Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 02:47:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717048.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_SRR9717048 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717048.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 02:47:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717048.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,060,950
Mapped reads	899,142 / 84.75%
Unmapped reads	161,808 / 15.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,375 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	18,267 / 1.72%
Duplication rate	1.45%
Clipped reads	902,111 / 85.03%

2.2. ACGT Content

Number/percentage of A's	11,695,982 / 23.2%
Number/percentage of C's	10,870,820 / 21.56%
Number/percentage of T's	14,653,448 / 29.07%
Number/percentage of G's	13,188,529 / 26.16%
Number/percentage of N's	1,525 / 0%
GC Percentage	47.73%

2.3. Coverage

Mean	0.0163

Standard Deviation	0.1581

2.4. Mapping Quality

Mean Mapping Quality	39.3

2.5. Mismatches and indels

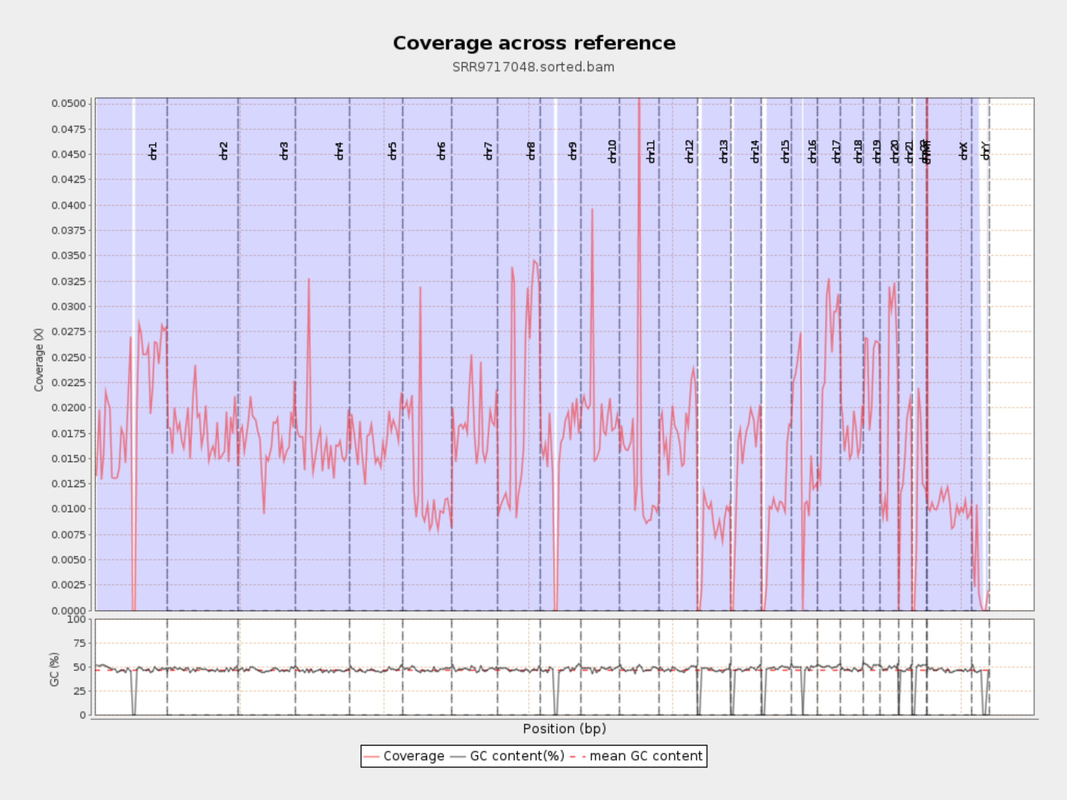
General error rate	0.54%
Mismatches	263,868
Insertions	3,172
Mapped reads with at least one insertion	0.35%
Deletions	8,482
Mapped reads with at least one deletion	0.93%
Homopolymer indels	35.17%

2.6. Chromosome stats

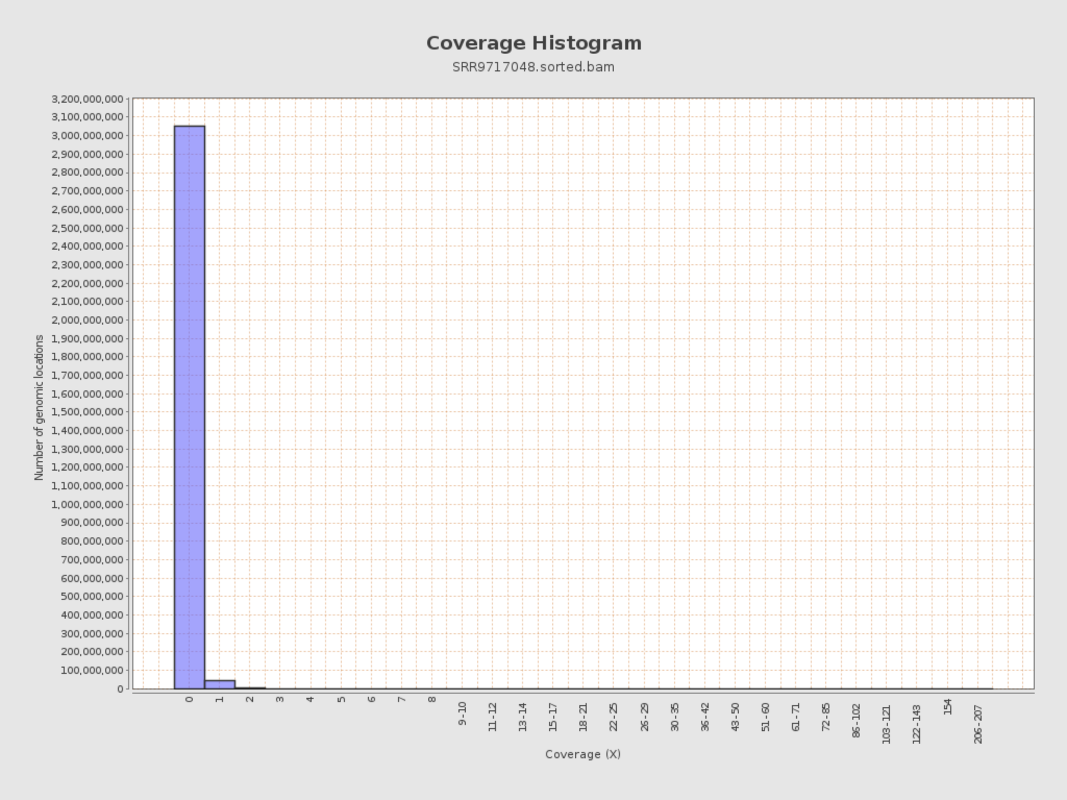
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4897075	0.0196	0.1915
chr2	243199373	4316112	0.0177	0.1869
chr3	198022430	3344184	0.0169	0.1441
chr4	191154276	3231828	0.0169	0.1562
chr5	180915260	3062762	0.0169	0.1403
chr6	171115067	2223628	0.013	0.1251
chr7	159138663	2936795	0.0185	0.1739

chr8	146364022	3052409	0.0209	0.1638
chr9	141213431	2174701	0.0154	0.1464
chr10	135534747	2685617	0.0198	0.2346
chr11	135006516	2051128	0.0152	0.1578
chr12	133851895	2433910	0.0182	0.1465
chr13	115169878	903074	0.0078	0.0957
chr14	107349540	1579935	0.0147	0.1363
chr15	102531392	981005	0.0096	0.1076
chr16	90354753	1397193	0.0155	0.143
chr17	81195210	2046994	0.0252	0.1797
chr18	78077248	1354946	0.0174	0.1718
chr19	59128983	1420123	0.024	0.1934
chr20	63025520	1303224	0.0207	0.1625
chr21	48129895	703205	0.0146	0.1452
chr22	51304566	577902	0.0113	0.117
chrMT	16571	1448	0.0874	0.3284
chrX	155270560	1585806	0.0102	0.1169
chrY	59373566	160172	0.0027	0.0895

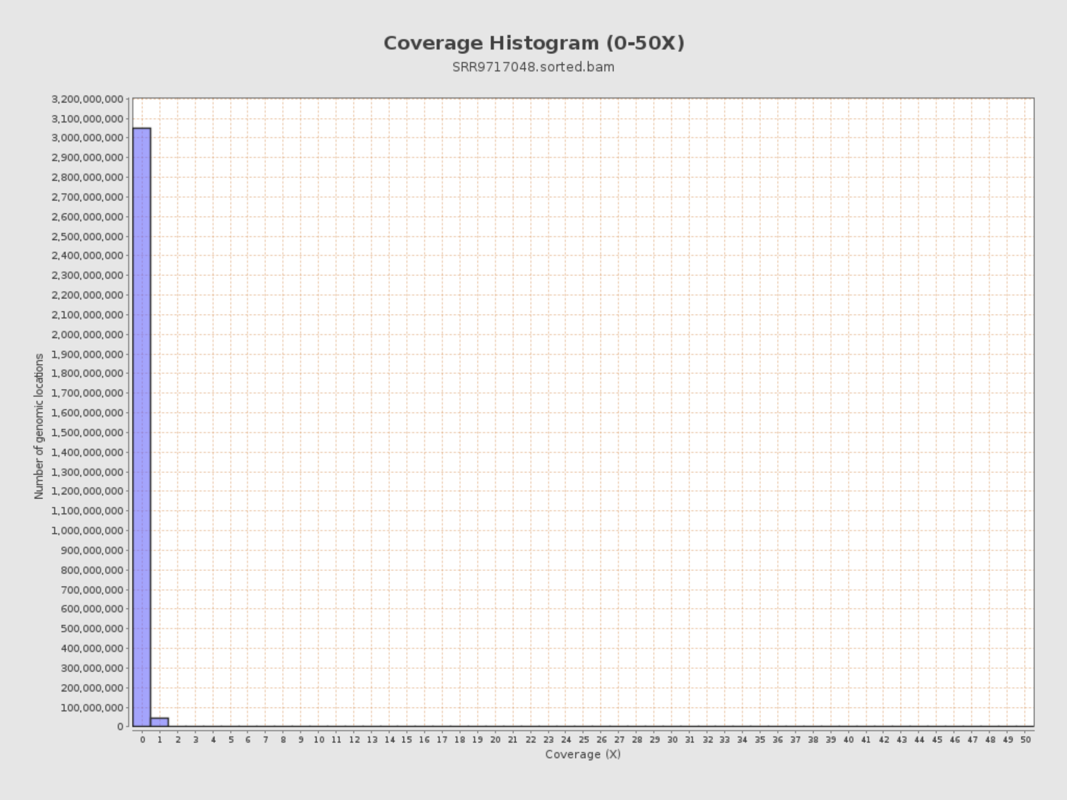
3. Results : Coverage across reference



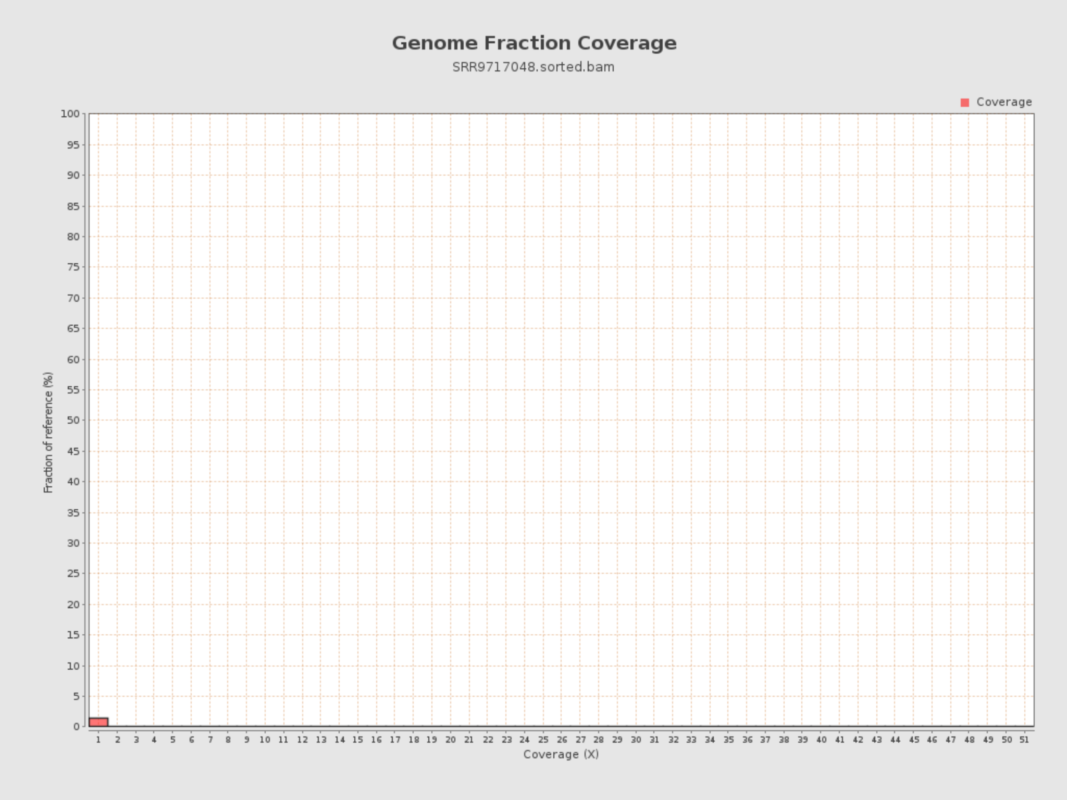
4. Results : Coverage Histogram



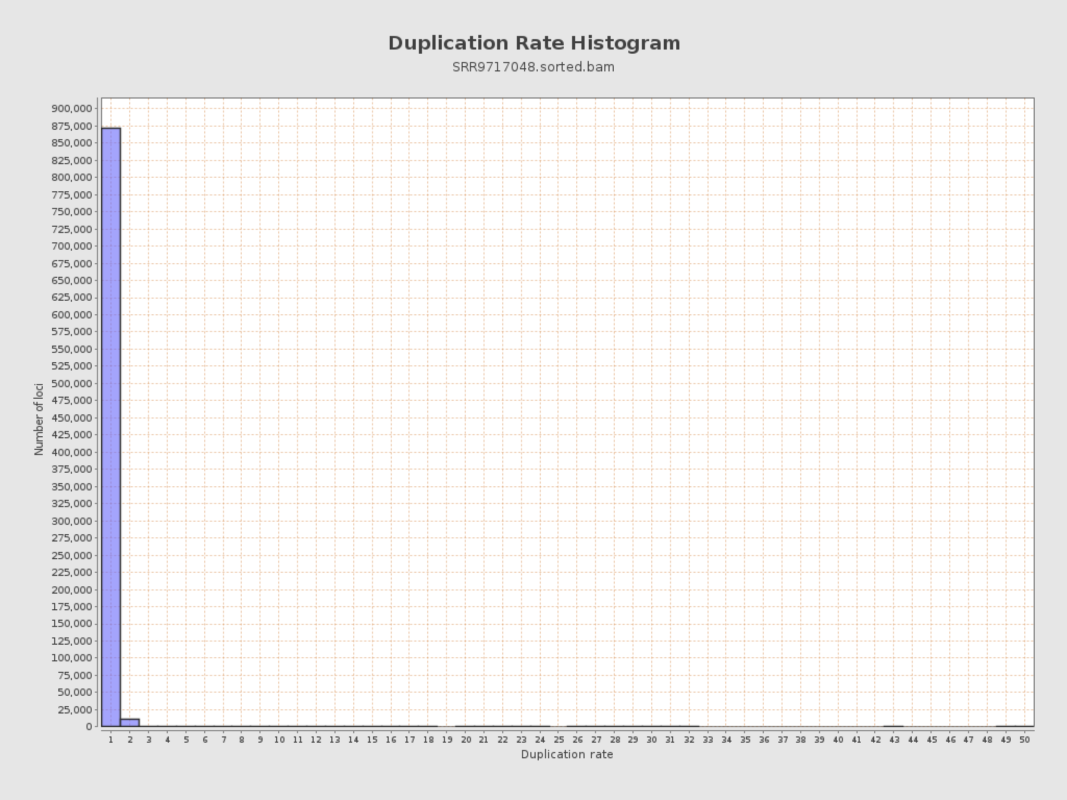
5. Results : Coverage Histogram (0-50X)



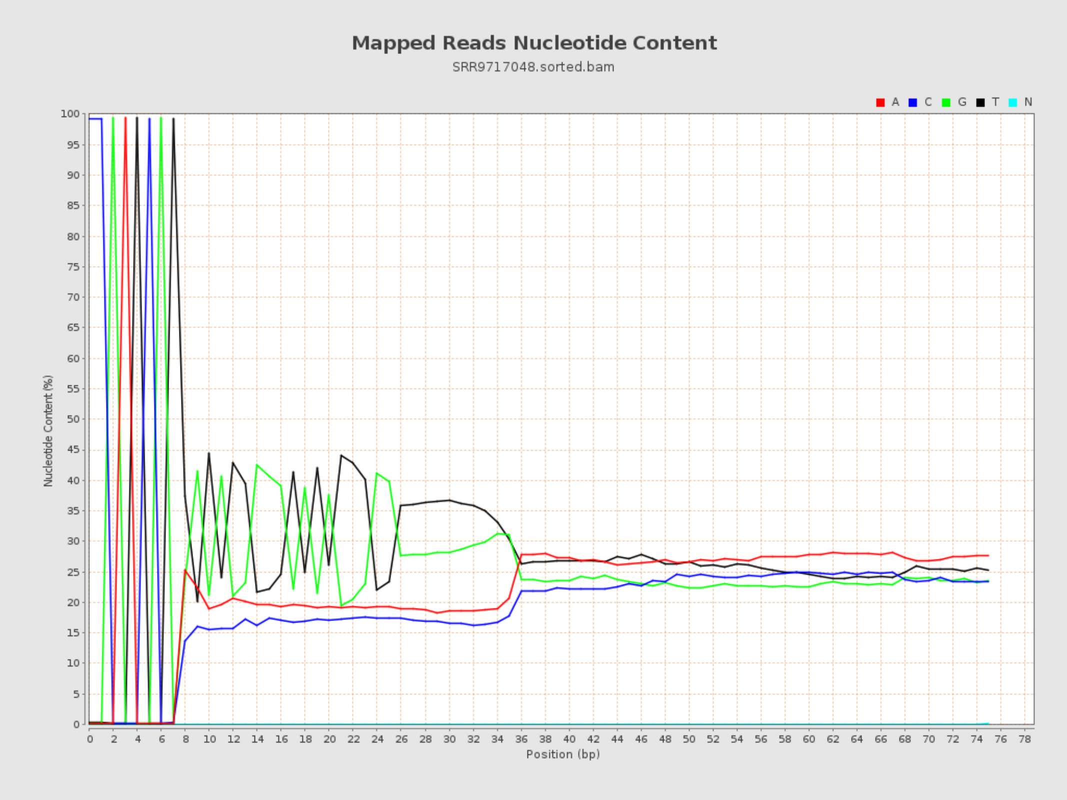
6. Results : Genome Fraction Coverage



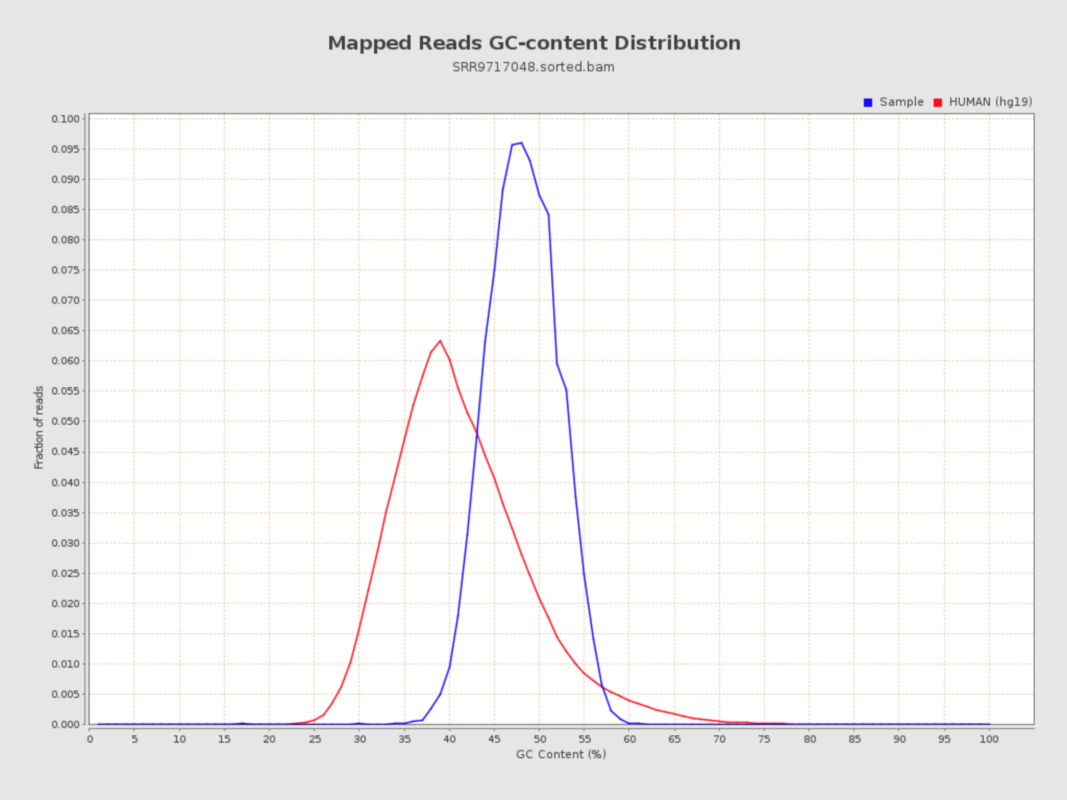
7. Results : Duplication Rate Histogram



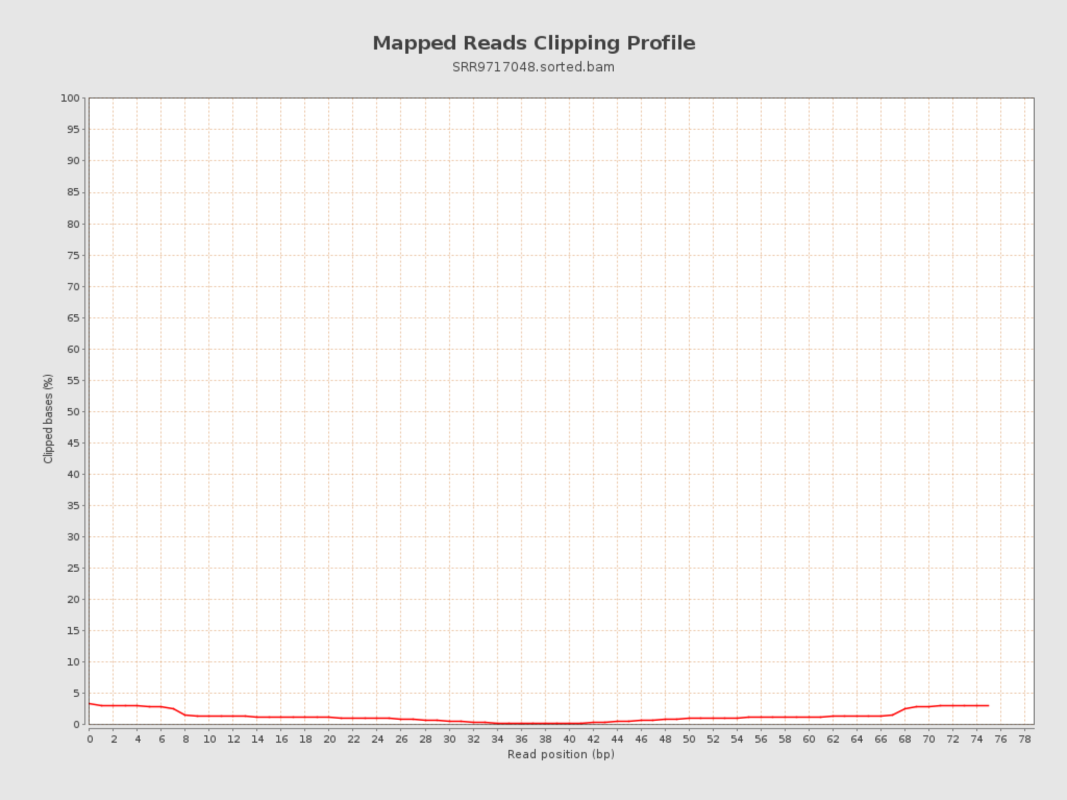
8. Results : Mapped Reads Nucleotide Content



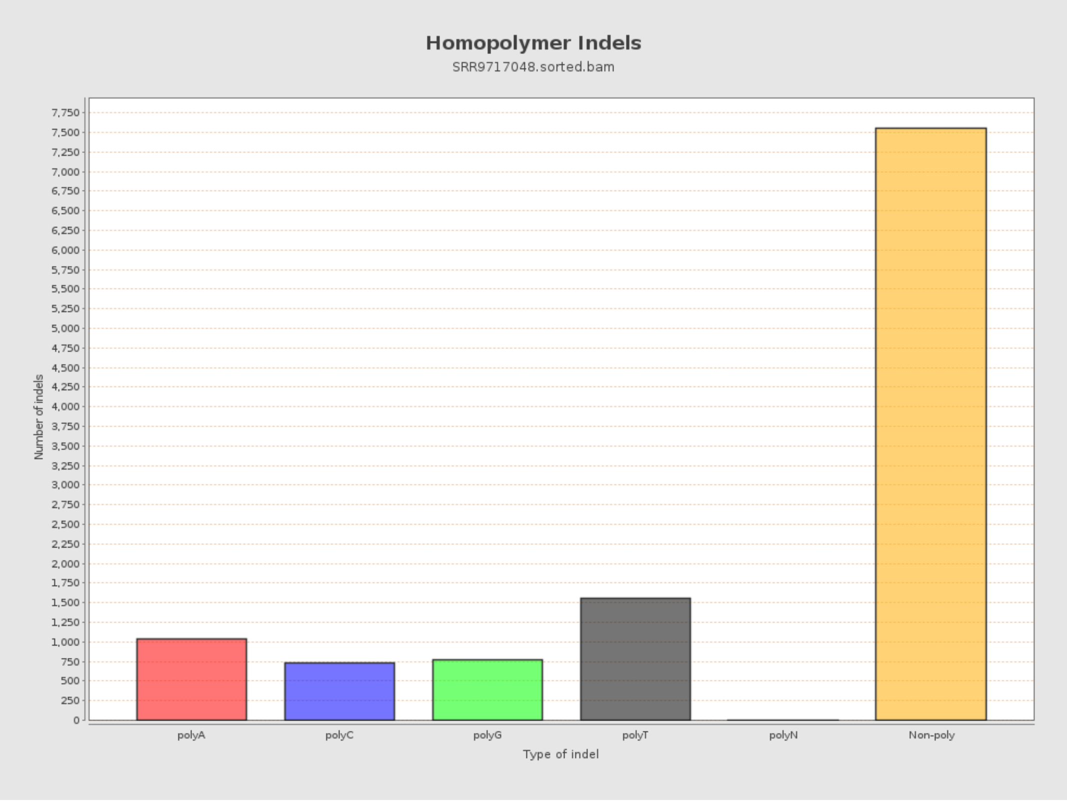
9. Results : Mapped Reads GC-content Distribution



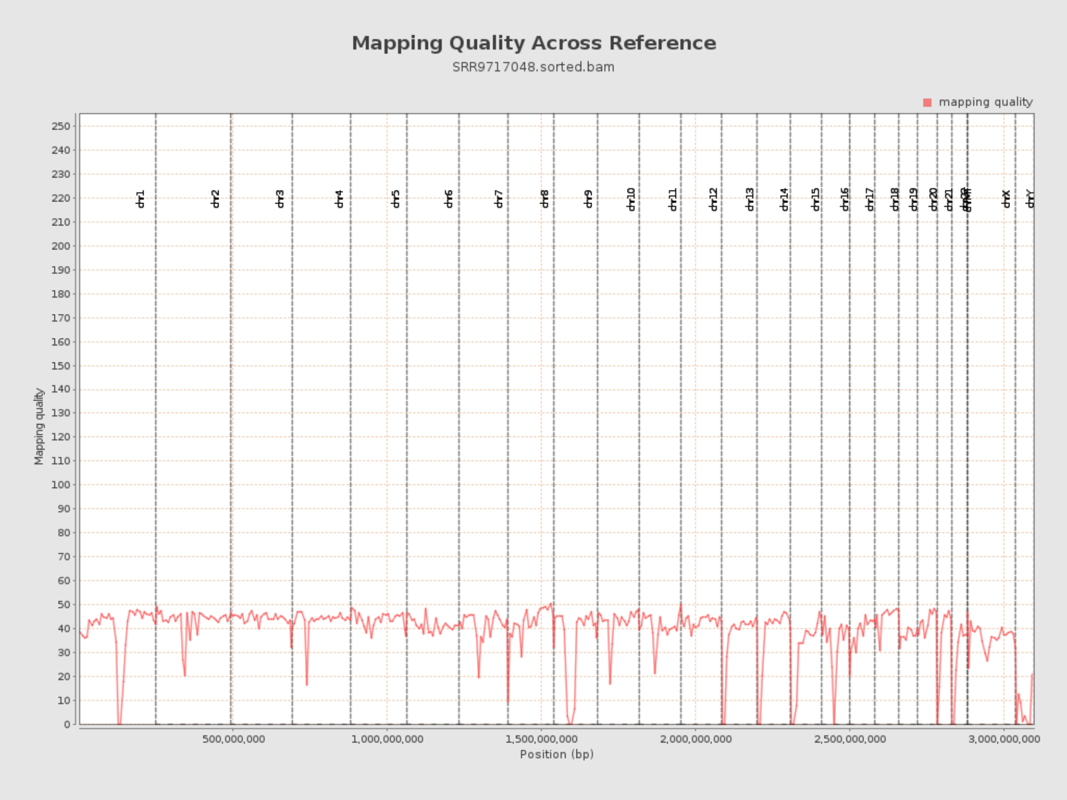
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram