Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 21:55:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524305.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_SRR10524305 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524305.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 21:55:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524305.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	523,689
Mapped reads	479,331 / 91.53%
Unmapped reads	44,358 / 8.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,973 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	7,203 / 1.38%
Duplication rate	1.05%
Clipped reads	480,138 / 91.68%

2.2. ACGT Content

Number/percentage of A's	6,752,189 / 24.33%
Number/percentage of C's	5,198,313 / 18.73%
Number/percentage of T's	8,910,701 / 32.1%
Number/percentage of G's	6,889,649 / 24.82%
Number/percentage of N's	4,099 / 0.01%
GC Percentage	43.55%

2.3. Coverage

Mean	0.009

Standard Deviation	0.1154

2.4. Mapping Quality

Mean Mapping Quality	43.8

2.5. Mismatches and indels

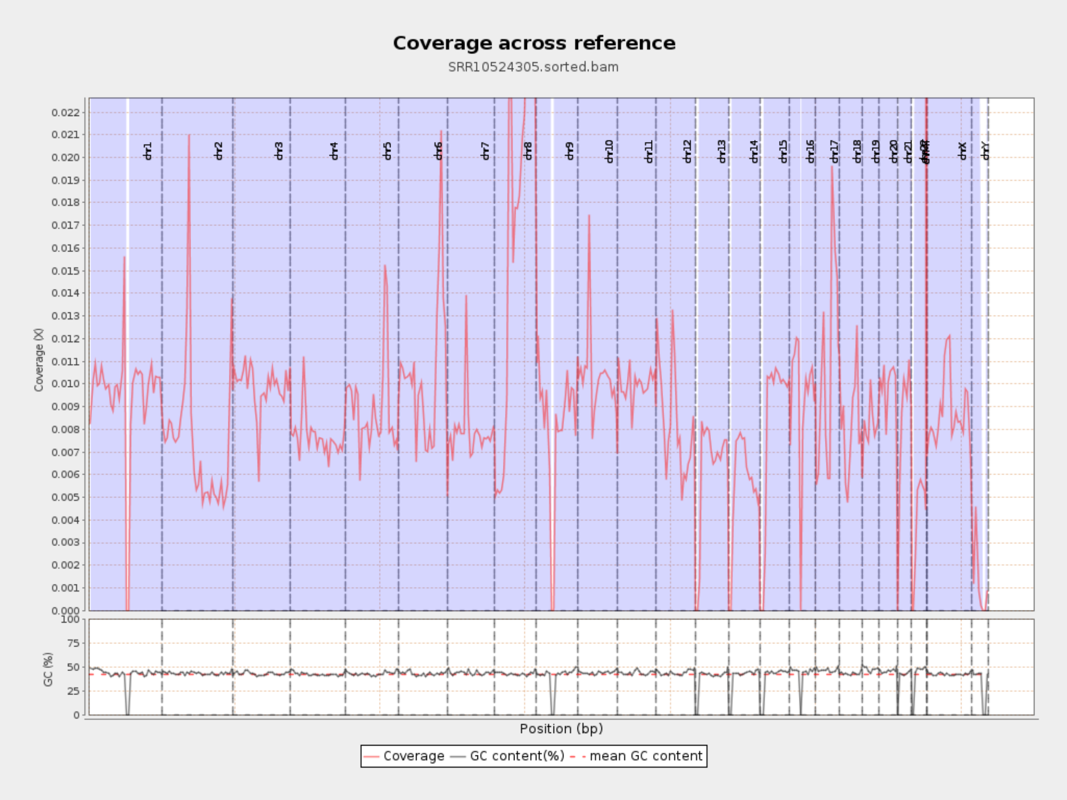
General error rate	0.52%
Mismatches	140,239
Insertions	1,851
Mapped reads with at least one insertion	0.38%
Deletions	4,740
Mapped reads with at least one deletion	0.98%
Homopolymer indels	43.16%

2.6. Chromosome stats

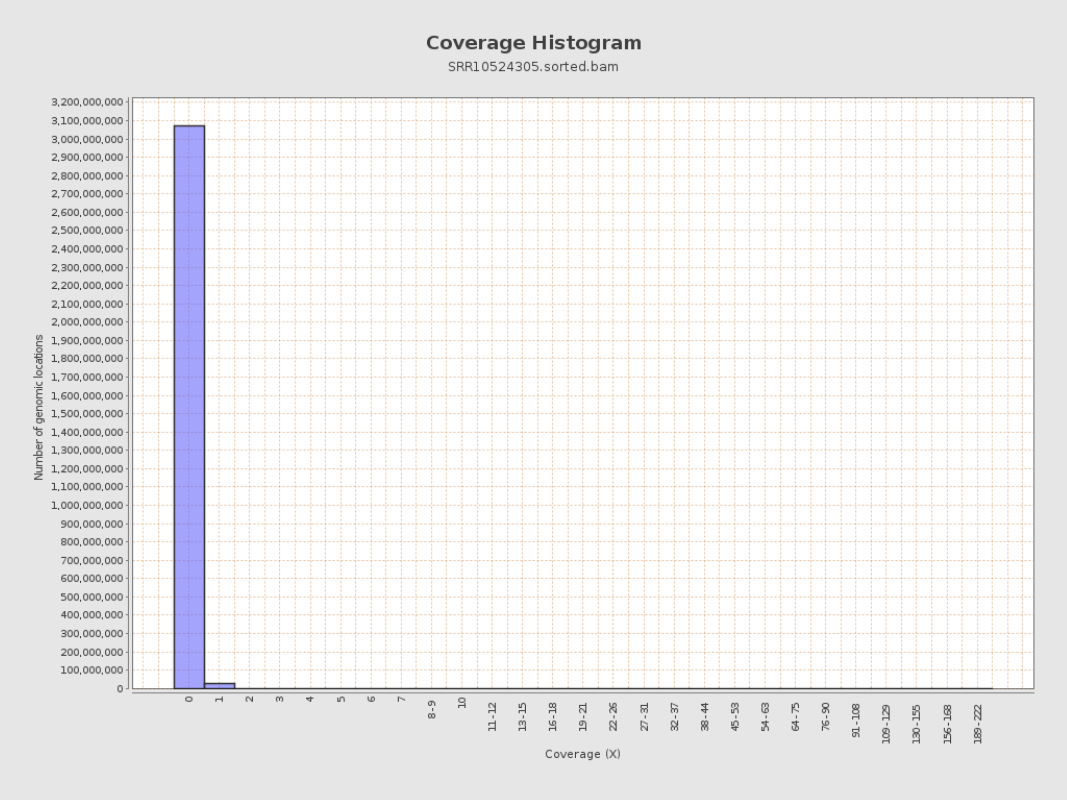
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2354422	0.0094	0.1751
chr2	243199373	1817273	0.0075	0.1283
chr3	198022430	1948192	0.0098	0.1023
chr4	191154276	1462304	0.0076	0.0924
chr5	180915260	1623282	0.009	0.0973
chr6	171115067	1782629	0.0104	0.1067
chr7	159138663	1267207	0.008	0.1288

chr8	146364022	2873502	0.0196	0.1576
chr9	141213431	1133426	0.008	0.1003
chr10	135534747	1407437	0.0104	0.1192
chr11	135006516	1340482	0.0099	0.1089
chr12	133851895	1107496	0.0083	0.0939
chr13	115169878	705618	0.0061	0.0808
chr14	107349540	588553	0.0055	0.0796
chr15	102531392	843392	0.0082	0.0936
chr16	90354753	849197	0.0094	0.1011
chr17	81195210	858709	0.0106	0.1096
chr18	78077248	652559	0.0084	0.1378
chr19	59128983	487560	0.0082	0.1357
chr20	63025520	623283	0.0099	0.1023
chr21	48129895	393240	0.0082	0.0949
chr22	51304566	196135	0.0038	0.0632
chrMT	16571	11908	0.7186	0.9762
chrX	155270560	1359942	0.0088	0.0998
chrY	59373566	74818	0.0013	0.0469

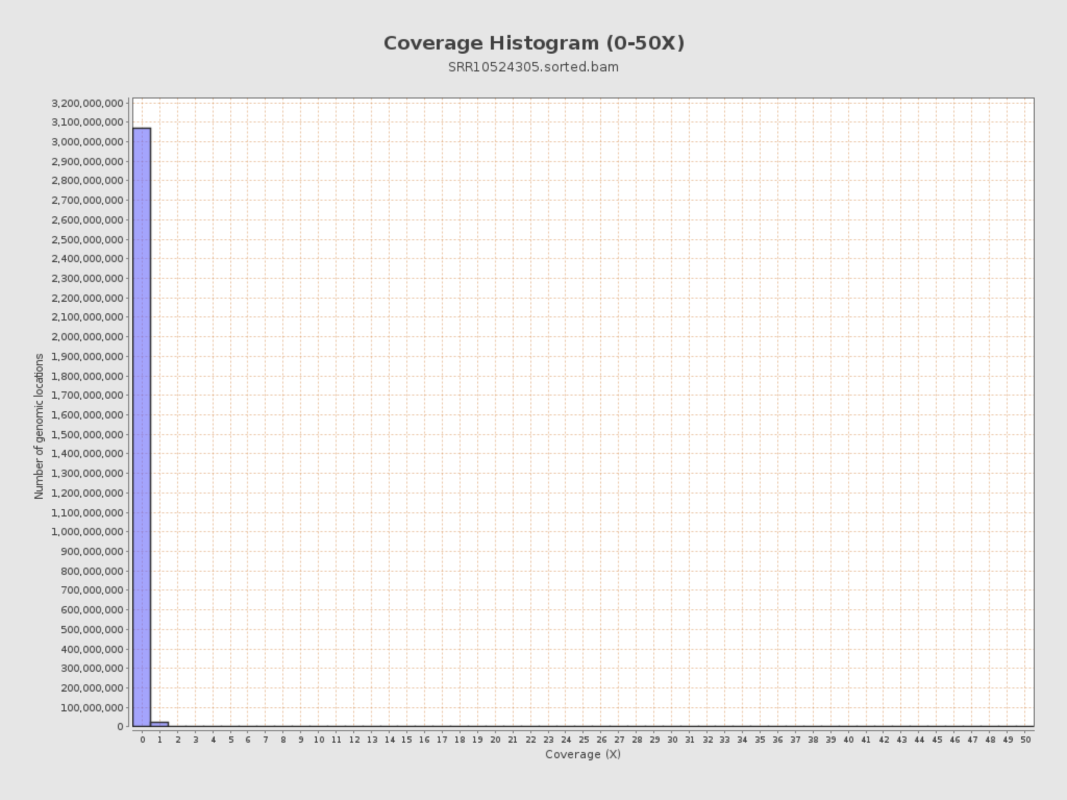
3. Results : Coverage across reference



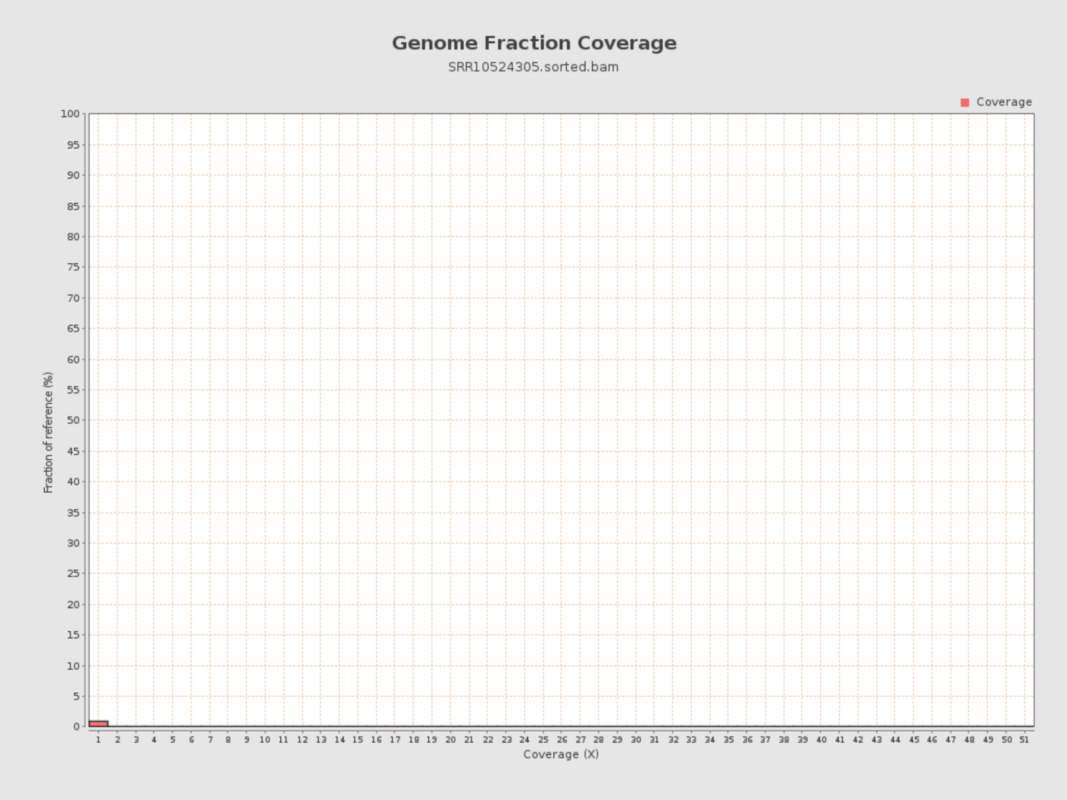
4. Results : Coverage Histogram



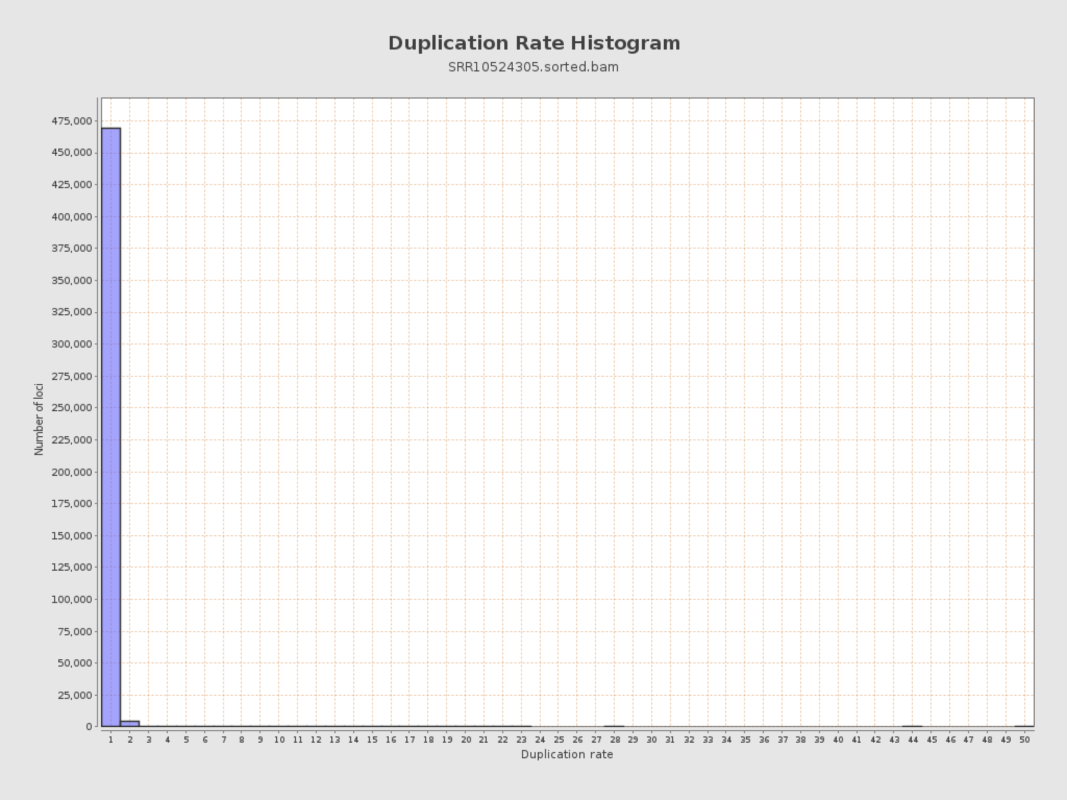
5. Results : Coverage Histogram (0-50X)



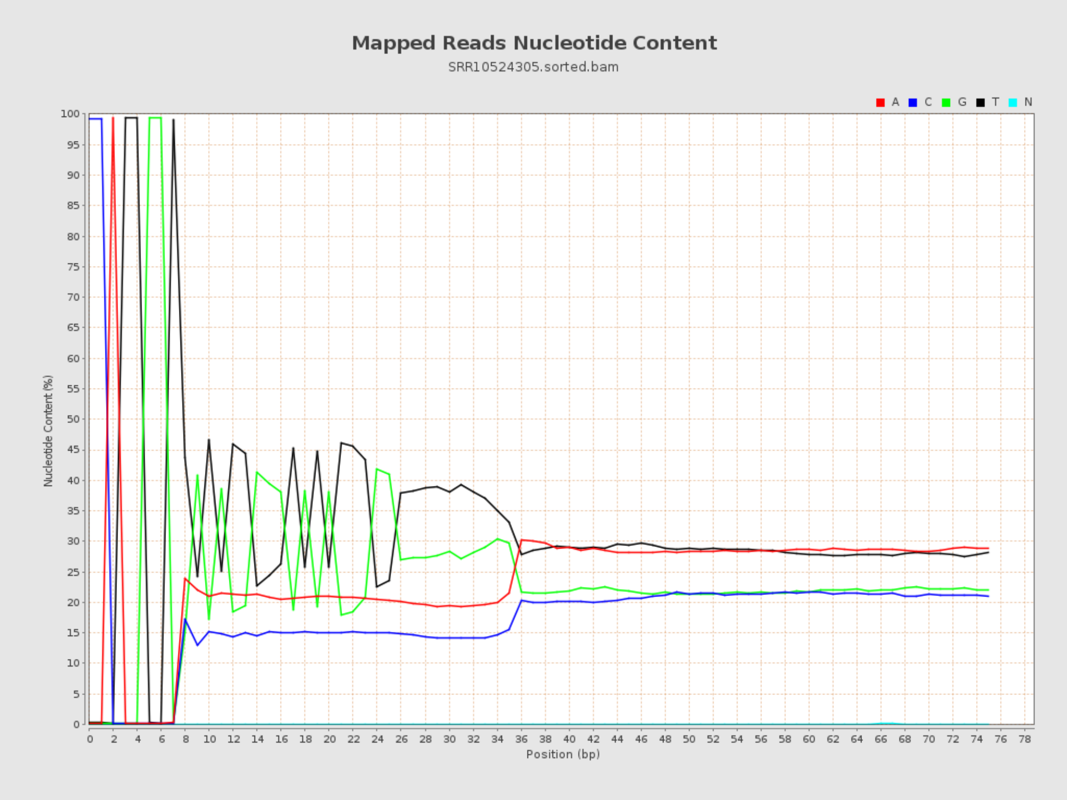
6. Results : Genome Fraction Coverage



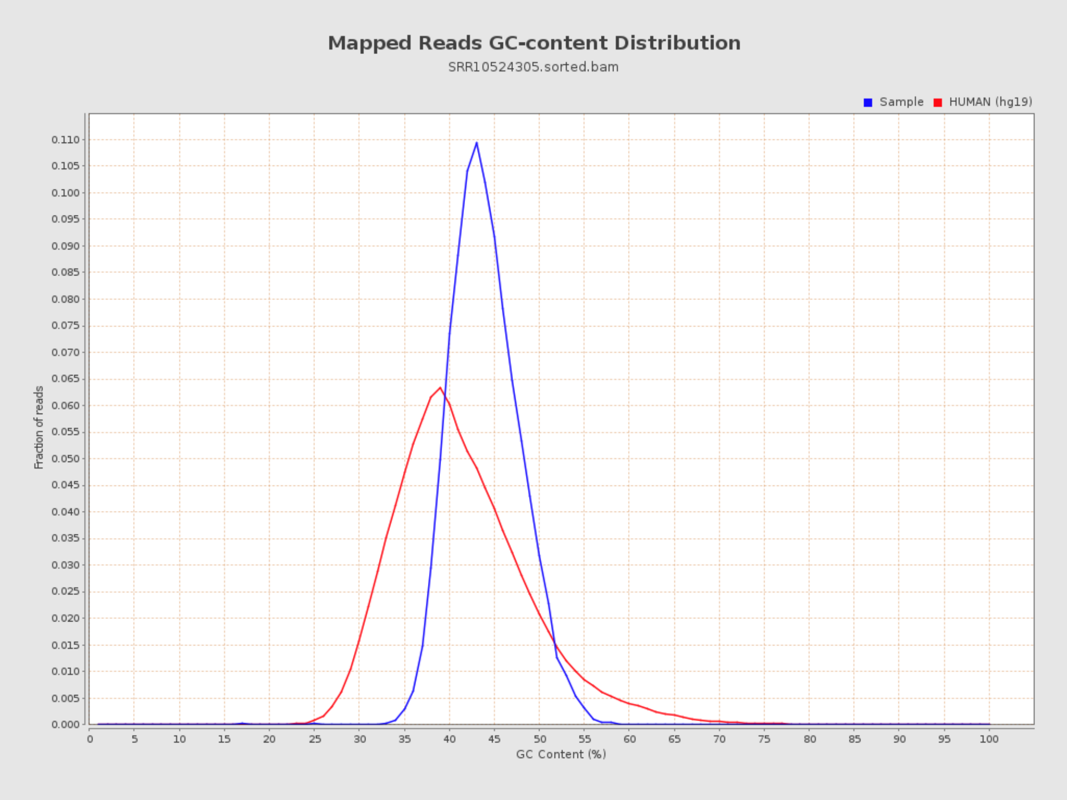
7. Results : Duplication Rate Histogram



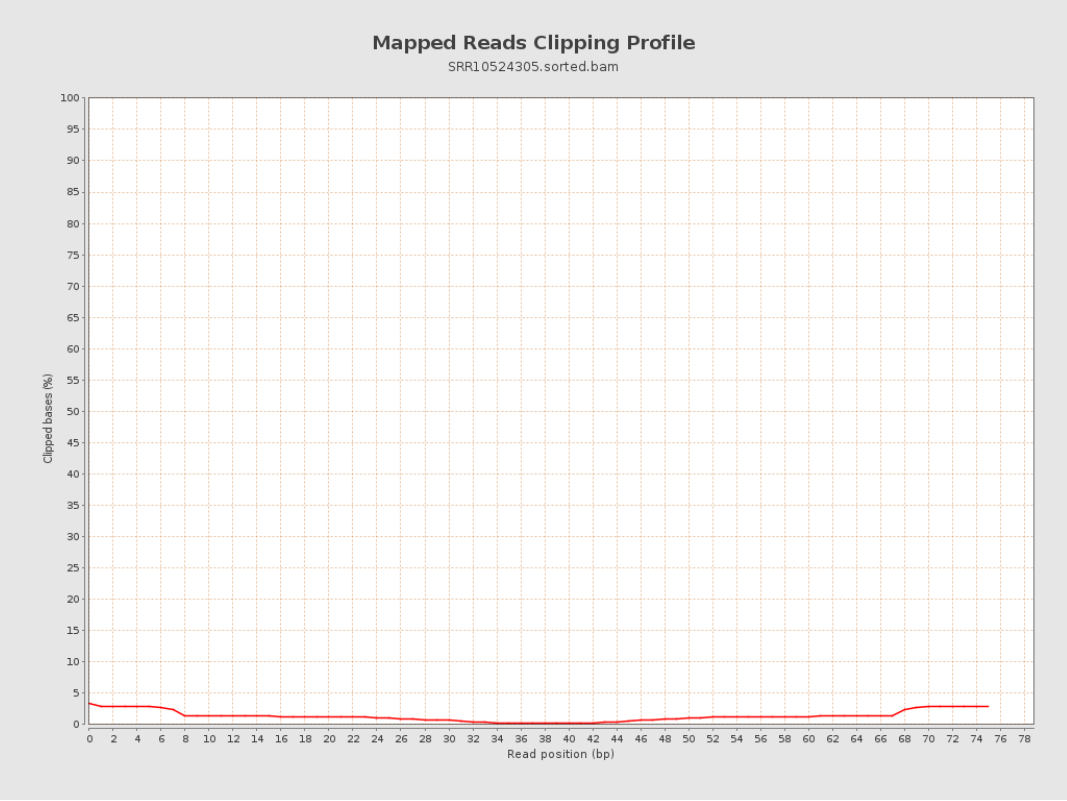
8. Results : Mapped Reads Nucleotide Content



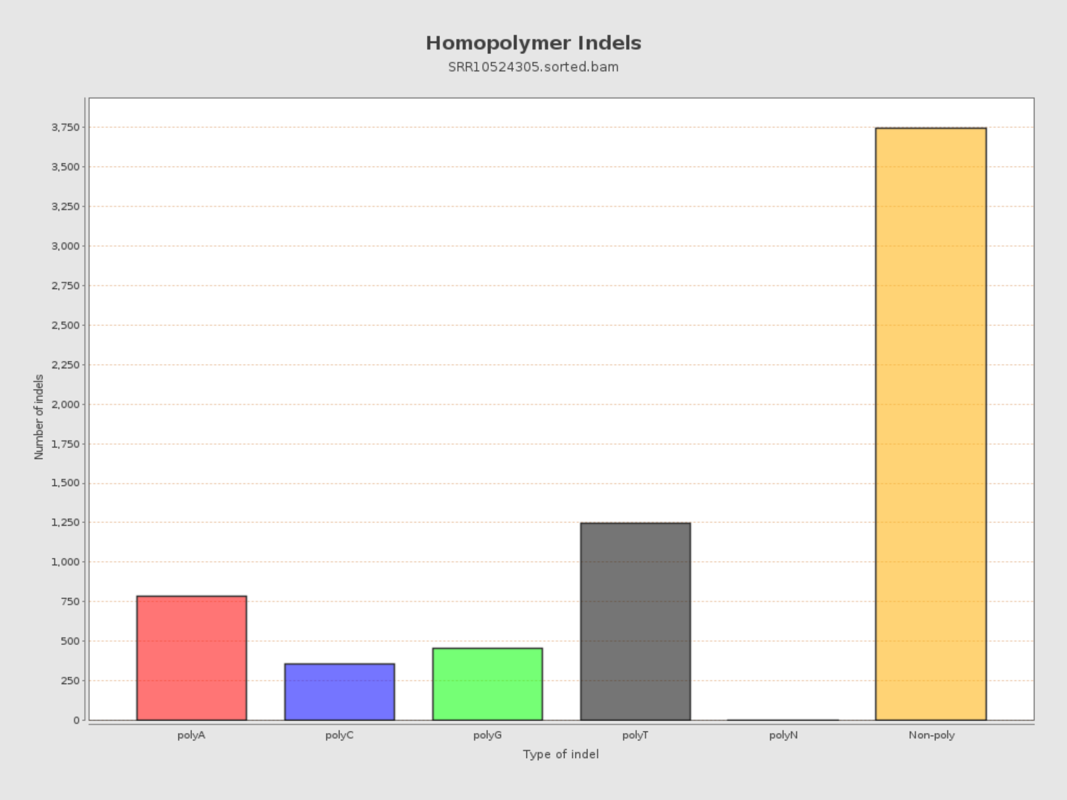
9. Results : Mapped Reads GC-content Distribution



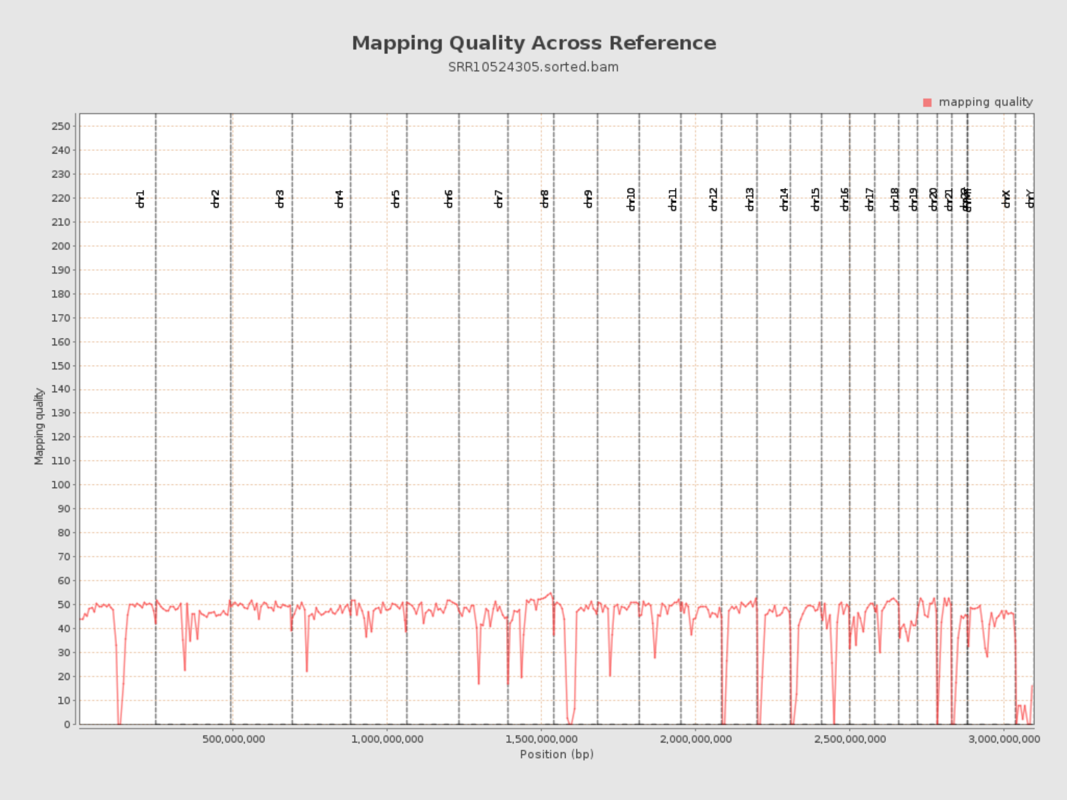
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram