Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 04:54:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717078.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_SRR9717078 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717078.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 04:54:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717078.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	513,492
Mapped reads	414,195 / 80.66%
Unmapped reads	99,297 / 19.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	958 / 0.19%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	7,125 / 1.39%
Duplication rate	1.3%
Clipped reads	414,087 / 80.64%

2.2. ACGT Content

Number/percentage of A's	5,880,025 / 24.32%
Number/percentage of C's	4,468,283 / 18.48%
Number/percentage of T's	7,785,208 / 32.2%
Number/percentage of G's	6,040,562 / 24.99%
Number/percentage of N's	274 / 0%
GC Percentage	43.47%

2.3. Coverage

Mean	0.0078

Standard Deviation	0.1057

2.4. Mapping Quality

Mean Mapping Quality	44.95

2.5. Mismatches and indels

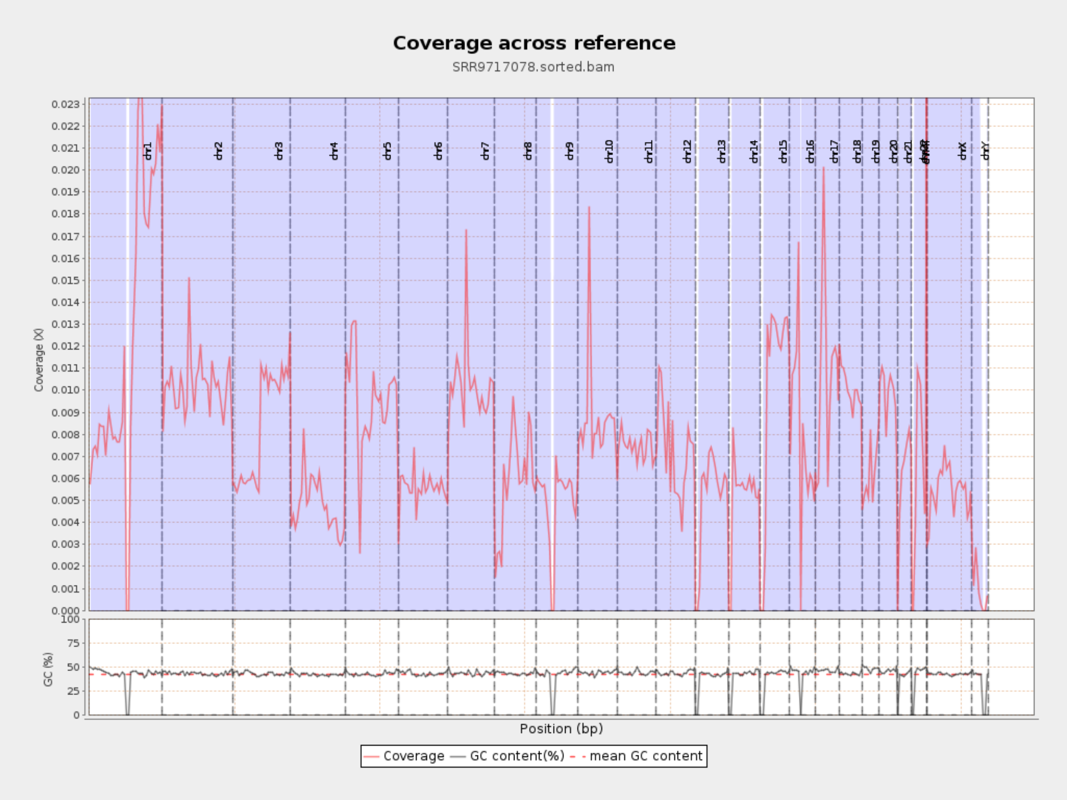
General error rate	0.5%
Mismatches	117,324
Insertions	1,531
Mapped reads with at least one insertion	0.37%
Deletions	4,881
Mapped reads with at least one deletion	1.17%
Homopolymer indels	42.86%

2.6. Chromosome stats

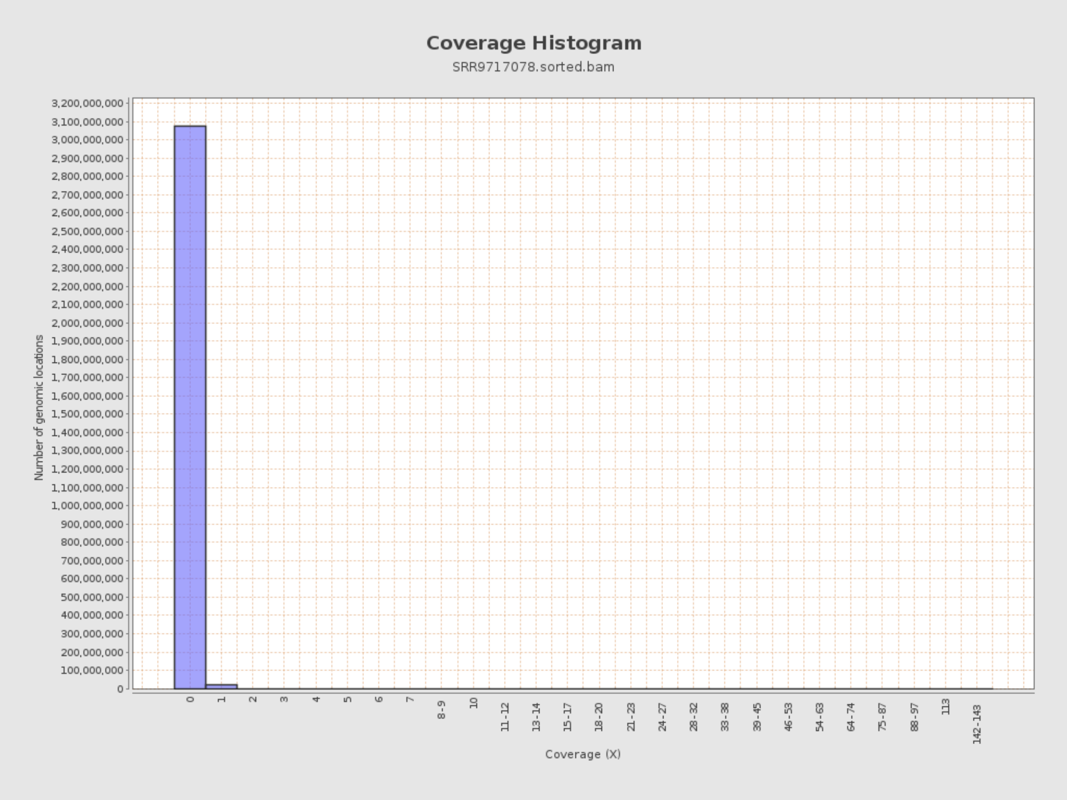
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3069660	0.0123	0.143
chr2	243199373	2492613	0.0102	0.1293
chr3	198022430	1645449	0.0083	0.0953
chr4	191154276	900637	0.0047	0.0726
chr5	180915260	1725103	0.0095	0.1004
chr6	171115067	953638	0.0056	0.0807
chr7	159138663	1646593	0.0103	0.1539

chr8	146364022	868424	0.0059	0.0872
chr9	141213431	689271	0.0049	0.0845
chr10	135534747	1182465	0.0087	0.1304
chr11	135006516	999050	0.0074	0.1012
chr12	133851895	961922	0.0072	0.0871
chr13	115169878	594753	0.0052	0.0739
chr14	107349540	546221	0.0051	0.0741
chr15	102531392	1043056	0.0102	0.104
chr16	90354753	714117	0.0079	0.0969
chr17	81195210	881378	0.0109	0.1092
chr18	78077248	790542	0.0101	0.1471
chr19	59128983	366169	0.0062	0.1189
chr20	63025520	621769	0.0099	0.1022
chr21	48129895	295223	0.0061	0.0816
chr22	51304566	294748	0.0057	0.0778
chrMT	16571	1071	0.0646	0.2724
chrX	155270560	843398	0.0054	0.0816
chrY	59373566	54892	0.0009	0.0369

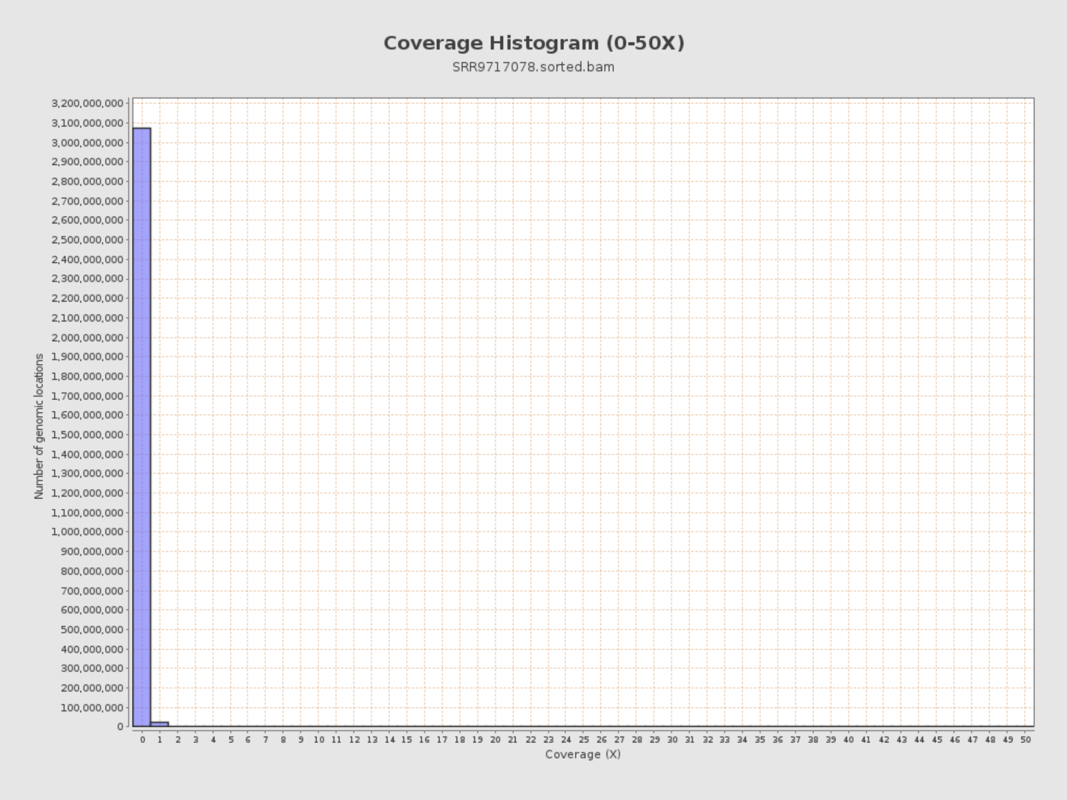
3. Results : Coverage across reference



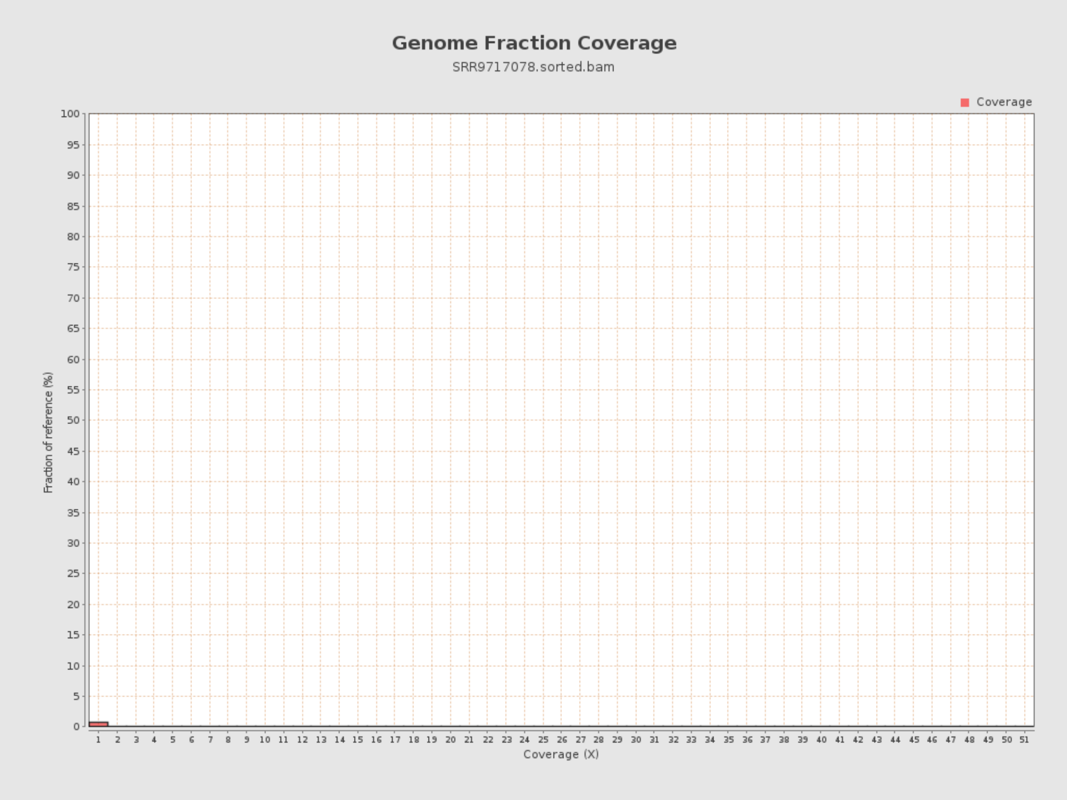
4. Results : Coverage Histogram



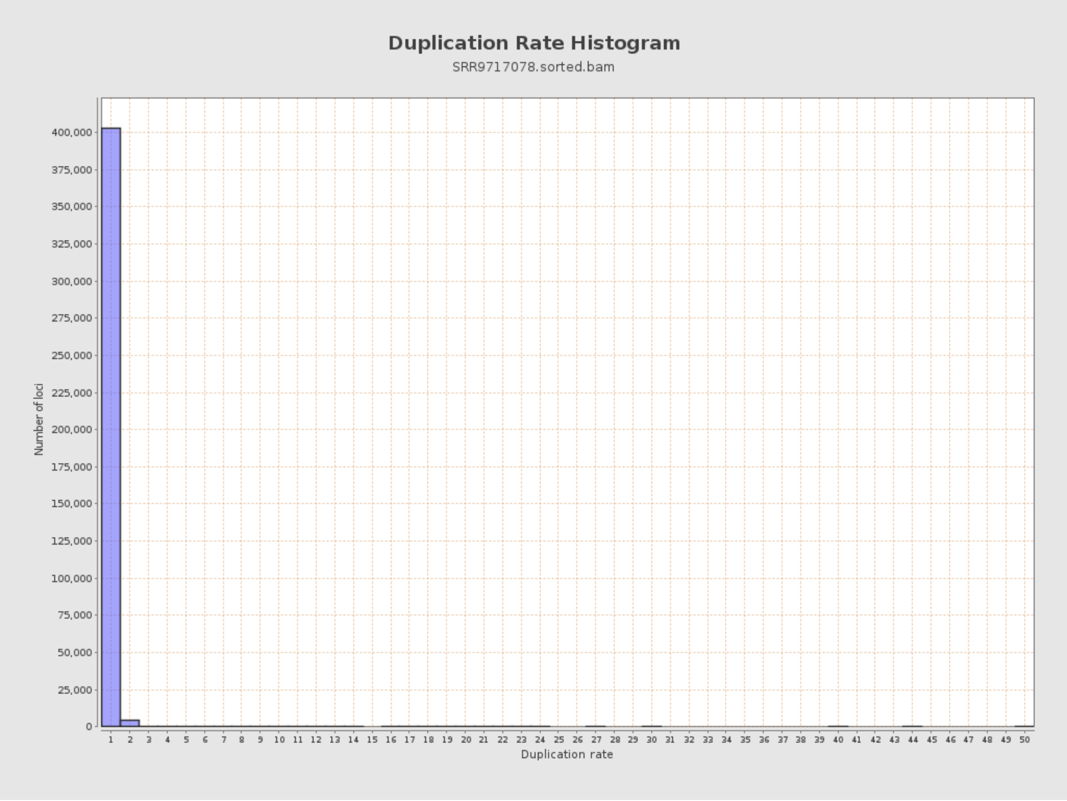
5. Results : Coverage Histogram (0-50X)



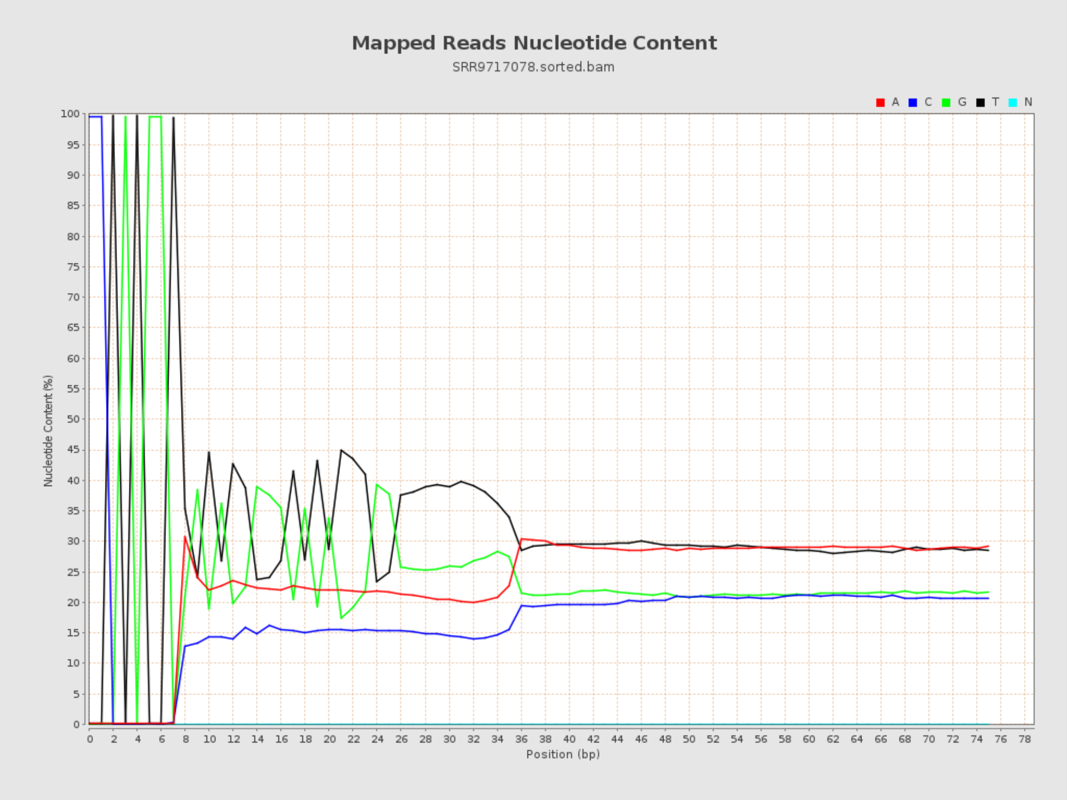
6. Results : Genome Fraction Coverage



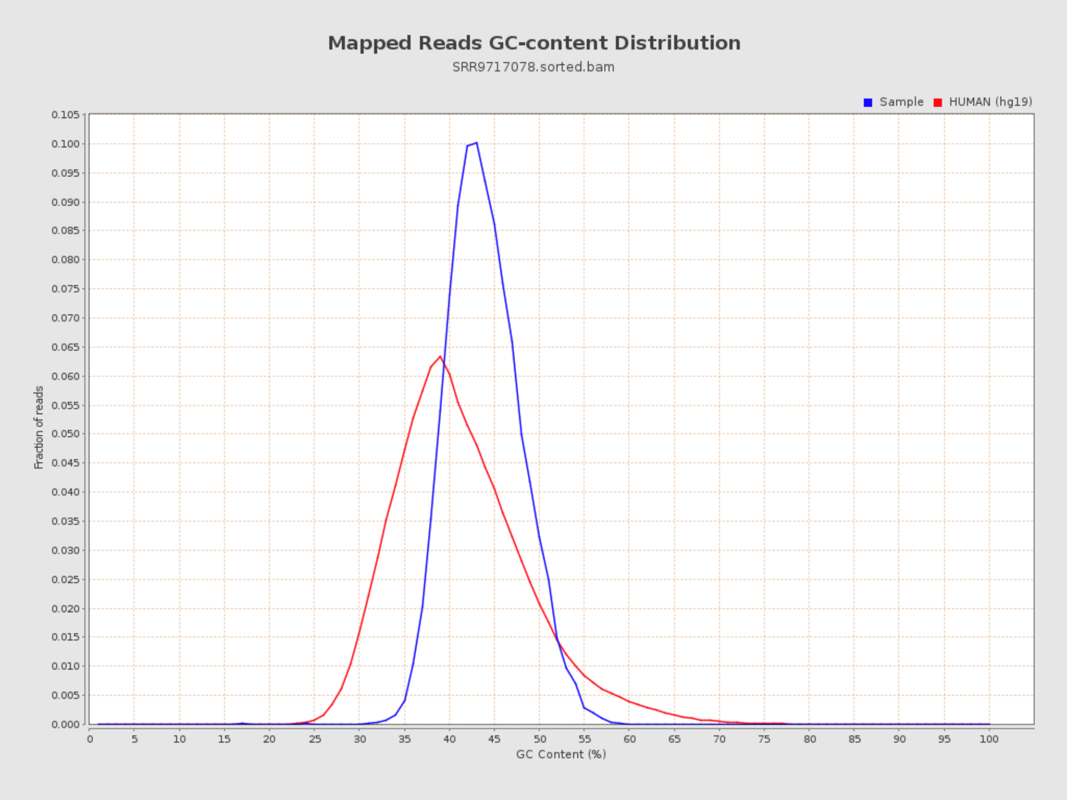
7. Results : Duplication Rate Histogram



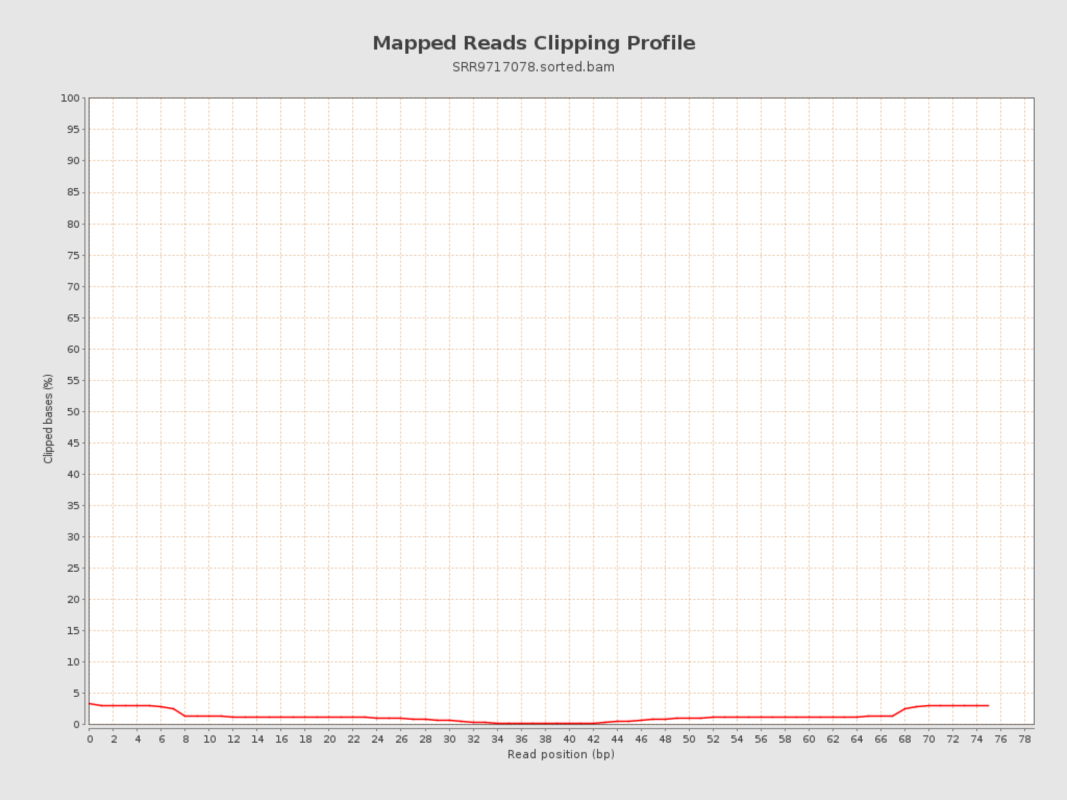
8. Results : Mapped Reads Nucleotide Content



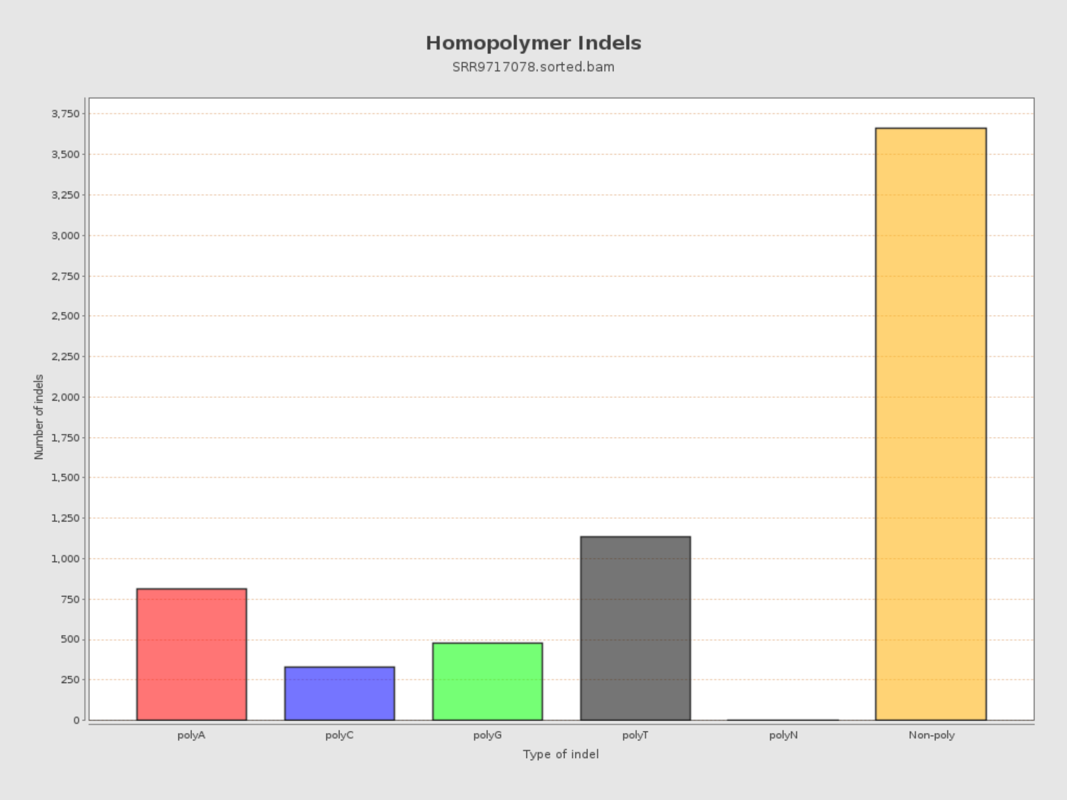
9. Results : Mapped Reads GC-content Distribution



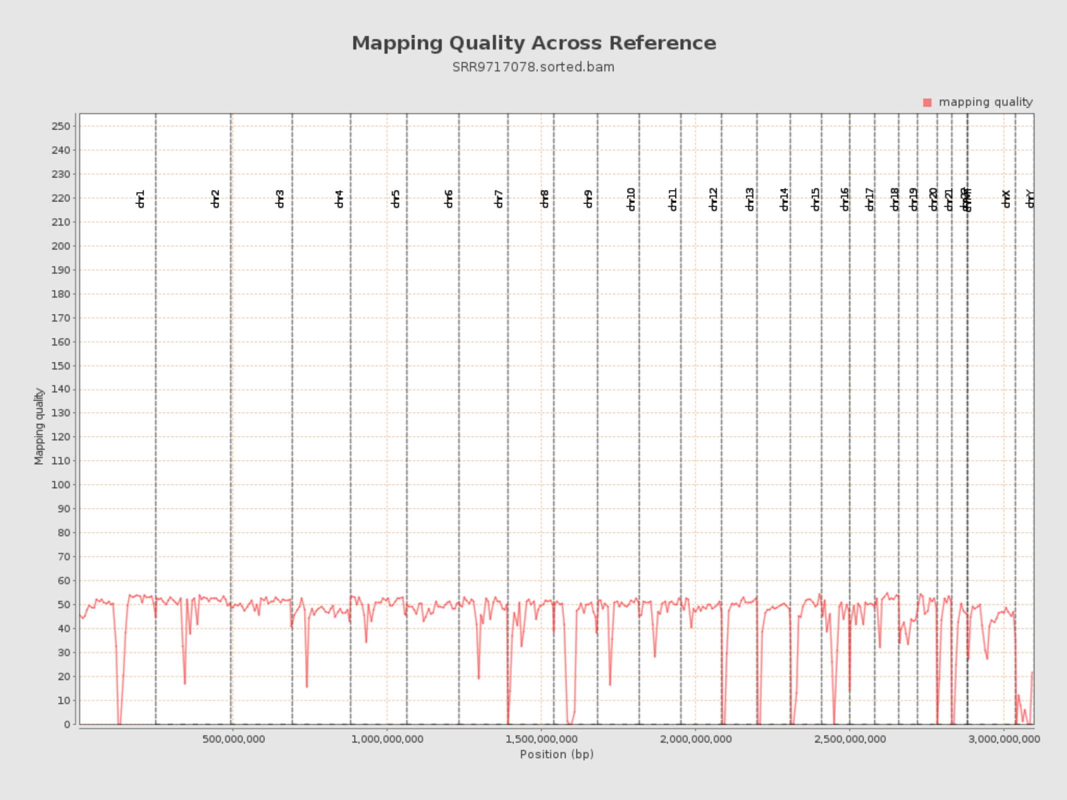
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram