

Supplementary Table 3 Relevant families of paralogous genes in *P. luminescens*

Family	Genes	Comments
<i>rhs</i> -like elements	<i>plu0353, plu3120, plu4278, plu4280</i>	<i>plu4278</i> is probably a pseudogene
<i>tcc</i> genes	<i>tccC1, tccC2, tccC3, tccC4, tccC5, tccC6, tccC7</i>	
<i>vgrG</i> -like genes, subfamily 1	<i>plu0355, plu0462, plu0821, plu0826, plu1492, plu1926, plu2295, plu3237, plu3246, plu3253, plu3305, plu4222, plu4601</i>	<i>plu3305</i> and <i>plu0821</i> are probably pseudogenes
<i>vgrG</i> -like genes, subfamily 2	<i>plu1660, plu1682, plu1701, plu1723, plu2392, plu2524</i>	
Two-partner secretion systems (<i>tpsA/tpsB</i>)	<i>phlA/phlB, plu0225/plu0226, plu0548/plu0549, plu1149/plu1150, plu1367/plu1368, plu3064/plu3065, plu3718/plu3719</i>	
	<i>plu3569</i>	No identified <i>tpsA</i> partner
	<i>plu3594, plu2453</i>	No identified <i>tpsB</i> partner
	<i>plu0537, plu0539, plu1130, plu1366, plu3584, plu3693, plu3701, plu3709</i>	Putative truncated genes showing similarities to the C-terminal domain of <i>tpsA</i>
<i>rtxA</i> genes	<i>plu1341, plu1344, plu3217, plu3324</i>	
	<i>plu1336/plu1337, plu1339/plu1340, plu1342/plu1343, plu3209/plu3207</i>	<i>rtxA</i> paralogs disrupted by frameshifts or IS
Bacteriocins/immunity	<i>plu4177</i>	Putative pyocin S3-like factor
	<i>plu4176 - plu4170</i>	Associated with <i>plu4177</i> , encode putative immunity proteins
	<i>plu0884</i>	Putative pyocin S3-like factor

	<i>plu0885 - plu0886</i>	Associated with <i>plu088</i> , encode putative immunity proteins
	<i>plu0887, plu0888, plu0889, plu0892</i>	Pseudogenes
	<i>plu0890, plu0891, plu0893, plu0894</i>	Putative immunity proteins
	<i>plu1894</i>	Putative colicin-like factor
	<i>plu1893</i>	Associated with <i>plu1894</i> , encode putative immunity proteins
	<i>plu1892</i>	Pseudogene (colicin-like factor)
	<i>plu1891, plu1890</i>	Putative immunity proteins
Iron/hemin/siderophore uptake systems (ABC transporter)	<i>plu2631 ; plu2632 - plu2637</i>	Hemin uptake (<i>hmu</i> locus of <i>Yersinia pestis</i>)
	<i>plu2850 - plu2853</i>	Hemin/siderophore uptake of <i>Yersinia pestis</i>
	<i>plu4621 - fepG</i>	Probable siderophore biosynthesis and uptake (YPO1538-YPO1532 of <i>Yersinia pestis</i>)
	<i>plu2315 – plu2324</i>	Yersiniabactin uptake of <i>Yersinia pestis</i> (high-pathogenicity island)
	<i>yfeA - yfeD</i>	Iron (chelated) uptake of <i>Yersinia pestis</i>
	<i>fecI - fecE</i>	Iron (III)-dicitrate transport system of <i>E. coli</i>
	<i>hemR, plu0739, plu2715 plu3513, plu3519, plu3838</i>	Putative receptors of the ISVH family
Putative genes encoding recombinases	<i>mrfI, xerC, xerD, plu0260, plu0419, plu0543, plu1125, plu1135, plu1143, plu1359, plu1991, plu3579, plu3588, plu3688, plu3696, plu3704, plu3713</i>	
Photopexins	<i>ppxA, ppxB, plu4230, plu4231, plu4224</i>	