Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 04:20:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717066.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_SRR9717066 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717066.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 04:20:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717066.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	824,676
Mapped reads	709,428 / 86.03%
Unmapped reads	115,248 / 13.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,138 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	11,708 / 1.42%
Duplication rate	1.17%
Clipped reads	710,370 / 86.14%

2.2. ACGT Content

Number/percentage of A's	9,693,154 / 24.2%
Number/percentage of C's	8,440,829 / 21.08%
Number/percentage of T's	11,284,650 / 28.18%
Number/percentage of G's	10,630,646 / 26.54%
Number/percentage of N's	1,132 / 0%
GC Percentage	47.62%

2.3. Coverage

Mean	0.0129

Standard Deviation	0.1365

2.4. Mapping Quality

Mean Mapping Quality	39.91

2.5. Mismatches and indels

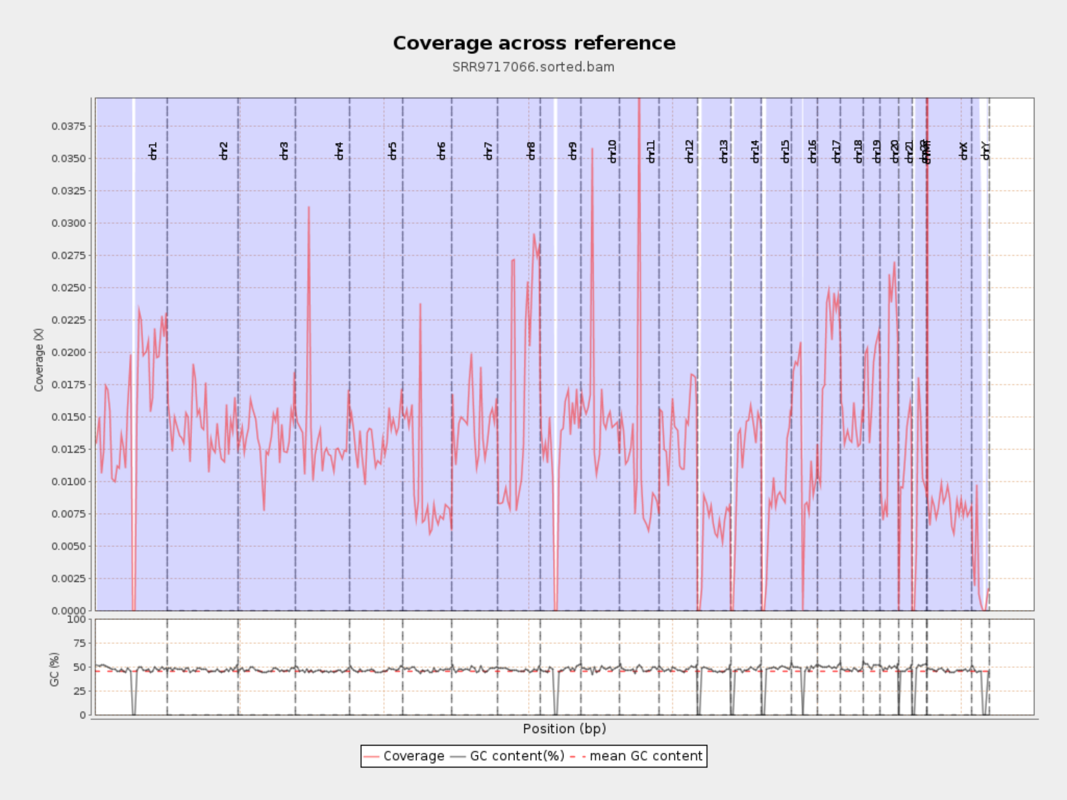
General error rate	0.55%
Mismatches	211,678
Insertions	3,619
Mapped reads with at least one insertion	0.51%
Deletions	6,787
Mapped reads with at least one deletion	0.95%
Homopolymer indels	33.53%

2.6. Chromosome stats

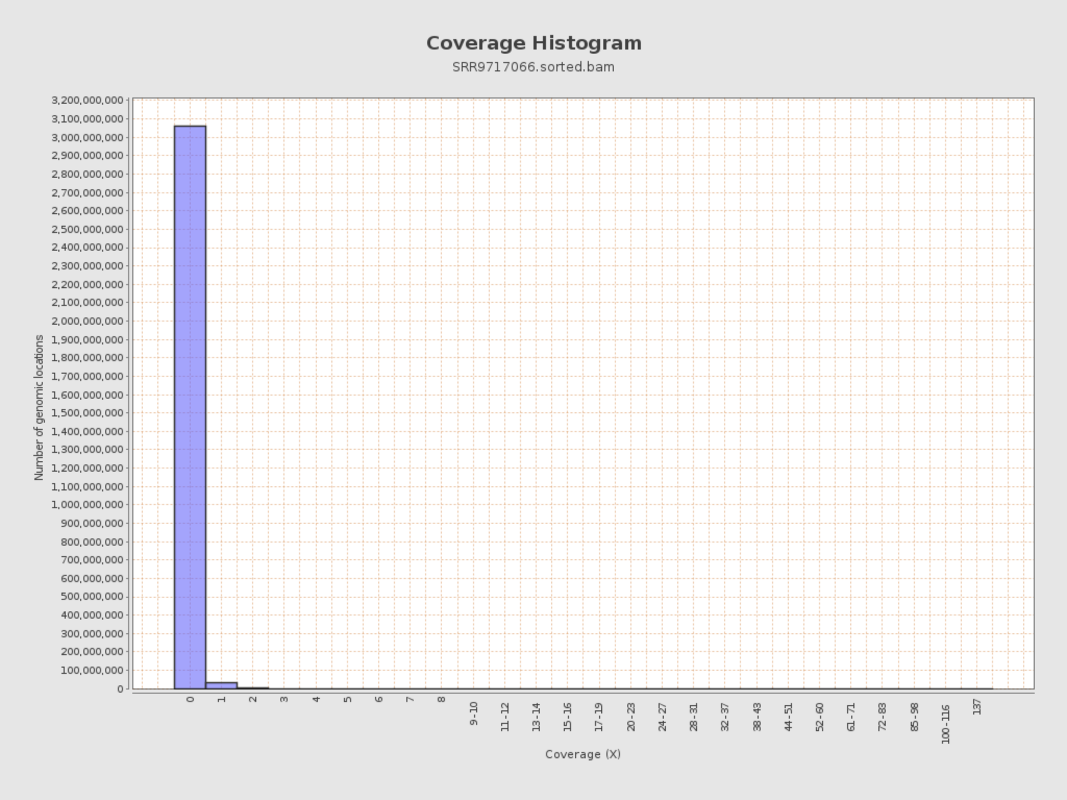
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3885779	0.0156	0.1551
chr2	243199373	3445251	0.0142	0.1593
chr3	198022430	2660215	0.0134	0.1255
chr4	191154276	2600991	0.0136	0.145
chr5	180915260	2398813	0.0133	0.1214
chr6	171115067	1677697	0.0098	0.1062
chr7	159138663	2327585	0.0146	0.1468

chr8	146364022	2475163	0.0169	0.1432
chr9	141213431	1758372	0.0125	0.1236
chr10	135534747	2135287	0.0158	0.2105
chr11	135006516	1637316	0.0121	0.1297
chr12	133851895	1895060	0.0142	0.1263
chr13	115169878	695837	0.006	0.0833
chr14	107349540	1246176	0.0116	0.1163
chr15	102531392	817301	0.008	0.0957
chr16	90354753	1103443	0.0122	0.1263
chr17	81195210	1605001	0.0198	0.1557
chr18	78077248	1097732	0.0141	0.1478
chr19	59128983	1090126	0.0184	0.1602
chr20	63025520	1069490	0.017	0.1465
chr21	48129895	545941	0.0113	0.1269
chr22	51304566	463435	0.009	0.1026
chrMT	16571	49597	2.993	2.9557
chrX	155270560	1241572	0.008	0.0986
chrY	59373566	139027	0.0023	0.09

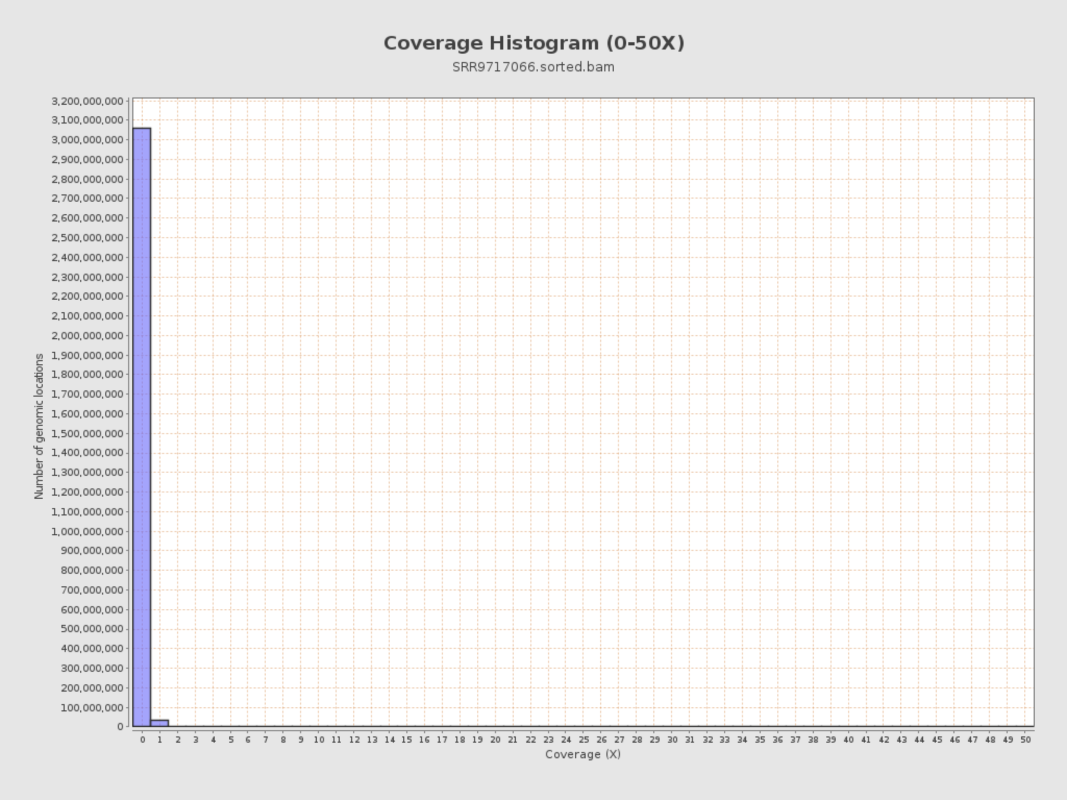
3. Results : Coverage across reference



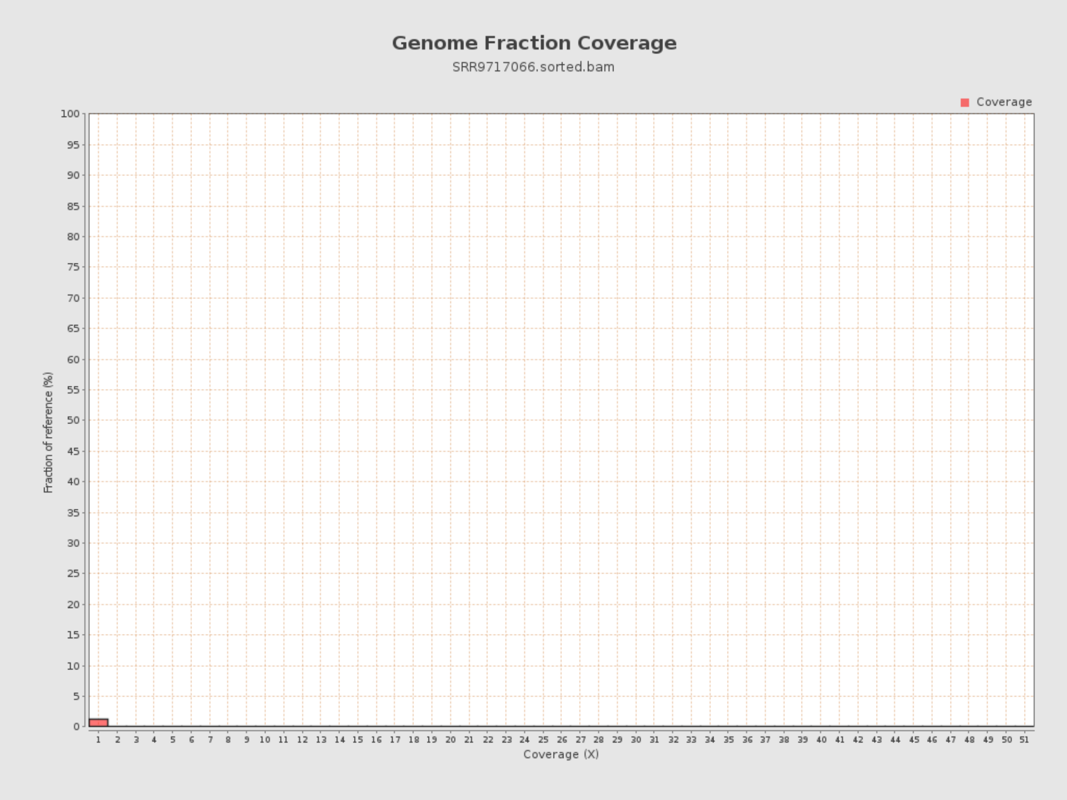
4. Results : Coverage Histogram



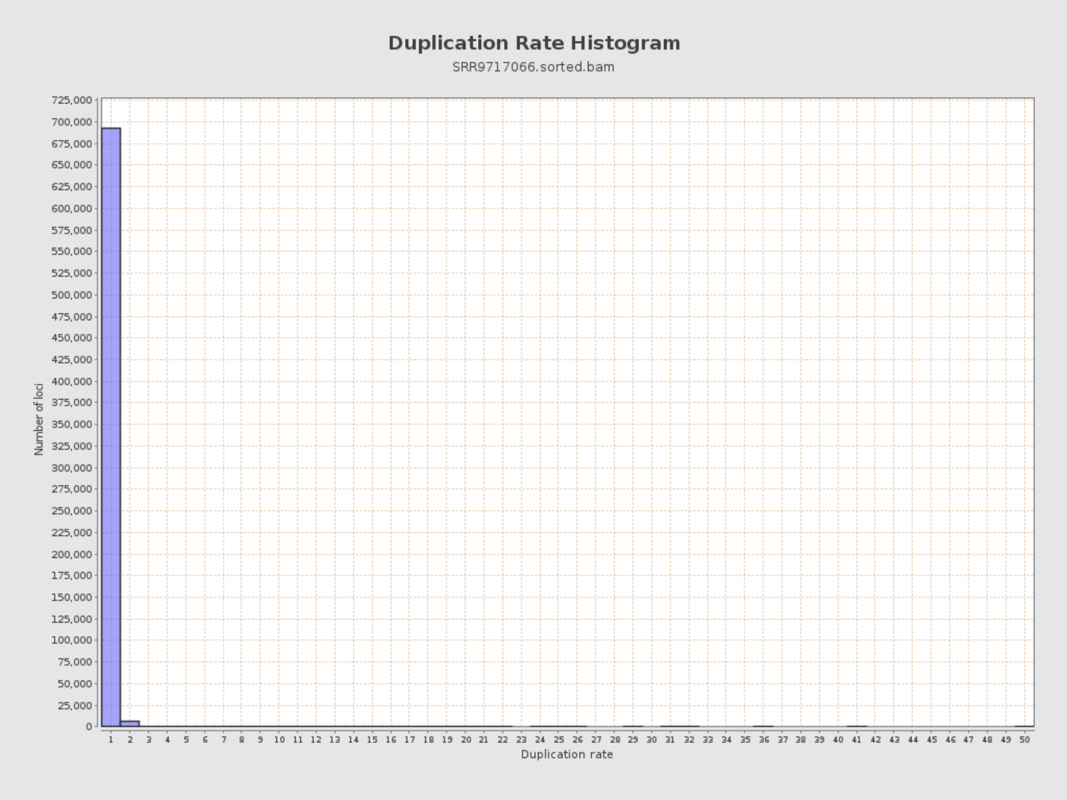
5. Results : Coverage Histogram (0-50X)



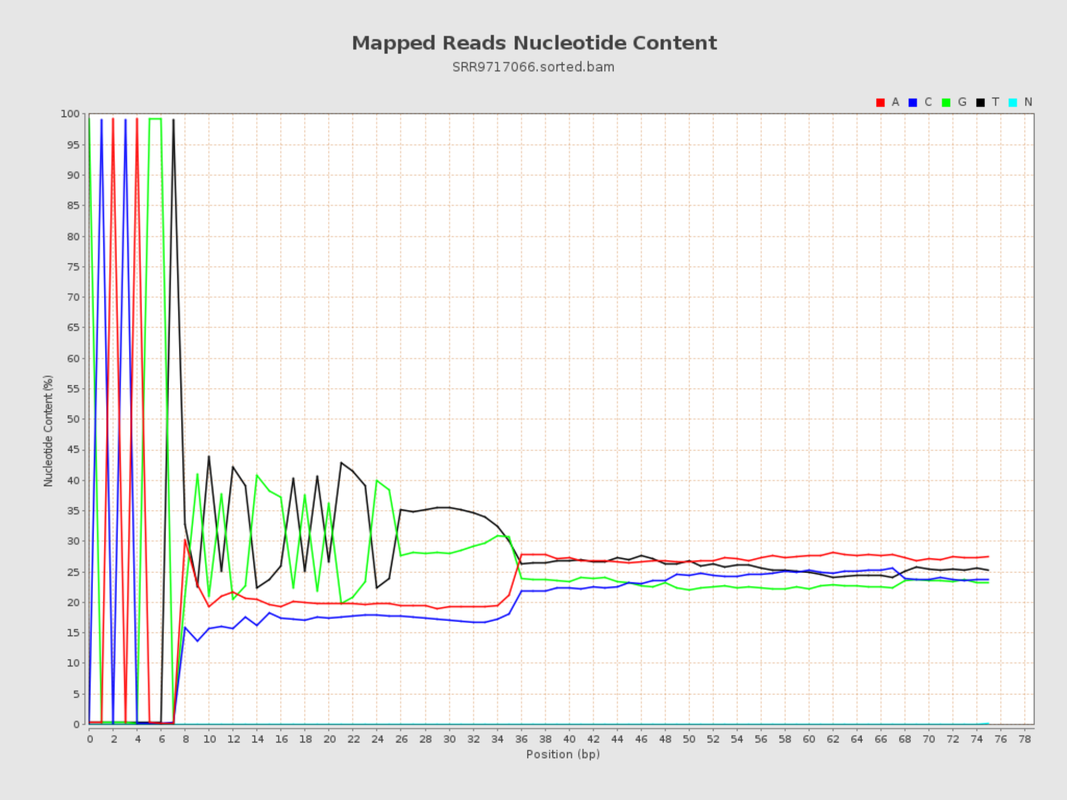
6. Results : Genome Fraction Coverage



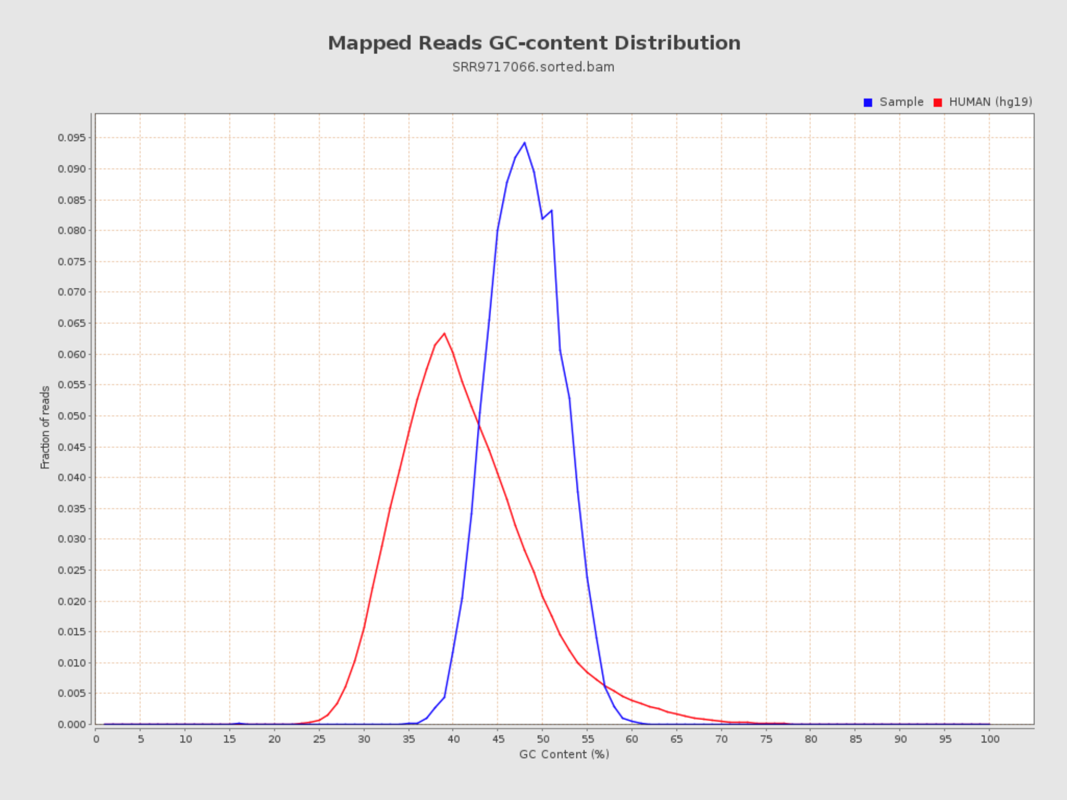
7. Results : Duplication Rate Histogram



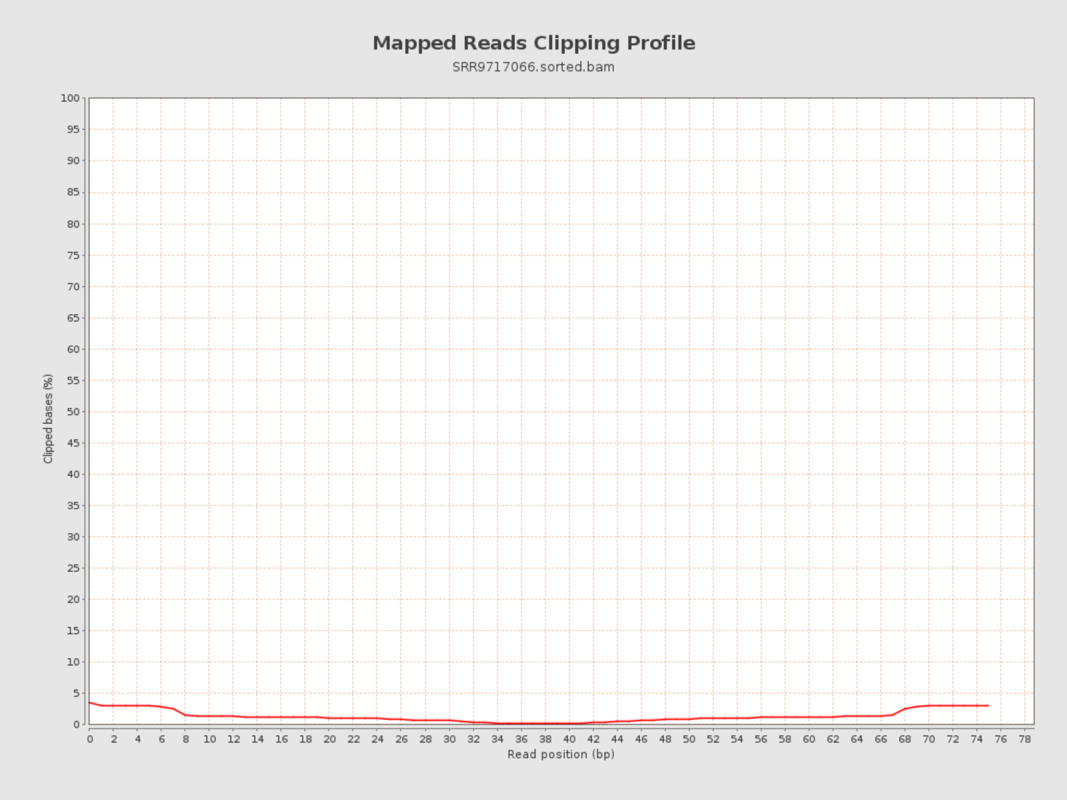
8. Results : Mapped Reads Nucleotide Content



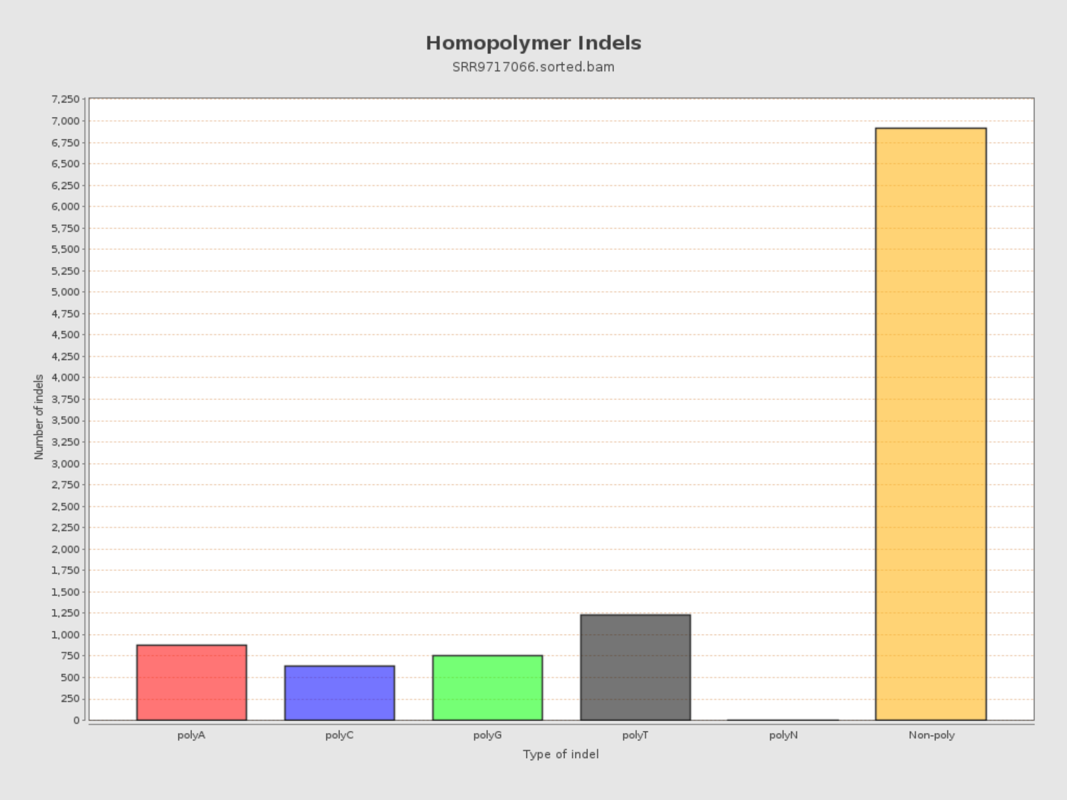
9. Results : Mapped Reads GC-content Distribution



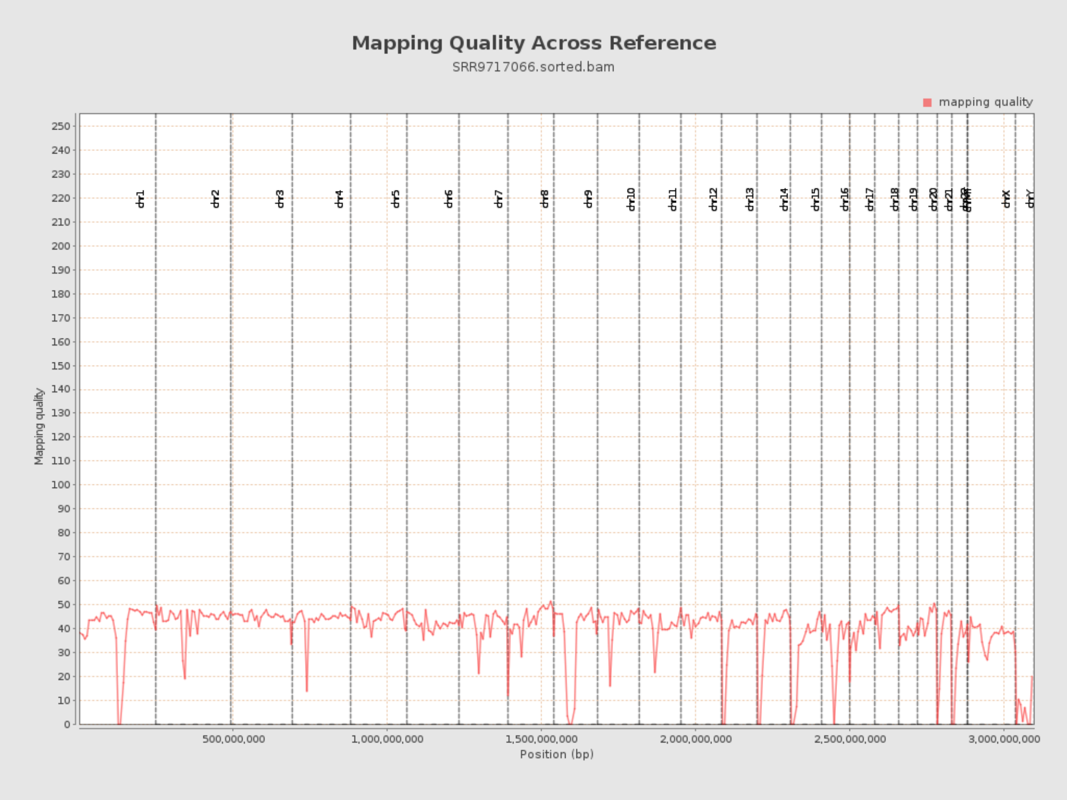
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram