

## **Whole-genome comparison between the type strain of *Halobacterium salinarum* (DSM 3754<sup>T</sup>) and the laboratory strains R1 and NRC-1.**

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Note: This document contains Supplementary Tables for the above manuscript. The legends use some terms which are only defined in the context of that manuscript. Here is one paragraph from that manuscript which briefly describes the content of the tables.

*Correlation of protein-coding genes among Halobacterium salinarum strains 91-R6<sup>T</sup>, R1, and NRC-1.* As an annotation principle, every gene encoding a protein on a matching genome segment in one strain must have a correlated gene in the other strain. The gene sets of the three strains have been correlated in detail (for details see Methods of the associated manuscript and Appendix 4 and Appendix 5). Proteins are classified as strain-specific only after validation by tBLASTn that they are not mere missing gene calls. Correlated proteins, encoded on the chromosome of strains 91-R6 and R1 are listed in Table S1 (1986 proteins). The corresponding proteins from strain NRC-1 are also listed. In addition, there are regions of very high similarity between the plasmids from strains 91-R6 and R1, and the resulting plasmid encoded correlated proteins are listed in Table S2. Furthermore, Table S2 lists proteins which are encoded on a plasmid in strain R1 but in a strain-specific region of the chromosome from strain 91-R6. Chromosomally encoded proteins from strain-specific regions of 91-R6 are listed in Table S3. In several cases, a homolog exists in R1 but the genes are not positionally correlated. Such homologs are also listed in Table S3. Residual proteins which are specific for the chromosome of strain R1 are listed in Table S4. Plasmid encoded proteins specific for strain 91-R6 are listed in Table S5, while plasmid encoded proteins specific for strain R1 are listed in Table S6. A few protein-coding genes exist in strain NRC-1 but are absent in both strains 91-R6 and R1. These are listed in Table S7. Finally, Table S8 lists ORFs which are annotated in the current version of the NRC-1 genome (AE004437, AE004438, AF016485) but which are considered not to code for a protein (spurious ORFs; for definition see Appendix 4 in the associated manuscript).

code (91-R6)	code (R1)	seq id (%)	serial	code (NRC-1)	gene	protein name	comment
HBSAL_00005	OE_4374R	99	m01	VNG_2406C	oapC	origin-associated protein OapC	-
HBSAL_00010	OE_4376R	100p	m01	VNG_2408C	oapB	origin-associated protein OapB	-
HBSAL_00015	OE_4377R	100p	m01	VNG_2410G	oapA	origin-associated GTP-binding protein OapA	-
HBSAL_00020	OE_4380F	99	m01	VNG_2411G	orc1	Orc1-type DNA replication protein	-
HBSAL_00025	OE_4382R	98	m01	VNG_2412H	-	uncharacterized protein	-
HBSAL_00030	OE_4384R	98	m01	VNG_2413H	-	DoxX domain protein	-
HBSAL_00035	OE_4385F	99	m01	VNG_2414H	-	HTH domain protein	-
HBSAL_00040	OE_4387F	100d	m01	VNG_2415H	-	uncharacterized protein	-
HBSAL_00045	OE_4388R	98	m01	VNG_2416G	sec11	signal peptidase I	-
HBSAL_00050	OE_4390F	99	m01	VNG_2417G	polD1	DNA-directed DNA polymerase D exonuclease subunit DP1	-
HBSAL_00055	OE_4391F	99	m01	VNG_2418G	-	pyridoxal phosphate-dependent aminotransferase	-
HBSAL_00060	OE_4393R	100p	m01	VNG_2419C	-	major facilitator superfamily transport protein	-
HBSAL_00065	OE_4397F	99	m01	VNG_2420G	metX	homoserine O-acetyltransferase	-
HBSAL_00070	OE_4398F	99	m01	VNG_2421G	metY	O-acetylhomoserine aminocarboxypropyltransferase (methionine synthase)	-
HBSAL_00075	OE_4399F	99	m01	VNG_2422G	-	FAD-dependent oxidoreductase (GlcD/DLD_GlcF/GlpC domain fusion protein)	-
HBSAL_00080	OE_4405R	99	m01	VNG_2423G	serB	phosphoserine phosphatase	-
HBSAL_00085	OE_4408F	99	m01	VNG_2424G	serA1	D-3-phosphoglycerate dehydrogenase	-
HBSAL_00090	OE_4410F	100p	m01	VNG_2426G	-	thioesterase domain protein	-
HBSAL_00095	OE_4411F	100p	m01	VNG_2429G	-	major facilitator superfamily transport protein	-
HBSAL_00100	OE_4412R	99	m01	VNG_2430G	thrC1	threonine synthase	-
HBSAL_00105	OE_4414R	98	m01	VNG_2431C	-	small CPxCG-related zinc finger protein	-
HBSAL_00110	OE_4416R	100p	m01	VNG_2432C	-	UPF0145 family protein	-
HBSAL_00115	OE_4418R	98	m01	VNG_2433H	-	homolog to acetylglutamate kinase	-
HBSAL_00120	OE_4419R	98	m01	VNG_2436G	argH	argininosuccinate lyase	-

HBSAL_00125	OE_4420R	99	m01	VNG_2437G	argG	argininosuccinate synthase	-
HBSAL_00130	OE_4421B1F	100p	m01	VNG_2439a	-	uncharacterized protein	-
HBSAL_00135	OE_4423F	99	m01	VNG_2440H	-	phosphodiesterase domain protein	-
HBSAL_00140	OE_4424R	99	m01	VNG_2441G	rad3b	DNA repair helicase Rad3	-
HBSAL_00145	OE_4426F	100p	m01	VNG_2442H	-	uncharacterized protein	-
HBSAL_00150	OE_4427R	100p	m01	VNG_2443G	dpsA	ferritin DpsA	-
HBSAL_00155	OE_4429F	99	m01	VNG_2444C	-	MJ0936 family phosphodiesterase	-
HBSAL_00160	OE_4432R	100p	m01	VNG_2445C	-	ArsR family transcription regulator	-
HBSAL_00165	OE_4435F	100d	m01	VNG_2446H	-	uncharacterized protein	-
HBSAL_00170	OE_4436R	98	m01	VNG_2447G	ltaE	threonine aldolase	-
HBSAL_00175	OE_4438F	100p	m01	VNG_2449G	pepB2	aminopeptidase (homolog to leucyl aminopeptidase / aminopeptidase T)	-
HBSAL_00180	OE_4440F	100d	m01	VNG_2451H	-	small CPxCG-related zinc finger protein	-
HBSAL_00185	OE_4442F	100p	m01	VNG_2452C	-	UPF0200 family protein	-
HBSAL_00190	OE_4444F	100p	m01	VNG_2454C	-	UPF0201 family protein	-
HBSAL_00195	OE_4446R	99	m01	VNG_2455C	-	uncharacterized protein	-
HBSAL_00200	OE_4448R	98	m01	VNG_2456C	-	MgtE family transport protein	-
HBSAL_00205	OE_4449R	100p	m01	VNG_2458C	-	MgtE family transport protein	-
HBSAL_00210	OE_4450R	99	m01	VNG_2459G	srp54	signal recognition particle 54K protein	-
HBSAL_00215	OE_4451F	100p	m01	VNG_2461H	-	uncharacterized protein	-
HBSAL_00220	OE_4454R	99	m01	VNG_2462G	ftsY	signal recognition particle receptor FtsY	-
HBSAL_00225	OE_4456R	100d	m01	VNG_2465C	pfdA	prefoldin alpha subunit	-
HBSAL_00230	OE_4458R	100p	m01	VNG_2466a	tif6	translation initiation factor aIF-6	-
HBSAL_00235	OE_4459R	100d	m01	VNG_2467G	rpl31e	50S ribosomal protein L31e	-
HBSAL_00240	OE_4460R	100d	m01	VNG_2469G	rpl39e	50S ribosomal protein L39e	-
HBSAL_00245	OE_4461F	100p	m01	VNG_2468C	-	tetratricopeptide repeat protein	-
HBSAL_00250	OE_4462F	100d	m01	VNG_2470C	-	DUF424 family protein	-
HBSAL_00255	OE_4463F	99	m01	VNG_2471G	sufS	cysteine desulfurase	-
HBSAL_00260	OE_4465F	100p	m01	VNG_2472G	iscU	iron-sulfur cluster assembly protein	-
HBSAL_00265	OE_4466R	100p	m01	VNG_2473G	radA	DNA repair and recombination protein RadA	-

HBSAL_00270	OE_4467F	99	m01	VNG_2474C	-	NMD3 family protein	-
HBSAL_00275	OE_4468F	99	m01	VNG_2475C	taw2	tRNA(Phe) (4-demethylwyosine(37)-C(7)) aminocarboxypropyltransferase	-
HBSAL_00280	OE_4470C1R	98	m01	VNG_2475a	-	uncharacterized protein	-
HBSAL_00285	OE_4471R	99	m01	VNG_2476C	-	helicase domain protein	-
HBSAL_00290	OE_4475R	98	m01	VNG_2477H	-	small CPxCG-related zinc finger protein	-
HBSAL_00295	OE_4476R	99	m01	VNG_2480H	phoU1	PhoU domain protein	-
HBSAL_00300	OE_4479R	97	m01	VNG_2482G	pstB1	ABC-type transport system ATP-binding protein (probable substrate phosphate)	-
HBSAL_00305	OE_4480R	99	m01	VNG_2483G	pstA1	ABC-type transport system permease protein (probable substrate phosphate)	-
HBSAL_00310	OE_4483R	100p	m01	VNG_2484G	pstC1	ABC-type transport system permease protein (probable substrate phosphate)	-
HBSAL_00315	OE_4485R	98	m01	VNG_2486G	pstS1	ABC-type transport system periplasmic substrate- binding protein (probable substrate phosphate)	-
HBSAL_00320	OE_4487F	100p	m01	VNG_2488C	-	arNOG08307 family NADH-binding domain protein	-
HBSAL_00325	OE_4488F	100p	m01	VNG_2490H	-	uncharacterized protein	-
HBSAL_00330	OE_4489B1R	100d	m01	VNG_2490a	-	uncharacterized protein	-
HBSAL_00335	OE_4490A1R	100d	m01	VNG_2490b	-	uncharacterized protein	-
HBSAL_00340	OE_4492F	99	m01	VNG_2493C	-	PHP domain protein	-
HBSAL_00345	OE_4491F	100d	m01	VNG_2495a	-	uncharacterized protein	-
HBSAL_00350	OE_4496R	100p	m01	VNG_2496G	fer4	ferredoxin (3Fe-4S)(4Fe-4S), zinc-containing	-
HBSAL_00355	OE_4498F	99	m01	VNG_2497H	-	cupin 2 barrel domain protein	-
HBSAL_00360	OE_4499F	99	m01	VNG_2498H	-	DUF393 family protein	-
HBSAL_00365	OE_4500R	100p	m01	VNG_2499G	acd6	glutaryl-CoA dehydrogenase	-
HBSAL_00370	OE_4502R	98	m01	VNG_2501C	guaAa2	glutamine amidotransferase (homolog to GMP synthase subunit A)	-
HBSAL_00375	OE_4504F	100p	m01	VNG_2502C	-	HD family hydrolase	-
HBSAL_00380	OE_4505F	96	m01	VNG_2504G	pheS	phenylalanine--tRNA ligase alpha subunit	-
HBSAL_00385	OE_4507F	99	m01	VNG_2505G	pheT	phenylalanine--tRNA ligase beta subunit	-

HBSAL_00390	OE_4508R	99	m01	VNG_2507G	pyrD	dihydroorotate dehydrogenase (quinone)	-
HBSAL_00395	OE_4509F	100d	m01	VNG_2508C	-	nonhistone chromosomal protein	-
HBSAL_00400	OE_4523F	99	m02	VNG_2509H	-	uncharacterized protein	-
HBSAL_00405	OE_4524F	100p	m02	VNG_2510H	-	uncharacterized protein	-
HBSAL_00410	OE_4526R	95	m02	VNG_2511H	-	uncharacterized protein	-
HBSAL_00415	OE_4527R	99	m02	VNG_2512G	-	beta-lactamase domain protein	-
HBSAL_00420	OE_4529F	100p	m02	VNG_2513G	aldH1	aldehyde dehydrogenase	-
HBSAL_00425	OE_4532F	100d	m02	VNG_2514G	rps6e	30S ribosomal protein S6e	-
HBSAL_00430	OE_4533F	98	m02	VNG_2515H	-	uncharacterized protein	-
HBSAL_00435	OE_4535F	98	m02	VNG_2516C	-	PfkB family kinase	-
HBSAL_00440	OE_4537R	98	m02	VNG_2518C	-	homolog to photosystem I biogenesis protein BtpA	-
HBSAL_00445	OE_4539R	100p	m02	VNG_2519H	-	uncharacterized protein	-
HBSAL_00450	OE_4540R	100d	m02	VNG_2520C	-	UspA domain protein	-
HBSAL_00455	OE_4541F	100p	m02	VNG_2521H	-	UspA domain protein	-
HBSAL_00460	OE_4543R	100p	m02	VNG_2522C	-	GNAT family acetyltransferase	-
HBSAL_00465	OE_4544R	100p	m02	VNG_2523H	-	UspA domain protein	-
HBSAL_00470	OE_4545F	100d	m02	VNG_2524H	-	uncharacterized protein	-
HBSAL_00475	OE_4549R	99	m02	VNG_2525H	-	uncharacterized protein	-
HBSAL_00480	OE_4550F	99	m02	VNG_2526G	dppDF2	ABC-type transport system ATP-binding protein (probable substrate dipeptide/oligopeptide)	-
HBSAL_00485	OE_4551F	99	m02	VNG_2527G	dppA2	ABC-type transport system periplasmic substrate-binding protein (probable substrate dipeptide/oligopeptide)	-
HBSAL_00490	OE_4552F	100p	m02	VNG_2529G	dppB2	ABC-type transport system permease protein (probable substrate dipeptide/oligopeptide)	-
HBSAL_00495	OE_4555F	99	m02	VNG_2531G	dppC2	ABC-type transport system permease protein (probable substrate dipeptide/oligopeptide)	-
HBSAL_00500	OE_4556F	97	m02	VNG_2532H	-	uncharacterized protein	-
HBSAL_00505	OE_4558R	99	m02	VNG_2533G	pyrC	dihydroorotase	-
HBSAL_00510	OE_4559R	98	m02	VNG_2536C	lpl3	lipoate--protein ligase domain protein	-
HBSAL_00515	OE_4560F	98	m02	VNG_2534C	-	peptidase M23 family protein	-

HBSAL_00520	OE_4561F	99	m02	VNG_2535H	-	PsiE domain protein	-
HBSAL_00525	OE_4562R	99	m02	VNG_2537G	entB2	isochorismatase family protein	-
HBSAL_00530	OE_4563F	99	m02	VNG_2539H	-	uncharacterized protein	-
HBSAL_00535	OE_4565F	99	m02	VNG_2541C	pncB	nicotinate phosphoribosyltransferase	-
HBSAL_00540	OE_4568R	100p	m02	VNG_2543C	-	AMMECR1 domain protein	-
HBSAL_00545	OE_4569R	77	m02	VNG_2544H	-	uncharacterized protein	LowSim
HBSAL_00550	OE_4571R	99	m02	VNG_2546G	pepB3	aminopeptidase (homolog to leucyl aminopeptidase / aminopeptidase T)	-
HBSAL_00555	OE_4572R	99	m02	VNG_2547G	valS	valine--tRNA ligase	-
HBSAL_00560	OE_4576F	96	m02	VNG_2549C	-	ABC-type transport system periplasmic substrate-binding protein	-
HBSAL_00565	OE_4577F	99	m02	VNG_2551G	-	ABC-type transport system permease protein	-
HBSAL_00570	OE_4579F	100p	m02	VNG_2552G	-	ABC-type transport system ATP-binding protein	-
HBSAL_00575	OE_4581F	99	m02	VNG_2553G	gndA	6-phosphogluconate dehydrogenase (NAD-dependent, decarboxylating)	-
HBSAL_00580	OE_4582R	100p	m02	VNG_2554H	-	ThiJ/PfpI domain protein	-
HBSAL_00585	OE_4583F	99	m02	VNG_2555C	fer5	ferredoxin (2Fe-2S)	-
HBSAL_00590	OE_4585R	98	m02	VNG_2556H	-	uncharacterized protein	-
HBSAL_00595	OE_4587R	100p	m02	VNG_2558G	-	ABC-type transport system ATP-binding protein	-
HBSAL_00600	OE_4591R	99	m02	VNG_2560G	-	ABC-type transport system permease protein	-
HBSAL_00605	OE_4593R	99	m02	VNG_2562H	-	ABC-type transport system periplasmic substrate-binding protein	-
HBSAL_00610	OE_4596R	99	m02	VNG_2563H	-	HTH domain protein	-
HBSAL_00615	OE_4599F	99	m02	VNG_2565G	trkH3	Trk-type transport system (probable substrate potassium)	-
HBSAL_00620	OE_4600F	96	m02	VNG_2565a	-	uncharacterized protein	-
HBSAL_00625	OE_4601F	98	m02	VNG_2566H	-	uncharacterized protein	-
HBSAL_00630	OE_4607R	98	m02	VNG_2567C	arlG2	ArlG2 protein (homolog to arl cluster protein ArlG)	-
HBSAL_00635	OE_4609F	100p	m02	VNG_2569H	-	uncharacterized protein	-
HBSAL_00640	OE_4610R	100p	m02	VNG_2570G	dut	dUTP diphosphatase	-
HBSAL_00645	OE_4612F	98	m02	VNG_2573G	hly	serine protease halolysin	-

HBSAL_00650	OE_4613F	100p	m02	VNG_2574G	citB	aconitate hydratase	-
HBSAL_00655	OE_4615F	100p	m02	VNG_2575G	-	GNAT family acetyltransferase	-
HBSAL_00660	OE_4614F	96	m02	VNG_2576H	-	uncharacterized protein	-
HBSAL_00665	OE_4617F	100d	m02	VNG_2577C	-	uncharacterized protein	-
HBSAL_00670	OE_4619R	99	m02	VNG_2579G	idr1	SirR/DtxR family transcription regulator Idr1	-
HBSAL_00675	OE_4621F	99	m02	VNG_2580C	-	NUDIX family hydrolase	-
HBSAL_00680	OE_4623F	98	m02	VNG_2581H	-	HMA domain protein	-
HBSAL_00685	OE_4622F	99	m02	VNG_2582H	-	rhodanese domain protein	-
HBSAL_00690	OE_4626R	100d	m02	VNG_2584C	tif1	translation initiation factor aIF-1 (SUI1 protein, bacterial-type IF3)	-
HBSAL_00695	OE_4627F	98	m02	VNG_2585H	-	uncharacterized protein	-
HBSAL_00700	OE_4628R	99	m02	VNG_2586C	cofE	coenzyme F420:L-glutamate ligase	-
HBSAL_00705	OE_4630R	99	m02	VNG_2587C	engB	probable GTP-binding protein EngB	-
HBSAL_00710	OE_4633F	99	m02	VNG_2589C	-	SIMPL domain protein	-
HBSAL_00715	OE_4634F	100p	m02	VNG_2591C	-	DUF389 family protein	-
HBSAL_00720	OE_4636F	99	m02	VNG_2593H	-	NifU C-terminal domain protein	-
HBSAL_00725	OE_4637R	99	m02	VNG_2595G	-	probable GTP-binding protein	-
HBSAL_00730	OE_4638F	100p	m02	VNG_2594C	-	uncharacterized protein	-
HBSAL_00735	OE_4641R	98	m02	VNG_2596G	hisE	phosphoribosyl-ATP pyrophosphatase	-
HBSAL_00740	OE_4643R	100p	m02	VNG_2597C	-	DUF151 family protein	-
HBSAL_00745	OE_4644R	100p	m02	VNG_2598G	pdxT	pyridoxal 5'-phosphate synthase subunit PdxT	-
HBSAL_00750	OE_4646R	100p	m02	VNG_2599H	secG	protein translocase subunit SecG	-
HBSAL_00755	OE_4648F	100d	m02	VNG_2600G	trxA2	thioredoxin	-
HBSAL_00760	OE_4649F	99	m02	VNG_2602G	arsB	DASS family transport protein	-
HBSAL_00765	OE_4650R	100p	m02	VNG_2603H	-	uncharacterized protein	-
HBSAL_00770	OE_4651F	100p	m02	VNG_2604G	thi4	adenosine diphosphate thiazole synthase, cysteine-dependent	-
HBSAL_00775	OE_4654F	99	m02	VNG_2606G	thiDN	phosphomethylpyrimidine kinase / phosphomethylpyrimidine phosphate kinase / thiamine-phosphate synthase	-

HBSAL_00780	OE_4655R	98	m02	VNG_2607C	npdG	F420H2:NADP oxidoreductase	-
HBSAL_00785	OE_4659R	99	m02	VNG_2608C	-	HAD superfamily hydrolase	-
HBSAL_00790	OE_4661R	99	m02	VNG_2608a	-	UPF0146 family protein	-
HBSAL_00795	OE_4663F	100p	m02	VNG_2610C	amzA	archaemetzincin	-
HBSAL_00800	OE_4665R	99	m02	VNG_2611G	hflX1	ribosome-associating GTPase HflX	-
HBSAL_00805	OE_4667R	99	m02	VNG_2612G	-	ABCE1 family ribosome recycling factor	-
HBSAL_00810	OE_4668R	98	m02	VNG_2613H	-	uncharacterized protein	-
HBSAL_00815	OE_4670F	100p	m02	VNG_2614H	-	NP_1176A family transcription regulator	-
HBSAL_00820	OE_4671R	100p	m02	VNG_2615C	-	arNOG04375 family protein (homolog to PilT-type ATPase)	-
HBSAL_00825	OE_4673F	100d	m02	VNG_2616G	cxp	metal-dependent carboxypeptidase	-
HBSAL_00830	OE_4674F	99	m02	VNG_2617G	adh2	alcohol dehydrogenase (NADP)	-
HBSAL_00835	OE_4676F	100d	m02	VNG_2619H	-	small CPxCG-related zinc finger protein	-
HBSAL_00840	OE_4677F	100p	m02	VNG_2620G	uvrD	repair helicase UvrD	-
HBSAL_00845	OE_4680F	99	m02	VNG_2622H	-	peptidase M24 family protein	-
HBSAL_00850	OE_4682A1R	100d	m02	VNG_2622a	-	uncharacterized protein	-
HBSAL_00855	OE_4683F	98	m02	VNG_2624G	ribE	riboflavin synthase	-
HBSAL_00860	OE_4685R	98	m02	VNG_2625C	-	PrsW family protein	-
HBSAL_00865	OE_4687F	96	m02	VNG_2626H	-	uncharacterized protein	-
HBSAL_00870	OE_4688F	99	m02	VNG_2627C	aubA	probable ribonuclease FAU-1	-
HBSAL_00875	OE_4689R	100p	m02	VNG_2628H	-	NifU C-terminal domain protein	-
HBSAL_00880	OE_4691R	99	m02	VNG_2629G	glcK	glucokinase	-
HBSAL_00885	OE_4693R	100p	m02	VNG_2631H	-	DUF124 family protein	-
HBSAL_00890	OE_4695F	99	m02	VNG_2632G	-	probable oxidoreductase (short-chain dehydrogenase family)	-
HBSAL_00895	OE_4696R	100p	m02	VNG_2633H	-	uncharacterized protein	-
HBSAL_00900	OE_4697R	98	m02	VNG_2634H	-	uncharacterized protein	-
HBSAL_00905	OE_4699F	99	m02	VNG_2636G	uvrA	UvrABC system protein A	-
HBSAL_00910	OE_4700F	99	m02	VNG_2637H	-	uncharacterized protein	-
HBSAL_00915	OE_4702F	100d	m02	VNG_2638G	-	FAD-dependent oxidoreductase (homolog to	-



						geranylgeranyl reductase)	
HBSAL_00920	OE_4703R	100p	m02	VNG_2639G	uae	probable nucleotide sugar epimerase	-
HBSAL_00925	OE_4705R	99	m02	VNG_2640G	-	homolog to glycine cleavage system protein T	-
HBSAL_00930	OE_4707R	100d	m02	VNG_2641H	-	uncharacterized protein	-
HBSAL_00935	OE_4709F	99	m02	VNG_2642H	-	uncharacterized protein	-
HBSAL_00940	OE_4712F	100p	m02	VNG_2643H	-	uncharacterized protein	-
HBSAL_00945	OE_4713R	100d	m02	VNG_2644C	sepF	probable SepF protein	-
HBSAL_00950	OE_4714F	100p	m02	VNG_2644a	-	DUF1028 family protein	-
HBSAL_00955	OE_4716R	100p	m02	VNG_2646C	-	PUA domain protein	-
HBSAL_00960	OE_4717F	98	m02	VNG_2645H	-	small CPxCG-related zinc finger protein	-
HBSAL_00965	OE_4718F	100p	m02	VNG_2647G	rnr	ribonuclease R	-
HBSAL_00970	OE_4720R	100d	m02	VNG_2648G	rps10a	30S ribosomal protein S10a	-
HBSAL_00975	OE_4721R	100p	m02	VNG_2649G	tef1a1	translation elongation factor aEF-1 alpha / peptide chain release factor aRF-3	-
HBSAL_00980	OE_4722R	98	m02	VNG_2650G	hom	homoserine dehydrogenase	-
HBSAL_00985	OE_4724R	97	m02	VNG_2650a	-	ACT domain protein	-
HBSAL_00990	OE_4726C1R	97	m02	VNG_2650b	-	uncharacterized protein	-
HBSAL_00995	OE_4729R	99	m03	VNG_2654G	tef2	translation elongation factor aEF-2	-
HBSAL_01000	OE_4732F	100p	m03	VNG_2656H	-	uncharacterized protein	-
HBSAL_01005	OE_4735R	100p	m03	VNG_2657G	rps7	30S ribosomal protein S7	-
HBSAL_01010	OE_4736R	100d	m03	VNG_2658G	rps12	30S ribosomal protein S12	-
HBSAL_01015	OE_4738R	100p	m03	VNG_2661G	nusA	transcription elongation factor NusA	-
HBSAL_01020	OE_4739R	99	m03	VNG_2662G	rpoA2	DNA-directed RNA polymerase subunit A''	-
HBSAL_01025	OE_4740R	100p	m03	VNG_2664G	rpoA1	DNA-directed RNA polymerase subunit A'	-
HBSAL_01030	OE_4741R	99	m03	VNG_2665G	rpoB1	DNA-directed RNA polymerase subunit B'	-
HBSAL_01035	OE_4742R	100p	m03	VNG_2666G	rpoB2	DNA-directed RNA polymerase subunit B''	-
HBSAL_01040	OE_4743R	100d	m03	VNG_2668G	rpoH	DNA-directed RNA polymerase subunit H	-
HBSAL_01045	OE_4745R	99	m03	VNG_2669G	artA	archaeosortase A	-
HBSAL_01050	OE_4748F	97	m03	[VNG_2669c; VNG_2669a]	-	uncharacterized protein	pseudo(NRC-1;split)

HBSAL_01055	OE_4752R	99	m03	VNG_2674H	-	uncharacterized protein	-
HBSAL_01060	OE_4753R	98	m03	VNG_2675C	-	TetR family transcription regulator	-
HBSAL_01065	OE_4755F	99	m03	VNG_2677H	-	probable secreted glycoprotein	-
HBSAL_01070	OE_4757R	96	m03	VNG_2678H	-	probable secreted glycoprotein	-
HBSAL_01075	OE_4759F	86	m03	VNG_2679G	csg	S-layer glycoprotein	LowSim
HBSAL_01080	OE_1001F	96	m03	VNG_0001H	-	uncharacterized protein	-
HBSAL_01085	OE_1004F	99	m03	VNG_0002G	-	ABC-type transport system ATP-binding protein (probable substrate macrolides)	-
HBSAL_01090	OE_1005F	97	m03	VNG_0003C	-	ABC-type transport system permease protein (probable substrate macrolides)	-
HBSAL_01095	OE_1008F	98	m03	VNG_0005H	-	uncharacterized protein	-
HBSAL_01100	OE_1013R	99	m03	VNG_0006G	glmS	glutamine--fructose-6-phosphate aminotransferase (isomerizing)	seqdiff(R1/NRC-1)
HBSAL_01105	OE_1014R	99	m03	VNG_0008G	graD5	sugar nucleotidyltransferase	-
HBSAL_01110	OE_1016R	100d	m03	VNG_0009G	graD2	sugar nucleotidyltransferase	-
HBSAL_01115	[OE_1018F]	83	m03/ d04	VNG_0011C	-	sugar transferase	pseudo(R1;split); traverse_junction
HBSAL_01355	OE_1136F	81	d04/ m04	VNG_0080H	-	VanZ family protein	traverse_junction
HBSAL_01360	OE_1139F	96	m04	VNG_0081G	moaE	molybdopterin synthase catalytic subunit	-
HBSAL_01365	OE_1140R	100p	m04	VNG_0084G	ubaA	SAMP-activating enzyme E1	-
HBSAL_01370	OE_1142F	99	m04	VNG_0085G	moaA	GTP 3',8-cyclase	-
HBSAL_01375	OE_1143R	99	m04	VNG_0086G	moeA2	molybdopterin molybdenumtransferase	-
HBSAL_01380	OE_1146R	99	m04	VNG_0090G	moeA1	molybdopterin molybdenumtransferase	-
HBSAL_01385	OE_1147R	99	m04	VNG_0089G	pimT1	protein-L-isoaspartate O-methyltransferase	-
HBSAL_01390	OE_1148R	99	m04	VNG_0091C	-	probable S-adenosylmethionine-dependent methyltransferase	-
HBSAL_01395	OE_1150R	100p	m04	VNG_0094C	-	UCP015877 family protein	-
HBSAL_01400	OE_1151R	99	m04	VNG_0096C	pepB4	aminopeptidase (homolog to leucyl aminopeptidase / aminopeptidase T)	-
HBSAL_01405	OE_1154F	100p	m04	VNG_0095G	gap	glyceraldehyde-3-phosphate dehydrogenase (NAD(P)) (phosphorylating)	-

HBSAL_01410	OE_1156F	100p	m04	VNG_0097G	hsp20A	Hsp20-type molecular chaperone	-
HBSAL_01415	OE_1158R	99	m04	VNG_0098G	-	ATP-grasp fold protein	-
HBSAL_01420	OE_1160R	100p	m04	VNG_0099G	rpl16	50S ribosomal protein L16	-
HBSAL_01425	OE_1162R	100d	m04	VNG_0101G	cspA1	cold shock protein	-
HBSAL_01430	OE_1164R	100p	m04	VNG_0102C	-	HAD superfamily hydrolase	-
HBSAL_01435	OE_1165R	99	m04	VNG_0104G	serA3	probable D-2-hydroxyacid dehydrogenase	-
HBSAL_01440	OE_1168R	98	m04	VNG_0105H	-	uncharacterized protein	-
HBSAL_01455	OE_1186A1F	92	m05	[VNG_0110d; VNG_0112a]	-	pilin Pila	LowSim; pseudo(NRC-1;split)
HBSAL_01460	OE_1188F	99	m05	VNG_0113H	-	HTH-10 family transcription regulator	-
HBSAL_01465	OE_1190F	99	m05	VNG_0115G	-	probable oxidoreductase (short-chain dehydrogenase family)	-
HBSAL_01470	OE_1201F	96	m06	VNG_0121H	-	DUF192 family protein	-
HBSAL_01475	OE_1202F	99	m06	VNG_0123G	-	ABC-type transport system ATP-binding/permease protein	-
HBSAL_01480	OE_1203F	99	m06	VNG_0124C	cre1	creatininase domain protein	-
HBSAL_01485	OE_1205R	99	m06	VNG_0125H	-	uncharacterized protein	-
HBSAL_01490	OE_1207R	100d	m06	VNG_0127C	mptD	dihydroneopterin aldolase, archaeal-type	-
HBSAL_01495	OE_1209F	100d	m06	VNG_0128C	azf	glucose-6-phosphate 1-dehydrogenase (NAD)	-
HBSAL_01500	OE_1211F	100d	m06	VNG_0129G	htpX	HtpX-like protease	-
HBSAL_01505	OE_1213F	100d	m06	VNG_0130H	-	uncharacterized protein	-
HBSAL_01510	OE_1215R	100d	m06	VNG_0132C	-	DUF309 family protein	-
HBSAL_01515	OE_1218F	100d	m06	VNG_0133G	rpa2	replication protein A	-
HBSAL_01520	OE_1220F	100d	m06	VNG_0134G	hstA	archaeal histone	-
HBSAL_01525	OE_1221F	100d	m06	VNG_0136G	hda1	HdaI-type histone deacetylase	-
HBSAL_01530	OE_1222R	100d	m06	VNG_0137G	cca	tRNA adenylyltransferase, CCA-adding	-
HBSAL_01535	OE_1224A1F	100d	m06	VNG_0137a	-	small CPxCG-related zinc finger protein	-
HBSAL_01540	OE_1225F	100d	m06	VNG_0138H	-	homolog to HGPV1-ORF14	pseudo(91-R6;R1;NRC-1)
HBSAL_01545	OE_1226F	100d	m06	VNG_0139H	-	uncharacterized protein	-
HBSAL_01550	OE_1227F	100d	m06	VNG_0140H	-	XerC/D-like integrase	pseudo(91-R6;R1;NRC-1)

HBSAL_01555	OE_1229R	100d	m06	VNG_0141H	-	uncharacterized protein	-
HBSAL_01560	[OE_1232R]	99	m06/ m07	VNG_0142C	-	TrmB family transcription regulator	pseudo(R1;split); traverse_junction
HBSAL_01565	OE_1234R	100d	m07	VNG_0143H	-	uncharacterized protein	-
HBSAL_01570	OE_1236F	100d	m07	VNG_0144H	-	DUF302 family protein	-
HBSAL_01575	OE_1239F	100d	m07	VNG_0146H	-	HTH domain protein	-
HBSAL_01580	OE_1241R	100d	m07	VNG_0147C	-	NikR family transcription regulator	-
HBSAL_01585	OE_1243R	100d	m07	VNG_0148H	-	uncharacterized protein	pseudo(91-R6;R1;NRC-1)
HBSAL_01590	OE_1245F	100d	m07	VNG_0149G	cadA	P-type transport ATPase (probable substrate zinc/cadmium)	-
HBSAL_01595	OE_1249R	100d	m07	VNG_0150H	-	homolog to cytochrome c-type biogenesis protein CcdA	-
HBSAL_01600	OE_1252R	100d	m07	VNG_0151C	trxA4	thioredoxin	-
HBSAL_01605	OE_1254R	100d	m07	VNG_0152G	-	SCO1/SenC/PrrC family protein	-
HBSAL_01610	OE_1259R	100d	m07	VNG_0153C	-	uncharacterized protein	-
HBSAL_01615	OE_1260R	100d	m07	VNG_0154G	-	bis-gamma-glutamylcystine reductase	-
HBSAL_01620	OE_1263F	100d	m07	VNG_0156C	-	HTH-10 family transcription regulator	-
HBSAL_01625	OE_1265F	100d	m07	VNG_0157G	-	major facilitator superfamily transport protein	-
HBSAL_01630	OE_1266R	100d	m07	VNG_0158G	kdgK	2-keto-3-deoxygluconate kinase	-
HBSAL_01635	OE_1267R	100d	m07	VNG_0159G	mutL	DNA mismatch repair protein MutL	-
HBSAL_01640	OE_1268F	100d	m07	VNG_0160G	boa1	sensor/bat box HTH-10 family transcription regulator	-
HBSAL_01645	OE_1269A1F	100d	m07	VNG_0160a	-	small CPxCG-related zinc finger protein	-
HBSAL_01650	OE_1270F	100d	m07	VNG_0161G	gdhA3	glutamate dehydrogenase (NAD)	-
HBSAL_01655	OE_1271F	100d	m07	VNG_0162G	acs4	acyl-CoA synthetase	-
HBSAL_01660	OE_1272R	100d	m07	VNG_0163G	mutS1b	DNA mismatch repair protein MutS	-
HBSAL_01665	OE_1274R	100d	m07	VNG_0164G	hypE2	HypE family protein	-
HBSAL_01670	OE_1275F	100d	m07	VNG_0166G	psmA	proteasome alpha subunit	-
HBSAL_01675	OE_1277F	100d	m07	VNG_0167H	trxA3	thioredoxin	-
HBSAL_01680	OE_1279R	100p	m07	VNG_0168H	rpoeps	DNA-directed RNA polymerase epsilon subunit	-
HBSAL_01685	OE_1283R	99	m07	VNG_0170C	-	thioredoxin domain protein	-

HBSAL_01690	OE_1285F	100p	m07	VNG_0171C	nucS1	endonuclease NucS	-
HBSAL_01695	OE_1286R	99	m07	VNG_0172G	mutS1a	DNA mismatch repair protein MutS	-
HBSAL_01700	OE_1288F	99	m07	VNG_0174G	cat1	transport protein (probable substrate cationic amino acids)	-
HBSAL_01705	OE_1290F	100p	m07	VNG_0175G	trkA1	TrkA domain protein	-
HBSAL_01710	OE_1291R	99	m07	VNG_0176H	-	GNAT family acetyltransferase	-
HBSAL_01715	OE_1294R	100p	m07	VNG_0177G	rpl15e	50S ribosomal protein L15e	-
HBSAL_01720	OE_1295R	100p	m07	VNG_0178H	-	homolog to restriction system mrr	-
HBSAL_01725	OE_1298R	99	m07	VNG_0179C	rio2	RIO-type serine/threonine protein kinase Rio2	-
HBSAL_01730	OE_1299R	100p	m07	VNG_0180G	hop	halorhodopsin	-
HBSAL_01735	OE_1302F	99	m07	VNG_0181G	lpl1	lipoate--protein ligase domain protein	-
HBSAL_01740	OE_1304F	100d	m07	VNG_0183G	apn1	endonuclease 4	-
HBSAL_01745	OE_1306F	100p	m07	VNG_0184H	-	probable S-adenosylmethionine-dependent methyltransferase	-
HBSAL_01750	OE_1309F	100d	m07	VNG_0186G	pepB1	aminopeptidase (homolog to leucyl aminopeptidase / aminopeptidase T)	-
HBSAL_01755	OE_1312R	100d	m07	VNG_0187H	-	uncharacterized protein	-
HBSAL_01760	OE_1314F	100d	m07	VNG_0188H	-	major facilitator superfamily transport protein	-
HBSAL_01765	OE_1317F	100d	m07	VNG_0189C	-	HD family hydrolase	-
HBSAL_01770	OE_1318F	100d	m07	VNG_0190C	ncsA	putative tRNA 2-thiolation protein NcsA	-
HBSAL_01775	OE_1319R	100d	m07	VNG_0192G	ftsZ2	cell division protein FtsZ, type II	-
HBSAL_01780	OE_1321R	100d	m07	VNG_0194H	-	CopG domain protein	-
HBSAL_01785	OE_1323R	100d	m07	VNG_0195H	-	DZR domain protein	-
HBSAL_01790	OE_1324R	100d	m07	VNG_0196H	-	uncharacterized protein	pseudo(91-R6;R1;NRC-1)
HBSAL_01795	OE_1326R	100d	m07	VNG_0197C	-	UPF0104 family protein	-
HBSAL_01800	OE_1328F	100d	m07	VNG_0197a	-	uncharacterized protein	-
HBSAL_01805	OE_1332R	100d	m07	VNG_0198H	-	uncharacterized protein	-
HBSAL_01810	OE_1334R	100d	m07	VNG_0199H	-	uncharacterized protein	-
HBSAL_01815	OE_1336R	100d	m07	VNG_0200C	-	uncharacterized protein	-
HBSAL_01820	OE_1339R	100d	m07	VNG_0200a	-	uncharacterized protein	-

HBSAL_01825	OE_1340R	100d	m07	VNG_0204H	-	probable secreted glycoprotein	-
HBSAL_01830	OE_1344R	99	m07	VNG_0205H	pilC2	type IV pilus biogenesis complex membrane subunit	pseudo(91-R6;R1;NRC-1)
HBSAL_01835	OE_1347R	99	m07	[VNG_0218G;VNG_0205a]	pilB2	type IV pilus biogenesis complex ATPase subunit	pseudo(NRC-1;split)
HBSAL_01840	OE_1352F	100d	m07	VNG_0219H	-	DUF4129 domain protein	-
HBSAL_01845	OE_1353F	100d	m07	VNG_0220H	-	uncharacterized protein	-
HBSAL_01850	OE_1356F	100d	m07	VNG_0222C	-	DUF11/DUF58 family protein	-
HBSAL_01855	OE_1357F	100d	m07	VNG_0222a	-	uncharacterized protein	-
HBSAL_01860	OE_1358R	100d	m07	VNG_0223G	moxR	AAA-type ATPase (MoxR subfamily)	-
HBSAL_01865	OE_1361F	100d	m07	VNG_0226G	degP	probable periplasmic serine protease	-
HBSAL_01870	OE_1362R	100d	m07	VNG_0227H	-	DUF192 family protein	-
HBSAL_01875	OE_1363F	100d	m07	VNG_0228G	guaAa1	GMP synthase (glutamine-hydrolyzing) subunit A	-
HBSAL_01880	OE_1365F	100d	m07	VNG_0230C	-	DUF2070 family protein	-
HBSAL_01885	OE_1366F	100d	m07	VNG_0231C	-	beta-lactamase domain protein	-
HBSAL_01890	OE_1368R	100d	m07	VNG_0233H	-	DUF3194 family protein	-
HBSAL_01895	OE_1371R	100d	m07	VNG_0234C	pfdB	prefoldin beta subunit	-
HBSAL_01900	OE_1371B1R	100d	m07	VNG_0234a	pcc1	KEOPS complex subunit Pcc1	-
HBSAL_01905	OE_1372R	100d	m07	VNG_0237H	rpoP	DNA-directed RNA polymerase subunit P	-
HBSAL_01910	OE_1373R	100d	m07	VNG_0239C	rpl43e	50S ribosomal protein L43e	-
HBSAL_01915	OE_1374F	100d	m07	VNG_0238H	-	uncharacterized protein	-
HBSAL_01920	OE_1376R	100d	m07	VNG_0240C	-	DUF2103 family protein	-
HBSAL_01925	OE_1378R	100d	m07	VNG_0243C	truD	tRNA pseudouridine(13) synthase TruD	-
HBSAL_01930	OE_1379R	100d	m07	VNG_0243a	pth	peptidyl-tRNA hydrolase	-
HBSAL_01935	OE_1382F	100d	m07	VNG_0244H	-	Yip1 domain protein	-
HBSAL_01940	OE_1384F	100d	m07	VNG_0245G	dcd	dCTP deaminase	-
HBSAL_01945	OE_1385F	100d	m07	VNG_0247C	thiR	transcription regulator ThiR	-
HBSAL_01950	OE_1388R	100d	m07	VNG_0248C	-	uncharacterized protein	-
HBSAL_01955	OE_1391R	100d	m07	VNG_0249G	hcpG	DUF5059 domain / halocyanin domain protein HcpG	-

HBSAL_01960	OE_1394R	100d	m07	VNG_0250C	-	4-phosphopantoate--beta-alanine ligase	-
HBSAL_01965	OE_1396R	100d	m07	VNG_0251C	-	pantoate kinase	-
HBSAL_01970	OE_1398R	99	m07	VNG_0252C	pcrB1	(S)-3-O-geranylgeranylglyceryl phosphate synthase 1	-
HBSAL_01975	OE_1399R	100d	m07	VNG_0254G	tfbA1	transcription initiation factor TFB	-
HBSAL_01980	OE_1400F	99	m07	VNG_0255C	rnhA2	ribonuclease H, type 1	pseudo(91-R6)
HBSAL_01985	OE_1403F	100d	m07	VNG_0256H	-	uncharacterized protein	-
HBSAL_01990	OE_1405R	100d	m07	VNG_0258H	rosR	PadR family transcription regulator RosR	-
HBSAL_01995	OE_1407F	100d	m07	VNG_0259G	ipp	inorganic pyrophosphatase	-
HBSAL_02000	OE_1409F	100d	m07	VNG_0261H	-	uncharacterized protein	-
HBSAL_02005	OE_1410F	100d	m07	VNG_0262C	-	DHH/RecJ family phosphoesterase	-
HBSAL_02010	OE_1412F	100d	m07	VNG_0264H	-	probable phosphodiesterase	-
HBSAL_02015	OE_1414R	100d	m07	VNG_0265G	cetZ2	FtsZ family protein CetZ, type III	-
HBSAL_02020	OE_1416F	100d	m07	VNG_0266H	-	uncharacterized protein	-
HBSAL_02025	OE_1417F	100d	m07	VNG_0267H	-	homolog to NAD-dependent epimerase/dehydratase	-
HBSAL_02030	OE_1418F	100d	m07	VNG_0268C	-	probable oxidoreductase (aldo-keto reductase family protein)	-
HBSAL_02035	OE_1420F	100d	m07	VNG_0270C	-	major facilitator superfamily transport protein	-
HBSAL_02040	OE_1422F	100d	m07	VNG_0271C	gtl5	probable glycosyltransferase, type 2	-
HBSAL_02045	OE_1424F	100d	m07	VNG_0272H	-	uncharacterized protein	-
HBSAL_02050	OE_1425F	100d	m07	VNG_0274C	-	NUDIX family hydrolase	-
HBSAL_02055	OE_1426F	100d	m07	VNG_0277G	-	probable flavin containing oxidoreductase (homolog to phytoene desaturase / monoamine oxidase)	-
HBSAL_02060	OE_1428F	100d	m07	VNG_0277a	-	uncharacterized protein	-
HBSAL_02065	OE_1430B1R	100d	m07	VNG_0280a	-	uncharacterized protein	-
HBSAL_02070	OE_1432F	99	m07	VNG_0281G	-	FAD-dependent oxidoreductase	-
HBSAL_02075	OE_1434R	100p	m07	VNG_0283C	hsp20D	Hsp20-type molecular chaperone	-
HBSAL_02080	OE_1435R	100d	m07	VNG_0282H	-	small CPxCG-related zinc finger protein	-
HBSAL_02085	OE_1435A1F	99	m07	VNG_0282a	-	uncharacterized protein	-

HBSAL_02090	OE_1438F	99	m07	VNG_0284C	-	radical SAM domain protein	-
HBSAL_02095	OE_1442R	95	m08	VNG_0287a	-	TRAM domain protein	-
HBSAL_02100	OE_1445R	99	m08	VNG_0289H	-	uncharacterized protein	-
HBSAL_02105	OE_1447R	99	m08	VNG_0291H	-	beta-lactamase domain protein	-
HBSAL_02110	OE_1448R	100p	m08	VNG_0293H	-	NP_1176A family transcription regulator	-
HBSAL_02115	OE_1451F	100p	m08	VNG_0294G	-	probable S-adenosylmethionine-dependent methyltransferase	-
HBSAL_02120	OE_1453F	100d	m08	VNG_0296H	gtl4	probable glycosyltransferase, type 2	-
HBSAL_02125	OE_1455R	100d	m08	VNG_0297H	-	amidohydrolase domain protein	-
HBSAL_02130	OE_1457R	100d	m08	VNG_0298H	-	UPF0126 family protein	-
HBSAL_02135	OE_1461R	100d	m08	VNG_0300C	-	S-adenosylmethionine hydroxide adenosyltransferase family protein	-
HBSAL_02140	OE_1462R	100d	m08	VNG_0301C	nadM	nicotinamide-nucleotide adenyltransferase	-
HBSAL_02145	OE_1465F	100p	m08	VNG_0303G	lon	ATP-dependent protease Lon	-
HBSAL_02150	OE_1467R	100d	m08	VNG_0306C	ogt	probable methylated-DNA--protein-cysteine methyltransferase	-
HBSAL_02155	OE_1469F	100d	m08	VNG_0305G	trpC	indole-3-glycerol-phosphate synthase	-
HBSAL_02160	OE_1470F	100d	m08	VNG_0307G	trpB	tryptophan synthase beta subunit	-
HBSAL_02165	OE_1471F	100d	m08	VNG_0308G	trpA	tryptophan synthase alpha subunit	-
HBSAL_02170	OE_1472F	100d	m08	VNG_0309C	fba2	2-amino-3,7-dideoxy-D-threo-hept-6-ulose synthase / fructose-bisphosphate aldolase	-
HBSAL_02175	OE_1474R	100d	m08	VNG_0311H	-	uncharacterized protein	-
HBSAL_02180	OE_1475F	100d	m08	VNG_0310C	aroB	3-dehydroquinate synthase, type II	-
HBSAL_02185	OE_1476R	100d	m08	VNG_0312H	-	small CPxCG-related zinc finger protein	-
HBSAL_02190	OE_1477R	100d	m08	VNG_0314G	aroD	3-dehydroquinate dehydratase	-
HBSAL_02195	OE_1478R	99	m08	VNG_0315G	tfbA2	transcription initiation factor TFB	-
HBSAL_02200	OE_1480F	100d	m08	VNG_0316C	-	ABC-type transport system periplasmic substrate-binding protein (probable substrate iron/cobalamin)	-
HBSAL_02205	OE_1482R	100d	m08	VNG_0318G	aglD	glycosyltransferase AglD	-
HBSAL_02210	OE_1488F	100d	m08	VNG_0319H	-	uncharacterized protein	-
HBSAL_02215	OE_1489R	100d	m08	VNG_0320H	-	HTH domain protein	-



HBSAL_02220	OE_1490R	100d	m08	VNG_0321G	-	stomatin family protein	-
HBSAL_02225	OE_1492R	100d	m08	VNG_0322H	-	NfeD domain protein	-
HBSAL_02230	OE_1494R	100d	m08	VNG_0323H	-	uncharacterized protein	-
HBSAL_02235	OE_1495R	100d	m08	VNG_0324G	pykA	pyruvate kinase	-
HBSAL_02240	OE_1496R	100d	m08	VNG_0326G	metS	methionine--tRNA ligase	-
HBSAL_02245	OE_1498R	100d	m08	VNG_0327G	panD	aspartate 1-decarboxylase	-
HBSAL_02250	OE_1499R	100d	m08	VNG_0329G	-	peptidase M48 family protein (homolog to CAAX prenyl protease)	-
HBSAL_02255	OE_1500R	100d	m08	VNG_0330G	ppsA	phosphoenolpyruvate synthase	-
HBSAL_02260	OE_1501F	100d	m08	VNG_0331H	-	uncharacterized protein	-
HBSAL_02265	OE_1502R	100d	m08	VNG_0332C	phzF1	PhzF family protein	-
HBSAL_02270	OE_1504F	100d	m08	VNG_0335G	gptA1	probable phosphoribosyltransferase	-
HBSAL_02275	[OE_1505F]	98	m08/ m09	[VNG_0335a; VNG_0337a]	-	probable 6-oxopurine nucleoside phosphorylase	pseudo(R1;split); pseudo(NRC-1;split); traverse_junction
HBSAL_02280	OE_1510F	100d	m09	VNG_0339H	-	uncharacterized protein	-
HBSAL_02285	OE_1512R	100d	m09	VNG_0340C	scpA	chromosome segregation and condensation protein ScpA	-
HBSAL_02290	OE_1515R	100d	m09	VNG_0342G	smc	chromosome segregation protein Smc	-
HBSAL_02295	OE_1520R	100d	m09	VNG_0343H	-	uncharacterized protein	-
HBSAL_02300	OE_1522F	100d	m09	VNG_0345G	gatB	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	-
HBSAL_02305	OE_1524R	100d	m09	VNG_0346H	-	uncharacterized protein	-
HBSAL_02310	OE_1526R	100d	m09	VNG_0347H	-	uncharacterized protein	-
HBSAL_02315	OE_1528F	100d	m09	VNG_0349G	topA	DNA topoisomerase 1	-
HBSAL_02320	OE_1529F	100d	m09	VNG_0351C	nreA	DNA repair protein NreA	-
HBSAL_02325	OE_1532F	100d	m09	VNG_0352H	-	homolog to Sec-independent protein translocase subunit TatA	-
HBSAL_02330	OE_1534F	100d	m09	VNG_0354C	-	Abi/CAAX domain protein	-
HBSAL_02335	OE_1536R	100d	m09	VNG_0355G	mpcT	transducer protein MpcT	-
HBSAL_02340	OE_1537B1R	100d	m09	VNG_0357a	-	uncharacterized protein	-

HBSAL_02345	OE_1539F	100d	m09	VNG_0359C	-	uncharacterized protein	-
HBSAL_02350	OE_1540R	100d	m09	VNG_0360C	-	uncharacterized protein	-
HBSAL_02355	OE_1541F	100d	m09	VNG_0361C	-	rhomboid family protease	-
HBSAL_02360	OE_1543F	100d	m09	VNG_0363G	nfi	endonuclease 5	-
HBSAL_02365	OE_1545F	100d	m09	VNG_0364G	-	probable oxidoreductase (short-chain dehydrogenase family)	-
HBSAL_02370	OE_1547R	100d	m09	VNG_0365G	arsA2	ArsA family ATPase	-
HBSAL_02375	OE_1549F	100d	m09	VNG_0367H	-	DUF1486 family protein	-
HBSAL_02380	OE_1550F	100d	m09	VNG_0368C	-	nicotinamide mononucleotide deamidase	-
HBSAL_02385	OE_1553F	100d	m09	VNG_0368a	-	DUF457 family protein	-
HBSAL_02390	OE_1554R	100d	m09	VNG_0370H	-	PHP domain protein	-
HBSAL_02395	OE_1555F	100d	m09	VNG_0371G	acd1	acyl-CoA dehydrogenase	-
HBSAL_02400	OE_1556F	100d	m09	VNG_0373H	-	homolog to small CPxCG-related zinc finger protein	-
HBSAL_02405	OE_1557R	100d	m09	VNG_0374G	spt5	transcription elongation factor Spt5	-
HBSAL_02410	OE_1558R	100d	m09	VNG_0375G	secE	protein translocase subunit SecE	-
HBSAL_02415	OE_1559R	100d	m09	VNG_0376G	ftsZ1	cell division protein FtsZ, type I	-
HBSAL_02420	OE_1560R	100d	m09	VNG_0378C	dtdA	D-aminoacyl-tRNA deacylase	-
HBSAL_02425	OE_1564R	100d	m09	VNG_0380G	-	homolog to sodium/calcium antiporter	-
HBSAL_02430	OE_1565F	100d	m09	VNG_0382G	aroE	shikimate dehydrogenase	-
HBSAL_02435	OE_1566F	100d	m09	VNG_0383H	-	uncharacterized protein	-
HBSAL_02440	OE_1568F	100d	m09	VNG_0384G	pabB	aminodeoxychorismate synthase component 1	-
HBSAL_02445	[OE_1570F]	98	m09/ m10	VNG_0386G	pabA	aminodeoxychorismate synthase component 2	pseudo(R1;split); traverse_junction
HBSAL_02450	OE_1574F	100d	m10	VNG_0387G	pabC	aminodeoxychorismate lyase	-
HBSAL_02455	OE_1576F	100d	m10	VNG_0388C	-	probable iron-sulfur protein (2Fe-2S)	-
HBSAL_02460	OE_1577R	100d	m10	VNG_0389C	-	HTH domain protein	-
HBSAL_02465	OE_1578F	100d	m10	VNG_0390G	graD1	sugar nucleotidyltransferase	-
HBSAL_02470	OE_1579R	100d	m10	VNG_0391C	dph6	diphthine--ammonia ligase	-
HBSAL_02475	OE_1582R	100d	m10	VNG_0393C	-	DUF373 family protein	-

HBSAL_02480	OE_1584R	100d	m10	VNG_0394C	-	uncharacterized protein	-
HBSAL_02485	OE_1587F	100d	m10	VNG_0396C	-	DUF371 family protein	-
HBSAL_02490	OE_1589F	100d	m10	VNG_0398G	nthB	endonuclease 3	-
HBSAL_02495	OE_1591R	100d	m10	VNG_0399H	-	uncharacterized protein	-
HBSAL_02500	OE_1592R	100d	m10	VNG_0401G	-	zinc-dependent nuclease	-
HBSAL_02505	OE_1593F	100d	m10	VNG_0401a	-	uncharacterized protein	-
HBSAL_02510	OE_1594R	100d	m10	VNG_0402H	-	uncharacterized protein	-
HBSAL_02515	OE_1595F	99	m10	VNG_0403G	proS1	proline--tRNA ligase	-
HBSAL_02520	OE_1597F	100d	m10	VNG_0404H	-	uncharacterized protein	-
HBSAL_02525	OE_1599F	100d	m10	VNG_0405C	-	GalE family epimerase/dehydratase	-
HBSAL_02530	OE_1602F	100d	m10	VNG_0406C	gldA2	glycerol-1-phosphate dehydrogenase (NAD(P))	-
HBSAL_02535	OE_1606R	100d	m10	VNG_0407H	-	UPF0104 family protein	-
HBSAL_02540	OE_1610R	100d	m10	VNG_0408H	-	peptidase M48 family protein	-
HBSAL_02545	OE_1613R	100d	m10	VNG_0409C	-	peptidase S9 family protein	-
HBSAL_02550	OE_1614F	100d	m10	VNG_0410G	gth3	probable glycosyltransferase, type 1	-
HBSAL_02555	OE_1615R	100d	m10	VNG_0412G	folCP	folypolyglutamate synthase / 7,8-dihydropteroate reductase / dihydropteroate synthase	-
HBSAL_02560	OE_1620R	100d	m10	VNG_0414G	purNH	phosphoribosylglycinamide formyltransferase / phosphoribosylaminoimidazolecarboxamide formyltransferase	-
HBSAL_02565	OE_1623F	100d	m10	VNG_0415G	purB	adenylosuccinate lyase	-
HBSAL_02570	OE_1625F	100d	m10	VNG_0417H	-	metallophosphoesterase domain protein	-
HBSAL_02575	OE_1626F	100d	m10	VNG_0419C	-	DUF88 family protein	-
HBSAL_02580	OE_1628R	100d	m10	VNG_0420H	-	uncharacterized protein	-
HBSAL_02585	OE_1629F	100d	m10	VNG_0421C	-	MiaB-like tRNA modifying enzyme	-
HBSAL_02590	OE_1632R	100d	m10	VNG_0422G	cyc	cytochrome P450	-
HBSAL_02595	OE_1633F	100d	m10	VNG_0424C	nac	nascent polypeptide-associated complex protein	-
HBSAL_02600	OE_1636F	100d	m10	VNG_0425G	trmI	tRNA (adenine-N(1))-methyltransferase TrmI	-
HBSAL_02605	OE_1637R	100d	m10	VNG_0426G	tfs1	transcription elongation factor TFS	-
HBSAL_02610	OE_1640F	100d	m10	VNG_0427G	-	major facilitator superfamily transport protein	-

HBSAL_02615	OE_1641R	99	m10	VNG_0428G	fadA2	enoyl-CoA hydratase	-
HBSAL_02620	OE_1643F	100d	m10	VNG_0429H	-	uncharacterized protein	-
HBSAL_02625	OE_1646R	100d	m10	VNG_0430H	-	uncharacterized protein	-
HBSAL_02630	OE_1648R	100d	m10	VNG_0431G	-	NUDIX family hydrolase	-
HBSAL_02635	OE_1651F	100d	m10	VNG_0433C	rps10b	30S ribosomal protein S10b	-
HBSAL_02640	OE_1652R	100d	m10	VNG_0435H	-	uncharacterized protein	-
HBSAL_02645	OE_1653R	99	m10	VNG_0436G	nhaC1	probable NhaC-type sodium/proton antiporter	-
HBSAL_02650	OE_1656F	100d	m10	VNG_0437C	-	M20 family amidohydrolase (homolog to indole-3-acetyl-aspartate hydrolase)	-
HBSAL_02655	OE_1657R	100d	m10	VNG_0439C	-	FAD-dependent oxidoreductase (homolog to geranylgeranyl reductase)	-
HBSAL_02660	OE_1658F	100d	m10	VNG_0438G	fer3	ferredoxin (2Fe-2S)	-
HBSAL_02665	OE_1659R	100d	m10	VNG_0440C	-	rhodanese domain protein / beta-lactamase domain protein	-
HBSAL_02670	OE_1661F	100d	m10	VNG_0441H	-	ferritin domain protein	-
HBSAL_02675	OE_1664R	100d	m10	VNG_0442G	gnaD	D-gluconate dehydratase	-
HBSAL_02680	OE_1665R	100d	m10	VNG_0444G	kdgA	2-dehydro-3-deoxy-(phospho)gluconate aldolase, archaeal-type	-
HBSAL_02685	OE_1668R	100d	m10	VNG_0447H	-	HAD superfamily hydrolase	-
HBSAL_02690	OE_1669F	100d	m10	VNG_0446G	gdh	glucose 1-dehydrogenase	-
HBSAL_02695	OE_1672F	100d	m10	VNG_0448G	pyrE1	homolog to orotate phosphoribosyltransferase	-
HBSAL_02700	OE_1673F	100d	m10	VNG_0450C	grx4	glutaredoxin	-
HBSAL_02705	OE_1674R	100d	m10	VNG_0451G	phoU2	PhoU domain protein	-
HBSAL_02710	OE_1675R	100d	m10	VNG_0452G	pstB2	ABC-type transport system ATP-binding protein (probable substrate phosphate)	-
HBSAL_02715	OE_1676R	100d	m10	VNG_0453G	pstA2	ABC-type transport system permease protein (probable substrate phosphate)	-
HBSAL_02720	OE_1678R	100d	m10	VNG_0455G	pstC2	ABC-type transport system permease protein (probable substrate phosphate)	-
HBSAL_02725	OE_1679R	100d	m10	VNG_0457G	pstS2	ABC-type transport system periplasmic substrate-binding protein (probable substrate phosphate)	-
HBSAL_02730	OE_1681F	100d	m10	VNG_0458G	phoU3	PhoU domain protein	-

HBSAL_02735	OE_1684F	100d	m10	VNG_0459G	-	homolog to sulfate adenylyltransferase small subunit	-
HBSAL_02740	OE_1687F	100d	m10	VNG_0461G	aspS	aspartate--tRNA(Asp/Asn) ligase	-
HBSAL_02745	OE_1688R	100d	m10	VNG_0462C	-	ArsR family transcription regulator	-
HBSAL_02750	OE_1691R	100d	m10	VNG_0463C	-	uncharacterized protein	-
HBSAL_02755	OE_1693R	100d	m10	VNG_0465G	-	probable ABC-type transport system ATP-binding protein	-
HBSAL_02760	OE_1695R	99	m10	VNG_0466C	-	ABC-type transport system permease protein	seqdiff(R1/NRC-1)
HBSAL_02765	OE_1698R	100d	m10	VNG_0467G	-	probable oxidoreductase (aldo-keto reductase family protein)	-
HBSAL_02770	OE_1699R	100d	m10	VNG_0468C	-	digeranylgeranylglycerophospholipid reductase	-
HBSAL_02775	OE_1702R	100d	m10	VNG_0469H	-	uncharacterized protein	-
HBSAL_02780	OE_1704R	100d	m10	VNG_0470G	-	ABC-type transport system ATP-binding protein	-
HBSAL_02785	OE_1707R	100d	m10	VNG_0471C	-	cro/C1 family transcription regulator	-
HBSAL_02790	OE_1708R	100d	m10	VNG_0472H	-	DUF2178 family protein	-
HBSAL_02795	OE_1709B1F	100d	m10	VNG_0472a	-	uncharacterized protein	pseudo(91-R6;R1;NRC-1)
HBSAL_02800	OE_1710R	100d	m10	VNG_0473G	korB	oxoglutarate--ferredoxin oxidoreductase beta subunit	-
HBSAL_02805	OE_1711R	100d	m10	VNG_0474G	korA	oxoglutarate--ferredoxin oxidoreductase alpha subunit	-
HBSAL_02810	OE_1713F	100d	m10	VNG_0475C	-	FAD-dependent oxidoreductase	-
HBSAL_02815	OE_1715F	100d	m10	VNG_0475a	-	NUDIX family hydrolase	-
HBSAL_02820	OE_1718R	100d	m10	VNG_0478C	mce	methylmalonyl-CoA epimerase	-
HBSAL_02825	OE_1719R	100d	m10	VNG_0479G	-	probable oxidoreductase (short-chain dehydrogenase family)	-
HBSAL_02830	OE_1721R	100d	m10	VNG_0481G	mmcA2	methylmalonyl-CoA mutase subunit A	-
HBSAL_02835	OE_1721G1R	100d	m10	VNG_0481a	-	peptidase S66 family protein	pseudo(91-R6;R1;NRC-1)
HBSAL_02840	OE_1722R	100d	m10	VNG_0482H	-	GNAT family acetyltransferase	-
HBSAL_02845	OE_1724R	100d	m10	VNG_0483C	-	LppX domain protein	-
HBSAL_02850	OE_1726F	100d	m10	VNG_0484G	acs1	acyl-CoA synthetase	-
HBSAL_02855	OE_1727R	100d	m10	VNG_0485H	-	NUDIX family hydrolase	-

HBSAL_02860	OE_1729R	100d	m10	VNG_0486G	-	GNAT family acetyltransferase	-
HBSAL_02865	OE_1730R	100d	m10	VNG_0487H	-	GNAT family acetyltransferase	-
HBSAL_02870	OE_1733R	100d	m10	VNG_0488H	-	uncharacterized protein	-
HBSAL_02875	OE_1736R	100d	m10	VNG_0489G	dnaJ	molecular chaperone DnaJ	-
HBSAL_02880	OE_1737R	100d	m10	VNG_0491G	dnaK	Hsp70-type molecular chaperone DnaK	-
HBSAL_02885	OE_1738R	100d	m10	VNG_0492H	-	alpha/beta hydrolase fold protein	-
HBSAL_02890	OE_1742R	100d	m10	VNG_0494G	grpE	DnaJ/DnaK ATPase stimulator GrpE	-
HBSAL_02895	OE_1743R	100d	m10	VNG_0496H	-	uncharacterized protein	-
HBSAL_02900	OE_1745R	100d	m10	VNG_0498C	-	uncharacterized protein	-
HBSAL_02905	OE_1748R	100d	m10	VNG_0499G	cna	tRNA/rRNA cytosine-C5-methylase	-
HBSAL_02910	OE_1752F	100d	m10	VNG_0500G	-	PAC2 family protein	-
HBSAL_02915	OE_1753R	100d	m10	VNG_0501G	-	major facilitator superfamily transport protein	-
HBSAL_02920	OE_1755F	100d	m10	VNG_0502G	aspC1	pyridoxal phosphate-dependent aminotransferase	-
HBSAL_02925	OE_1756F	100d	m10	VNG_0503C	-	probable S-adenosylmethionine-dependent methyltransferase	-
HBSAL_02930	OE_1757R	100d	m10	VNG_0504G	-	GTP-binding protein	-
HBSAL_02935	OE_1759F	100d	m10	VNG_0505C	-	DUF21/CBS domain protein	-
HBSAL_02940	OE_1760R	100d	m10	VNG_0506H	-	uncharacterized protein	-
HBSAL_02945	OE_1761R	100d	m10	VNG_0507C	-	DUF583 domain protein	-
HBSAL_02950	OE_1763F	100d	m10	VNG_0508H	-	uncharacterized protein	-
HBSAL_02955	OE_1764F	100d	m10	VNG_0509H	-	uncharacterized protein	-
HBSAL_02960	OE_1765R	100d	m10	VNG_0510G	pan2	proteasome-activating nucleotidase	-
HBSAL_02965	OE_1767F	100d	m10	VNG_0511H	-	NP_1176A family transcription regulator	-
HBSAL_02970	OE_1769F	100d	m10	VNG_0512G	mre11	DNA double-strand break repair protein Mre11	-
HBSAL_02975	OE_1770F	100d	m10	VNG_0514C	rad50	DNA double-strand break repair ATPase Rad50	-
HBSAL_02980	OE_1772F	100d	m10	VNG_0516H	-	uncharacterized protein	-
HBSAL_02985	OE_1772A1R	100d	m10	VNG_0516a	-	HTH domain protein	-
HBSAL_02990	OE_1774R	100d	m10	VNG_0518H	-	uncharacterized protein	-
HBSAL_02995	OE_1775R	100d	m10	VNG_0520H	-	uncharacterized protein	-
HBSAL_03000	OE_1777F	100d	m10	VNG_0521G	polB1	DNA-directed DNA polymerase B	-

HBSAL_03005	OE_1778R	100d	m10	VNG_0523G	-	probable oxidoreductase (short-chain dehydrogenase family)	-
HBSAL_03010	OE_1781F	100d	m10	VNG_0524G	sufC	Fe-S cluster assembly ATPase SufC	-
HBSAL_03015	OE_1782F	100d	m10	VNG_0525C	sufB1	SufB domain protein	-
HBSAL_03020	OE_1783F	100d	m10	VNG_0527C	sufB2	SufB domain protein	-
HBSAL_03025	OE_1785F	100d	m10	VNG_0527a	-	ferritin domain protein	-
HBSAL_03030	OE_1787F	100d	m10	VNG_0530G	-	SirR/DtxR family transcription regulator	-
HBSAL_03035	OE_1789R	100d	m10	VNG_0530a	-	small CPxCG-related zinc finger protein	-
HBSAL_03040	OE_1790A1F	100d	m10	VNG_0532a	-	uncharacterized protein	-
HBSAL_03045	OE_1792F	100d	m10	VNG_0533H	-	DUF124 family protein	-
HBSAL_03050	OE_1793F	100d	m10	VNG_0534C	-	HD family hydrolase	-
HBSAL_03055	OE_1794R	100d	m10	VNG_0535C	-	Gdt1 family protein	-
HBSAL_03060	OE_1797R	100d	m10	VNG_0536G	sirR	SirR/DtxR family transcription regulator SirR	-
HBSAL_03065	OE_1799R	100d	m10	VNG_0537C	-	TRAP-type transport system permease protein	-
HBSAL_03070	OE_1804R	100d	m10	VNG_0539C	-	TRAP-type transport system protein small subunit	-
HBSAL_03075	OE_1806R	100d	m10	VNG_0540G	-	TRAP-type transport system periplasmic substrate-binding protein	-
HBSAL_03080	OE_1807R	100d	m10	VNG_0541G	thrC2	threonine synthase	-
HBSAL_03085	OE_1808F	100d	m10	VNG_0542C	-	amine oxidase domain protein	-
HBSAL_03090	OE_1812R	100d	m10	VNG_0543H	-	probable phosphoesterase	-
HBSAL_03095	OE_1814R	100d	m10	VNG_0544a	-	DnaJ N-terminal domain protein	-
HBSAL_03100	OE_1816R	100d	m10	VNG_0546C	-	PAC2 family protein	-
HBSAL_03105	OE_1817R	100d	m10	VNG_0548C	nop10	tRNA/rRNA pseudouridine synthase complex protein Nop10	-
HBSAL_03110	OE_1818R	100d	m10	VNG_0549G	tif2a	translation initiation factor aIF-2 alpha subunit	-
HBSAL_03115	OE_1820R	100d	m10	VNG_0550G	rps27e	30S ribosomal protein S27e	-
HBSAL_03120	OE_1821R	100d	m10	VNG_0551G	rpl42e	50S ribosomal protein L42e	-
HBSAL_03125	OE_1823F	100d	m10	VNG_0553C	-	uncharacterized protein	seqdiff(R1/NRC-1)
HBSAL_03130	OE_1827F	100d	m10	VNG_0553a	-	uncharacterized protein	-
HBSAL_03135	OE_1829R	100d	m10	VNG_0555C	-	DUF2298 family protein	-

HBSAL_03140	OE_1835F	100d	m10	VNG_0556G	-	probable RfbX family transport protein	-
HBSAL_03145	OE_1838R	100d	m10	VNG_0557H	-	ThiJ/PfpI domain protein	-
HBSAL_03150	OE_1840R	100d	m10	VNG_0559G	apt1	purine phosphoribosyltransferase (adenine phosphoribosyltransferase, xanthine-guanine phosphoribosyltransferase)	-
HBSAL_03155	OE_1841R	100d	m10	VNG_0560C	mrpD2	Mrp-type sodium/proton antiporter system subunit D2	-
HBSAL_03160	OE_1842R	100d	m10	VNG_0562C	mrpD1	Mrp-type sodium/proton antiporter system subunit D1	-
HBSAL_03165	OE_1844R	100d	m10	VNG_0563G	mrpD3	Mrp-type sodium/proton antiporter system subunit D3	-
HBSAL_03170	OE_1847R	100d	m10	VNG_0565C	mrpC	Mrp-type sodium/proton antiporter system subunit C	-
HBSAL_03175	OE_1848R	100d	m10	VNG_0564H	mrpB2	Mrp-type sodium/proton antiporter system subunit B2	-
HBSAL_03180	OE_1849R	100d	m10	VNG_0566C	mrpB1	Mrp-type sodium/proton antiporter system subunit B1	-
HBSAL_03185	OE_1852R	100d	m10	VNG_0570H	mrpG	Mrp-type sodium/proton antiporter system subunit G	-
HBSAL_03190	OE_1853R	100d	m10	VNG_0568C	mrpF	Mrp-type sodium/proton antiporter system subunit F	-
HBSAL_03195	OE_1854R	100d	m10	VNG_0571C	mrpE	Mrp-type sodium/proton antiporter system subunit E	-
HBSAL_03200	OE_1856R	100d	m10	VNG_0572G	coaBC	phosphopantothencysteine decarboxylase / phosphopantothenate--cysteine ligase	-
HBSAL_03205	OE_1858F	100d	m10	VNG_0572a	-	START domain protein	-
HBSAL_03210	OE_1859R	100d	m10	VNG_0573C	hcpF	halocyanin HcpF	-
HBSAL_03215	OE_1860F	100d	m10	VNG_0574C	-	MTH865 family protein	-
HBSAL_03220	OE_1862F	100d	m10	VNG_0575G	ywaD1	probable M28 family peptidase (homolog to aminopeptidase YwaD)	-
HBSAL_03225	OE_1865F	100d	m10	VNG_0576C	nadK2	probable NAD kinase (polyphosphate/ATP)	-
HBSAL_03230	OE_1866F	100d	m10	VNG_0578H	-	uncharacterized protein	-
HBSAL_03235	OE_1867R	100d	m10	VNG_0579H	-	uncharacterized protein	-



HBSAL_03240	OE_1870R	100d	m10	VNG_0581H	-	uncharacterized protein	-
HBSAL_03245	OE_1872R	100d	m10	VNG_0582C	petD	cytochrome bc1 complex cytochrome b/c subunit	-
HBSAL_03250	OE_1874R	100d	m10	VNG_0583G	petB	cytochrome bc1 complex cytochrome b subunit	-
HBSAL_03255	OE_1876R	100d	m10	VNG_0584H	petA	cytochrome bc1 complex Rieske iron-sulfur protein	-
HBSAL_03260	OE_1878R	100d	m10	VNG_0585H	-	uncharacterized protein	-
HBSAL_03265	OE_1879R	100d	m10	VNG_0586C	hcpE	halocyanin HcpE	-
HBSAL_03270	OE_1882R	100d	m10	VNG_0587H	-	uncharacterized protein	-
HBSAL_03275	OE_1887F	100d	m10	VNG_0590H	-	uncharacterized protein	-
HBSAL_03280	OE_1888R	100d	m10	VNG_0591C	-	ArsR family transcription regulator	-
HBSAL_03285	OE_1890R	100d	m10	VNG_0592G	nthA	endonuclease 3	-
HBSAL_03290	OE_1893F	100d	m10	VNG_0593G	mvaD	phosphomevalonate decarboxylase	-
HBSAL_03295	OE_1896R	100d	m10	VNG_0593a	-	uncharacterized protein	-
HBSAL_03300	OE_1898A1F	100d	m10	VNG_0594H	-	uncharacterized protein	-
HBSAL_03305	OE_1899R	100d	m10	VNG_0595H	-	glyoxalase domain protein	-
HBSAL_03310	OE_1900F	100d	m10	VNG_0596H	-	DUF2797 family protein	-
HBSAL_03315	OE_1903F	100d	m10	VNG_0597H	-	glycine-rich protein	-
HBSAL_03320	OE_1905R	100d	m10	VNG_0598C	gth1	probable glycosyltransferase, type 1	-
HBSAL_03325	OE_1906R	100d	m10	VNG_0600C	gth2	probable glycosyltransferase, type 1	-
HBSAL_03330	OE_1907F	100d	m10	VNG_0599C	rnp4	ribonuclease P protein component 4	-
HBSAL_03335	OE_1909F	100d	m10	VNG_0601H	-	CRM domain protein	-
HBSAL_03340	OE_1911R	99	m10	VNG_0602C	-	UspA domain protein	-
HBSAL_03345	OE_1914A1F	100d	m10	VNG_0602a	-	homolog to tryptophan--tRNA ligase	pseudo(91-R6;R1;NRC-1)
HBSAL_03350	OE_1915F	100d	m10	VNG_0604H	-	uncharacterized protein	-
HBSAL_03355	OE_1916F	100d	m10	VNG_0606G	cysK1	cysteine synthase	seqdiff(R1/NRC-1)
HBSAL_03360	OE_1918R	100d	m10	VNG_0608C	-	YneT family protein	-
HBSAL_03365	OE_1919R	100d	m10	VNG_0609C	-	uncharacterized protein	-
HBSAL_03370	OE_1921R	100d	m10	VNG_0610G	ubiA2	(S)-2,3-di-O-geranylgeranylglycerol phosphate synthase	-
HBSAL_03375	OE_1923A1F	100d	m10	VNG_0610a	-	uncharacterized protein	pseudo(91-R6;R1;NRC-1)
HBSAL_03380	OE_1924F	100d	m10	VNG_0611H	-	uncharacterized protein	-

HBSAL_03385	OE_1925F	100d	m10	VNG_0611a	-	uncharacterized protein	-
HBSAL_03390	OE_1926R	100d	m10	VNG_0612H	-	uncharacterized protein	-
HBSAL_03395	OE_1928A1F	100d	m10	VNG_0613a	-	uncharacterized protein	-
HBSAL_03400	OE_1929R	100d	m10	VNG_0614G	htr16	transducer protein Htr16	-
HBSAL_03405	OE_1931R	100d	m10	VNG_0615C	pchA2	ion channel pore / TrkA domain protein	-
HBSAL_03410	OE_1932R	100d	m10	VNG_0617H	-	GATase domain protein	-
HBSAL_03415	OE_1934R	100d	m10	VNG_0620G	sppA	signal peptide peptidase SppA	-
HBSAL_03420	OE_1936R	100d	m10	VNG_0622H	-	flavin-containing amine-oxidoreductase	-
HBSAL_03425	OE_1939F	100d	m10	VNG_0623G	pccB1	propionyl-CoA carboxylase carboxyltransferase component	-
HBSAL_03430	OE_1940R	100d	m10	VNG_0624H	-	DoxX domain protein	-
HBSAL_03435	OE_1941R	100d	m10	VNG_0626G	maoC2	MaoC domain protein	-
HBSAL_03440	OE_1942F	100d	m10	VNG_0627G	citE	homolog to citrate lyase beta subunit	-
HBSAL_03445	OE_1943F	100d	m10	VNG_0628G	gdhA1	glutamate dehydrogenase (NADP)	-
HBSAL_03450	OE_1944R	100d	m10	VNG_0629G	aspC2	pyridoxal phosphate-dependent aminotransferase	-
HBSAL_03455	OE_1946R	100d	m10	VNG_0630G	ribH	6,7-dimethyl-8-ribityllumazine synthase	-
HBSAL_03460	OE_1947F	100d	m10	VNG_0631C	-	TIGR03663 family protein	-
HBSAL_03465	OE_1951F	100d	m10	VNG_0632G	purK	5-(carboxyamino)imidazole ribonucleotide synthase	-
HBSAL_03470	OE_1952F	100d	m10	VNG_0633G	purE	N5-carboxyaminoimidazole ribonucleotide mutase	-
HBSAL_03475	OE_1953F	100d	m10	VNG_0635G	nuoA	NADH dehydrogenase-like complex subunit A	-
HBSAL_03480	OE_1954F	100d	m10	VNG_0636G	nuoB	NADH dehydrogenase-like complex subunit B	-
HBSAL_03485	OE_1956F	100d	m10	VNG_0637G	nuoCD	NADH dehydrogenase-like complex subunit CD	-
HBSAL_03490	OE_1957F	100d	m10	VNG_0639G	nuoH	NADH dehydrogenase-like complex subunit H	-
HBSAL_03495	OE_1958F	100d	m10	VNG_0640G	nuoI	NADH dehydrogenase-like complex subunit I	-
HBSAL_03500	OE_1959F	100d	m10	VNG_0641C	nuoJ1	NADH dehydrogenase-like complex subunit J1	-
HBSAL_03505	OE_1960F	100d	m10	VNG_0642C	nuoJ2	NADH dehydrogenase-like complex subunit J2	-
HBSAL_03510	OE_1963F	100d	m10	VNG_0643G	nuoK	NADH dehydrogenase-like complex subunit K	-
HBSAL_03515	OE_1964F	100d	m10	VNG_0646G	nuoL	NADH dehydrogenase-like complex subunit L	-
HBSAL_03520	OE_1965F	100d	m10	VNG_0647G	nuoM	NADH dehydrogenase-like complex subunit M	-

HBSAL_03525	OE_1967F	100d	m10	VNG_0648G	nuoN	NADH dehydrogenase-like complex subunit N	-
HBSAL_03530	OE_1968F	100d	m10	VNG_0650C	-	DHH/RecJ family phosphoesterase	-
HBSAL_03535	OE_1969F	100d	m10	VNG_0651G	-	CBS/parB domain protein	-
HBSAL_03540	OE_1971F	100d	m10	VNG_0652H	-	ABC-type transport system permease protein	pseudo(91-R6;R1;NRC-1)
HBSAL_03545	OE_1972F	100d	m10	VNG_0653G	mmcA1	methylmalonyl-CoA mutase subunit A	-
HBSAL_03550	OE_1974R	100d	m10	VNG_0654C	-	GNAT family acetyltransferase	-
HBSAL_03555	OE_1978R	100d	m10	VNG_0656H	-	uncharacterized protein	-
HBSAL_03560	OE_1978A1F	100d	m10	VNG_0656a	-	uncharacterized protein	-
HBSAL_03565	OE_1979R	100d	m10	VNG_0657G	coxA1	cox-type terminal oxidase subunit I	-
HBSAL_03570	OE_1981R	100d	m10	VNG_0659H	-	uncharacterized protein	-
HBSAL_03575	OE_1982R	100d	m10	VNG_0660H	-	uncharacterized protein	-
HBSAL_03580	OE_1984F	100d	m10	VNG_0662G	coxC1	cox-type terminal oxidase subunit III	-
HBSAL_03585	OE_1987F	100d	m10	VNG_0664G	birA2	biotin--[acetyl-CoA-carboxylase] ligase	-
HBSAL_03590	OE_1988R	100d	m10	VNG_0665G	coxB1	cox-type terminal oxidase subunit II	-
HBSAL_03595	OE_1989F	100d	m10	VNG_0666G	ctaB	heme o synthase	-
HBSAL_03600	OE_1992F	100d	m10	VNG_0667G	-	uncharacterized protein	-
HBSAL_03605	OE_1994F	100d	m10	VNG_0668C	-	ABC-type transport system ATP-binding protein	-
HBSAL_03610	OE_1997F	100d	m10	VNG_0669H	-	ABC-type transport system permease protein	-
HBSAL_03615	OE_2000R	100d	m10	VNG_0670H	-	uncharacterized protein	-
HBSAL_03620	OE_2003R	100d	m10	VNG_0671H	-	DUF420 family protein	-
HBSAL_03625	OE_2005F	100d	m10	VNG_0673G	mmcB	methylmalonyl-CoA mutase subunit B (cobalamin-binding subunit)	-
HBSAL_03630	OE_2006F	100d	m10	VNG_0674C	ygfD	YgfD family GTPase	-
HBSAL_03635	OE_2007F	100d	m10	VNG_0675C	-	alpha/beta hydrolase fold protein	-
HBSAL_03640	OE_2010R	100d	m10	VNG_0676C	-	DUF35 family protein	-
HBSAL_03645	OE_2011R	100d	m10	VNG_0678G	acaB1	acetyl-CoA C-acetyltransferase	-
HBSAL_03650	OE_2012R	100d	m10	VNG_0677H	-	uncharacterized protein	-
HBSAL_03655	OE_2013R	100d	m10	VNG_0679G	acd4	acyl-CoA dehydrogenase	-
HBSAL_03660	OE_2014F	100d	m10	VNG_0680G	fdtT	squalene synthase	-
HBSAL_03665	OE_2015R	100d	m10	VNG_0681G	hbd1	3-hydroxyacyl-CoA dehydrogenase	-

HBSAL_03670	OE_2016F	100d	m10	VNG_0682C	-	uncharacterized protein	-
HBSAL_03675	OE_2019F	100d	m10	VNG_0683C	fba1	fructose-bisphosphate aldolase, class 1	-
HBSAL_03680	OE_2020F	100d	m10	VNG_0684G	fbp	fructose-1,6-bisphosphatase	-
HBSAL_03685	OE_2021F	100d	m10	VNG_0686C	-	UPF0361 family protein	-
HBSAL_03690	OE_2024F	100d	m10	VNG_0688H	-	HTH domain protein	-
HBSAL_03695	OE_2026F	100d	m10	VNG_0689G	-	ABC-type transport system ATP-binding protein	-
HBSAL_03700	OE_2027F	99	m10	VNG_0690C	-	ABC-type transport system permease protein	-
HBSAL_03705	OE_2032F	99	m10	VNG_0692C	-	ABC-type transport system permease protein	-
HBSAL_03710	OE_2037F	100p	m10	VNG_0694G	-	DUF123 domain protein	-
HBSAL_03715	[OE_2038R]	99	m10/ m11	[VNG_0697H ;VNG_0697a]	-	uncharacterized protein	pseudo(R1;split); pseudo(NRC-1;split); traverse_junction
HBSAL_03720	OE_2041R	100p	m11	VNG_0698H	-	uncharacterized protein	-
HBSAL_03725	OE_2042F	99	m11	VNG_0700G	copA	P-type transport ATPase (probable substrate copper/metal cation)	-
HBSAL_03730	OE_2044F	100p	m11	VNG_0702H	-	HMA domain protein	-
HBSAL_03735	OE_2046F	100p	m11	VNG_0703H	-	NP_1176A family transcription regulator	-
HBSAL_03740	OE_2047R	100p	m11	VNG_0704C	-	HxlR family transcription regulator	-
HBSAL_03745	OE_2049R	99	m11	VNG_0705C	phr3	homolog to cryptochrome/photo-lyase	-
HBSAL_03750	OE_2052F	99	m11	VNG_0707C	-	uracil-DNA glycosylase superfamily protein	-
HBSAL_03755	OE_2053F	100p	m11	VNG_0708H	-	uncharacterized protein	-
HBSAL_03760	OE_2054F	99	m11	VNG_0709C	-	beta-lactamase domain protein	-
HBSAL_03765	OE_2055F	97	m11	VNG_0711C	-	redoxin domain protein	-
HBSAL_03770	OE_2056F	98	m11	VNG_0713C	-	probable methyltransferase	-
HBSAL_03775	OE_2057F	100p	m11	VNG_0715G	thiC	phosphomethylpyrimidine synthase	-
HBSAL_03780	OE_2058R	98	m11	VNG_0716G	-	sensor box histidine kinase	-
HBSAL_03785	OE_2059F	100d	m11	VNG_0717H	-	uncharacterized protein	-
HBSAL_03790	OE_2060R	99	m11	VNG_0718C	-	phosphoglycolate phosphatase	-
HBSAL_03795	OE_2062F	99	m11	VNG_0719G	-	HAD superfamily hydrolase	-
HBSAL_03800	OE_2063R	99	m11	VNG_0720G	-	MATE efflux family protein	-

HBSAL_03805	OE_2065R	99	m11	VNG_0723G	pepQ	probable Xaa-Pro dipeptidase	-
HBSAL_03810	OE_2066F	98	m11	VNG_0724H	-	uncharacterized protein	-
HBSAL_03815	OE_2067F	99	m11	VNG_0725H	-	HTH domain protein	-
HBSAL_03820	OE_2071R	100p	m11	VNG_0726C	-	TetR family transcription regulator	-
HBSAL_03825	OE_2076F	100p	m11	VNG_0727C	-	MATE efflux family protein	-
HBSAL_03830	OE_2077F	99	m11	VNG_0729H	-	uncharacterized protein	-
HBSAL_03835	OE_2078R	99	m11	VNG_0730C	panE	2-dehydropantoate 2-reductase	-
HBSAL_03840	OE_2080F	98	m11	VNG_0731H	-	DUF422 family protein	-
HBSAL_03845	OE_2081R	100p	m11	VNG_0732G	rtcA	RNA 3'-terminal phosphate cyclase	-
HBSAL_03850	OE_2082F	99	m11	VNG_0733H	-	DUF1684 family protein	-
HBSAL_03855	OE_2084R	100p	m11	VNG_0734G	tfbA3	transcription initiation factor TFB	-
HBSAL_03860	OE_2086F	99	m11	VNG_0735G	-	receiver box response regulator	-
HBSAL_03865	OE_2088F	100p	m11	VNG_0736G	-	sensor box histidine kinase	-
HBSAL_03870	OE_2090R	100p	m11	VNG_0738H	-	uncharacterized protein	-
HBSAL_03875	OE_2092F	100d	m11	VNG_0737H	-	uncharacterized protein	-
HBSAL_03880	OE_2093R	99	m11	VNG_0740C	-	cyclase family protein	-
HBSAL_03885	OE_2094F	99	m11	VNG_0741H	-	uncharacterized protein	-
HBSAL_03890	OE_2095R	99	m11	VNG_0742H	-	DICT domain protein	-
HBSAL_03895	OE_2097F	100d	m11	VNG_0743H	-	UspA domain protein	-
HBSAL_03900	OE_2100R	99	m11	VNG_0745G	-	SpoVR family protein	-
HBSAL_03905	OE_2102R	99	m11	VNG_0746C	-	UPF0229 family protein	-
HBSAL_03910	OE_2103R	100p	m11	VNG_0748G	prkA2	probable PrkA-type serine/threonine protein kinase	-
HBSAL_03915	OE_2104R	100p	m11	VNG_0749G	prkA1	probable PrkA-type serine/threonine protein kinase	-
HBSAL_03920	OE_2105F	99	m11	VNG_0750C	-	GAF domain protein	-
HBSAL_03925	OE_2108F	100d	m11	VNG_0751C	-	PadR family transcription regulator	-
HBSAL_03930	OE_2110R	99	m11	VNG_0752G	-	GalE family epimerase/dehydratase	-
HBSAL_03935	OE_2113R	100p	m11	VNG_0753G	-	transport protein (probable substrate phosphate/sulfate)	-
HBSAL_03940	OE_2116R	100d	m11	VNG_0754C	-	glutamate/valine-rich protein	-
HBSAL_03945	OE_2117F	98	m11	VNG_0755C	trm56	tRNA (cytidine(56)-2'-O)-methyltransferase	-

HBSAL_03950	OE_2118F	100p	m11	VNG_0757G	tfeA	transcription initiation factor TFE alpha subunit	-
HBSAL_03955	OE_2120F	99	m11	VNG_0758C	-	DUF2110 family protein	-
HBSAL_03960	OE_2121F	100p	m11	VNG_0759H	-	uncharacterized protein	-
HBSAL_03965	OE_2122F	99	m11	VNG_0761G	-	ADP-ribose pyrophosphatase	-
HBSAL_03970	OE_2123R	100d	m11	VNG_0762H	-	uncharacterized protein	-
HBSAL_03975	OE_2124F	100p	m11	VNG_0763G	-	probable PAP2-type phosphatase	-
HBSAL_03980	OE_2126F	99	m11	VNG_0764C	-	homolog to NAD kinase	-
HBSAL_03985	OE_2127R	100p	m11	VNG_0765H	-	uncharacterized protein	-
HBSAL_03990	OE_2128F	100p	m11	VNG_0766G	phoU4	PhoU domain protein	-
HBSAL_03995	OE_2130F	100p	m11	VNG_0767H	-	uncharacterized protein	-
HBSAL_04000	OE_2131F	100d	m11	VNG_0768H	-	HTH domain protein	-
HBSAL_04005	OE_2132F	99	m11	VNG_0769H	-	START domain protein	-
HBSAL_04010	OE_2133R	100p	m11	VNG_0771G	aldH2	aldehyde dehydrogenase	-
HBSAL_04015	OE_2136R	100d	m11	VNG_0771a	-	RIO-type protein kinase domain protein	-
HBSAL_04020	OE_2138F	99	m11	VNG_0775G	acd2	acyl-CoA dehydrogenase	-
HBSAL_04025	OE_2139R	99	m11	VNG_0777G	ribL	FAD synthase	-
HBSAL_04030	OE_2140R	100p	m11	VNG_0778C	-	JAB domain protein	-
HBSAL_04035	OE_2141F	100p	m11	VNG_0779C	han	Hef-associated 3' exonuclease Han	seqdiff(R1/NRC-1)
HBSAL_04040	OE_2142R	99	m11	VNG_0779a	-	phospholipase D domain protein	-
HBSAL_04045	OE_2149R	99	m11	VNG_0782H	-	HEAT-PBS family protein	-
HBSAL_04050	OE_2155R	99	m11	VNG_0784G	assA	probable archaetidylserine synthase	-
HBSAL_04055	OE_2157F	98	m11	VNG_0786G	hcpH	halocyanin HcpH	-
HBSAL_04060	OE_2159R	99	m11	VNG_0787G	rps1e	30S ribosomal protein S1e	-
HBSAL_04065	OE_2160R	100d	m11	VNG_0788H	-	uncharacterized protein	-
HBSAL_04070	OE_2161R	100p	m11	VNG_0789C	recJ2	probable replication complex protein RecJ2	-
HBSAL_04075	OE_2165R	100p	m11	VNG_0790G	rps15	30S ribosomal protein S15	-
HBSAL_04080	OE_2168R	99	m11	VNG_0793G	htrVI	transducer protein HtrVI	-
HBSAL_04085	OE_2170R	99	m11	VNG_0794G	-	chemotactic signal transduction system periplasmic substrate-binding protein	-
HBSAL_04090	OE_2171F	100p	m11	VNG_0795G	hcpC	halocyanin HcpC	-

HBSAL_04095	OE_2173F	100p	m11	VNG_0796G	metB2	cystathionine synthase/lyase (cystathionine gamma-synthase, cystathionine gamma-lyase, cystathionine beta-lyase)	-
HBSAL_04100	OE_2175F	98	m11	VNG_0798H	-	uncharacterized protein	-
HBSAL_04105	OE_2179F	99	m11	VNG_0799C	-	ABC-type transport system ATP-binding protein	-
HBSAL_04110	OE_2182F	99	m11	VNG_0800H	-	ABC-type transport system permease protein	-
HBSAL_04115	OE_2186R	96	m11	VNG_0801C	tatA	Sec-independent protein translocase protein TatA	-
HBSAL_04120	OE_2187F	99	m11	VNG_0804C	-	HD family hydrolase	-
HBSAL_04125	OE_2189R	99	m11	VNG_0806G	htr4	transducer protein Htr4	-
HBSAL_04130	OE_2190R	99	m11	VNG_0808G	gabD	succinate-semialdehyde dehydrogenase	-
HBSAL_04135	OE_2191F	100p	m11	VNG_0810H	-	uncharacterized protein	-
HBSAL_04140	OE_2194R	100p	m11	VNG_0811H	-	uncharacterized protein	-
HBSAL_04145	OE_2195F	99	m11	VNG_0812G	htr18	transducer protein Htr18	-
HBSAL_04150	OE_2196F	100p	m11	VNG_0813G	-	chemotactic signal transduction system periplasmic substrate-binding protein	-
HBSAL_04155	OE_2197R	99	m11	VNG_0814C	-	homolog to NAD-dependent epimerase/dehydratase	-
HBSAL_04160	OE_2199F	100p	m11	VNG_0815G	qor2	NADPH:quinone reductase	-
HBSAL_04165	OE_2201F	99	m11	VNG_0816G	chiA1	chitinase	-
HBSAL_04170	OE_2205F	99	m11	VNG_0818C	chiA2	chitinase	-
HBSAL_04175	OE_2206F	98	m11	VNG_0819C	chiA3	chitin-binding domain protein	-
HBSAL_04180	OE_2210R	99	m11	VNG_0821C	trm9	tRNA (carboxymethyluridine(34)-5-O)-methyltransferase	-
HBSAL_04185	OE_2212R	99	m11	VNG_0822C	pilC1	type IV pilus biogenesis complex membrane subunit	-
HBSAL_04190	OE_2215R	100p	m11	VNG_0823G	pilB1	type IV pilus biogenesis complex ATPase subunit	-
HBSAL_04195	OE_2217R	98	m11	VNG_0824G	mobA	molybdenum cofactor guanylyltransferase	-
HBSAL_04200	OE_2219R	98	m11	VNG_0825C	mobB	molybdopterin-guanine dinucleotide biosynthesis adapter protein MobB	-
HBSAL_04205	OE_2220F	98	m11	VNG_0826C	dmsR	HTH-10 family transcription regulator DmsR	-
HBSAL_04210	OE_2222F	100d	m11	VNG_0828H	-	uncharacterized protein	-
HBSAL_05140	OE_2225F	86	m12	VNG_0830G	dmsB	dimethylsulfoxide reductase subunit B	LowSim

HBSAL_05145	OE_2227F	99	m12	VNG_0831G	dmsC	dimethylsulfoxide reductase subunit C	-
HBSAL_05150	OE_2229F	98	m12	VNG_0832C	dmsD	Tat proofreading chaperone DmsD	-
HBSAL_05155	OE_2230F	99	m12	VNG_0834C	-	DUF106 family protein	-
HBSAL_05160	OE_2231R	100p	m12	VNG_0835G	idr2	SirR/DtxR family transcription regulator Idr2	-
HBSAL_05165	OE_2232F	94	m12	VNG_0835a	-	probable halocin (homolog to halocin C8)	LowSim
HBSAL_05170	OE_2233F	97	m12	VNG_0835b	-	uncharacterized protein	-
HBSAL_05175	OE_2234F	92	m12	VNG_0836H	-	uncharacterized protein	LowSim; pseudo(91-R6)
HBSAL_05180	OE_2237F	100d	m12	VNG_0837H	-	uncharacterized protein	-
HBSAL_05185	OE_2239F	100d	m12	VNG_0838G	-	XerC/D-like integrase	-
HBSAL_05190	OE_2241R	100d	m12	VNG_0840H	-	HD family hydrolase	pseudo(91-R6;R1;NRC-1)
HBSAL_05195	OE_2243R	100d	m12	VNG_0841G	cynT	carbonic anhydrase	-
HBSAL_05200	OE_2244R	100d	m12	VNG_0845C	-	probable S-adenosylmethionine-dependent methyltransferase	-
HBSAL_05205	OE_2245F	100d	m12	VNG_0846C	-	VKGC domain protein	-
HBSAL_05210	OE_2247R	100d	m12	VNG_0847H	-	uncharacterized protein	-
HBSAL_05215	OE_2249R	100d	m12	VNG_0849C	-	probable coiled coil protein	-
HBSAL_05220	OE_2252R	100d	m12	VNG_0851C	-	metal-dependent hydrolase domain protein	-
HBSAL_05225	OE_2253F	100d	m12	VNG_0852C	-	HTH-10 family transcription regulator	-
HBSAL_05230	OE_2254R	100d	m12	VNG_0853C	-	DUF964 family protein	-
HBSAL_05235	OE_2257F	100d	m12	VNG_0854C	dph2	2-(3-amino-3-carboxypropyl)histidine synthase	-
HBSAL_05240	OE_2259F	100d	m12	VNG_0857C	-	probable rRNA methyltransferase	-
HBSAL_05245	OE_2260R	100d	m12	VNG_0858C	-	probable rhomboid family protease	-
HBSAL_05250	OE_2267F	100d	m12	VNG_0860G	rpoL	DNA-directed RNA polymerase subunit L	-
HBSAL_05255	OE_2268R	100d	m12	VNG_0862G	hisF	imidazole glycerol-phosphate synthase subunit HisF	-
HBSAL_05260	OE_2269F	100d	m12	VNG_0861H	-	UspA domain protein	-
HBSAL_05265	OE_2273F	100d	m12	VNG_0863H	-	uncharacterized protein	-
HBSAL_05270	OE_2274R	99	m12	VNG_0864G	purL	phosphoribosylformylglycinamide synthase subunit PurL	-
HBSAL_05275	OE_2276F	100d	m12	VNG_0865C	-	PHP domain protein	-



HBSAL_05280	OE_2278F	100d	m12	VNG_0867G	asnB	asparagine synthase (glutamine-hydrolyzing)	-
HBSAL_05285	OE_2280R	100d	m12	VNG_0868H	-	NUDIX family hydrolase	-
HBSAL_05290	OE_2281R	100d	m12	VNG_0869G	tfbA6	transcription initiation factor TFB	-
HBSAL_05295	OE_2283F	100d	m12	VNG_0870G	gatC	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C	-
HBSAL_05300	OE_2284F	100d	m12	VNG_0872G	gatA	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit A	-
HBSAL_05305	OE_2285R	100d	m12	VNG_0873G	-	thioesterase domain protein	-
HBSAL_05310	OE_2288F	100d	m12	VNG_0874G	traB	TraB family protein	-
HBSAL_05315	OE_2289F	100d	m12	VNG_0875C	-	M50 family metalloprotease	-
HBSAL_05320	OE_2292F	100d	m12	VNG_0876G	purM	phosphoribosylformylglycinamide cyclo-ligase	-
HBSAL_05325	OE_2293R	100d	m12	VNG_0878G	-	HTH/CBS domain protein	-
HBSAL_05330	OE_2294R	100d	m12	VNG_0879C	-	UPF0212 family protein	-
HBSAL_05335	OE_2296F	100d	m12	VNG_0880G	psmB	proteasome beta subunit	-
HBSAL_05340	OE_2298F	100d	m12	VNG_0881G	ligB	DNA ligase (ATP)	-
HBSAL_05345	OE_2299F	100p	m12	VNG_0882G	-	HAD superfamily hydrolase	-
HBSAL_05350	OE_2300F	99	m12	VNG_0883H	-	metal-dependent hydrolase domain protein	-
HBSAL_05355	OE_2301R	99	m12	VNG_0884G	top6A	DNA topoisomerase 6 subunit A	-
HBSAL_05360	OE_2302R	99	m12	VNG_0885G	top6B	DNA topoisomerase 6 subunit B	-
HBSAL_05365	OE_2303F	99	m12	VNG_0887G	gyrB	DNA gyrase subunit B	seqdiff(R1/NRC-1)
HBSAL_05370	OE_2304F	99	m12	VNG_0889G	gyrA	DNA gyrase subunit A	-
HBSAL_05375	OE_2306F	100d	m12	VNG_0890G	-	DUF293 domain protein	-
HBSAL_05380	OE_2307F	99	m12	VNG_0891G	ndh	probable NADH dehydrogenase	-
HBSAL_05385	OE_2309F	98	m12	VNG_0892H	-	uncharacterized protein	-
HBSAL_05390	OE_2310F	97	m12	VNG_0892a	-	UPF0157 family protein	-
HBSAL_05395	OE_2311R	100p	m12	VNG_0893G	udp2	uridine phosphorylase	-
HBSAL_05400	OE_2313R	100d	m12	VNG_0896G	cdd	cytidine deaminase	-
HBSAL_05405	OE_2314R	99	m12	VNG_0897G	tsgC	ABC-type transport system permease protein (probable substrate sugar)	-
HBSAL_05410	OE_2315R	100p	m12	VNG_0898G	tsgB	ABC-type transport system permease protein (probable substrate sugar)	-

HBSAL_05415	OE_2316R	99	m12	VNG_0901G	tsgD	ABC-type transport system ATP-binding protein (probable substrate sugar)	-
HBSAL_05420	OE_2317R	99	m12	VNG_0903C	tsgA	ABC-type transport system periplasmic substrate-binding protein (probable substrate sugar)	-
HBSAL_05425	OE_2318R	99	m12	VNG_0905G	pmm3	phosphohexomutase (phosphoglucomutase / phosphomannomutase)	-
HBSAL_05430	OE_2319R	100p	m12	VNG_0906H	-	uncharacterized protein	-
HBSAL_05435	OE_2321F	100d	m12	VNG_0907H	-	uncharacterized protein	-
HBSAL_05440	OE_2322F	99	m12	VNG_0908G	-	SSSF family transport protein	-
HBSAL_05445	OE_2324F	97	m12	VNG_0909H	-	uncharacterized protein	-
HBSAL_05450	OE_2325F	98	m12	VNG_0911H	-	uncharacterized protein	-
HBSAL_05455	OE_2328F	99	m12	VNG_0913H	-	uncharacterized protein	-
HBSAL_05460	OE_2330R	98	m12	VNG_0914H	-	uncharacterized protein	-
HBSAL_05465	OE_2332F	97	m12	VNG_0915G	kynU	kynureninase	-
HBSAL_05470	OE_2333R	99	m12	VNG_0916G	-	sensor box histidine kinase	-
[HBSAL_05485 ;HBSAL_05475 ]	OE_2334R	99	m12/ m13	VNG_0917G	-	receiver box response regulator	pseudo(91-R6;split); traverse_junction
HBSAL_05490	OE_2336F	100d	m13	VNG_0919G	gtl6	dolichyl-phosphate hexosyltransferase	-
HBSAL_05495	OE_2338R	99	m13	VNG_0920H	-	uncharacterized protein	-
HBSAL_05500	OE_2343R	99	m13	VNG_0921G	-	ABC-type transport system ATP-binding protein	-
HBSAL_05505	OE_2346R	100p	m13	VNG_0923G	-	ABC-type transport system permease protein	-
HBSAL_05510	OE_2348R	97	m13	VNG_0924G	-	ABC-type transport system periplasmic substrate-binding protein	-
HBSAL_05515	OE_2350R	99	m13	VNG_0925C	-	homolog to arabinopyranose mutase	-
HBSAL_05520	OE_2353R	100p	m13	VNG_0927C	-	uncharacterized protein	-
HBSAL_05525	OE_2354R	99	m13	VNG_0928G	-	ARM/HEAT repeat protein / protein kinase domain protein	-
HBSAL_05530	OE_2357F	99	m13	VNG_0930G	-	monooxygenase (homolog to alkanesulfonate monooxygenase)	-
HBSAL_05535	OE_2358F	100p	m13	VNG_0931G	acaB2	acetyl-CoA C-acetyltransferase catalytic subunit	-
HBSAL_05540	OE_2359F	99	m13	VNG_0932C	-	acetyl-CoA C-acetyltransferase small subunit	-

[HBSAL_05545 ;HBSAL_05570 ]	OE_2360R	99	m13/ m14	VNG_0933G	-	NamA family oxidoreductase	pseudo(91-R6;split); traverse_junction
HBSAL_05575	OE_2363R	100d	m14	VNG_0934H	-	uncharacterized protein	-
HBSAL_05580	OE_2364R	99	m14	VNG_0935G	-	nitroreductase family protein	-
HBSAL_05585	OE_2365R	98	m14	VNG_0936C	-	probable carbon-nitrogen hydrolase	-
HBSAL_05590	OE_2367F	99	m14	VNG_0937G	aldH3	aldehyde dehydrogenase	-
HBSAL_05595	OE_2370R	98	m14	VNG_0938G	gufA	GufA family transport protein (probable substrate zinc)	-
HBSAL_05600	OE_2372F	100p	m14	VNG_0940G	acdA	acetate--CoA ligase (ADP-forming)	-
HBSAL_05605	OE_2373F	99	m14	VNG_0941C	-	DRTGG domain protein	-
HBSAL_05610	OE_2374R	100p	m14	VNG_0942G	cheW2	purine-binding taxis protein CheW	-
HBSAL_05615	OE_2375F	100d	m14	VNG_0943C	-	HTH domain protein	-
HBSAL_05620	OE_2377F	100p	m14	VNG_0945H	-	uncharacterized protein	-
HBSAL_05625	OE_2378R	99	m14	VNG_0946G	-	ParA domain protein	-
HBSAL_05630	OE_2379R	99	m14	VNG_0947G	arlJ	archaellar motor/biogenesis protein ArlJ	-
HBSAL_05635	OE_2380R	99	m14	VNG_0949G	arlI	archaellar motor/biogenesis protein ArlI	-
HBSAL_05640	OE_2381R	100p	m14	VNG_0950G	arlH	arl cluster protein ArlH	-
HBSAL_05645	OE_2383R	99	m14	VNG_0950a	arlG	arl cluster protein ArlG	-
HBSAL_05650	OE_2385R	99	m14	VNG_0953C	arlF	arl cluster protein ArlF	-
HBSAL_05655	OE_2386R	99	m14	VNG_0954C	arlCE	arl cluster protein ArlCE	-
HBSAL_05660	OE_2390R	100d	m14	VNG_0955G	arlD	arl cluster protein ArlD	-
HBSAL_05665	OE_2392R	99	m14	VNG_0958G	htr15	transducer protein Htr15	-
HBSAL_05670	OE_2396R	98	m14	VNG_0959H	-	uncharacterized protein	-
HBSAL_05675	OE_2397F	97	m14	VNG_0960G	arlB1	archaellin B1	-
HBSAL_05680	OE_2398F	97	m14	VNG_0961G	arlB2	archaellin B2	-
HBSAL_05685	OE_2399F	100p	m14	VNG_0962G	arlB3	archaellin B3	-
HBSAL_05690	OE_2401F	100d	m14	VNG_0963G	-	HEAT-PBS family taxis protein	-
HBSAL_05695	OE_2402F	100d	m14	VNG_0964C	cheF1	taxis protein CheF1	-
HBSAL_05700	OE_2404R	100d	m14	VNG_0965C	cheF2	taxis protein CheF2	-

HBSAL_05705	OE_2406R	100p	m14	VNG_0966G	cheR	protein-glutamate O-methyltransferase CheR	-
HBSAL_05710	OE_2408R	99	m14	VNG_0967G	cheD	taxis cluster protein CheD	-
HBSAL_05715	OE_2410R	99	m14	VNG_0969H	cheC3	taxis cluster protein CheC	-
HBSAL_05720	OE_2414R	100d	m14	VNG_0970G	cheC1	taxis cluster protein CheC	-
HBSAL_05725	OE_2415R	99	m14	VNG_0971G	cheA	taxis sensor histidine kinase CheA	-
HBSAL_05730	OE_2416R	99	m14	VNG_0973G	cheB	protein-glutamate methylesterase / protein-glutamine glutaminase CheB	-
HBSAL_05735	OE_2417R	100d	m14	VNG_0974G	cheY	response regulator CheY	-
HBSAL_05740	OE_2419R	100d	m14	VNG_0976G	cheW1	purine-binding taxis protein CheW	-
HBSAL_05745	OE_2421R	99	m14	VNG_0978H	-	uncharacterized protein	-
HBSAL_05750	OE_2423F	99	m14	VNG_0979H	-	uncharacterized protein	-
HBSAL_05755	OE_2425F	100p	m14	VNG_0981C	aat1	pyridoxal phosphate-dependent aminotransferase (homolog to histidinol-phosphate aminotransferase / aspartate aminotransferase)	-
HBSAL_05760	OE_2427F	98	m14	VNG_0982C	-	PRC domain protein	-
HBSAL_05765	OE_2428R	99	m14	VNG_0983C	-	DHH/RecJ family phosphoesterase	-
HBSAL_05770	OE_2440F	92	m15	VNG_0990H	-	uncharacterized protein	LowSim
HBSAL_05775	OE_2443R	97	m16	VNG_0992H	-	uncharacterized protein	-
HBSAL_05780	OE_2443A1R	93	m16	VNG_0992a	-	ISH9-type transposase	LowSim; pseudo(91-R6;R1;NRC-1)
HBSAL_05795	OE_2445R	90	d16/ m17	[VNG_0994a; VNG_0993a]	-	homolog to phage PhiH1 repressor protein	LowSim; pseudo(NRC-1;split); traverse_junction
HBSAL_05800	OE_2446A1F	88	m17	VNG_0994b	bp4	basic protein bp4	LowSim; pseudo(91-R6)
HBSAL_05805	OE_2447F	100p	m17	VNG_0995H	-	small CPxCG-related zinc finger protein	-
HBSAL_05810	OE_2448F	99	m17	VNG_0996G	boa4	integrase family protein / bat box HTH-10 family transcription regulator	-
HBSAL_05815	OE_2450F	99	m17	VNG_0997G	acs2	acyl-CoA synthetase	-
HBSAL_05820	OE_2451R	99	m17	VNG_0998G	-	probable oxidoreductase (aldo-keto reductase family protein)	-
HBSAL_05825	OE_2453R	100p	m17	VNG_0999H	-	uncharacterized protein	-

HBSAL_05830	OE_2455F	100d	m17	VNG_0999a	-	CopG domain protein	-
HBSAL_05835	OE_2456F	99	m17	VNG_1000H	-	DUF2061 family protein	pseudo(91-R6)
HBSAL_05840	OE_2458R	99	m17	VNG_1001G	guaB1	inosine-5'-monophosphate dehydrogenase	-
HBSAL_05845	OE_2460F	99	m17	VNG_1002H	-	uncharacterized protein	-
HBSAL_05850	OE_2464F	100d	m17	VNG_1003H	-	small CPxCG-related zinc finger protein	-
HBSAL_05855	OE_2465R	100d	m17	VNG_1005H	-	uncharacterized protein	-
HBSAL_06295	OE_2548F	97	d17/ m18	VNG_1068G	aglB	dolichyl-monophosphooligosaccharide--protein glycotransferase AglB	traverse_junction
HBSAL_06300	OE_2551F	98	m18	VNG_1069C	-	DUF368 family protein	-
HBSAL_06305	OE_2553R	99	m18	VNG_1070G	glpA2	glycerol-3-phosphate dehydrogenase subunit A	-
HBSAL_06310	OE_2554R	100d	m18	VNG_1071G	tfeB	transcription initiation factor TFE beta subunit	-
HBSAL_06315	OE_2555R	99	m18	VNG_1073G	menE	o-succinylbenzoate--CoA ligase	-
HBSAL_06320	OE_2558R	97	m18	VNG_1074G	menC	o-succinylbenzoate synthase	-
HBSAL_06325	OE_2559R	99	m18	VNG_1075G	menA	1,4-dihydroxy-2-naphthoate polyprenyltransferase	-
HBSAL_06330	OE_2560R	100p	m18	VNG_1077G	opuD	compatible solute transport protein (probable substrate choline/glycine betaine)	-
HBSAL_06335	OE_2561R	100p	m18	VNG_1079G	menB	1,4-dihydroxy-2-naphthoyl-CoA synthase	-
HBSAL_06340	OE_2563R	99	m18	VNG_1081G	menD	2-succinyl-5-enolpyruvyl-6-hydroxy-3- cyclohexene-1-carboxylate synthase	-
HBSAL_06345	OE_2566R	99	m18	VNG_1083G	menF	isochorismate synthase	-
HBSAL_06350	OE_2569R	100p	m18	VNG_1084G	-	YuiH family molybdopterin-binding domain protein	-
HBSAL_06355	OE_2571F	100d	m18	VNG_1085H	-	uncharacterized protein	-
HBSAL_06360	OE_2572F	100d	m18	VNG_1086C	-	UPF0058 family protein	-
HBSAL_06365	OE_2573F	98	m18	VNG_1087C	-	uncharacterized protein	-
HBSAL_06370	OE_2577R	100d	m18	VNG_1088C	-	HTH domain protein	-
HBSAL_06375	OE_2579F	100p	m18	VNG_1089G	purA	adenylosuccinate synthase	-
HBSAL_06380	OE_2580F	100d	m18	VNG_1090H	trm112	methyltransferase activator Trm112	-
HBSAL_06385	OE_2582F	99	m18	VNG_1090a	-	uncharacterized protein	-
HBSAL_06390	OE_2583R	99	m18	VNG_1092C	-	uncharacterized protein	-
HBSAL_06395	OE_2585R	99	m18	VNG_1093C	cbiX2	sirohydrochlorin cobaltochelata	-

HBSAL_06400	OE_2586F	99	m18	VNG_1094H	-	LppX domain protein	-
HBSAL_06405	OE_2590R	100d	m18	VNG_1095H	-	uncharacterized protein	-
HBSAL_06410	OE_2591R	100d	m18	VNG_1096H	-	ArsR family transcription regulator	-
HBSAL_06415	OE_2594F	99	m18	VNG_1097G	cysS	cysteine--tRNA ligase	-
HBSAL_06425	OE_2595F	98	m19	VNG_1099C	-	YcgG family protein	-
HBSAL_06430	OE_2596F	98	m19	VNG_1100C	entB1	isochorismatase family protein	-
HBSAL_06435	OE_2597R	98	m19	VNG_1101C	-	DUF112 family protein	-
HBSAL_06440	OE_2600R	100p	m19	VNG_1103G	rpl12	50S ribosomal protein L12	-
HBSAL_06445	OE_2601R	98	m19	VNG_1104G	rpl10	50S ribosomal protein L10	-
HBSAL_06450	OE_2602R	100d	m19	VNG_1105G	rpl1	50S ribosomal protein L1	-
HBSAL_06455	OE_2603R	100d	m19	VNG_1108G	rpl11	50S ribosomal protein L11	-
HBSAL_06460	OE_2605R	98	m19	VNG_1110C	-	uncharacterized protein	-
HBSAL_06465	OE_2607F	100p	m19	VNG_1111G	drg	GTP-binding protein Drg	-
HBSAL_06470	OE_2608F	99	m19	VNG_1112H	-	TIGR04206 family protein	pseudo(91-R6)
HBSAL_06475	OE_2610F	100p	m19	VNG_1114G	-	glyoxalase domain protein	-
HBSAL_06480	OE_2612F	100p	m19	VNG_1115H	-	UPF0066 family protein	-
HBSAL_06485	OE_2613R	99	m19	VNG_1118G	dph5	diphthine synthase	-
HBSAL_06490	OE_2614F	99	m19	VNG_1117C	trm5	tRNA (guanine(37)-N(1))-methyltransferase	-
HBSAL_06495	OE_2616F	97	m19	VNG_1119H	-	uncharacterized protein	-
HBSAL_06500	OE_2618R	99	m19	VNG_1120H	-	START domain protein	-
HBSAL_06505	OE_2619F	100p	m19	VNG_1121G	aspC3	pyridoxal phosphate-dependent aminotransferase	-
HBSAL_06510	OE_2621R	100d	m19	VNG_1123G	lrpA1	Lrp/AsnC family transcription regulator LrpA1	-
HBSAL_06515	OE_2622R	100p	m19	VNG_1125G	porB	pyruvate--ferredoxin oxidoreductase beta subunit	-
HBSAL_06520	OE_2623R	100d	m19	VNG_1128G	porA	pyruvate--ferredoxin oxidoreductase alpha subunit	-
HBSAL_06525	OE_2625R	100d	m19	VNG_1130H	-	uncharacterized protein	-
HBSAL_06530	OE_2626R	100p	m19	VNG_1131G	apbC	Fe-S cluster carrier protein ApbC	-
HBSAL_06535	OE_2627F	100d	m19	VNG_1132G	rps13	30S ribosomal protein S13	-
HBSAL_06540	OE_2628F	100d	m19	VNG_1133G	rps4	30S ribosomal protein S4	-
HBSAL_06545	OE_2629F	100d	m19	VNG_1134G	rps11	30S ribosomal protein S11	-

HBSAL_06550	OE_2631F	100d	m19	VNG_1136G	rpoD	DNA-directed RNA polymerase subunit D	-
HBSAL_06555	OE_2632F	100d	m19	VNG_1137G	rpl18e	50S ribosomal protein L18e	-
HBSAL_06560	OE_2633F	100d	m19	VNG_1138G	rpl13	50S ribosomal protein L13	-
HBSAL_06565	OE_2635F	100d	m19	VNG_1139G	rps9	30S ribosomal protein S9	-
HBSAL_06570	OE_2637F	100d	m19	VNG_1140G	rpoN	DNA-directed RNA polymerase subunit N	-
HBSAL_06575	OE_2638F	100d	m19	VNG_1141G	rpoK	DNA-directed RNA polymerase subunit K	-
HBSAL_06580	OE_2640F	100d	m19	VNG_1142G	eno	enolase	-
HBSAL_06585	OE_2641F	100p	m19	VNG_1143G	rps2	30S ribosomal protein S2	-
HBSAL_06590	OE_2642R	100d	m19	VNG_1144H	-	glyoxalase domain protein	-
HBSAL_06595	OE_2645F	100p	m19	VNG_1145G	mvk	mevalonate kinase	-
HBSAL_06600	OE_2647F	99	m19	VNG_1148G	-	isopentenyl phosphate kinase	-
HBSAL_06605	OE_2648F	100p	m19	VNG_1149C	rnj	ribonuclease J	-
HBSAL_06610	OE_2650F	100p	m19	VNG_1150G	idsA1	bifunctional short chain isoprenyl diphosphate synthase	-
HBSAL_06615	OE_2651F	97	m19	VNG_1151H	-	uncharacterized protein	-
HBSAL_06620	OE_2652F	99	m19	VNG_1153G	gltS	glutamate--tRNA(Glu/Gln) ligase	-
HBSAL_06625	OE_2653R	100p	m19	VNG_1154H	-	DUF456 family protein	-
HBSAL_06630	OE_2656R	99	m19	VNG_1156G	tmcA	tRNA(Met) cytidine acetyltransferase TmcA	pseudo(91-R6)
HBSAL_06635	OE_2662F	100d	m19	VNG_1157G	rpl8e	50S ribosomal protein L8e	-
HBSAL_06640	OE_2664F	100d	m19	VNG_1158G	rps28e	30S ribosomal protein S28e	-
HBSAL_06645	OE_2665F	100d	m19	VNG_1159G	rpl24e	50S ribosomal protein L24e	-
HBSAL_06650	OE_2667F	100d	m19	VNG_1160G	ndk	nucleoside-diphosphate kinase	-
HBSAL_06655	OE_2668R	99	m19	VNG_1162H	metE	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (methionine synthase II)	-
HBSAL_06660	OE_2671R	100p	m19	VNG_1163G	prmC	release factor glutamine methyltransferase PrmC	-
HBSAL_06665	OE_2672R	99	m19	VNG_1164C	mscS1	mechanosensitive channel protein MscS	-
HBSAL_06670	OE_2674R	99	m19	VNG_1165G	ksgA	ribosome biogenesis protein KsgA, 16S rRNA-methylating	-
HBSAL_06675	OE_2676R	99	m19	VNG_1168C	-	putative tRNA-specific adenosine deaminase	-

HBSAL_06680	OE_2678R	100p	m19	VNG_1169C	rpoF	DNA-directed RNA polymerase subunit F	-
HBSAL_06685	OE_2679R	100d	m19	VNG_1170G	rpl21e	50S ribosomal protein L21e	-
HBSAL_06690	OE_2680B1R	100d	m19	VNG_1170a	-	small CPxCG-related zinc finger protein	-
HBSAL_06695	OE_2681F	99	m19	VNG_1172G	metB1	cystathionine synthase/lyase (cystathionine gamma-synthase, cystathionine gamma-lyase, cystathionine beta-lyase)	-
HBSAL_06700	OE_2683R	100p	m19	VNG_1173G	tef1b	translation elongation factor aEF-1 beta	-
HBSAL_06705	OE_2682A1R	100d	m19	VNG_1173a	-	small CPxCG-related zinc finger protein	-
HBSAL_06710	OE_2684R	99	m19	VNG_1175G	-	sensor box histidine kinase	pseudo(91-R6)
HBSAL_06715	OE_2685F	99	m19	VNG_1174G	nop5	rRNA/tRNA 2'-O-methyltransferase complex protein Nop5	-
HBSAL_06720	OE_2689F	99	m19	VNG_1176G	fib	fibrillarin-like rRNA/tRNA 2'-O-methyltransferase	-
HBSAL_06725	OE_2690R	98	m19	VNG_1178H	-	uncharacterized protein	-
HBSAL_06730	OE_2691R	99	m19	VNG_1179C	-	Lrp/AsnC family transcription regulator	-
HBSAL_06735	OE_2693F	99	m19	VNG_1180G	msrA	peptide methionine sulfoxide reductase MsrA (S-form specific)	-
HBSAL_06740	OE_2695F	99	m19	VNG_1181G	arlX	archaellin ArlX	-
HBSAL_06745	OE_2696F	99	m19	VNG_1182H	-	FMN-binding domain protein	-
HBSAL_06750	OE_2697R	100p	m19	VNG_1184G	ahbC	Fe-coproporphyrin synthase AhbC	-
HBSAL_06755	OE_2698R	100d	m19	VNG_1183H	-	TIGR04031 family protein	-
HBSAL_06760	OE_2700F	99	m19	VNG_1185G	ahbD	coproheme decarboxylase AhbD	-
HBSAL_06765	OE_2703F	99	m19	VNG_1187G	-	probable copper-containing oxidoreductase	-
HBSAL_06770	OE_2704F	99	m19	VNG_1188G	hcpD	halocyanin HcpD	-
HBSAL_06775	OE_2706R	98	m19	VNG_1189H	-	uncharacterized protein	-
HBSAL_06780	OE_2708R	99	m19	VNG_1190G	sod1	superoxide dismutase (Mn)	-
HBSAL_06785	OE_2710F	100p	m19	VNG_1191G	acd3	acyl-CoA dehydrogenase	-
HBSAL_06800	OE_2712R	100p	m20	VNG_1193C	-	histidine kinase	-
HBSAL_06805	OE_2715R	100d	m20	VNG_1194H	-	uncharacterized protein	-
HBSAL_06810	OE_2716R	99	m20	VNG_1196H	-	uncharacterized protein	-
HBSAL_06815	OE_2717R	100p	m20	VNG_1197G	-	peroxiredoxin	-



HBSAL_06820	OE_2720R	99	m20	VNG_1198C	-	FAD-dependent oxidoreductase (homolog to geranylgeranyl reductase)	-
HBSAL_06825	OE_2724F	100d	m20	VNG_1200H	-	uncharacterized protein	-
HBSAL_06830	OE_2725R	100p	m20	VNG_1201G	-	class II aldolase (homolog to L-fuculose-phosphate aldolase)	-
HBSAL_06835	OE_2727R	100p	m20	VNG_1202C	-	HAD superfamily hydrolase	-
HBSAL_06840	OE_2728R	100p	m20	VNG_1204G	gdhA2	glutamate dehydrogenase	-
HBSAL_06845	OE_2730R	99	m20	VNG_1205C	-	probable nucleoside deaminase	-
HBSAL_06850	OE_2731R	100d	m20	VNG_1205a	-	uncharacterized protein	-
HBSAL_06855	OE_2732R	99	m20	VNG_1207C	-	HTH-10 family transcription regulator	-
HBSAL_06860	OE_2734F	99	m20	VNG_1208G	hutU	urocanate hydratase	-
HBSAL_06865	OE_2736F	97	m20	VNG_1209G	hutG	formimidoylglutamase	-
HBSAL_06870	OE_2738F	99	m20	VNG_1211G	hutI	imidazolonepropionase	-
HBSAL_06875	OE_2739F	99	m20	VNG_1212G	hutH	histidine ammonia-lyase	-
HBSAL_06880	OE_2740F	100d	m20	VNG_1213C	-	ribonuclease H domain protein	-
HBSAL_06885	OE_2744R	99	m21	VNG_1215G	-	GNAT family acetyltransferase	-
HBSAL_06890	OE_2745R	99	m21	VNG_1216G	pgk	phosphoglycerate kinase	-
HBSAL_06895	OE_2747R	99	m21	VNG_1218C	-	CBS domain protein	-
HBSAL_06900	OE_2749F	99	m21	VNG_1219G	udk	uridine kinase	-
HBSAL_06905	OE_2750R	100p	m21	VNG_1220H	-	uncharacterized protein	-
HBSAL_06910	OE_2753F	100p	m21	VNG_1224G	orc10	Orc1-type DNA replication protein	-
HBSAL_06915	OE_2755R	98	m21	VNG_1227H	-	uncharacterized protein	-
HBSAL_06920	OE_2757F	98	m21	VNG_1226H	-	uncharacterized protein	-
HBSAL_06925	OE_2758R	99	m21	VNG_1228C	-	uracil-DNA glycosylase superfamily protein	-
HBSAL_06930	OE_2760F	100p	m21	VNG_1229H	-	uncharacterized protein	-
HBSAL_06935	OE_2761R	99	m21	VNG_1230G	aroC	chorismate synthase	-
HBSAL_06940	OE_2761D1F	76	m21/ d22/ m22/ d23	VNG_1230a	guaB2	inosine-5'-monophosphate dehydrogenase	LowSim; pseudo(R1;NRC-1); traverse_junction
HBSAL_06945	OE_2762R	97	m23	VNG_1232G	aroA	3-phosphoshikimate 1-carboxyvinyltransferase	-

HBSAL_06950	OE_2763F	99	m23	VNG_1233G	-	peptidase M24 family protein (homolog to Xaa-Pro dipeptidase)	-
HBSAL_06955	OE_2764R	99	m23	VNG_1234C	-	sensor box histidine kinase	-
HBSAL_06960	OE_2770F	98	m23	VNG_1235C	tyrA	prephenate dehydrogenase	-
HBSAL_06965	OE_2772F	99	m23	VNG_1236C	-	probable S-adenosylmethionine-dependent methyltransferase	-
HBSAL_06970	OE_2776F	100d	m23	VNG_1237C	-	Lrp/AsnC family transcription regulator	-
HBSAL_06975	OE_2780F	99	m23	VNG_1238C	-	TrkA-N domain protein	-
HBSAL_06980	OE_2779F	99	m23	VNG_1240G	cat3	transport protein (probable substrate cationic amino acids)	-
HBSAL_06985	OE_2782F	99	m23	VNG_1241G	surE	5'-nucleotidase SurE	-
HBSAL_06990	OE_2783A1R	100d	m23	VNG_1241a	-	NUDIX family hydrolase	pseudo(91-R6;R1;NRC-1)
HBSAL_06995	OE_2784R	100d	m23	VNG_1244C	aroQ	chorismate mutase	-
HBSAL_07000	OE_2785R	97	m23	VNG_1245C	aroK	shikimate kinase, archaeal-type	-
HBSAL_07005	OE_2786F	100p	m23	VNG_1246H	-	uncharacterized protein	-
HBSAL_07010	OE_2786B1R	100d	m23	VNG_1246a	-	small CPxCG-related zinc finger protein	-
HBSAL_07015	OE_2787R	99	m23	VNG_1247G	-	ABC-type transport system ATP-binding protein	-
HBSAL_07020	OE_2789R	98	m23	VNG_1249C	-	ABC-type transport system permease protein	-
HBSAL_07025	OE_2791R	98	m23	VNG_1250H	-	uncharacterized protein	-
HBSAL_07030	OE_2794R	99	m23	VNG_1251G	lhr	ATP-dependent DNA helicase	-
HBSAL_07035	OE_2798R	98	m23	VNG_1252G	rpe	rpa-associated phosphoesterase	-
HBSAL_07040	OE_2800R	98	m23	VNG_1253C	rpap1	rpa-associated protein	-
HBSAL_07045	OE_2801R	99	m23	VNG_1255C	rpa1	replication protein A	-
HBSAL_07050	OE_2802F	99	m23	VNG_1256G	arfC	2,5-diamino-6-(ribosylamino)-4(3H)-pyrimidinone 5'-phosphate reductase	-
HBSAL_07055	OE_2803R	100p	m23	VNG_1257H	-	uncharacterized protein	-
HBSAL_07060	OE_2805R	99	m23	VNG_1259G	trxB2	thioredoxin-disulfide reductase	-
HBSAL_07065	OE_2806F	100p	m23	VNG_1260C	-	DUF357 family protein	-
HBSAL_07070	OE_2808F	100d	m23	VNG_1261H	-	small CPxCG-related zinc finger protein	-
HBSAL_07075	OE_2809R	100p	m23	VNG_1262G	tif2b	translation initiation factor aIF-2 beta subunit	-
HBSAL_07080	OE_2811F	100p	m23	VNG_1263C	-	UPF0058 family protein	-

HBSAL_07085	OE_2813R	100d	m23	VNG_1264C	-	UPF0212 family protein	-
HBSAL_07090	OE_2814F	100p	m23	VNG_1266G	-	DNA N-glycosylase	-
HBSAL_07095	OE_2816F	98	m23	VNG_1268H	-	uncharacterized protein	-
HBSAL_07100	OE_2816B1R	96	m23	VNG_1268a	-	ISH14-type transposase	pseudo(91-R6;R1;NRC-1)
HBSAL_07105	OE_2818R	95	m23	VNG_1270H	-	uncharacterized protein	-
HBSAL_07110	OE_2818A1F	94	m23	VNG_1270a	-	ISH10-type transposase	LowSim; pseudo(91-R6;R1;NRC-1)
HBSAL_07115	OE_2820F	95	m23	VNG_1271H	-	uncharacterized protein	-
HBSAL_07120	OE_2821F	98	m23	VNG_1272C	nnrDE	bifunctional NAD(P)H-hydrate repair enzyme Nnr	-
HBSAL_07125	OE_2825F	96	m23/ d24	VNG_1273G	moaC	probable cyclic pyranopterin monophosphate synthase	traverse_junction
HBSAL_07135	OE_2827R	100p	m24	VNG_1275G	hflX2	ribosome-associating GTPase HflX	-
HBSAL_07140	OE_2828R	100p	m24	VNG_1276C	sdo1	ribosome maturation protein Sdo1	-
HBSAL_07145	OE_2832R	100p	m24	VNG_1279H	rnp2	ribonuclease P protein component 2	-
HBSAL_07150	OE_2833R	99	m24	VNG_1280C	-	probable S-adenosylmethionine-dependent methyltransferase	-
HBSAL_07155	OE_2834R	99	m24	VNG_1281H	rnp3	ribonuclease P protein component 3	-
HBSAL_07160	OE_2838R	100p	m24	VNG_1282G	trkA5	TrkA domain protein	-
HBSAL_07165	OE_2840R	100d	m24	VNG_1283H	-	uncharacterized protein	-
HBSAL_07170	OE_2841R	100d	m24	VNG_1284G	trkH1	Trk-type transport system (probable substrate potassium)	-
HBSAL_07175	OE_2844R	100d	m24	VNG_1285G	-	Lrp/AsnC family transcription regulator / TrkA domain protein	-
HBSAL_07180	OE_2845R	100d	m24	VNG_1287C	-	DUF54 family protein	-
HBSAL_07185	OE_2847R	100d	m24	VNG_1289H	-	DUF1918 family protein	-
HBSAL_07190	OE_2850R	100d	m24	VNG_1291H	-	glycoside hydrolase domain protein	-
HBSAL_07195	OE_2851R	100d	m24	VNG_1292H	-	uncharacterized protein	-
HBSAL_07200	OE_2853R	100d	m24	VNG_1294G	mtfK	FKBP-type peptidylprolyl isomerase	-
HBSAL_07205	OE_2854R	100d	m24	VNG_1295H	-	uncharacterized protein	-
HBSAL_07210	OE_2856F	100p	m24	VNG_1296C	-	adenylate cyclase domain protein	-
HBSAL_07215	OE_2857F	99	m24	VNG_1297C	mat	S-adenosylmethionine synthase	-

HBSAL_07220	OE_2858F	99	m24	VNG_1299C	thiI	tRNA uracil 4-sulfurtransferase	-
HBSAL_07225	OE_2859F	98	m24	VNG_1300H	-	uncharacterized protein	-
HBSAL_07230	OE_2860R	99	m24	VNG_1301G	cysK2	cysteine synthase	-
HBSAL_07235	OE_2862F	100p	m24	VNG_1302H	trxA5	thioredoxin	-
HBSAL_07240	OE_2863R	99	m24	VNG_1303C	-	YyaL family protein	-
HBSAL_07245	OE_2864F	98	m24	VNG_1305G	purD	phosphoribosylamine--glycine ligase	-
HBSAL_07250	OE_2865R	100p	m24	VNG_1306G	sdhA	succinate dehydrogenase subunit A	-
HBSAL_07255	OE_2866R	100d	m24	VNG_1308G	sdhB	succinate dehydrogenase subunit B	-
HBSAL_07260	OE_2867R	100d	m24	VNG_1309G	sdhD	succinate dehydrogenase subunit D	-
HBSAL_07265	OE_2868R	100d	m24	VNG_1310G	sdhC	succinate dehydrogenase subunit C	-
HBSAL_07270	OE_2870R	100d	m24	VNG_1311G	-	DNA N-glycosylase	-
HBSAL_07275	OE_2871F	100d	m24	VNG_1313G	hbd2	3-hydroxyacyl-CoA dehydrogenase / enoyl-CoA hydratase	-
HBSAL_07280	OE_2872F	100d	m24	VNG_1314H	-	uncharacterized protein	-
HBSAL_07285	OE_2874F	100d	m24	VNG_1315H	-	uncharacterized protein	-
HBSAL_07290	OE_2875R	100d	m24	VNG_1317H	-	uncharacterized protein	-
HBSAL_07295	OE_2878F	100d	m24	VNG_1318H	-	uncharacterized protein	-
HBSAL_07300	OE_2879R	100d	m24	VNG_1319H	-	uncharacterized protein	-
HBSAL_07305	OE_2887F	100d	m25	VNG_1320G	-	probable secreted glycoprotein	-
HBSAL_07310	OE_2891F	100d	m25	VNG_1323C	-	pectin lyase domain protein	-
HBSAL_07315	OE_2896R	100d	m25	VNG_1324C	-	GtrA family protein	-
HBSAL_07320	OE_2898R	100d	m25	VNG_1325C	thyX	thymidylate synthase ThyX	-
HBSAL_07325	OE_2900F	100d	m25	VNG_1326H	-	cupin 2 barrel domain protein	-
HBSAL_07330	OE_2902F	100d	m25	VNG_1327G	-	beta-lactamase domain protein	-
HBSAL_07335	OE_2903R	100d	m25	VNG_1329H	-	uncharacterized protein	-
HBSAL_07340	OE_2905F	100d	m25	VNG_1330H	-	uncharacterized protein	-
HBSAL_07345	OE_2906R	100d	m25	VNG_1332G	sod2	superoxide dismutase (Mn)	-
HBSAL_07350	OE_2907R	100d	m25	VNG_1335G	phr2	deoxyribodipyrimidine photo-lyase	-
HBSAL_07355	OE_2908R	100d	m25	VNG_1336C	-	Paal family protein	-
HBSAL_07360	OE_2909F	100d	m25	VNG_1337C	-	AlkP-core domain protein	-

HBSAL_07365	OE_2912F	100d	m25	VNG_1339C	acs3	acyl-CoA synthetase	-
HBSAL_07370	OE_2913R	100d	m25	VNG_1340C	-	beta-lactamase domain protein	-
HBSAL_07375	OE_2916F	100d	m25	VNG_1341G	-	probable oxidoreductase (short-chain dehydrogenase family)	-
HBSAL_07380	OE_2918F	100d	m25	VNG_1342G	-	probable F420-dependent oxidoreductase	-
HBSAL_07385	OE_2919R	100d	m25	VNG_1343C	mptE	6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase MptE	-
HBSAL_07390	OE_2921R	100d	m25	VNG_1344G	folP	dihydropteroate synthase	-
HBSAL_07395	OE_2922F	100d	m25	VNG_1345H	-	uncharacterized protein	-
HBSAL_07400	OE_2923F	100d	m25	VNG_1347C	-	tRNA (cytidine/uridine-2'-O-)-methyltransferase	-
HBSAL_07405	OE_2924R	100d	m25	VNG_1349C	maoC3	MaoC domain protein	-
HBSAL_07410	OE_2926R	100d	m25	VNG_1350C	-	DMT superfamily transport protein	-
HBSAL_07415	OE_2928F	100d	m25	VNG_1351G	-	Lrp/AsnC family transcription regulator	-
HBSAL_07420	OE_2929R	100d	m25	VNG_1352G	gatE	glutamyl-tRNA(Gln) amidotransferase subunit E	-
HBSAL_07425	OE_2930R	99	m25	VNG_1353C	-	DUF304 domain protein	-
HBSAL_07430	OE_2934R	100d	m25	VNG_1355H	-	DUF304 domain protein	-
HBSAL_07435	OE_2935R	100d	m25	VNG_1356G	fumC	fumarate hydratase	-
HBSAL_07440	OE_2937R	100d	m25	VNG_1357C	bolA	BolA family protein	-
HBSAL_07445	OE_2939R	100d	m25	VNG_1359G	fen1	flap endonuclease Fen1	-
HBSAL_07450	OE_2941R	100d	m25	VNG_1360H	-	GNAT family acetyltransferase	-
HBSAL_07455	OE_2944F	100d	m25	VNG_1362H	-	DUF3054 family protein	-
HBSAL_07460	OE_2945F	100d	m25	VNG_1364G	-	ornithine cyclodeaminase family protein	-
HBSAL_07465	OE_2946R	100d	m25	VNG_1365C	-	DUF1119 family protein	-
HBSAL_07470	OE_2948R	100d	m25	VNG_1366H	gar1	tRNA/rRNA pseudouridine synthase complex protein Gar1	-
HBSAL_07475	OE_2950R	100d	m25	VNG_1367G	srp19	signal recognition particle 19K protein	-
HBSAL_07480	OE_2951R	100d	m25	VNG_1369G	btuF	ABC-type transport system periplasmic substrate-binding protein (substrate cobalamin)	-
HBSAL_07485	OE_2952F	100d	m25	VNG_1370G	btuC	ABC-type transport system permease protein (substrate cobalamin)	-
HBSAL_07490	OE_2955F	99	m25	VNG_1371G	btuD	ABC-type transport system ATP-binding protein	-

						(substrate cobalamin)	
HBSAL_07495	OE_2956F	98	m25	VNG_1372C	-	probable secreted glycoprotein	-
HBSAL_07500	OE_2961F	99	m25	VNG_1374G	-	sensor box histidine kinase	seqdiff(R1/NRC-1)
HBSAL_07505	OE_2964F	98	m25	VNG_1375C	-	histidine kinase	-
HBSAL_07510	OE_2967R	98	m25	VNG_1376H	-	uncharacterized protein	-
HBSAL_07515	OE_2969R	100p	m25	VNG_1377G	-	Lrp/AsnC family transcription regulator	-
HBSAL_07520	OE_2970R	100p	m25	VNG_1379G	suhB	probable inositol-1(or 4)-monophosphatase / fructose-1,6-bisphosphatase, archaeal-type	-
HBSAL_07525	OE_2973F	100p	m25	VNG_1380H	-	uncharacterized protein	-
HBSAL_07530	OE_2975F	100p	m25	VNG_1381H	-	uncharacterized protein	-
HBSAL_07535	OE_2979F	97	m25	VNG_1382H	-	uncharacterized protein	-
HBSAL_07540	OE_2981F	99	m25	VNG_1383G	rad3a	DNA repair helicase Rad3	-
HBSAL_07545	OE_2983F	98	m25	VNG_1384H	-	uncharacterized protein	-
HBSAL_07550	OE_2985F	99	m25	VNG_1385G	yvoF	O-acetyltransferase (homolog to galactoside O-acetyltransferase)	-
HBSAL_07555	OE_2986R	100p	m25	VNG_1387H	-	uncharacterized protein	-
HBSAL_07560	OE_2988R	100d	m25	VNG_1388H	mscS2	mechanosensitive channel protein MscS	-
HBSAL_07565	OE_2989R	100d	m25	VNG_1389C	dacZ	diadenylate cyclase	-
HBSAL_07570	OE_2991F	100d	m25	VNG_1390H	-	cyclin domain protein	-
HBSAL_07575	OE_2992R	100d	m25	VNG_1390a	coaD	phosphopantetheine adenylyltransferase	-
HBSAL_07580	OE_2995R	100d	m25	VNG_1394H	-	TrmB family transcription regulator	-
HBSAL_07585	OE_2996R	100p	m25	VNG_1395G	htr9	transducer protein Htr9	-
HBSAL_07590	OE_2998R	100d	m25	VNG_1397C	gshA	glutamate--cysteine ligase	-
HBSAL_07595	OE_3000R	100d	m25	VNG_1398C	-	GNAT family acetyltransferase	-
HBSAL_07600	OE_3002R	100d	m25	VNG_1402H	-	DUF309 family protein	-
HBSAL_07605	OE_3004R	100d	m25	VNG_1401C	-	UPF0179 family protein	-
HBSAL_07615	OE_3006R	100d	m26	VNG_1403H	-	uncharacterized protein	-
HBSAL_07620	OE_3007R	100d	m26	VNG_1405C	-	HxlR family transcription regulator	-
HBSAL_07625	OE_3008F	100d	m26	VNG_1404G	msrB	peptide methionine sulfoxide reductase MsrB (R-form specific)	-

HBSAL_07630	OE_3009R	100d	m26	VNG_1404a	-	small CPxCG-related zinc finger protein	-
HBSAL_07635	OE_3010F	100d	m26	VNG_1406G	rad25c	DNA repair helicase Rad25	-
HBSAL_07640	OE_3015F	100d	m26	VNG_1407C	-	thioesterase domain protein	-
HBSAL_07645	OE_3017R	100d	m26	VNG_1408G	-	5'-nucleotidase family hydrolase	-
HBSAL_07650	OE_3018F	100d	m26	VNG_1409C	-	DUF63 family protein	-
HBSAL_07655	OE_3022R	100d	m26	VNG_1410H	-	DUF181 family protein	-
HBSAL_07660	OE_3028R	100d	m26	VNG_1412H	-	uncharacterized protein	-
HBSAL_07665	OE_3030R	100d	m26	VNG_1413H	-	uncharacterized protein	-
HBSAL_07670	OE_3036F	100d	m26	VNG_1414G	glyA	serine hydroxymethyltransferase	-
HBSAL_07675	OE_3038F	100p	m26	VNG_1416G	folD	methylenetetrahydrofolate dehydrogenase / methenyltetrahydrofolate cyclohydrolase	-
HBSAL_07680	OE_3040R	100d	m26	VNG_1417H	-	uncharacterized protein	-
HBSAL_07685	OE_3039F	100d	m26	VNG_1418C	-	alpha/beta hydrolase fold protein	-
HBSAL_07690	OE_3042F	100d	m26	VNG_1420H	-	uncharacterized protein	-
HBSAL_07695	OE_3045F	100d	m26	VNG_1422H	-	DUF1028 family protein	-
HBSAL_07700	OE_3047F	100d	m26	VNG_1423H	-	uncharacterized protein	-
HBSAL_07705	OE_3049R	100d	m26	VNG_1425H	-	uncharacterized protein	-
HBSAL_07710	OE_3050F	100d	m26	VNG_1426H	-	PadR family transcription regulator	-
HBSAL_07715	OE_3053F	100d	m26	VNG_1427H	-	uncharacterized protein	-
HBSAL_07720	OE_3054R	100d	m26	VNG_1428G	-	AI-2E family transport protein	-
HBSAL_07725	OE_3057F	100d	m26	VNG_1429C	cofD	2-phospho-L-lactate transferase	-
HBSAL_07730	OE_3058F	100d	m26	VNG_1431C	dpd	putative dihydropyrimidine dehydrogenase	-
HBSAL_07735	OE_3059F	100d	m26	VNG_1432G	dhs	deoxyhypusine synthase	-
HBSAL_07740	OE_3062F	100d	m26	VNG_1433G	rps17e	30S ribosomal protein S17e	-
HBSAL_07745	OE_3063F	100d	m26	VNG_1435G	asd	aspartate-semialdehyde dehydrogenase	-
HBSAL_07750	OE_3064F	100d	m26	VNG_1435a	-	uncharacterized protein	pseudo(91-R6;R1;NRC-1)
HBSAL_07755	OE_3065R	100d	m26	VNG_1437G	serA2	probable D-2-hydroxyacid dehydrogenase	-
HBSAL_07760	OE_3067F	100d	m26	VNG_1438H	-	uncharacterized protein	-
HBSAL_07765	OE_3067B1F	100d	m26	VNG_1438a	-	uncharacterized protein	-
HBSAL_07770	OE_3069R	100d	m26	VNG_1440H	-	uncharacterized protein	-

HBSAL_07775	OE_3070R	100d	m26	VNG_1442G	htrXII	transducer protein HtrXII	-
HBSAL_07780	OE_3071F	100d	m26	VNG_1444G	hisD	histidinol dehydrogenase	-
HBSAL_07785	OE_3073R	100d	m26	VNG_1446H	-	dodecin	-
HBSAL_07790	OE_3075R	100d	m26	VNG_1447H	-	DUF457 family protein	-
HBSAL_07795	OE_3078R	100d	m26	VNG_1448H	-	uncharacterized protein	-
HBSAL_07800	OE_3079F	100d	m26	VNG_1450G	-	5'-nucleotidase family hydrolase	-
HBSAL_07805	OE_3081F	100d	m26	VNG_1451C	trmB	TrmB family transcription regulator TrmB	-
HBSAL_07810	OE_3082R	100d	m26	VNG_1452G	-	eIF-2B domain protein	-
HBSAL_07815	OE_3084F	100d	m26	VNG_1453H	-	uncharacterized protein	-
HBSAL_07820	OE_3085R	100d	m26	VNG_1454C	rtcB	tRNA-splicing ligase RtcB	-
HBSAL_07825	OE_3087R	100d	m26	VNG_1455H	-	DoxX domain protein	-
HBSAL_07830	OE_3090R	100d	m26	VNG_1456H	-	homolog to archaease	-
HBSAL_07835	OE_3092F	100d	m26	VNG_1457C	-	GNAT family acetyltransferase	-
HBSAL_07840	OE_3093R	100d	m26	VNG_1458G	crtB1	phytoene synthase	-
HBSAL_07845	OE_3095R	100d	m26	VNG_1459H	-	small CPxCG-related zinc finger protein	-
HBSAL_07850	OE_3097R	100d	m26	VNG_1461H	-	uncharacterized protein	-
HBSAL_07855	OE_3098R	100d	m26	VNG_1462G	bac	bacterioopsin-associated chaperone	-
HBSAL_07860	OE_3100F	100d	m26	VNG_1463G	blp	bacterioopsin-linked protein Blp	-
HBSAL_07865	OE_3101R	100d	m26	VNG_1464G	bat	bacterioopsin activator Bat	-
HBSAL_07870	OE_3102R	100d	m26	VNG_1465G	brp	beta-carotene 15,15'-dioxygenase Brp	-
HBSAL_07875	OE_3104F	100d	m26	VNG_1466H	brz	transcription regulator Brz (CPxCG-related small zinc finger protein)	-
HBSAL_07880	OE_3105F	100d	m26	VNG_1466a	brb	bacteriorhodopsin-regulating basic protein	-
HBSAL_07890	OE_3106F	99	d26/ m27	VNG_1467G	bop	bacteriorhodopsin	traverse_junction
HBSAL_07895	OE_3107F	100d	m27	VNG_1468H	bap	bacterioopsin-associated protein	-
HBSAL_07900	OE_3108F	100d	m27	VNG_1470G	priS	DNA primase small subunit	-
HBSAL_07905	OE_3109F	100d	m27	VNG_1471C	ginS	DNA replication factor GINS	-
HBSAL_07910	OE_3112R	100d	m27	VNG_1472G	cdc48b	AAA-type ATPase (CDC48 subfamily)	-
HBSAL_07915	OE_3114R	100d	m27	VNG_1473H	-	uncharacterized protein	-



HBSAL_07920	OE_3115F	100d	m27	VNG_1474G	-	alpha/beta hydrolase fold protein	-
HBSAL_07925	OE_3116F	100d	m27	VNG_1475C	-	uncharacterized protein	-
HBSAL_07930	OE_3118F	100d	m27	VNG_1476C	-	RND superfamily permease	-
HBSAL_07935	OE_3119R	100d	m27	VNG_1478G	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	-
HBSAL_07940	OE_3120F	100d	m27	VNG_1479H	-	uncharacterized protein	-
HBSAL_07945	OE_3121R	100d	m27	VNG_1480C	-	HAD superfamily hydrolase	-
HBSAL_07950	OE_3122F	100d	m27	VNG_1481G	cysE	serine O-acetyltransferase	-
HBSAL_07955	OE_3123R	100d	m27	VNG_1482G	acd5	acyl-CoA dehydrogenase	-
HBSAL_07960	OE_3125R	100d	m27	VNG_1483C	-	cro/C1 family transcription regulator	-
HBSAL_07965	OE_3126F	100d	m27	VNG_1484H	-	uncharacterized protein	-
HBSAL_07970	OE_3131F	100d	m27	VNG_1486H	-	small CPxCG-related zinc finger protein	-
HBSAL_07975	OE_3130F	100d	m27	VNG_1486a	-	basic protein bp2	-
HBSAL_07980	OE_3132F	100d	m27	VNG_1487H	-	FMN-binding domain protein	-
HBSAL_07985	OE_3134F	100d	m27	VNG_1488G	boa2	HTH-10 family transcription regulator	-
HBSAL_07990	OE_3136F	100d	m27	VNG_1490H	-	HTH domain protein	-
HBSAL_07995	OE_3138F	100d	m27	VNG_1492C	-	DUF420 family protein	-
HBSAL_08000	OE_3139R	100d	m27	VNG_1493G	purF	amidophosphoribosyltransferase	-
HBSAL_08005	OE_3141R	100d	m27	VNG_1494G	rpl37e	50S ribosomal protein L37e	-
HBSAL_08010	OE_3142R	100d	m27	VNG_1496G	lsm	RNA-binding protein Lsm	-
HBSAL_08015	OE_3143R	100d	m27	VNG_1498G	-	peptidase M42 family protein	-
HBSAL_08020	OE_3144F	100d	m27	VNG_1498a	-	uncharacterized protein	-
HBSAL_08025	OE_3145F	100d	m27	VNG_1497C	-	DUF2342 family protein	-
HBSAL_08030	OE_3146R	100d	m27	VNG_1500H	-	uncharacterized protein	-
HBSAL_08035	OE_3147F	100d	m27	VNG_1501G	dna2	ATP-dependent DNA helicase Dna2	-
HBSAL_08040	OE_3149F	100d	m27	VNG_1503C	-	homolog to ribonuclease Z	-
HBSAL_08045	OE_3150R	100d	m27	VNG_1505G	hemAT	transducer protein HemAT	-
HBSAL_08050	OE_3152R	100d	m27	VNG_1506G	pelA	mRNA surveillance protein pelota	-
HBSAL_08055	OE_3153R	100d	m27	VNG_1508C	-	DUF814 domain protein	-
HBSAL_08060	OE_3154R	100d	m27	VNG_1510C	elp3	homolog to elongator complex protein ELP3	-

HBSAL_08065	OE_3155R	100d	m27	VNG_1511C	-	DHH/RecJ family phosphoesterase	-
HBSAL_08070	OE_3157R	100d	m27	VNG_1513H	-	uncharacterized protein	-
HBSAL_08075	OE_3158R	100d	m27	VNG_1514H	-	DUF649 family protein	-
HBSAL_08080	OE_3159R	100d	m27	VNG_1515G	tdk	thymidine kinase	-
HBSAL_08085	OE_3162F	100d	m27	VNG_1518H	-	UspA domain protein	-
HBSAL_08090	OE_3163R	100d	m27	VNG_1519H	-	DUF2892 family protein	-
HBSAL_08095	OE_3165R	100d	m27	VNG_1520G	mutY	A/G-specific adenine glycosylase	-
HBSAL_08100	OE_3164F	100d	m27	VNG_1520a	-	uncharacterized protein	-
HBSAL_08105	OE_3167F	100d	m27	VNG_1523G	htrVIII	transducer protein HtrVIII	-
HBSAL_08110	OE_3168R	100d	m27	VNG_1524C	-	pyridoxal phosphate-dependent aminotransferase	-
HBSAL_08115	OE_3169R	100d	m27	VNG_1525C	-	DUF4010 family protein	-
HBSAL_08120	OE_3171F	100d	m27	VNG_1526G	-	SNF family transport protein	-
HBSAL_08125	OE_3173F	100d	m27	VNG_1528G	-	SNF family transport protein	-
HBSAL_08130	OE_3175F	100d	m27	VNG_1529G	pccB2	propionyl-CoA carboxylase carboxyltransferase component	-
HBSAL_08135	OE_3176F	100d	m27	VNG_1530H	pccX	propionyl-CoA carboxylase small subunit	-
HBSAL_08140	OE_3177F	100d	m27	VNG_1532G	pccA2	propionyl-CoA carboxylase biotin carboxylase component	-
HBSAL_08145	OE_3178F	96	m27	VNG_1533H	-	uncharacterized protein	-
HBSAL_08150	OE_3184R	93	m27	VNG_1534H	-	uncharacterized protein	LowSim
HBSAL_08155	OE_3186F	99	m27	VNG_1534a	birA1	HTH domain protein / biotin--[acetyl-CoA-carboxylase] ligase	-
HBSAL_08160	OE_3187R	100p	m27	VNG_1536C	-	UspA domain protein	-
HBSAL_08165	OE_3188R	99	m27	VNG_1537C	-	HD family hydrolase	-
HBSAL_08170	OE_3190F	98	m27	VNG_1538H	-	uncharacterized protein	-
HBSAL_08175	OE_3194R	98	m27	VNG_1540G	-	probable oxidoreductase (short-chain dehydrogenase family)	-
HBSAL_08180	OE_3195F	99	m27	VNG_1541G	sucC	succinate--CoA ligase (ADP-forming) beta subunit	-
HBSAL_08185	OE_3196F	99	m27	VNG_1542G	sucD	succinate--CoA ligase (ADP-forming) alpha subunit	-
HBSAL_08190	OE_3197F	99	m27	VNG_1543G	zim	CTAG modification methylase	-

HBSAL_08195	OE_3200R	99	m27	VNG_1544G	clc	chloride channel protein	-
HBSAL_08200	OE_3203R	98	m27	VNG_1547C	pduO	ATP:cob(I)alamin adenosyltransferase	-
HBSAL_08205	OE_3204R	100p	m27	VNG_1546H	grx3	glutaredoxin	-
HBSAL_08210	OE_3205A1R	99	m27	VNG_1546a	-	DUF547 family protein	-
HBSAL_08215	OE_3206R	100p	m27	VNG_1548C	-	arNOG05395 family transcription regulator	-
HBSAL_08220	OE_3207F	100p	m27	VNG_1550G	cbiT	cobalt-precorrin-6B C15-methyltransferase (decarboxylating)	-
HBSAL_08225	OE_3209F	100p	m27	VNG_1551G	cbiL	cobalt-factor-II C20-methyltransferase	-
HBSAL_08230	OE_3212F	100p	m27	VNG_1553G	cbiF	cobalt-precorrin-4 C11-methyltransferase	-
HBSAL_08235	OE_3213F	99	m27	VNG_1554G	cbiG	cobalt-precorrin-5A hydrolase	-
HBSAL_08240	OE_3214F	99	m27	VNG_1555G	cbiH1	cobalt-factor-III C17-methyltransferase	-
HBSAL_08245	OE_3216F	95	m27	VNG_1557G	cbiH2	cobalt-factor-III C17-methyltransferase	insert(14aa;R1;NRC-1)
HBSAL_08250	OE_3219F	100d	m27	VNG_1558H	-	probable ferredoxin (4Fe-4S)	-
HBSAL_08255	OE_3218F	99	m27	VNG_1559H	-	uncharacterized protein	-
HBSAL_08260	OE_3221F	99	m27	VNG_1561C	cbiX1	sirohydrochlorin cobaltochelatase	-
HBSAL_08265	OE_3224F	99	m27	VNG_1562H	-	DUF3209 family protein	-
HBSAL_08270	OE_3227F	99	m27	VNG_1564H	-	PQQ repeat protein	-
HBSAL_08275	OE_3229R	98	m27	VNG_1565G	chlID	ATP-dependent cobaltochelatase subunit ChlID	-
HBSAL_08280	OE_3230F	99	m27	VNG_1566G	cobN	ATP-dependent cobaltochelatase subunit CobN	-
HBSAL_08285	OE_3237F	100d	m27	VNG_1567G	cbiC	cobalt-precorrin-8 methylmutase	-
HBSAL_08290	OE_3238F	100d	m27	VNG_1568G	cbiE	cobalt-precorrin-7 C5-methyltransferase	-
HBSAL_08295	OE_3239R	100d	m27	VNG_1570H	cbiX3	homolog to sirohydrochlorin cobaltochelatase	-
HBSAL_08300	OE_3242F	100d	m27	VNG_1572C	cobT	probable nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase	-
HBSAL_08305	OE_3243F	100d	m27	VNG_1573G	cbiA	cobyrrinate a,c-diamide synthase	-
HBSAL_08310	OE_3245F	100d	m27	VNG_1574G	cobA	cob(I)alamin adenosyltransferase	-
HBSAL_08315	OE_3246F	100d	m27	VNG_1576G	cbiP	adenosylcobyrate synthase	-
HBSAL_08320	OE_3249F	100d	m27	VNG_1577C	-	HAD superfamily hydrolase	-
HBSAL_08325	OE_3253F	100d	m27	VNG_1578H	cbiB	adenosylcobinamide-phosphate synthase	-
HBSAL_08330	OE_3255F	100d	m27	VNG_1580H	cobS	adenosylcobinamide-GDP ribazoletransferase	-

HBSAL_08335	OE_3257F	100d	m27	VNG_1581C	cobY	adenosylcobinamide-phosphate guanylyltransferase	-
HBSAL_08340	OE_3259F	100d	m27	VNG_1582G	cobD	L-threonine-O-3-phosphate decarboxylase	-
HBSAL_08345	OE_3261F	100d	m27	VNG_1583C	cbiZ	adenosylcobinamide amidohydrolase	-
HBSAL_08350	OE_3262R	99	m27	[VNG_1585C ;VNG_1587a]	-	DUF262/DUF1524 domain protein	pseudo(NRC-1;split)
HBSAL_08355	OE_3263R	100d	m27	VNG_1587c	-	ISH7-type transposase	pseudo(91-R6;R1;NRC-1)
HBSAL_08360	OE_3264F	100d	m27	VNG_1589C	-	uncharacterized protein	-
HBSAL_08365	OE_3265R	100d	m27	VNG_1590H	-	ISH7-type transposase	pseudo(91-R6;R1;NRC-1)
HBSAL_08370	OE_3268F	100d	m27	VNG_1591H	-	small CPxCG-related zinc finger protein	-
HBSAL_08375	OE_3269R	100d	m27	VNG_1592G	-	ABC-type transport system permease protein (probable substrate sulfate/thiosulfate/molybdate)	-
HBSAL_08380	OE_3270R	100d	m27	VNG_1595C	-	ABC-type transport system periplasmic substrate- binding protein (probable substrate sulfate/thiosulfate/molybdate)	-
HBSAL_08385	OE_3273F	100d	m27	VNG_1598a	tfx	Tfx-type DNA-binding protein	-
HBSAL_08390	OE_3274R	100d	m27	VNG_1601G	gcvP2	glycine cleavage system protein P beta subunit	-
HBSAL_08395	OE_3275R	100d	m27	VNG_1603G	gcvP1	glycine cleavage system protein P alpha subunit	-
HBSAL_08400	OE_3277R	100d	m27	VNG_1605G	gcvH	glycine cleavage system protein H	-
HBSAL_08405	OE_3278R	100d	m27	VNG_1606G	gcvT	glycine cleavage system protein T	-
HBSAL_08410	OE_3280R	100d	m27	VNG_1607G	cheC2	taxis cluster protein CheC	-
HBSAL_08415	OE_3283F	100d	m27	VNG_1608C	-	DUF88 family protein	-
HBSAL_08420	OE_3284R	100d	m27	VNG_1609C	-	DUF124 family protein	-
HBSAL_08425	OE_3286F	100d	m27	VNG_1610C	tatD	3'-5' ssDNA/RNA exonuclease TatD	-
HBSAL_08430	OE_3289F	100d	m27	VNG_1611C	-	DUF2150 family protein	-
HBSAL_08435	OE_3292F	100d	m27	VNG_1613H	-	probable secreted glycoprotein	-
HBSAL_08440	OE_3296F	100d	m27	VNG_1615G	hmgB	hydroxymethylglutaryl-CoA synthase	-
HBSAL_08445	OE_3297R	100d	m27	VNG_1618H	-	homolog to NAD(P)H dehydrogenase (quinone)	-
HBSAL_08450	OE_3299R	100d	m27	VNG_1616C	-	cro/C1 family transcription regulator	-
HBSAL_08455	OE_3300F	100d	m27	VNG_1617H	-	GNAT family acetyltransferase	-
HBSAL_08460	OE_3303R	100d	m27	VNG_1619H	-	uncharacterized protein	-

HBSAL_08465	OE_3304R	100d	m27	VNG_1621H	-	FMN-binding domain protein	-
HBSAL_08470	OE_3305F	100d	m27	VNG_1622G	rfcB	replication factor C large subunit	-
HBSAL_08475	OE_3306R	100d	m27	VNG_1623G	ctaA	heme A synthase	-
HBSAL_08480	OE_3308F	100d	m27	VNG_1624G	maeB	malate dehydrogenase (oxaloacetate-decarboxylating)	-
HBSAL_08485	OE_3309R	100d	m27	VNG_1625H	rnhA1	ribonuclease H, type 1	-
HBSAL_08490	OE_3311F	100d	m27	VNG_1626C	-	DMT superfamily transport protein	-
HBSAL_08495	OE_3312R	100d	m27	VNG_1628G	-	probable oxidoreductase (aldo-keto reductase family protein)	-
HBSAL_08500	OE_3314R	100d	m27	VNG_1630H	-	uncharacterized protein	-
HBSAL_08505	OE_3315R	100d	m27	VNG_1631G	cbiO	ABC-type transport system ATP-binding protein (probable substrate cobalt)	-
HBSAL_08510	OE_3317R	100d	m27	VNG_1632G	cbiQ	ABC-type transport system permease protein (probable substrate cobalt)	-
HBSAL_08515	OE_3318R	100d	m27	VNG_1634G	cbiN	ABC-type transport system protein CbiN (probable substrate cobalt)	-
HBSAL_08520	OE_3319R	100d	m27	VNG_1635G	cbiM	ABC-type transport system permease protein (probable substrate cobalt)	-
HBSAL_08525	OE_3320F	100d	m27	VNG_1637G	hcpA	halocyanin HcpA	-
HBSAL_08530	OE_3322F	100d	m27	VNG_1638H	-	uncharacterized protein	-
HBSAL_08535	OE_3324R	100d	m27	VNG_1640H	-	uncharacterized protein	-
HBSAL_08540	OE_3325F	100d	m27	VNG_1641H	-	uncharacterized protein	-
HBSAL_08545	OE_3327R	100d	m27	VNG_1642H	-	small CPxCG-related zinc finger protein	-
HBSAL_08550	OE_3328R	100d	m27	VNG_1644G	nrdJ	ribonucleoside-diphosphate reductase, adenosylcobalamin-dependent	-
HBSAL_08555	OE_3330F	100d	m27	VNG_1645H	-	uncharacterized protein	-
HBSAL_08560	OE_3331R	100d	m27	VNG_1646G	trpG1	anthranilate synthase component 2	-
HBSAL_08565	OE_3332R	100d	m27	VNG_1647G	trpE1	anthranilate synthase component 1	-
HBSAL_08570	OE_3333R	100d	m27	VNG_1648G	trpF	N-(5'-phosphoribosyl)anthranilate isomerase	-
HBSAL_08575	OE_3334R	100d	m27	VNG_1649G	trpD1	anthranilate phosphoribosyltransferase	-
HBSAL_08580	OE_3335R	100d	m27	VNG_1649a	-	uncharacterized protein	-

HBSAL_08590	OE_3338R	100d	m28/ m29	VNG_1650H	-	uncharacterized protein	seqdiff(R1/NRC-1); traverse_junction
HBSAL_08595	OE_3339R	100d	m29	VNG_1654G	aaa4	AAA-type ATPase core domain protein	-
HBSAL_08600	OE_3341A1R	100d	m29	VNG_1654a	-	zinc finger domain protein	pseudo(91-R6;R1;NRC-1)
HBSAL_08605	OE_3342R	100d	m29	VNG_1655H	-	uncharacterized protein	-
HBSAL_08610	OE_3343R	100d	m29	VNG_1657H	-	uncharacterized protein	-
HBSAL_08615	OE_3345F	100d	m29	VNG_1656H	-	uncharacterized protein	-
HBSAL_08620	OE_3346R	100d	m29	VNG_1658C	-	UspA domain protein	-
HBSAL_08625	OE_3347F	100d	m29	VNG_1659G	htrI	transducer protein HtrI	-
HBSAL_08630	OE_3348F	100d	m29	VNG_1660G	sopI	sensory rhodopsin I	-
HBSAL_08635	OE_3349F	100d	m29	VNG_1663C	-	CBS domain protein	-
HBSAL_08640	OE_3351F	100d	m29	VNG_1664H	-	uncharacterized protein	-
HBSAL_08645	OE_3352R	100d	m29	VNG_1665G	radB	DNA repair and recombination protein RadB	-
HBSAL_08650	OE_3355R	100d	m29	VNG_1666H	-	homolog to carbohydrate reductase	-
HBSAL_08655	OE_3356F	100d	m29	VNG_1667G	cdc48a	AAA-type ATPase (CDC48 subfamily)	-
HBSAL_08660	OE_3357R	100d	m29	VNG_1668G	rps8e	30S ribosomal protein S8e	-
HBSAL_08665	OE_3358F	100d	m29	VNG_1670C	-	DUF2240 family protein	-
HBSAL_08670	OE_3361F	100d	m29	VNG_1672H	-	uncharacterized protein	-
HBSAL_08675	OE_3363F	100d	m29	VNG_1673G	pyrF	orotidine-5'-phosphate decarboxylase	-
HBSAL_08680	OE_3365R	100d	m29	VNG_1674H	-	uncharacterized protein	-
HBSAL_08685	OE_3367F	100d	m29	VNG_1675H	-	DnaJ N-terminal domain protein	-
HBSAL_08690	OE_3369F	100d	m29	VNG_1675a	-	HAD superfamily hydrolase	-
HBSAL_08695	OE_3371F	100d	m29	VNG_1676G	-	homolog to translation elongation factor aEF-1 alpha subunit	-
HBSAL_08700	OE_3372F	100d	m29	VNG_1678H	-	uncharacterized protein	-
HBSAL_08705	OE_3374R	100d	m29	VNG_1679H	-	uncharacterized protein	-
HBSAL_08710	OE_3376F	100d	m29	VNG_1680G	crtB2	phytoene synthase	-
HBSAL_08715	OE_3377R	100d	m29	VNG_1681C	cruF	bisanhydrobacterioruberin hydratase	-
HBSAL_08720	OE_3380R	100d	m29	VNG_1682C	lyeJ	lycopene elongase/hydratase (dihydrobisanhydrobacterioruberin-forming)	-

HBSAL_08725	OE_3381R	100d	m29	VNG_1684G	crtD	carotenoid 3,4-desaturase	-
HBSAL_08730	OE_3383R	100d	m29	VNG_1686G	mch	probable methenyltetrahydrofolate cyclohydrolase	-
HBSAL_08735	OE_3384R	100d	m29	VNG_1687C	-	major facilitator superfamily transport protein	-
HBSAL_08795	OE_3386F	100d	m30	VNG_1688C	-	DUF171 family protein	-
HBSAL_08800	OE_3388F	100d	m30	VNG_1689G	rpl3	50S ribosomal protein L3	-
HBSAL_08805	OE_3389F	100d	m30	VNG_1690G	rpl4	50S ribosomal protein L4	-
HBSAL_08810	OE_3390F	100d	m30	VNG_1691G	rpl23	50S ribosomal protein L23	-
HBSAL_08815	OE_3392F	100d	m30	VNG_1692G	rpl2	50S ribosomal protein L2	-
HBSAL_08820	OE_3393F	100d	m30	VNG_1693G	rps19	30S ribosomal protein S19	-
HBSAL_08825	OE_3394F	100d	m30	VNG_1695G	rpl22	50S ribosomal protein L22	-
HBSAL_08830	OE_3395F	100d	m30	VNG_1697G	rps3	30S ribosomal protein S3	-
HBSAL_08835	OE_3396F	100d	m30	VNG_1698G	rpl29	50S ribosomal protein L29	-
HBSAL_08840	OE_3398F	100d	m30	VNG_1699C	rnp1	ribonuclease P protein component 1	-
HBSAL_08845	OE_3400F	100d	m30	VNG_1700G	rps17	30S ribosomal protein S17	-
HBSAL_08850	OE_3402F	100d	m30	VNG_1701G	rpl14	50S ribosomal protein L14	-
HBSAL_08855	OE_3404F	100d	m30	VNG_1702G	rpl24	50S ribosomal protein L24	-
HBSAL_08860	OE_3405F	100d	m30	VNG_1703G	rps4e	30S ribosomal protein S4e	-
HBSAL_08865	OE_3407F	100d	m30	VNG_1705G	rpl5	50S ribosomal protein L5	-
HBSAL_08870	OE_3408F	100d	m30	VNG_1706G	rps14	30S ribosomal protein S14	-
HBSAL_08875	OE_3410F	100d	m30	VNG_1707G	rps8	30S ribosomal protein S8	-
HBSAL_08880	OE_3411F	100d	m30	VNG_1709G	rpl6	50S ribosomal protein L6	-
HBSAL_08885	OE_3412F	100d	m30	VNG_1711G	rpl32e	50S ribosomal protein L32e	-
HBSAL_08890	OE_3413F	100d	m30	VNG_1713G	rpl19e	50S ribosomal protein L19e	-
HBSAL_08895	OE_3414F	100d	m30	VNG_1714G	rpl18	50S ribosomal protein L18	-
HBSAL_08900	OE_3415F	100d	m30	VNG_1715G	rps5	30S ribosomal protein S5	-
HBSAL_08905	OE_3416F	100d	m30	VNG_1716G	rpl30	50S ribosomal protein L30	-
HBSAL_08910	OE_3417F	100d	m30	VNG_1718G	rpl15	50S ribosomal protein L15	-
HBSAL_08915	OE_3418F	100d	m30	VNG_1719G	secY	protein translocase subunit SecY	-
HBSAL_08920	OE_3419F	100d	m30	VNG_1720H	-	ABC-type transport system periplasmic substrate-binding protein	-

HBSAL_08925	OE_3421A1F	100d	m30	VNG_1720a	-	Trk-type transport system	pseudo(91-R6;R1;NRC-1)
HBSAL_08930	OE_3422R	100d	m30	VNG_1721G	trkH2	Trk-type transport system (probable substrate potassium)	-
HBSAL_08935	OE_3424R	100d	m30	VNG_1723H	-	uncharacterized protein	-
HBSAL_08940	OE_3425F	100d	m30	VNG_1724G	adk1	adenylate kinase	-
HBSAL_08945	OE_3427F	100d	m30	VNG_1726G	-	DUF106 family protein	-
HBSAL_08950	OE_3429F	100d	m30	VNG_1727G	cmk	cytidylate kinase	-
HBSAL_08955	OE_3430F	100d	m30	VNG_1729G	cbf5	tRNA/rRNA pseudouridine synthase Cbf5	-
HBSAL_08960	OE_3432R	100d	m30	VNG_1732C	-	uncharacterized protein	-
HBSAL_08965	OE_3436R	100d	m30	VNG_1733G	htr17	transducer protein Htr17	-
HBSAL_08970	OE_3438R	100d	m30	VNG_1734H	-	uncharacterized protein	-
HBSAL_08975	OE_3439F	100d	m30	VNG_1735C	-	MOSC domain protein	-
HBSAL_08980	OE_3444F	100d	m30	VNG_1737H	-	uncharacterized protein	-
HBSAL_08985	OE_3445F	100d	m30	VNG_1739G	-	uncharacterized protein	-
HBSAL_08990	OE_3447F	100d	m30	VNG_1740C	-	uncharacterized protein	-
HBSAL_08995	OE_3451A1F	100d	m30	VNG_1740a	-	uncharacterized protein	-
HBSAL_09000	OE_3452F	100d	m30	VNG_1743C	tfs2	transcription elongation factor TFS	-
HBSAL_09005	OE_3453R	100d	m30	VNG_1744H	-	uncharacterized protein	-
HBSAL_09010	OE_3456F	100d	m30	VNG_1746C	-	DUF2071 family protein	-
HBSAL_09015	OE_3458R	100p	m30	VNG_1748C	-	probable oxidoreductase (short-chain dehydrogenase family)	-
HBSAL_09020	OE_3460F	99	m30	VNG_1749G	-	GTP-binding protein	-
HBSAL_09025	OE_3462R	100p	m30	VNG_1751H	-	receiver/sensor box protein	-
HBSAL_09030	OE_3466R	100d	m30	VNG_1752C	-	UspA domain protein	-
HBSAL_09035	OE_3467R	100p	m30	VNG_1754G	phr1	deoxyribodipyrimidine photo-lyase	-
HBSAL_09040	OE_3468R	100d	m30	VNG_1755G	crtI2	phytoene dehydrogenase (phytoene desaturase)	-
HBSAL_09045	OE_3470F	100d	m30	VNG_1756G	tif1A2	translation initiation factor aIF-1A	-
HBSAL_09050	OE_3472F	100d	m30	VNG_1758H	-	uncharacterized protein	-
HBSAL_09055	OE_3473F	100d	m30	VNG_1759G	htrVII	transducer protein HtrVII	-
HBSAL_09060	OE_3474R	100d	m30	VNG_1760G	cosT	transducer protein CosT	-



HBSAL_09065	OE_3476R	100d	m30	VNG_1762G	cosB	chemotactic signal transduction system periplasmic substrate-binding protein CosB	-
HBSAL_09070	OE_3478A1R	100d	m30	VNG_1762a	-	uncharacterized protein	-
HBSAL_09075	OE_3479R	100d	m30	VNG_1762b	-	uncharacterized protein	-
HBSAL_09080	OE_3480R	100d	m30	VNG_1764G	sopII	sensory rhodopsin II	-
HBSAL_09085	OE_3481R	100d	m30	VNG_1765G	htrII	transducer protein HtrII	-
HBSAL_09090	OE_3482R	100d	m30	VNG_1766C	-	GTP cyclohydrolase 1 domain protein	-
HBSAL_09095	OE_3486R	100d	m30	VNG_1767G	speB	agmatinase	-
HBSAL_09100	OE_3487R	100d	m30	VNG_1768G	tef5A	translation elongation factor aEF-5A	-
HBSAL_09105	OE_3488R	100d	m30	VNG_1769C	cre2	creatininase domain protein	-
HBSAL_09110	OE_3490R	100d	m30	VNG_1770C	-	UbiB family protein	-
HBSAL_09115	OE_3491R	100d	m30	VNG_1771C	hsp20C	Hsp20-type molecular chaperone	-
HBSAL_09120	OE_3492R	100d	m30	VNG_1772G	-	HAD superfamily hydrolase	-
HBSAL_09125	OE_3495R	100d	m30	VNG_1773G	cad	probable pterin-4-alpha-carbinolamine dehydratase	-
HBSAL_09130	OE_3496R	100d	m30	VNG_1774G	hemA	glutamyl-tRNA reductase	-
HBSAL_09135	OE_3498R	100d	m30	VNG_1775C	sirC	precorrin-2 oxidase / ferrochelatase	-
HBSAL_09140	OE_3500R	100d	m30	VNG_1776G	ahbB	siroheme decarboxylase AhbB	-
HBSAL_09145	OE_3501R	100d	m30	VNG_1777H	-	uncharacterized protein	-
HBSAL_09150	OE_3503F	100d	m30	VNG_1779C	uppS1	tritrans, polycis-undecaprenyl-diphosphate synthase (geranylgeranyl-diphosphate specific)	-
HBSAL_09155	OE_3505R	100d	m30	VNG_1781C	uppS2	tritrans, polycis-undecaprenyl-diphosphate synthase (geranylgeranyl-diphosphate specific)	-
HBSAL_09160	OE_3506F	100d	m30	VNG_1782C	-	DUF92 family protein	-
HBSAL_09165	OE_3509R	100d	m30	VNG_1784C	dnaG	DNA primase DnaG	-
HBSAL_09170	OE_3510F	100d	m30	VNG_1783H	-	DUF3311 family protein	-
HBSAL_09175	OE_3511F	100d	m30	VNG_1785G	-	SSSF family transport protein	-
HBSAL_09180	OE_3513R	100d	m30	VNG_1786H	-	PadR family transcription regulator	-
HBSAL_09185	OE_3515F	100d	m30	VNG_1787H	-	uncharacterized protein	-
HBSAL_09190	OE_3517F	100d	m30	VNG_1788C	-	uncharacterized protein	-
HBSAL_09195	OE_3520F	100d	m30	VNG_1790H	-	DsrE domain protein	-

HBSAL_09200	OE_3522R	100d	m30	VNG_1791C	-	DUF1405 family protein	-
HBSAL_09205	OE_3524F	100d	m30	VNG_1793C	pdxS	pyridoxal 5'-phosphate synthase subunit PdxS	-
HBSAL_09210	OE_3526R	100d	m30	VNG_1794C	-	endonuclease domain protein	-
HBSAL_09215	OE_3531R	100d	m30	VNG_1797G	thrB	homoserine kinase	-
HBSAL_09220	OE_3533F	100d	m30	VNG_1795C	-	amine oxidase domain protein	-
HBSAL_09225	OE_3534F	100d	m30	VNG_1796H	-	uncharacterized protein	-
HBSAL_09230	OE_3535A1R	100d	m30	VNG_1796a	-	uncharacterized protein	-
HBSAL_09235	OE_3537R	100d	m30	VNG_1798H	-	uncharacterized protein	-
HBSAL_09240	OE_3538R	100d	m30	VNG_1800H	-	uncharacterized protein	-
HBSAL_09245	OE_3541R	100d	m30	VNG_1801G	hsp20F	Hsp20-type molecular chaperone	-
HBSAL_09250	OE_3542R	100d	m30	VNG_1802H	-	glutamine-rich alkaline protein	-
HBSAL_09255	OE_3544F	100d	m30	VNG_1804G	-	flavin-dependent pyridine nucleotide oxidoreductase	-
HBSAL_09260	OE_3545F	100d	m30	VNG_1806H	-	uncharacterized protein	-
HBSAL_09265	OE_3547F	100d	m30	VNG_1807H	-	uncharacterized protein	-
HBSAL_09270	OE_3549F	100d	m30	VNG_1809H	-	uncharacterized protein	-
HBSAL_09275	OE_3551R	100d	m30	VNG_1811G	ereB	homolog to erythromycin esterase	-
HBSAL_09280	OE_3554F	100d	m30	VNG_1814G	carB	carbamoyl-phosphate synthase (glutamine-hydrolyzing) large subunit	-
HBSAL_09285	OE_3556R	100d	m30	VNG_1815G	carA	carbamoyl-phosphate synthase (glutamine-hydrolyzing) small subunit	-
HBSAL_09290	OE_3558F	100d	m30	VNG_1816G	-	Lrp/AsnC family transcription regulator	-
HBSAL_09295	OE_3560F	100d	m30	VNG_1818G	idiA	isopentenyl-diphosphate delta-isomerase, type I	-
HBSAL_09300	OE_3561F	100d	m30	VNG_1818a	jamm1	desampylase Jamm1	-
HBSAL_09305	OE_3562R	100d	m30	VNG_1820H	-	uncharacterized protein	-
HBSAL_09310	OE_3563R	100d	m30	VNG_1821G	qor1	NADPH:quinone reductase	-
HBSAL_09315	OE_3565F	100d	m30	VNG_1822G	moaB	molybdopterin adenylyltransferase	-
HBSAL_09320	OE_3566F	100d	m30	VNG_1823C	-	probable COG0212-type thiamine metabolism protein	-
HBSAL_09325	OE_3567F	100d	m30	VNG_1826H	-	uncharacterized protein	-
HBSAL_09330	OE_3569R	100d	m30	VNG_1827H	-	uncharacterized protein	-

HBSAL_09335	OE_3571R	100d	m30	VNG_1829G	guaAb	GMP synthase (glutamine-hydrolyzing) subunit B	-
HBSAL_09340	OE_3572R	100d	m30	VNG_1830G	pyrG	CTP synthase	-
HBSAL_09345	OE_3575R	100d	m30	VNG_1831H	-	uncharacterized protein	-
HBSAL_09350	OE_3578R	100d	m30	VNG_1833C	-	alpha/beta hydrolase fold protein	-
HBSAL_09355	OE_3579F	100d	m30	VNG_1834G	-	peroxiredoxin domain protein	-
HBSAL_09360	OE_3580R	100d	m30	VNG_1835G	thrS	threonine--tRNA ligase	-
HBSAL_09365	OE_3582F	100d	m30	VNG_1836G	cspA2	cold shock protein	-
HBSAL_09370	OE_3584R	100d	m30	VNG_1837G	-	homolog to dipeptide epimerase	-
HBSAL_09375	OE_3585R	100d	m30	VNG_1839H	-	DUF1611 family protein	-
HBSAL_09380	OE_3585A1F	100d	m30	VNG_1838H	-	small CPxCG-related zinc finger protein	-
HBSAL_09385	OE_3586R	100d	m30	VNG_1842H	-	uncharacterized protein	-
HBSAL_09390	OE_3588C1R	100d	m30	VNG_1842a	-	uncharacterized protein	-
HBSAL_09395	OE_3589F	100d	m30	VNG_1843C	-	ArsR family transcription regulator	-
HBSAL_09400	OE_3591F	100d	m30	VNG_1844G	gatD	glutamyl-tRNA(Gln) amidotransferase subunit D	-
[HBSAL_09405 ;HBSAL_09440 ]	OE_3592F	99	m30/ m31	VNG_1845C	-	GNAT family acetyltransferase	pseudo(91-R6;split); traverse_junction
HBSAL_09445	OE_3594R	100d	m31	VNG_1846C	glpQ	glycerophosphodiester phosphodiesterase	-
HBSAL_09450	OE_3595R	100d	m31	VNG_1848H	samp1	ubiquitin-like modifier protein SAMP1	-
HBSAL_09455	OE_3596F	100d	m31	VNG_1847G	pchA1	ion channel pore / TrkA domain protein	-
HBSAL_09460	OE_3597R	100d	m31	VNG_1849H	-	HPP domain protein	-
HBSAL_09465	OE_3603R	100d	m31	VNG_1850G	udp3	uridine phosphorylase	-
HBSAL_09470	OE_3606R	100d	m31	VNG_1851G	-	PfkB family kinase	-
HBSAL_09475	OE_3607R	100d	m31	VNG_1852H	-	DUF63 family protein	-
HBSAL_09480	OE_3610R	100d	m31	VNG_1853G	-	ribose-1,5-bisphosphate isomerase	-
HBSAL_09485	OE_3611R	100d	m31	VNG_1856G	basT	transducer protein BasT	-
HBSAL_09490	OE_3612R	100d	m31	VNG_1857C	basB	chemotactic signal transduction system periplasmic substrate-binding protein BasB	-
HBSAL_09495	OE_3616F	100d	m31	VNG_1859G	deoC	deoxyribose-phosphate aldolase	-
HBSAL_09500	OE_3617F	100d	m31	VNG_1861C	-	MiaB-like tRNA modifying enzyme	-

HBSAL_09505	OE_3619R	100d	m31	VNG_1862G	-	transport protein (probable substrate zinc/cadmium/cobalt)	-
HBSAL_09510	OE_3620R	100d	m31	VNG_1864G	hit2	histidine triad family protein (homolog to bis(5'-nucleosyl)-tetraphosphatase)	-
HBSAL_09515	OE_3621F	100d	m31	VNG_1865H	-	small CPxCG-related zinc finger protein	-
HBSAL_09520	OE_3623R	100d	m31	VNG_1866G	map	methionine aminopeptidase	-
HBSAL_09525	OE_3625R	100d	m31	VNG_1867G	-	ABC-type transport system permease protein	-
HBSAL_09530	OE_3627R	100d	m31	VNG_1868G	-	ABC-type transport system permease protein	-
HBSAL_09535	OE_3629R	100d	m31	VNG_1869C	-	ABC-type transport system periplasmic substrate-binding protein	-
HBSAL_09540	OE_3631F	100d	m31	VNG_1871G	-	ABC-type transport system ATP-binding protein	-
HBSAL_09545	OE_3633R	100d	m31	VNG_1872C	ansA	asparaginase family protein	-
HBSAL_09550	OE_3634F	100d	m31	VNG_1873G	icd	isocitrate dehydrogenase (NADP)	-
HBSAL_09555	OE_3636F	100d	m31	VNG_1874C	-	uncharacterized protein	-
HBSAL_09560	OE_3637R	100d	m31	VNG_1875G	hmgA	hydroxymethylglutaryl-CoA reductase (NADPH)	-
HBSAL_09565	OE_3639F	100d	m31	VNG_1877C	-	UPF0045 family protein	-
HBSAL_09570	OE_3641F	100d	m31	VNG_1879G	thiB2	ABC-type transport system periplasmic substrate-binding protein (probable substrate thiamine)	-
HBSAL_09575	OE_3642F	100d	m31	VNG_1880C	-	amidohydrolase domain protein	-
HBSAL_09580	OE_3644F	100d	m31	VNG_1882G	nadA	quinolinate synthase A	-
HBSAL_09585	OE_3646F	100d	m31	VNG_1883G	nadB	L-aspartate oxidase	-
HBSAL_09590	OE_3648F	100d	m31	VNG_1884G	nadC	nicotinate-nucleotide pyrophosphorylase (carboxylating)	-
HBSAL_09595	OE_3650R	100d	m31	VNG_1886C	-	TrmB family transcription regulator	-
HBSAL_09600	OE_3652F	100d	m31	VNG_1886a	-	Smr family transport protein	-
HBSAL_09605	OE_3653R	100d	m31	VNG_1887G	gpmI	phosphoglycerate mutase, 2,3-biphosphateglycerate-independent type	-
HBSAL_09610	OE_3654R	100d	m31	VNG_1889H	-	small CPxCG-related zinc finger protein	-
HBSAL_09615	OE_3655R	100d	m31	VNG_1890H	-	uncharacterized protein	-
HBSAL_09620	OE_3656F	100d	m31	VNG_1890a	-	uncharacterized protein	-
HBSAL_09625	OE_3659F	100d	m31	VNG_1891H	-	NurA domain protein	-

HBSAL_09630	OE_3661F	100d	m31	VNG_1893G	-	ABC-type transport system ATP-binding protein	-
HBSAL_09635	OE_3662F	100d	m31	VNG_1894C	-	uncharacterized protein	-
HBSAL_09640	OE_3665R	100d	m31	VNG_1895H	-	uncharacterized protein	-
HBSAL_09645	OE_3666F	100d	m31	VNG_1896C	-	arNOG05179 family protein (DUF87-related AAA-type ATPase)	-
HBSAL_09650	OE_3668F	100d	m31	VNG_1898C	-	UspA domain protein	-
HBSAL_09655	OE_3669R	100d	m31	VNG_1899G	-	KaiC domain protein	-
HBSAL_09660	OE_3671F	100d	m31	VNG_1900C	nadK1	probable NAD kinase (polyphosphate/ATP)	-
HBSAL_09665	OE_3673F	100d	m31	VNG_1901C	mptA	GTP cyclohydrolase MptA	-
HBSAL_09670	OE_3676R	100d	m31	VNG_1902H	-	DUF4870 family protein	-
HBSAL_09675	OE_3678R	100d	m31	VNG_1903C	-	TrmB family transcription regulator	-
HBSAL_09680	OE_3680R	100d	m31	VNG_1904H	-	uncharacterized protein	-
HBSAL_09685	OE_3681R	100d	m31	VNG_1905C	-	YyaL family protein	-
HBSAL_09690	OE_3682F	100d	m31	VNG_1906H	fxsA	FxsA domain protein	-
HBSAL_09695	OE_3686F	100d	m31	VNG_1907H	-	uncharacterized protein	-
HBSAL_09700	OE_3686A1F	100d	m31	VNG_1907a	-	uncharacterized protein	-
HBSAL_09705	OE_3687A1F	100d	m31	VNG_1907b	-	uncharacterized protein	-
HBSAL_09710	OE_3688F	100d	m31	VNG_1910H	-	uncharacterized protein	-
HBSAL_09715	OE_3689R	100d	m31	VNG_1911G	ahbA	siroheme decarboxylase AhbA	-
HBSAL_09720	OE_3691F	100d	m31	VNG_1912G	trpD2	probable phosphoribosyltransferase (homolog to anthranilate phosphoribosyltransferase)	-
HBSAL_09725	OE_3693F	100d	m31	VNG_1914G	ppiA	CYPL-type peptidylprolyl isomerase	-
HBSAL_09730	OE_3696F	100d	m31	VNG_1916H	-	uncharacterized protein	-
HBSAL_09735	OE_3695F	100d	m31	VNG_1917H	-	UCP030561 family protein	-
HBSAL_09740	OE_3699R	100d	m31	VNG_1918C	pcrB2	(S)-3-O-geranylgeranylglycerol phosphate synthase 2	-
HBSAL_09745	OE_3703R	100d	m31	VNG_1919H	crcB1	putative fluoride ion transport protein CrcB	-
HBSAL_09750	OE_3704R	100d	m31	VNG_1921H	crcB2	putative fluoride ion transport protein CrcB	-
HBSAL_09755	OE_3706F	100d	m31	VNG_1920H	-	uncharacterized protein	-
HBSAL_09760	OE_3708R	100d	m31	VNG_1922G	-	Lrp/AsnC family transcription regulator	-

HBSAL_09765	OE_3710R	100d	m31	VNG_1924G	trkA6	TrkA domain protein	-
HBSAL_09770	OE_3711F	100d	m31	VNG_1925H	-	Lrp/AsnC family transcription regulator	-
HBSAL_09775	OE_3712R	100d	m31	VNG_1926G	oxdhA2	probable branched-chain amino acid dehydrogenase E1 component alpha subunit	-
HBSAL_09780	OE_3714F	100d	m31	VNG_1927H	-	uncharacterized protein	-
HBSAL_09785	OE_3715R	100d	m31	VNG_1929G	tmk	thymidylate kinase	-
HBSAL_09790	OE_3717F	100d	m31	VNG_1932G	noIA	arNOG06768 family NADH-binding domain protein	-
HBSAL_09795	OE_3718F	100d	m31	VNG_1933G	cetZ1	FtsZ family protein CetZ, type III	-
HBSAL_09800	OE_3719F	100d	m31	VNG_1934H	-	uncharacterized protein	-
HBSAL_09805	OE_3721F	100d	m31	VNG_1935C	cofC	2-phospho-L-lactate guanylyltransferase	-
HBSAL_09810	OE_3722F	100d	m31	VNG_1937C	cofG	7,8-didemethyl-8-hydroxy-5-deazariboflavin synthase	-
HBSAL_09815	OE_3723R	100d	m31	VNG_1938C	cofH	5-amino-6-(D-ribitylamino)uracil--L-tyrosine 4-hydroxyphenyl transferase	-
HBSAL_09820	OE_3724F	100d	m31	VNG_1939G	purC	phosphoribosylaminoimidazole-succinocarboxamide synthase	-
HBSAL_09825	OE_3724D1F	100d	m31	VNG_1939a	-	VanZ family protein	pseudo(91-R6;R1;NRC-1)
HBSAL_09830	OE_3725F	100d	m31	VNG_1940H	-	uncharacterized protein	-
HBSAL_09835	OE_3726F	100d	m31	VNG_1941C	-	TIGR01210 family protein	-
HBSAL_09840	OE_3728R	100d	m31	VNG_1942H	-	uncharacterized protein	-
HBSAL_09845	OE_3730R	100d	m31	VNG_1943H	-	uncharacterized protein	-
HBSAL_09850	OE_3731R	100d	m31	VNG_1945G	purQ	phosphoribosylformylglycinamide synthase subunit PurQ	-
HBSAL_09855	OE_3732R	100d	m31	VNG_1944C	purS	phosphoribosylformylglycinamide synthase subunit PurS	-
HBSAL_09860	OE_3735F	100d	m31	VNG_1946G	purU	formyltetrahydrofolate deformylase	-
HBSAL_09865	OE_3738F	100d	m31	VNG_1948H	-	AlkP-core domain protein	-
HBSAL_09870	OE_3739R	100d	m31	VNG_1949G	-	CBS domain protein	-
HBSAL_09875	OE_3740R	100d	m31	VNG_1951G	-	S8 family serine protease	-
HBSAL_09880	OE_3741R	100d	m31	VNG_1952H	-	probable secreted glycoprotein	-

HBSAL_09885	OE_3744R	100d	m31	VNG_1953C	-	probable secreted glycoprotein	-
HBSAL_09890	OE_3746R	100d	m31	VNG_1954H	-	homolog to phage PhiH1 repressor protein	-
HBSAL_09895	OE_3747C1R	100d	m31	VNG_1956a	-	uncharacterized protein	-
HBSAL_09900	OE_3748R	100d	m31	VNG_1957G	arcS	archaeosine synthase	-
HBSAL_09905	OE_3749R	100d	m31	VNG_1959G	tgtA	tRNA-guanine(15) transglycosylase	-
HBSAL_09910	OE_3750R	100d	m31	VNG_1960H	-	uncharacterized protein	-
HBSAL_09915	OE_3752R	100d	m31	VNG_1962C	-	NUDIX family hydrolase	-
HBSAL_09920	OE_3755R	100d	m31	VNG_1963a	-	uncharacterized protein	-
HBSAL_09925	OE_3759R	100d	m31	VNG_1964H	orc1 l	Orc1-type DNA replication protein	-
HBSAL_09930	OE_3761R	100d	m31	VNG_1965H	-	uncharacterized protein	-
HBSAL_09935	OE_3762R	100d	m31	VNG_1967G	glpK	glycerol kinase	-
HBSAL_09940	OE_3763F	100d	m31	VNG_1969G	glpA1	glycerol-3-phosphate dehydrogenase subunit A	-
HBSAL_09945	OE_3764F	100d	m31	VNG_1971G	glpB	glycerol-3-phosphate dehydrogenase subunit B	-
HBSAL_09950	OE_3765F	100d	m31	VNG_1972G	glpC	glycerol-3-phosphate dehydrogenase subunit C	-
HBSAL_09955	OE_3766R	100d	m31	VNG_1973H	-	uncharacterized protein	-
HBSAL_09960	OE_3768F	100d	m31	VNG_1974H	-	DUF1628 domain protein	-
HBSAL_09965	OE_3769F	100d	m31	VNG_1976H	-	homolog to phage PhiH1 repressor protein	-
HBSAL_09970	OE_3770F	100d	m31	VNG_1977H	-	AAA-4 family protein	-
HBSAL_09975	OE_3771F	100d	m31	VNG_1978H	-	uncharacterized protein	-
HBSAL_09980	OE_3775R	100d	m31	VNG_1980C	trmY	tRNA (pseudouridine(54)-N(1))-methyltransferase	-
HBSAL_09985	OE_3777R	100d	m31	VNG_1983a	-	uncharacterized protein	-
HBSAL_09990	OE_3778F	100d	m31	VNG_1982C	pus10	tRNA pseudouridine synthase Pus10	-
HBSAL_09995	OE_3780F	100d	m31	VNG_1984G	rnhB	ribonuclease H, type 2	-
HBSAL_10000	OE_3782R	100d	m31	VNG_1985C	nhaC3	probable NhaC-type sodium/proton antiporter	-
HBSAL_10005	OE_3783F	100d	m31	VNG_1986C	nucS2	endonuclease NucS	-
HBSAL_10010	OE_3784R	100d	m31	VNG_1987G	secD	protein-export membrane protein SecD	-
HBSAL_10015	OE_3787R	100d	m31	VNG_1988G	secF	protein-export membrane protein SecF	-
HBSAL_10020	OE_3789R	100d	m31	VNG_1989H	-	uncharacterized protein	-
HBSAL_10025	OE_3790R	100d	m31	VNG_1991H	-	uncharacterized protein	-

HBSAL_10030	OE_3792F	100d	m31	VNG_1992G	pgi	glucose-6-phosphate isomerase	-
HBSAL_10035	OE_3794F	100d	m31	VNG_1993H	-	Abi/CAAX domain protein	-
HBSAL_10040	OE_3796R	100d	m31	VNG_1994C	nob1	rRNA maturation endonuclease Nob1	-
HBSAL_10045	OE_3798R	100d	m31	VNG_1995C	-	PRC domain protein	-
HBSAL_10050	OE_3800F	99	m31	VNG_1997G	tif5B	translation initiation factor aIF-5B (bacterial-type IF2)	-
HBSAL_10055	OE_3802R	100d	m31	VNG_1998H	-	uncharacterized protein	-
HBSAL_10060	OE_3803R	100d	m31	VNG_1999H	pdaD	pyruvoyl-dependent arginine decarboxylase	-
HBSAL_10065	OE_3805R	100d	m31	VNG_2000G	pan1	proteasome-activating nucleotidase	-
HBSAL_10070	OE_3807R	100d	m31	VNG_2001G	pepF	oligoendopeptidase PepF	-
HBSAL_10075	OE_3808F	100d	m31	VNG_2002H	ywaD2	probable M28 family peptidase (homolog to aminopeptidase YwaD)	-
HBSAL_10080	OE_3810R	100d	m31	VNG_2003G	truA	tRNA pseudouridine synthase TruA	-
HBSAL_10085	OE_3812R	100d	m31	VNG_2005G	hisS	histidine--tRNA ligase	-
HBSAL_10090	OE_3814R	100d	m31	VNG_2006C	-	uncharacterized protein	-
HBSAL_10095	OE_3815R	100d	m31	VNG_2008H	-	PDCD5 family DNA-binding protein	-
HBSAL_10100	OE_3817R	100d	m31	VNG_2010G	rps19e	30S ribosomal protein S19e	-
HBSAL_10105	OE_3818F	100d	m31	VNG_2011G	thiL	thiamine-monophosphate kinase	-
HBSAL_10110	OE_3820R	100d	m31	VNG_2012C	-	M50 family metalloprotease	-
HBSAL_10115	OE_3822R	100d	m31	VNG_2014H	-	uncharacterized protein	-
HBSAL_10120	OE_3822A1F	100d	m31	VNG_2014a	-	uncharacterized protein	-
HBSAL_10125	OE_3823F	100d	m31	VNG_2015C	pyrH	uridylate kinase	-
HBSAL_10130	OE_3826F	100d	m31	VNG_2017G	lysS	lysine--tRNA ligase	-
HBSAL_10135	OE_3828F	100d	m31	VNG_2019C	-	M50 family metalloprotease	-
HBSAL_10140	OE_3829R	100d	m31	VNG_2020C	-	PadR family transcription regulator	-
HBSAL_10145	OE_3832F	100d	m31	VNG_2021C	hemQ	coproheme decarboxylase HemQ	-
HBSAL_10150	OE_3832C1R	100d	m31	VNG_2021a	-	uncharacterized protein	-
HBSAL_10155	OE_3834R	100d	m31	VNG_2023G	-	probable oxidoreductase (aldo-keto reductase family protein)	-
HBSAL_10160	OE_3835F	100d	m31	VNG_2024H	-	uncharacterized protein	-



HBSAL_10165	OE_3836F	100d	m31	VNG_2025G	-	O-acetyltransferase (homolog to galactoside O-acetyltransferase)	-
HBSAL_10170	OE_3839F	100d	m31	VNG_2027H	-	small CPxCG-related zinc finger protein	-
HBSAL_10175	OE_3838F	100d	m31	VNG_2028H	-	uncharacterized protein	-
HBSAL_10180	OE_3842R	100d	m31	VNG_2029H	-	uncharacterized protein	-
HBSAL_10185	OE_3843F	100d	m31	VNG_2031G	nadE	NAD synthase, ammonia-dependent	-
HBSAL_10190	OE_3846R	100d	m31	VNG_2032G	fadA1	enoyl-CoA hydratase	-
HBSAL_10195	OE_3849F	100d	m31	VNG_2034a	-	uncharacterized protein	-
HBSAL_10200	OE_3852F	100d	m31	VNG_2035H	-	uncharacterized protein	-
HBSAL_10205	OE_3854R	100d	m31	VNG_2036G	-	receiver box response regulator	-
HBSAL_10210	OE_3855R	100d	m31	VNG_2037C	-	sensor box histidine kinase	-
HBSAL_10215	OE_3859F	100d	m31	VNG_2039H	-	uncharacterized protein	-
HBSAL_10220	OE_3859B1F	100d	m31	VNG_2041a	-	uncharacterized protein	-
HBSAL_10225	OE_3861F	100d	m31	VNG_2042H	-	uncharacterized protein	-
HBSAL_10230	OE_3863R	100d	m31	VNG_2043G	ham1	XTP/dITP diphosphatase	-
HBSAL_10235	OE_3864R	100d	m31	VNG_2044H	-	uncharacterized protein	-
HBSAL_10240	OE_3866R	100d	m31	VNG_2045G	kae1	KEOPS complex subunit Kae1/Bud32	-
HBSAL_10245	OE_3868R	100d	m31	VNG_2047G	rps31e	30S ribosomal protein S31e	-
HBSAL_10250	OE_3869R	100d	m31	VNG_2048G	rps24e	30S ribosomal protein S24e	-
HBSAL_10255	OE_3871R	100d	m31	VNG_2049C	-	UPF0218 family protein	-
HBSAL_10260	OE_3872R	100d	m31	VNG_2051G	spt4	transcription elongation factor Spt4	-
HBSAL_10265	OE_3874R	100d	m31	VNG_2053G	rpoE1	DNA-directed RNA polymerase subunit E	-
HBSAL_10270	OE_3875R	100d	m31	VNG_2054H	-	DUF188 family protein	-
HBSAL_10275	OE_3876R	100d	m31	VNG_2056G	tif2c	translation initiation factor aIF-2 gamma subunit	-
HBSAL_10280	OE_3879F	100d	m31	VNG_2059H	-	uncharacterized protein	-
HBSAL_10285	OE_3881R	100d	m31	VNG_2060G	-	beta-lactamase domain protein	-
HBSAL_10290	OE_3882R	100d	m31	VNG_2062G	aaa7	arNOG05511 family protein (AAA-type ATPase core domain protein)	-
HBSAL_10295	OE_3883R	100d	m31	VNG_2064H	-	TIGR03663 family protein	-
HBSAL_10300	OE_3884F	100d	m31	VNG_2063G	acaB3	acetyl-CoA C-acyltransferase	-

HBSAL_10305	OE_3887F	100d	m31	VNG_2065G	gtl3	probable glycosyltransferase, type 2	-
HBSAL_10310	OE_3888F	100d	m31	VNG_2067H	-	GtrA family protein	-
HBSAL_10315	OE_3889R	100d	m31	VNG_2068C	kef1	Kef-type transport system	-
HBSAL_10320	OE_3891R	100d	m31	VNG_2071G	acs5	acyl-CoA synthetase	-
HBSAL_10325	OE_3892R	100d	m31	VNG_2073C	-	beta-lactamase domain protein	-
HBSAL_10330	OE_3893F	100d	m31	VNG_2072G	serS	serine--tRNA ligase	-
HBSAL_10335	OE_3894R	100d	m31	VNG_2074H	-	DUF1486 family protein	-
HBSAL_10340	OE_3895F	100d	m31	VNG_2075C	-	probable 16S rRNA maturation protein	-
HBSAL_10345	OE_3898F	100d	m31	VNG_2076G	rpl40e	50S ribosomal protein L40e	-
HBSAL_10350	OE_3899R	100d	m31	VNG_2079G	-	NUDIX family hydrolase	-
HBSAL_10355	OE_3901R	100d	m31	VNG_2078G	-	GNAT family acetyltransferase	-
HBSAL_10360	OE_3902R	100d	m31	VNG_2080C	-	beta-lactamase domain protein	-
HBSAL_10365	OE_3903F	100d	m31	VNG_2081H	-	uncharacterized protein	-
HBSAL_10370	OE_3905F	100d	m31	VNG_2081a	-	UPF0215 family protein	-
HBSAL_10375	OE_3906F	100d	m31	VNG_2082G	udg	uracil-DNA glycosylase	-
HBSAL_10380	OE_3907R	100d	m31	VNG_2084G	phnE	ABC-type transport system permease protein (probable substrate phosphate/phosphonate)	-
HBSAL_10385	OE_3908R	100d	m31	VNG_2085G	phnC	ABC-type transport system ATP-binding protein (probable substrate phosphate/phosphonate)	-
HBSAL_10390	OE_3910R	100d	m31	VNG_2086G	phnD	ABC-type transport system periplasmic substrate-binding protein (probable substrate phosphate/phosphonate)	-
HBSAL_10395	OE_3913F	100d	m31	VNG_2087G	hisH	imidazole glycerol-phosphate synthase subunit HisH	-
HBSAL_10400	OE_3914R	100d	m31	VNG_2087a	-	SWIM zinc finger domain protein	-
HBSAL_10405	OE_3917F	100d	m31	VNG_2088G	trm1	tRNA (guanine(26)-N(2))-dimethyltransferase	-
HBSAL_10410	OE_3919F	100d	m31	VNG_2089H	-	uncharacterized protein	-
HBSAL_10415	OE_3921F	100d	m31	VNG_2091H	-	probable PAP2-type phosphatase	-
HBSAL_10420	OE_3922R	100d	m31	VNG_2093G	glnA	glutamine synthetase	-
HBSAL_10425	OE_3923F	100d	m31	VNG_2094G	lrp	Lrp/AsnC family global transcription regulator Lrp	-
HBSAL_10430	OE_3925R	100d	m31	VNG_2096G	ths2	thermosome subunit 2	-

HBSAL_10435	OE_3927F	100p	m31	VNG_2097C	-	DUF418 domain protein	-
HBSAL_10440	OE_3929R	98	m31	VNG_2098H	-	uncharacterized protein	-
HBSAL_10445	OE_3930R	100d	m31	VNG_2099C	ridA	enamine/imine deaminase	-
HBSAL_10450	OE_3931R	99	m31	VNG_2100G	ilvA	threonine ammonia-lyase	-
HBSAL_10455	OE_3933F	95	m31	VNG_2101H	-	uncharacterized protein	-
HBSAL_10460	OE_3934R	99	m31	VNG_2102G	citZ	citrate synthase	-
HBSAL_10465	OE_3936F	99	m31	VNG_2104G	pchB	PhoU/TrkA-C domain protein	-
HBSAL_10470	OE_3937R	100p	m31	VNG_2105H	-	uncharacterized protein	-
HBSAL_10475	OE_3940F	100p	m31	VNG_2106G	-	AstE domain protein	-
HBSAL_10480	OE_3941F	99	m31	VNG_2108G	thrC3	threonine synthase	-
HBSAL_10485	OE_3942R	100d	m31	VNG_2109H	-	uncharacterized protein	-
HBSAL_10490	OE_3943R	99	m31	VNG_2110C	tiaS	tRNA(Ile2) 2-agmatinylcytidine synthetase TiaS	-
HBSAL_10495	OE_3946F	100p	m31	VNG_2112C	-	cro/C1 family transcription regulator	-
HBSAL_10500	OE_3947R	99	m31	VNG_2113C	mscS3	mechanosensitive channel protein MscS	-
HBSAL_10505	OE_3949R	100d	m31	VNG_2115H	grx1	glutaredoxin	-
HBSAL_10510	OE_3950R	99	m31	VNG_2116C	uraA	xanthine/uracil permease family transport protein	-
HBSAL_10515	OE_3951R	100p	m31	VNG_2117C	apt2	purine phosphoribosyltransferase (adenine phosphoribosyltransferase, xanthine-guanine phosphoribosyltransferase)	-
HBSAL_10520	OE_3953R	100p	m31	VNG_2118G	pyrE2	orotate phosphoribosyltransferase	-
HBSAL_10525	OE_3954R	98	m31	VNG_2119C	carS	CDP-2,3-bis-(O-geranylgeranyl)-sn-glycerol synthase	-
HBSAL_10530	OE_3955F	100p	m31	VNG_2120G	fadM	proline dehydrogenase	-
HBSAL_10535	OE_3958F	99	m31	VNG_2121C	-	DUF502 family protein	-
HBSAL_10540	OE_3959R	100p	m31	VNG_2122G	ilvE2	branched-chain amino acid aminotransferase	-
HBSAL_10545	OE_3960F	99	m31	VNG_2123G	nhaC2	probable NhaC-type sodium/proton antiporter	-
HBSAL_10550	OE_3961R	99	m31	VNG_2124C	nhaC4	probable NhaC-type sodium/proton antiporter	-
HBSAL_10555	OE_3963R	100p	m31	VNG_2125G	ribB	3,4-dihydroxy-2-butanone 4-phosphate synthase	-
HBSAL_10560	OE_3964R	100p	m31	VNG_2126C	ribK	riboflavin kinase, CTP-dependent	-
HBSAL_10565	OE_3967R	99	m31	VNG_2128C	taw1	tRNA-(4-demethylwyosine) synthase, S-adenosyl-	-

						L-methionine-dependent	
HBSAL_10570	OE_3970R	100d	m31	VNG_2129H	-	uncharacterized protein	-
HBSAL_10575	OE_3971R	99	m31	VNG_2130G	-	ParA domain protein	-
HBSAL_10580	OE_3973F	100p	m31	VNG_2131G	arf1	peptide chain release factor aRF-1	-
HBSAL_10585	OE_3974R	99	m31	VNG_2132G	fer1	DnaJ N-terminal domain / ferredoxin fusion protein	-
HBSAL_10590	OE_3977R	99	m31	VNG_2133H	-	small CPxCG-related zinc finger protein	-
HBSAL_10595	OE_3978R	100d	m31	VNG_2135G	atpD	A-type ATP synthase subunit D	-
HBSAL_10600	OE_3980R	100p	m31	VNG_2136G	blh	beta-carotene 15,15'-dioxygenase Blh	-
HBSAL_10605	OE_3983R	98	m31	VNG_2137G	crtY	lycopene beta-cyclase	-
HBSAL_10610	OE_3984R	99	m31	VNG_2138G	atpB	A-type ATP synthase subunit B	-
HBSAL_10615	OE_3985R	100p	m31	VNG_2139G	atpA	A-type ATP synthase subunit A	-
HBSAL_10620	OE_3986R	100d	m31	VNG_2140G	atpF	A-type ATP synthase subunit F	-
HBSAL_10625	OE_3987R	99	m31	VNG_2141G	atpC	A-type ATP synthase subunit C	-
HBSAL_10630	OE_3988R	100p	m31	VNG_2142G	atpE	A-type ATP synthase subunit E	-
HBSAL_10635	OE_3989R	100d	m31	VNG_2143G	atpK	A-type ATP synthase subunit K	-
HBSAL_10640	OE_3991R	99	m31	VNG_2144G	atpI	A-type ATP synthase subunit I	-
HBSAL_10645	OE_3992R	100d	m31	VNG_2146H	atpH	A-type ATP synthase subunit H	-
HBSAL_10650	OE_3994F	100d	m31	VNG_2147G	menG	probable demethylmenaquinone methyltransferase	-
HBSAL_10655	OE_3996R	100p	m31	VNG_2147a	-	DUF1628 domain protein	-
HBSAL_10660	OE_3998R	99	m31	VNG_2148H	-	uncharacterized protein	-
HBSAL_10665	OE_4002F	98	m31	VNG_2149H	-	probable transmembrane glycoprotein / HTH domain protein	-
HBSAL_10670	OE_4005F	99	m31	VNG_2150G	etfB	electron transfer flavoprotein beta subunit	-
HBSAL_10675	OE_4007F	100p	m31	VNG_2151G	etfA	electron transfer flavoprotein alpha subunit	-
HBSAL_10680	OE_4008R	99	m31	VNG_2152C	-	UPF0098 family protein	-
HBSAL_10685	OE_4010F	99	m31	VNG_2153G	idsA2	bifunctional short chain isoprenyl diphosphate synthase	-
HBSAL_10690	OE_4011R	100p	m31	VNG_2154C	-	DUF373 family protein	-
HBSAL_10695	OE_4012F	99	m31	VNG_2155C	-	uncharacterized protein	-
HBSAL_10700	OE_4013R	98	m31	VNG_2156C	-	TIGR03663 family protein	-

HBSAL_10705	OE_4018F	100d	m31	VNG_2157C	-	TRAM domain protein	-
HBSAL_10710	OE_4021F	98	m31	VNG_2158G	-	probable oxidoreductase (short-chain dehydrogenase family)	-
HBSAL_10715	OE_4022R	99	m31	VNG_2159G	manC	mannose-1-phosphate guanylyltransferase	-
HBSAL_10720	OE_4023F	100p	m31	VNG_2160C	rpa3	replication protein A	-
HBSAL_10725	OE_4025F	99	m31	VNG_2162C	rpap3	rpa-associated protein	-
HBSAL_10730	OE_4027F	99	m31	VNG_2163H	-	CopG domain protein	-
HBSAL_10740	OE_4028R	99	m32	VNG_2164C	-	uncharacterized protein	-
HBSAL_10745	OE_4030F	99	m32	VNG_2165H	-	DUF4098 family protein	-
HBSAL_10750	OE_4032R	99	m32	VNG_2166C	-	probable oxidoreductase (homolog to saccharopine dehydrogenase)	-
HBSAL_10755	OE_4033R	98	m32	VNG_2167G	-	homolog to helicase	-
HBSAL_10760	OE_4034R	99	m32	VNG_2168C	-	M50 family metalloprotease	-
HBSAL_10765	OE_4036R	99	m32	VNG_2171G	-	probable oxidoreductase (iron-containing alcohol dehydrogenase family)	-
HBSAL_10770	OE_4039F	100p	m32	VNG_2170H	-	cupin 2 barrel domain protein	-
HBSAL_10775	OE_4040R	98	m32	VNG_2172C	-	APH family phosphotransferase	-
HBSAL_10780	OE_4041F	99	m32	VNG_2173G	ashA	archaea-specific helicase AshA	-
HBSAL_10795	OE_4047R	91	d33/ m33	VNG_2178H	-	homolog to phage PhiH1 repressor protein	LowSim; traverse_junction
HBSAL_10800	OE_4049R	99	m33	VNG_2178a	-	uncharacterized protein	-
HBSAL_10805	OE_4050F	99	m33	VNG_2179H	-	DUF1628 domain protein	-
HBSAL_10810	OE_4051R	99	m33	VNG_2180C	-	sensor box histidine kinase	-
HBSAL_10815	OE_4052F	99	m33	VNG_2181G	mcm	ATP-dependent DNA helicase MCM (intein-containing)	-
HBSAL_10820	OE_4054F	100d	m33	VNG_2182H	-	uncharacterized protein	-
HBSAL_10825	OE_4055F	98	m33	VNG_2183H	-	uncharacterized protein	-
HBSAL_10830	OE_4056R	100p	m33	VNG_2184G	tfbA7	transcription initiation factor TFB	-
HBSAL_10835	OE_4059F	99	m33	VNG_2185H	-	uncharacterized protein	-
HBSAL_10840	OE_4060R	99	m33	VNG_2185a	-	ParA domain protein	-
HBSAL_10845	OE_4065R	100p	m33	VNG_2186G	hit1	histidine triad family protein (homolog to bis(5'-	-

						nucleosyl)-tetraphosphatase)	
HBSAL_10850	OE_4067R	100p	m33	VNG_2187H	-	uncharacterized protein	-
HBSAL_10855	OE_4066F	100d	m33	VNG_2189H	-	uncharacterized protein	-
HBSAL_10860	OE_4068F	99	m33	VNG_2190G	ileS	isoleucine--tRNA ligase	-
HBSAL_10865	OE_4069R	100p	m33	VNG_2191H	-	uncharacterized protein	-
HBSAL_10870	OE_4070R	99	m33	VNG_2193G	cbaA	ba3-type terminal oxidase subunit I	-
HBSAL_10875	OE_4071R	100p	m33	VNG_2195G	cbaB	ba3-type terminal oxidase subunit II	-
HBSAL_10880	OE_4073R	99	m33	VNG_2196G	hcpB	halocyanin HcpB / cbaD domain protein	seqdiff(R1/NRC-1)
HBSAL_10885	OE_4077F	100p	m33	VNG_2197H	-	uncharacterized protein	-
HBSAL_10890	OE_4080F	99	m33	VNG_2199H	-	uncharacterized protein	-
HBSAL_10895	OE_4082F	99	m33	VNG_2201G	cpx	P-type transport ATPase (probable substrate copper/metal cation)	-
HBSAL_10900	OE_4083F	97	m33	VNG_2202H	-	uncharacterized protein	-
HBSAL_10905	OE_4085R	98	m33	VNG_2203G	prsA	ribose-phosphate pyrophosphokinase	-
HBSAL_10910	OE_4089R	100p	m34	VNG_2204H	-	uncharacterized protein	-
HBSAL_10915	OE_4093F	100d	m34	VNG_2205H	-	uncharacterized protein	-
HBSAL_10920	OE_4094F	100d	m34	VNG_2206G	pmm1	phosphohexomutase (phosphoglucomutase / phosphomannomutase)	-
HBSAL_10925	OE_4099R	100d	m34	VNG_2207H	-	uncharacterized protein	-
HBSAL_10930	OE_4101R	100d	m34	VNG_2208G	trpS1	tryptophan--tRNA ligase	-
HBSAL_10935	OE_4102R	100d	m34	VNG_2210G	endA	tRNA-splicing endonuclease	-
HBSAL_10940	OE_4103R	100d	m34	VNG_2211H	-	homolog to DNA topoisomerase 1	-
HBSAL_10945	OE_4105R	100d	m34	VNG_2213G	brr2	DEAD/DEAH box helicase	-
HBSAL_10950	OE_4110R	100d	m34	VNG_2214G	-	MATE efflux family protein	-
HBSAL_10955	OE_4111F	100d	m34	VNG_2216G	lipA	lipoate synthase	-
HBSAL_10960	OE_4113F	100d	m34	VNG_2217G	oxdhA1	2-oxo-3-methylvalerate dehydrogenase E1 component alpha subunit	-
HBSAL_10965	OE_4114F	100d	m34	VNG_2218G	oxdhB	2-oxo-3-methylvalerate dehydrogenase E1 component beta subunit	-
HBSAL_10970	OE_4115F	100d	m34	VNG_2219G	dsa	dihydrolipoamide S-acyltransferase	-
HBSAL_10975	OE_4116F	100d	m34	VNG_2220G	lpdA	dihydrolipoyl dehydrogenase	-

HBSAL_10980	OE_4117F	100d	m34	VNG_2222G	pheA	prephenate dehydratase	-
HBSAL_10985	OE_4118R	100d	m34	VNG_2223G	leuS	leucine--tRNA ligase	-
HBSAL_10990	OE_4121R	100d	m34	VNG_2224G	ala	alanine dehydrogenase	-
HBSAL_10995	OE_4122R	100d	m34	VNG_2226G	ths1	thermosome subunit 1	-
HBSAL_11000	OE_4124R	100d	m34	VNG_2227C	dim2	probable ribosome biogenesis protein Dim2	-
HBSAL_11005	OE_4127R	100d	m34	VNG_2230H	-	HTH domain protein	-
HBSAL_11010	OE_4129R	100d	m34	VNG_2231C	-	major facilitator superfamily transport protein	-
HBSAL_11015	OE_4132R	99	m34	VNG_2232G	trpS2	tryptophan--tRNA ligase	-
HBSAL_11020	OE_4133R	99	m34	VNG_2233C	rio1	RIO-type serine/threonine protein kinase Rio1	-
HBSAL_11025	OE_4136R	100d	m34	VNG_2234G	tif1A1	translation initiation factor aIF-1A	-
HBSAL_11030	OE_4137F	98	m34	VNG_2236H	-	uncharacterized protein	-
HBSAL_11040	OE_4139R	98	m35	VNG_2237G	tyrS	tyrosine--tRNA ligase	-
HBSAL_11050	OE_4140R	99	m36	VNG_2238C	-	DUF460 domain protein	-
HBSAL_11055	OE_4141R	100p	m36	VNG_2239C	rnz	ribonuclease Z	-
HBSAL_11060	OE_4142F	99	m36	VNG_2240G	rfcC	replication factor C small subunit	-
HBSAL_11065	OE_4143F	98	m36	VNG_2241H	-	uncharacterized protein	-
HBSAL_11070	OE_4144R	99	m36	VNG_2242C	trmG10	tRNA (guanine(10),N(2))-dimethyltransferase	-
HBSAL_11075	OE_4146F	100p	m36	VNG_2243G	tbp5	TATA-binding transcription initiation factor	-
HBSAL_11080	OE_4148F	96	m36	VNG_2244H	-	uncharacterized protein	-
HBSAL_11085	OE_4151F	100p	m36	VNG_2246H	-	uncharacterized protein	-
HBSAL_11090	OE_4152R	99	m36	VNG_2247G	hisG	ATP phosphoribosyltransferase	-
HBSAL_11095	OE_4153F	98	m36	VNG_2248H	-	uncharacterized protein	-
HBSAL_11100	OE_4157F	99	m36	VNG_2249G	mtaD	5-methylthioadenosine/S-adenosylhomocysteine deaminase	-
HBSAL_11105	OE_4159F	100p	m36	VNG_2251G	ahcY	adenosylhomocysteinase	-
HBSAL_11110	OE_4160F	100d	m36	VNG_2252G	hjc	Holliday junction resolvase Hjc	-
HBSAL_11115	OE_4162F	100d	m36	VNG_2253H	-	uncharacterized protein	-
HBSAL_11120	OE_4163R	100p	m36	VNG_2254C	priL	DNA primase large subunit	-
HBSAL_11125	OE_4164F	99	m36	VNG_2255C	psd	probable archaetidylserine decarboxylase	-
HBSAL_11130	OE_4165R	100p	m36	VNG_2256G	pcn	DNA polymerase sliding clamp	-

HBSAL_11135	OE_4167R	100p	m36	VNG_2257G	-	homolog to sodium/calcium antiporter	-
HBSAL_11140	OE_4169F	99	m36	VNG_2259C	ppcA	phosphoenolpyruvate carboxylase	-
HBSAL_11145	OE_4171R	99	m36	VNG_2260H	-	uncharacterized protein	-
HBSAL_11150	OE_4173F	100p	m36	VNG_2262H	-	uncharacterized protein	-
HBSAL_11155	OE_4176R	100p	m36	VNG_2262a	-	esterase domain protein	-
HBSAL_11160	OE_4177F	99	m36	VNG_2263G	rlmE	23S rRNA (uridine-2'-O-) methyltransferase	-
HBSAL_11165	OE_4178R	99	m36	VNG_2264C	-	probable transport protein (probable substrate queuosine precursor)	-
HBSAL_11170	OE_4179R	100p	m36	VNG_2268H	-	CopG domain protein	-
HBSAL_11175	OE_4181R	99	m36	VNG_2267G	tatC2	Sec-independent protein translocase protein TatC	-
HBSAL_11180	OE_4182F	99	m36	VNG_2269G	tatC1	Sec-independent protein translocase protein TatC	-
HBSAL_11185	OE_4183F	99	m36	VNG_2270G	mutS5a	DNA mismatch repair protein MutS	-
HBSAL_11190	OE_4184F	100p	m36	VNG_2271G	orc12	Orc1-type DNA replication protein	-
HBSAL_11195	OE_4185F	100p	m36	VNG_2272G	rpiA	ribose-5-phosphate isomerase	-
HBSAL_11200	OE_4187R	100d	m36	VNG_2273H	-	uncharacterized protein	-
HBSAL_11205	OE_4187B1F	100d	m36	VNG_2273a	-	small CPxCG-related zinc finger protein	-
HBSAL_11210	OE_4189F	100d	m36	VNG_2274C	-	UPF0213 family protein	-
HBSAL_11215	OE_4190F	99	m36	VNG_2276G	pmm2	phosphohexomutase (phosphoglucomutase / phosphomannomutase)	-
HBSAL_11220	OE_4192R	98	m36	VNG_2277H	-	GNAT family acetyltransferase	-
HBSAL_11225	OE_4193R	98	m36	VNG_2279H	samp2	ubiquitin-like modifier protein SAMP2	-
HBSAL_11230	OE_4195F	99	m36	VNG_2280G	rfcA	replication factor C small subunit	-
HBSAL_11235	OE_4196R	99	m36	VNG_2281C	-	YqjG-type gamma-glutamylcysteinyl-hydroquinone reductase	-
HBSAL_11240	OE_4197F	98	m36	VNG_2282C	-	thioredoxin domain protein	-
HBSAL_11245	OE_4198F	99	m36	VNG_2283G	alaS	alanine--tRNA ligase	-
HBSAL_11250	OE_4199R	99	m36	VNG_2284G	hisI	phosphoribosyl-AMP cyclohydrolase	-
HBSAL_11255	OE_4201R	100p	m36	VNG_2285C	pibD	prepilin/prearchaellin peptidase	-
HBSAL_11260	OE_4204F	100d	m36	VNG_2286G	mamA	methylaspartate mutase small subunit	-
HBSAL_11265	OE_4206F	99	m36	VNG_2288G	mamB	methylaspartate mutase large subunit	-



HBSAL_11270	OE_4207F	99	m36	VNG_2289G	mal	methylaspartate ammonia-lyase	-
HBSAL_11275	OE_4209F	100p	m36	VNG_2290G	maoC1	MaoC domain protein	-
HBSAL_11280	OE_4211F	99	m36	VNG_2291G	cat	probable succinyl-CoA transferase	-
HBSAL_11285	OE_4213R	99	m36	VNG_2292H	-	DUF2029 family protein	-
HBSAL_11290	OE_4217R	100d	m36	VNG_2293G	fdx	ferredoxin (2Fe-2S)	-
HBSAL_11295	OE_4218F	99	m36	VNG_2294G	hisA	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	-
HBSAL_11300	OE_4220F	99	m36	VNG_2295G	hisB	imidazoleglycerol-phosphate dehydratase	-
HBSAL_11305	OE_4221R	100p	m36	VNG_2297H	-	uncharacterized protein	-
HBSAL_11310	OE_4222F	100d	m36	VNG_2296C	-	ACT domain protein	-
HBSAL_11315	OE_4223R	99	m36	VNG_2298H	-	uncharacterized protein	-
HBSAL_11320	OE_4224F	99	m36	VNG_2298a	-	IMPACT family protein	-
HBSAL_11325	OE_4225F	99	m36/ d37/ m37	VNG_2299H	-	ABC-type transport system periplasmic substrate-binding protein	pseudo(R1;NRC-1; internal_deletion)
HBSAL_11330	OE_4227F	98	m37	VNG_2301G	trxB3	oxidoreductase (homolog to thioredoxin-disulfide reductase)	-
HBSAL_11335	OE_4230F	99	m37	VNG_2302G	-	peptidase S9 family protein	-
HBSAL_11340	OE_4231R	98	m37	VNG_2304H	-	small CPxCG-related zinc finger protein	-
HBSAL_11345	OE_4234R	100p	m37	VNG_2305C	upp	uracil phosphoribosyltransferase	-
HBSAL_11350	OE_4235F	100d	m37	VNG_2306H	-	uncharacterized protein	-
HBSAL_11355	OE_4236F	99	m37	VNG_2307C	-	transport protein (probable substrate phosphate/sulfate)	-
HBSAL_11360	OE_4238R	100p	m37	VNG_2308G	-	DUF21/CBS domain protein	-
HBSAL_11365	OE_4239F	100p	m37	VNG_2310H	grx2	glutaredoxin	-
HBSAL_11370	OE_4240F	98	m37	VNG_2311H	-	peroxiredoxin domain protein	-
HBSAL_11375	OE_4244F	100p	m37	VNG_2312C	yrdC	L-threonylcarbamoyladenylate synthase	-
HBSAL_11380	OE_4245R	99	m37	VNG_2312a	-	DUF83 domain protein	-
HBSAL_11385	OE_4248R	99	m37	VNG_2313H	-	uncharacterized protein	-
HBSAL_11390	OE_4250R	100d	m37	VNG_2314H	-	uncharacterized protein	-

HBSAL_11395	OE_4252R	99	m37	VNG_2315H	-	uncharacterized protein	-
HBSAL_11400	OE_4255F	99	m37	VNG_2316C	bioY	biotin transport protein BioY	-
HBSAL_11405	OE_4256F	100p	m37	VNG_2317G	bioM	ABC-type transport system ATP-binding protein (probable substrate biotin)	-
HBSAL_11410	OE_4257C1F	99	m37	VNG_2317a	bioN	ABC-type transport system permease protein (probable substrate biotin)	-
HBSAL_11415	OE_4258F	99	m37	VNG_2320G	-	iron-sulfur protein (4Fe-4S)	-
HBSAL_11420	OE_4260R	98	m37	VNG_2321G	-	GNAT family acetyltransferase	-
HBSAL_11425	OE_4262B1F	96	m37	VNG_2321a	-	uncharacterized protein	-
HBSAL_11430	OE_4262F	99	m37	VNG_2322G	hemB	porphobilinogen synthase	-
HBSAL_11435	OE_4263F	96	m37/d3 8	VNG_2323H	-	Abi/CAAX domain protein	-
HBSAL_11440	OE_4268F	99	m38	VNG_2326G	hemL	glutamate-1-semialdehyde 2,1-aminomutase	-
HBSAL_11445	OE_4271F	98	m38	VNG_2328H	-	uncharacterized protein	-
HBSAL_11450	OE_4272F	98	m38	VNG_2329C	-	uncharacterized protein	-
HBSAL_11455	OE_4276F	98	m38	VNG_2330G	hemC	hydroxymethylbilane synthase (porphobilinogen deaminase)	-
HBSAL_11460	OE_4277F	100d	m38	VNG_2331G	sirA	uroporphyrin-III C-methyltransferase	-
HBSAL_11465	OE_4281F	99	m38	VNG_2332G	hemD	uroporphyrinogen-III synthase	-
HBSAL_11470	OE_4282F	99	m38	VNG_2333C	recJ1	single-stranded-DNA-specific exonuclease RecJ1	-
HBSAL_11475	OE_4283R	99	m38	VNG_2334C	-	receiver/sensor box histidine kinase	-
HBSAL_11480	OE_4289F	99	m38	VNG_2335H	-	uncharacterized protein	-
HBSAL_11485	OE_4292F	100p	m38	VNG_2337C	-	NifU C-terminal domain protein	-
HBSAL_11490	OE_4293R	99	m38	VNG_2338G	polD2	DNA-directed DNA polymerase D large subunit (intein-containing)	-
HBSAL_11495	OE_4294R	100d	m38	VNG_2339C	-	DUF296 family protein	-
HBSAL_11500	OE_4295R	100d	m38	VNG_2339a	-	uncharacterized protein	-
HBSAL_11505	OE_4296F	99	m38	VNG_2340H	-	uncharacterized protein	-
HBSAL_11510	OE_4298R	100d	m38	VNG_2341H	-	uncharacterized protein	-
HBSAL_11515	OE_4300R	99	m38	VNG_2342H	-	uncharacterized protein	-
HBSAL_11520	OE_4301R	100p	m38	VNG_2343G	dppF1	ABC-type transport system ATP-binding protein	-

						(probable substrate dipeptide/oligopeptide)	
HBSAL_11525	OE_4302R	99	m38	VNG_2344G	dppD1	ABC-type transport system ATP-binding protein (probable substrate dipeptide/oligopeptide)	-
HBSAL_11530	OE_4303R	99	m38	VNG_2346G	dppC1	ABC-type transport system permease protein (probable substrate dipeptide/oligopeptide)	-
HBSAL_11535	OE_4304R	100p	m38	VNG_2347G	dppB1	ABC-type transport system permease protein (probable substrate dipeptide/oligopeptide)	-
HBSAL_11540	OE_4305R	100p	m38	VNG_2349G	dppA1	ABC-type transport system periplasmic substrate-binding protein (probable substrate dipeptide/oligopeptide)	-
HBSAL_11545	OE_4306F	100d	m38	VNG_2351C	-	CBS domain protein	-
HBSAL_11550	OE_4307F	100p	m38	VNG_2352G	glyS	glycine--tRNA ligase	-
HBSAL_11555	OE_4308F	99	m38	VNG_2353H	-	uncharacterized protein	-
HBSAL_11560	OE_4310F	99	m38	VNG_2356G	hef	ATP-dependent RNA helicase/nuclease Hef	-
HBSAL_11565	OE_4311F	97	m38	VNG_2358G	dppA3	ABC-type transport system periplasmic substrate-binding protein (probable substrate dipeptide/oligopeptide)	-
HBSAL_11570	OE_4313F	100p	m38	VNG_2359G	dppB3	ABC-type transport system permease protein (probable substrate dipeptide/oligopeptide)	-
HBSAL_11575	OE_4316F	99	m38	VNG_2361G	dppC3	ABC-type transport system permease protein (probable substrate dipeptide/oligopeptide)	-
HBSAL_11580	OE_4317F	99	m38	VNG_2363G	dppD3	ABC-type transport system ATP-binding protein (probable substrate dipeptide/oligopeptide)	-
HBSAL_11585	OE_4318F	99	m38	VNG_2365G	dppF3	ABC-type transport system ATP-binding protein (probable substrate dipeptide/oligopeptide)	-
HBSAL_11590	OE_4320R	99	m38	VNG_2366C	-	UPF0148 family protein	-
HBSAL_11595	OE_4323F	99	m38	VNG_2367G	mdh	malate dehydrogenase	-
HBSAL_11600	OE_4324R	98	m38	VNG_2370C	fer6	ferredoxin (4Fe-4S)	-
HBSAL_11605	OE_4325F	99	m38	VNG_2368G	hel308a	ATP-dependent DNA helicase Hel308	-
HBSAL_11610	OE_4326F	100p	m38	VNG_2369C	cgi121	KEOPS complex subunit Cgi121	-
HBSAL_11615	OE_4329F	99	m38	VNG_2371C	purO	inosine-5'-monophosphate cyclohydrolase, archaeal-type	-
HBSAL_11620	OE_4330F	100p	m38	VNG_2372G	-	MJ0936 family phosphodiesterase	-

HBSAL_11625	OE_4331R	99	m38	VNG_2373G	tnaA	tryptophanase	-
HBSAL_11630	OE_4333R	100p	m38	VNG_2374G	lysC	aspartate kinase	-
HBSAL_11635	OE_4335F	100p	m38	VNG_2376H	-	acetyltransferase domain protein	-
HBSAL_11640	OE_4336R	97	m38	VNG_2377G	-	ABC-type transport system permease protein	-
HBSAL_11645	OE_4339R	99	m38	VNG_2378G	-	ABC-type transport system ATP-binding protein	-
HBSAL_11650	OE_4341R	100p	m38	VNG_2379H	-	uncharacterized protein	-
HBSAL_11655	OE_4343R	99	m38	VNG_2380H	-	uncharacterized protein	-
HBSAL_11660	OE_4344F	99	m38	VNG_2381G	uvrC	UvrABC system protein C	-
HBSAL_11665	OE_4345R	99	m38	VNG_2383G	nrdB1	ribonucleoside-diphosphate reductase beta subunit	pseudo(91-R6)
HBSAL_11670	OE_4353R	99	m39	VNG_2390G	uvrB	UvrABC system protein B	-
HBSAL_11675	OE_4354R	100p	m39	VNG_2392H	-	ferritin domain protein	-
HBSAL_11680	OE_4355R	98	m39	VNG_2393G	tssA1	TtuD family sulfurtransferase	-
HBSAL_11685	OE_4356F	98	m39	VNG_2394G	tssA2	rhodanese domain protein	-
HBSAL_11690	OE_4357F	98	m39	VNG_2395C	thiB1	ABC-type transport system periplasmic substrate-binding protein (probable substrate thiamine)	-
HBSAL_11695	OE_4358F	99	m39	VNG_2396G	thiP	ABC-type transport system permease protein (probable substrate thiamine)	-
HBSAL_11700	OE_4359F	99	m39	VNG_2397G	thiQ	ABC-type transport system ATP-binding protein (probable substrate thiamine)	-
HBSAL_11705	OE_4360R	99	m39	VNG_2398G	-	probable S-adenosylmethionine-dependent methyltransferase (homolog to 24-sterol C-methyltransferase)	-
HBSAL_11710	OE_4363F	98	m39	VNG_2399H	-	DUF2391 family protein	-
HBSAL_11715	OE_4365F	99	m39	VNG_2400H	-	uncharacterized protein	-
HBSAL_11720	OE_4367R	100p	m39	VNG_2403H	-	uncharacterized protein	-
HBSAL_11725	OE_4369R	100d	m39	VNG_2402H	-	uncharacterized protein	-
HBSAL_11730	OE_4370R	99	m39	VNG_2404G	-	MATE efflux family protein	-

**Table S1: Protein-coding genes on matchSEGs from the chromosomes of strains 91-R6 and R1.** As a basic rule, every protein-coding gene encoded on a matchSEG between strains 91-R6 and R1 has to be annotated in both strains. The locus tag of the corresponding strain is provided as code (**code**). For each gene, the protein name (**protein name**) and, if assigned, the gene (**gene**) is provided. Most of the genes can also be correlated with those from strain NRC-1. Missing gene calls in NRC-1 were resolved by post-

prediction. A hyphen indicates that the gene is absent from the NRC-1 chromosome. The protein sequence identity is reported (**seq id**). If the protein sequences are identical, it is indicated if the coding sequences are identical ("100d", identity at the DNA level) or if there are silent mutations ("100p", coding sequences differ but all mutations are silent so that the resulting proteins are identical). Sequences with less than 95% seq id are flagged in the comment column by "LowSim". Coding sequences are identical between strains R1 and NRC-1 with only few exceptions. These are flagged in the comment column by "seqdiff(R1/NRC-1)". The matchSEG serial number (**serial**) is indicated, preceded by "m". Genes which traverse the end of a matchSEG are flagged in the comment column by "traverse\_junction". If the gene traverses between matchSEGs (in case of indel with an insert in the other strain) the two serial numbers are separated by a slash ("/"). If the gene traverses from a matchSEG into an adjacent divSEG, the serial number of the divSEG is given, preceded by "d". Disrupted genes are flagged in the comment column by "pseudo()" with the affected strain(s) indicated within parentheses. If the gene has been targeted by a MGE (transposon or MITE), this is flagged by adding the term "split" within the parenthesis following pseudo. The targeted gene/gene set is indicated by square brackets around the code(s). In strain R1, only a single code is assigned, and the coding region is discontinuous. Even though biologically correct, EMBL/GenBank reject this annotation (as they forbid the resulting "join" feature for prokaryotic genomes). Therefore, it was decided to annotate the fragments of a targeted gene as independent ORFs in strains 91-R6 and NRC-1. Such ORF pairs are indicated as two codes within one square bracket. One protein-coding gene is disrupted in strains R1 and NRC-1 due to a large internal deletion. This is flagged in the comment column by "pseudo(R1;NRC-1;internal\_deletion)". The regular gene from strain 91-R6 traverses the end of more than one matchSEG. One protein-coding gene has a highly conserved 14aa tandem duplication only in strains R1 and NRC-1. This is flagged in the comment column as "insert(14aa;R1;NRC-1)".

code (91-R6)	code (R1)	seq id (%)	serial or plasmid	code (NRC-1)	gene	protein name	comment
HBSAL_04240	OE_6051F	96	d12/pHS2	VNG_6371G	-	homolog to restriction system mrr	-
HBSAL_04245	OE_6049R	100d	d12/pHS2	VNG_6370H	-	homolog to antitoxin VapB	-
HBSAL_04250	OE_6047A1R	99	d12/pHS2	VNG_6368a	-	homolog to endonuclease VapC	-
HBSAL_04255	OE_6046F	92	d12/pHS2	VNG_6367a	-	ArsR family transcription regulator	LowSim
HBSAL_04260	OE_6041R	92	d12/pHS2	VNG_6365H	-	uncharacterized protein	LowSim
HBSAL_04265	OE_6037R	51	d12/pHS2	VNG_6363G	orc5	Orc1-type DNA replication protein	LowSim; seqdiff(R1/NRC-1)
HBSAL_04275	[OE_6182R]; [OE_7062R]	89	d12/pHS1+2	VNG_6050G; VNG_6476G; VNG_7038; VNG_7171	tbp1	TATA-binding transcription initiation factor	LowSim; pseudo(R1;split)
HBSAL_04280	OE_6177F; OE_7057F	87	d12/pHS1+2	VNG_6048H; VNG_6478H; VNG_7037d; VNG_7171a	-	PadR family transcription regulator	LowSim
HBSAL_04345	OE_6036F	99	d12/pHS2	VNG_6362G	polB2	DNA-directed DNA polymerase B2	pseudo(91-R6)
HBSAL_04365	OE_7219R	65	d12/pHS1	VNG_7117a	-	FMN-binding domain protein	LowSim
HBSAL_04415	OE_7215F; OE_8047F	100d	d12/pHS1+4	VNG_7115	-	HD family hydrolase	-
HBSAL_04505	OE_6210B1R; OE_7090B1R	90	d12/pHS1+2	VNG_6077H; VNG_6449H; VNG_7057a; VNG_7151a	-	uncharacterized protein	LowSim
HBSAL_04510	OE_6209R; OE_7089R	89	d12/pHS1+2	VNG_6076H; VNG_6450H; VNG_7056; VNG_7153	-	XerC/D-like integrase	LowSim
HBSAL_04550	[OE_6125F]	96	d12/pHS2	VNG_6438G	tbp3	TATA-binding transcription initiation factor	pseudo(R1;split)
HBSAL_04560	OE_6213R; OE_7093R	100d	d12/pHS1+2	VNG_6081G; VNG_6445G;	idiB	isopentenyl-diphosphate delta-isomerase, type II	-

				VNG_7060; VNG_7149			
HBSAL_04565	OE_6212B1F; OE_7092B1F	100d	d12/pHS1+2	VNG_6080H; VNG_6446H; VNG_7059a; VNG_7149a	-	uncharacterized protein	-
HBSAL_04595	OE_6004F	86	d12/pHS2	VNG_6334H	-	uncharacterized protein	LowSim
HBSAL_04650	OE_5395B1F	100d	d12/pHS3	-	-	uncharacterized protein	-
HBSAL_04655	OE_5396R	100d	d12/pHS3	-	-	uncharacterized protein	-
HBSAL_04660	OE_5396B1F	100d	d12/pHS3	-	-	uncharacterized protein	pseudo(91-R6;R1)
HBSAL_04665	OE_5396A1F	100d	d12/pHS3	-	-	exodeoxyribonuclease VII large subunit	pseudo(91-R6;R1)
HBSAL_04670	OE_5397A1F	100d	d12/pHS3	-	-	uncharacterized protein	-
HBSAL_04675	OE_5398A1F	100d	d12/pHS3	-	-	uncharacterized protein	-
HBSAL_04680	OE_5400F	99	d12/pHS3	-	-	probable secreted glycoprotein	pseudo(R1)
HBSAL_04685	OE_5404F	100d	d12/pHS3	-	-	probable secreted glycoprotein	-
HBSAL_04690	OE_5405F	99	d12/pHS3	-	-	uncharacterized protein	pseudo(R1; split+translocated; C-term_OE_5013R)
HBSAL_04695	OE_5010R	100d	d12/pHS3	VNG_6145H	-	uncharacterized protein	pNRC200
HBSAL_04700	OE_5009R	100d	d12/pHS3	VNG_6144G	-	uncharacterized protein	pNRC200
HBSAL_04705	OE_5004R	100d	d12/pHS3	VNG_6143H	-	uncharacterized protein	pNRC200
HBSAL_04710	OE_5001R	100d	d12/pHS3	VNG_6142C	-	uncharacterized protein	pNRC200
HBSAL_04715	OE_5446F	100d	d12/pHS3	VNG_7119a	-	IS1341-type transposase	pseudo(91-R6;R1;NRC-1); pNRC100
HBSAL_04720	OE_5445R	100d	d12/pHS3	VNG_7120	-	uncharacterized protein	pNRC100
HBSAL_04725	OE_5444F	100d	d12/pHS3	VNG_7121	arsM	probable arsenite(III)-methyltransferase	pNRC100
HBSAL_04730	OE_5443F	100d	d12/pHS3	VNG_7122	arsR2	ArsR family transcription regulator ArsR2	pNRC100
HBSAL_04735	OE_5442A1F	100d	d12/pHS3	VNG_7122a	-	uncharacterized protein	pNRC100
HBSAL_04740	OE_5442F	100d	d12/pHS3	VNG_7122b	-	DUF964 family protein	pNRC100

HBSAL_04745	OE_5440F	100d	d12/pHS3	VNG_7123	arsA1	ArsA-type transport ATPase (probable substrate arsenite)	pNRC100
HBSAL_04750	OE_5438F	100d	d12/pHS3	VNG_7124	arsD	transcription regulator ArsD	pNRC100
HBSAL_04755	OE_5437R	100d	d12/pHS3	VNG_7125	arsR	ArsR family transcription regulator ArsR	pNRC100
HBSAL_04760	OE_5436R	100d	d12/pHS3	VNG_7126	arsC	arsenate reductase (glutaredoxin)	pNRC100
HBSAL_04765	OE_5434R	100d	d12/pHS3	VNG_7127	-	uncharacterized protein	pNRC100
HBSAL_04770	[OE_5433C1R]	99	d12/pHS3	VNG_7127b	-	uncharacterized protein	pseudo(R1;split); pseudo(NRC-1;split; N-term_part_unannotated); pNRC100
HBSAL_04775	OE_5431B1R	100d	d12/pHS3	VNG_7128a	-	uncharacterized protein	pNRC100
HBSAL_04780	OE_5431A1R	100d	d12/pHS3	VNG_7128b	-	uncharacterized protein	pNRC100
HBSAL_04785	OE_5431R	100d	d12/pHS3	VNG_7130	-	uncharacterized protein	pNRC100
HBSAL_04790	OE_5429R	100d	d12/pHS3	VNG_7131	-	uncharacterized protein	pNRC100
HBSAL_04795	OE_5428R	100d	d12/pHS3	VNG_7132	-	uncharacterized protein	pNRC100
HBSAL_04800	OE_5424R	100d	d12/pHS3	VNG_7134	-	uncharacterized protein	pNRC100
HBSAL_04805	OE_5423R	100d	d12/pHS3	VNG_7135	-	uncharacterized protein	pseudo(91-R6;R1;NRC-1); pNRC100
HBSAL_04810	OE_5419R	99	d12/pHS3	VNG_7136	-	uncharacterized protein	pseudo(R1;NRC-1); pNRC100
HBSAL_04875	OE_5417A1F	100d	d12/pHS3	-	-	uncharacterized protein	-
HBSAL_04880	OE_5417R	100d	d12/pHS3	-	-	small CPxCG-related zinc finger protein	-
HBSAL_04885	OE_5416A1R	100d	d12/pHS3	-	-	small CPxCG-related zinc finger protein	-
HBSAL_04890	OE_5415R	100d	d12/pHS3	-	-	uncharacterized protein	-
HBSAL_04895	OE_5414R	100d	d12/pHS3	-	-	ArsR family transcription regulator	-
HBSAL_04900	OE_5413F	99	d12/pHS3	-	-	homolog to restriction system mrr	-
HBSAL_04905	OE_5412R	100d	d12/pHS3	-	-	uncharacterized protein	-
HBSAL_04910	OE_5411A1R	100d	d12/pHS3	-	-	CopG domain protein	-
HBSAL_04915	OE_5410A1R	100d	d12/pHS3	-	-	RelE family protein	-



HBSAL_04920	OE_5409B1R	100d	d12/pHS3	-	-	HNH endonuclease domain protein	pseudo(91-R6;R1)
HBSAL_04925	OE_5409A1R	100d	d12/pHS3	-	-	uncharacterized protein	pseudo(91-R6;R1)
HBSAL_04930	OE_5408A1F	100d	d12/pHS3	-	-	TrmB family transcription regulator	-
HBSAL_04935	OE_6201F; OE_7081F	87	d12/pHS1+2	VNG_6071C; VNG_6455C; VNG_7052; VNG_7157	-	TSUP family transport protein	LowSim; pseudo(91-R6)
HBSAL_04940	OE_6200A1F; OE_7080A1F	89	d12/pHS1+2	VNG_6070H; VNG_6456H; VNG_7051a; VNG_7157a	-	uncharacterized protein	LowSim
HBSAL_04945	OE_6196R; OE_7076R	82	d12/pHS1+2	VNG_6065G; VNG_6461G; VNG_7048; VNG_7161	-	HTH-10 family transcription regulator	LowSim; pseudo(91-R6)
HBSAL_04950	OE_6195F; OE_7075F	88	d12/pHS1+2	VNG_6064G; VNG_6462G; VNG_7047; VNG_7162	-	transport protein (probable substrate phosphate/sulfate)	LowSim
HBSAL_04955	OE_6194F; OE_7074F	92	d12/pHS1+2	VNG_6062H; VNG_6464H; VNG_7046; VNG_7164	-	DUF4341/DUF395 family protein	LowSim
HBSAL_04960	OE_6192F; OE_7072F	95	d12/pHS1+2	VNG_6061H; VNG_6465H; VNG_7044; VNG_7165	-	DUF4341/DUF395 family protein	-
HBSAL_04965	OE_6191F; OE_7071F	90	d12/pHS1+2	VNG_6060C; VNG_6466C; VNG_7043; VNG_7166	-	rhodanese domain protein / beta-lactamase domain protein	LowSim
HBSAL_04970	OE_6190R; OE_7070R	90	d12/pHS1+2	VNG_6059C; VNG_6467C; VNG_7042;	-	UPF0033 family protein	LowSim

				VNG_7167			
HBSAL_04975	OE_6188R; OE_7068R	92	d12/pHS1+2	VNG_6057C; VNG_6469C; VNG_7041; VNG_7168	-	DsrE domain protein	LowSim
HBSAL_05025	OE_5395R	100d	d12/pHS3	-	aaa9	AAA-type ATPase core domain protein	-
HBSAL_05030; [HBSAL_12805; HBSAL_12815]; [HBSAL_13495; HBSAL_13505]	[OE_5394R]	99	d12/pHS3	-	-	uncharacterized protein	pseudo(R1;split); pseudo(91-R6; split_twice+translocated)
HBSAL_05040	OE_5350R	58	d12/pHS3	-	pglX	BREX type 5 system DNA methyltransferase PglX	LowSim; pseudo(91-R6)
HBSAL_05045	OE_5378R	42	d12/pHS3	-	brxA	BREX type 5 system protein BrxA	LowSim
HBSAL_05050	OE_5371R	41	d12/pHS3	-	brxC1	BREX type 5 system protein BrxC	LowSim
HBSAL_05055	OE_5370R	52	d12/pHS3	-	brxB	BREX type 5 system protein BrxB	LowSim
HBSAL_05060	OE_5366R	38	d12/pHS3	-	brxC2	BREX type 5 system protein BrxC	LowSim
HBSAL_05065	OE_5345R	38	d12/pHS3	-	pglZ	BREX type 5 system protein PglZ	LowSim
HBSAL_05975	OE_6028R	56	d18/pHS2	VNG_6354G	-	beta-lactamase domain protein	LowSim
HBSAL_05980	OE_6027R	45	d18/pHS2	VNG_6353H	-	DUF3006 family protein	LowSim
HBSAL_05995	OE_5252C1R	85	d18/pHS3	-	-	uncharacterized protein	LowSim
HBSAL_06275	OE_6156F	69	d18/pHS2	-	-	probable HNH-type endonuclease	LowSim
HBSAL_06290	OE_6152R	52	d18/pHS2	-	-	uncharacterized protein	LowSim; pseudo(91-R6)
HBSAL_12005	OE_5069F	99	pHSAL1/pHS3	VNG_6187G	orc13	Orc1-type DNA replication protein	pseudo(91-R6;R1;NRC-1); pNRC200
HBSAL_12010	OE_5069A1R	100d	pHSAL1/pHS3	VNG_6187a	-	uncharacterized protein	pNRC200
HBSAL_12015	OE_5070R	100d	pHSAL1/pHS3	VNG_6188H	-	uncharacterized protein	pNRC200
HBSAL_12020	OE_5071F	100d	pHSAL1/pHS3	VNG_6189H	-	PQQ repeat protein	pseudo(91-R6;R1;NRC-1); pNRC200
HBSAL_12025	OE_5072R	100d	pHSAL1/pHS3	VNG_6191H	-	RelE family protein	pseudo(91-R6;R1;NRC-1);

							pNRC200
HBSAL_12030	OE_5074R	100d	pHSAL1/pHS3	VNG_6193H	-	CopG domain protein	pNRC200
HBSAL_12035	OE_5075F	100d	pHSAL1/pHS3	VNG_6194H	-	uncharacterized protein	pNRC200
HBSAL_12040	OE_5076R	100d	pHSAL1/pHS3	VNG_6195H	-	small CPxCG-related zinc finger protein	pNRC200
HBSAL_12045	OE_5078F	100d	pHSAL1/pHS3	VNG_6196G	-	transport protein (probable substrate phosphate/sulfate)	pseudo(91-R6;R1;NRC-1); pNRC200
HBSAL_12050	OE_5080F	100d	pHSAL1/pHS3	VNG_6197H	-	uncharacterized protein	pseudo(91-R6;R1;NRC-1); pNRC200
HBSAL_12055	OE_5082R	100d	pHSAL1/pHS3	VNG_6199G	cdc48d	AAA-type ATPase (CDC48 subfamily)	pNRC200
HBSAL_12060	OE_5083R	100d	pHSAL1/pHS3	VNG_6201G	hsp20E	Hsp20-type molecular chaperone	pNRC200
HBSAL_12065	OE_5085R	100d	pHSAL1/pHS3	VNG_6203H	-	uncharacterized protein	pNRC200
HBSAL_12070	OE_5086R	100d	pHSAL1/pHS3	VNG_6203a	-	chimeric protein	pseudo(91-R6;R1;NRC-1); pNRC200
HBSAL_12075	OE_5089F	100d	pHSAL1/pHS3	VNG_6205C	-	UspA domain protein	pNRC200
HBSAL_12080	OE_5090F	100d	pHSAL1/pHS3	VNG_6206H	-	uncharacterized protein	pNRC200
HBSAL_12085	OE_5091F	100d	pHSAL1/pHS3	VNG_6208C	-	stomatin family protein	pNRC200
HBSAL_12090	OE_5093F	100d	pHSAL1/pHS3	VNG_6209H	-	homolog to HGPV8-ORF82	pNRC200
HBSAL_12095	OE_5094F	100d	pHSAL1/pHS3	VNG_6210G	dat	diaminobutyrate--2-oxoglutarate aminotransferase	pNRC200
HBSAL_12100	OE_5095F	100d	pHSAL1/pHS3	VNG_6211G	bdb	diaminobutyrate decarboxylase	pNRC200
HBSAL_12105	OE_5096F	100d	pHSAL1/pHS3	VNG_6212G	iucA	siderophore biosynthesis protein IucA	pNRC200
HBSAL_12110	OE_5097F	100d	pHSAL1/pHS3	VNG_6213G	iucB	probable N4-hydroxy-1-aminopropane O-acetyltransferase	pNRC200
HBSAL_12115	OE_5098F	100d	pHSAL1/pHS3	VNG_6214G	iucD	probable 1,3-diaminopropane N-3-monooxygenase	pNRC200
HBSAL_12120	OE_5099F	100d	pHSAL1/pHS3	VNG_6216G	iucC	siderophore biosynthesis protein IucC	pNRC200
HBSAL_12125	OE_5100R	100d	pHSAL1/pHS3	VNG_6218G	trkA3	TrkA domain protein	pNRC200
HBSAL_12130	OE_5101R	100d	pHSAL1/pHS3	VNG_6220G	cat2	transport protein (probable substrate cationic amino acids)	pNRC200
HBSAL_12135	OE_5102R	100d	pHSAL1/pHS3	VNG_6221H	-	IS1341-type transposase HsIRS6	pNRC200

HBSAL_12140	OE_5104A1R	100d	pHSAL1/pHS3	VNG_6222a	-	IS200-type transposase HsIRS6	pseudo(91-R6;R1;NRC-1); pNRC200
HBSAL_12145	OE_5106F	100d	pHSAL1/pHS3	VNG_6223C	trkA7	TrkA domain protein	pNRC200
HBSAL_12150	OE_5107R	100d	pHSAL1/pHS3	VNG_6224H	-	uncharacterized protein	pNRC200
HBSAL_12155	OE_5108F	100d	pHSAL1/pHS3	VNG_6225C	-	ParA domain protein	pNRC200
HBSAL_12160	OE_5110F	100d	pHSAL1/pHS3	VNG_6226H	-	uncharacterized protein	pNRC200
HBSAL_12165	OE_5112R	100d	pHSAL1/pHS3	VNG_6226a	gvpM	gas-vesicle-associated protein GvpM	pNRC200
HBSAL_12170	OE_5113R	100d	pHSAL1/pHS3	VNG_6229G	gvpL	gas-vesicle-associated protein GvpL	pNRC200
HBSAL_12175	OE_5114R	100d	pHSAL1/pHS3	VNG_6230G	gvpK	gas-vesicle operon protein GvpK	pNRC200
HBSAL_12180	OE_5116R	100d	pHSAL1/pHS3	VNG_6232G	gvpJ	gas-vesicle-associated protein GvpJ	pNRC200
HBSAL_12185	OE_5118R	100d	pHSAL1/pHS3	VNG_6233G	gvpI	gas-vesicle operon protein GvpI	pNRC200
HBSAL_12190	OE_5119R	100d	pHSAL1/pHS3	VNG_6235G	gvpH	gas-vesicle operon protein GvpH	pNRC200
HBSAL_12195	OE_5121R	100d	pHSAL1/pHS3	VNG_6236G	gvpG	gas-vesicle-associated protein GvpG	pNRC200
HBSAL_12200	OE_5122R	100d	pHSAL1/pHS3	VNG_6237G	gvpF	gas-vesicle-associated protein GvpF	pNRC200
HBSAL_12205	OE_5123R	100d	pHSAL1/pHS3	VNG_6239G	gvpE	PadR family transcription activator GvpE	pNRC200
HBSAL_12210	OE_5124R	100d	pHSAL1/pHS3	VNG_6240G	gvpD	regulatory protein GvpD	pNRC200
HBSAL_12215	OE_5125F	100d	pHSAL1/pHS3	VNG_6241G	gvpA	gas-vesicle major structural protein GvpA	pNRC200
HBSAL_12220	OE_5127F	100d	pHSAL1/pHS3	VNG_6242G	gvpC	gas-vesicle minor protein GvpC	pNRC200
HBSAL_12225	OE_5128F	100d	pHSAL1/pHS3	VNG_6244G	gvpN	gas-vesicle operon protein GvpN	pNRC200
HBSAL_12230	OE_5129F	100d	pHSAL1/pHS3	VNG_6246G	gvpO	gas-vesicle operon protein GvpO	pNRC200
HBSAL_12235	OE_5130F	100d	pHSAL1/pHS3	VNG_6247G	trkA4	TrkA domain protein	pNRC200
HBSAL_12240	OE_5132F	100d	pHSAL1/pHS3	VNG_6250G	-	transport protein (probable substrate phosphate/sulfate)	pNRC200
HBSAL_12245	OE_5134F	100d	pHSAL1/pHS3	VNG_6251H	-	DUF2078 family protein	pNRC200
HBSAL_12250	OE_5136R	100d	pHSAL1/pHS3	VNG_6254C	-	homolog to autoinducer-2-degrading protein lsrG	pNRC200
HBSAL_12255	OE_5138F	100d	pHSAL1/pHS3	VNG_6255C	-	uncharacterized protein	pNRC200
HBSAL_12260	OE_5139F	100d	pHSAL1/pHS3	VNG_6256G	lp12	lipoate--protein ligase domain protein	pNRC200
HBSAL_12265	OE_5141R	100d	pHSAL1/pHS3	VNG_6258C	-	amidohydrolase domain protein	pNRC200

HBSAL_12270	OE_5142F	100d	pHSAL1/pHS3	VNG_6260G	ftsZ5	FtsZ family protein, noncanonical	pNRC200
HBSAL_12275	OE_5143F	100d	pHSAL1/pHS3	VNG_6261G	-	SNF family transport protein	pNRC200
HBSAL_12280	OE_5144R	100d	pHSAL1/pHS3	VNG_6262G	znuB	ABC-type transport system permease protein (probable substrate zinc)	pNRC200
HBSAL_12285	OE_5146R	100d	pHSAL1/pHS3	VNG_6264G	znuC	ABC-type transport system ATP-binding protein (probable substrate zinc)	pNRC200
HBSAL_12290	OE_5147R	100d	pHSAL1/pHS3	VNG_6265G	znuA	ABC-type transport system periplasmic substrate-binding protein (probable substrate zinc)	pNRC200
[HBSAL_12295; HBSAL_12305]	OE_5149R	99	pHSAL1/pHS3	VNG_6266H	-	uncharacterized protein	pseudo(91-R6;split); pNRC200
HBSAL_12310	OE_5157F	100d	pHSAL1/pHS3	VNG_6268C	-	OPT family transport protein	pNRC200
HBSAL_12315	OE_5158F	100d	pHSAL1/pHS3	VNG_6269C	-	uncharacterized protein	pNRC200
HBSAL_12320	OE_5160F	100d	pHSAL1/pHS3	VNG_6270G	gldA1	glycerol dehydrogenase	pNRC200
HBSAL_12325	OE_5162R	100d	pHSAL1/pHS3	VNG_6272G	orc14	Orc1-type DNA replication protein	pNRC200
HBSAL_12330	OE_5162D1F	100d	pHSAL1/pHS3	VNG_6275a	-	NifU C-terminal domain protein	pNRC200
HBSAL_12335	OE_5165R	100d	pHSAL1/pHS3	VNG_6276H	-	uncharacterized protein	pNRC200
HBSAL_12340	OE_5166F	100d	pHSAL1/pHS3	VNG_6277G	ugpB	ABC-type transport system periplasmic substrate-binding protein (probable substrate glycerol-3-phosphate)	pNRC200
HBSAL_12345	OE_5168F	100d	pHSAL1/pHS3	VNG_6279G	ugpA	ABC-type transport system permease protein (probable substrate glycerol-3-phosphate)	pNRC200
HBSAL_12350	OE_5169F	100d	pHSAL1/pHS3	VNG_6280G	ugpE	ABC-type transport system permease protein (probable substrate glycerol-3-phosphate)	pNRC200
HBSAL_12355	OE_5170F	100d	pHSAL1/pHS3	VNG_6281G	ugpC	ABC-type transport system ATP-binding protein (probable substrate glycerol-3-phosphate)	pNRC200
HBSAL_12360	OE_5171R	100d	pHSAL1/pHS3	VNG_6283H	-	uncharacterized protein	pNRC200
HBSAL_12365	OE_5174R	100d	pHSAL1/pHS3	VNG_6284H	-	chimeric protein	pseudo(91-R6;R1;NRC-1);

							pNRC200
HBSAL_12370	OE_5176R	100d	pHSAL1/pHS3	VNG_6286H	-	uncharacterized protein	pNRC200
HBSAL_12375	OE_5177F	100d	pHSAL1/pHS3	VNG_6287H	-	HTH domain protein	pNRC200
HBSAL_12380	OE_5178F	100d	pHSAL1/pHS3	VNG_6288C	-	CopG domain protein	pNRC200
HBSAL_12385	OE_5179B1F	100d	pHSAL1/pHS3	VNG_6288a	-	RelE family protein	pNRC200
HBSAL_12390	OE_5180F	100d	pHSAL1/pHS3	VNG_6290H	-	ISH7-type transposase	pseudo(91-R6;R1;NRC-1); pNRC200
HBSAL_12395	OE_5182R	100d	pHSAL1/pHS3	VNG_6291H	-	uncharacterized protein	pNRC200
HBSAL_12400	OE_5183R	100d	pHSAL1/pHS3	VNG_6292C	-	ISH14-type transposase HsIRS44	pNRC200
HBSAL_12405	OE_5184F	100d	pHSAL1/pHS3	VNG_6293C	-	DMT superfamily transport protein	pNRC200
HBSAL_12410	OE_5186R	100d	pHSAL1/pHS3	VNG_6294G	katG	catalase-peroxidase	pNRC200
HBSAL_12415	OE_5187R	100d	pHSAL1/pHS3	VNG_6296C	-	alpha/beta hydrolase fold protein	pNRC200
HBSAL_12420	OE_5188F	100d	pHSAL1/pHS3	VNG_6297C	-	PQQ repeat protein	pNRC200
HBSAL_12425	OE_5189F	100d	pHSAL1/pHS3	VNG_6298C	-	3-oxoacid CoA-transferase	pNRC200
HBSAL_12430	OE_5190R	100d	pHSAL1/pHS3	VNG_6299G	hypE1	HypE family protein	pNRC200
HBSAL_12435	OE_5192R	100d	pHSAL1/pHS3	VNG_6301G	aph	alkaline phosphatase	pNRC200
HBSAL_12440	OE_5193F	100d	pHSAL1/pHS3	VNG_6302C	-	DUF21/CBS domain protein	pNRC200
HBSAL_12445	OE_5195R	100d	pHSAL1/pHS3	VNG_6303G	queC	7-cyano-7-deazaguanine synthase	pNRC200
HBSAL_12450	OE_5197R	100d	pHSAL1/pHS3	VNG_6305C	queE	7-carboxy-7-deazaguanine synthase	pNRC200
HBSAL_12455	OE_5198R	100d	pHSAL1/pHS3	VNG_6306C	queD	6-carboxy-5,6,7,8-tetrahydropterin synthase	pNRC200
HBSAL_12460	OE_5200R	100d	pHSAL1/pHS3	VNG_6308G	gltP	SDF family transport protein (probable substrate glutamate/aspartate)	pNRC200
HBSAL_12465	OE_5201F	100d	pHSAL1/pHS3	VNG_6309G	pyrB	aspartate carbamoyltransferase catalytic subunit	pNRC200
HBSAL_12470	OE_5202F	100d	pHSAL1/pHS3	VNG_6311G	pyrI	aspartate carbamoyltransferase regulatory subunit	pNRC200
HBSAL_12475	OE_5203F	100d	pHSAL1/pHS3	VNG_6312G	argS	arginine--tRNA ligase	pNRC200
HBSAL_12480	OE_5204R	100d	pHSAL1/pHS3	VNG_6313G	arcD	arginine/ornithine antiporter	pNRC200
HBSAL_12485	OE_5205R	100d	pHSAL1/pHS3	VNG_6315G	arcB	ornithine carbamoyltransferase	pNRC200

HBSAL_12490	OE_5206R	100d	pHSAL1/pHS3	VNG_6316G	arcC	carbamate kinase	pNRC200
HBSAL_12495	OE_5208R	100d	pHSAL1/pHS3	VNG_6317G	arcA	arginine deiminase	pNRC200
HBSAL_12500	OE_5209R	100d	pHSAL1/pHS3	VNG_6318G	arcR	IclR family transcription regulator ArcR	pNRC200
HBSAL_12505	OE_5210F	100d	pHSAL1/pHS3	VNG_6318a	-	uncharacterized protein	pNRC200
HBSAL_12510	OE_5211F	100d	pHSAL1/pHS3	VNG_6319H	-	uncharacterized protein	pNRC200
HBSAL_12515	OE_5212F	100d	pHSAL1/pHS3	VNG_6320C	sph1	Smc-like protein Sph1	pNRC200
HBSAL_12520	OE_5215R	100d	pHSAL1/pHS3	VNG_6321H	-	XerC/D-like integrase	pNRC200
HBSAL_12525	OE_5217R	100d	pHSAL1/pHS3	VNG_6322H	-	uncharacterized protein	pNRC200
HBSAL_12530	OE_5219F	100d	pHSAL1/pHS3	VNG_6323H	-	uncharacterized protein	pNRC200
HBSAL_12535	OE_5220R	100d	pHSAL1/pHS3	VNG_6323a	-	IS1341-type transposase	pseudo(91-R6;R1;NRC-1); pNRC200
HBSAL_12540	OE_5220C1F	100d	pHSAL1/pHS3	VNG_6323b	-	uncharacterized protein	pseudo(91-R6;R1;NRC-1); pNRC200
HBSAL_12545	OE_5221A1F	100d	pHSAL1/pHS3	VNG_6323c	-	chimeric protein	pseudo(91-R6;R1;NRC-1); pNRC200
HBSAL_12550	OE_5221C1F	100d	pHSAL1/pHS3	VNG_6323d	-	uncharacterized protein	pseudo(91-R6;R1;NRC-1); pNRC200
-	OE_5222A1F	-	pHSAL1/pHS3	-	-	conserved hypothetical protein	pseudo(R1); unannotated(91- R6;NRC-1;very_short_pseudo)
HBSAL_12555	[OE_5228R]	99	pHSAL1/pHS3	VNG_6326G	-	ABC-type transport system ATP- binding protein	pseudo(R1;split); pNRC200
HBSAL_12560	OE_5230R	100d	pHSAL1/pHS3	VNG_6327H	-	uncharacterized protein	pNRC200
HBSAL_12570	OE_5231B1F	100d	pHSAL1/pHS3	VNG_6327a	-	uncharacterized protein	pseudo(91-R6;R1;NRC-1); pNRC200
HBSAL_12575	OE_5231A1F	100d	pHSAL1/pHS3	VNG_6327b	-	uncharacterized protein	pseudo(91-R6;R1;NRC-1); pNRC200
HBSAL_12580	OE_5232B1R	100d	pHSAL1/pHS3	VNG_6327c	-	uncharacterized protein	pNRC200
HBSAL_12585	[OE_5234R]	98	pHSAL1/pHS3	VNG_6329H	-	probable halocin (homolog to halocin C8)	pseudo(R1;split); pseudo(NRC-1;split; C-term_part_unannotated); pNRC200

HBSAL_12590	OE_5235F	100d	pHSAL1/pHS3	VNG_6330H	-	uncharacterized protein	pNRC200
HBSAL_12610	OE_5236F	100d	pHSAL1/pHS3	-	-	uncharacterized protein	pseudo(91-R6;R1)
HBSAL_12615	OE_5238R	100d	pHSAL1/pHS3	-	-	probable RfbX family transport protein	pseudo(91-R6;R1)
HBSAL_12710; HBSAL_13400	OE_6185F; OE_7065F	87	pHSAL1+2/pHS1 +2	VNG_6053G; VNG_6473G; VNG_7039; VNG_7170	cydA1	cytochrome bd ubiquinol oxidase subunit I	LowSim
HBSAL_12715; HBSAL_13405	OE_6186F; OE_7066F	84	pHSAL1+2/pHS1 +2	VNG_6055G; VNG_6471G; VNG_7040; VNG_7169	cydB1	cytochrome bd ubiquinol oxidase subunit II	LowSim
HBSAL_12820; HBSAL_13510	OE_5392F	100d	pHSAL1+2/pHS3	-	-	XerC/D-like integrase	-
HBSAL_12825; HBSAL_13515	OE_5391F	100d	pHSAL1+2/pHS3	-	-	uncharacterized protein	-
HBSAL_12830; HBSAL_13520	OE_5389F	100d	pHSAL1+2/pHS3	-	-	TrmB family transcription regulator	-
HBSAL_12835; HBSAL_13525	OE_5388B1F	100d	pHSAL1+2/pHS3	-	-	uncharacterized protein	pseudo(91-R6;R1)
HBSAL_13020	OE_7015F	94	pHSAL2/pHS1	VNG_6013a; VNG_7011a	-	uncharacterized protein	LowSim; pseudo(R1;NRC-1)
HBSAL_13025	OE_7014F	96	pHSAL2/pHS1	VNG_6013G; VNG_7011	repH	plasmid replication protein RepH	-
HBSAL_13095	OE_7212C1F; OE_8044C1F	94	pHSAL2/pHS1+4	VNG_7112d	-	small CPxCG-related zinc finger protein	LowSim
HBSAL_13100	OE_7212B1F; OE_8044B1F	100p	pHSAL2/pHS1+4	VNG_7112c	-	small CPxCG-related zinc finger protein	-
HBSAL_13105	OE_7211F; OE_8043F	95	pHSAL2/pHS1+4	VNG_7112b	-	uncharacterized protein	-
HBSAL_13110	OE_7210R; OE_8042R	93	pHSAL2/pHS1+4	VNG_7112a	-	small CPxCG-related zinc finger protein	LowSim
HBSAL_13115	OE_7209F; OE_8041F	92	pHSAL2/pHS1+4	VNG_7112	-	HTH domain protein	LowSim



HBSAL_13120	OE_7207F; OE_8039F	82	pHSAL2/pHS1+4	VNG_7110	-	uncharacterized protein	LowSim
HBSAL_13125	OE_7206F; OE_8038F	92	pHSAL2/pHS1+4	VNG_7109	-	uncharacterized protein	LowSim
HBSAL_13130	OE_7204F; OE_8036F	92	pHSAL2/pHS1+4	VNG_7108	-	uncharacterized protein	LowSim
HBSAL_13135	OE_7196F; OE_8027F	100d	pHSAL2/pHS1+4	VNG_7106	-	integrase family protein	-
HBSAL_13140	OE_7194F; OE_8025F	100d	pHSAL2/pHS1+4	VNG_7105	repJ1	plasmid replication protein RepJ	-
HBSAL_13145	OE_7192F; OE_8023F	100d	pHSAL2/pHS1+4	VNG_7104	-	uncharacterized protein	-
HBSAL_13150	OE_7190R; OE_8021R	100d	pHSAL2/pHS1+4	VNG_7103	-	uncharacterized protein	-
[HBSAL_13155; HBSAL_13165]	OE_7189F; OE_8020F	99	pHSAL2/pHS1+4	VNG_7102	-	PadR family transcription regulator	pseudo(91-R6;split)

**Table S2: Highly conserved protein-coding genes from strains 91-R6 and R1, at least one of which is encoded on a plasmid.** The 1<sup>st</sup> part of this table (up to HBSAL\_06290, column "code") lists proteins which are encoded on chromosomal divSEGs in strain 91-R6. The divSEG is indicated by "d" with a subsequent serial number in the "serial or plasmid" column. These proteins from strain 91-R6 match to a protein from one of the plasmids of strain R1 as indicated in the "serial or plasmid" column. It should be noted that the opposite, proteins from chromosomal divSEGs of strain R1 which match to plasmid proteins from strain 91-R6, has not been encountered. The 2<sup>nd</sup> part of this table (from HBSAL\_12005 onwards) lists proteins which are encoded on plasmids in both strains. Due to large-scale plasmid duplications, genes may be encoded on more than one plasmid (e.g. R1: pHS1+2 or 91-R6: pHSAL1+2). In that case, both locus tags are shown, separated by a semicolon ("code"). This should not be mixed up with multiple locus tags for genes which have been targeted by a MGE. For these, the two codes are within square brackets and the comment column notes "pseudo(91-R6;split)". Other disrupted genes are flagged in the comment column by "pseudo()" (see the legend to Table S1 for details). Matching sequence pairs cover a range of sequence identity values. For proteins with identical sequence, it is indicated if the coding sequences are identical ("100d") or if there are silent mutations ("100p") (see also the legend to Table S1). Proteins with less than 95% seq\_id are flagged in the comment column (LowSim). If possible, R1 codes have been matched to NRC-1 codes. With few exceptions, R1 and NRC-1 genes are identical, differences being notes flagged as "seqdiff(R1/NRC-1)". Due to even further plasmid duplications in NRC-1, up to four copies of a gene may exist. All locus tags are shown, separated by semicolons. For proteins from R1 plasmid pHS3 which correspond to a gene from strain NRC-1, a comment indicates if the NRC-1 gene is encoded on pNRC100 or on pNRC200. This table contains some special cases: (a) in some cases, a gene has been split but one fragment is very short and has not been annotated (flagged e.g. "N-term\_part\_unannotated"). (b) HBSAL\_04690: the R1 gene is split with a subsequent translocation due to a MGE-triggered genome inversion (OE\_5405F + OE\_5013R). (c) HBSAL\_05030; [HBSAL\_12805;HBSAL\_12815]; [HBSAL\_13495;HBSAL\_13505]: the gene has been targeted twice, more N-terminal by transposon ISH3B, more C-terminal by transposons ISHsal2. The N-terminal part upstream of ISH3B is encoded on the chromosome in divSEG12, while the C-terminal part, including its 2<sup>nd</sup> targeting MGE, has

been translocated to the plasmids, now being encoded on the duplicated part of pH<sub>SAL1</sub> and pH<sub>SAL2</sub>. (d) OE\_5222A1F. This pseudogene is very short (15 codons) and has not been annotated in strains 91-R6 and NRC-1 ("very\_short\_pseudo").

code (91-R6)	code (R1)	seq id (%)	serial	code (NRC-1)	gene	protein name	comment
HBSAL_01120	-	-	d04	-	-	uncharacterized protein	-
HBSAL_01125	-	-	d04	-	-	HTH domain protein	-
HBSAL_01130	-	-	d04	-	-	IS1341-type transposase	pseudo(91-R6)
HBSAL_01135	-	-	d04	-	-	uncharacterized protein	pseudo(91-R6)
HBSAL_01140	-	-	d04	-	-	HTH domain protein	-
HBSAL_01145	-	-	d04	-	-	uncharacterized protein	-
HBSAL_01150	-	-	d04	-	-	DUF234 domain protein	pseudo(91-R6)
HBSAL_01155	-	-	d04	-	-	ArsR family transcription regulator / DUF2204 family protein	-
HBSAL_01160	-	-	d04	-	-	IS200-type transposase ISH22	-
HBSAL_01165	-	-	d04	-	-	ISH9-type transposase ISH9	-
HBSAL_01170	-	-	d04	-	-	IS1341-type transposase	-
HBSAL_01175	OE_1036F	79	d04	VNG_0022H	-	uncharacterized protein	close_paralog
HBSAL_01180	OE_1037F	79	d04	VNG_0023H	-	uncharacterized protein	close_paralog
HBSAL_01185	-	-	d04	-	-	PIN domain protein	pseudo(91-R6)
HBSAL_01190	-	-	d04	-	-	uncharacterized protein	-
HBSAL_01195	-	-	d04	-	-	HTH domain protein	-
HBSAL_01200	-	-	d04	-	-	IS1341-type transposase	pseudo(91-R6)
HBSAL_01205	OE_1038R	86	d04	VNG_0024H	-	uncharacterized protein	close_paralog
HBSAL_01210	-	-	d04	-	-	probable HNH-type endonuclease	-
HBSAL_01215	OE_1041R	92	d04	VNG_0027H	-	uncharacterized protein	close_paralog; pseudo(91-R6)
HBSAL_01220	-	-	d04	-	-	uncharacterized protein	-
HBSAL_01225	-	-	d04	-	-	uncharacterized protein	-
HBSAL_01230	-	-	d04	-	-	uncharacterized protein	-
HBSAL_01235	-	-	d04	-	orc2	Orc1-type DNA replication protein	pseudo(91-R6)
HBSAL_01240	-	-	d04	-	-	IS1341-type transposase	pseudo(91-R6)

HBSAL_01245	-	-	d04	-	orc3	Orc1-type DNA replication protein	-
HBSAL_01255	-	-	d04	-	-	ISH10-type transposase ISH10	-
HBSAL_01260; HBSAL_01250	-	-	d04	-	-	ISHwa16-type transposase	pseudo(91-R6;split)
HBSAL_01265	-	-	d04	-	orc4	Orc1-type DNA replication protein	pseudo(91-R6)
HBSAL_01270	-	-	d04	-	-	glycoside hydrolase family protein	-
HBSAL_01275	-	-	d04	-	-	insertion element protein (MITEHsal2)	-
HBSAL_01280	-	-	d04	-	-	probable glycosyltransferase, type 1	-
HBSAL_01285	-	-	d04	-	-	probable glycosyltransferase, type 1	-
HBSAL_01290	-	-	d04	-	-	glycoside hydrolase family protein	-
HBSAL_01295	-	-	d04	-	-	ABC-type transport system ATP-binding/permease protein	-
HBSAL_01300	-	-	d04	-	-	uncharacterized protein	-
HBSAL_01305	-	-	d04	-	-	ISH8-type transposase ISH32	-
HBSAL_01310	-	-	d04	-	-	probable glycosyltransferase, type 1	-
HBSAL_01315	-	-	d04	-	-	probable glycosyltransferase, type 1	-
HBSAL_01320	-	-	d04	-	-	probable nucleotide sugar epimerase	-
HBSAL_01325	-	-	d04	-	-	probable nucleotide sugar dehydrogenase	-
HBSAL_01330	-	-	d04	-	-	GFO family oxidoreductase	-
HBSAL_01335	-	-	d04	-	-	DegT family aminotransferase	-
HBSAL_01340	-	-	d04	-	-	formyltransferase domain protein	-
HBSAL_01345	OE_1133F	76	d04	VNG_0077H	-	DUF4330 family protein	close_paralog
HBSAL_01350	OE_1134F	60	d04	VNG_0077a	-	uncharacterized protein	close_paralog
HBSAL_01445	-	-	d05	-	-	ISH14-type transposase	pseudo(91-R6)
HBSAL_01450	-	-	d05	-	-	conserved hypothetical protein	-
HBSAL_04215	OE_2223F	57	d12	VNG_0829G	dmsAa	dimethylsulfoxide reductase subunit A	close_paralog;pseudo(91-R6); C-term_far_away(HBSAL_05135)
HBSAL_04220	-	-	d12	-	-	insertion element protein (MITEHsal3)	-
HBSAL_04225	-	-	d12	-	-	small CPxCG-related zinc finger protein	-
HBSAL_04230	-	-	d12	-	-	uncharacterized protein	pseudo(91-R6)

HBSAL_04235	-	-	d12	-	-	uncharacterized protein	-
HBSAL_04270	-	-	d12	-	-	ISH11-type transposase	-
HBSAL_04285	-	-	d12	-	-	ISHwa16-type transposase	-
HBSAL_04290	-	-	d12	-	-	probable amidase	-
HBSAL_04300	-	-	d12	-	-	ISH3-type transposase	-
HBSAL_04305; HBSAL_04295	-	-	d12	-	tfbA4b	transcription initiation factor TFB	pseudo(91-R6;split)
HBSAL_04310	-	-	d12	-	-	uncharacterized protein	-
HBSAL_04315	-	-	d12	-	-	ISH4-type transposase	pseudo(91-R6)
HBSAL_04320	-	-	d12	-	-	ISH9-type transposase ISH9	pseudo(91-R6)
HBSAL_04325	-	-	d12	-	-	ISH7-type transposase	pseudo(91-R6)
HBSAL_04330	-	-	d12	-	-	DNA-directed DNA polymerase	pseudo(91-R6)
HBSAL_04335	-	-	d12	-	-	uncharacterized protein	-
HBSAL_04340	-	-	d12	-	-	uncharacterized protein	-
HBSAL_04350	-	-	d12	-	orc6	Orc1-type DNA replication protein	-
HBSAL_04355	-	-	d12	-	-	ISH3-type transposase	-
HBSAL_04360	-	-	d12	-	-	ISH8-type transposase	-
HBSAL_04370	-	-	d12	-	-	sensor box histidine kinase	-
HBSAL_04375	-	-	d12	-	-	ISHwa16-type transposase	-
HBSAL_04380	-	-	d12	-	tbp2	TATA-binding transcription initiation factor	-
HBSAL_04385	-	-	d12	-	-	PadR family transcription regulator	-
HBSAL_04390	-	-	d12	-	-	uncharacterized protein	-
HBSAL_04395	-	-	d12	-	-	conserved hypothetical protein	-
HBSAL_04400	-	-	d12	-	-	UvrD/REP family helicase	-
HBSAL_04405	-	-	d12	-	-	ISHwa16-type transposase	-
HBSAL_04410	-	-	d12	-	-	uncharacterized protein	-
HBSAL_04420	-	-	d12	-	-	uncharacterized protein	-
HBSAL_04425; HBSAL_04430	-	-	d12	-	-	uncharacterized protein	pseudo(91-R6;split)

HBSAL_04435	-	-	d12	-	-	uncharacterized protein	-
HBSAL_04440	-	-	d12	-	orc7	Orc1-type DNA replication protein	-
HBSAL_04445	-	-	d12	-	-	uncharacterized protein	-
HBSAL_04450	-	-	d12	-	-	UPF0395 family protein	-
HBSAL_04455	-	-	d12	-	-	small CPxCG-related zinc finger protein	-
HBSAL_04460	-	-	d12	-	-	uncharacterized protein	-
HBSAL_04465; HBSAL_04475	-	-	d12	-	-	ParA domain protein	pseudo(91-R6;split)
HBSAL_04470	-	-	d12	-	-	ISH3-type transposase	-
HBSAL_04480	-	-	d12	-	-	uncharacterized protein	-
HBSAL_04485	-	-	d12	-	-	uncharacterized protein	-
HBSAL_04490	-	-	d12	-	-	uncharacterized protein	pseudo(91-R6)
HBSAL_04495	-	-	d12	-	-	ISH9-type transposase	pseudo(91-R6)
HBSAL_04500	-	-	d12	-	-	ISH7-type transposase	pseudo(91-R6)
HBSAL_04515	-	-	d12	-	-	uncharacterized protein	-
HBSAL_04520	-	-	d12	-	-	HTH domain protein	-
HBSAL_04525	-	-	d12	-	-	ISH8-type transposase ISH8	-
HBSAL_04530	-	-	d12	-	-	probable S-adenosylmethionine- dependent methyltransferase	pseudo(91-R6)
HBSAL_04535	-	-	d12	-	-	ISH4-type transposase	-
HBSAL_04540	-	-	d12	-	-	uncharacterized protein	-
HBSAL_04545	-	-	d12	-	-	HTH domain protein	-
HBSAL_04555	-	-	d12	-	-	insertion element protein (MITEHsal2)	-
HBSAL_04570	-	-	d12	-	-	ISH7-type transposase	-
HBSAL_04575	-	-	d12	-	-	uncharacterized protein	-
HBSAL_04580	-	-	d12	-	-	ParA domain protein	-
HBSAL_04585	-	-	d12	-	-	HTH domain protein	-
HBSAL_04590	-	-	d12	-	-	uncharacterized protein	pseudo(91-R6)
HBSAL_04605	-	-	d12	-	-	ISH16-type transposase	-
HBSAL_04610;	-	-	d12	-	-	ISH8-type transposase ISH8	pseudo(91-R6;split)

HBSAL_04600							
HBSAL_04615	-	-	d12	-	-	uncharacterized protein	-
HBSAL_04620	-	-	d12	-	-	uncharacterized protein	-
HBSAL_04625	-	-	d12	-	-	uncharacterized protein	pseudo(91-R6)
HBSAL_04630	-	-	d12	-	-	TrmB family transcription regulator	-
HBSAL_04635	-	-	d12	-	-	integrase family protein	pseudo(91-R6)
HBSAL_04640	-	-	d12	-	-	HTH-10 family transcription regulator	pseudo(91-R6)
HBSAL_04645	-	-	d12	-	-	ISH3-type transposase	-
HBSAL_04815; HBSAL_04825	-	-	d12	-	-	uncharacterized protein	pseudo(91-R6;split)
HBSAL_04820	-	-	d12	-	-	ISH3-type transposase	-
HBSAL_04830	-	-	d12	-	-	uncharacterized protein	pseudo(91-R6)
HBSAL_04835	-	-	d12	-	tfbA5	transcription initiation factor TFB	-
HBSAL_04840	-	-	d12	-	-	insertion element protein (MITEHsal2)	-
HBSAL_04845	-	-	d12	-	-	death-on-curing family protein	-
HBSAL_04850	-	-	d12	-	-	uncharacterized protein	-
HBSAL_04855	-	-	d12	-	-	uncharacterized protein	pseudo(91-R6)
HBSAL_04860	-	-	d12	-	-	uncharacterized protein	-
HBSAL_04865	-	-	d12	-	-	major facilitator superfamily transport protein	pseudo(91-R6)
HBSAL_04870	-	-	d12	-	-	uncharacterized protein	pseudo(91-R6)
HBSAL_04980	-	-	d12	-	-	uncharacterized protein	pseudo(91-R6)
HBSAL_04985	-	-	d12	-	-	probable cysteine desulfurase	pseudo(91-R6)
HBSAL_04990	-	-	d12	-	-	DUF302 family protein	pseudo(91-R6)
HBSAL_04995	-	-	d12	-	-	probable S-adenosylmethionine-dependent methyltransferase	-
HBSAL_05000	-	-	d12	-	-	ABC-type transport system ATP-binding protein	pseudo(91-R6)
HBSAL_05005	-	-	d12	-	-	ABC-type transport system periplasmic substrate-binding protein	pseudo(91-R6)
HBSAL_05010	-	-	d12	-	-	ArsR family transcription regulator	-

HBSAL_05015	-	-	d12	-	-	uncharacterized protein	-
HBSAL_05020	-	-	d12	-	-	ISH3-type transposase	-
HBSAL_05035	-	-	d12	-	-	ISH3-type transposase ISH3	-
HBSAL_05070	-	-	d12	-	tbp4	TATA-binding transcription initiation factor	-
HBSAL_05075	-	-	d12	-	-	uncharacterized protein	-
HBSAL_05080	-	-	d12	-	-	uncharacterized protein	-
HBSAL_05085	-	-	d12	-	orc8	Orc1-type DNA replication protein	-
HBSAL_05090	-	-	d12	-	-	uncharacterized protein	-
HBSAL_05095	-	-	d12	-	-	uncharacterized protein	-
HBSAL_05100	-	-	d12	-	-	uncharacterized protein	-
HBSAL_05105	-	-	d12	-	-	uncharacterized protein	-
HBSAL_05110	-	-	d12	-	-	IS1341-type transposase	pseudo(91-R6)
HBSAL_05120	-	-	d12	-	-	ISH9-type transposase ISH1	-
HBSAL_05125; HBSAL_05115	-	-	d12	-	-	ISH8-type transposase ISH8	pseudo(91-R6;split)
HBSAL_05130	-	-	d12	-	-	insertion element protein (MITEHsal3)	pseudo(91-R6)
HBSAL_05135	-	-	d12	-	dmsAb	dimethylsulfoxide reductase subunit A	pseudo(91-R6)
HBSAL_05480	-	-	d13	-	-	ISH3-type transposase	-
HBSAL_05550	-	-	d14	-	-	uncharacterized protein	-
HBSAL_05555	-	-	d14	-	-	integrase family protein	-
HBSAL_05560	-	-	d14	-	-	uncharacterized protein	-
HBSAL_05565	-	-	d14	-	-	uncharacterized protein	-
HBSAL_05785	-	-	d17	-	-	ISH9-type transposase	pseudo(91-R6)
HBSAL_05790	-	-	d17	-	-	tetratricopeptide repeat protein	-
HBSAL_05860	-	-	d18	-	-	small CPxCG-related zinc finger protein	-
HBSAL_05865	-	-	d18	-	-	uncharacterized protein	-
HBSAL_05870	-	-	d18	-	-	uncharacterized protein	-
HBSAL_05875	-	-	d18	-	-	uncharacterized protein	-
HBSAL_05880	-	-	d18	-	-	uncharacterized protein	-



HBSAL_05885	-	-	d18	-	-	uncharacterized protein	-
HBSAL_05890	-	-	d18	-	-	uncharacterized protein	-
HBSAL_05895	-	-	d18	-	-	uncharacterized protein	-
HBSAL_05900	-	-	d18	-	orc9	Orc1-type DNA replication protein	-
HBSAL_05905	-	-	d18	-	-	uncharacterized protein	-
HBSAL_05910	-	-	d18	-	-	uncharacterized protein	-
HBSAL_05915	-	-	d18	-	-	uncharacterized protein	-
HBSAL_05920	-	-	d18	-	-	uncharacterized protein	-
HBSAL_05925	-	-	d18	-	-	uncharacterized protein	-
HBSAL_05930	-	-	d18	-	ilvD	dihydroxy-acid dehydratase	-
HBSAL_05935	-	-	d18	-	leuB	3-isopropylmalate dehydrogenase	-
HBSAL_05940	-	-	d18	-	leuD	3-isopropylmalate dehydratase small subunit	-
HBSAL_05945	-	-	d18	-	leuC	3-isopropylmalate dehydratase large subunit	-
HBSAL_05950	-	-	d18	-	-	uncharacterized protein	-
HBSAL_05955	-	-	d18	-	ilvC	ketol-acid reductoisomerase	-
HBSAL_05960	-	-	d18	-	ilvN	acetolactate synthase small subunit	-
HBSAL_05965	-	-	d18	-	ilvB	acetolactate synthase large subunit	-
HBSAL_05970	-	-	d18	-	leuA	2-isopropylmalate synthase	pseudo(91-R6)
HBSAL_05985	-	-	d18	-	-	uncharacterized protein	-
HBSAL_05990	OE_2469F	82	d18	VNG_1008G	arlA	archaellin A	close_paralog
HBSAL_06000	-	-	d18	-	-	homolog to quinoprotein glucose dehydrogenase	pseudo(91-R6)
HBSAL_06005	OE_2472F	82	d18	VNG_1011C	arfA1	GTP cyclohydrolase 3	close_paralog
HBSAL_06010	-	-	d18	-	rtcB	tRNA-splicing ligase RtcB	-
HBSAL_06015	-	-	d18	-	-	uncharacterized protein	-
HBSAL_06020	OE_2475F	78	d18	VNG_1014G	polY	DNA-directed DNA polymerase Y	close_paralog; pseudo(91-R6)
HBSAL_06025	-	-	d18	-	-	uncharacterized protein	-
HBSAL_06030	-	-	d18	-	-	uncharacterized protein	-

HBSAL_06035	OE_2500R	87	d18	VNG_1027G	tpiA	triosephosphate isomerase	close_paralog
HBSAL_06040	OE_2502R	76	d18	VNG_1029C	-	cro/C1 family transcription regulator	close_paralog
HBSAL_06045	OE_2503R	83	d18	VNG_1030G	agsA	probable archaetidylglycerolphosphate synthase	close_paralog
HBSAL_06050	OE_2506R	73	d18	VNG_1031C	adk2	probable adenylate kinase	close_paralog
HBSAL_06055	OE_2507R	81	d18	VNG_1033G	hisC	histidinol-phosphate aminotransferase	close_paralog
HBSAL_06060	-	-	d18	-	-	uncharacterized protein	-
HBSAL_06065	OE_2508F	80	d18	VNG_1034H	-	uncharacterized protein	close_paralog
HBSAL_06070	-	-	d18	-	-	probable iron-sulfur protein (2Fe-2S)	-
HBSAL_06075	-	-	d18	-	-	IS1341-type transposase	-
HBSAL_06080	-	-	d18	-	-	uncharacterized protein	-
HBSAL_06085	OE_2509R	81	d18	VNG_1035C	-	GMC family oxidoreductase	close_paralog
HBSAL_06090	OE_2510R	73	d18	VNG_1036H	-	LacC domain protein	close_paralog
HBSAL_06095	OE_2512R	77	d18	VNG_1037G	hpcE	fumarylacetoacetase family protein	close_paralog
HBSAL_06100	-	-	d18	-	-	probable oxidoreductase (aldo-keto reductase family protein)	-
HBSAL_06105	OE_2513F	75	d18	VNG_1038C	-	metal-dependent hydrolase domain protein	close_paralog
HBSAL_06110	-	-	d18	-	-	IS1341-type transposase	-
HBSAL_06115	OE_2515F	85	d18	VNG_1041a	-	OsmC domain protein	close_paralog
HBSAL_06120	OE_2519F	70	d18	VNG_1042H	-	uncharacterized protein	close_paralog
HBSAL_06125	OE_2521R	67	d18	VNG_1047H	-	uncharacterized protein	close_paralog
HBSAL_06130	OE_2522F	81	d18	VNG_1046H	-	uncharacterized protein	close_paralog
HBSAL_06135	-	-	d18	-	mazF	mRNA interferase MazF	-
HBSAL_06140	-	-	d18	-	-	homolog to antitoxin VapB	-
HBSAL_06145	OE_2524R	81	d18	VNG_1048G	aglM1	UDP-glucose 6-dehydrogenase AglM	close_paralog
HBSAL_06150	OE_2525R	72	d18	VNG_1050H	-	TRAM domain protein	close_paralog
HBSAL_06155	-	-	d18	-	-	glyoxalase domain protein	-
HBSAL_06160	-	-	d18	-	-	ISH11-type transposase	-
HBSAL_06170	-	-	d18	-	-	ISH3-type transposase ISH3	-

HBSAL_06175; HBSAL_06165	-	-	d18	-	-	IS1341-type transposase	pseudo(91-R6;split)
HBSAL_06180	-	-	d18	-	-	uncharacterized protein	-
HBSAL_06185	OE_2527F	73	d18	VNG_1052H	-	beta-lactamase domain protein	close_paralog
HBSAL_06190	OE_2528R	75	d18	VNG_1053G	aglJ	dolichyl-phosphate glucosyltransferase AglJ	close_paralog
HBSAL_06195	OE_2529F	64	d18	VNG_1054G	aglR	probable flippase AglR	close_paralog
HBSAL_06200	OE_2530F	89	d18	VNG_1055G	aglF2	UTP--glucose-1-phosphate uridylyltransferase AglF	close_paralog
HBSAL_06205	-	-	d18	-	-	ATP-grasp fold protein	-
HBSAL_06215	-	-	d18	-	-	ISH8-type transposase ISH8	-
HBSAL_06220; HBSAL_06210	-	-	d18	-	-	ISH14-type transposase	pseudo(91-R6;split)
HBSAL_06225	-	-	d18	-	-	AlkP-core domain protein	-
HBSAL_06230	-	-	d18	-	-	probable glycosyltransferase, type 2	-
HBSAL_06235	-	-	d18	-	-	probable glycosyltransferase, type 1	-
HBSAL_06240	-	-	d18	-	-	AlkP-core domain protein	-
HBSAL_06245	OE_2531F	48	d18	VNG_1056C	-	AlkP-core domain protein	close_paralog
HBSAL_06250	OE_2547R	81	d18	VNG_1067G	aglG	glucuronosyltransferase AglG	close_paralog
HBSAL_06255	-	-	d18	-	-	uncharacterized protein	-
HBSAL_06260	-	-	d18	-	-	uncharacterized protein	-
HBSAL_06265	-	-	d18	-	-	uncharacterized protein	-
HBSAL_06270	-	-	d18	-	-	uncharacterized protein	-
HBSAL_06280	-	-	d18	-	-	uncharacterized protein	-
HBSAL_06285	-	-	d18	-	-	ISH3-type transposase	-
HBSAL_06420	-	-	d19	-	-	ISH10-type transposase ISNpe8	-
HBSAL_06790	-	-	d20	-	-	PemK family protein	-
HBSAL_06795	-	-	d20	-	-	uncharacterized protein	-
HBSAL_07130	-	-	d24	-	-	uncharacterized protein	-
HBSAL_07610	-	-	d26	-	-	insertion element protein (MITEHsal2)	-
HBSAL_07885	-	-	d27	-	-	insertion element protein (MITEHsal2)	-

HBSAL_08585	-	-	d28	-	-	ISH10-type transposase ISH10	-
HBSAL_08740	-	-	d30	-	-	DUF2085 family protein	-
HBSAL_08745	-	-	d30	-	-	small CPxCG-related zinc finger protein	-
HBSAL_08750	-	-	d30	-	-	small CPxCG-related zinc finger protein	-
HBSAL_08755	-	-	d30	-	-	small CPxCG-related zinc finger protein	-
HBSAL_08760	-	-	d30	-	-	uncharacterized protein	-
HBSAL_08765	-	-	d30	-	-	SWIM zinc finger domain protein	-
HBSAL_08770	-	-	d30	-	-	uncharacterized protein	-
HBSAL_08775	-	-	d30	-	-	uncharacterized protein	-
HBSAL_08780	-	-	d30	-	-	uncharacterized protein	-
HBSAL_08785	-	-	d30	-	-	uncharacterized protein	-
HBSAL_08790	-	-	d30	-	-	XerC/D-like integrase	-
HBSAL_09410	-	-	d31	-	-	uncharacterized protein	-
HBSAL_09415	-	-	d31	-	-	uncharacterized protein	-
HBSAL_09420	-	-	d31	-	-	uncharacterized protein	-
HBSAL_09425	-	-	d31	-	-	uncharacterized protein	-
HBSAL_09430	-	-	d31	-	-	integrase family protein	-
HBSAL_09435	-	-	d31	-	-	uncharacterized protein	-
HBSAL_10735	-	-	d32	-	proS2	proline--tRNA ligase	traverse_junction (C-term_7aa_encoded_on_m32)
HBSAL_10785	-	-	d33	-	-	uncharacterized protein	pseudo(91-R6)
HBSAL_10790	-	-	d33	-	-	uncharacterized protein	-
HBSAL_11035	-	-	d35	-	-	uncharacterized protein	-
HBSAL_11045	-	-	d36	-	-	APH family phosphotransferase	-

**Table S3: Protein-coding genes on divSEGs from the chromosome of strain 91-R6.** Proteins encoded in divSEGs from strain 91-R6 are listed (**code**). The protein name (**protein name**) and, if assigned, the gene (**gene**) is given. If there is a paralog from strain R1, this is flagged in the comment column by "close\_paralog" and its code is given. If possible, the R1 gene is matched to a gene from strain NRC-1. The protein sequence identity is reported (**seq id**). The divSEG serial number (**serial**) is indicated, preceded by "d". This applies to the gene from strain 91-R6. If there is a paralog in strain R1, then the divSEG is a replacement and the R1 gene is found in the same divSEG. Disrupted genes are flagged in the comment column by "pseudo()" (see the legend to Table S1 for details). A special case is the *dmsA* gene which has been targeted by a transposon which was subsequently duplicated, associated with an insertion of >150 kb of DNA sequence. This is flagged in the comment column as "C-term\_far\_away(HBSAL\_05135)". Another

special case is the proS2 gene which traverses into the adjacent matchSEG on which the C-terminal heptapeptide is encoded. This is flagged in the comment column as "traverse\_junction (C-term\_7aa\_encoded\_on\_m32)".

code (R1)	serial	code (NRC-1)	gene	protein name	comment
OE_1019R	d04	VNG_0013C	-	IS1341-type transposase ISH37	-
OE_1020F	d04	VNG_0014C	leuC	3-isopropylmalate dehydratase large subunit	pseudo(R1;NRC-1)
OE_1021A1F	d04	VNG_0014a	-	ISH14-type transposase ISH29	pseudo(R1;NRC-1)
OE_1022R	d04	VNG_0015H	-	PemK family protein	-
OE_1023R	d04	VNG_0016H	-	HTH domain protein	-
OE_1025F	d04	VNG_0017H	-	RNase H domain protein	pseudo(R1;NRC-1)
OE_1028F	d04	VNG_0019H	-	hypothetical protein	-
OE_1029R	d04	VNG_0020H	-	Fido domain protein	-
OE_1031F	d04	VNG_0021H	-	ISH10-type transposase ISH10	-
OE_1039R	d04	VNG_0025H	-	conserved hypothetical protein	-
OE_1040R	d04	VNG_0026C	-	IS1341-type transposase ISH38	-
OE_1044F	d04	VNG_0027a	-	hypothetical protein	-
OE_1045F	d04	VNG_0028C	-	homolog to ISH16-type transposase	-
OE_1047R	d04	VNG_0029H	-	hypothetical protein	-
OE_1048F	d04	VNG_0029a	-	hypothetical protein	-
OE_1052F	d04	VNG_0030H	-	conserved hypothetical protein	-
OE_1053F	d04	VNG_0031H	-	conserved hypothetical protein	-
OE_1054F	d04	VNG_0032H	-	conserved hypothetical protein	-
OE_1055R	d04	VNG_0033H	-	conserved hypothetical protein	-
OE_1058R	d04	VNG_0035H	-	ISH9-type transposase ISH1	seqdiff(R1/NRC-1)
[OE_1059R]	d04	VNG_0034H; VNG_0035a	-	HTH domain protein	pseudo(R1;split); pseudo(NRC-1;split)
OE_1060F	d04	VNG_0037H	-	conserved hypothetical protein	-
OE_1062F	d04	VNG_0038H	-	UPF0395 family protein	-
OE_1063R	d04	VNG_0039H	-	HTH domain protein	-
OE_1064A1F	d04	VNG_0039a	-	conserved hypothetical protein	pseudo(R1;NRC-1)

OE_1065R	d04	VNG_0040C	-	HTH domain protein	-
OE_1067R	d04	VNG_0041C	-	conserved hypothetical protein	-
OE_1070R	d04	VNG_0042G	-	IS1341-type transposase ISH39	-
OE_1071F	d04	-	-	ISH4-type transposase ISH4	-
OE_1073F	d04	VNG_0043H	-	IS200-type transposase ISH12	-
OE_1074F	d04	VNG_0044H	-	IS1341-type transposase ISH12	-
OE_1076F	d04	VNG_0045C	orc9	Orc1-type DNA replication protein	-
OE_1077R	d04	VNG_0046G	aglM2	UDP-glucose 6-dehydrogenase AglM	has 67% seq_id to a paralog shared between strains R1 and 91-R6
OE_1078F	d04	VNG_0047G	aglF1	UTP--glucose-1-phosphate uridylyltransferase AglF	has 85% seq_id to a paralog shared between strains R1 and 91-R6
OE_1079F	d04	VNG_0049H	-	FkbM family methyltransferase	-
OE_1080F	d04	VNG_0050C	-	probable RfbX family transport protein	-
OE_1081R	d04	VNG_0051G	gth6	probable glycosyltransferase, type 1	-
OE_1083R	d04	VNG_0051a	-	ISH3-type transposase ISH3	seqdiff(R1/NRC-1)
[OE_1086A1F ]	d04	VNG_0053H	-	AlkP-core domain protein	pseudo(R1;split); pseudo(NRC-1;split; N-term_part_unannotated)
OE_1087R	d04	VNG_0052H	-	ISH8-type transposase ISH8	-
OE_1091R	d04	VNG_0054H	-	conserved hypothetical protein	-
OE_1094R	d04	VNG_0056H	-	ISH10-type transposase ISNpe8	-
OE_1097F	d04	VNG_0056a	-	pectin lyase domain protein	-
OE_1100F	d04	VNG_0057H	-	conserved hypothetical protein	-
OE_1101R	d04	VNG_0058H	-	conserved hypothetical protein	-
OE_1102R	d04	-	-	ISH8-type transposase ISH8	-
OE_1107R	d04	VNG_0058a	-	conserved hypothetical protein	pseudo(NRC-1;split; N-term_part_unannotated)
OE_1109R	d04	VNG_0060G	gth4	probable glycosyltransferase, type 1	-
OE_1110F	d04	VNG_0061C	-	AlkP-core domain protein	-
OE_1112R	d04	VNG_0062G	gth5	probable glycosyltransferase, type 1	-
OE_1113R	d04	VNG_0063G	-	GalE family epimerase/dehydratase	-

OE_1114F	d04	VNG_0064G	aglF3	UTP--glucose-1-phosphate uridylyltransferase AglF	-
OE_1115F	d04	VNG_0065G	-	GalE family epimerase/dehydratase	-
OE_1116F	d04	VNG_0066H	-	UPF0175 family protein	-
OE_1117F	d04	VNG_0067H	-	conserved hypothetical protein	pseudo(R1;NRC-1)
OE_1119F	d04	VNG_0068H	-	GalE family epimerase/dehydratase	pseudo(R1;NRC-1)
OE_1120F	d04	VNG_0069H	-	conserved hypothetical protein	-
OE_1121F	d04	VNG_0070H	-	conserved hypothetical protein	-
OE_1122A1F	d04	VNG_0070a	-	GalE family epimerase/dehydratase	pseudo(R1;NRC-1)
OE_1124R	d04	VNG_0072H	-	homolog to endonuclease VapC	-
OE_1126R	d04	VNG_0072a	-	conserved hypothetical protein	-
OE_1127F	d04	VNG_0073C	-	GalE family epimerase/dehydratase	pseudo(R1;NRC-1)
[OE_1128F]	d04	[VNG_0075H ;VNG_0075a]	-	HTH domain protein	pseudo(R1;split); pseudo(NRC-1;split)
OE_1129B1F	d04	VNG_0075b	-	conserved hypothetical protein	pseudo(R1;NRC-1)
OE_1169A1F	d05	-	-	integrase family protein	pseudo(R1) ; unannotated(NRC-1; very_short_pseudo)
[OE_1171F]	d05	VNG_0106G	rmeM	type I restriction-modification system DNA-methyltransferase RmeM	pseudo(R1;split)
OE_1173F	d05	-	-	ISH8-type transposase ISH8	-
OE_1177F	d05	VNG_0107G	rmeS	type I site-specific deoxyribonuclease subunit RmeS	-
OE_1178F	d05	VNG_0108G	rmeR	type I site-specific deoxyribonuclease subunit RmeR	-
OE_1182F	d05	VNG_0110C	-	DUF45 family protein	-
OE_1183F	d05	VNG_0110a	-	hypothetical protein	-
OE_1184R	d05	VNG_0110b	-	integrase family protein	pseudo(R1;NRC-1)
OE_1192R	d06	VNG_0116H	-	homolog to pHK2-ORF10	-
OE_1193F	d06	VNG_0116a	-	hypothetical protein	-
OE_1194R	d06	VNG_0117H	-	hypothetical protein	-
OE_1196R	d06	VNG_0118H	-	conserved hypothetical protein	-
OE_1197R	d06	VNG_0119H	-	hypothetical protein	-
OE_1198R	d06	VNG_0120H	-	hypothetical protein	-



OE_1231R	d07	-	-	insertion element protein (ISH2)	-
OE_1439F	d08	VNG_0285C	-	IS200-type transposase ISH22	-
OE_1440F	d08	VNG_0286C	-	IS1341-type transposase ISH22	-
OE_1506R	d09	VNG_0337H	-	ISH8-type transposase ISH8	-
OE_1572R	d10	-	-	ISH9-type transposase ISH1	-
OE_2430F	d15	VNG_0985H	-	HTH domain protein	-
OE_2432B1R	d15	VNG_0985a	-	conserved hypothetical protein	-
OE_2432C1F	d15	VNG_0986H	-	SWIM zinc finger domain protein	-
OE_2432F	d15	-	-	ISH3-type transposase ISH3	-
OE_2433A1F	d15	-	-	ISH3-type transposase ISH3	-
OE_2435F	d15	VNG_0987H	-	small CPxCG-related zinc finger protein	-
OE_2436B1F	d15	VNG_0987a	-	small CPxCG-related zinc finger protein	-
OE_2437F	d15	VNG_0988H	-	DUF2085 family protein	-
OE_2438R	d15	VNG_0989C	-	XerC/D-like integrase	-
OE_2442R	d16	VNG_0991H	-	hypothetical protein	-
OE_2444F	d17	VNG_0993H	-	hypothetical protein	-
OE_2466F	d18	VNG_1006H	-	conserved hypothetical protein	-
OE_2467R	d18	VNG_1007a	-	integrase family protein	-
OE_2470F	d18	VNG_1009G	arlA2	archaellin A2	shows 80% seq_id to R1:ArlA1 75% seq_id to 91-R6:ArlA
OE_2473F	d18	VNG_1012H	grx5	glutaredoxin	-
OE_2474R	d18	VNG_1013G	htrXIII	transducer protein HtrXIII	-
OE_2478R	d18	VNG_1015H	-	conserved hypothetical protein	-
OE_2481R	d18	VNG_1017H	gth8	probable glycosyltransferase, type 1	-
OE_2486F	d18	VNG_1018G	-	probable oxidoreductase (aldo-keto reductase family protein)	-
OE_2491F	d18	VNG_1020C	pgsA1	CDP-alcohol 1-archaetidyltransferase	-
OE_2492F	d18	VNG_1021C	arfA2	GTP cyclohydrolase 3	has 52% seq_id to a paralog shared between strains R1 and 91-R6
OE_2494F	d18	VNG_1023C	adh6	oxidoreductase (homolog to zinc-containing alcohol dehydrogenase / threonine 3-dehydrogenase)	-

OE_2495F	d18	VNG_1024C	-	PtpS family protein	-
OE_2497F	d18	VNG_1025H	-	homolog to S-adenosylmethionine-dependent methyltransferase	-
OE_2499F	d18	VNG_1026H	-	DUF457 family protein	-
OE_2514F	d18	VNG_1039H	-	hypothetical protein	-
OE_2532R	d18	VNG_1057C	-	AlkP-core domain protein	-
OE_2533F	d18	VNG_1058H	aglQ	AgIQ family protein	-
OE_2535R	d18	VNG_1059C	gth7	probable glycosyltransferase, type 1	-
OE_2536F	d18	VNG_1060H	-	FkbM family methyltransferase	-
OE_2537F	d18	VNG_1062G	aglE	glycosyltransferase AgIE	-
OE_2538R	d18	VNG_1063H	-	conserved hypothetical protein	-
OE_2540R	d18	VNG_1064H	-	ISH6-type transposase ISH6	seqdiff(R1/NRC-1)
OE_2545F	d18	VNG_1065C	-	probable hexuronic acid methyltransferase	-
OE_2546F	d18	VNG_1066C	aglI	glycosyltransferase AgII	-
OE_2741F	d21	VNG_1213a	-	integrase family protein	pseudo(R1;NRC-1)
OE_2743F	d21	VNG_1214H	-	conserved hypothetical protein	-
OE_2886R	d25	-	-	ISH9-type transposase ISH1	-
OE_3337F	d29	-	-	insertion element protein (ISH2)	-
OE_4042R	d33	VNG_2174H	-	hypothetical protein	-
OE_4043R	d33	[VNG_2176H ;VNG_2174a]	-	hypothetical protein	pseudo(NRC-1;split)
OE_4044R	d33	VNG_2177H	-	hypothetical protein	-
OE_4045R	d33	VNG_2177a	-	hypothetical protein	-
OE_4267F	d38	VNG_2324H	-	Abi/CAAX domain protein	-
OE_4346R	d39	VNG_2384G	nrdA1	ribonucleoside-diphosphate reductase alpha subunit	-
OE_4347F	d39	VNG_2385H	-	conserved hypothetical protein	-
OE_4348R	d39	VNG_2386C	-	UspA domain protein	-
OE_4350R	d39	VNG_2387a	-	TSUP family transport protein	-
OE_4727R	d03	VNG_2652H	-	IS1341-type transposase ISH34	-
OE_4728F	d03	VNG_2653C	-	IS200-type transposase ISH34	-

**Table S4: Protein-coding genes on divSEGs from the chromosome of strain R1.** Proteins encoded in divSEGs from strain R1 are listed (**code**). The protein name (**protein name**) and, if assigned, the gene (**gene**) is given. The genes can be correlated with those from strain NRC-1 except for genes encoded on strain-specific MGEs, and for one very short pseudogene. In some cases, the comment indicates that a paralog is shared between strains R1 and 91-R6.

code (91-R6)	gene	protein name	comment
HBSAL_12300	-	insertion element protein (MITEHsal3)	-
HBSAL_12565	-	ISH10-type transposase ISNpe8	-
[HBSAL_12595;HBSAL_12605]	-	ISH3-type transposase	pseudo(91-R6;split)
HBSAL_12600	-	ISH9-type transposase ISHsal6	-
[HBSAL_12620;HBSAL_12630];[HBSAL_13310;HBSAL_13320]	-	ISH8-type transposase ISH8	pseudo(91-R6;split)
HBSAL_12625;HBSAL_13315	-	ISH8-type transposase ISH32	-
HBSAL_12635;HBSAL_13325	-	AAA-type ATPase core domain protein	-
HBSAL_12640;HBSAL_13330	-	Mre11 family protein	-
HBSAL_12645	-	uncharacterized protein	pseudo(91-R6)
HBSAL_12650;HBSAL_13340	-	HTH domain protein	-
HBSAL_12655;HBSAL_13345	-	PemK family protein	-
[HBSAL_12660;HBSAL_12690];[HBSAL_13350;HBSAL_13380]	-	DUF21/CBS domain protein	pseudo(91-R6;split)
HBSAL_12665;HBSAL_13355	-	HTH domain protein	-
HBSAL_12670;HBSAL_13360	-	ISH7-type transposase	-
HBSAL_12675;HBSAL_13365	-	uncharacterized protein	-
HBSAL_12680;HBSAL_13370	-	uncharacterized protein	-
HBSAL_12685;HBSAL_13375	-	metallophosphoesterase domain protein	-
HBSAL_12695	-	small CPxCG-related zinc finger protein	pseudo(91-R6)
HBSAL_12700;HBSAL_13390	-	small CPxCG-related zinc finger protein	pseudo(91-R6)
HBSAL_12705;HBSAL_13395	-	ISH8-type transposase	pseudo(91-R6)
HBSAL_12720;HBSAL_13410	-	HTH-10 family transcription regulator	pseudo(91-R6)
HBSAL_12725;HBSAL_13415	-	uncharacterized protein	-
HBSAL_12730;HBSAL_13420	-	uncharacterized protein	-
HBSAL_12735;HBSAL_13425	-	uncharacterized protein	-
HBSAL_12740;HBSAL_13430	-	uncharacterized protein	-
HBSAL_12745;HBSAL_13435	-	uncharacterized protein	-
HBSAL_12750;HBSAL_13440	-	uncharacterized protein	-
HBSAL_12755;HBSAL_13445	-	uncharacterized protein	-

HBSAL_12760;HBSAL_13450	-	uncharacterized protein	-
HBSAL_12765;HBSAL_13455	-	homolog to ISH7-type transposase	pseudo(91-R6)
HBSAL_12770;HBSAL_13460	-	tetratricopeptide repeat protein	-
HBSAL_12775;HBSAL_13465	-	small CPxCG-related zinc finger protein	-
HBSAL_12780;HBSAL_13470	-	DUF4238 family protein	-
HBSAL_12785;HBSAL_13475	-	uncharacterized protein	-
HBSAL_12795;HBSAL_13485	-	ISH8-type transposase ISH5	-
[HBSAL_12800;HBSAL_12790];[HBSAL_13490;HBSAL_13480]	-	ISH3-type transposase ISH3	pseudo(91-R6;split)
HBSAL_12810;HBSAL_13500	-	ISH3-type transposase ISH3	-
HBSAL_12840;HBSAL_13530	-	uncharacterized protein	-
HBSAL_12845;HBSAL_13535	-	uncharacterized protein	pseudo(91-R6)
HBSAL_12850;HBSAL_13540	-	ISH9-type transposase ISH1	-
HBSAL_13005	-	chimeric protein	pseudo(91-R6)
HBSAL_13010	-	ISH8-type transposase ISH5	-
HBSAL_13015	-	uncharacterized protein	pseudo(91-R6)
HBSAL_13030	-	ISH7-type transposase	pseudo(91-R6)
HBSAL_13035	-	DUF234 domain protein	-
HBSAL_13045	-	ISH6-type transposase ISH6	-
[HBSAL_13050;HBSAL_13040]	-	uncharacterized protein (central)	pseudo(91-R6;split)
HBSAL_13055	-	ISH8-type transposase ISHsal4	-
HBSAL_13060	-	insertion element protein (MITEHsal2)	-
HBSAL_13065	-	uncharacterized protein	-
HBSAL_13070	-	ISH7-type transposase	-
HBSAL_13075	-	uncharacterized protein	pseudo(91-R6)
HBSAL_13080	-	uncharacterized protein	-
HBSAL_13085	-	PQQ repeat protein	-
HBSAL_13090	tbp6	TATA-binding transcription initiation factor	-
HBSAL_13160	-	insertion element protein (MITEHsal2)	-
HBSAL_13170	-	uncharacterized protein	-

HBSAL_13175	-	ISH8-type transposase ISH8	-
HBSAL_13180	-	ISH11-type transposase	-
HBSAL_13185	-	uncharacterized protein	-
HBSAL_13190	-	ISH9-type transposase	pseudo(91-R6)
HBSAL_13195	orc15	Orc1-type DNA replication protein	-
HBSAL_13200	-	uncharacterized protein	-
HBSAL_13205	-	ParA domain protein	-
HBSAL_13210	-	uncharacterized protein	-
HBSAL_13215	vapB	probable VapB/AbrB family antitoxin	-
HBSAL_13220	vapC	probable ribonuclease VapC	-
HBSAL_13225	-	metallophosphoesterase domain protein	-
HBSAL_13230	-	uncharacterized protein	-
HBSAL_13235	-	uncharacterized protein	-
HBSAL_13240	-	DUF457 family protein	-
HBSAL_13245	-	uncharacterized protein	-
HBSAL_13250	-	integrase family protein	-
HBSAL_13255	-	uncharacterized protein	pseudo(91-R6)
HBSAL_13260	-	probable DEAD/DEAH box helicase	-
HBSAL_13265	-	uncharacterized protein	-
HBSAL_13270	-	homolog to helicase	-
HBSAL_13280	-	insertion element protein (MITEHsal2)	-
[HBSAL_13285;HBSAL_13275]	-	homolog to modification methylase	pseudo(91-R6;split)
HBSAL_13290	-	uncharacterized protein	-
HBSAL_13300	-	ISH3-type transposase	-
[HBSAL_13305;HBSAL_13295]	-	DUF499 domain protein	pseudo(91-R6;split)
HBSAL_13335	-	uncharacterized protein	pseudo(91-R6)
HBSAL_13385	-	small CPxCG-related zinc finger protein	pseudo(91-R6)

**Table S5: Strain-specific protein-coding genes from plasmids of strain 91-R6.** This table lists proteins which are encoded on plasmids of strain 91-R6 but do not have homologs in strain R1. The protein name (**protein name**) and, if assigned, the gene (**gene**) is given.

code (R1)	code (NRC-1)	gene	protein name	comment
OE_5013R	VNG_6145a	-	conserved hypothetical protein	pseudo(R1;split+translocated;N-term_OE_5405F) pseudo(NRC-1;split+trunc)
OE_5015F	VNG_6147H	-	ISH8-type transposase ISH8	-
OE_5017R	VNG_6148H	-	ISH8-type transposase ISH32	-
OE_5018R	VNG_6149H	-	conserved hypothetical protein	-
OE_5019F	VNG_6150G	orc1	Orc1-type DNA replication protein	pseudo(R1;NRC-1)
OE_5020F	VNG_6152H	-	conserved hypothetical protein	pseudo(R1;NRC-1)
OE_5021F	VNG_6153G	parA3	ParA domain protein	-
OE_5022F	VNG_6155H	-	conserved hypothetical protein	-
OE_5025F	VNG_6156H	-	conserved hypothetical protein	pseudo(R1;NRC-1)
OE_5027R	VNG_6156a	-	ISH3-type transposase ISH3	-
OE_5029R	VNG_6156b	-	hypothetical protein	-
OE_5030R	VNG_6157H	-	conserved hypothetical protein	-
OE_5031R	VNG_6158H	-	conserved hypothetical protein	pseudo(R1;NRC-1)
OE_5032R	VNG_6159H	-	hypothetical protein	-
OE_5033R	[VNG_6162H ;VNG_6160H ]	-	conserved hypothetical protein	pseudo(NRC-1;split)
OE_5036F	VNG_6163H	-	chimeric protein (conserved hypothetical protein / DNA-directed DNA polymerase B2)	pseudo(R1;NRC-1)
OE_5037R	VNG_6164G	orc2	Orc1-type DNA replication protein	pseudo(R1;NRC-1)
OE_5039R	VNG_6165H	-	conserved hypothetical protein	-
OE_5040B1F	VNG_6165a	-	ArsR family transcription regulator	pseudo(R1;NRC-1)
OE_5042R	VNG_6166H	-	homolog to endonuclease VapC	-
OE_5043R	VNG_6168H	-	homolog to antitoxin VapB	-
OE_5045F	VNG_6168a	-	chimeric protein (IS1341-type transposase / UspA domain protein)	pseudo(R1;NRC-1)
OE_5048F	VNG_6171H	-	conserved hypothetical protein	-
OE_5049F	VNG_6173C	sph2	Smc-like protein Sph2	-

OE_5051A1F	VNG_6175a	kdpF	potassium-transporting ATPase subunit F	-
OE_5051R	VNG_6175G	trkA2	TrkA domain protein	-
OE_5052F	VNG_6176G	kdpA	potassium-transporting ATPase subunit A	-
OE_5053F	VNG_6177G	kdpB	potassium-transporting ATPase subunit B	-
OE_5054F	VNG_6178G	kdpC	potassium-transporting ATPase subunit C	-
OE_5055F	VNG_6179G	kdpQ	UspA domain protein KdpQ	-
OE_5058F	VNG_6180H	-	conserved hypothetical protein	-
OE_5061F	VNG_6180a	-	hypothetical protein	-
OE_5062R	VNG_6181H	-	IS1341-type transposase ISH35	-
OE_5063R	VNG_6182H	-	IS200-type transposase ISH35	-
OE_5065R	VNG_6183C	-	DHH/RecJ family phosphoesterase	-
OE_5066R	VNG_6184G	-	UspA domain protein	-
OE_5067R	VNG_6185H	-	hypothetical protein	-
OE_5068F	VNG_6186H	polB4	DNA-directed DNA polymerase B2	pseudo(R1;NRC-1)
OE_5225R	-	-	ISH3-type transposase ISH3	-
OE_5233F	VNG_6327e	-	ISH8-type transposase ISH30	-
OE_5243F	-	car	transducer protein Car	-
OE_5245F	-	-	ABC-type transport system ATP-binding protein	-
OE_5246R	-	-	ABC-type transport system permease protein	-
OE_5248F	-	-	conserved hypothetical protein	-
OE_5249F	-	-	RND superfamily permease	-
OE_5254F	-	-	UspA domain protein	-
OE_5255R	-	-	DASS family transport protein	-
OE_5257A1R	-	-	conserved hypothetical protein	-
OE_5260F	-	-	ISH10-type transposase ISH10	-
OE_5264F	-	-	ABC-type transport system ATP-binding protein	-
OE_5265F	-	-	conserved hypothetical protein	-
OE_5267R	-	-	conserved hypothetical protein	-
OE_5268R	-	-	ABC-type transport system ATP-binding protein	-



OE_5270R	-	-	ABC-type transport system permease protein	-
OE_5272R	-	-	ABC-type transport system permease protein	-
OE_5273R	-	-	ABC-type transport system periplasmic substrate-binding protein	-
OE_5275R	-	-	hypothetical protein	-
OE_5276F	-	-	ArsR family transcription regulator	-
OE_5280R	-	-	major facilitator superfamily transport protein	pseudo(R1)
OE_5282R	-	-	HTH domain protein	-
OE_5285R	-	-	RNase H domain protein	-
OE_5286R	-	-	probable DEAD/DEAH box helicase	-
OE_5289R	-	-	ribonuclease H domain protein	-
OE_5290R	-	-	hypothetical protein	-
OE_5291F	-	-	conserved hypothetical protein	-
OE_5293F	-	-	major facilitator superfamily transport protein	-
OE_5294R	-	-	hypothetical protein	-
OE_5295F	-	-	hypothetical protein	-
OE_5297A1R	-	apbE	flavin transferase ApbE	pseudo(R1)
OE_5297F	-	-	conserved hypothetical protein	pseudo(R1)
OE_5298F	-	trkA8	TrkA domain protein	-
OE_5301F	-	trkH4	Trk-type transport system (probable substrate potassium)	-
OE_5304A1F	-	-	homolog to helicase	pseudo(R1)
OE_5305R	-	-	HTH domain protein	-
OE_5307F	-	-	ABC-type transport system ATP-binding protein	-
OE_5308F	-	-	conserved hypothetical protein	pseudo(R1)
OE_5311R	-	-	conserved hypothetical protein	-
OE_5314F	-	-	conserved hypothetical protein	-
OE_5315R	-	-	hypothetical protein	-
OE_5317A1R	-	-	integrase family protein	pseudo(R1)
OE_5317B1F	-	-	conserved hypothetical protein	pseudo(R1)

OE_5317D1R	-	-	conserved hypothetical protein	pseudo(R1)
OE_5318F	-	-	conserved hypothetical protein	-
OE_5319B1R	-	-	ISH14-type transposase	pseudo(R1)
OE_5322A1R	-	-	ISH14-type transposase HsIRS4	pseudo(R1)
OE_5322B1R	-	-	IS1341-type transposase	pseudo(R1)
OE_5322R	-	-	conserved hypothetical protein	-
OE_5324A1F	-	-	ISH14-type transposase HsIRS2	pseudo(R1)
OE_5324F	-	-	IS1341-type transposase	pseudo(R1)
OE_5325F	-	-	HD family hydrolase	-
OE_5326R	-	-	conserved hypothetical protein	pseudo(R1)
OE_5328R	-	-	UvrD/REP family helicase	-
OE_5335R	-	-	homolog to nuclease subunit B	-
OE_5339R	-	-	ISH9-type transposase ISH1	-
[OE_5340R]	-	-	ISH8-type transposase ISH8	pseudo(R1;split)
[OE_5343R]	-	-	BREX type 5 system helicase BrxH2	pseudo(R1;split)
OE_5344R	-	-	conserved hypothetical protein	-
OE_5349R	-	-	conserved hypothetical protein	-
[OE_5358F]	-	-	conserved hypothetical protein	pseudo(R1;split)
OE_5359R	-	-	ISH3-type transposase ISH3	-
[OE_5361A1R ]	-	-	DUF2204 family protein	pseudo(R1;split)
OE_5361R	-	-	BREX type 5 system protein BrxC	pseudo(R1)
OE_5363R	-	-	insertion element protein (ISH2)	-
OE_5365R	-	-	ArsR family transcription regulator	-
OE_5381F	-	orc13	Orc1-type DNA replication protein	pseudo(R1)
OE_5383F	-	-	ISH3-type transposase ISH3	-
OE_5386R	-	-	homolog to deoxyhypusine synthase	pseudo(R1)
OE_5387F	-	-	ISH7-type transposase	-
OE_5393F	-	-	insertion element protein (ISH2)	-
OE_5406C1F	-	-	helicase domain protein	pseudo(R1)

OE_5406R	-	-	ISH8-type transposase ISH8	-
OE_5407F	-	-	ISH8-type transposase ISH8	-
OE_5408B1F	-	-	TSUP family transport protein	pseudo(R1)
OE_5418F	VNG_7136a	-	insertion element protein (ISH2)	-
OE_5433F	VNG_7127a	-	ISH3-type transposase ISH3	-
OE_6001R	VNG_6331H	-	ISH8-type transposase ISH8	-
[OE_6002R]	VNG_6332a	-	conserved hypothetical protein	pseudo(R1;split); pseudo(NRC-1;split+trunc)
OE_6006R	VNG_6335H	-	conserved hypothetical protein	-
OE_6008R	VNG_6337G	parA5	ParA domain protein	-
OE_6010F	VNG_6339H	-	conserved hypothetical protein	pseudo(R1;NRC-1)
OE_6011R	VNG_6340H	-	conserved hypothetical protein	-
OE_6012F	VNG_6341H	-	ISH6-type transposase ISH6	seqdiff(R1/NRC-1)
OE_6016C1R	VNG_6341d	-	homolog to histidine kinase	pseudo(R1;NRC-1)
OE_6016F	[VNG_6341a; VNG_6341c]	-	cysteine-rich protein	pseudo(NRC-1;split)
OE_6017B1R	VNG_6341e	tfs3	transcription elongation factor TFS	pseudo(R1;NRC-1)
OE_6018R	VNG_6343H	-	conserved hypothetical protein	pseudo(R1;NRC-1)
OE_6020R	[VNG_6346H ;VNG_6344H ]	-	conserved hypothetical protein	pseudo(NRC-1;split)
OE_6021F	VNG_6347H	-	conserved hypothetical protein	-
OE_6022A1R	VNG_6348a	-	small CPxCG-related zinc finger protein	-
OE_6022R	VNG_6348H	-	conserved hypothetical protein	-
OE_6023R	VNG_6349C	-	Fido domain protein	-
OE_6026R	VNG_6351G	tfbC	transcription initiation factor TFB	-
OE_6030R	VNG_6355H	-	conserved hypothetical protein	-
OE_6031A1F	-	-	probable DNA-directed DNA polymerase B2	pseudo(R1)
OE_6031B1F	VNG_6357a	-	conserved hypothetical protein	pseudo(R1;NRC-1)
OE_6031R	VNG_6357H	-	HTH domain protein	-

OE_6032F	VNG_6359H	-	conserved hypothetical protein	-
OE_6033R	VNG_6359a	-	conserved hypothetical protein	-
OE_6034F	VNG_6361G	-	IS1341-type transposase ISH40	-
OE_6040R	VNG_6364H	-	conserved hypothetical protein	-
[OE_6045R]	[VNG_6367H ;VNG_6366H ]	-	ISH3-type transposase ISH20	pseudo(R1;split); pseudo(NRC-1;split)
OE_6052R	VNG_6372H	-	conserved hypothetical protein	-
OE_6053F	VNG_6373G	-	homolog to phage PhiH1 repressor protein	-
OE_6055R	VNG_6375H	-	conserved hypothetical protein	-
OE_6057D1R	VNG_6377a	-	chimeric protein	pseudo(R1;NRC-1)
OE_6057R	VNG_6377H	-	TrmB family transcription regulator	-
OE_6059R	VNG_6379C	-	probable iron-sulfur protein (4Fe-4S)	-
OE_6062R	VNG_6381H	-	DUF162 family protein	-
OE_6063F	VNG_6383G	-	LctP family transport protein	-
OE_6066R	VNG_6384H	-	hypothetical protein	-
OE_6069R	VNG_6385a	vapC	probable ribonuclease VapC	-
OE_6070R	VNG_6387H	vapB	probable VapB/AbrB family antitoxin	-
OE_6071R	VNG_6389G	tfbE	transcription initiation factor TFB	-
OE_6073R	VNG_6390H	-	chimeric protein	-
OE_6074A1F	VNG_6393a	-	conserved hypothetical protein	-
OE_6075R	VNG_6395H	-	ISH8-type transposase ISH8	-
[OE_6079F]	VNG_6396H	-	PIN domain protein	pseudo(R1;split); pseudo(NRC-1;split;N-term_part_unannotated)
OE_6080F	VNG_6397H	-	HTH domain protein	-
OE_6083R	VNG_6400H	-	SWIM zinc finger domain protein	-
OE_6084R	VNG_6401H	-	conserved hypothetical protein	-
OE_6085R	VNG_6402H	-	HTH domain protein	-
OE_6087R	VNG_6403H	-	conserved hypothetical protein	-
OE_6089R	VNG_6406H	-	IS1341-type transposase HsIRS45	pseudo(R1;NRC-1)

OE_6092R	VNG_6407H	-	conserved hypothetical protein	-
OE_6093F	VNG_6408G	phzF2	PhzF family protein	-
OE_6095R	VNG_6409H	-	conserved hypothetical protein	-
OE_6096A1R	VNG_6411a	-	conserved hypothetical protein	-
OE_6097R	VNG_6412H	-	conserved hypothetical protein	-
OE_6098R	VNG_6413H	-	HTH domain protein	-
OE_6099F	VNG_6413a	-	conserved hypothetical protein	-
OE_6102R	VNG_6418H	-	conserved hypothetical protein	-
OE_6104R	VNG_6419H	-	conserved hypothetical protein	-
OE_6105R	VNG_6420H	-	conserved hypothetical protein	-
OE_6107R	VNG_6421H	-	ISH11-type transposase ISH11	-
OE_6108B1F	VNG_6421a	-	conserved hypothetical protein	pseudo(R1;NRC-1)
OE_6109B1F	VNG_6421b	-	HTH domain protein	-
OE_6111A1F	VNG_6427a	-	small CPxCG-related zinc finger protein	-
OE_6112F	VNG_6427b	-	small CPxCG-related zinc finger protein	-
OE_6113F	VNG_6427c	-	conserved hypothetical protein	-
OE_6115F	VNG_6430C	-	ISH14-type transposase ISH29	-
OE_6116R	VNG_6431H	-	hypothetical protein	-
OE_6118F	VNG_6432H	-	conserved hypothetical protein	-
OE_6120F	VNG_6432a	-	hypothetical protein	-
OE_6121F	VNG_6434H	-	small CPxCG-related zinc finger protein	-
OE_6124F	VNG_6437C	-	TRAM domain protein	-
OE_6126R	-	-	insertion element protein (ISH2)	-
OE_6128R	VNG_6439H	-	conserved hypothetical protein	-
OE_6130F	VNG_6441H	-	pilin PilA	-
OE_6133R	VNG_6442H	-	ISH10-type transposase ISH10	-
OE_6138F	-	-	homolog to restriction system mrr	-
OE_6139F	-	-	hypothetical protein	-
OE_6140R	-	tfbH	transcription initiation factor TFB	-

OE_6142R	-	-	conserved hypothetical protein	-
OE_6145R	-	-	sensor box histidine kinase	-
OE_6147R	-	-	conserved hypothetical protein	-
OE_6150R	-	-	TrmB family transcription regulator	-
OE_6151A1R	-	-	conserved hypothetical protein	pseudo(R1)
OE_6152A1R	-	-	conserved hypothetical protein	-
OE_6153F	-	-	HTH domain protein	pseudo(R1)
OE_6154F	-	-	hypothetical protein	-
OE_6157R	-	-	conserved hypothetical protein	-
OE_6165R	-	-	ISH3-type transposase ISH3	-
[OE_6166R]	-	-	conserved hypothetical protein	pseudo(R1;split)
OE_6168B1R	-	-	conserved hypothetical protein	-
OE_6170R	-	-	hypothetical protein	-
OE_6171A1R	-	-	ISH3-type transposase ISH3	-
OE_6171F	-	-	ISH3-type transposase ISH3	-
OE_6172F; OE_7052F	[VNG_6042H; ; VNG_6043a]; [VNG_6481a; VNG_6484H] ; [VNG_7035; VNG_7037]; [VNG_7172; VNG_7174]	-	ISH8-type transposase ISH5	pseudo(NRC-1;split)
OE_6174R; OE_7054R	VNG_6045H; VNG_6481H; VNG_7037a; VNG_7171d	-	conserved hypothetical protein	-
OE_6175A1R; OE_7055A1R	VNG_6046H; VNG_6480H; VNG_7037b;	-	conserved hypothetical protein	-

	VNG_7171c			
OE_6176A1R; OE_7056A1R	VNG_6047H; VNG_6479H; VNG_7037c; VNG_7171b	-	conserved hypothetical protein	-
OE_6180R; OE_7060R	-	-	insertion element protein (ISH2)	-
OE_6183A1R; OE_7063A1R	VNG_6051H; VNG_6475H; VNG_7038a; VNG_7170c	-	small CPxCG-related zinc finger protein	-
OE_6184A1R; OE_7064A1R	VNG_6052H; VNG_6474H; VNG_7038c; VNG_7170a	-	conserved hypothetical protein	-
OE_6184R; OE_7064R	VNG_6051a; VNG_6474a; VNG_7038b; VNG_7170b	-	hypothetical protein	-
OE_6197F; OE_7077F	VNG_6066C; VNG_6460C; VNG_7049; VNG_7160	-	rhodanese domain protein / beta-lactamase domain protein	-
OE_6199F; OE_7079F	VNG_6068C; VNG_6457C; VNG_7051; VNG_7158	-	major facilitator superfamily transport protein	-
OE_6202F; OE_7082F	VNG_6072C; VNG_6454C; VNG_7053; VNG_7156	-	TrmB family transcription regulator	-
OE_6204F; OE_7084F	VNG_6073G; VNG_6453G; VNG_7054; VNG_7155	trxA1b	thioredoxin	-

OE_6205F; OE_7085F	VNG_6074G; VNG_6452G; VNG_7055; VNG_7154	trxB1b	thioredoxin-disulfide reductase	pseudo(R1;NRC-1)
OE_6207A1F; OE_7087A1F	-	-	ISH14-type transposase	pseudo(R1)
OE_6212F; OE_7092F	VNG_6078H; VNG_6448H; VNG_7058a; VNG_7150a	-	conserved hypothetical protein	-
OE_6214F; OE_7094F	VNG_6082H; VNG_6444H; VNG_7061; VNG_7148	-	TrmB family transcription regulator	-
OE_6215F; OE_7095F	VNG_6083H; VNG_6443H; VNG_7062; VNG_7147	-	conserved hypothetical protein	-
OE_6217F; OE_7097F	VNG_6084H; VNG_7063; VNG_7146	-	ISH10-type transposase ISH10	-
OE_6219R; OE_7099R	VNG_6085H; VNG_7064; VNG_7145	-	conserved hypothetical protein	-
OE_6220R; OE_7100R	VNG_6086G; VNG_7065; VNG_7144	parA6b	ParA domain protein	-
OE_6221R; OE_7101R	VNG_6087C; VNG_7066; VNG_7143	-	DUF1814 family protein	-
OE_6222R; OE_7102R	VNG_6088C; VNG_7067; VNG_7142	-	DUF4095 family protein	-
OE_6224R; OE_7104R	VNG_6090C; VNG_7069;	-	TRAM domain protein	-



	VNG_7140			
OE_6225F; OE_7105F	VNG_6091G; VNG_7070; [VNG_7138; VNG_7139]	orc11b	Orc1-type DNA replication protein	copy_on_pNRC100_revDup_isSplit
OE_6226F; OE_7106F	[VNG_6091a; VNG_6094H] ; [VNG_7071; VNG_7071b]; [VNG_7136b; VNG_7137]	-	conserved hypothetical protein	pseudo(NRC-1;split)
OE_6227R; OE_7107R	VNG_6095C; VNG_7072	-	UPF0361 family protein	-
OE_6229R; OE_7109R	VNG_6098H; VNG_7073a	-	insertion element protein (ISH2)	-
[OE_6230R]; [OE_7110R]	VNG_6097C; VNG_7073	-	DUF262/DUF1524 domain protein	pseudo(R1;split); pseudo(NRC-1;split+trunc)
OE_6231F; OE_7111F	-	-	conserved hypothetical protein	-
OE_6233A1F; OE_7113A1F	-	-	conserved hypothetical protein	-
OE_6234F; OE_7114F	-	polB3b	probable DNA-directed DNA polymerase B2	-
OE_6235F; OE_7115F	-	orc10b	Orc1-type DNA replication protein	-
OE_6236B1R; OE_7116B1R	-	-	conserved hypothetical protein	-
OE_6238R; OE_7118R	-	-	SWIM zinc finger domain protein	-
OE_6240R; OE_7120R	-	-	conserved hypothetical protein	-
OE_6242R; OE_7122R	-	-	conserved hypothetical protein	-

OE_6244R; OE_7124R	-	-	conserved hypothetical protein	-
OE_6246R; OE_7126R	-	-	conserved hypothetical protein	-
OE_6247R; OE_7127R	-	-	conserved hypothetical protein	-
OE_6249F; OE_7129F	-	-	homolog to NAD-dependent epimerase/dehydratase	-
OE_6251A1R; OE_7131A1R	-	-	conserved hypothetical protein	-
OE_6251R; OE_7131R	-	-	small CPxCG-related zinc finger protein	-
OE_6252A1R; OE_7132A1R	-	-	conserved hypothetical protein	-
OE_6253F; OE_7133F	-	-	conserved hypothetical protein	-
OE_6254R; OE_7134R	-	-	conserved hypothetical protein	-
OE_6255R; OE_7135R	-	-	conserved hypothetical protein	-
OE_6256R; OE_7136R	-	-	conserved hypothetical protein	-
OE_6259B1R; OE_7139B1R	-	-	conserved hypothetical protein	-
OE_6259R; OE_7139R	-	-	conserved hypothetical protein	-
OE_6261R; OE_7141R	-	-	major facilitator superfamily transport protein	-
OE_6263R; OE_7143R	-	-	conserved hypothetical protein	-
OE_6264R; OE_7144R	-	-	HTH domain protein	-
OE_6265R; OE_7145R	-	-	HTH domain protein	-

OE_6266R; OE_7146R	-	tfb12	transcription initiation factor TFB	pseudo(R1)
OE_6267F; OE_7147F	VNG_6106H; VNG_7078a	-	ISH8-type transposase ISH8	-
OE_6268F; OE_7148F	VNG_6106a; VNG_7078b	-	hypothetical protein	pseudo(R1;NRC-1)
OE_6269F; OE_7149F	[VNG_6109a; VNG_6111a]; [VNG_7079; VNG_7079b]	-	hypothetical protein	pseudo(NRC-1;split)
OE_6270R; OE_7150R	VNG_6112H; VNG_7080	-	XerC/D-like integrase	-
OE_6272R; OE_7152R	VNG_6113H; VNG_7081	-	conserved hypothetical protein	-
OE_6274R; OE_7154R	VNG_6115H; VNG_7082	-	conserved hypothetical protein	-
OE_6275A1R; OE_7155A1R	VNG_6117H; VNG_7083a	-	conserved hypothetical protein	-
OE_6275R; OE_7155R	VNG_6116H; VNG_7083	-	HTH domain protein	-
OE_6277R	-	-	ISH7-type transposase	pseudo(R1)
OE_6278R	-	-	PQQ repeat protein	-
OE_6279R	-	-	ARM domain protein	-
OE_6280R	-	-	hypothetical protein	-
OE_6281R	-	-	hypothetical protein	-
OE_6282R	-	-	IS200-type transposase ISH36	pseudo(R1)
OE_6284A1F	-	-	conserved hypothetical protein	-
OE_6285F	-	-	IS1341-type transposase ISH36	-
OE_6288R	-	orc12	Orc1-type DNA replication protein	-
OE_6289R	-	-	chimeric protein	pseudo(R1)
OE_6290A1R	-	-	small CPxCG-related zinc finger protein	-
OE_6292R	-	-	ISH6-type transposase ISH6	-

OE_6296R	-	-	ISH8-type transposase ISH8	-
OE_6298A1R	-	-	insertion element protein (ISH2)	-
[OE_6298B1F ]	-	-	conserved hypothetical protein	pseudo(R1;split)
OE_6299F	-	-	ISH8-type transposase ISH8	-
OE_6301F	-	-	conserved hypothetical protein	-
OE_6303F	-	-	conserved hypothetical protein	-
OE_6308F	-	-	conserved hypothetical protein	-
OE_6309F	-	-	conserved hypothetical protein	-
OE_6311F	-	aaa10	AAA-type ATPase core domain protein	-
OE_6315F	-	-	PQQ repeat protein	-
OE_6321R	-	-	probable secreted glycoprotein	-
OE_6323R	-	-	conserved hypothetical protein	-
OE_6325R	-	-	conserved hypothetical protein	-
OE_6329R	-	ftsZ6	FtsZ family protein, noncanonical	-
OE_6332R	-	-	coiled-coil protein	-
OE_6335R	-	-	conserved hypothetical protein	-
OE_6337R	-	ftsZ7	FtsZ family protein, noncanonical	-
OE_6340R	-	-	conserved hypothetical protein	-
OE_6345R	-	ftsZ8	FtsZ family protein, noncanonical	-
OE_6347R	-	-	coiled-coil protein	-
OE_6351F	-	-	IS1341-type transposase HsIRS8	pseudo(R1)
OE_6353F	-	-	insertion element protein (ISH2)	-
OE_6356F	-	-	UPF0324 family protein	-
OE_6357F	-	-	conserved hypothetical protein	-
OE_7001R	VNG_6001H; VNG_7001	-	HTH domain protein	-
OE_7003R	VNG_6003H; VNG_7002	-	conserved hypothetical protein	-
OE_7004R	VNG_6005H; VNG_7003	-	hypothetical protein	pseudo(R1;NRC-1)

OE_7006R	VNG_6007H; VNG_7005	-	ISH7-type transposase ISH7	-
OE_7007F	VNG_6007a; VNG_7005a	-	hypothetical protein	-
OE_7008F	VNG_6008H; VNG_7006	-	conserved hypothetical protein	-
OE_7009F	VNG_6009H; VNG_7007	-	cro/C1 family transcription regulator	-
OE_7010R	VNG_6010G; VNG_7008	parA10	ParA domain protein	pseudo(R1;NRC-1)
OE_7011R	VNG_6011H; VNG_7009	-	conserved hypothetical protein	-
OE_7012R	VNG_6012H; VNG_7010	-	integrase family protein	-
OE_7017D1F	VNG_6015a; VNG_7011c	-	ABC-type transport system permease protein	pseudo(R1;NRC-1)
OE_7017R	VNG_6015H; VNG_7011b	-	ISH3-type transposase ISH3	-
OE_7019A1F	VNG_6016a; VNG_7012a	-	conserved hypothetical protein	pseudo(R1;NRC-1)
OE_7019F	VNG_6016H; VNG_7012	-	ISH8-type transposase ISH8	-
OE_7020F	VNG_6017H; VNG_7013	-	conserved hypothetical protein	pseudo(R1;NRC-1)
OE_7022R	VNG_6019G; VNG_7015	gvpM1	gas-vesicle-associated protein GvpM	-
OE_7023R	VNG_6020G; VNG_7016	gvpL1	gas-vesicle-associated protein GvpL	-
OE_7024R	VNG_6021G; VNG_7017	gvpK1	gas-vesicle operon protein GvpK	-
OE_7026R	VNG_6022G; VNG_7018	gvpJ1	gas-vesicle-associated protein GvpJ	-
OE_7027R	VNG_6023G; VNG_7019	gvpI1	gas-vesicle operon protein GvpI	-

OE_7028R	VNG_6024G; VNG_7020	gvpH1	gas-vesicle operon protein GvpH	-
OE_7030R	VNG_6025G; VNG_7021	gvpG1	gas-vesicle-associated protein GvpG	-
OE_7031R	VNG_6026G; VNG_7022	gvpF1	gas-vesicle-associated protein GvpF	-
OE_7032R	VNG_6027G; VNG_7023	gvpE1	PadR family transcription activator GvpE	-
OE_7033A1F	-	-	ISH3-type transposase ISH3	-
OE_7033R	VNG_6028G; VNG_7024	gvpD1	regulatory protein GvpD	-
OE_7034F	VNG_6029G; VNG_7025	gvpA1	gas-vesicle major structural protein GvpA	-
OE_7036F	VNG_6031G; VNG_7026	gvpC1	gas-vesicle minor protein GvpC	-
OE_7037F	VNG_6032G; VNG_7027	gvpN1	gas-vesicle operon protein GvpN	-
OE_7038F	VNG_6033G; VNG_7028	gvpO1	gas-vesicle operon protein GvpO	-
OE_7039F	VNG_6034G; VNG_7029	parA7	ParA domain protein	-
OE_7042K1R	VNG_6035a; VNG_7030a	-	small CPxCG-related zinc finger protein	pseudo(R1;NRC-1)
OE_7042R	VNG_6035G; VNG_7030	-	receiver/sensor box histidine kinase	-
OE_7043A1F	VNG_6036H; VNG_7030b	-	small CPxCG-related zinc finger protein	-
OE_7045A1R	VNG_6037a; VNG_7031a	-	homolog to resolvase	pseudo(R1;NRC-1)
OE_7045F	VNG_6037G; VNG_7031	tbpA	homolog to TATA-binding transcription initiation factor	-
OE_7046R	VNG_6038H; VNG_7032	-	ISH8-type transposase ISH8	-
OE_7048F	VNG_6038a; -	-	ISH3-type transposase ISH3	seqdiff(R1/NRC-1)

	VNG_7032a			
OE_7049R	VNG_6039H; VNG_6487H; VNG_7033; VNG_7176	-	helicase domain protein	pseudo(R1;NRC-1)
OE_7050A1R	VNG_6040a; VNG_6484a; VNG_7034a; VNG_7174a	-	conserved hypothetical protein	pseudo(R1;NRC-1)
OE_7050F	VNG_6040H; VNG_6486H; VNG_7034; VNG_7175	-	ISH9-type transposase ISH9	-
OE_7159R	VNG_6119H; VNG_7085	-	ISH7-type transposase ISH7	seqdiff(R1/NRC-1)
OE_7160R	VNG_6120H; VNG_7085a	-	conserved hypothetical protein	-
OE_7161R	VNG_6121H; VNG_7086	-	conserved hypothetical protein	-
OE_7162R	VNG_6123G; VNG_7087	parA8	ParA domain protein	-
OE_7164A1R	VNG_6123a; VNG_7088a	-	conserved hypothetical protein	-
OE_7165R	VNG_6125H; VNG_7089	-	conserved hypothetical protein	-
OE_7166F	VNG_6126H; VNG_7089a	-	PadR family transcription regulator	-
OE_7169A1F	-	-	ISH8-type transposase ISH8	-
OE_7169F	VNG_6126a; VNG_7089b	-	ISH3-type transposase ISH3	pseudo(R1;NRC-1)
OE_7170R	-	-	ISH4-type transposase ISH4	-
OE_7171F	VNG_6126b; VNG_7089c	-	conserved hypothetical protein	-
OE_7172F	VNG_6127H;	-	DUF2800 family protein	-

	VNG_7090			
OE_7173F	VNG_6128H; VNG_7091	-	conserved hypothetical protein	-
OE_7174R	VNG_6129C; VNG_7092	-	DUF790 family protein	-
OE_7176R	VNG_6130G; VNG_7093	rad25a	DNA repair helicase Rad25	-
OE_7177F	VNG_6131H; VNG_7094	-	conserved hypothetical protein	-
OE_7178F	VNG_6132G; VNG_7095	repI1	plasmid replication protein RepI	seqdiff(R1/NRC-1)
OE_7181B1F; OE_8012B1F	VNG_6134H; VNG_7095b	-	conserved hypothetical protein	-
OE_7182F; OE_8013F	[VNG_6135C ; VNG_6136H] ; [VNG_7096; VNG_7097]	-	probable restriction/modification enzyme	pseudo(NRC-1;split)
OE_7185F; OE_8016F	VNG_6139G; VNG_7099	-	ATP-dependent helicase	-
OE_7186F; OE_8017F	VNG_6140G; VNG_7100	tbpC1	TATA-binding transcription initiation factor	-
OE_7187F; OE_8018F	VNG_7101	-	YidE family protein	-
OE_7198F; OE_8030F	-	-	ISH8-type transposase ISH8	-
OE_7201R; OE_8033R	VNG_7107	-	ISH4-type transposase ISH4	-
OE_7214R; OE_8046R	VNG_7114	tbpD1	TATA-binding transcription initiation factor	-
OE_7216F	VNG_7116	-	integrase family protein	-
OE_7217F	VNG_7117	-	conserved hypothetical protein	pseudo(R1;NRC-1)
OE_7220F	VNG_7118	-	conserved hypothetical protein	pseudo(NRC-1)



OE_7222R	-	-	hypothetical protein	-
[OE_7223F]	VNG_6000a; VNG_7000a	-	conserved hypothetical protein	pseudo(R1;split); pseudo(NRC-1;split+trunc)
OE_7224R	-	-	insertion element protein (ISH2)	-
OE_8001F	-	-	UPF0157 family protein	-
OE_8002F	-	parA9	ParA domain protein	-
OE_8005B1R	-	-	conserved hypothetical protein	-
OE_8005C1R	-	-	conserved hypothetical protein	-
OE_8005F	-	-	conserved hypothetical protein	-
OE_8006A1F	-	-	ISH3-type transposase ISH3	-
OE_8006B1F	-	-	conserved hypothetical protein	-
OE_8006F	-	-	PadR family transcription regulator	-
OE_8007F	-	-	DUF2800 family protein	seqdiff(R1/NRC-1)
OE_8008F	-	-	conserved hypothetical protein	-
OE_8009R	-	-	DUF790 family protein	seqdiff(R1/NRC-1)
OE_8010B1F	-	-	conserved hypothetical protein	-
OE_8010G1F	-	repI2	plasmid replication protein RepI	-
OE_8010R	-	rad25b	DNA repair helicase Rad25	-
OE_8048F	-	-	integrase family protein	-
OE_8050F	-	-	conserved hypothetical protein	-

**Table S6: Strain-specific protein-coding genes from plasmids of strain R1.** Proteins encoded in strain specific plasmid regions of strain R1 are listed (**code**). The protein name (**protein name**) and, if assigned, the gene (**gene**) is given. If the plasmid region is also present strain NRC-1, the genes have been correlated except for genes encoded on R1 specific MGEs. Genes encoded on the 210 kb of plasmid unique to R1 and lacking in NRC-1 could not be correlated. Coding sequence differences are indicated in the comment column ("seqdiff(R1/NRC-1)"). Disrupted genes are flagged in the comment column by "pseudo()" (see the legend to Table S1 for details). In case of "split+trunc", the gene has been targeted in strains R1 and NRC-1 by the same MGE at an identical position, but the region on the other side of the MGE is lacking in the NRC-1 plasmid while it is present in the R1 plasmid unique regions. Up to four copies of NRC-1 genes are possible, due to large-scale duplications (four codes, separated by semicolons), because part of the region duplicated between pNRC100 and pNRC200 is further duplicated as an inverted repeat in each of the plasmids. The inverted repeat is longer in pNRC100 and thus some genes occur in three copies. In one such case, the copy on the inverted repeat is targeted by a MGE while the other two copies remained intact (indicated by "copy\_on\_pNRC100\_revDup\_isSplit").

code (NRC-1)	protein name	comment
VNG_0059H	ISH8-type transposase ISH8	strainspecific_MGE
VNG_0112H	ISH3-type transposase ISH3	strainspecific_MGE
VNG_0115a	ISH3-type transposase ISH3	strainspecific_MGE
VNG_0207H	uncharacterized protein	strainspecific_region
VNG_0208H	uncharacterized protein	strainspecific_region
VNG_0209H	XerC/D-like integrase	strainspecific_region
VNG_0210H	insertion element protein (ISH2)	strainspecific_region
[VNG_0212H;VNG_0213a]	DUF4352 domain protein	strainspecific_region;pseudo(NRC-1;split)
VNG_0213H	ISH11-type transposase	strainspecific_region
VNG_0214C	uncharacterized protein	strainspecific_region
VNG_0215C	phage primase domain protein	strainspecific_region
VNG_0216H	uncharacterized protein	strainspecific_region
VNG_0217H	uncharacterized protein	strainspecific_region
VNG_0918H	ISH4-type transposase ISH4	strainspecific_MGE
VNG_0994H	insertion element protein (ISH2)	strainspecific_MGE
VNG_1007H	insertion element protein (ISH2)	strainspecific_MGE
VNG_1587H	ISH11-type transposase	strainspecific_MGE
VNG_1587b	ISH3-type transposase ISH3	strainspecific_MGE
VNG_1651H	insertion element protein (ISH2)	strainspecific_MGE
VNG_1653H	ISH8-type transposase ISH8	strainspecific_MGE
VNG_2175H	ISH8-type transposase ISH8	strainspecific_MGE
VNG_2669b	ISH3-type transposase ISH3	strainspecific_MGE
VNG_6043H;VNG_6483H;VNG_7036;VNG_7173	ISH11-type transposase	strainspecific_MGE
VNG_6079H;VNG_6447H;VNG_7059;VNG_7150	ISH8-type transposase ISH8	strainspecific_MGE
VNG_6093H;VNG_7071a	insertion element protein (ISH2)	strainspecific_MGE
VNG_6099H;VNG_7074	uncharacterized protein	strainspecific_region; pseudo(NRC-1;split+trunc)

VNG_6101H;VNG_7075	probable secreted glycoprotein	strainspecific_region
VNG_6102H;VNG_7076	probable secreted glycoprotein	strainspecific_region
VNG_6103H;VNG_7077	uncharacterized protein	strainspecific_region
VNG_6105H;VNG_7078	uncharacterized protein	strainspecific_region
VNG_6111H;VNG_7079a	ISH3-type transposase ISH3	strainspecific_MGE
VNG_6132a;VNG_7095a	ISH3-type transposase ISH3	strainspecific_MGE
VNG_6135a;VNG_7096a	ISH3-type transposase ISH3	strainspecific_MGE
VNG_6141H	insertion element protein (ISH2)	strainspecific_MGE
VNG_6146H	insertion element protein (ISH2)	strainspecific_MGE
VNG_6149a	ISH3-type transposase ISH3	strainspecific_MGE
VNG_6161H	ISH8-type transposase ISH8	strainspecific_MGE
VNG_6327d	ISH3-type transposase ISH3	strainspecific_MGE
VNG_6341b	ISH3-type transposase ISH3	strainspecific_MGE
VNG_6345H	ISH8-type transposase ISH8	strainspecific_MGE
VNG_6391H	insertion element protein (ISH2)	strainspecific_MGE
VNG_6487a;VNG_7176a	ISH3-type transposase ISH3	strainspecific_MGE;pseudo(NRC-1;frameshift_at_N-term)
VNG_7119	ISH8-type transposase ISH8	strainspecific_MGE
VNG_7136c	ISH3-type transposase ISH3	strainspecific_MGE
VNG_7138a	insertion element protein (ISH2)	strainspecific_MGE

**Table S7: Strain-specific protein-coding genes from strain NRC-1.** Besides strain specific copies of MGEs, there are only two short genome regions, totalling to 15 kb, which are specific to strain NRC-1 and are missing in strain R1 (ref\_R1genome). A 10007 bp insertion was identified in the chromosome (extending from VNG\_0207H to VNG\_0217H). Among the encoded genes is a XerC/D-like integrase family and a phage primase domain protein, two genes typically associated with prophages. The insertion has targeted the *pilB2* gene from a disrupted type IV pilus biogenesis complex. In this complex, the *pilC* gene carries an in-frame stop codon. Interestingly, this complex, including the disruption of the *pilC* gene, is strictly conserved between strains R1 and 91-R6. This type IV pilus biogenesis complex has been partially characterized in several *Halobacterium* strains (Losensky, G., Vidakovic, L., Klingl, A., Pfeifer, F. & Fröls, S. 2015. Novel pili-like surface structures of *Halobacterium salinarum* strain R1 are crucial for surface adhesion. *Front Microbiol*, 5, 755). A 4527 bp strain-specific region, coding for VNG\_6099H to VNG\_6105H is found in pNRC100 and pNRC200 between the MGEs ISH2 and ISH8. The first gene, VNG\_6099H, has been targeted by the MGE but the C-terminal region has been lost. In strain R1 plasmids pHS1 and pHS2 is a 19365 bp region between the same pair of MGEs in an identical genomic context. This region codes for OE6230R to OE6266R. Also in R1, the first gene has been targeted but the C-terminal part (corresponding to VNG\_6097C) is encoded on the other side of the ISH2, an element which has a TSD only in R1. Thus, the R1 sequence represents the original version over that MGE. There is no suitable protein-coding gene across the ISH8 element at the other end but as this MGE lacks a TSD in both strains, this MGE may have been affected by genome rearrangements in both strains.

<b>code (R1)</b>	<b>code (NRC-1)</b>	<b>protein name</b>
OE_1092F	VNG_0055H	spurious ORF
OE_1131R	VNG_0076H	spurious ORF
OE_1135R	VNG_0079H	spurious ORF
OE_1429R	VNG_0280H	spurious ORF
OE_1441F	VNG_0287H	spurious ORF
OE_1538F	VNG_0357H	spurious ORF
OE_1786R	VNG_0529H	spurious ORF
OE_1790R	VNG_0532H	spurious ORF
OE_1813F	VNG_0544H	spurious ORF
OE_1928R	VNG_0613H	spurious ORF
OE_2137F	VNG_0772H	spurious ORF
OE_2351F	VNG_0926H	spurious ORF
OE_2516R	VNG_1041H	spurious ORF
OE_2778R	VNG_1239H	spurious ORF
OE_3271R	VNG_1598H	spurious ORF
OE_3576R	VNG_1832H	spurious ORF
OE_3747F	VNG_1956H	spurious ORF
OE_3754F	VNG_1963H	spurious ORF
OE_3776R	VNG_1983H	spurious ORF
OE_3848R	VNG_2034H	spurious ORF
OE_3860R	VNG_2041H	spurious ORF
OE_4349F	VNG_2387H	spurious ORF
OE_4422R	VNG_2439H	spurious ORF
OE_4457F	VNG_2466C	spurious ORF
OE_4494R	VNG_2495H	spurious ORF
OE_4750R	VNG_2673H	spurious ORF
OE_5046R	VNG_6170H	spurious ORF
OE_5087F	VNG_6204H	spurious ORF

OE_5103F	VNG_6222H	spurious ORF
OE_5163R	VNG_6275H	spurious ORF
OE_5222R	VNG_6325H	spurious ORF
OE_5425R	VNG_7133	spurious ORF
OE_5430F	VNG_7129	spurious ORF
OE_5432F	VNG_7128	spurious ORF
OE_6001D1F	VNG_6332H	spurious ORF
OE_6047R	VNG_6368H	spurious ORF
OE_6058F	VNG_6378H	spurious ORF
OE_6068R	VNG_6385H	spurious ORF
OE_6074R	VNG_6393H	spurious ORF
OE_6088R	VNG_6404H	spurious ORF
OE_6096F	VNG_6411H	spurious ORF
OE_6100R	VNG_6416H	spurious ORF
OE_6110R	VNG_6424H	spurious ORF
OE_6111R	VNG_6427H	spurious ORF
OE_6114R	VNG_6429H	spurious ORF
OE_6268A1R	VNG_6109H	spurious ORF
OE_7005F	VNG_7004	spurious ORF
OE_7021F	VNG_7014	spurious ORF
OE_7073R	VNG_7045;VNG_7163	spurious ORF
OE_7078R	VNG_7050;VNG_7159	spurious ORF
OE_7090F	VNG_7057;VNG_7152	spurious ORF
OE_7091F	VNG_7058;VNG_7151	spurious ORF
OE_7103F	VNG_7068;VNG_7141	spurious ORF
OE_7158F	VNG_7084	spurious ORF
OE_7164R	VNG_7088	spurious ORF
OE_7184R	VNG_7098	spurious ORF
OE_7208F	VNG_7111	spurious ORF

OE_7213F	VNG_7113	spurious ORF
OE_8011F	VNG_6133H	spurious ORF

**Table S8: Spurious ORFs from strain NRC-1.** This set of about 60 ORFs, which are annotated in strain NRC-1, are considered spurious and are named accordingly ("spurious ORF") in strain R1. Spurious ORFs are not represented in the R1 genome annotation but are retained in the TPA for strain NRC-1 to allow matching to the original annotation.