

Table S1: Summary of sequencing and processing statistics for samples EQ1 and ST

Analysis statistics	EQ1	ST
Upload: bp Count	3,771,611,986 bp	5,712,546,366 bp
Upload: Sequences Count	17,035,408	24,390,498
Upload: Mean Sequence Length	221 ± 39 bp	234 ± 40 bp
Mean GC percent	51 ± 10 %	59 ± 10 %
Artificial Duplicate Reads: Sequence Count	7,705,255	5,852,508
Post QC: bp Count	2,108,167,321 bp	4,382,885,342 bp
Post QC: Sequences Count	9,250,049	18,533,805
Post QC: Mean Sequence Length	228 ± 41 bp	236 ± 40 bp
Post QC: Mean GC percent	53 ± 10 %	59 ± 10 %
Processed: Predicted Protein Features	2,336,062	9,483,669
Processed: Predicted rRNA Features	6,880	22,144
Alignment: Identified Protein Features	1,354,729	5,754,737
Alignment: Identified rRNA Features	2,658	8,964