

Chr	Pos	ID	Ref	Alt	Filter	Variant_Typ	Normal_REF	Normal_ALT	Normal_Dep	Normal_Alle	Tumor_REF	Tumor_ALT	Tumor_Dep	Tumor_Alle	ig	ClinVar	Gene_Name	CDS_Chang	Amino_Acid_Change	TranscriptEffect
1	78390678		AC	A	non_homn	DEL	40	10	50	0.2	59	28	87	0.322	link	-	Sgpp2	c.423+36d	-	ENSMUST intron_variant
1	1.33E+08	rs2487306	AC	A	non_homn	DEL	265	54	319	0.169	317	86	403	0.213	link	-	Nfasc	c.2586+95-	-	ENSMUST intron_variant
10	56228606		CCATCC	C	PASS	DEL	259	0	259	0	197	47	244	0.193	link	-	Tbc1d32	c.9_26delT p.His3_Glu9delinsGln	-	ENSMUST disruptive_inframe_deletion
10	81622250		CCTA	C	weak_evid	DEL	4	0	4	0	1	7	8	0.875	link	-	Sirt6	c.*161_*16-	-	ENSMUST 3_prime_UTR_variant
10	99010505		ATTT	AT	multiallelic	DEL	15	1	17	0.059	17	5	26	0.192	link	-	Atp2b1	c.2336-15-	-	ENSMUST intron_variant
10	99010505		ATTT	A	multiallelic	DEL	15	1	17	0.059	17	4	26	0.154	link	-	Atp2b1	c.2336-15-	-	ENSMUST intron_variant
11	3894752		TG	T	non_homn	DEL	35	2	37	0.054	59	9	68	0.132	link	-	Dusp18	c.-2259del	-	ENSMUST upstream_gene_variant
11	3894752		TG	T	non_homn	DEL	35	2	37	0.054	59	9	68	0.132	link	-	4921536K	c.248+87d-	-	ENSMUST intron_variant
11	5063764		TG	T	non_homn	DEL	35	9	44	0.205	53	24	77	0.312	link	-	Ras10a	c.*3700del	-	ENSMUST downstream_gene_variant
11	5063764		TG	T	non_homn	DEL	35	9	44	0.205	53	24	77	0.312	link	-	Gas2l1	c.633+61d-	-	ENSMUST intron_variant
11	6028840		AC	A	alt_allele	j DEL	34	36	70	0.514	46	56	102	0.549	link	-	Camk2b	c.160+26d-	-	ENSMUST intron_variant
11	29821790		TC	T	non_homn	DEL	123	13	136	0.096	121	22	143	0.154	link	-	4931440F1c	c.*1700del	-	ENSMUST downstream_gene_variant
11	29821790		TC	T	non_homn	DEL	123	13	136	0.096	121	22	143	0.154	link	-	Enl6	c.1933-34-	-	ENSMUST intron_variant
11	58040460		TGG	T	non_homn	DEL	177	19	196	0.097	176	70	246	0.285	link	-	Larp1	c.417+20_	-	ENSMUST intron_variant
11	67286062	rs2389006	GT	G	non_homn	DEL	48	3	51	0.059	44	43	87	0.494	link	-	Myh8	c.1148-98-	-	ENSMUST intron_variant
11	69407147		TA	T	non_homn	DEL	315	35	350	0.1	281	53	334	0.159	link	-	Kdm6b	c.550-3del	-	ENSMUST splice_region_variant+intron_variant
11	69407147		TA	T	non_homn	DEL	315	35	350	0.1	281	53	334	0.159	link	-	Kdm6bos	n.*4448del	-	ENSMUST downstream_gene_variant
11	83070419		AC	A	non_homn	DEL	26	4	30	0.133	56	23	79	0.291	link	-	Sltf2	c.*98delC	-	ENSMUST 3_prime_UTR_variant
11	97343390		GGA	G	alt_allele	j DEL	25	26	51	0.51	4	16	20	0.8	link	-	Gpr179	c.1646-16_	-	ENSMUST intron_variant
11	1.07E+08		TG	T	non_homn	DEL	49	8	57	0.14	48	16	64	0.25	link	-	Ddx5	c.-1194del	-	ENSMUST upstream_gene_variant
11	1.07E+08		TG	T	non_homn	DEL	49	8	57	0.14	48	16	64	0.25	link	-	Cep95	c.19+143d	-	ENSMUST intron_variant
11	1.07E+08		AT	A	weak_evid	DEL	398	5	403	0.012	356	15	371	0.04	link	-	Bptf	c.3265delA p.Met1089fs	-	ENSMUST frameshift_variant
11	1.15E+08		G	GC	base_qual	INS	99	9	108	0.083	115	20	135	0.148	link	-	Gpr142	c.95-672d-	-	ENSMUST intron_variant
11	1.18E+08		CG	C	non_homn	DEL	34	9	43	0.209	41	28	69	0.406	link	-	Dnah17	c.3275+56-	-	ENSMUST intron_variant
12	17307555		T	TG	non_homn	INS	200	13	213	0.061	161	25	186	0.134	link	-	Atp6v1c2	c.284-56d-	-	ENSMUST intron_variant
12	31529423		TG	T	non_homn	DEL	67	27	94	0.287	91	55	146	0.377	link	-	Slc26a4	c.1803+35-	-	ENSMUST intron_variant
12	40180927	rs3870271	CA	C	non_homn	DEL	5	0	5	0	10	9	19	0.474	link	-	Lsmem1	c.128-154-	-	ENSMUST intron_variant
12	84604289		CGGG	C	non_homn	DEL	13	8	21	0.381	26	17	43	0.395	link	-	Abcd4	c.1559+41-	-	ENSMUST intron_variant
12	1.03E+08	rs3876513	TG	T	weak_evid	DEL	12	1	13	0.077	20	10	30	0.333	link	-	Unc79	c.1365+12-	-	ENSMUST intron_variant
13	17804427		CGCG	C	weak_evid	DEL	304	5	309	0.016	253	9	262	0.034	link	-	Cdk13	c.222_224(p.Ala75del)	-	ENSMUST disruptive_inframe_deletion
13	77030044		TC	T	non_homn	DEL	47	6	53	0.113	60	20	80	0.25	link	-	Mctp1	c.*104delC	-	ENSMUST 3_prime_UTR_variant
13	78198888		TC	T	PASS	DEL	31	2	33	0.061	17	10	27	0.37	link	-	Nr2f1	c.-316delG	-	ENSMUST 5_prime_UTR_variant
13	78198888		TC	T	PASS	DEL	31	2	33	0.061	17	10	27	0.37	link	-	A830082K	n.-3898del-	-	ENSMUST upstream_gene_variant
13	78198888		TC	T	PASS	DEL	31	2	33	0.061	17	10	27	0.37	link	-	A830082K	n.7819889-	-	intra-genic_variant
14	19417866		GA	G	weak_evid	DEL	396	12	408	0.029	120	9	129	0.07	link	-	Gm21738	c.161-501-	-	ENSMUST intron_variant
14	21848352		AC	A	non_homn	DEL	154	5	159	0.031	171	9	180	0.05	link	-	A430057M	n.-94delC	-	ENSMUST upstream_gene_variant
14	21848352		AC	A	non_homn	DEL	154	5	159	0.031	171	9	180	0.05	link	-	Vdac2	c.*3116del-	-	ENSMUST downstream_gene_variant
14	21848352		AC	A	non_homn	DEL	154	5	159	0.031	171	9	180	0.05	link	-	Comtd1	c.223-38d-	-	ENSMUST intron_variant
14	21848352		AC	A	non_homn	DEL	154	5	159	0.031	171	9	180	0.05	link	-	A430057M	n.2184836-	-	intra-genic_variant
14	42794463		A	AAGGAGG	low_frac	j INS	20	2	22	0.091	38	8	46	0.174	link	-	Gm10377	c.490+239	-	ENSMUST intron_variant
14	54550039		T	TAAAA	non_homn	INS	143	4	147	0.027	75	7	82	0.085	link	-	Haus4	c.56-7_56-	-	ENSMUST splice_region_variant+intron_variant
14	63017696		AC	A	alt_allele	j DEL	18	3	21	0.143	22	12	34	0.353	link	-	Defb43	c.59-70del	-	ENSMUST intron_variant
14	65731255		GC	G	non_homn	DEL	34	11	45	0.244	33	21	54	0.389	link	-	Scara5	c.916+73d-	-	ENSMUST intron_variant
15	9071392		TC	T	non_homn	DEL	20	13	33	0.394	15	21	36	0.583	link	-	Nadk2	c.-97delC	-	ENSMUST 5_prime_UTR_variant
15	9071392		TC	T	non_homn	DEL	20	13	33	0.394	15	21	36	0.583	link	-	Ranbp3l	c.*6386del-	-	ENSMUST downstream_gene_variant
15	9609543		AT	A	weak_evid	DEL	363	1	364	0.003	349	5	354	0.014	link	-	Spzf2	c.3894delA p.Lys1298fs	-	ENSMUST frameshift_variant
15	99524645		GC	G	non_homn	DEL	62	20	82	0.244	65	44	109	0.404	link	-	Faim2	c.214+55d-	-	ENSMUST intron_variant
15	1E+08		GC	G	non_homn	DEL	92	11	103	0.107	131	22	153	0.144	link	-	Slc11a2	c.-14242d-	-	ENSMUST upstream_gene_variant
15	1E+08		GC	G	non_homn	DEL	92	11	103	0.107	131	22	153	0.144	link	-	Gm5475	c.274-490-	-	ENSMUST intron_variant
16	42340621		TCCTC	T	weak_evid	DEL	56	1	57	0.018	92	7	99	0.071	link	-	Gap43	c.-123_-12-	-	ENSMUST 5_prime_UTR_variant
16	44449272		AC	A	non_homn	DEL	35	6	41	0.146	78	21	99	0.212	link	-	Cfap44	c.3573+76-	-	ENSMUST intron_variant
17	7326305		TG	T	alt_allele	j DEL	29	13	42	0.31	33	36	69	0.522	link	-	Tcp10a	c.106-63d-	-	ENSMUST intron_variant
17	23460746		C	CTTGTA	mapping	c INS	19	4	23	0.174	15	5	20	0.25	link	-	Vmn2r117	c.1655-15-	-	ENSMUST intron_variant
17	24441836		CG	C	non_homn	DEL	85	15	100	0.15	70	25	95	0.263	link	-	Ec1l	c.*2722del-	-	ENSMUST downstream_gene_variant
17	24441836		CG	C	non_homn	DEL	85	15	100	0.15	70	25	95	0.263	link	-	E4f1	c.*2144del-	-	ENSMUST downstream_gene_variant
17	24441836		CG	C	non_homn	DEL	85	15	100	0.15	70	25	95	0.263	link	-	Dnase1l2	c.531+21d-	-	ENSMUST intron_variant
17	25245069		CG	C	non_homn	DEL	21	9	30	0.3	36	28	64	0.438	link	-	Gnptg	c.-4959del-	-	ENSMUST upstream_gene_variant
17	25245069		CG	C	non_homn	DEL	21	9	30	0.3	36	28	64	0.438	link	-	Tsr3	c.*2409del-	-	ENSMUST downstream_gene_variant
17	25245069		CG	C	non_homn	DEL	21	9	30	0.3	36	28	64	0.438	link	-	Mir3547	n.*481delC	-	ENSMUST downstream_gene_variant
17	25245069		CG	C	non_homn	DEL	21	9	30	0.3	36	28	64	0.438	link	-	Baiap3	c.2745+67-	-	ENSMUST intron_variant
17	29690168		AC	A	alt_allele	j DEL	16	5	21	0.238	29	18	47	0.383	link	-	Cmtr1	c.1190-12-	-	ENSMUST intron_variant
17	29690168		AC	A	alt_allele	j DEL	16	5	21	0.238	29	18	47	0.383	link	-	Gm28043	c.*292-12-	-	ENSMUST intron_variant
17	29690168		AC	A	alt_allele	j DEL	16	5	21	0.238	29	18	47	0.383	link	-	Ccdc167	n.2969016-	-	intra-genic_variant
17	35874841		CTCCT	C	weak_evid	DEL	272	5	277	0.018	280	10	290	0.034	link	-	Ppp1r18	c.*853_*85-	-	ENSMUST 3_prime_UTR_variant
17	35874841		CTCCT	C	weak_evid	DEL	272	5	277	0.018	280	10	290	0.034	link	-	Dhx16	c.-5070_-5-	-	ENSMUST upstream_gene_variant
17	43064683		C	CTGTG	weak_evid	INS	5	0	5	0	3	4	7	0.571	link	-	Tnfrsf21	c.1244-23-	-	ENSMUST intron_variant
17	46538847		GC	G	non_homn	DEL	24	5	29	0.172	35	9	44	0.205	link	-	Gm26904	n.37-6106-	-	ENSMUST intron_variant
17	46538847		GC	G	non_homn	DEL	24	5	29	0.172	35	9	44	0.205	link	-	Cu19	c.1590+84-	-	ENSMUST intron_variant
17	74724609		CT	C	weak_evid	DEL	136	2	138	0.014	171	4	175	0.023	link	-	Ttc27	c.409-4del	-	ENSMUST splice_region_variant+intron_variant
17	84619594		AC	A	non_homn	DEL	29	4	33	0.121	27	16	43	0.372	link	-	Gm26066	n.-4807del-	-	ENSMUST upstream_gene_variant
17	84619594		AC	A	non_homn	DEL	29	4	33	0.121	27	16	43	0.372	link	-	Plekhh2	c.4291-18-	-	ENSMUST intron_variant
18	34628223		TG	T	PASS	DEL	87	10	97	0.103	96	27	123	0.22	link	-	Brd8	c.-3668del-	-	ENSMUST upstream_gene_variant
18	34628223		TG	T	PASS	DEL	87	10	97	0.103	96	27	123	0.22	link	-	Cdc23	c.*5770del-	-	ENSMUST downstream_gene_variant
18	34628223		TG	T	PASS	DEL	87	10	97	0.103	96	27	123	0.22	link	-	Klf20a	c.829+52d-	-	ENSMUST intron_variant
18	60808355	rs8255759	A	AG	non_homn	INS	135	20	1											

5	38739293 .	GAAAAC	G	weak_evid	DEL	411	2	413	0.005	302	8	310	0.026	link	-	Clnkos	n.46-2470,-	ENSMUST intron_variant
5	73421433 .	AC	A	non_homn	DEL	38	10	48	0.208	58	26	84	0.31	link	-	Cwh43	c.1061-10k-	ENSMUST intron_variant
5	1.09E+08 .	TC	T	non_homn	DEL	55	6	61	0.098	83	17	100	0.17	link	-	Idua	c.491-82di-	ENSMUST intron_variant
5	1.13E+08 .	TC	T	non_homn	DEL	20	2	22	0.091	43	15	58	0.259	link	-	Myo18b	c.2188+78-	ENSMUST intron_variant
5	1.16E+08 .	GCC	G	alt_allele_i	DEL	23	12	35	0.343	30	22	52	0.423	link	-	Cdc60	c.1029-76,-	ENSMUST intron_variant
5	1.18E+08 .	TG	T	non_homn	DEL	63	9	72	0.125	94	26	120	0.217	link	-	Gm26995	n..4233del-	ENSMUST upstream_gene_variant
5	1.18E+08 .	TG	T	non_homn	DEL	63	9	72	0.125	94	26	120	0.217	link	-	Nos1	c.3704-58k-	ENSMUST intron_variant
5	1.38E+08 .	GC	G	non_homn	DEL	48	9	57	0.158	63	20	83	0.241	link	-	Pcolce	c.797+72d-	ENSMUST intron_variant
6	5046089 .	C	CA	PASS	INS	152	2	154	0.013	104	56	160	0.35	link	-	Ppp1r9a	c.1531+21-	ENSMUST intron_variant
6	30614992 .	G	GTCTT	PASS	INS	77	0	77	0	47	23	70	0.329	link	-	Cpa5	c.199-35_1-	ENSMUST intron_variant
6	91950695 .	AC	A	non_homn	DEL	65	5	70	0.071	73	19	92	0.207	link	-	4930590J0	c.*56delC-	ENSMUST downstream_gene_variant
6	91950695 .	AC	A	non_homn	DEL	65	5	70	0.071	73	19	92	0.207	link	-	4930590J0	n.9195070-	- intragenic_variant
6	95117365 .	TGG	T	non_homn	DEL	186	15	201	0.075	191	24	215	0.112	link	-	Kbtbd8	c.-593_-59-	ENSMUST upstream_gene_variant
6	95117365 .	TGG	T	non_homn	DEL	186	15	201	0.075	191	24	215	0.112	link	-	Kbtbd8os	n.40+225,-	ENSMUST intron_variant
6	95117365 .	TGG	T	non_homn	DEL	186	15	201	0.075	191	24	215	0.112	link	-	Kbtbd8	n.9511737-	- intragenic_variant
6	1.25E+08 .	CG	C	non_homn	DEL	29	16	45	0.356	37	33	70	0.471	link	-	Cd27	c.*2840del-	ENSMUST downstream_gene_variant
6	1.25E+08 .	CG	C	non_homn	DEL	29	16	45	0.356	37	33	70	0.471	link	-	Mir8113	n.*214del-	ENSMUST downstream_gene_variant
6	1.25E+08 .	CG	C	non_homn	DEL	29	16	45	0.356	37	33	70	0.471	link	-	Tapbp1	c.308-53di-	ENSMUST intron_variant
6	1.25E+08 .	CG	C	non_homn	DEL	29	16	45	0.356	37	33	70	0.471	link	-	Vamp1	c.341-985i-	ENSMUST intron_variant
6	1.26E+08 .	T	TA	non_homn	INS	124	21	145	0.145	92	27	119	0.227	link	-	Vwfv	c.2187-34c-	ENSMUST intron_variant
6	1.29E+08 .	AAAAAC	A	PASS	DEL	210	1	211	0.005	134	19	153	0.124	link	-	Pzp	c.992-9_95-	ENSMUST splice_region_variant+intron_variant
6	1.37E+08 .	T	TG	non_homn	INS	176	20	196	0.102	190	23	213	0.108	link	-	Gucy2c	c.1085-5di-	ENSMUST splice_region_variant+intron_variant
7	34155756 rs2624914	TG	T	weak_evid	DEL	12	2	14	0.143	31	15	46	0.326	link	-	Uba2	c.871+128-	ENSMUST intron_variant
7	43792378 .	CG	C	non_homn	DEL	56	13	69	0.188	55	29	84	0.345	link	-	Klk9	c.200+55d-	ENSMUST intron_variant
7	43792378 .	CG	C	non_homn	DEL	56	13	69	0.188	55	29	84	0.345	link	-	2310002F	n.4379237-	- intragenic_variant
7	78916470 .	AG	A	non_homn	DEL	47	4	51	0.078	84	16	100	0.16	link	-	Isig20	c.229-53di-	ENSMUST intron_variant
7	1.32E+08 .	C	CGA	base_quali	INS	7	0	7	0	2	2	4	0.5	link	-	Hmx3	c.*439_*44-	ENSMUST downstream_gene_variant
7	1.32E+08 .	C	CGA	base_quali	INS	7	0	7	0	2	2	4	0.5	link	-	Fgfr2	n.1315450-	- intragenic_variant
8	27408258 .	C	CA	weak_evid	INS	89	9	98	0.092	66	18	84	0.214	link	-	Chrna6	c.374+56d-	ENSMUST intron_variant
8	45315794 rs2501327	TC	T	alt_allele_i	DEL	29	8	37	0.216	32	18	50	0.36	link	-	Cyp4v3	c.802-75di-	ENSMUST intron_variant
8	1.1E+08 .	CG	C	non_homn	DEL	26	4	30	0.133	27	15	42	0.357	link	-	Pmfbp1	c.2301+73-	ENSMUST intron_variant
9	3016097 .	GC	G	non_homn	DEL	225	3	228	0.013	66	4	70	0.057	link	-	Gm10719	c.-4057del-	ENSMUST upstream_gene_variant
9	3016097 .	GC	G	non_homn	DEL	225	3	228	0.013	66	4	70	0.057	link	-	Gm10721	c.*1754del-	ENSMUST downstream_gene_variant
9	3016097 .	GC	G	non_homn	DEL	225	3	228	0.013	66	4	70	0.057	link	-	Gm26870	n.219-174-	ENSMUST intron_variant
9	3016097 .	GC	G	non_homn	DEL	225	3	228	0.013	66	4	70	0.057	link	-	Gm10720	c.160+282-	ENSMUST intron_variant
9	3335527 .	C	CAT	PASS	INS	274	1	275	0.004	279	6	285	0.021	link	-	Alkbh8	c.-227_-22-	ENSMUST 5_prime_UTR_variant
9	44141904 .	AC	A	PASS	DEL	124	2	126	0.016	166	18	184	0.098	link	-	Mcam	c.*100delC-	ENSMUST 3_prime_UTR_variant
9	44141904 .	AC	A	PASS	DEL	124	2	126	0.016	166	18	184	0.098	link	-	Cbl	c.*9540del-	ENSMUST downstream_gene_variant
9	49517693 rs2637112	TG	T	alt_allele_i	DEL	21	5	26	0.192	47	19	66	0.288	link	-	Gm11149	c.-2463del-	ENSMUST upstream_gene_variant
9	49517693 rs2637112	TG	T	alt_allele_i	DEL	21	5	26	0.192	47	19	66	0.288	link	-	Ncam1	c.2020+23-	ENSMUST intron_variant
9	83836364 .	T	TAC	non_homn	INS	5	0	5	0	10	3	13	0.231	link	-	Ttk	c.136+486-	ENSMUST intron_variant
X	7947088 .	AC	A	alt_allele_i	DEL	96	35	131	0.267	46	118	164	0.72	link	-	Psmb6-ps	n.*3067del-	ENSMUST downstream_gene_variant
X	7947088 .	AC	A	alt_allele_i	DEL	96	35	131	0.267	46	118	164	0.72	link	-	Hdac6	c.90+36de-	ENSMUST intron_variant
X	1.02E+08 .	GC	G	non_homn	DEL	48	11	59	0.186	49	25	74	0.338	link	-	Taf1	c.412+28d-	ENSMUST intron_variant
X	1.3E+08 .	CG	C	base_quali	DEL	3	0	3	0	1	2	3	0.667	link	-	Diaph2	c.2352+43-	ENSMUST intron_variant
1	74784499 .	A	T	PASS	SNV	371	1	372	0.003	277	47	324	0.145	link	-	Wnt6	c.994A>C p.Ser332Cys	ENSMUST missense_variant
1	87929777 .	G	A	PASS	SNV	389	0	389	0	405	4	409	0.01	link	-	Dgkd	c.2210G>T p.Gly737Asp	ENSMUST missense_variant
1	1.18E+08 .	A	C	base_quali	SNV	306	7	313	0.022	304	12	316	0.038	link	-	Clasp1	c.907A>C p.Ile303Leu	ENSMUST missense_variant
1	1.35E+08 .	C	T	base_quali	SNV	218	27	245	0.11	124	36	160	0.225	link	-	Shisa4	c.20G>A p.Arg7His	ENSMUST missense_variant
1	1.63E+08 .	C	T	weak_evid	SNV	376	1	377	0.003	389	4	393	0.01	link	-	Fmo4	c.557G>A p.Arg186His	ENSMUST missense_variant
1	1.81E+08 .	C	T	weak_evid	SNV	360	1	361	0.003	352	4	356	0.011	link	-	Nvl	c.1847G>T p.Gly616Asp	ENSMUST missense_variant
10	58232188 rs1134013	C	T	mapping_c	SNV	260	12	272	0.044	331	29	360	0.081	link	-	Duxf3	c.488G>A p.Arg163Gln	ENSMUST missense_variant
10	1.3E+08 .	T	C	PASS	SNV	335	0	335	0	293	16	309	0.052	link	-	Oftr803	c.73A>G p.Ile25Val	ENSMUST missense_variant
11	23665783 .	C	T	base_quali	SNV	47	1	48	0.021	42	3	45	0.067	link	-	Pex13	c.62G>A p.Gly21Asp	ENSMUST missense_variant
11	72758596 .	T	G	alt_allele_i	SNV	156	5	161	0.031	166	15	181	0.083	link	-	Ankfy1	c.2919T>C p.Asn973Lys	ENSMUST missense_variant
11	73067741 .	A	C	base_quali	SNV	255	2	257	0.008	229	7	236	0.03	link	-	Ncbp3	c.726A>C p.Leu242Phe	ENSMUST missense_variant
11	83440296 .	C	A	base_quali	SNV	103	2	105	0.019	163	8	171	0.047	link	-	l700020L2	c.23C>A p.Thr8Asn	ENSMUST missense_variant
11	87583946 .	C	T	weak_evid	SNV	464	1	465	0.002	462	5	467	0.011	link	-	Sept4	c.383C>T p.Ala128Val	ENSMUST missense_variant
11	1.16E+08 .	T	A	weak_evid	SNV	228	1	229	0.004	210	5	215	0.023	link	-	Qrich2	c.3590A>T p.Lys119Met	ENSMUST missense_variant
12	31642767 .	A	C	base_quali	SNV	225	3	228	0.013	243	11	254	0.043	link	-	Dus4l	c.476T>G p.Ile159Arg	ENSMUST missense_variant
12	32038630 .	C	T	weak_evid	SNV	329	0	329	0	346	3	349	0.009	link	-	Prkar2b	c.329G>A p.Arg110His	ENSMUST missense_variant
12	89512059 .	A	C	PASS	SNV	302	0	302	0	338	14	352	0.04	link	-	Nrxn3	c.2921A>C p.Lys974Thr	ENSMUST missense_variant
14	1.21E+08 .	C	T	PASS	SNV	378	0	378	0	317	13	330	0.039	link	-	Farp1	c.2738C>T p.Thr913Met	ENSMUST missense_variant
15	39119411 .	T	C	weak_evid	SNV	463	1	464	0.002	432	4	436	0.009	link	-	Dcaf13	c.337C>T p.Arg113Trp	ENSMUST missense_variant
15	53885979 .	T	C	PASS	SNV	299	1	300	0.003	285	7	292	0.024	link	-	Gm7489	c.446T>C p.Leu149Pro	ENSMUST missense_variant
15	76477602 .	T	G	base_quali	SNV	124	12	136	0.088	126	13	139	0.094	link	-	Hsf1	c.2T>G p.Met17	ENSMUST start_lost
15	98480689 .	T	C	base_quali	SNV	49	3	52	0.058	31	8	39	0.205	link	-	Laiba	c.432A>G p.Ter144Tpxext*?	ENSMUST stop_loss
16	65827977 .	G	T	weak_evid	SNV	314	1	315	0.003	390	7	397	0.018	link	-	VglI3	c.210G>T p.Glu70Asp	ENSMUST missense_variant
17	33956172 .	A	G	weak_evid	SNV	404	1	405	0.002	381	4	385	0.01	link	-	Vps52	c.80A>G p.Glu27Gly	ENSMUST missense_variant
17	35684164 .	C	T	weak_evid	SNV	356	1	357	0.003	321	3	324	0.009	link	-	Ddr1	c.2141G>T p.Arg714His	ENSMUST missense_variant
17	42719520 .	A	C	base_quali	SNV	345	7	352	0.02	293	8	301	0.027	link	-	Adgrf2	c.47T>G p.Ile16Arg	ENSMUST missense_variant
18	34940222 .	A	C	base_quali	SNV	301	0	301	0	306	13	319	0.041	link	-	Hspa9	c.1608T>C p.Asp536Glu	ENSMUST missense_variant
18	84015497 .	T	A	base_quali	SNV	444	12	456	0.026	389	18	407	0.044	link	-	Tshz1	c.785C>T p.Thr262Met	ENSMUST missense_variant
19	47813953 .	G	C	weak_evid	SNV	274	0	274	0	219	3	222	0.014	link	-	Ctap43	c.986A>G p.Lys329Arg	ENSMUST missense_variant
2	19658140 .	G	A	PASS	SNV	319	1	320	0.003	344	5	349	0.014	link	-	Otod1	c.79G>A p.Ala27Thr	ENSMUST missense_variant
2	1.26E+08 .	G	A	weak_evid	SNV	300	1	301	0.003	332	3	335	0.009	link	-	Cep152	c.3497C>T p.Ala1166Val	ENSMUST missense_variant
2	1.64E+08 .	G	A	weak_evid	SNV	307	0	307	0	217	3	220	0.014	link	-	Pkig	c.97G>A p.Val33Met	ENSMUST missense_variant
2	1.68E+08 .	G	A	weak_evid	SNV	308	3	311	0.01	311	6	317	0.019	link	-	Cebpb	c.595G>A p.Ala199Thr	ENSMUST missense_variant
2	1.68E+08 .	C	T	PASS	SNV	378	1	379										

X	1.13E+08 .	G	A	PASS	SNV	232	0	232	0	206	5	211	0.024	link	-	Pof1b	c.1085C>T.p.Ala362Val	ENSMUST missense_variant
12	81971327 .	C	T	weak_evid	SNV	362	1	363	0.003	344	4	348	0.011	link	-	Pcnx	c.3958C>T.p.Gln1320*	ENSMUST stop_gained
1	5117012 .	A	C	base_qual	SNV	165	2	167	0.012	132	8	140	0.057	link	-	Atp6v1h	c.580-378/-	ENSMUST intron_variant
1	23866391 .	T	G	base_qual	SNV	97	3	100	0.03	97	4	101	0.04	link	-	Smap1	c.415-94C>	ENSMUST intron_variant
1	26687925 rs1134711	C	T	too_few_si	SNV	7	0	7	0	11	2	13	0.154	link	-	-	4931408C>c.-499G>A-	ENSMUST upstream_gene_variant
1	26687925 rs1134711	C	T	too_few_si	SNV	7	0	7	0	11	2	13	0.154	link	-	-	n.2668792-	- intergenic_region
1	38044624 .	C	T	mapping_c	SNV	36	3	39	0.077	27	2	29	0.069	link	-	Eif5b	c.2260-80/-	ENSMUST intron_variant
1	40345965 .	T	G	base_qual	SNV	58	8	66	0.121	73	7	80	0.087	link	-	Il1r2	c.733+88T-	ENSMUST intron_variant
1	43975407 .	A	C	base_qual	SNV	197	2	199	0.01	208	4	212	0.019	link	-	Tpp2	c.1914-9A/-	ENSMUST intron_variant
1	54550892 .	A	C	base_qual	SNV	49	5	54	0.093	58	17	75	0.227	link	-	Pgap1	c.301+85T-	ENSMUST intron_variant
1	59625291 .	T	G	base_qual	SNV	69	3	72	0.042	53	7	60	0.117	link	-	Gm24545	n.-1289T>-	ENSMUST upstream_gene_variant
1	59625291 .	T	G	base_qual	SNV	69	3	72	0.042	53	7	60	0.117	link	-	Gm973	c.1937+11-	ENSMUST intron_variant
1	59625291 .	T	G	base_qual	SNV	69	3	72	0.042	53	7	60	0.117	link	-	Sumo1	n.5962529-	- intragenic_variant
1	65205691 .	T	G	base_qual	SNV	221	12	233	0.052	254	18	272	0.066	link	-	Pikfyve	c.911+13T-	ENSMUST intron_variant
1	69684724 .	C	T	weak_evid	SNV	163	0	163	0	217	3	220	0.014	link	-	Ilkzf2	c.4-552G>-	ENSMUST intron_variant
1	70265065 .	C	T	PASS	SNV	201	4	205	0.02	150	84	234	0.359	link	-	Spag16	c.1238+16-	ENSMUST intron_variant
1	74622136 .	A	G	base_qual	SNV	85	2	87	0.023	90	9	99	0.091	link	-	Stk36	c.1381-60/-	ENSMUST intron_variant
1	74902095 .	A	C	base_qual	SNV	147	7	154	0.045	145	12	157	0.076	link	-	Ccdc108	c.*40T>G-	ENSMUST 3_prime_UTR_variant
1	74902095 .	A	C	base_qual	SNV	147	7	154	0.045	145	12	157	0.076	link	-	Gm15841	n.-276A>C-	ENSMUST upstream_gene_variant
1	74902095 .	A	C	base_qual	SNV	147	7	154	0.045	145	12	157	0.076	link	-	Mir375	n.-1374T>-	ENSMUST upstream_gene_variant
1	74904595 .	G	A	base_qual	SNV	109	5	114	0.044	139	12	151	0.079	link	-	Mir375	n.-3874C>-	ENSMUST upstream_gene_variant
1	74904595 .	G	A	base_qual	SNV	109	5	114	0.044	139	12	151	0.079	link	-	Ccdc108	c.4718+38-	ENSMUST intron_variant
1	74904595 .	G	A	base_qual	SNV	109	5	114	0.044	139	12	151	0.079	link	-	Gm15841	n.88-851G-	ENSMUST intron_variant
1	80536001 .	T	G	base_qual	SNV	224	3	227	0.013	169	17	186	0.091	link	-	Dock10	c.4394-36/-	ENSMUST intron_variant
1	85112004 rs1133202	G	A	weak_evid	SNV	185	0	185	0	190	10	200	0.05	link	-	A530032D	c.-2636C>-	ENSMUST upstream_gene_variant
1	85112004 rs1133202	G	A	weak_evid	SNV	185	0	185	0	190	10	200	0.05	link	-	Gm16038	n.-3315G>-	ENSMUST upstream_gene_variant
1	85112004 rs1133202	G	A	weak_evid	SNV	185	0	185	0	190	10	200	0.05	link	-	A530040E	n.896+45C-	ENSMUST intron_variant
1	85112004 rs1133202	G	A	weak_evid	SNV	185	0	185	0	190	10	200	0.05	link	-	C130026I2	n.8511200-	- intragenic_variant
1	85245213 rs1078675	C	A	weak_evid	SNV	7	1	8	0.125	9	4	13	0.308	link	-	Gm16028	n.-1638C>-	ENSMUST upstream_gene_variant
1	85245213 rs1078675	C	A	weak_evid	SNV	7	1	8	0.125	9	4	13	0.308	link	-	C130026I2	c.*1724G>-	ENSMUST downstream_gene_variant
1	85245213 rs1078675	C	A	weak_evid	SNV	7	1	8	0.125	9	4	13	0.308	link	-	Gm2619	n.379+691-	ENSMUST intron_variant
1	85245213 rs1078675	C	A	weak_evid	SNV	7	1	8	0.125	9	4	13	0.308	link	-	C130026I2	n.8524521-	- intragenic_variant
1	85246517 rs1083678	G	A	PASS	SNV	11	0	11	0	16	4	20	0.2	link	-	C130026I2	c.*420C>T-	ENSMUST 3_prime_UTR_variant
1	85246517 rs1083678	G	A	PASS	SNV	11	0	11	0	16	4	20	0.2	link	-	Gm16028	n.-334G>A-	ENSMUST upstream_gene_variant
1	85246517 rs1083678	G	A	PASS	SNV	11	0	11	0	16	4	20	0.2	link	-	Gm2619	n.379+678-	ENSMUST intron_variant
1	85247568 rs1133465	T	A	weak_evid	SNV	22	0	22	0	12	3	15	0.2	link	-	C130026I2	c.677-432/-	ENSMUST intron_variant
1	85247568 rs1133465	T	A	weak_evid	SNV	22	0	22	0	12	3	15	0.2	link	-	Gm16028	n.543+175-	ENSMUST intron_variant
1	85247568 rs1133465	T	A	weak_evid	SNV	22	0	22	0	12	3	15	0.2	link	-	Gm2619	n.379+667-	ENSMUST intron_variant
1	85247569 rs1135361	C	A	weak_evid	SNV	22	0	22	0	12	3	15	0.2	link	-	C130026I2	c.677-433/-	ENSMUST intron_variant
1	85247569 rs1135361	C	A	weak_evid	SNV	22	0	22	0	12	3	15	0.2	link	-	Gm16028	n.543+176-	ENSMUST intron_variant
1	85247569 rs1135361	C	A	weak_evid	SNV	22	0	22	0	12	3	15	0.2	link	-	Gm2619	n.379+667-	ENSMUST intron_variant
1	85257109 rs1076836	A	G	weak_evid	SNV	10	0	10	0	16	3	19	0.158	link	-	Gm16028	n.*1644A>-	ENSMUST downstream_gene_variant
1	85257109 rs1076836	A	G	weak_evid	SNV	10	0	10	0	16	3	19	0.158	link	-	C130026I2	c.451+277-	ENSMUST intron_variant
1	85257109 rs1076836	A	G	weak_evid	SNV	10	0	10	0	16	3	19	0.158	link	-	Gm2619	n.379+572-	ENSMUST intron_variant
1	85257150 .	G	T	PASS	SNV	19	0	19	0	37	6	43	0.14	link	-	Gm16028	n.*1685G>-	ENSMUST downstream_gene_variant
1	85257150 .	G	T	PASS	SNV	19	0	19	0	37	6	43	0.14	link	-	C130026I2	c.451+236-	ENSMUST intron_variant
1	85257150 .	G	T	PASS	SNV	19	0	19	0	37	6	43	0.14	link	-	Gm2619	n.379+572-	ENSMUST intron_variant
1	85513427 rs1132331	C	A	mapping_c	SNV	55	3	58	0.052	52	11	63	0.175	link	-	Gm16092	n.192-81G-	ENSMUST intron_variant
1	85513427 rs1132331	C	A	mapping_c	SNV	55	3	58	0.052	52	11	63	0.175	link	-	Gm2427	n.782+170-	ENSMUST intron_variant
1	85601210 .	T	C	low_frac_j	SNV	577	7	584	0.012	564	29	593	0.049	link	-	Sp110	c.-5102A>-	ENSMUST upstream_gene_variant
1	85601210 .	T	C	low_frac_j	SNV	577	7	584	0.012	564	29	593	0.049	link	-	Gm16094	n.*1371T>-	ENSMUST downstream_gene_variant
1	85601210 .	T	C	low_frac_j	SNV	577	7	584	0.012	564	29	593	0.049	link	-	Gm10552	n.*2875A>-	ENSMUST downstream_gene_variant
1	85601210 .	T	C	low_frac_j	SNV	577	7	584	0.012	564	29	593	0.049	link	-	Sp140	c.32+197T>-	ENSMUST intron_variant
1	85635109 .	A	C	weak_evid	SNV	8	0	8	0	9	3	12	0.25	link	-	Sp140	c.973-450/-	ENSMUST intron_variant
1	88231855 rs4784677	C	T	weak_evid	SNV	6	0	6	0	8	3	11	0.273	link	-	Mroh2a	c.557-389/-	ENSMUST intron_variant
1	88231886 rs5133683	C	T	PASS	SNV	9	0	9	0	14	4	18	0.222	link	-	Mroh2a	c.557-358/-	ENSMUST intron_variant
1	88232751 rs0119923	T	A	weak_evid	SNV	3	0	3	0	0	3	3	1	link	-	Mroh2a	c.655+409-	ENSMUST intron_variant
1	88238220 .	C	T	PASS	SNV	9	0	9	0	23	7	30	0.233	link	-	Mroh2a	c.1554+26-	ENSMUST intron_variant
1	88238261 .	C	T	weak_evid	SNV	5	0	5	0	12	6	18	0.333	link	-	Mroh2a	c.1554+30-	ENSMUST intron_variant
1	88239389 rs4724443	C	T	weak_evid	SNV	6	0	6	0	5	3	8	0.375	link	-	Mroh2a	c.1702+34-	ENSMUST intron_variant
1	88239452 rs4676275	T	C	weak_evid	SNV	8	0	8	0	2	3	5	0.6	link	-	Mroh2a	c.1702+41-	ENSMUST intron_variant
1	88245774 rs4998324	T	A	PASS	SNV	32	0	32	0	29	5	34	0.147	link	-	Mroh2a	c.2566-21/-	ENSMUST intron_variant
1	88260256 .	T	G	weak_evid	SNV	22	0	22	0	35	7	42	0.167	link	-	Mroh2a	c.*230T>G-	ENSMUST 3_prime_UTR_variant
1	88260256 .	T	G	weak_evid	SNV	22	0	22	0	35	7	42	0.167	link	-	Hjupr	c.*4925A>-	ENSMUST downstream_gene_variant
1	88501170 rs1134142	T	G	base_qual	SNV	320	3	323	0.009	212	8	220	0.036	link	-	Glrip1	c.506-28A/-	ENSMUST intron_variant
1	90959936 .	G	A	base_qual	SNV	56	2	58	0.034	58	9	67	0.134	link	-	Rab17	c.435+66C-	ENSMUST intron_variant
1	93561355 .	T	G	base_qual	SNV	20	2	22	0.091	31	6	37	0.162	link	-	Farp2	c.331+169-	ENSMUST intron_variant
1	1.31E+08 .	G	A	base_qual	SNV	307	5	312	0.016	286	16	302	0.053	link	-	Gm29427	c.513+32C-	ENSMUST intron_variant
1	1.31E+08 .	G	A	base_qual	SNV	307	5	312	0.016	286	16	302	0.053	link	-	Pikfb2	c.513+32C-	ENSMUST intron_variant
1	1.32E+08 .	T	G	base_qual	SNV	134	5	139	0.036	147	10	157	0.064	link	-	Slc41a1	c.477+70T-	ENSMUST intron_variant
1	1.35E+08 .	T	G	base_qual	SNV	204	7	211	0.033	157	11	168	0.065	link	-	Ube2t	c.109+65T-	ENSMUST intron_variant
1	1.36E+08 .	T	G	base_qual	SNV	187	18	205	0.088	166	22	188	0.117	link	-	Tmem9	c.158+24T-	ENSMUST intron_variant
1	1.36E+08 .	A	C	base_qual	SNV	23	3	26	0.115	42	6	48	0.125	link	-	Cacna1s	c.1394-11/-	ENSMUST intron_variant
1	1.54E+08 .	T	G	base_qual	SNV	93	2	95	0.021	79	9	88	0.102	link	-	C230024C	n.-3750A>-	ENSMUST upstream_gene_variant
1	1.54E+08 .	T	G	base_qual	SNV	93	2	95	0.021	79	9	88	0.102	link	-	Gm28513	n.*1973A>-	ENSMUST downstream_gene_variant
1	1.54E+08 .	T	G	base_qual	SNV	93	2	95	0.021	79	9	88	0.102	link	-	Rgs16	c.156-41T-	ENSMUST intron_variant
1	1.54E+08 .	T	G	alt_allele_j	SNV	14	4	18	0.222	18	8	26	0.308	link	-	Cacna1e	c.3562-16/-	ENSMUST intron_variant
1	1.56E+08 .	T	C	base_qual	SNV	18	1	19	0.053	12	8	20	0.4	link	-	Lhx4	c.*113A>C-	ENSMUST 3_prime_UTR_variant
1	1.56E+08 .	A	C	base_qual	SNV	33	5	38	0.132	55	9	64	0.141	link	-	Axdnd1	c.572+113-	ENSMUST intron_variant
1	1.56E+08 .	T	C	base_qual	SNV	38	4	42	0.095	37	8	45						

10	71277478	A	G	base_qual	SNV	145	0	145	0	121	7	128	0.055	link	-	Ube2d1	c.24+7623	-	ENSMUST intron_variant
10	79856311	A	C	base_qual	SNV	113	8	121	0.066	138	15	153	0.098	link	-	E130317F	n.-1355T>	-	ENSMUST upstream_gene_variant
10	79856311	A	C	base_qual	SNV	113	8	121	0.066	138	15	153	0.098	link	-	Ptbp1	c.9-193A>	-	ENSMUST intron_variant
10	80055192	G	T	base_qual	SNV	30	1	31	0.032	63	12	75	0.16	link	-	Sbno2	c.*2224C>	-	ENSMUST downstream_gene_variant
10	80055192	G	T	base_qual	SNV	30	1	31	0.032	63	12	75	0.16	link	-	Gpx4	c.644+73G	-	ENSMUST intron_variant
10	80836259	T	G	base_qual	SNV	10	1	11	0.091	18	3	21	0.143	link	-	Lingo3	c.-47-118A	-	ENSMUST intron_variant
10	85146971	T	G	base_qual	SNV	45	3	48	0.062	38	8	46	0.174	link	-	Cry1	c.685-95A	-	ENSMUST intron_variant
10	89414610	T	G	non_homn	SNV	20	2	22	0.091	14	7	21	0.333	link	-	Gas2l3	c.763-118I	-	ENSMUST intron_variant
10	92967391	A	C	base_qual	SNV	34	2	36	0.056	32	10	42	0.238	link	-	Cfap54	c.4699+89	-	ENSMUST intron_variant
10	93562974	T	G	base_qual	SNV	35	1	36	0.028	84	10	94	0.106	link	-	Ccdc38	c.533+80T	-	ENSMUST intron_variant
10	1.1E+08	T	C	base_qual	SNV	188	1	189	0.005	196	3	199	0.015	link	-	Nav3	c.6461+13	-	ENSMUST intron_variant
10	1.17E+08	A	C	base_qual	SNV	38	1	39	0.026	58	8	66	0.121	link	-	Myrf1	c.1368+76	-	ENSMUST intron_variant
10	1.18E+08	T	G	base_qual	SNV	11	0	11	0	34	5	39	0.128	link	-	Nup107	c.684-171T	-	ENSMUST intron_variant
10	1.19E+08	G	A	base_qual	SNV	231	0	231	0	201	8	209	0.038	link	-	Dyrk2	c.-79C>T	-	ENSMUST 5_prime_UTR_variant
10	1.2E+08	A	C	base_qual	SNV	164	9	173	0.052	125	18	143	0.126	link	-	Tmbim4	c.313-39A	-	ENSMUST intron_variant
10	1.27E+08	A	C	base_qual	SNV	90	2	92	0.022	62	9	71	0.127	link	-	Mettl21b	c.*70T>G	-	ENSMUST 3_prime_UTR_variant
10	1.27E+08	A	C	base_qual	SNV	90	2	92	0.022	62	9	71	0.127	link	-	Tsfm	c.-2038T>	-	ENSMUST upstream_gene_variant
10	1.27E+08	A	C	base_qual	SNV	112	2	114	0.018	168	14	182	0.077	link	-	Klf5a	c.445+69T	-	ENSMUST intron_variant
10	1.27E+08	A	C	base_qual	SNV	161	3	164	0.018	109	6	115	0.052	link	-	R3hdm2	c.208-47A	-	ENSMUST intron_variant
10	1.28E+08	G	A	base_qual	SNV	126	2	128	0.016	132	10	142	0.07	link	-	Ndufa4l2	c.*2595G>	-	ENSMUST downstream_gene_variant
10	1.28E+08	G	A	base_qual	SNV	126	2	128	0.016	132	10	142	0.07	link	-	Shmt2	c.857+27C	-	ENSMUST intron_variant
10	1.29E+08	T	G	base_qual	SNV	41	0	41	0	59	16	75	0.213	link	-	Ikzf4	c.866-88A	-	ENSMUST intron_variant
10	1.29E+08	T	G	base_qual	SNV	35	0	35	0	57	8	65	0.123	link	-	Ikzf4	c.866-98A	-	ENSMUST intron_variant
10	1.3E+08	T	C	PASS	SNV	335	0	335	0	293	16	309	0.052	link	-	Gm24717	n.-4011T>	-	ENSMUST upstream_gene_variant
11	3185600	A	G	weak_evid	SNV	97	1	98	0.01	74	5	79	0.063	link	-	Sfil	c.266+46S	-	ENSMUST intron_variant
11	5279653	A	C	non_homn	SNV	79	1	80	0.013	61	0	61	0	link	-	Znrf3	c.*71T>G	-	ENSMUST 3_prime_UTR_variant
11	6274377	A	C	base_qual	SNV	260	2	262	0.008	277	11	288	0.038	link	-	n-R5a67	n.*953A>C	-	ENSMUST downstream_gene_variant
11	6274377	A	C	base_qual	SNV	260	2	262	0.008	277	11	288	0.038	link	-	Tmed4	c.261+21T	-	ENSMUST upstream_gene_variant
11	23665783	C	T	base_qual	SNV	47	1	48	0.021	42	3	45	0.067	link	-	Pus10	c.-12+35C	-	ENSMUST intron_variant
11	23890162	A	C	base_qual	SNV	125	0	125	0	131	7	138	0.051	link	-	Gm12061	n.-4398A>	-	ENSMUST upstream_gene_variant
11	23890162	A	C	base_qual	SNV	125	0	125	0	131	7	138	0.051	link	-	Papogl	c.246+67T	-	ENSMUST intron_variant
11	32615991	G	T	base_qual	SNV	71	0	71	0	79	21	100	0.21	link	-	Stk10	c.2649+85	-	ENSMUST intron_variant
11	35675827	A	C	base_qual	SNV	148	4	152	0.026	126	11	137	0.08	link	-	Slit3	c.2943-18I	-	ENSMUST intron_variant
11	46389174	A	G	PASS	SNV	48	0	48	0	35	12	47	0.255	link	-	Itk	c.138+99T	-	ENSMUST intron_variant
11	53389793	T	G	alt_allele	JSNV	217	9	226	0.04	222	13	235	0.055	link	-	Gm25930	n.-609T>G	-	ENSMUST upstream_gene_variant
11	58981418	T	G	base_qual	SNV	52	1	53	0.019	65	5	70	0.071	link	-	1210058D	n.-3368A>	-	ENSMUST upstream_gene_variant
11	58981418	T	G	base_qual	SNV	52	1	53	0.019	65	5	70	0.071	link	-	Trim11	c.501+82T	-	ENSMUST intron_variant
11	59009461	A	C	base_qual	SNV	44	5	49	0.102	71	12	83	0.145	link	-	Gm10435	n.*2168A>	-	ENSMUST downstream_gene_variant
11	59009461	A	C	base_qual	SNV	44	5	49	0.102	71	12	83	0.145	link	-	Obscn	c.19349-8I	-	ENSMUST intron_variant
11	59063965	G	A	base_qual	SNV	6	0	6	0	11	3	14	0.214	link	-	Obscn	c.11071+2	-	ENSMUST intron_variant
11	67587022	A	G	base_qual	SNV	21	2	23	0.087	26	7	33	0.212	link	-	Gas7	c.3+207A>	-	ENSMUST intron_variant
11	69000403	G	T	base_qual	SNV	106	17	123	0.138	93	26	119	0.218	link	-	Gm25819	n.*4318G>	-	ENSMUST downstream_gene_variant
11	69000403	G	T	base_qual	SNV	106	17	123	0.138	93	26	119	0.218	link	-	Pfas	c.822-34C	-	ENSMUST intron_variant
11	70009741	T	C	too_few_s	SNV	9	0	9	0	18	2	20	0.1	link	-	Dvl2	c.*149T>C	-	ENSMUST 3_prime_UTR_variant
11	70009741	T	C	too_few_s	SNV	9	0	9	0	18	2	20	0.1	link	-	Mir324	n.-2302T>	-	ENSMUST upstream_gene_variant
11	70009741	T	C	too_few_s	SNV	9	0	9	0	18	2	20	0.1	link	-	Acadvl	c.*555A>G	-	ENSMUST downstream_gene_variant
11	71201009	A	C	base_qual	SNV	4	1	5	0.2	18	5	23	0.217	link	-	Nlrp1b	c.151+139	-	ENSMUST intron_variant
11	72065833	A	C	base_qual	SNV	70	1	71	0.014	86	7	93	0.075	link	-	Pitpnm3	c.1259-19I	-	ENSMUST intron_variant
11	72880769	T	G	base_qual	SNV	45	1	46	0.022	36	6	42	0.143	link	-	Gm26121	n.-1023T>	-	ENSMUST upstream_gene_variant
11	72880769	T	G	base_qual	SNV	45	1	46	0.022	36	6	42	0.143	link	-	Zze1f	c.4997+79	-	ENSMUST intron_variant
11	73176705	G	A	weak_evid	SNV	251	1	252	0.004	236	4	240	0.017	link	-	Emc6	c.-2C>T	-	ENSMUST 5_prime_UTR_variant
11	73176705	G	A	weak_evid	SNV	251	1	252	0.004	236	4	240	0.017	link	-	Tax1bp3	c.-599G>A	-	ENSMUST upstream_gene_variant
11	73176705	G	A	weak_evid	SNV	251	1	252	0.004	236	4	240	0.017	link	-	Pzrx5	c.*4871G>	-	ENSMUST downstream_gene_variant
11	73192970	A	C	base_qual	SNV	112	4	116	0.034	104	9	113	0.08	link	-	Ctns	c.140+85T	-	ENSMUST intron_variant
11	80029047	A	C	base_qual	SNV	49	0	49	0	25	7	32	0.219	link	-	Suz12	c.1602-10I	-	ENSMUST intron_variant
11	80029047	A	C	base_qual	SNV	49	0	49	0	25	7	32	0.219	link	-	Gm26563	n.300+52Z	-	ENSMUST intron_variant
11	80663538	T	G	base_qual	SNV	222	2	224	0.009	187	8	195	0.041	link	-	Myo1d	c.1539-42C	-	ENSMUST intron_variant
11	83440296	C	A	base_qual	SNV	103	2	105	0.019	163	8	171	0.047	link	-	Mmp28	c.*2255G>	-	ENSMUST downstream_gene_variant
11	94704043	A	C	base_qual	SNV	81	1	82	0.012	107	6	113	0.053	link	-	Gm11541	c.159+39T	-	ENSMUST intron_variant
11	96345571	C	T	weak_evid	SNV	417	4	421	0.01	458	5	463	0.011	link	-	Gm11536	n.-3463G>	-	ENSMUST upstream_gene_variant
11	96345571	C	T	weak_evid	SNV	417	4	421	0.01	458	5	463	0.011	link	-	Hoxb3os	n.2225G>I	-	ENSMUST non_coding_transcript_exon_variant
11	98582968	T	G	base_qual	SNV	26	0	26	0	42	7	49	0.143	link	-	Ormdl3	c.327-121I	-	ENSMUST intron_variant
11	99598238	G	C	too_few_s	SNV	11	0	11	0	17	2	19	0.105	link	-	Krtap9-3	c.-184C>G	-	ENSMUST upstream_gene_variant
11	99598238	G	C	too_few_s	SNV	11	0	11	0	17	2	19	0.105	link	-	Gm11938	c.*4634C>	-	ENSMUST downstream_gene_variant
11	99598238	G	C	too_few_s	SNV	11	0	11	0	17	2	19	0.105	link	-	-	n.9959823	-	intergenic_region
11	1.01E+08	G	A	base_qual	SNV	144	0	144	0	149	5	154	0.032	link	-	Stat5b	c.1473+50	-	ENSMUST intron_variant
11	1.01E+08	A	C	base_qual	SNV	141	2	143	0.014	150	5	155	0.032	link	-	Stat5b	c.1473+49	-	ENSMUST intron_variant
11	1.02E+08	A	C	base_qual	SNV	370	3	373	0.008	303	10	313	0.032	link	-	Tmub2	c.-47A>C	-	ENSMUST upstream_gene_variant
11	1.02E+08	A	C	base_qual	SNV	370	3	373	0.008	303	10	313	0.032	link	-	Atxn7l3	c.*6762T>	-	ENSMUST downstream_gene_variant
11	1.02E+08	A	C	base_qual	SNV	370	3	373	0.008	303	10	313	0.032	link	-	-	n.1022848	-	intergenic_region
11	1.03E+08	C	A	base_qual	SNV	28	2	30	0.067	47	11	58	0.19	link	-	Eftud2	c.-5595G>	-	ENSMUST upstream_gene_variant
11	1.03E+08	C	A	base_qual	SNV	28	2	30	0.067	47	11	58	0.19	link	-	Fam187a	c.-2063C>	-	ENSMUST upstream_gene_variant
11	1.03E+08	C	A	base_qual	SNV	28	2	30	0.067	47	11	58	0.19	link	-	Gfap	c.*5368G>	-	ENSMUST downstream_gene_variant
11	1.03E+08	C	A	base_qual	SNV	28	2	30	0.067	47	11	58	0.19	link	-	Ccdc103	c.276+103	-	ENSMUST intron_variant
11	1.03E+08	C	A	base_qual	SNV	28	2	30	0.067	47	11	58	0.19	link	-	Gm26668	n.3568+16	-	ENSMUST intron_variant
11	1.06E+08	A	C	base_qual	SNV	90	11	101	0.109	64	13	77	0.169	link	-	Ddx42	c.1301-85I	-	ENSMUST intron_variant
11	1.07E+08	A	C	base_qual	SNV	286	10	296	0.034	255	10	265	0.038	link	-	Cep95	c.-2913A>	-	ENSMUST upstream_gene_variant
11	1.07E+08	A	C	base_qual	SNV	286	10	296	0.034	255	10	265	0.038	link	-	Mir3064	n.-3687T>	-	ENSMUST upstream_gene_variant

12	80181345 .	G	A	base_qual	SNV	134	8	142	0.056	155	23	178	0.129	link	-	Actn1	c.1234+16-	ENSMUST intron_variant	
12	80181349 .	G	A	base_qual	SNV	146	6	152	0.039	154	28	182	0.154	link	-	Actn1	c.1234+12-	ENSMUST intron_variant	
12	83106735 .	A	C	base_qual	SNV	230	4	234	0.017	202	8	210	0.038	link	-	Rgs6	c.966-23A:-	ENSMUST intron_variant	
12	83776687 .	T	G	base_qual	SNV	34	1	35	0.029	30	8	38	0.211	link	-	Papln	c.1371+12-	ENSMUST intron_variant	
12	84114455 .	A	G	weak_evid	SNV	247	1	248	0.004	173	4	177	0.023	link	-	Acot6	c.*4916A>-	ENSMUST downstream_gene_variant	
12	84114455 .	A	G	weak_evid	SNV	247	1	248	0.004	173	4	177	0.023	link	-	DnaI1	c.3+56A>(-	ENSMUST intron_variant	
12	87224113 .	A	C	base_qual	SNV	70	3	73	0.041	96	6	102	0.059	link	-	Nxored1	c.688+45T-	ENSMUST intron_variant	
12	87286188 .	G	T	base_qual	SNV	17	0	17	0	21	1	22	0.045	link	-	Ism2	c.375+70T-	ENSMUST intron_variant	
12	87309690 .	T	A	too_few_s	SNV	4	0	4	0	10	2	12	0.167	link	-	Sptlc2	c.*211A>T-	ENSMUST 3_prime_UTR_variant	
12	87472182 .	C	T	weak_evid	SNV	213	1	214	0.005	203	3	206	0.015	link	-	Snnw1	c.14+66G>-	ENSMUST intron_variant	
12	89186983 .	A	C	base_qual	SNV	111	5	116	0.043	114	11	125	0.088	link	-	Nrxn3	c.758-39A:-	ENSMUST intron_variant	
12	1E+08 .	A	C	alt_allele	J_SNV	111	1	112	0.009	109	11	120	0.092	link	-	Psmc1	c.-76A>C-	ENSMUST upstream_gene_variant	
12	1E+08 .	A	C	alt_allele	J_SNV	111	1	112	0.009	109	11	120	0.092	link	-	-	n.1001101-	-	intergenic_region
12	1.03E+08 .	T	G	alt_allele	J_SNV	18	5	23	0.217	13	11	24	0.458	link	-	Btbd7	c.2572-12:-	ENSMUST intron_variant	
12	1.04E+08 .	A	C	base_qual	SNV	22	2	24	0.083	69	9	78	0.115	link	-	Serpina1b	c.*105T>G-	ENSMUST downstream_gene_variant	
12	1.04E+08 .	A	C	base_qual	SNV	22	2	24	0.083	69	9	78	0.115	link	-	-	n.1037281-	-	intergenic_region
12	1.05E+08 .	T	G	base_qual	SNV	112	3	115	0.026	113	10	123	0.081	link	-	Dicer1	c.2958-94/-	ENSMUST intron_variant	
12	1.06E+08 .	T	G	base_qual	SNV	143	3	146	0.021	117	11	128	0.086	link	-	Atg2b	c.5418-62/-	ENSMUST intron_variant	
12	1.06E+08 .	A	C	base_qual	SNV	18	3	21	0.143	30	6	36	0.167	link	-	Papola	c.332-125/-	ENSMUST intron_variant	
12	1.08E+08 .	C	T	weak_evid	SNV	347	1	348	0.003	230	4	234	0.017	link	-	Cyp46a1	c.283-37C:-	ENSMUST intron_variant	
12	1.11E+08 .	T	G	base_qual	SNV	19	4	23	0.174	24	5	29	0.172	link	-	Cdc42bpb	c.1141-16I-	ENSMUST intron_variant	
12	1.12E+08 .	A	C	base_qual	SNV	24	2	26	0.077	33	6	39	0.154	link	-	Gm15996	n.-1730T>-	ENSMUST upstream_gene_variant	
12	1.12E+08 .	A	C	base_qual	SNV	24	2	26	0.077	33	6	39	0.154	link	-	Apopt1	c.479+344-	ENSMUST intron_variant	
12	1.18E+08 .	A	C	base_qual	SNV	178	2	180	0.011	174	13	187	0.07	link	-	Dnah11	c.11118+1-	ENSMUST intron_variant	
13	3932588 .	T	G	base_qual	SNV	32	2	34	0.059	62	7	69	0.101	link	-	Tubal3	c.397-30T:-	ENSMUST intron_variant	
13	14193637 .	C	T	base_qual	SNV	103	5	108	0.046	82	9	91	0.099	link	-	Arid4b	c.3670+56-	ENSMUST intron_variant	
13	15660821 .	A	C	base_qual	SNV	139	2	141	0.014	136	9	145	0.062	link	-	Gli3	c.1243-60/-	ENSMUST intron_variant	
13	19350290 .	A	C	base_qual	SNV	239	3	242	0.012	202	9	211	0.043	link	-	Tcrg-C4	c.383-40A:-	ENSMUST intron_variant	
13	29849822 .	A	C	base_qual	SNV	12	0	12	0	20	4	24	0.167	link	-	Cdkal1	c.170+117-	ENSMUST intron_variant	
13	41109790 .	A	C	base_qual	SNV	64	2	66	0.03	85	8	93	0.086	link	-	Sycp2l	c.-4629A>-	ENSMUST upstream_gene_variant	
13	41109790 .	A	C	base_qual	SNV	64	2	66	0.03	85	8	93	0.086	link	-	Gcm2	c.90+75T>-	ENSMUST intron_variant	
13	46929671 .	G	A	weak_evid	SNV	136	1	137	0.007	103	3	106	0.028	link	-	Kif13a	c.-50C>T-	ENSMUST 5_prime_UTR_variant	
13	52841120 .	T	G	base_qual	SNV	106	6	112	0.054	117	14	131	0.107	link	-	Auh	c.581-56A:-	ENSMUST intron_variant	
13	58384699 rs1133271	G	A	base_qual	SNV	6	0	6	0	28	5	33	0.152	link	-	2210016F1c	c.331+125-	ENSMUST intron_variant	
13	58842674 .	A	C	too_few_s	SNV	3	0	3	0	11	2	13	0.154	link	-	Ntrk2	c.360-202/-	ENSMUST intron_variant	
13	59586378 .	T	G	base_qual	SNV	49	7	56	0.125	62	11	73	0.151	link	-	Naa35	c.124+97T-	ENSMUST intron_variant	
13	59731835 .	T	G	alt_allele	J_SNV	23	7	30	0.233	25	10	35	0.286	link	-	4930528D1c	c.-1810T>-	ENSMUST upstream_gene_variant	
13	59731835 .	T	G	alt_allele	J_SNV	23	7	30	0.233	25	10	35	0.286	link	-	Spta31d1	c.-115A>C-	ENSMUST upstream_gene_variant	
13	59731835 .	T	G	alt_allele	J_SNV	23	7	30	0.233	25	10	35	0.286	link	-	-	n.5973183-	-	intergenic_region
13	64111351 .	A	C	base_qual	SNV	19	3	22	0.136	36	11	47	0.234	link	-	Slc35d2	c.452+165-	ENSMUST intron_variant	
13	67728948 rs2310702	G	C	non_homn	SNV	16	1	17	0.059	20	7	27	0.259	link	-	Zfp65	c.6+113C>-	ENSMUST intron_variant	
13	77612768 .	T	G	base_qual	SNV	22	2	24	0.083	39	11	50	0.22	link	-	2210408I2	c.*124T>G-	ENSMUST 3_prime_UTR_variant	
13	85228826 .	T	G	base_qual	SNV	57	9	66	0.136	75	23	98	0.235	link	-	Rasa1	c.1750-61/-	ENSMUST intron_variant	
13	92221137 .	T	G	base_qual	SNV	87	5	92	0.054	112	9	121	0.074	link	-	Msh3	c.2875-52/-	ENSMUST intron_variant	
13	92847018 .	T	G	base_qual	SNV	88	2	90	0.022	90	13	103	0.126	link	-	Mtx3	c.321+65T-	ENSMUST intron_variant	
13	95104560 .	A	C	base_qual	SNV	68	5	73	0.068	121	9	130	0.069	link	-	Pde8b	c.590+93T-	ENSMUST intron_variant	
13	97093466 .	A	C	base_qual	SNV	38	5	43	0.116	36	11	47	0.234	link	-	Gm6169	c.*5313T>-	ENSMUST downstream_gene_variant	
13	97093466 .	A	C	base_qual	SNV	38	5	43	0.116	36	11	47	0.234	link	-	Fam169a	c.133-125/-	ENSMUST intron_variant	
13	1.03E+08 .	T	C	base_qual	SNV	130	5	135	0.037	171	10	181	0.055	link	-	Mast4	c.827+57A-	ENSMUST intron_variant	
13	1.03E+08 .	G	A	base_qual	SNV	137	7	144	0.049	164	21	185	0.114	link	-	Mast4	c.827+55C-	ENSMUST intron_variant	
13	1.03E+08 .	G	A	base_qual	SNV	145	6	151	0.04	177	15	192	0.078	link	-	Mast4	c.827+53C-	ENSMUST intron_variant	
13	1.13E+08 .	T	G	base_qual	SNV	21	1	22	0.045	36	5	41	0.122	link	-	SkiV2I2	c.2640-12:-	ENSMUST intron_variant	
14	14969313 .	A	C	base_qual	SNV	22	0	22	0	15	3	18	0.167	link	-	Nek10	c.2832-16:-	ENSMUST intron_variant	
14	20439595 .	A	C	base_qual	SNV	33	3	36	0.083	25	10	35	0.286	link	-	Cfap70	c.792+70T-	ENSMUST intron_variant	
14	30864663 .	T	G	base_qual	SNV	16	2	18	0.111	37	7	44	0.159	link	-	Tmem110	c.305+139-	ENSMUST intron_variant	
14	30920800 .	T	C	base_qual	SNV	253	3	256	0.012	207	15	222	0.068	link	-	Ith3	c.550-24A:-	ENSMUST intron_variant	
14	31117551 .	T	G	base_qual	SNV	8	1	9	0.111	19	10	29	0.345	link	-	Snim4	c.151+110-	ENSMUST intron_variant	
14	31117551 .	T	G	base_qual	SNV	8	1	9	0.111	19	10	29	0.345	link	-	Pbrm1	c.4942+13-	ENSMUST intron_variant	
14	33104713 .	T	G	base_qual	SNV	11	2	13	0.154	23	6	29	0.207	link	-	Wdyf4	c.3275-14:-	ENSMUST intron_variant	
14	33991952 .	T	G	base_qual	SNV	56	5	61	0.082	72	13	85	0.153	link	-	-	n.3399195-	-	intergenic_region
14	34588334 .	C	T	PASS	SNV	186	0	186	0	199	4	203	0.02	link	-	Opn4	c.*4415G>-	ENSMUST downstream_gene_variant	
14	34588334 .	C	T	PASS	SNV	186	0	186	0	199	4	203	0.02	link	-	Ldb3	c.93+43G>-	ENSMUST intron_variant	
14	35309196 .	A	C	base_qual	SNV	95	3	98	0.031	130	11	141	0.078	link	-	Grid1	c.781-36A:-	ENSMUST intron_variant	
14	37080072 .	T	G	base_qual	SNV	14	3	17	0.176	24	6	30	0.2	link	-	Cdhr1	c.2044-13I-	ENSMUST intron_variant	
14	43544077 rs5062591	A	C	mapping_c	SNV	14	1	15	0.067	12	5	17	0.294	link	-	Gm5799	c.130+304-	ENSMUST intron_variant	
14	46818258 .	G	A	alt_allele	J_SNV	35	8	43	0.186	32	7	39	0.179	link	-	Gmfb	c.4-776C>-	ENSMUST intron_variant	
14	51920411 .	A	C	base_qual	SNV	144	4	148	0.027	127	11	138	0.08	link	-	Rnase13	c.*1808T>-	ENSMUST downstream_gene_variant	
14	51920411 .	A	C	base_qual	SNV	144	4	148	0.027	127	11	138	0.08	link	-	Tppp2	c.328-16A:-	ENSMUST intron_variant	
14	51993923 .	A	C	base_qual	SNV	8	0	8	0	14	8	22	0.364	link	-	Arhgef40	c.2056-17I-	ENSMUST intron_variant	
14	51999694 .	A	C	base_qual	SNV	12	0	12	0	19	9	28	0.321	link	-	Arhgef40	c.3595-12I-	ENSMUST intron_variant	
14	52290899 .	A	G	base_qual	SNV	96	0	96	0	67	5	72	0.069	link	-	Mettl3	c.*4083T>-	ENSMUST downstream_gene_variant	
14	52290899 .	A	G	base_qual	SNV	96	0	96	0	67	5	72	0.069	link	-	Tox4	c.891+58A-	ENSMUST intron_variant	
14	54444129 .	T	G	base_qual	SNV	38	1	39	0.026	67	11	78	0.141	link	-	Mmp14	c.*3457T>-	ENSMUST downstream_gene_variant	
14	54444129 .	T	G	base_qual	SNV	38	1	39	0.026	67	11	78	0.141	link	-	-	n.5444412-	-	intergenic_region
14	55547900 .	T	G	base_qual	SNV	114	3	117	0.026	139	9	148	0.061	link	-	Pck2	c.1453+66-	ENSMUST intron_variant	
14	57037047 .	T	G	base_qual	SNV	31	1	32	0.031	45	8	53	0.151	link	-	Gja3	c.-17-117A-	ENSMUST intron_variant	
14	64990642 .	T	G	base_qual	SNV	234	3	237	0.013	203	10	213	0.047	link	-	Ints9	c.348+48T-	ENSMUST intron_variant	
14	66056277 .	T	C	weak_evid	SNV	9	0	9	0	23	3	26	0.115	link	-	Adam2	c.909+191-	ENSMUST intron_variant	
14	66988790 .	A	C	base_qual	SNV	70	6	76	0.079	73	8	81	0.099	link	-	Bnip3l	c.608+345-	ENSMUST intron_variant	
14	67700806 .	G	A	too_few_s	SNV	9	0	9	0	8	2	10	0.2						

15	76950219 .	A	C	base_qual	SNV	129	1	130	0.008	133	11	144	0.076	link	-	1110038F1c.530-30A>-	ENSMUST intron_variant	
15	77528954 .	T	G	base_qual	SNV	127	2	129	0.016	103	10	113	0.088	link	-	Apol7c c.141-46A>-	ENSMUST intron_variant	
15	78766938 .	T	G	base_qual	SNV	224	2	226	0.009	205	7	212	0.033	link	-	Mfng c.305-18A>-	ENSMUST intron_variant	
15	80375187 .	T	C	base_qual	SNV	83	3	86	0.035	104	16	120	0.133	link	-	Cacna1l c.3729-72>-	ENSMUST intron_variant	
15	81769256 .	T	G	base_qual	SNV	34	0	34	0	48	7	55	0.127	link	-	Zc3h7b c.285+75T>-	ENSMUST intron_variant	
15	85868629 .	A	C	base_qual	SNV	62	2	64	0.031	51	3	54	0.056	link	-	Gtse1 c.995-51A>-	ENSMUST intron_variant	
15	86125997 .	T	G	base_qual	SNV	37	2	39	0.051	70	13	83	0.157	link	-	Gramd4 c.790+115>-	ENSMUST intron_variant	
15	89773959 .	T	G	base_qual	SNV	387	2	389	0.005	336	11	347	0.032	link	-	-	intergenic_region	
15	90541156 .	A	C	base_qual	SNV	82	3	85	0.035	61	11	72	0.153	link	-	Cpne8 c.891+101>-	ENSMUST intron_variant	
15	98879700 rs1083545 C	A	PASS	SNV	SNV	100	4	104	0.038	118	13	131	0.099	link	-	Rhebl1 c.192+77G>-	ENSMUST intron_variant	
15	98917685 .	A	C	base_qual	SNV	18	2	20	0.1	32	7	39	0.179	link	-	Lmbr1l c.72+165T>-	ENSMUST intron_variant	
15	1.02E+08 .	T	G	base_qual	SNV	36	0	36	0	65	6	71	0.085	link	-	Krt79 c.469-85A>-	ENSMUST intron_variant	
16	13378197 .	A	C	base_qual	SNV	164	8	172	0.047	150	18	168	0.107	link	-	Mkl2 c.155-67A>-	ENSMUST intron_variant	
16	13378197 .	A	C	base_qual	SNV	164	8	172	0.047	150	18	168	0.107	link	-	Gm15738 n.354-122>-	ENSMUST intron_variant	
16	16342411 .	A	G	too_few_s	SNV	3	0	3	0	0	2	2	1	link	-	Dnm1l c.269-943>-	ENSMUST intron_variant	
16	17530519 .	T	G	base_qual	SNV	30	2	32	0.062	42	10	52	0.192	link	-	Lztr1 c.*4726T>-	ENSMUST downstream_gene_variant	
16	17530519 .	T	G	base_qual	SNV	30	2	32	0.062	42	10	52	0.192	link	-	Thap7 c.81-134A>-	ENSMUST intron_variant	
16	18899483 .	A	G	base_qual	SNV	180	1	181	0.006	173	11	184	0.06	link	-	Hira c.397+26A>-	ENSMUST intron_variant	
16	18899483 .	A	G	base_qual	SNV	180	1	181	0.006	173	11	184	0.06	link	-	Gm28539 c.*273+26>-	ENSMUST intron_variant	
16	22078818 .	T	G	base_qual	SNV	76	3	79	0.038	132	7	139	0.05	link	-	Igf2bp2 c.915-67A>-	ENSMUST intron_variant	
16	23125058 .	T	G	alt_allele	SNV	5	0	5	0	1	4	5	0.8	link	-	Rfc4 c.132-44A>-	ENSMUST intron_variant	
16	30545444 .	T	G	too_few_s	SNV	10	1	11	0.091	6	2	8	0.25	link	-	Tmem44 c.265-225>-	ENSMUST intron_variant	
16	31127612 .	T	G	base_qual	SNV	6	0	6	0	8	7	15	0.467	link	-	Acap2 c.745-179>-	ENSMUST intron_variant	
16	32827363 .	T	G	base_qual	SNV	153	2	155	0.013	141	11	152	0.072	link	-	Rubcn c.2079-11>-	ENSMUST intron_variant	
16	32979385 .	G	T	base_qual	SNV	73	0	73	0	89	4	93	0.043	link	-	Lrch3 c.1103-11>-	ENSMUST intron_variant	
16	33266934 .	C	T	base_qual	SNV	94	3	97	0.031	119	11	130	0.085	link	-	Snx4 c.399+49C>-	ENSMUST intron_variant	
16	35818592 .	A	C	base_qual	SNV	118	7	125	0.056	84	12	96	0.125	link	-	Hspbp1 c.742-87A>-	ENSMUST intron_variant	
16	35943328 .	C	T	non_homr	SNV	113	1	114	0.009	110	3	113	0.027	link	-	Dtx3l c.-4451G>-	ENSMUST upstream_gene_variant	
16	35943328 .	C	T	non_homr	SNV	113	1	114	0.009	110	3	113	0.027	link	-	Parp9 c.16-41C>-	ENSMUST intron_variant	
16	36955796 .	A	C	alt_allele	SNV	20	6	26	0.231	27	9	36	0.25	link	-	Hcls1 c.566-168>-	ENSMUST intron_variant	
16	38323628 .	C	T	PASS	SNV	328	5	333	0.015	323	4	327	0.012	link	-	Maats1 c.1015+50>-	ENSMUST intron_variant	
16	43981662 .	G	A	read_posit	SNV	4	0	4	0	1	2	3	0.667	link	-	Gramd1c c.*396C>T>-	ENSMUST 3_prime_UTR_variant	
16	43981662 .	G	A	read_posit	SNV	4	0	4	0	1	2	3	0.667	link	-	Zdhc23 c.-2612C>-	ENSMUST upstream_gene_variant	
16	45383566 .	A	G	base_qual	SNV	98	1	99	0.01	100	8	108	0.074	link	-	Cd200 c.*2-109T>-	ENSMUST intron_variant	
16	45678781 .	G	A	alt_allele	SNV	8	1	9	0.111	7	3	10	0.3	link	-	Tmprss7 c.1048+48>-	ENSMUST intron_variant	
16	72993573 .	A	C	base_qual	SNV	116	5	121	0.041	92	11	103	0.107	link	-	Robo1 c.2696-94>-	ENSMUST intron_variant	
16	79034363 .	T	G	base_qual	SNV	141	6	147	0.041	149	7	156	0.045	link	-	Tmprss15 c.1157-9A>-	ENSMUST intron_variant	
16	87424652 .	A	C	base_qual	SNV	13	3	16	0.188	22	4	26	0.154	link	-	Ltn1 c.629+177>-	ENSMUST intron_variant	
16	89488005 .	T	G	base_qual	SNV	33	3	36	0.083	56	9	65	0.138	link	-	Krtap8-1 c.-98A>C>-	ENSMUST upstream_gene_variant	
16	89488005 .	T	G	base_qual	SNV	33	3	36	0.083	56	9	65	0.138	link	-	-	n.8948800>-	intergenic_region
16	90746475 .	C	A	base_qual	SNV	49	0	49	0	41	9	50	0.18	link	-	Mrap c.107-104>-	ENSMUST intron_variant	
16	90968808 .	T	G	too_few_s	SNV	6	0	6	0	1	2	3	0.667	link	-	Synj1 c.1846+37>-	ENSMUST intron_variant	
16	93752790 .	C	A	base_qual	SNV	175	2	177	0.011	132	17	149	0.114	link	-	Dopey2 c.1015-45>-	ENSMUST intron_variant	
16	97865966 .	T	G	base_qual	SNV	190	1	191	0.005	210	4	214	0.019	link	-	C2cd2 c.1870+26>-	ENSMUST intron_variant	
17	6050660 .	C	T	base_qual	SNV	86	6	92	0.065	123	19	142	0.134	link	-	Serac1 c.1403+65>-	ENSMUST intron_variant	
17	7932415 .	T	G	base_qual	SNV	13	0	13	0	17	6	23	0.261	link	-	Tagap c.898+170>-	ENSMUST intron_variant	
17	7932415 .	T	G	base_qual	SNV	13	0	13	0	17	6	23	0.261	link	-	E430024P:n.963A>C>-	ENSMUST non_coding_transcript_exon_variant	
17	12264609 .	T	C	too_few_s	SNV	33	0	33	0	31	2	33	0.061	link	-	Map3k4 c.1681-46>-	ENSMUST intron_variant	
17	14680074 .	T	G	base_qual	SNV	89	1	90	0.011	89	4	93	0.043	link	-	Tlbs2 c.1652-36>-	ENSMUST intron_variant	
17	23343737 rs1134516 G	A	fragment	SNV	5	0	5	0	5	2	7	0.286	link	-	Vmn2r115 c.-240G>C>-	ENSMUST upstream_gene_variant		
17	23343737 rs1134516 G	A	fragment	SNV	5	0	5	0	5	2	7	0.286	link	-	-	n.2334373>-	intergenic_region	
17	23343747 rs1134786 C	A	fragment	SNV	7	0	7	0	6	2	8	0.25	link	-	Vmn2r115 c.-230C>A>-	ENSMUST upstream_gene_variant		
17	23343747 rs1134786 C	A	fragment	SNV	7	0	7	0	6	2	8	0.25	link	-	-	n.2334374>-	intergenic_region	
17	23343751 rs1132287 G	A	fragment	SNV	7	0	7	0	6	2	8	0.25	link	-	Vmn2r115 c.-226G>A>-	ENSMUST upstream_gene_variant		
17	23343751 rs1132287 G	A	fragment	SNV	7	0	7	0	6	2	8	0.25	link	-	-	n.2334375>-	intergenic_region	
17	23343757 rs1132204 C	T	fragment	SNV	7	0	7	0	6	2	8	0.25	link	-	Vmn2r115 c.-220C>T>-	ENSMUST upstream_gene_variant		
17	23343757 rs1132204 C	T	fragment	SNV	7	0	7	0	6	2	8	0.25	link	-	-	n.2334375>-	intergenic_region	
17	23343769 .	G	A	fragment	SNV	8	0	8	0	8	2	10	0.2	link	-	Vmn2r115 c.-208G>A>-	ENSMUST upstream_gene_variant	
17	23343769 .	G	A	fragment	SNV	8	0	8	0	8	2	10	0.2	link	-	-	n.2334376>-	intergenic_region
17	23343775 .	C	T	fragment	SNV	8	0	8	0	8	1	9	0.111	link	-	Vmn2r115 c.-202C>T>-	ENSMUST upstream_gene_variant	
17	23343775 .	C	T	fragment	SNV	8	0	8	0	8	1	9	0.111	link	-	-	n.2334377>-	intergenic_region
17	23343778 .	G	A	fragment	SNV	8	0	8	0	8	1	9	0.111	link	-	Vmn2r115 c.-199G>A>-	ENSMUST upstream_gene_variant	
17	23343778 .	G	A	fragment	SNV	8	0	8	0	8	1	9	0.111	link	-	-	n.2334377>-	intergenic_region
17	23343780 .	G	A	fragment	SNV	8	0	8	0	8	1	9	0.111	link	-	Vmn2r115 c.-197G>A>-	ENSMUST upstream_gene_variant	
17	23343780 .	G	A	fragment	SNV	8	0	8	0	8	1	9	0.111	link	-	-	n.2334378>-	intergenic_region
17	23343784 .	A	C	fragment	SNV	11	0	11	0	7	1	8	0.125	link	-	Vmn2r115 c.-193A>C>-	ENSMUST upstream_gene_variant	
17	23343784 .	A	C	fragment	SNV	11	0	11	0	7	1	8	0.125	link	-	-	n.2334378>-	intergenic_region
17	23343790 .	G	A	fragment	SNV	14	0	14	0	7	1	8	0.125	link	-	Vmn2r115 c.-187G>A>-	ENSMUST upstream_gene_variant	
17	23343790 .	G	A	fragment	SNV	14	0	14	0	7	1	8	0.125	link	-	-	n.2334379>-	intergenic_region
17	23343798 .	G	T	fragment	SNV	14	0	14	0	7	1	8	0.125	link	-	Vmn2r115 c.-179G>T>-	ENSMUST upstream_gene_variant	
17	23343798 .	G	T	fragment	SNV	14	0	14	0	7	1	8	0.125	link	-	-	n.2334379>-	intergenic_region
17	23343799 .	C	T	fragment	SNV	14	0	14	0	7	1	8	0.125	link	-	Vmn2r115 c.-178C>T>-	ENSMUST upstream_gene_variant	
17	23343799 .	C	T	fragment	SNV	14	0	14	0	7	1	8	0.125	link	-	-	n.2334379>-	intergenic_region
17	23357165 .	G	C	mapping	cSNV	87	0	87	0	96	7	103	0.068	link	-	Vmn2r115 c.1654+82>-	ENSMUST intron_variant	
17	23357196 .	C	T	mapping	cSNV	35	3	38	0.079	42	15	57	0.263	link	-	Vmn2r115 c.1654+11>-	ENSMUST intron_variant	
17	23357209 .	A	G	mapping	cSNV	22	3	25	0.12	31	9	40	0.225	link	-	Vmn2r115 c.1654+12>-	ENSMUST intron_variant	
17	23359088 .	A	G	mapping	cSNV	56	4	60	0.067	43	11	54	0.204	link	-	Vmn2r115 c.1655-12>-	ENSMUST intron_variant	
17	23460792 rs2254516 C	T	weak_evid	SNV	7	1	8	0.125	9	5	14	0.357	link	-	Vmn2r117 c.1655-19>-	ENSMUST intron_variant		
17	23478730 rs1132109 C	G	fragment	SNV	10	1	11	0.091	16	3	19	0.158	link	-	Vmn2r117 c.198-211>-	ENSMUST intron_variant		
17	23478794 rs1133232 A	G	weak_evid	SNV	5	0	5	0	6	5	11	0.455	link	-	Vmn2r117 c.198-275>-	ENSMUST intron_variant		
17	24038408 .	T	G	base_qual	SNV	231	2	233	0.009	252	4	256	0.016	link	-	Prss27 c.55+47T>-	ENSMUST intron_variant	
17	25189360 .	A	C	base_qual	SNV	16	0	16	0	21	5	26	0.192	link	-	BC003965 c.*4262A>-	ENSMUST downstream_gene_variant	
17	25189360 .	A	C	base_qual	SNV	16	0	16	0	21	5	26	0.192	link	-			

17	71638301	A	C	base_qual	SNV	302	6	308	0.019	241	13	254	0.051	link	-	Gm22858	n.-3283A>-	ENSMUST	upstream_gene_variant
17	73188055	T	G	base_qual	SNV	129	7	136	0.051	121	13	134	0.097	link	-	Gm9311	n.*2203A>-	ENSMUST	downstream_gene_variant
17	73188055	T	G	base_qual	SNV	129	7	136	0.051	121	13	134	0.097	link	-	Lclat1	c.511+34T>-	ENSMUST	intron_variant
17	74027174	T	G	base_qual	SNV	171	6	177	0.034	122	11	133	0.083	link	-	Srd5a2	c.282-33A>-	ENSMUST	intron_variant
17	74598353	T	C	too_few_s	SNV	4	0	4	0	12	2	14	0.143	link	-	Gm26749	n.1733+96-	ENSMUST	intron_variant
17	74598353	T	C	too_few_s	SNV	4	0	4	0	12	2	14	0.143	link	-	Birc6	c.3959+18-	ENSMUST	intron_variant
17	90208289	A	C	base_qual	SNV	77	6	83	0.072	90	10	100	0.1	link	-	Nrxn1	c.3739+34-	ENSMUST	intron_variant
18	9997907	T	G	base_qual	SNV	43	3	46	0.065	47	7	54	0.13	link	-	Thoc1	c.*4291T>-	ENSMUST	downstream_gene_variant
18	9997907	T	G	base_qual	SNV	43	3	46	0.065	47	7	54	0.13	link	-	Usp14	c.1165-13C>-	ENSMUST	intron_variant
18	12507172	T	G	base_qual	SNV	15	2	17	0.118	21	10	31	0.323	link	-	Gm29200	n.-2746A>-	ENSMUST	upstream_gene_variant
18	12507172	T	G	base_qual	SNV	15	2	17	0.118	21	10	31	0.323	link	-	Lama3	c.5103+13-	ENSMUST	intron_variant
18	12928378	A	G	base_qual	SNV	112	2	114	0.018	94	6	100	0.06	link	-	Osbpl1a	c.208-43T>-	ENSMUST	intron_variant
18	34247536	G	T	base_qual	SNV	64	8	72	0.111	60	11	71	0.155	link	-	Apc	c.-18-134E-	ENSMUST	intron_variant
18	34940191	A	C	base_qual	SNV	211	7	218	0.032	220	13	233	0.056	link	-	Gm22200	n.*1043T>-	ENSMUST	downstream_gene_variant
18	34940191	A	C	base_qual	SNV	211	7	218	0.032	220	13	233	0.056	link	-	Gm26109	n.*2453T>-	ENSMUST	downstream_gene_variant
18	34940222	A	C	base_qual	SNV	301	0	301	0	306	13	319	0.041	link	-	Gm22200	n.*1012T>-	ENSMUST	downstream_gene_variant
18	34940222	A	C	base_qual	SNV	301	0	301	0	306	13	319	0.041	link	-	Gm26109	n.*2422T>-	ENSMUST	downstream_gene_variant
18	43990649	A	C	base_qual	SNV	89	4	93	0.043	84	6	90	0.067	link	-	Spink5	c.1017-15I-	ENSMUST	intron_variant
18	43990653	A	C	base_qual	SNV	100	0	100	0	101	5	106	0.047	link	-	Spink5	c.1017-11I-	ENSMUST	intron_variant
18	44493608	G	T	base_qual	SNV	94	0	94	0	77	13	90	0.144	link	-	Mcc	c.983-63C>-	ENSMUST	intron_variant
18	53210272	A	C	base_qual	SNV	127	6	133	0.045	128	12	140	0.086	link	-	Snx2	c.799-58A>-	ENSMUST	intron_variant
18	61735775	C	T	base_qual	SNV	128	4	132	0.03	80	10	90	0.111	link	-	Afaf1l1	c.1976-29K-	ENSMUST	intron_variant
18	61735775	C	T	base_qual	SNV	128	4	132	0.03	80	10	90	0.111	link	-	1500015A(n.61735775	-	intragenic_variant	
18	61757948	G	A	too_few_s	SNV	9	0	9	0	9	2	11	0.182	link	-	Afaf1l1	c.146-213K-	ENSMUST	intron_variant
18	64508038	G	A	too_few_s	SNV	15	0	15	0	10	2	12	0.167	link	-	Nars	c.526-180K-	ENSMUST	intron_variant
18	67653142	A	C	base_qual	SNV	213	16	229	0.07	157	18	175	0.103	link	-	Psmg2	c.582-11A>-	ENSMUST	intron_variant
18	75125402	A	C	base_qual	SNV	191	9	200	0.045	176	8	184	0.043	link	-	Dym	c.1252-22I-	ENSMUST	intron_variant
18	90539829	A	C	base_qual	SNV	25	0	25	0	34	8	42	0.19	link	-	Tmx3	c.1114-11I-	ENSMUST	intron_variant
19	3392272	T	G	alt_allele	SNV	134	11	145	0.076	137	18	155	0.116	link	-	Mt5	c.543+11T>-	ENSMUST	intron_variant
19	5098210	G	T	base_qual	SNV	192	2	194	0.01	171	2	173	0.012	link	-	Rab1b	c.*2168C>-	ENSMUST	downstream_gene_variant
19	5981904	C	T	alt_allele	SNV	18	2	20	0.1	12	6	18	0.333	link	-	Slc22a20	c.804-151I-	ENSMUST	intron_variant
19	6085530	C	T	weak_evid	SNV	173	0	173	0	214	4	218	0.018	link	-	Zfp1l	c.-1077G>-	ENSMUST	upstream_gene_variant
19	6085530	C	T	weak_evid	SNV	173	0	173	0	214	4	218	0.018	link	-	Gm28374	c.-3275G>-	ENSMUST	upstream_gene_variant
19	6085530	C	T	weak_evid	SNV	173	0	173	0	214	4	218	0.018	link	-	Tmem262	c.*4826C>-	ENSMUST	downstream_gene_variant
19	6085530	C	T	weak_evid	SNV	173	0	173	0	214	4	218	0.018	link	-	Cdca5	c.138+41C-	ENSMUST	intron_variant
19	10253799	A	G	weak_evid	SNV	342	1	343	0.003	367	4	371	0.011	link	-	Dagla	c.1515-14I-	ENSMUST	intron_variant
19	11478052	C	G	alt_allele	SNV	2	0	2	0	1	5	6	0.833	link	-	BE692007	n.*2153G>-	ENSMUST	downstream_gene_variant
19	11478052	C	G	alt_allele	SNV	2	0	2	0	1	5	6	0.833	link	-	Ms4a6c	c.340-116I-	ENSMUST	intron_variant
19	11478052	C	G	alt_allele	SNV	2	0	2	0	1	5	6	0.833	link	-	BE692007	n.1147805	-	intragenic_variant
19	17565430	G	T	base_qual	SNV	121	6	127	0.047	142	9	151	0.06	link	-	Pcsk5	c.2289-65I-	ENSMUST	intron_variant
19	18691309	A	C	base_qual	SNV	24	4	28	0.143	25	3	28	0.107	link	-	Carrmt1	c.705-108I-	ENSMUST	intron_variant
19	18717175	A	C	base_qual	SNV	86	2	88	0.023	69	10	79	0.127	link	-	D030056L(c.337-44A>-	-	ENSMUST	intron_variant
19	22897902	T	G	base_qual	SNV	25	2	27	0.074	33	9	42	0.214	link	-	Trpm3	c.1815+92-	ENSMUST	intron_variant
19	26750963	G	T	base_qual	SNV	23	4	27	0.148	45	11	56	0.196	link	-	Smarca2	c.4015-86I-	ENSMUST	intron_variant
19	37969960	T	G	base_qual	SNV	278	3	281	0.011	283	8	291	0.027	link	-	Myof	c.1418-15I-	ENSMUST	intron_variant
19	41610958	C	A	PASS	SNV	297	0	297	0	356	9	365	0.025	link	-	Slit1	c.3109+44-	ENSMUST	intron_variant
19	45024633	A	G	weak_evid	SNV	62	0	62	0	17	5	22	0.227	link	-	Pdzd7	c.*2982T>-	ENSMUST	downstream_gene_variant
19	45024633	A	G	weak_evid	SNV	62	0	62	0	17	5	22	0.227	link	-	Lzts2	c.1072-86I-	ENSMUST	intron_variant
19	47660093	T	G	base_qual	SNV	167	14	181	0.077	142	13	155	0.084	link	-	Col17a1	c.2357-76I-	ENSMUST	intron_variant
19	53232337	G	T	non_homr	SNV	42	5	47	0.106	34	8	42	0.19	link	-	Add3	c.567+133-	ENSMUST	intron_variant
19	55076280	A	C	base_qual	SNV	228	9	237	0.038	278	7	285	0.025	link	-	Gpam	c.1980+11-	ENSMUST	intron_variant
19	55623702	G	T	base_qual	SNV	25	3	28	0.107	24	5	29	0.172	link	-	Vt1a	c.561-115I-	ENSMUST	intron_variant
19	55623706	A	C	base_qual	SNV	33	4	37	0.108	27	10	37	0.27	link	-	Vt1a	c.561-111I-	ENSMUST	intron_variant
19	55917333	A	C	base_qual	SNV	139	1	140	0.007	205	8	213	0.038	link	-	Tcf7l2	c.807-21A>-	ENSMUST	intron_variant
19	56592377	T	A	weak_evid	SNV	230	1	231	0.004	219	4	223	0.018	link	-	Nhlrc2	c.1372-16I-	ENSMUST	intron_variant
19	57706838	A	C	base_qual	SNV	56	0	56	0	68	9	77	0.117	link	-	Atrn1l	c.2816-77I-	ENSMUST	intron_variant
19	59015662	T	G	base_qual	SNV	151	0	151	0	175	10	185	0.054	link	-	Shtn1	c.1013-36I-	ENSMUST	intron_variant
19	61228508	T	C	base_qual	SNV	66	7	73	0.096	81	22	103	0.214	link	-	Csf2ra	c.-1143A>-	ENSMUST	upstream_gene_variant
19	61228508	T	C	base_qual	SNV	66	7	73	0.096	81	22	103	0.214	link	-	-	n.6122850	-	intergenic_region
2	5898683	G	A	weak_evid	SNV	283	1	284	0.004	212	4	216	0.019	link	-	Dhtkd1	c.*25C>T	ENSMUST	3_prime_UTR_variant
2	5898683	G	A	weak_evid	SNV	283	1	284	0.004	212	4	216	0.019	link	-	Sec61a2	c.-3420C>-	ENSMUST	upstream_gene_variant
2	5898683	G	A	weak_evid	SNV	283	1	284	0.004	212	4	216	0.019	link	-	Gm13267	n.130-96G>-	ENSMUST	intron_variant
2	10105816	T	G	base_qual	SNV	173	5	178	0.028	145	8	153	0.052	link	-	Ith2	c.1474-11I-	ENSMUST	intron_variant
2	11482661	T	G	base_qual	SNV	34	1	35	0.029	42	8	50	0.16	link	-	Pfkfb3	c.1084-87I-	ENSMUST	intron_variant
2	12357052	T	G	base_qual	SNV	75	4	79	0.051	84	8	92	0.087	link	-	Gm37289	n.*43A>C	ENSMUST	downstream_gene_variant
2	12357052	T	G	base_qual	SNV	75	4	79	0.051	84	8	92	0.087	link	-	Fam188a	c.953-75A>-	ENSMUST	intron_variant
2	14824356	G	T	base_qual	SNV	60	5	65	0.077	71	6	77	0.078	link	-	Cacnb2	c.202-504I-	ENSMUST	intron_variant
2	15029955	C	A	base_qual	SNV	72	0	72	0	75	11	86	0.128	link	-	Gm36930	n.*1846G>-	ENSMUST	downstream_gene_variant
2	15029955	C	A	base_qual	SNV	72	0	72	0	75	11	86	0.128	link	-	Nsun6	c.777+74G>-	ENSMUST	intron_variant
2	22668436	T	G	base_qual	SNV	95	5	100	0.05	115	10	125	0.08	link	-	Gm23636	n.*1684T>-	ENSMUST	downstream_gene_variant
2	22668436	T	G	base_qual	SNV	95	5	100	0.05	115	10	125	0.08	link	-	Gad2	c.1092+73-	ENSMUST	intron_variant
2	24734062	T	G	base_qual	SNV	183	4	187	0.021	158	6	164	0.037	link	-	Cacna1b	c.531-26A>-	ENSMUST	intron_variant
2	25501790	G	A	weak_evid	SNV	18	0	18	0	29	3	32	0.094	link	-	C8g	c.-1559C>-	ENSMUST	upstream_gene_variant
2	25501790	G	A	weak_evid	SNV	18	0	18	0	29	3	32	0.094	link	-	Fbxw5	c.-23-146C>-	ENSMUST	intron_variant
2	26315178	C	T	base_qual	SNV	5	0	5	0	6	2	8	0.25	link	-	Gpsm1	c.-4685C>-	ENSMUST	upstream_gene_variant
2	26315178	C	T	base_qual	SNV	5	0	5	0	6	2	8	0.25	link	-	-	n.2631517	-	intergenic_region
2	27009217	A	G	base_qual	SNV	167	0	167	0	141	13	154	0.084	link	-	Cacfd1	c.-771A>G	ENSMUST	upstream_gene_variant
2	27009217	A	G	base_qual	SNV	167	0	167	0	141	13	154	0.084	link	-	Adams13	c.4090-3		

2	1.57E+08 .	A	G	base_qual	SNV	39	8	47	0.17	26	12	38	0.316	link	-	Ghrh	c.*154T>C-	ENSMUST downstream_gene_variant
2	1.57E+08 .	A	G	base_qual	SNV	39	8	47	0.17	26	12	38	0.316	link	-	-	n.1573294-	- intergenic_region
2	1.61E+08 .	A	C	base_qual	SNV	101	3	104	0.029	150	12	162	0.074	link	-	Chd6	c.6936+10-	ENSMUST intron_variant
2	1.65E+08 .	C	A	base_qual	SNV	174	0	174	0	157	9	166	0.054	link	-	Cdh22	c.541+14C-	ENSMUST intron_variant
2	1.68E+08 .	G	A	weak_evid	SNV	308	3	311	0.01	311	6	317	0.019	link	-	A530013C.n.-1561G>-	-	ENSMUST upstream_gene_variant
2	1.68E+08 .	G	A	weak_evid	SNV	308	3	311	0.01	311	6	317	0.019	link	-	Tmem189	n.1676896-	- intragenic_variant
2	1.68E+08 .	C	T	PASS	SNV	378	1	379	0.003	255	57	312	0.183	link	-	Adnp	c.-22008G-	ENSMUST upstream_gene_variant
2	1.77E+08 rs5832657	A	G	mapping_c	SNV	119	4	123	0.033	132	13	145	0.09	link	-	Gm14407	n.*4901T>-	ENSMUST downstream_gene_variant
2	1.77E+08 rs5832657	A	G	mapping_c	SNV	119	4	123	0.033	132	13	145	0.09	link	-	Gm14401	c.4-3788A-	ENSMUST intron_variant
3	14039904 .	T	G	base_qual	SNV	51	7	58	0.121	50	12	62	0.194	link	-	Raly1	c.332+115-	ENSMUST intron_variant
3	15417278 rs4799594	G	C	mapping_c	SNV	67	7	74	0.095	62	5	67	0.075	link	-	Sirpb1a	c.74-85C>-	ENSMUST intron_variant
3	15848604 .	A	T	non_homr	SNV	18	3	21	0.143	27	13	40	0.325	link	-	Sirpb1c	c.-191T>A-	ENSMUST upstream_gene_variant
3	15848604 .	A	T	non_homr	SNV	18	3	21	0.143	27	13	40	0.325	link	-	-	n.1584860-	- intergenic_region
3	15848633 .	A	C	mapping_c	SNV	9	1	10	0.1	10	8	18	0.444	link	-	Sirpb1c	c.-220T>G-	ENSMUST upstream_gene_variant
3	15848633 .	A	C	mapping_c	SNV	9	1	10	0.1	10	8	18	0.444	link	-	-	n.1584863-	- intergenic_region
3	31238455 .	A	C	alt_allele	SNV	8	2	10	0.2	19	7	26	0.269	link	-	Slc7a14	c.541+139-	ENSMUST intron_variant
3	36089876 .	T	C	no_reliable	SNV	10	0	10	0	8	2	10	0.2	link	-	Acad9	c.1705-20C-	ENSMUST intron_variant
3	36089876 .	T	C	no_reliable	SNV	10	0	10	0	8	2	10	0.2	link	-	Gm43079	n.34+984T-	ENSMUST intron_variant
3	36553755 .	A	C	base_qual	SNV	71	3	74	0.041	65	6	71	0.085	link	-	Exosc9	c.162-51A-	ENSMUST intron_variant
3	54782039 .	G	A	too_few_s	SNV	12	0	12	0	15	2	17	0.118	link	-	Smad9	c.-206-11C-	ENSMUST intron_variant
3	55521693 .	A	C	base_qual	SNV	9	1	10	0.1	11	4	15	0.267	link	-	Gm42608	n.*2107A>-	ENSMUST downstream_gene_variant
3	55521693 .	A	C	base_qual	SNV	9	1	10	0.1	11	4	15	0.267	link	-	Dclk1	c.2106+47-	ENSMUST intron_variant
3	59245734 .	C	A	base_qual	SNV	285	0	285	0	192	19	211	0.09	link	-	Zfry12	c.-299+17I-	ENSMUST intron_variant
3	65725228 .	A	C	base_qual	SNV	79	3	82	0.037	47	8	55	0.145	link	-	Lekr1	n.6572522-	- intragenic_variant
3	66963606 .	A	G	base_qual	SNV	22	1	23	0.043	12	4	16	0.25	link	-	Rsrc1	c.195-159I-	ENSMUST intron_variant
3	87922920 rs2456340	A	C	base_qual	SNV	214	7	221	0.032	194	9	203	0.044	link	-	Rmad1	c.*871T>G-	ENSMUST 3_prime_UTR_variant
3	87922920 rs2456340	A	C	base_qual	SNV	214	7	221	0.032	194	9	203	0.044	link	-	Mrip24	c.384-15A-	ENSMUST intron_variant
3	89345875 .	A	C	base_qual	SNV	138	5	143	0.035	135	14	149	0.094	link	-	Dcst1	c.*4388T>-	ENSMUST downstream_gene_variant
3	89345875 .	A	C	base_qual	SNV	138	5	143	0.035	135	14	149	0.094	link	-	Adam15	c.679-38T-	ENSMUST intron_variant
3	89345875 .	A	C	base_qual	SNV	138	5	143	0.035	135	14	149	0.094	link	-	473141910	n.864A>C-	ENSMUST non_coding_transcript_exon_variant
3	90057034 .	C	T	non_homr	SNV	14	2	16	0.125	9	2	11	0.182	link	-	Ubpap2l	c.-9175G>-	ENSMUST upstream_gene_variant
3	90057034 .	C	T	non_homr	SNV	14	2	16	0.125	9	2	11	0.182	link	-	Gm16540	n.-225C>T-	ENSMUST upstream_gene_variant
3	90057034 .	C	T	non_homr	SNV	14	2	16	0.125	9	2	11	0.182	link	-	4933434Ec	c.340+452-	ENSMUST intron_variant
3	93395485 .	T	C	PASS	SNV	137	0	137	0	108	24	132	0.182	link	-	Gm37857	n.*589T>C-	ENSMUST downstream_gene_variant
3	93395485 .	T	C	PASS	SNV	137	0	137	0	108	24	132	0.182	link	-	Gm37245	n.217+139-	ENSMUST intron_variant
3	93395485 .	T	C	PASS	SNV	137	0	137	0	108	24	132	0.182	link	-	Rptn	c.139-15T-	ENSMUST intron_variant
3	1.01E+08 .	A	C	base_qual	SNV	21	2	23	0.087	33	12	45	0.267	link	-	Trim45	c.489-109I-	ENSMUST intron_variant
3	1.04E+08 .	A	C	base_qual	SNV	26	1	27	0.037	43	9	52	0.173	link	-	Mag3	c.947+109-	ENSMUST intron_variant
3	1.04E+08 .	T	G	base_qual	SNV	44	2	46	0.043	51	7	58	0.121	link	-	Gm43696	n.*3221A>-	ENSMUST downstream_gene_variant
3	1.04E+08 .	T	G	base_qual	SNV	44	2	46	0.043	51	7	58	0.121	link	-	Lrig2	c.1475-76I-	ENSMUST intron_variant
3	1.08E+08 .	T	G	base_qual	SNV	104	4	108	0.037	108	7	115	0.061	link	-	Sort1	c.1468+71-	ENSMUST intron_variant
3	1.17E+08 .	T	G	base_qual	SNV	291	10	301	0.033	212	16	228	0.07	link	-	Palmd	c.1613-9A-	ENSMUST intron_variant
3	1.19E+08 .	T	G	base_qual	SNV	80	3	83	0.036	92	4	96	0.042	link	-	Dpyd	c.1740+18-	ENSMUST intron_variant
3	1.29E+08 .	T	G	non_homr	SNV	71	2	73	0.027	61	5	66	0.076	link	-	Enpep	c.1486-84I-	ENSMUST intron_variant
3	1.33E+08 .	T	G	base_qual	SNV	160	1	161	0.006	153	10	163	0.061	link	-	Aimp1	c.416-9A>-	ENSMUST intron_variant
3	1.38E+08 .	T	G	alt_allele	SNV	13	4	17	0.235	21	7	28	0.25	link	-	Adh5a	c.828+133-	ENSMUST intron_variant
3	1.43E+08 .	G	T	base_qual	SNV	205	10	215	0.047	206	18	224	0.08	link	-	Kyat3	c.306+61C-	ENSMUST intron_variant
3	1.46E+08 .	A	C	base_qual	SNV	11	0	11	0	19	6	25	0.24	link	-	Znhit6	c.992+439-	ENSMUST intron_variant
3	1.49E+08 .	T	G	base_qual	SNV	340	7	347	0.02	280	12	292	0.041	link	-	Adgr12	c.402-925I-	ENSMUST intron_variant
4	3604987 .	C	T	weak_evid	SNV	38	0	38	0	58	3	61	0.049	link	-	Tgs1	c.2336+72-	ENSMUST intron_variant
4	9598368 .	A	G	base_qual	SNV	91	3	94	0.032	97	7	104	0.067	link	-	Asph	c.773-67A-	ENSMUST intron_variant
4	11192556 .	T	C	base_qual	SNV	36	2	38	0.053	40	11	51	0.216	link	-	Cone2	c.-23-125F-	ENSMUST intron_variant
4	12058743 .	C	T	base_qual	SNV	17	3	20	0.15	17	5	22	0.227	link	-	Tmem67	c.1717-16I-	ENSMUST intron_variant
4	15962293 .	A	C	base_qual	SNV	135	1	136	0.007	114	6	120	0.05	link	-	Nbn	c.38-18A>-	ENSMUST intron_variant
4	32696118 .	A	C	base_qual	SNV	25	3	28	0.107	38	3	41	0.073	link	-	Mdn1	c.3604-10A-	ENSMUST intron_variant
4	43566893 .	T	G	base_qual	SNV	34	2	36	0.056	35	11	46	0.239	link	-	Tin1	c.-1014A3-	ENSMUST upstream_gene_variant
4	43566893 .	T	G	base_qual	SNV	34	2	36	0.056	35	11	46	0.239	link	-	Gba2	c.*296A>C-	ENSMUST downstream_gene_variant
4	43566893 .	T	G	base_qual	SNV	34	2	36	0.056	35	11	46	0.239	link	-	Creb3	c.*96T>G-	ENSMUST downstream_gene_variant
4	46542440 .	T	G	base_qual	SNV	80	0	80	0	87	8	95	0.084	link	-	Gm16731	n.*2638T>-	ENSMUST downstream_gene_variant
4	46542440 .	T	G	base_qual	SNV	80	0	80	0	87	8	95	0.084	link	-	Coro2a	c.1025-93I-	ENSMUST intron_variant
4	47384041 .	A	G	base_qual	SNV	38	3	41	0.073	46	6	52	0.115	link	-	Tgfb1	c.331+47A-	ENSMUST intron_variant
4	57338708 .	A	C	base_qual	SNV	58	3	61	0.049	40	6	46	0.13	link	-	-	n.5733870-	- intergenic_region
4	60070462 .	T	C	mapping_c	SNV	30	6	36	0.167	44	8	52	0.154	link	-	Mup7	c.-162A>G-	ENSMUST 5_prime_UTR_premature_start_codon_gain_variant
4	60070462 .	T	C	mapping_c	SNV	30	6	36	0.167	44	8	52	0.154	link	-	Mup7	c.-162A>G-	ENSMUST 5_prime_UTR_variant
4	63730115 .	T	G	base_qual	SNV	79	4	83	0.048	91	14	105	0.133	link	-	Tnfrsf15	c.359-72A-	ENSMUST intron_variant
4	75944829 .	G	T	base_qual	SNV	26	2	28	0.071	31	9	40	0.225	link	-	Ptprd	c.*129C>A-	ENSMUST 3_prime_UTR_variant
4	89307373 .	A	G	base_qual	SNV	108	4	112	0.036	75	12	87	0.138	link	-	Cdkn2b	c.133-59T-	ENSMUST intron_variant
4	96558272 .	T	G	base_qual	SNV	223	4	227	0.018	253	10	263	0.038	link	-	Cyp2j6	c.-4821A>-	ENSMUST upstream_gene_variant
4	96558272 .	T	G	base_qual	SNV	223	4	227	0.018	253	10	263	0.038	link	-	-	n.9655827-	- intergenic_region
4	1.01E+08 .	C	G	base_qual	SNV	70	2	72	0.028	45	24	69	0.348	link	-	Cachd1	c.2137-64C-	ENSMUST intron_variant
4	1.05E+08 .	A	C	base_qual	SNV	66	4	70	0.057	80	12	92	0.13	link	-	Dab1	c.724-115I-	ENSMUST intron_variant
4	1.07E+08 .	T	G	base_qual	SNV	152	2	154	0.013	171	10	181	0.055	link	-	Mroh7	c.2830-31I-	ENSMUST intron_variant
4	1.08E+08 .	T	G	base_qual	SNV	30	2	32	0.062	28	8	36	0.222	link	-	Zyg11a	c.1003-90I-	ENSMUST intron_variant
4	1.09E+08 .	G	T	base_qual	SNV	28	0	28	0	56	13	69	0.188	link	-	Orc1	c.1418+10-	ENSMUST intron_variant
4	1.09E+08 .	G	T	base_qual	SNV	28	0	28	0	56	13	69	0.188	link	-	Gm12743	n.629-117I-	ENSMUST intron_variant
4	1.09E+08 .	G	T	base_qual	SNV	28	0	28	0	58	11	69	0.159	link	-	Orc1	c.1418+11-	ENSMUST intron_variant
4	1.09E+08 .	G	T	base_qual	SNV	28	0	28	0	58	11	69	0.159	link	-	Gm12743	n.629-118I-	ENSMUST intron_variant
4	1.09E+08 .	G	T	base_qual	SNV	27	0	27	0	61	10	71	0.141	link	-	Orc1	c.1418+11-	ENSMUST intron_variant
4	1.09E+08 .	G	T	base_qual	SNV	27	0	27	0	61	10	71	0.141	link	-	Gm12743	n.629-118I-	ENSMUST intron_variant
4	1.12E+08 .	A	C	base_qual	SNV	130	2	132	0.015	129	7	136	0.051	link	-	Agbl4	c.1268-67I-	ENSMUST intron_variant
4	1.13E+08 .	T	C	base_qual	SNV	59	4	63	0.063	54	12	66	0.182	link	-	Skint10	c.707-87A-	ENSMUST intron_variant

4	1.48E+08	rs1135284	C	T	mapping_c	SNV	103	4	107	0.037	101	21	122	0.172	link	-	Zfp534	c.*95G>A	-	ENSMUST_3_prime_UTR_variant
4	1.48E+08	rs1135284	C	T	mapping_c	SNV	103	4	107	0.037	101	21	122	0.172	link	-	Gm16211	c.-3276G>-	-	ENSMUST upstream_gene_variant
4	1.48E+08	rs1134898	T	C	mapping_c	SNV	121	5	126	0.04	120	23	143	0.161	link	-	Zfp534	c.*88A>G	-	ENSMUST_3_prime_UTR_variant
4	1.48E+08	rs1134898	T	C	mapping_c	SNV	121	5	126	0.04	120	23	143	0.161	link	-	Gm16211	c.-3283A>-	-	ENSMUST upstream_gene_variant
4	1.49E+08	.	A	C	base_qual	SNV	20	4	24	0.167	20	11	31	0.355	link	-	Nmnat1	c.-13920T>-	-	ENSMUST upstream_gene_variant
4	1.49E+08	.	A	C	base_qual	SNV	20	4	24	0.167	20	11	31	0.355	link	-	Gm13097	n.*4931A>-	-	ENSMUST downstream_gene_variant
4	1.49E+08	.	A	C	base_qual	SNV	20	4	24	0.167	20	11	31	0.355	link	-	Lzic	c.238-168/-	-	ENSMUST intron_variant
4	1.5E+08	.	G	T	base_qual	SNV	8	1	9	0.111	12	10	22	0.455	link	-	Clstn1	c.1520-17/-	-	ENSMUST intron_variant
4	1.52E+08	.	C	T	PASS	SNV	55	0	55	0	67	3	70	0.043	link	-	Rnf207	c.191+67G>-	-	ENSMUST intron_variant
5	14974231	rs2525766	G	A	mapping_c	SNV	44	3	47	0.064	35	14	49	0.286	link	-	Gm10354	c.*266C>T	-	ENSMUST_3_prime_UTR_variant
5	15473285	rs1134611	C	A	mapping_c	SNV	257	21	278	0.076	729	89	818	0.109	link	-	Gm21149	c.444-131(-	-	ENSMUST intron_variant
5	15473285	rs1134611	C	A	mapping_c	SNV	257	21	278	0.076	729	89	818	0.109	link	-	Gm43391	n.150+111-	-	ENSMUST intron_variant
5	15528304	.	T	A	weak_evid	SNV	105	3	108	0.028	131	7	138	0.051	link	-	Gm21847	n.222+237-	-	ENSMUST intron_variant
5	15528304	.	T	A	weak_evid	SNV	105	3	108	0.028	131	7	138	0.051	link	-	Gm21190	c.140-238/-	-	ENSMUST intron_variant
5	15528381	.	G	A	non_homn	SNV	121	3	124	0.024	106	12	118	0.102	link	-	Gm21847	n.222+244-	-	ENSMUST intron_variant
5	15528381	.	G	A	non_homn	SNV	121	3	124	0.024	106	12	118	0.102	link	-	Gm21190	c.140-315(-	-	ENSMUST intron_variant
5	15528439	.	T	A	mapping_c	SNV	128	1	129	0.008	87	12	99	0.121	link	-	Gm21847	n.222+250-	-	ENSMUST intron_variant
5	15528439	.	T	A	mapping_c	SNV	128	1	129	0.008	87	12	99	0.121	link	-	Gm21190	c.140-373(-	-	ENSMUST intron_variant
5	15528514	.	C	A	mapping_c	SNV	77	1	78	0.013	55	5	60	0.083	link	-	Gm21847	n.222+258-	-	ENSMUST intron_variant
5	15528514	.	C	A	mapping_c	SNV	77	1	78	0.013	55	5	60	0.083	link	-	Gm21190	c.140-448(-	-	ENSMUST intron_variant
5	15711884	rs1131741	C	T	mapping_c	SNV	238	11	249	0.044	338	31	369	0.084	link	-	Speed4cos	n.393+939-	-	ENSMUST intron_variant
5	15711884	rs1131741	C	T	mapping_c	SNV	238	11	249	0.044	338	31	369	0.084	link	-	Speed4c	c.300-216(-	-	ENSMUST intron_variant
5	21275777	.	T	C	too_few_s	SNV	5	0	5	0	6	2	8	0.25	link	-	Gm43214	n.*3493A>-	-	ENSMUST downstream_gene_variant
5	21275777	.	T	C	too_few_s	SNV	5	0	5	0	6	2	8	0.25	link	-	Gsap	c.1840-22/-	-	ENSMUST intron_variant
5	23811827	.	C	T	weak_evid	SNV	386	1	387	0.003	336	4	340	0.012	link	-	4933427G	n.*3791G>-	-	ENSMUST downstream_gene_variant
5	25954367	.	C	G	mapping_c	SNV	341	24	365	0.066	323	33	356	0.093	link	-	Gm21671	c.-23G>C	-	ENSMUST_5_prime_UTR_variant
5	25954367	.	C	G	mapping_c	SNV	341	24	365	0.066	323	33	356	0.093	link	-	Gm21168	n.-2259C>-	-	ENSMUST upstream_gene_variant
5	27781525	.	G	A	base_qual	SNV	294	16	310	0.052	211	16	227	0.07	link	-	Paxip1	c.261-40C>-	-	ENSMUST intron_variant
5	28245857	.	T	G	base_qual	SNV	156	2	158	0.013	177	8	185	0.043	link	-	-	n.2824585	-	intergenic_region
5	28464968	.	C	T	base_qual	SNV	114	2	116	0.017	98	6	104	0.058	link	-	Gm26894	n.-1406C>-	-	ENSMUST upstream_gene_variant
5	28464968	.	C	T	base_qual	SNV	114	2	116	0.017	98	6	104	0.058	link	-	9530036O	n.-2016C>-	-	ENSMUST upstream_gene_variant
5	28464968	.	C	T	base_qual	SNV	114	2	116	0.017	98	6	104	0.058	link	-	Shh	c.303+149-	-	ENSMUST intron_variant
5	28464968	.	C	T	base_qual	SNV	114	2	116	0.017	98	6	104	0.058	link	-	9530036O	n.2846496	-	intragenic_variant
5	31730689	.	T	G	base_qual	SNV	36	1	37	0.027	48	6	54	0.111	link	-	Bre	c.239+134-	-	ENSMUST intron_variant
5	32477998	.	A	C	base_qual	SNV	68	1	69	0.014	76	10	86	0.116	link	-	Gm15613	n.*1562T>-	-	ENSMUST downstream_gene_variant
5	32477998	.	A	C	base_qual	SNV	68	1	69	0.014	76	10	86	0.116	link	-	Ppp1cb	c.53-68A>-	-	ENSMUST intron_variant
5	32808475	.	C	T	base_qual	SNV	102	9	111	0.081	113	12	125	0.096	link	-	Gm20671	c.503+113-	-	ENSMUST intron_variant
5	32808475	.	C	T	base_qual	SNV	102	9	111	0.081	113	12	125	0.096	link	-	Prr14l	c.5543+11-	-	ENSMUST intron_variant
5	44063098	.	A	C	base_qual	SNV	164	12	176	0.068	167	10	177	0.056	link	-	Prom1	c.279+28T>-	-	ENSMUST intron_variant
5	45443586	.	T	G	base_qual	SNV	73	2	75	0.027	83	8	91	0.088	link	-	Qdpr	c.287-94A>-	-	ENSMUST intron_variant
5	45443586	.	T	G	base_qual	SNV	73	2	75	0.027	83	8	91	0.088	link	-	Gm42413	n.201-641(-	-	ENSMUST intron_variant
5	67315932	.	C	G	weak_evid	SNV	73	1	74	0.014	61	4	65	0.062	link	-	Slc30a9	c.271+87T>-	-	ENSMUST intron_variant
5	73191610	.	C	A	base_qual	SNV	150	0	150	0	133	16	149	0.107	link	-	Gm42571	n.-1193G>-	-	ENSMUST upstream_gene_variant
5	73191610	.	C	A	base_qual	SNV	150	0	150	0	133	16	149	0.107	link	-	Fryl	n.7319161(-	-	intragenic_variant
5	75576106	.	T	C	base_qual	SNV	230	12	242	0.05	142	18	160	0.113	link	-	Kit	c.67+988T>-	-	ENSMUST intron_variant
5	75942021	.	T	G	base_qual	SNV	73	4	77	0.052	52	8	60	0.133	link	-	Kdr	c.3505-60/-	-	ENSMUST intron_variant
5	76248471	.	T	G	base_qual	SNV	157	3	160	0.019	151	10	161	0.062	link	-	Clock	c.439-9A>-	-	ENSMUST intron_variant
5	87777234	.	A	C	base_qual	SNV	8	0	8	0	5	6	11	0.545	link	-	Csn1s2a	c.52-209A>-	-	ENSMUST intron_variant
5	90244617	.	T	G	base_qual	SNV	25	1	26	0.038	31	7	38	0.184	link	-	Ankrd17	c.5316-12(-	-	ENSMUST intron_variant
5	96534690	.	A	C	alt_allele_j	SNV	13	3	16	0.188	26	7	33	0.212	link	-	Fras1	c.214-169/-	-	ENSMUST intron_variant
5	1.02E+08	.	T	C	base_qual	SNV	79	1	80	0.013	117	20	137	0.146	link	-	Wdfy3	c.9204+57-	-	ENSMUST intron_variant
5	1.04E+08	.	T	G	alt_allele_j	SNV	17	4	21	0.19	15	10	25	0.4	link	-	Ptpn13	c.4116+14-	-	ENSMUST intron_variant
5	1.06E+08	.	A	C	alt_allele_j	SNV	167	6	173	0.035	167	8	175	0.046	link	-	Lrrc8dos	n.*3041T>-	-	ENSMUST downstream_gene_variant
5	1.17E+08	.	G	A	weak_evid	SNV	5	0	5	0	6	4	10	0.4	link	-	Taok3	c.988-168(-	-	ENSMUST intron_variant
5	1.17E+08	.	C	T	too_few_s	SNV	5	0	5	0	10	2	12	0.167	link	-	Rfc5	c.*5377G>-	-	ENSMUST downstream_gene_variant
5	1.17E+08	.	C	T	too_few_s	SNV	5	0	5	0	10	2	12	0.167	link	-	Wsb2	c.666+220-	-	ENSMUST intron_variant
5	1.22E+08	rs2273169	G	A	weak_evid	SNV	5	0	5	0	1	3	4	0.75	link	-	Gm15547	n.*2972C>-	-	ENSMUST downstream_gene_variant
5	1.22E+08	rs2273169	G	A	weak_evid	SNV	5	0	5	0	1	3	4	0.75	link	-	Mapkapk5	c.970-370(-	-	ENSMUST intron_variant
5	1.22E+08	rs2273169	G	A	weak_evid	SNV	5	0	5	0	1	3	4	0.75	link	-	Gm42878	c.970-370(-	-	ENSMUST intron_variant
5	1.22E+08	.	C	G	weak_evid	SNV	5	0	5	0	3	3	6	0.5	link	-	Gm15547	n.*2958G>-	-	ENSMUST downstream_gene_variant
5	1.22E+08	.	C	G	weak_evid	SNV	5	0	5	0	3	3	6	0.5	link	-	Mapkapk5	c.970-384(-	-	ENSMUST intron_variant
5	1.22E+08	.	C	G	weak_evid	SNV	5	0	5	0	3	3	6	0.5	link	-	Gm42878	c.970-384(-	-	ENSMUST intron_variant
5	1.24E+08	.	A	C	base_qual	SNV	152	1	153	0.007	157	8	165	0.048	link	-	B3gn4	c.-1084A>-	-	ENSMUST upstream_gene_variant
5	1.24E+08	.	A	C	base_qual	SNV	152	1	153	0.007	157	8	165	0.048	link	-	Lrrc43	c.*1322A>-	-	ENSMUST downstream_gene_variant
5	1.24E+08	.	A	C	base_qual	SNV	152	1	153	0.007	157	8	165	0.048	link	-	Diablo	c.*3021T>-	-	ENSMUST downstream_gene_variant
5	1.24E+08	.	A	C	base_qual	SNV	152	1	153	0.007	157	8	165	0.048	link	-	Gm15751	n.436+660-	-	ENSMUST intron_variant
5	1.24E+08	.	A	C	alt_allele_j	SNV	19	2	21	0.095	11	1	12	0.083	link	-	Kntc1	c.1546-17(-	-	ENSMUST intron_variant
5	1.24E+08	.	C	A	base_qual	SNV	36	3	39	0.077	25	7	32	0.219	link	-	Cdk2ap1	c.55+87G>-	-	ENSMUST intron_variant
5	1.24E+08	.	A	C	non_homn	SNV	12	2	14	0.143	9	3	12	0.25	link	-	Sbno1	c.745+219-	-	ENSMUST intron_variant
5	1.28E+08	.	C	A	base_qual	SNV	268	2	270	0.007	189	7	196	0.036	link	-	Gm43474	n.-179A>C	-	ENSMUST upstream_gene_variant
5	1.3E+08	.	G	A	too_few_s	SNV	8	0	8	0	13	2	15	0.133	link	-	Rabgef1	c.-169G>A	-	ENSMUST_5_prime_UTR_variant
5	1.3E+08	.	G	A	too_few_s	SNV	8	0	8	0	13	2	15	0.133	link	-	Gm15920	n.-1156G>-	-	ENSMUST upstream_gene_variant
5	1.3E+08	.	A	C	base_qual	SNV	91	0	91	0	102	5	107	0.047	link	-	Tywl1	c.1530-62/-	-	ENSMUST intron_variant
5	1.34E+08	.	T	C	base_qual	SNV	10	1	11	0.091	10	4	14	0.286	link	-	Gm24139	n.-2805T>-	-	ENSMUST upstream_gene_variant
5	1.34E+08	.	T	C	base_qual	SNV	10	1	11	0.091	10	4	14	0.286	link	-	Gtf2ird2	c.617+206-	-	ENSMUST intron_variant
5	1.34E+08	.	A	C</																

6	48743734 .	G	T	too_few_si	SNV	22	0	22	0	21	1	22	0.045	link	-	Gimap1os	n.-2290C>-	ENSMUST	upstream_gene_variant	
6	48743734 .	G	T	too_few_si	SNV	22	0	22	0	21	1	22	0.045	link	-	Gm28053	c.43>2317-	ENSMUST	intron_variant	
6	50353315 .	T	G	base_qual	SNV	3	0	3	0	0	8	8	1	link	-	Osbp13	c.94-214A>-	ENSMUST	intron_variant	
6	50353321 .	T	G	base_qual	SNV	3	0	3	0	0	8	8	1	link	-	Osbp13	c.94-220A>-	ENSMUST	intron_variant	
6	52259806 .	G	A	base_qual	SNV	79	5	84	0.06	60	10	70	0.143	link	-	Hottip	n.-2978G>-	ENSMUST	upstream_gene_variant	
6	52259806 .	G	A	base_qual	SNV	79	5	84	0.06	60	10	70	0.143	link	-	9530018H.n.-2346C>-	ENSMUST	upstream_gene_variant		
6	52259806 .	G	A	base_qual	SNV	79	5	84	0.06	60	10	70	0.143	link	-	Gm27280	n.-1348G>-	ENSMUST	upstream_gene_variant	
6	52259806 .	G	A	base_qual	SNV	79	5	84	0.06	60	10	70	0.143	link	-	Gm27985	n.-2786G>-	ENSMUST	upstream_gene_variant	
6	52259806 .	G	A	base_qual	SNV	79	5	84	0.06	60	10	70	0.143	link	-	Gm27383	n.-3252G>-	ENSMUST	upstream_gene_variant	
6	52259806 .	G	A	base_qual	SNV	79	5	84	0.06	60	10	70	0.143	link	-	Hoxa13	c.907+58C>-	ENSMUST	intron_variant	
6	55104571 .	G	A	alt_allele_i	SNV	10	3	13	0.231	22	10	32	0.312	link	-	Chrhr2	c.375+153-	ENSMUST	intron_variant	
6	82729045 .	A	G	base_qual	SNV	45	5	50	0.1	45	9	54	0.167	link	-	Hk2	c.2376-10C>-	ENSMUST	intron_variant	
6	82738571 .	T	G	base_qual	SNV	72	2	74	0.027	65	10	75	0.133	link	-	Hk2	c.1032-51C>-	ENSMUST	intron_variant	
6	83527241 .	A	C	base_qual	SNV	69	2	71	0.028	87	12	99	0.121	link	-	Actg2	c.126+75T>-	ENSMUST	intron_variant	
6	83711739 .	C	T	too_few_si	SNV	13	0	13	0	8	2	10	0.2	link	-	Vax2os	n.-807G>-	ENSMUST	upstream_gene_variant	
6	83711739 .	C	T	too_few_si	SNV	13	0	13	0	8	2	10	0.2	link	-	Gm27893	n.*807C>-T	ENSMUST	downstream_gene_variant	
6	83711739 .	C	T	too_few_si	SNV	13	0	13	0	8	2	10	0.2	link	-	Vax2	c.247+196-	ENSMUST	intron_variant	
6	83711739 .	C	T	too_few_si	SNV	13	0	13	0	8	2	10	0.2	link	-	Vax2os	n.8371173-	-	intragenic_variant	
6	88825814 .	A	G	weak_evid	SNV	92	2	94	0.021	144	4	148	0.027	link	-	Mgll	c.*38A>-G	ENSMUST	3_prime_UTR_variant	
6	89569480 .	G	A	non_homn	SNV	168	1	169	0.006	166	6	172	0.035	link	-	Chchd6	c.311-68C>-	ENSMUST	intron_variant	
6	91089760 .	A	C	base_qual	SNV	100	5	105	0.048	111	17	128	0.133	link	-	Nup210	c.533+75T>-	ENSMUST	intron_variant	
6	94606032 .	G	A	PASS	SNV	148	4	152	0.026	145	6	151	0.04	link	-	Slt25a26	c.*2363G>-	ENSMUST	downstream_gene_variant	
6	94606032 .	G	A	PASS	SNV	148	4	152	0.026	145	6	151	0.04	link	-	Mir7041	n.*332C>-T	ENSMUST	downstream_gene_variant	
6	94606032 .	G	A	PASS	SNV	148	4	152	0.026	145	6	151	0.04	link	-	Lrlg1	c.3032-29C>-	ENSMUST	intron_variant	
6	99692548 .	C	G	too_few_si	SNV	5	0	5	0	0	20	2	22	0.091	link	-	Gpr27	c.-131C>-G	ENSMUST	upstream_gene_variant
6	99692548 .	C	G	too_few_si	SNV	5	0	5	0	0	20	2	22	0.091	link	-	-	n.9969254-	-	intergenic_region
6	1.19E+08 rs2134583	C	A	weak_evid	SNV	33	0	33	0	56	6	62	0.097	link	-	Ankrd26	c.4422+67-	ENSMUST	intron_variant	
6	1.19E+08 .	T	C	base_qual	SNV	72	1	73	0.014	67	10	77	0.13	link	-	Fbx14	c.-32T>-C	ENSMUST	5_prime_UTR_variant	
6	1.19E+08 .	T	C	base_qual	SNV	72	1	73	0.014	67	10	77	0.13	link	-	Wnt5b	c.-18-315S>-	ENSMUST	intron_variant	
6	1.24E+08 .	C	A	base_qual	SNV	85	4	89	0.045	68	7	75	0.093	link	-	Pex5	c.183+54G>-	ENSMUST	intron_variant	
6	1.25E+08 .	G	C	too_few_si	SNV	5	0	5	0	5	2	7	0.286	link	-	Gpr162	c.-5791C>-	ENSMUST	upstream_gene_variant	
6	1.25E+08 .	G	C	too_few_si	SNV	5	0	5	0	5	2	7	0.286	link	-	Cd4	c.1156+18-	ENSMUST	intron_variant	
6	1.25E+08 .	G	T	base_qual	SNV	175	11	186	0.059	165	24	189	0.127	link	-	Ncapd2	c.1409-35C>-	ENSMUST	intron_variant	
6	1.27E+08 .	A	C	base_qual	SNV	30	0	30	0	27	6	33	0.182	link	-	Ndufa9	c.800+160-	ENSMUST	intron_variant	
6	1.28E+08 .	C	T	base_qual	SNV	17	3	21	0.143	5	9	28	0.321	link	-	Nrip2	c.*382C>-T	ENSMUST	3_prime_UTR_variant	
6	1.28E+08 .	C	T	base_qual	SNV	17	3	21	0.143	5	9	28	0.321	link	-	Itfg2	c.*1512G>-	ENSMUST	downstream_gene_variant	
6	1.28E+08 .	C	T	base_qual	SNV	17	3	21	0.143	5	9	28	0.321	link	-	Gm44596	c.*1327C>-	ENSMUST	downstream_gene_variant	
6	1.28E+08 .	C	G	base_qual	SNV	17	1	21	0.048	5	14	28	0.5	link	-	Nrip2	c.*382C>-C	ENSMUST	3_prime_UTR_variant	
6	1.28E+08 .	C	G	base_qual	SNV	17	1	21	0.048	5	14	28	0.5	link	-	Itfg2	c.*1512G>-	ENSMUST	downstream_gene_variant	
6	1.28E+08 .	C	G	base_qual	SNV	17	1	21	0.048	5	14	28	0.5	link	-	Gm44596	c.*1327C>-	ENSMUST	downstream_gene_variant	
6	1.29E+08 .	A	G	base_qual	SNV	4	0	4	0	16	9	25	0.36	link	-	Pzp	c.876+170-	ENSMUST	intron_variant	
6	1.29E+08 .	T	G	base_qual	SNV	106	9	115	0.078	115	12	127	0.094	link	-	Clec1b	c.545+71T>-	ENSMUST	intron_variant	
6	1.42E+08 .	T	G	base_qual	SNV	81	5	86	0.058	98	11	109	0.101	link	-	Recql	c.*2638A>-	ENSMUST	downstream_gene_variant	
6	1.42E+08 .	T	G	base_qual	SNV	81	5	86	0.058	98	11	109	0.101	link	-	Pyroxd1	c.1111-77C>-	ENSMUST	intron_variant	
6	1.42E+08 .	T	G	base_qual	SNV	81	5	86	0.058	98	11	109	0.101	link	-	Recql	n.1423600-	-	intragenic_variant	
6	1.44E+08 .	A	C	base_qual	SNV	198	5	203	0.025	164	8	172	0.047	link	-	Sox5	c.810+65T>-	ENSMUST	intron_variant	
6	1.44E+08 .	A	C	base_qual	SNV	198	5	203	0.025	164	8	172	0.047	link	-	Sox5os1	n.1197A>-C	ENSMUST	non_coding_transcript_exon_variant	
6	1.47E+08 .	T	G	base_qual	SNV	66	2	68	0.029	81	3	84	0.036	link	-	Asun	c.301-54A>-	ENSMUST	intron_variant	
7	4926625 .	G	T	base_qual	SNV	123	1	124	0.008	133	6	139	0.043	link	-	Zfp628	c.*4728G>-	ENSMUST	downstream_gene_variant	
7	4926625 .	G	T	base_qual	SNV	123	1	124	0.008	133	6	139	0.043	link	-	Nat14	c.*2174G>-	ENSMUST	downstream_gene_variant	
7	4926625 .	G	T	base_qual	SNV	123	1	124	0.008	133	6	139	0.043	link	-	Ssc5d	c.52+109G>-	ENSMUST	intron_variant	
7	12816046 .	A	C	base_qual	SNV	72	0	72	0	112	8	120	0.067	link	-	Zfp329	c.-72+277-	ENSMUST	intron_variant	
7	16273405 .	T	G	base_qual	SNV	18	3	21	0.143	33	9	42	0.214	link	-	Inafm1	c.-115A>-C	ENSMUST	5_prime_UTR_variant	
7	16273405 .	T	G	base_qual	SNV	18	3	21	0.143	33	9	42	0.214	link	-	Cdc9	c.*908A>-C	ENSMUST	downstream_gene_variant	
7	24987403 .	C	A	base_qual	SNV	113	1	114	0.009	114	6	120	0.05	link	-	Mir7047	n.*201G>-T	ENSMUST	downstream_gene_variant	
7	24987403 .	C	A	base_qual	SNV	113	1	114	0.009	114	6	120	0.05	link	-	Atp1a3	c.2263+32-	ENSMUST	intron_variant	
7	25244191 .	G	A	base_qual	SNV	59	2	61	0.033	88	20	108	0.185	link	-	Erf	c.*58C>-T	ENSMUST	3_prime_UTR_variant	
7	25297586 .	T	G	base_qual	SNV	34	5	39	0.128	52	16	68	0.235	link	-	Prr19	c.-5293T>-	ENSMUST	upstream_gene_variant	
7	25297586 .	T	G	base_qual	SNV	34	5	39	0.128	52	16	68	0.235	link	-	Cic	c.*4051T>-	ENSMUST	downstream_gene_variant	
7	25297586 .	T	G	base_qual	SNV	34	5	39	0.128	52	16	68	0.235	link	-	Pafah1b3	c.-18-116A>-	ENSMUST	intron_variant	
7	27036743 .	T	G	base_qual	SNV	36	1	37	0.027	51	11	62	0.177	link	-	Cyp2a12	c.*97T>-G	ENSMUST	3_prime_UTR_variant	
7	28005623 .	G	T	base_qual	SNV	61	1	62	0.016	88	6	94	0.064	link	-	Zfp850	c.161-306C>-	ENSMUST	intron_variant	
7	28544380 .	A	C	base_qual	SNV	94	2	96	0.021	88	8	96	0.083	link	-	Sycn	c.*2297A>-	ENSMUST	downstream_gene_variant	
7	28544380 .	A	C	base_qual	SNV	94	2	96	0.021	88	8	96	0.083	link	-	Nccrp1	c.735+42T>-	ENSMUST	intron_variant	
7	28544380 .	A	C	base_qual	SNV	94	2	96	0.021	88	8	96	0.083	link	-	Samd4b	c.-207+53-	ENSMUST	intron_variant	
7	29005960 .	T	G	base_qual	SNV	135	6	141	0.043	150	12	162	0.074	link	-	Map4k1	c.*2794T>-	ENSMUST	downstream_gene_variant	
7	29005960 .	T	G	base_qual	SNV	135	6	141	0.043	150	12	162	0.074	link	-	Ryr1	c.14638-3C>-	ENSMUST	intron_variant	
7	29051975 .	A	C	base_qual	SNV	155	1	156	0.006	156	6	162	0.037	link	-	Ryr1	c.11144+3-	ENSMUST	intron_variant	
7	29932288 .	A	C	base_qual	SNV	57	0	57	0	75	7	82	0.085	link	-	Zfp74	c.*1954T>-	ENSMUST	downstream_gene_variant	
7	29932288 .	A	C	base_qual	SNV	57	0	57	0	75	7	82	0.085	link	-	Gm44873	n.*1883A>-	ENSMUST	downstream_gene_variant	
7	29932288 .	A	C	base_qual	SNV	57	0	57	0	75	7	82	0.085	link	-	Zfp74	n.2993228-	-	intragenic_variant	
7	34747988 .	A	C	base_qual	SNV	79	5	84	0.06	77	11	88	0.125	link	-	Chst8	c.130+74T>-	ENSMUST	intron_variant	
7	42445303 .	A	T	PASS	SNV	162	0	162	0	165	32	197	0.162	link	-	493342110	c.*875T>-A	ENSMUST	downstream_gene_variant	
7	42445303 .	A	T	PASS	SNV	162	0	162	0	165	32	197	0.162	link	-	-	n.4244530-	-	intergenic_region	
7	45407099 .	T	G	base_qual	SNV	21	0	21	0	27	6	33	0.182	link	-	Kcna7	c.654+84T>-	ENSMUST	intron_variant	
7	45517397 .	C	T	too_few_si	SNV	5	0	5	0	2	2	4	0.5	link	-	RP23-218	n.-4830G>-	ENSMUST	upstream_gene_variant	
7	45517397 .	C	T	too_few_si	SNV	5	0	5	0	2	2	4	0.5	link	-	Tulp2	c.569-383C>-	ENSMUST	intron_variant	
7	51587535 .	A	C	base_qual	SNV	23	2	25	0.08	29	9	38	0.237	link	-	Ano5	c.2209-10C>-	ENSMUST	intron_variant	
7	51897192 .	A	C	base_qual	SNV	86	5	91	0.055	70	14									

8	3720726	C	T	weak_evid	SNV	103	0	103	0	124	4	128	0.031	link	-	Clec4g	c.-81G>A	-	ENSMUST	upstream_gene_variant
8	3720726	C	T	weak_evid	SNV	103	0	103	0	124	4	128	0.031	link	-	Gm16553	n.424+181-	-	ENSMUST	intron_variant
8	13584875	A	C	base_qual	SNV	156	4	160	0.025	134	11	145	0.076	link	-	Rasa3	c.1405+38-	-	ENSMUST	intron_variant
8	20122868	G	C	no_reliable	SNV	10	0	10	0	17	3	20	0.15	link	-	RP24-3661	n.*374G>C	-	ENSMUST	downstream_gene_variant
8	20122868	G	C	no_reliable	SNV	10	0	10	0	17	3	20	0.15	link	-	-	n.2012286-	-	-	intergenic_region
8	22631716	G	A	too_few_s	SNV	21	0	21	0	11	2	13	0.154	link	-	Dkk4	c.*4678G>-	-	ENSMUST	downstream_gene_variant
8	22631716	G	A	too_few_s	SNV	21	0	21	0	11	2	13	0.154	link	-	Polb	c.709-197(-	-	ENSMUST	intron_variant
8	23035205	G	A	weak_evid	SNV	319	0	319	0	272	3	275	0.011	link	-	Ank1	c.127-297(-	-	ENSMUST	intron_variant
8	33600102	C	T	base_qual	SNV	70	5	75	0.067	60	7	67	0.104	link	-	Ppp2cb	c.102+84C-	-	ENSMUST	intron_variant
8	41056693	T	G	alt_allele_j	SNV	121	7	128	0.055	102	20	122	0.164	link	-	Gm16193	n.214+337-	-	ENSMUST	intron_variant
8	41056693	T	G	alt_allele_j	SNV	121	7	128	0.055	102	20	122	0.164	link	-	Mtus1	c.2261-65(-	-	ENSMUST	intron_variant
8	41327797	T	C	too_few_s	SNV	15	0	15	0	17	2	19	0.105	link	-	Pcm1	c.5704+19-	-	ENSMUST	intron_variant
8	46740374	T	G	base_qual	SNV	250	3	253	0.012	224	2	226	0.009	link	-	Gm16675	n.-866A>C	-	ENSMUST	upstream_gene_variant
8	46740374	T	G	base_qual	SNV	250	3	253	0.012	224	2	226	0.009	link	-	Irf2	c.-7+438T-	-	ENSMUST	intron_variant
8	67720686	A	C	base_qual	SNV	13	2	15	0.133	28	11	39	0.282	link	-	Psd3	c.3365+11-	-	ENSMUST	intron_variant
8	68820585	A	C	base_qual	SNV	81	8	89	0.09	66	7	73	0.096	link	-	Ints10	c.1720-69(-	-	ENSMUST	intron_variant
8	71345899	A	C	base_qual	SNV	23	4	27	0.148	17	9	26	0.346	link	-	Myo9b	c.2689-13(-	-	ENSMUST	intron_variant
8	71535978	A	C	base_qual	SNV	26	3	29	0.103	23	16	39	0.41	link	-	Bst2	c.377-153(-	-	ENSMUST	intron_variant
8	71597549	A	C	weak_evid	SNV	6	1	7	0.143	13	6	19	0.316	link	-	Fam129c	c.-220A>C	-	ENSMUST	upstream_gene_variant
8	71597549	A	C	weak_evid	SNV	6	1	7	0.143	13	6	19	0.316	link	-	Pgls	c.*1358A>-	-	ENSMUST	downstream_gene_variant
8	71597549	A	C	weak_evid	SNV	6	1	7	0.143	13	6	19	0.316	link	-	Pgls	n.7159754-	-	-	intragenic_variant
8	79343987	T	G	base_qual	SNV	49	5	54	0.093	35	19	54	0.352	link	-	Smad1	c.998-77A(-	-	ENSMUST	intron_variant
8	79343990	C	A	alt_allele_j	SNV	46	7	53	0.132	27	23	50	0.46	link	-	Smad1	c.998-80G-	-	ENSMUST	intron_variant
8	84128739	C	T	too_few_s	SNV	90	0	90	0	92	0	92	0	link	-	Cc2d1a	c.*4498G>-	-	ENSMUST	downstream_gene_variant
8	84128739	C	T	too_few_s	SNV	90	0	90	0	92	0	92	0	link	-	Podnl1	c.651+13C-	-	ENSMUST	intron_variant
8	88132191	A	C	base_qual	SNV	189	3	192	0.016	148	7	155	0.045	link	-	Cnep1r1	c.337-159(-	-	ENSMUST	intron_variant
8	88706913	C	G	read_posit	SNV	3	0	3	0	10	2	12	0.167	link	-	Cyld	c.505-176(-	-	ENSMUST	intron_variant
8	91522722	A	C	base_qual	SNV	101	7	108	0.065	84	13	97	0.134	link	-	Fto	c.1231-50(-	-	ENSMUST	intron_variant
8	95730367	G	A	base_qual	SNV	62	2	64	0.031	83	6	89	0.067	link	-	Cnot1	c.5895+46-	-	ENSMUST	intron_variant
8	1.1E+08	G	A	weak_evid	SNV	13	0	13	0	5	5	10	0.5	link	-	Phlpp2	c.381-200(-	-	ENSMUST	intron_variant
8	1.11E+08	T	C	base_qual	SNV	51	4	55	0.073	49	14	63	0.222	link	-	Il13	c.28-160A-	-	ENSMUST	intron_variant
8	1.11E+08	T	C	base_qual	SNV	51	4	55	0.073	49	14	63	0.222	link	-	Gm15894	n.80T>C	-	ENSMUST	non_coding_transcript_exon_variant
8	1.11E+08	G	A	weak_evid	SNV	380	6	386	0.016	271	4	275	0.015	link	-	Aars	c.*1665G>-	-	ENSMUST	3_prime_UTR_variant
8	1.13E+08	A	C	base_qual	SNV	37	4	41	0.098	26	9	35	0.257	link	-	Cntnap4	c.2543-91(-	-	ENSMUST	intron_variant
8	1.22E+08	A	T	PASS	SNV	169	0	169	0	115	18	133	0.135	link	-	Gm20388	c.21+1643-	-	ENSMUST	intron_variant
8	1.22E+08	C	G	base_qual	SNV	196	6	202	0.03	144	7	151	0.046	link	-	Zcchc14	c.*68G>C	-	ENSMUST	3_prime_UTR_variant
8	1.22E+08	C	G	base_qual	SNV	196	6	202	0.03	144	7	151	0.046	link	-	Gm20388	c.21+1691-	-	ENSMUST	intron_variant
8	1.22E+08	G	T	weak_evid	SNV	225	2	227	0.009	198	3	201	0.015	link	-	BC048644	n.-282G>T	-	ENSMUST	upstream_gene_variant
8	1.22E+08	G	T	weak_evid	SNV	225	2	227	0.009	198	3	201	0.015	link	-	Gm20388	c.21+1996-	-	ENSMUST	intron_variant
8	1.23E+08	A	C	base_qual	SNV	130	4	134	0.03	100	14	114	0.123	link	-	Afg3l1	c.732-38A-	-	ENSMUST	intron_variant
8	1.23E+08	A	C	base_qual	SNV	130	4	134	0.03	100	14	114	0.123	link	-	Gm20388	c.22-8056A-	-	ENSMUST	intron_variant
8	1.25E+08	A	C	base_qual	SNV	210	7	217	0.032	116	6	122	0.049	link	-	Disc1	c.56-1185(-	-	ENSMUST	intron_variant
9	3007283	T	C	too_few_s	SNV	12	1	13	0.077	3	2	5	0.4	link	-	Gm10722	c.*4953T>-	-	ENSMUST	downstream_gene_variant
9	3007283	T	C	too_few_s	SNV	12	1	13	0.077	3	2	5	0.4	link	-	Gm11168	c.*2089T>-	-	ENSMUST	downstream_gene_variant
9	3007283	T	C	too_few_s	SNV	12	1	13	0.077	3	2	5	0.4	link	-	Gm26870	n.587-244(-	-	ENSMUST	intron_variant
9	3007284	G	A	too_few_s	SNV	12	1	13	0.077	3	2	5	0.4	link	-	Gm10722	c.*4954G>-	-	ENSMUST	downstream_gene_variant
9	3007284	G	A	too_few_s	SNV	12	1	13	0.077	3	2	5	0.4	link	-	Gm11168	c.*2090G>-	-	ENSMUST	downstream_gene_variant
9	3007284	G	A	too_few_s	SNV	12	1	13	0.077	3	2	5	0.4	link	-	Gm26870	n.587-244(-	-	ENSMUST	intron_variant
9	3007301	C	T	PASS	SNV	12	1	13	0.077	0	3	3	1	link	-	Gm10722	c.*4971C>-	-	ENSMUST	downstream_gene_variant
9	3007301	C	T	PASS	SNV	12	1	13	0.077	0	3	3	1	link	-	Gm11168	c.*2107C>-	-	ENSMUST	downstream_gene_variant
9	3007301	C	T	PASS	SNV	12	1	13	0.077	0	3	3	1	link	-	Gm26870	n.587-246(-	-	ENSMUST	intron_variant
9	3016085	T	C	weak_evid	SNV	218	1	219	0.005	72	3	75	0.04	link	-	Gm10719	c.-4070T>-	-	ENSMUST	upstream_gene_variant
9	3016085	T	C	weak_evid	SNV	218	1	219	0.005	72	3	75	0.04	link	-	Gm10721	c.*1741T>-	-	ENSMUST	downstream_gene_variant
9	3016085	T	C	weak_evid	SNV	218	1	219	0.005	72	3	75	0.04	link	-	Gm26870	n.219-172(-	-	ENSMUST	intron_variant
9	3016085	T	C	weak_evid	SNV	218	1	219	0.005	72	3	75	0.04	link	-	Gm10720	c.160+268-	-	ENSMUST	intron_variant
9	3016086	T	C	weak_evid	SNV	219	1	220	0.005	71	3	74	0.041	link	-	Gm10719	c.-4069T>-	-	ENSMUST	upstream_gene_variant
9	3016086	T	C	weak_evid	SNV	219	1	220	0.005	71	3	74	0.041	link	-	Gm10721	c.*1742T>-	-	ENSMUST	downstream_gene_variant
9	3016086	T	C	weak_evid	SNV	219	1	220	0.005	71	3	74	0.041	link	-	Gm26870	n.219-172(-	-	ENSMUST	intron_variant
9	3016086	T	C	weak_evid	SNV	219	1	220	0.005	71	3	74	0.041	link	-	Gm10720	c.160+269-	-	ENSMUST	intron_variant
9	3020585 rs1132057 T	A	A	non_homn	SNV	211	6	217	0.028	74	4	78	0.051	link	-	Gm26870	n.-2501A>-	-	ENSMUST	upstream_gene_variant
9	3020585 rs1132057 T	A	A	non_homn	SNV	211	6	217	0.028	74	4	78	0.051	link	-	Gm10718	c.-2962T>-	-	ENSMUST	upstream_gene_variant
9	3020585 rs1132057 T	A	A	non_homn	SNV	211	6	217	0.028	74	4	78	0.051	link	-	Gm10717	c.-4832T>-	-	ENSMUST	upstream_gene_variant
9	3020585 rs1132057 T	A	A	non_homn	SNV	211	6	217	0.028	74	4	78	0.051	link	-	Gm10720	c.*3375T>-	-	ENSMUST	downstream_gene_variant
9	3020585 rs1132057 T	A	A	non_homn	SNV	211	6	217	0.028	74	4	78	0.051	link	-	Gm10719	c.161-201(-	-	ENSMUST	intron_variant
9	3036676	T	C	no_reliable	SNV	73	1	74	0.014	9	3	12	0.25	link	-	Gm26870	n.3020585-	-	-	intragenic_variant
9	3036676	T	C	no_reliable	SNV	73	1	74	0.014	9	3	12	0.25	link	-	Gm10715	c.-435T>C	-	ENSMUST	upstream_gene_variant
9	3036676	T	C	no_reliable	SNV	73	1	74	0.014	9	3	12	0.25	link	-	Gm17535	c.*871T>C	-	ENSMUST	downstream_gene_variant
9	3036676	T	C	no_reliable	SNV	73	1	74	0.014	9	3	12	0.25	link	-	Mir101c	n.*1993A>-	-	ENSMUST	downstream_gene_variant
9	3036676	T	C	no_reliable	SNV	73	1	74	0.014	9	3	12	0.25	link	-	Gm26870	n.3036676-	-	-	intragenic_variant
9	15311516	A	C	base_qual	SNV	175	13	188	0.069	189	10	199	0.05	link	-	Gm25500	n.-1036A>-	-	ENSMUST	upstream_gene_variant
9	15311516	A	C	base_qual	SNV	175	13	188	0.069	189	10	199	0.05	link	-	Mir7650	n.-1095A>-	-	ENSMUST	upstream_gene_variant
9	15311516	A	C	base_qual	SNV	175	13	188	0.069	189	10	199	0.05	link	-	Gm24455	n.-2286A>-	-	ENSMUST	upstream_gene_variant
9	15311516	A	C	base_qual	SNV	175	13	188	0.069	189	10	199	0.05	link	-	Gm24299	n.-2558A>-	-	ENSMUST	upstream_gene_variant
9	15311516	A	C	base_qual	SNV	175	13	188	0.069	189	10	199	0.05	link	-	AC154296	n.-3326A>-	-	ENSMUST	upstream_gene_variant
9	15311516	A	C	base_qual	SNV	175	13	188	0.069	189	10	199	0.05	link	-	Gm25791	n.-3329A>-	-	ENSMUST	upstream_gene_variant
9	15311516	A	C	base_qual</																

X	7592506 .	A	C	too_few_si	SNV	11	0	11	0	13	2	15	0.133	link	-	Gm36995	n.3312+15-	ENSMUST intron_variant
X	9948794 .	G	T	base_qual	SNV	78	5	83	0.06	66	14	80	0.175	link	-	Syt15	c.832-18G-	ENSMUST intron_variant
X	59250900 .	G	A	weak_evid	SNV	187	0	187	0	165	3	168	0.018	link	-	Fgf13	n.5925090-	- intragenic_variant
X	73081737 .	T	G	base_qual	SNV	11	1	12	0.083	10	3	13	0.231	link	-	Xlr3a	c.*5391A>-	ENSMUST downstream_gene_variant
X	73081737 .	T	G	base_qual	SNV	11	1	12	0.083	10	3	13	0.231	link	-	Xlr4a	c.-31-136A-	ENSMUST intron_variant
X	98725978 .	G	A	too_few_si	SNV	88	0	88	0	87	1	88	0.011	link	-	Gm27554	n.*1337C>-	ENSMUST downstream_gene_variant
X	98725978 .	G	A	too_few_si	SNV	88	0	88	0	87	1	88	0.011	link	-	Ophn1	c.597+27C-	ENSMUST intron_variant
X	1.02E+08 .	A	C	base_qual	SNV	62	4	66	0.061	48	11	59	0.186	link	-	Taf1	c.3130-47I-	ENSMUST intron_variant
X	1.34E+08 .	A	C	base_qual	SNV	61	2	63	0.032	54	4	58	0.069	link	-	Mir3112	n.-2952A>-	ENSMUST upstream_gene_variant
X	1.34E+08 .	A	C	base_qual	SNV	61	2	63	0.032	54	4	58	0.069	link	-	Cstf2	c.890-772I-	ENSMUST intron_variant
X	1.4E+08 .	T	G	base_qual	SNV	124	5	129	0.039	116	8	124	0.065	link	-	Prps1	c.704+23T-	ENSMUST intron_variant
X	1.51E+08 .	A	C	base_qual	SNV	101	3	104	0.029	94	18	112	0.161	link	-	Alas2	c.305-29A-	ENSMUST intron_variant
X	1.51E+08 .	A	C	base_qual	SNV	101	3	104	0.029	94	18	112	0.161	link	-	Apex2	n.1505539-	- intragenic_variant
X	1.54E+08 .	A	C	base_qual	SNV	16	1	17	0.059	17	4	21	0.19	link	-	Z2100130C	c.*247-14C-	ENSMUST intron_variant
X	1.6E+08 .	T	G	base_qual	SNV	24	3	27	0.111	30	9	39	0.231	link	-	Sh3kbp1	c.858+65T-	ENSMUST intron_variant
X	1.63E+08 .	T	G	base_qual	SNV	31	4	35	0.114	35	10	45	0.222	link	-	Rbbp7	c.481+60T-	ENSMUST intron_variant
X	1.64E+08 .	A	G	weak_evid	SNV	6	0	6	0	5	5	10	0.5	link	-	Zrsr2	c.451-167I-	ENSMUST intron_variant
X	1.65E+08 .	G	A	base_qual	SNV	9	2	11	0.182	29	7	36	0.194	link	-	Glra2	c.68+125C-	ENSMUST intron_variant
Y	1134813 .	A	C	base_qual	SNV	44	3	47	0.064	51	9	60	0.15	link	-	Uty	c.2984+59-	ENSMUST intron_variant
Y	1134818 .	A	C	base_qual	SNV	50	1	51	0.02	58	9	67	0.134	link	-	Uty	c.2984+54-	ENSMUST intron_variant
Y	1444627 .	T	G	base_qual	SNV	104	2	106	0.019	92	5	97	0.052	link	-	Usp9y	c.323-12A-	ENSMUST intron_variant
GL456211 .	30146 .	T	C	non_homn	SNV	12	2	14	0.143	7	6	13	0.462	link	-	AC133103	c.*337A>-G-	ENSMUST downstream_gene_variant
GL456211 .	30146 .	T	C	non_homn	SNV	12	2	14	0.143	7	6	13	0.462	link	-	-	n.30146T>-	- intergenic_region
GL456211 .	82880 .	G	T	weak_evid	SNV	11	0	11	0	15	5	20	0.25	link	-	-	n.82880C>-	- intergenic_region
GL456211 .	168106 .	C	T	mapping_c	SNV	251	22	273	0.081	258	34	292	0.116	link	-	AC133103	c.32+118G-	ENSMUST intron_variant
GL456212 .	136325 .	C	T	non_homn	SNV	118	3	121	0.025	86	7	93	0.075	link	-	AC168977	c.973+204-	ENSMUST intron_variant
1	1.75E+08 .	C	T	PASS	SNV	184	0	184	0	137	6	143	0.042	link	-	Fmn2	c.3477C>-T.p.Leu1159Leu	ENSMUST synonymous_variant
1	1.8E+08 .	C	T	weak_evid	SNV	387	2	389	0.005	334	5	339	0.015	link	-	Cdc42bpa	c.3375C>-T.p.Cys1125Cys	ENSMUST synonymous_variant
11	53959356 .	C	T	PASS	SNV	469	0	469	0	369	9	378	0.024	link	-	Slc22a21	c.672G>-A p.Lys224Lys	ENSMUST synonymous_variant
11	96345571 .	C	T	weak_evid	SNV	417	4	421	0.01	458	5	463	0.011	link	-	Hoxb3	c.474C>-T p.Gly158Gly	ENSMUST synonymous_variant
11	1.01E+08 .	A	C	base_qual	SNV	253	6	259	0.023	253	11	264	0.042	link	-	Plekhh3	c.474T>-G p.Arg158Arg	ENSMUST synonymous_variant
12	8298327 .	G	A	base_qual	SNV	453	0	453	0	518	12	530	0.023	link	-	Gdf7	c.993C>-T p.Gly331Gly	ENSMUST synonymous_variant
12	1.11E+08 .	C	T	base_qual	SNV	399	5	404	0.012	274	9	283	0.032	link	-	Cdc42bpb	c.192G>-A p.Gln64Gln	ENSMUST synonymous_variant
13	1.13E+08 .	C	T	weak_evid	SNV	494	1	495	0.002	372	4	376	0.011	link	-	IL31ra	c.1188G>-T.p.Pro396Pro	ENSMUST synonymous_variant
14	21234964 .	G	A	read_posit	SNV	278	1	279	0.004	251	4	255	0.016	link	-	Adk	c.402G>-A p.Gln134Gln	ENSMUST synonymous_variant
14	66727861 .	C	T	base_qual	SNV	277	6	283	0.021	207	9	216	0.042	link	-	Adra1a	c.1299C>-T.p.Cys433Cys	ENSMUST synonymous_variant
16	63566737 .	T	A	PASS	SNV	288	1	289	0.003	301	13	314	0.041	link	-	Epha3	c.2535A>-T.p.Pro845Pro	ENSMUST synonymous_variant
17	32189349 .	G	A	base_qual	SNV	236	7	243	0.029	208	18	226	0.08	link	-	Ephx3	c.100C>-T p.Leu34Leu	ENSMUST synonymous_variant
18	20035382 .	A	C	base_qual	SNV	263	6	269	0.022	308	11	319	0.034	link	-	Dsc2	c.2019T>-C p.Thr673Thr	ENSMUST synonymous_variant
18	20533391 .	A	C	base_qual	SNV	215	4	219	0.018	216	5	221	0.023	link	-	Dsg3	c.1656A>-C p.Lys552Lys	ENSMUST synonymous_variant
19	5098210 .	G	T	base_qual	SNV	192	2	194	0.01	171	2	173	0.012	link	-	Cnih2	c.54C>-A p.Ala18Ala	ENSMUST synonymous_variant
19	5697633 .	T	C	PASS	SNV	358	1	359	0.003	373	5	378	0.013	link	-	Map3k11	c.1818T>-C p.Thr606Thr	ENSMUST synonymous_variant
2	27242861 .	C	T	weak_evid	SNV	209	0	209	0	203	3	206	0.015	link	-	Sardh	c.354G>-A p.Arg118Arg	ENSMUST synonymous_variant
2	1.28E+08 .	A	G	PASS	SNV	164	0	164	0	189	5	194	0.026	link	-	Bub1	c.1155T>-C p.Pro385Pro	ENSMUST synonymous_variant
3	19964505 .	A	T	PASS	SNV	223	0	223	0	221	6	227	0.026	link	-	Cp	c.372A>-T p.Val124Val	ENSMUST synonymous_variant
3	37029920 .	C	T	base_qual	SNV	248	1	249	0.004	250	15	265	0.057	link	-	4932438A	c.11485A>-p.Arg3829Arg	ENSMUST synonymous_variant
3	93074036 .	C	T	PASS	SNV	580	1	581	0.002	494	54	548	0.099	link	-	Gm4858	c.360C>-T p.Cys120Cys	ENSMUST synonymous_variant
4	1.05E+08 .	C	T	weak_evid	SNV	207	0	207	0	218	3	221	0.014	link	-	C8a	c.102G>-A p.Pro34Pro	ENSMUST synonymous_variant
4	1.41E+08 .	C	T	PASS	SNV	379	1	380	0.003	252	58	310	0.187	link	-	Spen	c.6060G>-f.p.Arg2020Arg	ENSMUST synonymous_variant
5	1.14E+08 .	A	G	base_qual	SNV	252	11	263	0.042	212	9	221	0.041	link	-	Foxn4	c.714T>-C p.Pro238Pro	ENSMUST synonymous_variant
7	1.05E+08 rs5819463	A	C	PASS	SNV	548	0	548	0	415	11	426	0.026	link	-	Usp17lb	c.153C>-T p.Cys51Cys	ENSMUST synonymous_variant
7	1.42E+08 .	G	A	base_qual	SNV	358	28	386	0.073	306	33	339	0.097	link	-	Dusp8	c.1474C>-T.p.Leu492Leu	ENSMUST synonymous_variant
9	35478640 .	G	A	weak_evid	SNV	416	0	416	0	361	4	365	0.011	link	-	Cdon	c.2589G>-f.p.Arg863Arg	ENSMUST synonymous_variant
X	8175903 .	C	T	base_qual	SNV	111	4	115	0.035	120	10	130	0.077	link	-	Tbc1d25	c.93G>-A p.Pro31Pro	ENSMUST synonymous_variant
1	84728123 .	A	C	base_qual	SNV	112	6	118	0.051	111	16	127	0.126	link	-	Trip12	c.5568+2T-	ENSMUST splice_donor_variant+intron_variant
1	84751717 .	T	G	base_qual	SNV	201	1	202	0.005	227	11	238	0.046	link	-	Trip12	c.3182-4A-	ENSMUST splice_region_variant+intron_variant
1	1.18E+08 .	A	C	base_qual	SNV	262	3	265	0.011	229	17	246	0.069	link	-	Clasp1	c.866-5A>-	ENSMUST splice_region_variant+intron_variant
1	1.2E+08 .	T	G	base_qual	SNV	142	1	143	0.007	128	3	131	0.023	link	-	Epb41I5	c.1523-2A-	ENSMUST splice_acceptor_variant+intron_variant
1	1.62E+08 .	A	C	base_qual	SNV	119	4	123	0.033	129	5	134	0.037	link	-	Suco	c.990+2T>-	ENSMUST splice_donor_variant+intron_variant
1	1.7E+08 .	T	G	base_qual	SNV	157	3	160	0.019	181	8	189	0.042	link	-	Uap1	c.662-2A>-	ENSMUST splice_acceptor_variant+intron_variant
1	1.72E+08 .	A	C	base_qual	SNV	216	4	220	0.018	103	7	110	0.064	link	-	Copa	c.3448-2A-	ENSMUST splice_acceptor_variant+intron_variant
10	12671932 .	T	G	base_qual	SNV	164	5	169	0.03	142	12	154	0.078	link	-	Utrn	c.4765-2A-	ENSMUST splice_acceptor_variant+intron_variant
10	41553071 .	A	C	base_qual	SNV	183	2	185	0.011	149	8	157	0.051	link	-	Gm29096	c.5811+2T-	ENSMUST splice_donor_variant+intron_variant
10	41553071 .	A	C	base_qual	SNV	183	2	185	0.011	149	8	157	0.051	link	-	Cdc162	c.1992+2T-	ENSMUST splice_donor_variant+intron_variant
10	1.12E+08 .	A	C	base_qual	SNV	242	2	244	0.008	240	5	245	0.02	link	-	Glpr1l2	c.695-4A>-	ENSMUST splice_region_variant+intron_variant
11	49635284 .	A	G	base_qual	SNV	256	7	263	0.027	209	14	223	0.063	link	-	Flt4	c.2406+4A-	ENSMUST splice_region_variant+intron_variant
11	53389793 .	T	G	alt_allele_i	SNV	217	9	226	0.04	222	13	235	0.055	link	-	Atf4	c.1072+2T-	ENSMUST splice_donor_variant+intron_variant
11	72758602 .	T	G	base_qual	SNV	154	2	156	0.013	161	10	171	0.058	link	-	Ankfy1	c.2923+2T-	ENSMUST splice_donor_variant+intron_variant
11	98822718 .	A	C	base_qual	SNV	177	3	180	0.017	185	13	198	0.066	link	-	Casc3	c.777-2A>-	ENSMUST splice_acceptor_variant+intron_variant
11	1.06E+08 .	T	G	base_qual	SNV	221	4	225	0.018	135	16	151	0.106	link	-	Kcnh6	c.2390+2T-	ENSMUST splice_donor_variant+intron_variant
11	1.07E+08 .	A	C	base_qual	SNV	286	10	296	0.034	255	10	265	0.038	link	-	Ddx5	c.307+2T>-	ENSMUST splice_donor_variant+intron_variant
11	1.1E+08 .	A	C	base_qual	SNV	292	3	295	0.01	308	3	311	0.01	link	-	Wip1l	c.163+2T>-	ENSMUST splice_donor_variant+intron_variant
12	31535248 .	A	C	base_qual	SNV	330	6	336	0.018	281	12	293	0.041	link	-	Slc26a4	c.1544+2T-	ENSMUST splice_donor_variant+intron_variant
12	83976626 .	A	C	base_qual	SNV	199	2	201	0.01	209	9	218	0.041	link	-	Heatr4	c.1252+2T-	ENSMUST splice_donor_variant+intron_variant
12	89187014 .	A	C	base_qual	SNV	179	8	187	0.043	190	14	204	0.069	link	-	Nrxn3	c.758-8A>-	ENSMUST splice_region_variant+intron_variant
13	24025943 .	T	G	base_qual	SNV	266	12	278	0.043	217	25	242	0.103	link	-	Lrrc16a	c.3556-8A-	ENSMUST splice_region_variant+intron_variant
13	58861248 .	A	C	base_qual	SNV	141	6	147	0.041	141	17	158	0.108	link	-	Ntrk2	c.854-2A>-	ENSMUST splice_acceptor_variant+intron_variant
13	76145198 .	A	C	base_qual	SNV	252	12	264	0.045	248	11	259	0.042					

8	1.06E+08	A	C	base_qual	SNV	229	7	236	0.03	148	8	156	0.051	link	-	Nfatc3	c.1405-2A	-	ENSMUST splice_acceptor_variant+intron_variant
8	1.22E+08	A	T	PASS	SNV	169	0	169	0	115	18	133	0.135	link	-	Fbxo31	c.955-7T>	-	ENSMUST splice_region_variant+intron_variant
9	82974925	A	C	base_qual	SNV	100	4	104	0.038	84	5	89	0.056	link	-	Phip	c.129+2T>	-	ENSMUST splice_donor_variant+intron_variant
9	1.12E+08	A	C	base_qual	SNV	125	2	127	0.016	129	15	144	0.104	link	-	Stac	c.1113+6T	-	ENSMUST splice_region_variant+intron_variant