

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 00:12:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094081.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_ERR2094081 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094081_1.fastq.gz ERR2094081_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 00:12:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094081.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	391,544
Mapped reads	380,891 / 97.28%
Unmapped reads	10,653 / 2.72%
Mapped paired reads	380,891 / 97.28%
Mapped reads, first in pair	191,437 / 48.89%
Mapped reads, second in pair	189,454 / 48.39%
Mapped reads, both in pair	378,126 / 96.57%
Mapped reads, singletons	2,765 / 0.71%
Secondary alignments	0
Supplementary alignments	13,084 / 3.34%
Read min/max/mean length	30 / 151 / 143.98
Duplicated reads (estimated)	363,118 / 92.74%
Duplication rate	48.62%
Clipped reads	140,368 / 35.85%

2.2. ACGT Content

Number/percentage of A's	13,127,247 / 26.18%
Number/percentage of C's	11,974,006 / 23.88%
Number/percentage of T's	12,608,465 / 25.14%
Number/percentage of G's	12,437,721 / 24.8%
Number/percentage of N's	568 / 0%

GC Percentage	48.68%
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2.3. Coverage

Mean	0.0166
Standard Deviation	4.7285

2.4. Mapping Quality

Mean Mapping Quality	39.48
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2.5. Insert size

Mean	392,961.36
Standard Deviation	5,664,478.28
P25/Median/P75	144 / 172 / 204

2.6. Mismatches and indels

General error rate	3.89%
Mismatches	1,879,097
Insertions	29,189
Mapped reads with at least one insertion	7.53%
Deletions	143,653
Mapped reads with at least one deletion	36.11%
Homopolymer indels	28.46%

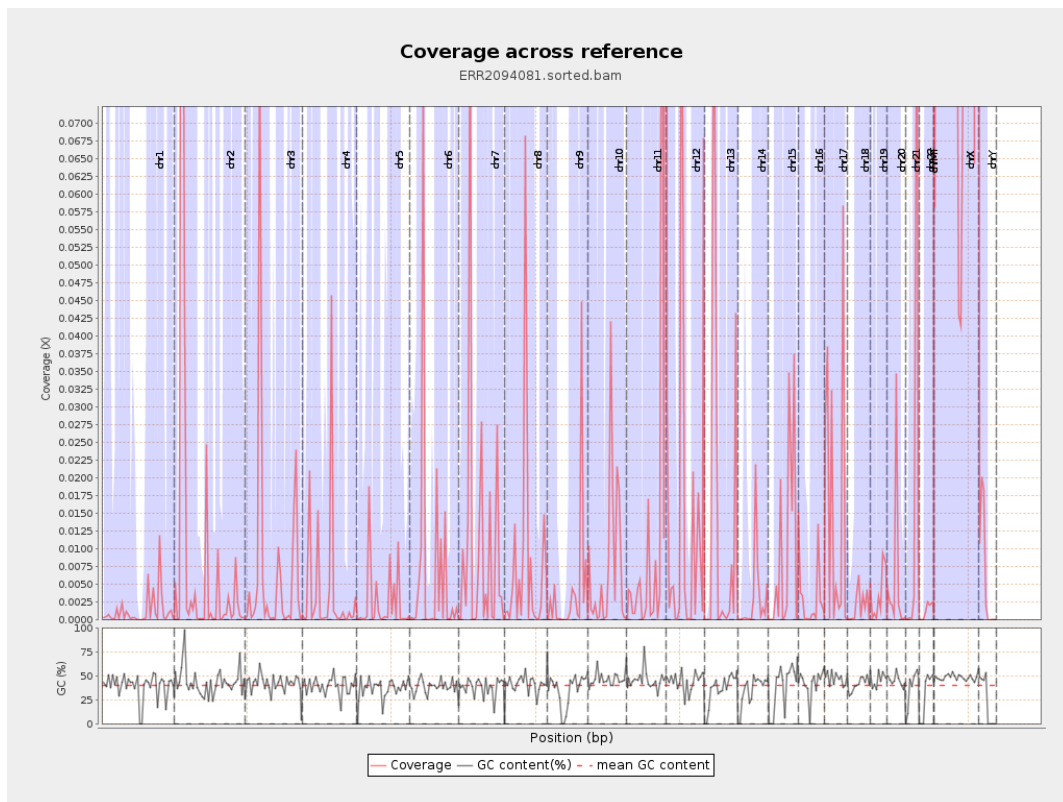
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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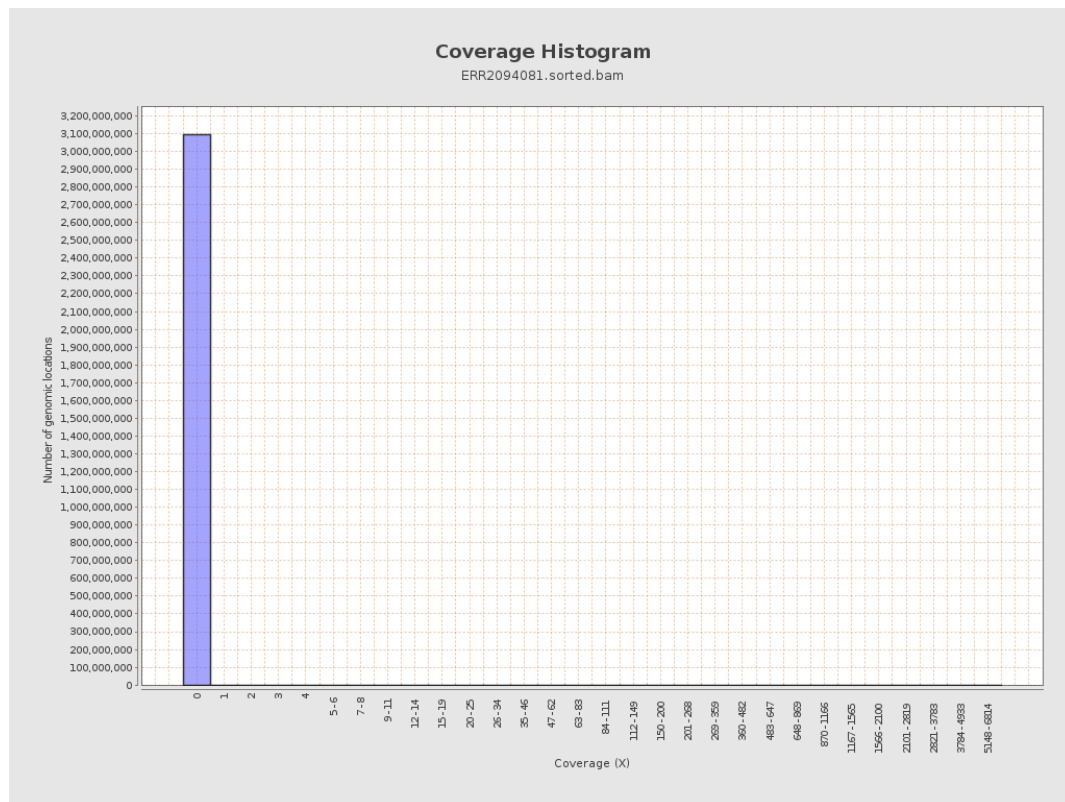
		bases	coverage	deviation
chr1	249250621	302057	0.0012	0.5661
chr2	243199373	2218492	0.0091	3.8413
chr3	198022430	1274663	0.0064	3.0441
chr4	191154276	767156	0.004	1.6378
chr5	180915260	417231	0.0023	1.0776
chr6	171115067	1129036	0.0066	3.8231
chr7	159138663	1620964	0.0102	3.839
chr8	146364022	1077471	0.0074	3.0585
chr9	141213431	570525	0.004	2.0748
chr10	135534747	1011530	0.0075	2.6464
chr11	135006516	1767370	0.0131	4.3461
chr12	133851895	1748690	0.0131	5.2984
chr13	115169878	1509421	0.0131	4.0087
chr14	107349540	311860	0.0029	1.3298
chr15	102531392	891197	0.0087	2.5856
chr16	90354753	279312	0.0031	0.9693
chr17	81195210	1274138	0.0157	4.9953
chr18	78077248	151052	0.0019	0.6248
chr19	59128983	192549	0.0033	0.7638
chr20	63025520	349243	0.0055	1.824
chr21	48129895	874059	0.0182	7.9918
chr22	51304566	62446	0.0012	0.2758
chrMT	16571	1897527	114.5089	548.1365
chrX	155270560	29170286	0.1879	15.1051

chrY	59373566	368035	0.0062	1.2502
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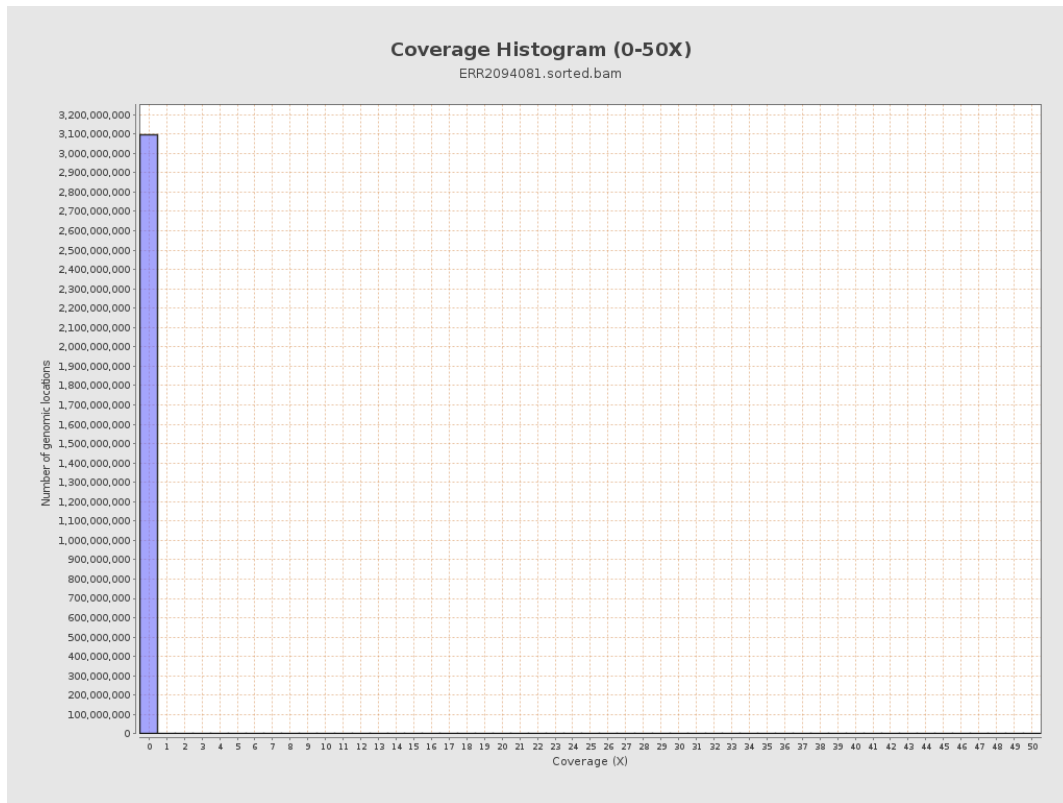
3. Results : Coverage across reference



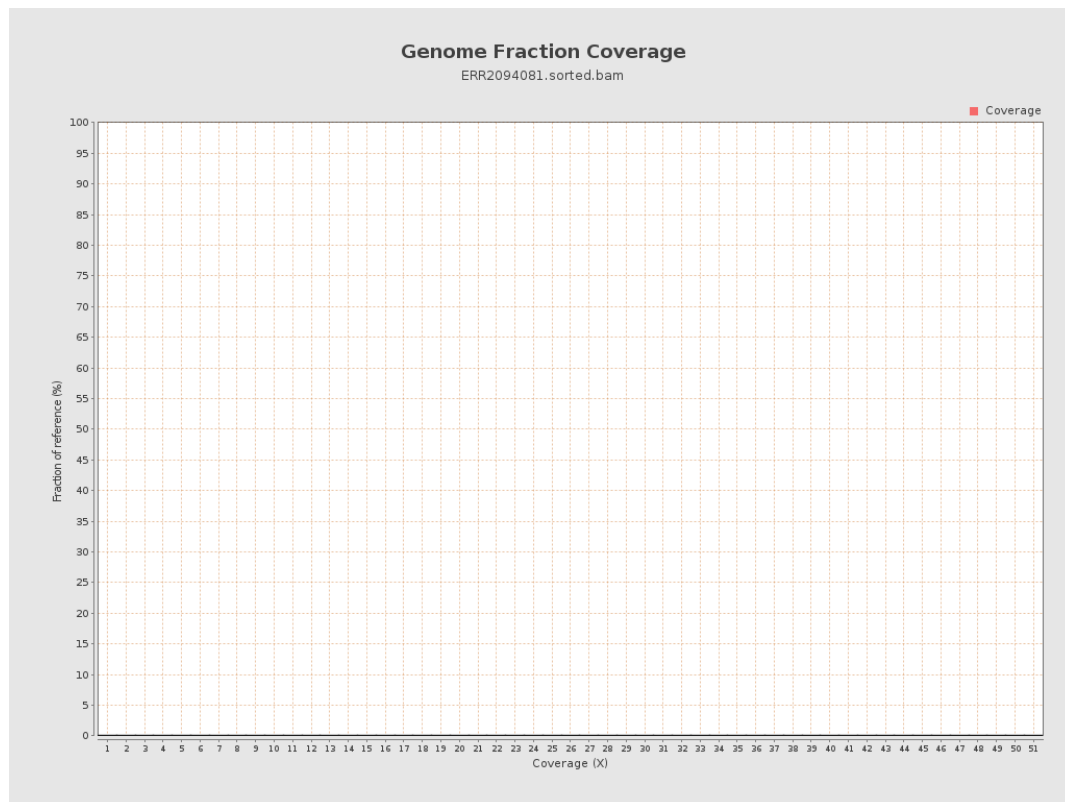
4. Results : Coverage Histogram



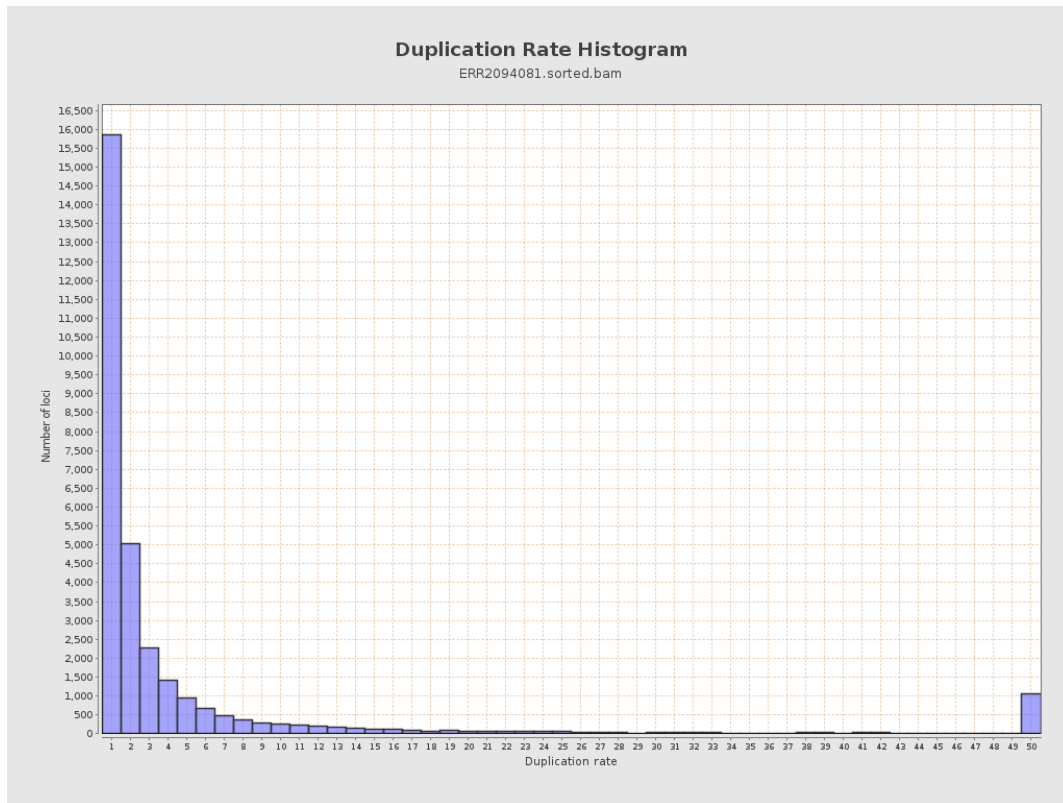
5. Results : Coverage Histogram (0-50X)



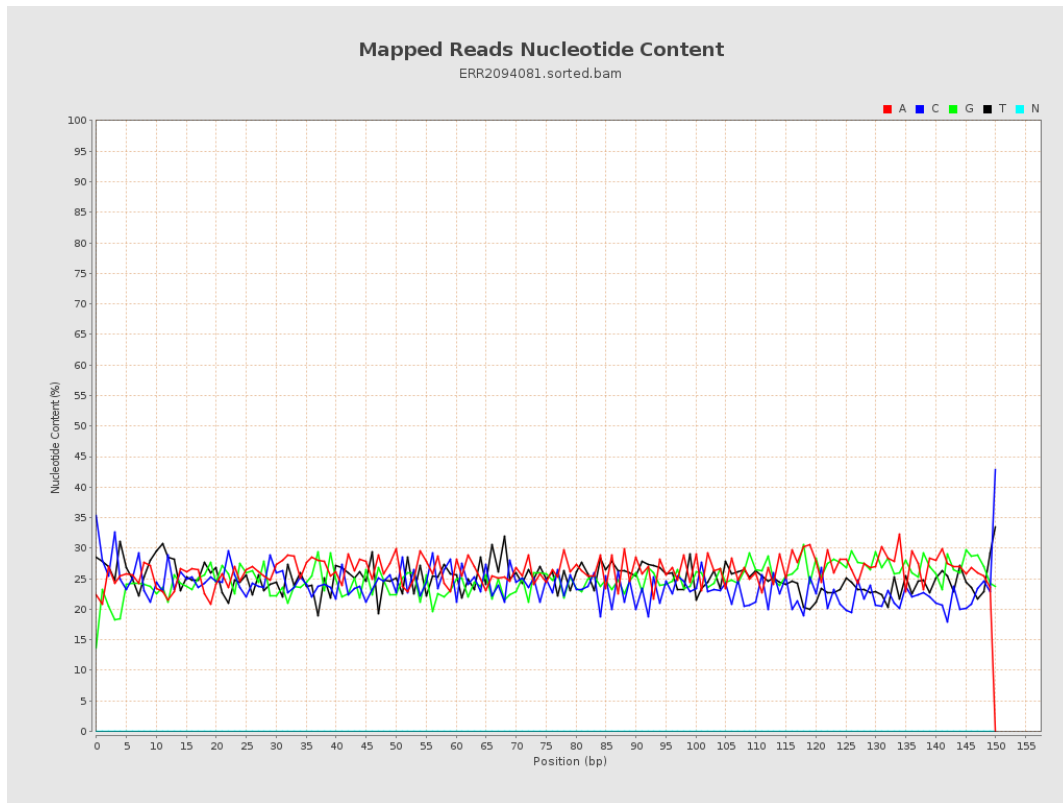
6. Results : Genome Fraction Coverage



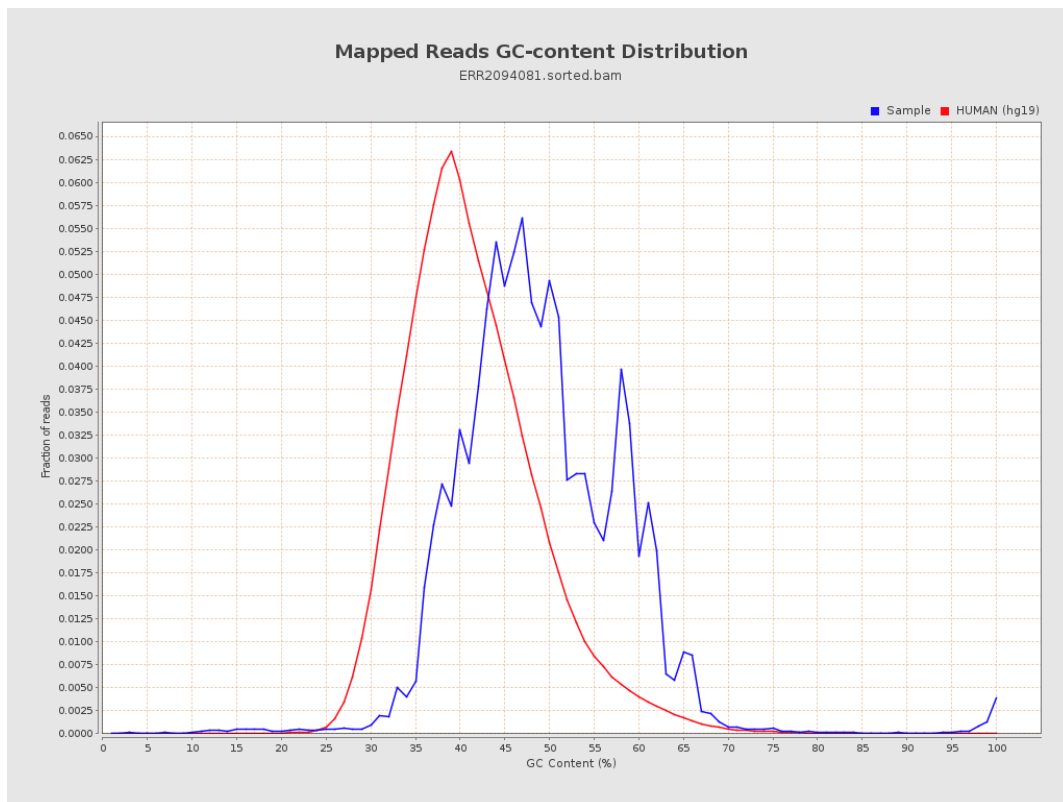
7. Results : Duplication Rate Histogram



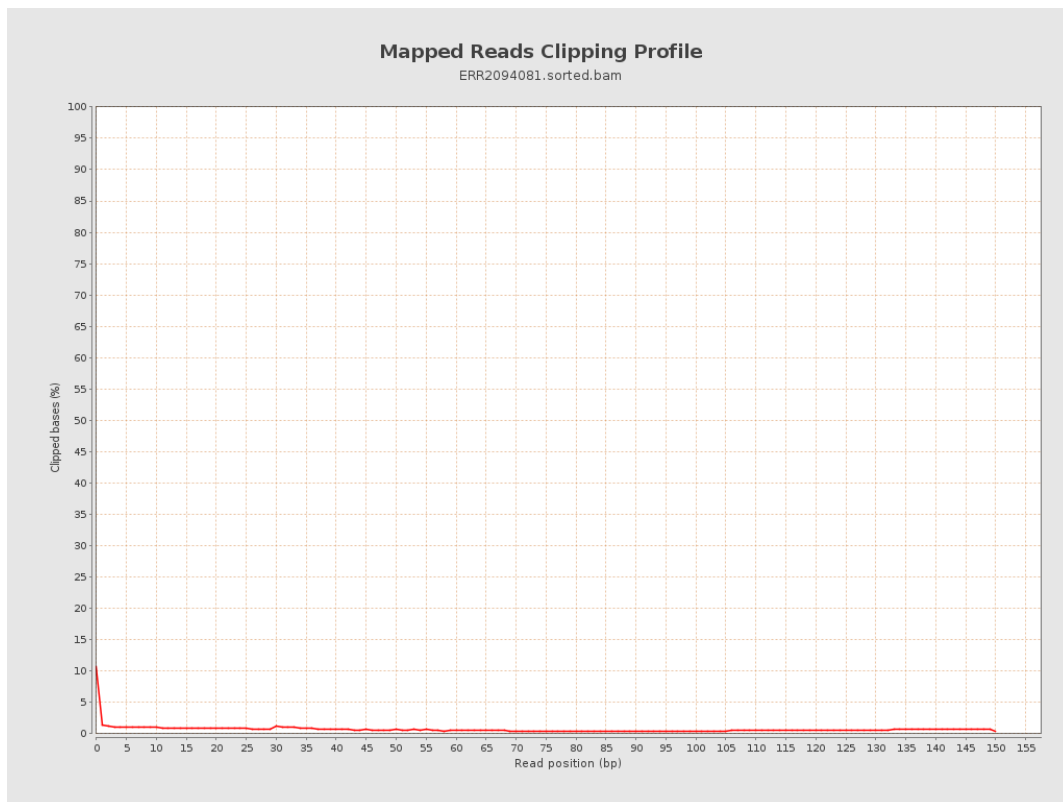
8. Results : Mapped Reads Nucleotide Content



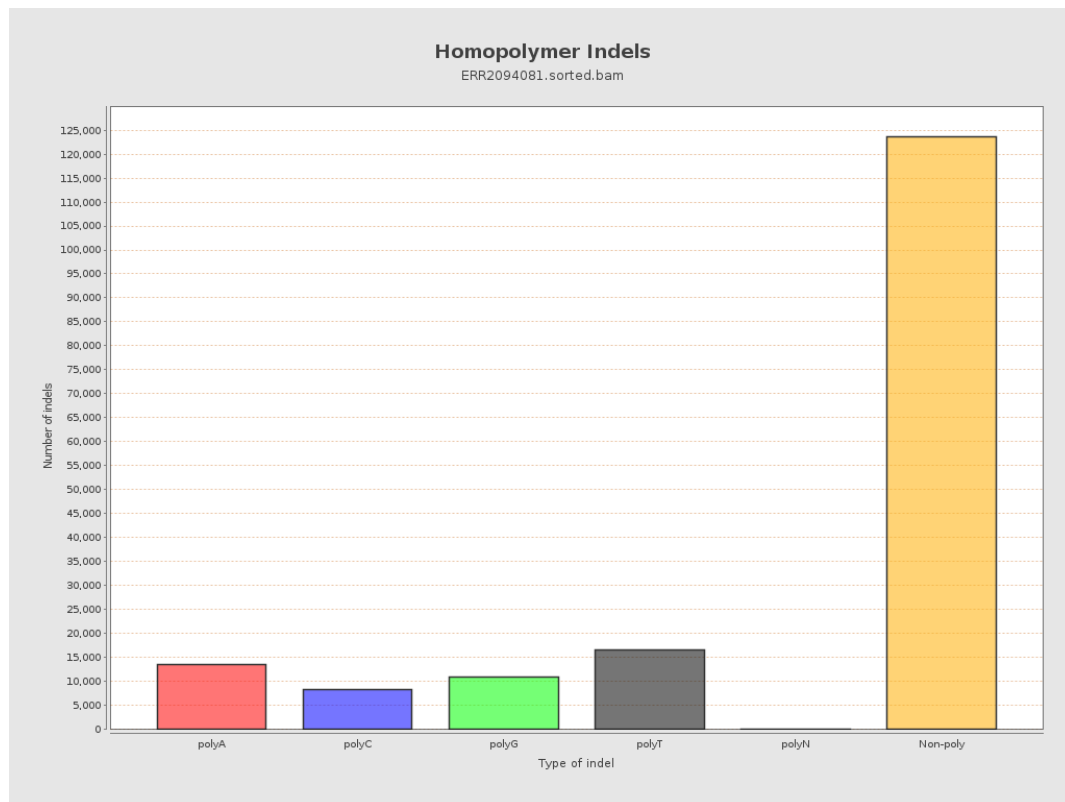
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



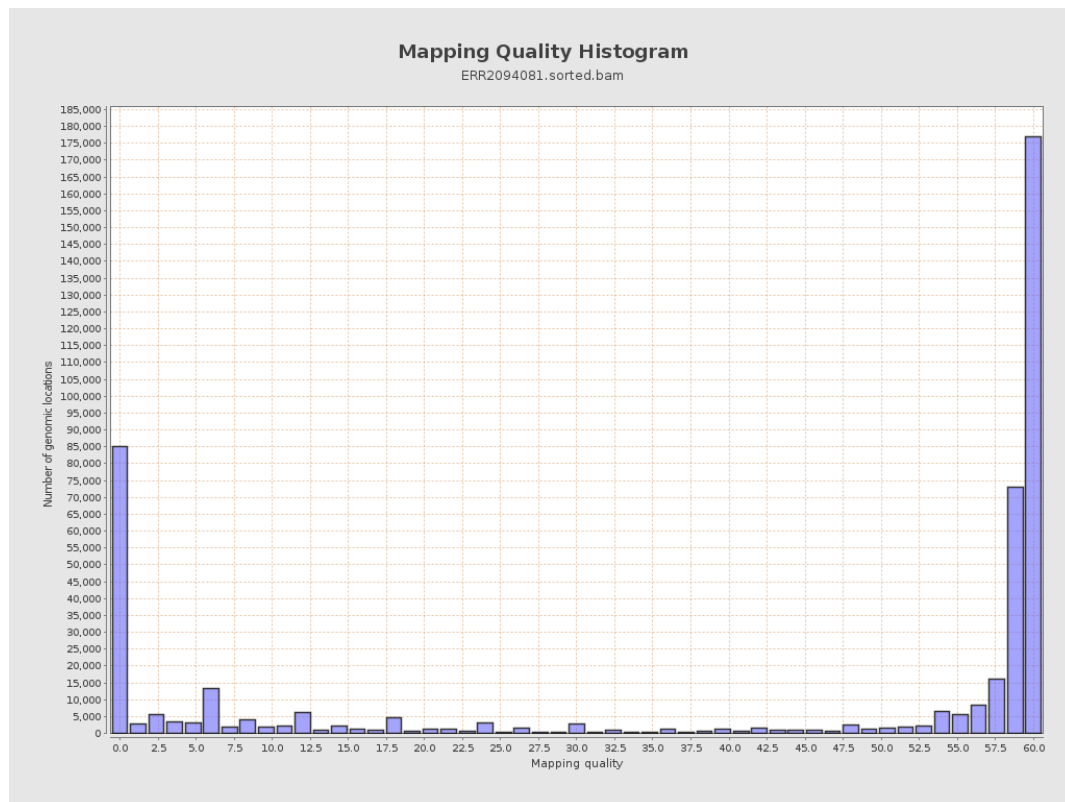
11. Results : Homopolymer Indels



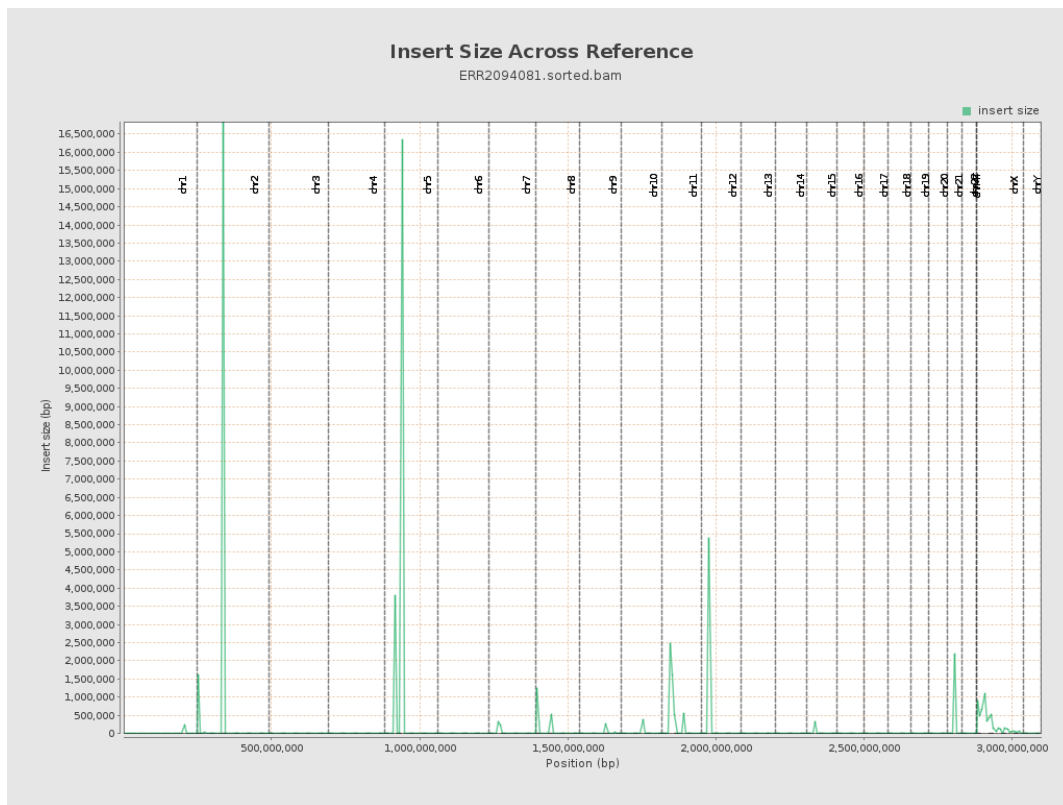
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

