:37107425	0.087	2.00E-09	6:37719901	0.107	1.45E-09
6:36966955	0.403	1.14E-06	6:37109146	0.096	2.75E-09	6:37720566	0.075	2.82E-06
6:36972708	0.24	6.04E-07	6:37110007	0.037	3.50E-07	6:37721941	0.244	1.17E-06
6:36973028	0.313	1.79E-12	6:37131598	0.08	4.03E-14	6:37741444	0.117	2.07E-09
6:36973237	0.119	1.17E-09	6:37133484	0.321	3.63E-11	6:37780331	0.338	7.88E-09
6:36977443	0.244	2.60E-09	6:37137051	0.114	2.01E-14	6:37791866	0.274	2.22E-06
6:36978296	0.486	2.18E-12	6:37138949	0.04	2.29E-06	6:37809426	0.46	2.69E-06
6:36978600	0.4	2.89E-13	6:37139057	0.232	3.04E-12	6:37842690	0.203	1.37E-06
6:36981217	0.024	2.07E-08	6:37142711	0.425	2.77E-07	6:37845320	0.453	1.65E-06
6:36981300	0.437	4.60E-12	6:37144813	0.013	3.00E-06	6:37918573	0.407	2.36E-06
6:36982070	0.419	1.13E-08	6:37145137	0.429	1.65E-12	6:37979645	0.294	6.44E-08
6:36986361	0.44	9.80E-07	6:37164390	0.042	2.11E-06	6:37979655	0.212	6.78E-07
6:36988131	0.496	9.75E-07	6:37166642	0.491	1.25E-06	6:37996275	0.262	2.03E-06
6:36988302	0.499	1.89E-14	6:37176390	0.327	2.89E-08	6:38005464	0.245	7.13E-07
6:36988707	0.381	1.13E-13	6:37226112	0.309	2.70E-07	6:38006817	0.259	6.90E-08
6:36989893	0.386	2.86E-16	6:37240753	0.067	4.92E-08	6:38006942	0.355	1.30E-08
6:36992705	0.04	1.14E-08	6:37247373	0.5	2.01E-07	6:38007578	0.468	2.14E-06
6:36998406	0.093	1.92E-12	6:37257975	0.425	2.24E-09	6:38008090	0.48	9.17E-07
6:37000524	0.437	1.47E-06	6:37334908	0.203	1.66E-06	6:38014752	0.282	2.18E-06
6:37003049	0.348	1.88E-08	6:37337876	0.444	2.47E-06	6:38033189	0.364	7.31E-07
6:37003412	0.047	4.43E-09	6:37353278	0.274	1.50E-07	6:38093707	0.343	6.38E-07
6:37005285	0.051	6.38E-08	6:37372676	0.061	1.00E-06	6:38218375	0.154	4.74E-07
6:37006436	0.397	7.23E-13	6:37448093	0.331	4.90E-07	6:38218903	0.444	4.44E-07
6:37009450	0.238	4.31E-07	6:37500865	0.212	1.68E-09	6:38223126	0.352	2.91E-06
6:37010465	0.479	1.44E-12	6:37539289	0.307	3.77E-08	6:38225971	0.155	3.09E-08
6:37010551	0.309	4.79E-12	6:37578424	0.3	2.59E-07	6:38229683	0.251	2.50E-07
6:37011023	0.11	3.42E-12	6:37581725	0.416	5.51E-10	6:38233138	0.088	1.14E-06
6:37011044	0.318	3.04E-13	6:37584836	0.225	4.03E-09	6:38234814	0.187	2.69E-10
6:37011080	0.072	1.01E-11	6:37641703	0.398	1.52E-06	6:38238491	0.123	3.13E-06
6:37012192	0.166	1.82E-07	6:37648758	0.104	1.39E-07	6:38252498	0.235	4.73E-07
6:37012272	0.486	2.70E-07	6:37665116	0.474	1.41E-06	6:38254822	0.339	1.09E-06
6:37012480	0.367	2.70E-10	6:37669807	0.045	7.54E-08	6:38260216	0.424	7.02E-07
6:37013810	0.453	3.46E-09	6:37669996	0.311	1.43E-09	6:38278215	0.461	9.52E-07
6:37014626	0.085	6.68E-12	6:37670760	0.216	3.21E-07	6:38288026	0.499	6.57E-07
6:37022135	0.152	1.71E-06	6:37674269	0.074	2.27E-10	6:38317608	0.433	8.10E-07
6:37022183	0.226	3.01E-07	6:37675450	0.441	2.43E-07	6:38411758	0.445	5.38E-07
6:37062449	0.042	6.09E-08	6:37681551	0.42	1.05E-06	6:38436284	0.253	2.83E-06
6:37063340	0.172	2.60E-06	6:37696908	0.318	5.33E-11	6:38455268	0.081	2.66E-06
6:37069087	0.047	1.41E-09	6:37697120	0.042	1.06E-06	6:38745328	0.243	7.62E-07

6:37071173	0.129	1.76E-13	6:37698503	0.422	1.59E-13	6:39185021	0.244	1.43E-06
6:37072037	0.071	1.19E-10	6:37705732	0.184	3.68E-09	6:39758586	0.038	2.39E-07
6:37074303	0.184	1.57E-14	6:37706793	0.081	1.84E-10	6:41091054	0.167	9.56E-07
6:37084369	0.118	9.25E-12	6:37707299	0.387	1.78E-12	6:43486592	0.332	1.82E-06

8-2-3. Selected SNP for CWT (continued)

SNP	MAF	p-value	SNP	MAF	p-value
6:60476752	0.007	2.97E-06	15:41223519	0.049	7.45E-07
7:24802409	0.01	1.28E-06	15:41260149	0.213	2.26E-06
7:44520812	0.098	5.91E-07	15:6645338	0.02	8.96E-08
7:56801220	0.088	2.53E-06	16:29500835	0.126	2.45E-06
7:56866134	0.088	1.23E-06	16:29516940	0.282	8.15E-07
8:14665693	0.127	1.66E-06	16:29563867	0.256	2.72E-06
9:2242823	0.368	1.80E-06	16:29628525	0.066	2.93E-06
9:56741389	0.052	2.90E-06	16:29646067	0.162	2.67E-06
9:62428563	0.056	7.35E-07	16:29677300	0.006	1.53E-07
9:7671239	0.011	2.72E-06	16:29680301	0.08	1.03E-06
11:25591690	0.47	2.39E-06	16:29705212	0.054	3.84E-07
11:25596636	0.338	1.04E-06	16:29804356	0.019	4.71E-07
11:25599296	0.267	1.33E-06	16:31681709	0.333	7.00E-07
11:26162350	0.19	1.42E-06	16:31994636	0.467	2.99E-06
11:26162501	0.119	1.65E-06	16:32008588	0.302	7.08E-07
11:26276300	0.309	4.66E-07	16:32009795	0.379	2.43E-06
11:26280657	0.457	2.75E-06	16:32016570	0.369	1.40E-06
11:26321365	0.193	2.24E-07	17:19357551	0.062	2.89E-06
11:26321380	0.304	2.82E-12	19:11372776	0.164	4.43E-07
11:26331988	0.354	8.03E-12	19:11377932	0.398	1.37E-06
11:26354892	0.2	2.36E-07	19:11378477	0.275	5.77E-07
11:26385750	0.165	1.69E-08	21:17750777	0.121	2.11E-06
11:26400563	0.396	2.55E-06	21:17898773	0.059	3.15E-06
11:26406181	0.397	2.34E-08	21:17898937	0.087	1.94E-06
11:26407996	0.291	1.40E-13	21:21848524	0.313	2.51E-06
11:26408018	0.042	4.66E-07	21:28718082	0.249	1.06E-06
11:26431075	0.162	1.71E-08	21:45116548	0.397	1.22E-07
11:26445930	0.213	1.06E-13	22:20856305	0.492	1.64E-06
11:27262894	0.041	5.73E-07	22:31310288	0.078	3.05E-07
11:27371976	0.284	1.64E-06	22:44834382	0.033	2.16E-06
11:27379277	0.219	9.82E-07	23:30011114	0.012	2.35E-06
11:27389736	0.359	1.82E-06	23:42698676	0.148	1.61E-06
11:49435338	0.208	2.77E-06	23:43896965	0.337	1.22E-07
11:49435377	0.335	1.29E-06	23:44258307	0.363	2.40E-06
12:19587271	0.236	1.45E-06	23:44493556	0.384	2.75E-06
12:19887485	0.036	2.42E-06	23:44867061	0.463	7.00E-07
13:10281660	0.012	2.84E-06	25:37694677	0.431	1.71E-07
13:17482029	0.389	3.12E-06	26:37615656	0.018	3.08E-06

13:57387621	0.011	2.79E-06	26:665754	0.022	3.19E-07
13:57758023	0.041	2.56E-06			
14:48137126	0.067	1.53E-06			
14:48261812	0.076	8.90E-07			
15:15482525	0.382	1.98E-07			
15:16939918	0.043	2.10E-07			
15:41215736	0.078	1.79E-07			

8-2-4. Selected SNP for DRESS

SNP	MAF	p-value	SNP	MAF	p-value	SNP	MAF	p-value
2:247491009	0.193	6.95E-07	6:36973028	0.302	5.11E-09	6:37621420	0.062	1.27E-08
3:43094665	0.067	2.30E-07	6:36973237	0.121	1.08E-09	6:37654053	0.073	2.57E-09
3:43094665	0.067	2.30E-07	6:36978600	0.417	1.06E-07	6:37698503	0.418	1.77E-07
6:35229559	0.252	1.44E-09	6:36979766	0.405	1.36E-14	6:37707299	0.411	1.20E-09
6:35236143	0.302	1.26E-07	6:36981159	0.418	5.98E-09	6:37718589	0.289	7.89E-08
6:35498049	0.452	3.69E-08	6:36981751	0.482	1.96E-15	6:37719901	0.107	3.70E-09
6:35554926	0.481	6.74E-08	6:36988707	0.367	1.14E-10	6:37721941	0.252	5.05E-08
6:35735779	0.46	6.30E-08	6:36989257	0.338	9.56E-09	6:37741444	0.12	2.64E-10
6:35743422	0.494	1.78E-09	6:36989381	0.5	6.09E-13	6:37754328	0.082	8.83E-10
6:35811216	0.356	1.68E-07	6:36989893	0.403	1.07E-12	6:37756468	0.043	2.97E-07
6:35869287	0.182	3.82E-09	6:36997883	0.4	2.42E-07	6:37757807	0.495	1.17E-07
6:35878794	0.242	1.81E-07	6:37006436	0.415	9.87E-09	6:37763397	0.438	8.99E-11
6:35913693	0.353	1.63E-07	6:37010465	0.473	7.22E-08	6:37763537	0.241	1.66E-08
6:35922466	0.139	1.58E-07	6:37011023	0.11	2.15E-07	6:37763969	0.104	1.28E-09
6:35929864	0.245	5.42E-08	6:37019549	0.104	1.13E-08	6:37780331	0.358	3.66E-10
6:36038584	0.421	3.67E-08	6:37022183	0.224	2.37E-09	6:37796547	0.083	2.65E-09
6:36087980	0.397	1.66E-07	6:37022629	0.119	7.29E-10	6:37810412	0.464	8.00E-08
6:36092348	0.487	2.00E-07	6:37023017	0.052	1.27E-07	6:37814517	0.412	4.95E-09
6:36349082	0.177	2.81E-07	6:37029801	0.347	2.31E-10	6:37817127	0.209	1.05E-08
6:36397120	0.388	5.19E-08	6:37032632	0.073	2.55E-09	6:37867955	0.073	6.90E-09
6:36397296	0.295	1.66E-07	6:37033477	0.189	4.27E-10	6:37902298	0.105	1.03E-07
6:36407873	0.367	8.86E-08	6:37051183	0.157	1.01E-07	6:37948509	0.319	3.69E-08
6:36416658	0.155	1.00E-08	6:37063340	0.171	5.25E-08	6:37979655	0.206	9.74E-08
6:36416848	0.266	1.49E-10	6:37071838	0.127	3.73E-10	6:37998720	0.298	3.19E-08
6:36465145	0.129	1.57E-07	6:37074303	0.182	3.03E-10	6:38031820	0.256	2.29E-07
6:36572923	0.499	1.63E-08	6:37074337	0.077	1.49E-09	6:38043172	0.459	4.99E-09
6:36783500	0.362	5.46E-08	6:37084369	0.118	1.03E-11	6:38086736	0.379	1.54E-07
6:36787319	0.283	2.18E-07	6:37102022	0.113	1.65E-08	6:38093707	0.362	1.30E-08
6:36789954	0.401	5.24E-08	6:37105197	0.082	1.10E-07	6:38218375	0.161	1.18E-07
6:36804256	0.287	1.19E-09	6:37109146	0.098	1.42E-10	6:38222811	0.371	4.59E-08
6:36840356	0.135	5.70E-10	6:37131598	0.082	2.95E-08	6:38234814	0.191	9.02E-12
6:36866012	0.327	2.60E-07	6:37133484	0.306	4.25E-09	6:38283997	0.075	2.12E-09
6:36879513	0.499	2.69E-10	6:37137051	0.115	4.64E-13	6:38295261	0.086	3.12E-07
6:36880062	0.288	1.13E-09	6:37139057	0.234	1.40E-12	6:38297721	0.335	1.05E-07
6:36887719	0.239	1.71E-07	6:37142711	0.406	1.01E-09	6:38319833	0.07	2.84E-08
6:36904664	0.335	3.04E-07	6:37145137	0.413	2.48E-12	6:38322543	0.124	2.87E-09

6:36910736	0.431	5.31E-09	6:37149869	0.051	2.46E-08	6:38358787	0.341	9.93E-08
6:36927951	0.455	2.69E-08	6:37180170	0.473	7.61E-09	6:38396772	0.245	1.59E-08
6:36928435	0.203	1.06E-09	6:37236177	0.315	2.06E-07	6:38454163	0.366	1.53E-08
6:36940386	0.105	1.12E-08	6:37334908	0.209	5.54E-09	6:38464721	0.497	1.41E-07
6:36940694	0.279	1.97E-12	6:37466821	0.054	1.07E-07	6:38478856	0.354	1.76E-07
6:36940978	0.42	1.05E-07	6:37528885	0.393	5.99E-08	6:38491846	0.47	5.64E-08
6:36941206	0.497	1.10E-07	6:37537732	0.048	4.52E-08	6:39969761	0.401	2.46E-07
6:36943520	0.306	3.40E-08	6:37578145	0.071	1.50E-08	6:41238229	0.013	2.34E-08
6:36950661	0.072	1.10E-08	6:37588825	0.329	2.69E-07	8:4888252	0.168	1.29E-07

8-2-4. Selected SNP for DRESS (continued)

SNP	MAF	p-value
11:26385750	0.171	1.00E-08
11:26426466	0.048	4.28E-08
14:16105153	0.01	1.92E-07
15:25913540	0.316	1.14E-07
15:25913540	0.316	1.14E-07
20:3694703	0.009	2.99E-07
20:3704861	0.008	4.84E-08

8-2-5. Selected SNP for IMF

SNP	MAF	p-value	SNP	MAF	p-value	SNP	MAF	p-value
1:104768172	0.26	2.05E-07	3:224074836	0.05	2.16E-07	10:25966671	0.296	3.34E-08
1:139426590	0.114	6.11E-07	3:36141168	0.008	4.46E-07	10:25968223	0.108	3.70E-09
1:139868420	0.315	9.47E-07	4:17283517	0.016	5.27E-07	10:25968398	0.224	6.40E-08
1:171598461	0.094	1.60E-07	5:5110296	0.414	5.59E-07	10:26038156	0.017	3.21E-07
1:171604642	0.011	8.20E-07	5:59470895	0.485	8.02E-08	10:26168122	0.028	1.46E-07
1:19648017	0.369	6.90E-07	6:25680997	0.07	4.35E-07	10:26252127	0.044	6.32E-08
1:19668677	0.435	2.16E-07	6:35503461	0.421	6.68E-07	10:26923660	0.057	8.46E-07
1:21892852	0.033	7.50E-07	6:36991143	0.493	7.83E-07	10:26958896	0.043	5.40E-08
1:30141355	0.124	4.94E-07	6:37009499	0.375	3.94E-08	10:27450048	0.026	2.06E-07
1:39302949	0.052	4.94E-07	6:37010465	0.48	4.11E-07	11:24288934	0.253	6.19E-07
1:69244732	0.025	9.84E-07	6:37011845	0.285	3.28E-07	11:7673849	0.161	2.34E-07
2:105520875	0.007	8.33E-07	6:37033477	0.19	6.83E-07	13:11869525	0.304	3.44E-07
2:109397462	0.034	4.52E-08	6:37070192	0.228	2.29E-07	13:3487653	0.317	7.16E-07
2:116082673	0.041	3.73E-08	6:37071173	0.13	9.96E-08	14:2232796	0.083	6.77E-07
2:116297787	0.076	2.02E-12	6:37083820	0.423	4.09E-07	14:42996731	0.276	8.85E-07
2:116739868	0.053	8.39E-07	6:37084369	0.119	7.13E-09	14:42999772	0.41	3.50E-07
2:116774703	0.042	1.42E-08	6:37126514	0.094	6.25E-07	15:23861645	0.034	6.01E-07
2:117376848	0.039	9.58E-07	6:37131598	0.081	7.00E-07	15:47047031	0.081	7.08E-07
2:117946614	0.076	8.87E-07	6:37137051	0.115	1.92E-07	16:14895299	0.024	4.92E-07
2:117958742	0.11	9.77E-07	6:37707299	0.389	1.70E-07	16:67968896	0.318	6.67E-07
2:118040948	0.051	4.08E-09	6:38440655	0.209	7.77E-07	17:25566869	0.259	5.50E-07
2:118041324	0.089	4.10E-07	6:68674304	0.045	1.84E-07	17:25593777	0.132	6.19E-07
2:118049723	0.039	4.88E-09	7:3068905	0.095	7.87E-07	17:9831431	0.406	7.18E-07
2:118207406	0.037	4.55E-08	8:24814018	0.012	2.43E-06	17:9835011	0.304	1.45E-07
2:118660954	0.051	5.35E-08	8:54571106	0.355	2.65E-06	18:59060634	0.124	5.02E-07
2:118894705	0.053	1.91E-07	9:8343807	0.083	2.21E-06	18:59732763	0.041	2.70E-07
2:118933616	0.084	2.65E-07	9:85516831	0.012	3.11E-06	18:60299766	0.086	2.50E-08
2:118987107	0.033	1.64E-07	10:25085791	0.146	2.11E-07	18:60647477	0.059	1.14E-07
2:119032157	0.031	2.30E-10	10:25147454	0.13	5.62E-07	18:60687304	0.091	8.67E-07
2:119077970	0.055	8.17E-08	10:25188745	0.017	2.94E-07	18:61126772	0.065	1.15E-08
2:119078854	0.037	3.02E-09	10:25430542	0.24	7.70E-07	18:61765478	0.123	1.80E-07
2:119780895	0.037	3.35E-09	10:25447955	0.352	6.99E-07	18:61768592	0.058	2.57E-11
2:119944747	0.036	3.19E-07	10:25688142	0.032	2.63E-07	18:61832952	0.055	5.90E-10
2:120110153	0.055	3.62E-07	10:25927155	0.092	2.52E-10	18:61836992	0.412	7.56E-07
2:120157774	0.059	7.30E-07	10:25931769	0.036	9.88E-14	18:61844228	0.315	9.66E-07
2:120571539	0.035	7.91E-10	10:25933500	0.133	5.99E-07	18:61928387	0.07	1.40E-08
2:120699592	0.039	4.35E-08	10:25934258	0.016	2.67E-07	18:61934217	0.069	2.53E-07
2:128887000	0.006	4.42E-07	10:25940059	0.281	1.78E-08	18:61951600	0.238	1.50E-07
2:227638749	0.446	9.20E-08	10:25943423	0.118	5.45E-08	18:61962193	0.247	3.75E-07
2:227642186	0.304	7.02E-08	10:25956478	0.079	4.87E-13	18:62009992	0.16	4.07E-07
2:227642923	0.451	2.31E-08	10:25960155	0.251	7.30E-07	18:62018110	0.083	7.27E-09
2:239057210	0.104	3.70E-07	10:25960279	0.399	2.06E-07	18:62019971	0.106	6.94E-07
2:245885201	0.181	5.32E-07	10:25962552	0.149	7.63E-12	18:62051469	0.162	1.53E-07

3:125666201	0.007	1.66E-07	10:25964557	0.09	1.63E-07	18:62056392	0.118	2.62E-07
3:145421484	0.008	4.51E-07	10:25966421	0.419	2.17E-07	18:62062548	0.139	1.96E-08

8-2-5. Selected SNP for IMF (continued)

SNP	MAF	p-value	SNP	MAF	p-value	SNP	MAF	p-value
18:62088046	0.144	5.18E-07	18:62894338	0.105	2.70E-08	18:63467543	0.412	3.38E-07
18:62140864	0.062	7.30E-14	18:62896471	0.075	5.95E-09	18:63536151	0.116	2.35E-08
18:62152926	0.052	6.17E-12	18:62902808	0.099	2.52E-09	18:63588112	0.086	8.03E-10
18:62242911	0.08	4.74E-08	18:62906363	0.082	3.00E-09	18:63588211	0.165	7.16E-10
18:62247785	0.094	4.92E-07	18:62910586	0.071	1.35E-09	18:63641756	0.307	5.41E-07
18:62297632	0.094	2.36E-08	18:62910942	0.199	7.93E-09	18:63667375	0.098	6.63E-08
18:62298959	0.22	8.86E-07	18:62915740	0.031	3.13E-07	18:63677840	0.202	4.31E-07
18:62306547	0.082	6.68E-07	18:62923903	0.097	3.04E-08	18:63677923	0.148	8.22E-09
18:62312428	0.262	1.04E-07	18:62961727	0.199	5.53E-07	18:63683934	0.393	3.93E-07
18:62312443	0.194	9.16E-08	18:63034904	0.11	2.99E-07	18:63691341	0.129	5.99E-08
18:62315940	0.066	1.12E-14	18:63083249	0.097	4.95E-07	18:63716856	0.137	7.95E-07
18:62316256	0.119	2.89E-08	18:63180318	0.051	2.69E-12	18:63755622	0.18	6.41E-07
18:62321316	0.06	1.77E-10	18:63222991	0.102	4.23E-07	18:63758005	0.404	6.14E-08
18:62324428	0.245	3.59E-07	18:63240136	0.087	4.41E-08	18:63809845	0.081	6.43E-07
18:62337083	0.086	7.15E-09	18:63250006	0.233	9.08E-07	18:63869449	0.474	4.14E-07
18:62356275	0.094	7.05E-12	18:63256971	0.127	8.27E-08	18:63869971	0.175	4.93E-09
18:62389560	0.056	2.81E-09	18:63265983	0.079	4.69E-11	18:63907079	0.062	3.65E-07
18:62417203	0.096	1.00E-08	18:63283833	0.181	3.48E-08	18:63921780	0.049	6.90E-17
18:62459691	0.151	3.50E-08	18:63290549	0.105	4.36E-07	18:63936191	0.416	5.97E-07
18:62464834	0.103	2.08E-09	18:63292767	0.138	5.77E-08	18:63943508	0.249	4.00E-08
18:62465646	0.437	9.45E-08	18:63307563	0.135	3.43E-07	18:63947780	0.387	5.64E-07
18:62498058	0.072	1.90E-09	18:63325969	0.042	4.75E-09	18:63951750	0.362	3.04E-09
18:62522139	0.103	2.40E-07	18:63328797	0.087	1.84E-08	18:63952211	0.27	1.32E-07
18:62596925	0.05	8.58E-16	18:63333519	0.155	7.77E-07	18:63958165	0.097	3.51E-10
18:62697549	0.183	3.68E-07	18:63339736	0.177	1.08E-10	18:63966392	0.022	9.88E-07
18:62709598	0.073	6.41E-08	18:63346504	0.058	3.66E-10	18:63970390	0.096	7.55E-07
18:62724787	0.11	8.26E-08	18:63368975	0.198	5.92E-07	18:63994768	0.17	3.46E-07

18:62749720	0.322	4.04E-08	18:63374804	0.126	8.39E-10	18:64009161	0.1	2.69E-17
18:62759793	0.217	2.08E-07	18:63375826	0.076	1.70E-11	18:64081180	0.236	7.18E-10
18:62760312	0.133	2.55E-07	18:63387064	0.254	7.87E-07	18:64081338	0.499	1.70E-10
18:62764990	0.211	3.19E-09	18:63393322	0.096	4.77E-07	18:64089099	0.308	2.73E-07
18:62765627	0.105	4.67E-12	18:63397346	0.149	4.06E-09	18:64089935	0.158	3.52E-10
18:62774897	0.263	8.55E-08	18:63398557	0.065	3.17E-12	18:64092006	0.079	1.93E-10
18:62820873	0.129	4.83E-07	18:63405701	0.251	6.01E-07	18:64096438	0.198	6.27E-07
18:62822546	0.114	4.01E-10	18:63406359	0.02	8.41E-07	18:64098846	0.085	9.49E-07
18:62822897	0.17	5.56E-08	18:63407107	0.064	9.36E-10	18:64103690	0.491	3.98E-07
18:62824050	0.187	2.60E-07	18:63408692	0.126	2.79E-07	18:64127307	0.137	2.10E-11
18:62833804	0.258	9.96E-07	18:63408699	0.091	2.29E-12	18:64128902	0.407	4.17E-08
18:62844263	0.051	1.66E-18	18:63410816	0.07	5.11E-09	18:64129131	0.074	1.67E-26
18:62851367	0.16	3.98E-10	18:63412579	0.287	4.12E-08	18:64129755	0.093	5.81E-13
18:62851485	0.247	1.87E-09	18:63413374	0.127	4.27E-09	18:64133604	0.194	2.09E-07
18:62851848	0.148	1.80E-09	18:63458413	0.152	4.47E-13	18:64140159	0.087	5.71E-20
18:62852866	0.067	1.44E-10	18:63459119	0.262	3.19E-09	18:64140171	0.218	7.27E-11
18:62858157	0.05	4.83E-13	18:63461702	0.207	1.09E-09	18:64142285	0.149	9.04E-19
18:62871503	0.081	2.63E-09	18:63463442	0.14	2.28E-11	18:64145123	0.347	2.09E-08

8-2-5. Selected SNP for IMF (continued)

SNP	MAF	p-value	SNP	MAF	p-value	SNP	MAF	p-value
18:64145927	0.156	6.12E-09	18:64441493	0.152	4.75E-15	18:64644740	0.277	4.40E-08
18:64151900	0.222	1.42E-07	18:64442181	0.274	2.19E-07	18:64648414	0.248	3.29E-08
18:64157616	0.305	5.23E-07	18:64442874	0.219	3.49E-15	18:64661729	0.234	3.58E-07
18:64162039	0.404	4.59E-07	18:64443120	0.102	7.03E-22	18:64675564	0.05	1.96E-11
18:64168341	0.31	2.09E-07	18:64444141	0.341	1.82E-07	18:64684563	0.307	4.37E-07
18:64168900	0.239	1.88E-07	18:64455141	0.105	3.36E-15	18:64685351	0.166	9.55E-07
18:64190428	0.112	6.34E-14	18:64464074	0.246	3.68E-08	18:64711408	0.055	6.69E-15
18:64190620	0.245	4.97E-07	18:64465606	0.275	9.85E-07	18:64759498	0.054	2.97E-17
18:64190878	0.132	2.41E-08	18:64465736	0.286	8.18E-08	18:64762186	0.11	6.57E-07
18:64192557	0.105	1.73E-11	18:64468635	0.119	1.28E-22	18:64839427	0.056	1.46E-13
18:64192699	0.068	6.19E-21	18:64477623	0.159	1.69E-17	18:64860596	0.133	6.79E-11
18:64196745	0.273	3.13E-11	18:64485507	0.168	9.10E-23	18:64866998	0.005	9.24E-07
18:64197287	0.194	8.41E-14	18:64486312	0.422	4.72E-07	18:64912779	0.087	6.25E-07
18:64197768	0.349	1.73E-09	18:64489866	0.137	7.92E-08	18:64957545	0.173	7.36E-09
18:64219551	0.158	5.06E-09	18:64494050	0.368	1.87E-13	18:64959539	0.273	2.90E-08

18:64272630	0.169	3.66E-08	18:64496250	0.408	9.75E-13	18:64960503	0.162	5.45E-08
18:64278207	0.157	6.39E-09	18:64499333	0.232	6.89E-15	18:64966109	0.118	2.65E-09
18:64291335	0.041	8.08E-10	18:64500030	0.268	2.52E-12	18:64971928	0.079	9.68E-09
18:64316482	0.164	1.65E-08	18:64500805	0.271	7.49E-08	18:64971969	0.041	4.16E-13
18:64338816	0.325	1.65E-08	18:64502808	0.275	4.78E-15	18:64988005	0.058	3.10E-08
18:64341672	0.304	4.00E-10	18:64507400	0.233	7.74E-10	18:65017420	0.079	8.27E-07
18:64342440	0.431	2.02E-08	18:64508318	0.165	3.19E-17	18:65019450	0.024	5.91E-07
18:64343333	0.201	5.67E-14	18:64510717	0.384	3.99E-07	18:65069389	0.007	1.02E-09
18:64343850	0.451	1.58E-08	18:64511907	0.288	2.97E-07	18:65094158	0.076	2.67E-09
18:64343959	0.146	3.47E-18	18:64512859	0.274	5.77E-08	18:65106605	0.155	6.88E-09
18:64344843	0.188	4.93E-10	18:64515350	0.317	8.07E-10	18:65124009	0.054	9.84E-12
18:64346151	0.285	1.78E-10	18:64515802	0.36	5.39E-07	18:65126367	0.079	3.44E-10
18:64346894	0.207	4.13E-14	18:64516776	0.335	3.30E-11	18:65128572	0.067	3.68E-08
18:64352826	0.456	8.48E-07	18:64519792	0.309	5.20E-09	18:65144709	0.095	1.88E-07
18:64353258	0.048	6.24E-07	18:64520092	0.255	1.09E-07	18:65152293	0.09	2.09E-07
18:64356404	0.032	2.63E-12	18:64523146	0.178	2.07E-09	18:65159510	0.056	1.06E-15
18:64357538	0.224	9.76E-11	18:64530703	0.059	3.35E-30	18:65162907	0.034	3.81E-20
18:64363304	0.276	8.94E-10	18:64531729	0.102	2.41E-09	18:65195913	0.062	4.50E-08
18:64364989	0.303	2.25E-10	18:64552442	0.128	7.55E-07	18:65283457	0.49	8.03E-08
18:64371724	0.186	5.58E-15	18:64555644	0.249	1.95E-08	18:65296316	0.446	8.85E-07
18:64394280	0.165	4.21E-17	18:64566847	0.217	1.59E-08	18:65312485	0.337	1.04E-07
18:64409041	0.15	8.42E-12	18:64574348	0.2	3.10E-07	18:65312551	0.47	2.40E-09
18:64413484	0.182	1.84E-12	18:64577124	0.134	1.21E-12	18:65312907	0.27	6.18E-07
18:64425930	0.19	1.94E-10	18:64577721	0.091	7.39E-16	18:65314462	0.055	1.02E-12
18:64430827	0.071	3.37E-32	18:64605680	0.192	8.77E-07	18:65332238	0.25	9.89E-07
18:64432480	0.306	3.68E-09	18:64626021	0.108	1.77E-18	18:65346702	0.448	5.01E-07
18:64433805	0.359	3.36E-07	18:64627288	0.385	5.71E-07	18:65370001	0.066	4.07E-09
18:64437483	0.096	8.82E-26	18:64628170	0.313	2.88E-07	18:65390325	0.036	5.35E-11
18:64437674	0.162	1.02E-20	18:64628672	0.208	3.93E-12	18:65391718	0.046	6.07E-15
18:64438969	0.487	3.24E-08	18:64640065	0.188	1.97E-07	18:65395020	0.073	5.96E-07

8-2-5. Selected SNP for IMF (continued)

SNP	MAF	p-value	SNP	MAF	p-value	SNP	MAF	p-value
18:65398815	0.49	4.21E-07	18:66279497	0.053	1.61E-07	18:68039771	0.107	4.14E-07
18:65406537	0.249	2.69E-07	18:66280558	0.097	4.95E-07	18:68431388	0.056	2.43E-07
18:65415035	0.054	1.41E-21	18:66363542	0.08	9.29E-07	18:68438329	0.045	1.48E-07
18:65416931	0.141	2.00E-09	18:66464994	0.295	9.11E-09	20:7168663	0.025	7.55E-07
18:65416967	0.209	3.64E-08	18:66478917	0.037	1.98E-08	22:35155507	0.034	2.40E-07
18:65423643	0.098	2.44E-10	18:66484603	0.489	2.60E-07	22:48689572	0.354	3.80E-08
18:65436431	0.064	1.40E-19	18:66488128	0.037	3.84E-10	23:33126187	0.029	1.07E-08
18:65438361	0.207	1.45E-07	18:66495463	0.378	6.46E-07	23:35070384	0.397	5.85E-07
18:65440359	0.096	1.18E-13	18:66521971	0.068	6.69E-07	23:35116790	0.442	9.96E-07
18:65440449	0.108	2.27E-13	18:66545885	0.052	4.08E-11	23:35170041	0.227	7.97E-07
18:65448678	0.044	1.03E-10	18:66686233	0.096	3.02E-11	23:36102678	0.274	2.18E-07
18:65468081	0.104	2.04E-07	18:66692573	0.07	5.22E-07	23:36349324	0.016	1.23E-07
18:65482025	0.045	7.65E-26	18:66693888	0.069	2.07E-09	23:40161528	0.019	6.66E-07

18:65483063	0.115	1.38E-07	18:66699677	0.205	2.20E-07	23:40442535	0.092	7.16E-07
18:65487810	0.119	2.54E-07	18:66709601	0.041	3.86E-13	23:42002952	0.05	2.25E-07
18:65504292	0.123	3.13E-07	18:66745708	0.192	1.18E-07	23:42054693	0.023	6.61E-09
18:65505874	0.19	6.76E-08	18:66764616	0.106	1.38E-10	23:42070786	0.014	1.18E-07
18:65506439	0.093	1.15E-08	18:66848634	0.068	5.21E-09	23:42087351	0.143	9.83E-07
18:65520347	0.064	9.27E-09	18:66938613	0.059	1.32E-09	23:42090578	0.047	7.69E-08
18:65577071	0.269	7.46E-07	18:66948241	0.087	4.02E-08	23:42117218	0.026	1.03E-09
18:65593686	0.046	2.07E-11	18:67007943	0.046	1.65E-09	23:42521945	0.011	7.81E-07
18:65602799	0.132	8.86E-11	18:67036794	0.036	1.36E-13	23:44619899	0.051	2.21E-09
18:65623153	0.152	5.13E-08	18:67036798	0.173	9.40E-07	23:44708118	0.047	2.13E-07
18:65627007	0.049	4.87E-10	18:67047789	0.109	1.66E-08	23:44746661	0.044	5.49E-08
18:65628436	0.088	7.13E-09	18:67156229	0.05	3.60E-07	23:44865981	0.032	5.38E-07
18:65716283	0.058	1.10E-11	18:67179158	0.066	1.93E-08	23:45991860	0.25	7.14E-07
18:65742059	0.045	3.36E-09	18:67182294	0.042	3.16E-09	23:46006228	0.209	9.97E-07
18:65816189	0.238	4.22E-08	18:67182355	0.048	3.86E-09	25:563440	0.025	7.26E-07
18:65816213	0.081	4.44E-08	18:67298832	0.039	5.78E-10	26:10781193	0.012	1.70E-06
18:65827345	0.05	3.18E-11	18:67518973	0.068	7.93E-07	26:12855735	0.119	1.74E-06
18:65846686	0.09	2.44E-07	18:67654136	0.05	2.98E-08			
18:65908210	0.053	1.16E-08	18:67654223	0.038	7.11E-10			
18:65919480	0.079	5.21E-07	18:67711401	0.076	2.25E-07			
18:65936720	0.082	8.02E-07	18:67713662	0.045	1.44E-11			
18:65950283	0.052	5.44E-10	18:67721919	0.371	8.20E-07			
18:65951766	0.095	1.41E-09	18:67726176	0.037	5.08E-12			
18:65962901	0.06	1.65E-10	18:67741805	0.064	1.96E-08			
18:65967001	0.045	1.43E-09	18:67774234	0.108	5.03E-07			
18:65977591	0.045	1.96E-11	18:67913809	0.066	3.23E-07			
18:65977596	0.071	6.58E-08	18:67937936	0.139	1.66E-07			
18:65983262	0.076	2.57E-07	18:67943328	0.041	1.23E-07			
18:65996880	0.045	2.46E-09	18:67994054	0.072	1.27E-07			
18:66179143	0.046	5.89E-07	18:68000919	0.04	1.10E-13			
18:66193341	0.053	5.81E-08	18:68000923	0.058	1.97E-10			
18:66197774	0.072	8.78E-07	18:68004486	0.047	1.08E-07			

8-2-6. Selected SNP for LMY

SNP	MAF	p-value	SNP	MAF	p-value	SNP	MAF	p-value
1:102055203	0.013	2.20E-06	6:36866916	0.387	3.85E-12	6:36978619	0.392	5.50E-11
1:102424619	0.014	8.54E-07	6:36867115	0.301	1.64E-10	6:36978958	0.494	7.36E-07
1:109547565	0.03	4.21E-07	6:36868055	0.149	2.71E-06	6:36979465	0.493	1.73E-07
1:12498670	0.01	8.57E-07	6:36868441	0.303	8.50E-10	6:36979766	0.412	4.50E-07
2:135750466	0.006	3.13E-06	6:36870173	0.488	1.21E-09	6:36979933	0.493	4.84E-09
2:232848741	0.016	1.30E-06	6:36879383	0.487	1.92E-09	6:36980718	0.299	3.32E-08
3:153351491	0.016	2.96E-06	6:36880013	0.402	5.42E-07	6:36981038	0.487	3.09E-08
3:77185761	0.171	1.28E-06	6:36880062	0.298	3.10E-08	6:36981159	0.412	2.85E-08
3:8422708	0.014	2.07E-06	6:36884735	0.268	1.12E-07	6:36981238	0.392	2.34E-08
5:103660749	0.021	2.00E-06	6:36886180	0.278	2.85E-08	6:36982545	0.491	1.73E-09
5:71599237	0.032	1.44E-06	6:36886299	0.31	1.24E-09	6:36982899	0.379	7.79E-07
5:71659355	0.028	1.60E-06	6:36887568	0.388	5.21E-09	6:36984153	0.491	1.10E-07

5:71695967	0.031	1.87E-06	6:36899027	0.307	1.22E-10	6:36984747	0.495	7.90E-10
6:33504319	0.282	6.04E-07	6:36900378	0.449	1.50E-06	6:36984985	0.494	1.90E-08
6:34332789	0.059	6.77E-07	6:36900601	0.073	2.94E-06	6:36986313	0.456	1.30E-06
6:34339236	0.072	1.09E-07	6:36904664	0.341	3.12E-08	6:36986361	0.47	3.92E-07
6:34358459	0.076	2.31E-08	6:36909193	0.378	1.95E-06	6:36988188	0.485	2.39E-08
6:35865240	0.271	1.70E-07	6:36909980	0.492	3.57E-10	6:36988302	0.464	3.64E-07
6:35870595	0.322	1.77E-06	6:36910736	0.435	1.22E-09	6:36988506	0.489	2.75E-07
6:35871196	0.266	2.98E-06	6:36911371	0.394	2.43E-13	6:36989202	0.475	2.93E-07
6:36155985	0.17	2.82E-06	6:36915939	0.309	4.95E-11	6:36989893	0.398	2.10E-12
6:36416658	0.168	2.07E-06	6:36923858	0.315	8.32E-12	6:36991000	0.385	2.14E-07
6:36416848	0.3	1.61E-06	6:36924192	0.34	3.36E-09	6:36991114	0.355	1.35E-07
6:36428727	0.145	1.48E-06	6:36928835	0.301	3.78E-11	6:36996476	0.337	8.96E-07
6:36461335	0.161	2.43E-07	6:36934675	0.363	5.24E-08	6:36997565	0.379	1.91E-07
6:36463650	0.153	1.46E-06	6:36935893	0.334	6.34E-09	6:37000219	0.38	3.44E-14
6:36463754	0.33	3.23E-07	6:36937956	0.359	3.38E-07	6:37000524	0.469	1.73E-06
6:36471430	0.393	1.28E-06	6:36939481	0.32	1.98E-08	6:37001731	0.37	1.06E-12
6:36572923	0.49	5.81E-09	6:36940694	0.287	1.02E-07	6:37001747	0.359	1.93E-07
6:36620367	0.314	2.19E-08	6:36940978	0.391	2.49E-08	6:37004974	0.383	1.63E-11
6:36623126	0.3	7.30E-09	6:36941206	0.5	2.25E-10	6:37006553	0.371	4.11E-13
6:36676760	0.297	1.10E-10	6:36941612	0.312	1.37E-09	6:37007016	0.462	1.22E-06
6:36789954	0.375	7.79E-07	6:36954317	0.454	2.86E-06	6:37008261	0.413	2.38E-07
6:36796272	0.359	2.54E-06	6:36960302	0.421	2.64E-06	6:37009499	0.397	7.29E-12
6:36804204	0.487	2.40E-07	6:36965594	0.385	1.83E-07	6:37010465	0.496	4.27E-10
6:36804256	0.277	1.40E-07	6:36965713	0.34	5.75E-07	6:37010551	0.343	1.40E-08
6:36813143	0.486	5.28E-07	6:36969028	0.307	2.84E-09	6:37010741	0.31	7.91E-12
6:36839109	0.28	4.51E-07	6:36971935	0.338	2.58E-06	6:37011023	0.139	1.13E-08
6:36841486	0.491	1.02E-06	6:36973028	0.303	2.11E-06	6:37011044	0.357	1.55E-11
6:36845573	0.488	5.46E-07	6:36976866	0.367	1.35E-06	6:37011845	0.308	5.22E-11
6:36855753	0.155	3.18E-07	6:36977365	0.386	1.76E-06	6:37012272	0.49	4.73E-07
6:36855848	0.151	1.08E-06	6:36977846	0.309	3.05E-09	6:37012301	0.108	2.19E-06
6:36864972	0.383	2.13E-08	6:36978379	0.497	6.76E-07	6:37012355	0.338	5.55E-08
6:36865319	0.157	1.00E-06	6:36978506	0.378	4.40E-07	6:37012416	0.466	1.05E-07
6:36866760	0.37	1.66E-06	6:36978600	0.428	5.59E-08	6:37012633	0.287	1.63E-12

8-2-6. Selected SNP for LMY (continued)

SNP2	MAF	p-value	SNP	MAF	p-value	SNP	MAF	p-value
6:37012743	0.328	1.39E-08	6:37131598	0.095	1.09E-07	6:37625722	0.486	2.66E-06
6:37013663	0.44	6.03E-09	6:37132520	0.241	2.00E-06	6:37639274	0.322	6.22E-11
6:37014402	0.111	2.22E-08	6:37133484	0.286	2.22E-07	6:37641703	0.43	1.33E-07
6:37017377	0.104	2.79E-06	6:37134706	0.105	2.65E-06	6:37646223	0.385	1.00E-06
6:37022629	0.142	7.96E-07	6:37137051	0.138	1.63E-08	6:37646228	0.433	5.51E-07
6:37023017	0.068	1.45E-06	6:37152822	0.286	1.35E-07	6:37646236	0.426	4.23E-08
6:37027217	0.054	3.09E-07	6:37174603	0.341	1.46E-09	6:37648835	0.411	3.19E-08
6:37031058	0.055	1.12E-06	6:37176390	0.301	2.80E-07	6:37649688	0.478	4.23E-07
6:37032632	0.079	2.62E-06	6:37180170	0.47	3.05E-06	6:37649710	0.343	5.80E-09
6:37035027	0.057	2.10E-06	6:37185976	0.354	1.01E-06	6:37651002	0.497	8.74E-07

6:37035542	0.224	3.62E-07	6:37204144	0.461	2.26E-07	6:37660927	0.291	1.55E-12
6:37038921	0.066	6.09E-07	6:37215463	0.296	5.60E-13	6:37663892	0.323	2.02E-08
6:37039495	0.363	1.47E-06	6:37218127	0.498	1.99E-06	6:37669757	0.342	6.43E-08
6:37041361	0.06	1.89E-06	6:37223597	0.329	3.22E-09	6:37676407	0.286	2.07E-13
6:37055967	0.238	1.43E-06	6:37231727	0.324	1.54E-09	6:37679480	0.419	3.11E-09
6:37055983	0.258	1.66E-07	6:37232730	0.317	4.17E-11	6:37679634	0.301	1.38E-08
6:37057090	0.11	3.49E-08	6:37234274	0.47	1.48E-06	6:37682091	0.441	8.13E-07
6:37062647	0.066	4.34E-07	6:37244292	0.325	1.05E-09	6:37687841	0.401	3.88E-11
6:37062804	0.098	1.18E-07	6:37246197	0.305	2.37E-09	6:37694401	0.349	4.50E-11
6:37064524	0.118	1.56E-07	6:37249737	0.306	6.66E-12	6:37694916	0.399	7.07E-11
6:37067851	0.099	7.48E-07	6:37257975	0.46	5.73E-08	6:37695541	0.324	1.05E-08
6:37068651	0.131	5.75E-09	6:37302029	0.307	8.85E-11	6:37696386	0.332	4.03E-10
6:37071127	0.159	2.28E-08	6:37371204	0.459	1.50E-07	6:37698503	0.457	1.45E-08
6:37071173	0.171	2.31E-09	6:37402245	0.294	3.69E-12	6:37701961	0.309	1.84E-07
6:37072532	0.328	4.95E-09	6:37411665	0.37	1.83E-06	6:37701980	0.357	3.68E-15
6:37073133	0.089	1.04E-06	6:37448093	0.364	1.23E-06	6:37704209	0.411	7.01E-12
6:37074271	0.068	1.61E-06	6:37461262	0.313	2.41E-11	6:37704960	0.298	3.23E-13
6:37074303	0.216	4.96E-10	6:37475062	0.296	1.06E-12	6:37707299	0.416	1.49E-11
6:37082977	0.141	6.69E-08	6:37517693	0.294	4.92E-13	6:37707553	0.344	4.96E-09
6:37083820	0.408	2.43E-06	6:37523721	0.456	6.03E-07	6:37708864	0.272	1.70E-13
6:37084369	0.147	1.57E-08	6:37528052	0.333	2.07E-08	6:37714980	0.321	2.97E-07
6:37086120	0.116	5.76E-07	6:37528885	0.416	1.07E-09	6:37718589	0.342	4.42E-08
6:37100478	0.097	1.71E-06	6:37539289	0.34	6.51E-07	6:37719901	0.149	3.14E-08
6:37102022	0.142	1.82E-08	6:37540148	0.333	1.03E-09	6:37721941	0.301	1.16E-07
6:37102378	0.116	2.79E-07	6:37557272	0.297	1.39E-07	6:37726861	0.293	1.22E-06
6:37108127	0.08	2.48E-07	6:37572760	0.309	2.63E-06	6:37732477	0.145	1.74E-06
6:37108293	0.086	2.47E-07	6:37578335	0.417	1.27E-08	6:37741444	0.155	2.75E-07
6:37109146	0.118	1.76E-07	6:37578424	0.322	3.78E-07	6:37766859	0.402	1.92E-06
6:37117256	0.267	1.33E-07	6:37579327	0.47	2.89E-06	6:37780331	0.35	1.02E-08
6:37118221	0.112	2.83E-06	6:37581725	0.447	1.33E-06	6:37791866	0.294	7.96E-08
6:37125266	0.085	2.14E-06	6:37586919	0.259	1.60E-13	6:37793428	0.479	9.77E-07

6:37126514	0.113	4.52E-08	6:37587663	0.263	1.20E-10	6:37819760	0.277	2.24E-08
6:37128230	0.095	2.49E-07	6:37588546	0.349	6.52E-08	6:37843942	0.389	1.57E-07
6:37128282	0.077	1.68E-06	6:37598575	0.364	1.28E-06	6:37862024	0.287	9.92E-08
6:37128650	0.248	2.07E-06	6:37625088	0.324	3.27E-10	6:37886775	0.314	2.07E-06

8-2-6. Selected SNP for LMY (continued)

SNP	MAF	p-value	SNP	MAF	p-value
6:37948535	0.329	6.87E-07	12:56943313	0.06	7.05E-07
6:37979645	0.325	1.69E-08	13:23840863	0.195	1.75E-06
6:37979762	0.268	3.35E-08	14:48383290	0.011	4.92E-07
6:37984521	0.246	6.70E-10	15:47576401	0.007	2.84E-06
6:37987765	0.229	2.49E-07	16:55378705	0.403	1.52E-06
6:37987789	0.261	1.33E-08	16:55380433	0.397	2.57E-06
6:37987793	0.272	4.58E-08	16:71039933	0.202	1.71E-06
6:37987807	0.289	7.92E-10	16:71040011	0.255	1.62E-07
6:37989335	0.256	1.66E-09	18:18695698	0.02	2.97E-06
6:37990158	0.267	1.23E-10	18:64941125	0.012	2.83E-06
6:37996569	0.241	3.75E-07	20:44983973	0.062	9.22E-08
6:37997898	0.279	6.19E-10	23:29577587	0.311	7.73E-07
6:37998720	0.301	1.16E-06	23:29589736	0.216	2.17E-06
6:37998827	0.264	3.00E-09	23:57868053	0.304	9.71E-07
6:38003500	0.257	8.32E-09			
6:38006817	0.275	1.99E-07			
6:38006942	0.379	6.99E-07			
6:38029892	0.243	1.08E-06			
6:38031139	0.255	3.17E-07			
6:38034949	0.364	1.18E-06			
6:38035107	0.336	7.48E-07			
6:38059144	0.234	1.55E-06			
6:38086736	0.378	4.65E-07			
6:38140404	0.233	4.88E-07			
6:38191739	0.089	8.30E-07			
6:38196373	0.483	2.22E-07			
6:38196512	0.371	2.92E-06			
6:38288170	0.091	1.84E-06			
6:38291990	0.103	1.33E-06			
6:38396772	0.248	6.32E-07			
6:38454163	0.37	1.17E-06			
6:38497995	0.479	1.11E-06			
6:38529980	0.414	5.60E-07			
6:38555845	0.228	5.64E-07			
6:38572760	0.247	2.79E-06			
6:88807138	0.479	2.60E-07			
6:88807888	0.487	2.42E-06			
6:88814205	0.426	1.74E-06			
6:94102042	0.446	2.13E-06			
7:47087745	0.181	1.30E-07			
8:33861947	0.015	1.54E-06			
8:46111281	0.143	1.38E-06			
11:26385750	0.161	2.17E-07			
11:26388169	0.144	2.71E-06			
11:7936077	0.009	2.97E-06			

8-2-7. Selected SNP for PCF

SNP	MAF	p-value	SNP	MAF	p-value
1:15250860	0.286	1.70E-06	11:39960334	0.323	5.63E-04
1:176934337	0.006	5.99E-07	11:44586136	0.491	3.28E-05
1:19247032	0.123	2.63E-06	11:4957615	0.08	2.26E-04
1:241463131	0.07	5.11E-07	13:21243575	0.034	9.30E-07
1:266366208	0.008	2.06E-08	13:25767074	0.007	2.06E-06
1:275591588	0.058	2.55E-06	13:26664001	0.386	3.76E-08
1:30621284	0.018	3.56E-08	13:46521518	0.074	7.57E-07
1:31493983	0.149	8.05E-05	14:10270116	0.198	8.21E-07
1:40670198	0.091	2.42E-47	14:18736989	0.027	9.90E-06
1:40937855	0.452	2.91E-10	15:66773839	0.019	4.59E-07
1:41469765	0.183	2.09E-10	16:13530968	0.055	1.11E-05
1:47379893	0.135	1.63E-04	16:18002639	0.043	6.40E-04
3:59704536	0.175	7.94E-07	16:21620943	0.15	2.31E-07
3:5971027	0.041	7.82E-07	16:32005123	0.416	2.39E-10
6:14725925	0.145	1.30E-04	16:33050047	0.035	1.44E-04
6:24453858	0.44	6.34E-04	16:34671805	0.33	5.40E-04
6:26863333	0.014	7.80E-11	18:12548653	0.052	1.18E-06
6:31990119	0.165	3.92E-04	18:13636735	0.01	4.30E-07
6:36819222	0.48	1.94E-14	19:26058416	0.38	5.51E-06
6:36968287	0.016	8.74E-21	19:28256173	0.084	2.41E-07
6:37013810	0.441	1.06E-10	19:29825703	0.1	1.08E-06
6:37516994	0.27	1.05E-29	19:39593299	0.234	3.72E-05
6:37708978	0.493	3.20E-07	20:28068276	0.023	2.84E-07
6:48076294	0.122	1.18E-04	20:32025940	0.042	1.27E-06
6:49901195	0.436	4.65E-04	21:7040988	0.01	9.70E-07
6:58350000	0.281	5.55E-05	22:6161861	0.008	4.85E-07
7:92499726	0.019	6.16E-08	23:25043582	0.29	4.93E-07
8:12484487	0.247	2.40E-05	23:29733600	0.454	1.84E-05
8:13555395	0.236	8.44E-07	23:39017018	0.043	4.25E-05
8:70517305	0.377	3.03E-05	23:55447703	0.237	7.21E-07
8:72555353	0.052	9.68E-04	24:25716192	0.214	6.17E-04
8:82257699	0.365	8.81E-08	24:27541648	0.19	8.39E-07
8:82583453	0.164	3.19E-07	24:35829455	0.121	7.67E-09
8:82897823	0.047	4.95E-20	24:831840	0.142	1.78E-07
8:87485545	0.332	1.51E-07	25:15035616	0.178	2.81E-07
9:20151547	0.033	5.94E-11	26:19926162	0.005	4.72E-07
9:23084752	0.043	5.08E-06	26:36410523	0.008	4.83E-10
9:36210627	0.246	1.86E-17			
9:38356183	0.27	1.74E-05			
10:72239780	0.04	1.31E-07			
11:11861613	0.316	9.00E-04			
11:21095364	0.167	3.14E-04			
11:25880037	0.245	1.21E-09			
11:26450446	0.223	3.89E-29			
11:36017659	0.078	3.44E-05			

8-2-8. Selected SNP for PEMD

SNP	MAF	p-value	SNP	MAF	p-value	SNP	MAF	p-value
1:105273500	0.041	9.99E-07	1:68864439	0.01	1.55E-07	4:15063543	0.356	8.19E-07
1:105274288	0.039	7.67E-07	1:69248603	0.012	3.12E-07	4:74264995	0.063	8.94E-07
1:114589843	0.05	1.19E-07	1:69646814	0.01	1.17E-07	5:77237846	0.023	1.93E-07
1:121416449	0.101	8.83E-07	1:70700999	0.092	1.97E-07	5:77257767	0.025	2.25E-07
1:121441082	0.139	8.24E-07	1:85881443	0.153	7.09E-07	5:77266550	0.03	3.50E-07
1:128711970	0.203	7.01E-07	1:90518773	0.273	7.61E-08	5:77267881	0.028	2.91E-07
1:128714785	0.201	5.18E-07	1:90521256	0.321	3.13E-07	5:77291290	0.024	7.60E-07
1:128717865	0.166	1.23E-07	1:90522038	0.36	7.28E-07	5:77302112	0.028	7.62E-07
1:128719432	0.196	2.94E-07	1:94388323	0.096	6.53E-07	5:89943438	0.021	2.50E-07
1:129815923	0.154	6.00E-07	2:116521844	0.037	9.33E-08	6:29279110	0.209	6.95E-07
1:129815968	0.161	2.93E-07	2:117025552	0.044	6.22E-07	6:33203818	0.042	8.86E-07
1:152259503	0.271	1.58E-07	2:117086763	0.039	5.91E-07	6:35455384	0.134	3.91E-07
1:152563808	0.182	1.62E-07	2:117803592	0.042	7.87E-07	6:35457551	0.096	3.53E-07
1:153452785	0.14	6.18E-08	2:117909043	0.097	4.82E-07	6:35504886	0.112	9.30E-07
1:163369181	0.007	4.22E-07	2:117946614	0.113	8.45E-07	6:35607168	0.144	2.46E-07
1:166418227	0.453	9.95E-07	2:117958011	0.098	1.86E-07	6:35634643	0.057	1.38E-07
1:17545601	0.031	6.26E-07	2:117984831	0.123	6.27E-07	6:35647279	0.044	6.85E-08
1:18207561	0.021	8.17E-07	2:118023195	0.115	5.54E-07	6:35729712	0.238	6.70E-07
1:191713332	0.017	2.73E-08	2:118023917	0.123	1.47E-07	6:35869287	0.148	7.98E-07
1:224324055	0.014	7.10E-08	2:118030455	0.108	1.64E-07	6:36015190	0.091	5.64E-08
1:224477300	0.013	7.05E-07	2:118034094	0.147	7.54E-07	6:36416658	0.117	7.49E-07
1:242588435	0.286	1.36E-08	2:118041407	0.135	8.75E-07	6:36442181	0.272	7.95E-07
1:242592899	0.32	2.45E-07	2:118043491	0.187	9.76E-07	6:36457753	0.155	4.96E-09
1:242592975	0.307	3.09E-07	2:118048807	0.158	7.25E-07	6:36461335	0.113	1.34E-09
1:254215277	0.079	9.53E-07	2:118049429	0.142	3.73E-07	6:36477029	0.145	2.46E-07
1:29158829	0.017	8.85E-07	2:118049523	0.117	6.04E-07	6:36544808	0.123	4.72E-07
1:29222167	0.026	8.52E-07	2:118049723	0.044	7.76E-08	6:36545220	0.133	2.24E-07
1:41485741	0.171	5.56E-07	2:118052483	0.125	1.47E-07	6:36545291	0.174	3.23E-10

1:41498428	0.13	7.72E-07	2:118052785	0.143	6.26E-08	6:36569337	0.221	9.07E-11
1:41514731	0.145	2.70E-07	2:118150665	0.042	3.48E-07	6:36572923	0.204	5.35E-10
1:41537749	0.091	4.02E-07	2:119245717	0.04	8.43E-07	6:36642513	0.221	5.10E-08
1:41551470	0.091	7.42E-07	2:119526055	0.042	6.79E-07	6:36812865	0.24	3.79E-07
1:41562700	0.099	9.13E-08	2:119927288	0.048	2.18E-07	6:36840356	0.098	1.49E-07
1:41590993	0.444	4.38E-07	2:120950028	0.038	9.19E-07	6:36841119	0.087	2.32E-08
1:41687131	0.129	8.56E-07	2:122576961	0.085	7.35E-07	6:36841486	0.234	6.31E-08
1:41689478	0.184	4.52E-09	2:86920138	0.005	8.79E-07	6:36851287	0.031	6.89E-07
1:41689536	0.098	2.54E-07	3:149434134	0.126	6.72E-07	6:36855753	0.087	7.77E-07
1:41689642	0.107	2.52E-07	3:177444952	0.078	9.90E-07	6:36855848	0.086	5.69E-07
1:41689856	0.213	1.90E-07	3:199139332	0.257	9.84E-07	6:36865319	0.095	2.05E-08
1:41689861	0.202	4.29E-07	3:199139413	0.247	8.08E-07	6:36866029	0.211	1.17E-07
1:41695826	0.186	5.94E-07	3:60133053	0.08	4.98E-07	6:36866675	0.304	5.16E-07
1:41769070	0.146	4.53E-07	3:6729084	0.021	4.23E-07	6:36876353	0.083	5.19E-08
1:41894406	0.184	2.59E-07	3:92704516	0.192	2.77E-07	6:36897622	0.019	3.06E-07
1:68388880	0.011	5.35E-07	3:92729283	0.088	7.42E-07	6:36904636	0.2	1.80E-07
1:68435541	0.01	9.31E-08	4:100684583	0.076	6.66E-07	6:36910736	0.195	8.39E-07

8-2-8. Selected SNP for PEMD (continue)

SNP	MAF	p-value	SNP	MAF	p-value	SNP	MAF	p-value
6:36938217	0.131	2.11E-07	6:37449673	0.084	1.59E-07	6:38101093	0.264	1.12E-07
6:36940100	0.177	5.95E-10	6:37461262	0.089	8.16E-07	6:38232761	0.055	4.58E-07
6:36941206	0.205	5.01E-09	6:37461262	0.093	2.15E-07	6:38233138	0.033	5.96E-08
6:36973028	0.41	8.35E-07	6:37485878	0.11	2.28E-08	6:38234814	0.113	3.21E-08
6:36977365	0.184	1.47E-07	6:37500865	0.1	4.20E-07	6:38237799	0.091	1.20E-07
6:36979766	0.456	2.58E-07	6:37513052	0.085	4.19E-08	6:38238491	0.076	5.16E-08
6:36980718	0.162	6.38E-07	6:37517693	0.084	3.68E-09	6:38240595	0.061	2.63E-07
6:36981159	0.165	1.60E-08	6:37529212	0.083	2.59E-07	6:38261511	0.029	3.79E-07
6:36983625	0.152	2.15E-08	6:37531171	0.166	4.33E-08	6:38261644	0.034	2.18E-07
6:36985004	0.114	2.70E-07	6:37534465	0.173	7.15E-08	6:38261644	0.084	6.72E-07

6:36986361	0.194	3.63E-08	6:37557272	0.121	3.89E-07	6:38262034	0.211	5.45E-07
6:36988188	0.176	3.20E-08	6:37566720	0.207	8.10E-07	6:38282752	0.181	4.59E-07
6:36988707	0.184	4.74E-07	6:37578424	0.131	2.97E-07	6:38297721	0.143	4.26E-07
6:36997023	0.069	3.36E-07	6:37581245	0.205	1.18E-07	6:38307658	0.073	7.91E-07
6:36998808	0.062	9.36E-07	6:37584836	0.109	5.11E-07	6:38322153	0.393	4.19E-07
6:37001747	0.177	4.00E-08	6:37586919	0.312	4.77E-10	6:38322543	0.043	4.78E-08
6:37006344	0.082	5.65E-07	6:37638154	0.083	8.84E-07	6:38322803	0.429	4.77E-08
6:37006436	0.211	9.29E-09	6:37646232	0.23	7.84E-08	6:38334283	0.058	1.27E-07
6:37019549	0.082	3.99E-07	6:37651124	0.052	1.16E-08	6:38411758	0.373	1.31E-08
6:37022183	0.15	9.90E-07	6:37665116	0.206	1.15E-08	6:38462659	0.041	2.01E-07
6:37029801	0.156	8.38E-07	6:37669686	0.179	1.48E-07	6:38464721	0.39	1.23E-07
6:37069409	0.125	8.21E-10	6:37687841	0.141	6.68E-07	6:38466372	0.388	1.57E-07
6:37071127	0.048	2.79E-07	6:37689350	0.082	2.53E-07	6:38659370	0.146	5.69E-07
6:37074303	0.104	8.21E-07	6:37696351	0.227	2.80E-07	6:38683509	0.143	8.03E-07
6:37083820	0.19	3.61E-09	6:37701980	0.131	5.19E-08	7:91808643	0.116	6.87E-07
6:37084369	0.046	4.97E-07	6:37707686	0.037	2.35E-07	8:1349607	0.232	1.04E-07
6:37084369	0.129	1.66E-08	6:37710922	0.293	9.46E-11	8:1678253	0.394	8.47E-07
6:37084849	0.103	2.44E-08	6:37718589	0.22	1.52E-07	8:1697484	0.354	4.78E-07
6:37102022	0.034	1.46E-07	6:37721941	0.196	1.77E-07	8:82225182	0.03	9.29E-07
6:37109146	0.038	5.00E-07	6:37729732	0.148	2.63E-07	8:82256561	0.025	7.21E-07
6:37128650	0.136	4.37E-07	6:37733115	0.158	5.52E-07	8:82296835	0.236	9.18E-07
6:37136493	0.123	1.25E-08	6:37763550	0.186	3.67E-07	8:82346099	0.035	6.31E-07
6:37137051	0.046	1.30E-07	6:37812394	0.229	1.51E-07	8:82486148	0.022	7.19E-08
6:37142711	0.165	2.23E-07	6:37831619	0.179	5.26E-08	8:82545228	0.022	1.85E-08
6:37152822	0.143	4.36E-07	6:37995728	0.331	1.37E-07	8:82675352	0.168	2.79E-07
6:37153392	0.203	9.93E-10	6:38005482	0.255	7.89E-07	8:82811585	0.157	1.02E-07
6:37161805	0.057	9.67E-07	6:38045053	0.043	9.71E-07	8:82815966	0.025	9.71E-07
6:37164263	0.168	2.03E-07	6:38046191	0.05	1.54E-07	8:82815966	0.156	6.46E-07
6:37176539	0.215	3.59E-09	6:38046301	0.055	2.37E-09	8:82897823	0.021	1.75E-10
6:37202037	0.2	2.29E-07	6:38056634	0.091	4.65E-07	8:82897823	0.14	1.20E-07
6:37250392	0.199	6.19E-08	6:38058791	0.043	8.99E-09	8:82939381	0.021	3.50E-10

6:37277129	0.083	4.70E-07	6:38059144	0.07	9.57E-07	8:82960169	0.021	2.52E-08
6:37334908	0.16	2.49E-09	6:38059144	0.422	9.19E-07	8:83666574	0.019	4.82E-07
6:37390425	0.082	5.53E-07	6:38093707	0.138	5.13E-07	9:92992207	0.215	4.85E-07
6:37448093	0.114	7.00E-07	6:38100353	0.229	4.78E-07	11:25768041	0.063	9.53E-07

8-2-8. Selected SNP for PEMD (continue)

SNP	MAF	p-value	SNP	MAF	p-value	SNP	MAF	p-value
11:25919732	0.069	3.57E-07	13:36373019	0.354	7.73E-07	18:64371468	0.178	4.77E-10
11:25931832	0.078	7.37E-08	13:65350966	0.015	9.88E-07	18:64371724	0.194	3.14E-09
11:25977352	0.181	2.13E-07	13:79200725	0.119	1.14E-07	18:64394280	0.217	2.14E-08
11:26185303	0.315	4.10E-07	13:79204371	0.128	1.32E-07	18:64408561	0.176	5.28E-10
11:26299991	0.469	4.86E-07	14:54415839	0.005	2.43E-07	18:64409041	0.201	4.89E-12
11:26311887	0.486	8.25E-07	15:44603128	0.099	8.50E-07	18:64413484	0.236	2.26E-09
11:26312315	0.284	3.47E-07	15:44643273	0.121	5.09E-07	18:64425930	0.23	9.74E-07
11:26320734	0.285	3.53E-07	15:44666688	0.454	5.44E-07	18:64430827	0.166	9.60E-14
11:26339111	0.347	9.52E-07	15:44668726	0.447	3.43E-07	18:64437372	0.198	2.84E-07
11:26339674	0.239	6.85E-07	15:44719312	0.344	1.20E-07	18:64437483	0.175	4.07E-11
11:26385750	0.077	3.29E-11	15:47572827	0.073	2.11E-07	18:64441000	0.192	4.22E-10
11:26388176	0.056	4.15E-07	15:47572906	0.071	5.36E-09	18:64449005	0.27	7.07E-07
11:26388176	0.069	1.36E-11	15:47572958	0.065	1.18E-08	18:64452599	0.296	8.60E-07
11:26399508	0.013	1.21E-07	16:31987469	0.421	2.12E-07	18:64455141	0.206	1.61E-08
11:26400661	0.013	2.55E-08	16:31995930	0.499	7.36E-07	18:64468635	0.184	4.45E-09
11:26402509	0.012	3.58E-08	16:69973148	0.136	6.51E-07	18:64477623	0.191	5.10E-10
11:26402860	0.014	1.66E-08	18:62267930	0.033	7.17E-07	18:64478234	0.137	1.61E-15
11:26403186	0.021	7.79E-08	18:62283560	0.024	1.80E-07	18:64485507	0.114	3.00E-08
11:26403540	0.02	6.86E-07	18:62854046	0.013	6.87E-07	18:64485507	0.21	3.17E-09
11:26419566	0.018	4.51E-07	18:62877138	0.015	5.22E-08	18:64500042	0.218	2.12E-08
11:26420149	0.216	6.23E-07	18:62902053	0.014	3.00E-07	18:64504714	0.288	5.27E-07
11:26434709	0.337	7.74E-07	18:62904073	0.012	5.26E-08	18:64508318	0.215	2.75E-11
11:26445930	0.071	2.38E-07	18:63180318	0.013	5.02E-07	18:64509653	0.301	1.67E-08

11:26445930	0.09	1.38E-10	18:63536151	0.221	2.39E-08	18:64512859	0.325	7.16E-08
11:26450446	0.15	3.83E-07	18:63921780	0.127	1.55E-07	18:64515964	0.447	2.50E-07
11:26464793	0.015	9.62E-08	18:63966986	0.118	1.37E-07	18:64516776	0.338	5.97E-09
11:27979452	0.045	1.02E-07	18:64120218	0.175	9.80E-07	18:64519792	0.335	8.06E-08
11:43151435	0.078	5.34E-07	18:64122145	0.113	7.99E-09	18:64520092	0.326	1.22E-07
11:43165283	0.055	7.77E-07	18:64140159	0.166	1.41E-07	18:64521038	0.314	7.50E-09
11:4667272	0.017	5.20E-07	18:64190878	0.152	1.76E-07	18:64523146	0.259	3.88E-08
12:20504658	0.473	9.73E-07	18:64192557	0.155	4.34E-07	18:64530703	0.143	7.75E-15
12:20508742	0.49	1.93E-07	18:64192699	0.132	3.43E-09	18:64531729	0.173	7.59E-08
12:20512428	0.481	8.05E-07	18:64196620	0.17	4.14E-09	18:64542455	0.145	6.39E-13
12:20517141	0.452	4.67E-07	18:64197287	0.185	1.18E-08	18:64552442	0.187	4.13E-09
12:20517236	0.42	8.17E-07	18:64341130	0.182	1.91E-07	18:64554827	0.257	7.62E-08
12:20519420	0.397	2.13E-07	18:64341472	0.194	1.97E-08	18:64559745	0.207	7.43E-08
12:20522576	0.438	1.89E-07	18:64343333	0.206	6.31E-07	18:64567047	0.157	1.20E-11
12:20524763	0.42	5.96E-08	18:64343959	0.185	3.15E-07	18:64574348	0.265	6.98E-08
12:25536803	0.352	4.55E-07	18:64346151	0.229	5.36E-07	18:64577124	0.205	8.53E-08
13:10269011	0.009	8.41E-07	18:64346894	0.2	7.55E-07	18:64577721	0.167	1.67E-09
13:10424389	0.016	5.24E-07	18:64347882	0.198	8.39E-07	18:64581413	0.203	1.80E-07
13:10424454	0.009	1.42E-07	18:64354671	0.174	3.33E-08	18:64584491	0.171	9.77E-10
13:10428737	0.012	9.89E-07	18:64356045	0.185	7.96E-08	18:64586296	0.187	7.20E-07
13:10513382	0.017	3.13E-07	18:64362177	0.197	1.47E-07	18:64586696	0.156	4.55E-08
13:20657240	0.006	8.89E-07	18:64363998	0.2	4.25E-07	18:64592190	0.211	6.18E-07

8-2-8. Selected SNP for PEMD (continue)

SNP	MAF	p-value	SNP	MAF	p-value
18:64595753	0.254	2.91E-08	23:22185921	0.416	8.32E-07
18:64596801	0.232	3.67E-08	23:22196130	0.394	3.29E-07
18:64601899	0.149	4.08E-07	23:22205547	0.381	3.87E-07
18:64609904	0.2	1.07E-09	23:22207204	0.472	9.97E-07
18:64626021	0.203	2.10E-09	23:22214043	0.4	2.27E-07
18:64759498	0.118	2.71E-07	23:22218058	0.433	5.39E-08
18:65143823	0.14	6.92E-07	23:22221379	0.365	2.43E-07
18:65144709	0.148	5.73E-08	23:22228269	0.365	5.33E-07
18:65198142	0.102	1.04E-08	23:22242994	0.378	7.74E-07
18:65413382	0.129	3.67E-08	23:22275222	0.408	6.32E-07
18:65415035	0.108	6.79E-09	23:22293699	0.495	5.45E-07
18:65418710	0.134	3.45E-08	23:22305650	0.344	1.37E-07
18:65423643	0.131	3.01E-07	23:22308256	0.374	7.13E-08
18:65424824	0.114	3.15E-08	23:22314923	0.395	2.16E-08
18:65426956	0.125	1.28E-08	23:22315986	0.377	1.33E-07
18:65428716	0.126	1.37E-07	23:22319978	0.407	9.05E-07
18:65434501	0.124	1.30E-07	23:22320833	0.364	2.25E-07
18:65440359	0.125	6.02E-07	23:24020009	0.452	9.54E-07
18:65441464	0.122	8.68E-09	23:24053247	0.467	4.38E-07
18:65482025	0.103	2.26E-09	23:24053984	0.422	1.33E-07
18:65523506	0.088	8.18E-07	23:24054005	0.384	2.16E-07
18:65948415	0.009	2.39E-07	23:24727067	0.496	3.35E-07
18:67492362	0.445	6.02E-07	23:24728313	0.479	8.94E-07
18:68257386	0.434	7.96E-07	23:24740967	0.458	6.44E-07
18:68322699	0.474	5.94E-08	23:26656874	0.373	7.02E-07
19:10259573	0.299	8.99E-07	23:26670278	0.392	4.76E-07
19:10262404	0.399	3.61E-07	23:31338594	0.487	7.31E-07
19:4141471	0.018	8.71E-08	23:31591677	0.199	5.91E-08
19:57017060	0.395	5.29E-07	23:40117053	0.335	1.15E-07
20:48396087	0.016	7.14E-07	23:41163236	0.303	6.13E-07
21:44698472	0.113	3.70E-07	23:44712954	0.428	8.55E-07
21:46892904	0.019	6.17E-07	23:55450334	0.259	7.32E-08
22:41796883	0.342	3.64E-07	23:55637223	0.34	8.07E-07
23:17194700	0.215	4.32E-07	23:59578545	0.035	5.24E-07
23:17359010	0.177	9.68E-07	26:15266840	0.066	3.60E-07
23:17362154	0.382	1.46E-07	26:16916368	0.028	1.34E-07
23:20178116	0.366	7.19E-07	26:16917372	0.031	2.55E-08
23:21203291	0.453	7.35E-07	26:1813748	0.015	2.13E-07
23:21554551	0.363	4.78E-07	26:27682068	0.051	9.68E-08
23:21554601	0.397	3.00E-07	26:27684268	0.066	5.02E-07
23:21568297	0.381	3.01E-07			
23:21596573	0.362	8.18E-07			
23:21814976	0.371	2.82E-07			
23:21972810	0.403	8.80E-07			
23:22100771	0.374	5.50E-07			

8-2-9. Selected SNP for PWT

SNP	MAF	p-value	SNP	MAF	p-value	SNP	MAF	p-value
1:104327367	0.06	3.99E-08	3:58947577	0.176	9.71E-08	3:59568326	0.158	2.07E-08
1:113307156	0.162	5.99E-01	3:58947588	0.09	7.57E-14	3:59611045	0.152	7.92E-09
1:117096941	0.344	2.00E-07	3:58957920	0.186	6.01E-08	3:59674434	0.074	9.26E-08
1:117097443	0.412	8.22E-01	3:58966132	0.144	3.20E-10	3:59704907	0.073	2.71E-09
1:125020902	0.122	1.66E-07	3:59002601	0.136	1.06E-10	3:59725226	0.141	4.46E-08
1:14817162	0.24	9.09E-08	3:59009512	0.168	4.14E-09	3:59766585	0.098	1.55E-07
1:15250975	0.49	2.79E-07	3:59021504	0.209	1.22E-07	3:59802845	0.072	1.96E-10
1:187170474	0.255	1.96E-07	3:59024445	0.149	8.84E-09	3:59931976	0.067	2.62E-10
1:1974221	0.073	2.60E-07	3:59034358	0.147	1.44E-09	3:59990896	0.491	2.58E-07
1:2142036	0.338	1.22E-07	3:59040425	0.079	1.19E-20	3:60000383	0.204	7.48E-08
1:21884750	0.156	1.28E-07	3:59042655	0.158	5.65E-08	3:60016803	0.142	7.45E-08
1:22010923	0.137	1.80E-07	3:59078646	0.088	2.86E-12	3:60032424	0.106	2.35E-12
1:22033328	0.131	2.06E-07	3:59083540	0.072	1.32E-13	3:60034871	0.209	3.01E-08
1:22034939	0.101	1.30E-07	3:59111937	0.235	1.80E-07	3:60045457	0.182	2.93E-08
1:95885026	0.192	1.19E-07	3:59137005	0.076	9.48E-13	3:60084743	0.131	1.60E-07
1:9861032	0.441	2.01E-07	3:59146314	0.183	1.18E-07	3:60133053	0.096	2.54E-10
3:126053108	0.16	2.82E-07	3:59149396	0.123	4.48E-13	3:60167791	0.081	5.74E-13
3:129867541	0.027	3.08E-07	3:59288222	0.198	2.46E-07	3:60171371	0.114	7.31E-08
3:202710636	0.149	9.25E-08	3:59298726	0.169	2.33E-07	3:60269304	0.094	4.24E-09
3:203072896	0.246	1.20E-07	3:59299954	0.089	1.46E-13	3:60299482	0.081	1.94E-07
3:209623856	0.187	1.36E-07	3:59321529	0.285	5.25E-08	3:60416807	0.116	1.02E-12
3:58648944	0.048	1.90E-08	3:59324740	0.143	3.13E-07	3:60430365	0.043	1.07E-11
3:58649008	0.068	4.07E-11	3:59328503	0.176	1.20E-07	3:60477228	0.032	1.89E-11
3:58705846	0.045	9.00E-10	3:59332637	0.402	1.21E-07	3:60498161	0.069	5.66E-08
3:58714579	0.084	4.94E-08	3:59351741	0.117	6.60E-13	3:60531520	0.077	2.12E-08
3:58729692	0.05	4.53E-17	3:59356706	0.129	1.16E-07	3:60639533	0.064	4.34E-09
3:58730947	0.211	6.95E-08	3:59376880	0.422	1.89E-10	3:60668122	0.075	4.26E-09
3:58749886	0.076	5.38E-12	3:59380440	0.093	1.49E-14	3:60956490	0.156	2.97E-07
3:58750656	0.047	8.23E-15	3:59381223	0.427	7.41E-08	3:61183351	0.052	2.89E-07

3:58761758	0.164	2.46E-08	3:59381424	0.106	2.92E-09	6:33002289	0.085	1.00E-07
3:58774086	0.114	1.97E-07	3:59381981	0.139	6.27E-13	6:33922303	0.447	1.19E-07
3:58788141	0.054	1.40E-12	3:59393438	0.185	2.56E-09	6:34118676	0.302	1.96E-07
3:58803239	0.034	1.61E-16	3:59400384	0.265	4.19E-08	6:34188567	0.301	2.03E-07
3:58820991	0.26	1.24E-07	3:59400469	0.085	1.74E-15	6:34223801	0.12	1.72E-07
3:58822407	0.169	4.58E-08	3:59400998	0.078	2.63E-13	6:34273621	0.473	1.22E-07
3:58844586	0.076	4.27E-08	3:59408959	0.151	9.09E-08	6:34287749	0.244	6.34E-09
3:58878657	0.103	1.11E-07	3:59417895	0.093	1.82E-11	6:34455307	0.214	1.75E-13
3:58903458	0.055	1.97E-13	3:59417919	0.177	2.19E-08	6:34495176	0.311	1.09E-07
3:58916180	0.066	6.30E-15	3:59439288	0.196	3.40E-08	6:34495460	0.126	3.69E-09
3:58924393	0.049	6.77E-13	3:59456740	0.459	2.56E-07	6:34601350	0.442	1.06E-07
3:58925704	0.203	4.22E-08	3:59461530	0.122	1.28E-10	6:34631060	0.101	1.86E-07
3:58929570	0.172	9.38E-08	3:59466209	0.159	1.45E-08	6:34637423	0.052	6.17E-08
3:58936329	0.172	1.07E-07	3:59479670	0.461	1.08E-07	6:34722555	0.256	2.20E-09
3:58939607	0.062	6.05E-15	3:59539635	0.176	4.18E-08	6:34792645	0.244	1.89E-10
3:58944400	0.183	6.06E-08	3:59568261	0.098	2.10E-07	6:34893011	0.334	1.35E-10

8-2-9. Selected SNP for PWT (continue)

SNP8	MAF9	p-value	SNP	MAF	p-value	SNP	MAF	p-value
6:34969146	0.215	4.86E-12	6:35805208	0.167	1.88E-08	6:36457753	0.169	4.47E-30
6:34969845	0.135	2.18E-07	6:35808656	0.059	2.95E-11	6:36460912	0.383	1.03E-09
6:35075464	0.25	1.62E-07	6:35812627	0.125	9.42E-15	6:36469985	0.465	4.12E-08
6:35088340	0.073	1.35E-07	6:35819875	0.08	4.77E-10	6:36477126	0.189	5.75E-10
6:35184703	0.174	1.86E-11	6:35844204	0.073	9.87E-15	6:36499723	0.192	2.22E-08
6:35191867	0.15	1.10E-10	6:35850703	0.175	6.44E-09	6:36522079	0.162	2.39E-17
6:35200173	0.262	5.78E-10	6:35852225	0.166	7.13E-10	6:36522278	0.097	1.23E-10
6:35203968	0.353	1.29E-12	6:35852305	0.058	2.81E-16	6:36523313	0.1	3.54E-17
6:35236143	0.233	5.17E-10	6:35852562	0.357	5.38E-08	6:36523763	0.057	1.41E-11
6:35355360	0.069	1.73E-07	6:35854812	0.122	2.23E-17	6:36545291	0.173	5.83E-25
6:35361806	0.115	2.44E-07	6:35869871	0.199	1.62E-26	6:36560534	0.072	4.82E-09
6:35418297	0.269	7.57E-08	6:35870869	0.358	5.02E-30	6:36567991	0.084	3.38E-13
6:35429074	0.484	1.01E-17	6:35917918	0.445	1.78E-07	6:36572600	0.061	2.27E-12
6:35453639	0.307	1.83E-08	6:35922466	0.122	8.18E-19	6:36572913	0.059	2.53E-09
6:35458701	0.154	2.92E-11	6:35945214	0.397	4.33E-08	6:36572943	0.09	1.37E-23
6:35468565	0.26	2.83E-11	6:35961305	0.057	1.33E-09	6:36603557	0.052	8.52E-09
6:35482430	0.317	3.56E-08	6:35963994	0.108	1.41E-11	6:36613648	0.078	4.94E-09
6:35504366	0.318	6.47E-18	6:35964237	0.218	8.12E-21	6:36620367	0.091	9.48E-05
6:35506600	0.062	1.95E-08	6:35967294	0.117	1.75E-07	6:36623126	0.084	2.87E-06
6:35516700	0.148	4.27E-16	6:35986307	0.074	1.26E-10	6:36627451	0.066	1.18E-11
6:35531805	0.262	3.81E-10	6:35991380	0.183	2.09E-15	6:36656453	0.063	2.55E-08
6:35535684	0.065	4.01E-12	6:35991763	0.064	1.40E-07	6:36662051	0.069	1.16E-07
6:35537890	0.073	2.13E-07	6:35992029	0.113	1.38E-13	6:36676760	0.081	3.92E-08

6:35543293	0.071	8.80E-11	6:35995724	0.211	3.02E-18	6:36776920	0.068	1.62E-07
6:35547420	0.074	5.09E-11	6:36015190	0.102	1.62E-11	6:36786078	0.105	5.15E-12
6:35570220	0.1	3.00E-15	6:36017835	0.092	2.37E-09	6:36787319	0.132	2.00E-30
6:35576253	0.067	3.41E-13	6:36038540	0.05	3.57E-14	6:36788660	0.39	1.47E-02
6:35576852	0.053	1.07E-10	6:36070176	0.058	2.58E-10	6:36795735	0.091	3.18E-12
6:35580956	0.141	1.84E-07	6:36095805	0.133	3.80E-08	6:36797255	0.139	1.64E-07
6:35604710	0.237	6.27E-08	6:36128399	0.162	2.15E-09	6:36803405	0.358	2.23E-07
6:35608123	0.337	7.75E-11	6:36155985	0.077	9.43E-03	6:36809566	0.415	8.01E-02
6:35626425	0.068	2.07E-11	6:36156044	0.06	2.97E-13	6:36813967	0.455	1.17E-05
6:35629877	0.278	4.08E-12	6:36166810	0.056	4.78E-11	6:36820145	0.077	8.62E-23
6:35630846	0.188	6.30E-11	6:36167496	0.076	7.96E-09	6:36826992	0.447	5.28E-06
6:35639358	0.056	1.66E-13	6:36169799	0.058	1.62E-11	6:36828895	0.119	2.35E-07
6:35656948	0.316	9.02E-08	6:36188854	0.055	5.04E-10	6:36832733	0.062	3.92E-10
6:35675156	0.128	7.77E-09	6:36244248	0.097	1.71E-11	6:36835643	0.36	1.73E-03
6:35735577	0.262	5.21E-17	6:36249917	0.052	1.59E-09	6:36839109	0.123	2.04E-07
6:35735779	0.13	2.73E-10	6:36252650	0.118	2.71E-07	6:36839119	0.392	1.20E-07
6:35744242	0.227	5.89E-08	6:36296088	0.093	2.66E-08	6:36839378	0.336	4.66E-03
6:35747059	0.14	1.56E-07	6:36349747	0.08	1.25E-12	6:36840440	0.282	2.58E-02
6:35752263	0.17	2.72E-13	6:36360596	0.174	4.38E-14	6:36845573	0.456	6.15E-06
6:35752300	0.237	3.15E-20	6:36365568	0.12	9.87E-11	6:36851287	0.061	3.02E-04
6:35753162	0.122	3.10E-07	6:36399881	0.068	3.15E-07	6:36855753	0.069	4.77E-06
6:35755917	0.233	5.66E-16	6:36428813	0.48	1.41E-08	6:36855848	0.065	9.85E-06

8-2-9. Selected SNP for PWT (continue)

SNP17	MAF	p-value	SNP	MAF	p-value	SNP	MAF	p-value
6:36865319	0.05	2.76E-09	6:36982426	0.09	6.52E-14	6:37133484	0.148	5.49E-09
6:36865620	0.104	2.79E-05	6:36984153	0.397	1.77E-07	6:37137293	0.057	1.09E-11
6:36867238	0.291	7.12E-07	6:36986354	0.064	1.00E-07	6:37137614	0.062	1.20E-19
6:36868441	0.104	1.24E-05	6:36988278	0.294	1.53E-09	6:37138570	0.054	4.89E-15
6:36878974	0.384	1.82E-02	6:36988302	0.386	1.54E-07	6:37148799	0.08	5.77E-08
6:36879203	0.127	6.91E-16	6:36988707	0.325	1.07E-09	6:37149869	0.071	1.10E-12
6:36879259	0.086	5.88E-10	6:36991000	0.224	2.05E-14	6:37153282	0.08	1.22E-11
6:36879383	0.398	2.30E-07	6:36991143	0.274	2.63E-07	6:37161805	0.059	1.92E-12
6:36880062	0.142	5.37E-08	6:36996211	0.093	1.47E-21	6:37164282	0.106	2.90E-25
6:36885131	0.129	1.81E-07	6:36996429	0.078	6.28E-11	6:37166764	0.059	8.05E-12
6:36886299	0.108	1.59E-03	6:36996476	0.097	8.48E-06	6:37174393	0.085	6.26E-18
6:36886858	0.397	1.76E-07	6:37000219	0.199	1.16E-07	6:37174437	0.143	2.15E-28
6:36898348	0.088	1.67E-23	6:37001731	0.295	4.29E-09	6:37176390	0.114	3.36E-34
6:36902145	0.065	5.31E-09	6:37002098	0.121	5.59E-19	6:37176922	0.093	2.60E-25
6:36905457	0.103	1.59E-05	6:37002913	0.119	4.94E-15	6:37182130	0.059	3.84E-17
6:36911780	0.081	2.00E-23	6:37004974	0.307	2.08E-08	6:37204144	0.148	4.42E-20
6:36925114	0.074	5.35E-11	6:37009450	0.116	6.56E-22	6:37204548	0.094	1.37E-12
6:36925216	0.124	2.20E-09	6:37009499	0.301	2.84E-07	6:37215463	0.082	5.28E-07
6:36926501	0.057	4.97E-11	6:37010741	0.085	6.54E-06	6:37249737	0.1	1.55E-04
6:36928435	0.117	9.52E-28	6:37011013	0.073	7.55E-13	6:37256245	0.102	1.40E-10
6:36934616	0.142	8.24E-15	6:37011023	0.1	5.09E-22	6:37277098	0.256	6.89E-01
6:36935287	0.123	2.90E-19	6:37011845	0.089	4.22E-07	6:37302029	0.087	4.19E-05
6:36935578	0.086	7.65E-10	6:37012633	0.081	4.57E-08	6:37334908	0.27	2.40E-01
6:36938297	0.075	6.69E-10	6:37012870	0.111	1.11E-11	6:37353278	0.123	1.03E-30
6:36939533	0.124	5.16E-24	6:37013810	0.176	1.54E-35	6:37356400	0.088	2.54E-05
6:36939803	0.101	2.52E-21	6:37014924	0.137	2.86E-11	6:37358037	0.072	2.03E-13
6:36940100	0.169	9.62E-29	6:37015823	0.094	1.12E-07	6:37364653	0.056	7.61E-08
6:36942044	0.126	8.09E-17	6:37017077	0.121	1.04E-17	6:37388901	0.126	2.72E-13
6:36950661	0.066	3.00E-19	6:37017377	0.058	1.05E-07	6:37402245	0.084	1.14E-05

6:36950870	0.085	8.52E-18	6:37019549	0.08	1.74E-16	6:37459157	0.152	2.40E-17
6:36958859	0.054	6.79E-09	6:37022699	0.08	9.19E-10	6:37461262	0.085	1.47E-05
6:36960295	0.115	8.22E-18	6:37025674	0.079	1.07E-10	6:37463855	0.116	6.09E-13
6:36961226	0.095	2.88E-10	6:37032632	0.093	1.71E-15	6:37475062	0.083	9.68E-07
6:36968179	0.071	1.14E-14	6:37043773	0.064	2.31E-16	6:37485878	0.1	5.25E-26
6:36969028	0.086	1.50E-05	6:37064444	0.072	3.92E-09	6:37492328	0.056	2.84E-11
6:36976884	0.137	7.94E-25	6:37071127	0.054	1.24E-13	6:37517693	0.081	7.40E-07
6:36977272	0.075	5.63E-14	6:37071173	0.057	3.42E-14	6:37522336	0.054	1.17E-07
6:36977667	0.086	1.15E-16	6:37072532	0.161	2.07E-11	6:37529212	0.08	3.53E-07
6:36977846	0.087	1.58E-05	6:37074303	0.139	1.32E-07	6:37540148	0.095	1.01E-07
6:36978619	0.3	3.28E-08	6:37074322	0.059	1.09E-11	6:37557272	0.125	2.74E-25
6:36978958	0.41	5.41E-08	6:37087893	0.08	3.47E-11	6:37577411	0.116	5.75E-26
6:36979766	0.352	9.56E-11	6:37090755	0.453	2.60E-07	6:37578145	0.058	1.35E-17
6:36980718	0.373	2.43E-07	6:37100043	0.308	4.94E-04	6:37584836	0.101	9.64E-26
6:36981387	0.299	3.00E-08	6:37105197	0.113	1.01E-11	6:37584956	0.219	2.42E-07
6:36982231	0.104	1.84E-11	6:37114757	0.314	1.95E-05	6:37586919	0.074	6.17E-07

8-2-9. Selected SNP for PWT (continue)

SNP26	MAF	p-value	SNP	MAF	p-value	SNP	MAF	p-value
6:37587663	0.075	1.91E-06	6:37794740	0.051	2.47E-13	6:38156116	0.171	1.73E-17
6:37593103	0.141	2.25E-10	6:37796547	0.107	6.26E-10	6:38156169	0.141	2.84E-07
6:37608435	0.084	8.44E-15	6:37814325	0.105	8.45E-14	6:38166349	0.085	5.77E-08
6:37612530	0.077	7.61E-22	6:37831619	0.172	7.07E-17	6:38167975	0.055	7.36E-08
6:37625024	0.051	3.09E-10	6:37837481	0.08	4.54E-11	6:38191739	0.056	3.17E-09
6:37625061	0.129	1.29E-18	6:37842690	0.129	4.19E-12	6:38201581	0.262	1.31E-07
6:37625084	0.088	7.16E-04	6:37867693	0.059	3.16E-09	6:38218375	0.073	5.43E-07
6:37625374	0.101	7.23E-16	6:37903049	0.094	1.74E-09	6:38223134	0.128	1.03E-13
6:37633299	0.082	8.60E-06	6:37923558	0.124	3.48E-13	6:38224632	0.075	3.41E-05
6:37641912	0.072	1.59E-14	6:37928056	0.117	1.99E-08	6:38225032	0.055	5.91E-05
6:37648429	0.084	1.96E-17	6:37930983	0.194	3.62E-08	6:38225971	0.091	1.80E-09
6:37650258	0.074	2.48E-12	6:37931205	0.197	3.57E-09	6:38226210	0.072	1.02E-09
6:37653198	0.159	9.20E-13	6:37939789	0.193	3.72E-17	6:38226853	0.08	4.19E-08
6:37656311	0.141	4.77E-18	6:37948509	0.194	7.94E-23	6:38229683	0.326	6.14E-07
6:37660618	0.063	2.73E-09	6:37953962	0.11	1.17E-16	6:38229914	0.067	1.71E-13
6:37663019	0.083	7.90E-05	6:37979270	0.141	2.33E-11	6:38232502	0.092	1.55E-13
6:37668421	0.078	5.23E-18	6:37979655	0.116	6.08E-17	6:38232761	0.067	2.21E-08
6:37668482	0.204	1.60E-13	6:37980923	0.208	1.96E-10	6:38234814	0.114	3.98E-15
6:37669996	0.118	4.93E-36	6:37985066	0.131	1.56E-08	6:38235587	0.146	1.44E-10
6:37671461	0.167	1.25E-21	6:37988009	0.161	9.44E-11	6:38237524	0.301	1.11E-09
6:37675450	0.19	6.83E-22	6:37992654	0.073	5.60E-06	6:38237583	0.098	1.47E-07
6:37677547	0.073	2.31E-20	6:38006729	0.056	3.09E-09	6:38237799	0.091	3.06E-11
6:37679480	0.318	4.69E-06	6:38006942	0.137	1.76E-07	6:38238491	0.158	1.57E-12
6:37681551	0.171	4.43E-21	6:38017511	0.124	3.84E-09	6:38246849	0.061	1.36E-08
6:37683420	0.11	1.26E-15	6:38017915	0.07	7.75E-06	6:38251399	0.05	2.30E-05
6:37687841	0.312	1.43E-07	6:38031139	0.079	1.38E-07	6:38251494	0.324	1.98E-06
6:37689350	0.081	1.37E-06	6:38038596	0.122	1.96E-07	6:38256294	0.208	3.30E-11
6:37697178	0.2	8.13E-57	6:38040900	0.142	9.47E-13	6:38259462	0.069	6.32E-09
6:37701980	0.304	7.01E-09	6:38056615	0.223	2.27E-09	6:38260171	0.064	8.50E-14
6:37704209	0.173	2.21E-07	6:38071961	0.16	3.58E-09	6:38260475	0.082	1.10E-09
6:37704294	0.069	3.80E-09	6:38072979	0.051	1.30E-07	6:38260650	0.113	3.79E-08
6:37705732	0.12	1.59E-22	6:38076696	0.123	3.30E-09	6:38262034	0.096	1.24E-16

6:37708182	0.156	1.82E-09	6:38079988	0.061	9.50E-08	6:38278215	0.239	6.17E-10
6:37708864	0.078	1.95E-06	6:38081740	0.097	7.12E-08	6:38286521	0.126	1.94E-21
6:37711273	0.054	1.65E-12	6:38083254	0.287	1.67E-10	6:38291247	0.055	7.53E-14
6:37713567	0.132	3.50E-18	6:38089953	0.29	3.94E-08	6:38293520	0.06	8.06E-09
6:37718589	0.15	2.59E-07	6:38101093	0.234	3.53E-08	6:38300862	0.113	3.27E-12
6:37726861	0.198	8.24E-27	6:38104879	0.056	2.65E-07	6:38306553	0.052	2.36E-08
6:37728071	0.08	2.20E-09	6:38106237	0.102	8.90E-14	6:38307327	0.113	2.13E-12
6:37728484	0.107	6.29E-10	6:38111955	0.193	1.28E-16	6:38320155	0.236	9.49E-08
6:37740649	0.133	8.48E-08	6:38112906	0.072	2.80E-11	6:38320207	0.247	9.46E-08
6:37748721	0.063	6.01E-09	6:38147798	0.221	1.06E-14	6:38325866	0.116	5.00E-11
6:37750331	0.087	9.16E-08	6:38148055	0.092	1.49E-10	6:38332324	0.056	1.26E-07
6:37757684	0.135	5.24E-10	6:38151217	0.106	4.54E-13	6:38333449	0.126	1.12E-11
6:37757807	0.214	1.90E-16	6:38152675	0.208	1.42E-09	6:38334728	0.311	5.95E-10

8-2-9. Selected SNP for PWT (continue)

SNP35	MAF	p-value	SNP	MAF	p-value	SNP	MAF	p-value
6:38342776	0.269	3.22E-09	6:39591542	0.229	1.10E-07	11:26435317	0.039	6.68E-04
6:38359443	0.062	3.12E-07	6:39603946	0.304	2.19E-08	11:26440354	0.164	7.43E-08
6:38407752	0.449	7.61E-08	6:94322306	0.056	2.44E-07	11:26445930	0.067	9.47E-06
6:38415393	0.235	1.05E-10	7:5167946	0.011	8.13E-01	11:26450446	0.314	1.23E-05
6:38426486	0.277	5.34E-09	7:81207564	0.036	3.09E-07	11:26451458	0.035	1.20E-02
6:38436284	0.164	2.12E-08	8:24452571	0.142	1.98E-07	11:26827137	0.277	3.22E-09
6:38442551	0.21	7.61E-09	9:36416350	0.226	2.45E-07	11:27992414	0.424	4.58E-08
6:38452446	0.291	2.31E-08	11:25973939	0.418	1.21E-07	12:54824291	0.483	5.93E-10
6:38477168	0.089	1.52E-08	11:25977352	0.297	2.22E-04	12:54848741	0.455	2.81E-07
6:38478856	0.189	7.82E-16	11:25977658	0.272	2.11E-04	12:55381977	0.158	8.87E-08
6:38499032	0.254	3.07E-08	11:25991229	0.059	2.34E-01	12:55425294	0.312	1.42E-07
6:38499078	0.248	2.21E-12	11:25996742	0.041	5.17E-01	12:55425684	0.493	1.61E-07
6:38506884	0.086	6.66E-08	11:25997163	0.216	2.49E-07	12:55443306	0.312	1.19E-07
6:38518229	0.308	5.63E-08	11:26007883	0.204	3.95E-08	12:55564482	0.332	1.81E-07
6:38546202	0.051	1.01E-08	11:26149175	0.371	2.24E-01	12:55605081	0.493	3.48E-09
6:38558204	0.06	2.53E-07	11:26162167	0.084	6.98E-02	12:55620735	0.334	2.02E-07
6:38584639	0.307	1.87E-07	11:26162350	0.086	2.11E-02	12:56713855	0.034	2.55E-07
6:38589794	0.227	1.75E-07	11:26162535	0.077	7.22E-02	12:60773593	0.127	9.09E-08
6:38593336	0.15	1.55E-08	11:26171099	0.109	1.54E-07	13:8393151	0.239	9.41E-09
6:38607532	0.328	2.13E-07	11:26252222	0.122	5.45E-08	16:29516940	0.117	1.30E-07
6:38615663	0.239	7.04E-08	11:26276300	0.302	1.86E-04	16:29563867	0.131	8.02E-01
6:38654881	0.052	5.16E-08	11:26307627	0.471	1.05E-03	16:31143958	0.143	1.99E-07
6:38658576	0.095	1.19E-09	11:26310509	0.433	2.70E-03	16:31229514	0.221	6.71E-11
6:38665271	0.086	1.79E-11	11:26316358	0.092	1.17E-07	16:31354487	0.238	1.62E-07
6:38697933	0.121	4.70E-10	11:26321365	0.082	2.64E-03	16:31393612	0.299	6.84E-09
6:38716991	0.094	1.16E-07	11:26321380	0.167	1.46E-05	16:31397967	0.149	1.62E-07
6:38749598	0.148	1.56E-08	11:26331800	0.289	4.49E-02	16:31466874	0.459	1.15E-07
6:38761277	0.161	1.35E-08	11:26331988	0.343	3.24E-07	16:31626724	0.093	2.24E-08
6:38765429	0.068	4.58E-09	11:26333173	0.156	1.61E-04	16:31681709	0.196	1.36E-08
6:38838326	0.145	1.11E-08	11:26338399	0.103	1.93E-07	16:31731858	0.359	2.64E-07
6:39154417	0.211	2.22E-10	11:26339111	0.328	6.63E-07	16:31770011	0.136	3.07E-07
6:39173843	0.258	6.45E-08	11:26339276	0.311	9.43E-06	16:31808197	0.147	1.48E-10
6:39185201	0.195	3.28E-08	11:26354892	0.087	1.38E-07	16:31880712	0.095	2.19E-07
6:39309689	0.207	6.41E-09	11:26361377	0.132	2.38E-07	16:31973270	0.23	4.08E-08
6:39343874	0.144	1.82E-07	11:26384545	0.111	1.34E-07	16:31982749	0.201	2.17E-08
6:39373871	0.071	7.63E-08	11:26385750	0.182	4.43E-17	16:31998863	0.497	2.17E-07
6:39381267	0.098	6.09E-08	11:26400676	0.035	9.10E-08	16:32005772	0.352	7.81E-16
6:39391221	0.157	5.28E-09	11:26407996	0.314	1.04E-06	16:32008588	0.141	9.39E-11

6:39428018	0.056	9.56E-08	11:26410417	0.296	1.91E-05	16:32009795	0.352	2.62E-10
6:39430247	0.14	8.14E-10	11:26412002	0.306	7.60E-06	16:32010258	0.481	9.85E-09
6:39438257	0.182	1.12E-08	11:26412807	0.301	1.92E-06	16:32010907	0.351	1.54E-15
6:39440721	0.105	9.90E-08	11:26419566	0.074	1.06E-07	16:32011750	0.2	7.26E-08
6:39460355	0.136	4.28E-09	11:26420149	0.248	2.81E-17	16:32018860	0.495	5.50E-09
6:39460579	0.169	2.97E-10	11:26422543	0.02	1.62E-07	16:32092533	0.167	1.19E-12
6:39543728	0.195	2.77E-07	11:26431075	0.048	8.72E-04	16:32167175	0.058	1.84E-08

8-2-9. Selected SNP for PWT (continue)

SNP44	MAF	p-value	SNP	MAF	p-value	SNP	MAF	p-value
16:32172066	0.327	4.44E-09	23:42738015	0.24	2.39E-08	23:43939977	0.14	5.48E-14
16:32294475	0.063	2.26E-08	23:42782648	0.445	3.35E-09	23:43944042	0.251	1.20E-16
16:32592330	0.295	7.85E-08	23:42790214	0.404	3.14E-07	23:43944062	0.036	3.75E-09
16:32619484	0.138	1.33E-08	23:42821382	0.409	1.51E-11	23:43949332	0.153	2.08E-20
16:32776987	0.371	6.09E-08	23:42842113	0.487	9.96E-10	23:43960491	0.075	3.59E-09
16:32808952	0.254	4.92E-09	23:42854990	0.059	2.00E-09	23:43971324	0.18	1.96E-08
16:32830530	0.345	7.74E-08	23:42865654	0.177	2.59E-08	23:43975487	0.461	8.15E-11
16:32975271	0.065	1.82E-07	23:42868647	0.386	9.36E-11	23:43982111	0.165	3.45E-10
16:33266956	0.085	1.59E-07	23:42869930	0.42	9.68E-20	23:44016724	0.456	2.29E-07
16:57329833	0.193	2.97E-01	23:42871956	0.325	7.98E-10	23:44071246	0.486	6.56E-11
16:69993188	0.109	3.13E-07	23:42910766	0.402	1.80E-07	23:44097299	0.477	3.00E-18
16:70015348	0.143	3.73E-09	23:42921272	0.227	6.60E-08	23:44097341	0.26	4.94E-16
17:60539998	0.176	1.31E-07	23:42931748	0.402	2.28E-08	23:44117370	0.108	1.25E-09
18:49560532	0.011	2.05E-07	23:42939199	0.039	1.95E-07	23:44124896	0.175	5.97E-11
18:50635113	0.044	3.08E-07	23:42948494	0.476	8.16E-09	23:44147932	0.265	1.25E-20
18:55906353	0.295	1.50E-07	23:42950582	0.267	6.03E-09	23:44149306	0.249	4.05E-11
22:26867359	0.179	1.83E-07	23:42954812	0.11	1.22E-09	23:44158925	0.31	1.81E-10
23:16977745	0.462	1.48E-08	23:42989517	0.217	1.26E-07	23:44167330	0.241	1.96E-13
23:30055112	0.488	2.18E-07	23:43118865	0.486	5.15E-09	23:44169589	0.098	8.48E-10
23:31244037	0.113	1.53E-07	23:43174327	0.31	6.37E-09	23:44202032	0.075	3.37E-08
23:36706015	0.28	2.77E-07	23:43396988	0.31	9.27E-10	23:44253381	0.084	1.43E-11
23:40463405	0.01	1.45E-07	23:43572323	0.145	2.96E-11	23:44296094	0.039	2.42E-08
23:41741901	0.289	2.66E-09	23:43635907	0.044	4.47E-09	23:44308821	0.467	2.73E-11
23:41793493	0.331	2.57E-07	23:43710957	0.096	1.93E-07	23:44317167	0.284	1.38E-08
23:42353254	0.475	4.60E-08	23:43741637	0.051	2.25E-07	23:44321574	0.17	2.04E-10
23:42376619	0.115	1.14E-08	23:43779460	0.061	3.44E-09	23:44325417	0.049	6.04E-08
23:42391678	0.373	6.75E-08	23:43785532	0.255	1.18E-13	23:44335221	0.478	3.10E-09
23:42399606	0.293	4.12E-09	23:43816766	0.144	2.73E-12	23:44345368	0.344	2.01E-09
23:42422938	0.369	6.01E-08	23:43816779	0.364	1.62E-09	23:44351584	0.409	2.09E-08
23:42425552	0.1	1.94E-08	23:43823225	0.365	1.95E-10	23:44351586	0.494	1.06E-10
23:42430175	0.169	3.20E-09	23:43828082	0.173	4.17E-14	23:44352704	0.433	4.00E-13
23:42446157	0.493	2.10E-07	23:43850992	0.138	2.94E-11	23:44373866	0.29	1.61E-09
23:42488734	0.064	2.67E-07	23:43854366	0.494	1.04E-20	23:44376656	0.136	1.34E-09
23:42514937	0.358	3.05E-11	23:43858365	0.044	2.97E-08	23:44384445	0.255	4.88E-14
23:42537676	0.148	1.57E-07	23:43859099	0.103	5.02E-14	23:44397694	0.467	9.04E-12
23:42552803	0.282	1.73E-07	23:43886430	0.213	8.41E-08	23:44420891	0.147	2.50E-08
23:42604469	0.265	2.61E-08	23:43887321	0.064	2.31E-07	23:44427379	0.169	4.11E-11
23:42638492	0.307	1.79E-07	23:43895306	0.435	3.41E-20	23:44432031	0.403	6.09E-21
23:42673603	0.146	1.56E-12	23:43907534	0.164	8.15E-17	23:44461530	0.337	3.44E-14
23:42694717	0.352	1.78E-12	23:43908319	0.096	1.02E-07	23:44467668	0.4	2.58E-13
23:42701457	0.483	6.97E-08	23:43908879	0.198	1.77E-09	23:44471073	0.227	1.49E-09
23:42704464	0.406	6.26E-08	23:43913257	0.172	6.95E-15	23:44472172	0.236	1.58E-11
23:42704916	0.153	1.49E-07	23:43919411	0.11	3.41E-08	23:44472293	0.128	8.88E-08
23:42707034	0.475	3.31E-10	23:43929415	0.183	2.55E-15	23:44473696	0.186	2.04E-11

23:42727350	0.445	2.70E-11	23:43934888	0.066	2.37E-13	23:44493038	0.051	4.24E-09

8-2-9. Selected SNP for PWT (continue)

SNP53	MAF	p-value	SNP	MAF	p-value
23:44524067	0.384	2.41E-12	25:34740390	0.224	6.24E-09
23:44526704	0.176	5.23E-10	25:34741069	0.294	5.78E-08
23:44532122	0.481	1.01E-22	25:34759747	0.297	2.29E-08
23:44534512	0.073	1.53E-07	25:34772185	0.25	1.11E-07
23:44535879	0.114	3.62E-08	25:34906694	0.279	2.11E-07
23:44539665	0.229	2.66E-07	25:34976759	0.224	3.74E-08
23:44539881	0.215	1.70E-11	25:35060280	0.222	4.98E-08
23:44542928	0.165	1.91E-15	25:35304025	0.247	1.16E-07
23:44543068	0.123	7.99E-13	25:35329840	0.249	2.43E-07
23:44543558	0.179	2.87E-08	25:35346934	0.214	2.42E-07
23:44556661	0.099	6.26E-11	25:35414033	0.248	7.95E-09
23:44556914	0.319	3.55E-08	25:35801489	0.289	2.03E-08
23:44557201	0.178	1.56E-09	25:35919902	0.205	2.02E-07
23:44561892	0.162	4.95E-09	25:36805074	0.229	2.82E-07
23:44562337	0.13	2.61E-08	26:19149932	0.464	2.07E-07
23:44562431	0.243	1.13E-10	26:20583246	0.015	2.57E-07
23:44564984	0.181	3.43E-10	26:27193568	0.472	1.53E-07
23:44569486	0.108	3.16E-08			
23:44604394	0.283	3.04E-07			
23:44619237	0.379	9.65E-10			
23:44625950	0.403	2.85E-08			
23:44631407	0.176	1.96E-07			
23:44643299	0.499	4.85E-11			
23:44654233	0.355	7.10E-08			
23:44669893	0.305	2.30E-07			
23:44674487	0.162	5.64E-10			
23:44682614	0.078	1.69E-07			
23:44684594	0.489	4.70E-10			
23:44704724	0.303	8.16E-08			
23:44707583	0.126	2.47E-07			
23:44709592	0.095	6.10E-09			
23:44709998	0.179	5.30E-09			
23:44732046	0.304	7.45E-08			
23:44735606	0.193	4.40E-10			
23:44744644	0.321	4.62E-10			
23:44747867	0.472	1.76E-07			
23:44748397	0.14	2.64E-13			
23:44823722	0.041	1.47E-07			
23:44906476	0.325	9.29E-11			
23:44921690	0.494	1.53E-07			
23:45460675	0.339	3.63E-08			
23:47072764	0.025	1.18E-07			
23:50327573	0.047	1.16E-07			
24:13493324	0.015	1.37E-07			
25:34258302	0.303	8.60E-08			

8-2-10. Selected SNP for SF5

SNP	MAF	p-value	SNP	MAF	p-value	SNP	MAF	p-value
1:108067046	0.145	3.10E-06	5:93421455	0.461	1.31E-06	5:93762527	0.259	2.17E-09
1:139485129	0.433	5.02E-07	5:93424949	0.255	4.94E-20	5:93765043	0.234	1.03E-07
1:139587273	0.284	6.75E-07	5:93430953	0.25	1.69E-08	5:93778224	0.277	1.07E-07
1:140205490	0.458	8.96E-07	5:93431002	0.466	3.44E-10	5:93789099	0.463	7.46E-07
1:140360238	0.114	3.03E-06	5:93431031	0.481	2.71E-13	5:93838166	0.362	2.14E-06
1:141214626	0.178	4.43E-07	5:93440434	0.358	9.57E-27	5:93850916	0.374	4.28E-07
1:142956565	0.132	1.90E-06	5:93440714	0.239	5.69E-13	5:93883118	0.439	1.05E-06
1:240360352	0.183	6.30E-07	5:93443960	0.197	8.40E-15	5:93958041	0.396	2.72E-06
1:48992138	0.164	2.95E-06	5:93450050	0.26	2.72E-12	5:94088468	0.469	3.14E-08
2:102562920	0.17	1.64E-06	5:93455073	0.199	4.12E-07	5:94091549	0.302	4.92E-08
2:131434157	0.269	1.93E-06	5:93455225	0.432	1.33E-14	5:94095140	0.309	2.97E-08
2:200391138	0.005	1.36E-06	5:93457572	0.486	7.10E-17	5:94095444	0.454	1.24E-08
2:21872728	0.476	2.50E-06	5:93458927	0.477	2.90E-18	5:94096561	0.237	1.74E-07
2:5880621	0.027	1.40E-06	5:93460118	0.483	3.73E-21	5:94100721	0.229	3.02E-07
2:9110282	0.312	1.97E-06	5:93463022	0.486	4.99E-16	5:94101117	0.304	8.32E-09
2:9118817	0.195	3.03E-06	5:93465037	0.451	2.65E-16	5:94109375	0.262	2.56E-06
3:17259565	0.238	1.61E-06	5:93466964	0.498	5.84E-07	5:94122148	0.421	1.81E-06
3:80555998	0.319	8.57E-07	5:93469260	0.282	1.46E-10	5:94129129	0.303	2.33E-06
3:82801081	0.464	1.00E-06	5:93470397	0.416	4.76E-12	5:94140030	0.475	7.52E-08
5:22621908	0.469	1.78E-06	5:93470571	0.458	4.75E-17	5:94149840	0.447	1.26E-06
5:83785127	0.32	1.96E-06	5:93470765	0.265	2.07E-09	5:94161287	0.229	8.55E-10
5:89651539	0.451	4.27E-07	5:93473819	0.371	4.78E-18	5:94161363	0.289	3.66E-07
5:91936730	0.498	7.15E-07	5:93482508	0.207	2.82E-06	5:94237138	0.275	2.17E-06
5:92012315	0.352	1.72E-06	5:93492626	0.247	6.84E-07	5:94254948	0.29	2.00E-07
5:92017947	0.228	1.13E-06	5:93553757	0.422	3.39E-08	5:94383136	0.278	1.80E-06
5:92081434	0.195	3.01E-07	5:93555096	0.241	2.41E-09	5:95021431	0.425	2.09E-06
5:92359168	0.467	2.82E-06	5:93557455	0.354	1.96E-08	6:37071173	0.128	2.51E-06
5:92924943	0.497	2.41E-06	5:93559259	0.478	1.19E-09	6:37084369	0.117	1.12E-07
5:92959145	0.332	1.82E-06	5:93560536	0.304	5.64E-07	6:37741444	0.117	8.80E-07

5:92970731	0.223	6.08E-07	5:93566745	0.397	3.24E-08	6:38232761	0.151	9.66E-07
5:92974709	0.392	9.99E-07	5:93568312	0.29	1.80E-08	6:42834880	0.246	1.72E-06
5:93024541	0.346	1.56E-06	5:93568661	0.226	1.93E-06	6:42912693	0.199	8.05E-07
5:93038152	0.264	1.40E-06	5:93579477	0.237	4.20E-07	7:88406397	0.019	2.26E-06
5:93078642	0.421	5.50E-07	5:93585574	0.393	2.46E-08	8:11672137	0.005	1.17E-06
5:93079399	0.353	2.09E-09	5:93595458	0.196	1.03E-06	8:41730173	0.459	6.05E-07
5:93080692	0.351	2.88E-06	5:93595571	0.268	2.17E-07	8:75897379	0.008	1.33E-07
5:93106168	0.444	3.20E-07	5:93595980	0.424	2.17E-06	9:87183739	0.237	1.84E-06
5:93135345	0.309	2.06E-06	5:93610589	0.224	1.87E-08	10:3142647	0.054	7.57E-07
5:93159374	0.302	2.77E-06	5:93610606	0.375	1.41E-06	11:32473968	0.026	1.12E-06
5:93160406	0.209	1.56E-06	5:93647712	0.218	5.29E-08	11:34054847	0.069	2.47E-06
5:93374758	0.5	4.53E-09	5:93670427	0.302	1.87E-06	11:57841850	0.072	8.64E-07
5:93402611	0.247	1.76E-07	5:93670805	0.42	6.44E-07	12:217416	0.013	5.81E-07
5:93409737	0.208	8.80E-12	5:93748949	0.207	3.37E-07	12:36561	0.062	2.74E-07
5:93416294	0.478	3.41E-19	5:93750358	0.291	1.11E-07	12:38019	0.031	1.81E-06
5:93417101	0.384	4.93E-21	5:93750881	0.464	2.22E-06	12:39660601	0.277	2.81E-06

8-2-10. Selected SNP for SF5 (continue)

SNP8	MAF	p-value	SNP	MAF	p-value	SNP	MAF	p-value
12:42166199	0.31	1.56E-06	18:62344851	0.117	9.72E-09	18:64096438	0.199	1.40E-06
12:42166330	0.164	2.64E-07	18:62506544	0.177	2.50E-06	18:64127307	0.138	5.72E-11
12:42202082	0.217	2.05E-06	18:62522139	0.103	5.93E-10	18:64133604	0.194	4.69E-07
12:42207097	0.149	2.51E-06	18:62724787	0.11	6.10E-08	18:64142285	0.15	1.79E-12
12:544759	0.013	6.78E-08	18:62765627	0.105	1.62E-06	18:64145689	0.497	3.14E-09
12:817531	0.047	7.41E-07	18:62822546	0.114	1.78E-07	18:64145898	0.388	1.04E-09
12:837458	0.014	2.59E-07	18:62822897	0.17	1.38E-06	18:64149918	0.183	4.64E-07
12:903825	0.036	7.62E-08	18:62851367	0.16	2.31E-06	18:64152977	0.21	1.45E-06
12:932543	0.014	1.48E-06	18:62851848	0.148	2.06E-08	18:64157220	0.137	4.20E-09
13:79683202	0.272	2.56E-06	18:62876375	0.167	2.82E-06	18:64157616	0.306	1.17E-07
14:3121702	0.245	2.66E-06	18:62902808	0.1	1.31E-06	18:64164465	0.225	7.87E-07
14:53970379	0.278	3.54E-07	18:62940780	0.105	4.05E-11	18:64165966	0.104	9.88E-07
14:53971323	0.489	9.10E-07	18:63061232	0.138	1.84E-06	18:64168341	0.311	3.79E-08
14:54029140	0.432	3.04E-06	18:63196886	0.153	1.51E-06	18:64168876	0.251	4.15E-07
14:54041967	0.485	1.68E-06	18:63222205	0.105	6.69E-08	18:64174741	0.307	1.46E-08
14:54473333	0.338	2.89E-06	18:63284059	0.161	1.92E-06	18:64190428	0.112	7.00E-10
15:26082088	0.302	3.10E-06	18:63292767	0.139	6.13E-08	18:64190878	0.132	2.72E-10
15:41835231	0.017	3.02E-06	18:63322733	0.107	1.13E-06	18:64192557	0.105	3.44E-07
15:41841697	0.029	1.62E-06	18:63368975	0.198	3.53E-08	18:64195515	0.298	1.45E-06

15:63033270	0.1	9.62E-07	18:63374804	0.125	9.61E-11	18:64197287	0.194	2.13E-06
15:69906135	0.047	2.02E-06	18:63397346	0.149	6.28E-08	18:64249211	0.419	2.73E-06
16:52756840	0.01	1.56E-06	18:63407138	0.207	1.27E-07	18:64272630	0.168	7.89E-08
17:3736366	0.01	3.14E-07	18:63413374	0.127	5.51E-09	18:64278207	0.157	7.03E-07
17:50889677	0.02	1.38E-06	18:63456929	0.242	1.99E-06	18:64316482	0.164	1.39E-06
17:63098036	0.458	2.52E-06	18:63458413	0.152	3.31E-12	18:64321863	0.113	7.61E-08
17:69378082	0.352	6.18E-07	18:63459119	0.262	2.85E-07	18:64339221	0.196	2.05E-06
17:69381281	0.217	6.77E-07	18:63461107	0.205	2.85E-06	18:64342129	0.263	2.48E-06
17:69387230	0.294	2.02E-06	18:63467568	0.129	1.48E-06	18:64343959	0.146	2.96E-10
17:72071048	0.364	1.62E-06	18:63536151	0.117	1.18E-08	18:64344843	0.188	3.14E-07
18:59484554	0.103	1.82E-07	18:63561640	0.199	6.17E-07	18:64346894	0.207	8.99E-08
18:59508576	0.164	1.46E-06	18:63563482	0.294	1.86E-07	18:64357538	0.224	2.49E-08
18:59599512	0.184	9.40E-07	18:63564004	0.292	3.09E-06	18:64363304	0.276	3.06E-07
18:61553882	0.137	2.05E-06	18:63576945	0.128	1.50E-06	18:64364989	0.303	1.16E-08
18:61604758	0.107	9.12E-07	18:63601500	0.199	2.90E-07	18:64371724	0.186	8.33E-09
18:61682972	0.194	9.71E-07	18:63677840	0.202	5.42E-09	18:64394280	0.166	1.39E-09
18:61765478	0.122	2.64E-07	18:63677923	0.147	3.89E-09	18:64408551	0.279	7.81E-07
18:62010464	0.111	1.58E-08	18:63691341	0.129	1.65E-08	18:64409041	0.15	7.17E-13
18:62011759	0.189	4.34E-07	18:63741409	0.132	1.57E-06	18:64413484	0.182	2.36E-09
18:62019971	0.106	2.32E-07	18:63864336	0.114	8.41E-11	18:64425930	0.189	5.54E-08
18:62039903	0.154	2.60E-06	18:63931808	0.153	1.28E-07	18:64437674	0.163	8.43E-10
18:62056392	0.118	1.53E-09	18:63931846	0.112	3.71E-09	18:64437727	0.21	1.57E-09
18:62078854	0.104	7.40E-07	18:63999908	0.176	2.87E-11	18:64441493	0.152	2.88E-09
18:62185674	0.114	5.00E-09	18:64009161	0.1	7.05E-15	18:64442181	0.274	1.64E-09
18:62262130	0.115	2.07E-06	18:64081180	0.237	9.23E-08	18:64443120	0.102	9.46E-18
18:62316256	0.119	5.65E-09	18:64089935	0.158	3.24E-10	18:64443165	0.169	4.40E-09

8-2-10. Selected SNP for SF5 (continue)

SNP17	MAF	p-value	SNP	MAF	p-value	SNP	MAF	p-value
18:64449005	0.2	2.64E-06	18:64860596	0.133	7.91E-08	18:66999449	0.18	5.32E-07
18:64455141	0.105	4.59E-14	18:64870290	0.275	1.35E-06	18:67029965	0.132	5.32E-07
18:64468635	0.119	7.16E-17	18:64876016	0.175	3.57E-08	18:67170374	0.385	1.18E-07
18:64475892	0.405	1.11E-08	18:64896195	0.1	3.00E-06	18:67937936	0.139	4.98E-07
18:64477393	0.402	1.43E-06	18:64908951	0.335	3.08E-06	18:68000328	0.247	1.48E-06
18:64477623	0.159	1.02E-19	18:64936731	0.467	1.32E-07	19:18628144	0.445	2.35E-06
18:64485507	0.168	1.87E-16	18:64940607	0.411	1.90E-06	20:12116615	0.031	1.68E-06
18:64486312	0.421	9.51E-09	18:64940914	0.141	1.92E-06	21:23172141	0.045	1.03E-06
18:64494050	0.367	6.16E-08	18:64941325	0.254	7.74E-08	21:41452017	0.194	2.36E-07
18:64499333	0.232	2.93E-12	18:64966109	0.118	2.58E-06	21:42262719	0.031	3.41E-08
18:64500030	0.268	2.09E-11	18:65017387	0.106	2.23E-09	21:42263495	0.046	5.41E-08
18:64502808	0.275	6.95E-09	18:65108231	0.149	2.30E-06	21:42679255	0.391	2.90E-06
18:64508318	0.165	7.64E-12	18:65149277	0.123	1.08E-06	21:42682394	0.184	1.65E-10
18:64512859	0.274	2.05E-09	18:65155263	0.134	9.37E-07	21:42719757	0.381	1.60E-06
18:64515350	0.318	1.38E-08	18:65342096	0.476	1.10E-06	21:42722506	0.112	2.30E-07
18:64515802	0.361	6.88E-07	18:65369971	0.237	1.74E-06	21:42737795	0.123	1.01E-06
18:64515964	0.346	1.19E-09	18:65416931	0.142	1.18E-10	21:42744073	0.174	2.74E-08
18:64518793	0.419	8.13E-07	18:65416967	0.209	3.61E-10	21:42744589	0.154	3.97E-08
18:64519792	0.31	2.42E-09	18:65423643	0.099	1.35E-11	21:42747479	0.401	6.15E-09
18:64520092	0.256	1.49E-08	18:65432609	0.23	5.92E-08	21:42749296	0.161	5.56E-08
18:64522723	0.224	3.14E-12	18:65436388	0.208	1.27E-06	21:42749491	0.344	1.46E-07
18:64522898	0.369	1.41E-06	18:65440449	0.108	9.19E-16	21:42749890	0.148	1.98E-06
18:64531729	0.102	1.91E-14	18:65441969	0.169	1.07E-06	21:42750438	0.436	1.34E-08
18:64532086	0.252	3.70E-07	18:65467043	0.175	5.69E-07	21:42752209	0.388	2.85E-06

18:64554827	0.201	2.61E-06	18:65467359	0.12	5.57E-09	21:42752272	0.491	2.74E-07
18:64559745	0.151	8.01E-07	18:65468081	0.105	7.37E-09	21:42759616	0.201	3.33E-07
18:64577124	0.135	4.39E-14	18:65476422	0.157	5.27E-07	21:42764636	0.317	2.55E-06
18:64584491	0.112	3.67E-11	18:65476545	0.128	4.16E-07	21:42784716	0.087	5.55E-07
18:64586296	0.152	1.23E-09	18:65476555	0.117	1.87E-09	21:42786234	0.216	5.90E-07
18:64592190	0.197	3.10E-09	18:65483063	0.115	1.36E-08	21:42806107	0.424	2.78E-06
18:64595753	0.191	6.89E-08	18:65522920	0.321	1.87E-06	21:42835681	0.491	1.88E-06
18:64605680	0.192	1.55E-06	18:66381175	0.251	9.49E-08	21:42886097	0.086	6.09E-07
18:64610412	0.297	1.96E-08	18:66510857	0.243	1.14E-06	21:42917162	0.064	5.72E-07
18:64619484	0.259	4.53E-07	18:66528108	0.133	2.02E-07	21:42966340	0.111	2.01E-06
18:64626021	0.109	1.90E-16	18:66691238	0.242	9.89E-07	21:43011291	0.073	1.09E-07
18:64628672	0.209	9.18E-08	18:66764616	0.106	8.97E-07	21:43146771	0.407	2.50E-08
18:64633367	0.215	2.97E-09	18:66910107	0.389	2.32E-06	21:43349188	0.324	2.09E-06
18:64640065	0.188	1.80E-08	18:66921244	0.307	2.40E-06	21:44244654	0.137	1.37E-07
18:64648414	0.248	6.27E-07	18:66933037	0.427	2.18E-06	21:44256953	0.03	1.19E-06
18:64684599	0.244	2.92E-06	18:66941685	0.32	2.62E-06	21:45241423	0.057	1.92E-06
18:64724522	0.19	8.89E-07	18:66942376	0.449	2.92E-06	22:41649596	0.01	1.95E-06
18:64765210	0.235	1.10E-06	18:66959880	0.244	5.18E-07			
18:64771859	0.216	3.10E-06	18:66982877	0.159	1.13E-08			
18:64807353	0.171	7.30E-08	18:66983851	0.486	4.63E-07			
18:64836854	0.236	2.73E-06	18:66998953	0.226	2.32E-06			

8-2-11. Selected SNP for AWT

SNP	MAF	p-value	SNP	MAF	p-value
1:140939235	0.357	2.64E-06	15:76538100	0.24	4.53E-06
1:169111727	0.367	7.68E-06	16:32108996	0.437	2.52E-07
1:212301166	0.077	9.42E-06	20:1347751	0.197	7.86E-07
1:234490273	0.301	1.55E-06	20:47414333	0.007	6.20E-07
1:40578216	0.353	3.96E-07	22:24348536	0.323	6.65E-07
1:40578216	0.353	3.96E-07	23:3332669	0.042	5.28E-07
1:53673300	0.215	5.50E-07	23:49383845	0.101	8.06E-06
1:53673300	0.215	5.50E-07	25:15833884	0.031	5.69E-07
1:8312711	0.336	7.03E-07			
2:181377001	0.431	9.01E-06			
2:88413408	0.028	9.59E-06			
3:1197913	0.358	1.55E-07			
3:1197913	0.358	1.55E-07			
3:220343094	0.106	6.17E-06			
3:58882574	0.028	3.98E-12			
4:100844823	0.485	2.87E-07			
4:104142836	0.088	2.58E-06			
4:65436128	0.225	3.55E-08			
4:74194223	0.445	4.63E-08			
4:77791648	0.464	1.28E-06			
4:99129923	0.21	1.28E-07			
5:16075452	0.005	7.03E-06			
5:1879517	0.023	4.34E-06			
5:2872093	0.329	3.97E-07			
6:26454199	0.066	6.84E-90			
6:37695238	0.334	3.50E-34			
6:37709806	0.055	1.51E-19			
6:37709806	0.055	7.89E-20			
6:85741411	0.031	1.14E-06			

8:15043584	0.296	7.53E-07			
8:48345878	0.157	1.18E-07			
8:48345878	0.157	9.81E-07			
8:49434910	0.178	4.52E-06			
8:73895627	0.22	5.98E-06			
9:51139489	0.305	1.17E-06			
10:47929322	0.008	9.39E-06			
10:70578322	0.453	8.73E-06			
11:16823737	0.033	1.36E-06			
11:26339363	0.388	7.16E-11			
11:26339363	0.388	8.42E-12			
11:26445930	0.327	1.14E-23			
11:26451458	0.161	4.40E-09			
12:64579599	0.088	2.06E-06			
12:74918193	0.236	1.59E-06			
14:37641348	0.014	9.84E-06			
14:62080378	0.116	5.63E-06			

8-2-12. Selected SNP for BSC

SNP	MAF	p-value	SNP	MAF	p-value
1:10825003	0.006	6.02E-07	18:17656421	0.006	7.97E-07
1:11596349	0.018	5.68E-07	18:23272250	0.059	4.57E-07
1:11731460	0.007	1.03E-07	19:23550068	0.005	8.50E-08
1:117556565	0.098	3.61E-07	19:26829089	0.006	1.45E-07
1:125647275	0.229	9.40E-07	19:5245573	0.085	7.41E-07
1:125663007	0.093	8.55E-07	20:28542766	0.021	4.10E-08
1:161313263	0.005	7.46E-07	22:12568110	0.038	9.28E-07
1:161317827	0.005	9.43E-07	23:42604469	0.258	5.67E-08
1:23286710	0.134	8.53E-07	23:43869558	0.38	6.97E-07
1:23525210	0.144	2.41E-07	23:44113095	0.389	6.42E-07
1:9748954	0.052	6.89E-07	23:44129421	0.401	6.53E-07
2:186184802	0.02	3.49E-07	23:44376654	0.379	1.01E-07
2:222547984	0.026	3.81E-07	23:44400178	0.362	3.98E-07
2:38912972	0.07	4.04E-08	23:44421542	0.301	2.16E-07
3:134445617	0.017	1.36E-07	23:44430236	0.257	4.18E-07
3:58729692	0.048	9.99E-07	23:44472147	0.319	6.13E-07
3:58803239	0.034	3.33E-07	23:44472172	0.244	1.97E-07
4:23215508	0.284	7.14E-08	23:44480704	0.348	8.16E-07
5:5204547	0.032	3.35E-07	23:44532122	0.472	1.74E-07
5:77960107	0.325	4.58E-08	23:60395049	0.373	2.51E-07
6:7747670	0.093	1.75E-07	23:61015285	0.352	3.76E-07
7:346151	0.018	6.92E-07	23:61015287	0.334	7.26E-07
7:88420532	0.009	8.60E-09	23:61441958	0.489	3.22E-07
8:11245715	0.007	9.23E-07	26:30244284	0.024	6.68E-08
8:33831062	0.488	3.93E-07	26:9301528	0.448	3.31E-08
8:83312543	0.136	1.05E-07			
8:87425145	0.036	1.94E-08			
9:49383752	0.114	2.12E-07			
10:3925471	0.006	2.94E-07			
11:45368810	0.014	4.13E-07			
12:30770373	0.228	5.83E-07			
14:16958134	0.025	3.22E-07			
14:16960989	0.026	9.50E-07			

14:16977366	0.023	7.74E-07
14:45673648	0.066	5.62E-07
14:45941941	0.106	3.75E-07
14:45951713	0.11	2.97E-07
14:46042763	0.119	7.24E-07
14:46109540	0.107	3.37E-07
14:46312410	0.056	1.40E-07
14:46438851	0.053	5.43E-07
15:13030890	0.007	2.40E-07
16:23054753	0.2	2.31E-07
16:4582449	0.118	8.27E-07
16:55460831	0.157	1.18E-07
18:15425063	0.006	1.83E-07

8-2-13. Selected SNP for YCON and CON

SNP	MAF	p-value	SNP	MAF	p-value	SNP	MAF	p-value
1:117033468	0.009	3.73E-07	9:4479703	0.012	1.28E-07	20:42660465	0.033	1.83E-07
1:163314443	0.073	1.09E-06	9:78653760	0.012	1.41E-07	20:42664648	0.036	7.34E-07
1:165842572	0.006	9.63E-07	9:78693486	0.009	2.45E-07	20:42669912	0.044	7.43E-07
1:181612858	0.024	3.73E-07	10:10099047	0.011	6.09E-07	20:42735086	0.046	9.69E-07
1:239407397	0.021	9.25E-07	10:33838945	0.03	7.99E-07	21:12287144	0.409	2.61E-06
1:239946553	0.087	9.32E-07	10:33839579	0.024	9.00E-07	21:14918853	0.13	6.06E-07
1:250198280	0.006	1.48E-07	10:83064253	0.009	1.76E-08	21:26064875	0.307	1.15E-07
1:43848773	0.005	7.89E-07	10:9068560	0.011	2.09E-09	21:27198523	0.035	9.82E-07
1:93350732	0.011	5.03E-07	11:13780092	0.1	6.29E-07	21:40380444	0.017	7.89E-07
1:94580809	0.039	4.38E-07	11:44111400	0.012	3.29E-07	21:6546648	0.229	4.89E-08
2:133963030	0.042	5.56E-08	11:7354290	0.069	3.92E-07	22:31705603	0.013	5.54E-07
2:133965393	0.041	2.70E-07	12:23369508	0.065	2.33E-06	22:35749780	0.012	2.96E-07
2:173054565	0.013	2.03E-07	12:2443069	0.442	2.08E-06	22:4941865	0.017	2.89E-07
2:173067780	0.017	1.92E-07	12:2470174	0.445	1.60E-06	23:29779492	0.012	9.09E-07
2:191858426	0.156	3.91E-07	12:25371152	0.105	1.80E-06	23:31486918	0.012	7.36E-07
2:206639168	0.038	4.31E-07	12:58770802	0.433	4.82E-07	23:32823114	0.006	2.85E-07
3:118294185	0.025	1.05E-06	13:21013384	0.014	8.53E-07	23:32976851	0.007	1.00E-06
3:118685649	0.196	2.43E-06	13:36371931	0.085	5.04E-07	23:33021303	0.213	4.14E-07
3:170027038	0.411	3.39E-07	13:38349542	0.019	8.70E-07	23:33821194	0.007	5.26E-07
3:170030010	0.466	1.99E-06	13:46116121	0.495	2.08E-06	23:34009830	0.007	7.06E-07

3:177038275	0.011	4.09E-09	13:48696547	0.028	4.08E-07	23:34264018	0.007	2.19E-07
3:196214902	0.149	9.22E-07	13:58186333	0.03	5.26E-07	23:34591980	0.013	2.39E-06
4:39691545	0.018	1.61E-07	14:1421248	0.047	6.63E-07	25:10068480	0.026	4.40E-07
4:84239316	0.163	2.59E-06	14:17120237	0.076	6.88E-07	25:10071645	0.029	4.30E-07
5:24160521	0.449	5.27E-07	14:20912935	0.39	8.29E-07	25:10091397	0.027	1.50E-07
5:24161157	0.452	4.03E-07	14:2361058	0.142	4.71E-07	25:28499269	0.039	5.57E-07
5:24161662	0.383	1.29E-06	14:30142241	0.014	6.99E-07	25:28505180	0.019	7.35E-07
5:24162152	0.432	1.55E-06	14:39726680	0.019	6.26E-07	25:39065794	0.125	5.23E-07
5:36132215	0.045	8.87E-07	14:4757334	0.019	9.88E-08	26:3299907	0.016	3.00E-07
5:36298113	0.013	4.78E-07	15:19828442	0.02	1.64E-07	26:43485768	0.07	9.56E-07
5:58341072	0.013	9.03E-07	15:73602158	0.013	2.11E-07			
5:69972866	0.198	8.62E-07	15:8780668	0.014	3.19E-08			
5:70279919	0.264	3.27E-07	15:8780910	0.014	4.65E-09			
5:89311974	0.08	7.31E-07	15:8782232	0.027	1.76E-07			
5:89320814	0.09	4.54E-07	15:8783544	0.01	2.73E-07			
5:89320882	0.097	4.70E-07	16:39518996	0.009	9.53E-07			
6:21600204	0.339	9.06E-07	16:45766900	0.01	1.69E-07			
6:25471374	0.036	3.05E-07	17:63384399	0.045	3.73E-07			
6:27367473	0.025	3.70E-07	18:33487293	0.448	5.17E-07			
6:41306664	0.152	6.21E-08	18:33487321	0.428	4.57E-07			
6:41308131	0.146	1.96E-07	18:47198266	0.025	3.63E-08			
8:2503214	0.009	1.49E-07	18:6221534	0.012	7.18E-07			
8:47184965	0.02	9.25E-08	19:33163137	0.01	8.98E-07			
8:7696280	0.152	2.05E-07	19:3506368	0.067	2.02E-07			
9:20725385	0.048	9.49E-07	19:40263985	0.271	2.92E-06			
9:21388388	0.006	2.15E-08	20:17862989	0.011	8.74E-07			

8-2-14. Selected SNP for YLS and LS

SNP	MAF	p-value	SNP	MAF	p-value	SNP	MAF	p-value
1:109028360	0.186	1.42E-07	7:65610400	0.078	3.71E-07	15:26933194	0.496	3.56E-07
1:177173056	0.058	1.56E-07	7:67108505	0.18	2.34E-07	15:26934222	0.434	7.78E-07
1:228939757	0.059	7.96E-06	7:76361649	0.012	5.46E-07	15:26939801	0.375	7.62E-07
1:40903044	0.016	3.70E-07	7:84411866	0.121	2.57E-16	15:26940768	0.495	3.77E-07
1:40931556	0.015	3.06E-07	7:93059686	0.083	5.01E-14	15:26940861	0.47	5.12E-07
1:50607431	0.05	1.46E-07	8:54888416	0.329	2.05E-10	15:63345228	0.037	2.50E-07
1:53612870	0.192	9.51E-07	8:67796973	0.115	4.08E-08	16:16727681	0.053	5.65E-07
2:131649234	0.31	3.07E-07	8:69952675	0.41	5.28E-06	16:17332703	0.124	6.98E-07
2:137363177	0.02	9.12E-06	8:88099034	0.034	2.61E-06	17:44492246	0.031	6.60E-08
2:151884049	0.025	1.47E-07	9:34798733	0.428	6.81E-07	18:17014362	0.067	3.44E-06
2:191262964	0.082	6.44E-06	9:56551087	0.01	2.27E-06	18:24308412	0.012	1.46E-06
2:214243867	0.386	3.91E-07	9:81648065	0.18	7.41E-07	18:43120325	0.022	5.86E-06
2:89204686	0.206	1.47E-06	9:84467917	0.062	8.99E-06	20:173415	0.08	6.72E-06
2:98854028	0.064	9.48E-09	10:81990650	0.025	7.42E-07	22:11017969	0.037	3.58E-06
3:117213550	0.071	9.09E-08	11:26001775	0.328	6.88E-07	22:22898045	0.352	5.62E-06
3:117476100	0.078	9.82E-07	11:35878939	0.08	6.07E-06	22:47139173	0.012	2.49E-07
3:117484048	0.093	1.15E-07	11:57570604	0.265	6.10E-06	23:11715377	0.115	3.92E-07
3:123712314	0.166	8.59E-06	11:57811826	0.019	9.66E-07	23:37130040	0.226	1.04E-07
3:151822210	0.016	2.69E-07	12:3942307	0.02	2.70E-06	24:12380748	0.127	2.59E-06
3:152295923	0.019	1.04E-07	12:42426722	0.016	8.57E-07	24:25418929	0.01	2.81E-06
3:160656494	0.225	5.95E-07	12:8472896	0.078	9.29E-07	24:37643644	0.019	3.23E-09
3:191320785	0.259	4.35E-06	12:8604079	0.084	7.41E-07	25:14979046	0.254	1.25E-06
3:205664696	0.063	5.04E-07	12:8604217	0.096	3.17E-07			
3:59304193	0.012	6.11E-07	12:8926850	0.062	9.27E-08			
4:109080643	0.375	7.24E-07	12:8961596	0.078	4.66E-07			
4:12016158	0.02	9.37E-06	12:9071327	0.078	4.66E-07			
4:95045369	0.087	3.52E-07	13:73867640	0.398	1.41E-08			
5:40740332	0.034	8.30E-07	13:76613561	0.019	6.90E-06			
5:41598599	0.029	2.95E-07	13:82076285	0.04	8.17E-08			
5:41837830	0.03	4.44E-07	14:1472821	0.417	7.85E-07			
5:42101316	0.029	9.62E-07	14:34618562	0.172	5.71E-07			

5:45107913	0.103	6.90E-07	14:34827943	0.202	6.31E-07
5:97976361	0.095	6.52E-07	14:34832773	0.197	2.40E-07
5:98041966	0.276	6.57E-07	14:34890598	0.176	9.00E-07
5:98097648	0.46	5.68E-08	14:35985801	0.119	5.45E-07
5:98101799	0.406	2.54E-07	14:36076228	0.13	5.54E-08
5:98227730	0.464	8.48E-07	14:36181667	0.138	5.35E-07
6:110656914	0.012	8.25E-07	14:36188885	0.124	8.78E-07
6:110957704	0.012	8.25E-07	14:36189078	0.163	5.18E-07
6:32773110	0.015	1.86E-07	14:36199239	0.196	6.68E-07
6:36840065	0.259	6.29E-07	14:36254844	0.201	8.52E-07
6:36864972	0.247	7.99E-07	14:36275077	0.145	4.91E-07
6:37689350	0.352	4.61E-07	14:43592145	0.106	1.30E-06
6:38034038	0.428	6.08E-07	14:54963432	0.028	7.52E-07
6:38034949	0.396	7.31E-07	14:55134314	0.053	2.65E-07
6:62772543	0.415	5.95E-06	14:55143434	0.06	7.07E-07

8-2-15. Selected SNP for tail Length

SNP	MAF	p-value	SNP	MAF	p-value
8:86908680	0.194	7.20E-08	19:7168810	0.379	1.64E-10
11:37064343	0.475	1.79E-08	19:7174905	0.312	3.81E-08
11:37081546	0.376	1.71E-08	19:7174936	0.371	2.63E-09
11:37089749	0.258	1.18E-10	19:7176931	0.315	6.36E-09
11:37099602	0.276	2.20E-09	19:7177221	0.336	6.44E-08
11:37146356	0.229	1.36E-08	19:7179470	0.36	8.85E-10
11:37170092	0.469	6.45E-08	19:7189571	0.341	4.64E-09
11:37188858	0.231	5.98E-08	19:7196597	0.327	7.02E-10
11:37210883	0.216	8.47E-10	19:7196660	0.376	1.37E-08
11:37310699	0.262	7.43E-11	19:7196719	0.303	9.87E-09
11:37316869	0.201	5.52E-32	19:7196956	0.344	4.73E-10
11:37319316	0.202	6.38E-31	19:7198252	0.377	3.58E-08
11:37321041	0.227	9.03E-21	19:7206027	0.353	9.40E-10
11:37321473	0.435	1.62E-12	19:7208472	0.354	6.58E-10
11:37326007	0.221	3.64E-35	19:7209832	0.357	6.68E-10
11:37327582	0.196	5.21E-29	19:7209879	0.356	1.13E-09
11:37335681	0.324	1.60E-25	19:7212816	0.339	1.21E-11
11:37341398	0.256	1.89E-24	19:7212951	0.443	1.21E-10
11:37387463	0.408	1.47E-10	19:7215175	0.381	3.42E-13
11:37393332	0.244	3.08E-08	19:7218254	0.409	6.01E-10
11:37398200	0.231	9.30E-09	19:7218429	0.28	3.30E-09
11:37592211	0.261	8.55E-08	19:7220499	0.346	1.74E-11

11:37627527	0.468	7.73E-08	19:7222181	0.408	3.40E-09
11:37776926	0.354	8.01E-08	19:7227140	0.312	9.74E-10
11:38000548	0.237	1.38E-09	19:7228001	0.334	2.90E-08
11:38021124	0.256	4.75E-08	19:7228199	0.364	2.95E-10
11:38026882	0.261	2.04E-09	19:7228397	0.455	6.70E-09
11:38239698	0.465	6.08E-10	19:7229902	0.364	5.60E-08
11:38240022	0.444	5.94E-09	19:7229927	0.292	1.57E-08
11:38240601	0.346	1.09E-09	19:7230345	0.338	9.07E-08
11:38249404	0.478	7.01E-09	19:7231656	0.372	2.00E-09
11:38256873	0.445	1.06E-08	19:7232796	0.41	4.89E-08
11:38257662	0.449	3.25E-09	19:7237413	0.365	6.88E-08
11:38261181	0.44	3.87E-08	19:7238107	0.44	3.84E-08
11:38262301	0.466	4.17E-08			
11:38262777	0.397	5.25E-08			
16:22289083	0.014	6.58E-08			
16:22291332	0.014	9.86E-08			
16:22302211	0.014	1.18E-08			
16:22303106	0.014	1.18E-08			
19:7141436	0.376	9.67E-08			
19:7151494	0.369	1.04E-08			
19:7154742	0.411	1.18E-09			
19:7156907	0.325	7.54E-08			
19:7164603	0.353	1.53E-08			
19:7168275	0.284	2.70E-08			

8.5 Abbreviated table of monogenic variants in sheep as downloaded from OMIA

OMIA ID(s)	Breed(s)	Variant Phenotype	Gene	Allele	Type of Variant	Deleterious?	Chr.	PubMed ID(s)
OMIA 000328-9940	White Dorper	Ehlers-Danlos syndrome, type VII (Dermatosparaxis)	ADAMTS2		nonsense (stop-gain)	yes	5	22497338
OMIA 000328-9940	White Dorper	Ehlers-Danlos syndrome, type VII (Dermatosparaxis)	ADAMTS2		nonsense (stop-gain)	yes	5	25354687
OMIA 000662-9940	Romney Marsh	Motor neuron disease, lower	AGTPBP1		missense	yes	2	22588130
OMIA 001672-9940	Zwartbles	Type 1 Primary Hyperoxaluria	AGXT		missense	yes	1	33003365
OMIA 000201-9940	Merino	White fleece	ASIP	Wt	insertion, gross (>20)	no	13	18493018
OMIA 000201-9940		Recessive black	ASIP	a	missense	no	13	18493018
OMIA 000201-9940		Recessive black	ASIP	a	deletion, small (<=20)	no	13	12354151
OMIA 001885-9940	Lacaune	Fecundity, Lacaune, FecL	B4GALNT2		regulatory	no	11	24086150
OMIA 001885-9940	Lacaune	Fecundity, Lacaune, FecL	B4GALNT2		regulatory	no	11	24086150
OMIA 001079-9940	SpÃ¦lsau	yellow fat	BCO2		insertion, gross (>20)	yes	15	34193038
OMIA 001079-9940	Norwegian White	Yellow fat	BCO2		nonsense (stop-gain)	yes	15	20122251
OMIA 002306-9940	Belclare, Irish Cambridge	Fecundity, Belclare	BMP15	FecX(B)	missense	no	X	14627550
OMIA 002306-9940	Olkuska	Fecundity, Olkuska	BMP15	FecX(O)	missense	no	X	23637641
OMIA 002306-9940	Lacaune	Fecundity, Lacaune	BMP15	FecX(L)	missense	no	X	17038554
OMIA 002306-9940	Grivette	Fecundity, Grivette	BMP15	FecX(Gr)	missense	no	X	23637641
OMIA 002306-9940	Romney Marsh	Fecundity, Inverdale	BMP15	FecX(I)	missense	no	X	10888873

OMIA 002306-9940	Romney Marsh	Fecundity, Hanna	BMP15	FecX(H)	nonsense (stop-gain)	no	X	10888873
OMIA 002306-9940	Irish Cambridge	Fecundity, Galway	BMP15	FecX(G)	nonsense (stop-gain)	no	X	14627550
OMIA 002306-9940	Rasa Aragonesa	Fecundity, Rasa Aragonesa	BMP15	FecX(R)	deletion, small (<=20)	no	X	18355397
OMIA 002306-9940	Tunisian Barbarine	Fecundity, Barbarine	BMP15	FecX(Bar)	complex rearrangement	no	X	28506298
OMIA 002306-9940	Rasa Aragonesa	Fecundity	BMP15	FecX(RA)	missense	unknown	X	31927415
OMIA 002306-9940	Blanche du Massif Central, Noire du Velay	Fecundity	BMP15	FecX(N)	regulatory	unknown	X	32636872
OMIA 000383-9940	Booroola, Han, small-tailed	Fecundity, Booroola	BMPR1B	FecB(B)	missense	no	6	11259271
OMIA 000698-9940	Rasa Aragonesa	Myotonia	CLCN1		missense	yes	4	25744800
OMIA 001482-9940	Borderdale	Neuronal ceroid lipofuscinosis, 5	CLN5		splicing	yes	10	17988881
OMIA 001443-9940	South Hampshire	Neuronal ceroid lipofuscinosis	CLN6		deletion, gross (>20)	yes	7	23338040
OMIA 001443-9940	Merino	Neuronal ceroid lipofuscinosis, 6	CLN6		missense	yes	7	17046213
OMIA 001481-9940	Awassi	Achromatopsia-2 (day blindness)	CNGA3		missense	yes	3	28282490
OMIA 001481-9940	Awassi	Achromatopsia-2 (day blindness)	CNGA3		nonsense (stop-gain)	yes	3	19874885
OMIA 001354-9940		Muscular hypertrophy (double muscling), Callipyge	DLK1		regulatory	unknown	18	12368241
OMIA 001542-9940	Corriedale	Hypophosphatemic rickets, autosomal recessive, 1	DMP1		nonsense (stop-gain)	yes	6	21747952
OMIA 001765-9940	Cameroon	Waardenburg syndrome, type 4A	EDNRB		deletion, gross (>20)	yes	10	23300849
OMIA 000437-9940	Swiss Alpine	Haemophilia A	F8		delins, small (<=20)	yes	X	19943872

OMIA 001723-9940	Romney Marsh	Familial episodic ataxia	FGF14		nonsense (stop-gain)	yes	10	29253853
OMIA 001703-9940	Suffolk	Chondrodysplasia, Spider lamb	FGFR3		missense	yes	6	16441300
OMIA 000405-9940	Southdown	Gaucher disease, type	GBA		missense	yes	1	29023809
OMIA 002362-9940	Cheviot	Fecundity, Thoka, FecG	GDF9	FecG(T)	missense	no	5	19713444
OMIA 002362-9940	Belclare, Irish Cambridge	Fecundity, High fertility, FecG	GDF9	FecG(H)	missense	no	5	14627550
OMIA 002362-9940	Norwegian White	Fecundity, Norwegian White Sheep	GDF9	FecG(F)	missense	no	5	23280002
OMIA 002362-9940	Brazilian Santa InÃªs, Mexican Pelibuey	Fecundity, Embrapa, FecG	GDF9	FecG(E)	missense	no	5	20528846
OMIA 002362-9940	Ile de France	Fecundity, Vacaria, FecG	GDF9	FecG(V)	missense	no	5	25039891
OMIA 000402-9940	Romney Marsh	Gangliosidosis, GM1	GLB1		missense	yes	19	Reference not in PubMed
OMIA 001461-9940	Jacob	Gangliosidosis, GM2, type I (B variant)	HEXA		splicing	yes	7	20817517
OMIA 001952-9940	Altay	Microtia	HMX1		duplication	yes	6	31691317
OMIA 000806-9940		Polyceraty	HOXD1		deletion, small (<=20)	no	2	33528505
OMIA 002229-9940	Valle del Belice	Hypotrichosis	HR		nonsense (stop-gain)	yes	2	12927087
OMIA 001528-9940	Romane	Fleece variation, woolly	IRF2BP2		insertion, gross (>20)	no	25	28379502
OMIA 001948-9940	Mouton Vendeen	Epidermolysis bullosa, junctionalis, ITGB4	ITGB4		nonsense (stop-gain)	yes	11	33225458
OMIA 001948-9940	Churra	Epidermolysis bullosa, junctionalis, ITGB4	ITGB4		deletion, small (<=20)	yes	11	25955497
OMIA 001678-9940	German Blackheaded Mutton	Epidermolysis bullosa, junctionalis, LAMC2-related	LAMC2		deletion, small (<=20)	yes	12	21573221

OMIA 001694-9940	Polypay	Resistance to lentivirus	LOC105603932		regulatory	no	20	24303974
OMIA 001505-9940	Swedish Landrace	Neuronal ceroid lipofuscinosis, 10	LOC443060		missense	yes	21	10856224
OMIA 001199-9940	Valle del Belice	Recessive pheomelanism	MC1R	e	missense	no	14	Reference not in PubMed
OMIA 001199-9940	Corriedale, Dala, Damara, Merino	Dominant black	MC1R	E^D	missense	no	14	9892731
OMIA 001199-9940	Massese	Dominant black	MC1R	E^D	missense	no	14	9892731
OMIA 001199-9940	Gotland, Gute, VÃ¤rmland	Dominant black	MC1R		missense	no	14	31475378
OMIA 000031-9940	Jacob	Lilac	MLPH		nonsense (stop-gain)	no	1	32512769
OMIA 001426-9940	Texel	Muscular hypertrophy (double muscling), Texel	MSTN		regulatory	yes	2	16751773
OMIA 001595-9940	Merino	Brachygnathia, cardiomegaly and renal hypoplasia syndrome	OBSL1		deletion, small (<=20)	yes	2	32933480
OMIA 002227-9940	Istrian Pramenka	Otocephaly	OTX2		nonsense (stop-gain)	yes	7	31969185
OMIA 000649-9940	Texel	Microphthalmia	PITX3		missense	yes	22	20084168
OMIA 002105-9940	Swaledale	Neuroaxonal dystrophy, PLA2G6-related	PLA2G6		nonsense (stop-gain)	yes	3	33159255
OMIA 002105-9940	Swaledale	Neuroaxonal dystrophy, PLA2G6-related	PLA2G6		splicing	unknown	3	33159255
OMIA 001504-9940		Neuronal ceroid lipofuscinosis, 1	PPT1		delins, small (<=20)	yes	1	31289301
OMIA 000944-9940	Ile de France, Romanov	Resistance to scrapie	PRNP	V	missense	yes	13	8094373
OMIA 000944-9940	Norwegian breeds	Resistance to scrapie, Nor98 type	PRNP	F	missense	yes	13	15604451
OMIA 000944-9940	Ile de France, Romanov	Resistance to scrapie	PRNP	H	missense	yes	13	8094373

OMIA 000944-9940	Suffolk	Resistance to scrapie	PRNP	Q	missense	yes	13	1969635
OMIA 001139-9940		Glycogen storage disease V	PYGM		splicing	yes	21	9267848
OMIA 001867-9940	Churra	Lissencephaly and cerebellar hypoplasia	RELN		deletion, gross (>20)	yes	4	24260534
OMIA 000483-9940	Numerous breeds	Polled	RXFP2		insertion, gross (>20)	no	10	26103004
OMIA 001400-9940	Texel	Chondrodysplasia, Texel	SLC13A1		deletion, small (<=20)	yes	4	22742499
OMIA 002176-9940	Coopworth, Perendale	Meckel-like hepatorenal fibrocystic dysplasia syndrome	TMEM67		haplotype	yes	9	28487520
OMIA 002285-9940	Merino	Ovine congenital progressive muscular dystrophy	TNNT1		deletion, small (<=20)	yes	14	32819427
OMIA 001249-9940		Brown	TYRP1		missense	no	2	23451726
OMIA 001249-9940	Valais Red	Brown	TYRP1	b^VS1	deletion, small (<=20)	no	2	31571241
OMIA 001249-9940	Soay	Tawny (light brown)	TYRP1	b^Soay	missense	no	2	17254985
OMIA 001249-9940	Valais Red	Brown	TYRP1	b^VS2	nonsense (stop-gain)	no	2	31571241
OMIA 001176-9940	German Blackface	Porphyria cutanea tarda	urod		missense	yes	1	16026339