

Supplementary Table 2 Genes affected by Mild-salt stress for 45 min, passed under fold change ≥ 1.5 and crt ≥ 1.15 cut off (122 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
RSP0031	Hypothetical protein	-1.2	0.6	-2.1	1.4	-2.0	1.3	-4.1	2.7
RSP0032	RNA polymerase sigma factor FlhA (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	Flagellar biosynthesis protein FlhA	-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
RSP0037	Hypothetical protein	1.3	1.0	-1.6	1.4	-1.2	1.1	-2.8	2.5
RSP0038	Hypothetical protein	-1.9	1.3	-2.7	1.9	-3.0	2.2	-32.4	22.6
RSP0040	Flagellar protein FlhS	1.6	1.2	-1.6	1.2	2.3	2.1	-1.8	1.5
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
RSP0046	Chemotaxis signal transduction protein CheW	-1.1	0.7	-2.0	1.4	-2.2	1.6	-13.3	7.9
RSP0048	Chemotaxis protein methyltransferase	1.1	0.7	-1.7	1.2	-2.3	1.8	-5.8	4.3
RSP0049	Chemotaxis protein histidine kinase and related kinases	-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
RSP0054	Flagellar motor switch protein FlgG	-1.8	1.2	-1.9	1.3	-3.2	2.1	-6.0	4.4
RSP0056	Flagellar ATPase-like component	-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 FlhL	-1.3	1.0	-2.2	1.7	-2.8	2.0	-9.5	7.0
RSP0060	Flagellar motor switch protein	-1.2	0.9	-1.5	1.2	-1.2	0.9	-2.2	1.7
RSP0061	Flagellar motor switch protein FlhN	-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 FlhP 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 FlhQ	-1.2	0.8	-2.0	1.3	-2.5	1.7	-4.3	2.7
RSP0065	Flagellar biosynthetic protein	-1.1	1.0	-1.7	1.4	-2.0	1.6	-2.5	2.2
RSP0066	Predicted membrane protein involved in flagellar biogenesis	-1.2	1.0	-1.7	1.4	-1.6	1.3	-2.1	1.7
RSP0067	Hypothetical protein	-1.4	1.0	-2.3	1.7	-2.1	1.7	-8.8	6.9
RSP0070	Flagellar hook-associated protein FlhD	1.2	1.0	-1.6	1.4	-1.1	0.9	-2.0	1.6
RSP0073	Flagellin and related hook-associated protein	-1.3	1.0	-2.0	1.6	-1.3	0.8	-4.0	2.6
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

Supplementary Table 2-----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
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 proteins	-1.3	1.2	-2.3	2.2	-2.7	2.5	-20.3	18.1
RSP0079	Flagellar basal body and hook proteins	-1.2	0.9	-2.1	1.6	-1.3	1.0	-11.0	8.7
RSP0080	Flagellar basal body and hook proteins	-1.2	0.9	-2.3	1.9	-2.0	1.5	-50.9	41.3
RSP0081	Flagellar hook capping protein	-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
RSP0084	Hypothetical protein	-1.3	1.0	-1.7	1.4	-1.8	1.5	-2.4	2.0
RSP0231	Flagellar motor protein MotB and related proteins	-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
RSP0263	bchC, 2-alpha-hydroxy ethyl bacteriochlorophyllide oxidase	1.4	1.2	1.5	1.4	1.5	1.2	2.9	2.6
RSP0271	CrtI, phytoene dehydrogenase	1.4	1.3	1.5	1.3	2.3	1.9	3.3	2.6
RSP0279	BchG; geranylgeranyl-bacteriochlorophyll synthetase	1.6	1.2	1.5	1.2	1.4	1.0	2.2	1.6
RSP0284	BchF; 2-vinyl bacteriochlorophyllide hydratase	1.6	1.2	1.6	1.2	1.5	1.2	2.2	1.5
RSP0295	Hypothetical protein	1.2	1.2	1.5	1.4	-1.7	1.5	1.1	0.9
RSP0319	Hypothetical protein	1.8	1.6	1.8	1.6	2.8	2.3	2.8	2.3
RSP0423	Predicted oxidoreductases (related to aryl-alcohol dehydrogena	1.6	1.3	1.7	1.4	1.3	1.0	2.9	2.3
RSP0697	Universal stress protein UspA	1.8	1.6	1.5	1.3	2.2	1.6	2.6	2.3
RSP0753	SspA	1.4	1.1	1.7	1.5	1.9	1.5	10.5	8.8
RSP0769	Glutathione-S-transferases	1.6	1.2	1.5	1.2	3.4	2.3	2.4	1.5
RSP0809	Nitroreductase family protein	1.7	1.3	1.6	1.3	-1.8	1.2	-1.4	1.0
RSP0871	PLP-dependent aminotransferases	1.6	1.3	1.6	1.2	1.4	1.1	1.9	1.5
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	-1.3	0.8	-2.0	1.3	-1.6	1.2	-32.4	21.8
RSP0912	Integral membrane protein	-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
RSP0983	Hypothetical protein	-1.9	1.4	-1.7	1.3	-3.4	2.5	-2.6	1.9
RSP1026	Hypothetical protein	1.4	1.2	1.5	1.3	1.1	0.8	3.0	2.4
RSP1180	Periplasmic sugar-binding protein	-1.0	1.0	-1.8	1.6	2.8	2.4	-3.0	2.7
RSP1249	Periplasmic sugar-binding protein	1.2	1.1	-1.5	1.3	1.0	0.7	-2.7	2.1
RSP1256	Enoyl-[acyl-carrier-protein] reductase (NADH)	1.8	1.5	1.5	1.3	1.6	1.3	2.7	1.8
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

Supplementary Table 2-----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
RSP1279	Predicted phosphatases	1.1	0.9	1.5	1.3	-2.6	2.1	1.2	1.0
RSP1379	Cytosol aminopeptidase	1.8	1.5	1.5	1.3	-1.5	1.0	-1.0	0.7
RSP1397	Glutathione S-transferase	1.5	1.2	1.6	1.3	1.5	1.2	1.8	1.4
RSP1420	Hypothetical protein	-1.3	1.0	-1.6	1.3	1.1	0.9	-2.4	2.0
RSP1492	2-Octaprenyl-6-methoxyphenol hydroxylase	1.5	1.3	1.5	1.4	1.1	1.0	1.9	1.6
RSP1583	Response regulator	1.4	1.0	-1.5	1.2	-2.6	2.0	-5.9	5.1
RSP1584	Chemotaxis protein histidine kinase	1.0	0.5	-2.1	1.4	-2.0	1.4	-6.5	3.8
RSP1589	Methyl-accepting chemotaxis protein	1.2	0.8	-1.6	1.2	-1.7	1.3	-3.8	3.1
RSP1860	Hypothetical protein	1.5	1.1	1.7	1.2	-1.2	0.8	2.4	1.7
RSP1870	Haloacid dehalogenase-like hydrolase	1.7	1.4	1.6	1.3	1.4	1.1	1.6	1.1
RSP1887	Ribosomal protein L33	-3.2	1.9	-2.4	1.3	-1.9	1.1	-1.5	0.9
RSP1895	Hypothetical protein	1.4	1.2	1.6	1.4	1.0	0.9	3.3	2.6
RSP1966	Hypothetical protein	1.3	0.9	1.5	1.2	5.3	3.5	2.0	1.1
RSP2085	Hypothetical protein	1.6	1.2	1.5	1.2	1.4	1.1	3.1	2.5
RSP2093	ATPases involved in chromosome partitioning	1.5	1.3	1.6	1.4	1.3	1.1	1.8	1.4
RSP2171	Transcriptional regulators	1.6	1.3	1.5	1.4	3.7	3.4	2.3	2.0
RSP2314	Aldo/keto reductases, related to diketoglucuronate reductase	1.1	1.0	1.5	1.2	-1.2	1.1	2.0	1.6
RSP2365	Periplasmic sugar-binding protein	1.2	1.0	-1.8	1.4	1.6	1.1	-2.4	2.2
RSP2663	Putative periplasmic binding ABC transporter	-1.7	0.8	-2.7	1.3	-1.6	0.7	-2.9	1.3
RSP2692	Predicted acyltransferase	1.9	1.5	1.9	1.4	4.6	3.6	2.6	1.8
RSP2764	Hypothetical protein	1.7	1.2	1.6	1.2	10.0	7.1	8.1	5.7
RSP2829	Hypothetical protein	1.0	0.7	1.6	1.2	-1.3	0.7	1.4	0.9
RSP2835	Putative enzyme of deoxyxylulose pathway (terpenoid biosynthe	1.6	1.4	1.6	1.4	-1.4	1.2	1.8	1.3
RSP2898	Hypothetical protein	1.4	1.2	1.5	1.2	1.3	1.0	1.4	0.9
RSP2967	Sugar (and other) transporter	1.2	1.0	1.5	1.2	-1.1	0.8	1.3	1.0
RSP2987	Predicted acetyltransferases	1.4	1.1	1.5	1.2	-1.6	1.0	1.1	0.8
RSP3058	Proline/glycine betaine ABC-type transport systems	2.0	1.4	2.4	1.7	3.9	2.6	45.3	31.1
RSP3059	Proline/glycine betaine ABC-type transport systems	2.1	1.1	2.9	1.5	9.6	4.3	50.1	22.7
RSP3075	Hypothetical protein	1.5	1.3	1.9	1.7	-1.1	1.0	3.6	2.9
RSP3076	Hypothetical protein	1.3	1.2	1.7	1.5	-1.3	0.9	2.9	2.5
RSP3080	Choline-glycine betaine transporter	1.8	1.3	2.0	1.5	1.1	0.7	4.0	2.9
RSP3083	Methyl-accepting chemotaxis protein	1.4	0.9	-1.7	1.3	1.3	0.9	-2.2	1.7
RSP3102	Sec-independent protein secretion pathway Tata	-3.3	2.6	-3.4	2.7	-3.2	2.4	-4.4	3.3
RSP3212	qxTA, cyt. bd subunit 1	1.2	1.0	1.5	1.3	2.2	1.7	1.9	1.6

Supplementary Table 2-----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
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
RSP3304	Hypothetical protein	-1.2	1.0	-1.5	1.3	1.0	0.8	-1.1	0.8
RSP3345	Hypothetical protein	1.6	1.2	1.6	1.3	-1.5	1.1	1.0	0.8
RSP3432	Probable methyl-accepting chemotaxis protein; BLAST	-1.8	1.3	-1.6	1.2	-1.7	1.2	-3.6	2.5
RSP3510	Hypothetical protein	1.5	1.0	1.6	1.2	2.5	1.5	2.0	1.2
RSP3511	Response regulator	1.5	1.2	1.6	1.4	2.5	2.0	1.7	1.6
RSP3539	Calcium-binding protein	-1.1	0.8	-1.5	1.3	1.2	0.8	-5.0	3.2
RSP3633	Hypothetical protein	1.7	1.5	1.7	1.4	16.2	12.4	8.1	6.2
RSP3732	ABC transporter, substrate binding protein [sugar]	-1.1	0.9	-1.6	1.4	5.1	3.7	-1.9	1.5
RSP3734	ABC transporter, membrane spanning protein [sugar]	1.1	0.9	-1.6	1.2	1.1	0.7	-2.0	1.5
RSP3893	Transcriptional regulator	1.4	1.1	1.5	1.3	1.3	1.0	1.4	1.2
RSP3917	Predicted integral membrane protein	1.6	1.2	1.5	1.2	-1.5	0.9	1.2	0.8
RSP4024	Hypothetical protein	1.5	1.3	1.6	1.4	-1.8	1.4	2.8	2.4
RSP4188	Hypothetical protein	1.4	1.2	1.6	1.4	21.5	17.8	8.5	6.3
RSP4203	Thiol-disulfide isomerase and thioredoxin	1.9	1.6	1.8	1.6	1.7	1.5	2.9	2.1
RSP4204	Hypothetical protein	1.9	1.4	1.8	1.3	1.1	0.8	2.6	1.7
RSP4209	Hypothetical protein	1.7	1.0	2.4	1.4	1.4	0.9	7.3	4.1
RSP4210	Protein-tyrosine-phosphatase	1.6	1.4	1.6	1.3	3.8	3.0	2.8	2.2
RSP4247	Hypothetical protein	1.6	1.3	1.6	1.2	1.1	0.7	2.5	1.5

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