Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 04:25:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717067.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_SRR9717067 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717067.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 04:25:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717067.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,057,677
Mapped reads	829,241 / 78.4%
Unmapped reads	228,436 / 21.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,166 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	16,409 / 1.55%
Duplication rate	1.4%
Clipped reads	829,684 / 78.44%

2.2. ACGT Content

Number/percentage of A's	11,039,720 / 24.1%
Number/percentage of C's	9,557,269 / 20.87%
Number/percentage of T's	13,705,123 / 29.92%
Number/percentage of G's	11,500,662 / 25.11%
Number/percentage of N's	1,313 / 0%
GC Percentage	45.97%

2.3. Coverage

Mean	0.0148

Standard Deviation	0.1506

2.4. Mapping Quality

Mean Mapping Quality	38.8

2.5. Mismatches and indels

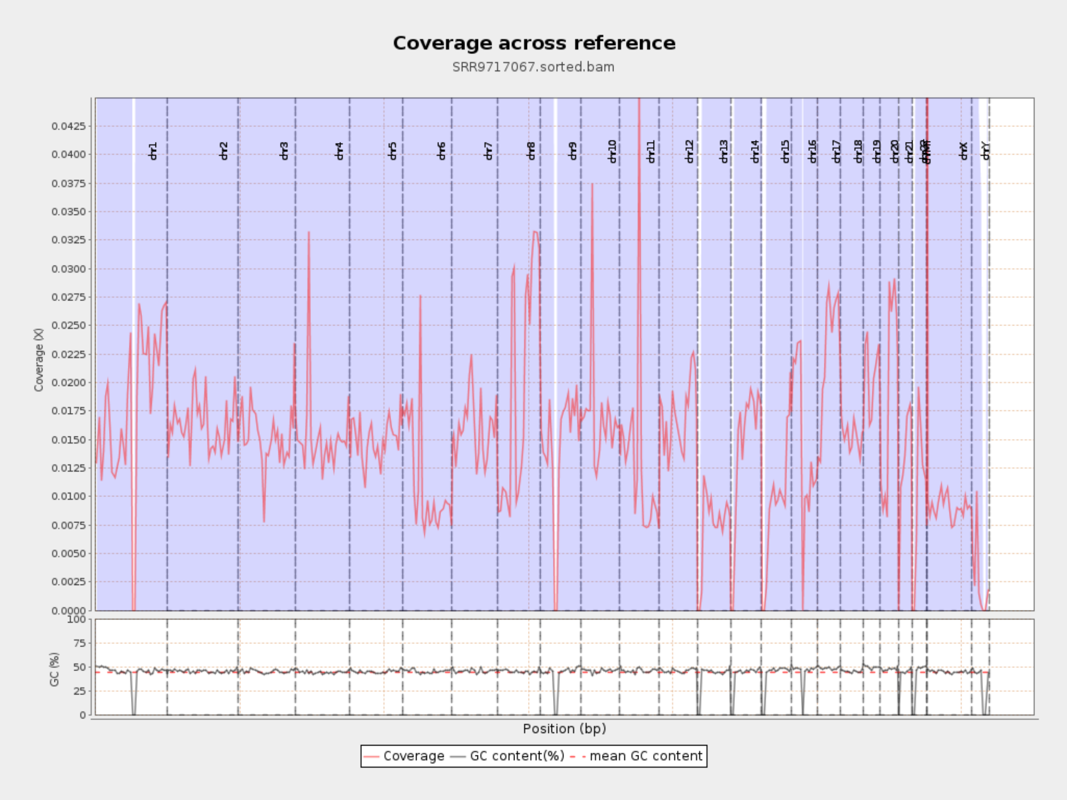
General error rate	0.56%
Mismatches	248,892
Insertions	4,279
Mapped reads with at least one insertion	0.51%
Deletions	7,911
Mapped reads with at least one deletion	0.94%
Homopolymer indels	34.8%

2.6. Chromosome stats

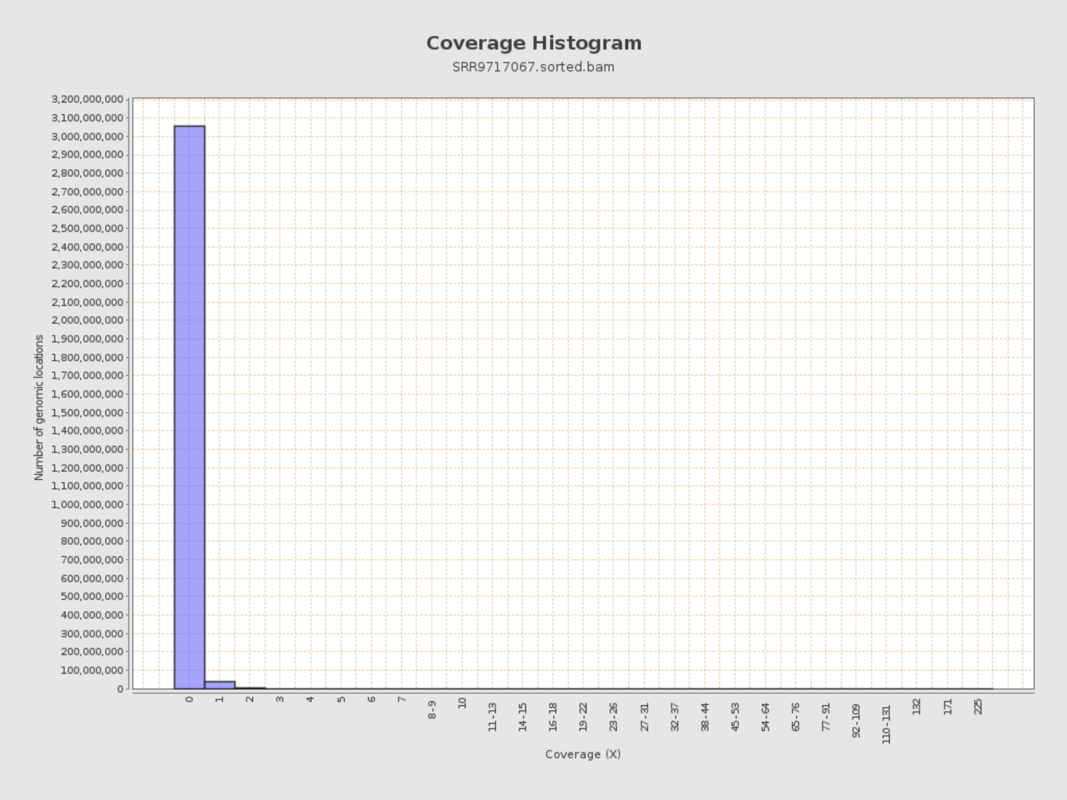
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4478279	0.018	0.1758
chr2	243199373	3974126	0.0163	0.1838
chr3	198022430	3010959	0.0152	0.1363
chr4	191154276	2944208	0.0154	0.1525
chr5	180915260	2734739	0.0151	0.1316
chr6	171115067	1952895	0.0114	0.1174
chr7	159138663	2557465	0.0161	0.1648

chr8	146364022	2870588	0.0196	0.156
chr9	141213431	2023811	0.0143	0.1378
chr10	135534747	2343524	0.0173	0.2309
chr11	135006516	1829119	0.0135	0.1451
chr12	133851895	2290730	0.0171	0.1418
chr13	115169878	841114	0.0073	0.0921
chr14	107349540	1536680	0.0143	0.1314
chr15	102531392	950346	0.0093	0.1035
chr16	90354753	1290216	0.0143	0.1393
chr17	81195210	1850126	0.0228	0.1714
chr18	78077248	1190512	0.0152	0.1571
chr19	59128983	1215950	0.0206	0.1771
chr20	63025520	1195408	0.019	0.1531
chr21	48129895	637307	0.0132	0.137
chr22	51304566	529367	0.0103	0.1103
chrMT	16571	5976	0.3606	0.6825
chrX	155270560	1408804	0.0091	0.1101
chrY	59373566	154829	0.0026	0.0957

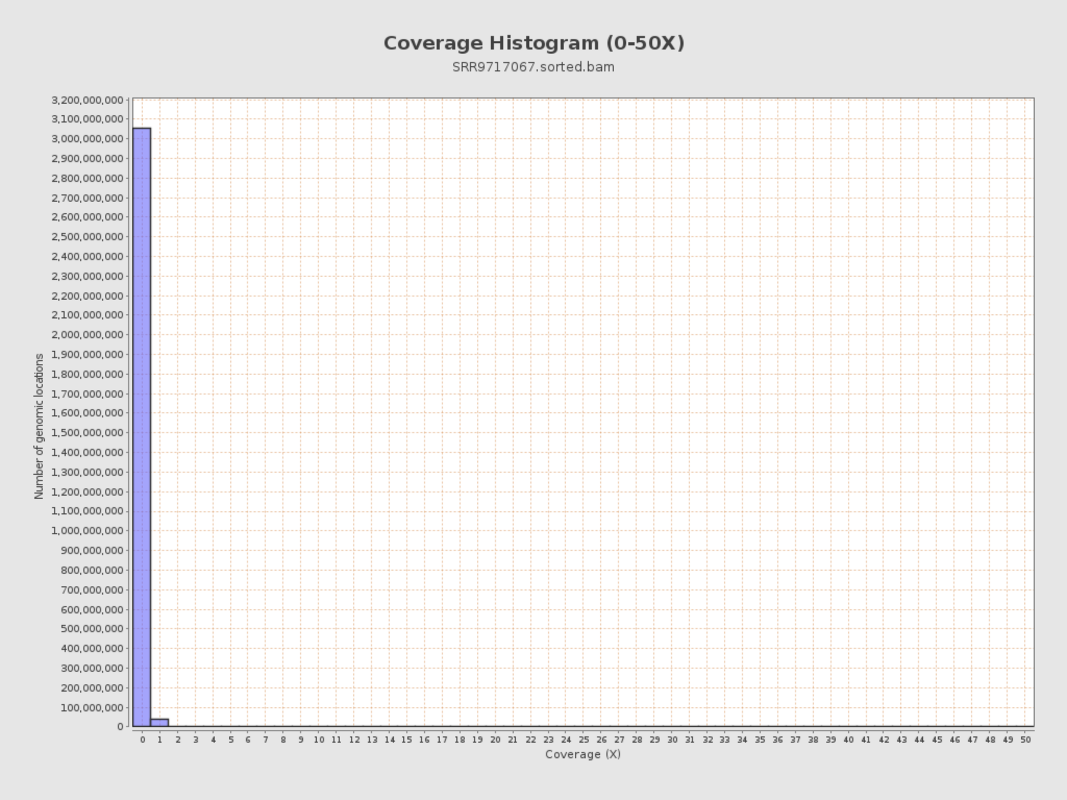
3. Results : Coverage across reference



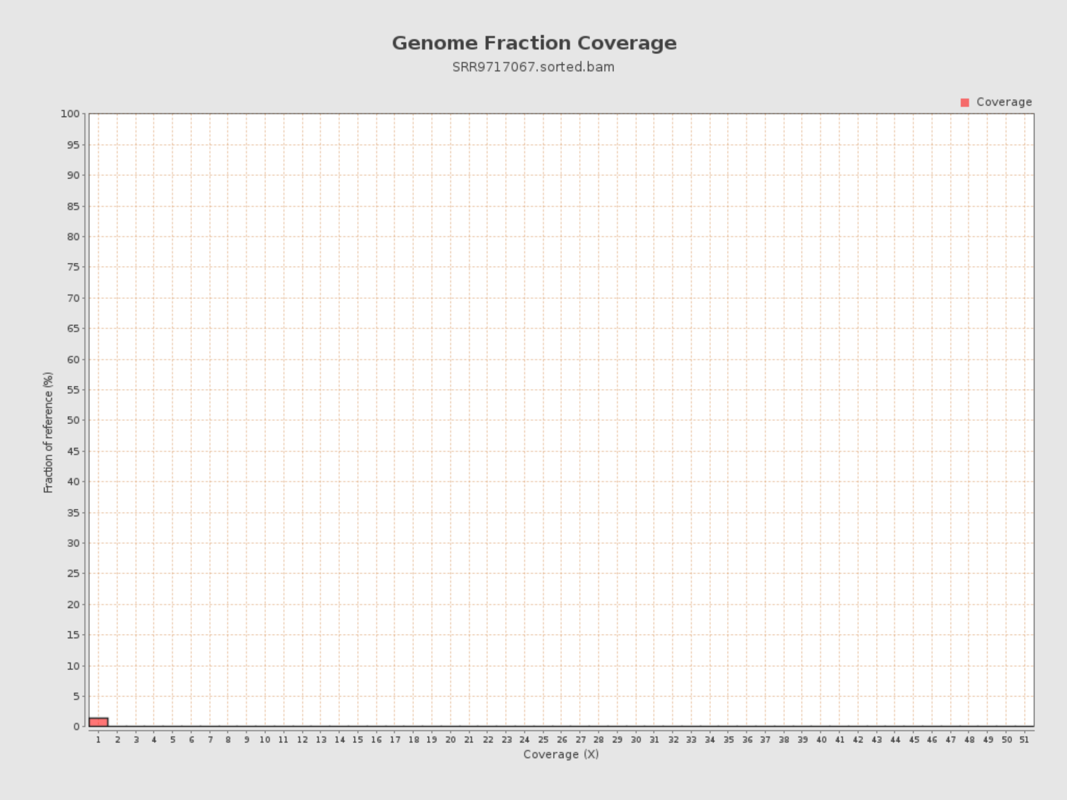
4. Results : Coverage Histogram



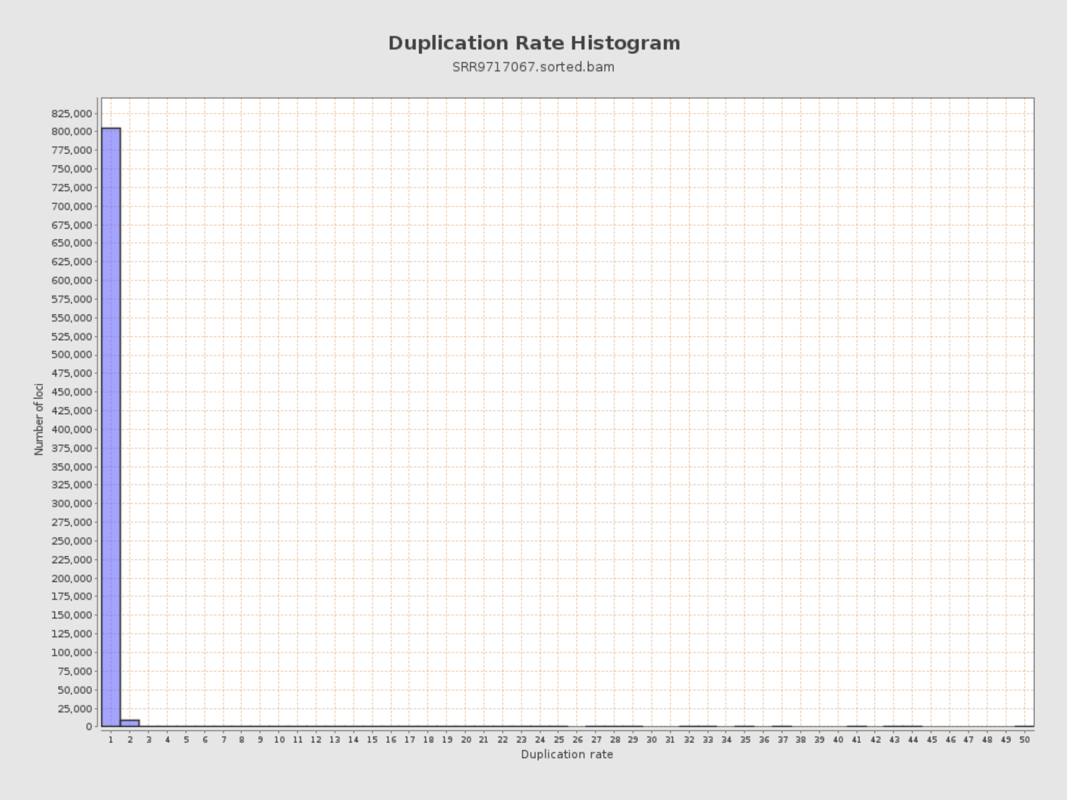
5. Results : Coverage Histogram (0-50X)



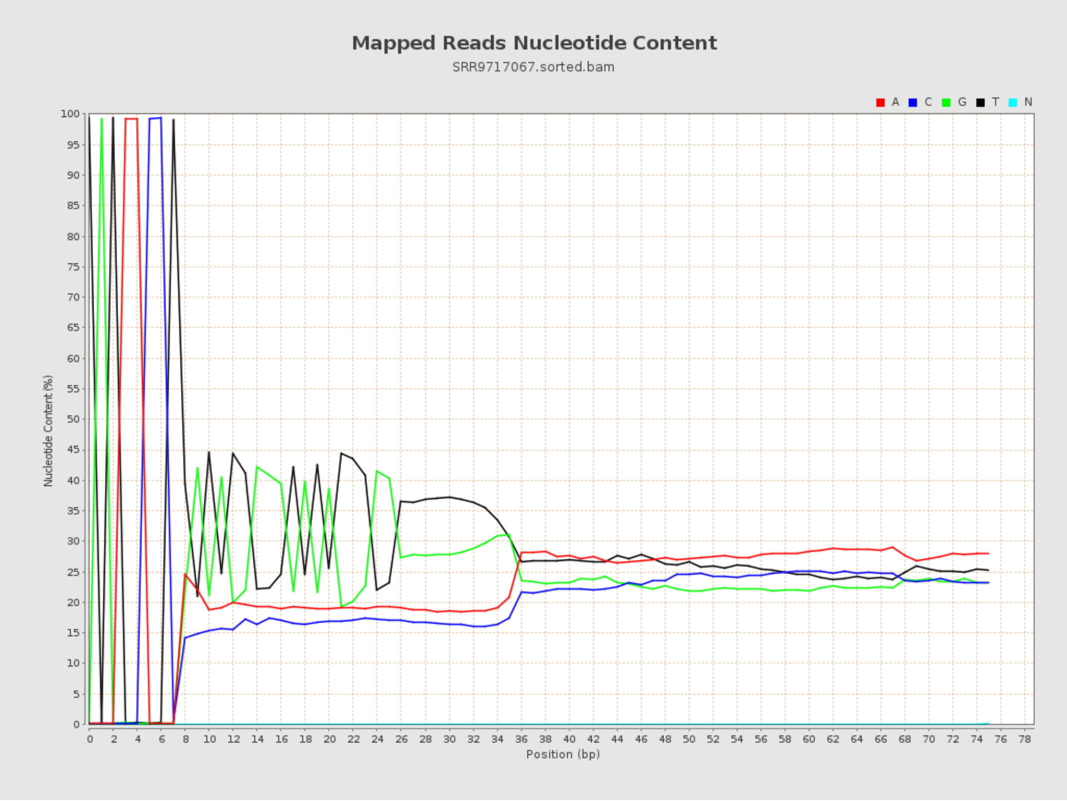
6. Results : Genome Fraction Coverage



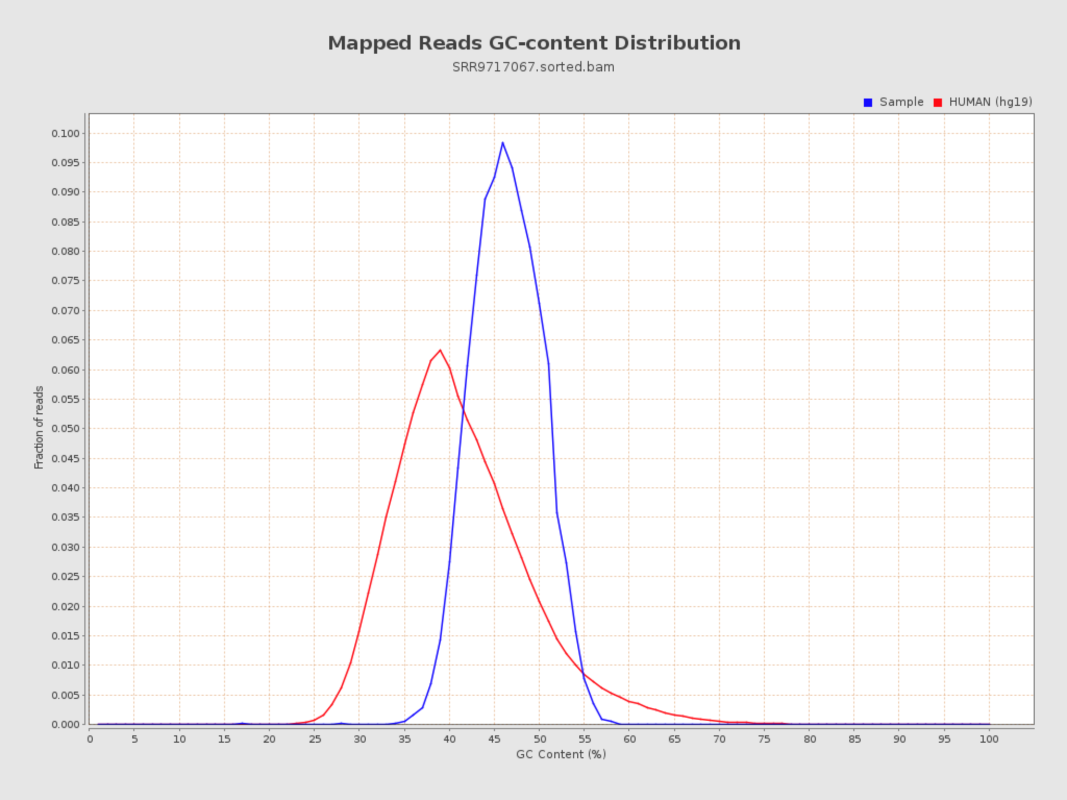
7. Results : Duplication Rate Histogram



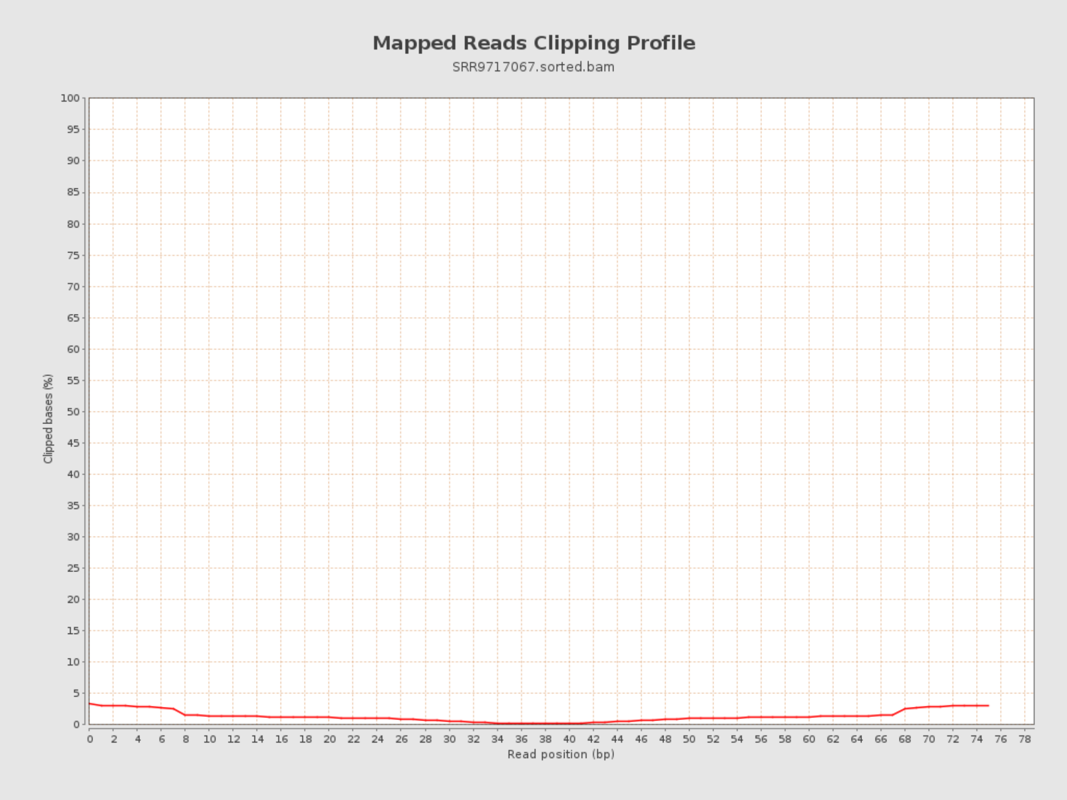
8. Results : Mapped Reads Nucleotide Content



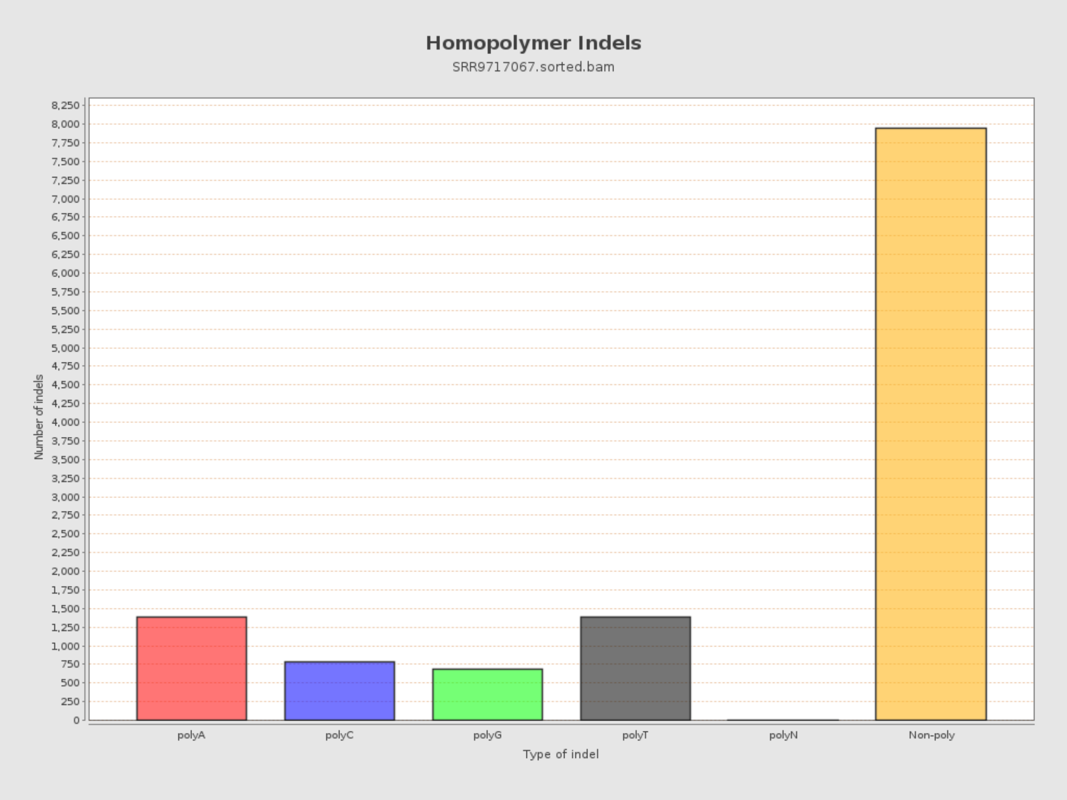
9. Results : Mapped Reads GC-content Distribution



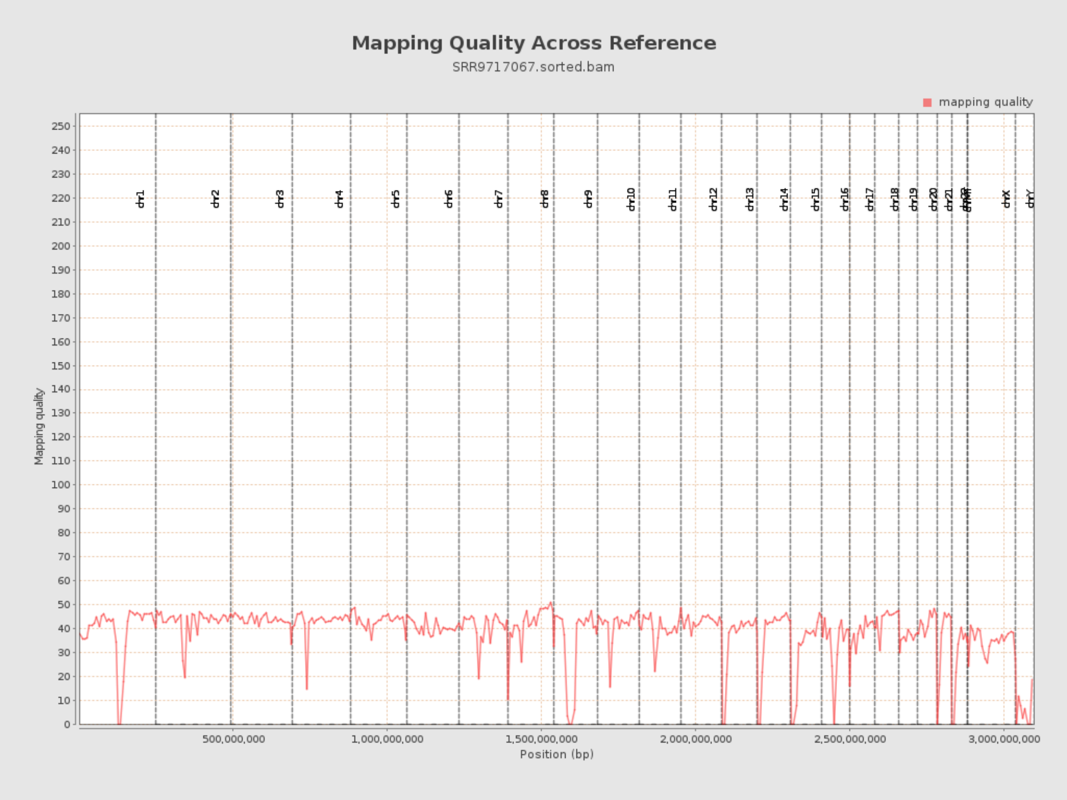
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram