

Evolutionary traits of Tick-borne encephalitis virus: Pervasive non-coding RNA structure conservation and molecular epidemiology – Supplementary Data –

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Table S1: Representative strains used in this study.

Accession	Subtype	Strain	Note	3'UTR length
MG599476.1	TBEV-Him	Himalaya-1	-	384
AB062063.2	TBEV-FE	Oshima 5-10	Cluster I	724
JQ825148.1	TBEV-FE	Primorye-82	Cluster I	509
KJ914682.1	TBEV-FE	Tomsk-PT14	Cluster I	404
AB062064.1	TBEV-FE	Sofjin-HO	Cluster II	518
KU761570.1	TBEV-FE	Primorye-949	Cluster II	466
JQ650523.1	TBEV-FE	Senzhang	Cluster III	408
MN615728.1	TBEV-FE	DXAL-T83	Cluster III	719
EF469661.1	TBEV-Bkl-1	178-79	-	488
KJ633033.1	TBEV-Bkl-2	886-84	-	539
MF774565.1	TBEV-Sib	TBEV-2871	Obskaya	725
DQ486861.1	TBEV-Sib	EK-328	Baltic	471
MG589939.1	TBEV-Sib	Kuutsalo_2	Baltic	727
AF527415.1	TBEV-Sib	Zausaev	Zausaev	455
MH645618.1	TBEV-Sib	TBEV-2836	Zausaev	730
MN114637.1	TBEV-Sib	1827-18	Vasilchenko	727
KM019545.1	TBEV-Sib	Tomsk-PT122	Vasilchenko	556
AF069066.1	TBEV-Sib	Vasilchenko	Vasilchenko	550
KJ626343.1	TBEV-Sib	Buzuuchuk	Bosnia	546
KJ000002.1	TBEV-Eur	Absettarov	-	720
MG210947.1	TBEV-Eur	KEM-127	-	617
KY069120.1	TBEV-Eur	118-71	-	528
FJ572210.1	TBEV-Eur	Salem	-	712
NC_001672.1	TBEV-Eur	Neudoerfl	-	764
U39292.1	TBEV-Eur	Hypr	-	458
MK801805.1	TBEV-Eur	Sipoo-8-Finland-2013	-	645
LC171402.1	TBEV-Eur	NL	W-Eur	442
MG243699.1	TBEV-Eur	N5-17	-	412

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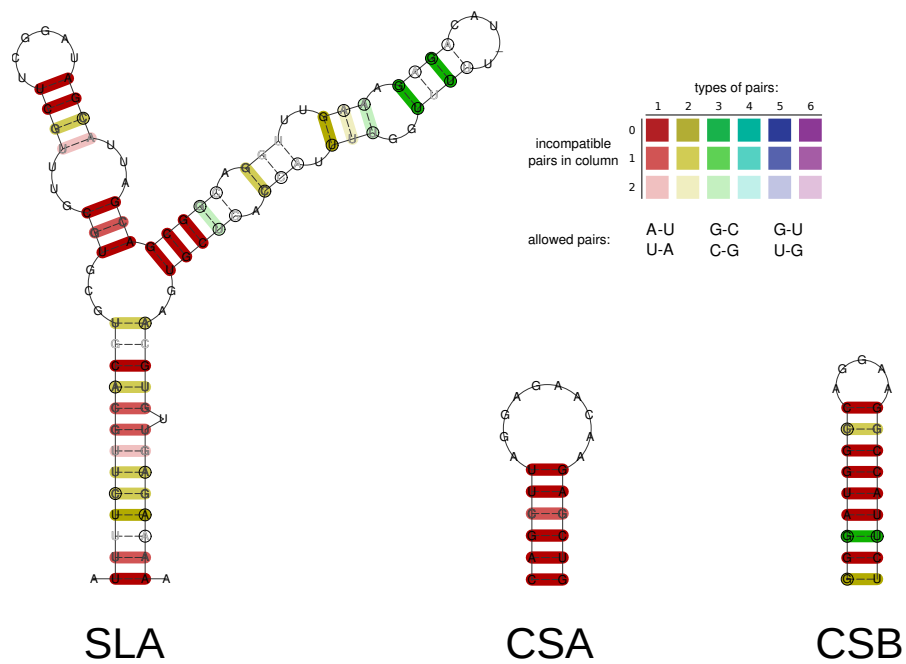


Figure S1: Consensus secondary structures of conserved RNA elements in the TBEV 5'UTRs. Base pair coloring indicates the level of covariation, following the default `RNAalifold` color scheme (top right). Circled nucleotides indicate compensatory mutations in the respective columns of the underlying multiple sequence alignments (MSAs). Structural MSAs for all elements shown here are available at the `viRNA` GitHub repository (<https://github.com/mtw/viRNA>).

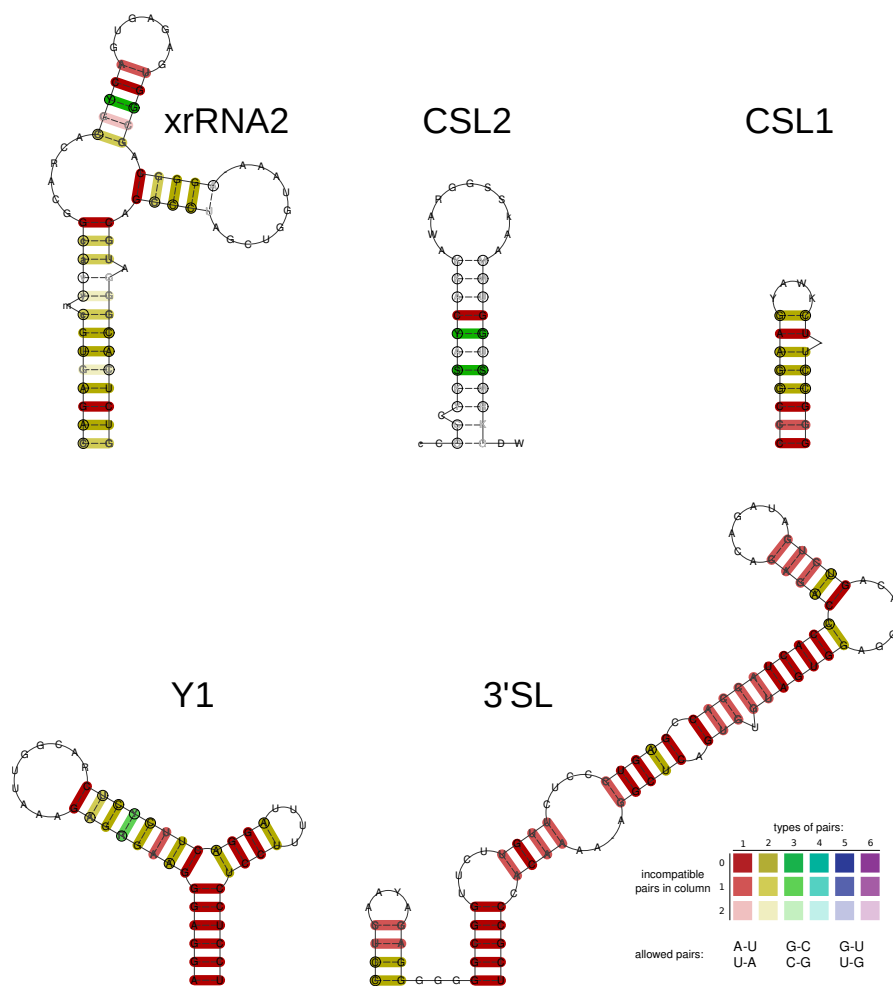


Figure S2: Consensus secondary structures of conserved RNA elements in the core region of TBEV 3'UTRs. See main text for details and Fig. S1 for a description of base pair coloring.

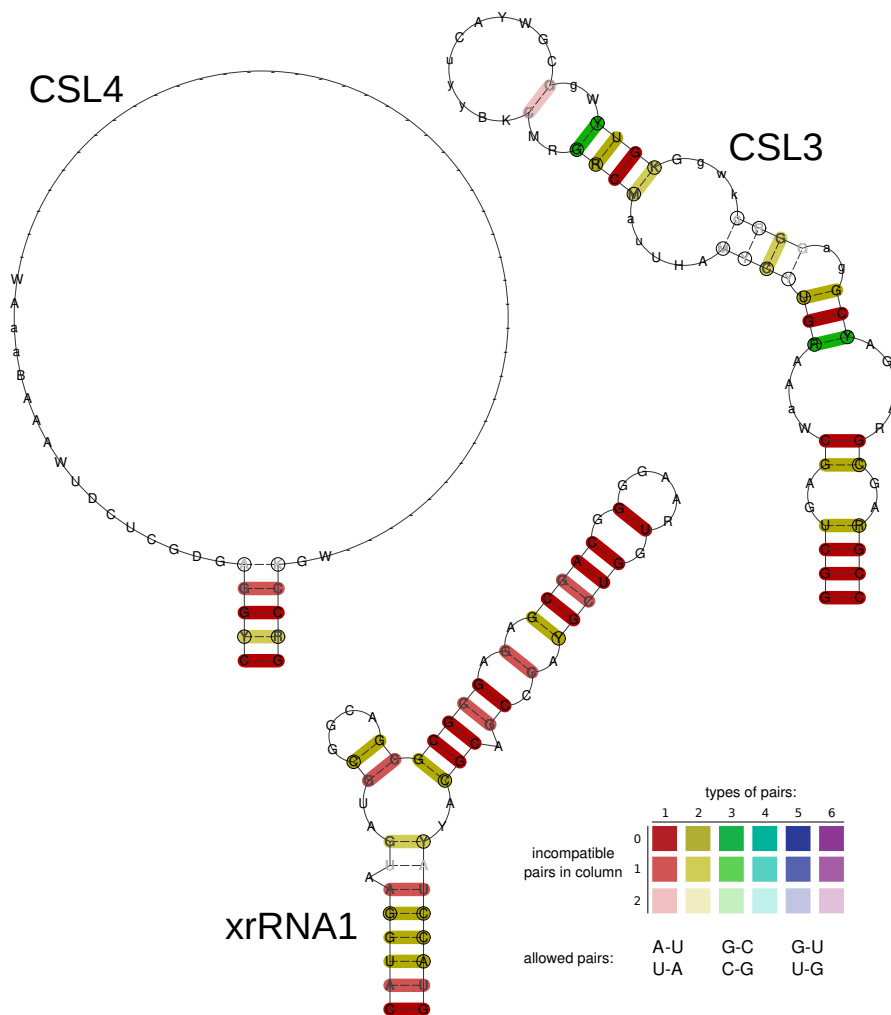


Figure S3: Consensus secondary structures of conserved RNA elements in the variable region of TBEV 3'UTRs. The large amount of gap characters in the hairpin loop of the CSL4 consensus structure is due to an insertion of a poly-A tract in one copy of the CSL4 element, observed in several TBFV-Eur strains. See main text for details and Fig. S1 for a description of base pair coloring.