

Table S3. Proteins encoded by the plasmid of “*Ca. N. fabula* KNB” and their closest homologs in the TrEMBL, Swiss-Prot, and NCBI nr databases.

Plasmid Gene	Predicted function	Database	Best hit, accession no.	Best hit, identity (%)	Best hit, predicted function	Best hit, organism
NITFABP_0001	Protein of unknown function	TrEMBL	A0A0F3GCT4	69	Uncharacterized protein	<i>Pseudomonas pseudoalcaligenes</i>
		Swiss-Prot	P20085	49	Mobilization protein MobL	<i>Acidithiobacillus ferrooxidans</i>
		nr	XP_012260969	99	uncharacterized protein LOC105688902	<i>Athalia rosae</i> ^a
NITFABP_0002	Putative protein involved in initiation of plasmid replication	TrEMBL	A0A1I3FIQ5	83	Initiator Replication protein	<i>Paracoccus aminovorans</i>
		Swiss-Prot	P17492	29	Replication protein	<i>Neisseria gonorrhoeae</i>
		nr	XP_012260970	100	uncharacterized protein LOC105688903	<i>Athalia rosae</i> ^a
NITFABP_0003	Conserved protein of unknown function	TrEMBL	A0A212B9I4	71	Uncharacterized protein	<i>Pseudomonas</i> sp. A46
		Swiss-Prot	No hit			
		nr	WP_088193532	71	hypothetical protein	<i>Pseudomonas</i> sp. A46
NITFABP_0004	Putative transcriptional regulator, TetR family	TrEMBL	A7KK53	100	Putative transcriptional regulator	<i>Delftia acidovorans</i>
		Swiss-Prot	P39897	34	HTH-type transcriptional regulator MtrR	<i>Neisseria gonorrhoeae</i>
		nr	WP_043008328	100	TetR/AcrR family transcriptional regulator	<i>Comamonas testosteronii</i>
NITFABP_0005	Quaternary ammonium compound-resistance protein EmrE	TrEMBL	A7TX95	100	Small multidrug resistance protein	<i>Delftia tsuruhatensis</i>
		Swiss-Prot	Q9X2N9	59	Quaternary ammonium compound-resistance protein QacF	<i>Klebsiella aerogenes</i>
		nr	WP_043008326	100	quaternary ammonium compound efflux SMR transporter QacF	<i>Comamonas testosteronii</i>
NITFABP_0006	Putative Mobilization protein, MobS-like	TrEMBL	A0A238DWW0	84	Uncharacterized protein	<i>Thiomonas</i> sp. X19
		Swiss-Prot	P20086	51	Mobilization protein MobS	<i>Acidithiobacillus ferrooxidans</i>
		nr	ART89884	70	hypothetical protein	uncultured bacterium

^aThe presence of these genes in the genome sequence of the insect *A. rosae* is interesting. However, since all genes on the plasmid of “*Ca. N. fabula*” have close homologs in members of the Proteobacteria, we consider the plasmid to be of proteobacterial origin.