

Table S1. Composition of the defined modules.**Module 1**

Halovirus HVTV-1 NC_020158'	'Caudovirales/Siphoviridae'
Halovirus HCTV-5 NC_021327'	'Caudovirales/Siphoviridae'
Halovirus HCTV-1 NC_021330'	'Caudovirales/Siphoviridae'

Module 2

Halorubrum virus HF2 NC_003345'	'Caudovirales/Myoviridae'
'Halovirus HF1 NC_004927'	'Caudovirales/Myoviridae'
'Halovirus HSTV-2 NC_020159'	'Caudovirales/Myoviridae'
'Halovirus HRTV-5 NC_021320'	'Caudovirales/Myoviridae'
'Halovirus HRTV-8 NC_021321'	'Caudovirales/Myoviridae'
'Halovirus HGTV-1 NC_021328'	'Caudovirales/Myoviridae'
'Halovirus HRTV-7 NC_021335'	'Caudovirales/Myoviridae'

Module 3

Nitrososphaera Pro-Nvie1 FR725450'	'Caudovirales/Proviruses'
ANMV-1 virus KP703175'	'metagenomics'
Methanosarcina acetivorans C2A NC_003552'	'Caudovirales/Proviruses'
'Methanocaldococcus fervens AG86 NC_013156'	'Caudovirales/Proviruses'
'Methanocaldococcus jannaschii DSM 2661 NC_000909'	'Caudovirales/Proviruses'
'Methanococcus maripaludis C6 NC_009975'	'Caudovirales/Proviruses'
'Methanothermococcus okinawensis IH1 NC_015636'	'Caudovirales/Proviruses'
Methanobrevibacter smithii ATCC 35061 NC_009515'	'Caudovirales/Proviruses'
'Methanocaldococcus vulcanius M7 NC_013407'	'Caudovirales/Proviruses'
Methanobacterium virus psiM2 NC_001902'	'Caudovirales/Siphoviridae'
Methanothermobacter virus psiM100 NC_002628'	'Caudovirales/Proviruses'
Natrialba virus PhiCh1 NC_004084'	'Caudovirales/Myoviridae'
'Archaeal BJ1 virus NC_008695'	'Caudovirales/Siphoviridae'
'Halovirus HCTV-2 NC_021319'	'Caudovirales/Siphoviridae'
'Halovirus HHTV-1 NC_021322'	'Caudovirales/Siphoviridae'
'Halovirus HRTV-4 NC_021329'	'Caudovirales/Siphoviridae'
'Halovirus HHTV-2 NC_021340'	'Caudovirales/Siphoviridae'
Halovirus HSTV-1 NC_021471'	'Caudovirales/Podoviridae'
Halorubrum virus CGphi46 NC_021537'	'Caudovirales'

Module 4

'Sulfolobus islandicus filamentous virus NC_003214'	'Lipothrixviridae'
'Acidianus filamentous virus 6 NC_010152'	'Lipothrixviridae'
'Acidianus filamentous virus 7 NC_010153'	'Lipothrixviridae'
'Acidianus filamentous virus 8 NC_010154'	'Lipothrixviridae'
'Acidianus filamentous virus 9 NC_010537'	'Lipothrixviridae'
'Acidianus filamentous virus 2 NC_009884'	'Lipothrixviridae'
'Acidianus filamentous virus 1 NC_005830'	'Lipothrixviridae'
'Stygiolobus rod-shaped virus FM164764'	'Rudiviridae'
'Sulfolobales Mexican rudivirus 1 JX944686'	'Rudiviridae'
'Acidianus rod-shaped virus 2 KP282675'	'Rudiviridae'

'Sulfolobus islandicus rod-shaped virus 2 NC_004086'
'Sulfolobus islandicus rod-shaped virus 1 NC_004087'
'Acidianus rod-shaped virus 1 NC_009965'

'Rudiviridae'
'Rudiviridae'
'Rudiviridae'

Module 5

'Acidianus bottle-shaped virus NC_009452'
Nitrosopumilus sp. AR NZ_AJVJ01000035'
'Candidatus Nitrosopumilus sp. AR2 NC_018656'
'Nitrosopumilus sp. SJ NZ_AJVI01000008'
His1 virus NC_007914'
'Acidianus bottle-shaped virus 3 NC_028787'
'Acidianus bottle-shaped virus 2 NC_028938'

'Ampullaviridae'
Casposons/Linked_to_Ampullaviridae_Salterprovirus'
Casposons/Linked_to_Ampullaviridae_Salterprovirus'
Casposons/Linked_to_Ampullaviridae_Salterprovirus'
Fuselloviridae/Salterprovirus'
'Ampullaviridae'
'Ampullaviridae'

Module 6

Haloarcula virus SH1 NC_007217'
'Haloarcula hispanica icosahedral virus 2 JN968479'
'Halovirus PH1 KC252997'
'Sulfolobus turreted icosahedral virus NC_005892'
'Sulfolobus turreted icosahedral virus 2 NC_014099'
Natrinema virus SNJ1 AY048850'
'Thermus thermophilus phage IN93 NC_004462'
Haloarcula saccharovororum plasmid pZMX101 NC_004531'
'Thermus thermophilus bacteriophage P23-77 NC_013197'
Methanosarcina acetivorans plasmid pC2A NC_002097'
Methanococcus voltae A3 provirus MVV NC_014222-2'
Pyrobaculum oguniense TE7 plasmid NC_016886'
Thermococcus kodakarensis KOD1 provirus TKV4 NC_006624'
Thermococcus nautili plasmid pTN3 NC_022527'

Sphaerolipoviridae/Alphashaerolipovirus'
Sphaerolipoviridae/Alphashaerolipovirus'
Sphaerolipoviridae/Alphashaerolipovirus'
'Turriviridae'
'Turriviridae'
Sphaerolipoviridae/Betasphaerolipovirus'
Sphaerolipoviridae/Gammasphaerolipovirus'
Plasmids/Linked_to_Betasphaerolipovirus'
Sphaerolipoviridae/Gammasphaerolipovirus'
'Plasmids/Linked_to_Betasphaerolipovirus'
Linked_to_Turriviridae/Proviruses'
'Plasmids/Linked_to_Turriviridae'
Linked_to_Turriviridae/Proviruses'
'Plasmids/Linked_to_Turriviridae'

Module 7

Thermococcus sp. CIR10 plasmid pCIR10 NC_019884'
Thermococcus sp. IRI48 plasmid pIRI48 NC_019883'
Thermococcus nautili plasmid pTN2 NC_014115'
Methanococcus voltae A3 provirus A3-VLP NC_014222-1'
Pyrococcus abyssi virus 1 NC_009597'

'Plasmids/Linked_to_PAV1'
'Plasmids/Linked_to_PAV1'
'Plasmids/Linked_to_PAV1'
Linked_to_Fuselloviridae/Proviruses'
'Fuselloviridae'

Module 8

'Sulfolobus virus 1 NC_001338'
'Sulfolobus virus 2 NC_005265'
'Sulfolobus virus Ragged Hills NC_005360'
'Sulfolobus virus Kamchatka 1 NC_005361'
'Sulfolobus spindle-shaped virus 4 NC_009986'
'Sulfolobus spindle-shaped virus 7 NC_013588'
'Acidianus spindle-shaped virus 1 NC_013585'
'Sulfolobus spindle-shaped virus 6 NC_013587'
'Aeropyrum pernix ovoid virus 1 HE580237'
Sulfolobus islandicus plasmid pSSVx NC_010011'

'Fuselloviridae'
'Fuselloviridae'
'Fuselloviridae'
'Fuselloviridae'
'Fuselloviridae'
'Fuselloviridae'
'Fuselloviridae'
'Fuselloviridae'
'Guttaviridae'
'Plasmids/Linked_to_Fuselloviridae'

Sulfolobus solfataricus P2 plasmid pSSVi NC_013777'	'Plasmids/Linked_to_Fuselloviridae'
Aeropyrum pernix spindle-shaped virus 1 HE580238'	'Fuselloviridae'
Thermococcus prieurii virus 1 NC_016899'	'Fuselloviridae'
'Sulfolobales Mexican fusellovirus 1 NC_020882'	'Fuselloviridae'
'Sulfolobus islandicus L.S.2.15 CP001399'	Fuselloviridae/Proviruses'
'Sulfolobus islandicus M.14.25 CP001400'	Fuselloviridae/Proviruses'
'Sulfolobus islandicus Y.G.57.14 CP001403'	Fuselloviridae/Proviruses'

Module 9

'Acidianus two-tailed virus NC_007409'	'Bicaudaviridae'
'Sulfolobales virus YNP1 KP282679'	'metagenomics'
'Sulfolobales Virus YNP2 KP282680'	'metagenomics'
'Hyperthermophilic Archaeal Virus 2 NC_014321'	'metagenomics'
'Sulfolobus monocaudavirus SMV1 HG322870'	'Bicaudaviridae'
'Sulfolobus virus STSV1 NC_006268'	'Bicaudaviridae'
'Sulfolobus virus STSV2 NC_020077'	'Bicaudaviridae'
'Sulfolobus monocaudavirus SMV2 NC_029020'	'Bicaudaviridae'
'Sulfolobus monocaudavirus SMV3 NC_029103'	'Bicaudaviridae'
'Acidianus tailed spindle virus NC_029316'	'Bicaudaviridae'

Module 10









Haloarcula hispanica pleomorphic virus 2 KF056323'	'Pleolipoviridae'
Halorubrum pleomorphic virus 1 NC_012558'	'Pleolipoviridae'
'Halorubrum pleomorphic virus 2 NC_017087'	'Pleolipoviridae'
'Halorubrum pleomorphic virus 6 NC_017089'	'Pleolipoviridae'
Archaeoglobus profundus plasmid pGS5 NC_012890'	'Plasmids/Linked_to_Pleolipoviridae'
Natrinema virus SNJ2 CP003412'	'Pleolipoviridae'
'Halorubrum pleomorphic virus 3 NC_017088'	'Pleolipoviridae'
Halogeometricum pleomorphic virus 1 NC_017090'	'Pleolipoviridae'
'His2 virus NC_007918'	'Pleolipoviridae'
Haloferax lucentense DSM 14919 plasmid pHK2 NC_019285'	Pleolipoviridae/Proviruses'
Thermococcus prieurii plasmid pTP2 NC_021208'	'Plasmids/Linked_to_Pleolipoviridae'

Unassigned

'Pyrobaculum spherical virus NC_005872'	'Globuloviridae'
'Hyperthermophilic Archaeal Virus 1 NC_014322'	'metagenomics'
'Aeropyrum spring-shaped virus HE681887'	'Spiraviridae'
'Pyrobaculum filamentous virus 1 KU307456'	'Tristromaviridae'
'Thermoproteus tenax virus 1 X14855'	'Tristromaviridae'
'Thermoproteus tenax spherical virus 1 NC_006556'	'Globuloviridae'
'Aeropyrum pernix bacilliform virus 1 AB537968'	'Clavaviridae'

Table S2. Complete list of core genes.

Family Nr.	Representative sequence	Annotation	Retention	Abund.	Module	Hallmark	Signature*	Comments
30578	'448260172'	' RHH domain'	0.740	0.310	8			* Signature genes of module 5 (Ampullaviridae) are absent in related casposons
24	'506497871'	Integrase	0.516	0.236	3			
5	'AAQ07582.1'	Terminase	0.960	0.234	3			
16	'BAK52950.1'	Portal protein	0.631	0.217	3			
13	'ABD90605.1'	Major capsid protein HK97-like	0.834	0.208	3			
11	'738838588'	DNA polymerase B	0.323	0.188	5			Core gene in the greater dsDNA virus network. It includes protein- and RNA-primed PolB. Protein-primed PolB is signature of Ampullaviridae.
30596	'448260216'	DnaA-like AAA+ ATPase (PHA00729)	0.999	0.188	8			
111	'NP_037700.1'	Protease (herpesvirus S21, phage U9/U35)	0.588	0.184	3			
30580	'146411830'	Glycosyl transferase (GT-B superfamily)	0.999	0.153	4			
12	'134287264'	A32-like packaging ATPase (FtsK/HerA)	0.999	0.144	6			
26	'ADF29313.1'	Phage mu protein F, putative minor head protein	0.733	0.138	3			
30576	'472438248'	Major capsid protein from fuselloviruses	0.999	0.136	8			
30577	'472438234'	' integrase [Sulfolobales Mexican fusellovirus 1]'	0.969	0.124	8			
36714	YP_007348292.1	AAA family ATPase	0.999	0.123	9			
27	'310831525'	HNHc endonuclease Bacteriophage HK97-gp10, putative tail-component	0.486	0.122	2			
22	'NP_945289.1'		0.683	0.104	3			
23	'9964588'	phage tail tape measure protein	0.163	0.098	3			Core gene in the greater dsDNA virus network
60	'YP_003929.1'	' Metallophosphatase'	0.770	0.098	2			
1045	'YP_319903.1'	Putative integrase	0.999	0.092	9			
30612	'448260199'	PHA02732 / hypothetical protein STSV2_52	0.999	0.092	9			
551	'NP_665939.1'	' HTH domain'	0.333	0.092	2			Core gene in the greater dsDNA virus network
30623	'448260185'	hypothetical protein STSV2_38	0.999	0.081	9			
30601	'270281838'	' zinc finger protein [Sulfolobus spindle-shaped virus 7]'	0.624	0.081	8			
30615	YP_001542641.1	MCP from Ligamenvirales	0.826	0.080	4			
30595	'171473698'	Glycosyltransferase (PHA01631)	0.999	0.080	4			
305	'CCE26327.1'	MoxR-like ATPase	0.663	0.075	9			
68	'738838596'	Double jelly-roll major capsid prot	0.999	0.072	6			
30579	'472438232'	PHA00728 (coiled-coil protein)	0.999	0.071	8			
26445	'YP_002791886.1'	Rolling-circle replication initiation endonuclease	0.063	0.071	10			Added to avoid disconnection of 'Archaeoglobus profundus NC_012890'
30581	'171473709'	SAM-dependent methyltransferase	0.794	0.070	4			
26471	'YP_919083.1'	'GI:119757041'	0.999	0.067	3			
69	'CBJ93956.1'	' PDDEXK nuclease; Cas4 superfamily'	0.999	0.066	2			
6697	YP_001429672.1'	' primase'	0.999	0.066	2			
19	'9628153'	' Ribonucleotide reductase large subunit'	0.063	0.064	2			Core gene in the greater dsDNA virus network
30641	'448260178'	' hypothetical protein STSV2_31 [Sulfolobus virus STSV2]'	0.999	0.064	9			
30649	'448260196'	' hypothetical protein STSV2_49 [Sulfolobus virus STSV2]'	0.999	0.064	9			
30696	'448260184'	Major capsid protein from Bicaudaviridae	0.999	0.064	9			
44	'BAK52969.1'	Baseplate J family protein	0.643	0.064	2			
19348	'NP_665955.1'	'GI:22091141'	0.643	0.064	2			

30913	'75750417'	'GI:75750417'	0.755	0.063	9	
30574	'472438231'	'hypothetical protein SMF1_0006 [Sulfolobales Mexican fusellovirus 1]'	0.999	0.061	8	
30575	'472438243'	'putative end-filament protein [Sulfolobales Mexican fusellovirus 1]'	0.999	0.061	8	
30587	'472438245'	'hypothetical protein SMF1_0020 [Sulfolobales Mexican fusellovirus 1]'	0.999	0.061	8	
30602	'472438229'	'hypothetical protein SMF1_0004 [Sulfolobales Mexican fusellovirus 1]'	0.999	0.061	8	
34324	'27819355'	'GI:27819355'	0.999	0.060	6	
34325	'27819354'	'GI:27819354'	0.999	0.060	6	
30907	'75750431'	'GI:75750431'	0.486	0.060	9	
30585	'171473711'	'hypothetical protein AFV9_gp63 [Acidianus filamentous virus 9]'	0.343	0.060	4	
30712	'171473720'	'hypothetical protein AFV9_gp72 [Acidianus filamentous virus 9]'	0.343	0.060	4	
31178	90403542'	ATP-dependent metalloprotease FtsH	0.999	0.059	10	
31182	90403538'	Spike protein (HRPV-1 VP4)	0.999	0.059	10	
30592	'270281809'	'hypothetical protein SSSV6_gp25 [Sulfolobus spindle-shaped virus 6]'	0.624	0.058	8	
30598	'472438246'	'putative transcriptional regulator [Sulfolobales Mexican fusellovirus 1]'	0.631	0.055	8	
30606	'472438230'	'hypothetical protein SMF1_0005 [Sulfolobales Mexican fusellovirus 1]'	0.631	0.055	8	
8	'134287171'	'DEAD-like helicase'	0.168	0.055	4	Core gene in the greater dsDNA virus network
30590	'157929288'	'hypothetical protein AFV2_gp15 [Acidianus filamentous virus 2]'	0.778	0.054	4	
30653	'448260181'	'GI:448260181'	0.444	0.054	9	
30616	'700075124'	'hypothetical protein [Stygiolobus rod-shaped virus]'	0.999	0.054	4	
50	'116326771'	Polynucleotide kinase/phosphatase	0.033	0.052	7	Core gene in the greater dsDNA virus network
34475	'AHF22118.1'	uncharacterized, GI:571033270	0.571	0.052	10	
34492	'YP_002791888.1'	Pleolipovirus integral membrane protein	0.571	0.052	10	
35205	'SNJ1_gp15'	'missing_db_xref_qualifer'	0.999	0.051	6	
271	'9628234'	'proliferating cell nuclear antigen'	0.087	0.051	3	Core gene in the greater dsDNA virus network
34677	'NP_542589.1'	'GI:18138485'	0.999	0.051	2	
34687	'NP_542607.1'	COG5484, YjcR	0.999	0.051	2	
32051	'937424876'	'38K [Perigonia lusca single nucleopolyhedrovirus]'	0.200	0.050	7	Core gene in the greater dsDNA virus network
545	'BAK52970.1'	'hypothetical protein'	0.643	0.050	2	
30608	'270281824'	'hypothetical protein SSSV7_gp02 [Sulfolobus spindle-shaped virus 7]'	0.208	0.049	8	Core gene in the greater dsDNA virus network
34839	'YP_007379058.1'	'GI:443404719'	0.999	0.048	1	
34655	'NP_542552.1'	'GI:18138450'	0.843	0.046	2	
34333	'478755957'	'hypothetical protein HhPH1_gp09 [Haloarcula hispanica virus PH1]'	0.999	0.045	6	
22541	'YP_003358951.1'	'hypothetical protein'	0.999	0.044	4	
30589	'171473670'	'hypothetical protein AFV9_gp22 [Acidianus filamentous virus 9]'	0.999	0.044	4	
30628	'171473671'	'hypothetical protein AFV9_gp23 [Acidianus filamentous virus 9]'	0.999	0.044	4	
30680	'171473690'	'hypothetical protein AFV9_gp42 [Acidianus filamentous virus 9]'	0.999	0.044	4	
186	'441432820'	'nucleotidase'	0.999	0.043	1	
273	'701447244'	'conserved ribonuclease H [Melbournevirus]'	0.999	0.043	1	
544	'ADQ52777.1'	'''' conserved hypothetical protein, range: 1..178 HHsearch against CDD matches: PRK04860:hypothetical protein;; PRK04351:hypothetic...' <Preview truncated at 128 characters>'	0.999	0.043	1	
34814	'YP_007379023.1'	'GI:443404684'	0.999	0.043	1	
35182	'YP_007195308.1'	Putative primase/polymerase	0.999	0.043	7	
35183	'YP_007195311.1'	Coiled-coil domain protein	0.999	0.041	7	
2376	'ADE87958.1'	'putative replicative DNA helicase'	0.559	0.040	3	

34554	'YP_003128847.1'	'GI:256811478'	0.559	0.040	3
34574	'YP_003128884.1'	'GI:256811515'	0.559	0.040	3
496	'134287225'	'transcription initiation factor IIB'	0.001	0.039	9
15	'134287325'	'S_TKc serine/threonine protein kinase'	0.015	0.039	1
3887	'ALM_ORF07'	'ALM_ORF07'	0.999	0.038	5
30837	'146411859'	GI:146411859'	0.999	0.038	5
30839	'146411857'	GI:146411857'	0.999	0.038	5
30840	'146411856'	GI:146411856'	0.999	0.038	5
30841	'146411854'	GI:146411854'	0.999	0.038	5
30842	'146411853'	GI:146411853'	0.999	0.038	5
30843	'146411852'	GI:146411852'	0.999	0.038	5
30844	'146411851'	GI:146411851'	0.999	0.038	5
30845	'146411850'	GI:146411850'	0.999	0.038	5
30846	'146411848'	GI:146411848'	0.999	0.038	5
30847	'146411847'	GI:146411847'	0.999	0.038	5
30848	'146411846'	GI:146411846'	0.999	0.038	5
30849	'146411845'	GI:146411845'	0.999	0.038	5
30850	'146411844'	GI:146411844'	0.999	0.038	5
30851	'146411843'	transcriptional regulator, winged helix-turn-helix motif'	0.999	0.038	5
30853	146411841'	'GI:146411841'	0.999	0.038	5
30854	146411839'	'GI:146411839'	0.999	0.038	5
30855	146411838'	'GI:146411838'	0.999	0.038	5
30856	146411837'	'GI:146411837'	0.999	0.038	5
30858	146411834'	'GI:146411834'	0.999	0.038	5
30861	146411829'	'GI:146411829'	0.999	0.038	5
30862	146411828'	'GI:146411828'	0.999	0.038	5
30864	146411826'	transcriptional regulator, RHH' HHpred hit (range 1..44) to 2cpg and pfam12651, P=95,3	0.999	0.038	5
30865	146411825'	GI:146411825'	0.999	0.038	5
30867	146411823'	'GI:146411823'	0.999	0.038	5
30870	146411820'	'GI:146411820'	0.999	0.038	5
311	NP_049763.1	Baseplate spike (PAAR domain)	0.999	0.037	2
3392	'AEA86265.1'	'hypothetical protein'	0.999	0.037	2
9354	'YP_418121.1'	'hypothetical protein'	0.999	0.037	2
11219	'YP_002898962.1'	'hypothetical protein'	0.999	0.037	2
20792	'YP_717710.1'	gp43, range: 1..122 HHsearch against CDD matches: (unmatched)'	0.999	0.037	2
34618	'NP_542506.1'	'GI:18138408'	0.999	0.037	2
34632	'NP_542523.1'	'GI:18138422'	0.999	0.037	2
34635	'NP_542527.1'	'GI:18138426'	0.999	0.037	2
34636	'NP_542528.1'	'GI:18138427'	0.999	0.037	2
34638	'NP_542531.1'	'GI:18138429'	0.999	0.037	2
34641	'NP_542534.1'	'GI:18138432'	0.999	0.037	2
34643	'NP_542536.1'	'GI:18138434'	0.999	0.037	2
34644	'NP_542539.1'	'GI:18138437'	0.999	0.037	2
34645	'NP_542540.1'	'GI:18138438'	0.999	0.037	2
34648	'NP_542544.1'	'GI:18138442'	0.999	0.037	2
34666	'NP_542575.1'	'GI:18138471'	0.999	0.037	2
34667	'NP_542576.1'	'GI:18138472'	0.999	0.037	2
34668	'NP_542579.1'	'GI:18138475'	0.999	0.037	2

Core gene in the greater dsDNA virus network
Core gene in the greater dsDNA virus network



34670	'NP_542582.1'	'GI:18138478'	0.999	0.037	2
34671	'NP_542583.1'	'GI:18138479'	0.999	0.037	2
34672	'NP_542584.1'	'GI:18138480'	0.999	0.037	2
34673	'NP_542585.1'	'GI:18138481'	0.999	0.037	2
34674	'NP_542586.1'	'GI:18138482'	0.999	0.037	2
34676	'NP_542588.1'	'GI:18138484'	0.999	0.037	2
34678	'NP_542590.1'	'GI:18138486'	0.999	0.037	2
34679	'NP_542591.1'	'GI:18138487'	0.999	0.037	2
34680	'NP_542592.1'	'GI:18138488'	0.999	0.037	2
34681	'NP_542593.1'	'GI:18138489'	0.999	0.037	2
34686	'NP_542605.1'	'GI:18138501'	0.999	0.037	2
36709	'NP_542598.1'	uncharacterized protein	0.999	0.037	2
30591	'700075128'	'hypothetical protein [Stygiolobus rod-shaped virus]'	0.999	0.036	4
30594	'700075126'	'hypothetical protein [Stygiolobus rod-shaped virus]'	0.999	0.036	4
30600	'700075122'	'hypothetical protein [Stygiolobus rod-shaped virus]'	0.999	0.036	4
30610	'700075129'	'hypothetical protein [Stygiolobus rod-shaped virus]'	0.999	0.036	4
30624	'700075127'	'hypothetical protein [Stygiolobus rod-shaped virus]'	0.999	0.036	4
30668	'700075121'	'hypothetical protein [Stygiolobus rod-shaped virus]'	0.999	0.036	4
30675	'700075104'	'hypothetical protein [Stygiolobus rod-shaped virus]'	0.999	0.036	4
30679	'700075120'	'hypothetical protein [Stygiolobus rod-shaped virus]'	0.999	0.036	4
30737	'700075125'	'hypothetical protein [Stygiolobus rod-shaped virus]'	0.999	0.036	4
30659	'295441845'	'GI:295441845'	0.999	0.035	6
30582	'171473676'	'hypothetical protein AFV9_gp28 [Acidianus filamentous virus 9]'	0.543	0.035	4
30611	'171473718'	'hypothetical protein AFV9_gp70 [Acidianus filamentous virus 9]'	0.543	0.035	4
30614	'171473662'	'hypothetical protein AFV9_gp14 [Acidianus filamentous virus 9]'	0.543	0.035	4
30620	'171473663'	'hypothetical protein AFV9_gp15 [Acidianus filamentous virus 9]'	0.543	0.035	4
30629	'171473654'	'hypothetical protein AFV9_gp06 [Acidianus filamentous virus 9]'	0.543	0.035	4
30630	'171473677'	'hypothetical protein AFV9_gp29 [Acidianus filamentous virus 9]'	0.543	0.035	4
30633	'171473679'	'hypothetical protein AFV9_gp31 [Acidianus filamentous virus 9]'	0.543	0.035	4
30636	'171473685'	'viral structural protein [Acidianus filamentous virus 9]'	0.543	0.035	4
30639	'171473655'	'putative RHH transcriptional regulator [Acidianus filamentous virus 9]'	0.543	0.035	4
30640	'171473712'	'viral structural protein [Acidianus filamentous virus 9]'	0.543	0.035	4
30643	'171473659'	'hypothetical protein AFV9_gp11 [Acidianus filamentous virus 9]'	0.543	0.035	4
30646	'171473660'	'viral structural protein [Acidianus filamentous virus 9]'	0.543	0.035	4
30662	'171473678'	'hypothetical protein AFV9_gp30 [Acidianus filamentous virus 9]'	0.543	0.035	4
30664	'171473682'	'hypothetical protein AFV9_gp34 [Acidianus filamentous virus 9]'	0.543	0.035	4
30673	'171473672'	'hypothetical protein AFV9_gp24 [Acidianus filamentous virus 9]'	0.543	0.035	4
30682	'171473675'	'hypothetical protein AFV9_gp27 [Acidianus filamentous virus 9]'	0.543	0.035	4
30703	'171473683'	'hypothetical protein AFV9_gp35 [Acidianus filamentous virus 9]'	0.543	0.035	4
21237	'YP_001429789.1'	'putative metalloprotein chaperonin subunit'	0.740	0.035	9
30900	'75750439'	'GI:75750439'	0.740	0.035	9
30921	'75750404'	'GI:75750404'	0.740	0.035	9
2418	'YP_112490.1'	'terminase small subunit'	0.999	0.033	3
31180	'90403540'	'GI:90403540'	0.491	0.033	10



34933	'YP_008058387.1'	'GI:509139494' 'putative capsid protein VP18 [Haloarcula hispanica virus PH1]'	0.999	0.033	3
34303	'478755997'	'hypothetical protein HhPH1_gp47 [Haloarcula hispanica virus PH1]'	0.999	0.033	6
34304	'478755995'	'hypothetical protein HhPH1_gp43 [Haloarcula hispanica virus PH1]'	0.999	0.033	6
34306	'478755991'	'hypothetical protein HhPH1_gp40 [Haloarcula hispanica virus PH1]'	0.999	0.033	6
34308	'478755988'	'hypothetical protein HhPH1_gp38 [Haloarcula hispanica virus PH1]'	0.999	0.033	6
34310	'478755986'	'hypothetical protein HhPH1_gp37 [Haloarcula hispanica virus PH1]'	0.999	0.033	6
34311	'478755985'	'hypothetical protein HhPH1_gp36 [Haloarcula hispanica virus PH1]'	0.999	0.033	6
34312	'478755984'	'hypothetical protein HhPH1_gp35 [Haloarcula hispanica virus PH1]'	0.999	0.033	6
34313	'478755983'	'hypothetical protein HhPH1_gp30 [Haloarcula hispanica virus PH1]'	0.999	0.033	6
34316	'478755978'	'capsid protein VP10 [Haloarcula hispanica virus PH1]'	0.999	0.033	6
34320	'478755974'	'capsid protein VP5 [Haloarcula hispanica virus PH1]'	0.999	0.033	6
34321	'478755973'	'capsid protein VP13 [Haloarcula hispanica virus PH1]'	0.999	0.033	6
34322	'478755971'	'hypothetical protein HhPH1_gp22 [Haloarcula hispanica virus PH1]'	0.999	0.033	6
34323	'478755970'	'capsid protein VP12 [Haloarcula hispanica virus PH1]'	0.999	0.033	6
34326	'478755967'	'hypothetical protein HhPH1_gp18 [Haloarcula hispanica virus PH1]'	0.999	0.033	6
34327	'478755966'	'hypothetical protein HhPH1_gp17 [Haloarcula hispanica virus PH1]'	0.999	0.033	6
34328	'478755965'	'hypothetical protein HhPH1_gp16 [Haloarcula hispanica virus PH1]'	0.999	0.033	6
34329	'478755964'	'hypothetical protein HhPH1_gp15 [Haloarcula hispanica virus PH1]'	0.999	0.033	6
34330	'478755963'	'hypothetical protein HhPH1_gp14 [Haloarcula hispanica virus PH1]'	0.999	0.033	6
34331	'478755962'	'capsid protein VP1 [Haloarcula hispanica virus PH1]'	0.999	0.033	6
34332	'478755960'	'hypothetical protein HhPH1_gp05 [Haloarcula hispanica virus PH1]'	0.999	0.033	6
34334	'478755953'	'hypothetical protein HhPH1_gp03 [Haloarcula hispanica virus PH1]'	0.999	0.033	6
34336	'478755951'	'putative glycosyltransferase [Megavirus lba]'	0.537	0.029	9
357	'448825509'	'GI:448260209'	0.537	0.029	9
30652	'448260209'	'GI:448260215'	0.537	0.029	9
30676	'448260215'	'GI:448260182'	0.537	0.029	9
30705	'448260182'	'GI:448260180'	0.537	0.029	9
30723	'448260180'	'GI:448260189'	0.537	0.029	9
30739	'448260189'	'GI:448260198'	0.537	0.029	9
30747	'448260198'	'GI:448260191'	0.537	0.029	9
30787	'448260191'	'GI:448260194'	0.537	0.029	9
30878	'448260194'	'GI:448260193'	0.537	0.029	9
30879	'448260193'	'GI:448260192'	0.537	0.029	9
30880	'448260192'	'putative HNH-family endonuclease [Melbournevirus]'	0.999	0.029	1
43	'701447394'	'alt RNA polymerase ADP-ribosylase'	0.999	0.029	1
257	'BAI83209.1'	'belonging to T4-LIKE GC: 843'	0.999	0.029	1
590	'YP_195178.1'	GTP cyclohydrolase	0.999	0.029	1
1582	'531034917'	Organic radical activating enzyme (radical SAM superfamily)	0.999	0.029	1
1841	YP_007378978.1'	'hypothetical protein, range: 1..185 HHsearch against CDD matches: (unmatched)'	0.999	0.029	1
1963	'ADF58194.1'	6-pyruvoyl tetrahydropterin synthase	0.999	0.029	1
6195	YP_007378981.1'	7-cyano-7-deazaguanine reductase	0.999	0.029	1
9116	'NP_899371.1'	'putative cobalamin biosynthesis protein CobT'	0.999	0.029	1
11110	'ADX87791.1'	'gp666'	0.999	0.029	1
19073	'AEO93909.1'				



21221	'YP_001429772.1'	'hypothetical protein'	0.999	0.029	1
24683	'AEL97961.1'	'gp52'	0.999	0.029	1
27604	'YP_003084174.1'	'minor head protein, range: 1..151 HHsearch against CDD matches: (unmatched)'	0.999	0.029	1
34764	'YP_007378914.1'	'GI:443404577'	0.999	0.029	1
34766	'YP_007378918.1'	'GI:443404580'	0.999	0.029	1
34767	'YP_007378919.1'	'GI:443404581'	0.999	0.029	1
34768	'YP_007378922.1'	'GI:443404583'	0.999	0.029	1
34769	'YP_007378923.1'	'GI:443404584'	0.999	0.029	1
34770	'YP_007378925.1'	'GI:443404586'	0.999	0.029	1
34771	'YP_007378926.1'	'GI:443404587'	0.999	0.029	1
34774	'YP_007378933.1'	'GI:443404594'	0.999	0.029	1
34775	'YP_007378935.1'	'GI:443404596'	0.999	0.029	1
34776	'YP_007378938.1'	'GI:443404599'	0.999	0.029	1
34778	'YP_007378945.1'	'GI:443404606'	0.999	0.029	1
34779	'YP_007378946.1'	'GI:443404607'	0.999	0.029	1
34782	'YP_007378955.1'	'GI:443404616'	0.999	0.029	1
34783	'YP_007378956.1'	'GI:443404617'	0.999	0.029	1
34784	'YP_007378958.1'	'GI:443404619'	0.999	0.029	1
34785	'YP_007378960.1'	'GI:443404621'	0.999	0.029	1
34787	'YP_007378965.1'	'GI:443404626'	0.999	0.029	1
34788	'YP_007378966.1'	'GI:443404627'	0.999	0.029	1
34789	'YP_007378969.1'	'GI:443404630'	0.999	0.029	1
34793	'YP_007378974.1'	'GI:443404635'	0.999	0.029	1
34794	'YP_007378976.1'	'GI:443404637'	0.999	0.029	1
34795	'YP_007378977.1'	'GI:443404638'	0.999	0.029	1
34796	'YP_007378984.1'	'GI:443404645'	0.999	0.029	1
34803	'YP_007378995.1'	'GI:443404656'	0.999	0.029	1
34804	'YP_007378999.1'	'GI:443404660'	0.999	0.029	1
34807	'YP_007379004.1'	'GI:443404665'	0.999	0.029	1
34808	'YP_007379006.1'	'GI:443404667'	0.999	0.029	1
34809	'YP_007379007.1'	'GI:443404668'	0.999	0.029	1
34811	'YP_007379009.1'	'GI:443404670'	0.999	0.029	1
34812	'YP_007379013.1'	'GI:443404674'	0.999	0.029	1
34817	'YP_007379026.1'	'GI:443404687'	0.999	0.029	1
34818	'YP_007379027.1'	'GI:443404688'	0.999	0.029	1
34819	'YP_007379028.1'	'GI:443404689'	0.999	0.029	1
34820	'YP_007379029.1'	'GI:443404690'	0.999	0.029	1
34833	'YP_007379049.1'	'GI:443404710'	0.999	0.029	1
34835	'YP_007379054.1'	'GI:443404715'	0.999	0.029	1
34842	'YP_007379061.1'	'GI:443404722'	0.999	0.029	1
34845	'YP_007379065.1'	'GI:443404726'	0.999	0.029	1
34846	'YP_007379067.1'	'GI:443404728'	0.999	0.029	1
34847	'YP_007379068.1'	'GI:443404729'	0.999	0.029	1
34848	'YP_007379069.1'	'GI:443404730'	0.999	0.029	1
34850	'YP_007379073.1'	'GI:443404734'	0.999	0.029	1
35104	'YP_007378980.1'	'GI:443404641'	0.999	0.029	1
36710	YP_007379010'	RadA recombinase	0.999	0.029	1
30	'134287277'	'UvrD-like helicase'	0.999	0.026	7



35184	'YP_007195317.1'	'GI:430721640'	0.999	0.026	7
36712	YP_007195312.1	transcriptional regulation (plasmid)	0.999	0.026	7
34501	'WP_016939979.1'	'GI:515506725'	0.999	0.024	5
34502	'WP_016939980.1'	'GI:515506726'	0.999	0.024	5
34503	'WP_016939981.1'	'GI:515506727'	0.999	0.024	5
34505	'WP_016939987.1'	'GI:515506733'	0.999	0.024	5
36711	NP_776202.1'	RepA	0.12	0.0233	6
84	'ACU41204.1'	'gp58, range: 1..64 HHsearch against CDD matches: pfam00057:Ldl_recept_a Low-den'	0.024	0.021	2

Shared by SNJ1, pZMX101 and pC2A
Core gene in the greater dsDNA virus network