

Illumina HiSeq 2000 data output & quality scores

GATC Biotech delivers high quality data, using TruSeq v3 Cluster and SBS kits, with specifications above Illuminas official parameters.

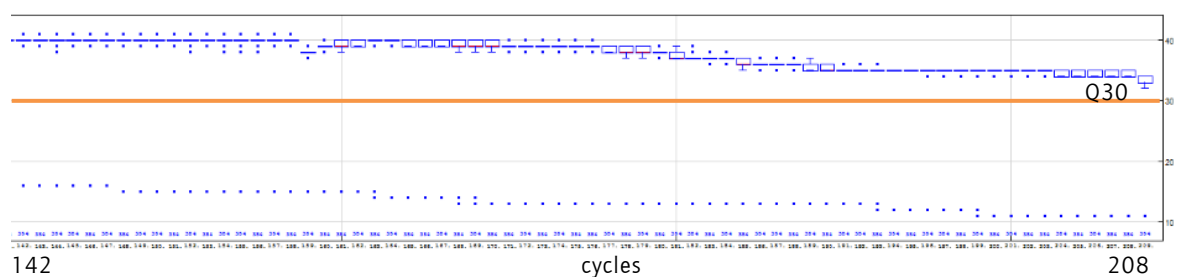
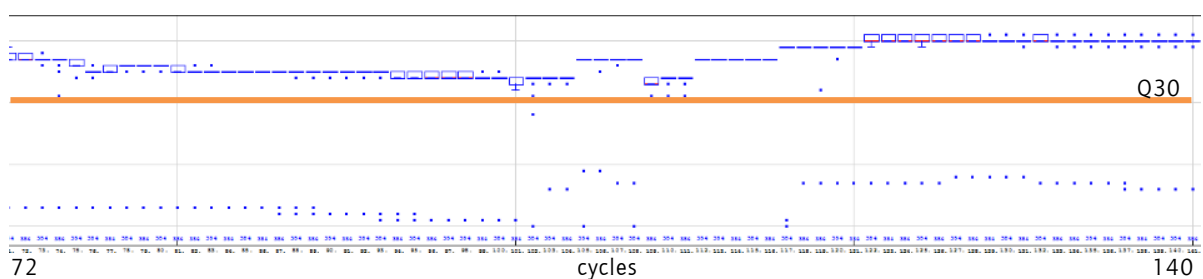
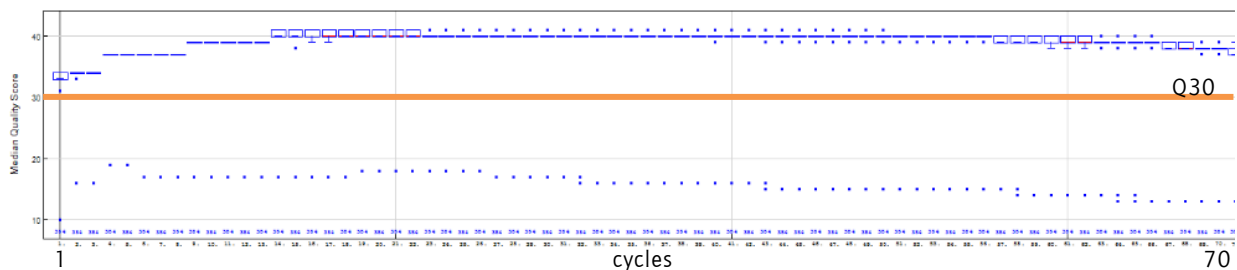


HiSeq 2000 System Performance Parameters

	output (2 x 100 bp)	clusters (reads) / lane passing filter	paired-end reads	perfect reads & bases (> Q30) at 2 x 100 bp
GATC Biotech using v3*	40 Gb / lane	up to 200 mio	up to 400 mio	greater than 80% bases higher than Q30
Illumina using v3*	37.5 Gb / lane	up to 180 mio	up to 360 mio	greater than 80% bases higher than Q30

GATC Biotech Median Quality Score (all lanes from one flowcell, per cycle)

In average 765K/mm² cluster, 698 K/mm² (91%) passed filter clusters - using TruSeq v3 Cluster & SBS kits

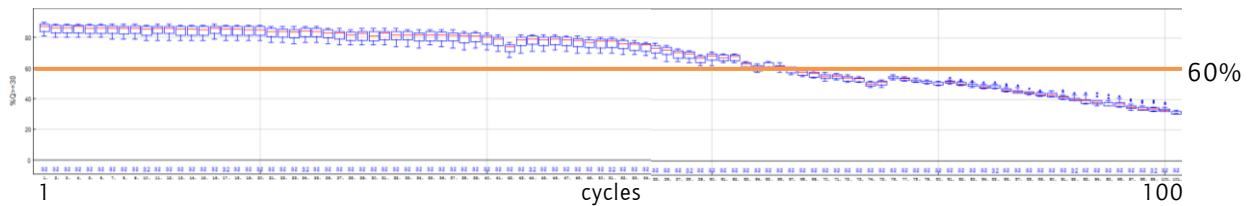


* for whole human genome; performance may vary based on sample quality, and other experimental factors

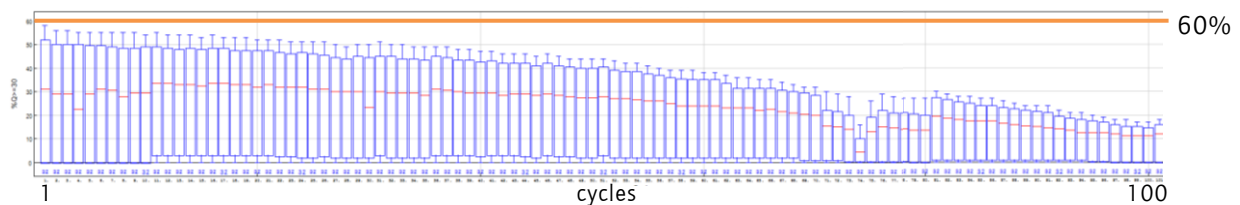
To get high quality data, the flowcell needs to be loaded in an appropriate cluster density which depends on the amount of loaded sample.
 Data output and data quality tremendously increases using v3 kits compared to v2 kits.

Percentage of clusters (per cycle) with a quality score higher than Q30

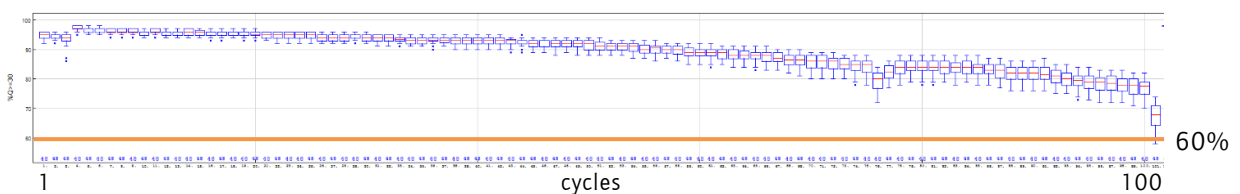
a) 743K/mm² cluster, 665K/mm² passed filter clusters (TruSeq v2 Cluster & SBS kits)



b) 1,034K/mm² cluster, 382K/mm² passed filter clusters (TruSeq v2 Cluster & SBS kits)



c) 841K/mm² cluster, 755K/mm² passed filter clusters (TruSeq v3 Cluster & SBS kits)



The density of 743K/mm² (example a) has a higher yield of passed filter clusters than the density of above 1,000 cluster (b). There is a limit in the amount of sample which should be loaded to get high quality data.

With v3, the cluster density can be increased (c), and the amount of clusters with a quality of above Q30 increases tremendously.