CheckM GC GC std Genome size ambiguous bases 2.0 2.0 9 1.5 1.5 3 6 1.0 1.0 3 0.5 0.5 0.0 0.050 0.42 0.43 0.44 0.45 0.46 0.03 0.04 0.05 90.0 -0.050 -0.0250.000.0 0.025 0.07 5.0e + 061.0e+071.5e+07 scaffolds Longest scaffold contigs Longest contig 5 2.0 2.0 5 4 4 1.5 1.5 3 3 1.0 1.0 2 2 0.5 0.5 1 1 2000 2000 6e+05 4e+05 3e+05 3e+05 6e+05 . 500 1000 1500 0 200 1000 1500 2e+05 5e+05 2e+05 4e+05 5e+05 Mean scaffold length N50 scaffolds N50 contigs Mean contig length 2.0 2.0 3 3 1.5 1.5 2 2 1.0 1.0 1 0.5 0.5 0.0 20000 50000 25000 75000 100000 25000 75000 100000 1e+05 2e+05 1e+05 2e+05 125000 125000 Coding density Translation table predicted genes 2.0 5 9 4 1.5 3 6 1.0 2 3 0.5 1 0.0 -10.950 0.8900 11.025 11.050 15000 0.8925 0.8950 0.8975 0.9000 10.975 11.000 5000 10000

Isolates

CheckM: Number of Contigs 5 4 3. 2. 0 Isolates 0







