Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 05:00:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717081.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_SRR9717081 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717081.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 05:00:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717081.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,000,695
Mapped reads	910,627 / 91%
Unmapped reads	90,068 / 9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,726 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	29,078 / 2.91%
Duplication rate	2.58%
Clipped reads	912,386 / 91.18%

2.2. ACGT Content

Number/percentage of A's	12,058,190 / 23.28%
Number/percentage of C's	10,261,451 / 19.81%
Number/percentage of T's	17,059,425 / 32.94%
Number/percentage of G's	12,409,688 / 23.96%
Number/percentage of N's	494 / 0%
GC Percentage	43.78%

2.3. Coverage

Mean	0.0167

Standard Deviation	0.1706

2.4. Mapping Quality

Mean Mapping Quality	44.67

2.5. Mismatches and indels

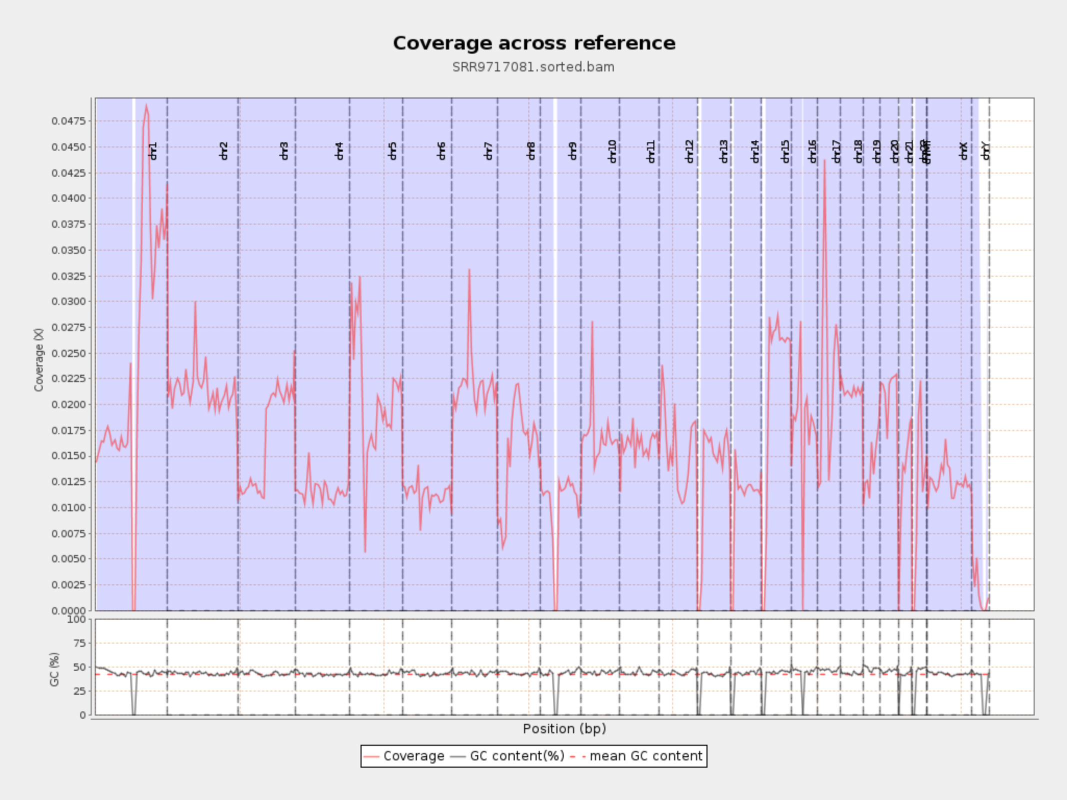
General error rate	0.49%
Mismatches	248,880
Insertions	2,935
Mapped reads with at least one insertion	0.32%
Deletions	9,693
Mapped reads with at least one deletion	1.06%
Homopolymer indels	44.84%

2.6. Chromosome stats

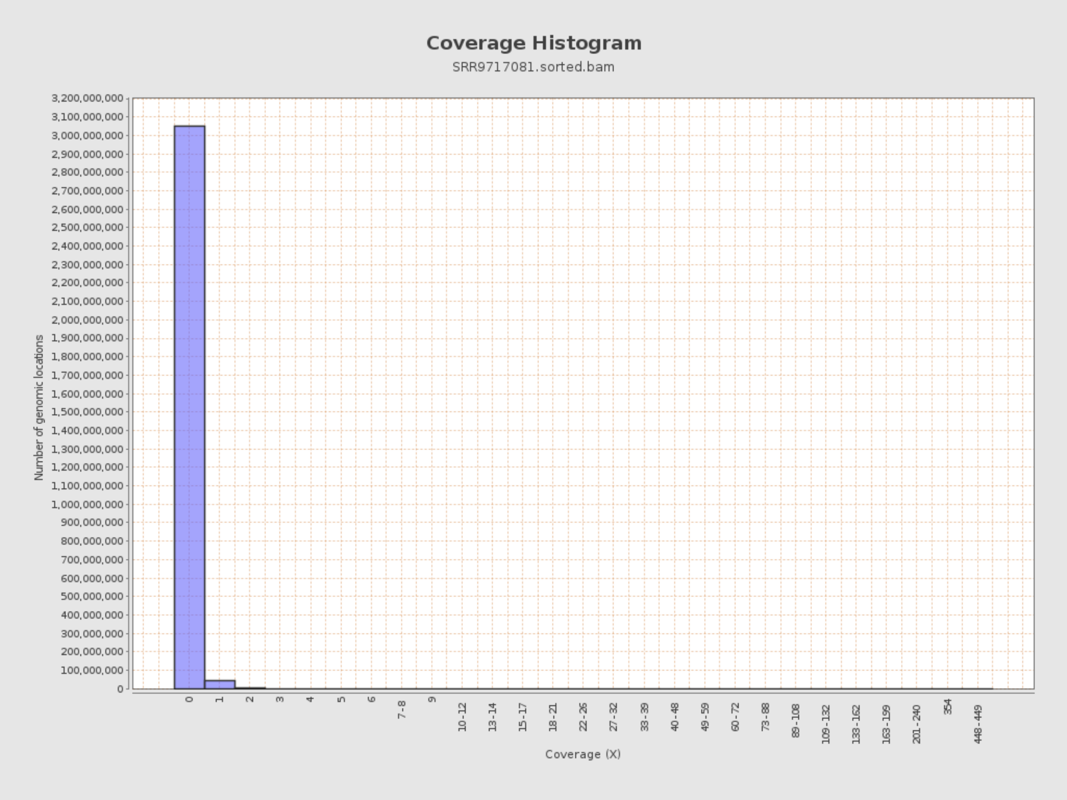
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6072032	0.0244	0.2371
chr2	243199373	5239018	0.0215	0.2463
chr3	198022430	3269119	0.0165	0.1385
chr4	191154276	2219762	0.0116	0.117
chr5	180915260	3752913	0.0207	0.1547
chr6	171115067	1939291	0.0113	0.1251
chr7	159138663	3502837	0.022	0.2491

chr8	146364022	2278853	0.0156	0.1454
chr9	141213431	1429116	0.0101	0.1313
chr10	135534747	2315426	0.0171	0.1805
chr11	135006516	2185703	0.0162	0.1619
chr12	133851895	2084681	0.0156	0.1342
chr13	115169878	1532165	0.0133	0.1238
chr14	107349540	1136695	0.0106	0.1119
chr15	102531392	2214317	0.0216	0.1592
chr16	90354753	1587789	0.0176	0.151
chr17	81195210	1909266	0.0235	0.1703
chr18	78077248	1666302	0.0213	0.2369
chr19	59128983	841616	0.0142	0.1763
chr20	63025520	1329479	0.0211	0.1561
chr21	48129895	634272	0.0132	0.1232
chr22	51304566	600252	0.0117	0.1158
chrMT	16571	250	0.0151	0.1219
chrX	155270560	1957006	0.0126	0.1309
chrY	59373566	106526	0.0018	0.0513

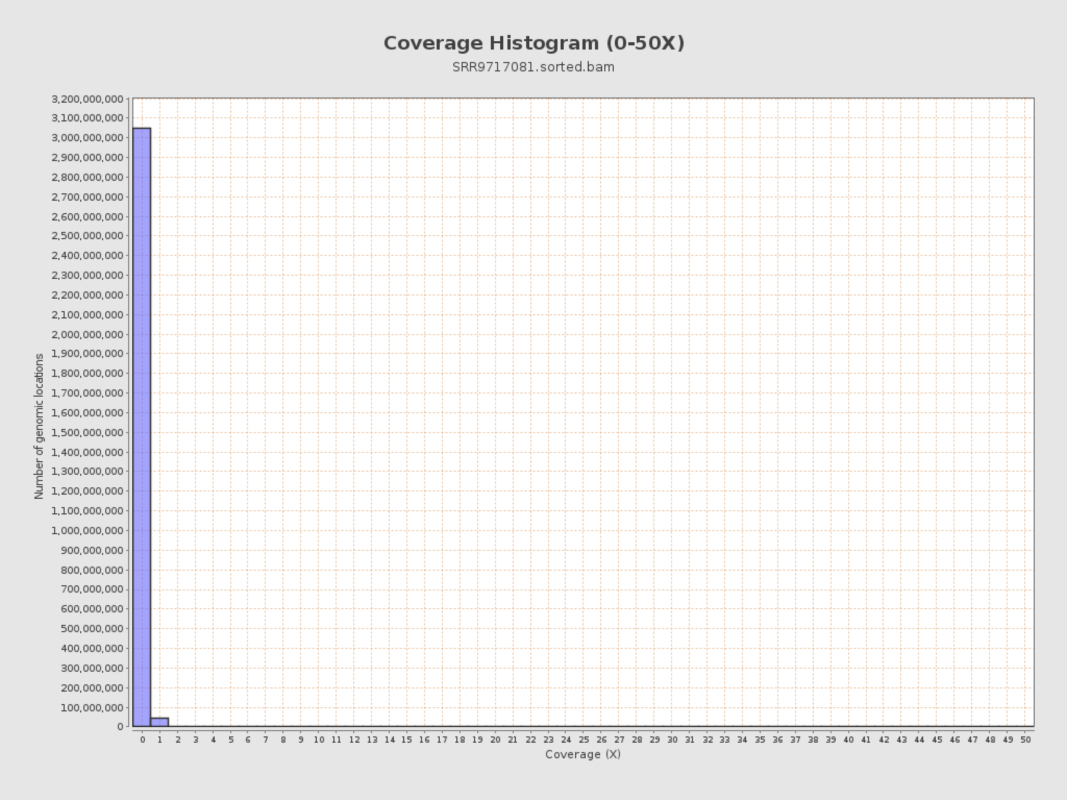
3. Results : Coverage across reference



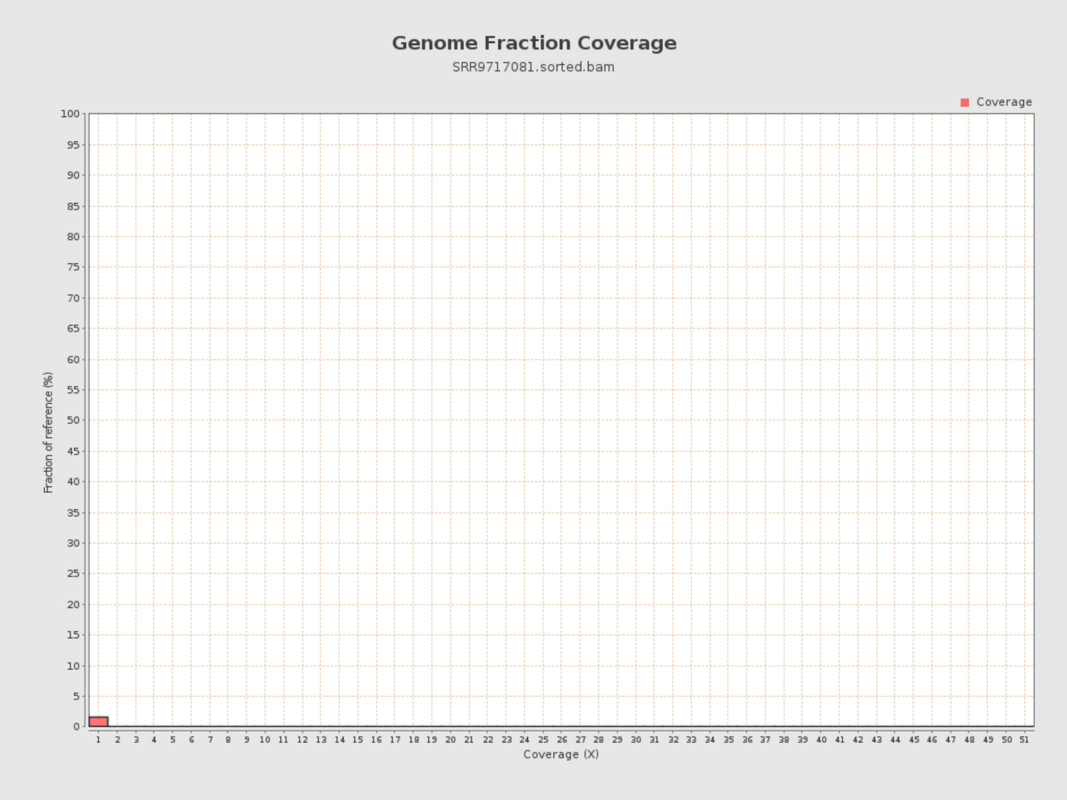
4. Results : Coverage Histogram



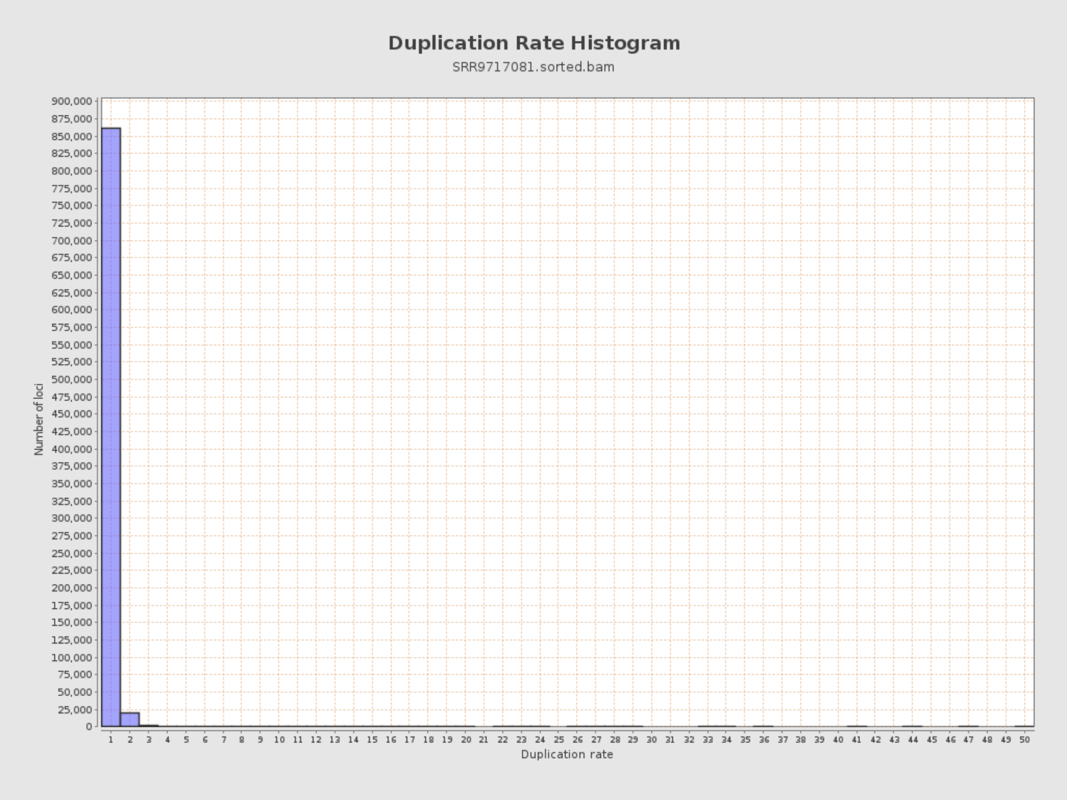
5. Results : Coverage Histogram (0-50X)



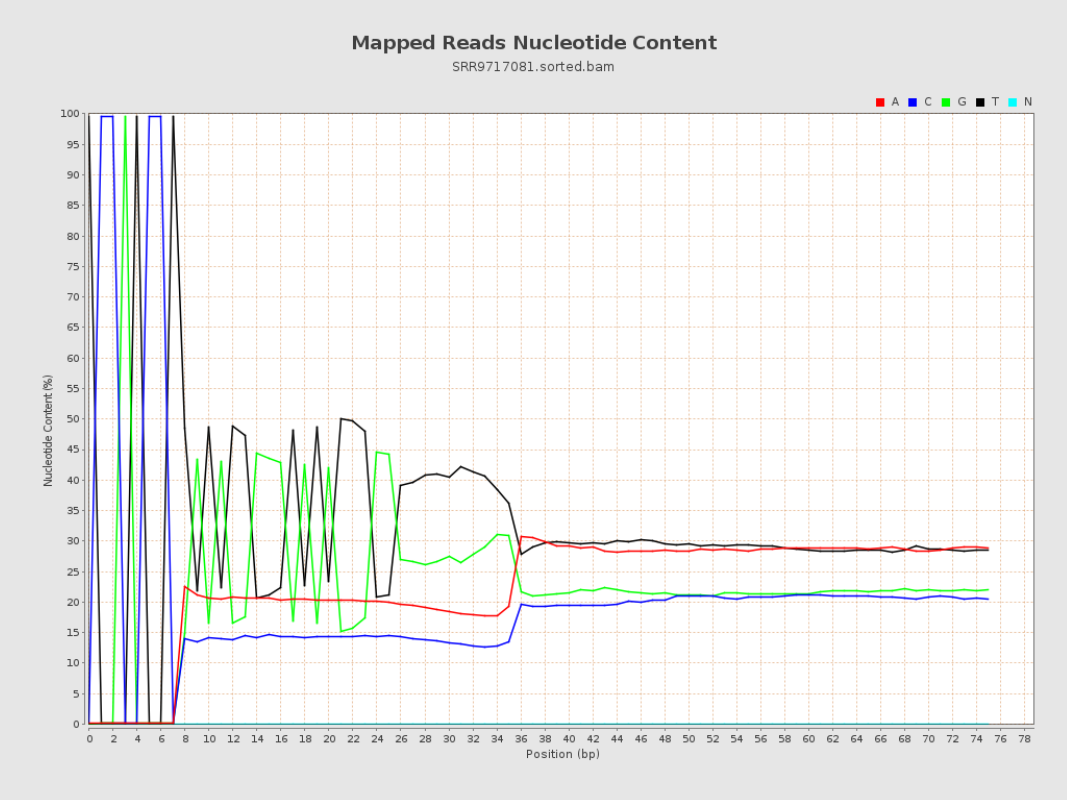
6. Results : Genome Fraction Coverage



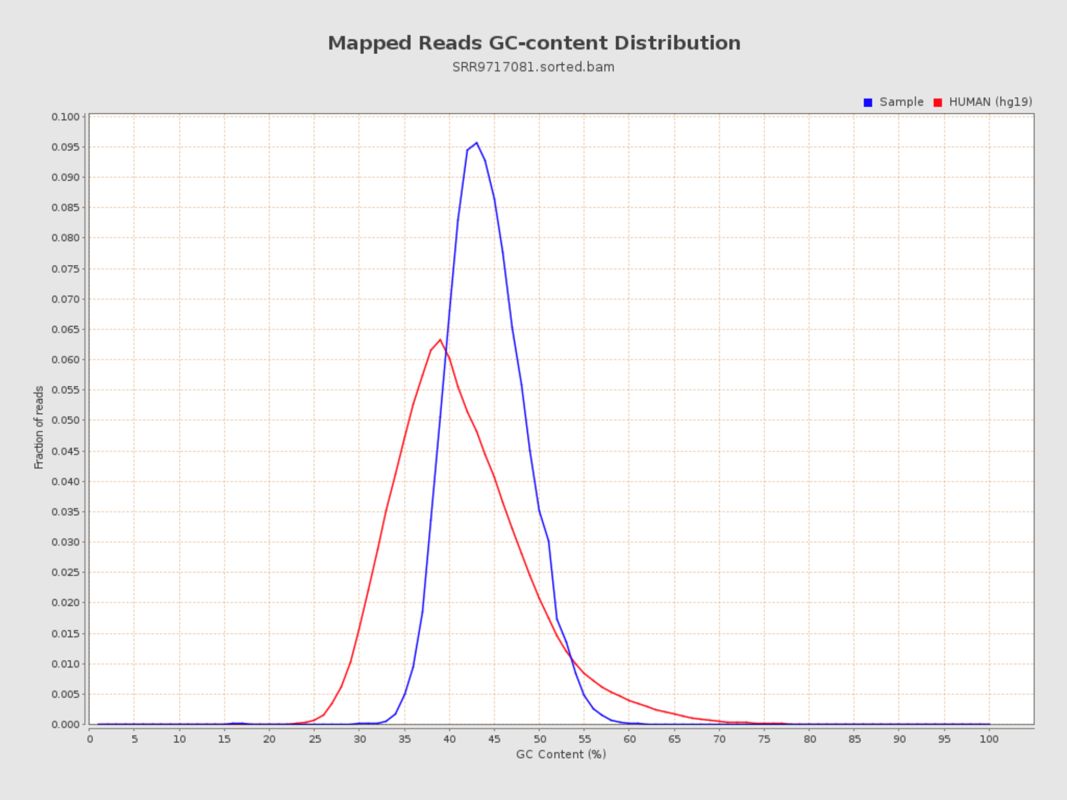
7. Results : Duplication Rate Histogram



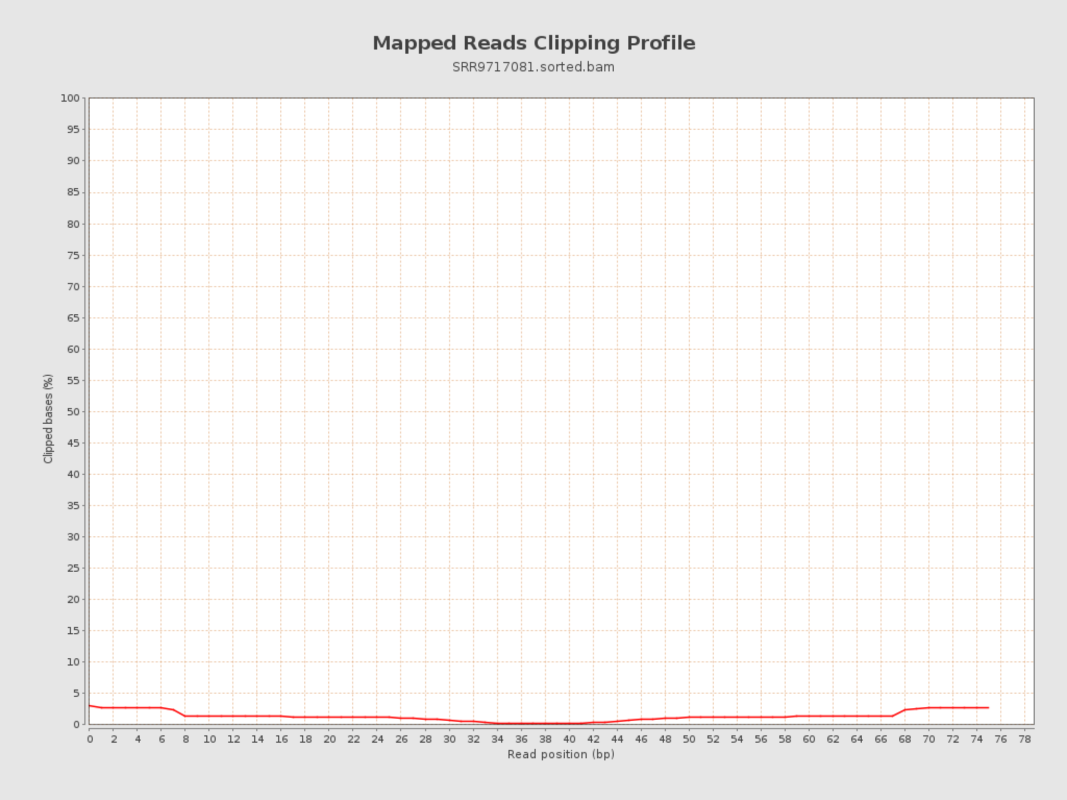
8. Results : Mapped Reads Nucleotide Content



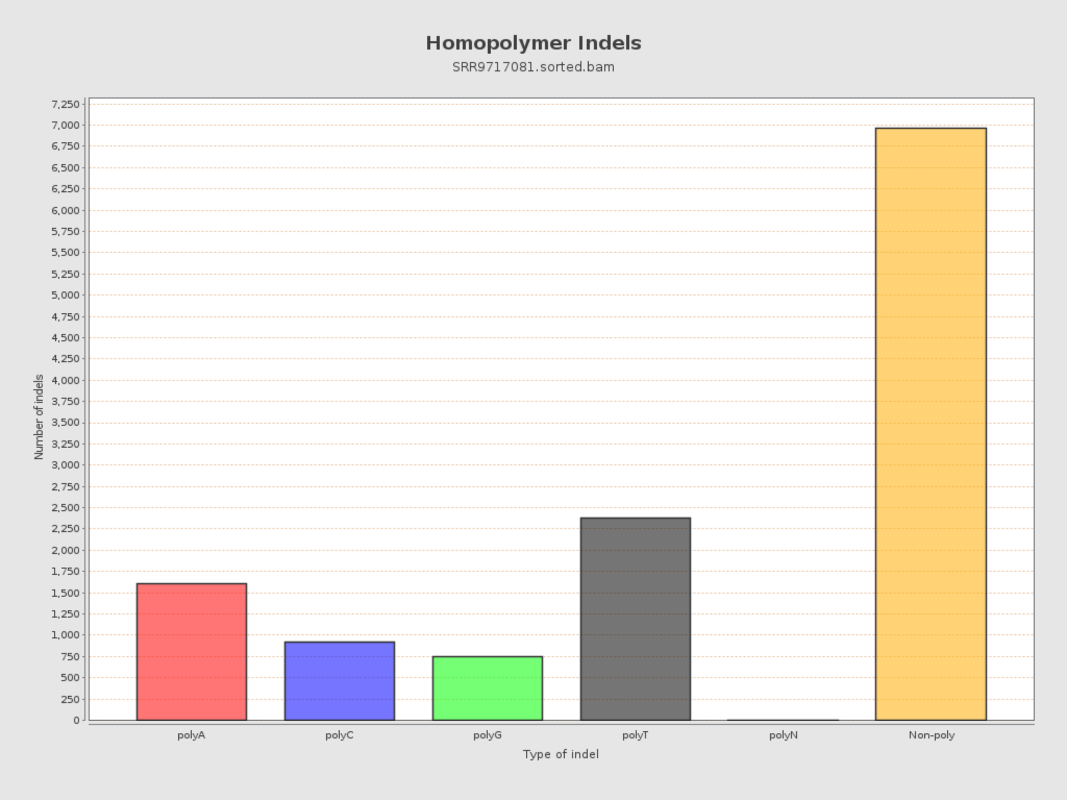
9. Results : Mapped Reads GC-content Distribution



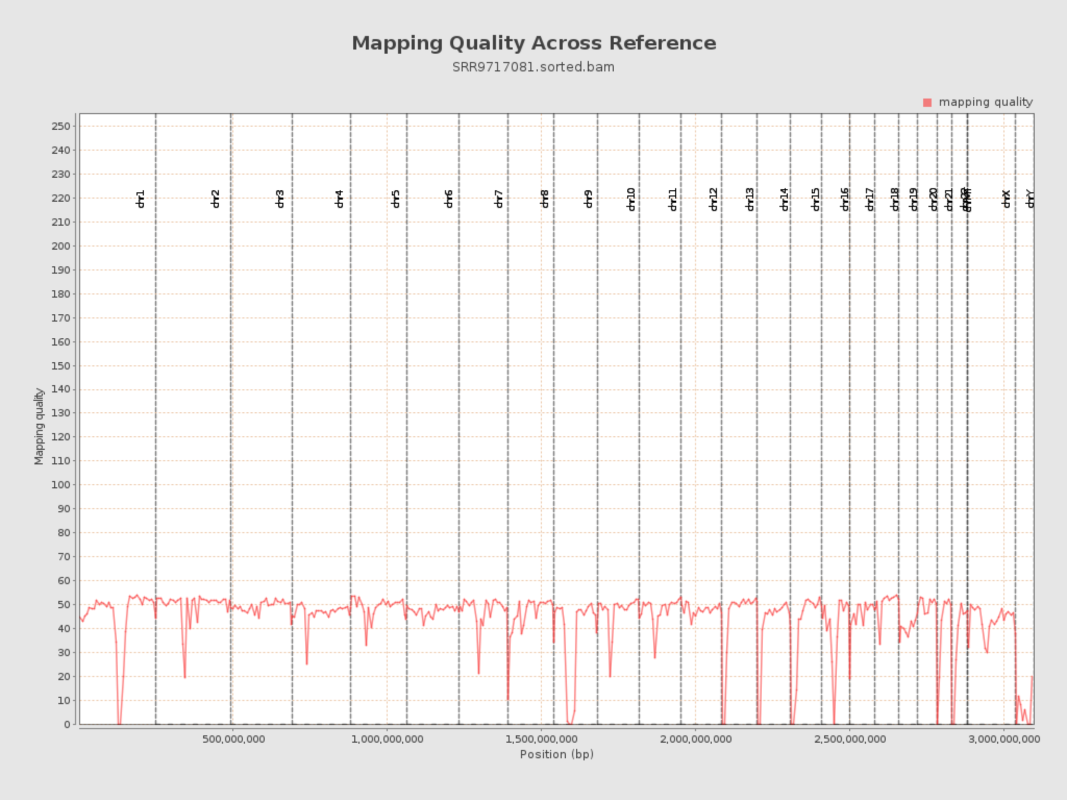
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram