Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 04:44:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717073.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_SRR9717073 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717073.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 04:44:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717073.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	537,985
Mapped reads	486,254 / 90.38%
Unmapped reads	51,731 / 9.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,891 / 0.54%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	14,585 / 2.71%
Duplication rate	2.49%
Clipped reads	488,461 / 90.79%

2.2. ACGT Content

Number/percentage of A's	7,141,882 / 24.9%
Number/percentage of C's	5,832,312 / 20.33%
Number/percentage of T's	8,708,628 / 30.36%
Number/percentage of G's	7,004,326 / 24.42%
Number/percentage of N's	195 / 0%
GC Percentage	44.75%

2.3. Coverage

Mean	0.0093

Standard Deviation	0.1167

2.4. Mapping Quality

Mean Mapping Quality	45.38

2.5. Mismatches and indels

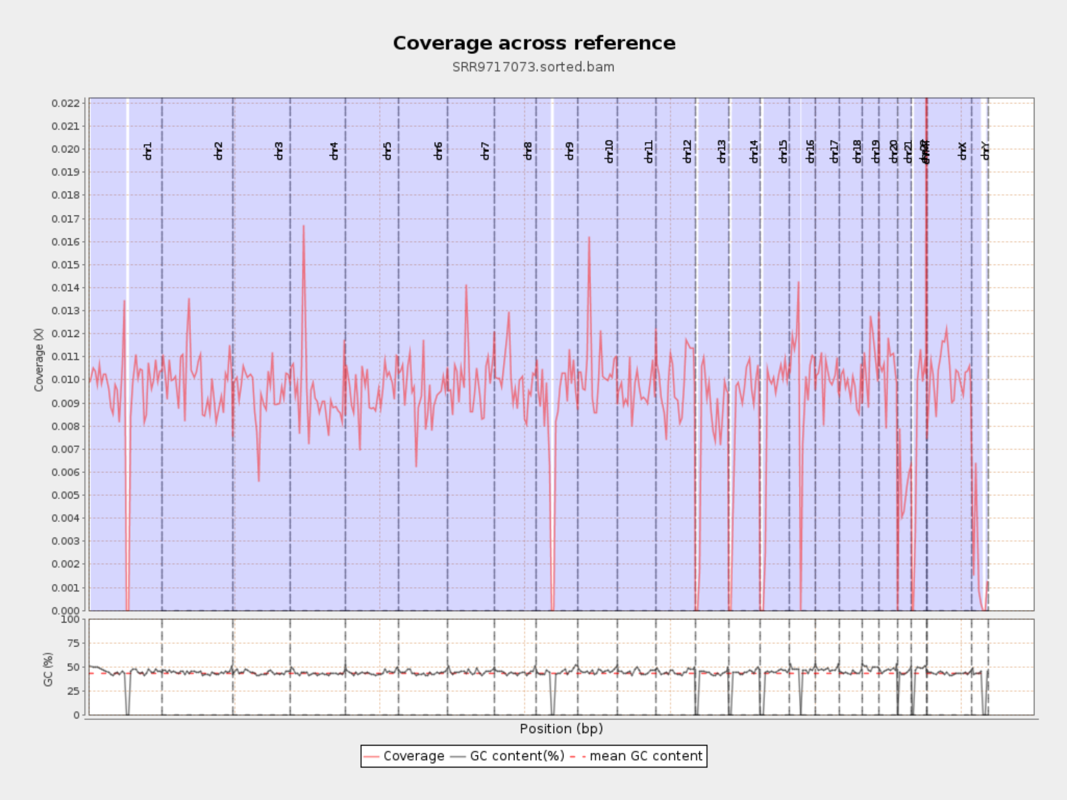
General error rate	0.5%
Mismatches	139,672
Insertions	1,762
Mapped reads with at least one insertion	0.36%
Deletions	5,006
Mapped reads with at least one deletion	1.02%
Homopolymer indels	43.42%

2.6. Chromosome stats

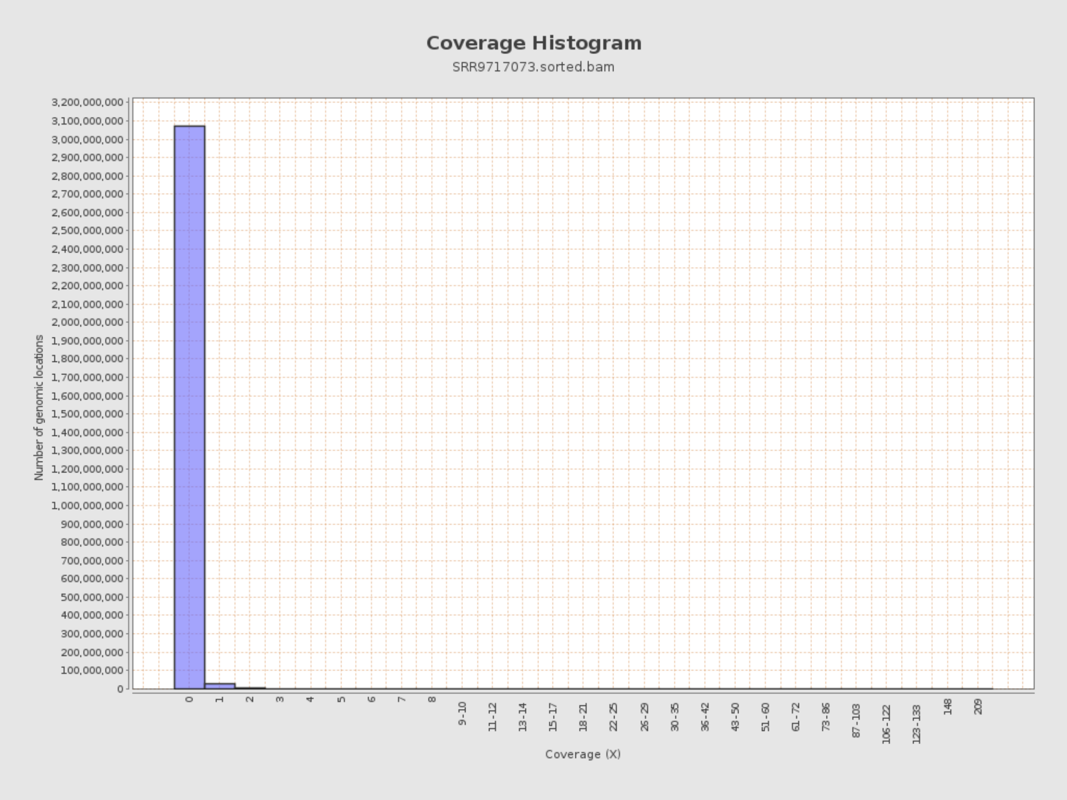
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2327964	0.0093	0.1461
chr2	243199373	2425492	0.01	0.14
chr3	198022430	1872081	0.0095	0.1033
chr4	191154276	1804609	0.0094	0.1114
chr5	180915260	1727702	0.0095	0.1033
chr6	171115067	1620752	0.0095	0.1061
chr7	159138663	1587635	0.01	0.134

chr8	146364022	1452569	0.0099	0.1334
chr9	141213431	1185397	0.0084	0.1038
chr10	135534747	1414243	0.0104	0.1296
chr11	135006516	1286677	0.0095	0.113
chr12	133851895	1326086	0.0099	0.1064
chr13	115169878	873322	0.0076	0.0929
chr14	107349540	880388	0.0082	0.0966
chr15	102531392	837296	0.0082	0.0962
chr16	90354753	895448	0.0099	0.1071
chr17	81195210	824170	0.0102	0.1093
chr18	78077248	756174	0.0097	0.1433
chr19	59128983	642126	0.0109	0.132
chr20	63025520	658116	0.0104	0.11
chr21	48129895	244585	0.0051	0.0856
chr22	51304566	371030	0.0072	0.0911
chrMT	16571	1222	0.0737	0.3064
chrX	155270560	1580884	0.0102	0.1093
chrY	59373566	99408	0.0017	0.0656

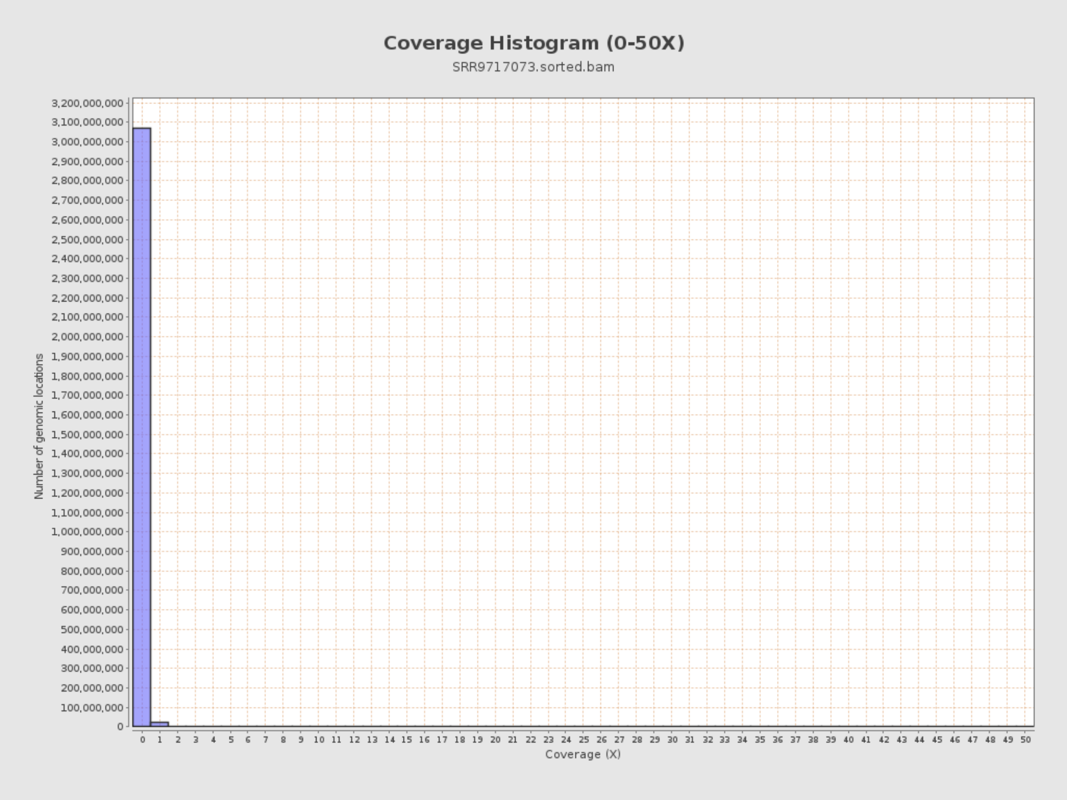
3. Results : Coverage across reference



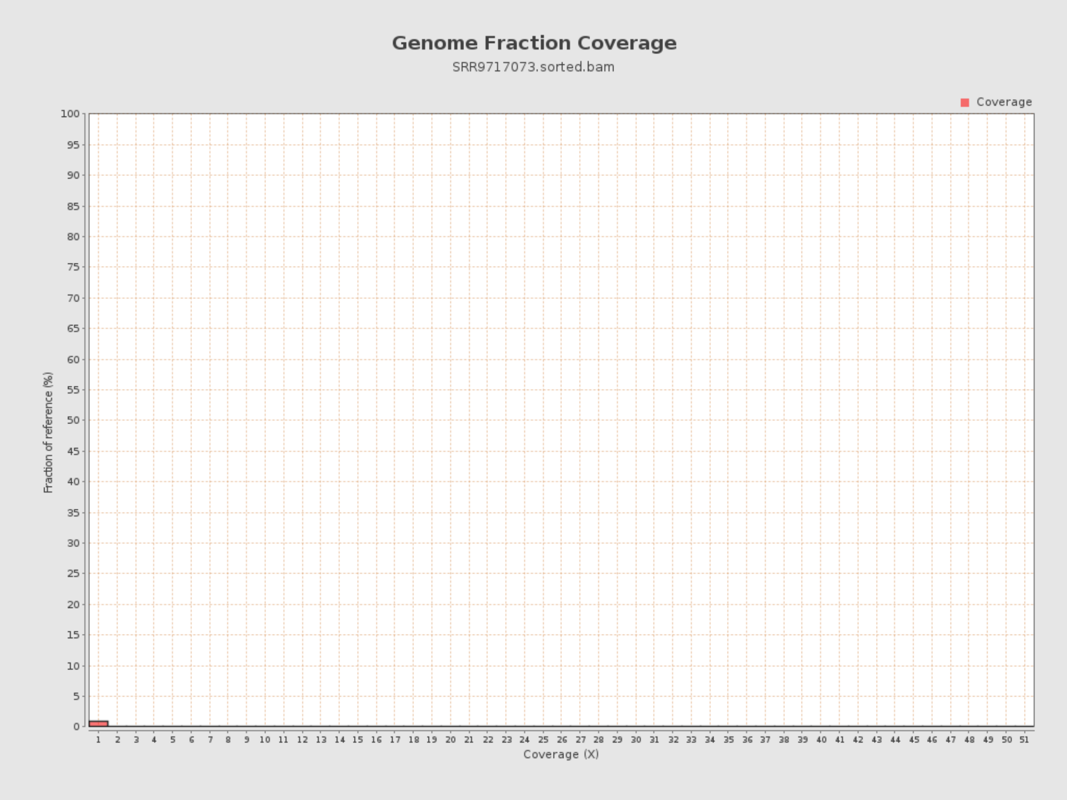
4. Results : Coverage Histogram



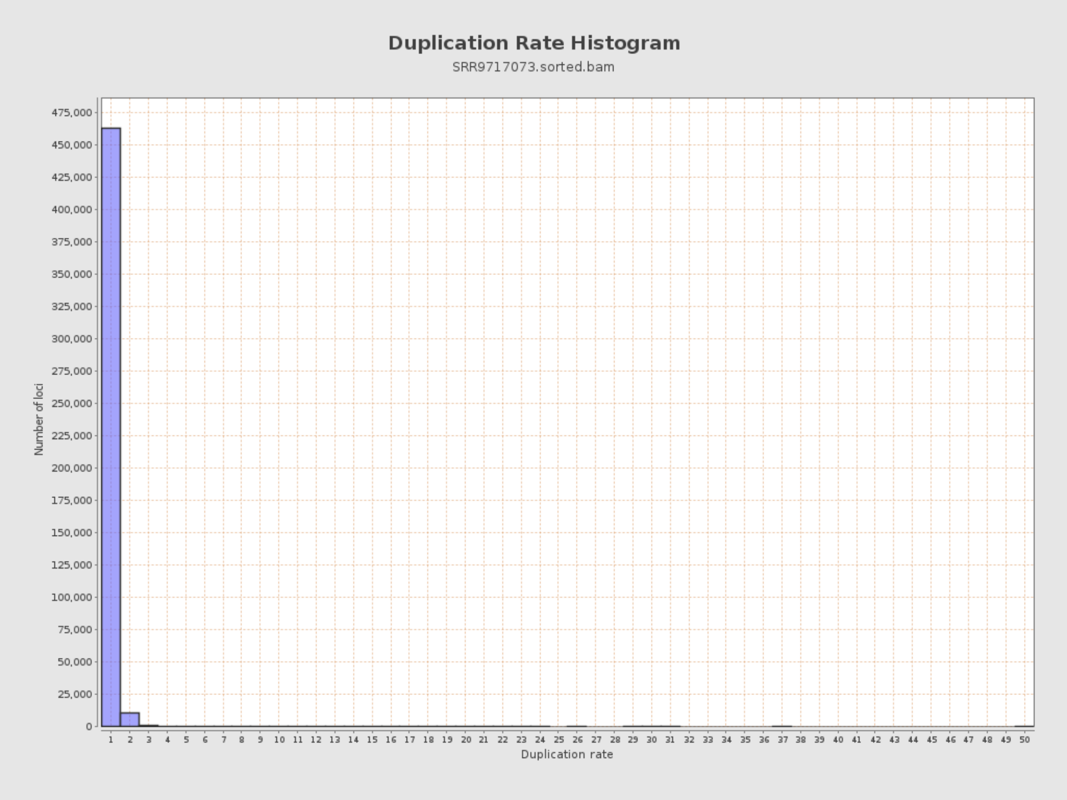
5. Results : Coverage Histogram (0-50X)



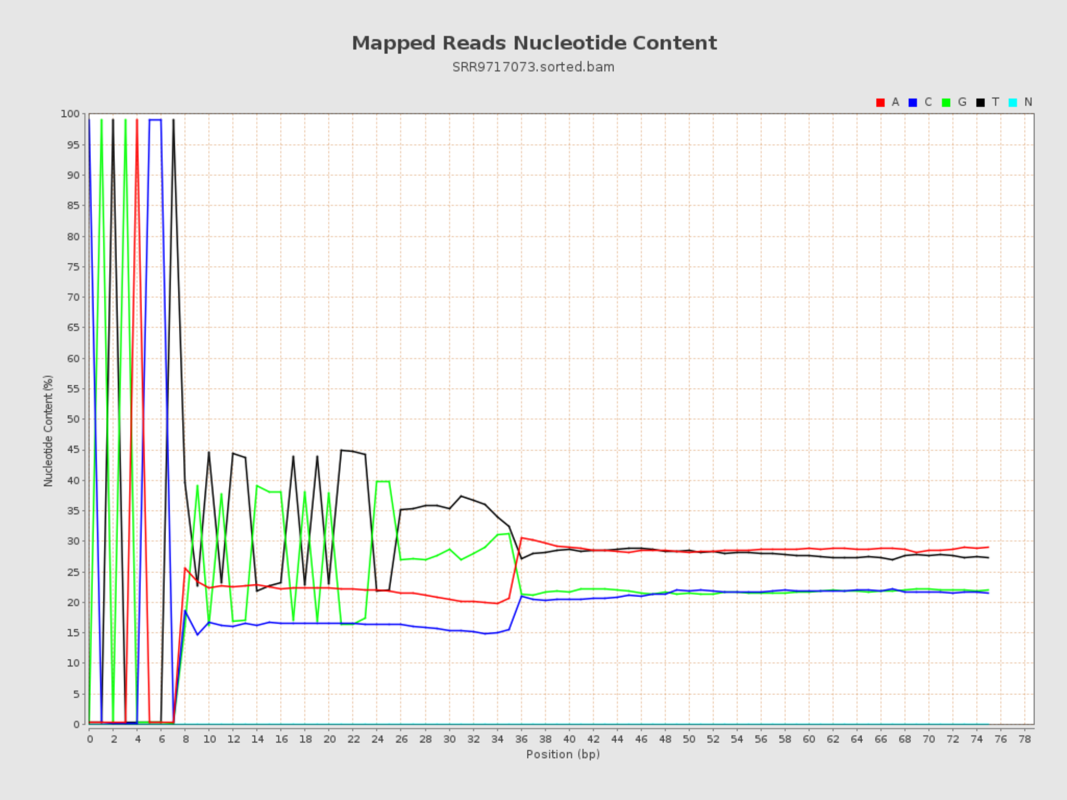
6. Results : Genome Fraction Coverage



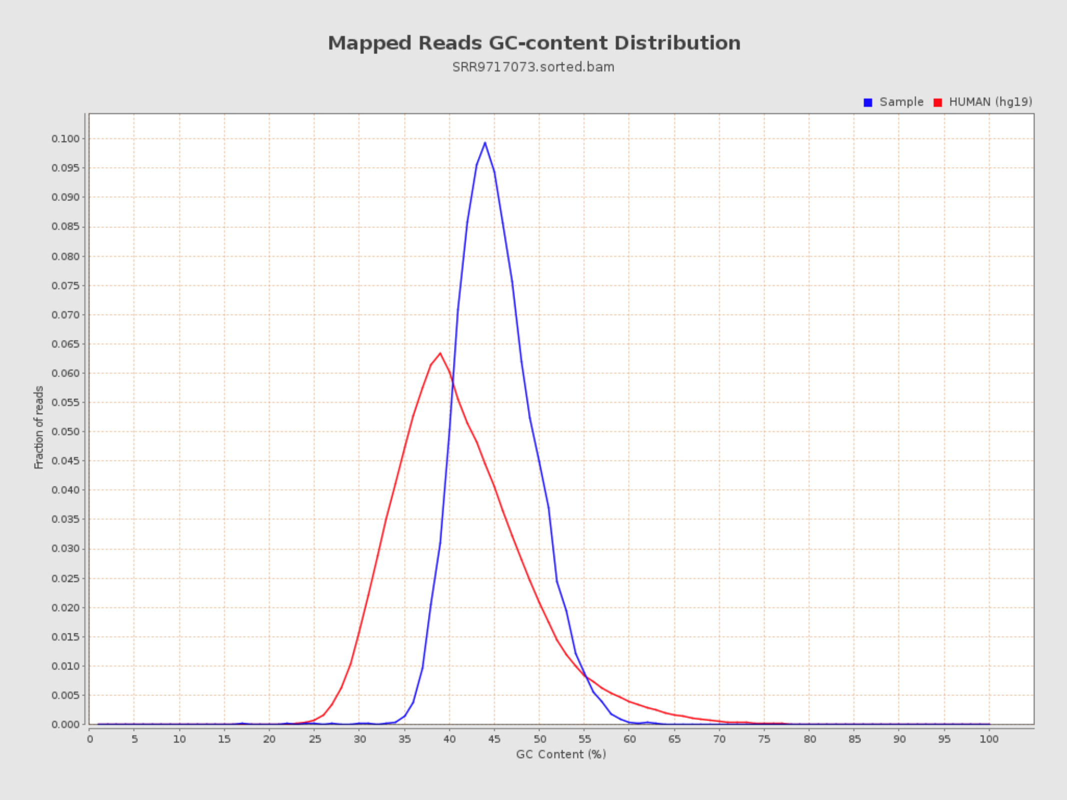
7. Results : Duplication Rate Histogram



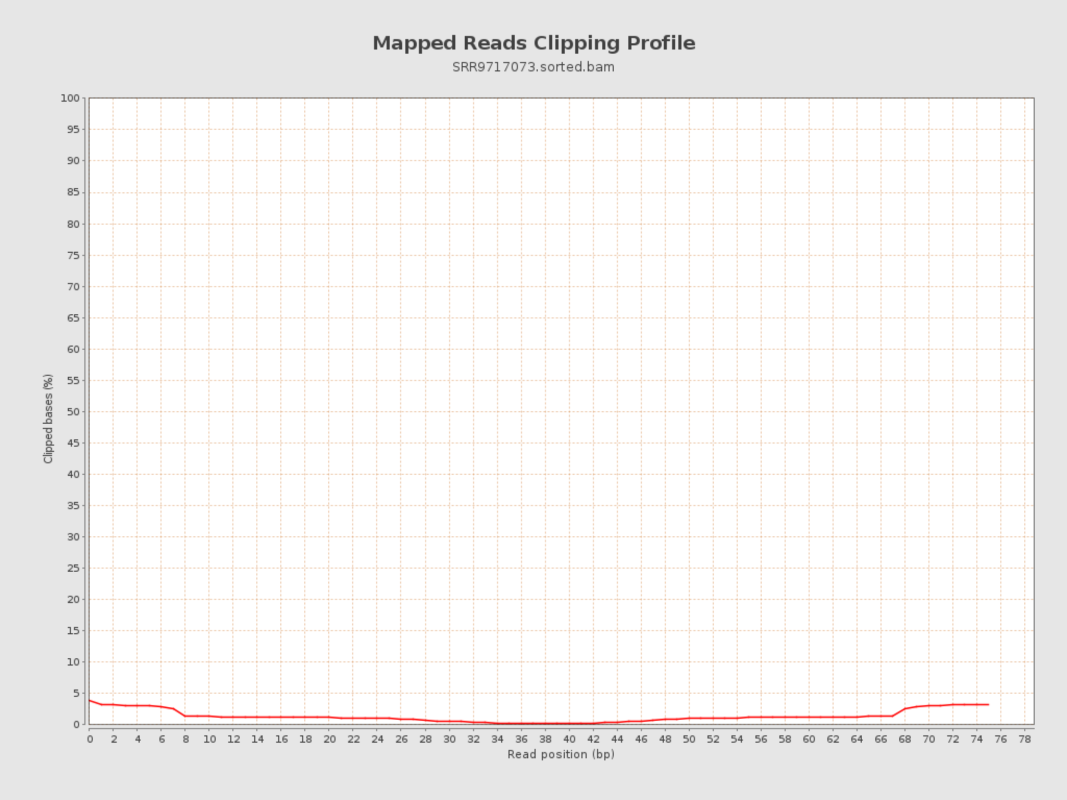
8. Results : Mapped Reads Nucleotide Content



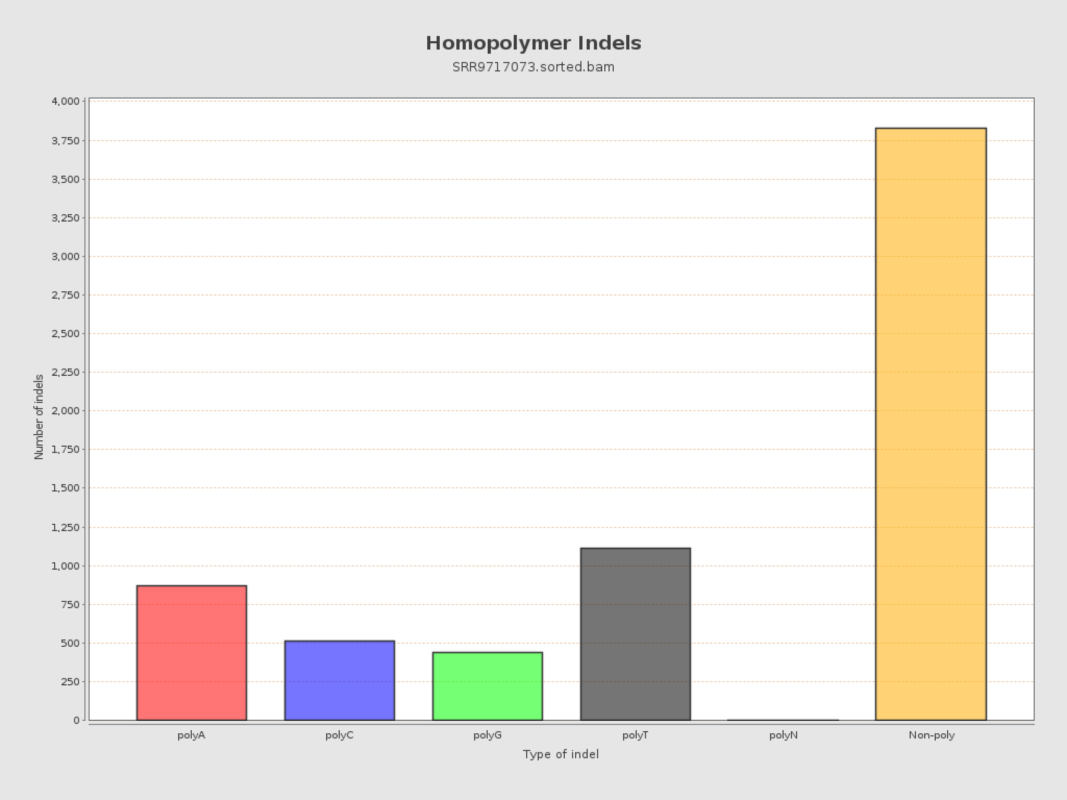
9. Results : Mapped Reads GC-content Distribution



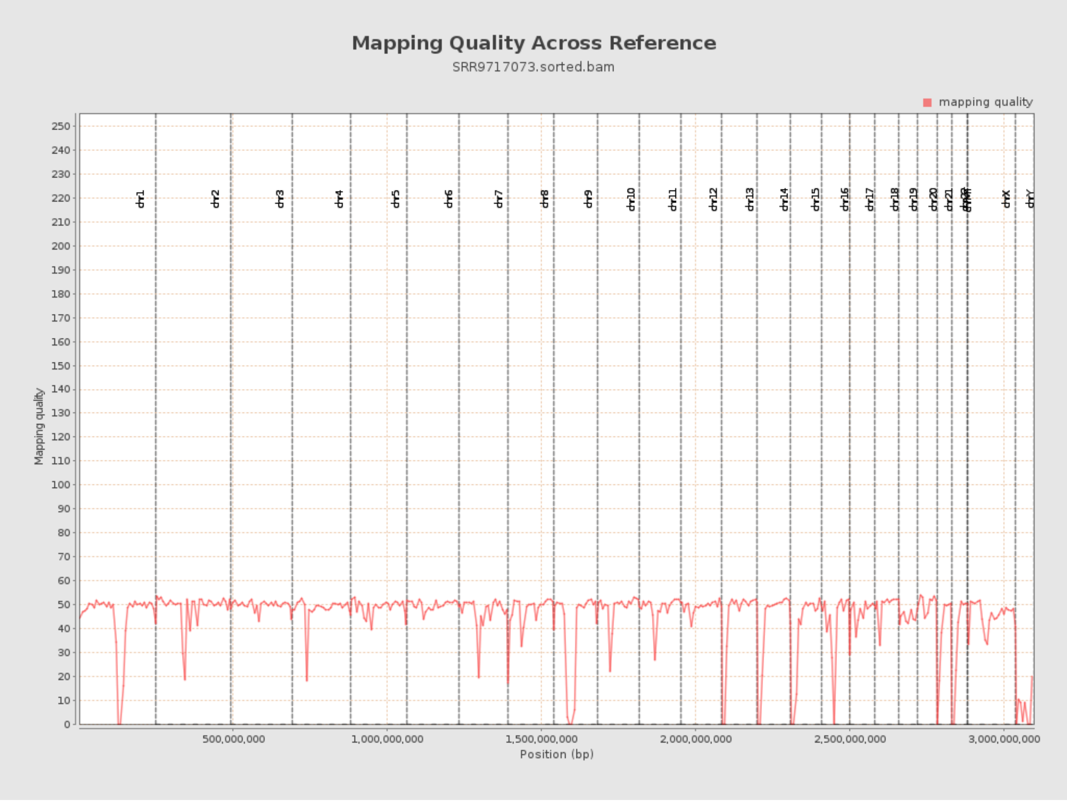
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram