Chr	Pos	ID	Ref	Alt	Filter	Variant_Typ	Normal_REF	Normal_ALT	Normal_Dep	Normal_Alle	Tumor_REF	Tumor_ALT	Tumor_Depl	Tumor_Allel	igv	ClinVar	Gene_Name	CDS_Chang	Amino_Acid	Transcript_I	Effect
1	85610347	.	CA	C	mapping_(	DEL	153	0	153	0	164	9	173	0.052	link	-	Sp140	c.196-389(	-	ENSMUST	intron_variant
1	85610347	.	CA	C	mapping_(	DEL	153	0	153	0	164	9	173	0.052	link	-	Gm10552	n.251-46d	-	ENSMUST	intron_variant
1	87853302	.	TGGC	T	weak_evid	DEL	75	1	76	0.013	77	5	82	0.061	link	-	Dgkd	c.14_16de	p.Ala5del	ENSMUST	disruptive_inframe_deletion
1	87853302	.	TGGC	T	weak_evid	DEL	75	1	76	0.013	77	5	82	0.061	link	-	Gm19582	n.*42_*44(	-	ENSMUST	downstream_gene_variant
1	88248226	.	A	ATGTG	non_homr	INS	17	2	19	0.105	20	4	24	0.167	link	-	Mroh2a	c.2851-30(	-	ENSMUST	intron_variant
1	1.35E+08	.	C	CAT	non_homr	INS	162	3	165	0.018	146	10	156	0.064	link	-	Nav1	c.2840+45(	-	ENSMUST	intron_variant
10	61482687	.	GGTTTT	G	too_few_s	DEL	11	0	11	0	15	2	17	0.118	link	-	Lrrc20	c.82+217_	-	ENSMUST	intron_variant
10	89480630	.	TG	T	non_homr	DEL	31	11	42	0.262	19	16	35	0.457	link	-	Nr1h4	c.632-4del	-	ENSMUST	splice_region_variant+intron_variant
10	97569121	rs2341260	GC	G	non_homr	DEL	60	7	67	0.104	43	14	57	0.246	link	-	Lum	c.862+26d	-	ENSMUST	intron_variant
10	1.11E+08	.	ATTTCT	A	PASS	DEL	130	0	130	0	129	4	133	0.03	link	-	Osbpl8	c.80-8_80-	-	ENSMUST	splice_region_variant+intron_variant
10	1.29E+08	rs1135172	AG	A	non_homr	DEL	61	12	73	0.164	51	21	72	0.292	link	-	Gm25494	n.-1882de	-	ENSMUST	upstream_gene_variant
10	1.29E+08	rs1135172	AG	A	non_homr	DEL	61	12	73	0.164	51	21	72	0.292	link	-	Itga7	c.998+18d	-	ENSMUST	intron_variant
11	8950548	.	AG	A	non_homr	DEL	48	8	56	0.143	30	10	40	0.25	link	-	Pkd1l1	c.1360-19(	-	ENSMUST	intron_variant
11	59031411	.	CTA	C	base_qual	DEL	6	0	6	0	14	1	15	0.067	link	-	Obscn	c.17771+1	-	ENSMUST	intron_variant
11	67349723	.	AC	A	non_homr	DEL	58	15	73	0.205	40	22	62	0.355	link	-	Myh13	c.2435+28	-	ENSMUST	intron_variant
11	80881713	.	TG	T	alt_allele_	DEL	39	22	61	0.361	35	28	63	0.444	link	-	Asic2	c.1522-33(	-	ENSMUST	intron_variant
11	95029812	.	GC	G	non_homr	DEL	122	24	146	0.164	93	31	124	0.25	link	-	Gm11513	n.-2946de	-	ENSMUST	upstream_gene_variant
11	95029812	.	GC	G	non_homr	DEL	122	24	146	0.164	93	31	124	0.25	link	-	Samd14	c.*5080del	-	ENSMUST	downstream_gene_variant
11	95029812	.	GC	G	non_homr	DEL	122	24	146	0.164	93	31	124	0.25	link	-	Pdk2	c.608-82d(	-	ENSMUST	intron_variant
11	98938276	.	G	GTGGTT	PASS	INS	25	0	25	0	24	9	33	0.273	link	-	Rara	c.-529+40	-	ENSMUST	intron_variant
11	1.03E+08	.	C	CG	non_homr	INS	81	6	87	0.069	54	18	72	0.25	link	-	Adam11	c.479+36d	-	ENSMUST	intron_variant
11	1.07E+08	rs2211011	AG	A	non_homr	DEL	82	18	100	0.18	59	27	86	0.314	link	-	Cep95	c.-2957del	-	ENSMUST	upstream_gene_variant
11	1.07E+08	rs2211011	AG	A	non_homr	DEL	82	18	100	0.18	59	27	86	0.314	link	-	Mir3064	n.-3643de	-	ENSMUST	upstream_gene_variant
11	1.07E+08	rs2211011	AG	A	non_homr	DEL	82	18	100	0.18	59	27	86	0.314	link	-	Gm25994	n.-3131de	-	ENSMUST	upstream_gene_variant
11	1.07E+08	rs2211011	AG	A	non_homr	DEL	82	18	100	0.18	59	27	86	0.314	link	-	Ddx5	c.308-43d(	-	ENSMUST	intron_variant
12	52024170	.	TG	T	PASS	DEL	194	0	194	0	197	20	217	0.092	link	-	Gpr33	c.84delC	p.Thr30fs	ENSMUST	frameshift_variant
13	6603014	.	TG	T	alt_allele_	DEL	79	35	114	0.307	50	48	98	0.49	link	-	Pfkp	c.1221+64	-	ENSMUST	intron_variant
13	21481470	.	TG	T	non_homr	DEL	23	3	26	0.115	19	11	30	0.367	link	-	Gm10065	c.-2030del	-	ENSMUST	upstream_gene_variant
13	21481470	.	TG	T	non_homr	DEL	23	3	26	0.115	19	11	30	0.367	link	-	Gm23779	n.*4867de	-	ENSMUST	downstream_gene_variant
13	21481470	.	TG	T	non_homr	DEL	23	3	26	0.115	19	11	30	0.367	link	-	Zkscan4	c.574+50d	-	ENSMUST	intron_variant
13	53110302	.	CCCT	C	weak_evid	DEL	205	4	209	0.019	260	16	276	0.058	link	-	Ror2	c.2750_27(	p.Glu917d	ENSMUST	disruptive_inframe_deletion
14	33624873	.	AT	A	non_homr	DEL	117	20	137	0.146	65	49	114	0.43	link	-	Ptpn20	c.511-12d(	-	ENSMUST	intron_variant
14	55758017	.	AG	A	alt_allele_	DEL	20	6	26	0.231	19	13	32	0.406	link	-	Ltb4r2	c.-3906del	-	ENSMUST	upstream_gene_variant
14	55758017	.	AG	A	alt_allele_	DEL	20	6	26	0.231	19	13	32	0.406	link	-	Nop9	c.*4220del	-	ENSMUST	downstream_gene_variant
14	55758017	.	AG	A	alt_allele_	DEL	20	6	26	0.231	19	13	32	0.406	link	-	Cideb	c.42-32del	-	ENSMUST	intron_variant
15	55519067	.	G	GT	alt_allele_	INS	45	54	99	0.545	51	65	116	0.56	link	-	Col14a1	c.5317+74	-	ENSMUST	intron_variant
17	13367891	.	C	CGT	non_homr	INS	32	4	36	0.111	38	13	51	0.255	link	-	Tcp10c	c.919-159_	-	ENSMUST	intron_variant
17	23344265	.	G	GAA	mapping_(	INS	66	0	66	0	72	7	79	0.089	link	-	Vmn2r115	c.197+92_	-	ENSMUST	intron_variant
17	23344267	.	ATG	A	mapping_(	DEL	65	0	65	0	71	7	78	0.09	link	-	Vmn2r115	c.197+95_	-	ENSMUST	intron_variant
17	35830829	.	TG	T	alt_allele_	DEL	37	11	48	0.229	29	22	51	0.431	link	-	Tubb5	c.*4152del	-	ENSMUST	downstream_gene_variant
17	35830829	.	TG	T	alt_allele_	DEL	37	11	48	0.229	29	22	51	0.431	link	-	Flot1	c.1089+49	-	ENSMUST	intron_variant
17	46304127	rs2173003	TG	T	non_homr	DEL	102	10	112	0.089	107	19	126	0.151	link	-	Dlk2	c.*1030del	-	ENSMUST	downstream_gene_variant
17	46304127	rs2173003	TG	T	non_homr	DEL	102	10	112	0.089	107	19	126	0.151	link	-	Abcc10	c.4305+29	-	ENSMUST	intron_variant
17	56614845	.	TG	T	alt_allele_	DEL	67	15	82	0.183	42	19	61	0.311	link	-	Rpl36	c.*633delC	-	ENSMUST	downstream_gene_variant
17	56614845	.	TG	T	alt_allele_	DEL	67	15	82	0.183	42	19	61	0.311	link	-	Lonp1	c.2505+28	-	ENSMUST	intron_variant
17	73350405	.	CCAGGCC	C	non_homr	DEL	100	0	100	0	100	6	106	0.057	link	-	Capn13	c.768+39_	-	ENSMUST	intron_variant
18	12472349	rs2607379	AC	A	non_homr	DEL	79	10	89	0.112	72	20	92	0.217	link	-	Lama3	c.3327+42	-	ENSMUST	intron_variant
18	76138101	.	GCCACA	G	too_few_s	DEL	5	0	5	0	2	2	4	0.5	link	-	Zbtb7c	c.1208+52	-	ENSMUST	intron_variant
2	88678616	.	AT	A	weak_evid	DEL	186	2	188	0.011	233	11	244	0.045	link	-	Olfr1193	c.768delT	p.Phe256f	ENSMUST	frameshift_variant
2	88678616	.	AT	A	weak_evid	DEL	186	2	188	0.011	233	11	244	0.045	link	-	Olfr1195	c.*4187del	-	ENSMUST	downstream_gene_variant
2	1.36E+08	.	G	GA	PASS	INS	26	0	26	0	22	13	35	0.371	link	-	Lamp5	c.665-113(	-	ENSMUST	intron_variant
2	1.52E+08	rs2399128	AG	A	non_homr	DEL	160	9	169	0.053	147	27	174	0.155	link	-	6820408C	c.11+34de	-	ENSMUST	intron_variant
2	1.74E+08	.	CCCGG	C	weak_evid	DEL	144	3	147	0.02	154	5	159	0.031	link	-	Slmo2	c.-80_-77c	-	ENSMUST	5_prime_UTR_variant
3	19628714	.	CT	C	weak_evid	DEL	267	2	269	0.007	269	9	278	0.032	link	-	1700064H	c.-107delA	-	ENSMUST	upstream_gene_variant
3	19628714	.	CT	C	weak_evid	DEL	267	2	269	0.007	269	9	278	0.032	link	-	-	n.1962871	-	-	intergenic_region
3	83032015	.	AC	A	alt_allele_	DEL	54	23	77	0.299	33	28	61	0.459	link	-	Fga	c.1660+49	-	ENSMUST	intron_variant
3	92080981	.	AGCC	A	weak_evid	DEL	354	5	359	0.014	435	18	453	0.04	link	-	Lor	c.994_996	p.Gly332d	ENSMUST	conservative_inframe_deletion
3	94480386	.	TC	T	non_homr	DEL	46	11	57	0.193	42	21	63	0.333	link	-	Celf3	c.228+48d	-	ENSMUST	intron_variant
3	1.27E+08	.	AG	A	alt_allele_	DEL	66	29	95	0.305	32	38	70	0.543	link	-	Ank2	c.1485+51	-	ENSMUST	intron_variant
3	1.33E+08	.	AG	A	non_homr	DEL	16	2	18	0.111	19	9	28	0.321	link	-	Gstcd	c.898-15d(	-	ENSMUST	intron_variant
4	43640003	.	C	CGTGT	weak_evid	INS	14	1	15	0.067	16	9	25	0.36	link	-	Npr2	c.874-109_	-	ENSMUST	intron_variant
4	43640003	.	C	CGTGT	weak_evid	INS	14	1	15	0.067	16	9	25	0.36	link	-	Gm12473	n.266+12(	-	ENSMUST	intron_variant
4	1.07E+08	.	TG	T	alt_allele_	DEL	60	16	76	0.211	54	31	85	0.365	link	-	Ttc22	c.623+38d	-	ENSMUST	intron_variant
4	1.13E+08	.	A	ATC	low_frac_i	INS	23	3	26	0.115	19	11	30	0.367	link	-	Skint6	c.3689-88_	-	ENSMUST	intron_variant
4	1.38E+08	.	A	AGG	base_qual	INS	15	3	18	0.167	15	6	21	0.286	link	-	Camk2n1	c.*200_*2(	-	ENSMUST	3_prime_UTR_variant
4	1.38E+08	.	A	AGGAGGA	base_qual	INS	17	1	18	0.056	16	5	21	0.238	link	-	Camk2n1	c.*202_*2(	-	ENSMUST	3_prime_UTR_variant
4	1.48E+08	.	AAAG	A	non_homr	DEL	68	3	71	0.042	94	11	105	0.105	link	-	Zfp985	c.158-140_	-	ENSMUST	intron_variant
5	14974027	.	AAG	A	mapping_(	DEL	6	0	6	0	10	2	12	0.167	link	-	Gm10354	c.*468_*4(	-	ENSMUST	downstream_gene_variant
5	14974027	.	AAG	A	mapping_(	DEL	6	0	6	0	10	2	12	0.167	link	-	-	n.1497402	-	-	intergenic_region
5	15029709	.	AC	A	mapping_(	DEL	37	0	37	0	45	6	51	0.118	link	-	Gm17019	c.625-283(	-	ENSMUST	intron_variant
5	23980469	.	AT	A	PASS	DEL	186	0	186	0	182	16	198	0.081	link	-	Fam126a	c.831+17d	-	ENSMUST	intron_variant
5	26021365	.	TTCAC	T	mapping_(	DEL	8	0	8	0	5	2	7	0.286	link	-	Gm5862	c.299+235	-	ENSMUST	intron_variant
5	1.13E+08	.	TCCTC	T	weak_evid	DEL	52	2	54	0.037	43	6	49	0.122	link	-	Myo18b	c.5638-43_	-	ENSMUST	intron_variant
5	1.15E+08	.	AC	A	alt_allele_	DEL	21	17	38	0.447	18	29	47	0.617	link	-	Msi1	c.791-92d(	-	ENSMUST	intron_variant
6	31432783	.	C	CCTAT	PASS	INS	11	0	11	0	13	6	19	0.316	link	-	Mkln1	c.511-110_	-	ENSMUST	intron_variant
6	1.42E+08	rs2237803	AAAAC	A	PASS	DEL	113	0	113	0	84	4	88	0.045	link	-	Gm6614	c.1438-10_	-	ENSMUST	splice_region_variant+intron_variant
6	1.42E+08	rs2237803	AAAAC	A	PASS	DEL	113	0	113	0	84	4	88	0.045	link	-	Gm23775	n.-2175_-2	-	ENSMUST	upstream_gene_variant
7	24112230	.	TG	T	alt_allele_	DEL	37	11	48	0.229	33	22	55	0.4	link	-	Zfp112	c.-6138del	-	ENSMUST	upstream_gene_variant
7	24112230	.	TG	T	alt_allele_	DEL	37	11	48	0.229	33	22	55	0.4	link	-	Zfp180	c.*6106del	-	ENSMUST	downstream_gene_variant
7	24112230	.	TG	T	alt_allele_	DEL	37	11	48	0.229	33	22	55	0.4	link	-	Gm44793	n.*223delC	-	ENSMUST	downstream_gene_variant
7	24112230	.	TG	T	alt_allele_	DEL	37	11	48	0.229	33	22	55	0.4	link	-	-	n.2411223	-	-	intergenic_region
7	34099671	rs2646431	CG	C	non_homr	DEL	49	12	61	0.197	37	16	53	0.302	link	-	Scgb1b30	c.62-23del	-	ENSMUST	intron_variant
7	80397715	.	TG	T	weak_evid	DEL	8	0	8	0	3	8	11	0.727	link	-	Furin	c.372+182	-	ENSMUST	intron_variant
7	98083261	.	GC	G	non_homr	DEL	43	10	53	0.189	31	23	54	0.426	link	-	Myo7a	c.2095-45(	-	ENSMUST	intron_variant
7	1.02E+08	.	ACC	A	too_few_s	DEL	5	0	5	0	0	2	2	1	link	-	Inppl1	c.*199_*2(	-	ENSMUST	3_prime_UTR_variant
7	1.02E+08	.	ACC	A	too_few_s	DEL	5	0	5	0	0	2	2	1	link	-	Phox2a	c.*968_*9(	-	ENSMUST	downstream_gene_variant
7	1.02E+08	.	TG	T	non_homr	DEL	12	9	21	0.429	12	13	25	0.52	link	-	Numa1	c.4665+10	-	ENSMUST	intron_variant
7	1.2E+08	.	T	TCTGCCT	weak_evid	INS	22	0	22	0	8	3	11	0.273	link	-	Dnah3	c.8360-35(	-	ENSMUST	intron_variant
7	1.2E+08	.	T	TCTGCCT	weak_evid	INS	22	0	22	0	8	3	11	0.273	link	-	Lyrm1	n.1199531	-	-	intragenic_variant
7	1.22E+08	rs2331294	GA	G	weak_evid	DEL	186	0	186	0	206	6	212	0.028	link	-	Ern2	c.304-10d(	-	ENSMUST	intron_variant
8	11441159	.	AC	A	non_homr	DEL	112	6	118	0.051	107	18	125	0.144	link	-	Col4a2	c.3620-53(	-	ENSMUST	intron_variant
8	36248765	.	AGGC	A	non_homr	DEL	253	3	256	0.012	250	13	263	0.049	link	-	Lonrf1	c.712_714	p.Ala238d	ENSMUST	conservative_inframe_deletion
8	70760256	rs2467108	T	TG	non_homr	INS	113	11	124	0.089	109	23	132	0.174	link	-	Rab3a	c.*2168_*2	-	ENSMUST	downstream_gene_variant
8	70760256	rs2467108	T	TG	non_homr	INS	113	11	124	0.089	109	23	132	0.174	link	-	Ifi30	c.*2718du	-	ENSMUST	downstream_gene_variant
8	70760256	rs2467108	T	TG	non_homr	INS	113	11	124	0.089	109	23	132	0.174	link	-	Mpv17l2	c.358+111	-	ENSMUST	intron_variant
8	79689188	.	AAAAC	A	weak_evid	DEL	239	1	240	0.004	246	7	253	0.028	link	-	Abce1	c.1205-9_:	-	ENSMUST	splice_region_variant+intron_variant
8	86527207	.	TG	T	non_homr	DEL	57	12	69	0.174	47	22	69	0.319	link	-	Abcc12	c.2891+55	-	ENSMUST	intron_variant
8	1.1E+08	rs2145861	C	CGT	PASS	INS	140	2	142	0.014	137	11	148	0.074	link	-	Tat	c.1125+32	-	ENSMUST	intron_variant
9	60602827	.	C	CT	PASS	INS	109	3	112	0.027	77	44	121	0.364	link	-	Lrrc49	c.1368-12(	-	ENSMUST	intron_variant
X	9265358	.	TA	T	too_few_s	DEL	9	0	9	0	3	2	5	0.4	link	-	Lancl3	c.1104-16(	-	ENSMUST	intron_variant
GL456212	95070	.	AT	A	mapping_(	DEL	124	0	124	0	133	4	137	0.029	link	-	-	n.95071de	-	-	intergenic_region
1	78499008	.	A	G	mapping_(	SNV	148	9	157	0.057	168	10	178	0.056	link	-	BC035947	c.886T>C	p.Ser296P	ENSMUST	missense_variant
1	1.74E+08	.	T	G	PASS	SNV	352	2	354	0.006	318	56	374	0.15	link	-	Pydc4	c.720A>C	p.Gln240H	ENSMUST	missense_variant
10	58224915	.	A	C	mapping_(	SNV	752	11	763	0.014	772	25	797	0.031	link	-	AW822073	c.16T>G	p.Trp6Gly	ENSMUST	missense_variant
10	81148404	.	T	G	base_qual	SNV	171	5	176	0.028	203	8	211	0.038	link	-	Zbtb7a	c.1679T>(	p.Val560G	ENSMUST	missense_variant
11	68556997	.	C	A	PASS	SNV	257	0	257	0	275	25	300	0.083	link	-	Mfsd6l	c.673C>A	p.Pro225T	ENSMUST	missense_variant
11	98372122	.	T	G	base_qual	SNV	170	2	172	0.012	150	15	165	0.091	link	-	Stard3	c.2T>G	p.Met1?	ENSMUST	start_lost

11	99540165	.	C	T	PASS	SNV	260	0	260	0	245	17	262	0.065	link	-	Krt40	c.757G>A	p.Asp253A	ENSMUST	missense_variant
11	1.02E+08	.	T	G	base_qual	SNV	138	4	142	0.028	160	12	172	0.07	link	-	Etv4	c.722A>C	p.Gln241P	ENSMUST	missense_variant
12	70887030	.	A	G	weak_evid	SNV	205	0	205	0	191	4	195	0.021	link	-	Frmd6	c.721A>G	p.Arg241G	ENSMUST	missense_variant
12	80181363	.	T	A	base_qual	SNV	125	6	131	0.046	113	9	122	0.074	link	-	Actn1	c.1232A>T	p.Asp411V	ENSMUST	missense_variant+splice_region_variant
14	12344374	.	T	G	weak_evid	SNV	136	0	136	0	166	4	170	0.024	link	-	Fezf2	c.812A>C	p.Asn271T	ENSMUST	missense_variant
14	19417270	.	C	G	non_homr	SNV	200	6	206	0.029	309	13	322	0.04	link	-	Gm21738	c.257G>C	p.Ser86Th	ENSMUST	missense_variant
14	24004089	.	C	T	PASS	SNV	311	1	312	0.003	378	8	386	0.021	link	-	Kcnma1	c.37G>A	p.Gly13Ser	ENSMUST	missense_variant
14	44858482	.	C	T	PASS	SNV	248	0	248	0	246	20	266	0.075	link	-	Ptgdr	c.772G>A	p.Glu258L	ENSMUST	missense_variant
14	51456291	.	A	G	mapping_c	SNV	293	5	298	0.017	311	3	314	0.01	link	-	Vmn2r89	c.1097A>C	p.Lys366A	ENSMUST	missense_variant
14	52006676	.	T	G	base_qual	SNV	85	9	94	0.096	79	18	97	0.186	link	-	Zfp219	c.2045A>C	p.Gln682P	ENSMUST	missense_variant
14	62674307	.	T	G	base_qual	SNV	220	0	220	0	188	29	217	0.134	link	-	Serpine3	c.717T>G	p.His239G	ENSMUST	missense_variant
15	76891116	.	T	A	PASS	SNV	266	0	266	0	206	97	303	0.32	link	-	Zfp7	c.1357T>A	p.Ser453T	ENSMUST	missense_variant
15	79828038	.	A	C	base_qual	SNV	184	2	186	0.011	196	5	201	0.025	link	-	Cbx6	c.1187T>C	p.Val396G	ENSMUST	missense_variant
17	15544089	rs5874052	T	G	base_qual	SNV	427	11	438	0.025	475	17	492	0.035	link	-	Prdm9	c.2428A>C	p.Lys810G	ENSMUST	missense_variant
17	23310616	.	G	T	mapping_c	SNV	249	1	250	0.004	267	11	278	0.04	link	-	Vmn2r114	c.511C>A	p.Pro171T	ENSMUST	missense_variant
17	23477455	.	T	C	mapping_c	SNV	55	3	58	0.052	89	8	97	0.082	link	-	Vmn2r117	c.977A>G	p.His326A	ENSMUST	missense_variant
17	32396867	.	T	G	base_qual	SNV	169	0	169	0	159	20	179	0.112	link	-	Rasal3	c.996A>C	p.Gln332H	ENSMUST	missense_variant
18	25001817	.	T	G	base_qual	SNV	231	0	231	0	194	20	214	0.093	link	-	Fhod3	c.984T>G	p.Asp328G	ENSMUST	missense_variant
18	36939510	.	A	G	PASS	SNV	483	0	483	0	444	92	536	0.172	link	-	Pcdha2	c.193A>G	p.Arg65Gly	ENSMUST	missense_variant
18	61310801	.	T	G	weak_evid	SNV	299	2	301	0.007	230	3	233	0.013	link	-	Ppargc1b	c.1338A>C	p.Glu446A	ENSMUST	missense_variant
19	4612149	.	A	C	base_qual	SNV	277	12	289	0.042	273	18	291	0.062	link	-	Lrfn4	c.1839T>C	p.His613G	ENSMUST	missense_variant
19	48767139	.	A	T	base_qual	SNV	118	5	123	0.041	99	13	112	0.116	link	-	Sorcs3	c.2717A>T	p.His906Le	ENSMUST	missense_variant
2	27452875	.	T	C	weak_evid	SNV	173	1	174	0.006	193	4	197	0.02	link	-	Brd3	c.1655A>C	p.Lys552A	ENSMUST	missense_variant
2	1.74E+08	.	G	A	PASS	SNV	286	0	286	0	291	26	317	0.082	link	-	Gnas	c.805G>A	p.Ala269Tl	ENSMUST	missense_variant
4	8838751	.	A	C	base_qual	SNV	174	2	176	0.011	172	18	190	0.095	link	-	Chd7	c.3949A>C	p.Ile1317L	ENSMUST	missense_variant
4	1.25E+08	.	T	G	weak_evid	SNV	145	1	146	0.007	189	6	195	0.031	link	-	Pou3f1	c.23T>G	p.Leu8Arg	ENSMUST	missense_variant
5	30796316	.	T	G	weak_evid	SNV	210	0	210	0	182	8	190	0.042	link	-	Dpysl5	c.1689T>C	p.Ile563Me	ENSMUST	missense_variant
5	33248597	.	T	G	base_qual	SNV	214	0	214	0	198	37	235	0.157	link	-	Ctbp1	c.1229A>C	p.His410P	ENSMUST	missense_variant
5	1.23E+08	.	T	G	base_qual	SNV	228	0	228	0	216	19	235	0.081	link	-	Setd1b	c.4250T>C	p.Leu1417	ENSMUST	missense_variant
6	1.14E+08	.	T	G	base_qual	SNV	247	0	247	0	209	20	229	0.087	link	-	Sec13	c.707A>C	p.Gln236P	ENSMUST	missense_variant+splice_region_variant
6	1.18E+08	.	C	T	weak_evid	SNV	260	1	261	0.004	260	4	264	0.015	link	-	Bms1	c.812G>A	p.Arg271H	ENSMUST	missense_variant
6	1.33E+08	.	A	C	base_qual	SNV	291	18	309	0.058	299	24	323	0.074	link	-	Prp2	c.706A>C	p.Thr236P	ENSMUST	missense_variant
7	83882197	.	T	G	base_qual	SNV	182	0	182	0	177	19	196	0.097	link	-	Mesdc1	c.1025A>C	p.Gln342P	ENSMUST	missense_variant
7	1.18E+08	.	C	T	weak_evid	SNV	233	0	233	0	261	4	265	0.015	link	-	Smg1	c.37G>A	p.Gly13Ser	ENSMUST	missense_variant
8	70518456	.	G	A	weak_evid	SNV	203	0	203	0	220	4	224	0.018	link	-	Kxd1	c.163C>T	p.Arg55Trp	ENSMUST	missense_variant
9	3020901	.	T	A	low_frac_i	SNV	55	5	60	0.083	86	14	100	0.14	link	-	Gm10719	c.276T>A	p.His92Gln	ENSMUST	missense_variant
9	3025937	.	A	C	weak_evid	SNV	172	3	175	0.017	315	11	326	0.034	link	-	Gm10717	c.521A>C	p.Gln174P	ENSMUST	missense_variant
9	42969733	.	G	A	PASS	SNV	257	0	257	0	221	4	225	0.018	link	-	Arhgef12	c.4604C>T	p.Ala1535V	ENSMUST	missense_variant
X	72269971	.	A	C	base_qual	SNV	156	2	158	0.013	176	11	187	0.059	link	-	Gabre	c.1221T>C	p.His407G	ENSMUST	missense_variant
X	74085565	.	C	T	weak_evid	SNV	104	1	105	0.01	105	3	108	0.028	link	-	Mecp2	c.22G>A	p.Ala8Thr	ENSMUST	missense_variant
X	1.01E+08	.	G	A	PASS	SNV	90	0	90	0	103	6	109	0.055	link	-	Pdzd11	c.77C>T	p.Pro26Le	ENSMUST	missense_variant
2	31898240	.	T	G	base_qual	SNV	145	0	145	0	122	16	138	0.116	link	-	Lamc3	c.411T>G	p.Tyr137*	ENSMUST	stop_gained
1	12841393	.	G	T	base_qual	SNV	131	1	132	0.008	118	3	121	0.025	link	-	Sulf1	c.2040-50(	-	ENSMUST	intron_variant
1	22428339	.	T	G	base_qual	SNV	19	1	20	0.05	24	3	27	0.111	link	-	Rims1	c.2315+12	-	ENSMUST	intron_variant
1	26686929	rs1133107	C	A	PASS	SNV	37	0	37	0	29	4	33	0.121	link	-	4931408C	c.186+312	-	ENSMUST	intron_variant
1	33835950	.	C	A	base_qual	SNV	45	4	49	0.082	59	6	65	0.092	link	-	Gm15455	n.*174G>T	-	ENSMUST	downstream_gene_variant
1	33835950	.	C	A	base_qual	SNV	45	4	49	0.082	59	6	65	0.092	link	-	-	n.3383595	-	-	intergenic_region
1	37262122	.	T	G	base_qual	SNV	61	4	65	0.062	46	7	53	0.132	link	-	Cnga3	c.*26T>G	-	ENSMUST	3_prime_UTR_variant
1	38129745	.	A	C	base_qual	SNV	91	4	95	0.042	102	8	110	0.073	link	-	Rev1	c.-21288T	-	ENSMUST	upstream_gene_variant
1	38129745	.	A	C	base_qual	SNV	91	4	95	0.042	102	8	110	0.073	link	-	Gm5099	n.-2338A>	-	ENSMUST	upstream_gene_variant
1	38129745	.	A	C	base_qual	SNV	91	4	95	0.042	102	8	110	0.073	link	-	Rev1	n.3812974	-	-	intragenic_variant
1	38129775	.	T	G	base_qual	SNV	129	9	138	0.065	118	9	127	0.071	link	-	Rev1	c.-21318A	-	ENSMUST	upstream_gene_variant
1	38129775	.	T	G	base_qual	SNV	129	9	138	0.065	118	9	127	0.071	link	-	Gm5099	n.-2308T>	-	ENSMUST	upstream_gene_variant
1	38129775	.	T	G	base_qual	SNV	129	9	138	0.065	118	9	127	0.071	link	-	Rev1	n.3812977	-	-	intragenic_variant
1	45384297	.	A	C	base_qual	SNV	10	1	11	0.091	7	3	10	0.3	link	-	Col5a2	c.3357+10	-	ENSMUST	intron_variant
1	55363126	.	A	C	base_qual	SNV	22	4	26	0.154	31	9	40	0.225	link	-	Boll	c.21+173T	-	ENSMUST	intron_variant
1	73991436	.	G	A	too_few_s	SNV	11	0	11	0	16	2	18	0.111	link	-	Tns1	c.920+239	-	ENSMUST	intron_variant
1	82839528	.	T	G	too_few_s	SNV	10	0	10	0	12	2	14	0.143	link	-	Agfg1	c.-207T>G	-	ENSMUST	upstream_gene_variant
1	82839528	.	T	G	too_few_s	SNV	10	0	10	0	12	2	14	0.143	link	-	Gm22396	n.*30T>G	-	ENSMUST	downstream_gene_variant
1	82839528	.	T	G	too_few_s	SNV	10	0	10	0	12	2	14	0.143	link	-	Agfg1	n.8283952	-	-	intragenic_variant
1	85100761	rs1132313	A	G	no_reliable	SNV	56	1	57	0.018	65	7	72	0.097	link	-	Gm10553	c.*226A>G	-	ENSMUST	downstream_gene_variant
1	85100761	rs1132313	A	G	no_reliable	SNV	56	1	57	0.018	65	7	72	0.097	link	-	A530032D	c.33-67T>	-	ENSMUST	intron_variant
1	85100761	rs1132313	A	G	no_reliable	SNV	56	1	57	0.018	65	7	72	0.097	link	-	C130026I2	n.8510076	-	-	intragenic_variant
1	85101442	.	G	A	weak_evid	SNV	39	2	41	0.049	50	9	59	0.153	link	-	A530040E	n.-4504G>	-	ENSMUST	upstream_gene_variant
1	85101442	.	G	A	weak_evid	SNV	39	2	41	0.049	50	9	59	0.153	link	-	Gm10553	c.*907G>A	-	ENSMUST	downstream_gene_variant
1	85101442	.	G	A	weak_evid	SNV	39	2	41	0.049	50	9	59	0.153	link	-	A530032D	c.33-748C	-	ENSMUST	intron_variant
1	85101442	.	G	A	weak_evid	SNV	39	2	41	0.049	50	9	59	0.153	link	-	C130026I2	n.8510144	-	-	intragenic_variant
1	85112106	.	C	G	non_homr	SNV	69	3	72	0.042	82	7	89	0.079	link	-	A530032D	c.-2738G>	-	ENSMUST	upstream_gene_variant
1	85112106	.	C	G	non_homr	SNV	69	3	72	0.042	82	7	89	0.079	link	-	Gm16038	n.-3213C>	-	ENSMUST	upstream_gene_variant
1	85112106	.	C	G	non_homr	SNV	69	3	72	0.042	82	7	89	0.079	link	-	A530040E	n.896+147	-	ENSMUST	intron_variant
1	85112106	.	C	G	non_homr	SNV	69	3	72	0.042	82	7	89	0.079	link	-	C130026I2	n.8511210	-	-	intragenic_variant
1	85245106	rs1132286	G	A	weak_evid	SNV	6	0	6	0	9	3	12	0.25	link	-	Gm16028	n.-1745G>	-	ENSMUST	upstream_gene_variant
1	85245106	rs1132286	G	A	weak_evid	SNV	6	0	6	0	9	3	12	0.25	link	-	C130026I2	c.*1831C>	-	ENSMUST	downstream_gene_variant
1	85245106	rs1132286	G	A	weak_evid	SNV	6	0	6	0	9	3	12	0.25	link	-	Gm2619	n.379+692	-	ENSMUST	intron_variant
1	85245106	rs1132286	G	A	weak_evid	SNV	6	0	6	0	9	3	12	0.25	link	-	C130026I2	n.8524510	-	-	intragenic_variant
1	85247615	rs1134411	T	A	weak_evid	SNV	13	0	13	0	14	3	17	0.176	link	-	C130026I2	c.677-479A	-	ENSMUST	intron_variant
1	85247615	rs1134411	T	A	weak_evid	SNV	13	0	13	0	14	3	17	0.176	link	-	Gm16028	n.543+222	-	ENSMUST	intron_variant
1	85247615	rs1134411	T	A	weak_evid	SNV	13	0	13	0	14	3	17	0.176	link	-	Gm2619	n.379+667	-	ENSMUST	intron_variant
1	85248521	rs1134785	C	T	no_reliable	SNV	38	0	38	0	75	6	81	0.074	link	-	C130026I2	c.596-142(	-	ENSMUST	intron_variant
1	85248521	rs1134785	C	T	no_reliable	SNV	38	0	38	0	75	6	81	0.074	link	-	Gm16028	n.543+112	-	ENSMUST	intron_variant
1	85248521	rs1134785	C	T	no_reliable	SNV	38	0	38	0	75	6	81	0.074	link	-	Gm2619	n.379+658	-	ENSMUST	intron_variant
1	85630228	rs1134029	G	T	PASS	SNV	23	1	24	0.042	17	6	23	0.261	link	-	Sp140	c.725-232(	-	ENSMUST	intron_variant
1	85635420	rs1132939	A	G	mapping_c	SNV	50	3	53	0.057	58	9	67	0.134	link	-	Sp140	c.973-139A	-	ENSMUST	intron_variant
1	85635443	rs1131757	A	G	mapping_c	SNV	69	3	72	0.042	64	8	72	0.111	link	-	Sp140	c.973-116A	-	ENSMUST	intron_variant
1	85638175	.	T	A	PASS	SNV	24	0	24	0	29	5	34	0.147	link	-	Gm17017	n.*3047A>	-	ENSMUST	downstream_gene_variant
1	85638175	.	T	A	PASS	SNV	24	0	24	0	29	5	34	0.147	link	-	Sp140	c.1062+31	-	ENSMUST	intron_variant
1	85638207	rs1083011	G	A	PASS	SNV	19	0	19	0	22	5	27	0.185	link	-	Gm17017	n.*3015C>	-	ENSMUST	downstream_gene_variant
1	85638207	rs1083011	G	A	PASS	SNV	19	0	19	0	22	5	27	0.185	link	-	Sp140	c.1062+34	-	ENSMUST	intron_variant
1	88244609	rs5025982	A	G	weak_evid	SNV	5	0	5	0	9	3	12	0.25	link	-	Mroh2a	c.2443-335	-	ENSMUST	intron_variant
1	88255755	.	A	C	base_qual	SNV	441	1	442	0.002	455	50	505	0.099	link	-	Mroh2a	c.4013+75	-	ENSMUST	intron_variant
1	88257866	.	G	A	PASS	SNV	884	0	884	0	893	27	920	0.029	link	-	Hjurp	c.*7315C>	-	ENSMUST	downstream_gene_variant
1	93286684	.	A	C	too_few_s	SNV	6	0	6	0	6	2	8	0.25	link	-	Sned1	c.3818-244	-	ENSMUST	intron_variant
1	1.08E+08	.	A	C	base_qual	SNV	130	0	130	0	107	19	126	0.151	link	-	Serpinb2	c.417+36A	-	ENSMUST	intron_variant
1	1.28E+08	.	A	C	base_qual	SNV	27	4	31	0.129	37	7	44	0.159	link	-	Gm38248	n.-3224T>	-	ENSMUST	upstream_gene_variant
1	1.28E+08	.	A	C	base_qual	SNV	27	4	31	0.129	37	7	44	0.159	link	-	Zranb3	c.1536+86	-	ENSMUST	intron_variant
1	1.32E+08	.	C	G	base_qual	SNV	84	1	85	0.012	63	10	73	0.137	link	-	Slc26a9	c.1389+36	-	ENSMUST	intron_variant
1	1.33E+08	.	T	G	base_qual	SNV	53	0	53	0	56	21	77	0.273	link	-	Plekha6	c.2394+86	-	ENSMUST	intron_variant
1	1.34E+08	.	A	T	too_few_s	SNV	10	0	10	0	10	2	12	0.167	link	-	Mybph	c.-4662A>	-	ENSMUST	upstream_gene_variant
1	1.34E+08	.	A	T	too_few_s	SNV	10	0	10	0	10	2	12	0.167	link	-	Chil1	c.921+165	-	ENSMUST	intron_variant
1	1.36E+08	.	G	A	too_few_s	SNV	9	0	9	0	9	2	11	0.182	link	-	9230116N	n.-3709C>	-	ENSMUST	upstream_gene_variant
1	1.36E+08	.	G	A	too_few_s	SNV	9	0	9	0	9	2	11	0.182	link	-	Ddx59	c.805-207(	-	ENSMUST	intron_variant
1	1.53E+08	.	A	C	base_qual	SNV	58	5	63	0.079	54	2	56	0.036	link	-	Lamc2	c.1861-30	-	ENSMUST	intron_variant
1	1.8E+08	.	T	G	base_qual	SNV	43	4	47	0.085	41	6	47	0.128	link	-	Psen2	c.887-137A	-	ENSMUST	intron_variant
1	1.82E+08	.	A	C	base_qual	SNV	17	0	17	0	20	5	25	0.2	link	-	Fbxo28	c.377+164	-	ENSMUST	intron_variant
1	1.87E+08	.	A	C	base_qual	SNV	93	9	102	0.088	90	13	103	0.126	link	-	Spata17	c.-415T>G	-	ENSMUST	upstream_gene_variant
1	1.87E+08	.	A	C	base_qual	SNV	93	9	102	0.088	90	13	103	0.126	link	-	Gpatch2	c.53+24A>	-	ENSMUST	intron_variant
1	1.93E+08	.	G	A	weak_evid	SNV	82	0	82	0	89	3	92	0.033	link	-	Syt14	c.13+115C	-	ENSMUST	intron_variant
10	8885527	.	T	G	base_qual	SNV	3	0	3	0	17	6	23	0.261	link	-	Sash1	c.135+197	-	ENSMUST	intron_variant

10	8885527	.	T	G	base_qual	SNV	3	0	3	0	17	6	23	0.261	link	-	Gm26674	n.206-111	-	ENSMUST	intron_variant
10	23123766	.	A	C	base_qual	SNV	31	5	36	0.139	45	9	54	0.167	link	-	Eya4	c.1212+86	-	ENSMUST	intron_variant
10	44447097	.	A	C	base_qual	SNV	63	5	68	0.074	64	16	80	0.2	link	-	Prdm1	c.508-53T	-	ENSMUST	intron_variant
10	58224915	.	A	C	mapping_(	SNV	752	11	763	0.014	772	25	797	0.031	link	-	Gm10807	n.*2942T>	-	ENSMUST	downstream_gene_variant
10	58225430	rs1080837	A	T	weak_evid	SNV	36	1	37	0.027	42	6	48	0.125	link	-	AW82207:	c.-500T>A	-	ENSMUST	upstream_gene_variant
10	58225430	rs1080837	A	T	weak_evid	SNV	36	1	37	0.027	42	6	48	0.125	link	-	Gm10807	n.*2427T>	-	ENSMUST	downstream_gene_variant
10	58225430	rs1080837	A	T	weak_evid	SNV	36	1	37	0.027	42	6	48	0.125	link	-	-	n.5822543	-	-	intergenic_region
10	58236848	.	A	G	weak_evid	SNV	15	1	16	0.062	16	3	19	0.158	link	-	Duxf3	c.-4173T>	-	ENSMUST	upstream_gene_variant
10	58236848	.	A	G	weak_evid	SNV	15	1	16	0.062	16	3	19	0.158	link	-	Gm4981	c.-458T>C	-	ENSMUST	upstream_gene_variant
10	58236848	.	A	G	weak_evid	SNV	15	1	16	0.062	16	3	19	0.158	link	-	Gm19459	n.*2760T>	-	ENSMUST	downstream_gene_variant
10	58236848	.	A	G	weak_evid	SNV	15	1	16	0.062	16	3	19	0.158	link	-	-	n.5823684	-	-	intergenic_region
10	61695473	.	T	G	base_qual	SNV	50	8	58	0.138	48	18	66	0.273	link	-	Tysnd1	c.-98T>G	-	ENSMUST	upstream_gene_variant
10	61695473	.	T	G	base_qual	SNV	50	8	58	0.138	48	18	66	0.273	link	-	Sar1a	c.*4072T>	-	ENSMUST	downstream_gene_variant
10	61695473	.	T	G	base_qual	SNV	50	8	58	0.138	48	18	66	0.273	link	-	-	n.6169547	-	-	intergenic_region
10	62286193	.	T	A	too_few_s	SNV	14	1	15	0.067	19	1	20	0.05	link	-	Hk1	c.1651+15	-	ENSMUST	intron_variant
10	63003117	.	A	C	base_qual	SNV	103	0	103	0	91	18	109	0.165	link	-	Gm16135	n.*3428A>	-	ENSMUST	downstream_gene_variant
10	63003117	.	A	C	base_qual	SNV	103	0	103	0	91	18	109	0.165	link	-	Rufy2	c.1205+83	-	ENSMUST	intron_variant
10	76797962	.	A	C	base_qual	SNV	135	0	135	0	98	20	118	0.169	link	-	Pcbp3	c.223-51T	-	ENSMUST	intron_variant
10	80006953	.	A	C	base_qual	SNV	133	3	136	0.022	122	8	130	0.062	link	-	Abca7	c.3514+31	-	ENSMUST	intron_variant
10	80534053	.	T	G	base_qual	SNV	28	3	31	0.097	30	7	37	0.189	link	-	Atp8b3	c.413+112	-	ENSMUST	intron_variant
10	81148404	.	T	G	base_qual	SNV	171	5	176	0.028	203	8	211	0.038	link	-	Pias4	c.*5697A>	-	ENSMUST	downstream_gene_variant
10	81212314	.	T	C	too_few_s	SNV	20	0	20	0	15	2	17	0.118	link	-	Atcayos	n.*1437T>	-	ENSMUST	downstream_gene_variant
10	81212314	.	T	C	too_few_s	SNV	20	0	20	0	15	2	17	0.118	link	-	Atcay	c.779+158	-	ENSMUST	intron_variant
10	81627370	.	A	C	alt_allele_i	SNV	23	5	28	0.179	27	5	32	0.156	link	-	Ankrd24	c.-2343A>	-	ENSMUST	upstream_gene_variant
10	81627370	.	A	C	alt_allele_i	SNV	23	5	28	0.179	27	5	32	0.156	link	-	Sirt6	c.66+102T	-	ENSMUST	intron_variant
10	85902106	.	T	G	too_few_s	SNV	5	0	5	0	7	2	9	0.222	link	-	Prdm4	c.1491-27	-	ENSMUST	intron_variant
10	92977117	.	T	G	base_qual	SNV	114	0	114	0	88	20	108	0.185	link	-	Cfap54	c.3986-33	-	ENSMUST	intron_variant
10	1.01E+08	.	A	C	base_qual	SNV	10	0	10	0	17	3	20	0.15	link	-	Cep290	c.4816-17	-	ENSMUST	intron_variant
10	1.03E+08	.	A	G	weak_evid	SNV	113	0	113	0	121	3	124	0.024	link	-	Alx1	c.532-30T	-	ENSMUST	intron_variant
10	1.07E+08	.	G	T	base_qual	SNV	30	3	33	0.091	41	13	54	0.241	link	-	Ppfia2	c.2925+95	-	ENSMUST	intron_variant
10	1.17E+08	.	C	A	base_qual	SNV	13	0	13	0	7	1	8	0.125	link	-	Cpsf6	c.1580+14	-	ENSMUST	intron_variant
10	1.17E+08	.	C	G	too_few_s	SNV	14	0	14	0	9	1	10	0.1	link	-	Cpsf6	c.1580+14	-	ENSMUST	intron_variant
10	1.2E+08	.	T	G	base_qual	SNV	28	7	35	0.2	32	14	46	0.304	link	-	Grip1	c.273-112	-	ENSMUST	intron_variant
10	1.2E+08	.	G	A	weak_evid	SNV	142	1	143	0.007	125	3	128	0.023	link	-	Grip1	c.872+13C	-	ENSMUST	intron_variant
10	1.23E+08	.	G	T	base_qual	SNV	56	5	61	0.082	61	14	75	0.187	link	-	Usp15	c.2764-68	-	ENSMUST	intron_variant
11	3185677	.	G	A	weak_evid	SNV	92	1	93	0.011	148	7	155	0.045	link	-	Sfi1	c.266+388	-	ENSMUST	intron_variant
11	3979005	.	T	G	base_qual	SNV	77	0	77	0	56	14	70	0.2	link	-	Pes1	c.*95T>G	-	ENSMUST	3_prime_UTR_variant
11	3979005	.	T	G	base_qual	SNV	77	0	77	0	56	14	70	0.2	link	-	4930556J2	c.-2603A>	-	ENSMUST	upstream_gene_variant
11	3979005	.	T	G	base_qual	SNV	77	0	77	0	56	14	70	0.2	link	-	Gal3st1	c.-17916T	-	ENSMUST	upstream_gene_variant
11	4490851	.	A	C	base_qual	SNV	23	0	23	0	10	6	16	0.375	link	-	Mtmr3	c.1671+12	-	ENSMUST	intron_variant
11	4490852	.	A	C	base_qual	SNV	23	0	23	0	12	5	17	0.294	link	-	Mtmr3	c.1671+12	-	ENSMUST	intron_variant
11	35564730	.	T	G	base_qual	SNV	151	4	155	0.026	153	14	167	0.084	link	-	Slit3	c.629+34T	-	ENSMUST	intron_variant
11	49811134	.	G	A	weak_evid	SNV	62	0	62	0	76	3	79	0.038	link	-	Gfpt2	c.399+112	-	ENSMUST	intron_variant
11	61378431	.	G	A	PASS	SNV	72	0	72	0	82	5	87	0.057	link	-	Slc47a1	c.-384C>T	-	ENSMUST	upstream_gene_variant
11	61378431	.	G	A	PASS	SNV	72	0	72	0	82	5	87	0.057	link	-	-	n.6137843	-	-	intergenic_region
11	65873873	.	T	G	weak_evid	SNV	5	0	5	0	1	3	4	0.75	link	-	Dnah9	c.11594+2	-	ENSMUST	intron_variant
11	67087107	.	T	C	PASS	SNV	24	0	24	0	31	8	39	0.205	link	-	Myh3	c.1142-13	-	ENSMUST	intron_variant
11	68556997	.	C	A	PASS	SNV	257	0	257	0	275	25	300	0.083	link	-	Pik3r6	c.*4953C>	-	ENSMUST	downstream_gene_variant
11	68998216	.	C	A	too_few_s	SNV	10	0	10	0	16	2	18	0.111	link	-	Gm25819	n.*2131C>	-	ENSMUST	downstream_gene_variant
11	68998216	.	C	A	too_few_s	SNV	10	0	10	0	16	2	18	0.111	link	-	Pfas	c.1076-17	-	ENSMUST	intron_variant
11	69846876	.	G	C	base_qual	SNV	23	3	26	0.115	25	14	39	0.359	link	-	Plscr3	c.-193G>C	-	ENSMUST	5_prime_UTR_variant
11	69846876	.	G	C	base_qual	SNV	23	3	26	0.115	25	14	39	0.359	link	-	Tnk1	c.*4726C>	-	ENSMUST	downstream_gene_variant
11	69902226	.	T	G	base_qual	SNV	107	8	115	0.07	89	10	99	0.101	link	-	2810408A	c.-1475A>	-	ENSMUST	upstream_gene_variant
11	69902226	.	T	G	base_qual	SNV	107	8	115	0.07	89	10	99	0.101	link	-	Neurl4	c.288+41T	-	ENSMUST	intron_variant
11	70845081	.	A	C	base_qual	SNV	42	3	45	0.067	58	8	66	0.121	link	-	Rabep1	c.34+73A	-	ENSMUST	intron_variant
11	74843440	.	A	C	base_qual	SNV	106	5	111	0.045	112	10	122	0.082	link	-	Mnt	c.*120A>C	-	ENSMUST	3_prime_UTR_variant
11	80389857	.	T	G	base_qual	SNV	141	0	141	0	154	11	165	0.067	link	-	Zfp207	c.599+36T	-	ENSMUST	intron_variant
11	93886441	.	T	G	base_qual	SNV	126	9	135	0.067	129	12	141	0.085	link	-	Utp18	c.-784A>C	-	ENSMUST	upstream_gene_variant
11	93886441	.	T	G	base_qual	SNV	126	9	135	0.067	129	12	141	0.085	link	-	Mbtd1	c.-47+379	-	ENSMUST	intron_variant
11	94242291	.	T	A	non_homr	SNV	17	1	18	0.056	31	0	31	0	link	-	Wfikkn2	c.195+64A	-	ENSMUST	intron_variant
11	1E+08	.	T	G	weak_evid	SNV	8	0	8	0	12	3	15	0.2	link	-	Krt17	c.-4990A>	-	ENSMUST	upstream_gene_variant
11	1E+08	.	T	G	weak_evid	SNV	8	0	8	0	12	3	15	0.2	link	-	Krt42	c.703-194	-	ENSMUST	intron_variant
11	1.02E+08	.	G	C	base_qual	SNV	59	2	61	0.033	60	9	69	0.13	link	-	Mpp2	c.1201+45	-	ENSMUST	intron_variant
11	1.03E+08	.	A	C	non_homr	SNV	37	4	41	0.098	59	5	64	0.078	link	-	Fzd2	c.-72A>C	-	ENSMUST	5_prime_UTR_variant
11	1.06E+08	.	A	C	weak_evid	SNV	35	0	35	0	46	4	50	0.08	link	-	Gm11651	n.157+415	-	ENSMUST	intron_variant
11	1.06E+08	.	A	C	weak_evid	SNV	35	0	35	0	46	4	50	0.08	link	-	Ace	c.2657-11	-	ENSMUST	intron_variant
11	1.06E+08	.	A	C	base_qual	SNV	53	3	56	0.054	47	11	58	0.19	link	-	Map3k3	c.-134A>C	-	ENSMUST	5_prime_UTR_variant
11	1.1E+08	.	T	G	base_qual	SNV	44	0	44	0	55	13	68	0.191	link	-	Abca8b	c.-6-120A	-	ENSMUST	intron_variant
11	1.15E+08	.	A	C	base_qual	SNV	19	0	19	0	14	5	19	0.263	link	-	Dnaic2	c.611-180	-	ENSMUST	intron_variant
11	1.15E+08	.	A	C	base_qual	SNV	65	0	65	0	53	12	65	0.185	link	-	Hid1	c.217-88T	-	ENSMUST	intron_variant
11	1.16E+08	.	C	T	weak_evid	SNV	37	0	37	0	45	3	48	0.062	link	-	Fbf1	c.*5059G>	-	ENSMUST	downstream_gene_variant
11	1.16E+08	.	C	T	weak_evid	SNV	37	0	37	0	45	3	48	0.062	link	-	Mrpl38	c.247+118	-	ENSMUST	intron_variant
11	1.21E+08	.	C	T	too_few_s	SNV	16	0	16	0	10	2	12	0.167	link	-	Rac3	c.-191C>T	-	ENSMUST	upstream_gene_variant
11	1.21E+08	.	C	T	too_few_s	SNV	16	0	16	0	10	2	12	0.167	link	-	Lrrc45	c.*602C>T	-	ENSMUST	downstream_gene_variant
11	1.21E+08	.	C	T	too_few_s	SNV	16	0	16	0	10	2	12	0.167	link	-	Dcxr	c.*4088G>	-	ENSMUST	downstream_gene_variant
11	1.21E+08	.	C	T	too_few_s	SNV	16	0	16	0	10	2	12	0.167	link	-	-	n.1207214	-	-	intergenic_region
12	31526422	.	C	A	base_qual	SNV	11	2	13	0.154	11	4	15	0.267	link	-	Slc26a4	c.2089+17	-	ENSMUST	intron_variant
12	55379133	.	C	A	alt_allele_i	SNV	6	1	7	0.143	12	4	16	0.25	link	-	1110008L	c.1416-14	-	ENSMUST	intron_variant
12	69250612	.	G	T	alt_allele_i	SNV	20	6	26	0.231	17	9	26	0.346	link	-	Klhdc1	c.97-141G	-	ENSMUST	intron_variant
12	73997876	.	T	G	base_qual	SNV	198	6	204	0.029	200	13	213	0.061	link	-	Syt16	c.13+13T	-	ENSMUST	intron_variant
12	1.04E+08	.	T	G	base_qual	SNV	69	0	69	0	57	12	69	0.174	link	-	Serpina3g	c.-376-22	-	ENSMUST	intron_variant
12	1.11E+08	.	C	G	weak_evid	SNV	31	3	34	0.088	27	4	31	0.129	link	-	Cdc42bpb	c.2347-15	-	ENSMUST	intron_variant
12	1.12E+08	.	T	G	base_qual	SNV	51	0	51	0	27	10	37	0.27	link	-	Klc1	c.1651-13	-	ENSMUST	intron_variant
13	3854823	.	A	C	base_qual	SNV	37	0	37	0	34	14	48	0.292	link	-	Calm5	c.*93A>C	-	ENSMUST	downstream_gene_variant
13	3854823	.	A	C	base_qual	SNV	37	0	37	0	34	14	48	0.292	link	-	Calm5	n.3854823	-	-	intragenic_variant
13	4191338	.	A	C	base_qual	SNV	237	0	237	0	212	22	234	0.094	link	-	Akr1c13	c.84+28A	-	ENSMUST	intron_variant
13	4581115	.	T	G	base_qual	SNV	104	0	104	0	94	18	112	0.161	link	-	Akr1c21	c.681-33T	-	ENSMUST	intron_variant
13	14270890	.	G	T	base_qual	SNV	100	2	102	0.02	92	6	98	0.061	link	-	Hecw1	c.3625+69	-	ENSMUST	intron_variant
13	17804822	.	T	G	base_qual	SNV	90	4	94	0.043	96	7	103	0.068	link	-	Cdk13	c.-171A>C	-	ENSMUST	5_prime_UTR_variant
13	17804822	.	T	G	base_qual	SNV	90	4	94	0.043	96	7	103	0.068	link	-	Gm24018	n.*4769A>	-	ENSMUST	downstream_gene_variant
13	41191764	.	T	G	alt_allele_i	SNV	31	7	38	0.184	22	11	33	0.333	link	-	Elovl2	c.333+124	-	ENSMUST	intron_variant
13	41197228	.	T	A	PASS	SNV	136	0	136	0	148	8	156	0.051	link	-	Elovl2	c.4-30A>T	-	ENSMUST	intron_variant
13	54762818	.	T	G	base_qual	SNV	117	1	118	0.008	103	4	107	0.037	link	-	Sncb	c.161-57A	-	ENSMUST	intron_variant
13	73689229	.	T	G	base_qual	SNV	84	4	88	0.045	92	14	106	0.132	link	-	Slc6a19	c.775-72A	-	ENSMUST	intron_variant
13	81687300	.	G	T	base_qual	SNV	49	3	52	0.058	36	10	46	0.217	link	-	Polr3g	c.308-124	-	ENSMUST	intron_variant
13	92503787	.	T	A	too_few_s	SNV	19	0	19	0	15	2	17	0.118	link	-	Zfyve16	c.3907+15	-	ENSMUST	intron_variant
13	1.12E+08	.	A	C	base_qual	SNV	83	3	86	0.035	80	1	81	0.012	link	-	Mier3	c.9+631A	-	ENSMUST	intron_variant
13	1.14E+08	.	C	G	alt_allele_i	SNV	18	5	23	0.217	16	12	28	0.429	link	-	Arl15	c.48+150C	-	ENSMUST	intron_variant
14	24308167	.	C	A	base_qual	SNV	62	3	65	0.046	92	5	97	0.052	link	-	E330034G	c.862-35C	-	ENSMUST	intron_variant
14	26855075	.	T	C	PASS	SNV	31	0	31	0	34	7	41	0.171	link	-	Dnah12	n.2685507	-	-	intragenic_variant
14	27480554	.	A	C	PASS	SNV	83	0	83	0	81	4	85	0.047	link	-	Ccdc66	c.*1962T>	-	ENSMUST	downstream_gene_variant
14	27480554	.	A	C	PASS	SNV	83	0	83	0	81	4	85	0.047	link	-	Fam208a	c.4442-88	-	ENSMUST	intron_variant
14	34220300	.	T	G	base_qual	SNV	86	0	86	0	95	11	106	0.104	link	-	Syt15	c.7+120T	-	ENSMUST	intron_variant
14	41642983	.	A	G	low_frac_i	SNV	10	0	10	0	8	4	12	0.333	link	-	Gm3676	c.490+224	-	ENSMUST	intron_variant
14	44858482	.	C	T	PASS	SNV	248	0	248	0	246	20	266	0.075	link	-	Gm16976	n.-189C>T	-	ENSMUST	upstream_gene_variant
14	50187262	.	T	C	PASS	SNV	140	0	140	0	113	5	118	0.042	link	-	Olfr730	c.-44A>G	-	ENSMUST	upstream_gene_variant
14	50187262	.	T	C	PASS	SNV	140	0	140	0	113	5	118	0.042	link	-	-	n.5018726	-	-	intergenic_region
14	51255968	.	T	G	base_qual	SNV	86	0	86	0	95	19	114	0.167	link	-	Rnase2a	c.-5-57A>	-	ENSMUST	intron_variant

14	51456291	.	A	G	mapping_q	SNV	293	5	298	0.017	311	3	314	0.01	link	-	Gm7247	c.255-655;	-	ENSMUST	intron_variant
14	52006676	.	T	G	base_qual	SNV	85	9	94	0.096	79	18	97	0.186	link	-	Arhgef40	c.*1646T>	-	ENSMUST	downstream_gene_variant
14	53444056	.	C	A	PASS	SNV	13	0	13	0	12	3	15	0.2	link	-	Trav7-3	c.*217C>A	-	ENSMUST	downstream_gene_variant
14	53444056	.	C	A	PASS	SNV	13	0	13	0	12	3	15	0.2	link	-	-	n.5344405	-	-	intergenic_region
14	55588346	.	T	G	base_qual	SNV	155	6	161	0.037	143	14	157	0.089	link	-	Emc9	c.-3237A>	-	ENSMUST	upstream_gene_variant
14	55588346	.	T	G	base_qual	SNV	155	6	161	0.037	143	14	157	0.089	link	-	Rnf31	c.-3538T>	-	ENSMUST	upstream_gene_variant
14	55588346	.	T	G	base_qual	SNV	155	6	161	0.037	143	14	157	0.089	link	-	Psme2	c.430-46A	-	ENSMUST	intron_variant
14	62674307	.	T	G	base_qual	SNV	220	0	220	0	188	29	217	0.134	link	-	Ints6	c.*19274A	-	ENSMUST	downstream_gene_variant
14	78849162	.	A	C	base_qual	SNV	52	2	54	0.037	56	5	61	0.082	link	-	Vwa8	c.-122A>C	-	ENSMUST	upstream_gene_variant
14	78849162	.	A	C	base_qual	SNV	52	2	54	0.037	56	5	61	0.082	link	-	-	n.7884916	-	-	intergenic_region
14	79197597	.	A	C	base_qual	SNV	68	0	68	0	59	10	69	0.145	link	-	Vwa8	c.5370+87	-	ENSMUST	intron_variant
14	79767545	.	C	T	PASS	SNV	275	0	275	0	222	29	251	0.116	link	-	Gm9748	n.-2363C>	-	ENSMUST	upstream_gene_variant
14	1.02E+08	.	A	C	weak_evid	SNV	8	0	8	0	11	3	14	0.214	link	-	Commd6	c.-242T>G	-	ENSMUST	5_prime_UTR_variant
15	10537735	.	A	C	base_qual	SNV	43	1	44	0.023	46	9	55	0.164	link	-	Ttc23l	c.522-74T	-	ENSMUST	intron_variant
15	34487393	.	C	T	too_few_s	SNV	5	0	5	0	1	2	3	0.667	link	-	Rida	c.226+349	-	ENSMUST	intron_variant
15	75900835	.	C	A	base_qual	SNV	73	4	77	0.052	62	12	74	0.162	link	-	Eef1d	c.1255-73(	-	ENSMUST	intron_variant
15	77098227	.	T	G	base_qual	SNV	16	0	16	0	13	4	17	0.235	link	-	1700109K	n.*1913T>	-	ENSMUST	downstream_gene_variant
15	77098227	.	T	G	base_qual	SNV	16	0	16	0	13	4	17	0.235	link	-	Rbfox2	c.959-143	-	ENSMUST	intron_variant
15	77755509	.	A	C	base_qual	SNV	10	2	12	0.167	13	5	18	0.278	link	-	Apol8	c.-2235T>	-	ENSMUST	upstream_gene_variant
15	77755509	.	A	C	base_qual	SNV	10	2	12	0.167	13	5	18	0.278	link	-	-	n.7775550	-	-	intergenic_region
15	78433146	.	A	C	non_homr	SNV	16	3	19	0.158	24	5	29	0.172	link	-	Kctd17	c.411+70A	-	ENSMUST	intron_variant
15	79623633	.	A	C	base_qual	SNV	22	4	26	0.154	17	8	25	0.32	link	-	Fam227a	c.1228-21	-	ENSMUST	intron_variant
15	79828038	.	A	C	base_qual	SNV	184	2	186	0.011	196	5	201	0.025	link	-	Npcd	c.537+650	-	ENSMUST	intron_variant
15	80014157	.	T	G	too_few_s	SNV	19	1	20	0.05	28	2	30	0.067	link	-	Pdgfb	c.-159A>C	-	ENSMUST	5_prime_UTR_premature_start_codon_gain_variant
15	80014157	.	T	G	too_few_s	SNV	19	1	20	0.05	28	2	30	0.067	link	-	Pdgfb	c.-159A>C	-	ENSMUST	5_prime_UTR_variant
15	80113375	.	A	C	base_qual	SNV	31	0	31	0	30	12	42	0.286	link	-	Syngr1	c.483+163	-	ENSMUST	intron_variant
15	80369534	.	T	G	weak_evid	SNV	84	5	89	0.056	61	13	74	0.176	link	-	Cacna1i	c.2019-48	-	ENSMUST	intron_variant
15	84950936	rs3235446	C	T	PASS	SNV	28	0	28	0	26	3	29	0.103	link	-	Mir1249	n.*590G>A	-	ENSMUST	downstream_gene_variant
15	84950936	rs3235446	C	T	PASS	SNV	28	0	28	0	26	3	29	0.103	link	-	5031439G	c.982-162	-	ENSMUST	intron_variant
15	97867105	.	A	C	base_qual	SNV	77	9	86	0.105	77	5	82	0.061	link	-	Vdr	c.740+12T	-	ENSMUST	intron_variant
15	98123964	.	T	G	too_few_s	SNV	44	2	46	0.043	20	2	22	0.091	link	-	Pfkm	c.1062+43	-	ENSMUST	intron_variant
15	99593436	.	T	G	base_qual	SNV	78	0	78	0	72	8	80	0.1	link	-	Aqp5	c.612+107	-	ENSMUST	intron_variant
15	1.01E+08	.	A	C	base_qual	SNV	49	4	53	0.075	38	14	52	0.269	link	-	Acvr1b	c.91+50A>	-	ENSMUST	intron_variant
15	1.02E+08	.	C	T	PASS	SNV	174	0	174	0	155	28	183	0.153	link	-	Krt71	c.444+14(	-	ENSMUST	intron_variant
15	1.03E+08	.	A	C	base_qual	SNV	16	3	19	0.158	38	6	44	0.136	link	-	Itga5	c.*168T>G	-	ENSMUST	3_prime_UTR_variant
16	17405760	.	G	A	weak_evid	SNV	234	1	235	0.004	261	4	265	0.015	link	-	Snap29	c.-363G>A	-	ENSMUST	upstream_gene_variant
16	17405760	.	G	A	weak_evid	SNV	234	1	235	0.004	261	4	265	0.015	link	-	Pi4ka	c.-19+495	-	ENSMUST	intron_variant
16	32246767	.	A	C	base_qual	SNV	146	5	151	0.033	145	18	163	0.11	link	-	Wdr53	c.-5072A>	-	ENSMUST	upstream_gene_variant
16	32246767	.	A	C	base_qual	SNV	146	5	151	0.033	145	18	163	0.11	link	-	Gm25848	n.-2912T>	-	ENSMUST	upstream_gene_variant
16	33062479	.	A	C	base_qual	SNV	62	1	63	0.016	79	8	87	0.092	link	-	Lmln	c.-70A>C	-	ENSMUST	upstream_gene_variant
16	33062479	.	A	C	base_qual	SNV	62	1	63	0.016	79	8	87	0.092	link	-	Rpl35a	c.*2358A>	-	ENSMUST	downstream_gene_variant
16	33062479	.	A	C	base_qual	SNV	62	1	63	0.016	79	8	87	0.092	link	-	Gm17106	n.147+459	-	ENSMUST	intron_variant
16	44520668	.	T	G	base_qual	SNV	19	0	19	0	9	4	13	0.308	link	-	Boc	c.83-165A	-	ENSMUST	intron_variant
16	46458397	.	C	A	too_few_s	SNV	15	0	15	0	19	2	21	0.095	link	-	Nectin3	c.800-166(	-	ENSMUST	intron_variant
16	56614541	.	A	C	base_qual	SNV	32	0	32	0	20	9	29	0.31	link	-	Abi3bp	c.1748-14!	-	ENSMUST	intron_variant
16	78301946	.	T	G	base_qual	SNV	116	10	126	0.079	136	17	153	0.111	link	-	Cxadr	c.43+72T>	-	ENSMUST	intron_variant
16	78301946	.	T	G	base_qual	SNV	116	10	126	0.079	136	17	153	0.111	link	-	RP23-299I	n.7830194	-	-	intragenic_variant
16	93752795	.	A	C	base_qual	SNV	119	4	123	0.033	127	14	141	0.099	link	-	Dopey2	c.1015-40	-	ENSMUST	intron_variant
16	95987042	.	T	C	too_few_s	SNV	12	0	12	0	11	2	13	0.154	link	-	Psmg1	c.459+251	-	ENSMUST	intron_variant
17	3115502	.	A	C	base_qual	SNV	29	0	29	0	33	7	40	0.175	link	-	Scaf8	c.30+84A>	-	ENSMUST	intron_variant
17	15731070	.	A	C	base_qual	SNV	63	3	66	0.045	83	10	93	0.108	link	-	Chd1	c.853+53A	-	ENSMUST	intron_variant
17	17374862	.	T	G	too_few_s	SNV	21	0	21	0	16	2	18	0.111	link	-	Chd1	n.1737486	-	-	intragenic_variant
17	18914164	.	C	A	base_qual	SNV	10	1	11	0.091	22	5	27	0.185	link	-	Vmn2r97	c.-158C>A	-	ENSMUST	upstream_gene_variant
17	18914164	.	C	A	base_qual	SNV	10	1	11	0.091	22	5	27	0.185	link	-	-	n.1891416	-	-	intergenic_region
17	23297057	rs2263706	T	C	mapping_q	SNV	93	4	97	0.041	101	10	111	0.09	link	-	Vmn2r114	c.1528-69	-	ENSMUST	intron_variant
17	23297063	rs2465486	A	G	mapping_q	SNV	88	4	92	0.043	97	10	107	0.093	link	-	Vmn2r114	c.1528-75'	-	ENSMUST	intron_variant
17	23297064	rs2655294	C	T	mapping_q	SNV	88	4	92	0.043	96	10	106	0.094	link	-	Vmn2r114	c.1528-76(	-	ENSMUST	intron_variant
17	23297126	.	T	G	mapping_q	SNV	28	1	29	0.034	43	9	52	0.173	link	-	Vmn2r114	c.1528-13(	-	ENSMUST	intron_variant
17	23309581	rs1131867	A	G	fragment_	SNV	6	0	6	0	8	3	11	0.273	link	-	Vmn2r114	c.1299+24	-	ENSMUST	intron_variant
17	23309609	rs1132234	G	A	fragment_	SNV	9	0	9	0	15	2	17	0.118	link	-	Vmn2r114	c.1299+21	-	ENSMUST	intron_variant
17	23344314	rs1133342	C	G	fragment_	SNV	33	0	33	0	33	7	40	0.175	link	-	Vmn2r115	c.197+141	-	ENSMUST	intron_variant
17	23345405	rs1132132	C	T	PASS	SNV	64	3	67	0.045	88	7	95	0.074	link	-	Vmn2r115	c.489+61C	-	ENSMUST	intron_variant
17	23345407	rs5199762	C	T	non_homr	SNV	65	3	68	0.044	88	6	94	0.064	link	-	Vmn2r115	c.489+63C	-	ENSMUST	intron_variant
17	23345428	rs2222125	A	G	weak_evid	SNV	47	3	50	0.06	81	6	87	0.069	link	-	Vmn2r115	c.489+84A	-	ENSMUST	intron_variant
17	23345437	rs1132480	A	T	weak_evid	SNV	46	3	49	0.061	81	6	87	0.069	link	-	Vmn2r115	c.489+93A	-	ENSMUST	intron_variant
17	23345453	rs1132901	G	A	non_homr	SNV	42	3	45	0.067	72	5	77	0.065	link	-	Vmn2r115	c.489+109	-	ENSMUST	intron_variant
17	23345454	rs1133839	T	A	non_homr	SNV	42	3	45	0.067	73	5	78	0.064	link	-	Vmn2r115	c.489+110	-	ENSMUST	intron_variant
17	23345458	rs1132589	T	C	non_homr	SNV	40	3	43	0.07	67	5	72	0.069	link	-	Vmn2r115	c.489+114	-	ENSMUST	intron_variant
17	23360541	.	A	C	weak_evid	SNV	5	0	5	0	2	4	6	0.667	link	-	Vmn2r115	c.*413A>C	-	ENSMUST	downstream_gene_variant
17	23360541	.	A	C	weak_evid	SNV	5	0	5	0	2	4	6	0.667	link	-	-	n.2336054	-	-	intergenic_region
17	23998324	.	T	G	weak_evid	SNV	7	0	7	0	4	4	8	0.5	link	-	Prss22	c.-320A>C	-	ENSMUST	upstream_gene_variant
17	23998324	.	T	G	weak_evid	SNV	7	0	7	0	4	4	8	0.5	link	-	-	n.2399832	-	-	intergenic_region
17	24250991	.	G	A	too_few_s	SNV	10	0	10	0	16	2	18	0.111	link	-	Ccnf	c.16+304C	-	ENSMUST	intron_variant
17	24689566	.	A	C	base_qual	SNV	22	2	24	0.083	21	6	27	0.222	link	-	Gfer	c.*4714T>	-	ENSMUST	downstream_gene_variant
17	24689566	.	A	C	base_qual	SNV	22	2	24	0.083	21	6	27	0.222	link	-	Syngr3	c.99+155T	-	ENSMUST	intron_variant
17	34190525	.	A	C	weak_evid	SNV	119	0	119	0	115	6	121	0.05	link	-	Psmb9	c.-3216T>	-	ENSMUST	upstream_gene_variant
17	34190525	.	A	C	weak_evid	SNV	119	0	119	0	115	6	121	0.05	link	-	Tap1	c.773-38A	-	ENSMUST	intron_variant
17	36020680	.	T	G	weak_evid	SNV	8	1	9	0.111	6	5	11	0.455	link	-	H2-T24	c.-169A>C	-	ENSMUST	upstream_gene_variant
17	36020680	.	T	G	weak_evid	SNV	8	1	9	0.111	6	5	11	0.455	link	-	A930015D	n.109-167	-	ENSMUST	intron_variant
17	42316279	.	A	G	weak_evid	SNV	286	1	287	0.003	266	4	270	0.015	link	-	Ptchd4	c.-26A>G	-	ENSMUST	5_prime_UTR_variant
17	45591947	.	T	C	PASS	SNV	18	0	18	0	25	5	30	0.167	link	-	Gm17080	n.*3570T>	-	ENSMUST	downstream_gene_variant
17	45591947	.	T	C	PASS	SNV	18	0	18	0	25	5	30	0.167	link	-	Slc29a1	c.29+232A	-	ENSMUST	intron_variant
17	53610751	.	C	A	base_qual	SNV	28	7	35	0.2	34	6	40	0.15	link	-	Kat2b	c.250-113(	-	ENSMUST	intron_variant
17	56040404	.	A	C	base_qual	SNV	87	3	90	0.033	87	5	92	0.054	link	-	Sh3gl1	c.-3945T>	-	ENSMUST	upstream_gene_variant
17	56040404	.	A	C	base_qual	SNV	87	3	90	0.033	87	5	92	0.054	link	-	Chaf1a	c.-108A>C	-	ENSMUST	upstream_gene_variant
17	56040404	.	A	C	base_qual	SNV	87	3	90	0.033	87	5	92	0.054	link	-	-	n.5604040	-	-	intergenic_region
17	57361789	.	T	G	weak_evid	SNV	120	2	122	0.016	121	4	125	0.032	link	-	Adgre1	c.94+55T>	-	ENSMUST	intron_variant
17	73345568	.	A	C	base_qual	SNV	21	2	23	0.087	15	4	19	0.211	link	-	Capn13	c.769-344	-	ENSMUST	intron_variant
17	74721493	.	C	A	base_qual	SNV	109	4	113	0.035	119	8	127	0.063	link	-	Ttc27	c.279-28C	-	ENSMUST	intron_variant
17	90036962	.	C	A	base_qual	SNV	23	1	24	0.042	33	4	37	0.108	link	-	Nrxn1	c.*115G>T	-	ENSMUST	3_prime_UTR_variant
18	13971343	.	A	C	base_qual	SNV	142	2	144	0.014	142	7	149	0.047	link	-	Zfp521	c.40+21T>	-	ENSMUST	intron_variant
18	35771947	.	T	G	base_qual	SNV	89	13	102	0.127	119	22	141	0.156	link	-	Ube2d2a	c.-42T>G	-	ENSMUST	5_prime_UTR_variant
18	35771947	.	T	G	base_qual	SNV	89	13	102	0.127	119	22	141	0.156	link	-	Gm16490	n.*1279T>	-	ENSMUST	downstream_gene_variant
18	36939510	.	A	G	PASS	SNV	483	0	483	0	444	92	536	0.172	link	-	Gm37751	n.-4361T>	-	ENSMUST	upstream_gene_variant
18	36939510	.	A	G	PASS	SNV	483	0	483	0	444	92	536	0.172	link	-	Pcdha1	c.2388+68	-	ENSMUST	intron_variant
18	38460779	.	T	G	base_qual	SNV	37	0	37	0	25	4	29	0.138	link	-	Ndfip1	c.*2+129T	-	ENSMUST	intron_variant
18	44104842	.	C	A	PASS	SNV	82	0	82	0	87	14	101	0.139	link	-	Spink12	c.115+71C	-	ENSMUST	intron_variant
18	44493607	.	T	G	base_qual	SNV	52	0	52	0	43	16	59	0.271	link	-	Mcc	c.983-62A	-	ENSMUST	intron_variant
18	60833206	.	A	C	base_qual	SNV	10	1	11	0.091	9	4	13	0.308	link	-	Tcof1	c.1098+21	-	ENSMUST	intron_variant
18	61707786	.	T	C	too_few_s	SNV	13	0	13	0	16	2	18	0.111	link	-	Pcyox1l	c.-205A>C	-	ENSMUST	upstream_gene_variant
18	61707786	.	T	C	too_few_s	SNV	13	0	13	0	16	2	18	0.111	link	-	Grpel2	c.*7977A>	-	ENSMUST	downstream_gene_variant
18	61707786	.	T	C	too_few_s	SNV	13	0	13	0	16	2	18	0.111	link	-	-	n.6170778	-	-	intergenic_region
18	70469359	.	C	A	base_qual	SNV	33	1	34	0.029	34	7	41	0.171	link	-	Stard6	c.-6745C>	-	ENSMUST	upstream_gene_variant
18	70469359	.	C	A	base_qual	SNV	33	1	34	0.029	34	7	41	0.171	link	-	4930503L	c.292+90(	-	ENSMUST	intron_variant
18	82405431	.	T	A	weak_evid	SNV	68	0	68	0	72	3	75	0.04	link	-	Galr1	c.663+57A	-	ENSMUST	intron_variant
19	4612149	.	A	C	base_qual	SNV	277	12	289	0.042	273	18	291	0.062	link	-	Pcx	c.1371+21	-	ENSMUST	intron_variant
19	6414920	.	A	C	weak_evid	SNV	62	2	64	0.031	62	3	65	0.046	link	-	Gm14965	n.*1890T>	-	ENSMUST	downstream_gene_variant
19	6414920	.	A	C	weak_evid	SNV	62	2	64	0.031	62	3	65	0.046	link	-	Rasgrp2	c.*4+66A>	-	ENSMUST	intron_variant

19	6414920	.	A	C	weak_evid	SNV	62	2	64	0.031	62	3	65	0.046	link	-	Gm14965	n.6414920	-	-	intragenic_variant
19	8756994	.	T	G	base_qual	SNV	13	3	16	0.188	6	5	11	0.455	link	-	Nxf1	c.-238T>C	-	ENSMUST	upstream_gene_variant
19	8756994	.	T	G	base_qual	SNV	13	3	16	0.188	6	5	11	0.455	link	-	Stx5a	c.*1697T>	-	ENSMUST	downstream_gene_variant
19	8756994	.	T	G	base_qual	SNV	13	3	16	0.188	6	5	11	0.455	link	-	-	n.8756994	-	-	intergenic_region
19	25060993	.	C	A	base_qual	SNV	16	3	19	0.158	27	10	37	0.27	link	-	Dock8	c.157-115(	-	ENSMUST	intron_variant
19	29949587	.	T	G	base_qual	SNV	67	3	70	0.043	74	9	83	0.108	link	-	Il33	c.-11-73T:	-	ENSMUST	intron_variant
19	45779204	.	G	A	PASS	SNV	44	0	44	0	37	8	45	0.178	link	-	Mgea5	c.200-121(	-	ENSMUST	intron_variant
19	53032204	.	T	G	base_qual	SNV	11	1	12	0.083	2	3	5	0.6	link	-	Xpnpep1	c.33-107A	-	ENSMUST	intron_variant
19	59060541	.	T	G	base_qual	SNV	81	3	84	0.036	45	4	49	0.082	link	-	Shtn1	c.111+90A	-	ENSMUST	intron_variant
2	11227016	.	A	C	base_qual	SNV	36	5	41	0.122	33	6	39	0.154	link	-	Gm37766	n.-281A>C	-	ENSMUST	upstream_gene_variant
2	11227016	.	A	C	base_qual	SNV	36	5	41	0.122	33	6	39	0.154	link	-	Prkcq	c.118+31A	-	ENSMUST	intron_variant
2	23120423	.	C	T	weak_evid	SNV	137	0	137	0	126	3	129	0.023	link	-	Mastl	c.2440+34	-	ENSMUST	intron_variant
2	26394898	.	A	C	base_qual	SNV	32	0	32	0	31	6	37	0.162	link	-	Inpp5e	c.*2941T>	-	ENSMUST	downstream_gene_variant
2	26394898	.	A	C	base_qual	SNV	32	0	32	0	31	6	37	0.162	link	-	Pmpca	c.1261-12'	-	ENSMUST	intron_variant
2	27452875	.	T	C	weak_evid	SNV	173	1	174	0.006	193	4	197	0.02	link	-	Mir7578	n.-2245A>	-	ENSMUST	upstream_gene_variant
2	32630487	.	T	G	PASS	SNV	13	0	13	0	4	5	9	0.556	link	-	Ak1	c.255+89T	-	ENSMUST	intron_variant
2	37786892	.	A	C	base_qual	SNV	97	1	98	0.01	110	6	116	0.052	link	-	Crb2	c.766+35A	-	ENSMUST	intron_variant
2	65748516	.	A	C	base_qual	SNV	47	7	54	0.13	58	12	70	0.171	link	-	Scn2a1	c.4449+85	-	ENSMUST	intron_variant
2	66493388	.	G	A	too_few_s	SNV	11	0	11	0	16	2	18	0.111	link	-	Gm13629	n.535+883	-	ENSMUST	intron_variant
2	66493388	.	G	A	too_few_s	SNV	11	0	11	0	16	2	18	0.111	link	-	Scn9a	c.4255-17(	-	ENSMUST	intron_variant
2	69873700	.	A	C	base_qual	SNV	14	0	14	0	12	6	18	0.333	link	-	Gm13625	n.-1498T>	-	ENSMUST	upstream_gene_variant
2	69873700	.	A	C	base_qual	SNV	14	0	14	0	12	6	18	0.333	link	-	Ssb	c.*2490A>	-	ENSMUST	downstream_gene_variant
2	69873700	.	A	C	base_qual	SNV	14	0	14	0	12	6	18	0.333	link	-	Mettl5	c.541+184	-	ENSMUST	intron_variant
2	69873703	.	A	C	PASS	SNV	14	0	14	0	12	8	20	0.4	link	-	Gm13625	n.-1501T>	-	ENSMUST	upstream_gene_variant
2	69873703	.	A	C	PASS	SNV	14	0	14	0	12	8	20	0.4	link	-	Ssb	c.*2493A>	-	ENSMUST	downstream_gene_variant
2	69873703	.	A	C	PASS	SNV	14	0	14	0	12	8	20	0.4	link	-	Mettl5	c.541+181	-	ENSMUST	intron_variant
2	82053713	.	A	C	base_qual	SNV	59	4	63	0.063	61	9	70	0.129	link	-	Zfp804a	c.-78A>C	-	ENSMUST	5_prime_UTR_variant
2	85353982	.	T	G	base_qual	SNV	79	1	80	0.013	91	12	103	0.117	link	-	Olfr988	c.-58A>C	-	ENSMUST	5_prime_UTR_variant
2	90580662	.	T	G	base_qual	SNV	60	3	63	0.048	66	10	76	0.132	link	-	Ptprj	c.-75A>C	-	ENSMUST	upstream_gene_variant
2	90580662	.	T	G	base_qual	SNV	60	3	63	0.048	66	10	76	0.132	link	-	-	n.9058066	-	-	intergenic_region
2	93434073	.	C	A	base_qual	SNV	22	2	24	0.083	15	4	19	0.211	link	-	Cd82	c.64-140G	-	ENSMUST	intron_variant
2	1.03E+08	.	T	C	PASS	SNV	134	0	134	0	123	19	142	0.134	link	-	Pamr1	c.821-29T	-	ENSMUST	intron_variant
2	1.03E+08	.	A	C	base_qual	SNV	219	12	231	0.052	218	24	242	0.099	link	-	Gm13872	n.*3814T>	-	ENSMUST	downstream_gene_variant
2	1.03E+08	.	A	C	base_qual	SNV	219	12	231	0.052	218	24	242	0.099	link	-	Gm13872	n.1027398	-	-	intragenic_variant
2	1.04E+08	.	C	A	base_qual	SNV	32	5	37	0.135	16	6	22	0.273	link	-	D430041D	c.2098-12'	-	ENSMUST	intron_variant
2	1.25E+08	.	A	C	too_few_s	SNV	8	1	9	0.111	11	2	13	0.154	link	-	Fbn1	c.3845-18(	-	ENSMUST	intron_variant
2	1.27E+08	.	C	T	too_few_s	SNV	6	0	6	0	21	2	23	0.087	link	-	1810024B	c.-24690G	-	ENSMUST	upstream_gene_variant
2	1.27E+08	.	C	T	too_few_s	SNV	6	0	6	0	21	2	23	0.087	link	-	Snrnp200	c.574+175	-	ENSMUST	intron_variant
2	1.28E+08	.	G	T	base_qual	SNV	88	1	89	0.011	100	4	104	0.038	link	-	Prom2	c.2043+75	-	ENSMUST	intron_variant
2	1.28E+08	.	A	C	base_qual	SNV	99	3	102	0.029	102	14	116	0.121	link	-	Bub1	c.1838-51'	-	ENSMUST	intron_variant
2	1.29E+08	.	T	G	base_qual	SNV	17	0	17	0	19	5	24	0.208	link	-	Zc3h6	c.741+177	-	ENSMUST	intron_variant
2	1.3E+08	.	C	A	base_qual	SNV	6	0	6	0	5	2	7	0.286	link	-	Tgm6	c.7+290C:	-	ENSMUST	intron_variant
2	1.36E+08	.	A	C	weak_evid	SNV	11	0	11	0	8	4	12	0.333	link	-	Plcb4	c.687-195(	-	ENSMUST	intron_variant
2	1.36E+08	.	A	C	base_qual	SNV	71	4	75	0.053	95	10	105	0.095	link	-	Plcb4	c.2779-12'	-	ENSMUST	intron_variant
2	1.52E+08	.	T	G	base_qual	SNV	7	0	7	0	7	2	9	0.222	link	-	Rspo4	c.79+252T	-	ENSMUST	intron_variant
2	1.54E+08	.	T	G	base_qual	SNV	15	0	15	0	8	6	14	0.429	link	-	Efcab8	n.1538414	-	-	intragenic_variant
2	1.56E+08	rs2204910	T	C	base_qual	SNV	28	7	35	0.2	24	8	32	0.25	link	-	Edem2	c.490+39A	-	ENSMUST	intron_variant
2	1.66E+08	.	T	G	base_qual	SNV	177	8	185	0.043	176	9	185	0.049	link	-	Slc2a10	c.4+38T>(	-	ENSMUST	intron_variant
2	1.68E+08	.	G	T	weak_evid	SNV	34	1	35	0.029	28	3	31	0.097	link	-	Rnf114	c.516+138	-	ENSMUST	intron_variant
2	1.74E+08	.	G	A	PASS	SNV	286	0	286	0	291	26	317	0.082	link	-	Nespas	n.-3230C>	-	ENSMUST	upstream_gene_variant
2	1.74E+08	.	G	A	PASS	SNV	286	0	286	0	291	26	317	0.082	link	-	Gm27869	n.*3474G>	-	ENSMUST	downstream_gene_variant
2	1.74E+08	.	G	A	PASS	SNV	286	0	286	0	291	26	317	0.082	link	-	Gm27849	n.*3205G>	-	ENSMUST	downstream_gene_variant
2	1.81E+08	.	G	A	too_few_s	SNV	10	0	10	0	13	2	15	0.133	link	-	Dido1	c.1153-18(	-	ENSMUST	intron_variant
3	15848049	.	G	A	weak_evid	SNV	6	0	6	0	8	6	14	0.429	link	-	Sirpb1c	c.73+292C	-	ENSMUST	intron_variant
3	15848659	.	C	T	mapping_(	SNV	8	0	8	0	13	3	16	0.188	link	-	Sirpb1c	c.-246G>A	-	ENSMUST	upstream_gene_variant
3	15848659	.	C	T	mapping_(	SNV	8	0	8	0	13	3	16	0.188	link	-	-	n.1584865	-	-	intergenic_region
3	35996084	.	C	A	too_few_s	SNV	16	0	16	0	15	2	17	0.118	link	-	Mccc1os	n.-3829C>	-	ENSMUST	upstream_gene_variant
3	35996084	.	C	A	too_few_s	SNV	16	0	16	0	15	2	17	0.118	link	-	Mccc1	c.125-167(	-	ENSMUST	intron_variant
3	52992686	.	T	C	PASS	SNV	68	0	68	0	52	11	63	0.175	link	-	Cog6	c.1584+69	-	ENSMUST	intron_variant
3	59276095	.	G	A	PASS	SNV	92	0	92	0	94	22	116	0.19	link	-	Gm43589	n.*4787G>	-	ENSMUST	downstream_gene_variant
3	59276095	.	G	A	PASS	SNV	92	0	92	0	94	22	116	0.19	link	-	Med12l	c.5856+61	-	ENSMUST	intron_variant
3	83356576	.	A	C	base_qual	SNV	27	0	27	0	27	8	35	0.229	link	-	Dchs2	c.*109A>C	-	ENSMUST	3_prime_UTR_variant
3	87789509	.	T	A	base_qual	SNV	46	3	49	0.061	64	14	78	0.179	link	-	Pear1	c.-70-291(	-	ENSMUST	intron_variant
3	87789509	.	T	A	base_qual	SNV	46	3	49	0.061	64	14	78	0.179	link	-	Ntrk1	c.428+108	-	ENSMUST	intron_variant
3	88115790	.	A	C	weak_evid	SNV	11	1	12	0.083	10	5	15	0.333	link	-	Iqgap3	c.4195-11(	-	ENSMUST	intron_variant
3	95190748	.	C	A	base_qual	SNV	87	3	90	0.033	66	9	75	0.12	link	-	Gabpb2	c.623-10G	-	ENSMUST	intron_variant
3	99984410	.	A	C	base_qual	SNV	110	3	113	0.027	106	18	124	0.145	link	-	Spag17	c.632-53A	-	ENSMUST	intron_variant
3	1.01E+08	.	T	G	base_qual	SNV	18	1	19	0.053	22	8	30	0.267	link	-	Vtcn1	c.725-148'	-	ENSMUST	intron_variant
3	1.03E+08	.	G	T	alt_allele_	SNV	15	3	18	0.167	32	11	43	0.256	link	-	Gm23820	n.*2375G>	-	ENSMUST	downstream_gene_variant
3	1.03E+08	.	G	T	alt_allele_	SNV	15	3	18	0.167	32	11	43	0.256	link	-	Ampd1	c.541+78(	-	ENSMUST	intron_variant
3	1.03E+08	.	T	G	base_qual	SNV	151	1	152	0.007	140	7	147	0.048	link	-	Trim33	c.-74T>G	-	ENSMUST	5_prime_UTR_variant
3	1.1E+08	.	T	G	base_qual	SNV	58	0	58	0	54	11	65	0.169	link	-	Ntng1	c.246+52A	-	ENSMUST	intron_variant
3	1.31E+08	.	A	C	base_qual	SNV	65	0	65	0	57	14	71	0.197	link	-	Etnppl	c.57-95A>	-	ENSMUST	intron_variant
3	1.39E+08	.	A	T	base_qual	SNV	62	4	66	0.061	61	7	68	0.103	link	-	Tspan5	c.82-101A	-	ENSMUST	intron_variant
3	1.42E+08	.	C	G	base_qual	SNV	42	7	49	0.143	30	11	41	0.268	link	-	Bmpr1b	c.586-86G	-	ENSMUST	intron_variant
3	1.54E+08	.	G	T	base_qual	SNV	51	2	53	0.038	68	8	76	0.105	link	-	Gm24395	n.-4001G>	-	ENSMUST	upstream_gene_variant
3	1.54E+08	.	G	T	base_qual	SNV	51	2	53	0.038	68	8	76	0.105	link	-	Msh4	c.2685+82	-	ENSMUST	intron_variant
4	3173761	rs1135307	G	A	mapping_(	SNV	22	1	23	0.043	18	9	27	0.333	link	-	Vmn1r2	c.*758G>A	-	ENSMUST	downstream_gene_variant
4	3173761	rs1135307	G	A	mapping_(	SNV	22	1	23	0.043	18	9	27	0.333	link	-	-	n.3173761	-	-	intergenic_region
4	3173808	rs1133793	C	G	mapping_(	SNV	14	0	14	0	13	5	18	0.278	link	-	Vmn1r2	c.*805C>G	-	ENSMUST	downstream_gene_variant
4	3173808	rs1133793	C	G	mapping_(	SNV	14	0	14	0	13	5	18	0.278	link	-	-	n.3173808	-	-	intergenic_region
4	3241918	.	C	T	mapping_(	SNV	167	6	173	0.035	192	11	203	0.054	link	-	AI838599	n.-4087C>	-	ENSMUST	upstream_gene_variant
4	3241918	.	C	T	mapping_(	SNV	167	6	173	0.035	192	11	203	0.054	link	-	-	n.3241918	-	-	intergenic_region
4	3241937	.	T	A	mapping_(	SNV	207	5	212	0.024	250	11	261	0.042	link	-	AI838599	n.-4068T>	-	ENSMUST	upstream_gene_variant
4	3241937	.	T	A	mapping_(	SNV	207	5	212	0.024	250	11	261	0.042	link	-	-	n.3241937	-	-	intergenic_region
4	40943739	.	A	C	base_qual	SNV	64	2	66	0.03	56	14	70	0.2	link	-	Chmp5	c.-4869A>	-	ENSMUST	upstream_gene_variant
4	40943739	.	A	C	base_qual	SNV	64	2	66	0.03	56	14	70	0.2	link	-	Bag1	c.611-32T	-	ENSMUST	intron_variant
4	45106512	.	T	G	base_qual	SNV	37	0	37	0	45	5	50	0.1	link	-	Tomm5	c.300+103	-	ENSMUST	intron_variant
4	47482918	.	T	G	base_qual	SNV	66	0	66	0	92	12	104	0.115	link	-	Sec61b	c.268-57T	-	ENSMUST	intron_variant
4	57088145	.	A	C	base_qual	SNV	91	0	91	0	84	12	96	0.125	link	-	Epb41l4b	c.455-81T	-	ENSMUST	intron_variant
4	58057769	.	C	A	non_homr	SNV	12	2	14	0.143	16	5	21	0.238	link	-	Svep1	c.9874+16	-	ENSMUST	intron_variant
4	59113833	.	T	A	PASS	SNV	63	1	64	0.016	80	6	86	0.07	link	-	AI481877	c.66+65A>	-	ENSMUST	intron_variant
4	63326364	.	G	T	base_qual	SNV	12	2	14	0.143	17	6	23	0.261	link	-	Col27a1	c.4827+21	-	ENSMUST	intron_variant
4	64006711	.	C	A	weak_evid	SNV	5	0	5	0	7	4	11	0.364	link	-	8030451A	n.137-172(	-	ENSMUST	intron_variant
4	64006711	.	C	A	weak_evid	SNV	5	0	5	0	7	4	11	0.364	link	-	Tnc	c.2951-20(	-	ENSMUST	intron_variant
4	83458024	.	T	G	base_qual	SNV	113	0	113	0	113	19	132	0.144	link	-	Snapc3	c.*4836T>	-	ENSMUST	downstream_gene_variant
4	83458024	.	T	G	base_qual	SNV	113	0	113	0	113	19	132	0.144	link	-	Psip1	c.1526+51	-	ENSMUST	intron_variant
4	83458024	.	T	G	base_qual	SNV	113	0	113	0	113	19	132	0.144	link	-	Snapc3	n.8345802	-	-	intragenic_variant
4	84884414	.	A	C	weak_evid	SNV	58	2	60	0.033	57	3	60	0.05	link	-	Cntln	c.-51A>C	-	ENSMUST	5_prime_UTR_variant
4	1.06E+08	.	C	T	low_norma	SNV	2	0	2	0	10	2	12	0.167	link	-	Usp24	c.-209C>T	-	ENSMUST	5_prime_UTR_variant
4	1.09E+08	.	T	G	base_qual	SNV	59	0	59	0	51	9	60	0.15	link	-	Orc1	c.1418+10	-	ENSMUST	intron_variant
4	1.09E+08	.	T	G	base_qual	SNV	59	0	59	0	51	9	60	0.15	link	-	Gm12743	n.629-117(	-	ENSMUST	intron_variant
4	1.17E+08	.	A	C	base_qual	SNV	15	3	18	0.167	41	12	53	0.226	link	-	Nasp	c.59+163T	-	ENSMUST	intron_variant
4	1.17E+08	.	A	C	too_few_s	SNV	15	0	15	0	22	2	24	0.083	link	-	Eif2b3	c.455-189(	-	ENSMUST	intron_variant
4	1.18E+08	.	G	T	base_qual	SNV	81	2	83	0.024	85	11	96	0.115	link	-	Klf17	c.845-21C	-	ENSMUST	intron_variant
4	1.18E+08	.	T	G	base_qual	SNV	103	0	103	0	111	17	128	0.133	link	-	Szt2	c.-3386A>	-	ENSMUST	upstream_gene_variant
4	1.18E+08	.	T	G	base_qual	SNV	103	0	103	0	111	17	128	0.133	link	-	Med8	c.411+83T>	-	ENSMUST	intron_variant
4	1.2E+08	.	T	G	base_qual	SNV	59	3	62	0.048	52	6	58	0.103	link	-	Guca2a	c.75+68T>	-	ENSMUST	intron_variant

4	1.23E+08	.	T	G	too_few_s	SNV	11	0	11	0	17	2	19	0.105	link	-	Gm25788	n.*4786T>	-	ENSMUST	downstream_gene_variant
4	1.23E+08	.	T	G	too_few_s	SNV	11	0	11	0	17	2	19	0.105	link	-	Gm22154	n.*2978T>	-	ENSMUST	downstream_gene_variant
4	1.23E+08	.	T	G	too_few_s	SNV	11	0	11	0	17	2	19	0.105	link	-	Pabpc4	c.1668+20	-	ENSMUST	intron_variant
4	1.24E+08	.	T	A	base_qual	SNV	55	2	57	0.035	70	10	80	0.125	link	-	Rhbdl2	c.-20-22T:	-	ENSMUST	intron_variant
4	1.25E+08	.	T	G	weak_evid	SNV	145	1	146	0.007	189	6	195	0.031	link	-	Gm27247	n.-560A>(	-	ENSMUST	upstream_gene_variant
4	1.26E+08	.	A	C	too_few_s	SNV	9	0	9	0	11	2	13	0.154	link	-	Trappc3	c.42+236A	-	ENSMUST	intron_variant
4	1.29E+08	.	A	C	base_qual	SNV	98	8	106	0.075	106	9	115	0.078	link	-	Csmd2	c.8147-12,	-	ENSMUST	intron_variant
4	1.29E+08	.	A	C	PASS	SNV	89	0	89	0	92	14	106	0.132	link	-	Zbtb8b	c.59+109T	-	ENSMUST	intron_variant
4	1.3E+08	.	C	A	base_qual	SNV	38	3	41	0.073	43	8	51	0.157	link	-	Snrnp40	c.862-132(	-	ENSMUST	intron_variant
4	1.34E+08	.	A	C	weak_evid	SNV	27	1	28	0.036	59	3	62	0.048	link	-	Gpn2	c.730-126,	-	ENSMUST	intron_variant
4	1.37E+08	.	A	C	base_qual	SNV	158	6	164	0.037	198	12	210	0.057	link	-	Cdc42	c.-51+454	-	ENSMUST	intron_variant
4	1.37E+08	.	A	C	base_qual	SNV	168	10	178	0.056	175	18	193	0.093	link	-	Cdc42	c.-51+68T	-	ENSMUST	intron_variant
4	1.38E+08	.	T	A	PASS	SNV	86	0	86	0	81	18	99	0.182	link	-	Eif4g3	c.4136-85'	-	ENSMUST	intron_variant
4	1.41E+08	.	A	C	base_qual	SNV	44	0	44	0	57	6	63	0.095	link	-	Padi4	c.273+32T	-	ENSMUST	intron_variant
4	1.42E+08	rs2488291	T	G	base_qual	SNV	115	8	123	0.065	133	6	139	0.043	link	-	AI507597	n.*2151T>	-	ENSMUST	downstream_gene_variant
4	1.42E+08	rs2488291	T	G	base_qual	SNV	115	8	123	0.065	133	6	139	0.043	link	-	Slc25a34	c.*2657A>	-	ENSMUST	downstream_gene_variant
4	1.42E+08	rs2488291	T	G	base_qual	SNV	115	8	123	0.065	133	6	139	0.043	link	-	Tmem82	c.89-43A>	-	ENSMUST	intron_variant
4	1.42E+08	.	T	G	base_qual	SNV	73	2	75	0.027	64	6	70	0.086	link	-	Fhad1	c.2586+26	-	ENSMUST	intron_variant
4	1.42E+08	.	A	C	base_qual	SNV	11	1	12	0.083	9	3	12	0.25	link	-	Kazn	c.816+202	-	ENSMUST	intron_variant
4	1.43E+08	.	G	T	alt_allele_	SNV	7	2	9	0.222	29	6	35	0.171	link	-	Pdpn	c.361+155	-	ENSMUST	intron_variant
4	1.46E+08	rs4765336	T	A	mapping_(	SNV	143	8	151	0.053	204	8	212	0.038	link	-	Zfp990	c.30+34T>	-	ENSMUST	intron_variant
4	1.46E+08	rs1133955	T	A	mapping_(	SNV	76	3	79	0.038	121	8	129	0.062	link	-	Zfp990	c.30+94T>	-	ENSMUST	intron_variant
4	1.46E+08	.	C	T	mapping_(	SNV	6	0	6	0	11	11	22	0.5	link	-	Gm13212	c.-76+738	-	ENSMUST	intron_variant
4	1.46E+08	.	G	A	mapping_(	SNV	29	3	32	0.094	29	16	45	0.356	link	-	Gm13212	c.-76+747	-	ENSMUST	intron_variant
4	1.46E+08	.	G	A	mapping_(	SNV	39	4	43	0.093	34	14	48	0.292	link	-	Gm13212	c.-76+748	-	ENSMUST	intron_variant
4	1.48E+08	rs1133479	A	T	mapping_(	SNV	135	3	138	0.022	159	5	164	0.03	link	-	Zfp985	c.31-623A	-	ENSMUST	intron_variant
4	1.48E+08	.	T	A	mapping_(	SNV	182	5	187	0.027	199	13	212	0.061	link	-	Zfp985	c.31-604T	-	ENSMUST	intron_variant
4	1.48E+08	.	T	A	non_homr	SNV	22	0	22	0	29	6	35	0.171	link	-	Zfp985	c.158-239'	-	ENSMUST	intron_variant
4	1.48E+08	rs1135049	G	C	weak_evid	SNV	46	2	48	0.042	63	4	67	0.06	link	-	Zfp985	c.*141G>(	-	ENSMUST	3_prime_UTR_variant
5	9422222	.	C	G	base_qual	SNV	90	7	97	0.072	78	17	95	0.179	link	-	9330182L(	c.998-80C	-	ENSMUST	intron_variant
5	14933603	.	G	A	weak_evid	SNV	8	1	9	0.111	22	6	28	0.214	link	-	Speer4e	c.*430C>1	-	ENSMUST	3_prime_UTR_variant
5	14933658	.	A	G	weak_evid	SNV	22	0	22	0	33	5	38	0.132	link	-	Speer4e	c.*375T>(	-	ENSMUST	3_prime_UTR_variant
5	14933671	.	C	T	non_homr	SNV	19	3	22	0.136	32	6	38	0.158	link	-	Speer4e	c.*362G>/	-	ENSMUST	3_prime_UTR_variant
5	14933673	rs1132176	T	C	mapping_(	SNV	22	0	22	0	33	6	39	0.154	link	-	Speer4e	c.*360A>(	-	ENSMUST	3_prime_UTR_variant
5	14973997	rs1132734	C	T	mapping_(	SNV	6	0	6	0	10	3	13	0.231	link	-	Gm10354	c.*500G>/	-	ENSMUST	downstream_gene_variant
5	14973997	rs1132734	C	T	mapping_(	SNV	6	0	6	0	10	3	13	0.231	link	-	-	n.1497399	-	-	intergenic_region
5	14978160	rs1134278	C	G	mapping_(	SNV	27	3	30	0.1	16	6	22	0.273	link	-	Gm10354	c.140-439(	-	ENSMUST	intron_variant
5	15029791	.	T	C	mapping_(	SNV	14	1	15	0.067	15	4	19	0.211	link	-	Gm17019	c.625-364,	-	ENSMUST	intron_variant
5	15525141	.	G	C	mapping_(	SNV	119	5	124	0.04	124	16	140	0.114	link	-	Gm21847	n.76-646G	-	ENSMUST	intron_variant
5	15525141	.	G	C	mapping_(	SNV	119	5	124	0.04	124	16	140	0.114	link	-	Gm21190	c.625-147(	-	ENSMUST	intron_variant
5	25954147	.	G	C	mapping_(	SNV	291	5	296	0.017	308	7	315	0.022	link	-	Gm21168	n.-2479G>	-	ENSMUST	upstream_gene_variant
5	25954147	.	G	C	mapping_(	SNV	291	5	296	0.017	308	7	315	0.022	link	-	Gm21671	c.139+59C	-	ENSMUST	intron_variant
5	26021202	.	C	T	weak_evid	SNV	8	1	9	0.111	5	3	8	0.375	link	-	Gm5862	c.299+402	-	ENSMUST	intron_variant
5	26021225	rs1133659	G	T	weak_evid	SNV	8	1	9	0.111	6	3	9	0.333	link	-	Gm5862	c.299+379	-	ENSMUST	intron_variant
5	26058549	rs1134243	G	A	mapping_(	SNV	128	4	132	0.03	136	15	151	0.099	link	-	Gm7347	c.-39C>T	-	ENSMUST	5_prime_UTR_variant
5	27262165	.	A	C	base_qual	SNV	6	0	6	0	19	4	23	0.174	link	-	Dpp6	c.226-120!	-	ENSMUST	intron_variant
5	31055488	.	A	C	alt_allele_	SNV	21	5	26	0.192	35	9	44	0.205	link	-	Atraid	c.*1121A>	-	ENSMUST	downstream_gene_variant
5	31055488	.	A	C	alt_allele_	SNV	21	5	26	0.192	35	9	44	0.205	link	-	Cad	c.222+106	-	ENSMUST	intron_variant
5	31193560	.	A	C	base_qual	SNV	63	1	64	0.016	61	11	72	0.153	link	-	Eif2b4	c.-584T>C	-	ENSMUST	upstream_gene_variant
5	31193560	.	A	C	base_qual	SNV	63	1	64	0.016	61	11	72	0.153	link	-	Snx17	c.63+95A>	-	ENSMUST	intron_variant
5	33389553	.	G	T	base_qual	SNV	34	4	38	0.105	37	10	47	0.213	link	-	Uvssa	c.551-89G	-	ENSMUST	intron_variant
5	34819087	.	A	C	base_qual	SNV	80	0	80	0	51	21	72	0.292	link	-	Htt	c.2179+53	-	ENSMUST	intron_variant
5	36071628	.	A	C	base_qual	SNV	7	0	7	0	5	3	8	0.375	link	-	Sorcs2	c.814-229'	-	ENSMUST	intron_variant
5	37194356	.	G	T	base_qual	SNV	93	1	94	0.011	84	10	94	0.106	link	-	Gm1043	c.4209+52	-	ENSMUST	intron_variant
5	64230583	.	A	C	base_qual	SNV	73	4	77	0.052	58	3	61	0.049	link	-	Gm43721	n.-3347A>	-	ENSMUST	upstream_gene_variant
5	64230583	.	A	C	base_qual	SNV	73	4	77	0.052	58	3	61	0.049	link	-	Tbc1d1	c.418-261'	-	ENSMUST	intron_variant
5	72660852	.	T	G	base_qual	SNV	191	1	192	0.005	172	18	190	0.095	link	-	Nipal1	c.370+401	-	ENSMUST	intron_variant
5	74395629	.	C	A	base_qual	SNV	28	1	29	0.034	28	4	32	0.125	link	-	Scfd2	c.1561+20	-	ENSMUST	intron_variant
5	88526313	.	T	G	base_qual	SNV	43	1	44	0.023	47	8	55	0.145	link	-	Jchain	c.65-94A>	-	ENSMUST	intron_variant
5	88639293	.	T	G	base_qual	SNV	7	0	7	0	13	8	21	0.381	link	-	Rufy3	c.1487+21	-	ENSMUST	intron_variant
5	89702871	.	T	C	PASS	SNV	82	0	82	0	87	18	105	0.171	link	-	Adamts3	c.1745+63	-	ENSMUST	intron_variant
5	92562613	.	T	G	base_qual	SNV	53	1	54	0.019	51	7	58	0.121	link	-	Fam47e	c.414+56T	-	ENSMUST	intron_variant
5	98186336	.	T	G	base_qual	SNV	156	6	162	0.037	177	16	193	0.083	link	-	A730035I1	n.-352A>(	-	ENSMUST	upstream_gene_variant
5	1.07E+08	.	A	C	base_qual	SNV	48	0	48	0	53	5	58	0.086	link	-	Tgfbr3	c.2326+14	-	ENSMUST	intron_variant
5	1.07E+08	.	A	C	base_qual	SNV	106	7	113	0.062	96	6	102	0.059	link	-	Brdt	c.2080+19	-	ENSMUST	intron_variant
5	1.1E+08	.	A	C	base_qual	SNV	114	0	114	0	90	23	113	0.204	link	-	Gtpbp6	c.*1886T>	-	ENSMUST	downstream_gene_variant
5	1.1E+08	.	A	C	base_qual	SNV	114	0	114	0	90	23	113	0.204	link	-	Plcxd1	c.496-41A	-	ENSMUST	intron_variant
5	1.14E+08	.	A	C	base_qual	SNV	38	5	43	0.116	36	7	43	0.163	link	-	Ssh1	c.825+69T	-	ENSMUST	intron_variant
5	1.15E+08	.	C	A	PASS	SNV	18	0	18	0	11	3	14	0.214	link	-	Gltp	c.163-158(	-	ENSMUST	intron_variant
5	1.15E+08	.	C	A	base_qual	SNV	30	0	30	0	45	8	53	0.151	link	-	Mlec	c.*85G>T	-	ENSMUST	3_prime_UTR_variant
5	1.15E+08	.	A	C	base_qual	SNV	99	6	105	0.057	127	12	139	0.086	link	-	Msi1	c.-113A>(	-	ENSMUST	5_prime_UTR_variant
5	1.15E+08	.	A	C	base_qual	SNV	99	6	105	0.057	127	12	139	0.086	link	-	Gm43231	n.-160T>(	-	ENSMUST	upstream_gene_variant
5	1.19E+08	.	T	G	base_qual	SNV	101	0	101	0	79	12	91	0.132	link	-	Med13l	c.5167-32'	-	ENSMUST	intron_variant
5	1.21E+08	.	T	G	base_qual	SNV	40	2	42	0.048	43	6	49	0.122	link	-	2510016D	n.*3582A>	-	ENSMUST	downstream_gene_variant
5	1.21E+08	.	T	G	base_qual	SNV	40	2	42	0.048	43	6	49	0.122	link	-	Tpcn1	c.1188-15(	-	ENSMUST	intron_variant
5	1.21E+08	.	A	T	weak_evid	SNV	5	0	5	0	8	3	11	0.273	link	-	Rph3a	c.1736+21	-	ENSMUST	intron_variant
5	1.22E+08	.	A	T	base_qual	SNV	51	3	54	0.056	53	7	60	0.117	link	-	Arpc3	c.*128A>T	-	ENSMUST	3_prime_UTR_variant
5	1.22E+08	.	A	T	base_qual	SNV	51	3	54	0.056	53	7	60	0.117	link	-	Gm42829	n.-2431A>	-	ENSMUST	upstream_gene_variant
5	1.23E+08	.	A	C	base_qual	SNV	52	0	52	0	51	7	58	0.121	link	-	Rhof	c.*4409T>	-	ENSMUST	downstream_gene_variant
5	1.23E+08	.	A	C	base_qual	SNV	52	0	52	0	51	7	58	0.121	link	-	Gm43413	n.*2760A>	-	ENSMUST	downstream_gene_variant
5	1.23E+08	.	A	C	base_qual	SNV	52	0	52	0	51	7	58	0.121	link	-	Tmem120	c.680-79A	-	ENSMUST	intron_variant
5	1.23E+08	.	A	C	base_qual	SNV	52	0	52	0	51	7	58	0.121	link	-	Gm26745	n.1850-67(	-	ENSMUST	intron_variant
5	1.23E+08	.	A	C	base_qual	SNV	52	0	52	0	51	7	58	0.121	link	-	Rhof	n.1231150	-	-	intragenic_variant
5	1.23E+08	.	T	A	base_qual	SNV	59	1	60	0.017	45	15	60	0.25	link	-	Rhof	c.*4402A>	-	ENSMUST	downstream_gene_variant
5	1.23E+08	.	T	A	base_qual	SNV	59	1	60	0.017	45	15	60	0.25	link	-	Gm43413	n.*2767T>	-	ENSMUST	downstream_gene_variant
5	1.23E+08	.	T	A	base_qual	SNV	59	1	60	0.017	45	15	60	0.25	link	-	Tmem120	c.680-72T	-	ENSMUST	intron_variant
5	1.23E+08	.	T	A	base_qual	SNV	59	1	60	0.017	45	15	60	0.25	link	-	Gm26745	n.1850-67(	-	ENSMUST	intron_variant
5	1.23E+08	.	T	A	base_qual	SNV	59	1	60	0.017	45	15	60	0.25	link	-	Rhof	n.1231150	-	-	intragenic_variant
5	1.23E+08	.	T	G	base_qual	SNV	34	4	38	0.105	31	8	39	0.205	link	-	Rhof	c.*3565A>	-	ENSMUST	downstream_gene_variant
5	1.23E+08	.	T	G	base_qual	SNV	34	4	38	0.105	31	8	39	0.205	link	-	Gm43413	n.*3604T>	-	ENSMUST	downstream_gene_variant
5	1.23E+08	.	T	G	base_qual	SNV	34	4	38	0.105	31	8	39	0.205	link	-	Tmem120	c.837+140	-	ENSMUST	intron_variant
5	1.23E+08	.	T	G	base_qual	SNV	34	4	38	0.105	31	8	39	0.205	link	-	Gm26745	n.1850-68	-	ENSMUST	intron_variant
5	1.23E+08	.	T	G	base_qual	SNV	34	4	38	0.105	31	8	39	0.205	link	-	Rhof	n.1231158	-	-	intragenic_variant
5	1.23E+08	.	T	G	base_qual	SNV	228	0	228	0	216	19	235	0.081	link	-	Gm26745	n.1849+68	-	ENSMUST	intron_variant
5	1.25E+08	.	T	G	base_qual	SNV	39	1	40	0.025	66	9	75	0.12	link	-	Tmed2	c.180+88T	-	ENSMUST	intron_variant
5	1.3E+08	.	C	T	too_few_s	SNV	21	0	21	0	16	2	18	0.111	link	-	Asl	c.1062+19	-	ENSMUST	intron_variant
5	1.34E+08	.	T	G	alt_allele_	SNV	35	6	41	0.146	40	6	46	0.13	link	-	Gatsl2	c.-62T>G	-	ENSMUST	5_prime_UTR_variant
5	1.34E+08	.	T	G	alt_allele_	SNV	35	6	41	0.146	40	6	46	0.13	link	-	Gm15627	n.-769A>(	-	ENSMUST	upstream_gene_variant
5	1.36E+08	.	T	G	base_qual	SNV	22	0	22	0	30	6	36	0.167	link	-	Srrm3	c.*112T>(	-	ENSMUST	3_prime_UTR_variant
5	1.36E+08	.	T	G	base_qual	SNV	22	0	22	0	30	6	36	0.167	link	-	Gm22450	n.-2237T>	-	ENSMUST	upstream_gene_variant
5	1.38E+08	.	T	G	base_qual	SNV	63	0	63	0	70	10	80	0.125	link	-	Lamtor4	c.-4745T>	-	ENSMUST	upstream_gene_variant
5	1.38E+08	.	T	G	base_qual	SNV	63	0	63	0	70	10	80	0.125	link	-	Nxpe5	c.1163-56'	-	ENSMUST	intron_variant
5	1.46E+08	rs5845261	T	G	weak_evid	SNV	5	0	5	0	5	4	9	0.444	link	-	Cyp3a44	c.72-270A	-	ENSMUST	intron_variant
5	1.5E+08	.	T	G	base_qual	SNV	10	2	12	0.167	14	6	20	0.3	link	-	Fry	c.1284-14;	-	ENSMUST	intron_variant
5	1.5E+08	.	C	G	base_qual	SNV	19	2	21	0.095	15	8	23	0.348	link	-	Fry	c.1284-12'	-	ENSMUST	intron_variant
6	13204811	.	G	A	too_few_s	SNV	9	0	9	0	18	2	20	0.1	link	-	Vwde	c.900+170	-	ENSMUST	intron_variant
6	21850830	.	C	A	base_qual	SNV	13	2	15	0.133	15	2	17	0.118	link	-	Gm42582	n.-1588C>	-	ENSMUST	upstream_gene_variant
6	21850830	.	C	A	base_qual	SNV	13	2	15	0.133	15	2	17	0.118	link	-	Gm3289	n.*2151G>	-	ENSMUST	downstream_gene_variant

6	21850830	.	C	A	base_qual	SNV	13	2	15	0.133	15	2	17	0.118	link	-	Tspan12	c.66+180C	-	ENSMUST	intron_variant
6	30545375	.	T	G	base_qual	SNV	45	1	46	0.022	46	6	52	0.115	link	-	Cpa2	c.283-129'	-	ENSMUST	intron_variant
6	40476658	.	G	T	base_qual	SNV	76	3	79	0.038	66	4	70	0.057	link	-	Ssbp1	c.227-90G	-	ENSMUST	intron_variant
6	41062310	.	A	G	PASS	SNV	205	0	205	0	172	4	176	0.023	link	-	Trbv5	c.-49A>G	-	ENSMUST	upstream_gene_variant
6	41062310	.	A	G	PASS	SNV	205	0	205	0	172	4	176	0.023	link	-	Trbv6	n.-4569A>	-	ENSMUST	upstream_gene_variant
6	41062310	.	A	G	PASS	SNV	205	0	205	0	172	4	176	0.023	link	-	5830405F(	n.*1166A>	-	ENSMUST	downstream_gene_variant
6	41062310	.	A	G	PASS	SNV	205	0	205	0	172	4	176	0.023	link	-	Trbv4	c.*2424A>	-	ENSMUST	downstream_gene_variant
6	41062310	.	A	G	PASS	SNV	205	0	205	0	172	4	176	0.023	link	-	5830405F(	n.4106231	-	-	intragenic_variant
6	42322956	.	T	G	base_qual	SNV	78	14	92	0.152	76	20	96	0.208	link	-	Fam131b	c.29-940A	-	ENSMUST	intron_variant
6	47671995	.	T	A	weak_evid	SNV	9	0	9	0	11	5	16	0.312	link	-	-	n.4767199	-	-	intergenic_region
6	52259812	.	A	C	base_qual	SNV	64	1	65	0.015	51	14	65	0.215	link	-	Hottip	n.-2972A>	-	ENSMUST	upstream_gene_variant
6	52259812	.	A	C	base_qual	SNV	64	1	65	0.015	51	14	65	0.215	link	-	9530018H	n.-2352T>	-	ENSMUST	upstream_gene_variant
6	52259812	.	A	C	base_qual	SNV	64	1	65	0.015	51	14	65	0.215	link	-	Gm27280	n.-1342A>	-	ENSMUST	upstream_gene_variant
6	52259812	.	A	C	base_qual	SNV	64	1	65	0.015	51	14	65	0.215	link	-	Gm27985	n.-2780A>	-	ENSMUST	upstream_gene_variant
6	52259812	.	A	C	base_qual	SNV	64	1	65	0.015	51	14	65	0.215	link	-	Gm27383	n.-3246A>	-	ENSMUST	upstream_gene_variant
6	52259812	.	A	C	base_qual	SNV	64	1	65	0.015	51	14	65	0.215	link	-	Hoxa13	c.907+52T	-	ENSMUST	intron_variant
6	72899806	.	C	G	non_homr	SNV	137	1	138	0.007	150	5	155	0.032	link	-	Kcmf1	c.-177G>(	-	ENSMUST	5_prime_UTR_variant
6	72899806	.	C	G	non_homr	SNV	137	1	138	0.007	150	5	155	0.032	link	-	D530018E	n.-3887G>	-	ENSMUST	upstream_gene_variant
6	83808730	.	G	C	read_posit	SNV	25	0	25	0	19	2	21	0.095	link	-	Paip2b	c.*106C>(	-	ENSMUST	3_prime_UTR_variant
6	92908385	.	C	A	base_qual	SNV	28	5	33	0.152	21	13	34	0.382	link	-	Adamts9	c.1316+92	-	ENSMUST	intron_variant
6	99666581	.	T	G	base_qual	SNV	123	3	126	0.024	125	8	133	0.06	link	-	Gm44104	n.-4363A>	-	ENSMUST	upstream_gene_variant
6	99666581	.	T	G	base_qual	SNV	123	3	126	0.024	125	8	133	0.06	link	-	Eif4e3	c.125+47A	-	ENSMUST	intron_variant
6	99666581	.	T	G	base_qual	SNV	123	3	126	0.024	125	8	133	0.06	link	-	Gm20696	c.125+47A	-	ENSMUST	intron_variant
6	99666591	.	A	C	base_qual	SNV	131	3	134	0.022	130	11	141	0.078	link	-	Gm44104	n.-4373T>	-	ENSMUST	upstream_gene_variant
6	99666591	.	A	C	base_qual	SNV	131	3	134	0.022	130	11	141	0.078	link	-	Eif4e3	c.125+37T	-	ENSMUST	intron_variant
6	99666591	.	A	C	base_qual	SNV	131	3	134	0.022	130	11	141	0.078	link	-	Gm20696	c.125+37T	-	ENSMUST	intron_variant
6	1.12E+08	.	T	G	base_qual	SNV	84	0	84	0	63	9	72	0.125	link	-	Ssu2	c.128-102/	-	ENSMUST	intron_variant
6	1.14E+08	.	T	G	base_qual	SNV	247	0	247	0	209	20	229	0.087	link	-	Gm44053	n.*4185T>	-	ENSMUST	downstream_gene_variant
6	1.16E+08	.	T	G	base_qual	SNV	47	5	52	0.096	38	9	47	0.191	link	-	H1foo	c.360+107	-	ENSMUST	intron_variant
6	1.21E+08	.	T	G	base_qual	SNV	198	0	198	0	192	10	202	0.05	link	-	Gm43915	n.130+315	-	ENSMUST	intron_variant
6	1.25E+08	.	T	C	too_few_s	SNV	19	0	19	0	22	2	24	0.083	link	-	Eno2	c.-6331A>	-	ENSMUST	upstream_gene_variant
6	1.25E+08	.	T	C	too_few_s	SNV	19	0	19	0	22	2	24	0.083	link	-	Lrrc23	c.613-171/	-	ENSMUST	intron_variant
6	1.25E+08	.	A	C	base_qual	SNV	122	0	122	0	110	19	129	0.147	link	-	Mlf2	c.*24A>C	-	ENSMUST	3_prime_UTR_variant
6	1.29E+08	.	C	A	weak_evid	SNV	90	0	90	0	115	3	118	0.025	link	-	BC048546	c.2132-48	-	ENSMUST	intron_variant
6	1.37E+08	.	A	G	too_few_s	SNV	7	0	7	0	19	2	21	0.095	link	-	Atf7ip	c.3206-18	-	ENSMUST	intron_variant
6	1.38E+08	.	T	G	base_qual	SNV	96	2	98	0.02	97	7	104	0.067	link	-	Slc15a5	c.954+30A	-	ENSMUST	intron_variant
6	1.48E+08	.	A	C	base_qual	SNV	69	1	70	0.014	69	4	73	0.055	link	-	Tmtc1	c.1430+96	-	ENSMUST	intron_variant
6	1.49E+08	.	G	T	base_qual	SNV	37	2	39	0.051	28	11	39	0.282	link	-	Fam60a	c.-19-73C	-	ENSMUST	intron_variant
7	18647095	rs5870635	A	C	PASS	SNV	84	1	85	0.012	82	19	101	0.188	link	-	Psg21	c.*106T>(	-	ENSMUST	3_prime_UTR_variant
7	23406968	.	G	A	weak_evid	SNV	15	0	15	0	23	3	26	0.115	link	-	Gm25196	n.-28G>A	-	ENSMUST	upstream_gene_variant
7	23406968	.	G	A	weak_evid	SNV	15	0	15	0	23	3	26	0.115	link	-	Nlrp5	c.149-493(	-	ENSMUST	intron_variant
7	23406971	.	T	C	weak_evid	SNV	16	0	16	0	24	3	27	0.111	link	-	Gm25196	n.-25T>C	-	ENSMUST	upstream_gene_variant
7	23406971	.	T	C	weak_evid	SNV	16	0	16	0	24	3	27	0.111	link	-	Nlrp5	c.149-490'	-	ENSMUST	intron_variant
7	23406972	.	G	C	weak_evid	SNV	16	0	16	0	24	3	27	0.111	link	-	Gm25196	n.-24G>C	-	ENSMUST	upstream_gene_variant
7	23406972	.	G	C	weak_evid	SNV	16	0	16	0	24	3	27	0.111	link	-	Nlrp5	c.149-489(	-	ENSMUST	intron_variant
7	23406978	.	G	A	weak_evid	SNV	16	0	16	0	25	3	28	0.107	link	-	Gm25196	n.-18G>A	-	ENSMUST	upstream_gene_variant
7	23406978	.	G	A	weak_evid	SNV	16	0	16	0	25	3	28	0.107	link	-	Nlrp5	c.149-483(	-	ENSMUST	intron_variant
7	23406986	.	C	T	weak_evid	SNV	16	0	16	0	26	3	29	0.103	link	-	Gm25196	n.-10C>T	-	ENSMUST	upstream_gene_variant
7	23406986	.	C	T	weak_evid	SNV	16	0	16	0	26	3	29	0.103	link	-	Nlrp5	c.149-475(	-	ENSMUST	intron_variant
7	23407018	.	G	A	weak_evid	SNV	19	0	19	0	22	3	25	0.12	link	-	Nlrp5	c.149-443(	-	ENSMUST	intron_variant
7	23407018	.	G	A	weak_evid	SNV	19	0	19	0	22	3	25	0.12	link	-	Gm25196	n.23G>A	-	ENSMUST	non_coding_transcript_exon_variant
7	23407034	.	G	C	too_few_s	SNV	21	0	21	0	19	2	21	0.095	link	-	Nlrp5	c.149-427(	-	ENSMUST	intron_variant
7	23407034	.	G	C	too_few_s	SNV	21	0	21	0	19	2	21	0.095	link	-	Gm25196	n.39G>C	-	ENSMUST	non_coding_transcript_exon_variant
7	23407035	.	G	T	too_few_s	SNV	21	0	21	0	19	2	21	0.095	link	-	Nlrp5	c.149-426(	-	ENSMUST	intron_variant
7	23407035	.	G	T	too_few_s	SNV	21	0	21	0	19	2	21	0.095	link	-	Gm25196	n.40G>T	-	ENSMUST	non_coding_transcript_exon_variant
7	23407041	.	C	T	weak_evid	SNV	20	0	20	0	17	3	20	0.15	link	-	Nlrp5	c.149-420(	-	ENSMUST	intron_variant
7	23407041	.	C	T	weak_evid	SNV	20	0	20	0	17	3	20	0.15	link	-	Gm25196	n.46C>T	-	ENSMUST	non_coding_transcript_exon_variant
7	23407052	.	T	G	weak_evid	SNV	18	0	18	0	18	3	21	0.143	link	-	Nlrp5	c.149-409'	-	ENSMUST	intron_variant
7	23407052	.	T	G	weak_evid	SNV	18	0	18	0	18	3	21	0.143	link	-	Gm25196	n.57T>G	-	ENSMUST	non_coding_transcript_exon_variant
7	23407065	.	T	C	weak_evid	SNV	18	0	18	0	18	3	21	0.143	link	-	Nlrp5	c.149-396'	-	ENSMUST	intron_variant
7	23407065	.	T	C	weak_evid	SNV	18	0	18	0	18	3	21	0.143	link	-	Gm25196	n.70T>C	-	ENSMUST	non_coding_transcript_exon_variant
7	23407105	.	T	C	too_few_s	SNV	19	0	19	0	11	2	13	0.154	link	-	Nlrp5	c.149-356'	-	ENSMUST	intron_variant
7	24547459	.	T	G	weak_evid	SNV	41	0	41	0	58	5	63	0.079	link	-	Pinlyp	c.-1466A>	-	ENSMUST	upstream_gene_variant
7	24547459	.	T	G	weak_evid	SNV	41	0	41	0	58	5	63	0.079	link	-	Xrcc1	c.51+100T	-	ENSMUST	intron_variant
7	24980409	.	T	G	base_qual	SNV	22	0	22	0	21	5	26	0.192	link	-	Atp1a3	c.2688+14	-	ENSMUST	intron_variant
7	27581254	.	T	G	base_qual	SNV	50	4	54	0.074	48	6	54	0.111	link	-	2310022A1	c.*417T>(	-	ENSMUST	3_prime_UTR_variant
7	28608151	.	T	G	PASS	SNV	33	0	33	0	39	9	48	0.188	link	-	Acp7	c.1426-14(	-	ENSMUST	intron_variant
7	29047135	.	C	A	base_qual	SNV	65	1	66	0.015	57	8	65	0.123	link	-	Gm44408	n.*1442C>	-	ENSMUST	downstream_gene_variant
7	29047135	.	C	A	base_qual	SNV	65	1	66	0.015	57	8	65	0.123	link	-	Ryr1	c.11372-5(	-	ENSMUST	intron_variant
7	29215633	.	A	C	base_qual	SNV	44	5	49	0.102	35	13	48	0.271	link	-	Catsperg1	c.-4719T>	-	ENSMUST	upstream_gene_variant
7	29215633	.	A	C	base_qual	SNV	44	5	49	0.102	35	13	48	0.271	link	-	-	n.2921563	-	-	intergenic_region
7	38865563	rs1132740	A	C	mapping_(	SNV	370	10	380	0.026	354	29	383	0.076	link	-	Gm21136	n.1209T>(	-	ENSMUST	non_coding_transcript_exon_variant
7	38865628	rs1134626	C	T	mapping_(	SNV	366	22	388	0.057	353	42	395	0.106	link	-	Gm21136	n.1144G>/	-	ENSMUST	non_coding_transcript_exon_variant
7	43778750	.	T	A	base_qual	SNV	85	1	86	0.012	89	8	97	0.082	link	-	Klk10	c.-2785T>	-	ENSMUST	upstream_gene_variant
7	43778750	.	T	A	base_qual	SNV	85	1	86	0.012	89	8	97	0.082	link	-	Klk11	c.679-35T	-	ENSMUST	intron_variant
7	43778750	.	T	A	base_qual	SNV	85	1	86	0.012	89	8	97	0.082	link	-	2310002F(	n.4377875	-	-	intragenic_variant
7	44004781	.	A	C	base_qual	SNV	128	1	129	0.008	127	26	153	0.17	link	-	Gm45195	n.-1918T>	-	ENSMUST	upstream_gene_variant
7	44004781	.	A	C	base_qual	SNV	128	1	129	0.008	127	26	153	0.17	link	-	Klk1b11	c.*4955A>	-	ENSMUST	downstream_gene_variant
7	44004781	.	A	C	base_qual	SNV	128	1	129	0.008	127	26	153	0.17	link	-	Klk1b12-p	n.44+97A:	-	ENSMUST	intron_variant
7	44623289	.	T	C	weak_evid	SNV	67	0	67	0	65	3	68	0.044	link	-	Myh14	c.4279-65/	-	ENSMUST	intron_variant
7	44715612	.	A	C	alt_allele_	SNV	18	5	23	0.217	30	7	37	0.189	link	-	Izumo2	c.539+161	-	ENSMUST	intron_variant
7	45353416	.	C	T	PASS	SNV	132	4	136	0.029	95	62	157	0.395	link	-	Ppfia3	c.1665+10	-	ENSMUST	intron_variant
7	45459458	.	A	C	base_qual	SNV	33	6	39	0.154	32	6	38	0.158	link	-	Gm22133	n.-1261T>	-	ENSMUST	upstream_gene_variant
7	45459458	.	A	C	base_qual	SNV	33	6	39	0.154	32	6	38	0.158	link	-	RP23-218	n.-11A>C	-	ENSMUST	upstream_gene_variant
7	45459458	.	A	C	base_qual	SNV	33	6	39	0.154	32	6	38	0.158	link	-	Gys1	c.*4091A>	-	ENSMUST	downstream_gene_variant
7	45459458	.	A	C	base_qual	SNV	33	6	39	0.154	32	6	38	0.158	link	-	Bax	c.*2404T>	-	ENSMUST	downstream_gene_variant
7	45459458	.	A	C	base_qual	SNV	33	6	39	0.154	32	6	38	0.158	link	-	Ftl1	c.102+72T	-	ENSMUST	intron_variant
7	46249277	.	G	A	too_few_s	SNV	10	0	10	0	22	2	24	0.083	link	-	Otog	c.656+162	-	ENSMUST	intron_variant
7	59770001	.	G	T	weak_evid	SNV	307	6	313	0.019	341	19	360	0.053	link	-	Gm23446	n.-3297C>	-	ENSMUST	upstream_gene_variant
7	59770001	.	G	T	weak_evid	SNV	307	6	313	0.019	341	19	360	0.053	link	-	Gm25210	n.-770C>A	-	ENSMUST	upstream_gene_variant
7	59770001	.	G	T	weak_evid	SNV	307	6	313	0.019	341	19	360	0.053	link	-	Gm22128	n.*1655C>	-	ENSMUST	downstream_gene_variant
7	59770001	.	G	T	weak_evid	SNV	307	6	313	0.019	341	19	360	0.053	link	-	Gm22851	n.*4189C>	-	ENSMUST	downstream_gene_variant
7	59770001	.	G	T	weak_evid	SNV	307	6	313	0.019	341	19	360	0.053	link	-	Snhg14	n.5977000	-	-	intragenic_variant
7	59770016	.	A	C	no_reliabl	SNV	255	3	258	0.012	274	9	283	0.032	link	-	Gm23446	n.-3312T>	-	ENSMUST	upstream_gene_variant
7	59770016	.	A	C	no_reliabl	SNV	255	3	258	0.012	274	9	283	0.032	link	-	Gm25210	n.-785T>(	-	ENSMUST	upstream_gene_variant
7	59770016	.	A	C	no_reliabl	SNV	255	3	258	0.012	274	9	283	0.032	link	-	Gm22128	n.*1640T>	-	ENSMUST	downstream_gene_variant
7	59770016	.	A	C	no_reliabl	SNV	255	3	258	0.012	274	9	283	0.032	link	-	Gm22851	n.*4174T>	-	ENSMUST	downstream_gene_variant
7	59770016	.	A	C	no_reliabl	SNV	255	3	258	0.012	274	9	283	0.032	link	-	Snhg14	n.5977001	-	-	intragenic_variant
7	79410957	.	G	T	base_qual	SNV	11	1	12	0.083	6	8	14	0.571	link	-	Gm16017	n.*1353C>	-	ENSMUST	downstream_gene_variant
7	79410957	.	G	T	base_qual	SNV	11	1	12	0.083	6	8	14	0.571	link	-	Fanci	c.883-204(	-	ENSMUST	intron_variant
7	80758059	.	C	A	base_qual	SNV	48	5	53	0.094	36	6	42	0.143	link	-	Iqgap1	c.913+115	-	ENSMUST	intron_variant
7	80758059	.	C	A	base_qual	SNV	48	5	53	0.094	36	6	42	0.143	link	-	Gm44649	n.272-190(	-	ENSMUST	intron_variant
7	80762666	.	T	G	base_qual	SNV	58	0	58	0	57	14	71	0.197	link	-	Gm44649	n.*4054T>	-	ENSMUST	downstream_gene_variant
7	80762666	.	T	G	base_qual	SNV	58	0	58	0	57	14	71	0.197	link	-	Iqgap1	c.468-101/	-	ENSMUST	intron_variant
7	83882197	.	T	G	base_qual	SNV	182	0	182	0	177	19	196	0.097	link	-	Gm44530	n.*4277T>	-	ENSMUST	downstream_gene_variant
7	97390763	.	A	G	weak_evid	SNV	12	2	14	0.143	14	5	19	0.263	link	-	Alg8	c.1277-12(	-	ENSMUST	intron_variant
7	97865752	.	C	T	too_few_s	SNV	12	0	12	0	22	2	24	0.083	link	-	Pak1	c.291+180	-	ENSMUST	intron_variant
7	1.05E+08	rs5211210	A	C	weak_evid	SNV	8	0	8	0	17	5	22	0.227	link	-	Usp17le	c.131-119(	-	ENSMUST	intron_variant

7	1.06E+08	.	G	T	base_qual	SNV	36	0	36	0	59	1	60	0.017	link	-	Gm15645	n.-1613G>	-	ENSMUST	upstream_gene_variant
7	1.06E+08	.	G	T	base_qual	SNV	36	0	36	0	59	1	60	0.017	link	-	Dchs1	c.5350+10	-	ENSMUST	intron_variant
7	1.06E+08	.	A	G	too_few_s	SNV	44	0	44	0	67	0	67	0	link	-	Gm15645	n.-1609A>	-	ENSMUST	upstream_gene_variant
7	1.06E+08	.	A	G	too_few_s	SNV	44	0	44	0	67	0	67	0	link	-	Dchs1	c.5350+10	-	ENSMUST	intron_variant
7	1.1E+08	.	C	A	base_qual	SNV	36	5	41	0.122	58	5	63	0.079	link	-	Dennd5a	c.2521+11	-	ENSMUST	intron_variant
7	1.13E+08	.	A	C	base_qual	SNV	134	0	134	0	115	16	131	0.122	link	-	Tead1	c.542+78A	-	ENSMUST	intron_variant
7	1.15E+08	.	G	T	PASS	SNV	60	1	61	0.016	55	8	63	0.127	link	-	Insc	c.1237+88	-	ENSMUST	intron_variant
7	1.16E+08	.	A	C	base_qual	SNV	28	0	28	0	28	10	38	0.263	link	-	Plekha7	c.2400+17	-	ENSMUST	intron_variant
7	1.16E+08	.	T	G	base_qual	SNV	99	0	99	0	93	13	106	0.123	link	-	Plekha7	c.2400+83	-	ENSMUST	intron_variant
7	1.18E+08	.	C	T	weak_evid	SNV	233	0	233	0	261	4	265	0.015	link	-	4930583K	n.-611C>1	-	ENSMUST	upstream_gene_variant
7	1.21E+08	.	C	A	base_qual	SNV	33	2	35	0.057	38	6	44	0.136	link	-	Cdr2	c.338+98C	-	ENSMUST	intron_variant
7	1.23E+08	.	C	A	too_few_s	SNV	16	0	16	0	14	2	16	0.125	link	-	Rbbp6	c.303+235	-	ENSMUST	intron_variant
7	1.23E+08	.	T	G	base_qual	SNV	77	0	77	0	82	14	96	0.146	link	-	Tnrc6a	c.5108-90	-	ENSMUST	intron_variant
7	1.34E+08	.	G	A	PASS	SNV	95	2	97	0.021	35	33	68	0.485	link	-	Adam12	c.1416+97	-	ENSMUST	intron_variant
7	1.4E+08	.	G	T	PASS	SNV	196	0	196	0	230	6	236	0.025	link	-	Fuom	c.-39C>A	-	ENSMUST	upstream_gene_variant
7	1.4E+08	.	G	T	PASS	SNV	196	0	196	0	230	6	236	0.025	link	-	Echs1	c.*3897C>	-	ENSMUST	downstream_gene_variant
7	1.4E+08	.	G	T	PASS	SNV	196	0	196	0	230	6	236	0.025	link	-	Fuom	n.1401024	-	-	intragenic_variant
7	1.41E+08	.	C	A	PASS	SNV	211	0	211	0	184	4	188	0.021	link	-	Psmd13	c.-618C>A	-	ENSMUST	upstream_gene_variant
7	1.41E+08	.	C	A	PASS	SNV	211	0	211	0	184	4	188	0.021	link	-	Sirt3	c.-143+30	-	ENSMUST	intron_variant
7	1.41E+08	.	T	G	base_qual	SNV	53	2	55	0.036	58	3	61	0.049	link	-	Cd151	c.-3833T>	-	ENSMUST	upstream_gene_variant
7	1.41E+08	.	T	G	base_qual	SNV	53	2	55	0.036	58	3	61	0.049	link	-	Gm10575	n.-398A>(	-	ENSMUST	upstream_gene_variant
7	1.41E+08	.	T	G	base_qual	SNV	53	2	55	0.036	58	3	61	0.049	link	-	Pnpla2	c.*5761T>	-	ENSMUST	downstream_gene_variant
7	1.41E+08	.	T	G	base_qual	SNV	53	2	55	0.036	58	3	61	0.049	link	-	Cracr2b	c.768+73T	-	ENSMUST	intron_variant
7	1.41E+08	.	T	G	base_qual	SNV	53	2	55	0.036	58	3	61	0.049	link	-	Gm10575	n.1414654	-	-	intragenic_variant
7	1.42E+08	.	T	G	base_qual	SNV	78	0	78	0	83	9	92	0.098	link	-	Ap2a2	c.1551-44	-	ENSMUST	intron_variant
7	1.42E+08	.	T	G	base_qual	SNV	78	0	78	0	83	9	92	0.098	link	-	Mir7063	n.48T>G	-	ENSMUST	non_coding_transcript_exon_variant
7	1.42E+08	.	G	A	weak_evid	SNV	150	0	150	0	142	3	145	0.021	link	-	Ap2a2	c.2121-33	-	ENSMUST	intron_variant
7	1.44E+08	.	A	C	too_few_s	SNV	15	0	15	0	9	0	9	0	link	-	Shank2	c.1854-20	-	ENSMUST	intron_variant
8	8667169	.	C	A	base_qual	SNV	50	5	55	0.091	57	13	70	0.186	link	-	Arglu1	c.*83G>T	-	ENSMUST	3_prime_UTR_variant
8	8667169	.	C	A	base_qual	SNV	50	5	55	0.091	57	13	70	0.186	link	-	4921522P	n.*2441C>	-	ENSMUST	downstream_gene_variant
8	12589379	.	T	G	base_qual	SNV	45	3	48	0.062	57	7	64	0.109	link	-	Spaca7	c.436+103	-	ENSMUST	intron_variant
8	12838171	.	T	G	weak_evid	SNV	12	1	13	0.077	15	5	20	0.25	link	-	Gm15350	n.-4306A>	-	ENSMUST	upstream_gene_variant
8	12838171	.	T	G	weak_evid	SNV	12	1	13	0.077	15	5	20	0.25	link	-	Atp11a	c.1815+15	-	ENSMUST	intron_variant
8	13248765	.	T	G	base_qual	SNV	61	1	62	0.016	67	3	70	0.043	link	-	Adprhl1	c.212-48A	-	ENSMUST	intron_variant
8	15081447	rs2203000	G	A	PASS	SNV	61	0	61	0	41	11	52	0.212	link	-	Myom2	c.1120+24	-	ENSMUST	intron_variant
8	20121939	rs1132003	T	A	weak_evid	SNV	9	0	9	0	5	8	13	0.615	link	-	RP24-366	n.-445T>A	-	ENSMUST	upstream_gene_variant
8	20121939	rs1132003	T	A	weak_evid	SNV	9	0	9	0	5	8	13	0.615	link	-	-	n.2012193	-	-	intergenic_region
8	20343143	rs1135021	G	A	weak_evid	SNV	8	0	8	0	9	4	13	0.308	link	-	Gm15319	c.878+253	-	ENSMUST	intron_variant
8	20343143	rs1135021	G	A	weak_evid	SNV	8	0	8	0	9	4	13	0.308	link	-	Gm26804	n.689+495	-	ENSMUST	intron_variant
8	27227144	.	A	C	too_few_s	SNV	16	1	17	0.059	13	2	15	0.133	link	-	RP23-118	n.-1542A>	-	ENSMUST	upstream_gene_variant
8	27227144	.	A	C	too_few_s	SNV	16	1	17	0.059	13	2	15	0.133	link	-	Adrb3	c.1163+11	-	ENSMUST	intron_variant
8	45800903	.	G	T	base_qual	SNV	125	6	131	0.046	142	4	146	0.027	link	-	Sorbs2	c.2935-62	-	ENSMUST	intron_variant
8	45800903	.	G	T	base_qual	SNV	125	6	131	0.046	142	4	146	0.027	link	-	Sorbs2os	n.193+182	-	ENSMUST	intron_variant
8	45900627	.	T	G	non_homr	SNV	36	4	40	0.1	23	4	27	0.148	link	-	Pdlim3	c.330+68T	-	ENSMUST	intron_variant
8	56538521	.	T	G	base_qual	SNV	61	2	63	0.032	56	11	67	0.164	link	-	Cep44	c.955+90A	-	ENSMUST	intron_variant
8	56591400	.	T	G	base_qual	SNV	83	0	83	0	99	14	113	0.124	link	-	Fbxo8	c.773-36T	-	ENSMUST	intron_variant
8	60534493	.	A	C	base_qual	SNV	95	0	95	0	107	8	115	0.07	link	-	Aadat	c.922-81A	-	ENSMUST	intron_variant
8	61374589	.	T	G	too_few_s	SNV	6	0	6	0	3	2	5	0.4	link	-	Sh3rf1	c.2154+22	-	ENSMUST	intron_variant
8	70493271	.	A	C	base_qual	SNV	127	6	133	0.045	127	11	138	0.08	link	-	Crlf1	c.-6A>C	-	ENSMUST	5_prime_UTR_variant
8	70493271	.	A	C	base_qual	SNV	127	6	133	0.045	127	11	138	0.08	link	-	RP23-423	n.*4202A>	-	ENSMUST	downstream_gene_variant
8	71143590	rs5827940	A	C	mapping_q	SNV	15	1	16	0.062	13	13	26	0.5	link	-	-	n.7114359	-	-	intergenic_region
8	71594591	.	T	G	base_qual	SNV	72	0	72	0	66	12	78	0.154	link	-	Fam129c	c.-3178T>	-	ENSMUST	upstream_gene_variant
8	71594591	.	T	G	base_qual	SNV	72	0	72	0	66	12	78	0.154	link	-	Pgls	c.397-78T	-	ENSMUST	intron_variant
8	79210498	.	A	C	base_qual	SNV	37	1	38	0.026	21	6	27	0.222	link	-	1700011L	c.*152T>(	-	ENSMUST	3_prime_UTR_variant
8	83995482	.	T	G	base_qual	SNV	50	5	55	0.091	43	16	59	0.271	link	-	Prkaca	c.*65T>G	-	ENSMUST	3_prime_UTR_variant
8	83995482	.	T	G	base_qual	SNV	50	5	55	0.091	43	16	59	0.271	link	-	Samd1	c.-2190T>	-	ENSMUST	upstream_gene_variant
8	84569782	.	T	G	base_qual	SNV	25	0	25	0	25	8	33	0.242	link	-	Cacna1a	c.3549-12	-	ENSMUST	intron_variant
8	84925157	.	A	C	base_qual	SNV	40	2	42	0.048	53	10	63	0.159	link	-	Gm24197	n.*368T>(	-	ENSMUST	downstream_gene_variant
8	84925157	.	A	C	base_qual	SNV	40	2	42	0.048	53	10	63	0.159	link	-	Mast1	c.1077+11	-	ENSMUST	intron_variant
8	85555399	.	A	C	base_qual	SNV	26	5	31	0.161	30	10	40	0.25	link	-	Dnaja2	c.-152T>C	-	ENSMUST	upstream_gene_variant
8	85555399	.	A	C	base_qual	SNV	26	5	31	0.161	30	10	40	0.25	link	-	-	n.8555539	-	-	intergenic_region
8	86557510	.	A	C	base_qual	SNV	29	4	33	0.121	23	6	29	0.207	link	-	Abcc12	c.982+87T	-	ENSMUST	intron_variant
8	94938747	.	A	C	base_qual	SNV	24	2	26	0.077	26	8	34	0.235	link	-	Adgrg5	c.1196+89	-	ENSMUST	intron_variant
8	1.05E+08	.	A	C	base_qual	SNV	158	0	158	0	163	10	173	0.058	link	-	E2f4	c.-2186A>	-	ENSMUST	upstream_gene_variant
8	1.05E+08	.	A	C	base_qual	SNV	158	0	158	0	163	10	173	0.058	link	-	RP23-127	n.*4237A>	-	ENSMUST	downstream_gene_variant
8	1.05E+08	.	A	C	base_qual	SNV	158	0	158	0	163	10	173	0.058	link	-	Exoc3l	c.34+71T>	-	ENSMUST	intron_variant
8	1.05E+08	.	A	C	base_qual	SNV	158	0	158	0	167	7	174	0.04	link	-	E2f4	c.-2185A>	-	ENSMUST	upstream_gene_variant
8	1.05E+08	.	A	C	base_qual	SNV	158	0	158	0	167	7	174	0.04	link	-	RP23-127	n.*4238A>	-	ENSMUST	downstream_gene_variant
8	1.05E+08	.	A	C	base_qual	SNV	158	0	158	0	167	7	174	0.04	link	-	Exoc3l	c.34+70T>	-	ENSMUST	intron_variant
8	1.05E+08	.	T	G	non_homr	SNV	78	2	80	0.025	49	3	52	0.058	link	-	E2f4	c.*2552T>	-	ENSMUST	downstream_gene_variant
8	1.05E+08	.	T	G	non_homr	SNV	78	2	80	0.025	49	3	52	0.058	link	-	Gm27320	n.*552A>(	-	ENSMUST	downstream_gene_variant
8	1.05E+08	.	T	G	non_homr	SNV	78	2	80	0.025	49	3	52	0.058	link	-	Mir328	n.*1124A>	-	ENSMUST	downstream_gene_variant
8	1.05E+08	.	T	G	non_homr	SNV	78	2	80	0.025	49	3	52	0.058	link	-	Elmo3	c.666-48T	-	ENSMUST	intron_variant
8	1.06E+08	.	A	C	PASS	SNV	18	1	19	0.053	6	5	11	0.455	link	-	Hsd11b2	c.-177A>(	-	ENSMUST	upstream_gene_variant
8	1.06E+08	.	A	C	PASS	SNV	18	1	19	0.053	6	5	11	0.455	link	-	-	n.1055186	-	-	intergenic_region
8	1.17E+08	.	A	C	base_qual	SNV	13	0	13	0	18	6	24	0.25	link	-	Cdyl2	c.24+162T	-	ENSMUST	intron_variant
8	1.21E+08	.	C	A	non_homr	SNV	39	4	43	0.093	43	6	49	0.122	link	-	Emc8	c.-1216G>	-	ENSMUST	upstream_gene_variant
8	1.21E+08	.	C	A	non_homr	SNV	39	4	43	0.093	43	6	49	0.122	link	-	Gm27021	c.-1216G>	-	ENSMUST	upstream_gene_variant
8	1.21E+08	.	C	A	non_homr	SNV	39	4	43	0.093	43	6	49	0.122	link	-	Cox4i1	c.-1-115C	-	ENSMUST	intron_variant
8	1.21E+08	.	C	A	non_homr	SNV	39	4	43	0.093	43	6	49	0.122	link	-	Gm20388	c.21+7582	-	ENSMUST	intron_variant
9	3000848	.	T	C	PASS	SNV	86	0	86	0	115	6	121	0.05	link	-	Gm10722	c.-74T>C	-	ENSMUST	upstream_gene_variant
9	3000848	.	T	C	PASS	SNV	86	0	86	0	115	6	121	0.05	link	-	Gm11168	c.-2498T>	-	ENSMUST	upstream_gene_variant
9	3000848	.	T	C	PASS	SNV	86	0	86	0	115	6	121	0.05	link	-	Gm26870	n.822-218	-	ENSMUST	intron_variant
9	3003006	.	T	A	weak_evid	SNV	13	0	13	0	14	3	17	0.176	link	-	Gm11168	c.-340T>A	-	ENSMUST	upstream_gene_variant
9	3003006	.	T	A	weak_evid	SNV	13	0	13	0	14	3	17	0.176	link	-	Gm10722	c.*676T>A	-	ENSMUST	downstream_gene_variant
9	3003006	.	T	A	weak_evid	SNV	13	0	13	0	14	3	17	0.176	link	-	Gm26870	n.821+160	-	ENSMUST	intron_variant
9	3003012	.	G	C	weak_evid	SNV	13	0	13	0	14	3	17	0.176	link	-	Gm11168	c.-334G>(	-	ENSMUST	upstream_gene_variant
9	3003012	.	G	C	weak_evid	SNV	13	0	13	0	14	3	17	0.176	link	-	Gm10722	c.*682G>(	-	ENSMUST	downstream_gene_variant
9	3003012	.	G	C	weak_evid	SNV	13	0	13	0	14	3	17	0.176	link	-	Gm26870	n.821+159	-	ENSMUST	intron_variant
9	3020563	.	T	G	weak_evid	SNV	100	2	102	0.02	138	9	147	0.061	link	-	Gm26870	n.-2479A>	-	ENSMUST	upstream_gene_variant
9	3020563	.	T	G	weak_evid	SNV	100	2	102	0.02	138	9	147	0.061	link	-	Gm10718	c.-2984T>	-	ENSMUST	upstream_gene_variant
9	3020563	.	T	G	weak_evid	SNV	100	2	102	0.02	138	9	147	0.061	link	-	Gm10717	c.-4854T>	-	ENSMUST	upstream_gene_variant
9	3020563	.	T	G	weak_evid	SNV	100	2	102	0.02	138	9	147	0.061	link	-	Gm10720	c.*3353T>	-	ENSMUST	downstream_gene_variant
9	3020563	.	T	G	weak_evid	SNV	100	2	102	0.02	138	9	147	0.061	link	-	Gm10719	c.161-223	-	ENSMUST	intron_variant
9	3020563	.	T	G	weak_evid	SNV	100	2	102	0.02	138	9	147	0.061	link	-	Gm26870	n.3020563	-	-	intragenic_variant
9	3020901	.	T	A	low_frac_i	SNV	55	5	60	0.083	86	14	100	0.14	link	-	Gm26870	n.-2817A>	-	ENSMUST	upstream_gene_variant
9	3020901	.	T	A	low_frac_i	SNV	55	5	60	0.083	86	14	100	0.14	link	-	Gm10718	c.-2646T>	-	ENSMUST	upstream_gene_variant
9	3020901	.	T	A	low_frac_i	SNV	55	5	60	0.083	86	14	100	0.14	link	-	Gm10717	c.-4516T>	-	ENSMUST	upstream_gene_variant
9	3020901	.	T	A	low_frac_i	SNV	55	5	60	0.083	86	14	100	0.14	link	-	Gm10720	c.*3691T>	-	ENSMUST	downstream_gene_variant
9	3020901	.	T	A	low_frac_i	SNV	55	5	60	0.083	86	14	100	0.14	link	-	Gm26870	n.3020901	-	-	intragenic_variant
9	3023523	.	A	G	mapping_q	SNV	761	32	793	0.04	1154	70	1224	0.057	link	-	Gm10718	c.-24A>G	-	ENSMUST	upstream_gene_variant
9	3023523	.	A	G	mapping_q	SNV	761	32	793	0.04	1154	70	1224	0.057	link	-	Gm10717	c.-1894A>	-	ENSMUST	upstream_gene_variant
9	3023523	.	A	G	mapping_q	SNV	761	32	793	0.04	1154	70	1224	0.057	link	-	Gm10719	c.*1930A>	-	ENSMUST	downstream_gene_variant
9	3023523	.	A	G	mapping_q	SNV	761	32	793	0.04	1154	70	1224	0.057	link	-	Gm26870	n.3023523	-	-	intragenic_variant
9	3025937	.	A	C	weak_evid	SNV	172	3	175	0.017	315	11	326	0.034	link	-	Gm10719	c.*4344A>	-	ENSMUST	downstream_gene_variant
9	3025937	.	A	C	weak_evid	SNV	172	3	175	0.017	315	11	326	0.034	link	-	Gm10718	c.*719A>(	-	ENSMUST	downstream_gene_variant
9	3025937	.	A	C	weak_evid	SNV	172	3	175	0.017	315	11	326	0.034	link	-	Gm26870	n.3025937	-	-	intragenic_variant
9	3025938	.	G	A	weak_evid	SNV	171	0	171	0	313	9	322	0.028	link	-	Gm10719	c.*4345G>	-	ENSMUST	downstream_gene_variant

9	3025938	.	G	A	weak_evid	SNV	171	0	171	0	313	9	322	0.028	link	-	Gm10718	c.*720G>A	-	ENSMUST	downstream_gene_variant
9	3025938	.	G	A	weak_evid	SNV	171	0	171	0	313	9	322	0.028	link	-	Gm26870	n.3025938	-	-	intragenic_variant
9	3031318	rs1133300	A	T	too_few_s	SNV	7	0	7	0	4	1	5	0.2	link	-	Gm17535	c.-3281A>	-	ENSMUST	upstream_gene_variant
9	3031318	rs1133300	A	T	too_few_s	SNV	7	0	7	0	4	1	5	0.2	link	-	Gm10717	c.*4931A>	-	ENSMUST	downstream_gene_variant
9	3031318	rs1133300	A	T	too_few_s	SNV	7	0	7	0	4	1	5	0.2	link	-	Gm26870	n.3031318	-	-	intragenic_variant
9	3031318	rs1133300	A	T	too_few_s	SNV	7	0	7	0	4	1	5	0.2	link	-	Gm10717	n.3031318	-	-	intragenic_variant
9	21928948	.	A	C	base_qual	SNV	18	2	20	0.1	30	3	33	0.091	link	-	Tmem205	c.-2600T>	-	ENSMUST	upstream_gene_variant
9	21928948	.	A	C	base_qual	SNV	18	2	20	0.1	30	3	33	0.091	link	-	Ccdc159	c.36-145A	-	ENSMUST	intron_variant
9	22018407	.	A	C	base_qual	SNV	23	1	24	0.042	24	7	31	0.226	link	-	Elavl3	c.*96T>G	-	ENSMUST	3_prime_UTR_variant
9	22018407	.	A	C	base_qual	SNV	23	1	24	0.042	24	7	31	0.226	link	-	Prkcsh	c.*5245A>	-	ENSMUST	downstream_gene_variant
9	22068628	.	A	G	too_few_s	SNV	13	0	13	0	6	2	8	0.25	link	-	Gm16845	n.-2404A>	-	ENSMUST	upstream_gene_variant
9	22068628	.	A	G	too_few_s	SNV	13	0	13	0	6	2	8	0.25	link	-	Ecsit	c.*3696T>	-	ENSMUST	downstream_gene_variant
9	22068628	.	A	G	too_few_s	SNV	13	0	13	0	6	2	8	0.25	link	-	Zfp653	c.294-437	-	ENSMUST	intron_variant
9	45731984	.	T	G	base_qual	SNV	121	0	121	0	106	18	124	0.145	link	-	Dscaml1	c.3743-43	-	ENSMUST	intron_variant
9	58019521	.	A	T	PASS	SNV	97	0	97	0	93	8	101	0.079	link	-	Cyp11a1	c.820+25A	-	ENSMUST	intron_variant
9	60614945	.	T	A	PASS	SNV	98	0	98	0	75	16	91	0.176	link	-	Lrrc49	c.1203+14	-	ENSMUST	intron_variant
9	64924248	.	C	T	too_few_s	SNV	14	0	14	0	19	2	21	0.095	link	-	Slc24a1	c.*173G>A	-	ENSMUST	3_prime_UTR_variant
9	64924248	.	C	T	too_few_s	SNV	14	0	14	0	19	2	21	0.095	link	-	Dennd4a	c.*7153C>	-	ENSMUST	downstream_gene_variant
9	72971863	.	C	G	base_qual	SNV	32	8	40	0.2	33	20	53	0.377	link	-	Gm23567	n.*2155C>	-	ENSMUST	downstream_gene_variant
9	72971863	.	C	G	base_qual	SNV	32	8	40	0.2	33	20	53	0.377	link	-	Gm37710	n.*422G>(	-	ENSMUST	downstream_gene_variant
9	72971863	.	C	G	base_qual	SNV	32	8	40	0.2	33	20	53	0.377	link	-	Dyx1c1	c.1042-11(	-	ENSMUST	intron_variant
9	72971863	.	C	G	base_qual	SNV	32	8	40	0.2	33	20	53	0.377	link	-	Gm44503	c.1042-11(	-	ENSMUST	intron_variant
9	79673877	.	T	A	too_few_s	SNV	20	0	20	0	13	2	15	0.133	link	-	Col12a1	c.4417+18	-	ENSMUST	intron_variant
9	83857219	.	C	A	base_qual	SNV	23	3	26	0.115	29	5	34	0.147	link	-	Ttk	c.1441-99	-	ENSMUST	intron_variant
9	95885321	.	C	A	base_qual	SNV	119	3	122	0.025	106	6	112	0.054	link	-	Atr	c.3451-21	-	ENSMUST	intron_variant
9	1.03E+08	.	G	T	base_qual	SNV	21	2	23	0.087	18	9	27	0.333	link	-	Topbp1	c.2811-13	-	ENSMUST	intron_variant
9	1.07E+08	.	T	G	base_qual	SNV	125	0	125	0	114	14	128	0.109	link	-	Rad54l2	c.2829+12	-	ENSMUST	intron_variant
9	1.08E+08	.	A	C	base_qual	SNV	79	3	82	0.037	62	6	68	0.088	link	-	Gm9917	n.*1421T>	-	ENSMUST	downstream_gene_variant
9	1.08E+08	.	A	C	base_qual	SNV	79	3	82	0.037	62	6	68	0.088	link	-	Rassf1	c.370-65A	-	ENSMUST	intron_variant
9	1.08E+08	.	A	C	too_few_s	SNV	104	4	108	0.037	100	2	102	0.02	link	-	Gm20529	n.*124A>(	-	ENSMUST	downstream_gene_variant
9	1.08E+08	.	A	C	too_few_s	SNV	104	4	108	0.037	100	2	102	0.02	link	-	Amigo3	c.*3810A>	-	ENSMUST	downstream_gene_variant
9	1.08E+08	.	A	C	too_few_s	SNV	104	4	108	0.037	100	2	102	0.02	link	-	Rnf123	c.2767+67	-	ENSMUST	intron_variant
9	1.09E+08	.	A	T	base_qual	SNV	9	0	9	0	8	3	11	0.273	link	-	Fbxw20	c.622-201	-	ENSMUST	intron_variant
9	1.11E+08	.	A	C	base_qual	SNV	77	0	77	0	72	8	80	0.1	link	-	Als2cl	c.667-89A	-	ENSMUST	intron_variant
9	1.12E+08	.	G	A	alt_allele_i	SNV	35	7	42	0.167	27	14	41	0.341	link	-	Arpp21	c.-35-20C:	-	ENSMUST	intron_variant
X	12048722	.	T	G	base_qual	SNV	19	1	20	0.05	20	9	29	0.31	link	-	Bcor	c.3512-75	-	ENSMUST	intron_variant
X	71376722	.	C	T	too_few_s	SNV	10	0	10	0	17	2	19	0.105	link	-	Mtmr1	c.265-647	-	ENSMUST	intron_variant
X	94387914	.	C	A	weak_evid	SNV	11	0	11	0	6	4	10	0.4	link	-	Apoo	c.334+195	-	ENSMUST	intron_variant
X	1.01E+08	.	G	A	PASS	SNV	90	0	90	0	103	6	109	0.055	link	-	Kif4	c.-1171G>	-	ENSMUST	upstream_gene_variant
GL456211	168106	.	G	T	mapping_(	SNV	185	24	209	0.115	220	39	259	0.151	link	-	AC133103	c.32+118(	-	ENSMUST	intron_variant
GL456221	57314	.	C	T	no_reliabl	SNV	26	1	27	0.037	16	5	21	0.238	link	-	AC132444	c.-1429C>	-	ENSMUST	upstream_gene_variant
GL456221	57314	.	C	T	no_reliabl	SNV	26	1	27	0.037	16	5	21	0.238	link	-	-	n.57314C>	-	-	intergenic_region
GL456221	112949	.	C	G	mapping_(	SNV	39	5	44	0.114	42	15	57	0.263	link	-	Csprs	c.*214G>(	-	ENSMUST	3_prime_UTR_variant
GL456210	956	.	G	A	no_reliabl	SNV	104	4	108	0.037	109	26	135	0.193	link	-	-	n.956G>A	-	-	intergenic_region
JH584292.	3962	.	T	G	mapping_(	SNV	20	3	23	0.13	21	1	22	0.045	link	-	Vmn2r122	c.206+136	-	ENSMUST	intron_variant
1	1.74E+08	.	G	A	PASS	SNV	282	0	282	0	242	40	282	0.142	link	-	Ifi204	c.1731C>T	p.Leu577L	ENSMUST	synonymous_variant
11	87101493	.	A	C	base_qual	SNV	187	4	191	0.021	185	6	191	0.031	link	-	Prr11	c.555T>G	p.Pro185P	ENSMUST	synonymous_variant
11	98982666	.	A	C	base_qual	SNV	141	4	145	0.028	160	14	174	0.08	link	-	Gjd3	c.351T>G	p.Arg117A	ENSMUST	synonymous_variant
11	1.02E+08	.	A	C	base_qual	SNV	140	7	147	0.048	155	19	174	0.109	link	-	Etv4	c.717T>G	p.Ala239A	ENSMUST	synonymous_variant
12	76603392	.	C	G	PASS	SNV	131	0	131	0	140	4	144	0.028	link	-	Sptb	c.5550G>(	p.Val1850	ENSMUST	synonymous_variant
14	79767545	.	C	T	PASS	SNV	275	0	275	0	222	29	251	0.116	link	-	Pcdh8	c.3039G>A	p.Leu1013	ENSMUST	synonymous_variant
15	76173124	.	A	C	base_qual	SNV	282	0	282	0	221	16	237	0.068	link	-	Plec	c.13122T>	p.Thr4374	ENSMUST	synonymous_variant
16	32246767	.	A	C	base_qual	SNV	146	5	151	0.033	145	18	163	0.11	link	-	Fbxo45	c.45T>G	p.Ala15Al	ENSMUST	synonymous_variant
17	74352008	.	A	G	weak_evid	SNV	212	1	213	0.005	223	4	227	0.018	link	-	Spast	c.468A>G	p.Lys156L	ENSMUST	synonymous_variant
19	46515162	.	T	G	base_qual	SNV	249	0	249	0	241	17	258	0.066	link	-	Trim8	c.1152T>(	p.Pro384P	ENSMUST	synonymous_variant
2	11254230	.	C	T	PASS	SNV	160	0	160	0	160	6	166	0.036	link	-	Prkcq	c.960C>T	p.Leu320L	ENSMUST	synonymous_variant
2	1.03E+08	.	A	C	base_qual	SNV	219	12	231	0.052	218	24	242	0.099	link	-	Slc1a2	c.459A>C	p.Leu153L	ENSMUST	synonymous_variant
3	5400849	.	T	A	weak_evid	SNV	148	1	149	0.007	117	5	122	0.041	link	-	Zfhx4	c.6141T>A	p.Pro2047	ENSMUST	synonymous_variant
3	1.08E+08	.	G	C	PASS	SNV	211	0	211	0	198	21	219	0.096	link	-	Gstm3	c.114C>G	p.Ala38Al	ENSMUST	splice_region_variant+synonymous_variant
4	45529904	.	G	C	weak_evid	SNV	197	1	198	0.005	188	5	193	0.026	link	-	Shb	c.357C>G	p.Gly119G	ENSMUST	synonymous_variant
5	3647455	.	A	C	base_qual	SNV	187	6	193	0.031	205	9	214	0.042	link	-	Gatad1	c.165T>G	p.Gly55Gl	ENSMUST	synonymous_variant
5	98186336	.	T	G	base_qual	SNV	156	6	162	0.037	177	16	193	0.083	link	-	Prdm8	c.1761T>(	p.Ala587A	ENSMUST	synonymous_variant
6	1.21E+08	.	T	G	base_qual	SNV	198	0	198	0	192	10	202	0.05	link	-	Mical3	c.4272A>(	p.Ser1424	ENSMUST	synonymous_variant
8	1.13E+08	.	C	T	PASS	SNV	154	0	154	0	172	33	205	0.161	link	-	Cntnap4	c.1476C>T	p.Val492V	ENSMUST	synonymous_variant
9	3025938	.	G	A	weak_evid	SNV	171	0	171	0	313	9	322	0.028	link	-	Gm10717	c.522G>A	p.Gln174G	ENSMUST	synonymous_variant
1	88257866	.	G	A	PASS	SNV	884	0	884	0	893	27	920	0.029	link	-	Mroh2a	c.4617+1(	-	ENSMUST	splice_donor_variant+intron_variant
15	85789122	.	G	A	no_reliabl	SNV	116	0	116	0	101	3	104	0.029	link	-	Ppara	c.508+5G:	-	ENSMUST	splice_region_variant+intron_variant
17	35887543	.	A	C	base_qual	SNV	53	3	56	0.054	51	6	57	0.105	link	-	Dhx16	c.2157+4A	-	ENSMUST	splice_region_variant+intron_variant
19	34040455	.	G	T	base_qual	SNV	116	8	124	0.065	146	8	154	0.052	link	-	Lipk	c.900+7G:	-	ENSMUST	splice_region_variant+intron_variant
2	65748436	.	G	T	base_qual	SNV	146	1	147	0.007	156	3	159	0.019	link	-	Scn2a1	c.4449+5(	-	ENSMUST	splice_region_variant+intron_variant
4	19553904	.	T	A	base_qual	SNV	101	6	107	0.056	101	10	111	0.09	link	-	Cpne3	c.133-7A>	-	ENSMUST	splice_region_variant+intron_variant
6	30370258	.	A	C	base_qual	SNV	115	3	118	0.025	129	6	135	0.044	link	-	Zc3hc1	c.1437+7T	-	ENSMUST	splice_region_variant+intron_variant
6	71238544	.	A	C	base_qual	SNV	132	0	132	0	116	20	136	0.147	link	-	Smyd1	c.528+4T>	-	ENSMUST	splice_region_variant+intron_variant
6	1.25E+08	.	A	C	base_qual	SNV	122	0	122	0	110	19	129	0.147	link	-	Mlf2	c.*24A>C	-	ENSMUST	splice_region_variant
7	23407105	.	T	C	too_few_s	SNV	19	0	19	0	11	2	13	0.154	link	-	Gm25196	n.110T>C	-	ENSMUST	splice_region_variant+non_coding_transcript_exon_variant
7	30241223	.	G	A	weak_evid	SNV	95	1	96	0.01	103	12	115	0.104	link	-	Wdr62	c.4174+8C	-	ENSMUST	splice_region_variant+intron_variant