

Supplemental Table 1: Sequence information, homologies, primers, and PCR product size of DNA sequences assigned in the cattle genome.

Symbol	Locus		SHC/ RH Ref	RH map				NCBI						PCR				
	Type	CV		SHC/ RH Ref	accum. cR	LOD	Loci Pl	Locus dist. cR	RF	BTA build 4.0 C Mb	HSA build 36.3 C Mb	sequence for primer design	Bovine Ref seq	Human Ref seq	Forward primer 5'-3'	Reverse primer 5'-3'	A °C	L bp
BTA27																		
<i>ERICH1</i>	G	0.94		0.0	2.18	P	18.0	0.26	27	0.31	8	0.60	NM_207332	XM_590664	NM_207332	TCCCAATAACATCCATGTAGAAC	55	95
<i>DLGAP2</i>	G	0.90		18.0	3.31	F	3.5	0.24	-	-	8	1.43	XM_600714	XM_600714	NM_004745	TTGTGGGGCCATCTGTGT	60	112
<i>CLN8</i>	G	0.94		21.5	0.39	P	25.3	0.23	27	1.09	8	1.48	NM_001075941	NM_001075941	NM_018941	CGGACCTCCATCCACTCC	58	175
<i>ARHGEF10</i>	G	0.94		46.8	2.38	P	6.5	0.29	27	0.98	8	1.76	NM_014629	XM_001788838	NM_014629	CGTCCCTGCTGTCATAGTGG	55	163
<i>MYOM2</i>	G	0.87		53.3	1.55	P	13.7	0.27	27	1.36	8	1.98	NM_003970	NM_001038140	NM_003970	CCCTTCATGTGTCCAATGC	55	100
<i>CSMD1</i>	G	0.84		66.9	1.57	P	74.8	0.27	27	2.11	8	2.78	NM_033225	XM_605201	NM_033225	ATCCAGGAGATGCAGGTGAA	55	139
<i>BM3507</i>	M		*	141.7	2.57	P	25.8	0.20	27	5.20	-	-	G18516	G18516	-	GCCCAAAGAAAGAAGTATGTGC	62	176
<i>BMS2168</i>	M		*	167.5	3.18	F	12.7	0.18	27	3.89	-	-	G18975	G18975	-	TAGTGGGAGTCAGTCATGTG	58	160
<i>BMS2104</i>	M		*	180.1	FCy	F	4.0	0.17	27	5.56	-	-	G18921	G18921	-	CCTTTATATAATCAGGGTTTCTGGA	58	170
<i>ANGPT2</i>	G	0.94		184.2	2.11	P	33.6	0.18	27	5.62	8	6.34	NM_001147	NM_001098855	NM_001147	CAAAGGAATCGAAAGCAGGA	55	156
<i>AGPAT5</i>	G	0.84		217.8	3.57	F	25.5	0.14	27	5.94	8	6.55	NM_018361	NM_001075932	NM_018361	TGTGCAAGTTTGCAAGTTCT	55	115
<i>BNBD4</i>	G		*	243.3	1.92	P	20.1	0.11	27	6.89	-	-	AF008307	NM_174775	-	GCTTGAGAATTACATCCAGGACA	62	153
<i>DEFB1</i>	G		*	263.4	FCy	F	19.4	0.13	27	7.55	8	6.71	NM_175703	NM_175703	NM_005218	TGGGCTTCAACATCGGTTA	62	164
<i>GPM6A</i>	G		*	282.8	2.04	P	32.2	0.13	27	8.06	4	176.79	AY273942	NM_001075309	NM_005277	ATCCTCTAAGCTGCCGTCTG	55	391
<i>WDR17</i>	G	0.74		315.0	0.24	P	9.8	0.11	27	8.36	4	177.34	XM_001789371	XM_001789371	NM_170710	CCGCAGTTTCTGTCTCTGCT	58	150
<i>SPATA4</i>	G	0.90		324.8	4.59	F	14.4	0.11	27	8.42	4	177.34	NM_001011677	NM_001011677	NM_144644	AGAGGCCCGCTGTTTCATC	55	118
<i>ASB5</i>	G	0.90		339.2	4.71	F	13.5	0.14	27	8.43	4	177.37	BC118205	NM_001075744	NM_080874	ACTTCCATCAACATGACCAAG	55	195
<i>SPCS3</i>	G	0.90		352.7	0.93	P	18.7	0.16	27	8.49	4	177.47	CK973844	NM_001076993	NM_021928	CTGTGCCAGTTATCCAACCT	55	101
<i>VEGFC</i>	G	0.87		371.4	2.79	P	4.6	0.13	27	8.74	4	177.84	BP110008	NM_174488	NM_005429	ATGTGATGGTGGAGGAAAA	55	155
<i>AGA</i>	G	0.87		376.0	3.76	F	9.8	0.10	27	9.46	4	178.58	CK981021	NM_001075511	NM_000027	CGTCTTGGGTTACTCCGTA	58	107

<i>NEIL3</i>	G	0.90	385.8	2.53	P	15.5	0.12	27	9.32	4	178.46	NM_001034490	NM_001034490	NM_018248	GGAGGAAATCCAACCACAGC TGTCCTTCCCATTCTGCAAC TTTATTCTGGCCCATTTTG	55	154
<i>ODZ3</i>	G	0.97	401.3	-	B	0.0	0.11	27	14.65	4	183.48	XM_865074	XM_865074	XM_371717	TGACCAACGTGACATTTCCA TTGAACCATGGGTGTAGAACGA	58	154
<i>DCTD</i>	G	*	401.3	FCy	F	9.8	0.11	27	15.19	4	184.04	AW482279	NM_001101292	NM_001012732	GTGCAGCCAGATTGTCTATTG TCCCAGTCTTCGGGAGATTT AGCTTCTGGAAGCCTCGT	58	97
<i>WWC2</i>	G	0.90	411.1	0.55	P	20.9	0.11	27	15.40	4	184.35	CK770006	XM_611687	NM_024949	GCAGAGTCGCCTCAACGAT AGCACTGCCTCTCAGGTGAC CGATCCACTTTGTTGTCTGG	58	126
<i>CDKN2A</i>	G	0.90	432.0	1.12	P	15.5	0.11	27	15.56	4	184.60	XM_590926	NM_001046143	NM_017632	TTTCCCCGTAAGCACTTGG TCGAGGACTGTGACGATCAG CATCAGGAATTTATCCATCC	58	159
<i>ING1L</i>	G	0.90	447.5	2.60	P	0.0	0.10	27	15.60	4	184.66	XM_586825	XM_874513	NM_001564	AGTTCGAGCACTTGGAAAGG TCACTGGAGACGATGGTCAG CTTTAATCAGCACACAGCTTCCCA	55	165
<i>CCDC111</i>	G	0.90	447.5	-	B	9.8	0.10	27	16.44	4	185.80	CB431232	NM_001075488	NM_152683	ATATGTGCTAGAAGTTTGGTCAACC	58	172
<i>C4orf41</i>	G	0.90	457.3	2.65	P	20.9	0.12	27	15.67	4	184.81	BM287361	NM_001102197	NM_021942	ATATGTGCTAGAAGTTTGGTCAACC	55	100
<i>TGLA179</i>	M S	*	478.3	2.46	P	16.1	0.10	27	12.58	-	-	STS:251232	STS:251232	-	TTTCCCCTAAGCACTTGGAAAGG TCACTGGAGACGATGGTCAG CTTTAATCAGCACACAGCTTCCCA	60	91
<i>CASP3</i>	G	0.90	494.4	FCy	F	15.5	0.09	27	16.44	4	185.78	CK958538	NM_001077840	NM_004346	ATATGTGCTAGAAGTTTGGTCAACC	52	169
<i>ACSL1</i>	G	*	509.8	0.16	P	42.1	0.12	27	16.49	4	185.91	AY273941	NM_001076085	NM_001995	TACTTTTCTGGCGAAATGC AATGCCAGAGCTGGTTGACT GCGTACCAGAAGGTGGTGAG	62	102
<i>SLC25A4</i>	G	0.84	551.9	2.05	P	40.3	0.17	27	16.80	4	186.30	NM_174658	NM_174658	NM_001151	GCCCTGGGAGACTGCTGGT GGCGCGGTAGATGATGATAC TCCAGGGCACATATGGTTAC	55	101
<i>UFSP2</i>	G	*	592.3	FCy	F	13.9	0.14	27	16.96	4	186.55	AW484589	NM_001076477	NM_018359	GGTGTTTGAACCAGGAGCAG AGTCGGATGTGTACCGGATG AGCGCCATCGTTCCTAGTT	60	103
<i>PDLIM3</i>	G	0.90	606.2	0.12	P	13.9	0.13	27	17.02	4	186.65	AW437727	NM_001034646	NM_014476	CGCCCTACAGTACCCAGTCA GCATCCTTAAACGCATTGGT TAGACCTCTCTATAATGGC	60	103
<i>SORBS2</i>	G	0.87	620.1	2.08	P	24.5	0.14	27	17.16	4	186.74	XM_865206	XM_865206	NM_003603	TCTTCTGGTGTAGTGAAGA GTTAAACGCTTCTTGGTTAACATGC GTACTGGAACAATGGCGATCTA	58	100
<i>TLR3</i>	G	*	644.6	1.96	P	14.4	0.13	27	17.48	4	187.22	NM_001008664	NM_001008664	NM_003265	TCGAGTCACCTAATGTGTTC AGTTTCAACAAGGCAATGTCA CCTGTCTCTGAAGCACACG	50	115
<i>CYP4V2</i>	G	0.90	659.0	0.49	P	19.4	0.12	27	17.56	4	187.34	CB424919	NM_001034373	NM_207352	CTCGACCACGTTGCTGTAAA ATTTTCATCGTTCGGATGCTC AAGTCTGGGGCTTCAGTTT	55	150
<i>KLKB1</i>	G	0.87	678.4	1.90	P	24.5	0.14	27	17.58	4	187.38	AY569316	NM_001046352	NM_000892	AGGGGGAACCTACAGCCTGAT CCACTCACGATGCTGAAGAA GTAGAAGTTAGTGACTGTCTCC	55	151
<i>F11</i>	G	*	702.9	0.40	P	9.5	0.13	27	17.60	4	187.42	U85057	NM_001008665	NM_000128	CCTCAGACCGTTGCTGTAAA ATTTTCATCGTTCGGATGCTC AAGTCTGGGGCTTCAGTTT	55	106
<i>MTNR1A</i>	G	*	712.4	0.48	P	4.7	0.11	27	17.73	4	187.69	U73327	XM_614283	NM_005958	AGGGGGAACCTACAGCCTGAT CCACTCACGATGCTGAAGAA GTAGAAGTTAGTGACTGTCTCC	60	118
<i>FAT2</i>	G	*	717.1	FCy	F	9.2	0.12	27	17.76	4	187.74	AW356960	XM_864984	NM_005245	AAGTCTGGGGCTTCAGTTT AGGGGGAACCTACAGCCTGAT CCACTCACGATGCTGAAGAA	58	125
<i>CA209</i>	M S	*	726.3	2.52	P	4.4	0.14	27	18.26	-	-	U32921	U32921	-	GTAGAAGTTAGTGACTGTCTCC CCTCAGAGCCCCATCATTTCC ACGCAGACCTTAGCATAGGAGA	58	115
<i>INRA016</i>	M S	0.90	730.7	2.59	P	14.4	0.13	27	18.47	-	-	X67828	X67828	-	GTCGCAATGAGTTGGACACAAC TTAACTGCCTGAAATGACG AGGGAAACAAACGAATGTGG	58	136
<i>CNOT7</i>	G	*	745.1	3.94	F	14.4	0.12	27	21.71	8	17.13	AW289341	NM_001034312	NM_013354	TTAACTGCCTGAAATGACG AGGGAAACAAACGAATGTGG	55	107

<i>PDGFRL</i>	G	*	759.5	2.20	P	9.2	0.13	27	21.34	8	17.47	AW313868	NM_001035301	NM_006207	CGCAGACCTCCAACTAAAAG CAAAAACCTTGCTCCTTTAATAGAAAAT	55	200
<i>MTMR7</i>	G	0.87	768.7	2.47	P	8.9	0.13	27	21.59	8	17.20	NM_001075641	NM_001075641	NM_004686	CCGAACTGTACGTTCCCAAG TCTTTATAGTAGTAAGAAAGGGCAGGA	58	103
<i>ZDHHC2</i>	G	0.94	777.6	2.59	P	13.5	0.15	27	21.73	8	17.05	XM_616436	XM_616436	NM_016353	GAGGCATTTAGAAGCCAGT CCTCTTCTCATCACCACAAAACC	58	102
<i>MTSG1</i>	G	*	791.0	2.58	P	9.2	0.14	27	21.27	8	17.70	AW654301	NM_001075692	NM_001001924	CATTTATGCCAAGGTGGACAG GAGATTGCCATGTGCTTGTGTC	55	108
<i>ASAH1</i>	G	*	800.2	FCy	F	4.6	0.12	27	20.82	8	17.95	AW463906	XM_587784	NM_004315	CGGTGTACACAGTCTTGATAGATG TGTGTGCTCACCACCCCTATG	60	93
<i>PCMI</i>	G	*	804.8	0.53	P	0.0	0.13	27	20.87	8	17.82	AW344602	XM_592336	NM_006197	AACCCTTTGCCTTTACCTTTAAC TATCAGGACTTCCAGCCAAAG	55	109
<i>MTUS1</i>	G	0.90	804.8	-	B	9.5	0.13	27	21.27	8	17.70	XM_614438	-	NM_001001924	TGAGGAAAAACCTCCAAAACC AGTTTTGAGAAAGTGCGTGTGA	55	100
<i>FGL1</i>	G	*	814.3	0.61	P	30.9	0.11	27	21.02	8	17.76	AW487058	NM_001034313	NM_004467	CTGCAAACCTGAATGGCTTC TTTCAAGGAATACCACCATCC	60	100
<i>MSR1</i>	G	*	845.2	2.56	P	0.0	0.16	27	22.86	8	16.01	AW461872	NM_174113	NM_002445	CAAGGATAACTCCCTGATCG TGCTGATGACTTGTCCAGAGA	60	119
<i>TUSC3</i>	G	0.94	845.2	-	B	8.9	0.16	27	23.23	8	15.44	AW485171	NM_001080914	NM_006765	TTCATGCTTTTAAAGTATTCACTCA TCTGTACAATCCCAAGAACTGC	50	101
<i>DLC1</i>	G	*	854.1	FCy	F	9.2	0.13	27	25.71	8	12.90	AW427798	NM_001102493	NM_006094	CAGCACCTCTGGGATGTAGACT ACATAGTCCCGAGCAGGATG	55	119
<i>KIAA1456</i>	G	0.94	863.3	0.35	P	4.4	0.13	27	25.98	8	12.85	AW632623	NM_001076832	NM_020844	GAAATGGCCAGGGTCTAGT CCAGGGAAACAAGCACGTC	58	105
<i>C8orf79</i>	G	0.97	867.7	0.46	P	9.2	0.14	27	25.98	8	12.85	AW632623	NM_001076832	NM_001099677	TCTGAAAGTGAACAGCCAGGT TGACGCCATATGGAGATGATG	58	158
<i>LONRF1</i>	G	*	876.9	2.95	F	4.6	0.12	27	26.21	8	12.62	AW445963	XM_001788551	NM_152271	AAATAGAGAACCTCCGGCAAC GCATTGATCCAAAGTCTGAA	55	114
<i>PPP1R3B</i>	G	0.97	881.4	3.32	F	19.4	0.13	27	27.18	8	9.03	XM_592275	NM_001103247	NM_024607	ATCGAGTGCCGGTACAGC ACACCCGCTTCTTACACCTTT	60	175
<i>PRAGMIN</i>	G	0.90	900.8	0.42	P	18.7	0.13	27	26.42	8	8.21	CK770308	XR_028156	XM_291277	GGTCCGGACAGTTAACACCT AGTCTGGGCTGCTCAGGTAG	55	158
<i>MFHAS1</i>	G	0.94	919.6	2.25	P	19.4	0.16	27	26.86	8	8.67	XR_027516	XR_027516	NM_004225	GCCGTCCATATGTTCCGGTAA ACAGCGTCCAGATCAACAAC	58	172
<i>FLJ39185</i>	G	*	939.0	2.56	P	35.0	0.11	27	26.85	8	8.68	AW669040	AW669040	AK096504	AGACTGTTTTGTACCCAGGAA TCGACTGTTAAAAATGCGGAAC	55	117
<i>THEX1</i>	G	0.77	973.9	1.97	P	17.0	0.19	27	27.06	8	8.89	CK775499	NM_001038192	NM_153332	TCAAGGGGAGAGCCAATAAA GGAGGGCATAATTGAATTCCT	55	158
<i>TNKS</i>	G	0.94	990.9	1.74	P	37.3	0.16	27	27.49	8	9.45	BE684244	XM_615006	NM_003747	TTTGGAGAAAGGACGTGGT AGTTATCCCTGGCGTTTGG	55	166
<i>DCTN6</i>	G	0.94	1028.2	1.54	P	38.7	0.19	27	28.40	8	30.13	NM_001075638	NM_001075638	NM_006571	CGTATGTGGGCAGAAATGTG GCAGGCAGTCTCCACCATAG	58	117
<i>RBPMS</i>	G	*	1067.0	1.86	P	8.9	0.14	27	28.58	8	30.22	AW462188	NM_001046535	NM_001008710	CGGGGAAGGGAGAGTGG TGTTCTCCTTCTCGGCTTTG	58	113
<i>GTF2E2</i>	G	*	1075.9	1.56	P	26.6	0.14	27	28.78	8	30.55	AW426828	NM_001046065	NM_002095	CGCTACTTCTCAGTGGCTCCT ATCTTTTGGAAATAAACAAATATTGCAT	58	100
<i>GSR</i>	G	0,87	1102.5	FCy	F	49.5	0.21	27	28.88	8	30.65	AW465212	XM_001788680	NM_000637	CAGGGAATTGGATGTGATGA AGCGAAGTGTGACCAGCTCT	55	130
<i>CSSM043</i>	M S	*	1152.0	FCy	F	18.9	0.16	27	30.07	-	-	U03824	U03824	-	AAAACCTGGGAACCTGAAAACCTA GTTACAAATTTAAGAGACAGAGTT	58	255

<i>NRG1</i>	G	0.94	1170.9	1.93	P		0.12	27	30.51	8	31.62	NM_174128	NM_174128	NM_013964	ACGGAAGCTTCATGACC ACCAGCTGCACGTTCTCG	60	117
						Av.	0.145										
BTAS																	
LG1																	
<i>ANXA10</i>	G	1.00	0.0	2.32	P	18.3	0.22	8	0.21	4	169.25	CK974509	XM_581595	NM_007193	GGCTTCCATAATAAAACCGTGA TGTCGTGGAAAAGGGACTTC	58	112
<i>PALLD</i>	G	1.00	18.3	3.77	F	11.3	0.19	8	0.42	4	169.65	CK947525	XM_869983	NM_016081	GGTGGCAAATAATGCTGCT TGGACCTCTCTTTCTTGCA	58	118
<i>AADAT</i>	G	1.00	29.6	3.52	F	3.7	0.16	8	1.67	4	172.21	CB455691	NM_001015551	NM_016228	TCTGTTCTGGAGAAGCTGAAGA TATTCATGCTTCCGGGATGT	58	93
<i>CBR4</i>	G	1.00	33.3	2.17	P	11.0	0.17	8	0.79	4	170.14	CK846272	NM_001083717	NM_032783	CAATGGACCCTCTCTGCTGT GAAGATATGCTCTCTCAGCTCCA	58	100
<i>CLCN3</i>	G	1.00	44.3	0.98	P	12.0	0.20	8	1.31	4	170.77	CK833623	XM_875593	NM_001829	GAGTACATCGTCCCTCAT TATGTCGTCCACCGTCAATG	58	228
<i>SH3RF1</i>	G	1.00	56.3	1.71	P	85.8	0.20	8	0.88	4	170.25	BF042386	NM_001098065	NM_020870	GAAGTGGTACCACGGAGAGG CAAACGGAGGCAATCTTTG	58	158
LG2																	
<i>HMGB2</i>	G	0.97	0.0	5.39	F	22.7	0.18	8	5.59	4	174.48	CK771774	NM_001037616	NM_002129	TCTTCGTACGCCTTCTTCGT CTCTCGGAACATTTCTTGGAA	58	104
<i>SCRGI</i>	G	1.00	22.7	5.39	F	32.4	0.22	8	5.64	4	174.54	CN441607	NM_001100370	NM_007281	CAACTGTCCAGCCTTCCAG CGCTGAAGTTGCAGTAACAGAC	58	116
<i>KIAA1712</i>	G	1.00	55.1	1.68	P	32.4	0.16	8	6.53	4	175.44	BI774464	NM_001076833	NM_030633	GAATGCCAAGAAAAGCTTAAGAA AGATAAAAGCATTTCTGTTTCAAGT	58	153
<i>FBXO8</i>	G	1.00	87.5	1.91	P	25.4	0.22	8	6.49	4	175.39	AW356344	NM_001015667	NM_012180	CTGTGGAGAGTGGCCAGAA TGGTGTGAGACATGTTGCTG	58	112
<i>HPGD</i>	G	*	112.9	3.40	F	35.8	0.23	8	6.72	4	175.64	BC102458	NM_001034419	NM_000860	TCCCATGTTTCTTCTTTTCAA TGGCTGCTAATCTTATGAACAGT	55	104
<i>GLRA3</i>	G	*	148.7	3.57	F	67.9	0.18	8	6.92	4	175.80	NM_006529	XM_866645	NM_006529	TCGTCAGAAATGGAATGATCC AGTTGGCACCCCTTTTCATTG	55	131
<i>CTSB</i>	G	*	216.6	1.68	P	23.3	0.31	8	7.45	8	11.73	NM_174031	NM_174031	NM_001908	CCTGTGAGCACCATGTGAAC TTCTTTGTAGGACGGGCTGT	55	107
<i>BLK</i>	G	1.00	239.9	5.32	F	17.1	0.23	8	7.70	8	11.38	BC123559	NM_001075968	NM_001715	AGGTGCCCTTTTCTCTGTCTGTG GGAGATGTAATAGCCGCCTTC	58	100
<i>XKR6</i>	G	1.00	257.0	5.39	F	26.0	0.24	8	8.02	8	10.79	XM_590278	XM_590278	NM_173683	AGGGCCCTCATTAAGATTG GAGCGAAGACTCATACTGTAGCA	58	181
<i>MTMR9</i>	G	0.97	283.0	3.39	F	15.2	0.19	8	7.87	8	11.17	XM_585423	NW_936823	NM_015458	CAGCAAGCAGAAGTGGGAAT ACTTTCATGTTGCCCAGGA	58	169
<i>SOX7</i>	G	1.00	298.2	0.60	P	15.2	0.17	8	8.71	8	10.61	XM_615317	XM_615317	NM_031439	TCGACCAGTACTTGAACACTCCT GGAATGAGGCTGGTCTCTG	58	116
<i>PINX1</i>	G	-	313.4	1.86	P	14.8	0.19	8	8.35	8	10.65	BE683974	NM_001034553	NM_017884	AGACTCCCCAGACAACAAGG CTTCCCTTTGTGAATTCATATAGT	55	100
<i>MSRA</i>	G	0.94	328.2	0.46	P	14.5	0.19	8	8.81	8	9.90	NM_174114	NM_174114	NM_012331	AGCATGGTTTTGGGCTGAT CTTTTAATACCAGGGGACAA	58	152
<i>RP1L1</i>	G	1.00	342.7	3.01	F	30.8	0.21	8	8.54	8	10.50	XM_867581	XM_867581	NM_178857	GATCATGAAGGCACTGATGG CTCACTTGTAGCGGGAGA	60	171
<i>EXTL3</i>	G	*	373.5	0.98	P	42.6	0.21	8	10.04	8	28.61	AW657227	NM_001082473	NM_001440	AGTCACTCACACAGCTCACGA CCTTGAATGGCAATCTGAAA	58	104
<i>CLU</i>	G	*	416.1	1.54	P	70.0	0.17	8	11.29	8	27.51	AW446457	NM_173902	NM_001831	AGCTGGCGGAGAAGTTTACAG	55	103

