

Table S2: Sequence variants of polled associated 932 kb haplotype in Holstein. Animals carrying the polled associated *indel* found in Simmental are not included. The remaining associated variants are highlighted in grey and the excluded variants shown in red.

UMD3.1 position	variant	reference allele	variant allele	ref/ref polled	ref/var polled	var/var polled	ref/ref horned	ref/var horned
1'583'414°	SNP	A	G		84	4	204	
1'584'650	SNP	C	T		1	2	55	1
1'587'758	SNP	C	T		76	4	200	1
1'596'777°	SNP	G	T		85	4	390	
1'603'747°	SNP	C	T		87	4	426	
1'606'620°	SNP	C	T		83	4	415	
1'607'675°	SNP	G	A			3*	41	
1'618'261°	SNP	T	C			3*	43	
1'623'157°	SNP	G	A		11	2	77	
1'623'573	SNP	G	C		77	4	368	
1'624'279°	SNP	C	T		82	2	417	
1'624'522°	SNP	T	G		85	2	411	
1'624'555°	SNP	T	C		81	1	408	
1'626'030°	SNP	T	C		84	4	425	
1'626'065°	SNP	G	C		84	4	421	
1'628'090°	SNP	A	G		60	4	384	
1'631'299°	SNP	A	G		86	4	424	
1'631'667°	SNP	C	T		87	4	429	
1'631'762°	SNP	G	A		87	4	429	
1'631'895°	SNP	T	C		87	4	427	
1'633'226°	SNP	T	A		77	4	420	
1'633'690°	SNP	C	T		79	4	422	
1'635'514°	SNP	G	C		76	4	414	
1'639'632°	SNP	A	G		82	3	396	
1'640'658°	SNP	G	T		86	4	432	
1'640'815°	SNP	T	C		85	3	420	
1642525° **	SNP	T	A			1	33	
1'645'083°	SNP	G	T		80	4	426	
1'645'296°	deletion	AT	A		76	4	422	
1645301°	SNP	T	A		75	4	423	
1'649'163 +	InDel	CGCATCA	TTCTCAGAATAG		85	3	415	
1'651'491°	SNP	C	T	6	12	3	203	
1'654'405 +	SNP	G	A		87	4	424	
1'655'463 +	SNP	C	T		86	4	429	
1'672'807	SNP	G	A		2	2	216	1
1'676'520	SNP	C	T		19	3	407	1
1'679'832	SNP	C	T		2	3	133	1
1'680'646	SNP	T	C		80	6	221	1
1'684'055°	SNP	G	C		85	4	416	
1'764'239°	SNP	T	C		85	4	409	
1'768'587 +	SNP	C	A	4***	152	25	443	
1'855'898°	SNP	G	A		87	4	408	
1'909'354+	80kbDup				105****		430	
2'028'953°	SNP	C	G			1	33	
2'248'958	SNP	G	A			1	33	
2'255'019	SNP	C	T			1	33	
2'261'830	SNP	T	C			1	33	
2'263'363	SNP	T	C			1	33	
2'267'616	deletion	CT	C			1	33	
2'268'463	SNP	G	A			1	33	
2'269'541	SNP	T	C			1	33	
2'270'224	SNP	C	T			1	33	
2'271'484	SNP	C	T			1	33	
2'274'411	SNP	C	T			1	33	
2'274'700	SNP	T	G			1	33	
2'275'244	SNP	G	A			1	33	
2'275'575	SNP	G	A			1	33	
2'275'606	SNP	C	G			1	33	
2'275'689	SNP	G	A			1	33	
2'278'133	SNP	A	C			1	33	
2'279'787	SNP	G	T			1	33	
2'279'861	SNP	A	G			1	33	

UMD3.1 position	variant	reference allele	variant allele	ref/ref polled	ref/var polled	var/var polled	ref/ref horned	ref/var horned
2'279'921	SNP	T	C			1	32	
2'279'996	SNP	G	A			1	32	
2'280'020	SNP	A	G			1	32	
2'280'142	SNP	C	T			1	32	
2'280'168	SNP	G	A			1	32	
2'280'378	SNP	T	C			1	32	
2'280'407	SNP	C	T			1	33	
2'280'428	InDel	CCT	CTCTAC			1	32	
2'280'522	SNP	T	C			1	33	
2'280'577	SNP	C	G			1	33	
2'280'612	SNP	C	T			1	33	
2'280'642	SNP	T	C			1	33	
2'280'673	SNP	C	A			1	33	
2'280'683	SNP	A	G			1	33	
2'280'702	SNP	C	T			1	33	
2'280'862	SNP	A	G			1	33	
2'280'879	SNP	A	G			1	33	
2'280'916	SNP	T	C			1	33	
2'280'926	SNP	G	C			1	33	
2'281'031	SNP	G	A			1	33	
2'281'058	SNP	C	G			1	33	
2'281'154	SNP	A	T			1	33	
2'281'262	SNP	T	C			1	33	
2'281'270	SNP	T	A			1	33	
2'281'440	SNP	A	T			1	33	
2'281'560	SNP	A	G			1	33	
2'281'590	SNP	T	C			1	33	
2'281'635	SNP	C	T			1	33	
2'282'082	SNP	A	G			1	33	
2'282'132	SNP	G	A			1	33	
2'282'187	SNP	T	C			1	33	
2'282'194	SNP	A	T			1	33	
2'282'315	SNP	A	G			1	33	
2'282'521	SNP	T	C			1	33	
2'282'761	SNP	A	G			1	33	
2'283'214	SNP	C	T			1	33	
2'283'224	SNP	G	A			1	33	
2'283'237	SNP	C	G			1	33	
2'283'539	SNP	G	A			1	33	
2'283'965	SNP	G	A			1	33	
2'283'992	SNP	C	A			1	33	
2'284'002	SNP	C	T			1	33	
2'284'720	SNP	C	G			1	33	
2'284'769	SNP	T	C			1	33	
2'285'147	insertion	G	GT			1	33	
2'285'345	SNP	G	A			1	33	
2'285'383	SNP	G	A			1	33	
2'286'301	SNP	T	G			1	33	
2'286'353	SNP	G	A			1	33	
2'286'400	SNP	T	G			1	33	
2'286'504	SNP	C	G			1	33	
2'286'523	SNP	C	A			1	33	
2'286'592	SNP	T	C			1	33	
2'286'604	SNP	G	A			1	33	
2'286'606	SNP	G	A			1	33	
2'286'988	SNP	A	G			1	33	
2'287'210	SNP	C	T			1	33	
2'287'370	SNP	A	G			1	33	
2'287'448	SNP	C	G			1	33	
2'287'529	insertion	A	AT			1	33	
2'287'596	insertion	C	CT			1	33	
2'287'746	SNP	T	C			1	33	
2'287'757	SNP	C	T			1	33	
2'287'765	SNP	T	C			1	33	
2'287'798	SNP	A	G			1	33	
2'287'996	SNP	G	C			1	33	
2'288'467	SNP	A	G			1	32	

UMD3.1 position	variant	reference allele	variant allele	ref/ref polled	ref/var polled	var/var polled	ref/ref horned	ref/var horned
2'288'990	SNP	A	G			1	32	
2'289'042	SNP	A	G			1	33	
2'289'346	SNP	G	A			1	33	
2'289'458	SNP	C	T			1	32	
2'289'716	SNP	C	T			1	33	
2'292'082	insertion	C	CACCT			1	33	
2'292'239	SNP	G	A			1	33	
2'292'304	SNP	G	A			1	33	
2'293'266	SNP	T	C			1	33	
2'293'846	SNP	G	A			1	33	
2'293'867	SNP	C	A			1	33	
2'293'870	SNP	T	C			1	33	
2'294'082	SNP	G	C			1	33	
2'294'184	SNP	C	T			1	33	
2'294'641	SNP	G	T			1	33	
2'294'647	SNP	T	C			1	33	
2'294'824	SNP	G	A			1	33	
2'294'855	SNP	C	T			1	33	
2'295'121	SNP	C	G			1	33	
2'295'487	SNP	G	A			1	33	
2'295'951	SNP	G	A			1	32	
2'297'070	SNP	C	T			1	33	
2'297'597	SNP	T	A			1	33	
2'298'042	SNP	A	G			1	33	
2'298'175	SNP	G	A			1	33	
2'298'226	SNP	C	A			1	33	
2'299'551	SNP	A	G			1	32	
2'299'669	SNP	C	G			1	33	
2'299'800	SNP	C	T			1	33	
2'299'901	SNP	A	G			1	33	
2'300'316	SNP	A	G			1	33	
2'300'391	deletion	TTAACTCACTGACAGTGAGTCGACAG	T			1	33	
2'300'451	SNP	C	T			1	33	
2'300'502	SNP	A	G			1	33	
2'300'761	SNP	G	A			1	33	
2'300'868	SNP	C	T			1	33	
2'300'871	SNP	G	A			1	33	
2'300'897	SNP	C	T			1	33	
2'300'924	SNP	G	A			1	33	
2'301'003	SNP	G	A			1	33	
2'301'036	SNP	T	C			1	33	
2'301'086	SNP	T	C			1	33	
2'301'104	SNP	T	A			1	33	
2'301'170	SNP	A	G			1	33	
2'301'257	SNP	T	C			1	33	
2'301'276	SNP	A	G			1	33	
2'301'300	SNP	A	G			1	33	
2'301'327	SNP	T	A			1	33	
2'301'358	SNP	G	A			1	33	
2'301'483	SNP	A	G			1	33	
2'301'520	deletion	AGAGAGAGC	A			1	33	
2'301'538	SNP	T	C			1	33	
2'301'708	SNP	G	A			1	32	
2'306'127	SNP	G	A			1	33	
2'306'341	SNP	G	A			1	31	
2'331'321	SNP	G	A			1	33	
2'335'134	insertion	A	AT			1	33	
2'336'578	SNP	T	G			1	33	
2'343'920	SNP	G	A			1	33	
2'354'603	SNP	T	A			1	33	
2'356'950	SNP	T	C			1	33	
2'381'155°	SNP	T	G			1	33	

* Variants were excluded because obligate heterozygous Pp polled animals carried two copies of the variant allele.

** Genotyping of additional animals for this variant was technically impossible.

*** One Simmental with polledness of unknown origin, two Limpurger with Scurs probably de novo mutation and one polled yak.

**** Differentiation between the heterozygous (ref/var) and homozygous (var/var) genotype not performed.

° Variants identified and ruled out by Allais-Bonnet et al. [3]

+ Variants identified by Allais-Bonnet et al. [3]