Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 11:35:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524581.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_SRR10524581 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524581.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 11:35:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524581.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,018,259
Mapped reads	902,887 / 88.67%
Unmapped reads	115,372 / 11.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,127 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	68,124 / 6.69%
Duplication rate	6.03%
Clipped reads	905,709 / 88.95%

2.2. ACGT Content

Number/percentage of A's	12,227,067 / 24.01%
Number/percentage of C's	9,414,473 / 18.49%
Number/percentage of T's	16,532,877 / 32.47%
Number/percentage of G's	12,741,527 / 25.02%
Number/percentage of N's	628 / 0%
GC Percentage	43.51%

2.3. Coverage

Mean	0.0165

Standard Deviation	0.191

2.4. Mapping Quality

Mean Mapping Quality	44.11

2.5. Mismatches and indels

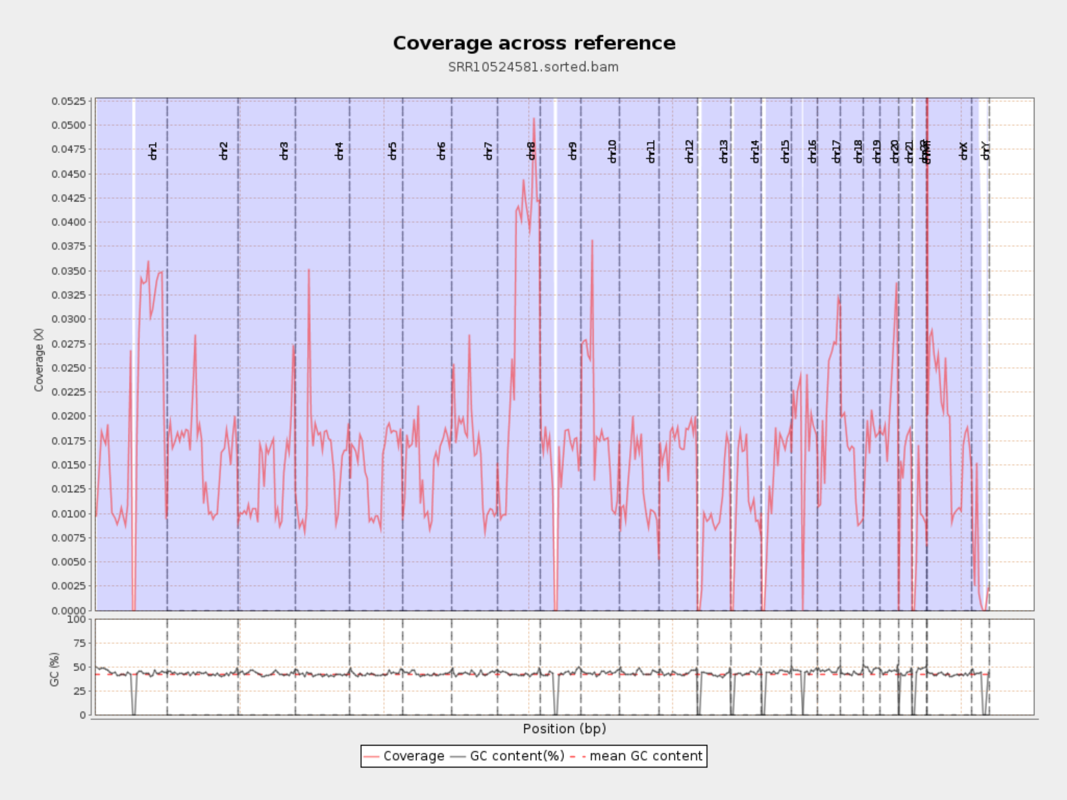
General error rate	0.58%
Mismatches	285,872
Insertions	3,456
Mapped reads with at least one insertion	0.38%
Deletions	11,394
Mapped reads with at least one deletion	1.25%
Homopolymer indels	42.73%

2.6. Chromosome stats

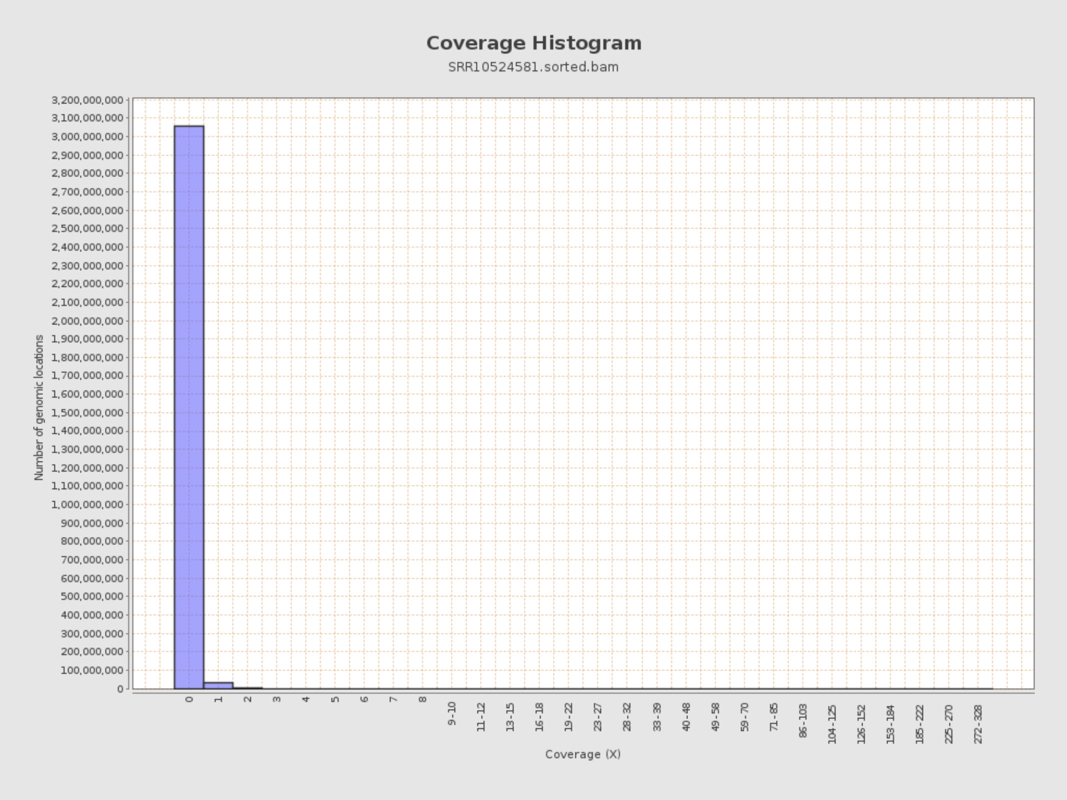
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4872036	0.0195	0.2795
chr2	243199373	4014538	0.0165	0.234
chr3	198022430	2688503	0.0136	0.1405
chr4	191154276	2989064	0.0156	0.1783
chr5	180915260	2733757	0.0151	0.1473
chr6	171115067	2575891	0.0151	0.158
chr7	159138663	2605893	0.0164	0.2121

chr8	146364022	4563867	0.0312	0.2402
chr9	141213431	2101698	0.0149	0.1629
chr10	135534747	2691431	0.0199	0.228
chr11	135006516	1716068	0.0127	0.1706
chr12	133851895	2345521	0.0175	0.1594
chr13	115169878	1099476	0.0095	0.1162
chr14	107349540	1192247	0.0111	0.1277
chr15	102531392	1323345	0.0129	0.1383
chr16	90354753	1643546	0.0182	0.1691
chr17	81195210	1791071	0.0221	0.1849
chr18	78077248	1169317	0.015	0.2445
chr19	59128983	1050019	0.0178	0.2151
chr20	63025520	1414077	0.0224	0.1832
chr21	48129895	718450	0.0149	0.1683
chr22	51304566	407724	0.0079	0.1056
chrMT	16571	39769	2.3999	2.3502
chrX	155270560	2971057	0.0191	0.174
chrY	59373566	217439	0.0037	0.1457

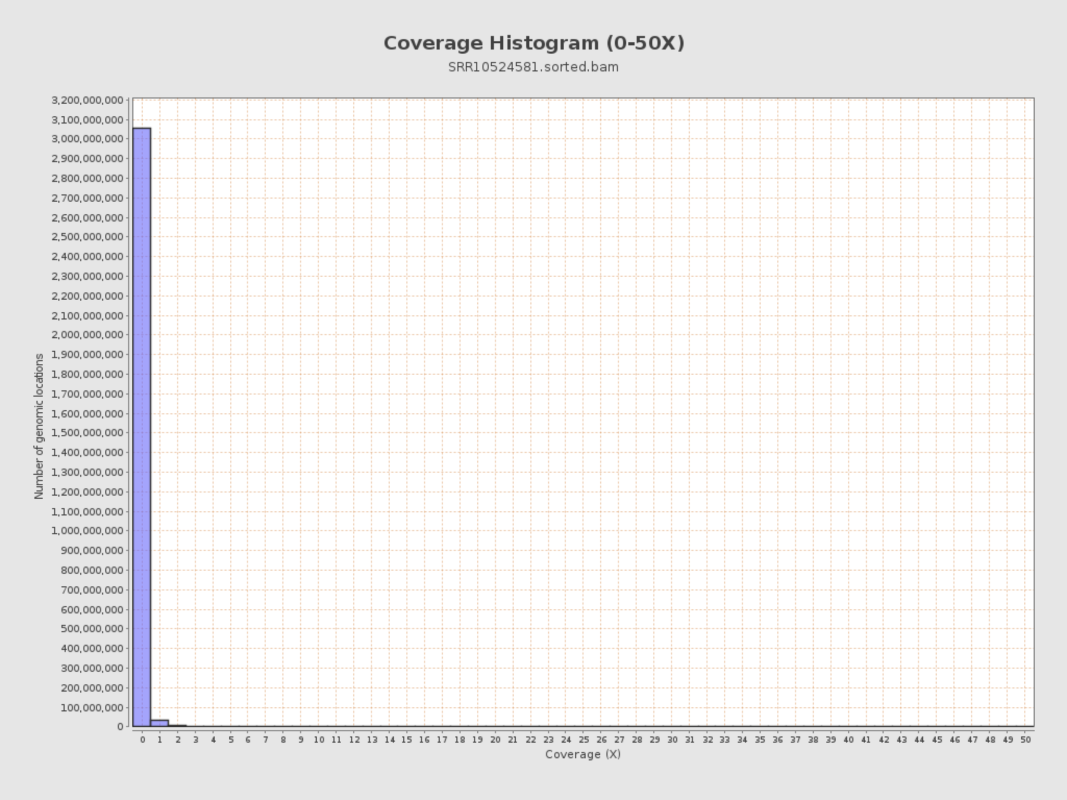
3. Results : Coverage across reference



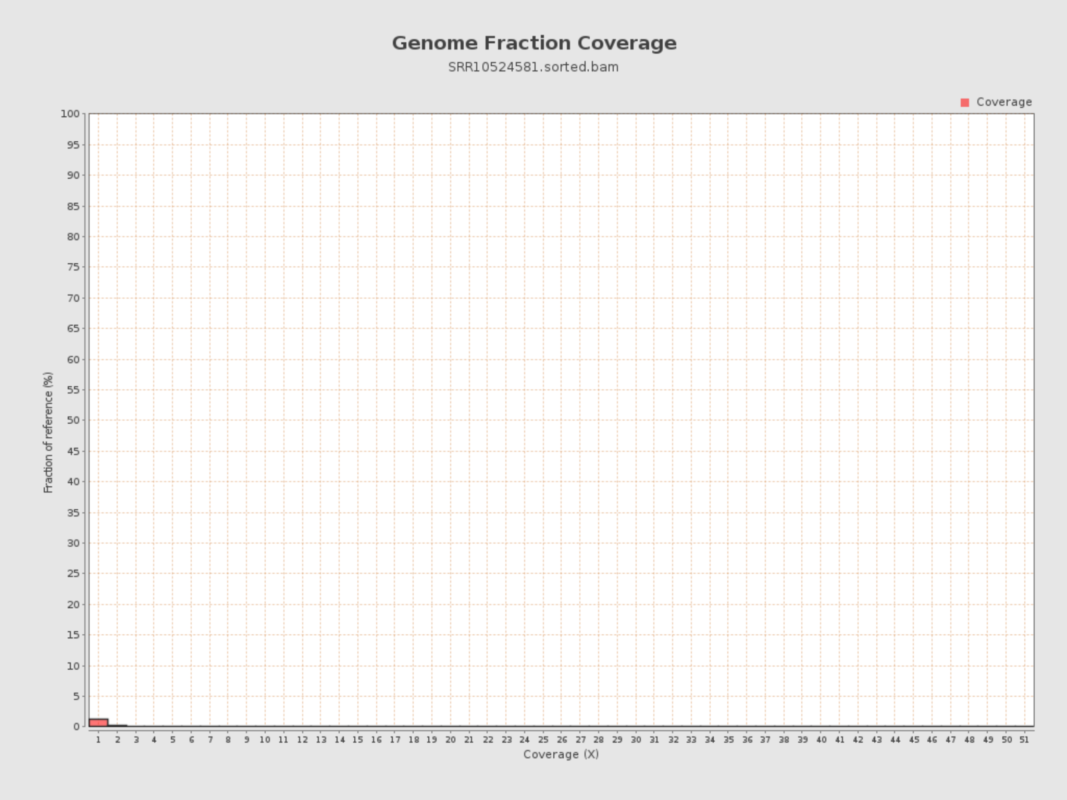
4. Results : Coverage Histogram



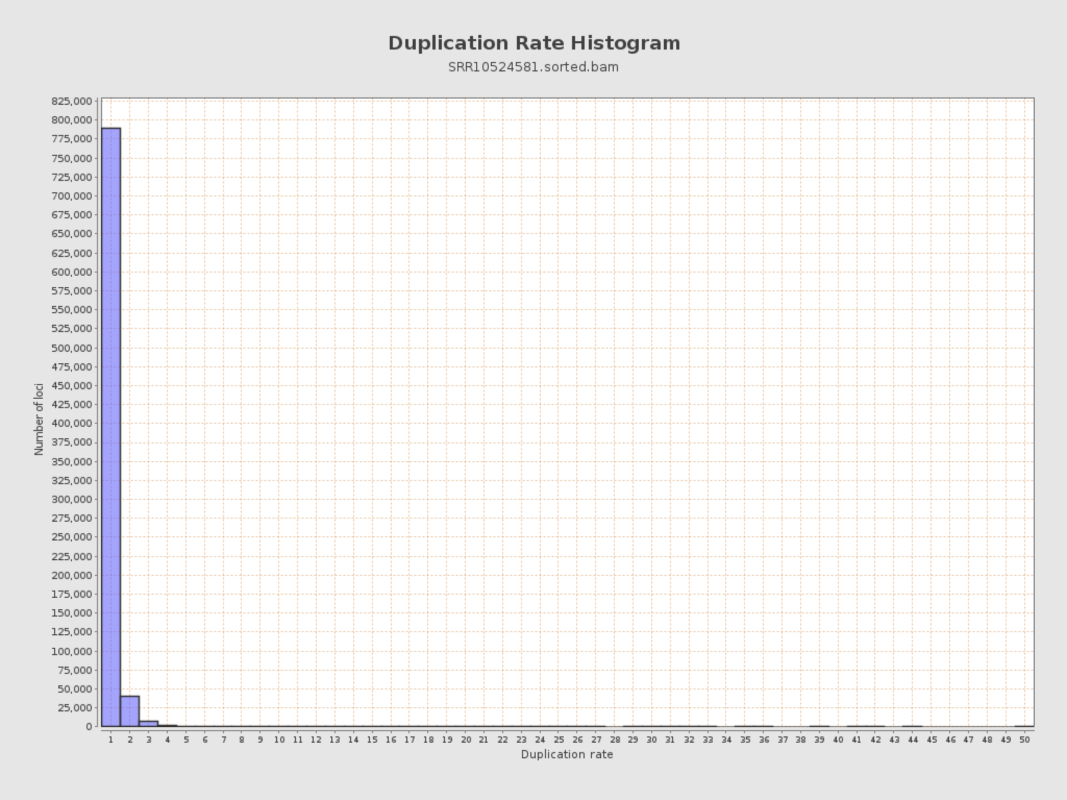
5. Results : Coverage Histogram (0-50X)



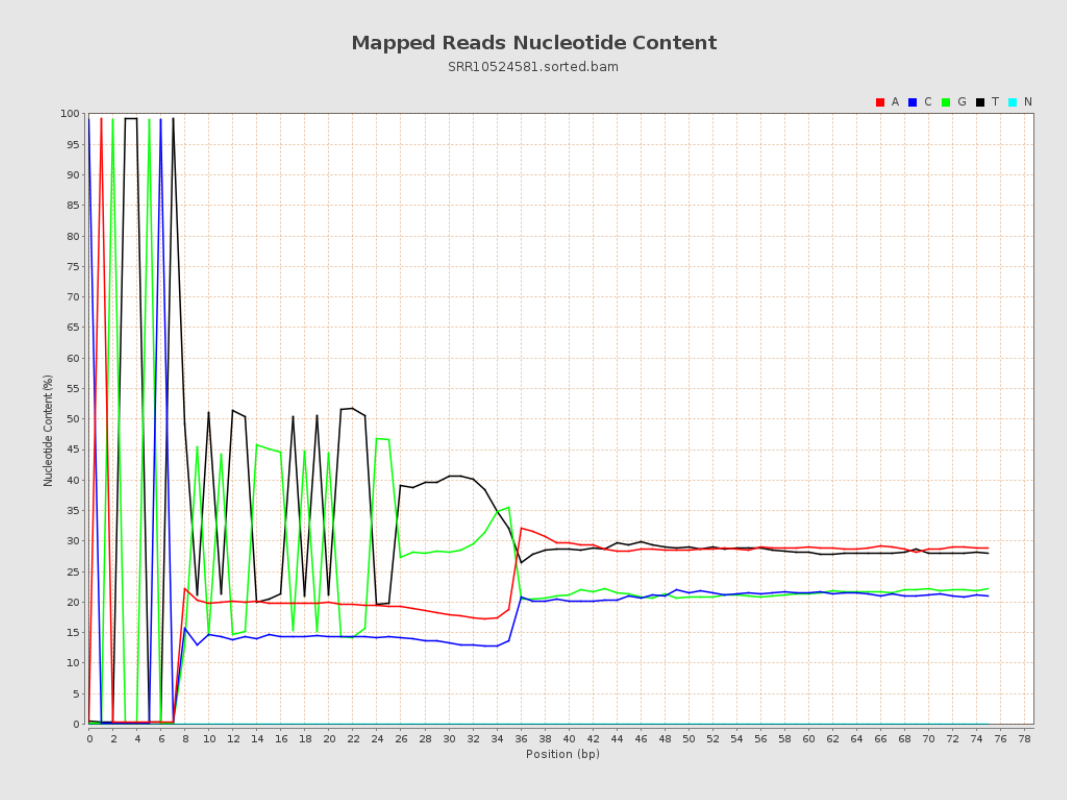
6. Results : Genome Fraction Coverage



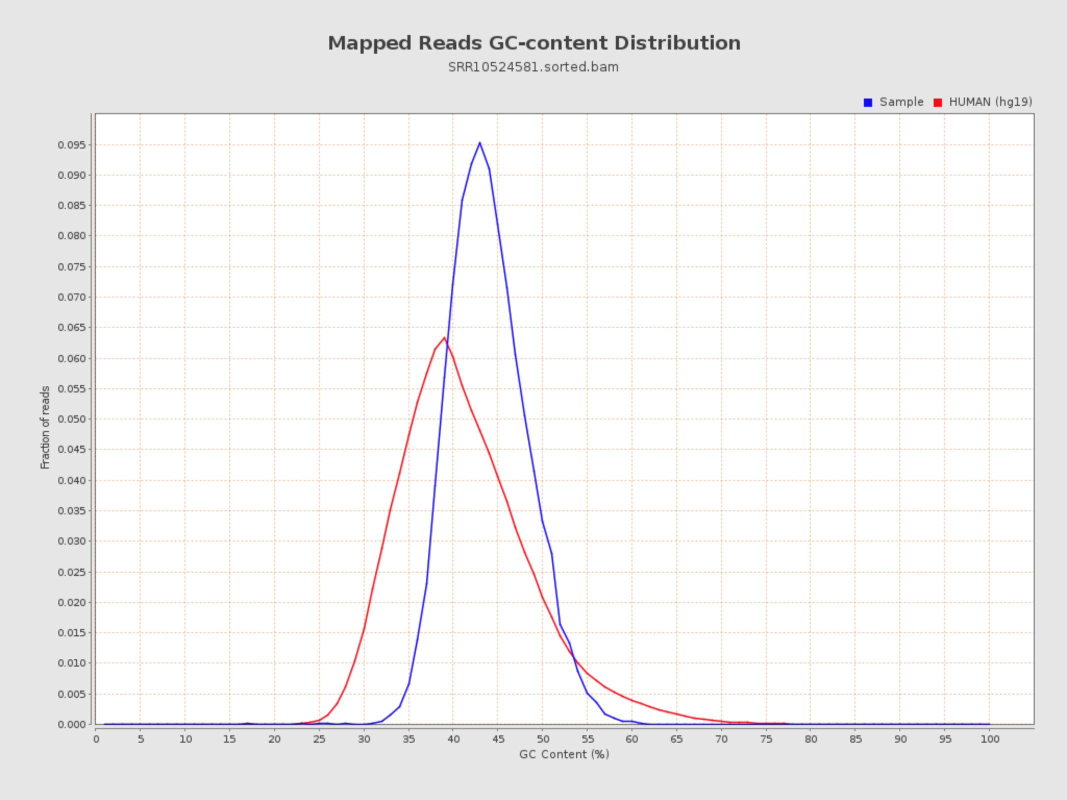
7. Results : Duplication Rate Histogram



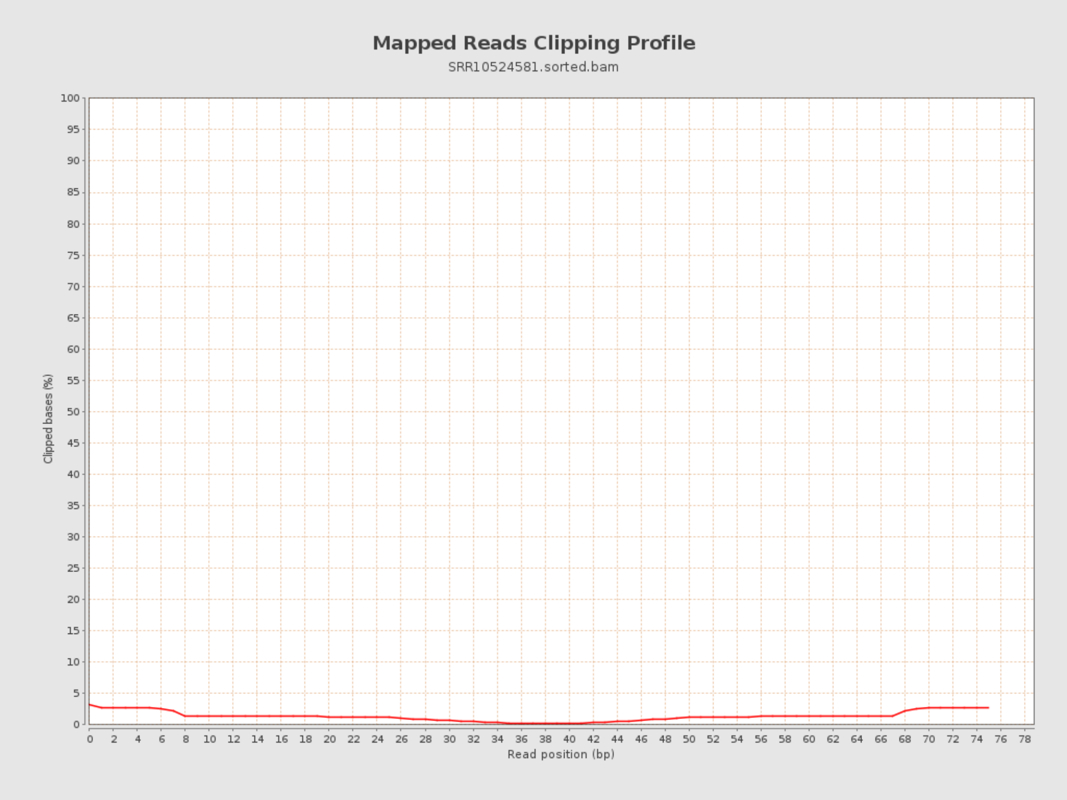
8. Results : Mapped Reads Nucleotide Content



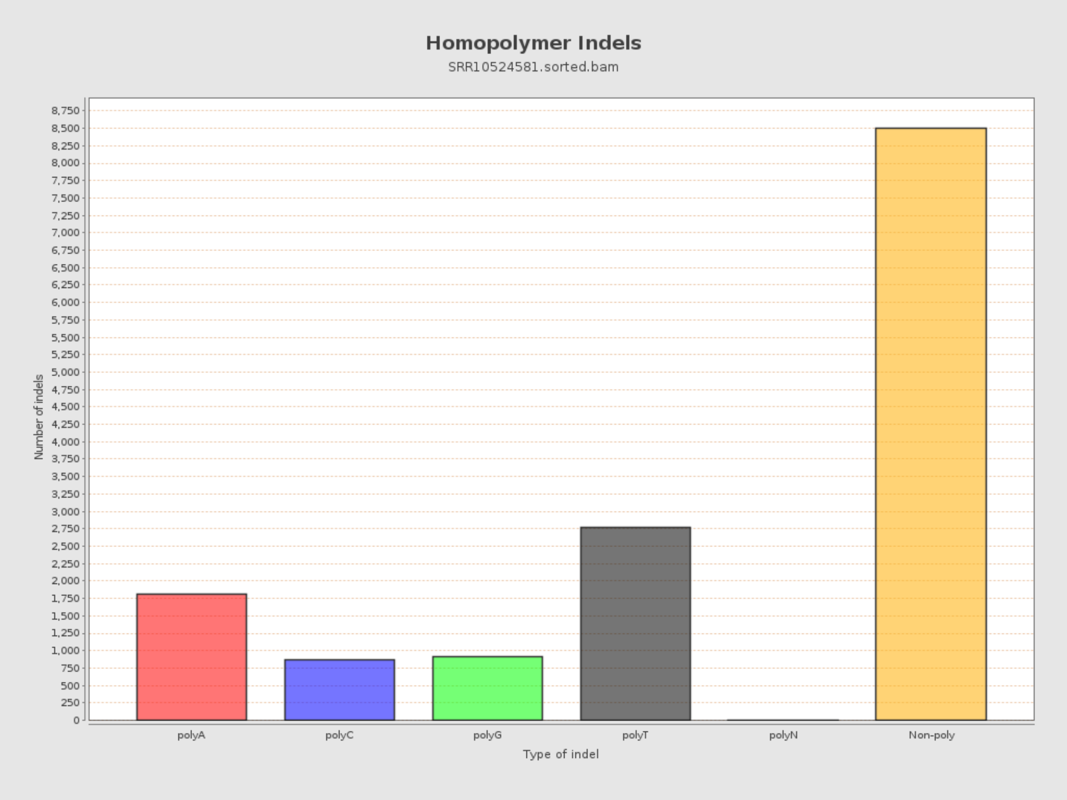
9. Results : Mapped Reads GC-content Distribution



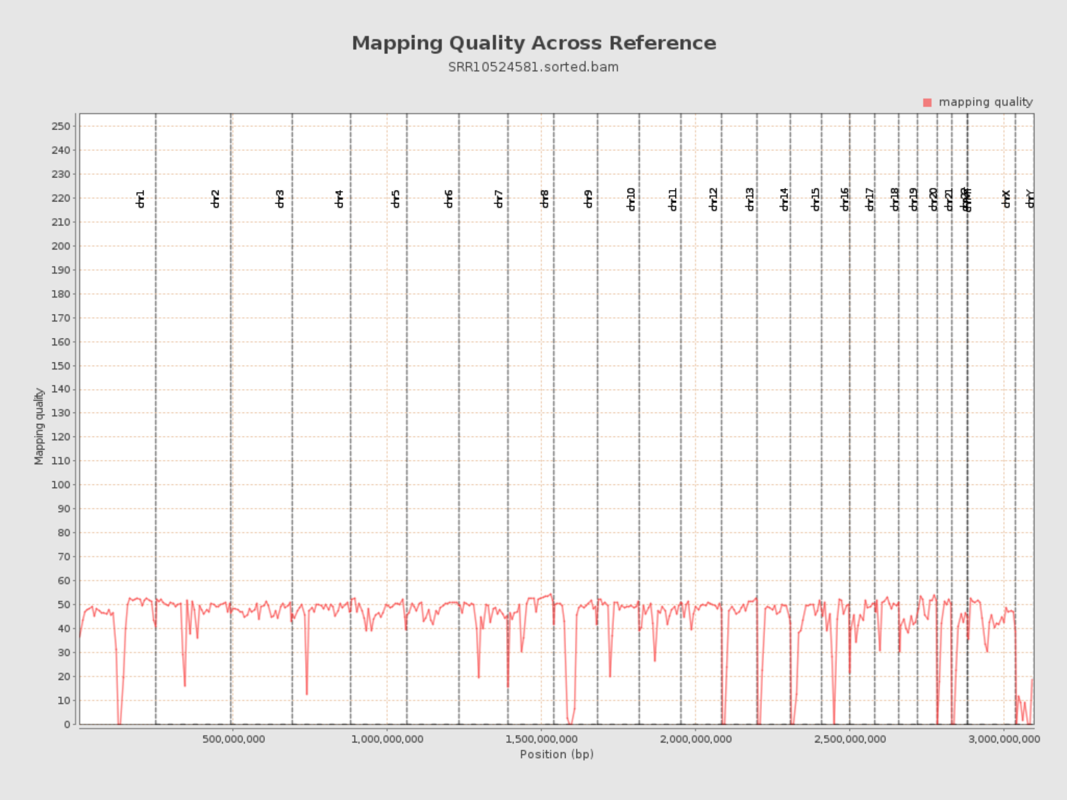
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram