Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 01:09:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524879.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_SRR10524879 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524879.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 01:09:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524879.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	886,711
Mapped reads	813,870 / 91.79%
Unmapped reads	72,841 / 8.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,557 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	18,016 / 2.03%
Duplication rate	1.48%
Clipped reads	814,341 / 91.84%

2.2. ACGT Content

Number/percentage of A's	11,817,450 / 24.89%
Number/percentage of C's	8,959,110 / 18.87%
Number/percentage of T's	15,871,775 / 33.43%
Number/percentage of G's	10,817,214 / 22.79%
Number/percentage of N's	6,860 / 0.01%
GC Percentage	41.66%

2.3. Coverage

Mean	0.0153

Standard Deviation	0.1822

2.4. Mapping Quality

Mean Mapping Quality	45.12

2.5. Mismatches and indels

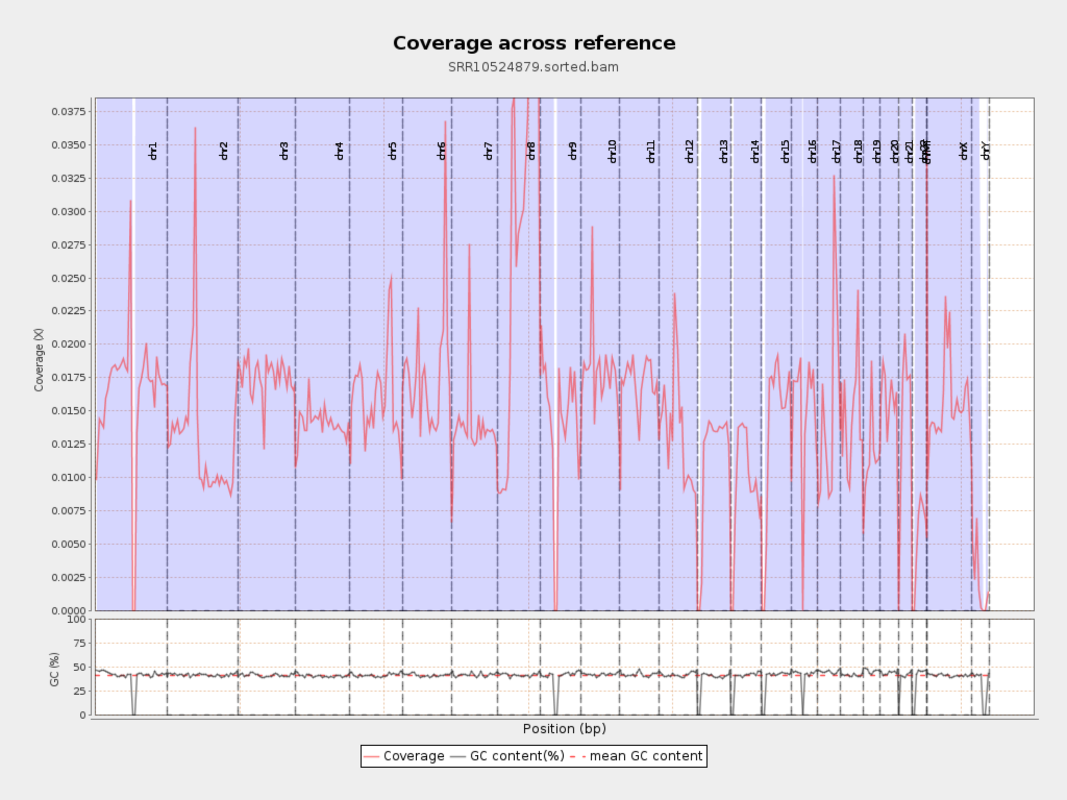
General error rate	0.5%
Mismatches	232,242
Insertions	3,605
Mapped reads with at least one insertion	0.44%
Deletions	9,108
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.38%

2.6. Chromosome stats

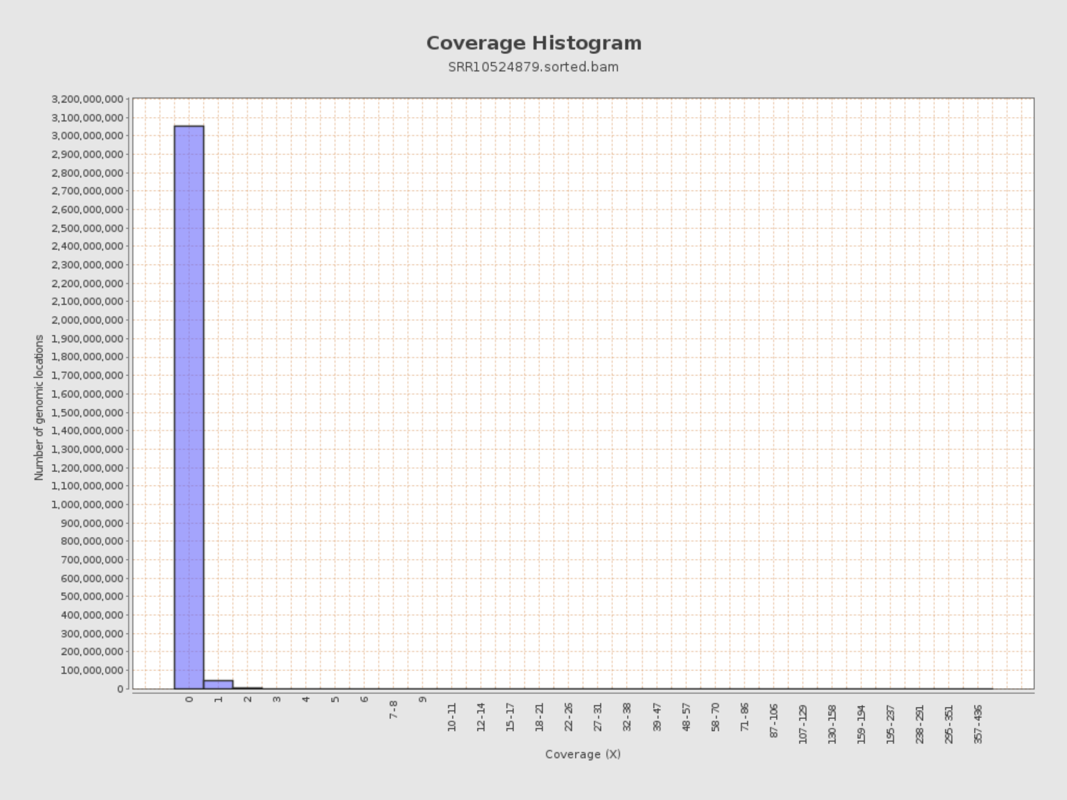
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4056963	0.0163	0.3431
chr2	243199373	3124453	0.0128	0.1755
chr3	198022430	3476491	0.0176	0.1374
chr4	191154276	2675934	0.014	0.1279
chr5	180915260	2938309	0.0162	0.1328
chr6	171115067	3010748	0.0176	0.1489
chr7	159138663	2220956	0.014	0.2271

chr8	146364022	4796751	0.0328	0.2362
chr9	141213431	1990777	0.0141	0.1584
chr10	135534747	2442015	0.018	0.175
chr11	135006516	2307234	0.0171	0.1678
chr12	133851895	1775342	0.0133	0.121
chr13	115169878	1291799	0.0112	0.1101
chr14	107349540	1009994	0.0094	0.1073
chr15	102531392	1410223	0.0138	0.1221
chr16	90354753	1329992	0.0147	0.1327
chr17	81195210	1254659	0.0155	0.1407
chr18	78077248	1147847	0.0147	0.2712
chr19	59128983	692640	0.0117	0.2409
chr20	63025520	994427	0.0158	0.1328
chr21	48129895	704880	0.0146	0.128
chr22	51304566	278990	0.0054	0.0761
chrMT	16571	573	0.0346	0.1905
chrX	155270560	2432019	0.0157	0.143
chrY	59373566	122559	0.0021	0.0646

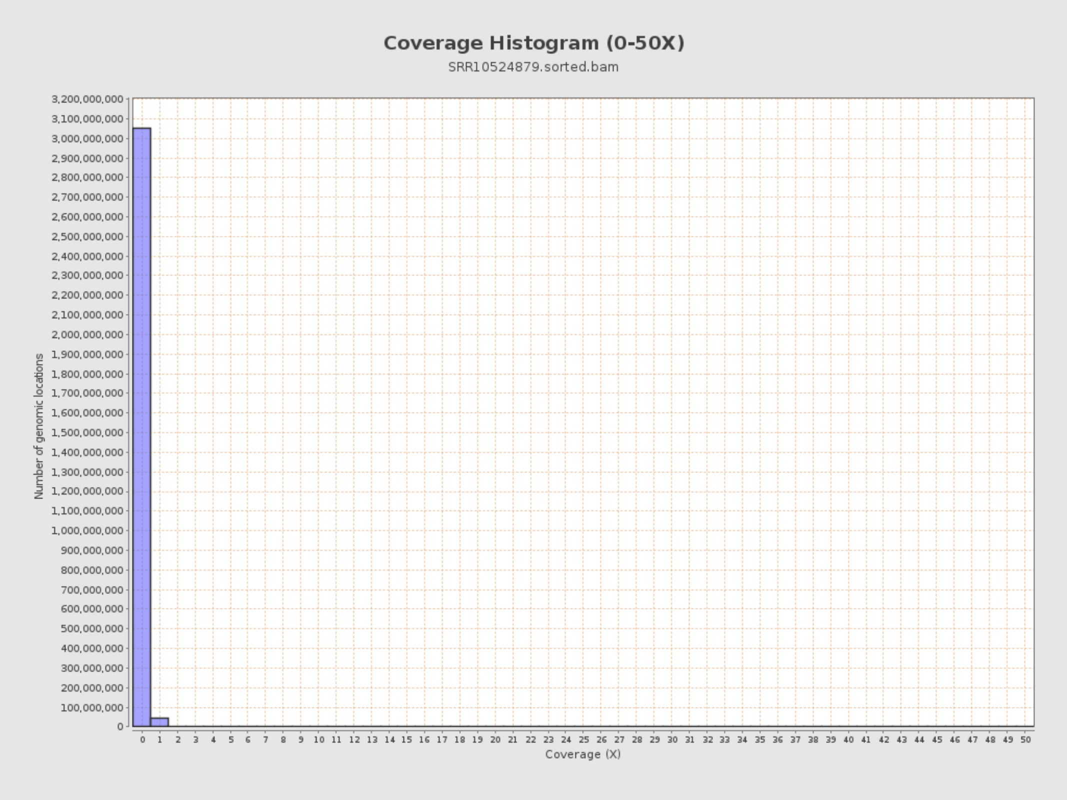
3. Results : Coverage across reference



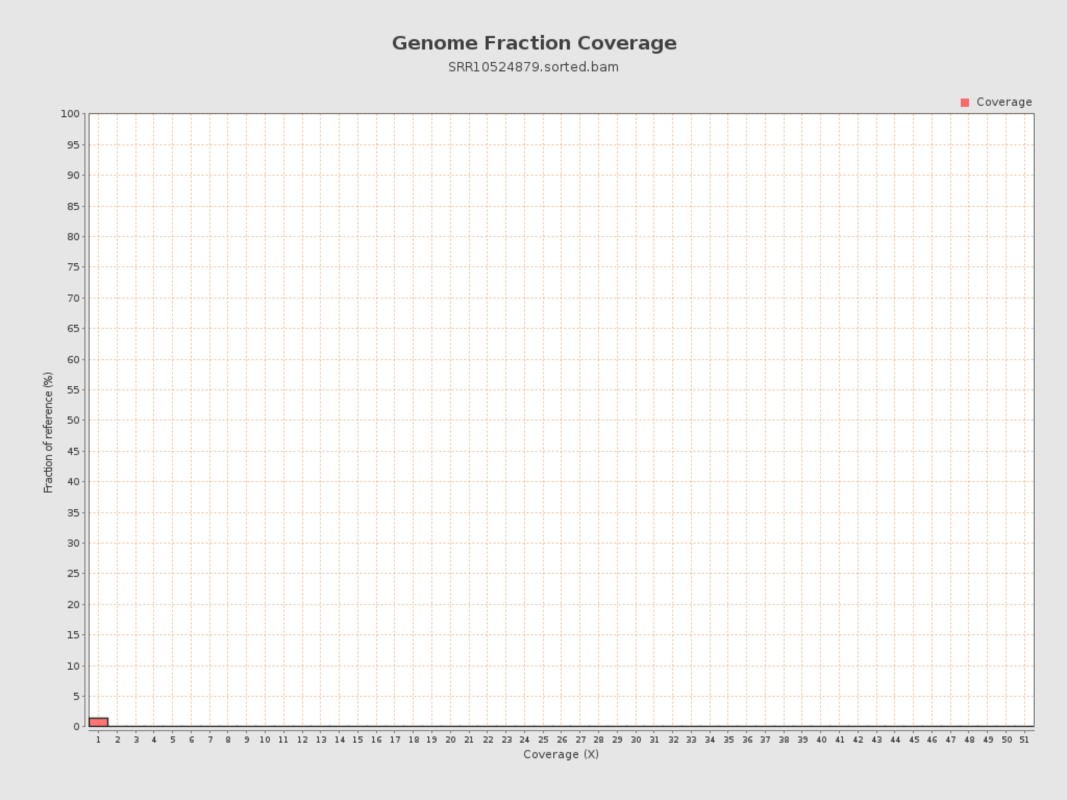
4. Results : Coverage Histogram



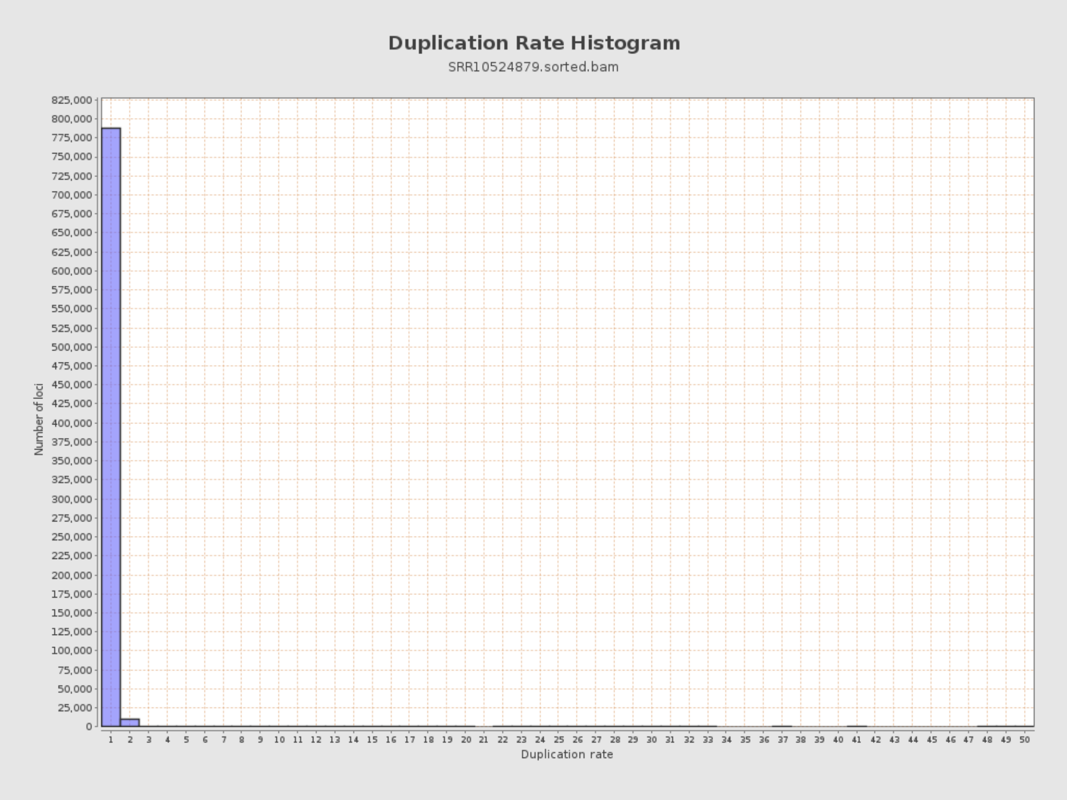
5. Results : Coverage Histogram (0-50X)



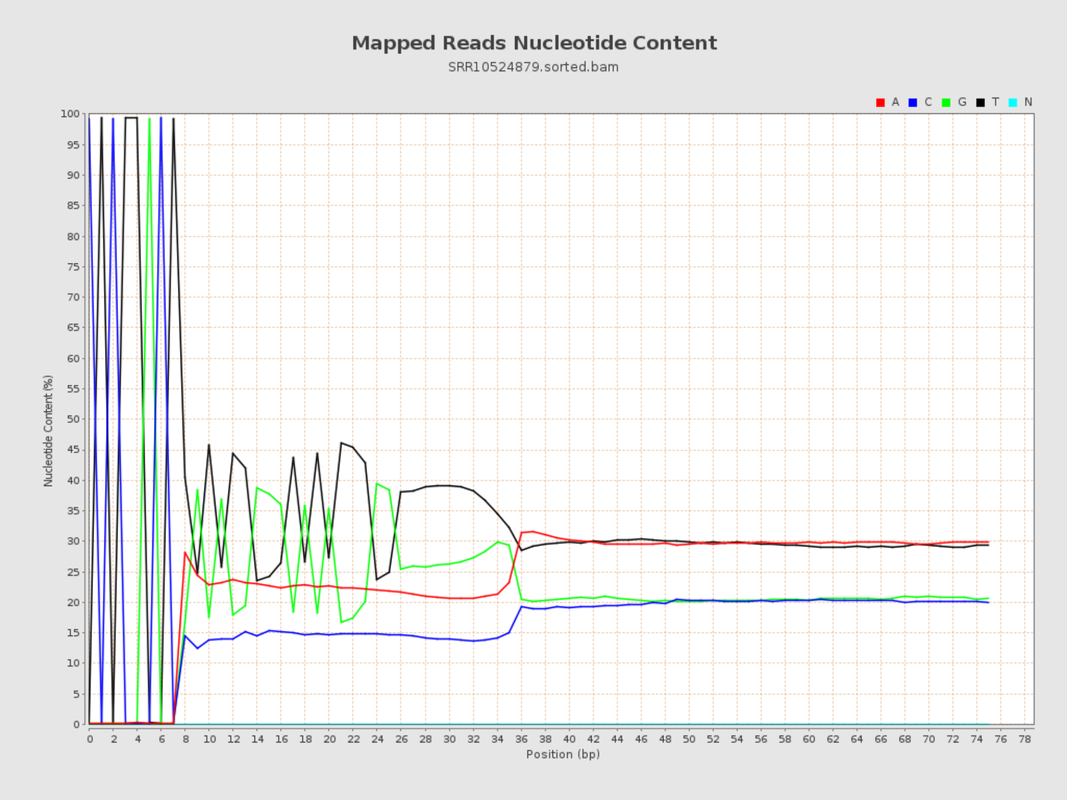
6. Results : Genome Fraction Coverage



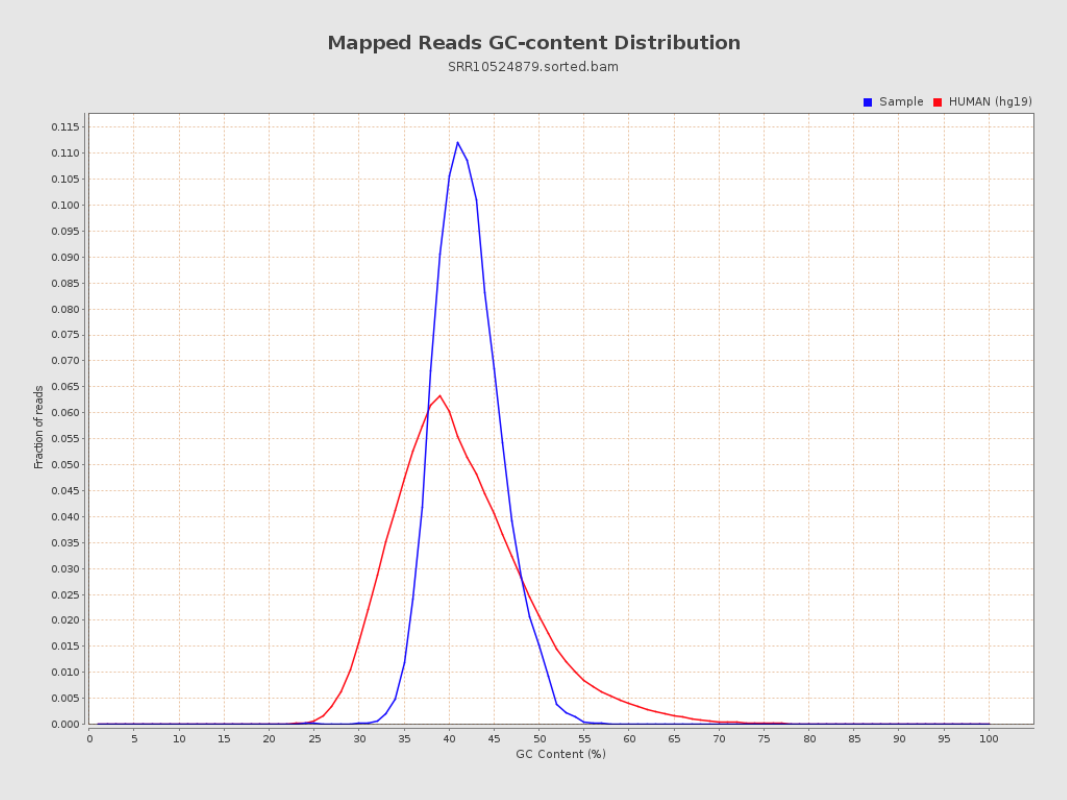
7. Results : Duplication Rate Histogram



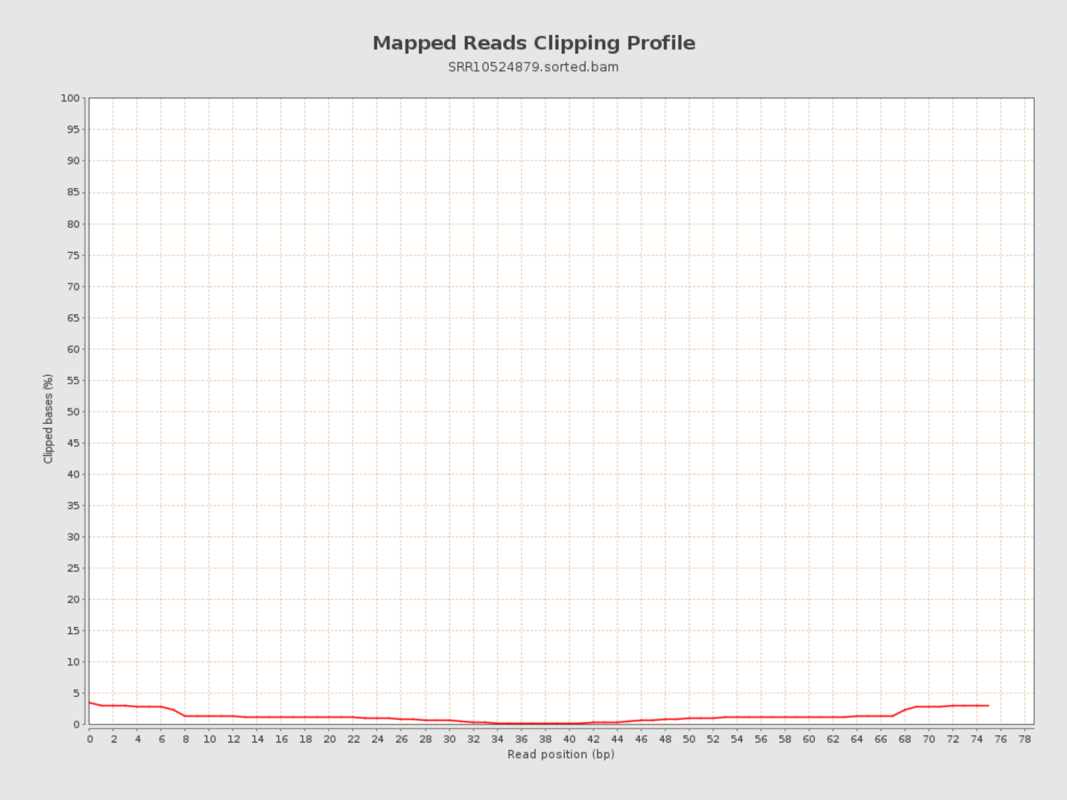
8. Results : Mapped Reads Nucleotide Content



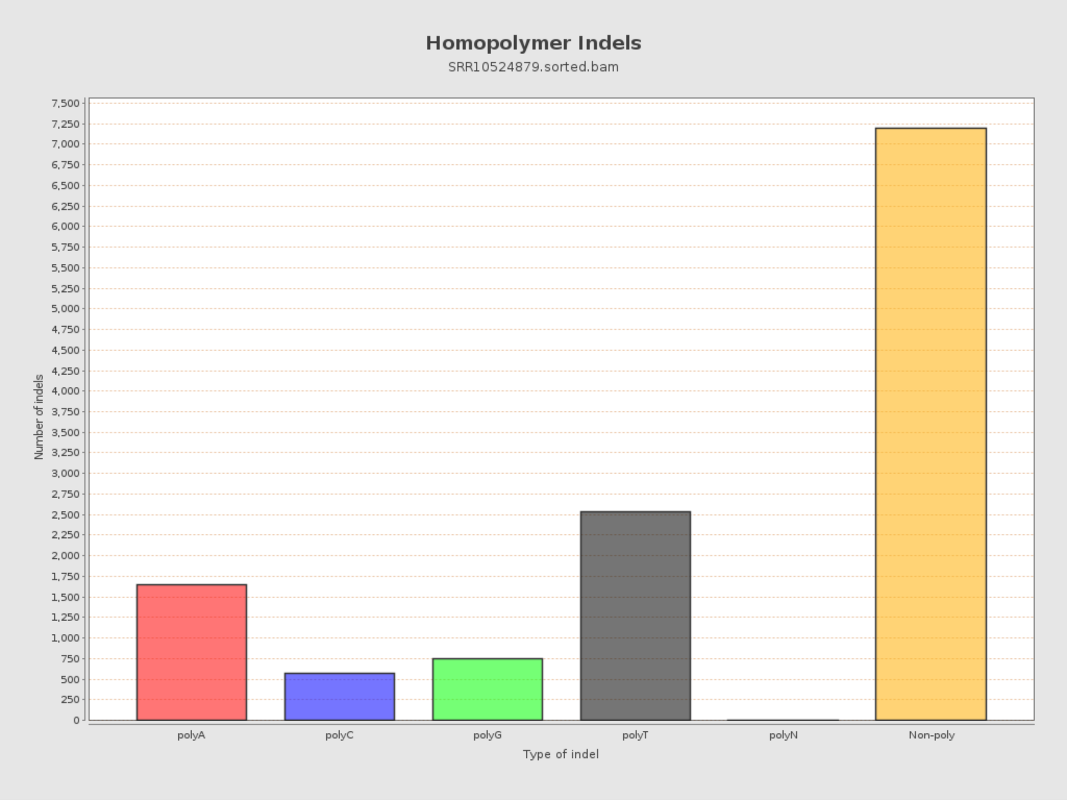
9. Results : Mapped Reads GC-content Distribution



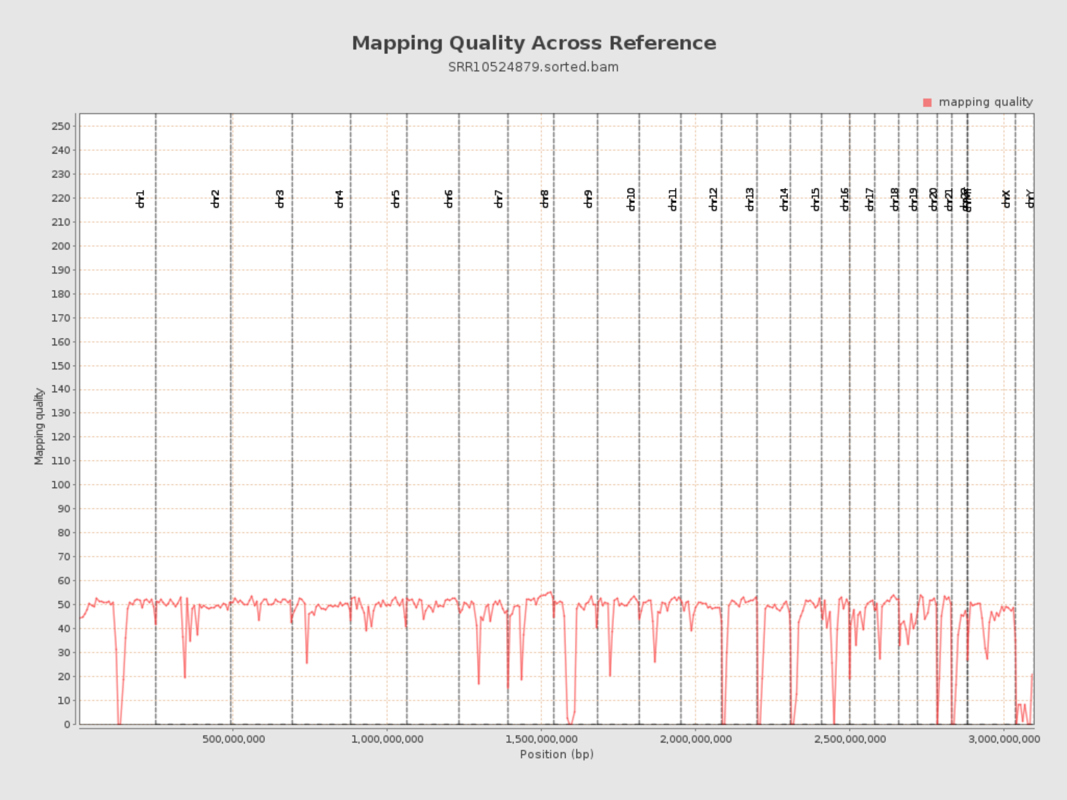
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram