Supplementary tables

Table S1. All predicted EcoR1 digestion fragments from VHS1.

All predicted digestion fragments							
Arranged by length				Arranged by order			
#	**Ends**	**Coordinates**	**Length (bp)**	**#**	**Ends**	**Coordinates**	**Length (bp)**
1	EcoRI-EcoRI	34915-56191	21277	1	EcoRI-EcoRI	2518-4012	1495
2	EcoRI-EcoRI	17918-27430	9513	2	EcoRI-EcoRI	4013-6526	2514
3	EcoRI-EcoRI	75916-2517	8110	3	EcoRI-EcoRI	6527-7206	680
4	EcoRI-EcoRI	27431-34914	7484	4	EcoRI-EcoRI	7207-9067	1861
5	EcoRI-EcoRI	65354-70742	5389	5	EcoRI-EcoRI	9068-9101	34
6	EcoRI-EcoRI	71916-75915	4000	6	EcoRI-EcoRI	9102-11876	2775
7	EcoRI-EcoRI	56192-59864	3673	7	EcoRI-EcoRI	11877-14349	2473
8	EcoRI-EcoRI	60278-63870	3593	8	EcoRI-EcoRI	14350-17234	2885
9	EcoRI-EcoRI	14350-17234	2885	9	EcoRI-EcoRI	17235-17917	683
10	EcoRI-EcoRI	9102-11876	2775	10	EcoRI-EcoRI	17918-27430	9513
11	EcoRI-EcoRI	4013-6526	2514	11	EcoRI-EcoRI	27431-34914	7484
12	EcoRI-EcoRI	11877-14349	2473	12	EcoRI-EcoRI	34915-56191	21277
13	EcoRI-EcoRI	7207-9067	1861	13	EcoRI-EcoRI	56192-59864	3673
14	EcoRI-EcoRI	2518-4012	1495	14	EcoRI-EcoRI	59865-60277	413
15	EcoRI-EcoRI	63871-65353	1483	15	EcoRI-EcoRI	60278-63870	3593
16	EcoRI-EcoRI	70743-71582	840	16	EcoRI-EcoRI	63871-65353	1483
17	EcoRI-EcoRI	17235-17917	683	17	EcoRI-EcoRI	65354-70742	5389
18	EcoRI-EcoRI	6527-7206	680	18	EcoRI-EcoRI	70743-71582	840
19	EcoRI-EcoRI	59865-60277	413	19	EcoRI-EcoRI	71583-71915	333
20	EcoRI-EcoRI	71583-71915	333	20	EcoRI-EcoRI	71916-75915	4000
21	EcoRI-EcoRI	9068-9101	34	21	EcoRI-EcoRI	75916-2517	8110

Table S2. All of the putative ORF from VHS1. Gray boxes indicate structural proteins.

ORF #	start	end	# Predic-tors	# Resi-dues	pI	MW	Domains	Homologues and thier functions
001	408	851	4	147	4.301	16695.7		
002	848	1024	3	58	5.036	6547.5		
003	1026	1430	4	134	6.860	15212.9		
004	1427	2152	5	241	10.694	27073.3		
005	2139	2954	5	271	10.291	30501.8		
006	2957	3268	5	103	8.736	11773.4	Pfam-B_1761	Similar to proteins of unknown function in *Vibrio* phage KVP40, *Vibrio* sp. 0908, *Vibrio harveyi* HY01, *Ralstonia solanacearum* GMI1000
007	3397	3903	3	168	6.006	18558.7		
008	3964	4563	4	199	5.341	22780.5	Protein of unknown function (DUF550)(PF 04447)	Similar to proteins of unknown function in *Mycobacterium* phage Kostya, *Pseudomonas aeruginosa* PA7, *Bordetella petrii* DSM 12804, *Burkholderia thailandensis* MSMB43 and *Dechloromonas aromatica* RCB
009	4825	5019	4	64	4.951	7312.4		
010	5034	5378	4	114	5.651	12890.7		
011	5451	5693	2	80	9.120	9254.8		
012	5699	6097	5	132	6.944	15548.5		
013	6178	6558	4	126	5.773	13846.7		
014	6609	6962	5	117	8.064	13242.0		
015	7095	7463	4	122	5.233	13642.4		
016	7469	7969	4	166	10.000	18688.2		
017	7956	8372	4	138	5.558	15816.9		
018	8512	8763	4	83	10.831	9719.4		
019	8813	9199	4	128	6.523	14092.8		
020	9196	9561	4	121	10.079	13610.7		
021	9849	10181	5	110	7.188	12231.1		
022	10239	10574	4	111	9.576	12274.8		
023	10628	11062	4	144	6.252	15799.7		
024	11052	11414	5	120	7.508	13163.0		
025	11547	11747	4	66	3.917	7608.7		
026	11789	12094	5	101	4.916	11460.9		
027	12098	12334	3	78	9.719	8965.0		
028	12347	12544	4	65	5.097	7655.7		
029	12547	12690	2	47	10.954	5409.4		
030	12813	13013	5	66	4.879	7169.3		
031	13600	15126	5	508	9.100	55745.5		
032	15233	16135	5	300	4.256	31257.4		
033	16202	17161	5	319	4.237	34397.8		
034	17289	17603	4	104	10.058	11820.5		
035	17608	18165	4	185	10.188	21600.8		
036	18240	18602	5	120	8.208	13829.9		
037	18652	18900	2	82	8.218	8824.4		
038	18902	19288	4	128	11.436	14113.2		
039	19285	19710	4	141	10.211	16111.1		
040	19781	20119	4	112	6.796	12336.9		
041	20132	20608	4	158	7.959	17891.4		
042	20633	21319	5	228	8.826	25167.6		
043	21329	21595	4	88	9.867	9524.9		
044	21729	22019	4	96	7.735	10605.1		
045	22029	22214	3	61	10.692	7202.4		
046	22344	22868	4	174	4.662	19673.2		
047	22868	23140	1	90	9.466	10591.9		
048	23211	23999	6	262	9.686	29722.9	Pfam-B_4580	conserved protein of unknown function
049	24037	25686	5	549	6.633	61247.9		
050	25758	26108	4	116	4.049	12396.7		

051	26237	26848	5	203	4.212	23234.7		Conserved protein of unknown function/N6 adenine-specific DNA methyltransferase [Haliangium ochraceum DSM 14365]
ORF #	start	end	# Predic-tors	# Resi-dues	pI	MW	Domains	Homologues and thier functions
052	26851	28032	5	393	3.959	41987.1		
053	28119	29072	6	317	9.818	35312.9	Phage capsid (PF05065)	Simialar to PBSX protein/capsid protein
054	29144	29431	4	95	4.340	10786.9		
055	29443	30081	4	212	5.246	22957.8		
056	30078	30542	4	154	9.483	17389.5		Y Similar to G protein in Mannheimia haemolytica serotype A2 str. BOVINE
057	30539	31030	4	163	6.522	18316.6		
058	31084	31878	6	264	4.358	28601.6	Pfam-B_3954	conserved protein of unknown function
059	31968	32390	4	140	4.960	14773.0		
060	32468	32590	1	40	10.680	4665.4		
061	32598	36737	6	1379	4.599	149916.6	PhageMin\ Tail (PF10145); Pfam-B_99; Pfam-B_5395	Similar to phage tail tape measure protein, TP901 family
062	36776	37120	5	114	10.106	12499.3		
063	37131	38120	5	329	5.738	35053.8		Similar to proteins of unknown function in Magnetococcus sp. MC-1
064	38132	39016	5	294	4.769	32677.4		Similar to proteins of unknown function in Magnetococcus sp. MC-1
065	39028	40326	5	432	5.078	47760.7	Pfam-B_4576	
066	40329	40853	4	174	4.358	18721.9		Similar to proteins of unknown functions in Denitrovibrio acetiphilus DSM 12809 and Magnetococcus sp. MC-1
067	40854	41156	4	100	4.428	11111.3		
068	41153	41380	3	75	4.879	7823.9		
069	41397	41804	4	135	7.572	14888.9		Conserved protein of unknown function
070	41807	42346	4	179	5.028	19958.9		Similar to protein of unknown function in Desulfotalea psychrophila LSv54 and Hahella chejuensis KCTC 2396
071	42470	43609	6	379	5.192	42444.4	AAA (PF00004)	AAA ATPase central domain protein, putative
072	44184	45674	5	496	9.297	54827.4		
073	45674	46330	3	218	9.742	24987.0		
074	46251	47696	5	481	4.650	54148.9	DnaB_C (PF03796)	Similar to replicative DNA helicase/DnaB helicase
075	47769	48233	5	154	10.999	16855.4		
076	48238	48351	2	37	10.402	4307.0		
077	48359	49330	5	323	6.376	36959.4		putative DNA primase
078	49341	50270	5	309	5.765	33478.4		
079	50318	51745	6	475	10.000	54044.3	ResIII (PF04851)	putative type III restriction protein res subunit/DEAD-DEAH box helicase/helicase
080	51841	52293	5	150	10.338	17409.3		
081	52301	52690	4	129	4.573	14461.9		

082	52704	53780	6	358	5.554	39978.5	RecA (PF00154)	putative recA protein
083	53761	54174	4	137	10.507	15365.7		
084	54164	55159	5	331	7.855	37525.4		
085	55160	55720	4	186	5.846	21107.9		conserved protein of unknown function
ORF #	start	end	# Predictors	# Residues	pI	MW	Domains	Homologues and thier functions
086	55822	56799	5	325	4.480	35854.9		Similar to proteins of unknown in Rhodomicrobium vannielii ATCC 17100 and Candidatus Cloacamonas acidaminovorans
087	56864	57154	3	96	10.381	11019.7		
088	57180	57923	5	247	8.797	28462.3		
089	58002	58733	5	243	4.560	27152.0		
090	58744	59553	5	269	6.391	30458.6		
091	59606	61522	5	638	8.539	72539.5		Similar to proteins of unknown function in Rhodococcus phage ReqiDocB7 (Teminase)
092	61534	61776	4	80	8.053	8841.2		
093	61878	62141	4	87	4.131	9870.0		
094	62186	62452	4	88	10.560	9836.4		
095	62442	62642	4	66	10.233	7402.5		
096	62644	62856	3	70	6.523	7825.0		
097	62889	64964	5	691	4.832	76634.4	PPDK_N (PF01326); PEP-utilizers (PF00391)	putative pyruvate phosphate dikinase
098	64969	65451	4	160	7.507	17263.6		
099	65502	65999	5	165	5.796	18394.1		putative phosphatase
100	66021	67031	5	336	7.784	37815.5		
101	67042	67584	5	180	4.385	19806.1		Similar to pyruvate decarboxylase and transporter
102	67634	67891	4	85	7.349	9644.9		
103	67903	70248	6	781	6.648	89490.9	3_5_exonuc (PF01612); DNA_pol_A (PF00476)	putative DNA polymerase I
104	70250	72127	5	625	4.334	68713.5	Phage_portal (PF04860)	putative capsid portal protein
105	72124	72585	4	153	4.611	17192.4		
106	72719	73210	4	163	4.580	18365.7		
107	73216	73866	6	216	7.307	25286.5	MT-A70 (PF05063)	putative Adenine-specific methyltransferase/putative MT-A70 family protein
108	74049	74456	4	135	6.511	14904.9		
109	74465	74920	4	151	8.201	16564.8		
110	75045	75413	3	122	7.003	14112.1		
111	75416	75601	3	61	11.103	7058.0		
112	75615	76001	4	128	9.006	15118.2		
113	76266	76499	3	77	5.654	8195.2		
114	76572	76754	2	60	9.779	6798.7		
115	76757	77041	4	94	4.217	10653.1		
116	77047	77346	4	99	4.023	11081.6		
117	77431	77739	5	102	4.468	11618.9		
118	77791	79131	5	446	4.777	49768.8		
119	79177	79512	4	111	4.261	12598.0		
120	79523	79903	4	126	10.527	14007.4	SEC-C (PF02810)	
121	79913	80371	3	152	10.016	17980.6		
122	80379	80882	4	167	3.972	18197.1		
123	80882	81130	4	82	10.478	9254.4		
124	81130	81309	3	59	10.205	6744.7		
125	81314	81448	2	44	3.376	4966.8		