Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 03:02:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717054.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_SRR9717054 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717054.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 03:02:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717054.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	933,610
Mapped reads	756,438 / 81.02%
Unmapped reads	177,172 / 18.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,177 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	12,680 / 1.36%
Duplication rate	1.2%
Clipped reads	757,730 / 81.16%

2.2. ACGT Content

Number/percentage of A's	10,351,127 / 24.37%
Number/percentage of C's	8,641,518 / 20.35%
Number/percentage of T's	12,264,908 / 28.88%
Number/percentage of G's	11,210,317 / 26.4%
Number/percentage of N's	1,286 / 0%
GC Percentage	46.74%

2.3. Coverage

Mean	0.0137

Standard Deviation	0.1411

2.4. Mapping Quality

Mean Mapping Quality	39.56

2.5. Mismatches and indels

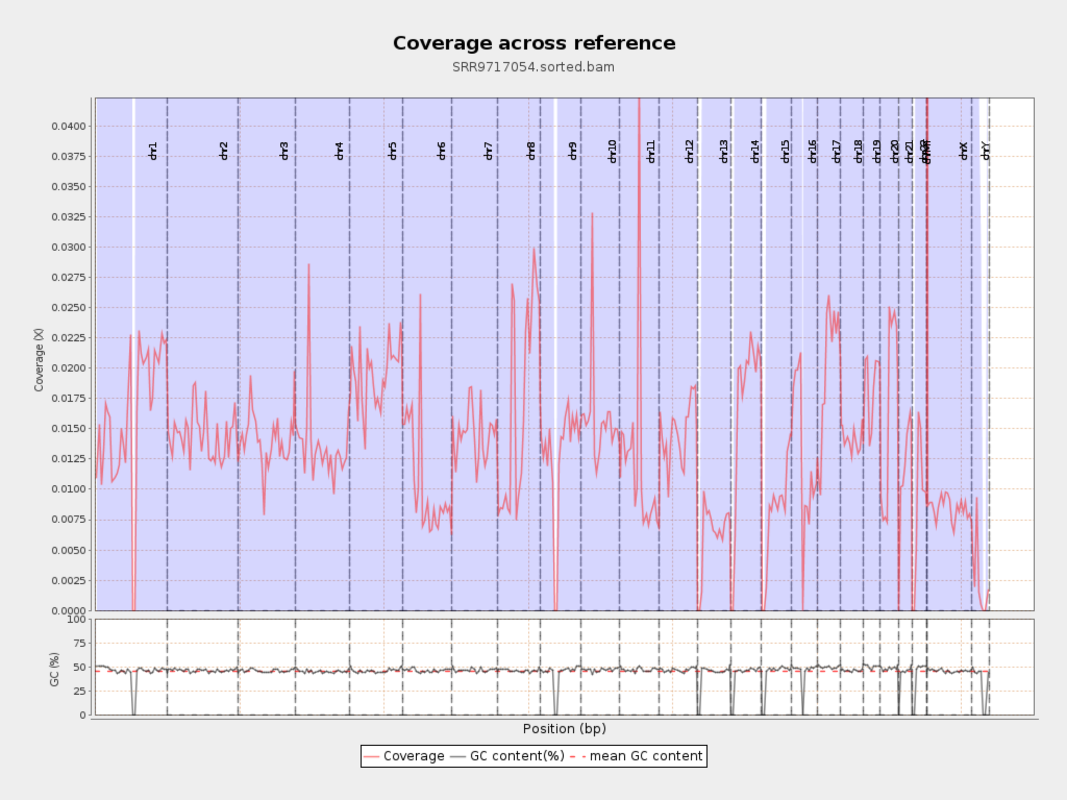
General error rate	0.54%
Mismatches	224,409
Insertions	3,358
Mapped reads with at least one insertion	0.44%
Deletions	7,272
Mapped reads with at least one deletion	0.95%
Homopolymer indels	34.48%

2.6. Chromosome stats

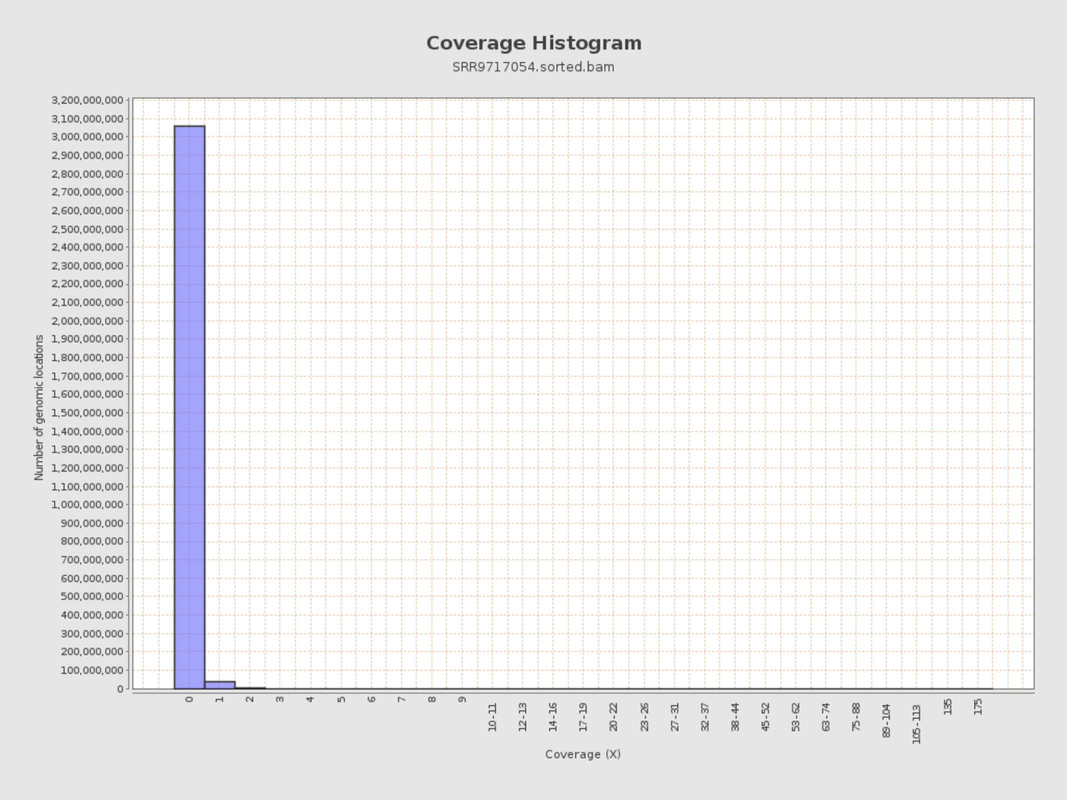
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3999354	0.016	0.1688
chr2	243199373	3512997	0.0144	0.1621
chr3	198022430	2772606	0.014	0.1284
chr4	191154276	2614772	0.0137	0.1409
chr5	180915260	3548179	0.0196	0.1497
chr6	171115067	1812141	0.0106	0.1109
chr7	159138663	2320789	0.0146	0.1525

chr8	146364022	2491866	0.017	0.1431
chr9	141213431	1793553	0.0127	0.1286
chr10	135534747	2161930	0.016	0.1965
chr11	135006516	1692058	0.0125	0.1373
chr12	133851895	1968151	0.0147	0.1298
chr13	115169878	712914	0.0062	0.0853
chr14	107349540	1804268	0.0168	0.1392
chr15	102531392	815267	0.008	0.0962
chr16	90354753	1121847	0.0124	0.1267
chr17	81195210	1630633	0.0201	0.1584
chr18	78077248	1098775	0.0141	0.1665
chr19	59128983	1083335	0.0183	0.1604
chr20	63025520	1038954	0.0165	0.1462
chr21	48129895	565814	0.0118	0.1277
chr22	51304566	454683	0.0089	0.1024
chrMT	16571	11133	0.6718	0.9424
chrX	155270560	1313218	0.0085	0.1022
chrY	59373566	142357	0.0024	0.0866

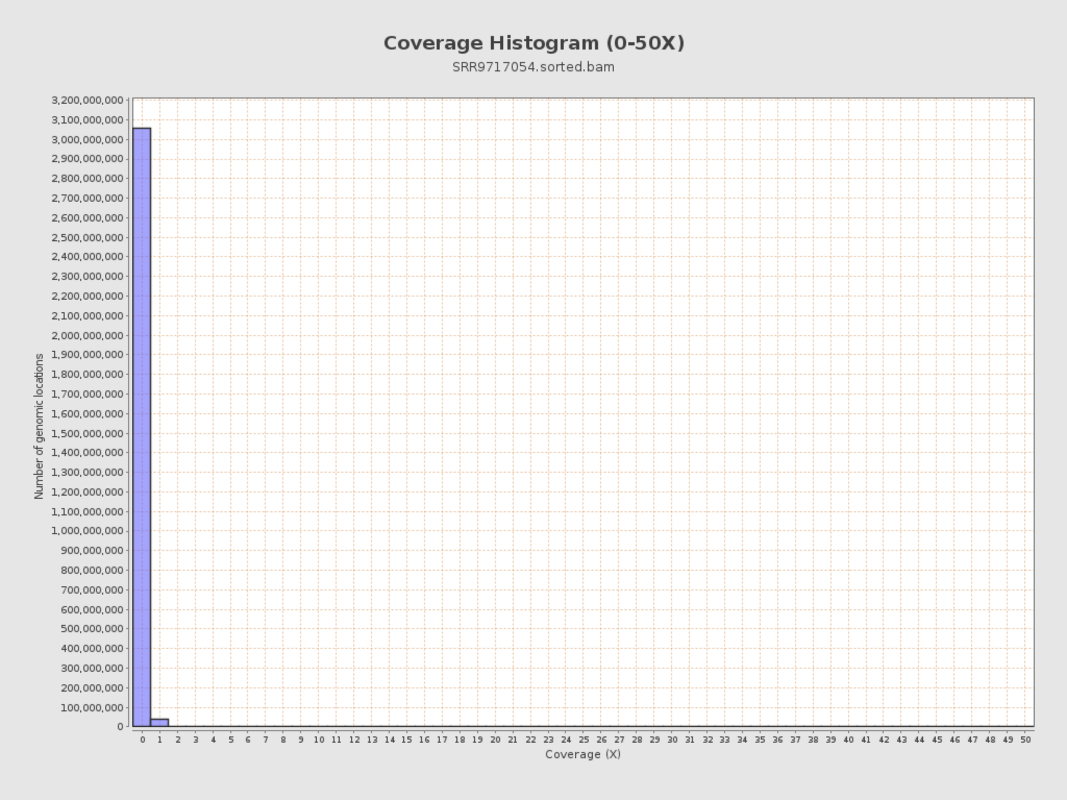
3. Results : Coverage across reference



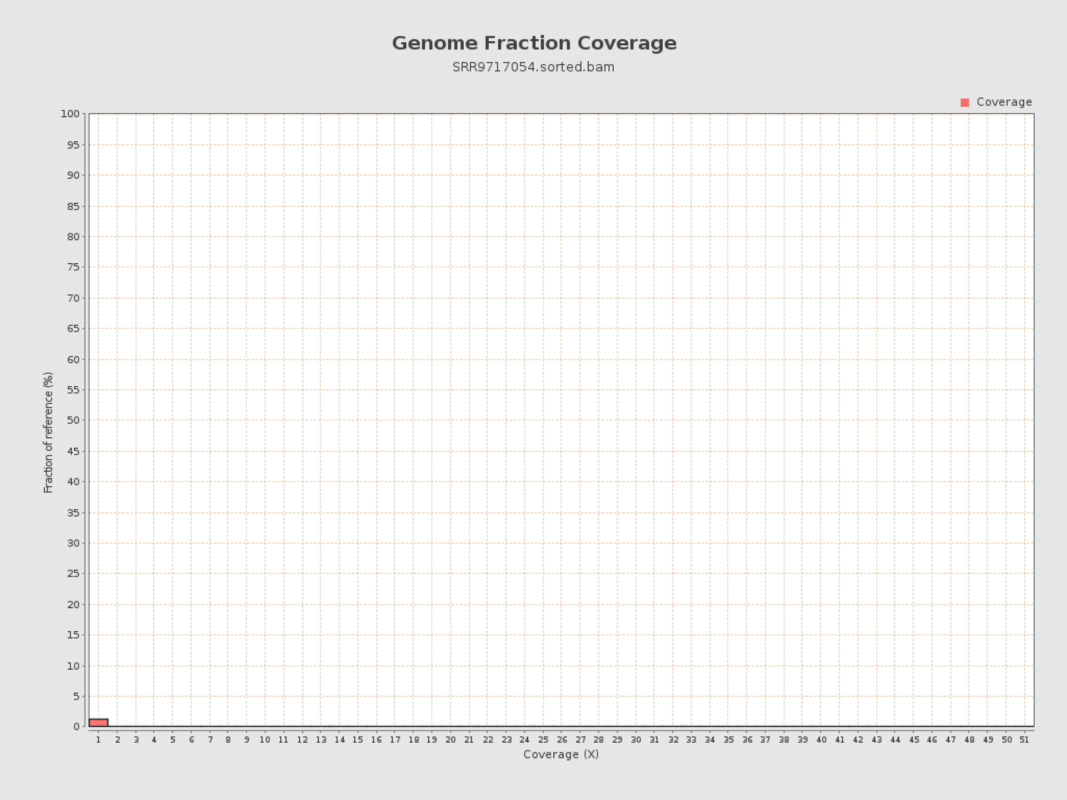
4. Results : Coverage Histogram



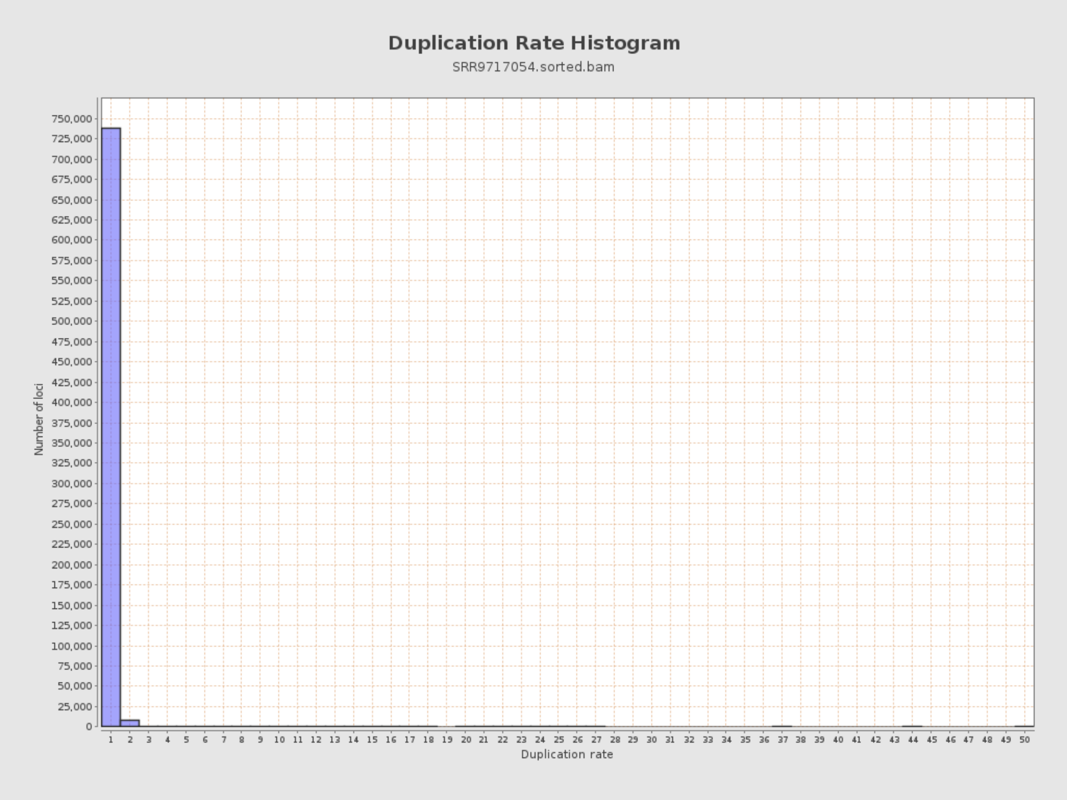
5. Results : Coverage Histogram (0-50X)



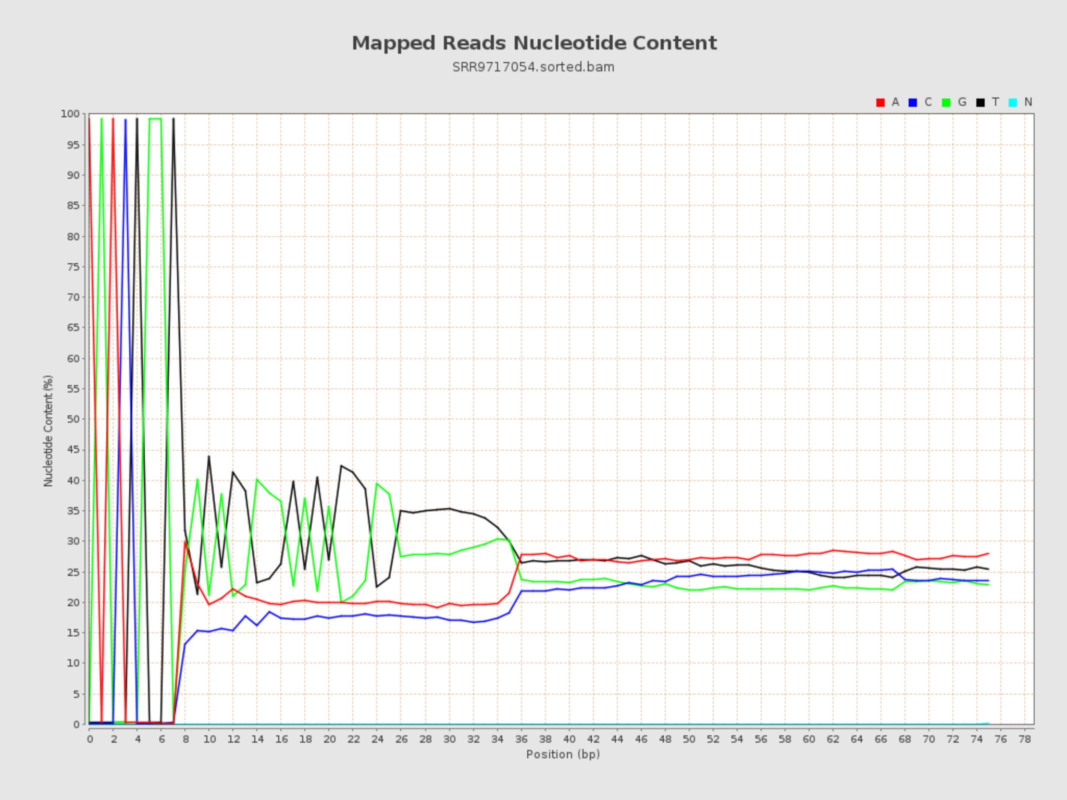
6. Results : Genome Fraction Coverage



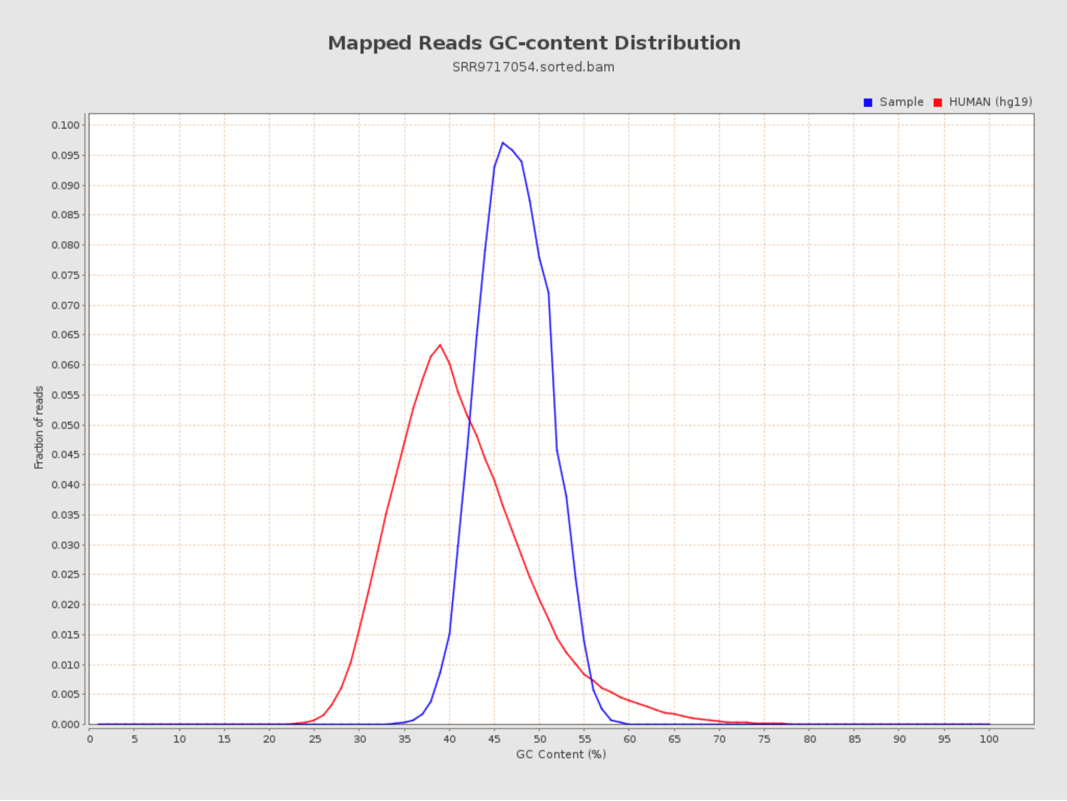
7. Results : Duplication Rate Histogram



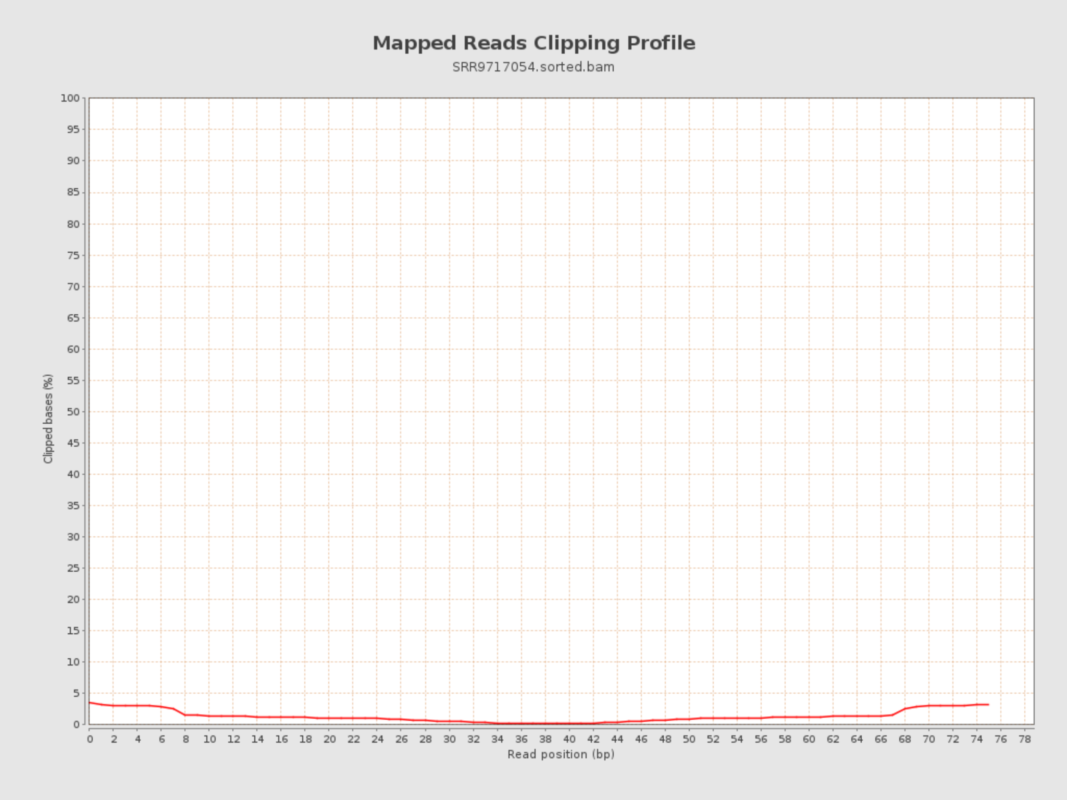
8. Results : Mapped Reads Nucleotide Content



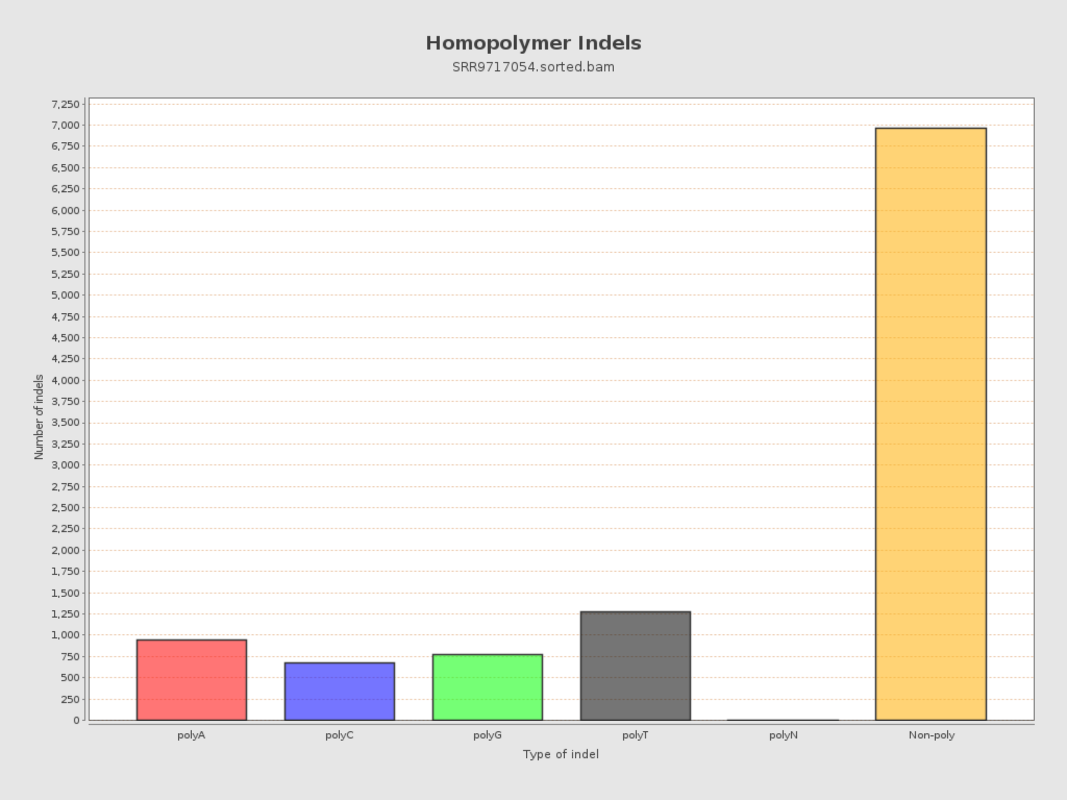
9. Results : Mapped Reads GC-content Distribution



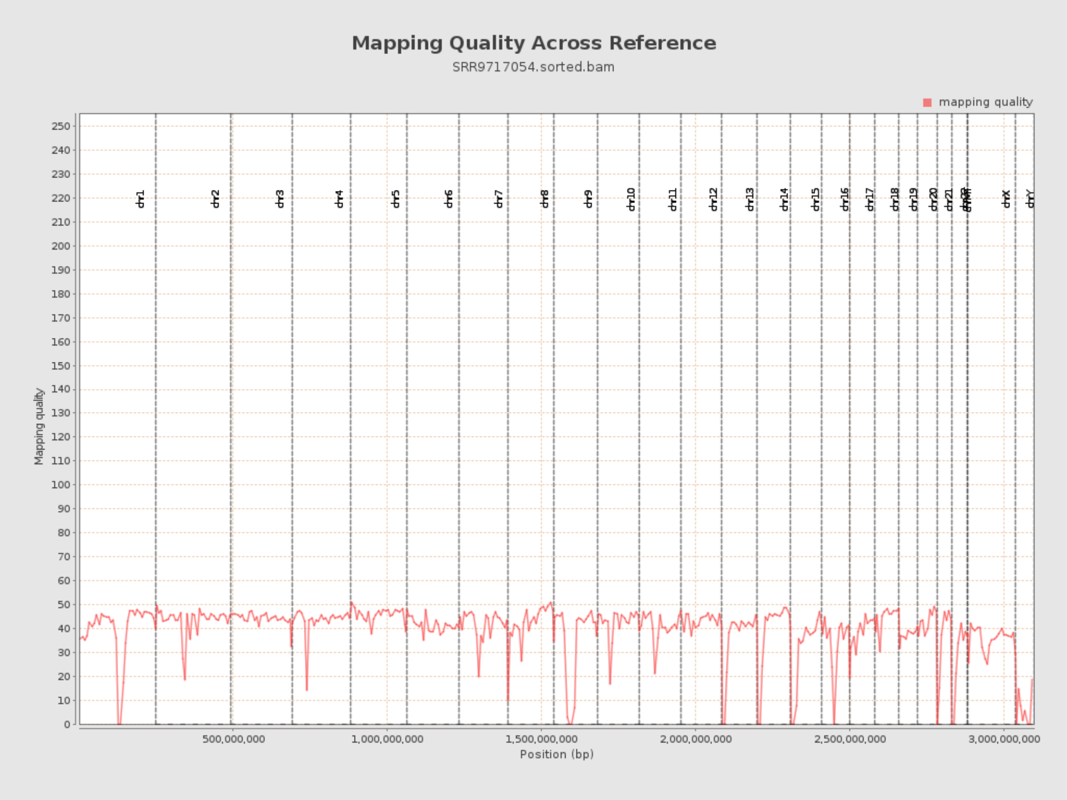
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram