Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 23:58:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524871.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_SRR10524871 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524871.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 23:58:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524871.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	735,017
Mapped reads	676,397 / 92.02%
Unmapped reads	58,620 / 7.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,218 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	13,532 / 1.84%
Duplication rate	1.38%
Clipped reads	678,469 / 92.31%

2.2. ACGT Content

Number/percentage of A's	10,013,945 / 25.45%
Number/percentage of C's	7,114,535 / 18.08%
Number/percentage of T's	12,818,550 / 32.58%
Number/percentage of G's	9,391,604 / 23.87%
Number/percentage of N's	5,476 / 0.01%
GC Percentage	41.95%

2.3. Coverage

Mean	0.0127

Standard Deviation	0.1534

2.4. Mapping Quality

Mean Mapping Quality	45.11

2.5. Mismatches and indels

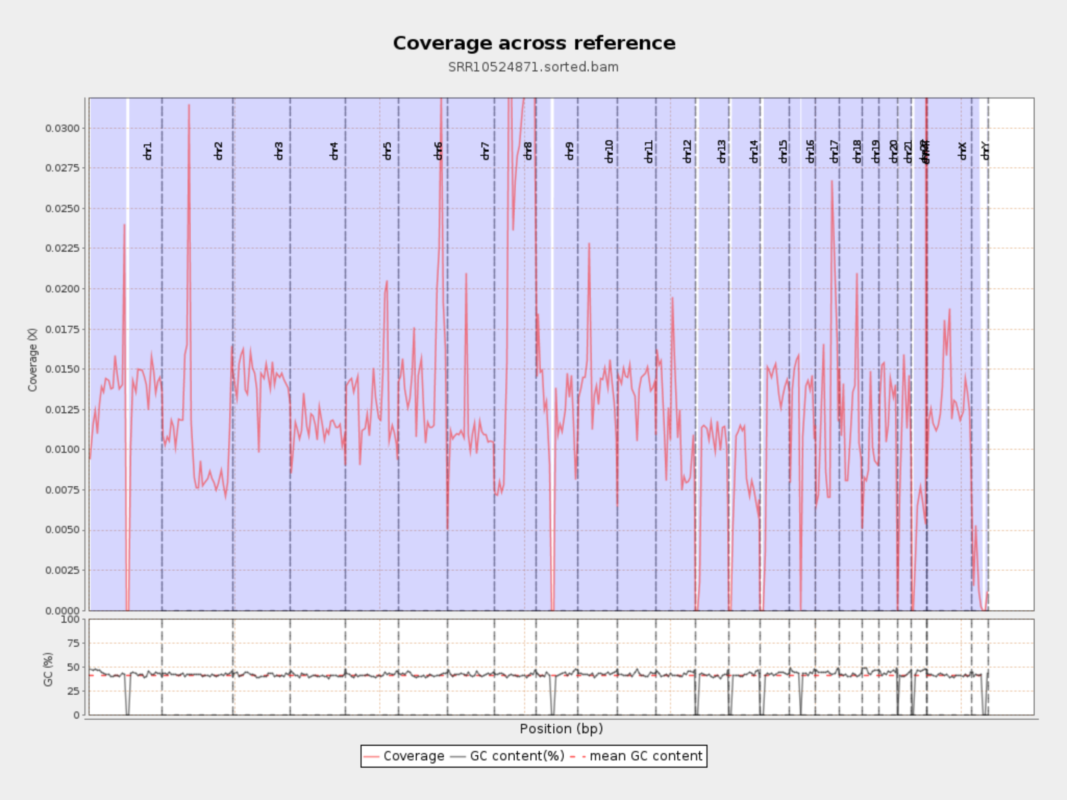
General error rate	0.49%
Mismatches	188,862
Insertions	2,436
Mapped reads with at least one insertion	0.36%
Deletions	7,410
Mapped reads with at least one deletion	1.09%
Homopolymer indels	44.25%

2.6. Chromosome stats

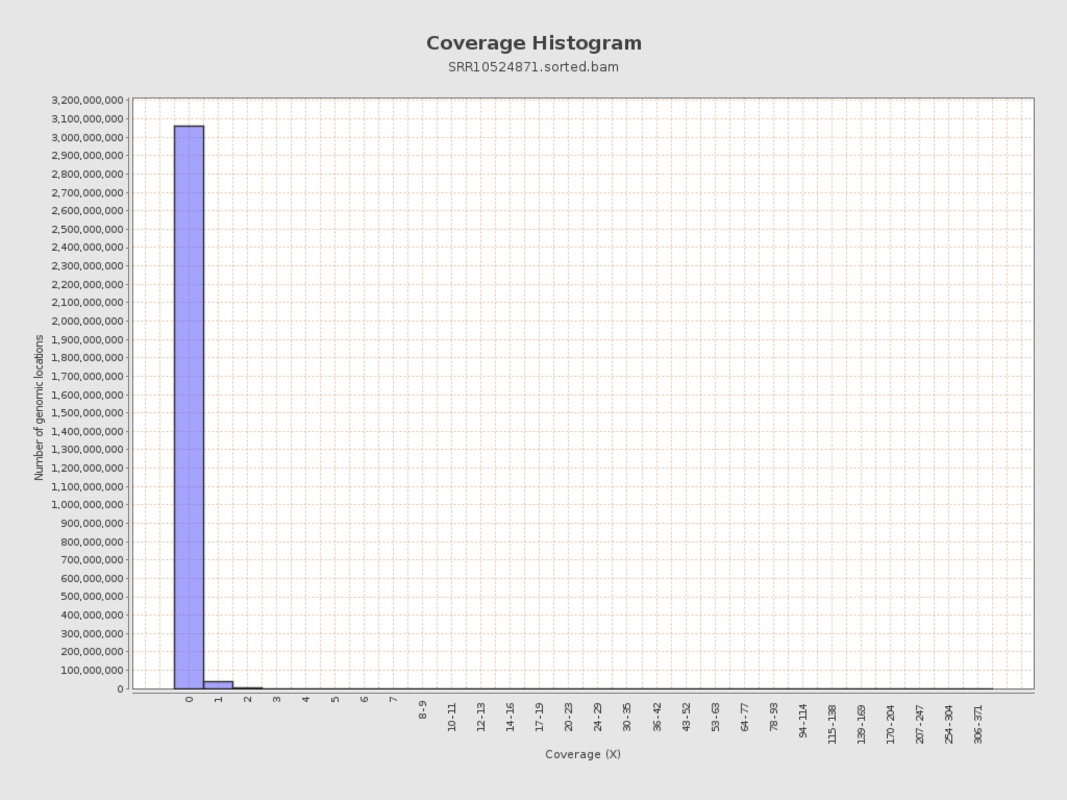
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3277574	0.0131	0.2702
chr2	243199373	2593063	0.0107	0.1461
chr3	198022430	2852844	0.0144	0.1239
chr4	191154276	2160177	0.0113	0.1135
chr5	180915260	2369797	0.0131	0.1183
chr6	171115067	2589518	0.0151	0.1352
chr7	159138663	1791482	0.0113	0.1831

chr8	146364022	4278155	0.0292	0.219
chr9	141213431	1612526	0.0114	0.1333
chr10	135534747	1945735	0.0144	0.1481
chr11	135006516	1885329	0.014	0.1431
chr12	133851895	1553588	0.0116	0.1122
chr13	115169878	1048026	0.0091	0.0985
chr14	107349540	822406	0.0077	0.0927
chr15	102531392	1171991	0.0114	0.1114
chr16	90354753	1114165	0.0123	0.1193
chr17	81195210	1055930	0.013	0.1256
chr18	78077248	960702	0.0123	0.214
chr19	59128983	564563	0.0095	0.1877
chr20	63025520	829462	0.0132	0.1196
chr21	48129895	513709	0.0107	0.1109
chr22	51304566	241667	0.0047	0.0703
chrMT	16571	3026	0.1826	0.445
chrX	155270560	2027062	0.0131	0.1267
chrY	59373566	93336	0.0016	0.0494

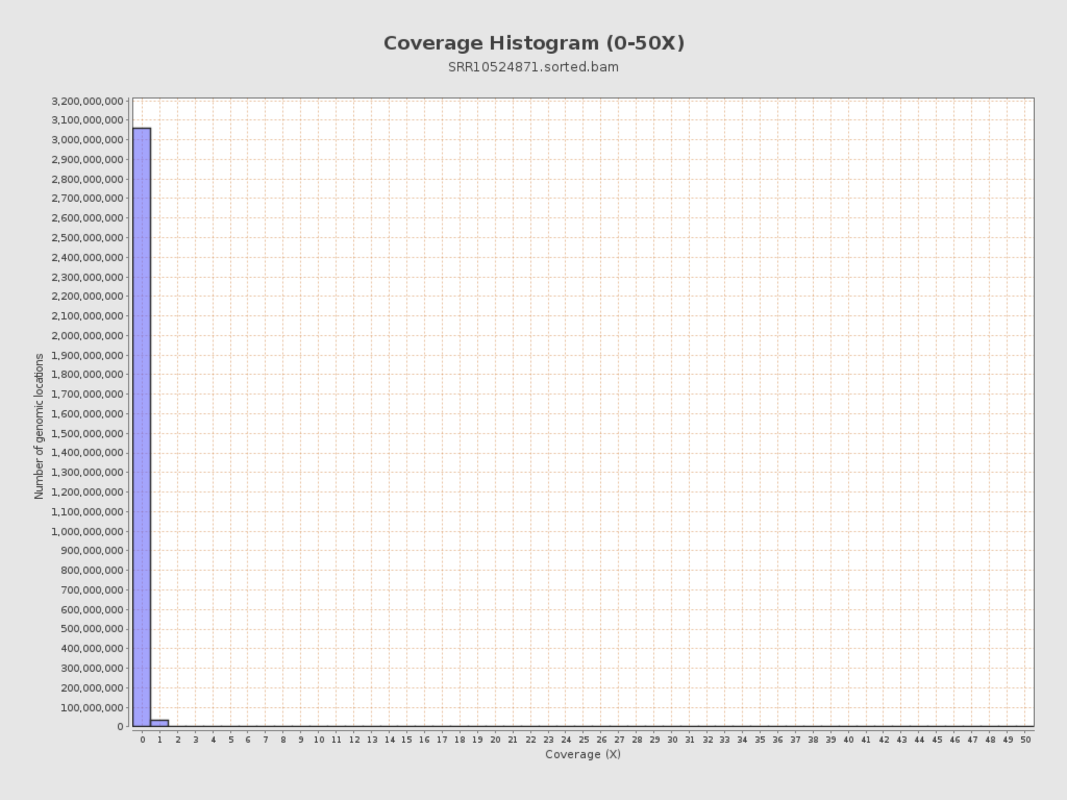
3. Results : Coverage across reference



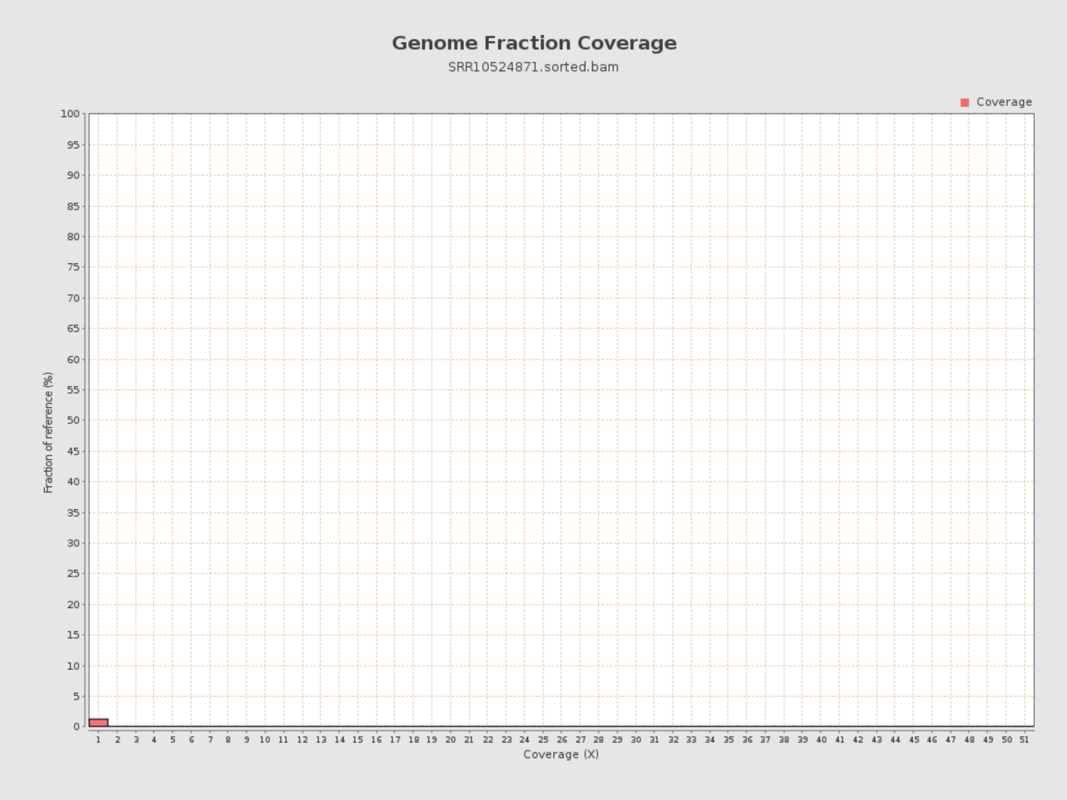
4. Results : Coverage Histogram



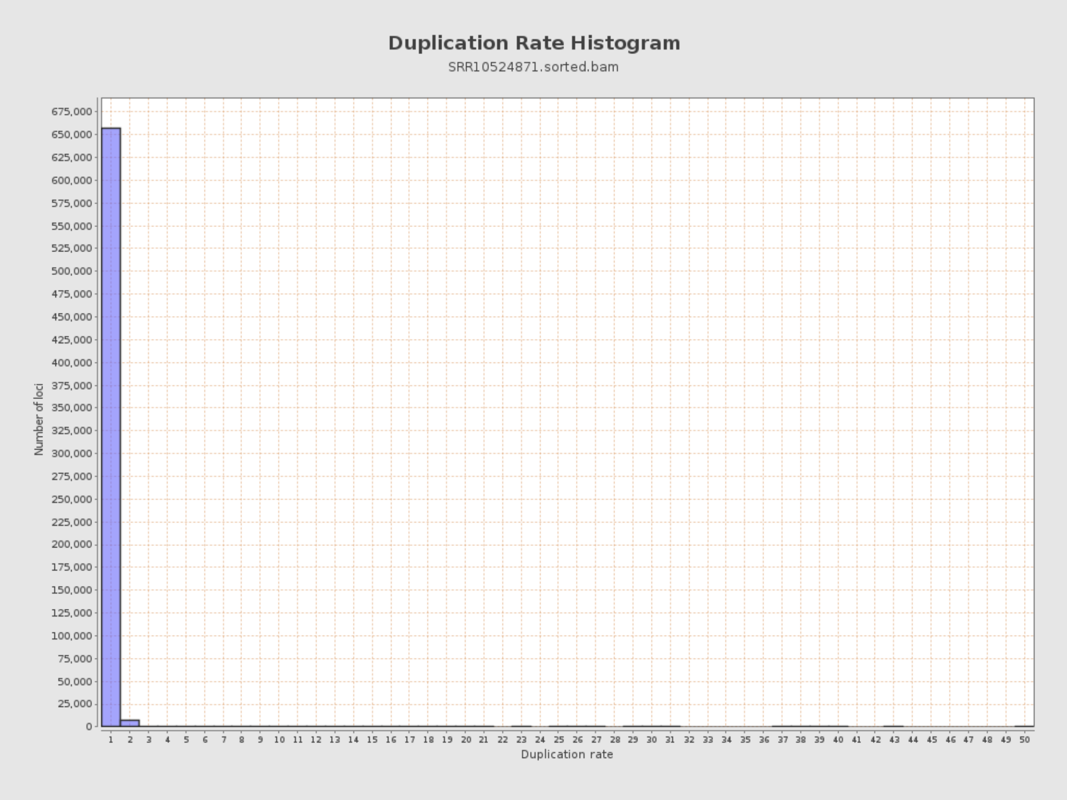
5. Results : Coverage Histogram (0-50X)



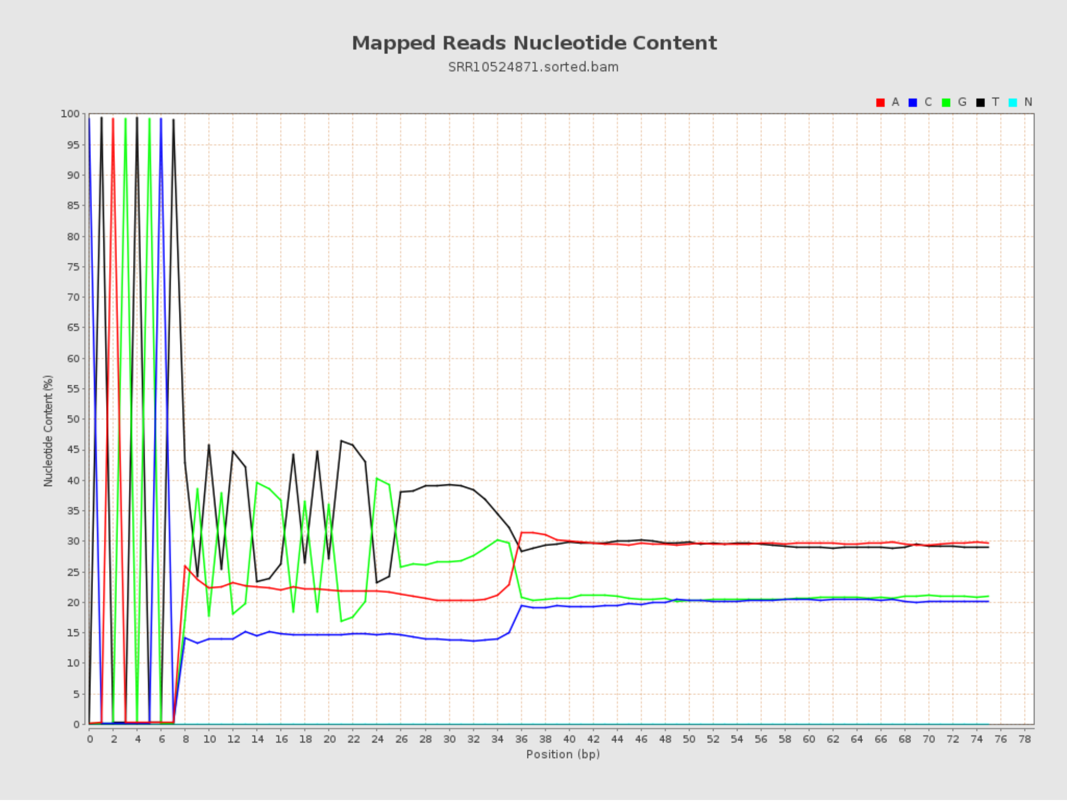
6. Results : Genome Fraction Coverage



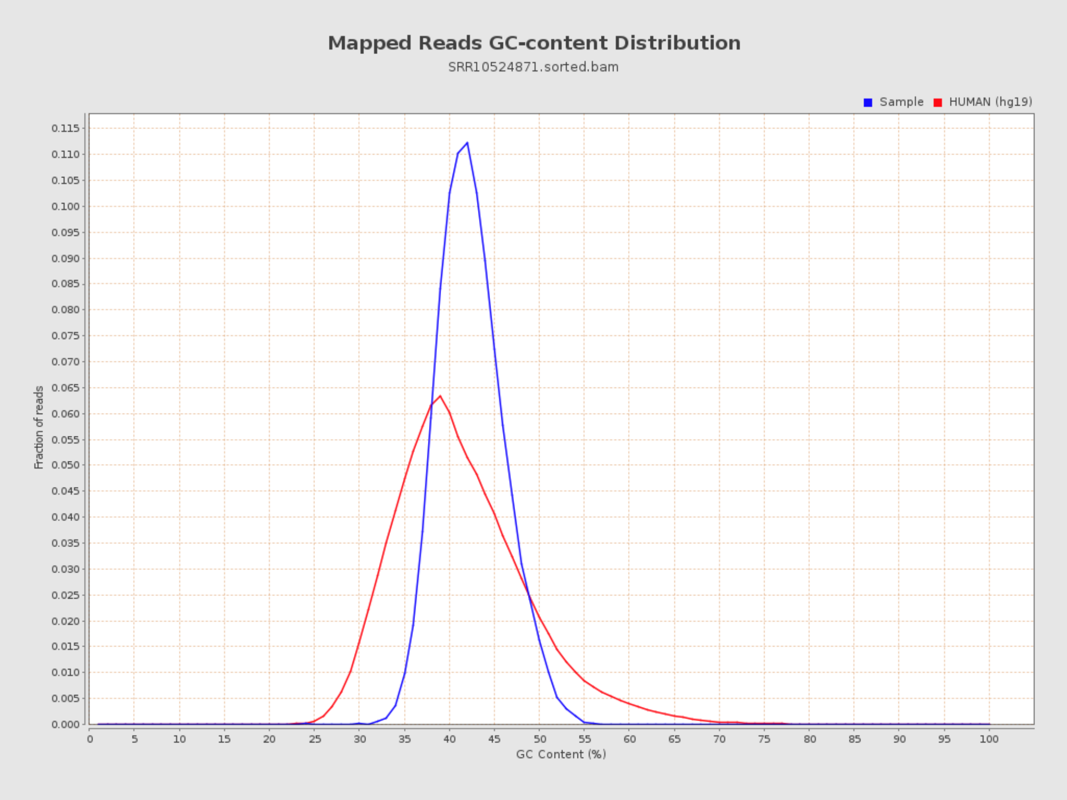
7. Results : Duplication Rate Histogram



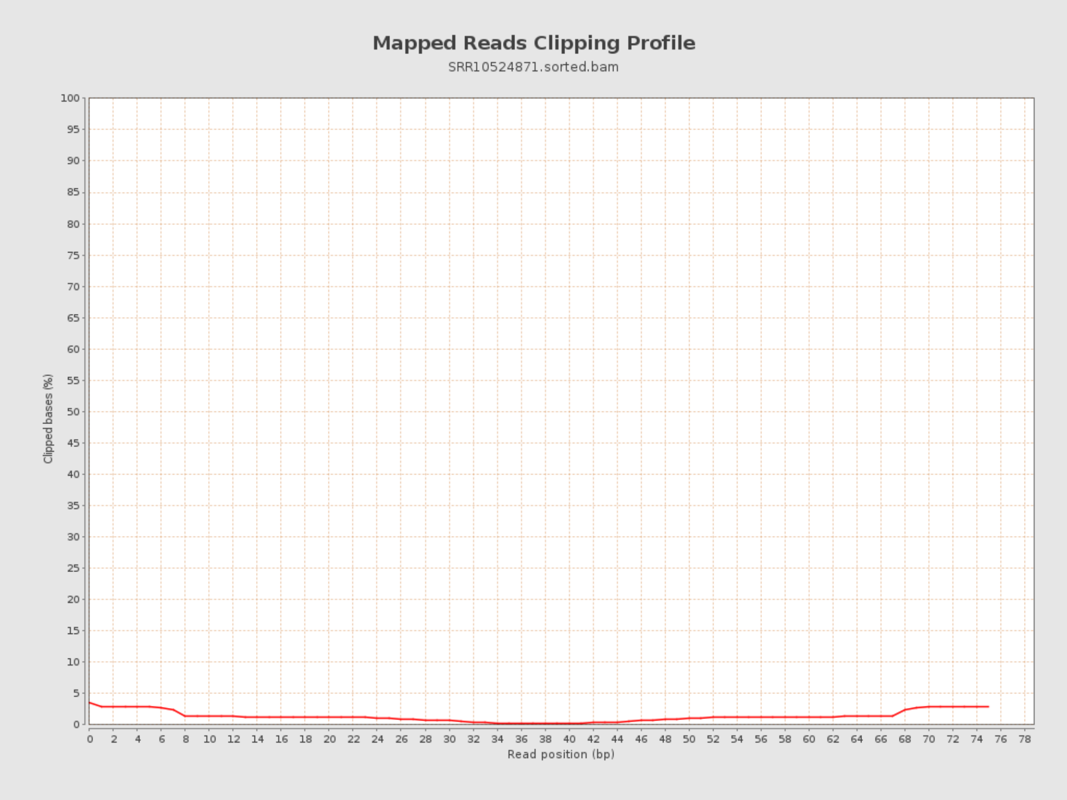
8. Results : Mapped Reads Nucleotide Content



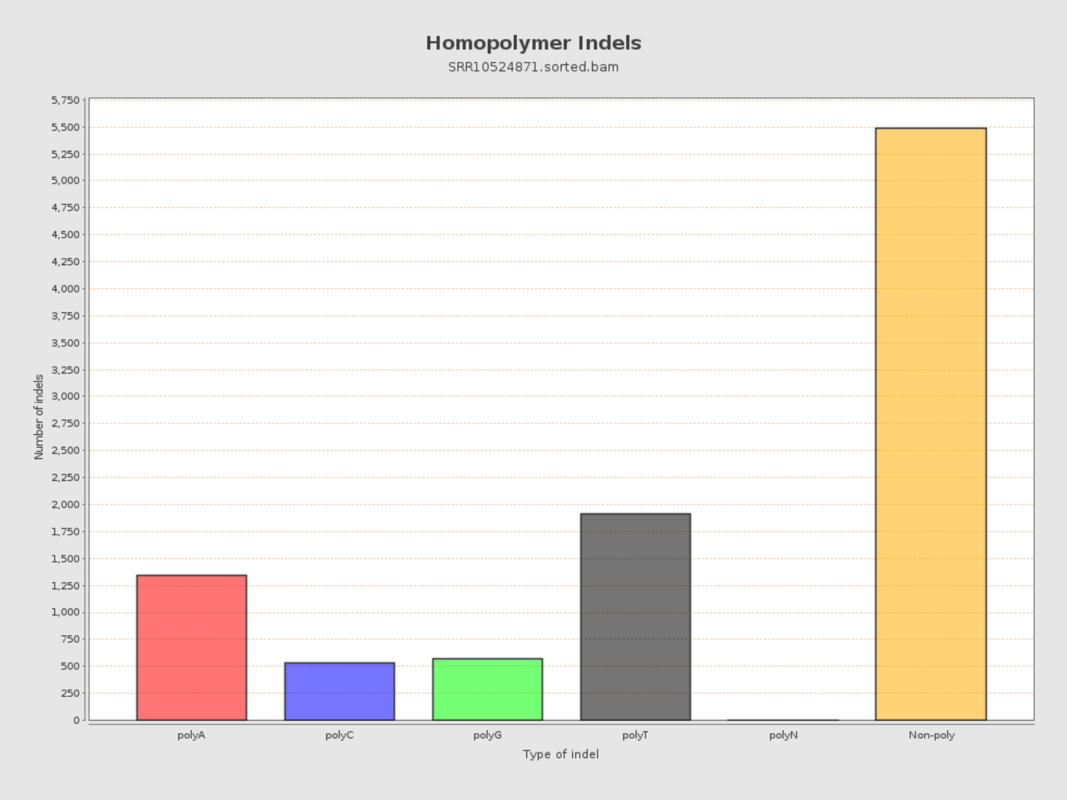
9. Results : Mapped Reads GC-content Distribution



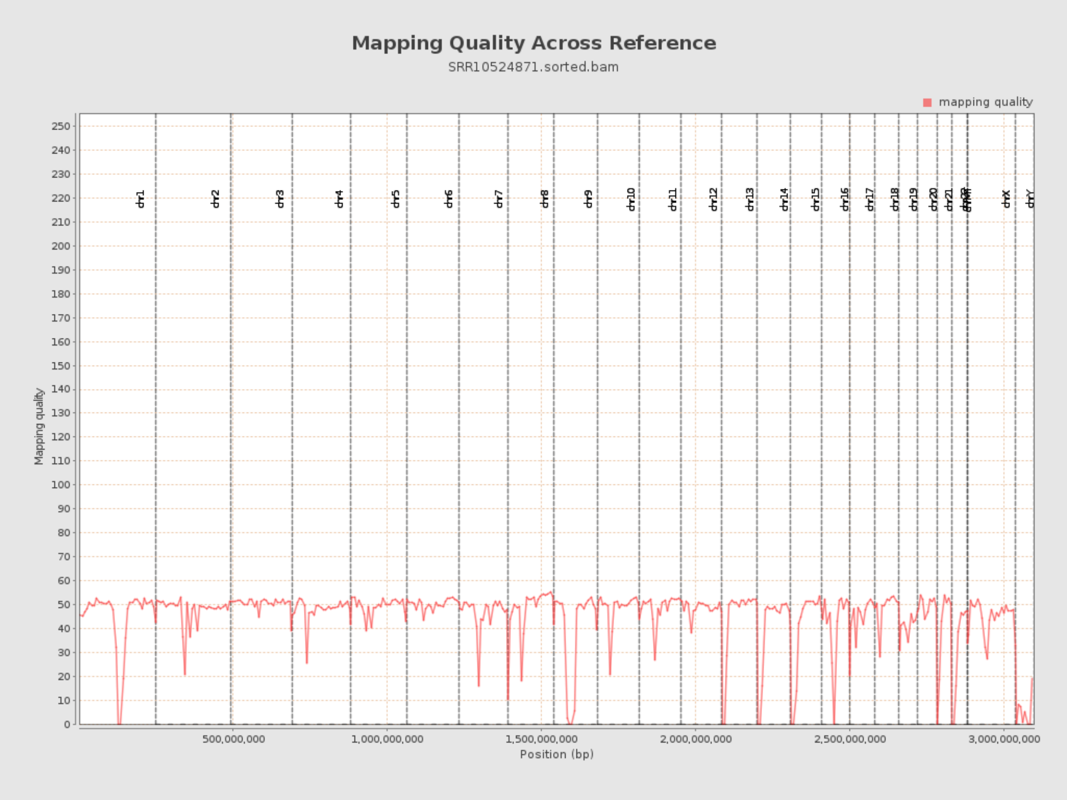
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram