Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 05:29:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524470.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_SRR10524470 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524470.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 05:29:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524470.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	713,410
Mapped reads	663,950 / 93.07%
Unmapped reads	49,460 / 6.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,599 / 0.22%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	15,494 / 2.17%
Duplication rate	1.77%
Clipped reads	664,238 / 93.11%

2.2. ACGT Content

Number/percentage of A's	9,454,342 / 24.26%
Number/percentage of C's	7,294,583 / 18.72%
Number/percentage of T's	12,397,351 / 31.82%
Number/percentage of G's	9,817,589 / 25.2%
Number/percentage of N's	906 / 0%
GC Percentage	43.92%

2.3. Coverage

Mean	0.0126

Standard Deviation	0.1441

2.4. Mapping Quality

Mean Mapping Quality	45.47

2.5. Mismatches and indels

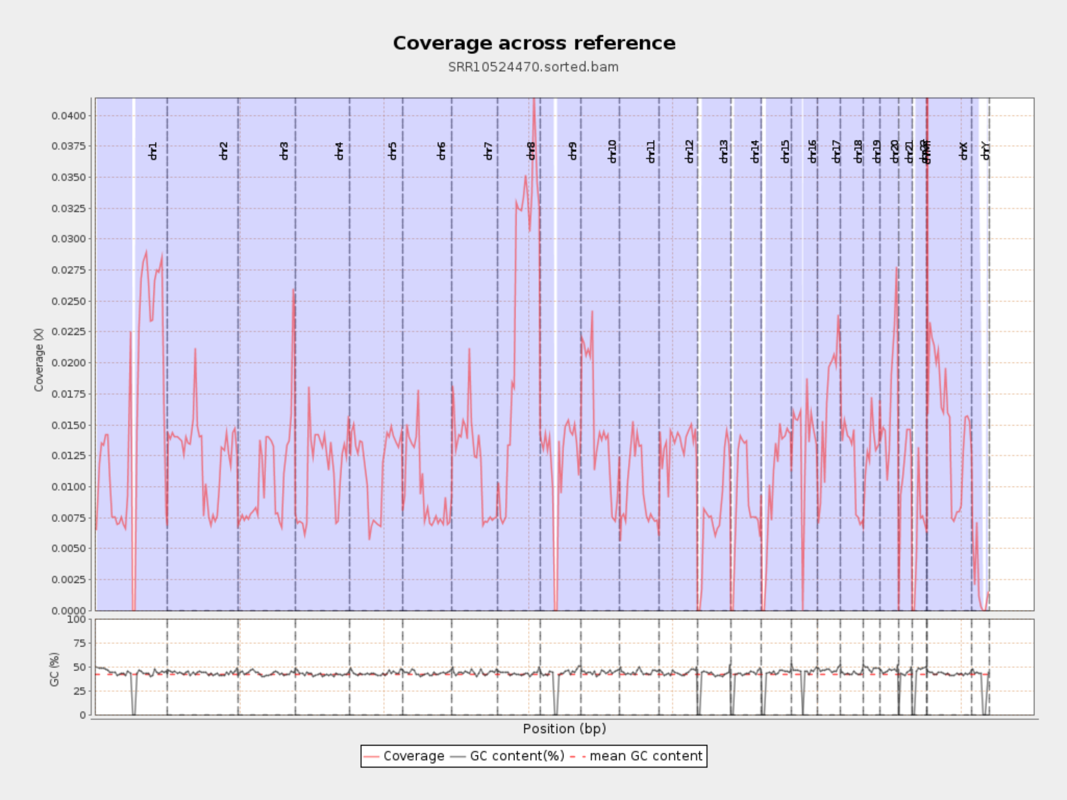
General error rate	0.47%
Mismatches	178,305
Insertions	2,327
Mapped reads with at least one insertion	0.35%
Deletions	7,193
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.12%

2.6. Chromosome stats

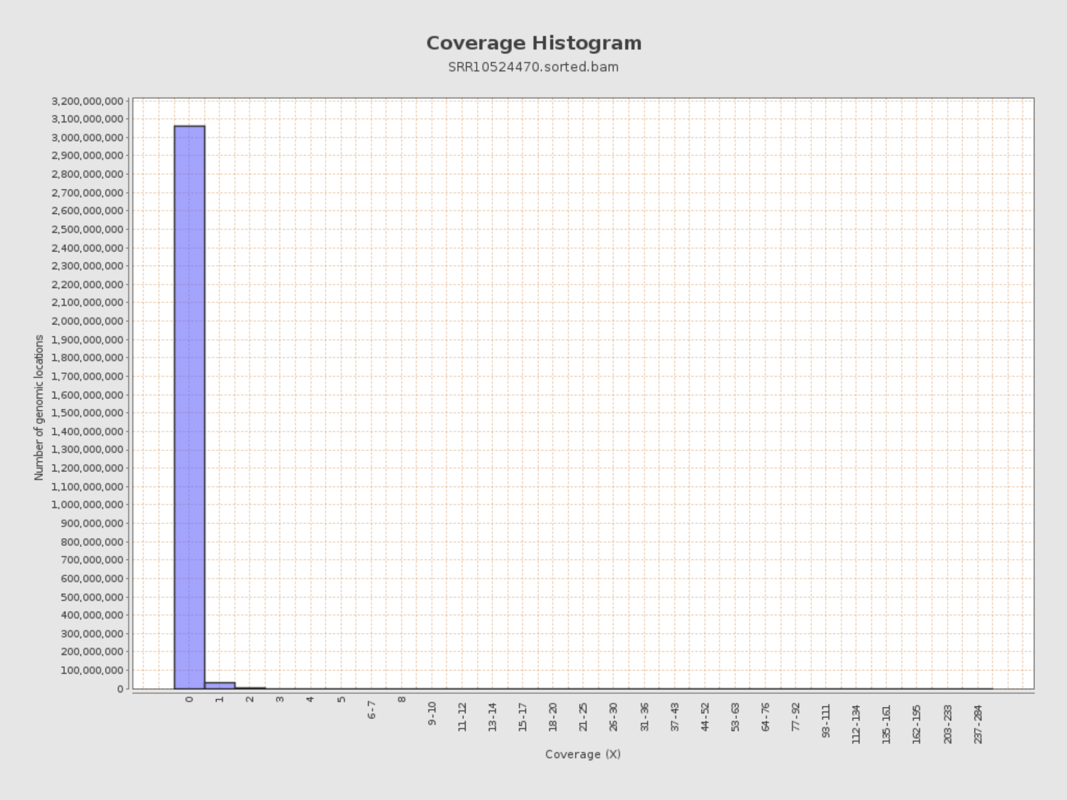
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3841105	0.0154	0.2343
chr2	243199373	3059915	0.0126	0.1542
chr3	198022430	2141165	0.0108	0.1091
chr4	191154276	2172938	0.0114	0.1187
chr5	180915260	2118143	0.0117	0.1135
chr6	171115067	1670155	0.0098	0.1147
chr7	159138663	1947963	0.0122	0.1647

chr8	146364022	3597578	0.0246	0.1764
chr9	141213431	1672884	0.0118	0.1332
chr10	135534747	2049632	0.0151	0.154
chr11	135006516	1328878	0.0098	0.1289
chr12	133851895	1807235	0.0135	0.122
chr13	115169878	876329	0.0076	0.0922
chr14	107349540	922165	0.0086	0.0973
chr15	102531392	1045048	0.0102	0.1083
chr16	90354753	1222897	0.0135	0.1258
chr17	81195210	1343006	0.0165	0.1379
chr18	78077248	920639	0.0118	0.1927
chr19	59128983	782197	0.0132	0.1799
chr20	63025520	1098123	0.0174	0.1391
chr21	48129895	541425	0.0112	0.1146
chr22	51304566	316666	0.0062	0.0824
chrMT	16571	4634	0.2796	0.5964
chrX	155270560	2369555	0.0153	0.1353
chrY	59373566	126842	0.0021	0.0684

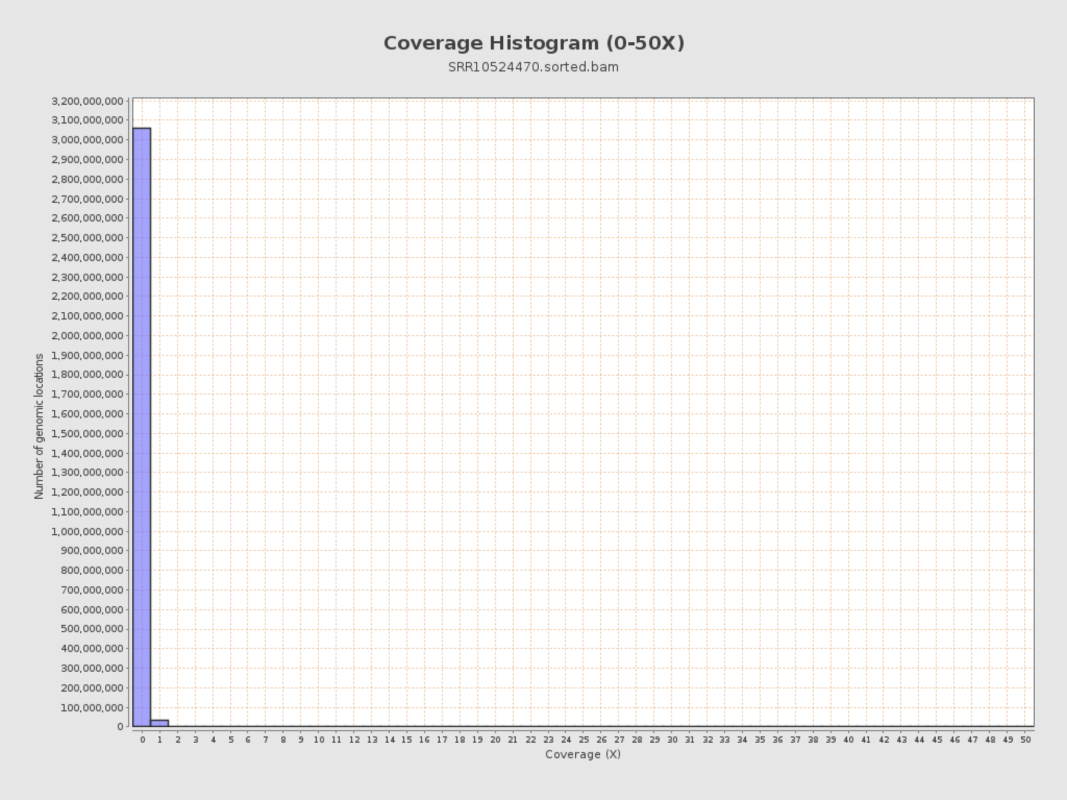
3. Results : Coverage across reference



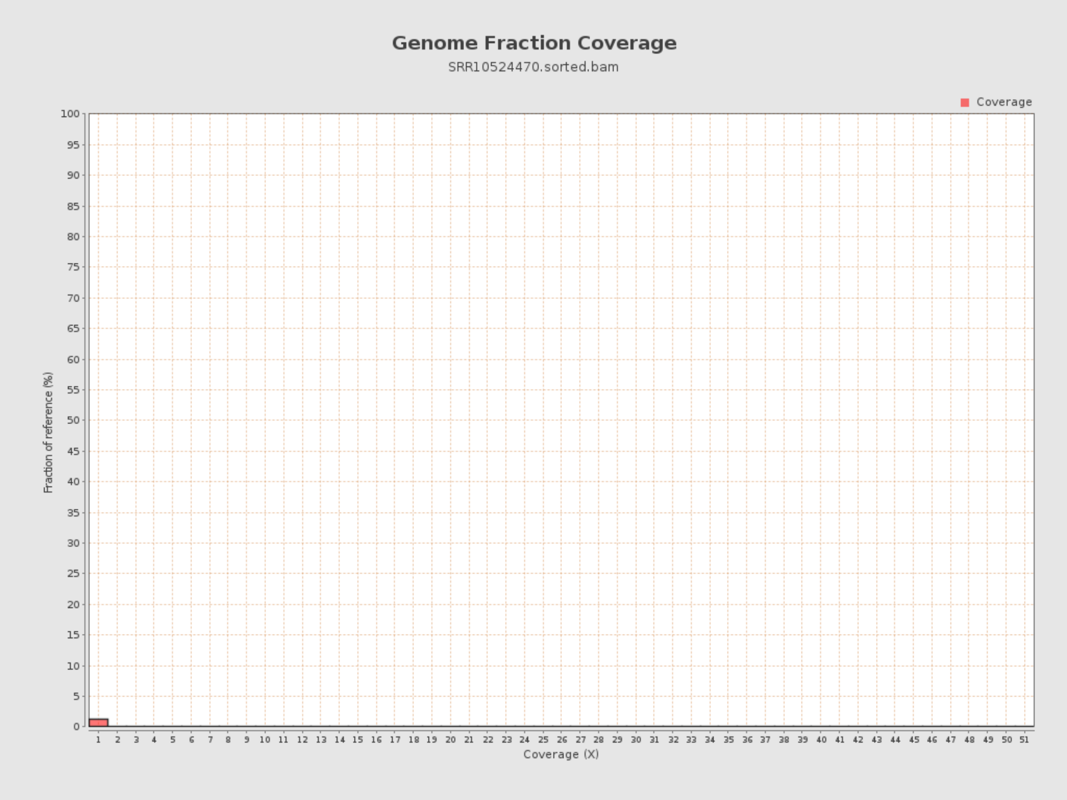
4. Results : Coverage Histogram



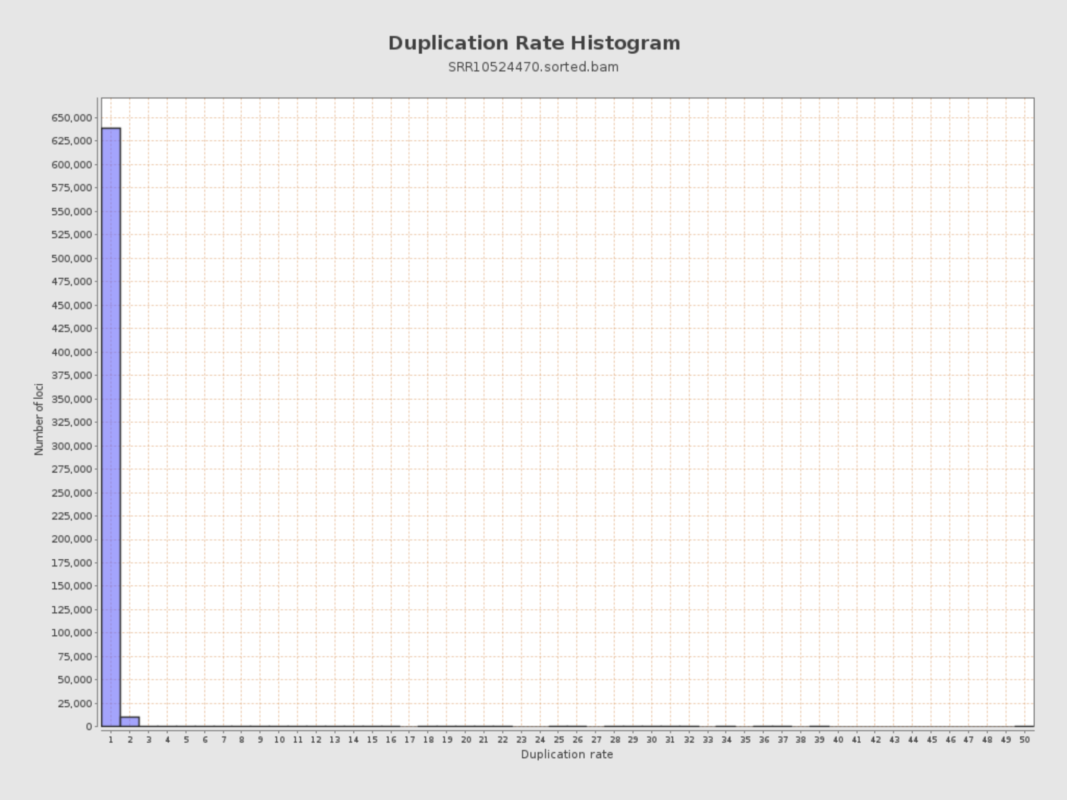
5. Results : Coverage Histogram (0-50X)



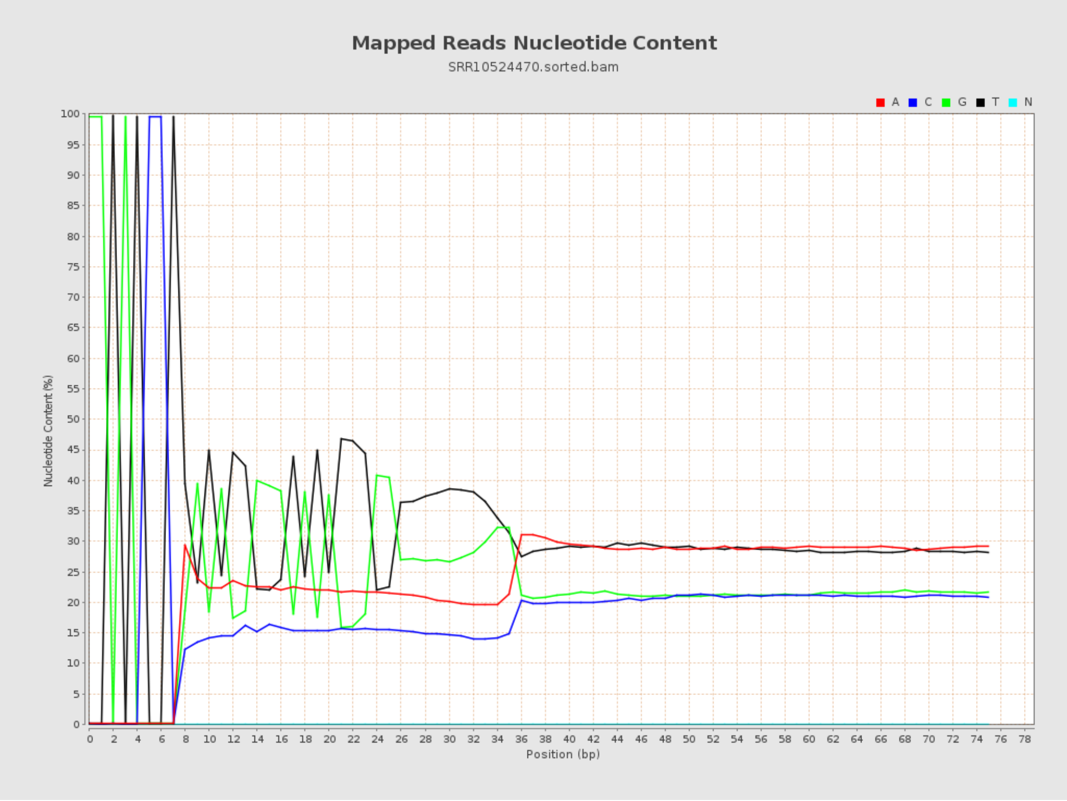
6. Results : Genome Fraction Coverage



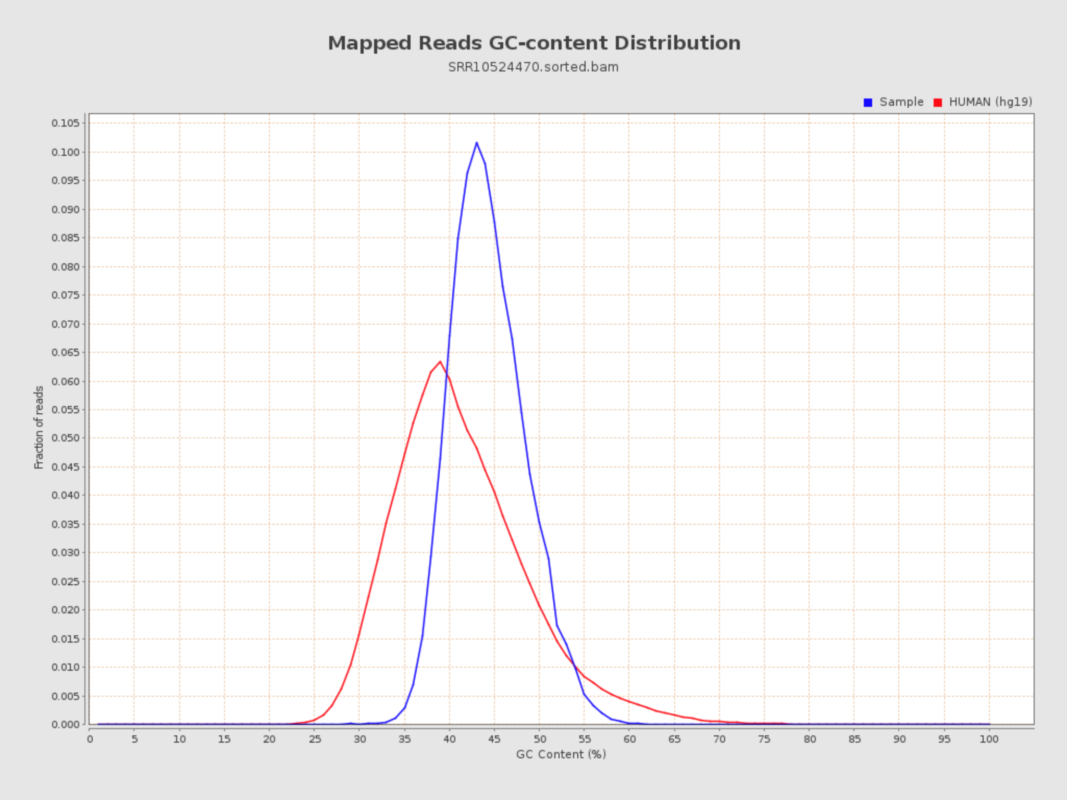
7. Results : Duplication Rate Histogram



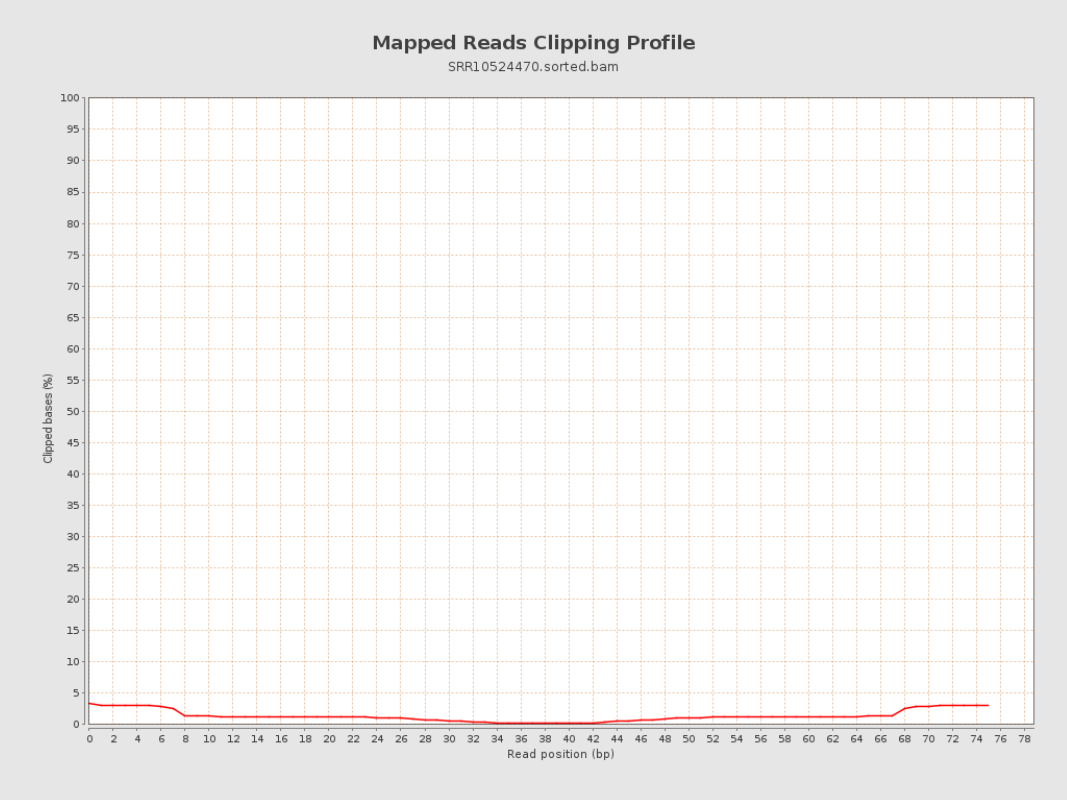
8. Results : Mapped Reads Nucleotide Content



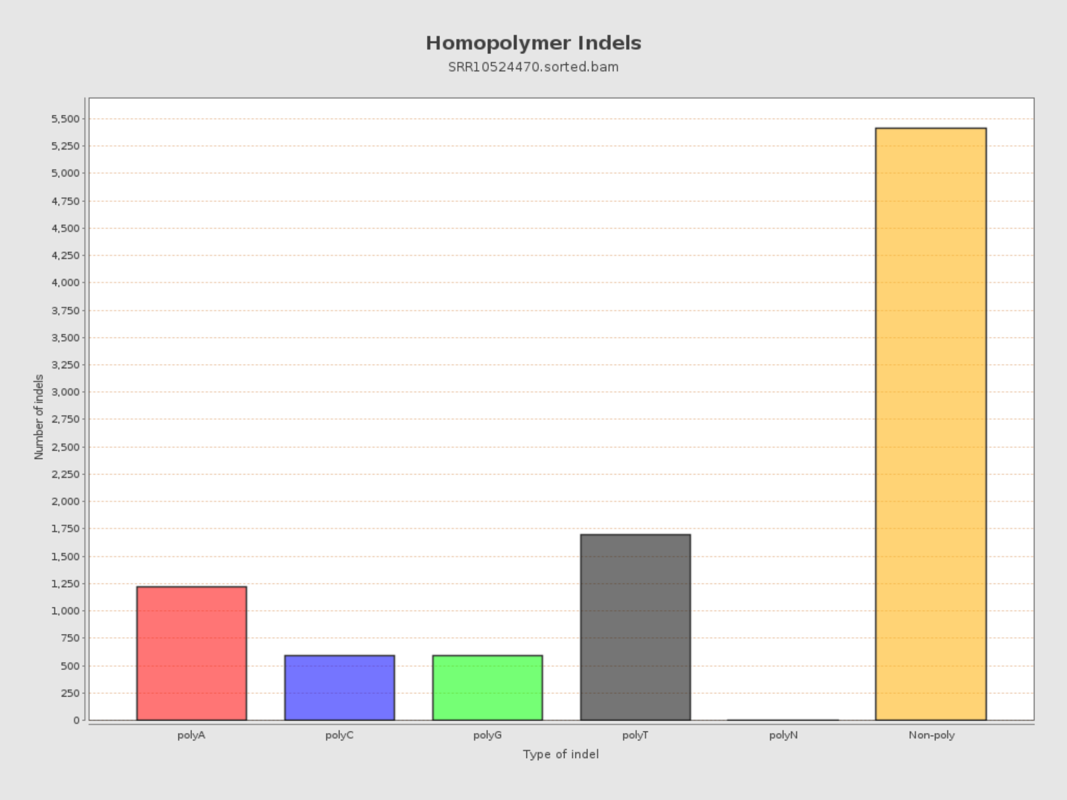
9. Results : Mapped Reads GC-content Distribution



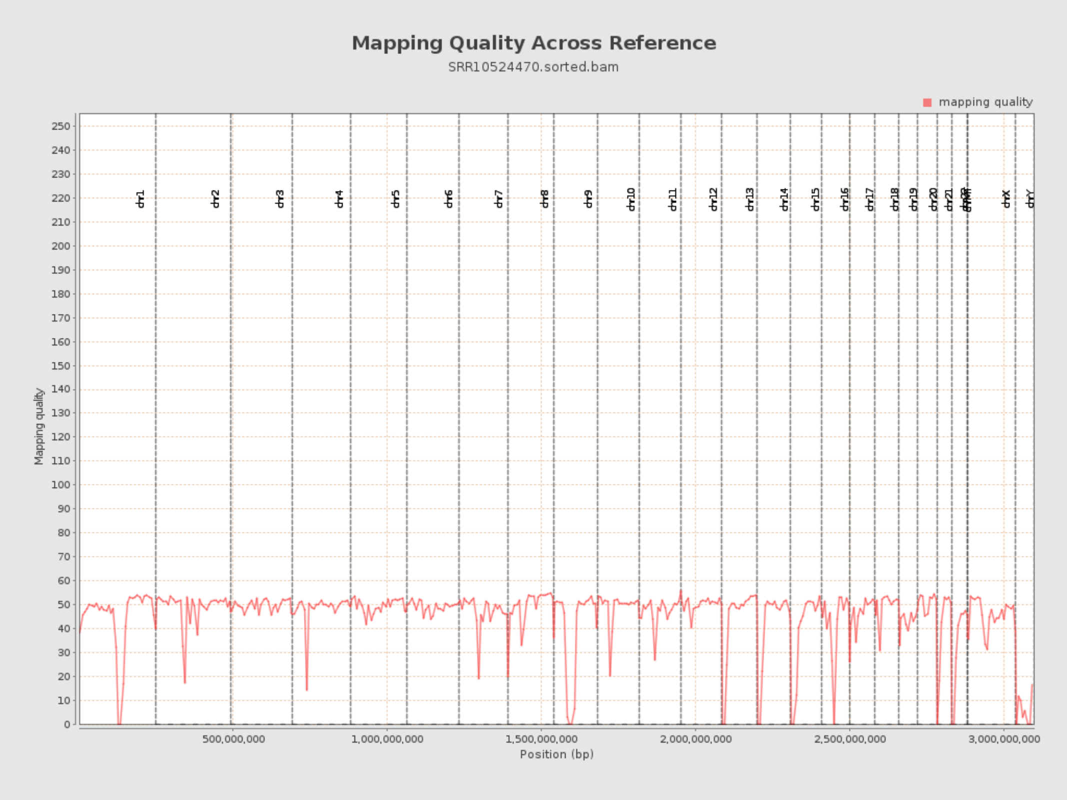
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram