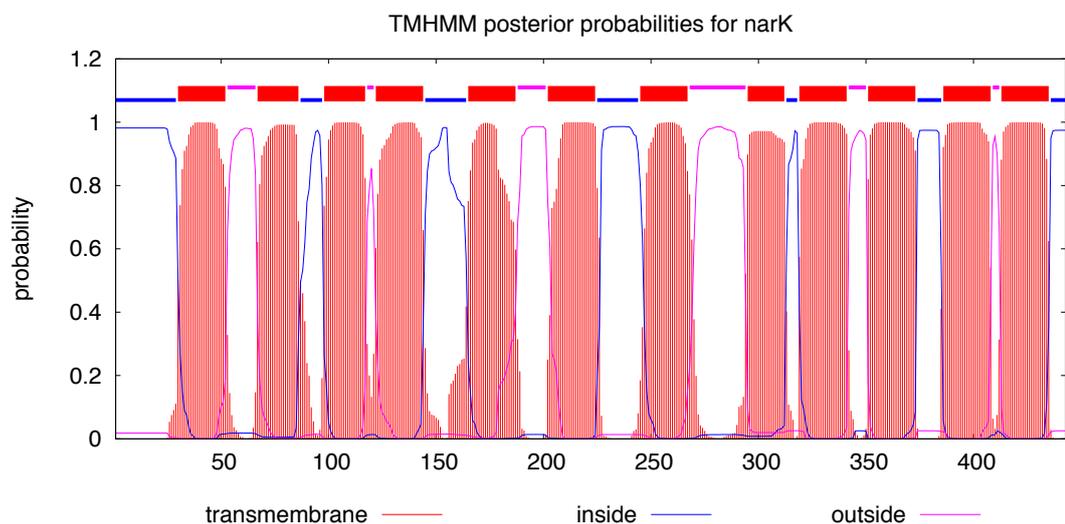


S1 Figure. Transmembrane helices in NarI protein from *C. pseudotuberculosis* biovar Equi.

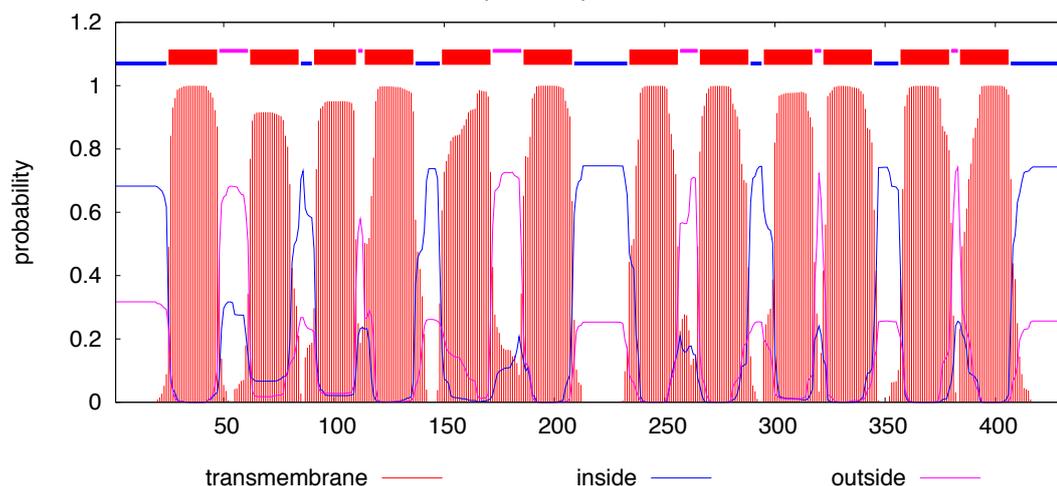
NarI presented 5 transmembrane helices. The probability of a given amino acid being in transmembrane regions in the cytoplasmic or extracellular face is recorded in red, blue and pink, respectively. Prediction was performed with TMHMM 2.0 (<http://www.cbs.dtu.dk/services/TMHMM/>).



S2 Figure. Transmembrane helices in NarK protein from *C. pseudotuberculosis* biovar Equi.

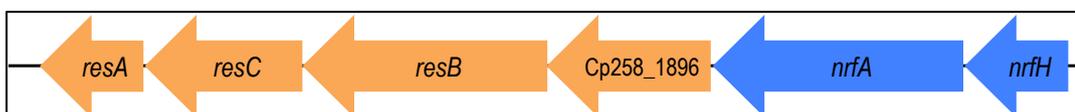
NarK presented 12 transmembrane helices. Prediction was performed with TMHMM 2.0 (<http://www.cbs.dtu.dk/services/TMHMM/>).

TMHMM posterior probabilities for narT



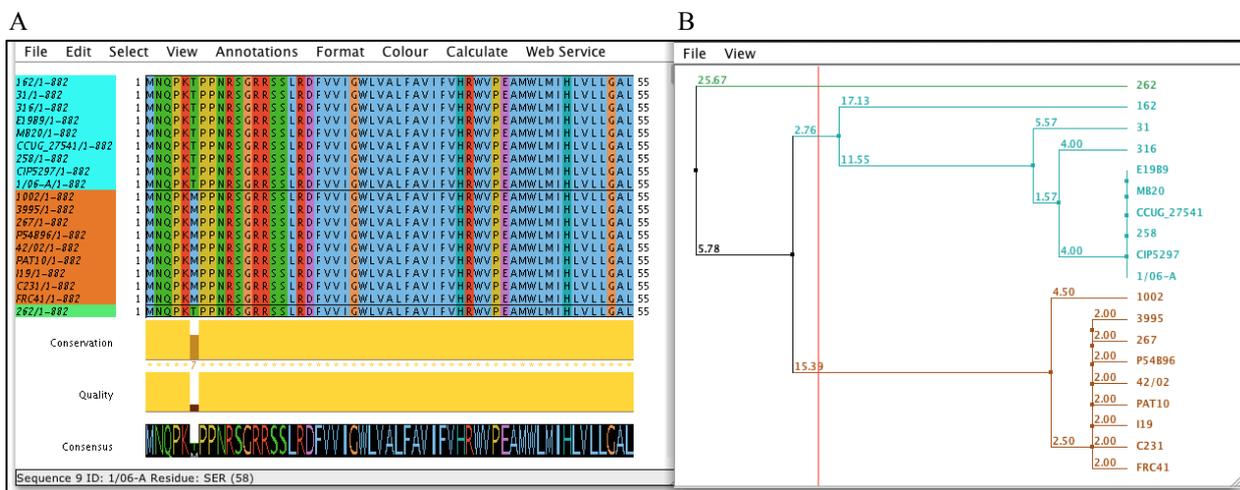
S3 Figure. Transmembrane helices in NarT protein from *C. pseudotuberculosis* biovar Equi.

NarT presented 12 transmembrane helices. Prediction was performed with TMHMM 2.0 (<http://www.cbs.dtu.dk/services/TMHMM/>).



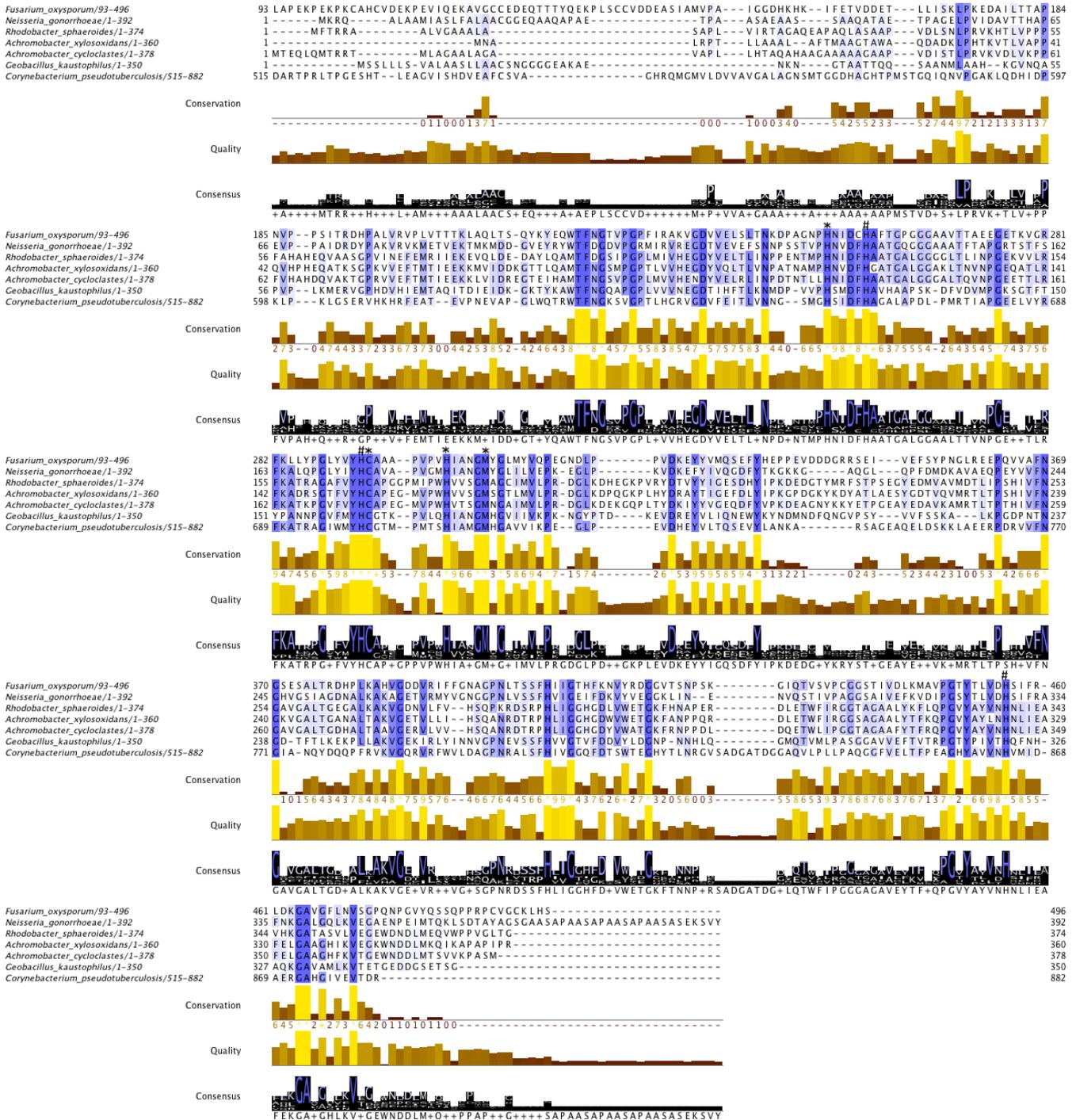
S4 Figure. Transcription unit for the *nrfHA* genes into *C. pseudotuberculosis* biovar Equi.

Genomic coordinate of 2046902 (*nrfH*) to 2052315 (*resA*). This region corresponds to 5414 pb length.



S5 Figure. Multiple Sequences alignment of *C. pseudotuberculosis* biovar Equi *nirK* gene.

In (A) multiple alignment using Clustal Omega with default settings. Alignment was visualized in Jalview. In (B) Phylogenetic trees of *nirK* inferred by Jalview program with the average distance using BLOSUM62. Sequences for each species have been deposited in the GenBank databases, access number Table 1.

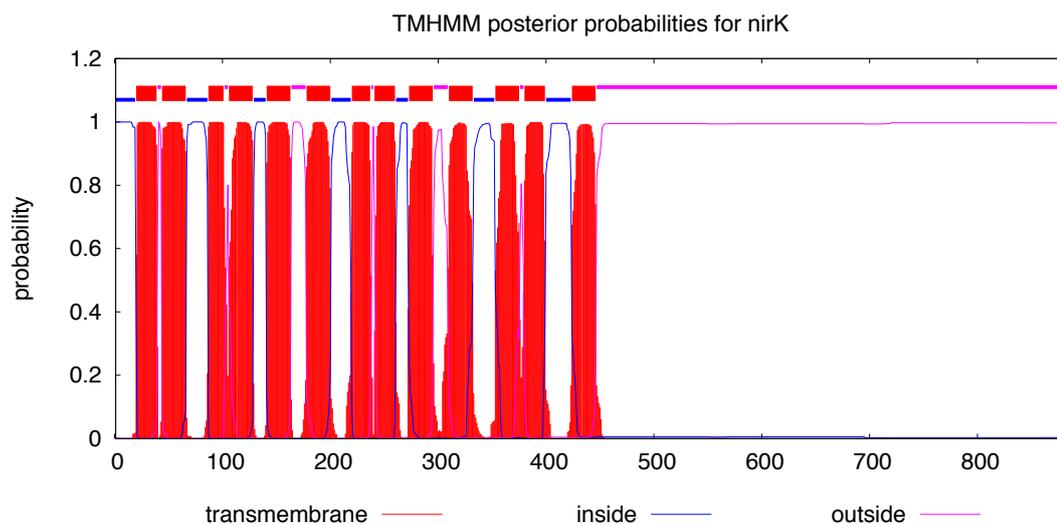


S6 Figure. Amino acid sequence alignment of bacterial NirKs.

Multiple alignment, the program used is ClustalO. Shading highlights amino acid residues of bacterial CuNiRs colored by percentage identity. Putative Cu-binding residues for type 1 and type 2 Cu are indicated by * and #, respectively. Accession numbers of the sequences shown here are as follows: *F. oxysporum* (EF600898); *N. gonorrhoeae* (GenBank M97926), *R. sphaeroides* (Rs) (GenBank U62291), *A. xylosoxidans* (EMBL AF051831), and *A. cycloclastes* (GenBank Z48635), *G. kaustophilus* (GenBank GAD15255.1). In B) Similarity sequence analysis between *nirk* from *C. pseudotuberculosis* and bacterial CuNiRs.

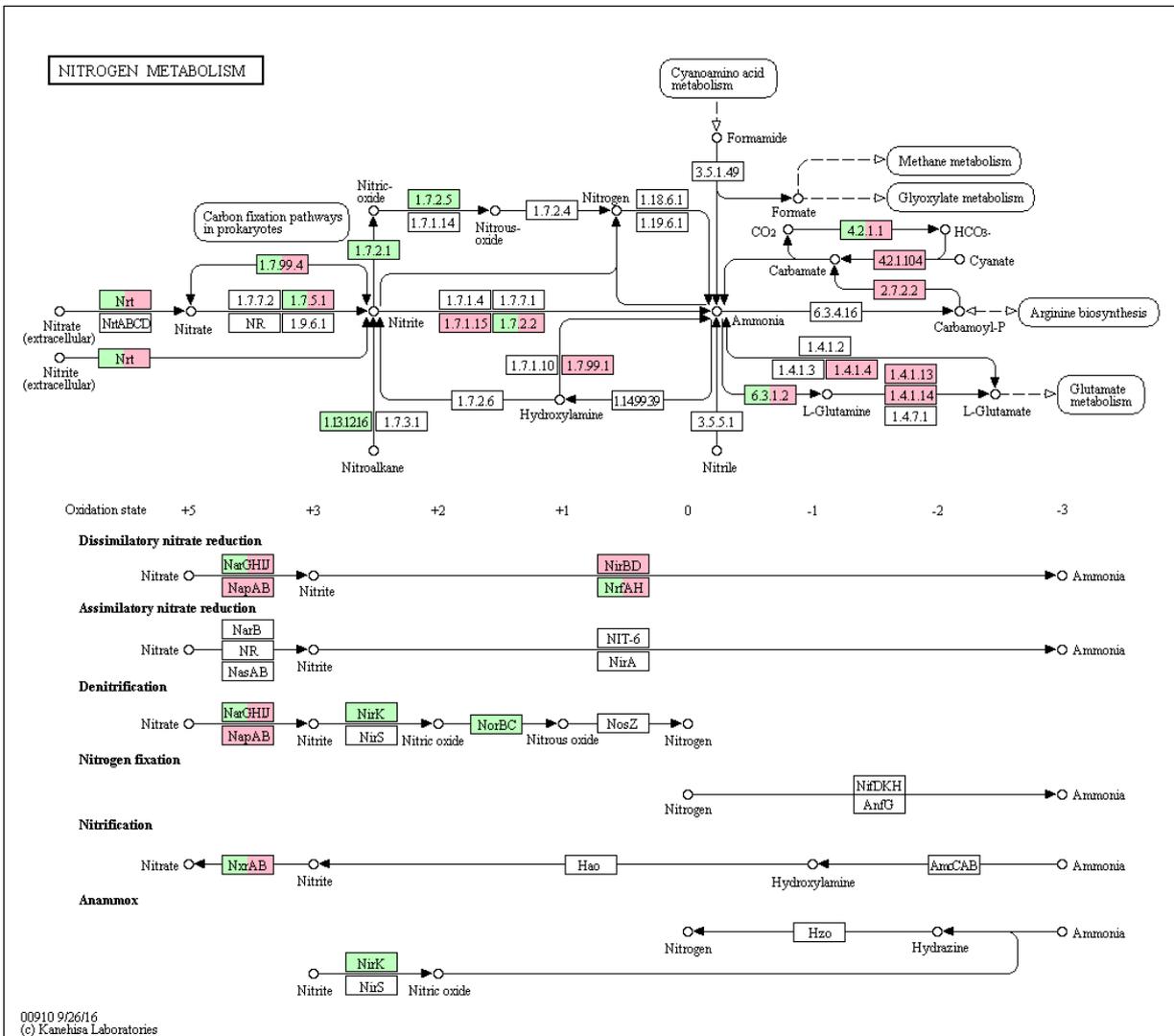
Table S1 – Similarity sequence analysis of *nirK* gene of *C. pseudotuberculosis* and bacterial CuNiRs

<i>C. pseudotuberculosis</i> Protein	Species	Length (aa)	ID (%)	Similarity (%)
Nitrite reductase enzyme likely dependent on copper (CuNIR) (<i>nirK</i>) - 882aa	<i>Fusarium oxysporum</i>	375	32	48
	<i>Neisseria gonorrhoeae</i>	392	33	50
	<i>Rhodobacter sphaeroides</i>	355	32	44
	<i>Achromobacter xylosoxidans</i>	360	30	44
	<i>Achromobacter Cycloclastes</i>	340	32	46
	<i>Geobacillus kaustophilus</i>	351	35	51
	<i>Corynebacterium durum</i>	867	40	54
	<i>Corynebacterium vitaeruminis</i>	845	40	54



S7 Figure. Transmembrane helices in *nirK* protein from *C. pseudotuberculosis* biovar Equi.

NirK presented 13 transmembrane helices. Prediction was performed with TMHMM 2.0 (<http://www.cbs.dtu.dk/services/TMHMM/>).



S8 Figure. Comparative nitrogen metabolism between *E.coli* and *C. pseudotuberculosis* biovar Equi. In red pathway to *E. coli*, in green to *C. pseudotuberculosis*. Prediction was performed with KEGG (<http://www.genome.jp/kegg/>).