

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 23:32:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094065.sorted.bam -c -nw 400 -hm 3
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1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_ERR2094065 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094065_1.fastq.gz ERR2094065_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 23:32:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094065.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	394,518
Mapped reads	368,403 / 93.38%
Unmapped reads	26,115 / 6.62%
Mapped paired reads	368,403 / 93.38%
Mapped reads, first in pair	185,004 / 46.89%
Mapped reads, second in pair	183,399 / 46.49%
Mapped reads, both in pair	365,634 / 92.68%
Mapped reads, singletons	2,769 / 0.7%
Secondary alignments	0
Supplementary alignments	13,417 / 3.4%
Read min/max/mean length	30 / 151 / 137.04
Duplicated reads (estimated)	351,471 / 89.09%
Duplication rate	49.47%
Clipped reads	147,257 / 37.33%

2.2. ACGT Content

Number/percentage of A's	12,453,668 / 26.56%
Number/percentage of C's	10,997,578 / 23.45%
Number/percentage of T's	11,783,489 / 25.13%
Number/percentage of G's	11,660,571 / 24.86%
Number/percentage of N's	534 / 0%

GC Percentage	48.32%
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2.3. Coverage

Mean	0.0155
Standard Deviation	4.2175

2.4. Mapping Quality

Mean Mapping Quality	37.73
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2.5. Insert size

Mean	341,548.29
Standard Deviation	5,272,061.29
P25/Median/P75	128 / 164 / 192

2.6. Mismatches and indels

General error rate	4.18%
Mismatches	1,891,291
Insertions	32,248
Mapped reads with at least one insertion	8.6%
Deletions	154,174
Mapped reads with at least one deletion	39.9%
Homopolymer indels	27.26%

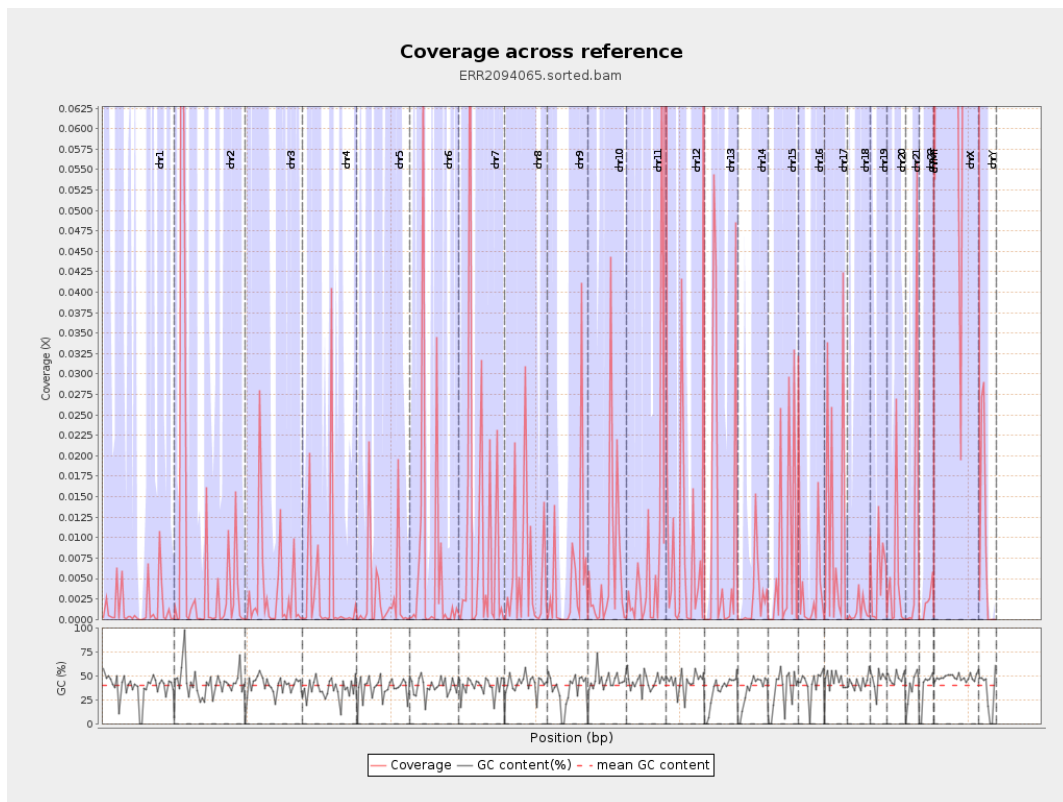
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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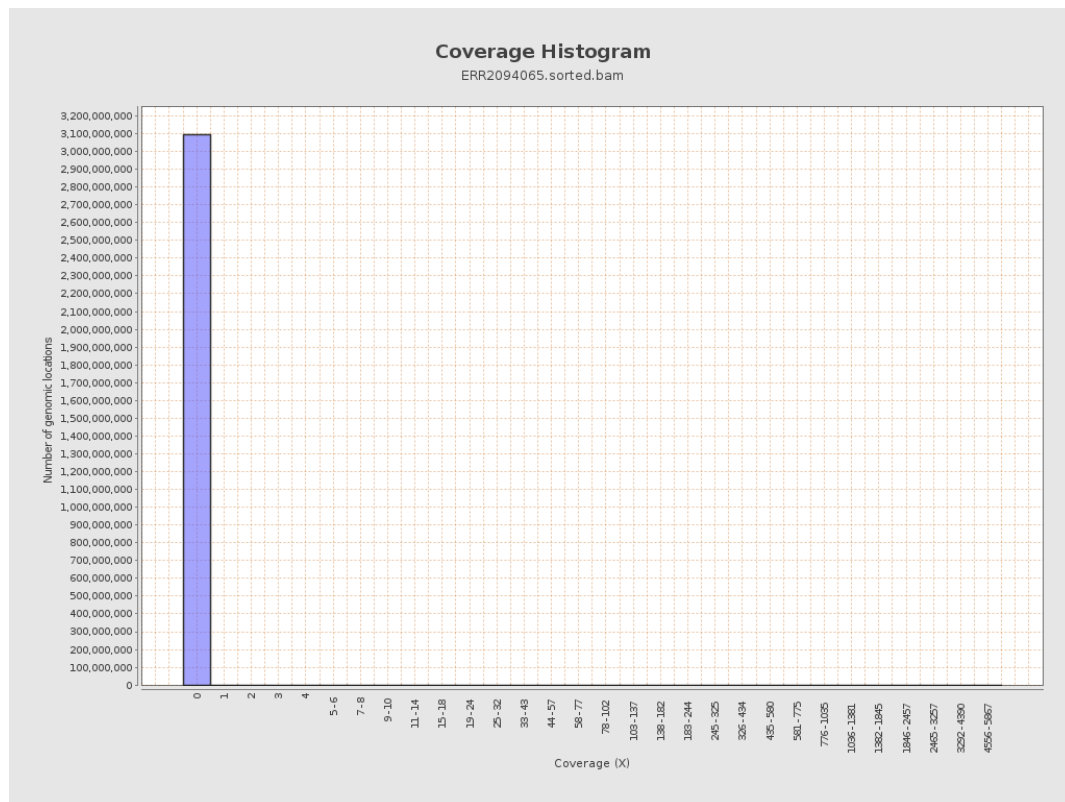
		bases	coverage	deviation
chr1	249250621	333552	0.0013	0.6036
chr2	243199373	1675943	0.0069	2.6281
chr3	198022430	614072	0.0031	1.0088
chr4	191154276	639132	0.0033	1.3315
chr5	180915260	492892	0.0027	1.391
chr6	171115067	1087738	0.0064	3.4636
chr7	159138663	1546096	0.0097	3.8448
chr8	146364022	840708	0.0057	2.0011
chr9	141213431	687681	0.0049	2.0847
chr10	135534747	860721	0.0064	2.5729
chr11	135006516	1141369	0.0085	2.5652
chr12	133851895	1173119	0.0088	2.7345
chr13	115169878	1226049	0.0106	3.2712
chr14	107349540	284149	0.0026	1.0328
chr15	102531392	754941	0.0074	2.352
chr16	90354753	392395	0.0043	1.7578
chr17	81195210	874614	0.0108	3.5857
chr18	78077248	85035	0.0011	0.3492
chr19	59128983	289480	0.0049	1.1713
chr20	63025520	304988	0.0048	1.6027
chr21	48129895	508019	0.0106	3.9711
chr22	51304566	96853	0.0019	0.578
chrMT	16571	934478	56.3924	260.719
chrX	155270560	30624073	0.1972	15.6879

chrY	59373566	514565	0.0087	2.4205
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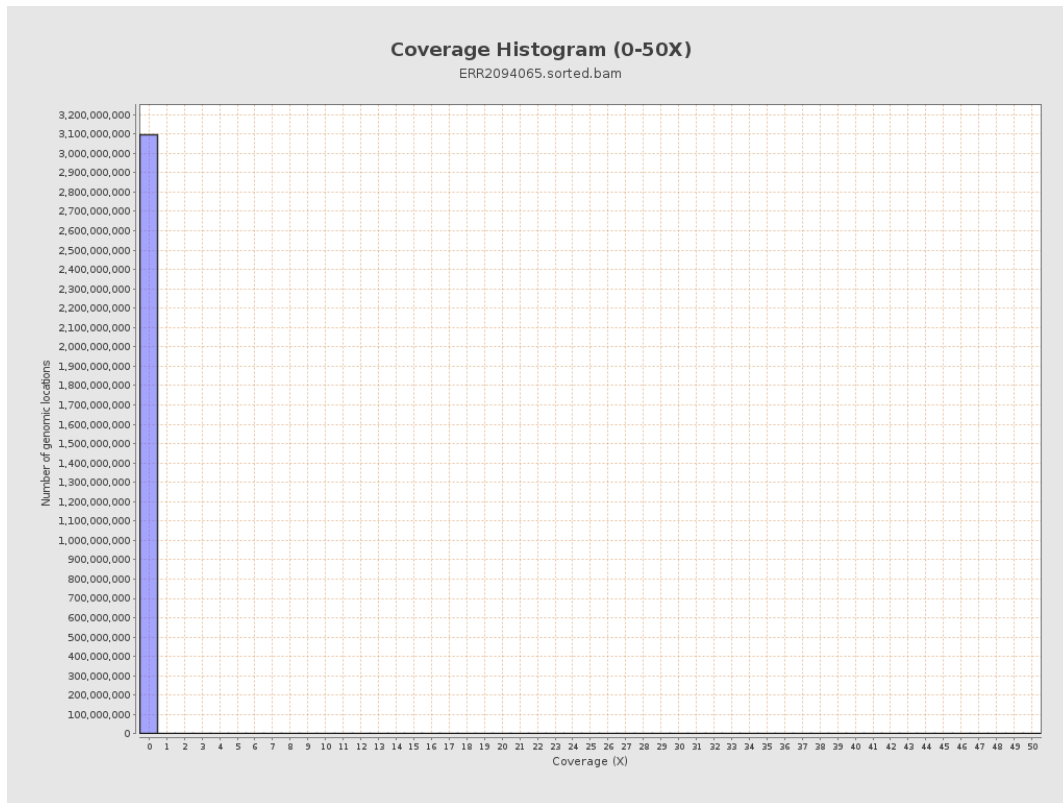
3. Results : Coverage across reference



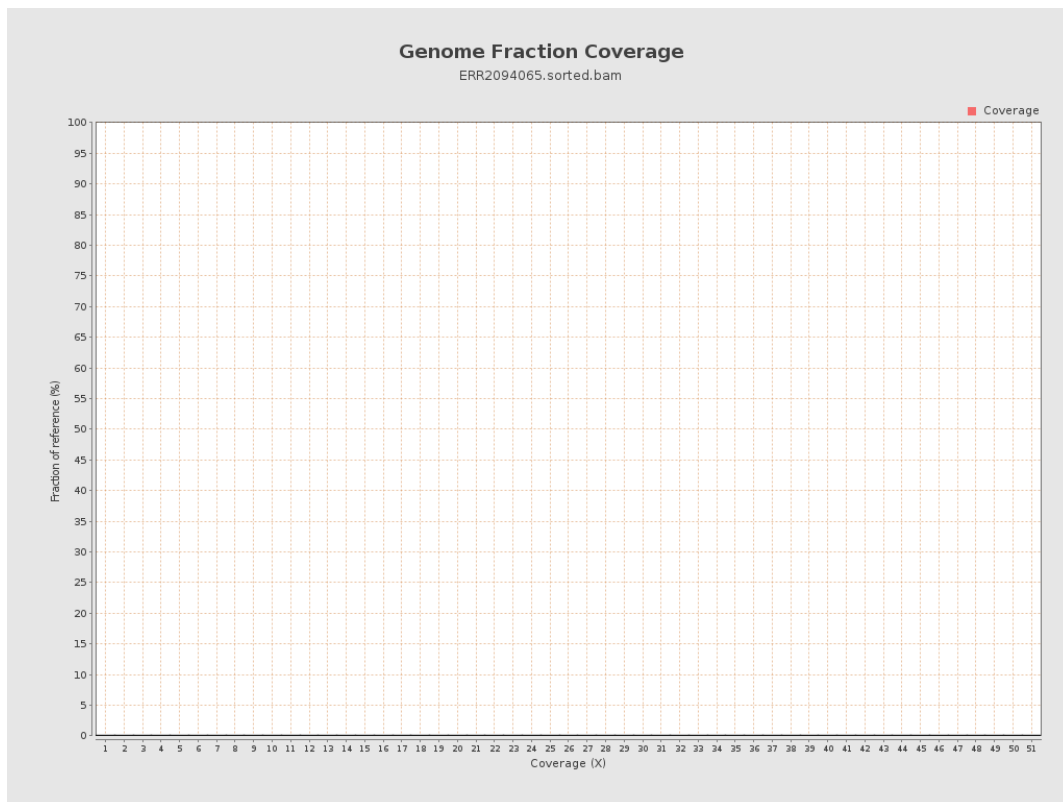
4. Results : Coverage Histogram



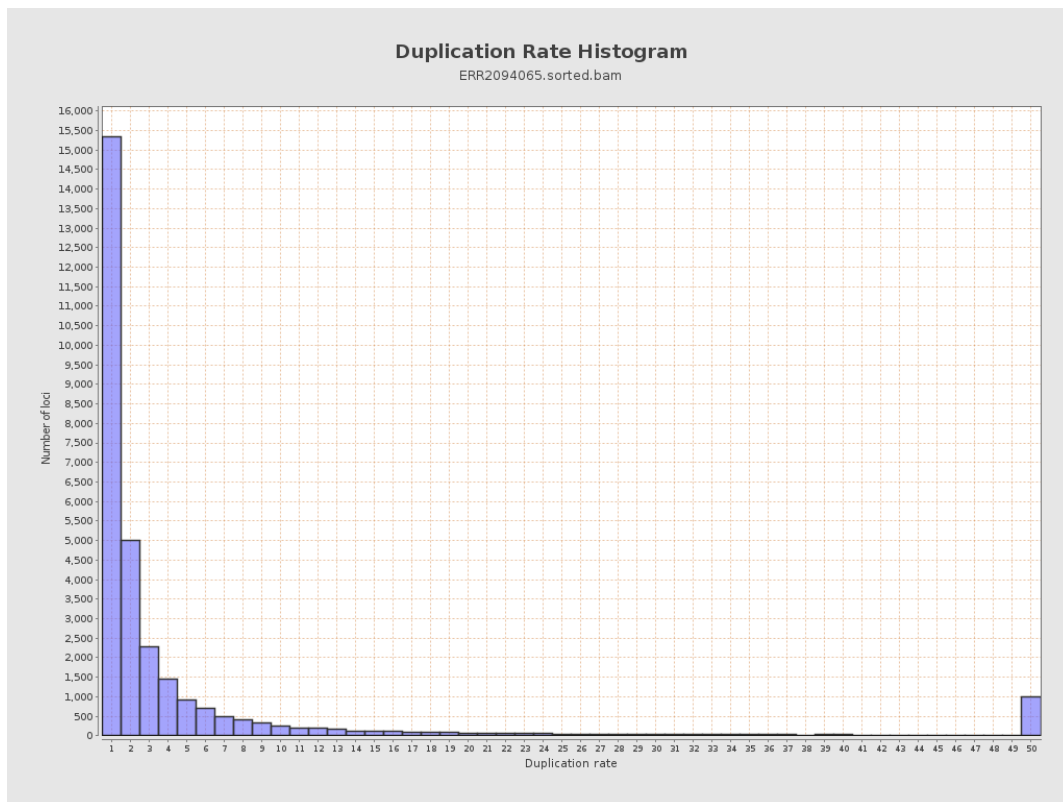
5. Results : Coverage Histogram (0-50X)



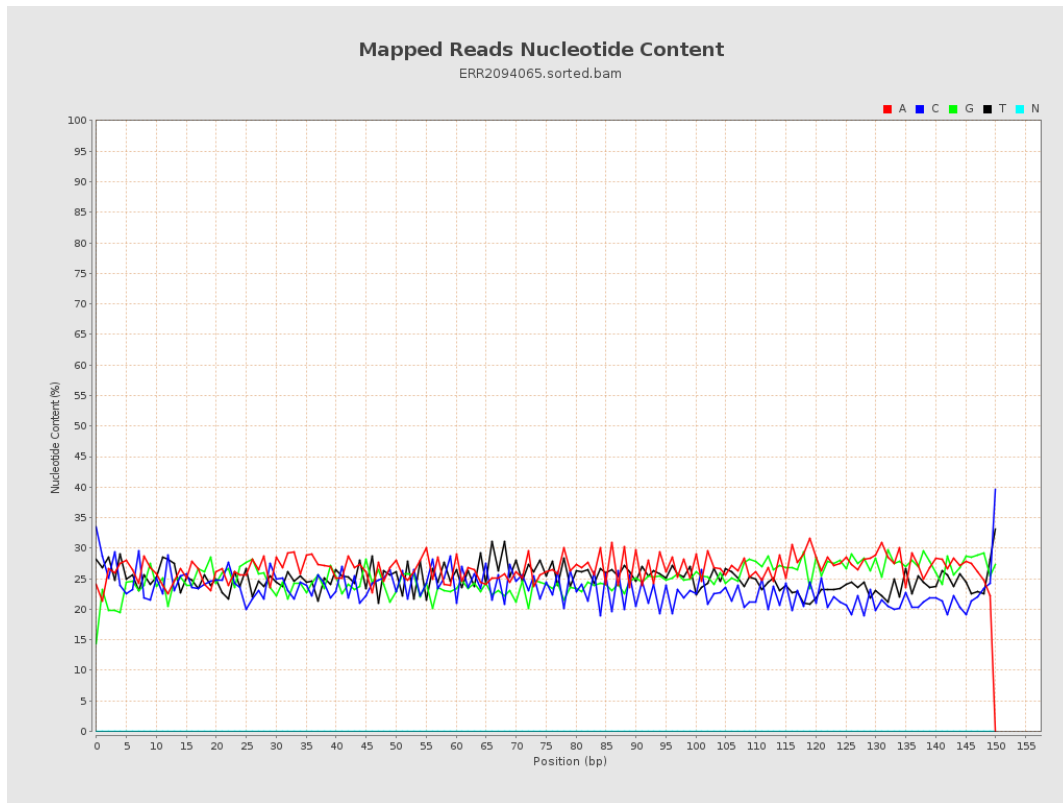
6. Results : Genome Fraction Coverage



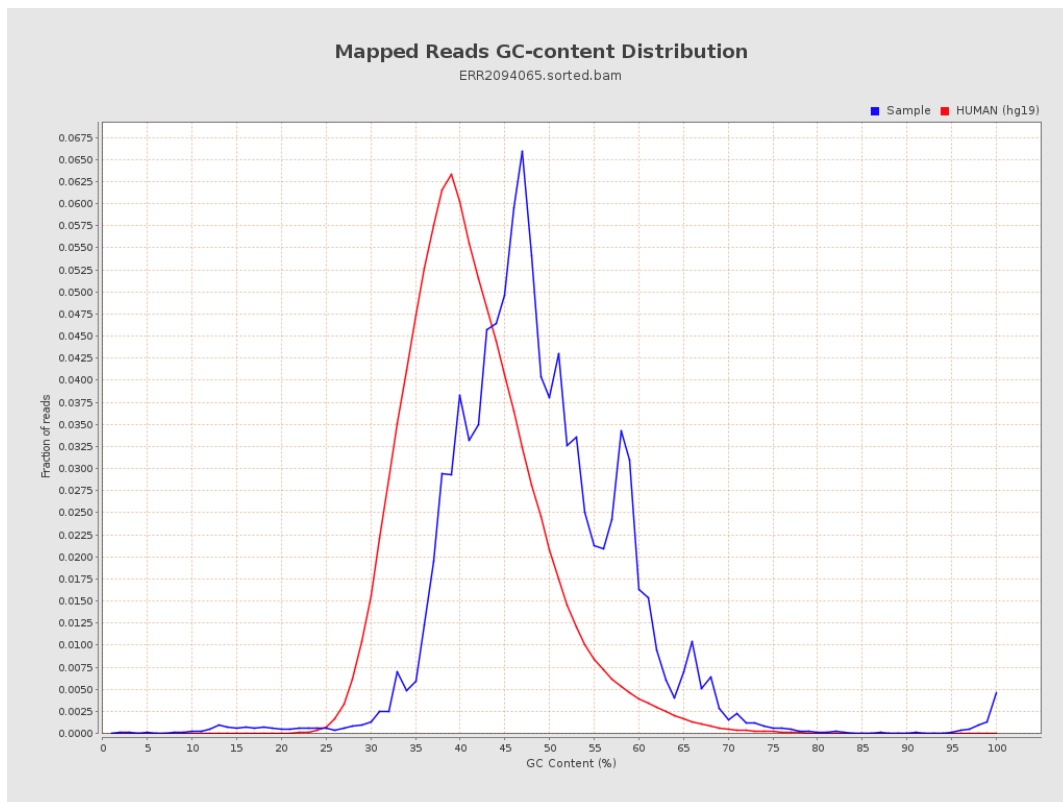
7. Results : Duplication Rate Histogram



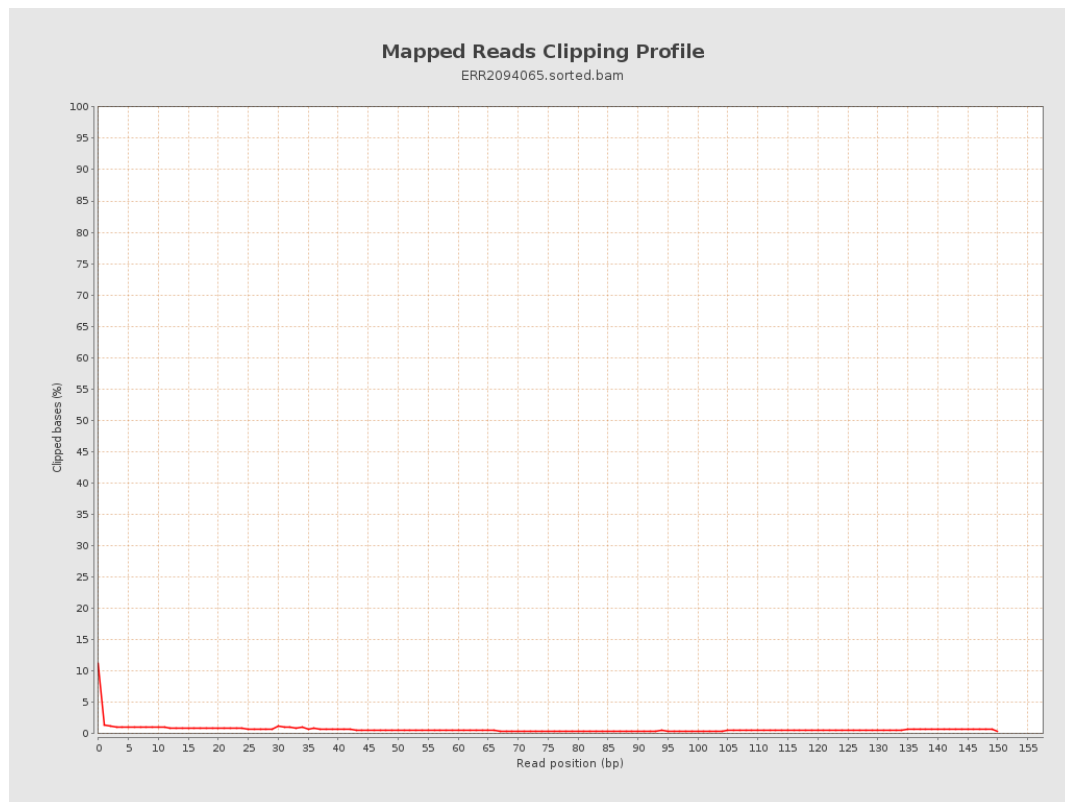
8. Results : Mapped Reads Nucleotide Content



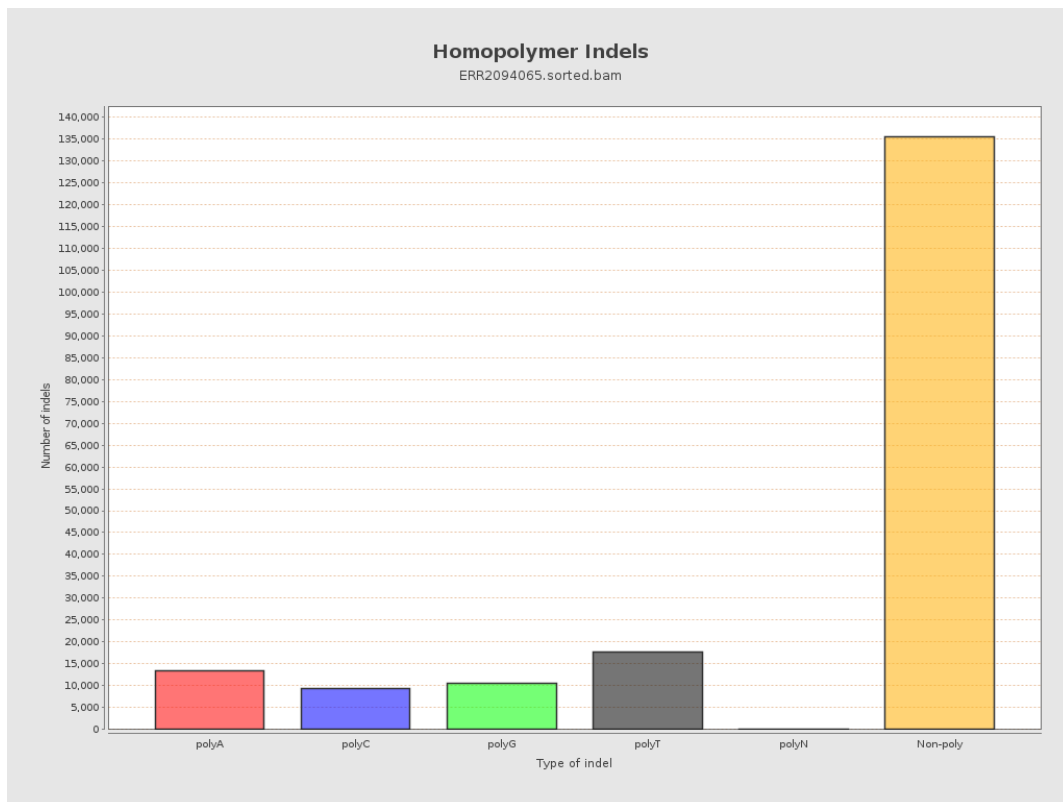
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



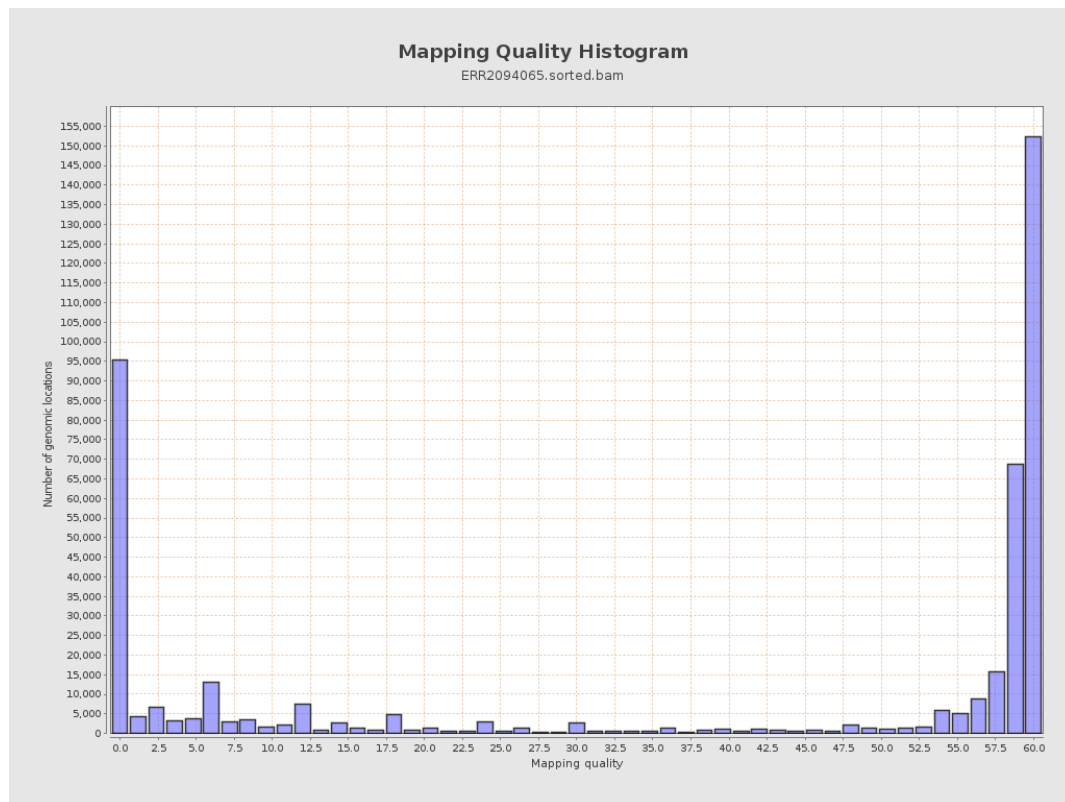
11. Results : Homopolymer Indels



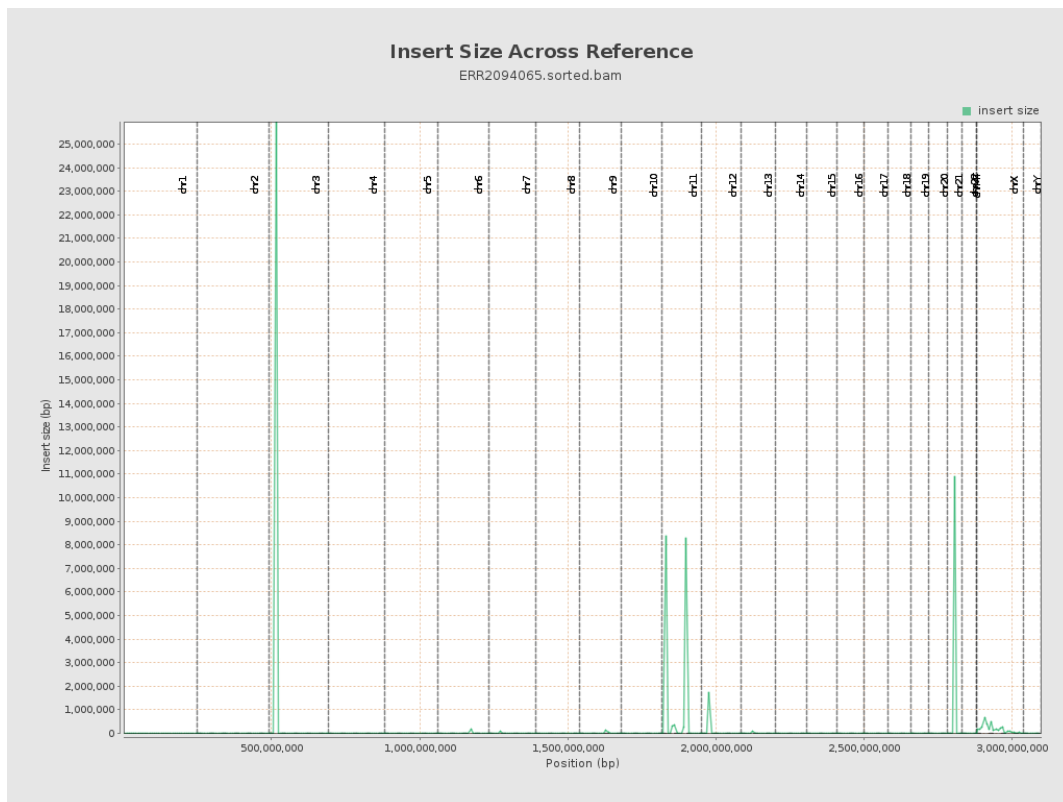
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

