

**Supplementary Table 3** Genes affected by Strong-salt stress for 7 min passed under fold change  $\geq 4.0$  and  $crt \geq 1.15$  cut off (145 genes)

Gene ID <sup>a</sup>	Function <sup>b</sup>	Mild-salt 7 min		Mild-salt 45min		Strong-salt 7 min		Strong-salt 45 min	
		Fold	crt	Fold	crt	Fold	crt	Fold	crt
RSP0051	Response 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
RSP0083	Flagellar basal-body rod protein FlgB	-1.6	0.9	-2.6	1.5	-4.3	2.6	-14.5	8.1
RSP0124	Hypothetical protein	1.1	0.9	1.1	0.9	4.8	4.0	-1.1	0.6
RSP0166	DnaK suppressor protein	1.3	0.8	1.1	0.7	4.2	2.8	1.9	1.1
RSP0171	Response regulator	-1.2	0.9	-1.4	1.0	6.2	4.4	1.8	1.4
RSP0184	Putative N-carbamyl-L-amino acid amidohydrolase	1.2	0.9	-1.1	0.9	5.3	4.2	2.4	1.8
RSP0189	NADPH-dependent glutamate synthase	1.2	1.0	-1.1	0.9	10.6	7.0	2.1	1.5
RSP0217	Phage integrase	1.5	1.1	1.4	1.0	29.6	24.0	6.5	4.6
RSP0250	Hypothetical protein	1.0	0.8	1.1	0.9	4.2	3.3	2.2	1.9
RSP0353	DNA-dependent DNA polymerase III alpha chain	1.1	0.8	1.1	0.9	9.8	6.2	3.2	2.4
RSP0589	Hypothetical protein	1.3	1.0	1.5	1.1	4.2	2.8	3.7	2.9
RSP0640	N-methylhydantoinase	1.2	1.2	1.1	1.0	21.6	20.8	5.5	4.1
RSP0641	Transcriptional regulator	-1.1	0.9	-1.0	0.9	5.4	4.4	2.7	2.0
RSP0751	Hypothetical protein	1.0	0.9	1.1	0.9	4.8	3.8	2.3	1.9
RSP0760	Transcriptional regulator	1.1	0.9	1.2	1.0	4.7	3.4	3.4	2.8
RSP0761	Hypothetical protein	1.1	1.0	1.1	0.9	4.7	3.8	3.5	3.1
RSP0762	Transcriptional regulator	1.1	0.8	1.1	0.8	6.0	4.6	3.5	2.6
RSP0766	Hypothetical protein	1.4	1.2	1.2	1.0	8.5	7.4	3.0	2.2
RSP0866	Hypothetical protein	1.0	0.7	1.1	0.8	4.4	3.2	1.6	1.2
RSP0868	Hypothetical protein	-1.1	0.6	-1.1	0.6	7.5	4.8	2.1	1.1
RSP0949	Trehalose-6-phosphatase (OtsA)	1.8	1.3	2.0	1.4	6.6	4.5	8.6	6.3
RSP0989	Ribose/xylose/arabinose/galactoside ABC-type transport systems	1.0	0.8	-1.2	1.0	7.9	4.0	-1.1	0.9
RSP0990	Periplasmic sugar-binding protein	-1.0	1.0	-1.2	1.2	23.0	19.9	-1.1	1.0
RSP0991	Transcriptional regulator	1.0	1.0	1.0	1.0	6.1	5.2	1.1	1.1
RSP1095	DNA mismatch repair enzyme (predicted ATPase)	1.0	1.0	1.2	1.1	9.9	9.3	5.5	4.7
RSP1184	tRNA-processing ribonuclease	1.1	0.8	1.1	0.8	6.2	4.6	3.8	2.7
RSP1220	Transcriptional regulators of heat shock genes	1.4	1.3	1.2	1.1	4.3	3.7	1.9	1.7
RSP1272	Specialized sigma subunits of RNA polymerase	1.5	1.1	1.6	1.1	5.6	3.5	3.9	2.7
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
RSP1308	Hypothetical protein	1.1	1.0	1.2	1.0	5.5	4.7	3.1	2.6
RSP1423	ATPases involved in chromosome partitioning	1.3	1.0	1.0	0.8	8.2	6.6	1.3	1.0
RSP1425	Hypothetical protein	1.2	1.0	1.3	1.0	6.8	5.8	2.5	2.0

Supplementary Table 3-----Continued 1

Gene ID <sup>a</sup>	Function <sup>b</sup>	Mild-salt 7 min		Mild-salt 45min		Strong-salt 7 min		Strong-salt 45 min	
		Fold	crt	Fold	crt	Fold	crt	Fold	crt
RSP1430	Hypothetical protein	1.6	1.3	1.4	1.3	6.7	5.7	2.8	2.6
RSP1431	Hypothetical protein	1.5	1.3	1.5	1.4	4.2	2.9	1.8	1.5
RSP1433	Hypothetical protein	1.3	1.1	1.3	1.1	6.9	5.5	4.2	3.2
RSP1434	NADPH:quinone reductase and related Zn-dependent oxidoreduc	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
RSP1436	Nucleotide binding/ATPase protein	-1.1	1.1	-1.1	1.1	13.4	8.6	1.1	1.1
RSP1486	Transcriptional regulator	1.1	1.0	1.1	1.1	15.5	14.6	3.4	3.0
RSP1487	Hypothetical protein	1.4	1.3	1.2	1.0	8.5	7.0	1.6	1.3
RSP1488	Glyoxalase Glyoxalase/Bleomycin resistance protein	1.1	0.9	-1.0	0.9	5.9	4.6	1.5	1.0
RSP1623	Hypothetical protein	-1.1	0.8	1.2	1.0	-5.0	3.6	-1.1	0.8
RSP1624	Hypothetical protein	1.4	1.0	1.3	1.0	7.5	5.7	2.6	1.8
RSP1709	Ribosomal protein S7	-1.1	1.0	1.0	0.9	-4.9	3.4	-1.8	1.6
RSP1890	Transcriptional regulator	1.2	0.9	-1.0	0.9	4.5	3.4	3.7	2.2
RSP1938	Hypothetical protein	1.0	0.9	1.2	1.0	4.6	4.1	3.6	3.1
RSP1943	Hypothetical protein	2.5	2.0	1.2	0.9	-5.1	2.9	-3.7	2.5
RSP1945	Transcriptional regulator	2.1	1.6	1.3	1.1	10.8	9.0	5.3	3.8
RSP1966	Hypothetical protein	1.3	0.9	1.5	1.2	5.3	3.5	2.0	1.1
RSP1990	Transcriptional regulator	-1.1	0.8	-1.0	0.8	5.7	5.1	1.9	1.4
RSP2075	Hypothetical protein	-1.0	0.9	-1.0	0.9	5.9	3.7	1.6	1.3
RSP2123	Hypothetical protein	-1.1	0.9	1.0	1.0	5.0	3.8	2.4	2.0
RSP2128	Phosphoribosylformylglycinamide (FGAM) synthase	1.1	0.8	1.2	1.0	-4.4	3.2	-1.6	1.4
RSP2231	Hypothetical protein	1.4	1.2	1.5	1.2	12.0	9.4	5.1	4.3
RSP2234	Hypothetical protein	1.1	1.0	1.1	1.1	6.7	6.5	2.9	2.8
RSP2258	Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR) sy	-1.0	0.7	1.2	1.0	-4.0	2.5	-3.8	2.4
RSP2338	Hypothetical protein	1.3	1.0	1.2	1.0	4.7	3.7	4.0	3.1
RSP2348	Hypothetical protein	1.7	1.2	1.3	1.1	4.3	3.2	3.7	2.3
RSP2349	Hypothetical protein	1.7	1.1	1.5	1.0	18.2	11.3	4.1	2.3
RSP2350	Hypothetical protein	1.6	0.9	1.4	0.9	15.4	9.9	3.8	2.2
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
RSP2476	Hypothetical protein	-1.0	1.0	1.0	1.0	4.3	4.0	2.2	2.1
RSP2484	Hypothetical protein	1.2	1.0	1.2	0.9	5.5	4.3	2.2	1.8
RSP2488	Hypothetical protein	-1.0	0.6	-1.1	0.7	8.1	5.2	1.7	1.0
RSP2489	Hypothetical protein	1.5	1.1	1.5	1.1	8.6	6.5	2.1	1.4

Supplementary Table 3-----Continued 2

Gene ID <sup>a</sup>	Function <sup>b</sup>	Mild-salt 7 min		Mild-salt 45min		Strong-salt 7 min		Strong-salt 45 min	
		Fold	crt	Fold	crt	Fold	crt	Fold	crt
RSP2506	Acyl-CoA dehydrogenases	1.0	0.8	-1.1	0.8	6.3	4.1	6.5	3.4
RSP2591	Response regulator	-1.1	0.7	-1.3	0.8	5.1	4.2	-2.0	1.2
RSP2604	Periplasmic phosphate-binding protein	1.6	1.2	1.3	1.0	4.2	2.9	3.5	2.3
RSP2610	Transcriptional regulator	1.3	1.2	1.3	1.1	4.6	3.8	1.9	1.8
RSP2611	Histone-like DNA-binding protein	1.2	1.0	1.2	1.0	5.0	4.4	1.9	1.6
RSP2624	Hypothetical protein	1.9	1.6	1.7	1.1	18.6	13.3	7.2	4.9
RSP2681	Specialized sigma subunits of RNA polymerase (sigma-24)	1.2	1.0	1.3	1.2	8.5	7.3	6.1	5.1
RSP2692	Predicted acyltransferases	1.9	1.5	1.9	1.4	4.6	3.6	2.6	1.8
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
RSP2765	Hypothetical protein	1.0	1.0	1.1	1.0	10.0	7.4	3.0	2.5
RSP2780	Transcriptional regulator	1.0	0.9	1.1	1.0	5.7	3.6	2.1	1.8
RSP2801	Transcriptional regulator	1.6	1.3	1.4	1.2	16.9	13.8	4.0	3.2
RSP2933	Cytosine deaminase and related metal-dependent hydrolase	1.0	0.9	-1.0	1.0	9.0	7.1	1.3	1.2
RSP3006	Hypothetical protein	1.1	0.9	1.2	1.0	5.8	4.2	4.2	3.3
RSP3007	Hypothetical protein	-1.1	0.6	-1.0	0.6	5.8	4.3	1.5	0.9
RSP3013	Hypothetical protein	-1.0	0.9	1.0	1.0	4.2	3.3	2.2	2.1
RSP3022	Transcriptional regulator	1.3	1.1	1.4	1.2	13.6	8.0	1.3	1.2
RSP3023	Hypothetical protein	-1.1	1.0	-1.0	0.9	4.3	2.1	-1.0	0.9
RSP3025	Flavodoxin	-1.1	1.0	-1.1	1.0	15.5	9.5	-1.0	0.9
RSP3059	Phosphoenolpyruvate carboxykinase	2.1	1.1	2.9	1.5	9.6	4.3	50.1	22.7
RSP3124	Transcriptional regulator	1.2	1.0	1.2	1.0	4.6	3.7	2.7	2.0
RSP3125	Transcriptional regulator	1.1	0.8	1.1	0.8	12.5	6.1	2.2	1.2
RSP3168	Putative taurine-binding periplasmic protein	1.2	1.1	-1.1	1.0	6.7	4.6	1.3	1.1
RSP3179	Ferric uptake regulation protein	1.0	0.6	-1.1	0.3	11.1	6.5	3.1	1.6
RSP3180	Transglutaminase-like enzymes	-1.1	1.0	-1.1	0.9	5.3	4.6	1.5	1.2
RSP3378	Hypothetical protein	1.3	0.8	1.2	0.8	10.7	6.5	4.9	2.8
RSP3379	Hypothetical protein	1.1	1.0	1.1	0.9	7.0	5.7	2.4	2.0
RSP3411	Hypothetical protein	1.4	1.2	1.1	0.9	7.2	6.0	1.4	1.2
RSP3606	Sigma-54 (RpoN) and related alternative sigma subunits	1.3	1.2	1.3	1.1	4.1	3.8	2.8	2.3
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
RSP3640	Hypothetical protein	-1.0	0.8	-1.2	0.9	-4.3	3.0	-3.9	3.0
RSP3642	Transcription regulator	-1.2	0.8	-1.3	0.9	-5.4	3.8	-4.5	2.9

Supplementary Table 3-----Continued 4

Gene ID <sup>a</sup>	Function <sup>b</sup>	Mild-salt 7 min		Mild-salt 45min		Strong-salt 7 min		Strong-salt 45 min	
		Fold	crt	Fold	crt	Fold	crt	Fold	crt
RSP3643	Hypothetical protein	-1.1	0.9	-1.1	0.9	-4.7	3.7	-3.1	2.4
RSP3644	dGTP triphosphohydrolase	-1.1	0.8	-1.2	0.9	-5.6	3.2	-2.7	1.9
RSP3646	Adenylate kinase/yeast uridylylate kinase	1.2	0.9	1.2	1.0	10.5	8.6	3.6	2.8
RSP3663	Putative ABC transporter	-1.0	0.9	-1.1	0.9	6.4	5.9	1.7	1.5
RSP3675	Acetyl esterase	1.0	1.0	1.1	1.0	5.4	4.4	-1.0	1.0
RSP3676	Transcriptional regulator	1.1	1.0	-1.0	1.0	8.2	7.1	1.1	1.0
RSP3677	Periplasmic sugar-binding protein	-1.1	1.0	-1.1	1.0	4.6	4.0	-1.2	1.1
RSP3701	Periplasmic sugar-binding protein	2.6	2.2	-1.3	0.8	11.8	9.3	-2.2	1.6
RSP3702	ABC-type sugar (aldose) transport system	1.8	1.2	-1.4	1.0	4.6	3.2	-1.5	1.1
RSP3731	Transcriptional regulators of sugar metabolism	-1.2	1.0	-1.1	1.0	4.3	3.6	1.8	1.3
RSP3732	ABC transporter, substrate binding protein [sugar]	-1.1	0.9	-1.6	1.4	5.1	3.7	-1.9	1.5
RSP3750	Hypothetical protein	1.0	0.9	1.0	0.8	-5.2	3.6	-1.1	0.9
RSP3751	Hypothetical protein	-1.0	0.7	1.0	0.7	-4.0	2.3	-1.3	0.8
RSP3756	ATP-dependent exoDNase (exonuclease V)	1.2	1.0	1.3	1.1	-4.8	3.1	1.4	0.9
RSP3814	Transcriptional regulator	-1.1	1.0	-1.1	1.0	4.3	2.5	-1.0	1.0
RSP3817	Hypothetical protein	-1.2	1.0	-1.1	0.9	5.2	2.5	1.0	0.8
RSP3840	ATPases involved in chromosome partitioning	-1.0	0.7	-1.0	0.8	11.5	9.0	3.7	2.6
RSP3861	Periplasmic sulfate/thiosulfate binding protein	2.0	1.4	1.3	1.0	4.4	3.5	1.2	0.9
RSP3925	Sulfotransfer Sulfotransferase protein	1.0	0.9	1.2	1.1	-4.8	3.2	-1.4	1.1
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
RSP3971	Transcriptional regulator	1.2	1.0	1.2	1.0	4.4	3.0	2.4	1.5
RSP4037	Sugar-binding periplasmic proteins	1.1	1.0	-1.1	1.0	7.5	6.8	1.1	1.0
RSP4038	Transcriptional regulators of sugar metabolism	1.1	0.9	1.2	1.0	4.8	2.8	2.0	1.5
RSP4075	Hypothetical protein	-1.2	0.9	-1.1	0.9	5.8	4.6	2.1	1.6
RSP4076	Hypothetical protein	1.0	0.9	1.1	1.0	4.3	3.6	2.8	2.4
RSP4081	Hypothetical protein	1.2	0.7	1.2	0.7	12.4	7.8	3.9	2.1
RSP4082	Hypothetical protein	1.3	1.0	1.2	0.9	9.1	7.2	4.4	3.5
RSP4090	Hypothetical protein	1.4	1.0	1.4	1.2	8.1	6.2	3.3	2.5
RSP4091	Transposase protein	1.3	1.1	1.2	1.2	14.1	11.8	4.6	4.3
RSP4092	Transposase protein	1.2	1.0	1.2	1.1	6.5	5.8	2.7	2.3
RSP4112	Hypothetical protein	1.1	1.0	1.1	1.0	10.7	9.5	3.2	3.0
RSP4139	Hypothetical protein	1.7	1.4	1.4	1.2	10.8	9.0	3.3	2.5
RSP4140	Hypothetical protein	1.5	1.3	1.2	1.1	4.3	3.9	2.9	2.4

Supplementary Table 3-----Continued 3

Gene ID <sup>a</sup>	Function <sup>b</sup>	Mild-salt 7 min		Mild-salt 45min		Strong-salt 7 min		Strong-salt 45 min	
		Fold	crt	Fold	crt	Fold	crt	Fold	crt
RSP4160	Hypothetical protein	1.3	0.9	-1.1	0.5	-5.1	1.9	1.2	0.6
RSP4186	ATPases involved in chromosome partitioning;	1.1	0.7	-1.2	0.8	5.6	3.8	2.6	1.6
RSP4188	Hypothetical protein	1.4	1.2	1.6	1.4	21.5	17.8	8.5	6.3
RSP4201	Transcriptional regulator	1.5	1.0	1.3	0.9	6.7	3.9	3.2	1.9
RSP4239	Hypothetical protein	1.4	1.3	1.4	1.2	4.6	3.7	4.1	3.4
RSP4260	Transcriptional regulator	1.1	1.0	1.1	1.0	14.5	13.4	2.5	1.7
RSP4278	Transcriptional regulator	1.3	1.1	1.3	1.1	5.0	4.0	1.7	1.3
RSP4281	Hypothetical protein	-1.2	0.8	-1.2	0.8	10.9	5.9	2.2	1.2
RSP4290	Hypothetical protein	-1.1	0.9	-1.0	0.8	7.4	4.3	1.2	0.8

<sup>a</sup> Sorted according to the *Rhodobacter* genome database. <sup>b</sup> Derived from Oak Ridge National Laboratory genome annotations.