

Table S1. Nucleotide variation*.

Locus category	basepairs	π	mean dS	mean dN	dN/dS
Protein coding	108261	0.00001 \pm 0.0000000	0.0000169	0.0000130	0.77
Non-coding	7909	0.00003 \pm 0.0000000	n. a.	n. a.	n. a.

* data based on 73 isolates; loci containing indels were excluded from these calculations;

π , the average number of nucleotide differences per site between sequences from two isolates; dS , the number of synonymous substitutions per synonymous site; dN , the number of non-synonymous substitutions per non-synonymous site;