Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 22:02:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524309.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_SRR10524309 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524309.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 22:02:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524309.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	687,278
Mapped reads	632,027 / 91.96%
Unmapped reads	55,251 / 8.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,781 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	11,402 / 1.66%
Duplication rate	1.32%
Clipped reads	633,541 / 92.18%

2.2. ACGT Content

Number/percentage of A's	8,699,983 / 23.52%
Number/percentage of C's	7,125,218 / 19.26%
Number/percentage of T's	11,664,959 / 31.53%
Number/percentage of G's	9,500,527 / 25.68%
Number/percentage of N's	5,325 / 0.01%
GC Percentage	44.94%

2.3. Coverage

Mean	0.012

Standard Deviation	0.1375

2.4. Mapping Quality

Mean Mapping Quality	44.33

2.5. Mismatches and indels

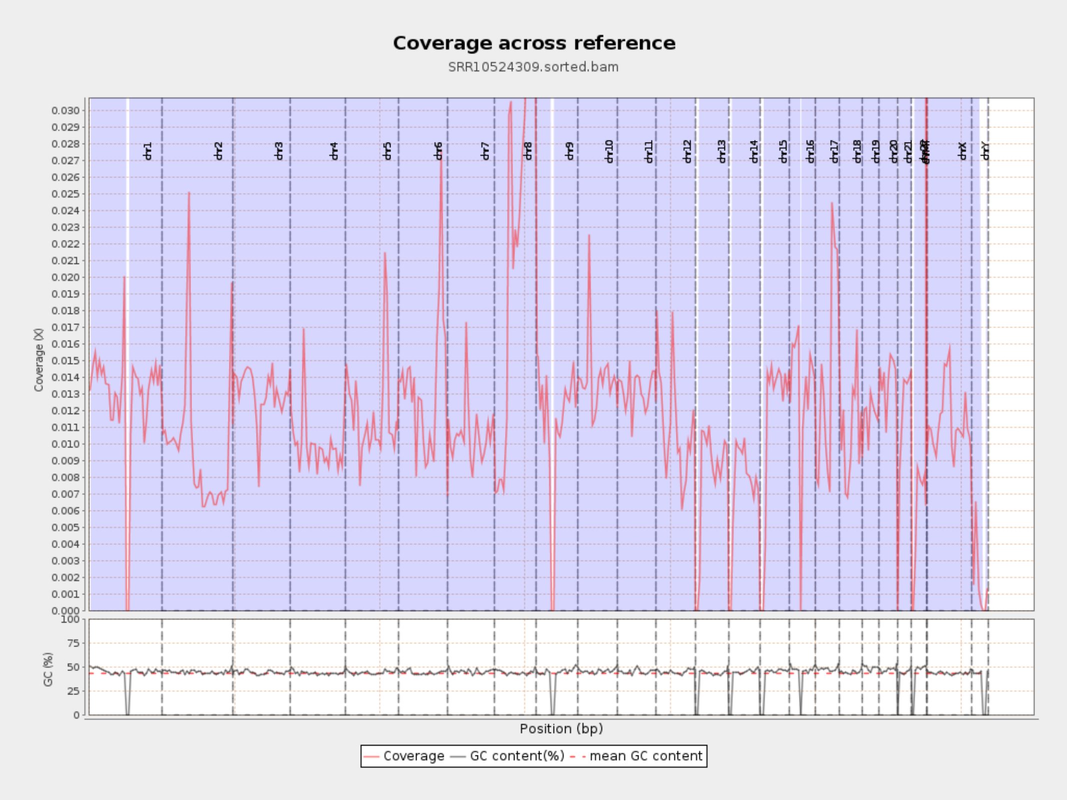
General error rate	0.52%
Mismatches	186,894
Insertions	2,381
Mapped reads with at least one insertion	0.38%
Deletions	5,855
Mapped reads with at least one deletion	0.92%
Homopolymer indels	42.31%

2.6. Chromosome stats

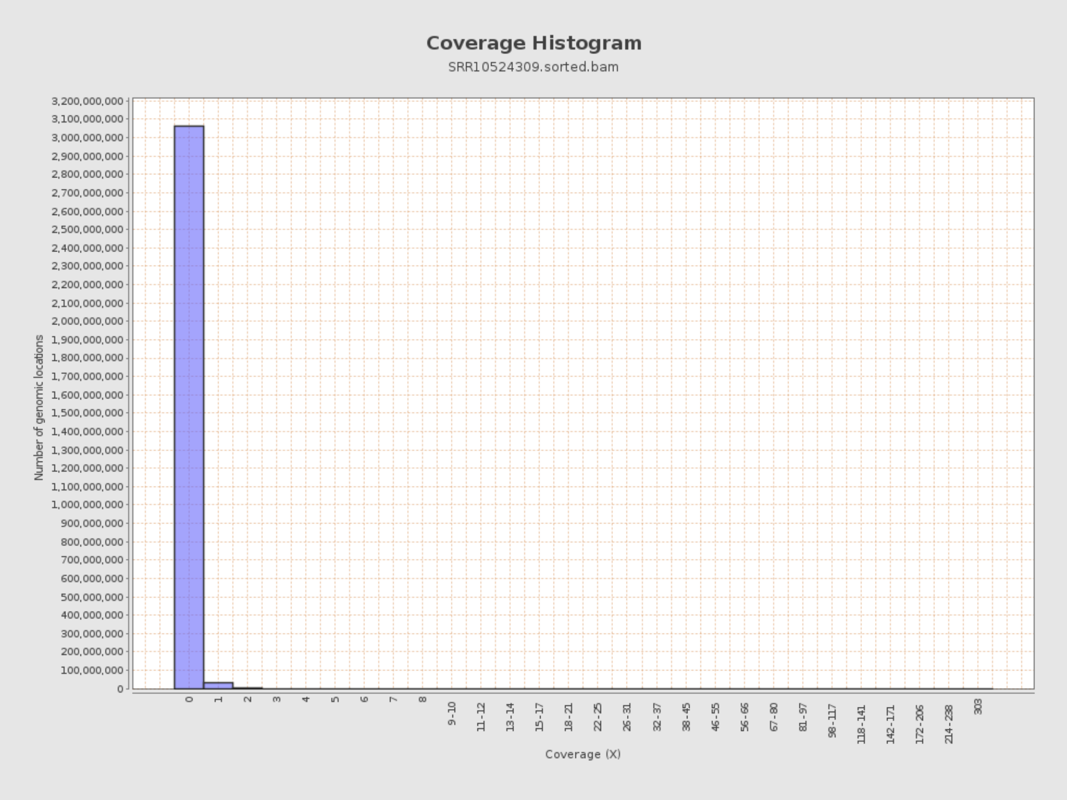
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3179642	0.0128	0.2122
chr2	243199373	2379604	0.0098	0.1627
chr3	198022430	2581177	0.013	0.1185
chr4	191154276	1898266	0.0099	0.1103
chr5	180915260	2159089	0.0119	0.1131
chr6	171115067	2296324	0.0134	0.1245
chr7	159138663	1685226	0.0106	0.1534

chr8	146364022	3803994	0.026	0.1849
chr9	141213431	1557787	0.011	0.1182
chr10	135534747	1891126	0.014	0.1408
chr11	135006516	1786466	0.0132	0.129
chr12	133851895	1479255	0.0111	0.1091
chr13	115169878	913484	0.0079	0.0917
chr14	107349540	785438	0.0073	0.0904
chr15	102531392	1141648	0.0111	0.1093
chr16	90354753	1199013	0.0133	0.1214
chr17	81195210	1137368	0.014	0.1263
chr18	78077248	860436	0.011	0.1691
chr19	59128983	692976	0.0117	0.1519
chr20	63025520	871153	0.0138	0.1242
chr21	48129895	542168	0.0113	0.1144
chr22	51304566	286175	0.0056	0.0771
chrMT	16571	16181	0.9765	1.0939
chrX	155270560	1754831	0.0113	0.1146
chrY	59373566	106743	0.0018	0.0602

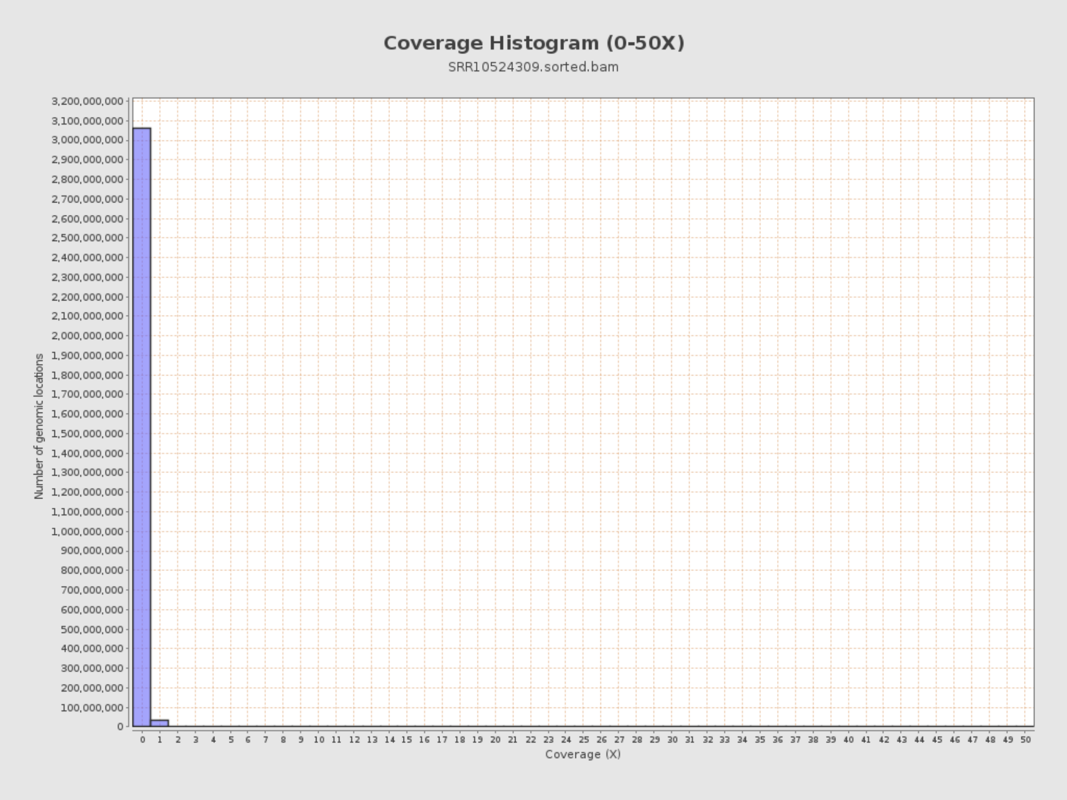
3. Results : Coverage across reference



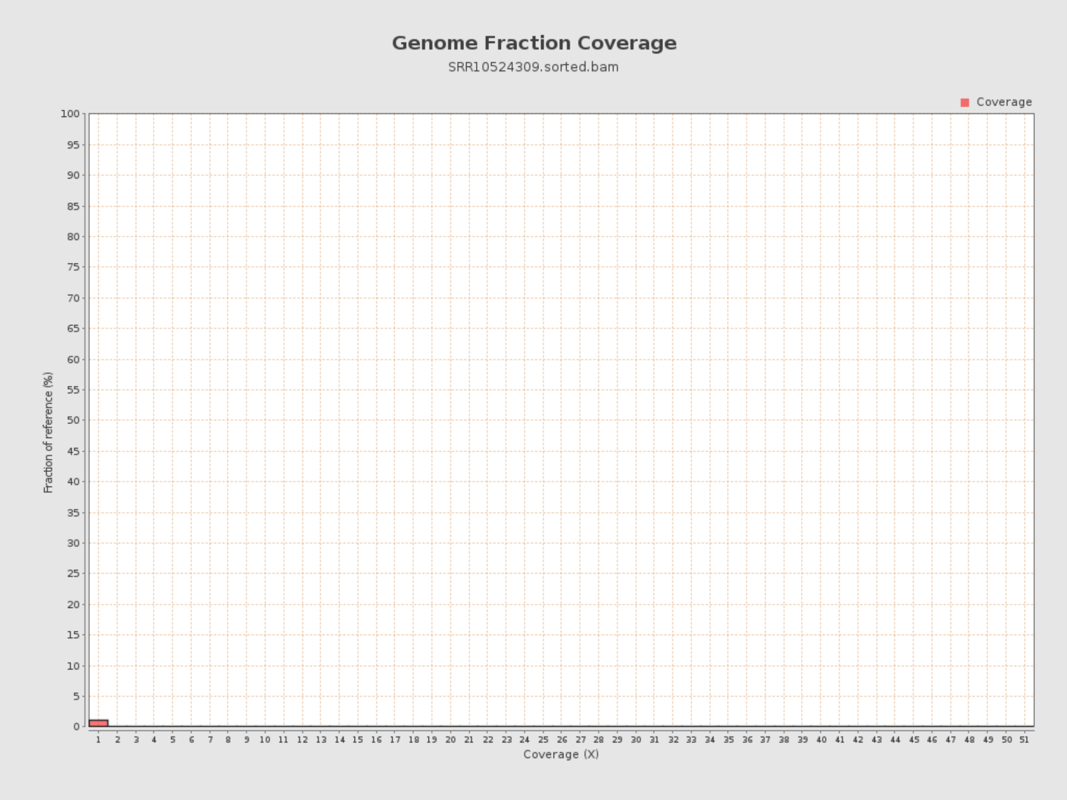
4. Results : Coverage Histogram



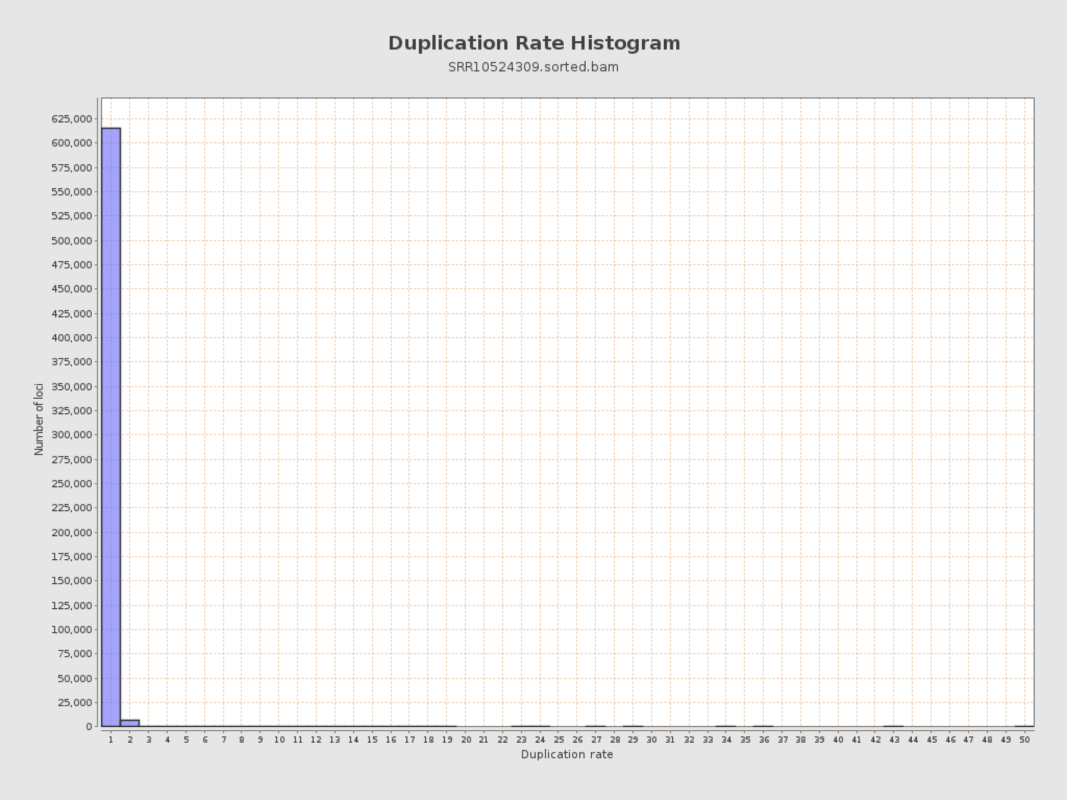
5. Results : Coverage Histogram (0-50X)



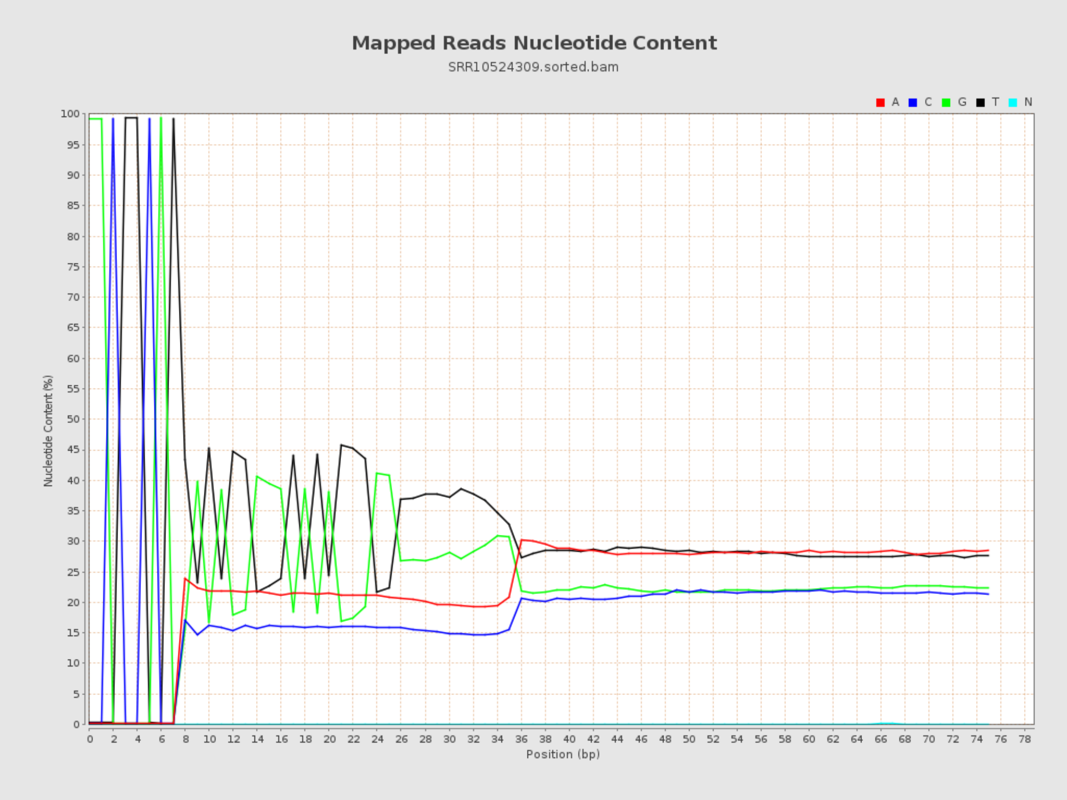
6. Results : Genome Fraction Coverage



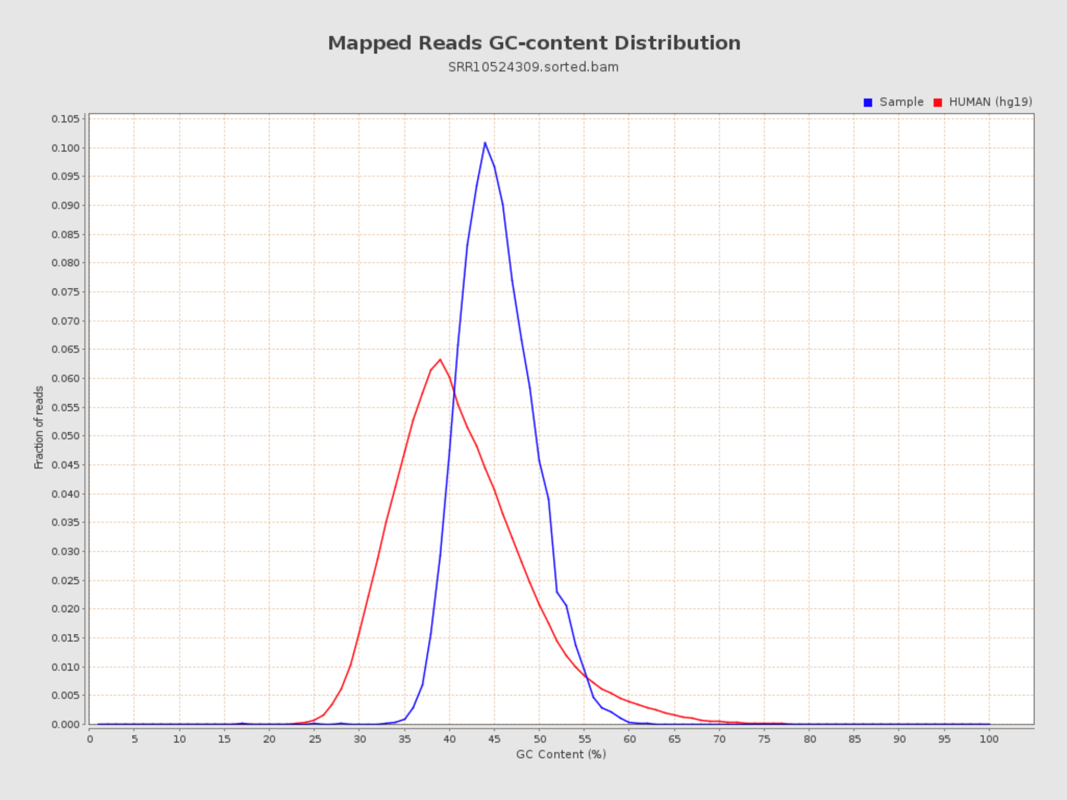
7. Results : Duplication Rate Histogram



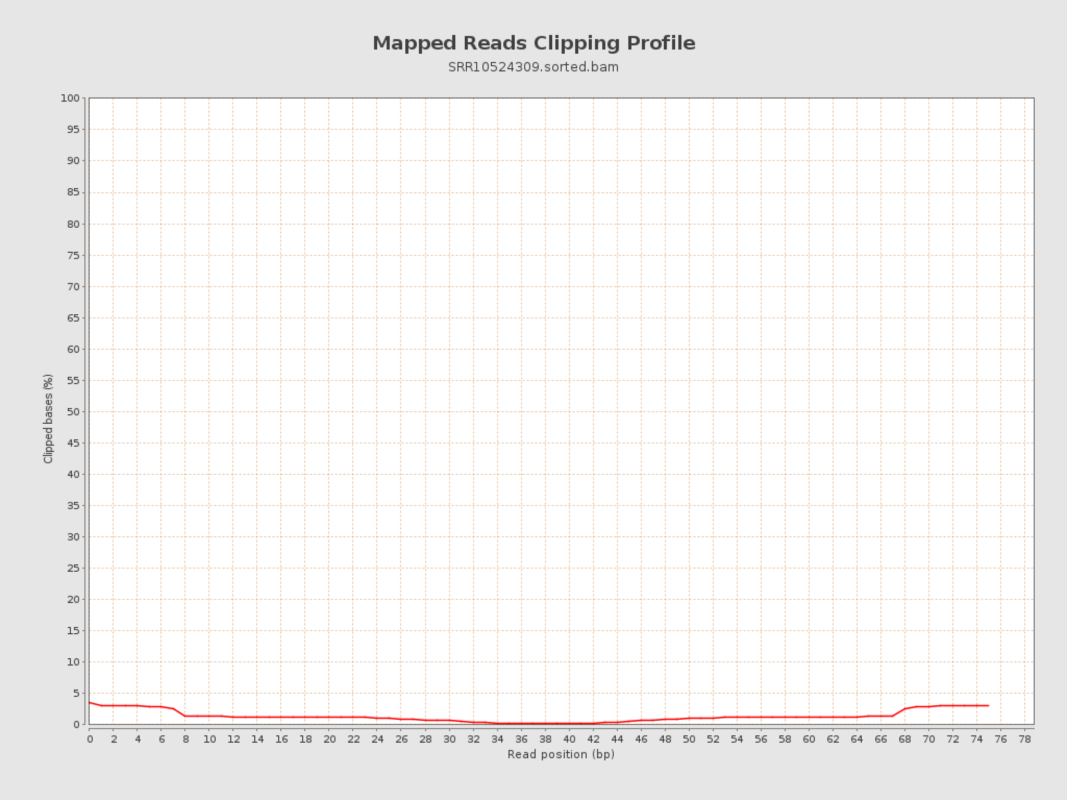
8. Results : Mapped Reads Nucleotide Content



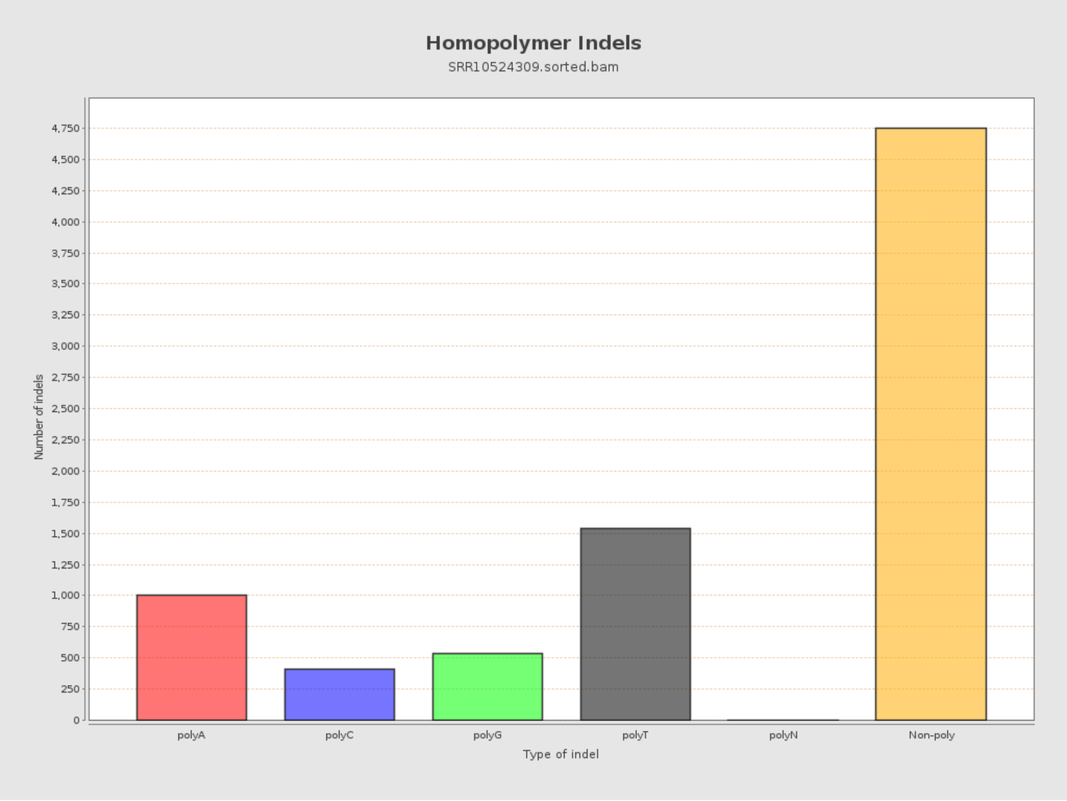
9. Results : Mapped Reads GC-content Distribution



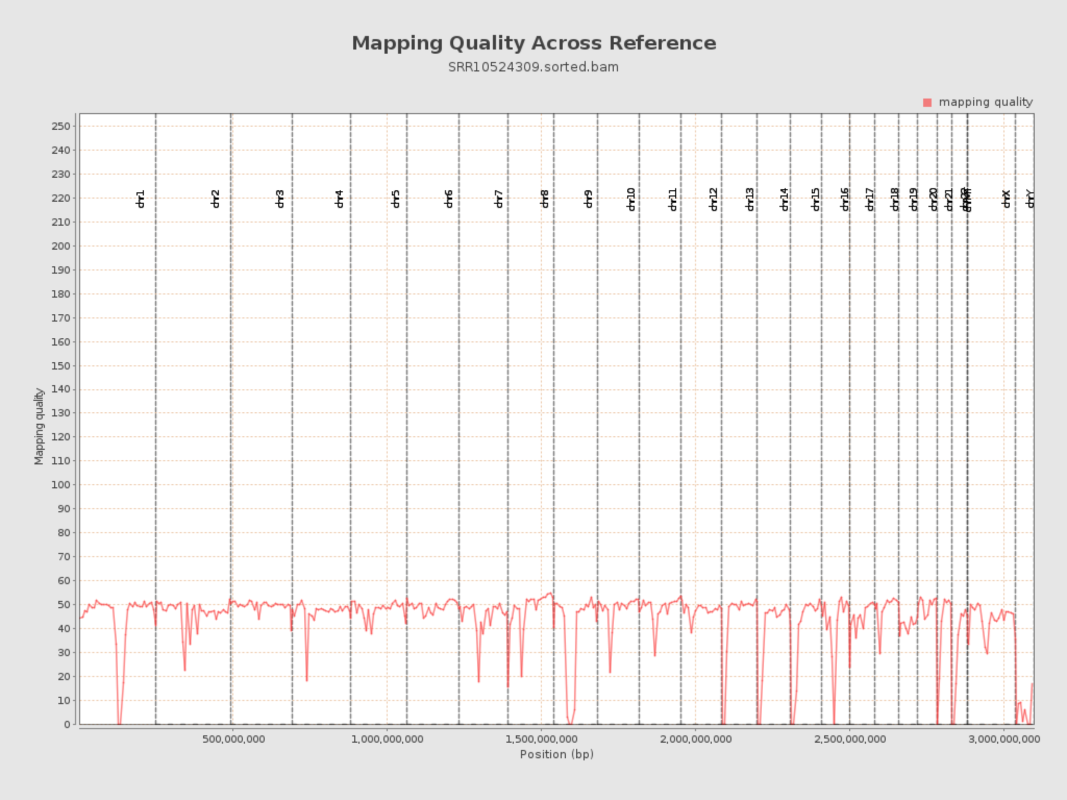
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram