Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 00:04:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717008.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_SRR9717008 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717008.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 00:04:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717008.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	486,762
Mapped reads	436,568 / 89.69%
Unmapped reads	50,194 / 10.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,965 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	5,660 / 1.16%
Duplication rate	1.01%
Clipped reads	437,345 / 89.85%

2.2. ACGT Content

Number/percentage of A's	6,103,573 / 24.56%
Number/percentage of C's	4,795,262 / 19.3%
Number/percentage of T's	7,814,773 / 31.45%
Number/percentage of G's	6,137,798 / 24.7%
Number/percentage of N's	496 / 0%
GC Percentage	43.99%

2.3. Coverage

Mean	0.008

Standard Deviation	0.1008

2.4. Mapping Quality

Mean Mapping Quality	44.35

2.5. Mismatches and indels

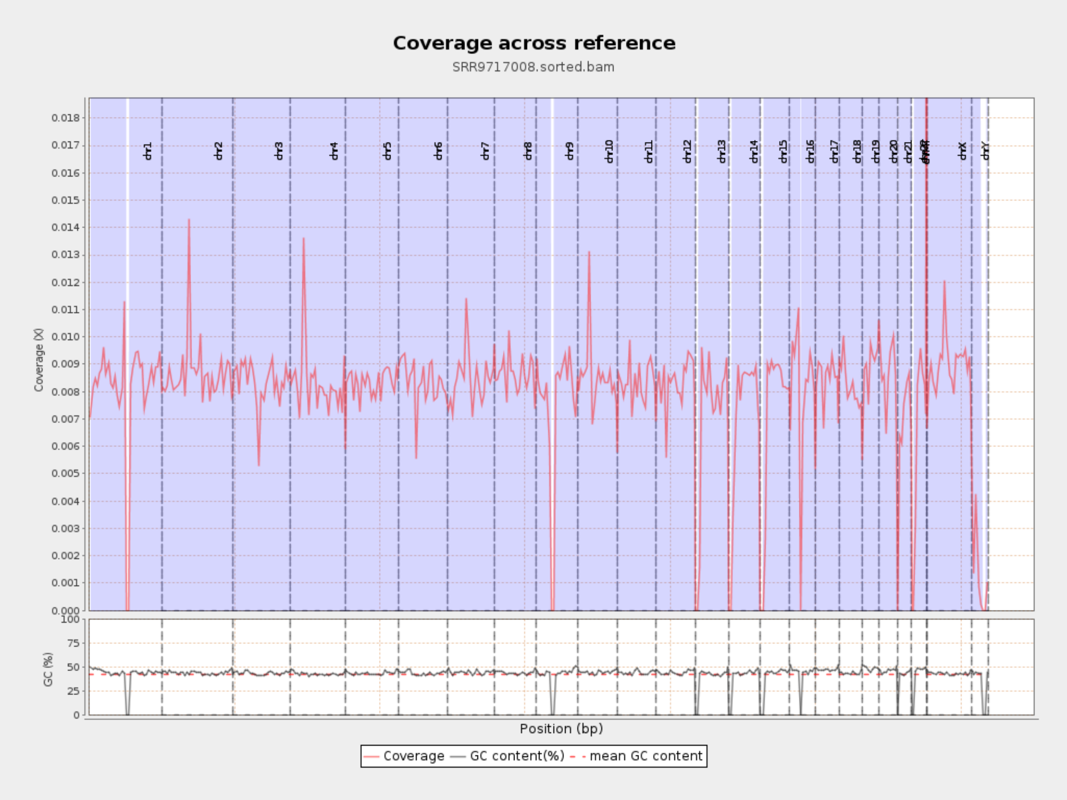
General error rate	0.51%
Mismatches	124,422
Insertions	1,582
Mapped reads with at least one insertion	0.36%
Deletions	4,086
Mapped reads with at least one deletion	0.93%
Homopolymer indels	40.93%

2.6. Chromosome stats

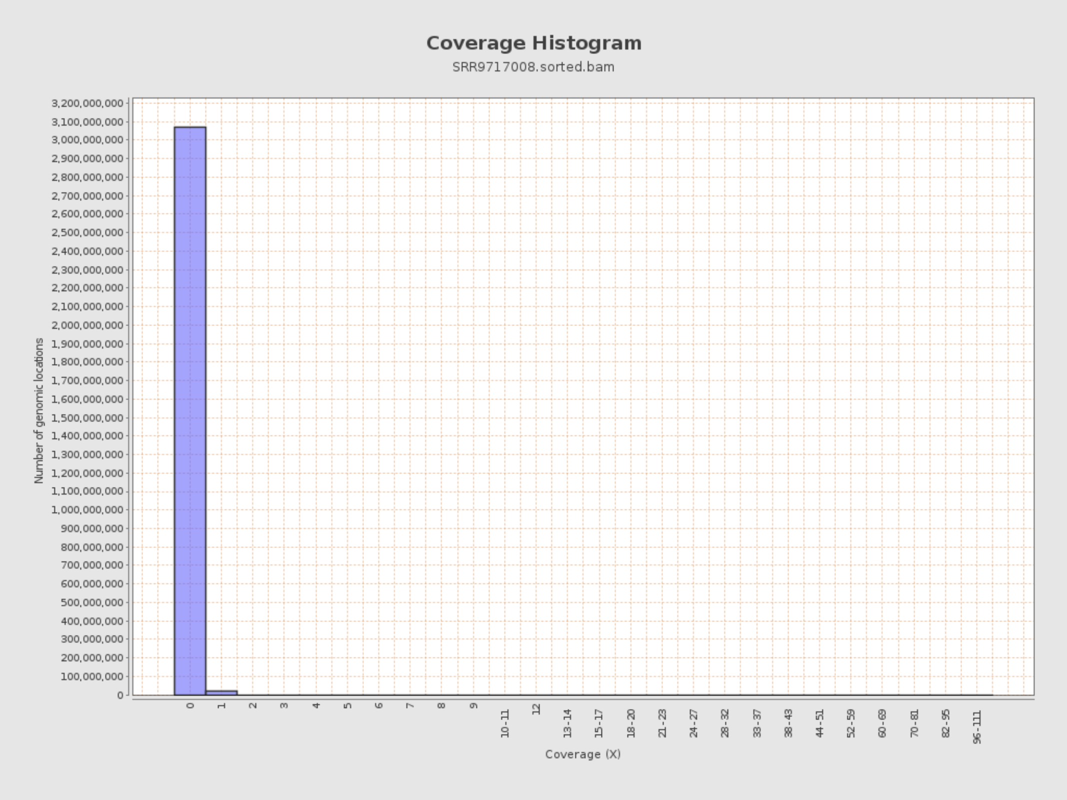
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2013780	0.0081	0.1236
chr2	243199373	2118268	0.0087	0.1096
chr3	198022430	1652294	0.0083	0.0937
chr4	191154276	1589580	0.0083	0.0966
chr5	180915260	1506855	0.0083	0.0939
chr6	171115067	1433373	0.0084	0.0954
chr7	159138663	1348384	0.0085	0.1064

chr8	146364022	1264842	0.0086	0.1002
chr9	141213431	1036971	0.0073	0.0988
chr10	135534747	1162496	0.0086	0.1041
chr11	135006516	1120096	0.0083	0.1029
chr12	133851895	1118176	0.0084	0.0939
chr13	115169878	796809	0.0069	0.0854
chr14	107349540	745629	0.0069	0.0872
chr15	102531392	716680	0.007	0.0859
chr16	90354753	734482	0.0081	0.0948
chr17	81195210	686189	0.0085	0.0961
chr18	78077248	647393	0.0083	0.1455
chr19	59128983	527734	0.0089	0.1121
chr20	63025520	539411	0.0086	0.0963
chr21	48129895	319656	0.0066	0.0864
chr22	51304566	307284	0.006	0.0794
chrMT	16571	1059	0.0639	0.2514
chrX	155270560	1395892	0.009	0.1007
chrY	59373566	75519	0.0013	0.0449

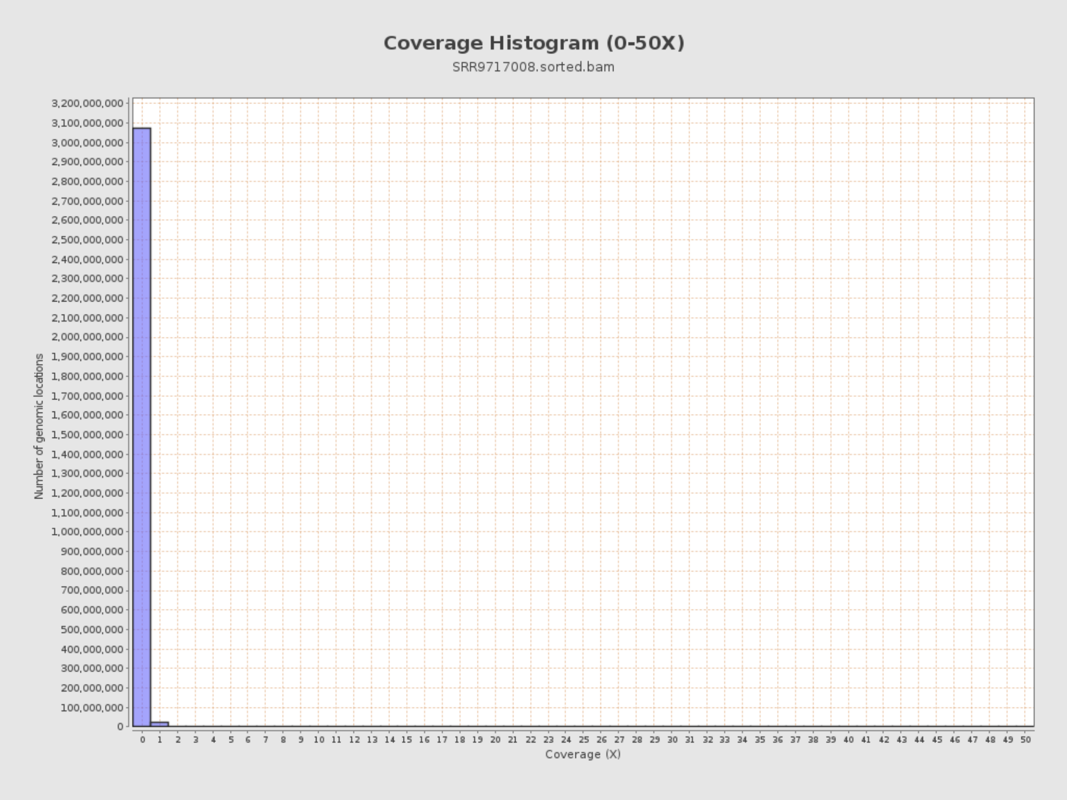
3. Results : Coverage across reference



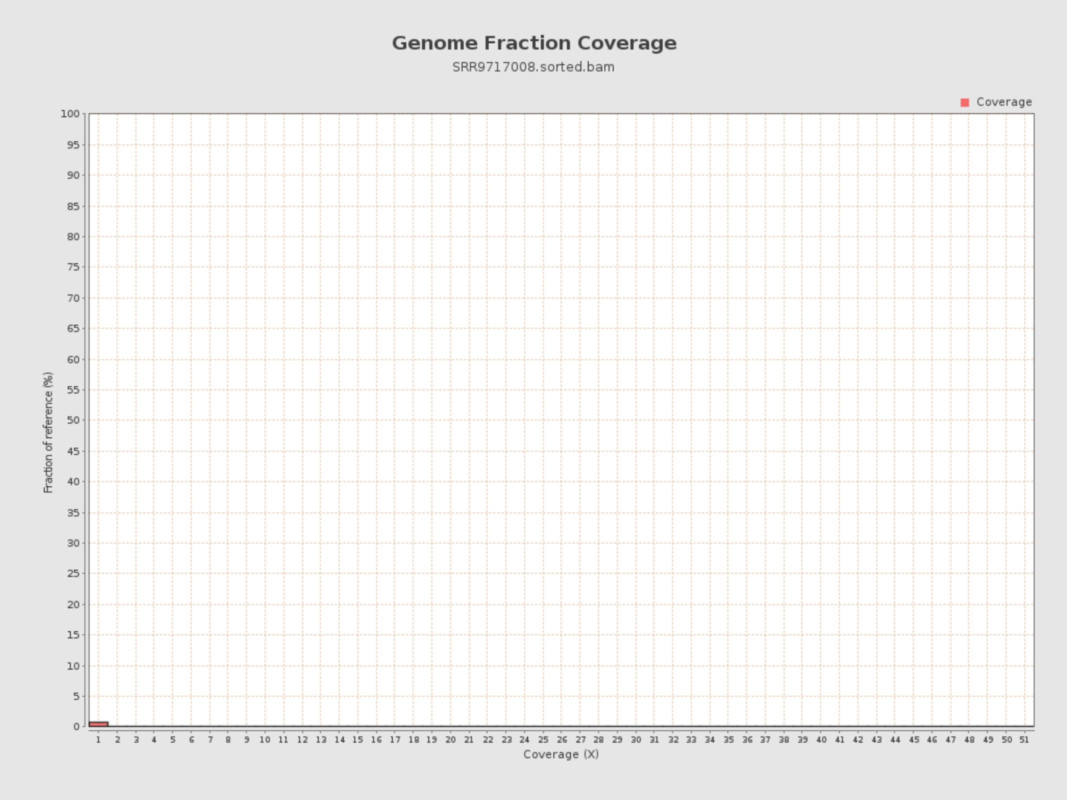
4. Results : Coverage Histogram



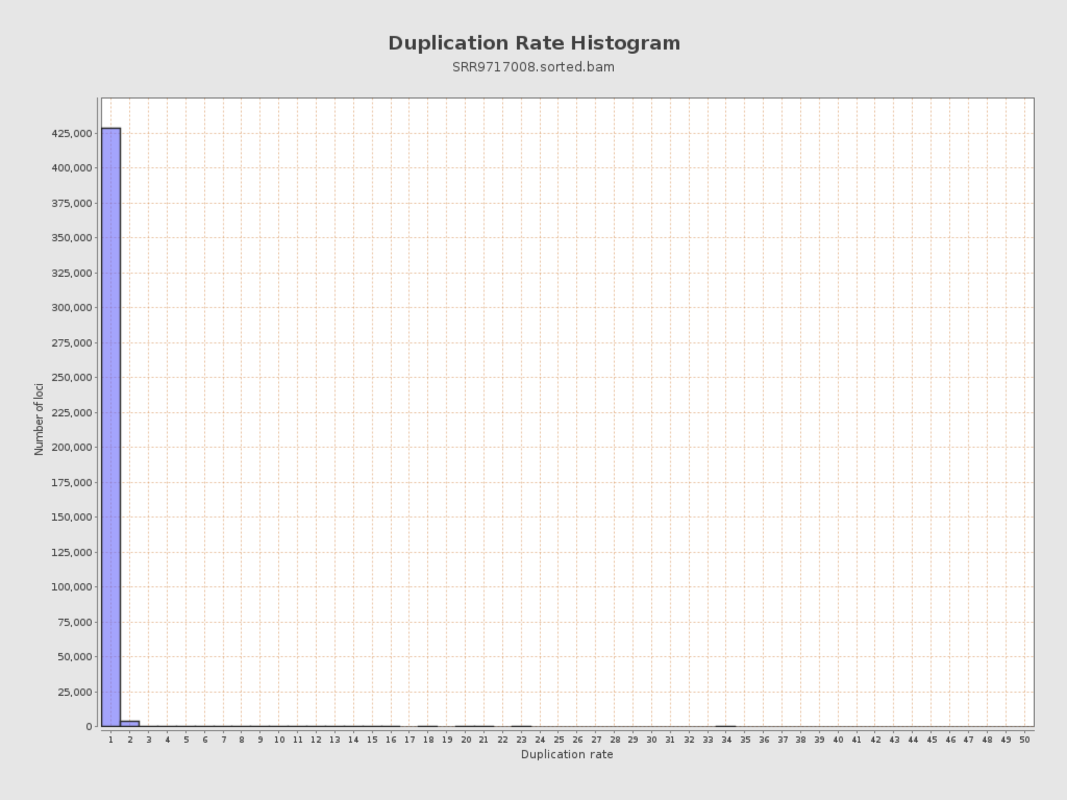
5. Results : Coverage Histogram (0-50X)



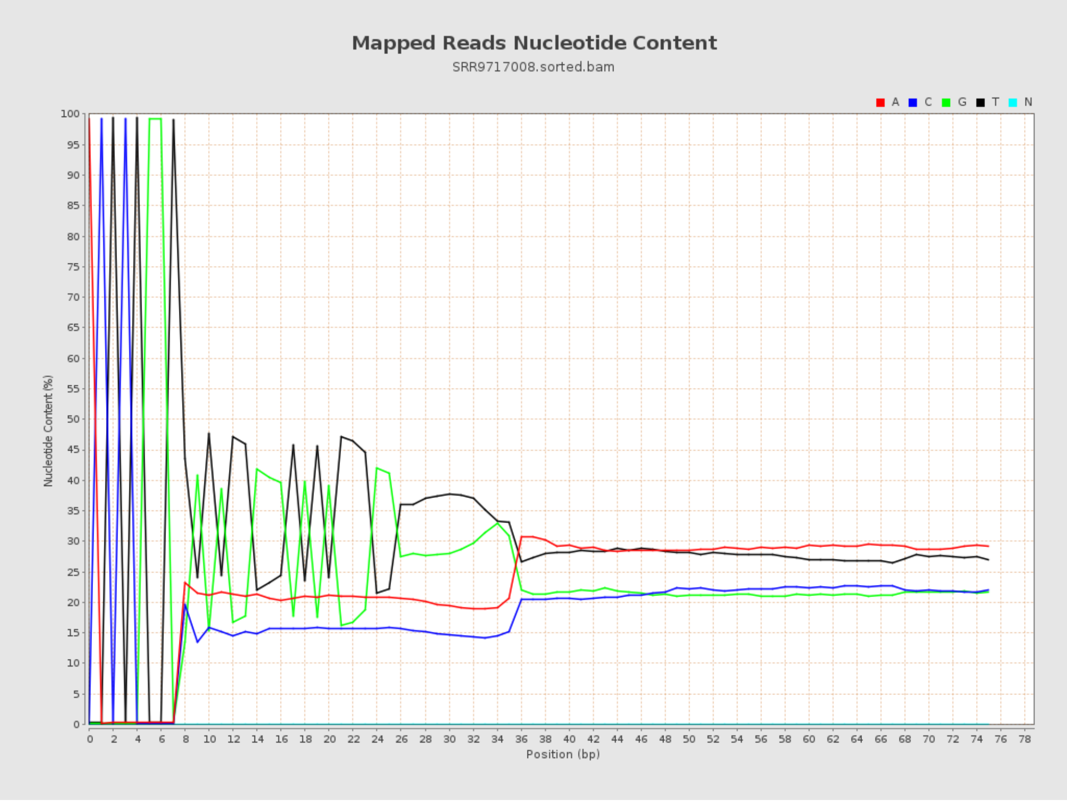
6. Results : Genome Fraction Coverage



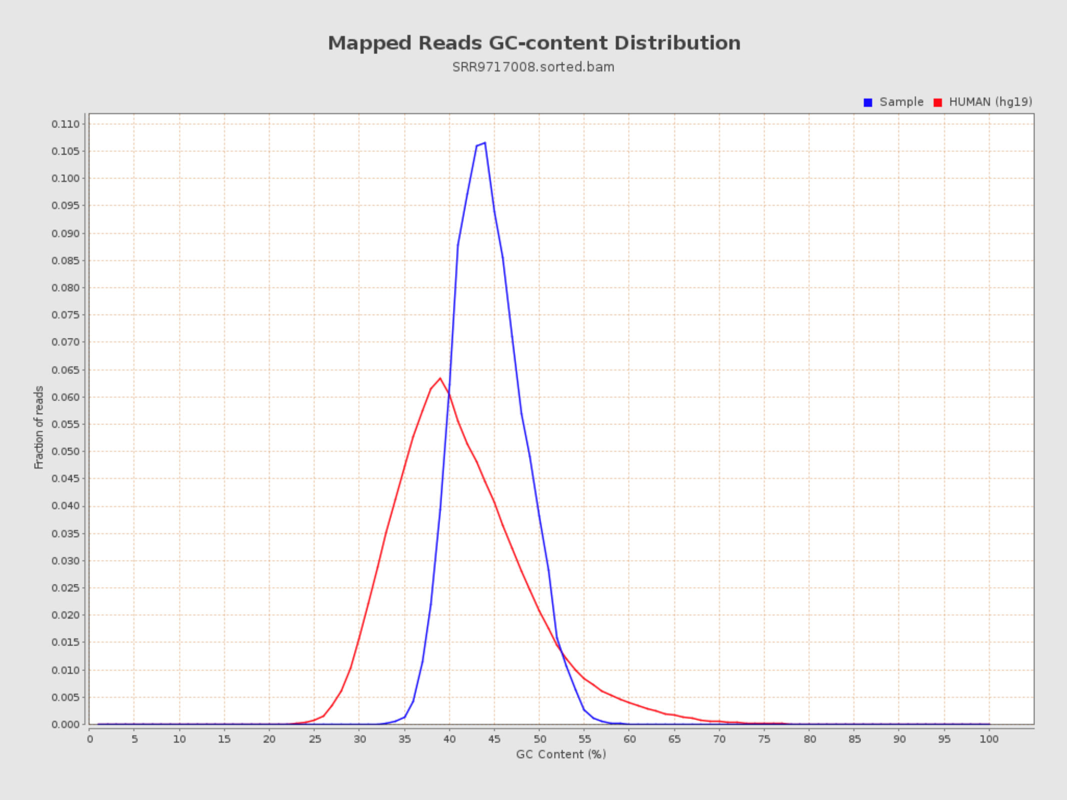
7. Results : Duplication Rate Histogram



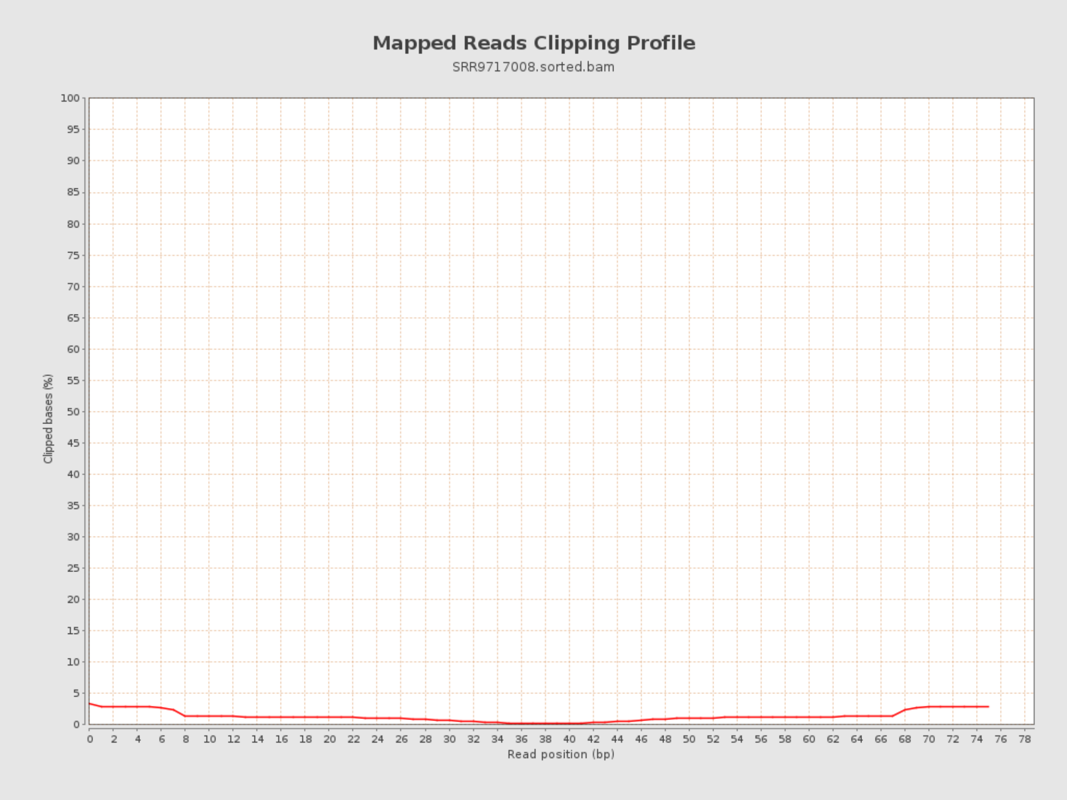
8. Results : Mapped Reads Nucleotide Content



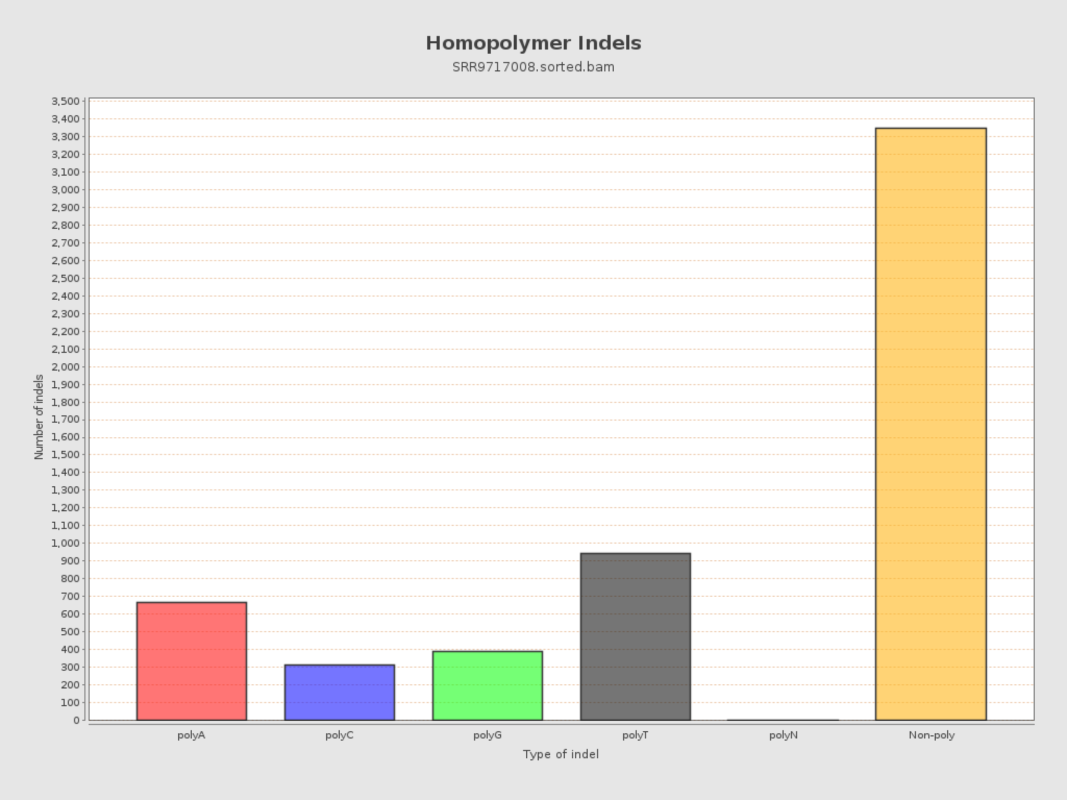
9. Results : Mapped Reads GC-content Distribution



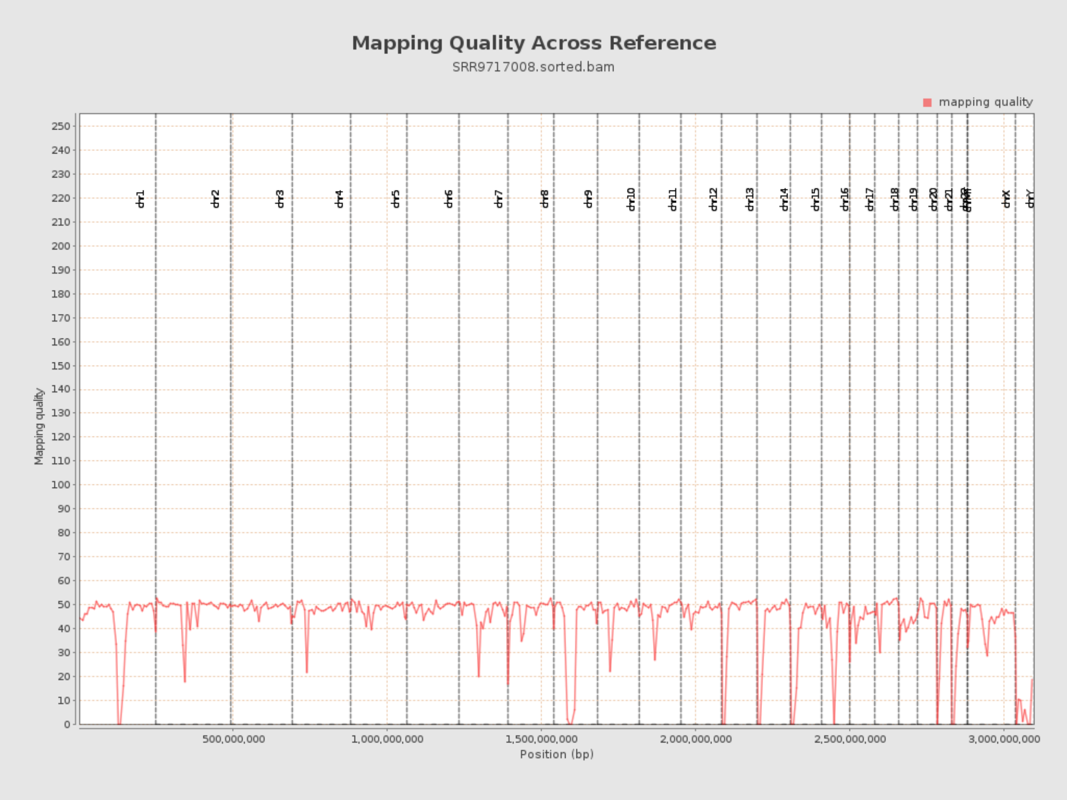
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram