Supplementary Materials: The Draft Genome Sequence of the *Yersinia entomophaga* Entomopathogenic Type Strain MH96T

Mark R. H. Hurst, Amy Beattie, Eric Altermann, Roger M. Moraga, Lincoln A. Harper, Joanne Calder and Aurelie Laugraud

Table S1. *Yersinia entomophaga* unique regions 1 and 2. For graphic depiction refer to Figure 2 of the associated manuscript.

Yersinia entomophaga unique region 1.

Locus (Amino Acid Residues)	Closest BlastP Orthologue [Species] Length: Amino Acid Length of Orthologue % Identity/% Similarity (Over the Indicated Range of Amino Acid Residues) in Relation to Target Sequence. Protein Domain	Accession Number
PL78_03820 (423)	branched-chain amino acid ABC transporter substrate-binding protein [*Yersinia nurmii*] Length: 423 95/97(423) 1–423	WP_049597723.1
	Aliphatic amidase expression-regulating protein [*Beauveria bassiana* D1-5] Length: 648 92/95(420) 226–645	gbKGQ13304.1
PL78_03825 (524)	urea ABC transporter permease [*Yersinia nurmii*] Length: 524 92/94(524) 1–524	WP_049597583.1
	MULTISPECIES: urea ABC transporter permease [*Enterobacteriaceae*] Length: 524 73/81(507) 1–524	WP_048332627.1
PL78_03830 (357)	amino acid ABC transporter permease [*Yersinia nurmii*] Length: 357 96/96(357) 1–357	WP_049597584.1
	amino acid ABC transporter permease [*Buttiauxella agrestis*] Length: 357 88/93(357) 1–357	WP_034495296.1

PL78_03835 (265)	urea ABC transporter ATP-binding protein [*Yersinia nurmii*] Length: 265 96/97(265)1–265	WP_049597585.1
	urea ABC transporter ATP-binding protein [*Cedecea neteri*] Length: 265 89/94(265) 1–265	WP_038472477.1
PL78_03840 (232)	urea ABC transporter ATP-binding protein [*Yersinia nurmii*] Length: 232 98/99(232) 1–232	WP_049597586.1
	urea ABC transporter ATP-binding protein [*Buttiauxella agrestis*] Length: 232 86/93(232) 1–232	WP_034455625.1
PL78_03845 (261)	LuxR family transcriptional regulator [*Yersinia nurmii*] Length: 247 98/99(247) 1–247	WP_049597724.1
	LuxR family transcriptional regulator [*Yersinia ruckeri*] Length: 247 80/89(246) 1–247	WP_004719049.1
PL78_03850 (216)	acyl-homoserine-lactone synthase [*Yersinia nurmii*] Length: 216 99/100(216)1–216	WP_049597587.1
	acyl-homoserine-lactone synthase [*Yersinia ruckeri*] Length: 216 87/92(216) 1–216	WP_038245616.1
PL78_03855 (237)	membrane protein [*Yersinia nurmii*] Length: 231 96/98(231) 1–231	WP_049597588.1
	hypothetical protein [*Yersinia intermedia*] Length: 237 72/87(236) 1–236	WP_050077576.1

PL78_03860 (238)	hypothetical membrane protein [*Azoarcus* sp. BH72] Length: 149 51/72(86) 68–149	embCAL95245.1
	hypothetical protein [*Photorhabdus luminescens*] Length: 207 31/49(209)13–207	WP_052739685.1
PL78_03862 (81)	hydrolase [*Mesorhizobium loti*] Length: 259 59/78(32)226–257	WP_027033575.1
	carbon monoxide dehydrogenase form II large subunit [uncultured bacterium] Length: 315 37/53(52) 14–65	gbAAW66018.1
PL78_03865 (100)	ERF family protein [uncultured Mediterranean phage uvMED] Length: 201 33/50(55) 41–94	dbjBAR33765.1
	PREDICTED: sarcoma antigen 1-like, partial [*Callithrix jacchus*] Length: 276 33/54(46) 169–213	XP_008989763.1
PL78_03870 (336)	glycosyl transferase [*Yersinia nurmii*] Length: 336 95/96(336) 1–336	WP_049597589.1
	glycosyl transferase [*Yersinia pseudotuberculosis*] Length: 326 70/83(325) 1–336	WP_012303433.1
PL78_03875 (723)	dipeptidyl carboxypeptidase II [*Yersinia nurmii*] Length: 723 95/97(723) 1–723	WP_049597590.1
	Dipeptidyl carboxypeptidase Dcp [*Yersinia ruckeri*] Length: 729 82/89(726) 1–726	embCEK27267.1

PL78_03880 (519)	hypothetical protein [*Yersinia nurmii*] Length: 519 97/97(519) 1–519	WP_049597591.1
	hypothetical protein [*Brenneria goodwinii*] Length: 534 62/79(516)1–516	WP_048636529.1
PL78_03885 (453)	malate permease [*Yersinia nurmii*] Length: 453 99/99(519) 1–453	WP_049597592.1
	malate permease [*Yersinia ruckeri*] Length: 453 92/96(452) 1–452	WP_045844043.1
PL78_03890 (239)	transcriptional regulator [*Yersinia nurmii*] Length: 239 99/99(239)1–239	WP_049597593.1
	transcriptional regulator [*Yersinia ruckeri*] Length: 239 93/96(239) 1–239	WP_038242277.1
PL78_03895 (543)	histidine kinase [*Yersinia nurmii*] Length: 543 97/98(543) 1–543	WP_049597594.1
	histidine kinase [*Yersinia ruckeri*] Length: 543 87/94(543) 1–543	WP_042524781.1
PL78_03900 (470)	2-oxoglutarate translocator [*Yersinia nurmii*] Length: 470 99/98(470) 1–470	WP_049597595.1
	2-oxoglutarate translocator [*Yersinia ruckeri*] Length: 470 91/95(470)1–470	WP_038275783.1

PL78_03905 (254)	iron reductase [*Yersinia aldovae*] Length: 254 94/96(254) 1–254	WP_042546885.1
	iron reductase [*Yersinia nurmii*] Length: 254 94/98(254) 1–254	WP_049597596.1
PL78_03910(519)	cytochrome C biogenesis protein CcmH [*Yersinia aldovae*] Length: 519 96/97(519) 1–519	WP_042546884.1
	cytochrome C biogenesis protein CcmH [*Yersinia nurmii*] Length: 519 96/97(519) 1–519	WP_049597597.1
PL78_03915 (434)	putative siderophore biosynthetic enzyme [*Yersinia aldovae*] Length: 434 97/98(434) 1–434	embCNL58692.1
	putative siderophore biosynthetic enzyme [*Yersinia nurmii*] Length: 434 95/96(434) 1–434	embCNE39394.1
PL78_03920 (190)	siderophore biosynthesis protein [*Yersinia aldovae*] Length: 198 95/97(197) 1–197	WP_049596217.1
	siderophore biosynthesis protein [*Yersinia aldovae*] Length: 198 95/97(197) 1–197	WP_042546883.1
PL78_03925 (612)	siderophore biosynthesis protein IucA [*Yersinia aldovae*] Length: 611 96/97(611) 1–611	WP_042839931.1
	siderophore biosynthesis protein IucA [*Yersinia aldovae*] Length: 611 96/97(611) 1–611	WP_042546882.1

PL78_03930 (287)	putative iron-siderophore transport system %2CATP-binding component [*Yersinia aldovae*] Length: 287 94/95(287) 1–287	embCNL53775.1
	putative iron-siderophore transport system %2CATP-binding component [*Yersinia aldovae*] Length: 287 94/95(287) 1–287	embCNL58815.1
PL78_03935 (346)	iron ABC transporter permease [*Yersinia aldovae*] Length: 346 97/97(216) 31–346	WP_049689070.1
	iron ABC transporter permease [*Yersinia nurmii*] Length: 346 96/98(206) 41–346	WP_049597600.1
PL78_03940 (339)	iron ABC transporter permease [*Yersinia nurmii*] Length: 339 94/95(339) 1–339	WP_049597601.1
	iron ABC transporter permease [*Yersinia aldovae*] Length: 339 95/96(336) 1–339	WP_042839929.1
PL78_03945 (341)	periplasmic binding family protein [*Yersinia aldovae* 670-83] Length: 37 96/97(376)1–376	gbAJJ64399.1
	iron-siderophore ABC transporter substrate-binding protein [*Yersinia aldovae*] Length: 362 97/98(362)1–362	WP_042546879.1
PL78_03950 (749)	TonB-dependent receptor [*Yersinia aldovae*] Length: 749 96/97(749) 1–749	WP_042839927.1
	TonB-dependent receptor [*Yersinia aldovae*] Length: 749 96/97(749) 1–749	WP_042546878.1

PL78_03955 (609)	IucA/IucC family protein [*Yersinia aldovae*] Length: 609 97/97(609) 1–609	WP_049596218.1
	siderophore biosynthesis protein IucA [*Yersinia aldovae*] Length: 609 96/97(609) 1–609	WP_042546877.1
PL78_03960 (478)	serine 3-dehydrogenase [*Yersinia intermedia*] Length: 479 86/93(478) 1–479	WP_050086263.1
	serine 3-dehydrogenase [*Yersinia nurmii*] Length: 478 96/97(478)1–478	WP_049597605.1
PL78_03965 (464)	serine 3-dehydrogenase [*Yersinia nurmii*] Length: 481 96/97(464) 18–481	WP_049597606.1
	serine 3-dehydrogenase [*Yersinia intermedia*] Length: 485 80/87(464)1–485	WP_005182588.1
PL78_03970 (482)	metalloprotease [*Yersinia nurmii*] Length: 482 93/95(482) 1–482	embCNE39855.1
	serine 3-dehydrogenase [*Yersinia ruckeri*] Length: 477 55/67(442) 40–477	WP_042524782.1
PL78_03975 (77)	No similarity	-
PL78_03980 (109)	Proteinase inhibitor precursor [*Yersinia nurmii*] Length: 138 97/100(109) 30–138	embCNE39896.1
	alkaline proteinase inhibitor [*Yersinia intermedia*] Length: 138 78/87(109) 30–138	WP_050086261.1

PL78_03985 (580)	peptidase [*Yersinia nurmii*] Length: 580 98/99(580) 1–580	WP_049597607.1
	peptidase [*Yersinia intermedia*] Length: 580 91/94(580) 1–580	WP_050312322.1
PL78_03990 (434)	hemolysin D [*Yersinia nurmii*] Length: 443 98/99(443) 1–443	WP_049597608.1
	hemolysin D [*Yersinia intermedia*] Length: 443 87/93(443) 1–443 pfam00529	WP_050312323.1
PL78_03995 (440)	peptidase [*Yersinia nurmii*] Length: 447 99/99(447) 1–447	WP_049597609.1
	peptidase [*Yersinia intermedia*] Length: 447 91/96(447) 1–447	WP_050086258.1
PL78_04000 (195)	cytochrome B561 [*Yersinia nurmii*] Length: 205 96/96 (2025) 1–205	WP_049597610.1
	cytochrome B561 [*Yersinia ruckeri*] Length: 206 84/90(205) 2–206	WP_042524786.1

PL78_04005 (262)	hypothetical protein [*Yersinia nurmii*] Length: 262 putative sulfite oxidase subunit YedY [*Yersinia nurmii*] Sequence ID: emb|CNE40096.1| Length: 262 Number of Matches: 97/98(262) 1–262	WP_049597611.1
	hypothetical protein [*Yersinia ruckeri*] Length: 262 90/94(262) 1–262	WP_042524787.1
PL78_04010 (112)	pentapeptide MXKDX repeat protein [*Yersinia nurmii*] Length: 123 89/90(123) 1–123	embCNE40130.1
	hypothetical protein [*Yersinia ruckeri*] Length: 112 77/90(112) 1–112	WP_042524788.1
PL78_04015 (300)	multidrug DMT transporter permease [*Yersinia nurmii*] Length: 300 96/98(300) 1–300	WP_049597612.1
	membrane protein [*Yersinia ruckeri*] Length: 300 87/93(289)	WP_004720598.1
PL78_04020 (292)	AraC family transcriptional regulator [*Yersinia nurmii*] Length: 292 99/99(292) 1–292	WP_049597613.1
	AraC family transcriptional regulator [*Yersinia ruckeri*] Length: 292 90/94(292) 1–292	WP_004720600.1

Yersinia entomophaga unique region 2

Locus (amino acid resides)	Closest BlastP Orthologue [Species] Length: Amino Acid Length of Orthologue % identity/% Similarity (over the Indicated Range of Amino Acid Residues) in Relation to Target Sequence. Protein Domain	Accession Number
PL78_09500 (239)	tRNA (guanine-N7)-methyltransferase [*Yersinia nurmii*] Length: 239 99/100(239) 1–239	WP_049599599.1
	tRNA (Guanine-N(7)-)-methyltransferase [*Yersinia ruckeri* ATCC 29473] Length: 252 94/96(239) 14–252	gbEEP99613.1
PL78_09505 (366)	A/G-specific adenine glycosylase [*Yersinia nurmii*] Length: 366 98/98(366) 1–366	WP_049599597.1
	A/G-specific adenine glycosylase [*Yersinia ruckeri*] Length: 366 93/96(366) 1–366	WP_045844287.1
PL78_09510 (90)	oxidative damage protection protein [*Yersinia nurmii*] Length: 90 99/98(90) 1–90	WP_049599595.1
	Fe(2+)-trafficking protein [*Yersinia massiliensis*] Length: 90 97/98(90) 1–90	WP_019211664.1
PL78_09515 (358)	murein transglycosylase [*Yersinia nurmii*] Length: 358 99/99(358) 1–358	WP_049599592.1
	murein transglycosylase [*Yersinia ruckeri*] Length: 358 99/99(358) 1–358	WP_004719291.1

PL78_09520 (249) Permease	permease [*Yersinia nurmii*] Length: 249 94/95(249) 1–249	WP_049599589.1
	Sulfite exporter TauE/SafE [*Yersinia bercovieri*] Length: 249 85/93(247) 1–247	embCNF01781.1
PL78_09525 (720)	ornithine decarboxylase [*Yersinia nurmii*] Length: 720 97/98(719) 1–719	WP_049599586.1
	ornithine decarboxylase [*Yersinia pekkanenii*] Length: 720 86/93(719) 1–719	WP_049615402.1
PL78_09550	tRNAphe	
PL78_09535 (176) Fimbrial protein	fimbrial protein [*Yersinia nurmii*] Length: 176 98/98(176) 1–176	WP_049597733.1
	fimbrial protein [*Yersinia intermedia*] Length: 176 91/96(176) 1–176	WP_050076821.1
PL78_09540 (243) Fimbrial chaperone	putative fimbrial chaperone [*Yersinia frederikseniir*] Length: 243 89/95(243) 1–243	embCFR11699.1
	fimbrial chaperone protein [*Yersinia nurmii*] Length: 242 98/97(242) 1–243	WP_049597734.1
PL78_09545 (887) Fimbrial protein	fimbrial protein [*Yersinia nurmii*] Length: 887 95/97(887) 1–887	WP_049597735.1
	fimbrial usher protein [*Yersinia frederikseniir*] Length: 887 88/95(888) 1–887	WP_004710087.1

PL78_09550 (424) Fimbrial usher protein StbD	putative fimbrial usher protein StbD [*Yersinia nurmii*] Length: 455 96/98(455)1–455	embCNE45478.1
	fimbrial family protein [*Yersinia frederikseniir* ATCC 33641] Length: 455 89/94(455) 1–455	gbKGA46118.1
PL78_09555 (243) Chaperone	molecular chaperone [*Yersinia nurmii*] Length: 255 95/97(243) 13–255	WP_049597737.1
	molecular chaperone [*Yersinia frederikseniir*] Length: 255 81/90(242) 14–255	WP_032911350.1
PL78_09560 (255)	nicotinamidase [*Salmonella enterica*] Length: 225 92/95(225) 1–225	WP_050178696.1
PL78_09565 (303) LysR	hypothetical protein [*Massilia niastensis*] Length: 302 74/85(301) 1–301	WP_020656025.1
	LysR family transcriptional regulator [*Aeromonas aquatica*] Length: 306 70/82(301) 1–301	WP_033130787.1
PL78_09570 (619) Transporters	potassium transporter KefC [*Yersinia nurmii*] Length: 619 98/98(619) 1–619	WP_049597738.1
	potassium transporter KefC [*Citrobacter amalonaticus*] Length: 620 86/91(619) 1–619	WP_046475364.1
PL78_09575 (176) Transporters	potassium transporter KefF [*Yersinia nurmii*] Length: 176 96/97(176) 1–176	WP_049597739.1
	MULTISPECIES: potassium transporter [*Enterobacteriaceae*] Length: 176 88/94(176) 1–176	WP_003018878.1

PL78_09575 (127)	hypothetical protein [*Yersinia nurmii*] Length: 129 96/99(129) 1–129	WP_049597740.1
	hypothetical protein [*Yersinia aldovae*] Length: 129 73/89(129) 1–129	WP_042546198.1
PL78_09580 (127)	hypothetical protein [*Yersinia nurmii*] Length: 129 96/99(127) 3–129	WP_049597740.1
	hypothetical protein [*Yersinia aldovae*] Length: 129 72/89(127) 2–129	WP_042546198.1
	hypothetical protein [*Photorhabdus luminescens*] Length: 123 50/64(119) 1–119	WP_011148526.1
PL78_09585 (96)	hypothetical protein [*Yersinia nurmii*] Length: 96 78/85(91) 1–91	WP_049597741.1
	hypothetical protein [*Yersinia intermedia*] Length: 112 52/67(87) 1–87	WP_050074814.1
PL78_09590 (137) PirA	hypothetical protein [*Yersinia intermedia*] Length: 136 79/88(137) 1–136	WP_032905692.1
	Uncharacterised protein [*Yersinia nurmii*] Length: 137 95/97(137) 1–137	embCNE45801.1

PL78_09595 (416) PirB	hypothetical protein [*Yersinia nurmii*] Length: 416 93/96(416) 1–416	WP_049597742.1
	hypothetical protein [*Yersinia intermedia*] Length: 416 86/94(416) 1–416	WP_050086266.1
	toxin PirB [*Photorhabdus luminescens*] Length: 419 47/66(396) 17–412	WP_046395117.1
PL78_09600 (426) Lipase	thermolabile hemolysin [*Yersinia intermedia*] Length: 426 82/91(426) 1–426	WP_050086267.1
	thermolabile hemolysin [*Yersinia nurmii*] Length: 426 95/97(426) 1–426 pfam00657: Lipase_GDSL	WP_049597743.1
PL78_09605 (255) Iron transporter	iron ABC transporter [*Erwinia toletana*] Length: 255 77/86(255) 1–255	WP_026111923.1
PL78_09610 (320) Iron transporter	iron-dicitrate transporter subunit FecD [*Rahnella aquatilis*] Length: 320 82/90(320) 1–320	WP_047607211.1
	Fe3+ dicitrate ABC transporter permease [*Rahnella aquatilis*] Length: 320 82/90(320) 1–320	WP_014341819.1
PL78_09615 (333) Iron transporter	iron ABC transporter [*Rahnella aquatilis*] Length: 334 85/91(333) 1–334	WP_014341818.1
PL78_09620 (302)	iron siderophore-binding protein [*Rahnella aquatilis*] Length: 301 80/88(289) 13–301	WP_014341817.1
PL78_09625 (785) Iron transporter	transporter [*Erwinia toletana*] Length: 786 83/91(784) 3–786	WP_017802701.1

PL78_09630 (321) Iron transporter	iron dicitrate transport regulator FecR [*Erwinia toletana*] Length: 309 69/82(309) 1–309	WP_051050855.1
	iron dicitrate transport regulator FecR [*Rahnella aquatilis*] Length: 323 68/81(323) 1–323	WP_047610250.1
PL78_09635 (175)	RNA polymerase sigma factor [*Rahnella aquatilis*] Length: 172 81/88(171) 1–171	WP_014341814.1
PL78_09645 (193)	MULTISPECIES: protein RclC [*Escherichia*] Length: 197 84/90(186) 1–186	WP_001355150.1
PL78_09650 (441)	pyridine nucleotide-disulfide oxidoreductase [*Escherichia coli*] Length: 441 73/85(441) 1–441	WP_038340583.1
PL78_09655 (288)	AraC family transcriptional regulator [*Ewingella americana*] Length: 284 61/74(282) 1–282	WP_034790889.1
PL78_09660(500)	glycine/betaine ABC transporter [*Yersinia nurmii*] Length: 500 100/100(500) 1–500	WP_049597746.1
	glycine/betaine ABC transporter [*Yersinia frederikseniir*] Length: 500 94/98(500) 1–500	WP_050108470.1
PL78_09665 (350)	6-O-methylguanine DNA methyltransferase [*Yersinia nurmii*] Length: 350 93/95(349) 1–349	WP_049597747.1
	hypothetical protein [*Serratia marcescens*] Length: 351 67/79(343) 11–351	WP_021504722.1

PL78_09670 (200)	DNA-3-methyladenine glycosidase [*Yersinia nurmii*] Length: 200 95/97(200) 1–200	WP_049597748.1
	DNA-3-methyladenine glycosidase [*Yersinia rohdei*] Length: 202 71/82(200) 1–200	WP_032817263.1
PL78_09675 (501)	peptide synthetase [*Yersinia nurmii*] Length: 501 96/98(500) 1–500	WP_049597749.1
	peptide synthetase [*Yersinia ruckeri*] Length: 501 76/83(500) 1–500	WP_042525915.1
PL78_09680 (248)	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase [*Yersinia nurmii*] Length: 248 96/98(248) 1–248	WP_049598095.1
	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase [*Yersinia ruckeri*] Length: 251 86/90(251) 1–251	gbKFE37680.1
PL78_09685 (294)	isochorismatase [*Yersinia nurmii*] Length: 294 97/97(294) 1–294	WP_049597750.1
	isochorismatase [*Yersinia ruckeri*] Length: 294 85/91(294) 1–294	WP_042525917.1
PL78_09690 (543)	enterobactin synthase subunit E [*Yersinia nurmii*] Length: 543 97/98(543) 1–543	WP_049597751.1
	enterobactin synthase subunit E [*Yersinia ruckeri*] Length: 544 86/91(540) 1–540	WP_038244834.1

PL78_09695 (389)	menaquinone-specific isochorismate synthase [*Yersinia nurmii*] Length: 415 96/97(415) 1–415	embCNE46363.1
	Enterobactin synthetase component C (Isochorismate synthase) [*Yersinia ruckeri* ATCC 29473] Length: 402 80/87(402) 1–402	gbEEP98231.1
PL78_09700 (346)	iron ABC transporter substrate-binding protein [*Yersinia nurmii*] Length: 349 95/96(346) 1–346	WP_049597752.1
	iron ABC transporter substrate-binding protein [*Yersinia ruckeri*] Length: 346 77/86(346) 1–346	WP_038244836.1
PL78_09705 (425)	POT family transporter [*Yersinia nurmii*] Length: 425 97/98(422) 1–425	WP_049597753.1
	POT family transporter [*Yersinia ruckeri*] Length: 422 91/96(422) 1–422	WP_038244838.1
PL78_09710 (312) Iron transporter	iron-enterobactin transporter membrane protein [*Yersinia nurmii*] Length: 351 97/98(351) 1–351	embCNE46474.1
	Ferric enterobactin transport protein [*Yersinia ruckeri* ATCC 29473] Length: 351 87/94(351) 1–351	gbEEP98234.1
PL78_09715 (347) Iron transporter	iron ABC transporter permease [*Yersinia nurmii*] Length: 347 97/97(347) 1–347	WP_049597754.1
	iron-enterobactin transporter permease [*Yersinia enterocolitica*] Length: 347 81/89(347) 1–347	WP_019079081.1

PL78_09720 (276) Iron transporter	iron-dicitrate transporter ATP-binding subunit [*Yersinia nurmii*] Length: 276 97/98(276) 1–276	WP_049597755.1
	iron-dicitrate transporter ATP-binding subunit [*Yersinia ruckeri*] Length: 275 86/94(271) 1–271	WP_045844292.1
PL78_09725 (219)	hypothetical protein [*Yersinia nurmii*] Length: 219 85/90(219) 1–219	WP_049597756.1
PL78_09730 (2399) chromophore lyase	chromophore lyase [*Yersinia nurmii*] Length: 2399 high molecular weight siderophore biosynthesis protein [*Yersinia nurmii*] Length: 2399 96/97(2399) 1–2399	WP_049597757.1 emb|CNE46596.1|
	chromophore lyase [*Yersinia ruckeri*] Length: 2386 72/83(2400) 1–2384	WP_038244849.1
PL78_09735 (73)	Uncharacterized protein conserved in bacteria [*Yersinia nurmii*] 97/98(74) 16–89	embCNE46635.1
	antibiotic synthesis protein MbtH [*Yersinia ruckeri*] Length: 74 81/89(74) 1–74	WP_038244851.1
	antibiotic synthesis protein MbtH [*Xenorhabdus cabanillasii*] Length: 84 56/67(73) 1–69	WP_051502373.1
PL78_09740 (435) Enterochelin esterase	enterochelin esterase [*Yersinia nurmii*] Length: 435 95/97(435) 1–435	WP_049597758.1
	enterochelin esterase [*Yersinia ruckeri*] Length: 439 80/87(435) 1–435	WP_042525934.1

PL78_09745 (736) Ferrichrysobactin receptor	ferrichrysobactin receptor [*Yersinia nurmii*] Length: 736 98/99(736) 1–736	WP_049597759.1
	ferrichrysobactin receptor [*Yersinia ruckeri*] Length: 735 88/94(736) 1–735	WP_004722010.1
PL78_09750 (139)	Uncharacterised protein [*Yersinia nurmii*] Length: 139 95/97(119) 21–139	embCNE46726.1
	hypothetical protein [*Yersinia mollaretii*] Length: 136 59/69(126)11–136	WP_049646990.1
PL78_09755 (112)	hypothetical protein [*Yersinia nurmii*] Length: 112 88/91(112) 1–112	WP_049597761.1
	putative efflux system protein [*Yersinia enterocolitica*] Length: 129 55/69(92) 38–128	embCFQ35865.1
PL78_09760 (426) Transporter	heavy metal RND transporter [*Yersinia nurmii*] Length: 426 93/95(424) 1–424	WP_049597762.1
	heavy metal RND transporter [*Yersinia intermedia*] Length: 432 75/84(432) 1–432	WP_050077138.1
PL78_09765 (503) Transporter	cobalt transporter [*Yersinia nurmii*] Length: 503 92/94(503) 1–503	WP_049597763.1
	cobalt transporter [*Yersinia frederikseniir*] Length: 509 71/83(509) 1–509	WP_050300177.1

PL78_09770 (1040) Transporter	cation transporter [*Yersinia nurmii*] Length: 1040 97/98(1040) 1–1040	WP_049597764.1
	putative cation efflux system protein [Yersinia kristensenii] Length: 1043 92/96(1039) 1–1039	embCFR25599.1
PL78_09775 (272)	shikimate dehydrogenase [*Yersinia nurmii*] Length: 272 97/98(272)1–272	WP_049597765.1
	shikimate dehydrogenase [*Yersinia ruckeri*] Length: 272 88/94(271) 1–271	WP_038244855.1
PL78_09780 (141) Transporter	biopolymer transporter ExbD [*Yersinia nurmii*] Length: 141 99/100(141) 1–141	WP_049597766.1
	biopolymer transporter ExbD [*Yersinia ruckeri*] Length: 141 91/96(141) 1–141	WP_004720996.1
PL78_09785 (238)	MotA/TolQ/ExbB proton channel family protein [*Yersinia nurmii*] Length: 339 97/97(341) 1–339	embCNE47005.1
	tonB-system energizer ExbB [*Yersinia ruckeri*] Length: 339 85/90(342) 1–339	gbAJI95450.1
PL78_09790 (402)	cystathionine beta-lyase [*Yersinia nurmii*] Length: 398 97/98(398) 1–398	WP_049597767.1
	cystathionine beta-lyase [*Yersinia ruckeri*] Length: 398 Rang88/95(394) 1–394	gbAJI94061.1

PL78_09795 (220)	membrane protein [*Yersinia nurmii*] Length: 220 99/100(220) 1–220	WP_049597768.1
	membrane protein [*Yersinia ruckeri*] Length: 220 92/95(220) 1–220	WP_004721003.1
PL78_09800 (297)	AraC family transcriptional regulator [*Yersinia nurmii*] Length: 297 96/96(297) 1–297	WP_049598101.1
	AraC family transcriptional regulator [*Yersinia ruckeri*] Length: 299 89/94(297) 1–297	WP_038244888.1

Table S2. *Yersinia entomophaga* Rhs associated regions 2–5. For graphic depiction refer to Figure 3 of the associated manuscript.

Yersinia entomophaga Rhs associated region 2.

Locus (Amino Acid Resides)	**Closest BlastP Orthologue [Species]** **Length: Amino Acid Length of Orthologue** **% Identity/% Similarity (over the Indicated Range of Amino acid Residues) in Relation to Target Sequence.** **Protein Domain**	**Accession Number**
PL78_18705(171) Ferritin	ferritin [*Yersinia nurmii*] Length: 171 99/99(171) 1–171	WP_049600522.1
	ferritin [*Yersinia ruckeri*] Length: 171 97/97(171) 1–171	WP_004721727.1
PL78_18710(128)	hypothetical protein [*Yersinia nurmii*] Length: 128 98/100(128) 1–128	WP_049600525.1
	hypothetical protein [*Yersinia ruckeri*] Length: 128 94/99(128) 1–128	WP_038243346.1
PL78_18715 (294) CopD	copper resistance protein CopD [*Yersinia nurmii*] Length: 294 96/97(294) 1–294	WP_049600528.1
	copper resistance protein CopD [*Yersinia ruckeri*] Length: 294 80/87(294) 1–94	WP_045844133.1
PL78_18720 (113)	hypothetical protein [*Yersinia nurmii*] Length: 113 97/98(113) 1–113	WP_049600531.1
	hypothetical protein [*Yersinia mollaretii*] Length: 113 81/90(113) 1–113	WP_004875990.1

PL78_18725 (263)	integrase [*Yersinia enterocolitica*] Length: 369 97/98(263) 107–369	WP_050876385.1
PL78_18730 (100)	MULTISPECIES: transposase [*Yersinia*] Length: 100 100/100(100) 1–100	WP_042526049.1
PL78_18735 (56)	IS911 orfB [*Shigella flexneri* 2a str. 2457T] Length: 52 82/90(51) 1–51	gbAAP16190.1
PL78_18740 (68)	Putative transposase [*Yersinia enterocolitica*] Length: 138 93/95(68) 71–138	embCFB70873.1
PL78_18745(155)	hypothetical protein [*Yersinia ruckeri*] Length: 542 99/98(253) 1–153	WP_038246006.1
PL78_18750 (220)	MULTISPECIES: hypothetical protein [*Serratia*] Length: 261 60/78(218) 44–260	WP_025122879.1
PL78_18755(91)	hypothetical protein [*Yersinia aldovae*] Length: 105 49/69(89) 17–105	WP_042546108.1
PL78_18760 (207) LopT	hypothetical protein [*Yersinia pekkanenii*] Length: 221 77/86(195) 12–206	WP_049615575.1
	cysteine protease [*Photorhabdus luminescens*] Length: 323 24/40(181) 131–297	WP_058589369.1
PL78_18765 (105)	hypothetical protein [*Yersinia nurmii*] Length: 105 92/96(104) 1–105	WP_049600537.1
	hypothetical protein [*Yersinia aldovae*] Length: 105 59/71(104) 1–105	WP_042546108.1

PL78_18770 (95)	hypothetical protein [*Yersinia aldovae*] Length: 268 61/74(94) 44–136	WP_042546107.1
PL78_18775 (120)	transposase [*Yersinia rohdei*] Length: 197 46/53(167) 1–167	embCNF45791.1
PL78_18780 (965) RhsA	rhsa toxin protein [*Yersinia nurmii*] Length: 963 87/90(965) 1–963	embCNE97220.1
	insecticidal toxin complex protein TccC3 [*Vibrio parahaemolyticus*] (tc_PAI_042) Length: 971 76/83(971) 1–971	gbAHZ10944.1
PL78_18785 (458)	hypothetical protein [*Photorhabdus luminescens*] Length: 462 45/64(457) 6–460	WP_049582883.1
	hypothetical protein [*Yersinia nurmii*] Length: 458 94/96(458) 1–458	WP_049600554.1
PL78_18790 (150) Ivy	inhibitor of vertebrate lysozyme precursor [*Salmonella enterica* subsp. VII] Length: 155 69/84(150) 6–155	embCAX67957.1
	Probable inhibitor of vertebrate lysozyme [*Erwinia tasmaniensis* Et1/99] Length: 154 62/76(150) 7–154	embCAO95555.1
PL78_18795(205) LyseE	lyseE threonine transporter [*Raoultella terrigena*] Length: 205 84/91(205) 1–205	WP_045857255.1
PL78_18800(182)	acetyltransferase [*Yersinia ruckeri*] Length: 182 92/98(182) 1–182	WP_038244025.1

Yersinia entomophaga Rhs associated region 3.

Locus (Amino Acid Residues)	**Closest BlastP Orthologue [Species]** **Length: Amino Acid Length of Orthologue** **% Identity/% Similarity (over the Indicated Range of Amino Acid Residues) in Relation to Target Sequence.** **Protein Domain**	**Accession Number**
PL78_00880 (249)	transposase [*Yersinia ruckeri*] Length: 249 99/100 (249) 1–249	WP_042527218.1
PL78_00885 (88)	transposase [*Yersinia enterocolitica*] Length: 96 100/100(88) 9–96	WP_011815814.1
PL78_00890 (252)	IS1329 transposase B [*Yersinia enterocolitica*] Length: 280 89/93(207) 1–207	embCRX47735.1
PL78_00895 (187)	hypothetical protein KOXM_28035 [*Klebsiella oxytoca* M5al] Length 116 87/93(187) 1–187	gbEKP24881.1
	MULTISPECIES: membrane protein [*Enterobacteriaceae*] Length: 187 87/93(87) 1–187	WP_024358370.1
	hypothetical protein [Serratia sp. Leaf51] Length: 187 94/97(187) 1–187	WP_056771403.1
PL78_00900 (172) Hcp	major exported protein [*Yersinia nurmii*] Length: 172 100/100(172) 1–172	WP_049602039.1
	hypothetical protein [*Photorhabdus temperata*] Length: 172 95/97(172) 1–172	WP_021323277.1

PL78_00905 (165)	type VI secretion protein [*Yersinia nurmii*] Length: 165 99/99(165) 1–165 “type VI secretion protein”	WP_049602042.1
PL78_00910 (493) ImpC	type VI secretion protein [*Yersinia nurmii*] Length: 493 100/100(493) 1–493	WP_049602045.1
	MULTISPECIES: type VI secretion protein [*Yersinia pseudotuberculosis* complex] Length: 493 93/96(493) 1–493	WP_025381701.1
PL78_00915 (146) Lys	lysozyme [*Yersinia nurmii*] Length: 146 98/98(146) 1–146	WP_049602048.1
	MULTISPECIES: lysozyme [Serratia] Length: 146 70/84(145) 1–146	WP_025123010.1
PL78_00920 (602) ImpG	type VI secretion protein [*Yersinia nurmii*] Length: 602 99/99(602) 1–602	WP_049602051.1
	type VI secretion protein [*Yersinia pekkanenii*] Length: 606 80/89(606) 1–602	WP_049612770.1
PL78_00925(347)	type VI secretion protein [*Yersinia nurmii*] Length: 347 100/100(335) 1–347	WP_049602054.1
	type VI secretion protein [*Yersinia pseudotuberculosis*] Length: 362 80/90(335) 1–347	WP_050136839.1
PL78_00930 (436)	phosphopeptide-binding protein [*Yersinia nurmii*] Length: 436 99/99(436) 1–436	WP_049602058.1
	MULTISPECIES: phosphopeptide-binding protein [*Yersinia pseudotuberculosis* complex] Length: 438 67/79(439) 1–436	WP_033852633.1

PL78_00935 (180)	type VI secretion protein [*Yersinia nurmii*] Length: 180 98/99(180) 1–180	WP_049602061.1
	type VI secretion protein [*Xenorhabdus khoisanae*] Length: 184 66/80(184) 1–180	WP_047964021.1
PL78_00940 (448) ImpJ	type VI secretion protein [*Yersinia nurmii*] Length: 448 99/99(448) 1–444	WP_049602062.1
	type VI secretion protein [*Yersinia aldovae*] Length: 448 83/91(448) 1–444	WP_049689231.1
PL78_00945 (255) MotB	membrane protein [*Yersinia nurmii*] Length: 255 97/98(255) 1–255	WP_049602063.1
	chemotaxis protein MotB [*Photorhabdus asymbiotica*] Length: 256 79/88(256) 1–256	WP_012776473.1
PL78_00950 (866) ClpV	Clp protease ClpV [*Yersinia nurmii*] Length: 866 98/99(866) 1–866	WP_049602066.1
	MULTISPECIES: Clp protease ClpV [*Yersinia pseudotuberculosis* complex] Length: 867 78/88(867) 1–866	WP_025381694.1
PL78_00955 (266) Fis	Fis family transcriptional regulator [*Yersinia nurmii*] Length: 266 96/98(266) 1–266	WP_049602068.1
	Fis family transcriptional regulator [*Yersinia aldovae*] Length: 265 71/83(266) 1–265	WP_042546926.1

PL78_00960 (218)	type VI secretion protein [*Yersinia nurmii*] Length: 218 96/96(218) 1–218	WP_049602071.1
	type VI secretion protein [*Yersinia aldovae*] Length: 219 63/73(192) 30–219	WP_042546925.1
PL78_00965 (470) ImpA	membrane protein [*Yersinia nurmii*] Length: 467 96/96(467) 1–467	WP_049602074.1
	MULTISPECIES: membrane protein [Serratia] Length: 462 60/73(471)1–467	WP_025123019.1
PL78_00970 (1183) IcmF Orf3	type VI secretion protein IcmF [*Yersinia nurmii*] Length: 1183 98/98(1183) 1–1183	WP_049602076.1
	lipoprotein [*Yersinia pseudotuberculosis*] Length: 1177 73/85(1176) 2–177	embCFV32787.1
	type VI secretion protein IcmF [*Photorhabdus luminescens*] Length: 1181 66/80(1168) 16–1181	WP_011144748.1
PL78_00975 (441) ImpA	membrane protein [*Yersinia nurmii*] Length: 441 97/98(441) 1–441	WP_049602079.1
	membrane protein [*Yersinia aldovae*] Length: 442 58/73(443) 1–441	WP_049634662.1
	hypothetical protein [*Photorhabdus luminescens*] Length: 459 34/51(466) 1–454	WP_011148302.1

PL78_00980 (770) VgR	type VI secretion protein Vgr [*Yersinia nurmii*] Length: 756 96/96(770) 1 to 756	WP_049602081.1
	type VI secretion protein Vgr [*Serratia fonticola*] Length: 743 72/80(705) 52–743	WP_037413087.1
	unnamed protein product [*Photorhabdus luminescens* subsp. laumondii TTO1] Length: 704 39/57(612) 3–604	embCAE12757.1
PL78_00985 (139) Orf5	hypothetical protein [*Yersinia nurmii*] Length: 139 98/98(138) 1–138	WP_049602084.1
	hypothetical protein [*Photorhabdus luminescens*] Length: 139 64/79(139) 1–139	WP_049584104.1
PL78_00990 (1444) Rhs	YD repeat-/RHS repeat-containing protein [*Yersinia nurmii*] Length: 1451 99/99(1320) 1–1320	embCNF22828.1
	type IV secretion protein Rhs [*Photorhabdus asymbiotica*] Length: 1451 59/72(1345) 1–1320	WP_012777142.1
PL78_00995 (123) Spt4	hypothetical protein [*Yersinia nurmii*] Length: 123 98/99(123) 1–123	WP_049602103.1
	hypothetical protein [*Leminorella grimontii*] Length: 123 100/100(13) 1–123 COG2093: Spt4	WP_027272928.1

PL78_01000 (117)	MULTISPECIES: hypothetical protein [*Yersinia pseudotuberculosis* complex] Length: 117 85/93(117) 1–117	WP_025381673.1
	Uncharacterised protein [*Yersinia similis*] Length: 117 85/92(117) 1–117	WP_054878057.1
	hypothetical protein [*Photorhabdus luminescens*] Length: 115 66/84(117) 1–115	WP_011147332.1
PL78_01005 (145)	type IV secretion protein Rhs [*Pectobacterium carotovorum*] Length: 1424 83/89(144) 1280–1423	WP_039503594.1
	hypothetical protein SK41_01880 [*Enterobacter aerogenes*] Length: 255 79/86(145) 111–254	gbKLV93059.1
PL78_01010 (147)	hypothetical protein [*Pectobacterium wasabiae*] Length: 145 61/64(142) 1–141	WP_025919449.1
	hypothetical protein [*Enterobacter cloacae*] Length: 141 60/78(132) 10–140	WP_047174021.1
PL78_01015 (67)	hypothetical protein [*Yersinia nurmii*] Length: 67 100/100(67) 1–67	WP_049602119.1
	hypothetical protein [Morganella morganii] Length: 284 75/95(67) 218–284	WP_052927290.1
PL78_01025 (159)	hypothetical protein [Lonsdalea quercina] Length: 159 94/96(159) 1–149	WP_036150158.1
PL78_01030 (97) TIGR03696: Rhs_assc_core	type IV secretion protein Rhs [Pantoea ananatis] Length: 1395 72/83(99) 1260–1358	WP_028723925.1

PL78_01035 (82)	hypothetical protein [*Yersinia nurmii*] Length: 82 98/100(82) 1–82	WP_049602116.1
	hypothetical protein [*Pantoea* sp. BL1] Length: 82 59/81(82) 1–82	WP_045834389.1
	hypothetical protein [Type-F symbiont of *Plautia stali*] Length: 82 59/82(82) 1–82	WP_058958422.1
PL78_01040 (139) AHH pfam14412	hypothetical protein [*Yersinia nurmii*] Length: 127 97/98(122) 6–127	WP_053215256.1
	hypothetical protein [*Serratia fonticola*] Length: 138 98/99(138) 1–138	WP_051363166.1
	hypothetical protein ECA4293 [*Pectobacterium atrosepticum* SCRI1043] Length: 150 74/83(139) 12–150	embCAG77190.1
	type IV secretion protein Rhs [*Serratia fonticola*] Length: 1487 99/99(139) 1349–1487	WP_046808161.1
PL78_01045 (173)	hypothetical protein [*Serratia fonticola*] Length: 173 99/99(173) 1–173	P_046808162.1
	hypothetical protein [*Yersinia nurmii*] Length: 173 95/97(173) 1–173	WP_049596802.1
	hypothetical protein [*Photorhabdus luminescens*] Length: 177 34/57(173) 5–174	WP_036812017.1
PL78_01050 (321)	membrane protein [*Yersinia nurmii*] Length: 321 98/99(284) 38–321	WP_049596801.1
	putative membrane protein [*Yersinia intermedia*] Length: 284 83/93(284) 1–284	gbAJJ19515.1

Yersinia entomophaga Rhs associated region 4.

Locus (Amino Acid Residues)	Closest BlastP Orthologue [Species] Length: Amino Acid Length of Orthologue % Identity/% Similarity (over the Indicated Range of Amino Acid Residues) in Relation to Target Sequence. Protein Domain	Accession Number
PL78_11955 (317)	ketodeoxygluconokinase [*Yersinia nurmii*] Length: 317 95/96(317) 1–317	WP_049597328.1
	ketodeoxygluconokinase [*Yersinia ruckeri*] Length: 317 86/92(315) 1–315	WP_049689687.1
PL78_11960 (515)	peptidase [*Yersinia nurmii*] Length: 515 96/97(515) 1–515	WP_049597329.1
	peptidase [*Yersinia ruckeri*] Length: 496 90/94(490) 1–490	WP_042526849.1
PL78_11965 (430)	C4-dicarboxylate transporter [*Yersinia nurmii*] Length: 430 99/99(430) 1–430	WP_049597330.1
	C4-dicarboxylate ABC transporter [*Yersinia ruckeri*] Length: 430 97/98(430) 1–430	WP_004723244.1
PL78_11970 (655)	biofilm formation regulator HmsP [*Yersinia nurmii*] Length: 666 98/99(655) 12–666	embCNE26472.1
	biofilm formation regulator HmsP [*Yersinia ruckeri*] Length: 655 81/90(655) 1–655	WP_038242966.1

PL78_11975 (1159) CelC	cellulose synthase [*Yersinia ruckeri*] Length: 1160 86/92(1160) 1–1160	WP_042526844.1
	cellulose synthase [*Yersinia ruckeri*] Length: 1160 86/92(1160) 1–1160	WP_038242904.1
PL78_11980 (377) CelD	endoglucanase [*Yersinia nurmii*] Length: 377 97/97(377) 1–377	WP_049597332.1
	endoglucanase [*Yersinia ruckeri*] Length: 376 86/91(377) 1–376	WP_004723238.1
PL78_11985 (770) CelB	cellulose synthase [*Yersinia nurmii*] Length: 770 96/97(770) 1–770	WP_049597464.1
	cellulose synthase [*Yersinia ruckeri*] Length: 770 90/94(770) 1–770	WP_042528353.1
PL78_11990 (875) CelA	cellulose synthase [*Yersinia nurmii*] Length: 875 98/98(875) 1–875	WP_049597333.1
	cellulose synthase [*Yersinia ruckeri*] Length: 875 91/95(875) 1–875	WP_038276495.1
PL78_11995 (243) CelT	cell division protein [*Yersinia nurmii*] Length: 243 95/98(243) 1–243	WP_049597334.1
	cell division protein [*Yersinia ruckeri*] Length: 245 79/87(245) 1–245	WP_038276497.1

PL78_12000 (63) CelS	hypothetical protein [*Yersinia nurmii*] Length: 63 90/92(63) 1–63	WP_049597335.1
	hypothetical protein [*Yersinia ruckeri*] Length: 63 90/95(63) 1–63	WP_038242910.1
PL78_12005 (518) CelP	cellulose biosynthesis protein BcsE [*Yersinia ruckeri*] Length: 518 84/92(518) 1–518	WP_042526838.1
WP_042526824.1	WP_042526824.1	WP_042526824.1
	membrane protein [*Yersinia ruckeri*] Length: 546 84/91(553) 1–546	WP_042526834.1
PL78_12020 (334)	dipeptide transporter ATP-binding subunit [*Yersinia nurmii*] Length: 341 98/98(334) 8–334	embCNE26976.1
	dipeptide transporter ATP-binding subunit [*Yersinia enterocolitica*] Length: 341 98/98(333) 8–340	embCFQ43661.1
PL78_12025 (326)	peptide ABC transporter ATP-binding protein [*Yersinia nurmii*] Length: 326 99/100(1–326) 1–326	WP_049597338.1
	peptide ABC transporter ATP-binding protein [*Yersinia ruckeri*] Length: 326 98/98(326) 1–326	WP_042526832.1
PL78_12030 (300)	peptide transporter [*Yersinia nurmii*] Length: 300 99/100(300) 1–300	WP_049597339.1
	peptide ABC transporter [*Yersinia ruckeri*] Length: 300 98/99(300) 1–300	WP_004718359.1

PL78_12035 (339)	hypothetical protein [*Yersinia nurmii*] Length: 339 99/99(339) 1–339	WP_049597340.1
	hypothetical protein [*Yersinia ruckeri*] Length: 339 99/99(33) 1–339	WP_038242913.1
PL78_12040 (536)	peptide ABC transporter substrate-binding protein [*Yersinia nurmii*] Length: 536 99/99(536) 1–536	WP_049597341.1
	peptide ABC transporter substrate-binding protein [*Yersinia ruckeri*] Length: 536 97/98(536) 1–536	WP_004718354.1
PL78_12050 (443)	MFS transporter [*Yersinia nurmii*] Length: 443 99/100(443) 1–443	WP_049597342.1
	hypothetical protein [*Yersinia ruckeri*] Length: 445 97/98(443) 1–443	WP_004718352.1
PL78_12045 tRNA-Pro		
PL78_12050 (443)	MFS transporter [*Yersinia nurmii*] Length: 443 99/100(443) 1–443	WP_049597342.1
	hypothetical protein [*Yersinia ruckeri*] Length: 445 97/98(443) 1–443	WP_004718352.1
PL78_12055 (509)	histidine kinase [*Yersinia nurmii*] Length: 509 99/99(509) 1–509	WP_049597343.1
	histidine kinase [*Yersinia ruckeri*] Length: 509 91/95(509) 1–509	WP_038242914.1

PL78_12060 (196)	DNA-binding response regulator [*Yersinia nurmii*] Length: 196 99/99(196) 1–196	WP_049597344.1
	DNA-binding response regulator [*Yersinia ruckeri*] Length: 196 95/98(196) 1–196	WP_038242915.1
PL78_12065 (563)	phosphoethanolamine transferase [*Yersinia nurmii*] Length: 563 98/99(563) 1–563	WP_049597345.1
	phosphoethanolamine transferase [*Yersinia ruckeri*] Length: 563 91/95(561) 1–561	WP_042528351.1
PL78_12070 (141)	organic hydroperoxide resistance protein [*Yersinia nurmii*] Length: 141 98/98(141) 1–141	WP_049597346.1
	MULTISPECIES: organic hydroperoxide resistance protein [*Yersinia*] Length: 141 95/91(1410) 1–141	WP_038637498.1
PL78_12075 (149)	homoprotocatechuate degradative operon repressor [*Yersinia nurmii*] Length: 144 95/97(144) 1–144	embCNE27397.1
	Transcriptional regulator, MarR family [*Yersinia frederikseniir* ATCC 33641] Length: 144 85/93(143) 1–143	gbEEQ15729.1
PL78_12080 (487)	membrane protein [*Yersinia nurmii*] Length: 487 98/99(487) 1–487	WP_049597348.1
	membrane protein [*Yersinia ruckeri*] Length: 487 93/96(487) 1–497	WP_038242916.1

PL78_12085 (175)	membrane protein [*Yersinia nurmii*] Length: 175 97/97(175) 1–175	WP_049597349.1
	membrane protein [*Yersinia ruckeri*] Length 84/90(172) 1–172	WP_004718344.1
PL78_12090 (464	proline-specific permease [*Yersinia nurmii*] Length: 464 99/100 1–464	WP_049597350.1
	proline-specific permease [*Yersinia ruckeri*] Length: 464 95/97(463) 1–463	WP_042526824.1
PL78_12095 (511)	histidine ammonia-lyase [*Yersinia nurmii*] Length: 511 98/98(511) 1–511	WP_049597351.1
	histidine ammonia-lyase [*Yersinia ruckeri*] Length: 511 95/97(510) 1–510	WP_038276502.1
PL78_12100 (563) Uhyd	urocanate hydratase [*Yersinia nurmii*] Length: 563 99/99(562) 1–562	WP_049597352.1
	urocanate hydratase [*Yersinia ruckeri*] Length: 563 98/99(563) 1–563	WP_038242919.1
PL78_12105 (592) IcmF	hypothetical protein [*Yersinia nurmii*] Length: 592 90/94(592) 1–592	WP_049597353.1
	type VI secretion protein IcmF [*Pantoea* sp. MBLJ3] Length: 1145 32/50(560) 409–950	WP_039659128.1

PL78_12110 (205) VasF	hypothetical protein [*Yersinia nurmii*] Length: 207 90/96(196) 6–201	WP_049597354.1
	hypothetical protein [*Yersinia mollaretii*] Length: 207 39/60(207) 1–198	WP_032813416.1
PL78_12115 (176)	hypothetical protein [*Serratia fonticola*] Length: 176 86/91(175) 1–175	WP_037411404.1
	hypothetical protein [*Xenorhabdus cabanillasii*] Length: 164 40–58(172) 1–162	WP_038263077.1
	hypothetical protein [*Photorhabdus luminescens*] Length: 164 38/58(170) 1–160	WP_040154291.1
PL78_12120 (131)	hypothetical protein [*Yersinia pseudotuberculosis*] Length: 131 88/94(131) 1–131	WP_0503212031
PL78_12125(138) T4SS	type IV secretion protein Rhs [*Yersinia similis*] Length: 457 92/96(132) 326–457	gbAHK18882.1
PL78_12130(204) T3SS	type III secretion system effector protein, partial [*Xanthomonas campestris* pv. musacearum NCPPB 4379] locus, KWO_0111025 Length: 82 37/46(52) 18–69	gbKFA09649.1
	hypothetical protein [*Photorhabdus luminescens*] Length: 201 46/56(203) 4–201	WP_049584090.1

PL78_12135 (1400) Rhs	RHS/YD repeat-containing protein [*Yersinia nurmii*] Length: 1395 95/96(1257) 1–1297	embCND85328.1
	RHS/YD repeat-containing protein wapA_1 [*Yersinia pseudotuberculosis*] Length: 1406 86/90(1297) 1–1297	embCNB75225.1
PL78_12140 (144)	hypothetical protein [*Yersinia nurmii*] Length: 144 97/98(144) 1–144	WP_049596388.1
	hypothetical protein [*Serratia fonticola*] Length: 144 84/88(144) 1–144	WP_021181280.1
	hypothetical protein [*Photorhabdus luminescens*] Length: 141 53/71(135) 6–140	WP_049583043.1
PL78_12145 (249)	integrase core domain protein [*Yersinia ruckeri*] Length: 264 99/99(249) 16–264	gbAJI95622.1
	IS1400 transposase B [*Yersinia enterocolitica* subsp. enterocolitica WA-314] Length: 249 97/98(249) 1–249	gbEKA28335.1
PL78_12150 (89)	transposase [*Yersinia enterocolitica*] Length: 96 100/100(88) 9–96	WP_011815814.1
	transposase [*Citrobacter youngae* ATCC 29220] Length: 95 100/100(88) 8–95	gbEFE06341.1

PL78_12155 (110)	aldehyde dehydrogenase [*Yersinia enterocolitica*] Length: 110 91/94(110) 1–110	WP_050130145.1
PL78_12160 (141)	hypothetical protein [*Yersinia massiliensis*] Length: 141 99/98(141) 1–141	WP_049607925.1
	hypothetical protein [*Photorhabdus luminescens*] Length: 141 48/78(141) 1–141	WP_049583905.1
PL78_12165 (619)	helicase [*Yersinia massiliensis*] Length: 619 99/99(619) 1–619	WP_049607923.1

Yersinia entomophaga Rhs associated region 5.

Locus (Amino Acid Residues)	**Closest BlastP Orthologue [Species]** **Length: Amino Acid Length of Orthologue** **% Identity/% Similarity (over the Indicated Range of Amino Acid Residues) in Relation to Target Sequence.** **Protein Domain**	**Accession Number**
PL78_15035(306) LysR	LysR family transcriptional regulator [*Yersinia nurmii*] Length: 306 97/98(306) 1–306	WP_049602006.1
	LysR family transcriptional regulator [*Yersinia ruckeri*] Length: 306 94/96(306) 1–306	WP_004721488.1
PL78_15040 (115)	hypothetical protein [*Yersinia nurmii*] Length: 293 57/68(89) 186–274	WP_049602009.1
	hypothetical protein [*Yersinia frederikseniir*] Length: 291 37/58(114) 161–274	WP_050083633.1
PL78_15045 (93)	hypothetical protein [*Chromobacterium violaceum*] Length: 89 47/67(86) 1–86	WP_011135095.1
	hypothetical protein [*Photorhabdus luminescens*] Length: 81 45/64(77) 1–77	WP_036775687.1
PL78_15050 (265)	hypothetical protein [*Chromobacterium violaceum*] Length: 265 39/59(268) 1–264	WP_011135094.1
PL78_15055 (416) 3-o-ACP	3-oxoacyl-ACP synthase [*Chromobacterium violaceum*] Length: 416 76/83(416) 1–416	WP_045050403.1

PL78_15060 (321)	unnamed protein product [*Photorhabdus luminescens* subsp. laumondii TTO1] Length: 340 28/21(351) 9–329	embCAE14514.1
PL78_15065 (181)	hypothetical protein [*Photorhabdus luminescens*] Length: 186 32/52(170) 14–179	WP_049581660.1
	PREDICTED: xaa-Pro dipeptidase isoform X1 [Xenopus (Silurana) tropicalis] Length: 554 25/42(146) 121–265	XP_012816407.1
PL78_15070 (1584) Rhs	type IV secretion protein Rhs [Pseudomonas fluorescens] Length: 1577 40/58(1449) 1–1433	WP_034134568.1
PL78_15075 (160) NusG	hypothetical protein [*Yersinia intermedia*] Length: 160 58/76(159) 1–159	WP_050074372.1
	NusG-type transcription antiterminator [Serratia entomophila] Length: 160 53/73(159) 1–159	WP_010895762.1
PL78_15080 (214) AmpC	CMY/LAT/MOX/ACT/MIR/FOX family class C beta-lactamase [*Yersinia ruckeri*] Length: 381 96/97(212) 1–212	WP_004721718.1
PL78_15085 (92)	ISEhe3 transposase A [*Yersinia ruckeri* ATCC 29473] Length: 94 95/96(92) 3–94	gbEEP97487.1
PL78_15090 (283)	transposase [*Yersinia pekkanenii*] Length: 283 99/99(283) 1–283	WP_049615490.1
PL78_15095 (283)	MULTISPECIES: hypothetical protein [*Enterobacteriaceae*] Length: 283 100/100(283) 1–283	WP_048990909.1

PL78_15100 (68)	hypothetical protein [*Escherichia coli*] Length: 68 100/100(68)1–68	WP_001071601.1
	DNA binding protein [*Plautia stali symbiont*] Length: 70 99/100(68) 3–70	dbjBAN95392.1
PL78_15105 (169)	hypothetical protein [*Escherichia coli*] Length: 169 96/97(133) 1–133	WP_001610849.1
PL78_15110 (189)	MULTISPECIES: hypothetical protein [*Enterobacteriaceae*] Length: 189 97/98(189) 1–189	WP_001610847.1
PL78_15115 (90)	hypothetical protein E1470_c27270 [*Escherichia coli* ECC-1470] Length: 92 100//100(90) 3–92	gbAJG09638.1
	His-Xaa-Ser system protein HxsD [*Photorhabdus luminescens*] Length: 90 96/98(90)1–90	WP_058588807.1
PL78_15120 (462)	His-Xaa-Ser system radical SAM maturase HxsB [*Escherichia coli*] Length: 462 99/100(462) 1–462	WP_023567064.1

Table S3. *Yersinia entomophaga* Type II and III associated regions. For graphic depiction refer to Figure 4 of the associated manuscript.

Yersinia entomophaga T3SSYE1.

Locus (Amino Acid Resides)	Closest BlastP Orthologue [Species] Length: Amino Acid Length of Orthologue % Identity/% Similarity (over the Indicated Range of Amino Acid Residues) in Relation to Target Sequence. Protein Domain	Accession Number
PL78_18070 (296) LuxR	hypothetical protein SLIQ_15070 [Serratia liquefaciens FK01] Length: 209 33/55(202) 5–206	dbjGAK27997.1
	hypothetical protein [*Yersinia nurmii*] Length: 296 85/91(296) 1–296	WP_049596354.1
PL78_18075 (2347) Intimim	hypothetical protein [*Yersinia nurmii*] Length: 2359 92/94(2337) 1–2336	WP_049596353.1
	hypothetical protein [*Hafnia alvei*] Length: 2332 44/61(2355) 1–2319	WP_051874183.1
	invasin [*Xenorhabdus bovienii*] Length: 2217 43/60(1607) 16–1595	WP_012988596.1
	invasin [*Sodalis praecaptivus*] Length: 934 46/53(900) 17–905	WP_025423285.1
PL78_18080 (151)	hypothetical protein [*Yersinia nurmii*] Length: 151 79/86(151) 1–151	WP_049596352.1
	alpha-N-arabinofuranosidase [*Cellvibrio japonicus*] Length: 375 27/47(100) 93–176	WP_012488648.1

PL78_18085 (241)	hypothetical protein [*Yersinia frederikseniir*] Length: 345 33/51(129) 210–316	WP_050318901.1
	hypothetical protein [*Yersinia nurmii*] Length: 241 75/87(160) 82–241	WP_049596351.1
PL78_18090 (371)	DUF218 domain [*Yersinia nurmii*] Length: 455 93/95(455) 1–455	embCND83898.1
	hypothetical protein [Pseudomonas sp. UW4] Length: 435 54/70(391) 44–433	WP_015095362.1
PL78_18095 (139) IaGB	invasion protein IagB [*Yersinia nurmii*] Length: 143 97/98(143) 1–143	WP_049596806.1
	invasion protein IagB [*Serratia fonticola*] Length: 146 64/80(136) 4–139	WP_046808476.1
PL78_18100 (69)	NA	
PL78_18105 (193) InvF	hypothetical protein [*Serratia fonticola*] Length: 263 45/62(264) 1–263)	WP_024486144.1
	hypothetical protein [*Yersinia nurmii*] Length: 255 96/98(255) 1–255	WP_049596350.1
PL78_18110 (549) InvG	type III secretion system outer membrane pore InvG [*Serratia fonticola*] Length: 564 72/84(564) 1–563	WP_024486143.1
	type III secretion system protein [*Yersinia nurmii*] Length: 562 99/99(562) 1–562 1–562	embCND83797.1

PL78_18115 (367) InvE	hypothetical protein [*Yersinia nurmii*] Length: 381 96/97(380) 1–380	WP_049596349.1
	hypothetical protein [*Serratia fonticola*] Length: 381 64/80(332) 35–366	WP_024486142.1
PL78_18120 (681) InvA	type III secretion system protein InvA [*Yersinia nurmii*] Length: 682 98/98(682) 1–682	WP_049596348.1
	type III secretion system protein InvA [*Serratia fonticola*] Length: 685 76/88(685) 1–685	WP_024486141.1
PL78_18125 (133) SpaK	hypothetical protein [*Serratia fonticola*] Length: 134 59/81(133) 2–134	WP_024486140.1
	hypothetical protein [*Yersinia nurmii*] Length: 133 97/100(133) 1–133	WP_049596347.1
PL78_18130 (430) InvC ATP synthase	ATP synthase [*Serratia fonticola*] Length: 430 81/88(430) 1–430	WP_024486139.1
	ATP synthase [*Yersinia nurmii*] Length: 430 97/98(430) 1–430	WP_049596346.1
PL78_18135 (151) SpaM	hypothetical protein [*Serratia fonticola*] Length: 151 44/66(151) 1–151	WP_037413054.1
	hypothetical protein [*Yersinia nurmii*] Length: 151 92/94(151) 1–151	WP_049596345.1

PL78_18140 (358) SpaN	hypothetical protein [*Serratia fonticola*] Length: 328 39/55(84) 254–328	WP_024486137.1
	hypothetical protein [*Yersinia nurmii*] Length: 358 87/91(358) 1–358	WP_049596344.1
PL78_18145 (317) SpaO	hypothetical protein [*Serratia fonticola*] Length: 286 51/68(289) 1–286	WP_037413052.1
	hypothetical protein [*Yersinia nurmii*] Length: 317 91/96(317) 1–317	WP_049596343.1
PL78_18150(219) FilP	type III secretion system protein [*Yersinia nurmii*] Length: 219 99/100(219)1–219	WP_049596342.1
PL78_18155(84) SpaQ	type III secretion system protein SpaQ [*Yersinia nurmii*] Length: 84 100/100(84) 1–84	WP_049596341.1
	surface presentation of antigens protein SpaQ [*Cedecea davisae*] Length: 85 83/93(83) 1–83	WP_016537922.1
PL78_18160 (254) SpaR	hypothetical protein [*Serratia fonticola*] Length: 254 76/85(253) 1–253	WP_024486133.1
	type III secretion apparatus SpaR [*Yersinia nurmii*] Length: 254 97/99(254) 1–254	WP_049596340.1
PL78_18165 (350) SpaS	type III secretion system protein SpaS [*Serratia fonticola*] Length: 355 72/88(346) 1–346	WP_046808151.1
	type III secretion system protein SpaS [*Yersinia nurmii*] Length: 350 97/98(350) 1–350	WP_049596339.1

PL78_18170 (164) SicA	chaperone protein SicA [*Yersinia nurmii*] Length: 164 98/100(164) 1–164	WP_049596338.1
	chaperone protein SicA [*Serratia fonticola*] Length: 158 71/90(151) 1–151	WP_037412608.1
PL78_18175 (630) SipB	hypothetical protein [*Yersinia nurmii*] Length: 630 95/98(630) 1–630	WP_049596337.1
	hypothetical protein [*Serratia fonticola*] Length: 609 47/67(604) 12–605	WP_046808152.1
PL78_18180 (400) SipC	hypothetical protein [*Yersinia nurmii*] Length: 400 96/97(399)1–399	WP_049596336.1
	hypothetical protein [*Serratia fonticola*] Length: 364 33/51(281) 47–323	WP_024485265.1
PL78_18185 (408) SipD	cell invasion protein SipD, partial [*Chromobacterium violaceum*] Length: 283 47/66(212)74–281	WP_045050982.1
	hypothetical protein [*Yersinia nurmii*] Length: 407 89/92(409) 1–407	WP_049596335.1
PL78_18190 (752) SipA	hypothetical protein [*Yersinia nurmii*] Length: 805 86/91(444) 1–443	WP_049596334.1
	hypothetical protein [*Serratia fonticola*] Length: 733 28/48(194) 60–247	WP_024485266.1

PL78_18195(85)	hypothetical protein [*Yersinia nurmii*] Length: 77 92/97(77) 1–77	WP_049596333.1
	acyl carrier protein [Candidatus Regiella insecticola] Length: 91 43/69(75) 2–76	WP_039908335.1
PL78_18205 (402) PrgH	type III secretion system needle complex protein PrgH [*Yersinia nurmii*] Length: 402 96/98(402) 1–402	embCND83112.1
	hypothetical protein [*Serratia fonticola*] Length: 401 46/66(401) 2–401	WP_046808154.1
PL78_18210 (87) PrgI	type III secretion system needle complex protein PrgI [*Yersinia nurmii*] Length: 87 92/95(87) 1–87	WP_049596331.1
	type III secretion apparatus needle protein [*Cedecea davisae* DSM 4568] Length: 90 76/81(76) 15–90	gbEPF14983.1
PL78_18215 (100) PrgJ	hypothetical protein [*Yersinia nurmii*] Length: 100 97/98(100)1–100	WP_049596330.1
	hypothetical protein [*Serratia fonticola*] Length: 97 53/80(96) 2–97	WP_024485270.1
PL78_18220(244) PrgK	pathogenicity island 1 effector protein [*Yersinia nurmii*] Length: 244 98/98(244) 1–244	WP_049596329.1
	type III secretion apparatus lipoprotein [*Serratia fonticola*] Length: 235 66/83(229) 2–230	WP_024485271.1
PL78_18225 (190) OrgA	hypothetical protein [*Yersinia nurmii*] Length: 190 94/97(190)1–190	WP_049596328.1
	hypothetical protein [*Serratia fonticola*] Length: 199 46/63(182) 15–196	WP_024485272.1

PL78_18230 (233) OrgB	hypothetical protein [*Yersinia nurmii*] Length: 233 95/98(233) 1–233	WP_049596327.1
	hypothetical protein [*Serratia fonticola*] Length: 230 42/65(149) 1–226	WP_024485273.1
PL78_18235 (73)	hypothetical protein [*Yersinia nurmii*] Length: 70 97/99(58) 1–70 Sequence ID: emb|CND82903.1| Length: 70 81/90(70) 1–70	WP_049596326.1
	hypothetical protein [*Serratia fonticola*] Length: 71 48/68(58) 14–71	WP_024485274.1
PL78_18240 (197)	Uncharacterised protein [*Yersinia nurmii*] Length: 196 91/94(196) 1–196	embCND82874.1
	hypothetical protein [*Serratia fonticola*] Length: 197 44/61(201) 1–196	WP_024485275.1
PL78_18245 (438)	oxidoreductase [*Yersinia nurmii*] Length: 438 97/98(438) 1–438	WP_049596324.1
	oxidoreductase [*Serratia fonticola*] Length: 438 80/90(438) 1–438	WP_046808249.1
PL78_18250 (367)	agmatine deiminase [*Yersinia nurmii*] Length: 367 91/95(367) 1–367	WP_049596323.1
	agmatine deiminase [*Marinomonas mediterranea*] Length: 367 67/78(366) 1–365	WP_013660875.1

Yersinia entomophaga T3SSYE2.

Locus (Amino Acid Residues)	Closest BlastP Orthologue [Species] Length: Amino Acid Length of Orthologue % Identity/% similarity (over the Indicated Range of Amino Acid Residues) in Relation to Target Sequence. Protein Domain	Accession Number
PL78_14480 (851)	DNA mismatch repair protein MutS [*Yersinia nurmii*] Length: 851 99/99(851) 1–851	WP_049601201.1
PL78_14490 (147)	membrane protein [*Yersinia nurmii*] Length: 147 90/93(147) 1–147	embCNF08019.1
	hypothetical protein BD65_2656 [*Yersinia ruckeri*] Length: 149 63/75(149) 1–149	gbAJI94952.1
PL78_14495 (120)	lytic transglycosylase [*Yersinia nurmii*] Length: 159 81/91(159) 1–159	WP_049601195.1
	lytic transglycosylase [*Yersinia ruckeri*] Length: 158 61/77(145) 11–155	WP_038244579.1
PL78_14500 (117)	helicase [*Halomonas* sp. TG39a] Length: 907 31/47(122) 82–199	WP_035576868.1
	Uncharacterised protein [*Yersinia nurmii*] Length: 138 73/83(138) 1–138	embCNF07957.1
PL78_14505 (224) OrgB	invasion protein OrgB [*Yersinia nurmii*] Length: 224 82/90(224) 1–224	embCNF07929.1
	hypothetical protein [*Yersinia ruckeri*] Length: 222 40/60(213) 10–222	WP_042527542.1

PL78_14510 (181)	hypothetical protein [*Yersinia nurmii*] Length: 181 84/91(160) 21–180	WP_049601187.1
	hypothetical protein [*Yersinia ruckeri*] Length: 176 44/67(158) 17–174	WP_038251258.1
PL78_14515 (248) Prgk	type III secretion protein [*Yersinia nurmii*] Length: 247 91/94(247) 1–247	WP_049601185.1
	type III secretion protein [*Yersinia ruckeri*] Length: 252 69/80(247) 1–243	WP_042527545.1
PL78_14520 (101) PrgJ	hypothetical protein [*Yersinia ruckeri*] Length: 100 44/61(101) 1–100	WP_042527547.1
	hypothetical protein [*Yersinia nurmii*] Length: 101 94/97(101) 1–101	WP_049601183.1
PL78_14525 (100) PrgI	hypothetical protein [*Yersinia nurmii*] Length: 99 36/51(97) 1–99	WP_049601181.1
	hypothetical protein [*Yersinia ruckeri*] Length: 104 36/51(97) 8–103	WP_042527549.1
PL78_14530 (422) PrgH	type III secretion system needle complex protein PrgH [*Yersinia nurmii*] Length: 422 85/92(422) 1–422	embCNF07697.1
	hypothetical protein [*Yersinia ruckeri*] Length: 395 39/59(411) 3–395	WP_042527551.1

PL78_14535 (150) AraC	hypothetical protein [*Yersinia ruckeri*] Length: 264 42/57(143) 14–156	WP_052470857.1
	hypothetical protein [*Yersinia nurmii*] Length: 261 83/89(131) 7–137	WP_049601175.1
PL78_14540 (567) InvG Ysac	type III secretion system protein [*Yersinia nurmii*] Length: 567 95/97(567) 1–567	WP_049601173.1
	type III secretion system protein [*Yersinia ruckeri*] Length: 570 74/86(565) 5–569	WP_042527553.1
PL78_14545 (366) InvE Ysaw	hypothetical protein [*Yersinia nurmii*] Length: 366 90/95(366) 1–366	WP_049601168.1
	hypothetical protein [*Yersinia ruckeri*] Length: 368 67/82(357) 1–357	WP_038244567.1
PL78_14550 (691) InvA	type III secretion system protein InvA [*Yersinia ruckeri*] Length: 689 80/88(689) 1–689	WP_045844472.1
	type III secretion system protein InvA [*Yersinia nurmii*] Length: 689 95/97(689) 1–689	WP_049601166.1
PL78_14555 (140) InvB Ysak	type III secretion system protein [*Yersinia nurmii*] Length: 135 91/95(135) 1–135	WP_049601164.1
	type III secretion system protein [*Yersinia ruckeri*] Length: 135 66/78(134) 1–134	WP_042527558.1

PL78_14560 (430) SpaL InvC	ATP synthase SpaL [*Yersinia nurmii*] Length: 399 92/96(399) 1–399	embCNF07457.1
	ATP synthase [*Yersinia nurmii*] Length: 430 92/96(430) 1–430	WP_049601162.1
PL78_14565 (153)	hypothetical protein [*Yersinia nurmii*] Length: 153 82/90(153) 1–153	WP_049601160.1
	hypothetical protein [*Yersinia ruckeri*] Length: 159 49/70(152) 1–152	WP_038244563.1
PL78_14570 (365)	hypothetical protein [*Yersinia ruckeri*] Length: 411 53/73(75) 335–409	WP_042527563.1
	hypothetical protein [*Yersinia nurmii*] Length: 365 75/82(365) 1–365	WP_049601159.1
PL78_14575 (310) SpoA Ysaq	hypothetical protein [*Yersinia nurmii*] Length: 310 84/92(310) 1–310	WP_049601155.1
	hypothetical protein [*Yersinia ruckeri*] Length: 308 51/67(310) 1–308	WP_038244561.1
PL78_14580 (218) Spap YsaR	type III secretion system protein [*Yersinia nurmii*] Length: 218 96/98(218) 1–218	WP_049601152.1
	type III secretion system protein [*Yersinia ruckeri*] Length: 218 83/92(218) 1–218	WP_042527567.1

PL78_14585 (87) Spaq	type III secretion apparatus protein [*Yersinia nurmii*] Length: 87 94/97(87) 1–87	WP_049601148.1
	hypothetical protein [*Yersinia ruckeri*] Length: 87 88/97(86) 1–86	WP_004722103.1
PL78_14590 (264) SpaR YscT	type III secretion system protein [*Yersinia nurmii*] Length: 264 94/96(264) 1–264	WP_049601145.1
	type III secretion system protein [*Yersinia ruckeri*] Length: 264 79/90(264) 1–264	WP_042527569.1
PL78_14595 (376) SpaS	type III secretion system protein [*Yersinia ruckeri*] Length: 386 76/89(377) 1–374	WP_042527571.1
	type III secretion system protein [*Yersinia nurmii*] Length: 376 94/98(376) 1–376	WP_049601142.1
PL78_14600 (170) SicA	type III secretion protein [*Yersinia ruckeri*] Length: 170 84/91(167) 1–167	gbKFE37947.1
	type III secretion protein [*Yersinia nurmii*] Length: 170 96/97(170) 1–170	WP_049601141.1
PL78_14605 (643) SipB Ysp1	hypothetical protein [*Yersinia nurmii*] Length: 643 89/93(643) 1–643	WP_049601136.1
	hypothetical protein [*Yersinia ruckeri*] Length: 659 43/64(676) 1–643	WP_042527573.1

PL78_14610 (410) SipC Yspc	hypothetical protein [*Yersinia nurmii*] Length: 410 84/91(410) 1–410	WP_049601135.1
	hypothetical protein [*Yersinia ruckeri*] Length: 503 30/54(337) 179–503	WP_038275434.1
PL78_14615 (682) SipD	hypothetical protein [*Yersinia nurmii*] Length: 341 86/92(341) 1–341	WP_049601131.1
	hypothetical protein [*Yersinia ruckeri*] Length: 365 44/64(226) 143–365	WP_038275436.1
PL78_14620 (93)	acyl carrier protein [*Yersinia nurmii*] Length: 91 84/90(92) 1–89	embCNF06932.1
	hypothetical protein [*Yersinia ruckeri*] Length: 94 55/75(73) 19–91	WP_052470858.1
PL78_14625 (128)	secretion protein [*Yersinia nurmii*] Length: 128 93/95(128) 1–128	WP_049601130.1
	secretion protein [*Yersinia mollaretii*] Length: 128 54/72(128) 1–128	WP_004874038.1
PL78_14630 (547)	fumarate hydratase [*Yersinia ruckeri*] Length: 547 98/98(547) 1–547	WP_004722663.1
	fumarate hydratase [*Yersinia nurmii*] Length: 547 99/99(547) 1–547	WP_049601127.1

Yersinia entomophaga general secretion pathway protein T2SS.

Locus (Amino Acid Residues)	**Closest BlastP Orthologue [Species]** **Length: Amino Acid Length of Orthologue** **% Identity/% Similarity (over the Indicated Range of Amino Acid Residues) in Relation to Target Sequence.** **Protein Domain**	**Accession Number**
PL78_08915 (222) LysR	transcriptional regulator [*Yersinia nurmii*] Length: 222 93/95(222) 1–222	WP_049599794.1
	hypothetical protein [*Yersinia ruckeri*] Length: 222 59/76(222) 1–222	WP_042525802.1
PL78_08920 (98)	transposase [*Yersinia enterocolitica*] Length: 180 74/75(97) 22–118	WP_050927038.1
	transposase [Serratia sp. Leaf51] Length: 180 74/75(96) 22–117	WP_056779158.1
PL78_08925 (65)	transposase [Pluralibacter gergoviae] Length: 88 82/88(60) 1–60	WP_048282832.1
	transposase [*Yersinia enterocolitica*] Length: 88 82/88(60) 1–60	WP_050927036.1
PL78_08930 (280) GspK	general secretion pathway protein K [*Yersinia nurmii*] Length: 259 78/87(256) 1–256	embCNE84927.1
	hypothetical protein [*Yersinia ruckeri*] Length: 321 33/52(315) 5–317	WP_038276190.1

PL78_08935 (204) GspJ	type II secretion system protein GspJ [*Yersinia nurmii*] Length: 213 87/94(204) 10–213	WP_049599786.1
	general secretion pathway protein J [*Serratia marcescens* FGI94] Length: 202 34/56(198) 11–200	gbAGB84035.1
PL78_08940 (127) GspI	type II secretion system protein GspI [*Yersinia nurmii*] Length: 127 82/87(127) 1–127	WP_049599784.1
	general secretion pathway protein I [Aeromonas diversa CDC 2478–85] Length: 119 32/61(108) 2–104	gbENY71267.1
PL78_08945 (185)	hypothetical protein [*Yersinia nurmii*] Length: 183 81/90(182) 1–182	WP_049599781.1
	hypothetical protein [*Yersinia ruckeri*] Length: 192 29/48(173) 6–171	WP_038241044.1
PL78_08950 (102) GspI	type II secretion system protein GspG [*Yersinia nurmii*] Length: 150 93/96(150) 1–150	WP_049599778.1
	type II secretion system protein GspG [*Yersinia ruckeri*] Length: 149 76/85(143) 1–143	WP_038241042.1
PL78_08955 (399)	hypothetical protein [*Yersinia nurmii*] Length: 399 93/97(399) 1–399	WP_049599774.1
	hypothetical protein [*Yersinia ruckeri*] Length: 395 50/71(397) 1–393	WP_042525816.1

PL78_08960 (495) GspE	type II secretion system protein GspE [*Yersinia nurmii*] Length: 502 96/98(495) 8–502	WP_049599771.1
	type II secretion system protein E [*Yersinia ruckeri* ATCC 29473] Length: 491 71/85(491) 1–491	gbKGA50644.1
PL78_08965 (651) GspD	general secretion pathway protein GspD [*Yersinia nurmii*] Length: 680 94/96(645) 29–673	WP_053215274.1
	type II secretion system protein GspD [*Yersinia ruckeri*] Length: 650 68/83(633) 21–650	WP_038241119.1
PL78_08970 (187) GspC	hypothetical protein [*Yersinia nurmii*] Length: 189 79/90(188) 1–188	WP_049599768.1
	General secretion pathway protein C [*Yersinia ruckeri* ATCC 29473] Length: 188 32/50(186)	gbEEP93904.1
PL78_08975 (139)	hypothetical protein [*Yersinia nurmii*] Length: 139 100/100(139) 1–139	WP_049599767.1
	hypothetical protein yruck0001_4150 [*Yersinia ruckeri* ATCC 29473] Length: 157 194/97(139) 19–157	gbEEP99541.1
PL78_08980 (94)	No significant similarity	
PL78_08985 tRNA–Gly		

Table S4. *Yersinia entomophaga* accessory virulence determinants: Repeats in Toxin cluster, CdtAB, VIP2, adenylate cyclase, chitinase and chitin binding protein associated regions and putative hemolysins. For graphic depiction refer to Figure 5 of the associated manuscript.

Yersinia entomophaga Repeats in Toxin associated cluster.

Locus (Amino Acid Residues)	**Closest BlastP Orthologue [Species]** **Length: Amino Acid Length of Orthologue** **% Identity/% Similarity (over the Indicated Range of Amino Acid Residues) in Relation to Target Sequence.** **Protein Domain**	**Accession Number**
PL78_16895 (216)	transcriptional regulator [*Yersinia nurmii*] Length: 216 99/100(216) 1–216	WP_049597066.1
	transcriptional regulator [*Yersinia ruckeri*] Length: 216 99/100(216) 1–216	WP_042525316.1
PL78_16900 (907)	tRNA(5–methylaminomethyl–2–thiouridylate) methyltransferase [*Yersinia nurmii*] Length: 907 96/98(907) 1–907	WP_049597067.1
	tRNA(5–methylaminomethyl–2–thiouridylate) methyltransferase [*Yersinia ruckeri*] Length: 907 85/91(907) 1–907	WP_042525315.1
PL78_16905 (384) MFS transporter	MFS transporter [*Yersinia nurmii*] Length: 384 98/99(384)1–384	WP_049597068.1
	MFS transporter [*Yersinia ruckeri*] Length: 384 90/95(384) 1–384	WP_042528242.1
PL78_16910 (4660) RTX	autotransporter adhesin [*Yersinia nurmii*] Length: 4660 93/95(4661) 1–4659	WP_049597069.1
	adhesin [*Yersinia enterocolitica*] Length: 4221 58/72(4103) 179–4220	WP_050915363.1

PL78_16915 (461)	outer membrane channel protein [*Yersinia nurmii*] Length: 461 98/99(461) 1–461	embCNE14355.1
	MULTISPECIES: type I secretion system outer membrane protein [Yersinia] Length: 461 85/91(463) 1–461	WP_050142178.1
PL78_16920 (713) T1SS (CyaE)	putative toxin transport protein [*Yersinia nurmii*] Length: 713 97/98(713) 1–713	embCNE14391.1
	putative toxin transport protein [*Yersinia massiliensis*] Length: 760 87/92(712) 51–760	embCNH58774.1
PL78_16925 (389) HlyD	secretion protein HlyD [*Yersinia nurmii*] Length: 389 99/99(389) 1–289	WP_049597070.1
	secretion protein HlyD [*Yersinia frederikseniir*] Length: 389 88/95(389) 1–389	WP_050140418.1
PL78_16930 (370)	membrane protein [*Yersinia nurmii*] Length: 370 97/98(370)1–370	WP_049597071.1
	membrane protein [*Yersinia ruckeri*] Length: 376 90/94(376)1–376	WP_038251489.1
PL78_16945 (183)	GNAT family acetyltransferase [*Yersinia nurmii*] Length: 183 97/98(183) 1–183	WP_049597072.1
	GNAT family acetyltransferase [*Yersinia ruckeri*] Length: 178 81/88(178) 1–178	WP_042525312.1

PL78_16950 (376)	beta–lactam binding protein AmpH [*Yersinia nurmii*] Length: 376 99/98(367)10–376	embCNE14590.1
	beta–lactam–binding protein [*Yersinia ruckeri*] Length: 381 91/94(367)15–381	WP_042525310.1
PL78_16955 (475)	hypothetical protein yinte0001_11730 [*Yersinia intermedia* ATCC 29909] Length: 512 87/91(485) 5–489	gbEEQ17977.1
	MULTISPECIES: MFS transporter [Yersinia] Length: 508 87/91(485) 1–485	WP_032907368.1
PL78_16960 (330)	MBL fold hydrolase [*Yersinia nurmii*] Length: 330 94/96(330) 1–330	WP_045844204.1
	MBL fold metallo–hydrolase [*Yersinia ruckeri*] Length: 330 83/89(330) 1–330	WP_049597075.1
PL78_16965 (325)	hypothetical protein [*Yersinia nurmii*] Length: 325 98/98(325) 1–325	WP_050475862.1
	hypothetical protein [Herbaspirillum rhizosphaerae] Length: 326 71/82(324) 1–324	WP_049597076.1

Yersinia entomophaga putative virulence cluster CdtAB.

Locus (Amino Acid Residues)	Closest BlastP orthologue [Species] Length: Amino Acid Length of Orthologue % Identity/% Similarity (over The Indicated Range of Amino Acid Residues) in Relation to Target Sequence. Protein Domain	Accession Number
PL78_18410	hypothetical protein [*Yersinia nurmii*] Length: 241 96/97(241) 1–241	WP_049600373.1
	hypothetical protein [*Serratia fonticola*] Length: 249 46/63(241) 12–249	WP_059200486.1
PL78_18415 (371)	D–alanine—D–alanine ligase [*Yersinia nurmii*] Length: 371 98/99(371) 1–367	WP_049600376.1
	D–alanine—D–alanine ligase [*Yersinia ruckeri*] Length: 368 92/97(367) 1–367	WP_038276041.1
PL78_18420 (211)	yheo–like PAS domain [*Yersinia nurmii*] Length: 220 95/97(220) 1–220	embCNE94733.1
	yheo–like PAS domain [*Yersinia frederikseniir*] Length: 230 6/92(217) 12–228	embCNK81303.1
PL78_18425 (323)	serine dehydratase [*Yersinia nurmii*] Length: 323 97/98(323) 1–323	WP_049600379.1
	serine dehydratase [*Yersinia intermedia*] Length: 322 79/88(321) 1–321	WP_050077290.1

PL78_18430 (293)	alpha/beta hydrolase [*Yersinia nurmii*] Length: 293 95/96(293) 1–293	WP_049600386.1
	alpha/beta hydrolase [*Serratia marcescens*] Length: 294 63/77(294) 1–294 pfam00561; COG1075	WP_033635162.1
PL78_18435 (108)	acid–resistance protein [*Yersinia nurmii*] Length: 108 95/98(108) 1–108	WP_049600389.1
	acid–resistance protein [*Yersinia rohdei*] Length: 110 76/86(110) 1–110	WP_032816440.1
PL78_18440 (190) CdtA	hypothetical protein [*Yersinia nurmii*] Length: 190 83/90(189) 1–189	WP_049600392.1
	hypothetical protein [*Yersinia ruckeri*] Length: 191 59/74(182) 10–189 pfam03498: CDtoxinA	WP_052470825.1
PL78_18445 (296) CdtB	cytolethal distending toxin subunit B [*Yersinia ruckeri*] Length: 298 64/78(294)1–294	embCNB14664.1
	hypothetical protein [*Yersinia nurmii*] Length: 296 91/96(296) 1–296	WP_049600395.1
PL78_18450 (466)	hypothetical protein [*Yersinia nurmii*] Length: 466 94/97(466) 1–466	WP_049600397.1
	hypothetical protein [*Yersinia ruckeri*] Length: 463 73/85(466) 1–463	WP_049689405.1

PL78_18455 (282)	kinase [*Yersinia nurmii*] Length: 282 99/99(282) 1–282	WP_049600400.1
	serine/threonine protein kinase [*Yersinia ruckeri*] Length: 282 93/96(282) 1–282	WP_004721381.1

Yersinia entomophaga putative VIP2 associated region.

Locus (Amino Acid Residues)	**Closest BlastP Orthologue [Species]** **Length: Amino Acid Length of Orthologue** **% Identity/% Similarity (over the Indicated Range of Amino Acid Residues) in Relation to Target Sequence.** **Protein Domain**	**Accession Number**
PL78_16130 (293)	transcriptional regulator [*Yersinia nurmii*] Length: 293 96/96(293) 1–293	WP_049596942.1
	transcriptional regulator [*Yersinia ruckeri*] Length: 287 86/92(287) 1–287	WP_042525447.1
PL78_16135 (158)	Na(+)–translocating NADH–quinone reductase subunit E [*Yersinia nurmii*] Length: 158 99/99(158) 1–158	WP_049596943.1
	a+–translocating NADH–quinone reductase subunit E [*Yersinia ruckeri*] Length: 158 91/93(158) 1–158	WP_004717931.1
PL78_16140 (321)	glucokinase [*Yersinia nurmii*] Length: 321 96/97(321) 1–321	WP_049596944.1
	glucokinase [*Yersinia ruckeri*] Length: 321 90/94(321) 1–321	WP_042525445.1
PL78_16145 (402) VIPA	hypothetical protein [*Yersinia enterocolitica*] Length: 400 50–67(403) 1–400	WP_005175826.1
	NAD:arginine ADP–ribosyltransferase [*Yersinia enterocolitica*] Length: 402 50/66(399) 9–402 (pfam01129)	embCRY18359.1

PL78_16150 (414)	membrane protein [*Yersinia nurmii*] Length: 414 98/99(414) 1–414	WP_049596945.1
	membrane protein [*Yersinia ruckeri*] Length 415 92/95(415) 1–415	WP_004717929.1

Yersinia entomophaga putative virulence cluster adenylate cyclase associated region.

Locus (Amino Acid Residues)	**Closest BlastP Orthologue [Species]** **Length: Amino Acid Length of Orthologue** **% Identity/% Similarity (over the Indicated Range of Amino Acid Residues) in Relation to Target Sequence.** **Protein Domain**	**Accession number**
PL78_08385 (330)	serine/threonine dehydratase [*Yersinia nurmii*] Length: 330 99/100(330) 1–330	WP_049599166.1
	serine/threonine dehydratase [*Yersinia aldovae*] ength: 330 94/97(330) 1–330	WP_004699735.1
PL78_08390 (61)	Nil similarity	
PL78_08395 (351)	toxin protein [*Yersinia nurmii*] Length: 402 89/95(350)52–401	embCNE75600.1
	adenylate cyclase [Serratia sp. Leaf50] Length: 369 56/76(356) 13–402	WP_055772549.1
	adenylate cyclase–1 [Candidatus Hamiltonella defensa] Length: 437 55/74(345) 77–415	WP_015873608.1
	calmodulin–sensitive adenylate cyclase [Bacillus anthracis] Length: 800 35/52(201) 306–503 pfam03497 Anthrax_toxA	WP_000197748.1

PL78_08400 (931)	peptidase M16 [*Yersinia nurmii*] Length: 931 94/96(931)1–931	WP_049599163.1
	peptidase M16 [*Yersinia enterocolitica*] Length: 927 77/87(931) 1–927	WP_050157122.1

Yersinia entomophaga chitinase.

Locus (Amino Acid Residues)	Closest BlastP Orthologue [Species] Length: Amino Acid Length of Orthologue % Identity/% Similarity (over the Indicated Range of Amino Acid Residues) in Relation to Target Sequence. Protein Domain	Accession Number
PL78_11905 (450)	glutathione–disulfide reductase [*Yersinia nurmii*] Length: 450 99/99(450) 1–450	WP_049597320.1
	glutathione–disulfide reductase [*Yersinia intermedia*] Length: 450 97/98(450) 1–450	WP_050073664.1
PL78_11910 (351)	glycosyl hydrolase family protein [*Yersinia nurmii*] Length: 352 98/98(352)1–352	embCNE26027.1
	chitinase [Paenibacillus dauci] Length: 414 60/77(341) 13–351	WP_052714100.1
PL78_11915 (396)	cystathionine beta–lyase [*Yersinia nurmii*] Length: 396 97/98(396) 1–396	WP_049597321.1
	cystathionine beta–lyase [*Yersinia ruckeri*] Length: 396 96/98(396) 1–396	WP_038242896.1

Yersinia entomophaga chitin binding fimbrial cluster, Chi–Fim.

Locus (Amino Acid Residues)	**Closest BlastP Orthologue [Species]** **Length: Amino Acid Length of Orthologue** **% Identity/% Similarity (over the Indicated Range Of Amino Acid Residues) in Relation to Target Sequence.** **Protein Domain**	**Accession Number**
PL78_08260 (176)	outer membrane lipoprotein Blc [*Yersinia nurmii*] Length: 176 98/99(176) 1–176	embCNE76662.1
	membrane protein [*Yersinia ruckeri*] Length: 180 89/96(174) 1–174	WP_042528366.1
PL78_08265 (104)	multidrug transporter [*Yersinia nurmii*] 99/100(104) 1–104	WP_049599231.1
	multidrug transporter [*Yersinia ruckeri*] 95/99(104) 1–104	WP_038241885.1
PL78_08270 (174)	fimbrial protein [*Yersinia nurmii*] Length: 174 99/99(174) 1–174	WP_049599227.1
	fimbrial protein [*Yersinia ruckeri*] Length: 174 89/95(174) 1–174	WP_042527048.1
PL78_08275 (660)	pilus assembly protein [*Yersinia nurmii*] Length: 805 99/99(660) 128–787	WP_049599224.1
	pilus assembly protein [*Yersinia ruckeri*] Length: 803 85/92(659) 126–784	WP_052470850.1

PL78_08280(244)	fimbrial protein [*Yersinia nurmii*] Length: 244 Legth: 244 97/97(244) 1–244	WP_049599223.1
	fimbrial protein [*Yersinia ruckeri*] Length: 244 81/89(244) 1–244	WP_042527047.1
PL78_08285 (330) pfam00419	hypothetical protein [*Yersinia nurmii*] Length: 330 97/98(330) 1–330	WP_049599220.1
	fimbrial family protein [*Yersinia ruckeri*] Length: 330 88/93(330) 1–330	gbAJI95306.1
PL78_08290 (203)	helix–turn–helix transcriptional regulator [*Yersinia ruckeri*] 97/98(202) 1–202	WP_038241888.1
PL78_08295 (197)	chitin–binding protein [*Yersinia ruckeri*] Length: 197 89/93(196) 1–196	WP_052470849.1
PL78_08300 (160)	elongation factor P [*Yersinia ruckeri*] Length: 188 100/100(160) 1–160	WP_004722438.1
	elongation factor P [*Yersinia nurmii*] Length: 188 99/99(160) 1–160	WP_049599212.1

Yersinia entomophaga putative chitin binding fimbrial cluster, Chi–SrfAB.

Locus (Amino Acid Residues)	**Closest BlastP Orthologue [Species]** **Length: Amino Acid Length of Orthologue** **% Identity/% Similarity (over the Indicated Range of Amino Acid Residues) in Relation To Target Sequence.** **Protein Domain**	**Accession Number**
PL78_05305 (216)	Vat family streptogramin A O–acetyltransferase [*Yersinia nurmii*] Length: 216 95/96(216) 1–216	WP_049598340.1
	streptogramin A acetyl transferase [Enterobacter sp. 638] Length: 216 74/90(210) 1–216	gbABP59079.1
PL78_05310 (216)	chitin–binding protein [*Yersinia nurmii*] Length: 216 93/95(216)–1–216	WP_049598342.1
	chitin–binding protein [*Yersinia intermedia*] Length: 216 71/78(215)–1–215	WP_005183097.1
PL78_05315 (464) SrfA	virulence factor [*Yersinia nurmii*] Length: 444 91/92(451)1–444	embCNE60077.1
	virulence effector protein [*Yersinia ruckeri*] Length: 442 65/71(471)1–442	WP_004717438.1
PL78_05320 (994) SrfB	virulence factor SrfB [*Yersinia nurmii*] Length: 994 98/98(994) 1–994	WP_049598346.1
	virulence factor SrfB [*Yersinia ruckeri*] Length 994 87/93(994) 1–994	WP_038242595.1

PL78_10835 (460) virulence factor	virulence factor [*Yersinia nurmii*] Length: 816 94/96(433) 1–433	WP_049598348.1
	virulence factor [*Yersinia ruckeri*] Length: 816 72/83(433) 1–433 pfam10139: Virul_Fac putative bacterial virulence factor	WP_038275949.1
PL78_05330 (189)	hypothetical protein [*Yersinia nurmii*] Length 189 96/97(189) 1–189	WP_049598349.1
	serine hydrolase family protein [*Yersinia ruckeri*] Length: 186 78/87(185) 1–185	gbAJI94666.1
	hypothetical protein [Xenorhabdus doucetiae] Length: 185 87/73(186) 1–185	WP_045973197.1
PL78_05335 (195)	Uncharacterized distant relative of cell wall–associated hydrolases [*Yersinia nurmii*] Length: 196 98/98(195) 2–196	embCNE60215.1
	hypothetical protein MU9_2339 [Morganella morganii subsp. morganii KT] 63/79(188) 9–196	gbAGG31384.1

Yersinia entomophaga putative hemolysin's.

Locus (Amino Acid Residues)	Closest BlastP Orthologue [Species] Length: Amino Acid Length of Orthologue % identity/% Similarity (over the Indicated Range of Amino Acid Residues) in Relation to Target Sequence. Protein Domain	Accession Number
PL78_04365 (1624)	hemolysin [*Yersinia nurmii*] Length: 1625 96/97(1625)1–1625	WP_049597670.1
	hemolysin [*Yersinia ruckeri*] Length: 1630 57/93 (1630)1–1628	WP_045844326.1
	hemolysin [Serratia proteamaculans] Length: 1615 57/71(1646) 1–1615	WP_012147176.1
PL78_11060 (1645)	hemolysin [*Yersinia nurmii*] Length: 1645 95/97(1645)1–1645	WP_049598079.1
	hemolysin [*Yersinia ruckeri*] Length: 1630 70/82(1637)1–1627	WP_004719456.1
	hemolysin [Serratia liquefaciens] Length: 1615 53/69(1–1615) 1–1615	WP_046372512.1
PL78_09050(221)	hemolysin III family protein [*Yersinia nurmii*] Length: 221 98/100(221) 1–221	WP_049600002.1
	hemolysin III [*Yersinia intermedia*] Length: 237 83/89(237) 1–237	embCQJ63471.1

Table S5. *Yersinia entomophaga* cell adhesins, fimbriae, Lipopolysaccharide and cellulose encoding clusters. For graphic depiction refer to Figure 7 of the associated manuscript.

Yersinia entomophaga fimbrial associated region.

Locus (Amino Acid Residues)	**Closest BlastP Orthologue [Species]** **Length: Amino Acid Length of Orthologue** **% identity/% Similarity (over the Indicated Range of Amino Acid Residues) in Relation to Target Sequence.** **Protein Domain**	**Accession Number**
PL78_08255 (118)	fumarate reductase [*Yersinia nurmii*] Length: 118 99/100(118) 1–118	WP_049599234.1
	fumarate reductase subunit D [*Yersinia ruckeri*] 97/100(118) 1–118	WP_004722457.1
PL78_08260 (176)	outer membrane lipoprotein Blc [*Yersinia nurmii*] Length: 176 98/99(176) 1–176	embCNE76662.1
	membrane protein [*Yersinia ruckeri*] Length: 180 89/96(174) 1–174	WP_042528366.1
PL78_08265 (104)	multidrug transporter [*Yersinia nurmii*] Length: 104 99/100(104) 1–104	WP_049599231.1
	multidrug transporter [*Yersinia ruckeri*] Length: 104 95/99(104) 1–104	WP_038241885.1
PL78_08270 (174)	fimbrial protein [*Yersinia nurmii*] Length: 174 99/99(174) 1–174	WP_049599227.1
	fimbrial protein [*Yersinia ruckeri*] Length: 174 90/95(174) 1–174	WP_042527048.1

PL78_08275 (678) FimD/PapC	pilus assembly protein [*Yersinia nurmii*] Length: 805 98/99(678) 128–805	WP_049599224.1
	pilus assembly protein [*Yersinia ruckeri*] Length: 803 84/91(678) 126–803	WP_052470850.1
PL78_08280 (244) PapD	fimbrial protein [*Yersinia nurmii*] Length: 244 97/97(244) 1–244	WP_049599223.1
	fimbrial protein [*Yersinia ruckeri*] Length: 244 81/89(244) 1–244	WP_042527047.1
PL78_08285 (330)	hypothetical protein [*Yersinia nurmii*] Length: 330 97/98(330) 1–330	WP_049599220.1
	fimbrial family protein [*Yersinia ruckeri*] Length: 330 88/93(330) 1–330	gbAJI95306.1
PL78_08290 (203)	helix–turn–helix transcriptional regulator [*Yersinia nurmii*] Length: 199 77/86(202)1–198	WP_049599217.1
	helix–turn–helix transcriptional regulator [*Yersinia ruckeri*] Length: 203 97/98(202) 1–202	WP_038241888.1
PL78_08295 (197)	chitin–binding protein [*Yersinia ruckeri*] Length: 197 89/93(196) 1–196	WP_052470849.1
PL78_08300 (188)	elongation factor P [*Yersinia nurmii*] Length: 188 99/100(188) 1–188	WP_049599212.1
	elongation factor P [*Yersinia ruckeri*] Length: 188 99/99(188) 1–188	WP_004722438.1

PL78_0805 (342)	lysine 2,3–aminomutase [*Yersinia nurmii*] Length: 342 99/99(342) 1–342	WP_049599209.1
	EF–P beta–lysylation protein EpmB [*Yersinia ruckeri*] Length: 342 93/95(341) 1–341	WP_042527045.1

Yersinia entomophaga fimbrial associated island FAI$_{YE96}$.

Locus (Amino Acid Residues)	**Closest BlastP Orthologue [Species]** **Length: Amino acid Length of Orthologue** **% identity/% Similarity (over the Indicated Range of Amino Acid Residues) in Relation to Target Sequence.** **Protein Domain**	**Accession Number**
PL78_17260 tRNA–Asn	tRNA–Asn aagcaaaaaacccgactaagtttccttaatcgggcttctctaatatggctcctctgactggactcgaaccagtgacatacggatt aacagtccgccgttctaccgactgaactacagaggaatcgtgtgaacggggcg	
PL78_17265 (425)	Raffinose permease [*Yersinia rohdei*] Length: 430 92/95(422) 9–430	WP_004716742.1
	galactoside permease [Serratia sp. Leaf51] Length: 428 73/86(406) 7–412	WP_056775892.1
PL78_17270 (708)	alpha–galactosidase [*Yersinia rohdei*] Length: 707 80/89(708) 1–707	WP_049616652.1
	alpha–galactosidase [*Serratia fonticola*] Length: 708 75/85(708) 1–708	WP_024483295.1

PL78_17275 (336) Reg	transcriptional regulator [*Yersinia rohdei*] Length: 336 75/82(333) 1–333	WP_004716744.1
	transcriptional regulator [*Sodalis praecaptivus*] Length: 336 64/75(331) 1–329	WP_025421693.1
	transcriptional regulator [*Serratia fonticola*] Length: 335 63/76(326) 1–324	WP_024527340.1
PL78_17280 (236) Chap	molecular chaperone [*Yersinia nurmii*] Length: 236 93/97(236) 1–236	WP_049597187.1
	molecular chaperone [*Yersinia frederikseniir*] Length: 250 62/74(239) 7–244	WP_050141295.1
PL78_17285 (421) StbD	putative fimbrial usher protein StbD [*Yersinia nurmii*] Length: 440 98/98(421) 20–440	embCNE17004.1
	hypothetical protein [*Yersinia enterocolitica*] Length: 444 81/90(416) 29–444	WP_019082823.1
PL78_17290 (856) Fim	fimbrial protein [*Yersinia nurmii*] Length: 858 96/98(858) 1–858	WP_049597131.1
	fimbrial protein [*Yersinia enterocolitica*] Length: 874 65/77(876) 1–874	WP_050160997.1
PL78_17295 (244) PapD	pilus assembly protein [*Yersinia nurmii*] Length: 244 96/96(244) 1–244	WP_049597132.1
	pilus assembly protein [*Yersinia mollaretii*] Length: 243 73/82(244) 1–243	WP_049648727.1

PL78_17300 (176) Fim	fimbrial protein [*Yersinia nurmii*] Length: 176 98/98(176) 1–176	WP_049597133.1
	fimbrial protein [*Yersinia pekkanenii*] Length: 176 76/88(176) 1–176	WP_049613690.1
PL78_17305 (1207)	histidine kinase [*Yersinia nurmii*] Length: 1207 95/97(1207) 1–1207	WP_049613690.1
	putative virulence sensor protein [*Yersinia intermedia*] Length: 1288 68/81(1234) 22–1273	embCRY76056.1
PL78_17310 (209) LuxR	putative two–component response regulator [*Yersinia nurmii*] Length: 209 98/99(209) 1–209	embCNE17197.1
	DNA–binding response regulator [*Yersinia intermedia*] Length: 210 93/96(208) 3–210	WP_050075308.1
PL78_17315 (59)	hypothetical protein [*Yersinia nurmii*] Length: 59 91/93(58) 1–58	WP_049597134.1
PL78_17320 tRNA–Asn	tRNA–Asn aagcaaaaaacccgactaagtttccttaatcgggcttctctaatatggctcctctgactggactcgaaccagtgacatacggatt aacagtccgccgttctaccgactgaactacagaggaatcgtgtgaacggggcg	

Yersinia entomophaga lipopolysaccharide cluster.

Locus (Amino Acid Residues)	**Closest BlastP Orthologue [Species]** **Length: Amino Acid Length of Orthologue** **% Identity/% Similarity (over the Indicated Range of Amino Acid Residues) in Relation to Target Sequence.** **Protein Domain**	**Accession Number**
PL78_00680 (327) DdhD	CDP–6–deoxy–delta–3,4–glucoseen reductase [*Yersinia nurmii*] Length: 327 97/99(327) 1–327	WP_049598615.1
	CDP–6–deoxy–delta–3,4–glucoseen reductase [*Yersinia similis*] Length: 329 83/94(329) 1–329	WP_054878293.1
PL78_00685 (257) DdhA	cytidylyltransferase [*Yersinia nurmii*] Length: 257 100/100(257) 1–257	WP_049598616.1
	glucose–1–phosphate cytidylyltransferase [*Yersinia ruckeri*] Length: 257 99/99(257) 1–257	WP_038275604.1
PL78_00690 (299) DdhB	C CDP–glucose 4%2C6–dehydratase [*Yersinia nurmii*] Length: 357N 99/99(357) 1–357	embCNE67016.1
	CDP–glucose 4,6–dehydratase [*Yersinia pseudotuberculosis* IP 31758] Length: 391 90/94(357)35–391	gbABS48236.1
PL78_00695 (437) DdhC	lipopolysaccharide biosynthesis protein RfbH [*Yersinia nurmii*] Length: 437 99/100(437) 1–437	WP_049598618.1
	CDP–4–keto–6–deoxy–D–glucose–3–dehydrase [*Yersinia pseudotuberculosis*] Length: 437 97/98(437) 1–437	gbADI59424.1
PL78_00700 (283) Prt	paratose synthase [*Yersinia enterocolitica*] Length: 285 70/84(283) 1–283	WP_057647476.1

PL78_00705 (338)	CDP–paratose 2–epimerase [*Yersinia mollaretii*] Length: 338 84/92(338)1–338	ref_049608459.1
PL78_00710 (438) Wzx	CDP–paratose 2–epimerase [*Yersinia mollaretii*] Length: 338 84/92(338) 1–338	WP_049608459.1
PL78_00715 (333) WbcC	hypothetical protein [*Yersinia nurmii*] Length: 336 77/90(333) 4–336	WP_049598623.1
	putative glycosyltransferase [*Yersinia pseudotuberculosis*] Length: 339 59/75(331) 4–334	embCNK90709.1
PL78_00720 (417) Wzy O antigen	histidine kinase [*Yersinia pseudotuberculosis*] Length: 406 51/70(404) 1–404	WP_050103368.1
PL78_00725 (337) WbyK RfaB	mannosyltransferase [*Yersinia nurmii*] Length: 337 Range 1: 1 to 337 0/337(0%)	WP_049598627.1
	mannosyltransferase [*Yersinia pseudotuberculosis*] Length: 337 78/88(337)1–337	WP_012304490.1
PL78_00730 (373) Gmd	GDP–mannose 4,6–dehydratase [*Yersinia nurmii*] Length: 373 100/100(373) 1–373	WP_049598628.1
	GDP–mannose 4,6–dehydratase [*Yersinia pseudotuberculosis*] Length: 373 96/98(373) 1–373	P_011191888.1

PL78_00735 (321) Fcl	GDP–L–fucose synthetase [*Yersinia nurmii*] Length: 323 98/99(321) 3–323	embCNE67246.1
	GDP–fucose synthetase [*Yersinia similis*] Length: 321 90/94(321) 1–321	WP_054878416.1
PL78_00740 (154) Gmm	GDP–mannose mannosyl hydrolase [*Yersinia nurmii*] Length: 154 97/97(154) 1–154	WP_049598631.1
	GDP–mannose mannosyl hydrolase [*Photorhabdus temperata*] Length: 154 65/81(154) 1–154	WP_023043826.1
PL78_00745 (468) ManC	mannose–1–phosphate guanyltransferase [*Yersinia nurmii*] Length: 468 99/98(468) 1–468	WP_049598633.1
	mannose–1–phosphate guanyltransferase [*Yersinia enterocolitica*] Length: 468 87/94(468)1–468	WP_050142517.1
PL78_00750 (247) WbyL	glycosyl transferase [*Yersinia nurmii*] Length: 247 98/98(247) 1–247	WP_049598721.1
	glycosyl transferase [*Yersinia mollaretii*] Length: 247 76/88(247) 1–247	WP_004873391.1
PL78_00755 (256) ManB	phosphomannomutase [*Yersinia nurmii*] Length: 456 99/99(455)1–456	WP_049598635.1
	phosphomannomutase [*Yersinia pseudotuberculosis*] Length: 457 85/91(455) 1–455	WP_050093032.1

PL78_00760 (384) Wzz	chain–length determining protein [*Yersinia nurmii*] Length: 384 96/98(384)1–384	WP_049598637.1
	chain–length determining protein [*Yersinia ruckeri*] Length: 384 76/90(382)1–382	WP_038275531.1
PL78_00765 (436)	inosine/guanosine kinase [*Yersinia nurmii*] Length: 436 99/99(436)1–436	WP_049598639.1
	inosine/guanosine kinase [*Yersinia ruckeri*] ength: 436 96/98(436)1–436	WP_038243753.1
PL78_00770 (563)	cation:proton antiport protein [*Yersinia nurmii*] Length: 563 99/100(563)1–563	WP_049598641.1
	cation:proton antiport protein [*Yersinia intermedia*] Length: 563 94/97 (563) 1 to 563	WP_042569300.1
PL78_00775 (404)	fosmidomycin resistance protein [*Yersinia nurmii*] Sequence ID: Length: 404 98/98(404)1–404	WP_049598644.1
	fosmidomycin resistance protein [*Yersinia enterocolitica*] Length: 410 86/91(410)1–410	WP_050155900.1
PL78_00780 (550) UshA	bifunctional UDP–sugar hydrolase/5'–nucleotidase [*Yersinia nurmii*] Length: 550 99/99(550)1–550	WP_049598646.1
	bifunctional UDP–sugar hydrolase/5'–nucleotidase [*Yersinia ruckeri*] Length: 550 97/98(550) 1–550	WP_038275532.1

Table S6. *Yersinia entomophaga* countermeasures: ColicinV, Sod, and non–ribosomal peptide synthetase.

Yersinia entomophaga Colicin V.

Locus (Amino Acid Residues)	Closest BlastP Orthologue [Species] Length: Amino Acid Length of Orthologue % Identity/% Similarity (over the Indicated Range of Amino Acid Residues) in Relation to Target Sequence. Protein Domain	Accession Number
PL78_16520 (246) Colicin V	cell division protein DedD [*Yersinia nurmii*] Length: 246 95/96(245)1–246	WP_049597003.1
	cell division protein DedD [*Yersinia ruckeri*] Length: 241 80/86(247)1–241	WP_038244265.1
PL78_16525 (169)	colicin V production protein [*Yersinia nurmii*] Length: 169 99/100(169)1–169	WP_049597004.1
	colicin V production protein [*Yersinia frederikseniir*] Length: 169 98/99(169)1–169	WP_050106079.1
PL78_16530 (486)	amidophosphoribosyltransferase [*Yersinia nurmii*] Length: 505 99/99(505)1–505	WP_049597005.1
	amidophosphoribosyltransferase [*Yersinia ruckeri*] Length: 505 98/99(505)1–505	WP_004717879.1

Yersinia entomophaga superoxide dismutase.

Locus (Amino Acid Residues)	Closest BlastP Orthologue [Species] Length: Amino Acid Length of Orthologue % Identity/% Similarity (over the Indicated Range of Amino Acid Residues) in Relation to Target Sequence. Protein Domain	Accession Number
PL78_05910 (192) SodB	superoxide dismutase [*Yersinia nurmii*] Length: 192 99/100(192)1–192	WP_049600140.1
	superoxide dismutase [*Yersinia ruckeri*] Length: 192 91/96(192) 1–192	WP_004717636.1
PL78_12235 (208) SodA	superoxide dismutase [*Yersinia nurmii*] Length: 208 99/100(208)1–208	WP_049597374.1
	Superoxide dismutase [Mn] [*Yersinia ruckeri* ATCC 29473] Length: 210 96/98(208)3–210	gb|EEQ00149.1
PL78_14360 (174) Sod	superoxide dismutase [*Yersinia nurmii*] Length: 174 95/95(174) 1–174	WP_049601253.1
	superoxide dismutase [*Yersinia enterocolitica*] Length: 174 81/89(174)1–174	WP_046051564.1

Yersinia entomophaga non–ribosomal peptide synthetase.

Locus (Amino Acid Residues)	Closest BlastP Orthologue [Species] Length: Amino Acid Length of Orthologue % Identity/% Similarity (over the Indicated Range of Amino Acid Residues) in Relation to Target Sequence. Protein Domain	Accession Number
PL78_15600 (350)	hydroxymethylpyrimidine/phosphomethylpyrimidine kinase [*Yersinia nurmii*] Length: 266 97/98(266) 1–266	WP_049597164.1
	hydroxymethylpyrimidine/phosphomethylpyrimidine kinase [*Yersinia ruckeri*] Length: 266 88/93(288) 1–266	WP_038241377.1
PL78_15605 (288)	hypothetical protein [*Yersinia nurmii*] Length: 288 95/96(288) 1–288	WP_049596853.1
	hypothetical protein [*Yersinia ruckeri*] Length: 288 80/88(288) 1–288	WP_004717978.1
PL78_15610 (152) Ivy	hypothetical protein [*Yersinia nurmii*] Length: 152 95/96(152) 1–152	WP_049596854.1
	Inhibitor of vertebrate lysozyme [*Yersinia ruckeri* ATCC 29473] Length: 153 84/92(152) 1–153	gb|EEQ00208.1
PL78_15615 (3939) non–ribosomal peptide synthetase	non–ribosomal peptide synthetase [*Yersinia nurmii*] Length: 3941 94/96(3944) 1–3941	WP_049596855.1
	hypothetical protein [*Serratia marcescens*] Length: 4849 40/57(3581) 2–3497	WP_060448349.1

PL78_15620 (189)	transposon DNA–invertase [*Yersinia nurmii*] Length: 189 99/99(189) 1–189	WP_049596856.1
	DNA invertase [Methylophaga aminisulfidivorans] Length: 191 74/87(187)1–187	WP_007143928.1
	DNA invertase [Methylophaga aminisulfidivorans] Length: 191 74/87(187)1–187	WP_007143928.1

Yersinia entomophaga non–ribosomal peptide synthetase.

Locus (Amino Acid Residues)	**Closest BlastP Orthologue [Species]** **Length: Amino Acid Length of Orthologue** **% Identity/% Similarity (over the Indicated Range of Amino Acid Residues) in Relation to Target Sequence.** **Protein Domain**	**Accession Number**
PL78_04160 (191)	HutD family protein [*Yersinia nurmii*] Length: 191 88/93(191)1–191	WP_049597639.1
	HutD family protein [*Yersinia ruckeri*] Length: 190 72/82(187) 1–186	WP_042524807.1
PL78_04165 (1844) non–ribosomal peptide synthetase	non–ribosomal peptide synthetase [*Yersinia nurmii*] Length: 1844 92/95(1844)1–1844	WP_049597640.1
	pyochelin synthetase [Brevibacillus laterosporus] Length: 1838 47/65(1838)8–1837	WP_031412270.1

PL78_04170 (78)	MULTISPECIES: transposase [*Enterobacteriaceae*] Length: 92 97/98(92)1–92	WP_012442396.1
	transposase [*Yersinia ruckeri*] Length: 92 95/96(92)1–92	WP_038245923.1
PL78_04175 (283)	transposase [*Yersinia pekkanenii*] Length: 283 99/99(283) 1–283	WP_049615490.1
	integrase [*Erwinia tasmaniensis*] Length: 283 99/99(283) 1–283	WP_012442397.1