Table S1. Salt-responsive genes.

	7 min	45 min		
ID	Fold change	Fold change	Gene ID	Description of **upregulated** genes
RSP0006	2.61	3.46	3720260	DMT family permease
RSP0018	2.47	8.62	3720153	GntR family transcriptional regulator
RSP0019	2.71	8.22	3720154	hypothetical protein RSP_0019
RSP0091	2.50	0.37	3719922	ABC sorbitol/mannitol transporter, periplasmic binding protein
RSP0100	2.93	3.03	3719932	putative NADH dehydrogenase I chain A
RSP0101	2.29	3.44	3719933	NADH dehydrogenase (ubiquinone), 20 kDa subunit
RSP0102	NC	2.26	3719934	bifunctional NADH:ubiquinone oxidoreductase subunit C/D
RSP0103	NC	2.81	3719705	NADH dehydrogenase subunit E
RSP0104	NC	2.87	3719706	respiratory-chain NADH dehydrogenase, 51 kDa subunit
RSP0105	NC	2.12	3719707	NADH dehydrogenase subunit G
RSP0106	NC	2.14	3719708	putative NADH dehydrogenase I chain H
RSP0107	NC	2.14	3719709	NADH dehydrogenase subunit I
RSP0108	NC	2.51	3719710	NADH dehydrogenase I chain J
RSP0109	NC	2.65	3719711	putative NADH dehydrogenase I chain K
RSP0110	NC	2.00	3719712	NADH-ubiquinone oxidoreductase, chain 5
RSP0123	2.18	NC	3719690	autoinducer synthesis protein
RSP0124	4.78	NC	3719691	hypothetical protein RSP_0124
RSP0152	NC	2.39	3719572	P-loop ATPase
RSP0166	4.23	2.52	3719551	DnaK suppressor protein
RSP0170	2.47	NC	3719555	hypothetical protein RSP_0170
RSP0171	5.82	2.16	3719498	response regulator receiver protein
RSP0175	2.79	NC	3719502	lactate dehydrogenase and related dehydrogenase
RSP0183	NC	2.29	3719510	phenylhydantoinase
RSP0184	5.53	2.67	3719511	allantoate amidohydrolase
RSP0187	NC	3.11	3719514	dihydropyrimidine dehydrogenase
RSP0189	6.77	2.45	3719516	putative oxidoreductase
RSP0217	30.03	7.85	3719375	phage-related integrase
RSP0237	2.10	NC	3719417	acetylornithine deacetylase
RSP0243	2.16	NC	3719385	putative lipoprotein
RSP0244	NC	2.05	3719386	glutamine amidotransferase
RSP0250	3.74	2.20	3719392	hypothetical protein RSP_0250
RSP0254	NC	2.61	3719396	1-deoxy-D-xylulose-5-phosphate synthase
RSP0261	NC	3.19	3719271	chlorophyllide reductase, BchY subunit
RSP0262	NC	2.33	3719272	chlorophyllide reductase, BchX subunit
RSP0263	NC	2.98	3719273	chlorophyll synthesis pathway, bchC
RSP0264	NC	2.85	3719274	hydroxyneurosporene-O-methyltransferase
RSP0266	NC	2.32	3719276	methoxyneurosporene dehydrogenase
RSP0269	NC	2.67	3719278	tryptophan rich sensory protein
RSP0270	NC	2.29	3719279	phytoene synthase
RSP0271	2.30	3.10	3719280	phytoene dehydrogenase
RSP0275	NC	2.26		putative protein
RSP0278	NC	2.26	3719287	putative light-harvesting 1 (B870) complex assembly protein PucC
RSP0279	NC	2.24	3719288	bacteriochlorophyll/chlorophyll a synthase
RSP0281	NC	2.25	3719193	magnesium-protoporphyrin IX monomethylester oxidative cyclase, 66 kDa subunit (bchE)
RSP0283	NC	2.38	3719195	regulatory protein, PpaA

RSP0284	NC	2.02	3719196	2-vinyl bacteriochlorophyllide hydratase
RSP0285	NC	2.00	3719197	light-independent protochlorophyllide reductase subunit N
RSP0316	2.14	NC	3719076	LuxR family transcriptional regulator
RSP0319	2.26	2.81	3719079	NnrU
RSP0320	2.37	2.28	3719080	hypothetical protein RSP_0320
RSP0329	2.32	2.19	3719089	diguanylate cyclase with GAF sensor
RSP0351	NC	2.38	3719032	D-threo-aldose 1-dehydrogenase
RSP0354	2.34	NC	3719035	hypothetical protein RSP_0354
RSP0370	NC	2.00	3718994	hypothetical protein RSP_0370
RSP0379	2.79	2.31	3718887	aminotransferase
RSP0381	NC	2.03	3718889	hypothetical protein
RSP0402	NC	2.18	3718871	TetR family transcriptional regulator
RSP0423	NC	2.24	3718838	aldo/keto reductase
RSP0427	2.43	NC	3718842	hypothetical protein RSP_0427
RSP0442	2.84	3.43	3718815	putative aminotransferase
RSP0443	2.59	2.81	3718816	BadM/Rrf2 family transcriptional regulator
RSP0458	2.69	NC	3718737	hypothetical protein RSP_0458
RSP0465	NC	2.20	3718744	putative protease
RSP0466	NC	2.25	3718745	hypothetical protein RSP_0466
RSP0467	NC	2.01	3718746	3-octaprenyl-4hydroxybenzoate decarboxylase
RSP0527	NC	3.61	3718440	sigma-54 factor (RpoN1)
RSP0589	3.12	3.58	3718003	hypothetical protein RSP_0589
RSP0590	NC	2.35	3718005	hypothetical protein RSP_0590
RSP0601	3.58	4.29	3718015	RNA polymerase factor sigma-32
RSP0634	NC	6.66	3718264	TRAP dicarboxylate family transporter DctM subunit
RSP0635	NC	17.70	3718265	TRAP dicarboxylate family transporter DctQ subunit
RSP0636	NC	12.12	3718266	TRAP dicarboxylate family transporter DctP subunit
RSP0637	NC	3.95	3718267	hypothetical protein RSP_0637
RSP0638	NC	3.60	3718268	putative FAD dependent oxidoreductase protein
RSP0639	NC	5.47	3718288	putative N-methylhydantoinase B
RSP0640	23.44	7.10	3718289	putative N-methylhydantoinase A
RSP0641	4.51	2.84	3718290	XRE family transcriptional regulator
RSP0660	NC	2.53	3718270	hypothetical protein RSP_0660
RSP0664	NC	2.18	3718274	hypothetical protein RSP_0664
RSP0674	NC	3.29	3718285	DNA polymerase III subunit delta'
RSP0685	NC	2.58	3718335	16S rRNA m(2)G 1207 methyltransferase
RSP0686	NC	2.23	3718336	ATP-dependent Clp protease adaptor protein clpS
RSP0688	2.71	NC	3718338	penicillin-binding protein
RSP0697	NC	2.49	3718175	universal stress protein
RSP0723	2.91	NC	3718087	L-alanine dehydrogenase
RSP0724	NC	2.08	3718088	large-conductance mechanosensitive channel
RSP0751	4.00	NC	3718116	hypothetical protein RSP_0751
RSP0753	2.06	9.87	3718120	Salt-stress induced outer membrane protein
RSP0760	4.29	3.45	3718128	MarR family transcriptional regulator
RSP0761	3.93	3.43	3718129	hypothetical protein RSP_0761
RSP0762	4.74	3.19	3718130	XRE family transcriptional regulator
RSP0765	3.18	2.29	3718133	SAM-dependent methyltransferase
RSP0766	7.38	3.53	3718134	hypothetical protein RSP_0766
RSP0769	3.07	NC	3718137	glutathione S-transferase
RSP0775	2.18	NC	3718141	class I monoheme cytochrome c
RSP0785	2.54	NC	3718151	putative heat shock protein DnaJ
RSP0786	3.05	2.79	3718152	endonuclease/exonuclease/phosphatase fa

RSP0846	NC	2.21	3718152	endonuclease/exonuclease/phosphatase family
RSP0850	NC	2.46	3718311	GTP cyclohydrolase II
RSP0864	NC	2.22	3718316	hypothetical protein RSP_0850
RSP0865	2.87	NC	3718218	hypothetical protein RSP_0864
RSP0866	4.59	NC	3718220	hypothetical protein RSP_0866
RSP0868	7.19	2.24	3718222	putative transcriptional regulator
RSP0880	NC	2.01	3718348	oxidoreductase
RSP0887	NC	2.02	3718356	glycosyl transferase family protein
RSP0935	NC	2.12	3717922	MiaB-like radical SAM protein
RSP0936	NC	2.27	3717923	diaminopimelate epimerase
RSP0937	2.19	NC	3720765	alpha amylase domain-containing protein
RSP0938	2.50	2.40	3720766	hypothetical protein RSP_0938
RSP0940	NC	2.38	3720768	ABC transporter, periplasmic substrate binding protein
RSP0948	2.81	16.19	3720777	OtsA trehalose-6-phosphate synthase
RSP0949	6.45	11.77	3720778	putative trehalose-6-phosphate phosphatase
RSP0959	NC	2.50	3720750	ATPase
RSP0989	4.70	NC	3720743	ABC sugar transporter, inner membrane subunit
RSP0990	14.33	NC	3720744	ABC sugar transporter, periplasmic sugar binding subunit
RSP0991	4.26	NC	3720707	ROK family transcriptional regulator
RSP1007	NC	2.15	3720723	16S ribosomal RNA methyltransferase RsmE
RSP1025	NC	3.18	3720993	hypothetical protein RSP_1025
RSP1026	NC	2.57	3720994	hypothetical protein RSP_1026
RSP1078	2.08	NC	3720893	formate dehydrogenase subunit gamma
RSP1083	3.73	NC	3720842	two component transcriptional regulator
RSP1094	NC	2.87	3720853	hypothetical protein RSP_1094
RSP1095	8.20	4.77	3720854	DNA mismatch repair protein
RSP1125	2.10	NC	3720823	membrane bound lytic murein transglycosylase B
RSP1133	3.44	NC	3720831	hypothetical protein RSP_1133
RSP1139	2.52	NC	3720837	MarR family transcriptional regulator
RSP1141	2.78	2.16	3720839	hypothetical protein RSP_1141
RSP1180	2.35	0.35	3718173	ABC sugar (xylose) transporter, periplasmic binding protein
RSP1184	5.70	3.94	3718848	ribonuclease BN
RSP1191	NC	2.12	3718855	MarR family transcriptional regulator
RSP1204	NC	2.94	3720232	ABC multidrug efflux pump, fused ATPase and inner membrane subunits
RSP1220	3.85	NC	3719668	heat-inducible transcription repressor
RSP1233	NC	2.50	3719681	putative Maf/YceF/YhdE family protein
RSP1254	NC	2.44	3718552	acetate kinase
RSP1255	NC	3.61	3718553	bifunctional enoyl-CoA hydratase/phosphate acetyltransferase
RSP1256	NC	3.59	3718554	enoyl-(acyl carrier protein) reductase
RSP1257	3.47	3.58	3718555	putative polyhydroxyalkanoic synthase, PHA synthase
RSP1261	2.38	NC	3718464	BLUF blue-light receptor
RSP1270	NC	3.46	3718473	hypothetical protein RSP_1270
RSP1271	NC	3.59	3718474	periplasmic sensor signal transduction histidine kinase
RSP1272	5.44	4.41	3718475	RNA polymerase sigma factor
RSP1273	3.76	2.79	3718476	hypothetical protein RSP_1273
RSP1274	2.83	2.36	3718477	two-component response regulator

RSP1275	3.10	4.57	3718479	CrpO
RSP1276	7.43	8.97	3718480	hypothetical protein RSP_1276
RSP1286	7.61	3.63	3718200	RuBisCO operon transcriptional regulator, CbbR
RSP1297	NC	2.52	3718211	LysR family transcriptional regulator
RSP1308	5.01	3.03	3720969	hypothetical protein RSP_1308
RSP1345	2.32	NC	3720871	hypothetical protein RSP_1345
RSP1382	NC	3.66	3720789	radical SAM superfamily protein
RSP1385	2.42	2.54	3720792	hypothetical protein RSP_1385
RSP1403	2.21	NC	3718491	hypothetical protein RSP_1403
RSP1422	2.12	NC	3721987	ParB-like nuclease
RSP1423	8.06	NC	3721988	ParA family ATPase
RSP1425	6.32	2.58	3721989	plasmid replication initiation protein
RSP1428	2.35	NC	3718797	Pre (Mob) type recombination enzyme
RSP1430	7.28	2.66	3718798	hypothetical protein RSP_1430
RSP1433	5.74	4.81	3718800	hypothetical protein RSP_1433
RSP1434	17.09	7.08	3718801	putative Zn-dependent oxidoreductase
RSP1435	38.77	5.58	3718802	TetR family regulatory protein
RSP1436	9.13	NC	3718803	ABC transporter ATPase
RSP1437	2.03	NC	3718804	ABC Fe+3 hydroxamate (ferrichrome) transporter, ATPase subunit
RSP1439	2.42	NC	3718772	ABC Fe+3 hydroxamate (ferrichrome) transporter, periplasmic siderophore binding protein
RSP1441	2.22	NC	3718774	GntR family regulatory protein
RSP1442	2.16	NC	3718775	ABC sugar transporter, periplasmic sugar-binding protein
RSP1443	2.39	NC	3718776	ABC sugar transporter, inner membrane subunit
RSP1467	NC	2.02	3718762	alkane 1-monooxygenase
RSP1471	NC	2.64	3718765	hypothetical protein RSP_1471
RSP1473	2.51	NC	3718768	hypothetical protein RSP_1473
RSP1486	13.04	3.32	3718723	TetR family transcriptional regulator
RSP1487	6.75	NC	3718724	hypothetical protein RSP_1487
RSP1488	5.35	NC	3718725	glyoxalase
RSP1490	NC	2.01	3718727	putative ATP-dependent protease La, LON
RSP1496	2.89	NC	3718696	hypothetical protein RSP_1496
RSP1502	2.77	2.29	3718701	GAF domain-containing protein
RSP1551	2.86	NC	3718618	putative glyoxalase family protein
RSP1607	3.96	NC	3718560	GntR family transcriptional regulator
RSP1624	6.63	2.13	3718520	hypothetical protein RSP_1624
RSP1666	NC	2.07	3717932	4-hydroxy-3-methylbut-2-enyl diphosphate reductase
RSP1706	NC	2.01	3718905	putative acetyltransferase
RSP1759	NC	3.17	3718965	hypothetical protein RSP_1759
RSP1760	NC	3.62	3718966	hypothetical protein RSP_1760
RSP1769	NC	2.03	3718975	mandelate racemase/muconate lactonizing protein
RSP1770	2.69	2.98	3718976	hypothetical protein
RSP1785	NC	2.18	3719011	LacI family transcription regulator
RSP1786	2.58	NC	3719012	phosphoenolpyruvate--protein phosphotransferase
RSP1790	2.70	2.18	3719016	transcriptional regulator
RSP1812	2.12	NC	3719058	hypothetical protein
RSP1860	NC	2.64	3719127	hypothetical protein RSP_1860
RSP1873	2.60	3.80	3719141	hypothetical protein RSP_1873
RSP1890	4.62	4.80	3719177	LysR family transcriptional regulator
RSP1895	NC	2.95	3719182	small-conductance mechanosensitive ion channel

RSP1896	2.41	NC	3719183	guanine deaminase
RSP1926	NC	2.18	3719235	tRNA-dihydrouridine synthase A
RSP1938	3.97	3.62	3719248	hypothetical protein RSP_1938
RSP1945	11.31	6.55	3719255	AsnC family transcriptional regulator
RSP1952	2.91	3.11	3719262	cold-shock DNA-binding protein family protein
RSP1956	NC	2.57	3719266	hypothetical protein RSP_1956
RSP1963	2.07	NC	3719293	hypothetical protein RSP_1963
RSP1966	3.19	2.02	3719297	ISSod13, transposase
RSP1973	2.27	3.06	3719304	SufE protein
RSP1974	2.05	2.96	3719305	hypothetical protein RSP_1974
RSP1990	5.08	NC	3719323	AsnC family transcriptional regulator
RSP1997	2.34	NC	3719330	LexA repressor
RSP2007	NC	2.09	3719340	hypothetical protein RSP_2007
RSP2024	2.40	2.15	3719358	cold-shock DNA-binding protein family protein
RSP2038	NC	2.71	3719428	acetyltransferase
RSP2053	2.16	NC	3719442	RarD family protein
RSP2075	3.96	NC	3719468	putative transcriptional regulator
RSP2084	NC	2.01	3719517	hypothetical protein RSP_2084
RSP2085	NC	2.69	3719518	hypothetical protein RSP_2085
RSP2087	NC	3.27	3719520	hypothetical protein RSP_2087
RSP2092	3.21	2.52	3719525	ATP-dependent DNA helicase Rep
RSP2111	3.73	NC	3719582	D-alanine--D-alanine ligase
RSP2115	2.44	3.37	3719586	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase
RSP2123	3.87	2.55	3719593	radical SAM domain-containing protein
RSP2171	3.36	NC	3719640	LysR family transcriptional regulator
RSP2186	NC	3.04	3719656	MerR family transcriptional regulator
RSP2231	11.52	5.40	3719761	hypothetical protein RSP_2231
RSP2234	4.96	2.44	3719763	DNA-binding protein
RSP2236	NC	2.83	3719765	MarR family transcriptional regulator
RSP2237	NC	2.95	3719766	membrane fusion protein (MFP) family protein
RSP2238	NC	3.21	3719767	major facilitator superfamily multidrug-efflux transporter
RSP2286	2.06	NC	3719818	hypothetical protein
RSP2305	2.82	NC	3719836	MaoC family protein
RSP2312	NC	2.14	3719843	hypothetical protein RSP_2312
RSP2320	NC	2.29	3719851	TRAP-T family transporter periplasmic binding protein
RSP2321	NC	2.52	3719852	TRAP-T family transporter
RSP2322	NC	2.45	3719853	TRAP dicarboxylate family transporter DctQ subunit
RSP2323	3.42	3.42	3719854	hypothetical protein RSP_2323
RSP2324	2.12	NC	3719855	RpiR family transcriptional regulator
RSP2331	NC	2.00	3719863	PpaZ, a novel pseudoazurin precursor (blue copper protein)
RSP2334	2.35	NC	3719866	6-phosphofructokinase
RSP2338	4.58	5.40	3719871	hypothetical protein RSP_2338
RSP2339	2.82	2.51	3719872	hypothetical protein RSP_2339
RSP2348	3.96	3.36	3719882	hypothetical protein RSP_2348
RSP2349	16.19	5.11	3719884	hypothetical protein RSP_2349
RSP2350	14.36	4.03	3719885	hypothetical protein RSP_2350
RSP2378	NC	2.64	3719914	putative fatty acid beta hydroxylase (cytochrome P450)
RSP2379	9.34	8.15	3719915	hypothetical protein

RSP2380	NC	2.89	3719974	catalase
RSP2384	NC	2.16	3719981	hypothetical protein RSP_2384
RSP2395	5.61	5.68	3719992	BCCP, cytochrome c peroxidase
RSP2414	NC	2.19	3719992	BCCP, cytochrome c peroxidase
RSP2425	3.11	NC	3720022	CarD family transcriptional regulator
RSP2445	NC	5.15	3720042	putative Alpha amylase
RSP2446	NC	3.49	3720043	putative trehalose synthase
RSP2448	NC	2.89	3720044	glycogen branching enzyme
RSP2449	NC	2.23	3720045	putative glycosyl hydrolase
RSP2476	4.24	2.28	3720093	hypothetical protein RSP_2476
RSP2481	2.32	2.22	3720098	serine O-acetyltransferase
RSP2482	NC	2.34	3711864	TonB-dependent receptor protein
RSP2484	5.11	2.17	3711861	hypothetical protein RSP_2484
RSP2505	NC	2.69	3720064	CreA family protein
RSP2506	4.75	4.77	3720065	isovaleryl-CoA dehydrogenase
RSP2508	NC	3.34	3720067	methylcrotonyl-CoA carboxylase beta chain
RSP2509	NC	3.16	3720068	3-methylcrotonoyl-CoA carboxylase, alpha subunit
RSP2510	NC	3.60	3720069	hydroxymethylglutaryl-CoA lyase
RSP2511	NC	3.17	3720070	enoyl-CoA hydratase
RSP2543	2.29	NC	3720178	peptidoglycan-binding LysM (peptidase)
RSP2547	2.80	NC	3720181	exopolysaccharide production protein exoY
RSP2548	2.23	NC	3720182	Outer membrane polysaccharide export protein, exoF
RSP2555	2.18	NC	3720189	hypothetical protein RSP_2555
RSP2563	NC	2.15	3720197	glycosyl transferase family protein
RSP2572	NC	2.04	3720205	crpK, Fnr-type transcriptional regulator
RSP2591	4.64	NC	3720224	two component LuxR family transcriptional regulator
RSP2599	NC	2.96	3720271	phosphate regulon transcriptional regulator, PhoR
RSP2600	NC	2.14	3720272	phosphate uptake regulator, PhoU
RSP2601	NC	2.59	3720273	ABC phosphate transporter, ATPase subunit PstB
RSP2602	NC	2.24	3720274	ABC phosphate transporter, inner membrane subunit PstA
RSP2603	NC	2.77	3720275	ABC phosphate transporter, inner membrane subunit PstC
RSP2604	3.61	4.38	3720276	ABC phosphate transporter, periplasmic phosphate-binding protein
RSP2610	3.99	NC	3720283	MerR family transcriptional regulator
RSP2611	4.67	NC	3720284	integration host factor subunit alpha
RSP2624	16.44	8.10	3720297	hypothetical protein
RSP2629	NC	2.11	3720301	tRNA (uracil-5-)-methyltransferase Gid
RSP2655	2.20	NC	3720347	hypothetical protein RSP_2655
RSP2670	4.08	NC	3720360	glycerol-3-phosphate dehydrogenase
RSP2674	3.36	5.79	3720364	hypothetical protein RSP_2674
RSP2681	8.35	5.55	3720372	sigma factor, RpoE
RSP2688	NC	2.11	3720379	putative sarcosine oxidase delta subunit protein
RSP2692	4.68	2.76	3720421	acyltransferase domain-containing protein
RSP2709	NC	3.27	3720438	1-deoxy-D-xylulose 5-phosphate reductoisomerase
RSP2722	3.72	3.40	3720452	cysteinyl-tRNA synthetase
RSP2723	NC	2.33	3720453	putative alpha-isopropylmalate/homocitrate synthase
RSP2729	2.27	NC	3720459	restriction endonuclease
RSP2741	NC	3.68	3720471	class I diheme cytochrome c4
RSP2763	9.26	7.24	3720494	hypothetical protein RSP_2763
RSP2764	8.78	7.55	3720495	hypothetical protein RSP_2764

RSP2765	8.37	3.08	3720496	hypothetical protein RSP_2765
RSP2771	2.79	NC	3720504	putative exopolyphosphatase
RSP2780	3.75	2.38	3720513	LysR family transcriptional regulator
RSP2787	NC	2.32	3720520	hypothetical protein RSP_2787
RSP2801	16.04	4.65	3720592	TetR family transcriptional regulator
RSP2802	2.92	2.13	3720591	multidrug/cation efflux pump, membrane fusion
RSP2839	NC	2.07	3720547	nitrogen regulation protein, NtrY, Signal transduction
RSP2847	3.24	NC	3720539	hypothetical protein RSP_2847
RSP2864	NC	2.67	3720523	ribulose-5-phosphate 3-epimerase
RSP2865	2.23	2.51	3720522	putative transposase
RSP2932	2.12	NC	3720672	GntR family transcriptional regulator
RSP2933	7.39	NC	3720673	N-formimino-L-glutamate deiminase
RSP2934	2.47	NC	3720674	imidazolonepropionase
RSP2961	3.47	NC	3720414	CBS domain-containing proteins
RSP2982	NC	2.20	3720396	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase
RSP3004	2.38	4.53	3721591	protein kinase
RSP3006	6.71	4.45	3721593	hypothetical protein RSP_3006
RSP3007	4.45	NC	3721594	hypothetical protein RSP_3007
RSP3014	2.19	NC	3721599	putative aldolase protein
RSP3018	2.44	NC	3721603	putative acyl-CoA dehydrogenase
RSP3021	2.59	NC	3721606	putative catechol 2,3-dioxygenase
RSP3022	8.49	NC	3721607	TetR family transcriptional regulator
RSP3023	2.15	NC	3721608	hypothetical protein RSP_3023
RSP3025	8.43	NC	3721609	NAD(P)H oxidoreductase
RSP3039	NC	2.04	3721624	ABC permidine/putrescine transporter, inner membrane subunit
RSP3041	2.84	NC	3721626	ABC permidine/putrescine transporter, ATPase subunit
RSP3042	NC	2.99	3721627	LuxR family transcriptional regulator
RSP3057	NC	17.45	3721644	ABC proline/glycine betaine transporter, ATPase subunit
RSP3058	3.73	56.40	3721645	ABC proline/glycine betaine transporter, inner
RSP3059	8.86	53.55	3721646	ABC proline/glycine betaine transporter, periplasmic substrate-binding protein
RSP3060	NC	4.23	3721647	O-acetylserine synthase
RSP3061	NC	3.22	3721648	hypothetical protein RSP_3061
RSP3062	NC	5.50	3721649	3-oxoacyl-(acyl-carrier-protein) reductase
RSP3070	NC	3.17	3721347	hypothetical protein RSP_3070
RSP3075	NC	3.52	3721351	hypothetical protein RSP_3075
RSP3076	NC	2.61	3721352	hypothetical protein RSP_3076
RSP3080	NC	4.03	3721356	BCCT family choline/carnitine/betaine transporter
RSP3113	2.29	5.59	3721388	D-amino acid dehydrogenase small subunit
RSP3124	3.60	2.65	3721579	LysR family transcriptional regulator
RSP3125	10.22	2.93	3721580	ArsR family transcriptional regulator
RSP3126	2.80	NC	3721581	ACR3 family arsenite efflux pump
RSP3168	4.22	NC	3721460	ABC transporter, periplasmic binding protein
RSP3170	2.35	NC	3721462	demethylmenaquinone methyltransferase
RSP3179	10.59	3.39	3721470	ferric-uptake regulator
RSP3180	4.36	NC	3721471	transglutaminase-like enzyme
RSP3225	NC	2.12	3721832	periplasmic sensor signal transduction histidine kinase
RSP3226	2.32	NC	3721833	NAD-dependent deacetylase

RSP3272	NC	3.17	3721873	gamma-glutamyltransferase 1
RSP3290	2.61	NC	3721890	ABC glycerol-3-phosphate transporter, periplasmic binding protein, UgpB
RSP3291	2.29	2.27	3721991	putative Na+/phosphate symporter
RSP3297	2.39	NC	3721998	ABC branched-chain amino acid transporter, periplasmic binding protein
RSP3305	2.52	2.72	3722007	putative ubiquinol-cytochrome-c reductase assembly protein
RSP3324	2.38	2.51	3722024	LuxR family transcriptional regulator
RSP3351	2.20	6.06	3722051	hypothetical protein RSP_3351
RSP3353	NC	3.37	3722055	Phage related tail protein
RSP3378	7.86	4.96	3722080	hypothetical protein RSP_3378
RSP3379	6.04	2.71	3722081	hypothetical protein RSP_3379
RSP3384	NC	2.49	3721669	mandelate racemase/muconate lactonizing enzyme family protein
RSP3385	2.11	NC	3721670	LysR family transcriptional regulator
RSP3386	2.12	NC	3721671	TRAP-T family transporter periplasmic binding protein
RSP3405	2.14	NC	3721690	GntR family transcriptional regulator
RSP3410	2.44	NC	3721695	TRAP-T family transporter periplasmic binding protein
RSP3411	5.71	NC	3721696	TRAP-T family transporter small inner membrane subunit
RSP3453	3.34	NC	3721739	TRAP-T family transporter periplasmic binding protein
RSP3494	2.60	NC	3721909	OmpA/MotB domain-containing protein
RSP3503	2.01	NC	3721920	sugar ABC transporter ATPase
RSP3509	3.04	NC	3721925	hemolysin-type calcium-binding region, RTX
RSP3537	NC	2.98	3721951	alcohol dehydrogenase, zinc-containing
RSP3538	2.57	NC	3721952	hypothetical protein RSP_3538
RSP3547	2.22	2.72	3721961	ribonucleotide reductase
RSP3569	NC	2.00	3722084	Zinc-uptake regulator, Zur
RSP3594	NC	3.03	3722111	antifreeze protein, type I
RSP3604	NC	2.30	3721762	tRNA 2-selenouridine synthase
RSP3606	4.15	3.15	3721764	sigma-54 factor (RpoN3)
RSP3619	2.04	NC	3721786	hypothetical protein
RSP3621	2.78	3.23	3721788	cold-shock DNA-binding protein
RSP3632	2.72	NC	3722121	hypothetical protein RSP_3632
RSP3634	13.21	4.87	3722123	hypothetical protein RSP_3634
RSP3646	10.86	3.47	3722135	DNA topology modulation kinase FlaR, putative
RSP3661	NC	2.06	3722150	TRAP-T family transporter periplasmic binding protein
RSP3662	2.21	NC	3722151	TRAP-T family transporter large inner membrane subunit
RSP3663	5.82	NC	3722152	TRAP-T family transporter small inner membrane subunit
RSP3675	4.24	NC	3722164	esterase/lipase/thioesterase
RSP3676	6.91	NC	3722165	GntR family transcriptional regulator
RSP3677	3.94	NC	3722166	ABC sugar transporter, ATPase subunit
RSP3700	2.92	NC	3722190	LacI family transcription regulator
RSP3701	8.40	0.42	3722191	ABC sugar transporter, periplasmic binding protein
RSP3702	4.14	NC	3722192	ABC sugar transporter, ATPase subunit
RSP3731	3.36	NC	3721492	DeoR family transcriptional regulator

RSP3732	4.31	NC	3721493	ABC sugar transporter, periplasmic binding protein
RSP3808	2.94	NC	3721661	hypothetical protein RSP_3808
RSP3812	2.39	NC	3722118	recombinase
RSP3814	4.93	NC	3721395	hypothetical protein RSP_3814
RSP3816	3.46	NC	3721396	hypothetical protein RSP_3816
RSP3821	5.27	4.30	3721402	putative acetyltransferase
RSP3822	2.25	NC	3721403	GTPase ObgE
RSP3823	2.69	NC	3721404	gamma-glutamyl kinase
RSP3824	2.12	NC	3721405	glutamate-5-semialdehyde dehydrogenase
RSP3833	2.36	NC	3721415	enoyl-CoA hydratase
RSP3840	11.96	4.90	4796457	ATPase, ParA type
RSP3860	3.25	NC	4796542	sulfate/molybdate ABC transporter inner membrane protein
RSP3861	4.24	NC	4796445	sulfate/molybdate ABC transporter periplasmic ligand-binding protein
RSP3865	2.78	2.73	4796516	BadM/Rrf2 family transcriptional regulator
RSP3866	NC	3.24	4796539	hypothetical protein RSP_3866
RSP3927	3.90	11.65	4796463	hypothetical protein RSP_3927
RSP3970	2.79	NC	3712014	3-hydroxyacyl-CoA dehydrogenase
RSP3971	3.56	2.62	3712013	GntR family transcriptional regulator
RSP3972	3.39	2.45	3712012	3-ketoacyl-(acyl-carrier-protein) reductase
RSP3974	NC	2.04	3711824	transketolase
RSP3981	NC	2.39	3711816	hypothetical protein RSP_3981
RSP4000	3.22	NC	3711787	glycine betaine/L-proline ABC transporter ATPase
RSP4022	NC	2.33	3712039	ParB-like partition protein
RSP4023	NC	2.95	3712038	ATPase, ParA type
RSP4024	NC	2.38	3712037	hypothetical protein RSP_4024
RSP4037	6.31	NC	3711799	ABC sugar transporter, periplasmic lignad binding protein
RSP4038	3.51	NC	3711798	DeoR family transcriptional regulator
RSP4047	2.26	2.48	3720101	pyruvate dehydrogenase E1 component, alpha subunit
RSP4049	NC	2.60	3720100	pyruvate dehydrogenase subunit beta
RSP4050	NC	2.31	3720099	branched-chain alpha-keto acid dehydrogenase subunit E2
RSP4051	4.67	3.37	3711921	hypothetical protein RSP_4051
RSP4076	3.34	3.21	3711951	plamid maintenance protein
RSP4081	10.36	4.00	3711955	hypothetical protein RSP_4081
RSP4082	8.91	5.28	3711956	hypothetical protein RSP_4082
RSP4098	2.75	NC	3711965	glycosyl transferase, group 1
RSP4112	9.71	3.86	3711828	hypothetical protein RSP_4112
RSP4113	2.62	NC	3711829	NapE component of periplasmic nitrate reductase
RSP4124	2.04	3.42	3711839	hypothetical protein RSP_4124
RSP4139	8.57	3.32	3711988	partition parA like-protein
RSP4154	NC	3.01	3711873	putative transposase
RSP4172	2.88	NC	3711887	hypothetical protein RSP_4172
RSP4186	5.11	2.22	3711974	RepA partitioning protein/ATPase, ParA type
RSP4188	22.75	9.61	3711976	hypothetical protein RSP_4188
RSP4189	NC	2.16	3711977	TonB-dependent receptor protein
RSP4190	3.41	2.79	3711978	Heme oxygenase
RSP4201	6.55	4.16	3711894	ArsR family transcriptional regulator
RSP4202	3.16	4.78	3711895	transporter

RSP4203	NC	2.47	3711896	putative glutaredoxin family protein/Thio-disulfide isomerase
RSP4204	NC	2.31	3711897	hypothetical protein RSP_4204
RSP4209	NC	6.61	3711901	acyltransferase
RSP4210	3.04	2.45	3711902	ArsR family transcriptional regulator
RSP4211	2.04	2.22	3711903	glyceraldehyde-3-phosphate dehydrogenase
RSP4212	NC	2.15	3711904	putative multidrug-efflux transporter
RSP4246	NC	2.30	3711914	putative SinR-like protein
RSP4247	NC	2.93	3711916	hypothetical protein RSP_4247
RSP4248	NC	2.55	3711917	hypothetical protein RSP_4248
RSP4254	3.34	2.81	4796553	nucleoside diphosphate kinase regulator
RSP4255	2.28	NC	4796484	mechanosensitive (MS) ion channel protein
RSP4260	13.33	2.49	4796456	LysR family transcriptional regulator
RSP4277	2.34	NC	4796525	MerR family transcriptional regulator
RSP4278	4.35	NC	4796488	AraC family transcriptional regulator
RSP6029	2.09	NC	3719350	hypothetical protein RSP_6029
RSP6045	5.57	3.81	3719868	hypothetical protein RSP_6045
RSP6048	2.45	3.13	3719975	hypothetical protein RSP_6048
RSP6070	4.07	2.23	3720497	hypothetical protein RSP_6070
RSP6102	12.72	5.72	3719374	hypothetical protein RSP_6102
RSP6134	2.35	2.78	3718398	hypothetical protein RSP_6134
RSP6154	3.03	2.34	3720962	hypothetical protein RSP_6154
RSP6166	6.17	2.03	3721449	hypothetical protein RSP_6166
RSP6172	NC	3.25	3718478	hypothetical protein RSP_6152
RSP6198	2.71	3.85	3722174	hypothetical protein RSP_6198
RSP6220	NC	4.22	3719521	hypothetical protein RSP_6220
RSP7172	4.89	2.17	3711807	hypothetical protein RSP_7172

ID	**7 min Fold change**	**45 min Fold change**	**Gene ID**	**Description of downregulated genes**
RSP0005	0.39	0.29	3720259	GMP synthase
RSP0007	NC	0.44	3720261	putative outer membrane protein
RSP0009	0.48	NC	3720263	hypothetical protein RSP_0009
RSP0010	0.42	NC	3720264	homoserine O-succinyltransferase
RSP0015	NC	0.33	3720150	ABC spermidine/putrescine transporter, ATPase subunit
RSP0016	0.36	NC	3720151	ABC spermidine/putrescine transporter, inner membrane subunit
RSP0021	NC	0.44	3720156	30S ribosomal protein S9
RSP0022	NC	0.47	3720157	50S ribosomal protein L13
RSP0030	0.45	0.23	3720165	diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s)
RSP0032	0.49	0.18	3720168	sigma factor FliA (sigma-28 group, flagellar)
RSP0033	NC	0.14	3720111	hypothetical protein RSP_0033
RSP0034	0.48	0.14	3720112	flagellar biosynthesis protein, FlhA
RSP0035	0.35	0.15	3720113	hypothetical protein RSP_0035
RSP0036	NC	0.24	3720115	flagellar basal-body P-ring formation protein FlgA
RSP0037	NC	0.38	3720116	putative FlgM, negative regulator of flagellin synthesis
RSP0038	0.30	0.04	3720121	hypothetical protein RSP_0038
RSP0041	NC	0.23	3720124	hypothetical protein RSP_0041
RSP0042	NC	0.13	3720125	chemotaxis histidine protein kinase, CheA3
RSP0043	NC	0.04	3720126	chemotaxis response regulator, CheY6

RSP0044	NC	0.05	3720127	putative cytoplasmic chemoreceptor, TlpT
RSP0045	NC	0.10	3720128	Slp
RSP0046	0.43	0.07	3720129	CheW protein
RSP0047	NC	0.21	3719954	chemotaxis methylesterase, CheB2
RSP0048	0.44	0.21	3719955	MCP methyltransferase, CheR-type
RSP0049	0.42	0.24	3719956	chemotaxis histidine protein kinase, CheA4
RSP0051	0.14	0.05	3719958	Torf protein
RSP0052	0.18	0.09	3719959	flagellar protein FliE
RSP0053	0.37	0.18	3719960	flagellar FliF M-ring protein
RSP0054	0.28	0.18	3719961	flagellar motor switch protein FliG
RSP0056	NC	0.24	3719963	flagellum-specific ATPase FliI
RSP0057	0.41	0.28	3719964	flagellar protein FliJ
RSP0058	0.35	0.14	3719965	FliK, flagellar hook-length control protein
RSP0059	0.35	0.13	3719966	flagellar biosynthesis protein, FliL
RSP0061	0.32	0.18	3719968	flagellar motor switch FliN protein
RSP0062	0.31	0.05	3719969	flagellar protein FliO
RSP0063	0.32	0.19	3719970	flagellar biosynthesis protein FliP
RSP0064	0.47	0.30	3719971	flagellar protein FliQ
RSP0065	NC	0.44	3719972	flagellar protein FliR
RSP0067	0.49	0.14	3719935	hypothetical protein RSP_0067
RSP0068	0.31	0.09	3719937	sigma-54 factor (RpoN2)
RSP0069	NC	0.48	3719938	flagellar filament protein
RSP0070	NC	0.46	3719939	flagellar hook-associated protein 2 (filament cap protein)
RSP0071	0.40	0.28	3719940	sigma-54 dependent transcriptional regulator
RSP0072	NC	0.34	3719941	invasion protein
RSP0073	NC	0.29	3719942	flagellar hook-associated protein 3 FlgL
RSP0074	NC	0.10	3719943	FlgK flagellar hook-associated protein 1
RSP0076	NC	0.14	3719945	flagellar basal body P-ring protein
RSP0077	0.40	0.11	3719946	flagellar L-ring protein
RSP0078	0.36	0.05	3719947	flagellar distal rod protein
RSP0079	NC	0.13	3719948	flagellar proximal rod protein FlgF
RSP0080	0.49	0.02	3719949	flagellar hook protein FlgE
RSP0081	0.31	0.08	3719950	flagellar scaffolding protein FlgD
RSP0082	0.37	0.11	3719951	flagellar basal-body rod protein FlgC
RSP0083	0.24	0.07	3719952	flagellar proximal rod protein FlgB
RSP0084	NC	0.44	3719953	hypothetical protein RSP_0084
RSP0085	NC	0.49	3719916	PAS/PAC sensor hybrid histidine kinase
RSP0086	NC	0.33	3719917	hypothetical protein RSP_0086
RSP0087	NC	0.43	3719918	two component transcriptional regulator, LuxR
RSP0092	NC	0.48	3719923	ABC sorbitol/mannitol transporter, inner membrane subunit
RSP0094	NC	0.30	3719925	ABC sorbitol/mannitol transporter, ATPase subunit
RSP0095	NC	0.37	3719926	sorbitol dehydrogenase
RSP0097	NC	0.26	3719929	TRAP-T family sorbitol/mannitol periplasmic binding protein SmoM
RSP0099	0.46	0.14	3719931	TRAP dicarboxylate family transporter DctQ subunit
RSP0125	0.41	NC	3719692	glucan biosynthesis protein G
RSP0129	0.35	0.36	3719697	ABC D-methionine uptake transporter, ATPase subunit
RSP0132	NC	0.28	3719699	ABC D-methionine uptake transporter, substrate-binding protein
RSP0146	NC	0.46	3719567	nitrogen regulatory protein P-II

RSP0147	NC	0.50	3719568	L-glutamine synthetase
RSP0154	NC	0.42	3719538	3-hydroxyisobutyrate dehydrogenase
RSP0155	NC	0.46	3719539	enoyl-CoA hydratase
RSP0156	NC	0.44	3719540	Acyl-CoA dehydrogenase
RSP0164	0.36	NC	3719549	hypothetical protein RSP_0164
RSP0173	NC	0.39	3719500	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1 7·dioic acid hydratase
RSP0190	0.37	NC	3719479	biotin carboxyl carrier protein
RSP0191	0.44	NC	3719480	acetyl-CoA carboxylase biotin carboxylase subunit
RSP0205	NC	0.43	3719495	hypothetical protein RSP_0205
RSP0230	0.48	0.25	3719409	neutral zinc metallopeptidase
RSP0231	0.48	0.15	3719411	flagellar MotB protein
RSP0233	0.35	0.06	3719412	flagellar motor protein MotA
RSP0246	0.47	NC	3719388	ABC lipid efflux transporter, fused ATPase and inner membrane subunits
RSP0248	0.30	NC	3719390	elongation factor P
RSP0282	0.44	NC	3719194	transcriptional regulator PpsR
RSP0294	0.45	NC	3719207	magnesium-protoporphyrin IX monomethyl ester cyclase
RSP0296	NC	0.45	3719209	cytochrome c2
RSP0377	0.50	NC	3718885	L-glutamine synthetase
RSP0385	NC	0.38	3718893	threonyl-tRNA synthetase / Ser-tRNA(Thr) hydrolase
RSP0395	0.43	NC	3718865	RNA polymerase sigma factor RpoD
RSP0396	0.42	NC	3718864	hypothetical protein RSP_0396
RSP0404	0.45	0.45	3718873	fructose 1,6-bisphosphatase II
RSP0420	0.50	NC	3718835	hypothetical protein
RSP0425	0.43	NC	3718840	methionyl-tRNA synthetase
RSP0431	0.49	NC	3718808	putative selenocysteine lyase
RSP0445	0.47	NC	3718818	hypothetical protein RSP_0445
RSP0448	NC	0.44	3718821	EF-Tu; elongation factor Tu
RSP0450	NC	0.45	3718823	hypothetical protein RSP_0450
RSP0457	0.47	NC	3718735	glycerol-3-phosphate regulon repressor
RSP0474	NC	0.47	3718637	cytochrome c'
RSP0479	0.37	NC	3718642	elongation factor P
RSP0487	NC	0.40	3718649	TRAP dicarboxylate family transporter DctP subunit
RSP0513	0.32	0.14	3718426	hypothetical protein RSP_0513
RSP0557	0.42	NC	3717950	hypothetical protein RSP_0557
RSP0571	0.49	NC	3718023	tRNA pseudouridine synthase A
RSP0576	NC	0.14	3718028	Na+/solute symporter
RSP0577	NC	0.16	3718029	hypothetical protein RSP_0577
RSP0623	0.32	NC	3718251	hypothetical protein RSP_0623
RSP0629	NC	0.43	3718257	hypothetical protein RSP_0629
RSP0651	NC	0.41	3718300	putative inositol monophosphatase protein
RSP0652	NC	0.42	3718301	UDP-galactose 4-epimerase
RSP0653	0.47	0.40	3718302	UDP-glucose 6-dehydrogenase
RSP0655	0.35	0.46	3718304	hypothetical protein RSP_0655
RSP0657	0.45	NC	3718306	hypothetical protein
RSP0669	NC	0.47	3718279	translocation protein TolB
RSP0671	NC	0.49	3718281	ExbD/TolR family protein
RSP0676	0.46	0.40	3718287	PhnP-like protein
RSP0687	NC	0.45	3718337	HAD superfamily hydrolase
RSP0706	0.40	NC	3718184	prephenate dehydratase
RSP0714	0.50	NC	3718078	hypothetical protein RSP_0714

RSP0728	0.39	NC	3718092	hypothetical protein RSP_0728
RSP0739	0.50	NC	3718103	branched chain amino acid efflux pump, large (AzlC) subunit
RSP0745	NC	0.29	3718111	acetyl-CoA acetyltransferase
RSP0747	NC	0.34	3718112	3-oxoacyl-[acyl-carrier-protein] reductase
RSP0768	0.49	0.44	3718136	LuxR family transcriptional regulator
RSP0776	NC	0.35	3718142	ABC lipoprotein efflux transporter, ATPase subunit, LolD
RSP0777	NC	0.49	3718143	ABC lipoprotein efflux transporter, inner membrane subunit, LolE
RSP0778	0.45	0.48	3718144	prolyl-tRNA synthetase
RSP0780	NC	0.49	3718146	hypothetical protein RSP_0780
RSP0818	NC	0.47	3718396	carbamoyl phosphate synthase large subunit
RSP0831	0.43	NC	3718371	tryptophan synthase subunit alpha
RSP0832	0.43	NC	3718373	GTP-dependent nucleic acid-binding protein EngD
RSP0841	0.45	NC	3718382	hypothetical protein RSP_0841
RSP0859	NC	0.49	3718212	3-isopropylmalate dehydrogenase
RSP0872	0.27	NC	3718226	peptide deformylase
RSP0873	0.36	NC	3718227	N-formylmethionyl tRNA deformylase
RSP0874	0.34	NC	3718228	formylmethionine deformylase
RSP0885	0.38	NC	3718352	thiosulfate sulfurtransferase, rhodanese-like
RSP0899	NC	0.38	3717962	thiol peroxidase (atypical 2-Cys peroxiredoxin)
RSP0902	NC	0.46	3717965	hydrolase, haloacid dehalogenase-like hydrolase
RSP0910	NC	0.06	3717973	TRAP dicarboxylate family transporter DctP subunit
RSP0911	NC	0.04	3717974	TRAP dicarboxylate family transporter DctQ subunit
RSP0912	NC	0.06	3717975	TRAP dicarboxylate family transporter DctM subunit
RSP0929	0.46	NC	3717916	acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha
RSP0930	0.48	NC	3717917	folylpolyglutamate synthetase
RSP0944	0.43	0.41	3720772	Locus tag
RSP0956	0.43	NC	3720747	hypothetical protein RSP_0956
RSP0968	NC	0.47	3720759	malate dehydrogenase
RSP0970	NC	0.43	3720761	putative citrate lyase beta chain
RSP0971	NC	0.45	3720762	hypothetical protein
RSP0972	NC	0.42	3720763	hypothetical protein RSP_0972
RSP0983	0.32	0.39	3720736	hypothetical protein RSP_0983
RSP0998	NC	0.31	3720714	Na+/H+ antiporter, NhaD
RSP1001	0.40	NC	3720717	hypothetical protein RSP_1001
RSP1002	0.32	NC	3720718	aspartate carbamoyltransferase catalytic subunit
RSP1003	NC	0.44	3720719	dihydroorotase
RSP1009	NC	0.45	3720725	OmpA family outer membrane protein
RSP1033	NC	0.50	3720943	OmpA family protein
RSP1035	NC	0.37	3720945	F0F1 ATP synthase subunit B
RSP1036	NC	0.34	3720946	F0F1 ATP synthase subunit B'
RSP1037	NC	0.27	3720947	F0F1 ATP synthase subunit C
RSP1038	0.39	0.30	3720948	F0F1 ATP synthase subunit A
RSP1039	0.35	0.48	3720949	FoF1 ATP synthase, subunit I
RSP1041	NC	0.50	3720951	malonyl-CoA synthase
RSP1047	NC	0.49	3720957	16S rRNA-processing protein RimM
RSP1048	NC	0.38	3720900	30S ribosomal protein S16
RSP1049	NC	0.34	3720901	chorismate mutase
RSP1064	0.36	0.46	3720917	putative inner membrane protein translocase component YidC

RSP1068	0.40	NC	3720883	acetylglutamate kinase
RSP1073	0.47	NC	3720888	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
RSP1100	0.50	NC	3720859	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase
RSP1106	0.45	NC	3720690	ribosome-binding factor A
RSP1109	NC	0.36	3720693	cysteine synthase
RSP1140	NC	0.31	3720838	branched-chain amino acid aminotransferase
RSP1146	NC	0.32	3718061	glutamate synthase (NADPH) large subunit
RSP1147	NC	0.21	3718062	hypothetical protein RSP_1147
RSP1148	NC	0.23	3718063	hypothetical protein RSP_1148
RSP1152	0.24	NC	3718068	ribonuclease D
RSP1153	0.48	NC	3718069	sugar phosphate isomerase
RSP1161	0.35	NC	3718154	3'-phosphadenosine 5'-phosphosulfate 3'-phosphatase
RSP1168	NC	0.46	3718161	PpiC-type peptidyl-prolyl cis-trans isomerase
RSP1169	0.50	NC	3718162	preprotein translocase subunit SecA
RSP1175	0.43	NC	3718168	3-demethylubiquinone-9 3-methyltransferase
RSP1179	NC	0.46	3718172	ABC sugar (xylose) transporter, inner membrane subunit
RSP1212	0.44	NC	3720240	argininosuccinate synthase
RSP1222	0.42	0.41	3719670	putative deoxyribonucleotide triphosphate pyrophosphatase
RSP1223	NC	0.43	3719671	YjgF family translation initiation inhibitor
RSP1231	0.47	NC	3719679	transcription termination factor Rho
RSP1249	NC	0.35	3718547	ABC ribose transporter, periplasmic solute-binding protein
RSP1279	0.49	NC	3718193	CbbY family protein
RSP1280	0.39	NC	3718194	CbbX protein
RSP1283	0.46	NC	3718197	fructose-1,6-bisphosphate aldolase
RSP1284	0.48	NC	3718198	phosphoribulokinase
RSP1291	NC	0.40	3718205	branched chain amino acid ABC transporter periplasmic substrate-binding protein
RSP1337	0.47	NC	3720863	2-octaprenylphenol hydroxylase
RSP1340	0.37	NC	3720866	short chain enoyl-CoA hydratase
RSP1341	0.45	NC	3720867	30S ribosomal protein S20
RSP1351	NC	0.33	3720876	phosphoserine aminotransferase
RSP1352	NC	0.22	3720877	D-3-phosphoglycerate dehydrogenase
RSP1359	0.50	NC	3720805	DEAD/DEAH box helicase
RSP1360	0.37	0.48	3720806	hypothetical protein RSP_1360
RSP1365	NC	0.46	3720811	hypothetical protein RSP_1365
RSP1369	0.43	NC	3720815	Short-chain dehydrogenase/reductase SDR
RSP1376	NC	0.38	3720783	aspartate-semialdehyde dehydrogenase
RSP1377	0.41	0.34	3720784	carbonic anhydrase
RSP1389	0.40	0.41	3720796	chorismate synthase
RSP1419	NC	0.50	3721984	TRAP-T family transporter small inner membrane subunit
RSP1420	NC	0.42	3721985	TRAP-T family transporter periplasmic binding protein
RSP1460	0.40	NC	3718755	hypothetical protein RSP_1460
RSP1464	0.41	NC	3718759	periplasmic thiol-disulphide interchange protein

RSP1476	NC	0.49	3718712	heavy metal-(Cd/Co/Hg/Pb/Zn)-translocating P-type ATPase
RSP1480	0.47	NC	3718716	ABC oligopeptide transporter, inner membrane subunit OppB
RSP1512	NC	0.31	3718676	hypothetical protein RSP_1512
RSP1547	NC	0.48	3718671	bacterioferritin-associated ferredoxin
RSP1570	0.47	NC	3718597	phosphoribosylaminoimidazole carboxylase ATPase subunit
RSP1575	0.44	0.20	3718603	bifunctional sulfate adenylyltransferase subunit 1/adenylylsulfate kinase protein
RSP1576	NC	0.50	3718604	thioredoxin reductase
RSP1577	NC	0.34	3718605	AsnC family transcriptional regulator
RSP1582	NC	0.29	3718610	putative sulfate transporter/antisigma-factor antagonist
RSP1583	0.32	0.19	3718611	chemotaxis response regulator, CheY3
RSP1584	NC	0.20	3718612	chemotaxis histidine protein kinase
RSP1585	NC	0.21	3718613	chemotaxis protein, CheW2
RSP1586	NC	0.21	3718614	chemotaxis protein, CheW3
RSP1587	0.39	0.17	3718615	chemotaxis methyltransferase, CheR2
RSP1588	NC	0.35	3718577	chemotaxis methylesterase, CheB1
RSP1589	NC	0.33	3718578	transducer-like protein, TlpC
RSP1592	NC	0.34	3718582	acyl-CoA sythetase
RSP1599	NC	0.45	3718591	AMP-binding protein
RSP1605	NC	0.25	3718558	TRAP dicarboxylate family transporter DctP subunit
RSP1613	NC	0.35	3718566	TRAP dicarboxylate family transporter DctP subunit
RSP1623	0.26	NC	3718576	hypothetical protein RSP_1623
RSP1628	0.45	NC	3718524	sensor histidine protein kinase
RSP1670	0.46	NC	3717936	RelA/SpoT family protein
RSP1674	0.41	NC	3717940	signal peptidase I
RSP1691	NC	0.48	3717996	electron transfer flavoprotein subunit beta
RSP1700	NC	0.40	3718912	50S ribosomal protein L7/L12
RSP1705	0.46	NC	3718907	preprotein translocase subunit SecE
RSP1709	0.31	NC	3718917	30S ribosomal protein S7
RSP1710	0.39	NC	3718916	30S ribosomal protein S12
RSP1716	NC	0.40	3718921	50S ribosomal protein L3
RSP1717	NC	0.39	3718922	50S ribosomal protein L4
RSP1718	NC	0.46	3718923	50S ribosomal protein L23
RSP1720	NC	0.45	3718925	30S ribosomal protein S19
RSP1721	NC	0.48	3718926	50S ribosomal protein L22
RSP1722	NC	0.47	3718927	30S ribosomal protein S3
RSP1723	NC	0.38	3718928	50S ribosomal protein L16
RSP1725	NC	0.48	3718931	50S ribosomal protein L14
RSP1726	NC	0.45	3718932	50S ribosomal protein L24
RSP1727	NC	0.41	3718933	50S ribosomal protein L5
RSP1728	NC	0.44	3718934	30S ribosomal protein S14
RSP1729	NC	0.46	3718935	30S ribosomal protein S8
RSP1730	NC	0.43	3718936	50S ribosomal protein L6
RSP1731	NC	0.38	3718937	50S ribosomal protein L18
RSP1732	NC	0.42	3718938	30S ribosomal protein S5
RSP1733	NC	0.35	3718939	50S ribosomal protein L30
RSP1735	NC	0.46	3718941	preprotein translocase subunit SecY
RSP1736	NC	0.30	3718942	adenylate kinase

RSP1750	NC	0.38	3718956	ABC glutamate/glutamine/aspartate/asparagine transporter, ATPase subunit bztD
RSP1754	0.50	NC	3718960	hypothetical protein
RSP1763	0.49	NC	3718969	phenylalanyl-tRNA synthetase subunit alpha
RSP1803	0.47	NC	3719048	ABC heme exporter, inner membrane subunit CcmC
RSP1815	0.48	NC	3719061	glutathione synthetase
RSP1837	0.46	NC	3719104	5'-methylthioadenosine phosphorylase
RSP1843	0.44	NC	3719110	Signal recognition particle-docking protein FtsY
RSP1846	0.39	NC	3719113	hypothetical protein RSP_1846
RSP1851	NC	0.46	3719118	O-succinylhomoserine sulfhydrylase
RSP1856	0.43	NC	3719123	glycyl-tRNA synthetase subunit alpha
RSP1857	0.34	NC	3719124	hypothetical protein RSP_1857
RSP1865	NC	0.27	3719132	ketol-acid reductoisomerase
RSP1903	NC	0.38	3719190	putative Flp pilus assembly protein TadC
RSP1904	NC	0.33	3719191	putative Flp pilus assembly protein TadB
RSP1905	NC	0.40	3719211	putative Flp pilus assembly protein ATPase CpaF
RSP1912	NC	0.24	3719219	hypothetical protein RSP_1912
RSP1913	NC	0.18	3719220	butyryl-CoA:acetate CoA transferase
RSP1914	NC	0.21	3719221	3-ketoacid CoA transferase alpha subunit
RSP1929	0.50	0.34	3719238	orotate phosphoribosyltransferase
RSP1930	0.43	NC	3719239	dihydroorotase
RSP1940	0.46	0.30	3719250	hypothetical protein RSP_1940
RSP1941	0.42	0.39	3719251	phosphoadenosine phosphosulfate reductase
RSP1942	0.39	0.40	3719252	sulfite/nitrite reductase hemoprotein subunit
RSP1943	0.19	0.26	3719253	hypothetical protein RSP_1943
RSP1944	0.47	0.45	3719254	uroporphyrinogen-III C-methyltransferase
RSP1969	0.39	NC	3719300	phosphoribosylaminoimidazole synthetase
RSP1987	0.42	0.46	3719320	hypothetical protein RSP_1987
RSP1991	NC	0.45	3719324	putative ornithine decarboxylase
RSP1995	0.48	NC	3719328	glutamyl-tRNA synthetase
RSP2045	0.45	NC	3719435	hypothetical protein RSP_2045
RSP2047	0.42	NC	3719437	ThiF family protein
RSP2098	0.42	NC	3719532	cell division protein FtsI/penicillin-binding protein 2
RSP2099	0.28	NC	3719533	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase
RSP2124	NC	0.46	3719594	methionine synthase I
RSP2125	NC	0.42	3719595	hypothetical protein RSP_2125
RSP2127	0.42	NC	3719597	component of phosphoribosylformylglycinamidine (FGAM) synthetase
RSP2128	0.31	NC	3719598	phosphoribosylformylglycinamidine synthase I
RSP2131	0.45	NC	3719601	RNAse E
RSP2192	NC	0.49	3719665	methylmalonyl-CoA mutase
RSP2209	NC	0.46	3719738	ABC sugar transporter, inner membrane subunit
RSP2221	NC	0.39	3719751	adenylosuccinate lyase
RSP2242	0.34	NC	3719772	imidazole glycerol phosphate synthase subunit HisF
RSP2243	0.30	0.35	3719773	1-(5-phosphoribosyl)-5-[(5-
RSP2246	0.49	NC	3719776	imidazoleglycerol-phosphate dehydratase
RSP2256	0.35	0.31	3719785	D-tyrosyl-tRNA(Tyr) deacylase
RSP2257	0.39	0.26	3719786	putative fructokinase
RSP2258	0.29	0.21	3719787	phosphoribosylaminoimidazole-succinocarboxamide synthase
RSP2270	0.38	NC	3719800	aspartyl/glutamyl-tRNA amidotransferase subunit A

RSP2275	NC	0.50	3719806	branched chain amino acid ABC transporter periplasmic substrate-binding protein
RSP2296	0.30	NC	3719827	ATPase, delta (OSCP) subunit
RSP2298	NC	0.47	3719829	F0F1 ATP synthase subunit gamma
RSP2301	0.34	0.49	3719832	phosphoribosyl pyrophosphate synthetase
RSP2308	0.43	0.37	3719839	hypothetical protein RSP_2308
RSP2310	NC	0.33	3719841	co-chaperonin GroES
RSP2311	NC	0.33	3719842	chaperonin GroEL
RSP2328	NC	0.45	3719859	rod shape-determining protein MreC
RSP2329	0.35	0.43	3719860	rod shape-determining protein MreB
RSP2342	0.38	0.43	3719875	xanthine-guanine phosphoribosyltransferase
RSP2343	0.46	0.45	3719876	RhtB family threonine efflux protein
RSP2344	0.40	NC	3719877	enoyl-(acyl carrier protein) reductase
RSP2356	NC	0.49	3719892	hypothetical protein RSP_2356
RSP2365	NC	0.37	3719902	ABC sugar (ribose) transporter, periplasmic substrate-binding subunit
RSP2398	0.42	NC	3719995	ABC putrescine transporter, inner membrane subunit
RSP2399	0.49	NC	3719996	ABC putrescine transporter, inner membrane subunit
RSP2402	NC	0.46	3719999	putative TonB dependent vitamin B12 outer membrane receptor
RSP2408	0.47	NC	3720005	hypothetical protein
RSP2428	NC	0.38	3720024	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase
RSP2430	NC	0.35	3720027	hypothetical protein RSP_2430
RSP2453	0.50	NC	3720049	putative oxidoreductase (NAD/NADP dependent)
RSP2454	NC	0.34	3720050	amidophosphoribosyltransferase
RSP2455	0.36	0.43	3720051	putative colicin V production protein, dedE
RSP2458	NC	0.45	3720074	ABC transporter, ATPase subunit
RSP2459	NC	0.50	3720075	ABC transporter, inner membrane subunit
RSP2460	0.38	NC	3720076	alanine racemase
RSP2463	0.43	0.45	3720078	acyl carrier protein
RSP2494	0.43	NC	3720054	FUR family manganese uptake regulator
RSP2537	0.41	NC	3720171	peptide chain release factor 3
RSP2540	0.43	NC	3720174	twin-arginine translocation system protein, TatA
RSP2541	0.36	NC	3720175	twin-arginine translocation system protein, TatB
RSP2584	NC	0.45	3720217	hypothetical protein RSP_2584
RSP2585	NC	0.30	3720218	hypothetical protein RSP_2585
RSP2595	NC	0.50	3720267	hypothetical protein RSP_2595
RSP2613	0.45	NC	3720286	putative glycerol-3-phosphate acyltransferase PlsX
RSP2615	0.19	NC	3720288	hypothetical protein RSP_2615
RSP2619	0.47	NC	3720292	tRNA-specific 2-thiouridylase MnmA
RSP2654	0.31	0.45	3720345	DnaK suppressor protein
RSP2683	NC	0.47	3720374	hypothetical protein RSP_2683
RSP2686	0.47	0.44	3720377	putative sarcosine oxidase beta subunit
RSP2712	0.49	NC	3720443	(3R)-hydroxymyristoyl-ACP dehydratase
RSP2737	NC	0.37	3720466	putative ssRNA endoribonuclease L-PSP
RSP2738	0.42	0.35	3720467	rhodanese-related sulfurtransferase
RSP2739	NC	0.47	3720468	hypothetical protein RSP_2739
RSP2747	NC	0.44	3720477	glycosyltransferase
RSP2781	0.44	0.41	3720514	peroxiredoxin/glutaredoxin family protein
RSP2783	0.49	NC	3720516	lipoyl synthase

RSP2805	NC	0.45	3720588	putative NADH-flavin oxidoreductase
RSP2822	NC	0.45	3720568	putative precorrin methylase
RSP2828	0.42	NC	3720561	cobalamin synthesis protein CobW
RSP2848	0.42	NC	3720538	delta-aminolevulinic acid dehydratase
RSP2852	0.45	NC	3720534	polyketide biosynthesis associated protein
RSP2860	NC	0.34	3720526	30S ribosomal protein S2
RSP2861	NC	0.31	3720525	elongation factor Ts
RSP2868	NC	0.42	3720608	inosine-5'-monophosphate dehydrogenase
RSP2875	0.47	NC	3720615	glucokinase
RSP2876	NC	0.41	3720616	putative carbon monoxide dehydrogenase medium chain
RSP2877	NC	0.22	3720617	xanthine dehydrogenase, molybdenum binding subunit apoprotein
RSP2878	NC	0.13	3720618	putative carbon-monoxide dehydrogenase small chain
RSP2879	NC	0.49	3720619	hypothetical protein RSP_2879
RSP2886	NC	0.45	3720626	glucose-1-phosphate adenylyltransferase
RSP2894	NC	0.48	3720633	nucleoside diphosphate kinase
RSP2895	0.44	NC	3720634	putative ABC transporter, fused ATPase subunits
RSP2908	0.47	NC	3720648	hypothetical protein RSP_2908
RSP2910	0.36	NC	3720650	metal-dependent amidase/aminoacylase/carboxypeptidase
RSP2913	0.48	NC	3720652	ABC Fe+3 siderophore transporter, periplasmic substrate-binding protein
RSP2918	0.48	0.44	3720657	ferripyochelin binding protein
RSP2919	0.43	NC	3720658	guanylate kinase
RSP2921	NC	0.47	3720661	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase
RSP2922	0.49	NC	3720662	transcriptional regulator
RSP2950	NC	0.23	3720402	LysR family transcriptional regulator
RSP2951	NC	0.41	3720403	phosphoribosylformylglycinamidine synthase II
RSP2956	NC	0.38	3720408	transketolase
RSP2959	NC	0.32	3720411	glyceraldehyde-3-phosphate dehydrogenase
RSP2974	0.35	0.41	3720388	putative metalopeptidase
RSP2975	0.37	0.38	3720389	hypothetical protein RSP_2975
RSP2985	0.47	NC	3720399	hypothetical protein RSP_2985
RSP3003	0.44	NC	3721590	hypothetical protein
RSP3083	NC	0.41	3721359	methyl accepting chemotaxis protein
RSP3090	0.36	NC	3721366	putative alkylphosphonate uptake protein, phnA
RSP3102	0.42	0.29	3721377	Sec-independent protein translocase TatE
RSP3136	NC	0.22	3721428	hypothetical protein
RSP3161	NC	0.45	3721453	hypothetical protein RSP_3161
RSP3174	NC	0.34	3721465	NCS1 nucleoside transporter
RSP3186	NC	0.41	3721477	hypothetical protein RSP_3186
RSP3187	0.49	0.12	3721479	glucan biosynthesis protein D
RSP3302	0.46	0.12	3722004	chemotaxis response regulator, CheY4
RSP3303	0.47	0.28	3722005	putative methyl accepting chemotaxis protein, McpG
RSP3349	0.41	NC	3722049	hypothetical protein
RSP3361	0.44	NC	3722061	putative restriction endonuclease or methylase
RSP3382	NC	0.48	3721667	hypothetical protein RSP_3382
RSP3432	NC	0.29	3721718	methyl-accepting chemotaxis protein
RSP3500	NC	0.40	3721917	ABC sugar transporter, periplasmic binding protein
RSP3513	0.48	NC	3721929	diguanylate cyclase with GAF sensor

RSP3539	NC	0.20	3721953	hemolysin-type calcium-binding region, RTX
RSP3540	0.45	0.16	3721954	putative adhesin or RTX toxin
RSP3551	0.47	NC	3721965	histidyl-tRNA synthetase
RSP3557	NC	0.44	3721971	ABC transporter ATPase
RSP3593	NC	0.41	3722110	tRNA (guanine-N(7))-methyltransferase
RSP3600	0.48	NC	3722117	tRNA-i(6)A37 thiotransferase enzyme MiaB
RSP3640	0.33	0.28	3722129	hypothetical protein RSP_3640
RSP3641	0.32	0.35	3722130	pfkB family carbohydrate kinase
RSP3642	0.33	0.39	3722131	putative ExsB
RSP3643	0.36	0.49	3722132	hypothetical protein RSP_3643
RSP3644	0.29	0.34	3722133	metal dependent phosphohydrolase
RSP3696	0.40	NC	3722186	ABC sulfate/thiosulfate transporter, ATPase subunit CysA
RSP3750	0.25	NC	3721509	hypothetical protein RSP_3750
RSP3751	0.35	NC	3721510	hypothetical protein RSP_3751
RSP3752	0.29	NC	3721511	hypothetical protein RSP_3752
RSP3755	0.31	NC	3721514	hypothetical protein
RSP3756	0.25	NC	3721515	hypothetical protein RSP_3756
RSP3768	NC	0.48	3721523	hypothetical protein RSP_3768
RSP3825	0.42	NC	3721406	hypothetical protein RSP_3825
RSP3835	0.41	NC	3721417	hypothetical protein RSP_3835
RSP3838	0.36	0.50	4796555	capsule polysaccharide export protein
RSP3844	0.50	NC	4796551	dTDP-glucose 4,6-dehydratase
RSP3924	0.43	0.48	4796490	hypothetical protein RSP_3924
RSP3925	0.23	NC	4796526	hypothetical protein RSP_3925
RSP3982	NC	0.43	3711815	hypothetical protein RSP_3982
RSP3983	NC	0.36	3711814	circadian clock KaiB-like protein
RSP3985	NC	0.32	3711812	hypothetical protein RSP_3985
RSP3986	0.49	0.42	3711811	hypothetical protein RSP_3986
RSP3988	0.35	NC	3711810	glycosyltransferase
RSP3989	0.42	NC	3711808	NAD-dependent epimerase/dehydratase
RSP4039	0.49	0.37	3711797	hypothetical protein RSP_4039
RSP4039	0.49	0.37	3720104	phosphoglycerate kinase
RSP4044	NC	0.43	3720101	pyruvate dehydrogenase E1 component, alpha subunit
RSP4068	0.49	NC	3711942	hypothetical protein
RSP4070	0.37	NC	3711944	putative signal peptide protein
RSP4159	0.46	NC	3711877	isopropylmalate/homocitrate synthase
RSP4160	0.22	NC	3711878	hypothetical protein RSP_4160
RSP4161	0.37	NC	3711879	O-acetylhomoserine sulfhydrylase
RSP4195	0.39	NC	3711983	response regulator receiver protein
RSP4219	NC	0.39	3711909	hypothetical protein RSP_4219
RSP4220	0.47	0.41	3711910	hypothetical protein RSP_4220
RSP4221	0.48	0.42	3711997	hypothetical protein RSP_4221
RSP4242	NC	0.47	3711914	hemolysin-type calcium-binding protein
RSP6025	NC	0.08	3719217	hypothetical protein RSP_6025
RSP6078	0.47	NC	3720645	hypothetical protein RSP_6078
RSP6086	0.40	0.20	3720114	hypothetical protein RSP_6086
RSP6087	NC	0.33	3720117	hypothetical protein RSP_6087
RSP6092	NC	0.26	3719936	hypothetical protein RSP_6092
RSP6098	0.29	0.33	3719541	hypothetical protein RSP_6098
RSP6151	NC	0.27	3718549	hypothetical protein RSP_6151
RSP6212	0.29	NC	3718384	hypothetical protein RSP_6212

RSP7124	0.47	NC	3711809	hypothetical protein RSP_7124
RSP7252	0.44	0.43	3711936	hypothetical protein RSP_7252

All genes that passed the selection criteria (FDR<0.05 and fold-change in average values =<0.5 or >=2.0 compared to 0 min NaCl) at least at one time point are shown.

NC, genes that did not pass the selection criteria are shown as 'not changed'.