G3 Genes | Genomes | Genetics

Supplementary File 1

Analyses of Compact *Trichinella* Kinomes Reveal a MOS-like Protein Kinase with a Unique N-terminal Domain

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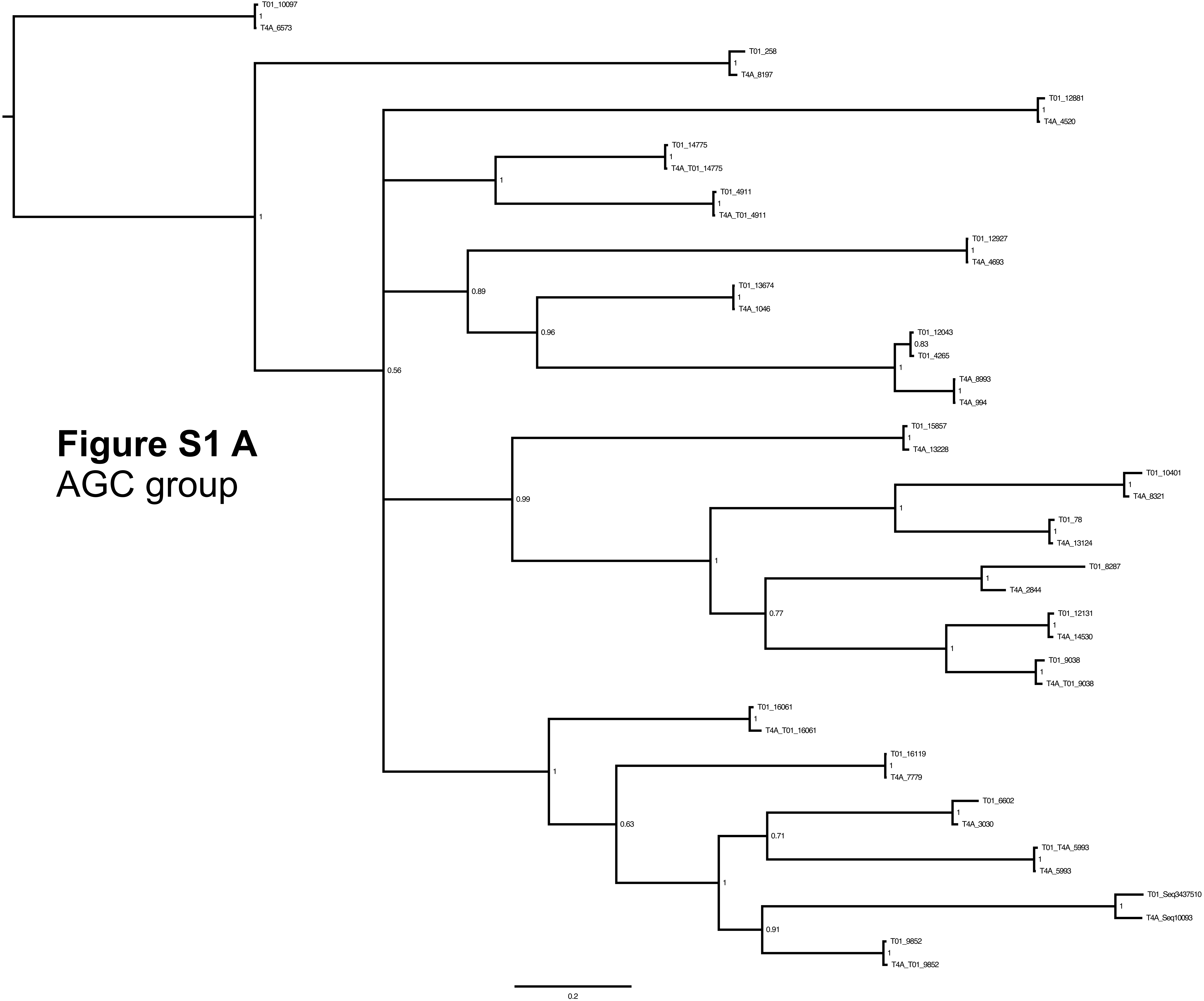
Figure S1 Trees representing the phylogenetic relationship of eukaryotic protein kinase (ePK) sequences between *Trichinella spiralis* (T1) and *T. pseudospiralis* (T4A). Each ePK group is represented by an individual tree (**A-I**). Nodal support values (Bayesian inference) and sequence identifiers are given at the nodes and tips, respectively

S1 A	Protein kinases A, G and C, and other nucleoside-regulated kinases (AGC group)
S1 B	Ca^{2+}/calmodulin-dependent kinases (CAMK group)
S1 C	Casein kinase 1 (CK1 group)
S1 D	Cyclin-dependent kinases (CDKs), mitogen-activated protein kinases (MAPKs), glycogen synthase kinases (GSKs) and CDK-like kinases (CMGC group)
S1 E	“Other” protein kinases (Other group)
S1 F	Receptor guanylate cyclases (RGC group)
S1 G	MAPK cascade kinases (STE group)
S1 H	Tyrosine kinases (TK group)
S1 I	Tyrosine kinase-like kinases (TKL group)

Figure S1 A
AGC group



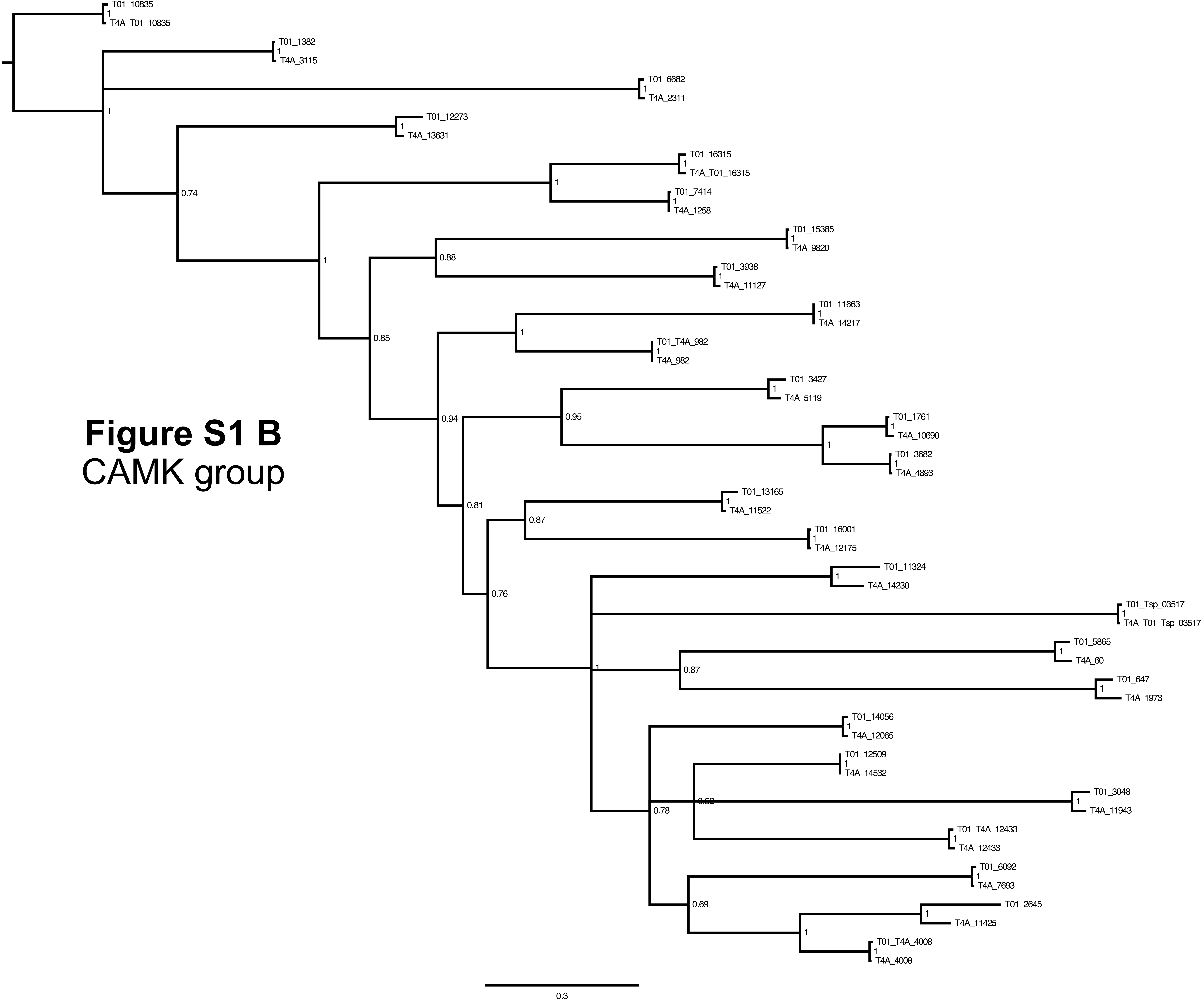


Figure S1 B
CAMK group

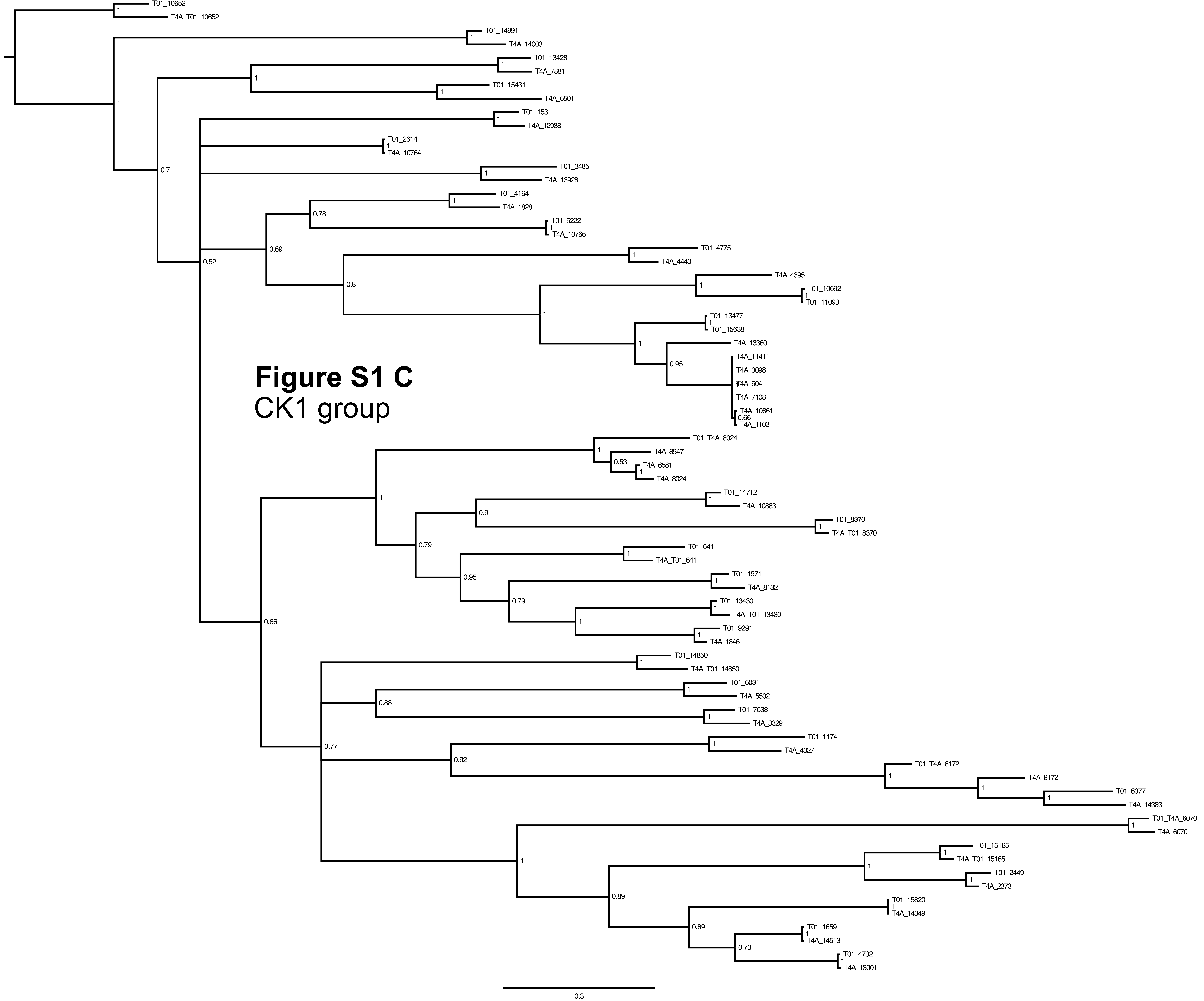


Figure S1 C

CK1 group

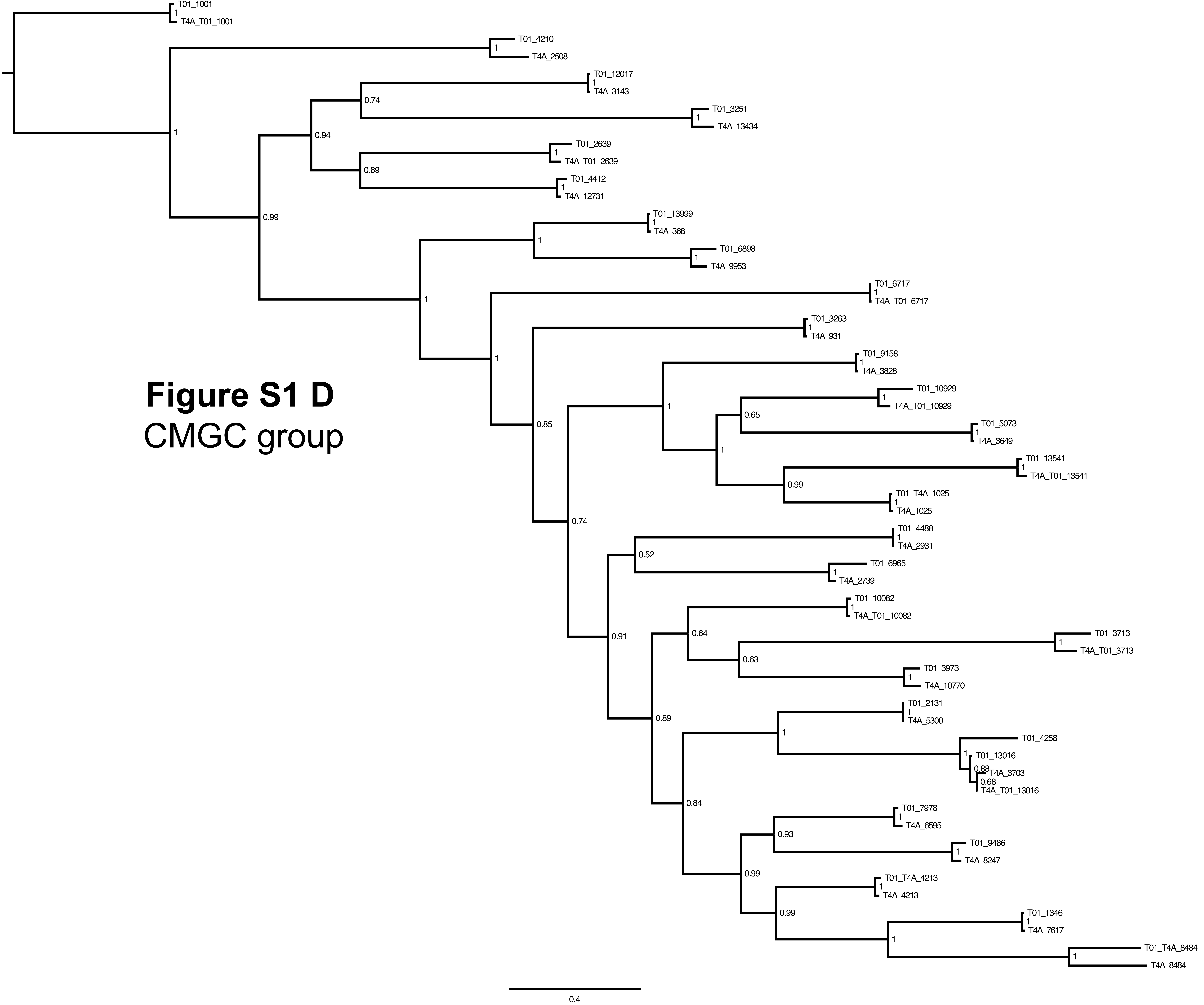


Figure S1 D

CMGC group

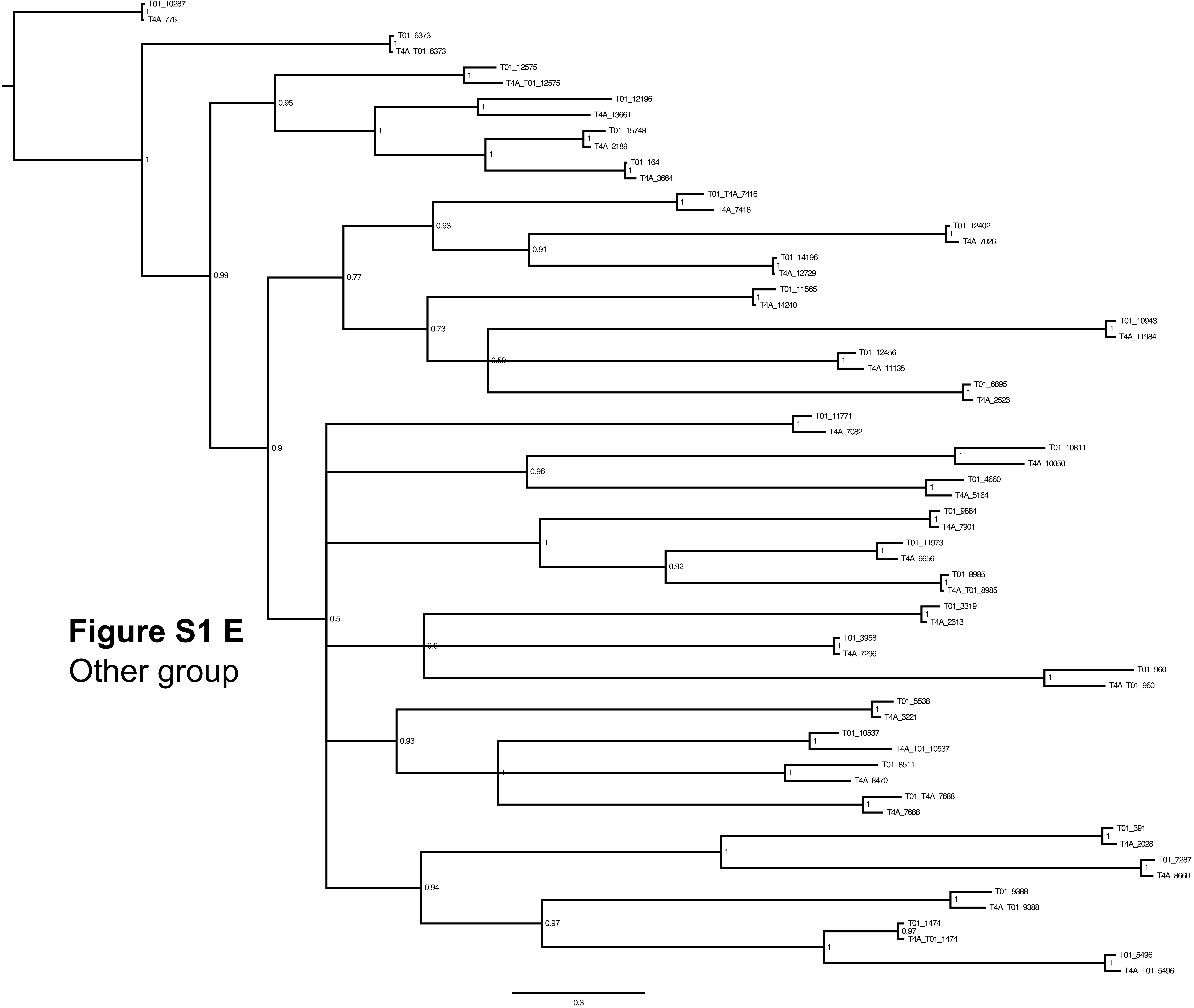
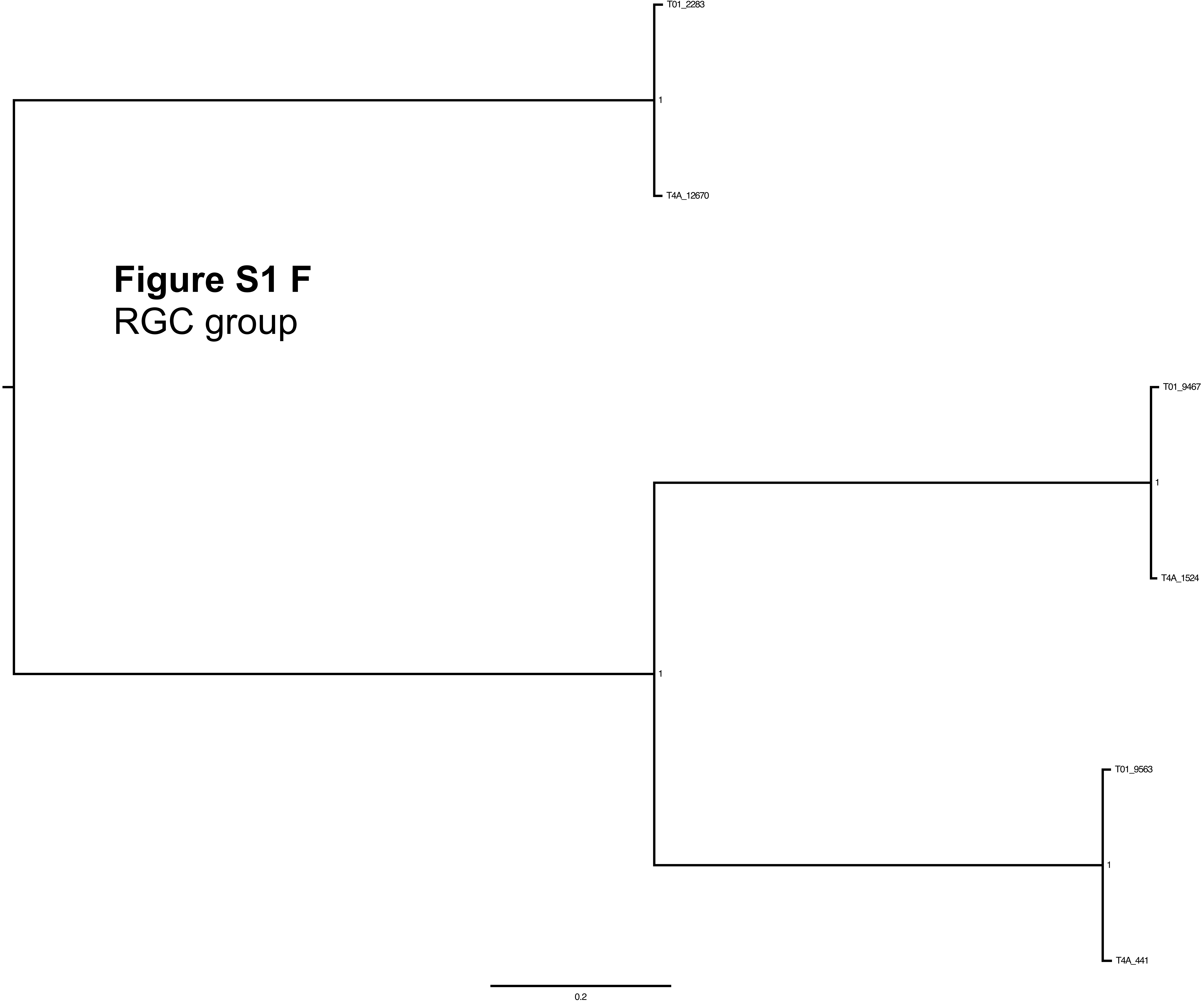


Figure S1 E
Other group

Figure S1 F
RGC group



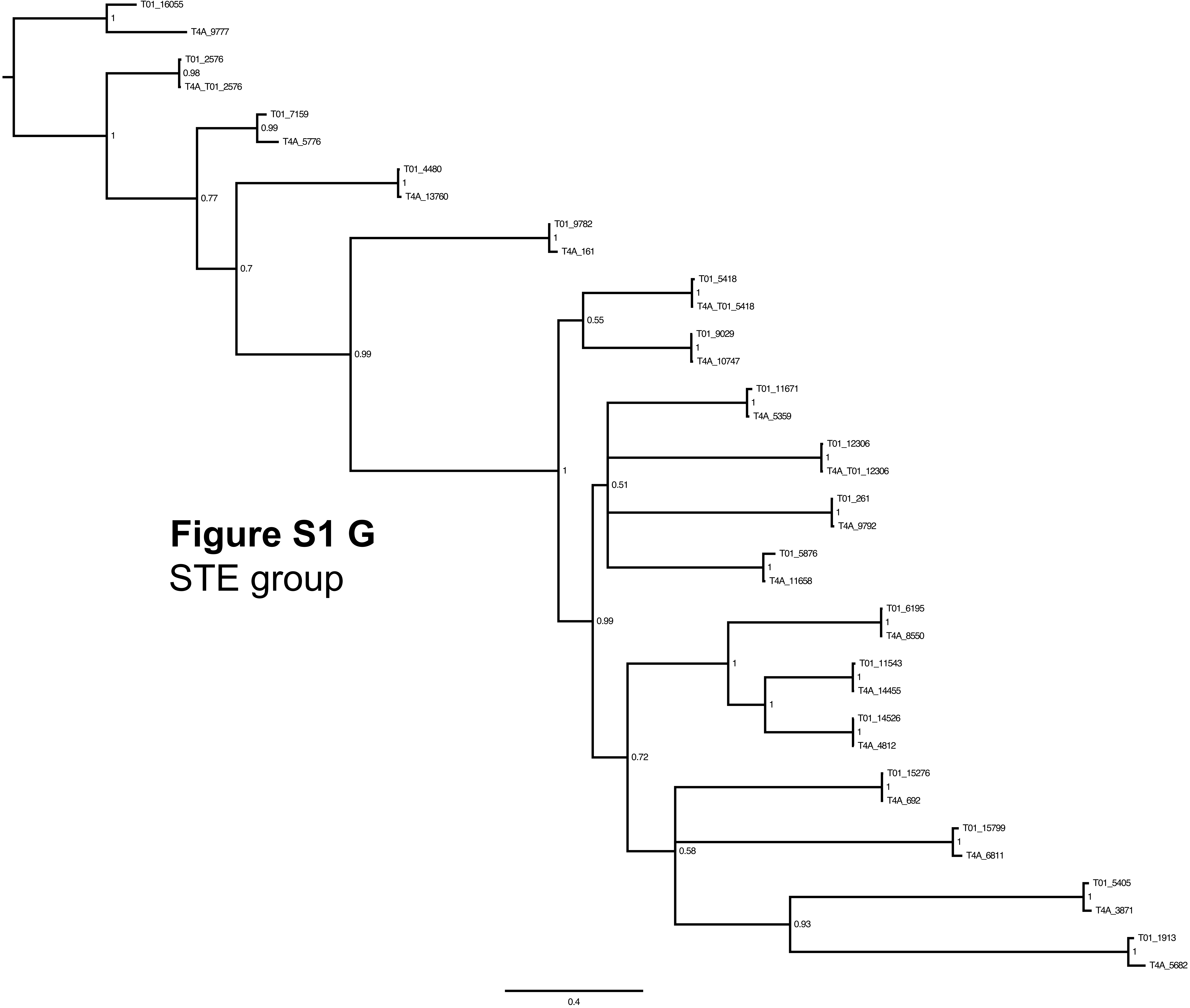


Figure S1 G
STE group

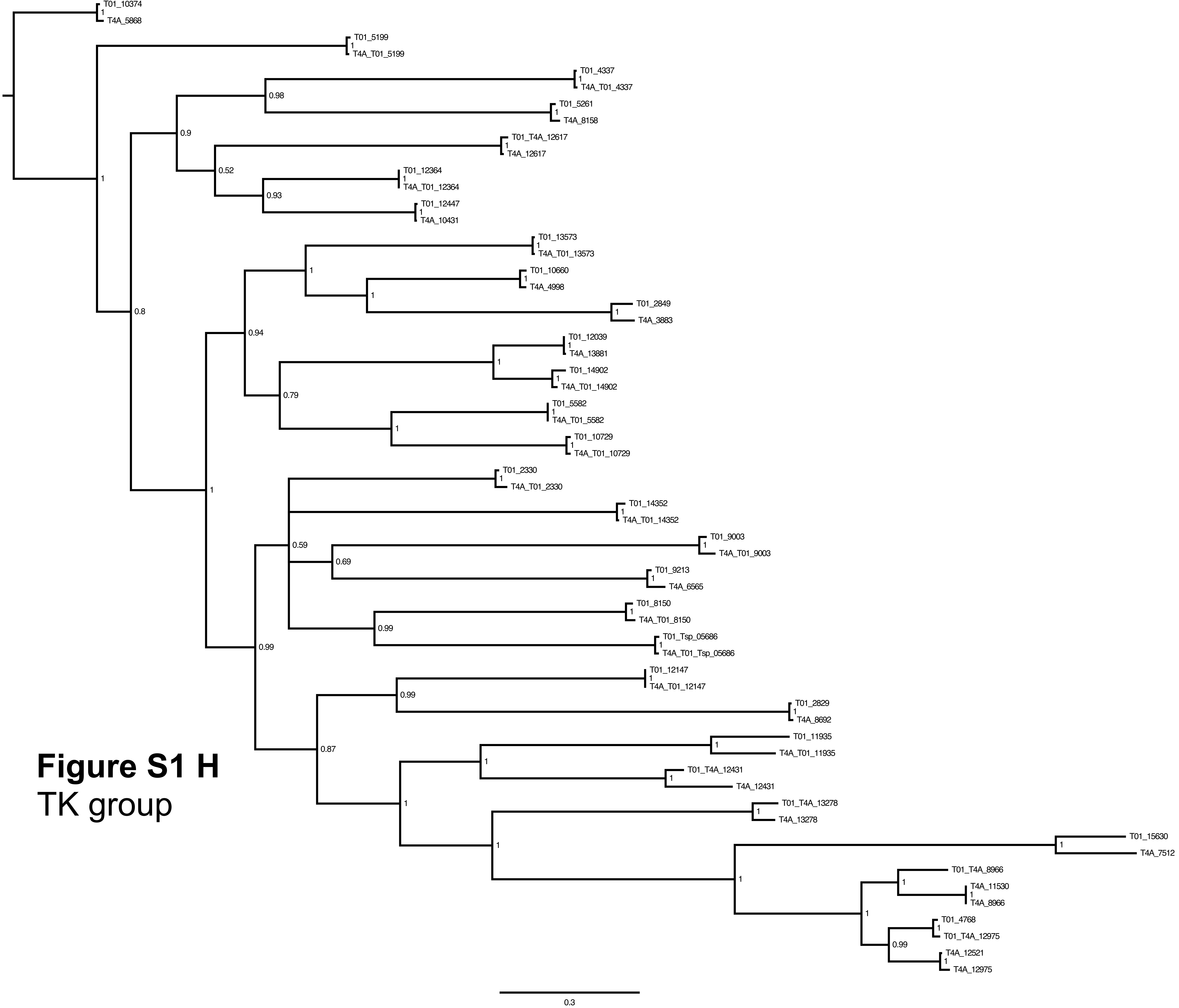


Figure S1 H
TK group

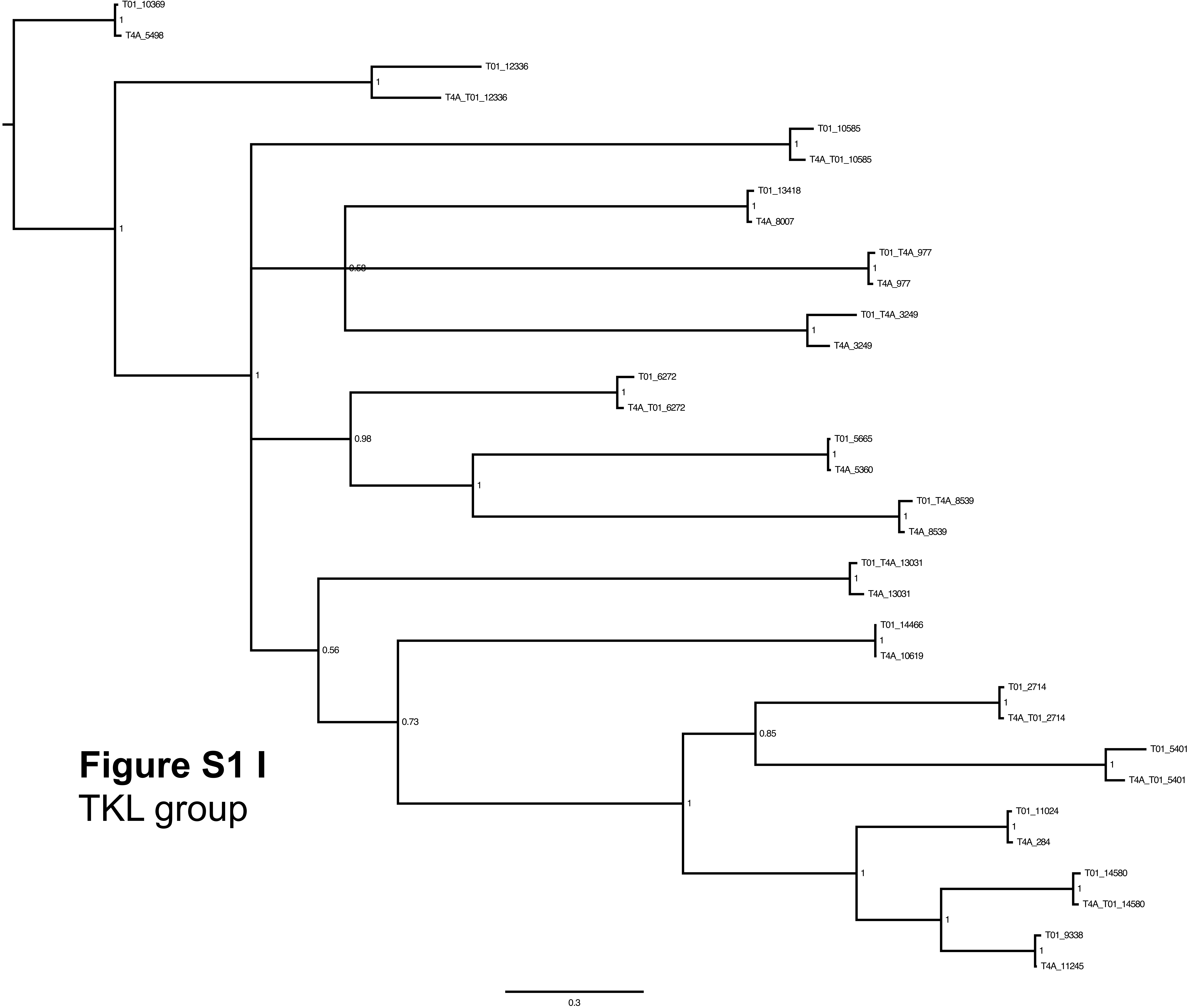


Figure S1 I
TKL group