

S1 Table. Multiple sequence alignment of the HCV IRES region spanning nts 301–341

Genotype	Name	Sequence ^a	GenBank No	Clone No
1a	H77	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCACC	NC_004102	139
	US.BID-V182	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAAC	EU234064	2
	HEC278830	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAUC	AJ278830	1
	US.BID-V411	CGUGCAC CGAGUGCCCCG GGAGGUCUCGUAGACCGUGCACC	EU155311	1
1a/2a	WO0075338-9	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCACC	AX057094	1
1b/2k	RJ.N687	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAUC	AY587845	1
1b	Con1	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCACC	AJ238799	183
	CN.AY587016	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAUC	AY587016	38
	JP.MD6-675	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAAC	AF165056	1
	US.BID-V341	GCGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCACC	EU155300	1
	MD27	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGUCGUGCAUC	AF207768	1
	JP.MD9-1012	GUGCUUGCGAG AG CCCCG GGAGGUCUCGUAGACCGUGCAUC	AF165062	1
	MD26	GUGCUUGCGAG G CCCCG GGAGGUCUCGUAGUCGUGCAC	AF207767	1
1c	IN.Khajal	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCACC	AY651061	3
1	GQ.AJ851228	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCACC	AJ851228	1
2a	JP.AY746460	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCACC	AY746460	9
	G2AK1	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAUC	AF169003	4
	JFH-1	GCGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCACC	AB047639	1
2b	JP.MD2b1-2	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAUC	AY232731	12
	JPUT971017	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCACC	AB030907	1
2c	BEBE1	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAUC	D50409	1
2k	MD.VAT96	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCACC	AB031663	1
3a	DE.HCVCENS1	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAAC	X76918	3
	K3A	GCGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGUAAC	D28917	1
3b	JP.HCV-Tr	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAAC	D49374	2
3k	ID.JK049	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAUC	D63821	1
4a	EG.ED43	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCACC	Y11604	9
4d	03-18	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCACC	DQ418786	2
5a	GB.EUH1480	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCACC	Y13184	2
	ZA.SA13	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAAC	AF064490	1
6a	HK.6a35	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAUC	DQ480513	13
	HK.6a33	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAUC	AY859526	1
	HK.6a74	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAUC	DQ480524	1
6b	Th580	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAAC	NC_009827	1
6c	TH.Th846	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAUC	EF424629	1
6d	VN.VN235	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAUC	D84263	1
6e	CN.GX004	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAUC	DQ314805	1
6f	TH.C-0044	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAUC	DQ835760	2
6g	HK.HK6554	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAUC	DQ314806	2
6h	VN.VN004	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAUC	D84265	1
6i	TH.C-0159	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAUC	DQ835762	1
	TH.Th602	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAUC	DQ835770	1
6j	TH.C-0667	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAUC	DQ835761	2
6k	CN.KM41	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCACC	DQ278893	1
	CN.KM45	GUGCUUGC A AGUGCCCCG GGAGGUCUCGUAGACCGUGCACC	DQ278891	1
	VN.VN405	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAAC	D84264	1
6l	US.537796	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAUC	EF424628	1
6m	TH.B4/92	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCACC	DQ835767	2
	TH.C-0185	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAAC	DQ835765	1
	TH.C-0192	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAUC	DQ835766	1
6n	CN.KM42	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAAC	AY878652	2
6o	CA.QC227	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAAC	EF424627	1
6p	CA.QC216	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAUC	EF424626	1
6q	CA.QC99	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAAC	EF424625	1
6	CN.GZ52557	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCAUC	DQ278892	1
7	CA.QC69	GUGCUUGCGAGUGCCCCG GGAGGUCUCGUAGACCGUGCACC	EF108306	1

^aA total of 468 HCV sequences available on the HCV database web server (<http://hcv.lanl.gov/content/index>) operated by Los Alamos National Security were analyzed to align the IRES region, spanning nts 301–341, by using ALIGN0 and QuickAlign v1 programs provided by the server. Five clones representing 1.02% of aligned sequences showed a single nucleotide change, with two clones harboring a C to U change that can still make a G:U wobble base-pairing with siIE22 guide strand. The siIE22 target is shown in blue and the residues not conserved among the aligned sequences are shown in red.