Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:38:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717030.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_SRR9717030 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717030.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:38:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717030.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	963,877
Mapped reads	876,938 / 90.98%
Unmapped reads	86,939 / 9.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,350 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	18,891 / 1.96%
Duplication rate	1.52%
Clipped reads	880,313 / 91.33%

2.2. ACGT Content

Number/percentage of A's	12,780,708 / 24.98%
Number/percentage of C's	9,886,724 / 19.33%
Number/percentage of T's	16,099,093 / 31.47%
Number/percentage of G's	12,392,564 / 24.22%
Number/percentage of N's	568 / 0%
GC Percentage	43.55%

2.3. Coverage

Mean	0.0165

Standard Deviation	0.1729

2.4. Mapping Quality

Mean Mapping Quality	44.31

2.5. Mismatches and indels

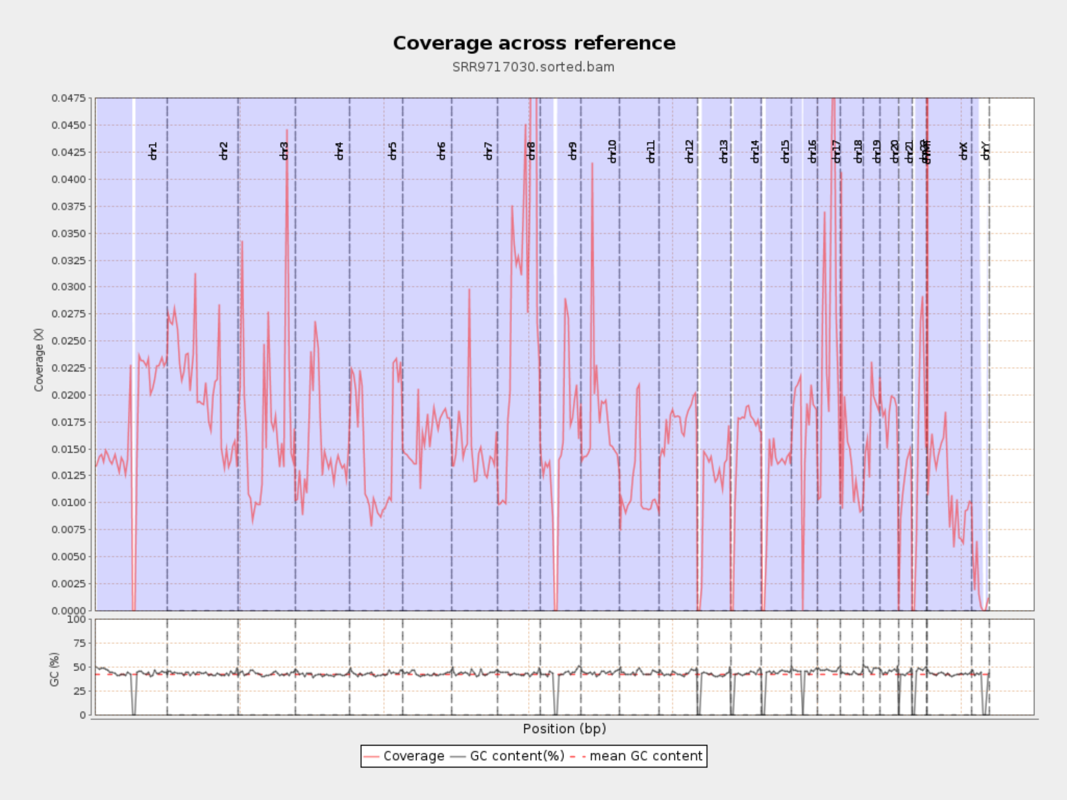
General error rate	0.51%
Mismatches	254,934
Insertions	2,983
Mapped reads with at least one insertion	0.34%
Deletions	9,259
Mapped reads with at least one deletion	1.05%
Homopolymer indels	41.24%

2.6. Chromosome stats

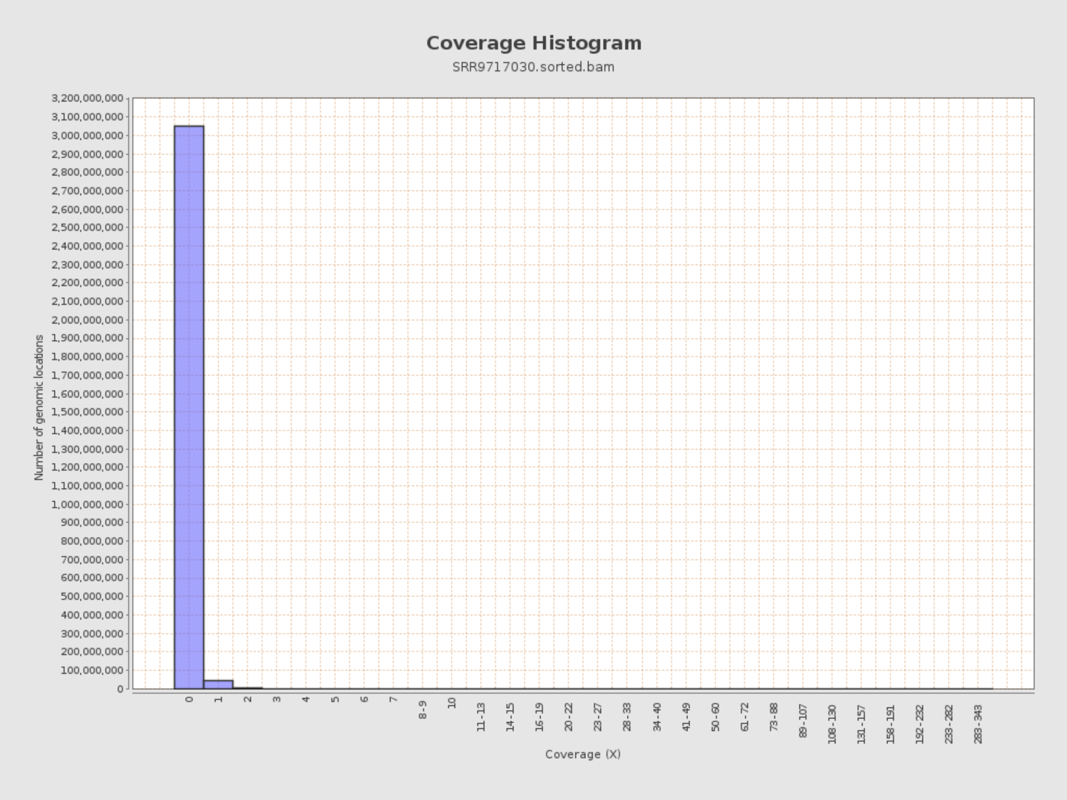
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4203017	0.0169	0.2481
chr2	243199373	5043937	0.0207	0.2159
chr3	198022430	3455367	0.0174	0.1414
chr4	191154276	2847978	0.0149	0.1341
chr5	180915260	2706592	0.015	0.1283
chr6	171115067	2782128	0.0163	0.1401
chr7	159138663	2412810	0.0152	0.2313

chr8	146364022	4931900	0.0337	0.2368
chr9	141213431	2106257	0.0149	0.1399
chr10	135534747	2443008	0.018	0.2223
chr11	135006516	1535098	0.0114	0.1289
chr12	133851895	2332832	0.0174	0.1461
chr13	115169878	1313930	0.0114	0.1115
chr14	107349540	1615925	0.0151	0.1308
chr15	102531392	1191802	0.0116	0.1137
chr16	90354753	1559964	0.0173	0.142
chr17	81195210	2153274	0.0265	0.1752
chr18	78077248	1081999	0.0139	0.1963
chr19	59128983	1033288	0.0175	0.225
chr20	63025520	1151893	0.0183	0.1466
chr21	48129895	537647	0.0112	0.1173
chr22	51304566	768357	0.015	0.128
chrMT	16571	74558	4.4993	3.245
chrX	155270560	1774522	0.0114	0.1212
chrY	59373566	116203	0.002	0.0617

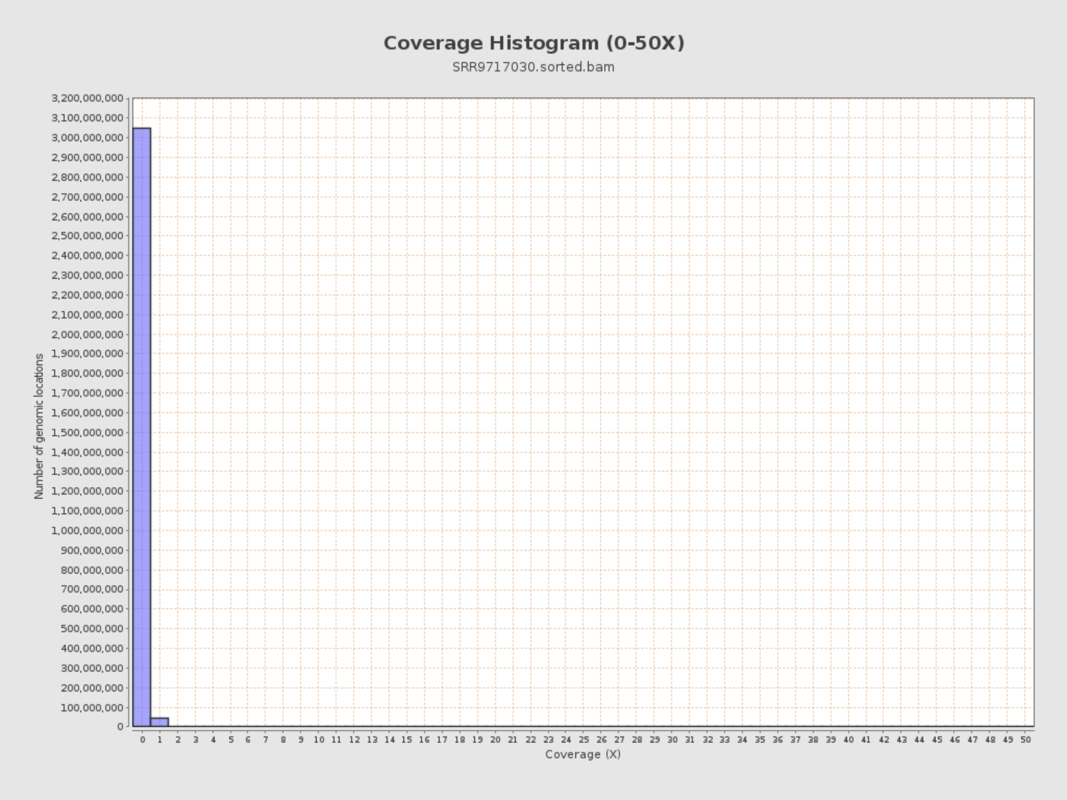
3. Results : Coverage across reference



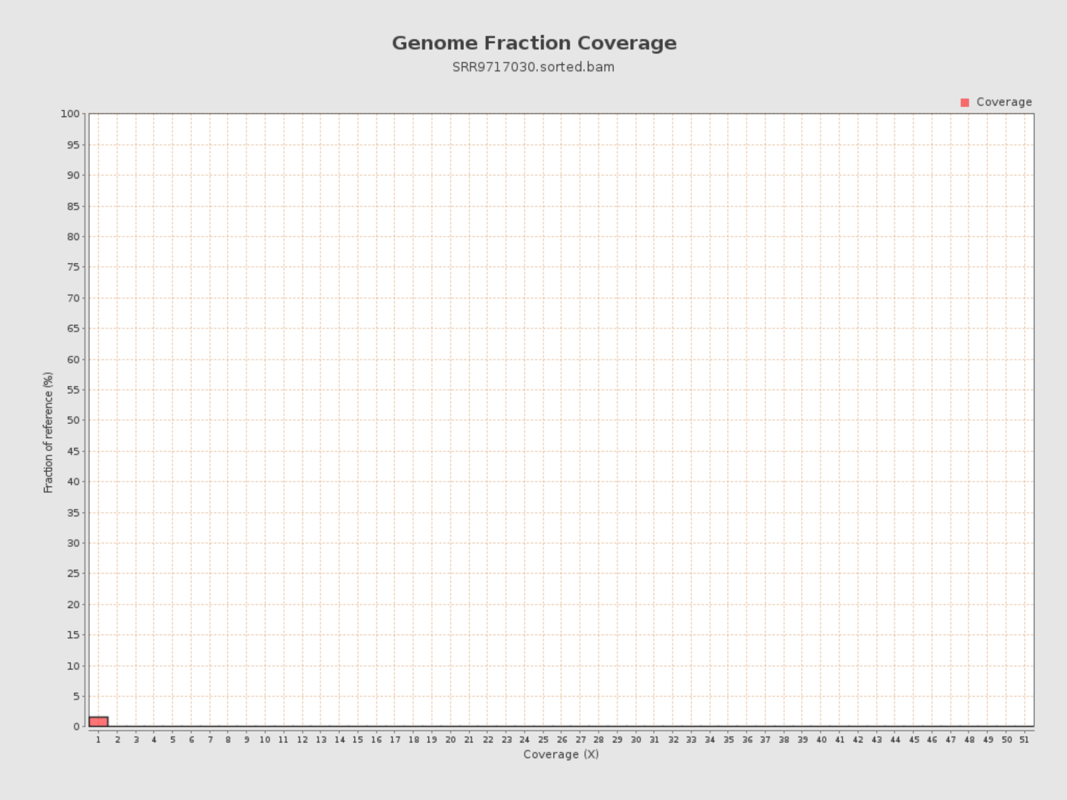
4. Results : Coverage Histogram



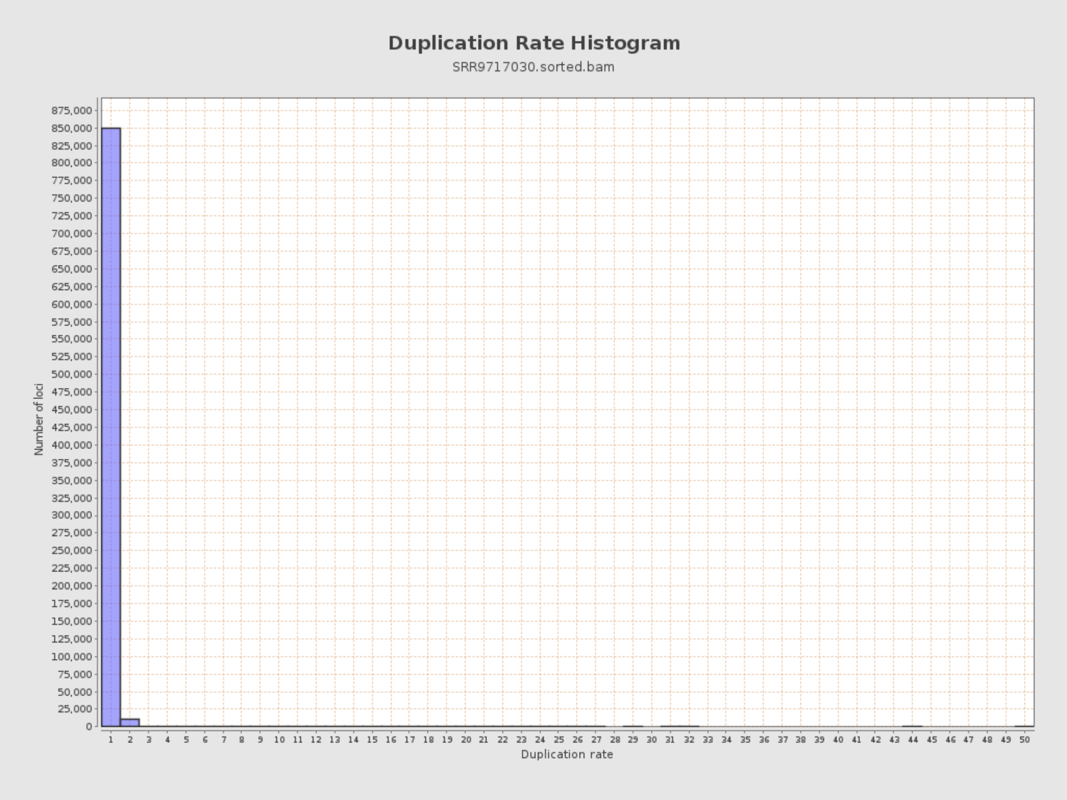
5. Results : Coverage Histogram (0-50X)



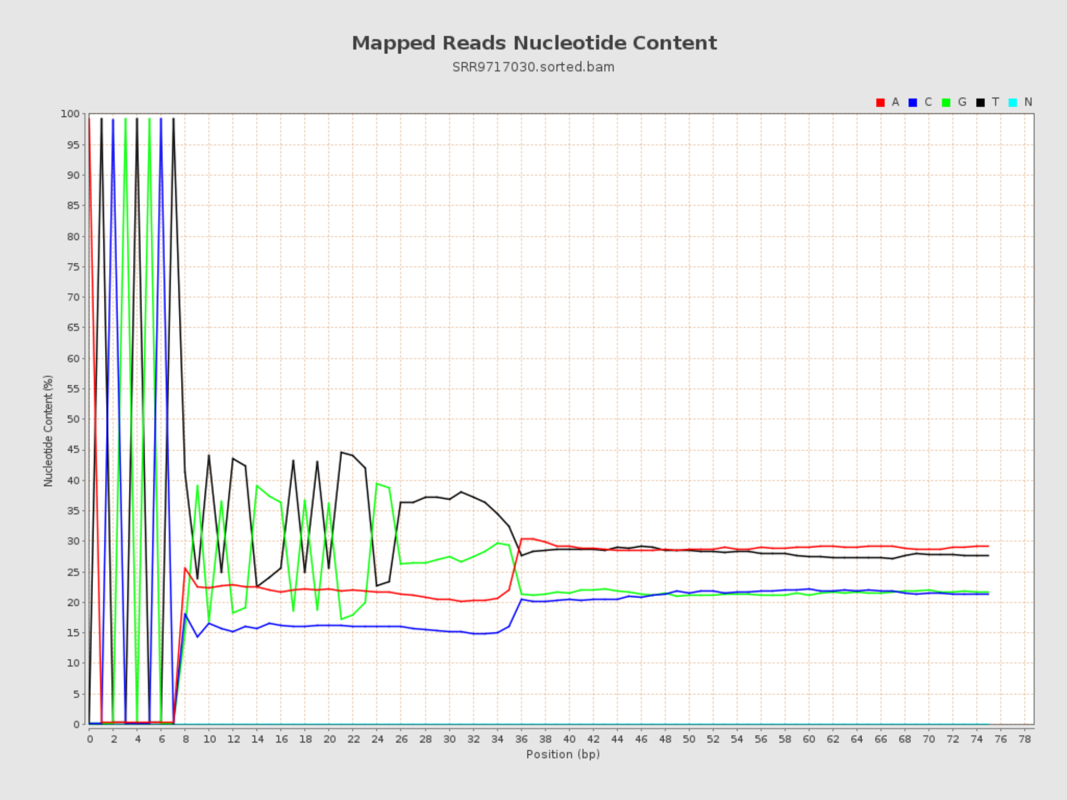
6. Results : Genome Fraction Coverage



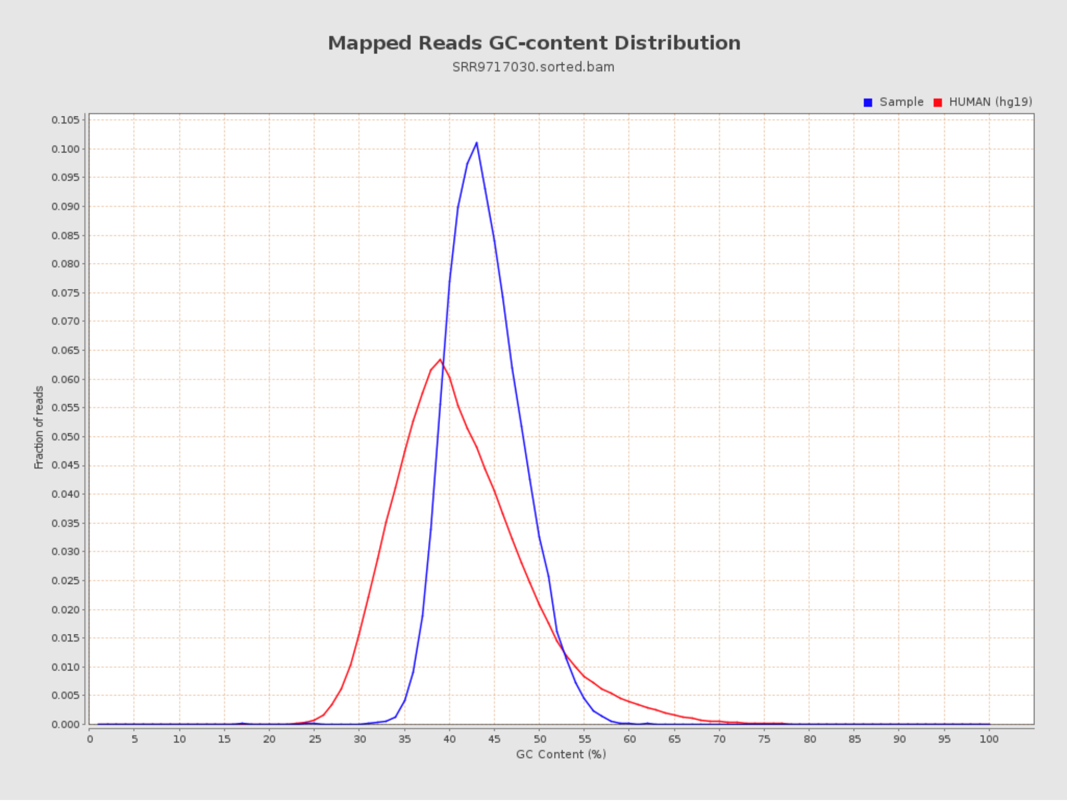
7. Results : Duplication Rate Histogram



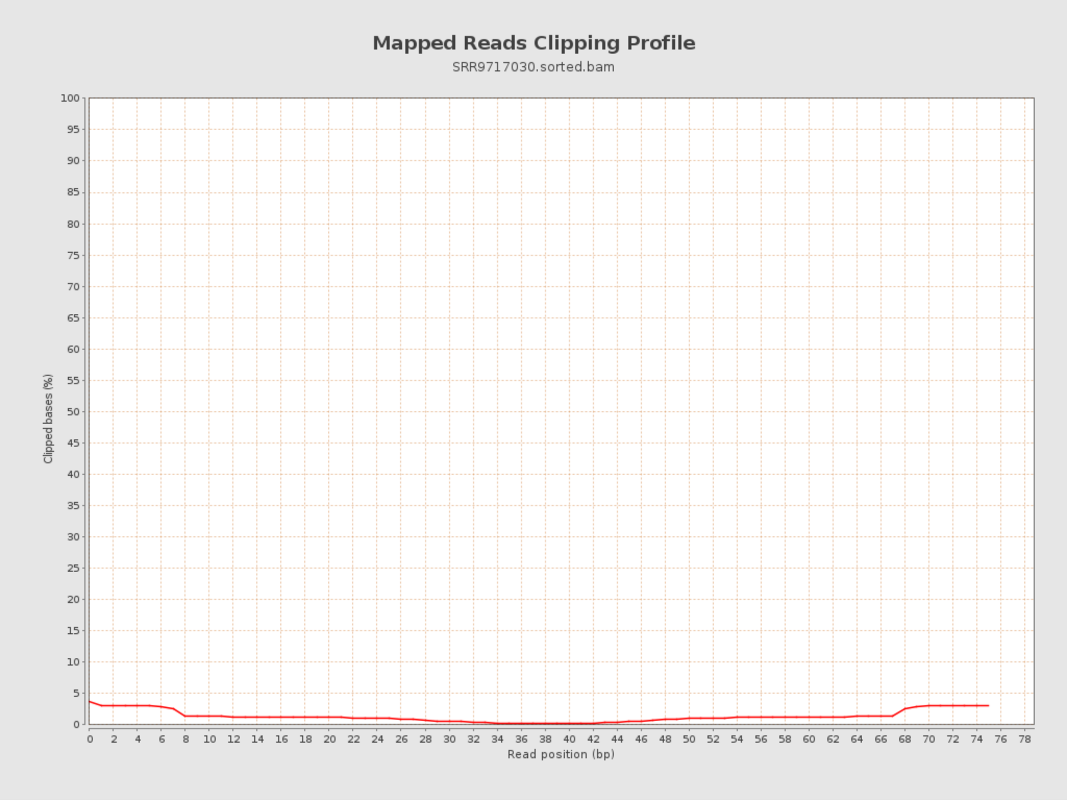
8. Results : Mapped Reads Nucleotide Content



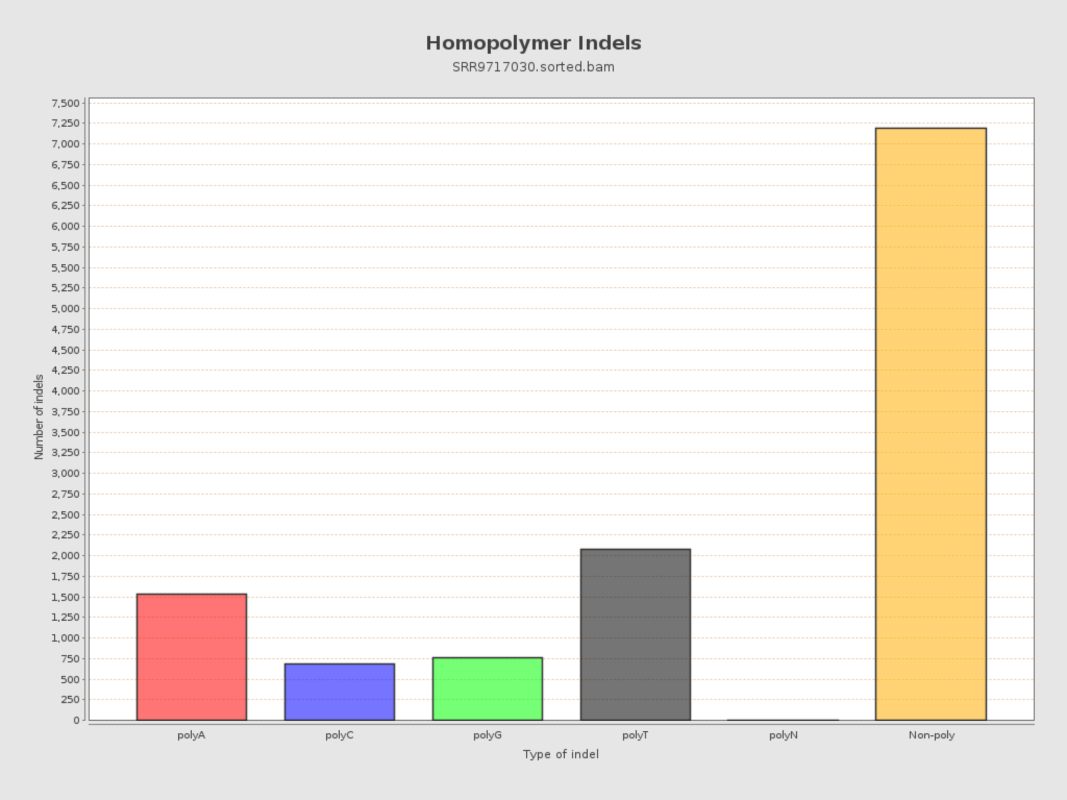
9. Results : Mapped Reads GC-content Distribution



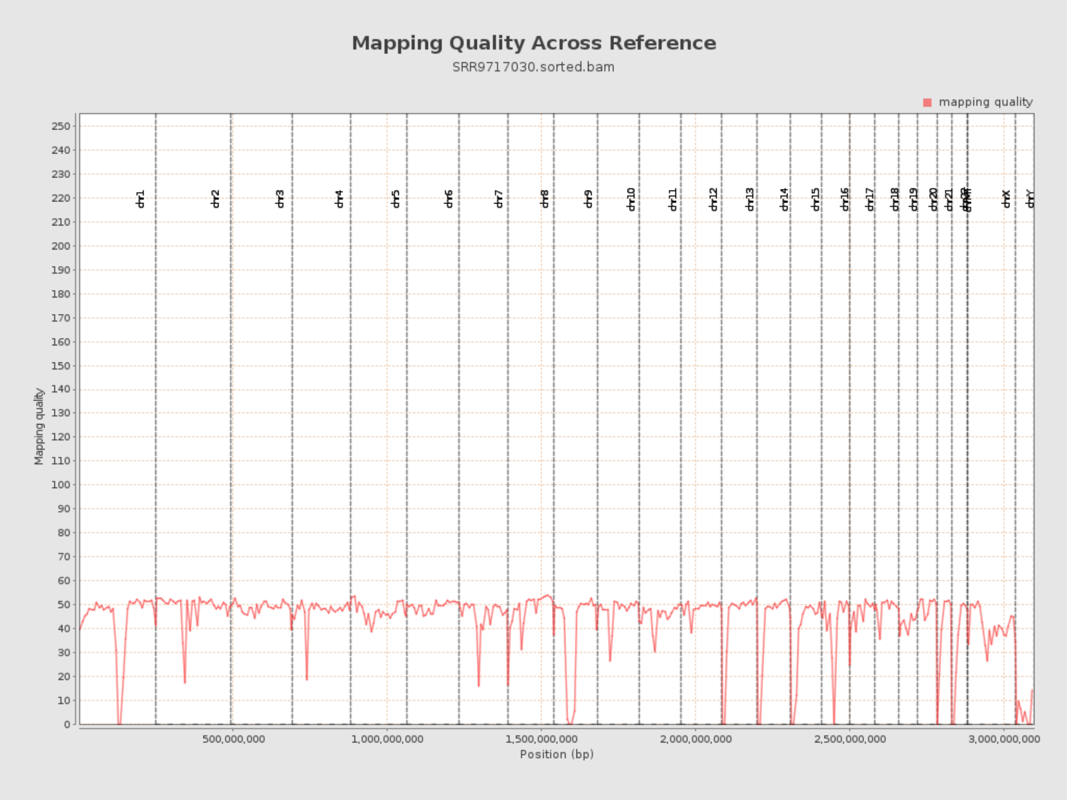
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram