Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 02:26:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524905.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_SRR10524905 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524905.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 02:26:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524905.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,110,972
Mapped reads	1,027,716 / 92.51%
Unmapped reads	83,256 / 7.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,913 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	43,187 / 3.89%
Duplication rate	3.3%
Clipped reads	1,028,912 / 92.61%

2.2. ACGT Content

Number/percentage of A's	14,587,276 / 24.44%
Number/percentage of C's	10,637,243 / 17.82%
Number/percentage of T's	19,757,389 / 33.11%
Number/percentage of G's	14,695,039 / 24.62%
Number/percentage of N's	480 / 0%
GC Percentage	42.45%

2.3. Coverage

Mean	0.0193

Standard Deviation	0.1998

2.4. Mapping Quality

Mean Mapping Quality	44.86

2.5. Mismatches and indels

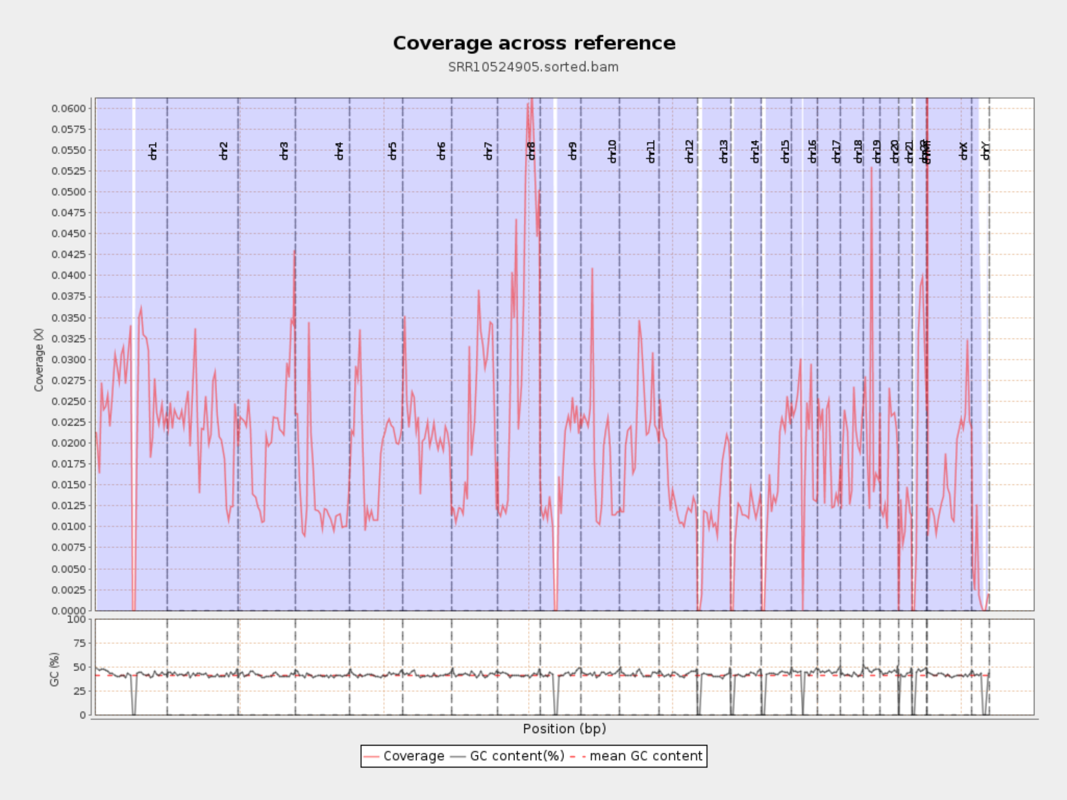
General error rate	0.52%
Mismatches	304,341
Insertions	4,208
Mapped reads with at least one insertion	0.41%
Deletions	11,416
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.38%

2.6. Chromosome stats

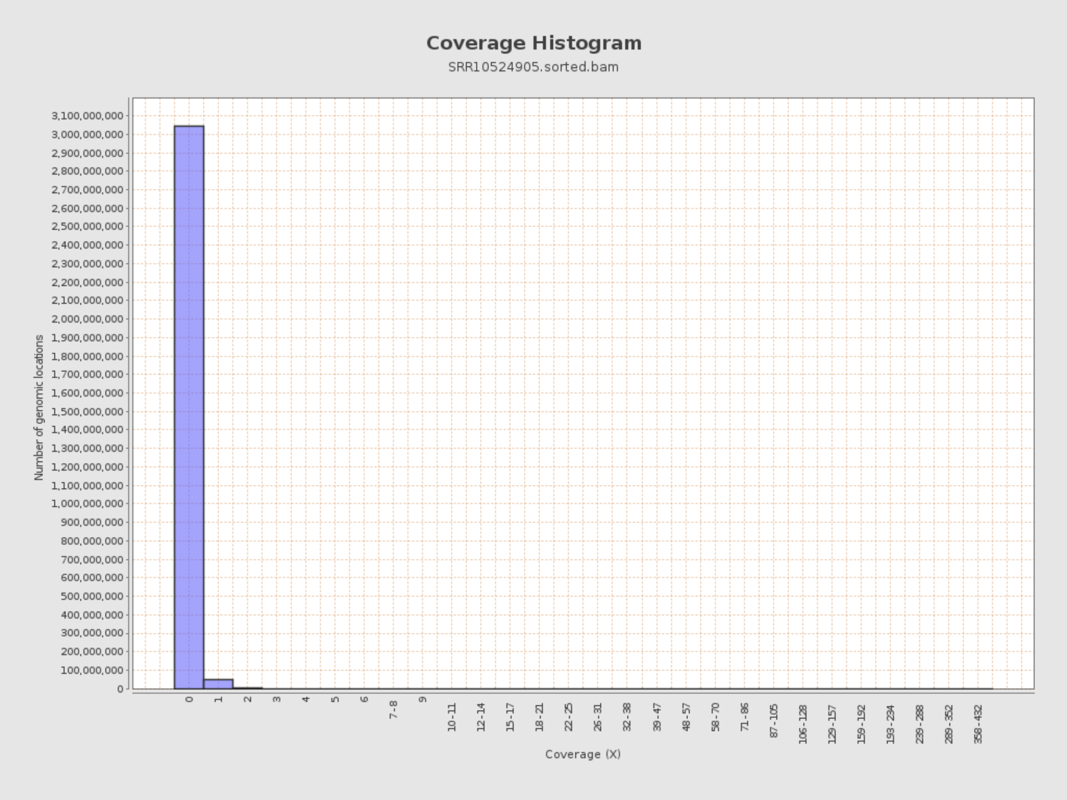
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6193275	0.0248	0.3457
chr2	243199373	5291701	0.0218	0.2441
chr3	198022430	4236558	0.0214	0.1593
chr4	191154276	2623010	0.0137	0.1548
chr5	180915260	3491888	0.0193	0.1506
chr6	171115067	3738626	0.0218	0.1666
chr7	159138663	3581927	0.0225	0.2381

chr8	146364022	5164831	0.0353	0.2623
chr9	141213431	2163731	0.0153	0.1563
chr10	135534747	2554517	0.0188	0.2146
chr11	135006516	2984927	0.0221	0.1777
chr12	133851895	1926901	0.0144	0.1338
chr13	115169878	1339240	0.0116	0.1176
chr14	107349540	1114654	0.0104	0.1151
chr15	102531392	1545680	0.0151	0.1341
chr16	90354753	1836518	0.0203	0.1608
chr17	81195210	1496267	0.0184	0.1525
chr18	78077248	1531583	0.0196	0.2466
chr19	59128983	1334332	0.0226	0.2439
chr20	63025520	1126153	0.0179	0.1481
chr21	48129895	498107	0.0103	0.1319
chr22	51304566	1181632	0.023	0.1654
chrMT	16571	6265	0.3781	0.7476
chrX	155270560	2554667	0.0165	0.1493
chrY	59373566	179535	0.003	0.1219

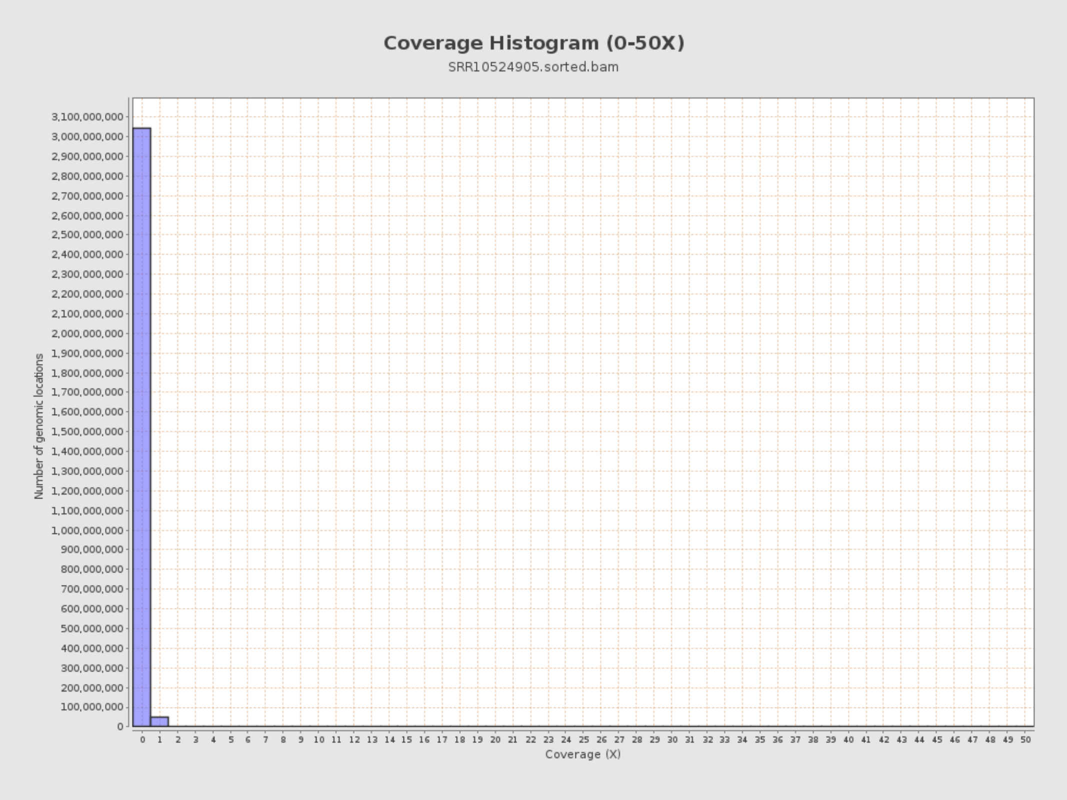
3. Results : Coverage across reference



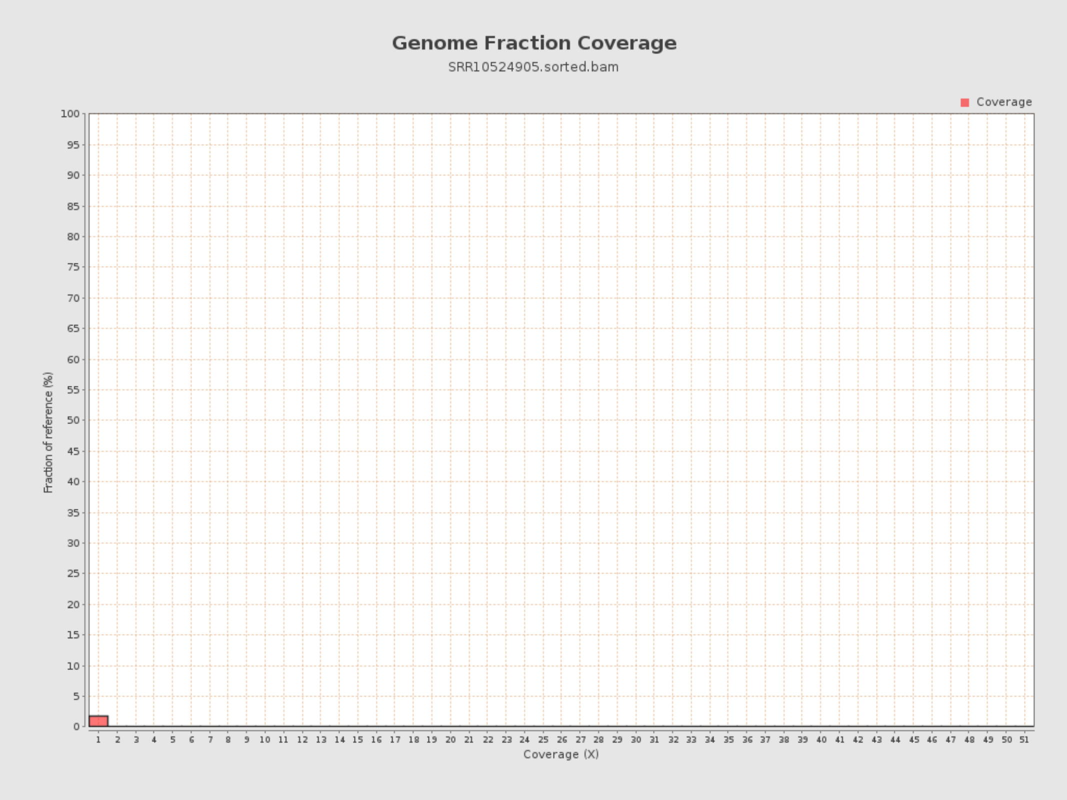
4. Results : Coverage Histogram



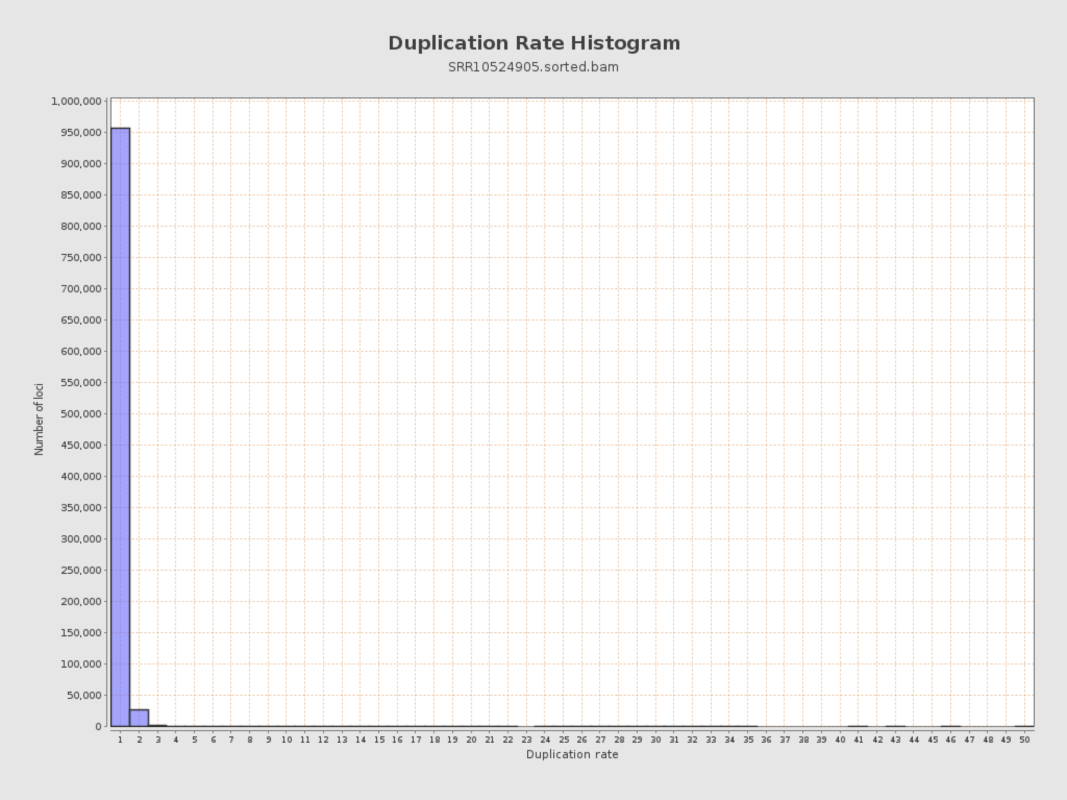
5. Results : Coverage Histogram (0-50X)



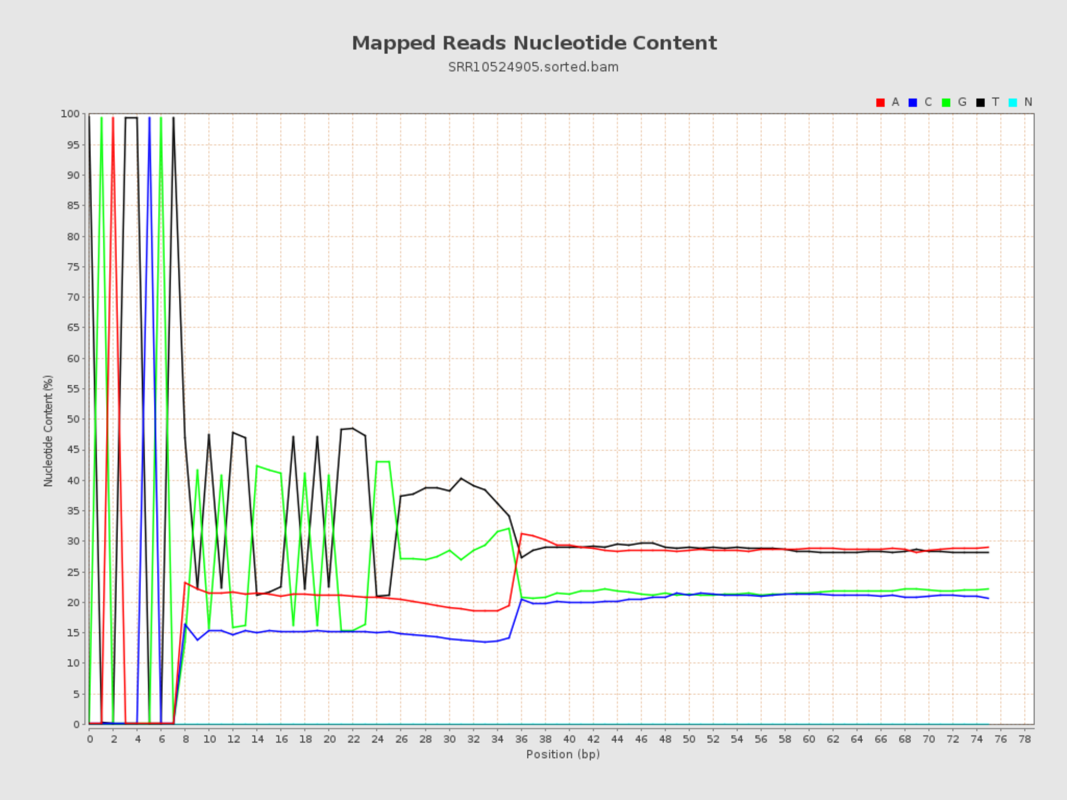
6. Results : Genome Fraction Coverage



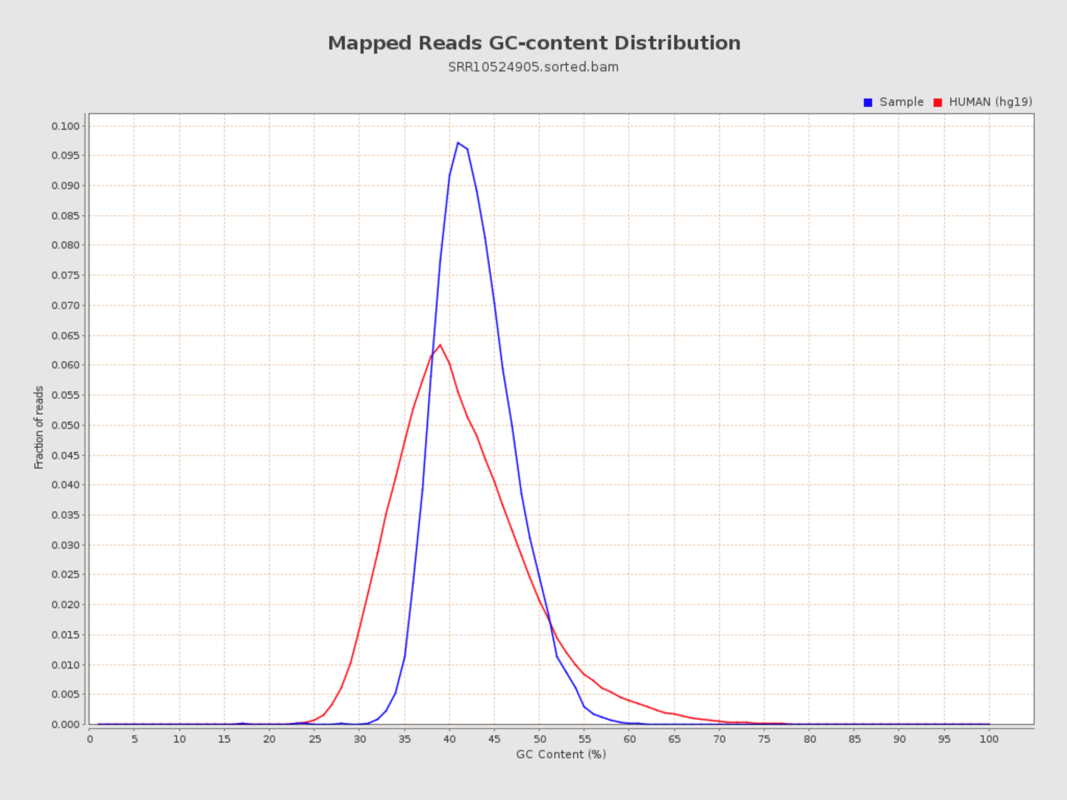
7. Results : Duplication Rate Histogram



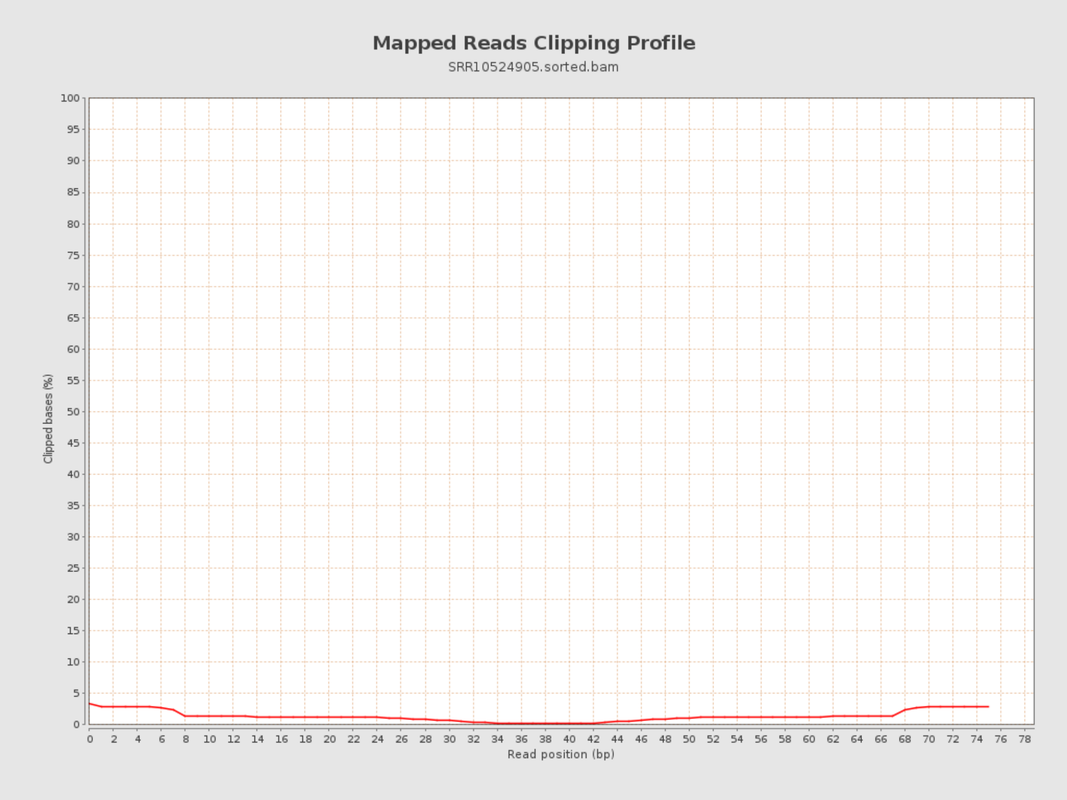
8. Results : Mapped Reads Nucleotide Content



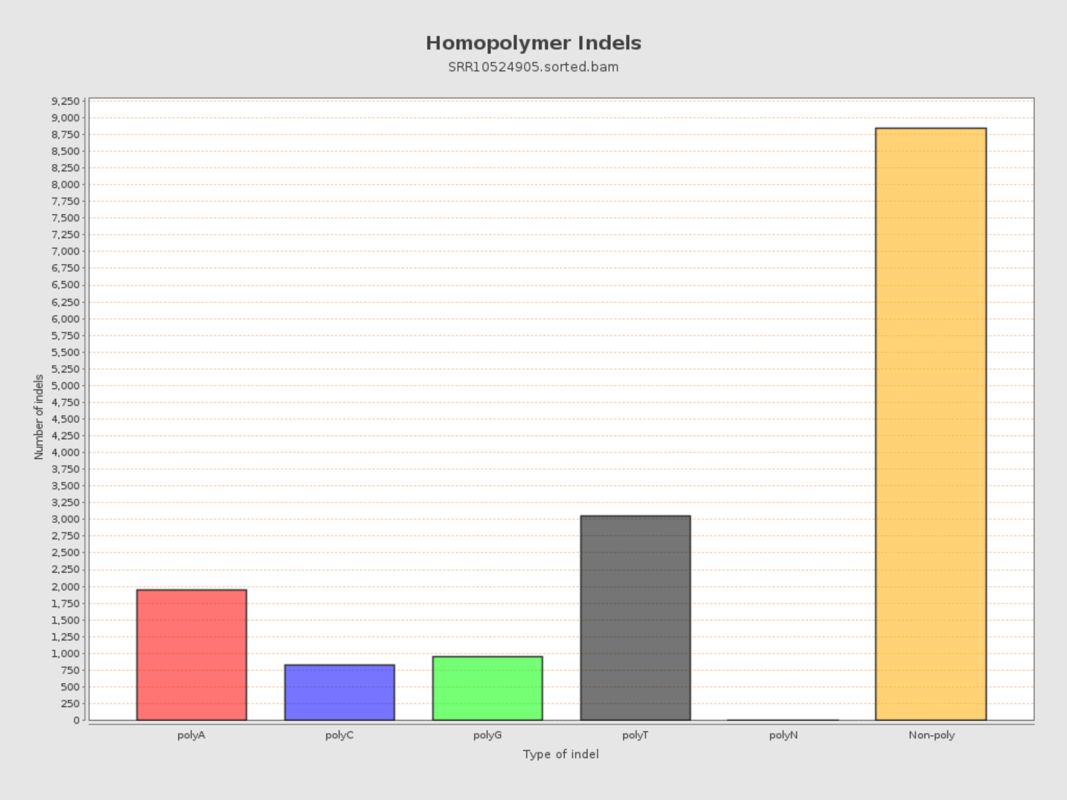
9. Results : Mapped Reads GC-content Distribution



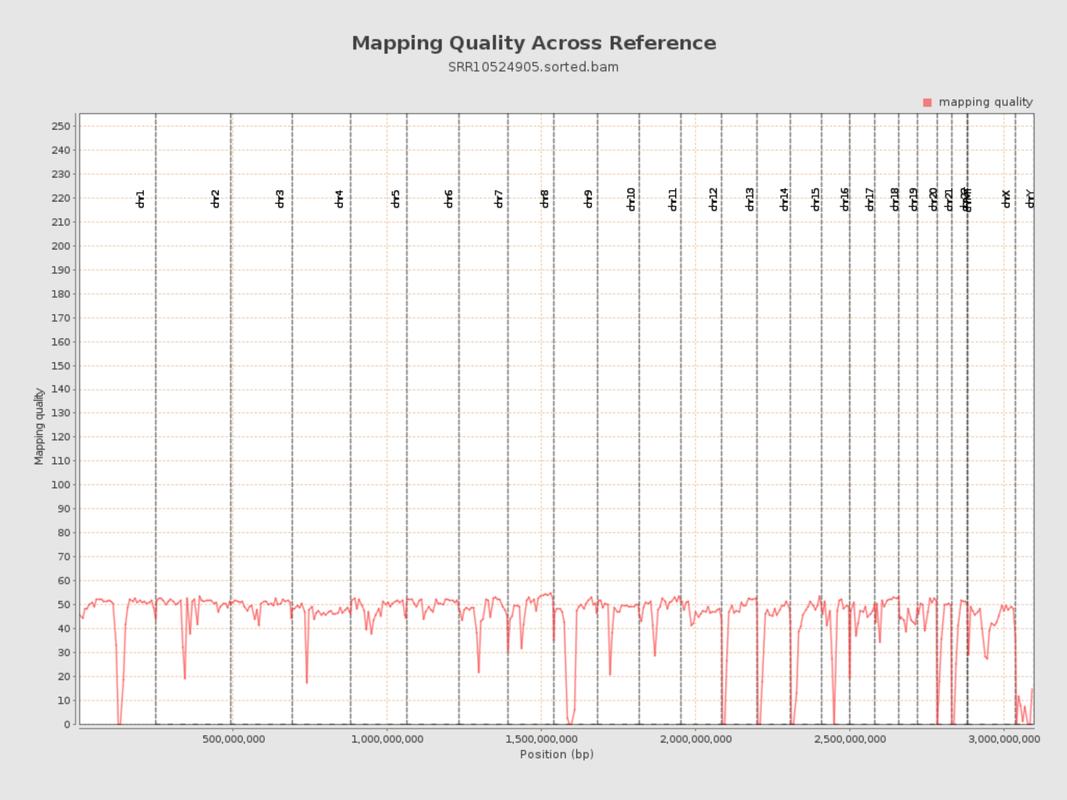
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram