Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 04:56:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717079.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_SRR9717079 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717079.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 04:56:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717079.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	582,696
Mapped reads	484,334 / 83.12%
Unmapped reads	98,362 / 16.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	938 / 0.16%
Read min/max/mean length	30 / 76 / 76.05
Duplicated reads (estimated)	9,273 / 1.59%
Duplication rate	1.42%
Clipped reads	483,817 / 83.03%

2.2. ACGT Content

Number/percentage of A's	6,501,315 / 23.46%
Number/percentage of C's	4,802,068 / 17.33%
Number/percentage of T's	9,340,185 / 33.7%
Number/percentage of G's	7,067,805 / 25.5%
Number/percentage of N's	242 / 0%
GC Percentage	42.83%

2.3. Coverage

Mean	0.009

Standard Deviation	0.1165

2.4. Mapping Quality

Mean Mapping Quality	44.29

2.5. Mismatches and indels

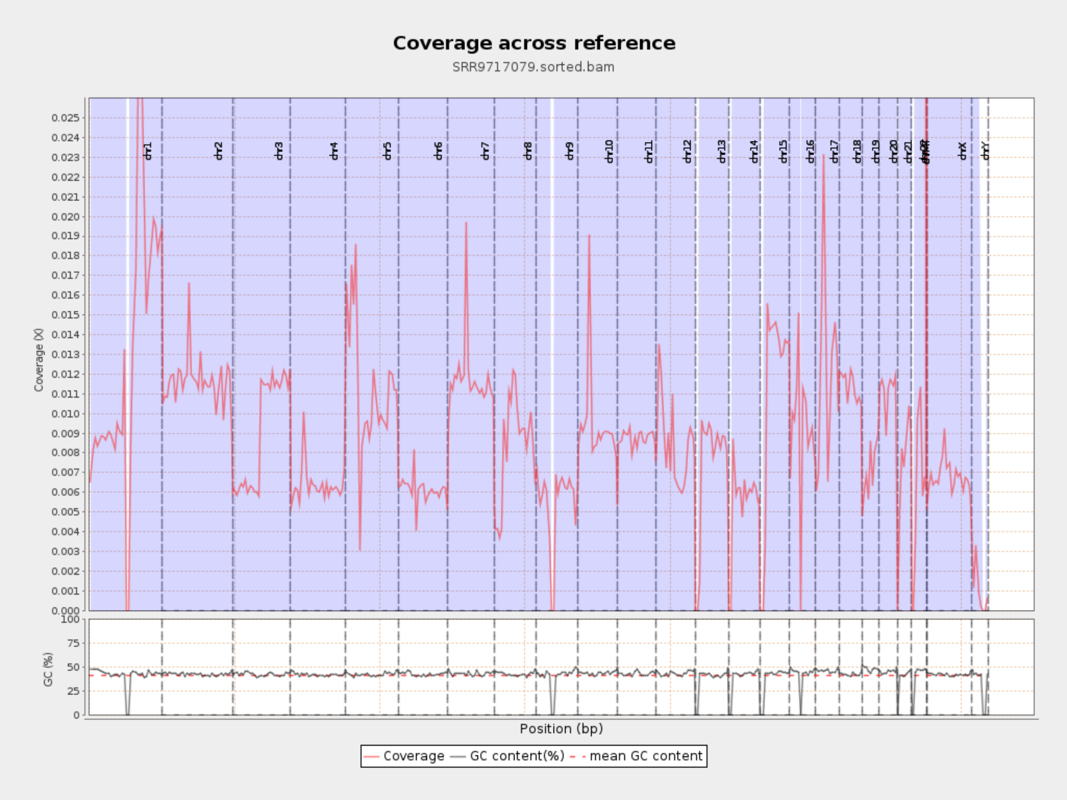
General error rate	0.5%
Mismatches	136,712
Insertions	1,845
Mapped reads with at least one insertion	0.38%
Deletions	5,649
Mapped reads with at least one deletion	1.16%
Homopolymer indels	44.38%

2.6. Chromosome stats

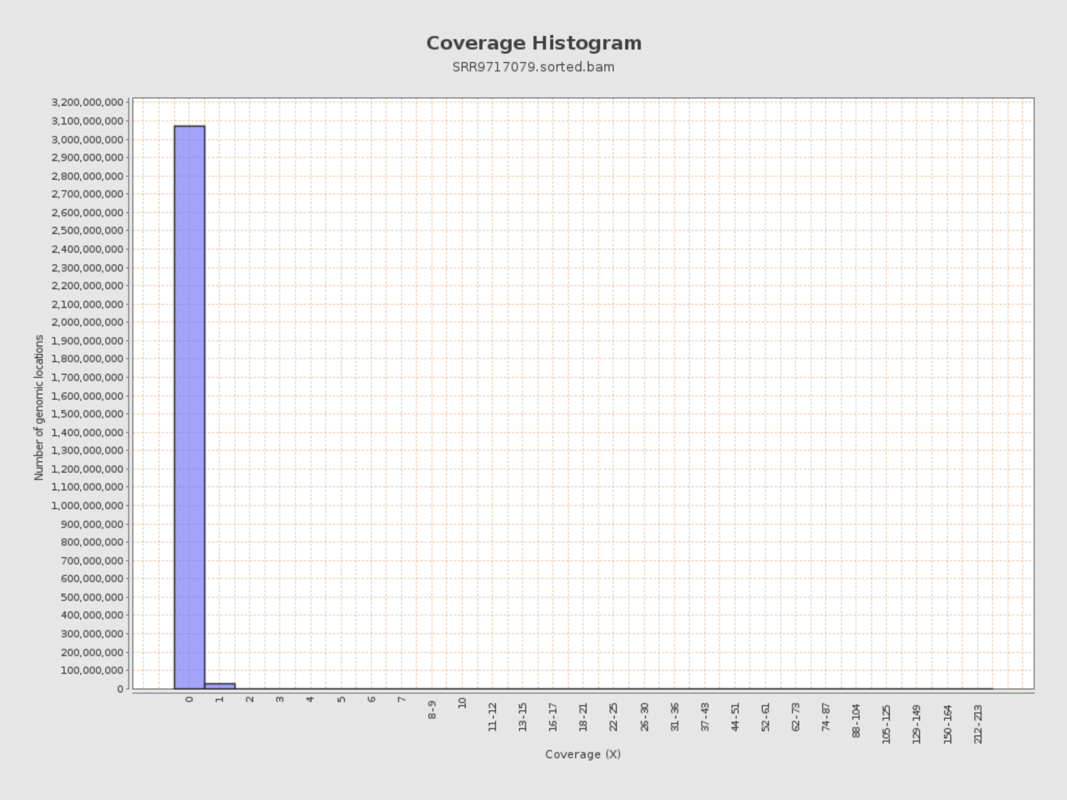
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3186563	0.0128	0.1625
chr2	243199373	2828911	0.0116	0.1481
chr3	198022430	1778491	0.009	0.0988
chr4	191154276	1212841	0.0063	0.0834
chr5	180915260	2044800	0.0113	0.1098
chr6	171115067	1048103	0.0061	0.0863
chr7	159138663	1883383	0.0118	0.1782

chr8	146364022	1230768	0.0084	0.1036
chr9	141213431	755128	0.0053	0.088
chr10	135534747	1281389	0.0095	0.1315
chr11	135006516	1174073	0.0087	0.109
chr12	133851895	1121022	0.0084	0.0948
chr13	115169878	838291	0.0073	0.088
chr14	107349540	582194	0.0054	0.0775
chr15	102531392	1152513	0.0112	0.1099
chr16	90354753	826268	0.0091	0.1047
chr17	81195210	994867	0.0123	0.1172
chr18	78077248	889512	0.0114	0.16
chr19	59128983	424257	0.0072	0.1145
chr20	63025520	691349	0.011	0.1078
chr21	48129895	353700	0.0073	0.0898
chr22	51304566	299665	0.0058	0.0786
chrMT	16571	7205	0.4348	0.7255
chrX	155270560	1055022	0.0068	0.0926
chrY	59373566	60307	0.001	0.0365

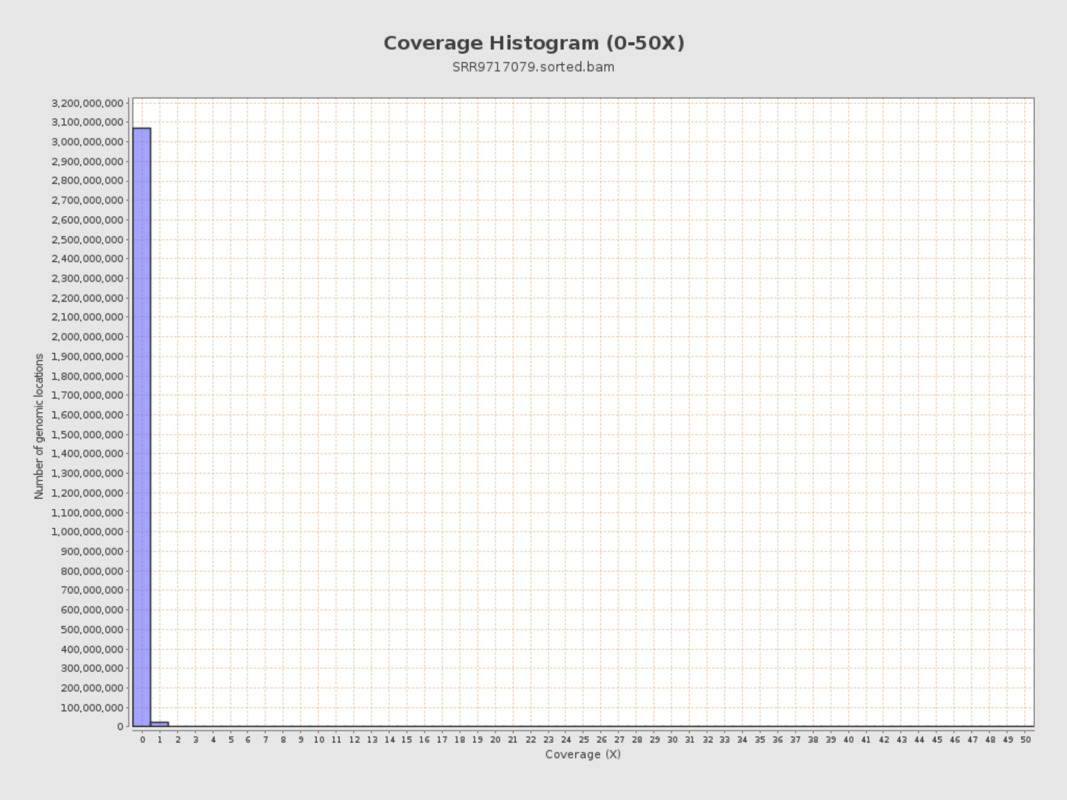
3. Results : Coverage across reference



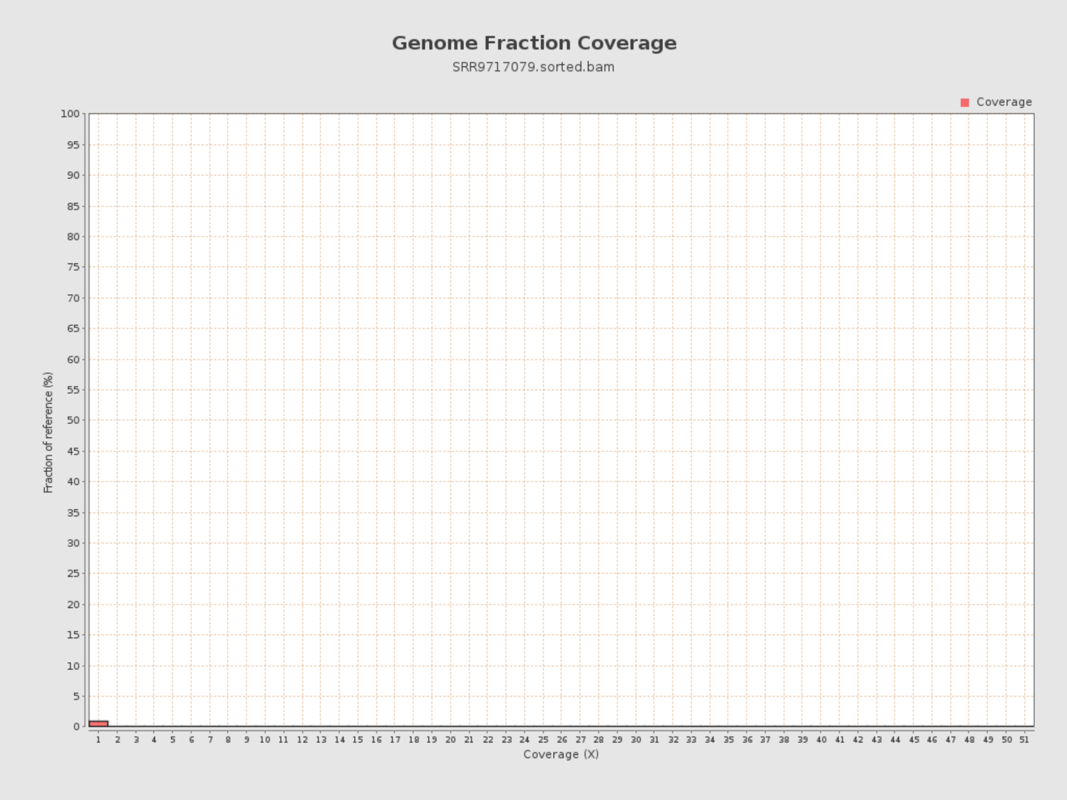
4. Results : Coverage Histogram



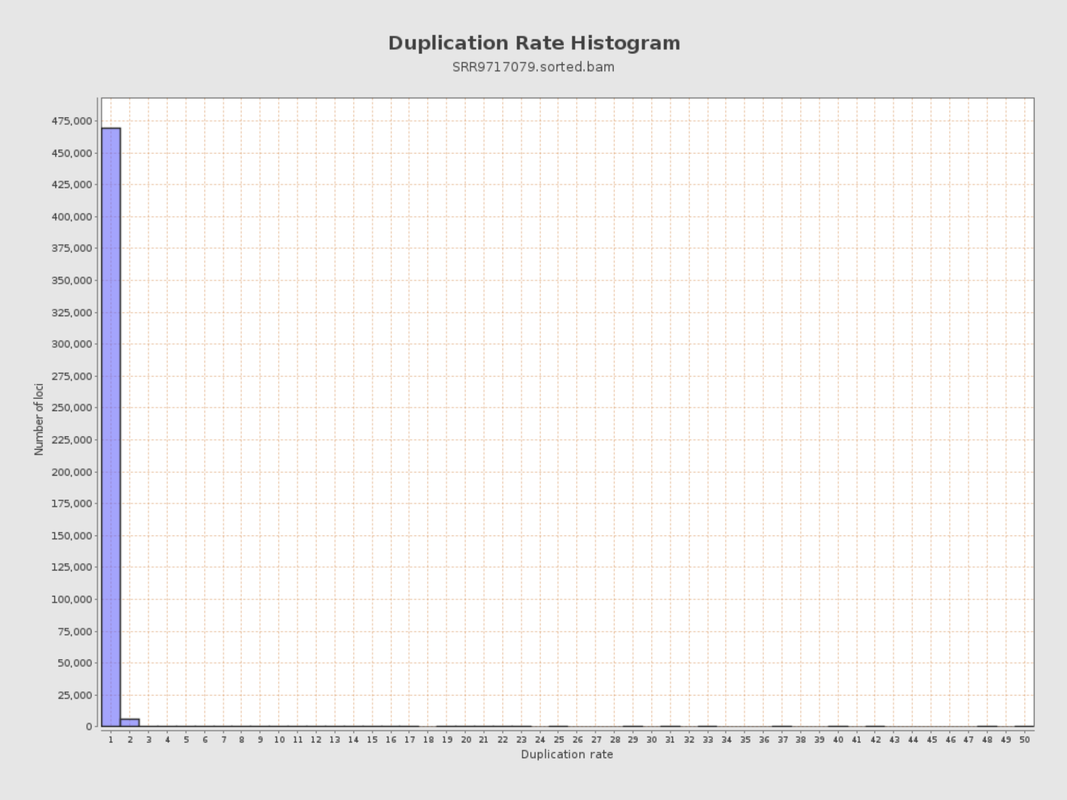
5. Results : Coverage Histogram (0-50X)



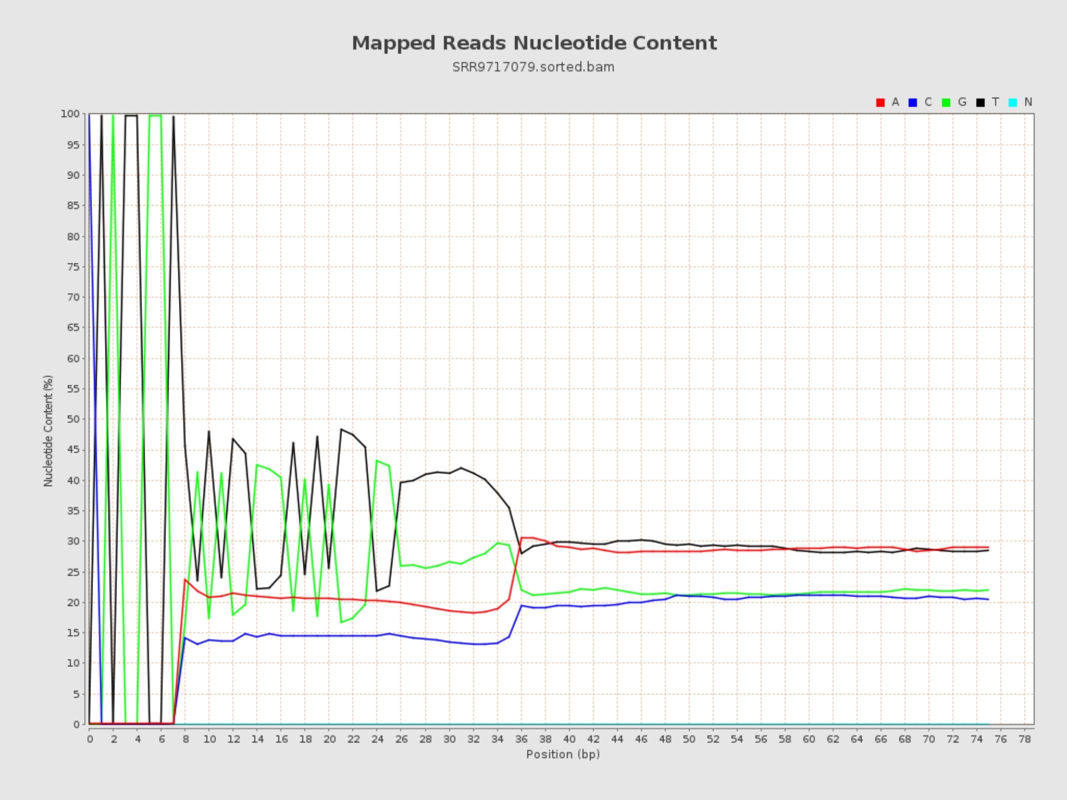
6. Results : Genome Fraction Coverage



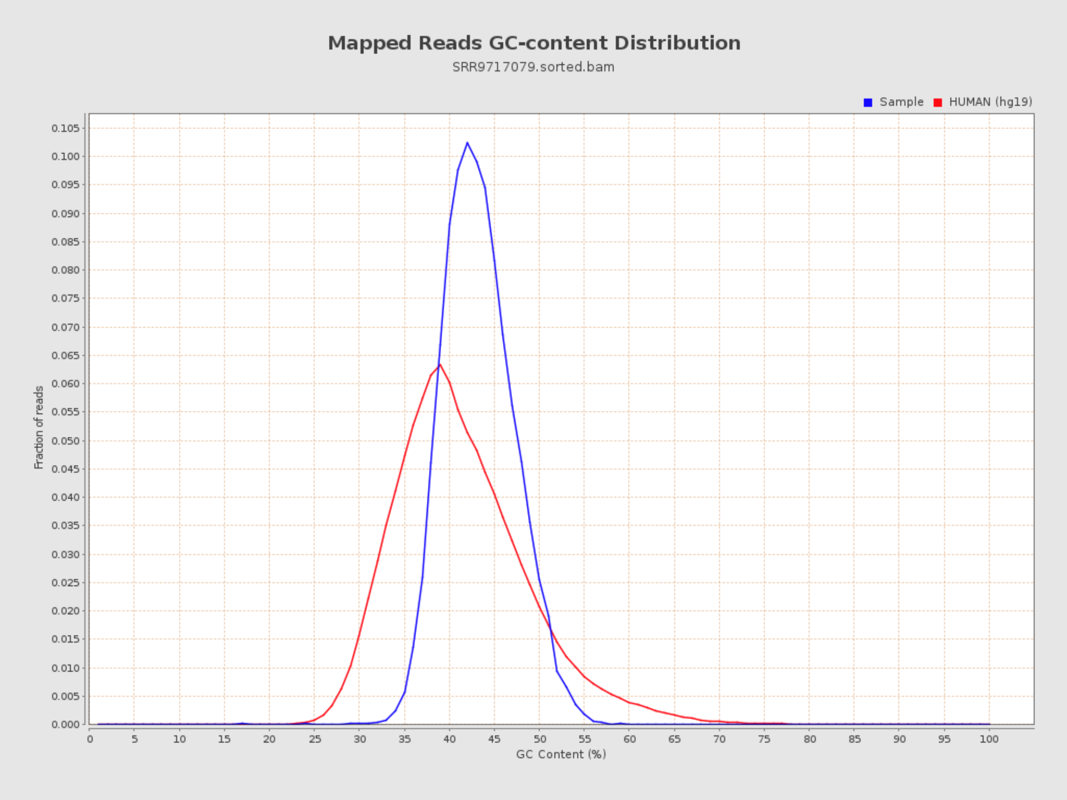
7. Results : Duplication Rate Histogram



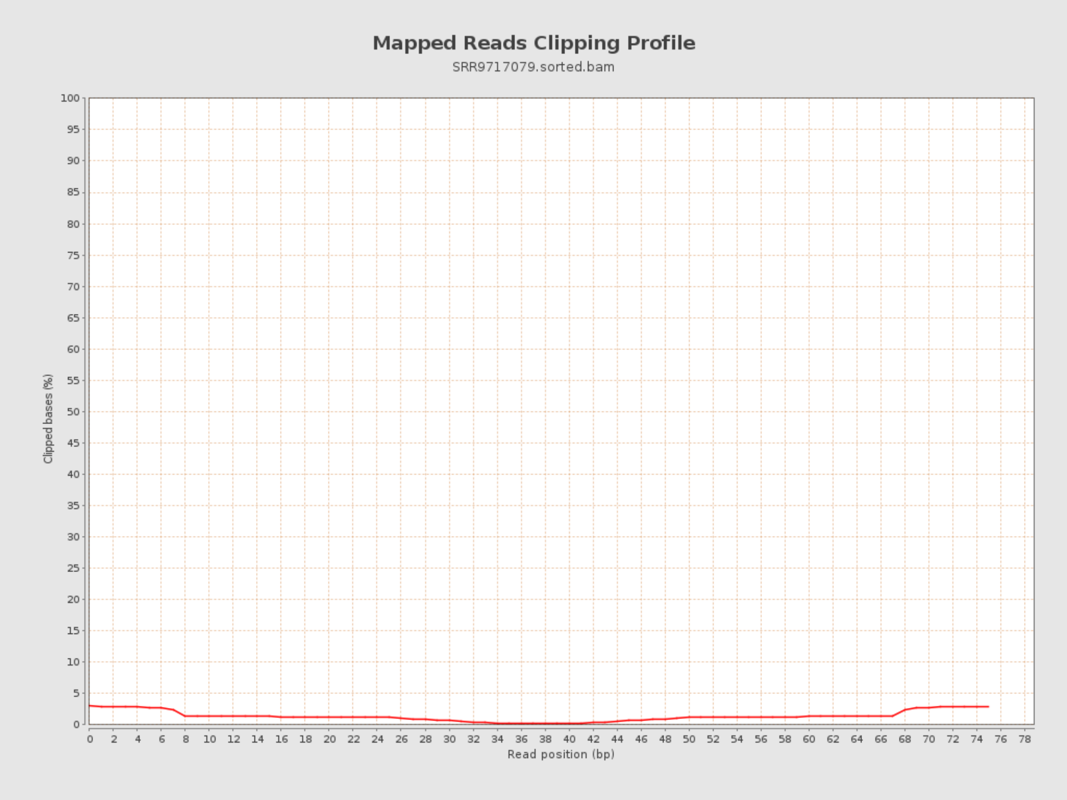
8. Results : Mapped Reads Nucleotide Content



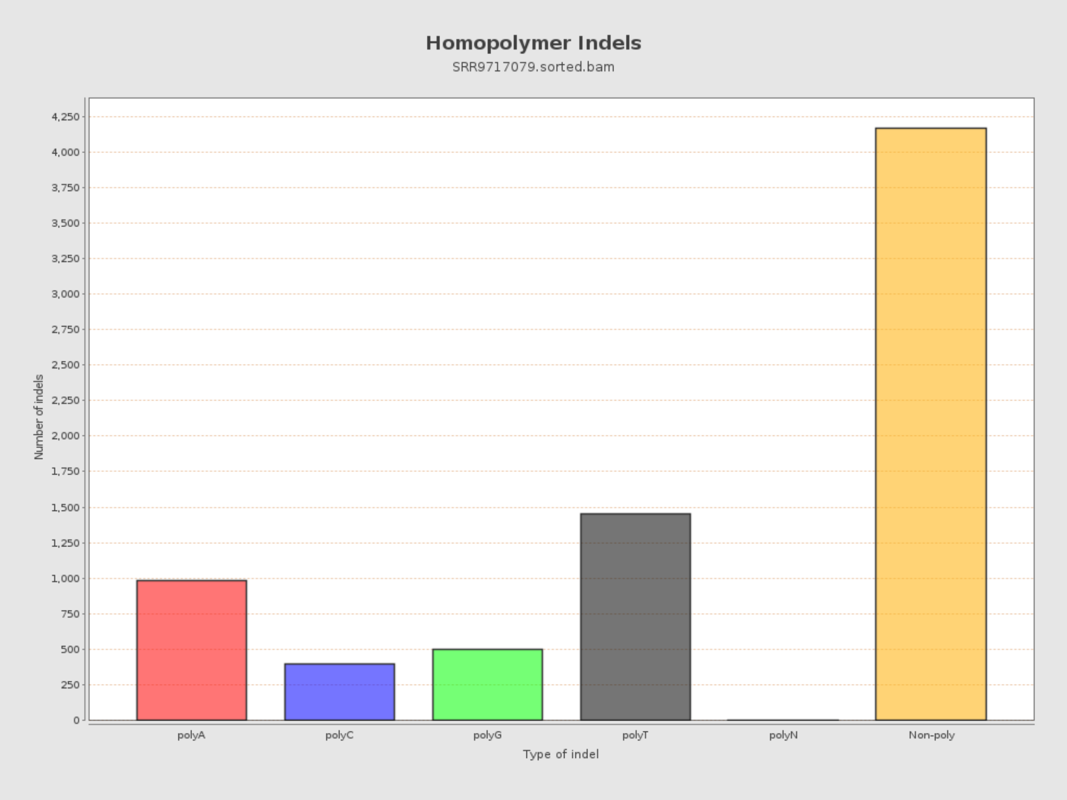
9. Results : Mapped Reads GC-content Distribution



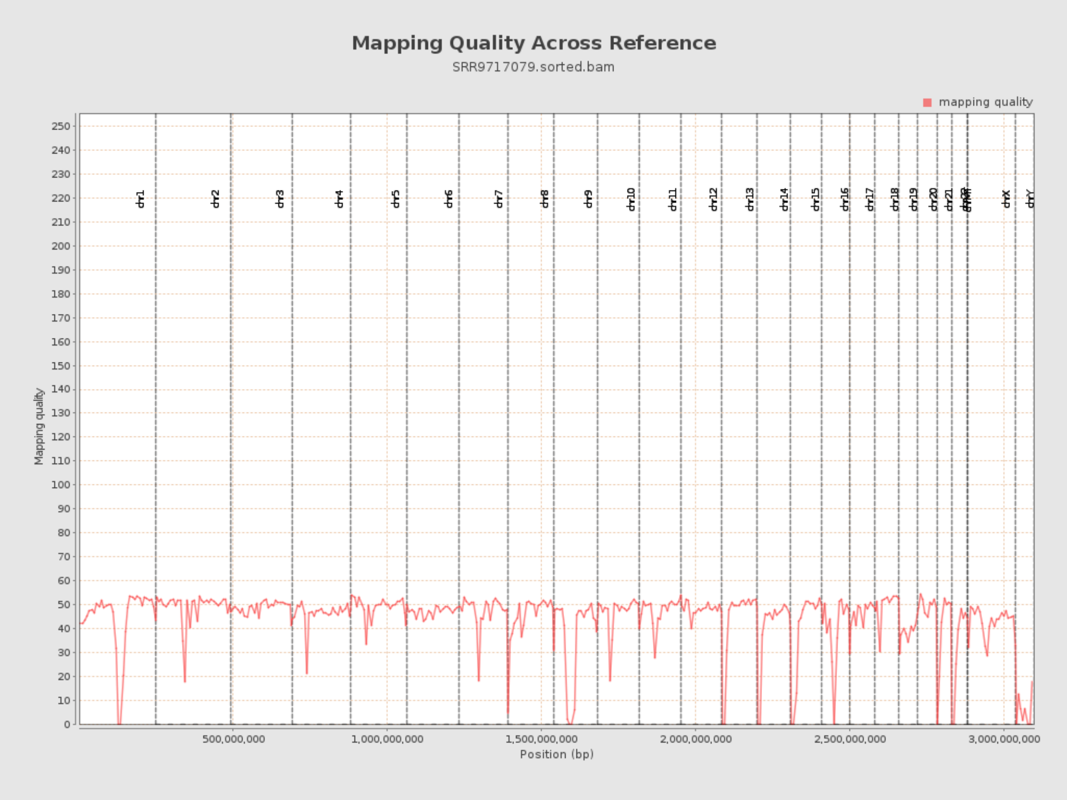
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram