Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:34:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717028.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_SRR9717028 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717028.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:34:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717028.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,787,177
Mapped reads	2,563,024 / 91.96%
Unmapped reads	224,153 / 8.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,293 / 0.51%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	116,246 / 4.17%
Duplication rate	3.2%
Clipped reads	2,572,460 / 92.3%

2.2. ACGT Content

Number/percentage of A's	36,371,976 / 24.27%
Number/percentage of C's	29,085,023 / 19.41%
Number/percentage of T's	46,982,468 / 31.35%
Number/percentage of G's	37,441,255 / 24.98%
Number/percentage of N's	1,892 / 0%
GC Percentage	44.39%

2.3. Coverage

Mean	0.0484

Standard Deviation	0.4348

2.4. Mapping Quality

Mean Mapping Quality	44.48

2.5. Mismatches and indels

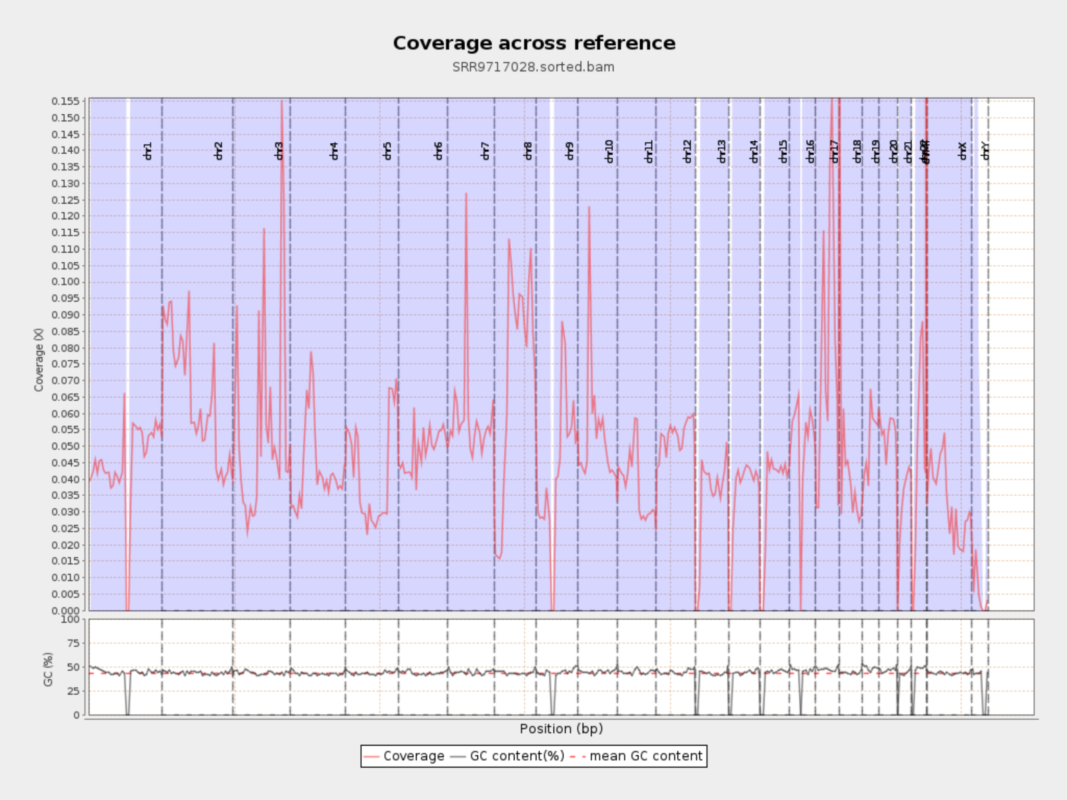
General error rate	0.52%
Mismatches	764,044
Insertions	9,682
Mapped reads with at least one insertion	0.38%
Deletions	28,067
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.28%

2.6. Chromosome stats

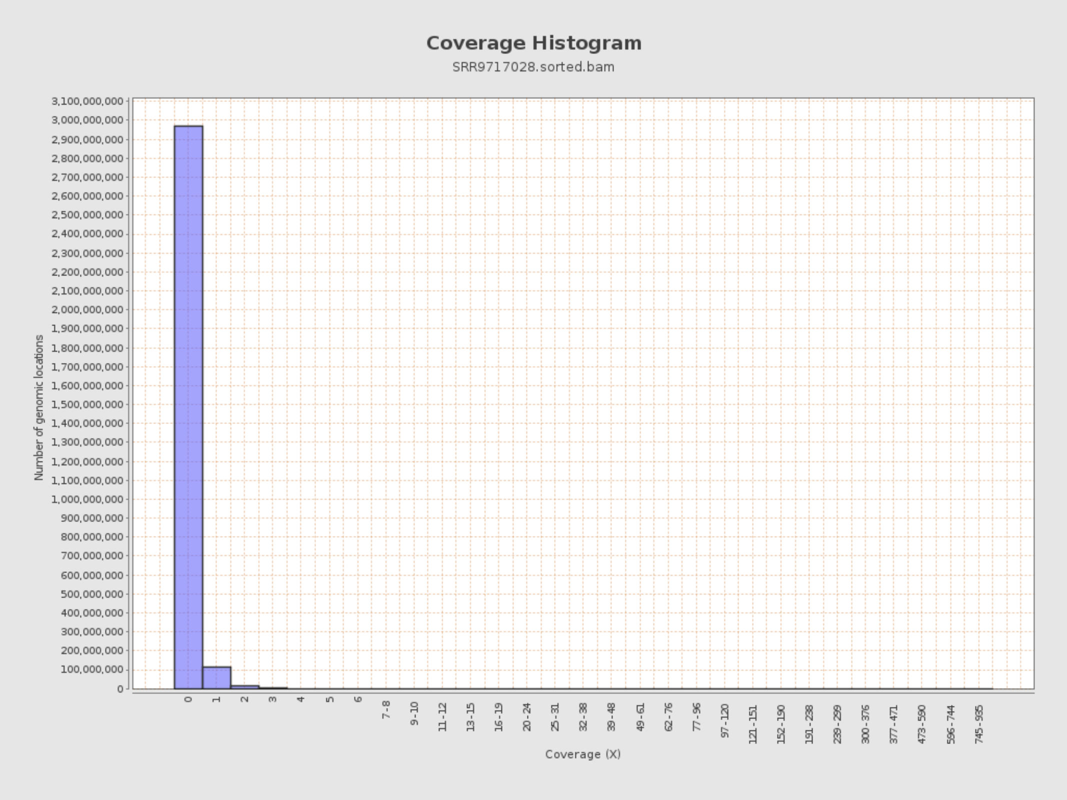
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11159540	0.0448	0.5887
chr2	243199373	15965881	0.0656	0.5205
chr3	198022430	11206154	0.0566	0.295
chr4	191154276	8288176	0.0434	0.2673
chr5	180915260	7550564	0.0417	0.2323
chr6	171115067	8371889	0.0489	0.2774
chr7	159138663	9380948	0.0589	1.0283

chr8	146364022	10640641	0.0727	0.4551
chr9	141213431	5912124	0.0419	0.2888
chr10	135534747	7243015	0.0534	0.6161
chr11	135006516	5139422	0.0381	0.2988
chr12	133851895	7108244	0.0531	0.3112
chr13	115169878	3908432	0.0339	0.2073
chr14	107349540	3765770	0.0351	0.225
chr15	102531392	3640797	0.0355	0.2186
chr16	90354753	4661888	0.0516	0.2772
chr17	81195210	6484855	0.0799	0.3422
chr18	78077248	3494554	0.0448	0.4786
chr19	59128983	3046499	0.0515	0.5725
chr20	63025520	3409215	0.0541	0.2861
chr21	48129895	1554867	0.0323	0.2231
chr22	51304566	2286002	0.0446	0.2403
chrMT	16571	117191	7.0721	4.876
chrX	155270560	5250256	0.0338	0.2498
chrY	59373566	340172	0.0057	0.1454

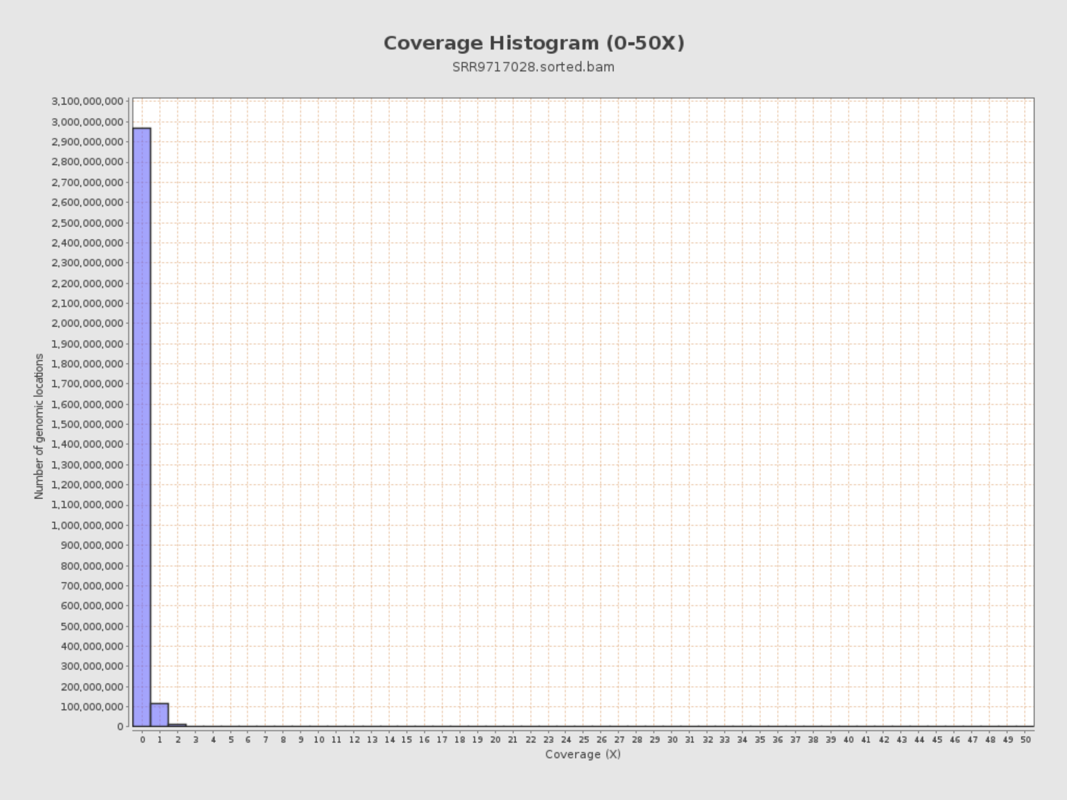
3. Results : Coverage across reference



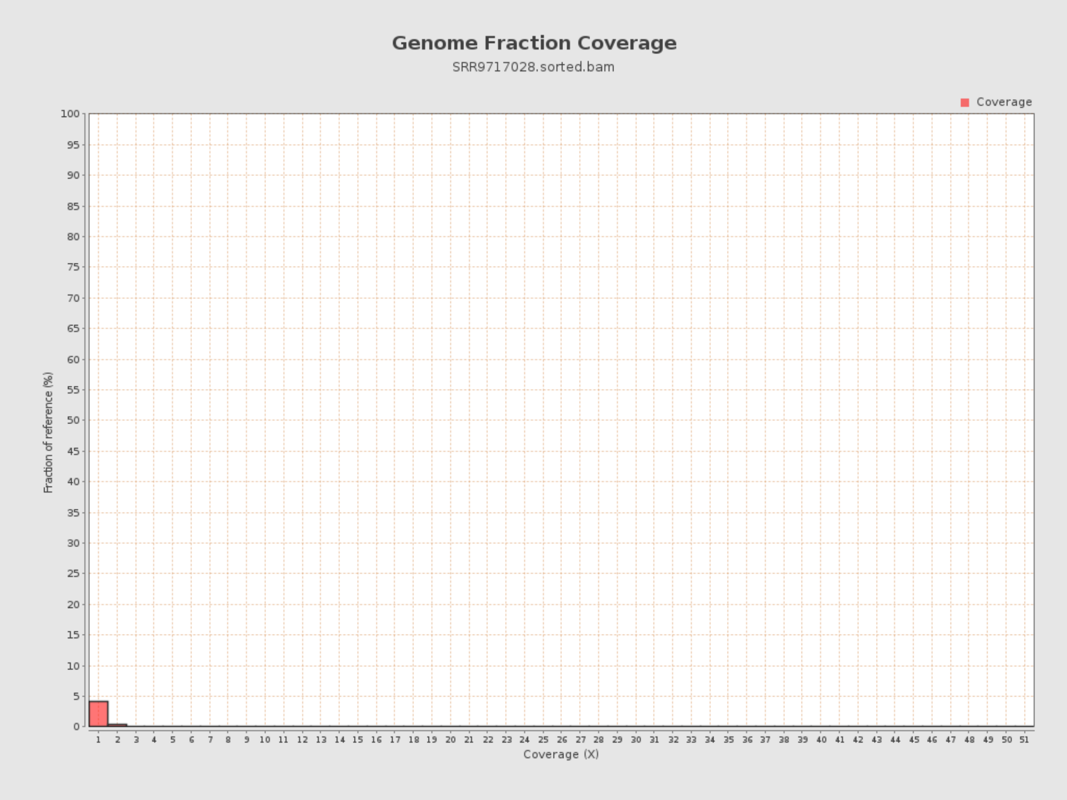
4. Results : Coverage Histogram



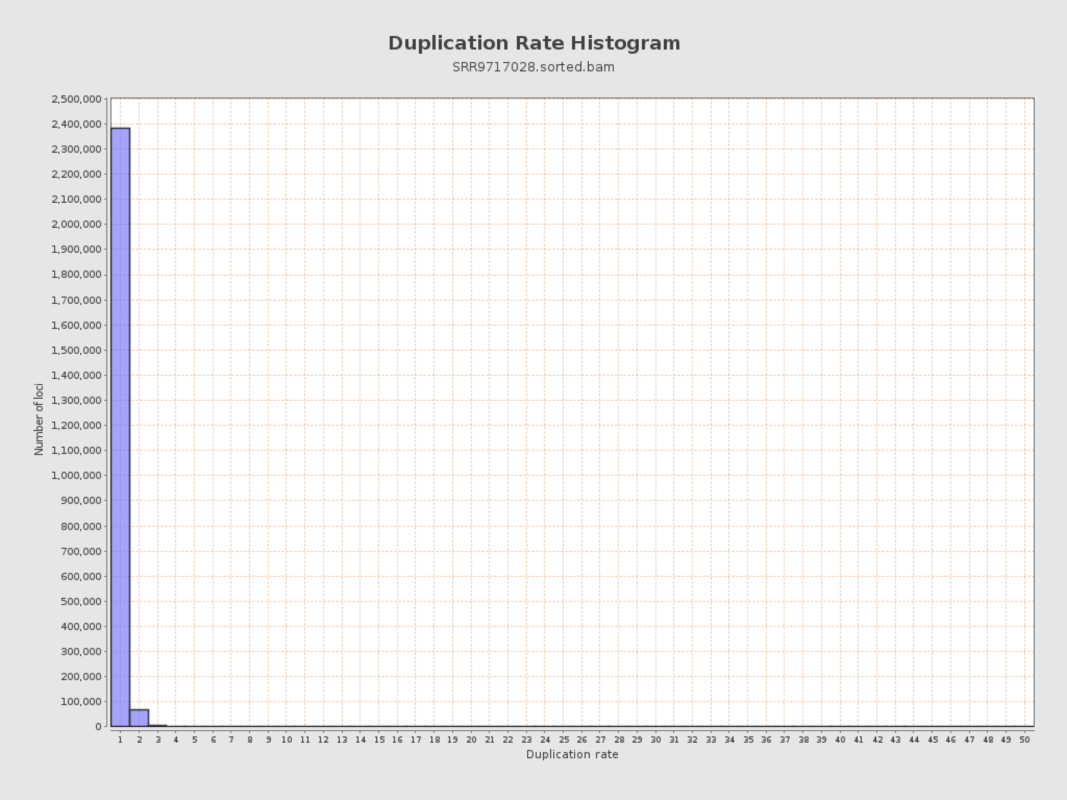
5. Results : Coverage Histogram (0-50X)



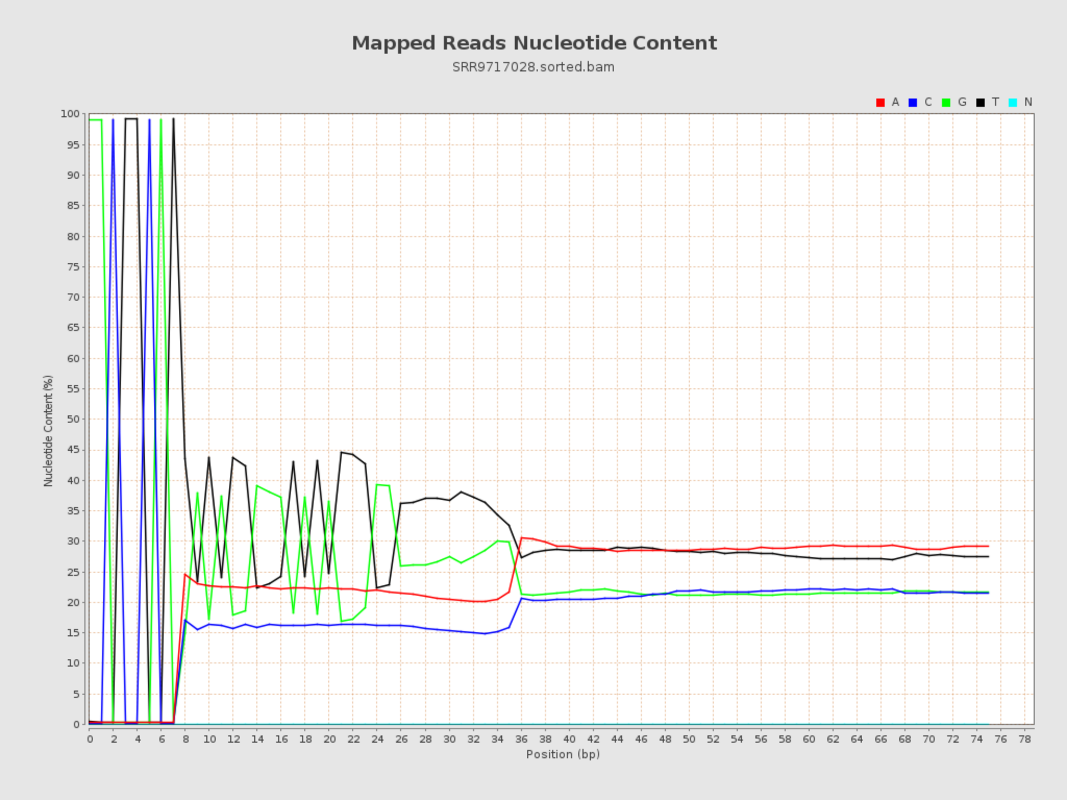
6. Results : Genome Fraction Coverage



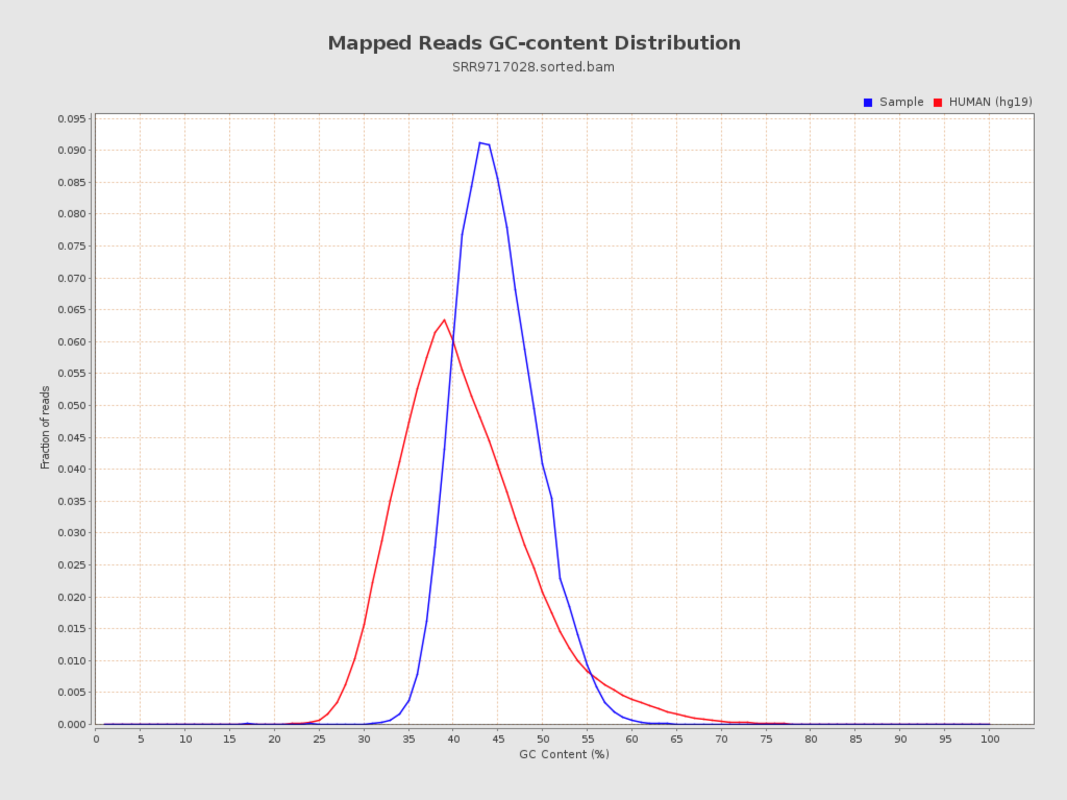
7. Results : Duplication Rate Histogram



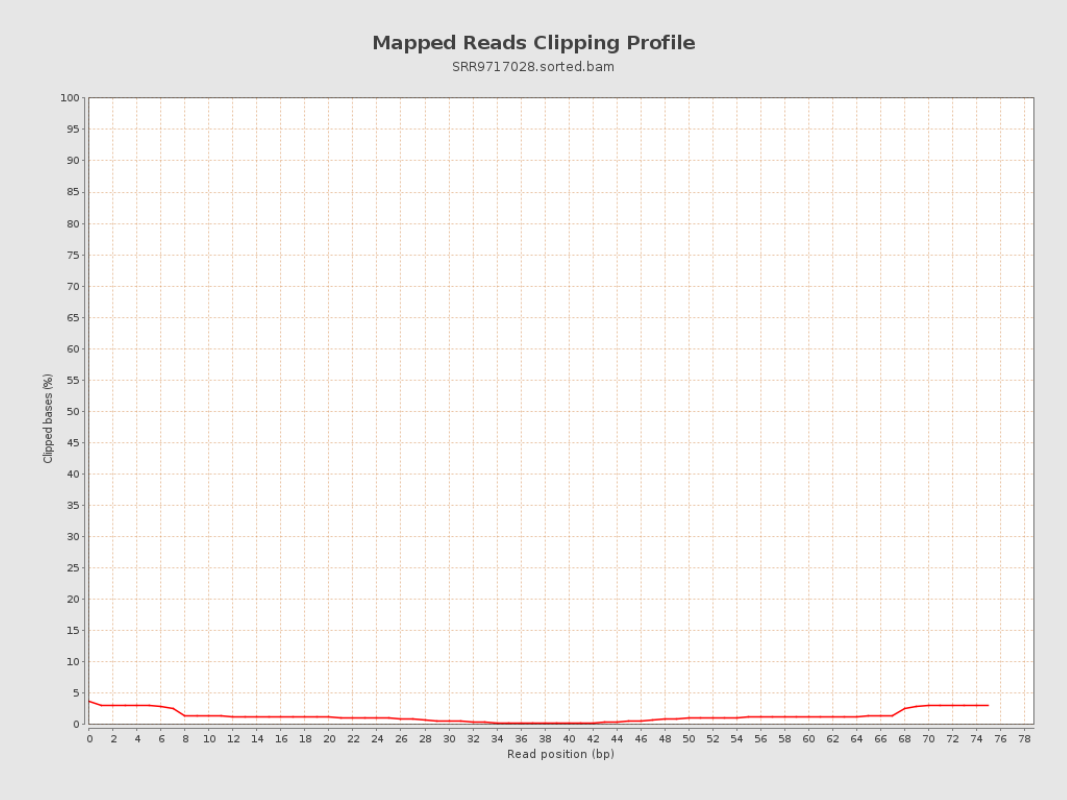
8. Results : Mapped Reads Nucleotide Content



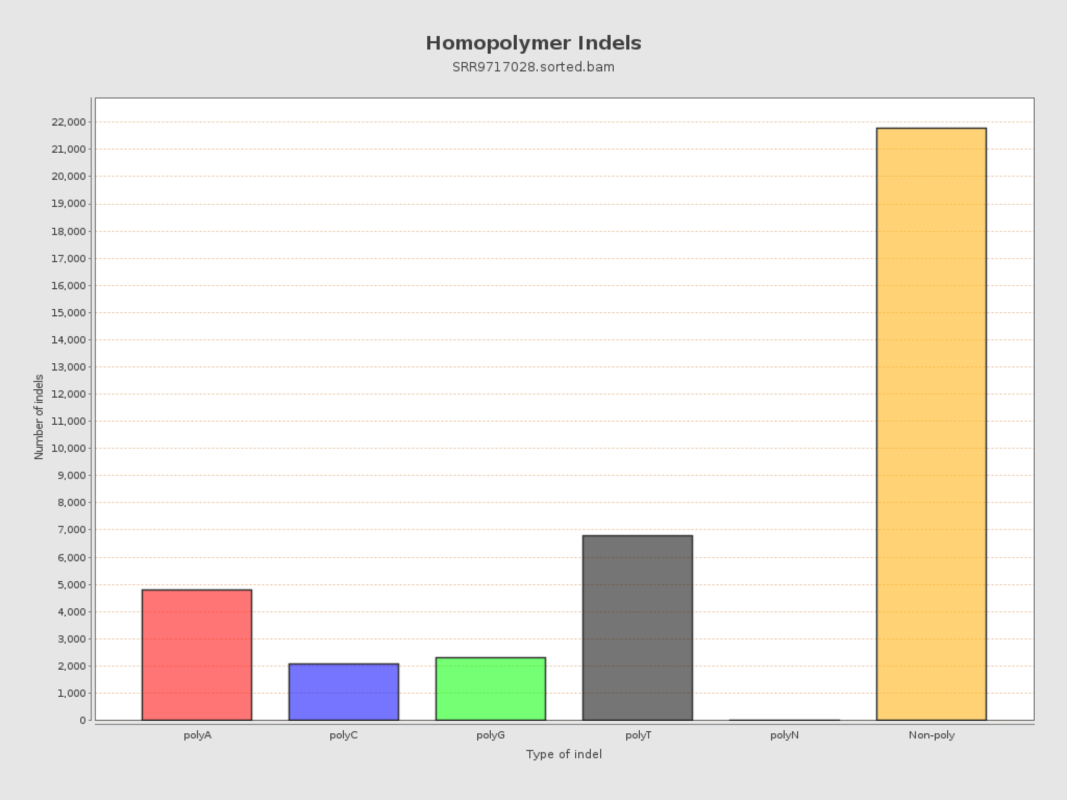
9. Results : Mapped Reads GC-content Distribution



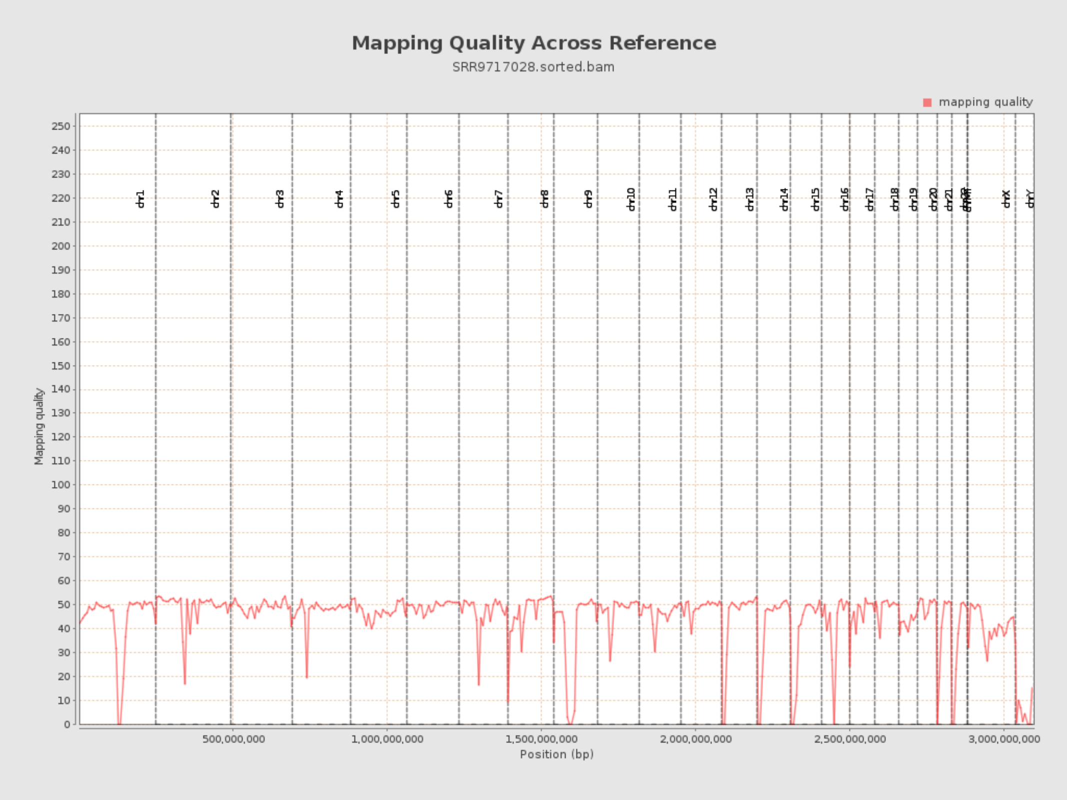
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram