Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 02:55:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717051.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_SRR9717051 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717051.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 02:54:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717051.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	973,247
Mapped reads	759,285 / 78.02%
Unmapped reads	213,962 / 21.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,830 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	12,955 / 1.33%
Duplication rate	1.23%
Clipped reads	760,695 / 78.16%

2.2. ACGT Content

Number/percentage of A's	10,340,930 / 24.21%
Number/percentage of C's	9,244,041 / 21.64%
Number/percentage of T's	12,417,828 / 29.07%
Number/percentage of G's	10,709,930 / 25.07%
Number/percentage of N's	1,146 / 0%
GC Percentage	46.72%

2.3. Coverage

Mean	0.0138

Standard Deviation	0.1421

2.4. Mapping Quality

Mean Mapping Quality	39.96

2.5. Mismatches and indels

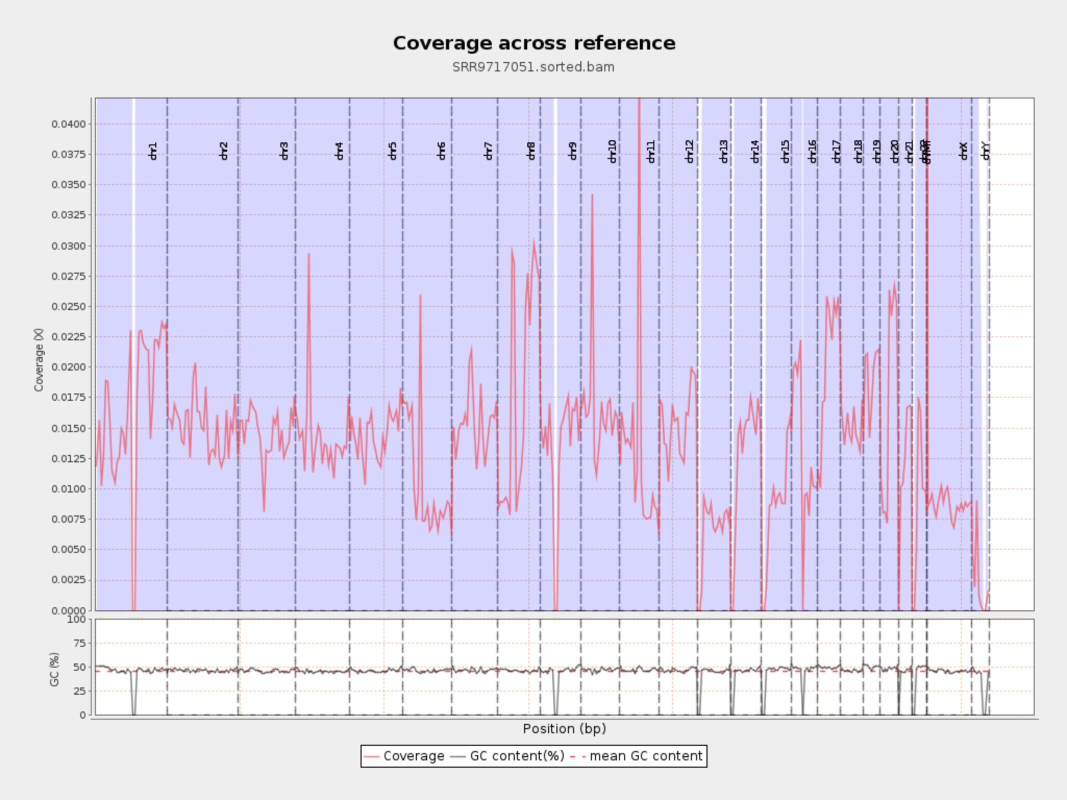
General error rate	0.53%
Mismatches	219,106
Insertions	3,634
Mapped reads with at least one insertion	0.48%
Deletions	7,028
Mapped reads with at least one deletion	0.91%
Homopolymer indels	32.42%

2.6. Chromosome stats

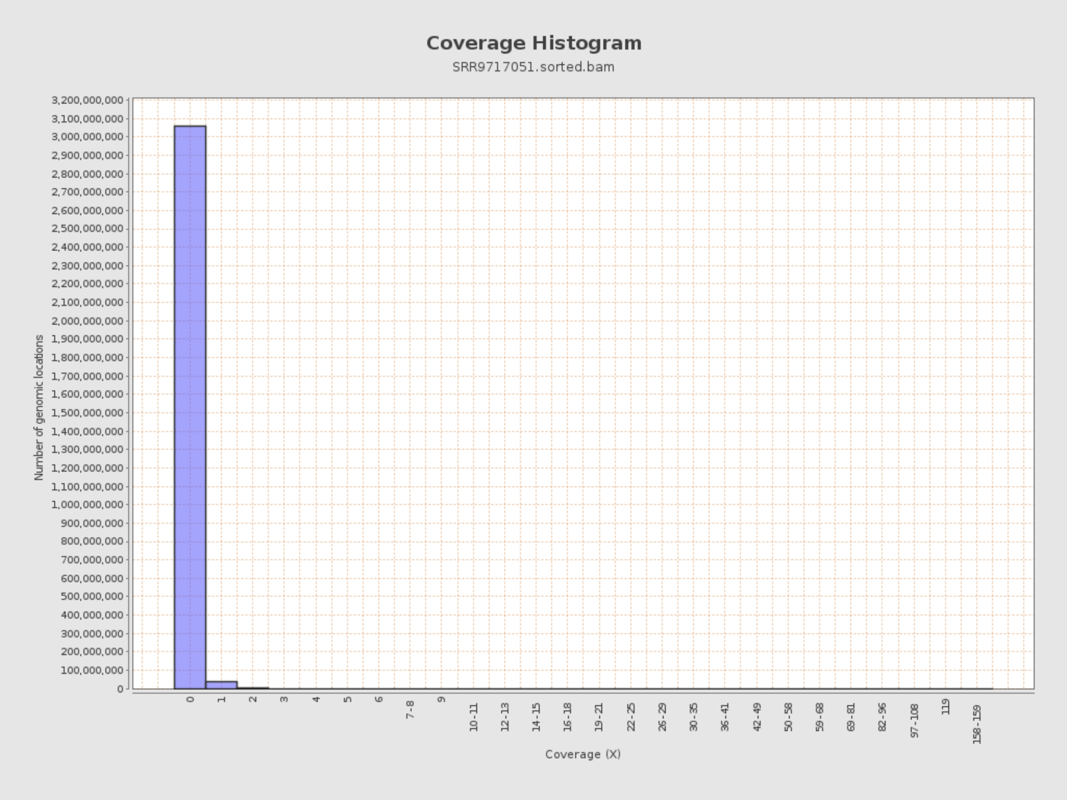
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4117569	0.0165	0.169
chr2	243199373	3684994	0.0152	0.1659
chr3	198022430	2870235	0.0145	0.1311
chr4	191154276	2750669	0.0144	0.1453
chr5	180915260	2634703	0.0146	0.1279
chr6	171115067	1825499	0.0107	0.1123
chr7	159138663	2461407	0.0155	0.1612

chr8	146364022	2642068	0.0181	0.1481
chr9	141213431	1884889	0.0133	0.1313
chr10	135534747	2250782	0.0166	0.2086
chr11	135006516	1771402	0.0131	0.1381
chr12	133851895	2076710	0.0155	0.1338
chr13	115169878	744159	0.0065	0.086
chr14	107349540	1371155	0.0128	0.1223
chr15	102531392	856263	0.0084	0.0984
chr16	90354753	1165780	0.0129	0.1276
chr17	81195210	1668499	0.0205	0.1585
chr18	78077248	1165435	0.0149	0.1566
chr19	59128983	1131170	0.0191	0.1708
chr20	63025520	1098042	0.0174	0.1467
chr21	48129895	596267	0.0124	0.1329
chr22	51304566	469638	0.0092	0.1046
chrMT	16571	1851	0.1117	0.3393
chrX	155270560	1351610	0.0087	0.1042
chrY	59373566	134922	0.0023	0.0819

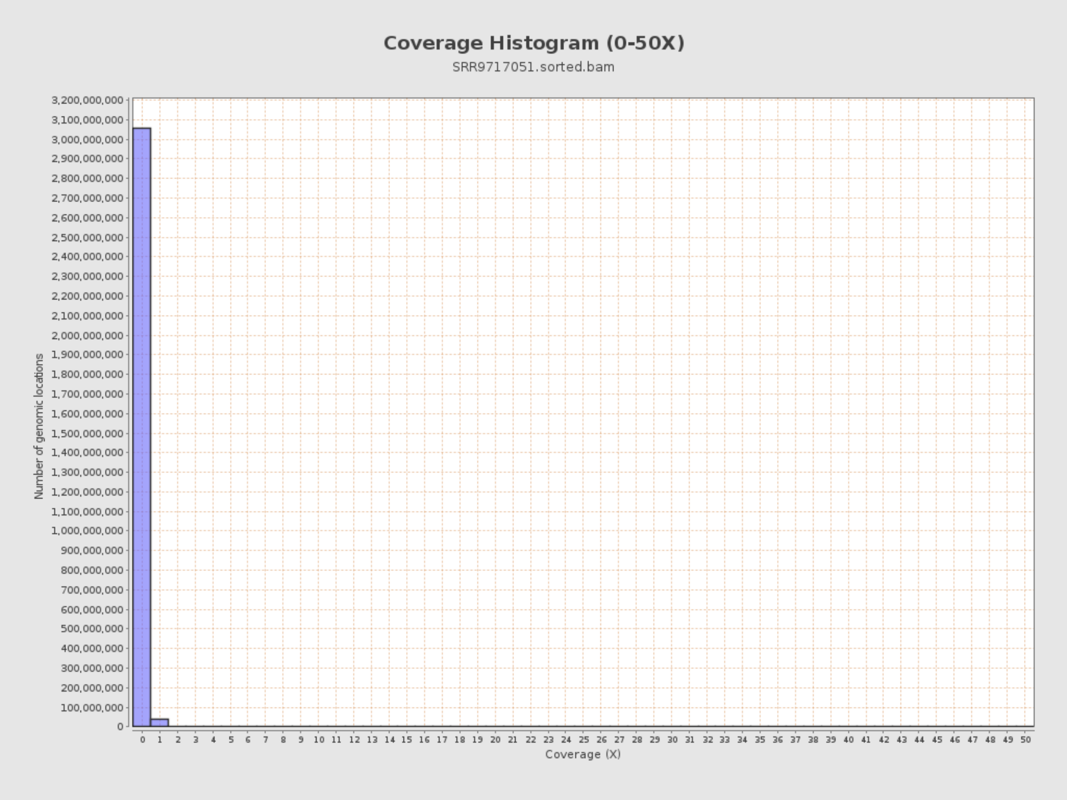
3. Results : Coverage across reference



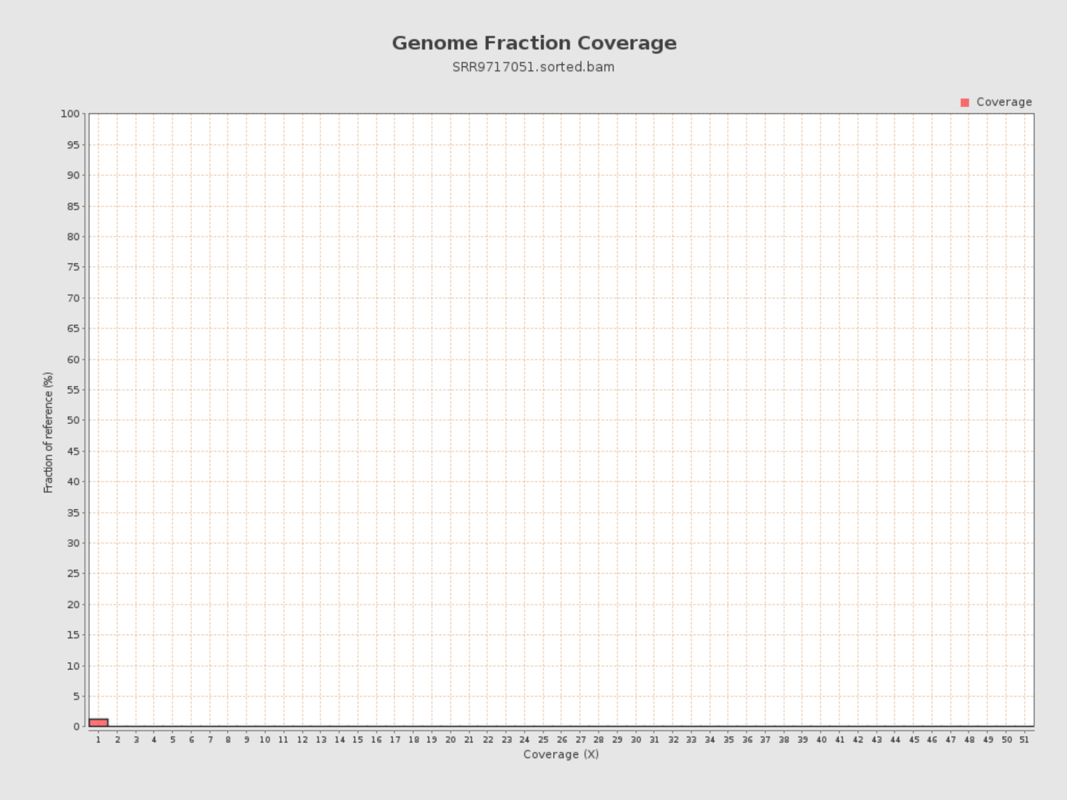
4. Results : Coverage Histogram



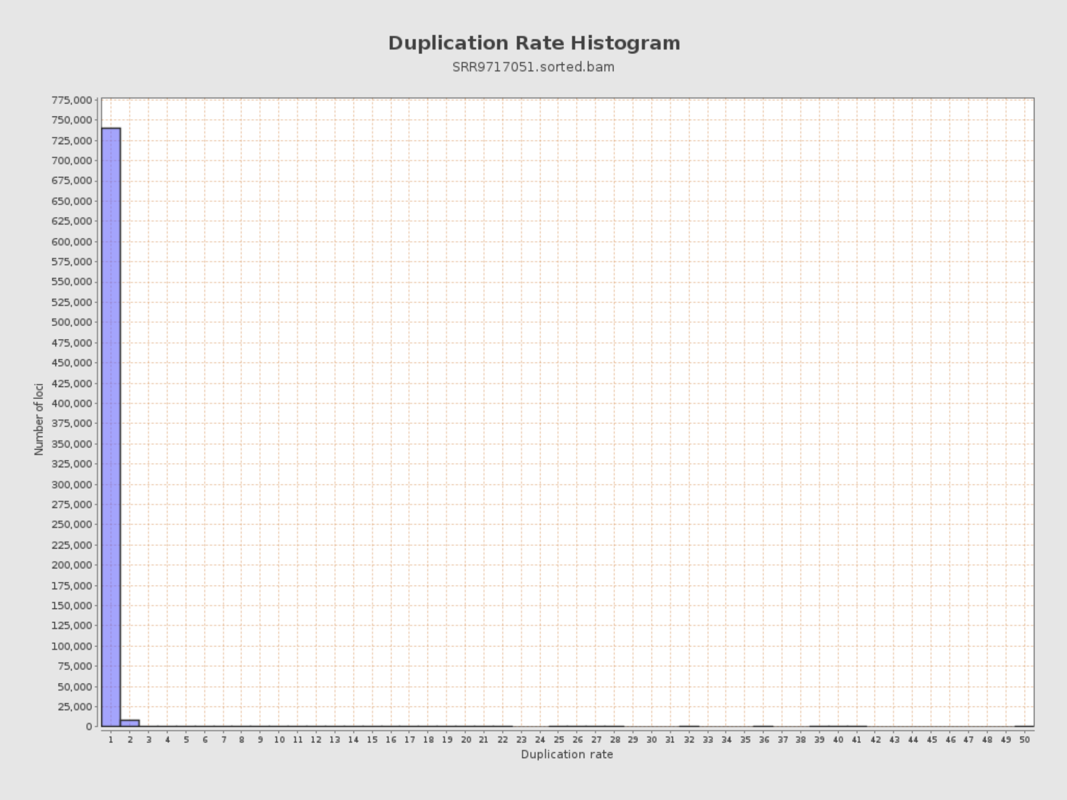
5. Results : Coverage Histogram (0-50X)



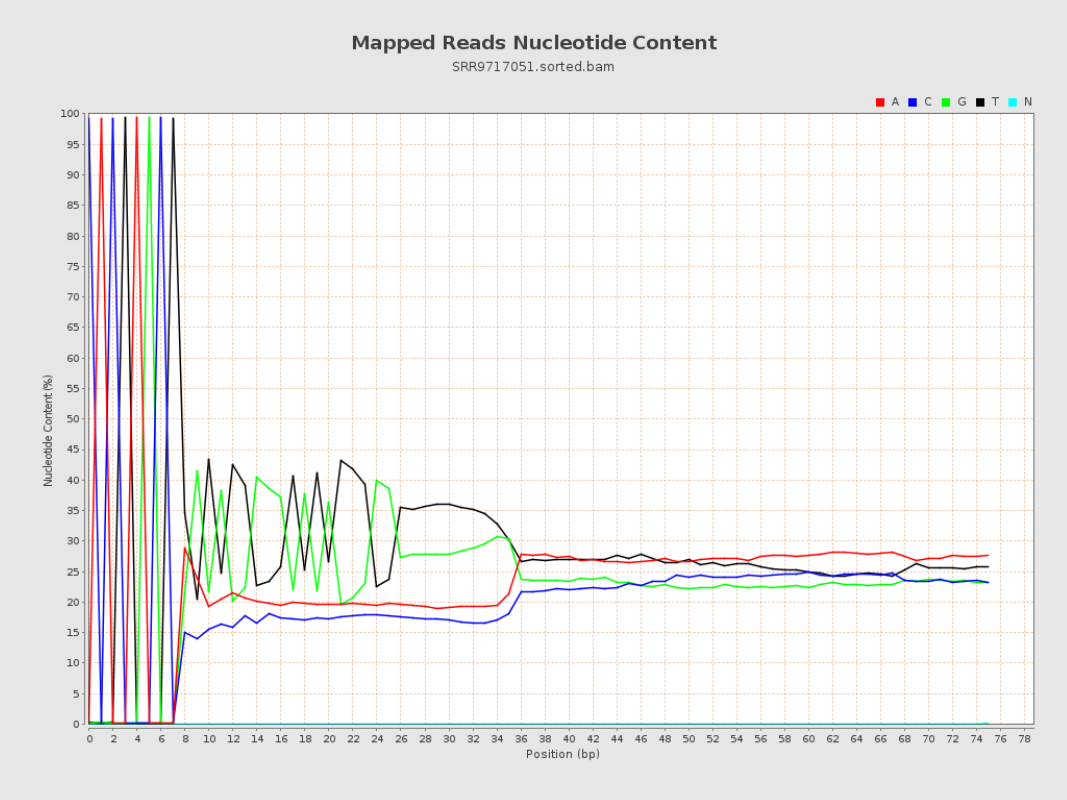
6. Results : Genome Fraction Coverage



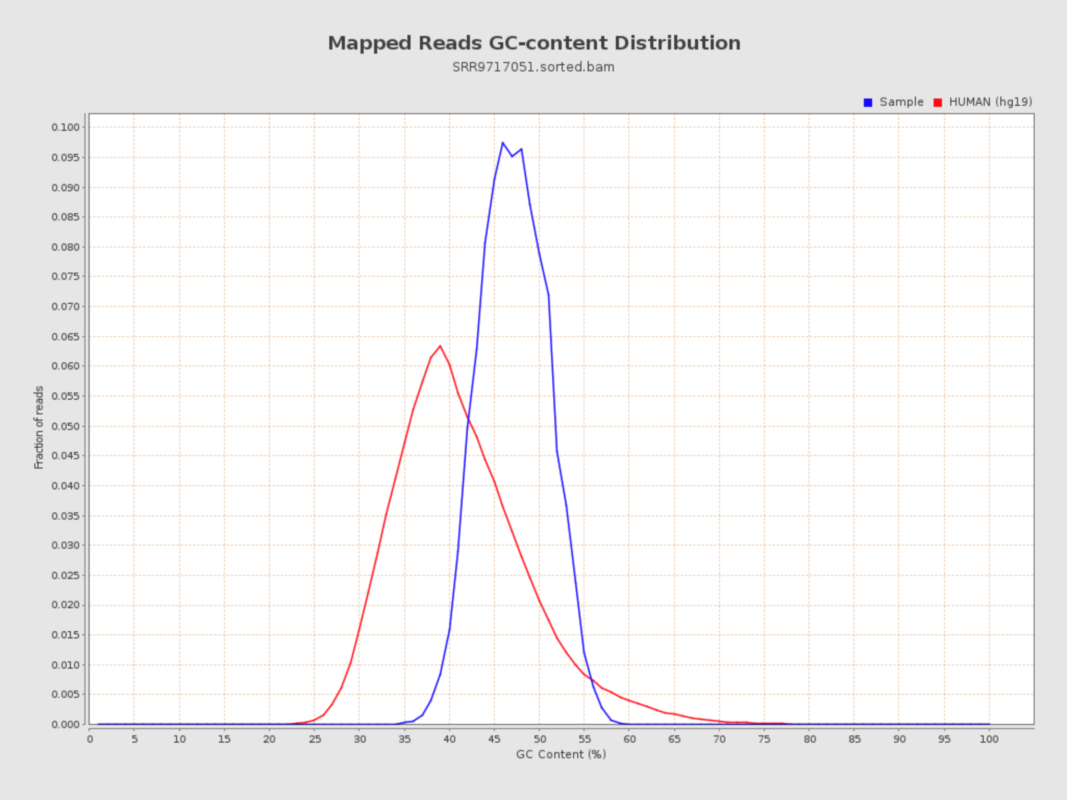
7. Results : Duplication Rate Histogram



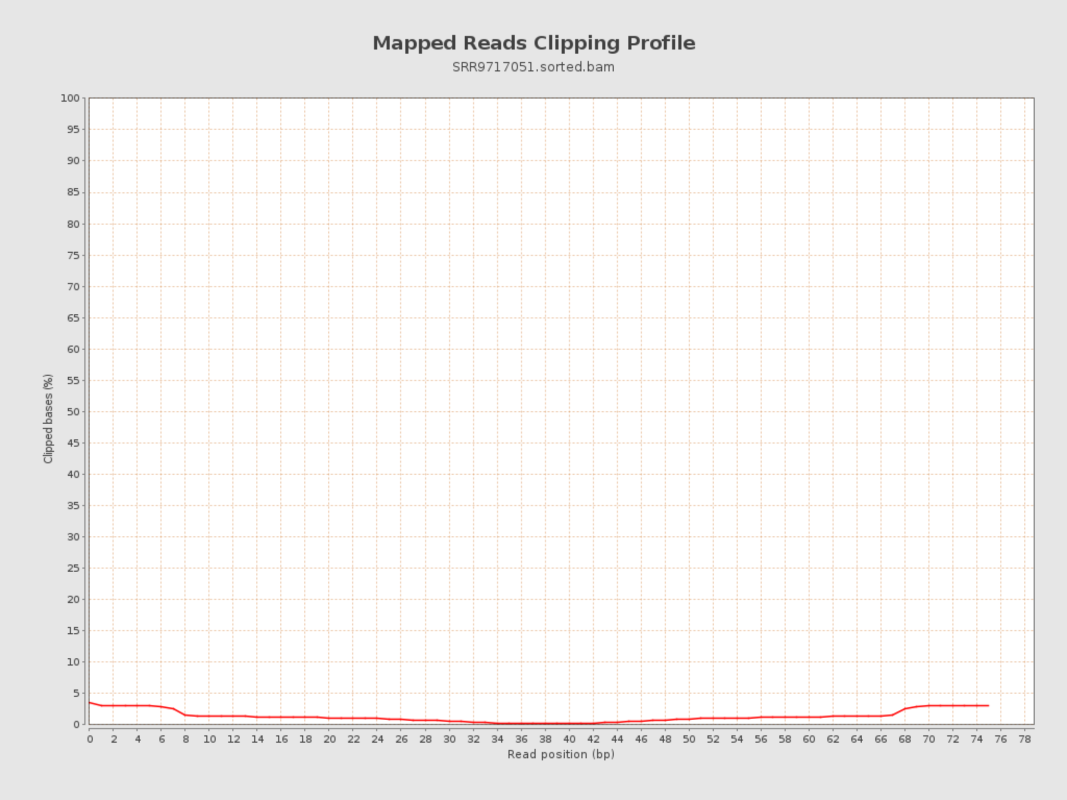
8. Results : Mapped Reads Nucleotide Content



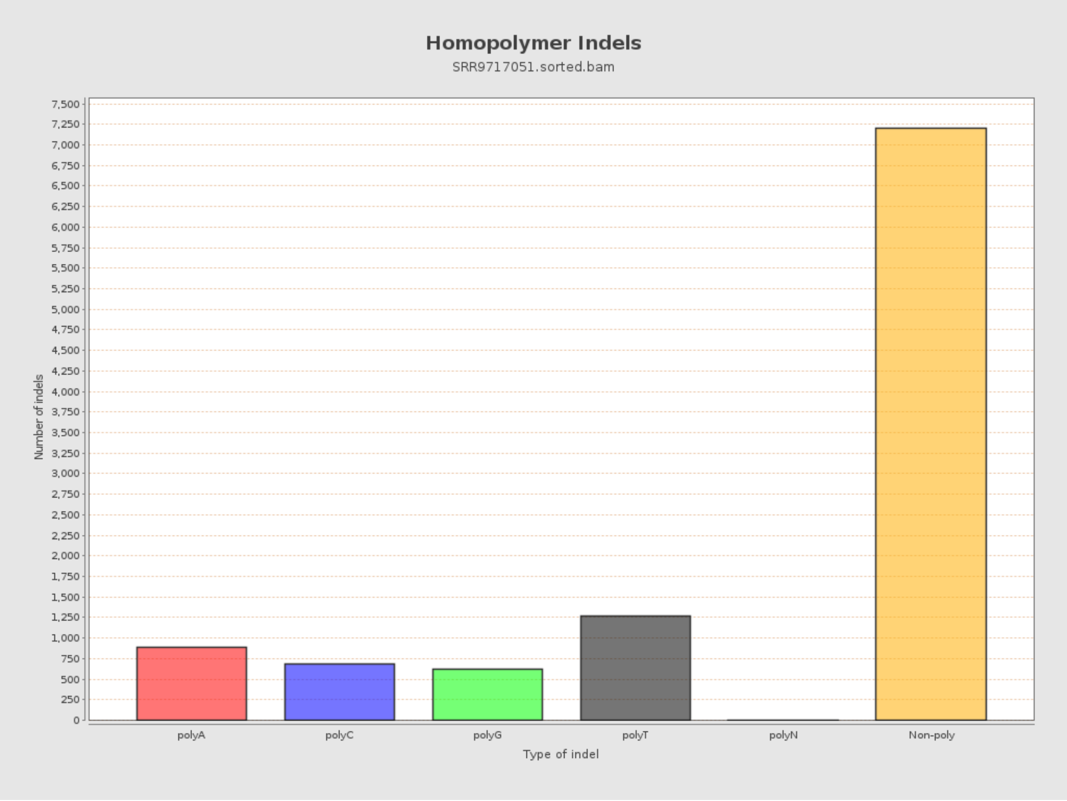
9. Results : Mapped Reads GC-content Distribution



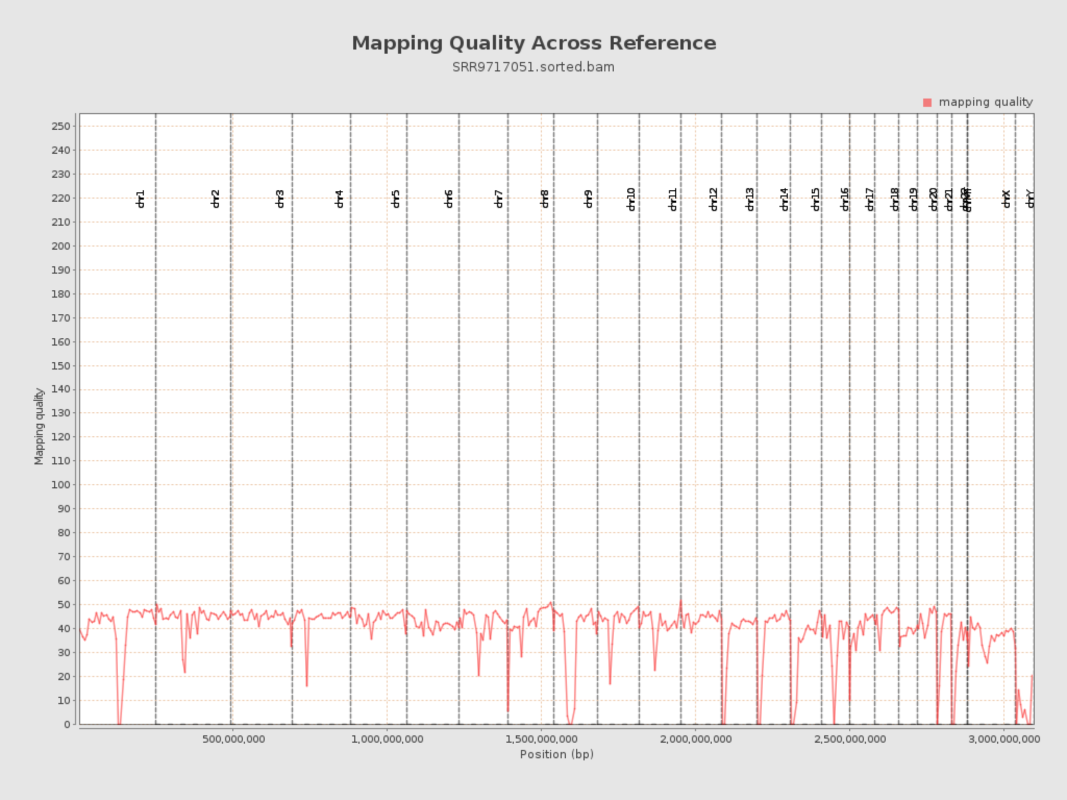
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram