

Table S7 Cluster of Orthologous Genes (COGs) categories assigned by eggNOG mapper

	COG	Description	Example functions/proteins and associated genes
Information Storage and Processing	J	Translation, ribosomal structure and biogenesis	tRNA-synthetases: <i>glnS</i> , <i>proS</i> , <i>ileS</i> , <i>leuS</i> Ribosome components: <i>rpl</i> genes, <i>rpm</i> genes, <i>rps</i> genes Initiation, elongation, and peptide chain release factors: <i>infA</i> , <i>efp</i> , <i>prfAH</i> , <i>pth</i> RNA chaperones: <i>proQ</i> , <i>hfq</i>
	A	RNA processing and modification	RNA 3'-terminal phosphate cyclase: <i>rtcA</i> Oligoribonuclease (3'-5' exoribonuclease): <i>orn</i>
	K	Transcription	RNA polymerase: <i>rpoABC</i> Sigma factors: <i>rpoESD</i> Anti- and termination factors: <i>nusBAG</i> Initiation, elongation, termination factors Transcriptional regulators: <i>hns</i> , <i>fnr</i> , <i>hilA</i> Nucleoid-associated proteins: <i>hns</i> Response regulators of two-component systems (TCS): <i>phoP</i> Cold shock proteins <i>csp</i>
	L	Replication, recombination and repair	Primosome-associated: <i>dnaGAC</i> , <i>priABC</i> , <i>rep</i> , <i>ssb</i> DNA polymerase III: <i>dnaEN</i> , <i>holABCE</i> DNA polymerase II: <i>polB</i> DNA polymerase I: <i>polA</i> Gyrase and topoisomerases: <i>gyrAB</i> , <i>parCE</i> Endo- and exonucleases: <i>mthHLMT</i> , <i>rnh</i> , <i>ruvAC</i> , <i>uvrABCD</i> Transposase, integrase
Cellular Processes and Signalling	D	Cell cycle control, cell division, chromosome partitioning	Cell division proteins: <i>damX</i> , <i>ftsAEUKLNQWXYZ</i> , <i>sula</i> Chromosome partitioning: <i>mukBEF</i> Cell partitioning: <i>minCD</i>
	V	Defense mechanisms	Transporters and efflux pumps: <i>sapBC</i> , <i>acrDEF</i> Restriction enzymes: <i>hsdMRS</i> Beta-lactam-associated: <i>ampEDH</i>
	T	Signal transduction mechanisms	Sensor kinases of TCS: <i>envZ</i> , <i>phoQ</i> , <i>arcB</i> , <i>baeS</i> , <i>ssrA</i>
	M	Cell wall / membrane / envelope biogenesis	Peptidoglycan synthesis: <i>murABCDEFGFI</i> , <i>mraY</i> Lipopolysaccharide biosynthesis: <i>rfaBCFGIJKLQ</i> O-antigen biosynthesis: <i>rfb</i> genes Colanic acid polysaccharide capsule biosynthetic genes: <i>wca</i> genes
	N	Cell motility	Fimbrial proteins: <i>bcdDEFG</i> , <i>fimADFHI</i> , <i>pegABD</i> , <i>stbACD</i> Flagella biosynthesis & components: <i>flgABCDEFGHIJKLMN</i> , <i>flhABE</i> , <i>fliCDEFGH</i> , <i>motAB</i>

	COG	Description	Example functions/proteins and associated genes
			SPI secretion system apparatus proteins: <i>spaOS</i> (SPI-1), <i>ssaCKNQ</i> (SPI-2)
	W	Extracellular structures	Autotransporter adhesin: <i>sadA</i> Outer membrane usher protein <i>fimD</i>
	U	Intracellular trafficking, secretion, and vesicular transport	Sec translocase SPI-1 TTSS (<i>spaPQR</i>) SPI-2 TTSS (<i>ssaJRSTUV</i>)
	O	Post-translational modification, protein turnover, chaperones	<i>ccm</i> genes <i>clpABPX</i> Molecular chaperones: <i>dnaAK</i> Fe-S cluster: <i>sufBCD</i> Lon protease: <i>lon</i> <i>ppiBAC</i>
Metabolism	C	Energy production and conversion	ATP synthase: <i>atpBEFGH</i> Cytochrome: <i>cybBC</i> , <i>cydABCD</i> <i>nuo</i> genes
	G	Carbohydrate transport and metabolism	Galactose metabolism and transport: <i>galKMPT</i> Galactarate metabolism and transport: <i>garDKL</i> Mannose metabolism and transport: <i>manAXYZ</i>
	E	Amino acid transport and metabolism	Arginine biosynthesis: <i>argACDEH</i> , Aromatic amino acids biosynthesis: <i>aroABCDEF</i>
	F	Nucleotide transport and metabolism	Purine metabolism: <i>purABCDEFGH</i>
	H	Coenzyme transport and metabolism	Heme biosynthesis: <i>hem</i> genes Aspartate pathway: <i>nadABCDE</i> <i>ribABDEF</i> genes
	I	Lipid transport and metabolism	<i>accABCD</i> Fatty acid biosynthesis: <i>fabABDFGH</i>
	P	Inorganic ion transport and metabolism	<i>fhu</i> genes Catalase genes: <i>kat</i> genes Magnesium transport: <i>mgtABC</i>
	Q	Secondary metabolites biosynthesis, transport and catabolism	Siderophore (enterobactin) synthesis: <i>entBCDEF</i> genes <i>pduACEJKLNTX</i> (although some are also classified under category C)
Poorly Characterised	S	Function unknown	Includes many genes associated with Regions of Difference (RODs), prophage regions and SPIs

Note: eggNOG-mapper uses only 20 of the 26 functional categories from the NCBI COG database (<https://www.ncbi.nlm.nih.gov/research/cog>). An "N/A" category was added to group all genes that were not assigned a COG category by eggNOG-mapper.