Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 09:32:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524946.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_SRR10524946 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524946.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 09:31:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524946.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	974,439
Mapped reads	906,840 / 93.06%
Unmapped reads	67,599 / 6.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,350 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	20,414 / 2.09%
Duplication rate	1.57%
Clipped reads	906,744 / 93.05%

2.2. ACGT Content

Number/percentage of A's	12,997,652 / 24.4%
Number/percentage of C's	9,902,021 / 18.59%
Number/percentage of T's	16,887,949 / 31.71%
Number/percentage of G's	13,475,327 / 25.3%
Number/percentage of N's	628 / 0%
GC Percentage	43.89%

2.3. Coverage

Mean	0.0172

Standard Deviation	0.183

2.4. Mapping Quality

Mean Mapping Quality	44.93

2.5. Mismatches and indels

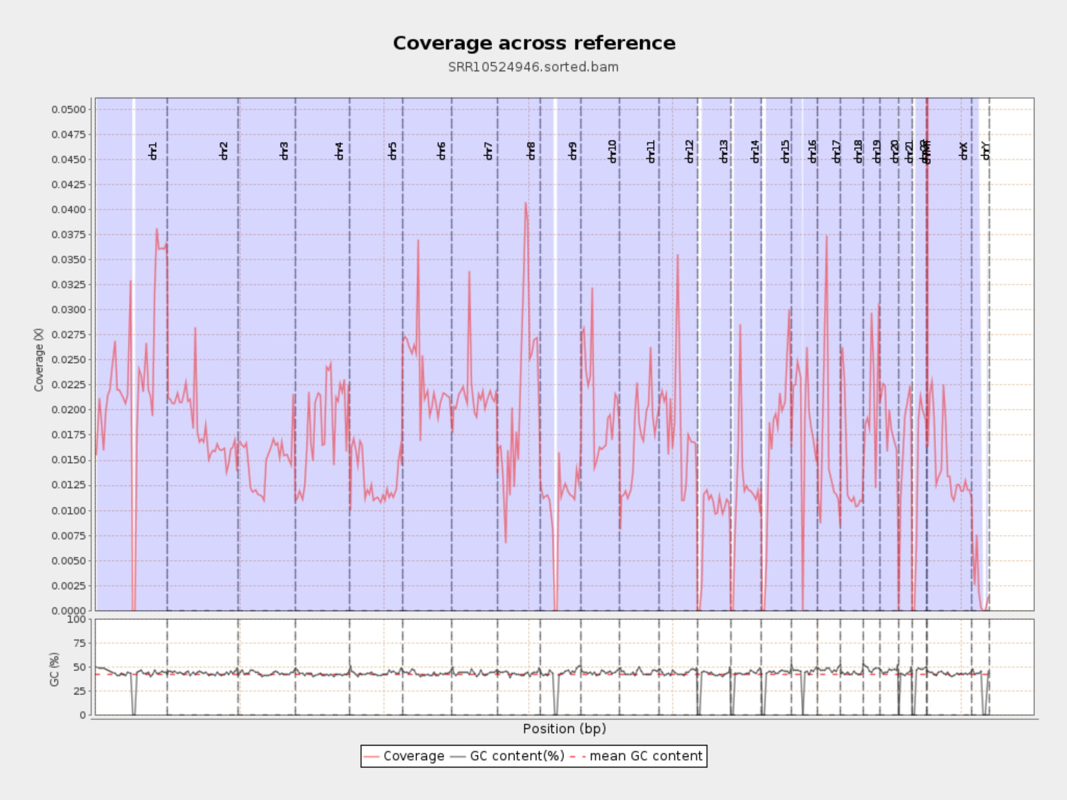
General error rate	0.49%
Mismatches	255,561
Insertions	3,141
Mapped reads with at least one insertion	0.34%
Deletions	10,399
Mapped reads with at least one deletion	1.14%
Homopolymer indels	44.57%

2.6. Chromosome stats

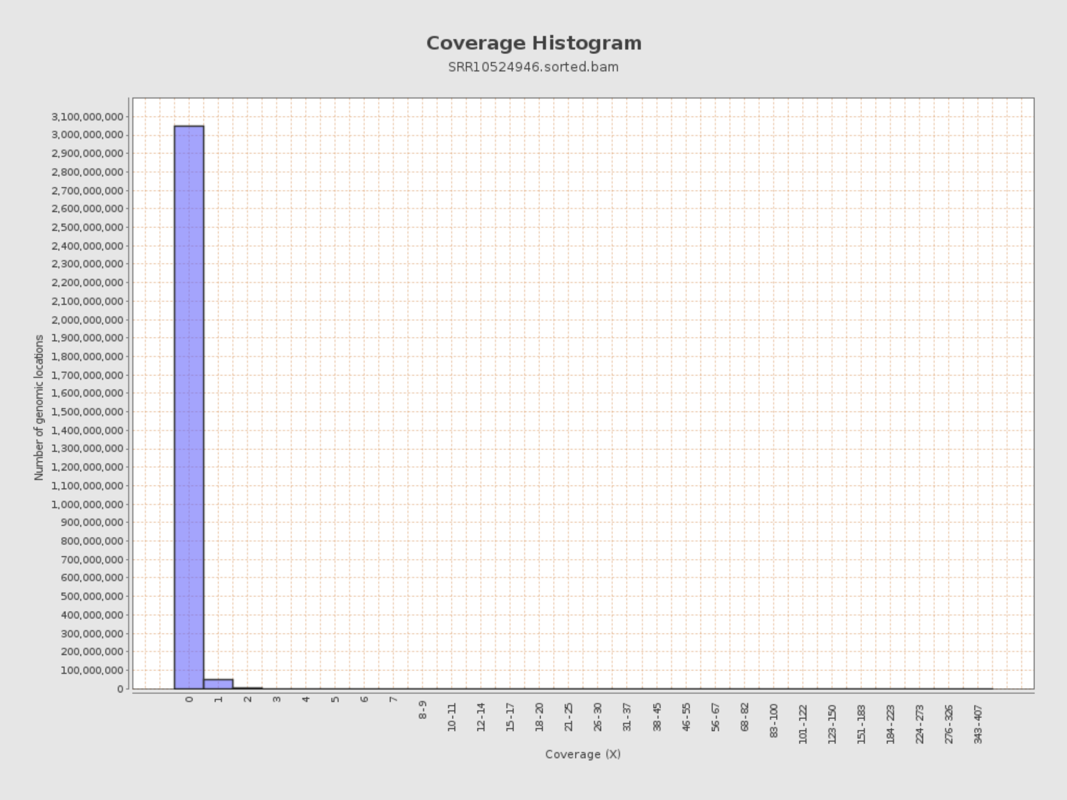
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5778749	0.0232	0.327
chr2	243199373	4460307	0.0183	0.201
chr3	198022430	2975276	0.015	0.1287
chr4	191154276	3525100	0.0184	0.1485
chr5	180915260	2373474	0.0131	0.1213
chr6	171115067	3990199	0.0233	0.2051
chr7	159138663	3449169	0.0217	0.2474

chr8	146364022	3153657	0.0215	0.1894
chr9	141213431	1499679	0.0106	0.142
chr10	135534747	2777394	0.0205	0.1777
chr11	135006516	2282598	0.0169	0.1704
chr12	133851895	2492182	0.0186	0.1437
chr13	115169878	1041156	0.009	0.0998
chr14	107349540	1245584	0.0116	0.1141
chr15	102531392	1734323	0.0169	0.1419
chr16	90354753	1699815	0.0188	0.1486
chr17	81195210	1307981	0.0161	0.1585
chr18	78077248	1117807	0.0143	0.2071
chr19	59128983	1266226	0.0214	0.214
chr20	63025520	1178171	0.0187	0.1437
chr21	48129895	778576	0.0162	0.1366
chr22	51304566	697332	0.0136	0.1215
chrMT	16571	21243	1.2819	1.4508
chrX	155270560	2294993	0.0148	0.1403
chrY	59373566	140398	0.0024	0.0643

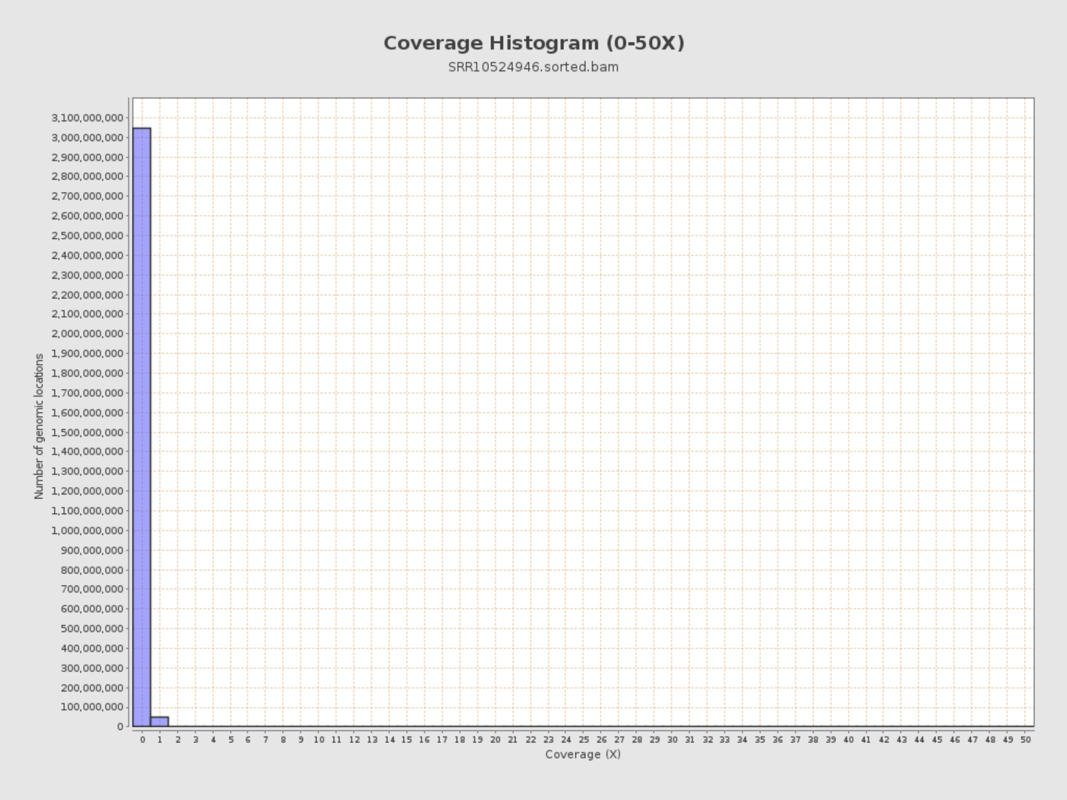
3. Results : Coverage across reference



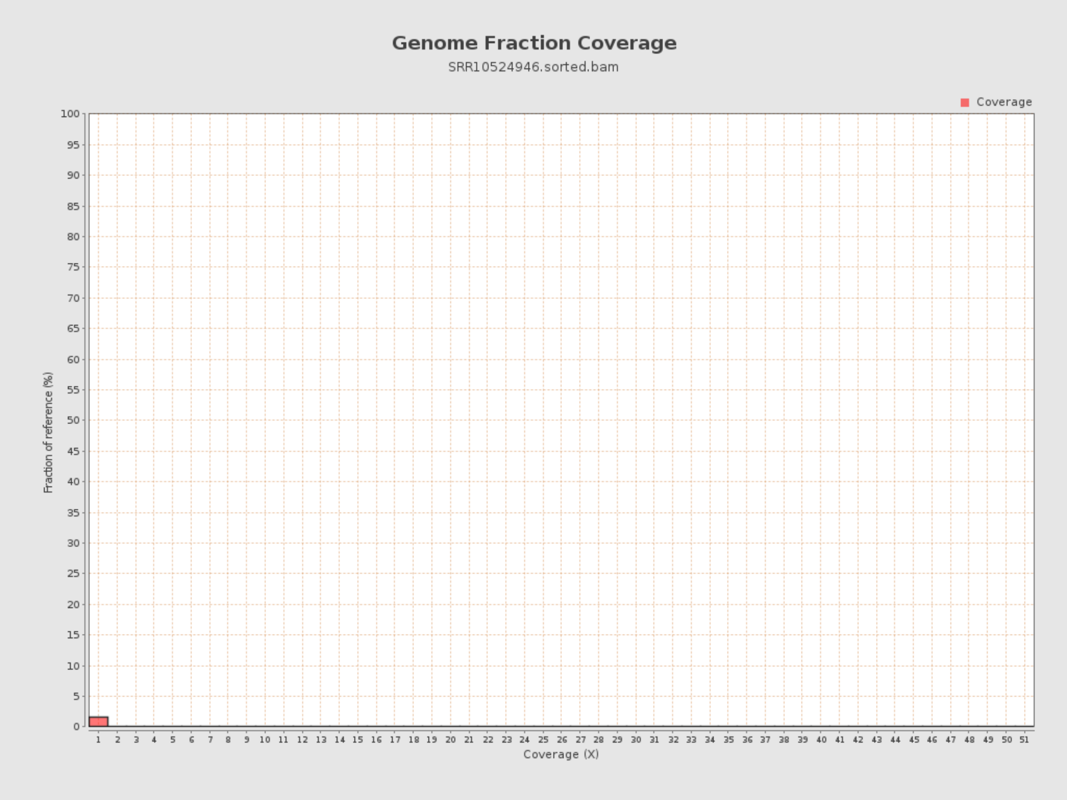
4. Results : Coverage Histogram



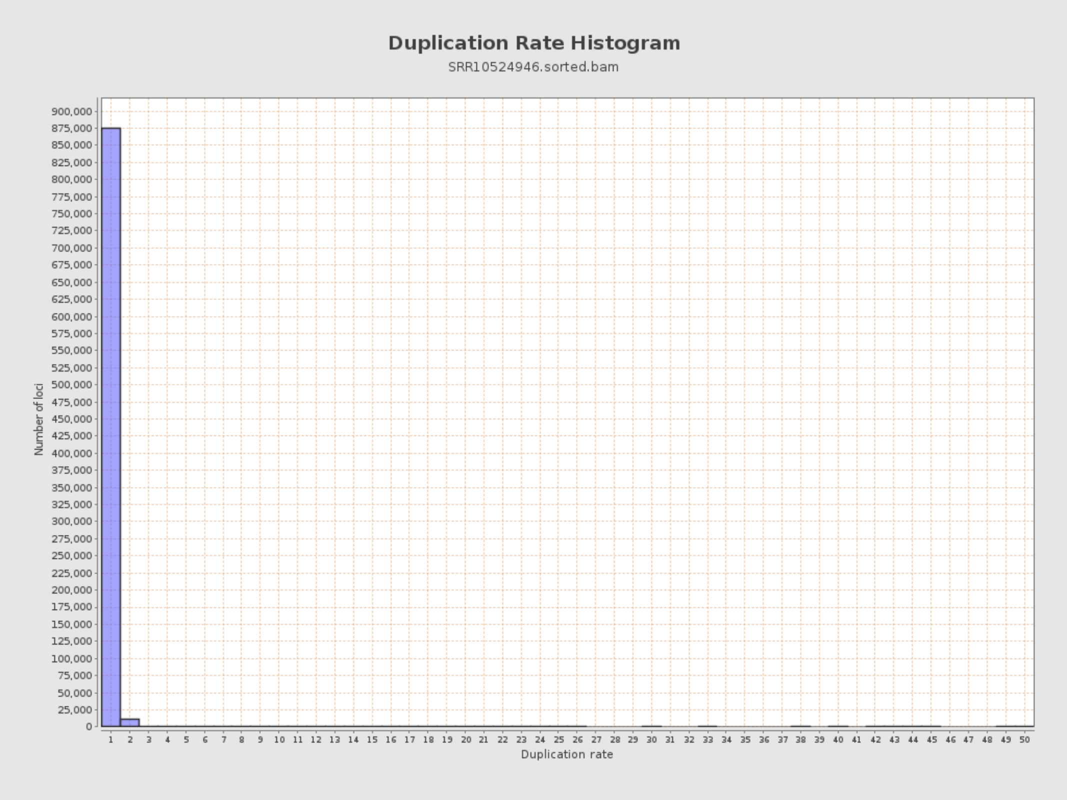
5. Results : Coverage Histogram (0-50X)



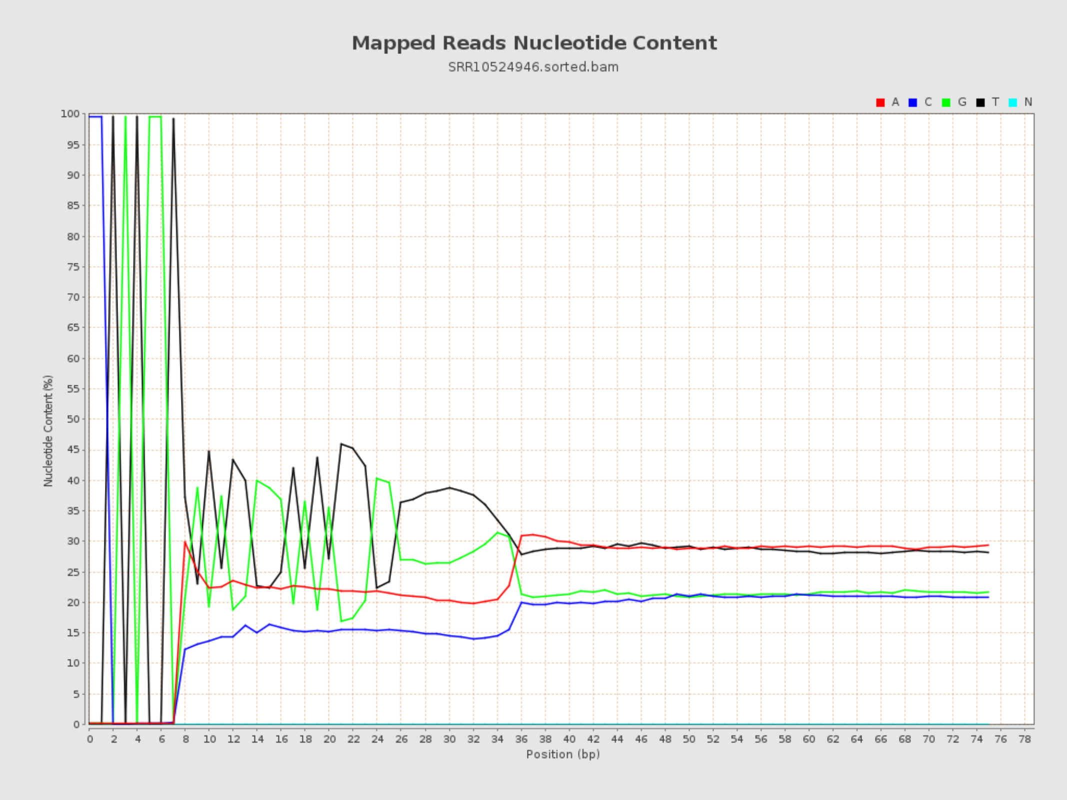
6. Results : Genome Fraction Coverage



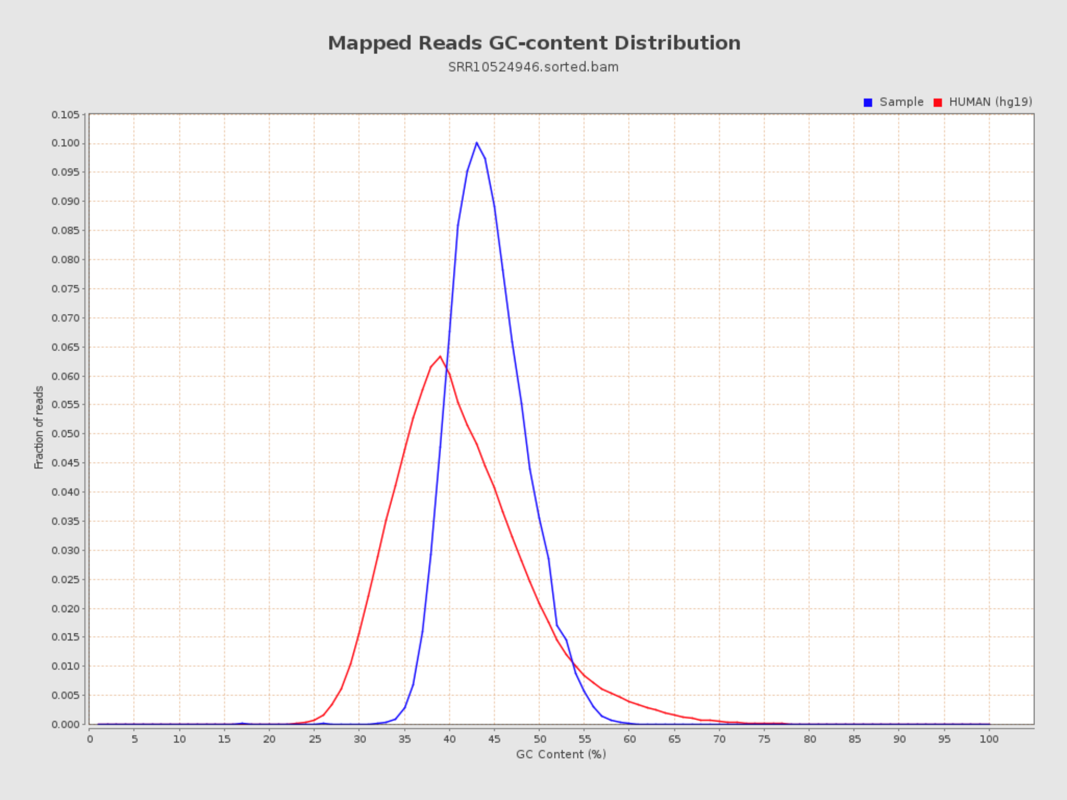
7. Results : Duplication Rate Histogram



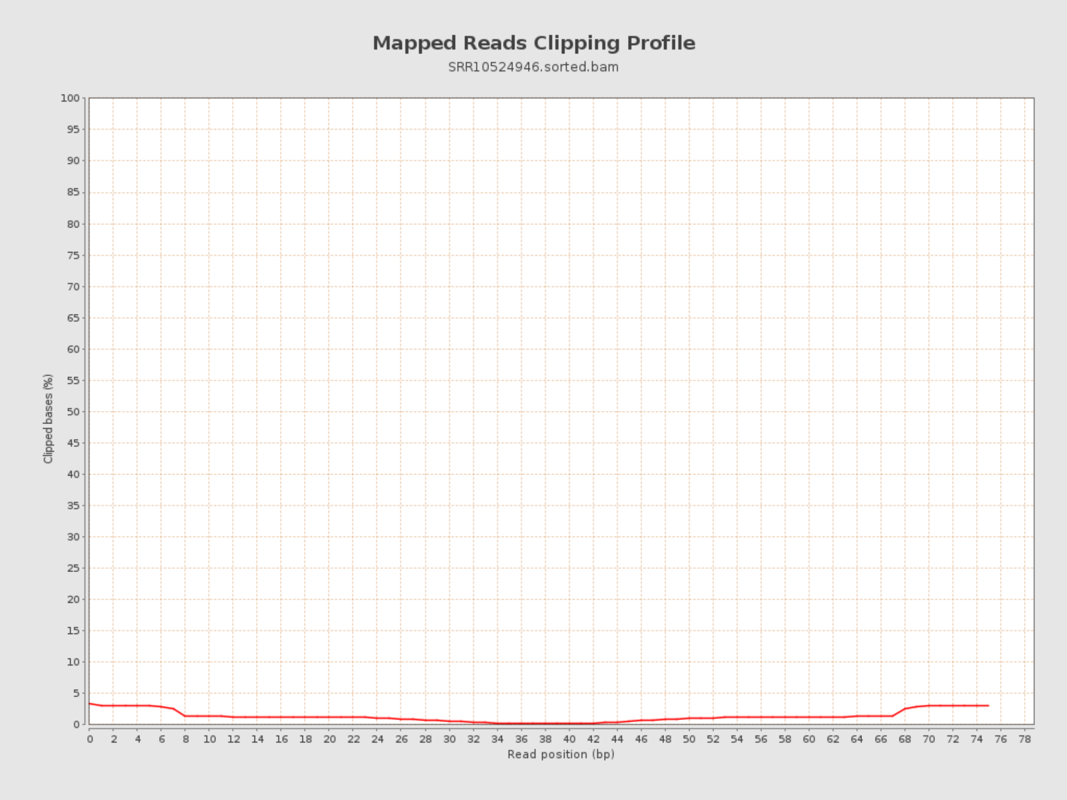
8. Results : Mapped Reads Nucleotide Content



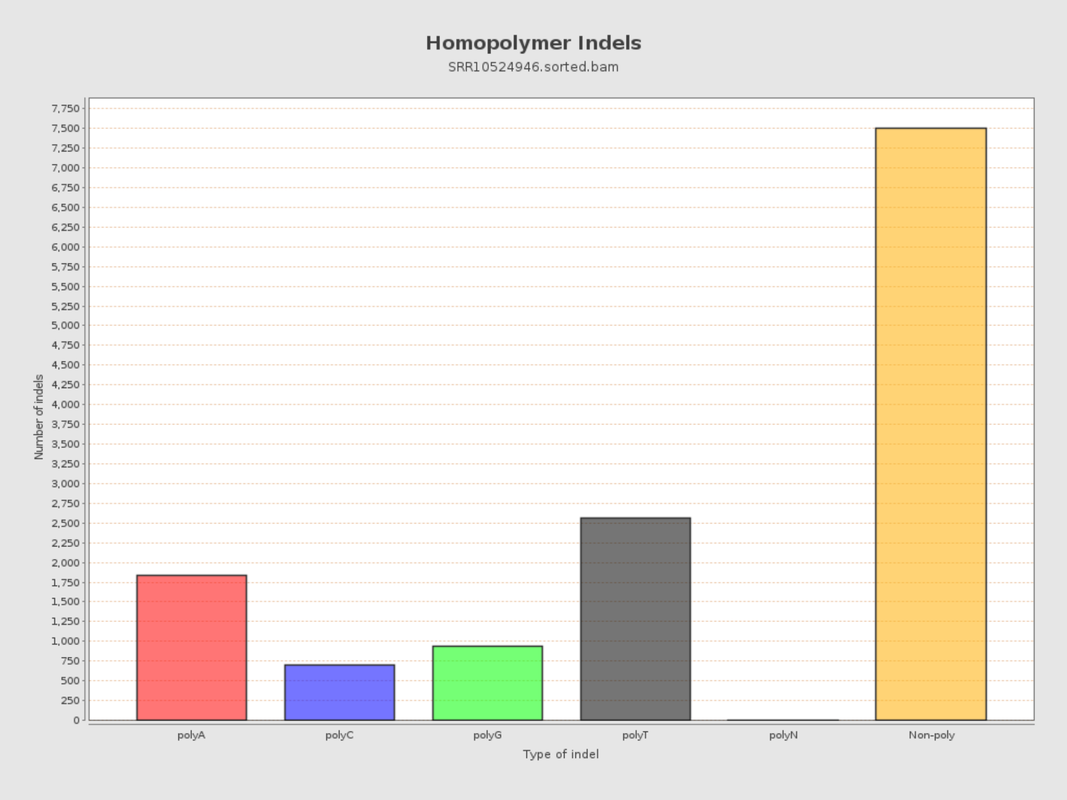
9. Results : Mapped Reads GC-content Distribution



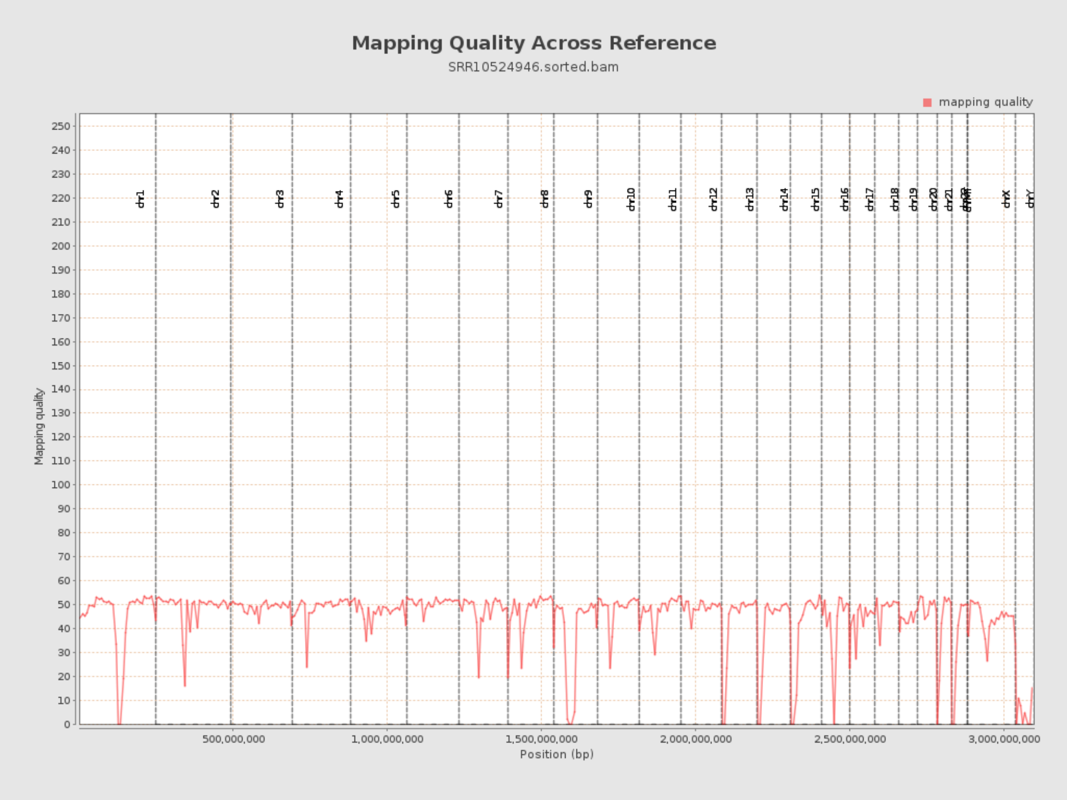
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram