Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 03:44:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717063.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_SRR9717063 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717063.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 03:44:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717063.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,453,248
Mapped reads	920,158 / 63.32%
Unmapped reads	533,090 / 36.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,612 / 0.18%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	19,889 / 1.37%
Duplication rate	1.57%
Clipped reads	921,319 / 63.4%

2.2. ACGT Content

Number/percentage of A's	12,375,749 / 24.59%
Number/percentage of C's	9,944,995 / 19.76%
Number/percentage of T's	14,881,989 / 29.57%
Number/percentage of G's	13,124,146 / 26.08%
Number/percentage of N's	1,481 / 0%
GC Percentage	45.84%

2.3. Coverage

Mean	0.0163

Standard Deviation	0.1579

2.4. Mapping Quality

Mean Mapping Quality	39.04

2.5. Mismatches and indels

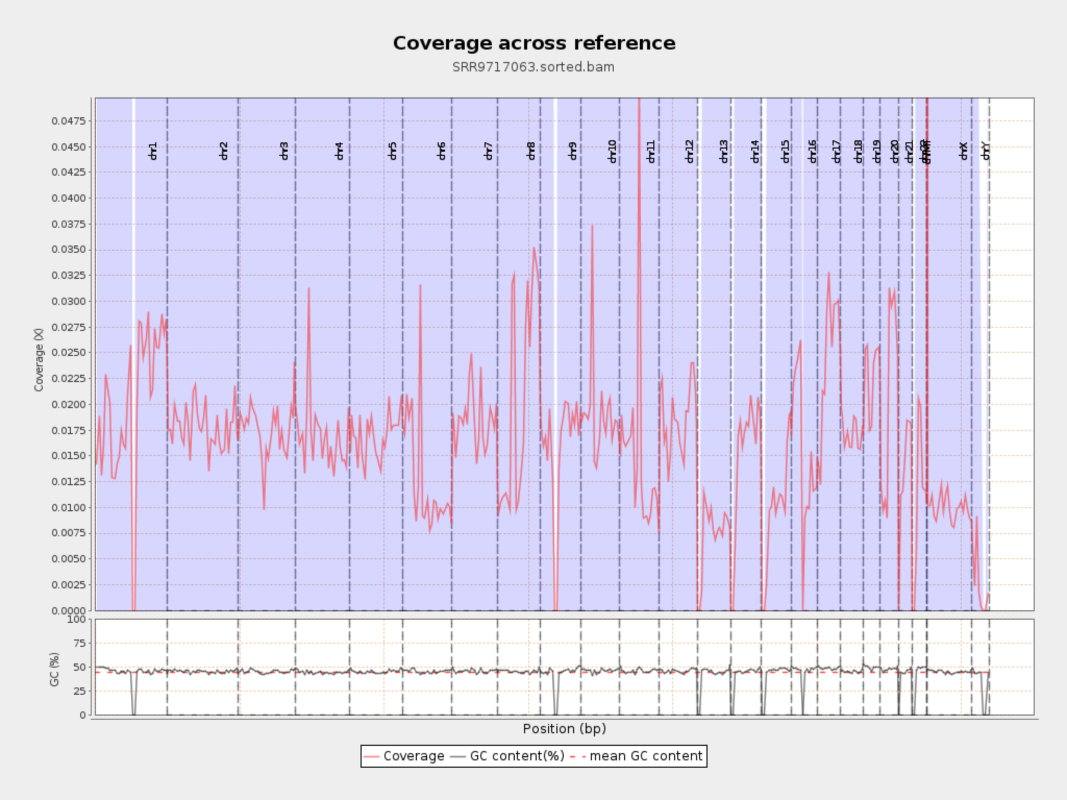
General error rate	0.54%
Mismatches	266,227
Insertions	3,510
Mapped reads with at least one insertion	0.38%
Deletions	8,258
Mapped reads with at least one deletion	0.89%
Homopolymer indels	35.1%

2.6. Chromosome stats

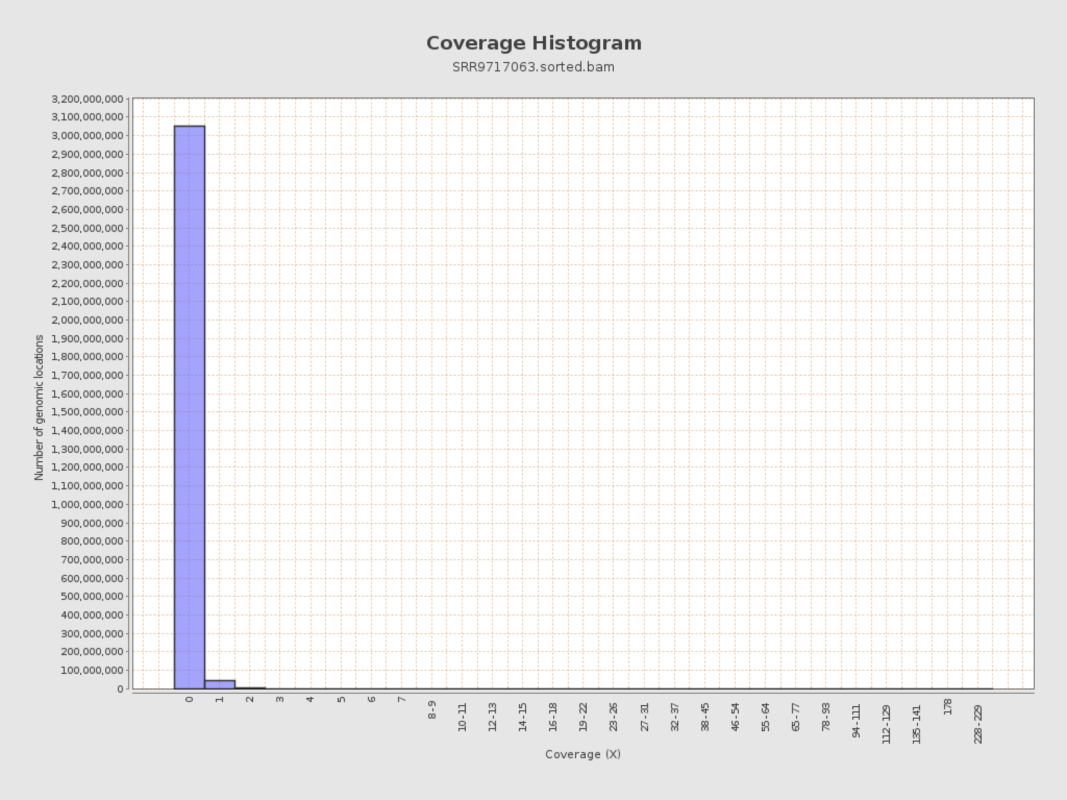
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4970760	0.0199	0.1865
chr2	243199373	4333724	0.0178	0.1884
chr3	198022430	3451440	0.0174	0.1483
chr4	191154276	3255407	0.017	0.1544
chr5	180915260	3083214	0.017	0.1409
chr6	171115067	2179570	0.0127	0.124
chr7	159138663	2953529	0.0186	0.183

chr8	146364022	3016017	0.0206	0.1628
chr9	141213431	2194099	0.0155	0.1451
chr10	135534747	2601798	0.0192	0.2338
chr11	135006516	2096044	0.0155	0.1585
chr12	133851895	2491659	0.0186	0.1485
chr13	115169878	842347	0.0073	0.0933
chr14	107349540	1607122	0.015	0.1349
chr15	102531392	994692	0.0097	0.1102
chr16	90354753	1355751	0.015	0.1435
chr17	81195210	2001578	0.0247	0.1774
chr18	78077248	1335853	0.0171	0.1716
chr19	59128983	1346230	0.0228	0.1838
chr20	63025520	1293554	0.0205	0.1638
chr21	48129895	664261	0.0138	0.1375
chr22	51304566	560791	0.0109	0.1158
chrMT	16571	8229	0.4966	0.8134
chrX	155270560	1552578	0.01	0.1173
chrY	59373566	151965	0.0026	0.0792

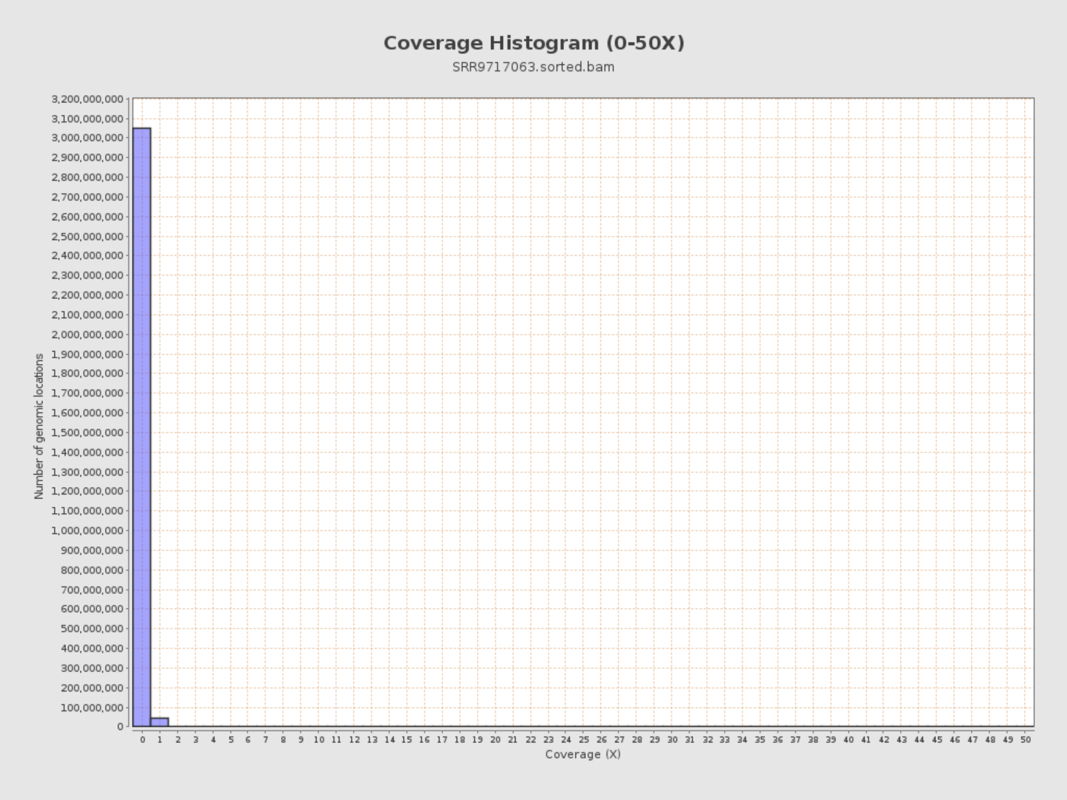
3. Results : Coverage across reference



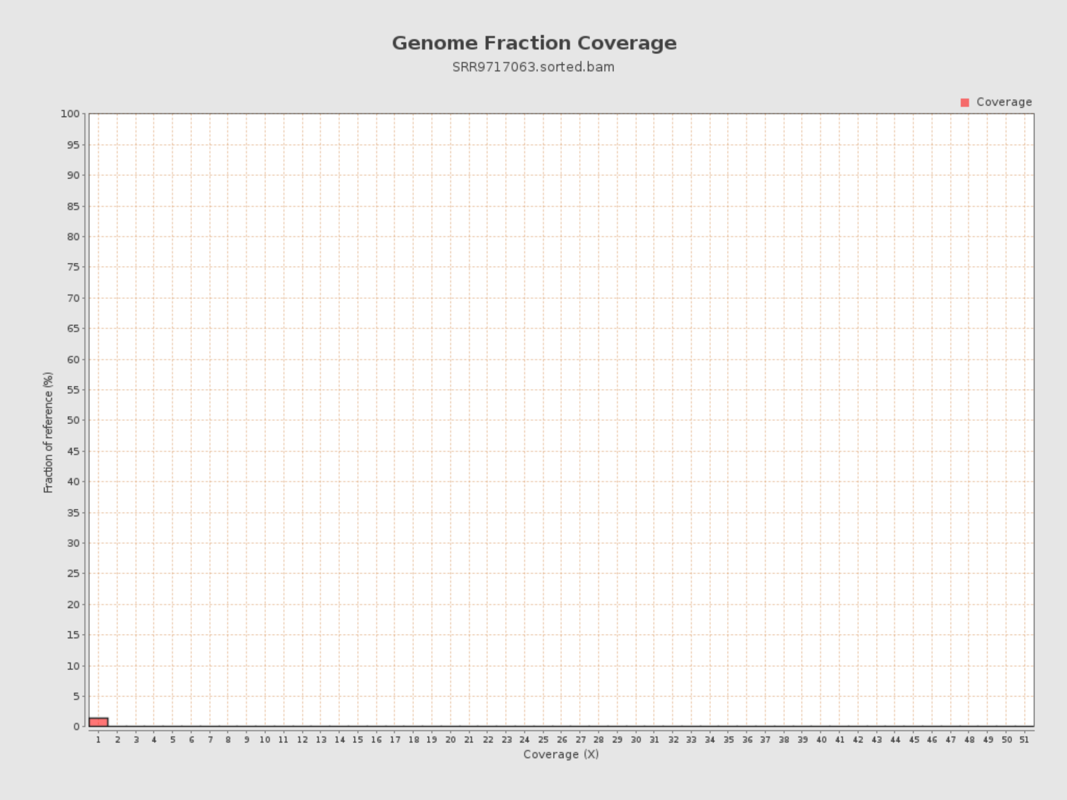
4. Results : Coverage Histogram



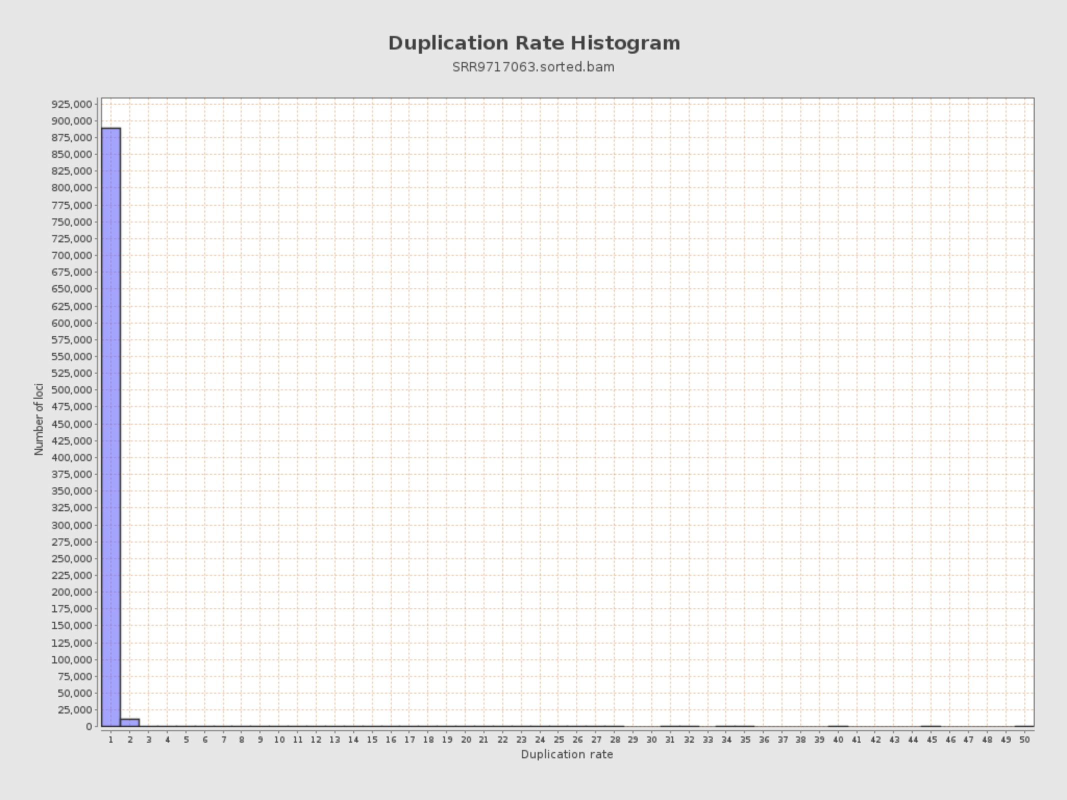
5. Results : Coverage Histogram (0-50X)



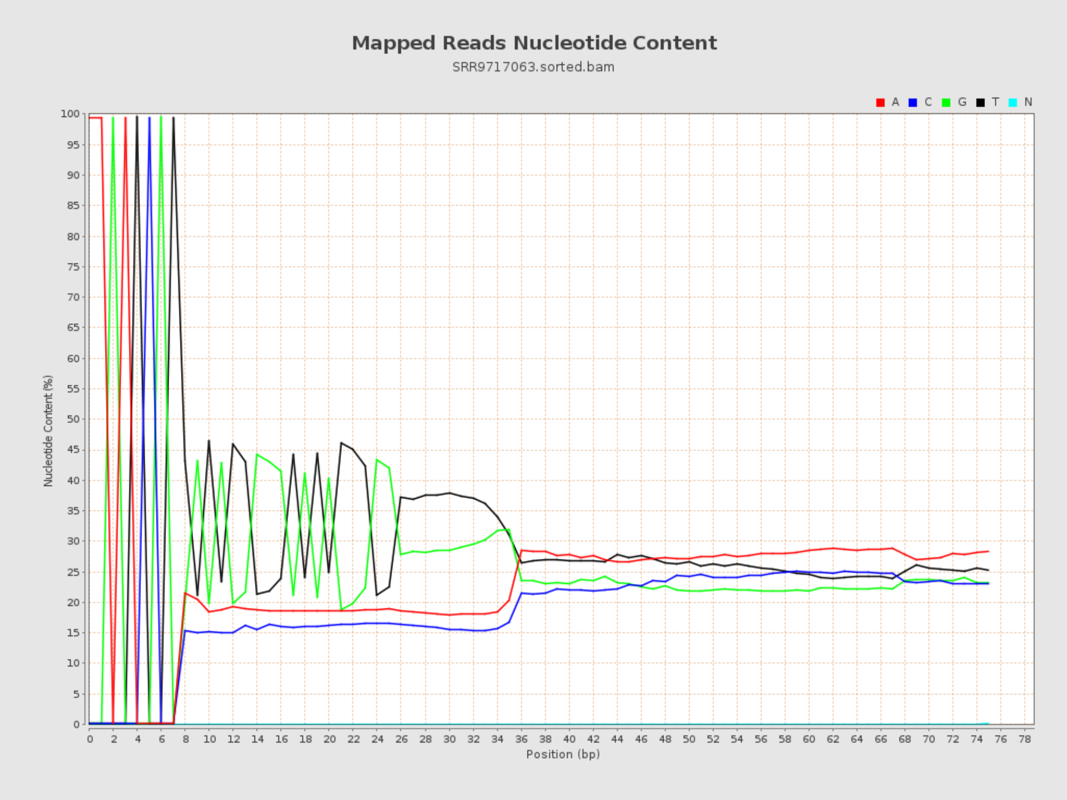
6. Results : Genome Fraction Coverage



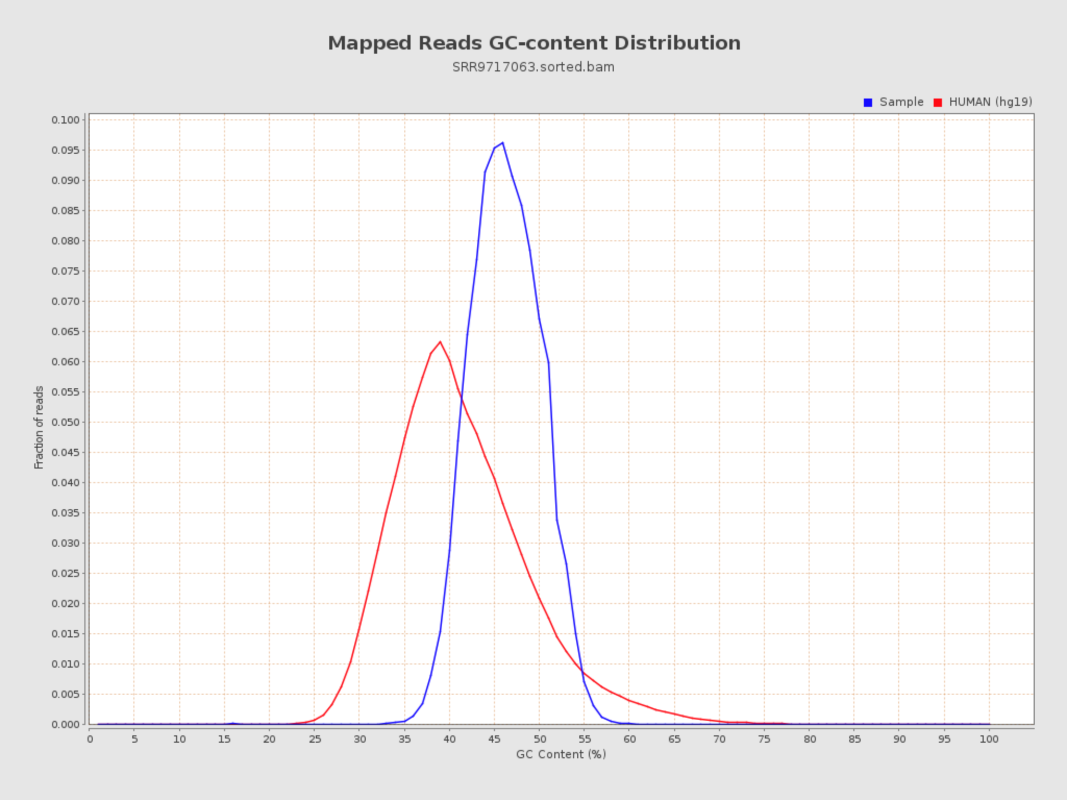
7. Results : Duplication Rate Histogram



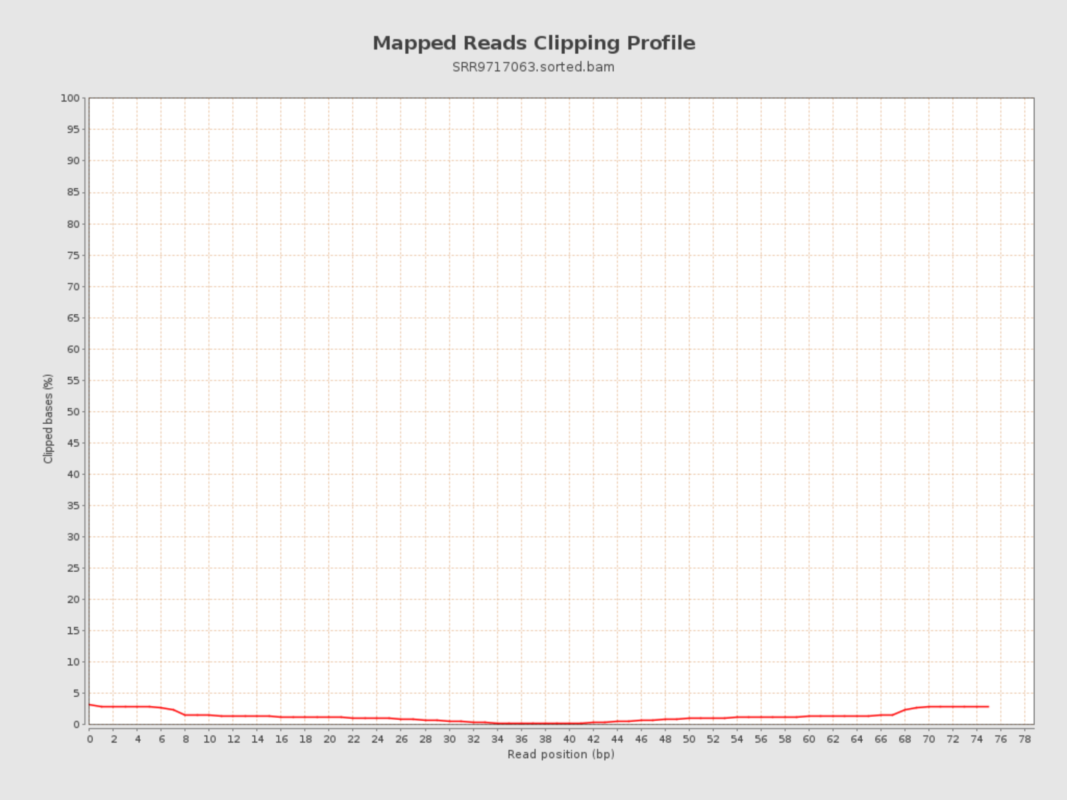
8. Results : Mapped Reads Nucleotide Content



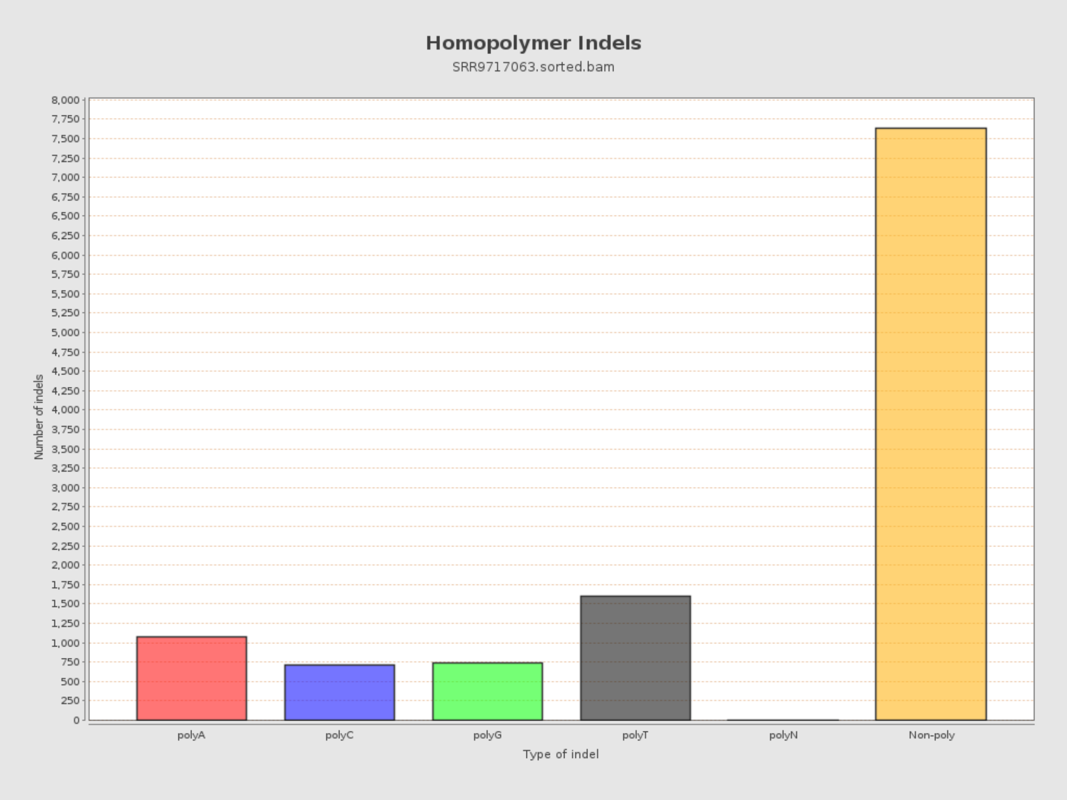
9. Results : Mapped Reads GC-content Distribution



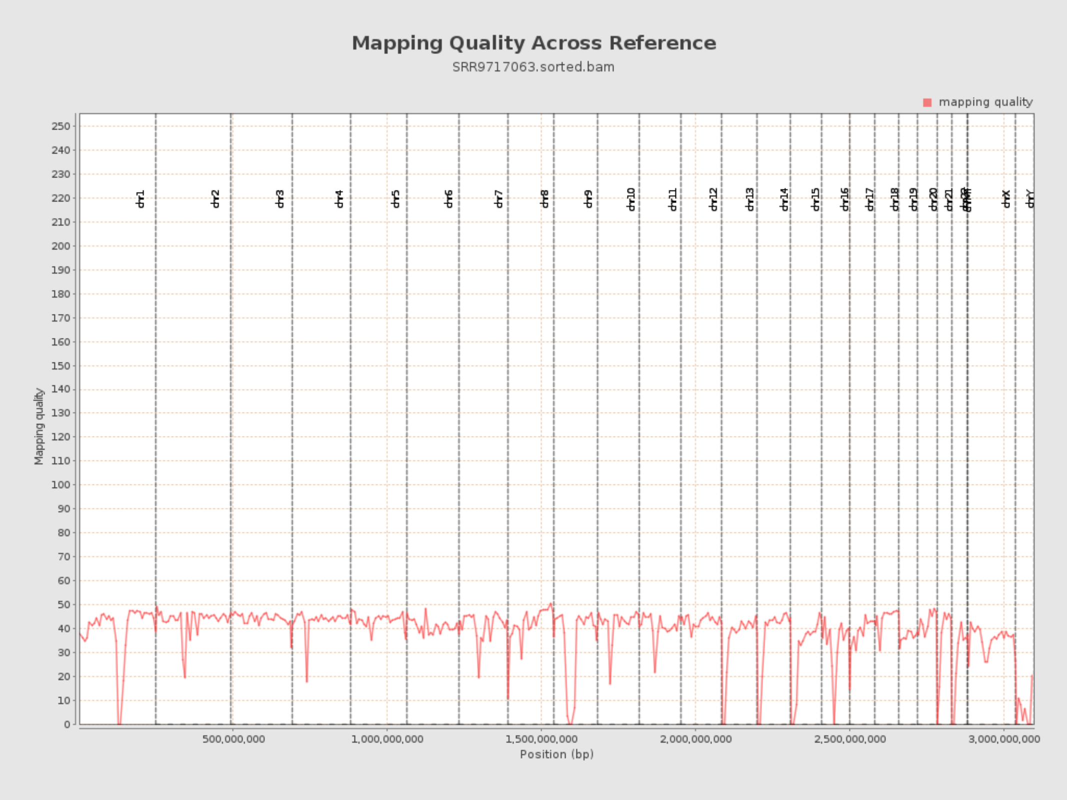
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram