Table S1. Chikungunya virus 3'-UTR Elements. Alignment of nucleotides 11,921-11,964 in strain AF15561, which is deleted in plaque isolates from the serum of persistently-infected *Rag1* -/- mice, with similar elements found in the 3'-UTRs of other CHIKV strains.

		Strain	Accession Number		Percent ID
CHIKV	Asian	**AF15561 (11,921-11,964)**	**EF452493**	**aagcttcctaaaagcagccgaactcactttgagatgtaggcata**	**100**
		AF15561 (11,728-11,768)	EF452493	aagcttcctaaaagcagccgaactcgctttgagatgtaggcgta	95.45
		MY021IMR/06/BP	EU703762	aagcttcctaaaagcagccgaactcactttgagatgtaggcata	100
		MY002IMR/06/BP	EU703759	aagcttcctaaaagcagccgaactcactttgagatgtaggcata	100
		MY003IMR/06/BP	EU703760	aagcttcctaaaagcagccgaactcactttgagatgtaggcata	100
		MY019IMR/06/BP	EU703761	aagcttcctaaaagcagccgaactcactttgagatgtaggcata	100
		0706aTw	FJ807897	aagcttcttaaaagcagccgaactcactttgagatgtaggcata	97.73
		PhH15483	HM045790	aagcttcctaaaagcagccgaactcactttgagatgtaggcata	100
		Hu/85/NR/001	HM045800	aagcttcctaaaagcagccgaactcactttgagatgtaggcata	100
		JKT23574	HM045791	aagcttcctaaaagcagccgaactcactttgagatgtaggcata	100
		RSU1	HM045797	aagcttcctaaaagcagccgaactcactttgagatgtaggcata	100
		SV0444-95	HM045787	aagcttcctaaaagtagccgaactcactttgagacgtaggcata	95.45
		CO392-95	HM045796	aagcttcctaaaagcagccgaactcgctttgagatgtaggcgta	95.45
		6441-88	HM045789	aagcttcctaaaagcagccgaactcgctttgagatgtaggcgta	95.45
		3412-78	HM045808	aagcttcctaaaagcagccgaactcactttgagatgtaggcata	100
		1455-75	HM045814	aagcttcctaaaagcagccgaactcactttgagatgtaggcata	100
		TH35	HM045810	aagcttcctaaaagcagccgaactcactttgagatgtaggcata	100
		IND-73-MH5	EF027141	aagcttcctaaaagcagccgaactcgcttt--gatgtaggcata	93
		P0731460	HM045788	aagcttcctaaaagcagccgaactcactttgagatgtaggcata	100
		Gibbs 63-263	HM045813	aagcttcctaaaagcagccgaactcactttgagatgtaggcata	100
		IND-63-WB1	EF027140	aagcttcctaaaagcagccgaactcgctttgagatgtaggcata	97.73
		I-634029	HM045803	aagcttcctaaaagcagccgaactcgctttgagatgtaggcata	97.73
	Indian Ocean Lineage	IND-KR51	FJ000066	aagcttcctaaaagcagccgaactcactttgagaagtaggcata	97.72
		0611aTw	FJ807896	aagcttcctaaaagcagccgaactcactttgagaagtaggcata	97.72
		INF-KA51	FJ000068	aagcttcctaaaagcagccgaactcactttgagaagtaggcata	97.72
		SL10571	AB455494	aagcttcctaaaagcagccgaactcactttgagaagtaggcata	97.72
		RGCB120/KL07	GQ428213	aagcttcctaaaagcagccgaactcactttgagaagtaggcata	97.72
		0810bTw	FJ807899	aagcttcctaaaagcagccgaactcactttgagaagtaggcata	97.72
		RGCB80/KL07	GQ428212	aagcttcctaaaagcagccgaactcactttgagaagtaggcata	97.72
		IND-06-RJ1	EF027137	aagcttcctaaaagcagccgaactcactttgagaagtaggcata	97.72
		IND-06-KA15	EF027135	aagcttcctaaaagcagccgaactcactttgagaagtaggcata	97.72
		IND-GJ51	FJ000064	aagcttcctaaaagcagccgaactcactttgagaagtaggcata	97.72
		IND-06-AP3	EF027134	aagcttcctaaaagcagccgaactcactttgagaagtaggcata	97.72
		RGCB356/KL08	GQ428215	aagcttcctaaaagcagccgaactcactttgagaagtaggcata	97.72
		OPY4	KP003809	aagcttcctaaaagcagccgaactcactttgagaagtaggcata	97.72
		TM25	EU564334	aagcttcctaaaagcagccgaactcactttgagaagtaggcata	97.72
		SL15649	GU189061	aagcttcctaaaagcagccgaactcactttgagaagtaggcata	97.72
	East, Central, South African	DakAr B 16878	HM045784	aagcttcctaaaagcagccgaactcactttgagatgtaggcata	100
		UgAg4155	HM045812	aagcttcctaaaagcagccgaactcgctttgagatgtaggcata	100
		HB78	HM045822	aagcttcctaaaagcagccgaactcactttgagatgtaggcata	100
		SAH2123	HM045795	aagcttcctaaaagcagccgaactcactttgagatgtaggcata	100
		AR 18211	HM045805	aagcttcctaaaagcagccgaactcactttgagatgtaggcata	100
		Ross low-psg	HM045811	aagcttcctaaaagcagccgaactcactttgagatgtaggcata	100
		A301	HM045821	aagcttcctaaaagcagccgaactcactttgagatgtaggcata	100
		Vereening	HM045792	aagcttcctaaaagcagccgaactcactttgagatgtaggcata	100
		LFSF	HM045809	aagcttcctaaaagcagccgaactcactttgagatgtaggcata	100
	West African	ArA 2657	HM045818	aagcttcctaaaagcagccgaactcactttgagacgtaggcata	97.72
		ArD 93229	HM045819	aagcttcctaaaagcagccgaactcactttgagacgtaggcata	97.72
		ArA 30548	HM045820	aagcttcctaaaagcagccgaactcactttgagacgtaggcata	97.72
		HD 180760	HM045817	aagcttcctaaaagcagccgaactcactttgagacgtaggcata	97.72
		37997	AY726732	aagcttcctaaaagcagccgaactcactttgagacgtaggcata	97.72
		IbH35	HM045786	aagcttcctaaaagcagccgaactcactttgagacgtaggcata	97.72
		IbAn4824	HM045807	aagcttcctaaaagcagccgaactcactttgagacgtaggcata	97.72
		SH2830	HM045798	aagcttcctaaaagcagccgaactcactttgagacgtaggcata	97.72
		PM2951	HM045785	aagcttcctaaaagcagccgaactcactttgagacgtaggcata	97.72
		ArD 30237	HM045815	aagcttcctaaaagcagccgaactcactttgagacgtaggcata	97.72
		Sh 3013	HM045816	aagcttcctaaaagcagccgaactcactttgagacgtaggcata	97.72