

A**SRR13129036****General**

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|-------------------------------------|--|
| 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

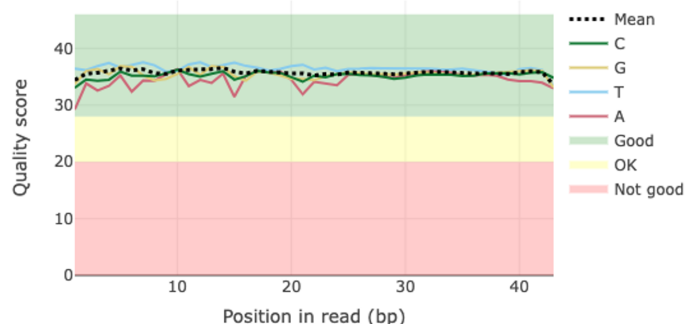
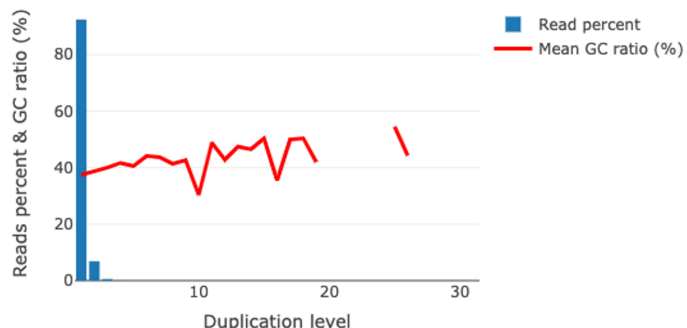
| | |
|--------------------|----------------------|
| Total reads | 11451376 |
| Total bases | 492409168 |
| Q20 bases | 463828448 (94.1957%) |
| Q30 bases | 436401257 (88.6257%) |
| GC content | 52.99% |

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**