Table S1: salient feature of whole genome sequence of *K. quasipneumoniae*

Genome ID	570.5897
Genome Name	*K. quasipneumoniae* (Marine isolate)
Reference Genomes	573.17795
Coarse consistency (%)	99.5
Fine consistency (%)	91.8
Completeness (%)	99.9
Contamination (%)	6.5
Evaluation Group	R200 (Kluyvera ascorbata ATCC 33433)
Contig count	1
DNA size (bp)	5,255,929
Contigs N50 (bp)	5,255,929
Contigs L50	1
Overpresent Roles	126
Underpresent Roles	15
Predicted Roles	1744
Completeness Roles	898
Total Distinct Roles	4023
Protein-Encoding Genes with Functional Assignment	6661

Table S2: Genome similarity between marine isolate and human isolate

id	**isolate**	**species**	**species_match**	**contig_count**	**N50**	**largest_contig**	**total_size**	**ambiguous_bases**	**ST**
10512	BS54-A	*Klebsiella quasipneumoniae subsp. quasipneumoniae*	strong	149	254752	1011343	5253055	no	ST4549

ARO term	AMR gene family	Marine isolate	Human Isolate
FosA6	fosfomycin thiol transferase	🟩	🟩
leuO	major facilitator superfamily (MFS) antibiotic efflux pump	🟩	🟩
Shigella flexneri acrA	resistance-nodulation-cell division (RND) antibiotic efflux pump	🟩	🟩
msbA	ATP-binding cassette (ABC) antibiotic efflux pump	🟩	🟩
OmpA	General Bacterial Porin with reduced permeability to peptide antibiotics	🟩	🟩
Klebsiella pneumoniae OmpK37	General Bacterial Porin with reduced permeability to beta-lactams	🟩	🟩
Klebsiella pneumoniae KpnE	small multidrug resistance (SMR) antibiotic efflux pump	🟩	🟩
Klebsiella pneumoniae KpnF	small multidrug resistance (SMR) antibiotic efflux pump	🟩	🟩
OKP-A-8	OKP beta-lactamase	🟩	🟩
marA	resistance-nodulation-cell division (RND) antibiotic efflux pump,	🟩	🟩
MdtQ	Outer Membrane Porin (Opr)	🟩	🟩

oqxA	resistance-nodulation-cell division (RND) antibiotic efflux pump	🟩	🟩
adeF	resistance-nodulation-cell division (RND) antibiotic efflux pump	🟩	🟩
emrR	major facilitator superfamily (MFS) antibiotic efflux pump	🟩	🟩
Klebsiella pneumoniae KpnG	major facilitator superfamily (MFS) antibiotic efflux pump	🟩	🟩
Klebsiella pneumoniae KpnH	major facilitator superfamily (MFS) antibiotic efflux pump	🟩	🟩
rsmA	resistance-nodulation-cell division (RND) antibiotic efflux pump	🟩	🟩
CRP	resistance-nodulation-cell division (RND) antibiotic efflux pump	🟩	🟩
ArnT	pmr phosphoethanolamine transferase	🟩	🟩
eptB	pmr phosphoethanolamine transferase	🟩	🟩
Escherichia coli EF-Tu mutants conferring resistance to Pulvomycin	elfamycin resistant EF-Tu	🟩	🟩
Klebsiella pneumoniae acrR with mutation conferring multidrug antibiotic resistance	resistance-nodulation-cell division (RND) antibiotic efflux pump	🟩	🟩
Escherichia coli EF-Tu mutants conferring resistance to Pulvomycin	elfamycin resistant EF-Tu	🟩	🟩
Escherichia coli UhpT with mutation conferring resistance to fosfomycin	antibiotic-resistant UhpT	🟩	🟩
Escherichia coli AcrAB-TolC with MarR mutations conferring resistance to ciprofloxacin and tetracycline	resistance-nodulation-cell division (RND) antibiotic efflux pump	🟩	🟩
Klebsiella pneumoniae acrR with mutation conferring multidrug antibiotic resistance	resistance-nodulation-cell division (RND) antibiotic efflux pump	🟩	🟩

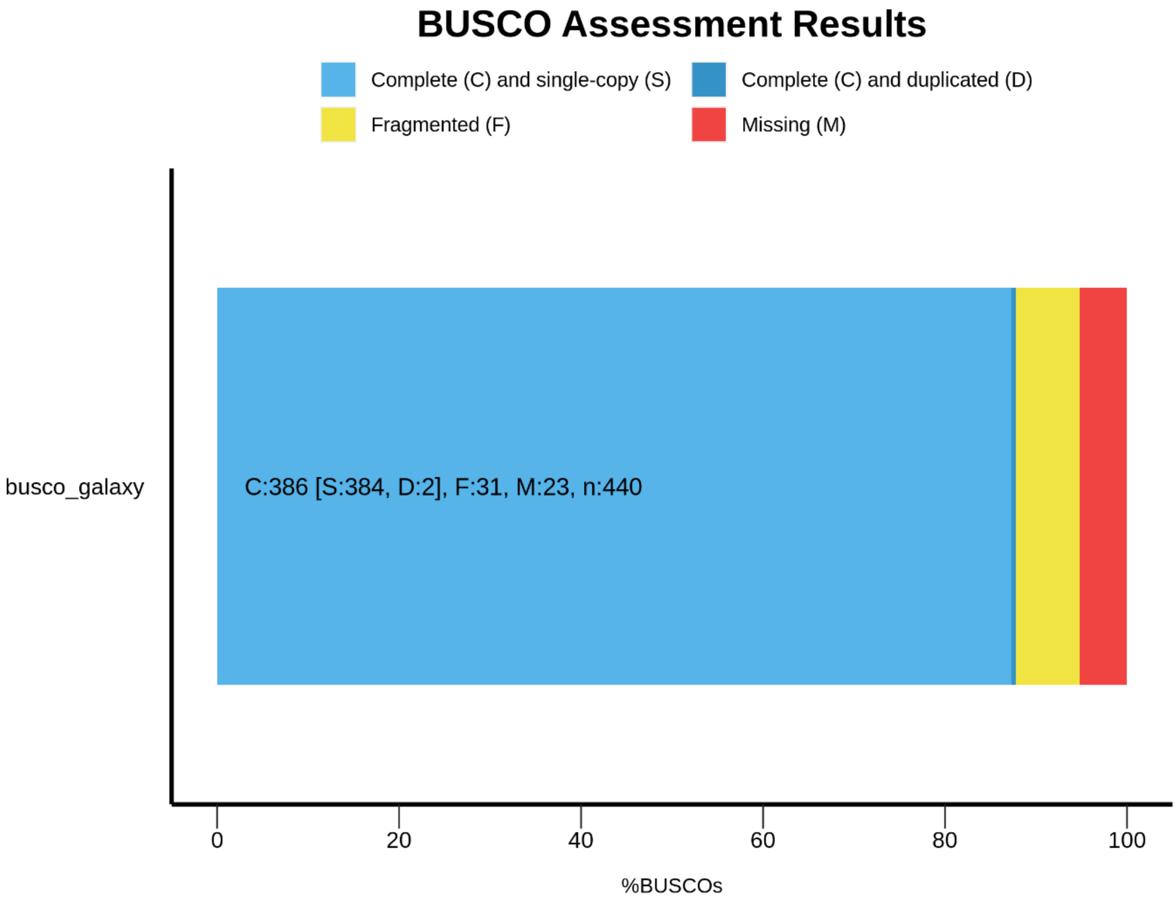

Figure S1 Graphical representation of BUSCO analysis on the genome of *K. quasipneumoniae*_ BARC01 to determine the quality of the genome.