

Table 1S. Sequence polymorphism analyses of the individual and concatenated 16 bovine *C. pecorum* HK gene fragments sequences used in this study

Gene fragment	Sequence length (bp)	No. of non-synonymous substitutions	$d_n^{\wedge}$	No. of synonymous substitutions	$d_s^{\wedge}$	d_n/d_s	Δnt	N haplotypes	Haplotype diversity (H^x)
<i>gatA</i>	425	2	0.00267	4	0.01724	0.15487	6	4	0.650
<i>oppA_3</i>	483	0	0	1	0.00117	0	1	2	0.125
<i>hflX</i>	435	1	0.00071	3	0.00539	0.13173	4	5	0.667
<i>gidA</i>	474	1	0.00091	3	0.00818	0.11125	4	4	0.592
<i>enoA</i>	381	2	0.00261	8	0.02974	0.08776	10	6	0.675
<i>hemN</i>	432	0	0	1	0.00398	0	1	2	0.400
<i>fumC</i>	465	0	0	2	0.00466	0	2	2	0.233
Concatenated sequence	3095	6	0.00690	22	0.07036	0.09810	28	6	0.675

$d_s^{\wedge}$ and $d_n^{\wedge}$: the average number of synonymous substitutions per synonymous site and non-synonymous substitutions per non-synonymous site, respectively (Jukes - Cantor corrected); Δnt : No. of polymorphic sites; N haplotypes: No. of unique sequences according to the gene; H^x : measure of uniqueness of a particular haplotype in a given population (ranging from 0 (low haplotype diversity) to 1 (highly diverse)).