Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 06:45:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524503.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_SRR10524503 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524503.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 06:45:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524503.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	565,328
Mapped reads	504,155 / 89.18%
Unmapped reads	61,173 / 10.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,711 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	33,020 / 5.84%
Duplication rate	5.4%
Clipped reads	504,592 / 89.26%

2.2. ACGT Content

Number/percentage of A's	6,723,094 / 23.73%
Number/percentage of C's	5,183,011 / 18.3%
Number/percentage of T's	9,246,248 / 32.64%
Number/percentage of G's	7,173,604 / 25.32%
Number/percentage of N's	537 / 0%
GC Percentage	43.62%

2.3. Coverage

Mean	0.0092

Standard Deviation	0.1289

2.4. Mapping Quality

Mean Mapping Quality	44.53

2.5. Mismatches and indels

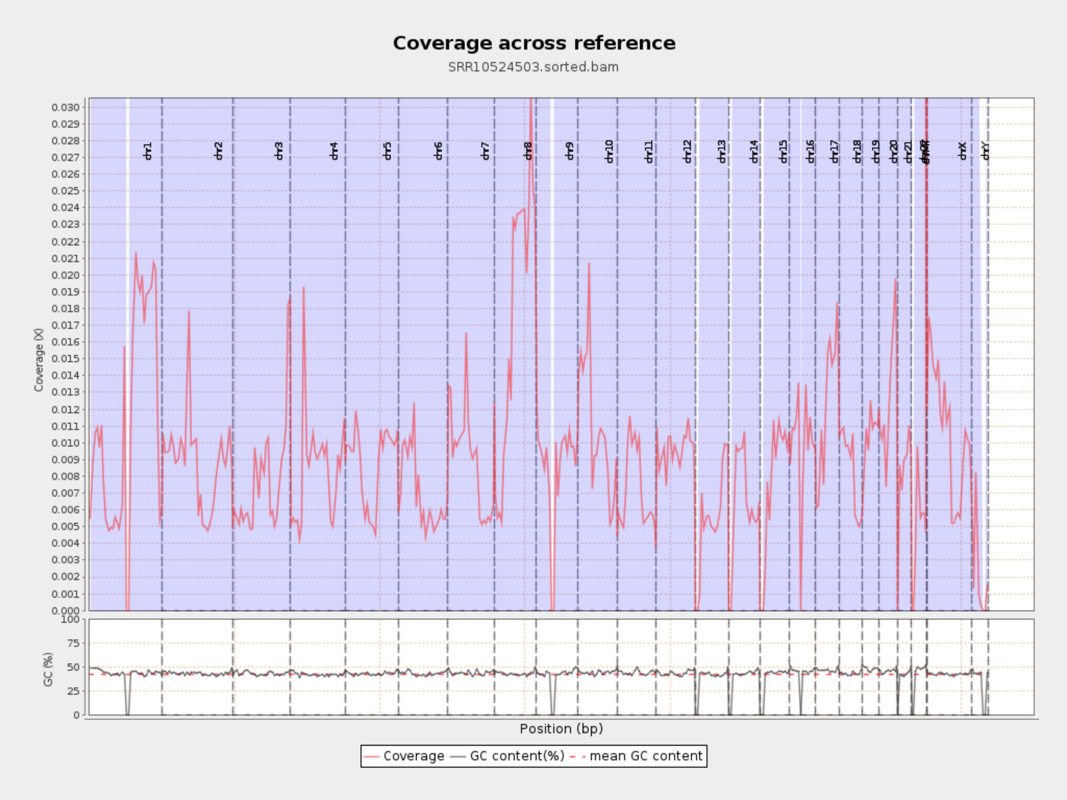
General error rate	0.58%
Mismatches	160,669
Insertions	1,784
Mapped reads with at least one insertion	0.35%
Deletions	8,105
Mapped reads with at least one deletion	1.59%
Homopolymer indels	41.72%

2.6. Chromosome stats

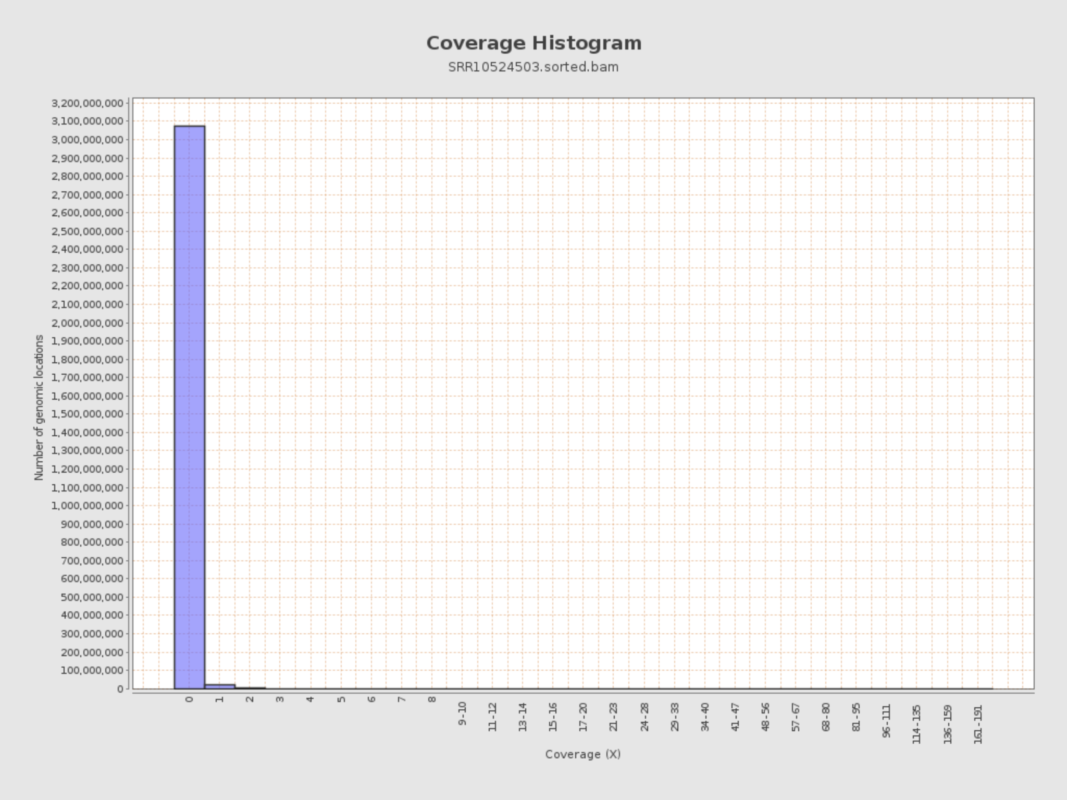
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2804971	0.0113	0.1798
chr2	243199373	2176907	0.009	0.1523
chr3	198022430	1510399	0.0076	0.101
chr4	191154276	1605257	0.0084	0.1183
chr5	180915260	1587596	0.0088	0.1079
chr6	171115067	1190347	0.007	0.1034
chr7	159138663	1433558	0.009	0.1484

chr8	146364022	2588127	0.0177	0.1641
chr9	141213431	1173848	0.0083	0.1153
chr10	135534747	1489600	0.011	0.1507
chr11	135006516	980292	0.0073	0.1143
chr12	133851895	1289067	0.0096	0.1138
chr13	115169878	629130	0.0055	0.0847
chr14	107349540	678090	0.0063	0.0921
chr15	102531392	777766	0.0076	0.1016
chr16	90354753	888462	0.0098	0.1178
chr17	81195210	1014909	0.0125	0.133
chr18	78077248	659253	0.0084	0.1488
chr19	59128983	619093	0.0105	0.1385
chr20	63025520	812221	0.0129	0.134
chr21	48129895	395054	0.0082	0.1117
chr22	51304566	241219	0.0047	0.0795
chrMT	16571	6800	0.4104	0.7589
chrX	155270560	1667940	0.0107	0.1231
chrY	59373566	120294	0.002	0.0815

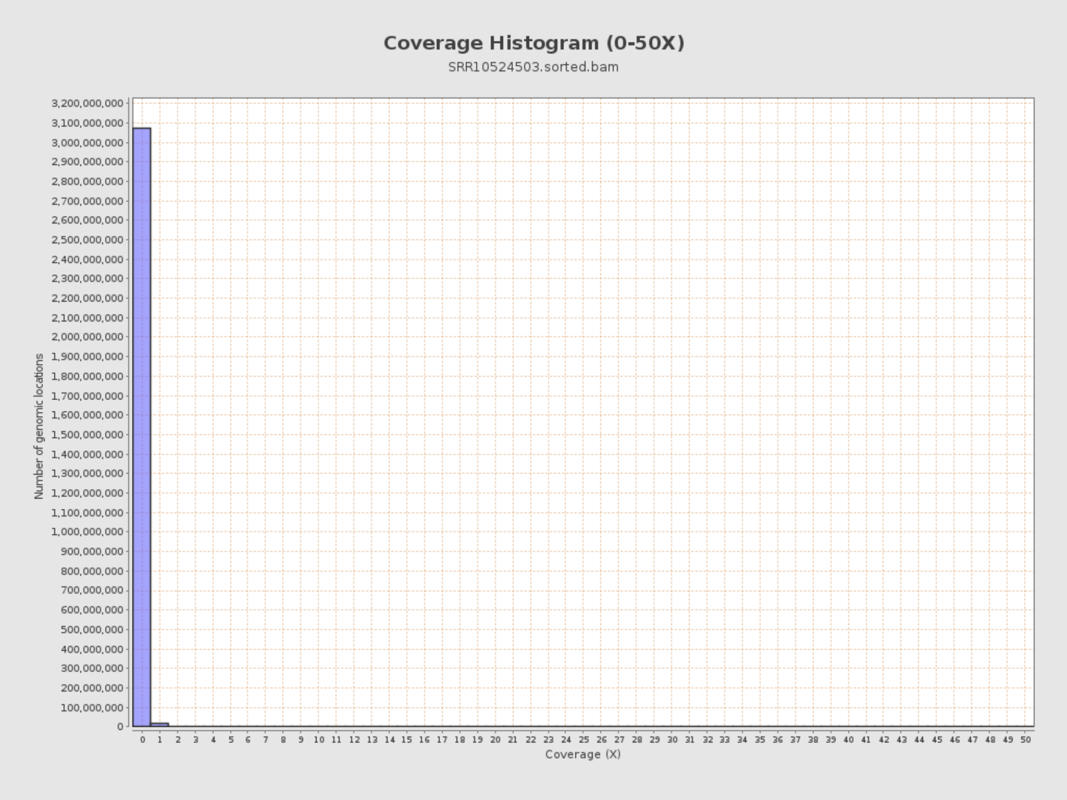
3. Results : Coverage across reference



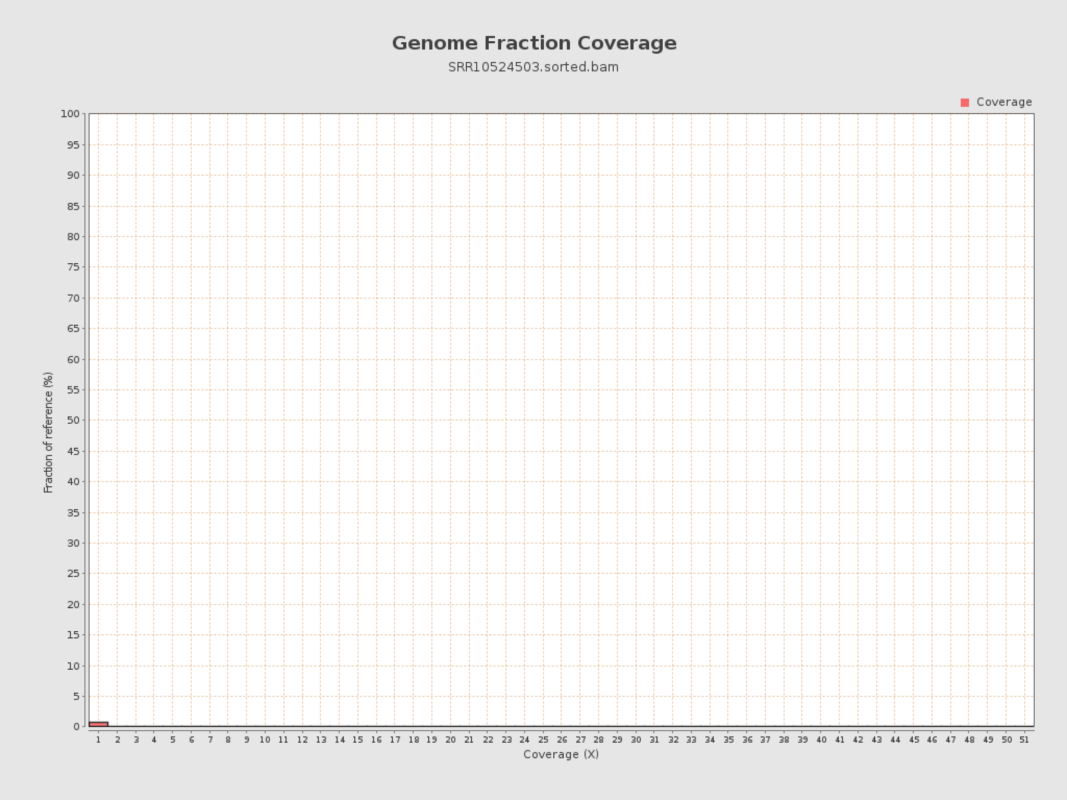
4. Results : Coverage Histogram



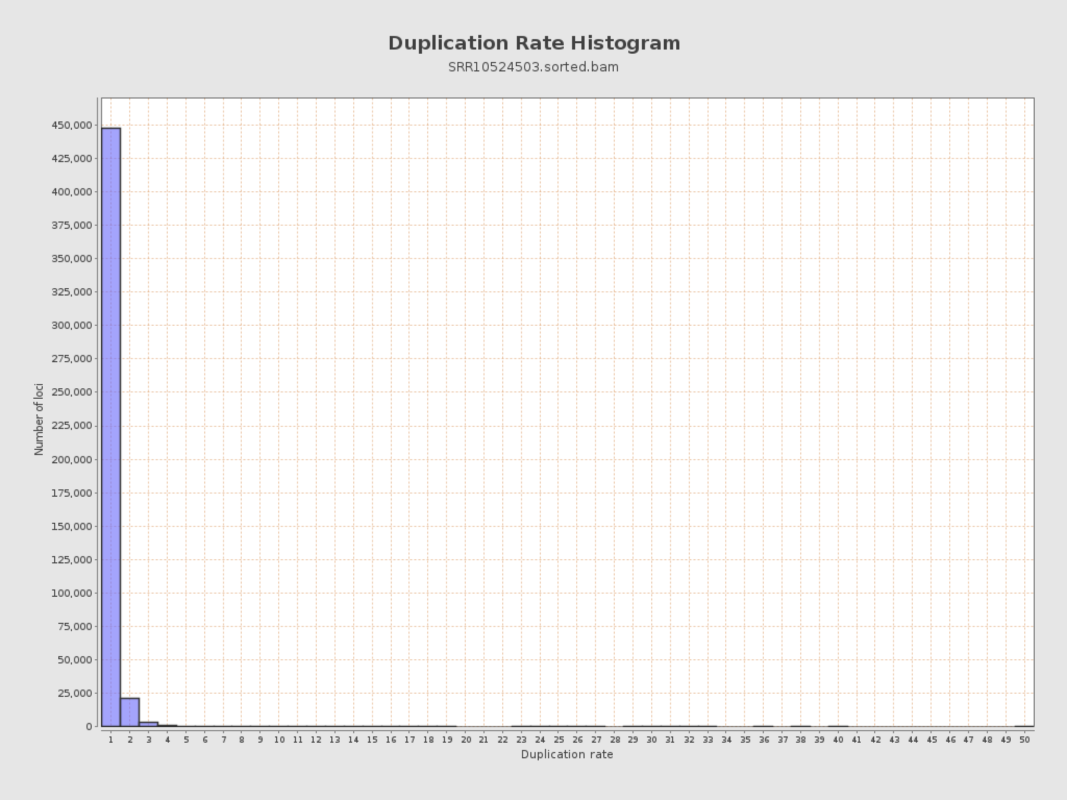
5. Results : Coverage Histogram (0-50X)



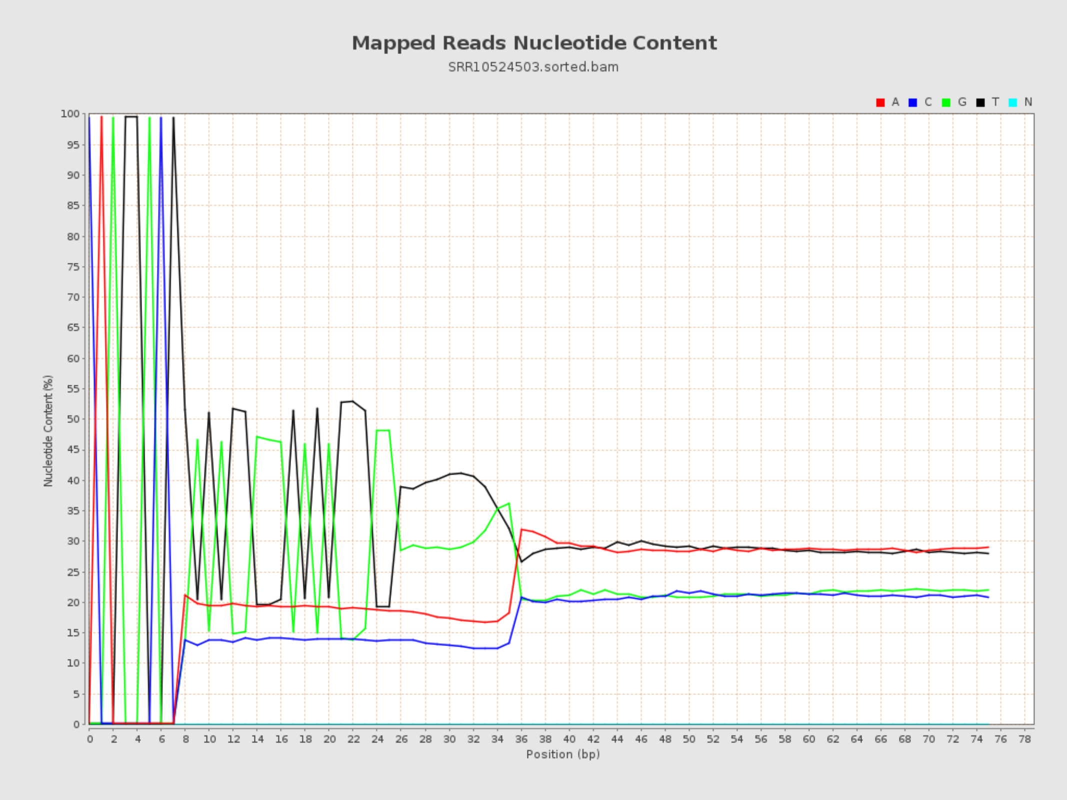
6. Results : Genome Fraction Coverage



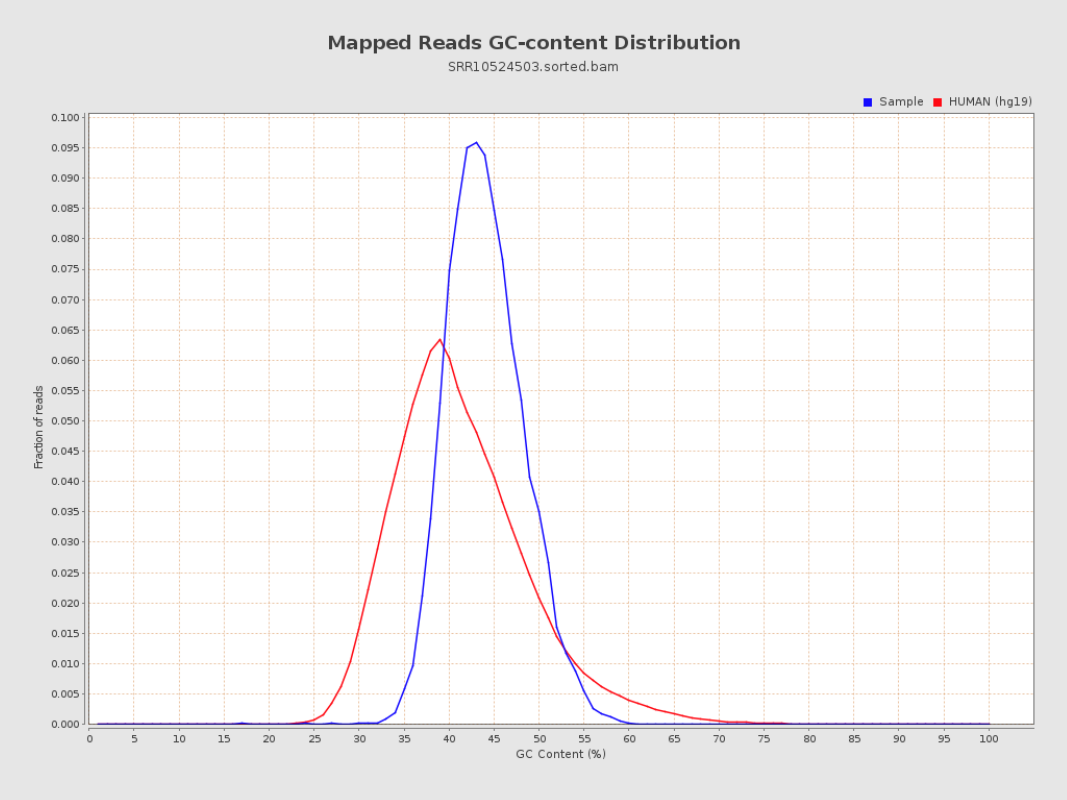
7. Results : Duplication Rate Histogram



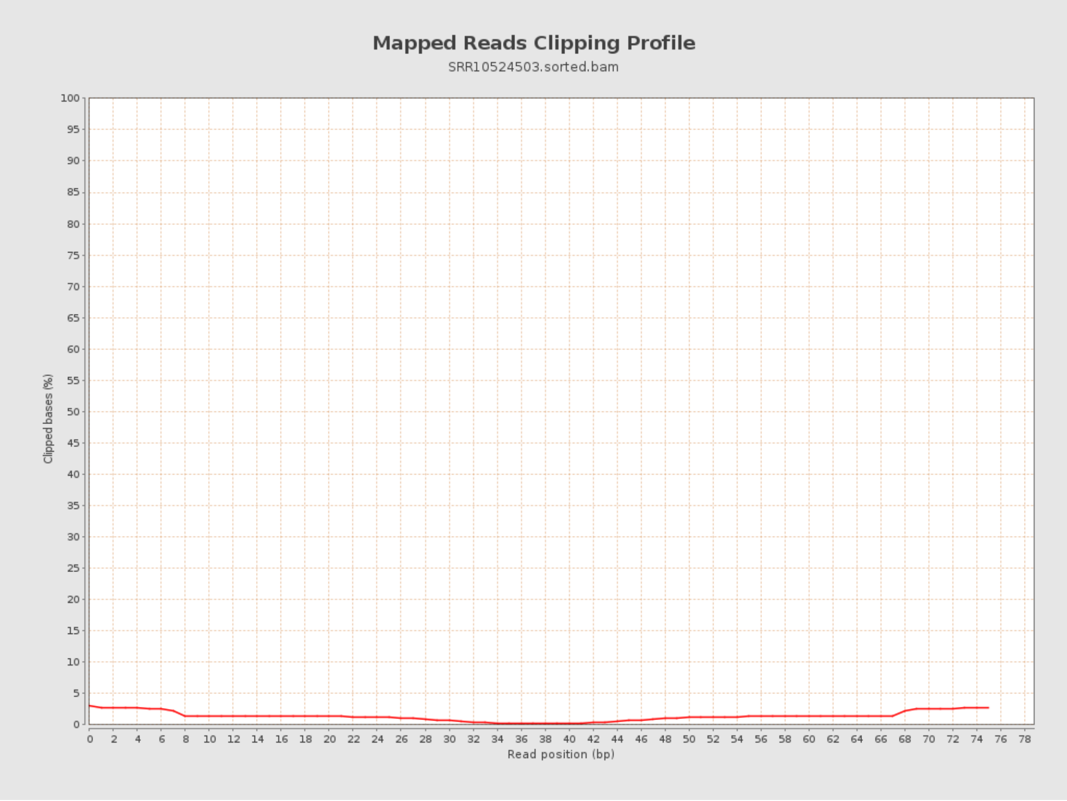
8. Results : Mapped Reads Nucleotide Content



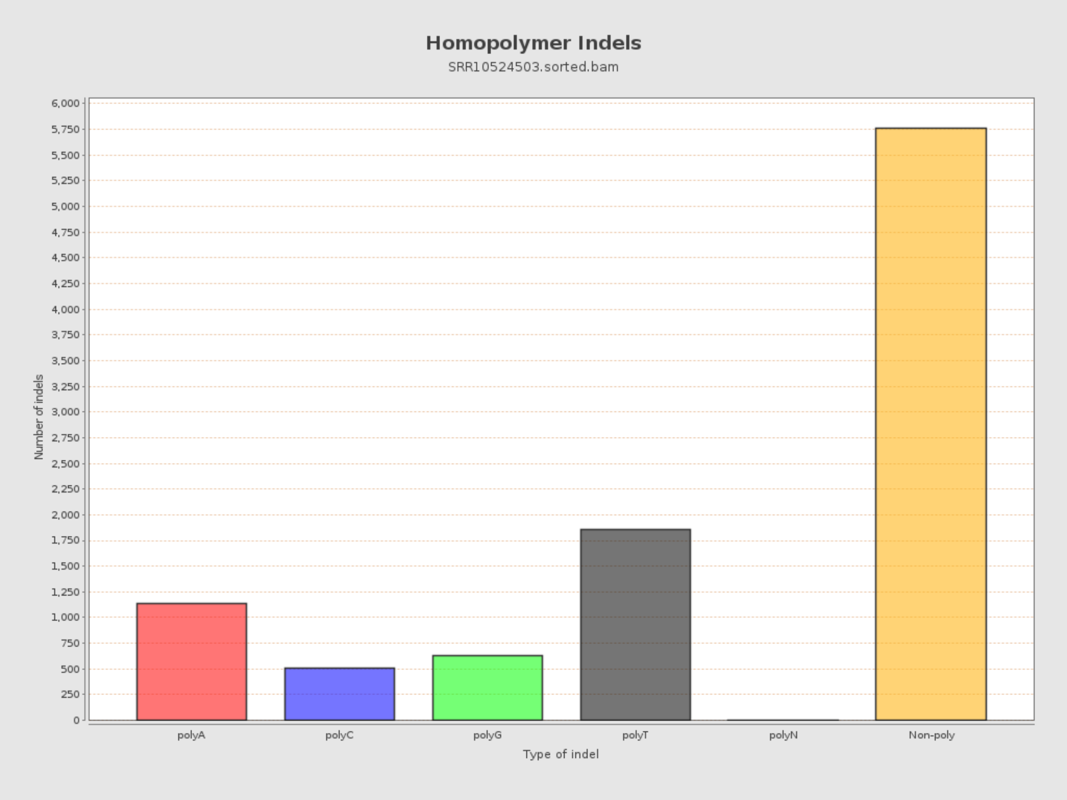
9. Results : Mapped Reads GC-content Distribution



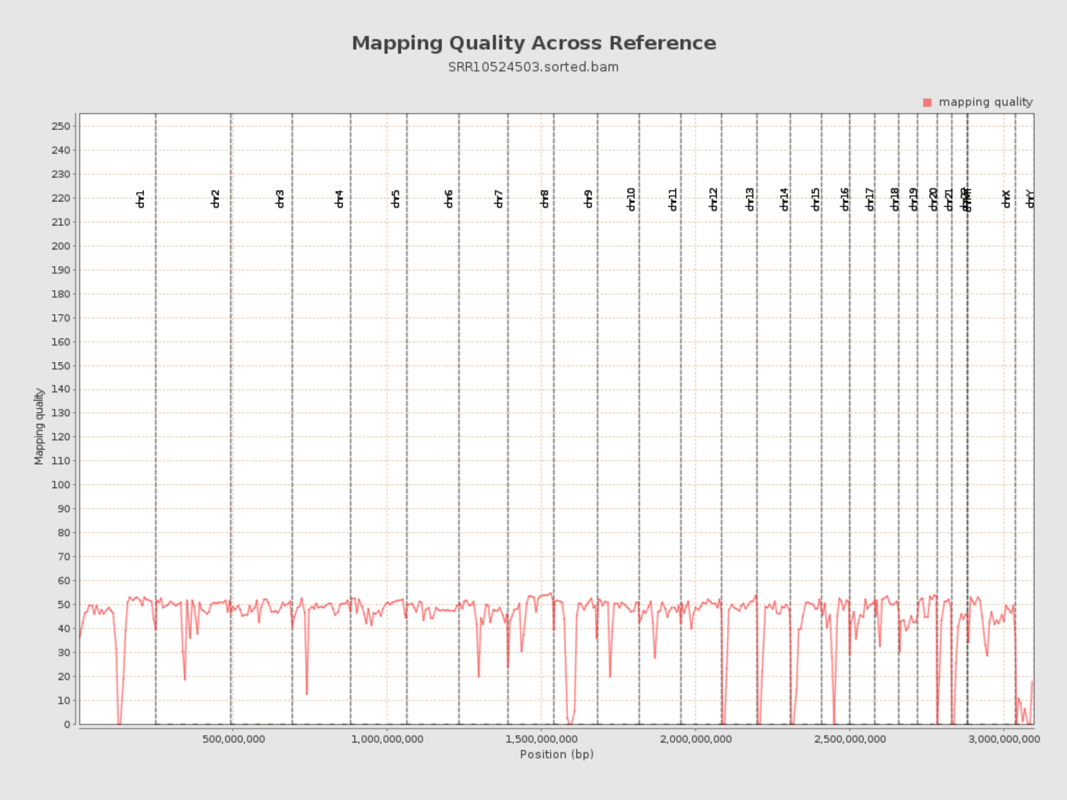
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram