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Genomic Evaluation and Variance Component Estimation of Additive and Dominance Effects Using Single Nucleotide Polymorphism Markers in Heterogeneous Stock Mice

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Supplementary Online Material (SOM)

Table S1. Top ten SNP markers (additive) significantly associated with the traits (MAD)

Trait	SNP	Location		$-\log_{10}$ P
		chr	(mbp)	
End weight	**rs13479293**	**7**	**30.62735**	**14.73755**
	rs6310696	8	71.88783	14.73755
	rs6196597	10	61.25074	14.73755
	CEL-15_81685254	15	40.50697	14.73755
	rs3653699	18	4.288372	14.73755
	rs3708073	8	71.79651	5.47237
	rs13479443	7	56.37176	4.863279
	rs6243527	9	15.50942	4.465974
	rs3720735	7	19.29459	4.432974
	rs4151940	16	56.91535	4.219683
Growth slope	**rs3653699**	**18**	**4.288372**	**18.7264386**
	rs8255002	18	4.615448	6.48535265
	rs6173740	5	61.43063	6.42895394
	rs6335021	6	81.70352	6.42895394
	CEL-14_90299389	14	40.24828	6.42895394
	rs13482478	15	7.965041	6.25484156
	CEL-17_92336158	17	63.01656	6.20773378
	rs13480482	10	0.992045	6.09445614
	rs4230147	14	0.087722	5.79175783
	rs6196597	10	61.25074	5.70364507
Body mass index	**rs6400423**	**8**	**77.80948168**	**17.81984888**
	rs4228381	10	50.45353345	17.81984888
	rs4231494	17	19.91676064	17.81984888
	rs3669949	18	48.85017531	17.81984888
	rs6392739	5	7.180780605	8.489351924
	rs3679284	8	40.23559378	6.271496879
	rs3023347	12	26.64905761	6.041210237
	rs6161057	9	58.3351552	6.009400647
	rs6405821	1	40.78344037	5.892262751
	rs13479476	7	63.59200161	5.821454398
Body length	**rs6400423**	**8**	**77.80948168**	**16.1650958**
	rs4231494	17	19.91676064	16.1650958
	rs3669949	18	48.85017531	16.1650958
	rs6392739	5	7.180780605	5.637041457
	rs13482528	15	14.41382501	5.460455467
	gnf03.073.308	3	34.54450466	5.096298198
	rs13482527	15	14.34718365	4.986398163
	rs3669366	12	33.35638445	4.802774042
	rs13481524	12	33.43698228	4.802774042
	rs6245977	13	45.12567607	4.735451806

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Table S2. Top ten SNP markers (dominance) significantly associated with the traits (MAD)

Trait	SNP	Location		$-\log_{10}$ P
		chr	(mbp)	
End weight	**rs13479293**	**7**	**30.62735**	**18.52724**
	rs6310696	8	71.88783	18.52724
	rs6196597	10	61.25074	18.52724
	CEL-15_81685254	15	40.50697	18.52724
	rs3653699	18	4.288372	18.52724
	rs6392739	5	7.180781	6.011441
	rs13482899	17	7.984049	5.987163
	rs3667809	17	8.443918	5.987163
	rs13482914	17	8.450262	5.987163
	CEL-17_20610264	17	8.477446	5.987163
Growth slope	**rs3653699**	**18**	**4.288372**	**22.16599567**
	rs13478049	4	95.94017	8.652117172
	UT_4_148.695258	4	95.93255	8.650878341
	rs3695426	4	95.90605	8.646870595
	rs13482899	17	7.984049	7.864588726
	rs3667809	17	8.443918	7.864588726
	rs13482914	17	8.450262	7.864588726
	CEL-17_20610264	17	8.477446	7.864588726
	rs3697826	1	65.66521	7.602986199
	rs3698067	1	65.60968	7.602712792
Body mass index	**rs6400423**	**8**	**77.80948168**	**21.6800967**
	rs4228381	10	50.45353345	21.6800967
	rs4231494	17	19.91676064	21.6800967
	rs3669949	18	48.85017531	21.6800967
	rs6392739	5	7.180780605	12.64966358
	rs3680085	8	30.40233682	8.620252253
	rs13479795	8	30.41282447	8.620252253
	rs13478487	5	75.83209957	8.176697305
	mCV25130934	5	75.86959957	8.176697305
	gnf05.114.391	5	76.21047258	8.176697305
Body length	**rs6400423**	**8**	**77.80948168**	**20.01195269**
	rs4231494	17	19.91676064	20.01195269
	rs3669949	18	48.85017531	20.01195269
	rs6392739	5	7.180780605	9.7846652
	rs3711532	2	61.36540539	6.659019793
	rs3697826	1	65.66521228	6.3586317
	rs4137908	1	65.7830299	6.358233484
	rs3698067	1	65.60968345	6.357637981
	rs3718687	19	51.00444705	6.344968711
	CEL-15_58115663	15	25.43679543	6.235179333

Table S3. Top ten SNP markers (additive) significantly associated with the traits (MA)

Trait	SNP	Location		$-\log_{10}$ P
		chr	(mbp)	
End weight	rs13479293	7	30.62735	**15.05302**
	rs6310696	8	71.88783	15.05302
	rs6196597	10	61.25074	15.05302
	CEL-15_81685254	15	40.50697	15.05302
	rs3653699	18	4.288372	15.05302
	rs3658927	2	66.44203	5.137606
	rs13480088	9	4.7	4.208585
	rs3088801	9	8.634818	4.182828
	rs13481565	12	43.39202	4.134308
	rs3678312	13	60.61242	4.100315
Growth slope	**rs3653699**	**18**	**4.288372**	**18.77287745**
	rs3711381	9	78.67545	6.163134809
	rs13479437	7	55.36992	6.029361119
	rs3705078	11	43.20887	5.931340756
	rs3716382	15	63.21584	5.825131407
	rs6209043	4	54.66185	5.781227982
	rs4139403	9	18.9921	5.770029577
	rs13475744	1	4.866112	5.746834826
	rs3721918	14	23.92071	5.679363591
	rs13481841	13	30.97403	5.522975749
Body mass index	rs6400423	8	77.80948168	**18.20804577**
	rs4228381	10	50.45353345	18.20804577
	rs4231494	17	19.91676064	18.20804577
	rs3669949	18	48.85017531	18.20804577
	rs6392739	5	7.180780605	8.712944823
	rs13479569	7	89.49601307	6.344955544
	rs6194426	19	44.74910173	6.332033109
	rs13475920	1	38.74528574	6.212985242
	rs13482420	15	1.934444444	5.935711269
	rs3677347	7	71.17722509	5.802048803
Body length	**rs6400423**	**8**	**77.80948168**	**16.22115**
	rs4231494	17	19.91676064	16.22115
	rs3669949	18	48.85017531	16.22115
	rs13482948	17	14.51933581	6.021307
	rs3675505	1	52.85447579	5.750904
	rs6392739	5	7.180780605	5.610044
	rs4184315	16	33.80698736	5.208256
	rs3670489	6	17.44913252	4.990883
	rs3662693	1	56.12254108	4.927349
	rs4137718	17	57.12447885	4.879368

Table S4. Top ten SNP markers (dominance) significantly associated with the traits (MD)

Trait	SNP	Location		$-\log_{10}$ P
		chr	(mbp)	
End weight	rs13479293	**7**	**30.62735465**	**18.98583**
	rs6310696	8	71.88782704	18.98583
	rs6196597	10	61.25073613	18.98583
	CEL-15_81685254	15	40.50697146	18.98583
	rs3653699	18	4.288371777	18.98583
	rs6392739	5	7.180780605	6.537468
	rs13482899	17	7.98404922	5.23438
	rs3667809	17	8.443917848	5.23438
	rs13482914	17	8.450262472	5.23438
	CEL-17_20610264	17	8.477445799	5.23438
Growth slope	**rs3653699**	**18**	**4.288372**	**21.7046**
	mCV23574676	2	20.50012	7.948158
	rs6392739	5	7.180781	7.154413
	rs3155343	14	18.56903	7.144513
	rs3697826	1	65.66521	6.96681
	rs4137908	1	65.78303	6.966347
	rs3698067	1	65.60968	6.96622
	rs13478049	4	95.94017	6.881616
	UT_4_148.695258	4	95.93255	6.88126
	rs3695426	4	95.90605	6.880276
Body mass index	rs6400423	**8**	**77.80948168**	**21.57345035**
	rs4228381	10	50.45353345	21.57345035
	rs4231494	17	19.91676064	21.57345035
	rs3669949	18	48.85017531	21.57345035
	rs6392739	5	7.180780605	11.74701791
	rs13478487	5	75.83209957	7.447920122
	mCV25130934	5	75.86959957	7.447920122
	gnf05.114.391	5	76.21047258	7.447920122
	gnf05.114.515	5	76.3247583	7.447920122
	rs13478492	5	76.43904401	7.447920122
Body length	**rs6400423**	**8**	**77.80948168**	**19.82695424**
	rs4231494	17	19.91676064	19.82695424
	rs3669949	18	48.85017531	19.82695424
	rs6392739	5	7.180780605	9.170930101
	rs13477408	3	65.46020185	6.803798106
	UT_3_135.243811	3	65.46118561	6.799204476
	rs3710354	3	65.44617369	6.771392554
	rs13461066	9	5.741155627	5.892631949
	rs13482263	14	34.03197025	5.816173762
	rs3665356	14	34.13197025	5.816173762

Table S5. Number of significant SNPs for end weight ($P < 10^{-4}$)

Model	MAD^a			MA^b			MD^c		
Chromosome	A^d	D^d	A&D^d	A	D	A&D	A	D	A&D
1	1	17	1	–	–	–	–	15	–
2	–	4	–	2	–	–	–	–	–
3	–	17	–	–	–	–	–	16	–
4	–	6	–	1	–	–	–	4	–
5	–	7	–	–	–	–	–	6	–
6	–	1	–	–	–	–	–	1	–
7	3	2	–	1	–	–	–	2	–
8	2	5	2	1	–	–	–	2	–
9	1	2	1	2	–	–	–	1	–
10	1	6	1	1	–	–	–	4	–
11	1	3	–		–	–	–	–	–
12	–	–	–	1	–	–	–	–	–
13	–	5	–	1	–	–	–	4	–
14	–	6	–	1	–	–	–	–	–
15	1	6	1	1	–	–	–	2	–
16	1	2	–	–	–	–	–	–	–
17	–	6	–	–	–	–	–	4	–
18	1	3	1	1	–	–	–	2	–
19	–	2	–	–	–	–	–	–	–
Sum	12	100	7	13	–	–	–	63	–

[a] MAD is an SNP marker model considering both additive and dominance effects, [b] MA is an SNP marker model considering just additive effect, [c] MD is an SNP marker model considering just dominance model, [d] A, D and A&D are the numbers of SNPs that had significant additive, dominance, and both effects respectively

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Table S6. Number of significant SNPs for growth slope ($P < 10^{-4}$)

Model	MAD[a]			MA[b]			MD[c]		
Chromosome	A[d]	D[d]	A&D[d]	A	D	A&D	A	D	A&D
1	38	124	9	34	–	–	–	77	–
2	28	38	–	18	–	–	–	22	–
3	25	86	1	15	–	–	–	42	–
4	19	70	5	18	–	–	–	28	–
5	17	85	10	10	–	–	–	43	–
6	24	47	7	15	–	–	–	24	–
7	20	53	9	26	–	–	–	26	–
8	32	54	9	28	–	–	–	23	–
9	18	55	7	15	–	–	–	18	–
10	28	58	11	14	–	–	–	32	–
11	6	58	2	18	–	–	–	15	–
12	12	22	–	19	–	–	–	21	–
13	29	82	7	12	–	–	–	52	–
14	24	90	11	32	–	–	–	64	–
15	28	50	9	11	–	–	–	30	–
16	15	25	1	12	–	–	–	7	–
17	38	66	16	20	–	–	–	25	–
18	15	42	9	18	–	–	–	23	–
19	8	15	3	10	–	–	–	14	–
Sum	424	1120	126	343	–	–	–	586	–

[a]MAD is an SNP marker model considering both additive and dominance effects, [b]MA is an SNP marker model considering just additive effect, [c]MD is an SNP marker model considering just dominance model, [d]A, D and A&D are the numbers of SNPs that had significant additive, dominance, and both effects respectively

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Table S7. Number of significant SNPs for body mass index ($P < 10^{-4}$)

Model	MAD[a]			MA[b]			MD[c]		
Chromosome	A[d]	D[d]	A&D[d]	A	D	A&D	A	D	A&D
1	54	354	31	57	–	–	–	136	–
2	28	202	8	30	–	–	–	37	–
3	37	223	7	31	–	–	–	87	–
4	20	195	9	29	–	–	–	52	–
5	52	250	33	42	–	–	–	147	–
6	47	140	23	40	–	–	–	41	–
7	51	200	28	47	–	–	–	56	–
8	33	226	24	34	–	–	–	66	–
9	33	163	14	35	–	–	–	48	–
10	26	139	22	28	–	–	–	40	–
11	46	171	21	50	–	–	–	66	–
12	25	139	9	24	–	–	–	54	–
13	33	220	21	31	–	–	–	99	–
14	33	198	23	40	–	–	–	104	–
15	32	175	22	33	–	–	–	72	–
16	23	91	8	26	–	–	–	30	–
17	34	171	19	30	–	–	–	40	–
18	45	133	24	37	–	–	–	44	–
19	27	100	11	35	–	–	–	21	–
Sum	677	3490	357	679	–	–	–	1240	–

[a]MAD is an SNP marker model considering both additive and dominance effects, [b]MA is an SNP marker model considering just additive effect, [c]MD is an SNP marker model considering just dominance model, [d]A, D and A&D are the numbers of SNPs that had significant additive, dominance, and both effects respectively

Table S8. Number of significant SNPs for body length ($P < 10^{-4}$)

Model	MAD[a]			MA[b]			MD[c]		
Chromosome	A[d]	D[d]	A&D[d]	A	D	A&D	A	D	A&D
1	2	70	–	4	–	–	–	30	–
2	2	22	–	–	–	–	–	2	–
3	2	51	–	–	–	–	–	34	–
4	–	27	–	1	–	–	–	5	–
5	2	47	2	1	–	–	–	23	–
6	4	13	–	2	–	–	–	4	–
7	1	12	–	3	–	–	–	4	–
8	3	19	1	1	–	–	–	4	–
9	1	22	9	3	–	–	–	12	–
10	–	17	–	1	–	–	–	4	–
11	3	17	1	11	–	–	–	7	–
12	3	24	–	–	–	–	–	3	–
13	2	38	–	1	––	––	––	19	––
14	–	34	–	2	–	–	–	16	–
15	5	25	–	1	–	–	–	16	–
16	–	7	–	3	–	–	–	1	–
17	5	13	2	6	–	–	–	9	–
18	1	15	1	3	–	–	–	10	–
19	–	8	–	–	–	–	–	5	–
Sum	36	481	8	33	–	–	–	208	–

[a]MAD is an SNP marker model considering both additive and dominance effects, [b]MA is an SNP marker model considering just additive effect, [c]MD is an SNP marker model considering just dominance model, [d]A, D and A&D are the numbers of SNPs that had significant additive, dominance, and both effects respectively