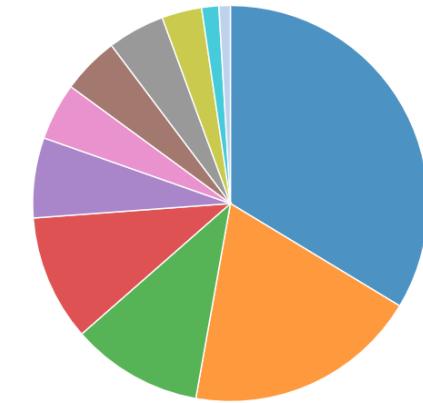
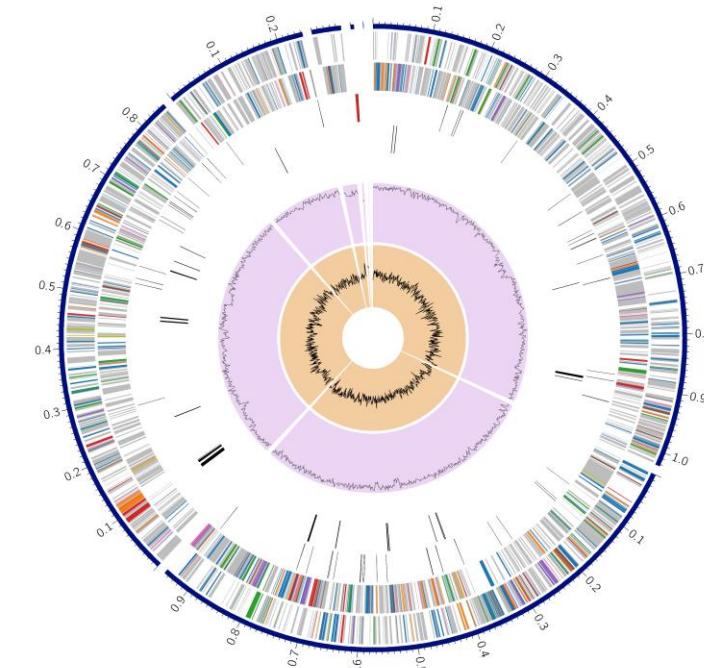


Quality of Genome Assembly and Annotation:Results from indigenously developed **BHARAT** analysis pipeline: (**Bacterial Hybrid genome Assembly and Rapid Annotation Toolset**)**Subsystem Analysis****Subsystem (Subsystems, Genes)**

METABOLISM	(72, 479)
PROTEIN PROCESSING	(41, 195)
ENERGY	(23, 155)
STRESS RESPONSE, DEFENSE, VIRULENCE	(22, 85)
DNA PROCESSING	(14, 60)
RNA PROCESSING	(10, 40)
MEMBRANE TRANSPORT	(10, 42)
CELLULAR PROCESSES	(10, 32)
CELL ENVELOPE	(7, 14)
MISCELLANEOUS	(3, 6)
REGULATION AND CELL SIGNALING	(2, 3)

Genome Assembly**Table 3: Antimicrobial Resistance Genes**

AMR Mechanism	Genes
Antibiotic target in susceptible species	Alr, Ddl, dxr, EF-G, EF-Tu, folA, Dfr, folP, gyrA, gyrB, Iso-tRNA, kasA, MurA, rho, rpoB, rpoC, S10p, S12p
Antibiotic target replacement protein	FabL-like
Protein altering cell wall charge conferring antibiotic resistance	GdpD, PgsA
Regulator modulating expression of antibiotic resistance genes	MtrA, MtrB