Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 10:19:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524956.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_SRR10524956 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524956.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 10:19:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524956.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,164,118
Mapped reads	2,917,207 / 92.2%
Unmapped reads	246,911 / 7.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,660 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	124,731 / 3.94%
Duplication rate	3.09%
Clipped reads	2,928,873 / 92.57%

2.2. ACGT Content

Number/percentage of A's	40,653,740 / 24.19%
Number/percentage of C's	33,004,869 / 19.64%
Number/percentage of T's	52,135,540 / 31.02%
Number/percentage of G's	42,280,534 / 25.16%
Number/percentage of N's	4,904 / 0%
GC Percentage	44.79%

2.3. Coverage

Mean	0.0543

Standard Deviation	0.4258

2.4. Mapping Quality

Mean Mapping Quality	45.17

2.5. Mismatches and indels

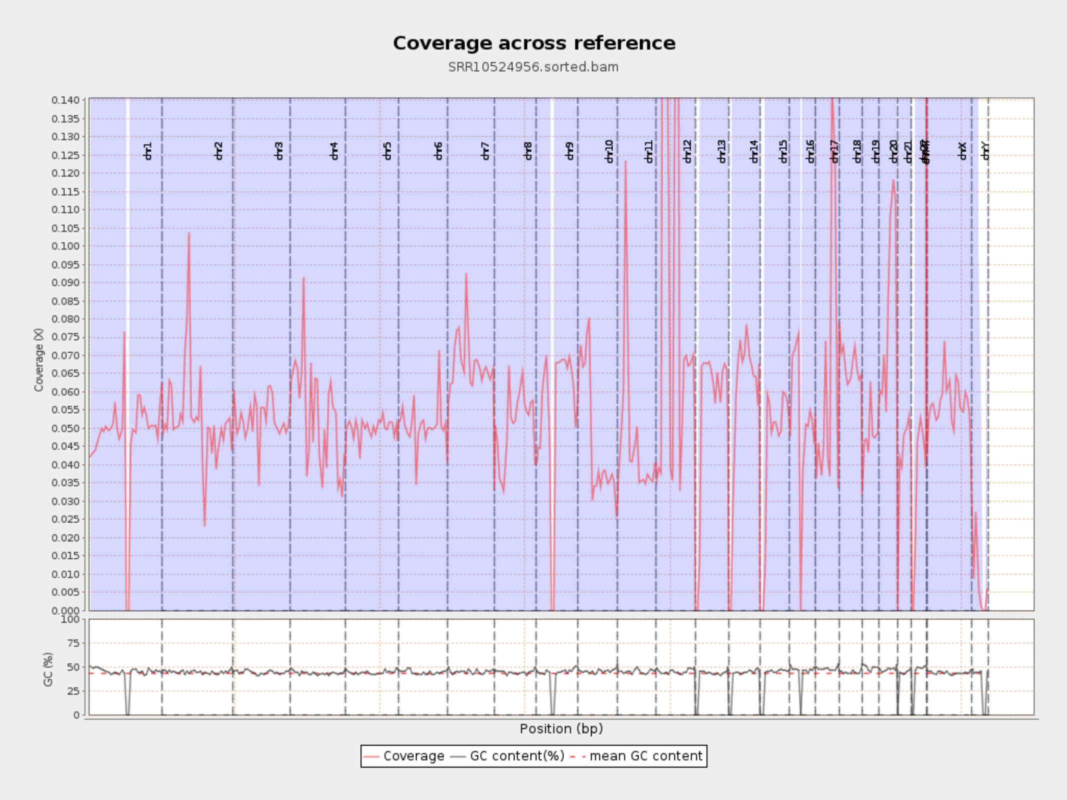
General error rate	0.48%
Mismatches	790,838
Insertions	8,910
Mapped reads with at least one insertion	0.3%
Deletions	26,005
Mapped reads with at least one deletion	0.89%
Homopolymer indels	43.32%

2.6. Chromosome stats

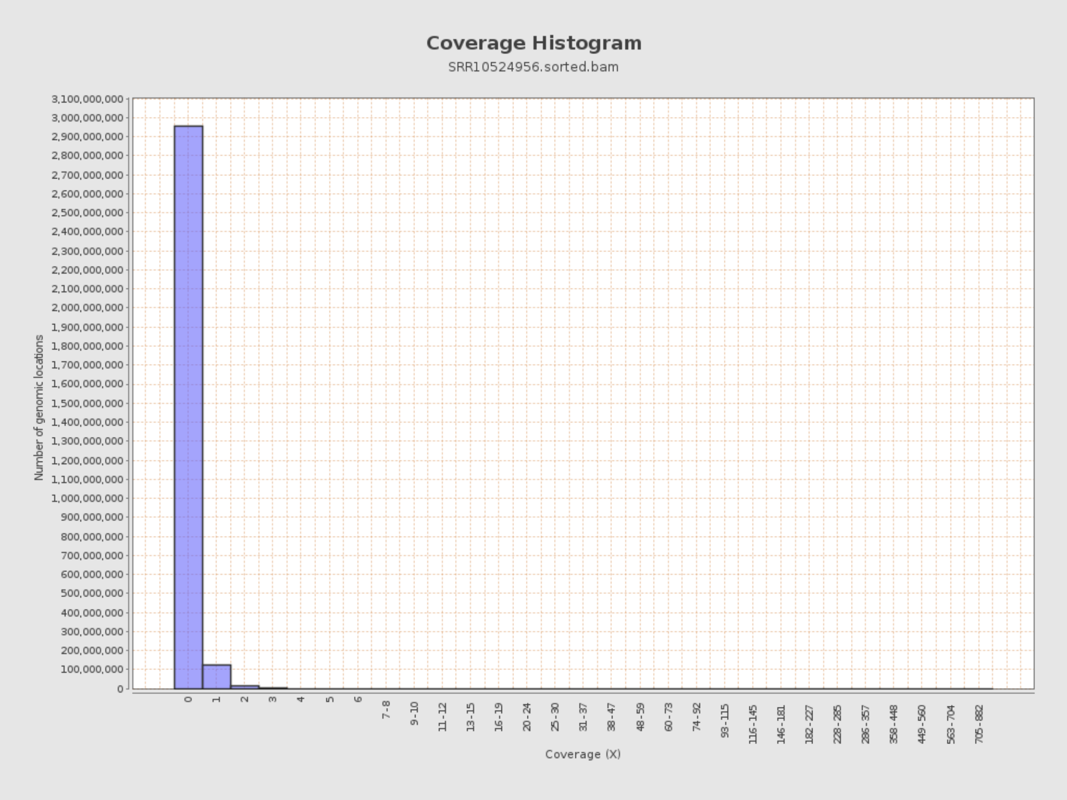
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11985149	0.0481	0.7294
chr2	243199373	12959452	0.0533	0.4788
chr3	198022430	10408118	0.0526	0.259
chr4	191154276	10251630	0.0536	0.3089
chr5	180915260	9048088	0.05	0.2576
chr6	171115067	8726524	0.051	0.2862
chr7	159138663	10883365	0.0684	0.594

chr8	146364022	7497330	0.0512	0.4041
chr9	141213431	7751775	0.0549	0.4564
chr10	135534747	6429570	0.0474	0.4285
chr11	135006516	6435596	0.0477	0.3595
chr12	133851895	12677891	0.0947	0.4197
chr13	115169878	6237571	0.0542	0.2627
chr14	107349540	6027190	0.0561	0.3027
chr15	102531392	4453750	0.0434	0.2373
chr16	90354753	4771501	0.0528	0.2883
chr17	81195210	5073279	0.0625	0.2997
chr18	78077248	5284480	0.0677	0.7938
chr19	59128983	2870418	0.0485	0.567
chr20	63025520	5299531	0.0841	0.3454
chr21	48129895	2017507	0.0419	0.2896
chr22	51304566	1707297	0.0333	0.2043
chrMT	16571	5983	0.3611	0.666
chrX	155270560	8840017	0.0569	0.331
chrY	59373566	480993	0.0081	0.1863

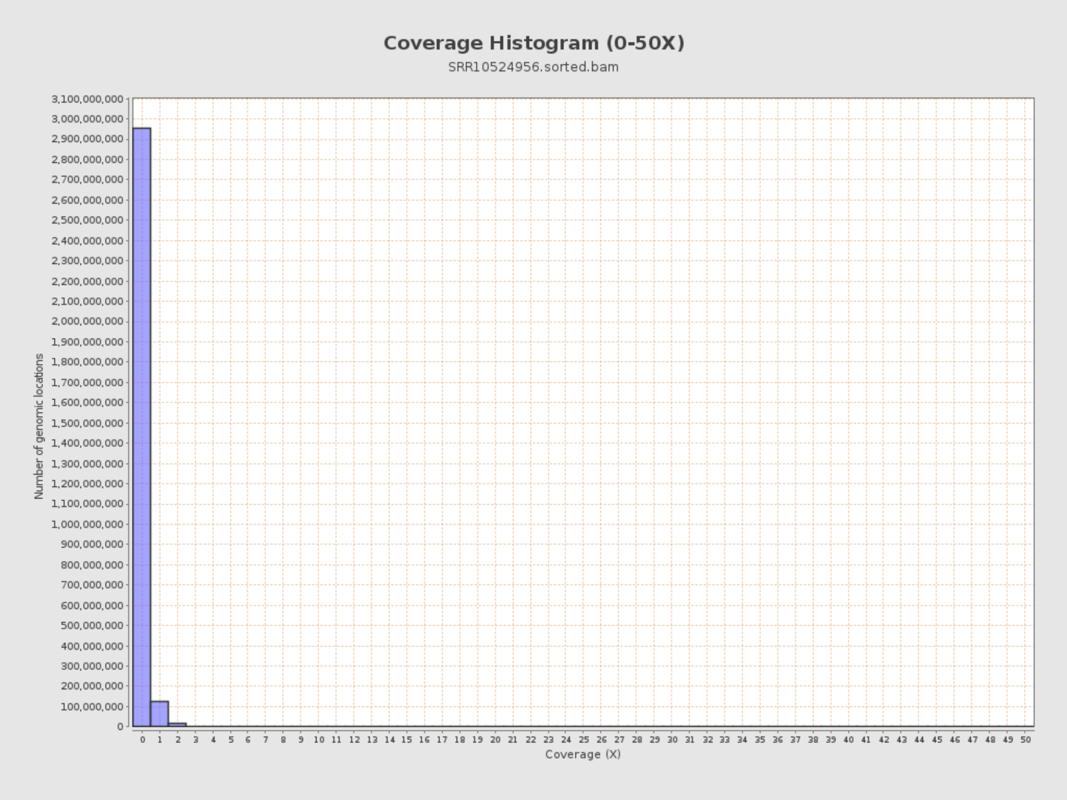
3. Results : Coverage across reference



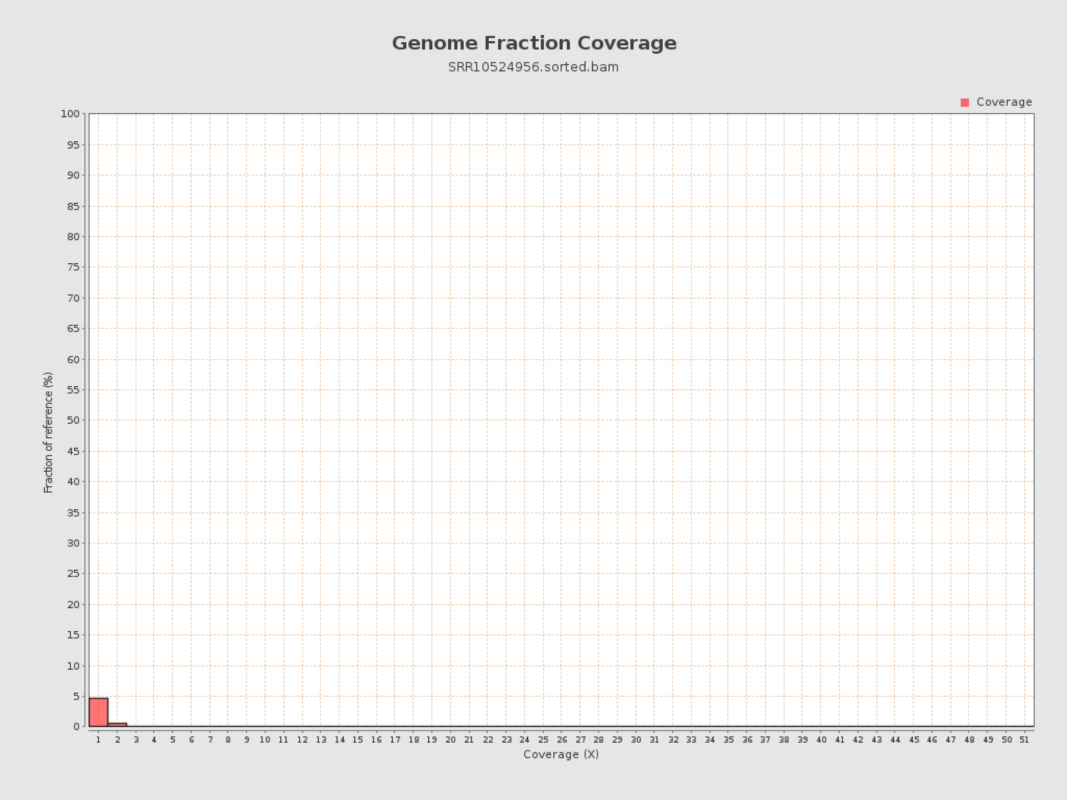
4. Results : Coverage Histogram



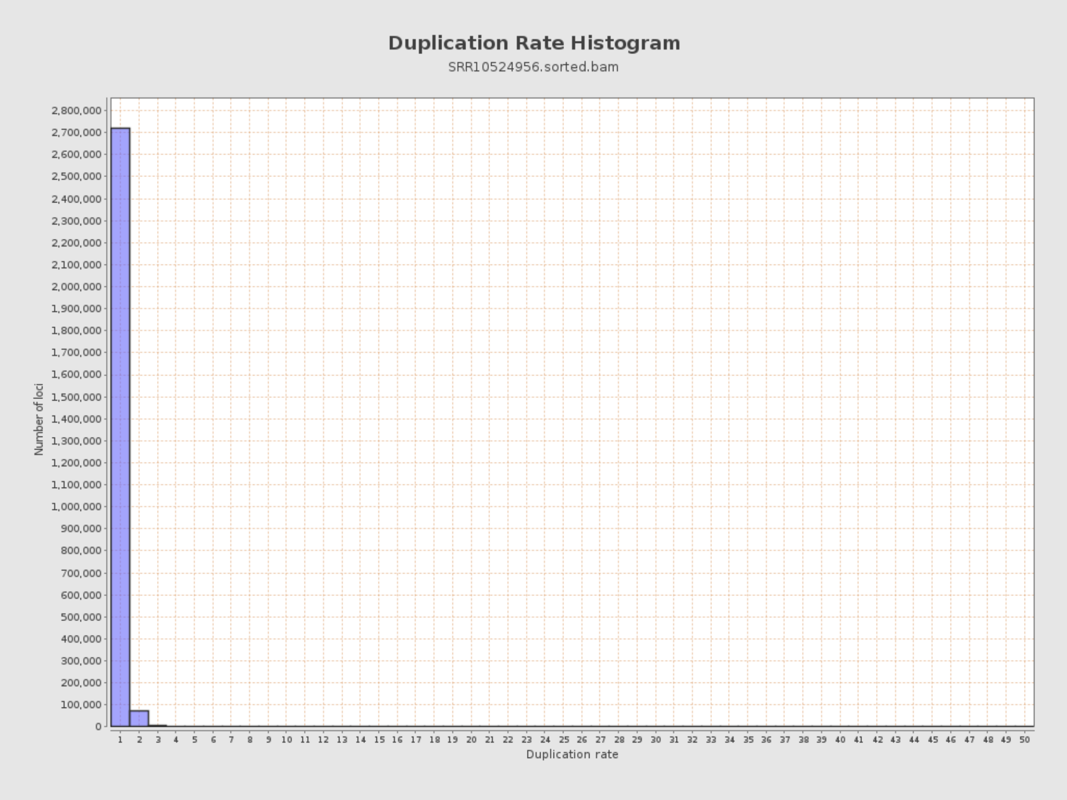
5. Results : Coverage Histogram (0-50X)



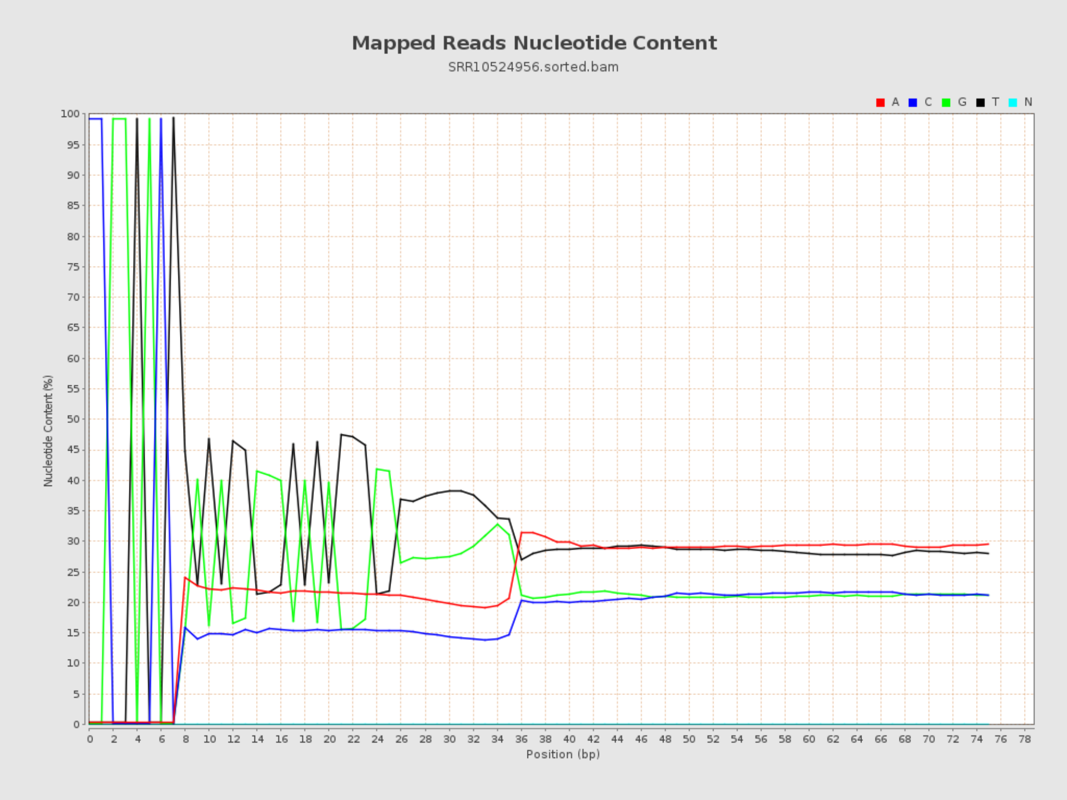
6. Results : Genome Fraction Coverage



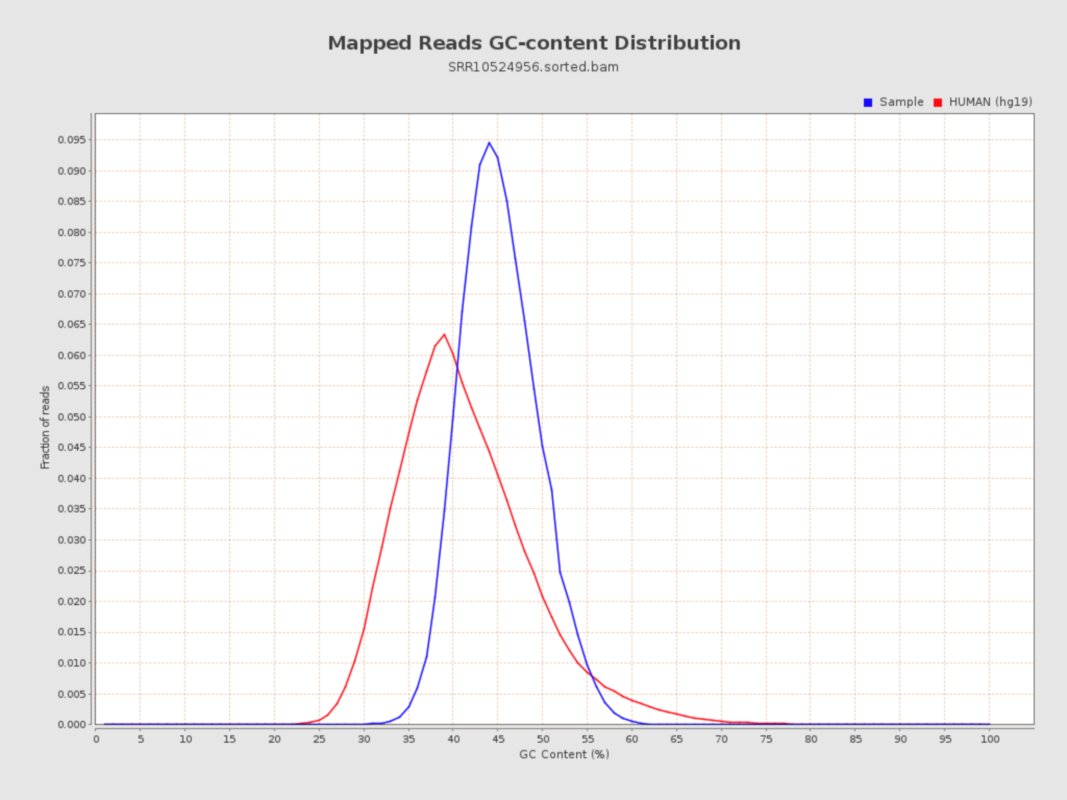
7. Results : Duplication Rate Histogram



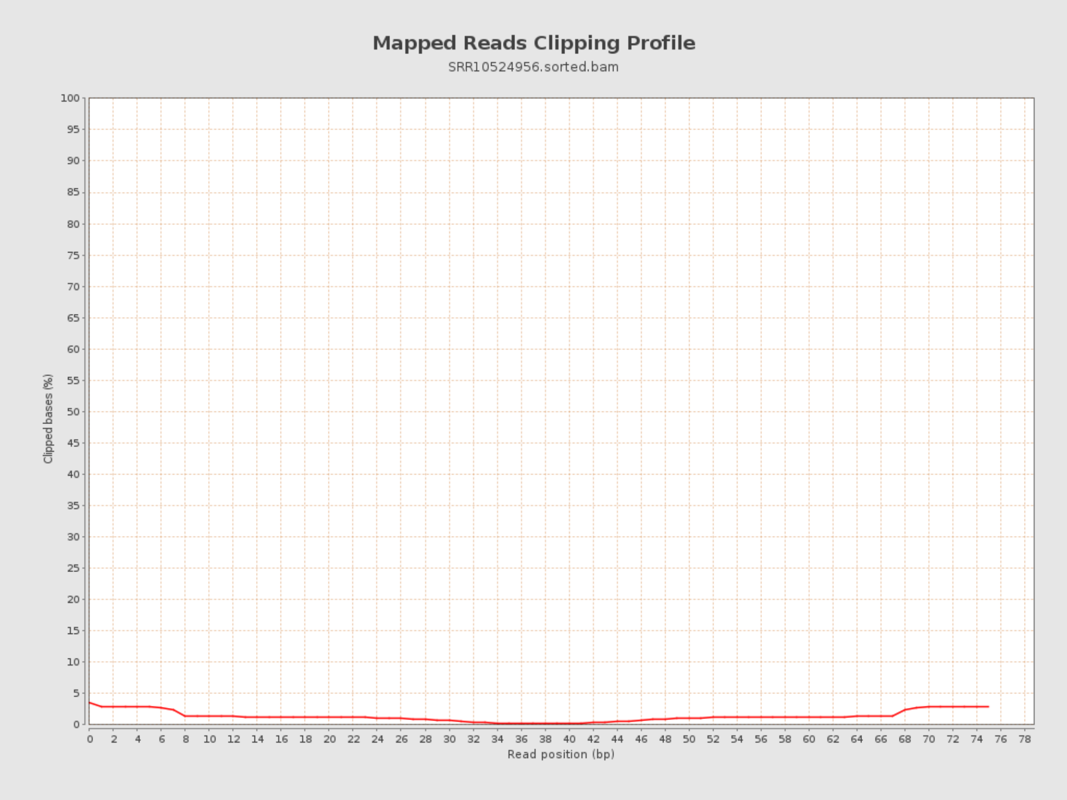
8. Results : Mapped Reads Nucleotide Content



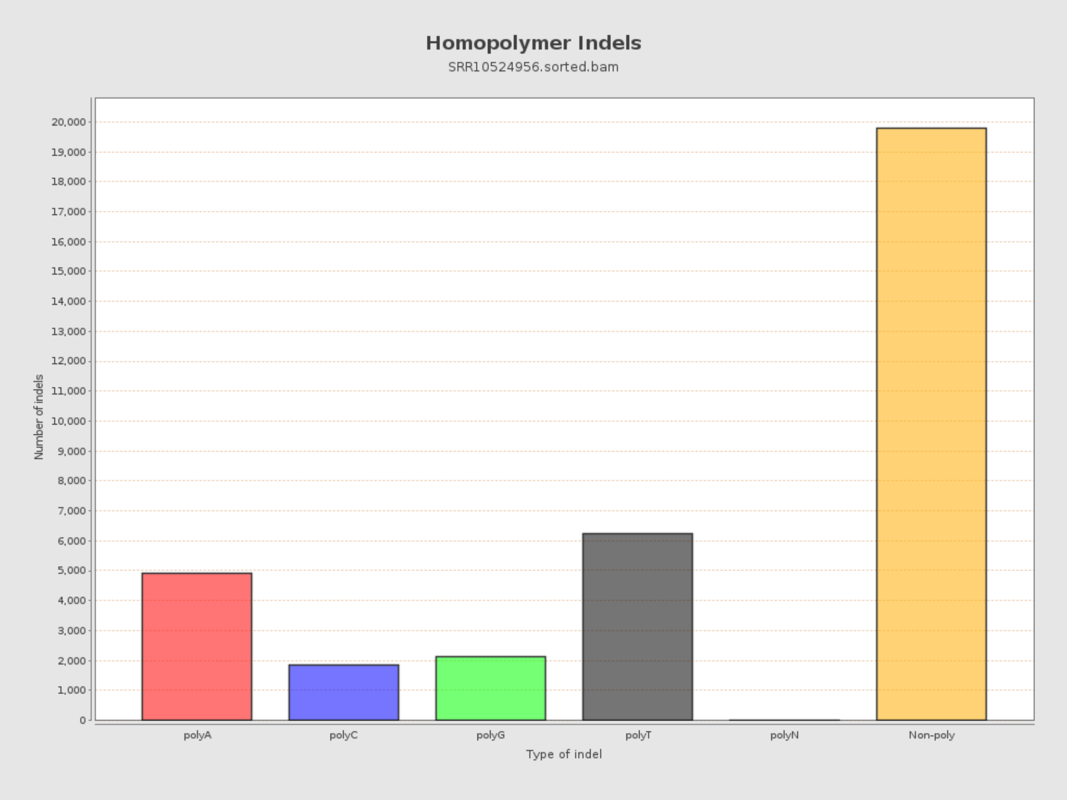
9. Results : Mapped Reads GC-content Distribution



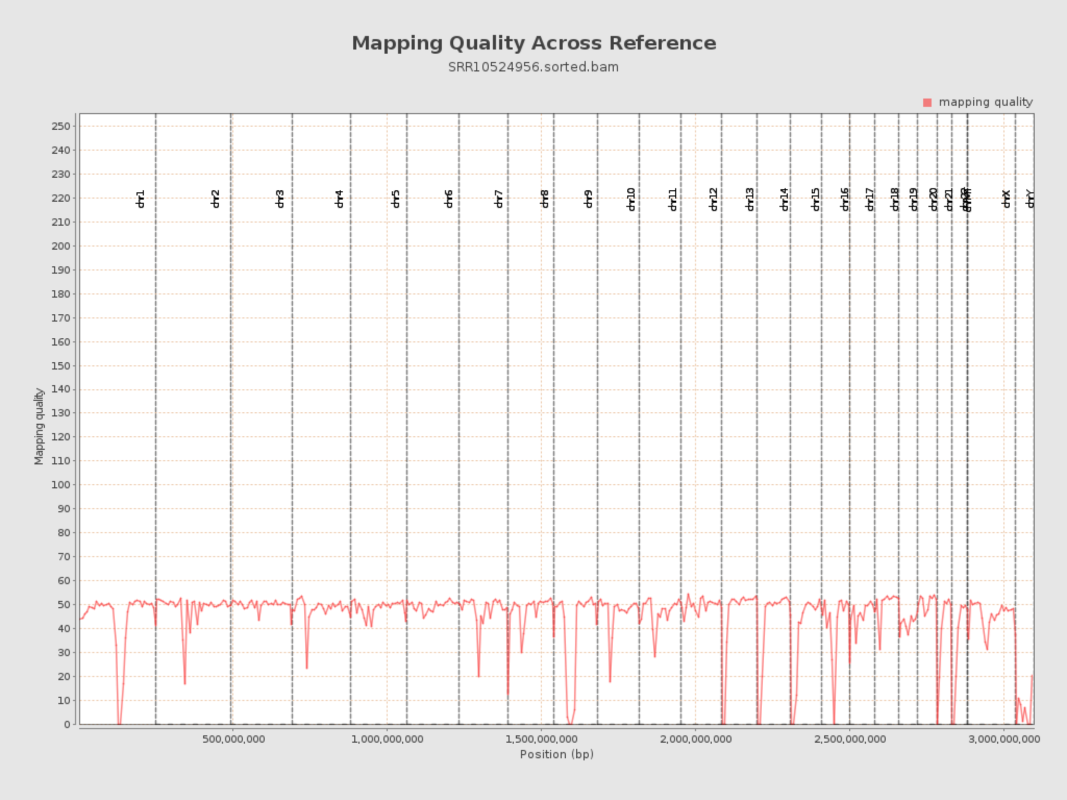
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram