

Chr	Pos	ID	Ref	Alt	Filter	Variant_Typ	Normal_REF	Normal_ALT	Normal_Dep	Normal_Alle	Tumor_REF	Tumor_ALT	Tumor_Dep	Tumor_Alle	igv	ClinVar	Gene_Name	CDS_Chang	Amino_Acid	Transcript	Effect
1	26686757	.	C	CTTCCTC	non_homr	INS	11	0	11	0	15	3	18	0.167	link	-	4931408C	c.186+483-		ENSMUST	intron_variant
1	85638309	.	C	CTAGTTT	too_few_s	INS	11	0	11	0	5	2	7	0.286	link	-	Gm17017	n.*2912,*1-		ENSMUST	downstream_gene_variant
1	85638309	.	C	CTAGTTT	too_few_s	INS	11	0	11	0	5	2	7	0.286	link	-	Sp140	c.1062+44-		ENSMUST	intron_variant
1	88236388	.	A	AGTAAGG	PASS	INS	20	0	20	0	26	8	34	0.235	link	-	Mroh2a	c.1247-26-		ENSMUST	intron_variant
1	88236391	.	T	GTATA	non_homr	INS	19	0	19	0	20	6	26	0.231	link	-	Mroh2a	c.1247-26-		ENSMUST	intron_variant
1	88237173	rs2651159A	AG	weak_evid	INS		9	0	9	0	32	4	36	0.111	link	-	Mroh2a	c.1324-29-		ENSMUST	intron_variant
1	88269887	.	A	AT	weak_evid	INS	4	0	4	0	15	6	21	0.286	link	-	Hjurp	c.354+314-		ENSMUST	intron_variant
1	1.5E+08	.	TG	T	non_homr	DEL	91	16	107	0.15	79	24	103	0.233	link	-	Pla2g4a	c.33+84de		ENSMUST	intron_variant
10	61884868	rs2277493ACC	A	weak_evid	DEL		12	1	13	0.077	15	5	20	0.25	link	-	Col13a1	c.937-159-		ENSMUST	intron_variant
10	69926338	.	GA	G	base_qual	DEL	29	3	32	0.094	25	22	47	0.468	link	-	Ank3	n.6992635-		-	intragenic_variant
10	1.3E+08	.	C	CAG	low_frac_j	INS	12	0	12	0	22	4	26	0.154	link	-	Olfr809	c.-179_-17-		ENSMUST	upstream_gene_variant
10	1.3E+08	.	C	CAG	low_frac_j	INS	12	0	12	0	22	4	26	0.154	link	-	Olfr809	c.-134_-11-		ENSMUST	upstream_gene_variant
10	1.3E+08	.	C	CAG	low_frac_j	INS	12	0	12	0	22	4	26	0.154	link	-	Olfr809	n.1297757-		-	intragenic_variant
11	3188470	.	ATCTTT	A	low_frac_j	DEL	17	4	21	0.19	29	10	39	0.256	link	-	Sfi1	c.23+466-		ENSMUST	intron_variant
11	3188470	.	ATCTTT	A	low_frac_j	DEL	17	4	21	0.19	29	10	39	0.256	link	-	Drg1	n.3188475-		-	intragenic_variant
11	3188475	.	T	TAAAA	weak_evid	INS	20	1	21	0.048	31	4	35	0.114	link	-	Sfi1	c.23+465-		ENSMUST	intron_variant
11	3188475	.	T	TAAAA	weak_evid	INS	20	1	21	0.048	31	4	35	0.114	link	-	Drg1	n.3188476-		-	intragenic_variant
11	29563976	.	GTAGA	G	non_homr	DEL	59	6	65	0.092	60	14	74	0.189	link	-	Clhc1	c.1039+62-		ENSMUST	intron_variant
11	68494619	.	AG	A	non_homr	DEL	44	9	53	0.17	24	20	44	0.455	link	-	Pik3r5	c.2107+75-		ENSMUST	intron_variant
11	69369349	.	TCTC	T	non_homr	DEL	167	12	179	0.067	143	15	158	0.095	link	-	Chd3	c.40_42de p.Glu14de		ENSMUST	conservative_inframe_deletion
11	69369349	.	TCTC	T	non_homr	DEL	167	12	179	0.067	143	15	158	0.095	link	-	Gm17305	c.467_469p.Pro156d		ENSMUST	disruptive_inframe_deletion
11	96272263	.	AC	A	too_few_s	DEL	6	0	6	0	3	2	5	0.4	link	-	Hoxb9	c.517+211-		ENSMUST	intron_variant
11	97664895	.	T	TG	non_homr	INS	76	3	79	0.038	103	14	117	0.12	link	-	Gm11613	n.-4529du-		ENSMUST	upstream_gene_variant
11	97664895	.	T	TG	non_homr	INS	76	3	79	0.038	103	14	117	0.12	link	-	Gm24158	n.-4569du-		ENSMUST	upstream_gene_variant
11	97664895	.	T	TG	non_homr	INS	76	3	79	0.038	103	14	117	0.12	link	-	Mlt6	c.110-51d-		ENSMUST	intron_variant
11	97986767	.	GC	G	weak_evid	DEL	4	0	4	0	3	3	6	0.5	link	-	Plxdc1	c.-452d(C-		ENSMUST	upstream_gene_variant
11	97986767	.	GC	G	weak_evid	DEL	4	0	4	0	3	3	6	0.5	link	-	Arl5c	c.*3523dc-		ENSMUST	downstream_gene_variant
11	97986767	.	GC	G	weak_evid	DEL	4	0	4	0	3	3	6	0.5	link	-	-	n.9798676-		-	intergenic_region
11	1.2E+08	.	TG	T	weak_evid	DEL	44	6	50	0.12	24	14	38	0.368	link	-	Endov	c.714+53d-		ENSMUST	intron_variant
12	33147794	.	GA	G	weak_evid	DEL	236	1	237	0.004	228	6	234	0.026	link	-	Atxn7l1	c.44del(A p.Lys15fs		ENSMUST	frameshift_variant
12	33147794	.	GA	G	weak_evid	DEL	236	1	237	0.004	228	6	234	0.026	link	-	F730043M	n.-209del1-		ENSMUST	upstream_gene_variant
13	31820379	.	C	CTCTTTC	low_frac_j	INS	5	0	5	0	15	4	19	0.211	link	-	Gmds	c.988-177-		ENSMUST	intron_variant
13	33334212	.	G	GTT	alt_allele	INS	44	12	56	0.214	47	37	84	0.44	link	-	Serpinh9f	c.727-4_7i-		ENSMUST	splice_acceptor_variant+intron_variant
13	1.19E+08	.	G	CGGGGCT	low_normr	INS	2	0	2	0	0	4	4	1	link	-	Tmem267	c.-4062_-4-		ENSMUST	upstream_gene_variant
13	1.19E+08	.	G	CGGGGCT	low_normr	INS	2	0	2	0	0	4	4	1	link	-	3110070M	c.-366_-3C-		ENSMUST	upstream_gene_variant
13	1.19E+08	.	G	CGGGGCT	low_normr	INS	2	0	2	0	0	4	4	1	link	-	4833420G	c.*2656,*1-		ENSMUST	downstream_gene_variant
13	1.19E+08	.	G	CGGGGCT	low_normr	INS	2	0	2	0	0	4	4	1	link	-	Tmem267	n.1194885-		-	intragenic_variant
14	41383125	.	G	GA	PASS	INS	94	0	94	0	122	8	130	0.062	link	-	Gm7945	c.471-134-		ENSMUST	intron_variant
14	43343148	.	G	GACACAC	weak_evid	INS	9	0	9	0	7	3	10	0.3	link	-	1700001F	c.491-423-		ENSMUST	intron_variant
14	67008580	.	CCCACT	C	base_qual	DEL	18	1	19	0.053	21	5	26	0.192	link	-	Bnip3l	c.97+103-		ENSMUST	intron_variant
15	3282642	.	CA	C	weak_evid	DEL	15	0	15	0	41	3	44	0.068	link	-	Sepp1	c.*2933dc-		ENSMUST	downstream_gene_variant
15	3282642	.	CA	C	weak_evid	DEL	15	0	15	0	41	3	44	0.068	link	-	Ccdc152	c.558+175-		ENSMUST	intron_variant
15	3282644	.	GATCAAG	G	weak_evid	DEL	20	0	20	0	43	3	46	0.065	link	-	Sepp1	c.*2935,*1-		ENSMUST	downstream_gene_variant
15	3282644	.	GATCAAG	G	weak_evid	DEL	20	0	20	0	43	3	46	0.065	link	-	Ccdc152	c.558+164-		ENSMUST	intron_variant
15	54860103	rs2119781G	GA	non_homr	INS		179	15	194	0.077	147	24	171	0.14	link	-	Enpp2	c.1882-10-		ENSMUST	intron_variant
15	58661041	rs2416992G	GAGAT	weak_evid	INS		5	0	5	0	6	3	9	0.333	link	-	Fer1l6	c.5402+24-		ENSMUST	intron_variant
15	66286150	.	CCCG	C	weak_evid	DEL	249	6	255	0.024	238	14	252	0.056	link	-	Kcnq3	c.72_74de p.Gly25del		ENSMUST	disruptive_inframe_deletion
15	66286150	.	CCCG	C	weak_evid	DEL	249	6	255	0.024	238	14	252	0.056	link	-	Gm27242	n.-766_-7E-		ENSMUST	upstream_gene_variant
16	15632258	.	GA	G	weak_evid	DEL	189	2	191	0.01	240	5	245	0.02	link	-	Mcm4	c.908delT p.Phe303f		ENSMUST	frameshift_variant
16	44332266	rs2185897TG	T	alt_allele	DEL		34	18	52	0.346	36	28	64	0.438	link	-	Sid1t	c.222+40d-		ENSMUST	intron_variant
16	44332266	rs2185897TG	T	alt_allele	DEL		34	18	52	0.346	36	28	64	0.438	link	-	Gm26732	n.2282del(C-		ENSMUST	non_coding_transcript_exon_variant
17	17318985	.	T	TA	non_homr	INS	228	11	239	0.046	273	25	298	0.084	link	-	Gm6712	n.*881,*8I-		ENSMUST	downstream_gene_variant
17	17318985	.	T	TA	non_homr	INS	228	11	239	0.046	273	25	298	0.084	link	-	Chd1	n.1731899-		-	intragenic_variant
17	17318985	.	T	TA	non_homr	INS	228	11	239	0.046	273	25	298	0.084	link	-	Gm6712	n.1731899-		-	intragenic_variant
17	25856829	.	A	AAAAAAA	weak_evid	INS	16	2	18	0.111	18	3	21	0.143	link	-	Gm26694	n.1888+6C-		ENSMUST	intron_variant
17	25856829	.	A	AAAAAAA	weak_evid	INS	16	2	18	0.111	18	3	21	0.143	link	-	Wdr90	c.1677+13-		ENSMUST	intron_variant
17	36128871	.	CG	C	non_homr	DEL	116	4	120	0.033	104	14	118	0.119	link	-	Gm19684	c.*293del(C-		ENSMUST	3_prime_UTR_variant
17	36128871	.	CG	C	non_homr	DEL	116	4	120	0.033	104	14	118	0.119	link	-	Gm7030	c.346+23d-		ENSMUST	intron_variant
17	45587523	rs2314956TG	T	weak_evid	DEL		58	7	65	0.108	50	18	68	0.265	link	-	Slc29a1	c.973+38d-		ENSMUST	intron_variant
17	45587523	rs2314956TG	T	weak_evid	DEL		58	7	65	0.108	50	18	68	0.265	link	-	Gm17080	n.635-667-		ENSMUST	intron_variant
17	45675472	rs2658797AC	A	non_homr	DEL		129	17	146	0.116	97	25	122	0.205	link	-	Tmem63b	c.370-50d-		ENSMUST	intron_variant
17	65783467	.	CCCGGGC	C	non_homr	DEL	146	1	147	0.007	104	3	107	0.028	link	-	Ppp4r1	c.7+27_8-		ENSMUST	intron_variant
19	5706645	.	TG	T	alt_allele	DEL	44	8	52	0.154	59	19	78	0.244	link	-	Map3k11	c.*4302de-		ENSMUST	downstream_gene_variant
19	5706645	.	TG	T	alt_allele	DEL	44	8	52	0.154	59	19	78	0.244	link	-	Ehbp1l1	c.*1680de-		ENSMUST	downstream_gene_variant
19	5706645	.	TG	T	alt_allele	DEL	44	8	52	0.154	59	19	78	0.244	link	-	Kcnk7	c.719-47d-		ENSMUST	intron_variant
19	11275655	.	TG	T	non_homr	DEL	175	13	188	0.069	182	19	201	0.095	link	-	4930526L	n.149-169-		ENSMUST	intron_variant
19	11275655	.	TG	T	non_homr	DEL	175	13	188	0.069	182	19	201	0.095	link	-	Ms4a5	c.492+954-		ENSMUST	intron_variant
19	34583479	rs1133281AC	A	non_homr	DEL		53	9	62	0.145	49	20	69	0.29	link	-	Ifit3	c.-120del(C-		ENSMUST	upstream_gene_variant
19	34583479	rs1133281AC	A	non_homr	DEL		53	9	62	0.145	49	20	69	0.29	link	-	-	n.3458348-		-	intergenic_region
19	34964496	.	CTTTTGT	C	weak_evid	DEL	162	1	163	0.006	152	4	156	0.026	link	-	Mir1950	n.-899_-8S-		ENSMUST	upstream_gene_variant
19	34964496	.	CTTTTGT	C	weak_evid	DEL	162	1	163	0.006	152	4	156	0.026	link	-	Kif20b	c.4366-15-		ENSMUST	intron_variant
19	45636173	.	TAA	T	non_homr	DEL	33	3	36	0.083	38	8	46	0.174	link	-	Fbxw4	c.536+88-		ENSMUST	intron_variant
2	91184916	rs2442222TC	T	alt_allele	DEL		62	19	81	0.235	34	30	64	0.469	link	-	Madd	c.-5680del-		ENSMUST	upstream_gene_variant

6	1.25E+08 .	GCC	G	non_homr	DEL	6	0	6	0	15	5	20	0.25	link	-	Ncapd2	c.*1997.*1-	ENSMUSTdownstream_gene_variant
6	1.25E+08 .	GCC	G	non_homr	DEL	6	0	6	0	15	5	20	0.25	link	-	Gapdh	c.60+157.-	ENSMUSTintron_variant
7	4925998 .	TG	T	non_homr	DEL	45	9	54	0.167	44	19	63	0.302	link	-	Zfp628	c.*14102de-	ENSMUSTdownstream_gene_variant
7	4925998 .	TG	T	non_homr	DEL	45	9	54	0.167	44	19	63	0.302	link	-	Nat14	c.*1548de-	ENSMUSTdownstream_gene_variant
7	4925998 .	TG	T	non_homr	DEL	45	9	54	0.167	44	19	63	0.302	link	-	Ssc5d	c.25+30de-	ENSMUSTintron_variant
7	18890366 .	TC	T	non_homr	DEL	60	9	69	0.13	56	17	73	0.233	link	-	Pglyrp1	c.*35delC	ENSMUST3_prime_UTR_variant
7	18890366 .	TC	T	non_homr	DEL	60	9	69	0.13	56	17	73	0.233	link	-	Ccdc61	c.*709delC	ENSMUSTdownstream_gene_variant
7	30481612 .	TC	T	non_homr	DEL	114	15	129	0.116	92	31	123	0.252	link	-	Rps12-ps4/n.*3088de-	ENSMUSTdownstream_gene_variant	
7	30481612 .	TC	T	non_homr	DEL	114	15	129	0.116	92	31	123	0.252	link	-	Nphs1	c.3329-19i-	ENSMUSTintron_variant
7	34099671 rs2646431	CG	C	alt_allele_	DEL	52	13	65	0.2	35	25	60	0.417	link	-	Scgb1b30	c.62-23del	ENSMUSTintron_variant
7	35195334 rs2118992	AG	A	base_qual	DEL	28	3	31	0.097	26	10	36	0.278	link	-	Slc7a10	c.374+53d-	ENSMUSTintron_variant
7	43496776 rs2524534	TG	T	alt_allele_	DEL	46	10	56	0.179	33	21	54	0.389	link	-	49314068	c.998+103-	ENSMUSTintron_variant
7	1.02E+08 .	AC	A	alt_allele_	DEL	44	12	56	0.214	31	17	48	0.354	link	-	Xndc1	c.*2316de-	ENSMUSTdownstream_gene_variant
7	1.02E+08 .	AC	A	alt_allele_	DEL	44	12	56	0.214	31	17	48	0.354	link	-	Trpc2	c.735+20d-	ENSMUSTintron_variant
7	1.02E+08 .	AC	A	alt_allele_	DEL	44	12	56	0.214	31	17	48	0.354	link	-	Xntrpc	c.1857+20-	ENSMUSTintron_variant
8	61940364 .	AT	A	non_homr	INS	94	29	123	0.236	90	78	168	0.464	link	-	Ddx60	c.71+20de-	ENSMUSTintron_variant
8	86510117 .	C	CCG	weak_evid	INS	6	0	6	0	6	4	10	0.4	link	-	Abcc12	c.3307-24i-	ENSMUSTintron_variant
9	3020229 .	CA	C	mapping_c	DEL	36	0	36	0	28	6	34	0.176	link	-	Gm10719	c.73delA p.Tr25fs	ENSMUSTframeshift_variant
9	3020229 .	CA	C	mapping_c	DEL	36	0	36	0	28	6	34	0.176	link	-	Gm26870	n.-2146de-	ENSMUSTupstream_gene_variant
9	3020229 .	CA	C	mapping_c	DEL	36	0	36	0	28	6	34	0.176	link	-	Gm10718	c.-3317del-	ENSMUSTupstream_gene_variant
9	3020229 .	CA	C	mapping_c	DEL	36	0	36	0	28	6	34	0.176	link	-	Gm10720	c.*3020de-	ENSMUSTdownstream_gene_variant
9	3020229 .	CA	C	mapping_c	DEL	36	0	36	0	28	6	34	0.176	link	-	Gm26870	n.3020230-	- intragenic_variant
9	21838684 .	TC	T	alt_allele_	DEL	52	14	66	0.212	49	23	72	0.319	link	-	Angptl8	c.*1598de-	ENSMUSTdownstream_gene_variant
9	21838684 .	TC	T	alt_allele_	DEL	52	14	66	0.212	49	23	72	0.319	link	-	Dock6	c.1637+66-	ENSMUSTintron_variant
9	31847061 rs2646210	TGG	T	weak_evid	DEL	33	2	35	0.057	20	10	30	0.333	link	-	Barx2	c.586-8_5i-	ENSMUSTsplice_region_variant+intron_variant
9	95637941 .	T	TC	non_homr	INS	104	3	107	0.028	64	33	97	0.34	link	-	Pcolce2	c.80+77du-	ENSMUSTintron_variant
9	95637941 .	T	TC	non_homr	INS	104	3	107	0.028	64	33	97	0.34	link	-	Gm16126	n.211+508-	ENSMUSTintron_variant
9	95637941 .	T	TC	non_homr	INS	104	3	107	0.028	64	33	97	0.34	link	-	Gm16127	n.149+175-	ENSMUSTintron_variant
9	1.11E+08 rs2199239	CTTTG	C	low_norm	DEL	1	0	1	0	12	2	14	0.143	link	-	Setd2	c.6031+27-	ENSMUSTintron_variant
X	7947088 .	AC	A	non_homr	DEL	61	13	74	0.176	57	29	86	0.337	link	-	Psmb6-ps	n.*3067de-	ENSMUSTdownstream_gene_variant
X	7947088 .	AC	A	non_homr	DEL	61	13	74	0.176	57	29	86	0.337	link	-	Hdac6	c.90+36de-	ENSMUSTintron_variant
X	1.01E+08 .	CAAAAT	C	too_few_s	DEL	6	0	6	0	1	2	3	0.667	link	-	Slc7a3	c.370+170-	ENSMUSTintron_variant
X	1.09E+08 .	TTTTG	T	PASS	DEL	95	0	95	0	110	6	116	0.052	link	-	Sh3bgrl	c.313-12_-i-	ENSMUSTintron_variant
GL456212	136195 .	T	TA	mapping_c	INS	24	0	24	0	29	3	32	0.094	link	-	AC168977	c.973+333-	ENSMUSTintron_variant
GL456212	136199 .	T	TA	mapping_c	INS	25	0	25	0	30	3	33	0.091	link	-	AC168977	c.973+329-	ENSMUSTintron_variant
1	1.32E+08 .	A	C	base_qual	SNV	197	5	202	0.025	204	11	215	0.051	link	-	Dstyk	c.17A>C p.Gln6Pro	ENSMUSTmissense_variant
1	1.72E+08 .	C	G	PASS	SNV	222	1	223	0.004	208	33	241	0.137	link	-	Atp1a2	c.1683G>p.Lys561A	ENSMUSTmissense_variant
1	1.75E+08 .	G	A	PASS	SNV	214	0	214	0	215	7	222	0.032	link	-	Fmn2	c.3796G>p.Asp1266	ENSMUSTmissense_variant
10	58223007 rs2493491	G	A	mapping_c	SNV	142	7	149	0.047	166	69	235	0.294	link	-	AW822075	c.1924C>p.Pro642S	ENSMUSTmissense_variant
10	58231613 .	C	T	weak_evid	SNV	418	11	429	0.026	753	16	769	0.021	link	-	Dux3	c.1063G>p.Asp355A	ENSMUSTmissense_variant
11	69589821 .	C	A	base_qual	SNV	144	5	149	0.034	172	16	188	0.085	link	-	Trp53	c.943C>A p.Gln315L	ENSMUSTmissense_variant
11	72536588 .	G	T	too_few_s	SNV	227	1	228	0.004	230	2	232	0.009	link	-	Spns3	c.875C>A p.Ala292A	ENSMUSTmissense_variant
11	1E+08 .	G	T	base_qual	SNV	254	0	254	0	208	11	219	0.05	link	-	Krt35	c.888C>A p.Asn296L	ENSMUSTmissense_variant
11	1.21E+08 .	A	C	base_qual	SNV	146	1	147	0.007	196	5	201	0.025	link	-	Arhgdia	c.346T>G p.Phe116V	ENSMUSTmissense_variant
12	21244864 .	G	A	weak_evid	SNV	167	0	167	0	151	3	154	0.019	link	-	Asap2	c.1735G>p.Ala579T	ENSMUSTmissense_variant
13	27774668 .	A	C	PASS	SNV	157	0	157	0	148	19	167	0.114	link	-	Prf1c1	c.377T>G p.Ile126S	ENSMUSTmissense_variant
13	53472652 .	A	C	base_qual	SNV	256	4	260	0.015	235	10	245	0.041	link	-	Msx2	c.59T>G p.Val20Gly	ENSMUSTmissense_variant
14	51413051 rs1133490	G	A	mapping_c	SNV	216	9	225	0.04	267	14	281	0.05	link	-	Vmn2r88	c.220G>A p.Glu74Lys	ENSMUSTmissense_variant
14	51457511 rs1132854	A	T	mapping_c	SNV	368	10	378	0.026	402	19	421	0.045	link	-	Vmn2r89	c.1447A>p.Ile483Le	ENSMUSTmissense_variant
14	63495853 .	A	C	base_qual	SNV	181	0	181	0	174	15	189	0.079	link	-	Tdh	c.488T>G p.Val163G	ENSMUSTmissense_variant
16	32753567 .	A	T	mapping_c	SNV	464	24	488	0.049	460	47	507	0.093	link	-	Muc4	c.3442A>p.Trp1148	ENSMUSTmissense_variant
17	15544089 rs5874052	T	G	PASS	SNV	428	5	433	0.012	442	17	459	0.037	link	-	Prdm9	c.2428A>(p.Lys181G)	ENSMUSTmissense_variant
18	77399061 .	G	A	weak_evid	SNV	208	0	208	0	237	4	241	0.017	link	-	Loxhd1	c.3841G>p.Gly1281	ENSMUSTmissense_variant
19	45021810 .	A	C	base_qual	SNV	185	0	185	0	183	18	201	0.09	link	-	Lzts2	c.382A>C p.Ile128Le	ENSMUSTmissense_variant
2	26351859 .	T	G	base_qual	SNV	242	12	254	0.047	212	17	229	0.074	link	-	Dnlz	c.154A>C p.Ser52Ar	ENSMUSTmissense_variant
2	26975765 .	A	C	base_qual	SNV	166	0	166	0	144	10	154	0.065	link	-	Adams13	c.331A>C p.Asn111F	ENSMUSTmissense_variant
2	28610030 .	T	G	base_qual	SNV	144	1	145	0.007	142	21	163	0.129	link	-	Gfi1b	c.1087A>(p.Lys363G)	ENSMUSTmissense_variant
2	33172464 .	G	A	weak_evid	SNV	264	1	265	0.004	279	4	283	0.014	link	-	Ralgps1	c.796C>T p.Arg266C	ENSMUSTmissense_variant
2	60252484 .	G	T	base_qual	SNV	115	4	119	0.034	119	7	126	0.056	link	-	Cd302	c.495C>A p.His165G	ENSMUSTmissense_variant
2	82991731 .	T	G	PASS	SNV	277	0	277	0	358	8	366	0.022	link	-	Fsfp2	c.1780T>p.Ile5936S	ENSMUSTmissense_variant
2	1.45E+08 .	T	C	weak_evid	SNV	242	1	243	0.004	252	4	256	0.016	link	-	Rbbp9	c.86A>G p.Lys29Ar	ENSMUSTmissense_variant
3	87922937 .	A	C	weak_evid	SNV	139	1	140	0.007	126	17	143	0.119	link	-	Mrlp24	c.386A>C p.Lys129T	ENSMUSTmissense_variant+splice_region_variant
3	1.25E+08 .	T	C	PASS	SNV	279	0	279	0	272	18	290	0.062	link	-	Ndst4	c.809T>C p.Leu270F	ENSMUSTmissense_variant
4	1.47E+08 rs1132667	T	A	mapping_c	SNV	94	14	108	0.13	134	33	167	0.198	link	-	Zfp991	c.67T>A p.Ser237H	ENSMUSTmissense_variant
5	1.37E+08 .	C	A	base_qual	SNV	185	0	185	0	178	6	184	0.033	link	-	Zan	c.631G>T p.Val211P	ENSMUSTmissense_variant+splice_region_variant
6	89870384 .	C	T	PASS	SNV	366	0	366	0	342	24	366	0.066	link	-	Vmn1r43	c.119G>A p.Gly40As	ENSMUSTmissense_variant
7	19395374 .	C	G	base_qual	SNV	148	2	150	0.013	144	12	156	0.077	link	-	Klc3	c.1225G>(p.Ala409P)	ENSMUSTmissense_variant
7	55058109 .	A	G	weak_evid	SNV	226	0	226	0	231	4	235	0.017	link	-	Luzp2	c.244A>G p.Arg82G	ENSMUSTmissense_variant
7	80505843 .	C	A	weak_evid	SNV	174	0	174	0	197	3	200	0.015	link	-	Blm	c.1087G>p.Ala363S	ENSMUSTmissense_variant
7	1.03E+08 .	A	G	PASS	SNV	310	0	310	0	278	28	306	0.092	link	-	Olfr573-ps	c.755T>C p.Ile252T	ENSMUSTmissense_variant
8	43625839 .	A	T	PASS	SNV	342	0	342	0	357	10	367	0.027	link	-	Gm5346	c.1347T>p.Phe449L	ENSMUSTmissense_variant
8	70808604 .	T	C	PASS	SNV	219	0	219	0	162	24	186	0.129	link	-	Il12rb1	c.53T>C p.Leu18Pr	ENSMUSTmissense_variant
8	95075208 .	T	G	base_qual	SNV	170	0	170	0	147	10	157	0.064	link	-	Drc7	c.2096T>(p.Leu699A)	ENSMUSTmissense_variant
8	1.25E+08 .	T	G	base_qual	SNV	197	0	197	0	203	14	217	0.065	link	-	Capn9	c.498T>G p.Asn166L	ENSMUSTmissense_variant
9	36936459 .	A	C	base_qual	SNV	204	0	204	0	168	10	178	0.056	link	-	Pknox2	c.261T>G p.Phe87Le	ENSMUSTmissense_variant
9	64909511 .	C	A	base_qual	SNV	102	4	106	0.038	93	5	98	0.051	link	-	Dennd4a	c.4657C>p.Leu1553	ENSMUSTmissense_variant
9	1.21E+08 .	A	T	PASS	SNV	243	0	243	0	219	6	225	0.027	link	-	Ulk4	c.2450T>p.Ile817As	ENSMUSTmissense_variant
X	53746977 .	A	G	PASS	SNV	111	0	111	0	86	6	92	0.065	link	-	1700013H	c.616	

1	85101243	rs1134636	T	G	no_reliabl	SNV	8	1	9	0.111	5	2	7	0.286	link	-	Gm10553	c.*708T>C-	ENSMUSTdownstream_gene_variant
1	85101243	rs1134636	T	G	no_reliabl	SNV	8	1	9	0.111	5	2	7	0.286	link	-	A530032D	c.33-549A-	ENSMUSTintron_variant
1	85101243	rs1134636	T	G	no_reliabl	SNV	8	1	9	0.111	5	2	7	0.286	link	-	C130026I2	n.8510124-	- intragenic_variant
1	85101295	rs1132311	C	T	weak_evid	SNV	10	1	11	0.091	6	3	9	0.333	link	-	A530040E	n.-4651C>-	ENSMUSTupstream_gene_variant
1	85101295	rs1132311	C	T	weak_evid	SNV	10	1	11	0.091	6	3	9	0.333	link	-	Gm10553	c.*760C>T-	ENSMUSTdownstream_gene_variant
1	85101295	rs1132311	C	T	weak_evid	SNV	10	1	11	0.091	6	3	9	0.333	link	-	A530032D	c.33-601G-	ENSMUSTintron_variant
1	85101295	rs1132311	C	T	weak_evid	SNV	10	1	11	0.091	6	3	9	0.333	link	-	C130026I2	n.8510129-	- intragenic_variant
1	85101317	rs1132624	G	T	no_reliabl	SNV	9	1	10	0.1	8	3	11	0.273	link	-	A530040E	n.-4629G>-	ENSMUSTupstream_gene_variant
1	85101317	rs1132624	G	T	no_reliabl	SNV	9	1	10	0.1	8	3	11	0.273	link	-	Gm10553	c.*782G>T-	ENSMUSTdownstream_gene_variant
1	85101317	rs1132624	G	T	no_reliabl	SNV	9	1	10	0.1	8	3	11	0.273	link	-	A530032D	c.33-623C-	ENSMUSTintron_variant
1	85101317	rs1132624	G	T	no_reliabl	SNV	9	1	10	0.1	8	3	11	0.273	link	-	C130026I2	n.8510131-	- intragenic_variant
1	85112207	rs1081203	T	C	PASS	SNV	60	1	61	0.016	106	9	115	0.078	link	-	A530032D	c.-2839A>-	ENSMUSTupstream_gene_variant
1	85112207	rs1081203	T	C	PASS	SNV	60	1	61	0.016	106	9	115	0.078	link	-	Gm16038	n.-3112T>-	ENSMUSTupstream_gene_variant
1	85112207	rs1081203	T	C	PASS	SNV	60	1	61	0.016	106	9	115	0.078	link	-	A530040E	n.897-244-	ENSMUSTintron_variant
1	85112207	rs1081203	T	C	PASS	SNV	60	1	61	0.016	106	9	115	0.078	link	-	C130026I2	n.8511220-	- intragenic_variant
1	85245179	rs1134097	C	A	too_few_s	SNV	11	0	11	0	6	2	8	0.25	link	-	Gm16028	n.-1672C>-	ENSMUSTupstream_gene_variant
1	85245179	rs1134097	C	A	too_few_s	SNV	11	0	11	0	6	2	8	0.25	link	-	C130026I2	c.*1758G>-	ENSMUSTdownstream_gene_variant
1	85245179	rs1134097	C	A	too_few_s	SNV	11	0	11	0	6	2	8	0.25	link	-	Gm2619	n.379+691-	ENSMUSTintron_variant
1	85245179	rs1134097	C	A	too_few_s	SNV	11	0	11	0	6	2	8	0.25	link	-	C130026I2	n.8524517-	- intragenic_variant
1	85254878	.	T	G	no_reliabl	SNV	17	0	17	0	33	7	40	0.175	link	-	C130026I2	c.452-302-	ENSMUSTintron_variant
1	85254878	.	T	G	no_reliabl	SNV	17	0	17	0	33	7	40	0.175	link	-	Gm16028	n.544-241-	ENSMUSTintron_variant
1	85254878	.	T	G	no_reliabl	SNV	17	0	17	0	33	7	40	0.175	link	-	Gm2619	n.379+594-	ENSMUSTintron_variant
1	85257109	rs1076836	A	G	no_reliabl	SNV	14	0	14	0	46	4	50	0.08	link	-	Gm16028	n.*1644A>-	ENSMUSTdownstream_gene_variant
1	85257109	rs1076836	A	G	no_reliabl	SNV	14	0	14	0	46	4	50	0.08	link	-	C130026I2	c.451+277-	ENSMUSTintron_variant
1	85257109	rs1076836	A	G	no_reliabl	SNV	14	0	14	0	46	4	50	0.08	link	-	Gm2619	n.379+572-	ENSMUSTintron_variant
1	85257150	.	G	T	no_reliabl	SNV	35	2	37	0.054	69	7	76	0.092	link	-	Gm16028	n.*1685G>-	ENSMUSTdownstream_gene_variant
1	85257150	.	G	T	no_reliabl	SNV	35	2	37	0.054	69	7	76	0.092	link	-	C130026I2	c.451+236-	ENSMUSTintron_variant
1	85257150	.	G	T	no_reliabl	SNV	35	2	37	0.054	69	7	76	0.092	link	-	Gm2619	n.379+572-	ENSMUSTintron_variant
1	85513536	rs2134620	A	G	mapping_c	SNV	36	3	39	0.077	44	14	58	0.241	link	-	Gm16092	n.192-190-	ENSMUSTintron_variant
1	85513536	rs2134620	A	G	mapping_c	SNV	36	3	39	0.077	44	14	58	0.241	link	-	Gm2427	n.782+275-	ENSMUSTintron_variant
1	85577467	.	A	T	mapping_c	SNV	43	1	44	0.023	71	7	78	0.09	link	-	G530012D	c.*172A>T-	ENSMUSTdownstream_gene_variant
1	85577467	.	A	T	mapping_c	SNV	43	1	44	0.023	71	7	78	0.09	link	-	Sp110	c.1285-12-	ENSMUSTintron_variant
1	85630351	rs1131852	A	G	non_homr	SNV	59	4	63	0.063	74	9	83	0.108	link	-	Sp140	c.725-109-	ENSMUSTintron_variant
1	85638287	.	G	T	too_few_s	SNV	12	0	12	0	10	2	12	0.167	link	-	Gm17017	n.*2935C>-	ENSMUSTdownstream_gene_variant
1	85638287	.	G	T	too_few_s	SNV	12	0	12	0	10	2	12	0.167	link	-	Sp140	c.1062+42-	ENSMUSTintron_variant
1	85638288	.	G	T	too_few_s	SNV	11	0	11	0	10	2	12	0.167	link	-	Gm17017	n.*2934C>-	ENSMUSTdownstream_gene_variant
1	85638288	.	G	T	too_few_s	SNV	11	0	11	0	10	2	12	0.167	link	-	Sp140	c.1062+42-	ENSMUSTintron_variant
1	88217844	.	C	T	weak_evid	SNV	4	0	4	0	10	4	14	0.286	link	-	Ugt1a10	c.1296-28-	ENSMUSTintron_variant
1	88217844	.	C	T	weak_evid	SNV	4	0	4	0	10	4	14	0.286	link	-	Ugt1a9	c.1290-28-	ENSMUSTintron_variant
1	88217844	.	C	T	weak_evid	SNV	4	0	4	0	10	4	14	0.286	link	-	Ugt1a7c	c.1299-28-	ENSMUSTintron_variant
1	88217844	.	C	T	weak_evid	SNV	4	0	4	0	10	4	14	0.286	link	-	Ugt1a6a	c.1299-28-	ENSMUSTintron_variant
1	88217844	.	C	T	weak_evid	SNV	4	0	4	0	10	4	14	0.286	link	-	Ugt1a5	c.1293-28-	ENSMUSTintron_variant
1	88217844	.	C	T	weak_evid	SNV	4	0	4	0	10	4	14	0.286	link	-	Ugt1a2	c.1305-28-	ENSMUSTintron_variant
1	88217844	.	C	T	weak_evid	SNV	4	0	4	0	10	4	14	0.286	link	-	Ugt1a1	c.1311-28-	ENSMUSTintron_variant
1	88217844	.	C	T	weak_evid	SNV	4	0	4	0	10	4	14	0.286	link	-	Ugt1a6b	c.1299-28-	ENSMUSTintron_variant
1	88217844	.	C	T	weak_evid	SNV	4	0	4	0	10	4	14	0.286	link	-	Gm20528	n.274+437-	ENSMUSTintron_variant
1	88217844	.	C	T	weak_evid	SNV	4	0	4	0	10	4	14	0.286	link	-	Ugt1a8	c.1296-28-	ENSMUSTintron_variant
1	88235821	rs4788929	G	A	too_few_s	SNV	5	0	5	0	12	2	14	0.143	link	-	Mroh2a	c.1246+33-	ENSMUSTintron_variant
1	88238261	.	C	T	PASS	SNV	8	0	8	0	27	8	35	0.229	link	-	Mroh2a	c.1554+30-	ENSMUSTintron_variant
1	88239253	rs5044606	T	C	weak_evid	SNV	30	1	31	0.032	59	14	73	0.192	link	-	Mroh2a	c.1702+21-	ENSMUSTintron_variant
1	88244432	.	G	T	too_few_s	SNV	6	0	6	0	12	2	14	0.143	link	-	Mroh2a	c.2442+34-	ENSMUSTintron_variant
1	88245479	rs4664378	C	G	weak_evid	SNV	7	0	7	0	5	4	9	0.444	link	-	Mroh2a	c.2565+41-	ENSMUSTintron_variant
1	88246818	.	A	G	PASS	SNV	10	0	10	0	24	6	30	0.2	link	-	Mroh2a	c.2646-31-	ENSMUSTintron_variant
1	88251772	rs5173056	A	T	too_few_s	SNV	11	0	11	0	12	2	14	0.143	link	-	Mroh2a	c.3351+37-	ENSMUSTintron_variant
1	88254510	rs4586156	C	T	weak_evid	SNV	5	0	5	0	7	5	12	0.417	link	-	Mroh2a	c.3507-34-	ENSMUSTintron_variant
1	88264745	rs4768619	G	A	too_few_s	SNV	4	0	4	0	6	2	8	0.25	link	-	Hjurp	c.*436C>T-	ENSMUST3_prime_UTR_variant
1	88264745	rs4768619	G	A	too_few_s	SNV	4	0	4	0	6	2	8	0.25	link	-	Mroh2a	c.*4719G>-	ENSMUSTdownstream_gene_variant
1	88264748	rs4687299	T	C	too_few_s	SNV	4	0	4	0	5	2	7	0.286	link	-	Hjurp	c.*433A>C-	ENSMUST3_prime_UTR_variant
1	88264748	rs4687299	T	C	too_few_s	SNV	4	0	4	0	5	2	7	0.286	link	-	Mroh2a	c.*4722T>-	ENSMUSTdownstream_gene_variant
1	88264760	rs5178294	C	T	too_few_s	SNV	4	0	4	0	7	2	9	0.222	link	-	Hjurp	c.*421G>A-	ENSMUST3_prime_UTR_variant
1	88264760	rs5178294	C	T	too_few_s	SNV	4	0	4	0	7	2	9	0.222	link	-	Mroh2a	c.*4734C>-	ENSMUSTdownstream_gene_variant
1	88269884	rs1134164	C	G	weak_evid	SNV	4	0	4	0	15	5	20	0.25	link	-	Hjurp	c.354+318-	ENSMUSTintron_variant
1	91205386	.	T	G	base_qual	SNV	132	2	134	0.015	126	12	138	0.087	link	-	Ramp1	c.191+847-	ENSMUSTintron_variant
1	91250582	.	T	G	base_qual	SNV	25	0	25	0	24	6	30	0.2	link	-	Ube2f	c.-85+145-	ENSMUSTintron_variant
1	91526128	.	A	C	base_qual	SNV	86	5	91	0.055	84	10	94	0.106	link	-	Traf3ip1	c.1799+26-	ENSMUSTintron_variant
1	91964655	.	T	A	base_qual	SNV	40	3	43	0.07	48	12	60	0.2	link	-	Hdac4	c.2241+12-	ENSMUSTintron_variant
1	93135218	.	A	T	PASS	SNV	73	0	73	0	73	13	86	0.151	link	-	Agxt	c.-76A>T-	ENSMUSTupstream_gene_variant
1	93135218	.	A	T	PASS	SNV	73	0	73	0	73	13	86	0.151	link	-	-	n.9313521-	- intergenic_region
1	96839375	.	G	T	base_qual	SNV	73	4	77	0.052	58	6	64	0.094	link	-	Slco4c1	c.1007-90-	ENSMUSTintron_variant
1	1.19E+08	.	A	C	base_qual	SNV	16	2	18	0.111	20	9	29	0.31	link	-	Inhbb	c.460+153-	ENSMUSTintron_variant
1	1.28E+08	.	A	C	base_qual	SNV	28	4	32	0.125	23	6	29	0.207	link	-	Gm38248	n.-3204T>-	ENSMUSTupstream_gene_variant
1	1.28E+08	.	A	C	base_qual	SNV	28	4	32	0.125	23	6	29	0.207	link	-	Zranb3	c.1536+10-	ENSMUSTintron_variant
1	1.31E+08	.	T	G	base_qual	SNV	10	0	10	0	6	2	8	0.25	link	-	Gm29427	c.-3471A>-	ENSMUSTupstream_gene_variant
1	1.31E+08	.	T	G	base_qual	SNV	10	0	10	0	6	2	8	0.25	link	-	Pfkfb2	c.-3471A>-	ENSMUSTupstream_gene_variant
1	1.31E+08	.	T	G	base_qual	SNV	10	0	10	0	6	2	8	0.25	link	-	Yod1	c.328+216-	ENSMUSTintron_variant
1	1.31E+08	.	T	G	base_qual	SNV	10	0	10	0	6	2	8	0.25	link	-	Pfkfb2	n.1307180-	- intragenic_variant
1	1.32E+08	.	G	T	base_qual	SNV	55	1	56	0.018	62	7	69	0.101	link	-	Rab7b	c.54-40G>-	ENSMUSTintron_variant
1	1.32E+08	.	T	G	too_few_s	SNV	8	1	9	0.111	15	2	17	0.118	link	-	Rbbp5	c.1166+25-	ENSMUSTintron_variant
1	1.51E+08	.	A	T	PASS	SNV	174	0	174										

10	29313900 .	A	C	base_qual SNV	20	0	20	0	42	8	50	0.16	link	-	Echdc1	c.67+167A-	ENSMUSTintron_variant	
10	41694124 .	G	A	too_few_s SNV	7	0	7	0	9	2	11	0.182	link	-	Gm29096	c.137+227-	ENSMUSTintron_variant	
10	41887406 .	T	G	base_qual SNV	30	5	35	0.143	30	6	36	0.167	link	-	Sesn1	c.280-663-	ENSMUSTintron_variant	
10	45107510 .	T	G	base_qual SNV	144	0	144	0	148	19	167	0.114	link	-	Prep	c.718-262-	ENSMUSTintron_variant	
10	53596698 .	A	C	base_qual SNV	29	2	31	0.065	32	3	35	0.086	link	-	Asf1a	c.-492A>C-	ENSMUSTupstream_gene_variant	
10	53596698 .	A	C	base_qual SNV	29	2	31	0.065	32	3	35	0.086	link	-	Mcm9	c.1618+14-	ENSMUSTintron_variant	
10	58222956 rs2310783 A	G	G	mapping_c SNV	70	7	77	0.091	83	72	155	0.465	link	-	AW82207c	c.*16T>C-	ENSMUSTdownstream_gene_variant	
10	58222956 rs2310783 A	G	G	mapping_c SNV	70	7	77	0.091	83	72	155	0.465	link	-	Gm10807	n.*4901T>-	ENSMUSTdownstream_gene_variant	
10	58222956 rs2310783 A	G	G	mapping_c SNV	70	7	77	0.091	83	72	155	0.465	link	-	-	n.5822295-	-	intergenic_region
10	58223007 rs2493491 G	A	A	mapping_c SNV	142	7	149	0.047	166	69	235	0.294	link	-	Gm10807	n.*4850C>-	ENSMUSTdownstream_gene_variant	
10	58231613 .	C	T	weak_evid SNV	418	11	429	0.026	753	16	769	0.021	link	-	Gm10807	n.-2962G>-	ENSMUSTupstream_gene_variant	
10	58231613 .	C	T	weak_evid SNV	418	11	429	0.026	753	16	769	0.021	link	-	Gm4981	c.*3902G>-	ENSMUSTdownstream_gene_variant	
10	62393633 .	A	C	base_qual SNV	78	6	84	0.071	58	6	64	0.094	link	-	Hkdc1	c.2210+54-	ENSMUSTintron_variant	
10	76177946 .	T	C	weak_evid SNV	21	0	21	0	28	3	31	0.097	link	-	Slc5a4a	c.1130-14-	ENSMUSTintron_variant	
10	77038605 .	T	G	base_qual SNV	95	3	98	0.031	83	12	95	0.126	link	-	Slc19a1	c.183+26T-	ENSMUSTintron_variant	
10	79914246 .	A	C	non_homr SNV	125	4	129	0.031	118	5	123	0.041	link	-	Kiss1r	c.-4428A>-	ENSMUSTupstream_gene_variant	
10	79914246 .	A	C	non_homr SNV	125	4	129	0.031	118	5	123	0.041	link	-	Gm24019	n.*4945A>-	ENSMUSTdownstream_gene_variant	
10	79914246 .	A	C	non_homr SNV	125	4	129	0.031	118	5	123	0.041	link	-	Gm26602	c.*3106A>-	ENSMUSTdownstream_gene_variant	
10	79914246 .	A	C	non_homr SNV	125	4	129	0.031	118	5	123	0.041	link	-	R3hdm4	c.63-535T-	ENSMUSTintron_variant	
10	80055131 .	T	G	base_qual SNV	118	4	122	0.033	111	9	120	0.075	link	-	Sbno2	c.*2285A>-	ENSMUSTdownstream_gene_variant	
10	80055131 .	T	G	base_qual SNV	118	4	122	0.033	111	9	120	0.075	link	-	Gpx4	c.644+12T-	ENSMUSTintron_variant	
10	81577631 .	T	G	base_qual SNV	248	0	248	0	195	18	213	0.085	link	-	Gm15917	n.-1691A>-	ENSMUSTupstream_gene_variant	
10	89088072 rs5273694 G	A	A	base_qual SNV	31	3	34	0.088	27	10	37	0.27	link	-	Ano4	c.557+12T-	ENSMUSTintron_variant	
10	94124689 .	A	G	too_few_s SNV	4	0	4	0	1	0	1	0	link	-	Fgd6	c.3175-20-	ENSMUSTintron_variant	
10	1.11E+08 .	A	C	base_qual SNV	116	8	124	0.065	82	11	93	0.118	link	-	Zdhhc17	c.-38T>G-	ENSMUSTupstream_gene_variant	
10	1.11E+08 .	A	C	base_qual SNV	116	8	124	0.065	82	11	93	0.118	link	-	-	n.1110100-	-	intergenic_region
10	1.12E+08 .	G	A	PASS SNV	12	0	12	0	15	4	19	0.211	link	-	Caps2	c.837-200-	ENSMUSTintron_variant	
10	1.16E+08 .	A	C	base_qual SNV	59	0	59	0	84	9	93	0.097	link	-	Tspan8	c.655-114-	ENSMUSTintron_variant	
10	1.23E+08 .	C	A	base_qual SNV	63	6	69	0.087	63	14	77	0.182	link	-	Usp15	c.2764-63-	ENSMUSTintron_variant	
10	1.27E+08 .	T	G	base_qual SNV	30	5	35	0.143	40	19	59	0.322	link	-	R3hdm2	c.810+112-	ENSMUSTintron_variant	
10	1.28E+08 .	T	G	base_qual SNV	25	4	29	0.138	18	5	23	0.217	link	-	Nxph4	c.-152A>C-	ENSMUSTupstream_gene_variant	
10	1.28E+08 .	T	G	base_qual SNV	25	4	29	0.138	18	5	23	0.217	link	-	Lrp1	c.*4366A>-	ENSMUSTdownstream_gene_variant	
10	1.28E+08 .	T	G	base_qual SNV	25	4	29	0.138	18	5	23	0.217	link	-	-	n.1275345-	-	intergenic_region
10	1.28E+08 .	T	G	base_qual SNV	217	15	232	0.065	167	12	179	0.067	link	-	Gm26308	n.*551A>C-	ENSMUSTdownstream_gene_variant	
10	1.28E+08 .	T	G	base_qual SNV	217	15	232	0.065	167	12	179	0.067	link	-	Ankrd52	c.277>3T-	ENSMUSTintron_variant	
10	1.29E+08 .	A	T	alt_allele_ SNV	10	1	11	0.091	9	5	14	0.357	link	-	Ilkzf4	c.-187>1A-	ENSMUSTupstream_gene_variant	
10	1.29E+08 .	A	T	alt_allele_ SNV	10	1	11	0.091	9	5	14	0.357	link	-	Gm26876	n.37+74A>-	ENSMUSTintron_variant	
11	5799405 .	G	A	weak_evid SNV	85	0	85	0	118	3	121	0.025	link	-	Pgam2	c.*2268C>-	ENSMUSTdownstream_gene_variant	
11	5799405 .	G	A	weak_evid SNV	85	0	85	0	118	3	121	0.025	link	-	Dbnl	c.1171+66-	ENSMUSTintron_variant	
11	7208627 .	T	G	base_qual SNV	30	0	30	0	56	7	63	0.111	link	-	Igfbp3	c.754-119-	ENSMUSTintron_variant	
11	8886901 .	T	G	base_qual SNV	22	0	22	0	31	4	35	0.114	link	-	Gm11991	n.-1605A>-	ENSMUSTupstream_gene_variant	
11	8886901 .	T	G	base_qual SNV	22	0	22	0	31	4	35	0.114	link	-	Pkd1l1	c.4007-13-	ENSMUSTintron_variant	
11	28388767 .	T	G	base_qual SNV	62	0	62	0	69	18	87	0.207	link	-	Ccdc85a	c.*92A>C-	ENSMUST3_prime_UTR_variant	
11	50638391 .	T	G	weak_evid SNV	11	1	12	0.083	11	3	14	0.214	link	-	Adams2	c.532-296-	ENSMUSTintron_variant	
11	51650758 .	A	C	base_qual SNV	4	0	4	0	10	3	13	0.231	link	-	N4bp3	c.-111T>G-	ENSMUST5_prime_UTR_variant	
11	51650758 .	A	C	base_qual SNV	4	0	4	0	10	3	13	0.231	link	-	D930048Nc	c.-226A>C-	ENSMUSTupstream_gene_variant	
11	54324274 .	G	T	base_qual SNV	11	0	11	0	14	6	20	0.3	link	-	Acs16	c.450+220-	ENSMUSTintron_variant	
11	58177489 .	C	T	too_few_s SNV	10	0	10	0	22	2	24	0.083	link	-	Mrpl22	c.409+203-	ENSMUSTintron_variant	
11	60753987 .	A	C	base_qual SNV	180	0	180	0	179	18	197	0.091	link	-	Top3a	c.916-26T-	ENSMUSTintron_variant	
11	63889860 .	C	A	base_qual SNV	19	4	23	0.174	43	15	58	0.259	link	-	Hs3st3b1	c.555-115-	ENSMUSTintron_variant	
11	63889864 rs2502669 C	A	A	base_qual SNV	20	1	21	0.048	40	15	55	0.273	link	-	Hs3st3b1	c.555-119-	ENSMUSTintron_variant	
11	65041310 .	A	C	base_qual SNV	20	0	20	0	27	6	33	0.182	link	-	Gm12294	n.-3769T>-	ENSMUSTupstream_gene_variant	
11	65041310 .	A	C	base_qual SNV	20	0	20	0	27	6	33	0.182	link	-	Arhgap44	c.651+132-	ENSMUSTintron_variant	
11	72155583 .	A	C	base_qual SNV	18	1	19	0.053	19	8	27	0.296	link	-	4933427D	c.2763-14-	ENSMUSTintron_variant	
11	74925784 .	T	G	alt_allele_ SNV	41	10	51	0.196	31	21	52	0.404	link	-	Srr	c.-396A>C-	ENSMUST5_prime_UTR_variant	
11	74925784 .	T	G	alt_allele_ SNV	41	10	51	0.196	31	21	52	0.404	link	-	Smg6	c.-132T>C-	ENSMUSTupstream_gene_variant	
11	74925799 .	A	C	base_qual SNV	62	6	68	0.088	40	18	58	0.31	link	-	Srr	c.-12670T-	ENSMUSTupstream_gene_variant	
11	74925799 .	A	C	base_qual SNV	62	6	68	0.088	40	18	58	0.31	link	-	Smg6	c.-117A>C-	ENSMUSTupstream_gene_variant	
11	74925799 .	A	C	base_qual SNV	62	6	68	0.088	40	18	58	0.31	link	-	Srr	n.7492579-	-	intragenic_variant
11	75679832 .	G	A	too_few_s SNV	16	0	16	0	19	2	21	0.095	link	-	Crk	c.241+168-	ENSMUSTintron_variant	
11	76809031 .	C	A	base_qual SNV	14	0	14	0	26	6	32	0.188	link	-	Cpd	c.1847-15-	ENSMUSTintron_variant	
11	80881753 .	T	G	base_qual SNV	45	1	46	0.022	32	5	37	0.135	link	-	Asic2	c.1522-72-	ENSMUSTintron_variant	
11	87737376 .	G	A	too_few_s SNV	8	0	8	0	10	2	12	0.167	link	-	Supt4a	c.-224G>A-	ENSMUSTupstream_gene_variant	
11	87737376 .	G	A	too_few_s SNV	8	0	8	0	10	2	12	0.167	link	-	Rnf43	c.*317TG>-	ENSMUSTdownstream_gene_variant	
11	87737376 .	G	A	too_few_s SNV	8	0	8	0	10	2	12	0.167	link	-	-	n.8773737-	-	intergenic_region
11	95283831 .	G	T	too_few_s SNV	9	0	9	0	15	2	17	0.118	link	-	Kat7	c.1161+19-	ENSMUSTintron_variant	
11	96345559 .	T	G	base_qual SNV	216	9	225	0.04	208	12	220	0.055	link	-	Gm11536	n.-3451A>-	ENSMUSTupstream_gene_variant	
11	96345559 .	T	G	base_qual SNV	216	9	225	0.04	208	12	220	0.055	link	-	Hoxb3os	n.2237A>C-	ENSMUSTnon_coding_transcript_exon_variant	
11	96345574 .	T	G	base_qual SNV	232	14	246	0.057	222	16	238	0.067	link	-	Gm11536	n.-3466A>-	ENSMUSTupstream_gene_variant	
11	96345574 .	T	G	base_qual SNV	232	14	246	0.057	222	16	238	0.067	link	-	Hoxb3os	n.2222A>C-	ENSMUSTnon_coding_transcript_exon_variant	
11	97575108 .	C	G	base_qual SNV	39	2	41	0.049	36	7	43	0.163	link	-	Srcin1	c.-119G>C-	ENSMUST5_prime_UTR_variant	
11	1E+08 .	C	A	too_few_s SNV	10	0	10	0	20	2	22	0.091	link	-	Krt17	c.-203G>T-	ENSMUSTupstream_gene_variant	
11	1E+08 .	C	A	too_few_s SNV	10	0	10	0	20	2	22	0.091	link	-	Krt42	c.*1902G>-	ENSMUSTdownstream_gene_variant	
11	1E+08 .	C	A	too_few_s SNV	10	0	10	0	20	2	22	0.091	link	-	-	n.1002611-	-	intergenic_region
11	1E+08 .	G	A	PASS SNV	278	0	278	0	242	38	280	0.136	link	-	Krt42	c.545+13C-	ENSMUSTintron_variant	
11	1E+08 .	T	G	alt_allele_ SNV	23	3	26	0.115	26	4	30	0.133	link	-	P3h4	c.-99A>C-	ENSMUST5_prime_UTR_variant	
11	1E+08 .	T	G	alt_allele_ SNV	23	3	26	0.115	26	4	30	0.133	link	-	Fkbp10	c.-1029T>-	ENSMUSTupstream_gene_variant	
11	1.02E+08 .	T	A	base_qual SNV	11	1	12	0.083	13	12	25	0.48	link	-	Hdac5	c.1911+13-	ENSMUSTintron_variant	
11	1.06E+08 .	A	C	base_qual SNV	59	7	66	0.106	49	9	58	0.155	link	-	Map3k3	c.-134A>C-	ENSMUST5_prime_UTR_variant	
11	1.1E+08 .	G	T	alt_allele_ SNV	18	3	21	0.143	23	12	35	0.343	link	-	Abca5	c.4416-11-	ENSMUSTintron_variant	
11	1.14E+08 .	A	C	weak_evid SNV	21	0	21	0	23	3	26	0.115	link	-	Sdk2	c.2983+11-	ENSMUSTintron_variant	
11	1.16E+08 .	G	C	base_qual SNV	14	0	14	0	17	2	19	0.105	link	-	Itgb4	c.*4328G>-	ENSMUSTdownstream_gene_variant	
11	1.16E+08 .	G	C	base_qual SNV	14	0	14	0	17	2	1							

12	31928799 .	G	T	alt_allele_SNV	30	5	35	0.143	33	5	38	0.132	link	-	Cog5	c.*32+300-	ENSMUSTintron_variant
12	31928799 .	G	T	alt_allele_SNV	30	5	35	0.143	33	5	38	0.132	link	-	Hbp1	c.1422-741-	ENSMUSTintron_variant
12	75176326 .	A	C	read_positSNV	12	1	13	0.077	12	2	14	0.143	link	-	Kcnh5	c.73+1307-	ENSMUSTintron_variant
12	76214301 .	C	A	base_qual SNV	35	2	37	0.054	36	6	42	0.143	link	-	Tex21	c.960+112-	ENSMUSTintron_variant
12	87336286 .	A	C	base_qual SNV	28	0	28	0	33	8	41	0.195	link	-	Gm26764	n.*631A>-C-	ENSMUSTdownstream_gene_variant
12	87336286 .	A	C	base_qual SNV	28	0	28	0	33	8	41	0.195	link	-	Sptlc2	c.1171-121-	ENSMUSTintron_variant
12	98231556 .	G	T	base_qual SNV	97	3	100	0.03	88	8	96	0.083	link	-	Galc	c.909-16C-	ENSMUSTintron_variant
12	98784796 .	A	C	base_qual SNV	28	2	30	0.067	31	8	39	0.205	link	-	Emf5	c.*5554T>-	ENSMUSTdownstream_gene_variant
12	98784796 .	A	C	base_qual SNV	28	2	30	0.067	31	8	39	0.205	link	-	Zc3h14	c.1869-121-	ENSMUSTintron_variant
12	1.09E+08 .	A	C	base_qual SNV	27	0	27	0	34	6	40	0.15	link	-	Wdr25	c.1075-141-	ENSMUSTintron_variant
12	1.11E+08 .	A	C	too_few_s SNV	4	0	4	0	14	2	16	0.125	link	-	Cdc42bbp	c.3312+23-	ENSMUSTintron_variant
12	1.12E+08 .	T	G	base_qual SNV	93	0	93	0	84	8	92	0.087	link	-	Klc1	c.-17500T-	ENSMUSTupstream_gene_variant
12	1.12E+08 .	T	G	base_qual SNV	93	0	93	0	84	8	92	0.087	link	-	Apopt1	c.569-144'-	ENSMUSTintron_variant
12	1.12E+08 .	T	G	base_qual SNV	56	0	56	0	36	17	53	0.321	link	-	Klc1	c.1651-131-	ENSMUSTintron_variant
12	1.12E+08 .	G	A	weak_evid SNV	71	0	71	0	84	3	87	0.034	link	-	Ppp1r13b	c.631+75C-	ENSMUSTintron_variant
13	3932598 .	T	G	base_qual SNV	27	6	33	0.182	22	7	29	0.241	link	-	Tubal3	c.397-20T-	ENSMUSTintron_variant
13	14248555 .	T	G	PASS SNV	46	0	46	0	32	18	50	0.36	link	-	Hecw1	c.4014-111-	ENSMUSTintron_variant
13	16027182 .	C	A	base_qual SNV	52	1	53	0.019	54	7	61	0.115	link	-	Inhba	c.*53C>A-	ENSMUST3_prime_UTR_variant
13	21423674 .	A	C	base_qual SNV	50	2	52	0.038	50	3	53	0.057	link	-	Pgbd1	c.399-50T-	ENSMUSTintron_variant
13	33038220 .	A	C	base_qual SNV	61	0	61	0	55	11	66	0.167	link	-	Serpinb9b	c.723+93A-	ENSMUSTintron_variant
13	49702795 .	T	C	too_few_s SNV	6	0	6	0	18	2	20	0.1	link	-	lars	c.894+247-	ENSMUSTintron_variant
13	59586394 .	G	C	base_qual SNV	29	6	35	0.171	26	8	34	0.235	link	-	Naa35	c.124+113-	ENSMUSTintron_variant
13	63513522 .	A	C	alt_allele_SNV	25	2	27	0.074	19	3	22	0.136	link	-	Ptch1	c.3762+39-	ENSMUSTintron_variant
13	68447828 rs5847705	A	G	mapping_cSNV	155	3	158	0.019	146	7	153	0.046	link	-	-	n.6844782-	- intergenic_region
13	73982529 .	T	G	base_qual SNV	52	0	52	0	63	22	85	0.259	link	-	Zdhc11	c.794-68T-	ENSMUSTintron_variant
13	95961104 .	C	T	too_few_s SNV	9	0	9	0	12	2	14	0.143	link	-	Sv2c	c.*176G>-J-	ENSMUST3_prime_UTR_variant
13	96516487 .	A	C	base_qual SNV	24	6	30	0.2	43	8	51	0.157	link	-	Polk	c.252+152-	ENSMUSTintron_variant
13	98206151 .	A	C	base_qual SNV	5	0	5	0	4	3	7	0.429	link	-	Arhgef28	c.-90T>G-	ENSMUST5_prime_UTR_variant
13	1E+08 .	C	G	non_homrSNV	20	0	20	0	36	6	42	0.143	link	-	Naip2	c.802+137-	ENSMUSTintron_variant
13	1.04E+08 .	C	A	base_qual SNV	16	2	18	0.111	28	7	35	0.2	link	-	Ppwd1	c.*117G>1-	ENSMUST3_prime_UTR_variant
13	1.04E+08 .	C	A	base_qual SNV	16	2	18	0.111	28	7	35	0.2	link	-	Trim23	c.*3977C>-	ENSMUSTdownstream_gene_variant
14	20566211 .	C	A	base_qual SNV	16	0	16	0	19	5	24	0.208	link	-	18100620	n.259+116-	ENSMUSTintron_variant
14	20566211 .	C	A	base_qual SNV	16	0	16	0	19	5	24	0.208	link	-	Usp54	c.2189-141-	ENSMUSTintron_variant
14	20566217 .	A	T	base_qual SNV	13	1	14	0.071	16	5	21	0.238	link	-	18100620	n.259+117-	ENSMUSTintron_variant
14	20566217 .	A	T	base_qual SNV	13	1	14	0.071	16	5	21	0.238	link	-	Usp54	c.2189-151-	ENSMUSTintron_variant
14	20566219 .	G	T	base_qual SNV	13	1	14	0.071	15	6	21	0.286	link	-	18100620	n.259+117-	ENSMUSTintron_variant
14	20566219 .	G	T	base_qual SNV	13	1	14	0.071	15	6	21	0.286	link	-	Usp54	c.2189-151-	ENSMUSTintron_variant
14	20929306 .	A	C	weak_evid SNV	4	0	4	0	7	3	10	0.3	link	-	Vcl	c.-215A>-C-	ENSMUSTupstream_gene_variant
14	20929306 .	A	C	weak_evid SNV	4	0	4	0	7	3	10	0.3	link	-	-	n.2092930-	- intergenic_region
14	27335992 .	A	C	base_qual SNV	14	0	14	0	27	4	31	0.129	link	-	Arhgef3	c.115-2671-	ENSMUSTintron_variant
14	49052456 .	G	T	base_qual SNV	75	4	79	0.051	115	5	120	0.042	link	-	Exoc5	c.28-64C>-	ENSMUSTintron_variant
14	51413041 rs1132076	T	A	mapping_cSNV	195	9	204	0.044	248	14	262	0.053	link	-	Gm7247	c.254+475-	ENSMUSTintron_variant
14	51413041 rs1132076	T	A	mapping_cSNV	195	9	204	0.044	248	14	262	0.053	link	-	Vmn2r-ps.-n.5141304-	- intragenic_variant	
14	51413051 rs1133490	G	A	mapping_cSNV	216	9	225	0.04	267	14	281	0.05	link	-	Gm7247	c.254+475-	ENSMUSTintron_variant
14	51413051 rs1133490	G	A	mapping_cSNV	216	9	225	0.04	267	14	281	0.05	link	-	Vmn2r-ps.-n.5141305-	- intragenic_variant	
14	51457511 rs1132854	A	T	mapping_cSNV	368	10	378	0.026	402	19	421	0.045	link	-	Gm7247	c.255-6431-	ENSMUSTintron_variant
14	54894251 .	T	G	base_qual SNV	238	8	246	0.033	245	14	259	0.054	link	-	Gm20521	c.433-597-	ENSMUSTintron_variant
14	63495853 .	A	C	base_qual SNV	181	0	181	0	174	15	189	0.079	link	-	Gm17232	n.72-1750-	ENSMUSTintron_variant
14	65593099 .	A	C	base_qual SNV	62	1	63	0.016	75	13	88	0.148	link	-	Elp3	c.-99T>G-	ENSMUST5_prime_UTR_variant
14	65731253 .	A	C	base_qual SNV	37	2	39	0.051	39	9	48	0.188	link	-	Scara5	c.916+58A-	ENSMUSTintron_variant
14	66077618 .	T	A	base_qual SNV	107	13	120	0.108	98	11	109	0.101	link	-	Adam2	c.73-32A>-	ENSMUSTintron_variant
14	66637452 .	A	C	weak_evid SNV	12	2	14	0.143	17	4	21	0.19	link	-	Adra1a	c.-126A>-C-	ENSMUST5_prime_UTR_variant
14	67822520 .	T	G	base_qual SNV	173	0	173	0	154	31	185	0.168	link	-	Dock5	c.1443+26-	ENSMUSTintron_variant
14	75906760 .	A	C	base_qual SNV	118	2	120	0.017	135	21	156	0.135	link	-	Gtf2i2	c.630+23T-	ENSMUSTintron_variant
14	96382051 .	G	T	base_qual SNV	33	2	35	0.057	55	4	59	0.068	link	-	Klhl1	c.507-98C-	ENSMUSTintron_variant
14	1.03E+08 .	G	T	base_qual SNV	70	5	75	0.067	84	10	94	0.106	link	-	Mycbp2	c.1571-101-	ENSMUSTintron_variant
14	1.18E+08 .	T	G	base_qual SNV	77	4	81	0.049	71	10	81	0.123	link	-	Mir6239	n.*2415A>-	ENSMUSTdownstream_gene_variant
14	1.18E+08 .	T	G	base_qual SNV	77	4	81	0.049	71	10	81	0.123	link	-	Gpc6	c.1319+54-	ENSMUSTintron_variant
15	3282630 .	G	A	weak_evid SNV	12	0	12	0	33	3	36	0.083	link	-	Sepp1	c.*2920G>-	ENSMUSTdownstream_gene_variant
15	3282630 .	G	A	weak_evid SNV	12	0	12	0	33	3	36	0.083	link	-	Ccdc152	c.558+188-	ENSMUSTintron_variant
15	4101307 .	C	A	base_qual SNV	61	5	66	0.076	58	12	70	0.171	link	-	Oxct1	c.1172+10-	ENSMUSTintron_variant
15	8137640 .	A	G	too_few_s SNV	5	0	5	0	12	2	14	0.143	link	-	Nup155	c.2092-211-	ENSMUSTintron_variant
15	8518285 .	C	A	base_qual SNV	544	7	551	0.013	493	18	511	0.035	link	-	Gm2310	c.*398G>1-	ENSMUSTdownstream_gene_variant
15	8518285 .	C	A	base_qual SNV	544	7	551	0.013	493	18	511	0.035	link	-	-	n.8518285-	- intergenic_region
15	10325780 .	T	G	base_qual SNV	73	0	73	0	83	16	99	0.162	link	-	Prlr	c.671-87T-	ENSMUSTintron_variant
15	10325780 .	T	G	base_qual SNV	73	0	73	0	83	16	99	0.162	link	-	Gm21973	c.32-87T>-	ENSMUSTintron_variant
15	13041504 .	A	C	base_qual SNV	126	3	129	0.023	108	36	144	0.25	link	-	Cdh6	c.1513-40'-	ENSMUSTintron_variant
15	35869468 .	G	T	base_qual SNV	60	4	64	0.062	59	11	70	0.157	link	-	Vps13b	c.8091+26-	ENSMUSTintron_variant
15	44533672 .	G	T	weak_evid SNV	68	0	68	0	100	3	103	0.029	link	-	Pkhd11i	c.6023-711-	ENSMUSTintron_variant
15	57920286 .	T	C	too_few_s SNV	3	0	3	0	10	2	12	0.167	link	-	Tbc1d31	c.340+240-	ENSMUSTintron_variant
15	75996661 .	T	G	base_qual SNV	20	0	20	0	21	6	27	0.222	link	-	Fam83b	c.*5196A>-	ENSMUSTdownstream_gene_variant
15	75996661 .	T	G	base_qual SNV	20	0	20	0	21	6	27	0.222	link	-	Mapk15	c.724+147-	ENSMUSTintron_variant
15	78983030 .	A	C	base_qual SNV	97	4	101	0.04	104	8	112	0.071	link	-	Triobp	c.4308+42-	ENSMUSTintron_variant
15	82003626 rs1132975	C	A	base_qual SNV	43	4	47	0.085	67	9	76	0.118	link	-	Desi1	c.110+132-	ENSMUSTintron_variant
15	82003626 rs1132975	C	A	base_qual SNV	43	4	47	0.085	67	9	76	0.118	link	-	Xrcc6	n.8200362-	- intragenic_variant
15	84260585 .	A	C	base_qual SNV	63	4	67	0.06	54	10	64	0.156	link	-	Parvb	c.116-106-	ENSMUSTintron_variant
15	86185640 .	T	G	base_qual SNV	153	0	153	0	146	5	151	0.033	link	-	Gm15569	n.-88T>G-	ENSMUSTupstream_gene_variant
15	88863790 .	T	G	too_few_s SNV	5	0	5	0	6	2	8	0.25	link	-	Pim3	c.616+242-	ENSMUSTintron_variant
15	90948927 .	T	G	base_qual SNV	127	0	127	0	116	14	130	0.108	link	-	Kif21a	c.3953+79-	ENSMUSTintron_variant
15	98862763 .	A	C	base_qual SNV	197	0	197	0	198	12	210	0.057	link	-	Kmt2d	c.2692-13-	ENSMUSTintron_variant
15	99794305 .	T	A	weak_evid SNV	33	0	33	0	36	6	42	0.143	link	-	Lima1	c.1134+10-	ENSMUSTintron_variant
15	1.01E+08 .	T	G	alt_allele_SNV	29	4	33	0.121	29	7	36	0.194	link	-	Acvr1b	n.91+66T>-	ENSMUSTintron_variant
15	1.02E+08 .	T	G	base_qual SNV	112	0	112	0	128	12	140	0.086	link	-	Gm27406	n.*4726T>-	ENSMUSTdownstream_gene_variant
15	1.02E+08 .	T															

16	87411956 .	C	A	base_qual SNV	22	3	25	0.12	21	6	27	0.222 link	-	Ltn1	c.2351-98I-	ENSMUSTintron_variant
16	93844832 .	T	G	base_qual SNV	37	1	38	0.026	39	8	47	0.17 link	-	Morc3	c.246-308-	ENSMUSTintron_variant
16	95987596 .	C	T	too_few_s SNV	5	0	5	0	14	2	16	0.125 link	-	Psmg1	c.397-241I-	ENSMUSTintron_variant
17	6050147 .	A	C	base_qual SNV	73	0	73	0	66	12	78	0.154 link	-	Serac1	c.1404-87-	ENSMUSTintron_variant
17	8964872 .	A	C	base_qual SNV	7	0	7	0	14	9	23	0.391 link	-	Pde10a	c.1656+15-	ENSMUSTintron_variant
17	10319900 .	T	G	base_qual SNV	245	21	266	0.079	193	18	211	0.085 link	-	Qk	c.-1027A>-	ENSMUSTupstream_gene_variant
17	10319900 .	T	G	base_qual SNV	245	21	266	0.079	193	18	211	0.085 link	-	1700110C	n.-4702T>-	ENSMUSTupstream_gene_variant
17	10319900 .	T	G	base_qual SNV	245	21	266	0.079	193	18	211	0.085 link	-	-	n.1031990-	intergenic_region
17	12659396 .	T	G	base_qual SNV	8	1	9	0.111	9	6	15	0.4 link	-	Slc22a1	c.1279+15-	ENSMUSTintron_variant
17	23357165 .	G	C	mapping_c SNV	86	0	86	0	109	8	117	0.068 link	-	Vmn2r115	c.1654+82-	ENSMUSTintron_variant
17	23470983 rs5799638A	G	G	mapping_c SNV	10	2	12	0.167	17	6	23	0.261 link	-	Vmn2r117	c.1654+19-	ENSMUSTintron_variant
17	23471007 rs1135191T	C	C	mapping_c SNV	13	2	15	0.133	22	6	28	0.214 link	-	Vmn2r117	c.1654+17-	ENSMUSTintron_variant
17	23478596 .	C	T	non_homr SNV	81	0	81	0	92	2	94	0.021 link	-	Vmn2r117	c.198-77G-	ENSMUSTintron_variant
17	23478598 .	G	C	non_homr SNV	78	0	78	0	88	2	90	0.022 link	-	Vmn2r117	c.198-79C-	ENSMUSTintron_variant
17	24883444 .	A	C	base_qual SNV	34	0	34	0	52	11	63	0.175 link	-	Spsb3	c.-3236A>-	ENSMUSTupstream_gene_variant
17	24883444 .	A	C	base_qual SNV	34	0	34	0	52	11	63	0.175 link	-	Igfals	c.*1696A>-	ENSMUSTupstream_gene_variant
17	24883444 .	A	C	base_qual SNV	34	0	34	0	52	11	63	0.175 link	-	Nubp2	c.683-130-	ENSMUSTintron_variant
17	25744368 .	C	A	base_qual SNV	43	3	46	0.065	55	10	65	0.154 link	-	Msln	c.*4374G>-	ENSMUSTdownstream_gene_variant
17	25744368 .	C	A	base_qual SNV	43	3	46	0.065	55	10	65	0.154 link	-	Gm25083	n.*2420G>-	ENSMUSTdownstream_gene_variant
17	25744368 .	C	A	base_qual SNV	43	3	46	0.065	55	10	65	0.154 link	-	Msln	c.923-96C-	ENSMUSTintron_variant
17	26123472 .	A	C	base_qual SNV	31	4	35	0.114	29	6	35	0.171 link	-	Mrpl28	c.-90A>-C	ENSMUSTintron_variant
17	26123472 .	A	C	base_qual SNV	31	4	35	0.114	29	6	35	0.171 link	-	Tmem8	c.*1238A>-	ENSMUSTdownstream_gene_variant
17	26123472 .	A	C	base_qual SNV	31	4	35	0.114	29	6	35	0.171 link	-	-	n.2612347-	intergenic_region
17	28350697 .	A	C	base_qual SNV	47	4	51	0.078	49	11	60	0.183 link	-	Tead3	c.-102T>-G-	ENSMUSTupstream_gene_variant
17	28350697 .	A	C	base_qual SNV	47	4	51	0.078	49	11	60	0.183 link	-	Tulp1	c.*1172T>-	ENSMUSTdownstream_gene_variant
17	28350697 .	A	C	base_qual SNV	47	4	51	0.078	49	11	60	0.183 link	-	Tead3	n.2835069-	intergenic_region
17	28775495 .	T	G	base_qual SNV	68	5	73	0.068	85	15	100	0.15 link	-	Mapk13	c.418-59T-	ENSMUSTintron_variant
17	28859154 .	A	T	base_qual SNV	34	0	34	0	48	5	53	0.094 link	-	Pnpla1os	n.28-100T-	ENSMUSTintron_variant
17	28859154 .	A	T	base_qual SNV	34	0	34	0	48	5	53	0.094 link	-	Pnpla1	c.205+83A-	ENSMUSTintron_variant
17	28962532 .	A	C	base_qual SNV	21	2	23	0.087	19	5	24	0.208 link	-	Kctd20	c.435-278-	ENSMUSTintron_variant
17	30192387 .	A	C	too_few_s SNV	8	0	8	0	14	2	16	0.125 link	-	Zfand3	c.296-176-	ENSMUSTintron_variant
17	31265705 .	T	A	base_qual SNV	12	1	13	0.077	9	11	20	0.55 link	-	Rsph1	c.501+109-	ENSMUSTintron_variant
17	31632784 .	A	C	base_qual SNV	75	1	76	0.013	70	4	74	0.054 link	-	Cbs	c.200+44T-	ENSMUSTintron_variant
17	34182992 .	A	C	base_qual SNV	42	3	45	0.067	37	10	47	0.213 link	-	Tap1	c.-4888A>-	ENSMUSTupstream_gene_variant
17	34182992 .	A	C	base_qual SNV	42	3	45	0.067	37	10	47	0.213 link	-	Psmb9	c.532+97T-	ENSMUSTintron_variant
17	35223747 .	G	T	base_qual SNV	28	2	30	0.067	39	8	47	0.17 link	-	Gm16181	c.-110G>-1	ENSMUST5_prime_UTR_variant
17	35223747 .	G	T	base_qual SNV	28	2	30	0.067	39	8	47	0.17 link	-	Nfkbi1	c.338-238I-	ENSMUSTintron_variant
17	35887802 .	C	A	base_qual SNV	56	1	57	0.018	49	11	60	0.183 link	-	231006110	c.*5051G>-	ENSMUSTdownstream_gene_variant
17	35887802 .	C	A	base_qual SNV	56	1	57	0.018	49	11	60	0.183 link	-	Dhx16	c.2158-33I-	ENSMUSTintron_variant
17	36949728 .	A	C	base_qual SNV	16	2	18	0.111	27	6	33	0.182 link	-	Rnf39	c.*2092A>-	ENSMUSTdownstream_gene_variant
17	36949728 .	A	C	base_qual SNV	16	2	18	0.111	27	6	33	0.182 link	-	Znrd1	c.*4800T>-	ENSMUSTintron_variant
17	36949728 .	A	C	base_qual SNV	16	2	18	0.111	27	6	33	0.182 link	-	Ppp1r11	c.193+149-	ENSMUSTintron_variant
17	37046587 .	A	C	base_qual SNV	80	5	85	0.059	63	12	75	0.16 link	-	Gabbr1	c.1-108A>-	ENSMUSTintron_variant
17	42876386 .	A	C	base_qual SNV	109	6	115	0.052	108	8	116	0.069 link	-	Cd2ap	c.-70T>-G	ENSMUST5_prime_UTR_variant
17	46526821 .	C	T	read_posit SNV	117	0	117	0	92	3	95	0.032 link	-	Gm26904	n.36+5528-	ENSMUSTintron_variant
17	46526821 .	C	T	read_posit SNV	117	0	117	0	92	3	95	0.032 link	-	Cul9	c.2810-13I-	ENSMUSTintron_variant
17	46858302 .	T	G	base_qual SNV	16	4	20	0.2	9	12	21	0.571 link	-	-	n.4685830-	intergenic_region
17	51785472 .	C	G	alt_allele SNV	23	5	28	0.179	18	8	26	0.308 link	-	Satb1	c.751+57C-	ENSMUSTintron_variant
17	71517457 .	C	A	base_qual SNV	41	0	41	0	40	1	41	0.024 link	-	Ndc80	c.669+87C-	ENSMUSTintron_variant
17	74294540 .	A	C	alt_allele SNV	19	5	24	0.208	9	5	14	0.357 link	-	Dpy30	c.*5212T>-	ENSMUSTdownstream_gene_variant
17	74294540 .	A	C	alt_allele SNV	19	5	24	0.208	9	5	14	0.357 link	-	Memo1	c.61+152T-	ENSMUSTintron_variant
17	78627009 .	T	G	base_qual SNV	19	1	20	0.05	10	5	15	0.333 link	-	Vit	c.*86T>-G	ENSMUST3_prime_UTR_variant
17	85613547 .	T	G	weak_evid SNV	32	1	33	0.03	38	6	44	0.136 link	-	Gm27610	n.-1115T>-	ENSMUSTupstream_gene_variant
17	85613547 .	T	G	weak_evid SNV	32	1	33	0.03	38	6	44	0.136 link	-	Gm27283	n.-1413T>-	ENSMUSTupstream_gene_variant
17	85613547 .	T	G	weak_evid SNV	32	1	33	0.03	38	6	44	0.136 link	-	Gm27275	n.-3155T>-	ENSMUSTupstream_gene_variant
17	85613547 .	T	G	weak_evid SNV	32	1	33	0.03	38	6	44	0.136 link	-	Gm27502	n.-4520T>-	ENSMUSTupstream_gene_variant
17	85613547 .	T	G	weak_evid SNV	32	1	33	0.03	38	6	44	0.136 link	-	Gm27435	n.*1784T>-	ENSMUSTdownstream_gene_variant
17	85613547 .	T	G	weak_evid SNV	32	1	33	0.03	38	6	44	0.136 link	-	Six3os1	n.538-55T-	ENSMUSTintron_variant
17	85613547 .	T	G	weak_evid SNV	32	1	33	0.03	38	6	44	0.136 link	-	Gm27801	n.166T>-G	ENSMUSTnon_coding_transcript_exon_variant
18	13717588 .	T	G	base_qual SNV	162	0	162	0	154	15	169	0.089 link	-	Zfp521	c.3790+28-	ENSMUSTintron_variant
18	34845114 .	A	C	base_qual SNV	21	4	25	0.16	34	8	42	0.19 link	-	Reep2	c.183-138-	ENSMUSTintron_variant
18	34909341 .	A	T	weak_evid SNV	35	0	35	0	50	4	54	0.074 link	-	Etf1	c.733-69T-	ENSMUSTintron_variant
18	36786416 .	C	T	too_few_s SNV	9	0	9	0	17	2	19	0.105 link	-	Hars	c.-3316G>-	ENSMUSTupstream_gene_variant
18	36786416 .	C	T	too_few_s SNV	9	0	9	0	17	2	19	0.105 link	-	Hars2	c.396+210-	ENSMUSTintron_variant
18	42275652 .	T	G	base_qual SNV	63	4	67	0.06	51	11	62	0.177 link	-	Rbm27	c.59+60T>-	ENSMUSTintron_variant
18	56572892 .	T	G	base_qual SNV	30	1	31	0.032	28	11	39	0.282 link	-	Phax	c.-148T>-C	ENSMUST5_prime_UTR_variant
18	56572892 .	T	G	base_qual SNV	30	1	31	0.032	28	11	39	0.282 link	-	Aldh7a1	n.5657289-	intergenic_region
18	58836658 .	G	C	base_qual SNV	18	0	18	0	16	4	20	0.2 link	-	Adams19	c.-149G>-C	ENSMUSTupstream_gene_variant
18	58836658 .	G	C	base_qual SNV	18	0	18	0	16	4	20	0.2 link	-	-	n.5883665-	intergenic_region
18	58836662 .	G	C	base_qual SNV	20	1	21	0.048	20	2	22	0.091 link	-	Adams19	c.-145G>-C	ENSMUSTupstream_gene_variant
18	58836662 .	G	C	base_qual SNV	20	1	21	0.048	20	2	22	0.091 link	-	-	n.5883666-	intergenic_region
18	65749549 .	C	A	base_qual SNV	68	1	69	0.014	64	8	72	0.111 link	-	Oacyl	c.1790-76I-	ENSMUSTintron_variant
18	69966720 .	T	G	base_qual SNV	78	0	78	0	51	26	77	0.338 link	-	49304480	n.-2957T>-	ENSMUSTupstream_gene_variant
18	69966720 .	T	G	base_qual SNV	78	0	78	0	51	26	77	0.338 link	-	Ccdc68	c.868-70T-	ENSMUSTintron_variant
18	69966720 .	T	G	base_qual SNV	78	0	78	0	51	26	77	0.338 link	-	1700061H	n.130+276-	ENSMUSTintron_variant
18	77426016 .	C	T	too_few_s SNV	8	0	8	0	9	2	11	0.182 link	-	Loxhd1	c.5434+26-	ENSMUSTintron_variant
19	3935428 .	T	G	base_qual SNV	20	2	22	0.091	15	4	19	0.211 link	-	Unc93b1	c.159+76T-	ENSMUSTintron_variant
19	3936205 .	T	G	base_qual SNV	76	0	76	0	54	15	69	0.217 link	-	Unc93b1	c.302-64T-	ENSMUSTintron_variant
19	4394719 .	C	A	base_qual SNV	66	3	69	0.043	84	7	91	0.077 link	-	Kdm2a	c.42+73G>-	ENSMUSTintron_variant
19	6443482 .	T	G	base_qual SNV	58	0	58	0	54	11	65	0.169 link	-	Nrxn2	c.731-149-	ENSMUSTintron_variant
19	6488953 .	T	G	base_qual SNV	6	0	6	0	13	6	19	0.316 link	-	Nrxn2	c.2416+14-	ENSMUSTintron_variant
19	10871625 .	A	C	weak_evid SNV	21	0	21	0	28	3	31	0.097 link	-	Tmem109	c.*133T>-C	ENSMUST3_prime_UTR_variant
19	10871625 .	A	C	weak_evid SNV	21	0	21	0	28	3	31	0.097 link	-	Tmem132	c.-1999T>-	ENSMUSTupstream_gene_variant
19	18589877 .	G	T	base_qual SNV	33	4	37	0.108	33	15	48	0.312 link	-	Ostf1	c.359-123I-	ENSMUSTintron_variant
19	42740588 .	T	G	base_qual SNV	37	7	44	0.159	56	15	71	0.211 link	-	Pyrox2	c.472-100-	ENSMUSTintron_variant
19	46271364 .	C	A	base_qual SNV	10	0	10	0	19	4	23	0.174 link	-	Gm16726	n.-3695G>-	ENSMUSTupstream_gene_variant
19	46271364 .	C	A	base_qual SNV	10	0										

2	26351859 .	T	G	base_qual SNV	242	12	254	0.047	212	17	229	0.074	link	-	Gm13562	n.-786T>C-	ENSMUSTupstream_gene_variant
2	26351859 .	T	G	base_qual SNV	242	12	254	0.047	212	17	229	0.074	link	-	Gpsm1	c.*4846T>-	ENSMUSTdownstream_gene_variant
2	26351859 .	T	G	base_qual SNV	242	12	254	0.047	212	17	229	0.074	link	-	Card9	c.*453A>C-	ENSMUSTdownstream_gene_variant
2	28610030 .	T	G	base_qual SNV	144	1	145	0.007	142	21	163	0.129	link	-	Gm22824	n.*1744T>-	ENSMUSTdownstream_gene_variant
2	31918397 .	T	G	base_qual SNV	103	1	104	0.01	98	23	121	0.19	link	-	Lamc3	c.2195>31-	ENSMUSTintron_variant
2	32578681 .	A	C	alt_allele_SNV	16	3	19	0.158	15	5	20	0.25	link	-	9430097D	c.-3896T>-	ENSMUSTupstream_gene_variant
2	32578681 .	A	C	alt_allele_SNV	16	3	19	0.158	15	5	20	0.25	link	-	Pip5k1l	c.565+77A-	ENSMUSTintron_variant
2	36104962 .	G	C	base_qual SNV	22	4	26	0.154	22	12	34	0.353	link	-	Lhx6	c.84+162C-	ENSMUSTintron_variant
2	52221095 .	G	T	base_qual SNV	50	2	52	0.038	43	8	51	0.157	link	-	Neb	c.13044+1-	ENSMUSTintron_variant
2	57356042 .	C	A	alt_allele_SNV	28	7	35	0.2	20	8	28	0.286	link	-	Gpd2	c.1476+10-	ENSMUSTintron_variant
2	59943049 rs2799899A	T	PASS	SNV	140	0	140	0	115	22	137	0.161	link	-	Baz2b	c.2429>19'-	ENSMUSTintron_variant
2	60252484 .	G	T	base_qual SNV	115	4	119	0.034	119	7	126	0.056	link	-	March7	c.*4575G>-	ENSMUSTdownstream_gene_variant
2	69885451 .	A	T	base_qual SNV	34	4	38	0.105	14	7	21	0.333	link	-	Mettl5	c.-94T>A -	ENSMUST5_prime_UTR_variant
2	69885451 .	A	T	base_qual SNV	34	4	38	0.105	14	7	21	0.333	link	-	Mettl5os	n.-277A>T-	ENSMUSTupstream_gene_variant
2	74522007 .	C	A	base_qual SNV	56	1	57	0.018	58	6	64	0.094	link	-	Lnplk1	c.*52G>T -	ENSMUST3_prime_UTR_variant
2	92989767 .	A	C	base_qual SNV	18	3	21	0.143	34	10	44	0.227	link	-	Prdm11	c.554+359-	ENSMUSTintron_variant
2	93704197 .	G	T	base_qual SNV	7	1	8	0.125	14	5	19	0.263	link	-	Ext2	c.1935>28-	ENSMUSTintron_variant
2	1.04E+08 .	A	C	base_qual SNV	57	1	58	0.017	57	9	66	0.136	link	-	D430041D	c.4002+91-	ENSMUSTintron_variant
2	1.1E+08 .	T	A	base_qual SNV	124	5	129	0.039	153	10	163	0.061	link	-	Lgr4	c.830+80T-	ENSMUSTintron_variant
2	1.19E+08 .	A	C	base_qual SNV	149	0	149	0	164	29	193	0.15	link	-	Picb2	c.1700>39-	ENSMUSTintron_variant
2	1.2E+08 .	A	C	base_qual SNV	182	0	182	0	153	12	165	0.073	link	-	Vps39	c.*6179T>-	ENSMUSTupstream_gene_variant
2	1.2E+08 .	A	C	base_qual SNV	182	0	182	0	153	12	165	0.073	link	-	Pla2g4f	c.448>51T-	ENSMUSTintron_variant
2	1.28E+08 .	A	C	too_few_s SNV	6	0	6	0	4	2	6	0.333	link	-	Zfp661	c.274+279-	ENSMUSTintron_variant
2	1.31E+08 .	C	A	base_qual SNV	33	4	37	0.108	40	21	61	0.344	link	-	Gm24893	n.-3691G>-	ENSMUSTupstream_gene_variant
2	1.31E+08 .	C	A	base_qual SNV	33	4	37	0.108	40	21	61	0.344	link	-	4930402H	c.3422>69-	ENSMUSTintron_variant
2	1.53E+08 .	A	C	base_qual SNV	92	1	93	0.011	78	16	94	0.17	link	-	Tpx2	c.1942>58-	ENSMUSTintron_variant
2	1.55E+08 .	T	G	base_qual SNV	34	5	39	0.128	35	10	45	0.222	link	-	a	c.*97T>G -	ENSMUST3_prime_UTR_variant
2	1.55E+08 .	T	G	base_qual SNV	25	0	25	0	23	6	29	0.207	link	-	a	c.*110T>C-	ENSMUST3_prime_UTR_variant
2	1.55E+08 .	G	A	too_few_s SNV	7	0	7	0	11	2	13	0.154	link	-	Pigu	c.256>241(-	ENSMUSTintron_variant
2	1.58E+08 .	G	A	weak_evid SNV	5	0	5	0	5	6	11	0.545	link	-	Ctnnb1	c.1603>29-	ENSMUSTintron_variant
2	1.64E+08 .	T	G	base_qual SNV	11	1	12	0.083	13	6	19	0.316	link	-	Rims4	c.-415A>C-	ENSMUSTupstream_gene_variant
2	1.64E+08 .	T	G	base_qual SNV	11	1	12	0.083	13	6	19	0.316	link	-	-	n.1639190	- intergenic_region
2	1.65E+08 .	T	G	base_qual SNV	35	0	35	0	33	15	48	0.312	link	-	Slc13a3	c.1488+13-	ENSMUSTintron_variant
2	1.75E+08 rs4957000G	A	mapping_c SNV	160	1	161	0.006	157	13	170	0.076	link	-	Gm14393	c.-103C>T-	ENSMUSTupstream_gene_variant	
2	1.75E+08 rs4957000G	A	mapping_c SNV	160	1	161	0.006	157	13	170	0.076	link	-	Gm14439	n.*4929G>-	ENSMUSTdownstream_gene_variant	
2	1.75E+08 rs4957000G	A	mapping_c SNV	160	1	161	0.006	157	13	170	0.076	link	-	-	n.1750678	- intergenic_region	
2	1.75E+08 rs4840184A	T	mapping_c SNV	157	1	158	0.006	147	14	161	0.087	link	-	Gm14393	c.-108T>A-	ENSMUSTupstream_gene_variant	
2	1.75E+08 rs4840184A	T	mapping_c SNV	157	1	158	0.006	147	14	161	0.087	link	-	Gm14439	n.*4934A>-	ENSMUSTdownstream_gene_variant	
2	1.75E+08 rs4840184A	T	mapping_c SNV	157	1	158	0.006	147	14	161	0.087	link	-	-	n.1750678	- intergenic_region	
2	1.75E+08 rs2763440C	G	mapping_c SNV	88	0	88	0	97	8	105	0.076	link	-	Gm14393	c.-147G>C-	ENSMUSTupstream_gene_variant	
2	1.75E+08 rs2763440C	G	mapping_c SNV	88	0	88	0	97	8	105	0.076	link	-	Gm14439	n.*4973C>-	ENSMUSTdownstream_gene_variant	
2	1.75E+08 rs2763440C	G	mapping_c SNV	88	0	88	0	97	8	105	0.076	link	-	-	n.1750678	- intergenic_region	
3	7528697 .	T	G	base_qual SNV	212	0	212	0	206	12	218	0.055	link	-	Zc2hc1a	c.701+13T-	ENSMUSTintron_variant
3	9439666 .	A	C	base_qual SNV	49	5	54	0.093	52	13	65	0.2	link	-	Zfp704	c.1589+11-	ENSMUSTintron_variant
3	14545799 .	G	T	base_qual SNV	13	0	13	0	22	9	31	0.29	link	-	Lrrcc1	c.1106>10-	ENSMUSTintron_variant
3	15541909 rs2468447A	T	mapping_c SNV	24	2	26	0.077	13	8	21	0.381	link	-	Sirpb1	c.1081>23-	ENSMUSTintron_variant	
3	28049142 rs2283303G	T	base_qual SNV	61	4	65	0.062	63	16	79	0.203	link	-	Pld1	c.1062>67(-	ENSMUSTintron_variant	
3	36553758 .	G	T	base_qual SNV	63	9	72	0.125	78	9	87	0.103	link	-	Exosc9	c.162>48G-	ENSMUSTintron_variant
3	36570027 .	A	C	PASS SNV	137	0	137	0	94	32	126	0.254	link	-	Exosc9	c.*4520A>-	ENSMUSTdownstream_gene_variant
3	36570027 .	A	C	PASS SNV	137	0	137	0	94	32	126	0.254	link	-	Bbs7	c.*3462T>-	ENSMUSTdownstream_gene_variant
3	36570027 .	A	C	PASS SNV	137	0	137	0	94	32	126	0.254	link	-	Ccna2	c.430+709-	ENSMUSTintron_variant
3	41762946 .	T	G	base_qual SNV	32	2	34	0.059	31	8	39	0.205	link	-	D3Etd751c	*6813T>-	ENSMUSTdownstream_gene_variant
3	41762946 .	T	G	base_qual SNV	32	2	34	0.059	31	8	39	0.205	link	-	D3Etd751n	c.4176294-	- intragenic_variant
3	55050444 .	G	T	base_qual SNV	27	1	28	0.036	45	5	50	0.1	link	-	4931419H	n.-4798G>-	ENSMUSTupstream_gene_variant
3	55050444 .	G	T	base_qual SNV	27	1	28	0.036	45	5	50	0.1	link	-	Ccna1	c.537+102-	ENSMUSTintron_variant
3	68596051 .	G	T	base_qual SNV	48	4	52	0.077	56	14	70	0.2	link	-	Schp1	c.751>99G-	ENSMUSTintron_variant
3	68596051 .	G	T	base_qual SNV	48	4	52	0.077	56	14	70	0.2	link	-	Gm21949	c.976>99G-	ENSMUSTintron_variant
3	79836488 .	T	G	base_qual SNV	40	0	40	0	21	10	31	0.323	link	-	Gm26420	n.*1453T>-	ENSMUSTdownstream_gene_variant
3	79836488 .	T	G	base_qual SNV	40	0	40	0	21	10	31	0.323	link	-	Tmem144	c.110>132(-	ENSMUSTintron_variant
3	79836490 .	T	G	base_qual SNV	38	0	38	0	20	10	30	0.333	link	-	Gm26420	n.*1455T>-	ENSMUSTdownstream_gene_variant
3	79836490 .	T	G	base_qual SNV	38	0	38	0	20	10	30	0.333	link	-	Tmem144	c.110>134(-	ENSMUSTintron_variant
3	79836491 .	T	G	base_qual SNV	37	0	37	0	17	12	29	0.414	link	-	Gm26420	n.*1456T>-	ENSMUSTdownstream_gene_variant
3	79836491 .	T	G	base_qual SNV	37	0	37	0	17	12	29	0.414	link	-	Tmem144	c.110>135(-	ENSMUSTintron_variant
3	86107087 .	C	T	PASS SNV	137	0	137	0	163	6	169	0.036	link	-	Sh3d19	c.1308+49-	ENSMUSTintron_variant
3	86138177 .	A	C	base_qual SNV	57	8	65	0.123	70	8	78	0.103	link	-	Gm37933	n.-4580A>-	ENSMUSTupstream_gene_variant
3	86138177 .	A	C	base_qual SNV	57	8	65	0.123	70	8	78	0.103	link	-	Snord73a	n.*614T>C-	ENSMUSTdownstream_gene_variant
3	86138177 .	A	C	base_qual SNV	57	8	65	0.123	70	8	78	0.103	link	-	Rnu73b	n.*2441T>-	ENSMUSTdownstream_gene_variant
3	86138177 .	A	C	base_qual SNV	57	8	65	0.123	70	8	78	0.103	link	-	Rps3a1	c.674>67T-	ENSMUSTintron_variant
3	87922937 .	A	C	weak_evid SNV	139	1	140	0.007	126	17	143	0.119	link	-	Rrnad1	c.*854T>C-	ENSMUST3_prime_UTR_variant
3	87989036 .	A	C	base_qual SNV	47	2	49	0.041	57	12	69	0.174	link	-	Bcan	c.2220>13-	ENSMUSTintron_variant
3	89418016 .	A	C	base_qual SNV	7	1	8	0.125	4	5	9	0.556	link	-	Shc1	c.-3835A>-	ENSMUSTupstream_gene_variant
3	89418016 .	A	C	base_qual SNV	7	1	8	0.125	4	5	9	0.556	link	-	Cks1b	c.59+139T-	ENSMUSTintron_variant
3	89945893 .	G	A	weak_evid SNV	93	0	93	0	118	3	121	0.025	link	-	Atp8b2	c.2358>28-	ENSMUSTintron_variant
3	89957410 .	T	G	base_qual SNV	138	5	143	0.035	135	8	143	0.056	link	-	Atp8b2	c.439>42A-	ENSMUSTintron_variant
3	90274248 .	T	G	base_qual SNV	132	0	132	0	126	29	155	0.187	link	-	Mir7012	n.*4036T>-	ENSMUSTdownstream_gene_variant
3	90274248 .	T	G	base_qual SNV	132	0	132	0	126	29	155	0.187	link	-	Dennd4b	c.2473>41-	ENSMUSTintron_variant
3	95190748 .	C	A	base_qual SNV	73	3	76	0.039	91	6	97	0.062	link	-	Gabpb2	c.623>10G-	ENSMUSTintron_variant
3	98111506 .	T	G	base_qual SNV	93	2	95	0.021	90	22	112	0.196	link	-	Notch2	c.2027>44-	ENSMUSTintron_variant
3	1.05E+08 .	T	G	base_qual SNV	9	0	9	0	20	5	25	0.2	link	-	Fam19a3	c.-8239A>-	ENSMUSTupstream_gene_variant
3	1.05E+08 .	T	G	base_qual SNV	9	0	9	0	20	5	25	0.2	link	-	Ppm1j	c.324>430'-	ENSMUSTintron_variant
3	1.07E+08 .	C	A	base_qual SNV	26	3	29	0.103	19	5	24	0.208	link	-	Gm43071	n.-1686C>-	ENSMUSTupstream_gene_variant
3	1.07E+08 .	C	A	base_qual SNV	26	3	29	0.103	19	5	24	0.208	link	-	Dram2	c.200>126(-	ENSMUSTintron_variant
3	1.27E+08 .	A	G	too_few_s SNV	5	0	5	0	5	2	7	0.286	link	-	Camk2d	c.342>295-	ENSMUSTintron_variant

4	59892374 .	A	C	base_qual SNV	49	2	51	0.039	54	13	67	0.194	link	-	Snx30	c.1015-88;-	ENSMUSTintron_variant
4	59892374 .	A	C	base_qual SNV	49	2	51	0.039	54	13	67	0.194	link	-	Gm12542	n.111-185;-	ENSMUSTintron_variant
4	62965590 .	C	T	weak_evidSNV	145	1	146	0.007	80	5	85	0.059	link	-	Zfp618	c.-84C>T	ENSMUST5_prime_UTR_variant
4	84546514 .	T	G	alt_allele_SNV	10	3	13	0.231	20	5	25	0.2	link	-	Bnc2	c.130-109;-	ENSMUSTintron_variant
4	1.02E+08 .	G	T	base_qual SNV	21	1	22	0.045	19	7	26	0.269	link	-	Dnajc6	c.661-125;-	ENSMUSTintron_variant
4	1.07E+08 .	A	C	base_qual SNV	56	2	58	0.034	83	11	94	0.117	link	-	Acot11	c.93+60T>-	ENSMUSTintron_variant
4	1.12E+08 .	T	G	base_qual SNV	38	0	38	0	43	9	52	0.173	link	-	Skint8	c.818-94T-	ENSMUSTintron_variant
4	1.13E+08 .	A	C	too_few_s SNV	6	0	6	0	6	2	8	0.25	link	-	Skint6	c.424+250-	ENSMUSTintron_variant
4	1.18E+08 .	T	G	base_qual SNV	121	1	122	0.008	129	10	139	0.072	link	-	Ipo13	c.84+74A>-	ENSMUSTintron_variant
4	1.18E+08 .	A	T	too_few_s SNV	18	0	18	0	15	2	17	0.118	link	-	Szt2	c.7341+17-	ENSMUSTintron_variant
4	1.21E+08 .	T	G	base_qual SNV	113	1	114	0.009	97	7	104	0.067	link	-	Mir30f	n.-3703T>-	ENSMUSTupstream_gene_variant
4	1.21E+08 .	T	G	base_qual SNV	113	1	114	0.009	97	7	104	0.067	link	-	Mir30c-1	n.*631A>-C-	ENSMUSTdownstream_gene_variant
4	1.21E+08 .	T	G	base_qual SNV	113	1	114	0.009	97	7	104	0.067	link	-	Mir30e	n.*3703A>-	ENSMUSTdownstream_gene_variant
4	1.21E+08 .	T	G	base_qual SNV	83	0	83	0	68	9	77	0.117	link	-	Col9a2	c.415-27T-	ENSMUSTintron_variant
4	1.25E+08 .	G	A	too_few_s SNV	12	0	12	0	14	2	16	0.125	link	-	Snip1	c.-3395G>-	ENSMUSTupstream_gene_variant
4	1.25E+08 .	G	A	too_few_s SNV	12	0	12	0	14	2	16	0.125	link	-	Dnal1	c.397+195-	ENSMUSTintron_variant
4	1.27E+08 .	T	G	base_qual SNV	34	1	35	0.029	32	12	44	0.273	link	-	Tfap2e	c.786-126-	ENSMUSTintron_variant
4	1.27E+08 .	T	G	base_qual SNV	20	2	22	0.091	21	6	27	0.222	link	-	Tfap2e	c.786-146-	ENSMUSTintron_variant
4	1.27E+08 .	C	A	base_qual SNV	11	0	11	0	12	10	22	0.455	link	-	Gm25600	n.*1578G>-	ENSMUSTdownstream_gene_variant
4	1.27E+08 .	C	A	base_qual SNV	11	0	11	0	12	10	22	0.455	link	-	Zmym6	c.1570+16-	ENSMUSTintron_variant
4	1.36E+08 .	T	G	base_qual SNV	10	2	12	0.167	12	6	18	0.333	link	-	Myom3	c.3156+15-	ENSMUSTintron_variant
4	1.41E+08 .	G	T	base_qual SNV	20	2	22	0.091	16	5	21	0.238	link	-	Crocc	c.1297-16-	ENSMUSTintron_variant
4	1.41E+08 .	A	C	base_qual SNV	39	4	43	0.093	45	18	63	0.286	link	-	Gm13075	n.-1717A>-	ENSMUSTupstream_gene_variant
4	1.41E+08 .	A	C	base_qual SNV	39	4	43	0.093	45	18	63	0.286	link	-	Clncka	c.229+90T-	ENSMUSTintron_variant
4	1.42E+08 rs2488291	T	G	base_qual SNV	99	6	105	0.057	100	9	109	0.083	link	-	Al507597	n.*2151T>-	ENSMUSTdownstream_gene_variant
4	1.42E+08 rs2488291	T	G	base_qual SNV	99	6	105	0.057	100	9	109	0.083	link	-	Slc25a34	c.*2657A>-	ENSMUSTdownstream_gene_variant
4	1.42E+08 rs2488291	T	G	base_qual SNV	99	6	105	0.057	100	9	109	0.083	link	-	Tmem82	c.89-43A>-	ENSMUSTintron_variant
4	1.45E+08 .	G	C	base_qual SNV	8	0	8	0	24	2	26	0.077	link	-	Vps13d	c.12171+1-	ENSMUSTintron_variant
4	1.46E+08 .	T	C	mapping_cSNV	35	3	38	0.079	65	21	86	0.244	link	-	Gm26763	n.181-143-	ENSMUSTintron_variant
4	1.46E+08 .	T	C	mapping_cSNV	35	3	38	0.079	65	21	86	0.244	link	-	Zfp980	c.75+216T-	ENSMUSTintron_variant
4	1.47E+08 rs1132667	T	A	mapping_cSNV	94	14	108	0.13	134	33	167	0.198	link	-	Gm26624	n.1897+38-	ENSMUSTintron_variant
4	1.47E+08 rs1132667	T	A	mapping_cSNV	94	14	108	0.13	134	33	167	0.198	link	-	C230088H	n.1516+43-	ENSMUSTintron_variant
4	1.47E+08 .	C	G	mapping_cSNV	17	3	20	0.15	27	17	44	0.386	link	-	Gm26624	n.1907+83-	ENSMUSTintron_variant
4	1.47E+08 .	C	G	mapping_cSNV	17	3	20	0.15	27	17	44	0.386	link	-	C230088H	n.1321+34-	ENSMUSTintron_variant
4	1.47E+08 .	C	G	mapping_cSNV	17	3	20	0.15	27	17	44	0.386	link	-	Zfp988	c.-74-134C-	ENSMUSTintron_variant
4	1.48E+08 rs5839116	A	G	alt_allele_SNV	11	2	13	0.154	12	7	19	0.368	link	-	Zfp979	c.202+188-	ENSMUSTintron_variant
4	1.48E+08 .	T	C	mapping_cSNV	231	1	232	0.004	291	10	301	0.033	link	-	Zfp534	c.*61A>-G	ENSMUST3_prime_UTR_variant
4	1.48E+08 .	T	C	mapping_cSNV	231	1	232	0.004	291	10	301	0.033	link	-	Gm16211	n.-3310A>-	ENSMUSTupstream_gene_variant
4	1.48E+08 rs1132217	A	C	mapping_cSNV	314	2	316	0.006	375	12	387	0.031	link	-	Zfp534	c.*39T>-G	ENSMUST3_prime_UTR_variant
4	1.48E+08 rs1132217	A	C	mapping_cSNV	314	2	316	0.006	375	12	387	0.031	link	-	Gm16211	n.-3332T>-	ENSMUSTupstream_gene_variant
4	1.5E+08 .	A	G	too_few_s SNV	7	0	7	0	18	2	20	0.1	link	-	Gpr157	c.*186A>-C-	ENSMUST3_prime_UTR_variant
4	1.5E+08 .	T	C	PASS SNV	72	0	72	0	62	12	74	0.162	link	-	Gm13092	n.*17A>-G	ENSMUSTdownstream_gene_variant
4	1.5E+08 .	T	C	PASS SNV	72	0	72	0	62	12	74	0.162	link	-	Rere	c.-145+33-	ENSMUSTintron_variant
4	1.52E+08 .	G	C	base_qual SNV	85	4	89	0.045	54	13	67	0.194	link	-	Espn	c.1900+12-	ENSMUSTintron_variant
4	1.55E+08 .	T	A	base_qual SNV	128	7	135	0.052	85	10	95	0.105	link	-	Plch2	c.*3590A>-	ENSMUSTdownstream_gene_variant
4	1.55E+08 .	T	A	base_qual SNV	128	7	135	0.052	85	10	95	0.105	link	-	Pank4	c.2109-22-	ENSMUSTintron_variant
5	3956396 .	A	C	base_qual SNV	53	0	53	0	48	13	61	0.213	link	-	Akap9	c.636+84A-	ENSMUSTintron_variant
5	3970840 .	T	G	base_qual SNV	61	0	61	0	83	18	101	0.178	link	-	Akap9	c.3447+10-	ENSMUSTintron_variant
5	14975226 .	G	T	mapping_cSNV	345	3	348	0.009	423	14	437	0.032	link	-	Gm10354	c.627+159-	ENSMUSTintron_variant
5	14975269 .	G	T	mapping_cSNV	474	5	479	0.01	579	22	601	0.037	link	-	Gm10354	c.627+116-	ENSMUSTintron_variant
5	14977277 rs1132479	T	C	no_reliable SNV	14	1	15	0.067	23	7	30	0.233	link	-	Gm10354	c.299+285-	ENSMUSTintron_variant
5	15529329 .	C	T	mapping_cSNV	725	39	764	0.051	1042	74	1116	0.066	link	-	Gm21190	c.-1116>-A-	ENSMUSTupstream_gene_variant
5	15529329 .	C	T	mapping_cSNV	725	39	764	0.051	1042	74	1116	0.066	link	-	Gm21847	n.222+335-	ENSMUSTintron_variant
5	15529608 .	A	T	weak_evidSNV	21	0	21	0	42	7	49	0.143	link	-	Gm21190	c.-390T>-A-	ENSMUSTupstream_gene_variant
5	15529608 .	A	T	weak_evidSNV	21	0	21	0	42	7	49	0.143	link	-	Gm21847	n.222+367-	ENSMUSTintron_variant
5	15529702 .	G	A	weak_evidSNV	32	1	33	0.03	41	6	47	0.128	link	-	Gm21190	c.-484C>-T	ENSMUSTupstream_gene_variant
5	15529702 .	G	A	weak_evidSNV	32	1	33	0.03	41	6	47	0.128	link	-	Gm21847	n.222+376-	ENSMUSTintron_variant
5	15577286 .	G	A	mapping_cSNV	457	6	463	0.013	524	28	552	0.051	link	-	Gm21083	c.-51G>-A-	ENSMUSTupstream_gene_variant
5	15577286 .	G	A	mapping_cSNV	457	6	463	0.013	524	28	552	0.051	link	-	Gm21847	n.222+513-	ENSMUSTintron_variant
5	15577286 .	G	A	mapping_cSNV	457	6	463	0.013	524	28	552	0.051	link	-	Gm30613	n.358-217-	ENSMUSTintron_variant
5	15713500 rs1081773	C	T	weak_evidSNV	17	1	18	0.056	16	3	19	0.158	link	-	Speer4cos	n.394-407-	ENSMUSTintron_variant
5	15713500 rs1081773	C	T	weak_evidSNV	17	1	18	0.056	16	3	19	0.158	link	-	Speer4c	c.140-452-	ENSMUSTintron_variant
5	15713523 .	G	T	no_reliable SNV	22	1	23	0.043	22	4	26	0.154	link	-	Speer4cos	n.394-384-	ENSMUSTintron_variant
5	15713523 .	G	T	no_reliable SNV	22	1	23	0.043	22	4	26	0.154	link	-	Speer4c	c.140-475-	ENSMUSTintron_variant
5	15713544 rs1133421	G	C	weak_evidSNV	30	0	30	0	24	3	27	0.111	link	-	Speer4cos	n.394-363-	ENSMUSTintron_variant
5	15713544 rs1133421	G	C	weak_evidSNV	30	0	30	0	24	3	27	0.111	link	-	Speer4c	c.140-496-	ENSMUSTintron_variant
5	25969577 .	C	T	mapping_cSNV	23	4	27	0.148	32	13	45	0.289	link	-	Gm21680	c.443+218-	ENSMUSTintron_variant
5	26021241 rs1132623	G	T	weak_evidSNV	7	0	7	0	6	7	13	0.538	link	-	Gm5862	c.299+363-	ENSMUSTintron_variant
5	27500935 .	C	A	PASS SNV	17	1	18	0.056	14	9	23	0.391	link	-	Dpp6	c.609+314-	ENSMUSTintron_variant
5	27500935 .	C	A	PASS SNV	17	1	18	0.056	14	9	23	0.391	link	-	Speer4b	c.139+294-	ENSMUSTintron_variant
5	30394800 .	A	C	base_qual SNV	107	0	107	0	91	19	110	0.173	link	-	Otof	c.895-96T-	ENSMUSTintron_variant
5	31094106 .	C	A	base_qual SNV	13	3	16	0.188	15	8	23	0.348	link	-	Slc30a3	c.-749G>-T	ENSMUSTupstream_gene_variant
5	31094106 .	C	A	base_qual SNV	13	3	16	0.188	15	8	23	0.348	link	-	Gm9924	n.-788C>-A-	ENSMUSTupstream_gene_variant
5	31094106 .	C	A	base_qual SNV	13	3	16	0.188	15	8	23	0.348	link	-	Slc30a3	n.3109410-	- intragenic_variant
5	31697325 .	T	A	base_qual SNV	11	0	11	0	11	8	19	0.421	link	-	Bre	c.-4525T>-	ENSMUSTupstream_gene_variant
5	31697325 .	T	A	base_qual SNV	11	0	11	0	11	8	19	0.421	link	-	Rbks	c.92+185A-	ENSMUSTintron_variant
5	31697325 .	T	A	base_qual SNV	11	0	11	0	11	8	19	0.421	link	-	Gm43809	n.192-450-	ENSMUSTintron_variant
5	36807074 .	T	G	base_qual SNV	85	17	102	0.167	79	21	100	0.21	link	-	Man2b2	c.*42A>-C	ENSMUST3_prime_UTR_variant
5	36931169 .	T	G	base_qual SNV	73	0	73	0	86	12	98	0.122	link	-	Ppp2r2c	c.448-67T-	ENSMUSTintron_variant
5	38742205 rs2123033	A	PASS SNV	65	0	65	0	67	8	75	0.107	link	-	Clnk	c.636+137-	ENSMUSTintron_variant	
5	38742205 rs2123033	A	PASS SNV	65	0	65	0	67	8	75	0.107	link	-	Clnkos	n.236+225-	ENSMUSTintron_variant	
5	77407341 .	A	C	non_homr_SNV	35	1	36	0.028	36	10	46	0.217	link	-	Igfbp7	c.475+199-	ENSMUSTintron_variant
5	88639211 .	G	T	weak_evidSNV	33	1											

5	1.25E+08 .	T	G	base_qual	SNV	66	0	66	0	66	22	88	0.25	link	-	Dnah10	c.*86T>G	-	ENSMUST3_prime_UTR_variant
5	1.25E+08 .	T	G	base_qual	SNV	66	0	66	0	66	22	88	0.25	link	-	Ccdc92	c.*1308A>-	-	ENSMUSTdownstream_gene_variant
5	1.25E+08 .	T	G	base_qual	SNV	19	2	21	0.095	13	2	15	0.133	link	-	Dhx37	c.*969-64A	-	ENSMUSTintron_variant
5	1.34E+08 .	T	A	base_qual	SNV	15	1	16	0.062	21	4	25	0.16	link	-	Gtf2ird1	c.1916+14-	-	ENSMUSTintron_variant
5	1.36E+08 .	T	A	weak_evid	SNV	108	1	109	0.009	94	6	100	0.06	link	-	Prkrip1	c.205+55A-	-	ENSMUSTintron_variant
5	1.37E+08 .	C	T	PASS	SNV	45	0	45	0	46	13	59	0.22	link	-	Zan	c.13491+8-	-	ENSMUSTintron_variant
5	1.37E+08 .	A	C	base_qual	SNV	9	2	11	0.182	19	9	28	0.321	link	-	Zan	c.6150+14-	-	ENSMUSTintron_variant
5	1.38E+08 .	T	G	base_qual	SNV	100	2	102	0.02	97	6	103	0.058	link	-	Tsc22d4	c.954+309-	-	ENSMUSTintron_variant
5	1.43E+08 .	A	C	base_qual	SNV	36	1	37	0.027	33	5	38	0.132	link	-	Spdye4a	c.434-162'-	-	ENSMUSTintron_variant
5	1.45E+08 rs5853732	G	T	mapping_	SNV	9	1	10	0.1	24	6	30	0.2	link	-	Cyp3a16	c.166-208(-	-	ENSMUSTintron_variant
5	1.45E+08 rs1133102	G	A	weak_evid	SNV	6	0	6	0	15	7	22	0.318	link	-	Cyp3a16	c.166-245(-	-	ENSMUSTintron_variant
5	1.46E+08 rs1132429	G	A	mapping_	SNV	94	12	106	0.113	102	31	133	0.233	link	-	Cyp3a41b	c.-100C>T-	-	ENSMUSTupstream_gene_variant
5	1.46E+08 rs1132429	G	A	mapping_	SNV	94	12	106	0.113	102	31	133	0.233	link	-	-	n.1455847-	-	intergenic_region
5	1.46E+08 rs3648566	T	C	mapping_	SNV	92	12	104	0.115	99	30	129	0.233	link	-	Cyp3a41b	c.-101A>C-	-	ENSMUSTupstream_gene_variant
5	1.46E+08 rs3648566	T	C	mapping_	SNV	92	12	104	0.115	99	30	129	0.233	link	-	-	n.1455847-	-	intergenic_region
5	1.46E+08 rs1134737	G	T	mapping_	SNV	82	12	94	0.128	92	29	121	0.24	link	-	Cyp3a41b	c.-106C>A-	-	ENSMUSTupstream_gene_variant
5	1.46E+08 rs1134737	G	T	mapping_	SNV	82	12	94	0.128	92	29	121	0.24	link	-	-	n.1455847-	-	intergenic_region
5	1.46E+08 rs1132633	A	T	mapping_	SNV	81	12	93	0.129	90	31	121	0.256	link	-	Cyp3a41b	c.-107T>A-	-	ENSMUSTupstream_gene_variant
5	1.46E+08 rs1132633	A	T	mapping_	SNV	81	12	93	0.129	90	31	121	0.256	link	-	-	n.1455847-	-	intergenic_region
5	1.46E+08 rs1135273	T	C	mapping_	SNV	75	15	90	0.167	84	32	116	0.276	link	-	Cyp3a41b	c.-116A>C-	-	ENSMUSTupstream_gene_variant
5	1.46E+08 rs1135273	T	C	mapping_	SNV	75	15	90	0.167	84	32	116	0.276	link	-	-	n.1455847-	-	intergenic_region
5	1.46E+08 rs5833119	A	G	mapping_	SNV	71	15	86	0.174	78	33	111	0.297	link	-	Cyp3a41b	c.-122T>C-	-	ENSMUSTupstream_gene_variant
5	1.46E+08 rs5833119	A	G	mapping_	SNV	71	15	86	0.174	78	33	111	0.297	link	-	-	n.1455847-	-	intergenic_region
5	1.47E+08 .	A	C	base_qual	SNV	63	7	70	0.1	75	9	84	0.107	link	-	Gsx1	c.409+54A-	-	ENSMUSTintron_variant
5	1.47E+08 .	A	C	base_qual	SNV	100	5	105	0.048	83	22	105	0.21	link	-	Gm43461	n.*2167A>-	-	ENSMUSTdownstream_gene_variant
5	1.47E+08 .	A	C	base_qual	SNV	100	5	105	0.048	83	22	105	0.21	link	-	Gm43460	n.*1014A>-	-	ENSMUSTdownstream_gene_variant
5	1.49E+08 .	A	C	base_qual	SNV	129	2	131	0.015	126	25	151	0.166	link	-	Ubl3	c.28-35T>-	-	ENSMUSTintron_variant
6	5784248 .	A	C	base_qual	SNV	11	1	12	0.083	37	10	47	0.213	link	-	Dync1i1	c.366-191(-	-	ENSMUSTintron_variant
6	23033574 .	C	A	base_qual	SNV	72	7	79	0.089	81	15	96	0.156	link	-	Ptptr21	c.5792+68-	-	ENSMUSTintron_variant
6	34172500 .	A	C	weak_evid	SNV	15	1	16	0.062	24	3	27	0.111	link	-	Gm13856	n.1578-15-	-	ENSMUSTintron_variant
6	34172500 .	A	C	weak_evid	SNV	15	1	16	0.062	24	3	27	0.111	link	-	Slc35b4	c.78-1926'-	-	ENSMUSTintron_variant
6	34392214 .	A	C	base_qual	SNV	115	0	115	0	127	18	145	0.124	link	-	Akr1b10	c.552+75A-	-	ENSMUSTintron_variant
6	41304970 .	C	A	PASS	SNV	391	0	391	0	337	71	408	0.174	link	-	Gm18964	n.*1233G>-	-	ENSMUSTdownstream_gene_variant
6	41680692 .	A	C	base_qual	SNV	128	0	128	0	124	13	137	0.095	link	-	Trpv5	c.-37T>G	-	ENSMUST5_prime_UTR_variant
6	41680692 .	A	C	base_qual	SNV	128	0	128	0	124	13	137	0.095	link	-	17000340	c.-3826A>-	-	ENSMUSTupstream_gene_variant
6	50194522 .	C	T	PASS	SNV	110	0	110	0	136	4	140	0.029	link	-	Dfna5	n.5019452-	-	intragenic_variant
6	71336537 .	C	A	base_qual	SNV	29	1	30	0.033	30	9	39	0.231	link	-	Gm44110	n.*2349G>-	-	ENSMUSTdownstream_gene_variant
6	71336537 .	C	A	base_qual	SNV	29	1	30	0.033	30	9	39	0.231	link	-	Cd8b1	c.630-173(-	-	ENSMUSTintron_variant
6	72234383 .	T	G	base_qual	SNV	148	4	152	0.026	142	14	156	0.09	link	-	Atoh8	c.771+11A-	-	ENSMUSTintron_variant
6	72630981 .	G	A	weak_evid	SNV	114	1	115	0.009	103	3	106	0.028	link	-	Gm37969	n.*4166C>-	-	ENSMUSTdownstream_gene_variant
6	72630981 .	G	A	weak_evid	SNV	114	1	115	0.009	103	3	106	0.028	link	-	Tcf7l1	c.1290-31-	-	ENSMUSTintron_variant
6	72630981 .	G	A	weak_evid	SNV	114	1	115	0.009	103	3	106	0.028	link	-	Gm15401	n.146-130(-	-	ENSMUSTintron_variant
6	83188958 .	A	C	base_qual	SNV	8	0	8	0	4	8	12	0.667	link	-	Dctn1	c.454-119(-	-	ENSMUSTintron_variant
6	85333242 .	A	C	base_qual	SNV	129	1	130	0.008	116	20	136	0.147	link	-	Rab11fp5	c.*3781T>-	-	ENSMUSTdownstream_gene_variant
6	85333242 .	A	C	base_qual	SNV	129	1	130	0.008	116	20	136	0.147	link	-	Mir705	n.*3050T>-	-	ENSMUSTdownstream_gene_variant
6	85333242 .	A	C	base_qual	SNV	129	1	130	0.008	116	20	136	0.147	link	-	Sfxn5	c.108+661-	-	ENSMUSTintron_variant
6	1.01E+08 .	C	G	base_qual	SNV	75	3	78	0.038	53	8	61	0.131	link	-	Pdzrn3	c.-17G>C	-	ENSMUSTupstream_gene_variant
6	1.01E+08 .	C	G	base_qual	SNV	75	3	78	0.038	53	8	61	0.131	link	-	-	n.1013779-	-	intergenic_region
6	1.04E+08 .	C	A	base_qual	SNV	77	6	83	0.072	66	4	70	0.057	link	-	Chl1	n.1037463-	-	intragenic_variant
6	1.16E+08 .	A	C	base_qual	SNV	66	0	66	0	66	16	82	0.195	link	-	9530062Kl	n.-429T>C-	-	ENSMUSTupstream_gene_variant
6	1.16E+08 .	A	C	base_qual	SNV	66	0	66	0	66	16	82	0.195	link	-	Fam21	c.123+93A-	-	ENSMUSTintron_variant
6	1.18E+08 .	T	G	base_qual	SNV	46	2	48	0.042	25	3	28	0.107	link	-	Ret	c.1654-52-	-	ENSMUSTintron_variant
6	1.2E+08 .	T	G	base_qual	SNV	28	0	28	0	23	6	29	0.207	link	-	Rad52	c.471-169'-	-	ENSMUSTintron_variant
6	1.22E+08 .	T	G	base_qual	SNV	56	7	63	0.111	58	10	68	0.147	link	-	Mug2	c.1464+85-	-	ENSMUSTintron_variant
6	1.25E+08 .	T	G	weak_evid	SNV	209	0	209	0	218	13	231	0.056	link	-	Zfp384	c.352+391-	-	ENSMUSTintron_variant
6	1.25E+08 .	T	G	weak_evid	SNV	209	0	209	0	218	13	231	0.056	link	-	Gm43989	n.141+238-	-	ENSMUSTintron_variant
6	1.27E+08 .	T	G	base_qual	SNV	12	2	14	0.143	19	5	24	0.208	link	-	Parp11	c.127-170'-	-	ENSMUSTintron_variant
6	1.36E+08 .	A	C	base_qual	SNV	68	1	69	0.014	72	16	88	0.182	link	-	Grin2b	c.1501-70-	-	ENSMUSTintron_variant
6	1.42E+08 .	A	C	base_qual	SNV	26	1	27	0.037	34	11	45	0.244	link	-	Slco1a5	c.1272-10(-	-	ENSMUSTintron_variant
7	3694499 .	T	G	base_qual	SNV	111	4	115	0.035	105	10	115	0.087	link	-	Mboat7	c.-2384A>-	-	ENSMUSTupstream_gene_variant
7	3694499 .	T	G	base_qual	SNV	111	4	115	0.035	105	10	115	0.087	link	-	Tsen34	c.-103T>C-	-	ENSMUSTupstream_gene_variant
7	3694499 .	T	G	base_qual	SNV	111	4	115	0.035	105	10	115	0.087	link	-	Tsen34	n.3694499-	-	intragenic_variant
7	4778011 .	A	C	alt_allele	SNV	116	7	123	0.057	120	11	131	0.084	link	-	Il11	c.-25T>G	-	ENSMUST5_prime_UTR_variant
7	4778011 .	A	C	alt_allele_SNV	SNV	116	7	123	0.057	120	11	131	0.084	link	-	Tmem190	c.-4972A>-	-	ENSMUSTupstream_gene_variant
7	15950817 .	A	C	base_qual	SNV	88	0	88	0	87	10	97	0.103	link	-	Gltscr2	c.-4764T>-	-	ENSMUSTupstream_gene_variant
7	15950817 .	A	C	base_qual	SNV	88	0	88	0	87	10	97	0.103	link	-	Gm24576	n.*4322A>-	-	ENSMUSTdownstream_gene_variant
7	15950817 .	A	C	base_qual	SNV	88	0	88	0	87	10	97	0.103	link	-	Ehd2	c.1081-25'-	-	ENSMUSTintron_variant
7	16150518 .	T	G	base_qual	SNV	208	1	209	0.005	200	14	214	0.065	link	-	Slc8a2	c.1868-56'-	-	ENSMUSTintron_variant
7	16313129 .	A	C	base_qual	SNV	74	0	74	0	67	7	74	0.095	link	-	Bbc3	c.275-498(-	-	ENSMUSTintron_variant
7	18903339 .	T	A	base_qual	SNV	41	2	43	0.047	33	5	38	0.132	link	-	Ccdc61	c.231+131-	-	ENSMUSTintron_variant
7	19395374 .	C	G	base_qual	SNV	148	2	150	0.013	144	12	156	0.077	link	-	Erc22	c.*930C>C-	-	ENSMUST3_prime_UTR_variant
7	19395374 .	C	G	base_qual	SNV	148	2	150	0.013	144	12	156	0.077	link	-	Gm26852	n.-2656G>-	-	ENSMUSTupstream_gene_variant
7	19758394 .	C	G	base_qual	SNV	64	2	66	0.03	88	11	99	0.111	link	-	Gm45114	n.*2512G>-	-	ENSMUSTdownstream_gene_variant
7	19758394 .	C	G	base_qual	SNV	64	2	66	0.03	88	11	99	0.111	link	-	Bcam	c.1745+30-	-	ENSMUSTintron_variant
7	24884706 .	A	C	base_qual	SNV	81	2	83	0.024	86	10	96	0.104	link	-	Rps19	c.-1+39A>-	-	ENSMUSTintron_variant
7	28179328 .	T	G	base_qual	SNV	13	0	13	0	32	6	38	0.158	link	-	Dyrklb	c.-1020T>-	-	ENSMUSTupstream_gene_variant
7	28179328 .	T	G	base_qual	SNV	13	0	13	0	32	6	38	0.158	link	-	Fbl	c.*173T>C-	-	ENSMUSTdownstream_gene_variant
7	28179328 .</																		

7	1.01E+08	C	A	base_qual	SNV	69	4	73	0.055	79	9	88	0.102	link	-	RP24-126.n.*3539G>-	ENSMUSTdownstream_gene_variant
7	1.01E+08	C	A	base_qual	SNV	69	4	73	0.055	79	9	88	0.102	link	-	Stard10 c.679-47C-	ENSMUSTintron_variant
7	1.04E+08	A	C	base_qual	SNV	41	2	43	0.047	37	7	44	0.159	link	-	Olfr5 c.*777>-G	ENSMUST3_prime_UTR_variant
7	1.04E+08	A	C	base_qual	SNV	41	2	43	0.047	37	7	44	0.159	link	-	Ubqlnl c.-3399T>-	ENSMUSTupstream_gene_variant
7	1.05E+08	T	C	PASS	SNV	21	0	21	0	27	4	31	0.129	link	-	Olfr692 c.*137T>-C	ENSMUSTdownstream_gene_variant
7	1.05E+08	T	C	PASS	SNV	21	0	21	0	27	4	31	0.129	link	-	Olfr692 c.*137T>-C	ENSMUSTdownstream_gene_variant
7	1.05E+08	T	C	PASS	SNV	21	0	21	0	27	4	31	0.129	link	-	-	n.1053694- intergenic_region
7	1.1E+08	T	G	base_qual	SNV	11	0	11	0	24	7	31	0.226	link	-	Swap70 c.1651+12-	ENSMUSTintron_variant
7	1.1E+08	T	G	base_qual	SNV	11	0	11	0	24	7	31	0.226	link	-	RP24-83E n.492+155-	ENSMUSTintron_variant
7	1.2E+08	A	T	base_qual	SNV	60	4	64	0.062	67	6	73	0.082	link	-	Acsm1 c.980+91A-	ENSMUSTintron_variant
7	1.26E+08	A	C	base_qual	SNV	29	0	29	0	32	14	46	0.304	link	-	Gm45141 n.-4340A>-	ENSMUSTupstream_gene_variant
7	1.26E+08	A	C	base_qual	SNV	29	0	29	0	32	14	46	0.304	link	-	Nfatc2jp c.434-124'-	ENSMUSTintron_variant
7	1.27E+08	T	G	base_qual	SNV	94	3	97	0.031	86	7	93	0.075	link	-	Mapk3 c.173+61T-	ENSMUSTintron_variant
7	1.27E+08	A	C	base_qual	SNV	34	0	34	0	49	7	56	0.125	link	-	Doc2a c.*1077A>-	ENSMUSTdownstream_gene_variant
7	1.27E+08	A	C	base_qual	SNV	34	0	34	0	49	7	56	0.125	link	-	Ino80e c.685-122'-	ENSMUSTintron_variant
7	1.31E+08	A	C	base_qual	SNV	163	1	164	0.006	133	13	146	0.089	link	-	Tacc2 c.33+66A>-	ENSMUSTintron_variant
7	1.31E+08	A	C	base_qual	SNV	163	1	164	0.006	133	13	146	0.089	link	-	Fgfr2 n.1305775-	- intragenic_variant
7	1.31E+08	T	G	base_qual	SNV	34	6	40	0.15	52	10	62	0.161	link	-	Btdb16 c.709-117-	ENSMUSTintron_variant
7	1.31E+08	T	G	base_qual	SNV	34	6	40	0.15	52	10	62	0.161	link	-	Fgfr2 n.1307968-	- intragenic_variant
7	1.31E+08	A	C	base_qual	SNV	69	5	74	0.068	66	11	77	0.143	link	-	5430419D c.763+116-	ENSMUSTintron_variant
7	1.31E+08	A	C	base_qual	SNV	69	5	74	0.068	66	11	77	0.143	link	-	Fgfr2 n.1312235-	- intragenic_variant
7	1.33E+08	A	G	too_few_s	SNV	7	0	7	0	14	2	16	0.125	link	-	RP24-69E n.*773T>-C	ENSMUSTdownstream_gene_variant
7	1.33E+08	A	G	too_few_s	SNV	7	0	7	0	14	2	16	0.125	link	-	Mettl10 c.399+175-	ENSMUSTintron_variant
7	1.33E+08	A	G	too_few_s	SNV	7	0	7	0	14	2	16	0.125	link	-	Fgfr2 n.1328369-	- intragenic_variant
7	1.42E+08	T	G	base_qual	SNV	26	5	31	0.161	17	7	24	0.292	link	-	Gm20501 n.-2829A>-	ENSMUSTupstream_gene_variant
7	1.42E+08	T	G	base_qual	SNV	26	5	31	0.161	17	7	24	0.292	link	-	Brsk2 c.94+167T-	ENSMUSTintron_variant
8	3541213	A	C	base_qual	SNV	45	1	46	0.022	39	10	49	0.204	link	-	Pnpla6 c.3338-78-	ENSMUSTintron_variant
8	11201975	C	A	base_qual	SNV	12	1	13	0.077	15	8	23	0.348	link	-	Col4a1 c.4756-14-	ENSMUSTintron_variant
8	11201975	C	A	base_qual	SNV	12	1	13	0.077	15	8	23	0.348	link	-	Gm15418 n.357+383-	ENSMUSTintron_variant
8	13356999	T	G	base_qual	SNV	175	0	175	0	148	28	176	0.159	link	-	Tfdp1 c.13-44T>-	ENSMUSTintron_variant
8	19933348	C	G	mapping_c	SNV	37	12	49	0.245	32	51	83	0.614	link	-	-	n.1993334- intergenic_region
8	22302625	T	A	base_qual	SNV	26	0	26	0	18	5	23	0.217	link	-	Tpte c.114-177-	ENSMUSTintron_variant
8	33600072	T	G	base_qual	SNV	93	2	95	0.021	94	5	99	0.051	link	-	Ppp2cb c.102+54T-	ENSMUSTintron_variant
8	47822604	T	G	base_qual	SNV	144	1	145	0.007	145	26	171	0.152	link	-	Cldn22 c.-1925T>-	ENSMUSTupstream_gene_variant
8	47822604	T	G	base_qual	SNV	144	1	145	0.007	145	26	171	0.152	link	-	RP24-423n c.-4383A>-	ENSMUSTupstream_gene_variant
8	47822604	T	G	base_qual	SNV	144	1	145	0.007	145	26	171	0.152	link	-	Wwc2 c.*6114A>-	ENSMUSTdownstream_gene_variant
8	83271595	T	G	base_qual	SNV	190	2	192	0.01	149	20	169	0.118	link	-	RP23-630 n.*3968T>-	ENSMUSTdownstream_gene_variant
8	84257328	T	G	weak_evid	SNV	51	0	51	0	48	4	52	0.077	link	-	Mri1 c.-68A>-C	ENSMUSTupstream_gene_variant
8	84257328	T	G	weak_evid	SNV	51	0	51	0	48	4	52	0.077	link	-	Ccdc130 c.*1153A>-	ENSMUSTdownstream_gene_variant
8	84257328	T	G	weak_evid	SNV	51	0	51	0	48	4	52	0.077	link	-	-	n.8425732- intergenic_region
8	84937362	T	G	base_qual	SNV	156	1	157	0.006	117	10	127	0.079	link	-	Mast1 c.-85A>-C	ENSMUSTupstream_gene_variant
8	84937362	T	G	base_qual	SNV	156	1	157	0.006	117	10	127	0.079	link	-	-	n.8493736- intergenic_region
8	85336359	A	C	base_qual	SNV	119	4	123	0.033	104	9	113	0.08	link	-	AA672651 n.-2984A>-	ENSMUSTupstream_gene_variant
8	85336359	A	C	base_qual	SNV	119	4	123	0.033	104	9	113	0.08	link	-	Myk13 c.2042+9T-	ENSMUSTintron_variant
8	87582800	T	G	base_qual	SNV	34	0	34	0	33	5	38	0.132	link	-	4933402JC c.412+178-	ENSMUSTintron_variant
8	88521272	T	G	base_qual	SNV	5	0	5	0	4	4	8	0.5	link	-	Nkd1 c.-235T>-C	ENSMUSTupstream_gene_variant
8	88521272	T	G	base_qual	SNV	5	0	5	0	4	4	8	0.5	link	-	-	n.8852127- intergenic_region
8	95260610	C	A	weak_evid	SNV	201	0	201	0	161	5	166	0.03	link	-	Cnbg1 c.2445+14-	ENSMUSTintron_variant
8	1.06E+08	T	G	base_qual	SNV	35	0	35	0	25	20	45	0.444	link	-	Slc7a6 c.1023-66'-	ENSMUSTintron_variant
8	1.07E+08	A	T	base_qual	SNV	22	0	22	0	23	5	28	0.179	link	-	Sntb2 c.1088+13-	ENSMUSTintron_variant
8	1.07E+08	T	C	too_few_s	SNV	4	0	4	0	6	2	8	0.25	link	-	Nqo1 c.-295A>-C	ENSMUSTupstream_gene_variant
8	1.07E+08	T	C	too_few_s	SNV	4	0	4	0	6	2	8	0.25	link	-	-	n.1074033- intergenic_region
8	1.13E+08	T	G	base_qual	SNV	51	0	51	0	45	12	57	0.211	link	-	Cntnap4 c.3360+95-	ENSMUSTintron_variant
8	1.13E+08	T	G	base_qual	SNV	50	0	50	0	50	6	56	0.107	link	-	Cntnap4 c.3360+96-	ENSMUSTintron_variant
8	1.17E+08	A	C	base_qual	SNV	18	2	20	0.1	10	2	12	0.167	link	-	Cdyl2 c.24+162T-	ENSMUSTintron_variant
8	1.21E+08	C	A	base_qual	SNV	41	5	46	0.109	66	12	78	0.154	link	-	Emc8 c.-1216G>-	ENSMUSTupstream_gene_variant
8	1.21E+08	C	A	base_qual	SNV	41	5	46	0.109	66	12	78	0.154	link	-	Gm27021 c.-1216G>-	ENSMUSTupstream_gene_variant
8	1.21E+08	C	A	base_qual	SNV	41	5	46	0.109	66	12	78	0.154	link	-	Cox41l c.-1-115C-	ENSMUSTintron_variant
8	1.21E+08	C	A	base_qual	SNV	41	5	46	0.109	66	12	78	0.154	link	-	Gm20388 c.21+7582-	ENSMUSTintron_variant
8	1.22E+08	A	C	base_qual	SNV	73	7	80	0.087	56	12	68	0.176	link	-	Cyba c.-1390T>-	ENSMUSTupstream_gene_variant
8	1.22E+08	A	C	base_qual	SNV	73	7	80	0.087	56	12	68	0.176	link	-	Mvd c.1126-82'-	ENSMUSTintron_variant
8	1.22E+08	A	C	base_qual	SNV	73	7	80	0.087	56	12	68	0.176	link	-	Gm20388 c.22-1861-	ENSMUSTintron_variant
8	1.25E+08	T	G	base_qual	SNV	26	4	30	0.133	28	18	46	0.391	link	-	Gnpat c.694-124'-	ENSMUSTintron_variant
8	1.26E+08	A	C	too_few_s	SNV	9	0	9	0	5	2	7	0.286	link	-	Ntpcr c.35-494A-	ENSMUSTintron_variant
9	3001493	C	G	mapping_c	SNV	348	5	353	0.014	423	12	435	0.028	link	-	Gm11168 c.-1853C>-	ENSMUSTupstream_gene_variant
9	3001493	C	G	mapping_c	SNV	348	5	353	0.014	423	12	435	0.028	link	-	Gm26870 n.822-863-	ENSMUSTupstream_gene_variant
9	3001493	C	G	mapping_c	SNV	348	5	353	0.014	423	12	435	0.028	link	-	Gm10722 c.519+49C-	ENSMUSTintron_variant
9	5327031	A	C	base_qual	SNV	12	1	13	0.077	17	5	22	0.227	link	-	Casp4 c.770-145-	ENSMUSTintron_variant
9	15341001	G	T	base_qual	SNV	141	5	146	0.034	153	11	164	0.067	link	-	Cep295 c.947-20C-	ENSMUSTintron_variant
9	25252790	T	G	base_qual	SNV	104	6	110	0.055	85	12	97	0.124	link	-	Sept7 c.61+91T>-	ENSMUSTintron_variant
9	40330488	A	C	weak_evid	SNV	69	1	70	0.014	67	4	71	0.056	link	-	1700110K n.-2986A>-	ENSMUSTupstream_gene_variant
9	40330488	A	C	weak_evid	SNV	69	1	70	0.014	67	4	71	0.056	link	-	Gramd1b c.666+295-	ENSMUSTintron_variant
9	40330488	A	C	weak_evid	SNV	69	1	70	0.014	67	4	71	0.056	link	-	1700110K n.4033048-	- intragenic_variant
9	41992206	A	C	base_qual	SNV	9	1	10	0.1	19	4	23	0.174	link	-	Sorl1 c.4651+98-	ENSMUSTintron_variant
9	43326876	T	G	base_qual	SNV	28	0	28	0	28	13	41	0.317	link	-	Trim29 c.1436-16I-	ENSMUSTintron_variant
9	45055393	T	G	base_qual	SNV	79	1	80	0.013	62	9	71	0.127	link	-	Mpzl2 c.*5678T>-	ENSMUSTdownstream_gene_variant
9	45055393	T	G	base_qual	SNV	79	1	80	0.013	62	9	71	0.127	link	-	Mpzl3 c.76+75T>-	ENSMUSTintron_variant
9	53450750	G	T	base_qual	SNV	54	2	56	0.036	55	13	68	0.191	link	-	Atm c.8182-11I-	ENSMUSTintron_variant
9	55149896	A	C	base_qual	SNV	38	6	44	0.136	30	11	41	0.268	link	-	Ube2q2 c.192+70A-	ENSMUSTintron_variant
9	55149904	T	G	base_qual	SNV	31	6	37	0.162	28	9	37	0.243	link	-	Ube2q2 c.192+78T-	ENSMUSTintron_variant
9	55208982	T	G	base_qual	SNV	58	2	60	0.033	62	10	72	0.139	link	-	Fbxo22 c.-70T>-G	ENSMUST5_prime_UTR_variant
9	55208982	T	G	base_qual	SNV	58	2	60	0.033	62	10	72	0.139	link	-	Ube2q2 c.*2991T>-	ENSMUSTdownstream_gene_variant
9	57022127	T	G	base_qual	SNV	66	0	66	0	66	11	77	0.143	link	-	Ptpn9 c.208-81T-	ENSMUSTintron_variant
9	57117676	G	T	base_qual	SNV	26	2	28	0.071	37	8	45	0.178	link	-	Sin3a c.3198+12-	

9	1.09E+08 .	A	G	too_few_s SNV	3	0	3	0	7	2	9	0.222 link	-	Gm42494	n.-3139A>-	ENSMUSTupstream_gene_variant
9	1.09E+08 .	A	G	too_few_s SNV	3	0	3	0	7	2	9	0.222 link	-	Fbxw16	c.992-231'-	ENSMUSTintron_variant
9	1.09E+08 .	C	A	PASS SNV	103	0	103	0	92	21	113	0.186 link	-	Fbxw16	c.-99G>T	ENSMUSTupstream_gene_variant
9	1.09E+08 .	C	A	PASS SNV	103	0	103	0	92	21	113	0.186 link	-	Gm42493	n.123+44C-	ENSMUSTintron_variant
9	1.11E+08 .	G	T	base_qual SNV	32	2	34	0.059	40	20	60	0.333 link	-	Trank1	c.1765+79-	ENSMUSTintron_variant
9	1.14E+08 .	G	T	base_qual SNV	71	2	73	0.027	77	13	90	0.144 link	-	-	n.1141879-	- intergenic_region
9	1.15E+08 .	C	T	PASS SNV	88	0	88	0	77	12	89	0.135 link	-	Osbp10	c.1252-37I-	ENSMUSTintron_variant
9	1.19E+08 .	G	T	non_homn SNV	80	3	83	0.036	82	4	86	0.047 link	-	RP24-257I/n.	*4266C>-	ENSMUSTdownstream_gene_variant
9	1.19E+08 .	G	T	non_homn SNV	80	3	83	0.036	82	4	86	0.047 link	-	Golga4	c.6426+93-	ENSMUSTintron_variant
X	8587576 .	T	A	weak_evid SNV	80	1	81	0.012	67	5	72	0.069 link	-	Ssxb3	c.324+74A-	ENSMUSTintron_variant
X	53774597 .	A	C	base_qual SNV	199	18	217	0.083	213	22	235	0.094 link	-	Gm14593	n.*1468A>-	ENSMUSTdownstream_gene_variant
X	73196132 .	T	G	base_qual SNV	15	0	15	0	17	6	23	0.261 link	-	Xlr3b	c.211+156-	ENSMUSTintron_variant
X	73196132 .	T	G	base_qual SNV	15	0	15	0	17	6	23	0.261 link	-	Xlr5a	n.7319613-	- intragenic_variant
X	99137036 .	T	G	base_qual SNV	80	0	80	0	68	5	73	0.068 link	-	Efnb1	c.128+23T-	ENSMUSTintron_variant
X	1.37E+08 .	C	A	base_qual SNV	13	0	13	0	21	6	27	0.222 link	-	Rab9b	c.*48G>T	ENSMUST3_prime_UTR_variant
X	1.68E+08 .	T	G	base_qual SNV	17	0	17	0	26	5	31	0.161 link	-	Frmpd4	c.573+12S-	ENSMUSTintron_variant
X	1.69E+08 .	A	C	weak_evid SNV	100	0	100	0	109	8	117	0.068 link	-	Arhgap6	c.592-377I-	ENSMUSTintron_variant
X	1.69E+08 .	A	C	base_qual SNV	102	0	102	0	111	7	118	0.059 link	-	Arhgap6	c.592-377I-	ENSMUSTintron_variant
Y	90825633 .	A	G	non_homn SNV	205	3	208	0.014	193	7	200	0.035 link	-	-	n.9082563-	- intergenic_region
GL456221	114409 .	T	A	mapping_c SNV	5	0	5	0	2	4	6	0.667 link	-	Csprs	c.-23-333I-	ENSMUSTintron_variant
GL456210	33797 .	A	G	mapping_c SNV	134	4	138	0.029	165	8	173	0.046 link	-	AC125149	c.-78-236S-	ENSMUSTintron_variant
GL456212	137560 .	A	T	mapping_c SNV	33	2	35	0.057	38	18	56	0.321 link	-	AC168977	c.820+280-	ENSMUSTintron_variant
GL456212	139452 .	C	A	weak_evid SNV	10	0	10	0	9	5	14	0.357 link	-	AC168977	c.662-360I-	ENSMUSTintron_variant
GL456212	145404 .	C	T	weak_evid SNV	9	0	9	0	12	5	17	0.294 link	-	AC168977	c.316+440-	ENSMUSTintron_variant
GL456216	35213 .	G	C	base_qual SNV	138	18	156	0.115	147	24	171	0.14 link	-	DHR5X	c.80S-20G-	ENSMUSTintron_variant
10	81577631 .	T	G	base_qual SNV	248	0	248	0	195	18	213	0.085 link	-	Tle2	c.303T>G p.Ala101A	ENSMUSTsplice_region_variant+synonymous_variant
11	21885017 .	G	A	non_homn SNV	215	2	217	0.009	245	8	253	0.032 link	-	Wdpcp	c.2019G>p.Glu673G	ENSMUSTsynonymous_variant
11	96345559 .	T	G	base_qual SNV	216	9	225	0.04	208	12	220	0.055 link	-	Hoxb3	c.462T>G p.Gly154G	ENSMUSTsynonymous_variant
11	96345574 .	T	G	base_qual SNV	232	14	246	0.057	222	16	238	0.067 link	-	Hoxb3	c.477T>G p.Gly159G	ENSMUSTsynonymous_variant
14	51413041 rs1132076	T	A	mapping_c SNV	195	9	204	0.044	248	14	262	0.053 link	-	Vmn2r88	c.210T>A p.Ile70Ile	ENSMUSTsynonymous_variant
14	54894251 .	T	G	base_qual SNV	238	8	246	0.033	245	14	259	0.054 link	-	Pabpn1	c.96T>G p.Gly32Gly	ENSMUSTsynonymous_variant
15	86185640 .	T	G	base_qual SNV	153	0	153	0	146	5	151	0.033 link	-	Cerk	c.9A>C p.Ala3Ala	ENSMUSTsynonymous_variant
15	88965439 .	G	A	PASS SNV	265	0	265	0	254	5	259	0.019 link	-	Mlc1	c.690C>T p.Asn230A	ENSMUSTsynonymous_variant
16	32753575 .	T	C	mapping_c SNV	457	30	487	0.062	444	59	503	0.117 link	-	Muc4	c.3450T>(p.Ser1150)	ENSMUSTsynonymous_variant
16	91170382 .	A	C	base_qual SNV	191	9	200	0.045	154	10	164	0.061 link	-	Gm9881	c.453T>G p.Pro151P	ENSMUSTsynonymous_variant
18	90592082 .	C	T	mapping_c SNV	227	4	231	0.017	269	6	275	0.022 link	-	CH25-588	c.1443C>T p.Gly481G	ENSMUSTsynonymous_variant
5	1.47E+08 .	A	C	base_qual SNV	100	5	105	0.048	83	22	105	0.21 link	-	Pan3	c.321A>C p.Gly107G	ENSMUSTsynonymous_variant
6	41304970 .	C	A	PASS SNV	391	0	391	0	337	71	408	0.174 link	-	Try4	c.489C>A p.Ala163A	ENSMUSTsynonymous_variant
7	73417952 .	C	T	weak_evid SNV	260	2	262	0.008	249	6	255	0.024 link	-	Rgma	c.1284C>T p.Ala428A	ENSMUSTsynonymous_variant
8	47822604 .	T	G	base_qual SNV	144	1	145	0.007	145	26	171	0.152 link	-	Cldn24	c.462T>G p.Pro154P	ENSMUSTsynonymous_variant
8	83271595 .	T	G	base_qual SNV	190	2	192	0.01	149	20	169	0.118 link	-	Tbc1d9	c.3780T>(p.Ser1260)	ENSMUSTsynonymous_variant
8	1.09E+08 .	T	G	base_qual SNV	283	6	289	0.021	224	5	229	0.022 link	-	Zfhx3	c.10932T>p.Ala3644)	ENSMUSTsynonymous_variant
16	8706593 .	A	C	weak_evid SNV	136	0	136	0	114	27	141	0.191 link	-	Usp7	c.974+6T>-	ENSMUSTsplice_region_variant+intron_variant
16	8706595 .	A	C	PASS SNV	140	0	140	0	118	24	142	0.169 link	-	Usp7	c.974+4T>-	ENSMUSTsplice_region_variant+intron_variant
4	1.21E+08 .	T	G	base_qual SNV	113	1	114	0.009	97	7	104	0.067 link	-	Nfyc	c.388-4A>-	ENSMUSTsplice_region_variant+intron_variant
5	1.5E+08 .	T	G	base_qual SNV	148	0	148	0	120	15	135	0.111 link	-	B3glct	c.1037+6T-	ENSMUSTsplice_region_variant+intron_variant
6	13205731 .	A	C	base_qual SNV	115	0	115	0	81	17	98	0.173 link	-	Vwde	c.810+6T>-	ENSMUSTsplice_region_variant+intron_variant
6	50194522 .	C	T	PASS SNV	110	0	110	0	136	4	140	0.029 link	-	Mpp6	c.1154-4C-	ENSMUSTsplice_region_variant+intron_variant
7	44521673 .	A	C	base_qual SNV	133	0	133	0	111	10	121	0.083 link	-	Mybp2	c.451+2T>-	ENSMUSTsplice_donor_variant+intron_variant
9	1.1E+08 .	T	G	weak_evid SNV	137	0	137	0	119	12	131	0.092 link	-	Smarcc1	c.915+4T>-	ENSMUSTsplice_region_variant+intron_variant
9	1.1E+08 .	T	G	weak_evid SNV	134	2	136	0.015	116	11	127	0.087 link	-	Smarcc1	c.915+5T>-	ENSMUSTsplice_region_variant+intron_variant
9	1.1E+08 .	T	G	base_qual SNV	133	0	133	0	121	9	130	0.069 link	-	Smarcc1	c.915+6T>-	ENSMUSTsplice_region_variant+intron_variant
X	1.69E+08 .	A	C	weak_evid SNV	100	0	100	0	109	8	117	0.068 link	-	Amelx	c.147+6T>-	ENSMUSTsplice_region_variant+intron_variant
X	1.69E+08 .	A	C	base_qual SNV	102	0	102	0	111	7	118	0.059 link	-	Amelx	c.147+4T>-	ENSMUSTsplice_region_variant+intron_variant