Locus on BTA6	BAC ID with insert size and BAC position on BTA6 scaffold [Mb]	ETS_ID	Similarity to bovine genome sequence	Position [Mb]	Similarity to other transcripts	Similarity to other genome sequences
FBNS4	BBI_750F05243 (99 Kb) NW_001495159.2: 41.414-41.513	20835	NW_001495159.2, KCNIP4 (NM_001076935, exon 5),	BTA6: 41.423	Exon 13 of human KCNIP4	
		20849	NW_001495159.2, KCNIP4, exon 2	BTA6: 41.440	Exon 9 of human KCNIP4	
		20853	NW_001495159.2, KCNIP4, intron 1	BTA6: 41.464		
		20858	NW_001495159.2, KCNIP4, intron 1	BTA6: 41.495		Intron 4 of human KCNIP4
		20837	NW_001495159.2, KCNIP4, intron 1	BTA6: 41.508		Human genomic contigs, e.g. NW_921665, altern. assembly
		20866	-----------------------------	UN	11 bovine ESTs (e.g. DY055462), exons 11 and 12 of human KCNIP4	
BMS382	BBI_750F06108 (110 Kb) NW_001495159.2: 42.091-42.201	25626	NW_001495159.2, 584.6 Kb 5' to KCNIP4	BTA6: 42.107	Ovine EST EE834255, Bovine predicted transcript hmn 107334 (gnomon model)	
		25624	NW_001495159.2, 586.2 Kb 5' to KCNIP4	BTA6: 42.109	Ovine EST EE834255, Bovine predicted transcript hmm 107334 (gnomon model)	
		25316	NW_001495159.2, 591 Kb 5' to KCNIP4	BTA6: 42.114	Ovine EST EE834255	Human genomic contigs, e.g. NW_923238, altern. assembly
		25618	NW_001495159.2, 592.9 Kb 5' to KCNIP4	BTA6: 42.116	Ovine EST EE834255	
		25599	NW_001495159.2, 594.7 Kb 5' to KCNIP4	BTA6: 42.119	Ovine EST EE834255	
		25609	NW_001495159.2, 611.4 Kb 5' to KCNIP4	BTA6: 42.134	Bovine ESTs DY149610, DY194833, DY1944707 assigned to NW_00149515 Ovine EST EE834255	
		25315	NW_001495159.2, 622.5 Kb 5' to KCNIP4	BTA6: 42.145	Ovine EST EE834255	
		25319	NW_001495159.2, 649.2 Kb 5' to KCNIP4	BTA6: 42.172	Ovine ESTs EE834255 and EE870115	Human genomic contigs on multiple chromosomes
		25314	NW_001495159.2, 652.9 Kb 5' to KCNIP4	BTA6: 42.176	Ovine EST EE834255	
		25324	NW_001495159.2, 655.2 Kb 5' to KCNIP4	BTA6: 42.178	Ovine EST EE834255	
		25614	NW_001495159.2, 658.5 Kb 5' to KCNIP4	BTA6: 42.182		
		25619	NW_001495159.2, 662.3 Kb 5' to KCNIP4	BTA6: 42.186		
		25313	-----------------------------	UN		
		25612	-----------------------------	UN		
		25613	-----------------------------	UN		
FBN12	BBI_750M16218 (64 Kb) NW_001495159.2: 43.3825-43.4460	20687	NW_001495159.2, 29.8 Kb 5' to GPR125, (XM_614752.3)	BTA6: 43.383		Human genomic contigs, e.g. NW_921594, NW_922185, altern. assembly
		20708	NW_001495159.2, 44.1 Kb 5' to GPR125, 44.4 Kb 3' to GBA3 (NM_001787544.3)	BTA6: 43.397		Human genomic contigs, e.g. NW_922099, altern. assembly
		21395	NW_001495159.2, 63 Kb 5' to GPR125, 25.5 Kb 3' to GBA3	BTA6: 43.416	Bovine predicted transcript hmm 133334 (gnomon model)	
		25598	NW_001495159.2, 70.4 (78.3) Kb 5' to GPR125, 18.1 (10.2) Kb 3' to predicted	BTA6: 43.423 and 43.431	Bovine predicted transcript hmm 133334 (gnomon model)	Human genomic contig, NW_921914, altern. Assembly

			GBA3 (XM_)			Mouse genomic contig NT_39305 on MMU5, 107 Kb 5’ to Gpr125, 1.29 Mb 3’ to pargc1a
		20309	NW_001495159.2, 76 Kb 5’ to GPR125, 12.5 Kb 3’ to GBA3	BTA6: 43.429	Bovine predicted transcript hmm 133334 (gnomon model)	
		20308	NW_001495159.2, 77 Kb 5’ to GPR125, 11.5 Kb 3’ to GBA3	BTA6: 43.4301	Bovine predicted transcript hmm 133334 (gnomon model)	
		20311	NW_001495159.2, 77.1 Kb 5’ to GPR125, 11.4 Kb 3’ to GBA3	BTA6: 43.4302	Bovine predicted transcript hmm 133334 (gnomon model)	Human genomic contigs, e.g. NW_921594, altern. assembly
		20565	NW_001495159.2, 79 Kb 5’ to GPR125, 9.4 Kb 3’ to GBA3	BTA6: 43.432		Human genomic contigs on HSA18 and HSA12
		20691	UN, partiell repetitive	UN		
BM143	BBI_750F22162 (76 Kb) NW_001495167.2: 44.107-44.183	21697	NW_001495167.2	BTA6: 44.114		
		21696	NW_001495167.2	BTA6: 44.1165 and 44.118		Human genomic contig NT_006316 on HSA4, 442 Kb 5’ to LOC643751 , 625 Kb 3’ to PPARGC1A, Mouse genomic contig NT_39305 on MMU5, 733 Kb 5’ to Gpr125, 663 Kb 3’ to Ppargc1a
		21688	NW_001495167.2	BTA6: 44.1178		Human genomic contigs, e.g. NW_922185, altern. assembly
		20396	NW_001495167.2	BTA6: 44.134		
		21685	NW_001495167.2	BTA6: 44.141		
		20400	NW_001495167.2	BTA6: 44.168		
		20395	NW_001495167.2	BTA6: 44.170		
		21687	NW_001495167.2	BTA6: 44.175		Human genomic contigs, e.g. NW_922900, altern. assembly
FBNS10	BBI_750J07162 (66 Kb) NW_001495167.2: 45.374-45.440	25285	NW_001495167.2, 554.4 Kb 5’ to PPARGC1A (NM_177945.3)	BTA6: 45.393		
		25657	NW_001495167.2, 77.9 Kb 3’ to DHX15 (NM_001098018.3)	BTA6: 45.407		
		25310	NW_001495167.2, 73.6 Kb 3’ to DHX15	BTA6: 45.411		Human genomic contig NT_006316 on HSA4, 544 Kb 5’ to PPARGC1A, 37 Kb 3’ to LOC729175
		25303	NW_001495167.2, 580.3 (581.1, 581.5) Kb 5’ to PPARGC1A, 65.8 (65.1, 64.7) Kb 3’ to DHX15	BTA6: 45.4191, 45.4198, and 45.4202		Human genomic contig NT_006316 on HSA4, 552 Kb 5’ to PPARGC1A, 29 Kb 3’ to LOC729175
		25299	NW_001495167.2, 59.8 Kb 3’ to DHX15	BTA6: 45.425		Human genomic contig NT_006316 on HSA4, 560 Kb 5’ to PPARGC1A, 22 Kb 3’ to LOC729175 Mouse genomic contig NT_39305 on MMU5, 240 Kb 5’ to Ppargc1a, 56 Kb 3’ to Dhx15
		25292	NW_001495167.2, 54.6 Kb 3’ to DHX15	BTA6: 45.430		

		25283	NW_001495167.2, 49.3 Kb 3’ to DHX15	BTA6: 45.435		
		25294	NW_001495167.2, 47.8 Kb 3’ to DHX15	BTA6: 45.437	Bovine EST DY067729 Bovine predicted transcript hmm 183334 (gnomon model)	
BL1099	BBI_750C04346 (60 Kb) NW_001495169.2: 49.074-49.134	26271	NW_001495169.2	BTA6: 49.080	Bovine predicted transcript hmm 281334 (gnomon model)	Human genomic contig NW_922643, altern. assembly
		22258	NW_001495169.2	BTA6: 49.088		
		26268	NW_001495169.2	BTA6: 49.118		
		26267	NW_001495169.2	BTA6: 49.123		
FBNS13	BBI_750K15348 (865 Kb) NW_001495170.2: 50.439-51.304	25328	NW_001495170.2, 228.8 Kb 3’ to PCDH7 (XM_864701)	BTA6: 51.287		
		25329	NW_001495170.2, 274.5 Kb 3’ to PCDH7	BTA6: 51.241		
		25336	NW_001495170.2, 268.5 Kb 3’ to PCDH7	BTA6: 51.247		
BMS518	BBI_750E20138 (50 Kb) NW_001495170.2: 51.287-51.337	25582	NW_001495170.2, 208.3 (209.0) Kb 3’ to PCDH7	BTA6: 51.3069 and 51.3075		
		25584	NW_001495170.2, 202.4 Kb 3’ to PCDH7,	BTA6: 51.313		
		26352	NW_001495170.2, 191.1 Kb 3’ to PCDH7	BTA6: 51.3248		
		26342	NW_001495170.2, 191 Kb 3’ to PCDH7	BTA6: 51.325		
		26308	NW_001495170.2, 184.4 Kb 3’ to PCDH7	BTA6: 51.332	Bovine ESTs assigned to a number of chromosomes	Human genomic contigs, e.g. NW_921858, altern. assembly
TGLA37	BBI_750E07177 (77 Kb) NW_001495170.2: 52.453-52.530	16065	NW_001495170.2, 467.3 Kb 5’ to PCDH7	BTA6: 52.467		
		15338	NW_001495170.2, 514.9 Kb 5’ to PCDH7	BTA6: 52.5145		Human genomic contig NW_921594, altern. assembly
		15335	NW_001495170.2, 516.9 Kb 5’ to PCDH7	BTA6: 52.516		
		16062	NW_001495170.2, 523.2 Kb 5’ to PCDH7	BTA6: 52.523		Human genomic contig NW_921594, altern. assembly
TGLA37	BBI_750B13346 (72 Kb) NW_001495170.2: 52.458-52.530	26263	NW_001495170.2, 469.4 (468.9) Kb 5’ to PCDH7	BTA6: 52.4687 and 52.4683)		
		26264	NW_001495170.2, 524.5 Kb 5’ to PCDH7	BTA6: 52.524		
		22268	NW_001495170.2, 1,013.6 Kb 5’ to PCDH7	BTA6: 53.013		Human genomic contig NW_921789, altern. assembly
		22269	NW_001495170.2, 1,060.3 Kb 5’ to PCDH7	BTA6: 53.059		Human genomic contigs, e.g. NW_921858, NW_921665, altern. assembly
		22277	NW_001503872.2	UN	Bovine predicted transcript hmm 2103723 (gnomon model)	Mouse genomic contig NT_39606 on MMU14, Polr3d
FBN13	BBI_750M0258 (198 Kb) NW_001495175.2: 56.090-56.288	15498	NW_001495175.2, partial repetitive sequence	BTA6: 56.100		Human genomic contig NW_921594, altern. assembly
		15495	NW_001495175.2 and NW_001495179.2	BTA6: 56.115 and 56.253		Human genomic contig NW_921914, altern. assembly
		14638	NW_001495179.2	BTA6: 56.278		
FBN13	BBI_750B0172 (92/83 or 48/222Kb) NW_001495175.2/NW_001495179.2: 56.128/56.267-56.175/56.350	16042	NW_001495179.2	BTA6: 56.280		Human genomic contig NW_921699, altern. assembly

		16037	NW_00149517.2	BTA6: 56.2878 and 56.2883		Human genomic contig NW_922974, altern. assembly
		15239	NW_001495179.2	BTA6: 56.289		
		15246	NW_001495179.2	BTA6:56.292	Bovine ESTs DN840825, DN845774	
		16035	NW_001495179.2	BTA6: 56.302	Porcine EST EW1959132	
		16667	NW_001495179.2	BTA6: 56.304	Bovine predicted transcript hmm 37344 (gnomon model) and hypothetical locus LOC100140872	Human genomic contigs on HSA10 and HSA8, PHYHIPL Mouse genomic contigs on MMU10 and MMU14, Phyhipl
		16041	--------------------------	UN		Human genomic contigs NW_921665, NW_921517, altern. assembly
BM4528	BBI_750A1391 (33 Kb) NW_001495186.2: 65.832-65.865	20748	NW_001495186.2, 8.0 Kb 5' to KCTD8, (XM_590048)	BTA6: 65.588	Bovine predicted transcript hmm 325344 (gnomon model)	
		20751	NW_001495186.2, KCTD8, intron	BTA6: 65.835		Human genomic contigs on HSA6, HSA12, HSA5
		20746	NW_001495186.2, KCTD8, intron	BTA6: 65.853		Human genomic contig, NW_922610, altern. assembly, pred Hmm438037
		23447	NW_001495186.2, KCTD8, intron	BTA6: 65.8545		
		23435	NW_001495186.2, KCTD8, intron	BTA6: 65.860		Human genomic contigs, e.g. NW_922226, altern. assembly
		20758	NW_001495186.2, KCTD8, intron	BTA6: 65.865		Human genomic contigs, e.g. NW_921858,, NW_921665 altern. assembly
		20749	NW_001495186.2, KCTD8, intron	BTA6: 65.879		
		23438	NW_001495186.2, 2.0 Kb 5' to KCTD8	BTA6: 65.882	Bovine predicted transcript hmm 325344 (gnomon model)	
		23437	NW_001503872.1	UN	Bovine predicted transcript hmm 2102733 (gnomon model) and hypothetical locus LOC788223	Mouse genomic contig NT_39606 on MMU14, Pol3rd
		23434	NW_001502282, NW_001501795, NW_001495173.1	UN BTA6:46.99	Repetitive motifs in bovine ESTs assigned to multiple chromosomes	Human genomic contigs, e.g. NW_921858,, NW_921665 altern. assembly
FBN14	BBI_750C1821 (83 Kb) NW_001495201.2: 78.415-78.498	16053	NW_001495201.2	BTA6: 78.430		
		16662	NW_001495201.2	BTA6: 78.435		Human genomic contigs, e.g. NW_921665 and Mouse genomic contig NW_001037873, altern. assemblies
		16048	NW_001495201.2	BTA6: 78.448		Human genomic contigs, e.g. NW_921665 altern. assembly
		15328	NW_001495201.2	BTA6: 78.4574/78.4576 and 78.4612/78.4614		Human genomic contig NT_022778 on HSA4, 144 Kb 5' to LOC644419, 1.2 Mb 3' to LOC644484
		16050	NW_001495201.2	BTA6: 78.471		Human genomic contigs, e.g. NW_922185, altern. assembly