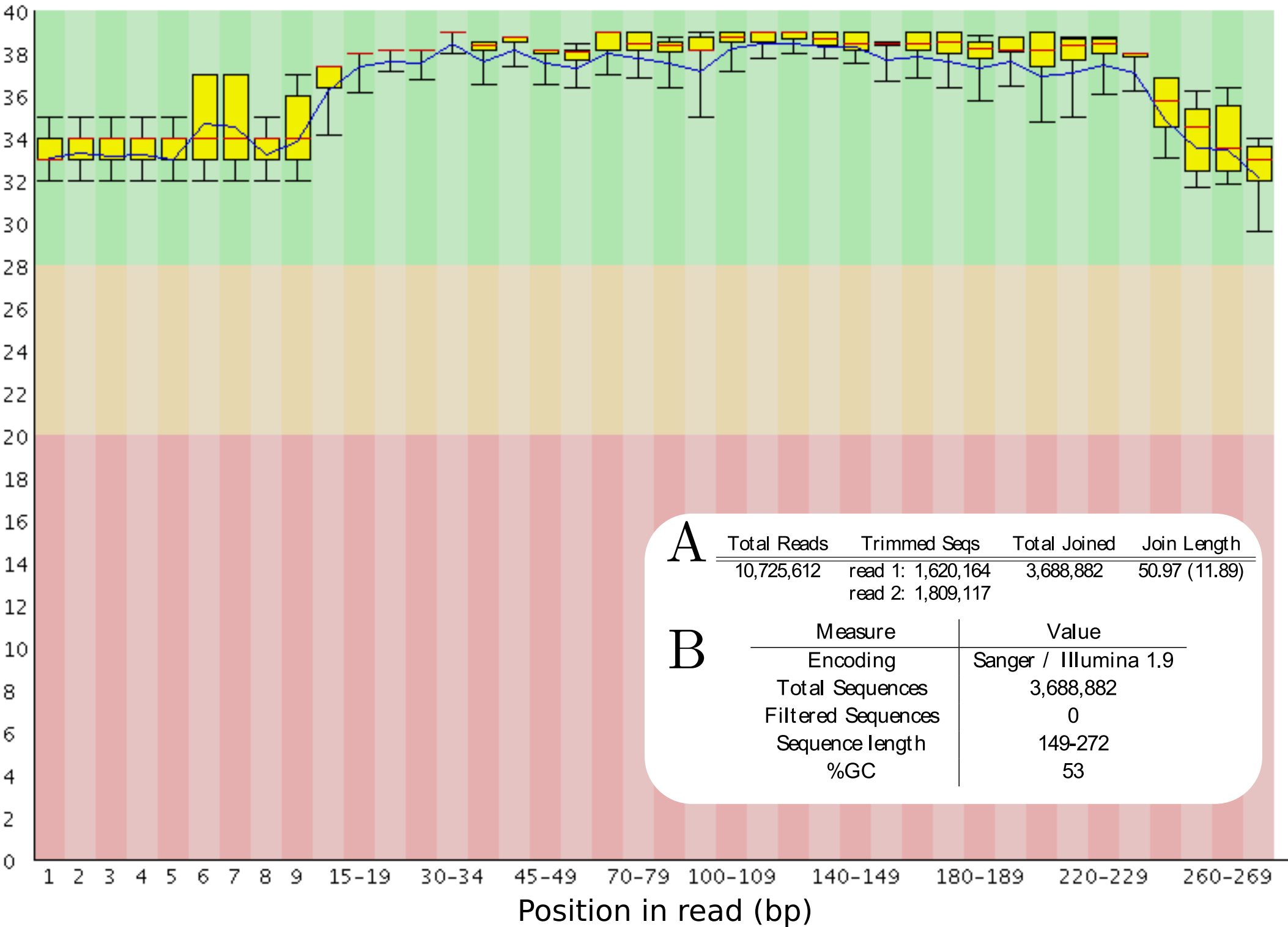


**C**

Quality scores across all bases (Sanger / Illumina 1.9 encoding)

**A**

Total Reads	Trimmed Seqs	Total Joined	Join Length
10,725,612	read 1: 1,620,164 read 2: 1,809,117	3,688,882	50.97 (11.89)

**B**

Measure	Value
Encoding	Sanger / Illumina 1.9
Total Sequences	3,688,882
Filtered Sequences	0
Sequence length	149-272
%GC	53