Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 05:27:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524469.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_SRR10524469 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524469.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 05:27:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524469.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	524,511
Mapped reads	487,467 / 92.94%
Unmapped reads	37,044 / 7.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,020 / 0.19%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	11,554 / 2.2%
Duplication rate	1.88%
Clipped reads	487,341 / 92.91%

2.2. ACGT Content

Number/percentage of A's	7,044,898 / 24.74%
Number/percentage of C's	5,796,734 / 20.35%
Number/percentage of T's	8,638,995 / 30.33%
Number/percentage of G's	7,000,034 / 24.58%
Number/percentage of N's	645 / 0%
GC Percentage	44.93%

2.3. Coverage

Mean	0.0092

Standard Deviation	0.117

2.4. Mapping Quality

Mean Mapping Quality	45.56

2.5. Mismatches and indels

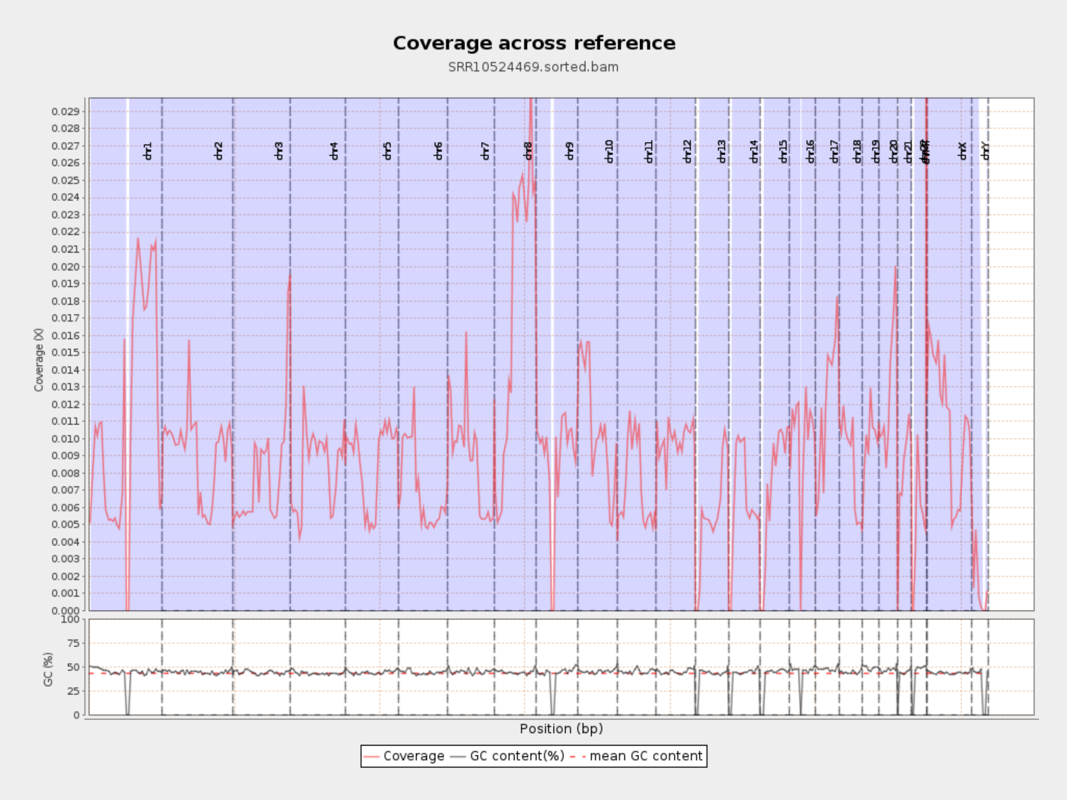
General error rate	0.48%
Mismatches	132,599
Insertions	1,877
Mapped reads with at least one insertion	0.38%
Deletions	5,185
Mapped reads with at least one deletion	1.05%
Homopolymer indels	43.49%

2.6. Chromosome stats

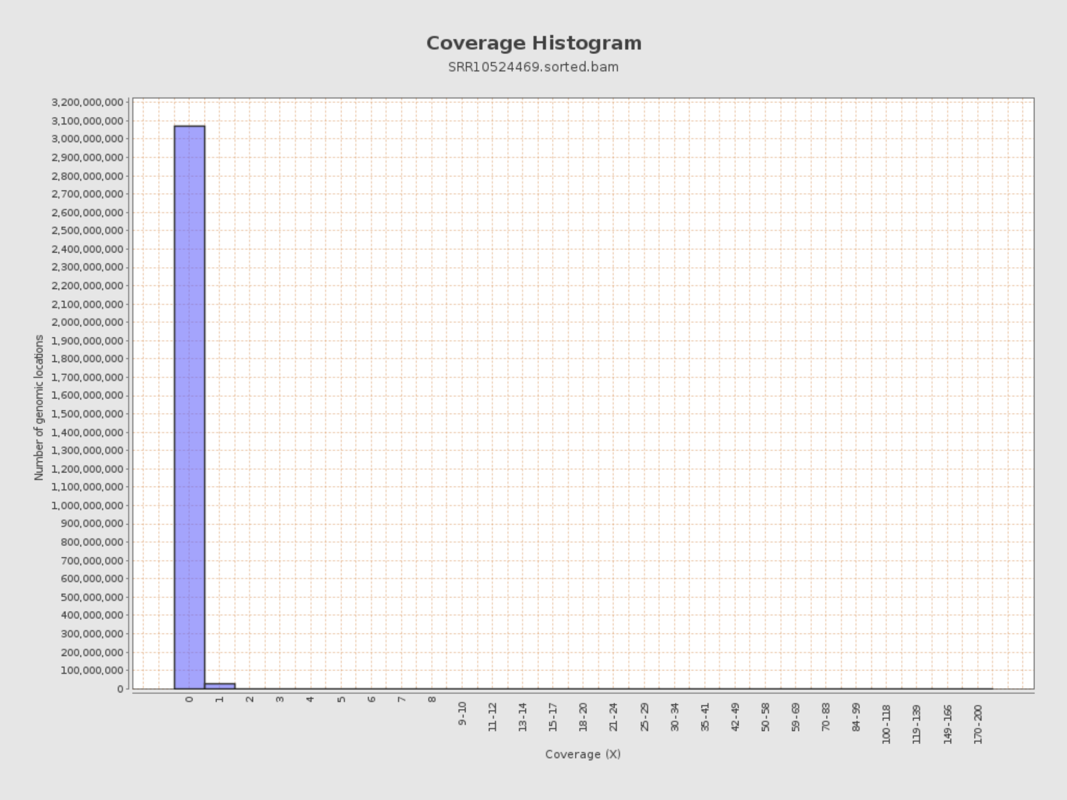
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2847485	0.0114	0.1753
chr2	243199373	2246716	0.0092	0.1272
chr3	198022430	1546100	0.0078	0.0923
chr4	191154276	1589372	0.0083	0.1001
chr5	180915260	1572255	0.0087	0.0976
chr6	171115067	1206226	0.007	0.0953
chr7	159138663	1409570	0.0089	0.1325

chr8	146364022	2616337	0.0179	0.1485
chr9	141213431	1215331	0.0086	0.1085
chr10	135534747	1458758	0.0108	0.121
chr11	135006516	983940	0.0073	0.1064
chr12	133851895	1333495	0.01	0.1045
chr13	115169878	629162	0.0055	0.0776
chr14	107349540	682191	0.0064	0.0839
chr15	102531392	741006	0.0072	0.0898
chr16	90354753	895310	0.0099	0.1061
chr17	81195210	995309	0.0123	0.118
chr18	78077248	678861	0.0087	0.1495
chr19	59128983	588051	0.0099	0.1487
chr20	63025520	817335	0.013	0.1195
chr21	48129895	387477	0.0081	0.0957
chr22	51304566	243684	0.0047	0.0719
chrMT	16571	2166	0.1307	0.4127
chrX	155270560	1718212	0.0111	0.1138
chrY	59373566	85849	0.0014	0.0519

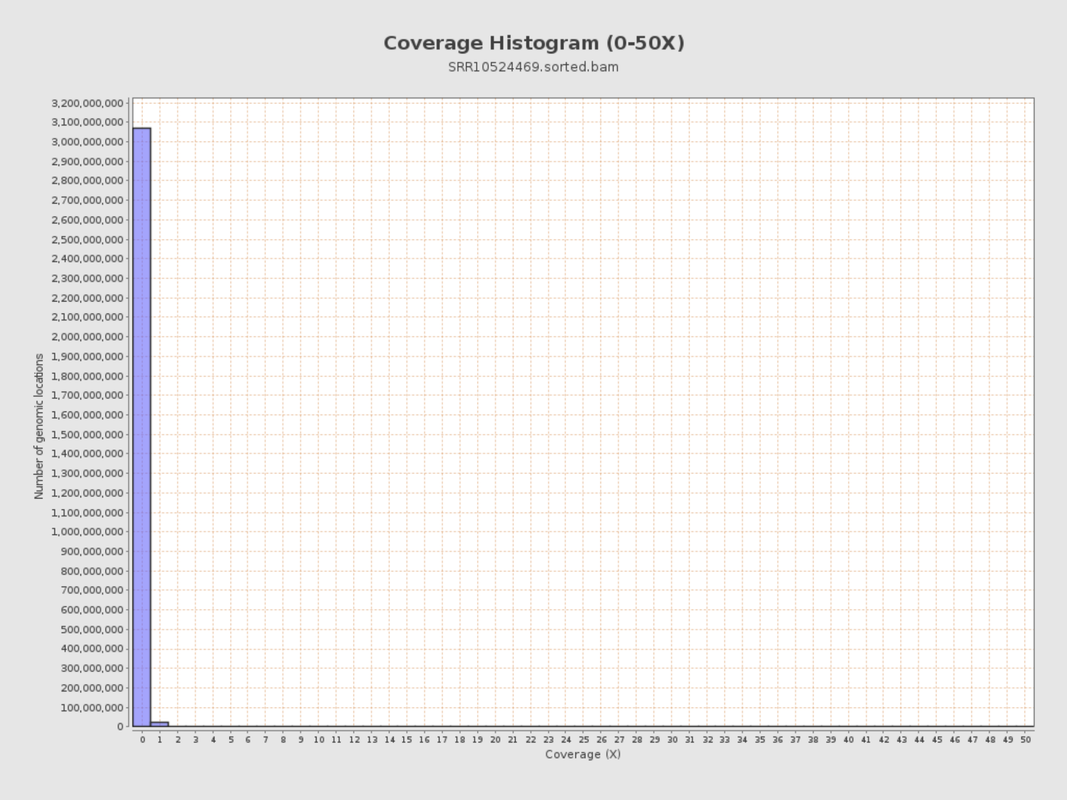
3. Results : Coverage across reference



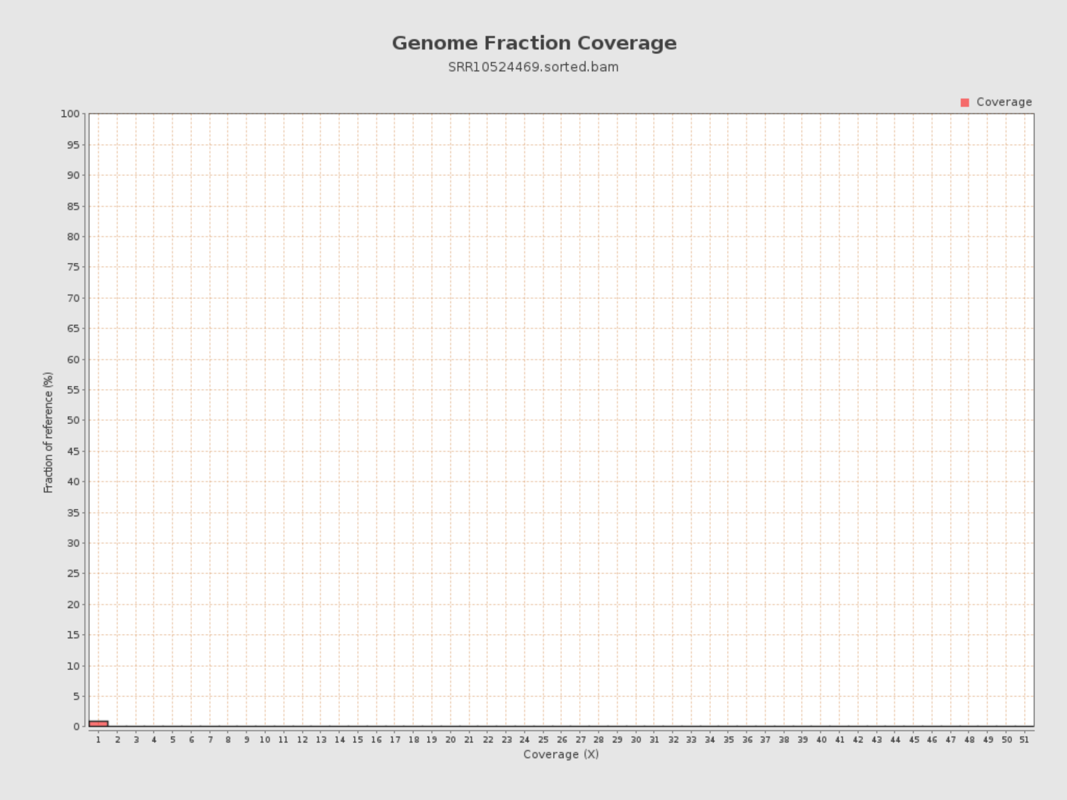
4. Results : Coverage Histogram



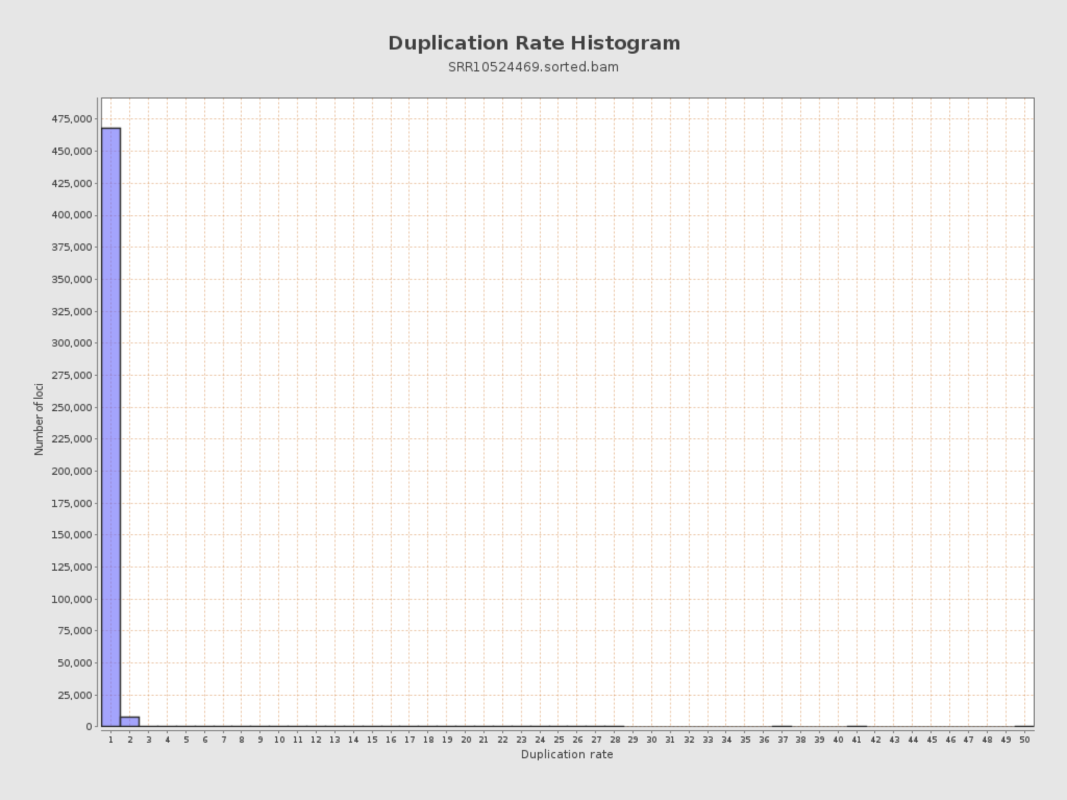
5. Results : Coverage Histogram (0-50X)



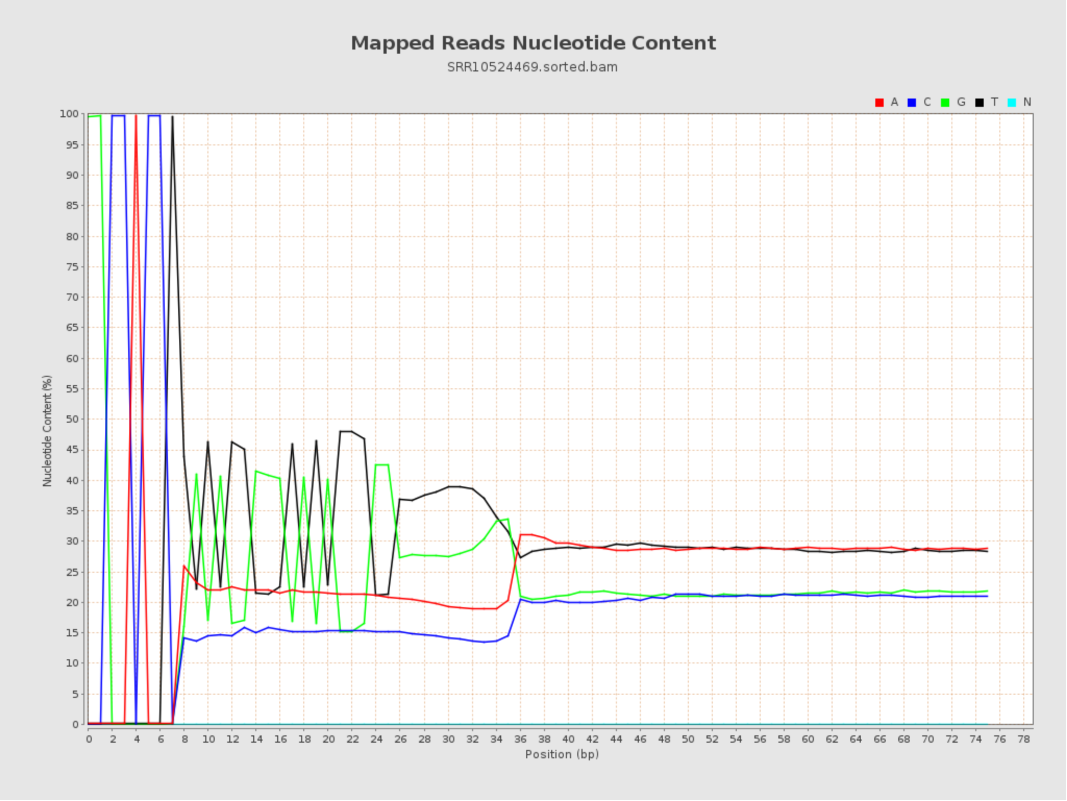
6. Results : Genome Fraction Coverage



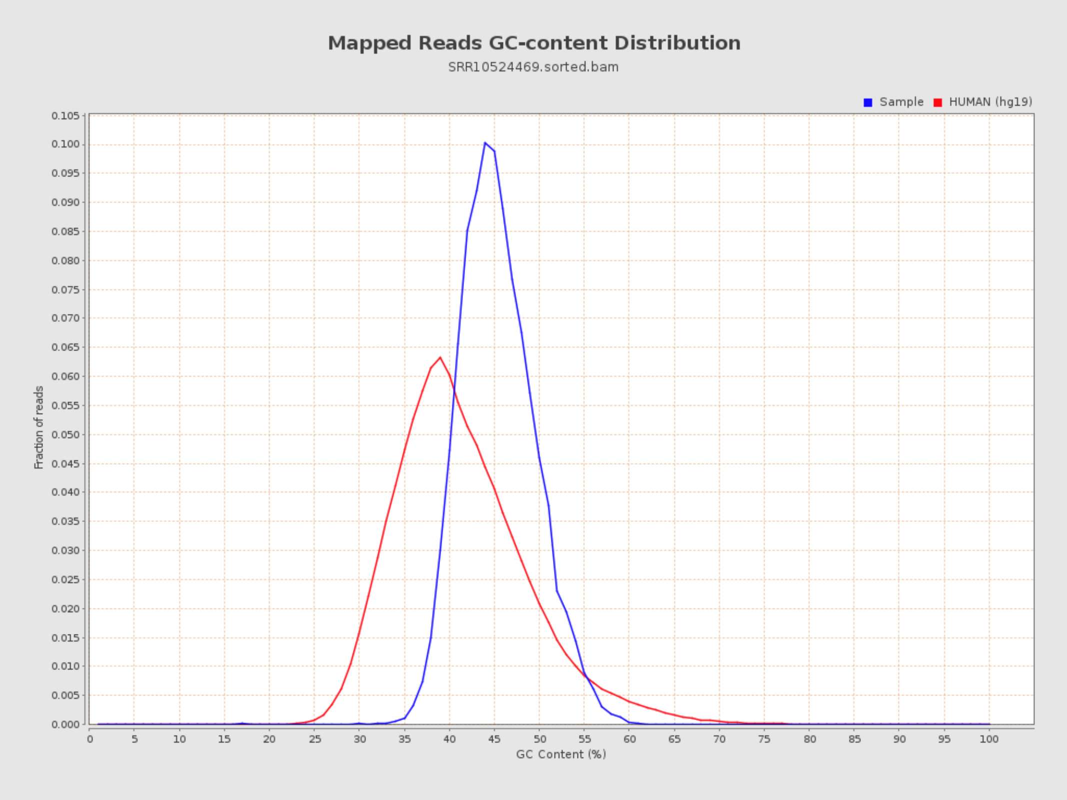
7. Results : Duplication Rate Histogram



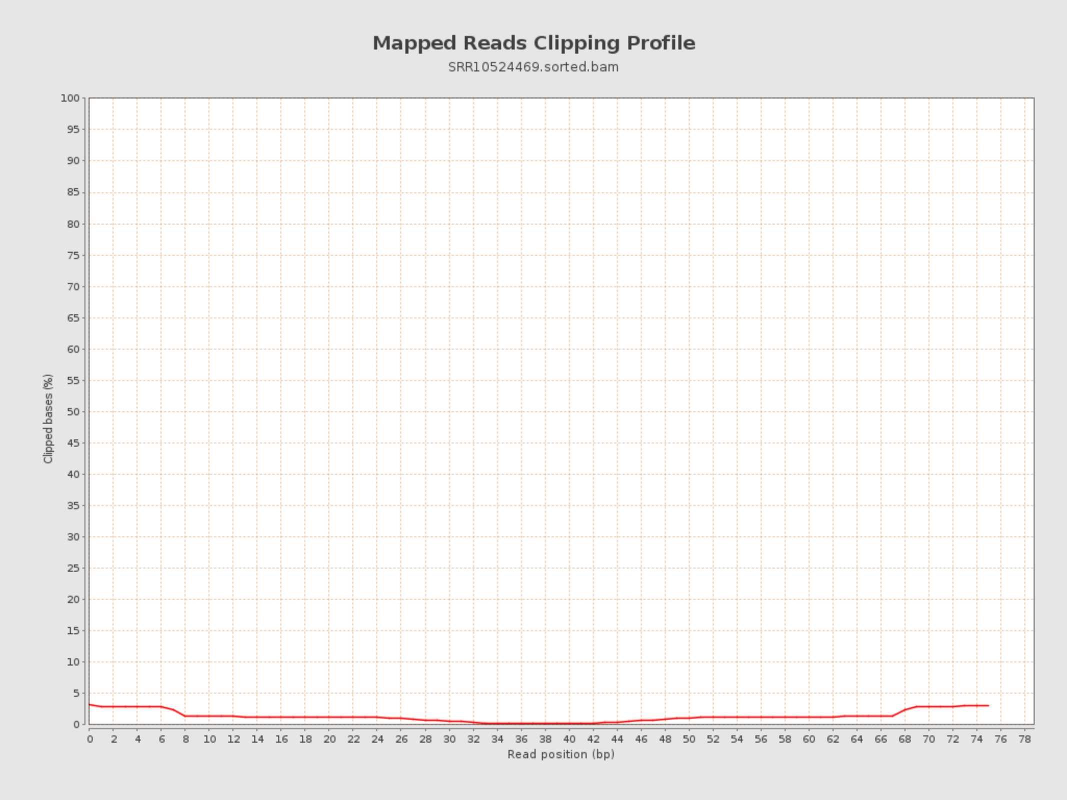
8. Results : Mapped Reads Nucleotide Content



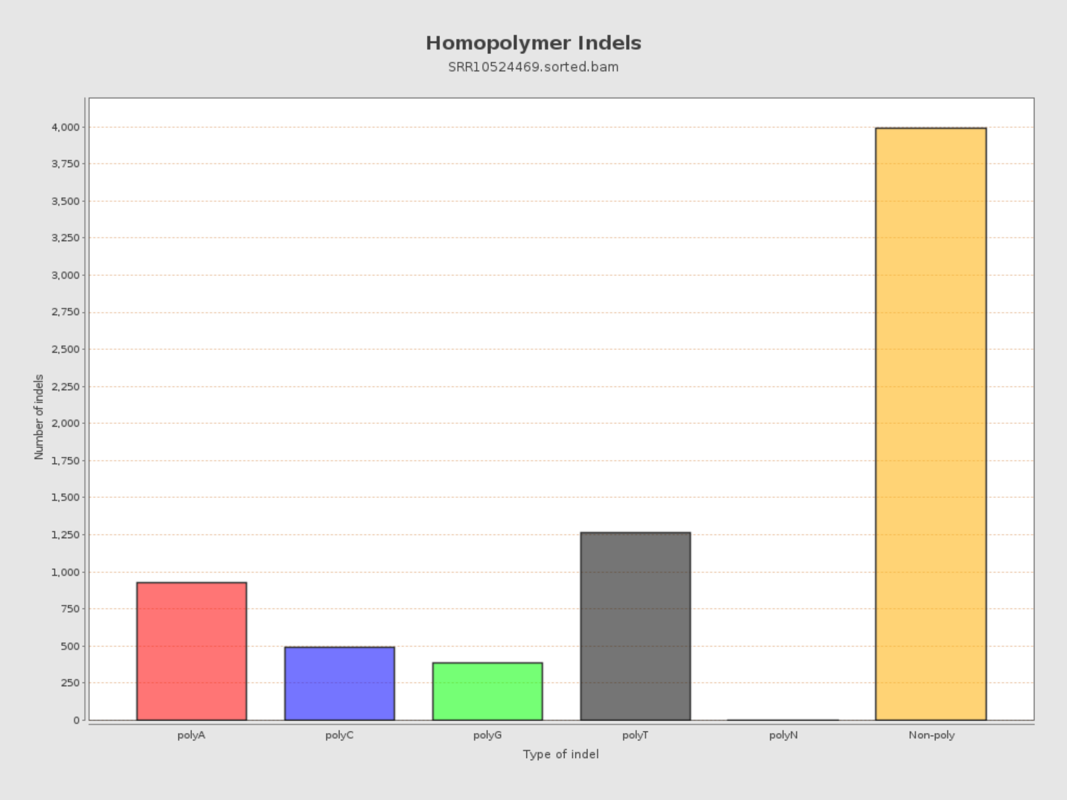
9. Results : Mapped Reads GC-content Distribution



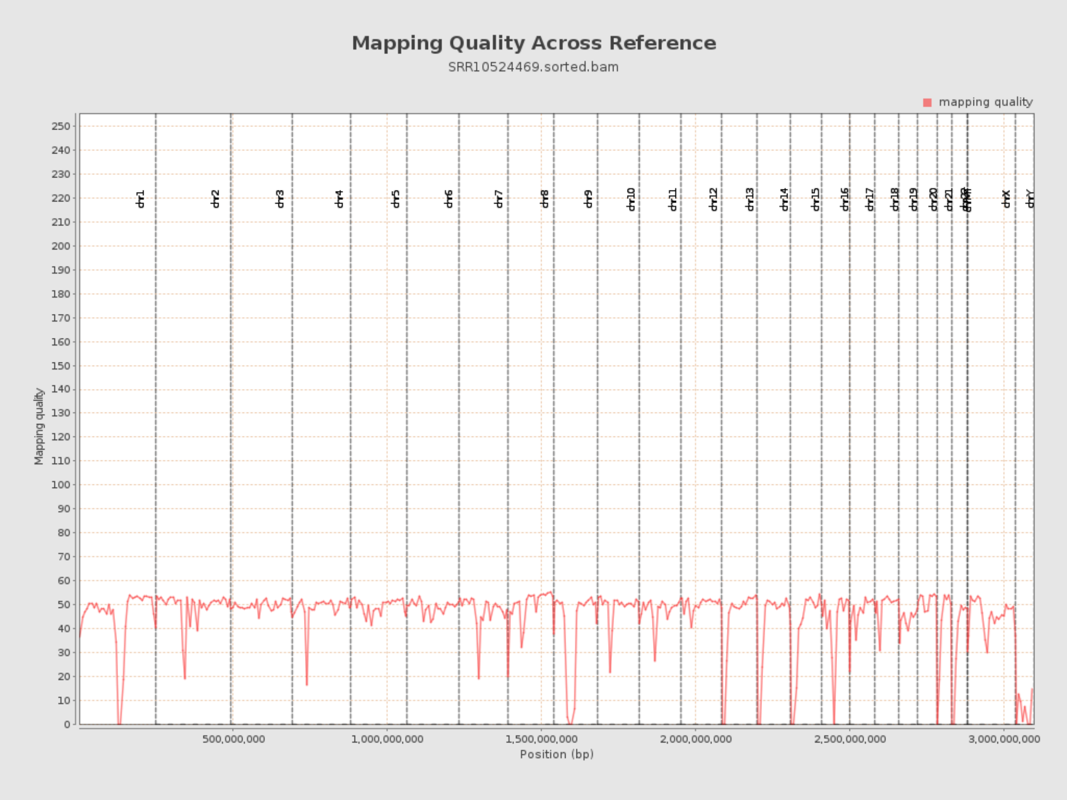
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram