

Supplemental Table S2. Missense variants detected in candidate genes in Gotland cattle, showing chromosome, position, reference genome and alternate alleles, gene symbol, genotype in the two Gotland cattle samples (coded as 00 for homozygous reference, 01 for heterozygote and 11 for homozygous alternate), alternate allele counts out of total number of chromosomes for the other breeds, and potential consequences for protein sequence as predicted by VEP. When multiple splice variants lead to proteins with the same amino acid substitution in the same position, the table only gives one transcript accession. Note that due to the risk of allelic drop-out, homozygotes may not have been accurately distinguished from heterozygotes in the Gotland cattle samples.

Chr	Position	REF	ALT	gene	Gotlandsko1	Gotlandsko2	Bohuskulla	Fjäll	Fjällnära	Rödkulla	Ringamåläko	Väneko	SRB	Potential consequences
3	116981583	A	G	MLPH	11	..	2 / 6	4 / 14	4 / 8	9 / 18	3 / 4	2 / 10	3 / 16	ENSBTAP00000000837:p.Met113Val
3	116981637	C	A	MLPH	11	00	0 / 6	4 / 14	4 / 8	5 / 18	3 / 4	2 / 10	2 / 16	ENSBTAP00000000837:p.His131Asn
3	116981638	A	G	MLPH	11	00	2 / 6	4 / 14	4 / 8	9 / 18	3 / 4	2 / 10	5 / 16	ENSBTAP00000000837:p.His131Arg
3	116981649	G	A	MLPH	11	00	0 / 6	4 / 14	1 / 8	4 / 18	0 / 4	1 / 10	2 / 14	ENSBTAP00000000837:p.Ala135Thr
3	116996878	T	C	MLPH	11	00	0 / 6	4 / 14	2 / 8	4 / 18	0 / 4	1 / 10	4 / 16	ENSBTAP00000058971:p.Met387Thr, ENSBTAP00000000837:p.Met393Thr, XP_024845194.1:p.Met400Thr, XP_024845193.1:p.Met402Thr
3	116997197	G	A	MLPH	00	01	0 / 6	4 / 14	2 / 8	4 / 18	0 / 4	1 / 10	5 / 16	ENSBTAP00000058971:p.Arg419Gln, ENSBTAP00000000837:p.Arg425Gln, XP_024845194.1:p.Arg432Gln, XP_024845193.1:p.Arg434Gln
3	117002401	A	G	MLPH	11	00	0 / 6	4 / 14	2 / 8	4 / 18	0 / 4	1 / 10	3 / 16	ENSBTAP00000058971:p.Thr565Ala, ENSBTAP00000000837:p.Thr571Ala, XP_024845194.1:p.Thr578Ala, XP_024845193.1:p.Thr580Ala
4	27814937	G	T	TWIST1	11	11	6 / 6	11 / 14	8 / 8	16 / 18	4 / 4	7 / 10	14 / 16	XP_024846774.1:p.Trp64Leu
6	70214244	T	C	KIT	11	11	6 / 6	10 / 14	8 / 8	18 / 18	4 / 4	10 / 10	16 / 16	ENSBTAP00000003498:p.Met258Thr
6	85451132	C	G	CSN2	11	11	6 / 6	12 / 14	8 / 8	17 / 18	4 / 4	10 / 10	14 / 16	XP_015327157.2:p.Arg129Ser, ENSBTAP00000003409:p.Arg172Ser
6	85451298	T	G	CSN2	00	11	2 / 6	7 / 14	5 / 8	7 / 18	3 / 4	5 / 10	9 / 16	ENSBTAP00000003409:p.His117Pro, XP_015327157.2:p.His74Pro
6	85536434	G	T	CSNIS2	01	11	0 / 6	0 / 14	0 / 8	2 / 18	0 / 4	0 / 10	1 / 16	XP_015327143.1:p.Glu65Asp, ENSBTAP00000006590:p.Glu74Asp
6	85656736	T	C	CSN3	01	00	0 / 6	3 / 14	4 / 8	9 / 18	4 / 4	8 / 10	1 / 14	ENSBTAP00000065313:p.Ile146Thr, ENSBTAP00000028685:p.Ile157Thr
6	85656772	C	A	CSN3	01	01	0 / 6	3 / 14	4 / 8	9 / 18	4 / 4	8 / 10	2 / 12	ENSBTAP00000065313:p.Ala158Asp, ENSBTAP00000028685:p.Ala169Asp
8	31639069	C	T	TYRP1	00	01	1 / 6	8 / 14	3 / 8	14 / 18	4 / 4	4 / 10	11 / 16	ENSBTAP00000027945:p.Glu329Lys, XP_015327928.2:p.Glu362Lys
8	31647440	G	C	TYRP1	00	01	0 / 6	0 / 14	0 / 8	0 / 18	0 / 4	3 / 10	0 / 16	ENSBTAP00000027945:p.Thr112Ser, XP_015327928.2:p.Thr145Ser
11	103257950	G	A	LBG	11	00	3 / 6	4 / 14	0 / 8	3 / 18	2 / 4	8 / 10	7 / 16	ENSBTAP00000019538:p.Gly80Asp
11	103259232	C	T	LBG	11	11	3 / 6	4 / 14	0 / 8	3 / 18	2 / 4	8 / 10	3 / 16	ENSBTAP00000019538:p.Ala134Val
11	103260219	T	C	LBG	11	00	3 / 6	4 / 14	0 / 8	3 / 18	2 / 4	8 / 10	6 / 16	XP_024854027.1:p.Leu238Pro
19	40977156	A	G	KRT27	00	11	2 / 6	6 / 14	1 / 8	9 / 18	1 / 4	6 / 10	7 / 16	ENSBTAP00000040718:p.Ser446Pro
19	40977827	C	A	KRT27	01	11	0 / 6	3 / 14	0 / 8	3 / 18	0 / 4	0 / 10	0 / 16	ENSBTAP00000040718:p.Gly404Cys
19	40978227	G	A	KRT27	01	00	0 / 6	0 / 14	2 / 8	1 / 18	0 / 4	0 / 10	1 / 16	ENSBTAP00000040718:p.Thr333Met
19	40982347	C	G	KRT27	01	00	0 / 6	2 / 14	2 / 8	3 / 18	0 / 4	0 / 10	2 / 14	ENSBTAP00000040718:p.Gly60Ala
20	31869993	G	A	GHR	11	00	6 / 6	14 / 14	8 / 8	18 / 18	4 / 4	10 / 10	16 / 16	ENSBTAP00000065441:p.Thr541Ile, ENSBTAP00000001758:p.Thr563Ile, ENSBTAP00000058520:p.Thr570Ile, ENSBTAP00000065610:p.Thr620Ile
20	39789981	C	T	SLC45A2	00	01	0 / 6	0 / 14	0 / 8	0 / 18	1 / 4	0 / 10	0 / 16	ENSBTAP00000024272:p.Leu64Phe
20	39792306	T	A	SLC45A2	00	01	1 / 6	4 / 14	2 / 8	2 / 18	1 / 4	2 / 10	4 / 16	ENSBTAP00000024272:p.Phe230Tyr