Supplementary Figure 5 Synteny (X-alignment) between *P. luminescens* TT01 and *Y. pestis* CO92 (A); *E. coli* K12 (C); *P. aeruginosa* (D) and genes present in *Y. pestis* CO92 but absent from *E. coli K12* (B). (1) Island 4 of strain W14 (encoding macrophage-like toxins and PhlB/A); (2) NADH-quinone reductase (*nqr* locus); (3) 4-hydroxyphenylacetate catabolism (*hpc* locus); (4) urease (*ure* locus); (5) yersiniabactine (HPI locus); (6) iron uptake (*yfe* locus); (7) ribonuclease; (8) hemin/siderophore uptake; (9) hemin uptake (*hmu* locus); (10) probable siderophore biosynthesis and uptake (YPO1538-YPO1532). Each diamond represents one gene having an ortholog in the other genome with co-ordinates corresponding to the position in bp in each genome. Orthologs were defined as genes showing bi-directional best-hits by *P. luminescens* proteome BLASTP comparisons. The threshold was set to a minimum of 50% sequence similarity and an overlap corresponding to at least 80% of the smallest protein.