

# Eldholm et al 2016 – Supplementary Tables and Figures

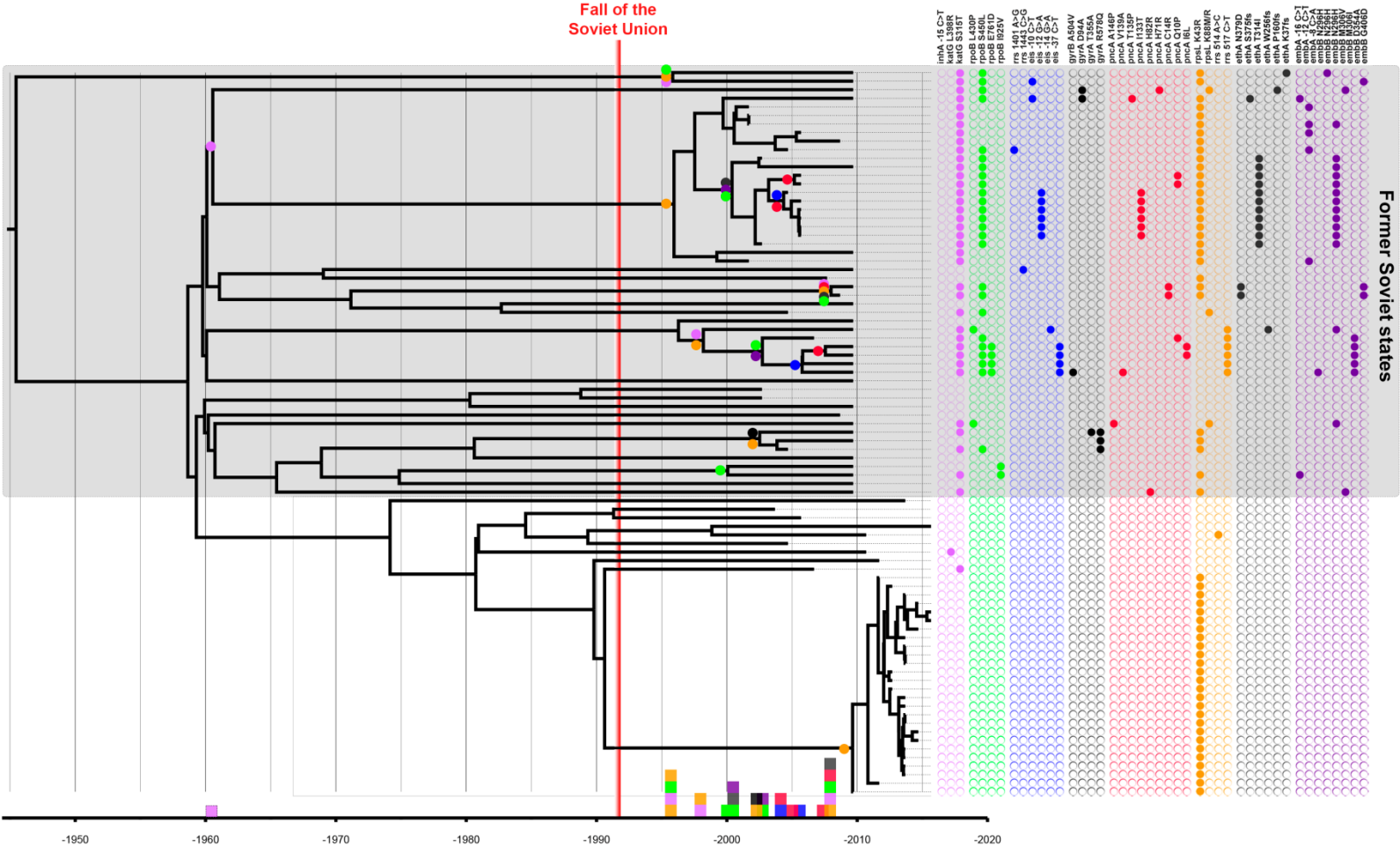


Figure S1. Timed phylogeny with resistance mutations mapped to nodes. Only mutations present in at least two isolates were mapped. The colored boxes at the bottom time-bar indicate the timing of individual mutation events.

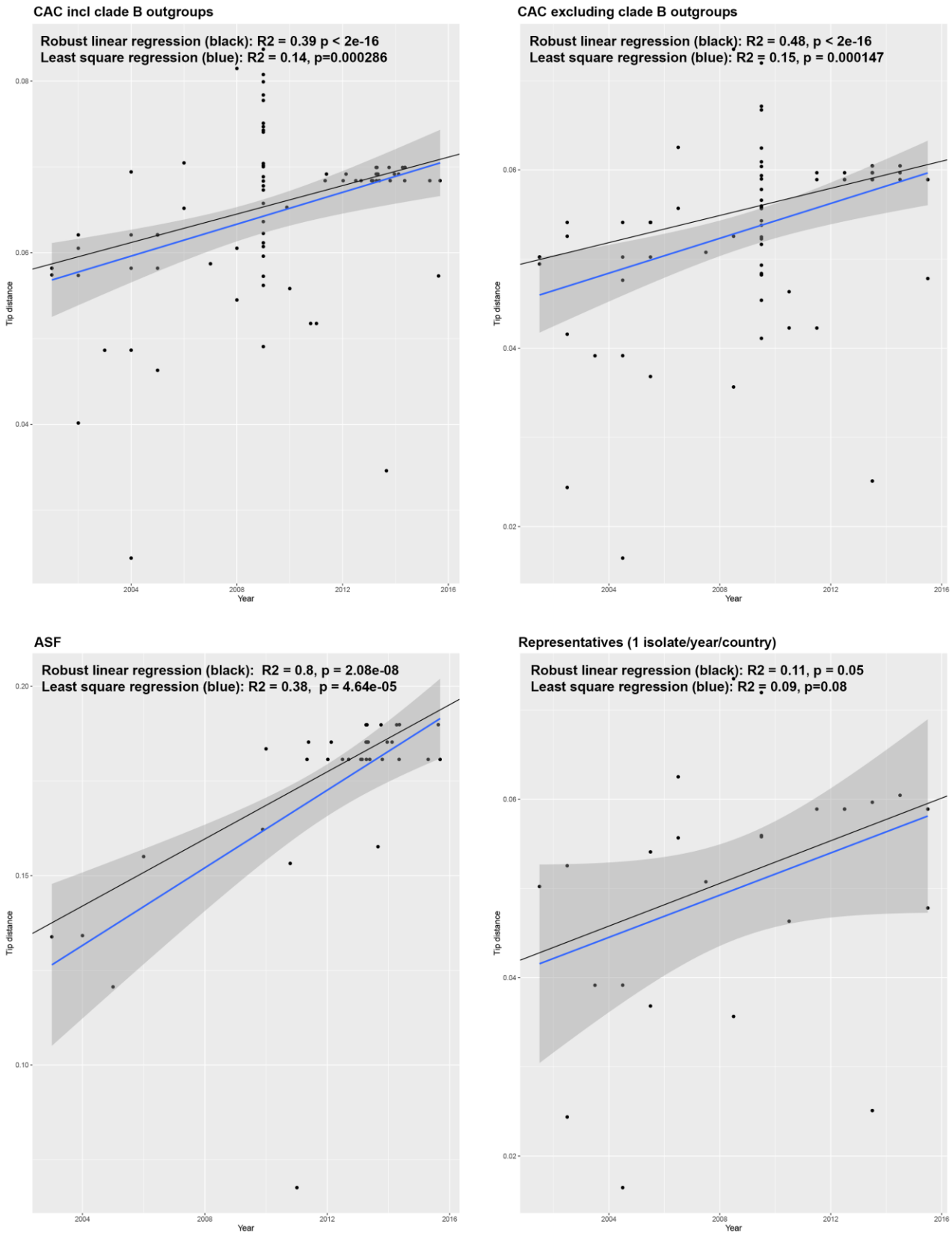


Figure S2. Root-to-tip regression including various sample sets.

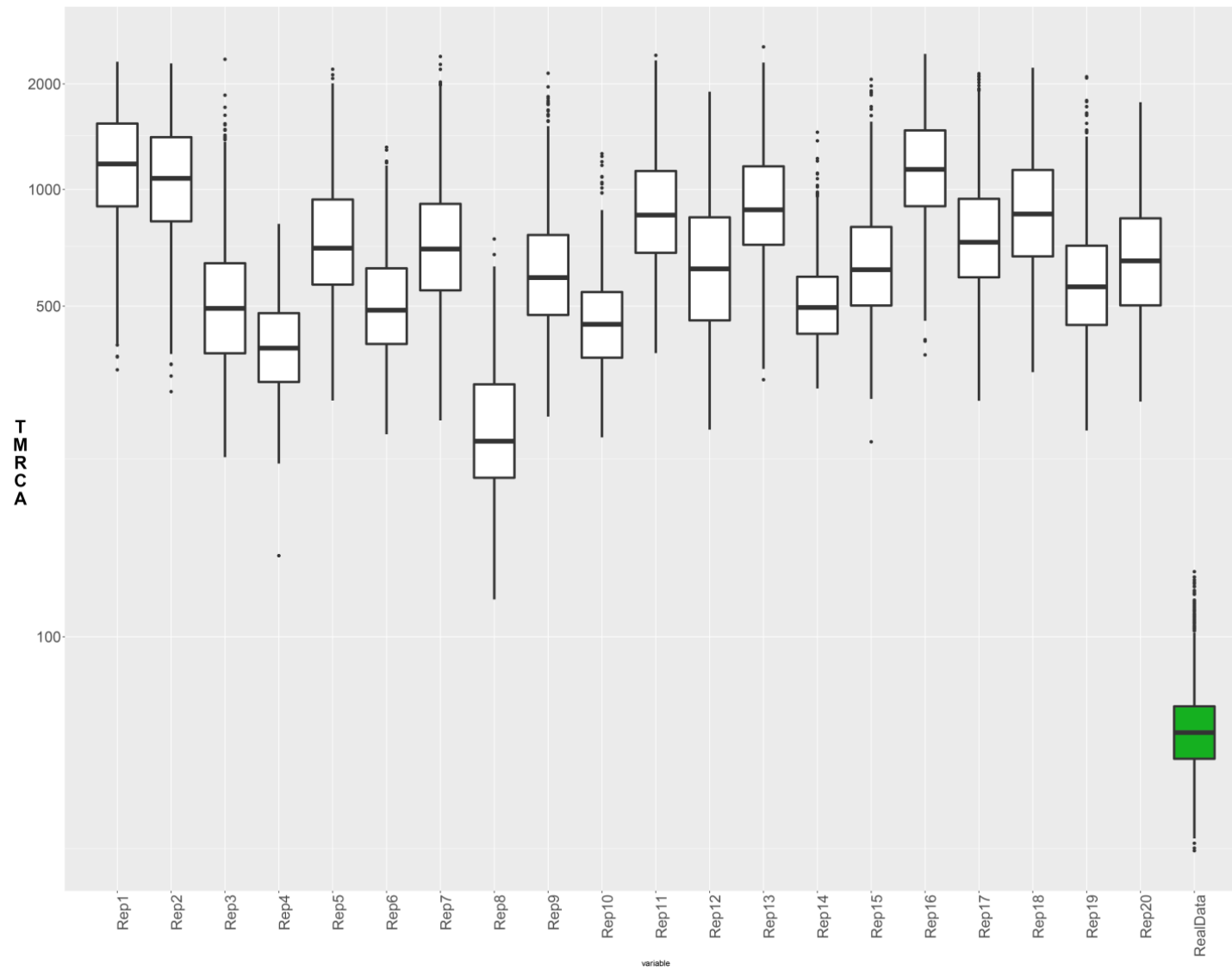


Figure S3. Calculated TMRCA of all isolates following tip-randomization.

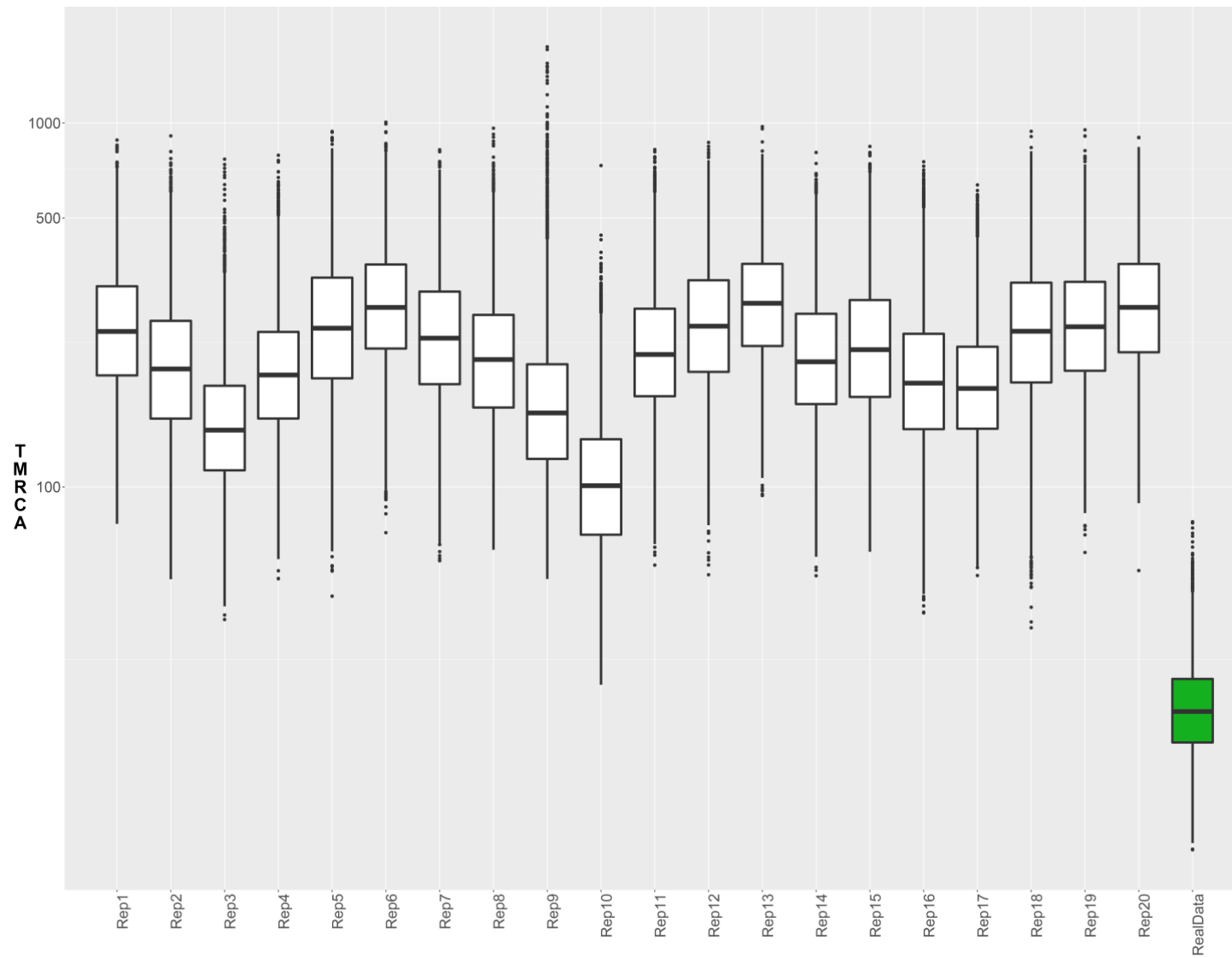


Figure S4. Calculated TMRCA of the Afghan strain family following tip-randomization.

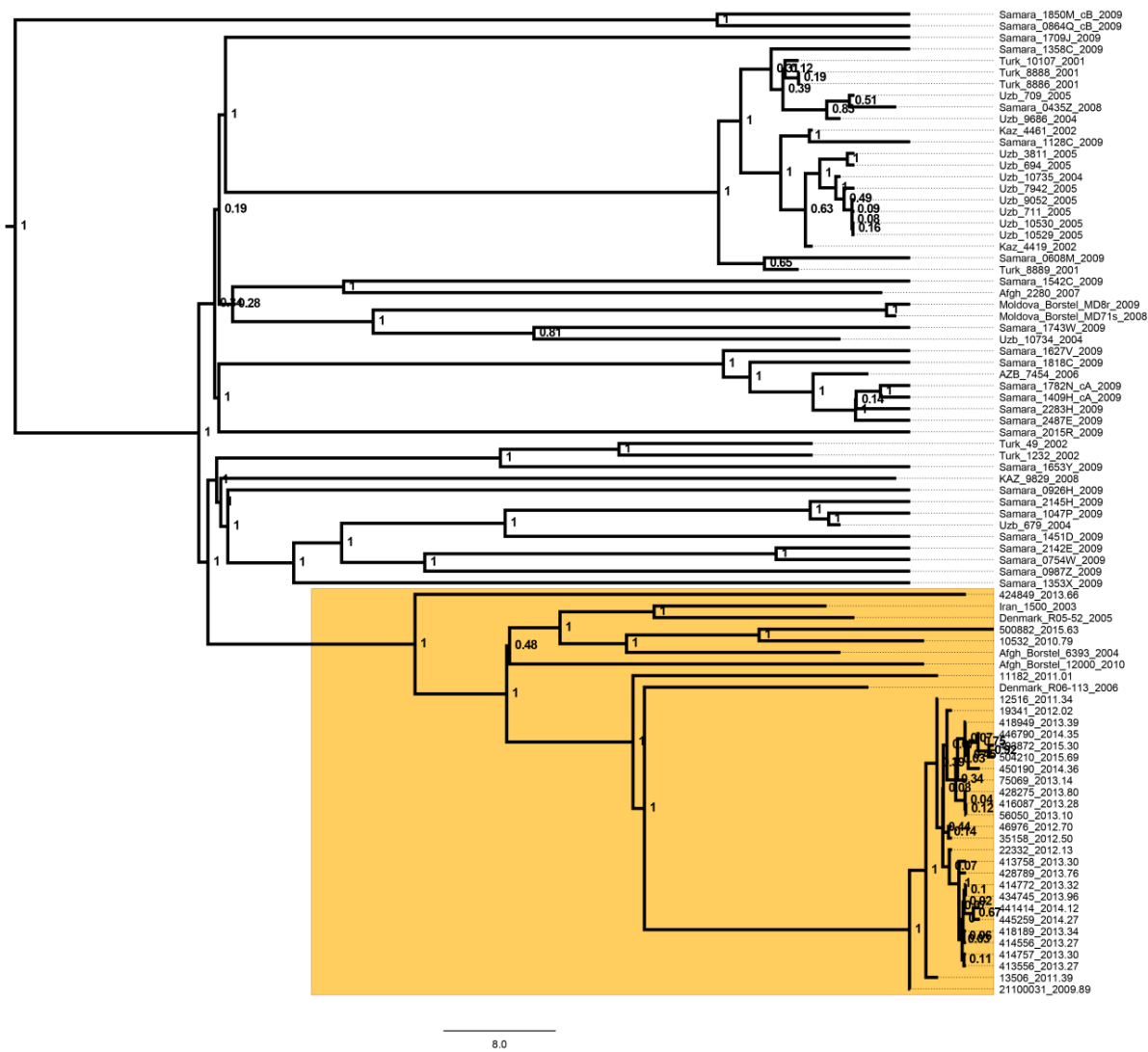


Figure S5. Tipdate-calibrated Beast phylogeny including all 85 isolates showing posterior probabilities of individual nodes

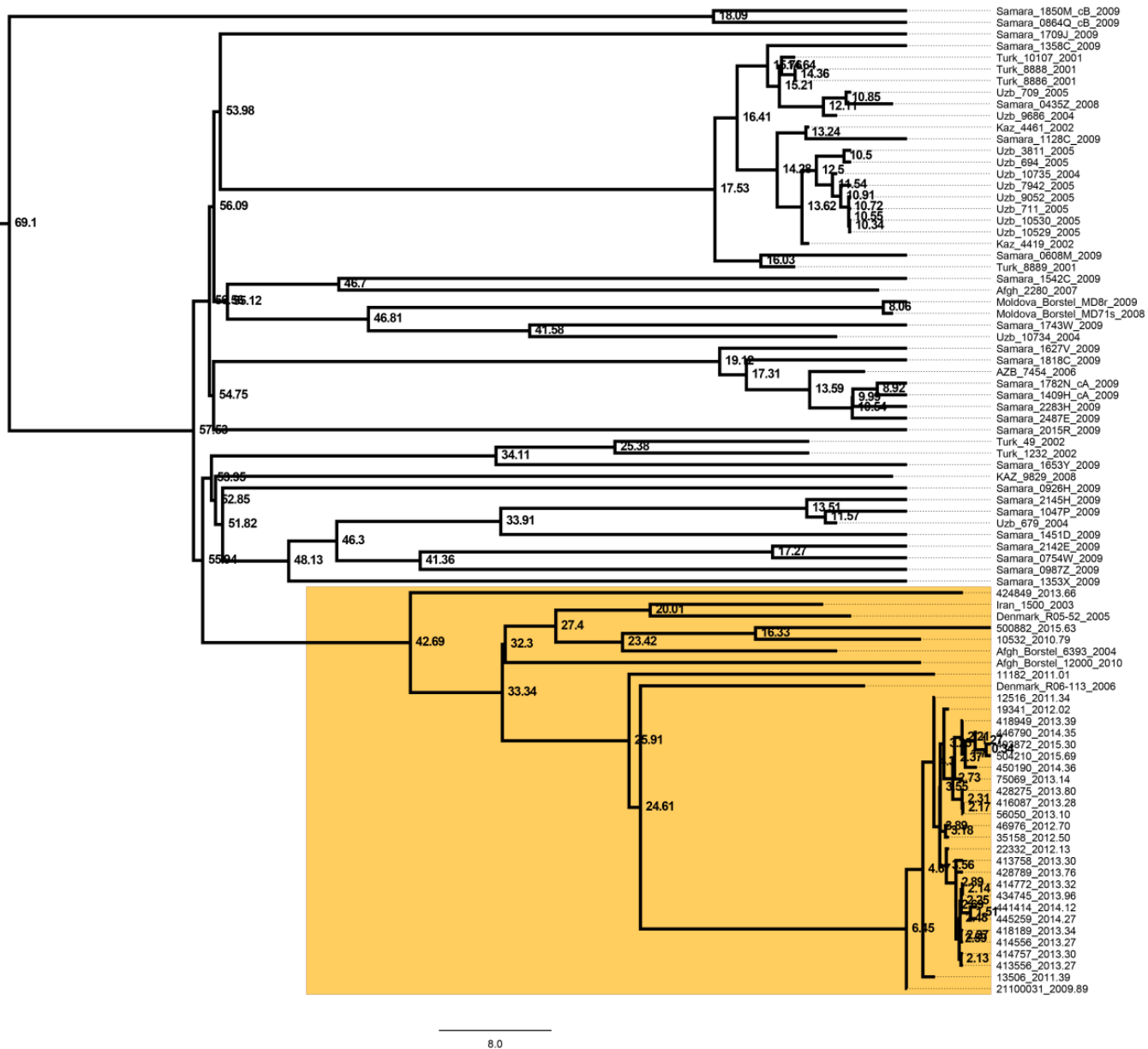


Figure S6. Tiptdate-calibrated Beast phylogeny including all 85 isolates showing individual node ages.

**Supplementary table S1. Model comparison using posterior simulation-based analog of Akaike's information criterion (AICM)**

Afghan strain family							
Demographic model comparison							
	AICM	S.E.	Constant	Exponential	Logistic	Skyride	Expansion
Constant	32398179.2	+/- 0.133	-	-14.315	1.663	-28.481	-8.517
Exponential	32398164.9	+/- 0.148	14.315	-	15.978	-14.166	5.798
Logistic	32398180.9	+/- 0.154	-1.663	-15.978	-	-30.144	-10.18
Skyride	32398150.7	+/- 0.111	28.481	14.166	30.144	-	19.964
Expansion	32398170.7	+/- 0.128	8.517	-5.798	10.18	-19.964	-
Clock model comparison							
			Strict	Lognorm relaxed			
Strict	32398150.7	+/- 0.077	-	5.61			
Lognorm relaxed	32398156.3	+/- 0.039	-5.61	-			
Central Asian Clade							
Clock model comparison							
			Strict	Lognorm relaxed			
Strict	32433074.8	+/- 0.165	-	-32.735			
Lognorm relaxed	32433042.1	+/- 0.257	32.735	-			