Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:36:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717029.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_SRR9717029 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717029.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:36:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717029.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	439,474
Mapped reads	393,457 / 89.53%
Unmapped reads	46,017 / 10.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,791 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	5,895 / 1.34%
Duplication rate	1.06%
Clipped reads	394,104 / 89.68%

2.2. ACGT Content

Number/percentage of A's	5,959,804 / 25.97%
Number/percentage of C's	4,404,018 / 19.19%
Number/percentage of T's	7,245,134 / 31.57%
Number/percentage of G's	5,340,040 / 23.27%
Number/percentage of N's	308 / 0%
GC Percentage	42.46%

2.3. Coverage

Mean	0.0074

Standard Deviation	0.1057

2.4. Mapping Quality

Mean Mapping Quality	44.59

2.5. Mismatches and indels

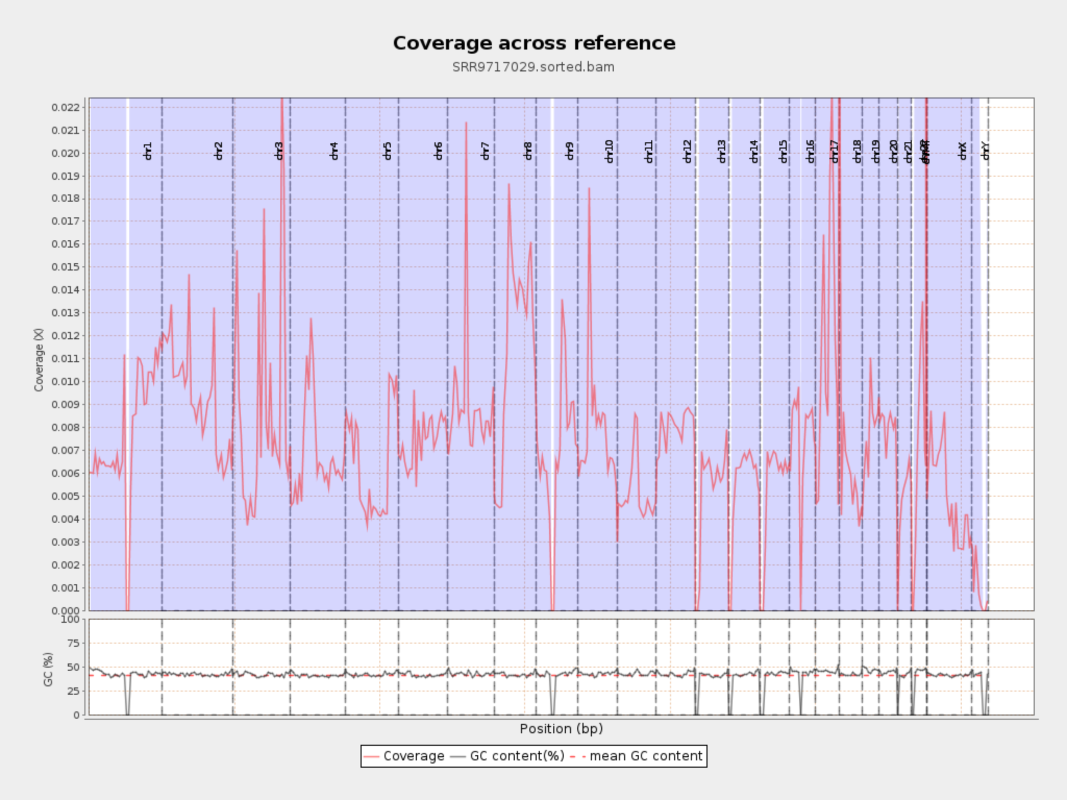
General error rate	0.51%
Mismatches	114,027
Insertions	1,753
Mapped reads with at least one insertion	0.44%
Deletions	4,392
Mapped reads with at least one deletion	1.11%
Homopolymer indels	39.8%

2.6. Chromosome stats

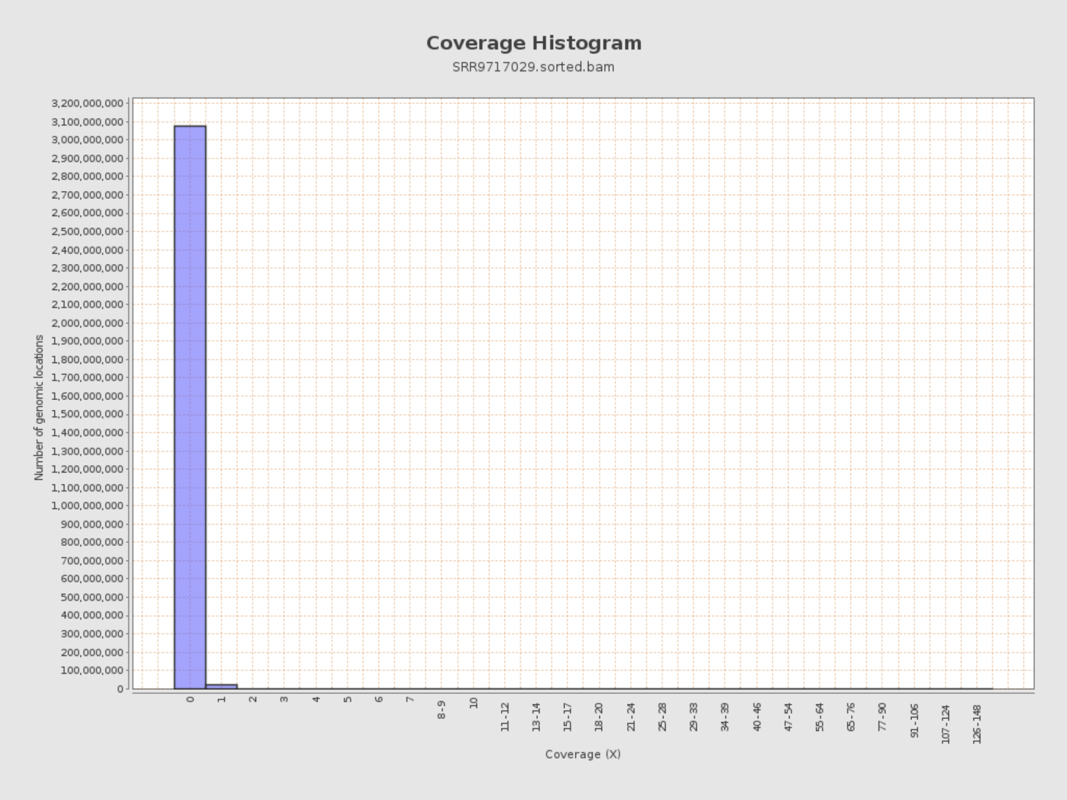
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1910343	0.0077	0.1302
chr2	243199373	2299676	0.0095	0.1182
chr3	198022430	1746120	0.0088	0.0976
chr4	191154276	1309387	0.0068	0.0874
chr5	180915260	1145862	0.0063	0.0813
chr6	171115067	1279164	0.0075	0.0901
chr7	159138663	1440879	0.0091	0.1948

chr8	146364022	1731071	0.0118	0.1256
chr9	141213431	962365	0.0068	0.0893
chr10	135534747	1080681	0.008	0.12
chr11	135006516	686370	0.0051	0.0782
chr12	133851895	1077077	0.008	0.0954
chr13	115169878	604173	0.0052	0.074
chr14	107349540	582387	0.0054	0.0754
chr15	102531392	542791	0.0053	0.0748
chr16	90354753	683743	0.0076	0.0911
chr17	81195210	935226	0.0115	0.111
chr18	78077248	529476	0.0068	0.1056
chr19	59128983	462194	0.0078	0.1231
chr20	63025520	506391	0.008	0.0931
chr21	48129895	229822	0.0048	0.072
chr22	51304566	337083	0.0066	0.083
chrMT	16571	25925	1.5645	1.4649
chrX	155270560	795457	0.0051	0.0771
chrY	59373566	52444	0.0009	0.0355

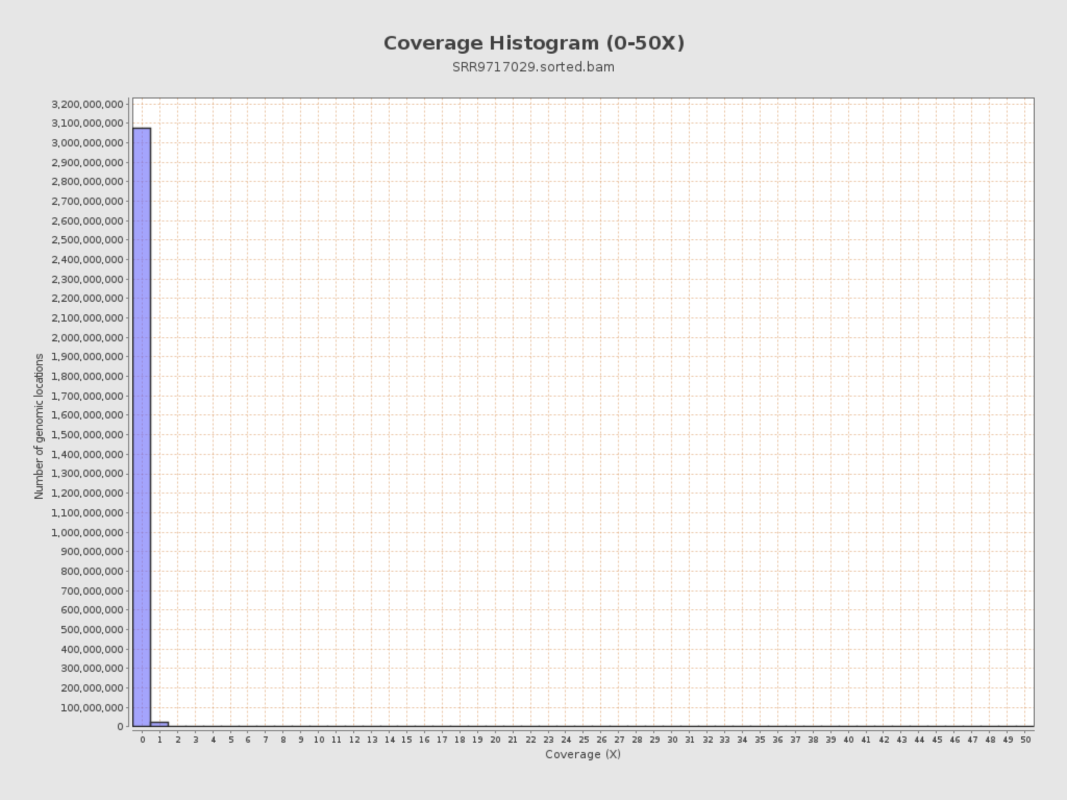
3. Results : Coverage across reference



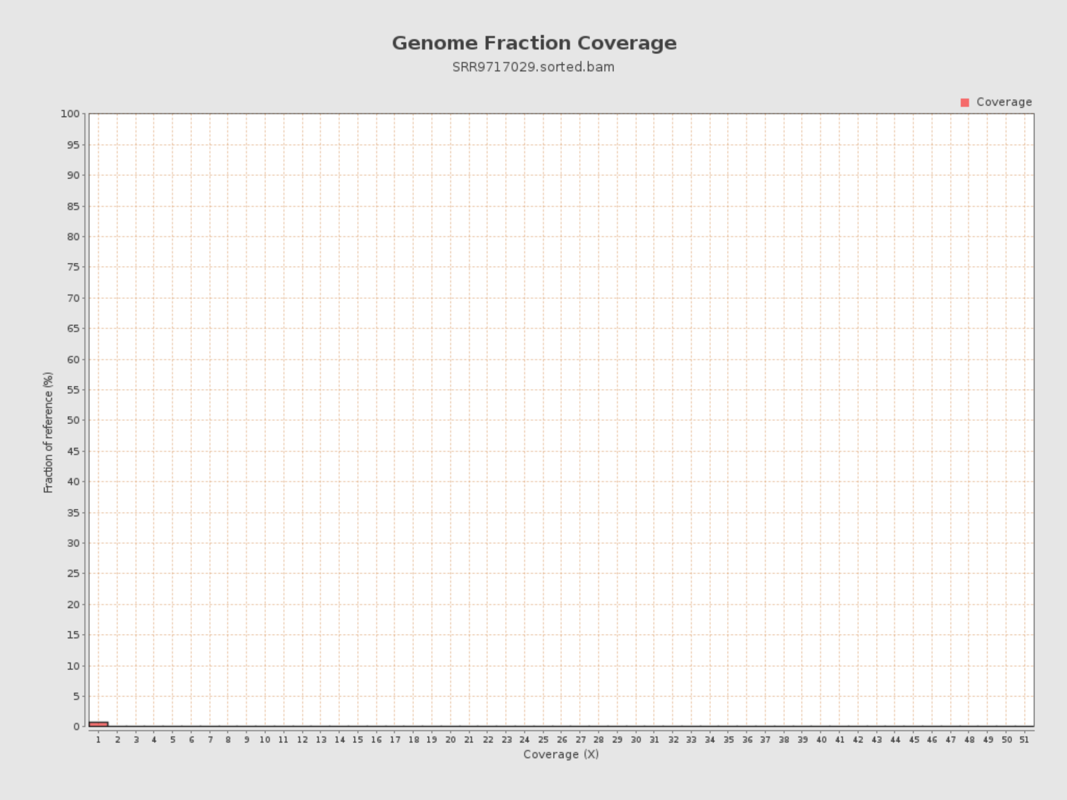
4. Results : Coverage Histogram



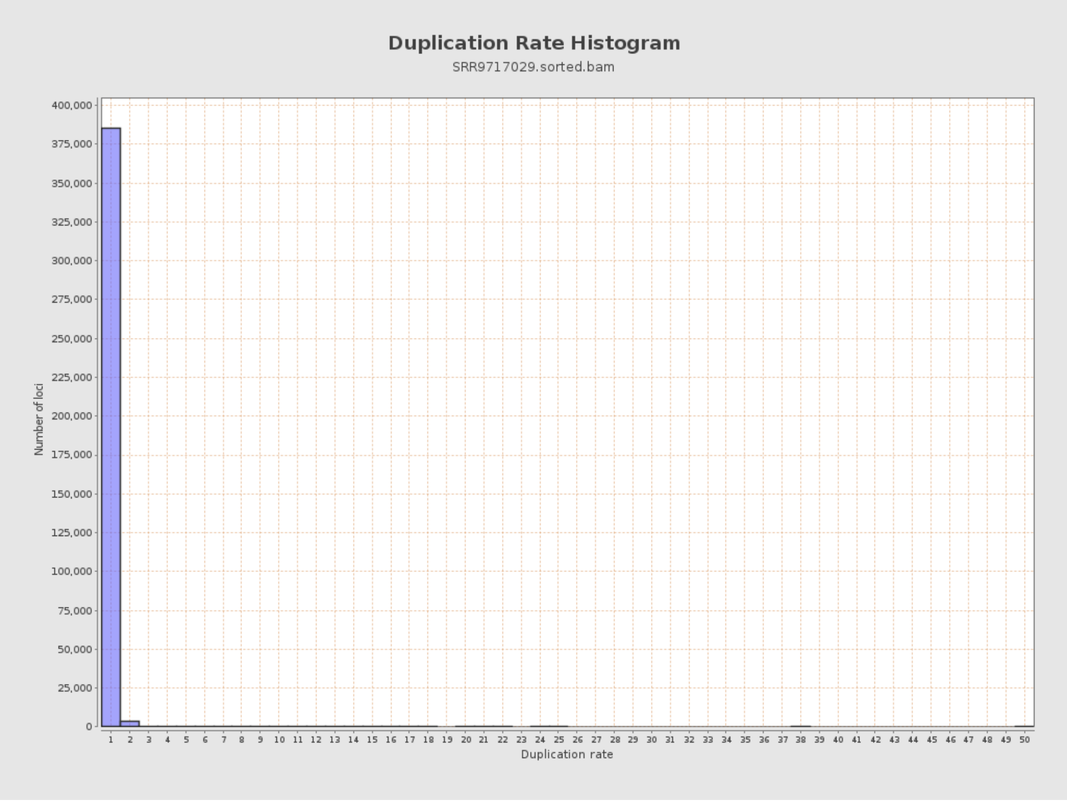
5. Results : Coverage Histogram (0-50X)



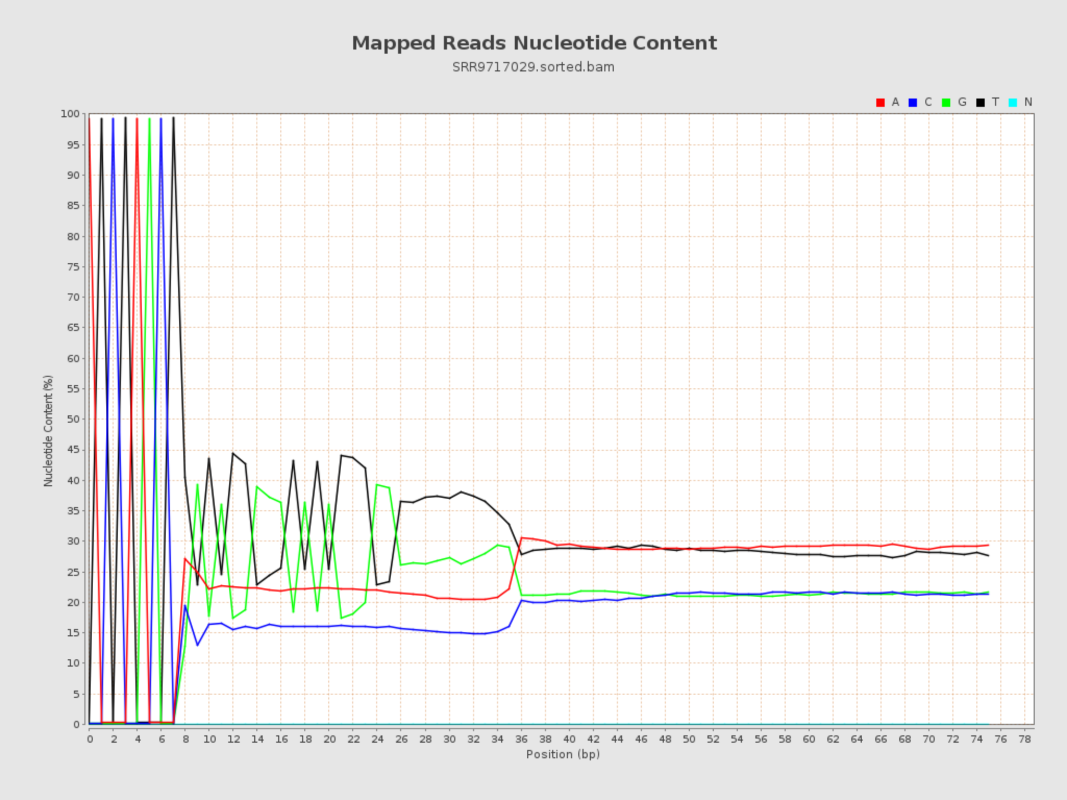
6. Results : Genome Fraction Coverage



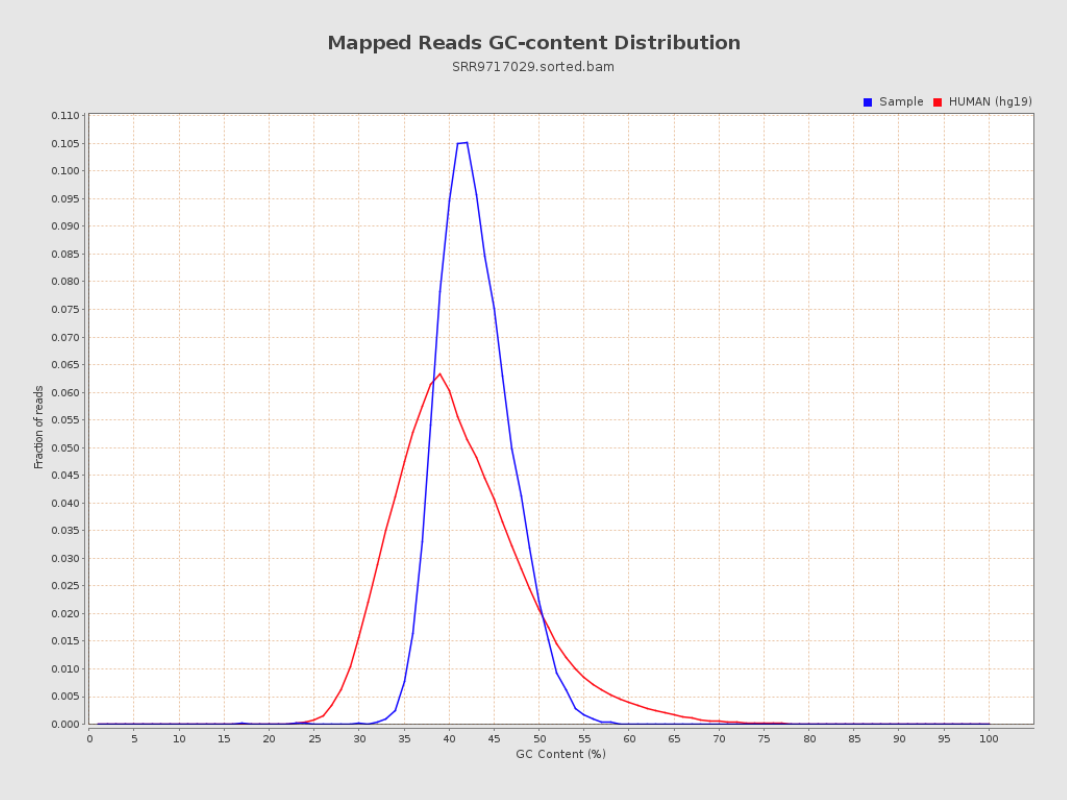
7. Results : Duplication Rate Histogram



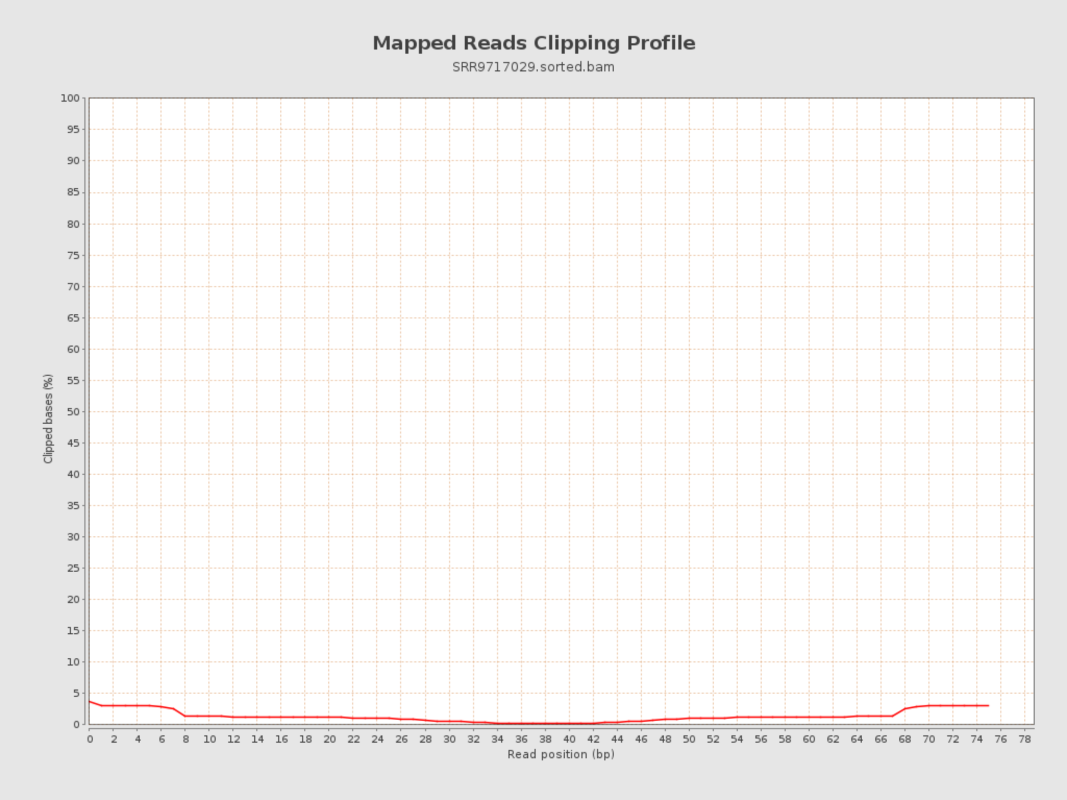
8. Results : Mapped Reads Nucleotide Content



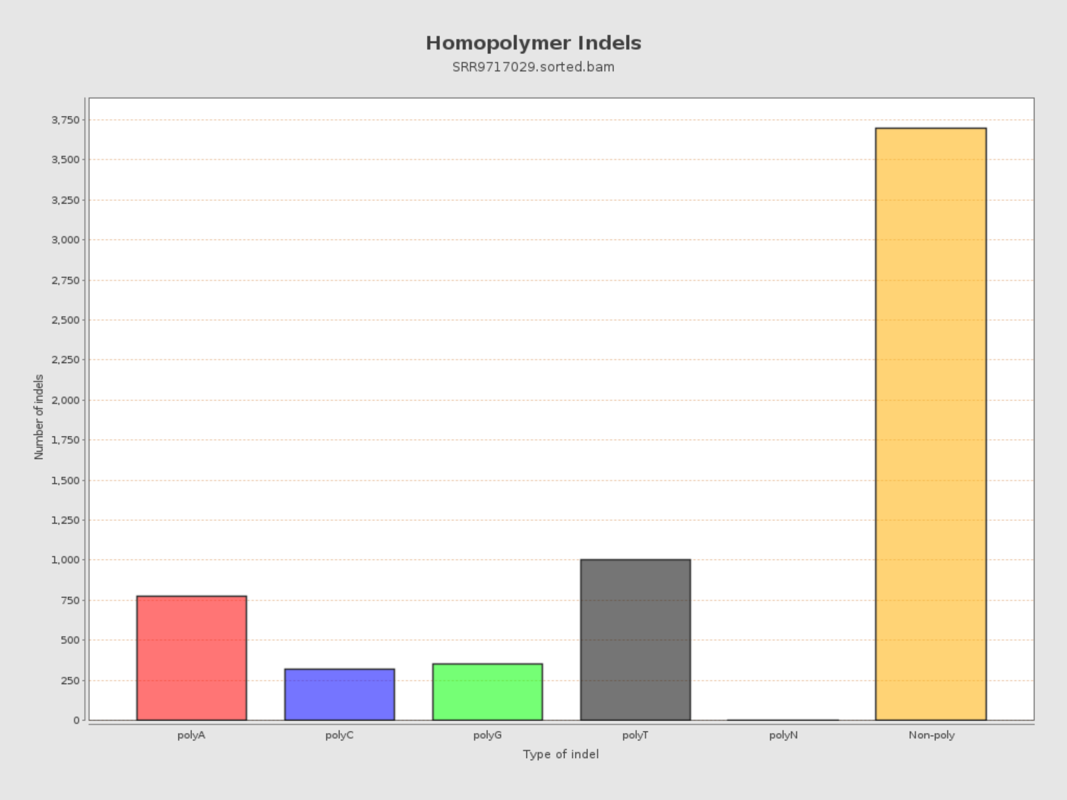
9. Results : Mapped Reads GC-content Distribution



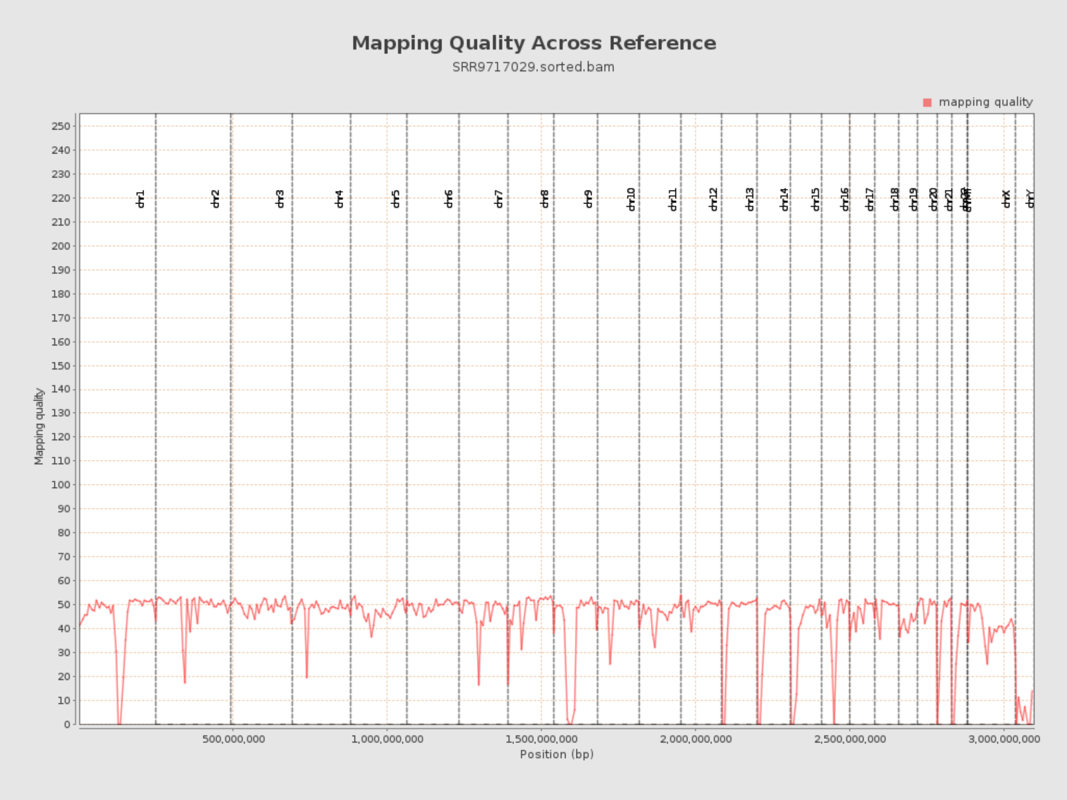
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram