

Table S4: Validations of productive RpoN binding

Group#	Locus tag*	Gene function	Expression compared to <i>Y. pseudotuberculosis</i> WT	
			$\Delta rpoN$	Binding site mutant
	YPK_0329	N-acetyltransferase	↙	↙
	YPK_1886	Putative tripeptide transporter permease, TppB	↗	↗
	YPK_1894	Phage shock protein, PspA	↙	↙
A	YPK_2909	Zinc resistance protein, ZraP	↗	↗
	YPK_2908	Sensor kinase, ZraS	↙	↙
	YPK_2927	Asparagine synthetase B, AsnB	↙	-
	YPK_3010	Glutamate and aspartate transporter subunit, GltI	↙	↙
	YPK_2997	Glucosamine-6-phosphate deaminase, NagB	↗	↗
	YPK_3962	Glycerol-3-phosphate transporter , UgpB	↗	↗
D	YPK_3075	2,5-didehydrogluconate reductase, DkgA	↗	↗
	YPK_3613	Soluble lytic murein transglycosylase, Slt	↗	↗
	YPK_3887	NmrA family protein	↗	-

grouping of binding sites depending on position (A) intergenic sense strand (D) intragenic anti sense strand

*locus tag for downstream gene (A) or gene on corresponding sense strand

↙ = Down-regulated in $\Delta rpoN$ /WT

↗ = Up-regulated in RpoN binding site mutant/WT

- = No change in relative expression