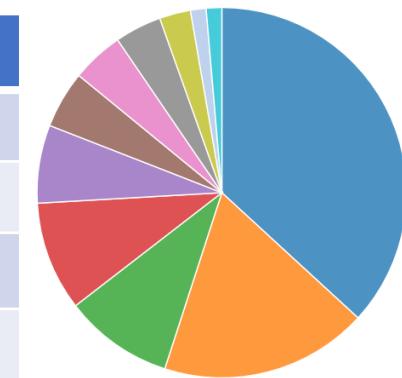


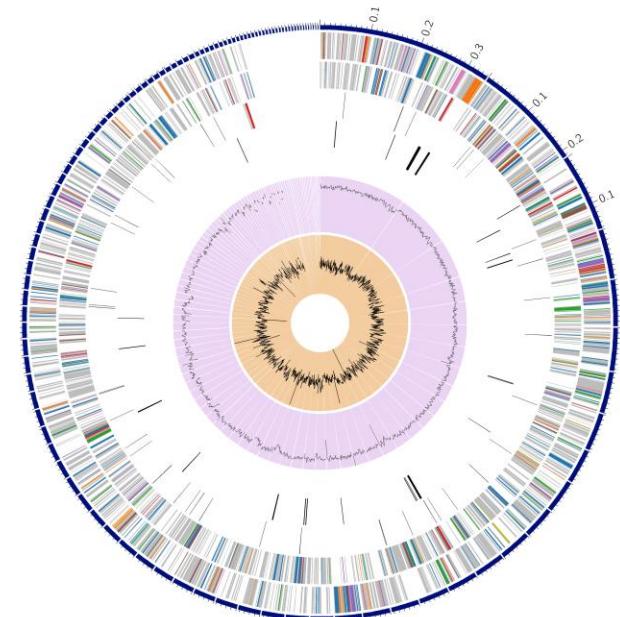
Quality of Genome Assembly and Annotation:Results from indigenously developed **BHARAT** analysis pipeline: (**Bacterial Hybrid genome Assembly and Rapid Annotation Toolset**)

Table 1: Assembly Details	
Contigs	110
GC Content	68.52
Contig L50	17
Genome length	3,236,374 bp
Contig N50	52,576

Table 2: Annotated Genome Features	
CDS	3,167
tRNA	50
Repeat Regions	0
rRNA	4

**Subsystem Analysis**

- METABOLISM (81, 496)
- PROTEIN PROCESSING (40, 204)
- ENERGY (21, 137)
- STRESS RESPONSE, DEFENSE, VIRULENCE (21, 82)
- DNA PROCESSING (15, 67)
- MEMBRANE TRANSPORT (11, 51)
- RNA PROCESSING (10, 39)
- CELLULAR PROCESSES (9, 30)
- CELL ENVELOPE (6, 15)
- REGULATION AND CELL SIGNALING (3, 6)
- MISCELLANEOUS (3, 9)

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

AMR Mechanism	Genes
Antibiotic target in susceptible species	Alr, Ddl, dxr, EF-G, EF-Tu, 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