

A

## SRR13129036

## General

Sequencing	single-end (43 cycles)
Mean length before filtering	43
Mean length after filtering	30
Duplication rate	7.73% (may be overestimated since this is SE data)

## Before QC

Total reads	11451376
Total bases	492409168
Q20 bases	463828448 (94.1957%)
Q30 bases	436401257 (88.6257%)
GC content	52.99%

## After QC

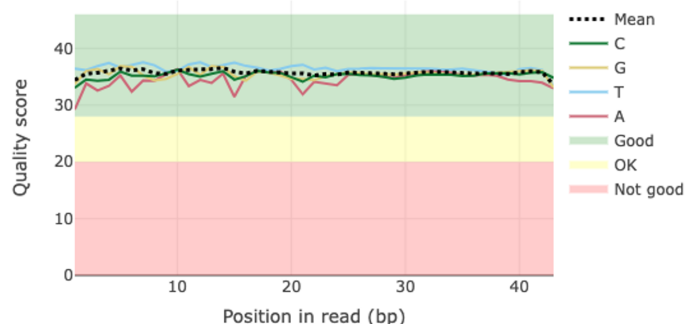
Total reads	11102724
Total bases	340958795
Q20 bases	324750375 (95.2462%)
Q30 bases	307362232 (90.1464%)
GC content	53.66%

## Filtering

Reads passed filters	11102724 (96.96%)
Reads with low quality	126063 (1.1%)
Reads with too many N	1 (0%)
Reads too short	222588 (1.94%)
Reads too long	0 (96.96%)

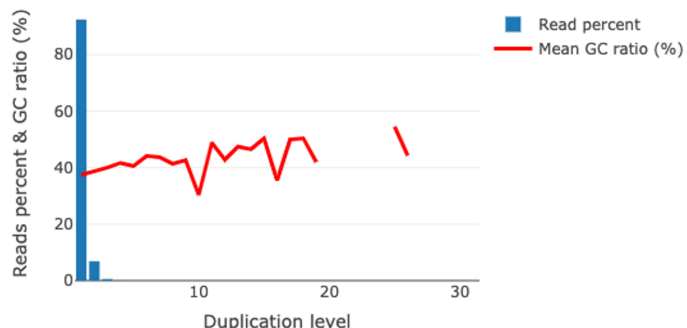
B

## Per base sequence quality



C

## Duplication rate: 7.73%



D

## Histogram of read length distribution

