

Summary

Basic Statistics

Per base sequence quality

Per tile sequence quality

Per sequence quality scores

Per base sequence content

Per sequence GC content

Per_base_N_content

Sequence_Length_Distribution

Sequence Duplication Levels

Overrepresented sequences

Adapter Content

Basic Statistics

Measure	Value
Filename	LR13_HHH23DSXX_L3_1.fq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	8994262
Sequences flagged as poor quality	0
Sequence length	150
%GC	38

Per base sequence quality



