Table S2: Coding and non-coding lengths for the Turkey RABV genome sequence dataset.

Region	Length in nucleotides (nts)	
	Clade 1 (and other Turkey genomes)	Clade 2
3' UTR	70	70
N protein	1353	1353
N-P	90	90
P protein	894	894
P-M	88	88
M protein	609	609
M-G	**211**	**212**
G protein	1575	1575
G-L	**518**	**518^**
L protein	6384	6384
5' UTR	131	131
Total	11923 (10,815)	11924-5 (10,815)

The total genome length is indicated, concatenated coding length in brackets. The regions with differences between the dataset are in bold. All clade 2 viruses have an extra base (A) at position 3193 in the M-G intergenic region (See Table 3 for deep sequence analysis of this position). ^RV3160F and Sub5792D have extra base (A) at position 5348 (See Table S5 for deep sequence analysis of this position).