Chapter 6 Conclusions and future work

This thesis attempted to improve our understanding of the genetic architecture of complex traits in sheep populations. The work focussed on two different quantitative traits: body weight (BW, 6 – 10 months) and gene expression (longissimus lumborum muscle). Genetic architecture can be seen as the collective outcome of factors that include linkage disequilibrium, distribution of allele frequencies, number of loci affecting a trait and effects of gene-gene and gene-environment interactions on the trait. From this standpoint, in chapter 2, we estimated and compared linkage disequilibrium (LD) and various other genetic diversity parameters such as gene diversity (H_e) and fixation index (F_{st}) between five Australian sheep populations – three pure breeds and two crossbred populations. We found that LD decays rapidly as genetic distances increase but that this varies significantly between these sheep populations. Genome-wide LD information is used in genomic selection (GS) where genetic markers covering the whole genome are used to predict genomic estimated breeding values (GEBV). In genomic selection, the accuracy of GEBV largely depends on the heritability of the trait, genetic architecture and the effective size of the targeted populations. The low levels of LD observed in these populations suggest that accuracies of prediction in sheep will be lower than in other populations with higher LD under similar trait/population scenarios. As proposed by Kijas et al. (Kijas et al. 2014), denser marker panels may help offset the effects of low LD. Larger datasets with more animals than the numbers used in e.g. cattle or pig may also be needed to obtain similar levels of prediction accuracy as those observed in these other species. The results from this study improve our understanding of the genetic diversity and structure of the three main Australian commercial sheep breeds and can help guide future effective GWAS. In addition, the results provide insights into the effects of artificial selection within these breeds and can help guide the design of genomic selection studies that aim to improve the accuracy of genomic estimated breeding values (GEBV) based on genome-wide markers.

In chapter 3, a genome wide association studies (GWAS) for body weight involving a population of 1,781 Merino sheep was conducted. Our GWAS identified 39 SNP that are associated with body weight in sheep and found a major QTL region on OAR6. The results include both previously reported and several new QTL regions for the body weight traits. Results suggest that body weight trait in sheep is polygenic though there are some QTL of large effects. These findings are particularly useful for marker assisted selection and prediction models could put more emphasis on selection in these QTL regions. Furthermore, this analysis can be considered a first step in the process of identifying the causal gene (and variants) that have a sizeable effect on body weight. Given the synteny observed across species, this is an ancient adaptation which could be of broader biological interest.

Next, Chapter 4 proposed a new best linear unbiased prediction method to estimate breeding values which tries to identify a relationship matrix based on a subset of SNP that are potentially functionally associated to the trait, which we called TBLUP. A heuristic approach based on Differential evolution (DE) was used to evolve SNP subsets. Using simulated data for different scenarios, we showed that the proposed method performed better or was at least equivalent to GBLUP and a Bayesian method when the traits are controlled by a relatively small number of QTL. The proposed method has potential for applications in genomic selection. However, further experimentation with real datasets on various traits is needed to fully assess the performance of TBLUP.

GWAS has been widely used to identify QTL regions of complex traits. However, by and large, the sum of effects of the statistically significant loci identified by GWAS explains a very small proportion of additive heritability. Even when all the SNP in high-density panels are used the estimates are still below pedigree based estimates of heritability. The gap between the two estimates has come to be known as missing heritability (pedigree heritability is correct – there's something missing in the SNP data) or phantom heritability (pedigree heritability is over-inflated, SNP estimates probably more accurate). In chapter 5, we estimated the heritability of gene expression in sheep half-sib families using the pedigree information and then using SNP data. As with other studies, results showed that the heritability based on pedigree is much higher than the heritability based on SNP and the latter only captured part of the additive variance in gene expression. This led us to postulate that interactions play a much more significant role in estimates of heritability than current consensus suggests. In effect and in agreement with the phantom heritability notion, we are over-estimating additive heritability because it is based on close relationships through pedigree but in reality it is the truly additive effects plus a proportion of the epistatic effect that are being used to estimate h^2. This work has implications for genomic selection and provides additional insights as to why prediction equations have to be re-calibrated, why accuracies are higher in closely related populations and why predictions across breeds are less reliable.

Significant progress has been made in the past decade to understand genetic architecture and how it gives raise to complex traits but there still are large gaps and limitations in our knowledge of the relationship between genome and phenotype; and even the true nature of inheritance seems murkier now (because of different postulates regarding the inheritance of complex traits) that we know more than in the past. In this thesis, we have documented a series of studies that help inform our knowledge of this exciting field. We hope some of this work will find its way into practical applications and, even if in a small way, be of some use to society.

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Appendix 1 Supplementary tables and figures for chapter 2

Table 2.S1 Summary of statistics for SNP, average minor allele frequency and heterozygosity.

OAR	Size (Mbp)	SNP	Mean distance between SNP(kb)	BL		PD		MER		BxM		BxMxP	
				MAF	Het	MAF	Het	MAF	Het	MAF	Het	MAF	Het
1	275.61	5484	50.26	0.230	0.308	0.262	0.345	0.295	0.383	0.285	0.405	0.296	0.404
2	248.99	5123	48.58	0.220	0.293	0.259	0.342	0.293	0.381	0.280	0.403	0.292	0.403
3	224.28	4637	48.35	0.224	0.302	0.255	0.337	0.289	0.376	0.282	0.405	0.293	0.405
4	119.26	2510	47.53	0.231	0.307	0.253	0.338	0.290	0.379	0.284	0.404	0.293	0.406
5	107.9	2192	48.8	0.225	0.302	0.263	0.345	0.296	0.384	0.283	0.404	0.297	0.402
6	117.03	2410	48.54	0.221	0.296	0.257	0.338	0.290	0.378	0.276	0.399	0.290	0.400
7	100.08	2094	47.8	0.217	0.293	0.262	0.343	0.297	0.384	0.286	0.413	0.297	0.409
8	90.7	1915	47.26	0.235	0.314	0.255	0.337	0.296	0.385	0.286	0.410	0.296	0.408
9	94.73	1980	47.84	0.229	0.305	0.271	0.356	0.293	0.380	0.284	0.404	0.296	0.403
10	86.45	1717	50.36	0.214	0.292	0.261	0.346	0.292	0.381	0.278	0.406	0.293	0.401
11	62.25	1103	56.29	0.230	0.305	0.255	0.337	0.273	0.358	0.274	0.390	0.286	0.388
12	79.1	1583	49.89	0.227	0.306	0.270	0.355	0.291	0.381	0.283	0.404	0.295	0.404
13	83.08	1561	53.24	0.227	0.297	0.259	0.341	0.297	0.381	0.284	0.404	0.294	0.408
14	62.72	1088	57.67	0.231	0.304	0.246	0.325	0.289	0.372	0.279	0.394	0.287	0.401
15	80.92	1553	52.06	0.232	0.309	0.252	0.332	0.289	0.380	0.284	0.399	0.288	0.400
16	71.72	1448	49.45	0.247	0.327	0.256	0.337	0.285	0.375	0.288	0.401	0.294	0.406
17	72.29	1321	54.64	0.219	0.289	0.257	0.340	0.296	0.385	0.282	0.407	0.297	0.410
18	68.6	1316	52.09	0.226	0.303	0.269	0.352	0.292	0.377	0.281	0.396	0.295	0.402
19	60.46	1152	52.46	0.236	0.309	0.247	0.324	0.289	0.376	0.283	0.401	0.286	0.399
20	51.18	1050	48.56	0.245	0.319	0.261	0.340	0.294	0.382	0.284	0.394	0.289	0.395
21	50.07	821	61.01	0.239	0.312	0.268	0.343	0.291	0.378	0.282	0.394	0.295	0.401
22	50.83	1008	50.47	0.225	0.303	0.255	0.337	0.287	0.377	0.285	0.406	0.294	0.407
23	62.33	1054	59.16	0.232	0.309	0.256	0.344	0.297	0.386	0.285	0.403	0.298	0.410
24	42.03	683	61.62	0.226	0.306	0.257	0.332	0.289	0.374	0.283	0.404	0.291	0.396
25	45.37	931	48.75	0.242	0.318	0.265	0.337	0.293	0.376	0.288	0.401	0.292	0.397
26	44.08	865	50.93	0.236	0.315	0.256	0.338	0.293	0.382	0.286	0.406	0.300	0.412

A summary of statistics for the SNP that passed quality control within each chromosome and chromosome-wise average minor allele frequency (MAF) and heterozygosity (Het) for each breed.

Table 2.S2 Mean linkage disequilibrium in five populations over different map distances.

	r^2					D’				
	BL	PD	MER	BxM	BxMxP	BL	PD	MER	BxM	BxMxP
10Kb	0.335	0.334	0.27	0.288	0.300	0.846	0.839	0.744	0.784	0.781
10-20Kb	0.276	0.259	0.202	0.213	0.215	0.806	0.786	0.675	0.698	0.689
20-40Kb	0.223	0.206	0.141	0.152	0.156	0.754	0.728	0.573	0.603	0.597
40-60Kb	0.189	0.174	0.103	0.115	0.118	0.717	0.692	0.506	0.539	0.533
60-100Kb	0.160	0.146	0.075	0.084	0.088	0.681	0.656	0.445	0.478	0.476
100-200Kb	0.133	0.120	0.049	0.058	0.063	0.644	0.620	0.382	0.418	0.420
200-500Kb	0.104	0.099	0.033	0.041	0.046	0.593	0.577	0.33	0.368	0.372
500Kb-1Mb	0.075	0.079	0.025	0.030	0.036	0.528	0.526	0.292	0.324	0.334
1-2Mb	0.047	0.058	0.018	0.021	0.027	0.456	0.467	0.254	0.279	0.295
2-5Mb	0.023	0.035	0.011	0.012	0.018	0.374	0.384	0.208	0.229	0.249
5-10Mb	0.013	0.019	0.008	0.008	0.013	0.320	0.311	0.177	0.199	0.217
10-20Mb	0.009	0.011	0.006	0.007	0.010	0.293	0.261	0.159	0.184	0.195
20-50Mb	0.007	0.007	0.005	0.006	0.008	0.279	0.224	0.148	0.174	0.178
50Mb+	0.006	0.005	0.005	0.006	0.007	0.275	0.211	0.145	0.172	0.172
Non-syntenic	0.009	0.011	0.006	0.007	0.009	0.292	0.244	0.174	0.183	0.188

Table 2.S3 Average linkage disequilibrium (r^2) between adjacent markers for each autosome (OAR).

OAR	BL		PD		MER		BxM		BxMxP	
	Mean	Median	Mean	Median	Mean	Median	Mean	Median	Mean	Median
1	0.21	0.081	0.196	0.089	0.13	0.048	0.142	0.056	0.147	0.062
2	0.226	0.083	0.208	0.097	0.143	0.057	0.156	0.060	0.153	0.065
3	0.222	0.084	0.204	0.088	0.134	0.055	0.150	0.059	0.148	0.062
4	0.211	0.08	0.202	0.094	0.137	0.056	0.146	0.055	0.151	0.061
5	0.212	0.075	0.192	0.082	0.124	0.048	0.134	0.046	0.143	0.056
6	0.21	0.079	0.19	0.087	0.124	0.05	0.142	0.057	0.141	0.06
7	0.229	0.078	0.205	0.089	0.129	0.053	0.153	0.064	0.155	0.067
8	0.216	0.084	0.196	0.085	0.128	0.051	0.142	0.061	0.144	0.061
9	0.211	0.077	0.187	0.081	0.128	0.049	0.137	0.056	0.141	0.061
10	0.246	0.087	0.21	0.088	0.148	0.054	0.166	0.061	0.162	0.07
11	0.175	0.058	0.173	0.067	0.111	0.038	0.114	0.037	0.123	0.043
12	0.219	0.083	0.182	0.08	0.126	0.044	0.138	0.055	0.145	0.06
13	0.209	0.069	0.198	0.084	0.137	0.052	0.139	0.049	0.142	0.055
14	0.184	0.054	0.182	0.069	0.11	0.041	0.117	0.041	0.116	0.037
15	0.195	0.072	0.2	0.087	0.124	0.049	0.130	0.049	0.138	0.056
16	0.185	0.073	0.192	0.088	0.121	0.047	0.124	0.051	0.138	0.063
17	0.218	0.078	0.188	0.082	0.117	0.047	0.142	0.051	0.135	0.049
18	0.195	0.07	0.188	0.09	0.127	0.049	0.131	0.046	0.14	0.054
19	0.204	0.072	0.192	0.077	0.137	0.049	0.141	0.051	0.141	0.051
20	0.18	0.067	0.166	0.074	0.109	0.043	0.115	0.045	0.117	0.042
21	0.188	0.064	0.182	0.069	0.108	0.036	0.125	0.046	0.122	0.043
22	0.206	0.085	0.196	0.075	0.118	0.04	0.133	0.049	0.142	0.064
23	0.174	0.067	0.184	0.079	0.108	0.04	0.107	0.043	0.118	0.042
24	0.195	0.064	0.162	0.06	0.109	0.035	0.118	0.040	0.122	0.041
25	0.197	0.073	0.195	0.087	0.114	0.044	0.124	0.046	0.136	0.056
26	0.184	0.075	0.176	0.072	0.107	0.04	0.115	0.045	0.12	0.054

Table 2.S4 Average linkage disequilibrium (|D’|) between adjacent markers for each autosome (OAR).

OAR	BL		PD		MER		BxM		BxMxP	
	Mean	Median	Mean	Median	Mean	Median	Mean	Median	Mean	Median
1	0.732	0.883	0.701	0.836	0.543	0.517	0.584	0.592	0.576	0.581
2	0.755	0.926	0.733	0.896	0.568	0.564	0.604	0.627	0.587	0.599
3	0.749	0.912	0.73	0.889	0.567	0.564	0.607	0.638	0.586	0.598
4	0.733	0.88	0.728	0.874	0.563	0.546	0.592	0.592	0.583	0.594
5	0.736	0.897	0.696	0.816	0.543	0.507	0.559	0.541	0.567	0.556
6	0.743	0.9	0.722	0.86	0.546	0.524	0.594	0.623	0.583	0.593
7	0.752	0.913	0.727	0.882	0.536	0.494	0.599	0.615	0.584	0.603
8	0.74	0.885	0.707	0.85	0.532	0.502	0.567	0.562	0.558	0.548
9	0.753	0.905	0.698	0.846	0.543	0.53	0.580	0.571	0.572	0.565
10	0.765	0.921	0.722	0.889	0.571	0.563	0.598	0.613	0.59	0.604
11	0.719	0.859	0.696	0.823	0.547	0.519	0.546	0.558	0.547	0.548
12	0.752	0.905	0.687	0.809	0.542	0.53	0.575	0.583	0.563	0.568
13	0.721	0.886	0.716	0.862	0.548	0.521	0.556	0.525	0.555	0.552
14	0.723	0.88	0.714	0.849	0.523	0.493	0.546	0.514	0.53	0.491
15	0.726	0.879	0.744	0.902	0.544	0.516	0.560	0.544	0.569	0.566
16	0.716	0.865	0.718	0.866	0.549	0.525	0.555	0.539	0.573	0.569
17	0.718	0.858	0.694	0.805	0.516	0.464	0.567	0.561	0.549	0.517
18	0.713	0.859	0.701	0.841	0.542	0.52	0.563	0.544	0.564	0.562
19	0.735	0.901	0.747	0.899	0.547	0.525	0.571	0.568	0.577	0.588
20	0.709	0.855	0.683	0.803	0.506	0.464	0.533	0.499	0.532	0.513
21	0.718	0.852	0.69	0.834	0.481	0.419	0.542	0.513	0.531	0.512
22	0.724	0.873	0.72	0.85	0.529	0.478	0.565	0.554	0.586	0.595
23	0.707	0.827	0.679	0.78	0.505	0.457	0.523	0.493	0.516	0.473
24	0.698	0.821	0.667	0.762	0.503	0.47	0.509	0.457	0.532	0.506
25	0.728	0.882	0.707	0.834	0.517	0.464	0.551	0.510	0.551	0.552
26	0.723	0.872	0.696	0.82	0.524	0.479	0.540	0.499	0.551	0.55

Table 2.S5 Chromosome wise average linkage disequilibrium (r^2) in five populations.

OAR	BL		PD		MER		BxM		BxMxP	
	Mean	Median	Mean	Median	Mean	Median	Mean	Median	Mean	Median
1	0.008	0.003	0.008	0.003	0.005	0.002	0.006	0.003	0.008	0.003
2	0.009	0.003	0.009	0.003	0.006	0.002	0.007	0.003	0.008	0.004
3	0.009	0.003	0.009	0.003	0.006	0.002	0.007	0.003	0.009	0.004
4	0.01	0.003	0.013	0.004	0.006	0.003	0.007	0.003	0.010	0.004
5	0.01	0.003	0.012	0.004	0.006	0.003	0.007	0.003	0.010	0.004
6	0.012	0.004	0.012	0.004	0.006	0.003	0.008	0.003	0.010	0.004
7	0.011	0.003	0.012	0.004	0.006	0.003	0.008	0.003	0.011	0.004
8	0.011	0.004	0.014	0.004	0.007	0.003	0.008	0.003	0.010	0.004
9	0.011	0.004	0.012	0.004	0.006	0.003	0.008	0.003	0.010	0.004
10	0.014	0.004	0.015	0.004	0.007	0.003	0.009	0.003	0.012	0.005
11	0.011	0.003	0.014	0.004	0.007	0.003	0.008	0.003	0.010	0.004
12	0.012	0.004	0.013	0.004	0.007	0.003	0.008	0.003	0.010	0.004
13	0.012	0.004	0.013	0.004	0.007	0.003	0.008	0.003	0.011	0.004
14	0.011	0.003	0.014	0.004	0.007	0.003	0.008	0.003	0.010	0.004
15	0.011	0.003	0.014	0.004	0.007	0.003	0.008	0.003	0.011	0.004
16	0.011	0.004	0.015	0.004	0.007	0.003	0.008	0.003	0.012	0.005
17	0.013	0.004	0.015	0.004	0.007	0.003	0.009	0.003	0.011	0.004
18	0.012	0.004	0.015	0.004	0.007	0.003	0.008	0.003	0.011	0.004
19	0.012	0.004	0.014	0.004	0.008	0.003	0.008	0.003	0.011	0.004
20	0.012	0.004	0.016	0.005	0.007	0.003	0.008	0.003	0.011	0.005
21	0.013	0.004	0.017	0.005	0.007	0.003	0.009	0.003	0.011	0.004
22	0.014	0.004	0.019	0.005	0.007	0.003	0.009	0.003	0.012	0.005
23	0.012	0.004	0.016	0.004	0.007	0.003	0.008	0.003	0.012	0.005
24	0.013	0.004	0.014	0.004	0.008	0.003	0.009	0.003	0.011	0.004
25	0.014	0.004	0.017	0.005	0.008	0.003	0.009	0.003	0.012	0.005
26	0.013	0.004	0.018	0.005	0.007	0.003	0.009	0.003	0.012	0.005

Table 2.S6 Chromosome wise average linkage disequilibrium (D') in five populations.

OAR	BL		PD		MER		BxM		BxMxP	
	Mean	Median	Mean	Median	Mean	Median	Mean	Median	Mean	Median
1	0.276	0.152	0.222	0.127	0.15	0.094	0.176	0.110	0.176	0.114
2	0.299	0.168	0.236	0.133	0.151	0.094	0.181	0.113	0.184	0.120
3	0.288	0.16	0.241	0.135	0.156	0.097	0.183	0.114	0.188	0.122
4	0.278	0.159	0.262	0.155	0.161	0.1	0.182	0.114	0.189	0.124
5	0.299	0.168	0.238	0.144	0.158	0.098	0.183	0.115	0.192	0.125
6	0.312	0.182	0.251	0.146	0.158	0.1	0.195	0.121	0.200	0.131
7	0.322	0.187	0.252	0.145	0.152	0.096	0.184	0.115	0.195	0.128
8	0.283	0.165	0.266	0.159	0.153	0.098	0.176	0.115	0.186	0.125
9	0.299	0.174	0.236	0.137	0.159	0.099	0.184	0.117	0.184	0.123
10	0.32	0.186	0.267	0.157	0.165	0.103	0.197	0.123	0.203	0.135
11	0.304	0.172	0.282	0.164	0.199	0.116	0.208	0.127	0.214	0.134
12	0.29	0.169	0.253	0.151	0.161	0.102	0.186	0.118	0.190	0.127
13	0.3	0.175	0.264	0.152	0.167	0.102	0.186	0.117	0.196	0.132
14	0.317	0.179	0.282	0.167	0.168	0.104	0.196	0.122	0.208	0.133
15	0.298	0.169	0.28	0.166	0.168	0.105	0.189	0.119	0.201	0.132
16	0.281	0.16	0.287	0.175	0.176	0.11	0.183	0.117	0.203	0.137
17	0.308	0.184	0.263	0.163	0.158	0.102	0.195	0.123	0.193	0.130
18	0.296	0.176	0.264	0.16	0.173	0.107	0.198	0.124	0.200	0.131
19	0.31	0.175	0.306	0.179	0.175	0.11	0.196	0.123	0.211	0.139
20	0.299	0.172	0.275	0.173	0.161	0.102	0.185	0.118	0.203	0.135
21	0.305	0.178	0.286	0.175	0.166	0.106	0.192	0.124	0.200	0.132
22	0.299	0.177	0.29	0.184	0.168	0.107	0.194	0.124	0.208	0.139
23	0.294	0.175	0.266	0.162	0.166	0.104	0.187	0.121	0.200	0.134
24	0.307	0.183	0.284	0.167	0.181	0.111	0.200	0.125	0.210	0.138
25	0.31	0.178	0.281	0.178	0.176	0.109	0.197	0.123	0.213	0.140
26	0.293	0.172	0.276	0.173	0.168	0.105	0.185	0.121	0.198	0.134

Table 2.S7 Chromosome wise haplotype analysis summary.

Breed	Chromosome	Number of Blocks	Total block length (kb)	% of chromosome length in blocks	Min block length (kb)	Max block length (kb)	Number of SNP in blocks	% of SNP in blocks
BL	1	303	19711.34	7.15	2.97	462.71	861	15.70
BL	2	289	23471.07	9.43	3.66	481.76	895	17.47
BL	3	258	19500.66	8.69	3.27	493.11	771	16.63
BL	4	134	9479.03	7.95	3.91	373.78	405	16.14
BL	5	116	7058.86	6.54	4.76	489.39	325	14.83
BL	6	118	9166.13	7.83	4.97	475.06	357	14.81
BL	7	114	11824.49	11.82	6.05	498.58	393	18.77
BL	8	99	5366.45	5.92	2.62	408.97	272	14.20
BL	9	120	8296.02	8.76	4.18	470.45	349	17.63
BL	10	99	9910.07	11.46	3.95	493.36	315	18.35
BL	11	56	2658.05	4.27	3.87	283.53	146	13.24
BL	12	99	5834.46	7.38	1.95	394.87	274	17.31
BL	13	77	7686.51	9.25	3.75	476.38	262	16.78
BL	14	44	2424.21	3.87	3.56	449.88	118	10.85
BL	15	64	3939.06	4.87	2.13	458.02	171	11.01
BL	16	65	3689.49	5.14	4.62	304.22	179	12.36
BL	17	63	4632.88	6.41	4.81	428.87	183	13.85
BL	18	57	3002.75	4.38	5.08	243.19	155	11.78
BL	19	54	4536.79	7.50	5.73	436.40	164	14.24
BL	20	43	1651.83	3.23	6.33	202.95	111	10.57
BL	21	38	3020.14	6.03	4.88	499.13	106	12.91
BL	22	58	2353.13	4.63	2.32	300.62	154	15.28
BL	23	44	3286.40	5.27	6.60	370.09	121	11.48
BL	24	32	1591.10	3.79	4.38	413.60	83	12.15
BL	25	40	1783.64	3.93	5.51	408.69	105	11.28
BL	26	27	1865.04	4.23	3.05	386.45	79	9.13
BxM	1	191	3779.53	1.37	3.10	309.66	416	7.59
BxM	2	195	4768.56	1.92	4.84	473.56	432	8.43
BxM	3	148	3352.31	1.49	4.05	259.01	333	7.18
BxM	4	87	1847.98	1.55	2.89	226.81	191	7.61
BxM	5	72	1717.52	1.59	3.73	286.25	159	7.25
BxM	6	82	1536.67	1.31	3.72	207.77	178	7.39
BxM	7	66	1188.49	1.19	2.20	172.38	141	6.73

BxM	8	61	766.88	0.85	4.16	20.91	126	6.58
BxM	9	72	1891.31	2.00	3.66	286.93	158	7.98
BxM	10	68	3831.75	4.43	3.95	493.36	171	9.96
BxM	11	30	592.28	0.95	5.63	152.43	64	5.80
BxM	12	58	1433.21	1.81	1.95	378.21	127	8.02
BxM	13	47	888.59	1.07	3.75	144.14	103	6.60
BxM	14	32	472.07	0.75	5.21	36.06	67	6.16
BxM	15	38	782.09	0.97	2.13	357.20	79	5.09
BxM	16	34	651.00	0.91	5.62	178.25	77	5.32
BxM	17	33	482.42	0.67	4.36	122.78	68	5.15
BxM	18	42	571.39	0.83	5.08	99.97	87	6.61
BxM	19	31	504.67	0.83	5.73	110.19	66	5.73
BxM	20	30	440.24	0.86	6.33	99.75	64	6.10
BxM	21	25	306.19	0.61	2.84	24.91	53	6.46
BxM	22	43	670.58	1.32	2.32	82.99	91	9.03
BxM	23	28	397.01	0.64	6.60	26.49	59	5.60
BxM	24	16	166.84	0.40	4.38	18.32	33	4.83
BxM	25	32	460.39	1.01	5.35	85.22	68	7.30
BxM	26	20	233.02	0.53	3.05	17.88	40	4.62
BxMxP	1	230	4065.53	1.48	3.10	238.07	502	9.15
BxMxP	2	205	5981.95	2.40	3.66	473.56	474	9.25
BxMxP	3	160	3879.36	1.73	4.10	464.91	365	7.87
BxMxP	4	98	2624.25	2.20	2.89	265.74	227	9.04
BxMxP	5	83	1733.78	1.61	3.73	286.25	180	8.21
BxMxP	6	94	1726.91	1.48	4.80	281.31	200	8.30
BxMxP	7	84	1458.43	1.46	2.20	172.38	178	8.50
BxMxP	8	80	1035.34	1.14	2.62	20.91	163	8.51
BxMxP	9	87	2251.14	2.38	4.18	286.93	197	9.95
BxMxP	10	80	3908.01	4.52	3.95	493.36	205	11.94
BxMxP	11	34	525.28	0.84	5.55	175.09	72	6.53
BxMxP	12	69	1440.31	1.82	1.95	249.39	150	9.48
BxMxP	13	59	1200.42	1.44	3.75	238.55	130	8.33
BxMxP	14	38	637.37	1.02	3.56	118.51	82	7.54
BxMxP	15	54	805.03	0.99	3.39	135.05	113	7.28
BxMxP	16	38	630.65	0.88	3.41	103.76	83	5.73
BxMxP	17	41	1134.17	1.57	4.81	162.27	97	7.34
BxMxP	18	46	698.30	1.02	5.08	186.87	95	7.22

BxMxP	19	35	535.18	0.89	6.50	53.96	73	6.34
BxMxP	20	29	614.82	1.20	6.36	185.01	63	6.00
BxMxP	21	27	409.42	0.82	2.84	99.92	58	7.06
BxMxP	22	45	1026.98	2.02	2.32	229.60	99	9.82
BxMxP	23	23	696.40	1.12	6.60	393.23	51	4.84
BxMxP	24	18	201.89	0.48	4.38	27.11	39	5.71
BxMxP	25	33	713.25	1.57	5.35	167.48	75	8.06
BxMxP	26	20	232.48	0.53	3.05	19.53	40	4.62
MER	1	250	4202.71	1.52	1.39	168.04	535	9.76
MER	2	257	6358.13	2.55	3.66	473.56	577	11.26
MER	3	190	3678.32	1.64	3.99	246.35	418	9.01
MER	4	106	2160.60	1.81	2.89	226.81	231	9.20
MER	5	98	2108.58	1.95	0.06	310.86	217	9.90
MER	6	102	1788.89	1.53	3.72	228.13	218	9.05
MER	7	103	2329.15	2.33	2.20	322.01	225	10.74
MER	8	78	1102.24	1.22	2.62	80.23	163	8.51
MER	9	97	2254.96	2.38	3.66	392.39	216	10.91
MER	10	88	4255.97	4.92	2.46	493.36	223	12.99
MER	11	35	1054.53	1.69	5.78	312.82	84	7.62
MER	12	67	901.16	1.14	1.95	86.44	140	8.84
MER	13	60	1137.76	1.37	3.75	188.44	131	8.39
MER	14	38	643.11	1.03	0.16	118.51	82	7.54
MER	15	58	813.33	1.01	2.13	107.41	120	7.73
MER	16	47	919.77	1.28	4.38	178.25	104	7.18
MER	17	47	1186.32	1.64	3.36	275.76	106	8.02
MER	18	53	872.17	1.27	5.08	129.02	115	8.74
MER	19	52	773.47	1.28	5.73	77.46	107	9.29
MER	20	39	642.83	1.26	3.21	119.13	84	8.00
MER	21	28	500.87	1.00	2.84	178.05	61	7.43
MER	22	45	888.33	1.75	2.32	229.60	98	9.72
MER	23	33	500.19	0.80	6.27	62.12	71	6.74
MER	24	21	234.09	0.56	4.38	18.98	42	6.15
MER	25	36	796.73	1.76	4.20	308.34	82	8.81
MER	26	20	207.54	0.47	1.04	17.69	40	4.62
PD	1	321	13623.07	4.94	2.97	446.63	810	14.77
PD	2	294	17712.33	7.11	3.16	495.44	818	15.97
PD	3	233	12716.85	5.67	3.27	485.56	643	13.87

PD	4	126	6621.48	5.55	2.89	395.86	350	13.94
PD	5	126	5551.59	5.15	3.73	411.00	320	14.60
PD	6	118	6370.30	5.44	4.80	463.58	331	13.73
PD	7	129	5827.82	5.82	3.49	279.39	337	16.09
PD	8	95	3430.33	3.78	4.16	303.84	237	12.38
PD	9	114	6072.24	6.41	4.18	396.99	300	15.15
PD	10	106	8875.84	10.27	2.46	495.61	326	18.99
PD	11	53	1716.96	2.76	5.13	220.13	125	11.33
PD	12	90	3637.74	4.60	1.95	362.30	230	14.53
PD	13	73	4977.02	5.99	1.67	414.73	216	13.84
PD	14	57	3160.23	5.04	3.56	494.13	149	13.69
PD	15	79	4468.57	5.52	2.13	439.89	210	13.52
PD	16	55	3377.67	4.71	3.41	448.60	159	10.98
PD	17	59	3266.64	4.52	4.81	335.30	157	11.88
PD	18	63	2526.58	3.68	5.08	341.82	154	11.70
PD	19	55	2961.80	4.90	5.73	341.54	145	12.59
PD	20	47	1870.49	3.65	3.21	332.01	114	10.86
PD	21	37	1212.40	2.42	2.84	212.17	92	11.21
PD	22	59	3933.26	7.74	2.32	441.51	174	17.26
PD	23	41	2166.66	3.48	6.91	486.27	105	9.96
PD	24	30	1577.27	3.75	4.38	476.83	74	10.83
PD	25	43	1744.98	3.85	6.02	205.28	116	12.46
PD	26	31	1126.87	2.56	1.04	196.46	77	8.90

Table 2.S8 Range of inbreeding coefficients in five populations.

Breed	F_1		F_2		F_3	
	Min	*Max*	*Min*	*Max*	*Min*	*Max*
BL	-0.22	1.18	-1.3	0.29	-0.07	0.13
PD	-0.24	0.68	-1.25	0.23	-0.31	0.1
MER	-.067	0.26	-0.27	0.057	-0.06	0.05
BxM	-0.13	-0.04	-0.17	-0.04	-0.14	-0.05
BxMxP	-0.14	0.11	-0.12	-0.01	-0.09	0.01

Inbreeding coefficients were calculated for each individual using the GCTA program. F_1 is calculated based on the variance of the additive genotype; F_2 is calculated based on the excess of homozygosity; and F_3 is calculated based on the correlation between uniting gametes.

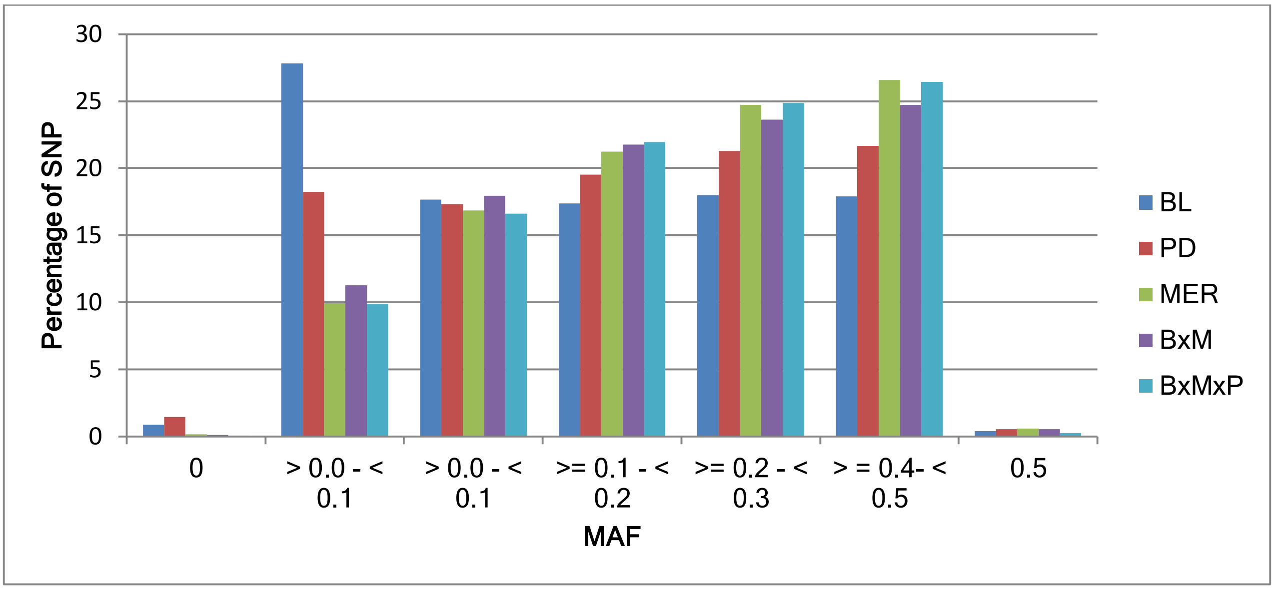

Figure 2.S1 Distribution of minor allele frequency (MAF) in five populations. The percentage of SNP is plotted for each frequency bin.

Appendix 2 Supplementary tables for chapter 3

Table 3.S1 Distribution of SNP before and after quality control and the average distances between adjacent SNP on each chromosome

Chromosome	Length of chromosome (Mbp)	No. SNP		Average distance (Kb)	
		Before QC	After QC	Before QC	After QC
1	275.61	5930	5494	46.48	54.48
2	248.99	5474	5111	45.46	51.15
3	224.28	5008	4647	44.77	52.19
4	119.26	2680	2508	44.51	50.36
5	107.9	2363	2199	45.57	52.41
6	117.03	2592	2413	45.13	53.35
7	100.08	2252	2094	44.45	47.55
8	90.7	2057	1916	44.08	47.22
9	94.73	2141	1983	44.25	50.2
10	86.45	1851	1719	46.71	52.91
11	62.25	1180	1104	52.62	59.13
12	79.1	1723	1583	45.9	54.07
13	83.08	1696	1565	49	54.16
14	62.72	1174	1094	53.44	61.13
15	80.92	1694	1555	47.63	57.05
16	71.72	1580	1450	45.4	53.05
17	72.29	1420	1320	50.83	59.57
18	68.6	1413	1318	48.52	54.22
19	60.46	1248	1153	48.42	56
20	51.18	1148	1050	44.41	48.36
21	50.07	898	825	55.77	66.15
22	50.83	1097	1005	46.37	55.01
23	62.33	1128	1056	55.28	58.76
24	42.03	741	679	56.79	65.47
25	45.37	1001	931	45.34	48.66
26	44.08	924	868	47.68	50.56

Table 3.S2 All 39 SNP showing significant association with body weight in 1,743 Merino sheep

SNP	Chr	Position	P.value	Adjusted P-value	n0	n1	n2	p	q	v_g	**β (kg)**
OAR6_41936490.1	6	37694563	2.37E-16	1.15E-11	119	706	918	0.270797	0.729203	6.1721	2.116
s17946.1	6	37164383	7.97E-14	3.87E-09	83	630	1030	0.228342	0.771658	5.87533	-2.132
OAR6_41877997.1	6	37640732	2.48E-12	1.21E-07	110	650	983	0.24957	0.75043	6.0518	-1.876
OAR3_128968872.1	3	1.21E+08	2.16E-11	1.05E-06	313	861	569	0.426563	0.573437	5.86187	-1.626
OAR6_41003295.1	6	36819342	2.40E-11	1.17E-06	150	722	871	0.293173	0.706827	6.50054	-1.741
OAR14_57922732.1	14	57922732	3.21E-10	1.56E-05	22	321	1400	0.104705	0.895295	6.53851	2.28
OAR6_42945420.1	6	38567455	3.21E-10	1.56E-05	22	321	1400	0.104705	0.895295	6.53851	2.28
OAR12_19764133.1	12	16922406	5.82E-10	2.83E-05	288	853	602	0.409925	0.590075	6.49044	-1.477
s41303.1	7	77974470	8.80E-10	4.28E-05	233	766	744	0.353414	0.646586	6.45232	-1.471
OAR6_40449774.1	6	36234302	7.94E-09	3.86E-04	20	378	1345	0.119908	0.880092	6.61587	-2.079
OAR14_33804119.1	14	32425979	1.10E-08	5.35E-04	36	433	1274	0.144865	0.855135	6.58181	-1.942
OAR6_41558126.1	6	37334387	1.12E-08	5.44E-04	79	574	1090	0.209983	0.790017	6.29639	1.686
OAR10_28234413.1	10	28220524	1.23E-08	5.98E-04	362	839	542	0.448365	0.551635	6.93535	1.35
OAR3_170046187.1	3	1.59E+08	2.14E-08	1.04E-03	118	655	970	0.255594	0.744406	6.52127	1.542
s10875.1	19	55289603	2.29E-08	1.11E-03	51	476	1216	0.165806	0.834194	6.30989	-1.69
OAR3_79625099.1	3	75408156	2.54E-08	1.23E-03	125	634	984	0.253586	0.746414	5.59996	1.472
OAR6_40409402.1	6	36192023	3.30E-08	1.60E-03	9	254	1480	0.078026	0.921974	6.64712	2.337
OAR2_200781582.1	2	1.89E+08	3.31E-08	1.61E-03	49	367	1327	0.133391	0.866609	6.35177	1.852
OAR6_40370293.1	6	36155169	3.39E-08	1.65E-03	110	641	992	0.246988	0.753012	6.25208	-1.589
s64523.1	1	12775585	3.73E-08	1.81E-03	121	622	1000	0.247849	0.752151	6.20749	-1.478
OAR6_42247197.1	6	37987281	4.04E-08	1.96E-03	60	512	1171	0.181297	0.818703	6.51561	-1.645
OAR10_62872792.1	10	61341529	4.49E-08	2.18E-03	408	858	477	0.480207	0.519793	6.35358	1.283
s66267.1	23	58323699	4.72E-08	2.29E-03	237	781	725	0.360011	0.639989	6.46201	-1.295
OAR12_2311264.1	12	3371387	5.44E-08	2.64E-03	44	510	1189	0.171543	0.828457	6.7511	-1.729
OAR8_49852851.1	8	46382226	5.48E-08	2.66E-03	354	832	557	0.441767	0.558233	6.38024	1.233

OAR2_33892911.1	2	32570329	5.55E-08	2.70E-03	104	658	981	0.248422	0.751578	5.72961	-1.472
OAR7_88735490.1	7	81383811	6.82E-08	3.31E-03	115	704	924	0.267929	0.732071	6.65625	1.444
OAR6_40724811_X.1	6	36522166	7.41E-08	3.60E-03	18	385	1340	0.120769	0.879231	6.26261	-1.914
OAR1_141580492.1	1	1.31E+08	1.07E-07	5.20E-03	267	829	647	0.390993	0.609007	6.39115	-1.27
s36305.1	13	61597135	1.08E-07	5.25E-03	34	415	1294	0.138554	0.861446	7.04824	-1.793
OAR7_81534131.1	7	74570199	1.11E-07	5.39E-03	313	855	575	0.424842	0.575158	6.43876	1.265
s29813.1	14	52182942	1.11E-07	5.39E-03	413	898	432	0.49455	0.50545	7.10285	1.286
s43545.1	15	74500105	1.15E-07	5.59E-03	1	92	1650	0.026965	0.973035	6.56781	-3.486
OAR6_40855809.1	6	36655091	1.16E-07	5.64E-03	53	448	1242	0.158921	0.841079	6.33587	1.612
s40612.1	2	1.82E+08	1.24E-07	6.03E-03	281	823	639	0.397303	0.602697	6.33904	1.256
s35115.1	3	14572165	1.42E-07	6.90E-03	61	454	1228	0.165232	0.834768	6.00704	1.699
s38098.1	14	23489233	1.70E-07	8.26E-03	18	327	1398	0.104131	0.895869	6.23655	-2.021
OAR6_41768532.1	6	37533664	1.85E-07	8.99E-03	64	521	1158	0.186173	0.813827	6.45921	1.542
s05777.1	8	30348320	2.00E-07	9.72E-03	89	626	1028	0.230637	0.769363	6.33963	1.475

A total of 39 SNP were identified as genome-wide significant for Bonferroni-corrected p-value threshold of 1.15×10^{-11}. *Vg* indicates the proportion of the genetic variance attributable to each SNP estimated by ASReml. β is the allele substitution effect. SNP positions are based on Oar_v3.1 assembly of the ovine genome sequence.

Table 3.S3. The percentage of genetic variance explained by each chromosome

OAR	Length (Mb)	Explained variance	SE	LRT
1	275.61	1.85	0.03	196.55
2	248.99	1.42	0.03	174.27
3	224.28	2.64	0.03	201.89
4	119.26	1.78	0.02	170.21
5	107.9	1.72	0.02	137.00
6	117.03	7.71	0.03	197.89
7	100.08	0.96	0.02	146.22
8	90.7	4.47	0.02	146.94
9	94.73	0.84	0.02	150.94
10	86.45	3.35	0.02	161.66
11	62.25	8.54	0.02	171.35
12	79.1	8.91	0.03	179.09
13	83.08	1.46	0.02	128.49
14	62.72	2.73	0.02	142.41
15	80.92	0.00	0.02	117.15
16	71.72	2.02	0.02	134.54
17	72.29	0.00	0.02	101.71
18	68.6	0.00	0.02	117.04
19	60.46	0.58	0.02	105.54
20	51.18	2.12	0.02	114.54
21	50.07	0.00	0.02	103.32
22	50.83	0.00	0.02	106.36
23	62.33	3.71	0.02	131.95
24	42.03	2.92	0.02	95.49
25	45.37	5.74	0.02	148.08
26	44.08	1.50	0.02	95.45

Explained variance is given in percentage and was standardized according to each chromosome length. SE is the standard error. Likelihood ratio test (LRT) was calculated in GCTA fitting each chromosome individually.