Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 04:41:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717072.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_SRR9717072 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717072.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 04:41:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717072.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	837,968
Mapped reads	510,210 / 60.89%
Unmapped reads	327,758 / 39.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,001 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	14,669 / 1.75%
Duplication rate	2.39%
Clipped reads	511,868 / 61.08%

2.2. ACGT Content

Number/percentage of A's	7,957,310 / 26.64%
Number/percentage of C's	5,605,065 / 18.76%
Number/percentage of T's	9,077,173 / 30.39%
Number/percentage of G's	7,230,058 / 24.21%
Number/percentage of N's	255 / 0%
GC Percentage	42.97%

2.3. Coverage

Mean	0.0097

Standard Deviation	0.1191

2.4. Mapping Quality

Mean Mapping Quality	45.18

2.5. Mismatches and indels

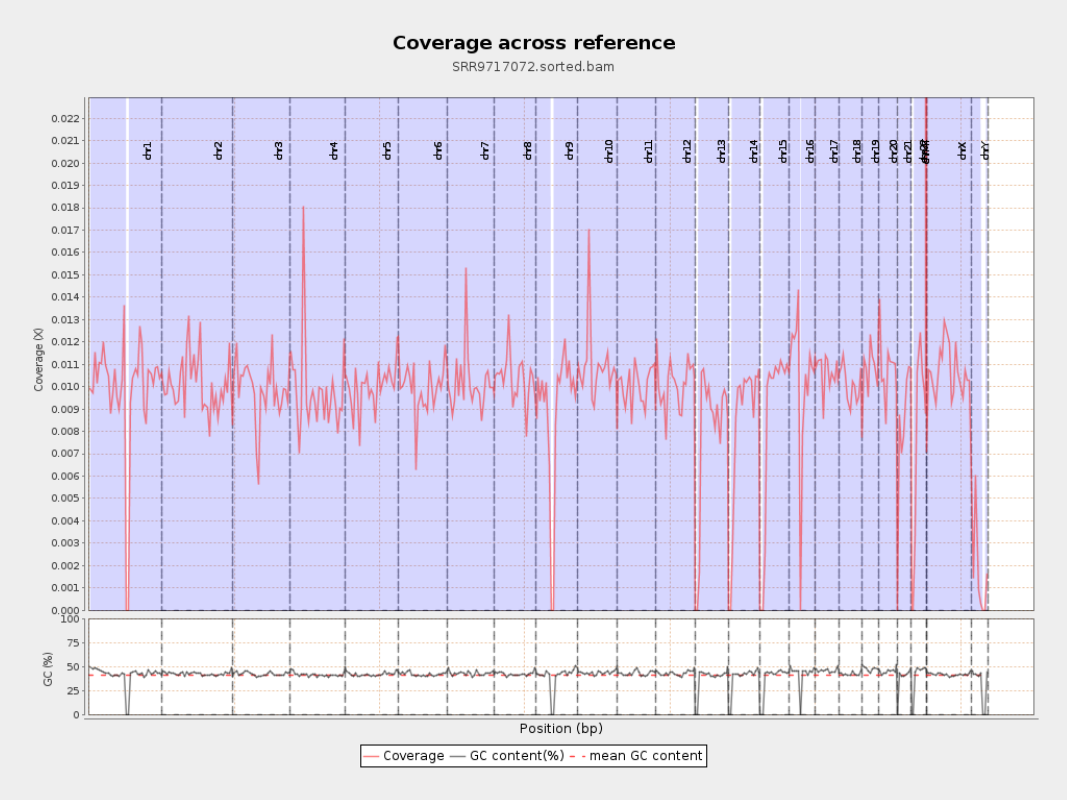
General error rate	0.51%
Mismatches	148,444
Insertions	2,171
Mapped reads with at least one insertion	0.42%
Deletions	5,073
Mapped reads with at least one deletion	0.99%
Homopolymer indels	40.32%

2.6. Chromosome stats

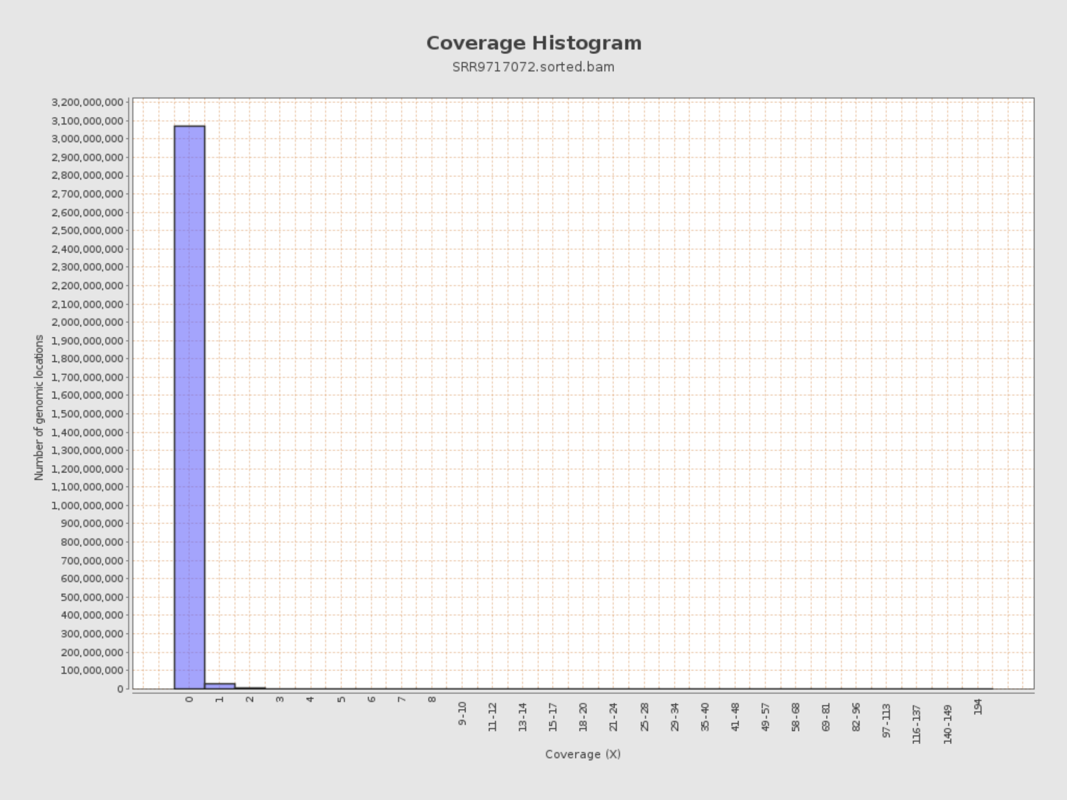
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2455541	0.0099	0.1494
chr2	243199373	2461681	0.0101	0.139
chr3	198022430	1942033	0.0098	0.1052
chr4	191154276	1861431	0.0097	0.1136
chr5	180915260	1798203	0.0099	0.1059
chr6	171115067	1708402	0.01	0.109
chr7	159138663	1615704	0.0102	0.1397

chr8	146364022	1517369	0.0104	0.135
chr9	141213431	1251607	0.0089	0.1061
chr10	135534747	1477583	0.0109	0.1306
chr11	135006516	1353025	0.01	0.1164
chr12	133851895	1354578	0.0101	0.1076
chr13	115169878	901240	0.0078	0.094
chr14	107349540	875470	0.0082	0.0969
chr15	102531392	875771	0.0085	0.0984
chr16	90354753	928094	0.0103	0.1095
chr17	81195210	863477	0.0106	0.1129
chr18	78077248	789708	0.0101	0.1535
chr19	59128983	640387	0.0108	0.1315
chr20	63025520	680398	0.0108	0.1121
chr21	48129895	399703	0.0083	0.102
chr22	51304566	379221	0.0074	0.0917
chrMT	16571	5135	0.3099	0.5988
chrX	155270560	1642636	0.0106	0.1115
chrY	59373566	99680	0.0017	0.0599

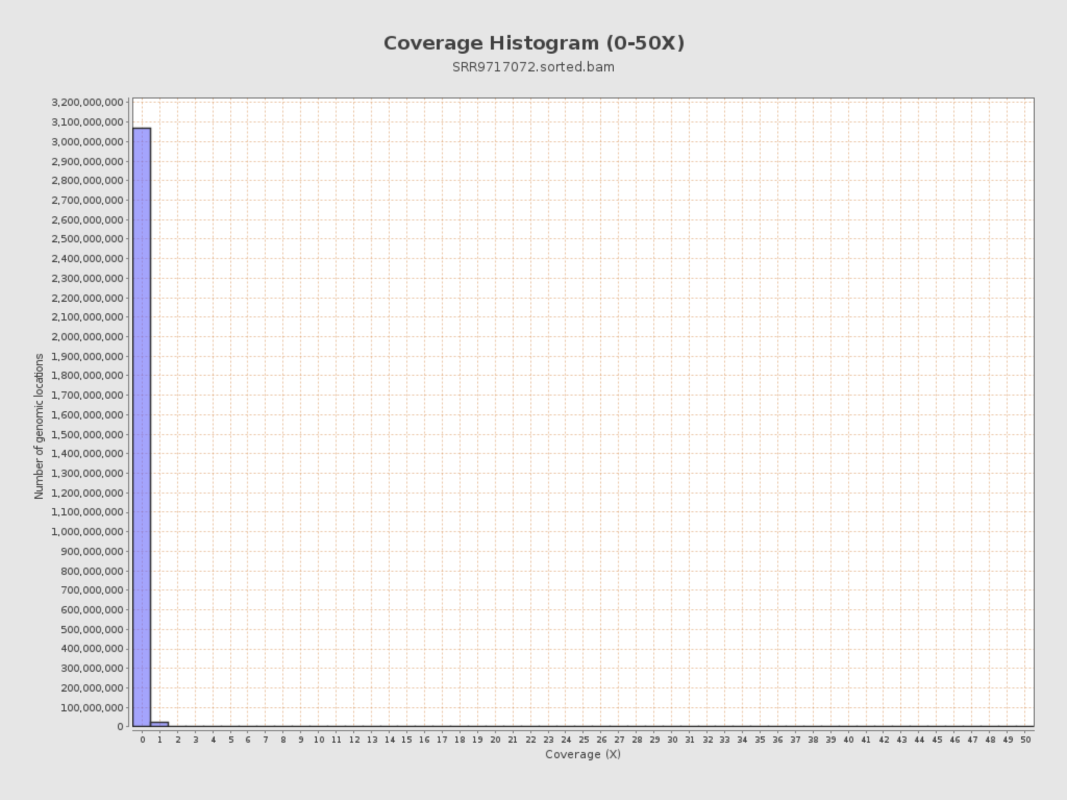
3. Results : Coverage across reference



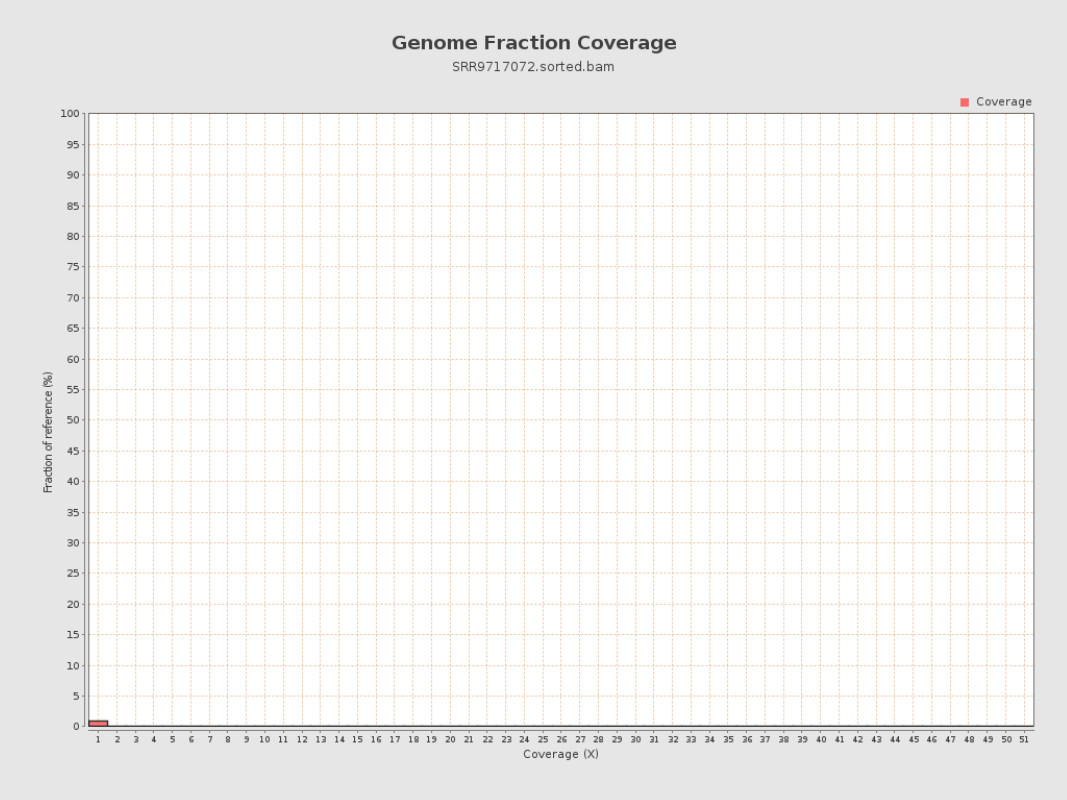
4. Results : Coverage Histogram



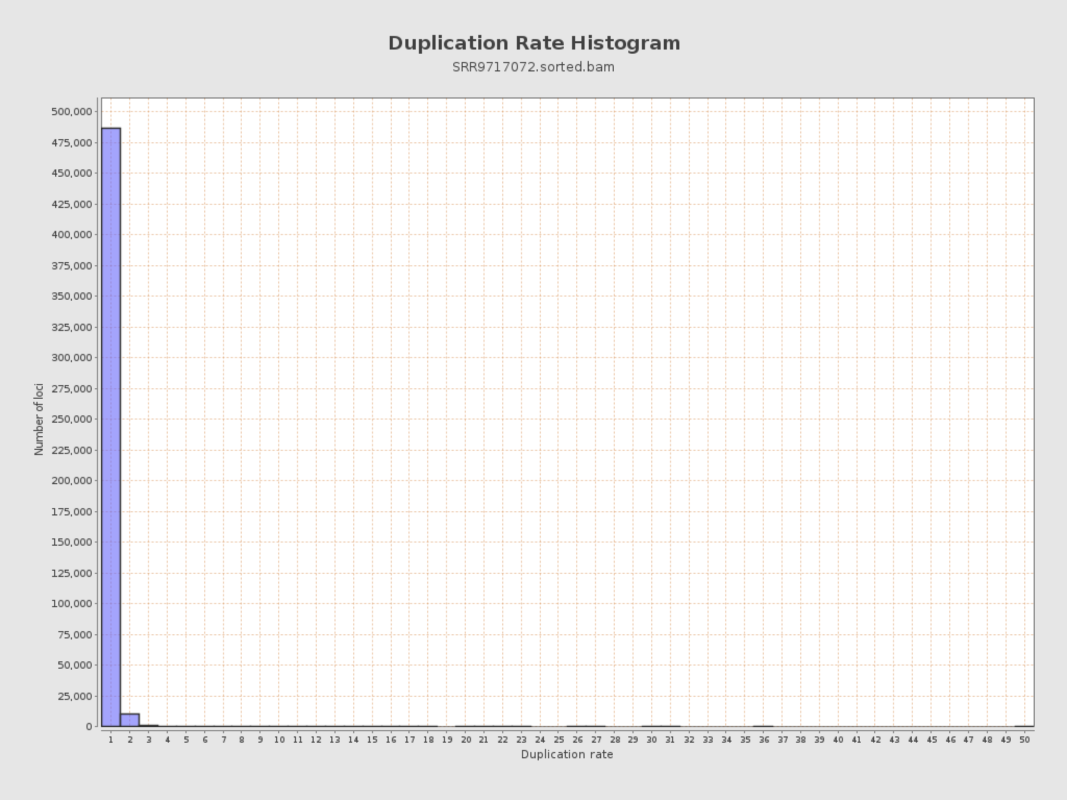
5. Results : Coverage Histogram (0-50X)



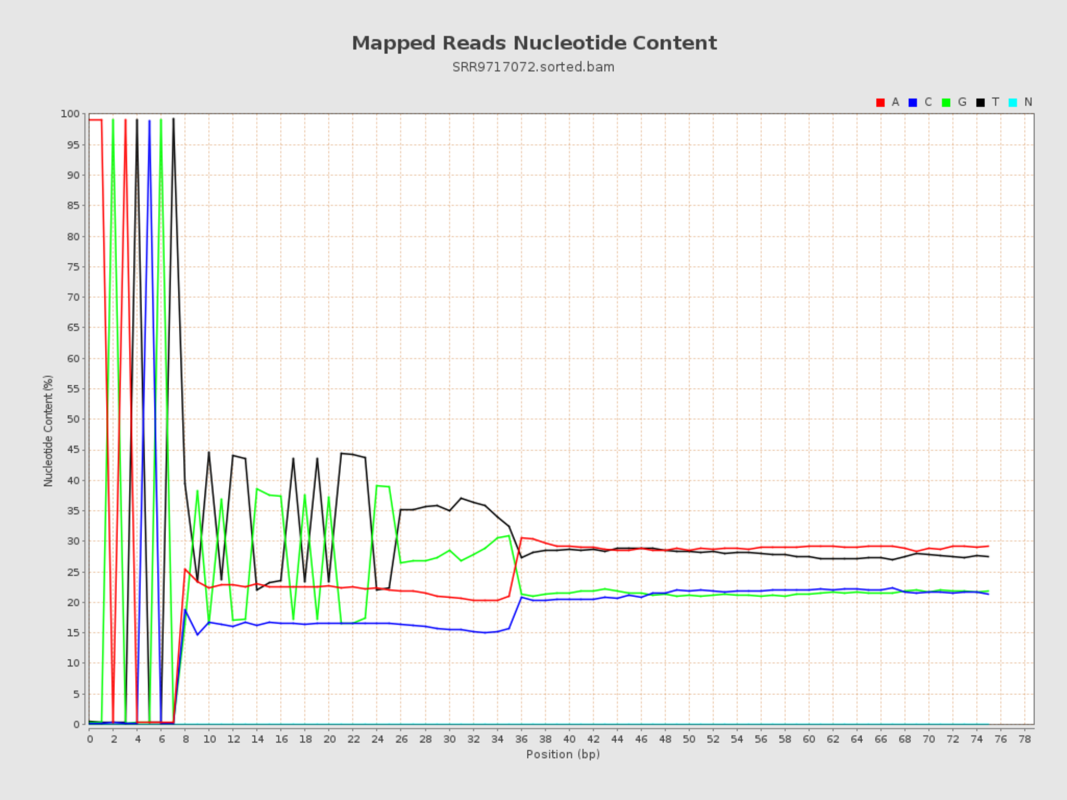
6. Results : Genome Fraction Coverage



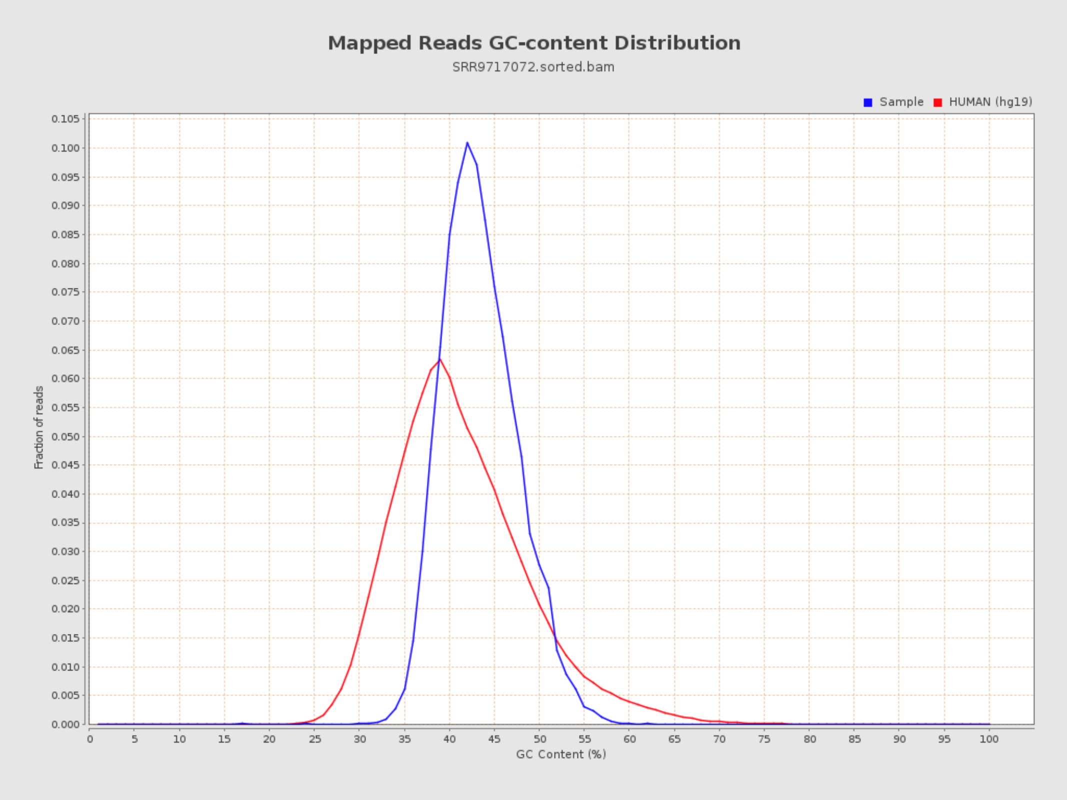
7. Results : Duplication Rate Histogram



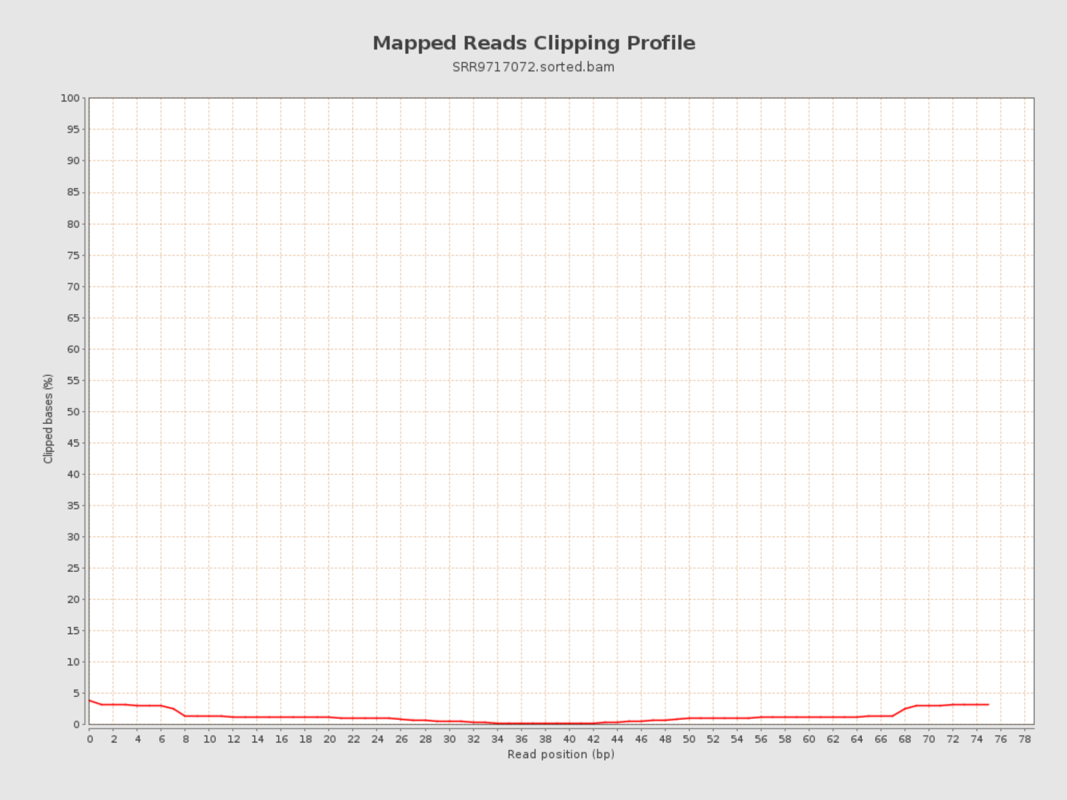
8. Results : Mapped Reads Nucleotide Content



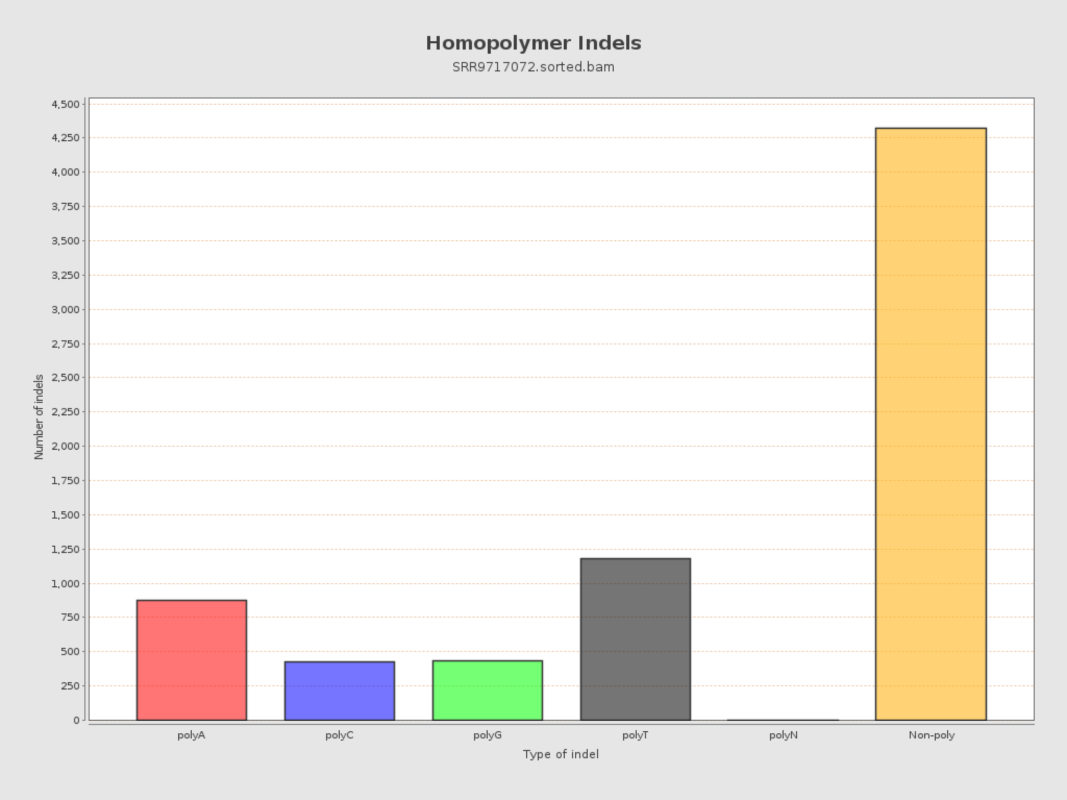
9. Results : Mapped Reads GC-content Distribution



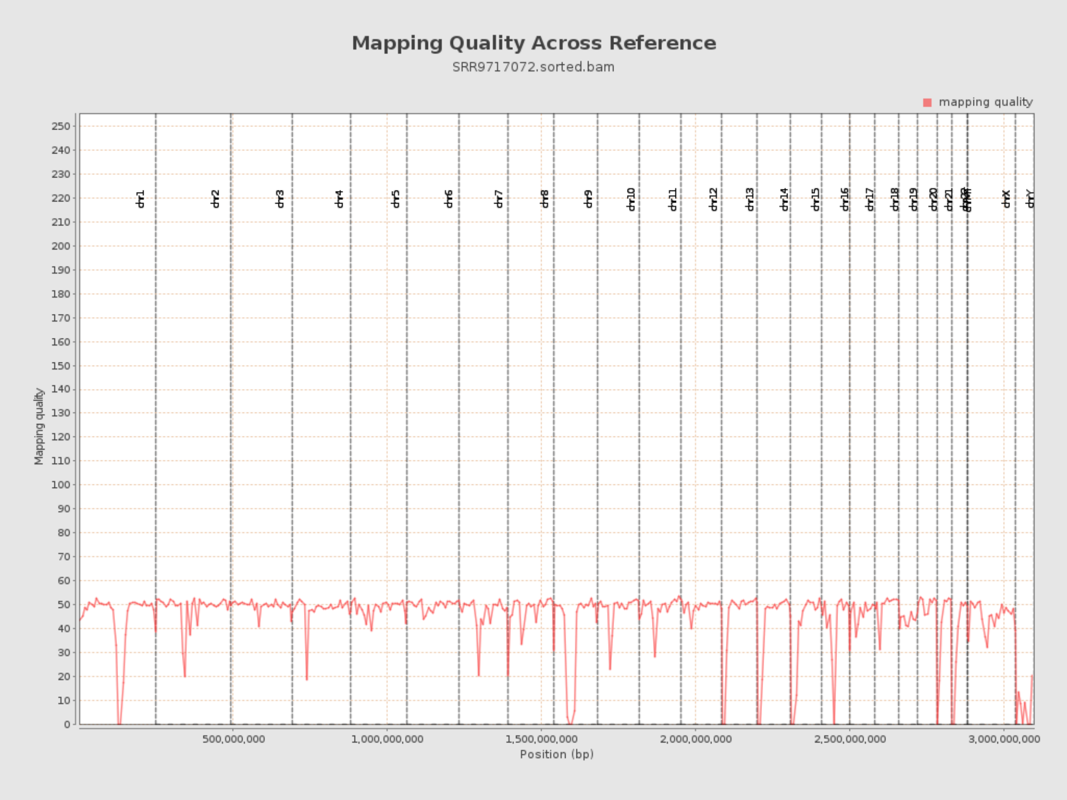
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram