Haplotype analysis improved evidence for candidate genes for intramuscular fat percentage from a genome wide association study of cattle

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Supplementary Tables

Table S4. Haplotype counts for each gene in each pure breed

		Haplotypes							
Gene	Breed	111	112	121	122	211	212	221	222
ADIPOQ	ANG	0	0	0	356	0	1	0	83
	HFD	0	0	28	245	10	2	0	7
	MGY	0	0	0	103	0	0	0	7
	SHN	0	0	0	153	0	0	0	9
	BEL	0	0	1	169	0	5	0	155
	SGT	0	0	0	184	0	0	0	68
	BRM	0	0	0	39	0	0	0	117
CAPN1	ANG	0	175	62	129	0	0	36	38
	HFD	9	52	25	135	0	0	13	58
	MGY	0	48	0	22	0	0	26	14
	SHN	0	0	38	3	0	0	121	0
	BEL	5	139	109	29	0	0	20	28
	SGT	39	27	101	61	0	0	17	7
	BRM	2	2	127	16	0	1	5	3
CAPN3	ANG	2	0	152	0	236	0	6	44
	HFD	0	0	90	0	68	0	134	0
	MGY	0	0	19	0	43	0	27	21
	SHN	0	0	60	0	59	0	35	8
	BEL	11	0	54	14	101	0	141	9
	SGT	5	0	41	51	61	0	81	13
	BRM	0	0	2	47	3	0	73	31
CAST	ANG	0	0	58	85	297	0	0	0
	HFD	0	0	55	12	225	0	0	0
	MGY	0	0	15	48	47	0	0	0
	SHN	0	0	111	0	50	1	0	0
	BEL	0	0	9	60	203	16	4	38
	SGT	0	1	8	52	121	29	22	19
	BRM	1	0	1	1	43	33	9	68
CEBPA	ANG	0	0	12	0	122	286	0	20
	HFD	0	0	19	0	3	184	25	61
	MGY	0	0	7	0	2	93	0	8
	SHN	0	0	0	0	6	124	1	31
	BEL	0	0	11	29	3	103	1	183
	SGT	0	0	0	0	1	180	0	71
	BRM	0	0	0	18	0	12	5	121
CPE	ANG	98	149	4	129	12	48	0	0
	HFD	0	176	49	65	1	1	0	0

	MGY	55	14	1	11	0	20	0	9
	SHN	8	48	1	49	0	6	0	50
	BEL	1	135	13	106	2	51	5	17
	SGT	2	71	2	68	2	83	0	24
	BRM	2	4	4	21	5	80	2	38
CRH	ANG	0	0	1	62	0	86	118	173
	HFD	0	0	0	82	0	141	4	65
	MGY	0	0	0	5	0	49	32	24
	SHN	0	0	0	90	0	14	14	44
	BEL	0	8	55	135	0	67	12	53
	SGT	0	3	23	97	0	88	15	26
	BRM	0	4	18	33	0	40	10	51
CXCR4	ANG	0	0	0	1	0	25	216	198
	HFD	0	0	0	0	0	89	14	189
	MGY	0	0	0	0	0	5	56	49
	SHN	0	0	0	0	0	1	12	149
	BEL	0	0	0	17	0	11	21	281
	SGT	0	0	0	3	0	54	11	184
	BRM	0	0	0	6	0	8	12	130
DECR1	ANG	38	68	1	1	5	0	282	45
	HFD	28	41	0	0	75	29	18	101
	MGY	13	14	0	0	2	0	52	29
	SHN	1	50	0	6	23	5	54	23
	BEL	48	93	11	0	49	11	96	22
	SGT	34	175	0	2	13	1	21	6
	BRM	72	69	0	0	1	0	6	8
DGAT1	ANG	0	0	0	0	0	428	0	12
	HFD	0	0	0	0	29	263	0	0
	MGY	0	0	0	0	0	104	0	6
	SHN	0	0	0	0	0	162	0	0
	BEL	0	0	0	0	7	199	0	124
	SGT	0	0	0	0	1	130	0	121
	BRM	0	0	0	1	0	27	0	128
FABP4	ANG	0	0	0	83	22	74	210	51
	HFD	0	0	7	39	71	22	108	45
	MGY	0	0	0	39	5	36	15	15
	SHN	0	1	44	22	1	72	10	12
	BEL	0	9	59	28	35	110	36	53
	SGT	0	3	48	27	10	72	12	80
	BRM	0	31	2	7	8	80	16	12
FASN	ANG	0	117	6	1	27	184	104	1
	HFD	0	0	50	0	0	142	48	52
	MGY	0	26	1	0	12	30	30	11
	SHN	0	1	0	0	8	97	37	19
	BEL	0	0	18	0	5	30	207	70
	SGT	0	0	2	0	1	26	190	33
	BRM	0	0	2	0	0	0	149	5
FGF8	ANG	84	16	224	0	116	0	0	0

	HFD	210	29	32	0	21	0	0	0
	MGY	0	0	69	0	41	0	0	0
	SHN	115	26	10	0	10	0	1	0
	BEL	266	8	11	0	36	1	8	0
	SGT	187	27	29	0	9	0	0	0
	BRM	142	9	3	0	2	0	0	0
GH1	ANG	38	150	54	89	28	2	79	0
	HFD	60	67	33	2	3	16	109	2
	MGY	6	67	7	14	14	0	2	0
	SHN	16	2	45	63	35	0	0	1
	BEL	67	13	3	20	19	6	18	184
	SGT	7	26	26	86	12	1	9	85
	BRM	4	25	2	27	8	2	21	67
GHR	ANG	31	63	0	294	0	52	0	0
	HFD	104	0	0	140	0	37	0	11
	MGY	0	28	0	63	0	19	0	0
	SHN	14	12	0	104	0	25	0	7
	BEL	12	2	0	301	0	15	0	0
	SGT	12	1	0	162	0	77	0	0
	BRM	3	0	0	148	0	5	0	0
IGF2	ANG	0	0	6	268	1	85	0	80
	HFD	0	0	47	132	0	11	20	82
	MGY	0	0	0	56	0	20	13	21
	SHN	0	0	4	100	0	2	0	56
	BEL	0	0	4	57	41	14	9	205
	SGT	0	0	19	128	1	19	1	84
	BRM	0	0	0	13	0	13	1	129
LEP	ANG	1	196	23	0	0	59	149	12
	HFD	0	114	0	19	0	126	33	0
	MGY	0	14	19	1	0	23	53	0
	SHN	2	37	1	1	0	116	5	0
	BEL	0	170	7	21	0	103	20	9
	SGT	1	148	2	26	0	73	2	0
	BRM	0	38	9	89	0	14	6	0
RORC	ANG	0	0	0	121	0	95	117	107
	HFD	0	0	0	0	47	214	26	5
	MGY	0	0	0	46	0	38	6	20
	SHN	0	0	0	50	1	104	4	3
	BEL	0	0	0	10	19	134	25	142
	SGT	0	0	0	58	2	103	21	68
	BRM	0	0	0	2	1	7	50	96
SCD	ANG	0	1	0	0	0	133	44	262
	HFD	0	0	0	53	0	0	6	233
	MGY	0	0	0	0	0	12	20	78
	SHN	0	0	0	4	0	32	0	126
	BEL	0	0	1	51	0	35	0	243
	SGT	0	0	0	14	0	38	4	196
	BRM	0	0	0	18	0	15	0	123

SREBF1	ANG	208	0	0	0	50	2	2	178
	HFD	112	2	0	0	31	0	0	147
	MGY	29	0	0	0	0	0	2	79
	SHN	84	0	0	0	1	32	0	45
	BEL	27	0	0	0	14	7	1	281
	SGT	42	0	0	0	3	8	0	199
	BRM	10	0	0	0	1	0	0	145
TCAP	ANG	0	337	79	11	12	1	0	0
	HFD	5	179	44	0	64	0	0	0
	MGY	1	48	45	16	0	0	0	0
	SHN	0	122	1	39	0	0	0	0
	BEL	29	121	53	6	102	0	19	0
	SGT	1	136	1	64	36	0	14	0
	BRM	1	10	4	2	60	0	79	0
TG	ANG	0	112	184	0	17	127	0	0
	HFD	0	104	31	13	0	52	86	6
	MGY	0	32	21	0	0	57	0	0
	SHN	0	64	86	3	0	7	2	0
	BEL	0	43	52	4	0	154	17	60
	SGT	0	43	89	1	1	14	12	92
	BRM	0	4	10	0	0	15	3	124

Note that for the gene *CXCR4*, this gene is the closest gene to the significant SNPs, but these are not located within the gene itself.