Sequencing, Mapping, and Variant Calling QC Report

Case ID: case0019

Sequence ID: PG0002847-DNA

Summary metrics

Raw quality

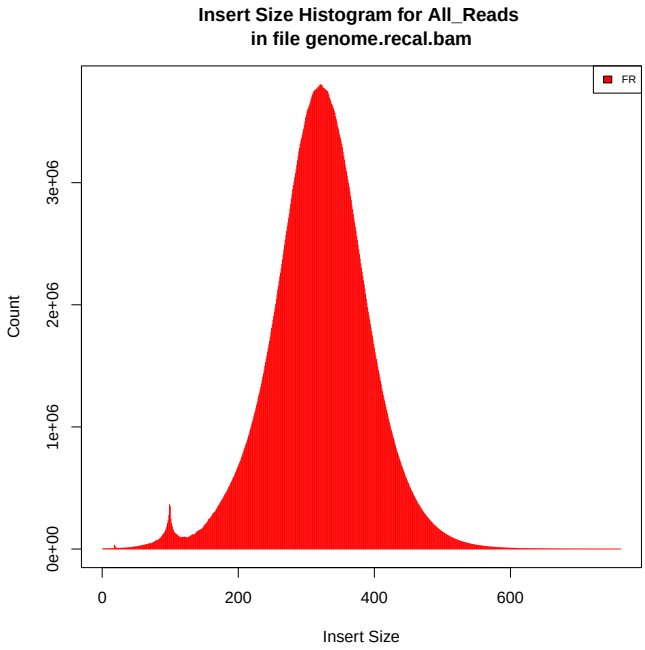

Figure 1: Insert size

Table 1: Insert Size Metrics

MEDIAN_INSERT_SIZE	322
MEDIAN_ABSOLUTE_DEVIATION	44
MIN_INSERT_SIZE	1
MAX_INSERT_SIZE	249230453
MEAN_INSERT_SIZE	319.181717
STANDARD_DEVIATION	72.530818
READ_PAIRS	613603753
PAIR_ORIENTATION	FR
WIDTH_OF_10_PERCENT	17
WIDTH_OF_20_PERCENT	33
WIDTH_OF_30_PERCENT	51
WIDTH_OF_40_PERCENT	69
WIDTH_OF_50_PERCENT	89
WIDTH_OF_60_PERCENT	113
WIDTH_OF_70_PERCENT	141
WIDTH_OF_80_PERCENT	181
WIDTH_OF_90_PERCENT	245
WIDTH_OF_99_PERCENT	2947
SAMPLE	
LIBRARY	
READ_GROUP	

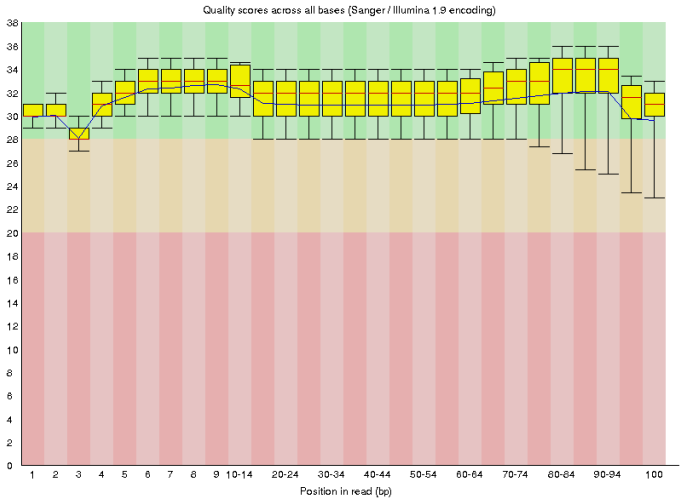

Figure 2: Read quality

Alignment quality

Table 2: Mapped read metrics

total	1337704436
duplicates	27545068
mapped	1320357652
paired in sequencing	1337704436
read1	668853080
read2	668851356
properly paired	1260655004
with itself and mate mapped	1309602873
singletons	10754779
with mate mapped to a different chr	15003068
with mate mapped to a different chr (mapQ>=5)	3296218

Coverage

Variant quality

Table 3: Variant Ti/Tv metrics

VariantType	nTi	nTv	TiTvRatio
SNP	41108	16937	2.43

Table 4: Variant count metrics

VariantType	nProcessedLoci	nVariantLoci	nSNPs	nMNPs	nInsertions	nDeletions	nComplex	nNoCalls	nHets	nHomVar	hetHomRatio
INDEL	76442373	9302	0	0	4465	4475	362	0	5509	3793	1.45
SNP	76442373	58062	58062	0	0	0	0	0	34530	23532	1.47

Detailed metrics

Raw quality

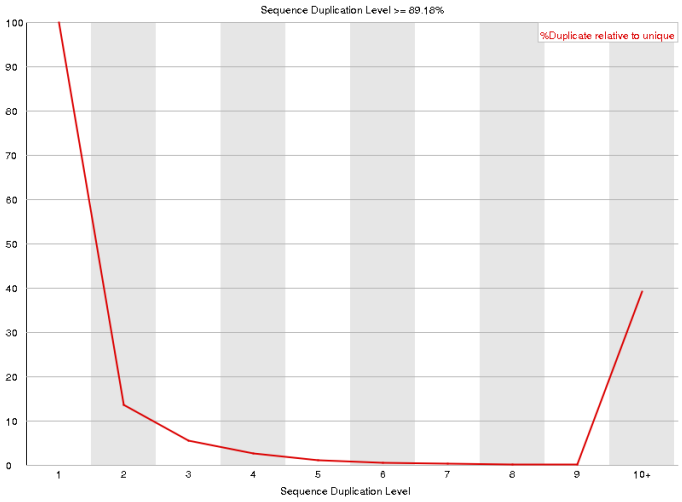

Figure 3: Duplication levels

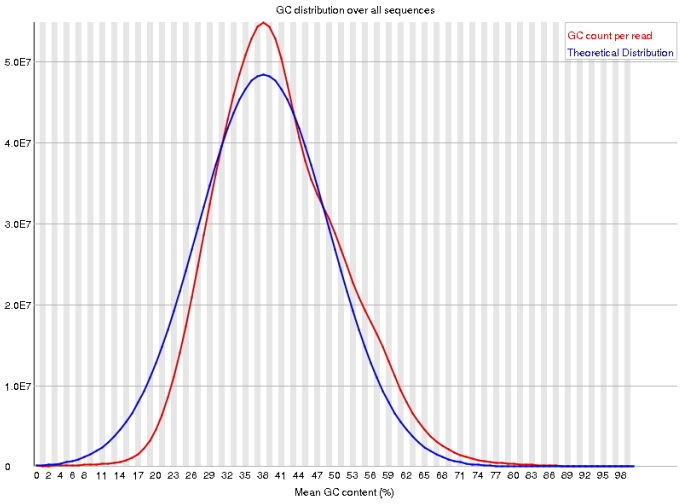

Figure 4: Per-sequence GC content

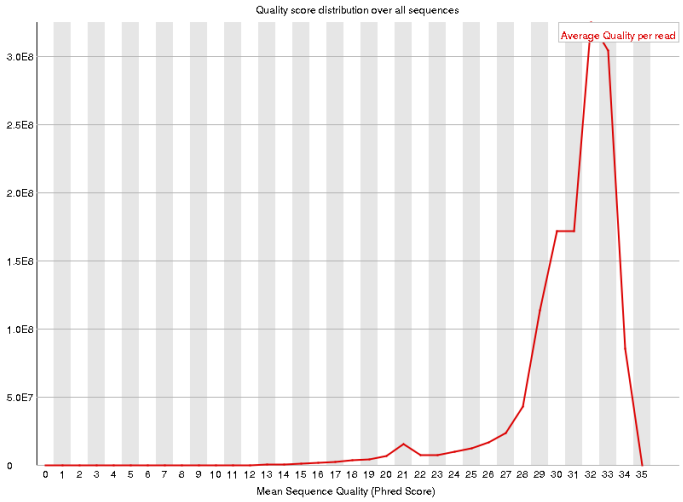

Figure 5: Per-sequence quality score

Alignment quality

Coverage

Variant quality

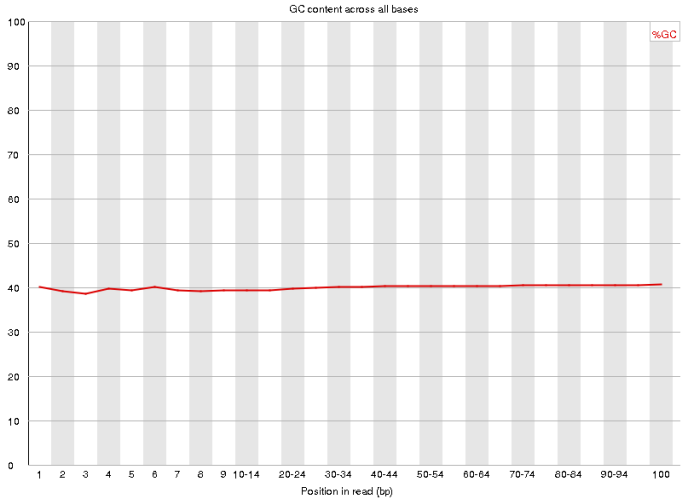

Figure 6: Per-base GC content

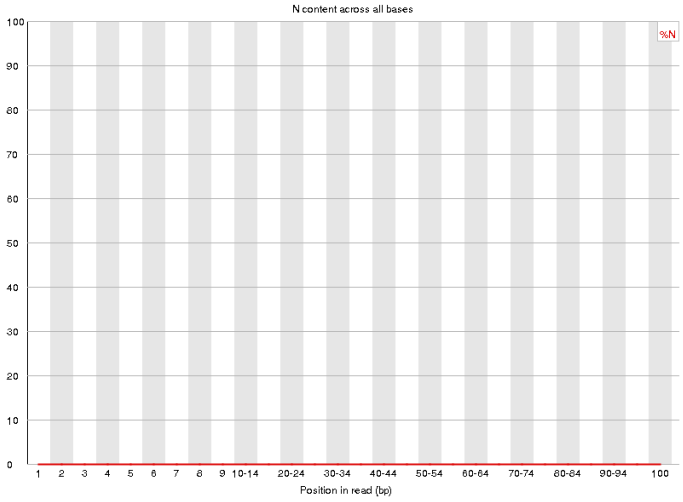

Figure 7: Per-base N content

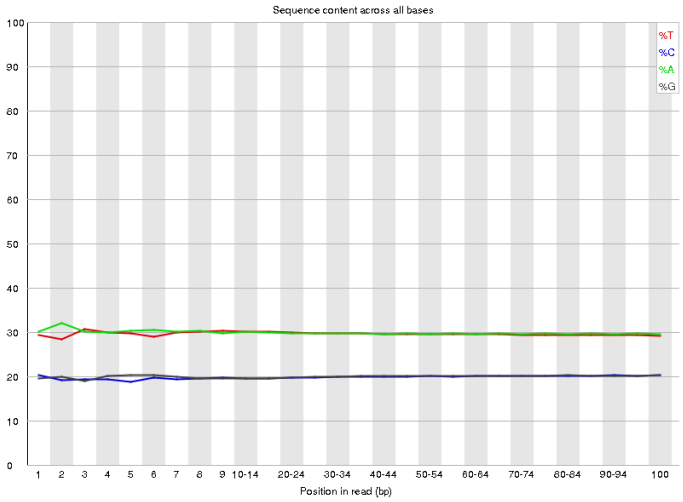

Figure 8: Per-base sequence content

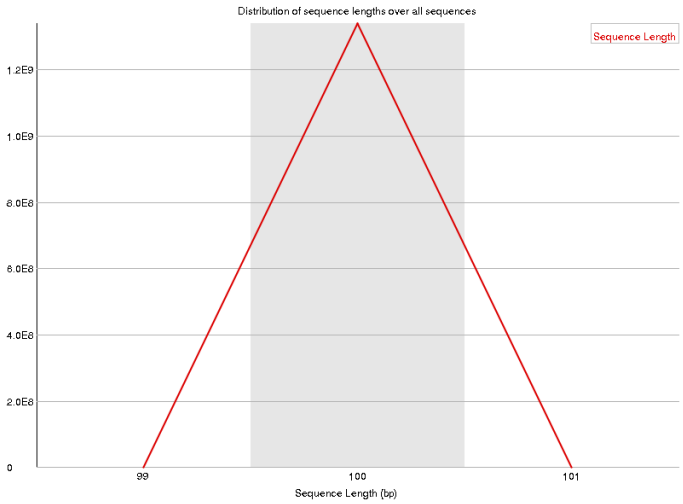

Figure 9: Sequence length distribution