Species 1	**Species 2**	**Dist**	**%**
KR025413.1_*Entamoeba*_*invadens*_VK-1	AY769863.1_*Entamoeba*_*invadens*	0.000	0
KR025413.1_*Entamoeba*_*invadens*_VK-1	AF149905.1_*Entamoeba*_*invadens*	0.004	0.4
AY769863.1_*Entamoeba*_*invadens*	AF149905.1_*Entamoeba*_*invadens*	0.004	0.4
KR025413.1_*Entamoeba*_*invadens*_VK-1	MK652887_*Entamoeba*_VJ1	0.034	3.4
AY769863.1_*Entamoeba*_*invadens*	MK652887_*Entamoeba*_VJ1	0.034	3.4
AF149905.1_*Entamoeba*_*invadens*	MK652887_*Entamoeba*_VJ1	0.038	3.8
KR025413.1_*Entamoeba*_*invadens*_VK-1	MK652888_*Entamoeba*_VJ2	0.034	3.4
AY769863.1_*Entamoeba*_*invadens*	MK652888_*Entamoeba*_VJ2	0.034	3.4
AF149905.1_*Entamoeba*_*invadens*	MK652888_*Entamoeba*_VJ2	0.038	3.8
MK652887_*Entamoeba*_VJ1	MK652888_*Entamoeba*_VJ2	0.000	0

Table. Estimates of Evolutionary Divergence between Sequences

The number of base substitutions per site from between sequences are shown. Analyses were conducted using the Kimura 2-parameter model [1]. The analysis involved 5 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated. There were a total of 1847 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 [2].