

## Supplementary table

### Human phenotypes present in the two genomic regions that are homologue to cattle break-point containing regions

<u>Gene/locus<sup>a</sup></u>	<u>MIM<sup>b</sup></u>	<u>Chr<sup>c</sup></u>	<u>bp<sup>d</sup></u>	<u>Mutation<sup>e</sup></u>	<u>Phenotype<sup>f</sup></u>
ZAP50	176947	2	97,696,463	Yes	Immunodeficiency due to Selective T-cell defect
CNGA3	600053	2	98,352,832	Yes	Rod Monochromacy
GLC1B	606689	2	85,140,603-101,786,053	Linkage	glaucoma 1, open angle, B (adult-onset)
BAFME2	607876	2	85,140,603-105,912,854	Linkage	Epilepsy, myoclonic, benign adult familial, type 2
SLEN2	607976	2	101,938,508	Linkage	systemic lupus erythematosus with nephritis 2
SUMO4	608829	6	149,763,188	Yes	Diabetes mellitus, insulin dependent, 5
LNCR1	608935	6	36,184,520-159,947,125	Linkage	Lung cancer 1
ESR1	133430	6	152,170,379	Yes	Estrogen resistance
OPRM1	600018	6	154,402,136	Yes	Epilepsy, idiopathic generalized
DUH	127500	6	149,621,101-155,110,683	Linkage	Dyschromatosis universalis hereditaria
BPPV	193007	6	155,338,031*	Linkage	Vestibulopathy, familial
STQTL1	606255	6	157,982,868*	Linkage	Stature QTL1
GTF2H5	608780	6	158,511,489	Yes	Trichothiodystrophy (TTD)
BMIQ3	607446	6	137,343,885- 162,115,304	Linkage	body mass index QTL 3
IGF2R	147280	6	160,310,121	Yes	Hepatocellular carcinoma
LPA	152200	6	161,005,281	Yes	Lipoprotein(a) deficiency, congenital
PLG	173350	6	161,043,273	Yes	Dysplasminogemia

a = genes or locus name

b= OMIM database number

c= human chromosome

d= bp position

e= mutation: this indicates that mutations in the gene are responsible for the phenotype. Linkage: this indicates that up to date only a genetic linkage between the phenotype and the reported genome region have been established

f= described phenotype