Table S3. Characteristics of the polymorphic chromosomal genes under positive selection analysed in the present study from three porcine *C. pecorum* L1, L17, and L71 strains

Annotation and sequence length (bp)	**Locus tag in L1**	**Predicted function/product***	**Δnt in protein coding region***	**No. of non-synonymous substitutions**	**No. of synonymous substitutions**	**dn/ds ratio^**	**Base coordinates in L1**
Hypothetical protein (1912 bp)	cpL1_0291	*C. pneumoniae* 76kDa orthologue/wall surface anchor SrpA1 protein	159	87	72	1.11	327 – 332kbp
Conserved hypothetical protein (1089 bp)	cpL1_0338	Chlamydial T3SS effector protein/*C. psittaci* SINC orthologue	174	107	67	1.30	381.5 – 383.5kbp
Conserved hypothetical protein (2406 bp)	cpL1_0441	T3SS effector *Tar*p homologue	105	56	49	1.11	475.5 – 478.5kbp
Conserved hypothetical protein (1683 bp)	cpL1_0538	Chlamydial conserved protein	517	324	193	1.88	587 – 591.5kbp
Conserved hypothetical protein (2246 bp)	cpL1_0539	Chlamydial conserved protein/transcriptional regulator	575	385	190	1.33	587 – 591.5kbp
Conserved hypothetical protein (1460 bp)	cpL1_0645	Chlamydial conserved protein	61	39	22	1.66	725 – 729.5kbp
Conserved hypothetical protein (1794 bp)	cpL1_0646	Chlamydial conserved protein	101	75	26	1.56	725 – 729.5kbp
Macro domain protein (1140 bp)	cpL1_0675	ADP-ribose binding domain	189	122	67	1.72	756.5 – 758.5kbp

*: function predicted based on blastn and tblastx comparison; *: Δnt (No. of polymorphic sites), excluding gaps in the alignment; ^: ratio of the average number of non-synonymous substitutions per non-synonymous site and synonymous substitutions per synonymous site (Jukes - Cantor corrected), estimated excluding gaps in the alignment.