Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 18:59:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524463.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_SRR10524463 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524463.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 18:59:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524463.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	800,628
Mapped reads	737,909 / 92.17%
Unmapped reads	62,719 / 7.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,547 / 0.19%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	20,783 / 2.6%
Duplication rate	2.17%
Clipped reads	739,028 / 92.31%

2.2. ACGT Content

Number/percentage of A's	10,754,160 / 24.95%
Number/percentage of C's	8,394,216 / 19.47%
Number/percentage of T's	13,437,319 / 31.17%
Number/percentage of G's	10,522,392 / 24.41%
Number/percentage of N's	812 / 0%
GC Percentage	43.88%

2.3. Coverage

Mean	0.0139

Standard Deviation	0.1587

2.4. Mapping Quality

Mean Mapping Quality	45.2

2.5. Mismatches and indels

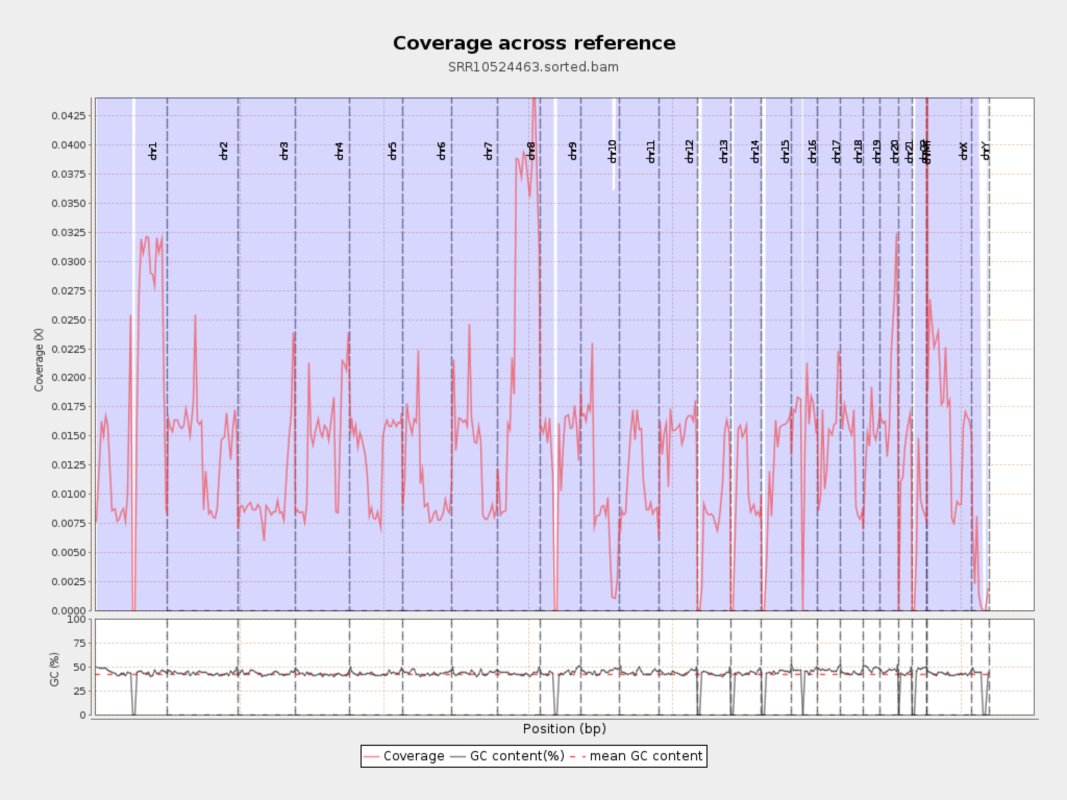
General error rate	0.48%
Mismatches	203,551
Insertions	2,171
Mapped reads with at least one insertion	0.29%
Deletions	7,835
Mapped reads with at least one deletion	1.05%
Homopolymer indels	44.85%

2.6. Chromosome stats

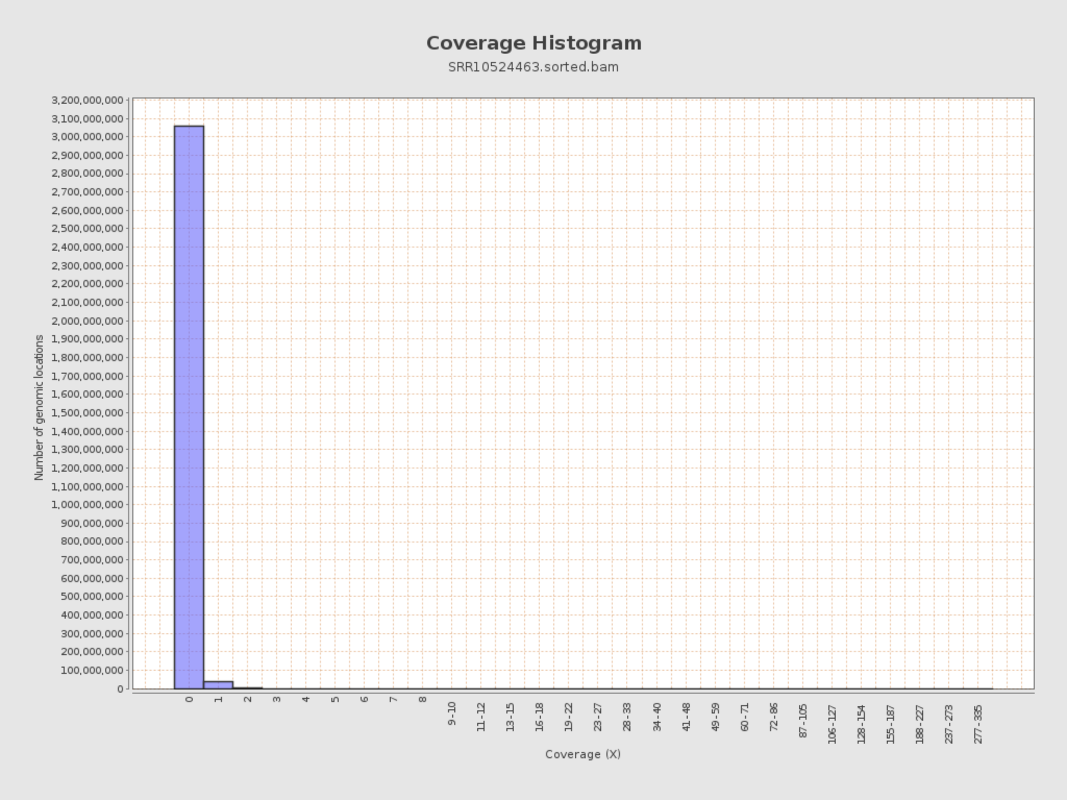
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4416177	0.0177	0.2655
chr2	243199373	3528939	0.0145	0.1715
chr3	198022430	1975836	0.01	0.106
chr4	191154276	2780215	0.0145	0.1354
chr5	180915260	2435449	0.0135	0.1229
chr6	171115067	1937204	0.0113	0.1303
chr7	159138663	2224930	0.014	0.194

chr8	146364022	4060693	0.0277	0.1907
chr9	141213431	1903512	0.0135	0.1461
chr10	135534747	1392655	0.0103	0.1414
chr11	135006516	1541456	0.0114	0.1474
chr12	133851895	2083155	0.0156	0.1321
chr13	115169878	989081	0.0086	0.0982
chr14	107349540	1065875	0.0099	0.1065
chr15	102531392	1185319	0.0116	0.1164
chr16	90354753	1411647	0.0156	0.1364
chr17	81195210	1192580	0.0147	0.1331
chr18	78077248	1050888	0.0135	0.2255
chr19	59128983	881417	0.0149	0.1967
chr20	63025520	1282782	0.0204	0.153
chr21	48129895	608129	0.0126	0.1245
chr22	51304566	371264	0.0072	0.0898
chrMT	16571	2080	0.1255	0.3477
chrX	155270560	2656503	0.0171	0.1493
chrY	59373566	144741	0.0024	0.073

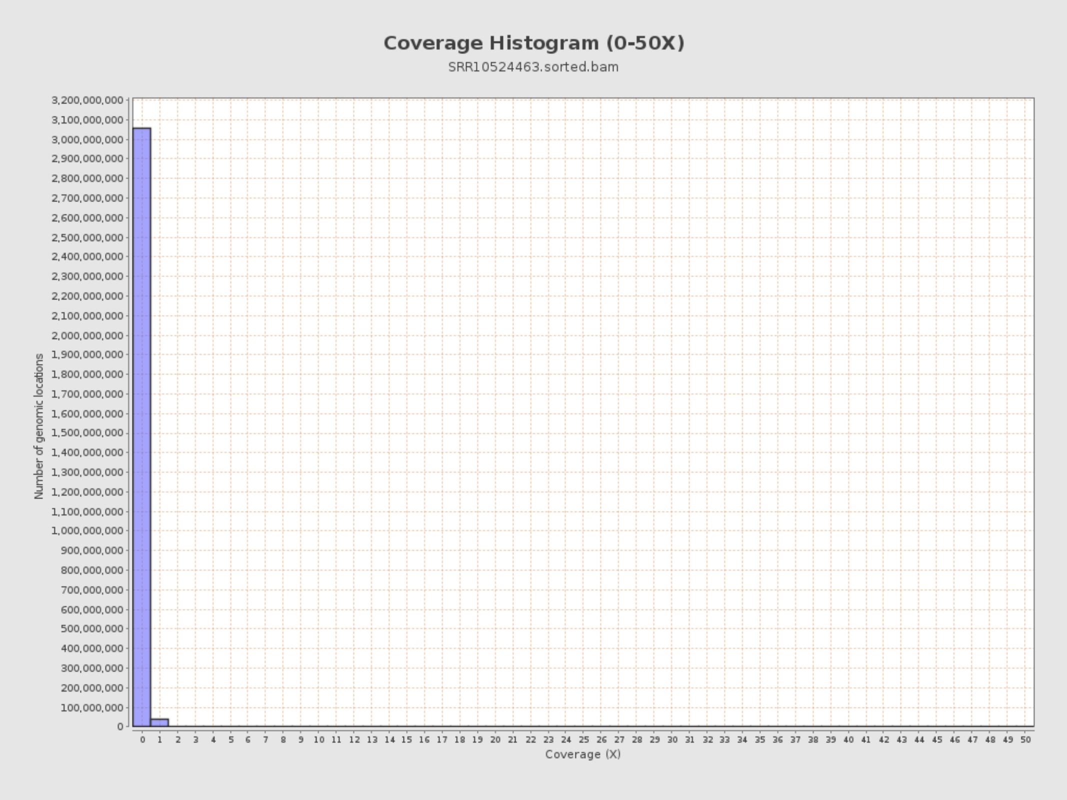
3. Results : Coverage across reference



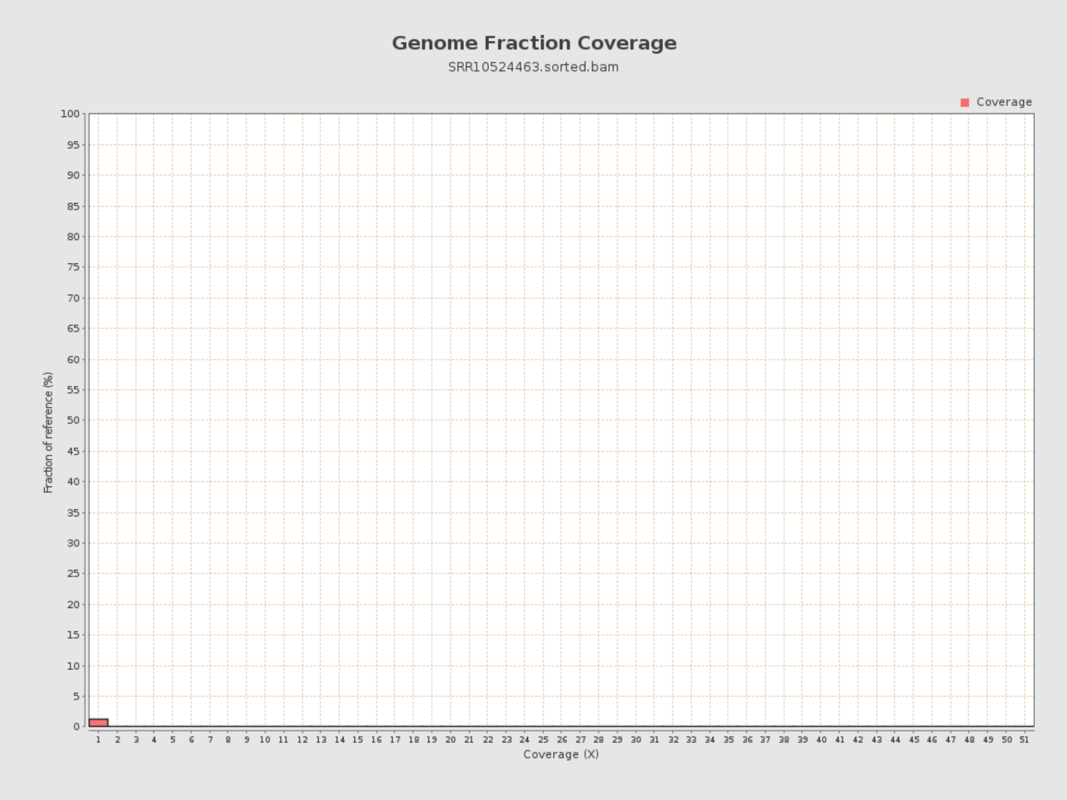
4. Results : Coverage Histogram



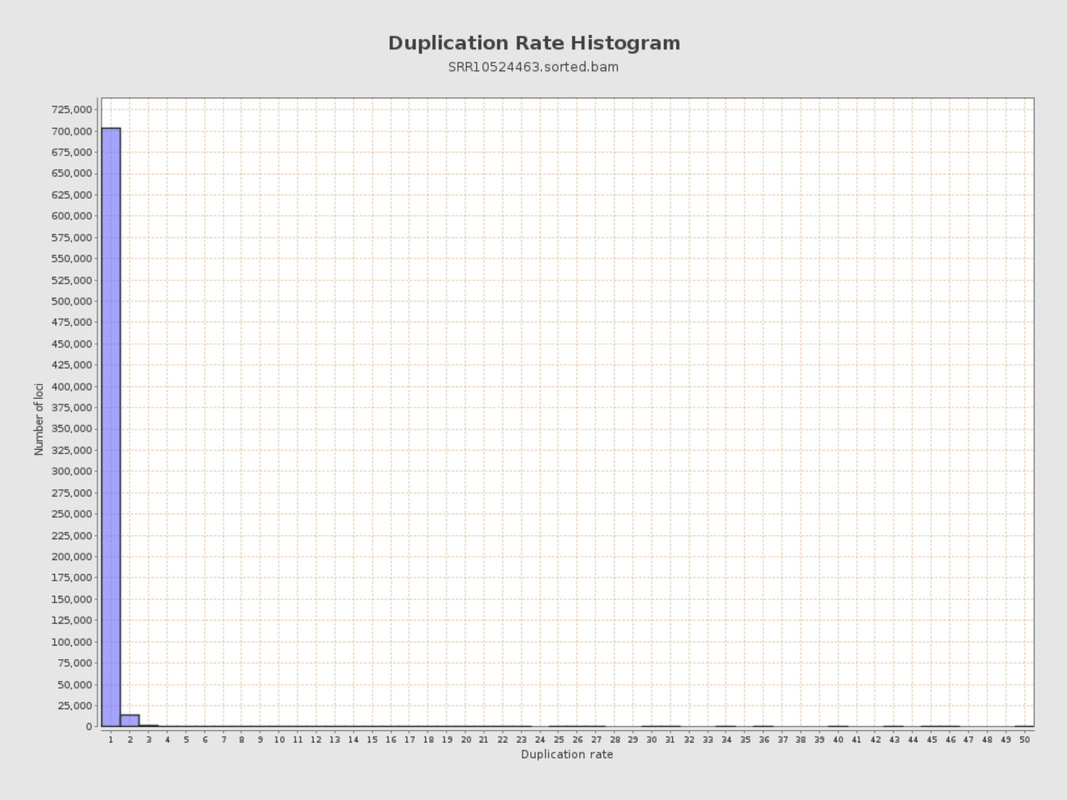
5. Results : Coverage Histogram (0-50X)



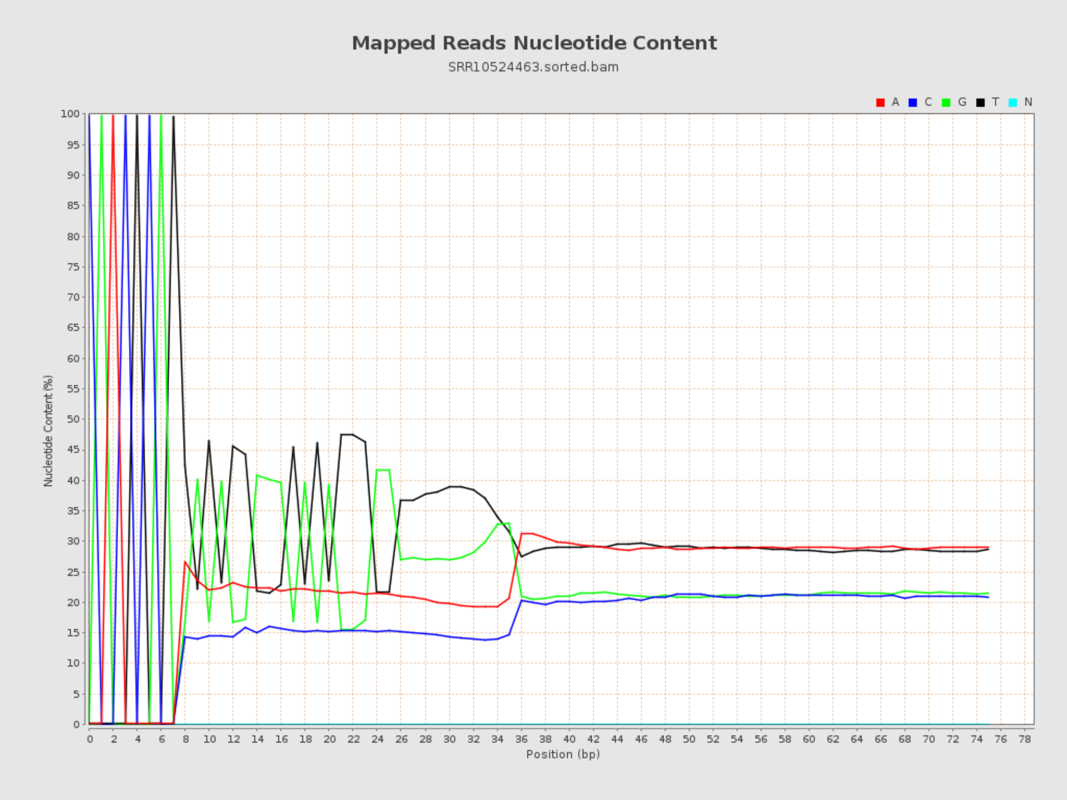
6. Results : Genome Fraction Coverage



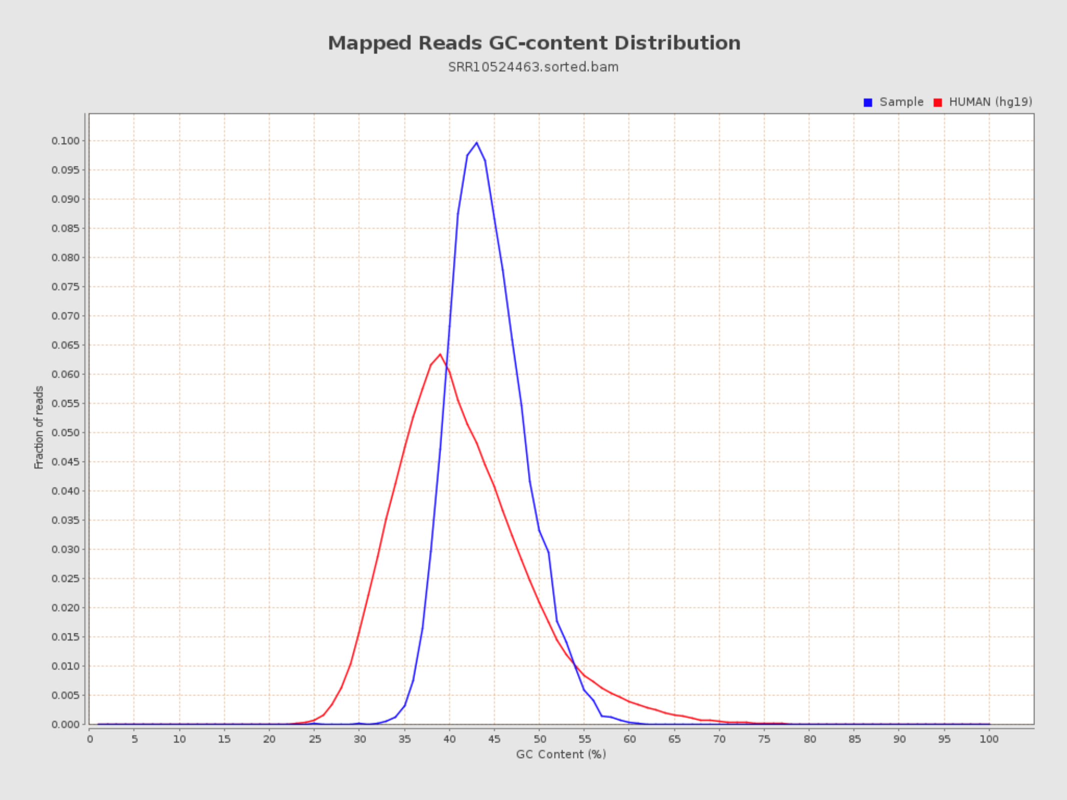
7. Results : Duplication Rate Histogram



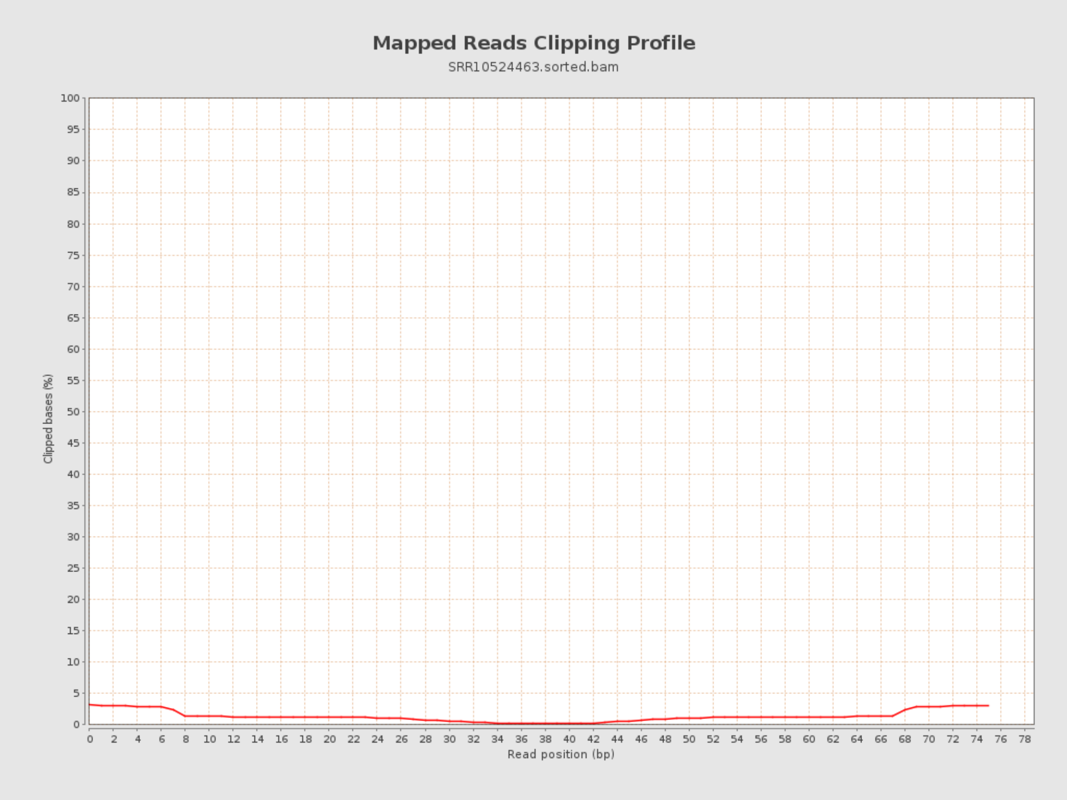
8. Results : Mapped Reads Nucleotide Content



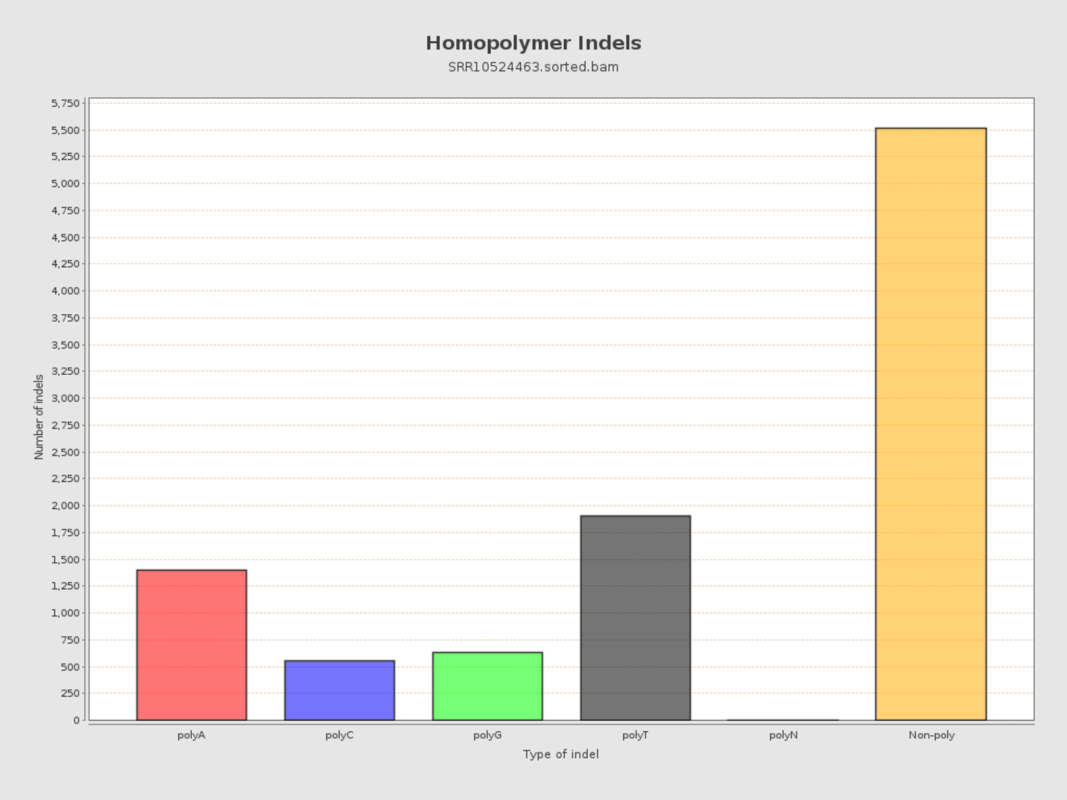
9. Results : Mapped Reads GC-content Distribution



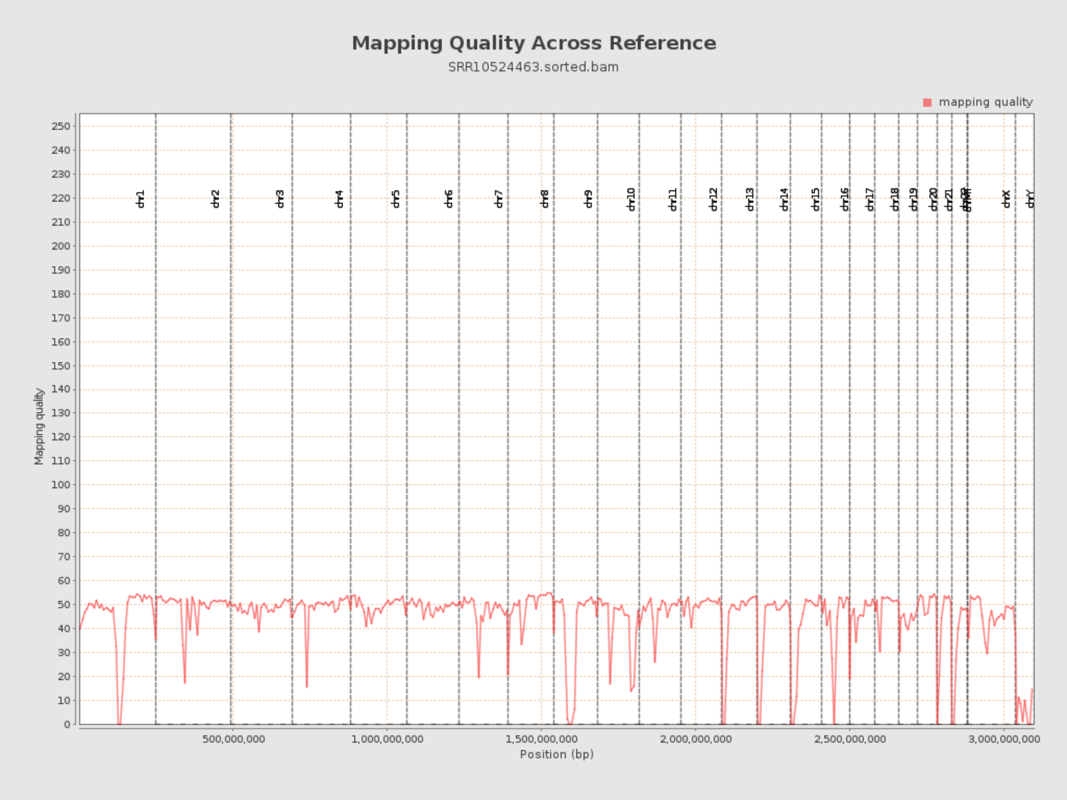
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram