

Supplementary Table 4 Genes affected by Strong-salt stress for 45 min passed under fold change ≥ 4.0 and crt ≥ 1.15 cut off (140 genes)

Gene ID ^a	Function ^b	Mild-salt 7 min		Mild-salt 45min		Strong-salt 7 min		Strong-salt 45 min	
		Fold	crt	Fold	crt	Fold	crt	Fold	crt
RSP0018	Transcriptional regulator	1.3	1.1	1.0	0.8	2.8	2.1	9.0	7.3
RSP0019	Hypothetical protein	1.6	0.8	1.3	0.8	3.5	1.8	8.4	3.6
RSP0030	Diguanylate cyclase/phosphodiesterase	-1.5	1.0	-1.3	0.8	-2.0	1.3	-4.1	2.7
RSP0031	Hypothetical protein	-1.2	0.6	-2.1	1.4	-2.0	1.3	-4.1	2.7
RSP0032	RNA polymerase sigma factor FlIA (Sigma-28 group, flagellar)	-1.4	1.1	-2.4	2.0	-2.0	1.5	-5.7	4.8
RSP0033	Hypothetical protein	-1.0	0.7	-1.8	1.3	-1.1	0.7	-8.4	6.6
RSP0034	Membrane protein involved in flagellum assembly	-1.5	1.1	-2.8	2.1	-2.3	1.8	-8.5	6.1
RSP0035	Hypothetical protein	-1.2	0.8	-1.8	1.4	-2.9	2.2	-10.2	7.7
RSP0036	Flagella basal body P ring formation protein FlgA	-1.2	1.0	-1.9	1.5	-2.0	1.7	-4.7	3.7
RSP0038	Hypothetical protein	-1.9	1.3	-2.7	1.9	-3.0	2.2	-32.4	22.6
RSP0041	Hypothetical protein	1.1	0.8	-1.3	0.9	-1.2	0.8	-4.8	3.4
RSP0042	Chemotaxis protein histidine kinase and related kinases	-1.1	0.6	-2.0	1.1	-1.0	0.5	-15.2	7.7
RSP0043	Chemotaxis response regulator CheB	1.1	0.8	-1.7	1.4	-1.2	1.0	-24.1	18.1
RSP0044	Methyl-accepting chemotaxis protein	1.1	0.6	-1.8	1.4	-1.3	0.9	-17.8	11.1
RSP0045	ATPases involved in chromosome partitioning	1.2	0.9	-1.5	1.0	-1.4	1.0	-9.9	6.7
RSP0046	Chemotaxis signal transduction protein CheW	-1.1	0.7	-2.0	1.4	-2.2	1.6	-13.3	7.9
RSP0048	Methylase of chemotaxis methyl-accepting protein	1.1	0.7	-1.7	1.2	-2.3	1.8	-5.8	4.3
RSP0049	Chemotaxis protein histidine kinase and related kinase	-1.0	0.8	-1.9	1.4	-3.0	2.4	-4.5	3.3
RSP0051	Transcriptional regulator	-1.5	1.1	-1.9	1.4	-6.6	4.8	-20.9	15.6
RSP0052	Flagellar hook-basal body protein FlIE	-1.3	0.9	-1.5	1.0	-5.0	3.4	-10.4	7.6
RSP0053	Flagellar basal body M-ring protein	-1.7	1.0	-1.7	1.1	-2.6	1.8	-4.4	2.9
RSP0054	Flagellar motor switch protein	-1.8	1.2	-1.9	1.3	-3.2	2.1	-6.0	4.4
RSP0056	Flagellar ATPase-like componen	-1.4	0.9	-1.8	1.3	-2.5	1.7	-5.3	4.0
RSP0057	Hypothetical protein	-1.5	1.0	-2.1	1.3	-2.6	1.6	-5.1	3.4
RSP0058	Hypothetical protein	-1.4	1.1	-2.3	1.9	-2.7	2.0	-8.4	7.0
RSP0059	Flagellar basal body-associated protein FlIL	-1.3	1.0	-2.2	1.7	-2.8	2.0	-9.5	7.0
RSP0061	Flagellar motor switch protein	-1.1	0.9	-2.2	1.6	-2.9	2.0	-8.2	6.0
RSP0062	Hypothetical protein	-1.5	1.0	-3.0	2.1	-2.7	1.7	-22.0	16.4
RSP0063	Membrane protein FlIP involved in flagellar biogenesis	1.0	0.6	-1.8	1.4	-3.0	2.4	-7.3	6.0
RSP0064	Flagellar biosynthesis/export protein FlIQ	-1.2	0.8	-2.0	1.3	-2.5	1.7	-4.3	2.7
RSP0067	Hypothetical protein	-1.4	1.0	-2.3	1.7	-2.1	1.7	-8.8	6.9
RSP0068	Sigma-54 (RpoN) and related alternative sigma subunits	-1.0	0.7	-1.3	1.1	-3.2	2.5	-10.0	7.4
RSP0071	Transcriptional regulator	-1.4	1.1	-1.3	1.0	-3.2	2.5	-4.8	3.8
RSP0073	Flagellin and related hook-associated protein	-1.3	1.0	-2.0	1.6	-1.3	0.8	-4.0	2.6

Supplementary Table 4-----Continued 1

Gene ID ^a	Function ^b	Mild-salt 7 min		Mild-salt 45min		Strong-salt 7 min		Strong-salt 45 min	
		Fold	crt	Fold	crt	Fold	crt	Fold	crt
RSP0074	Flagellar hook-associated protein	-1.2	1.1	-2.1	2.0	-1.1	1.0	-9.8	8.3
RSP0075	Hypothetical protein	-1.4	1.1	-2.7	1.9	-1.2	0.8	-6.2	4.6
RSP0076	Flagellar basal-body P-ring protein	-1.6	0.9	-3.1	1.8	-2.9	1.8	-6.6	4.0
RSP0076	Flagellar basal-body P-ring protein	-1.5	0.9	-2.9	1.7	-2.3	1.5	-11.2	7.1
RSP0077	Flagellar basal body L-ring protein	-1.4	1.0	-2.3	1.8	-2.7	2.1	-12.1	8.6
RSP0078	Flagellar basal body and hook protein	-1.3	1.2	-2.3	2.2	-2.7	2.5	-20.3	18.1
RSP0079	Flagellar basal body and hook protein	-1.2	0.9	-2.1	1.6	-1.3	1.0	-11.0	8.7
RSP0080	Flagellar basal body and hook protein	-1.2	0.9	-2.3	1.9	-2.0	1.5	-50.9	41.3
RSP0081	Flagellar hook capping protein FlgD	-1.2	0.9	-2.0	1.6	-3.3	2.5	-19.6	15.2
RSP0082	Flagellar basal body rod protein	-1.4	1.1	-2.3	1.9	-3.2	2.7	-11.1	9.0
RSP0083	Flagellar basal body protein	-1.6	0.9	-2.6	1.5	-4.3	2.6	-14.5	8.1
RSP0097	Periplasmic mannitol-binding protein	1.0	0.9	-1.3	1.1	-1.1	0.9	-4.3	3.4
RSP0098	Hypothetical protein	-1.1	0.9	-1.4	1.1	-1.1	0.9	-6.0	4.5
RSP0099	Hypothetical protein	-1.2	0.9	-1.4	1.1	-2.2	1.8	-7.8	6.0
RSP0187	Dihydroorotate dehydrogenase	1.3	1.2	-1.0	1.0	1.4	1.2	4.0	2.7
RSP0217	Phage integrase	1.5	1.1	1.4	1.0	29.6	24.0	6.5	4.6
RSP0230	Ccalcium-binding protein	-1.2	1.0	-1.1	0.9	-2.5	2.0	-4.8	3.8
RSP0231	Flagellar motor protein MotB	-1.4	1.1	-2.3	1.8	-2.3	1.9	-6.2	4.2
RSP0233	Flagellar motor protein MotA	-1.2	0.9	-2.0	1.6	-3.0	2.3	-23.9	19.1
RSP0513	Glycosyl hydrolases	-1.6	1.4	-1.3	1.2	-3.8	3.2	-6.8	5.4
RSP0576	Na ⁺ /proline, Na ⁺ /panthothenate symporter	1.8	1.4	-1.2	0.9	1.6	1.1	-7.7	5.8
RSP0577	Hypothetical protein	1.4	1.2	-1.5	1.1	1.7	1.0	-7.4	5.8
RSP0634	Hypothetical protein	1.3	1.0	1.0	0.9	-1.1	0.8	7.6	6.3
RSP0635	Hypothetical protein	2.5	1.9	1.3	1.1	-1.0	0.9	17.1	13.6
RSP0636	Dicarboxylate-binding periplasmic protein	1.7	1.5	1.1	1.0	1.1	1.0	10.5	7.8
RSP0639	N-methylhydantoinase	1.2	1.0	1.0	0.9	1.2	0.9	4.2	2.5
RSP0640	N-methylhydantoinase	1.2	1.2	1.1	1.0	21.6	20.8	5.5	4.1
RSP0753	SspA	1.4	1.1	1.7	1.5	1.9	1.5	10.5	8.8
RSP0910	Dicarboxylate-binding periplasmic protein	-1.2	1.0	-1.7	1.3	-1.3	1.1	-17.5	14.9
RSP0911	C4-dicarboxylate transport protein DctQ	-1.3	0.8	-2.0	1.3	-1.6	1.2	-32.4	21.8
RSP0912	C4-dicarboxylate transport protein DctQ	-1.1	0.8	-1.9	1.3	-1.3	1.0	-17.4	12.9
RSP0948	Trehalose-6-phosphate synthase (OtsA)	1.7	1.3	1.9	1.4	2.3	1.5	11.0	8.1
RSP0949	Trehalose-6-phosphatase (OtsB)	1.8	1.3	2.0	1.4	6.6	4.5	8.6	6.3

Supplementary Table 4-----Continued 2

Gene ID ^a	Function ^b	Mild-salt 7 min		Mild-salt 45min		Strong-salt 7 min		Strong-salt 45 min	
		Fold	crt	Fold	crt	Fold	crt	Fold	crt
RSP1037	FoF1-type ATP synthase	-1.4	1.2	-1.4	1.1	-1.8	1.5	-4.1	3.4
RSP1095	DNA mismatch repair enzyme (predicted ATPase)	1.0	1.0	1.2	1.1	9.9	9.3	5.5	4.7
RSP1147	Hypothetical protein	-1.2	0.8	-1.0	0.8	-1.8	1.3	-4.9	3.2
RSP1148	Hypothetical protein	-1.2	1.1	-1.1	1.0	-1.6	1.4	-4.4	4.2
RSP1275	Transcriptional regulator	1.5	1.1	1.8	1.2	2.7	1.9	4.2	3.1
RSP1276	Hypothetical protein	1.4	1.2	1.8	1.5	7.7	6.4	8.9	7.4
RSP1286	Transcriptional regulator	1.3	1.1	1.3	1.1	8.3	7.5	4.3	3.6
RSP1352	Phosphoglycerate dehydrogenase	-1.5	0.9	1.1	0.7	-2.3	1.2	-5.5	3.2
RSP1433	Hypothetical protein	1.3	1.1	1.3	1.1	6.9	5.5	4.2	3.2
RSP1434	NADPH:quinone reductase	1.4	1.1	1.4	1.1	19.6	12.8	5.8	4.0
RSP1435	Transcriptional regulator	1.2	1.1	1.2	1.1	47.7	42.6	4.8	2.9
RSP1575	Adenylylsulfate kinase	1.2	0.9	-1.1	0.8	-3.0	1.7	-5.2	3.8
RSP1583	Response regulator	1.4	1.0	-1.5	1.2	-2.6	2.0	-5.9	5.1
RSP1584	Chemotaxis protein histidine kinase and related kinase	1.0	0.5	-2.1	1.4	-2.0	1.4	-6.5	3.8
RSP1585	Chemotaxis signal transduction protein CheW	1.4	0.8	-1.6	1.0	-1.2	0.8	-5.5	3.1
RSP1586	Chemotaxis signal transduction protein CheW	1.2	0.7	-1.6	1.1	-1.6	1.0	-5.8	3.9
RSP1587	Response regulator for chemotaxis	1.6	1.0	-1.3	1.0	-2.0	1.3	-5.9	4.2
RSP1865	Ketol-acid reductoisomerase (isoleucine biosynthesis)	-1.2	1.0	-1.4	1.2	-1.1	0.9	-4.7	3.8
RSP1873	Hypothetical protein	1.1	1.1	1.2	1.1	3.2	3.0	4.4	4.1
RSP1913	3-oxoadipate CoA-transferase	1.1	1.0	-1.3	1.2	-1.4	1.4	-5.7	5.4
RSP1914	Acyl-CoA:acetate CoA transferase	-1.0	0.8	-1.3	1.0	-1.3	1.0	-5.9	4.1
RSP1945	Transcriptional regulator	2.1	1.6	1.3	1.1	10.8	9.0	5.3	3.8
RSP2231	Hypothetical protein	1.4	1.2	1.5	1.2	12.0	9.4	5.1	4.3
RSP2338	Hypothetical protein	1.3	1.0	1.2	1.0	4.7	3.7	4.0	3.1
RSP2349	Hypothetical protein	1.7	1.1	1.5	1.0	18.2	11.3	4.1	2.3
RSP2379	Hypothetical protein	1.1	0.8	1.5	1.2	9.6	7.8	10.4	7.7
RSP2395	Cytochrome c peroxidase	1.5	1.1	1.3	0.9	5.3	3.7	5.5	3.9
RSP2445	Alpha amylase	1.2	1.0	1.4	1.1	2.1	1.7	5.8	4.7
RSP2506	Acyl-CoA dehydrogenase	1.0	0.8	-1.1	0.8	6.3	4.1	6.5	3.4
RSP2508	Acetyl-CoA carboxylase	1.2	0.8	1.0	0.7	-1.1	0.6	5.7	2.8
RSP2509	Biotin carboxylase	1.4	1.0	-1.2	0.8	-1.0	0.6	4.9	3.0
RSP2510	Isopropylmalate/homocitrate/citramalate synthases	2.0	1.3	-1.0	0.6	1.0	0.8	5.2	3.3
RSP2511	Enoyl-CoA hydratase/carnithine racemase	2.5	2.0	-1.1	0.7	1.2	0.9	4.5	3.2
RSP2624	Hypothetical protein	1.9	1.6	1.7	1.1	18.6	13.3	7.2	4.9

Supplementary Table 4-----Continued 3

Gene ID ^a	Function ^b	Mild-salt 7 min		Mild-salt 45min		Strong-salt 7 min		Strong-salt 45 min	
		Fold	crt	Fold	crt	Fold	crt	Fold	crt
RSP2674	Hypothetical protein	1.2	0.6	1.4	0.8	3.3	1.5	5.6	2.5
RSP2680	Hypothetical protein	1.0	0.9	1.1	0.9	2.2	2.0	4.9	4.2
RSP2681	Specialized sigma subunits of RNA polymerase Sigma70	1.2	1.0	1.3	1.2	8.5	7.3	6.1	5.1
RSP2741	Probable oxidoreductase	-1.1	0.8	1.1	0.8	-1.4	1.2	5.4	4.7
RSP2763	Hypothetical protein	1.6	1.0	1.4	0.9	11.4	7.6	7.0	3.7
RSP2764	Hypothetical protein	1.7	1.2	1.6	1.2	10.0	7.1	8.1	5.7
RSP2801	Transcriptional regulator	1.6	1.3	1.4	1.2	16.9	13.8	4.0	3.2
RSP2877	Aerobic-type carbon monoxide dehydrogenase	1.1	0.9	1.0	0.6	1.5	1.1	-4.8	3.7
RSP2878	Aerobic-type carbon monoxide dehydrogenase	-1.5	0.9	-1.2	0.7	-1.1	0.7	-9.4	5.9
RSP2950	Transcriptional regulator	-1.7	1.1	-1.3	0.8	-1.5	1.0	-4.2	2.6
RSP3006	Hypothetical protein	1.1	0.9	1.2	1.0	5.8	4.2	4.2	3.3
RSP3057	ABC-type proline/glycine betaine transport systems	1.2	1.0	1.3	1.0	1.1	0.8	16.4	12.8
RSP3058	ABC-type proline/glycine betaine transport systems	2.0	1.4	2.4	1.7	3.9	2.6	45.3	31.1
RSP3059	ABC-type proline/glycine betaine transport systems	2.1	1.1	2.9	1.5	9.6	4.3	50.1	22.7
RSP3060	Serine acetyltransferase	-1.1	0.9	1.1	0.9	1.7	1.4	5.0	4.0
RSP3062	Short-chain alcohol dehydrogenases	-1.0	1.0	1.1	1.0	1.0	1.0	4.6	4.0
RSP3080	Choline-glycine betaine transporter	1.8	1.3	2.0	1.5	1.1	0.7	4.0	2.9
RSP3102	Sec-independent protein secretion pathway TataA	-3.3	2.6	-3.4	2.7	-3.2	2.4	-4.4	3.3
RSP3113	D-amino-acid dehydrogenase	1.7	1.5	-1.0	0.8	2.5	2.0	4.6	3.6
RSP3136	Hypothetical protein	-1.5	1.0	-1.0	0.7	-1.7	0.9	-5.5	3.6
RSP3187	Hypothetical protein	-1.3	1.0	-1.2	0.9	-3.0	1.7	-10.5	8.0
RSP3302	Response regulator	1.4	0.9	-1.8	1.2	-2.0	1.4	-8.0	5.4
RSP3303	Methyl-accepting chemotaxis protein	1.4	0.7	-1.8	1.2	-2.2	1.4	-4.5	3.4
RSP3351	Hypothetical protein	1.0	0.8	1.3	1.0	2.1	1.5	5.7	3.9
RSP3378	Hypothetical protein	1.3	0.8	1.2	0.8	10.7	6.5	4.9	2.8
RSP3539	Calcium-binding protein	-1.1	0.8	-1.5	1.3	1.2	0.8	-5.0	3.2
RSP3540	Probable phosphoesterase	-1.1	0.8	-1.3	1.1	-2.3	2.0	-6.0	4.8
RSP3633	Hypothetical protein	1.7	1.5	1.7	1.4	16.2	12.4	8.1	6.2
RSP3634	Hypothetical protein	1.9	1.1	1.5	0.9	19.5	10.7	5.2	2.3
RSP3642	Transcriptional regulator	-1.2	0.8	-1.3	0.9	-5.4	3.8	-4.5	2.9
RSP3927	Hypothetical protein	-1.1	0.7	1.3	0.9	6.9	2.8	14.4	8.6
RSP3928	Hypothetical protein	-1.2	1.0	1.0	0.9	4.4	4.0	8.7	6.7
RSP4082	Hypothetical protein	1.3	1.0	1.2	0.9	9.1	7.2	4.4	3.5
RSP4091	Transposase protein	1.3	1.1	1.2	1.2	14.1	11.8	4.6	4.3

Supplementary Table 4-----Continued 4

Gene ID ^a	Function ^b	Mild-salt 7 min		Mild-salt 45min		Strong-salt 7 min		Strong-salt 45 min	
		Fold	crt	Fold	crt	Fold	crt	Fold	crt
RSP4124	Hypothetical protein	1.2	1.0	1.1	1.0	2.6	1.9	4.2	3.6
RSP4082	Hypothetical protein	1.3	1.0	1.2	0.9	9.1	7.2	4.4	3.5
RSP4091	Transposase protein	1.3	1.1	1.2	1.2	14.1	11.8	4.6	4.3
RSP4124	Hypothetical protein	1.2	1.0	1.1	1.0	2.6	1.9	4.2	3.6
RSP4188	Hypothetical protein	1.4	1.2	1.6	1.4	21.5	17.8	8.5	6.3
RSP4202	Hypothetical protein	1.7	1.2	1.6	1.1	3.6	2.2	4.1	2.9
RSP4209	Hypothetical protein	1.7	1.0	2.4	1.4	1.4	0.9	7.3	4.1
RSP4239	Hypothetical protein	1.4	1.3	1.4	1.2	4.6	3.7	4.1	3.4

^a Sorted according to the *Rhodobacter* genome database. ^b Derived from Oak ridge National Laboratory genome annotations.