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✓ Basic Statistics

Measure	Value
Filename	7Q-SU+UV_CGCTCATT_L005_R1_001.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	32874428
Sequences flagged as poor quality	0
Sequence length	51
%GC	61

✗ Per base sequence quality

