

Table S2: *Sequence similarities between TconTS-LDs*

	TconTS1-LD	TconTS2-LD	TconTS3-LD	TconTS4-LD
TconTS-LD1	-	42.3% (54.6%)	41.0% (57.7%)	40.7% (51.8%)
TconTS-LD2	42.3% (54.6%)	-	39.9% (54.4%)	37.4% (55.1%)
TconTS-LD3	41.0% (57.7%)	39.9% (54.4%)	-	45.4% (61.7%)
TconTS-LD4	40.7% (51.8%)	37.4% (55.1%)	45.4% (61.7%)	-

The amino acid sequences of TconTS-LD were pairwise aligned using the Blosum62 matrix with a gap opening penalty of 12 and a gap extension penalty of 5. Shown are the percent of positions with identical or similar (giving a positive value in the Blosum62 matrix; in brackets) amino acids.