Table 2 Estimates of Evolutionary Divergence between Sequences

	Fox Texas	Dog Nigeria	Cat Ghana	Dog Ghana	Dog Niger	Wolf Pakistan	Cow India	Dog India	Dog Brazil	Dog Argentina
Fox Texas	-									
Dog Nigeria	.605 (.030)	-								
Cat Ghana	.590(.029)	.130(.020)	-							
Dog Ghana	.590(.029)	.130(.020)	.000	-						
Dog Niger	.670(.029)	.613(.029)	.613(.029)	.613(.029)	-					
Wolf Pakistan	.682(.029)	.613(.020)	.605(.029)	.605(.029)	.146(.023)	-				
Cow India	.594(030)	.165(.022)	.149(.022)	.149(.022)	.617(.029)	.609(.031)	-			
Dog India	..613(.030)	.069(.015)	.107(.019)	.107(.019)	.628(.029)	.625(.030)	.146(.021)	-		
Dog Brazil	.192(.025)	.594(.029)	.586(.029)	.586(.029)	.621(.030)	.617.030)	.605(.030)	.617(.030)	-	
Dog Argentina	.146(,022)	.613(029)	.594(.029)	.594(.029)	.678(.029)	.655(.030)	.598(.020)	.625(.029)	.150(.024)	-

Note: The number of base differences per site from between sequences are shown with Standard error estimate(s). The analysis involved 10 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated. There were a total of 261 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 (Tamura et al., 2011)