

Suppl. Fig. 1. Chromosome homology between BTA4 break point containing region and human genome. Only a part of the genes located in this region is shown. The analysis shows that the cattle 4q14 region is homologous to 2 separated human regions, both located on HSA7, HSA7p21 and HSA7q21. All genes examined followed the right expected orientation, except gene RUNDC3B (this is probably ascribable to a genome assembly error).

				HSA	cdsStart	name
				chr7	7.676.630	RPA3
			1-	chr7	8.008.981	GLCCH
			$ / \rightarrow$	chr7	8.153.552	ICA1
_	cdsStart	name	1/	chr7	8.475.343	HXPH1
÷	16.005.576	RPA3	//	chr7	9.675.447	PER4
	16.399.052	GLCCH 4		chr7	10.973.262	NDUFA4
1	16.510.379	ICA1	1	chr7	11.013.950	PHF14
1	16.841.314	NXPH1	1-	chr7	11.415.420	THSD7A
-	19.458.240	IIDUFA4	1-	chr7	12.254.436	TMEM106B
	19.482.853	PHF14	1-	chr7	12.370.808	VWDE
6	20.166.359	THSDTA		chr7	12.610.412	SCIII
5	21.088.099	TMEM106B	//	chr7	12.727.879	ARL4A
1	21.157.667	WWDE 4	1/-	chr7	13.935.490	ETV1
	21.344.946	SCIN	//	chr7	14.188.755	DGKB
	21.573.935	ARL 4A	1-	chr7	15.240.909	TMEM195
	23.073.858	ETV1	//	chr7	15.652.011	MEOX2
	23.366.180	DGKB		chr7	16.131.319	LOC729920 SOSTDC1
	24.580.091 25.060.618	MEOX2	// :	chr7 chr7	16.502.172 16.572.119	DT932641(est)
1		LOC729920		chr7	16.640.385	
	25.649.177 26.098.540	SOSTDC14	1	chr7	16.705.068	AIIKMY2 BZW2
	26.160.871	MGC165762	//	chr7	16.793.592	TSPAH13
3	26.227.139	ANKMY2	1	chr7	16.832.531	AGR2
	26.283.679	BZW2	/	chr7	17.338.888	AHR
	26.381.143	TSPAII13	$ \rightarrow $	chr7	17.833.668	SIIX13
	26.426.658	AGR2	1-	chr7	18.066.448	PRPS1L1
	27.033.125	AHR 4	/	cht7	18,535,925	HDACS
	27.605.197	SNX13	/	chr7	19.156.335	TWIST1
	27.783.692	PRPS1L1	1-	chr7	19.184.484	FERD3L
	28,419,105	HDAC9	1-	chr7	19.737.938	TWISTIN
	29.018.354	TWISTI		chr7	19.761.697	TMEM196
	29.054.935	FERD3L	1-	chr7	20,180,568	MACCI
	29.683.377	TWISTIN	1/	chr7	20.371.429	ITG88
1	29.706.843	TIMEN/196	1-	chr7	20.691.045	ABCB5
	30.047.668	MACCI	1-	chr7	20.823.908	SP8
1.5	30.314.026	ITGB8		chr7	20.867.439	RPL23P8
	30.677.519	ABCB5	-	chr7	21.467.869	SP4
1	30.712.760	SP8	/	chr7	21.582.863	DIIAH11
F. I	31,521.627	SP4		chr7	21.941.939	CDCA7L
K	31.608.413	DNAH11	/	chr7	22.162.023	RAPGEF5
13	31.980.426	CDCA7L+		chr7	22.766.881	IL6
1	32,203,709	RAPGEFS		chi T	22,852,788	TOMM7
	32.756.596	IL6		chr7	22.896.304	SHORD93
	32.839.149	SNORD93		chr7	22.985.207	FAM126A
	32.901.052	FAM126A		chr7	23.157.529	KLHL7
	33.077.868	KLHL7		chr7	23.221.704	NUPL2
-	33.155.286	NUPL2		chr7	23.286.476	GPHMB
10	33.202.570	GPNMB		chr7	23.338.971	C7orf30
	33.249.243	C7orf30		chr7	23.351.980	IGF2BP3
	33.271.245	IGF2BP3		chi T	23.531.029	RPSZP32
	33.442.905	TRA2A 4	-	chr7	23.545.177	TRA2A
1	33.560.973	CCDC126	-	chr7	23.626.146	CLK2P
	33.611.934	DBF4		chr7	23.650.934	CCDC126
	33.688.752	SLC25A40	1	abe 7	00 204 404	GRM3
	33.880.578 33.759.374	ABCB1	1	chr7 chr7	86.394.461 86.509.786	KIAA1324L
	34.036.015	ABCB4	1/	chr7	86.800.342	DMTF1
6	34.214.940	CROT 4		chr7	86.825.951	C7orf23
	34.302.504	C7orf23		chr7	86.974.808	TP53TG1
	34.323.001	DMITES 4		chr7	86.978.384	CROT
	34.689.023	KIAA1324L		chr7	87.031.411	ABCB4
	34.710.429	GRM3		chr7	87.133.558	ABCB1
	241110142.3	orano 4		chr7	87.258.139	RUNDC3B
				chr7	87.465.563	SLC25A40
				chr7	87.506.047	DBF4

Suppl. Fig. 2. Genes present in BTA4 and HSA7 homologous regions. Genes classified as RefSeq in both cattle and human genomes are in pink. The gene classified as RefSeq in cattle and mapped in human by BLAT comparison software is in red. Genes in black are RefSeq in human and they do not show homology in the cattle genome. Finally human RefSeq genes that map to a different cattle genome chromosome than BTA4 are indicated in green. cdsStart = position of ATG start codon.