

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 22:56:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094056.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_ERR2094056 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094056_1.fastq.gz ERR2094056_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 22:56:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094056.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	392,084
Mapped reads	377,072 / 96.17%
Unmapped reads	15,012 / 3.83%
Mapped paired reads	377,072 / 96.17%
Mapped reads, first in pair	189,395 / 48.3%
Mapped reads, second in pair	187,677 / 47.87%
Mapped reads, both in pair	374,650 / 95.55%
Mapped reads, singletons	2,422 / 0.62%
Secondary alignments	0
Supplementary alignments	12,725 / 3.25%
Read min/max/mean length	30 / 151 / 142.42
Duplicated reads (estimated)	355,192 / 90.59%
Duplication rate	50.38%
Clipped reads	150,666 / 38.43%

2.2. ACGT Content

Number/percentage of A's	13,536,357 / 27.34%
Number/percentage of C's	11,209,032 / 22.64%
Number/percentage of T's	13,134,969 / 26.53%
Number/percentage of G's	11,622,895 / 23.48%
Number/percentage of N's	587 / 0%

GC Percentage	46.12%
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2.3. Coverage

Mean	0.0164
Standard Deviation	4.3793

2.4. Mapping Quality

Mean Mapping Quality	44.84
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2.5. Insert size

Mean	548,853.1
Standard Deviation	6,654,140.84
P25/Median/P75	143 / 172 / 204

2.6. Mismatches and indels

General error rate	4.28%
Mismatches	2,049,339
Insertions	37,315
Mapped reads with at least one insertion	9.75%
Deletions	161,883
Mapped reads with at least one deletion	39.9%
Homopolymer indels	30.08%

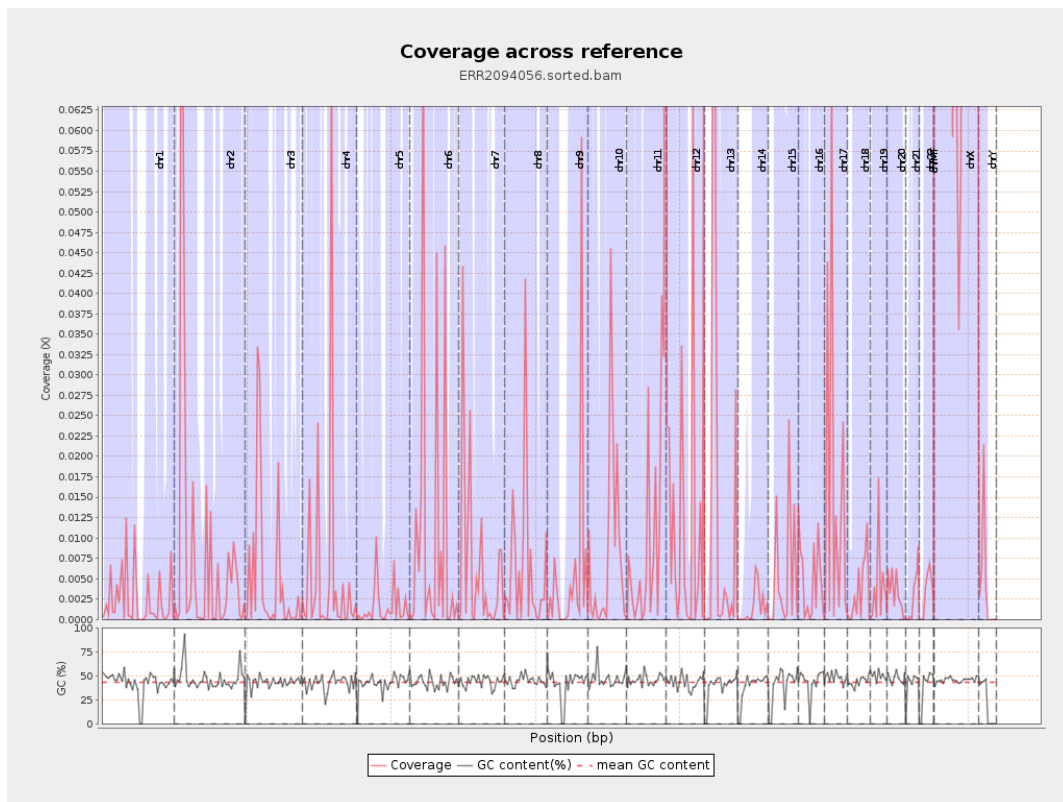
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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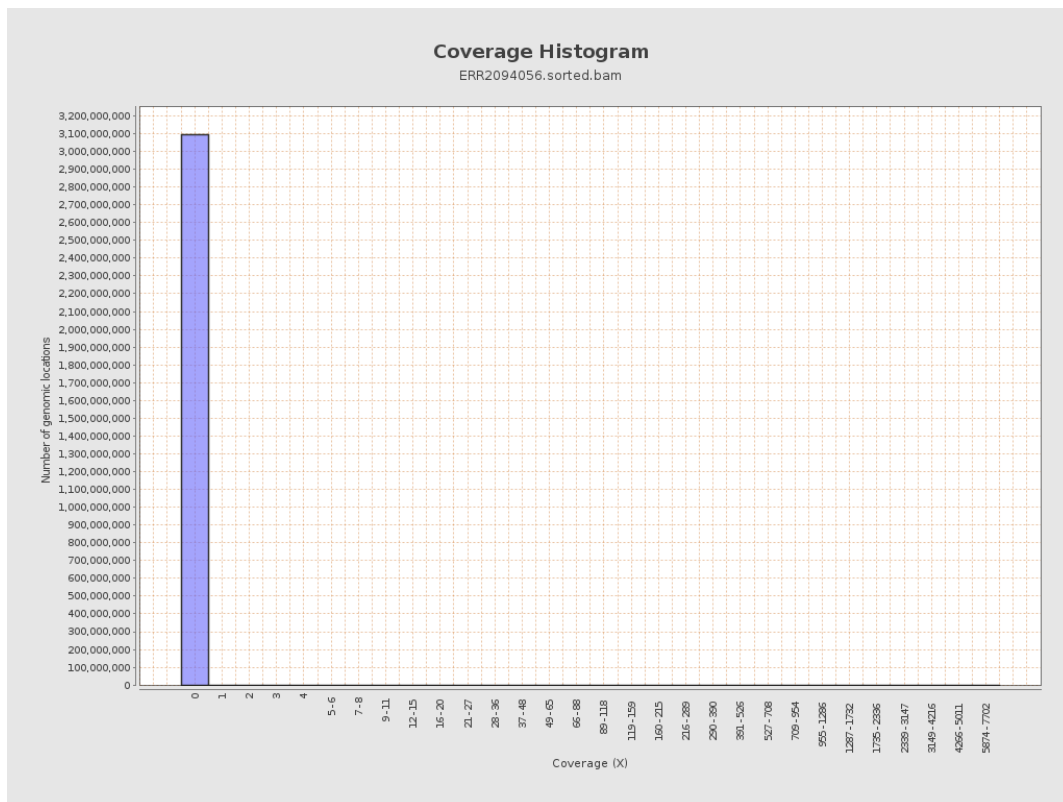
		bases	coverage	deviation
chr1	249250621	582917	0.0023	0.8206
chr2	243199373	1813972	0.0075	2.3545
chr3	198022430	938236	0.0047	1.5832
chr4	191154276	1100387	0.0058	2.53
chr5	180915260	293947	0.0016	0.5474
chr6	171115067	1756041	0.0103	4.494
chr7	159138663	995242	0.0063	2.2484
chr8	146364022	910013	0.0062	1.9101
chr9	141213431	787251	0.0056	2.7831
chr10	135534747	1135345	0.0084	2.7683
chr11	135006516	1481332	0.011	2.7467
chr12	133851895	1699248	0.0127	4.1692
chr13	115169878	1446253	0.0126	3.9808
chr14	107349540	161777	0.0015	0.5221
chr15	102531392	514486	0.005	1.5406
chr16	90354753	438843	0.0049	1.1917
chr17	81195210	1309047	0.0161	4.3283
chr18	78077248	282860	0.0036	0.999
chr19	59128983	243661	0.0041	1.2644
chr20	63025520	204437	0.0032	0.7236
chr21	48129895	125461	0.0026	0.5028
chr22	51304566	157500	0.0031	0.6799
chrMT	16571	3842958	231.9086	957.8903
chrX	155270560	28211488	0.1817	12.8363

chrY	59373566	256757	0.0043	1.5148
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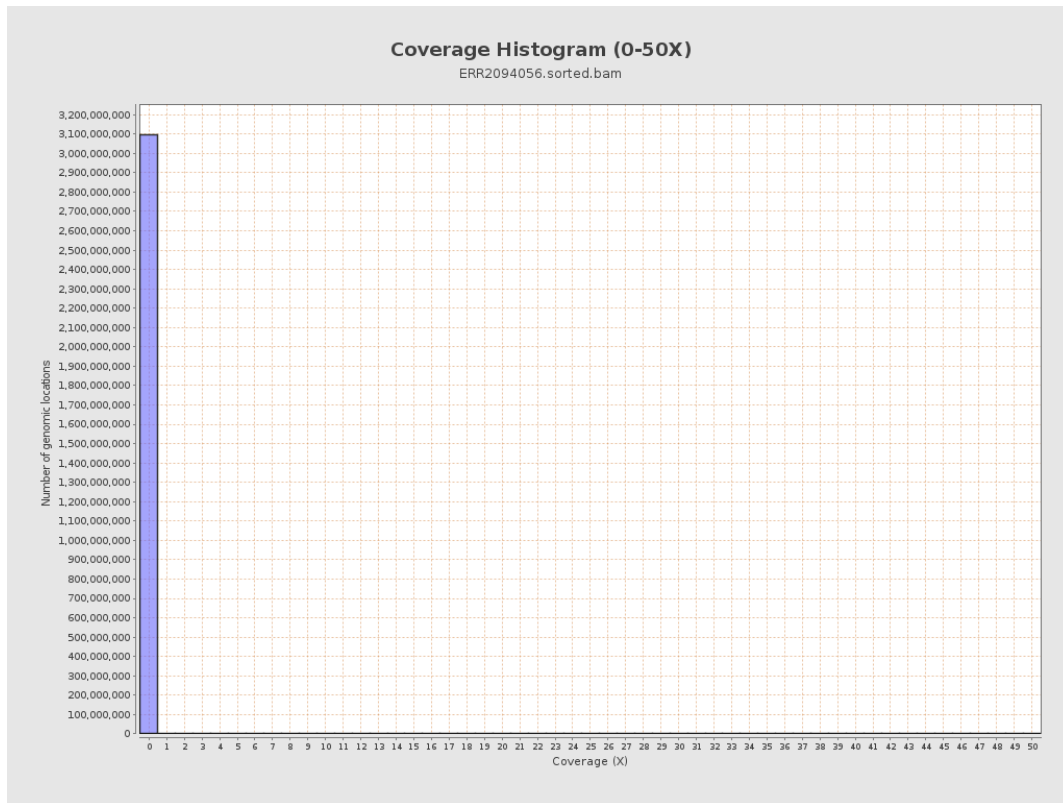
3. Results : Coverage across reference



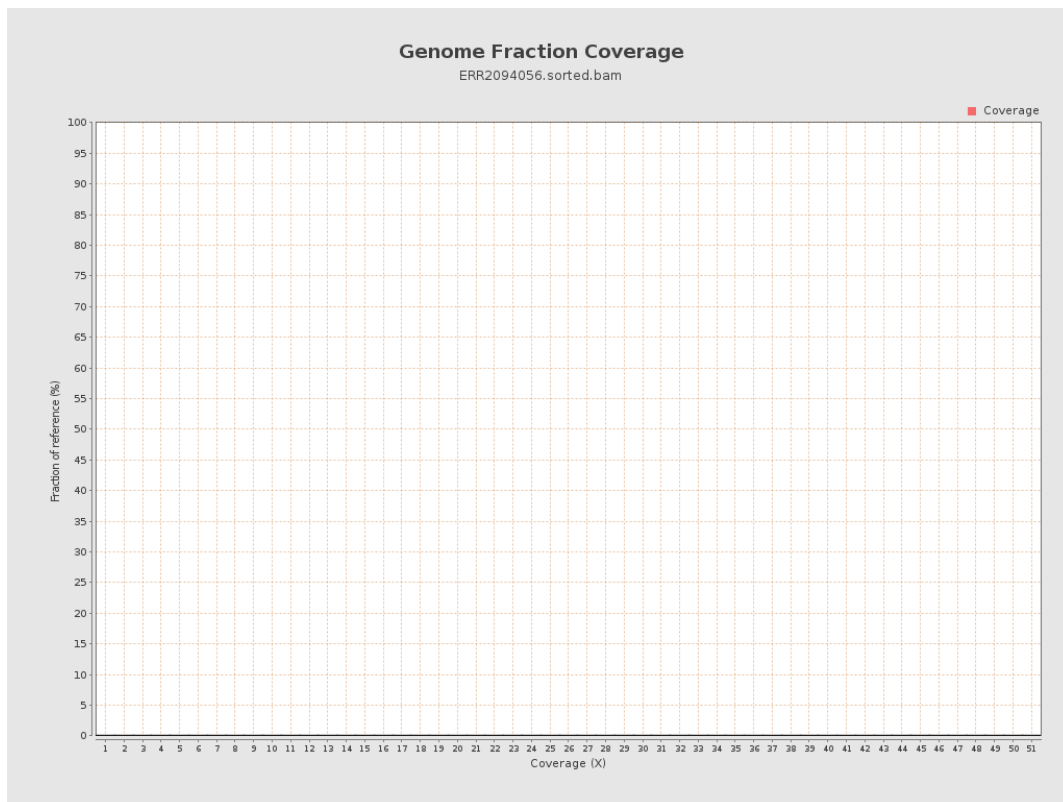
4. Results : Coverage Histogram



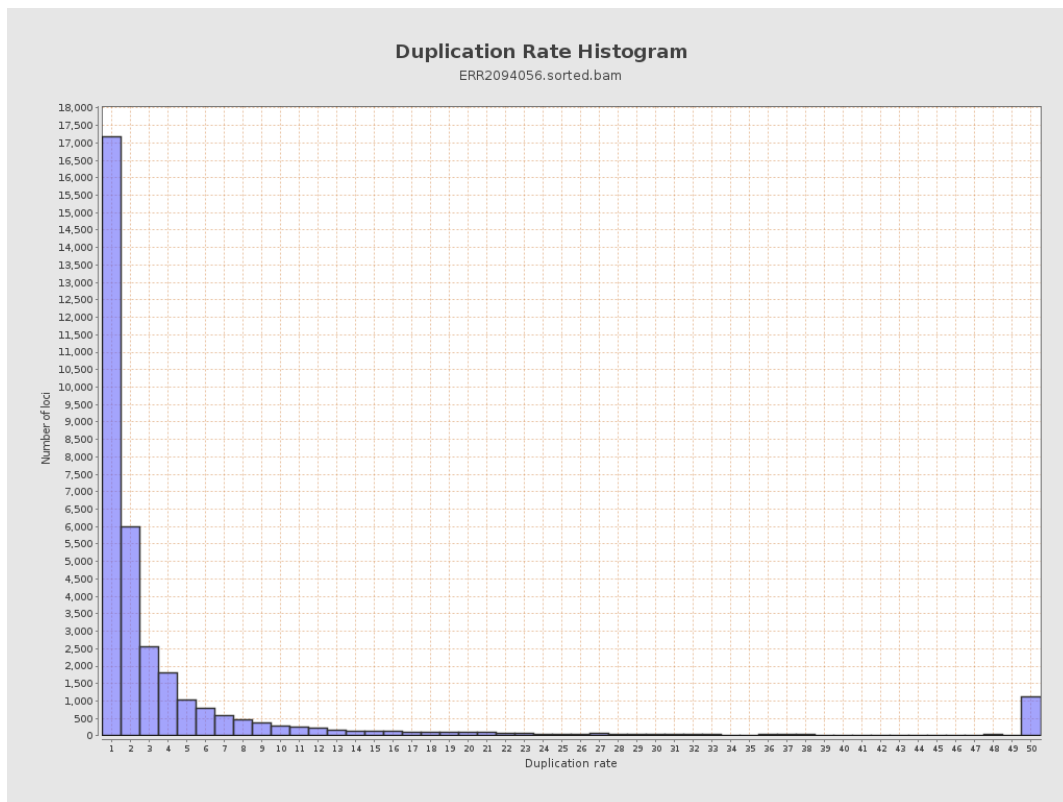
5. Results : Coverage Histogram (0-50X)



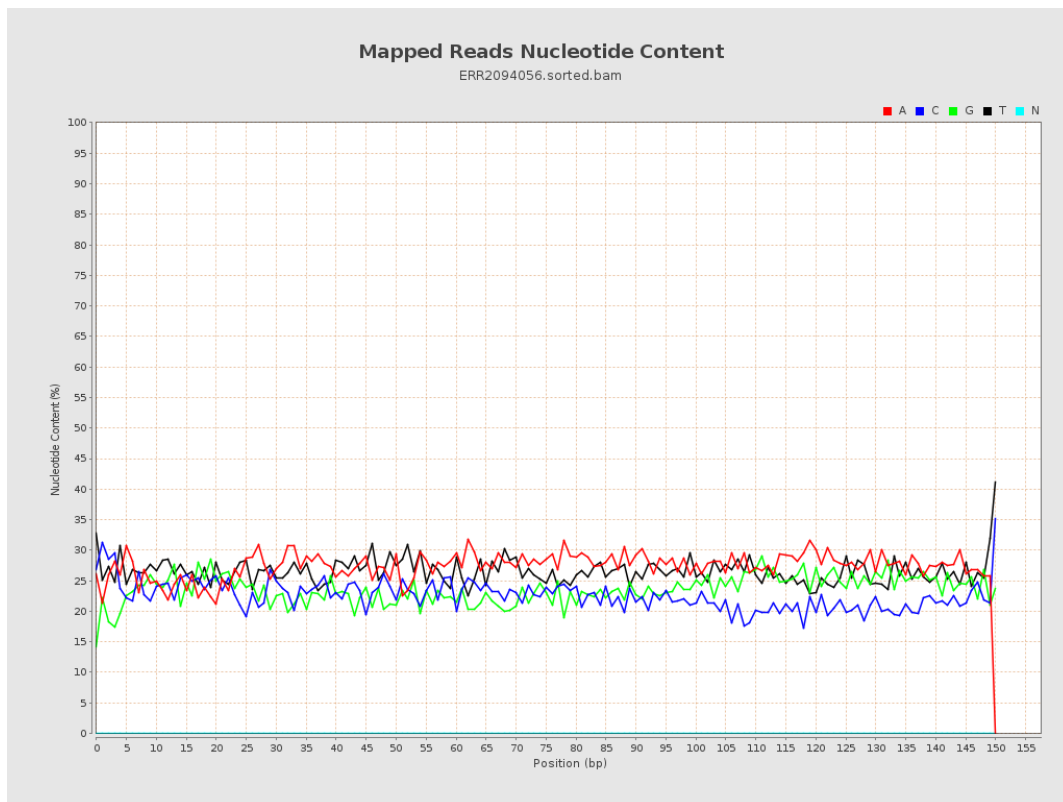
6. Results : Genome Fraction Coverage



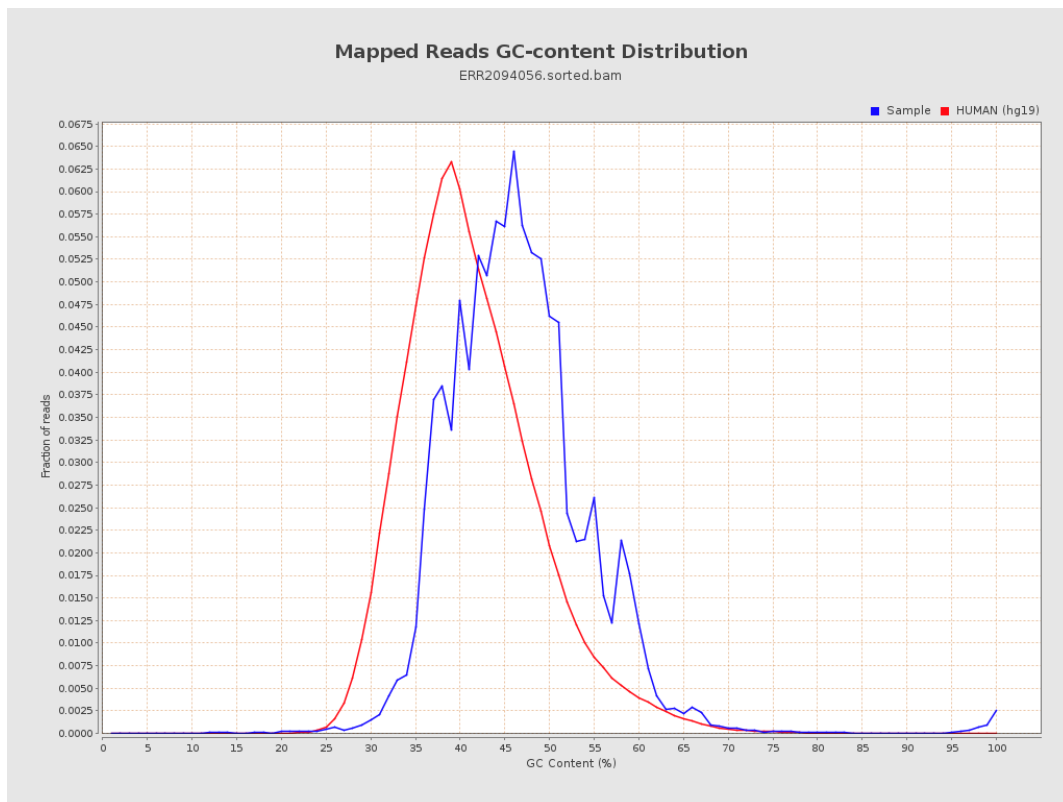
7. Results : Duplication Rate Histogram



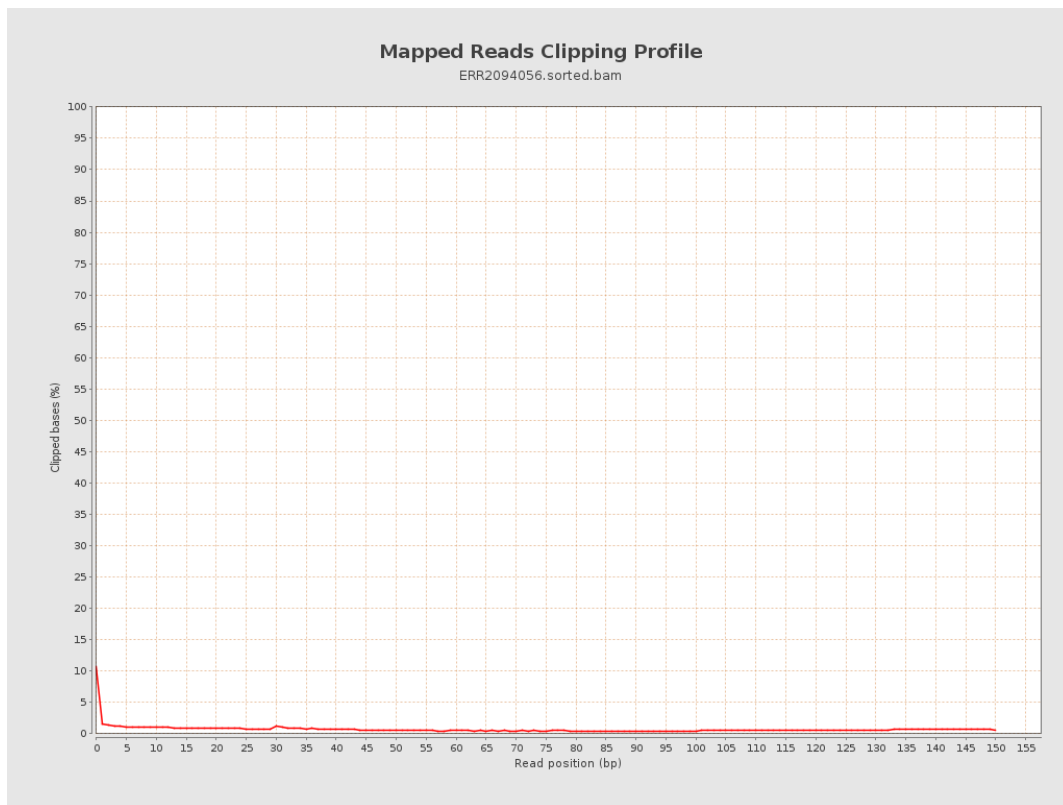
8. Results : Mapped Reads Nucleotide Content



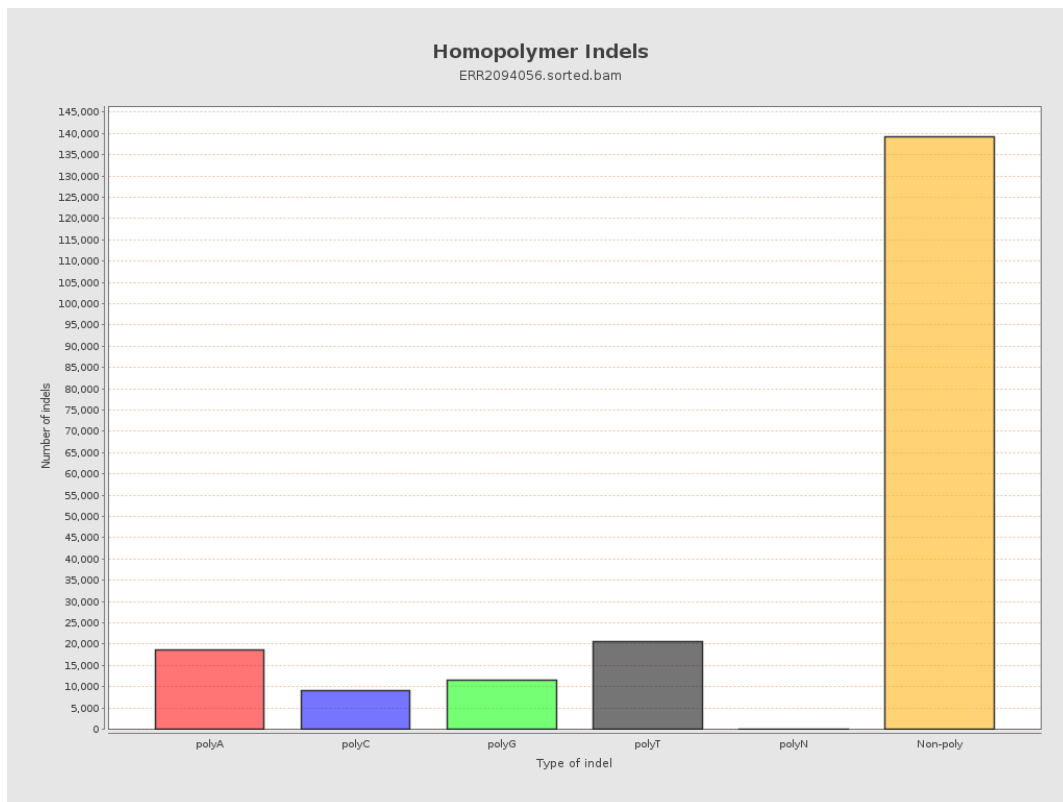
9. Results : Mapped Reads GC-content Distribution



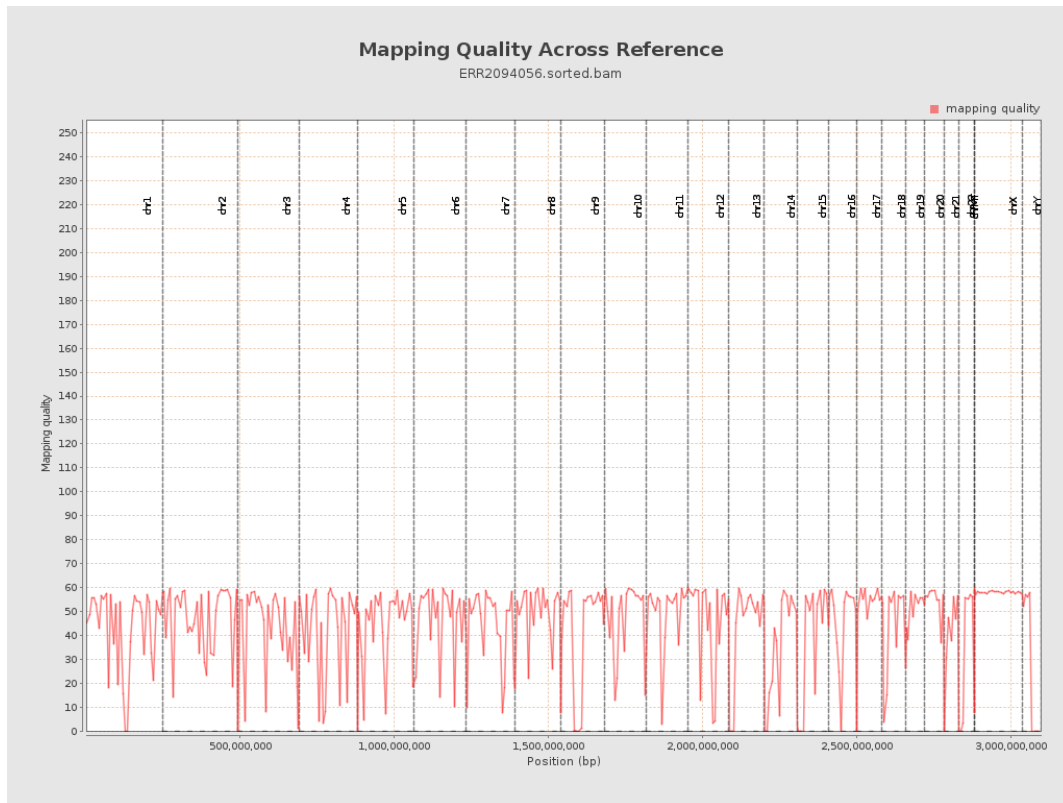
10. Results : Mapped Reads Clipping Profile



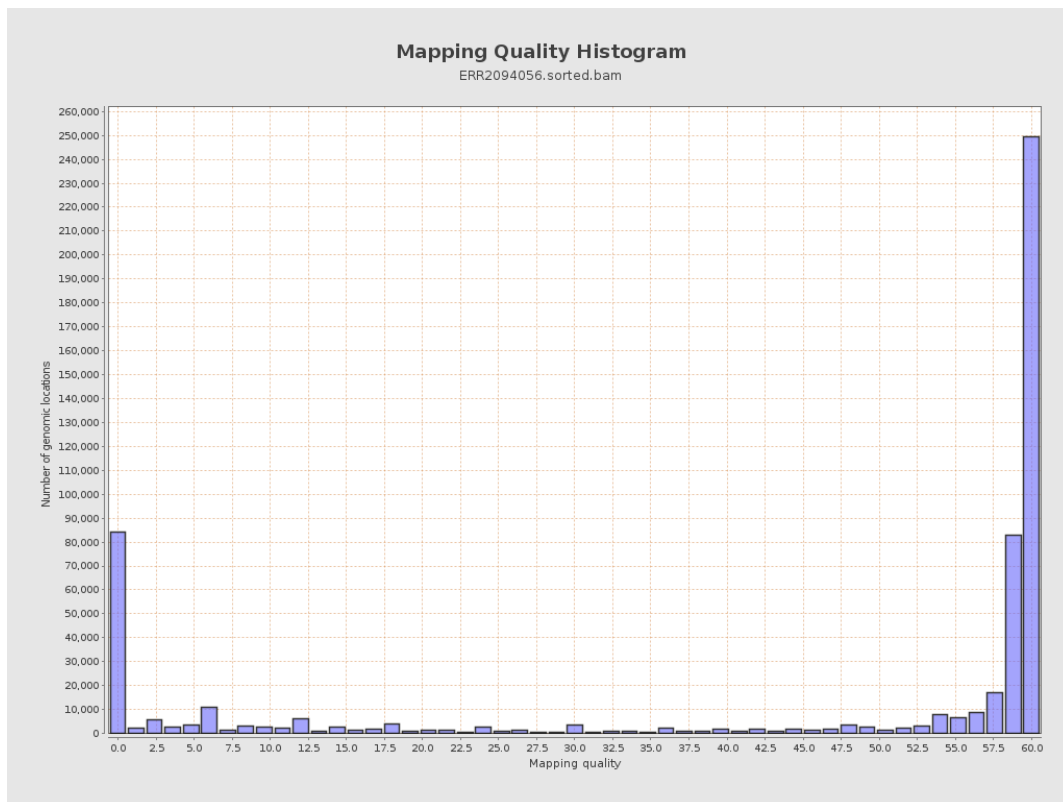
11. Results : Homopolymer Indels



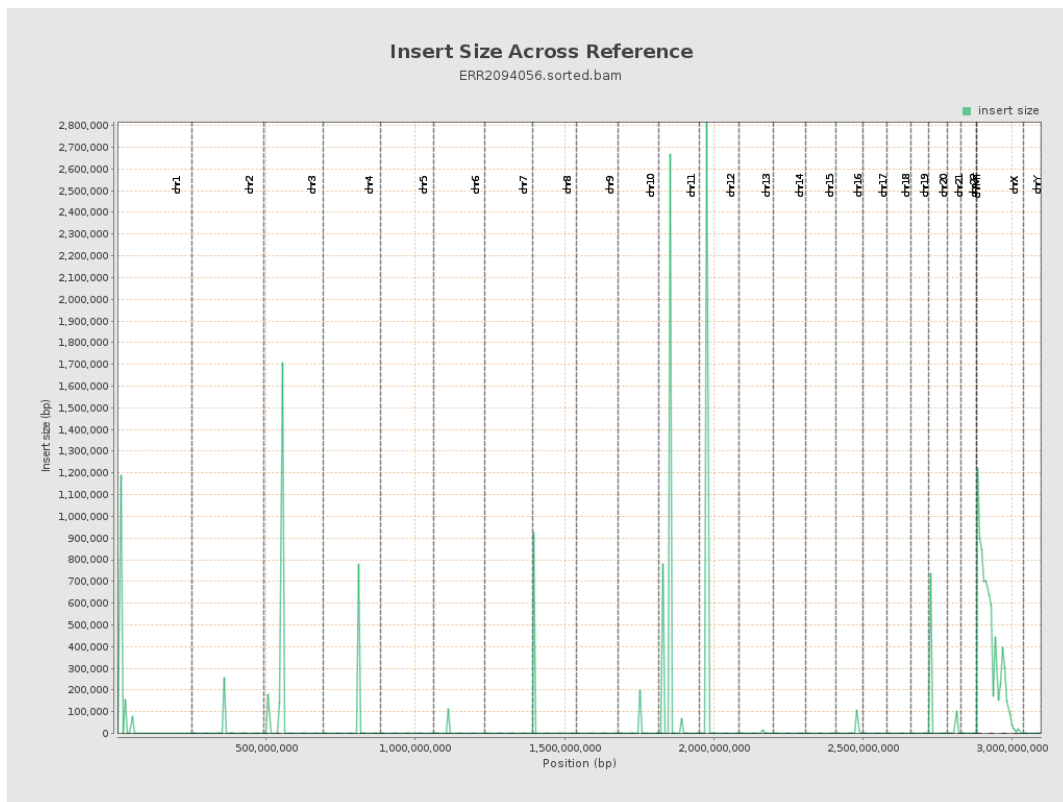
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

