Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 21:17:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524805.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_SRR10524805 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524805.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 21:17:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524805.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,505,998
Mapped reads	1,369,382 / 90.93%
Unmapped reads	136,616 / 9.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,217 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	58,554 / 3.89%
Duplication rate	3.29%
Clipped reads	1,373,370 / 91.19%

2.2. ACGT Content

Number/percentage of A's	19,532,044 / 24.98%
Number/percentage of C's	15,083,270 / 19.29%
Number/percentage of T's	24,728,125 / 31.63%
Number/percentage of G's	18,830,505 / 24.09%
Number/percentage of N's	9,128 / 0.01%
GC Percentage	43.38%

2.3. Coverage

Mean	0.0253

Standard Deviation	0.2375

2.4. Mapping Quality

Mean Mapping Quality	44.34

2.5. Mismatches and indels

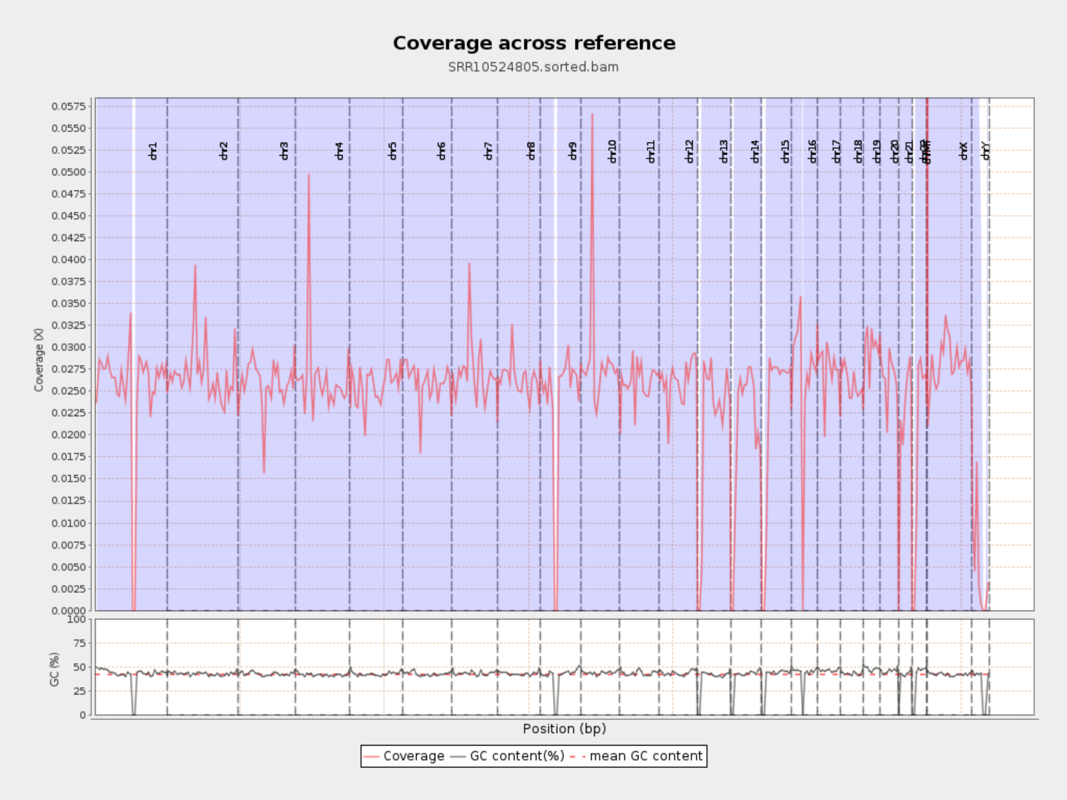
General error rate	0.52%
Mismatches	397,656
Insertions	4,932
Mapped reads with at least one insertion	0.36%
Deletions	15,450
Mapped reads with at least one deletion	1.12%
Homopolymer indels	42.98%

2.6. Chromosome stats

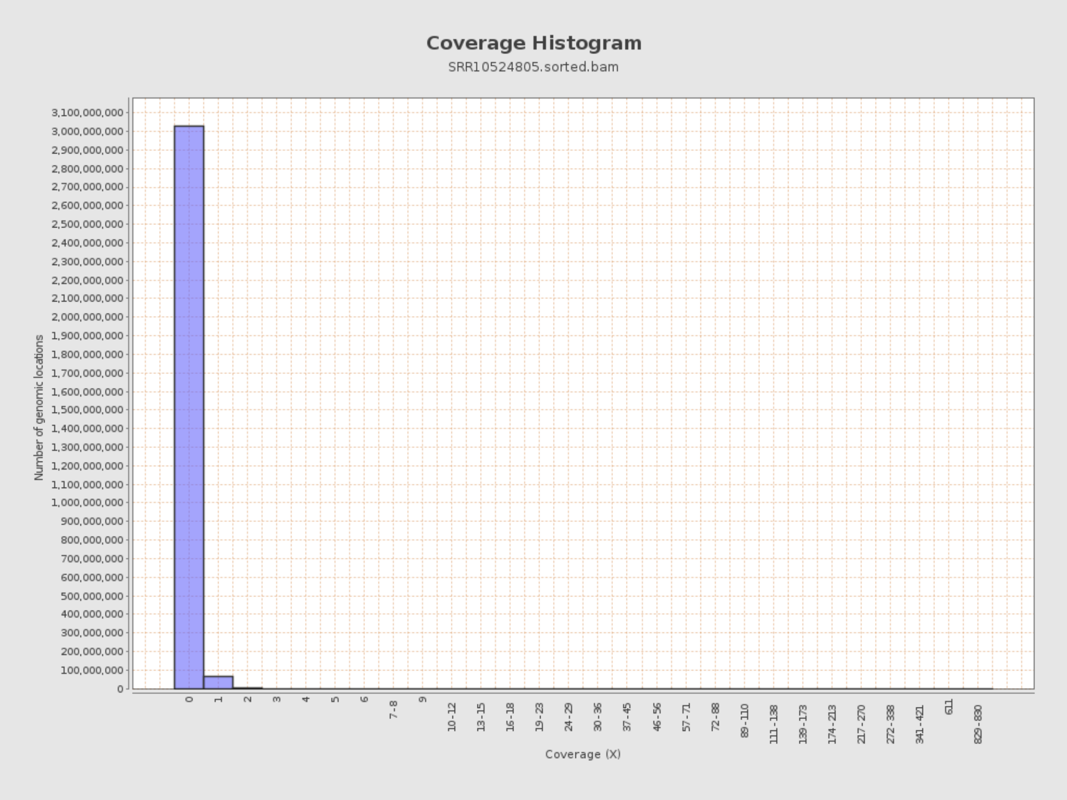
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6272181	0.0252	0.3196
chr2	243199373	6566140	0.027	0.3947
chr3	198022430	5123363	0.0259	0.1794
chr4	191154276	5070088	0.0265	0.2062
chr5	180915260	4685587	0.0259	0.1777
chr6	171115067	4463586	0.0261	0.203
chr7	159138663	4342482	0.0273	0.2765

chr8	146364022	3866869	0.0264	0.2213
chr9	141213431	3314874	0.0235	0.2025
chr10	135534747	3879325	0.0286	0.2847
chr11	135006516	3527271	0.0261	0.2043
chr12	133851895	3502434	0.0262	0.1805
chr13	115169878	2416192	0.021	0.1607
chr14	107349540	2152494	0.0201	0.1616
chr15	102531392	2275212	0.0222	0.1648
chr16	90354753	2369200	0.0262	0.1969
chr17	81195210	2223393	0.0274	0.1893
chr18	78077248	2026979	0.026	0.2848
chr19	59128983	1761311	0.0298	0.2737
chr20	63025520	1661249	0.0264	0.1873
chr21	48129895	1050151	0.0218	0.1797
chr22	51304566	973297	0.019	0.1543
chrMT	16571	27880	1.6825	1.5671
chrX	155270560	4382703	0.0282	0.1968
chrY	59373566	273740	0.0046	0.1365

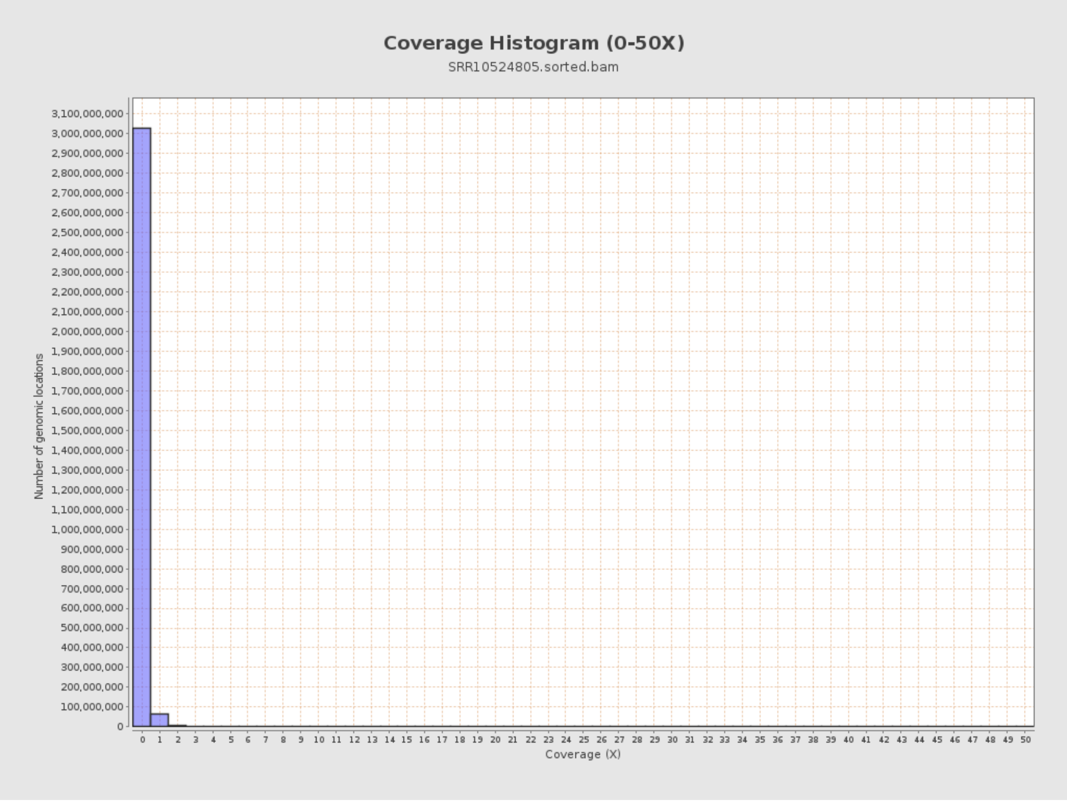
3. Results : Coverage across reference



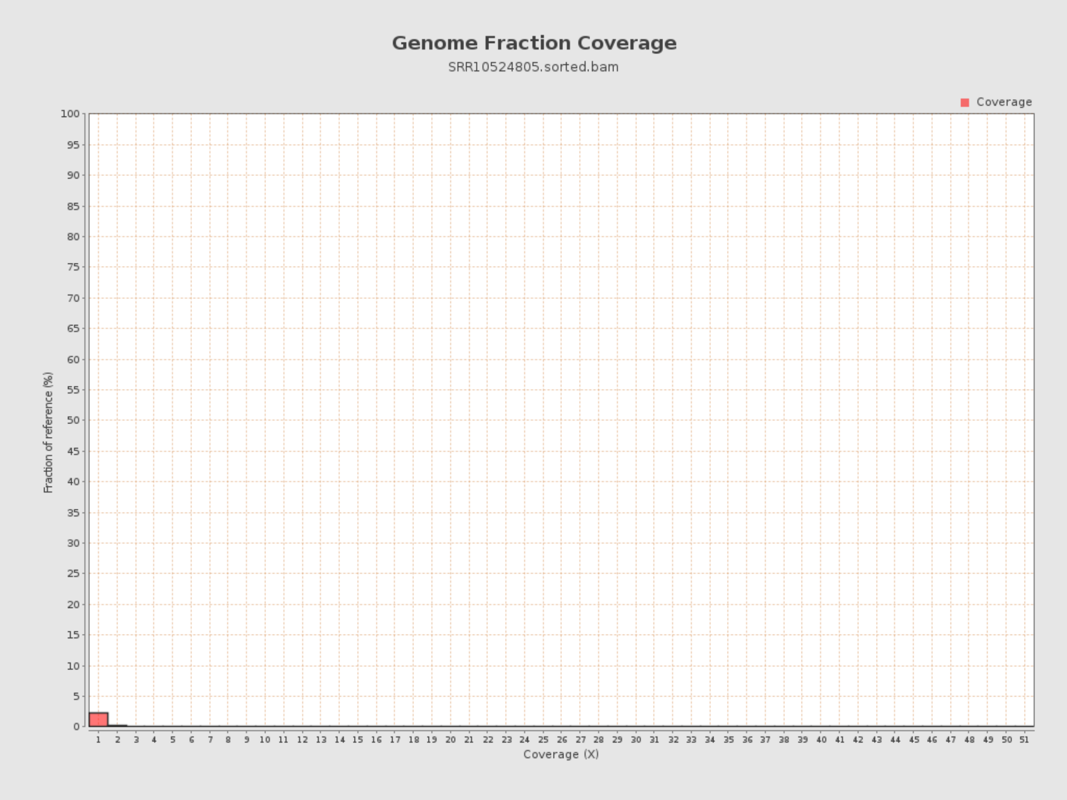
4. Results : Coverage Histogram



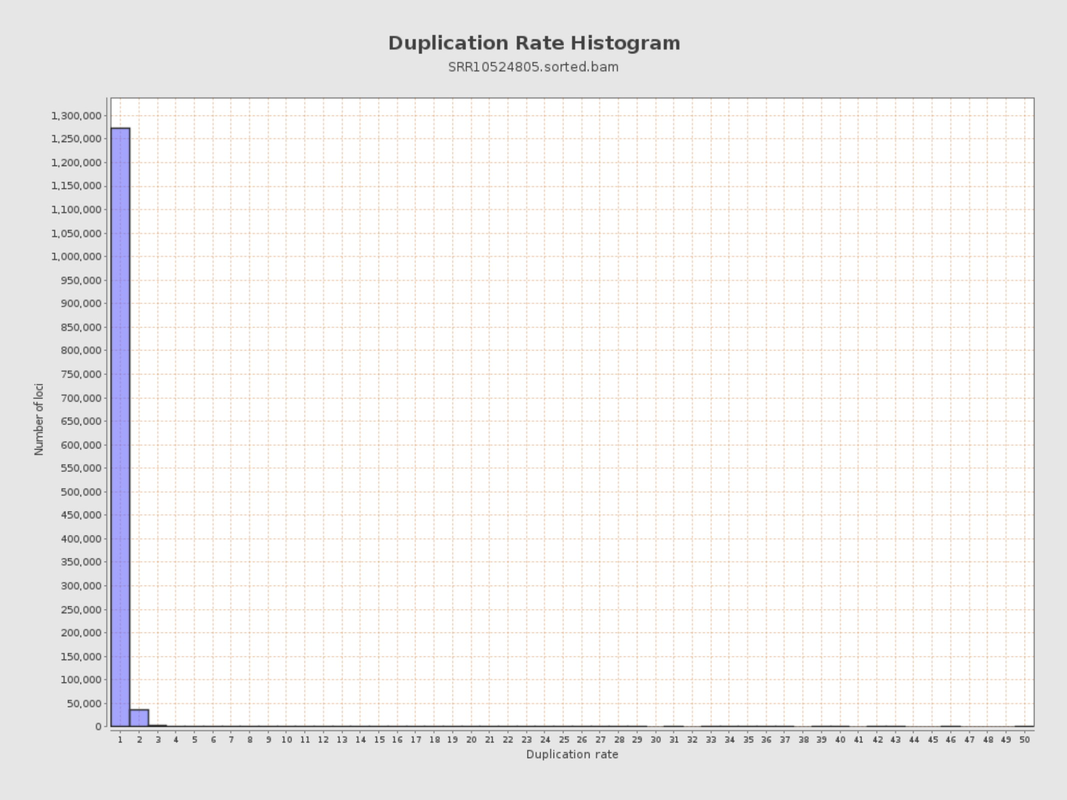
5. Results : Coverage Histogram (0-50X)



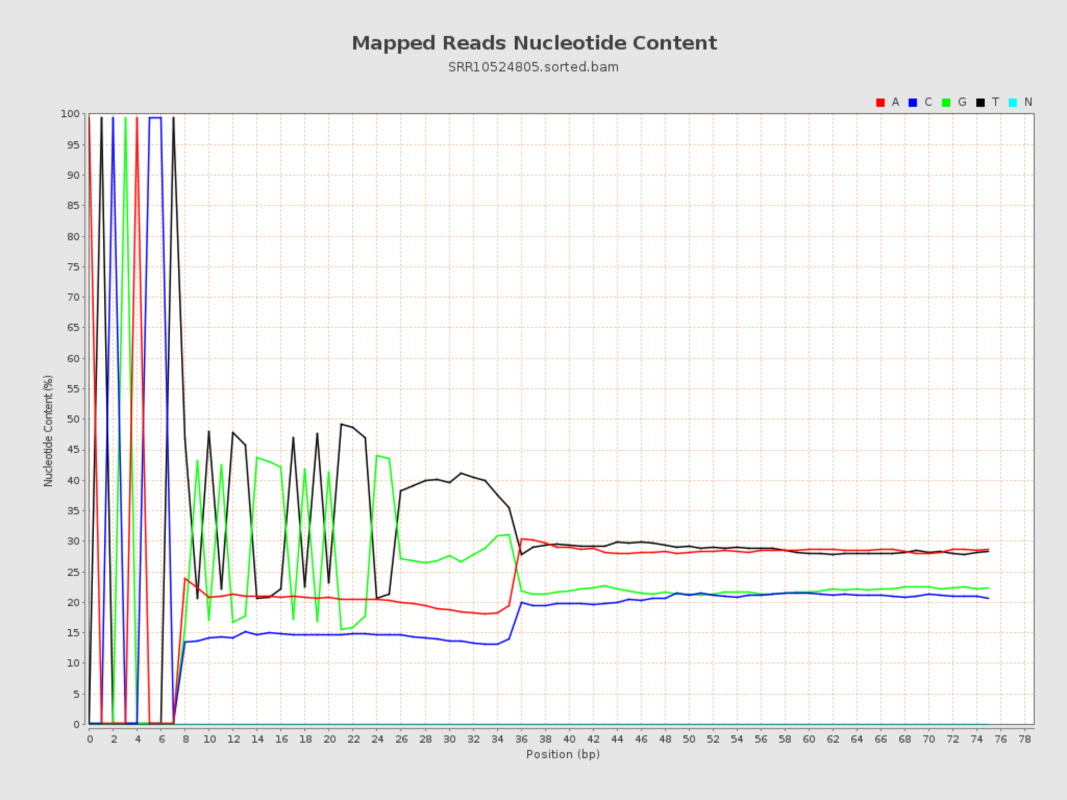
6. Results : Genome Fraction Coverage



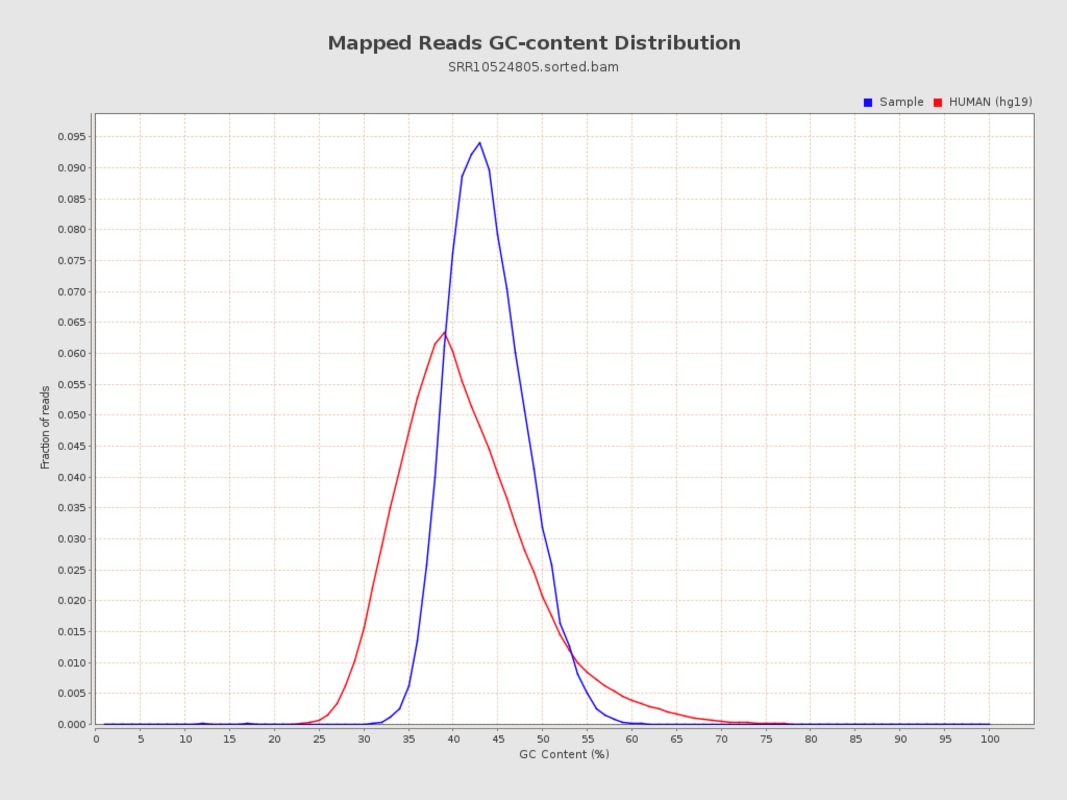
7. Results : Duplication Rate Histogram



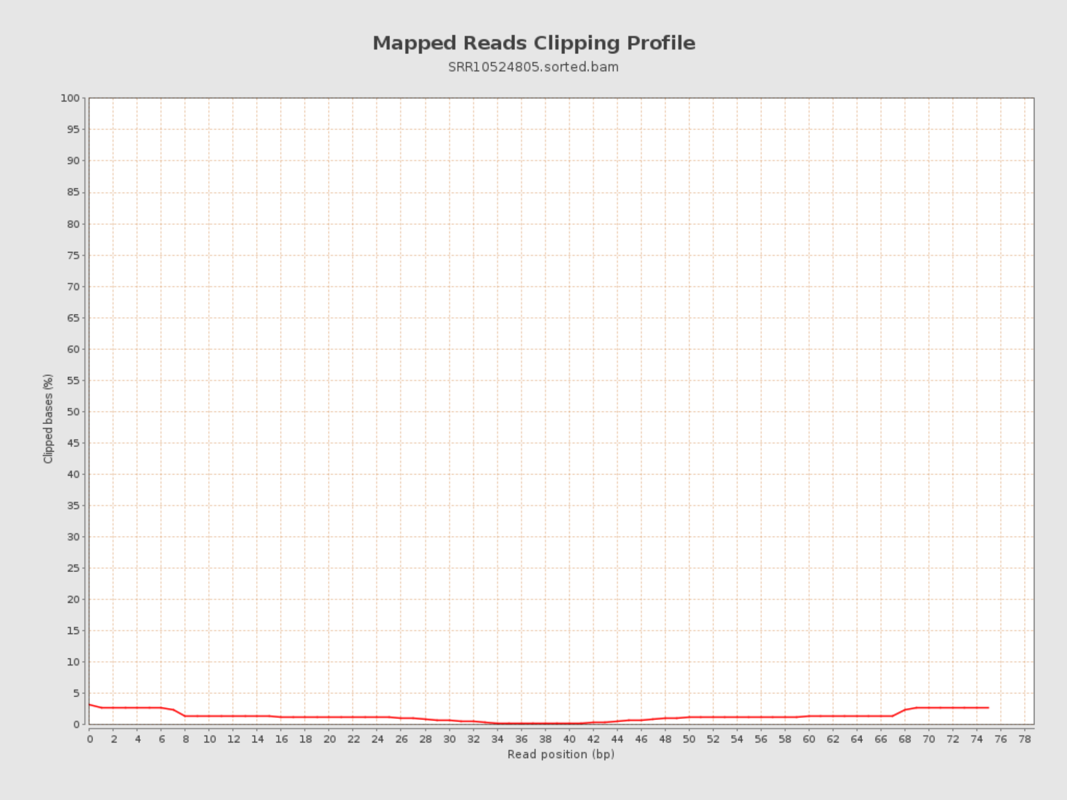
8. Results : Mapped Reads Nucleotide Content



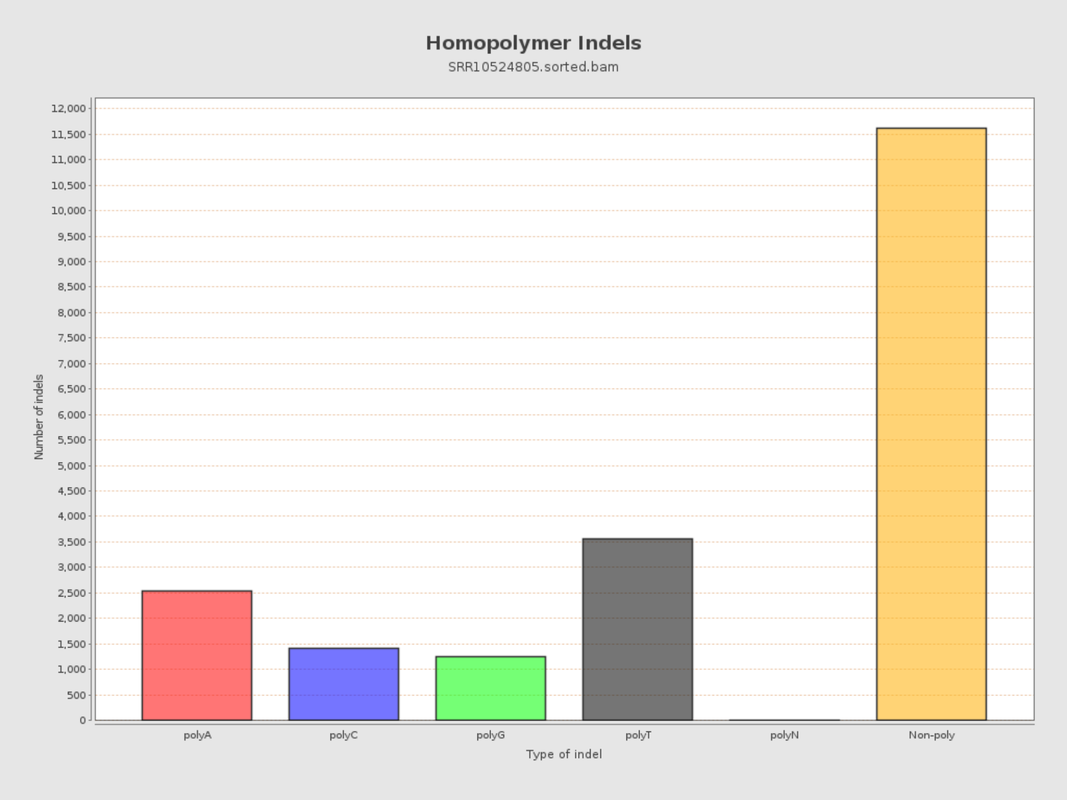
9. Results : Mapped Reads GC-content Distribution



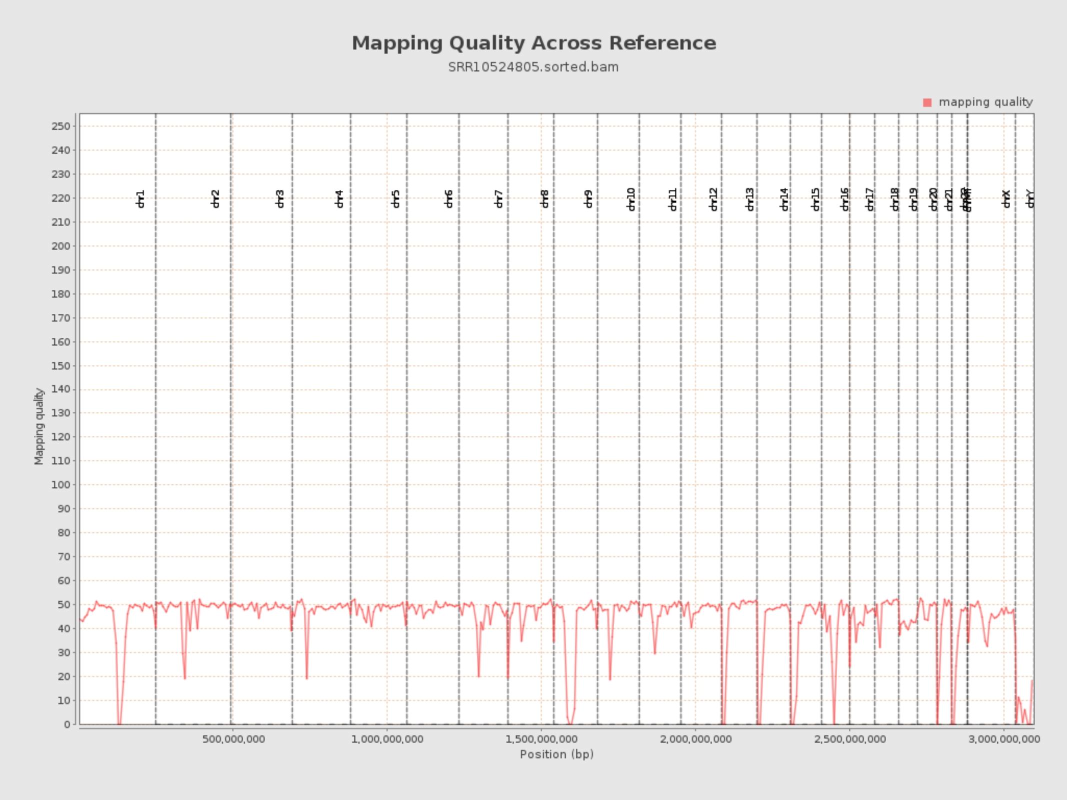
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram