Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 03:23:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717060.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_SRR9717060 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717060.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 03:23:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717060.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,131,697
Mapped reads	1,024,109 / 90.49%
Unmapped reads	107,588 / 9.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,167 / 0.46%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	25,727 / 2.27%
Duplication rate	1.73%
Clipped reads	1,026,179 / 90.68%

2.2. ACGT Content

Number/percentage of A's	14,393,358 / 24.33%
Number/percentage of C's	10,939,640 / 18.49%
Number/percentage of T's	19,093,150 / 32.28%
Number/percentage of G's	14,724,093 / 24.89%
Number/percentage of N's	701 / 0%
GC Percentage	43.39%

2.3. Coverage

Mean	0.0191

Standard Deviation	0.2075

2.4. Mapping Quality

Mean Mapping Quality	44.43

2.5. Mismatches and indels

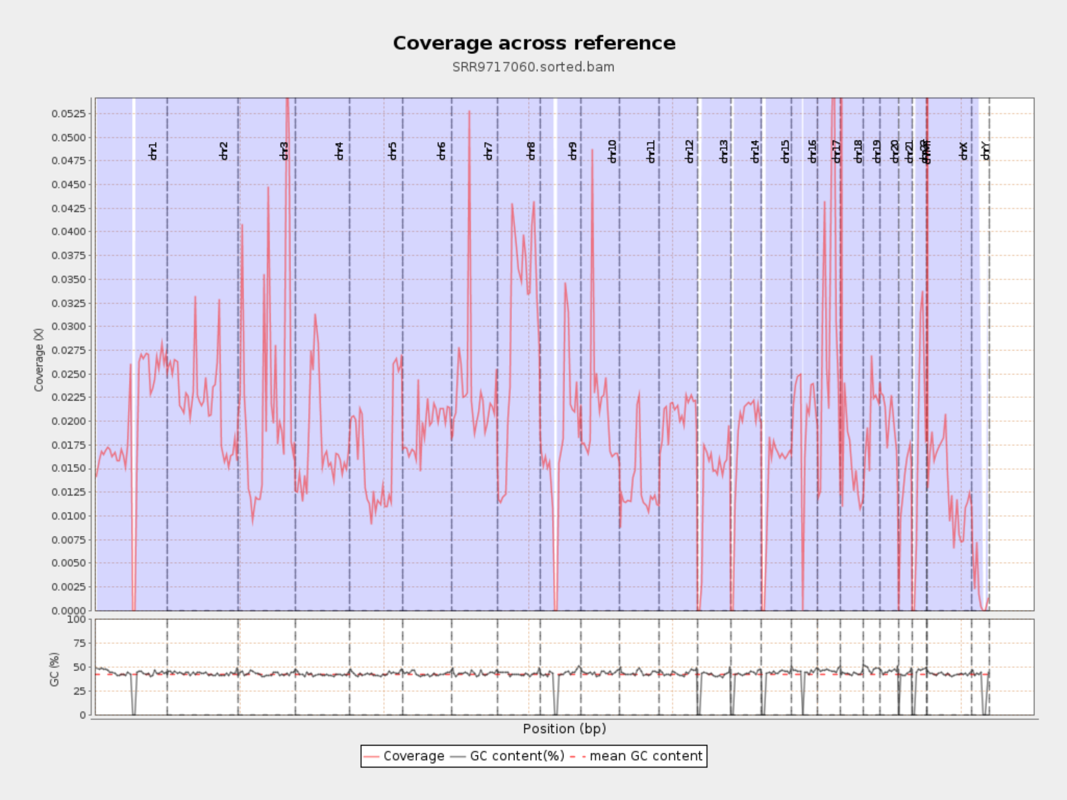
General error rate	0.51%
Mismatches	296,120
Insertions	4,191
Mapped reads with at least one insertion	0.41%
Deletions	11,099
Mapped reads with at least one deletion	1.08%
Homopolymer indels	41.01%

2.6. Chromosome stats

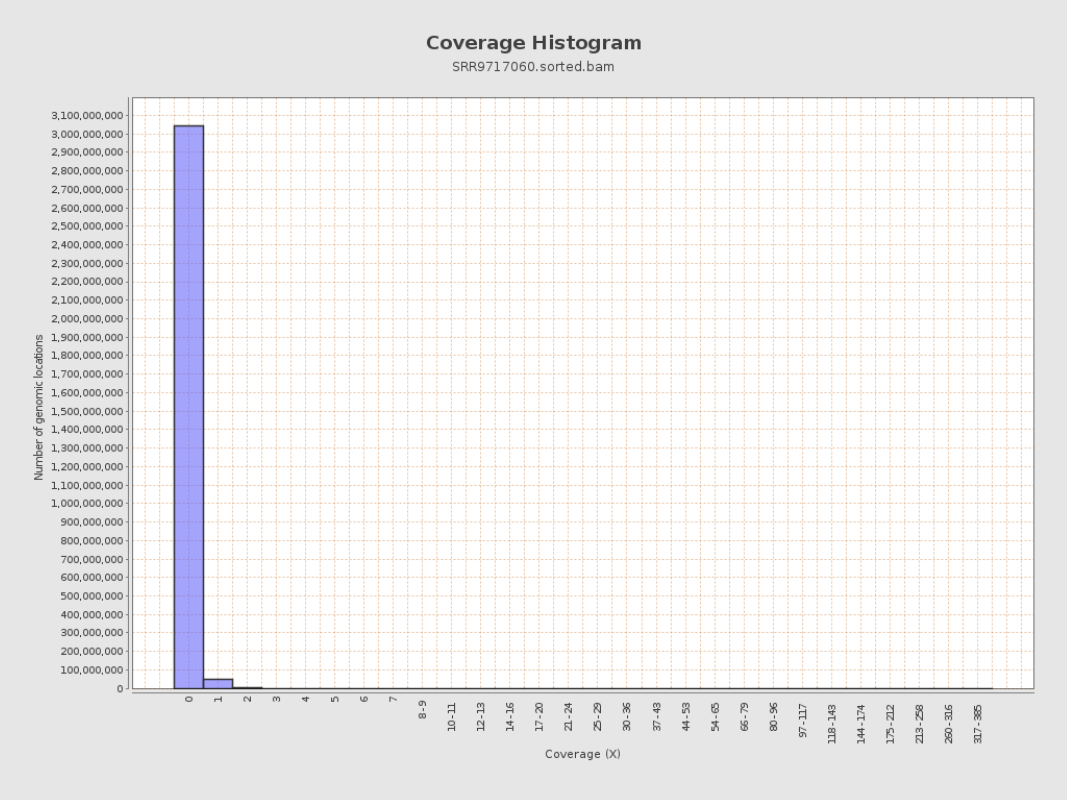
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4879173	0.0196	0.2711
chr2	243199373	5399254	0.0222	0.2299
chr3	198022430	4519383	0.0228	0.165
chr4	191154276	3331308	0.0174	0.1478
chr5	180915260	2961610	0.0164	0.1351
chr6	171115067	3308048	0.0193	0.1564
chr7	159138663	3726040	0.0234	0.458

chr8	146364022	4413709	0.0302	0.2265
chr9	141213431	2462094	0.0174	0.1525
chr10	135534747	2861512	0.0211	0.2561
chr11	135006516	1766331	0.0131	0.1395
chr12	133851895	2780915	0.0208	0.1633
chr13	115169878	1541145	0.0134	0.1227
chr14	107349540	1897464	0.0177	0.1428
chr15	102531392	1400160	0.0137	0.1266
chr16	90354753	1808200	0.02	0.1555
chr17	81195210	2473642	0.0305	0.1899
chr18	78077248	1402488	0.018	0.2357
chr19	59128983	1205484	0.0204	0.2605
chr20	63025520	1258261	0.02	0.1537
chr21	48129895	621994	0.0129	0.1267
chr22	51304566	893375	0.0174	0.1392
chrMT	16571	58445	3.5269	2.462
chrX	155270560	2063144	0.0133	0.1345
chrY	59373566	135113	0.0023	0.068

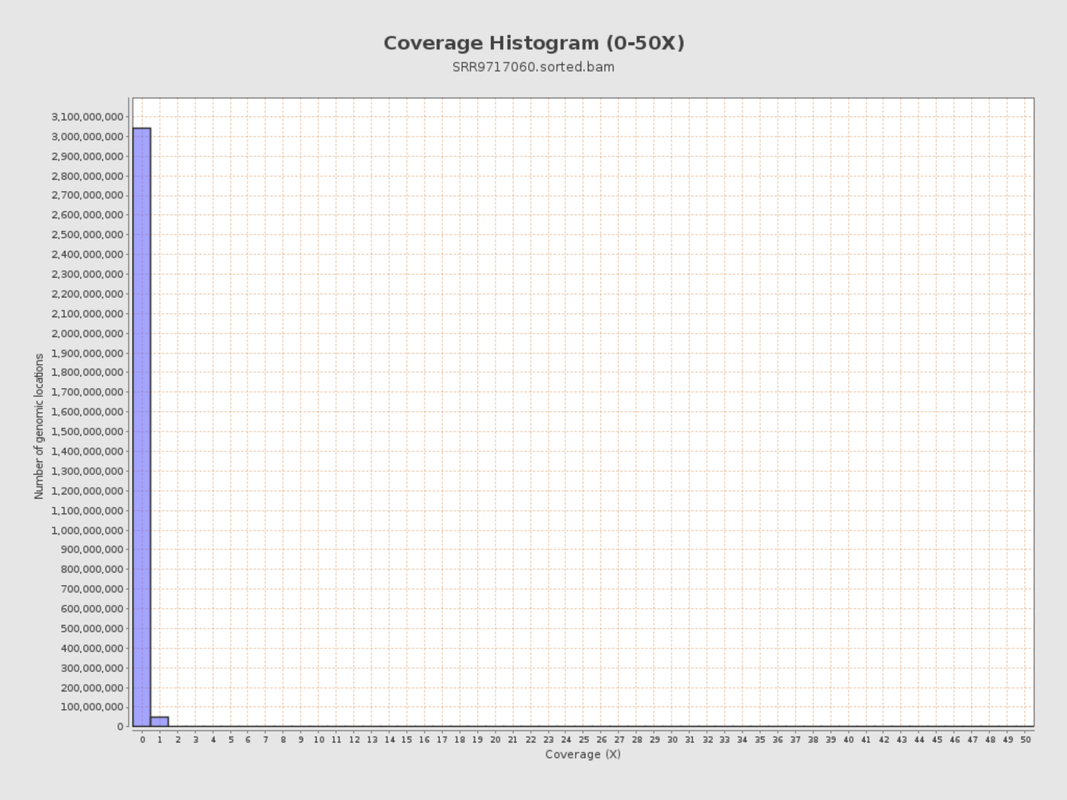
3. Results : Coverage across reference



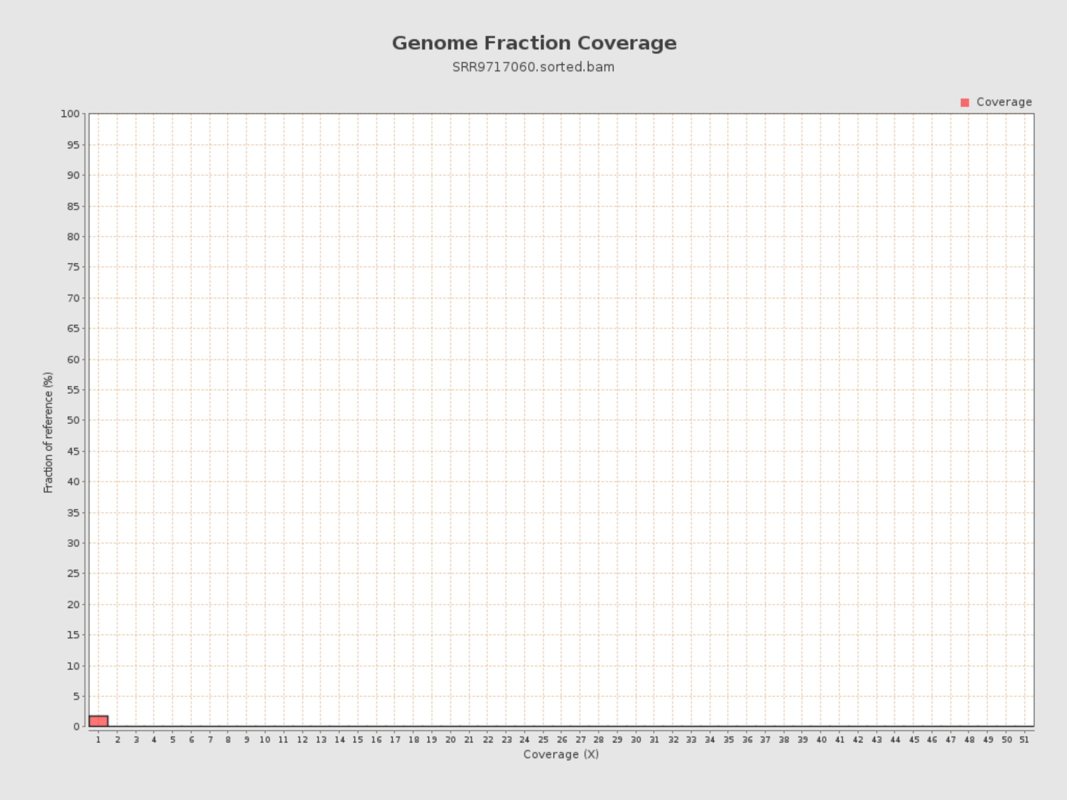
4. Results : Coverage Histogram



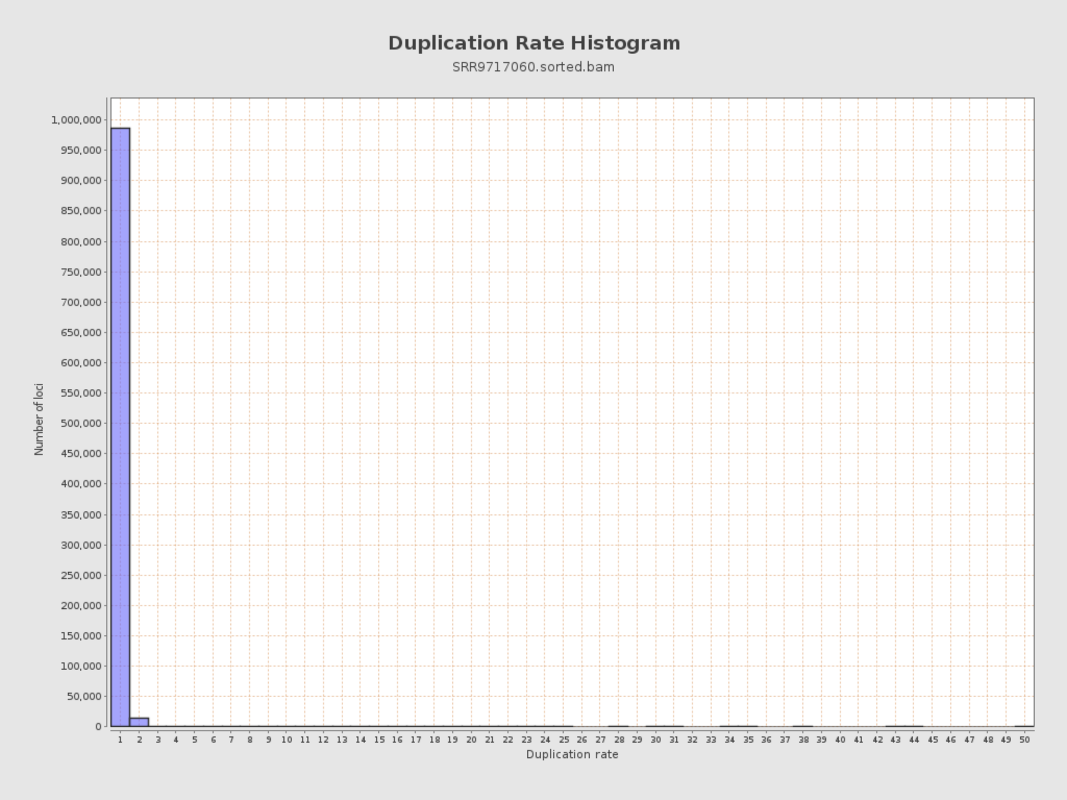
5. Results : Coverage Histogram (0-50X)



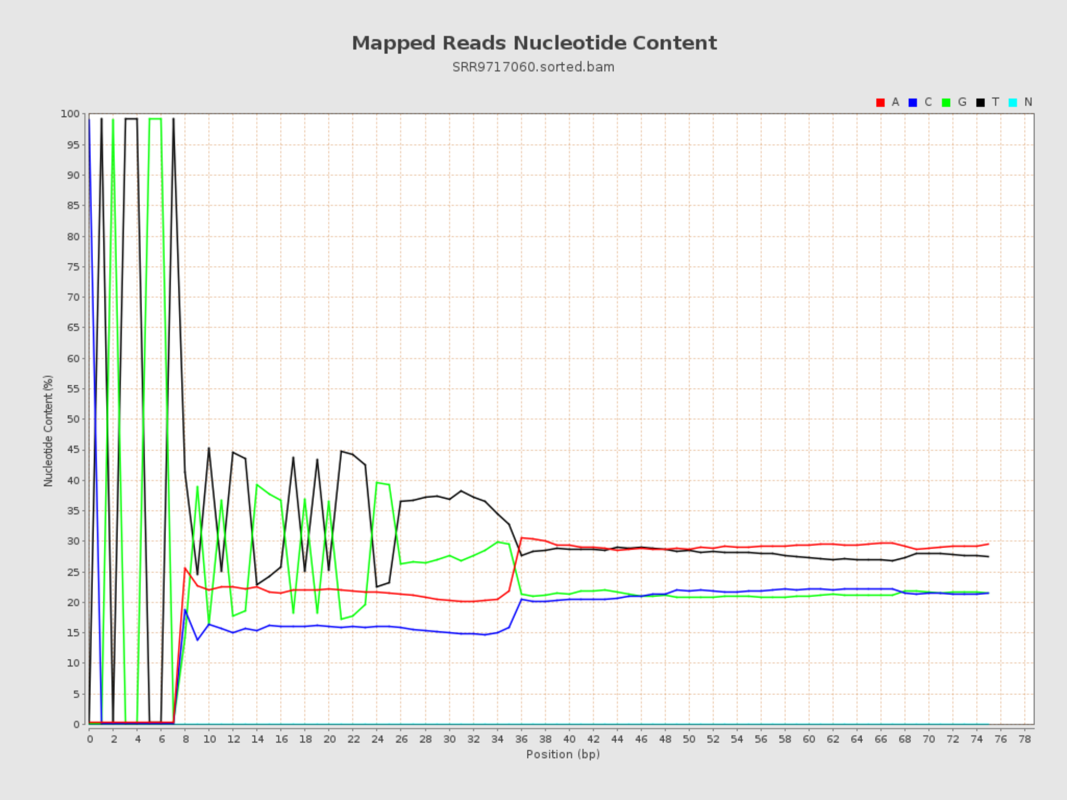
6. Results : Genome Fraction Coverage



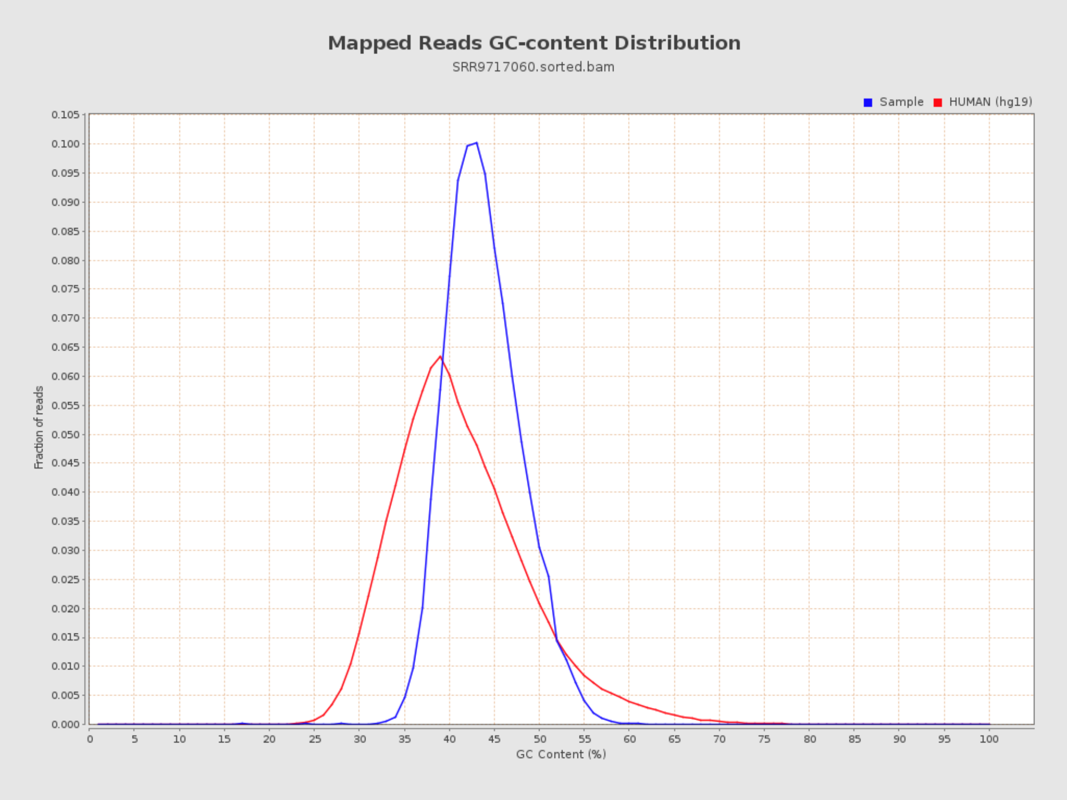
7. Results : Duplication Rate Histogram



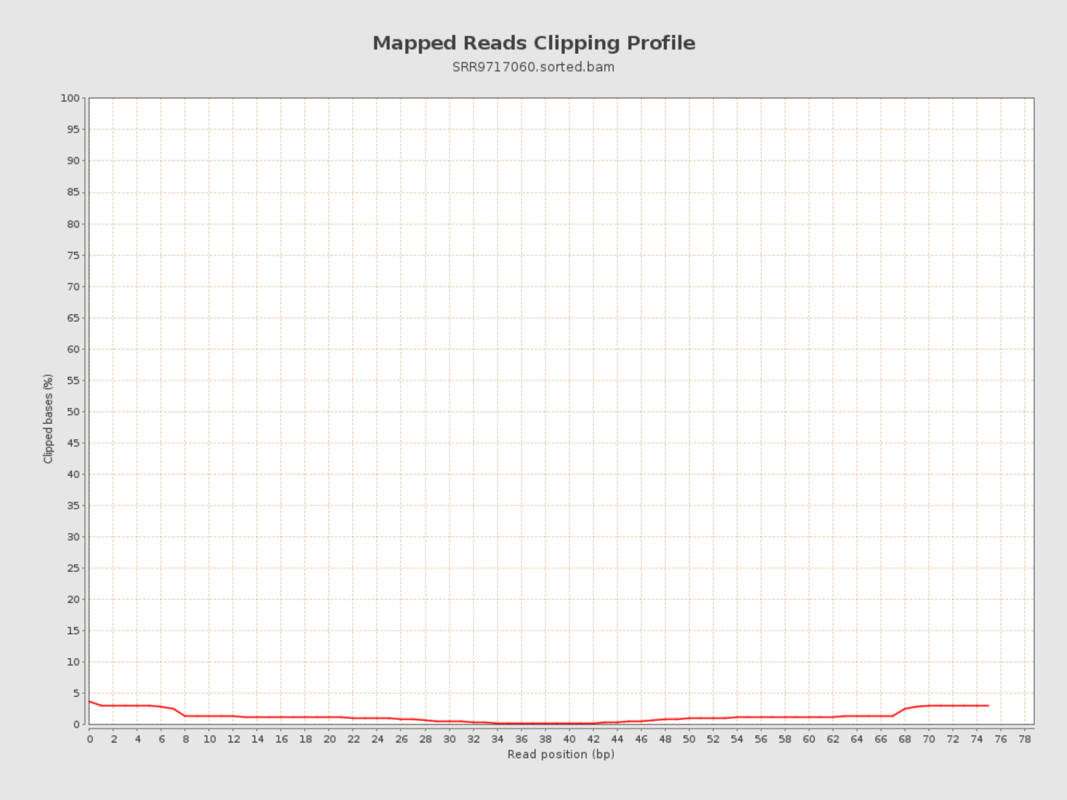
8. Results : Mapped Reads Nucleotide Content



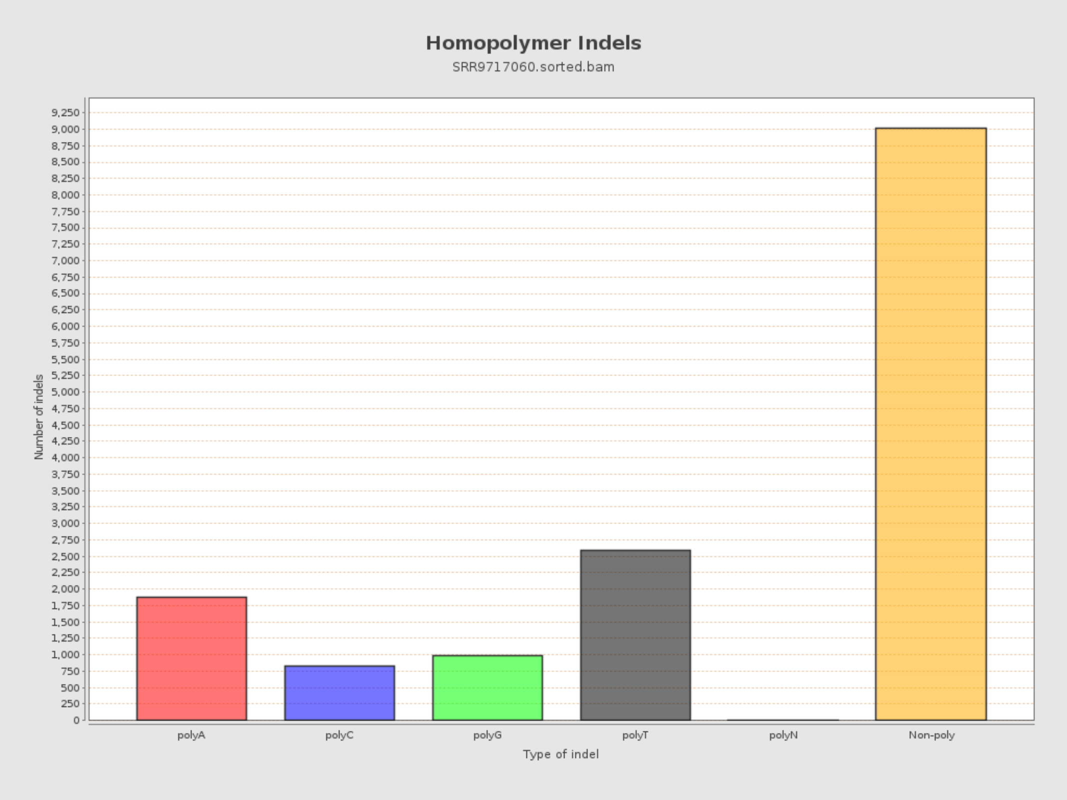
9. Results : Mapped Reads GC-content Distribution



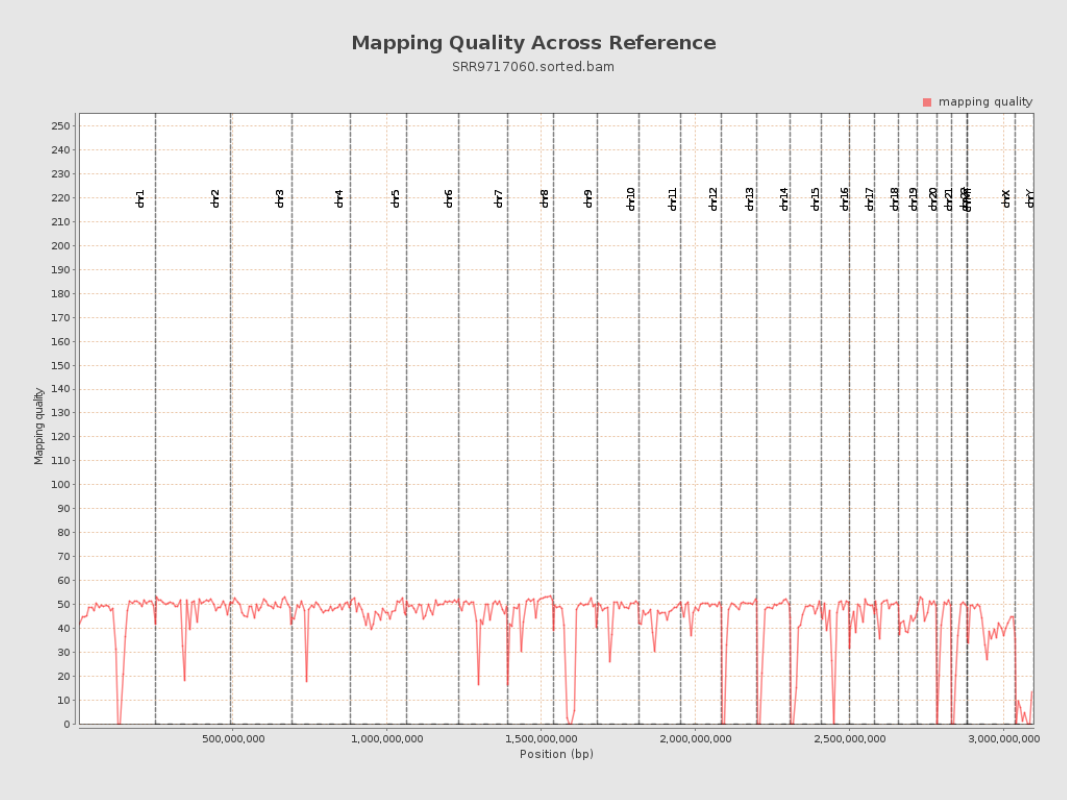
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram