Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 05:02:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717082.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_SRR9717082 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717082.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 05:02:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717082.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	428,506
Mapped reads	380,076 / 88.7%
Unmapped reads	48,430 / 11.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,644 / 1.32%
Read min/max/mean length	30 / 101 / 101.48
Duplicated reads (estimated)	8,881 / 2.07%
Duplication rate	1.43%
Clipped reads	385,080 / 89.87%

2.2. ACGT Content

Number/percentage of A's	7,424,465 / 25.12%
Number/percentage of C's	5,600,799 / 18.95%
Number/percentage of T's	9,345,450 / 31.62%
Number/percentage of G's	7,183,165 / 24.3%
Number/percentage of N's	1,843 / 0.01%
GC Percentage	43.25%

2.3. Coverage

Mean	0.0096

Standard Deviation	0.1389

2.4. Mapping Quality

Mean Mapping Quality	44.14

2.5. Mismatches and indels

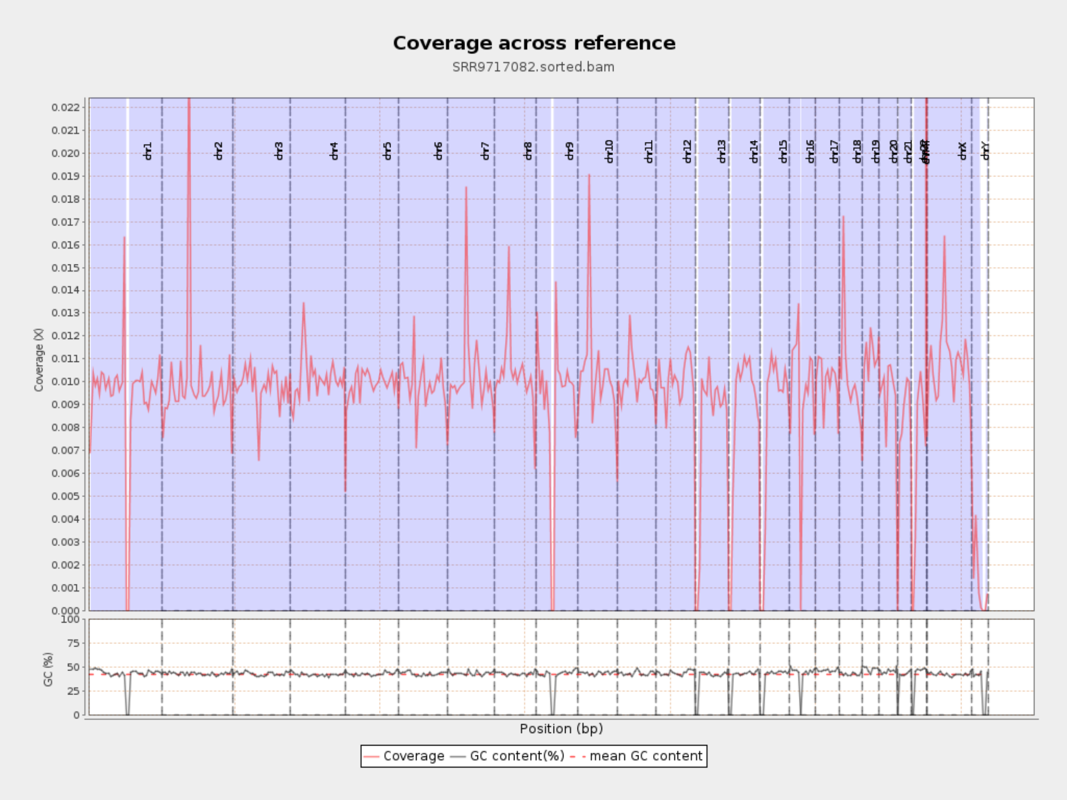
General error rate	0.92%
Mismatches	265,942
Insertions	2,823
Mapped reads with at least one insertion	0.73%
Deletions	7,358
Mapped reads with at least one deletion	1.91%
Homopolymer indels	42.22%

2.6. Chromosome stats

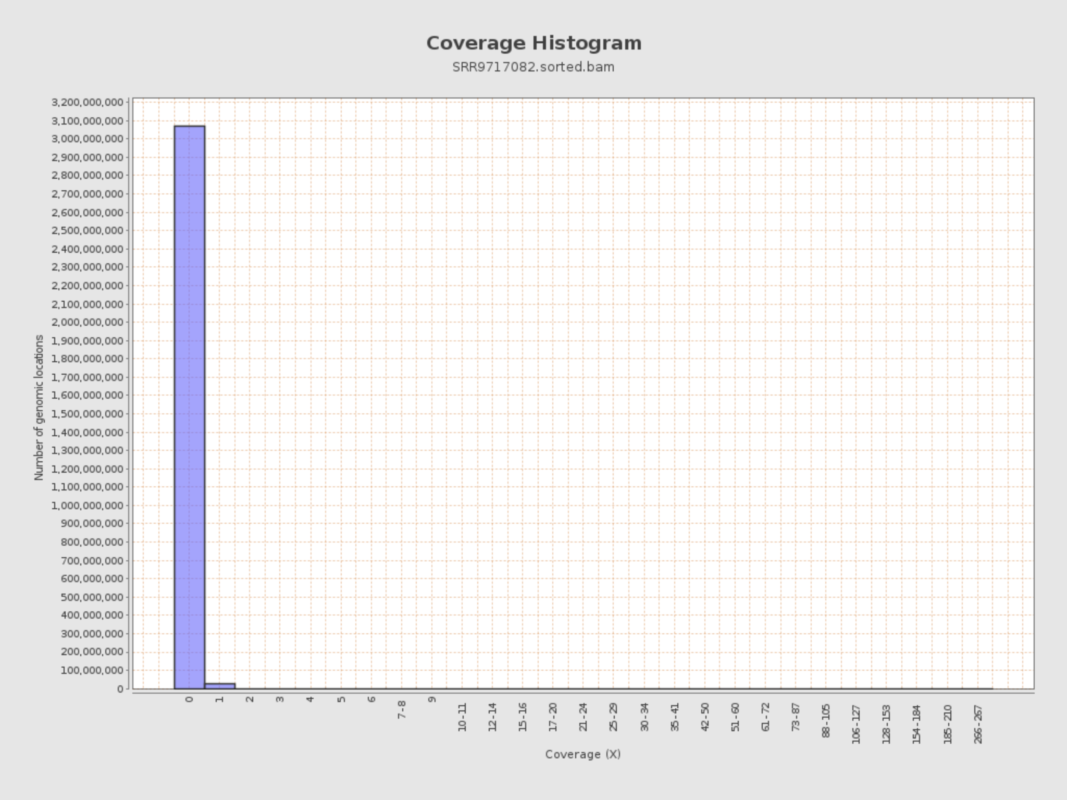
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2327422	0.0093	0.1802
chr2	243199373	2454265	0.0101	0.1995
chr3	198022430	1936904	0.0098	0.103
chr4	191154276	1938222	0.0101	0.1065
chr5	180915260	1798950	0.0099	0.1043
chr6	171115067	1691365	0.0099	0.1136
chr7	159138663	1645165	0.0103	0.1621

chr8	146364022	1515602	0.0104	0.1797
chr9	141213431	1265312	0.009	0.144
chr10	135534747	1418782	0.0105	0.1365
chr11	135006516	1354143	0.01	0.134
chr12	133851895	1345755	0.0101	0.1052
chr13	115169878	908549	0.0079	0.092
chr14	107349540	914948	0.0085	0.1069
chr15	102531392	844561	0.0082	0.0953
chr16	90354753	859772	0.0095	0.106
chr17	81195210	813278	0.01	0.1068
chr18	78077248	814154	0.0104	0.2444
chr19	59128983	649093	0.011	0.1615
chr20	63025520	595797	0.0095	0.1053
chr21	48129895	376150	0.0078	0.0946
chr22	51304566	325226	0.0063	0.0822
chrMT	16571	1747	0.1054	0.341
chrX	155270560	1697003	0.0109	0.1233
chrY	59373566	76487	0.0013	0.0453

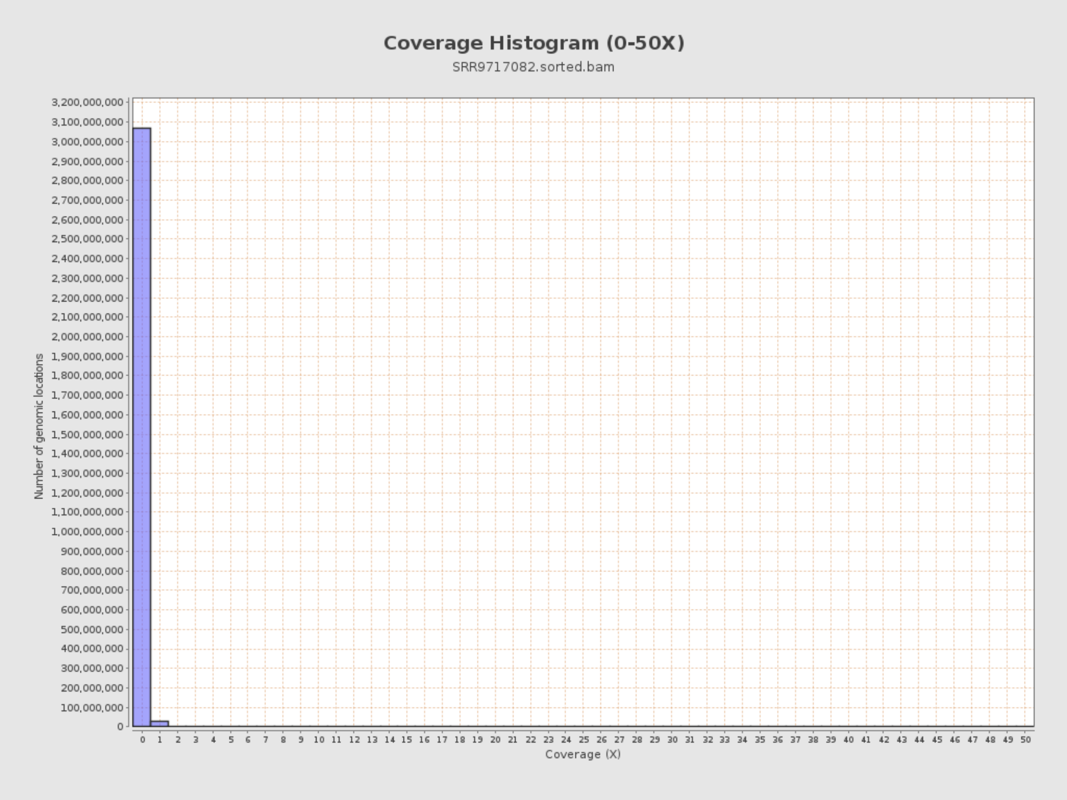
3. Results : Coverage across reference



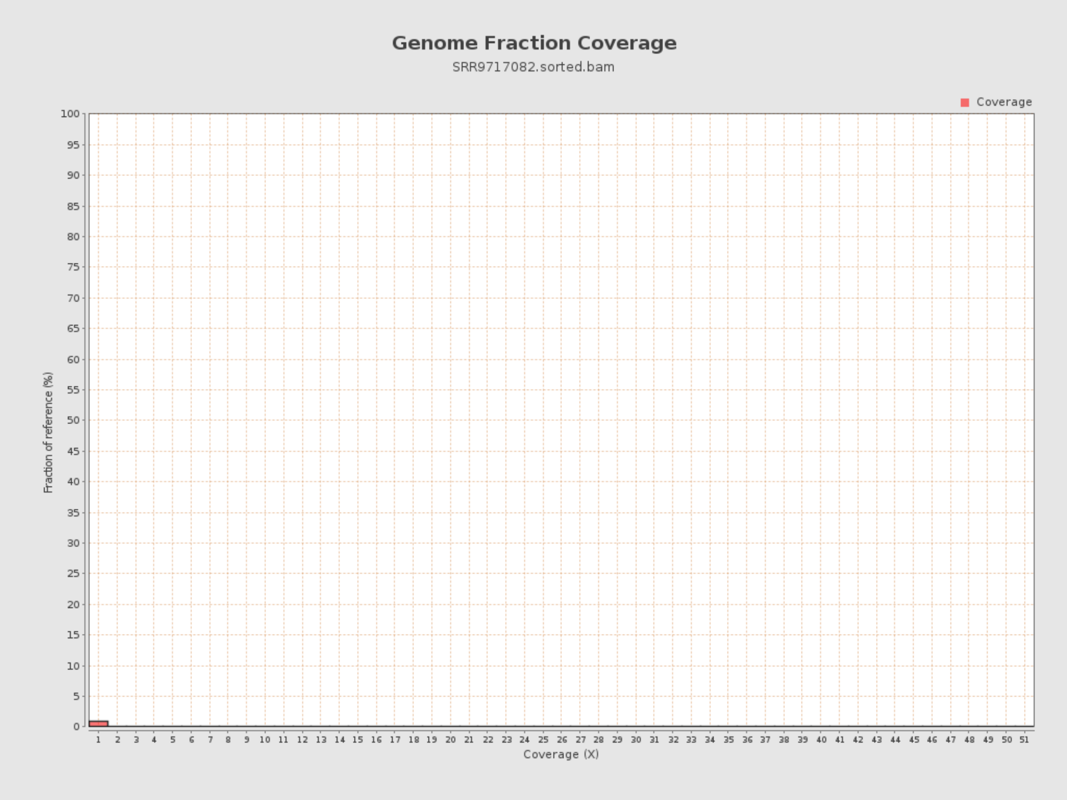
4. Results : Coverage Histogram



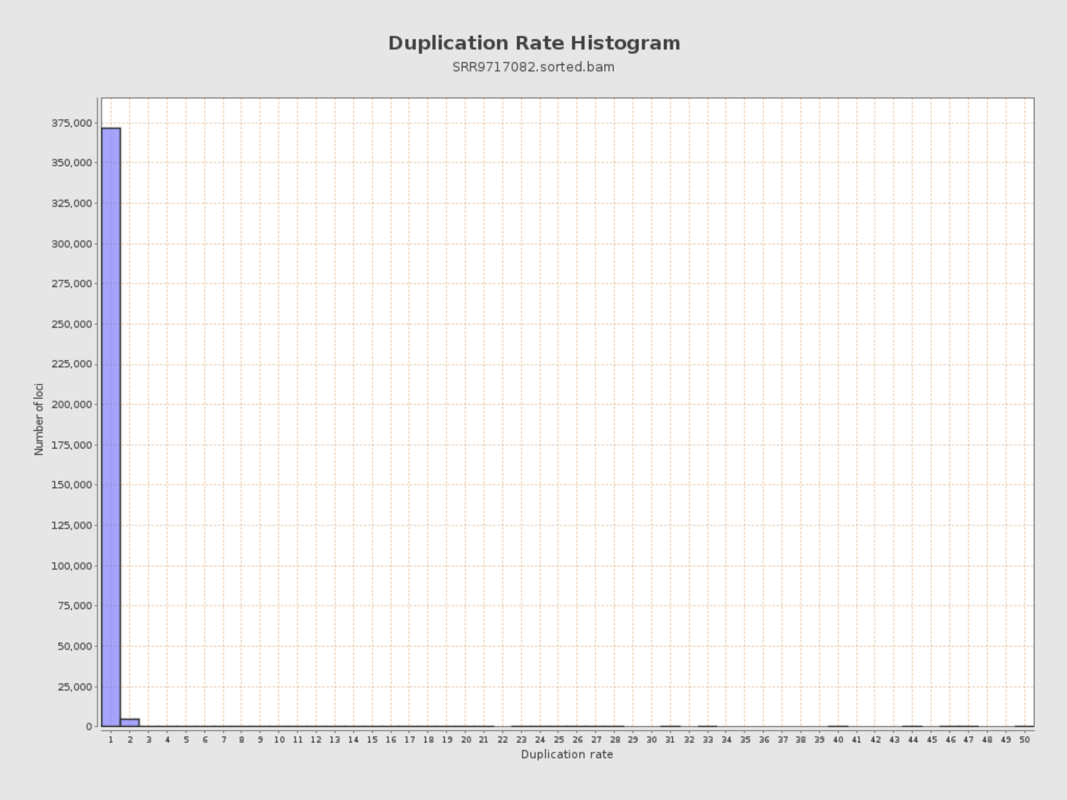
5. Results : Coverage Histogram (0-50X)



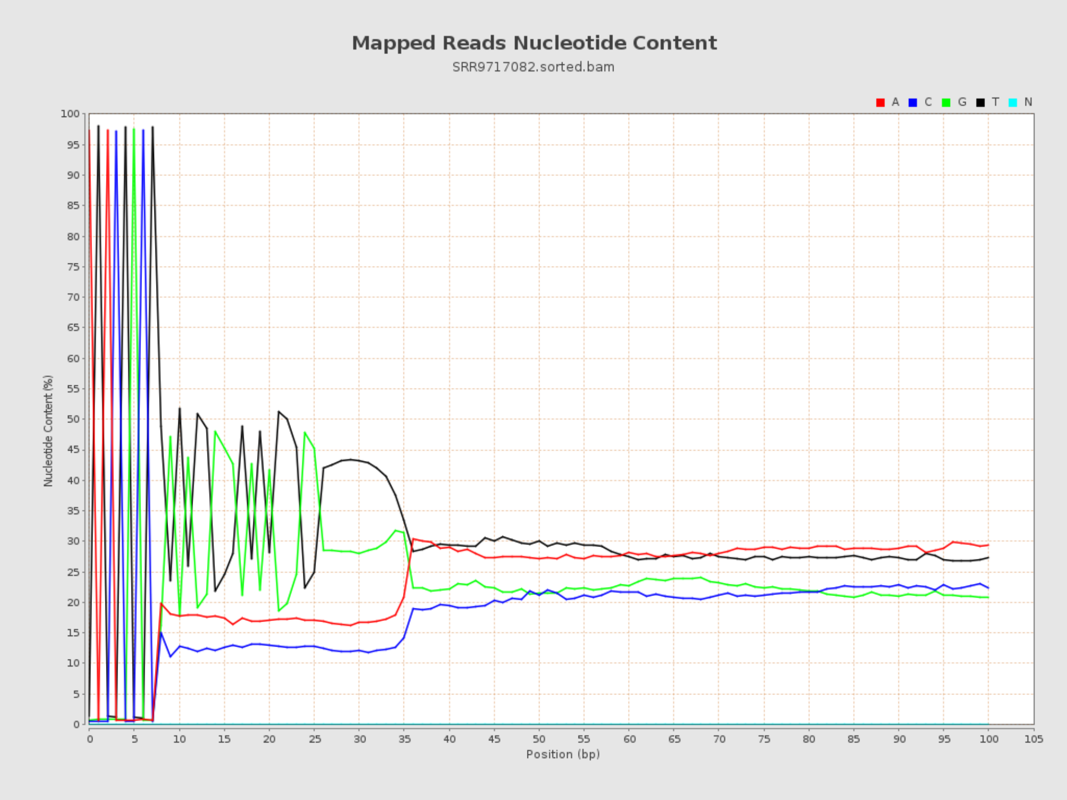
6. Results : Genome Fraction Coverage



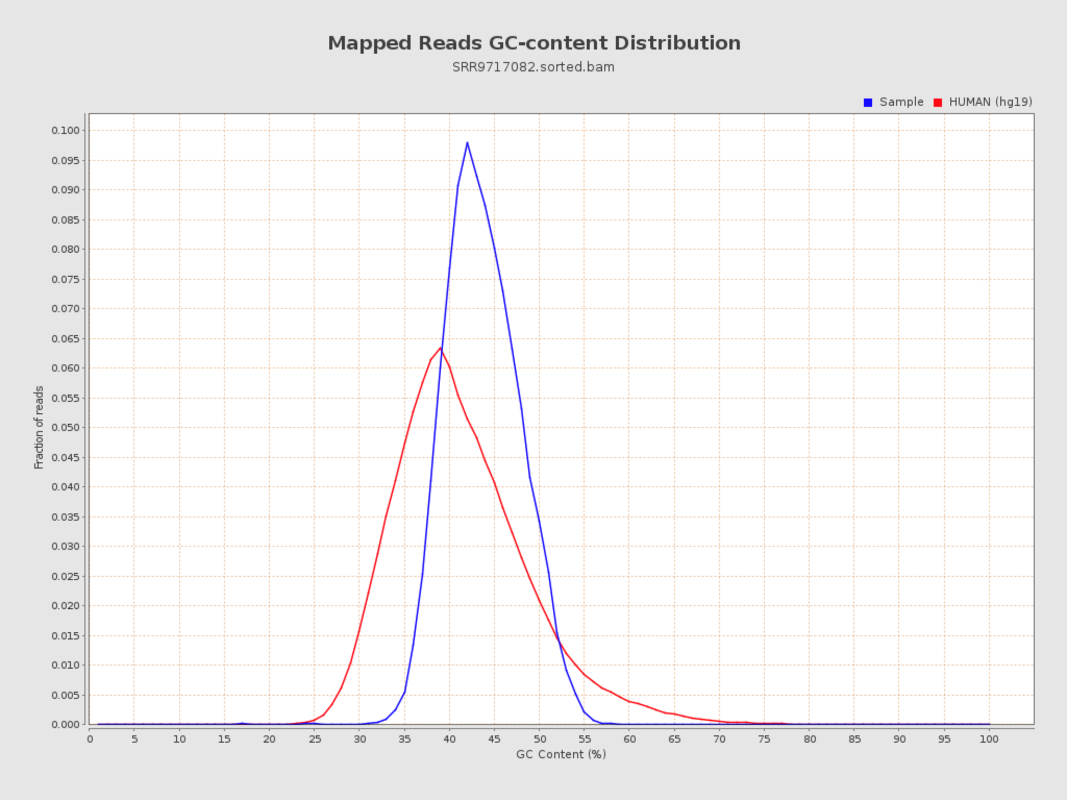
7. Results : Duplication Rate Histogram



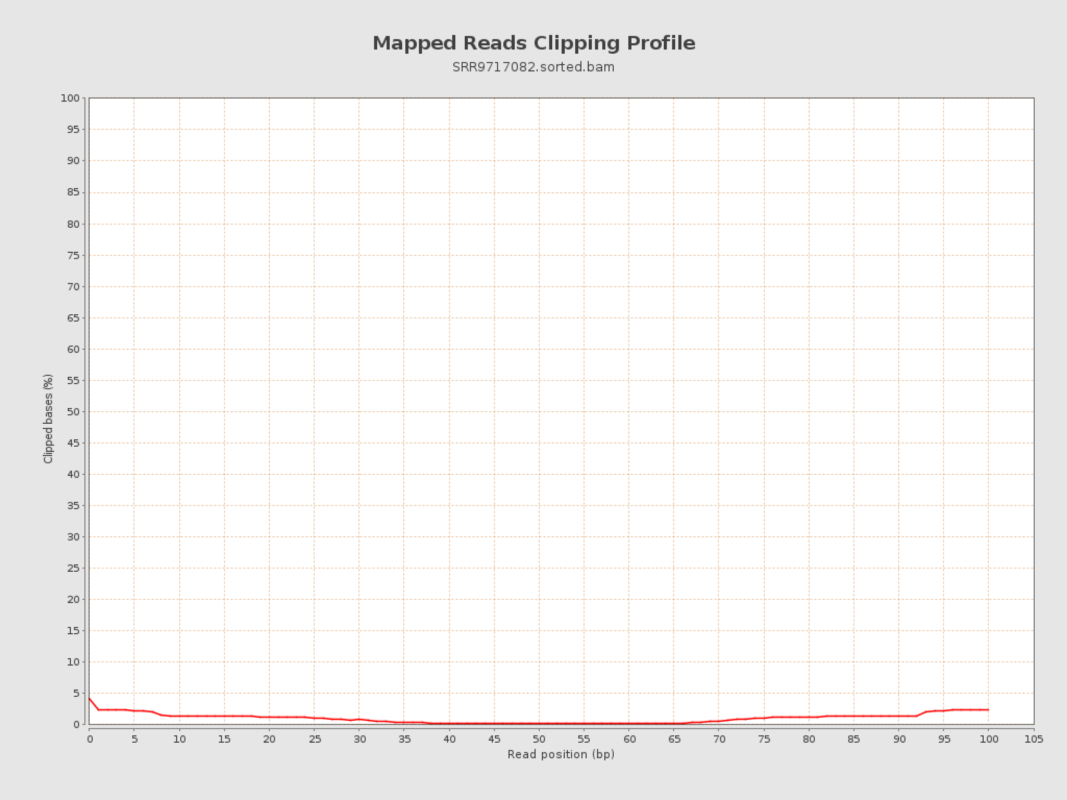
8. Results : Mapped Reads Nucleotide Content



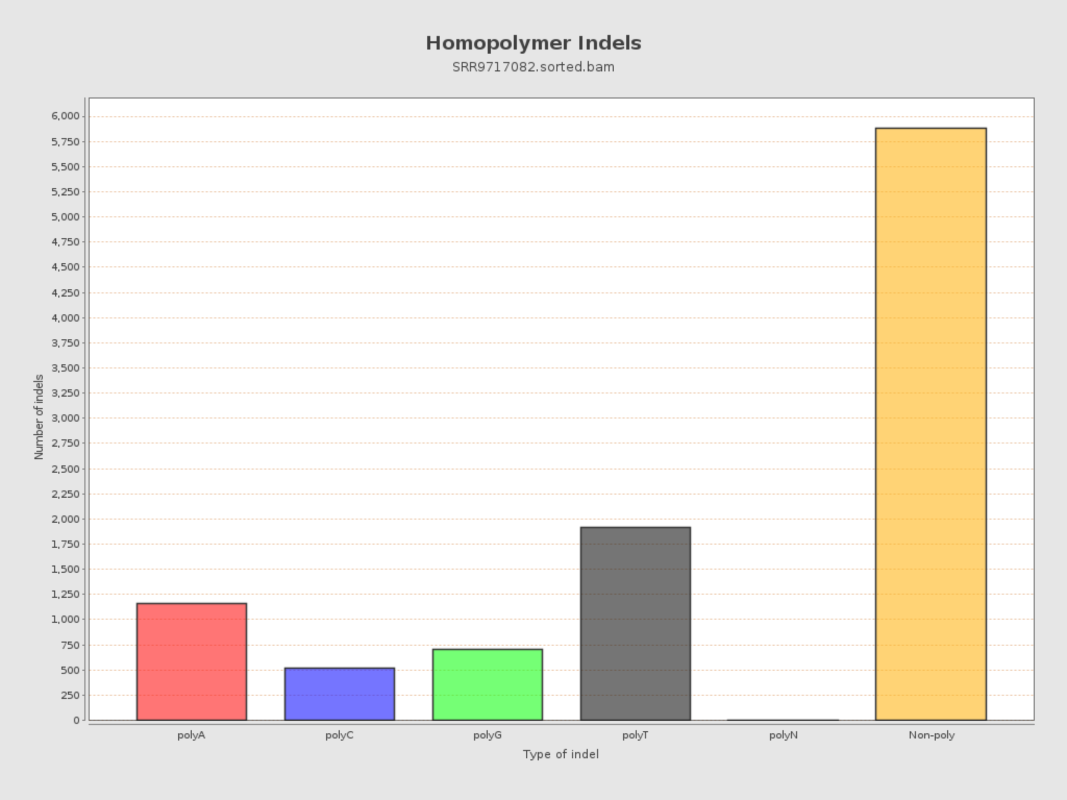
9. Results : Mapped Reads GC-content Distribution



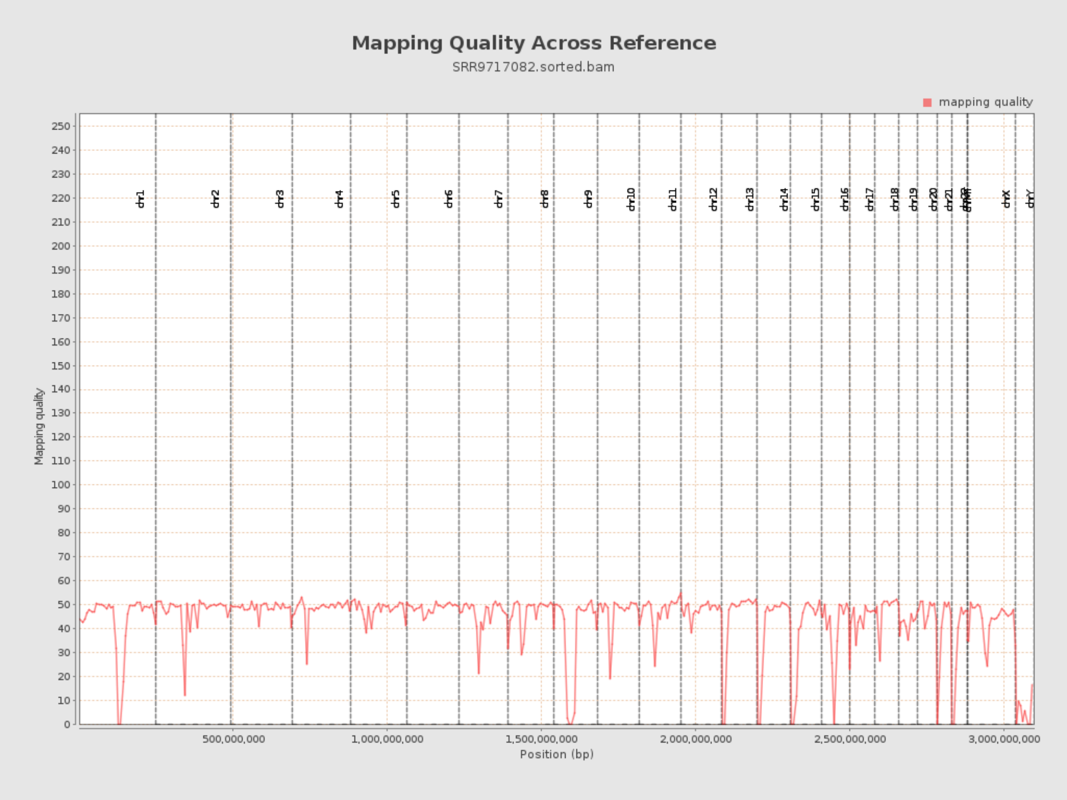
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram