

**A****SRR13129036****General**

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

**Before QC**

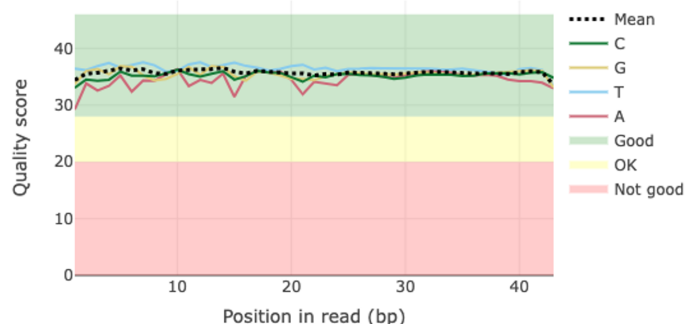
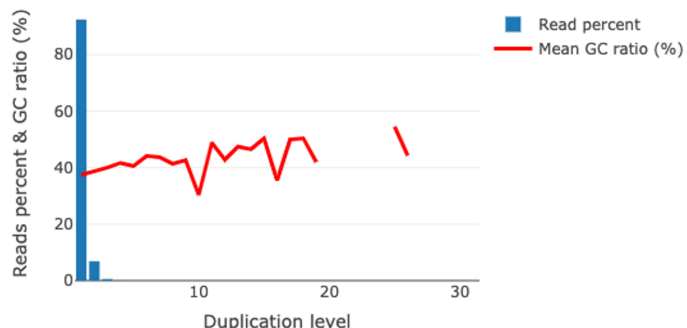
<b>Total reads</b>	11451376
<b>Total bases</b>	492409168
<b>Q20 bases</b>	463828448 (94.1957%)
<b>Q30 bases</b>	436401257 (88.6257%)
<b>GC content</b>	52.99%

**After QC**

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

**Filtering**

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

**B****Per base sequence quality****C****Duplication rate: 7.73%****D****Histogram of read length distribution**