

Supplementary Materials

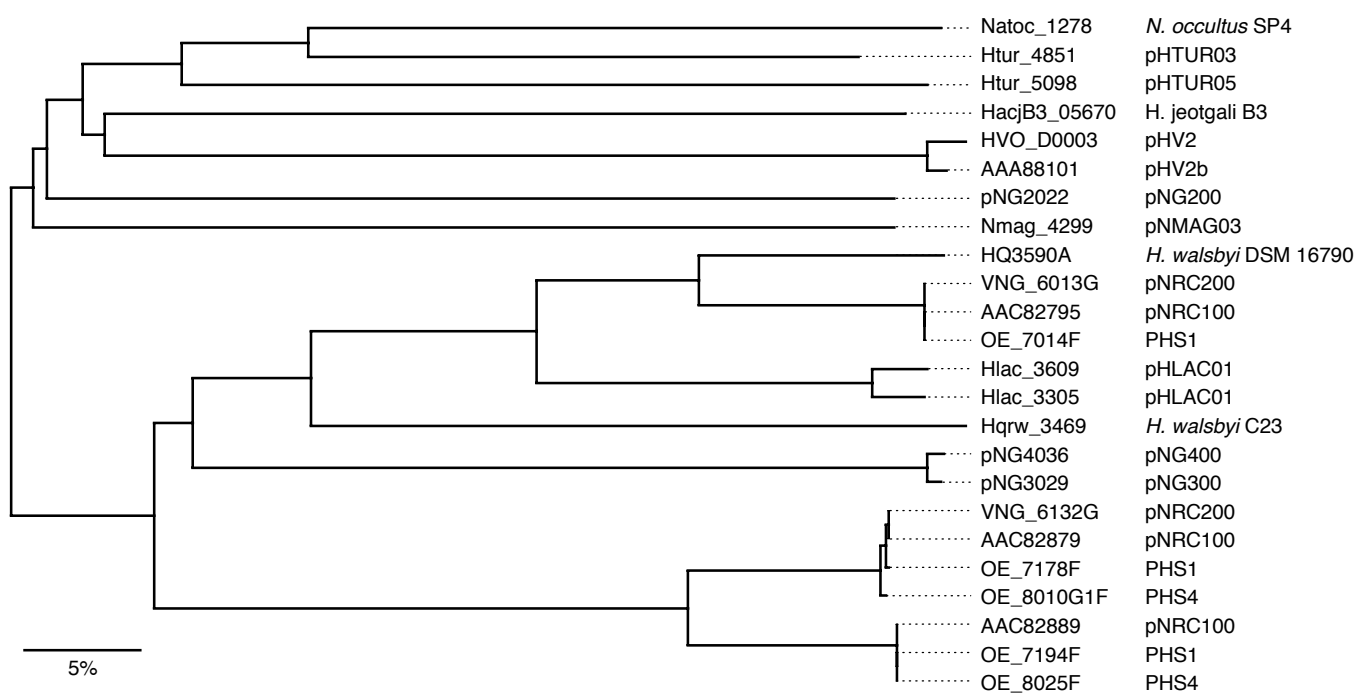


Fig. S1 A phylogenetic tree of RepH homologs of haloarchaeal plasmids.

The dendrogram is based on the similarities of protein sequences of RepH identified in the GenBank databases. The ruler in the bottom indicates the branch length corresponding to 5 % dissimilarity, while plasmids which do share sequences are separated by smaller branch lengths. Each RepH is indicated by its gene annotation and name of the plasmid.

II. Supplementary tables

Table S1. Archaeal viruses¹

Viron morphology	Taxonomy		Virus	Species name	Host	Genome			References
	Family	Genus				Size(kb)	Type ²	int	
Spindle	<i>Fuselloviridae</i>	<i>Alphafusellovirus</i>	SSV1	<i>Sulfolobus</i> spindle-shaped virus 1	<i>Sulfolobus</i>	15.4	ds, C	+	(1, 2)
			SSV2	<i>Sulfolobus</i> spindle-shaped virus 2	<i>Sulfolobus</i>	14.7	ds, C	+	(3)
			SSV4	<i>Sulfolobus</i> spindle-shaped virus 4	<i>Sulfolobus</i>	15.1	ds, C	+	(4)
			SSV5	<i>Sulfolobus</i> spindle-shaped virus 5	<i>Sulfolobus</i>	15.3	ds, C	+	(4)
			SSV7	<i>Sulfolobus</i> spindle-shaped virus 7	<i>Sulfolobus</i>	17.6	ds, C	+	(4)
			SSV8	<i>Sulfolobus</i> spindle-shaped virus 8	<i>Sulfolobus</i>	16.4	ds, C	+	(5)
			SSV9	<i>Sulfolobus</i> spindle-shaped virus 9	<i>Sulfolobus</i>	17.4	ds, C	+	(5)
			SSV6	<i>Sulfolobus</i> spindle-shaped virus 6	<i>Sulfolobus</i>	15.6	ds, C	+	(4)
			ASV1	<i>Acidianus</i> spindle-shaped virus 1	<i>Acidianus</i>	24.1	ds, C	+	(4)
	<i>Bicaudaviridae</i>	<i>Bicaudavirus</i>	ATV	<i>Acidianus</i> two-tailed virus	<i>Acidianus</i>	62.7	ds, C	+	(6, 7)
	Unclassified	<i>Salterprovirus</i>	His1	His virus 1	<i>Haloarcula</i>	14.4	ds, L	-	(8, 9)
			His2	His virus 2	<i>Haloarcula</i>	16.1	ds, L	-	(8, 9)
	Unclassified	Unclassified	STSV1	<i>Sulfolobus tengchongensis</i> spindle-shaped 1	<i>Sulfolobus</i>	75.3	ds, C	+	(10)
			STSV2	<i>Sulfolobus tengchongensis</i> spindle-shaped 2	<i>Sulfolobus</i>	76.1	ds, C	+	(11)
PAV1			<i>Pyrococcus abyssi</i> virus 1	<i>Pyrococcus</i>	18.1	ds, C	-	(12, 13)	
TPV1			<i>Thermococcus prieurii</i> virus 1	<i>Thermococcus</i>	21.5	ds, C	+	(14)	

	Unclassified		ACV	<i>Aeropyrum</i> coil-shaped virus	<i>Aeropyrum</i>	24.9	ss, D	-	(18)	
Droplet	<i>Guttaviridae</i>		<i>Alphaguttavirus</i>	SNDV	<i>Sulfolobus neozealandicus</i> droplet-shaped virus	<i>Sulfolobus</i>	~20	ds, C	-	(19)
			<i>Betaguttavirus</i>	APOV1	<i>Aeropyrum pernix</i> ovoid virus 1	<i>Aeropyrum</i>	13.8	ds, C	+	(15)
³ Linear	<i>Ligamenvirales</i>	<i>Lipothrixviridae</i>	<i>Alphalipothrixvirus</i>	TTV1	<i>Thermoproteus tenax</i> virus 1	<i>Thermoproteus</i>	15.9	ds, L	-	(20)
			<i>Betalipothrixvirus</i>	SIFV	<i>Sulfolobus islandicus</i> filamentous virus	<i>Sulfolobus</i>	40.8	ds, L	-	(21)
				AFV3	<i>Acidianus</i> filamentous virus 3	<i>Acidianus</i>	40.4	ds, L	-	(22)
				AFV6	<i>Acidianus</i> filamentous virus 6	<i>Acidianus</i>	39.5	ds, L	-	(22)
				AFV7	<i>Acidianus</i> filamentous virus 7	<i>Acidianus</i>	36.8	ds, L	-	(22)
				AFV8	<i>Acidianus</i> filamentous virus 8	<i>Acidianus</i>	38.1	ds, L	-	(22)
			AFV9	<i>Acidianus</i> filamentous virus 9	<i>Acidianus</i>	41.1	ds, L	-	(23)	
			<i>Gammalipthrixvirus</i>	AFV1	<i>Acidianus</i> filamentous virus 1	<i>Acidianus</i>	20.9	ds, L	-	(24)
	<i>Deltalipothrixvirus</i>	AFV2	<i>Acidianus</i> filamentous virus 2	<i>Acidianus</i>	31.7	ds, L	-	(25)		
	<i>Rudiviridae</i>	<i>Rudivirus</i>	SIRV2	<i>Sulfolobus islandicus</i> rod-shaped virus 2	<i>Sulfolobus</i>	35.4	ds, L	-	(26, 27)	
			SIRV1	<i>Sulfolobus islandicus</i> rod-shaped virus 1	<i>Sulfolobus</i>	32.3	ds, L	-	(26, 27)	
ARV1			<i>Acidianus</i> rod-shaped virus 1	<i>Acidianus</i>	24.6	ds, L	-	(28)		
Unclassified		SRV	<i>Stygiolobus</i> rod-shaped virus	<i>Stygiolobus</i>	28.1	ds, L	-	(29)		
Spherical	<i>Globulaviridae</i>	<i>Globulovirus</i>	PSV	<i>Pyrobaculum</i> spherical virus	<i>Pyrobaculum</i>	28.3	ds, L	-	(30)	
			TTSV1	<i>Thermoproteus tenax</i> spherical virus 1	<i>Thermoproteus</i>	21.6	ds, L	-	(31)	
	Unclassified	Unclassified	STIV	<i>Sulfolobus</i> turreted icosahedral virus	<i>Sulfolobus</i>	16.6	ds, C	-	(32)	
			STIV2	<i>Sulfolobus</i> turreted icosahedral virus 2	<i>Sulfolobus</i>	17.6	ds, C	-	(11)	
			SH1	Spherical halovirus 1	<i>Haloarcula/Haloferax/Halorubrum</i>	30.9	ds, L	-	(33)	
			HHIV-2	<i>Haloarcula hispanica</i> icosahedral virus 2	<i>Haloarcula</i>	30.6	ds, L	-	(34)	
PH1	Pink Lake <i>Har. hiapanica</i> virus 1	<i>Haloarcula</i>	28.1	ds, L	-	(35)				
Pleomorphic	Unclassified	Unclassified	HHPV-1	<i>Haloarcula hispanica</i> pleomorphic virus 1	<i>Haloarcula</i>	8.1	ds, C	-	(36)	
			HHPV-2	<i>Haloarcula hispanica</i> pleomorphic	<i>Haloarcula</i>	8.2	ss, C	-	(37)	

				virus 2					
			HRPV-1	<i>Halorubrum</i> pleomorphic virus 1	<i>Halorubrum</i> , ³	7.0	ss, C	-	(38)
			HGPV-1	<i>Halogeometricum</i> pleomorphic virus 1	<i>Halogeometricum</i>	9.7	ds, C	-	(39, 40)
			HRPV-2	<i>Halorubrum</i> pleomorphic virus 2	<i>Halorubrum</i>	10.7	ss, C	-	(39, 40)
			HRPV-3	<i>Halorubrum</i> pleomorphic virus 3	<i>Halorubrum</i>	8.8	ds, C	-	(39, 40)
			HRPV-6	<i>Halorubrum</i> pleomorphic virus 6	<i>Halorubrum</i>	8.5	ss, C	-	(39, 40)
Head-tail	<i>Myoviridae</i>	<i>Phihlikevirus</i>	phiH	<i>Halobacterium</i> phage phiH	<i>Halobacterium</i>	~59	ds, L	+	(41)
		Unclassified	phiCh1	phiCh1	<i>Natrialba</i>	58.5	ds, L	-	(42)
	<i>Siphoviridae</i>	<i>Psimunalikevirus</i>	psiM1	<i>Methanobacterium</i> phage psiM1	<i>Methanobacterium</i>	30.4	ds, L	?	(43)
		Unclassified	psiM2	<i>Methanobacterium</i> phage psiM2	<i>Methanobacterium</i>	26.1	ds, L	+	(44)
			psiM100	<i>Methanothermobacter</i> prophage psiM100	<i>Methanothermobacter</i>	28.8	ds, L	+	(45)
			BJ1	BJ1	<i>Halorubrum</i>	42.3	ds, C	+	(46, 47)
	Unclassified	Unclassified	SNJ1	SNJ1	<i>Natrinema</i>	16.3	ds, C	-	(39, 48, 49)
			HF1	HF1	<i>Halobrum</i>	75.9	L	+	(41, 50, 51)
			HF2	HF2	<i>Halobacterium</i>	77.7	L	+	(52, 53)

¹ This table is prepared in accordance with the 2012 version of the ICTV catalogue.

² The genome type is indicated as follows: ds, double-stranded DNA genome; ss, single-stranded DNA genome; L, linear genome; C, circular genome.

³ Linear viruses are assigned to the only order of archaeal viruses Ligamenvirales.

Table S2. Archaeal plasmids

Order/Family	Type	Classification	Name	Size (kb)	Host	Main features	Refs	
Sulfolobaceae	Cryptic plasmids	pRN family	pDL10	7.6	<i>Acidianus ambivalens</i>	Putative Pri/Pol domain replicase of pRN family	(54)	
			pRN1	5.3	<i>Sulfolobus islandicus</i>	Pri/Pol domain replicase of pRN family, shuttle vector pC etc.	(55-57)	
			pRN2	6.9	<i>S. islandicus</i>	Putative Pri/Pol domain replicase of pRN family, shuttle vector pHZ2, pZC1, expression plasmid pSeSD, pEXA	(56, 58-61)	
			pHEN7	7.8	<i>S. islandicus</i>	Putative Pri/Pol domain replicase of pRN family	(62)	
		Unclassified	pIT3	4.9	<i>Sulfolobus solfataricus</i>	Putative Pri/Pol domain replicase	(63)	
			pXZ1	6.9	<i>S. islandicus</i> strain ARN3/6	Putative Pri/Pol domain replicase	(64)	
			pTIK4	13.6	<i>Sulfolobus neozealandicus</i>	Putative Pri/Pol domain replicase	(65)	
			pTAU4	7.2	<i>S. neozealandicus</i>	MCM as putative replicase	(65)	
			pORA1	9.7	<i>S. neozealandicus</i>	Putative Pri/Pol domain replicase	(65)	
			Virus satellites	pRN family	pSSVx	5.7	<i>S. islandicus</i>	Plasmid-virus hybrid, Pri/Pol domain replicase of pRN family
	Unclassified	pSSVi		5.7	<i>S. solfataricus</i>	Plasmid-virus hybrid, SF III Helicase	(67)	
	Conjugative plasmids			pAH1	28.6	<i>Acidianus hospitalis</i> strain W1	Conjugative	(68)
				pARN3	26.2	<i>S. islandicus</i>	Conjugative	(69)
				pARN4	26.5	<i>S. islandicus</i>	Conjugative	(69)
				pHVE14	35.4	<i>S. islandicus</i>	Conjugative	(69)
				pING1	24.5	<i>S. islandicus</i>	Conjugative	(70)
pKEF9				28.9	<i>S. islandicus</i>	Conjugative CRISPR	(69)	
pSOG1				29	<i>S. islandicus</i>	Conjugative	(71)	
pSOG2				25.9	<i>S. islandicus</i>	Conjugative	(71)	

			pLD8501	26.6	<i>S. islandicus</i> L.D.8.5	Conjugative, identified from genome sequencing	Reno et al., unpublished
			pYN01	42.2	<i>S. islandicus</i> Y.N.15.51	Conjugative, identified from genome sequencing	(72)
			pNOB8	41.2	<i>Sulfolobus</i> sp. NOB8H2 conjugative	Conjugative, carrying a CRISPR array, ParA and ParB implicated in plasmid segregation	(73, 74)
			pTC	20.4	<i>Sulfolobus tengchongensis</i>	Conjugative plasmid, lacking an integrase	Xiang and Huang, unpublished
Host unknown	Enrichment culture		pHA1	33.8	Archaeon enrichment culture clone 1	Conjugative plasmid identified from metagenomics	(75)
Thermoproteaceae			pTPEN01	31.5	<i>Thermofilum pendens</i> Hrk 5		Copeland et al., unpublished
Haloarchaeaceae	Small plasmids	θ family	pZMX101	3.9	<i>Halorubrum saccharovororum</i>	Shuttle vector pZMX108, RepA, minimal replicon	(76)
			pSCM201	3.4	<i>Haloarcula</i> sp. AS7094	Unidirectional theta mechanism, minimal replicon defined, expression vector pPbop	(77, 78)
		RCR family	pZMX201	1.6	<i>Natrinema</i> sp. CX2021	RCR mechanism, RepZ	(79)
			pNB101	2.5	<i>Natronobacterium</i> sp. AS-7091	RCR mechanism, RepN	(80)
			pSN	2.2	<i>Haloterrigena thermotolerans</i> strain H13		You and Lai, unpublished
			pEHSP	1.7	<i>Halobacterium halobium</i>	Putative RCR replicase,	(81)
			pHGN1	1.7	<i>Halobacterium</i> sp. GN101	Putative RCR replicase, similar to pHSB	(82)
			pGRB1	1.8	<i>Halobacterium</i> GRB	Putative RCR replicase, Rep	(83-85)
			pHSB1	1.7	<i>Halobacterium</i> strain SB3/strain GRB	Putative RCR replicase, shuttle vector	(81, 86)
			pHK2	10.8	<i>Haloferax</i> Aa2.2/ <i>Haloarcula</i>	Putative RCR replicase, shuttle vector pMLH3, pMDS20	(87-89)

		Unclassified	pHV2b	6.3	<i>hispanica</i> <i>Haloferax volcanii</i> DS2	Replicase unknown, Shuttle vector pTA963	(90, 91)
			pHV2	6.3	<i>H. volcanii</i> DS2	Replicase unknown, shuttle vectors	(90, 92)
			PL6A	6.1	<i>Haloquadratum walsbyi</i> C23	Genome sequencing	(93)
			PL6B	6	<i>H.walsbyi</i> C23	Genome sequencing	(93)
			pHJ6	6.9	<i>Halalkalicoccus jeotgali</i> B3	Genome sequencing	(94)
Thermococcaceae	Cryptic plasmids	pGT5 RCR family	pGT5	3.4	<i>Pyrococcus abyssi</i> GE5	RCR mechanism, Rep75, Shuttle vector pAG1 series; pYS2	(95-97)
			pTN1	3.6	<i>Thermococcus nautilus</i> 30-1	RCR mechanism, Rep74, Shuttle vector pLC64	(98, 99)
			pTP1	3.1	<i>Thermococcus prieurii</i>	RCR mechanism, homologous to pGT5, RepTP1	(100)
			pTP2	2	<i>Thermococcus prieurii</i>	Putative RCR plasmid	(100)
		Unclassified	pAMT11	20.5	<i>Thermococcus</i> sp. AMT11	From black smokers of the East Pacific Rise,	(101)
			pRT1	3.3	<i>Pyrococcus</i> sp. JT1		(102)
		pT26-2 family	pT26-2	21.5	<i>Thermococcus</i> sp. 26/2	Integrative,	(103)
		pTN2 family	pTN2	13	<i>Thermococcus nautilus</i> strain 30/1	Encoding a novel Pri/Pol replicase	(103)
			pCIR10	13.3	<i>Thermococcus</i> sp. CIR10	pTN2-like Pri/Pol replicase	(104)
			pP12-1	12.2	<i>Pyrococcus</i> sp. 12/1	pTN2-like Pri/Pol replicase	(103)
			pIR48	12.9	<i>Thermococcus</i> sp. IR48	pTN2-like Pri/Pol replicase	(104)
		pEXT9a family	pAMT7	8.5	<i>Thermococcus</i> sp. AMT7	Novel type of replicase	(104)
			pEXT9a	10.5	<i>Thermococcus</i> sp. EXT9	Novel type of replicase	(104)
pIRI33	11		<i>Thermococcus</i> sp. IRI33	Novel type of replicase	(104)		
Methanogen plasmids	Methanococcaeae	pT26-2 family	pMEFER01	22.2	<i>Methanocaldococcus fervens</i> AG86	Genome sequencing, Acc. No. CP001697	Lucas et al. unpublished

			pURB500	8.3	<i>Methanococcus maripaludis</i>	Shuttle vector pDLT44	(105)
			pMMC501	8.3	<i>Methanococcus maripaludis</i> C5	Genome sequencing, Acc. No. CP000610	Copeland et al. unpublished
		pEXT9a family	pMETVU01	10.7	<i>Methanocaldococcus vulcanius</i> M7	Genome sequencing, Acc. No. CP001788	Lucas et al. unpublished
		Unclassified	pMETVU02	4.7	<i>Methanocaldococcus vulcanius</i> M7	Genome sequencing, Acc. No. CP001789	Lucas et al. unpublished
			pMJ-ECE2	58.4	<i>Methanocaldococcus jannaschii</i> DSM 2661	Genome sequencing, Acc. No. L77118	(106)
			pMJ-ECE1	16.5	<i>Methanocaldococcus jannaschii</i> DSM 2661	Genome sequencing, Acc. No. L77119	(106)
			pFS01	12.2	<i>Methanocaldococcus</i> sp. FS406-22	Genome sequencing, Acc. No. CP001902	Lucas et al. unpublished
	Methanobacteriaceae	Unclassified	pMETEV01	163.9	<i>Methanohalobium evestigatum</i> Z-7303	Genome sequencing, Acc. No. CP002070	Lucas et al. unpublished
			pMTBMA4	4.4	<i>Methanothermobacter marburgensis</i> str. Marburg	Genome sequencing, Acc. No. CP001711	(107)
			pMP1	~7	Methanogen PL-12/M	Cryptic	(108)
			pME2001	4.4	<i>Methanothermobacter autotrophicum</i> Marburg	Cryptic	(109-111)
			pME2200	6.2	<i>Methanothermobacter autotrophicum</i> strain ZH3	Cryptic	(111)
			pFV1	13.5	<i>M. thermoformicum</i> THF	Orc1/Cdc6 as the putative replicase, Type II R-M	(112, 113)
			pFZ1	11	<i>M. thermoformicum</i> Z245	Orc1/Cdc6 as the putative replicase, Type II R-M	(112)
	Methanosarcinaceae	Unclassified	pC2A	5.4	<i>Methanosarcina acetivorans</i>	Integrative, shuttle vector pWM307 etc	(114, 115)
			p1	36.3	<i>Methanosarcina</i>	Genome sequencing, Acc. No.	(116)

				<i>barkeri</i> str. Fusaro	CP000098	
Other plasmids	pPO1	7.6	<i>Picrophilus oshimae</i>	Orc1/Cdc6 as the putative replicase, encoding a putative R-M system	(117)	
	pGS5	2.8	<i>Archaeoglobus profundus</i> strain AV18	Cryptic plasmid, negative supercoiled	(118)	
	pArcpr01	2.8	<i>Archaeoglobus profundus</i> DSM 5631	Cryptic plasmid, similar to pGS5	(119)	

Table S3 Extrachromosomal genetic elements: host, size and integrase

Viruses/plasmids	Host	Size	Integrase	Reference
SSV1	<i>S. shibatae</i>	15.4	SSV1-type integrase Integrate at a tRNA ^{Arg} gene.	(120-126) (127)
SSV2	<i>S. islandicus</i>	14.7	SSV1-type integrase Integrated at a tRNA ^{Gly} gene	(3, 128)
SSV4	<i>S. islandicus</i>	15.1	SSV1-type integrase Integrated at a tRNA ^{Glu} gene	(4, 64)
SSV5	<i>S. islandicus</i>	15.3	SSV1-type integrase	(4)
SSV7	<i>S. islandicus</i>	17.6	SSV1-type integrase	(4)
SSV8	<i>S. solfataricus</i> P2, natural host unknown	16.4	SSV1-type integrase Integrate at a non-tRNA gene	(5)
SSV9	<i>S. solfataricus</i> P2, natural host unknown	17.3	SSV1-type integrase	(5)
SSV6	<i>Sulfolobus</i> species	15.6	SSV1-type integrase	(4)
SMF1	Unknown <i>Sulfolobus</i> strains	14.8	Putitive integrase	(129)
ASV1	<i>Acidianus</i> species	24.1	SSV1-type integrase	(4)
STSV1	<i>S. tenchongensis</i>	75.3	Putative integrase	(130)
STSV2	<i>S. tenchongensis</i> HB25	76.1	Putative integrase	(131)
ATV	<i>Acidianus</i> species	62.7	Putative integrase	(132)
APSV1	<i>Aeropyrum pernix</i> K1	38	SSV1-type integrase	(133)
APOV1	<i>Aeropyrum pernix</i> K1	13.8	SSV1-type integrase	(133)
phiCh1	<i>Natrialba magadii</i>	58.5	Putative integrases 1 and 2	(134, 135)
BJ1	<i>Halorubrum</i> BJ1 B11	42.2	Putative integrase	(46)
psiM1	<i>Methanobacterium</i>	30.4	Putative integrase	(136)
psiM2	<i>Methanothermobacter</i>	26.1	Tyrosine recombinase	(44)
psiM100	<i>Methanothermobacter</i>	28.8	Putative integrase	(45)
HF1		75.9	Putative integrase	(41, 50, 137)
HF2		77.7	Putative integrase	
TPV1	<i>Thermococcus</i> <i>prieurii</i>	21.5	SSV1-type integrase	(138)
HCTV-5	<i>Halorcula</i>	102.1	Putative integrase	(139)
HRTV-5	<i>Halorubrum</i>	76.1	Putative integrase	(139)
HRTV-7	<i>Halorubrum</i>	69.0	Putative integrase	(139)
HRTV-8	<i>Halorubrum</i>	74.5	Putative integrase	(139)
pSSVi	<i>S. solfataricus</i>	5.7	SSV1-type integrase	(67)
pXZ1	<i>S. islandicus</i> strain ARN3/6	7.0	SSV1-type integrase	(64)
pNOB8	<i>Sulfolobus</i> sp. NOB8H2 conjugative		pNOB8-type integrase Integrate at tRNA ^{Glu} genes	(73, 74, 140)
pAH1	<i>Acidianus hospitalis</i> strain W1	28.6	pNOB8-type integrase	(68)
pARN3	<i>S. islandicus</i>	26.2	pNOB8-type integrase	(69)
pARN4	<i>S. islandicus</i>	26.5	pNOB8-type integrase	(69)
pHVE14	<i>S. islandicus</i>	35.4	pNOB8-type integrase	(69)
pING1	<i>S. islandicus</i>	24.6	pNOB8-type integrase	(70)
pKEF9	<i>S. islandicus</i>	28.9	pNOB8-type integrase Integrate at tRNA ^{Glu} genes	(69) (Q. She unpublished data)
pSOG1	<i>S. islandicus</i>	29.0	pNOB8-type integrase	(71)
pSOG2	<i>S. islandicus</i>	26.0	pNOB8-type integrase	(71)
pLD8501	<i>S. islandicus</i> L.D.8.5	26.6	Putative integrase	(72)
pYN01	<i>S. islandicus</i> Y.N.15.51	42.2	Putative integrase	(72)

pHA1	archaeal enrichment culture clone 1	33.8	Integrase?	(75)
pT26-2	<i>Thermococcus</i> sp. 26/2	21.6	SSV1-type integrase	(103)
pC2A	<i>Methanosarcina acetivorans</i>	5.5	pNOB8-type integrase	(114, 115)

References

1. **Martin A, Yeats S, Janekovic D, Reiter WD, Aicher W, Zillig W.** 1984. Sav-1, a Temperate UV-Inducible DNA Virus-Like Particle from the Archaeobacterium *Sulfolobus*-*Acidocaldarius* Isolate B-12. *Embo Journal* **3**:2165-2168.
2. **Palm P, Schleper C, Grampp B, Yeats S, McWilliam P, Reiter WD, Zillig W.** 1991. Complete nucleotide sequence of the virus SSV1 of the archaeobacterium *Sulfolobus shibatae*. *Virology* **185**:242-250.
3. **Stedman KM, She Q, Phan H, Arnold HP, Holz I, Garrett RA, Zillig W.** 2003. Relationships between fuselloviruses infecting the extremely thermophilic archaeon *Sulfolobus*: SSV1 and SSV2. *Res Microbiol* **154**:295-302.
4. **Redder P, et al.** 2009. Four newly isolated fuselloviruses from extreme geothermal environments reveal unusual morphologies and a possible intervirial recombination mechanism. *Environ Microbiol* **11**:2849-2862.
5. **Wiedenheft B, Stedman K, Roberto F, Willits D, Gleske AK, Zoeller L, Snyder J, Douglas T, Young M.** 2004. Comparative genomic analysis of hyperthermophilic archaeal Fuselloviridae viruses. *J Virol* **78**:1954-1961.
6. **Haring M, Vestergaard G, Rachel R, Chen L, Garrett RA, Prangishvili D.** 2005. Virology: independent virus development outside a host. *Nature* **436**:1101-1102.
7. **Prangishvili D, Vestergaard G, Haring M, Aramayo R, Basta T, Rachel R, Garrett RA.** 2006. Structural and genomic properties of the hyperthermophilic archaeal virus ATV with an extracellular stage of the reproductive cycle. *Journal of Molecular Biology* **359**:1203-1216.
8. **Bath C, Cukalac T, Porter K, Dyll-Smith ML.** 2006. His1 and His2 are distantly related, spindle-shaped haloviruses belonging to the novel virus group, Salterprovirus. *Virology* **350**:228-239.
9. **Bath C, Dyll-Smith ML.** 1998. His1, an archaeal virus of the Fuselloviridae family that infects *Haloarcula hispanica*. *Journal of Virology* **72**:9392-9395.
10. **Xiang XY, Chen LM, Huang XX, Luo YM, She QX, Huang L.** 2005. *Sulfolobus tengchongensis* spindle-shaped virus STSV1: Virus-host interactions and genomic features. *Journal of Virology* **79**:8677-8686.
11. **Erdmann S, et al.** 2014. A novel single-tailed fusiform *Sulfolobus* virus STSV2 infecting model *Sulfolobus* species. *Extremophiles* **18**:51-60.
12. **Geslin C, Gaillard M, Flament D, Rouault K, Le Romancer M, Prieur D, Erauso G.** 2007. Analysis of the first genome of a hyperthermophilic marine virus-like particle, PAV1, isolated from *Pyrococcus abyssi*. *Journal of Bacteriology* **189**:4510-4519.
13. **Geslin C, Le Romancer M, Erauso G, Gaillard M, Perrot G, Prieur D.** 2003. PAV1, the first virus-like particle isolated from a hyperthermophilic euryarchaeote, "*Pyrococcus abyssi*". *J Bacteriol* **185**:3888-3894.
14. **Gorlas A, Koonin EV, Bienvenu N, Prieur D, Geslin C.** 2012. TPV1, the first virus isolated from the hyperthermophilic genus *Thermococcus*. *Environmental Microbiology* **14**:503-516.
15. **Mochizuki T, Sako Y, Prangishvili D.** 2011. Provirus Induction in Hyperthermophilic Archaea: Characterization of *Aeropyrum pernix* Spindle-Shaped Virus 1 and *Aeropyrum pernix* Ovoid Virus 1. *Journal of Bacteriology* **193**:5412-5419.
16. **Haring M, Rachel R, Peng X, Garrett RA, Prangishvili D.** 2005. Viral diversity in hot springs of Pozzuoli, Italy, and characterization of a unique archaeal virus, acidianus bottle-shaped virus, from a new family, the Ampullaviridae. *Journal of Virology* **79**:9904-9911.

17. **Mochizuki T, Yoshida T, Tanaka R, Forterre P, Sako Y, Prangishvili D.** 2010. Diversity of viruses of the hyperthermophilic archaeal genus *Aeropyrum*, and isolation of the *Aeropyrum pernix* bacilliform virus 1, APBV1, the first representative of the family Clavaviridae. *Virology* **402**:347-354.
18. **Mochizuki T, Krupovic M, Pehau-Arnaudet G, Sako Y, Forterre P, Prangishvili D.** 2012. Archaeal virus with exceptional virion architecture and the largest single-stranded DNA genome. *Proceedings of the National Academy of Sciences of the United States of America* **109**:13386-13391.
19. **Arnold HP, Ziese U, Zillig W.** 2000. SNDV, a novel virus of the extremely thermophilic and acidophilic archaeon *Sulfolobus*. *Virology* **272**:409-416.
20. **Janekovic D, Wunderl S, Holz I, Zillig W, Gierl A, Neumann H.** 1983. TTV1, TTV2 AND TTV3, A FAMILY OF VIRUSES OF THE EXTREMELY THERMOPHILIC, ANAEROBIC, SULFUR REDUCING ARCHAEABACTERIUM THERMOPROTEUS-TENAX. *Molecular & General Genetics* **192**:39-45.
21. **Arnold HP, et al.** 2000. A novel lipothrixvirus, SIFV, of the extremely thermophilic crenarchaeon *Sulfolobus*. *Virology* **267**:252-266.
22. **Vestergaard G, et al.** 2008. Structure of the acidianus filamentous virus 3 and comparative genomics of related archaeal lipothrixviruses. *J Virol* **82**:371-381.
23. **Bize A, Peng X, Prokofeva M, MacLellan K, Lucas S, Forterre P, Garrett RA, Bonch-Osmolovskaya EA, Prangishvili D.** 2008. Viruses in acidic geothermal environments of the Kamchatka Peninsula. *Research in Microbiology* **159**:358-366.
24. **Bettstetter M, Peng X, Garrett RA, Prangishvili D.** 2003. AFV1, a novel virus infecting hyperthermophilic archaea of the genus acidianus. *Virology* **315**:68-79.
25. **Haring M, Vestergaard G, Brugger K, Rachel R, Garrett RA, Prangishvili D.** 2005. Structure and genome organization of AFV2, a novel archaeal lipothrixvirus with unusual terminal and core structures. *J Bacteriol* **187**:3855-3858.
26. **Prangishvili D, Arnold HP, Gotz D, Ziese U, Holz I, Kristjansson JK, Zillig W.** 1999. A novel virus family, the Rudiviridae: Structure, virus-host interactions and genome variability of the sulfolobus viruses SIRV1 and SIRV2. *Genetics* **152**:1387-1396.
27. **Peng X, Blum H, She QX, Mallok S, Brugger K, Garrett RA, Zillig W, Prangishvili D.** 2001. Sequences and replication of genomes of the archaeal rudiviruses SIRV1 and SIRV2: Relationships to the archaeal lipothrixvirus SIFV and some eukaryal viruses. *Virology* **291**:226-234.
28. **Vestergaard G, Haring M, Peng X, Rachel R, Garrett RA, Prangishvili D.** 2005. A novel rudivirus, ARV1, of the hyperthermophilic archaeal genus Acidianus. *Virology* **336**:83-92.
29. **Vestergaard G, et al.** 2008. Stygiolobus rod-shaped virus and the interplay of crenarchaeal rudiviruses with the CRISPR antiviral system. *Journal of Bacteriology* **190**:6837-6845.
30. **Haring M, Peng X, Brugger K, Rachel R, Stetter KO, Garrett RA, Prangishvili D.** 2004. Morphology and genome organization of the virus PSV of the hyperthermophilic archaeal genera *Pyrobaculum* and *Thermoproteus*: a novel virus family, the *Globuloviridae*. *Virology* **323**:233-242.
31. **Ahn DG, Kim SI, Rhee JK, Kim KP, Pan JG, Oh JW.** 2006. TTSV1, a new virus-like particle isolated from the hyperthermophilic crenarchaeote *Thermoproteus tenax*. *Virology* **351**:280-290.
32. **Rice G, Tang L, Stedman K, Roberto F, Spuhler J, Gillitzer E, Johnson JE, Douglas T, Young M.** 2004. The structure of a thermophilic archaeal virus shows a double-stranded DNA viral capsid type that spans all domains of life. *Proceedings of the National Academy of Sciences of the United States of America* **101**:7716-7720.
33. **Porter K, Kukkaro P, Bamford JK, Bath C, Kivela HM, Dyall-Smith ML, Bamford DH.** 2005. SH1: A novel, spherical halovirus isolated from an Australian hypersaline lake. *Virology* **335**:22-33.
34. **Jaakkola ST, Penttinen RK, Vilen ST, Jalasvuori M, Ronnholm G, Bamford JKH, Bamford DH, Oksanen HM.** 2012. Closely Related Archaeal Haloarcula hispanica Icosahedral Viruses HHIV-2 and SH1 Have Nonhomologous Genes Encoding Host Recognition Functions. *Journal of Virology* **86**:4734-4742.

35. **Porter K, Tang SL, Chen CP, Chiang PW, Hong MJ, Dyall-Smith M.** 2013. PH1: An Archaeovirus of *Haloarcula hispanica* Related to SH1 and HHIV-2. *Archaea-an International Microbiological Journal*.
36. **Roine E, Kukkaro P, Paulin L, Laurinavicius S, Domanska A, Somerharju P, Bamford DH.** 2010. New, Closely Related Haloarchaeal Viral Elements with Different Nucleic Acid Types. *Journal of Virology* **84**:3682-3689.
37. **Ming L, Rui W, Dahe Z, Hua X.** 2013. Adaptation of the *Haloarcula hispanica* CRISPR-Cas system to a purified virus strictly requires a priming process. *Nucleic Acids Research*.
38. **Pietila MK, Roine E, Paulin L, Kalkkinen N, Bamford DH.** 2009. An ssDNA virus infecting archaea: a new lineage of viruses with a membrane envelope. *Molecular Microbiology* **72**:307-319.
39. **Atanasova NS, Roine E, Oren A, Bamford DH, Oksanen HM.** 2012. Global network of specific virus-host interactions in hypersaline environments. *Environmental Microbiology* **14**:426-440.
40. **Sencilo A, Paulin L, Kellner S, Helm M, Roine E.** 2012. Related haloarchaeal pleomorphic viruses contain different genome types. *Nucleic Acids Research* **40**:5523-5534.
41. **Nuttall SD, Dyallsmith ML.** 1993. Hf1 and Hf2 - Novel Bacteriophages of Halophilic Archaea. *Virology* **197**:678-684.
42. **Witte A, Baranyi U, Klein R, Sulzner M, Luo C, Wanner G, Kruger DH, Lubitz W.** 1997. Characterization of *Natronobacterium magadii* phage Phi Ch1, a unique archaeal phage containing DNA and RNA. *Molecular Microbiology* **23**:603-616.
43. **Meile L, Jenal U, Studer D, Jordan M, Leisinger T.** 1989. CHARACTERIZATION OF PSI-M1, A VIRULENT PHAGE OF METHANOBACTERIUM-THERMOAUTOTROPHICUM MARBURG. *Archives of Microbiology* **152**:105-110.
44. **Pfister P, Wasserfallen A, Stettler R, Leisinger T.** 1998. Molecular analysis of *Methanobacterium* phage psiM2. *Mol Microbiol* **30**:233-244.
45. **Luo YN, Pfister P, Leisinger T, Wasserfallen A.** 2001. The genome of archaeal prophage Psi M100 encodes the lytic enzyme responsible for autolysis of *Methanothermobacter wolfeii*. *Journal of Bacteriology* **183**:5788-5792.
46. **Pagaling E, Haigh RD, Grant WD, Cowan DA, Jones BE, Ma Y, Ventosa A, Heaphy S.** 2007. Sequence analysis of an Archaeal virus isolated from a hypersaline lake in Inner Mongolia, China. *BMC Genomics* **8**.
47. **Kukkaro P, Bamford DH.** 2009. Virus-host interactions in environments with a wide range of ionic strengths. *Environmental Microbiology Reports* **1**:71-77.
48. **Mei YJ, Chen D, Sun DC, Yang Y, Shen P, Chen XD.** 2007. Induction and preliminary characterization of a novel halophage SNJ1 from lysogenic *Natrinema* sp F5. *Canadian Journal of Microbiology* **53**:1106-1110.
49. **Zhang ZQ, et al.** 2012. Temperate membrane-containing halophilic archaeal virus SNJ1 has a circular dsDNA genome identical to that of plasmid pHH205. *Virology* **434**:233-241.
50. **Nuttall SD, Dyall-Smith ML.** 1995. Halophage HF2: genome organization and replication strategy. *J Virol* **69**:2322-2327.
51. **Tang SL, Nuttall S, Ngui K, Fisher C, Lopez P, Dyall-Smith M.** 2002. HF2: a double-stranded DNA tailed haloarchaeal virus with a mosaic genome. *Molecular Microbiology* **44**:283-296.
52. **Schnabel H, Schramm E, Schnabel R, Zillig W.** 1982. STRUCTURAL VARIABILITY IN THE GENOME OF PHAGE PHI-H OF HALOBACTERIUM-HALOBIIUM. *Molecular & General Genetics* **188**:370-377.
53. **Schnabel H, Zillig W, Pfaffle M, Schnabel R, Michel H, Delius H.** 1982. HALOBACTERIUM-HALOBIIUM PHAGE PHI-H. *Embo Journal* **1**:87-92.
54. **Kletz A, Lieke A, Urich T, Charlebois RL, Sensen CW.** 1999. Molecular analysis of pDL10 from *Acidianus ambivalens* reveals a family of related plasmids from extremely thermophilic and acidophilic archaea. *Genetics* **152**:1307-1314.
55. **Keeling PJ, Klenk HP, Singh RK, Feeley O, Schleper C, Zillig W, Doolittle WF, Sensen CW.** 1996. Complete nucleotide sequence of the *Sulfolobus islandicus* multicopy plasmid pRN1. *Plasmid* **35**:141-144.

56. **Keeling PJ, Klenk HP, Singh RK, Schenk ME, Sensen CW, Zillig W, Doolittle WF.** 1998. *Sulfolobus islandicus* plasmids pRN1 and pRN2 share distant but common evolutionary ancestry. *Extremophiles* **2**:391-393.
57. **Berkner S, Grogan D, Albers SV, Lipps G.** 2007. Small multicopy, non-integrative shuttle vectors based on the plasmid pRN1 for *Sulfolobus acidocaldarius* and *Sulfolobus solfataricus*, model organisms of the (cren-)archaea. *Nucleic Acids Res* **35**:e88.
58. **Deng L, Zhu H, Chen Z, Liang YX, She Q.** 2009. Unmarked gene deletion and host-vector system for the hyperthermophilic crenarchaeon *Sulfolobus islandicus*. *Extremophiles* **13**:735-746.
59. **Peng N, Xia Q, Chen Z, Liang YX, She Q.** 2009. An upstream activation element exerting differential transcriptional activation on an archaeal promoter. *Mol Microbiol* **74**:928-939.
60. **Gudbergsdottir S, Deng L, Chen Z, Jensen JV, Jensen LR, She Q, Garrett RA.** 2011. Dynamic properties of the *Sulfolobus* CRISPR/Cas and CRISPR/Cmr systems when challenged with vector-borne viral and plasmid genes and protospacers. *Mol Microbiol* **79**:35-49.
61. **Peng N, Deng L, Mei Y, Jiang D, Hu Y, Awayez M, Liang Y, She Q.** 2012. A synthetic arabinose-inducible promoter confers high levels of recombinant protein expression in hyperthermophilic archaeon *Sulfolobus islandicus*. *Appl Environ Microbiol* **78**:5630-5637.
62. **Peng X, Holz I, Zillig W, Garrett RA, She Q.** 2000. Evolution of the family of pRN plasmids and their integrase-mediated insertion into the chromosome of the crenarchaeon *Sulfolobus solfataricus*. *J Mol Biol* **303**:449-454.
63. **Prato S, Cannio R, Klenk HP, Contursi P, Rossi M, Bartolucci S.** 2006. pIT3, a cryptic plasmid isolated from the hyperthermophilic crenarchaeon *Sulfolobus solfataricus* IT3. *Plasmid* **56**:35-45.
64. **Peng X.** 2008. Evidence for the horizontal transfer of an integrase gene from a fusellovirus to a pRN-like plasmid within a single strain of *Sulfolobus* and the implications for plasmid survival. *Microbiology* **154**:383-391.
65. **Greve B, Jensen S, Phan H, Brugger K, Zillig W, She Q, Garrett RA.** 2005. Novel RepA-MCM proteins encoded in plasmids pTAU4, pORA1 and pTIK4 from *Sulfolobus neozealandicus*. *Archaea* **1**:319-325.
66. **Arnold HP, She Q, Phan H, Stedman K, Prangishvili D, Holz I, Kristjansson JK, Garrett R, Zillig W.** 1999. The genetic element pSSVx of the extremely thermophilic crenarchaeon *Sulfolobus* is a hybrid between a plasmid and a virus. *Mol Microbiol* **34**:217-226.
67. **Wang Y, Duan Z, Zhu H, Guo X, Wang Z, Zhou J, She Q, Huang L.** 2007. A novel *Sulfolobus* non-conjugative extrachromosomal genetic element capable of integration into the host genome and spreading in the presence of a fusellovirus. *Virology* **363**:124-133.
68. **Basta T, Smyth J, Forterre P, Prangishvili D, Peng X.** 2009. Novel archaeal plasmid pAH1 and its interactions with the lipothrixvirus AFV1. *Mol Microbiol* **71**:23-34.
69. **Greve B, Jensen S, Brugger K, Zillig W, Garrett RA.** 2004. Genomic comparison of archaeal conjugative plasmids from *Sulfolobus*. *Archaea* **1**:231-239.
70. **Stedman KM, She Q, Phan H, Holz I, Singh H, Prangishvili D, Garrett R, Zillig W.** 2000. pING family of conjugative plasmids from the extremely thermophilic archaeon *Sulfolobus islandicus*: insights into recombination and conjugation in Crenarchaeota. *J Bacteriol* **182**:7014-7020.
71. **Erauso G, Stedman KM, van de Werken HJ, Zillig W, van der Oost J.** 2006. Two novel conjugative plasmids from a single strain of *Sulfolobus*. *Microbiology* **152**:1951-1968.
72. **Reno ML, Held NL, Fields CJ, Burke PV, Whitaker RJ.** 2009. Biogeography of the *Sulfolobus islandicus* pan-genome. *Proc Natl Acad Sci U S A* **106**:8605-8610.
73. **Schleper C, Holz I, Janekovic D, Murphy J, Zillig W.** 1995. A multicopy plasmid of the extremely thermophilic archaeon *Sulfolobus* effects its transfer to recipients by mating. *J Bacteriol* **177**:4417-4426.
74. **She Q, Phan H, Garrett RA, Albers SV, Stedman KM, Zillig W.** 1998. Genetic profile of pNOB8 from *Sulfolobus*: the first conjugative plasmid from an archaeon. *Extremophiles* **2**:417-425.

75. **Garrett RA, Prangishvili D, Shah SA, Reuter M, Stetter KO, Peng X.** 2010. Metagenomic analyses of novel viruses and plasmids from a cultured environmental sample of hyperthermophilic neutrophiles. *Environ Microbiol* **12**:2918-2930.
76. **Zhou LG, Zhou MX, Sun CM, Xiang H, Tan HR.** 2007. Genetic analysis of a novel plasmid pZMX101 from *Halorubrum saccharovorum*: determination of the minimal replicon and comparison with the related haloarchaeal plasmid pSCM201. *FEMS Microbiol Lett* **270**:104-108.
77. **Sun C, Zhou M, Li Y, Xiang H.** 2006. Molecular characterization of the minimal replicon and the unidirectional theta replication of pSCM201 in extremely halophilic archaea. *J Bacteriol* **188**:8136-8144.
78. **Sun C, Li Y, Mei S, Lu Q, Zhou L, Xiang H.** 2005. A single gene directs both production and immunity of halocin C8 in a haloarchaeal strain AS7092. *Mol Microbiol* **57**:537-549.
79. **Zhou L, Zhou MX, Sun CM, Han J, Lu QH, Zhou J, Xiang H.** 2008. Precise determination, cross-recognition, and functional analysis of the double-strand origins of the rolling-circle replication plasmids in haloarchaea. *J Bacteriol* **190**:5710-5719.
80. **Zhou MX, Xiang H, Sun CM, Li Y, Liu JF, Tan HR.** 2004. Complete sequence and molecular characterization of pNB101, a rolling-circle replicating plasmid from the haloalkaliphilic archaeon *Natronobacterium* sp strain AS7091. *Extremophiles* **8**:91-98.
81. **Kagramanova VK, Derckacheva NI, Mankin AS.** 1988. The complete nucleotide sequence of the archaeobacterial plasmid pHSB from *Halobacterium*, strain SB3. *Nucleic Acids Res* **16**:4158.
82. **Hall MJ, Hackett NR.** 1989. DNA sequence of a small plasmid from *Halobacterium* strain GN101. *Nucleic Acids Res* **17**:10501.
83. **Hackett NR, Krebs MP, DasSarma S, Goebel W, RajBhandary UL, Khorana HG.** 1990. Nucleotide sequence of a high copy number plasmid from *Halobacterium* strain GRB. *Nucleic Acids Res* **18**:3408.
84. **Ilyina TV, Koonin EV.** 1992. Conserved sequence motifs in the initiator proteins for rolling circle DNA replication encoded by diverse replicons from eubacteria, eucaryotes and archaeobacteria. *Nucleic Acids Res* **20**:3279-3285.
85. **Sioud M, Baldacci G, Forterre P, de Recondo AM.** 1988. Novobiocin induces accumulation of a single strand of plasmid pGRB-1 in the archaeobacterium *Halobacterium* GRB. *Nucleic Acids Res* **16**:7833-7842.
86. **Hackett NR, DasSarma S.** 1989. Characterization of the small endogenous plasmid of *Halobacterium* strain SB3 and its use in transformation of *Halobacterium halobium*. *Can J Microbiol* **35**:86-91.
87. **Holmes M, Pfeifer F, Dyall-Smith M.** 1994. Improved shuttle vectors for *Haloferax volcanii* including a dual-resistance plasmid. *Gene* **146**:117-121.
88. **Holmes ML, Dyall-Smith ML.** 1990. A plasmid vector with a selectable marker for halophilic archaeobacteria. *J Bacteriol* **172**:756-761.
89. **Holmes ML, Pfeifer F, Dyall-Smith ML.** 1995. Analysis of the halobacterial plasmid pHK2 minimal replicon. *Gene* **153**:117-121.
90. **Charlebois RL, Lam WL, Cline SW, Doolittle WF.** 1987. Characterization of pHV2 from *Halobacterium volcanii* and its use in demonstrating transformation of an archaeobacterium. *Proc Natl Acad Sci U S A* **84**:8530-8534.
91. **Allers T, Barak S, Liddell S, Wardell K, Mevarech M.** 2010. Improved strains and plasmid vectors for conditional overexpression of His-tagged proteins in *Haloferax volcanii*. *Appl Environ Microbiol* **76**:1759-1769.
92. **Hartman AL, et al.** 2010. The complete genome sequence of *Haloferax volcanii* DS2, a model archaeon. *PLoS One* **5**:e9605.
93. **Dyall-Smith ML, Pfeiffer F, Klee K, Palm P, Gross K, Schuster SC, Rampp M, Oesterhelt D.** 2011. *Haloquadratum walsbyi*: limited diversity in a global pond. *PLoS One* **6**:e20968.
94. **Roh SW, Nam YD, Nam SH, Choi SH, Park HS, Bae JW.** 2010. Complete genome sequence of *Halalkalicoccus jeotgali* B3(T), an extremely halophilic archaeon. *J Bacteriol* **192**:4528-4529.

95. **Erauso G, Marsin S, Benbouzid-Rollet N, Baucher MF, Barbeyron T, Zivanovic Y, Prieur D, Forterre P.** 1996. Sequence of plasmid pGT5 from the archaeon *Pyrococcus abyssi*: evidence for rolling-circle replication in a hyperthermophile. *J Bacteriol* **178**:3232-3237.
96. **Aravalli RN, Garrett RA.** 1997. Shuttle vectors for hyperthermophilic archaea. *Extremophiles* **1**:183-191.
97. **Lucas S, Toffin L, Zivanovic Y, Charlier D, Moussard H, Forterre P, Prieur D, Erauso G.** 2002. Construction of a shuttle vector for, and spheroplast transformation of, the hyperthermophilic archaeon *Pyrococcus abyssi*. *Appl Environ Microbiol* **68**:5528-5536.
98. **Soler N, Justome A, Quevillon-Cheruel S, Lorieux F, Le Cam E, Marguet E, Forterre P.** 2007. The rolling-circle plasmid pTN1 from the hyperthermophilic archaeon *Thermococcus nautilus*. *Mol Microbiol* **66**:357-370.
99. **Santangelo TJ, Cubonova L, Reeve JN.** 2008. Shuttle vector expression in *Thermococcus kodakaraensis*: contributions of cis elements to protein synthesis in a hyperthermophilic archaeon. *Appl Environ Microbiol* **74**:3099-3104.
100. **Gorlas A, Krupovic M, Forterre P, Geslin C.** 2013. Living Side by Side with a Virus: Characterization of Two Novel Plasmids from *Thermococcus prieurii*, a Host for the Spindle-Shaped Virus TPV1. *Appl Environ Microbiol* **79**:3822-3828.
101. **Gonnet M, Erauso G, Prieur D, Le Romancer M.** 2011. pAMT11, a novel plasmid isolated from a *Thermococcus* sp. strain closely related to the virus-like integrated element TKV1 of the *Thermococcus kodakaraensis* genome. *Res Microbiol* **162**:132-143.
102. **Ward DE, Revet IM, Nandakumar R, Tuttle JH, de Vos WM, van der Oost J, DiRuggiero J.** 2002. Characterization of plasmid pRT1 from *Pyrococcus* sp. strain JT1. *J Bacteriol* **184**:2561-2566.
103. **Soler N, Marguet E, Cortez D, Desnoues N, Keller J, van Tilbeurgh H, Sezonov G, Forterre P.** 2010. Two novel families of plasmids from hyperthermophilic archaea encoding new families of replication proteins. *Nucleic Acids Res* **38**:5088-5104.
104. **Krupovic M, Gonnet M, Ben Hania W, Forterre P, Erauso G.** 2013. Insights into Dynamics of Mobile Genetic Elements in Hyperthermophilic Environments from Five New *Thermococcus* Plasmids. *Plos One* **8**.
105. **Tumbula DL, Bowen TL, Whitman WB.** 1997. Characterization of pURB500 from the archaeon *Methanococcus maripaludis* and construction of a shuttle vector. *J Bacteriol* **179**:2976-2986.
106. **Bult CJ, et al.** 1996. Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*. *Science* **273**:1058-1073.
107. **Liesegang H, Kaster AK, Wiezer A, Goenrich M, Wollherr A, Seedorf H, Gottschalk G, Thauer RK.** 2010. Complete genome sequence of *Methanothermobacter marburgensis*, a methanoarchaeon model organism. *J Bacteriol* **192**:5850-5851.
108. **Thomm M, Altenbuchner J, Stetter KO.** 1983. Evidence for a plasmid in a methanogenic bacterium. *J Bacteriol* **153**:1060-1062.
109. **Bokranz M, Klein A, Meile L.** 1990. Complete nucleotide sequence of plasmid pME2001 of *Methanobacterium thermoautotrophicum* (Marburg). *Nucleic Acids Res* **18**:363.
110. **Meile L, Madon J, Leisinger T.** 1988. Identification of a transcript and its promoter region on the archaeobacterial plasmid pME2001. *J Bacteriol* **170**:478-481.
111. **Luo Y, Leisinger T, Wasserfallen A.** 2001. Comparative sequence analysis of plasmids pME2001 and pME2200 of *Methanothermobacter marburgensis* strains Marburg and ZH3. *Plasmid* **45**:18-30.
112. **Nolling J, van Eeden FJ, Eggen RI, de Vos WM.** 1992. Modular organization of related Archaeal plasmids encoding different restriction-modification systems in *Methanobacterium thermoformicicum*. *Nucleic Acids Res* **20**:6501-6507.
113. **Nolling J, de Vos WM.** 1992. Characterization of the archaeal, plasmid-encoded type II restriction-modification system MthTI from *Methanobacterium thermoformicicum* THF: homology to the bacterial NgoPII system from *Neisseria gonorrhoeae*. *J Bacteriol* **174**:5719-5726.

114. **Metcalf WW, Zhang JK, Apolinario E, Sowers KR, Wolfe RS.** 1997. A genetic system for Archaea of the genus *Methanosarcina*: liposome-mediated transformation and construction of shuttle vectors. *Proc Natl Acad Sci U S A* **94**:2626-2631.
115. **Sowers KR, Gunsalus RP.** 1988. Plasmid DNA from the acetotrophic methanogen *Methanosarcina acetivorans*. *J Bacteriol* **170**:4979-4982.
116. **Maeder DL, et al.** 2006. The *Methanosarcina barkeri* genome: comparative analysis with *Methanosarcina acetivorans* and *Methanosarcina mazei* reveals extensive rearrangement within methanosarcinal genomes. *J Bacteriol* **188**:7922-7931.
117. **Angelov A, Voss J, Liebl W.** 2011. Characterization of plasmid pPO1 from the hyperacidophile *Picrophilus oshimae*. *Archaea* **2011**:723604.
118. **Lopez-Garcia P, Forterre P, van der Oost J, Erauso G.** 2000. Plasmid pGS5 from the hyperthermophilic archaeon *Archaeoglobus profundus* is negatively supercoiled. *J Bacteriol* **182**:4998-5000.
119. **von Jan M, et al.** 2010. Complete genome sequence of *Archaeoglobus profundus* type strain (AV18). *Stand Genomic Sci* **2**:327-346.
120. **Reiter WD, Palm P, Yeats S.** 1989. Transfer RNA genes frequently serve as integration sites for prokaryotic genetic elements. *Nucleic Acids Res* **17**:1907-1914.
121. **Schleper C, Kubo K, Zillig W.** 1992. The particle SSV1 from the extremely thermophilic archaeon *Sulfolobus* is a virus: demonstration of infectivity and of transfection with viral DNA. *Proc Natl Acad Sci U S A* **89**:7645-7649.
122. **Muskhelishvili G, Palm P, Zillig W.** 1993. SSV1-encoded site-specific recombination system in *Sulfolobus shibatae*. *Mol Gen Genet* **237**:334-342.
123. **Serre MC, Letzelter C, Garel JR, Duguet M.** 2002. Cleavage properties of an archaeal site-specific recombinase, the SSV1 integrase. *J Biol Chem* **277**:16758-16767.
124. **Letzelter C, Duguet M, Serre MC.** 2004. Mutational analysis of the archaeal tyrosine recombinase SSV1 integrase suggests a mechanism of DNA cleavage in trans. *J Biol Chem* **279**:28936-28944.
125. **Eilers BJ, Young MJ, Lawrence CM.** 2012. The structure of an archaeal viral integrase reveals an evolutionarily conserved catalytic core yet supports a mechanism of DNA cleavage in trans. *J Virol* **86**:8309-8313.
126. **Zhan Z, Ouyang S, Liang W, Zhang Z, Liu ZJ, Huang L.** 2012. Structural and functional characterization of the C-terminal catalytic domain of SSV1 integrase. *Acta Crystallogr D Biol Crystallogr* **68**:659-670.
127. **Palm P, Schleper C, Grampp B, Yeats S, McWilliam P, Reiter WD, Zillig W.** 1991. Complete Nucleotide-Sequence of the Virus SSV1 of the Archaeobacterium *Sulfolobus shibatae*. *Virology* **185**:242-250.
128. **Contursi P, Jensen S, Aucelli T, Rossi M, Bartolucci S, She Q.** 2006. Characterization of the *Sulfolobus* host-SSV2 virus interaction. *Extremophiles* **10**:615-627.
129. **Servin-Garciduenas LE, Peng X, Garrett RA, Martinez-Romero E.** 2013. Genome sequence of a novel archaeal fusellovirus assembled from the metagenome of a mexican hot spring. *Genome Announc* **1**:e0016413.
130. **Xiang X, Chen L, Huang X, Luo Y, She Q, Huang L.** 2005. *Sulfolobus tengchongensis* spindle-shaped virus STSV1: virus-host interactions and genomic features. *J. Virol.* **79**:8677-8686.
131. **Erdmann S, et al.** 2014. A novel single-tailed fusiform *Sulfolobus* virus STSV2 infecting model *Sulfolobus* species. *Extremophiles* **18**:51-60.
132. **Prangishvili D, Vestergaard G, Haring M, Aramayo R, Basta T, Rachel R, Garrett RA.** 2006. Structural and genomic properties of the hyperthermophilic archaeal virus ATV with an extracellular stage of the reproductive cycle. *J Mol Biol* **359**:1203-1216.
133. **Mochizuki T, Sako Y, Prangishvili D.** 2011. Provirus Induction in Hyperthermophilic Archaea: Characterization of *Aeropyrum pernix* Spindle-Shaped Virus 1 and *Aeropyrum pernix* Ovoid Virus 1. *J Bacteriol* **193**:5412-5419.
134. **Klein R, Baranyi U, Rössler N, Greineder B, Scholz H, Witte A.** 2002. *Natrialba magadii* virus phiCh1: first complete nucleotide sequence and functional organization of a virus infecting a haloalkaliphilic archaeon. *Mol Microbiol* **45**:851-863.

135. **Witte A, Baranyi U, Klein R, Sulzner M, Luo C, Wanner G, Kruger DH, Lubitz W.** 1997. Characterization of *Natronobacterium magadii* phage Phi Ch1, a unique archaeal phage containing DNA and RNA. *Mol Microbiol* **23**:603-616.
136. **Meile L, Jenal U, Studer D, Jordan M, Leisinger T.** 1989. Characterization of Psi-M1, a Virulent Phage of *Methanobacterium-Thermoautotrophicum* Marburg. *Arch Microbiol* **152**:105-110.
137. **Tang SL, Nuttall S, Ngui K, Fisher C, Lopez P, Dyall-Smith M.** 2002. HF2: a double-stranded DNA tailed haloarchaeal virus with a mosaic genome. *Mol Microbiol* **44**:283-296.
138. **Gorlas A, Koonin EV, Bienvenu N, Prieur D, Geslin C.** 2012. TPV1, the first virus isolated from the hyperthermophilic genus *Thermococcus*. *Environ Microbiol* **14**:503-516.
139. **Atanasova NS, Roine E, Oren A, Bamford DH, Oksanen HM.** 2012. Global network of specific virus-host interactions in hypersaline environments. *Environ Microbiol* **14**:426-440.
140. **She Q, Shen B, Chen L.** 2004. Archaeal integrases and mechanisms of gene capture. *Biochem Soc Trans* **32**:222-226.