

Chr	Pos	ID	Ref	Alt	Filter	Variant_Type	Normal_REF	Normal_ALT	Normal_Dep	Normal_Allele	Tumor_REF	Tumor_ALT	Tumor_Dep	Tumor_Allele	igv	ClinVar	Gene_Name	CDS_Chang	Amino_Acid_Change	Transcript1Effect
1	10142391.		GGGGGGG		low_normaDEL	2	0	2	0	13	2	15	0.133	link	-	Arfge1	c.5119+17-		ENSMUST1intron_variant	
1	37911010.		C	CA	alt_allele_iINS	63	14	77	0.182	74	27	101	0.267	link	-	Lyg2	c.187+48d-		ENSMUST1intron_variant	
1	45340451.		TG	T	non_homrDEL	28	7	35	0.2	37	24	61	0.393	link	-	Col3a1	c.2604+15-		ENSMUST1intron_variant	
1	74286149 rs2334631	AG	A		weak_evid DEL	13	2	15	0.133	23	14	37	0.378	link	-	Aamp	c.-1527del-		ENSMUST1upstream_gene_variant	
1	74286149 rs2334631	AG	A		weak_evid DEL	13	2	15	0.133	23	14	37	0.378	link	-	Tmbim1	c.*3222del-		ENSMUST1downstream_gene_variant	
1	74286149 rs2334631	AG	A		weak_evid DEL	13	2	15	0.133	23	14	37	0.378	link	-	Gm28364	n.*4284del-		ENSMUST1downstream_gene_variant	
1	74286149 rs2334631	AG	A		weak_evid DEL	13	2	15	0.133	23	14	37	0.378	link	-	Gm37503	n.*1392del-		ENSMUST1downstream_gene_variant	
1	74286149 rs234631	AG	A		weak_evid DEL	13	2	15	0.133	23	14	37	0.378	link	-	Prkcd	c.236+151-		ENSMUST1intron_variant	
1	74890409.		TC	T	non_homrDEL	13	3	16	0.188	24	12	36	0.333	link	-	Fev	c.-5200del-		ENSMUST1upstream_gene_variant	
1	74890409.		TC	T	non_homrDEL	13	3	16	0.188	24	12	36	0.333	link	-	Cryba2	c.446+121-		ENSMUST1intron_variant	
1	81087326.		CT	C	weak_evid DEL	318	1	319	0.003	315	7	322	0.022	link	-	Nypa2	c.59delT	p.Phe20fs	ENSMUST1frameshift_variant	
1	85584067.		A	AAAAAGAA	weak_evid INS	3	0	3	0	1	3	4	0.75	link	-	Sp110	c.971-495,-		ENSMUST1intron_variant	
1	87853348.		TCCG	T	weak_evid DEL	186	1	187	0.005	253	8	261	0.031	link	-	Dgkd	c.60_62del p.Pro21del		ENSMUST1disruptive_inframe_deletion	
1	87853348.		TCCG	T	weak_evid DEL	186	1	187	0.005	253	8	261	0.031	link	-	Gm19582	n.837_839c-		ENSMUST1splice_region_variant+non_coding_transcript_exon_variant	
1	88238229.		G	GGA	non_homrINS	14	0	14	0	52	0	52	0	link	-	Mroh2a	c.1554+27-		ENSMUST1intron_variant	
1	88241890.		T	TTTTTTT	low_frac_iINS	11	1	12	0.083	32	15	47	0.319	link	-	Mroh2a	c.2046+24-		ENSMUST1intron_variant	
1	88251620.		A	AAAG	PASS INS	19	0	19	0	39	15	54	0.278	link	-	Mroh2a	c.3351+22-		ENSMUST1intron_variant	
1	88267615 rs2392254	A	AG		weak_evid INS	4	0	4	0	18	8	26	0.308	link	-	Hjupr	c.526+332-		ENSMUST1intron_variant	
1	90798307.		TG	T	non_homrDEL	25	3	28	0.107	30	7	37	0.189	link	-	Col6a3	c.5909-111-		ENSMUST1intron_variant	
1	93190738.		CG	C	non_homrDEL	29	5	34	0.147	56	23	79	0.291	link	-	Crocc2	c.1323+70-		ENSMUST1intron_variant	
1	1.31E+08 rs1135129	TG	T		non_homrDEL	94	5	99	0.051	92	18	110	0.164	link	-	Pigr	c.1042+34-		ENSMUST1intron_variant	
1	1.32E+08.		AC	A	non_homrDEL	60	5	65	0.077	77	12	89	0.135	link	-	Mfsd4a	c.681+43d-		ENSMUST1intron_variant	
1	1.32E+08.		AC	A	non_homrDEL	60	5	65	0.077	77	12	89	0.135	link	-	Gm26892	n.1395-101-		ENSMUST1intron_variant	
1	1.33E+08.		TG	T	non_homrDEL	39	8	47	0.17	63	26	89	0.292	link	-	Sox13	c.640-75dc-		ENSMUST1intron_variant	
1	1.36E+08.		AT	A	non_homrDEL	32	10	42	0.238	48	32	80	0.4	link	-	Mroh3	c.2103+96-		ENSMUST1intron_variant	
1	1.58E+08.		TG	T	non_homrDEL	31	8	39	0.205	37	18	55	0.327	link	-	Brnp2	c.776-52dc-		ENSMUST1intron_variant	
1	1.74E+08.		T	TACAC	non_homrINS	5	0	5	0	4	0	4	0	link	-	Spta1	c.1107-195-		ENSMUST1intron_variant	
1	1.78E+08.		AC	A	non_homrDEL	148	12	160	0.075	181	20	201	0.1	link	-	Gm16432	c.68+45dc-		ENSMUST1intron_variant	
1	1.78E+08.		AC	A	non_homrDEL	148	12	160	0.075	181	20	201	0.1	link	-	Gm37313	n.47-171bc-		ENSMUST1intron_variant	
10	61218683.		A	ACT	low_frac_iINS	3	0	3	0	10	5	15	0.333	link	-	Adamt5	c.1719-15c-		ENSMUST1intron_variant	
10	80676191.		TGCCGCC	T	non_homrDEL	353	5	358	0.014	613	14	627	0.022	link	-	Mknk2	c.-204,-17-		ENSMUST15_prime_UTR_variant	
10	88982346.		GC	G	non_homrDEL	52	9	61	0.148	83	19	102	0.186	link	-	Ano4	c.1739-59c-		ENSMUST1intron_variant	
10	1.28E+08.		CG	C	non_homrDEL	71	26	97	0.268	105	45	150	0.3	link	-	Ndufa4i2	c.*2576del-		ENSMUST1downstream_gene_variant	
10	1.28E+08.		CG	C	non_homrDEL	71	26	97	0.268	105	45	150	0.3	link	-	Shmt2	c.857+46d-		ENSMUST1intron_variant	
11	5063764.		TG	T	PASS DEL	56	10	66	0.152	66	30	96	0.312	link	-	Rasl10a	c.*3700del-		ENSMUST1downstream_gene_variant	
11	5063764.		TG	T	PASS DEL	56	10	66	0.152	66	30	96	0.312	link	-	Gas2l1	c.633+61d-		ENSMUST1intron_variant	
11	61487293.		CG	C	alt_allele_iDEL	31	23	54	0.426	31	37	68	0.544	link	-	Mapk7	c.*1823del-		ENSMUST1downstream_gene_variant	
11	61487293.		CG	C	alt_allele_iDEL	31	23	54	0.426	31	37	68	0.544	link	-	Mfap4	c.598-46d-		ENSMUST1intron_variant	
11	67299152.		CCCTT	C	non_homrDEL	25	2	27	0.074	45	13	58	0.224	link	-	Myl8	c.373bc-62,-		ENSMUST1intron_variant	
11	69657662.		TAC	T	non_homrDEL	148	29	177	0.164	237	63	300	0.21	link	-	Fxr2	c.*4964.*4-		ENSMUST1downstream_gene_variant	
11	69657662.		TAC	T	non_homrDEL	148	29	177	0.164	237	63	300	0.21	link	-	Sox15	c.*1042.*1-		ENSMUST1downstream_gene_variant	
11	69657662.		TAC	T	non_homrDEL	148	29	177	0.164	237	63	300	0.21	link	-	Mpdu1	c.507+61,-		ENSMUST1intron_variant	
11	98389961 rs1133692	AG	A		non_homrDEL	65	17	82	0.207	74	32	106	0.302	link	-	Pgap3	c.*76delC-		ENSMUST13_prime_UTR_variant	
11	98389961 rs1133692	AG	A		non_homrDEL	65	17	82	0.207	74	32	106	0.302	link	-	Pgmt	c.*1865del-		ENSMUST1downstream_gene_variant	
11	1E+08.		TG	T	weak_evid DEL	4	0	4	0	1	6	7	0.857	link	-	Jup	c.707+265-		ENSMUST1intron_variant	
11	1.01E+08 rs3871683	TC	T		non_homrDEL	57	10	67	0.149	75	25	100	0.25	link	-	Kcnh4	c.829+48d-		ENSMUST1intron_variant	
11	1.16E+08.		CG	C	non_homrDEL	20	11	31	0.355	36	54	90	0.6	link	-	Ligl2	c.-12972dc-		ENSMUST1upstream_gene_variant	
11	1.16E+08.		CG	C	non_homrDEL	20	11	31	0.355	36	54	90	0.6	link	-	Tsen54	c.1311-13c-		ENSMUST1intron_variant	
11	1.18E+08 rs2391229	TC	T		alt_allele_iDEL	29	9	38	0.237	54	33	87	0.379	link	-	Dnah17	c.11764-1c-		ENSMUST1intron_variant	
11	1.18E+08 rs2501790	AC	A		non_homrDEL	36	7	43	0.163	50	18	68	0.265	link	-	Dnah17	c.4215+12-		ENSMUST1intron_variant	
12	86744520.		AT	A	weak_evid DEL	8	0	8	0	9	3	12	0.25	link	-	Lrrc47a	c.551-474c-		ENSMUST1intron_variant	
12	1E+08.		AG	A	non_homrDEL	72	20	92	0.217	88	35	123	0.285	link	-	Ttc7b	c.1967-36c-		ENSMUST1intron_variant	
12	1.04E+08.		AG	A	non_homrDEL	99	12	111	0.108	132	28	160	0.175	link	-	Serpina1a	c.698-73dc-		ENSMUST1intron_variant	
12	1.07E+08.		CTCCTCT	C	low_frac_iDEL	139	6	145	0.041	177	15	192	0.078	link	-		n.10711111-		- intergenic_region	
12	1.09E+08.		CGAC	C	weak_evid DEL	298	8	306	0.026	442	23	465	0.049	link	-	Yy1	c.141_143cp.Glu47del		ENSMUST1disruptive_inframe_deletion	
12	1.14E+08.		T	TG	non_homrINS	141	13	154	0.084	147	30	177	0.169	link	-	Gm7003	n.-4501_4-		ENSMUST1upstream_gene_variant	
12	1.14E+08.		T	TG	non_homrINS	141	13	154	0.084	147	30	177	0.169	link	-	Ighv2-7	c.-87_-86ir-		ENSMUST1upstream_gene_variant	
12	1.14E+08.		T	TG	non_homrINS	141	13	154	0.084	147	30	177	0.169	link	-		n.1138078c-		- intergenic_region	
13	93144271.		TG	T	non_homrDEL	43	14	57	0.246	65	43	108	0.398	link	-	Papd4	c.*3319del-		ENSMUST1downstream_gene_variant	
13	93144271.		TG	T	non_homrDEL	43	14	57	0.246	65	43	108	0.398	link	-	Cmya5	c.149+86d-		ENSMUST1intron_variant	
13	98145443 rs1132873	GC	G		non_homrDEL	48	9	57	0.158	38	10	48	0.208	link	-	Arhgef2f	c.33+108d-		ENSMUST1intron_variant	
14	13899688.		GT	G	weak_evid DEL	114	1	115	0.009	124	8	132	0.061	link	-	Gm281	c.241-9del-		ENSMUST1intron_variant	
14	20264127.		AGG	A	low_frac_iDEL	48	11	59	0.186	82	30	112	0.268	link	-	Kcnk16	c.495+31,-		ENSMUST1intron_variant	
14	23336074.		G	GT	weak_evid INS	362	1	363	0.003	307	7	314	0.022	link	-	Kcnma1	c.3028+87-		ENSMUST1intron_variant	
14	56060155.		AC	A	non_homrDEL	108	9	117	0.077	137	34	171	0.199	link	-	Mcp4	c.598-56dc-		ENSMUST1intron_variant	
14	63017696.		AC	A	non_homrDEL	21	4	25	0.16	16	12	28	0.429	link	-	Defb43	c.59-70del-		ENSMUST1intron_variant	
14	64075698.		CT	C	weak_evid DEL	333	3	336	0.009	338	10	348	0.029	link	-	Prss55	c.735delA	p.Gly246fs	ENSMUST1frameshift_variant	
14	67008604.		AC	A	non_homrDEL	33	12	45	0.267	74	34	108	0.315	link	-	Bnip3l	c.97+83dc-		ENSMUST1intron_variant	
14	70493039 rs2221378	TG	T		non_homrDEL	14	3	17	0.176	21	9	30	0.3	link	-	Bmp1	c.1196-14c-		ENSMUST1intron_variant	
14	78949762.		TTTTG	T	too_few_sDEL	9	0	9	0	13	2	15	0.133	link	-	Vwa8	c.1422+20-		ENSMUST1intron_variant	
15	33381280 rs2217221	T	TTTA		weak_evid INS	92	1	93	0.011	65	6	71	0.085	link	-	Cpq	c.844-8_84-		ENSMUST1splice_region_variant+intron_variant	
15	84032874.		AC	A	non_homrDEL	46	16	62	0.258	39	23	62	0.371	link	-	Rpl31-ps2n.*2200del-			ENSMUST1disruptive_inframe_deletion	
15	84032874.		AC	A	non_homrDEL	46	16	62	0.258	39	23	62	0.371	link	-	Efcab6	c.429+54d-		ENSMUST1intron_variant	
15	91182564.		AG	A	alt_allele_iDEL	20	6	26	0.231	38	23	61	0.377	link	-	Abcd2	c.1242+11-		ENSMUST1intron_variant	
15	97979015 rs2165853	AC	A		non_homrDEL	102	16	118	0.136	156	35	191	0.183	link	-	Col2a1	c.3436-85c-		ENSMUST1intron_variant	
15	98721392.		CTGTGTG	C	base_quali DEL	6	0	6	0	9	1	10	0.1	link	-	Fkbp11	c.*2961.*2-		ENSMUST1downstream_gene_variant	
15	98721392.		CTGTGTG	C	base_quali DEL	6	0	6	0	9	1	10	0.1	link	-					

19	5874821	TG	T	PASS	DEL	199	14	213	0.066	248	45	293	0.154	link	-	Slc25a45	c.-3833del-	ENSMUSTupstream_gene_variant
19	5874821	TG	T	PASS	DEL	199	14	213	0.066	248	45	293	0.154	link	-	Frmcd8	c.1-28delC-	ENSMUSTintron_variant
19	6857598	GC	G	non_homr	DEL	115	6	121	0.05	135	11	146	0.075	link	-	Ccdc88b	c.218+35d-	ENSMUSTintron_variant
19	10638235	AC	A	non_homr	DEL	46	15	61	0.246	84	46	130	0.354	link	-	Vwce	c.424+68d-	ENSMUSTintron_variant
19	32652131	G	GA	weak_evid	INS	106	6	112	0.054	120	21	141	0.149	link	-	Papsa2	c.1089+40-	ENSMUSTintron_variant
19	42147489	CGGAGCA	C	too_few_s	DEL	26	0	26	0	44	2	46	0.043	link	-	Marveld1	c.-103_-86-	ENSMUST5_prime_UTR_variant
19	46306712	CGG	C	alt_allele_i	DEL	33	28	61	0.459	51	67	118	0.568	link	-	Nfkfb2	c.145+43de-	ENSMUSTintron_variant
2	26470016	AG	A	weak_evid	DEL	356	3	359	0.008	439	10	449	0.022	link	-	Notch1	c.3685delCp.Asp1230fs	ENSMUSTframeshift_variant
2	26470016	AG	A	weak_evid	DEL	356	3	359	0.008	439	10	449	0.022	link	-	Mir6996	n.*42delC-	ENSMUSTdownstream_gene_variant
2	85042220	AC	A	non_homr	DEL	81	7	88	0.08	103	16	119	0.134	link	-	Ssrp1	c.1224-13c-	ENSMUSTintron_variant
2	1.17E+08	AG	A	alt_allele_i	DEL	42	9	51	0.176	77	43	120	0.358	link	-	Rasgrp1	c.2253+35-	ENSMUSTintron_variant
2	1.21E+08	TC	T	weak_evid	DEL	160	1	161	0.006	242	5	247	0.02	link	-	AV039307	n.-305delC-	ENSMUSTupstream_gene_variant
2	1.21E+08	TC	T	weak_evid	DEL	160	1	161	0.006	242	5	247	0.02	link	-	Ttbk2	c.66+56de-	ENSMUSTintron_variant
2	1.3E+08 rs1134907	AC	A	non_homr	DEL	35	14	49	0.286	47	34	81	0.42	link	-	Tmem239	c.*110delC-	ENSMUST3_prime_UTR_variant
2	1.3E+08 rs1134907	AC	A	non_homr	DEL	35	14	49	0.286	47	34	81	0.42	link	-	Gm28372	c.*75delC-	ENSMUST3_prime_UTR_variant
2	1.3E+08 rs1134907	AC	A	non_homr	DEL	35	14	49	0.286	47	34	81	0.42	link	-	1700020A	c.*1259del-	ENSMUSTdownstream_gene_variant
2	1.52E+08 rs1134349	AC	A	non_homr	DEL	63	11	74	0.149	32	13	45	0.289	link	-	Rad21l	c.1392+10-	ENSMUSTintron_variant
2	1.58E+08	CG	G	non_homr	DEL	61	8	69	0.116	81	27	108	0.25	link	-	Bpi	c.533+49d-	ENSMUSTintron_variant
2	1.65E+08	CG	C	alt_allele_i	DEL	28	17	45	0.378	51	38	89	0.427	link	-	Pcif1	c.*3372del-	ENSMUSTdownstream_gene_variant
2	1.65E+08	CG	C	alt_allele_i	DEL	28	17	45	0.378	51	38	89	0.427	link	-	Zfp335	c.3189+36-	ENSMUSTintron_variant
2	1.67E+08	TG	T	non_homr	DEL	24	6	30	0.2	51	21	72	0.292	link	-	Prex1	c.2625+92-	ENSMUSTintron_variant
2	1.74E+08	TC	T	alt_allele_i	DEL	16	27	43	0.628	21	28	49	0.571	link	-	Ankrd60	c.-62delG-	ENSMUSTupstream_gene_variant
2	1.74E+08	TC	T	alt_allele_i	DEL	16	27	43	0.628	21	28	49	0.571	link	-	Ppp4r1l-prn	*2035del-	ENSMUSTdownstream_gene_variant
2	1.74E+08	TC	T	alt_allele_i	DEL	16	27	43	0.628	21	28	49	0.571	link	-	-	n.1735784d-	intergenic_region
3	95764220	AG	A	weak_evid	DEL	240	3	243	0.012	334	12	346	0.035	link	-	Rprd2	c.3869delCp.Pro1290fs	ENSMUSTframeshift_variant
3	96647382	GC	G	PASS	DEL	271	0	271	0	293	55	348	0.158	link	-	Gm42957	c.738delC p.Trp247fs	ENSMUSTframeshift_variant
3	96647382	GC	G	PASS	DEL	271	0	271	0	293	55	348	0.158	link	-	Itga10	c.183delC p.Trp62fs	ENSMUSTframeshift_variant
3	96647382	GC	G	PASS	DEL	271	0	271	0	293	55	348	0.158	link	-	Pex11b	c.*3403del-	ENSMUSTdownstream_gene_variant
3	1.06E+08	C	CTGTGTG	multiallelic	INS	3	0	3	0	2	3	5	0.6	link	-	Chia1	c.1177+39-	ENSMUSTintron_variant
3	1.06E+08	C	CTGTG	multiallelic	INS	3	0	3	0	4	1	5	0.2	link	-	Chia1	c.1177+40-	ENSMUSTintron_variant
3	1.07E+08	AT	A	alt_allele_i	DEL	27	12	39	0.308	36	36	72	0.5	link	-	Prok1	c.*2775del-	ENSMUSTdownstream_gene_variant
3	1.07E+08	AT	A	alt_allele_i	DEL	27	12	39	0.308	36	36	72	0.5	link	-	A6300761	c.84+132d-	ENSMUSTintron_variant
3	1.38E+08	A	AT	non_homr	INS	6	0	6	0	6	4	10	0.4	link	-	Ddit4l	c.*176dup-	ENSMUST3_prime_UTR_variant
4	3173957	CTG	C	weak_evid	DEL	7	0	7	0	7	3	10	0.3	link	-	Vmn1r2	c.*955_*95-	ENSMUSTdownstream_gene_variant
4	3173957	CTG	C	weak_evid	DEL	7	0	7	0	7	3	10	0.3	link	-	-	n.3173958-	intergenic_region
4	8828216	GC	G	alt_allele_i	DEL	81	29	110	0.264	111	52	163	0.319	link	-	Chd7	c.3172-3de-	ENSMUSTsplice_region_variant+intron_variant
4	1.14E+08	CT	C	non_homr	DEL	25	6	31	0.194	19	21	40	0.525	link	-	Skint5	c.2792-124-	ENSMUSTintron_variant
4	1.18E+08	C	CG	non_homr	INS	207	14	221	0.063	218	51	269	0.19	link	-	Cdc20	c.*1596dup-	ENSMUSTdownstream_gene_variant
4	1.18E+08	C	CG	non_homr	INS	207	14	221	0.063	218	51	269	0.19	link	-	Elovl1	c.376-33de-	ENSMUSTintron_variant
4	1.34E+08	AC	A	alt_allele_i	DEL	25	39	64	0.609	30	45	75	0.6	link	-	Catsper4	c.-1581del-	ENSMUSTupstream_gene_variant
4	1.34E+08	AC	A	alt_allele_i	DEL	25	39	64	0.609	30	45	75	0.6	link	-	Cnksr1	c.1833+21-	ENSMUSTintron_variant
4	1.48E+08	TA	TA	mapping_c	INS	64	1	65	0.015	110	15	125	0.12	link	-	Zfp982	c.157+117-	ENSMUSTintron_variant
4	1.48E+08	GAGAGAAG	A	non_homr	DEL	32	4	36	0.111	38	17	55	0.309	link	-	Zfp534	c.31-477_3-	ENSMUSTintron_variant
4	1.52E+08	TCTCC	T	weak_evid	DEL	15	0	15	0	45	3	48	0.062	link	-	Dnajc11	c.*3167_*3-	ENSMUSTdownstream_gene_variant
4	1.52E+08	TCTCC	T	weak_evid	DEL	15	0	15	0	45	3	48	0.062	link	-	Thap3	c.268-162-	ENSMUSTintron_variant
4	1.56E+08	AC	A	non_homr	DEL	35	6	41	0.146	63	23	86	0.267	link	-	Isig15	c.*50delG-	ENSMUST3_prime_UTR_variant
4	1.56E+08	AC	A	non_homr	DEL	35	6	41	0.146	63	23	86	0.267	link	-	Agri	c.-2114del-	ENSMUSTupstream_gene_variant
4	1.56E+08	AC	A	non_homr	DEL	35	6	41	0.146	63	23	86	0.267	link	-	AW011738	c.-3774del-	ENSMUSTupstream_gene_variant
5	14976083	AC	A	mapping_c	DEL	256	0	256	0	336	8	344	0.023	link	-	Gm10354	c.443+115-	ENSMUSTintron_variant
5	15581038	AC	A	mapping_c	DEL	74	0	74	0	98	6	104	0.058	link	-	Gm21847	n.222+551-	ENSMUSTintron_variant
5	15581038	AC	A	mapping_c	DEL	74	0	74	0	98	6	104	0.058	link	-	Gm30613	n.211-271c-	ENSMUSTintron_variant
5	15581038	AC	A	mapping_c	DEL	74	0	74	0	98	6	104	0.058	link	-	Gm21083	c.627+215-	ENSMUSTintron_variant
5	15621567	CAG	C	mapping_c	DEL	69	0	69	0	92	2	94	0.021	link	-	Gm21847	n.223-342c-	ENSMUSTintron_variant
5	15621567	CAG	C	mapping_c	DEL	69	0	69	0	92	2	94	0.021	link	-	Speer4d	c.168-96_1-	ENSMUSTintron_variant
5	31643310	AC	A	non_homr	DEL	68	13	81	0.16	79	34	113	0.301	link	-	Rbks	c.798+441-	ENSMUSTintron_variant
5	31643310	AC	A	non_homr	DEL	68	13	81	0.16	79	34	113	0.301	link	-	Mrp133	c.149-6981-	ENSMUSTintron_variant
5	31643310	AC	A	non_homr	DEL	68	13	81	0.16	79	34	113	0.301	link	-	Gm43809	n.191+268-	ENSMUSTintron_variant
5	35043063 rs2124468	TG	T	alt_allele_i	DEL	14	3	17	0.176	45	19	64	0.297	link	-	Rgs12	c.*3675del-	ENSMUSTdownstream_gene_variant
5	35043063 rs2124468	TG	T	alt_allele_i	DEL	14	3	17	0.176	45	19	64	0.297	link	-	Hgfac	c.466+139-	ENSMUSTintron_variant
5	65453141	AC	A	non_homr	DEL	46	13	59	0.22	79	34	113	0.301	link	-	Gm43552	c.75+152c-	ENSMUSTintron_variant
5	65453141	AC	A	non_homr	DEL	46	13	59	0.22	79	34	113	0.301	link	-	Smin14	c.267+44d-	ENSMUSTintron_variant
5	92409197	TG	T	non_homr	DEL	79	17	96	0.177	107	42	149	0.282	link	-	Art3	c.904-61de-	ENSMUSTintron_variant
5	1.15E+08	TC	T	non_homr	DEL	68	8	76	0.105	74	22	96	0.229	link	-	2610524H	c.-74delG-	ENSMUSTupstream_gene_variant
5	1.15E+08	TC	T	non_homr	DEL	68	8	76	0.105	74	22	96	0.229	link	-	Gm20499	c.-74delG-	ENSMUSTupstream_gene_variant
5	1.15E+08	TC	T	non_homr	DEL	68	8	76	0.105	74	22	96	0.229	link	-	-	n.1148235-	intergenic_region
5	1.37E+08	CG	C	non_homr	DEL	82	20	102	0.196	84	43	127	0.339	link	-	Serpine1	c.1-53del-	ENSMUSTintron_variant
5	1.38E+08	GC	G	non_homr	DEL	46	9	55	0.164	90	26	116	0.224	link	-	Pcolce	c.797+72d-	ENSMUSTintron_variant
5	1.4E+08 rs2493274	TC	T	non_homr	DEL	38	9	47	0.191	62	32	94	0.34	link	-	Mir7037	n.-670delG-	ENSMUSTupstream_gene_variant
5	1.4E+08 rs2493274	TC	T	non_homr	DEL	38	9	47	0.191	62	32	94	0.34	link	-	Ints1	c.1920-111-	ENSMUSTintron_variant
5	1.4E+08	GAAA	G	weak_evid	DEL	6	0	6	0	9	4	13	0.308	link	-	Gm42805	n.-2806_-2-	ENSMUSTupstream_gene_variant
5	1.4E+08	GAAA	G	weak_evid	DEL	6	0	6	0	9	4	13	0.308	link	-	Gm4869	c.199-198-	ENSMUSTintron_variant
5	1.43E+08	G	GTTTTTTT	base_quali	INS	84	7	91	0.077	76	15	91	0.165	link	-	Daglb	c.248-22_2-	ENSMUSTintron_variant
5	29938958	G	GCCCCC	too_few_s	INS	27	0	27	0	33	0	33	0	link	-	Strip2	c.1680-76-	ENSMUSTintron_variant
6	38077076	T	TAC	non_homr	INS	3	0	3	0	7	4	11	0.364	link	-	Atp6v0a4	c.1030-24c-	ENSMUSTintron_variant
6	40387360	TGA	T	weak_evid	DEL	30	0	30	0	37	7	44	0.159	link	-	Agk	c.875-70_8-	ENSMUSTintron_variant
6	48613057	TC	T	weak_evid	DEL	42	8	50	0.16	48	18	66	0.273	link	-	Zfp775	c.-171delC-	ENSMUSTupstream_gene_variant
6	48613057	TC	T	weak_evid	DEL	42	8	50	0.16	48	18	66	0.273	link	-	Gm44119	n.*915delC-	ENSMUSTdownstream_gene_variant
6	48613057	TC	T	weak_evid	DEL	42	8	50	0.16	48	18	66	0.273	link	-	Gm44965	c.151-109c-	ENSMUSTintron_variant
6	48613057	TC	T	weak_evid	DEL	42	8	50	0.16	48	18	66	0.273	link	-	Gm45021	c.-51-109d-	ENSMUSTintron_variant
6	48613057	TC	T	weak_evid	DEL	42	8	50	0.16	48	18	66	0.273	link	-	Zfp775	n.4861306l-	intragenic_variant
6	54842540	GCCC	G	weak														

8	1.07E+08.	CT	C	weak_evid	DEL	260	1	261	0.004	304	7	311	0.023	link	-	Cog8	c.*3797del-	ENSMUST	downstream_gene_variant
8	1.07E+08.	CT	C	weak_evid	DEL	260	1	261	0.004	304	7	311	0.023	link	-	Pdf	c.*2103del-	ENSMUST	downstream_gene_variant
8	1.07E+08.	CT	C	weak_evid	DEL	260	1	261	0.004	304	7	311	0.023	link	-	Vps4a	c.1213-24c-	ENSMUST	intron_variant
8	1.07E+08.	CT	C	weak_evid	DEL	260	1	261	0.004	304	7	311	0.023	link	-	Pdf	n.1070450-	-	intragenic_variant
8	1.14E+08 rs1133198	TC	T	non_homr	DEL	93	6	99	0.061	96	12	108	0.111	link	-	Vat1l	c.1072-34c-	ENSMUST	intron_variant
9	3027600.	CT	C	too_few_s	DEL	13	0	13	0	3	2	5	0.4	link	-	Gm10718	c.*2383del-	ENSMUST	downstream_gene_variant
9	3027600.	CT	C	too_few_s	DEL	13	0	13	0	3	2	5	0.4	link	-	Gm10717	c.*1214del-	ENSMUST	downstream_gene_variant
9	3027600.	CT	C	too_few_s	DEL	13	0	13	0	3	2	5	0.4	link	-	Gm26870	n.3027601-	ENSMUST	intragenic_variant
9	3027600.	CT	C	too_few_s	DEL	13	0	13	0	3	2	5	0.4	link	-	Gm10717	n.3027605-	ENSMUST	intragenic_variant
9	21485535 rs2314181	AG	A	non_homr	DEL	31	12	43	0.279	47	37	84	0.44	link	-	Dnm2	c.1423-104-	ENSMUST	intron_variant
9	21732198.	TCACACA	T	weak_evid	DEL	48	2	50	0.04	51	30	81	0.37	link	-	Ldfr	c.191-71_1-	ENSMUST	intron_variant
9	35047192 rs2270498	ACC	A	non_homr	DEL	3	0	3	0	1	5	6	0.833	link	-	Slc3a4	c.*239_+24-	ENSMUST	3_prime_UTR_variant
9	37417160.	AG	A	non_homr	DEL	69	14	83	0.169	84	31	115	0.27	link	-	Robo4	c.*3774del-	ENSMUST	downstream_gene_variant
9	37417160.	AG	A	non_homr	DEL	69	14	83	0.169	84	31	115	0.27	link	-	Robo3	c.3973+16-	ENSMUST	intron_variant
9	38499572.	TA	T	PASS	DEL	193	0	193	0	110	55	165	0.333	link	-	Olfir907	c.910delA p.Thr304fs	ENSMUST	frameshift_variant
9	51076255.	AC	A	weak_evid	DEL	38	5	43	0.116	41	17	58	0.293	link	-	Layn	c.109+66d-	ENSMUST	intron_variant
9	56995880.	CG	C	weak_evid	DEL	8	0	8	0	10	11	21	0.524	link	-	Ptpn9	c.63+237d-	ENSMUST	intron_variant
9	58032602.	TG	T	non_homr	DEL	71	9	80	0.113	129	26	155	0.168	link	-	Ccdc33	c.2275+79-	ENSMUST	intron_variant
9	58032602.	TG	T	non_homr	DEL	71	9	80	0.113	129	26	155	0.168	link	-	Gm16130	n.243+97d-	ENSMUST	intron_variant
9	65488934 rs2269634	GC	G	weak_evid	DEL	129	4	133	0.03	143	12	155	0.077	link	-	Spq21	c.*1986del-	ENSMUST	downstream_gene_variant
9	65488934 rs2269634	GC	G	weak_evid	DEL	129	4	133	0.03	143	12	155	0.077	link	-	-	n.6548893!	-	intergenic_region
9	1.08E+08.	CG	C	non_homr	DEL	170	21	191	0.11	180	36	216	0.167	link	-	Cacna2d2	c.1782+32-	ENSMUST	intron_variant
9	1.08E+08 rs2545454	AC	A	non_homr	DEL	159	23	182	0.126	212	49	261	0.188	link	-	Usp19	c.1839+25-	ENSMUST	intron_variant
9	1.09E+08.	GC	G	weak_evid	DEL	69	10	79	0.127	71	22	93	0.237	link	-	Mir171	n.*2120del-	ENSMUST	downstream_gene_variant
9	1.09E+08.	GC	G	weak_evid	DEL	69	10	79	0.127	71	22	93	0.237	link	-	Col7a1	c.5754+59-	ENSMUST	intron_variant
X	1.02E+08.	TG	T	non_homr	DEL	94	3	97	0.031	125	10	135	0.074	link	-	Gm14858	n.-2192del-	ENSMUST	upstream_gene_variant
X	1.02E+08.	TG	T	non_homr	DEL	94	3	97	0.031	125	10	135	0.074	link	-	Gm26318	n.*4971del-	ENSMUST	downstream_gene_variant
X	1.02E+08.	TG	T	non_homr	DEL	94	3	97	0.031	125	10	135	0.074	link	-	Cited1	c.-66+157l-	ENSMUST	intron_variant
X	1.41E+08.	TG	T	alt_allele_i	DEL	20	8	28	0.286	8	28	36	0.778	link	-	Col4a6	c.1429+42-	ENSMUST	intron_variant
X	1.43E+08.	TGCC	T	weak_evid	DEL	170	20	190	0.105	172	31	203	0.153	link	-	Ammecr1	c.268_270c.p.Gly90del	ENSMUST	conservative_inframe_deletion
X	1.43E+08.	TGCC	T	weak_evid	DEL	170	20	190	0.105	172	31	203	0.153	link	-	Gm44351	n.-3749_-3-	ENSMUST	upstream_gene_variant
X	1.54E+08.	C	CT	non_homr	INS	3	0	3	0	5	5	10	0.5	link	-	Z2100130;c.*247-181-	-	ENSMUST	intron_variant
X	1.6E+08.	TCC	T	non_homr	DEL	9	0	9	0	13	7	20	0.35	link	-	Sh3kbp1	c.858+100-	ENSMUST	intron_variant
Y	2786902.	AAAGGGA	A	weak_evid	DEL	22	0	22	0	36	11	47	0.234	link	-	Gm4064	c.737+160-	ENSMUST	intron_variant
GL456210.	130509.	AACAAAC(A	A	long_indel	DEL	456	0	456	0	508	0	508	0	link	-	AC125149.c.*4720_+4-	-	ENSMUST	downstream_gene_variant
GL456210.	130509.	AACAAAC(A	A	long_indel	DEL	456	0	456	0	508	0	508	0	link	-	-	n.130510_-	-	intergenic_region
JH584292.	3788.	T	TTATACT	too_few_s	INS	385	0	385	0	374	0	374	0	link	-	Vmn2r122	c.168_169p.p.Ile57fs	ENSMUST	frameshift_variant
1	6244849.	C	G	PASS	SNV	312	0	312	0	259	52	311	0.167	link	-	Rb1cc1	c.1225C>C p.Pro409Ala	ENSMUST	missense_variant
10	78036761.	C	T	PASS	SNV	456	0	456	0	322	73	395	0.185	link	-	Aire	c.1025G>A p.Cys342Tyr	ENSMUST	missense_variant
11	116E+08.	C	T	PASS	SNV	226	0	226	0	199	7	206	0.034	link	-	Gga3	c.488G>A p.Arg163Gln	ENSMUST	missense_variant
14	4779246.	C	A	PASS	SNV	158	0	158	0	131	59	190	0.311	link	-	Gm9602	c.463C>A p.Leu155Ile	ENSMUST	missense_variant
14	14850891.	T	C	PASS	SNV	317	0	317	0	298	7	305	0.023	link	-	Nek10	c.935T>C p.Ile312Thr	ENSMUST	missense_variant
14	70422643.	G	A	PASS	SNV	279	0	279	0	251	14	265	0.053	link	-	Piwil2	c.404C>T p.Ser135Phe	ENSMUST	missense_variant
15	59359307.	C	T	PASS	SNV	282	0	282	0	292	4	296	0.014	link	-	E430025E;c.1106G>A p.Cys369Tyr	-	ENSMUST	missense_variant
15	76065020.	G	C	PASS	SNV	384	0	384	0	392	67	459	0.146	link	-	Scrib	c.1163C>C p.Ala388Gly	ENSMUST	missense_variant
16	10731784.	C	T	PASS	SNV	196	0	196	0	220	7	227	0.031	link	-	Clec16a	c.2720C>T p.Ser907Phe	ENSMUST	missense_variant
18	12909903.	T	G	PASS	SNV	261	1	262	0.004	225	12	237	0.051	link	-	Osbp1a	c.580A>C p.Lys194Gln	ENSMUST	missense_variant
2	1.27E+08.	A	G	PASS	SNV	261	0	261	0	272	4	276	0.014	link	-	Slc27a2	c.521A>G p.Lys174Arg	ENSMUST	missense_variant
3	32837857.	G	A	PASS	SNV	316	0	316	0	300	10	310	0.032	link	-	Usp13	c.184G>A p.Val62Ile	ENSMUST	missense_variant
3	1.05E+08.	C	T	PASS	SNV	208	0	208	0	220	4	224	0.018	link	-	Cttnbp2nl	c.307G>A p.Ala103Thr	ENSMUST	missense_variant
4	49450658.	A	G	PASS	SNV	222	1	223	0.004	225	5	230	0.022	link	-	Acnat1	c.452T>C p.Leu151Pro	ENSMUST	missense_variant
5	1.16E+08.	C	T	PASS	SNV	341	0	341	0	338	5	343	0.015	link	-	Gcn1l1	c.3946C>T p.Arg1316Trp	ENSMUST	missense_variant
5	1.29E+08.	C	T	PASS	SNV	329	0	329	0	247	38	285	0.133	link	-	Adgrd1	c.1672C>T p.Leu558Phe	ENSMUST	missense_variant
7	45549897.	T	C	PASS	SNV	289	0	289	0	265	5	270	0.019	link	-	Plekha4	c.1846T>C p.Ser616Pro	ENSMUST	missense_variant
8	1.06E+08.	G	A	PASS	SNV	374	0	374	0	415	5	420	0.012	link	-	Smpd3	c.1933C>T p.Arg645Trp	ENSMUST	missense_variant
1	1.36E+08.	C	T	PASS	SNV	409	0	409	0	496	10	506	0.02	link	-	Igfn1	c.2346G>A p.Trp782*	ENSMUST	stop_gained
11	5948297.	C	T	PASS	SNV	304	0	304	0	352	5	357	0.014	link	-	Med9	c.31C>T p.Gln111*	ENSMUST	stop_gained
5	37309110.	G	A	PASS	SNV	390	1	391	0.003	305	4	309	0.013	link	-	Evc	c.2371C>T p.Gln791*	ENSMUST	stop_gained
1	3670384.	T	G	weak_evid	SNV	7	0	7	0	23	4	27	0.148	link	-	Xkr4	c.797+168-	ENSMUST	intron_variant
1	6233950.	A	C	base_quali	SNV	157	4	161	0.025	147	7	154	0.045	link	-	Rb1cc1	c.72-11A>-	ENSMUST	intron_variant
1	16645611.	G	A	base_quali	SNV	47	3	50	0.06	54	12	66	0.182	link	-	Toeb1	c.214+75C-	ENSMUST	intron_variant
1	23849599.	C	T	base_quali	SNV	17	1	18	0.056	19	3	22	0.136	link	-	B3gat2	c.*4412C>-	ENSMUST	downstream_gene_variant
1	23849599.	C	T	base_quali	SNV	17	1	18	0.056	19	3	22	0.136	link	-	Smap1	c.715-131(-	ENSMUST	intron_variant
1	30943394.	T	G	base_quali	SNV	119	10	129	0.078	96	16	112	0.143	link	-	Ptp4a1	c.405-71A(-	ENSMUST	intron_variant
1	36429598.	T	G	base_quali	SNV	50	7	57	0.123	53	14	67	0.209	link	-	Lman2l	c.505-143(-	ENSMUST	intron_variant
1	36599977.	A	C	base_quali	SNV	35	6	41	0.146	43	17	60	0.283	link	-	Gm5428	n.-1825A>-	ENSMUST	upstream_gene_variant
1	36599977.	A	C	base_quali	SNV	35	6	41	0.146	43	17	60	0.283	link	-	Fam178b	c.1094+14-	ENSMUST	intron_variant
1	37123870.	A	C	base_quali	SNV	58	3	61	0.049	58	9	67	0.134	link	-	Vwa3b	c.1654-81(-	ENSMUST	intron_variant
1	37890423.	T	G	base_quali	SNV	32	0	32	0	51	3	54	0.056	link	-	Mtld1	c.-113A>C-	ENSMUST	upstream_gene_variant
1	37890423.	T	G	base_quali	SNV	32	0	32	0	51	3	54	0.056	link	-	Mrpl30	c.-3542T>-	ENSMUST	upstream_gene_variant
1	37890423.	T	G	base_quali	SNV	32	0	32	0	51	3	54	0.056	link	-	-	n.3789042(-	-	intergenic_region
1	44126339.	A	C	base_quali	SNV	68	2	70	0.029	78	17	95	0.179	link	-	Blvm	c.-53A>C-	ENSMUST	5_prime_UTR_variant
1	45407385.	T	G	base_quali	SNV	25	0	25	0	35	7	42	0.167	link	-	Col5a2	c.1252-10(-	ENSMUST	intron_variant
1	45423443 rs272610	G	A	weak_evid	SNV	5	0	5	0	3	3	6	0.5	link	-	Col5a2	c.684+239-	ENSMUST	intron_variant
1	55052762.	A	C	base_quali	SNV	17	2	19	0.105	22	13	35	0.371	link	-	Coq10b	c.-113A>C-	ENSMUST	upstream_gene_variant
1	55052762.	A	C	base_quali	SNV	17	2	19	0.105	22	13	35	0.371	link	-	E330011M	n.351T>G-	ENSMUST	non_coding_transcript_exon_variant
1	55052763.	G	A	base_quali	SNV	20	1	21	0.048	29	8	37	0.216	link	-	Coq10b	c.-112G>A-	ENSMUST	upstream_gene_variant
1	55052763.	G	A	base_quali	SNV	20	1	21											

1	85272813 rs1131831	C	T	mapping_cSNV	10	1	11	0.091	7	8	15	0.533	link	-	Gm2619	n.379+415-	ENSMUST intron_variant
1	85272813 rs1131831	C	T	mapping_cSNV	10	1	11	0.091	7	8	15	0.533	link	-	Gm16026	n.266+304-	ENSMUST intron_variant
1	85615442 rs2343937	A	C	mapping_cSNV	62	0	62	0	59	7	66	0.106	link	-	Gm10552	n.-3546T>	ENSMUST upstream_gene_variant
1	85615442 rs2343937	A	C	mapping_cSNV	62	0	62	0	59	7	66	0.106	link	-	Sp140	c.502+171-	ENSMUST intron_variant
1	85615481	T	A	mapping_cSNV	36	1	37	0.027	47	9	56	0.161	link	-	Gm10552	n.-3585A>	ENSMUST upstream_gene_variant
1	85615481	T	A	mapping_cSNV	36	1	37	0.027	47	9	56	0.161	link	-	Sp140	c.502+210-	ENSMUST intron_variant
1	85620192 rs1080602	G	A	mapping_cSNV	233	4	237	0.017	267	12	279	0.043	link	-	Sp140	c.604+35G-	ENSMUST intron_variant
1	85644247 rs1133741	T	C	weak_evid_SNV	5	0	5	0	2	4	6	0.667	link	-	Sp140	c.1507-33I-	ENSMUST intron_variant
1	85644247 rs1133741	T	C	weak_evid_SNV	5	0	5	0	2	4	6	0.667	link	-	Gm17017	n.192-812I-	ENSMUST intron_variant
1	88217844	C	T	weak_evid_SNV	13	0	13	0	37	6	43	0.14	link	-	Ugt1a10	c.1296-28I-	ENSMUST intron_variant
1	88217844	C	T	weak_evid_SNV	13	0	13	0	37	6	43	0.14	link	-	Ugt1a9	c.1290-28I-	ENSMUST intron_variant
1	88217844	C	T	weak_evid_SNV	13	0	13	0	37	6	43	0.14	link	-	Ugt1a7c	c.1299-28I-	ENSMUST intron_variant
1	88217844	C	T	weak_evid_SNV	13	0	13	0	37	6	43	0.14	link	-	Ugt1a6a	c.1299-28I-	ENSMUST intron_variant
1	88217844	C	T	weak_evid_SNV	13	0	13	0	37	6	43	0.14	link	-	Ugt1a5	c.1293-28I-	ENSMUST intron_variant
1	88217844	C	T	weak_evid_SNV	13	0	13	0	37	6	43	0.14	link	-	Ugt1a2	c.1305-28I-	ENSMUST intron_variant
1	88217844	C	T	weak_evid_SNV	13	0	13	0	37	6	43	0.14	link	-	Ugt1a1	c.1311-28I-	ENSMUST intron_variant
1	88217844	C	T	weak_evid_SNV	13	0	13	0	37	6	43	0.14	link	-	Ugt1a6b	c.1299-28I-	ENSMUST intron_variant
1	88217844	C	T	weak_evid_SNV	13	0	13	0	37	6	43	0.14	link	-	Gm20528	n.274+437-	ENSMUST intron_variant
1	88217844	C	T	weak_evid_SNV	13	0	13	0	37	6	43	0.14	link	-	Ugt1a8	c.1296-28I-	ENSMUST intron_variant
1	88218833	A	G	weak_evid_SNV	5	0	5	0	3	6	9	0.667	link	-	Ugt1a10	c.*409A>G-	ENSMUST3_prime_UTR_variant
1	88218833	A	G	weak_evid_SNV	5	0	5	0	3	6	9	0.667	link	-	Ugt1a9	c.*409A>G-	ENSMUST3_prime_UTR_variant
1	88218833	A	G	weak_evid_SNV	5	0	5	0	3	6	9	0.667	link	-	Ugt1a7c	c.*409A>G-	ENSMUST3_prime_UTR_variant
1	88218833	A	G	weak_evid_SNV	5	0	5	0	3	6	9	0.667	link	-	Ugt1a6a	c.*409A>G-	ENSMUST3_prime_UTR_variant
1	88218833	A	G	weak_evid_SNV	5	0	5	0	3	6	9	0.667	link	-	Ugt1a5	c.*409A>G-	ENSMUST3_prime_UTR_variant
1	88218833	A	G	weak_evid_SNV	5	0	5	0	3	6	9	0.667	link	-	Ugt1a2	c.*409A>G-	ENSMUST3_prime_UTR_variant
1	88218833	A	G	weak_evid_SNV	5	0	5	0	3	6	9	0.667	link	-	Ugt1a1	c.*409A>G-	ENSMUST3_prime_UTR_variant
1	88218833	A	G	weak_evid_SNV	5	0	5	0	3	6	9	0.667	link	-	Ugt1a6b	c.*409A>G-	ENSMUST3_prime_UTR_variant
1	88218833	A	G	weak_evid_SNV	5	0	5	0	3	6	9	0.667	link	-	Ugt1a8	c.*409A>G-	ENSMUST3_prime_UTR_variant
1	88227655 rs4641301	G	T	low_normaSNV	1	0	1	0	10	2	12	0.167	link	-	Gm20528	n.-279T>C-	ENSMUST upstream_gene_variant
1	88230029 rs4650528	T	A	too_few_sI_SNV	4	0	4	0	13	2	15	0.133	link	-	Mroh2a	c.-14-399C-	ENSMUST intron_variant
1	88231886 rs5133683	C	T	too_few_sI_SNV	10	0	10	0	10	2	12	0.167	link	-	Mroh2a	c.262-313I-	ENSMUST intron_variant
1	88235812 rs4788929	G	A	weak_evid_SNV	3	0	3	0	10	4	14	0.286	link	-	Mroh2a	c.557-358C-	ENSMUST intron_variant
1	88244609 rs5025982	A	G	too_few_sI_SNV	6	0	6	0	24	2	26	0.077	link	-	Mroh2a	c.2443-33I-	ENSMUST intron_variant
1	88245374	G	A	PASS SNV	11	0	11	0	22	4	26	0.154	link	-	Mroh2a	c.2565+30-	ENSMUST intron_variant
1	88251008	T	C	too_few_sI_SNV	9	0	9	0	15	2	17	0.118	link	-	Mroh2a	c.3199-23I-	ENSMUST intron_variant
1	88257356 rs1084011	C	T	too_few_sI_SNV	8	0	8	0	13	2	15	0.133	link	-	Mroh2a	c.4462-35A-	ENSMUST intron_variant
1	88260295 rs4954938	T	C	PASS SNV	15	0	15	0	37	9	46	0.196	link	-	Mroh2a	c.*269T>C-	ENSMUST3_prime_UTR_variant
1	88260295 rs4954938	T	C	PASS SNV	15	0	15	0	37	9	46	0.196	link	-	Hjurp	c.*4886A>	ENSMUST downstream_gene_variant
1	88260380 rs4696621	C	T	too_few_sI_SNV	6	0	6	0	17	2	19	0.105	link	-	Mroh2a	c.*354C>T-	ENSMUST3_prime_UTR_variant
1	88260380 rs4696621	C	T	too_few_sI_SNV	6	0	6	0	17	2	19	0.105	link	-	Hjurp	c.*4801G>	ENSMUST downstream_gene_variant
1	88264722 rs4700904	C	G	too_few_sI_SNV	6	0	6	0	3	2	5	0.4	link	-	Hjurp	c.*459G>C-	ENSMUST3_prime_UTR_variant
1	88264722 rs4700904	C	G	too_few_sI_SNV	6	0	6	0	3	2	5	0.4	link	-	Mroh2a	c.*4696C>	ENSMUST downstream_gene_variant
1	88264913 rs4715892	G	T	PASS SNV	8	0	8	0	27	7	34	0.206	link	-	Hjurp	c.*268C>A-	ENSMUST3_prime_UTR_variant
1	88264913 rs4715892	G	T	PASS SNV	8	0	8	0	27	7	34	0.206	link	-	Mroh2a	c.*4887G>	ENSMUST downstream_gene_variant
1	88264914 rs4962688	G	A	PASS SNV	8	0	8	0	27	7	34	0.206	link	-	Hjurp	c.*267C>T-	ENSMUST3_prime_UTR_variant
1	88264914 rs4962688	G	A	PASS SNV	8	0	8	0	27	7	34	0.206	link	-	Mroh2a	c.*4888G>	ENSMUST downstream_gene_variant
1	88267620	C	T	weak_evid_SNV	5	0	5	0	20	8	28	0.286	link	-	Hjurp	c.526+328-	ENSMUST intron_variant
1	90778634	G	A	base_quali_SNV	24	1	25	0.04	38	5	43	0.116	link	-	Col6a3	c.8455+12-	ENSMUST intron_variant
1	1.06E+08	A	C	base_quali_SNV	21	1	22	0.045	12	3	15	0.2	link	-	Tnfrsf11a	c.734-189I-	ENSMUST intron_variant
1	1.07E+08	T	G	base_quali_SNV	65	3	68	0.044	87	12	99	0.121	link	-	Serpinb11	c.348+93T-	ENSMUST intron_variant
1	1.2E+08	G	A	weak_evid_SNV	268	2	270	0.007	271	5	276	0.018	link	-	Marco	c.467-27C-	ENSMUST intron_variant
1	1.28E+08	A	C	base_quali_SNV	95	3	98	0.031	96	11	107	0.103	link	-	Ubxn4	c.334-58A-	ENSMUST intron_variant
1	1.31E+08	T	G	weak_evid_SNV	9	0	9	0	9	7	16	0.438	link	-	Fcamr	c.265+194-	ENSMUST intron_variant
1	1.32E+08	A	C	base_quali_SNV	256	2	258	0.008	211	11	222	0.05	link	-	Lemd1	c.277-68A-	ENSMUST intron_variant
1	1.34E+08	T	G	base_quali_SNV	84	2	86	0.023	121	7	128	0.055	link	-	Tmem183c	c.200-55A-	ENSMUST intron_variant
1	1.35E+08	A	C	base_quali_SNV	287	4	291	0.014	282	13	295	0.044	link	-	Mir1231	n.-3176T>	ENSMUST upstream_gene_variant
1	1.35E+08	A	C	base_quali_SNV	287	4	291	0.014	282	13	295	0.044	link	-	Nav1	c.3642+53-	ENSMUST intron_variant
1	1.36E+08	G	A	base_quali_SNV	33	1	34	0.029	48	8	56	0.143	link	-	Nav1	c.1235+22-	ENSMUST intron_variant
1	1.36E+08	T	G	base_quali_SNV	52	2	54	0.037	95	13	108	0.12	link	-	Igfn1	c.124-81A-	ENSMUST intron_variant
1	1.36E+08	T	G	base_quali_SNV	47	5	52	0.096	67	27	94	0.287	link	-	Igfn1	c.124-87A-	ENSMUST intron_variant
1	1.37E+08 rs2348254	C	T	weak_evid_SNV	143	1	144	0.007	130	3	133	0.023	link	-	Gm29485	n.*2556C>	ENSMUST downstream_gene_variant
1	1.37E+08 rs2348254	C	T	weak_evid_SNV	143	1	144	0.007	130	3	133	0.023	link	-	Klf14	c.4522-54C-	ENSMUST intron_variant
1	1.53E+08	A	C	base_quali_SNV	31	0	31	0	45	5	50	0.1	link	-	Rgl1	c.-93712T>	ENSMUST upstream_gene_variant
1	1.53E+08	A	C	base_quali_SNV	31	0	31	0	45	5	50	0.1	link	-	Arpc5	c.144-158I-	ENSMUST intron_variant
1	1.54E+08	T	G	base_quali_SNV	8	0	8	0	11	5	16	0.312	link	-	Npl	c.778+167-	ENSMUST intron_variant
1	1.54E+08	T	G	alt_allele_I_SNV	11	3	14	0.214	29	14	43	0.326	link	-	Cacna1e	c.3562-16C-	ENSMUST intron_variant
1	1.6E+08	A	C	base_quali_SNV	95	4	99	0.04	87	11	98	0.112	link	-	Tnn	c.3964+84-	ENSMUST intron_variant
1	1.61E+08	C	T	too_few_sI_SNV	5	0	5	0	19	2	21	0.095	link	-	Cenpl	c.424-166C-	ENSMUST intron_variant
1	1.65E+08	A	C	base_quali_SNV	18	2	20	0.1	31	3	34	0.088	link	-	Dcaf6	c.688+99T-	ENSMUST intron_variant
1	1.68E+08	A	C	base_quali_SNV	245	2	247	0.008	241	12	253	0.047	link	-	Rxrg	c.-42A>C-	ENSMUST5_prime_UTR_variant
1	1.68E+08	A	C	base_quali_SNV	56	4	60	0.067	56	12	68	0.176	link	-	Lmx1a	c.818-117I-	ENSMUST intron_variant
1	1.7E+08	G	T	base_quali_SNV	129	0	129	0	162	10	172	0.058	link	-	Ddr2	c.186-18C-	ENSMUST intron_variant
1	1.7E+08	A	C	base_quali_SNV	23	2	25	0.08	45	4	49	0.082	link	-	Nos1ap	c.927+188-	ENSMUST intron_variant
1	1.71E+08	A	C	base_quali_SNV	168	3	171	0.018	192	14	206	0.068	link	-	Fcrlb	c.307+26T-	ENSMUST intron_variant
1	1.74E+08	G	T	weak_evid_SNV	132	0	132	0	147	4	151	0.026	link	-	Spta1	c.3370-56C-	ENSMUST intron_variant
1	1.75E+08	T	G	base_quali_SNV	22	4	26	0.154	17	9	26	0.346	link	-	Fmn2	c.4152+12-	ENSMUST intron_variant
1	1.76E+08	G	T	base_quali_SNV	18	1	19	0.053	24	9	33	0.273	link	-	Pid5	c.607+131-	ENSMUST intron_variant
1	1.81E+08	G	A	low_normaSNV	2	0	2	0	16	2	18	0.111	link	-	Tmem63a	c.1568+25-	ENSMUST intron_variant
1	1.82E+08	A	G	base_quali_SNV	89	6	95	0.063	95	10	105	0.095	link	-	Dnah14	c.9486+24-	ENSMUST intron_variant
1	1.82E+08	A	C	base_quali_SNV	176	5	181	0.028	181	24	205	0.117	link	-	Dnah14	c.9934-11I-	ENSMUST intron_variant
1	1.82E+08	G	A	too_few_sI_SNV	5	0	5	0	14	2	16	0.125	link	-	Gm37089	n.-4836G>	ENSMUST upstream_gene_variant
1	1.82E+08	G	A	too_few_sI_SNV	5	0	5	0	14	2	16	0.125	link	-	Capn2	c.814-241C-	ENSMUST intron_variant
1	1.82E+08	G	A	too_few_sI_SNV	5	0	5	0	14	2	16	0.125	link	-	Gm37885	n.258-522C-	ENSMUST intron_variant
1	1.83E+08	T	G	base_quali_SNV	173	3	176	0.017	150	11	161	0.068	link	-	Capn8	c.2030-77C-	ENSMUST intron_variant
1	1.85E+08	G	T	base_quali_SNV													

10	58630226	A	G	base_qualiSNV	107	4	111	0.036	143	15	158	0.095	link	-	Edar	c.-18-94T>-	ENSMUSTintron_variant
10	60098032	A	C	base_qualiSNV	131	10	141	0.071	132	10	142	0.07	link	-	Ascc1	c.955-61A>-	ENSMUSTintron_variant
10	60329773	A	C	base_qualiSNV	238	2	240	0.008	221	14	235	0.06	link	-	Cdh23	c.5820+33-	ENSMUSTintron_variant
10	61336798	G	T	too_few_sSNV	3	0	3	0	7	2	9	0.222	link	-	Pald1	c.2271+24-	ENSMUSTintron_variant
10	61783401	C	T	base_qualiSNV	315	20	335	0.06	311	35	346	0.101	link	-	H2afy2	c.-60+382(-	ENSMUSTintron_variant
10	62299493	C	T	too_few_sSNV	4	0	4	0	9	2	11	0.182	link	-	Hk1	c.388-224(-	ENSMUSTintron_variant
10	62995496	T	G	base_qualiSNV	82	2	84	0.024	82	15	97	0.155	link	-	Gm16135	n.-3283T>-	ENSMUSTupstream_gene_variant
10	62995496	T	G	base_qualiSNV	82	2	84	0.024	82	15	97	0.155	link	-	Rufy2	c.720+117-	ENSMUSTintron_variant
10	63316477	T	C	too_few_sSNV	5	0	5	0	12	2	14	0.143	link	-	Sirt1	c.*159A>-	ENSMUSTdownstream_gene_variant
10	63316477	T	C	too_few_sSNV	5	0	5	0	12	2	14	0.143	link	-	Herc4	c.2839-22(-	ENSMUSTintron_variant
10	67237996	A	C	base_qualiSNV	40	2	42	0.048	71	8	79	0.101	link	-	Gm26359	n.-2035T>-	ENSMUSTupstream_gene_variant
10	67237996	A	C	base_qualiSNV	40	2	42	0.048	71	8	79	0.101	link	-	Jmjd1c	c.5621-11(-	ENSMUSTintron_variant
10	67255406	A	C	base_qualiSNV	113	3	116	0.026	141	5	146	0.034	link	-	Jmjd1c	c.7507-42(-	ENSMUSTintron_variant
10	70256368	C	T	base_qualiSNV	18	0	18	0	19	4	23	0.174	link	-	Slc16a9	c.196+176-	ENSMUSTintron_variant
10	70925106	rs1132281A	C	base_qualiSNV	12	1	13	0.077	31	6	37	0.162	link	-	Bicc1	c.*139T>G-	ENSMUST3_prime_UTR_variant
10	76221217	rs5806773C	A	alt_allele_iSNV	44	6	50	0.12	55	18	73	0.247	link	-	Prmt2	c.526-55(-	ENSMUSTintron_variant
10	76268709	T	G	base_qualiSNV	23	6	29	0.207	38	15	53	0.283	link	-	Dip2a	c.4093-14(-	ENSMUSTintron_variant
10	76392029	A	G	too_few_sSNV	17	0	17	0	22	2	24	0.083	link	-	1700094J0	n.267+246-	ENSMUSTintron_variant
10	76392029	A	G	too_few_sSNV	17	0	17	0	22	2	24	0.083	link	-	Pcnt	c.5136+16-	ENSMUSTintron_variant
10	77072280	T	G	base_qualiSNV	7	1	8	0.125	26	6	32	0.188	link	-	Col18a1	c.3232-21(-	ENSMUSTintron_variant
10	79856311	A	C	base_qualiSNV	160	7	167	0.042	186	21	207	0.101	link	-	E130317f	n.-1355T>-	ENSMUSTupstream_gene_variant
10	79856311	A	C	base_qualiSNV	160	7	167	0.042	186	21	207	0.101	link	-	Ptbp1	c.9-193A>-	ENSMUSTintron_variant
10	79895286	A	C	base_qualiSNV	119	4	123	0.033	124	5	129	0.039	link	-	Cld	c.*2700A>-	ENSMUSTdownstream_gene_variant
10	80138139	G	T	base_qualiSNV	66	4	70	0.057	94	14	108	0.13	link	-	Atp5d	c.-4327G>-	ENSMUSTintron_variant
10	80138139	G	T	base_qualiSNV	66	4	70	0.057	94	14	108	0.13	link	-	Cbap	c.-777C>A-	ENSMUSTupstream_gene_variant
10	80138139	G	T	base_qualiSNV	66	4	70	0.057	94	14	108	0.13	link	-	Cbap	n.8013813(-	- intragenic_variant
10	81239339	G	A	base_qualiSNV	51	2	53	0.038	92	14	106	0.132	link	-	Zfr2	c.289-91(-	ENSMUSTintron_variant
10	81247593	G	A	too_few_sSNV	3	0	3	0	15	2	17	0.118	link	-	Zfr2	c.1902+20-	ENSMUSTintron_variant
10	83281211	T	C	base_qualiSNV	18	1	19	0.053	24	12	36	0.333	link	-	Slc41a2	c.1255+15-	ENSMUSTintron_variant
10	83362269	T	G	base_qualiSNV	29	3	32	0.094	30	11	41	0.268	link	-	D10Wsu10c	c.202+136-	ENSMUSTintron_variant
10	84869103	T	G	base_qualiSNV	13	1	14	0.071	39	7	46	0.152	link	-	Rfx4	c.1351+14-	ENSMUSTintron_variant
10	85929049	A	G	base_qualiSNV	15	2	17	0.118	25	7	32	0.219	link	-	Ascl4	c.*124A>G-	ENSMUST3_prime_UTR_variant
10	86866747	A	G	too_few_sSNV	153	2	155	0.013	137	2	139	0.014	link	-	Gm16268	n.372-495(-	ENSMUSTintron_variant
10	89414610	T	G	base_qualiSNV	14	3	17	0.176	24	2	26	0.077	link	-	Gas2l3	c.763-118A-	ENSMUSTintron_variant
10	89597241	G	A	too_few_sSNV	4	0	4	0	21	2	23	0.087	link	-	Slc17a8	c.715+204-	ENSMUSTintron_variant
10	93048201	T	G	base_qualiSNV	23	0	23	0	35	14	49	0.286	link	-	Ctcfp54	c.814-124(-	ENSMUSTintron_variant
10	93226480	T	C	low_normaSNV	1	0	1	0	21	2	23	0.087	link	-	Cdk17	c.811-233(-	ENSMUSTintron_variant
10	93562644	C	T	base_qualiSNV	47	6	53	0.113	53	21	74	0.284	link	-	Ccdc38	c.370-87(-	ENSMUSTintron_variant
10	95828185	A	G	base_qualiSNV	152	11	163	0.067	123	15	138	0.109	link	-	RP23-234f	c.-1-55T>(-	ENSMUSTintron_variant
10	95843138	G	A	too_few_sSNV	6	0	6	0	12	2	14	0.143	link	-	RP23-234f	c.-15009(-	ENSMUSTupstream_gene_variant
10	95843138	G	A	too_few_sSNV	6	0	6	0	12	2	14	0.143	link	-	-	n.9584313(-	- intergenic_region
10	1.01E+08	A	C	base_qualiSNV	22	0	22	0	27	7	34	0.206	link	-	1700017N	c.175-146(-	ENSMUSTintron_variant
10	1.01E+08	A	C	base_qualiSNV	23	0	23	0	32	4	36	0.111	link	-	1700017N	c.175-139(-	ENSMUSTintron_variant
10	1.08E+08	T	G	weak_evid	173	6	179	0.034	149	5	154	0.032	link	-	Ptpqr	c.4613-52(-	ENSMUSTintron_variant
10	1.08E+08	A	C	base_qualiSNV	6	1	7	0.143	14	4	18	0.222	link	-	Otogl	c.3306+18-	ENSMUSTintron_variant
10	1.08E+08	G	A	base_qualiSNV	260	3	263	0.011	214	18	232	0.078	link	-	Otogl	c.208+48(-	ENSMUSTintron_variant
10	1.12E+08	T	C	alt_allele_iSNV	27	0	27	0	23	3	26	0.115	link	-	Gilpr1l1	c.629-195(-	ENSMUSTintron_variant
10	1.16E+08	T	C	base_qualiSNV	72	3	75	0.04	104	8	112	0.071	link	-	Cnot2	c.1536+50-	ENSMUSTintron_variant
10	1.17E+08	G	T	base_qualiSNV	73	0	73	0	113	15	128	0.117	link	-	Myrf1	c.2554-12(-	ENSMUSTintron_variant
10	1.17E+08	T	G	base_qualiSNV	5	1	6	0.167	14	5	19	0.263	link	-	Frs2	c.-26-183A-	ENSMUSTintron_variant
10	1.2E+08	A	C	base_qualiSNV	135	12	147	0.082	126	36	162	0.222	link	-	Tmbim4	c.313-32A(-	ENSMUSTintron_variant
10	1.27E+08	G	A	alt_allele_iSNV	32	7	39	0.179	52	20	72	0.278	link	-	Gil1	c.*921C>T-	ENSMUSTdownstream_gene_variant
10	1.27E+08	G	A	alt_allele_iSNV	32	7	39	0.179	52	20	72	0.278	link	-	Arhgap9	c.1250+14-	ENSMUSTintron_variant
10	1.28E+08	A	C	base_qualiSNV	119	3	122	0.025	155	10	165	0.061	link	-	Naca	c.71-28A>-	ENSMUSTintron_variant
10	1.28E+08	A	C	base_qualiSNV	125	2	127	0.016	166	11	177	0.062	link	-	Naca	c.71-23A>-	ENSMUSTintron_variant
10	1.29E+08	C	T	weak_evid	381	1	382	0.003	373	6	379	0.016	link	-	Rdh5	c.-1453G>-	ENSMUSTupstream_gene_variant
10	1.29E+08	C	T	weak_evid	381	1	382	0.003	373	6	379	0.016	link	-	Rdh5	n.1289200(-	- intragenic_variant
10	1.3E+08	T	G	alt_allele_iSNV	60	5	65	0.077	55	8	63	0.127	link	-	Olfr810	c.-64A>C-	ENSMUSTupstream_gene_variant
10	1.3E+08	T	G	alt_allele_iSNV	60	5	65	0.077	55	8	63	0.127	link	-	-	n.1297916(-	- intergenic_region
11	4670505	T	C	PASS_SNV	83	0	83	0	98	43	141	0.305	link	-	Ascc2	c.1347+43-	ENSMUSTintron_variant
11	5070745	T	G	base_qualiSNV	250	4	254	0.016	226	17	243	0.07	link	-	Ewrs1	c.1596-22(-	ENSMUSTintron_variant
11	6437702	G	T	base_qualiSNV	8	0	8	0	7	4	11	0.364	link	-	H2afv	c.81+1674-	ENSMUSTintron_variant
11	9007429	C	T	PASS_SNV	105	0	105	0	125	10	135	0.074	link	-	Hus1	c.468+65(-	ENSMUSTintron_variant
11	11967372	A	C	base_qualiSNV	12	1	13	0.077	22	5	27	0.185	link	-	Grb10	c.348+160-	ENSMUSTintron_variant
11	20080645	A	C	alt_allele_iSNV	131	8	139	0.058	116	13	129	0.101	link	-	Actr2	c.585+177-	ENSMUSTintron_variant
11	21998622	T	G	base_qualiSNV	38	10	48	0.208	46	20	66	0.303	link	-	Otx1	c.98-101A(-	ENSMUSTintron_variant
11	23354799	A	C	base_qualiSNV	122	4	126	0.032	122	9	131	0.069	link	-	Usp34	c.1134-46(-	ENSMUSTintron_variant
11	29805925	T	G	base_qualiSNV	27	4	31	0.129	72	9	81	0.111	link	-	Em16	c.2439-11(-	ENSMUSTintron_variant
11	29805949	T	G	base_qualiSNV	16	4	20	0.2	41	20	61	0.328	link	-	Em16	c.2439-13(-	ENSMUSTintron_variant
11	29893166	A	C	base_qualiSNV	215	6	221	0.027	201	4	205	0.02	link	-	Em16	c.525+22(-	ENSMUSTintron_variant
11	32604321	G	A	PASS_SNV	168	0	168	0	164	65	229	0.284	link	-	Stk10	c.1986+21-	ENSMUSTintron_variant
11	32742422	A	G	weak_evid	98	4	102	0.039	96	4	100	0.04	link	-	Fbxw11	c.1531-37(-	ENSMUSTintron_variant
11	43445520	C	T	base_qualiSNV	244	8	252	0.032	223	20	243	0.082	link	-	Slu7	c.1578+48-	ENSMUSTintron_variant
11	50385080	A	C	base_qualiSNV	150	4	154	0.026	147	9	156	0.058	link	-	Rufy1	c.*4735T>-	ENSMUSTdownstream_gene_variant
11	50385080	A	C	base_qualiSNV	150	4	154	0.026	147	9	156	0.058	link	-	Hnmrph1	c.1300+34-	ENSMUSTintron_variant
11	50864425	G	A	base_qualiSNV	82	3	85	0.035	102	9	111	0.081	link	-	Grm6	c.2419-36(-	ENSMUSTintron_variant
11	51721963	T	G	base_qualiSNV	93	2	95	0.021	59	8	67	0.119	link	-	Sec24a	c.1596-30(-	ENSMUSTintron_variant
11	52037296	A	C	base_qualiSNV	59	2	61	0.033	86	7	93	0.075	link	-	Gm12205	n.*1554T>-	ENSMUSTdownstream_gene_variant
11	52037296	A	C	base_qualiSNV	59	2	61	0.033	86	7	93	0.075	link	-	Gm26551	n.2397+83-	ENSMUSTintron_variant
11	52037296	A	C	base_qualiSNV	59	2	61	0.033	86	7	93	0.075	link	-	Cdk13	c.1800-13(-	ENSMUSTintron_variant
11	52375059	C	T	PASS_SNV	117	0	117	0	125	13	138	0.094	link	-	Vdac1	c.156+92(-	ENSMUSTintron_variant
11	54028107	A	G	base_qualiSNV	31	3	34	0.088	62	17	79	0.215	link	-	Slc22a4	c.-131T>C-	ENSMUSTupstream_gene_variant
11	54028107	A	G	base_qualiSNV	31	3	34	0.088	62	17	79	0.215	link	-	-	n.5402810(-	- intergenic_region
11	54496730	G	A	PASS_S													

11	75342348	T	G	base_qualiSNV	12	1	13	0.077	33	15	48	0.312	link	-	Rpa1	c.34-154A>-	ENSMUSTintron_variant
11	76117302	C	T	base_qualiSNV	44	4	48	0.083	69	17	86	0.198	link	-	Vps53	c.832-101C>-	ENSMUSTintron_variant
11	78335376	A	C	base_qualiSNV	92	4	96	0.042	124	9	133	0.068	link	-	Pigs	c.469-51A>-	ENSMUSTintron_variant
11	79250916	T	C	base_qualiSNV	55	2	57	0.035	114	11	125	0.088	link	-	Wsb1	c.209+65A>-	ENSMUSTintron_variant
11	79559261	G	T	base_qualiSNV	10	2	12	0.167	17	4	21	0.19	link	-	Nf1	c.7464-14A>-	ENSMUSTintron_variant
11	86214690	T	C	base_qualiSNV	8	1	9	0.111	13	3	16	0.188	link	-	Brip1os	n.*3498T>-	ENSMUSTdownstream_gene_variant
11	86214690	T	C	base_qualiSNV	8	1	9	0.111	13	3	16	0.188	link	-	Ints2	c.3250+22>-	ENSMUSTintron_variant
11	86214690	T	C	base_qualiSNV	8	1	9	0.111	13	3	16	0.188	link	-	Brip1os	n.8621469/-	- intragenic_variant
11	86785191	C	A	base_qualiSNV	5	0	5	0	12	3	15	0.2	link	-	Dhx40	c.1425-15/-	ENSMUSTintron_variant
11	88988206	T	G	alt_allele_iSNV	32	4	36	0.111	50	9	59	0.153	link	-	Gm11496	n.*4834A>-	ENSMUSTdownstream_gene_variant
11	88988206	T	G	alt_allele_iSNV	32	4	36	0.111	50	9	59	0.153	link	-	Coil	c.1647+13>-	ENSMUSTintron_variant
11	94414813	C	A	base_qualiSNV	25	3	28	0.107	46	10	56	0.179	link	-	Cacna1g	c.5931+11>-	ENSMUSTintron_variant
11	97059575	G	A	base_qualiSNV	7	0	7	0	12	6	18	0.333	link	-	Mir8103	n.-4193G>-	ENSMUSTupstream_gene_variant
11	97059575	G	A	base_qualiSNV	7	0	7	0	12	6	18	0.333	link	-	Osbp17	c.1714+38>-	ENSMUSTintron_variant
11	97864886	C	A	weak_evid	7	0	7	0	16	3	19	0.158	link	-	Fbxo47	c.616+173>-	ENSMUSTintron_variant
11	98337338	A	C	base_qualiSNV	172	7	179	0.039	169	14	183	0.077	link	-	-	n.9833733/-	- intergenic_region
11	98969954	G	A	too_few_s_iSNV	5	0	5	0	13	2	15	0.133	link	-	Rara	c.470-203C>-	ENSMUSTintron_variant
11	99240362 rs5864369A	A	C	base_qualiSNV	15	1	16	0.062	16	12	28	0.429	link	-	Krt222	c.225+131>-	ENSMUSTintron_variant
11	1.01E+08	A	G	base_qualiSNV	39	5	44	0.114	51	18	69	0.261	link	-	Atpfv0a1	c.117+111>-	ENSMUSTintron_variant
11	1.01E+08	A	C	base_qualiSNV	211	9	220	0.041	194	26	220	0.118	link	-	Atpfv0a1	c.1494-50/-	ENSMUSTintron_variant
11	1.01E+08 rs2451563A	A	C	base_qualiSNV	211	6	217	0.028	195	18	213	0.085	link	-	Gm11615	n.-2365T>-	ENSMUSTupstream_gene_variant
11	1.01E+08 rs2451563A	A	C	base_qualiSNV	211	6	217	0.028	195	18	213	0.085	link	-	Wnk4	c.1733-35/-	ENSMUSTintron_variant
11	1.02E+08	T	C	alt_allele_iSNV	9	0	9	0	16	6	22	0.273	link	-	Cd300lg	c.509-155/-	ENSMUSTintron_variant
11	1.05E+08	G	A	base_qualiSNV	12	2	14	0.143	25	6	31	0.194	link	-	Iltg3	c.359-126C>-	ENSMUSTintron_variant
11	1.05E+08	T	G	base_qualiSNV	34	2	36	0.056	41	6	47	0.128	link	-	Gm11639	c.5116+11>-	ENSMUSTintron_variant
11	1.05E+08	C	T	base_qualiSNV	12	0	12	0	21	5	26	0.192	link	-	Gm11639	c.7036+20>-	ENSMUSTintron_variant
11	1.05E+08	T	G	base_qualiSNV	88	4	92	0.043	90	3	93	0.032	link	-	Gm11621	n.*1279T>-	ENSMUSTdownstream_gene_variant
11	1.05E+08	T	G	base_qualiSNV	88	4	92	0.043	90	3	93	0.032	link	-	Gm11639	c.10054+6>-	ENSMUSTintron_variant
11	1.05E+08 rs2390247C	G	G	too_few_s_iSNV	12	1	13	0.077	13	2	15	0.133	link	-	Gm24290	n.-2760C>-	ENSMUSTupstream_gene_variant
11	1.05E+08 rs2390247C	G	G	too_few_s_iSNV	12	1	13	0.077	13	2	15	0.133	link	-	Mettl2	c.961+670>-	ENSMUSTintron_variant
11	1.05E+08	T	G	base_qualiSNV	31	0	31	0	27	2	29	0.069	link	-	Gm24290	n.-2750T>-	ENSMUSTupstream_gene_variant
11	1.05E+08	T	G	base_qualiSNV	31	0	31	0	27	2	29	0.069	link	-	Mettl2	c.961+680>-	ENSMUSTintron_variant
11	1.06E+08	G	A	too_few_s_iSNV	6	0	6	0	18	2	20	0.1	link	-	Kcnh6	c.-220G>A>-	ENSMUSTupstream_gene_variant
11	1.06E+08	G	A	too_few_s_iSNV	6	0	6	0	18	2	20	0.1	link	-	Ace3	c.*2540G>-	ENSMUSTdownstream_gene_variant
11	1.06E+08	G	A	too_few_s_iSNV	6	0	6	0	18	2	20	0.1	link	-	-	n.1060079/-	- intergenic_region
11	1.07E+08	T	G	base_qualiSNV	15	0	15	0	20	7	27	0.259	link	-	Polg2	c.-3399A>-	ENSMUSTupstream_gene_variant
11	1.07E+08	T	G	base_qualiSNV	15	0	15	0	20	7	27	0.259	link	-	Mir3064	n.-82A>C>-	ENSMUSTupstream_gene_variant
11	1.07E+08	T	G	base_qualiSNV	15	0	15	0	20	7	27	0.259	link	-	Gm25994	n.*330A>C>-	ENSMUSTdownstream_gene_variant
11	1.07E+08	T	G	base_qualiSNV	15	0	15	0	20	7	27	0.259	link	-	Ddx5	c.1217-14/-	ENSMUSTintron_variant
11	1.07E+08	T	G	base_qualiSNV	6	0	6	0	12	5	17	0.294	link	-	Bptf	c.9075-10/-	ENSMUSTintron_variant
11	1.08E+08	A	C	base_qualiSNV	96	7	103	0.068	84	13	97	0.134	link	-	Helz	c.2181-44/-	ENSMUSTintron_variant
11	1.08E+08	T	G	base_qualiSNV	149	10	159	0.063	134	7	141	0.05	link	-	Prkca	c.530-26A>-	ENSMUSTintron_variant
11	1.14E+08	C	A	base_qualiSNV	9	1	10	0.1	18	9	27	0.333	link	-	Fam104a	c.-161G>T>-	ENSMUSTupstream_gene_variant
11	1.14E+08	C	A	base_qualiSNV	9	1	10	0.1	18	9	27	0.333	link	-	D11Wsu47c	-3535C>-	ENSMUSTupstream_gene_variant
11	1.14E+08	C	A	base_qualiSNV	9	1	10	0.1	18	9	27	0.333	link	-	Gm11693	n.*4915C>-	ENSMUSTdownstream_gene_variant
11	1.14E+08	C	A	base_qualiSNV	9	1	10	0.1	18	9	27	0.333	link	-	-	n.1136842/-	- intergenic_region
11	1.15E+08	G	A	base_qualiSNV	34	4	38	0.105	51	11	62	0.177	link	-	Hid1	c.*152C>T>-	ENSMUST3_prime_UTR_variant
11	1.15E+08	G	A	base_qualiSNV	34	4	38	0.105	51	11	62	0.177	link	-	Otop3	c.*1872G>-	ENSMUSTdownstream_gene_variant
11	1.15E+08	T	C	base_qualiSNV	40	4	44	0.091	58	13	71	0.183	link	-	Hid1	c.*145A>G>-	ENSMUST3_prime_UTR_variant
11	1.15E+08	T	C	base_qualiSNV	40	4	44	0.091	58	13	71	0.183	link	-	Otop3	c.*1879T>-	ENSMUSTdownstream_gene_variant
11	1.15E+08	A	C	base_qualiSNV	177	2	179	0.011	201	10	211	0.047	link	-	Ict1os	n.-1090T>-	ENSMUSTupstream_gene_variant
11	1.15E+08	A	C	base_qualiSNV	177	2	179	0.011	201	10	211	0.047	link	-	Ict1	c.224-76A>-	ENSMUSTintron_variant
11	1.15E+08	A	G	too_few_s_iSNV	13	0	13	0	15	2	17	0.118	link	-	Kctd2	c.-3029A>-	ENSMUSTupstream_gene_variant
11	1.15E+08	A	G	too_few_s_iSNV	13	0	13	0	15	2	17	0.118	link	-	Ict1	c.*6417A>-	ENSMUSTdownstream_gene_variant
11	1.15E+08	A	G	too_few_s_iSNV	13	0	13	0	15	2	17	0.118	link	-	Atpf5h	c.220-215/-	ENSMUSTintron_variant
11	1.16E+08	A	C	too_few_s_iSNV	4	0	4	0	16	2	18	0.111	link	-	Gga3	c.*5477T>-	ENSMUSTdownstream_gene_variant
11	1.16E+08	A	C	too_few_s_iSNV	4	0	4	0	16	2	18	0.111	link	-	Nup85	c.1095-25/-	ENSMUSTintron_variant
11	1.16E+08	A	C	base_qualiSNV	245	0	245	0	225	9	234	0.038	link	-	Llg12	c.-12842A>-	ENSMUSTupstream_gene_variant
11	1.16E+08	A	C	base_qualiSNV	245	0	245	0	225	9	234	0.038	link	-	Tsen54	c.1311-13/-	ENSMUSTintron_variant
11	1.16E+08	C	A	base_qualiSNV	14	1	15	0.067	32	7	39	0.179	link	-	Unk	c.623-155/-	ENSMUSTintron_variant
11	1.17E+08	T	G	base_qualiSNV	17	0	17	0	27	10	37	0.27	link	-	Sphk1	c.*3893T>-	ENSMUSTdownstream_gene_variant
11	1.17E+08	T	G	base_qualiSNV	17	0	17	0	27	10	37	0.27	link	-	Ube2o	c.2938-14/-	ENSMUSTintron_variant
11	1.19E+08	G	A	base_qualiSNV	76	5	81	0.062	95	13	108	0.12	link	-	Ccdc40	c.1006-90/-	ENSMUSTintron_variant
11	1.19E+08 rs2930436A	T	weak_evid	231	0	231	0	241	6	247	0.024	link	-	Card14	c.*2939A>-	ENSMUSTdownstream_gene_variant	
11	1.21E+08	C	T	alt_allele_iSNV	7	0	7	0	10	2	12	0.167	link	-	Aspsrc1	c.1225+31>-	ENSMUSTintron_variant
11	1.21E+08	C	T	alt_allele_iSNV	7	0	7	0	10	2	12	0.167	link	-	Gm17178	n.226+625/-	ENSMUSTintron_variant
12	3732469	T	C	base_qualiSNV	36	2	38	0.053	24	5	29	0.172	link	-	Dtnb	c.1080-14/-	ENSMUSTintron_variant
12	3772502	A	C	base_qualiSNV	45	3	48	0.062	75	19	94	0.202	link	-	Dtnb	c.1555-85/-	ENSMUSTintron_variant
12	4774358	G	T	base_qualiSNV	150	11	161	0.068	158	12	170	0.071	link	-	Pfn4	c.118-34G>-	ENSMUSTintron_variant
12	4865104	G	A	base_qualiSNV	89	2	91	0.022	109	9	118	0.076	link	-	Mfsd2b	c.1460+33>-	ENSMUSTintron_variant
12	8744184	A	C	base_qualiSNV	21	2	23	0.087	39	7	46	0.152	link	-	Pum2	c.2226-15/-	ENSMUSTintron_variant
12	11246064	T	G	too_few_s_iSNV	11	0	11	0	9	2	11	0.182	link	-	Gen1	c.1261+22>-	ENSMUSTintron_variant
12	11279866	T	G	base_qualiSNV	20	3	23	0.13	24	9	33	0.273	link	-	Smc6	c.499+125>-	ENSMUSTintron_variant
12	16990076	T	G	base_qualiSNV	10	0	10	0	23	8	31	0.258	link	-	Rock2	c.*5435T>-	ENSMUSTdownstream_gene_variant
12	16990076	T	G	base_qualiSNV	10	0	10	0	23	8	31	0.258	link	-	Pqlc3	c.518-181/-	ENSMUSTintron_variant
12	17407035	T	G	base_qualiSNV	19	4	23	0.174	41	8	49	0.163	link	-	Nol10	c.1422+13>-	ENSMUSTintron_variant
12	20987776	A	G	weak_evid	14	0	14	0	25	6	31	0.194	link	-	Gm21989	n.-2683A>-	ENSMUSTupstream_gene_variant
12	20987776	A	G	weak_evid	14	0	14	0	25	6	31	0.194	link	-	-	n.2098777/-	- intergenic_region
12	24581850	T	G	base_qualiSNV	16	3	19	0.158	30	12	42	0.286	link	-	Grhl1	c.669+132>-	ENSMUSTintron_variant
12	26317983	T	G	base_qualiSNV	5	0	5	0	15	4	19	0.211	link	-	Rnf144a	c.510-187/-	ENSMUSTintron_variant
12	30005665	A	C	base_qualiSNV	120	2	122	0.016	131	12	143	0.084	link	-	Pxdn	c.3600-51/-	ENSMUSTintron_variant
12	31466761	T	G	base_qualiSNV	21	1	22	0.045	18	5	23	0.217	link	-	Sic26a3	c.1986+13>-	ENSMUSTintron_variant
12	54185529	A	C	base_qualiSNV	170	3	173	0.017	232	5	237	0.021	link	-	Egln3	c.477+12	

13	49859263	C	A	PASS	SNV	428	0	428	0	285	136	421	0.323	link	-	-	n.4985926:-	-	intergenic_region
13	54106765	C	A	alt_allele	_SNV	10	2	12	0.167	15	15	30	0.5	link	-	Sfxn1	c.*162C>A-	-	ENSMUST3_prime_UTR_variant
13	58181027	T	G	base_quali	SNV	32	4	36	0.111	50	7	57	0.123	link	-	Ublqnl1	c.1231-12:-	-	ENSMUSTintron_variant
13	58384699 rs1133271	G	A	base_quali	SNV	16	0	16	0	19	4	23	0.174	link	-	2210016F1c.331+125-	-	ENSMUSTintron_variant	
13	59731806	T	G	base_quali	SNV	75	3	78	0.038	91	15	106	0.142	link	-	4930528D(n.-1839T>-	-	ENSMUSTupstream_gene_variant	
13	59731806	T	G	base_quali	SNV	75	3	78	0.038	91	15	106	0.142	link	-	Spata31d1 c.-86A>C	-	ENSMUSTupstream_gene_variant	
13	59731806	T	G	base_quali	SNV	75	3	78	0.038	91	15	106	0.142	link	-	-	n.5973180:-	-	intergenic_region
13	59731835	T	G	base_quali	SNV	31	3	34	0.088	37	19	56	0.339	link	-	4930528D(n.-1810T>-	-	ENSMUSTupstream_gene_variant	
13	59731835	T	G	base_quali	SNV	31	3	34	0.088	37	19	56	0.339	link	-	Spata31d1 c.-115A>C	-	ENSMUSTupstream_gene_variant	
13	59731835	T	G	base_quali	SNV	31	3	34	0.088	37	19	56	0.339	link	-	-	n.5973183:-	-	intergenic_region
13	63565187	A	C	base_quali	SNV	14	0	14	0	31	8	39	0.205	link	-	A930032L(n.*1911T>-	-	ENSMUSTdownstream_gene_variant	
13	63565187	A	C	base_quali	SNV	14	0	14	0	31	8	39	0.205	link	-	Ptch1	c.159+175-	-	ENSMUSTintron_variant
13	64225367	A	C	base_quali	SNV	6	0	6	0	11	5	16	0.312	link	-	Cdc14b	c.497+205-	-	ENSMUSTintron_variant
13	64764379	G	T	base_quali	SNV	47	1	48	0.021	60	9	69	0.13	link	-	Cntnap3	c.2087-79C-	-	ENSMUSTintron_variant
13	64764379	C	T	alt_allele	_SNV	29	1	30	0.033	48	9	57	0.158	link	-	Cntnap3	c.2087-98C-	-	ENSMUSTintron_variant
13	76271124	A	C	base_quali	SNV	29	7	36	0.194	42	11	53	0.208	link	-	Fam81b	c.168+138-	-	ENSMUSTintron_variant
13	89678269	T	G	base_quali	SNV	45	7	52	0.135	57	23	80	0.287	link	-	Vcan	c.9527-11:-	-	ENSMUSTintron_variant
13	90104309	A	C	base_quali	SNV	162	3	165	0.018	184	16	200	0.08	link	-	Tmem167	c.149-66A:-	-	ENSMUSTintron_variant
13	91796957	T	C	base_quali	SNV	14	2	16	0.125	17	4	21	0.19	link	-	Zcchc9	c.*179A>G-	-	ENSMUST3_prime_UTR_variant
13	93049189	T	G	base_quali	SNV	3	0	3	0	14	4	18	0.222	link	-	Cmya5	c.10511-21-	-	ENSMUSTintron_variant
13	93083096	A	C	base_quali	SNV	102	4	106	0.038	133	14	147	0.095	link	-	Cmya5	c.9789+55-	-	ENSMUSTintron_variant
13	94210741	T	G	base_quali	SNV	68	3	71	0.042	78	11	89	0.124	link	-	Scamp1	c.633-63A:-	-	ENSMUSTintron_variant
13	94814992	A	C	base_quali	SNV	73	5	78	0.064	74	8	82	0.098	link	-	Tbca	c.54-1736E-	-	ENSMUSTintron_variant
13	96866171	C	T	too_few	_sSNV	10	0	10	0	26	2	28	0.071	link	-	Ankrd31	c.3457-16:-	-	ENSMUSTintron_variant
13	1E+08	T	G	base_quali	SNV	42	1	43	0.023	67	13	80	0.163	link	-	Bdp1	c.2370-82/-	-	ENSMUSTintron_variant
13	1.01E+08	T	G	base_quali	SNV	32	0	32	0	54	8	62	0.129	link	-	Ocln	c.724-109/-	-	ENSMUSTintron_variant
13	1.01E+08	T	G	base_quali	SNV	35	0	35	0	47	10	57	0.175	link	-	Ccdc125	c.682+99T-	-	ENSMUSTintron_variant
13	1.01E+08	T	G	base_quali	SNV	43	3	46	0.065	46	3	49	0.061	link	-	Cdk7	c.715-95A:-	-	ENSMUSTintron_variant
13	1.12E+08	A	C	base_quali	SNV	90	4	94	0.043	117	11	128	0.086	link	-	Ankrd55	c.794+280-	-	ENSMUSTintron_variant
13	1.13E+08 rs2924700	A	C	base_quali	SNV	10	2	12	0.167	26	4	30	0.133	link	-	Skiv2l2	c.-2086T>-	-	ENSMUSTupstream_gene_variant
13	1.13E+08 rs2924700	A	C	base_quali	SNV	10	2	12	0.167	26	4	30	0.133	link	-	Dhx29	c.182-184/-	-	ENSMUSTintron_variant
13	1.13E+08	G	A	alt_allele	_SNV	9	0	9	0	4	3	7	0.429	link	-	Gzma	c.215+215-	-	ENSMUSTintron_variant
13	1.14E+08	T	G	base_quali	SNV	109	3	112	0.027	136	12	148	0.081	link	-	Snx18	c.1595-30/-	-	ENSMUSTintron_variant
14	4000224	A	C	base_quali	SNV	21	1	22	0.045	17	5	22	0.227	link	-	Gm3099	c.294-237/-	-	ENSMUSTintron_variant
14	4166821	A	C	base_quali	SNV	11	0	11	0	14	8	22	0.364	link	-	Gm3127	c.294-251/-	-	ENSMUSTintron_variant
14	4398825	G	A	too_few	_sSNV	1	0	31	0	21	2	23	0.087	link	-	Gm3159	c.293+222-	-	ENSMUSTintron_variant
14	7884480	G	T	base_quali	SNV	96	1	97	0.01	110	11	121	0.091	link	-	Flnb	c.1148-70C-	-	ENSMUSTintron_variant
14	12551092	T	G	base_quali	SNV	8	1	9	0.111	11	6	17	0.353	link	-	Cadps	c.1320-17C-	-	ENSMUSTintron_variant
14	13899690	T	G	base_quali	SNV	109	7	116	0.06	125	11	136	0.081	link	-	Gm281	c.241-10A:-	-	ENSMUSTintron_variant
14	13954394	C	A	base_quali	SNV	53	2	55	0.036	68	19	87	0.218	link	-	Gm11100	n.*4836C>-	-	ENSMUSTdownstream_gene_variant
14	13954394	C	A	base_quali	SNV	53	2	55	0.036	68	19	87	0.218	link	-	Thoc7	c.137-145-	-	ENSMUSTintron_variant
14	13962004	T	G	base_quali	SNV	27	3	30	0.1	34	7	41	0.171	link	-	Thoc7	c.-801A>C-	-	ENSMUSTupstream_gene_variant
14	13962004	T	G	base_quali	SNV	27	3	30	0.1	34	7	41	0.171	link	-	-	n.1396200:-	-	intergenic_region
14	18238513	C	T	too_few	_sSNV	6	0	6	0	14	2	16	0.125	link	-	Nr1d2	c.16+298G-	-	ENSMUSTintron_variant
14	20381945	T	G	base_quali	SNV	44	6	50	0.12	57	6	63	0.095	link	-	Dnajc9	c.*3417A>-	-	ENSMUSTdownstream_gene_variant
14	20381945	T	G	base_quali	SNV	44	6	50	0.12	57	6	63	0.095	link	-	Fam149b	c.1669+12-	-	ENSMUSTintron_variant
14	20565115	T	G	base_quali	SNV	95	3	98	0.031	93	19	112	0.17	link	-	18100620(n.259+68T-	-	ENSMUSTintron_variant	
14	20565115	T	G	base_quali	SNV	95	3	98	0.031	93	19	112	0.17	link	-	Usp54	c.2309-52/-	-	ENSMUSTintron_variant
14	20655186	A	C	base_quali	SNV	91	6	97	0.062	96	11	107	0.103	link	-	Synpo2l	c.*5115T>-	-	ENSMUSTdownstream_gene_variant
14	20655186	A	C	base_quali	SNV	91	6	97	0.062	96	11	107	0.103	link	-	Myoz1	c.73+90T>-	-	ENSMUSTintron_variant
14	21686566	A	C	base_quali	SNV	77	9	86	0.105	122	16	138	0.116	link	-	Dupd1	c.418+49T-	-	ENSMUSTintron_variant
14	23289398	A	C	base_quali	SNV	187	5	192	0.026	180	10	190	0.053	link	-	A830039N(n.*2893T>-	-	ENSMUSTdownstream_gene_variant	
14	23289398	A	C	base_quali	SNV	187	5	192	0.026	180	10	190	0.053	link	-	-	n.2328939:-	-	intergenic_region
14	24150111	C	A	base_quali	SNV	191	0	191	0	186	23	209	0.11	link	-	Dlg5	c.4322+28-	-	ENSMUSTintron_variant
14	24165940	G	A	too_few	_sSNV	4	0	4	0	6	2	8	0.25	link	-	Dlg5	c.1881+22-	-	ENSMUSTintron_variant
14	26871883	C	T	base_quali	SNV	115	2	117	0.017	91	6	97	0.062	link	-	Dnah12	n.2687188:-	-	intergenic_variant
14	27093964	A	C	base_quali	SNV	9	0	9	0	21	5	26	0.192	link	-	Il17rd	c.814-214/-	-	ENSMUSTintron_variant
14	31475221	A	C	base_quali	SNV	64	5	69	0.072	67	10	77	0.13	link	-	Mettl6	c.*4414T>-	-	ENSMUSTdownstream_gene_variant
14	31475221	A	C	base_quali	SNV	64	5	69	0.072	67	10	77	0.13	link	-	-	n.3147522:-	-	intergenic_region
14	34424845	A	C	base_quali	SNV	29	1	30	0.033	54	8	62	0.129	link	-	Bmpr1a	c.868+101-	-	ENSMUSTintron_variant
14	34597550	T	G	base_quali	SNV	105	3	108	0.028	103	7	110	0.064	link	-	Opn4	c.288-57A:-	-	ENSMUSTintron_variant
14	34691593	A	C	base_quali	SNV	28	5	33	0.152	30	14	44	0.318	link	-	Wapl	c.500-89A:-	-	ENSMUSTintron_variant
14	34740932	A	C	base_quali	SNV	39	0	39	0	45	6	51	0.118	link	-	Wapl	c.3353-12C-	-	ENSMUSTintron_variant
14	42849405	A	T	no_reliable	SNV	178	1	179	0.006	205	9	214	0.042	link	-	Gm21977	c.633+494-	-	ENSMUSTintron_variant
14	44201703	G	T	alt_allele	_SNV	119	4	123	0.033	131	4	135	0.03	link	-	Gm8212	c.633+478-	-	ENSMUSTintron_variant
14	46818258	G	A	base_quali	SNV	22	4	26	0.154	48	8	56	0.143	link	-	Gmfb	c.4-776C>-	-	ENSMUSTintron_variant
14	47087600	A	C	base_quali	SNV	18	1	19	0.053	21	10	31	0.323	link	-	Samd4	c.1695-15C-	-	ENSMUSTintron_variant
14	49052474	T	G	base_quali	SNV	105	6	111	0.054	91	10	101	0.099	link	-	Exoc5	c.28-82A>-	-	ENSMUSTintron_variant
14	51716453	T	G	base_quali	SNV	20	0	20	0	45	4	49	0.082	link	-	Gm5800	c.17-313A:-	-	ENSMUSTintron_variant
14	51891890	T	G	non_homr	SNV	13	3	16	0.188	27	6	33	0.182	link	-	Slc39a2	c.-1910T>-	-	ENSMUSTupstream_gene_variant
14	51891890	T	G	non_homr	SNV	13	3	16	0.188	27	6	33	0.182	link	-	Mettl17	c.*155T>G-	-	ENSMUSTdownstream_gene_variant
14	51891890	T	G	non_homr	SNV	13	3	16	0.188	27	6	33	0.182	link	-	Mettl17	n.5189189:-	-	intragenic_variant
14	51999694	A	C	base_quali	SNV	15	3	18	0.167	19	7	26	0.269	link	-	Arhgef40	c.3595-12C-	-	ENSMUSTintron_variant
14	53487971	A	C	base_quali	SNV	60	2	62	0.032	75	9	84	0.107	link	-	Trav9-1	c.-135A>C-	-	ENSMUSTupstream_gene_variant
14	53487971	A	C	base_quali	SNV	60	2	62	0.032	75	9	84	0.107	link	-	Trav6-5	c.-3181A>-	-	ENSMUSTupstream_gene_variant
14	53487971	A	C	base_quali	SNV	60	2	62	0.032	75	9	84	0.107	link	-	-	n.5348797:-	-	intergenic_region
14	55674704	A	C	base_quali	SNV	6	0	6	0	19	8	27	0.296	link	-	Nedd8	c.-2892T>-	-	ENSMUSTupstream_gene_variant
14	55674704	A	C	base_quali	SNV	6	0	6	0	19	8	27	0.296	link	-	Tinf2	c.*4634T>-	-	ENSMUSTdownstream_gene_variant

15	34584886	C	T	base_qualiSNV	20	3	23	0.13	37	7	44	0.159 link	-	Nipal2	c.656-121(-	ENSMUSTintron_variant
15	44376696	T	G	base_qualiSNV	152	7	159	0.044	145	22	167	0.132 link	-	Nudcd1	c.1457-10(-	ENSMUSTintron_variant
15	47695603	A	G	PASS SNV	69	0	69	0	61	6	67	0.09 link	-	Gm16300	n.*4106T>-	ENSMUSTdownstream_gene_variant
15	47695603	A	G	PASS SNV	69	0	69	0	61	6	67	0.09 link	-	Csmd3	c.7165+98-	ENSMUSTintron_variant
15	48287659	T	G	PASS SNV	65	0	65	0	63	5	68	0.074 link	-	Csmd3	c.1421-87(-	ENSMUSTintron_variant
15	58034179	G	A	weak_evid SNV	373	4	377	0.011	398	5	403	0.012 link	-	Gm29394	c.22-3079(-	ENSMUSTintron_variant
15	58322680	A	C	no_reliableSNV	8	1	9	0.111	28	4	32	0.125 link	-	Sgle	c.720-156(-	ENSMUSTintron_variant
15	59359182	A	C	base_qualiSNV	65	4	69	0.058	73	11	84	0.131 link	-	E430025E	c.1150+81-	ENSMUSTintron_variant
15	64122147	T	G	base_qualiSNV	206	12	218	0.055	220	17	237	0.072 link	-	Asap1	c.2110-32(-	ENSMUSTintron_variant
15	66674179	T	A	PASS SNV	19	0	19	0	35	17	52	0.327 link	-	Tg	c.641+108-	ENSMUSTintron_variant
15	66792459	T	G	base_qualiSNV	40	1	41	0.024	32	12	44	0.273 link	-	Tg	c.7236+18-	ENSMUSTintron_variant
15	66792459	T	G	base_qualiSNV	40	1	41	0.024	32	12	44	0.273 link	-	Sla	c.210-148(-	ENSMUSTintron_variant
15	73566962	C	A	base_qualiSNV	118	0	118	0	133	13	146	0.089 link	-	Dennd3	c.3249-71(-	ENSMUSTintron_variant
15	76065020	G	C	PASS SNV	384	0	384	0	392	67	459	0.146 link	-	Mir6952	n.-132C>G-	ENSMUSTupstream_gene_variant
15	79251037	A	C	base_qualiSNV	26	2	28	0.071	58	9	67	0.134 link	-	Slc16a8	c.*91T>G -	ENSMUST3_prime_UTR_variant
15	79251037	A	C	base_qualiSNV	26	2	28	0.071	58	9	67	0.134 link	-	Lgals1-ps	n.-453TA>-	ENSMUSTupstream_gene_variant
15	79251037	A	C	base_qualiSNV	26	2	28	0.071	58	9	67	0.134 link	-	Pick1	c.979+274-	ENSMUSTintron_variant
15	79420051	T	G	base_qualiSNV	162	9	171	0.053	216	10	226	0.044 link	-	Csnk1e	c.1219-83(-	ENSMUSTintron_variant
15	80929044	T	C	base_qualiSNV	100	7	107	0.065	81	11	92	0.12 link	-	Tnrc6b	c.5046-451-	ENSMUSTintron_variant
15	81023817	T	G	base_qualiSNV	8	1	9	0.111	10	4	14	0.286 link	-	Mkl1	c.169-200(-	ENSMUSTintron_variant
15	81686203	A	C	base_qualiSNV	233	1	234	0.004	258	8	266	0.03 link	-	Chad1	c.*212T>G-	ENSMUST3_prime_UTR_variant
15	82223299	T	G	base_qualiSNV	189	2	191	0.01	218	16	234	0.068 link	-	Tnfrsf13c	c.458-56A(-	ENSMUSTintron_variant
15	82283347	C	T	non_homrSNV	95	1	96	0.01	129	5	134	0.037 link	-	Sept3	c.292+60C-	ENSMUSTintron_variant
15	83783911	A	C	base_qualiSNV	325	8	333	0.024	268	13	281	0.046 link	-	Mpped1	c.-82+380-	ENSMUSTintron_variant
15	86158947	A	C	base_qualiSNV	11	1	12	0.083	22	5	27	0.185 link	-	Cerk	c.505+147-	ENSMUSTintron_variant
15	88957969	G	A	PASS SNV	22	0	22	0	46	3	49	0.061 link	-	Ttl8	c.-3894C>-	ENSMUSTupstream_gene_variant
15	88957969	G	A	PASS SNV	22	0	22	0	46	3	49	0.061 link	-	Mlc1	c.1092+95-	ENSMUSTintron_variant
15	89126987	T	G	base_qualiSNV	302	6	308	0.019	323	6	329	0.018 link	-	Tubgcp6	c.-4170A>-	ENSMUSTupstream_gene_variant
15	89126987	T	G	base_qualiSNV	302	6	308	0.019	323	6	329	0.018 link	-	Mapk12	c.*4152A>-	ENSMUSTdownstream_gene_variant
15	91182586	A	C	base_qualiSNV	68	3	71	0.042	80	7	87	0.08 link	-	Abcd2	c.1242+95-	ENSMUSTintron_variant
15	94282097	T	G	base_qualiSNV	74	4	78	0.051	86	17	103	0.165 link	-	Adams20	c.5301-78(-	ENSMUSTintron_variant
15	94554604	A	C	base_qualiSNV	52	4	56	0.071	66	14	80	0.175 link	-	Irak4	c.491-82A(-	ENSMUSTintron_variant
15	94554616	A	C	base_qualiSNV	67	1	68	0.015	85	9	94	0.096 link	-	Irak4	c.491-70A(-	ENSMUSTintron_variant
15	98125414	C	A	base_qualiSNV	55	0	55	0	71	11	82	0.134 link	-	Pfkm	c.1128-13(-	ENSMUSTintron_variant
15	98595848	A	C	base_qualiSNV	8	1	9	0.111	12	6	18	0.333 link	-	Gm29331	n.*4758A>-	ENSMUSTdownstream_gene_variant
15	98595848	A	C	base_qualiSNV	8	1	9	0.111	12	6	18	0.333 link	-	Adcy6	c.2621+19-	ENSMUSTintron_variant
15	1E+08	G	A	PASS SNV	190	0	190	0	238	5	243	0.021 link	-	Dip2b	c.-169G>A-	ENSMUSTupstream_gene_variant
15	1E+08	G	A	PASS SNV	190	0	190	0	238	5	243	0.021 link	-	-	n.1000386(-	- intergenic_region
15	1.01E+08	A	C	base_qualiSNV	18	0	18	0	26	13	39	0.333 link	-	Gm27209	n.-3697A>-	ENSMUSTupstream_gene_variant
15	1.01E+08	A	C	base_qualiSNV	18	0	18	0	26	13	39	0.333 link	-	Pou6f1	c.241+122-	ENSMUSTintron_variant
15	1.01E+08	A	C	base_qualiSNV	18	0	18	0	26	13	39	0.333 link	-	Gm20680	n.641-170(-	ENSMUSTintron_variant
15	1.01E+08	A	C	base_qualiSNV	18	2	20	0.1	31	9	40	0.225 link	-	Gm27209	n.-3694A>-	ENSMUSTupstream_gene_variant
15	1.01E+08	A	C	base_qualiSNV	18	2	20	0.1	31	9	40	0.225 link	-	Pou6f1	c.241+119-	ENSMUSTintron_variant
15	1.01E+08	A	C	base_qualiSNV	18	2	20	0.1	31	9	40	0.225 link	-	Gm20680	n.641-167(-	ENSMUSTintron_variant
15	1.01E+08	A	C	base_qualiSNV	47	5	52	0.096	85	12	97	0.124 link	-	C330013E	n.-4170T>-	ENSMUSTupstream_gene_variant
15	1.01E+08	A	C	base_qualiSNV	47	5	52	0.096	85	12	97	0.124 link	-	Smagp	c.*2568T>-	ENSMUSTdownstream_gene_variant
15	1.01E+08	A	C	base_qualiSNV	47	5	52	0.096	85	12	97	0.124 link	-	Dazap2	c.379-88A(-	ENSMUSTintron_variant
15	1.01E+08	T	G	base_qualiSNV	14	1	15	0.067	28	4	32	0.125 link	-	Scn8a	c.614+150-	ENSMUSTintron_variant
15	1.01E+08	T	G	base_qualiSNV	8	0	8	0	9	4	13	0.308 link	-	Ankrd33	c.292+244-	ENSMUSTintron_variant
15	1.03E+08	T	G	base_qualiSNV	137	3	140	0.021	173	15	188	0.08 link	-	Atpsg2	c.40-74A>-	ENSMUSTintron_variant
15	1.03E+08	G	C	PASS SNV	232	0	232	0	207	4	211	0.019 link	-	Calcoco1	c.850-17C(-	ENSMUSTintron_variant
15	1.03E+08	T	G	alt_allele_iSNV	18	5	23	0.217	37	16	53	0.302 link	-	Nckap1	c.2156+12-	ENSMUSTintron_variant
15	1.04E+08	T	G	base_qualiSNV	200	1	201	0.005	186	8	194	0.041 link	-	Pde1b	c.110+366-	ENSMUSTintron_variant
15	1.04E+08 rs3246356A	G	G	low_normaSNV	2	0	2	0	14	2	16	0.125 link	-	Muc12	c.*283T>C-	ENSMUSTdownstream_gene_variant
15	1.04E+08 rs3246356A	G	G	low_normaSNV	2	0	2	0	14	2	16	0.125 link	-	-	n.1038957(-	- intergenic_region
15	1.04E+08 rs1133742T	A	A	too_few_sSNV	4	0	4	0	17	2	19	0.105 link	-	Muc12	c.*272A>T-	ENSMUSTdownstream_gene_variant
15	1.04E+08 rs1133742T	A	A	too_few_sSNV	4	0	4	0	17	2	19	0.105 link	-	-	n.1038957(-	- intergenic_region
15	1.04E+08 rs11332996C	A	A	weak_evid SNV	11	0	11	0	33	4	37	0.108 link	-	Muc12	c.*234G>T-	ENSMUSTdownstream_gene_variant
15	1.04E+08 rs11332996C	A	A	weak_evid SNV	11	0	11	0	33	4	37	0.108 link	-	-	n.1038957(-	- intergenic_region
16	4483387	T	G	base_qualiSNV	22	3	25	0.12	34	8	42	0.19 link	-	Srl	c.1922-10(-	ENSMUSTintron_variant
16	14151110	A	C	base_qualiSNV	97	4	101	0.04	121	11	132	0.083 link	-	Marf1	c.1003+32-	ENSMUSTintron_variant
16	14256094	A	C	too_few_sSNV	16	0	16	0	24	2	26	0.077 link	-	Myh11	c.530+391-	ENSMUSTintron_variant
16	17654038	G	T	base_qualiSNV	252	0	252	0	213	25	238	0.105 link	-	Ccdc74a	c.*3428G>-	ENSMUSTdownstream_gene_variant
16	17654038	G	T	base_qualiSNV	252	0	252	0	213	25	238	0.105 link	-	Med15	c.1740-47(-	ENSMUSTintron_variant
16	17654039	G	T	base_qualiSNV	248	0	248	0	227	19	246	0.077 link	-	Ccdc74a	c.*3429G>-	ENSMUSTdownstream_gene_variant
16	17654039	G	T	base_qualiSNV	248	0	248	0	227	19	246	0.077 link	-	Med15	c.1740-48(-	ENSMUSTintron_variant
16	17671415	A	C	base_qualiSNV	16	2	18	0.111	28	11	39	0.282 link	-	Med15	c.1164+13-	ENSMUSTintron_variant
16	20157155	C	G	PASS SNV	93	0	93	0	110	10	120	0.083 link	-	Yeats2	c.537+23C-	ENSMUSTintron_variant
16	20680263	T	G	alt_allele_iSNV	12	1	13	0.077	9	1	10	0.1 link	-	Snord66	n.-3976T>-	ENSMUSTupstream_gene_variant
16	20680263	T	G	alt_allele_iSNV	12	1	13	0.077	9	1	10	0.1 link	-	Eif4g1	c.1531+23-	ENSMUSTintron_variant
16	22265550	C	A	base_qualiSNV	10	1	11	0.091	28	9	37	0.243 link	-	Tra2b	c.36+191G-	ENSMUSTintron_variant
16	25871248	C	T	base_qualiSNV	21	3	24	0.125	38	9	47	0.191 link	-	Trp63	c.1349+11-	ENSMUSTintron_variant
16	30348140	T	G	base_qualiSNV	186	6	192	0.031	240	8	248	0.032 link	-	Atp13a3	c.1486-29(-	ENSMUSTintron_variant
16	32087214	G	A	base_qualiSNV	23	1	24	0.042	42	5	47	0.106 link	-	Pigx	c.520+80C-	ENSMUSTintron_variant
16	33106999	A	C	base_qualiSNV	138	3	141	0.021	134	10	144	0.069 link	-	Mir1947	n.*1554A>-	ENSMUSTdownstream_gene_variant
16	33106999	A	C	base_qualiSNV	138	3	141	0.021	134	10	144	0.069 link	-	Lmln	c.1444-15(-	ENSMUSTintron_variant
16	33106999	A	C	base_qualiSNV	138	3	141	0.021	134	10	144	0.069 link	-	Gm17106	n.147+145-	ENSMUSTintron_variant
16	34013471	T	C	alt_allele_iSNV	14	4	18	0.222	30	7	37	0.189 link	-	Kalrn	c.7109+48-	ENSMUSTintron_variant
16	34677063	A	C	base_qualiSNV	50	1	51	0.02	65	8	73	0.11 link	-	Ropn1	c.397-73A(-	ENSMUSTintron_variant
16	35456202	A	G	base_qualiSNV	205	7	212	0.033	239	11	250	0.044 link	-	Pdia5	c.336-61T(-	ENSMUSTintron_variant
16	35664437	C	T	base_qualiSNV	165	3	168	0.018	135	14	149	0.094 link	-	Sema5b	c.*1162C>-	ENSMUSTdownstream_gene_variant
16	35664437	C	T	base_qualiSNV	165	3	168	0.018	135	14	149	0.094 link	-	Sema5b	n.3566443(-	- intragenic_variant
16	35719213	G	A	base_qualiSNV	40	2	42	0.048	63	7	70	0.1 link	-	Gm25967	n.*2874C>-	ENSMUSTdownstream_gene_variant
16	35719213	G	A	base_qualiSNV	40	2	42	0.048	63	7	70	0.1 link	-	Dir2	c.1138+99-	ENSMUSTintron_variant
16	36255838	T	G	alt_allele_iSNV	8	0	8	0	16	3	19	0.158 link	-	Gm24569	n.*1672A>-	ENSMUSTdownstream_gene_variant
16	36255838	T	G	alt_allele_iSNV	8	0	8	0	16	3	19	0.158 link	-			

17	13902398 .	A	C	base_qualiSNV	32	1	33	0.03	47	8	55	0.145 link	-	MIH4	c.5246-13i-	ENSMUST intron_variant
17	13902416 .	A	C	base_qualiSNV	45	1	46	0.022	54	11	65	0.169 link	-	MIH4	c.5246-114-	ENSMUST intron_variant
17	23347626 .	A	T	weak_evid SNV	9	0	9	0	20	6	26	0.231 link	-	Vmn2r115	c.1303-19i-	ENSMUST intron_variant
17	23357109 rs1132173T	G	G	mapping_cSNV	221	12	233	0.052	179	40	219	0.183 link	-	Vmn2r115	c.1654+26-	ENSMUST intron_variant
17	23357118 rs1132846G	A	A	mapping_cSNV	197	11	208	0.053	159	35	194	0.18 link	-	Vmn2r115	c.1654+35-	ENSMUST intron_variant
17	23357120 rs1132124G	A	A	mapping_cSNV	191	12	203	0.059	156	35	191	0.183 link	-	Vmn2r115	c.1654+37-	ENSMUST intron_variant
17	23357125 .	C	A	mapping_cSNV	171	10	181	0.055	163	19	182	0.104 link	-	Vmn2r115	c.1654+42-	ENSMUST intron_variant
17	23357132 .	T	C	mapping_cSNV	155	11	166	0.066	131	35	166	0.211 link	-	Vmn2r115	c.1654+49-	ENSMUST intron_variant
17	23357166 .	G	A	mapping_cSNV	71	10	81	0.123	86	34	120	0.283 link	-	Vmn2r115	c.1654+83-	ENSMUST intron_variant
17	23357192 .	G	A	mapping_cSNV	35	5	40	0.125	56	20	76	0.263 link	-	Vmn2r115	c.1654+10-	ENSMUST intron_variant
17	23357196 .	C	T	mapping_cSNV	35	5	40	0.125	52	16	68	0.235 link	-	Vmn2r115	c.1654+11-	ENSMUST intron_variant
17	23357209 .	A	G	mapping_cSNV	23	3	26	0.115	37	15	52	0.288 link	-	Vmn2r115	c.1654+12-	ENSMUST intron_variant
17	23475728 rs1134571C	T	T	mapping_cSNV	9	0	9	0	15	6	21	0.286 link	-	Vmn2r117	c.1303-15i-	ENSMUST intron_variant
17	23478598 .	G	C	non_homrctSNV	98	0	98	0	98	1	99	0.01 link	-	Vmn2r117	c.198-79C-	ENSMUST intron_variant
17	23478601 .	G	T	too_few_srsSNV	93	0	93	0	94	1	95	0.011 link	-	Vmn2r117	c.198-82C-	ENSMUST intron_variant
17	23668064 .	C	T	PASS SNV	315	0	315	0	274	51	325	0.157 link	-	Thoc6	c.*742G>A-	ENSMUST downstream_gene_variant
17	23668064 .	C	T	PASS SNV	315	0	315	0	274	51	325	0.157 link	-	Ccdc64b	c.1363-39C-	ENSMUST intron_variant
17	24650313 .	G	A	too_few_srsSNV	9	0	9	0	28	2	30	0.067 link	-	Slc9a3r2	c.-163C>T-	ENSMUST upstream_gene_variant
17	24650313 .	G	A	too_few_srsSNV	9	0	9	0	28	2	30	0.067 link	-	-	n.2465031-	- intergenic_region
17	27029365 .	A	C	base_qualiSNV	40	2	42	0.048	46	13	59	0.22 link	-	Ggnbp1	c.-94A>C-	ENSMUST 5_prime_UTR_variant
17	27029365 .	A	C	base_qualiSNV	40	2	42	0.048	46	13	59	0.22 link	-	Bak1	c.c3509T>-	ENSMUST upstream_gene_variant
17	27715157 .	T	G	base_qualiSNV	29	5	34	0.147	38	13	51	0.255 link	-	Pacsin1	c.*6622T>-	ENSMUST downstream_gene_variant
17	27715157 .	T	G	base_qualiSNV	29	5	34	0.147	38	13	51	0.255 link	-	Spdef	c.800-111/-	ENSMUST intron_variant
17	29036177 .	A	C	base_qualiSNV	102	3	105	0.029	131	5	136	0.037 link	-	Srsf3	c.-2-64A>-/-	ENSMUST intron_variant
17	29378264 .	A	C	base_qualiSNV	145	11	156	0.071	155	11	166	0.066 link	-	Fgd2	c.1606-49/-	ENSMUST intron_variant
17	30524988 .	T	G	base_qualiSNV	149	7	156	0.045	145	14	159	0.088 link	-	Btdb9	c.550-11A-	ENSMUST intron_variant
17	30854789 .	A	C	base_qualiSNV	111	3	114	0.026	115	10	125	0.08 link	-	Dnah8	c.13444-1i-	ENSMUST intron_variant
17	32525010 .	T	G	base_qualiSNV	198	3	201	0.015	234	11	245	0.045 link	-	Cyp4f17	c.1115+46-	ENSMUST intron_variant
17	33630506 .	T	G	base_qualiSNV	251	7	258	0.027	267	13	280	0.046 link	-	Gm20507	n.-253T>G-	ENSMUST upstream_gene_variant
17	33630506 .	T	G	base_qualiSNV	251	7	258	0.027	267	13	280	0.046 link	-	Zfp414	c.394+32T-	ENSMUST intron_variant
17	34028662 .	A	G	base_qualiSNV	27	3	30	0.1	49	12	61	0.197 link	-	Slc39a7	c.*134T>C-	ENSMUST 3_prime_UTR_variant
17	34028662 .	A	G	base_qualiSNV	27	3	30	0.1	49	12	61	0.197 link	-	Ring1	c.c4296T>-	ENSMUST upstream_gene_variant
17	34028662 .	A	G	base_qualiSNV	27	3	30	0.1	49	12	61	0.197 link	-	H2-Ke6	c.-615T>C-	ENSMUST upstream_gene_variant
17	34028662 .	A	G	base_qualiSNV	27	3	30	0.1	49	12	61	0.197 link	-	Rxbp	c.-3336A>-	ENSMUST upstream_gene_variant
17	34028662 .	A	G	base_qualiSNV	27	3	30	0.1	49	12	61	0.197 link	-	Gm26940	n.-3592T>-	ENSMUST upstream_gene_variant
17	34028662 .	A	G	base_qualiSNV	27	3	30	0.1	49	12	61	0.197 link	-	Mir219a-1	n.-3570T>-	ENSMUST upstream_gene_variant
17	34028662 .	A	G	base_qualiSNV	27	3	30	0.1	49	12	61	0.197 link	-	Mir219c	n.*3591A>-	ENSMUST downstream_gene_variant
17	34028662 .	A	G	base_qualiSNV	27	3	30	0.1	49	12	61	0.197 link	-	Gm20427	n.1683T>C-	ENSMUST non_coding_transcript_exon_variant
17	34333578 .	T	G	base_qualiSNV	95	3	98	0.031	84	8	92	0.087 link	-	H2-Eb2	c.367+29T-	ENSMUST intron_variant
17	34843072 .	T	G	base_qualiSNV	145	7	152	0.046	190	17	207	0.082 link	-	Mir6971	n.-1201A>-	ENSMUST upstream_gene_variant
17	34843072 .	T	G	base_qualiSNV	145	7	152	0.046	190	17	207	0.082 link	-	Dxo	c.*3935T>-	ENSMUST downstream_gene_variant
17	34843072 .	T	G	base_qualiSNV	145	7	152	0.046	190	17	207	0.082 link	-	Mir6970	n.*2029A>-	ENSMUST downstream_gene_variant
17	34843072 .	T	G	base_qualiSNV	145	7	152	0.046	190	17	207	0.082 link	-	Skiv2i	c.1963-30/-	ENSMUST intron_variant
17	35265684 .	A	C	base_qualiSNV	75	4	79	0.051	131	11	142	0.077 link	-	H2-D1	c.620-100/-	ENSMUST intron_variant
17	35265687 .	T	C	base_qualiSNV	85	3	88	0.034	132	15	147	0.102 link	-	H2-D1	c.620-97T/-	ENSMUST intron_variant
17	35684342 .	T	G	base_qualiSNV	138	6	144	0.042	132	10	142	0.07 link	-	Ddr1	c.1992-29/-	ENSMUST intron_variant
17	35688505 .	G	A	PASS SNV	231	0	231	0	240	9	249	0.036 link	-	Ddr1	c.1341+34-	ENSMUST intron_variant
17	35887565 .	G	C	base_qualiSNV	53	10	63	0.159	45	29	74	0.392 link	-	Dhx16	c.2157+26-	ENSMUST intron_variant
17	42377782 .	G	T	base_qualiSNV	6	1	7	0.143	27	5	32	0.156 link	-	Ptchd4	c.1072+14-	ENSMUST intron_variant
17	42594574 .	A	C	too_few_srsSNV	13	0	13	0	13	2	15	0.133 link	-	Opn5	c.422-155i-	ENSMUST intron_variant
17	42596683 .	T	G	alt_allele_iSNV	30	5	35	0.143	46	5	51	0.098 link	-	Opn5	c.251-110/-	ENSMUST intron_variant
17	43617073 .	G	A	weak_evid SNV	184	1	185	0.005	173	3	176	0.017 link	-	Pla2g7	c.*5094G>-	ENSMUST downstream_gene_variant
17	43617073 .	G	A	weak_evid SNV	184	1	185	0.005	173	3	176	0.017 link	-	Tdrd6	c.6331+9T-	ENSMUST intron_variant
17	43953148 .	A	C	base_qualiSNV	6	1	7	0.143	5	2	7	0.286 link	-	Rcan2	c.226-646i-	ENSMUST intron_variant
17	44639843 .	T	G	base_qualiSNV	163	1	164	0.006	209	9	218	0.041 link	-	n-R5e27	n.*1182A>-	ENSMUST downstream_gene_variant
17	44639843 .	T	G	base_qualiSNV	163	1	164	0.006	209	9	218	0.041 link	-	Runx2	c.1085-17/-	ENSMUST intron_variant
17	44639891 .	T	G	base_qualiSNV	71	9	80	0.113	84	17	101	0.168 link	-	n-R5e27	n.*1134A>-	ENSMUST downstream_gene_variant
17	44639891 .	T	G	base_qualiSNV	71	9	80	0.113	84	17	101	0.168 link	-	Runx2	c.1085-65/-	ENSMUST intron_variant
17	46238797 .	G	A	base_qualiSNV	50	5	55	0.091	55	16	71	0.225 link	-	Xpo5	c.2823-93C-	ENSMUST intron_variant
17	46527537 .	C	T	too_few_srsSNV	6	0	6	0	4	2	6	0.333 link	-	Gm26904	n.36+5600-	ENSMUST intron_variant
17	46527537 .	C	T	too_few_srsSNV	6	0	6	0	4	2	6	0.333 link	-	CuI9	c.2809+36-	ENSMUST intron_variant
17	50741797 .	C	T	too_few_srsSNV	9	0	9	0	25	2	27	0.074 link	-	Tbcd5	c.2005-17i-	ENSMUST intron_variant
17	56011199 .	T	G	base_qualiSNV	54	1	55	0.018	125	19	144	0.132 link	-	Gm16276	n.*3084A>-	ENSMUST downstream_gene_variant
17	56011199 .	T	G	base_qualiSNV	54	1	55	0.018	125	19	144	0.132 link	-	Mpnd	c.625+88T-	ENSMUST intron_variant
17	56438149 .	T	G	base_qualiSNV	58	3	61	0.049	59	8	67	0.119 link	-	Ptptr	c.680-94A/-	ENSMUST intron_variant
17	56660073 rs1076919T	C	C	base_qualiSNV	73	3	76	0.039	95	16	111	0.144 link	-	Catsperd	c.1551-98i-	ENSMUST intron_variant
17	57041388 .	C	A	base_qualiSNV	24	1	25	0.04	46	10	56	0.179 link	-	Gm17168	n.-387C>A-	ENSMUST upstream_gene_variant
17	57041388 .	C	A	base_qualiSNV	24	1	25	0.04	46	10	56	0.179 link	-	Slc25a23	c.*4091G>-	ENSMUST downstream_gene_variant
17	57041388 .	C	A	base_qualiSNV	24	1	25	0.04	46	10	56	0.179 link	-	Slc25a41	c.18+186G-	ENSMUST intron_variant
17	58932598 .	T	G	base_qualiSNV	56	3	59	0.051	71	10	81	0.123 link	-	Pdzph1	c.2804-70/-	ENSMUST intron_variant
17	64713436 .	A	C	alt_allele_iSNV	15	4	19	0.211	19	6	25	0.24 link	-	Man2a1	c.2332-12i-	ENSMUST intron_variant
17	71121048 .	G	A	base_qualiSNV	151	4	155	0.026	106	4	110	0.036 link	-	Myom1	c.4632-78C-	ENSMUST intron_variant
17	71121048 .	G	A	base_qualiSNV	151	4	155	0.026	106	4	110	0.036 link	-	Gm26561	n.184+164-	ENSMUST intron_variant
17	74561936 .	A	G	base_qualiSNV	93	4	97	0.041	99	13	112	0.116 link	-	Birc6	c.961-83A/-	ENSMUST intron_variant
17	74585868 .	A	C	base_qualiSNV	53	3	56	0.054	51	8	59	0.136 link	-	Gm26749	n.1734-10i-	ENSMUST intron_variant
17	74585868 .	A	C	base_qualiSNV	53	3	56	0.054	51	8	59	0.136 link	-	Birc6	c.2885-85/-	ENSMUST intron_variant
17	74646932 .	T	G	base_qualiSNV	36	2	38	0.053	29	3	32	0.094 link	-	Birc6	c.10049+1-	ENSMUST intron_variant
17	74690162 .	A	G	too_few_srsSNV	10	0	10	0	22	2	24	0.083 link	-	Birc6	c.13577-1i-	ENSMUST intron_variant
17	75226766 .	A	C	base_qualiSNV	4	0	4	0	3	7	10	0.7 link	-	Ltpb1	c.1403-20i-	ENSMUST intron_variant
17	78936117 .	G	A	base_qualiSNV	68	4	72	0.056	52	5	57	0.088 link	-	Ndufaf7	c.-1048G>-	ENSMUST upstream_gene_variant
17	78936117 .	G	A	base_qualiSNV	68	4	72	0.056	52	5	57	0.088 link	-	Cebpz	c.157-50C/-	ENSMUST intron_variant
17	79857271 .	T	G	base_qualiSNV	157	1	158	0.006	169	8	177	0.045 link	-	Ati2	c.805-25A/-	ENSMUST intron_variant
17	80045205 .	T	G	base_qualiSNV	8	0	8	0	27	6	33	0.182 link	-	Hnrnp1l	c.950-640/-	ENSMUST intron_variant
17	81428084 .	A	C	base_qualiSNV	78	4	82	0.049	104	11	115	0.096 link	-	Slc8a1	c.2260+98-	ENSMUST intron_variant
17	83832555 .	T	G	base_qualiSNV	22	2	24	0.083	31	12	43	0.279 link	-	Haao	c.6	

18	69966719 .	A	C	base_qualiSNV	115	6	121	0.05	115	17	132	0.129	link	-	1700061H.n.130+276-	ENSMUSTintron_variant
18	70467567 .	T	G	base_qualiSNV	83	5	88	0.057	105	12	117	0.103	link	-	Stard6 c.-8537T>-	ENSMUSTupstream_gene_variant
18	70467567 .	T	G	base_qualiSNV	83	5	88	0.057	105	12	117	0.103	link	-	4930503L1c.1052-82/-	ENSMUSTintron_variant
18	73747505 .	C	T	too_few_sSNV	14	0	14	0	35	2	37	0.054	link	-	Elac1 c.-8-174G>-	ENSMUSTintron_variant
18	74217000 .	A	C	base_qualiSNV	11	1	12	0.083	32	6	38	0.158	link	-	Ccxc1 c.4-167A>-	ENSMUSTintron_variant
18	75286423 .	A	T	too_few_sSNV	8	0	8	0	19	2	21	0.095	link	-	Dym c.1861-19/-	ENSMUSTintron_variant
18	80137666 .	G	T	base_qualiSNV	71	8	79	0.101	69	20	89	0.225	link	-	Adnp2 c.109-93C>-	ENSMUSTintron_variant
19	3268064 .	A	C	base_qualiSNV	8	0	8	0	16	5	21	0.238	link	-	Ighmbp2 c.1534+23-	ENSMUSTintron_variant
19	5424751 .	G	A	weak_evid SNV	216	1	217	0.005	339	7	346	0.02	link	-	Dras1 c.-37C>T	ENSMUST5_prime_UTR_variant
19	5424751 .	G	A	weak_evid SNV	216	1	217	0.005	339	7	346	0.02	link	-	A1837181 c.-418G>A-	ENSMUSTupstream_gene_variant
19	5424751 .	G	A	weak_evid SNV	216	1	217	0.005	339	7	346	0.02	link	-	4930481A1n.*1904G>-	ENSMUSTdownstream_gene_variant
19	5478345 .	T	G	base_qualiSNV	135	9	144	0.062	123	25	148	0.169	link	-	Mus81 c.*4618A>-	ENSMUSTdownstream_gene_variant
19	5478345 .	T	G	base_qualiSNV	135	9	144	0.062	123	25	148	0.169	link	-	Eltemp2 c.784+25T-	ENSMUSTintron_variant
19	6537550 .	T	C	base_qualiSNV	62	2	64	0.031	70	10	80	0.125	link	-	Nrxn2 c.*5402T>-	ENSMUSTdownstream_gene_variant
19	6537550 .	T	C	base_qualiSNV	62	2	64	0.031	70	10	80	0.125	link	-	Slc22a12 c.1285+88-	ENSMUSTintron_variant
19	6537550 .	T	C	base_qualiSNV	62	2	64	0.031	70	10	80	0.125	link	-	Nrxn2 n.6537550-	- intragenic_variant
19	6933673 .	C	T	too_few_sSNV	6	0	6	0	11	2	13	0.154	link	-	Gpr137 c.*4697G>-	ENSMUSTdownstream_gene_variant
19	6933673 .	C	T	too_few_sSNV	6	0	6	0	11	2	13	0.154	link	-	Kcnk4 c.-78+675/-	ENSMUSTintron_variant
19	7280041 .	T	G	base_qualiSNV	323	1	324	0.003	346	10	356	0.028	link	-	Rcor2 c.*5384T>-	ENSMUSTdownstream_gene_variant
19	7280041 .	T	G	base_qualiSNV	323	1	324	0.003	346	10	356	0.028	link	-	Mark2 c.1925+95-	ENSMUSTintron_variant
19	7597898 .	A	C	base_qualiSNV	16	0	16	0	19	4	23	0.174	link	-	Lgals12 c.*127T>G-	ENSMUST3_prime_UTR_variant
19	8743195 .	G	A	base_qualiSNV	217	15	232	0.065	298	11	309	0.036	link	-	Wdr74 c.*2617G>-	ENSMUSTdownstream_gene_variant
19	8743195 .	G	A	base_qualiSNV	217	15	232	0.065	298	11	309	0.036	link	-	1700092M c.*2039G>-	ENSMUSTdownstream_gene_variant
19	8743195 .	G	A	base_qualiSNV	217	15	232	0.065	298	11	309	0.036	link	-	Mir6992 n.*116G>A-	ENSMUSTdownstream_gene_variant
19	8743195 .	G	A	base_qualiSNV	217	15	232	0.065	298	11	309	0.036	link	-	RP23-620' c.*2039G>-	ENSMUSTdownstream_gene_variant
19	8743195 .	G	A	base_qualiSNV	217	15	232	0.065	298	11	309	0.036	link	-	St5a5 c.352+60G-	ENSMUSTintron_variant
19	10638213 .	T	G	base_qualiSNV	183	1	184	0.005	215	13	228	0.057	link	-	Vwce c.424+33T-	ENSMUSTintron_variant
19	11942430 .	A	C	base_qualiSNV	5	0	5	0	17	4	21	0.19	link	-	Patl1 c.c.2050-19/-	ENSMUSTintron_variant
19	16699166 .	T	G	base_qualiSNV	51	1	52	0.019	64	5	69	0.072	link	-	Vps13a c.3496-54/-	ENSMUSTintron_variant
19	16760145 .	T	G	alt_allele_iSNV	18	6	24	0.25	31	10	41	0.244	link	-	Vps13a c.188-109/-	ENSMUSTintron_variant
19	17560539 .	A	C	alt_allele_iSNV	6	1	7	0.143	17	7	24	0.292	link	-	Pcsk5 c.2632+32-	ENSMUSTintron_variant
19	18717175 .	A	C	base_qualiSNV	75	3	78	0.038	63	12	75	0.16	link	-	D030056L1c.337-44A/-	ENSMUSTintron_variant
19	24267433 .	T	G	base_qualiSNV	164	5	169	0.03	194	18	212	0.085	link	-	Fxn c.376-34A/-	ENSMUSTintron_variant
19	28945953 .	T	G	base_qualiSNV	42	5	47	0.106	70	14	84	0.167	link	-	443040211c.394-122/-	ENSMUSTintron_variant
19	29321850 .	T	G	alt_allele_iSNV	20	5	25	0.2	25	8	33	0.242	link	-	Insl6 c.272-111/-	ENSMUSTintron_variant
19	31992126 .	C	T	weak_evid SNV	192	0	192	0	199	3	202	0.015	link	-	Asah2 c.1993-36/-	ENSMUSTintron_variant
19	37968143 .	A	C	base_qualiSNV	4	0	4	0	17	5	22	0.227	link	-	Myof c.1542+18-	ENSMUSTintron_variant
19	40047677 .	A	G	base_qualiSNV	146	9	155	0.058	132	17	149	0.114	link	-	Cyp2c54 c.820-32T/-	ENSMUSTintron_variant
19	40788215 .	C	A	alt_allele_iSNV	34	4	38	0.105	17	7	24	0.292	link	-	Cc2d2b c.1452-20/-	ENSMUSTintron_variant
19	40792948 .	T	G	base_qualiSNV	74	2	76	0.026	69	2	71	0.028	link	-	Cc2d2b c.1794+15-	ENSMUSTintron_variant
19	44192472 .	T	G	base_qualiSNV	10	0	10	0	20	4	24	0.167	link	-	Pkd21l c.-198A>C-	ENSMUSTupstream_gene_variant
19	44192472 .	T	G	base_qualiSNV	10	0	10	0	20	4	24	0.167	link	-	- n.4419247/-	- intergenic_region
19	44938326 .	A	C	base_qualiSNV	133	0	133	0	157	8	165	0.048	link	-	Fam178a c.919-39A/-	ENSMUSTintron_variant
19	45155769 .	A	C	weak_evid SNV	18	1	19	0.053	50	3	53	0.057	link	-	Tlx1 c.780-125/-	ENSMUSTintron_variant
19	45155769 .	A	C	weak_evid SNV	18	1	19	0.053	50	3	53	0.057	link	-	Tlx1os n.396-148/-	ENSMUSTintron_variant
19	45560563 .	A	C	base_qualiSNV	81	1	82	0.012	144	9	153	0.059	link	-	Poll c.-872T>G-	ENSMUSTupstream_gene_variant
19	45560563 .	A	C	base_qualiSNV	81	1	82	0.012	144	9	153	0.059	link	-	Gm17018 c.-81A>C-	ENSMUSTupstream_gene_variant
19	45560563 .	A	C	base_qualiSNV	81	1	82	0.012	144	9	153	0.059	link	-	- n.4556056/-	- intergenic_region
19	46305853 rs2597385A	C	C	base_qualiSNV	73	1	74	0.014	127	14	141	0.099	link	-	Nfk2 c.-74-77A>-	ENSMUSTintron_variant
19	46306734 .	T	C	base_qualiSNV	132	11	143	0.077	140	21	161	0.13	link	-	Nfk2b c.145-37T/-	ENSMUSTintron_variant
19	46379512 .	T	G	base_qualiSNV	172	6	178	0.034	155	9	164	0.055	link	-	Mfsd13a c.*4798T>-	ENSMUSTdownstream_gene_variant
19	46379512 .	T	G	base_qualiSNV	172	6	178	0.034	155	9	164	0.055	link	-	Actr1a c.926-38A/-	ENSMUSTintron_variant
19	47109897 .	G	T	base_qualiSNV	24	4	28	0.143	22	16	38	0.421	link	-	Pdcd11 c.2497+12-	ENSMUSTintron_variant
19	47109897 .	G	T	base_qualiSNV	24	4	28	0.143	22	16	38	0.421	link	-	Calhm2 n.4710989'-	- intragenic_variant
19	47510690 .	T	C	too_few_sSNV	3	0	3	0	14	2	16	0.125	link	-	Gm19557 n.-2292T>-	ENSMUSTupstream_gene_variant
19	47510690 .	T	C	too_few_sSNV	3	0	3	0	14	2	16	0.125	link	-	Obfcl1 c.784-233/-	ENSMUSTintron_variant
19	47669214 .	A	C	base_qualiSNV	199	8	207	0.039	230	11	241	0.046	link	-	Col17a1 c.1492+24-	ENSMUSTintron_variant
19	55912721 .	T	G	base_qualiSNV	106	3	109	0.028	147	10	157	0.064	link	-	Tcf7l2 c.806+76T-	ENSMUSTintron_variant
2	5795746 .	T	G	base_qualiSNV	94	2	96	0.021	83	12	95	0.126	link	-	Cdc123 c.847-60A/-	ENSMUSTintron_variant
2	6872513 .	C	T	non_homrecSNV	172	1	173	0.006	148	3	151	0.02	link	-	Cell2 c.107+123-	ENSMUSTintron_variant
2	10097286 .	A	G	base_qualiSNV	115	3	118	0.025	159	12	171	0.07	link	-	Kin c.*4769A>-	ENSMUSTdownstream_gene_variant
2	10097286 .	A	G	base_qualiSNV	115	3	118	0.025	159	12	171	0.07	link	-	Ith2 c.2421-37T/-	ENSMUSTintron_variant
2	10105816 .	T	G	base_qualiSNV	157	7	164	0.043	150	9	159	0.057	link	-	Ith2 c.1474-11/-	ENSMUSTintron_variant
2	12194580 .	T	G	base_qualiSNV	29	3	32	0.094	26	16	42	0.381	link	-	Itha8 c.1551-14/-	ENSMUSTintron_variant
2	22867163 .	G	T	base_qualiSNV	10	1	11	0.091	37	6	43	0.14	link	-	Apbb1lp c.c.1263+17-	ENSMUSTintron_variant
2	24429386 .	A	C	base_qualiSNV	31	1	32	0.031	52	6	58	0.103	link	-	Pax8 c.1210+14-	ENSMUSTintron_variant
2	24632053 .	T	G	base_qualiSNV	136	8	144	0.056	146	17	163	0.104	link	-	Cacna1b c.5071-27/-	ENSMUSTintron_variant
2	25232354 .	T	C	base_qualiSNV	164	11	175	0.063	183	40	223	0.179	link	-	Rnf224 c.*3515A>-	ENSMUSTdownstream_gene_variant
2	25232354 .	T	C	base_qualiSNV	164	11	175	0.063	183	40	223	0.179	link	-	Slc34a3 c.301+26A-	ENSMUSTintron_variant
2	25616968 .	C	A	base_qualiSNV	118	11	129	0.085	110	18	128	0.141	link	-	Tmem141 c.*3549G>-	ENSMUSTdownstream_gene_variant
2	25616968 .	C	A	base_qualiSNV	118	11	129	0.085	110	18	128	0.141	link	-	Ccdc183 c.192+18G-	ENSMUSTintron_variant
2	25616968 .	C	A	base_qualiSNV	118	11	129	0.085	110	18	128	0.141	link	-	Fcnaos n.558C>A-	ENSMUSTnon_coding_transcript_exon_variant
2	26413872 .	T	G	base_qualiSNV	46	1	47	0.021	76	11	87	0.126	link	-	Inpp5e c.-5285A>-	ENSMUSTupstream_gene_variant
2	26413872 .	T	G	base_qualiSNV	46	1	47	0.021	76	11	87	0.126	link	-	Sec16a c.6928-134-	ENSMUSTintron_variant
2	26419465 .	A	C	base_qualiSNV	16	0	16	0	20	6	26	0.231	link	-	Sec16a c.6372+15-	ENSMUSTintron_variant
2	26509751 .	T	G	base_qualiSNV	109	4	113	0.035	157	16	173	0.092	link	-	Notch1 n.2650975/-	- intragenic_variant
2	27062175 rs1346557T	G	G	PASS SNV	229	1	230	0.004	224	6	230	0.026	link	-	Tmem8c c.*13A>C-	ENSMUST3_prime_UTR_variant
2	27961979 .	A	C	base_qualiSNV	109	5	114	0.044	105	15	120	0.125	link	-	Col5a1 c.1570-83/-	ENSMUSTintron_variant
2	30022378 .	A	C	base_qualiSNV	158	5	163	0.031	157	10	167	0.06	link	-	Sptan1 c.5734-62/-	ENSMUSTintron_variant
2	30435802 .	G	T	base_qualiSNV	34	0	34	0	55	5	60	0.083	link	-	Ptpa c.460+121-	ENSMUSTintron_variant
2	31615448 .	C	A	base_qualiSNV	90	3	93	0.032	97	14	111	0.126	link	-	Mir6998 n.*2964C>-	ENSMUSTdownstream_gene_variant
2	31615448 .	C	A	base_qualiSNV	90	3	93	0.032	97	14	111	0.126	link	-	Fubp3 c.1574-50C-	ENSMUSTintron_variant
2	32206707 .	G	T	base_qualiSNV	39	6	45	0.133	67	16	83	0.193	link	-	Prrc2b c.1962+12-	ENSMUSTintron_variant
2	34901413 .	A	G	low_normaSNV	2	0	2	0	1	8	9	0.889	link	-	Phf19 c.895-286T-	ENSMUSTintron_variant
2	34903982 .	G	T	base_qualiSNV	74											

2	84620499	T	G	base_quali	SNV	98	3	101	0.03	86	20	106	0.189	link	-	Gm28635	c.421-45A>-	ENSMUST intron_variant
2	91142952	C	T	base_quali	SNV	195	1	196	0.005	203	17	220	0.077	link	-	Madd	c.4571-90C>-	ENSMUST intron_variant
2	91930272	T	G	base_quali	SNV	27	2	29	0.069	47	9	56	0.161	link	-	Dgkz	c.*1317A>-	ENSMUST downstream_gene_variant
2	91930272	T	G	base_quali	SNV	27	2	29	0.069	47	9	56	0.161	link	-	Chrm4	c.*1584T>-	ENSMUST downstream_gene_variant
2	91930272	T	G	base_quali	SNV	27	2	29	0.069	47	9	56	0.161	link	-	Mdk	c.398-157/-	ENSMUST intron_variant
2	93677080	A	G	base_quali	SNV	14	1	15	0.067	26	8	34	0.235	link	-	Alx4	c.871-152/-	ENSMUST intron_variant
2	93677080	A	G	base_quali	SNV	14	1	15	0.067	26	8	34	0.235	link	-	Ext2	n.9367708/-	- intragenic_variant
2	93677081	A	G	base_quali	SNV	15	0	15	0	25	9	34	0.265	link	-	Alx4	c.871-151/-	ENSMUST intron_variant
2	93677081	A	G	base_quali	SNV	15	0	15	0	25	9	34	0.265	link	-	Ext2	n.9367708/-	- intragenic_variant
2	1.02E+08	A	C	base_quali	SNV	8	0	8	0	21	7	28	0.25	link	-	Rag2	c.-25-119A>-	ENSMUST intron_variant
2	1.02E+08	A	C	base_quali	SNV	8	0	8	0	21	7	28	0.25	link	-	B230118Hn	n.1016292/-	- intragenic_variant
2	1.04E+08	T	C	base_quali	SNV	79	6	85	0.071	100	15	115	0.13	link	-	D430041D	c.3476-66/-	ENSMUST intron_variant
2	1.13E+08	T	C	base_quali	SNV	62	4	66	0.061	90	8	98	0.082	link	-	Ryr3	c.7569+92/-	ENSMUST intron_variant
2	1.16E+08	A	C	base_quali	SNV	37	2	39	0.051	74	10	84	0.119	link	-	Meis2	c.-1303T>-	ENSMUST upstream_gene_variant
2	1.16E+08	A	C	base_quali	SNV	37	2	39	0.051	74	10	84	0.119	link	-	G630016G	n.-1852A>-	ENSMUST upstream_gene_variant
2	1.16E+08	A	C	base_quali	SNV	37	2	39	0.051	74	10	84	0.119	link	-	Z700033N	n.*102T>G>-	ENSMUST downstream_gene_variant
2	1.16E+08	A	C	base_quali	SNV	37	2	39	0.051	74	10	84	0.119	link	-	-	n.1160661/-	- intergenic_region
2	1.19E+08	T	C	base_quali	SNV	25	2	27	0.074	31	7	38	0.184	link	-	Ino80	c.3841+12>-	ENSMUST intron_variant
2	1.2E+08 rs2432693	A	C	base_quali	SNV	14	2	16	0.125	19	7	26	0.269	link	-	Nusap1	c.1079-161/-	ENSMUST intron_variant
2	1.2E+08	T	G	base_quali	SNV	11	0	11	0	15	6	21	0.286	link	-	Mapkbp1	c.330-242>-	ENSMUST intron_variant
2	1.2E+08	C	T	base_quali	SNV	18	2	20	0.1	34	12	46	0.261	link	-	Tmem87a	c.417+134>-	ENSMUST intron_variant
2	1.21E+08	T	C	weak_evid	SNV	142	2	144	0.014	181	5	186	0.027	link	-	Ppip5k1	c.3169+29>-	ENSMUST intron_variant
2	1.25E+08	T	G	base_quali	SNV	38	2	40	0.05	55	21	76	0.276	link	-	Myef2	c.1352-92/-	ENSMUST intron_variant
2	1.25E+08	T	G	base_quali	SNV	27	0	27	0	44	19	63	0.302	link	-	Myef2	c.1352-10/-	ENSMUST intron_variant
2	1.26E+08	A	G	base_quali	SNV	91	0	91	0	85	10	95	0.105	link	-	Fgf7	c.*58A>G>-	ENSMUST 3_prime_UTR_variant
2	1.26E+08	A	G	base_quali	SNV	91	0	91	0	85	10	95	0.105	link	-	Fam227b	c.976+112>-	ENSMUST intron_variant
2	1.28E+08	A	C	base_quali	SNV	27	2	29	0.069	40	12	52	0.231	link	-	Mrps5	c.938-109/-	ENSMUST intron_variant
2	1.29E+08	A	G	base_quali	SNV	45	3	48	0.062	73	10	83	0.12	link	-	Tmem87b	c.505-117/-	ENSMUST intron_variant
2	1.29E+08	T	G	base_quali	SNV	48	4	52	0.077	69	11	80	0.138	link	-	Gm14023	n.108-209/-	ENSMUST intron_variant
2	1.29E+08	T	G	base_quali	SNV	48	4	52	0.077	69	11	80	0.138	link	-	Il1a	c.500-65A>-	ENSMUST intron_variant
2	1.29E+08	T	G	base_quali	SNV	40	0	40	0	66	8	74	0.108	link	-	Gm14023	n.108-208/-	ENSMUST intron_variant
2	1.29E+08	T	G	base_quali	SNV	40	0	40	0	66	8	74	0.108	link	-	Il1a	c.500-73A>-	ENSMUST intron_variant
2	1.31E+08	T	C	base_quali	SNV	38	2	40	0.05	45	6	51	0.118	link	-	Ptptra	c.416-1301/-	ENSMUST intron_variant
2	1.31E+08	A	C	base_quali	SNV	38	2	40	0.05	45	8	53	0.151	link	-	Ptptra	c.416-129/-	ENSMUST intron_variant
2	1.31E+08	A	G	alt_allele	_jSNV	17	5	22	0.227	24	10	34	0.294	link	-	Atrn	c.3467-14/-	ENSMUST intron_variant
2	1.32E+08	G	A	too_few	_sSNV	6	0	6	0	12	2	14	0.143	link	-	-	n.1315304/-	- intergenic_region
2	1.35E+08 rs2574231	C	A	base_quali	SNV	18	2	20	0.1	30	9	39	0.231	link	-	Tmx4	c.280+294>-	ENSMUST intron_variant
2	1.36E+08	T	G	base_quali	SNV	90	6	96	0.062	116	10	126	0.079	link	-	Pak7	c.-442A>C>-	ENSMUST 5_prime_UTR_variant
2	1.52E+08	A	C	base_quali	SNV	39	3	42	0.071	69	17	86	0.198	link	-	Slc52a3	c.1047-10/-	ENSMUST intron_variant
2	1.53E+08	A	C	base_quali	SNV	13	1	14	0.071	21	4	25	0.16	link	-	Mylik2	c.528-161/-	ENSMUST intron_variant
2	1.54E+08	A	C	base_quali	SNV	21	0	21	0	28	9	37	0.243	link	-	Sun5	c.453+156>-	ENSMUST intron_variant
2	1.54E+08	A	C	base_quali	SNV	27	2	29	0.069	37	11	48	0.229	link	-	Sun5	c.453+143>-	ENSMUST intron_variant
2	1.54E+08	T	G	base_quali	SNV	6	0	6	0	15	10	25	0.4	link	-	Bpifa2	c.121+164>-	ENSMUST intron_variant
2	1.54E+08	T	A	PASS	SNV	39	0	39	0	61	11	72	0.153	link	-	Bpifa9b	c.266-1111/-	ENSMUST intron_variant
2	1.54E+08	A	C	base_quali	SNV	21	4	25	0.16	37	17	54	0.315	link	-	Cdk5rap1	c.1389+11>-	ENSMUST intron_variant
2	1.55E+08	T	G	base_quali	SNV	9	0	9	0	36	6	42	0.143	link	-	1700003F1c	-3431T>-	ENSMUST upstream_gene_variant
2	1.55E+08	T	G	base_quali	SNV	9	0	9	0	36	6	42	0.143	link	-	Necab3	c.942-165/-	ENSMUST intron_variant
2	1.56E+08	A	C	base_quali	SNV	19	2	21	0.095	59	13	72	0.181	link	-	Edem2	c.1114+97>-	ENSMUST intron_variant
2	1.56E+08	T	G	base_quali	SNV	101	2	103	0.019	170	9	179	0.05	link	-	Fer1f4	c.325-80A>-	ENSMUST intron_variant
2	1.56E+08	T	C	base_quali	SNV	13	0	13	0	24	12	36	0.333	link	-	Phf20	c.340+178>-	ENSMUST intron_variant
2	1.57E+08	G	T	base_quali	SNV	237	12	249	0.048	260	20	280	0.071	link	-	Dlgap4	c.2011-42/-	ENSMUST intron_variant
2	1.57E+08	T	G	base_quali	SNV	26	1	27	0.037	44	12	56	0.214	link	-	Mroh8	c.1360-10/-	ENSMUST intron_variant
2	1.59E+08	T	G	base_quali	SNV	5	0	5	0	26	9	35	0.257	link	-	Dhx35	c.1347+18>-	ENSMUST intron_variant
2	1.63E+08	G	C	too_few	_sSNV	8	0	8	0	20	2	22	0.091	link	-	Tox2	c.1087-20/-	ENSMUST intron_variant
2	1.64E+08	A	C	base_quali	SNV	22	4	26	0.154	48	11	59	0.186	link	-	Hnf4a	c.386-142/-	ENSMUST intron_variant
2	1.64E+08	C	A	base_quali	SNV	85	5	90	0.056	98	15	113	0.133	link	-	Wisp2	c.277+76C>-	ENSMUST intron_variant
2	1.64E+08	T	G	base_quali	SNV	77	7	84	0.083	96	13	109	0.119	link	-	Wisp2	c.277+81T>-	ENSMUST intron_variant
2	1.67E+08	A	G	base_quali	SNV	29	5	34	0.147	48	10	58	0.172	link	-	Cse1l	c.675+119>-	ENSMUST intron_variant
2	1.68E+08	T	G	base_quali	SNV	35	5	40	0.125	32	17	49	0.347	link	-	Mocs3	c.*105T>G>-	ENSMUST 3_prime_UTR_variant
2	1.68E+08	T	G	base_quali	SNV	35	5	40	0.125	32	17	49	0.347	link	-	Dpm1	c.-1769A>-	ENSMUST upstream_gene_variant
2	1.68E+08	T	G	base_quali	SNV	35	5	40	0.125	32	17	49	0.347	link	-	Gm20716	c.-1769A>-	ENSMUST upstream_gene_variant
2	1.73E+08	A	C	base_quali	SNV	214	5	219	0.023	196	20	216	0.093	link	-	Spo11	c.335-16A>-	ENSMUST intron_variant
2	1.8E+08	T	G	base_quali	SNV	85	2	87	0.023	120	4	124	0.032	link	-	Cdh4	c.2535+50>-	ENSMUST intron_variant
2	1.81E+08	A	G	base_quali	SNV	239	3	242	0.012	324	4	328	0.012	link	-	Abhd16b	c.*2651A>-	ENSMUST downstream_gene_variant
2	1.81E+08	A	G	base_quali	SNV	239	3	242	0.012	324	4	328	0.012	link	-	Tpds212	c.19+50A>-	ENSMUST intron_variant
2	1.82E+08	C	T	weak_evid	SNV	177	0	177	0	215	4	219	0.018	link	-	Gm25184	n.-874C>T>-	ENSMUST upstream_gene_variant
2	1.82E+08	C	T	weak_evid	SNV	177	0	177	0	215	4	219	0.018	link	-	Tpds212	c.545+61C>-	ENSMUST intron_variant
3	10321940	T	G	too_few	_sSNV	4	0	4	0	19	2	21	0.095	link	-	Impa1	c.458-220/-	ENSMUST intron_variant
3	10321940	T	G	too_few	_sSNV	4	0	4	0	19	2	21	0.095	link	-	Gm38303	c.*142-220>-	ENSMUST intron_variant
3	10328222	A	C	base_quali	SNV	31	4	35	0.114	46	9	55	0.164	link	-	Slc10a5	c.*6072T>-	ENSMUST downstream_gene_variant
3	10328222	A	C	base_quali	SNV	31	4	35	0.114	46	9	55	0.164	link	-	Impa1	c.197+123>-	ENSMUST intron_variant
3	10328222	A	C	base_quali	SNV	31	4	35	0.114	46	9	55	0.164	link	-	Gm38303	c.211-203/-	ENSMUST intron_variant
3	14602765	T	G	base_quali	SNV	137	3	140	0.021	133	8	141	0.057	link	-	1810022K1c	*3581A>-	ENSMUST downstream_gene_variant
3	14602765	T	G	base_quali	SNV	137	3	140	0.021	133	8	141	0.057	link	-	E2f5	c.588+53T>-	ENSMUST intron_variant
3	15410981 rs1078982	G	A	weak_evid	SNV	9	0	9	0	21	12	33	0.364	link	-	Sirpb1a	c.748+208>-	ENSMUST intron_variant
3	15848604	A	T	non_homr	SNV	24	5	29	0.172	42	26	68	0.382	link	-	Sirpb1c	c.-191T>A>-	ENSMUST upstream_gene_variant
3	15848604	A	T	non_homr	SNV	24	5	29	0.172	42	26	68	0.382	link	-	-	n.1584860/-	- intergenic_region
3	15848633	A	C	mapping_cSNV		11	2	13	0.154	36	13	49	0.265	link	-	Sirpb1c	c.-220T>G>-	ENSMUST upstream_gene_variant
3	15848633	A	C	mapping_cSNV		11	2	13	0.154	36	13	49	0.265	link	-	-	n.1584863/-	- intergenic_region
3	15848643	A	G	mapping_cSNV		10	2	12	0.167	30	8	38	0.211	link	-	Sirpb1c	c.-230T>C>-	ENSMUST upstream_gene_variant
3	15848643	A	G	mapping_cSNV		10	2	12	0.167	30	8	38	0.211	link	-	-	n.1584864/-	- intergenic_region
3	327																	

3	1.19E+08.	A	C	base_quali_SNV	55	7	62	0.113	97	28	125	0.224	link	-	Dpyd	c.-147A>C-	ENSMUST5_prime_UTR_variant
3	1.23E+08.	T	G	base_quali_SNV	43	2	45	0.044	42	10	52	0.192	link	-	Synpo2	c.106-107/-	ENSMUSTintron_variant
3	1.3E+08.	C	T	base_quali_SNV	31	3	34	0.088	33	7	40	0.175	link	-	Egl	c.1743-11/-	ENSMUSTintron_variant
3	1.3E+08.	T	G	base_quali_SNV	90	2	92	0.022	110	7	117	0.06	link	-	Egl	c.1208-73/-	ENSMUSTintron_variant
3	1.35E+08.	G	A	base_quali_SNV	35	2	37	0.054	55	15	70	0.214	link	-	4930539J0	n.-2190C>-	ENSMUSTupstream_gene_variant
3	1.35E+08.	G	A	base_quali_SNV	35	2	37	0.054	55	15	70	0.214	link	-	Gm43379	n.-4061C>-	ENSMUSTupstream_gene_variant
3	1.35E+08.	G	A	base_quali_SNV	35	2	37	0.054	55	15	70	0.214	link	-	Ube2d3	c.24+151G-	ENSMUSTintron_variant
3	1.38E+08.	G	C	base_quali_SNV	11	0	11	0	19	7	26	0.269	link	-	Dnajb14	c.-2054G>-	ENSMUSTupstream_gene_variant
3	1.38E+08.	G	C	base_quali_SNV	11	0	11	0	19	7	26	0.269	link	-	Gm43403	n.-1496C>-	ENSMUSTupstream_gene_variant
3	1.38E+08.	G	C	base_quali_SNV	11	0	11	0	19	7	26	0.269	link	-	H2afz	c.196-141(-	ENSMUSTintron_variant
3	1.38E+08 rs5805839G	A	A	base_quali_SNV	8	1	9	0.111	14	6	20	0.3	link	-	Gm16559	n.-1804C>-	ENSMUSTdownstream_gene_variant
3	1.38E+08 rs5805839G	A	A	base_quali_SNV	8	1	9	0.111	14	6	20	0.3	link	-	Adh1	c.19-127G/-	ENSMUSTintron_variant
3	1.39E+08.	C	T	too_few_s_SNV	9	0	9	0	27	2	29	0.069	link	-	Mir1956	n.-191C>T-	ENSMUSTdownstream_gene_variant
3	1.39E+08.	C	T	too_few_s_SNV	9	0	9	0	27	2	29	0.069	link	-	Eif4e	c.-30+382(-	ENSMUSTintron_variant
3	1.42E+08.	T	G	base_quali_SNV	82	0	82	0	109	8	117	0.068	link	-	Unc5c	c.1790+70-	ENSMUSTintron_variant
3	1.45E+08.	G	A	too_few_s_SNV	11	0	11	0	21	2	23	0.087	link	-	C1ca3a2	c.2126-204-	ENSMUSTintron_variant
3	1.45E+08.	A	C	base_quali_SNV	197	7	204	0.034	188	22	210	0.105	link	-	Odft2l	c.502-15A>-	ENSMUSTintron_variant
3	1.45E+08.	T	G	base_quali_SNV	69	4	73	0.055	74	11	85	0.129	link	-	Odft2l	c.914+85T-	ENSMUSTintron_variant
3	1.46E+08.	T	C	base_quali_SNV	28	3	31	0.097	35	7	42	0.167	link	-	Mcoln3	c.-131T>C-	ENSMUSTupstream_gene_variant
3	1.46E+08.	T	C	base_quali_SNV	28	3	31	0.097	35	7	42	0.167	link	-	Mcoln3	n.1461216(-	- intragenic_variant
3	1.47E+08.	A	C	base_quali_SNV	56	4	60	0.067	53	13	66	0.197	link	-	Ttll7	c.2619-35/-	ENSMUSTintron_variant
3	1.52E+08.	A	C	base_quali_SNV	60	9	69	0.13	71	13	84	0.155	link	-	Usp33	c.639-140/-	ENSMUSTintron_variant
3	1.52E+08.	A	C	base_quali_SNV	90	4	94	0.043	92	13	105	0.124	link	-	Usp33	c.639-113/-	ENSMUSTintron_variant
3	1.55E+08.	A	C	base_quali_SNV	27	2	29	0.069	36	11	47	0.234	link	-	Cryz	c.-10593A>-	ENSMUSTupstream_gene_variant
3	1.55E+08.	A	C	base_quali_SNV	27	2	29	0.069	36	11	47	0.234	link	-	Tyw3	c.255+142-	ENSMUSTintron_variant
3	1.55E+08.	A	C	base_quali_SNV	18	3	21	0.143	21	7	28	0.25	link	-	Tnni3k	c.333+174-	ENSMUSTintron_variant
4	3184052 rs1131832C	A	A	mapping_c_SNV	35	0	35	0	66	27	93	0.29	link	-	Vmn1r3	c.*333G>T-	ENSMUSTdownstream_gene_variant
4	3184052 rs1131832C	A	A	mapping_c_SNV	35	0	35	0	66	27	93	0.29	link	-	-	n.3184052(-	- intergenic_region
4	3241768 rs5825756A	G	G	mapping_c_SNV	6	0	6	0	31	7	38	0.184	link	-	Ai838599	n.-4237A>-	ENSMUSTupstream_gene_variant
4	3241768 rs5825756A	G	G	mapping_c_SNV	6	0	6	0	31	7	38	0.184	link	-	-	n.3241768(-	- intergenic_region
4	25280804.	A	G	base_quali_SNV	97	9	106	0.085	93	16	109	0.147	link	-	Uf1l	c.78-36T>-	ENSMUSTintron_variant
4	25280805.	T	G	base_quali_SNV	92	7	99	0.071	86	22	108	0.204	link	-	Uf1l	c.78-37A>-	ENSMUSTintron_variant
4	32771772.	T	A	non_homcr_SNV	147	3	150	0.02	139	8	147	0.054	link	-	Mdn1	c.16375-6/-	ENSMUSTintron_variant
4	33045300.	T	G	base_quali_SNV	32	3	35	0.086	37	12	49	0.245	link	-	Ube2j1	c.678+101-	ENSMUSTintron_variant
4	33208960.	G	A	base_quali_SNV	31	3	34	0.088	29	9	38	0.237	link	-	Srsf12	c.-122G>A-	ENSMUSTupstream_gene_variant
4	33208960.	G	A	base_quali_SNV	31	3	34	0.088	29	9	38	0.237	link	-	-	n.3320896(-	- intergenic_region
4	34571627.	A	C	base_quali_SNV	39	1	40	0.025	53	10	63	0.159	link	-	Akirin2	c.*5402A>-	ENSMUSTdownstream_gene_variant
4	34571627.	A	C	base_quali_SNV	39	1	40	0.025	53	10	63	0.159	link	-	Orc3	c.2042+10-	ENSMUSTintron_variant
4	34674942.	C	A	alt_allele_i_SNV	20	6	26	0.231	32	10	42	0.238	link	-	Slc35a1	c.507+88G-	ENSMUSTintron_variant
4	43656314.	G	A	base_quali_SNV	96	7	103	0.068	190	19	209	0.091	link	-	Spag8	c.-2773C>-	ENSMUSTupstream_gene_variant
4	43656314.	G	A	base_quali_SNV	96	7	103	0.068	190	19	209	0.091	link	-	Fam221b	c.*3341C>-	ENSMUSTdownstream_gene_variant
4	43656314.	G	A	base_quali_SNV	96	7	103	0.068	190	19	209	0.091	link	-	Hint2	c.81+45C>-	ENSMUSTintron_variant
4	46502301.	A	C	alt_allele_i_SNV	14	1	15	0.067	10	23	33	0.697	link	-	Trim14	c.*4591T>-	ENSMUSTdownstream_gene_variant
4	46502301.	A	C	alt_allele_i_SNV	14	1	15	0.067	10	23	33	0.697	link	-	Nans	c.871-134/-	ENSMUSTintron_variant
4	46502301.	A	C	alt_allele_i_SNV	14	1	15	0.067	10	23	33	0.697	link	-	Trim14	n.4650230(-	- intragenic_variant
4	48048882.	A	C	alt_allele_i_SNV	7	2	9	0.222	23	8	31	0.258	link	-	Nr4a3	c.-234A>C-	ENSMUSTupstream_gene_variant
4	48048882.	A	C	alt_allele_i_SNV	7	2	9	0.222	23	8	31	0.258	link	-	Nr4a3	n.4804888(-	- intragenic_variant
4	49448940.	G	T	base_quali_SNV	8	1	9	0.111	19	4	23	0.174	link	-	Acnat1	c.669+156-	ENSMUSTintron_variant
4	52440111.	A	C	base_quali_SNV	5	0	5	0	7	6	13	0.462	link	-	Smc2os	n.-1146T>-	ENSMUSTupstream_gene_variant
4	52440111.	A	C	base_quali_SNV	5	0	5	0	7	6	13	0.462	link	-	Tmc4-ps	n.*3804T>-	ENSMUSTdownstream_gene_variant
4	52440111.	A	C	base_quali_SNV	5	0	5	0	7	6	13	0.462	link	-	Smc2	c.-55-90A>-	ENSMUSTintron_variant
4	56925423.	C	T	too_few_s_SNV	5	0	5	0	16	2	18	0.111	link	-	Tmem245	c.905-208(-	ENSMUSTintron_variant
4	58805810.	T	G	base_quali_SNV	18	1	19	0.053	20	5	25	0.2	link	-	Ai314180	c.5117-164-	ENSMUSTintron_variant
4	58836399.	T	G	base_quali_SNV	15	1	16	0.062	20	9	29	0.31	link	-	Ai314180	c.2083-14/-	ENSMUSTupstream_gene_variant
4	62054177.	G	T	alt_allele_i_SNV	3	0	3	0	6	10	16	0.625	link	-	Mup20	c.-128C>A-	ENSMUSTupstream_gene_variant
4	62054177.	G	T	alt_allele_i_SNV	3	0	3	0	6	10	16	0.625	link	-	-	n.6205417(-	- intergenic_region
4	62423166.	A	C	base_quali_SNV	86	0	86	0	112	10	122	0.082	link	-	Rnf183	c.*4821T>-	ENSMUSTdownstream_gene_variant
4	62423166.	A	C	base_quali_SNV	86	0	86	0	112	10	122	0.082	link	-	Prpf4	c.1373-52/-	ENSMUSTintron_variant
4	82966572 rs5807120G	A	A	too_few_s_SNV	4	0	4	0	4	2	6	0.333	link	-	Frem1	c.3547-40/-	ENSMUSTintron_variant
4	89179245.	A	C	base_quali_SNV	7	0	7	0	12	4	16	0.25	link	-	Gm26490	n.*3736T>-	ENSMUSTdownstream_gene_variant
4	89179245.	A	C	base_quali_SNV	7	0	7	0	12	4	16	0.25	link	-	Mtap	c.814-223/-	ENSMUSTintron_variant
4	94919905.	G	A	base_quali_SNV	135	3	138	0.022	91	11	102	0.108	link	-	Egtn	c.641+18C-	ENSMUSTintron_variant
4	1E+08.	A	G	base_quali_SNV	13	0	13	0	32	8	40	0.2	link	-	Ror1	c.611-135/-	ENSMUSTintron_variant
4	1.03E+08.	A	C	base_quali_SNV	50	3	53	0.057	28	4	32	0.125	link	-	Sgfp1	c.484-145/-	ENSMUSTintron_variant
4	1.07E+08.	T	G	base_quali_SNV	173	1	174	0.006	228	9	237	0.038	link	-	Mroh7	c.2830-31/-	ENSMUSTintron_variant
4	1.08E+08.	C	A	base_quali_SNV	34	0	34	0	69	9	78	0.115	link	-	Slc1a7	c.825-108(-	ENSMUSTintron_variant
4	1.09E+08.	A	C	base_quali_SNV	79	4	83	0.048	111	7	118	0.059	link	-	Prpf38a	c.722+757-	ENSMUSTintron_variant
4	1.1E+08.	T	G	base_quali_SNV	165	2	167	0.012	116	8	124	0.065	link	-	Elavf4	c.266-43A>-	ENSMUSTintron_variant
4	1.13E+08.	A	C	base_quali_SNV	31	0	31	0	43	12	55	0.218	link	-	Skinf6	c.1963+11-	ENSMUSTintron_variant
4	1.13E+08.	T	G	base_quali_SNV	100	6	106	0.057	102	7	109	0.064	link	-	Skinf5	c.4391-62/-	ENSMUSTintron_variant
4	1.13E+08.	T	G	base_quali_SNV	95	4	99	0.04	89	9	98	0.092	link	-	Skinf5	c.4391-68/-	ENSMUSTintron_variant
4	1.15E+08.	A	C	base_quali_SNV	46	2	48	0.042	58	12	70	0.171	link	-	Stil	c.753-125/-	ENSMUSTintron_variant
4	1.16E+08.	A	C	base_quali_SNV	20	2	22	0.091	32	6	38	0.158	link	-	Faah	c.309+119-	ENSMUSTintron_variant
4	1.19E+08.	A	C	base_quali_SNV	196	4	200	0.02	202	9	211	0.043	link	-	Zmynd12	c.595-13A>-	ENSMUSTintron_variant
4	1.19E+08.	T	G	alt_allele_i_SNV	9	3	12	0.25	29	7	36	0.194	link	-	Zmynd12	c.829+175-	ENSMUSTintron_variant
4	1.21E+08.	T	G	base_quali_SNV	61	3	64	0.047	49	9	58	0.155	link	-	Gm8439	c.171+98T-	ENSMUSTintron_variant
4	1.23E+08.	A	C	base_quali_SNV	53	6	59	0.102	62	18	80	0.225	link	-	Ppt1	c.-102A>C-	ENSMUSTupstream_gene_variant
4	1.23E+08.	A	C	base_quali_SNV	53	6	59	0.102	62	18	80	0.225	link	-	-	n.1228361(-	- intergenic_region
4	1.23E+08.	C	T	too_few_s_SNV	5	0	5	0	16	2	18	0.111	link	-	Ppt1	c.536+136-	ENSMUSTintron_variant
4	1.25E+08.	T	G	base_quali_SNV	213	5	218	0.023	201	12	213	0.056	link	-	Mir697	n.-3232T>-	ENSMUSTupstream_gene_variant
4	1.25E+08.	T	G	base_quali_SNV	213	5	218	0.023	201	12	213	0.056	link	-	Sf3a3	c.1261+33-	ENSMUSTintron_variant
4	1.26E+08.	G	A	too_few_s_SNV	4	0	4	0	20	2	22	0.091	link	-	Oscp1	c.435+196-	ENSMUSTintron_variant
4	1.26E+08.	C	T	too_few_s_SNV	5	0	5	0	18	2	20	0.1	link	-	Ago3	c.1029+20-	ENSMUSTintron_variant
4	1.28E+08.	A	C	base_quali_SNV	12	1	13	0.077	27	11	38	0.289	link	-	CK137956	c.1440+15-	ENSMUSTintron_variant
4	1.29E+08.	T	C	base_quali													

4	1.48E+08	rs1134898	T	C	mapping_cSNV	114	6	120	0.05	155	26	181	0.144	link	-	Gm16211	n.-3283A>-	ENSMUSTupstream_gene_variant
4	1.48E+08		T	C	too_few_sSNV	5	0	5	0	20	2	22	0.091	link	-	Gm13156	n.*4837T>-	ENSMUSTdownstream_gene_variant
4	1.48E+08		T	C	too_few_sSNV	5	0	5	0	20	2	22	0.091	link	-	Mfn2	c.-4-188A>-	ENSMUSTintron_variant
4	1.5E+08		A	G	base_qualiSNV	23	3	26	0.115	33	11	44	0.25	link	-	Pik3cd	c.*6361T>-	ENSMUSTdownstream_gene_variant
4	1.5E+08		A	G	base_qualiSNV	23	3	26	0.115	33	11	44	0.25	link	-	Ctln1	c.2110+81-	ENSMUSTintron_variant
4	1.5E+08		C	T	base_qualiSNV	206	14	220	0.064	226	18	244	0.074	link	-	Rere	c.396+20C-	ENSMUSTintron_variant
4	1.51E+08		A	C	base_qualiSNV	64	4	68	0.059	60	13	73	0.178	link	-	Camta1	c.4188+67-	ENSMUSTintron_variant
4	1.52E+08		T	G	base_qualiSNV	65	4	69	0.058	73	14	87	0.161	link	-	Nol9	c.2010+77-	ENSMUSTintron_variant
4	1.55E+08		A	G	base_qualiSNV	62	1	63	0.016	88	9	97	0.093	link	-	Pdpm16	c.38-45T>-	ENSMUSTintron_variant
4	1.55E+08		T	G	base_qualiSNV	44	0	44	0	57	14	71	0.197	link	-	Pdpm16	c.38-61A>-	ENSMUSTintron_variant
5	4893876		A	C	base_qualiSNV	5	0	5	0	15	5	20	0.25	link	-	Cdk14	c.1294+15-	ENSMUSTintron_variant
5	5451919		A	C	base_qualiSNV	115	5	120	0.042	116	18	134	0.134	link	-	1700015F1	c.442+90T-	ENSMUSTintron_variant
5	5683092		T	G	base_qualiSNV	44	1	45	0.022	52	13	65	0.2	link	-	Steap2	c.-33-37A>-	ENSMUSTintron_variant
5	8947518		A	G	base_qualiSNV	59	7	66	0.106	41	23	64	0.359	link	-	Abcb4	c.2915+81-	ENSMUSTintron_variant
5	13580944		A	C	base_qualiSNV	99	8	107	0.075	93	6	99	0.061	link	-	Sema3a	c.1495-48A-	ENSMUSTintron_variant
5	14230098		A	C	base_qualiSNV	131	3	134	0.022	107	8	115	0.07	link	-	Sema3e	c.999-9A>-	ENSMUSTintron_variant
5	14978327	rs1133473	A	C	mapping_cSNV	37	2	39	0.051	50	9	59	0.153	link	-	Gm10354	c.139+410-	ENSMUSTintron_variant
5	15528304		T	A	weak_evid_SNV	110	1	111	0.009	154	7	161	0.043	link	-	Gm21847	n.222+237-	ENSMUSTintron_variant
5	15528304		T	A	weak_evid_SNV	110	1	111	0.009	154	7	161	0.043	link	-	Gm21190	c.140-238A-	ENSMUSTintron_variant
5	15528381		G	A	non_homrSNV	105	3	108	0.028	121	8	129	0.062	link	-	Gm21847	n.222+244-	ENSMUSTintron_variant
5	15528381		G	A	non_homrSNV	105	3	108	0.028	121	8	129	0.062	link	-	Gm21190	c.140-315C-	ENSMUSTintron_variant
5	15529309		C	G	mapping_cSNV	700	25	725	0.034	1217	52	1269	0.041	link	-	Gm21190	c.-91G>C-	ENSMUSTupstream_gene_variant
5	15529309		C	G	mapping_cSNV	700	25	725	0.034	1217	52	1269	0.041	link	-	Gm21847	n.222+337-	ENSMUSTintron_variant
5	16296726		C	A	base_qualiSNV	10	0	10	0	16	4	20	0.2	link	-	Cacna2d1	c.880-320C-	ENSMUSTintron_variant
5	16613634		A	C	base_qualiSNV	40	3	43	0.07	35	8	43	0.186	link	-	Hgf	c.1545-12C-	ENSMUSTintron_variant
5	17377043		C	T	PASS_SNV	14	1	15	0.067	19	5	24	0.208	link	-	Gm21999	n.-3530C>-	ENSMUSTupstream_gene_variant
5	17377043		C	T	PASS_SNV	14	1	15	0.067	19	5	24	0.208	link	-	Speer4f2	c.607-34A(-	ENSMUSTintron_variant
5	17377045		C	T	PASS_SNV	14	1	15	0.067	19	5	24	0.208	link	-	Gm21999	n.-3528C>-	ENSMUSTupstream_gene_variant
5	17377045		C	T	PASS_SNV	14	1	15	0.067	19	5	24	0.208	link	-	Speer4f2	c.607-342(-	ENSMUSTintron_variant
5	17377050		G	C	PASS_SNV	14	0	14	0	21	5	26	0.192	link	-	Gm21999	n.-3523G>-	ENSMUSTupstream_gene_variant
5	17377050		G	C	PASS_SNV	14	0	14	0	21	5	26	0.192	link	-	Speer4f2	c.607-337(-	ENSMUSTintron_variant
5	17377051		C	A	PASS_SNV	14	0	14	0	21	5	26	0.192	link	-	Gm21999	n.-3522C>-	ENSMUSTupstream_gene_variant
5	17377051		C	A	PASS_SNV	14	0	14	0	21	5	26	0.192	link	-	Speer4f2	c.607-336(-	ENSMUSTintron_variant
5	17377054		A	T	PASS_SNV	15	0	15	0	20	5	25	0.2	link	-	Gm21999	n.-3519A>-	ENSMUSTupstream_gene_variant
5	17377054		A	T	PASS_SNV	15	0	15	0	20	5	25	0.2	link	-	Speer4f2	c.607-333A-	ENSMUSTintron_variant
5	23503151		T	G	base_qualiSNV	25	1	26	0.038	27	8	35	0.229	link	-	Kmt2e	c.*104T>G-	ENSMUST3_prime_UTR_variant
5	23503151		T	G	base_qualiSNV	25	1	26	0.038	27	8	35	0.229	link	-	Srpk2	c.*4385A>-	ENSMUSTdownstream_gene_variant
5	25350014		C	A	base_qualiSNV	72	4	76	0.053	67	7	74	0.095	link	-	Kmt2c	c.3695-74C-	ENSMUSTintron_variant
5	25941885		A	T	mapping_cSNV	41	2	43	0.047	67	9	76	0.118	link	-	Gm21663	c.139+283-	ENSMUSTintron_variant
5	26003606		G	A	mapping_cSNV	392	60	452	0.133	400	100	500	0.2	link	-	Gm5067	n.-3421G>-	ENSMUSTupstream_gene_variant
5	26003606		G	A	mapping_cSNV	392	60	452	0.133	400	100	500	0.2	link	-	Gm1979	c.140-100C-	ENSMUSTintron_variant
5	26004022	rs182535A	T		weak_evid_SNV	5	0	5	0	11	7	18	0.389	link	-	Gm5067	n.-3005A>-	ENSMUSTupstream_gene_variant
5	26004022	rs182535A	T		weak_evid_SNV	5	0	5	0	11	7	18	0.389	link	-	Gm1979	c.140-426T-	ENSMUSTintron_variant
5	26021176	rs1134189G	C		weak_evid_SNV	5	0	5	0	2	7	9	0.778	link	-	Gm5862	c.299+428-	ENSMUSTintron_variant
5	26088952	rs1134862T	A		mapping_cSNV	71	4	75	0.053	104	35	139	0.252	link	-	Gm10471	c.94+133A-	ENSMUSTintron_variant
5	27262182		T	C	base_qualiSNV	86	3	89	0.034	95	10	105	0.095	link	-	Dpp6	c.226-120T-	ENSMUSTintron_variant
5	27500935		C	A	mapping_cSNV	31	2	33	0.061	36	6	42	0.143	link	-	Dpp6	c.609+314-	ENSMUSTintron_variant
5	27500935		C	A	mapping_cSNV	31	2	33	0.061	36	6	42	0.143	link	-	Speer4b	c.139+294-	ENSMUSTintron_variant
5	27501580		A	T	mapping_cSNV	71	2	73	0.027	94	8	102	0.078	link	-	Speer4b	c.-213T>A-	ENSMUSTupstream_gene_variant
5	27501580		A	T	mapping_cSNV	71	2	73	0.027	94	8	102	0.078	link	-	Dpp6	c.609+320-	ENSMUSTintron_variant
5	30667481		A	C	base_qualiSNV	50	3	53	0.057	81	18	99	0.182	link	-	Cenpa	c.85+368A-	ENSMUSTintron_variant
5	32341738		G	C	non_homrSNV	20	0	20	0	31	0	31	0	link	-	Gm36840	n.134+130-	ENSMUSTintron_variant
5	32341738		G	C	non_homrSNV	20	0	20	0	31	0	31	0	link	-	Pt1b1	c.3208-164-	ENSMUSTintron_variant
5	34350277		T	C	too_few_sSNV	4	0	4	0	12	2	14	0.143	link	-	Rnf4	c.386+206-	ENSMUSTintron_variant
5	34730128		T	G	base_qualiSNV	94	2	96	0.021	93	12	105	0.114	link	-	Mir467g	n.*2725A>-	ENSMUSTdownstream_gene_variant
5	34730128		T	G	base_qualiSNV	94	2	96	0.021	93	12	105	0.114	link	-	Grk4	c.967+86T-	ENSMUSTintron_variant
5	34866471		G	T	base_qualiSNV	20	4	24	0.167	16	10	26	0.385	link	-	Htt	c.5166-104-	ENSMUSTintron_variant
5	36661739		T	G	base_qualiSNV	161	4	165	0.024	197	19	216	0.088	link	-	Gm24878	n.*4670A>-	ENSMUSTdownstream_gene_variant
5	36661739		T	G	base_qualiSNV	161	4	165	0.024	197	19	216	0.088	link	-	D5Erdt579	c.231+110-	ENSMUSTintron_variant
5	37120757		A	C	base_qualiSNV	7	0	7	0	23	6	29	0.207	link	-	Jakmp1	c.1561-184-	ENSMUSTintron_variant
5	37324001		T	C	too_few_sSNV	7	0	7	0	25	2	27	0.074	link	-	Evc	c.703-204A-	ENSMUSTintron_variant
5	41834008		T	G	base_qualiSNV	7	1	8	0.125	13	3	16	0.188	link	-	Bod1l	c.363-160A-	ENSMUSTintron_variant
5	48380463		A	G	too_few_sSNV	7	0	7	0	16	2	18	0.111	link	-	5730480H	c.609+232-	ENSMUSTintron_variant
5	48889588		G	T	base_qualiSNV	59	0	59	0	67	10	77	0.13	link	-	Kcnip4	c.62-3798T-	ENSMUSTintron_variant
5	53268021		A	C	base_qualiSNV	380	4	384	0.01	356	15	371	0.04	link	-	Smm20	c.115+663-	ENSMUSTintron_variant
5	62643017		T	G	base_qualiSNV	51	2	53	0.038	79	12	91	0.132	link	-	Arap2	c.3741-75A-	ENSMUSTintron_variant
5	69519044	rs2211949	A	C	weak_evid_SNV	9	0	9	0	19	3	22	0.136	link	-	Yipf7	c.602+149-	ENSMUSTintron_variant
5	69562998		A	C	base_qualiSNV	54	3	57	0.053	62	12	74	0.162	link	-	Gul1	c.885-85A>-	ENSMUSTintron_variant
5	69563009		A	C	base_qualiSNV	66	1	67	0.015	78	10	88	0.114	link	-	Gul1	c.885-74A>-	ENSMUSTintron_variant
5	72612311		G	A	base_qualiSNV	335	3	338	0.009	352	10	362	0.028	link	-	Cnga1	c.315-40C>-	ENSMUSTintron_variant
5	76901471		C	T	too_few_sSNV	11	0	11	0	25	2	27	0.074	link	-	Aasdh	c.231-190C-	ENSMUSTintron_variant
5	89443290		A	C	base_qualiSNV	26	3	29	0.103	29	8	37	0.216	link	-	Gc	c.473+115-	ENSMUSTintron_variant
5	92411316		T	G	base_qualiSNV	68	4	72	0.056	61	10	71	0.141	link	-	Nup54	c.*4894A>-	ENSMUSTdownstream_gene_variant
5	92411316		T	G	base_qualiSNV	68	4	72	0.056	61	10	71	0.141	link	-	Art3	c.990+121-	ENSMUSTintron_variant
5	93171205		A	C	base_qualiSNV	64	15	79	0.19	52	24	76	0.316	link	-	Sept11	c.1275-22E-	ENSMUSTintron_variant
5	97965618		A	C	base_qualiSNV	106	4	110	0.036	120	10	130	0.077	link	-	Antxr2	c.945+64T-	ENSMUSTintron_variant
5	98879979		T	G	base_qualiSNV	57	4	61	0.066	61	9	70	0.129	link	-	Bmp3	c.*117T>G-	ENSMUST3_prime_UTR_variant
5	98947693		T	G	base_qualiSNV	18	0	18	0	29	7	36	0.194	link	-	Prkg2	c.1777-15C-	ENSMUSTintron_variant
5	1E+08		T	G	base_qualiSNV	12	0	12	0	12	3	15	0.2	link	-	Sec31a	c.403-205A-	ENSMUSTintron_variant
5	1.01E+08		T	G	base_qualiSNV	133	2	135	0.015	116	11	127	0.087	link	-	Gm15777	n.*2983T>-	ENSMUSTdownstream_gene_variant
5	1.01E+08		T	G	base_qualiSNV	133	2	135	0.015	116	11	127	0.087	link	-	Hpse	c.1449-58A-	ENSMUSTintron_variant
5	1.01E+08		A	G	base_qualiSNV	61	5	66	0.076	62								

5	1.37E+08.	A	G	base_qualiSNV	107	6	113	0.053	160	16	176	0.091	link	-	Fis1	c.361+53A-	ENSMUSTintron_variant
5	1.37E+08.	T	C	base_qualiSNV	13	0	13	0	19	12	31	0.387	link	-	Zan	c.11310+1-	ENSMUSTintron_variant
5	1.37E+08.	A	C	base_qualiSNV	23	3	26	0.115	41	7	48	0.146	link	-	Rpl36-ps9	n.-4723A>-	ENSMUSTupstream_gene_variant
5	1.37E+08.	A	C	base_qualiSNV	23	3	26	0.115	41	7	48	0.146	link	-	Zan	c.7501+11-	ENSMUSTintron_variant
5	1.38E+08.	G	A	weak_evid	174	1	175	0.006	211	4	215	0.019	link	-	Trf2	c.1980+19-	ENSMUSTintron_variant
5	1.4E+08.	T	C	base_qualiSNV	25	2	27	0.074	55	13	68	0.191	link	-	Tmem184	c.72+134A-	ENSMUSTintron_variant
5	1.4E+08.	T	C	base_qualiSNV	25	2	27	0.074	55	13	68	0.191	link	-	Gm26938	c.217-727/-	ENSMUSTintron_variant
5	1.41E+08.	C	T	too_few_s1SNV	4	0	4	0	23	2	25	0.08	link	-	Ttyh3	c.1501-224-	ENSMUSTintron_variant
5	1.41E+08.	A	G	PASS_SNV	162	0	162	0	184	27	211	0.128	link	-	lqce	c.-3705T>-	ENSMUSTupstream_gene_variant
5	1.41E+08.	A	G	PASS_SNV	162	0	162	0	184	27	211	0.128	link	-	Brat1	c.119-31A->	ENSMUSTintron_variant
5	1.45E+08.	A	C	base_qualiSNV	259	4	263	0.015	297	9	306	0.029	link	-	Arpc1b	c.65-24A>-	ENSMUSTintron_variant
5	1.45E+08 rs3346602	A	C	mapping_cSNV	40	1	41	0.024	55	10	65	0.154	link	-	Cyp3a16	c.166-161/-	ENSMUSTintron_variant
5	1.46E+08.	C	A	mapping_cSNV	6	0	6	0	10	4	14	0.286	link	-	Cyp3a41b	c.-253G>T-	ENSMUSTupstream_gene_variant
5	1.46E+08.	C	A	mapping_cSNV	6	0	6	0	10	4	14	0.286	link	-	-	n.1455848/-	intergenic_region
5	1.46E+08.	G	C	mapping_cSNV	15	2	17	0.118	15	17	32	0.531	link	-	Cyp3a41a	c.319-186/-	ENSMUSTintron_variant
5	1.46E+08.	A	C	base_qualiSNV	98	2	100	0.02	122	6	128	0.047	link	-	Cyp3a11	c.1029+60-	ENSMUSTintron_variant
5	1.48E+08.	T	G	too_few_s1SNV	5	0	5	0	23	2	25	0.08	link	-	Pomp	c.*3928T>-	ENSMUSTdownstream_gene_variant
5	1.48E+08.	T	G	too_few_s1SNV	5	0	5	0	23	2	25	0.08	link	-	Slc46a3	c.1301-23-	ENSMUSTintron_variant
5	1.49E+08.	A	G	base_qualiSNV	29	0	29	0	38	9	47	0.191	link	-	Gm15406	n.190-149/-	ENSMUSTintron_variant
5	1.49E+08.	A	G	base_qualiSNV	29	0	29	0	38	9	47	0.191	link	-	Gm42791	c.-15+108/-	ENSMUSTintron_variant
6	755483.	A	C	base_qualiSNV	25	1	26	0.038	39	7	46	0.152	link	-	Tac1	c.9-122A>-	ENSMUSTintron_variant
6	13678036.	T	G	base_qualiSNV	15	2	17	0.118	19	5	24	0.208	link	-	Bmt2	c.-203A>C-	ENSMUSTupstream_gene_variant
6	13678036.	T	G	base_qualiSNV	15	2	17	0.118	19	5	24	0.208	link	-	-	n.1367803/-	intergenic_region
6	17553085.	A	C	base_qualiSNV	20	1	21	0.048	20	7	27	0.259	link	-	Met	c.3023-154-	ENSMUSTintron_variant
6	18429272.	T	G	base_qualiSNV	74	5	79	0.063	63	14	77	0.182	link	-	Gm15594	n.*1387T>-	ENSMUSTdownstream_gene_variant
6	18429272.	T	G	base_qualiSNV	74	5	79	0.063	63	14	77	0.182	link	-	Gm43843	n.*387A>C-	ENSMUSTdownstream_gene_variant
6	18429272.	T	G	base_qualiSNV	74	5	79	0.063	63	14	77	0.182	link	-	Ctnnb2	c.2039-16/-	ENSMUSTintron_variant
6	22059778.	A	C	base_qualiSNV	49	2	51	0.039	50	10	60	0.167	link	-	Cped1	c.541-99A->	ENSMUSTintron_variant
6	22059778.	A	C	base_qualiSNV	49	2	51	0.039	50	10	60	0.167	link	-	Gm26719	n.2075+58-	ENSMUSTintron_variant
6	22339467.	T	G	base_qualiSNV	111	4	115	0.035	115	10	125	0.08	link	-	Fam3c	c.74-90A>-	ENSMUSTintron_variant
6	30381893.	T	G	base_qualiSNV	224	4	228	0.018	210	14	224	0.062	link	-	n-R5s161	n.*2679T>-	ENSMUSTdownstream_gene_variant
6	30381893.	T	G	base_qualiSNV	224	4	228	0.018	210	14	224	0.062	link	-	Zc3hc1	c.410-29A/-	ENSMUSTintron_variant
6	30861611.	T	G	base_qualiSNV	18	1	19	0.053	34	6	40	0.15	link	-	Ccpg2	c.400-151/-	ENSMUSTintron_variant
6	34930262.	A	C	base_qualiSNV	72	2	74	0.027	89	11	100	0.11	link	-	Stra8	c.193-99A->	ENSMUSTintron_variant
6	35307170.	A	C	alt_allele_iSNV	7	3	10	0.3	30	4	34	0.118	link	-	Slc13a4	c.99+188T-	ENSMUSTintron_variant
6	40347345.	A	C	base_qualiSNV	163	12	175	0.069	172	16	188	0.085	link	-	Agk	c.102-67A/-	ENSMUSTintron_variant
6	47667716 rs1081788	A	A	non_homrSNV	12	0	12	0	34	6	40	0.15	link	-	-	n.4766771/-	intergenic_region
6	48450236.	C	T	base_qualiSNV	112	4	116	0.034	141	10	151	0.066	link	-	Sspo	c.841+66C->	ENSMUSTintron_variant
6	48571637.	A	C	base_qualiSNV	26	0	26	0	62	6	68	0.088	link	-	Lrrc61	c.*2613A>-	ENSMUSTdownstream_gene_variant
6	48571637.	A	C	base_qualiSNV	26	0	26	0	62	6	68	0.088	link	-	Rarres2	c.285+146-	ENSMUSTintron_variant
6	48989075.	T	G	base_qualiSNV	16	4	20	0.2	29	13	42	0.31	link	-	4930563H	n.416-224/-	ENSMUSTintron_variant
6	48989075.	T	G	base_qualiSNV	16	4	20	0.2	29	13	42	0.31	link	-	Svs1	c.1882+13-	ENSMUSTintron_variant
6	55381485.	A	C	too_few_s1SNV	5	0	5	0	22	2	24	0.083	link	-	Ghrhr	c.465-219/-	ENSMUSTintron_variant
6	57209805.	A	C	base_qualiSNV	39	3	42	0.071	58	6	64	0.094	link	-	Vmn1r13	c.-53A>C-	ENSMUSTupstream_gene_variant
6	57209805.	A	C	base_qualiSNV	39	3	42	0.071	58	6	64	0.094	link	-	-	n.5720980/-	intergenic_region
6	68736941.	G	T	PASS_SNV	18	0	18	0	41	7	48	0.146	link	-	Gm40414	n.-2280C>-	ENSMUSTupstream_gene_variant
6	68736941.	G	T	PASS_SNV	18	0	18	0	41	7	48	0.146	link	-	Igkv19-93	c.-177C>A-	ENSMUSTupstream_gene_variant
6	68736941.	G	T	PASS_SNV	18	0	18	0	41	7	48	0.146	link	-	-	n.6873694/-	intergenic_region
6	71216026.	C	T	base_qualiSNV	29	2	31	0.065	42	15	57	0.263	link	-	Smyd1	c.1315-117/-	ENSMUSTintron_variant
6	71322232.	C	T	base_qualiSNV	8	0	8	0	8	3	11	0.273	link	-	Cd8b1	c.-625C>T-	ENSMUSTdownstream_gene_variant
6	71322232.	C	T	base_qualiSNV	8	0	8	0	8	3	11	0.273	link	-	Smyd1	n.7132223/-	intragenic_variant
6	71892547.	G	A	PASS_SNV	277	0	277	0	297	5	302	0.077	link	-	Ptcd3	c.1094-28C-	ENSMUSTintron_variant
6	72630147.	T	G	base_qualiSNV	89	9	98	0.092	84	16	100	0.16	link	-	Gm37969	n.*5000A>-	ENSMUSTdownstream_gene_variant
6	72630147.	T	G	base_qualiSNV	89	9	98	0.092	84	16	100	0.16	link	-	Tc7f11	c.1291-11/-	ENSMUSTintron_variant
6	83506250 rs5875000	G	T	base_qualiSNV	18	0	18	0	17	4	21	0.19	link	-	Dguok	c.142+498-	ENSMUSTintron_variant
6	83814710.	A	C	base_qualiSNV	197	4	201	0.02	199	16	215	0.074	link	-	Paip2b	c.177+127-	ENSMUSTintron_variant
6	84574128.	G	T	base_qualiSNV	11	2	13	0.154	9	9	18	0.5	link	-	Cyp26b1	c.*139C>A-	ENSMUST3_prime_UTR_variant
6	85448322.	A	C	base_qualiSNV	11	1	12	0.083	44	9	53	0.17	link	-	Cct7	c.-3800A>-	ENSMUSTupstream_gene_variant
6	85448322.	A	C	base_qualiSNV	11	1	12	0.083	44	9	53	0.17	link	-	Smyd5	c.*3106A>-	ENSMUSTdownstream_gene_variant
6	85448322.	A	C	base_qualiSNV	11	1	12	0.083	44	9	53	0.17	link	-	Pradcl	c.168+169-	ENSMUSTintron_variant
6	92063002.	T	G	base_qualiSNV	108	3	111	0.027	145	15	160	0.094	link	-	Fgd5	c.3558+98-	ENSMUSTintron_variant
6	97288595.	T	G	base_qualiSNV	32	5	37	0.135	33	13	46	0.283	link	-	Frmdd4b	c.2988-11/-	ENSMUSTintron_variant
6	1.01E+08.	T	G	base_qualiSNV	37	2	39	0.051	41	10	51	0.196	link	-	Shq1	c.144-143/-	ENSMUSTintron_variant
6	1.15E+08.	G	A	too_few_s1SNV	17	1	18	0.056	34	2	36	0.056	link	-	Atg7	c.*5710G>-	ENSMUSTdownstream_gene_variant
6	1.15E+08.	G	A	too_few_s1SNV	17	1	18	0.056	34	2	36	0.056	link	-	Vgll4	c.273-854/-	ENSMUSTintron_variant
6	1.16E+08.	A	C	base_qualiSNV	42	1	43	0.023	43	7	50	0.14	link	-	Cand2	c.*1542A>-	ENSMUST3_prime_UTR_variant
6	1.16E+08.	A	C	base_qualiSNV	42	1	43	0.023	43	7	50	0.14	link	-	Rpl32	c.*153T>G-	ENSMUSTdownstream_gene_variant
6	1.16E+08.	A	C	base_qualiSNV	42	1	43	0.023	43	7	50	0.14	link	-	Snora7a	n.*2569T>-	ENSMUSTdownstream_gene_variant
6	1.16E+08.	A	C	base_qualiSNV	13	1	14	0.071	7	9	16	0.562	link	-	Itf122	c.1489-14/-	ENSMUSTintron_variant
6	1.18E+08.	T	G	base_qualiSNV	71	2	73	0.027	78	14	92	0.152	link	-	Bms1	c.3469-44/-	ENSMUSTintron_variant
6	1.2E+08.	A	C	base_qualiSNV	51	6	57	0.105	61	12	73	0.164	link	-	Kdm5a	c.4075-77/-	ENSMUSTintron_variant
6	1.23E+08.	A	C	base_qualiSNV	72	8	80	0.1	59	9	68	0.132	link	-	Dppa3	c.-99A>C-	ENSMUST5_prime_UTR_variant
6	1.23E+08.	A	C	base_qualiSNV	72	8	80	0.1	59	9	68	0.132	link	-	Gm26168	n.*2766A>-	ENSMUSTdownstream_gene_variant
6	1.25E+08.	T	G	base_qualiSNV	37	0	37	0	74	5	79	0.063	link	-	Lrrc23	c.*3366A>-	ENSMUSTdownstream_gene_variant
6	1.25E+08.	T	G	base_qualiSNV	37	0	37	0	74	5	79	0.063	link	-	Eno2	c.241-134/-	ENSMUSTintron_variant
6	1.25E+08.	A	G	base_qualiSNV	47	3	50	0.06	48	17	65	0.262	link	-	Gpr162	c.*2476T>-	ENSMUSTdownstream_gene_variant
6	1.25E+08.	A	G	base_qualiSNV	47	3	50	0.06	48	17	65	0.262	link	-	P3h3	c.493-97T->	ENSMUSTintron_variant
6	1.25E+08.	A	G	base_qualiSNV	8	0	8	0	10	11	21	0.524	link	-	Scn1a	c.-873A>G-	ENSMUSTupstream_gene_variant
6	1.25E+08.	A	G	base_qualiSNV	8	0	8	0	10	11	21	0.524	link	-	Scn1a	n.1253210/-	intragenic_variant
6	1.26E+08.	T	G	base_qualiSNV	111	4	115	0.035	136	12	148	0.081	link	-	Vwf	c.6901+72-	ENSMUSTintron_variant
6	1.26E+08.	G	T	base_qualiSNV	22	3	25	0.12	45	4	49	0.082	link	-	Ano2	c.208-337/-	ENSMUSTintron_variant
6	1.29E+08.	G	A	low_normaSNV	2	0	2	0	20	2	22	0.091	link	-	Cd69	c.-229C>T-	ENSMUSTupstream_gene_variant
6	1.29E+08.	G	A	low_normaSNV	2	0	2	0	20	2	22	0.091	link	-	-	n.1292755/-	intergenic_region
6	1.29E+08.	T	G	base_qualiSNV	100	4	104	0.038	121	11	132	0.083	link	-	Clec1b	c.545	

7	27532192	G	A	base_qualiSNV	23	4	27	0.148	40	12	52	0.231	link	-	Hipk4	c.*1325G>-	ENSMUST downstream_gene_variant
7	28301141	C	A	weak_evid_SNV	15	0	15	0	34	4	38	0.105	link	-	Timm50	c.*4788G>-	ENSMUST downstream_gene_variant
7	28301141	C	A	weak_evid_SNV	15	0	15	0	34	4	38	0.105	link	-	Dil3	c.345+143-	ENSMUST intron_variant
7	28405366	A	C	base_qualiSNV	19	1	20	0.05	44	14	58	0.241	link	-	Samd4b	c.1628+12-	ENSMUST intron_variant
7	28740787	T	G	base_qualiSNV	246	3	249	0.012	293	9	302	0.03	link	-	Sars2	c.-1229T>-	ENSMUST upstream_gene_variant
7	28740787	T	G	base_qualiSNV	246	3	249	0.012	293	9	302	0.03	link	-	Fbxo17	c.*3305T>-	ENSMUST downstream_gene_variant
7	28740787	T	G	base_qualiSNV	246	3	249	0.012	293	9	302	0.03	link	-	Mrops12	c.50-548A>-	ENSMUST intron_variant
7	28797512	T	C	base_qualiSNV	95	2	97	0.021	137	15	152	0.099	link	-	Rin1	c.1484-481-	ENSMUST intron_variant
7	28896441	T	C	too_few_s1SNV	5	0	5	0	22	2	24	0.083	link	-	Capn12	c.*3453T>-	ENSMUST downstream_gene_variant
7	28896441	T	C	too_few_s1SNV	5	0	5	0	22	2	24	0.083	link	-	Actn4	c.2194-206-	ENSMUST intron_variant
7	29000353	T	G	base_qualiSNV	89	10	99	0.101	77	10	87	0.115	link	-	Ryr1	c.*3105A>-	ENSMUST downstream_gene_variant
7	29000353	T	G	base_qualiSNV	89	10	99	0.101	77	10	87	0.115	link	-	Map4k1	c.1959+59-	ENSMUST intron_variant
7	29169501	C	T	PASS_SNV	306	0	306	0	394	8	402	0.02	link	-	Spred3	c.-1532G>-	ENSMUST upstream_gene_variant
7	29169501	C	T	PASS_SNV	306	0	306	0	394	8	402	0.02	link	-	Ggn	c.-1588C>-	ENSMUST upstream_gene_variant
7	29169501	C	T	PASS_SNV	306	0	306	0	394	8	402	0.02	link	-	Psmd8	c.*5109G>-	ENSMUST downstream_gene_variant
7	29169501	C	T	PASS_SNV	306	0	306	0	394	8	402	0.02	link	-	Spred3	n.2916950-	- intragenic_variant
7	29308132	C	T	PASS_SNV	218	1	219	0.005	226	7	233	0.03	link	-	Dplf1	c.33-1279C-	ENSMUST intron_variant
7	30508337	T	C	base_qualiSNV	202	5	207	0.024	204	20	224	0.089	link	-	Prodh2	c.1002-14-	ENSMUST intron_variant
7	30744308	T	G	base_qualiSNV	22	6	28	0.214	24	9	33	0.273	link	-	Gapdhs	c.-654A>C-	ENSMUST upstream_gene_variant
7	30744308	T	G	base_qualiSNV	22	6	28	0.214	24	9	33	0.273	link	-	Tmem147	n.896-124-	ENSMUST intron_variant
7	30744308	T	G	base_qualiSNV	22	6	28	0.214	24	9	33	0.273	link	-	RP24-63G	n.177+834-	ENSMUST intron_variant
7	30744308	T	G	base_qualiSNV	22	6	28	0.214	24	9	33	0.273	link	-	Gm26935	n.131-374-	ENSMUST intron_variant
7	30909417	A	G	base_qualiSNV	15	1	16	0.062	23	3	26	0.115	link	-	Mag	c.416-1451-	ENSMUST intron_variant
7	32335643	T	G	base_qualiSNV	10	0	10	0	18	7	25	0.28	link	-	Scgb1b12	c.*261T>G-	ENSMUST downstream_gene_variant
7	32335643	T	G	base_qualiSNV	10	0	10	0	18	7	25	0.28	link	-	-	n.3233564-	- intergenic_region
7	33737669 rs2380270	A	G	weak_evid_SNV	205	1	206	0.005	198	4	202	0.02	link	-	Scgb2b24	c.244-2271-	ENSMUST intron_variant
7	38522092 rs5803244	A	G	mapping_cSNV	434	65	499	0.13	429	131	560	0.234	link	-	Gm29087	n.290-672C-	ENSMUST intron_variant
7	38866033 rs1134799	T	G	mapping_cSNV	396	5	401	0.012	391	25	416	0.06	link	-	Gm21136	n.776-37A>-	ENSMUST intron_variant
7	44943272	G	A	weak_evid_SNV	143	1	144	0.007	130	3	133	0.023	link	-	Tsk5	c.-12G>A-	ENSMUST 5_prime_UTR_variant
7	45549897	T	C	PASS_SNV	289	0	289	0	265	5	270	0.019	link	-	Hsd17b14	c.-5082T>-	ENSMUST upstream_gene_variant
7	45549897	T	C	PASS_SNV	289	0	289	0	265	5	270	0.019	link	-	AC151602	n.*637A>G-	ENSMUST downstream_gene_variant
7	50176346	T	G	base_qualiSNV	167	2	169	0.012	144	15	159	0.094	link	-	Nell1	c.603+25T-	ENSMUST intron_variant
7	51554132	G	A	too_few_s1SNV	8	0	8	0	23	2	25	0.08	link	-	Ano5	c.738+189-	ENSMUST intron_variant
7	51658912	T	G	base_qualiSNV	49	1	50	0.02	44	5	49	0.102	link	-	Slc17a6	c.891+92T-	ENSMUST intron_variant
7	55773402	C	T	too_few_s1SNV	9	0	9	0	34	2	36	0.056	link	-	Siglech	c.934+820-	ENSMUST intron_variant
7	59285977	A	C	base_qualiSNV	34	7	41	0.171	42	11	53	0.208	link	-	Gm44560	n.*75T>G-	ENSMUST downstream_gene_variant
7	59285977	A	C	base_qualiSNV	34	7	41	0.171	42	11	53	0.208	link	-	Ube3a	c.1748-77/-	ENSMUST intron_variant
7	70357568	G	A	base_qualiSNV	15	0	15	0	7	2	9	0.222	link	-	Nr2f2	c.970+195-	ENSMUST intron_variant
7	79684469	T	G	base_qualiSNV	5	0	5	0	12	4	16	0.25	link	-	Ticrr	c.2710+20-	ENSMUST intron_variant
7	79931590	A	C	base_qualiSNV	5	0	5	0	17	4	21	0.19	link	-	Arpin	c.168+213-	ENSMUST intron_variant
7	80249939	A	C	base_qualiSNV	24	2	26	0.077	36	5	41	0.122	link	-	Tll13	c.299-181/-	ENSMUST intron_variant
7	80306328	A	C	base_qualiSNV	58	3	61	0.049	73	18	91	0.198	link	-	Prc1	c.823-47A>-	ENSMUST intron_variant
7	80306328	A	C	base_qualiSNV	58	3	61	0.049	73	18	91	0.198	link	-	Rccd1	n.8030632-	- intragenic_variant
7	80947645	T	G	base_qualiSNV	7	1	8	0.125	23	6	29	0.207	link	-	Sec11a	c.-193A>C-	ENSMUST upstream_gene_variant
7	80947645	T	G	base_qualiSNV	7	1	8	0.125	23	6	29	0.207	link	-	Sec11a	n.8094764-	- intragenic_variant
7	89517974	C	T	base_qualiSNV	308	0	308	0	283	16	299	0.054	link	-	Prss23	c.-7115G>-	ENSMUST upstream_gene_variant
7	89517974	C	T	base_qualiSNV	308	0	308	0	283	16	299	0.054	link	-	Prss23	n.8951797-	- intragenic_variant
7	96797400	G	A	weak_evid_SNV	481	0	481	0	514	4	518	0.008	link	-	Gm15413	n.261-160-	ENSMUST intron_variant
7	97400145	A	C	base_qualiSNV	119	2	121	0.017	154	8	162	0.049	link	-	Ndufc2	c.-44A>C-	ENSMUST 5_prime_UTR_variant
7	98703304	G	A	base_qualiSNV	42	7	49	0.143	58	19	77	0.247	link	-	Pkrir1	c.-86G>A-	ENSMUST 5_prime_UTR_variant
7	98703304	G	A	base_qualiSNV	42	7	49	0.143	58	19	77	0.247	link	-	Gm15506	n.-416C>T-	ENSMUST upstream_gene_variant
7	99317670	T	G	base_qualiSNV	265	1	266	0.004	217	8	225	0.036	link	-	RP23-239	n.-3530T>-	ENSMUST upstream_gene_variant
7	1E+08	T	G	too_few_s1SNV	27	1	28	0.036	29	0	29	0	link	-	Ppme1	c.289-155/-	ENSMUST intron_variant
7	1E+08	G	A	PASS_SNV	72	0	72	0	59	3	62	0.048	link	-	C2cd3	c.1179-104-	ENSMUST intron_variant
7	1.01E+08	T	G	base_qualiSNV	56	1	57	0.018	60	8	68	0.118	link	-	Gm20476	n.*346A>C-	ENSMUST downstream_gene_variant
7	1.01E+08	T	G	base_qualiSNV	56	1	57	0.018	60	8	68	0.118	link	-	Stard10	c.3+151T-	ENSMUST intron_variant
7	1.01E+08	G	T	base_qualiSNV	13	2	15	0.133	40	19	59	0.322	link	-	RP24-126	n.*1931C>-	ENSMUST downstream_gene_variant
7	1.01E+08	G	T	base_qualiSNV	13	2	15	0.133	40	19	59	0.322	link	-	Stard10	c.797-157C-	ENSMUST intron_variant
7	1.01E+08	G	A	base_qualiSNV	34	2	36	0.056	41	8	49	0.163	link	-	Pde2a	c.561+80G-	ENSMUST intron_variant
7	1.01E+08	G	A	base_qualiSNV	34	2	36	0.056	41	8	49	0.163	link	-	Pde2a	c.513+80G-	ENSMUST intron_variant
7	1.03E+08	A	C	base_qualiSNV	60	2	62	0.032	68	9	77	0.117	link	-	Olfir583	c.-75A>C-	ENSMUST upstream_gene_variant
7	1.03E+08	A	C	base_qualiSNV	60	2	62	0.032	68	9	77	0.117	link	-	-	n.1030512-	- intergenic_region
7	1.05E+08	G	A	PASS_SNV	358	0	358	0	289	40	329	0.122	link	-	Usp17lb	c.-10C>T-	ENSMUST upstream_gene_variant
7	1.05E+08	G	A	PASS_SNV	358	0	358	0	289	40	329	0.122	link	-	Usp17lb	n.1048425-	- intragenic_variant
7	1.07E+08	C	A	base_qualiSNV	120	3	123	0.024	138	11	149	0.074	link	-	Olfir697	c.*30G>T-	ENSMUST 3_prime_UTR_variant
7	1.07E+08	A	C	base_qualiSNV	142	4	146	0.027	163	9	172	0.052	link	-	Olfir697	c.*18T>G-	ENSMUST 3_prime_UTR_variant
7	1.11E+08	C	A	base_qualiSNV	234	5	239	0.021	310	5	315	0.016	link	-	Adm	c.248+17C-	ENSMUST intron_variant
7	1.11E+08	C	A	base_qualiSNV	234	5	239	0.021	310	5	315	0.016	link	-	Gm28863	n.126-186/-	ENSMUST intron_variant
7	1.12E+08	T	G	base_qualiSNV	9	1	10	0.1	24	7	31	0.226	link	-	Usp47	c.1711+18-	ENSMUST intron_variant
7	1.13E+08	T	G	base_qualiSNV	34	1	35	0.029	55	10	65	0.154	link	-	Parva	c.867+139-	ENSMUST intron_variant
7	1.18E+08	T	G	weak_evid_SNV	11	2	13	0.154	17	10	27	0.37	link	-	-	n.1184490-	- intergenic_region
7	1.2E+08	T	G	base_qualiSNV	10	0	10	0	28	7	35	0.2	link	-	2610020H	c.1674+16-	ENSMUST intron_variant
7	1.22E+08	A	C	base_qualiSNV	119	3	122	0.025	133	9	142	0.063	link	-	Dnah3	c.2267+47-	ENSMUST intron_variant
7	1.21E+08	T	G	base_qualiSNV	74	5	79	0.063	82	10	92	0.109	link	-	Uqcrc2	c.*100T>G-	ENSMUST 3_prime_UTR_variant
7	1.21E+08	T	G	base_qualiSNV	74	5	79	0.063	82	10	92	0.109	link	-	Pdzd9	c.*759A>C-	ENSMUST 3_prime_UTR_variant
7	1.21E+08	A	C	too_few_s1SNV	13	0	13	0	22	2	24	0.083	link	-	Gm5737	c.941-206/-	ENSMUST intron_variant
7	1.22E+08	A	C	base_qualiSNV	9	0	9	0	6	6	12	0.5	link	-	Gm44987	n.-510A>C-	ENSMUST upstream_gene_variant
7	1.22E+08	A	C	base_qualiSNV	9	0	9	0	6	6	12	0.5	link	-	Cog7	c.169+166-	ENSMUST intron_variant
7	1.22E+08	A	C	base_qualiSNV	16	2	18	0.111	26	9	35	0.257	link	-	Ern2	c.*106T>G-	ENSMUST 3_prime_UTR_variant
7	1.22E+08	A	C	base_qualiSNV	16	2	18	0.111	26	9	35	0.257	link	-	Gm44985	n.-1916T>-	ENSMUST upstream_gene_variant
7	1.22E+08	A	C	base_qualiSNV	16	2	18	0.111	26	9	35	0.257	link	-	Pik1	c.*370A>C-	ENSMUST downstream_gene_variant
7	1.22E+08	T	G	base_qualiSNV	170	6	176	0.034	173	14	187	0.075	link	-	Ern2	c.-52A>C-	ENSMUST 5_prime_UTR_variant
7	1.23E+08	A	C	base_qualiSNV	35	0	35	0	44	7	51	0.137	link	-	Tnrc6a	c.*842A>C-	ENSMUST 3_prime_UTR_variant
7	1.23E+08	C	T	base_qualiSNV	80	2	82	0.024	74	13	87	0.149	link	-	Slc5a11	c.664+98C-	ENSMUST intron_variant
7	1.26E+08																

8	31168684	C	T	PASS	SNV	321	0	321	0	336	3	339	0.009	link	-	Tti2	c.*6811C>-	ENSMUST downstream_gene_variant
8	33685393	G	T	base_quali	SNV	8	0	8	0	16	1	17	0.059	link	-	Gsr	c.817-151C>	ENSMUST intron_variant
8	40423941	G	A	base_quali	SNV	21	2	23	0.087	52	14	66	0.212	link	-	Zdhhc2	c.-102G>A-	ENSMUST 5_prime_UTR_variant
8	41280299	T	G	base_quali	SNV	13	0	13	0	21	6	27	0.222	link	-	Pcm1	c.2433+14-	ENSMUST intron_variant
8	47202971	G	A	alt_allele	_ISNV	11	3	14	0.214	34	13	47	0.277	link	-	Stox2	c.511+150-	ENSMUST intron_variant
8	47202984	A	C	base_quali	SNV	22	3	25	0.12	34	20	54	0.37	link	-	Stox2	c.511+137-	ENSMUST intron_variant
8	47887021	A	C	base_quali	SNV	179	9	188	0.048	179	9	188	0.048	link	-	Wwc2	c.602+51T-	ENSMUST intron_variant
8	61016470	T	G	base_quali	SNV	15	1	16	0.062	27	4	31	0.129	link	-	Nek1	c.396+164-	ENSMUST intron_variant
8	61354073	T	A	too_few_s	SNV	4	0	4	0	14	2	16	0.125	link	-	Sh3f1	c.1179+22-	ENSMUST intron_variant
8	64812026	C	T	too_few_s	SNV	5	0	5	0	13	2	15	0.133	link	-	CH25-5011n	..2888G>-	ENSMUST upstream_gene_variant
8	64812026	C	T	too_few_s	SNV	5	0	5	0	13	2	15	0.133	link	-	Kih12	c.260-225C>	ENSMUST intron_variant
8	68000935	T	G	base_quali	SNV	56	4	60	0.067	55	12	67	0.179	link	-	Psd3	c.781-110A-	ENSMUST intron_variant
8	68820538	A	C	alt_allele	_ISNV	24	6	30	0.2	39	18	57	0.316	link	-	Ints10	c.1720-11T>	ENSMUST intron_variant
8	70373441	T	C	base_quali	SNV	42	3	45	0.067	75	9	84	0.107	link	-	Comp	c.-131T>C>-	ENSMUST upstream_gene_variant
8	70373441	T	C	base_quali	SNV	42	3	45	0.067	75	9	84	0.107	link	-	-	n.70373441-	- intergenic_region
8	70400416	A	G	too_few_s	SNV	11	0	11	0	28	2	30	0.067	link	-	Crtc1	c.624+203-	ENSMUST intron_variant
8	71171680 rs2269442	C	T	low_norma	SNV	2	0	2	0	1	10	11	0.909	link	-	-	n.71171681-	- intergenic_region
8	71409500	C	T	base_quali	SNV	29	1	30	0.033	53	8	61	0.131	link	-	Ankle1	c.*101C>T-	ENSMUST 3_prime_UTR_variant
8	71409500	C	T	base_quali	SNV	29	1	30	0.033	53	8	61	0.131	link	-	Babam1	c.*5102C>-	ENSMUST downstream_gene_variant
8	71503391	G	A	PASS	SNV	216	0	216	0	238	7	245	0.029	link	-	Pivap	c.1310+34-	ENSMUST intron_variant
8	72345753	A	C	non_homr	SNV	12	0	12	0	7	2	9	0.222	link	-	Eps15l1	c.2580+21-	ENSMUST intron_variant
8	72653370	A	C	base_quali	SNV	51	3	54	0.056	68	5	73	0.068	link	-	Nwd1	c.-2-116A>-	ENSMUST intron_variant
8	73116594	T	G	base_quali	SNV	80	4	84	0.048	109	14	123	0.114	link	-	Large	c.409-109A-	ENSMUST intron_variant
8	75022054	T	G	base_quali	SNV	9	0	9	0	20	15	35	0.429	link	-	RP23-4781n	..*2043A>-	ENSMUST downstream_gene_variant
8	75022054	T	G	base_quali	SNV	9	0	9	0	20	15	35	0.429	link	-	Hmgxb4	c.1341+18-	ENSMUST intron_variant
8	75022063	T	G	base_quali	SNV	6	0	6	0	17	10	27	0.37	link	-	RP23-4781n	..*2034A>-	ENSMUST downstream_gene_variant
8	75022063	T	G	base_quali	SNV	6	0	6	0	17	10	27	0.37	link	-	Hmgxb4	c.1341+19-	ENSMUST intron_variant
8	79178725	A	C	base_quali	SNV	11	0	11	0	24	4	28	0.143	link	-	RP24-1631n	..*1562A>-	ENSMUST downstream_gene_variant
8	79178725	A	C	base_quali	SNV	11	0	11	0	24	4	28	0.143	link	-	Zfp827	c.2513-181-	ENSMUST intron_variant
8	79727117	A	C	base_quali	SNV	16	1	17	0.059	20	7	27	0.259	link	-	Anapc10	c.207-201C>	ENSMUST intron_variant
8	83436226	G	T	weak_evid	SNV	4	0	4	0	16	5	21	0.238	link	-	Scoc	c.236-186C>	ENSMUST intron_variant
8	92831581	G	A	base_quali	SNV	29	1	30	0.033	46	8	54	0.148	link	-	Mmp2	c.381-104C>	ENSMUST intron_variant
8	92874111	A	G	base_quali	SNV	42	3	45	0.067	71	6	77	0.078	link	-	Lpcat2	c.704-122A-	ENSMUST intron_variant
8	92972673	A	C	base_quali	SNV	46	3	49	0.061	79	15	94	0.16	link	-	Slc6a2	c.407-79A>-	ENSMUST intron_variant
8	92996956	C	A	base_quali	SNV	158	0	158	0	189	18	207	0.087	link	-	Slc6a2	c.1759-58C>	ENSMUST intron_variant
8	94028675	A	C	base_quali	SNV	17	0	17	0	27	8	35	0.229	link	-	Nudt21	c.471+160-	ENSMUST intron_variant
8	94560079	A	C	base_quali	SNV	249	2	251	0.008	241	12	253	0.047	link	-	Cpne2	c.1062-30A-	ENSMUST intron_variant
8	94671498	T	G	base_quali	SNV	59	4	63	0.063	89	18	107	0.168	link	-	RP24-97K	n.-4108T>-	ENSMUST upstream_gene_variant
8	94671498	T	G	base_quali	SNV	59	4	63	0.063	89	18	107	0.168	link	-	Pilp	c.*4665A>-	ENSMUST downstream_gene_variant
8	94671498	T	G	base_quali	SNV	59	4	63	0.063	89	18	107	0.168	link	-	Ar12bp	c.293+118-	ENSMUST intron_variant
8	95271133	T	G	alt_allele	_ISNV	14	2	16	0.125	22	6	28	0.214	link	-	Cngb1	c.1601-16E>	ENSMUST intron_variant
8	95271137	T	G	base_quali	SNV	16	1	17	0.059	18	9	27	0.333	link	-	Cngb1	c.1601-17I>	ENSMUST intron_variant
8	95730361	T	C	base_quali	SNV	77	0	77	0	91	7	98	0.071	link	-	Cnot1	c.5895+52-	ENSMUST intron_variant
8	1.06E+08	G	A	PASS	SNV	374	0	374	0	415	5	420	0.012	link	-	Prrnt7	c.*3645G>-	ENSMUST downstream_gene_variant
8	1.06E+08	G	A	PASS	SNV	374	0	374	0	415	5	420	0.012	link	-	Gm26786	n.6223-17I>	ENSMUST intron_variant
8	1.1E+08	A	C	base_quali	SNV	18	2	20	0.1	11	6	17	0.353	link	-	Phlpp2	c.706-170A-	ENSMUST intron_variant
8	1.1E+08 rs5822946	G	A	base_quali	SNV	33	1	34	0.029	29	15	44	0.341	link	-	Gm17720	c.6+134C>-	ENSMUST intron_variant
8	1.12E+08	A	C	base_quali	SNV	190	2	192	0.01	270	11	281	0.039	link	-	Wdr59	c.54+49T>-	ENSMUST intron_variant
8	1.17E+08	C	T	base_quali	SNV	44	5	49	0.102	46	9	55	0.164	link	-	Gan	c.1236+78-	ENSMUST intron_variant
8	1.17E+08	A	G	base_quali	SNV	32	2	34	0.059	40	8	48	0.167	link	-	Gan	c.1236+86-	ENSMUST intron_variant
8	1.17E+08	T	C	base_quali	SNV	12	0	12	0	29	3	32	0.094	link	-	Cmpip	c.301-279C>	ENSMUST intron_variant
8	1.19E+08	G	A	PASS	SNV	24	0	24	0	37	7	44	0.159	link	-	Cdh13	c.1284+15-	ENSMUST intron_variant
8	1.2E+08	C	T	base_quali	SNV	37	1	38	0.026	57	6	63	0.095	link	-	Atp2c2	c.2475+96-	ENSMUST intron_variant
8	1.21E+08	T	C	too_few_s	SNV	5	0	5	0	23	2	25	0.08	link	-	Irf8	c.982+192-	ENSMUST intron_variant
8	1.21E+08	T	C	too_few_s	SNV	5	0	5	0	23	2	25	0.08	link	-	Gm20388	c.21+8429-	ENSMUST intron_variant
8	1.23E+08	G	A	weak_evid	SNV	402	1	403	0.002	381	3	384	0.008	link	-	Gm20388	c.22-1205C>	ENSMUST intron_variant
8	1.23E+08	A	C	base_quali	SNV	196	0	196	0	227	8	235	0.034	link	-	Mir7080	n.-1557A>-	ENSMUST upstream_gene_variant
8	1.23E+08	A	C	base_quali	SNV	196	0	196	0	227	8	235	0.034	link	-	Cpne7	c.925-29A>-	ENSMUST intron_variant
8	1.23E+08	A	C	base_quali	SNV	196	0	196	0	227	8	235	0.034	link	-	Gm20388	c.22-1166E>	ENSMUST intron_variant
8	1.24E+08	A	C	base_quali	SNV	6	0	6	0	12	3	15	0.2	link	-	Urb2	c.4378-20C>	ENSMUST intron_variant
8	1.24E+08	A	C	base_quali	SNV	6	0	6	0	12	3	15	0.2	link	-	Gm20388	c.22-2484E>	ENSMUST intron_variant
8	1.24E+08	A	C	base_quali	SNV	6	0	6	0	12	3	15	0.2	link	-	RP23-4301n	..473+103-	ENSMUST intron_variant
8	1.25E+08	C	A	alt_allele	_ISNV	13	1	14	0.071	12	6	18	0.333	link	-	Cog2	c.1911-10I>	ENSMUST intron_variant
8	1.25E+08	T	G	base_quali	SNV	51	4	55	0.073	37	9	46	0.196	link	-	Ttc13	c.398-141A-	ENSMUST intron_variant
8	1.26E+08	T	C	base_quali	SNV	38	1	39	0.026	71	4	75	0.053	link	-	BC021891	c.1779-10T>	ENSMUST intron_variant
9	3003580	A	T	non_homr	SNV	196	10	206	0.049	53	6	59	0.102	link	-	Gm10722	c.*1250A>-	ENSMUST downstream_gene_variant
9	3003580	A	T	non_homr	SNV	196	10	206	0.049	53	6	59	0.102	link	-	Gm26870	n.821+102-	ENSMUST intron_variant
9	13792969	A	C	base_quali	SNV	8	2	10	0.2	20	7	27	0.259	link	-	Mtmr2	c.571-180A-	ENSMUST intron_variant
9	21245240	T	G	base_quali	SNV	4	0	4	0	13	7	20	0.35	link	-	Slpr5	c.-75-37A>-	ENSMUST intron_variant
9	35474325	T	G	base_quali	SNV	7	0	7	0	20	9	29	0.31	link	-	Gm25630	n.-560T>G>	ENSMUST upstream_gene_variant
9	35474325	T	G	base_quali	SNV	7	0	7	0	20	9	29	0.31	link	-	Cdon	c.2146+76-	ENSMUST intron_variant
9	36782363	C	T	base_quali	SNV	250	13	263	0.049	222	14	236	0.059	link	-	Gm26787	n.271C>T-	ENSMUST non_coding_transcript_exon_variant
9	37531804	T	G	base_quali	SNV	39	3	42	0.071	47	9	56	0.161	link	-	Esam	c.258+129-	ENSMUST intron_variant
9	37746025	A	C	base_quali	SNV	34	1	35	0.029	57	14	71	0.197	link	-	Olfr874	c.-111A>C>-	ENSMUST upstream_gene_variant
9	37746025	A	C	base_quali	SNV	34	1	35	0.029	57	14	71	0.197	link	-	-	n.37746021-	- intergenic_region
9	38368717	G	A	too_few_s	SNV	11	0	11	0	14	2	16	0.125	link	-	Olfr250	c.*174G>A-	ENSMUST downstream_gene_variant
9	38368717	G	A	too_few_s	SNV	11	0	11	0	14	2	16	0.125	link	-	-	n.38368711-	- intergenic_region
9	39599519	T	A	weak_evid	SNV	27	3	30	0.1	32	8	40	0.2	link	-	AW551984	c.645+126-	ENSMUST intron_variant
9	44160631	T	G	base_quali	SNV	5	0	5	0	12	3	15	0.2	link	-	Cbl	c.1426-15C>	ENSMUST intron_variant
9	44242164	C	T	too_few_s	SNV	7	0	7	0	7	2	9	0.222	link	-	Ccdc153	c.136+47T>	ENSMUST intron_variant
9	46127197	T	G	base_quali	SNV	35	0	35	0	78	5	83	0.06	link	-	Slk3	c.454+124-	ENSMUST intron_variant
9	49523503	G	A	base_quali	SNV	98	3	101	0.03	116	4	120	0.033	link	-	Gm11149	c.100+324-	ENSMUST intr

9	73693108.	G	A	alt allele_iSNV	13	1	14	0.071	36	8	44	0.182	link	-	Unc13c	c.4256+97-	ENSMUST intron_variant
9	74953699.	A	C	base_qualiSNV	144	8	152	0.053	172	9	181	0.05	link	-	Fam214a	n.74953699-	- intragenic_variant
9	75151865.	A	C	base_qualiSNV	135	7	142	0.049	168	5	173	0.029	link	-	Myo5a	c.1402-28/-	ENSMUST intron_variant
9	78101800.	T	G	base_qualiSNV	27	1	28	0.036	22	19	41	0.463	link	-	Fbxo9	c.91-114A/-	ENSMUST intron_variant
9	79758411.	T	C	base_qualiSNV	60	2	62	0.032	96	6	102	0.059	link	-	Cox7a2	c.108+79A-	ENSMUST intron_variant
9	80300809.	T	G	alt allele_iSNV	14	1	15	0.067	21	9	30	0.3	link	-	Myo6	c.3439+14-	ENSMUST intron_variant
9	83636636.	G	A	too_few_sSNV	26	0	26	0	32	2	34	0.059	link	-	Sh3bgrl2	c.*495G>A-	ENSMUST3_prime_UTR_variant
9	92488520.	A	C	base_qualiSNV	60	4	64	0.062	60	17	77	0.221	link	-	Plscr4	c.613-74A/-	ENSMUST intron_variant
9	92593653.	G	T	base_qualiSNV	44	7	51	0.137	67	28	95	0.295	link	-	Plod2	c.880-92C/-	ENSMUST intron_variant
9	99321945.	A	C	base_qualiSNV	29	1	30	0.033	35	6	41	0.146	link	-	1700008A2n.-881A>-C-		ENSMUST upstream_gene_variant
9	99321945.	A	C	base_qualiSNV	29	1	30	0.033	35	6	41	0.146	link	-	Esyf3	c.1320+15-	ENSMUST intron_variant
9	99698694.	A	C	base_qualiSNV	19	0	19	0	39	5	44	0.114	link	-	Cldn18	c.385+115-	ENSMUST intron_variant
9	1.03E+08.	T	G	base_qualiSNV	46	2	48	0.042	63	15	78	0.192	link	-	Ryk	c.1266+84-	ENSMUST intron_variant
9	1.05E+08.	A	C	base_qualiSNV	4	0	4	0	17	4	21	0.19	link	-	Aste1	c.*1618A>-	ENSMUST downstream_gene_variant
9	1.05E+08.	A	C	base_qualiSNV	4	0	4	0	17	4	21	0.19	link	-	Atp2c1	c.*6127T>-	ENSMUST downstream_gene_variant
9	1.05E+08.	A	C	base_qualiSNV	4	0	4	0	17	4	21	0.19	link	-	Aste1	n.1054069;-	- intragenic_variant
9	1.05E+08.	A	C	base_qualiSNV	4	0	4	0	17	4	21	0.19	link	-	Atp2c1	n.1054069;-	- intragenic_variant
9	1.05E+08.	G	T	base_qualiSNV	49	0	49	0	56	1	57	0.018	link	-	Atp2c1	c.524+89C-	ENSMUST intron_variant
9	1.09E+08 rs8643206/G	T		non_homrSNV	27	3	30	0.1	37	9	46	0.196	link	-	Slc25a20	c.105+62G-	ENSMUST intron_variant
9	1.09E+08.	A	C	base_qualiSNV	202	6	208	0.029	213	8	221	0.036	link	-	Slc25a20	c.536-35A/-	ENSMUST intron_variant
9	1.09E+08.	A	C	base_qualiSNV	59	0	59	0	65	5	70	0.071	link	-	Fbxw22	c.1295+41-	ENSMUST intron_variant
9	1.11E+08.	G	T	base_qualiSNV	117	6	123	0.049	141	8	149	0.054	link	-	Fbxw27	c.625+33C-	ENSMUST intron_variant
9	1.11E+08.	C	A	base_qualiSNV	209	0	209	0	220	8	228	0.035	link	-	Prss50	c.-2010C-	ENSMUST upstream_gene_variant
9	1.11E+08.	C	A	base_qualiSNV	209	0	209	0	220	8	228	0.035	link	-	Prss46	c.691-19C-	ENSMUST intron_variant
9	1.18E+08.	G	C	too_few_sSNV	5	0	5	0	16	2	18	0.111	link	-	Rbms3	c.51+228C-	ENSMUST intron_variant
9	1.19E+08.	A	C	base_qualiSNV	43	3	46	0.065	90	8	98	0.082	link	-	Villl	c.457-91A/-	ENSMUST intron_variant
9	1.19E+08.	A	C	base_qualiSNV	17	1	18	0.056	28	4	32	0.125	link	-	Slc22a14	c.1679+15-	ENSMUST intron_variant
9	1.24E+08.	A	C	base_qualiSNV	190	2	192	0.01	181	12	193	0.062	link	-	Limd1	c.1801-72/-	ENSMUST intron_variant
9	1.24E+08.	A	C	base_qualiSNV	62	2	64	0.031	122	18	140	0.129	link	-	Ppp2r3d	c.244-322/-	ENSMUST intron_variant
X	7166516.	T	G	base_qualiSNV	48	2	50	0.04	45	15	60	0.25	link	-	Clnf5	c.934-80A/-	ENSMUST intron_variant
X	7595076.	T	C	weak_evid SNV	131	0	131	0	162	4	166	0.024	link	-	Foxp3	c.*2033T>-	ENSMUST3_prime_UTR_variant
X	7595076.	T	C	weak_evid SNV	131	0	131	0	162	4	166	0.024	link	-	Ccdc22	c.1540-21/-	ENSMUST intron_variant
X	7595076.	T	C	weak_evid SNV	131	0	131	0	162	4	166	0.024	link	-	Gm36995	n.2940-21/-	ENSMUST intron_variant
X	13161037.	G	C	alt allele_iSNV	13	4	17	0.235	27	7	34	0.206	link	-	Usp9x	c.6751+10-	ENSMUST intron_variant
X	48401665.	A	C	base_qualiSNV	36	1	37	0.027	36	6	42	0.143	link	-	Bcorl1	c.4913-94/-	ENSMUST intron_variant
X	57388645.	T	G	base_qualiSNV	129	4	133	0.033	162	10	172	0.058	link	-	Snord61	n.*2804A>-	ENSMUST downstream_gene_variant
X	59165904.	A	C	base_qualiSNV	25	0	25	0	35	2	37	0.054	link	-	Fgf113	n.5916590-	- intragenic_variant
X	74243192.	C	T	weak_evid SNV	107	0	107	0	119	3	122	0.025	link	-	Flna	c.374-27G/-	ENSMUST intron_variant
X	93777586.	T	G	base_qualiSNV	7	1	8	0.125	6	7	13	0.538	link	-	Pdk3	c.964-164/-	ENSMUST intron_variant
X	98803009.	A	C	base_qualiSNV	32	3	35	0.086	39	8	47	0.17	link	-	Ophn1	c.250+76T-	ENSMUST intron_variant
X	1E+08.	T	G	base_qualiSNV	20	2	22	0.091	39	10	49	0.204	link	-	Awat2	c.86-88A>-	ENSMUST intron_variant
X	1.02E+08.	A	C	base_qualiSNV	49	4	53	0.075	68	4	72	0.056	link	-	Taf1	c.3130-47/-	ENSMUST intron_variant
X	1.02E+08.	T	G	base_qualiSNV	123	7	130	0.054	111	10	121	0.083	link	-	Gm14858	n.-2050T>-	ENSMUST upstream_gene_variant
X	1.02E+08.	T	G	base_qualiSNV	123	7	130	0.054	111	10	121	0.083	link	-	Gm26318	n.*4829A>-	ENSMUST downstream_gene_variant
X	1.02E+08.	T	G	base_qualiSNV	123	7	130	0.054	111	10	121	0.083	link	-	Cited1	c.-66+143/-	ENSMUST intron_variant
X	1.03E+08.	T	G	alt allele_iSNV	16	4	20	0.2	19	9	28	0.321	link	-	Phka1	c.1570-82/-	ENSMUST intron_variant
X	1.21E+08.	T	C	too_few_sSNV	15	0	15	0	8	2	10	0.2	link	-	Pcdh11x	c.3037-15/-	ENSMUST intron_variant
X	1.34E+08.	A	C	base_qualiSNV	48	0	48	0	55	4	59	0.068	link	-	Mir3112	n.-2952A>-	ENSMUST upstream_gene_variant
X	1.34E+08.	A	C	base_qualiSNV	48	0	48	0	55	4	59	0.068	link	-	Cstf2	c.890-772/-	ENSMUST intron_variant
X	1.36E+08.	G	T	non_homrSNV	15	2	17	0.118	20	2	22	0.091	link	-	Nxf7	c.*127C>A-	ENSMUST downstream_gene_variant
X	1.36E+08.	G	T	non_homrSNV	15	2	17	0.118	20	2	22	0.091	link	-	Nxf7	n.1355796/-	- intragenic_variant
X	1.36E+08.	G	T	base_qualiSNV	16	2	18	0.111	22	4	26	0.154	link	-	Nxf7	c.*124C>A-	ENSMUST downstream_gene_variant
X	1.36E+08.	G	T	base_qualiSNV	16	2	18	0.111	22	4	26	0.154	link	-	Nxf7	n.1355796/-	- intragenic_variant
X	1.36E+08.	A	T	weak_evid SNV	143	0	143	0	155	3	158	0.019	link	-	Bhlhb9	n.1358027;-	- intragenic_variant
X	1.42E+08.	A	C	no_reliableSNV	117	0	117	0	91	3	94	0.032	link	-	Col4a5	c.4995-9A/-	ENSMUST intron_variant
X	1.52E+08.	G	A	weak_evid SNV	213	2	215	0.009	216	3	219	0.014	link	-	Gpr173	c.*6385C>-	ENSMUST downstream_gene_variant
X	1.61E+08.	T	G	base_qualiSNV	14	0	14	0	21	7	28	0.25	link	-	Cdkl5	c.2377-10/-	ENSMUST intron_variant
X	1.62E+08.	A	C	alt allele_iSNV	6	0	6	0	13	5	18	0.278	link	-	Nhs	c.843+150-	ENSMUST intron_variant
GL456211.	55552.	C	A	base_qualiSNV	252	10	262	0.038	283	25	308	0.081	link	-	AC133103.c.-712G>T-		ENSMUST upstream_gene_variant
GL456211.	55552.	C	A	base_qualiSNV	252	10	262	0.038	283	25	308	0.081	link	-	-	n.55552C>-	- intergenic_region
GL456211.	83828.	C	G	too_few_sSNV	5	0	5	0	4	2	6	0.333	link	-	-	n.83828C>-	- intergenic_region
GL456210.	20850.	A	T	mapping_cSNV	193	9	202	0.045	251	28	279	0.1	link	-	AC125149.c.-78-1074-		ENSMUST intron_variant
GL456210.	33708.	A	C	mapping_cSNV	99	3	102	0.029	132	22	154	0.143	link	-	AC125149.c.-78-2360-		ENSMUST intron_variant
GL456212.	137560.	A	T	mapping_cSNV	24	0	24	0	42	13	55	0.236	link	-	AC168977.c.820+280-		ENSMUST intron_variant
GL456212.	137576.	T	C	mapping_cSNV	25	1	26	0.038	49	18	67	0.269	link	-	AC168977.c.820+264-		ENSMUST intron_variant
GL456216.	33934.	C	T	low_frac_iSNV	7	0	7	0	16	1	17	0.059	link	-	DHR5X	c.389-204/-	ENSMUST intron_variant
1	1.75E+08.	C	A	weak_evid SNV	192	1	193	0.005	225	9	234	0.038	link	-	Fmn2	c.2925C>A.p.Gly975Gly	ENSMUST synonymous_variant
1	1.85E+08.	T	G	base_qualiSNV	203	5	208	0.024	187	9	196	0.046	link	-	lars2	c.282A>C p.Ser94Ser	ENSMUST synonymous_variant
10	1.29E+08.	C	T	weak_evid SNV	381	1	382	0.003	373	6	379	0.016	link	-	Bloc1s1	c.360G>A p.Leu120Leu	ENSMUST synonymous_variant
11	69801467.	G	A	base_qualiSNV	347	6	353	0.017	417	21	438	0.048	link	-	Fgf111	c.159C>T p.Cys53Cys	ENSMUST synonymous_variant
11	1.01E+08.	A	C	base_qualiSNV	246	8	254	0.031	321	14	335	0.042	link	-	Plekhh3	c.474T>G p.Arg158Arg	ENSMUST synonymous_variant
11	1.07E+08.	A	C	base_qualiSNV	330	1	331	0.003	293	5	298	0.017	link	-	Bptf	c.4569T>G.p.Ser1523Ser	ENSMUST synonymous_variant
12	1.02E+08.	A	C	base_qualiSNV	344	6	350	0.017	374	17	391	0.043	link	-	Rin3	c.412A>C p.Arg138Arg	ENSMUST synonymous_variant
13	3556995.	C	T	weak_evid SNV	245	0	245	0	237	4	241	0.017	link	-	Gdi2	c.657C>T p.Tyr219Tyr	ENSMUST synonymous_variant
13	55828458.	G	T	PASS SNV	337	0	337	0	348	11	359	0.031	link	-	Ptx1	c.387C>A p.Leu129Leu	ENSMUST synonymous_variant
13	73763805.	C	A	base_qualiSNV	343	2	345	0.006	416	4	420	0.01	link	-	Slc12a7	c.39C>A p.Arg13Arg	ENSMUST synonymous_variant
14	41486387 rs1134879/G	A		mapping_cSNV	463	22	485	0.045	452	41	493	0.083	link	-	Gm3486	c.366C>T p.His122His	ENSMUST synonymous_variant
15	26552757.	G	A	weak_evid SNV	419	1	420	0.002	420	5	425	0.012	link	-	Fbw17	c.423C>T p.Cys141Cys	ENSMUST synonymous_variant
15	58034179.	G	A	weak_evid SNV	373	4	377	0.011	398	5	403	0.012	link	-	9130401M.c.22C>T	p.Leu8Leu	ENSMUST synonymous_variant
15	63861675.	A	T	PASS SNV	259	0	259	0	215	24	239	0.1	link	-	Gsdmc3	c.666T>A p.Pro222Pro	ENSMUST synonymous_variant
15	98851075.	C	T	PASS SNV	554	1	555	0.002	574	13	587	0.022	link	-	Kmt2d	c.8367G>A.p.Gln2789Gln	ENSMUST synonymous_variant
16	20499021.	G	A	base_qualiSNV	141	10	151	0.066	193	17	210	0.081	link	-	Eif2b5	c.108G>A p.Pro36Pro	ENSMUST synonymous_variant
16	32979403.	T	C	base_qualiSNV	161	0	161	0	138	3	141	0.02					

3	37029899 .	A	C	base_qualiSNV	152	5	157	0.032	144	16	160	0.1 link	-	4932438A1c.11466-2/-	ENSMUST splice_acceptor_variant+intron_variant
3	83031981 .	T	G	base_qualiSNV	227	8	235	0.034	252	20	272	0.074 link	-	Fga c.1660+2T -	ENSMUST splice_donor_variant+intron_variant
4	32741315 .	A	C	base_qualiSNV	124	6	130	0.046	146	12	158	0.076 link	-	Mdn1 c.11424-8/-	ENSMUST splice_region_variant+intron_variant
4	48181495 .	A	C	base_qualiSNV	132	2	134	0.015	150	3	153	0.02 link	-	Stx17 c.667-4A> -	ENSMUST splice_region_variant+intron_variant
4	1.18E+08 .	A	C	base_qualiSNV	265	7	272	0.026	237	32	269	0.119 link	-	Tie1 c.3333+2T -	ENSMUST splice_donor_variant+intron_variant
5	1.24E+08 .	T	G	alt_allele_iSNV	37	3	40	0.075	47	11	58	0.19 link	-	Pitpnm2 c.-98-2A>(-	ENSMUST splice_acceptor_variant+intron_variant
6	72630147 .	T	G	base_qualiSNV	89	9	98	0.092	84	16	100	0.16 link	-	Gm15401 n.145+2T> -	ENSMUST splice_donor_variant+intron_variant
7	99317670 .	T	G	base_qualiSNV	265	1	266	0.004	217	8	225	0.036 link	-	Map6 c.1703+2T -	ENSMUST splice_donor_variant+intron_variant
8	1.25E+08 .	A	C	base_qualiSNV	342	2	344	0.006	300	13	313	0.042 link	-	Gnpat c.694-2A> -	ENSMUST splice_acceptor_variant+intron_variant
X	1.02E+08 .	T	C	base_qualiSNV	90	1	91	0.011	86	12	98	0.122 link	-	Taf1 c.412+8T> -	ENSMUST splice_region_variant+intron_variant
X	1.71E+08 .	G	A	base_qualiSNV	145	7	152	0.046	154	11	165	0.067 link	-	Asmt c.581-4G> -	ENSMUST splice_region_variant+intron_variant