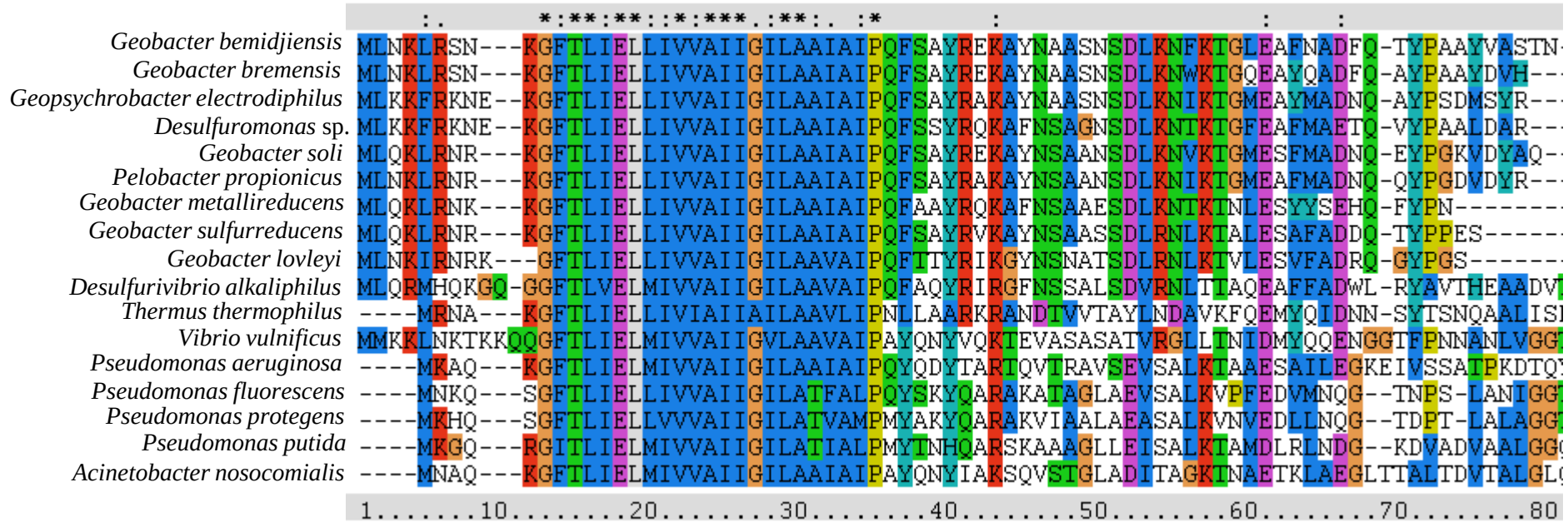

Figure S1 Amino acid sequence alignment of pilin domain protein SE37_07695 from Geobacter soli GSS01 and those from other bacteria. Amino acid sequence alignments were generated using the Clustal X (1.8).

Different amino acid residues were assigned to one of a number of groups (by chemical similarity) and each group was assigned a colour.

The GenBank accession number of the sequences used for the alignment analysis were ACH39598 for *G. bemidji*ensis, WP_026840453 for *G. bremensis*, WP_020676438 for *Geopsychrobacter electrodiphilus*, WP_027714750 for *Desulfuromonas* sp., ABK99270 for *Pelobacter propionicus*, ABB31633 for *G. metallireducens*, WP_049786599 for G. sulfurreducedns, ACD95812 for *G. lovleyi*, ADH86948 for *Desulfurivibrio alkaliphilus*, AAS81202 for *Thermus thermophilus*, ACK37858 for *Vibrio vulnificus*, ABN80239 for *Pseudomonas aeruginosa*, AEV64986 for *Ps. fluorescens*, AAY94501 for *Ps. protegens*, AAN66259 for *Ps. putida*, and CDG73934 for *Acinetobacter nosocomialis.*