Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:03:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524772.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_SRR10524772 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524772.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:03:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524772.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,137,709
Mapped reads	1,040,519 / 91.46%
Unmapped reads	97,190 / 8.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,958 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	29,992 / 2.64%
Duplication rate	2.17%
Clipped reads	1,043,281 / 91.7%

2.2. ACGT Content

Number/percentage of A's	14,056,706 / 23.49%
Number/percentage of C's	11,171,368 / 18.67%
Number/percentage of T's	19,244,145 / 32.15%
Number/percentage of G's	15,371,829 / 25.68%
Number/percentage of N's	7,340 / 0.01%
GC Percentage	44.35%

2.3. Coverage

Mean	0.0193

Standard Deviation	0.1872

2.4. Mapping Quality

Mean Mapping Quality	44.83

2.5. Mismatches and indels

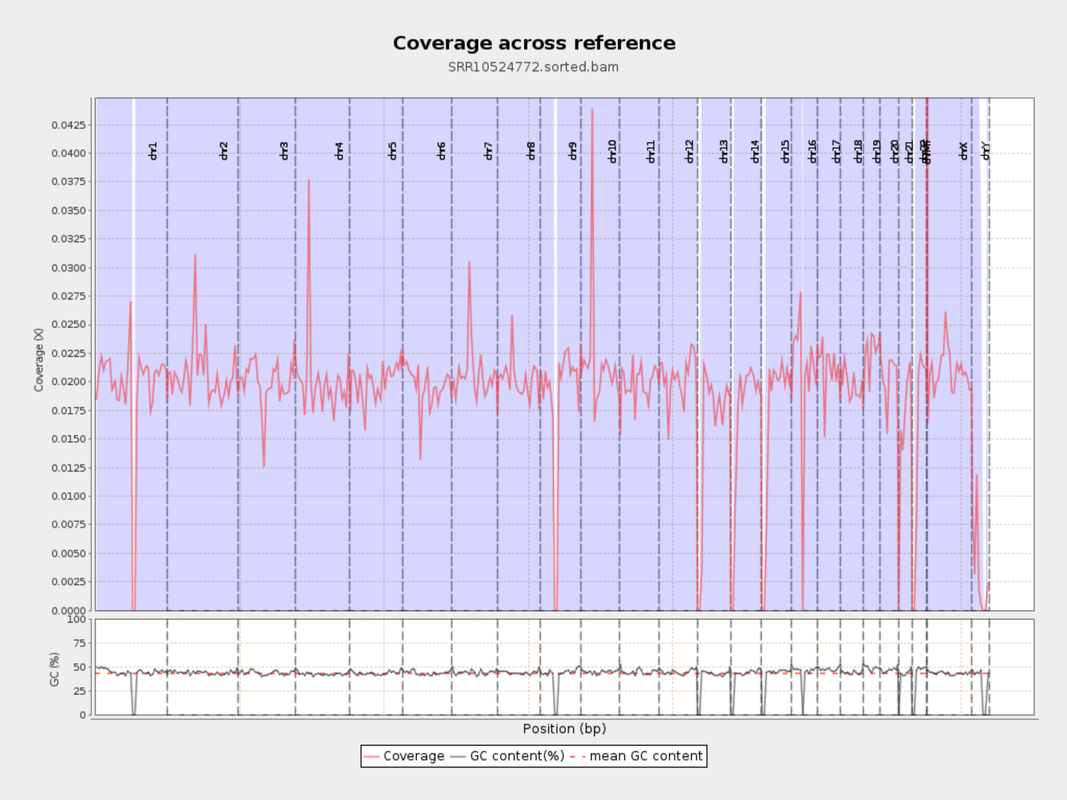
General error rate	0.52%
Mismatches	302,887
Insertions	3,696
Mapped reads with at least one insertion	0.35%
Deletions	11,638
Mapped reads with at least one deletion	1.11%
Homopolymer indels	42.73%

2.6. Chromosome stats

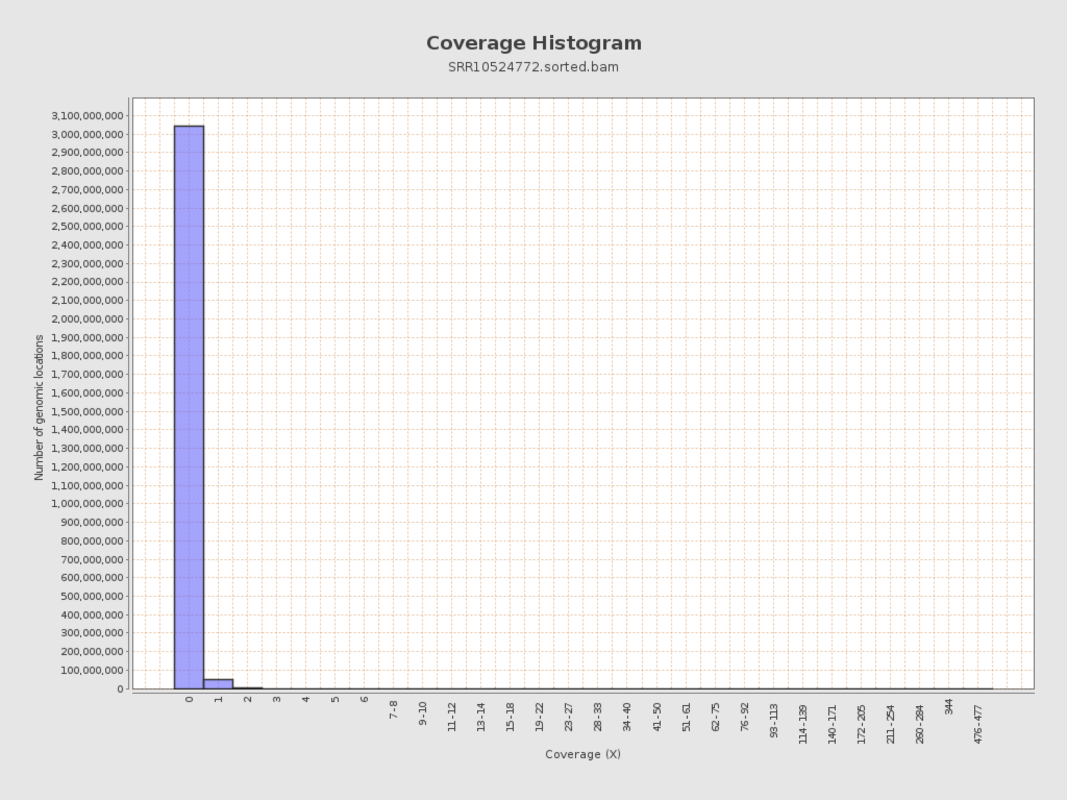
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4815591	0.0193	0.2464
chr2	243199373	5038446	0.0207	0.2649
chr3	198022430	3936574	0.0199	0.1549
chr4	191154276	3859501	0.0202	0.1692
chr5	180915260	3640191	0.0201	0.1516
chr6	171115067	3363388	0.0197	0.1568
chr7	159138663	3318754	0.0209	0.2247

chr8	146364022	2961928	0.0202	0.1788
chr9	141213431	2577391	0.0183	0.1668
chr10	135534747	2961805	0.0219	0.2354
chr11	135006516	2696005	0.02	0.1752
chr12	133851895	2725886	0.0204	0.1543
chr13	115169878	1810809	0.0157	0.1339
chr14	107349540	1767835	0.0165	0.1404
chr15	102531392	1699608	0.0166	0.1375
chr16	90354753	1838730	0.0204	0.1681
chr17	81195210	1711392	0.0211	0.1607
chr18	78077248	1537819	0.0197	0.2416
chr19	59128983	1336481	0.0226	0.2109
chr20	63025520	1274127	0.0202	0.1589
chr21	48129895	777517	0.0162	0.1472
chr22	51304566	757879	0.0148	0.1308
chrMT	16571	14488	0.8743	1.1103
chrX	155270560	3250085	0.0209	0.1623
chrY	59373566	198183	0.0033	0.0978

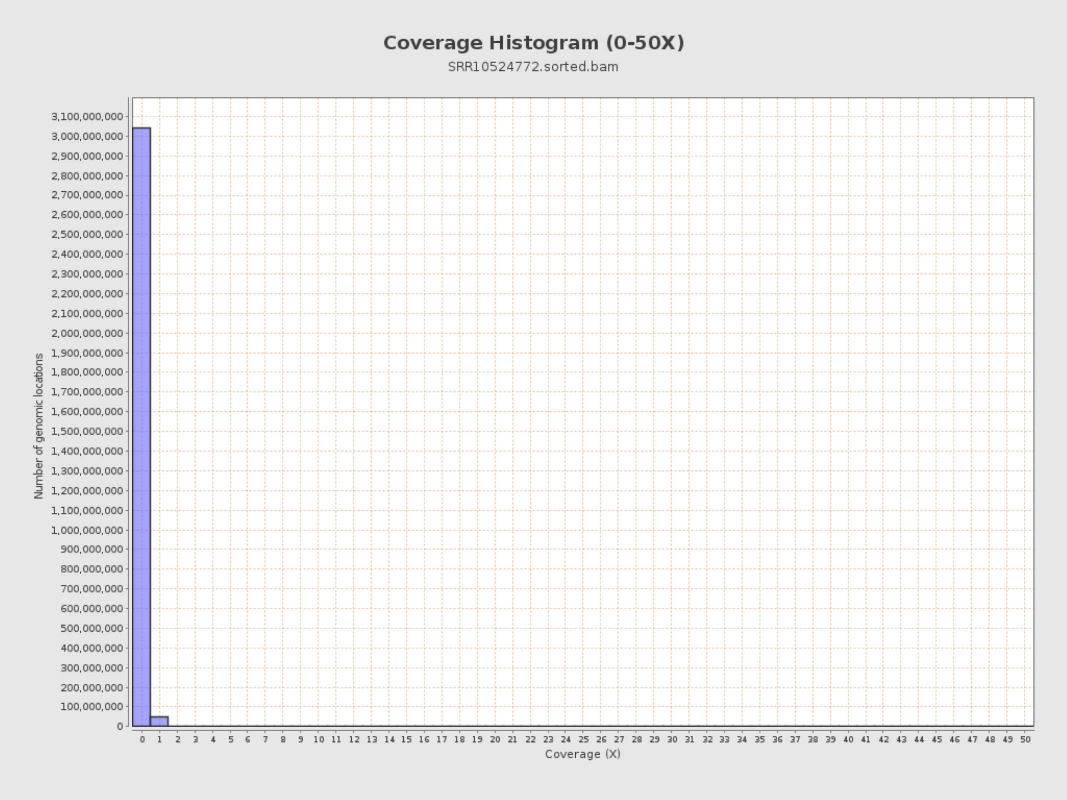
3. Results : Coverage across reference



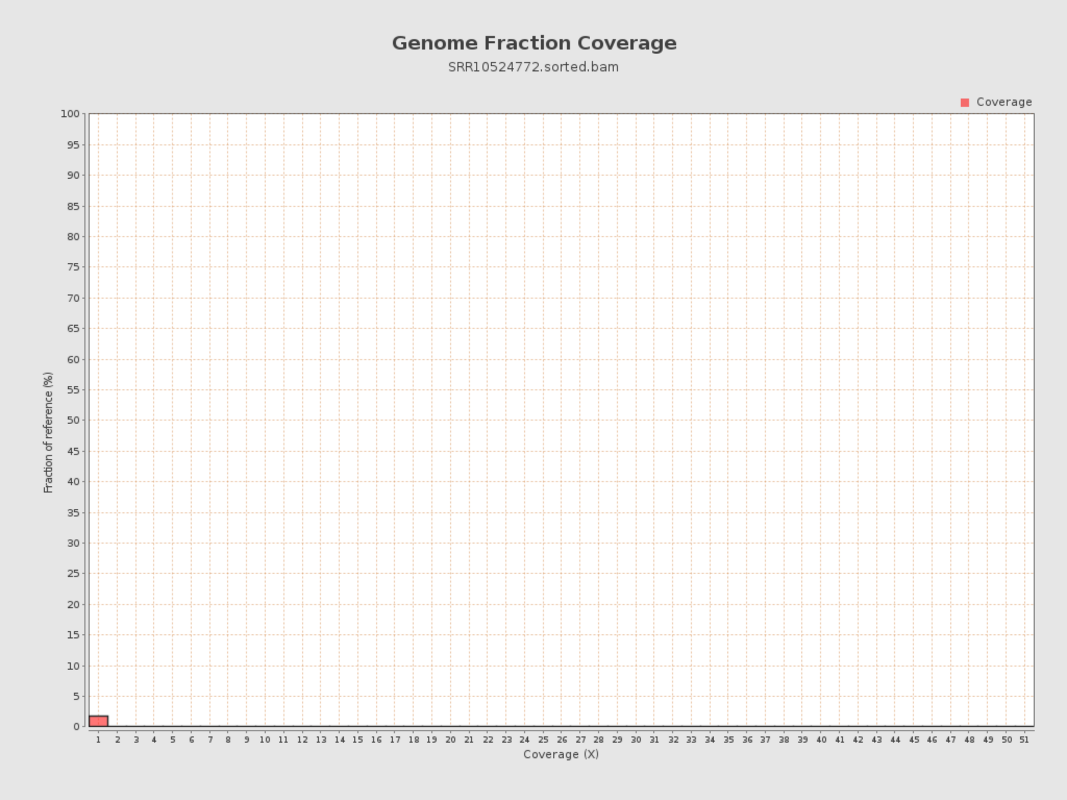
4. Results : Coverage Histogram



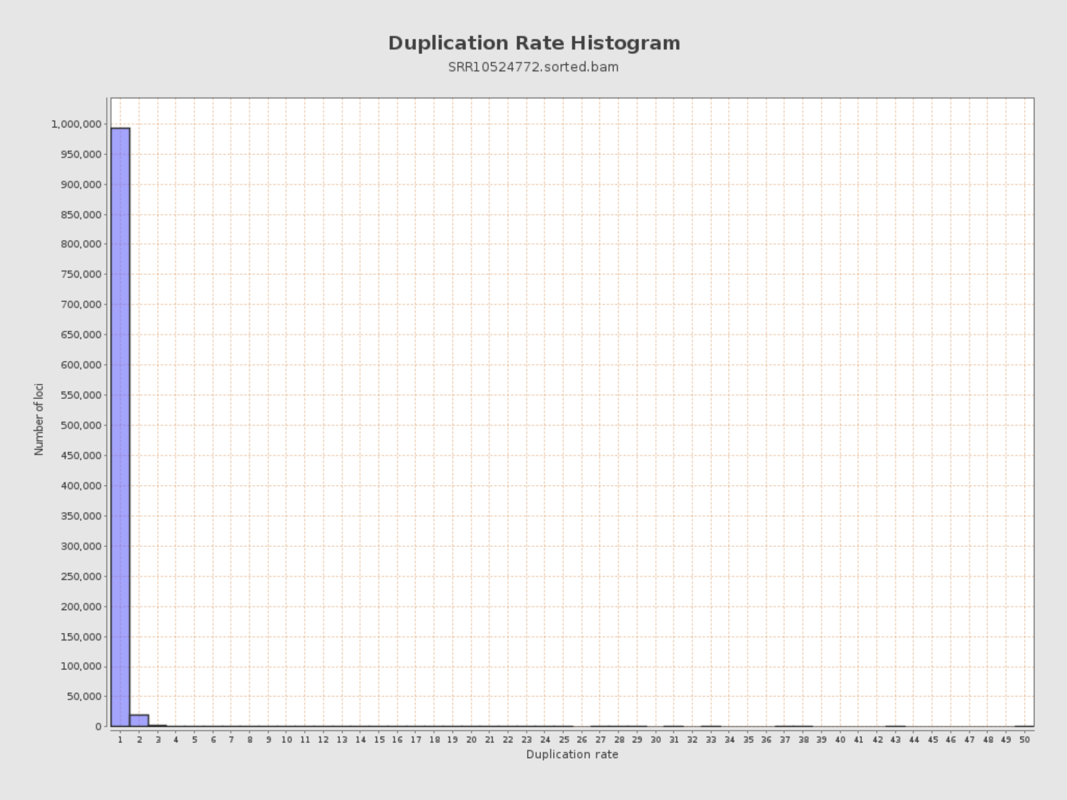
5. Results : Coverage Histogram (0-50X)



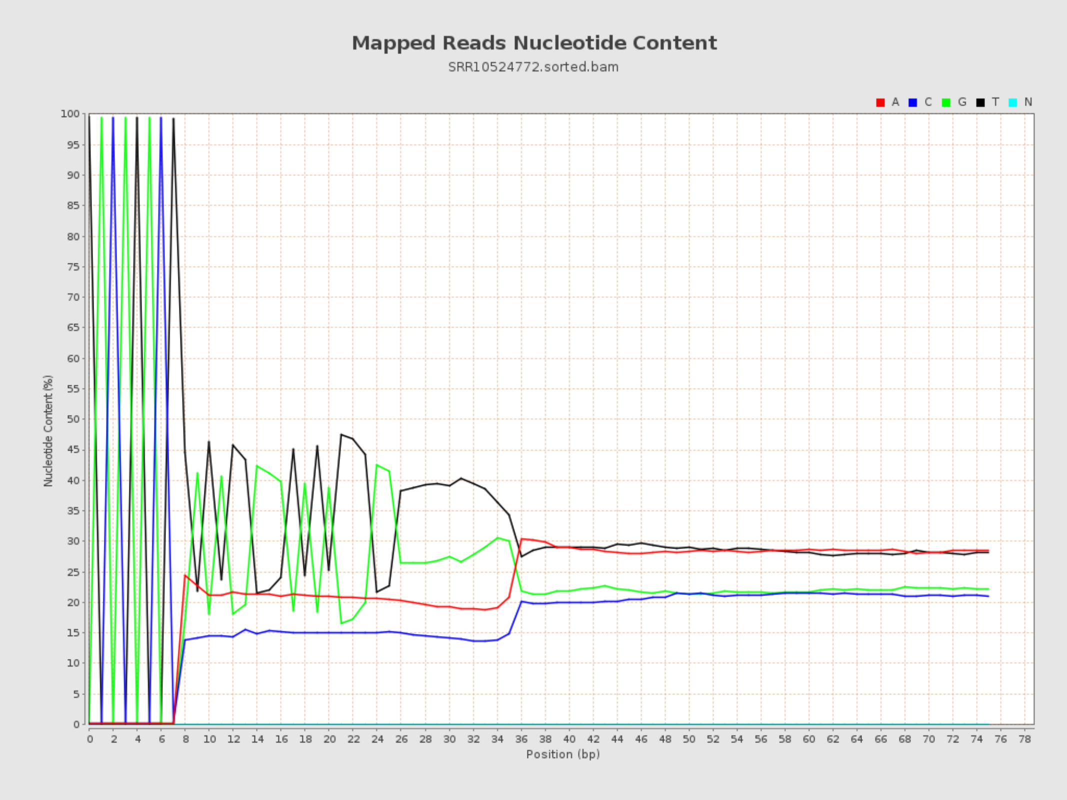
6. Results : Genome Fraction Coverage



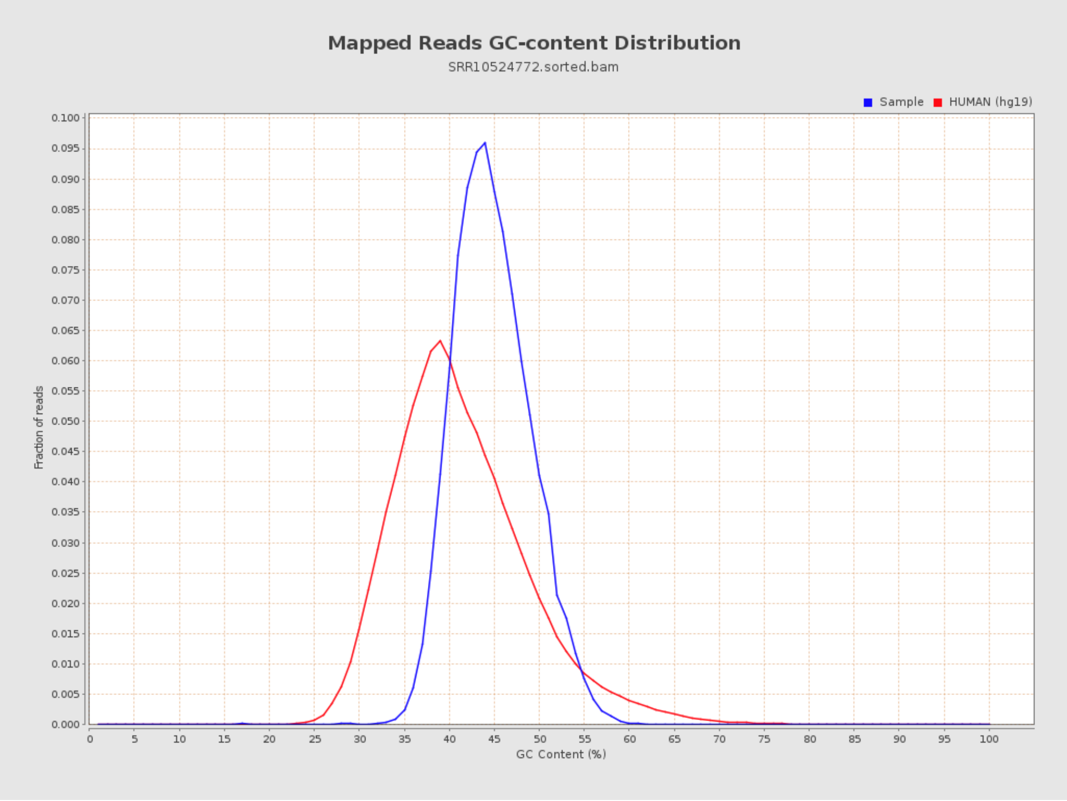
7. Results : Duplication Rate Histogram



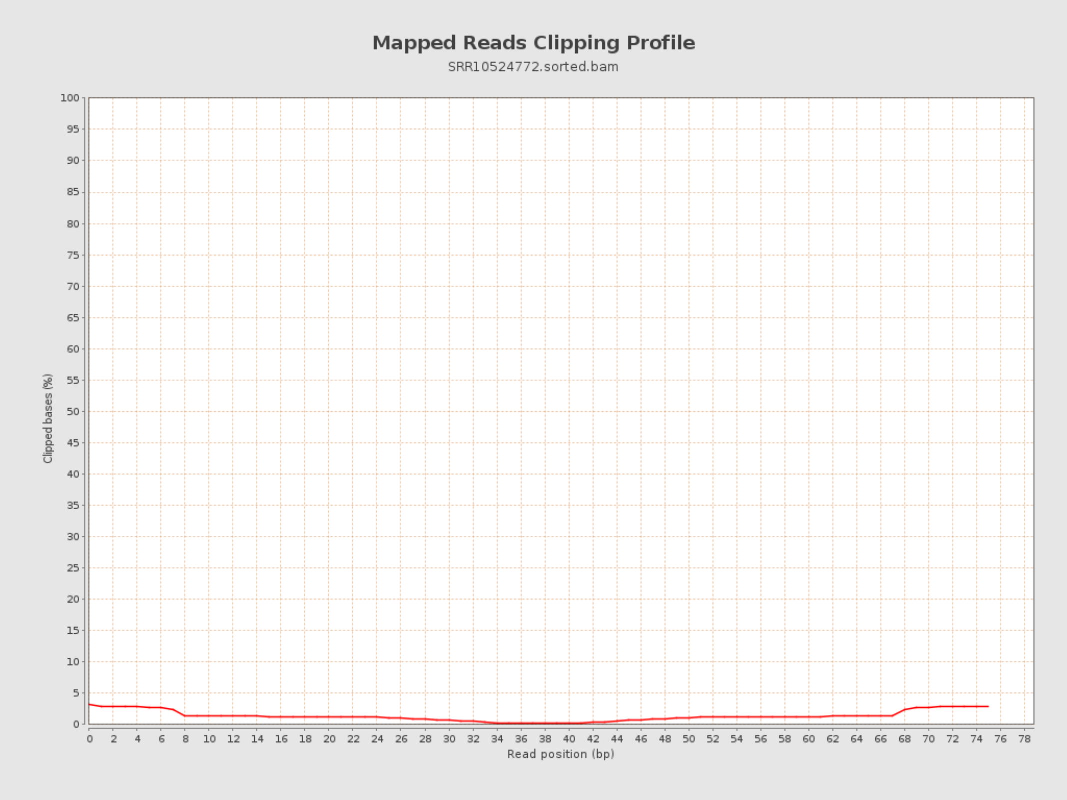
8. Results : Mapped Reads Nucleotide Content



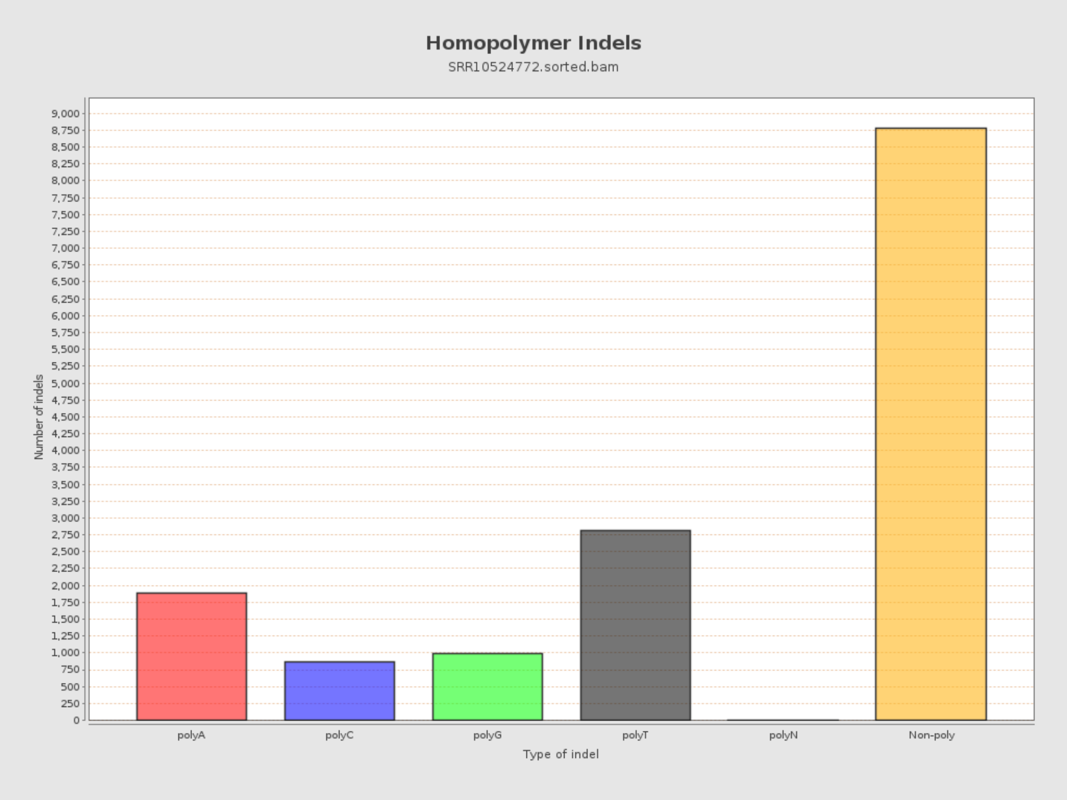
9. Results : Mapped Reads GC-content Distribution



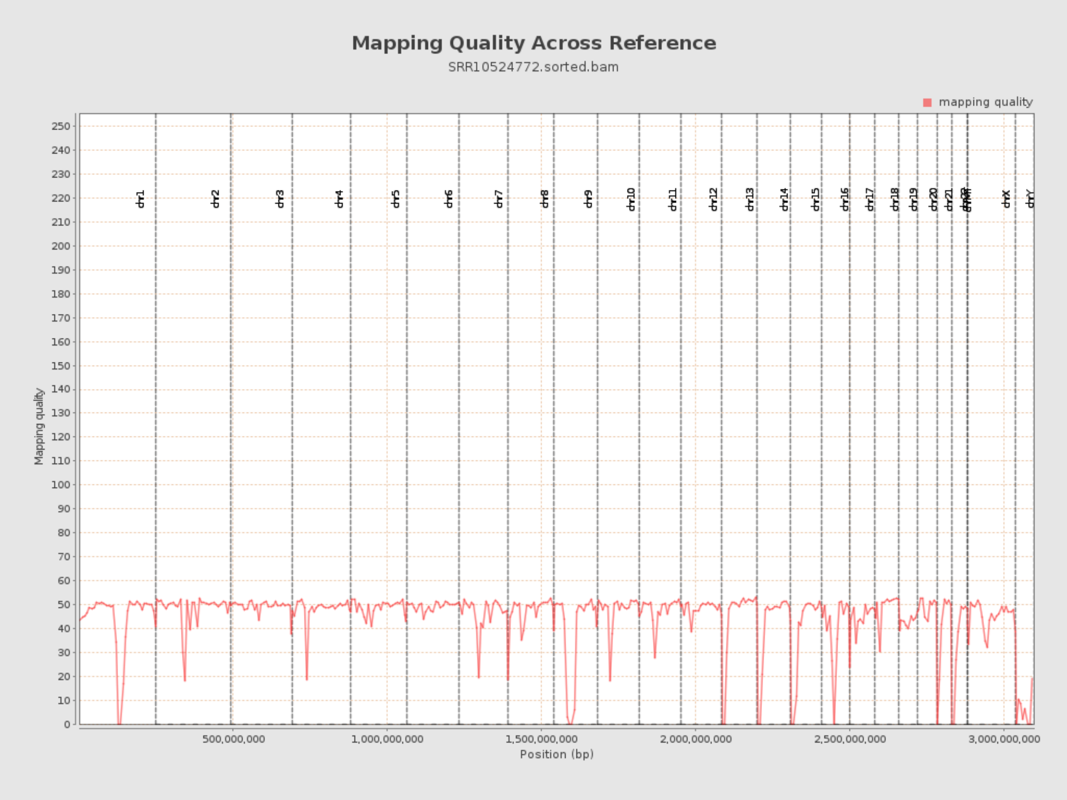
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram