

1 **Lysogenization of *Staphylococcus aureus* RN450 by phages  $\phi$ 11 and  $\phi$ 80 $\alpha$  leads to**  
2 **the activation of the SigB regulon**

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4 Running Title: Transcriptome of *Staphylococcus aureus* lysogens

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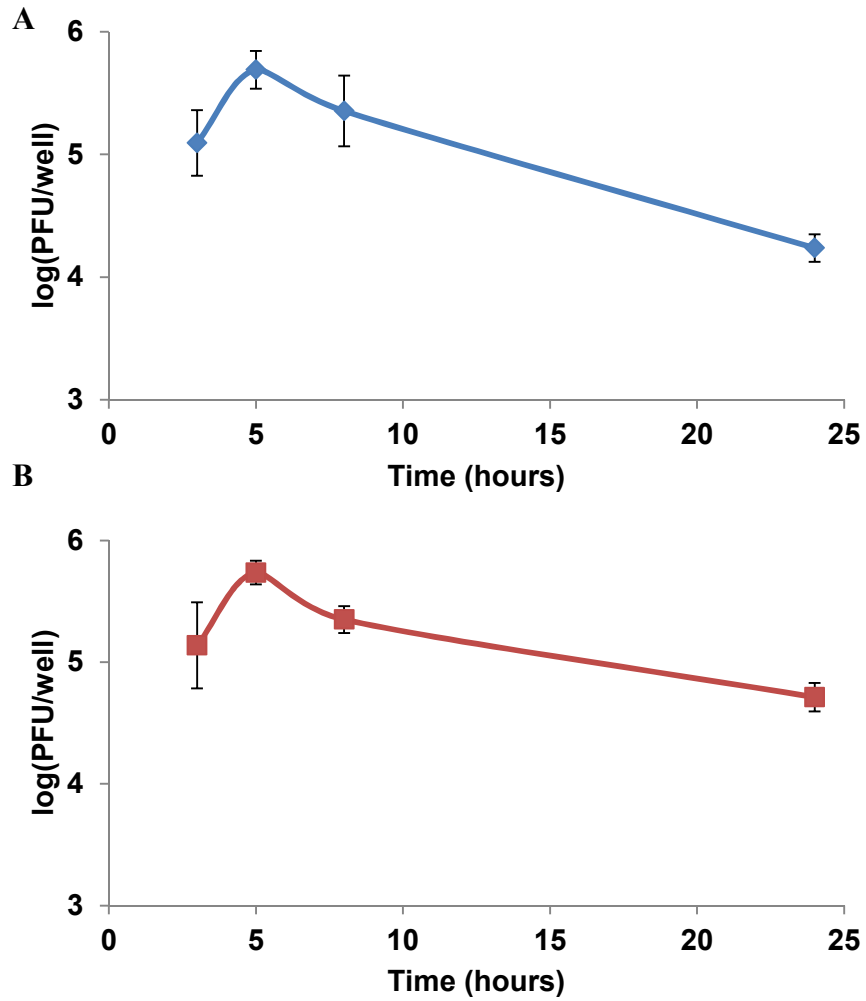
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**Figure S1. Analysis of phage release throughout biofilm development in lysogenic strains RN450- $\phi$ 11 and RN450- $\phi$ 80 $\alpha$ .** Biofilms were formed for 3, 5, 8 or 24 hours by strains RN450-f80a (A) or RN450-f11 (B). Then, free phage particles in the adhered phase (biofilm) were titrated using strain *S. aureus* RN4220 as a host.



**Table S1. Full list of genes dysregulated in biofilms formed by the lysogenic strain RN450-Φ11 compared to the non-lysogenic strain RN4**

Gene ID*	Gene name	Gene product	Fold-change	padj
SAOUHSC_02163			-5.22	9.41E-10
SAOUHSC_02906	SAOUHSC_02906	Putative uncharacterized protein	-3.24	5.66E-08
SAOUHSC_02240			-3.21	8.61E-06
SAOUHSC_02967	SAOUHSC_02967	"Arginine/ornithine antiporter, putative"	-3.06	7.63E-09
SAOUHSC_00401	SAOUHSC_00401	Putative uncharacterized protein	-2.99	4.41E-04
SAOUHSC_02969	arcA	Arginine deiminase	-2.98	6.10E-07
SAOUHSC_02965	arcC2	Carbamate kinase 2	-2.94	9.53E-12
SAOUHSC_02907	SAOUHSC_02907	Putative uncharacterized protein	-2.89	1.29E-05
SAOUHSC_02905	SAOUHSC_02905	Putative uncharacterized protein	-2.83	5.78E-08
SAOUHSC_01942	splA	Serine protease SplA	-2.75	4.30E-04
SAOUHSC_02968	argF	Ornithine carbamoyltransferase	-2.66	2.81E-06
SAOUHSC_02452	lacD	"Tagatose 1,6-diphosphate aldolase"	-2.60	1.07E-05
SAOUHSC_02453	lacC	Tagatose-6-phosphate kinase	-2.56	2.50E-06
SAOUHSC_01941	splB	Serine protease SplB	-2.51	1.33E-02
SAOUHSC_02454	lacB	Galactose-6-phosphate isomerase subunit LacB	-2.49	4.14E-03
SAOUHSC_01135	SAOUHSC_01135	Putative uncharacterized protein	-2.49	1.91E-03
SAOUHSC_02260	hld	Delta-hemolysin	-2.48	1.54E-04
SAOUHSC_02090	SAOUHSC_02090	Conserved hypothetical phage protein	-2.45	1.21E-15
SAOUHSC_02964	arcR	HTH-type transcriptional regulator ArcR	-2.41	8.50E-06
SAOUHSC_01136	SAOUHSC_01136	Putative uncharacterized protein	-2.27	2.43E-03
SAOUHSC_02451	SAOUHSC_02451	"PTS system lactose-specific IIA component, putative"	-2.26	1.21E-02
SAOUHSC_02266	SAOUHSC_02266	Putative uncharacterized protein	-2.25	4.99E-06
SAOUHSC_02620	SAOUHSC_02620	Putative uncharacterized protein	-2.24	6.23E-06
SAOUHSC_02971	SAOUHSC_02971	"Aureolysin, putative"	-2.21	4.19E-11
SAOUHSC_01950	SAOUHSC_01950	"Flavoprotein, epiD, putative"	-2.20	1.19E-04
SAOUHSC_01945	SAOUHSC_01945	"Membrane protein, putative"	-2.17	7.81E-06
SAOUHSC_01935	splF	Serine protease SplF	-2.15	9.18E-04
SAOUHSC_01939	splC	Serine protease SplC	-2.14	1.53E-03
SAOUHSC_01949	SAOUHSC_01949	"Intracellular serine protease, putative"	-2.10	2.50E-05
SAOUHSC_00257	SAOUHSC_00257	Putative uncharacterized protein	-2.09	1.13E-05
SAOUHSC_01952	SAOUHSC_01952	"Lantibiotic epidermin biosynthesis protein EpiB, putative"	-2.07	2.41E-04
SAOUHSC_01951	SAOUHSC_01951	"Epidermin biosynthesis protein EpiC, authentic point mutatio	-2.07	1.21E-04
SAOUHSC_02970			-2.06	5.66E-04
SAOUHSC_01513	SAOUHSC_01513	Putative uncharacterized protein	-2.03	1.42E-05
SAOUHSC_00988	sspA	Glutamyl endopeptidase	-2.03	1.95E-04
SAOUHSC_02455	lacA	Galactose-6-phosphate isomerase subunit LacA	-2.01	1.42E-02
SAOUHSC_02261	agrB	Accessory gene regulator protein B	-2.00	1.08E-04
SAOUHSC_02265	SAOUHSC_02265	Accessory gene regulator protein A	-2.00	8.54E-06
SAOUHSC_01018	purD	Phosphoribosylamine--glycine ligase	2.00	1.69E-03
SAOUHSC_01918	SAOUHSC_01918	Putative uncharacterized protein	2.01	1.13E-02
SAOUHSC_00632	mnhG2	Putative antiporter subunit mnhG2	2.04	5.53E-05
SAOUHSC_00630	SAOUHSC_00630	Putative uncharacterized protein	2.05	6.38E-06
SAOUHSC_02848	glcB	PTS system glucoside-specific EIICBA component	2.07	1.21E-04
SAOUHSC_00655	SAOUHSC_00655	Putative uncharacterized protein	2.07	4.88E-02
SAOUHSC_00629	mnhE2	Putative antiporter subunit mnhE2	2.08	1.37E-05
SAOUHSC_03032	SAOUHSC_03032	Putative uncharacterized protein	2.09	4.16E-03
SAOUHSC_00625	mnhA2	Putative antiporter subunit mnhA2	2.10	2.46E-08
SAOUHSC_02597	SAOUHSC_02597	"PTS system component, putative"	2.12	1.07E-02
SAOUHSC_00627	mnhC2	Putative antiporter subunit mnhC2	2.13	2.68E-04
SAOUHSC_00626	mnhB2	Putative antiporter subunit mnhB2	2.14	7.06E-05
SAOUHSC_00628	mnhD2	Putative antiporter subunit mnhD2	2.14	5.08E-08
SAOUHSC_02877	crtN	Dehydrosqualene desaturase	2.14	2.28E-11
SAOUHSC_02137	sdcS	Sodium-dependent dicarboxylate transporter SdcS	2.15	7.79E-06
SAOUHSC_01017	purH	Bifunctional purine biosynthesis protein PurH	2.17	2.39E-02
SAOUHSC_01318	SAOUHSC_01318	Putative uncharacterized protein	2.18	1.61E-03
SAOUHSC_02729	SAOUHSC_02729	"Amino acid ABC transporter-like protein, putative"	2.20	2.19E-02
SAOUHSC_01603	SAOUHSC_01603	Putative uncharacterized protein	2.21	2.71E-02
SAOUHSC_01921	SAOUHSC_01921	Putative uncharacterized protein	2.21	1.54E-03
SAOUHSC_02822	fbp	"Fructose-1,6-bisphosphatase class 3"	2.31	4.20E-02
SAOUHSC_00160	SAOUHSC_00160	Putative uncharacterized protein	2.31	3.00E-02

SAOUHSC_00291	SAOUHSC_00291	"PfkB family carbohydrate kinase family, putative"	2.32	2.99E-02
SAOUHSC_02772	SAOUHSC_02772	Putative uncharacterized protein	2.32	6.38E-06
SAOUHSC_03028	SAOUHSC_03028	Putative uncharacterized protein	2.34	1.12E-04
SAOUHSC_01920	SAOUHSC_01920	Putative uncharacterized protein	2.35	1.72E-04
SAOUHSC_00061	SAOUHSC_00061	Putative uncharacterized protein	2.35	8.91E-11
SAOUHSC_02425	SAOUHSC_02425	UPF0457 protein SAOUHSC_02425	2.39	1.50E-02
SAOUHSC_00156	SAOUHSC_00156	Putative uncharacterized protein	2.47	5.99E-03
SAOUHSC_02908	SAOUHSC_02908	Putative uncharacterized protein	2.49	3.11E-13
SAOUHSC_02815	SAOUHSC_02815	Putative uncharacterized protein	2.63	1.37E-03
SAOUHSC_01602	SAOUHSC_01602	"Transcriptional regulator, putative"	2.67	2.41E-03
SAOUHSC_01601	SAOUHSC_01601	"Alpha-glucosidase, putative"	2.70	2.45E-03
SAOUHSC_00624	SAOUHSC_00624	"Integrase/recombinase, putative"	2.72	4.42E-10
SAOUHSC_00317	SAOUHSC_00317	Glycerol-3-phosphate transporter	2.81	2.54E-05
SAOUHSC_00196	SAOUHSC_00196	Putative uncharacterized protein	2.82	3.92E-02
SAOUHSC_02882	crtO	"Glycosyl-4,4'-diaponeurosporenoate acyltransferase"	2.93	3.13E-03
SAOUHSC_02771	SAOUHSC_02771	Putative uncharacterized protein	2.96	2.96E-06
SAOUHSC_00846	SAOUHSC_00846	Putative uncharacterized protein	2.97	4.87E-17
SAOUHSC_02812	SAOUHSC_02812	Putative uncharacterized protein	3.00	1.36E-16
SAOUHSC_02881	crtP	Diapolycopene oxygenase	3.08	1.46E-03
SAOUHSC_00157	murQ	N-acetylmuramic acid 6-phosphate etherase	3.13	2.71E-03
SAOUHSC_01910	pckA	Phosphoenolpyruvate carboxykinase [ATP]	3.14	2.47E-03
SAOUHSC_00070	sarS	HTH-type transcriptional regulator SarS	3.26	5.67E-06
SAOUHSC_02403	mtlD	Mannitol-1-phosphate 5-dehydrogenase	3.27	2.51E-06
SAOUHSC_02387	SAOUHSC_02387	Putative uncharacterized protein	3.30	1.70E-22
SAOUHSC_02400	SAOUHSC_02400	"PTS system, mannitol-specific component, putative"	3.31	6.11E-04
SAOUHSC_00158	SAOUHSC_00158	PTS system EIIBC component SAOUHSC_00158	3.39	1.23E-03
SAOUHSC_02879	crtM	Dehydrosqualene synthase	3.46	7.53E-23
SAOUHSC_00831	SAOUHSC_00831	Organic hydroperoxide resistance protein-like	3.48	4.53E-14
SAOUHSC_02401	SAOUHSC_02401	Putative uncharacterized protein	3.63	2.55E-04
SAOUHSC_00069	spa	Immunoglobulin G-binding protein A	3.70	3.06E-06
SAOUHSC_00183	SAOUHSC_00183	"Membrane protein, putative"	3.72	4.68E-05
SAOUHSC_01794	SAOUHSC_01794	"Glyceraldehyde-3-phosphate dehydrogenase, type I"	3.77	2.50E-06
SAOUHSC_02880	crtQ	"4,4'-diaponeurosporenoate glycosyltransferase"	3.88	2.54E-12
SAOUHSC_00356	SAOUHSC_00356	Putative uncharacterized protein	3.96	1.13E-25
SAOUHSC_02402	SAOUHSC_02402	"PTS system, mannitol-specific IIa component, putative"	4.08	7.79E-06
SAOUHSC_00358	SAOUHSC_00358	Putative uncharacterized protein	4.67	3.86E-41
SAOUHSC_02444	SAOUHSC_02444	"Osmoprotectant transporter, BCCT family, opuD-like protein,	4.99	1.19E-39
SAOUHSC_A00354	SAOUHSC_00358.1	Putative uncharacterized protein	5.17	3.74E-17
SAOUHSC_02862	clpL	ATP-dependent Clp protease ATP-binding subunit ClpL	5.24	1.68E-66
SAOUHSC_00619	SAOUHSC_00619	Putative uncharacterized protein	5.66	1.56E-60
SAOUHSC_01730	SAOUHSC_01730	UPF0337 protein SAOUHSC_01730	6.31	4.25E-33
SAOUHSC_01729	SAOUHSC_01729	Putative uncharacterized protein	7.55	3.12E-31
SAOUHSC_02442	SAOUHSC_02442	Putative uncharacterized protein	7.60	4.64E-86
SAOUHSC_02443	SAOUHSC_02443	Putative uncharacterized protein	8.17	7.15E-89
SAOUHSC_00845	SAOUHSC_00845	UPF0337 protein SAOUHSC_00845	8.90	8.31E-61
SAOUHSC_02441	asp23	Alkaline shock protein 23	9.56	2.20E-91

\* Genes highlighted in grey correspond to genes dysregulated in this lysogen but not in the phi80alpha lysogenic strain

**Table S2. Full list of genes dysregulated in biofilms formed by the lysogenic strain RN450-Φ80α compared to the non-lysogenic strain RN**

Gene ID*	Gene name	Gene product	Fold-change	padj
SAOUHSC_02260	hld	Delta-hemolysin	-25.60	2.36E-92
SAOUHSC_01135	SAOUHSC_01135	Putative uncharacterized protein	-17.63	4.45E-106
SAOUHSC_01136	SAOUHSC_01136	Putative uncharacterized protein	-16.54	1.11E-100
SAOUHSC_02163			-11.84	5.09E-20
SAOUHSC_02240			-9.04	3.86E-18
SAOUHSC_02907	SAOUHSC_02907	Putative uncharacterized protein	-7.37	7.77E-32
SAOUHSC_02906	SAOUHSC_02906	Putative uncharacterized protein	-7.29	2.90E-26
SAOUHSC_02905	SAOUHSC_02905	Putative uncharacterized protein	-6.71	3.86E-32
SAOUHSC_00401	SAOUHSC_00401	Putative uncharacterized protein	-6.40	2.49E-10
SAOUHSC_02262	SAOUHSC_02262	Putative uncharacterized protein	-6.04	9.89E-47
SAOUHSC_02261	agrB	Accessory gene regulator protein B	-5.98	9.95E-55
SAOUHSC_02264	SAOUHSC_02264	Accessory gene regulator protein C	-5.60	2.13E-53
SAOUHSC_02970			-5.20	2.91E-18
SAOUHSC_02265	SAOUHSC_02265	Accessory gene regulator protein A	-5.03	5.09E-71
SAOUHSC_02969	arcA	Arginine deiminase	-4.59	4.43E-21
SAOUHSC_02967	SAOUHSC_02967	"Arginine/ornithine antiporter, putative"	-4.55	1.80E-36
SAOUHSC_02968	argF	Ornithine carbamoyltransferase	-4.51	1.91E-25
SAOUHSC_02965	arcC2	Carbamate kinase 2	-4.25	3.20E-25
SAOUHSC_02964	arcR	HTH-type transcriptional regulator ArcR	-4.19	3.74E-35
SAOUHSC_01953	SAOUHSC_01953	"Gallidermin superfamily epiA, putative"	-4.17	4.26E-23
SAOUHSC_02266	SAOUHSC_02266	Putative uncharacterized protein	-4.17	1.82E-40
SAOUHSC_02620	SAOUHSC_02620	Putative uncharacterized protein	-4.09	3.78E-31
SAOUHSC_01584	SAOUHSC_01584	Putative uncharacterized protein	-4.03	9.78E-44
SAOUHSC_01942	splA	Serine protease SplA	-3.91	1.68E-07
SAOUHSC_01583	SAOUHSC_01583	Conserved hypothetical phage protein	-3.89	8.70E-36
SAOUHSC_01513	SAOUHSC_01513	Putative uncharacterized protein	-3.80	5.79E-21
SAOUHSC_01512	SAOUHSC_01512	Putative uncharacterized protein	-3.77	3.14E-26
SAOUHSC_00256	SAOUHSC_00256	Putative uncharacterized protein	-3.74	7.77E-32
SAOUHSC_02462	SAOUHSC_02462	Putative uncharacterized protein	-3.69	3.21E-02
SAOUHSC_00257	SAOUHSC_00257	Putative uncharacterized protein	-3.59	1.73E-15
SAOUHSC_01511	SAOUHSC_01511	Putative uncharacterized protein	-3.43	5.25E-19
SAOUHSC_02241	SAOUHSC_02241	Uncharacterized leukocidin-like protein 1	-3.40	1.27E-25
SAOUHSC_02971	SAOUHSC_02971	"Aureolysin, putative"	-3.37	1.69E-32
SAOUHSC_01510	SAOUHSC_01510	Putative uncharacterized protein	-3.37	2.94E-29
SAOUHSC_00272	SAOUHSC_00272	Putative uncharacterized protein	-3.36	2.99E-09
SAOUHSC_01952	SAOUHSC_01952	"Lantibiotic epidermin biosynthesis protein EpiB, putative"	-3.31	2.37E-24
SAOUHSC_01951	SAOUHSC_01951	"Epidermin biosynthesis protein EpiC, authentic point mutatio	-3.24	6.66E-23
SAOUHSC_01508	SAOUHSC_01508	Putative uncharacterized protein	-3.24	1.09E-25
SAOUHSC_02243	SAOUHSC_02243	Uncharacterized leukocidin-like protein 2	-3.20	1.11E-28
SAOUHSC_01950	SAOUHSC_01950	"Flavoprotein, epiD, putative"	-3.15	1.70E-25
SAOUHSC_00988	sspA	Glutamyl endopeptidase	-3.11	8.34E-10
SAOUHSC_01941	splB	Serine protease SplB	-3.10	6.38E-05
SAOUHSC_00274	SAOUHSC_00274	Putative uncharacterized protein	-3.05	5.24E-13
SAOUHSC_00259	SAOUHSC_00259	Putative uncharacterized protein	-3.03	6.68E-12
SAOUHSC_00258	SAOUHSC_00258	Putative uncharacterized protein	-3.03	7.93E-16
SAOUHSC_00260	SAOUHSC_00260	Putative uncharacterized protein	-2.94	1.47E-12
SAOUHSC_00267	SAOUHSC_00267	Putative uncharacterized protein	-2.87	1.64E-19
SAOUHSC_00266	SAOUHSC_00266	Putative uncharacterized protein	-2.85	2.64E-22
SAOUHSC_02709	hlgC	Gamma-hemolysin component C	-2.85	1.58E-09
SAOUHSC_01949	SAOUHSC_01949	"Intracellular serine protease, putative"	-2.78	2.01E-15
SAOUHSC_00262	SAOUHSC_00262	Putative uncharacterized protein	-2.75	3.54E-09

SAOUHSC_00261	SAOUHSC_00261	Putative uncharacterized protein	-2.75	5.72E-11
SAOUHSC_02161	SAOUHSC_02161	MHC class II analog protein	-2.72	5.19E-03
SAOUHSC_00264	SAOUHSC_00264	Putative uncharacterized protein	-2.72	1.81E-08
SAOUHSC_02706	sbi	Immunoglobulin-binding protein sbi	-2.69	1.12E-03
SAOUHSC_01944	SAOUHSC_01944	Putative uncharacterized protein	-2.65	2.97E-04
SAOUHSC_00961	SAOUHSC_00961	Putative uncharacterized protein	-2.63	8.10E-08
SAOUHSC_00265	SAOUHSC_00265	Putative uncharacterized protein	-2.60	1.72E-09
SAOUHSC_00717	SAOUHSC_00717	Putative uncharacterized protein	-2.59	8.28E-03
SAOUHSC_00275	SAOUHSC_00275	Putative uncharacterized protein	-2.57	5.72E-09
SAOUHSC_00280	SAOUHSC_00280	Putative uncharacterized protein	-2.55	2.68E-14
SAOUHSC_T0003			-2.53	3.24E-03
SAOUHSC_00055	SAOUHSC_00055	Uncharacterized lipoprotein SAOUHSC_00055	-2.50	1.88E-16
SAOUHSC_A01912	SAOUHSC_01993.3	Putative uncharacterized protein	-2.46	8.49E-03
SAOUHSC_01945	SAOUHSC_01945	"Membrane protein, putative"	-2.46	1.27E-13
SAOUHSC_00561	SAOUHSC_00561	Putative uncharacterized protein	-2.46	1.88E-16
SAOUHSC_00054	SAOUHSC_00054	Uncharacterized lipoprotein SAOUHSC_00054	-2.45	3.30E-12
SAOUHSC_00053	SAOUHSC_00053	Uncharacterized lipoprotein SAOUHSC_00053	-2.43	1.11E-16
SAOUHSC_02707	SAOUHSC_02707	Putative uncharacterized protein	-2.40	3.17E-02
SAOUHSC_01121	hly	Alpha-hemolysin	-2.38	3.50E-05
SAOUHSC_02795	SAOUHSC_02795	Putative uncharacterized protein	-2.38	5.58E-10
SAOUHSC_02710	hlgB	Gamma-hemolysin component B	-2.37	4.00E-13
SAOUHSC_01948	SAOUHSC_01948	ABC transporter domain protein	-2.36	6.55E-17
SAOUHSC_02872	SAOUHSC_02872	Putative uncharacterized protein	-2.36	3.93E-04
SAOUHSC_02108	ftnA	Ferritin	-2.34	1.30E-02
SAOUHSC_01947	SAOUHSC_01947	"Membrane protein, putative"	-2.33	3.30E-18
SAOUHSC_00986	sspC	Staphostatin B	-2.29	8.68E-05
SAOUHSC_T00029			-2.29	5.69E-03
SAOUHSC_00279	SAOUHSC_00279	Putative uncharacterized protein	-2.27	2.33E-12
SAOUHSC_00987	sspB	Staphopain B	-2.26	5.87E-04
SAOUHSC_02312	kdpA	Potassium-transporting ATPase A chain	-2.25	1.06E-04
SAOUHSC_02452	lacD	"Tagatose 1,6-diphosphate aldolase"	-2.23	4.99E-04
SAOUHSC_00052	SAOUHSC_00052	Uncharacterized lipoprotein SAOUHSC_00052	-2.23	2.36E-12
SAOUHSC_02109	SAOUHSC_02109	Putative uncharacterized protein	-2.22	2.34E-02
SAOUHSC_01936	spIE	Serine protease SpIE	-2.21	2.89E-05
SAOUHSC_02692	SAOUHSC_02692	Putative uncharacterized protein	-2.21	6.50E-04
SAOUHSC_00807	SAOUHSC_00807	Putative uncharacterized protein	-2.21	2.93E-12
SAOUHSC_00975	SAOUHSC_00975	Putative uncharacterized protein	-2.20	3.16E-07
SAOUHSC_00047	SAOUHSC_00047	Putative uncharacterized protein	-2.19	2.06E-10
SAOUHSC_00818	SAOUHSC_00818	Thermonuclease	-2.17	4.60E-07
SAOUHSC_00277	SAOUHSC_00277	Putative uncharacterized protein	-2.16	4.87E-11
SAOUHSC_00918	SAOUHSC_00918	Truncated MHC class II analog protein	-2.14	3.54E-10
SAOUHSC_00276	SAOUHSC_00276	Putative uncharacterized protein	-2.14	1.16E-06
SAOUHSC_03003	icaD	"Poly-beta-1,6-N-acetyl-D-glucosamine synthesis protein IcaD"	-2.14	1.69E-03
SAOUHSC_02794	SAOUHSC_02794	Putative uncharacterized protein	-2.13	3.17E-07
SAOUHSC_00808	SAOUHSC_00808	Putative uncharacterized protein	-2.13	2.62E-12
SAOUHSC_01939	spIC	Serine protease SpIC	-2.12	3.12E-05
SAOUHSC_01935	spIF	Serine protease SpIF	-2.11	9.33E-05
SAOUHSC_02160	SAOUHSC_02160	Putative uncharacterized protein	-2.10	3.73E-02
SAOUHSC_02865	SAOUHSC_02865	Putative uncharacterized protein	-2.09	2.53E-09
SAOUHSC_01180	SAOUHSC_01180	Putative uncharacterized protein	-2.09	9.16E-12
SAOUHSC_02691	SAOUHSC_02691	Putative uncharacterized protein	-2.07	3.38E-03
SAOUHSC_00268	SAOUHSC_00268	Putative uncharacterized protein	-2.06	7.68E-12

SAOUHSC_02451	SAOUHSC_02451	"PTS system lactose-specific IIA component, putative"	-2.06	1.05E-02
SAOUHSC_03004	icaB	"Poly-beta-1,6-N-acetyl-D-glucosamine N-deacetylase"	-2.05	7.71E-05
SAOUHSC_02999	SAOUHSC_02999	Capsular polysaccharide biosynthesis protein Cap5B	-2.04	1.66E-05
SAOUHSC_00806	SAOUHSC_00806	Putative uncharacterized protein	-2.04	2.93E-11
SAOUHSC_02453	lacC	Tagatose-6-phosphate kinase	-2.03	4.34E-05
SAOUHSC_00191	SAOUHSC_00191	Putative uncharacterized protein	-2.02	2.09E-02
SAOUHSC_03000	SAOUHSC_03000	"Capsular polysaccharide biosynthesis, capA, putative"	-2.00	2.55E-03
SAOUHSC_00716	SAOUHSC_00716	Putative uncharacterized protein	-2.00	2.78E-02
SAOUHSC_03023	drp35	Lactonase drp35	2.01	9.53E-05
SAOUHSC_01014	SAOUHSC_01014	Amidophosphoribosyltransferase	2.01	3.90E-02
SAOUHSC_02763	SAOUHSC_02763	"Peptide ABC transporter, ATP-binding protein, putative"	2.01	6.83E-07
SAOUHSC_02820	SAOUHSC_02820	Putative uncharacterized protein	2.01	1.26E-08
SAOUHSC_02767	SAOUHSC_02767	"Peptide ABC transporter, peptide-binding protein, putative"	2.01	5.23E-05
SAOUHSC_01087	SAOUHSC_01087	"Iron compound ABC transporter, permease protein"	2.02	1.16E-03
SAOUHSC_02994	SAOUHSC_02994	Putative uncharacterized protein	2.02	1.06E-11
SAOUHSC_01088	SAOUHSC_01088	Putative uncharacterized protein	2.02	7.59E-04
SAOUHSC_00532	SAOUHSC_00532	Putative uncharacterized protein	2.03	4.41E-03
SAOUHSC_01082	isdC	Iron-regulated surface determinant protein C	2.03	1.17E-03
SAOUHSC_01079	isdB	Iron-regulated surface determinant protein B	2.03	2.93E-09
SAOUHSC_00155	ptsG	PTS system glucose-specific EIICBA component	2.04	9.04E-13
SAOUHSC_02830	SAOUHSC_02830	"D-lactate dehydrogenase, putative"	2.05	3.89E-08
SAOUHSC_02330	SAOUHSC_02330	Phosphomethylpyrimidine kinase	2.05	1.83E-13
SAOUHSC_00205	SAOUHSC_00205	Putative uncharacterized protein	2.06	3.77E-03
SAOUHSC_00604	SAOUHSC_00604	Putative uncharacterized protein	2.06	1.44E-03
SAOUHSC_00139	SAOUHSC_00139	Putative uncharacterized protein	2.07	2.46E-03
SAOUHSC_02466	SAOUHSC_02466	Truncated MHC class II analog protein	2.07	3.50E-07
SAOUHSC_00748	SAOUHSC_00748	Putative uncharacterized protein	2.08	1.67E-06
SAOUHSC_02331	tenA	Putative thiaminase-2	2.08	2.25E-14
SAOUHSC_00153	SAOUHSC_00153	"Indolepyruvate decarboxylase, putative"	2.09	1.35E-02
SAOUHSC_02936	SAOUHSC_02936	Putative uncharacterized protein	2.11	5.93E-06
SAOUHSC_00152	SAOUHSC_00152	Putative uncharacterized protein	2.12	1.10E-02
SAOUHSC_01854	SAOUHSC_01854	Putative uncharacterized protein	2.12	9.48E-15
SAOUHSC_02821	SAOUHSC_02821	"Membrane spanning protein, putative"	2.13	1.77E-10
SAOUHSC_00737	SAOUHSC_00737	Putative uncharacterized protein	2.13	3.54E-03
SAOUHSC_00848	SAOUHSC_00848	Putative uncharacterized protein	2.15	2.19E-09
SAOUHSC_02363	SAOUHSC_02363	Putative aldehyde dehydrogenase SAOUHSC_02363	2.17	8.45E-08
SAOUHSC_00371	SAOUHSC_00371	Putative uncharacterized protein	2.17	3.44E-04
SAOUHSC_02754	SAOUHSC_02754	"ABC transporter, ATP-binding protein, putative"	2.18	2.13E-03
SAOUHSC_00291	SAOUHSC_00291	"PfkB family carbohydrate kinase family, putative"	2.18	5.68E-03
SAOUHSC_00749	SAOUHSC_00749	Putative uncharacterized protein	2.19	3.21E-10
SAOUHSC_01855	SAOUHSC_01855	UPF0478 protein SAOUHSC_01855	2.22	1.02E-19
SAOUHSC_02975	SAOUHSC_02975	"PTS system, fructose-specific IIAABC component, putative"	2.22	1.86E-03
SAOUHSC_02329	thiM	Hydroxyethylthiazole kinase	2.23	1.85E-13
SAOUHSC_00895	SAOUHSC_00895	Glutamate dehydrogenase	2.23	3.60E-04
SAOUHSC_01847	SAOUHSC_01847	Putative uncharacterized protein	2.24	4.98E-03
SAOUHSC_02663	SAOUHSC_02663	Putative uncharacterized protein	2.24	4.44E-04
SAOUHSC_02803	fnbA	Fibronectin-binding protein A	2.25	5.29E-09
SAOUHSC_00285	SAOUHSC_00285	Putative uncharacterized protein	2.26	3.68E-12
SAOUHSC_00690	SAOUHSC_00690	Putative uncharacterized protein	2.26	7.59E-18
SAOUHSC_01849	SAOUHSC_01849	Putative uncharacterized protein	2.26	9.57E-04
SAOUHSC_03006	lipA	Lipase 1	2.29	2.09E-03
SAOUHSC_01416	odhB	Dihydrolipoyllysine-residue succinyltransferase component of	2.29	3.42E-04

SAOUHSC_00180	SAOUHSC_00180	Putative uncharacterized protein	2.30	1.01E-02
SAOUHSC_02608	SAOUHSC_02608	Putative uncharacterized protein	2.31	1.24E-03
SAOUHSC_00847	SAOUHSC_00847	"ABC transporter, ATP-binding protein, putative"	2.31	1.95E-16
SAOUHSC_01844	SAOUHSC_01844	Putative uncharacterized protein	2.31	4.94E-02
SAOUHSC_02661	SAOUHSC_02661	"PTS system sucrose-specific IIBC component, putative"	2.33	7.38E-14
SAOUHSC_02409	SAOUHSC_02409	Arginase	2.34	2.42E-02
SAOUHSC_01015	purM	Phosphoribosylformylglycinamide cyclo-ligase	2.34	3.00E-02
SAOUHSC_01027	SAOUHSC_01027	Putative uncharacterized protein	2.35	4.50E-14
SAOUHSC_01922	SAOUHSC_01922	Putative uncharacterized protein	2.36	9.54E-09
SAOUHSC_01018	purD	Phosphoribosylamine--glycine ligase	2.43	2.75E-06
SAOUHSC_02013	SAOUHSC_02013	Uncharacterized protein SAOUHSC_02013	2.43	1.98E-19
SAOUHSC_00747	SAOUHSC_00747	Putative uncharacterized protein	2.45	4.87E-12
SAOUHSC_02662	SAOUHSC_02662	PTS system sucrose-specific IIBC component	2.46	2.00E-19
SAOUHSC_01275	SAOUHSC_01275	Putative uncharacterized protein	2.48	1.73E-03
SAOUHSC_01318	SAOUHSC_01318	Putative uncharacterized protein	2.48	4.04E-05
SAOUHSC_01016	SAOUHSC_01016	"Phosphoribosylglycinamide formyltransferase, putative"	2.51	1.99E-02
SAOUHSC_00296	SAOUHSC_00296	ROK family protein	2.51	3.38E-02
SAOUHSC_00658	SAOUHSC_00658	Putative uncharacterized protein	2.53	1.40E-03
SAOUHSC_00294	SAOUHSC_00294	Putative uncharacterized protein	2.54	3.90E-02
SAOUHSC_01017	purH	Bifunctional purine biosynthesis protein PurH	2.57	7.82E-04
SAOUHSC_01418	odhA	2-oxoglutarate dehydrogenase E1 component	2.57	3.40E-05
SAOUHSC_02774	SAOUHSC_02774	Putative uncharacterized protein	2.60	1.24E-11
SAOUHSC_00746	SAOUHSC_00746	Putative uncharacterized protein	2.62	2.50E-08
SAOUHSC_00656	SAOUHSC_00656	Putative uncharacterized protein	2.64	4.91E-03
SAOUHSC_00310	SAOUHSC_00310	Putative uncharacterized protein	2.66	2.15E-03
SAOUHSC_00894	rocD	Ornithine aminotransferase	2.66	1.66E-04
SAOUHSC_02339	SAOUHSC_02339	Putative uncharacterized protein	2.67	3.51E-05
SAOUHSC_02899	SAOUHSC_02899	Putative uncharacterized protein	2.68	1.37E-23
SAOUHSC_02607	hutU	Urocanate hydratase	2.72	2.66E-03
SAOUHSC_00037	SAOUHSC_00037	Putative uncharacterized protein	2.72	1.19E-21
SAOUHSC_01921	SAOUHSC_01921	Putative uncharacterized protein	2.74	4.33E-09
SAOUHSC_00655	SAOUHSC_00655	Putative uncharacterized protein	2.76	9.29E-04
SAOUHSC_00199	SAOUHSC_00199	Acetate CoA-transferase YdiF	2.76	1.60E-03
SAOUHSC_01918	SAOUHSC_01918	Putative uncharacterized protein	2.89	1.22E-06
SAOUHSC_01603	SAOUHSC_01603	Putative uncharacterized protein	2.89	3.31E-04
SAOUHSC_02848	glcB	PTS system glucoside-specific EIICBA component	2.90	2.77E-13
SAOUHSC_02597	SAOUHSC_02597	"PTS system component, putative"	2.90	9.53E-06
SAOUHSC_00383	SAOUHSC_00383	Putative uncharacterized protein	2.90	1.03E-11
SAOUHSC_00309	SAOUHSC_00309	Putative uncharacterized protein	2.92	3.45E-32
SAOUHSC_00071	SAOUHSC_00071	"Lipoprotein, SirC, putative"	2.97	1.76E-21
SAOUHSC_03035	SAOUHSC_03035	Putative uncharacterized protein	3.01	1.98E-23
SAOUHSC_02610	hutG	Formimidoylglutamase	3.02	1.95E-23
SAOUHSC_02925	SAOUHSC_02925	Putative uncharacterized protein	3.06	2.90E-08
SAOUHSC_02097	SAOUHSC_02097	Putative uncharacterized protein	3.12	3.23E-21
SAOUHSC_02729	SAOUHSC_02729	"Amino acid ABC transporter-like protein, putative"	3.14	6.25E-05
SAOUHSC_02665	SAOUHSC_02665	Putative uncharacterized protein	3.14	1.54E-18
SAOUHSC_01919	SAOUHSC_01919	Putative uncharacterized protein	3.15	3.38E-08
SAOUHSC_02137	sdcS	Sodium-dependent dicarboxylate transporter SdcS	3.17	4.72E-17
SAOUHSC_02822	fbp	"Fructose-1,6-bisphosphatase class 3"	3.17	1.14E-03
SAOUHSC_00156	SAOUHSC_00156	Putative uncharacterized protein	3.18	4.41E-05
SAOUHSC_01920	SAOUHSC_01920	Putative uncharacterized protein	3.23	1.38E-15
SAOUHSC_02425	SAOUHSC_02425	UPF0457 protein SAOUHSC_02425	3.26	4.86E-05



SAOUHSC_02799	sarT	HTH-type transcriptional regulator SarT	3.35	5.41E-05
SAOUHSC_02753	SAOUHSC_02753	"Membrane protein, putative"	3.38	1.44E-13
SAOUHSC_00632	mnhG2	Putative antiporter subunit mnhG2	3.42	8.90E-17
SAOUHSC_00160	SAOUHSC_00160	Putative uncharacterized protein	3.46	2.96E-07
SAOUHSC_02930	SAOUHSC_02930	Putative uncharacterized protein	3.46	4.53E-16
SAOUHSC_00630	SAOUHSC_00630	Putative uncharacterized protein	3.51	1.99E-20
SAOUHSC_00629	mnhE2	Putative antiporter subunit mnhE2	3.58	2.47E-15
SAOUHSC_02869	rocA	1-pyrroline-5-carboxylate dehydrogenase	3.59	4.63E-04
SAOUHSC_00198	SAOUHSC_00198	Putative uncharacterized protein	3.66	6.96E-04
SAOUHSC_A02680	SAOUHSC_02822.1	Putative uncharacterized protein	3.69	7.84E-04
SAOUHSC_00626	mnhB2	Putative antiporter subunit mnhB2	3.70	2.15E-15
SAOUHSC_00628	mnhD2	Putative antiporter subunit mnhD2	3.75	2.23E-25
SAOUHSC_00317	SAOUHSC_00317	Glycerol-3-phosphate transporter	3.78	6.90E-10
SAOUHSC_00736	SAOUHSC_00736	Putative lipid kinase SAOUHSC_00736	3.78	3.09E-28
SAOUHSC_00812	clfA	Clumping factor A	3.82	4.54E-23
SAOUHSC_00627	mnhC2	Putative antiporter subunit mnhC2	3.97	1.02E-19
SAOUHSC_02863	SAOUHSC_02863	Putative uncharacterized protein	3.97	1.68E-30
SAOUHSC_01602	SAOUHSC_01602	"Transcriptional regulator, putative"	3.98	3.59E-06
SAOUHSC_01024	SAOUHSC_01024	Putative uncharacterized protein	4.03	5.53E-06
SAOUHSC_01601	SAOUHSC_01601	"Alpha-glucosidase, putative"	4.10	1.90E-07
SAOUHSC_00196	SAOUHSC_00196	Putative uncharacterized protein	4.12	4.20E-04
SAOUHSC_00157	murQ	N-acetylmuramic acid 6-phosphate etherase	4.18	1.77E-06
SAOUHSC_01846	SAOUHSC_01846	"Acetyl-CoA synthetase, putative"	4.19	4.25E-05
SAOUHSC_00625	mnhA2	Putative antiporter subunit mnhA2	4.29	4.23E-46
SAOUHSC_00569	SAOUHSC_00569	Putative uncharacterized protein	4.33	7.03E-40
SAOUHSC_00158	SAOUHSC_00158	PTS system EIIBC component SAOUHSC_00158	4.35	1.09E-07
SAOUHSC_01884	SAOUHSC_01884	Putative uncharacterized protein	4.36	1.36E-04
SAOUHSC_00179	SAOUHSC_00179	Putative uncharacterized protein	4.37	1.80E-04
SAOUHSC_00825	SAOUHSC_00825	Putative uncharacterized protein	4.37	2.78E-36
SAOUHSC_02815	SAOUHSC_02815	Putative uncharacterized protein	4.38	2.90E-08
SAOUHSC_02900	SAOUHSC_02900	Uncharacterized hydrolase SAOUHSC_02900	4.43	2.82E-60
SAOUHSC_03032	SAOUHSC_03032	Putative uncharacterized protein	4.46	6.47E-21
SAOUHSC_02604	SAOUHSC_02604	Putative uncharacterized protein	4.64	1.19E-64
SAOUHSC_00070	sarS	HTH-type transcriptional regulator SarS	4.73	7.12E-10
SAOUHSC_02809	SAOUHSC_02809	"Gluconate operon transcriptional repressor, putative"	4.82	2.57E-06
SAOUHSC_02440	SAOUHSC_02440	Putative uncharacterized protein	4.88	1.12E-04
SAOUHSC_01910	pckA	Phosphoenolpyruvate carboxykinase [ATP]	4.92	7.37E-07
SAOUHSC_00061	SAOUHSC_00061	Putative uncharacterized protein	4.97	3.31E-57
SAOUHSC_00175	SAOUHSC_00175	"Multiple sugar-binding transport ATP-binding protein, putativ	5.19	4.97E-06
SAOUHSC_00311	SAOUHSC_00311	Putative uncharacterized protein	5.24	1.73E-04
SAOUHSC_00069	spa	Immunoglobulin G-binding protein A	5.40	8.93E-13
SAOUHSC_02771	SAOUHSC_02771	Putative uncharacterized protein	5.46	2.23E-18
SAOUHSC_01794	SAOUHSC_01794	"Glyceraldehyde-3-phosphate dehydrogenase, type I"	5.80	6.92E-11
SAOUHSC_02908	SAOUHSC_02908	Putative uncharacterized protein	5.89	8.09E-49
SAOUHSC_00826	SAOUHSC_00826	Putative uncharacterized protein	5.92	5.39E-51
SAOUHSC_02877	crtN	Dehydrosqualene desaturase	5.93	2.91E-51
SAOUHSC_02808	SAOUHSC_02808	Gluconate kinase	6.39	6.98E-03
SAOUHSC_03028	SAOUHSC_03028	Putative uncharacterized protein	6.42	3.48E-34
SAOUHSC_02772	SAOUHSC_02772	Putative uncharacterized protein	6.49	7.77E-32
SAOUHSC_00312	SAOUHSC_00312	Putative uncharacterized protein	6.73	2.78E-02
SAOUHSC_02806	SAOUHSC_02806	"Gluconate permease, putative"	7.11	2.21E-08
SAOUHSC_00624	SAOUHSC_00624	"Integrase/recombinase, putative"	7.23	2.68E-57

SAOUHSC_00183	SAOUHSC_00183	"Membrane protein, putative"	7.31	1.18E-15
SAOUHSC_00176	SAOUHSC_00176	"Bacterial extracellular solute-binding protein, putative"	7.77	2.08E-02
SAOUHSC_02812	SAOUHSC_02812	Putative uncharacterized protein	7.98	1.32E-72
SAOUHSC_02400	SAOUHSC_02400	"PTS system, mannitol-specific component, putative"	8.23	1.50E-13
SAOUHSC_00177	SAOUHSC_00177	"Maltose ABC transporter, permease protein, putative"	8.41	7.15E-03
SAOUHSC_00846	SAOUHSC_00846	Putative uncharacterized protein	8.59	6.06E-82
SAOUHSC_00178	SAOUHSC_00178	"Maltose ABC transporter, permease protein"	8.60	3.24E-03
SAOUHSC_02403	mtID	Mannitol-1-phosphate 5-dehydrogenase	8.74	2.87E-23
SAOUHSC_02882	crtO	"Glycosyl-4,4'-diaponeurosporenoate acyltransferase"	8.93	4.56E-14
SAOUHSC_00831	SAOUHSC_00831	Organic hydroperoxide resistance protein-like	9.45	2.42E-60
SAOUHSC_02401	SAOUHSC_02401	Putative uncharacterized protein	9.77	1.99E-14
SAOUHSC_02881	crtP	Diapolycopene oxygenase	10.10	1.13E-13
SAOUHSC_02879	crtM	Dehydrosqualene synthase	10.17	6.60E-88
SAOUHSC_02402	SAOUHSC_02402	"PTS system, mannitol-specific IIa component, putative"	11.06	3.94E-20
SAOUHSC_02387	SAOUHSC_02387	Putative uncharacterized protein	11.15	5.60E-97
SAOUHSC_00356	SAOUHSC_00356	Putative uncharacterized protein	11.49	2.50E-66
SAOUHSC_00358	SAOUHSC_00358	Putative uncharacterized protein	12.22	7.92E-85
SAOUHSC_02880	crtQ	"4,4'-diaponeurosporenoate glycosyltransferase"	13.11	1.33E-52
SAOUHSC_A00354	SAOUHSC_00358.1	Putative uncharacterized protein	13.93	9.78E-44
SAOUHSC_02862	clpL	ATP-dependent Clp protease ATP-binding subunit ClpL	16.79	1.28E-231
SAOUHSC_01729	SAOUHSC_01729	Putative uncharacterized protein	18.24	1.86E-105
SAOUHSC_01730	SAOUHSC_01730	UPF0337 protein SAOUHSC_01730	19.71	3.15E-197
SAOUHSC_02444	SAOUHSC_02444	"Osmoprotectant transporter, BCCT family, opuD-like protein,	19.92	1.15E-144
SAOUHSC_00619	SAOUHSC_00619	Putative uncharacterized protein	21.10	2.64E-196
SAOUHSC_02442	SAOUHSC_02442	Putative uncharacterized protein	27.27	1.58E-186
SAOUHSC_02441	asp23	Alkaline shock protein 23	28.18	2.18E-286
SAOUHSC_02443	SAOUHSC_02443	Putative uncharacterized protein	29.88	1.28E-231
SAOUHSC_00845	SAOUHSC_00845	UPF0337 protein SAOUHSC_00845	31.38	5.63E-205

\* Genes highlighted in grey correspond to genes dysregulated in this lysogen but not in the phi11 lysogenic strain

Table S3. Normalized mean reads per kilobase million (RPKM) values corresponding to the different open reading frames (ORFs) of  $\Phi$ 11 genome in samples of strain RN450- $\Phi$ 11

gene_ID	start_coord	end_coord	phi11-1 Reads	phi11-2 Reads	phi11-3 Reads	phi11-1 RPKM	phi11-2 RPKM	phi11-3 RPKM	RPKM MEAN	RPKM ESTAND.gene_name
phi11_01	83	1129	2506	2033	1083	12992	9385	6630	9669	3190.494162 integrase
phi11_02	1241	1441	896	822	569	24196	19765	18144	20701.66667	3132.83966 excisionase
phi11_03	1378	2283	10055	9648	6842	60240	51468	48402	53370	6143.920898 PV83 orf 3-like protei
phi11_04	2319	2504	1764	1411	1186	51477	36664	40868	43003	7633.800561 PV83 orf 4-like protei
phi11_05	2901	3620	7063	6399	5458	53246	42954	48586	48262	5153.644148 cl-like repressor
phi11_06	3762	3980	1307	1493	1062	32394	32949	31081	32141.33333	959.289494 cro-like repressor
phi11_07	4427	5251	5420	5923	4727	35660	34699	36723	35694	1012.428269 anti-repressor
phi11_08	5252	5476	1262	1222	1082	30444	26249	30822	29171.66667	2538.150179 phi11_08
phi11_09	5518	5967	3391	4156	3029	40902	44637	43142	42893.66667	1879.842635 phi PV83 orf 10-like p
phi11_10	5981	6202	3158	4051	2895	77213	88194	83581	82996	5513.824353 phi PV83 orf 12-like p
phi11_11	6696	7016	473	657	482	7998	9892	9624	9171.333333	1024.933819 phi PVL orf 39-like pr
phi11_12	7566	8345	4210	4701	3756	29297	29129	30863	29763	956.3242128 phi ETA orf 17-like pr
phi11_13	8375	8929	3324	4191	2975	32509	36497	34356	34454	1995.805351 ssb
phi11_14	8942	9634	3489	4338	3094	27327	30254	28615	28732	1467.003408 phi PV83 orf 19-like p
phi11_15	9606	10412	3879	4462	3441	26090	26723	27329	26714	619.5490295 phi PV83 orf 20-like p
phi11_16	10765	12006	7167	8479	6286	31322	32995	32439	32252	852.0322764 helicase DnaB
phi11_17	12222	12443	1146	1316	999	28020	28650	28842	28504	430.0093022 phi ETA orf 24-like pr
phi11_18	12454	12858	1524	2095	1519	20425	25001	24039	23155	2412.682325 phi ETA orf 25-like pr
phi11_19	12863	13048	844	1122	917	24630	29155	31599	28461.33333	3535.904458 PV83 orf 23-like prote
phi11_20	13049	13318	1079	1421	1147	21691	25437	27228	24785.33333	2825.437016 HTH DNA binding pro
phi11_21	13319	13678	1168	1494	1276	17610	20058	22717	20128.33333	2554.226367 phi PVL orf 50-like pr
phi11_22	13679	13927	1276	1523	1120	27815	29562	28829	28735.33333	877.2584188 phi PVL orf 51-like pr
phi11_23	13933	14187	1365	1562	1325	29055	29605	33303	30654.33333	2310.238372 phi PVL orf 52-like pr
phi11_24	14184	14426	1082	1300	1120	24169	25856	29541	26522	2747.22824 ETA orf 33-like protei
phi11_25	14419	14928	2671	3217	2772	28427	30487	34836	31250	3271.917939 dUTPase
phi11_26	15037	15210	407	471	420	12696	13083	15471	13750	1502.938122 phi SLT orf 81b-like pi
phi11_27	15558	15746	703	872	706	20189	22299	23942	22143.33333	1881.336316 rinB
phi11_28	15917	16339	1912	2743	2030	24535	31341	30759	28878.33333	3772.67668 rinA
phi11_29	16526	16966	385	686	552	4739	7518	8023	6760	1768.357147 small terminase
phi11_30	16887	18230	1581	2634	2267	6385	9472	10811	8889.333333	2269.800505 large terminase
phi11_31	18241	19776	2389	3576	2971	8442	11252	12397	10697	2035.073709 phi Mu50B-like prote
phi11_32	19894	20778	1302	1930	1840	7985	10540	13326	10617	2671.332439 phi Mu50B-like prote
phi11_33	21115	21750	3419	5277	5138	29179	40101	51778	40352.66667	11301.60176 phi Mu50B-like prote
phi11_34	21764	22738	4957	8108	6858	27596	40192	45082	37623.33333	9021.562245 head protein
phi11_35	22760	23047	874	1562	1304	16472	26213	29020	23901.66667	6585.573045 phi Mu50B-like prote
phi11_36	23056	23388	1095	2097	1726	17848	30436	33221	27168.33333	8190.880071 phi Mu50B-like prote
phi11_37	23687	24034	1713	2852	2472	26718	39609	45528	37285	9617.939332 phi Mu50B-like prote
phi11_38	24046	24429	1522	2280	1859	21514	28697	31028	27079.66667	4958.918666 phi Mu50B-like prote
phi11_39	24448	25029	2594	3798	3421	24192	31540	37674	31135.33333	6750.103505 structural phi Mu50B
phi11_40	25091	25456	991	1571	1443	14697	20746	25269	20237.33333	5304.323928 phi11_40
phi11_41	25486	25830	994	1641	1482	15639	22989	27532	22053.33333	6001.455351 phi11_41
phi11_42	26582	29314	8024	11459	9620	15936	20265	22560	19587	3363.644898 tape measure proteir
phi11_43	29327	30274	2796	3880	3386	16009	19781	22892	19560.66667	3446.785797 phi ETA orf 54-like pr
phi11_44	30283	32184	3977	5271	4712	11349	13394	15878	13540.33333	2268.043283 phi ETA orf 55-like pr
phi11_45	32199	34109	3926	5698	4762	11151	14411	15971	13844.33333	2459.457935 phi ETA orf 56-like pr
phi11_46	35932	36309	532	689	608	7639	8810	10309	8919.333333	1338.353591 phi105 orf 44-like prc

phi11_47	36313	36486	211	241	211	6582	6694	7772	<b>7016</b>	657.1057754	phi ETA orf 58-like pr
phi11_48	36526	36825	342	550	448	6188	8861	9571	<b>8206.666667</b>	1783.896391	phi SLT orf 99-like prc
phi11_49	36962	38860	3200	5130	4143	9147	13056	13983	<b>12062</b>	2566.66145	cell wall hydrolase
phi11_50	38873	40045	2234	3125	2565	10337	12876	14015	<b>12409.33333</b>	1882.884578	tail fiber
phi11_51	40051	40446	1378	1990	1505	18888	24288	24359	<b>22511.66667</b>	3138.388174	phi ETA orf 63-like pr
phi11_52	40502	40939	863	1228	1050	10695	13550	15365	<b>13203.33333</b>	2354.221386	holin
phi11_53	40920	42365	3572	4509	3873	13408	15071	17167	<b>15215.33333</b>	1883.651861	amidase

Table S4. Normalized mean reads per kilobase million (RPKM) values corresponding to the different open reading frames (ORFs) of  $\Phi$ 80 $\alpha$  genome in samples of strain RN450- $\Phi$ 80 $\alpha$

gene_ID	start_coord	end_coord	phi80-1 Reads	phi80-2 Reads	phi80-3 Reads	phi80-1 RPKM	phi80-2 RPKM	phi80-3 RPKM	RPKM MEAN	RPKM ESTAND.gene_name
SPV-80A_gp01	32	1417	17180	8997	6710	59202	34948	26071	<b>40073.66667</b>	17149.93103 int
SPV-80A_gp02	1525	1725	5870	4017	4490	139482	107594	120296	<b>122457.33333</b>	16053.49362 xis
SPV-80A_gp03	1662	2567	66096	55552	55700	348435	330107	331075	<b>336539</b>	10313.60112 hypothetical protein
SPV-80A_gp04	2603	2788	15034	12040	10498	386044	348495	303944	<b>346161</b>	41099.73439 hypothetical protein
SPV-80A_gp05	2948	3115	19816	17151	15551	563355	549621	498481	<b>537152.33333</b>	34187.12777 hypothetical protein
SPV-80A_gp06	3185	3901	85840	78565	76483	571802	589920	574441	<b>578721</b>	9787.966132 Cl-like repressor
SPV-80A_gp07	4065	4307	2183	1450	1127	42906	32125	24976	<b>33335.66667</b>	9026.101613 cro-like repressor
SPV-80A_gp08	4323	5111	10593	6984	5787	64123	47655	39498	<b>50425.33333</b>	12544.07096 antirepressor
SPV-80A_gp09	5127	5321	2347	1680	1349	57485	46383	37254	<b>47040.66667</b>	10131.52182 hypothetical protein
SPV-80A_gp10	5374	5550	1400	1208	1193	37777	36743	36297	<b>36939</b>	759.2180188 hypothetical protein
SPV-80A_gp11	5525	5755	2510	2584	3177	51896	60223	74064	<b>62061</b>	11197.71133 hypothetical protein
SPV-80A_gp12	5814	5942	1286	993	976	47613	41442	40744	<b>43266.33333</b>	3780.467476 hypothetical protein
SPV-80A_gp13	5935	6096	983	655	464	28981	21768	15424	<b>22057.66667</b>	6783.1403 hypothetical protein
SPV-80A_gp14	6188	6448	1797	1154	1002	32884	23804	20674	<b>25787.33333</b>	6342.021234 hypothetical protein
SPV-80A_gp15	6458	6679	1879	1344	1110	40425	32593	26926	<b>33314.66667</b>	6778.373871 hypothetical protein
SPV-80A_gp16	6672	7295	4461	3097	2342	34145	26720	20212	<b>27025.66667</b>	6971.527547 e12
SPV-80A_gp17	7295	7723	3165	2049	1638	35236	25714	20562	<b>27170.66667</b>	7444.660995 ssb
SPV-80A_gp18	7737	8411	5083	3431	2738	35966	27365	21844	<b>28391.66667</b>	7116.758696 hypothetical protein
SPV-80A_gp19	8517	9374	33807	37725	44525	188189	236714	279458	<b>234787</b>	45665.00396 hypothetical protein
SPV-80A_gp20	9439	10209	3785	3010	2626	23447	21018	18342	<b>20935.66667</b>	2553.495709 hypothetical protein
SPV-80A_gp21	10219	10998	3490	2534	2149	21370	17490	14837	<b>17899</b>	3285.648033 DnaC
SPV-80A_gp22	10992	11150	703	496	415	21117	16795	14056	<b>17322.66667</b>	3559.951451 hypothetical protein
SPV-80A_gp23	11163	11384	996	696	579	21428	16879	14045	<b>17450.66667</b>	3724.550219 hypothetical protein
SPV-80A_gp24	11394	11801	1337	1016	890	15651	13407	11747	<b>13601.66667</b>	1959.266529 RusA
SPV-80A_gp25	11801	11986	511	375	348	13121	10854	10075	<b>11350</b>	1582.416191 hypothetical protein
SPV-80A_gp26	11987	12346	807	604	509	10706	9033	7614	<b>9117.666667</b>	1547.737812 hypothetical protein
SPV-80A_gp27	12347	12595	774	614	501	14846	13276	10835	<b>12985.66667</b>	2021.200221 hypothetical protein
SPV-80A_gp28	12610	13011	1061	749	648	12606	10031	8681	<b>10439.33333</b>	1994.105898 hypothetical protein
SPV-80A_gp29	13008	13355	880	679	672	12078	10504	10399	<b>10993.66667</b>	940.5266255 hypothetical protein
SPV-80A_gp30	13352	13660	388	304	261	5997	5297	4549	<b>5281</b>	724.1325845 53 ORF 49-like protei
SPV-80A_gp31	13653	13889	409	285	256	8242	6474	5817	<b>6844.333333</b>	1254.199479 hypothetical protein
SPV-80A_gp32	13894	14406	736	630	588	6852	6612	6172	<b>6545.333333</b>	344.8671242 dUTPase
SPV-80A_gp33	14443	14649	246	170	161	5676	4421	4188	<b>4761.666667</b>	800.3601273 hypothetical protein
SPV-80A_gp34	14646	14849	216	144	148	5057	3800	3907	<b>4254.666667</b>	696.8976491 hypothetical protein
SPV-80A_gp35	14842	15078	354	281	258	7134	6383	5862	<b>6459.666667</b>	639.4562795 hypothetical protein
SPV-80A_gp36	15071	15457	888	813	645	10959	11310	8975	<b>10414.66667</b>	1259.079161 hypothetical protein
SPV-80A_gp37	15454	15627	291	231	187	7988	7147	5788	<b>6974.333333</b>	1110.117261 rinB
SPV-80A_gp38	15628	15774	313	243	199	10170	8900	7290	<b>8786.666667</b>	1443.341032 rinMiddle
SPV-80A_gp39	15798	16220	1003	841	762	11325	10704	9701	<b>10576.66667</b>	819.4536798 rinA
SPV-80A_gp40	16407	16847	640	690	688	6931	8424	8401	<b>7918.666667</b>	855.4217284 terminase small subu
SPV-80A_gp41	16768	18111	2279	2895	3002	8099	11597	12028	<b>10574.66667</b>	2154.793339 terminase large subu
SPV-80A_gp42	18122	19657	2347	3147	3528	7298	11030	12369	<b>10232.33333</b>	2627.920154 portal protein
SPV-80A_gp43	19545	19730	63	66	77	1618	1910	2229	<b>1919</b>	305.599411 hypothetical protein
SPV-80A_gp44	19664	20659	1332	1968	2112	6387	10638	11419	<b>9481.333333</b>	2708.073916 minor head protein
SPV-80A_gp45	20732	20902	271	345	363	7569	10862	11432	<b>9954.333333</b>	2085.326433 hypothetical protein
SPV-80A_gp46	21011	21631	2539	3360	3645	19527	29129	31609	<b>26755</b>	6381.268526 scaffold protein

SPV-80A_gp47	21645	22619	3744	4966	5704	18340	27421	31505	<b>25755.33333</b>	6738.704648	major head protein
SPV-80A_gp48	22641	22928	568	739	876	9420	13814	16380	<b>13204.66667</b>	3519.782001	hypothetical protein
SPV-80A_gp49	22937	23269	796	867	964	11417	14017	15590	<b>13674.66667</b>	2107.457315	hypothetical protein
SPV-80A_gp50	23266	23568	1117	1185	1310	17607	21055	23282	<b>20648</b>	2859.308133	hypothetical protein
SPV-80A_gp51	23568	23915	1240	1342	1503	17018	20761	23258	<b>20345.66667</b>	3140.664951	hypothetical protein
SPV-80A_gp52	23927	24310	1014	1096	1294	12612	15366	18147	<b>15375</b>	2767.510976	hypothetical protein
SPV-80A_gp53	24329	24910	1825	1922	2127	14977	17779	19681	<b>17479</b>	2366.305982	major tail protein
SPV-80A_gp54	24972	25337	541	639	672	7060	9399	9888	<b>8782.333333</b>	1511.490765	hypothetical protein
SPV-80A_gp55	25367	25711	563	627	638	7794	9784	9959	<b>9179</b>	1202.632529	hypothetical protein
SPV-80A_gp56	25728	29192	3497	3833	4244	4820	5956	6596	<b>5790.666667</b>	899.4694733	tape measure protein
SPV-80A_gp57	27980	28372	188	213	248	2285	2918	3398	<b>2867</b>	558.249944	inside tape protein
SPV-80A_gp58	29205	30152	1872	1980	2049	9431	11244	11639	<b>10771.33333</b>	1177.444832	hypothetical protein
SPV-80A_gp59	30161	32062	2315	2447	2644	5813	6926	7486	<b>6741.666667</b>	851.5963441	hypothetical protein
SPV-80A_gp60	31875	32084	89	78	68	2024	2000	1744	<b>1922.666667</b>	155.1945016	hypothetical protein
SPV-80A_gp61	32077	33987	2476	2484	2654	6188	6998	7479	<b>6888.333333</b>	652.4494872	minor structure prote
SPV-80A_gp62	33987	35810	1827	1753	1975	4784	5174	5831	<b>5263</b>	529.1436478	hypothetical protein
SPV-80A_gp63	35284	35505	48	0	0	1033	0	0	<b>344.3333333</b>	596.4028281	hypothetical protein
SPV-80A_gp64	35810	36187	398	299	346	5029	4259	4929	<b>4739</b>	418.6884283	hypothetical protein
SPV-80A_gp65	36188	36370	131	109	116	3419	3207	3414	<b>3346.666667</b>	120.9807147	hypothetical protein
SPV-80A_gp66	36411	36710	237	241	272	3773	4325	4883	<b>4327</b>	555.0027027	hypothetical protein
SPV-80A_gp67	36847	38745	2046	2048	2160	5146	5806	6125	<b>5692.333333</b>	499.2998431	lyz
SPV-80A_gp68	38758	39930	1110	1160	1143	4520	5324	5247	<b>5030.333333</b>	443.6353608	tail fiber protein
SPV-80A_gp69	39936	40331	599	585	585	7224	7953	7955	<b>7710.666667</b>	421.4668828	hypothetical protein
SPV-80A_gp70	40387	40689	216	214	230	3405	3802	4088	<b>3765</b>	343	holin
SPV-80A_gp71	40701	42155	1095	1068	1043	3594	3952	3860	<b>3802</b>	185.9139586	lyt2
SPV-80A_gp72	42409	42636	3138	5168	5804	65734	122031	137086	<b>108283.6667</b>	37610.08982	hypothetical protein
SPV-80A_gp73	42770	43606	13354	12330	10659	76201	79309	68579	<b>74696.33333</b>	5520.981917	hypothetical protein