Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 14:35:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524643.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_SRR10524643 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524643.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 14:35:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524643.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,318,186
Mapped reads	1,210,430 / 91.83%
Unmapped reads	107,756 / 8.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,211 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	49,991 / 3.79%
Duplication rate	3.2%
Clipped reads	1,212,494 / 91.98%

2.2. ACGT Content

Number/percentage of A's	16,778,076 / 23.78%
Number/percentage of C's	12,638,704 / 17.91%
Number/percentage of T's	23,301,915 / 33.02%
Number/percentage of G's	17,842,091 / 25.29%
Number/percentage of N's	561 / 0%
GC Percentage	43.2%

2.3. Coverage

Mean	0.0228

Standard Deviation	0.2225

2.4. Mapping Quality

Mean Mapping Quality	44.92

2.5. Mismatches and indels

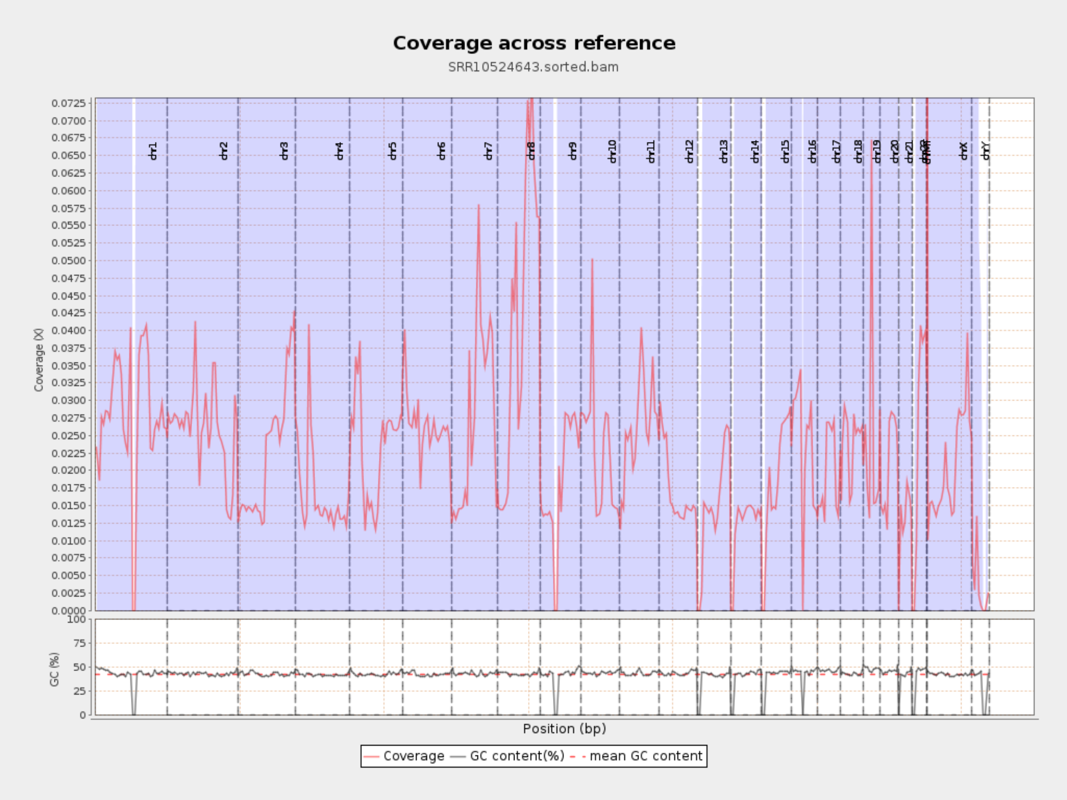
General error rate	0.51%
Mismatches	350,340
Insertions	4,694
Mapped reads with at least one insertion	0.39%
Deletions	13,753
Mapped reads with at least one deletion	1.13%
Homopolymer indels	42.62%

2.6. Chromosome stats

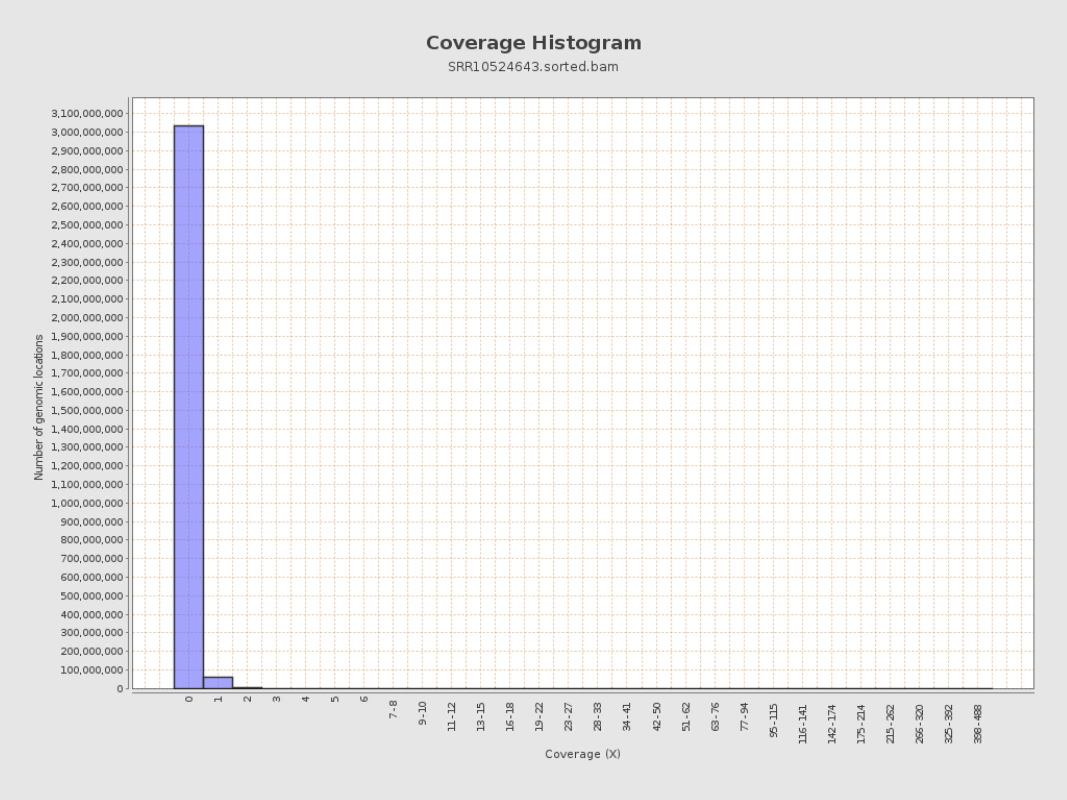
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6925295	0.0278	0.393
chr2	243199373	6334589	0.026	0.2662
chr3	198022430	4453792	0.0225	0.1656
chr4	191154276	3219551	0.0168	0.169
chr5	180915260	4271798	0.0236	0.1677
chr6	171115067	4536277	0.0265	0.1872
chr7	159138663	4438233	0.0279	0.2607

chr8	146364022	6237891	0.0426	0.2814
chr9	141213431	2562011	0.0181	0.1796
chr10	135534747	3155679	0.0233	0.2512
chr11	135006516	3571697	0.0265	0.2043
chr12	133851895	2314297	0.0173	0.1468
chr13	115169878	1715067	0.0149	0.134
chr14	107349540	1304054	0.0121	0.1244
chr15	102531392	1841109	0.018	0.1469
chr16	90354753	2118981	0.0235	0.1761
chr17	81195210	1589093	0.0196	0.1576
chr18	78077248	1866514	0.0239	0.2829
chr19	59128983	1454127	0.0246	0.2863
chr20	63025520	1316949	0.0209	0.161
chr21	48129895	634478	0.0132	0.1466
chr22	51304566	1303915	0.0254	0.1747
chrMT	16571	6423	0.3876	0.7162
chrX	155270560	3209737	0.0207	0.1681
chrY	59373566	203244	0.0034	0.1236

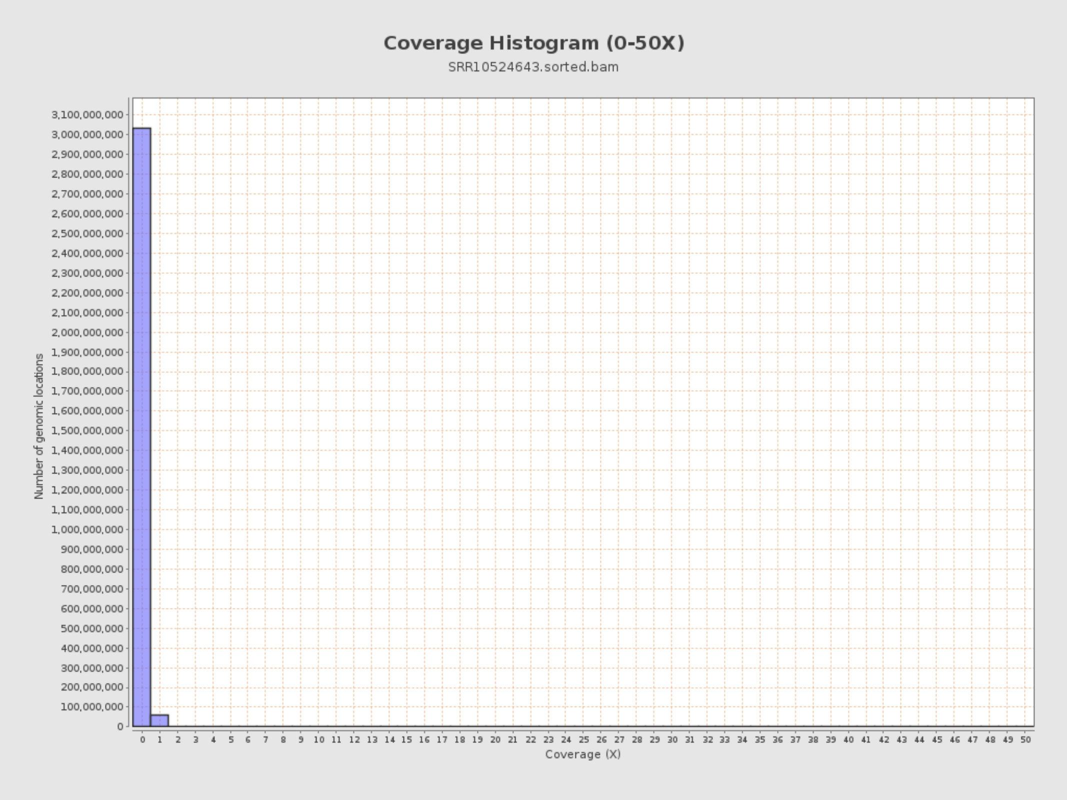
3. Results : Coverage across reference



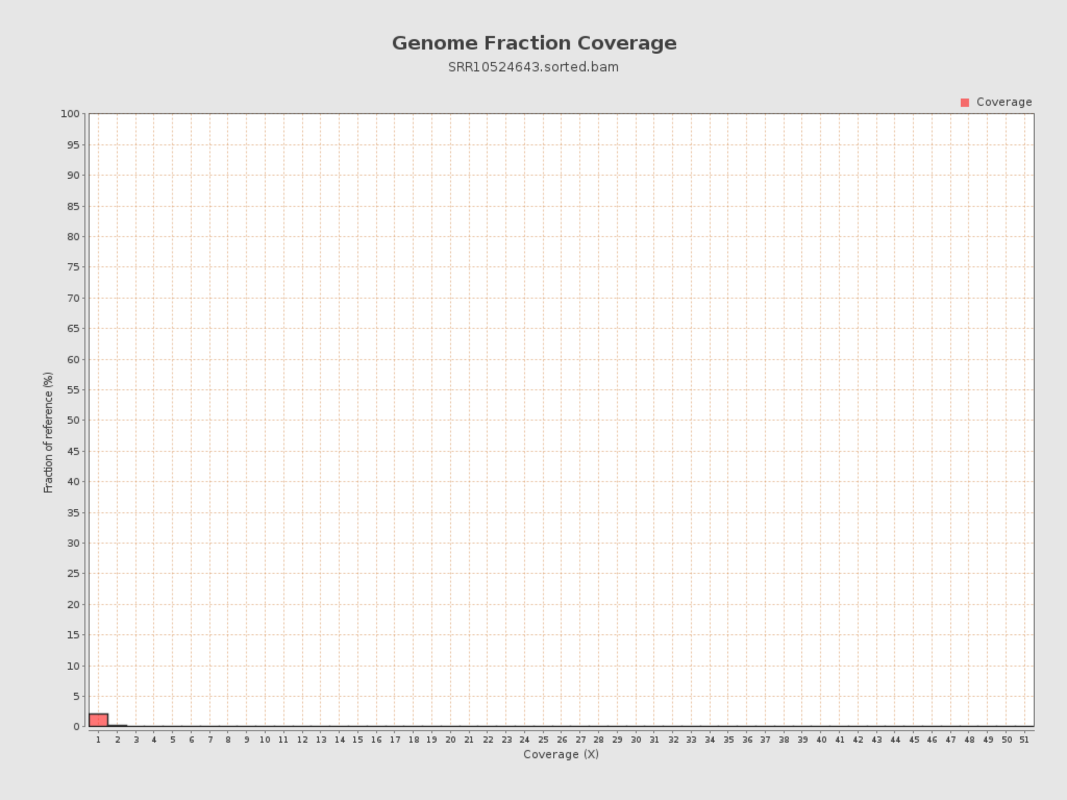
4. Results : Coverage Histogram



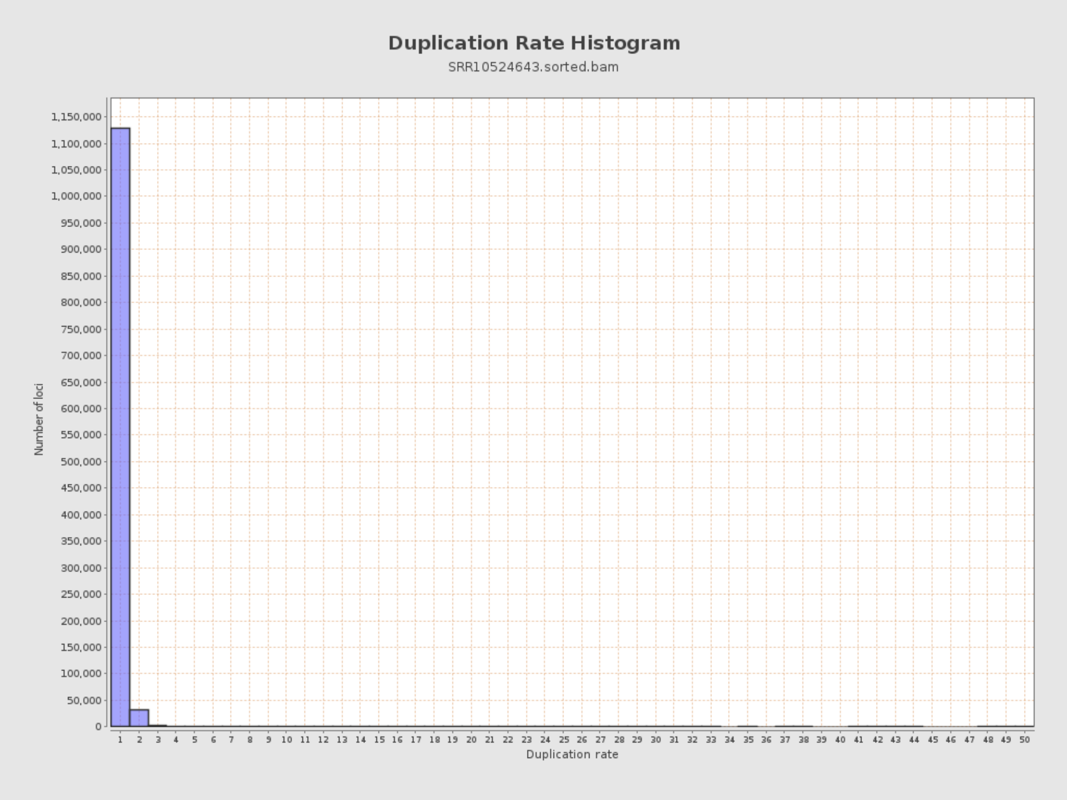
5. Results : Coverage Histogram (0-50X)



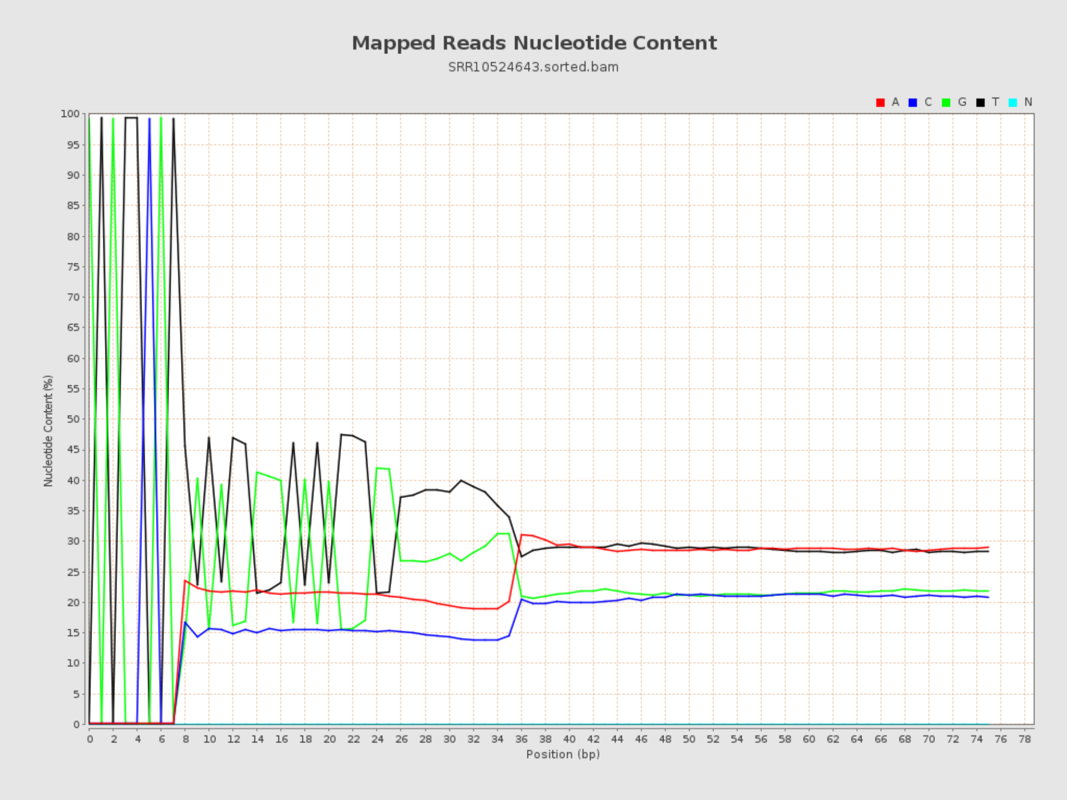
6. Results : Genome Fraction Coverage



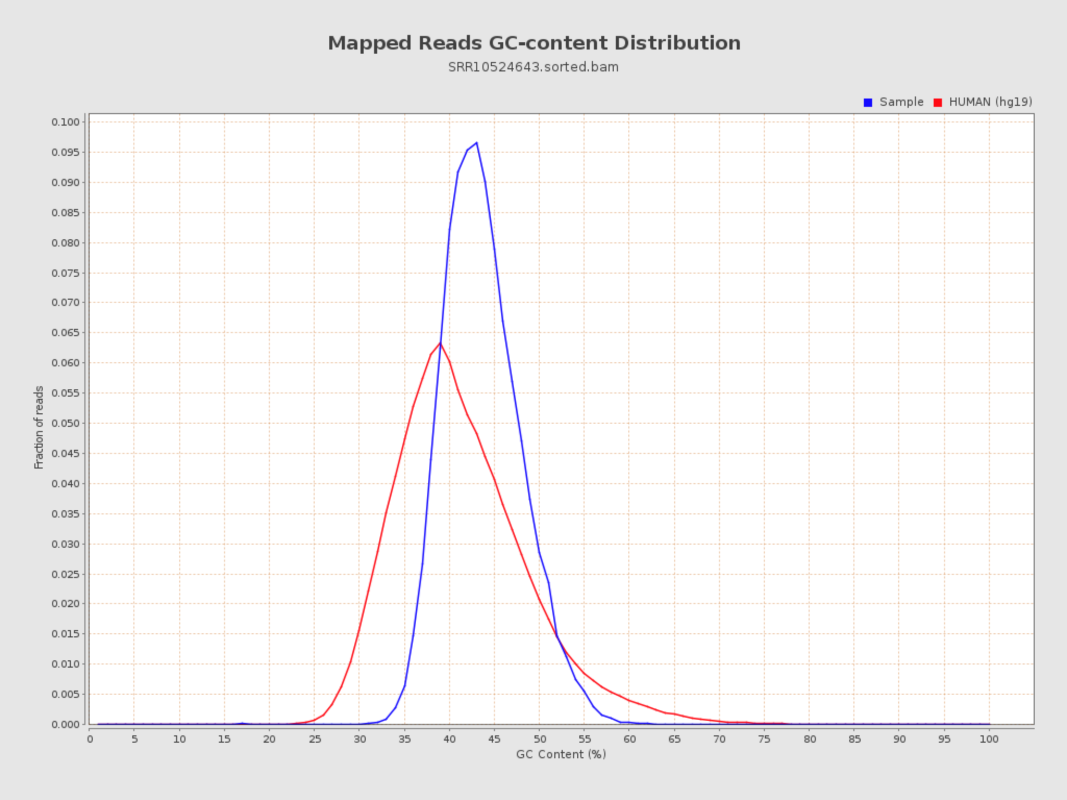
7. Results : Duplication Rate Histogram



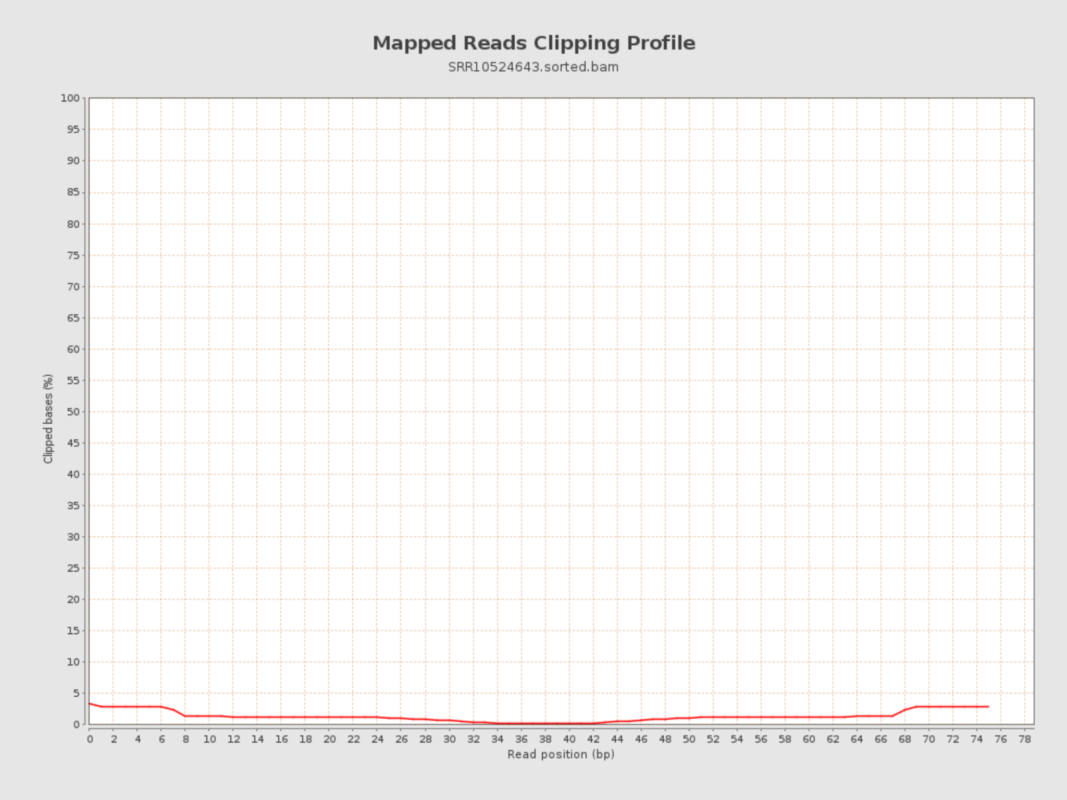
8. Results : Mapped Reads Nucleotide Content



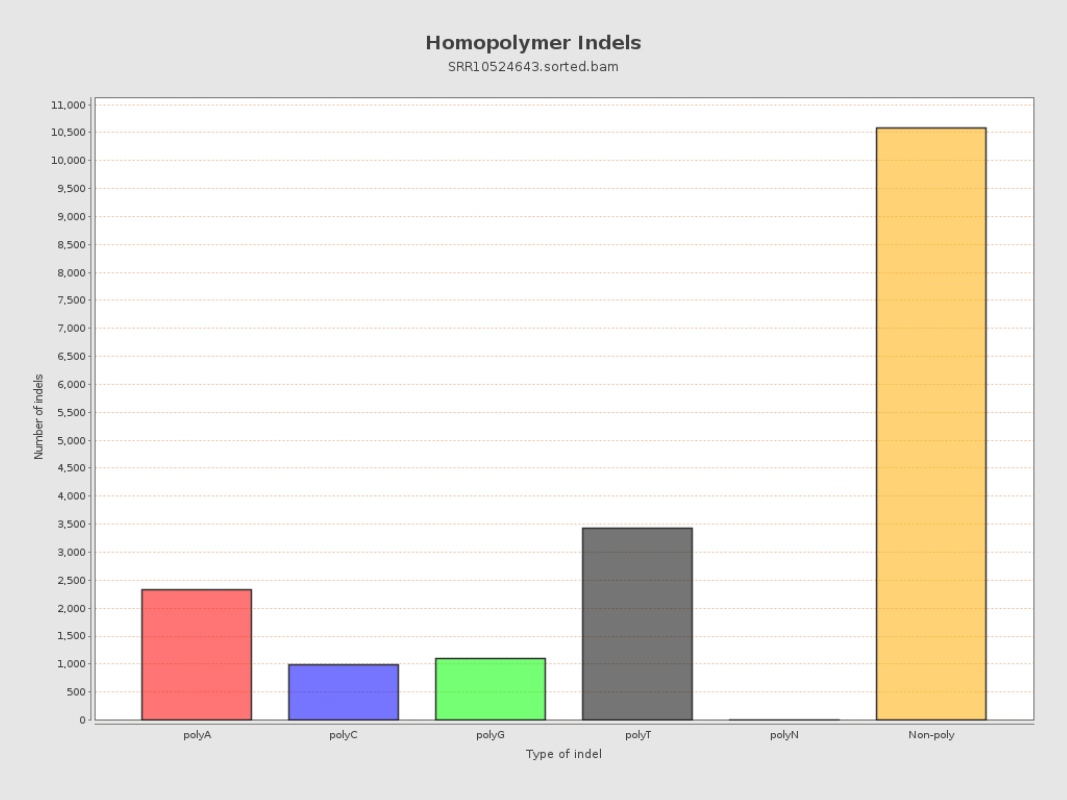
9. Results : Mapped Reads GC-content Distribution



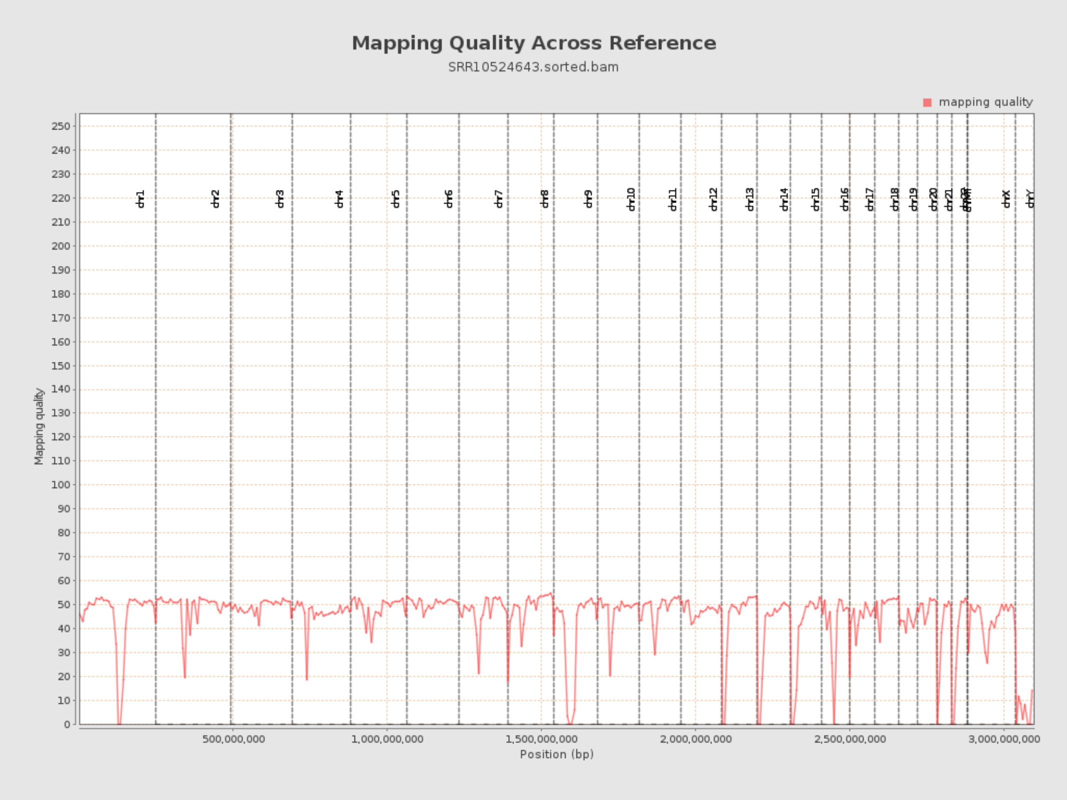
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram