Table S1. Summary of open reading frames and putative functions from plasmids harvested from *Edwardsiella piscicida* isolates from different hosts and geographic origins. Conserved domains and putative product/function of plasmid-encoded ORFs were predicted using BLASTX, with an e-value cut-off of 1e-02 or lower. Physical maps of complete nucleotide sequences of plasmids harvested from *E. piscicida* are displayed in Figure 7.

Plasmid Source	**ORF**	**Location (+/-)**	**Conserved domain; putative product; function**	**alignment and identity**	**E-value**
F373.2 HL1 HL25 HL32 RBR8 ACC69 CAQ 8.10 CAQ 10.10 CAQ 39	Group - 1	493..1134 (+)	RloB superfamily; hypothetical protein of unknown function; most similar to hypothetical protein [*Klebsiella pneumoniae*]; GenBank WP_048991273.1	115/202 (57%)	4.00E-77
	Group - 2	1152..1337 (+)	hypothetical protein of unknown function; most similar to hypothetical protein G972_04939 [*Escherichia coli* UMEA 3355-1]; GenBank EQZ07072.1	37/51 (78%)	7.00E-13
	Group - 3	1298..1453 (-)	replication initiation factor; most similar to replication initiation protein [*Enterobacter cloacae*]; GenBank WP_048210874.1	34/56 (61%)	1.00E-10
	Group - 4	1915..2091 (-)	Rop superfamily; RNA polymerase; most similar to RNA polymerase [*Edwardsiella tarda*]; GenBank WP_035607970.1	40/56 (71%)	5.00E-09
	Group - 5	3013..499 (+)	P-loop NTPase superfamily; hypothetical protein of unknown function; most similar to hypothetical protein [*Klebsiella pneumoniae*]; GenBank WP_048991271.1	215/419 (51%)	8.00E-155
PB 07-309	PB07-309-1	677..1144 (+)	hypothetical protein of unknown function; most similar to hypothetical protein [Enterobacteriaceae]; GenBank WP_039023474.1	127/151 (84%)	1.00E-89
	PB07-309-2	1328..1483 (-)	hypothetical protein of unknown function; most similar to replication initiation protein [Enterobacter]; GenBank WP_052684121.1	29/42 (69%)	9.00E-10
	PB07-309-3	1946..2242 (-)	hypothetical protein of unknown function; most similar to hypothetical protein [*Edwardsiella tarda*]; GenBank WP_034166090.1	24/36 (67%)	1.00E-08

	PB07-309-4	2744..279 (-)	hypothetical protein of unknown function; most similar to hypothetical protein [*Escherichia coli*]; GenBank WP_052266651.1	170/192 (89%)	1.00E-122
S11-285	S11-285-1	10..606 (+)	hypothetical protein of unknown function; most similar to hypothetical protein [*Edwardsiella tarda*]; GenBank WP_034166090.1	140/147 (95%)	2.00E-91
	S11-285-2	879..1529 (+)	hypothetical protein of unknown function; most similar to hypothetical protein [*Pectobacterium carotovorum*]; GenBank WP_039520268.1	181/216 (84%)	4.00E-133
	S11-285-3	1596..2534 (-)	Replicase superfamily; replicase protein most similar to replicase [Enterobacteriaceae]; GenBank WP_038870790.1	257/308 (83%)	2.00E-179
SC 09-03	SC09-03-1	397..702 (-)	hypothetical protein of unknown function; most similar to hypothetical protein [uncultured bacterium]; GenBank AET87465.1	101/101 (100%)	8.00E-65
	SC09-03-2	734..880 (-)	hypothetical protein of unknown function; most similar to Resolvase (plasmid) [*Citrobacter freundii*]; GenBank AKJ18929.1	47/48 (98%)	4.00E-25
	SC09-03-3	968..1096 (+)	PFL_4706 family; conjugal transfer protein most similar to hypothetical protein, partial [*Bacillus cereus*]; GenBank WP_000306031.1	43/43 (100%)	3.00E-21
	SC09-03-4	1152..2417 (-)	MFS superfamily; tetracycline resistance protein most similar to tetracycline resistance protein A [*Laribacter hongkongensis*]; GenBank AAW83817.1	421/421 (100%)	0.0
	SC09-03-5	2421..3128 (+)	TetR superfamily; tetracycline repressor protein most similar to tetracycline repressor protein TetR [*Plesiomonas* sp. ZOR0011]; GenBank WP_047706566.1	202/203 (99%)	2.00E-133
	SC09-03-6	3133..3270 (+)	plasmid replication protein most similar to replication protein C [*Candidatus snodgrassella* sp. T4_34144]; GenBank AFV98734.1	46/46 (100%)	3.00E-24

SC09-03-7	3439..3879 (+)	Rep_3 superfamily; plasmid replication protein most similar to MULTISPECIES: hypothetical protein [Chlamydia]; GenBank WP_030122376.1	145/146 (99%)	1.00E-100
SC09-03-8	4037..4915 (-)	P-loop_NTPase superfamily; replication protein most similar to RepA [*Chlamydia suis*]; GenBank AAR96040.1	292/292 (100%)	0.0
SC09-03-9	4944..5270 (-)	hypothetical protein of unknown function; most similar to hypothetical protein [*Gulbenkiania indica*]; GenBank WP_055434597.1	107/108 (99%)	2.00E-52
SC09-03-10	5267..5593 (-)	PemK superfamily; growth inhibitor protein most similar to putative PemK-like protein [*Chlamydia trachomatis* RC-F(s)/852]; GenkBank AGR96051.1	108/108 (100%)	1.00E-70
SC09-03-11	5590..5814 (-)	DUF3018 superfamily; hypothetical protein of unknown function most similar to MULTISPECIES: hypothetical protein [Proteobacteria]; GenBank WP_043149934.1	74/74 (100%)	9.00E-46
SC09-03-12	5881..8553 (-)	Relaxase superfamily; mobilization protein most similar to mobilization protein [*Enterobacter* sp. GN02768]; GenBank WP_047353284.1	890/890 (100%)	0.0
SC09-03-13	8543..8857	mobilization protein; most similar to mobilization protein B [*Aeromonas salmonicida* subsp. *salmonicida*]; GenBank AIM49702.1	104/104 (100%)	6.00E-68
SC09-03-14	9149..9526 (+)	mobilization protein; most similar to MobC [*Chlamydia suis*]; GenBank AAR96037.1	124/125 (99%)	2.00E-59
SC09-03-15	9539..10222 (+)	mobilization protein; most similar to MULTISPECIES: protein mobD [Bacteria]; GenBank WP_009873358.1	227/227 (100%)	6.00E-148
SC09-03-16	10215..10853 (+)	mobilization protein; most similar to MULTISPECIES: protein mobE [Bacteria]; GenBank WP_009873359.1	212/212 (100%)	8.00E-117

	SC09-03-17	10850..11602 (+)	hypothetical protein of unknown function; most similar to MULTISPECIES: OfxX fusion product [Bacteria]; GenBank WP_009873360.1	250/250 (100%)	2.00E-128
43644	43644-1	184..594 (+)	hypothetical protein of unknown function; most similar to hypothetical protein [*Escherichia coli*]; GenBank WP_044864692.1	129/136 (94%)	5.00E-84
	43644-2	854..1417 (+)	DnaK domain; molecular chaperone involved in posttranslational modification and protein turnover; most similar to hypothetical protein [Enterobacteriaceae]; GenBank WP_001749520.1	159/187 (85%)	1.00E-112
	43644-3	1452..1934 (-)	hypothetical protein of unknown function; most similar to hypothetical protein [Enterobacteriaceae]; GenBank WP_000043122.1	134/151 (89%)	2.00E-90
	43644-4	2915..3358 (-)	hypothetical protein of unknown function; most similar to hypothetical protein [*Edwardsiella tarda*]; GenBank WP_034166090.1	142/147 (97%)	2.00E-95