

T1SS conventional PCR conditions and concentrations:

PCR was performed in 25 µl reactions containing 2 µl of DNA template (concentration not determined), 0.2mM each dNTP, 0.2 µM each primer, 1X PCR buffer (5 prime), and 1 U *Taq* polymerase (5 prime). Amplifications were performed in a Mastercycler 5331 (Eppendorf, Hamburg, Germany) programmed for an initial denaturing step of 94°C for 4 min; followed by 36 cycles of 94°C for 30 seconds, 55°C for 30 sec, and 72°C for 2min; and a final extension step of 72°C for 5min. For a positive control, *H. defensa* 5AT or *R. insecticola* 5.15 DNA was preformed in each reaction. Amplified DNA was visualized after electrophoresis on a 1% agarose gel stained with ethidium bromide (run at ~4.9 V/cm for at least 1 h). Amplified DNA was cleaned using the Wizard® PCR Preps DNA Purification System (Promega, Madison, WI, USA) and Sanger sequenced in both directions at the Yale University DNA Analysis Facility. T1SS primers are described in the table below.

APSE conventional PCR conditions and concentrations:

Thermocycler conditions and PCR concentrations for APSE- phage PCR were conducted as in Degnan and Moran (2008a). APSE primers are described in the table below.

T1SS primers

Primer reference

Hamiltonella defensa RTX primers

1	T1SS-351F: 5 -ATC CGC CAT TAA TGC TCT TG- 3
1	T1SS-640F: 5 -AAA ATT TGA CCG CTT TGT GG- 3
1	T1SS-815F: 5 -CGA TAC GAC CTG CAC TCT GA- 3
1	T1SS-2216F: 5 -TAA CGT TCC CTC ATC GCT TC- 3
1	T1SS-2309F: 5 -ACC GAC ATA CCC GCA GAT AG- 3
1	T1SS-2537F: 5 -ACC ATG GCT TCA ATT TCC AG- 3
1	T1SS-2902F: 5 -TGC GAT AGA CTG CGT TTT TG- 3

1	T1SS-4019F: 5 -CAA AGG CGC TGT AGG AAA AG- 3
1	T1SS-1635R: 5 -GGC GAT GAT AGG ATT GGC TA- 3
1	T1SS-2112R: 5 -GTT GGG TTT GCC GAT AGA GA- 3
1	T1SS-3253R: 5 -GCT TGA GCT TAA TCC GGT TG- 3
1	T1SS-3590R: 5 -TGA AAT TTT TGC AGG CCT TT- 3
1	T1SS-3926R: 5 -GGG GGA TCT TCT CTT TCA GG- 3
1	T1SS-4707R: 5 -CCT GAA AAG CTT GGC GTT AG- 3
1	T1SS-5450R: 5 -AGC GGG CAT AAA TCA ACA AC- 3
1	T1SS-5663R: 5 -TGG ATT GCA TCC GAT CAG TA- 3

Regiella insecticola RTX primers

1	T1SS-381F: 5 -GTT GTG CCC GAA AAA CAA CT- 3
1	T1SS-530F: 5 -ATT GGC GCG AAT TAA TGA AG- 3
1	T1SS-1530F: 5 -CAA CAA AGT ATT CGC GCT CA- 3
1	T1SS-1716F: 5 -CAC GCA GGT GAA CAT ATT GG- 3
1	T1SS-2406F: 5 -ATC AAC GCA TAG TGC AAT GG- 3
1	T1SS-3132F: 5 -GCT CAC TCA ATG GTC AGC AA- 3
1	T1SS-3825F: 5 -TGT TTT GAT TTG GCG ATT GA- 3
1	T1SS-4285F: 5 -TGG TCT CGC TAT TGT TGC AG- 3
1	T1SS-1428R: 5 -ATG CGC CTA AAA CAA TCA CC- 3
1	T1SS-1549R: 5 -TGA GCG CGA ATA CTT TGT TG- 3
1	T1SS-3492R: 5 -TTT ACT TCA ACC GGC TGT CC- 3
1	T1SS-5244R: 5 -GAT AAC GGA AAC GCA CCT GT- 3
1	T1SS-5806R: 5 -TTG AGA CGA TGG GCA ATA CA- 3

Phage APSE

primers

1	P17F1	APSE8624F	5'-stgggcatgtgtgtsc-3'
1	P18R1	APSE9293R	5'-TTCMGCTTCHTCHACCC-3'
1	P23F2	APSE13227F	5'-tytmatcatgcatgctga-3'
1	P24R2	APSE14752R	5'-AAAGAAATGMCCVCCCAT-3'

2	P45	APSE 30.6F	5'-AGTGCAGAAGGGTAACAAAGAC-3'
2	P51	APSE 34.9R	5'-GATAAAACATCGCCGTTTGC-3'
2	P35	APSE20.8F	5'-GCCGCGGGGCGTGTTATTGACG-3'
2	P41	APSE26.0R	5'-ATCATTCCGGTTACGCAAAG-3'

Reference 1= this paper, 2= Degnan and Moran 2008a

***H. defensa* and *R. insecticola* strain information:** The *Regiella insecticola* strain UK102 was kindly sent by Charles Godfray. All other strain information on insect host species and location collected can be found in Degnan and Moran (2008b).

For the O-antigen (*rfb* gene) phylogeny, we retrieved homologues of four *R. insecticola* 5.15 core genes (*rfbA*, *rfbB*, *rfbC* and *rfbD*) from GenBank for fourteen bacterial strains (S_table 3). The four genes were concatenated into a single 1,096 amino acid alignment. For the enteric single copy ortholog tree we retrieved orthologs of four genes (*accD*, *rpS*, *gyrB*, and *murE*) from GenBank for 34 species (S_table 4), and concatenated these sequences into a 1,639 amino acid alignment. For the *phoP* and *phoQ* phylogeny, we retrieved homologues of *R. insecticola* *phoP* and *phoQ* genes from GenBank for 66 and 62 bacterial strains respectively (S_table 5). For all phylogenetic analyses we aligned nucleotide and protein sequences with MacClade 4.06 OSX (Maddison and Maddison, 2008), and the phylogeny and 100 non-parametric bootstraps were estimated using RAxML Blackbox 7.2.7 (Stamatakis et al. 2008) on the CIPRES Science Gateway V. 3.1 (Miller et al. 2009).

454 homopolymer/pseudogene quality checks

For homopolymer/pseudogene quality checks we screened a total of 48 regions for PCR amplification and Sanger sequencing (96 reads), starting from fresh samples of genomic DNA (no MDA step). PCR conditions and concentrations similar to above for RTX reactions except for amplicons <800 annealing (56°C for 30 sec), and extension (72°C for 1:30min), and for amplicons >800 annealing (56°C for 45 sec), and extension (72°C for 2min). All primers used were designed in this study and are presented below in (S_Table 6).

S_table 3. NCBI GI numbers for *rfb* genes in S_Figure 1.

Strain name	<i>rfbA</i> (GI#)	<i>rfbB</i> (GI#)	<i>rfbC</i> (GI#)	<i>rfbD</i> (GI#)
<i>Mycobacterium smegmatis</i> str. MC2 155	118470588	118467903	118469056	118472789
<i>Escherichia coli</i> str. K-12 substr. W3110	89108859	89108861	89108858	89108860
<i>Salmonella enterica</i> subsp. enterica serovar Typhi str. CT18	16761027	16761029	16761026	16761028
<i>Acidovorax delafieldii</i> 2AN	241763425	241763176	241763426	241763422
<i>Polaromonas</i> sp. JS666	91789858	91789862	91789857	91789861
<i>Acidovorax ebreus</i> TPSY	222109771	222109769	222109772	222109770
<i>Acidovorax</i> sp. JS42	121592969	222109769	121592970	121592968
<i>Methylobacterium album</i> BG8	334110446	334110444	334110447	334110445
<i>Achromobacter piechaudii</i> ATCC 43553	293602506	293602503	293602507	293602505
<i>Pseudomonas aeruginosa</i> PAO1	15600356	15600354	15600357	15600355
<i>Burkholderia vietnamiensis</i> G4	134297305	134297308	134297304	134297306
<i>Variovorax paradoxus</i> S110	239813763	239813761	239813764	239813762
<i>Methylobacter tundripaludum</i> SV96	307825027	307826124	307825026	307825028
<i>Gallionella capsiferriformans</i> ES-2	302880020	302880022	302880019	302880021

S_table 4. NCBI GI numbers for Enteric single copy orthologs in S_Figure 2.

Strain name	<i>accD</i>	<i>rpoS</i>	<i>gyrB</i>	<i>murE</i>
<i>Sphingomonas wittichii</i> RW1	148555640	148553355	148555711	148556853
Candidatus <i>Hamiltonella defensa</i> 5AT	238897979	238898782	238898809	238898850
Candidatus <i>Regiella insecticola</i> LSR1	304413210	304413872	304414285	304413638
<i>Cronobacter turicensis</i> z3032	260598736	260599105	260595833	260596510
<i>Dickeya dadantii</i> 3937	307131842	307132339	307133244	307132588
<i>Dickeya zeae</i> Ech1591	251788990	251788478	251787656	251788245
<i>Enterobacter aerogenes</i> KCTC 2190	336251378	336246873	336247897	336248730
<i>Enterobacter cloacae</i> SCF1	311278723	311278284	311277336	311280935
<i>Enterobacter hormaechei</i> ATCC 49162	334124975	334125373	334121946	334123461
<i>Enterobacter</i> sp. 638	146312507	146312853	146309671	146310295
<i>Enterobacteriaceae bacterium</i> 9 2 54FAA	317492659	317493947	317494670	317493284
<i>Erwinia billingiae</i> Eb661	300717684	300718097	300719138	300715303
<i>Escherichia albertii</i> TW07627	170767162	170765845	170766845	170768391
<i>Klebsiella pneumoniae</i> NTUH-K2044	238895836	238896221	238897209	238893065
<i>Pantoea vagans</i> C9-1	308187624	308187918	308188762	308185654
<i>Pectobacterium atrosepticum</i> SCRI1043	50121979	50122451	50123356	50122742
<i>Pectobacterium carotovorum</i> subsp. <i>carotovorum</i> PC1	253689174	253689710	253686413	253689958
<i>Pectobacterium wasabiae</i> WPP163	261820767	261822742	261819374	261823021

<i>Photorhabdus asymbiotica</i> subsp. <i>asymbiotica</i> ATCC 43949	253988934	253988173	253987487	253988589
<i>Rahnella</i> sp. Y9602	322831953	322831414	322830737	322834425
<i>Salmonella enterica</i> subsp. <i>arizonae</i> serovar 62:z4,z23:-- str. RSK2980	161502489	161502017	161505634	161504755
<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Typhi str. CT18	16761291	16761696	16762490	16759118
<i>Serratia odorifera</i> 4Rx13	270262838	270264030	270264122	270263954
<i>Serratia proteamaculans</i> 568]	157371569	157369077	157368284	157369001
<i>Serratia symbiotica</i> str. Tucson	320540466	320538977	320539857	320540410
<i>Shigella boydii</i> Sb227	82544797	82545186	82546037	82542689
<i>Shigella dysenteriae</i> Sd197	82777727	82778108	82779228	82775492
<i>Yersinia bercovieri</i> ATCC 43970	238785194	238786006	238783051	238784573
<i>Yersinia intermedia</i> ATCC 29909	238791910	238791265	238793146	238791168
<i>Yersinia kristensenii</i> ATCC 33638	238763891	238761664	238765067	238761552
<i>Yersinia mollaretii</i> ATCC 43969	238797426	238797130	238797842	238797711
<i>Yersinia pestis</i> KIM 10	21958392	22124745	22127978	22127505
<i>Yersinia pseudotuberculosis</i> IP 32953	51596935	51595126	51598224	51595033
<i>Yersinia rohdei</i> ATCC 43380	238751278	238750591	238750286	238752427
<i>Yersinia ruckeri</i> ATCC 29473	238753784	238754524	238754008	238754431
<i>Escherichia coli</i> str. K-12 substr. MG1655	16130251	16130648	49176395	16128078

S_table 5. NCBI GI numbers for *phoP* and *phoQ* genes in S_Figures 3 and 4.

Strain name	PhoP (GI#)	PhoQ (GI#)
Citrobacter koseri ATCC BAA-895	157146166	157146167
Citrobacter rodentium ICC168	283784940	283784939
Citrobacter sp. 30 2	237731111	237731110
Citrobacter youngae ATCC 29220	283833495	283833496
Cronobacter sakazakii ATCC BAA-894	156934385	-
Cronobacter turicensis z3032	260597499	-
Dickeya dadantii 3937	307131191	307131192
Dickeya dadantii Ech586	271500465	271500464
Dickeya dadantii Ech703	242239495	242239496
Dickeya zeae Ech1591	251789546	251789545
Edwardsiella ictaluri 93-146	238920215	238920216
Edwardsiella tarda ATCC 23685	294636784	294636785
Edwardsiella tarda EIB202	269139404	269139405
Enterobacter aerogenes KCTC 2190	336249792	-
Enterobacter cancerogenus ATCC 35316	288549514	261339430
Enterobacter cloacae SCF1	311279965	-
Enterobacter cloacae subsp. cloacae ATCC 13047	296102850	-
Enterobacter cloacae subsp. cloacae NCTC 9394	-	295096185
Enterobacter hormaechei ATCC 49162	334122430	334122431
Enterobacter sp. 638	146311299	146311298
Enterobacteriaceae bacterium 9 2 54FAA	317491839	317491838
Erwinia amylovora CFBP1430	292488012	292488011
Erwinia billingiae Eb661	300716267	300716266
Erwinia pyrifoliae Ep1/96	259908742	-
Erwinia pyrifoliae DSM 12163	-	283478716
Erwinia chrysanthemi	-	27526280
Erwinia tasmaniensis Et1/99	188534102	188534103
Escherichia albertii TW07627	170768311	170768304

Escherichia coli str. K-12 substr. MG1655	16129093	16129092
Escherichia coli O157:H7	-	85692731
Escherichia fergusonii ATCC 35469	218549147	218549148
Klebsiella pneumoniae subsp. pneumoniae MGH 78578	152969690	-
Xenorhabdus bovienii Mg+	290475831	-
Pantoea ananatis LMG 20103	291617065	291617064
Pantoea sp. aB	304397248	304397247
Pantoea sp. At-9b	317047742	317047741
Pantoea vagans C9-1	-	308186445
Pectobacterium atrosepticumSCRI1043	50121372	50121373
Pectobacterium carotovorum subsp. brasiliensis PBR1692	227111566	227111567
Pectobacterium carotovorum subsp. carotovorum WPP14	227327067	227327068
Pectobacterium carotovorum subsp. carotovorum	4103328	4103329
Pectobacterium wasabiae WPP163	261821426	261821425
Photorhabdus asymbiotica subsp. asymbiotica ATCC 43949	-	253989213
Photorhabdus luminescens subsp. laumondii TTO1	37526697	37526698
Plautia stali symbiont	329297168	329297169
Proteus mirabilis HI4320	197284770	-
Proteus penneri ATCC 35198	226330499	-
Providencia alcalifaciens DSM 30120	212712838	212712837
Providencia rettgeri DSM 1131	268589246	268589245
Providencia rustigianii DSM 4541	261346014	261346015
Providencia stuartii ATCC 25827	183599453	183599454
Rahnella sp. Y9602	322833622	322833623
Salmonella bongori	109453374	339512426
Salmonella enterica subsp. arizonae serovar 62:z4,z23:-- str. RSK2980	161503675	161503676
Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67	62179752	-
Salmonella enterica subsp. enterica	-	16760105

serovar Typhi str. CT18		
Serratia odorifera 4Rx13	270261453	270261452
Serratia proteamaculans 568	157370255	157370254
Serratia symbiotica str. Tucson	320540374	-
Serratia sp. AS12	-	333926822
Shigella dysenteriae Sd197	-	82777260
Shigella flexneri 2a str. 301	332759462	24112548
Sodalis glossinidius str. "morsitans"	85059060	85059059
Xenorhabdus nematophila ATCC 19061	300723604	300723605
Yersinia aldovae ATCC 35236	238758418	238758417
Yersinia bercovieri ATCC 43970	238783795	238783794
Yersinia enterocolitica subsp. enterocolitica 8081	123442021	123442020
Yersinia frederiksenii ATCC 33641	238789085	238789086
Yersinia intermedia ATCC 29909	238791834	238791835
Yersinia kristensenii ATCC 33638	238762221	238762220
Yersinia mollaretii ATCC 43969	238796000	238795999
Yersinia pestis KIM 10	22125688	22125687
Yersinia pseudotuberculosis YPIII	170023956	170023955
Yersinia rohdei ATCC 43380	238749640	238749641
Yersinia ruckeri ATCC 29473	238754408	238754407

S_table 6. Primers used for screening homopolymer errors/candidate pseudogenes

Gene ID #s correspond to JGI's version 1 of *R. insecticola*'s genome.

Gene ID	Gene name	Homopolymers 6 and > long	Homopolymer error within gene	Forward primer 5'-3'	Reverse primer 5'-3'
Virulence related genes					
Rin_00010840	rfbA	3	none	rfbA_F, ATGAAACGTAAAGGTATTATTCTCG	rfbA_R, GGTGAGTACGCGTAGCAGAT
Rin_00010860	rfbB	2	none	H6_rfbB_F, GTCCTCGTGCGGTTATCAAT	H6_rfbB_R, TGCCAGATACCACTCCACTG
Rin_00010830	rfbC	0	NA	-	-
Rin_00010850	rfbD	1	none	H6_rfbD_F, ACCTCTGGGTGAAGTGATGG	H6_rfbD_R, ACGATCAGCATGGATCTTCC

Rin_00007440	rtxB2	5	none	See RTX primers above	See RTX primers above
Rin_00007430	rtxD	5	none	See RTX primers above	See RTX primers above
Rin_00007420	rtxB1	2	none	See RTX primers above	See RTX primers above
Rin_00011530	RTX toxin	6	none	H6_rtx_Toxin_F1, CCGCAGGAGTAGCAAAAGTC	H6_rtx_Toxin_R1, TGAAC TGGCATAATCGGTGA
				H6_rtx_Toxin_F2, CGAGACGGGACTGATACCAT	H6_rtx_Toxin_R2, TGCAACAATACCGGATACGA
				H6_rtx_Toxin_F3, CACTTTGTATGGTGGCGATG	H6_rtx_Toxin_R3, TTATGCCCTGCATTTCCTTC
Rin_00019350	prgK	2	none	T1_PrgK_F, TTGTATCCAAGCCGAAAC	T1_PrgK_R, TTTACCGCAATGTCAACTGC
				T2_PrgK_F, TCATGTGTATCGGCACCACT	T2_PrgK_R, GGAAAAGTTTGGGGGCTTAT
				prgK_F: TCAACAACAAGCGAATGAGG	prgK_R: CATGATGCTGCTCCTGGTTA
Rin_00000910	prgI	1	none	PrgL_F, TCTTTGTCCGGTGACTTGTG	PrgL_R, ATGTTGTCTGCGTTGTCGTC
Rin_00008330	prgH	3	1	prgH_F: TTGGGAAAGAATCGGATGTT	prgH_R: CCAGGCCATCTCTTTGTCAT
Rin_00008340	lagB	4	none	lagB_F: AATAAGCCCTTTCGCTCAGG	lagB_R: CAACCGCTTCCCAAGAATAA
Rin_00006440	SpaM	1	none	H6_spaM_F, CAGCAGAAGTGAGCTGTATGC	H6_spaM_R, TAAGACGACGTGACCGTTTG
Rin_00006450	SpaN	9	none	H6_spaN_F2, TGTCACCGATGATCCTTACG	H6_spaN_R2, TATCATGATTGACCGGCTGA
Rin_00006460	spaO	7	none	H6_SpaO_F2, TGCGTGATTGGTTTCATCAT	H6_SpaO_R2, ATTACCCCTTGGCGATAGTG
Rin_00006470	spaP	2	none	H6_spaP_F, TTGCGTTTTTGCTTTTTCT	H6_spaP_R, TTCTCGGCTAACGTCCACTT
Rin_00006480	spaQ	0	NA	SpaO_F: GTTGCCGTTGCCACTTTTAT	SpaO_R: ATTACCCCTTGGCGATAGTG
Rin_00018330	invA	3	none	H6_invA_F, TGATGATCGTCTCGATGTTGA	H6_invA_R, GATCATGACGCGATTTTCAG
Rin_00018340	invB	0	NA	-	-
Rin_00018350	invC	0	NA	-	-
Rin_00019410	yopJ/P	5	none	YopJ_F: TTTTGGATAGAGGGGATCCAT	YopJ_R: TGTCTCTCAACGAGGGCTTT
Rin_00009550	sopD	4	none	SopD_F: TTTTGCAGCCGATTATTTC	SopD_R: TTAAATCCTGCATCGCTTCC
				H6_sopD_F2,	H6_sopD_R2,

Rin_00014090	lpa	4	none	AGAATGATTGAAGGCGATCC lpa_F: GGGCAACTTCTCCTGTGAA	GAATAATCGGCTCGCAAAA lpa_R: TTGCTCCGACGACTCTTTTT
Rin_00014100	lpa	0	NA	-	-
Rin_00018380	phoP	1	none	H6_PhoPQ_F, AATTGCGTGAAAGCCATACC	H6_PhoPQ_R, GTAATTGAGGGTGGCAGGA
Rin_00018390	phoQ	2	none	phoQ_F: CGCAAGAATTACAACGCTCA	phoQ_R: ATCAGTTCTCGTTGGCTTGG
Rin_00015460	pqaA	3	none	pqaA_F: ATCCCACTAAATGGCAGCAC	pqaA_R: ACGTGCCAACGGATTTTTAG
Rin_00023870	hmuR	1	none	hmuR_F: CGTCGTTTGTGCACTACCAT	hmuR_R: ACCACTAGCTCCGAGACCAA
Rin_00004790	hmuV	1	none	H6_hmuVU_F,	H6_hmuVU_R,
Rin_00004800	hmuU	1	none	GGTTTGCTCCATCACCTGTT	GCGCCAATTTTCTTTATGGA
Rin_00004810	hmuT	1	none	H6_hmuT_F2, TACGAAAAGAAAGCGGCAGT	H6_hmuT_R2, TCGACAGCGGTGTTAAAGTG
Rin_00004820	hmuS	1	none		
Rin_00004830	hmuS	0	NA		
Rin_00004840	hmuR	2	none	hmuR_Fb: GCCAGAGAACCCACAACAAT H6_hmuRb_F2, TCCTGAAAGAAGGCGAAAAA	hmuR_Rb: ACCCAACCGGTAGAAAATCC H6_hmuRb_R2, TTCCTTGAAAATGGCTTTGG
Candidate pseudogenes					
Gene IDs	Gene annotation	Homopolymers errors?	Concatenated genes	Forward primer 5'-3'	Reverse primer 5'-3'
Rin_00001380	HipA	None	NA	P_HipA_F: CAAAGCGAAACGGCTAAAAG	P_HipA_R: GCCAGAAAAACGCTGAAAAG
Rin_00001390					
Rin_00023060	FL_ring	1	Rin_00023060	P_FL_ring_F: AGCATCAGCCATTTTTCACC	P_FL_ring_R: TGGAGGAGCTATGGAATGG
Rin_00023070			Rin_00023070		
Rin_00023080	FHook	None	NA	P_FHook_F: GCAACATGCATCTCATCACC	P_FHook_R: GCAGGTAGGGCAAAATGTGT
Rin_00023090					
Rin_00023100					
Rin_00021180	autotrans	1	Rin_00021180	P_autotrans_F: CCCATCGAGCTTATTGGAGA	P_autotrans_R: TGAGATGACAGCGTTCAAGG
Rin_00021190			Rin_00021190		
Rin_00021200					
Rin_00018770	pulF	1	Rin_00018770	P_PulF_F: TGCACAACACCAAGGGAATA	P_PulF_R: GACTGAGACATCTGCCACGA
Rin_00018780			Rin_00018780		
Rin_00016550	NAcet	1	Rin_00016550	P_NAcet_F: GGCCACTCGAACTTTTAACG	P_NAcet_R: AAACCGTGCGGATAGTGTTC
Rin_00016560			Rin_00016560		
Rin_00011350	TraK	None	NA	P_TraK_F: CGTTGTTATCATTGCCATCG	P_TraK_R:CCAAAAATCCGGCTC TGTTA
Rin_00011360					
Rin_00011300	T4SS	1	Rin_00011300	P_T4SS_F: AAGTTACCGCGTCACATTCC	P_T4SS_R: TTCTGTCTACACACTGGCGATT
Rin_00011310			Rin_00011310		

Rin_00008320	PrgH	1	Rin_00008320	P_PrgH_F:	P_PrgH_R:
Rin_00008330			Rin_00008330	GGTGATCGTGGCGTTTCTAT	TTATTCTTGGGAAGCGGTTG
Rin_00004820	hmuS	None	NA	P_hmuS_F:	P_hmuS_R:
Rin_00004830				GAAACGTCACCGCCAATAGT	TCGATATGCCATCCAACAGA
Rin_00003100	M30	None	NA	P_M30_F:	P_M30_R:
Rin_00003110				CCCTCAGGCATACCCTTACA	CACCTCGGGATGGGTATATG
Rin_00003120					
Rin_00002140	Chrom1	1	Rin_00002140	P_ChroP1_F:	P_ChroP1_R:
Rin_00002150			Rin_00002150	TCCTCATCACTCTGCACCAA	ACGATATCGCTGTGGACGAT
Rin_00002170					
				P_ChromP2_F:	P_ChromP2_R:
				GCAGCCATGGTAGTGGATTT	AAATTTGCCAACAGCTCACC
Rin_00019400	YopJ	None	NA	P_YopJ_F:	P_YopJ_R:
Rin_00019410				GGTCATGCCTCACCTTTCAT	TGTCTCTCAACGAGGGCTTT
Rin_00015390	ABC	1	Rin_00015390	P_ABC_F:	P_ABC_R:
Rin_00015400			Rin_00015400	ACGGATACGGATCAAACCAA	TTTGTGTCTCTCGGCAGTG
Rin_00002720	hisK	None	NA	hisK_2_F, TTAACGAGCTTTCGCCCTAA	hisK_2_R,
Rin_00002730					TCGACTGCAACTGGAAGATG

Citations:

- Degnan PH, Moran NA. 2008a. Diverse phage-encoded toxins in a protective insect endosymbiont. *Applied and Environmental Microbiology* **74**: 6782-6791.
- Degnan PH, Moran NA. 2008b. Evolutionary genetics of a defensive facultative symbiont of insects: exchange of toxin-encoding bacteriophage. *Molecular Ecology* **17**: 916-929.