

Supplement

Supplementary Tables

Table 1: Indel summary for bench-top reads against *E. coli* 280 - 454 FLX+ reference

	insertions	deletions	indels_per_100	indels_per_read
454 GS Junior (1)	158750	52771	0.37	1.70
454 GS Junior (1+2)	317503	105543	0.37	1.70
454 GS Junior (2)	158753	52772	0.37	1.70
Illumina MiSeq (280)	341	1452	0.00	0.00
Ion Torrent (1)	1810437	1779715	1.45	1.67
Ion Torrent (1+2)	3359935	3480896	1.50	1.72
Ion Torrent (2)	1549498	1701181	1.55	1.77

Table 2: Indel summary for bench-top reads against *E. coli* 55989 (Sanger sequenced) reference

	insertions	deletions	indels_per_100	indels_per_read
454 GS Junior (1)	160105	56257	0.38	1.72
454 GS Junior (1+2)	322649	109595	0.37	1.71
454 GS Junior (2)	162544	53338	0.37	1.69
Illumina MiSeq (c236-11)	2036	4589	0.01	0.01
Ion Torrent (1)	1680237	1656164	1.44	1.67
Ion Torrent (1+2)	3120133	3241258	1.49	1.71
Ion Torrent (2)	1439896	1585094	1.55	1.76

Table 3: Indel summary for bench-top reads against *E. coli* c236-11 - Illumina + PacBio reference

	insertions	deletions	indels_per_100	indels_per_read
454 GS Junior (1)	173457	61880	0.38	1.75
454 GS Junior (1+2)	348464	120232	0.38	1.74
454 GS Junior (2)	175007	58352	0.38	1.72
Illumina MiSeq (c236-11)	845	3512	0.00	0.00
Ion Torrent (1)	1850024	1827451	1.45	1.68
Ion Torrent (1+2)	3431462	3572351	1.50	1.72
Ion Torrent (2)	1581438	1744900	1.56	1.78

Supplementary Excel File 1. **Assembly_comparison_supplemental.xlsx** Statistics from Mauve Assembly Metrics comparing each of the assemblies produced from bench-top instrument data.

Supplementary Excel File 2. **BLAST_searches.xlsx** Result of BLAST searches for important pathogen biology genes.

Supplementary Figures

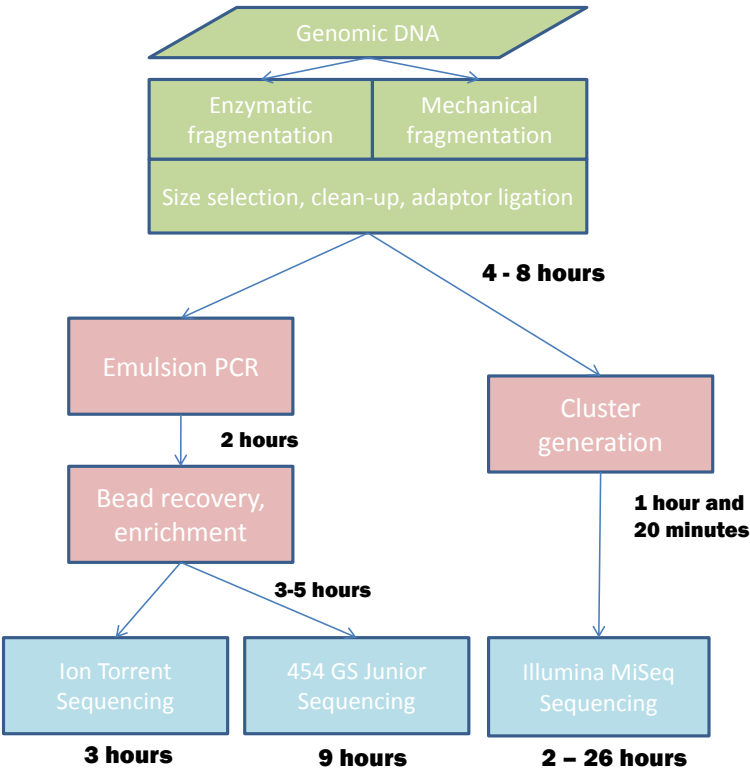


Figure 1: Simplified workflow for bench-top sequencing

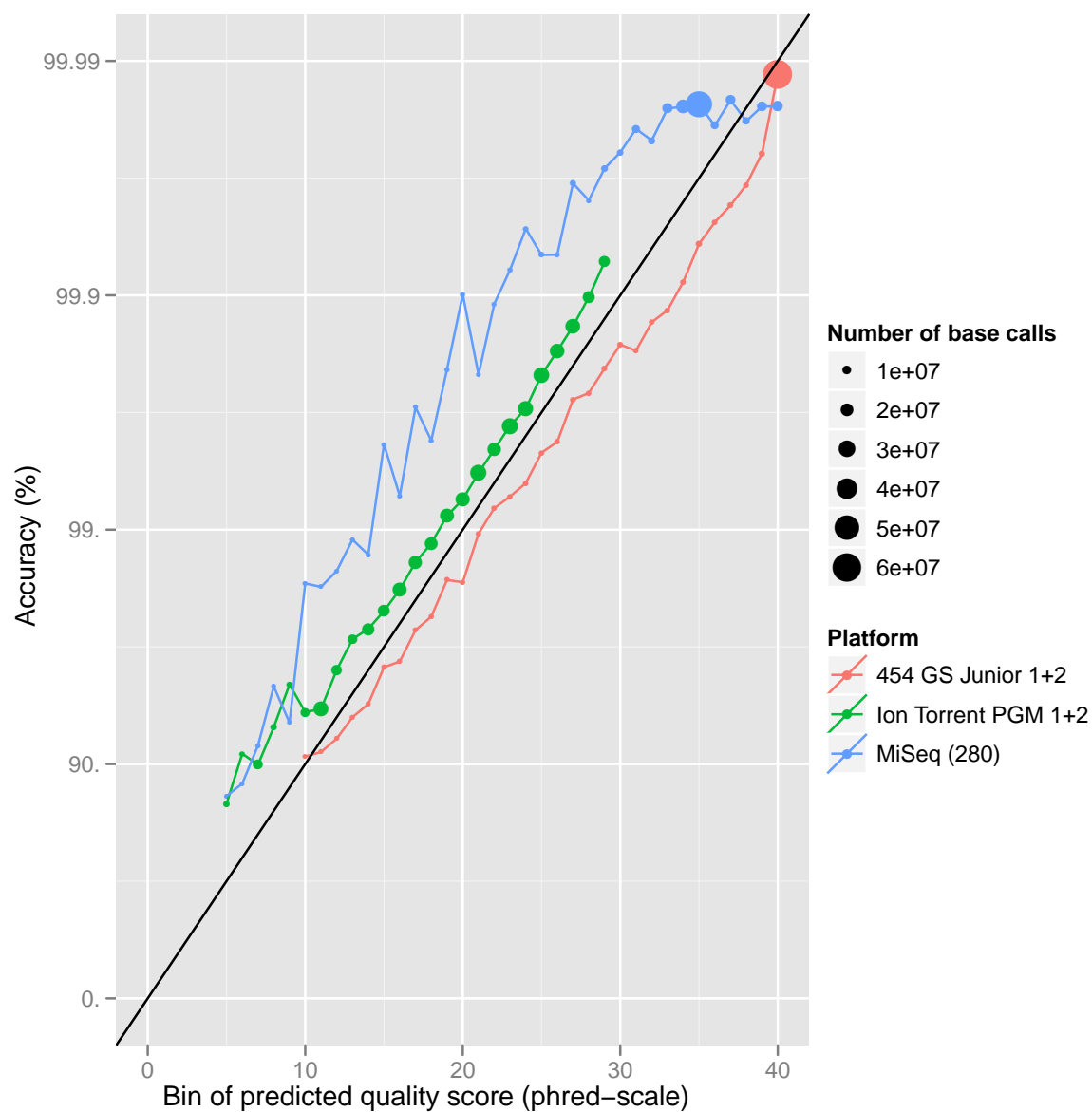


Figure 2: Chart showing the relationship between predicted quality scores and measured base accuracy. The area of each point shows the number of aligned bases in the predicted quality score bin. The diagonal slope indicates the relationship between base quality scores and accuracy.

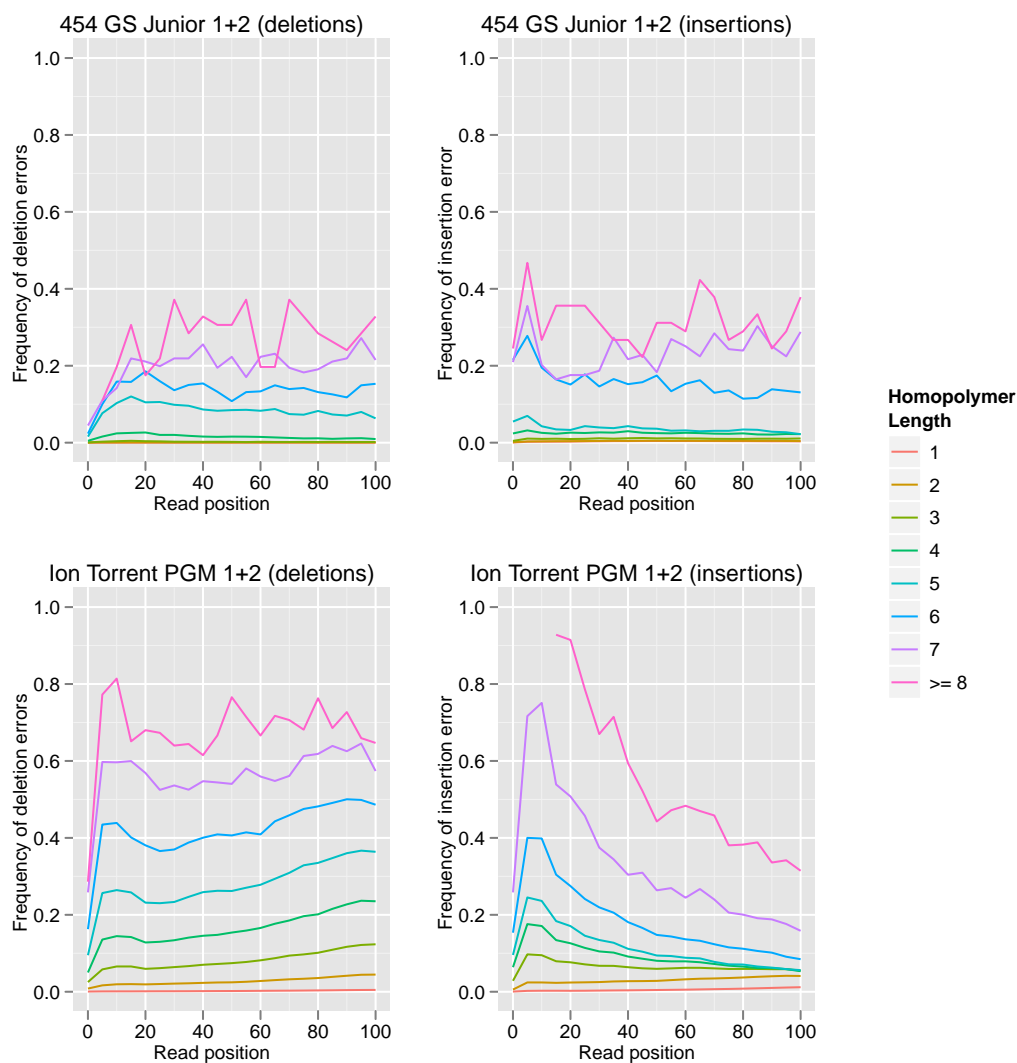


Figure 3: Comparison of homopolymer tract accuracy between 454 GS Junior and Ion Torrent. Charts show the frequency of erroneous insertions or deletions associated with homopolymeric tracts in the reference genome of lengths 1-7, and 8 or greater.

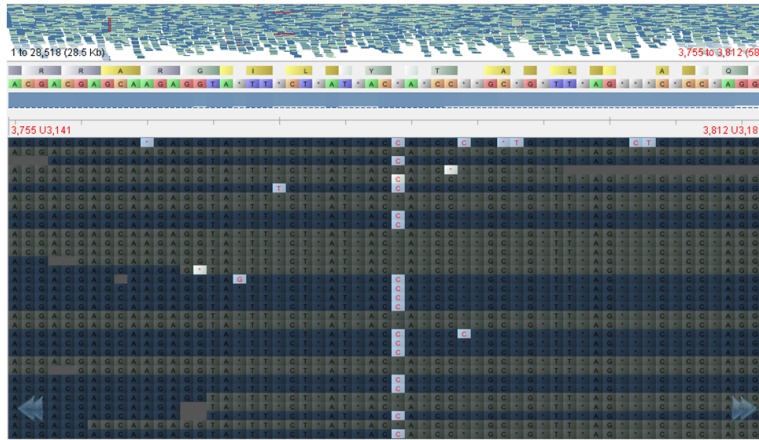


Figure 4: Homopolymeric tract error demonstrating strand bias (light blue is forward strand, dark blue is reverse strand)

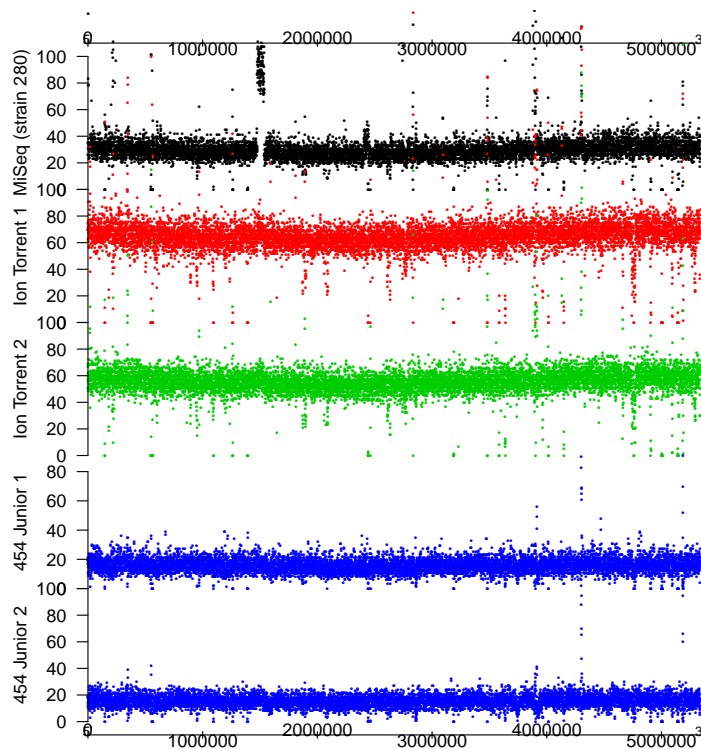


Figure 5: Depth of coverage plot for reads from each bench-top instrument against the *E. coli* strain 280 reference chromosome. In the MiSeq plot the large peak at 1.5 megabases corresponds to the Shiga-toxin producing phage, indicating the phage was likely undergoing lysis when DNA was being prepared. A smaller peak can be seen at the same position in the Ion Torrent PGM data.)