Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 02:50:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717049.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_SRR9717049 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717049.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 02:50:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717049.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,040,352
Mapped reads	896,066 / 86.13%
Unmapped reads	144,286 / 13.87%
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)	17,364 / 1.67%
Duplication rate	1.42%
Clipped reads	898,414 / 86.36%

2.2. ACGT Content

Number/percentage of A's	11,424,829 / 22.62%
Number/percentage of C's	10,041,279 / 19.88%
Number/percentage of T's	15,527,804 / 30.74%
Number/percentage of G's	13,522,401 / 26.77%
Number/percentage of N's	1,439 / 0%
GC Percentage	46.64%

2.3. Coverage

Mean	0.0163

Standard Deviation	0.1571

2.4. Mapping Quality

Mean Mapping Quality	40.19

2.5. Mismatches and indels

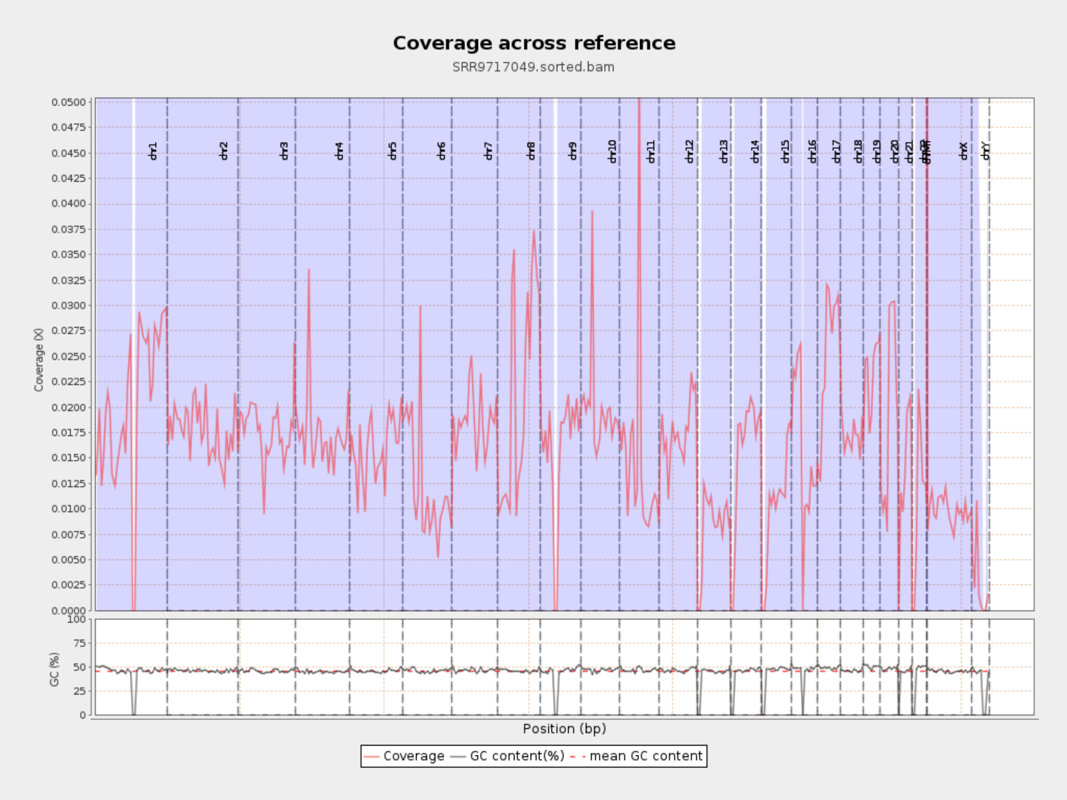
General error rate	0.53%
Mismatches	262,022
Insertions	3,289
Mapped reads with at least one insertion	0.36%
Deletions	8,678
Mapped reads with at least one deletion	0.96%
Homopolymer indels	38.16%

2.6. Chromosome stats

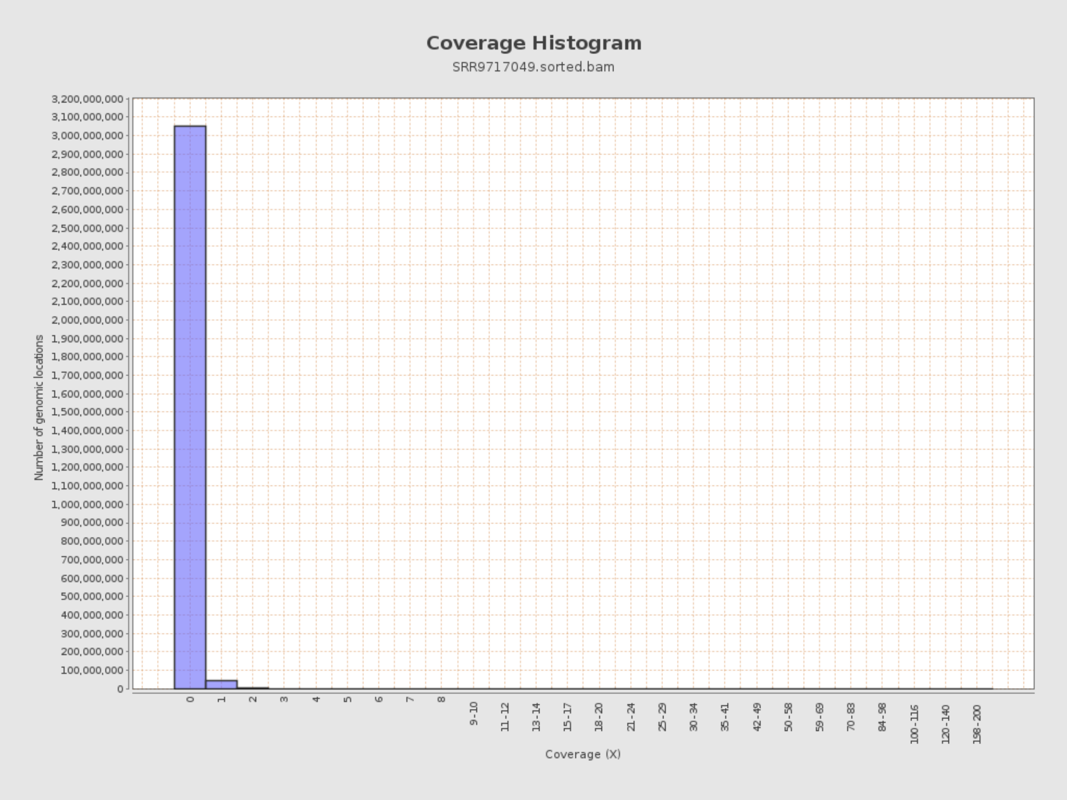
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5055626	0.0203	0.1925
chr2	243199373	4297192	0.0177	0.1764
chr3	198022430	3475642	0.0176	0.1482
chr4	191154276	3366376	0.0176	0.1584
chr5	180915260	2892945	0.016	0.1358
chr6	171115067	2129665	0.0124	0.1223
chr7	159138663	2985173	0.0188	0.184

chr8	146364022	3086706	0.0211	0.1631
chr9	141213431	2226271	0.0158	0.1419
chr10	135534747	2707177	0.02	0.2357
chr11	135006516	2045974	0.0152	0.1551
chr12	133851895	2334984	0.0174	0.1426
chr13	115169878	940954	0.0082	0.0979
chr14	107349540	1655422	0.0154	0.1349
chr15	102531392	1040776	0.0102	0.1087
chr16	90354753	1384733	0.0153	0.1441
chr17	81195210	2050726	0.0253	0.1784
chr18	78077248	1340600	0.0172	0.1727
chr19	59128983	1370869	0.0232	0.1935
chr20	63025520	1212694	0.0192	0.1549
chr21	48129895	670286	0.0139	0.1374
chr22	51304566	574889	0.0112	0.1153
chrMT	16571	2672	0.1612	0.4339
chrX	155270560	1529045	0.0098	0.1141
chrY	59373566	155264	0.0026	0.0904

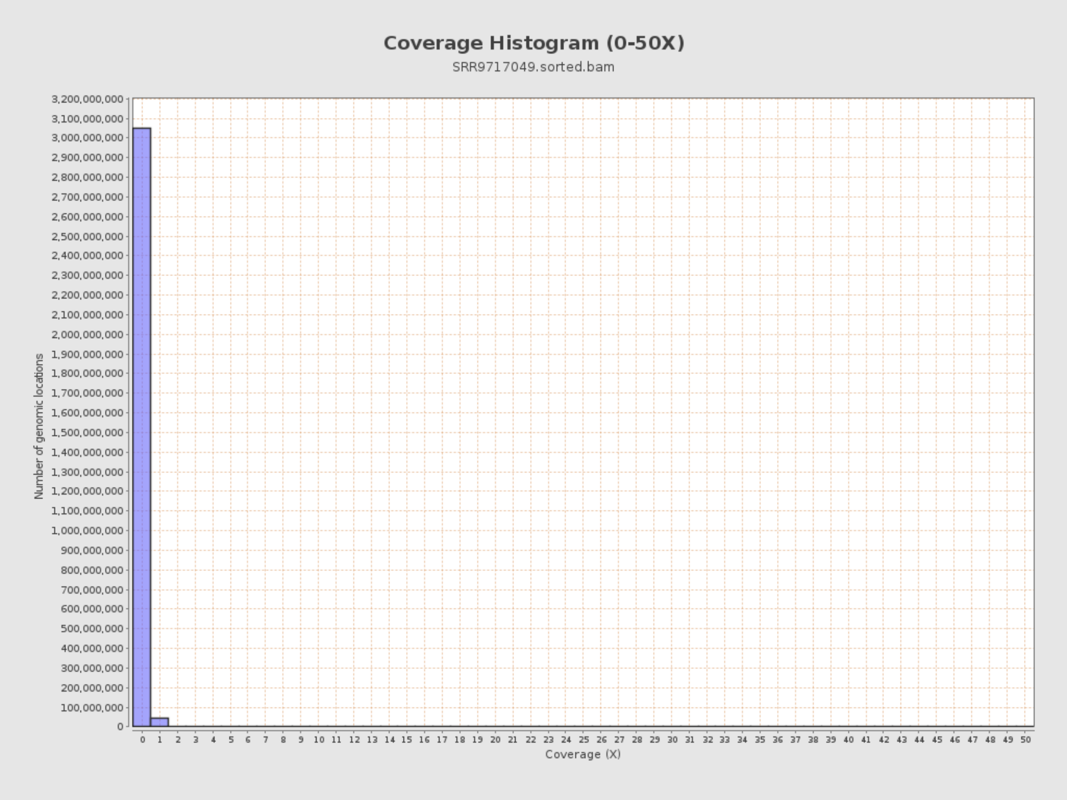
3. Results : Coverage across reference



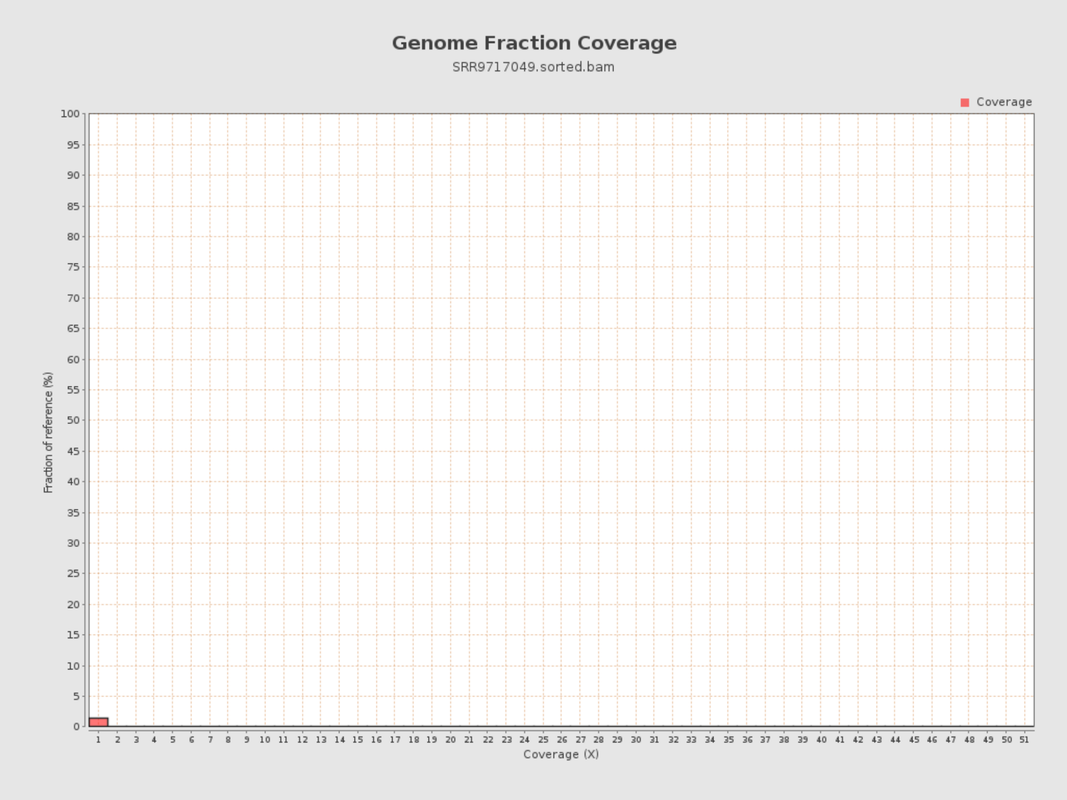
4. Results : Coverage Histogram



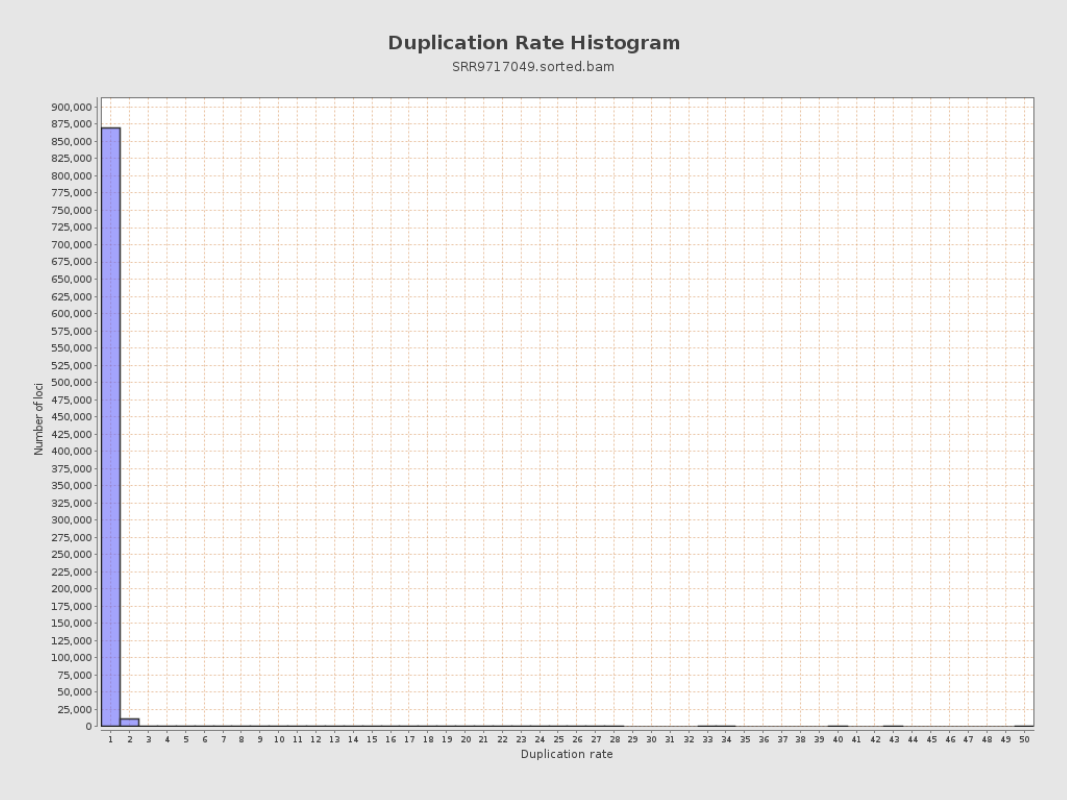
5. Results : Coverage Histogram (0-50X)



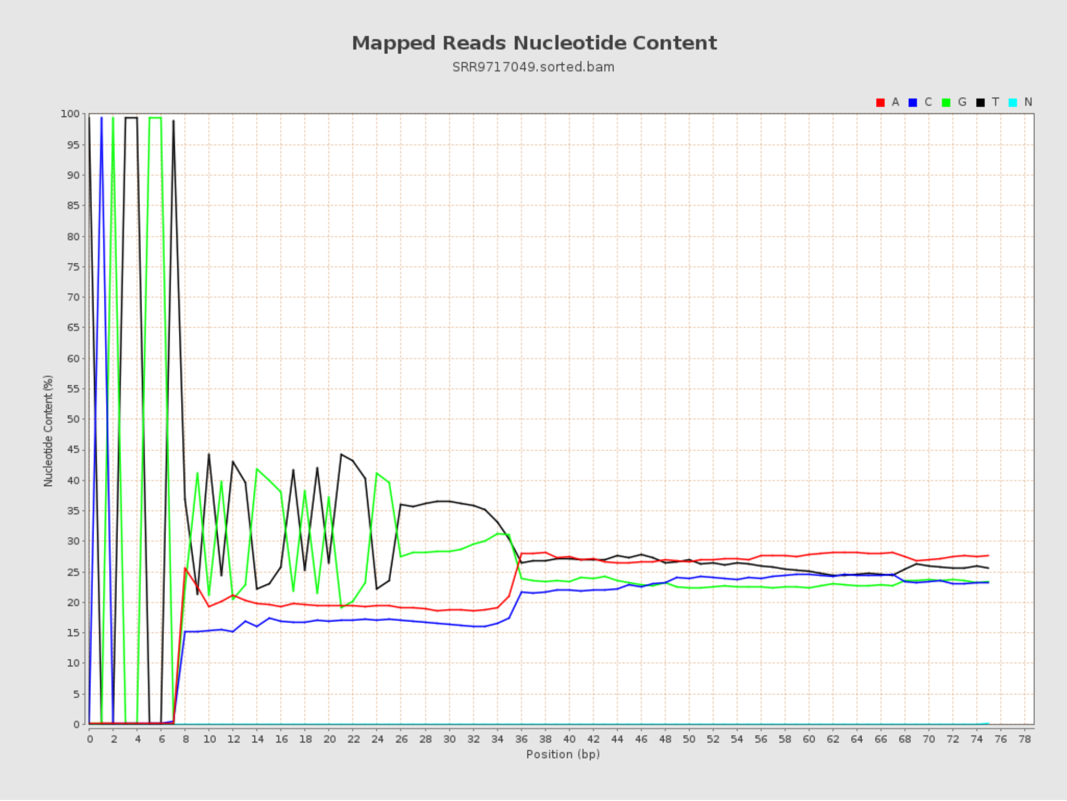
6. Results : Genome Fraction Coverage



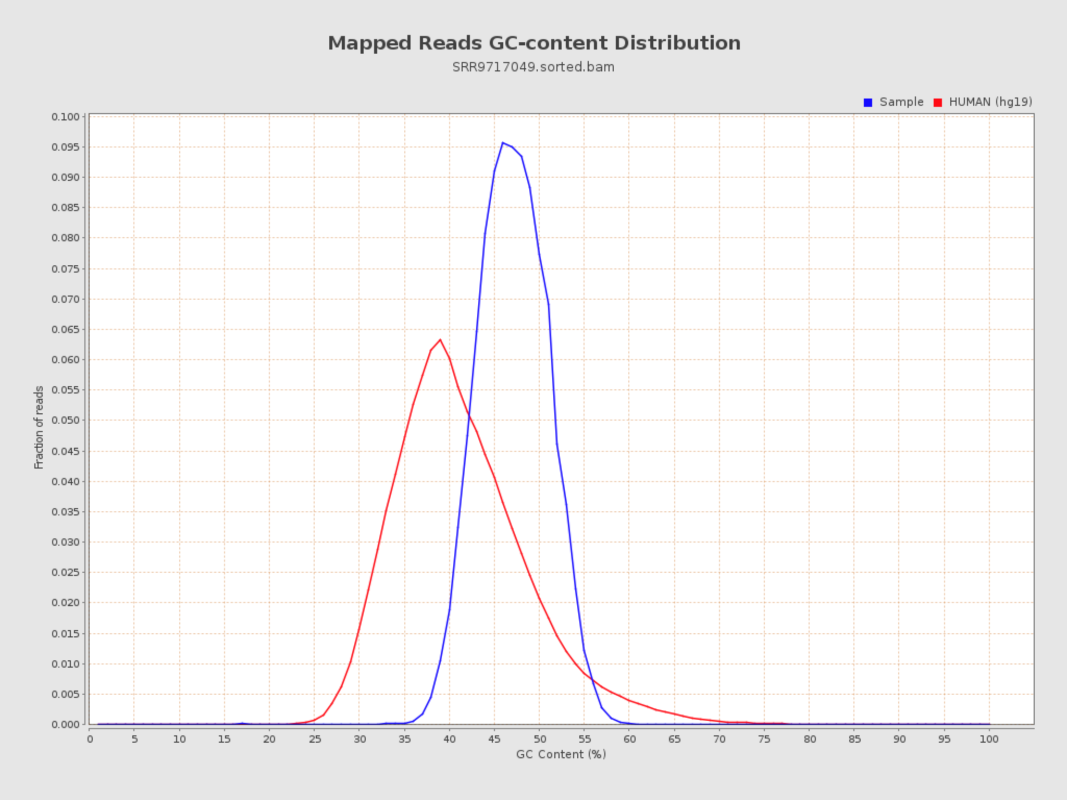
7. Results : Duplication Rate Histogram



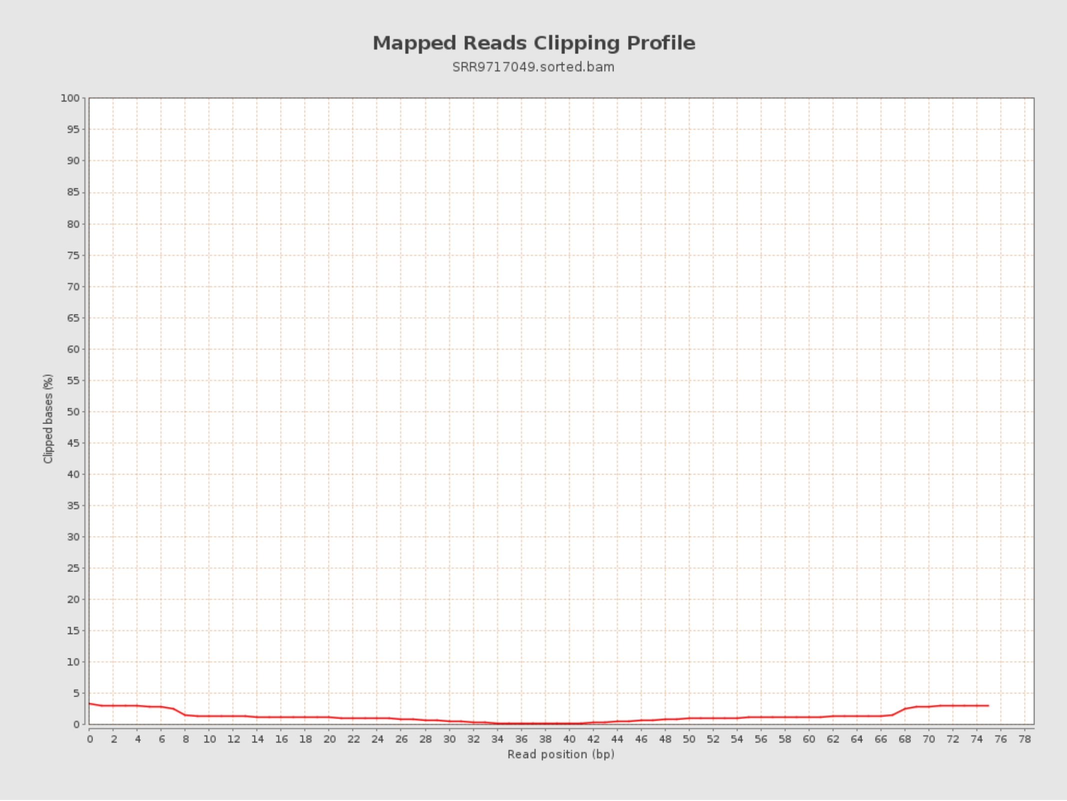
8. Results : Mapped Reads Nucleotide Content



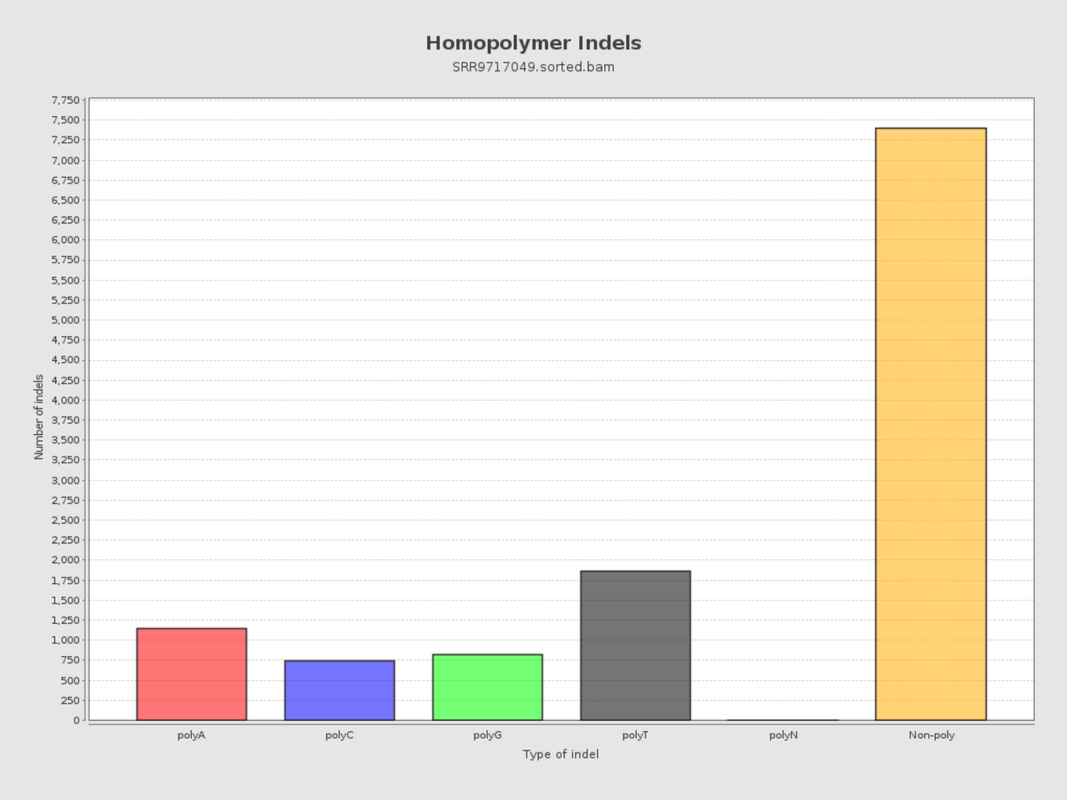
9. Results : Mapped Reads GC-content Distribution



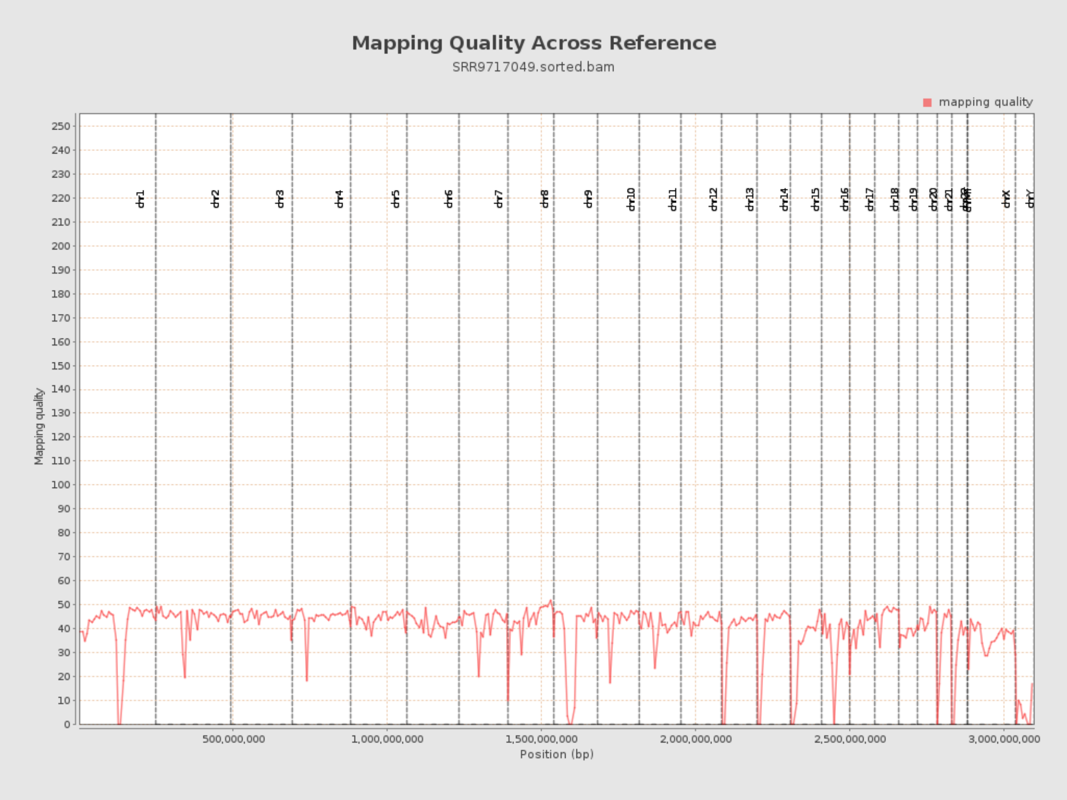
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram