Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:15:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094024.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_ERR2094024 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094024_1.fastq.gz ERR2094024_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:15:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094024.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	474,992
Mapped reads	442,617 / 93.18%
Unmapped reads	32,375 / 6.82%
Mapped paired reads	442,617 / 93.18%
Mapped reads, first in pair	222,579 / 46.86%
Mapped reads, second in pair	220,038 / 46.32%
Mapped reads, both in pair	436,730 / 91.94%
Mapped reads, singletons	5,887 / 1.24%
Secondary alignments	0
Supplementary alignments	22,847 / 4.81%
Read min/max/mean length	30 / 151 / 141.91
Duplicated reads (estimated)	414,853 / 87.34%
Duplication rate	45.74%
Clipped reads	212,554 / 44.75%

2.2. ACGT Content

Number/percentage of A's	15,518,325 / 27.67%
Number/percentage of C's	12,533,581 / 22.35%
Number/percentage of T's	14,903,490 / 26.58%
Number/percentage of G's	13,121,145 / 23.4%
Number/percentage of N's	539 / 0%

GC Percentage	45.75%

2.3. Coverage

Mean	0.0185
Standard Deviation	6.1548

2.4. Mapping Quality

Mean Mapping Quality	44.89

2.5. Insert size

Mean	470,427.05
Standard Deviation	6,294,096.83
P25/Median/P75	133 / 166 / 204

2.6. Mismatches and indels

General error rate	3.93%
Mismatches	2,146,909
Insertions	34,007
Mapped reads with at least one insertion	7.53%
Deletions	154,453
Mapped reads with at least one deletion	33.71%
Homopolymer indels	27.56%

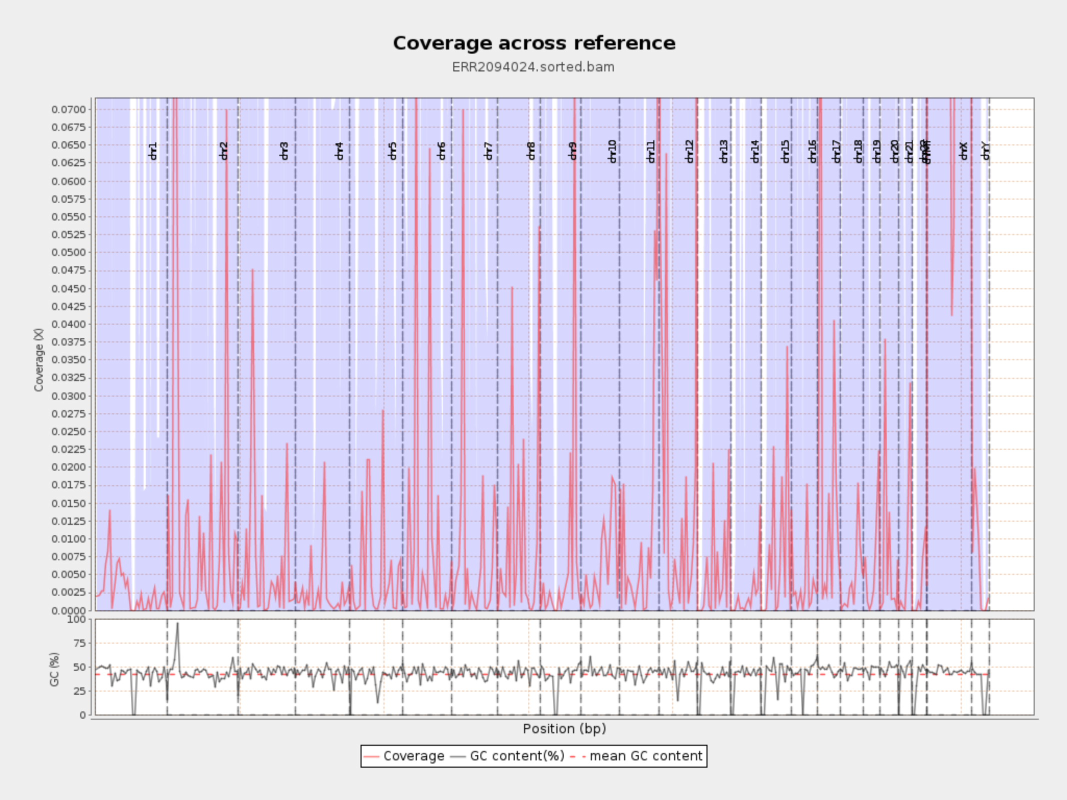
2.7. Chromosome stats

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

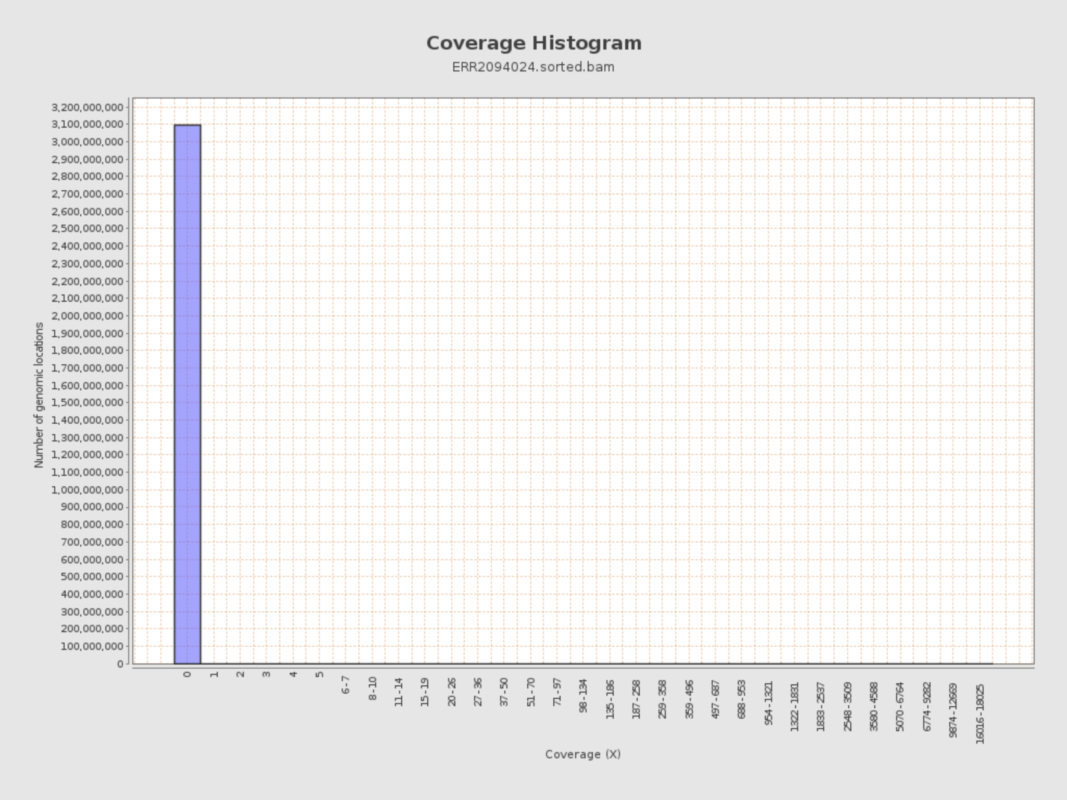
		bases	coverage	deviation
chr1	249250621	706103	0.0028	0.6822
chr2	243199373	3092431	0.0127	3.7244
chr3	198022430	1227552	0.0062	1.8252
chr4	191154276	530345	0.0028	0.5775
chr5	180915260	1011459	0.0056	1.8531
chr6	171115067	1764044	0.0103	4.2485
chr7	159138663	1334488	0.0084	2.3684
chr8	146364022	1436876	0.0098	2.6814
chr9	141213431	1034632	0.0073	2.845
chr10	135534747	856668	0.0063	1.3199
chr11	135006516	1549974	0.0115	2.8053
chr12	133851895	2121026	0.0158	4.1459
chr13	115169878	619294	0.0054	1.6759
chr14	107349540	242812	0.0023	0.4576
chr15	102531392	813540	0.0079	2.2187
chr16	90354753	352206	0.0039	1.1045
chr17	81195210	1709461	0.0211	5.1595
chr18	78077248	357366	0.0046	1.2579
chr19	59128983	363037	0.0061	1.2887
chr20	63025520	478626	0.0076	2.9644
chr21	48129895	373428	0.0078	2.3572
chr22	51304566	166669	0.0032	0.5126
chrMT	16571	8133048	490.8001	2,073.6854
chrX	155270560	26682712	0.1718	12.2102

chrY	59373566	398122	0.0067	1.201

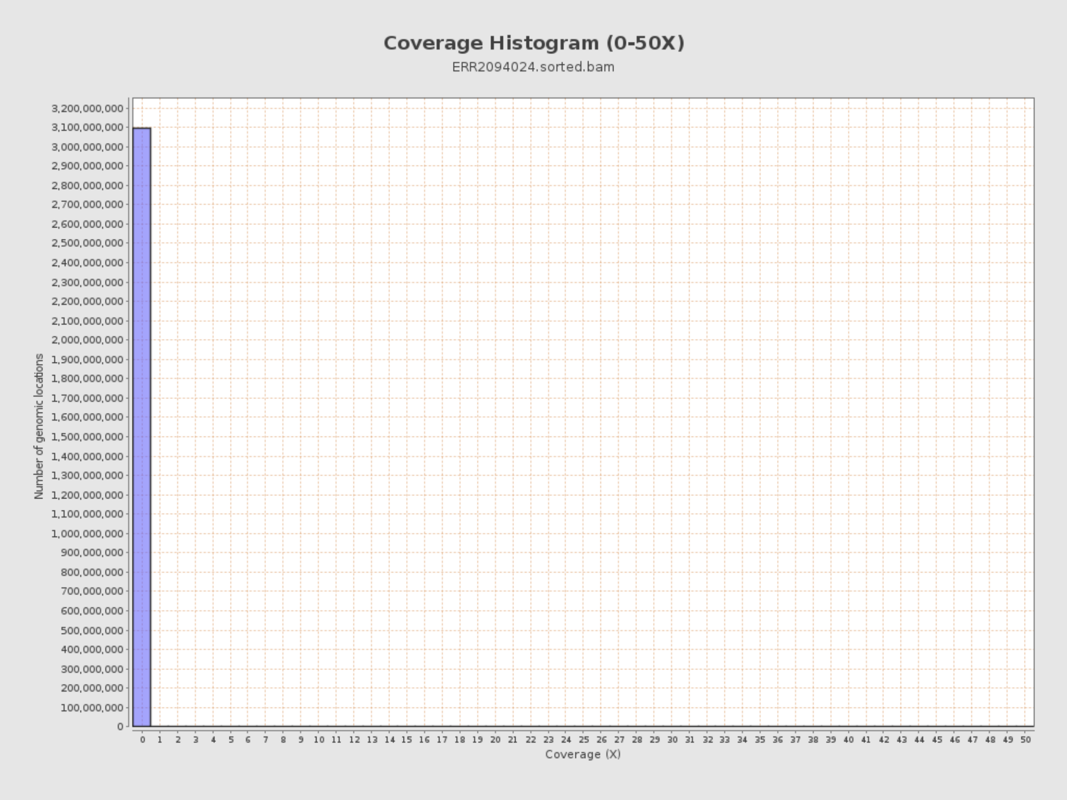
3. Results : Coverage across reference



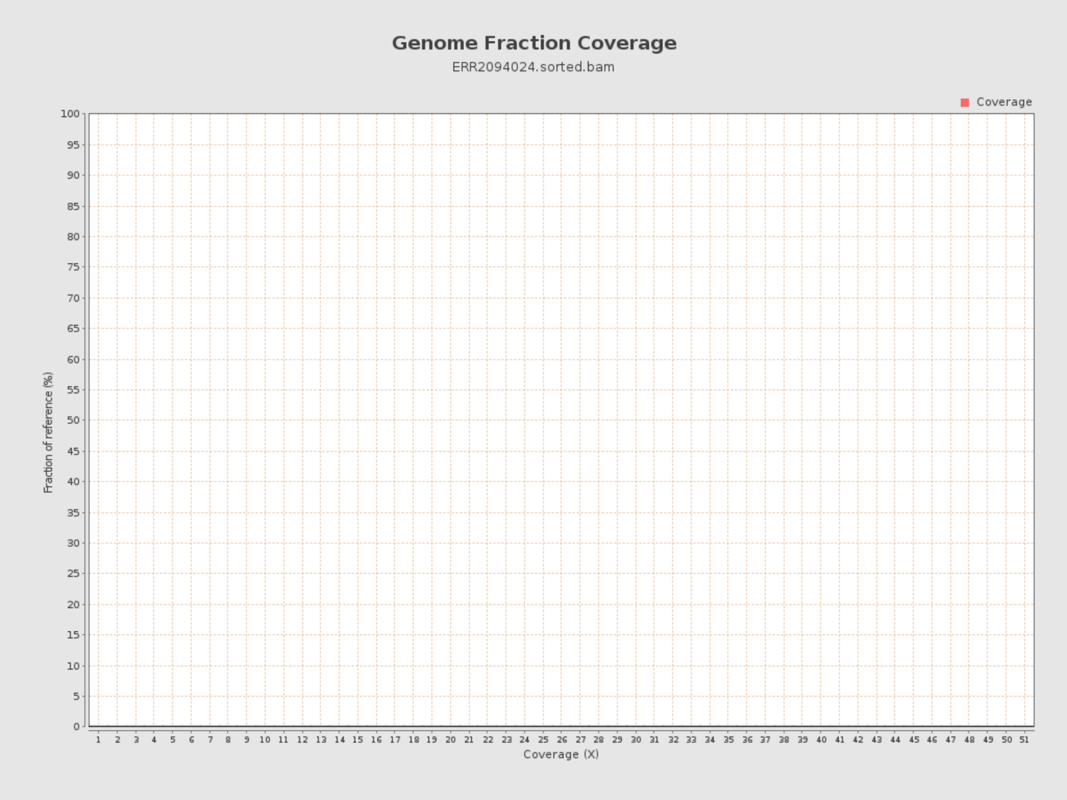
4. Results : Coverage Histogram



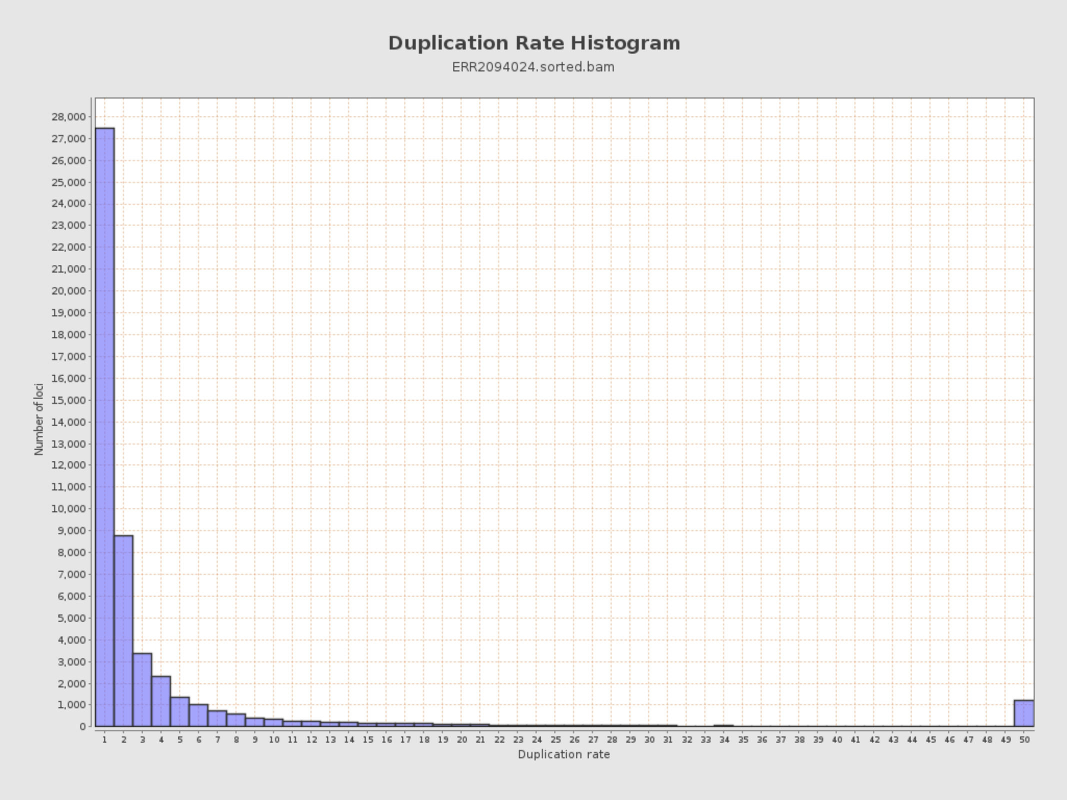
5. Results : Coverage Histogram (0-50X)



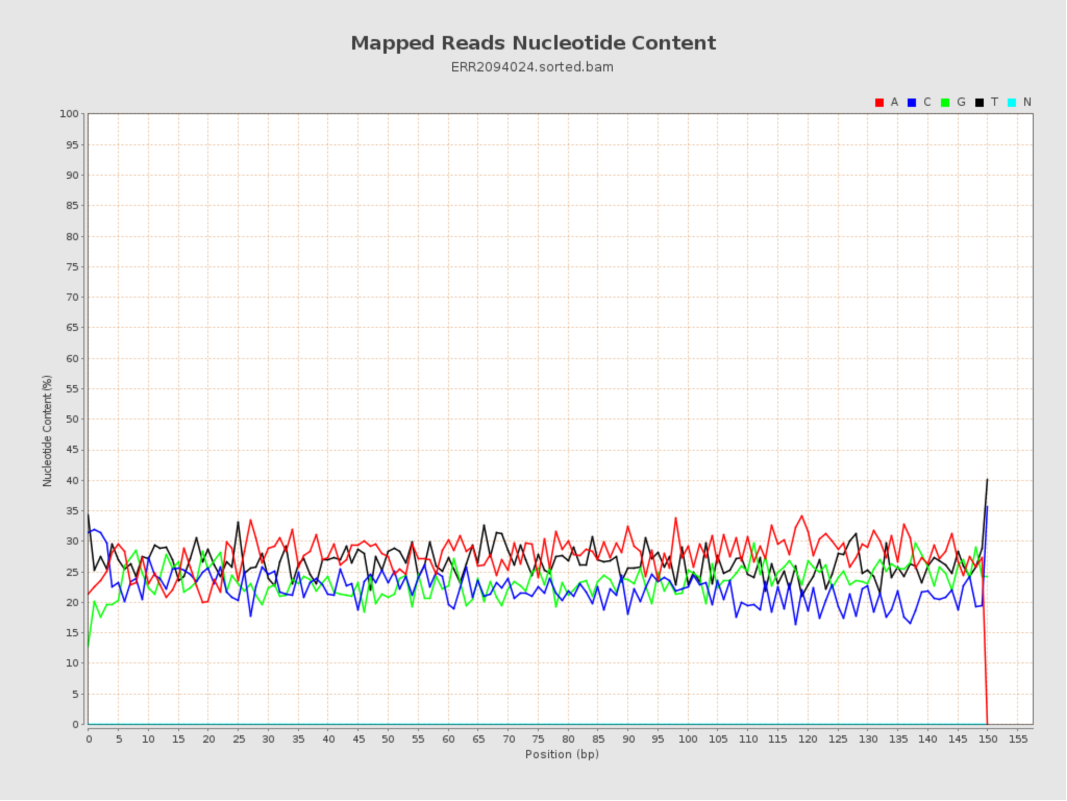
6. Results : Genome Fraction Coverage



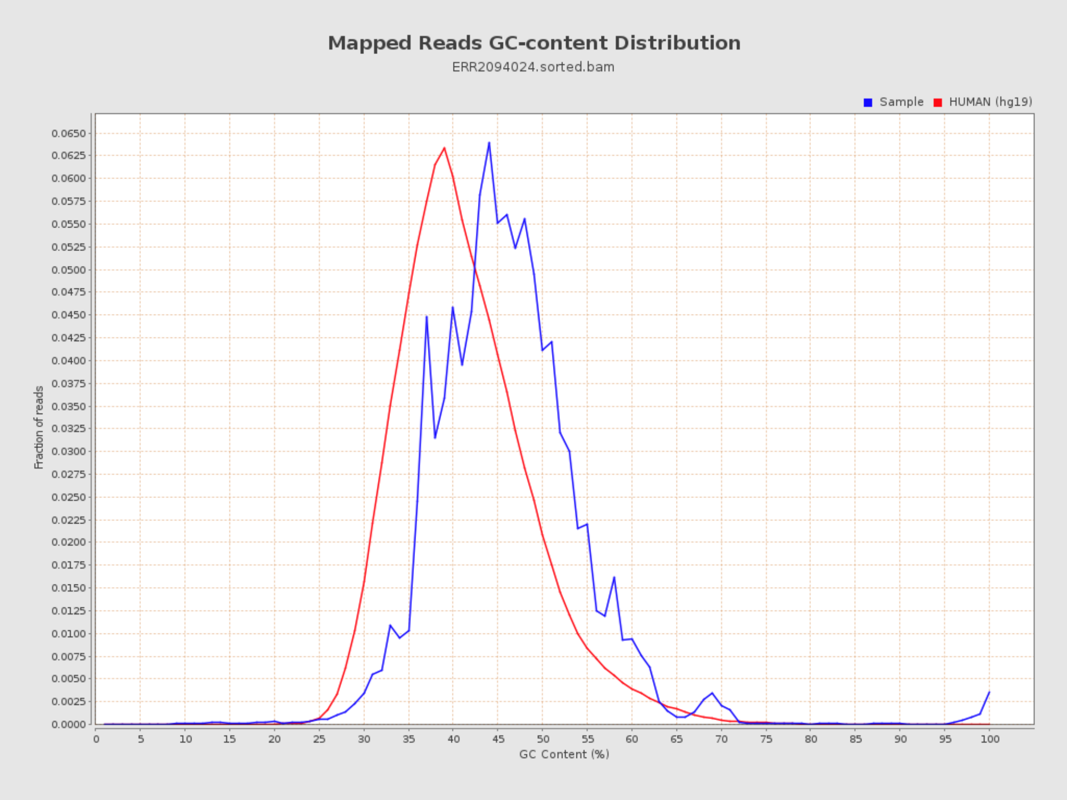
7. Results : Duplication Rate Histogram



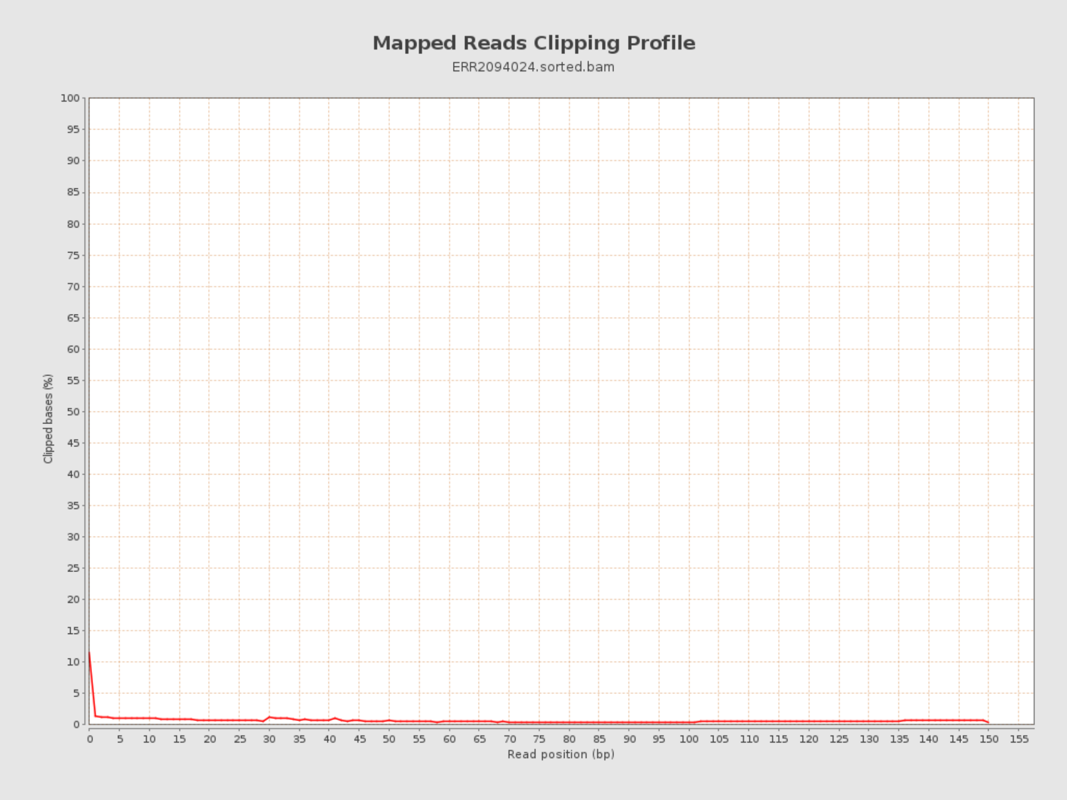
8. Results : Mapped Reads Nucleotide Content



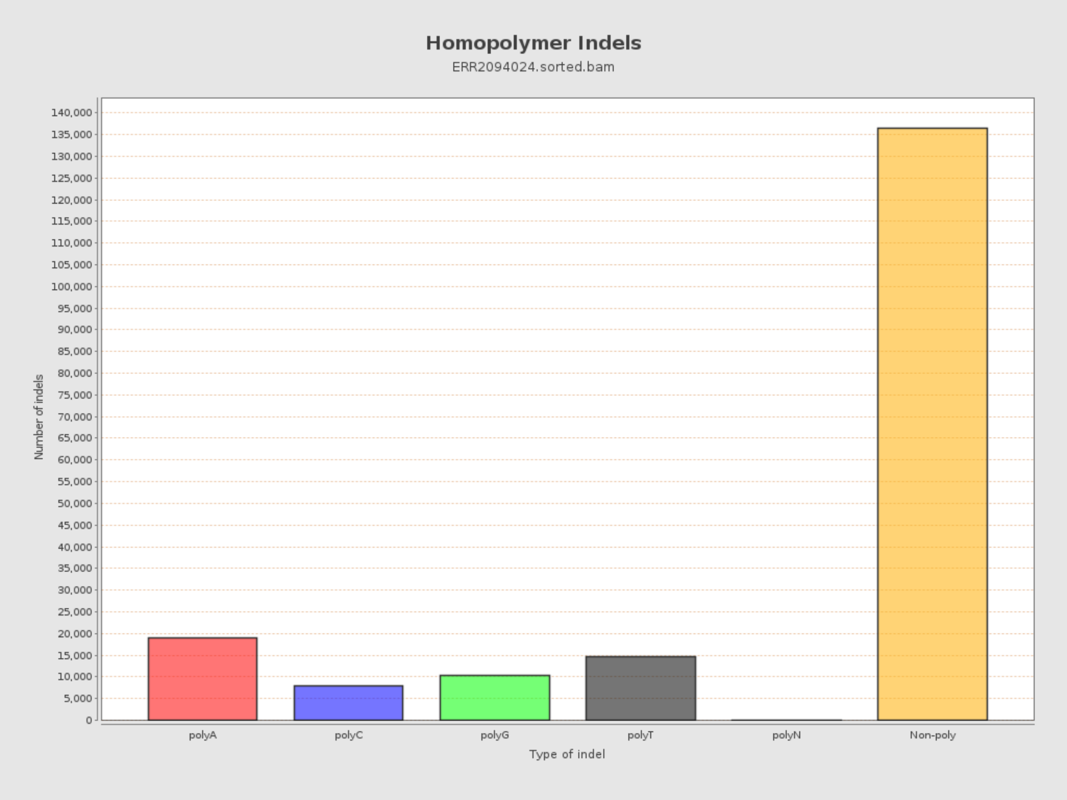
9. Results : Mapped Reads GC-content Distribution



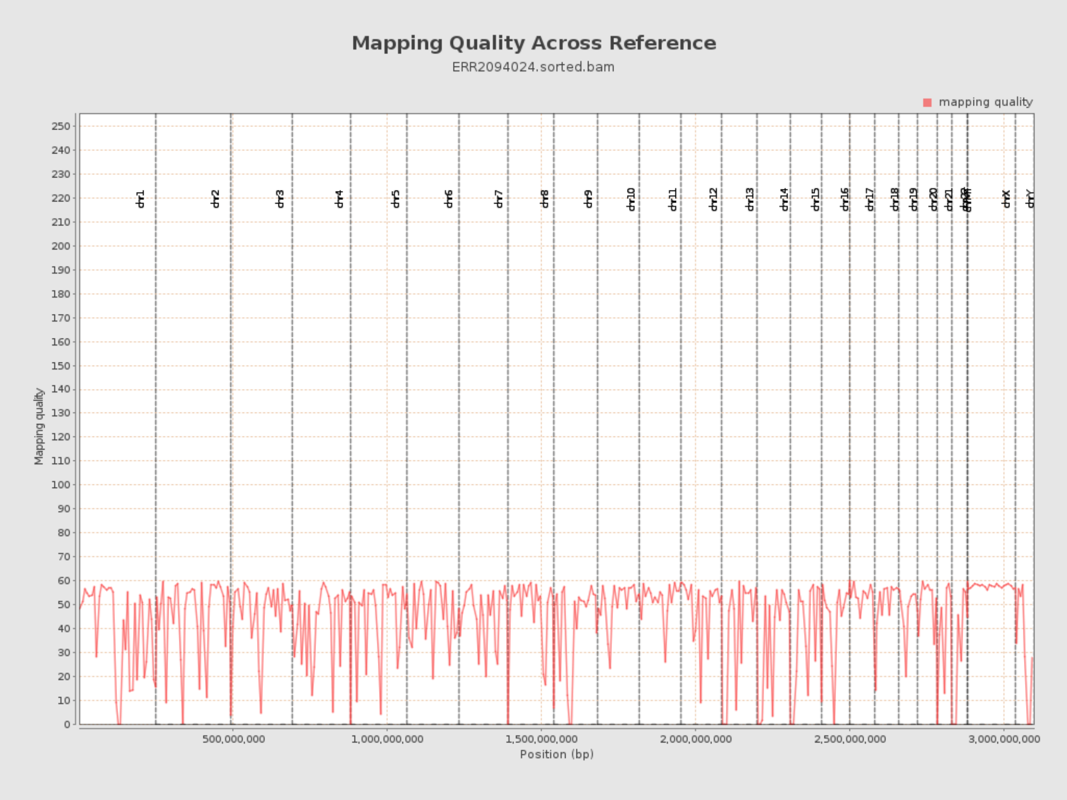
10. Results : Mapped Reads Clipping Profile



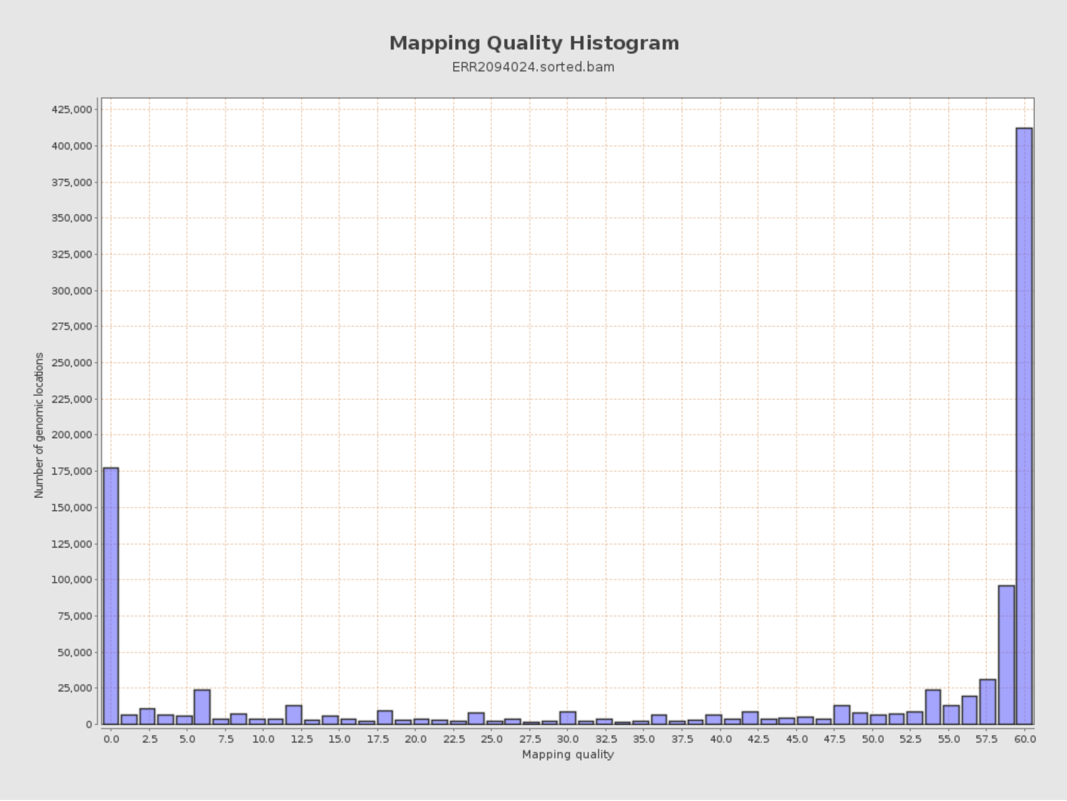
11. Results : Homopolymer Indels



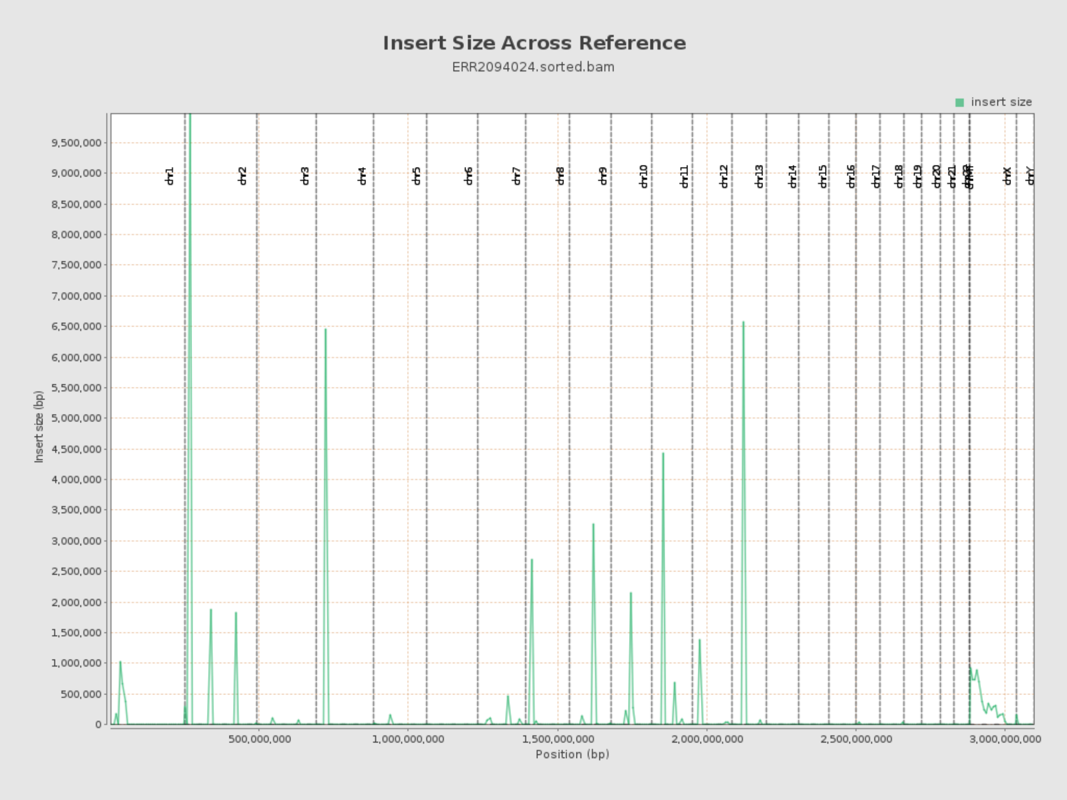
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram