Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 18:19:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524734.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_SRR10524734 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524734.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 18:19:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524734.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,161,660
Mapped reads	1,061,703 / 91.4%
Unmapped reads	99,957 / 8.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,984 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	38,730 / 3.33%
Duplication rate	2.84%
Clipped reads	1,063,133 / 91.52%

2.2. ACGT Content

Number/percentage of A's	14,069,761 / 23.19%
Number/percentage of C's	10,677,876 / 17.6%
Number/percentage of T's	20,246,148 / 33.37%
Number/percentage of G's	15,666,222 / 25.82%
Number/percentage of N's	7,051 / 0.01%
GC Percentage	43.42%

2.3. Coverage

Mean	0.0196

Standard Deviation	0.1931

2.4. Mapping Quality

Mean Mapping Quality	44.58

2.5. Mismatches and indels

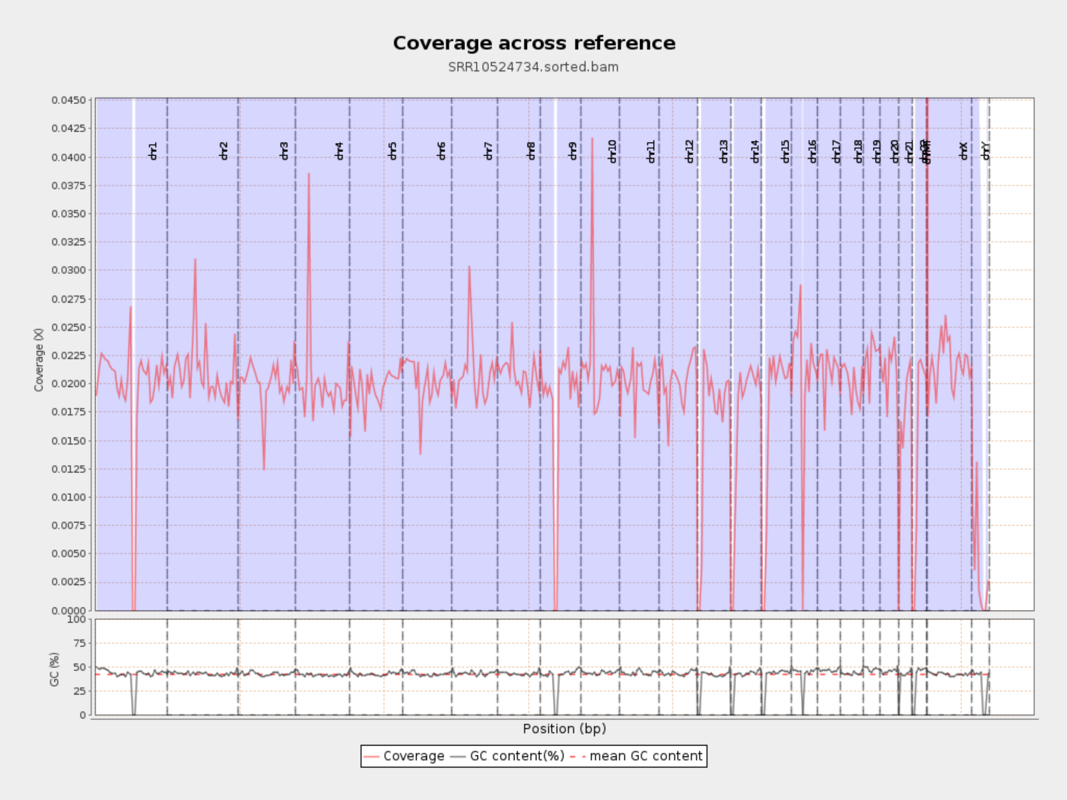
General error rate	0.52%
Mismatches	305,870
Insertions	4,248
Mapped reads with at least one insertion	0.4%
Deletions	11,688
Mapped reads with at least one deletion	1.09%
Homopolymer indels	43.15%

2.6. Chromosome stats

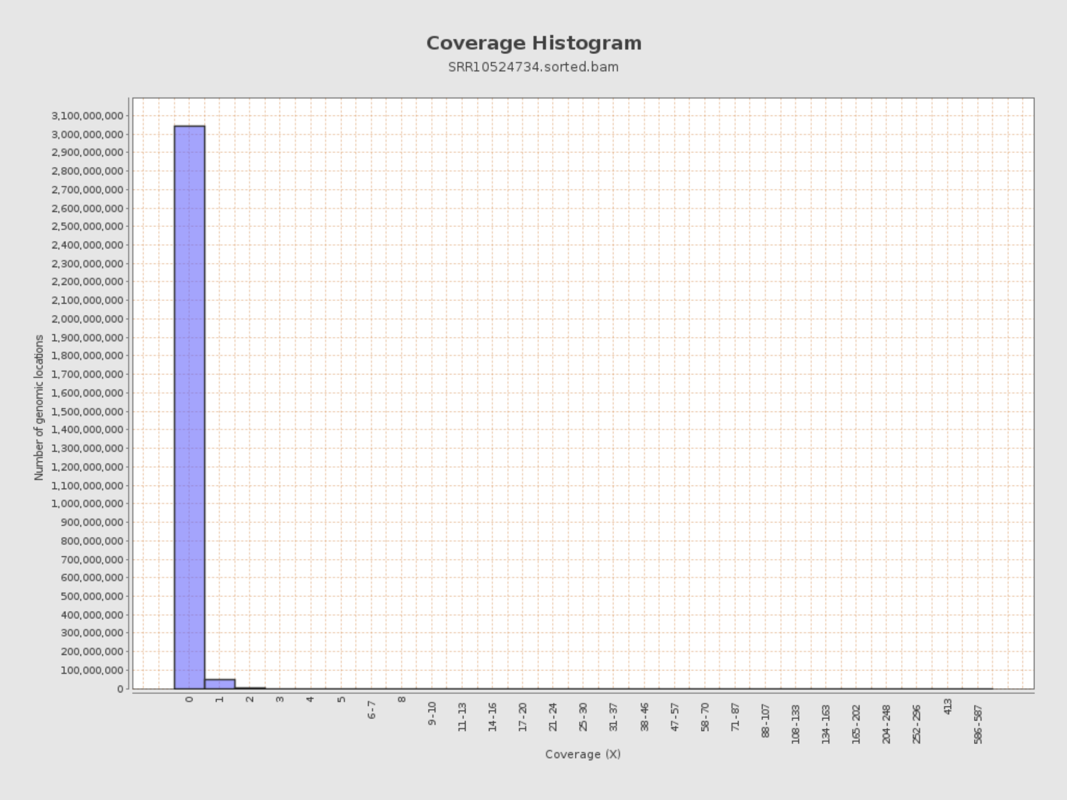
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4871143	0.0195	0.2576
chr2	243199373	5093848	0.0209	0.294
chr3	198022430	3961337	0.02	0.1551
chr4	191154276	3885610	0.0203	0.1729
chr5	180915260	3603889	0.0199	0.1524
chr6	171115067	3481285	0.0203	0.1652
chr7	159138663	3338937	0.021	0.2186

chr8	146364022	3053191	0.0209	0.1872
chr9	141213431	2550755	0.0181	0.17
chr10	135534747	2948113	0.0218	0.2269
chr11	135006516	2747294	0.0203	0.1741
chr12	133851895	2722150	0.0203	0.155
chr13	115169878	1877902	0.0163	0.1388
chr14	107349540	1804237	0.0168	0.1448
chr15	102531392	1766033	0.0172	0.1431
chr16	90354753	1866257	0.0207	0.1692
chr17	81195210	1722917	0.0212	0.1618
chr18	78077248	1561495	0.02	0.2393
chr19	59128983	1324534	0.0224	0.2174
chr20	63025520	1330997	0.0211	0.1658
chr21	48129895	802771	0.0167	0.1544
chr22	51304566	756729	0.0147	0.1322
chrMT	16571	19941	1.2034	1.2089
chrX	155270560	3379928	0.0218	0.168
chrY	59373566	214703	0.0036	0.1066

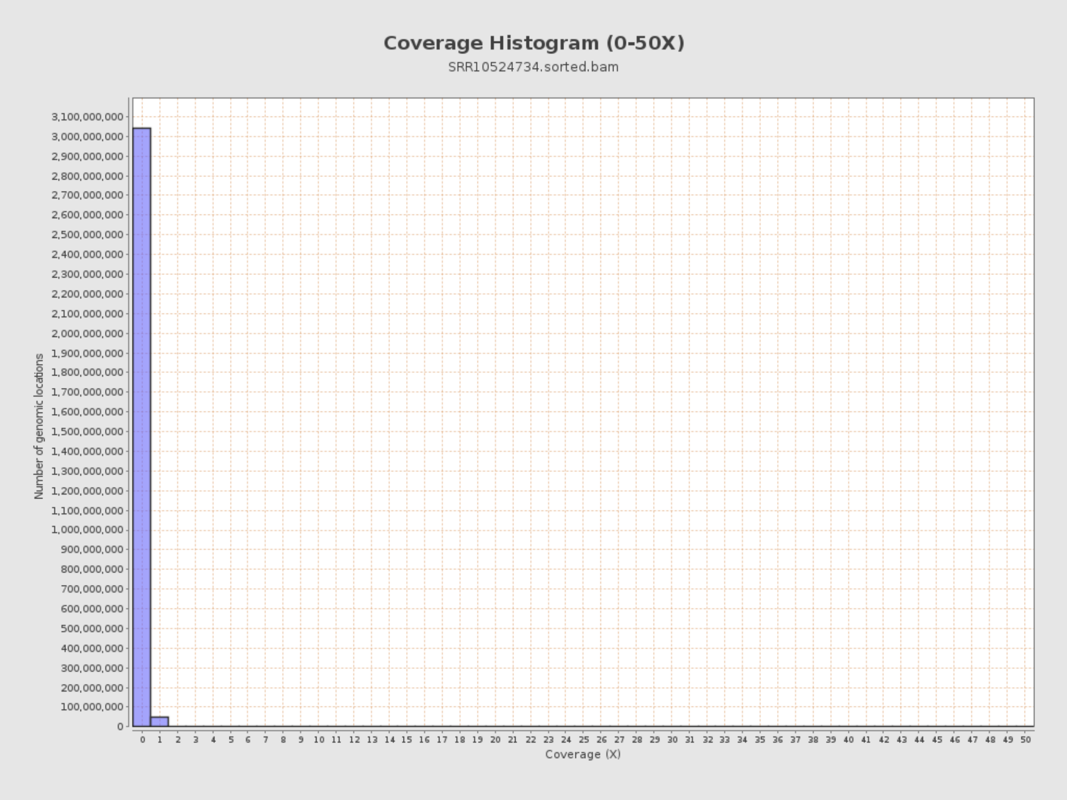
3. Results : Coverage across reference



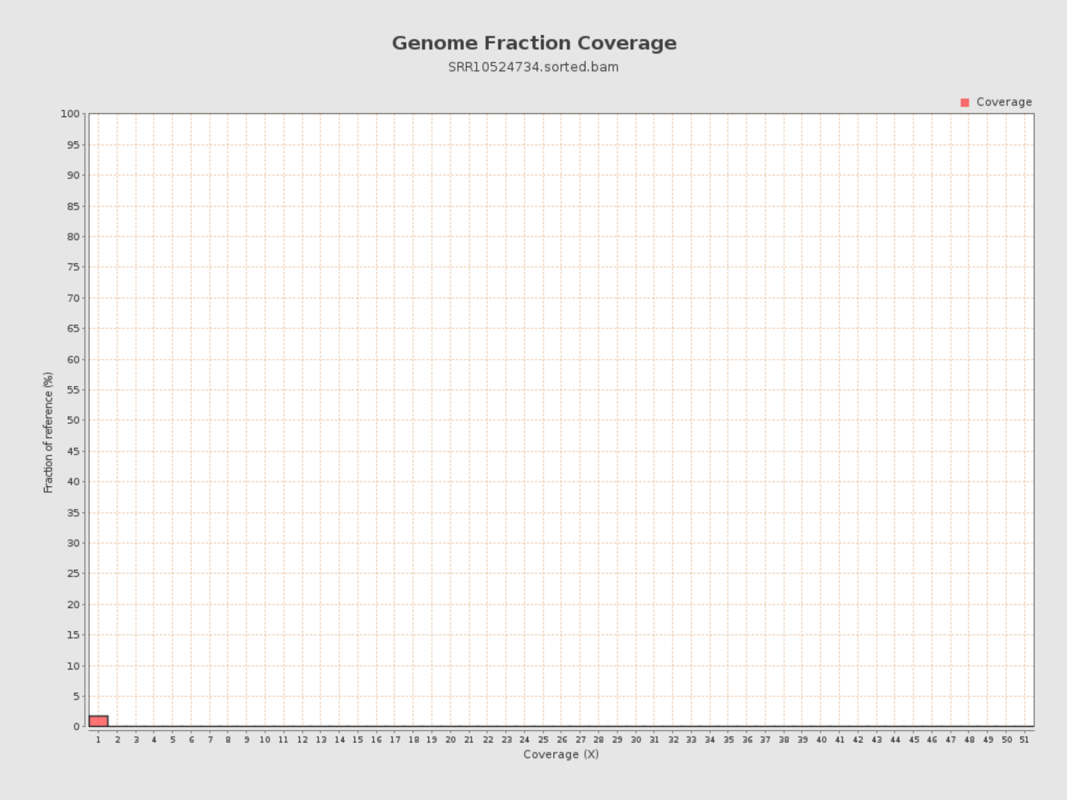
4. Results : Coverage Histogram



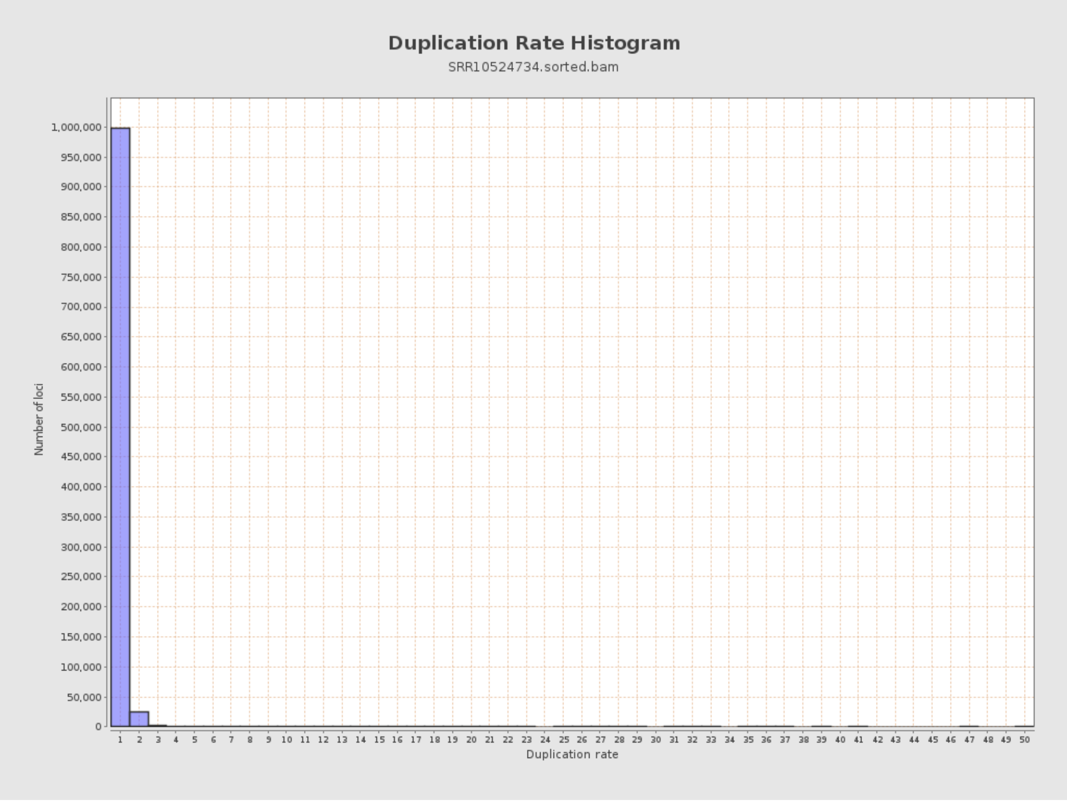
5. Results : Coverage Histogram (0-50X)



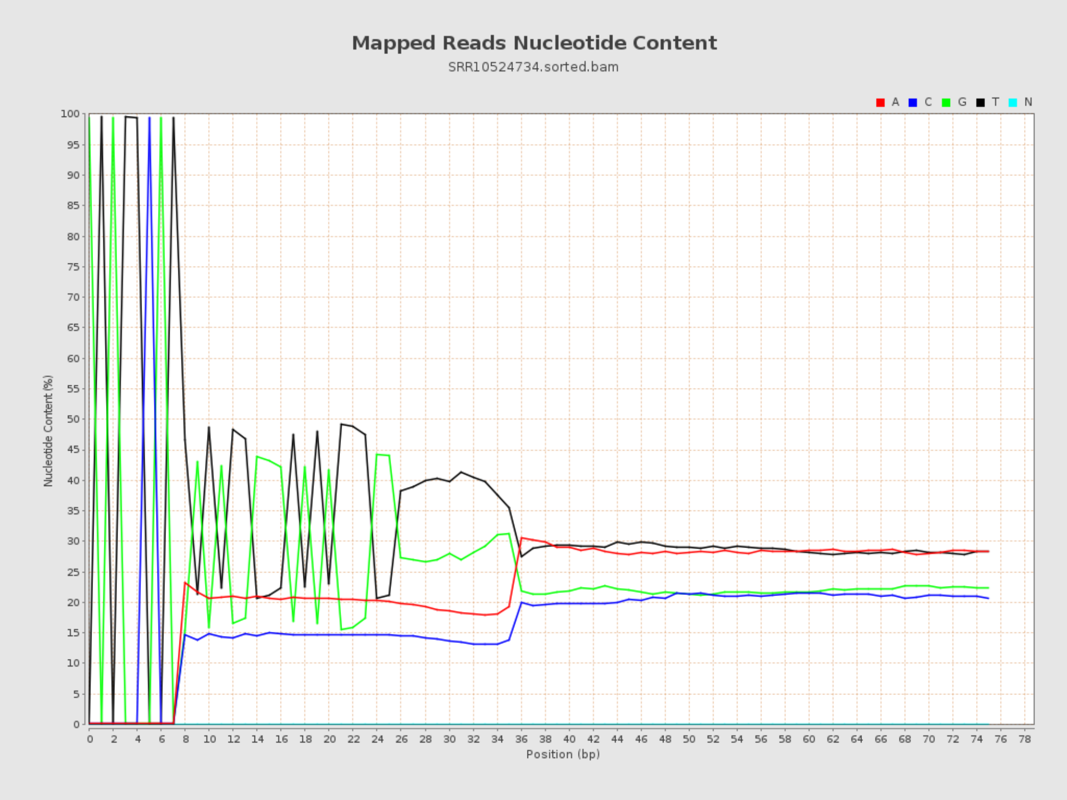
6. Results : Genome Fraction Coverage



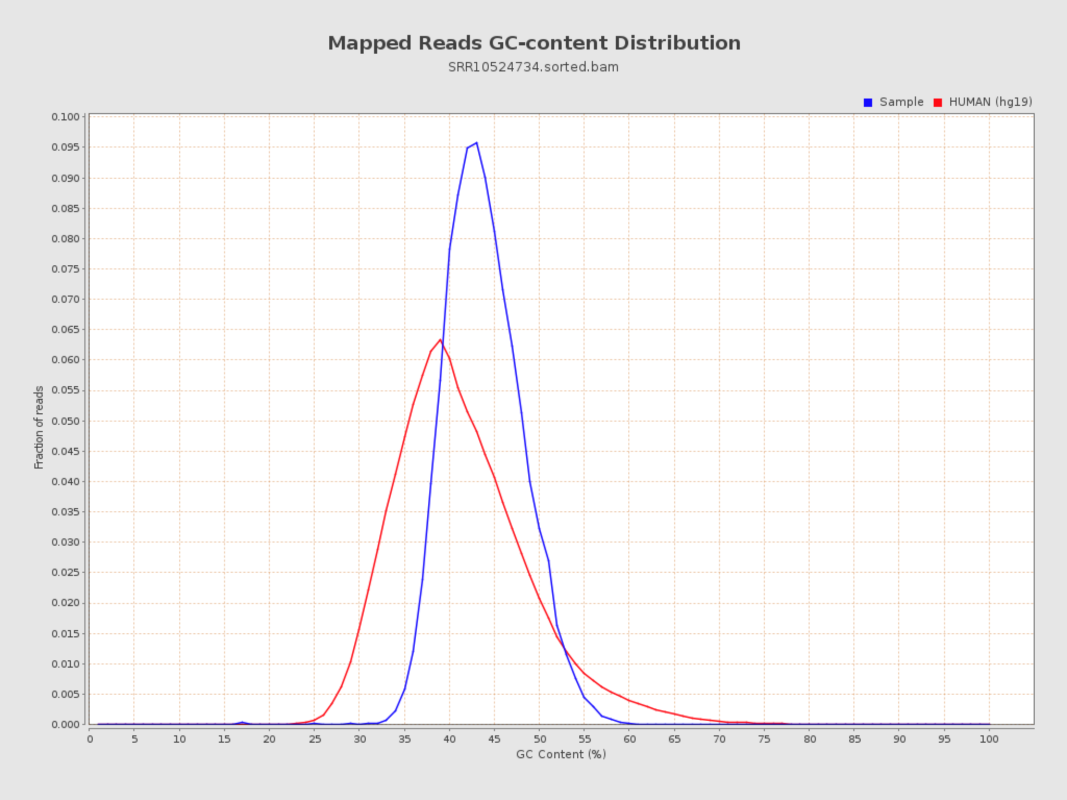
7. Results : Duplication Rate Histogram



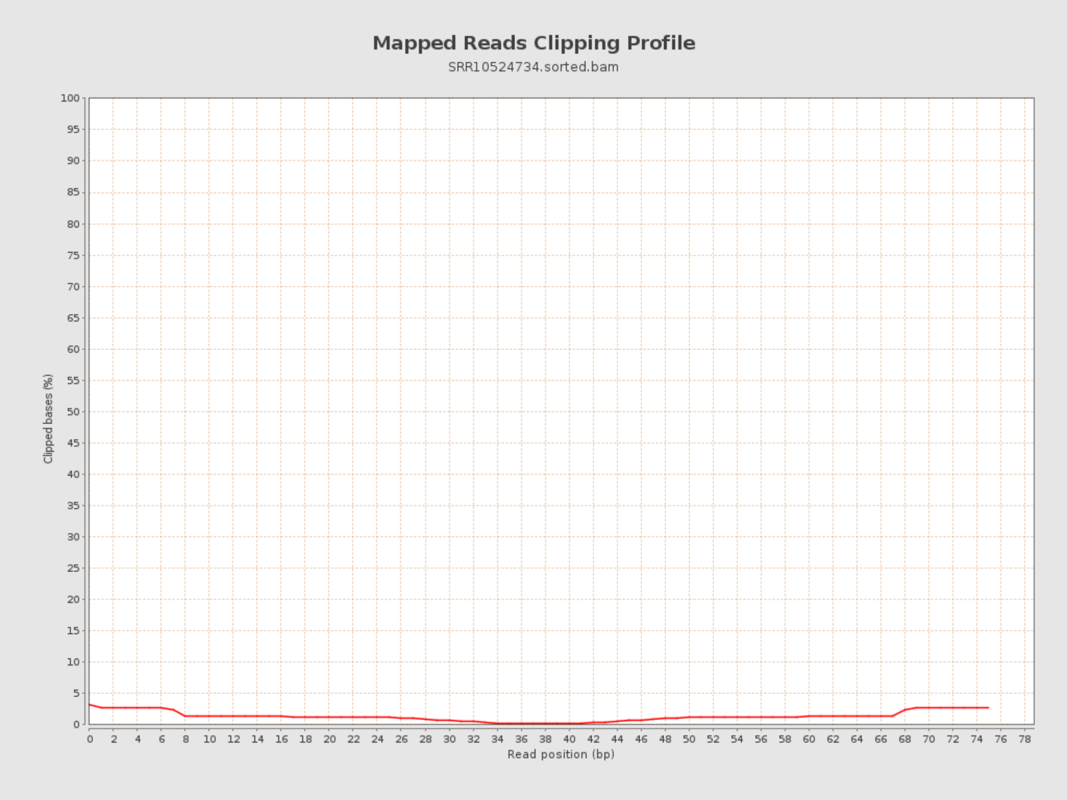
8. Results : Mapped Reads Nucleotide Content



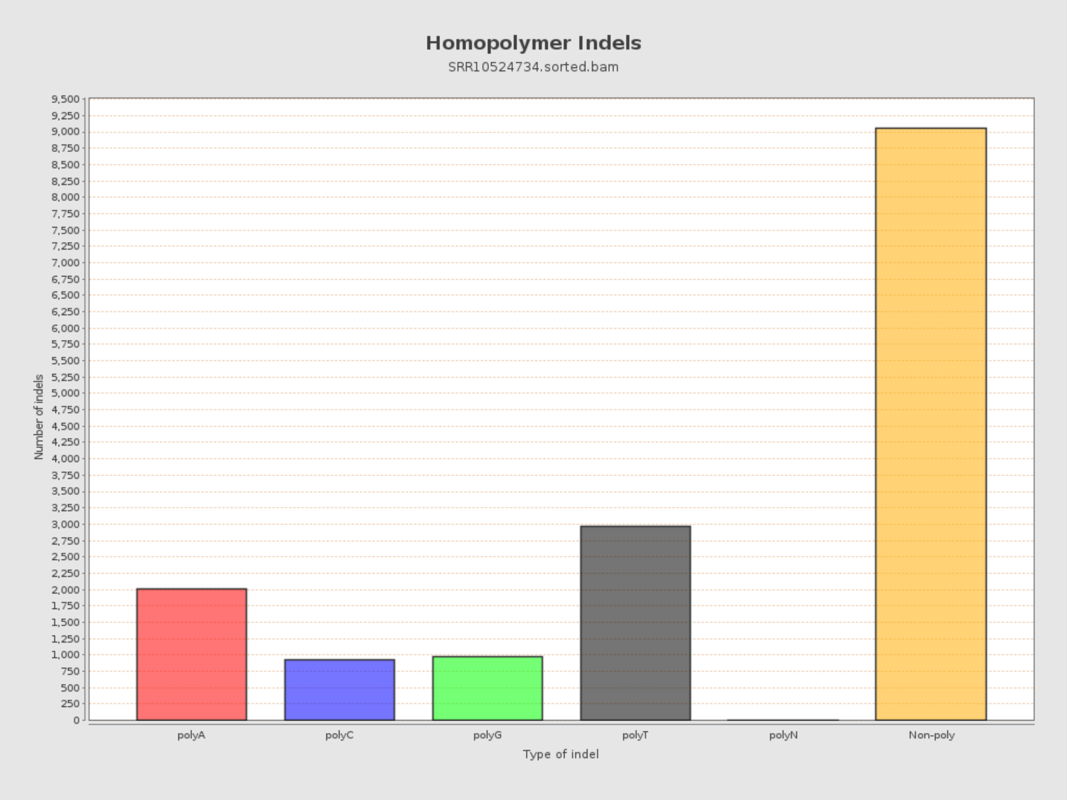
9. Results : Mapped Reads GC-content Distribution



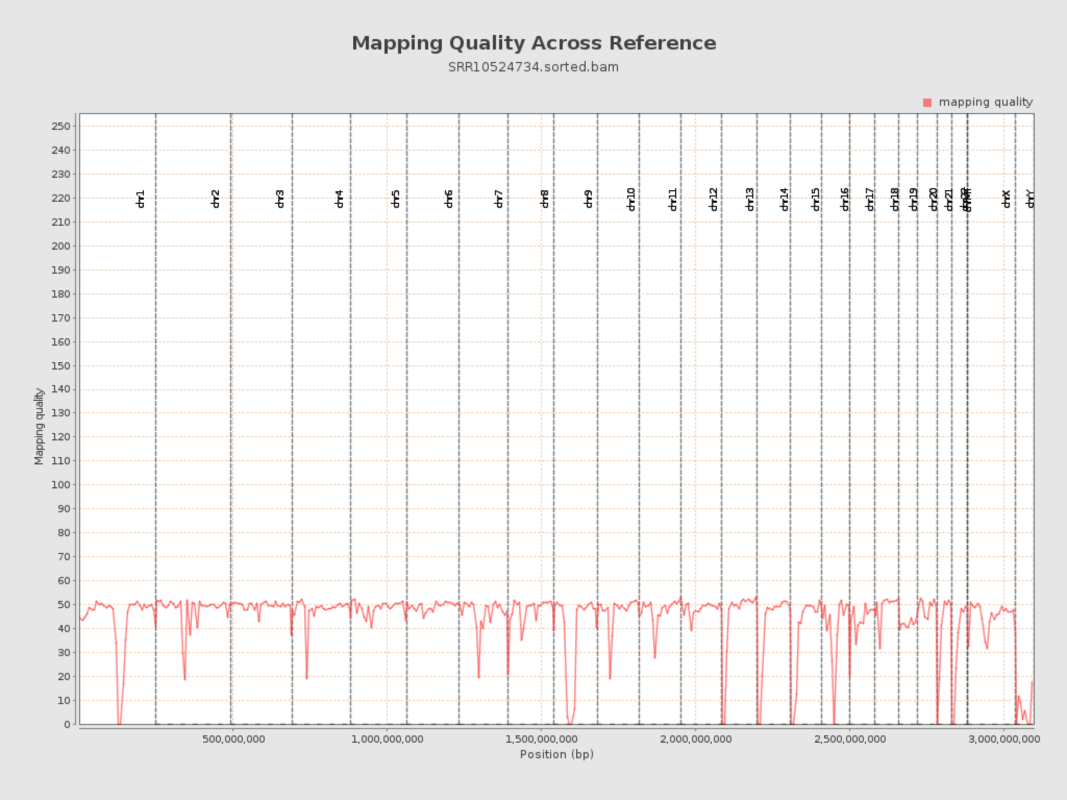
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram