Chr	Pos	ID	Ref	Alt	Filter	Variant_Typ	Normal_REF	Normal_ALT	Normal_Dep	Normal_Alle	Tumor_REF	Tumor_ALT	Tumor_Dep	Tumor_Allel	igv	ClinVar	Gene_Name	CDS_Chang	Amino_Acid	Transcript_I	Effect
1	88269887	.	A	AT	too_few_si	INS	4	0	4	0	1	2	3	0.667	link	-	Hjurp	c.354+314	-	ENSMUST	intron_variant
8	45934596	.	TC	T	non_homre	DEL	52	31	83	0.373	46	49	95	0.516	link	-	Ccdc110	c.-108delC	-	ENSMUST	upstream_gene_variant
8	45934596	.	TC	T	non_homre	DEL	52	31	83	0.373	46	49	95	0.516	link	-	-	n.4593459	-	-	intergenic_region
2	25566570	.	TG	T	alt_allele_i	DEL	51	19	70	0.271	37	37	74	0.5	link	-	Mamdc4	c.1985-3d	-	ENSMUST	splice_region_variant+intron_variant
2	25566570	.	TG	T	alt_allele_i	DEL	51	19	70	0.271	37	37	74	0.5	link	-	Edf1	c.*4659del	-	ENSMUST	downstream_gene_variant
5	26035532	.	T	TA	mapping_c	INS	6	0	6	0	1	1	2	0.5	link	-	Speer4a	c.627+333	-	ENSMUST	intron_variant
8	84872125	.	CG	C	non_homre	DEL	58	19	77	0.247	40	36	76	0.474	link	-	Syce2	c.-101delG	-	ENSMUST	5_prime_UTR_variant
8	84872125	.	CG	C	non_homre	DEL	58	19	77	0.247	40	36	76	0.474	link	-	Farsa	c.*3122del	-	ENSMUST	downstream_gene_variant
8	84872125	.	CG	C	non_homre	DEL	58	19	77	0.247	40	36	76	0.474	link	-	Mir7069	n.*4118del	-	ENSMUST	downstream_gene_variant
14	32193509	.	TA	T	non_homre	DEL	113	25	138	0.181	67	53	120	0.442	link	-	Gm23946	n.-1460del	-	ENSMUST	upstream_gene_variant
14	32193509	.	TA	T	non_homre	DEL	113	25	138	0.181	67	53	120	0.442	link	-	Timm23	c.260-23d	-	ENSMUST	intron_variant
15	83102530	.	AC	A	alt_allele_i	DEL	69	36	105	0.343	63	50	113	0.442	link	-	Serhl	c.341-82d	-	ENSMUST	intron_variant
15	83102530	.	AC	A	alt_allele_i	DEL	69	36	105	0.343	63	50	113	0.442	link	-	Gm17206	n.269-151	-	ENSMUST	intron_variant
13	1.13E+08	.	TGGG	T	non_homre	DEL	19	1	20	0.05	8	6	14	0.429	link	-	Dhx29	c.3066+69	-	ENSMUST	intron_variant
11	3188470	.	ATCTTT	A	low_frac_ir	DEL	17	5	22	0.227	11	8	19	0.421	link	-	Sfi1	c.23+466_	-	ENSMUST	intron_variant
11	3188470	.	ATCTTT	A	low_frac_ir	DEL	17	5	22	0.227	11	8	19	0.421	link	-	Drg1	n.3188475	-	-	intragenic_variant
13	51449154	rs2333696	GC	G	alt_allele_i	DEL	58	10	68	0.147	25	18	43	0.419	link	-	Shc3	c.841+72d	-	ENSMUST	intron_variant
8	78393185	.	T	TTA	base_qualii	INS	13	0	13	0	14	9	23	0.391	link	-	Ttc29	c.1397+94	-	ENSMUST	intron_variant
5	1.2E+08	.	AG	A	alt_allele_i	DEL	35	10	45	0.222	22	14	36	0.389	link	-	Gm27199	n.-4487del	-	ENSMUST	upstream_gene_variant
5	1.2E+08	.	AG	A	alt_allele_i	DEL	35	10	45	0.222	22	14	36	0.389	link	-	Lhx5	c.676-43d	-	ENSMUST	intron_variant
4	1.48E+08	.	TAAA	T	weak_evid	DEL	21	2	23	0.087	8	5	13	0.385	link	-	Zfp982	c.31-227_3	-	ENSMUST	intron_variant
9	29012066	rs2479449	TG	T	non_homre	DEL	97	17	114	0.149	59	37	96	0.385	link	-	Ntm	c.782+34d	-	ENSMUST	intron_variant
7	1.35E+08	.	TG	T	alt_allele_i	DEL	33	8	41	0.195	28	17	45	0.378	link	-	Dock1	c.130+70d	-	ENSMUST	intron_variant
4	1.48E+08	.	GAGAAGA	G	mapping_c	DEL	46	9	55	0.164	29	17	46	0.37	link	-	Zfp534	c.31-477_3	-	ENSMUST	intron_variant
4	1.48E+08	.	A	ATT	non_homre	INS	19	2	21	0.095	8	4	12	0.333	link	-	Zfp982	c.31-227_3	-	ENSMUST	intron_variant
5	1.41E+08	.	CTTTT	C	too_few_si	DEL	4	0	4	0	4	2	6	0.333	link	-	Iqce	c.631-347_	-	ENSMUST	intron_variant
10	78583854	.	CT	C	non_homre	DEL	85	15	100	0.15	56	27	83	0.325	link	-	Syde1	c.*1647del	-	ENSMUST	downstream_gene_variant
10	78583854	.	CT	C	non_homre	DEL	85	15	100	0.15	56	27	83	0.325	link	-	Ilvbl	c.1615-11	-	ENSMUST	intron_variant
19	34583479	rs1133281	AC	A	non_homre	DEL	51	8	59	0.136	34	16	50	0.32	link	-	Ifit3	c.-120delC	-	ENSMUST	upstream_gene_variant
19	34583479	rs1133281	AC	A	non_homre	DEL	51	8	59	0.136	34	16	50	0.32	link	-	-	n.3458348	-	-	intergenic_region
7	1.31E+08	.	GC	G	weak_evid	DEL	40	3	43	0.07	32	15	47	0.319	link	-	Nsmce4a	c.362-51d	-	ENSMUST	intron_variant
7	1.31E+08	.	GC	G	weak_evid	DEL	40	3	43	0.07	32	15	47	0.319	link	-	Fgfr2	n.1305428	-	-	intragenic_variant
4	1.46E+08	.	TA	T	mapping_c	DEL	9	0	9	0	15	7	22	0.318	link	-	Zfp992	c.31-235d	-	ENSMUST	intron_variant
4	1.46E+08	.	TA	T	mapping_c	DEL	9	0	9	0	15	7	22	0.318	link	-	Gm26573	n.1421-17	-	ENSMUST	intron_variant
19	4139188	.	AC	A	weak_evid	DEL	19	2	21	0.095	32	14	46	0.304	link	-	Gpr152	c.-3273del	-	ENSMUST	upstream_gene_variant
19	4139188	.	AC	A	weak_evid	DEL	19	2	21	0.095	32	14	46	0.304	link	-	Cabp4	c.354+14d	-	ENSMUST	intron_variant
7	1.26E+08	.	GC	G	non_homre	DEL	43	11	54	0.204	35	15	50	0.3	link	-	Gm44876	n.-3169del	-	ENSMUST	upstream_gene_variant
7	1.26E+08	.	GC	G	non_homre	DEL	43	11	54	0.204	35	15	50	0.3	link	-	Il4ra	c.902+108	-	ENSMUST	intron_variant
4	1.15E+08	.	AGG	A	low_frac_ir	DEL	53	7	60	0.117	36	15	51	0.294	link	-	Trabd2b	c.1349+19	-	ENSMUST	intron_variant
1	62764998	.	AG	A	non_homre	DEL	64	12	76	0.158	49	20	69	0.29	link	-	Nrp2	c.1786+15	-	ENSMUST	intron_variant
3	1.21E+08	rs2340670	GC	G	weak_evid	DEL	49	7	56	0.125	42	16	58	0.276	link	-	Cnn3	c.*3978del	-	ENSMUST	downstream_gene_variant
3	1.21E+08	rs2340670	GC	G	weak_evid	DEL	49	7	56	0.125	42	16	58	0.276	link	-	Slc44a3	c.1630-66	-	ENSMUST	intron_variant
4	47257308	.	CG	C	non_homre	DEL	46	5	51	0.098	21	8	29	0.276	link	-	Col15a1	c.1059+49	-	ENSMUST	intron_variant
1	1.5E+08	.	TG	T	non_homre	DEL	92	17	109	0.156	69	23	92	0.25	link	-	Pla2g4a	c.33+84de	-	ENSMUST	intron_variant
13	55724670	rs2511814	CT	C	non_homre	DEL	67	12	79	0.152	72	24	96	0.25	link	-	Pcbd2	c.-2702del	-	ENSMUST	upstream_gene_variant
13	55724670	rs2511814	CT	C	non_homre	DEL	67	12	79	0.152	72	24	96	0.25	link	-	Txndc15	c.838+44d	-	ENSMUST	intron_variant
11	32614511	.	TC	T	non_homre	DEL	68	12	80	0.15	80	26	106	0.245	link	-	Stk10	c.2335-3d	-	ENSMUST	splice_region_variant+intron_variant
11	84962558	rs2287441	CTT	C	weak_evid	DEL	34	2	36	0.056	30	9	39	0.231	link	-	Car4	c.109+132	-	ENSMUST	intron_variant
12	3982145	.	AC	A	non_homre	DEL	66	7	73	0.096	49	14	63	0.222	link	-	Efr3b	c.850-41d	-	ENSMUST	intron_variant
7	1.05E+08	.	T	TCTTC	low_frac_ir	INS	5	0	5	0	7	2	9	0.222	link	-	Usp17le	c.131-121	-	ENSMUST	intron_variant
8	4245878	rs2234285	AC	A	non_homre	DEL	64	7	71	0.099	77	20	97	0.206	link	-	Tgfbr3l	c.-2404del	-	ENSMUST	upstream_gene_variant
8	4245878	rs2234285	AC	A	non_homre	DEL	64	7	71	0.099	77	20	97	0.206	link	-	Map2k7	c.1304+63	-	ENSMUST	intron_variant
8	4245878	rs2234285	AC	A	non_homre	DEL	64	7	71	0.099	77	20	97	0.206	link	-	Map2k7	c.1304+63	-	ENSMUST	intron_variant
8	1.2E+08	.	TG	T	PASS	DEL	79	4	83	0.048	51	13	64	0.203	link	-	Adad2	c.1461-85	-	ENSMUST	intron_variant
14	43343148	.	G	GACACAC	multiallelic	INS	9	0	9	0	10	3	16	0.188	link	-	1700001F(	c.491-423_	-	ENSMUST	intron_variant
14	43343148	.	G	GACAC	base_qualii	INS	9	0	9	0	10	3	16	0.188	link	-	1700001F(	c.491-421_	-	ENSMUST	intron_variant
13	54105818	.	G	GT	non_homre	INS	158	19	177	0.107	131	30	161	0.186	link	-	Sfxn1	c.872+33d	-	ENSMUST	intron_variant
1	26686757	.	C	CTTCCTC	non_homre	INS	11	0	11	0	9	2	11	0.182	link	-	4931408C(	c.186+483	-	ENSMUST	intron_variant
15	1.01E+08	.	TGCCAGT	T	too_few_si	DEL	9	0	9	0	9	2	11	0.182	link	-	Krt7	c.*4969_*4	-	ENSMUST	downstream_gene_variant
15	1.01E+08	.	TGCCAGT	T	too_few_si	DEL	9	0	9	0	9	2	11	0.182	link	-	Krt87	c.1263-26	-	ENSMUST	intron_variant
7	1.23E+08	.	ACC	A	non_homre	DEL	32	5	37	0.135	45	10	55	0.182	link	-	Tnrc6a	c.53+92_5	-	ENSMUST	intron_variant
7	1.23E+08	.	ACC	A	non_homre	DEL	32	5	37	0.135	45	10	55	0.182	link	-	RP23-243(	n.304-447	-	ENSMUST	intron_variant
4	1.52E+08	rs2551877	AG	A	PASS	DEL	105	0	105	0	111	22	133	0.165	link	-	Kcnab2	c.119+49d	-	ENSMUST	intron_variant
17	34578164	.	AG	A	non_homre	DEL	80	6	86	0.07	87	17	104	0.163	link	-	Notch4	c.2853+41	-	ENSMUST	intron_variant
5	36153773	.	TCATA	T	non_homre	DEL	80	7	87	0.08	80	15	95	0.158	link	-	Sorcs2	c.648+46_	-	ENSMUST	intron_variant
18	76965416	.	C	CTG	too_few_si	INS	7	0	7	0	11	2	13	0.154	link	-	Hdhd2	c.612+193	-	ENSMUST	intron_variant
15	1.01E+08	.	GTC	G	too_few_si	DEL	17	0	17	0	13	2	15	0.133	link	-	Krt7	c.*4949_*4	-	ENSMUST	downstream_gene_variant
15	1.01E+08	.	GTC	G	too_few_si	DEL	17	0	17	0	13	2	15	0.133	link	-	Krt87	c.1263-24(	-	ENSMUST	intron_variant
X	7812132	.	AAAAAC	A	too_few_si	DEL	13	0	13	0	14	2	16	0.125	link	-	Mir1198	n.*4912_*4	-	ENSMUST	downstream_gene_variant
X	7812132	.	AAAAAC	A	too_few_si	DEL	13	0	13	0	14	2	16	0.125	link	-	Gripap1	c.1588-13(	-	ENSMUST	intron_variant
17	30719085	.	TGAGG	T	non_homre	DEL	21	2	23	0.087	30	4	34	0.118	link	-	Dnah8	c.4917+33	-	ENSMUST	intron_variant
7	45054470	.	TC	T	non_homre	DEL	61	3	64	0.047	94	11	105	0.105	link	-	Prr12	c.-1590del	-	ENSMUST	upstream_gene_variant
7	45054470	.	TC	T	non_homre	DEL	61	3	64	0.047	94	11	105	0.105	link	-	Prrg2	c.578+48d	-	ENSMUST	intron_variant
14	34353504	.	TCCTC	T	base_qualii	DEL	22	0	22	0	23	2	25	0.08	link	-	Fam25c	c.136+190	-	ENSMUST	intron_variant
2	1.29E+08	.	TTTTC	T	base_qualii	DEL	11	0	11	0	24	2	26	0.077	link	-	Gm10762	c.*117_*12	-	ENSMUST	3_prime_UTR_variant
2	1.29E+08	.	TTTTC	T	base_qualii	DEL	11	0	11	0	24	2	26	0.077	link	-	Zc3h6	c.-845_-84	-	ENSMUST	upstream_gene_variant
15	89300420	.	CCT	C	PASS	DEL	228	1	229	0.004	225	18	243	0.074	link	-	Sbf1	c.3290_32	p.Glu1097f	ENSMUST	frameshift_variant
11	97574993	.	GCGGGGC	G	long_indel	DEL	141	0	141	0	103	5	108	0.046	link	-	Srcin1	c.-118_-5d	-	ENSMUST	5_prime_UTR_variant
5	38739293	.	GAAAAC	G	weak_evid	DEL	202	2	204	0.01	198	8	206	0.039	link	-	Clnk	c.655+44_	-	ENSMUST	intron_variant
5	38739293	.	GAAAAC	G	weak_evid	DEL	202	2	204	0.01	198	8	206	0.039	link	-	Clnkos	n.46-2470_	-	ENSMUST	intron_variant
4	1.35E+08	.	CGAG	C	weak_evid	DEL	142	1	143	0.007	152	6	158	0.038	link	-	Srrm1	c.1757_17	p.Pro586d	ENSMUST	disruptive_inframe_deletion
10	80024842	.	CA	C	weak_evid	DEL	174	1	175	0.006	157	6	163	0.037	link	-	Hmha1	c.1400delA	p.Asn467fs	ENSMUST	frameshift_variant
11	50170653	.	CTTTGT	C	too_few_si	DEL	50	0	50	0	59	2	61	0.033	link	-	3010026O(	c.-4232_-4	-	ENSMUST	upstream_gene_variant
11	50170653	.	CTTTGT	C	too_few_si	DEL	50	0	50	0	59	2	61	0.033	link	-	Tbc1d9b	c.3082-29_	-	ENSMUST	intron_variant
13	1.02E+08	.	TCAAAA	T	weak_evid	DEL	116	1	117	0.009	120	4	124	0.032	link	-	Pik3r1	c.635-14_6	-	ENSMUST	intron_variant
15	93398064	.	TCGAGGC	T	weak_evid	DEL	179	1	180	0.006	182	5	187	0.027	link	-	Pphln1	c.-12647_-	-	ENSMUST	upstream_gene_variant
15	93398064	.	TCGAGGC	T	weak_evid	DEL	179	1	180	0.006	182	5	187	0.027	link	-	Zcrb1	c.-3+75_-3	-	ENSMUST	intron_variant
17	65783467	.	CCCGGGC	C	weak_evid	DEL	142	1	143	0.007	153	4	157	0.025	link	-	Ppp4r1	c.7+27_8	-	ENSMUST	intron_variant
4	46389300	.	CT	C	PASS	DEL	234	0	234	0	203	5	208	0.024	link	-	Hemgn	c.*5296del	-	ENSMUST	downstream_gene_variant
4	46389300	.	CT	C	PASS	DEL	234	0	234	0	203	5	208	0.024	link	-	Trmo	c.76+17de	-	ENSMUST	intron_variant
15	84120672	.	CG	C	weak_evid	DEL	250	1	251	0.004	260	6	266	0.023	link	-	Pnpla5	c.476delC	p.Pro159fs	ENSMUST	frameshift_variant
16	89047223	.	G	GAACACA	multiallelic	INS	6	0	6	0	4	0	4	0	link	-	Krtap6-5	c.*383_*38	-	ENSMUST	downstream_gene_variant
16	89047223	.	G	GAACACA	multiallelic	INS	6	0	6	0	4	0	4	0	link	-	-	n.8904722	-	-	intergenic_region
16	89047223	.	G	GAACACA	multiallelic	INS	6	0	6	0	4	0	4	0	link	-	Krtap6-5	c.*383_*38	-	ENSMUST	downstream_gene_variant
16	89047223	.	G	GAACACA	multiallelic	INS	6	0	6	0	4	0	4	0	link	-	-	n.8904722	-	-	intergenic_region
19	37402761	.	T	TGGGGGC	too_few_si	INS	4	0	4	0	1	0	1	0	link	-	Kif11	c.1302+47	-	ENSMUST	intron_variant
10	58224401	.	C	A	mapping_c	SNV	540	7	547	0.013	525	15	540	0.028	link	-	AW822073	c.530G>T	p.Arg177Le	ENSMUST	missense_variant
10	79716801	.	A	C	base_qualii	SNV	184	1	185	0.005	198	7	205	0.034	link	-	Hcn2	c.133A>C	p.Thr45Pr	ENSMUST	missense_variant
11	16981861	.	G	A	PASS	SNV	238	0	238	0	244	5	249	0.02	link	-	Plek	c.989C>T	p.Ala330Va	ENSMUST	missense_variant
11	1.01E+08	.	T	G	base_qualii	SNV	237	3	240	0.013	295	7	302	0.023	link	-	Plekhh3	c.1631A>C	p.Gln544P	ENSMUST	missense_variant
12	4820612	.	G	A	PASS	SNV	204	0	204	0	200	5	205	0.024	link	-	Sf3b6	c.49G>A	p.Val17Ile	ENSMUST	missense_variant
12	1.13E+08	.	A	C	base_qualii	SNV	189	0	189	0	145	12	157	0.076	link	-	Cep170b	c.4111A>C	p.Ile1371L	ENSMUST	missense_variant
14	52792698	.	C	A	base_qualii	SNV	302	3	305	0.01	305	21	326	0.064	link	-	Trav9d-1	c.258C>A	p.Ser86Arg	ENSMUST	missense_variant

15	78885298	.	T	G	base_quali	SNV	122	7	129	0.054	137	12	149	0.081	link	-	Gga1	c.470T>G	p.Phe157C	ENSMUST	missense_variant
15	1.01E+08	.	G	A	weak_evid	SNV	169	0	169	0	153	3	156	0.019	link	-	Tfcp2	c.1159C>T	p.Arg387T	ENSMUST	missense_variant
16	74045884	.	G	T	PASS	SNV	328	0	328	0	260	8	268	0.03	link	-	Robo2	c.605C>A	p.Thr202A	ENSMUST	missense_variant
2	26351859	.	T	G	base_quali	SNV	235	15	250	0.06	185	18	203	0.089	link	-	Dnlz	c.154A>C	p.Ser52Arg	ENSMUST	missense_variant
2	40879482	.	T	A	PASS	SNV	239	0	239	0	180	40	220	0.182	link	-	Lrp1b	c.8504A>T	p.Asp2835	ENSMUST	missense_variant
2	1.12E+08	.	G	A	PASS	SNV	309	0	309	0	262	9	271	0.033	link	-	Olfr1307	c.412C>T	p.Pro138S	ENSMUST	missense_variant
2	1.56E+08	.	C	T	PASS	SNV	175	0	175	0	179	6	185	0.032	link	-	Fer1l4	c.4511G>A	p.Ser1504	ENSMUST	missense_variant
3	63993891	.	C	T	weak_evid	SNV	193	0	193	0	227	3	230	0.013	link	-	Gmps	c.1130C>T	p.Ala377Va	ENSMUST	missense_variant
3	87922936	.	A	C	base_quali	SNV	138	0	138	0	123	12	135	0.089	link	-	Mrpl24	c.385A>C	p.Lys129G	ENSMUST	missense_variant+splice_region_variant
3	87922937	.	A	C	base_quali	SNV	139	1	140	0.007	114	19	133	0.143	link	-	Mrpl24	c.386A>C	p.Lys129T	ENSMUST	missense_variant+splice_region_variant
3	1.1E+08	.	T	A	PASS	SNV	257	0	257	0	226	5	231	0.022	link	-	Vav3	c.1666T>A	p.Leu556M	ENSMUST	missense_variant
4	1.36E+08	.	T	A	base_quali	SNV	173	4	177	0.023	136	5	141	0.035	link	-	6030445D	c.56T>A	p.Val19Asp	ENSMUST	missense_variant
6	97247676	.	T	A	base_quali	SNV	255	5	260	0.019	235	14	249	0.056	link	-	Lmod3	c.1183A>T	p.Met395L	ENSMUST	missense_variant
6	1.13E+08	.	T	G	weak_evid	SNV	383	3	386	0.008	317	38	355	0.107	link	-	Prrt3	c.1328A>C	p.Asn443T	ENSMUST	missense_variant
8	1.25E+08	.	A	C	base_quali	SNV	195	4	199	0.02	216	6	222	0.027	link	-	Ttc13	c.77T>G	p.Leu26Ar	ENSMUST	missense_variant
9	3025910	.	G	T	non_homre	SNV	200	4	204	0.02	170	7	177	0.04	link	-	Gm10717	c.494G>T	p.Ser165Il	ENSMUST	missense_variant
9	3026361	.	A	G	non_homre	SNV	17	2	19	0.105	17	3	20	0.15	link	-	Gm10717	c.658A>G	p.Ile220Va	ENSMUST	missense_variant
9	46308915	.	T	G	weak_evid	SNV	177	0	177	0	145	6	151	0.04	link	-	4931429L1	c.318A>C	p.Lys106A	ENSMUST	missense_variant
9	46308916	.	T	G	weak_evid	SNV	176	1	177	0.006	145	6	151	0.04	link	-	4931429L1	c.317A>C	p.Lys106T	ENSMUST	missense_variant
9	46308917	.	T	G	weak_evid	SNV	177	0	177	0	144	6	150	0.04	link	-	4931429L1	c.316A>C	p.Lys106G	ENSMUST	missense_variant
X	7008880	.	G	A	weak_evid	SNV	111	0	111	0	122	3	125	0.024	link	-	Ccnb3	c.1459C>T	p.Pro487S	ENSMUST	missense_variant
1	21166339	.	G	A	too_few_si	SNV	15	0	15	0	20	2	22	0.091	link	-	-	n.2116633	-	-	intergenic_region
1	37864876	.	T	G	base_quali	SNV	135	2	137	0.015	130	7	137	0.051	link	-	Gm26805	n.-423T>G	-	ENSMUST	upstream_gene_variant
1	37864876	.	T	G	base_quali	SNV	135	2	137	0.015	130	7	137	0.051	link	-	Tsga10	c.-529+14	-	ENSMUST	intron_variant
1	38836077	.	T	G	base_quali	SNV	188	3	191	0.016	171	8	179	0.045	link	-	Lonrf2	n.3883607	-	-	intragenic_variant
1	39347421	.	T	G	base_quali	SNV	16	1	17	0.059	12	5	17	0.294	link	-	Npas2	c.1840-70	-	ENSMUST	intron_variant
1	58336287	rs5812189	T	A	too_few_si	SNV	4	0	4	0	1	1	2	0.5	link	-	Aox2	c.2587-31	-	ENSMUST	intron_variant
1	85112207	rs1081203	T	C	weak_evid	SNV	59	1	60	0.017	66	8	74	0.108	link	-	A530032D	c.-2839A>	-	ENSMUST	upstream_gene_variant
1	85112207	rs1081203	T	C	weak_evid	SNV	59	1	60	0.017	66	8	74	0.108	link	-	Gm16038	n.-3112T>	-	ENSMUST	upstream_gene_variant
1	85112207	rs1081203	T	C	weak_evid	SNV	59	1	60	0.017	66	8	74	0.108	link	-	A530040E	n.897-244	-	ENSMUST	intron_variant
1	85112207	rs1081203	T	C	weak_evid	SNV	59	1	60	0.017	66	8	74	0.108	link	-	C130026I2	n.8511220	-	-	intragenic_variant
1	85245213	rs1078675	C	A	too_few_si	SNV	8	1	9	0.111	10	2	12	0.167	link	-	Gm16028	n.-1638C>	-	ENSMUST	upstream_gene_variant
1	85245213	rs1078675	C	A	too_few_si	SNV	8	1	9	0.111	10	2	12	0.167	link	-	C130026I2	c.*1724G>	-	ENSMUST	downstream_gene_variant
1	85245213	rs1078675	C	A	too_few_si	SNV	8	1	9	0.111	10	2	12	0.167	link	-	Gm2619	n.379+691	-	ENSMUST	intron_variant
1	85245213	rs1078675	C	A	too_few_si	SNV	8	1	9	0.111	10	2	12	0.167	link	-	C130026I2	n.8524521	-	-	intragenic_variant
1	85576884	rs1135171	T	A	mapping_c	SNV	79	6	85	0.071	61	11	72	0.153	link	-	Sp110	c.*408A>T	-	ENSMUST	downstream_gene_variant
1	85576884	rs1135171	T	A	mapping_c	SNV	79	6	85	0.071	61	11	72	0.153	link	-	G530012D	c.29-20T>	-	ENSMUST	intron_variant
1	85584703	rs1132598	G	T	mapping_c	SNV	33	4	37	0.108	27	11	38	0.289	link	-	Sp110	c.970+200	-	ENSMUST	intron_variant
1	85630787	rs1135212	A	G	non_homre	SNV	14	2	16	0.125	14	7	21	0.333	link	-	Sp140	c.829+223	-	ENSMUST	intron_variant
1	85638175	.	T	A	too_few_si	SNV	14	0	14	0	12	2	14	0.143	link	-	Gm17017	n.*3047A>	-	ENSMUST	downstream_gene_variant
1	85638175	.	T	A	too_few_si	SNV	14	0	14	0	12	2	14	0.143	link	-	Sp140	c.1062+31	-	ENSMUST	intron_variant
1	87681296	.	T	C	too_few_si	SNV	13	0	13	0	18	2	20	0.1	link	-	Inpp5d	c.763-193	-	ENSMUST	intron_variant
1	87821548	.	A	T	base_quali	SNV	16	2	18	0.111	9	5	14	0.357	link	-	Sag	c.503+165	-	ENSMUST	intron_variant
1	88217844	.	C	T	too_few_si	SNV	4	0	4	0	10	2	12	0.167	link	-	Ugt1a10	c.1296-28	-	ENSMUST	intron_variant
1	88217844	.	C	T	too_few_si	SNV	4	0	4	0	10	2	12	0.167	link	-	Ugt1a9	c.1290-28	-	ENSMUST	intron_variant
1	88217844	.	C	T	too_few_si	SNV	4	0	4	0	10	2	12	0.167	link	-	Ugt1a7c	c.1299-28	-	ENSMUST	intron_variant
1	88217844	.	C	T	too_few_si	SNV	4	0	4	0	10	2	12	0.167	link	-	Ugt1a6a	c.1299-28	-	ENSMUST	intron_variant
1	88217844	.	C	T	too_few_si	SNV	4	0	4	0	10	2	12	0.167	link	-	Ugt1a5	c.1293-28	-	ENSMUST	intron_variant
1	88217844	.	C	T	too_few_si	SNV	4	0	4	0	10	2	12	0.167	link	-	Ugt1a2	c.1305-28	-	ENSMUST	intron_variant
1	88217844	.	C	T	too_few_si	SNV	4	0	4	0	10	2	12	0.167	link	-	Ugt1a1	c.1311-28	-	ENSMUST	intron_variant
1	88217844	.	C	T	too_few_si	SNV	4	0	4	0	10	2	12	0.167	link	-	Ugt1a6b	c.1299-28	-	ENSMUST	intron_variant
1	88217844	.	C	T	too_few_si	SNV	4	0	4	0	10	2	12	0.167	link	-	Gm20528	n.274+437	-	ENSMUST	intron_variant
1	88217844	.	C	T	too_few_si	SNV	4	0	4	0	10	2	12	0.167	link	-	Ugt1a8	c.1296-28	-	ENSMUST	intron_variant
1	88218726	.	C	T	too_few_si	SNV	6	0	6	0	7	2	9	0.222	link	-	Ugt1a10	c.*302C>T	-	ENSMUST	3_prime_UTR_variant
1	88218726	.	C	T	too_few_si	SNV	6	0	6	0	7	2	9	0.222	link	-	Ugt1a9	c.*302C>T	-	ENSMUST	3_prime_UTR_variant
1	88218726	.	C	T	too_few_si	SNV	6	0	6	0	7	2	9	0.222	link	-	Ugt1a7c	c.*302C>T	-	ENSMUST	3_prime_UTR_variant
1	88218726	.	C	T	too_few_si	SNV	6	0	6	0	7	2	9	0.222	link	-	Ugt1a6a	c.*302C>T	-	ENSMUST	3_prime_UTR_variant
1	88218726	.	C	T	too_few_si	SNV	6	0	6	0	7	2	9	0.222	link	-	Ugt1a5	c.*302C>T	-	ENSMUST	3_prime_UTR_variant
1	88218726	.	C	T	too_few_si	SNV	6	0	6	0	7	2	9	0.222	link	-	Ugt1a2	c.*302C>T	-	ENSMUST	3_prime_UTR_variant
1	88218726	.	C	T	too_few_si	SNV	6	0	6	0	7	2	9	0.222	link	-	Ugt1a1	c.*302C>T	-	ENSMUST	3_prime_UTR_variant
1	88218726	.	C	T	too_few_si	SNV	6	0	6	0	7	2	9	0.222	link	-	Ugt1a6b	c.*302C>T	-	ENSMUST	3_prime_UTR_variant
1	88218726	.	C	T	too_few_si	SNV	6	0	6	0	7	2	9	0.222	link	-	Ugt1a8	c.*302C>T	-	ENSMUST	3_prime_UTR_variant
1	88218726	.	C	T	too_few_si	SNV	6	0	6	0	7	2	9	0.222	link	-	Gm20528	n.-172G>A	-	ENSMUST	upstream_gene_variant
1	88238261	.	C	T	weak_evid	SNV	8	0	8	0	9	4	13	0.308	link	-	Mroh2a	c.1554+30	-	ENSMUST	intron_variant
1	88243085	rs5084670	C	T	PASS	SNV	18	0	18	0	10	6	16	0.375	link	-	Mroh2a	c.2289+29	-	ENSMUST	intron_variant
1	88244432	.	G	T	too_few_si	SNV	6	0	6	0	5	2	7	0.286	link	-	Mroh2a	c.2442+34	-	ENSMUST	intron_variant
1	88264745	rs4768619	G	A	too_few_si	SNV	4	0	4	0	1	2	3	0.667	link	-	Hjurp	c.*436C>T	-	ENSMUST	3_prime_UTR_variant
1	88264745	rs4768619	G	A	too_few_si	SNV	4	0	4	0	1	2	3	0.667	link	-	Mroh2a	c.*4719G>	-	ENSMUST	downstream_gene_variant
1	88264760	rs5178294	C	T	too_few_si	SNV	4	0	4	0	1	2	3	0.667	link	-	Hjurp	c.*421G>A	-	ENSMUST	3_prime_UTR_variant
1	88264760	rs5178294	C	T	too_few_si	SNV	4	0	4	0	1	2	3	0.667	link	-	Mroh2a	c.*4734C>	-	ENSMUST	downstream_gene_variant
1	88269884	rs1134164	C	G	too_few_si	SNV	4	0	4	0	1	2	3	0.667	link	-	Hjurp	c.354+318	-	ENSMUST	intron_variant
1	1.21E+08	rs5817106	T	C	base_quali	SNV	150	4	154	0.026	178	11	189	0.058	link	-	2210011K	n.89+1345	-	ENSMUST	intron_variant
1	1.21E+08	.	C	A	non_homre	SNV	155	4	159	0.025	177	9	186	0.048	link	-	2210011K	n.89+1327	-	ENSMUST	intron_variant
1	1.21E+08	.	C	A	non_homre	SNV	154	3	157	0.019	170	9	179	0.05	link	-	2210011K	n.89+1318	-	ENSMUST	intron_variant
1	1.21E+08	.	C	A	non_homre	SNV	143	3	146	0.021	149	9	158	0.057	link	-	2210011K	n.89+1309	-	ENSMUST	intron_variant
1	1.21E+08	.	T	C	weak_evid	SNV	134	2	136	0.015	134	9	143	0.063	link	-	2210011K	n.89+1299	-	ENSMUST	intron_variant
1	1.21E+08	.	G	A	weak_evid	SNV	134	2	136	0.015	129	8	137	0.058	link	-	2210011K	n.89+1298	-	ENSMUST	intron_variant
1	1.3E+08	.	C	T	weak_evid	SNV	35	0	35	0	35	6	41	0.146	link	-	Gm29428	n.-3245C>	-	ENSMUST	upstream_gene_variant
1	1.3E+08	.	C	T	weak_evid	SNV	35	0	35	0	35	6	41	0.146	link	-	Thsd7b	c.4461+99	-	ENSMUST	intron_variant
1	1.3E+08	.	C	A	base_quali	SNV	96	1	97	0.01	62	4	66	0.061	link	-	Thsd7b	c.4655-61	-	ENSMUST	intron_variant
1	1.32E+08	.	T	G	base_quali	SNV	12	3	15	0.2	13	7	20	0.35	link	-	Nuak2	c.365-179	-	ENSMUST	intron_variant
1	1.35E+08	.	G	T	too_few_si	SNV	4	0	4	0	8	2	10	0.2	link	-	Lgr6	c.999-263	-	ENSMUST	intron_variant
1	1.56E+08	.	G	A	weak_evid	SNV	84	0	84	0	74	3	77	0.039	link	-	Axdnd1	c.1487+66	-	ENSMUST	intron_variant
1	1.67E+08	.	A	C	base_quali	SNV	144	10	154	0.065	130	18	148	0.122	link	-	Fam78b	c.-3A>C	-	ENSMUST	5_prime_UTR_variant
1	1.67E+08	.	A	C	base_quali	SNV	144	10	154	0.065	130	18	148	0.122	link	-	Gm16701	n.-1835T>	-	ENSMUST	upstream_gene_variant
1	1.67E+08	.	A	C	base_quali	SNV	144	10	154	0.065	130	18	148	0.122	link	-	Gm16701	n.-722T>G	-	ENSMUST	upstream_gene_variant
1	1.67E+08	.	A	T	base_quali	SNV	6	1	7	0.143	0	4	4	1	link	-	Gm37982	n.-4681A>	-	ENSMUST	upstream_gene_variant
1	1.67E+08	.	A	T	base_quali	SNV	6	1	7	0.143	0	4	4	1	link	-	Uck2	c.100-128	-	ENSMUST	intron_variant
1	1.71E+08	.	G	A	PASS	SNV	199	0	199	0	181	4	185	0.022	link	-	Nos1ap	c.177+28C	-	ENSMUST	intron_variant
10	5358184	.	C	A	too_few_si	SNV	17	0	17	0	17	2	19	0.105	link	-	Gm23573	n.*905C>A	-	ENSMUST	downstream_gene_variant
10	5358184	.	C	A	too_few_si	SNV	17	0	17	0	17	2	19	0.105	link	-	Syne1	c.2220+15	-	ENSMUST	intron_variant
10	14423119	.	C	G	weak_evid	SNV	40	0	40	0	40	6	46	0.13	link	-	Adgrg6	c.2933-35	-	ENSMUST	intron_variant
10	33444263	.	C	A	base_quali	SNV	21	3	24	0.125	11	3	14	0.214	link	-	Trdn	c.1651+18	-	ENSMUST	intron_variant
10	40349569	.	G	A	weak_evid	SNV	103	0	103	0	100	3	103	0.029	link	-	Cdk19	c.-25G>A	-	ENSMUST	5_prime_UTR_variant
10	40349569	.	G	A	weak_evid	SNV	103	0	103	0	100	3	103	0.029	link	-	Cdk19os	n.63C>T	-	ENSMUST	non_coding_transcript_exon_variant
10	58224401	.	C	A	mapping_c	SNV	540	7	547	0.013	525	15	540	0.028	link	-	Gm10807	n.*3456G>	-	ENSMUST	downstream_gene_variant
10	76285841	.	A	T	base_quali	SNV	12	2	14	0.143	6	7	13	0.538	link	-	Dip2a	c.2368-188	-	ENSMUST	intron_variant
10	76712996	.	A	C	base_quali	SNV	126	0	126	0	89	18	107	0.168	link	-	Col6a1	c.1811-125	-	ENSMUST	intron_variant
10	77989079	.	T	G	weak_evid	SNV	24	2	26	0.077	21	9	30	0.3	link	-	1810043G	c.*4532T>	-	ENSMUST	downstream_gene_variant
10	77989079	.	T	G	weak_evid	SNV	24	2	26	0.077	21	9	30	0.3	link	-	Pfkl	c.1990-115	-	ENSMUST	intron_variant
10	79716801	.	A	C	base_quali	SNV	184	1	185	0.005	198	7	205	0.034	link	-	Bsg	c.*5244A>	-	ENSMUST	downstream_gene_variant
10	80006953	.	A	C	base_quali	SNV	142	5	147	0.034	116	11	127	0.087	link	-	Abca7	c.3514+31	-	ENSMUST	intron_variant
10	96913617	.	G	C	too_few_si	SNV	8	0	8	0	4	2	6	0.333	link	-	-	n.9691361	-	-	intergenic_region
10	1.07E+08	.	T	G	base_quali	SNV	107	1	108	0.009	92	15	107	0.14	link	-	Ppfia2	c.2643-108	-	ENSMUST	intron_variant

11	6028840	rs2547416	A	C	base_quali	SNV	33	4	37	0.108	20	20	40	0.5	link	-	Camk2b	c.160+27T	-	ENSMUST	intron_variant
11	6674634	.	A	C	base_quali	SNV	30	0	30	0	27	7	34	0.206	link	-	Ramp3	c.56-129A	-	ENSMUST	intron_variant
11	18884528	.	A	C	base_quali	SNV	96	4	100	0.04	74	6	80	0.075	link	-	Gm37818	n.*95T>G	-	ENSMUST	downstream_gene_variant
11	18884528	.	A	C	base_quali	SNV	96	4	100	0.04	74	6	80	0.075	link	-	2900018N	n.*3733T>	-	ENSMUST	downstream_gene_variant
11	18884528	.	A	C	base_quali	SNV	96	4	100	0.04	74	6	80	0.075	link	-	Meis1	c.1025-52	-	ENSMUST	intron_variant
11	61309066	.	G	T	base_quali	SNV	24	4	28	0.143	23	8	31	0.258	link	-	Slc47a2	c.1134-13	-	ENSMUST	intron_variant
11	69122081	.	T	G	base_quali	SNV	69	2	71	0.028	81	5	86	0.058	link	-	Aloxe3	c.-4322T>	-	ENSMUST	upstream_gene_variant
11	69122081	.	T	G	base_quali	SNV	69	2	71	0.028	81	5	86	0.058	link	-	9130213A	c.-35+459	-	ENSMUST	intron_variant
11	69122081	.	T	G	base_quali	SNV	69	2	71	0.028	81	5	86	0.058	link	-	Hes7	c.139-62T	-	ENSMUST	intron_variant
11	72759750	.	T	G	base_quali	SNV	29	0	29	0	12	9	21	0.429	link	-	Ankfy1	c.2924-16	-	ENSMUST	intron_variant
11	74925784	.	T	G	alt_allele_i	SNV	41	10	51	0.196	32	17	49	0.347	link	-	Srr	c.-396A>C	-	ENSMUST	5_prime_UTR_variant
11	74925784	.	T	G	alt_allele_i	SNV	41	10	51	0.196	32	17	49	0.347	link	-	Smg6	c.-132T>G	-	ENSMUST	upstream_gene_variant
11	83942015	.	T	G	weak_evid	SNV	9	0	9	0	4	3	7	0.429	link	-	Ddx52	c.-163T>G	-	ENSMUST	upstream_gene_variant
11	83942015	.	T	G	weak_evid	SNV	9	0	9	0	4	3	7	0.429	link	-	-	n.8394201	-	-	intergenic_region
11	84445884	.	G	T	too_few_si	SNV	9	2	11	0.182	18	2	20	0.1	link	-	Aatf	c.1365-17	-	ENSMUST	intron_variant
11	99346470	.	A	C	base_quali	SNV	166	1	167	0.006	150	16	166	0.096	link	-	Krt27	c.1210+15	-	ENSMUST	intron_variant
11	1.01E+08	.	T	G	base_quali	SNV	237	3	240	0.013	295	7	302	0.023	link	-	Tubg2	c.*2793T>	-	ENSMUST	downstream_gene_variant
11	1.03E+08	.	G	A	PASS	SNV	23	0	23	0	19	6	25	0.24	link	-	Gm20511	n.-3225C>	-	ENSMUST	upstream_gene_variant
11	1.03E+08	.	G	A	PASS	SNV	23	0	23	0	19	6	25	0.24	link	-	1700023F	c.*2840C>	-	ENSMUST	downstream_gene_variant
11	1.03E+08	.	G	A	PASS	SNV	23	0	23	0	19	6	25	0.24	link	-	Fmnl1	c.2503-14	-	ENSMUST	intron_variant
12	4774349	.	A	C	base_quali	SNV	53	6	59	0.102	43	7	50	0.14	link	-	Pfn4	c.118-43A	-	ENSMUST	intron_variant
12	31652544	.	G	T	base_quali	SNV	29	1	30	0.033	19	5	24	0.208	link	-	Cog5	c.-2346G>	-	ENSMUST	upstream_gene_variant
12	31652544	.	G	T	base_quali	SNV	29	1	30	0.033	19	5	24	0.208	link	-	Dus4l	c.-35-103	-	ENSMUST	intron_variant
12	51393993	.	A	T	non_homre	SNV	64	2	66	0.03	51	5	56	0.089	link	-	Scfd1	c.604+83A	-	ENSMUST	intron_variant
12	54690509	.	G	A	too_few_si	SNV	20	0	20	0	17	2	19	0.105	link	-	Eapp	c.352+149	-	ENSMUST	intron_variant
12	76100784	.	C	T	too_few_si	SNV	11	0	11	0	7	2	9	0.222	link	-	Syne2	c.19301-2	-	ENSMUST	intron_variant
12	85782807	.	C	A	too_few_si	SNV	10	0	10	0	8	2	10	0.2	link	-	Mfsd7c	c.739-150	-	ENSMUST	intron_variant
12	1.05E+08	.	A	C	base_quali	SNV	67	8	75	0.107	49	6	55	0.109	link	-	Clmn	c.144+117	-	ENSMUST	intron_variant
12	1.05E+08	.	T	G	base_quali	SNV	83	1	84	0.012	72	14	86	0.163	link	-	Syne3	c.1446+54	-	ENSMUST	intron_variant
13	11700210	.	G	T	base_quali	SNV	86	4	90	0.044	79	7	86	0.081	link	-	Ryr2	c.8433+38	-	ENSMUST	intron_variant
13	14248555	.	T	G	base_quali	SNV	46	0	46	0	21	12	33	0.364	link	-	Hecw1	c.4014-11	-	ENSMUST	intron_variant
13	49191015	.	T	G	base_quali	SNV	50	0	50	0	46	9	55	0.164	link	-	Ninj1	c.76-70T>	-	ENSMUST	intron_variant
13	68447286	.	A	G	too_few_si	SNV	13	0	13	0	10	2	12	0.167	link	-	-	n.6844728	-	-	intergenic_region
13	68447828	rs5847705	A	G	mapping_c	SNV	158	3	161	0.019	173	5	178	0.028	link	-	-	n.6844782	-	-	intergenic_region
13	90899335	.	C	A	base_quali	SNV	28	1	29	0.034	18	4	22	0.182	link	-	Atp6ap1l	c.198+159	-	ENSMUST	intron_variant
13	1.15E+08	.	T	G	weak_evid	SNV	104	4	108	0.037	107	4	111	0.036	link	-	Mocs2	c.-47-11T	-	ENSMUST	intron_variant
14	4504335	.	A	C	base_quali	SNV	38	0	38	0	20	9	29	0.31	link	-	Gm3173	n.4504335	-	-	intragenic_variant
14	7450768	.	A	T	weak_evid	SNV	94	0	94	0	75	3	78	0.038	link	-	Gm3755	c.55+93T>	-	ENSMUST	intron_variant
14	7450768	.	A	T	weak_evid	SNV	94	0	94	0	75	3	78	0.038	link	-	4933406F	n.7450768	-	-	intragenic_variant
14	14969344	.	C	A	base_quali	SNV	21	3	24	0.125	20	5	25	0.2	link	-	Nek10	c.2832-13	-	ENSMUST	intron_variant
14	18893548	.	T	G	base_quali	SNV	28	1	29	0.034	25	5	30	0.167	link	-	Ube2e2	n.1889354	-	-	intragenic_variant
14	19417584	.	A	T	too_few_si	SNV	35	0	35	0	23	2	25	0.08	link	-	Gm21738	c.161-218	-	ENSMUST	intron_variant
14	34740960	.	C	A	base_quali	SNV	52	6	58	0.103	45	6	51	0.118	link	-	Wapl	c.3353-97	-	ENSMUST	intron_variant
14	49172549	.	A	C	base_quali	SNV	106	6	112	0.054	86	10	96	0.104	link	-	Naa30	c.-68A>C	-	ENSMUST	upstream_gene_variant
14	49172549	.	A	C	base_quali	SNV	106	6	112	0.054	86	10	96	0.104	link	-	Naa30	n.4917254	-	-	intragenic_variant
14	50777085	.	A	T	too_few_si	SNV	15	0	15	0	13	2	15	0.133	link	-	Ttc5	c.547+177	-	ENSMUST	intron_variant
14	51920426	.	G	T	base_quali	SNV	82	3	85	0.035	66	9	75	0.12	link	-	Rnase13	c.*1793C>	-	ENSMUST	downstream_gene_variant
14	52792698	.	C	A	base_quali	SNV	302	3	305	0.01	305	21	326	0.064	link	-	Trav6d-5	c.-2467C>	-	ENSMUST	upstream_gene_variant
14	57857586	.	G	C	weak_evid	SNV	161	0	161	0	153	3	156	0.019	link	-	Zdhhc20	c.473+42C	-	ENSMUST	intron_variant
14	62361190	.	C	G	base_quali	SNV	23	6	29	0.207	17	4	21	0.19	link	-	Rnaseh2b	c.502-139	-	ENSMUST	intron_variant
14	65731253	.	A	C	base_quali	SNV	37	2	39	0.051	38	7	45	0.156	link	-	Scara5	c.916+58A	-	ENSMUST	intron_variant
14	1.03E+08	.	G	T	base_quali	SNV	70	5	75	0.067	56	10	66	0.152	link	-	Mycbp2	c.1571-10	-	ENSMUST	intron_variant
15	54839260	rs2365639	C	A	base_quali	SNV	11	1	12	0.083	8	7	15	0.467	link	-	Enpp2	c.*106G>T	-	ENSMUST	3_prime_UTR_variant
15	76079549	.	T	G	base_quali	SNV	73	3	76	0.039	58	10	68	0.147	link	-	Puf60	c.24+1301	-	ENSMUST	intron_variant
15	81786182	.	C	A	too_few_si	SNV	6	0	6	0	10	2	12	0.167	link	-	Zc3h7b	c.2037+21	-	ENSMUST	intron_variant
15	88821231	.	A	C	base_quali	SNV	58	7	65	0.108	62	18	80	0.225	link	-	Alg12	c.-5000T>	-	ENSMUST	upstream_gene_variant
15	89069511	.	C	T	PASS	SNV	134	0	134	0	149	4	153	0.026	link	-	1810021B	n.*1687G>	-	ENSMUST	downstream_gene_variant
15	89069511	.	C	T	PASS	SNV	134	0	134	0	149	4	153	0.026	link	-	Panx2	c.1691-23	-	ENSMUST	intron_variant
15	91049778	.	C	T	weak_evid	SNV	139	0	139	0	138	3	141	0.021	link	-	Kif21a	c.-76G>A	-	ENSMUST	5_prime_UTR_variant
15	1.01E+08	rs1132067	G	A	too_few_si	SNV	17	0	17	0	16	2	18	0.111	link	-	Krt7	c.*4945G>	-	ENSMUST	downstream_gene_variant
15	1.01E+08	rs1132067	G	A	too_few_si	SNV	17	0	17	0	16	2	18	0.111	link	-	Krt87	c.1263-23	-	ENSMUST	intron_variant
15	1.01E+08	rs2630595	T	C	too_few_si	SNV	15	0	15	0	13	2	15	0.133	link	-	Krt7	c.*4953T>	-	ENSMUST	downstream_gene_variant
15	1.01E+08	rs2630595	T	C	too_few_si	SNV	15	0	15	0	13	2	15	0.133	link	-	Krt87	c.1263-24	-	ENSMUST	intron_variant
15	1.01E+08	rs1133479	T	C	too_few_si	SNV	13	0	13	0	12	2	14	0.143	link	-	Krt7	c.*4959T>	-	ENSMUST	downstream_gene_variant
15	1.01E+08	rs1133479	T	C	too_few_si	SNV	13	0	13	0	12	2	14	0.143	link	-	Krt87	c.1263-24	-	ENSMUST	intron_variant
15	1.01E+08	rs2263609	C	T	too_few_si	SNV	9	0	9	0	11	2	13	0.154	link	-	Krt7	c.*4964C>	-	ENSMUST	downstream_gene_variant
15	1.01E+08	rs2263609	C	T	too_few_si	SNV	9	0	9	0	11	2	13	0.154	link	-	Krt87	c.1263-25	-	ENSMUST	intron_variant
16	13810458	.	T	G	base_quali	SNV	111	0	111	0	86	15	101	0.149	link	-	Rrn3	c.1548-46	-	ENSMUST	intron_variant
16	15770213	.	C	A	too_few_si	SNV	7	0	7	0	4	2	6	0.333	link	-	Prkdc	c.7749+21	-	ENSMUST	intron_variant
16	17531017	.	G	A	too_few_si	SNV	14	0	14	0	15	2	17	0.118	link	-	Lztr1	c.*5224G>	-	ENSMUST	downstream_gene_variant
16	37855695	.	A	C	PASS	SNV	23	0	23	0	18	10	28	0.357	link	-	n-R5s34	n.*798A>C	-	ENSMUST	downstream_gene_variant
16	37855695	.	A	C	PASS	SNV	23	0	23	0	18	10	28	0.357	link	-	Gm36028	c.583+126	-	ENSMUST	intron_variant
16	37855696	.	A	C	PASS	SNV	22	0	22	0	15	13	28	0.464	link	-	n-R5s34	n.*799A>C	-	ENSMUST	downstream_gene_variant
16	37855696	.	A	C	PASS	SNV	22	0	22	0	15	13	28	0.464	link	-	Gm36028	c.583+125	-	ENSMUST	intron_variant
16	37855697	.	A	C	base_quali	SNV	22	0	22	0	24	6	30	0.2	link	-	n-R5s34	n.*800A>C	-	ENSMUST	downstream_gene_variant
16	37855697	.	A	C	base_quali	SNV	22	0	22	0	24	6	30	0.2	link	-	Gm36028	c.583+124	-	ENSMUST	intron_variant
16	59542181	.	A	C	base_quali	SNV	80	0	80	0	73	13	86	0.151	link	-	Crybg3	c.1807-86	-	ENSMUST	intron_variant
16	78985823	.	T	A	base_quali	SNV	37	4	41	0.098	52	5	57	0.088	link	-	Tmprss15	c.2300+52	-	ENSMUST	intron_variant
16	94289946	.	G	A	too_few_si	SNV	24	0	24	0	19	2	21	0.095	link	-	Hlcs	c.-21359C	-	ENSMUST	upstream_gene_variant
16	94289946	.	G	A	too_few_si	SNV	24	0	24	0	19	2	21	0.095	link	-	Hlcs	n.9428994	-	-	intragenic_variant
17	7931257	.	T	G	base_quali	SNV	21	0	21	0	22	6	28	0.214	link	-	Tagap	c.588-115	-	ENSMUST	intron_variant
17	7931257	.	T	G	base_quali	SNV	21	0	21	0	22	6	28	0.214	link	-	E430024P	n.2121A>C	-	ENSMUST	non_coding_transcript_exon_variant
17	23297171	rs1132418	T	C	alt_allele_i	SNV	10	2	12	0.167	17	4	21	0.19	link	-	Vmn2r114	c.1528-18	-	ENSMUST	intron_variant
17	23297174	rs1134947	T	C	alt_allele_i	SNV	10	2	12	0.167	14	4	18	0.222	link	-	Vmn2r114	c.1528-18	-	ENSMUST	intron_variant
17	23297178	rs1086402	A	C	alt_allele_i	SNV	10	2	12	0.167	12	4	16	0.25	link	-	Vmn2r114	c.1528-19	-	ENSMUST	intron_variant
17	24418723	.	T	G	base_quali	SNV	24	0	24	0	33	9	42	0.214	link	-	D330041H	n.-4296A>	-	ENSMUST	upstream_gene_variant
17	24418723	.	T	G	base_quali	SNV	24	0	24	0	33	9	42	0.214	link	-	Rnps1	c.227+111	-	ENSMUST	intron_variant
17	25991857	rs4767552	A	G	PASS	SNV	89	0	89	0	90	4	94	0.043	link	-	1700022N	n.*3388A>	-	ENSMUST	downstream_gene_variant
17	25991857	rs4767552	A	G	PASS	SNV	89	0	89	0	90	4	94	0.043	link	-	Rab11fip3	c.2731-57	-	ENSMUST	intron_variant
17	26946425	.	A	C	weak_evid	SNV	9	1	10	0.1	8	3	11	0.273	link	-	Mir3083	n.*1631T>	-	ENSMUST	downstream_gene_variant
17	26946425	.	A	C	weak_evid	SNV	9	1	10	0.1	8	3	11	0.273	link	-	Syngap1	c.190-208	-	ENSMUST	intron_variant
17	27887763	.	T	G	non_homre	SNV	40	3	43	0.07	46	4	50	0.08	link	-	Uhrf1bp1	c.3191+71	-	ENSMUST	intron_variant
17	28350682	.	A	C	alt_allele_i	SNV	62	9	71	0.127	65	23	88	0.261	link	-	Tead3	c.-87T>G	-	ENSMUST	upstream_gene_variant
17	28350682	.	A	C	alt_allele_i	SNV	62	9	71	0.127	65	23	88	0.261	link	-	Tulp1	c.*1187T>	-	ENSMUST	downstream_gene_variant
17	28350682	.	A	C	alt_allele_i	SNV	62	9	71	0.127	65	23	88	0.261	link	-	Tead3	n.2835068	-	-	intragenic_variant
17	37050826	.	A	C	base_quali	SNV	127	4	131	0.031	142	9	151	0.06	link	-	Gabbr1	c.494-173	-	ENSMUST	intron_variant
17	49452895	.	T	G	base_quali	SNV	158	6	164	0.037	141	9	150	0.06	link	-	Daam2	c.*5631A>	-	ENSMUST	downstream_gene_variant
17	49452895	.	T	G	base_quali	SNV	158	6	164	0.037	141	9	150	0.06	link	-	Mocs1	c.1150+53	-	ENSMUST	intron_variant
17	50509561	.	C	G	weak_evid	SNV	166	1	167	0.006	154	4	158	0.025	link	-	Plcl2	c.-47C>G	-	ENSMUST	5_prime_UTR_variant
17	64292763	.	A	C	alt_allele_i	SNV	36	5	41	0.122	34	8	42	0.19	link	-	Pja2	c.1649+76	-	ENSMUST	intron_variant
17	85090593	.	A	C	base_quali	SNV	38	5	43	0.116	44	6	50	0.12	link	-	Prepl	c.-2041T>	-	ENSMUST	upstream_gene_variant
17	85090593	.	A	C	base_quali	SNV	38	5	43	0.116	44	6	50	0.12	link	-	Camkmt	c.-133A>C	-	ENSMUST	upstream_gene_variant
17	85090593	.	A	C	base_quali	SNV	38	5	43	0.116	44	6	50	0.12	link	-	-	n.8509059	-	-	intergenic_region
17	88530237	.	A	C	weak_evid	SNV	126	3	129	0.023	92	5	97	0.052	link	-	Ppp1r21	c.-25A>C	-	ENSMUST	5_prime_UTR_variant

17	88530237	.	A	C	weak_evid	SNV	126	3	129	0.023	92	5	97	0.052	link	-	Gm38109	n.-2790A>	-	ENSMUST	upstream_gene_variant
18	42732017	.	A	C	base_quali	SNV	34	0	34	0	22	7	29	0.241	link	-	Ppp2r2b	c.344-118	-	ENSMUST	intron_variant
18	73798120	.	C	G	too_few_s	SNV	12	0	12	0	11	2	13	0.154	link	-	Me2	c.243-142	-	ENSMUST	intron_variant
18	75435090	.	T	C	PASS	SNV	47	0	47	0	34	11	45	0.244	link	-	Ctif	c.*104A>G	-	ENSMUST	3_prime_UTR_variant
19	3649777	.	C	T	too_few_s	SNV	14	0	14	0	12	2	14	0.143	link	-	Lrp5	c.684-177	-	ENSMUST	intron_variant
19	4439113	.	T	G	base_quali	SNV	57	0	57	0	38	15	53	0.283	link	-	Rhod	c.132+107	-	ENSMUST	intron_variant
19	4439113	.	T	G	base_quali	SNV	57	0	57	0	38	15	53	0.283	link	-	A930001C	n.4439113	-	-	intragenic_variant
19	12795034	.	C	T	PASS	SNV	301	0	301	0	322	14	336	0.042	link	-	Lpxn	c.-3633C>	-	ENSMUST	upstream_gene_variant
19	25131905	.	T	A	base_quali	SNV	16	1	17	0.059	11	6	17	0.353	link	-	Dock8	c.2609-15	-	ENSMUST	intron_variant
19	38123917	.	C	A	base_quali	SNV	48	2	50	0.04	38	17	55	0.309	link	-	Rbp4	c.487+112	-	ENSMUST	intron_variant
19	44948828	.	A	C	too_few_s	SNV	18	0	18	0	20	2	22	0.091	link	-	Gm25482	n.*3700A>	-	ENSMUST	downstream_gene_variant
19	44948828	.	A	C	too_few_s	SNV	18	0	18	0	20	2	22	0.091	link	-	Fam178a	c.2136-14	-	ENSMUST	intron_variant
19	56722175	.	G	A	PASS	SNV	68	0	68	0	67	6	73	0.082	link	-	Adrb1	c.-197G>A	-	ENSMUST	upstream_gene_variant
19	56722175	.	G	A	PASS	SNV	68	0	68	0	67	6	73	0.082	link	-	-	n.5672217	-	-	intergenic_region
2	6884972	.	G	T	base_quali	SNV	161	4	165	0.024	150	9	159	0.057	link	-	Celf2	c.-14C>A	-	ENSMUST	5_prime_UTR_variant
2	6884972	.	G	T	base_quali	SNV	161	4	165	0.024	150	9	159	0.057	link	-	Gm13389	n.60+643	-	ENSMUST	intron_variant
2	11248374	rs2347824	A	C	weak_evid	SNV	137	1	138	0.007	109	3	112	0.027	link	-	Prkcq	c.790+44A	-	ENSMUST	intron_variant
2	26351859	.	T	G	base_quali	SNV	235	15	250	0.06	185	18	203	0.089	link	-	Gm13562	n.-786T>G	-	ENSMUST	upstream_gene_variant
2	26351859	.	T	G	base_quali	SNV	235	15	250	0.06	185	18	203	0.089	link	-	Gpsm1	c.*4846T>	-	ENSMUST	downstream_gene_variant
2	26351859	.	T	G	base_quali	SNV	235	15	250	0.06	185	18	203	0.089	link	-	Card9	c.*453A>C	-	ENSMUST	downstream_gene_variant
2	36104962	.	G	C	base_quali	SNV	22	5	27	0.185	10	8	18	0.444	link	-	Lhx6	c.84+162C	-	ENSMUST	intron_variant
2	69732825	rs5870122	A	G	weak_evid	SNV	194	1	195	0.005	185	4	189	0.021	link	-	Gm13622	n.*4532T>	-	ENSMUST	downstream_gene_variant
2	91559235	.	T	A	weak_evid	SNV	56	0	56	0	80	4	84	0.048	link	-	Ckap5	c.978+73T	-	ENSMUST	intron_variant
2	98663693	.	T	C	too_few_s	SNV	10	0	10	0	6	2	8	0.25	link	-	Gm10800	c.*2854A>	-	ENSMUST	downstream_gene_variant
2	98663693	.	T	C	too_few_s	SNV	10	0	10	0	6	2	8	0.25	link	-	Gm10801	c.292-113	-	ENSMUST	intron_variant
2	1.12E+08	.	C	A	base_quali	SNV	54	5	59	0.085	36	11	47	0.234	link	-	Olfr1312	c.*65G>T	-	ENSMUST	downstream_gene_variant
2	1.12E+08	.	C	A	base_quali	SNV	54	5	59	0.085	36	11	47	0.234	link	-	-	n.1120420	-	-	intergenic_region
2	1.16E+08	.	A	C	base_quali	SNV	45	4	49	0.082	28	8	36	0.222	link	-	Meis2	c.-1294T>	-	ENSMUST	upstream_gene_variant
2	1.16E+08	.	A	C	base_quali	SNV	45	4	49	0.082	28	8	36	0.222	link	-	G630016G	n.-1861A>	-	ENSMUST	upstream_gene_variant
2	1.16E+08	.	A	C	base_quali	SNV	45	4	49	0.082	28	8	36	0.222	link	-	2700033N	n.*111T>G	-	ENSMUST	downstream_gene_variant
2	1.16E+08	.	A	C	base_quali	SNV	45	4	49	0.082	28	8	36	0.222	link	-	-	n.1160661	-	-	intergenic_region
2	1.22E+08	.	C	A	too_few_s	SNV	16	0	16	0	17	2	19	0.105	link	-	Slc28a2	c.1866-16	-	ENSMUST	intron_variant
2	1.42E+08	.	G	T	weak_evid	SNV	9	0	9	0	7	3	10	0.3	link	-	Macrod2	c.1114+23	-	ENSMUST	intron_variant
2	1.53E+08	.	A	C	base_quali	SNV	14	0	14	0	19	4	23	0.174	link	-	Xkr7	c.585-978	-	ENSMUST	intron_variant
2	1.65E+08	.	T	A	base_quali	SNV	75	9	84	0.107	87	10	97	0.103	link	-	Pcif1	c.*3405T>	-	ENSMUST	downstream_gene_variant
2	1.77E+08	.	C	G	too_few_s	SNV	22	0	22	0	17	2	19	0.105	link	-	Gm14295	c.-3240C>	-	ENSMUST	upstream_gene_variant
2	1.77E+08	.	C	G	too_few_s	SNV	22	0	22	0	17	2	19	0.105	link	-	Gm14295	n.1767989	-	-	intragenic_variant
3	68698228	.	G	A	too_few_s	SNV	14	0	14	0	18	2	20	0.1	link	-	Il12a	c.*178G>A	-	ENSMUST	3_prime_UTR_variant
3	85872273	.	C	A	base_quali	SNV	42	2	44	0.045	36	9	45	0.2	link	-	Gm37240	c.-455+14	-	ENSMUST	intron_variant
3	85872273	.	C	A	base_quali	SNV	42	2	44	0.045	36	9	45	0.2	link	-	Glt28d2	c.-26-83G:	-	ENSMUST	intron_variant
3	86138177	.	A	C	base_quali	SNV	57	8	65	0.123	49	10	59	0.169	link	-	Gm37933	n.-4580A>	-	ENSMUST	upstream_gene_variant
3	86138177	.	A	C	base_quali	SNV	57	8	65	0.123	49	10	59	0.169	link	-	Snord73a	n.*614T>G	-	ENSMUST	downstream_gene_variant
3	86138177	.	A	C	base_quali	SNV	57	8	65	0.123	49	10	59	0.169	link	-	Rnu73b	n.*2441T>	-	ENSMUST	downstream_gene_variant
3	86138177	.	A	C	base_quali	SNV	57	8	65	0.123	49	10	59	0.169	link	-	Rps3a1	c.674-67T:	-	ENSMUST	intron_variant
3	87922936	.	A	C	base_quali	SNV	138	0	138	0	123	12	135	0.089	link	-	Rrnad1	c.*855T>G	-	ENSMUST	3_prime_UTR_variant
3	87922937	.	A	C	base_quali	SNV	139	1	140	0.007	114	19	133	0.143	link	-	Rrnad1	c.*854T>G	-	ENSMUST	3_prime_UTR_variant
3	87993762	.	T	G	too_few_s	SNV	6	0	6	0	4	2	6	0.333	link	-	Bcan	c.1283-12	-	ENSMUST	intron_variant
3	90118316	.	C	A	weak_evid	SNV	6	0	6	0	6	3	9	0.333	link	-	Nup210l	c.461-217	-	ENSMUST	intron_variant
3	96262956	.	T	G	base_quali	SNV	112	8	120	0.067	109	9	118	0.076	link	-	Hist2h4	c.*37A>C	-	ENSMUST	3_prime_UTR_variant
3	96262956	.	T	G	base_quali	SNV	112	8	120	0.067	109	9	118	0.076	link	-	Gm38227	n.-829T>G	-	ENSMUST	upstream_gene_variant
3	96262956	.	T	G	base_quali	SNV	112	8	120	0.067	109	9	118	0.076	link	-	Gm20628	n.*4119A>	-	ENSMUST	downstream_gene_variant
3	1.04E+08	.	C	A	base_quali	SNV	43	1	44	0.023	39	6	45	0.133	link	-	Gm43696	n.*3233G>	-	ENSMUST	downstream_gene_variant
3	1.04E+08	.	C	A	base_quali	SNV	43	1	44	0.023	39	6	45	0.133	link	-	Lrig2	c.1475-64	-	ENSMUST	intron_variant
3	1.06E+08	.	A	C	base_quali	SNV	27	1	28	0.036	14	2	16	0.125	link	-	I830077J0	c.*6291T>	-	ENSMUST	downstream_gene_variant
3	1.06E+08	.	A	C	base_quali	SNV	27	1	28	0.036	14	2	16	0.125	link	-	Tmigd3	c.550+74A	-	ENSMUST	intron_variant
3	1.27E+08	.	T	A	PASS	SNV	165	0	165	0	115	43	158	0.272	link	-	Ank2	c.10831+1	-	ENSMUST	intron_variant
3	1.49E+08	.	G	T	alt_allele_i	SNV	9	2	11	0.182	11	3	14	0.214	link	-	Adgrl2	c.1609-16	-	ENSMUST	intron_variant
3	1.54E+08	.	G	T	weak_evid	SNV	285	0	285	0	268	4	272	0.015	link	-	Slc44a5	c.2029+21	-	ENSMUST	intron_variant
4	9598350	.	C	A	weak_evid	SNV	94	1	95	0.011	81	5	86	0.058	link	-	Asph	c.773-49G	-	ENSMUST	intron_variant
4	41508479	.	C	A	base_quali	SNV	125	2	127	0.016	130	6	136	0.044	link	-	1110017D	c.393+38G	-	ENSMUST	intron_variant
4	47353473	.	T	G	weak_evid	SNV	107	4	111	0.036	99	10	109	0.092	link	-	Tgfbr1	c.85+77T>	-	ENSMUST	intron_variant
4	62965590	.	C	T	weak_evid	SNV	141	1	142	0.007	119	5	124	0.04	link	-	Zfp618	c.-84C>T	-	ENSMUST	5_prime_UTR_variant
4	70337576	.	G	A	weak_evid	SNV	107	0	107	0	98	3	101	0.03	link	-	Cdk5rap2	c.1087-17	-	ENSMUST	intron_variant
4	99035021	.	T	G	base_quali	SNV	74	0	74	0	49	14	63	0.222	link	-	Angptl3	c.931+97T	-	ENSMUST	intron_variant
4	99035021	.	T	G	base_quali	SNV	74	0	74	0	49	14	63	0.222	link	-	Dock7	c.1683-115	-	ENSMUST	intron_variant
4	1.03E+08	.	G	T	alt_allele_i	SNV	26	8	34	0.235	16	12	28	0.429	link	-	4921539E1	c.335-139	-	ENSMUST	intron_variant
4	1.16E+08	.	G	T	read_posit	SNV	6	0	6	0	6	2	8	0.25	link	-	Mknk1	c.198+496	-	ENSMUST	intron_variant
4	1.26E+08	.	T	G	base_quali	SNV	99	3	102	0.029	85	15	100	0.15	link	-	Sh3d21	c.-4208A>	-	ENSMUST	upstream_gene_variant
4	1.26E+08	.	T	G	base_quali	SNV	99	3	102	0.029	85	15	100	0.15	link	-	Thrap3	c.2490+34	-	ENSMUST	intron_variant
4	1.29E+08	.	G	A	too_few_s	SNV	10	0	10	0	10	2	12	0.167	link	-	Zbtb8a	c.972+174	-	ENSMUST	intron_variant
4	1.3E+08	.	A	G	too_few_s	SNV	18	0	18	0	12	2	14	0.143	link	-	Hcrtr1	c.-39-99T:	-	ENSMUST	intron_variant
4	1.39E+08	.	A	C	base_quali	SNV	34	0	34	0	39	1	40	0.025	link	-	Pla2g2d	c.38-62A>	-	ENSMUST	intron_variant
4	1.52E+08	.	A	C	base_quali	SNV	31	4	35	0.114	20	8	28	0.286	link	-	Kcnab2	c.415+153	-	ENSMUST	intron_variant
5	3980766	.	G	A	too_few_s	SNV	17	0	17	0	6	2	8	0.25	link	-	Akap9	c.3981-352	-	ENSMUST	intron_variant
5	14933658	.	A	G	mapping_c	SNV	28	2	30	0.067	22	6	28	0.214	link	-	Speer4e	c.*375T>C	-	ENSMUST	3_prime_UTR_variant
5	14974902	.	G	C	no_reliable	SNV	217	8	225	0.036	189	7	196	0.036	link	-	Gm10354	c.628-262	-	ENSMUST	intron_variant
5	15033416	.	G	T	weak_evid	SNV	10	0	10	0	8	4	12	0.333	link	-	Gm17019	c.-478C>A	-	ENSMUST	upstream_gene_variant
5	15033416	.	G	T	weak_evid	SNV	10	0	10	0	8	4	12	0.333	link	-	-	n.1503341	-	-	intergenic_region
5	15474404	rs1135081	C	A	weak_evid	SNV	5	0	5	0	9	5	14	0.357	link	-	Gm21149	c.300-476	-	ENSMUST	intron_variant
5	15474404	rs1135081	C	A	weak_evid	SNV	5	0	5	0	9	5	14	0.357	link	-	Gm43391	n.151-874	-	ENSMUST	intron_variant
5	15529253	.	A	C	base_quali	SNV	1469	3	1472	0.002	1206	159	1365	0.116	link	-	Gm21190	c.-35T>G	-	ENSMUST	upstream_gene_variant
5	15529253	.	A	C	base_quali	SNV	1469	3	1472	0.002	1206	159	1365	0.116	link	-	Gm21847	n.222+332	-	ENSMUST	intron_variant
5	24348574	.	T	G	base_quali	SNV	31	1	32	0.031	25	3	28	0.107	link	-	Kcnh2	c.77-33A>	-	ENSMUST	intron_variant
5	25941885	.	A	T	mapping_c	SNV	36	3	39	0.077	36	10	46	0.217	link	-	Gm21663	c.139+283	-	ENSMUST	intron_variant
5	25941891	rs1135030	T	G	mapping_c	SNV	42	3	45	0.067	37	10	47	0.213	link	-	Gm21663	c.139+277	-	ENSMUST	intron_variant
5	25941930	rs1134412	C	G	mapping_c	SNV	63	2	65	0.031	45	10	55	0.182	link	-	Gm21663	c.139+238	-	ENSMUST	intron_variant
5	26021225	rs1133659	G	T	weak_evid	SNV	7	1	8	0.125	5	8	13	0.615	link	-	Gm5862	c.299+379	-	ENSMUST	intron_variant
5	26021241	rs1132623	G	T	weak_evid	SNV	7	0	7	0	5	8	13	0.615	link	-	Gm5862	c.299+363	-	ENSMUST	intron_variant
5	27500901	.	A	G	mapping_c	SNV	10	0	10	0	14	3	17	0.176	link	-	Dpp6	c.609+314	-	ENSMUST	intron_variant
5	27500901	.	A	G	mapping_c	SNV	10	0	10	0	14	3	17	0.176	link	-	Speer4b	c.139+328	-	ENSMUST	intron_variant
5	64827416	.	G	A	too_few_s	SNV	18	0	18	0	15	2	17	0.118	link	-	Klf3	c.853+146	-	ENSMUST	intron_variant
5	72823637	.	G	A	PASS	SNV	100	0	100	0	70	24	94	0.255	link	-	Tec	c.-44C>T	-	ENSMUST	5_prime_UTR_premature_start_codon_gain_variant
5	72823637	.	G	A	PASS	SNV	100	0	100	0	70	24	94	0.255	link	-	Tec	c.-44C>T	-	ENSMUST	5_prime_UTR_variant
5	90563723	.	C	T	too_few_s	SNV	6	0	6	0	7	2	9	0.222	link	-	Gm2602	n.*4304C>	-	ENSMUST	downstream_gene_variant
5	90563723	.	C	T	too_few_s	SNV	6	0	6	0	7	2	9	0.222	link	-	Gm43448	n.353-102	-	ENSMUST	intron_variant
5	90563723	.	C	T	too_few_s	SNV	6	0	6	0	7	2	9	0.222	link	-	5830473C1	c.86-252C:	-	ENSMUST	intron_variant
5	1.1E+08	.	A	C	base_quali	SNV	32	1	33	0.03	23	6	29	0.207	link	-	Crlf2	c.-124T>G	-	ENSMUST	upstream_gene_variant
5	1.1E+08	.	A	C	base_quali	SNV	32	1	33	0.03	23	6	29	0.207	link	-	Gm8493	n.-4851T>	-	ENSMUST	upstream_gene_variant
5	1.1E+08	.	A	C	base_quali	SNV	32	1	33	0.03	23	6	29	0.207	link	-	-	n.1095590	-	-	intergenic_region
5	1.18E+08	.	T	G	base_quali	SNV	60	2	62	0.032	32	6	38	0.158	link	-	Tesc	c.210-85T:	-	ENSMUST	intron_variant
5	1.2E+08	.	T	A	too_few_s	SNV	13	0	13	0	12	2	14	0.143	link	-	Gm10390	n.*3473A>	-	ENSMUST	downstream_gene_variant
5	1.2E+08	.	T	A	too_few_s	SNV	13	0	13	0	12	2	14	0.143	link	-	Rbm19	c.1271-172	-	ENSMUST	intron_variant
5	1.2E+08	.	T	A	too_few_s	SNV	13	0	13	0	12	2	14	0.143	link	-	Gm10390	n.1201280	-	-	intragenic_variant
5	1.21E+08	.	A	C	base_quali	SNV	76	5	81	0.062	50	14	64	0.219	link	-	Gm15800	c.6973+66	-	ENSMUST	intron_variant

5	1.23E+08	.	A	C	weak_evid	SNV	18	2	20	0.1	25	3	28	0.107	link	-	P2rx4	c.525-159A	-	ENSMUST	intron_variant
5	1.23E+08	.	G	C	base_quali	SNV	54	4	58	0.069	51	8	59	0.136	link	-	Gm43412	n.*2200G>	-	ENSMUST	downstream_gene_variant
5	1.23E+08	.	G	C	base_quali	SNV	54	4	58	0.069	51	8	59	0.136	link	-	Morn3	c.303+66C	-	ENSMUST	intron_variant
5	1.25E+08	.	G	A	weak_evid	SNV	95	0	95	0	100	3	103	0.029	link	-	Ncor2	c.6091+13	-	ENSMUST	intron_variant
5	1.36E+08	.	T	G	weak_evid	SNV	8	1	9	0.111	3	3	6	0.5	link	-	Lrwd1	c.1448+28	-	ENSMUST	intron_variant
5	1.45E+08	.	A	C	base_quali	SNV	62	3	65	0.046	62	5	67	0.075	link	-	Smurf1	c.55+53T>	-	ENSMUST	intron_variant
5	1.46E+08	rs3648566	T	C	mapping_c	SNV	92	12	104	0.115	72	12	84	0.143	link	-	Cyp3a41b	c.-101A>G	-	ENSMUST	upstream_gene_variant
5	1.46E+08	rs3648566	T	C	mapping_c	SNV	92	12	104	0.115	72	12	84	0.143	link	-	-	n.1455847	-	-	intergenic_region
5	1.46E+08	rs1134737	G	T	mapping_c	SNV	82	12	94	0.128	68	12	80	0.15	link	-	Cyp3a41b	c.-106C>A	-	ENSMUST	upstream_gene_variant
5	1.46E+08	rs1134737	G	T	mapping_c	SNV	82	12	94	0.128	68	12	80	0.15	link	-	-	n.1455847	-	-	intergenic_region
5	1.46E+08	rs1132633	A	T	mapping_c	SNV	81	12	93	0.129	68	12	80	0.15	link	-	Cyp3a41b	c.-107T>A	-	ENSMUST	upstream_gene_variant
5	1.46E+08	rs1132633	A	T	mapping_c	SNV	81	12	93	0.129	68	12	80	0.15	link	-	-	n.1455847	-	-	intergenic_region
5	1.46E+08	rs5833119	A	G	mapping_c	SNV	71	15	86	0.174	55	13	68	0.191	link	-	Cyp3a41b	c.-122T>C	-	ENSMUST	upstream_gene_variant
5	1.46E+08	rs5833119	A	G	mapping_c	SNV	71	15	86	0.174	55	13	68	0.191	link	-	-	n.1455847	-	-	intergenic_region
6	3707410	.	G	C	base_quali	SNV	77	11	88	0.125	60	22	82	0.268	link	-	Calcr	c.810+79C	-	ENSMUST	intron_variant
6	38941144	.	T	C	too_few_si	SNV	8	0	8	0	14	2	16	0.125	link	-	Gm42962	n.431+174	-	ENSMUST	intron_variant
6	38941144	.	T	C	too_few_si	SNV	8	0	8	0	14	2	16	0.125	link	-	Tbxas1	c.90-7398	T	ENSMUST	intron_variant
6	39725757	.	G	T	too_few_si	SNV	4	0	4	0	7	2	9	0.222	link	-	Braf	c.-462C>A	-	ENSMUST	upstream_gene_variant
6	39725757	.	G	T	too_few_si	SNV	4	0	4	0	7	2	9	0.222	link	-	-	n.3972575	-	-	intergenic_region
6	42363530	.	T	G	base_quali	SNV	44	4	48	0.083	36	10	46	0.217	link	-	Zyx	c.*5574T>	-	ENSMUST	downstream_gene_variant
6	42363530	.	T	G	base_quali	SNV	44	4	48	0.083	36	10	46	0.217	link	-	Epha1	c.1774+32	-	ENSMUST	intron_variant
6	47681530	.	C	A	mapping_c	SNV	279	12	291	0.041	261	20	281	0.071	link	-	-	n.4768153	-	-	intergenic_region
6	47681557	.	C	T	non_homre	SNV	226	13	239	0.054	222	17	239	0.071	link	-	-	n.4768155	-	-	intergenic_region
6	52622803	.	A	C	base_quali	SNV	125	0	125	0	109	14	123	0.114	link	-	Hibadh	c.359+48T	-	ENSMUST	intron_variant
6	1.13E+08	.	T	G	weak_evid	SNV	383	3	386	0.008	317	38	355	0.107	link	-	Creld1	c.*2981T>	-	ENSMUST	downstream_gene_variant
6	1.26E+08	.	T	C	weak_evid	SNV	170	0	170	0	152	3	155	0.019	link	-	Ano2	c.1434+32	-	ENSMUST	intron_variant
6	1.27E+08	.	G	A	PASS	SNV	257	0	257	0	216	3	219	0.014	link	-	Dyrk4	c.132+573	-	ENSMUST	intron_variant
6	1.49E+08	.	G	T	alt_allele_i	SNV	23	7	30	0.233	13	10	23	0.435	link	-	Caprin2	c.178-137(	-	ENSMUST	intron_variant
7	17054658	.	A	C	base_quali	SNV	54	4	58	0.069	57	4	61	0.066	link	-	4833404L0	n.-3876A>	-	ENSMUST	upstream_gene_variant
7	17054658	.	A	C	base_quali	SNV	54	4	58	0.069	57	4	61	0.066	link	-	Hif3a	c.363+24T	-	ENSMUST	intron_variant
7	25627998	.	A	G	too_few_si	SNV	22	0	22	0	15	2	17	0.118	link	-	Atp5sl	c.*3106A>	-	ENSMUST	downstream_gene_variant
7	25627998	.	A	G	too_few_si	SNV	22	0	22	0	15	2	17	0.118	link	-	Bckdha	c.*2265T>	-	ENSMUST	downstream_gene_variant
7	25627998	.	A	G	too_few_si	SNV	22	0	22	0	15	2	17	0.118	link	-	B3gnt8	c.-32-1174	A	ENSMUST	intron_variant
7	27807328	.	T	G	base_quali	SNV	108	7	115	0.061	98	12	110	0.109	link	-	Zfp626	c.33+92T>	-	ENSMUST	intron_variant
7	29070744	.	C	A	weak_evid	SNV	74	0	74	0	70	3	73	0.041	link	-	Gm26604	n.-893C>A	-	ENSMUST	upstream_gene_variant
7	29070744	.	C	A	weak_evid	SNV	74	0	74	0	70	3	73	0.041	link	-	Ryr1	c.7930-48(	-	ENSMUST	intron_variant
7	30508300	.	T	G	base_quali	SNV	29	2	31	0.065	19	7	26	0.269	link	-	Prodh2	c.1002-14(	-	ENSMUST	intron_variant
7	30957147	.	T	G	base_quali	SNV	19	3	22	0.136	21	6	27	0.222	link	-	Usf2	c.-390A>C	-	ENSMUST	upstream_gene_variant
7	30957147	.	T	G	base_quali	SNV	19	3	22	0.136	21	6	27	0.222	link	-	Gm4673	n.-262T>G	-	ENSMUST	upstream_gene_variant
7	30957147	.	T	G	base_quali	SNV	19	3	22	0.136	21	6	27	0.222	link	-	Lsr	c.*719A>C	-	ENSMUST	downstream_gene_variant
7	30957147	.	T	G	base_quali	SNV	19	3	22	0.136	21	6	27	0.222	link	-	Gm17077	n.168-746	T	ENSMUST	intron_variant
7	30957147	.	T	G	base_quali	SNV	19	3	22	0.136	21	6	27	0.222	link	-	Gm4673	n.3095714	-	-	intragenic_variant
7	38019427	.	G	A	weak_evid	SNV	308	1	309	0.003	309	5	314	0.016	link	-	Uri1	c.117+400	-	ENSMUST	intron_variant
7	44602023	.	T	G	base_quali	SNV	140	5	145	0.034	146	7	153	0.046	link	-	Kcnc3	c.*18T>G	-	ENSMUST	3_prime_UTR_variant
7	44602023	.	T	G	base_quali	SNV	140	5	145	0.034	146	7	153	0.046	link	-	Myh14	c.*4187A>	-	ENSMUST	downstream_gene_variant
7	45980118	.	T	G	base_quali	SNV	61	0	61	0	65	13	78	0.167	link	-	Abcc6	c.3868-84/	-	ENSMUST	intron_variant
7	46065973	.	A	C	too_few_si	SNV	6	0	6	0	5	2	7	0.286	link	-	Nomo1	c.2031-18	-	ENSMUST	intron_variant
7	59770001	.	G	T	weak_evid	SNV	297	5	302	0.017	310	10	320	0.031	link	-	Gm23446	n.-3297C>	-	ENSMUST	upstream_gene_variant
7	59770001	.	G	T	weak_evid	SNV	297	5	302	0.017	310	10	320	0.031	link	-	Gm25210	n.-770C>A	-	ENSMUST	upstream_gene_variant
7	59770001	.	G	T	weak_evid	SNV	297	5	302	0.017	310	10	320	0.031	link	-	Gm22128	n.*1655C>	-	ENSMUST	downstream_gene_variant
7	59770001	.	G	T	weak_evid	SNV	297	5	302	0.017	310	10	320	0.031	link	-	Gm22851	n.*4189C>	-	ENSMUST	downstream_gene_variant
7	59770001	.	G	T	weak_evid	SNV	297	5	302	0.017	310	10	320	0.031	link	-	Snhg14	n.5977000	-	-	intragenic_variant
7	81454102	.	T	G	base_quali	SNV	51	2	53	0.038	51	11	62	0.177	link	-	Cpeb1os1	n.-1793T>	-	ENSMUST	upstream_gene_variant
7	81454102	.	T	G	base_quali	SNV	51	2	53	0.038	51	11	62	0.177	link	-	Cpeb1	c.15+532A	-	ENSMUST	intron_variant
7	88035927	.	A	G	too_few_si	SNV	17	0	17	0	12	2	14	0.143	link	-	Grm5	c.1392-14(	-	ENSMUST	intron_variant
7	97558438	.	A	G	too_few_si	SNV	6	0	6	0	4	2	6	0.333	link	-	Aamdc	c.217-212(	-	ENSMUST	intron_variant
7	1.02E+08	.	T	G	base_quali	SNV	88	8	96	0.083	87	8	95	0.084	link	-	Pde2a	c.2320-71(	-	ENSMUST	intron_variant
7	1.02E+08	.	T	G	base_quali	SNV	88	8	96	0.083	87	8	95	0.084	link	-	Pde2a	c.2272-71(	-	ENSMUST	intron_variant
7	1.1E+08	.	T	A	non_homre	SNV	100	3	103	0.029	88	5	93	0.054	link	-	RP23-462(	n.*1223T>	-	ENSMUST	downstream_gene_variant
7	1.1E+08	.	T	A	non_homre	SNV	100	3	103	0.029	88	5	93	0.054	link	-	1600010M	n.712+246	-	ENSMUST	intron_variant
7	1.1E+08	.	T	A	non_homre	SNV	100	3	103	0.029	88	5	93	0.054	link	-	Wee1	c.576+38T	-	ENSMUST	intron_variant
7	1.2E+08	.	T	G	base_quali	SNV	91	0	91	0	77	16	93	0.172	link	-	2610020H(	c.461-50T:	-	ENSMUST	intron_variant
7	1.41E+08	rs2652526	T	G	base_quali	SNV	23	2	25	0.08	23	7	30	0.233	link	-	Tmem80	c.*115T>G	-	ENSMUST	3_prime_UTR_variant
7	1.41E+08	rs2652526	T	G	base_quali	SNV	23	2	25	0.08	23	7	30	0.233	link	-	Eps8l2	c.-5766T>	-	ENSMUST	upstream_gene_variant
8	83271595	.	T	G	base_quali	SNV	190	2	192	0.01	136	13	149	0.087	link	-	RP23-63O	n.*3968T>	-	ENSMUST	downstream_gene_variant
8	88362012	.	T	G	base_quali	SNV	74	6	80	0.075	86	7	93	0.075	link	-	Brd7	c.-58A>C	-	ENSMUST	5_prime_UTR_variant
8	1.22E+08	.	A	C	base_quali	SNV	89	1	90	0.011	95	18	113	0.159	link	-	Slc7a5	c.1484-10(	-	ENSMUST	intron_variant
8	1.22E+08	.	A	C	base_quali	SNV	89	1	90	0.011	95	18	113	0.159	link	-	Gm20388	c.21+1972	-	ENSMUST	intron_variant
8	1.22E+08	.	A	C	base_quali	SNV	58	0	58	0	40	11	51	0.216	link	-	RP23-354I	n.-3792T>	-	ENSMUST	upstream_gene_variant
8	1.22E+08	.	A	C	base_quali	SNV	58	0	58	0	40	11	51	0.216	link	-	Snai3	c.683-80T:	-	ENSMUST	intron_variant
8	1.22E+08	.	A	C	base_quali	SNV	58	0	58	0	40	11	51	0.216	link	-	Gm20388	c.22-1840(	-	ENSMUST	intron_variant
8	1.25E+08	.	A	C	base_quali	SNV	195	4	199	0.02	216	6	222	0.027	link	-	Arv1	c.-298A>C	-	ENSMUST	upstream_gene_variant
8	1.27E+08	.	A	C	base_quali	SNV	25	4	29	0.138	25	9	34	0.265	link	-	Tomm20	c.-122T>G	-	ENSMUST	upstream_gene_variant
8	1.27E+08	.	A	C	base_quali	SNV	25	4	29	0.138	25	9	34	0.265	link	-	Gm26397	n.-866T>G	-	ENSMUST	upstream_gene_variant
8	1.27E+08	.	A	C	base_quali	SNV	25	4	29	0.138	25	9	34	0.265	link	-	Rbm34	c.*3389T>	-	ENSMUST	downstream_gene_variant
8	1.27E+08	.	A	C	base_quali	SNV	25	4	29	0.138	25	9	34	0.265	link	-	-	n.1269458	-	-	intergenic_region
8	1.29E+08	.	C	T	weak_evid	SNV	8	0	8	0	8	3	11	0.273	link	-	Ccdc7a	c.-51-97G:	-	ENSMUST	intron_variant
9	3025910	.	G	T	non_homre	SNV	200	4	204	0.02	170	7	177	0.04	link	-	Gm10719	c.*4317G>	-	ENSMUST	downstream_gene_variant
9	3025910	.	G	T	non_homre	SNV	200	4	204	0.02	170	7	177	0.04	link	-	Gm10718	c.*692G>T	-	ENSMUST	downstream_gene_variant
9	3025910	.	G	T	non_homre	SNV	200	4	204	0.02	170	7	177	0.04	link	-	Gm26870	n.3025910	-	-	intragenic_variant
9	3026361	.	A	G	non_homre	SNV	17	2	19	0.105	17	3	20	0.15	link	-	Gm10719	c.*4768A>	-	ENSMUST	downstream_gene_variant
9	3026361	.	A	G	non_homre	SNV	17	2	19	0.105	17	3	20	0.15	link	-	Gm10718	c.*1143A>	-	ENSMUST	downstream_gene_variant
9	3026361	.	A	G	non_homre	SNV	17	2	19	0.105	17	3	20	0.15	link	-	Gm26870	n.3026361	-	-	intragenic_variant
9	3027215	.	C	T	PASS	SNV	59	0	59	0	57	6	63	0.095	link	-	Gm10718	c.*1997C>	-	ENSMUST	downstream_gene_variant
9	3027215	.	C	T	PASS	SNV	59	0	59	0	57	6	63	0.095	link	-	Gm10717	c.*828C>T	-	ENSMUST	downstream_gene_variant
9	3027215	.	C	T	PASS	SNV	59	0	59	0	57	6	63	0.095	link	-	Gm26870	n.3027215	-	-	intragenic_variant
9	3027215	.	C	T	PASS	SNV	59	0	59	0	57	6	63	0.095	link	-	Gm10717	n.3027215	-	-	intragenic_variant
9	9008276	.	T	G	base_quali	SNV	17	0	17	0	17	6	23	0.261	link	-	Arhgap42	c.1609-16/	-	ENSMUST	intron_variant
9	14718211	.	T	G	base_quali	SNV	162	0	162	0	123	10	133	0.075	link	-	Piwil4	c.1394+25	-	ENSMUST	intron_variant
9	14718211	.	T	G	base_quali	SNV	162	0	162	0	123	10	133	0.075	link	-	Gm10706	n.1471T>(	-	ENSMUST	non_coding_transcript_exon_variant
9	21927361	.	T	G	base_quali	SNV	139	2	141	0.014	100	25	125	0.2	link	-	Tmem205	c.-79A>C	-	ENSMUST	5_prime_UTR_variant
9	21927361	.	T	G	base_quali	SNV	139	2	141	0.014	100	25	125	0.2	link	-	Ccdc159	c.-347T>G	-	ENSMUST	upstream_gene_variant
9	42541748	.	G	A	weak_evid	SNV	59	0	59	0	63	3	66	0.045	link	-	Grik4	c.2266+74	-	ENSMUST	intron_variant
9	43176251	.	T	G	PASS	SNV	171	0	171	0	159	23	182	0.126	link	-	Pou2f3	c.132+35A	-	ENSMUST	intron_variant
9	45869635	.	G	T	base_quali	SNV	62	5	67	0.075	50	9	59	0.153	link	-	Rnf214	c.1146-91(	-	ENSMUST	intron_variant
9	59328831	.	C	A	too_few_si	SNV	14	0	14	0	21	2	23	0.087	link	-	Bbs4	c.643-183(	-	ENSMUST	intron_variant
9	60587572	.	T	G	base_quali	SNV	12	1	13	0.077	10	2	12	0.167	link	-	Lrrc49	c.*116A>C	-	ENSMUST	3_prime_UTR_variant
9	65135041	.	A	C	base_quali	SNV	52	5	57	0.088	40	13	53	0.245	link	-	Igdcc4	c.3484-71/	-	ENSMUST	intron_variant
9	66592651	.	T	G	alt_allele_i	SNV	25	4	29	0.138	29	8	37	0.216	link	-	Usp3	c.91+133A	-	ENSMUST	intron_variant
9	70430804	.	A	C	base_quali	SNV	36	0	36	0	22	10	32	0.312	link	-	Rnf111	c.2724+12	-	ENSMUST	intron_variant
9	1.03E+08	.	T	G	weak_evid	SNV	28	2	30	0.067	22	5	27	0.185	link	-	Slco2a1	c.*96T>G	-	ENSMUST	3_prime_UTR_variant
9	1.08E+08	.	A	C	too_few_si	SNV	13	0	13	0	9	2	11	0.182	link	-	Rbm5	c.855+139	-	ENSMUST	intron_variant
9	1.1E+08	.	G	C	base_quali	SNV	22	4	26	0.154	18	6	24	0.25	link	-	Cdc25a	c.-89G>C	-	ENSMUST	5_prime_UTR_variant
9	1.14E+08	.	T	G	base_quali	SNV	155	0	155	0	116	8	124	0.065	link	-	Clasp2	c.845+52T	-	ENSMUST	intron_variant

9	1.14E+08	.	T	G	base_quali	SNV	155	0	155	0	110	13	123	0.106	link	-	Clasp2	c.845+53T	-	ENSMUST	intron_variant
9	1.14E+08	.	T	G	base_quali	SNV	150	0	150	0	119	8	127	0.063	link	-	Clasp2	c.845+55T	-	ENSMUST	intron_variant
9	1.22E+08	.	A	C	base_quali	SNV	80	6	86	0.07	79	5	84	0.06	link	-	Deb1	c.-43A>C	-	ENSMUST	upstream_gene_variant
9	1.22E+08	.	A	C	base_quali	SNV	80	6	86	0.07	79	5	84	0.06	link	-	-	n.1217103	-	-	intergenic_region
9	1.23E+08	.	G	A	too_few_si	SNV	24	0	24	0	12	2	14	0.143	link	-	Zdhhc3	c.-24-123(	-	ENSMUST	intron_variant
9	1.24E+08	.	A	C	base_quali	SNV	30	4	34	0.118	28	7	35	0.2	link	-	Fyco1	c.*147T>G	-	ENSMUST	3_prime_UTR_variant
9	1.24E+08	.	A	C	base_quali	SNV	30	4	34	0.118	28	7	35	0.2	link	-	Gm17021	n.-1588T>	-	ENSMUST	upstream_gene_variant
GL456211.	82880	.	C	T	non_homre	SNV	18	4	22	0.182	13	5	18	0.278	link	-	-	n.82880C>	-	-	intergenic_region
GL456221.	114409	.	T	A	mapping_c	SNV	5	0	5	0	2	5	7	0.714	link	-	Csprs	c.-23-333A	-	ENSMUST	intron_variant
GL456212.	138220	.	G	T	no_reliable	SNV	11	1	12	0.083	14	5	19	0.263	link	-	AC168977.	c.740-300(	-	ENSMUST	intron_variant
14	77582475	.	T	C	PASS	SNV	168	0	168	0	135	30	165	0.182	link	-	Enox1	c.669T>C	p.Asp223A	ENSMUST	synonymous_variant
15	98851075	.	C	T	weak_evid	SNV	328	2	330	0.006	298	6	304	0.02	link	-	Kmt2d	c.8367G>A	p.Gln2789(	ENSMUST	synonymous_variant
16	42144573	.	T	G	base_quali	SNV	215	3	218	0.014	172	18	190	0.095	link	-	Lsamp	c.843T>G	p.Leu281L	ENSMUST	synonymous_variant
16	62802730	.	A	G	weak_evid	SNV	280	1	281	0.004	312	4	316	0.013	link	-	Arl13b	c.1128T>C	p.Pro376P	ENSMUST	synonymous_variant
17	4995865	.	C	A	weak_evid	SNV	285	2	287	0.007	307	8	315	0.025	link	-	Arid1b	c.771C>A	p.Gly257G	ENSMUST	synonymous_variant
19	12795034	.	C	T	PASS	SNV	301	0	301	0	322	14	336	0.042	link	-	Zfp91	c.300G>A	p.Ala100Al	ENSMUST	synonymous_variant
2	69732825	rs5870122	A	G	weak_evid	SNV	194	1	195	0.005	185	4	189	0.021	link	-	Ppig	c.144A>G	p.Lys48Ly:	ENSMUST	synonymous_variant
2	76908341	.	T	C	PASS	SNV	262	0	262	0	237	9	246	0.037	link	-	Ttn	c.11991A>	p.Ala3997/	ENSMUST	synonymous_variant
2	1.67E+08	.	T	G	base_quali	SNV	151	5	156	0.032	127	17	144	0.118	link	-	Prex1	c.4498A>C	p.Arg1500/	ENSMUST	splice_region_variant+synonymous_variant
7	1.04E+08	.	A	G	PASS	SNV	238	0	238	0	215	7	222	0.032	link	-	Olfr619	c.279A>G	p.Gln93Glr	ENSMUST	synonymous_variant
7	1.23E+08	.	C	T	weak_evid	SNV	375	2	377	0.005	378	5	383	0.013	link	-	Arhgap17	c.2058G>A	p.Gln686G	ENSMUST	synonymous_variant
7	1.27E+08	.	A	C	base_quali	SNV	295	4	299	0.013	311	20	331	0.06	link	-	Atxn2l	c.192T>G	p.Ala64Ala	ENSMUST	synonymous_variant
8	11244401	.	G	T	PASS	SNV	157	0	157	0	189	5	194	0.026	link	-	Col4a1	c.555C>A	p.Gly185G	ENSMUST	splice_region_variant+synonymous_variant
8	83271595	.	T	G	base_quali	SNV	190	2	192	0.01	136	13	149	0.087	link	-	Tbc1d9	c.3780T>C	p.Ser1260!	ENSMUST	synonymous_variant
14	51920426	.	G	T	base_quali	SNV	82	3	85	0.035	66	9	75	0.12	link	-	Tppp2	c.328-1G>T	-	ENSMUST	splice_acceptor_variant+intron_variant
15	88821231	.	A	C	base_quali	SNV	58	7	65	0.108	62	18	80	0.225	link	-	Creld2	c.409+5A>C	-	ENSMUST	splice_region_variant+intron_variant
16	8706593	.	A	C	weak_evid	SNV	136	0	136	0	131	22	153	0.144	link	-	Usp7	c.974+6T>G	-	ENSMUST	splice_region_variant+intron_variant
16	8706595	.	A	C	base_quali	SNV	140	0	140	0	151	12	163	0.074	link	-	Usp7	c.974+4T>G	-	ENSMUST	splice_region_variant+intron_variant
16	17531017	.	G	A	too_few_si	SNV	14	0	14	0	15	2	17	0.118	link	-	Thap7	c.-1+8C>T	-	ENSMUST	splice_region_variant+intron_variant
16	97568890	rs4707516	G	A	PASS	SNV	124	0	124	0	110	28	138	0.203	link	-	Tmprss2	c.1069+4C	-	ENSMUST	splice_region_variant+intron_variant
2	1.65E+08	.	T	A	base_quali	SNV	75	9	84	0.107	87	10	97	0.103	link	-	Zfp335	c.3189+3A	-	ENSMUST	splice_region_variant+intron_variant