

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 01:14:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094104.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_ERR2094104 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094104_1.fastq.gz ERR2094104_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 01:14:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094104.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	469,218
Mapped reads	437,446 / 93.23%
Unmapped reads	31,772 / 6.77%
Mapped paired reads	437,446 / 93.23%
Mapped reads, first in pair	219,705 / 46.82%
Mapped reads, second in pair	217,741 / 46.41%
Mapped reads, both in pair	433,906 / 92.47%
Mapped reads, singletons	3,540 / 0.75%
Secondary alignments	0
Supplementary alignments	29,433 / 6.27%
Read min/max/mean length	30 / 151 / 135.1
Duplicated reads (estimated)	420,348 / 89.58%
Duplication rate	52.36%
Clipped reads	223,165 / 47.56%

2.2. ACGT Content

Number/percentage of A's	15,376,872 / 29.1%
Number/percentage of C's	11,231,427 / 21.25%
Number/percentage of T's	14,413,406 / 27.27%
Number/percentage of G's	11,825,591 / 22.38%
Number/percentage of N's	572 / 0%

GC Percentage	43.63%
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2.3. Coverage

Mean	0.0174
Standard Deviation	3.6281

2.4. Mapping Quality

Mean Mapping Quality	41.85
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2.5. Insert size

Mean	1,663,545.75
Standard Deviation	11,539,229.41
P25/Median/P75	112 / 145 / 172

2.6. Mismatches and indels

General error rate	3.49%
Mismatches	1,778,601
Insertions	35,116
Mapped reads with at least one insertion	7.94%
Deletions	139,727
Mapped reads with at least one deletion	30.99%
Homopolymer indels	26.36%

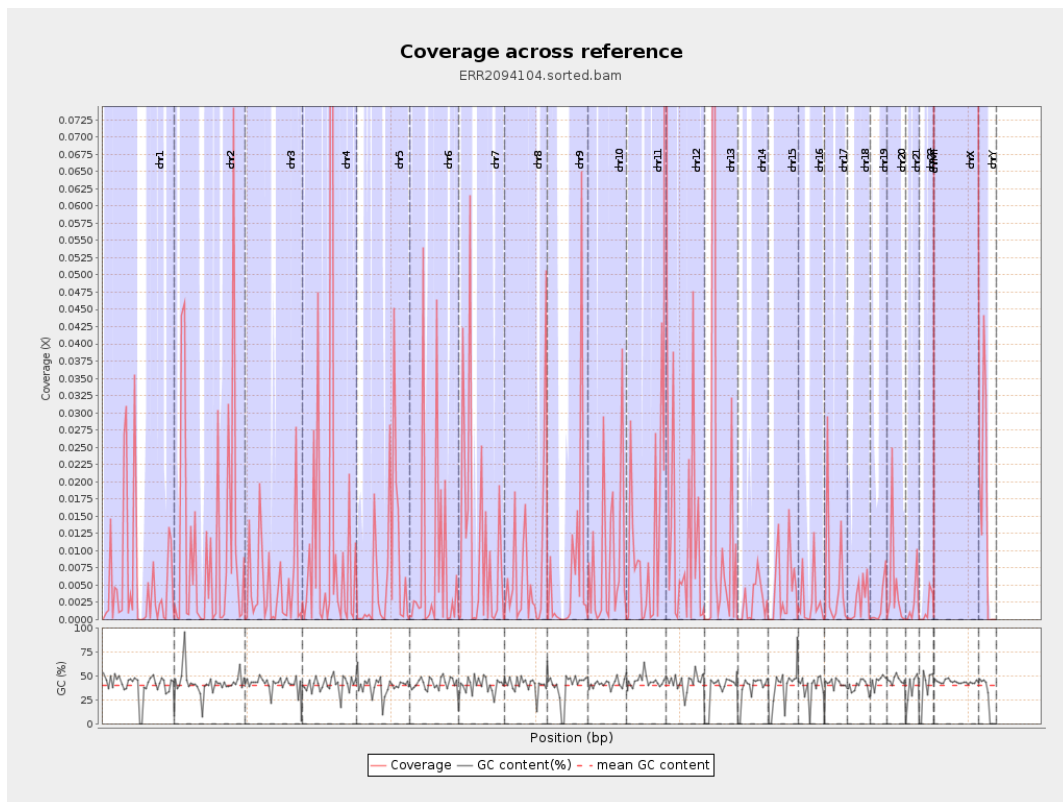
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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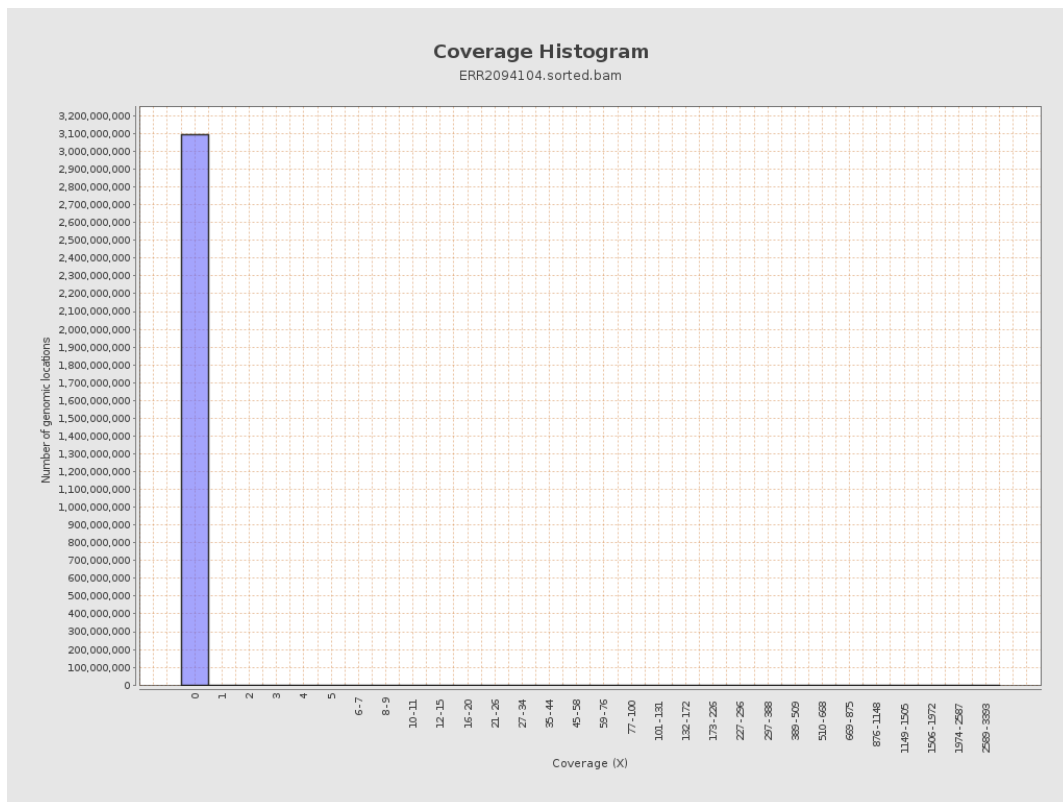
		bases	coverage	deviation
chr1	249250621	1368137	0.0055	2.3387
chr2	243199373	2556651	0.0105	3.4411
chr3	198022430	947573	0.0048	1.5734
chr4	191154276	2779562	0.0145	4.1751
chr5	180915260	1245552	0.0069	3.0203
chr6	171115067	1292297	0.0076	2.917
chr7	159138663	1673927	0.0105	2.9267
chr8	146364022	1123600	0.0077	2.6298
chr9	141213431	922933	0.0065	2.7542
chr10	135534747	1110144	0.0082	2.5944
chr11	135006516	1678703	0.0124	3.3279
chr12	133851895	1653996	0.0124	2.9373
chr13	115169878	1712582	0.0149	4.0425
chr14	107349540	269561	0.0025	0.8339
chr15	102531392	458943	0.0045	1.0067
chr16	90354753	247828	0.0027	0.9547
chr17	81195210	435735	0.0054	2.0818
chr18	78077248	212537	0.0027	0.7645
chr19	59128983	116610	0.002	0.6567
chr20	63025520	303123	0.0048	1.901
chr21	48129895	116061	0.0024	0.6064
chr22	51304566	77370	0.0015	0.4386
chrMT	16571	188802	11.3935	51.4781
chrX	155270560	30595857	0.197	11.1437

chrY	59373566	797045	0.0134	2.6386
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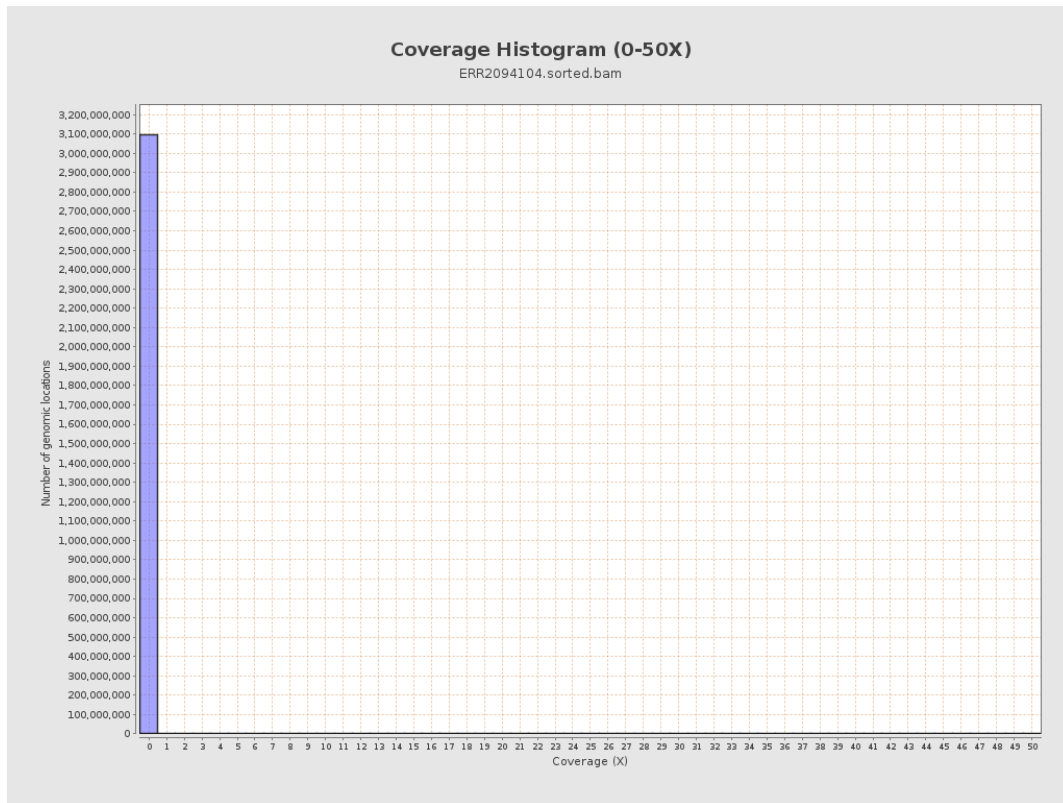
3. Results : Coverage across reference



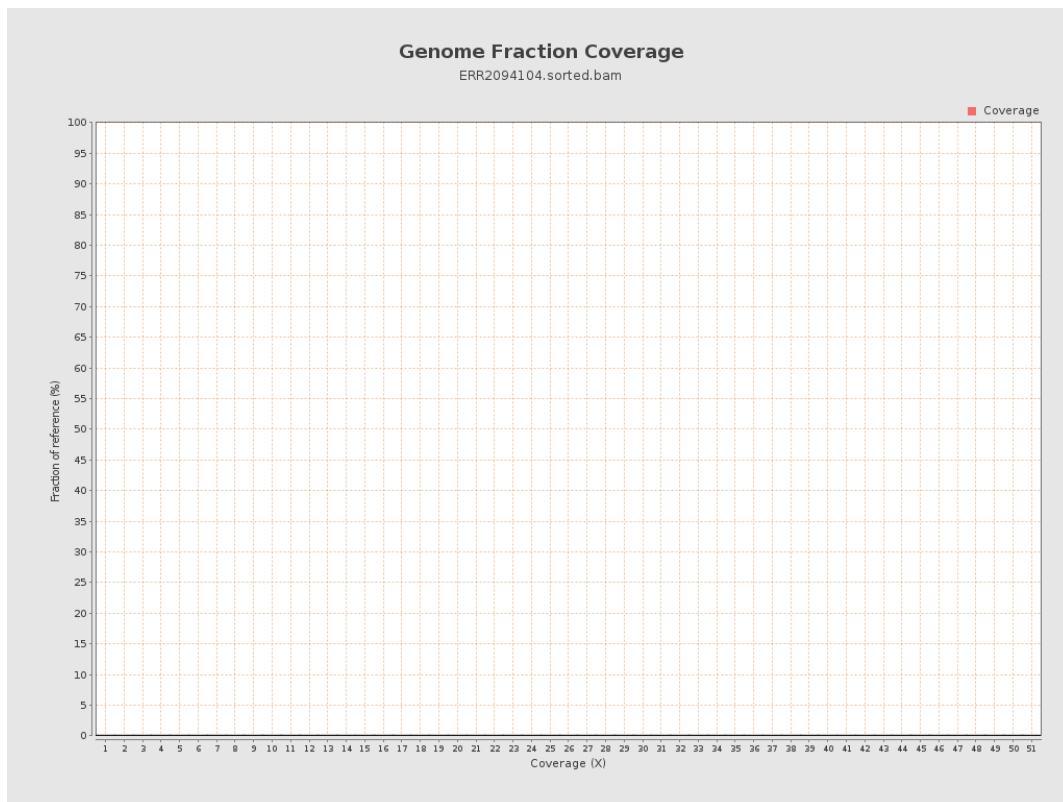
4. Results : Coverage Histogram



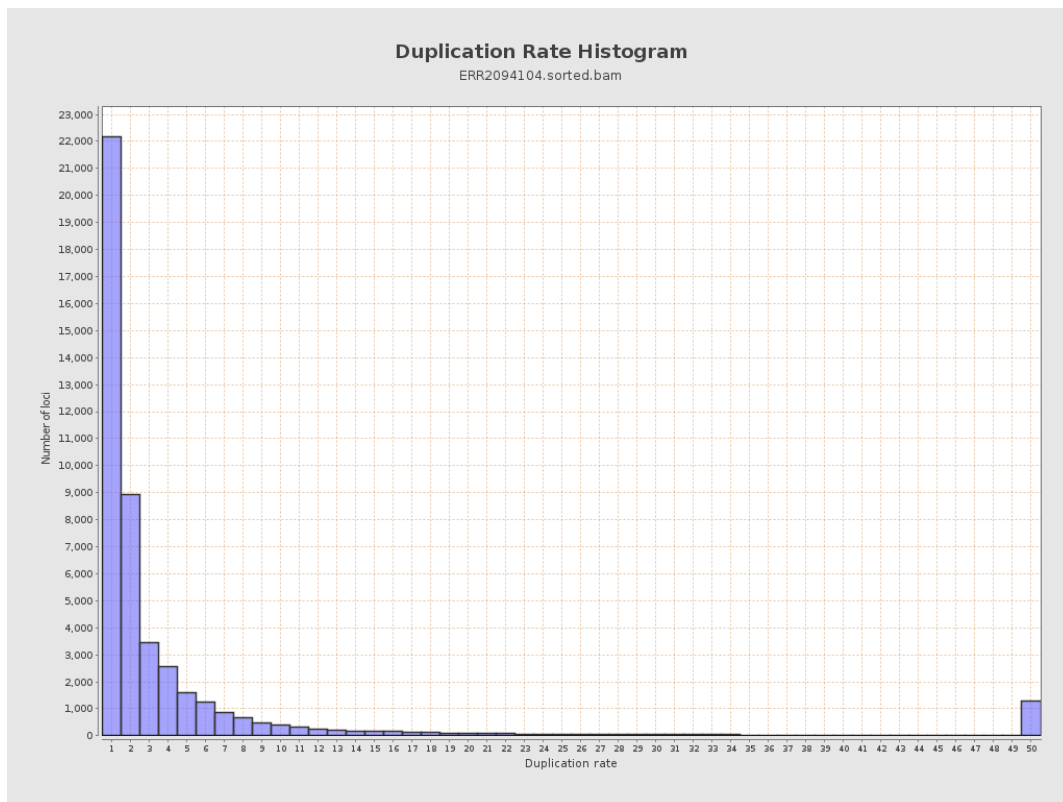
5. Results : Coverage Histogram (0-50X)



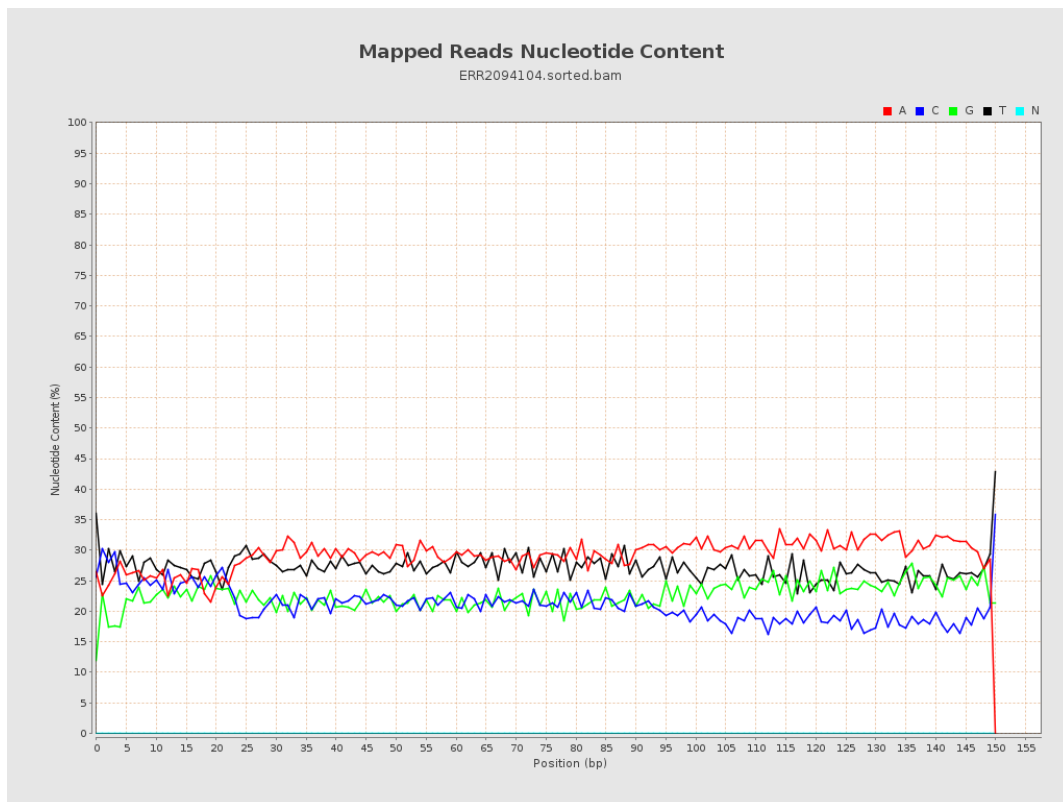
6. Results : Genome Fraction Coverage



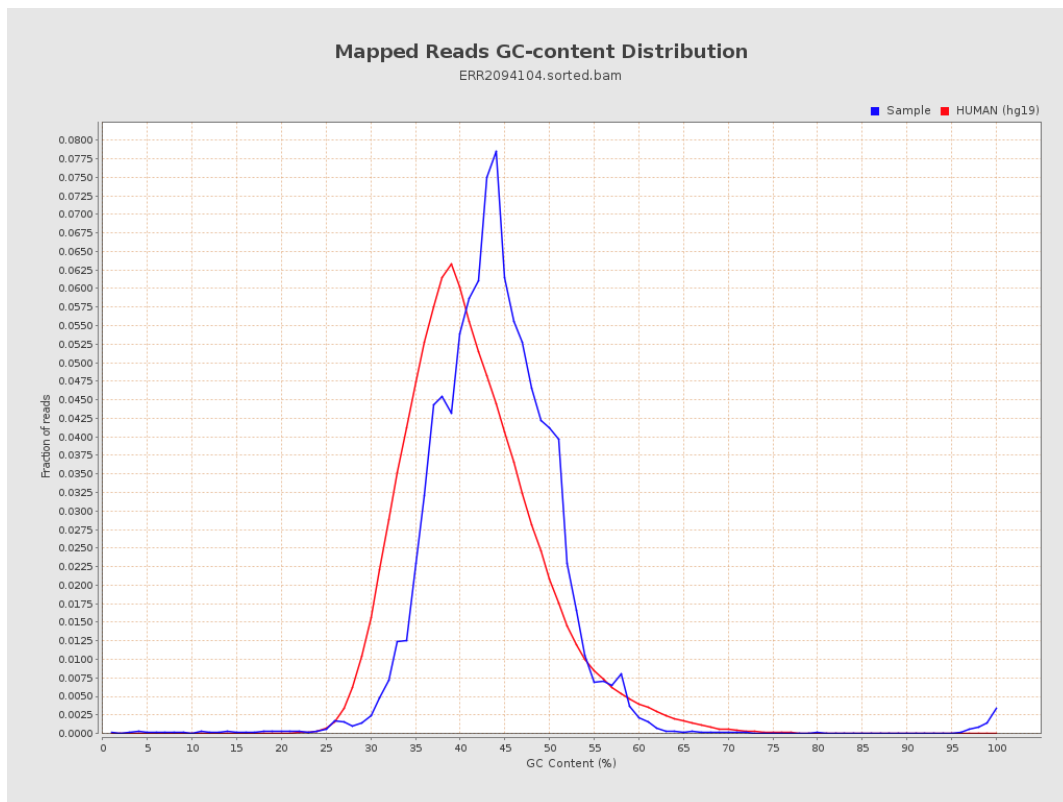
7. Results : Duplication Rate Histogram



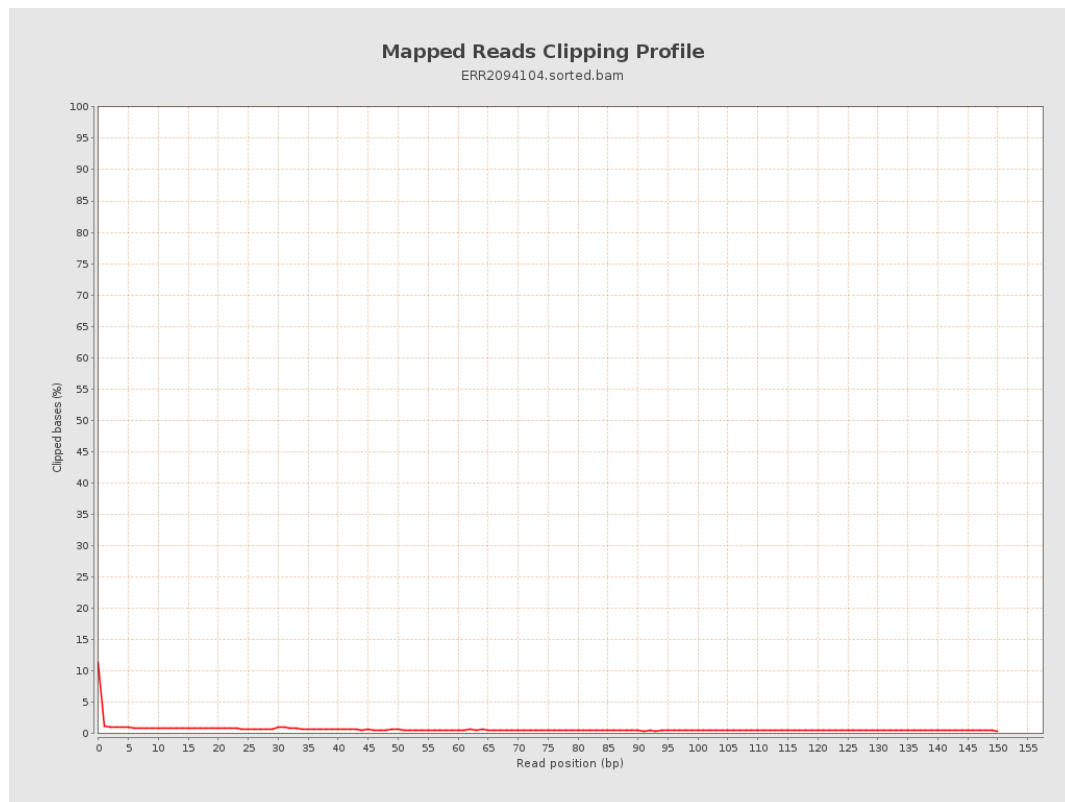
8. Results : Mapped Reads Nucleotide Content



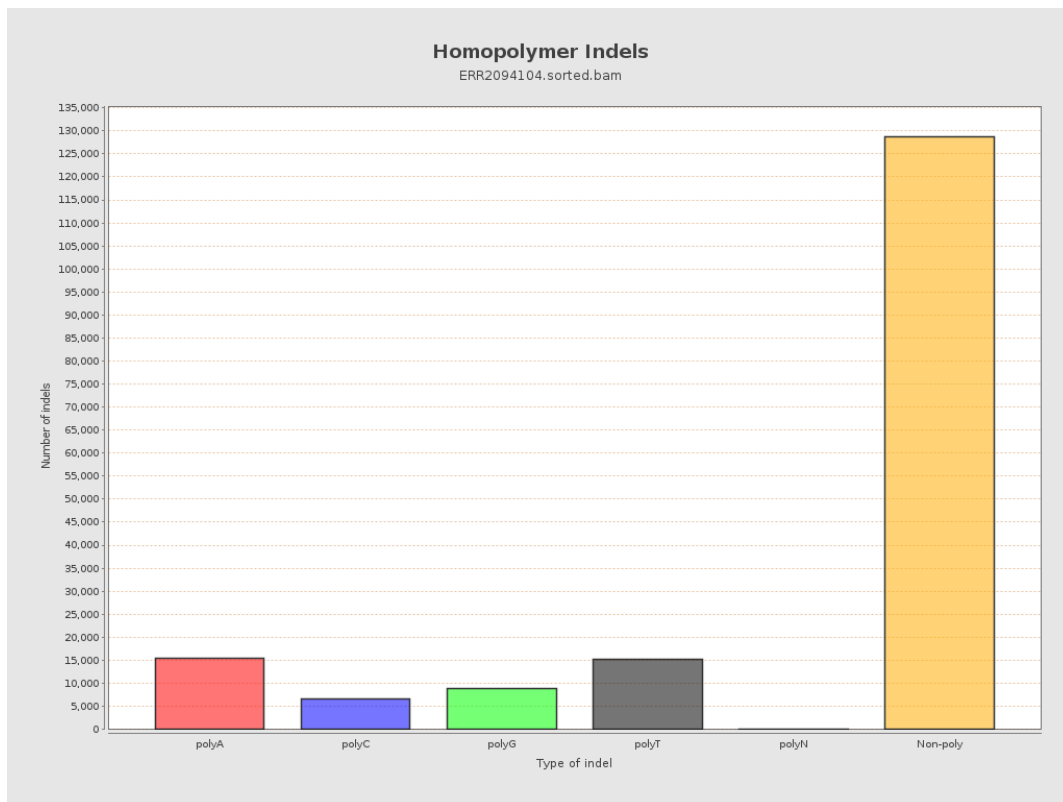
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



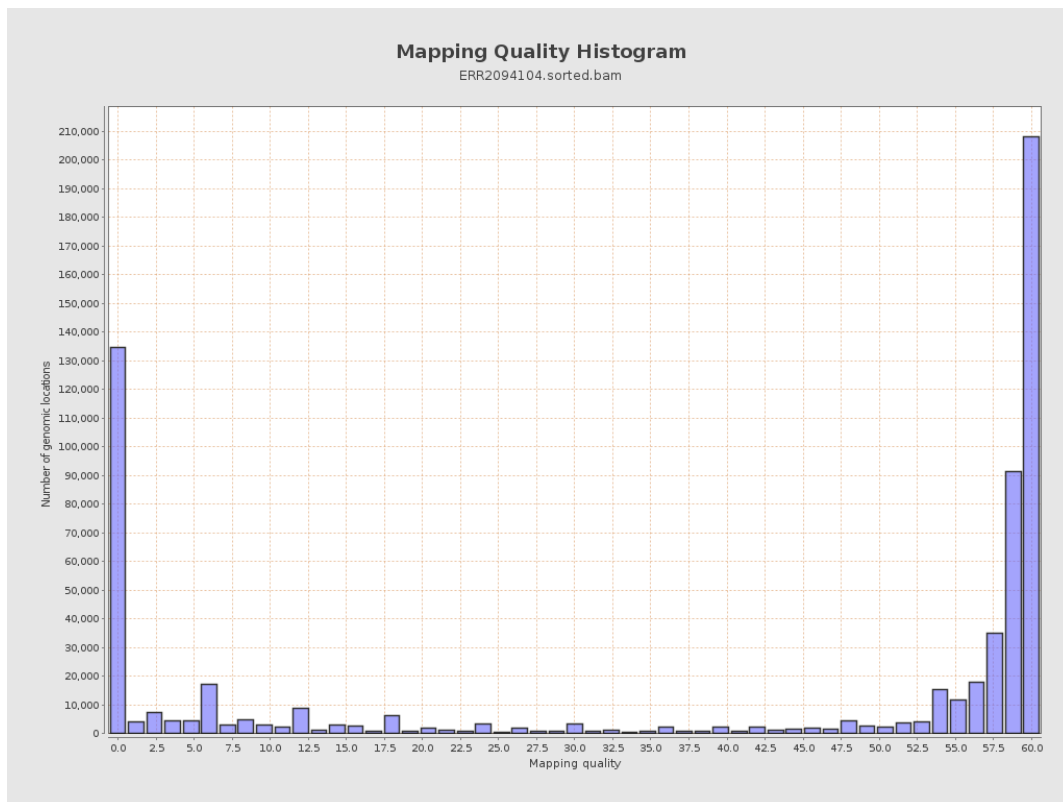
11. Results : Homopolymer Indels



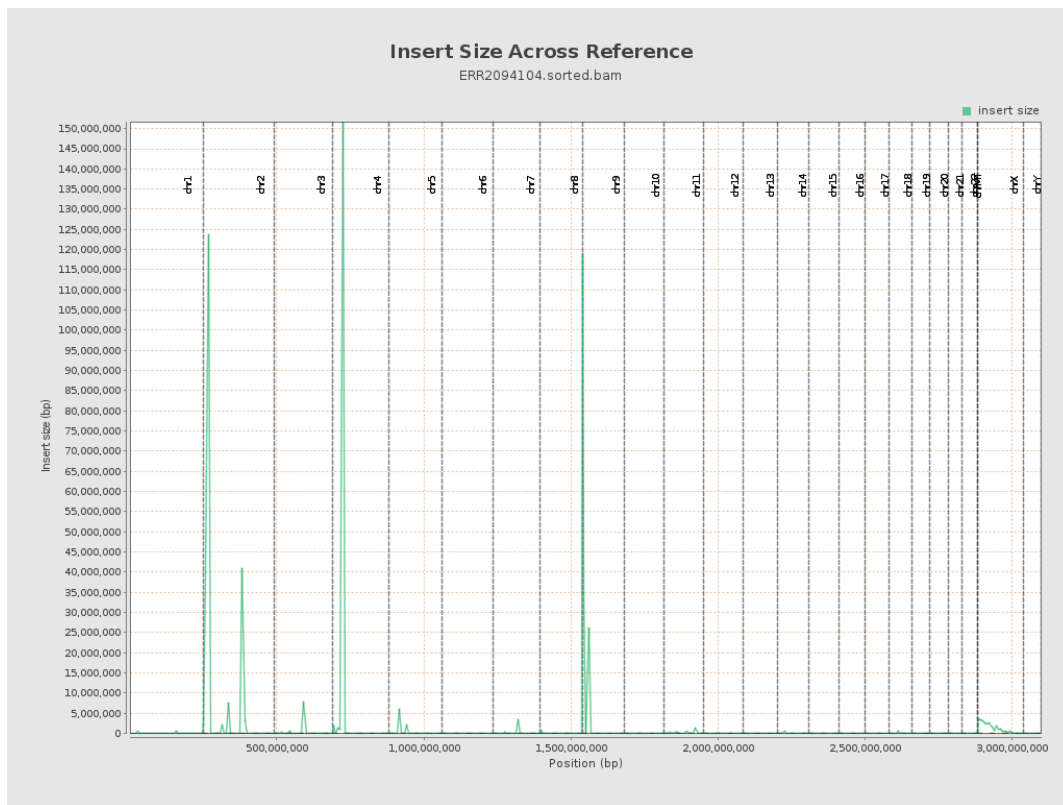
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

