

Supplementary material:

Table 1: Algorithms or rules for rational design of siRNA molecules

Ui-Tei Rules	Amarzguioui Rules	Reynolds Rules
A/U at the 5' terminus of the sense strand	Duplex End A/U differential > 0. Strong binding of 5' sense strand	Each rule is assigned a score which is summed up to a total duplex score to improve the efficacy of siRNA.
G/C at the 5' terminus of the antisense strand	No U at position 1. Presence of A at position 6.	
At least 4 A/U residues in the 5' terminal 7 bp of sense strand	Weak binding of 3' sense strand. No G at position 19	
No GC stretch longer than 9nt		

Table 2: Worldwide, genome isolates of HDV

Group	Genome isolate	Country	Accession No	Location of coding region in genome	Length (Base pair)
Group I	Cagliri	Cagliri	X85253	1008-1595	1676
	China	China	X77627	82-666	1674
	Ethiopia	Ethiopia	U81989	1011-1598	1679
	IR-1	Iran	AY633627	1007-1594	1676
	Italy	Italy	X04451	950-1618	1678
	Lebanon1	Lebanon	M84917	Not Available	1678
	Nauru	Nauru	M58629	952-1598	1678
	Somalia	Somalia	U81988	1006-1593	1674
	Taiwan	Taiwan	M92448	951-1595	1682
	TW2667	Taiwan	AF104263	951-1595	167
	US-1	US	D01075	1013-1600	1682
	US-2	US	L22066	1013-1600	1681
	Nagasaki-2	Nagasaki	AB118849	950-1594	1675
	OA	Turkey	EF514905	950-1594	1676
	NK	Turkey	EF514904	950-1594	1676
	SO	Turkey	EF514906	950-1594	1676
	ZA	Turkey	EF514907	950-1594	1676
	CB	Turkey	EF514903	950-1594	1676
	W5	Italy	AJ307077	954-1598	1679
	TW3678#25	Taiwan	AY648959	1006-1593	1674
	TW5132#24	Taiwan	AY648957	1007-1594	1675
	TW1573#4	Taiwan	AY648958	1006-1593	1674
	TW1435#47	Taiwan	AY648956	1007-1594	1675
JN	China	HM046802	952-1596	1677	
Group II	Japan	Japan	X60193	1013-1600	1683
	Yakut-26	Russia	AJ309879	964-1605	1685
	Yakut-62	Russia	AJ309880	964-1605	1688
	TW2476	Taiwan	AF104264	956-1600	1684
Group III	3	Taiwan	U19598	949-1593	1676
	Miyako-37	Japan	AB118846	952-1596	1678
	Peru-1	Peru	L22063	953-1597	1677
	VnzD8375	Venezuela	AB037947	1007-1591	1672
	VnzD8349	Venezuela	AB037948	1008-1592	1673
Group IV	VnzD8624	Venezuela	A B037949	1009-1593	1674
	Miyako	Japan	AF309420	1011-1595	1676
Group V	L215	Japan	AB088679	961-1602	1682
	Miyako-36	Japan	AB118845	955-1596	1677
	Taiwan TW-2b	Taiwan	AF018077	1012-1596	1676
	AF209859	Taiwan	AF209859	1013-1597	1678
	Tokiyo	Japan	AB118847	957-1598	1678
	TW3038#25	Taiwan	AY648955	1014-1598	1678
	2621#56	Taiwan	AY648953	1014 -1598	1678
	TW1025#14	Taiwan	AY648954	1014-1598	1678
	TWD62#16	Taiwan	AY648952	1014-1598	1678
	dFr2005	Guinea	AM183331	958-1602	1687
dFr2600	Togo	AM183326	963-1607	1691	
dFr47	Not Available	AX741149	Not Available	1697	
dFr910	Mali	AX741159	Not Available	1697	
dFr-73	Not Available	AX741154	Not Available	1697	
dFr-2703	Senegal	AM183328	1017-1604	1688	

Group VI	dFr48	Poland	AX741164	Not Available	1687
	dFr2139	Central African Republic	AM183332	951-1592	1677
	dFr2627	Nigeria	AM183329	956-1597	1680
Group VII	dFr45	Not Available	AX741144	Not Available	1672
	dFr2158	Cameroon	AM183333	949-1593	1674
Group VIII	dFr2072	Senegal	AM183330	1011-1598	1681
	dFr644	Cogo-Brazzaville	AX741169	Not Available	1680
	dFr2736	Cote d' Ivoire	AM183327	954-1598	1681
Group IX	HDV-DN79	Gabon	GU177114	1010-1597	1679
	Isolate- 1	Turkey	HQ005370	785-1372	1679
	Isolate- 2	Turkey	HQ005371	785-1372	1679
	Isolate- 3	Turkey	HQ005372	774-1361	1673
	Isolate- 4	Turkey	HQ005369	786-1373	1684
	Isolate- 5	Turkey	HQ005364	730-1374	1681
	Isolate- 6	Turkey	HQ005366	786-1373	1683
	Isolate- 7	Turkey	HQ005365	729-1373	1682
	Isolate-8	Turkey	HQ005367	730-1374	1685
	Isolate -9	Turkey	HQ005368	786-1373	1681

Table 3: Predicted siRNA target for genome isolates of HDV, worldwide

Accession No	Target	Location of target within gene	siRNA target sequence within gene
X85253	Target-1	412-434	TCCGAGAATTCCTTTGATGTTTC
	Target-2	451-473	GTCCTCTAACTTCTTGATTTTCT
U81989	Target-3	454-476	CTCGAGTTTCTTGATCTTCTTCT
AY633627	Target-4	408-430	TCCGAGAATTCCTTTGATGTTTC
X04451	Target-5	472-494	TCCGAGAATTCCTTTGATGTTCC
M92448	Target-6	469-491	TCCGAGAATTCCTTTGATGTTTC
AF104263	Target-7	412-434	TCCGAGAATTCCTTTGATGTTTC
	Target-8	469-491	TCCGAGAATTCCTTTGATGTTTC
D01075	Target-9	412-434	TCCGAGAATTCCTTTGATGTTTC
L22066	Target-10	412-434	TCCGAGAATTCCTTTGATGTTTC
AB118849	Target-11	511-533	CTCAAGTATCTTGATATTCTTCT
EF514905	Target-12	454-476	CTCGAGTTTCTTGATCTTCTTCC
	Target-13	511-533	CTCGAGTTTCTTGATCTTCTTCC
EF514904	Target-14	454-476	CTCGAGTTTCTTGATCTTCTTCC
	Target-15	511-533	CTCGAGTTTCTTGATCTTCTTCC
EF514906	Target-16	454-476	CTCGAGTTTCTTGATCTTCTTCC
	Target-17	511-533	CTCGAGTTTCTTGATCTTCTTCC
EF514907	Target-18	454-476	CTCGAGTTTCTTGATCTTCTTCC
	Target-19	511-533	CTCGAGTTTCTTGATCTTCTTCC
EF514903	Target-20	454-476	CTCGAGTTTCTTGATCTTCTTCC
	Target-21	511-533	CTCGAGTTTCTTGATCTTCTTCC
AJ307077	Target-22	412-434	TCCGAGAATTCCTTTGATGTTCC
	Target-23	441-463	AGGGATTTTCGTCCTCTATCTTC
	Target-24	451-473	GTCCCTATCTTCTTGAGTTTCT
AY648959	Target-25	412-434	TCCGAGTATTCCTTTGATGTTTC
AY648957	Target-26	412-434	TCCGAGAATTCCTTTGATGTTTC
AY648958	Target-27	412-434	TCCGAGAATTCCTTTGATGTTTC
AY648956	Target-28	412-434	TCCGAGAATTCCTTTGATGTTTC

HM046802	Target-29	412-434	TCCGAGAATTCCTTTGATGTTCC
	Target-30	441-463	AGGGATTTTCGTCCTCTATCTTC
	Target-31	451-476	GTCCCTCTATCTTCTTGAGTTTCT
	Target-32	469-491	TCCGAGAATTCCTTTGATGTTCC
	Target-33	498-520	AGGGATTTTCGTCCTCTATCTTC
	Target-34	508-530	GTCCCTCTATCTTCTTGAGTTTCT
AB118845	Target-35	48-70	GAGGGTTAACCTACGGAAATTC
AB118847	Target-36	48-70	GAGGGTTAACCTACGGAAATTC
AM183332	Target-37	551-573	TCGAGTTCATCTCGATTTTTTCT
HQ005370	Target-38	237-259	CTCCAGAAAGTTGCTTCTTCTTG
	Target-39	412-434	TCCGAGAATTCCTTTGATGTTCC
HQ005371	Target-40	410-432	TCCGAGAATTCCTTTGATGTTCC
	Target-41	494-516	TCGAGTTCCTTAACTTTTTCT
HQ005372	Target-42	237-259	CTCCAGATAGTTGCTTCTTCTTG
	Target-43	412-434	TCCGAGAATTCCTTTGATGTTCC
HQ005364	Target-44	469-491	TCCGAGAATTCCTTTGATGTTCC
HQ005366	Target-45	412-434	TCCGAGAATTCCTTTGATGTTCC
HQ005365	Target-46	469-491	TCCGAGAATTCCTTTGATGTTCC
	Target-47	554-576	TCGAGTTCATCGGCTCTTTTTCT
HQ005367	Target-48	469-491	TCCGAGAATTCCTTTGATGTTCC

Table 4: Two effective siRNA molecule with GC%, free energy of folding and free energy of binding with target

Target	Location of target within mRNA	siRNA target within in consensus	Predicted siRNA duplex	GC%	Free energy of folding of siRNA candidate at 37°C	Free energy of Binding with target
Consensus Target-1	478-501	TCCGAGAATTCCTTTGATGTTCT	AACAUCAAGGAAUUCUCG GA CGAGAAUUCUUUGAUGUU UC	47.1	0.15	-21.21
Consensus Target-2	508-530	GTCCCTCTATCTTCTTGATTTTCT	AAAAUCAAGAAGAUAGAGG AC CCUCUAUCUUCUUGAUUUU CU	36.8	-0.82	-9.41