Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 11:12:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524970.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_SRR10524970 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524970.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 11:12:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524970.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	844,552
Mapped reads	780,090 / 92.37%
Unmapped reads	64,462 / 7.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,133 / 0.25%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	15,689 / 1.86%
Duplication rate	1.4%
Clipped reads	780,085 / 92.37%

2.2. ACGT Content

Number/percentage of A's	12,005,234 / 26.13%
Number/percentage of C's	8,953,960 / 19.49%
Number/percentage of T's	14,174,434 / 30.85%
Number/percentage of G's	10,806,291 / 23.52%
Number/percentage of N's	549 / 0%
GC Percentage	43.01%

2.3. Coverage

Mean	0.0148

Standard Deviation	0.1644

2.4. Mapping Quality

Mean Mapping Quality	44.57

2.5. Mismatches and indels

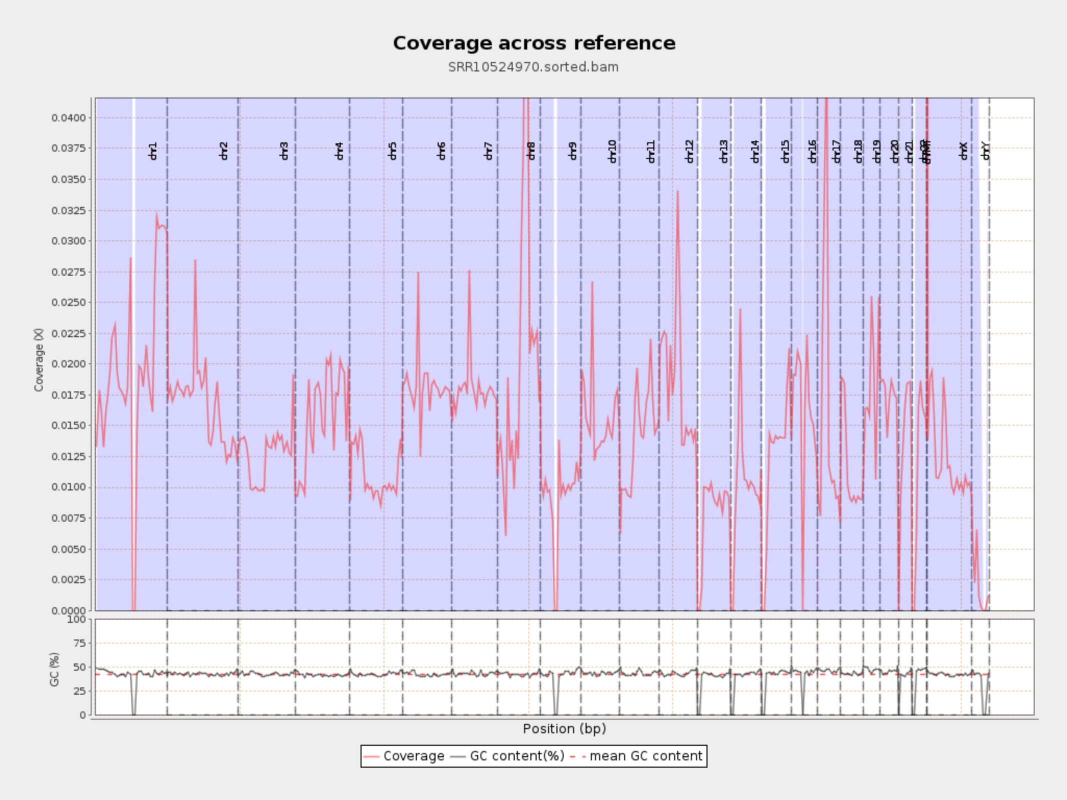
General error rate	0.5%
Mismatches	224,229
Insertions	2,887
Mapped reads with at least one insertion	0.37%
Deletions	8,896
Mapped reads with at least one deletion	1.13%
Homopolymer indels	43.57%

2.6. Chromosome stats

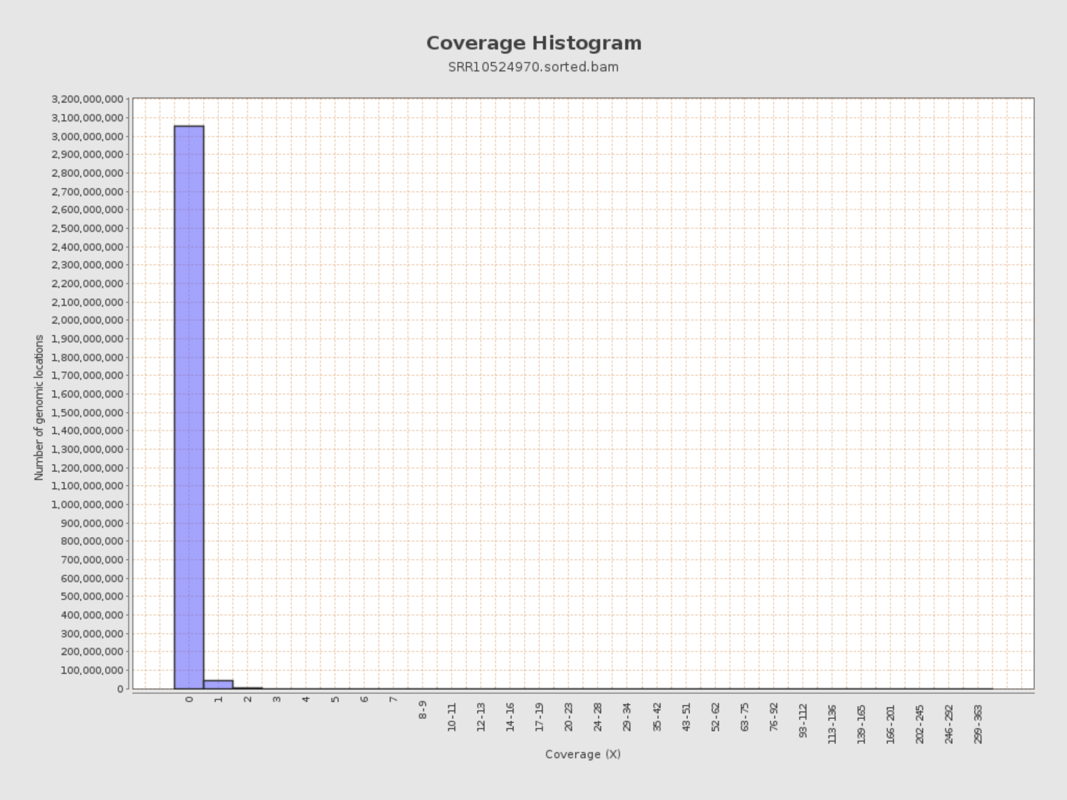
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4876752	0.0196	0.2919
chr2	243199373	4081194	0.0168	0.1781
chr3	198022430	2521346	0.0127	0.1178
chr4	191154276	3020544	0.0158	0.1346
chr5	180915260	2016142	0.0111	0.1103
chr6	171115067	3109580	0.0182	0.1704
chr7	159138663	2876033	0.0181	0.211

chr8	146364022	3162273	0.0216	0.1764
chr9	141213431	1293374	0.0092	0.13
chr10	135534747	2138144	0.0158	0.1587
chr11	135006516	1918402	0.0142	0.1463
chr12	133851895	2505182	0.0187	0.1439
chr13	115169878	898245	0.0078	0.0919
chr14	107349540	1076243	0.01	0.1074
chr15	102531392	1255484	0.0122	0.1164
chr16	90354753	1451368	0.0161	0.1368
chr17	81195210	1363716	0.0168	0.1728
chr18	78077248	900374	0.0115	0.1981
chr19	59128983	1088449	0.0184	0.1933
chr20	63025520	1080273	0.0171	0.1369
chr21	48129895	664694	0.0138	0.1254
chr22	51304566	594436	0.0116	0.1114
chrMT	16571	5954	0.3593	0.6576
chrX	155270560	1938756	0.0125	0.1258
chrY	59373566	118544	0.002	0.057

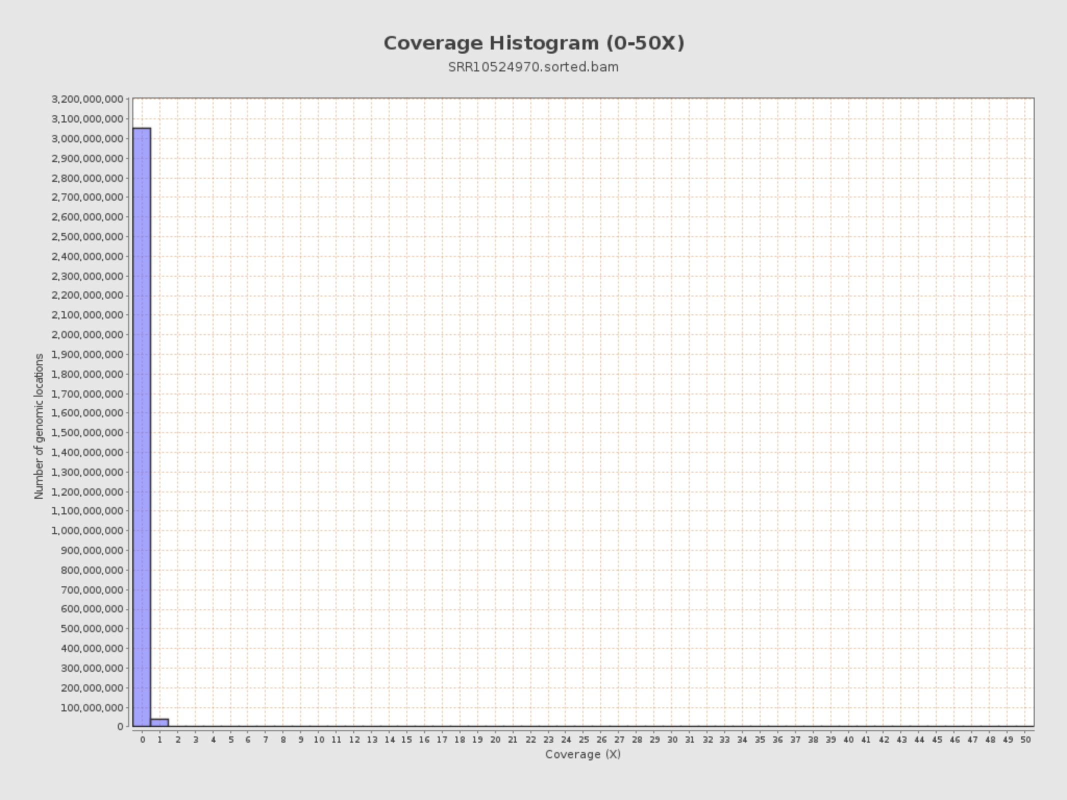
3. Results : Coverage across reference



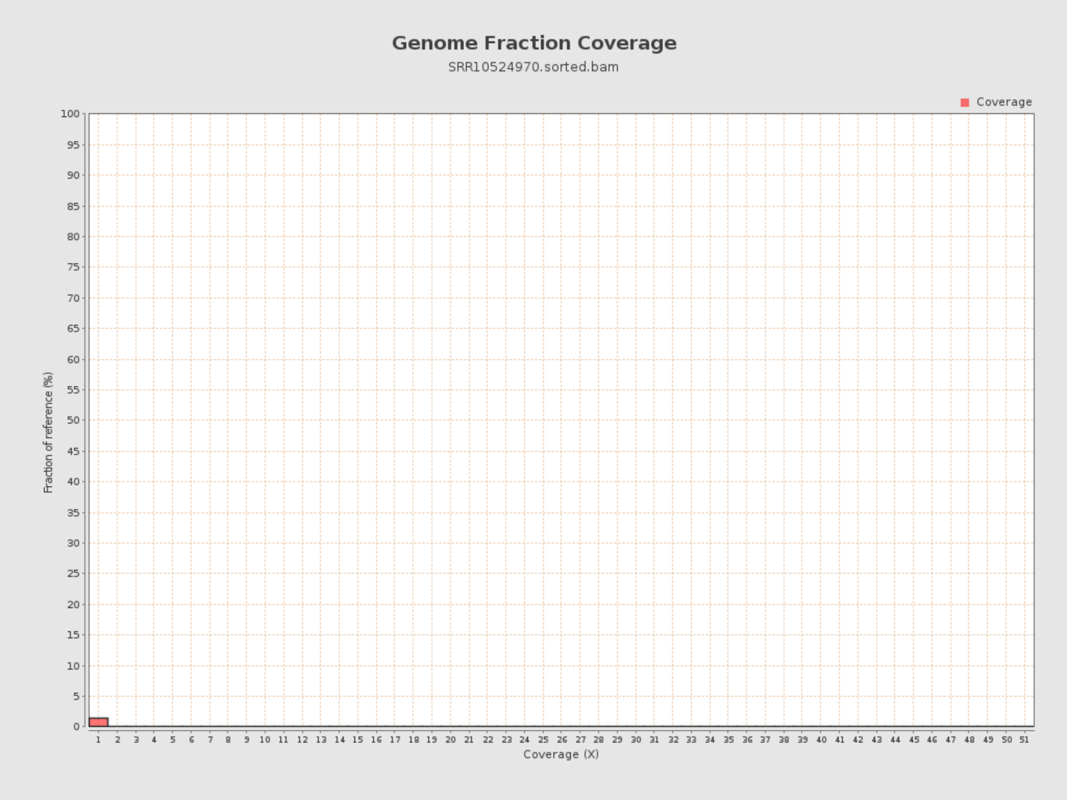
4. Results : Coverage Histogram



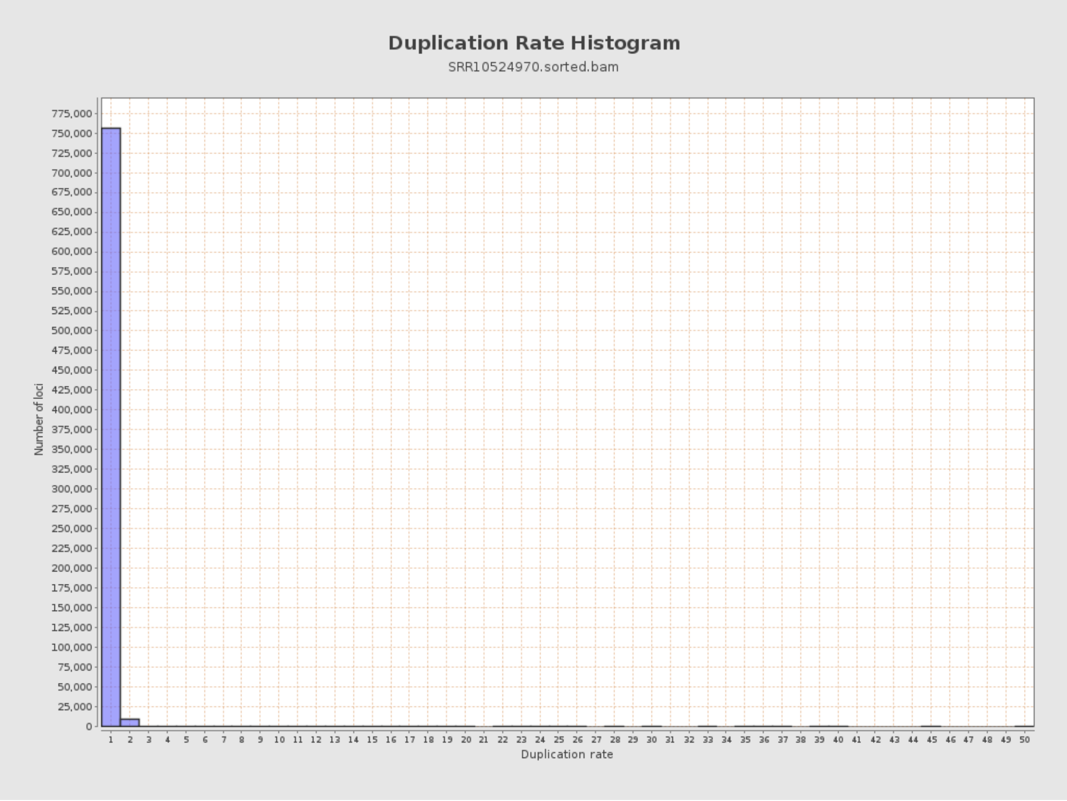
5. Results : Coverage Histogram (0-50X)



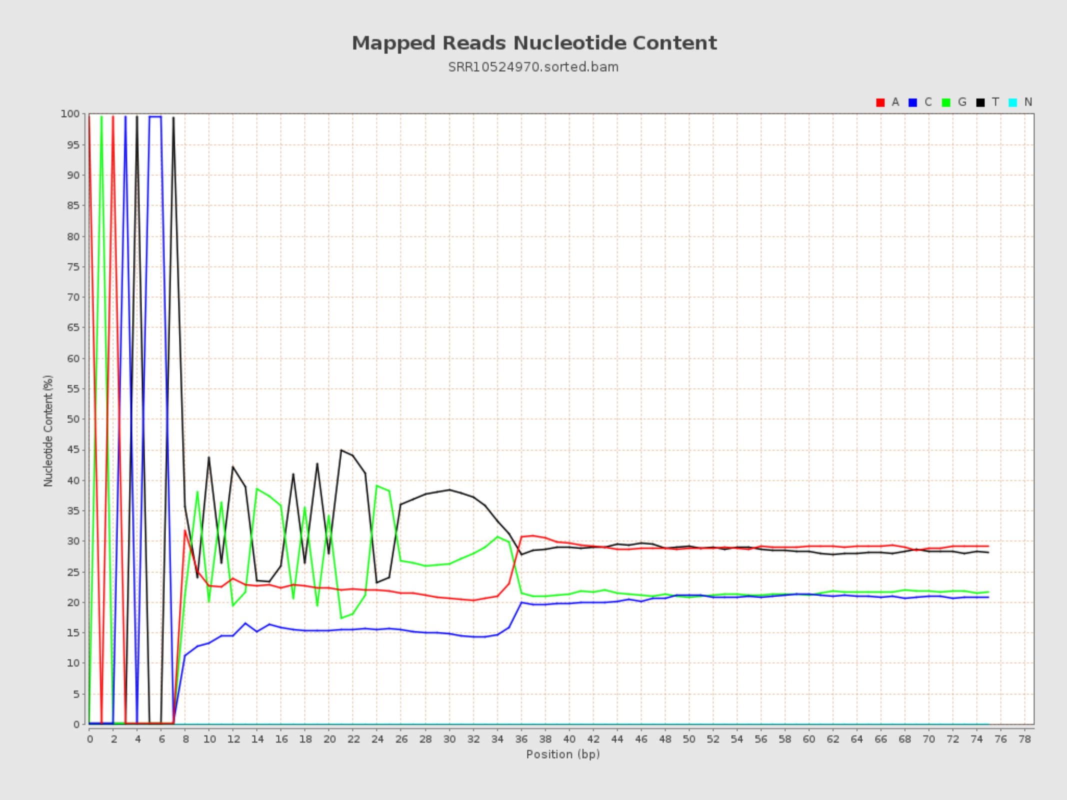
6. Results : Genome Fraction Coverage



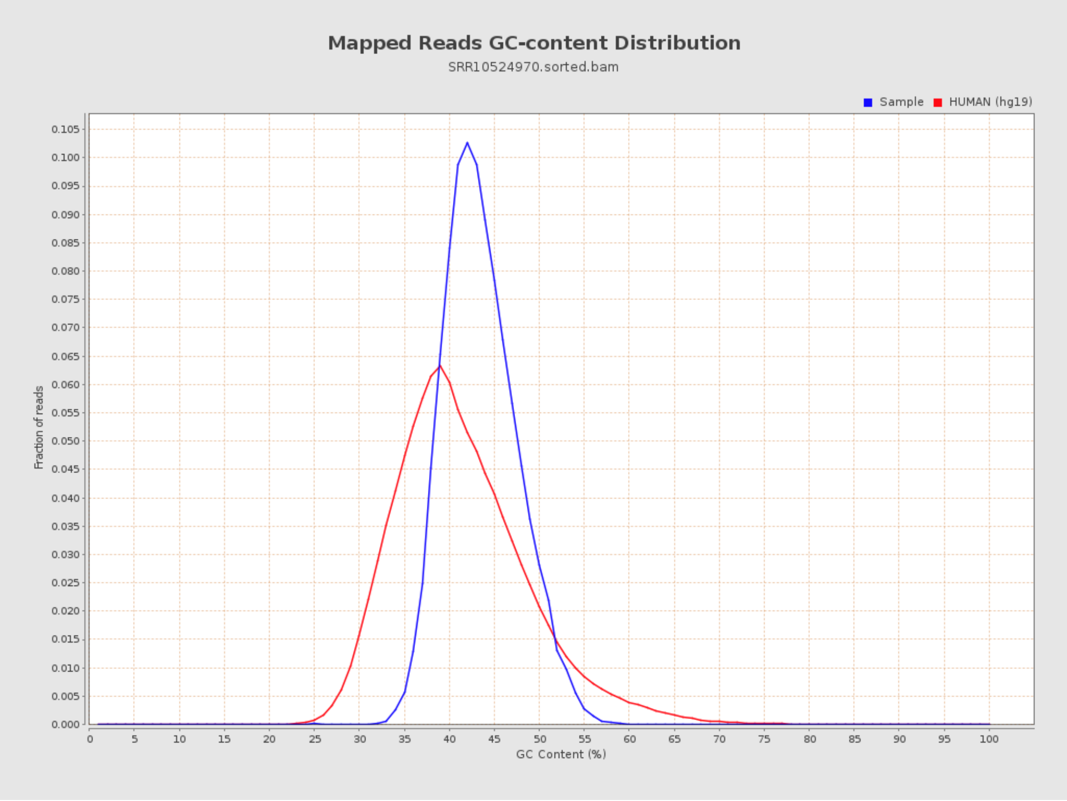
7. Results : Duplication Rate Histogram



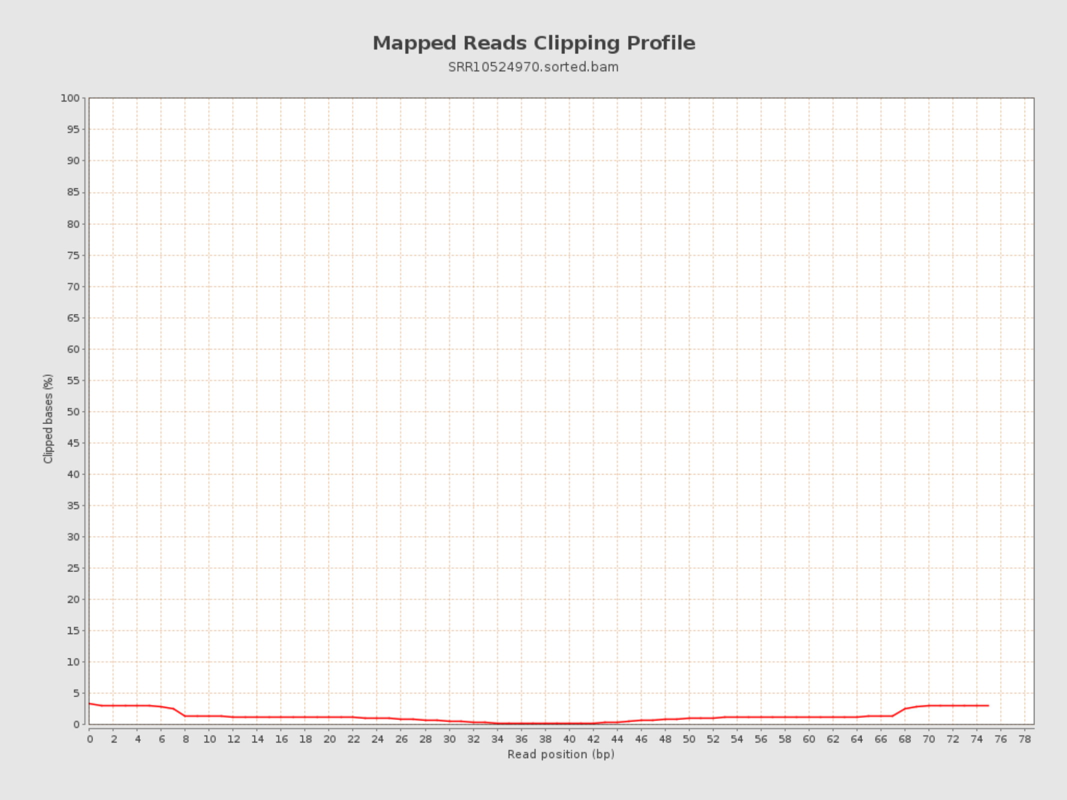
8. Results : Mapped Reads Nucleotide Content



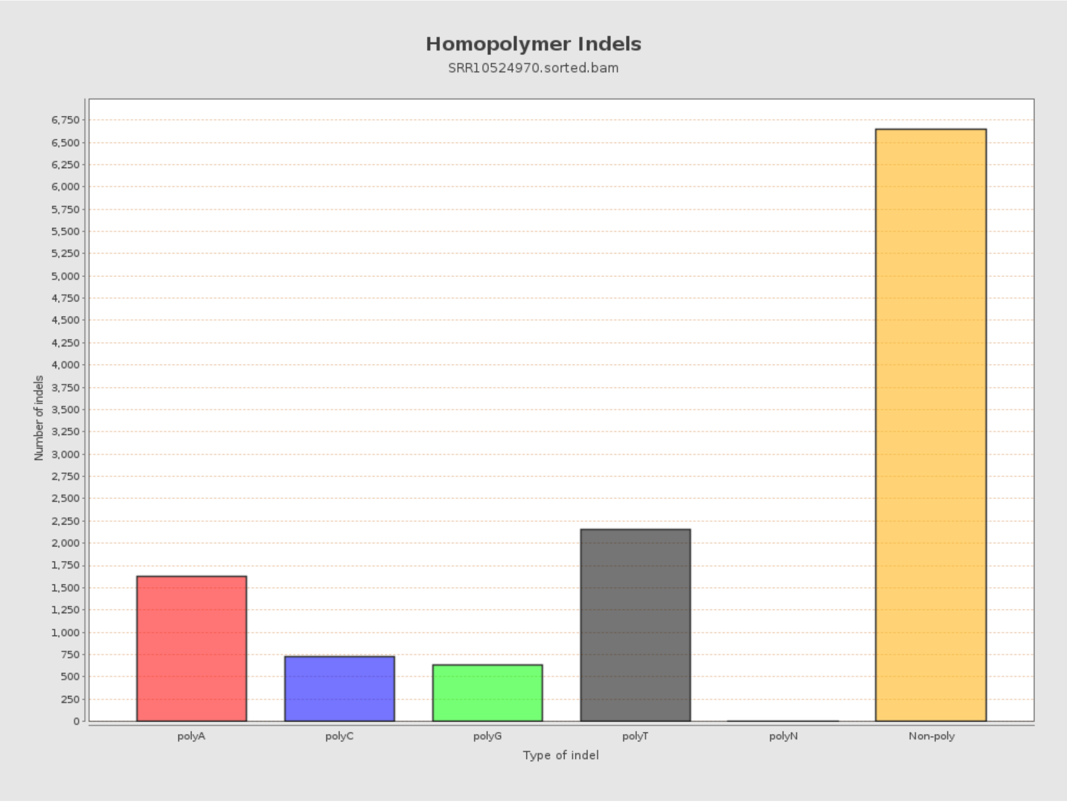
9. Results : Mapped Reads GC-content Distribution



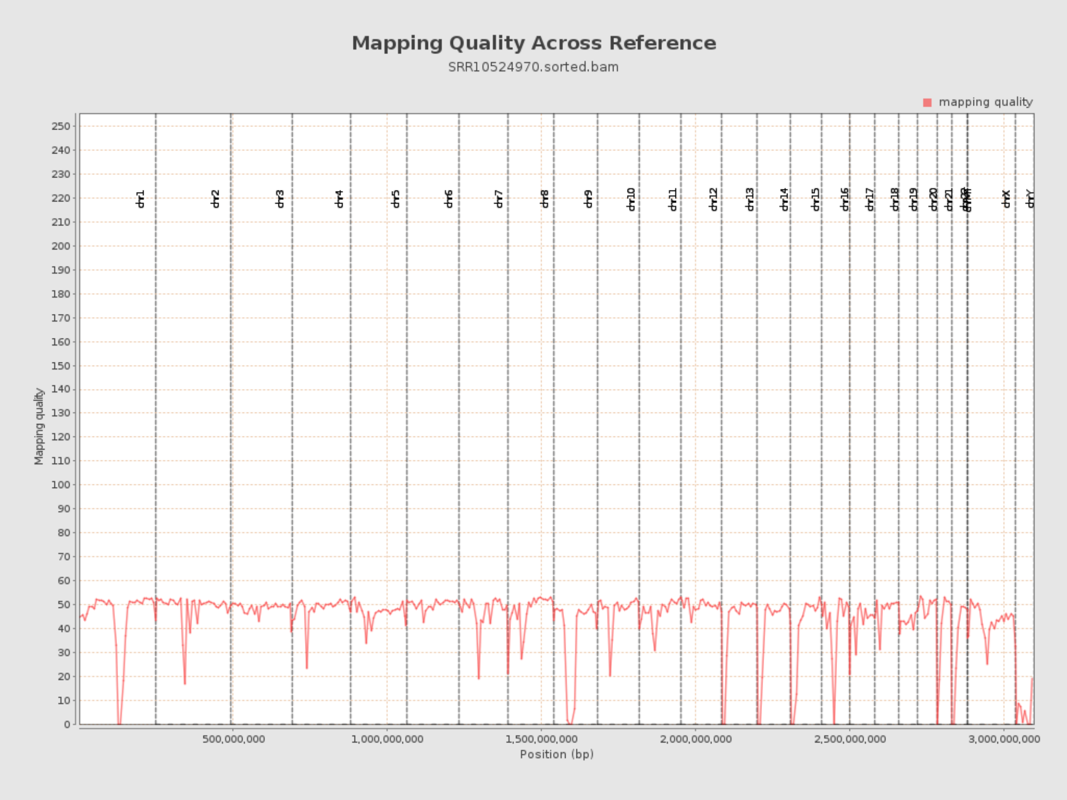
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram