Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:31:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094003.sorted.bam -c -nw 400 -hm 3
```

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_ERR2094003 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094003_1.fastq.gz ERR2094003_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:31:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094003.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	365,900
Mapped reads	150,403 / 41.1%
Unmapped reads	215,497 / 58.9%
Mapped paired reads	150,403 / 41.1%
Mapped reads, first in pair	74,608 / 20.39%
Mapped reads, second in pair	75,795 / 20.71%
Mapped reads, both in pair	147,288 / 40.25%
Mapped reads, singletons	3,115 / 0.85%
Secondary alignments	0
Supplementary alignments	900 / 0.25%
Read min/max/mean length	30 / 151 / 93.27
Duplicated reads (estimated)	147,108 / 40.2%
Duplication rate	31.16%
Clipped reads	26,668 / 7.29%

2.2. ACGT Content

Number/percentage of A's	6,190,469 / 29.15%
Number/percentage of C's	4,190,820 / 19.73%
Number/percentage of T's	6,252,478 / 29.44%
Number/percentage of G's	4,604,860 / 21.68%
Number/percentage of N's	284 / 0%

GC Percentage	41.41%

2.3. Coverage

Mean	0.0069
Standard Deviation	14.8191

2.4. Mapping Quality

Mean Mapping Quality	24.96

2.5. Insert size

Mean	36,971.66
Standard Deviation	2,010,457.9
P25/Median/P75	212 / 217 / 237

2.6. Mismatches and indels

General error rate	2.38%
Mismatches	500,683
Insertions	3,775
Mapped reads with at least one insertion	2.4%
Deletions	21,692
Mapped reads with at least one deletion	14.12%
Homopolymer indels	41.49%

2.7. Chromosome stats

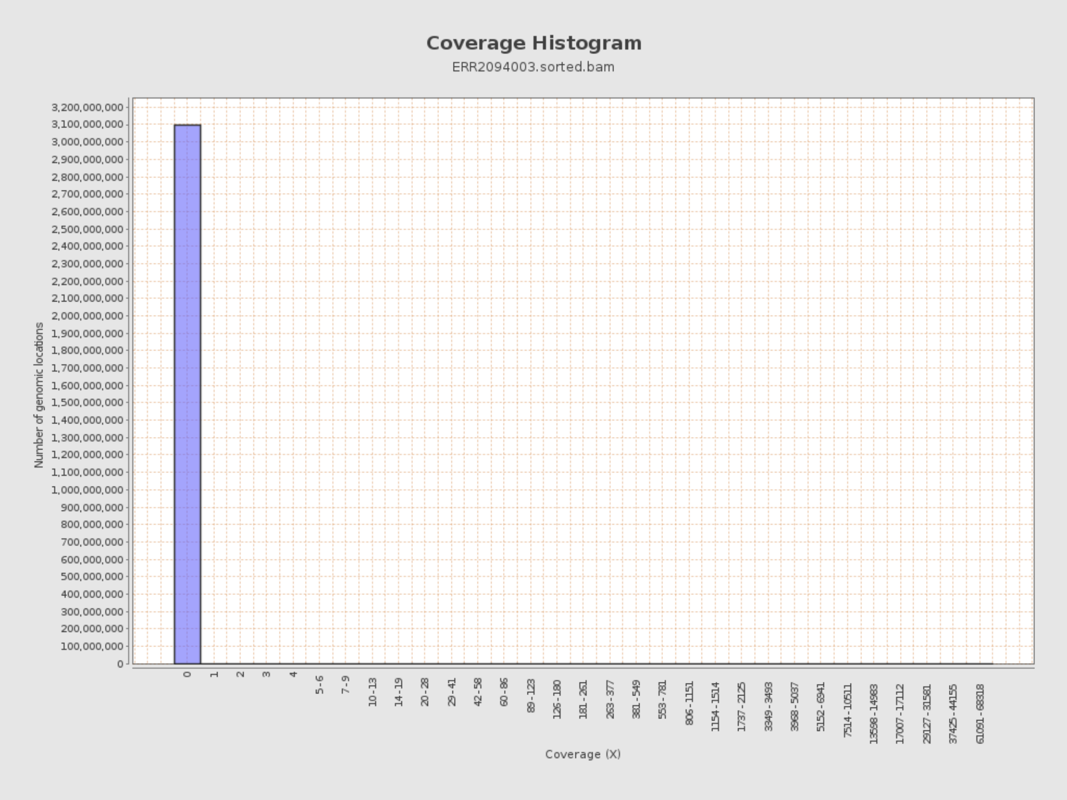
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	coverage	deviation
chr1	249250621	14794	0.0001	0.0139
chr2	243199373	264409	0.0011	0.9302
chr3	198022430	227743	0.0012	1.0259
chr4	191154276	765257	0.004	4.3682
chr5	180915260	16005	0.0001	0.0345
chr6	171115067	15793	0.0001	0.0425
chr7	159138663	12029	0.0001	0.0174
chr8	146364022	16766	0.0001	0.0355
chr9	141213431	6804	0	0.0104
chr10	135534747	7520	0.0001	0.0136
chr11	135006516	60201	0.0004	0.3098
chr12	133851895	94577	0.0007	0.44
chr13	115169878	16863	0.0001	0.0703
chr14	107349540	50164	0.0005	0.3137
chr15	102531392	7946	0.0001	0.0312
chr16	90354753	3242	0	0.0079
chr17	81195210	7271	0.0001	0.0215
chr18	78077248	3672	0	0.0119
chr19	59128983	99758	0.0017	0.9994
chr20	63025520	3766	0.0001	0.0101
chr21	48129895	4950	0.0001	0.0163
chr22	51304566	2871	0.0001	0.012
chrMT	16571	17075227	1,030.4283	6,240.5088
chrX	155270560	2630527	0.0169	9.0551

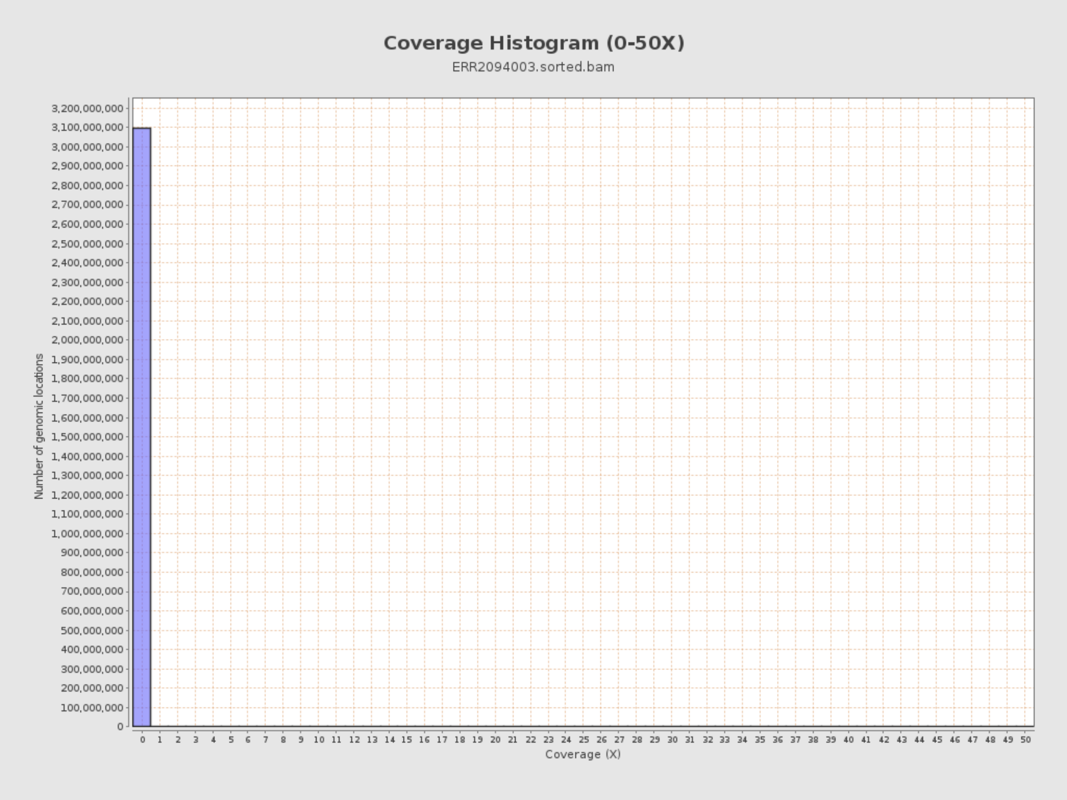
chrY	59373566	7683	0.0001	0.0388

3. Results : Coverage across reference

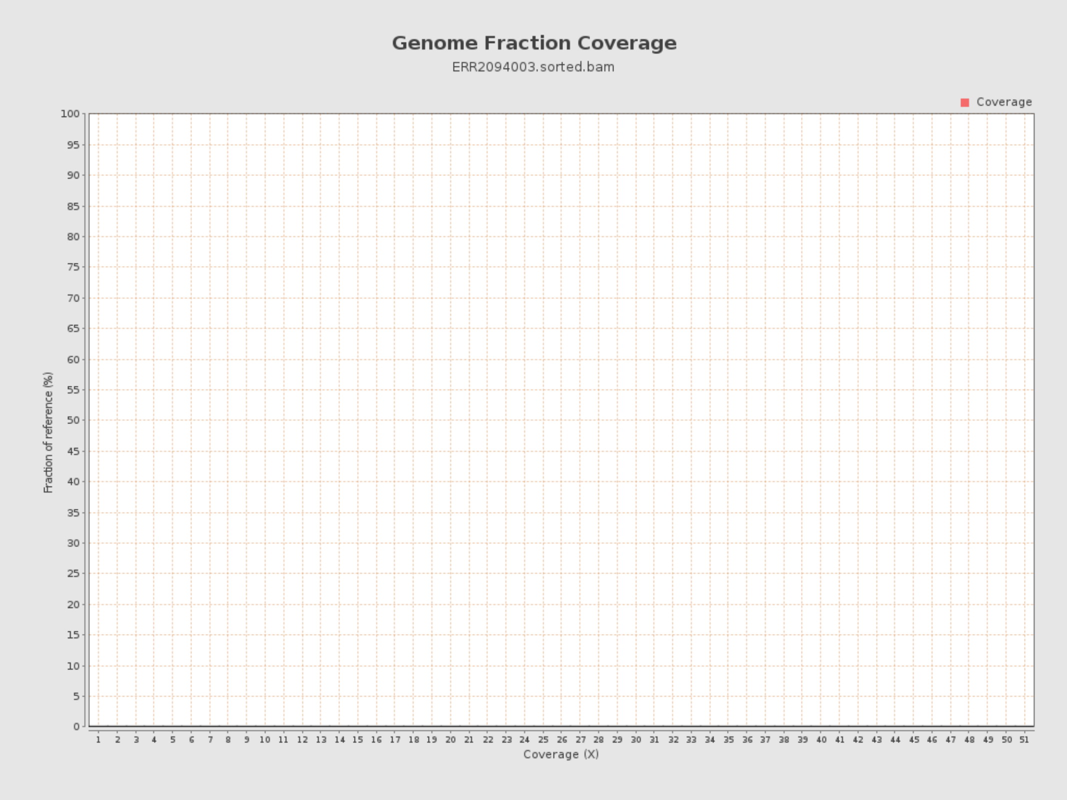
4. Results : Coverage Histogram



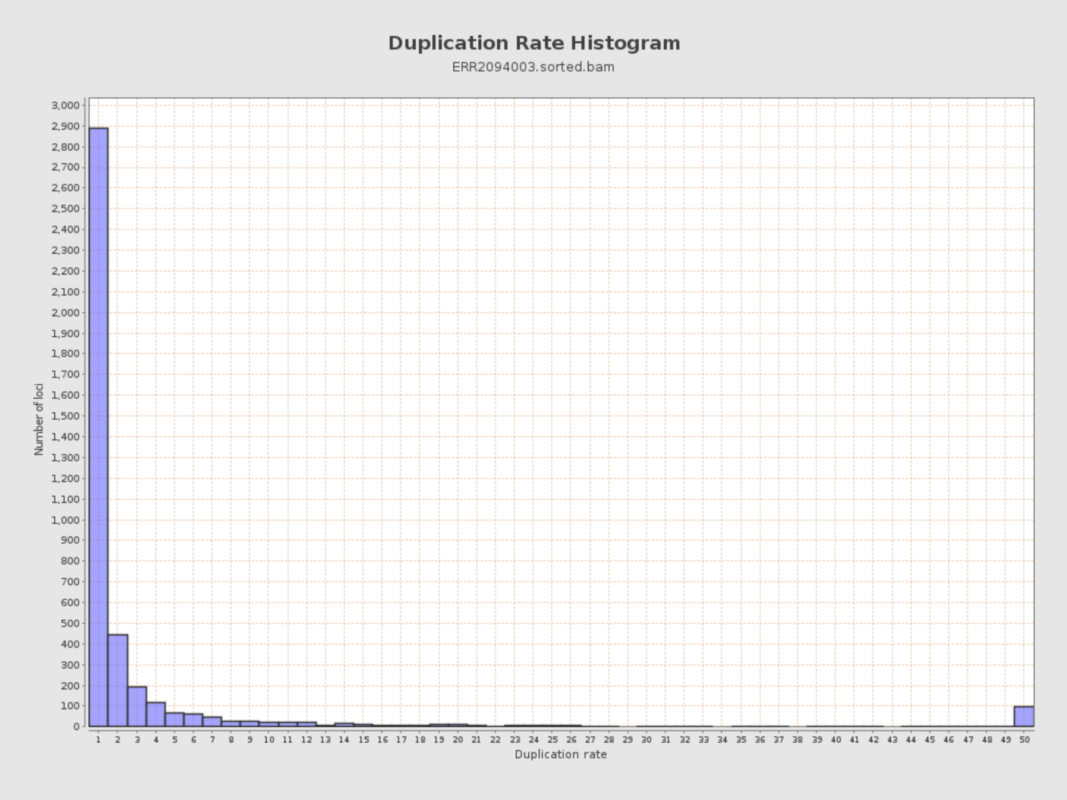
5. Results : Coverage Histogram (0-50X)



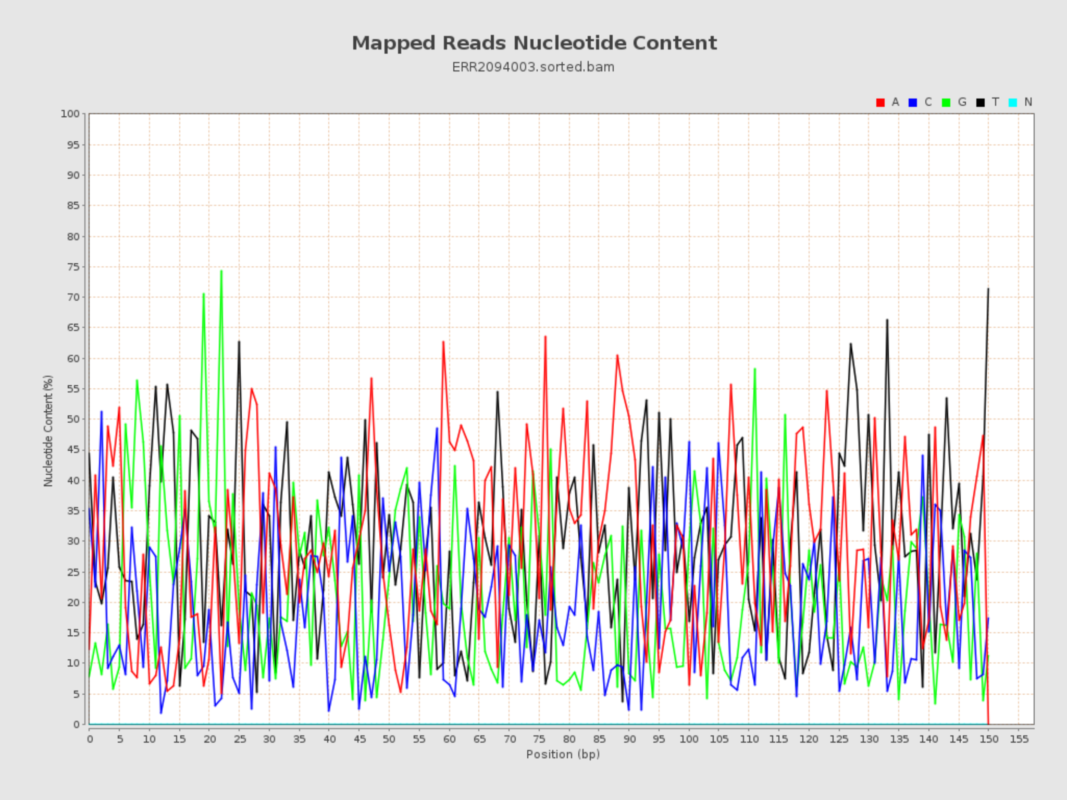
6. Results : Genome Fraction Coverage



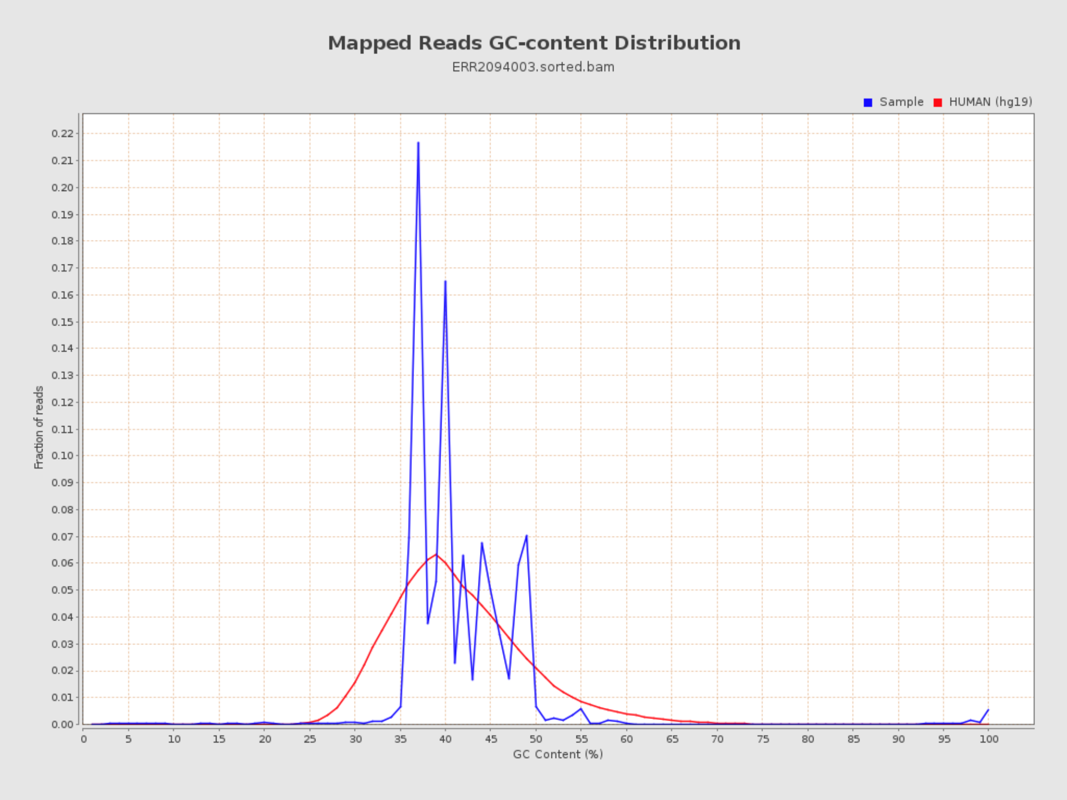
7. Results : Duplication Rate Histogram



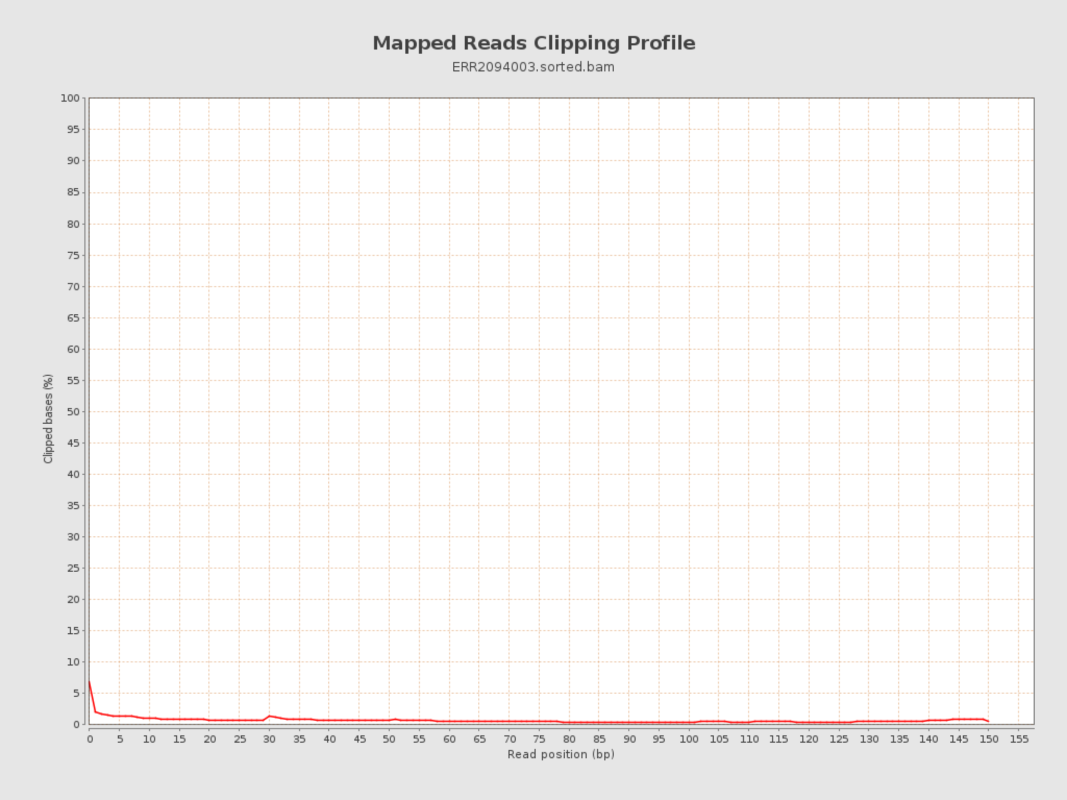
8. Results : Mapped Reads Nucleotide Content



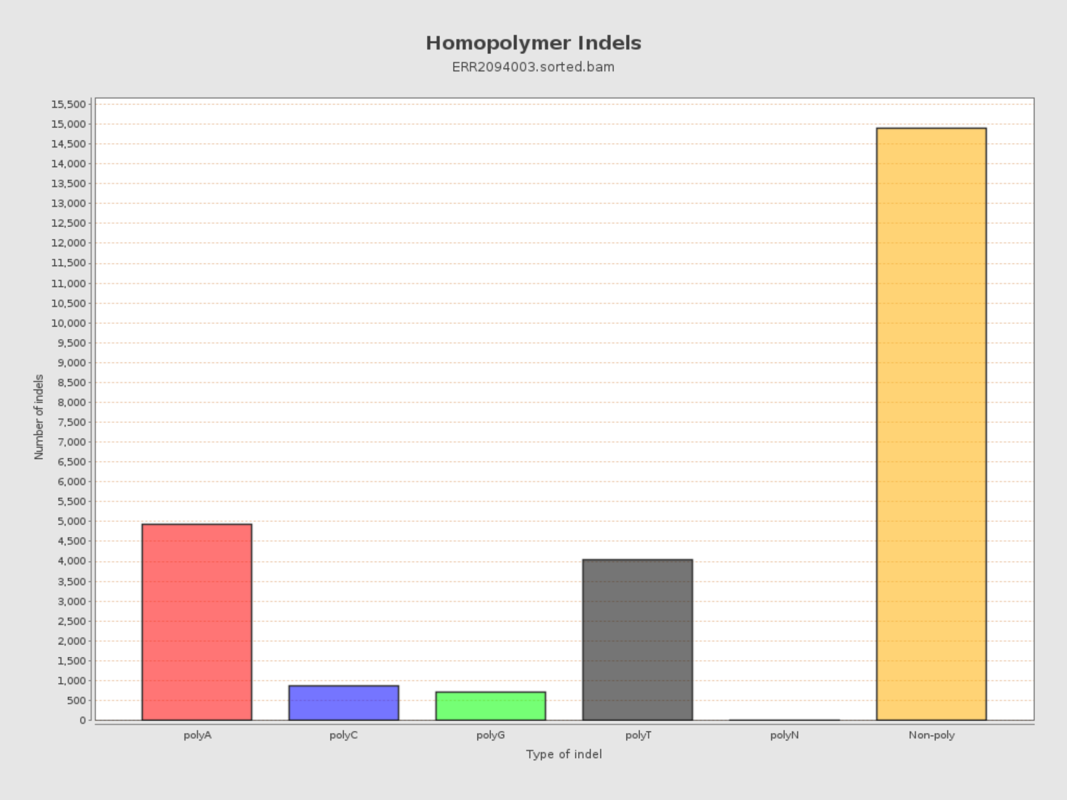
9. Results : Mapped Reads GC-content Distribution



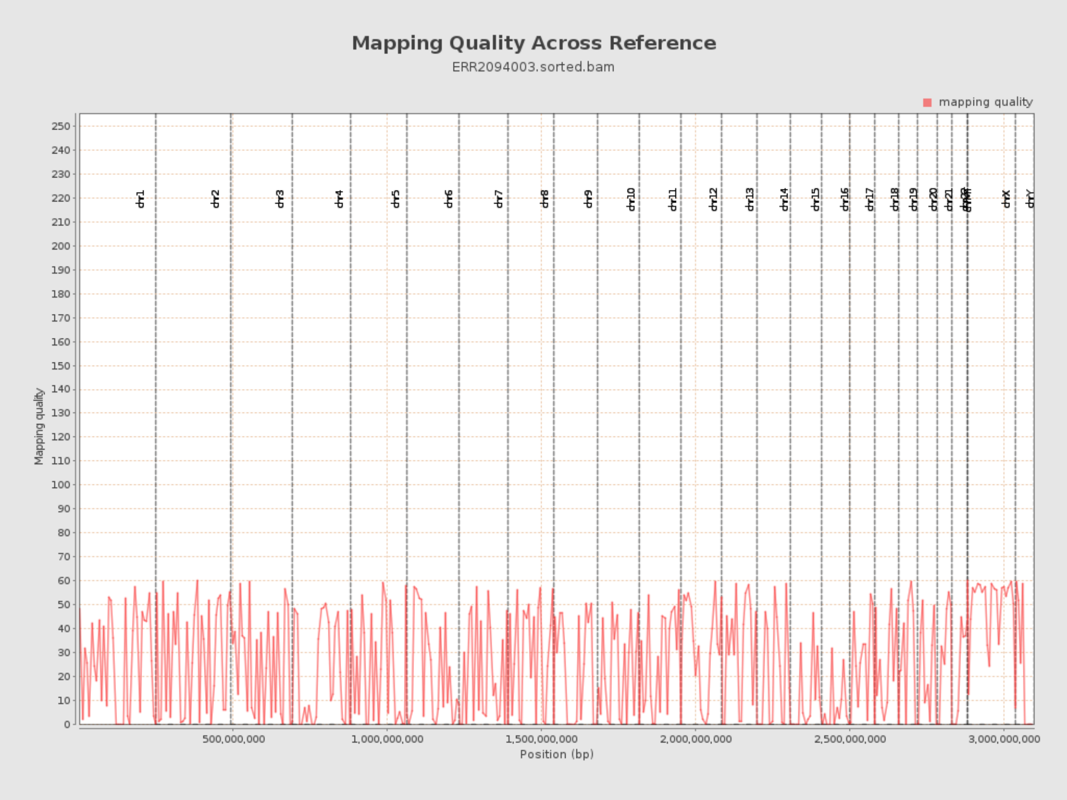
10. Results : Mapped Reads Clipping Profile



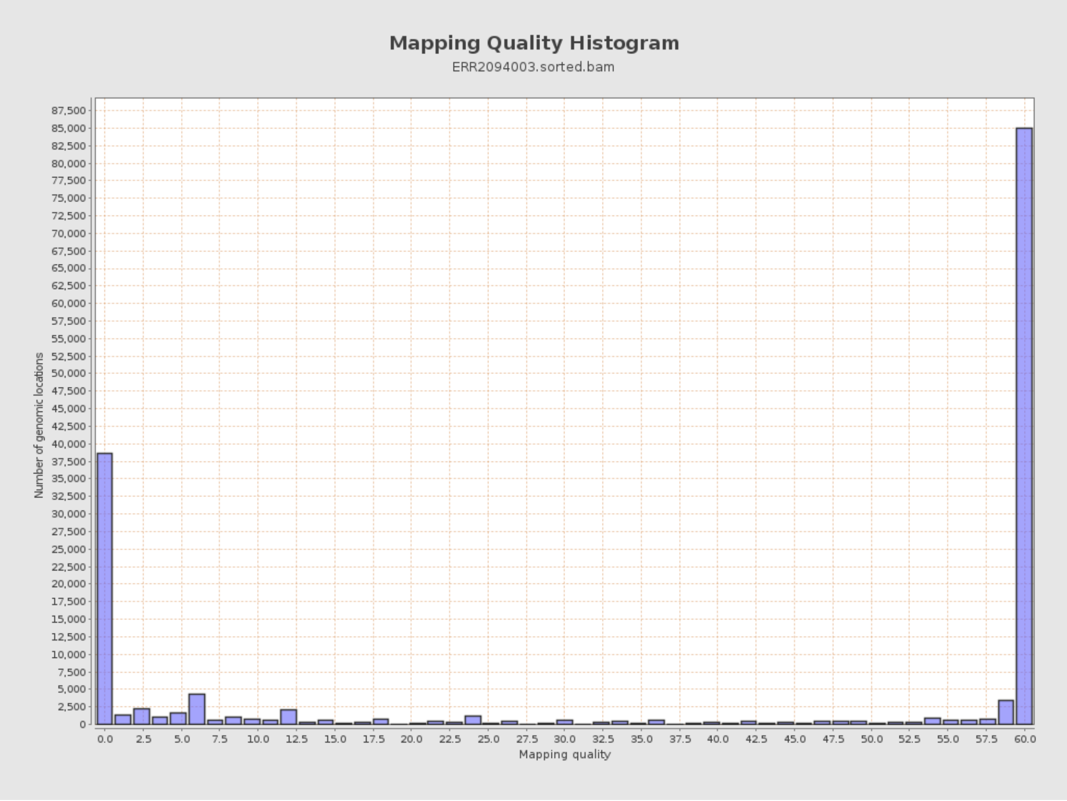
11. Results : Homopolymer Indels



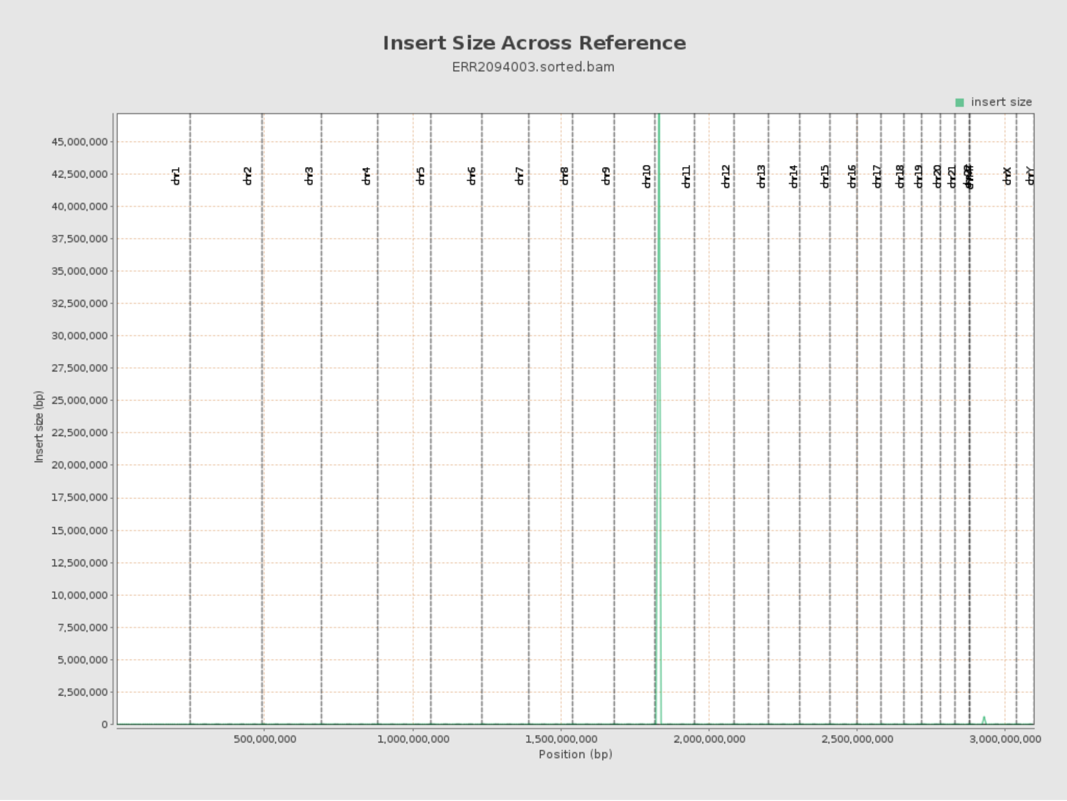
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram