

TABLE S4. Conserved domains in HCIV-1 predicted proteins.

HCIV-1 (putative) proteins	Domain hit <sup>a</sup>				
	Name	Accession	Description	Amino acid Coordinates	BLAST e- value
VP1	PCNA	<a href="#">cd00577</a>	Proliferating Cell Nuclear Antigen (PCNA) domain found in eukaryotes and archaea	376-601	4.51e-20
	PCNA	<a href="#">cd00577</a>	Proliferating Cell Nuclear Antigen (PCNA) domain found in eukaryotes and archaea	5-223	3.22e-10
	PRK01115	<a href="#">PRK01115</a>	DNA polymerase sliding clamp	363-602	2.15e-31
	PRK01115	<a href="#">PRK01115</a>	DNA polymerase sliding clamp	3-247	2.43e-09
	DnaN	<a href="#">COG0592</a>	DNA polymerase sliding clamp subunit (PCNA homolog)	376-516	1.42e-04
	TIGR03491	<a href="#">TIGR03491</a>	RecB family nuclease, putative, TM0106 family	91-159	6.96e-04
Putative ATPase	AAA_10	<a href="#">pfam12846</a>	AAA-like domain	92-192	1.39e-07
	Yjgr	<a href="#">COG0433</a>	Archaeal DNA helicase HerA or a related bacterial ATPase	119-211	2.51e-04
VP5	cpdB	<a href="#">PRK09420</a>	Bifunctional 2',3'-cyclic nucleotide 2'-phosphodiesterase/3'-nucleotidase periplasmic precursor protein	167-264	9.99e-03
Putative protein 32	phenyl_P_alpha	<a href="#">TIGR02723</a>	Phenylphosphate carboxylase, alpha subunit	7-50	2.69e-03
Putative protein 33	PRK14293	<a href="#">PRK14293</a>	Chaperon protein DnaJ	38-71	7.25e-03
Putative protein 34	SIR2	<a href="#">COG0846</a>	NAD-dependent protein deacetylases, SIR2 family	2-50	1.77e-03
	PRK06082	<a href="#">PRK06082</a>	4-aminobutyrate aminotransferase	30-49	5.24e-03
	SIR2-fam	<a href="#">cd01407</a>	Sir2 proteins (gene regulators)	10-50	9.46e-03
Putative protein 41	DUF4326	<a href="#">pfam14216</a>	Domain of unknown function (DUF4326)	206-279	1.74e-10
	PTZ00121	<a href="#">PTZ00121</a>	MAEBL	3-227	4.11e-04
Putative protein 42	TPMT	<a href="#">pfam05724</a>	Thiopurine S-methyltransferase (TPMT)	83-164	2.04e-03
Putative protein 44	Sigma70_r4_2	<a href="#">pfam08281</a>	Sigma-70, region 4	65-108	1.18e-07
	Sigma70_r4	<a href="#">cd06171</a>	Sigma70, region (SR) 4	65-105	3.36e-05
	txf	<a href="#">PRK03975</a>	Putative transcriptional regulator	60-134	5.58e-09
	SigX5	<a href="#">TIGR02960</a>	RNA polymerase sigma-70 factor, TIGR02960 family	32-127	2.28e-07
	RpoE	<a href="#">COG1595</a>	DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog	10-105	3.08e-07
Putative protein 46	HypA	<a href="#">pfam01155</a>	Hydrogenase expression/synthesis hypA family	6-37	3.00e-04
	hypA	<a href="#">PRK00564</a>	Hydrogenase nickel incorporation protein	5-31	9.57e-03
	PriA	<a href="#">COG1198</a>	Primosomal protein N' (replication factor Y) - superfamily II helicase	3-34	3.74e-05

<sup>a</sup> Hits were found with BLASTp program, search dated 21 March 2016 (e-value threshold 0.01).