Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 05:01:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524456.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_SRR10524456 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524456.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 05:01:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524456.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,084,168
Mapped reads	1,005,735 / 92.77%
Unmapped reads	78,433 / 7.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,276 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	38,001 / 3.51%
Duplication rate	2.99%
Clipped reads	1,005,966 / 92.79%

2.2. ACGT Content

Number/percentage of A's	14,450,798 / 24.66%
Number/percentage of C's	11,421,512 / 19.49%
Number/percentage of T's	18,291,186 / 31.21%
Number/percentage of G's	14,445,406 / 24.65%
Number/percentage of N's	1,220 / 0%
GC Percentage	44.13%

2.3. Coverage

Mean	0.0189

Standard Deviation	0.1923

2.4. Mapping Quality

Mean Mapping Quality	45.45

2.5. Mismatches and indels

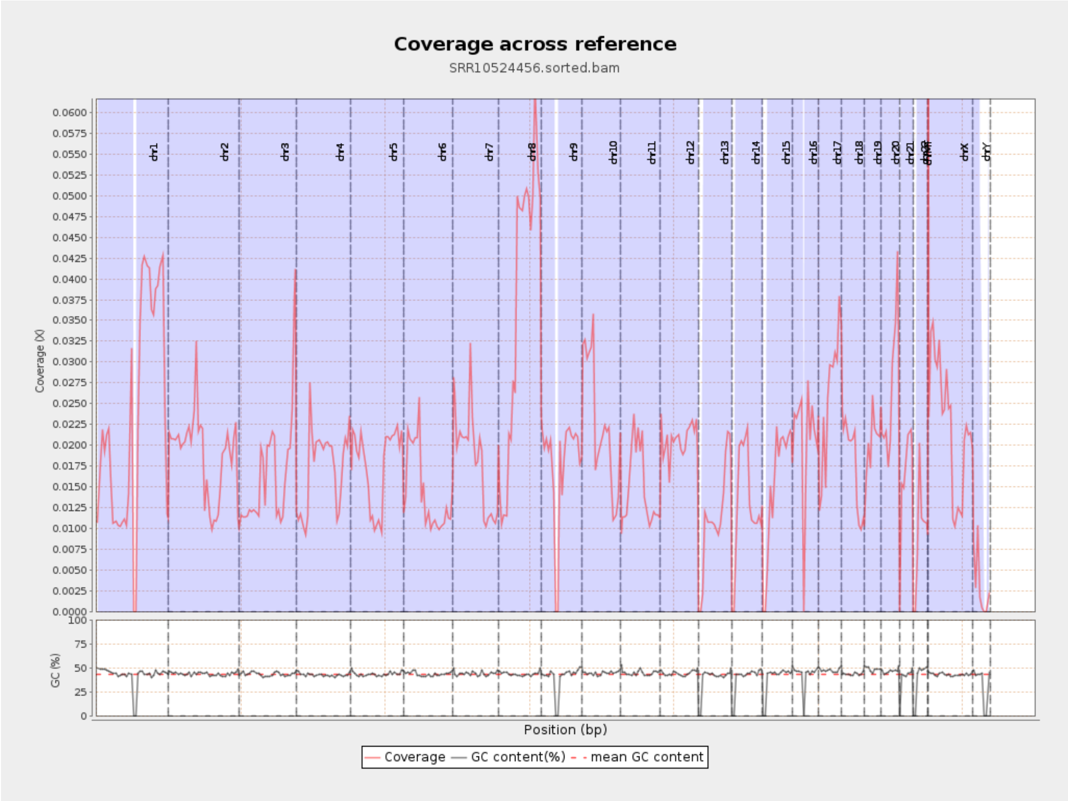
General error rate	0.48%
Mismatches	272,714
Insertions	3,428
Mapped reads with at least one insertion	0.34%
Deletions	10,987
Mapped reads with at least one deletion	1.08%
Homopolymer indels	44.16%

2.6. Chromosome stats

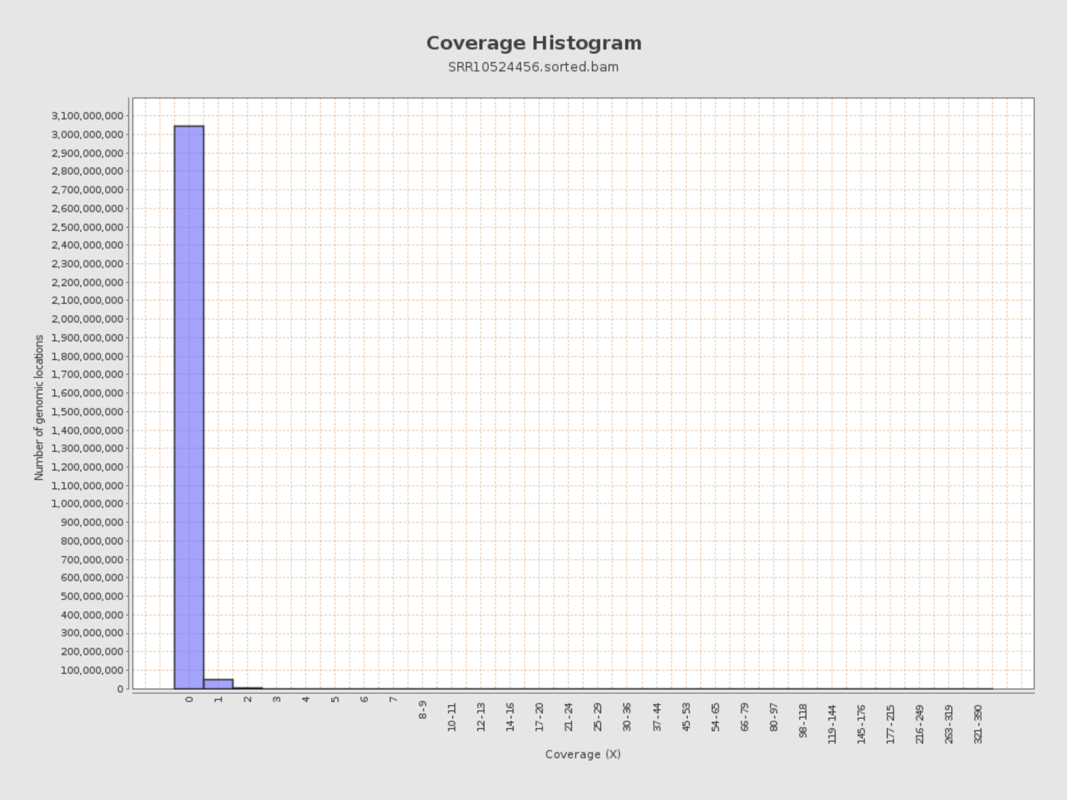
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5759834	0.0231	0.3124
chr2	243199373	4591065	0.0189	0.2168
chr3	198022430	3206419	0.0162	0.1378
chr4	191154276	3304201	0.0173	0.1577
chr5	180915260	3199451	0.0177	0.1441
chr6	171115067	2455405	0.0143	0.1512
chr7	159138663	2917961	0.0183	0.2374

chr8	146364022	5407192	0.0369	0.2286
chr9	141213431	2480818	0.0176	0.1768
chr10	135534747	3093553	0.0228	0.204
chr11	135006516	2025447	0.015	0.1794
chr12	133851895	2763990	0.0206	0.1565
chr13	115169878	1298322	0.0113	0.1145
chr14	107349540	1395985	0.013	0.1244
chr15	102531392	1556095	0.0152	0.1357
chr16	90354753	1860422	0.0206	0.1616
chr17	81195210	2063420	0.0254	0.179
chr18	78077248	1393591	0.0178	0.2747
chr19	59128983	1198242	0.0203	0.2357
chr20	63025520	1680508	0.0267	0.1786
chr21	48129895	802644	0.0167	0.148
chr22	51304566	479997	0.0094	0.1046
chrMT	16571	3194	0.1927	0.5095
chrX	155270560	3511654	0.0226	0.1768
chrY	59373566	179467	0.003	0.0868

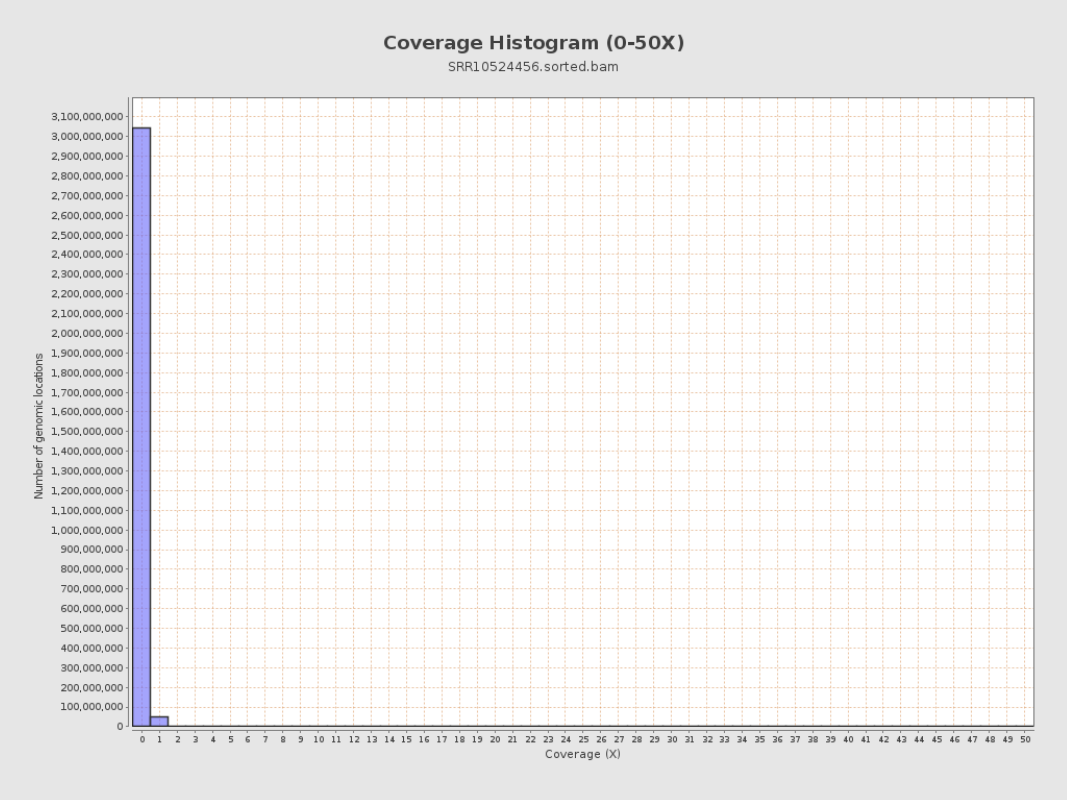
3. Results : Coverage across reference



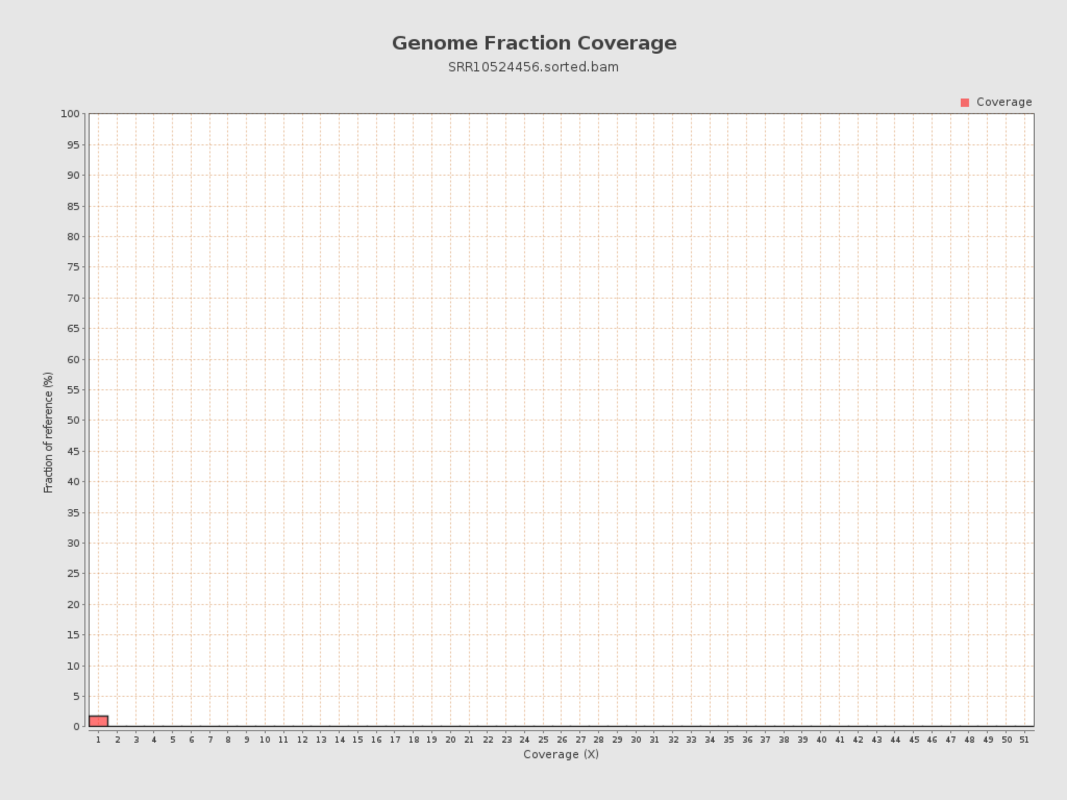
4. Results : Coverage Histogram



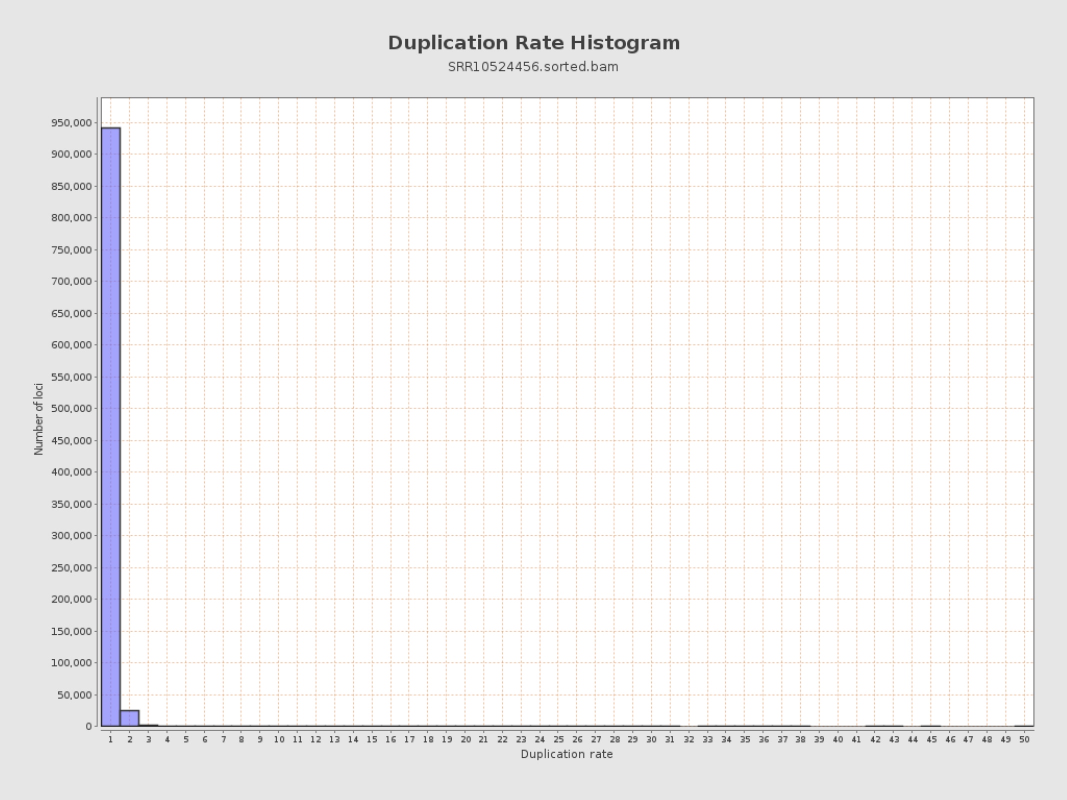
5. Results : Coverage Histogram (0-50X)



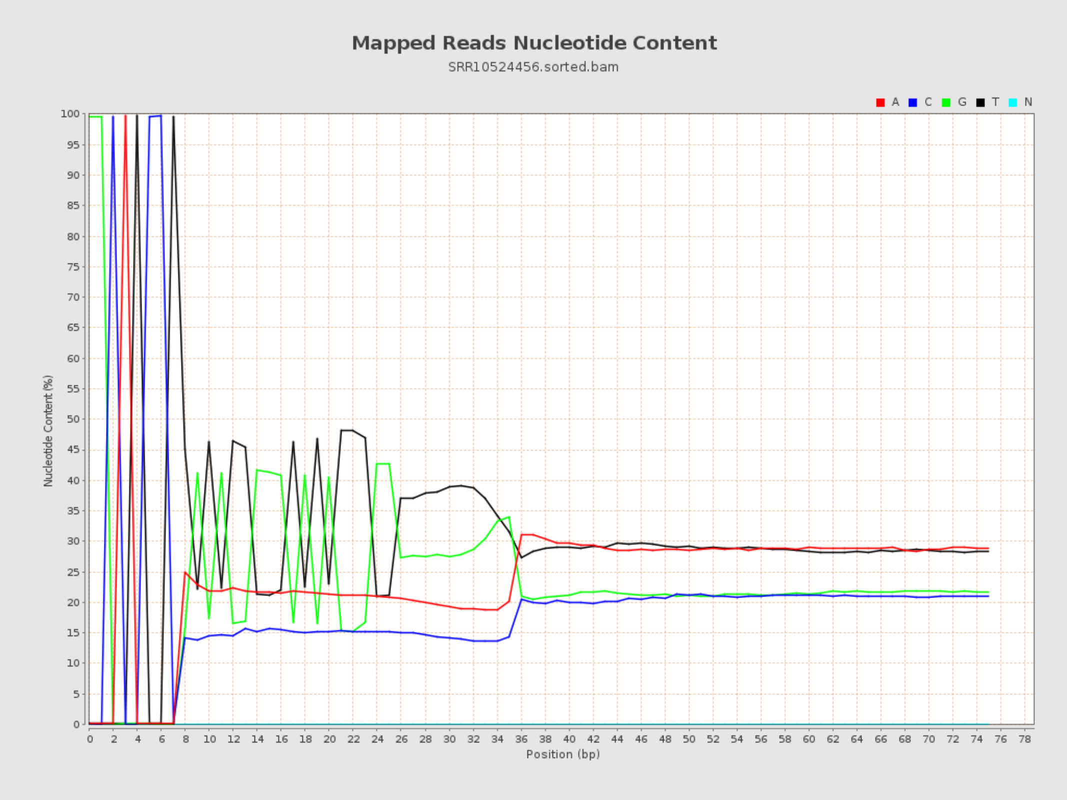
6. Results : Genome Fraction Coverage



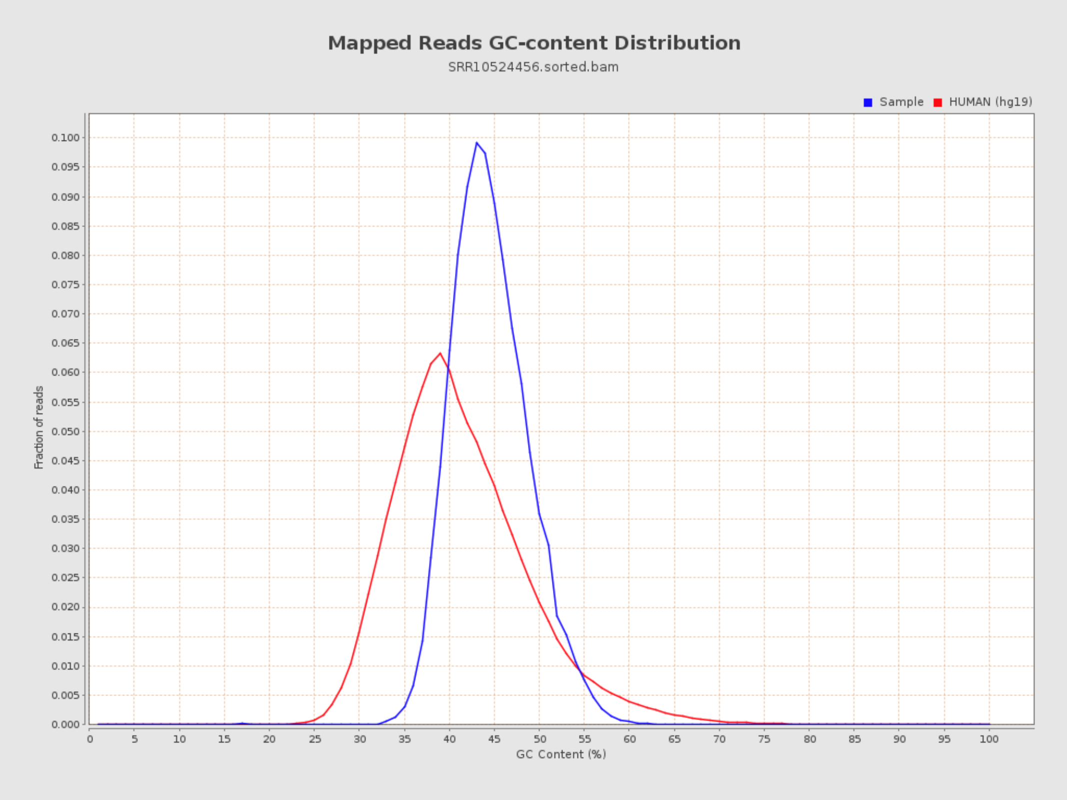
7. Results : Duplication Rate Histogram



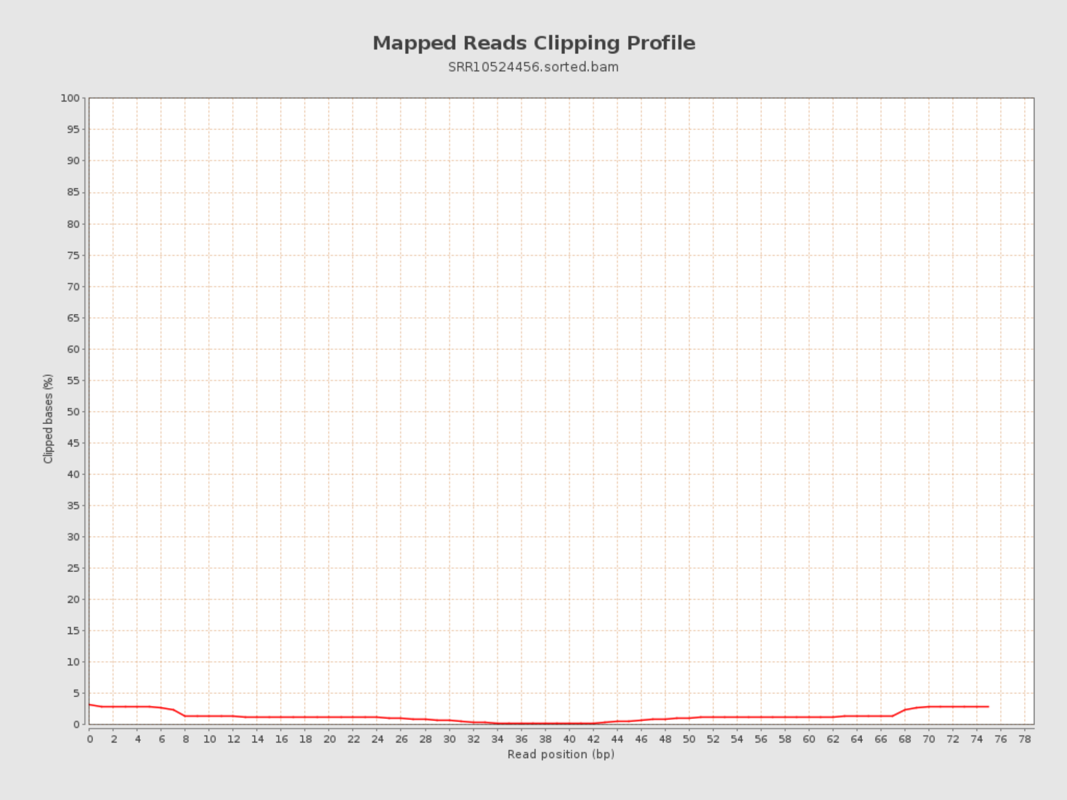
8. Results : Mapped Reads Nucleotide Content



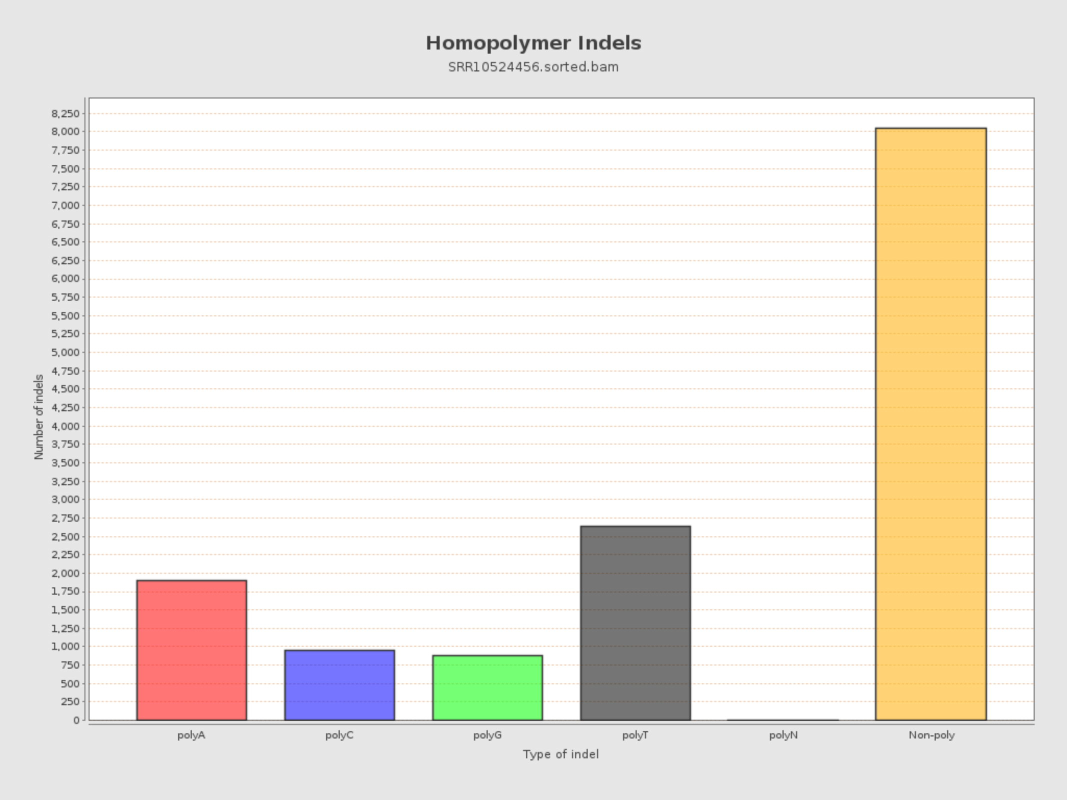
9. Results : Mapped Reads GC-content Distribution



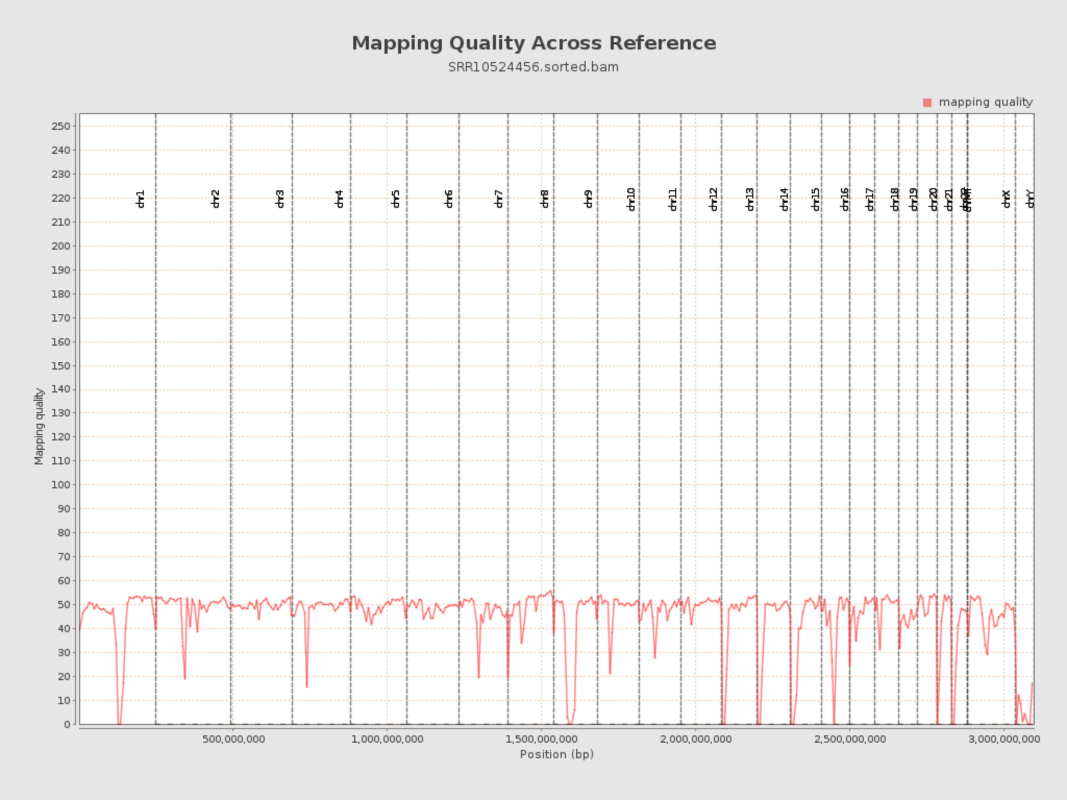
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram