Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 02:45:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717047.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_SRR9717047 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717047.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 02:45:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717047.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	786,941
Mapped reads	634,736 / 80.66%
Unmapped reads	152,205 / 19.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,472 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	10,685 / 1.36%
Duplication rate	1.17%
Clipped reads	635,598 / 80.77%

2.2. ACGT Content

Number/percentage of A's	8,182,269 / 23.22%
Number/percentage of C's	7,787,360 / 22.09%
Number/percentage of T's	10,575,519 / 30.01%
Number/percentage of G's	8,698,812 / 24.68%
Number/percentage of N's	956 / 0%
GC Percentage	46.78%

2.3. Coverage

Mean	0.0114

Standard Deviation	0.1269

2.4. Mapping Quality

Mean Mapping Quality	38.73

2.5. Mismatches and indels

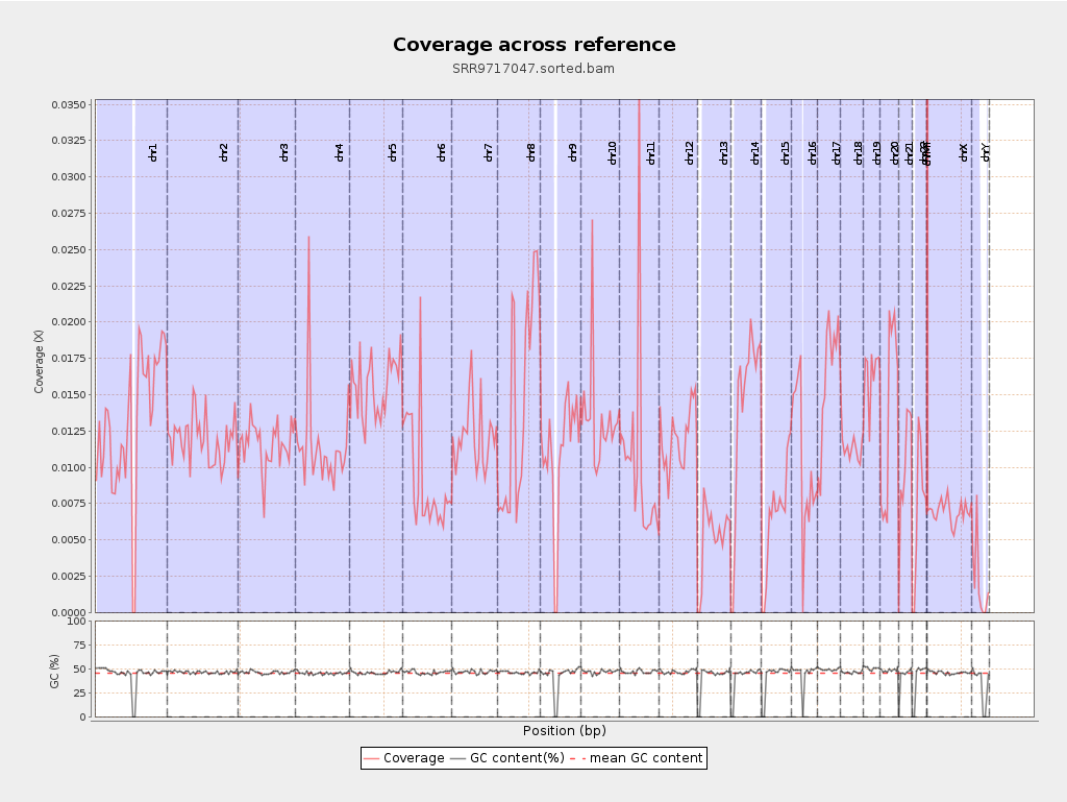
General error rate	0.56%
Mismatches	191,322
Insertions	3,037
Mapped reads with at least one insertion	0.47%
Deletions	6,268
Mapped reads with at least one deletion	0.98%
Homopolymer indels	34.55%

2.6. Chromosome stats

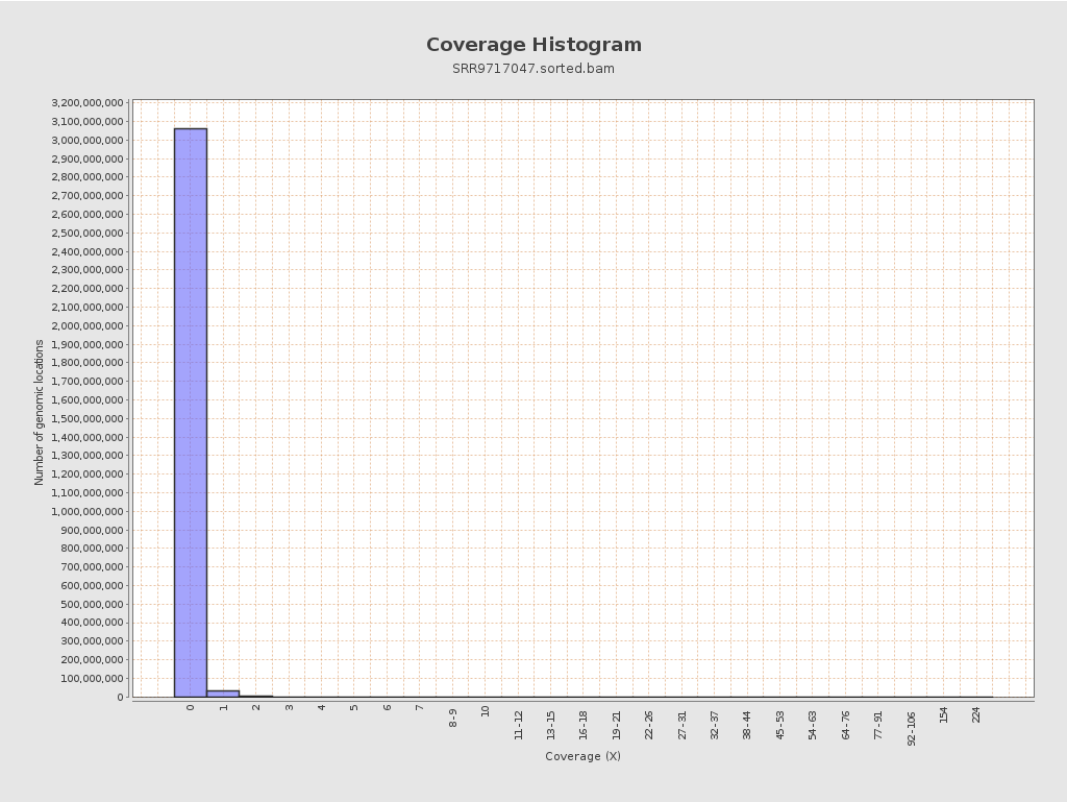
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3271429	0.0131	0.1451
chr2	243199373	2892945	0.0119	0.1561
chr3	198022430	2288336	0.0116	0.1156
chr4	191154276	2203064	0.0115	0.1263
chr5	180915260	2845955	0.0157	0.133
chr6	171115067	1557145	0.0091	0.1026
chr7	159138663	1933774	0.0122	0.1361

chr8	146364022	2109238	0.0144	0.1319
chr9	141213431	1540858	0.0109	0.1172
chr10	135534747	1813842	0.0134	0.1751
chr11	135006516	1411067	0.0105	0.1244
chr12	133851895	1603712	0.012	0.1155
chr13	115169878	588583	0.0051	0.0759
chr14	107349540	1512946	0.0141	0.1271
chr15	102531392	682522	0.0067	0.0875
chr16	90354753	919767	0.0102	0.1127
chr17	81195210	1314645	0.0162	0.1393
chr18	78077248	884573	0.0113	0.1336
chr19	59128983	962972	0.0163	0.1524
chr20	63025520	857007	0.0136	0.1282
chr21	48129895	481281	0.01	0.1127
chr22	51304566	373516	0.0073	0.0922
chrMT	16571	6299	0.3801	0.6798
chrX	155270560	1079071	0.0069	0.0948
chrY	59373566	121102	0.002	0.0725

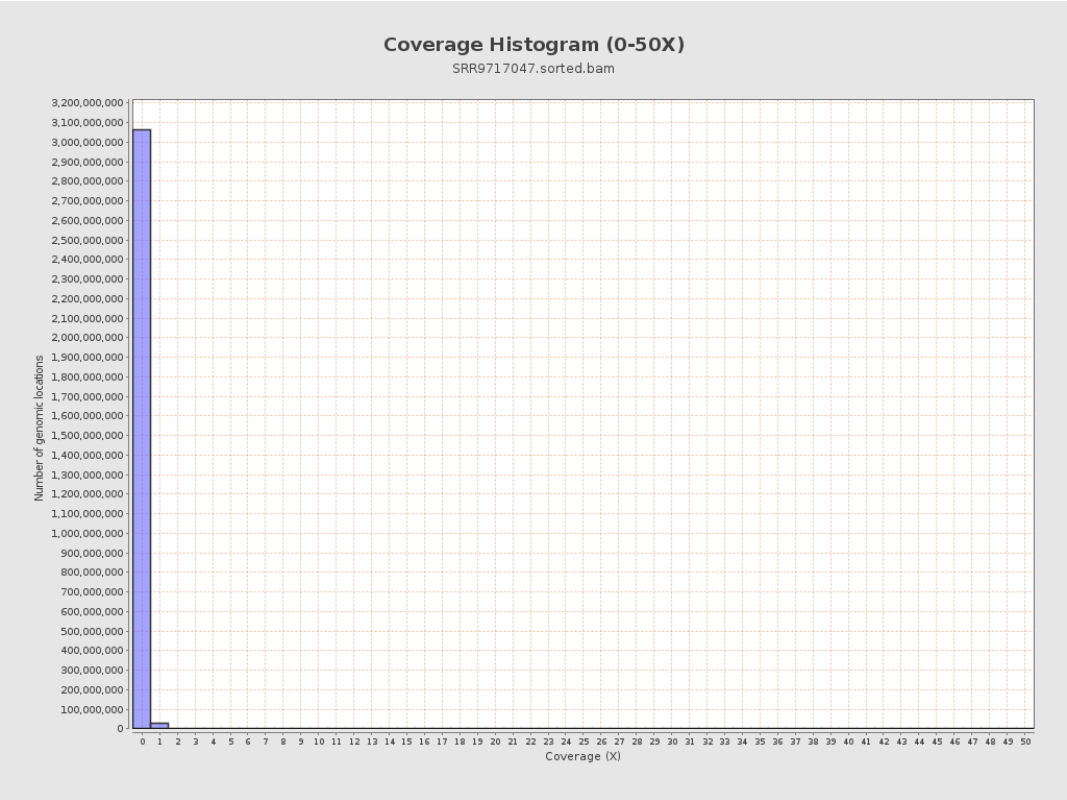
3. Results : Coverage across reference



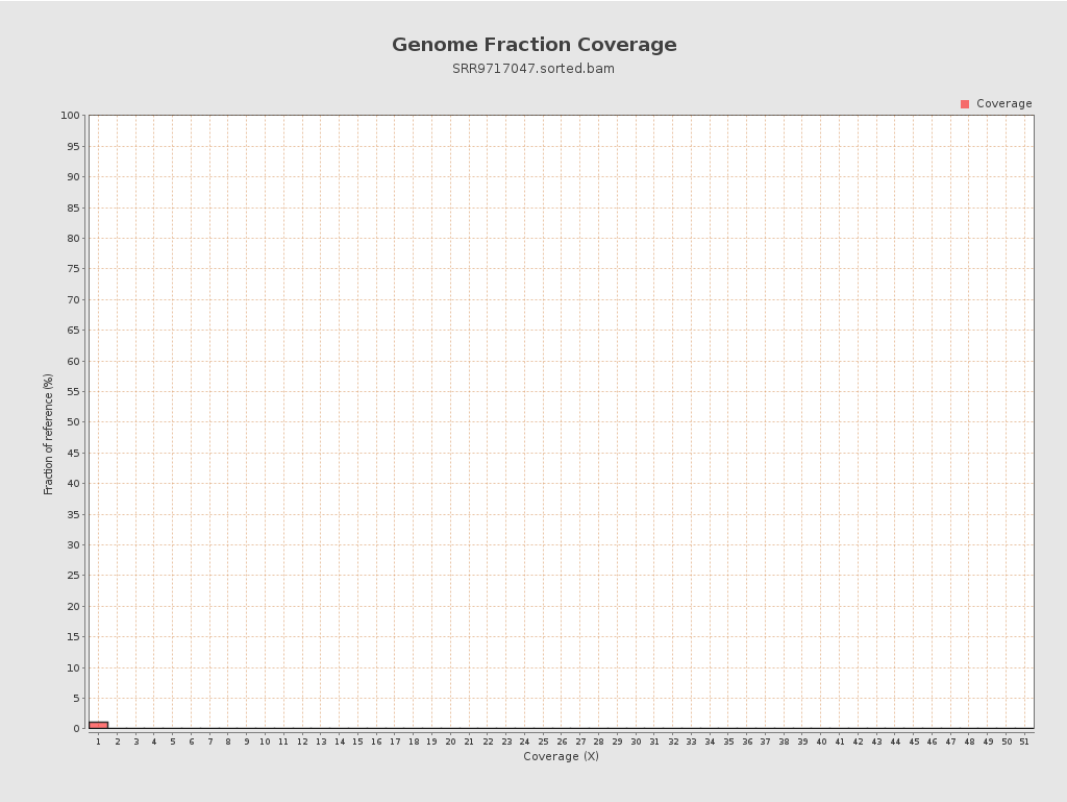
4. Results : Coverage Histogram



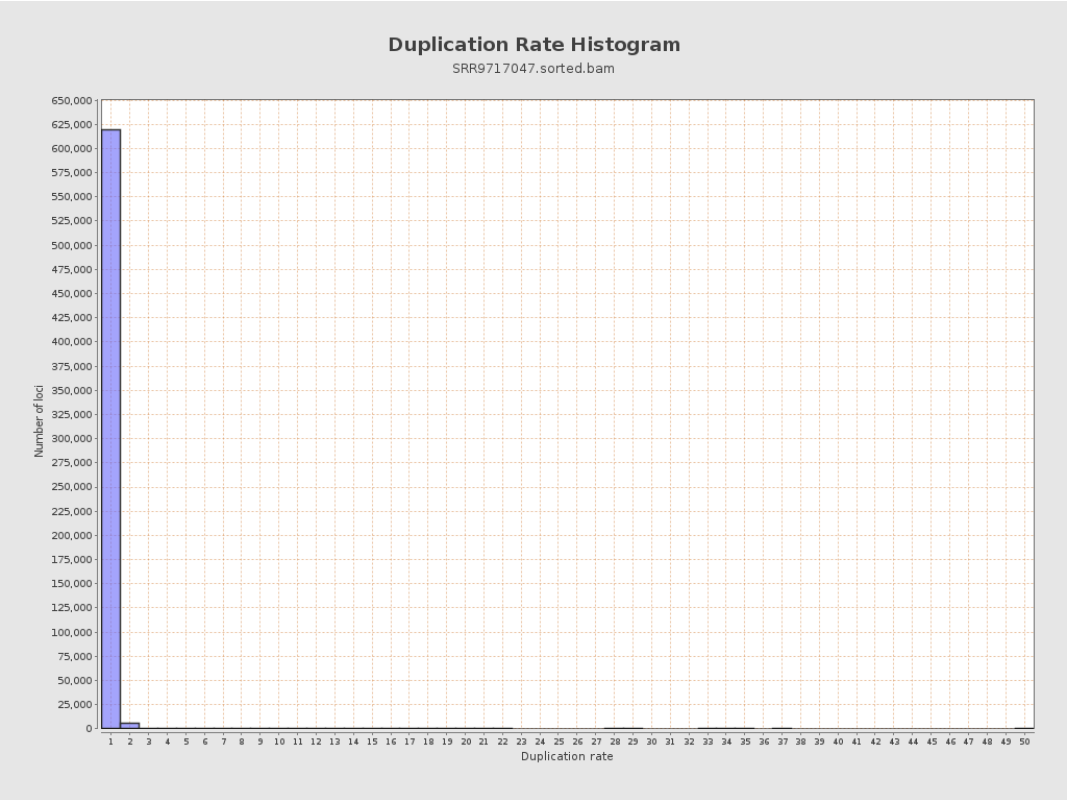
5. Results : Coverage Histogram (0-50X)



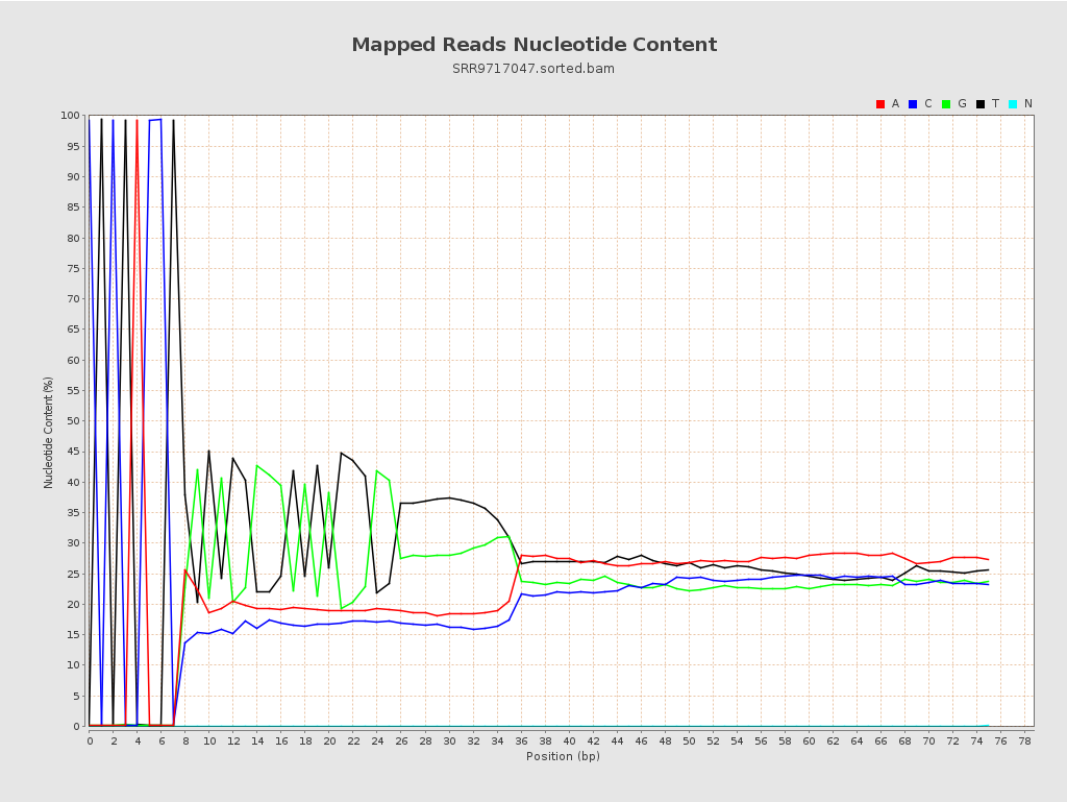
6. Results : Genome Fraction Coverage



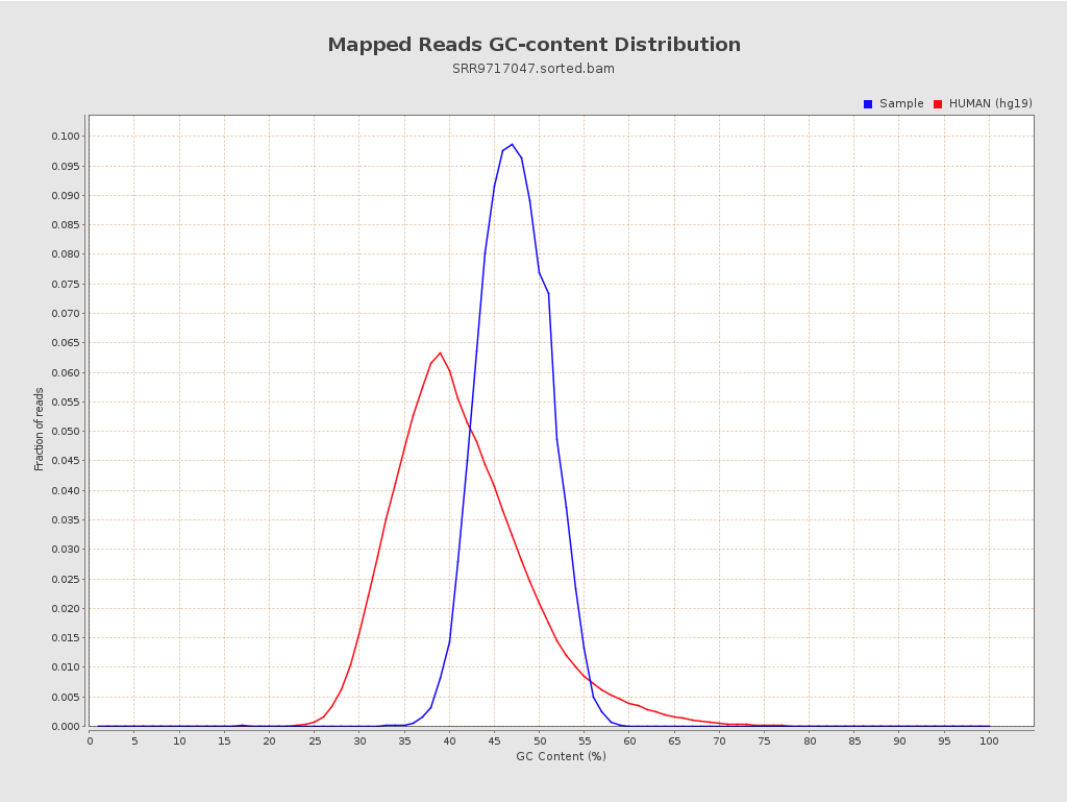
7. Results : Duplication Rate Histogram



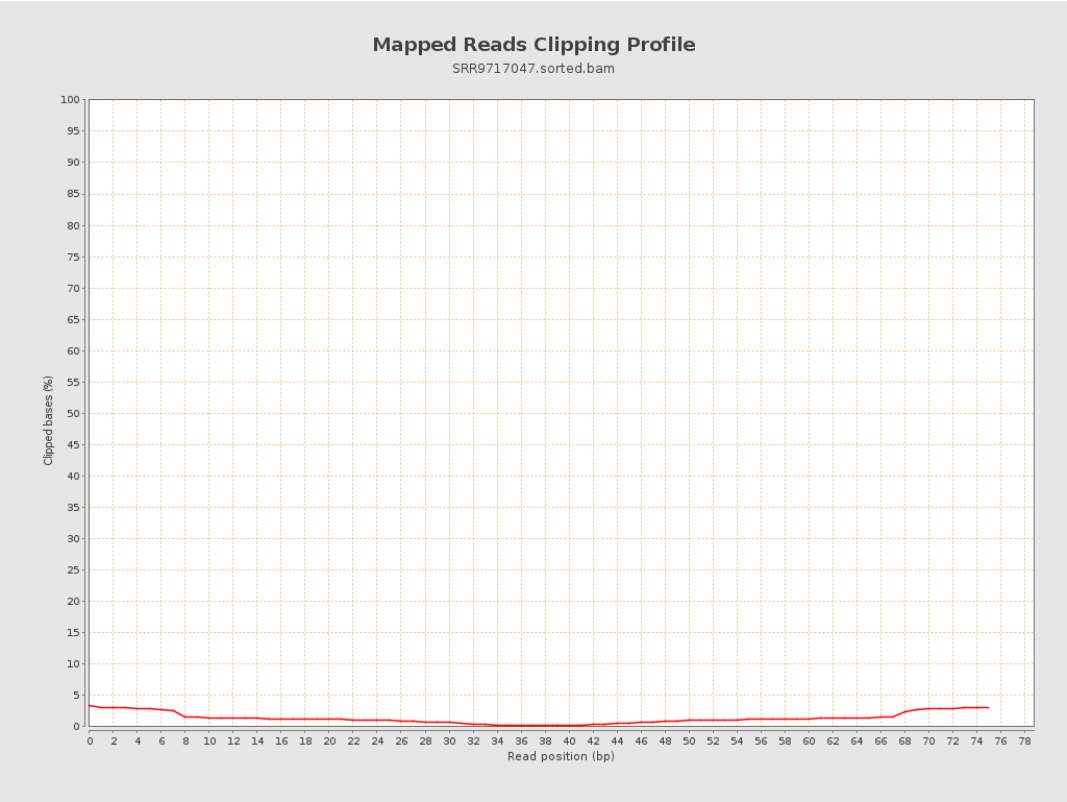
8. Results : Mapped Reads Nucleotide Content



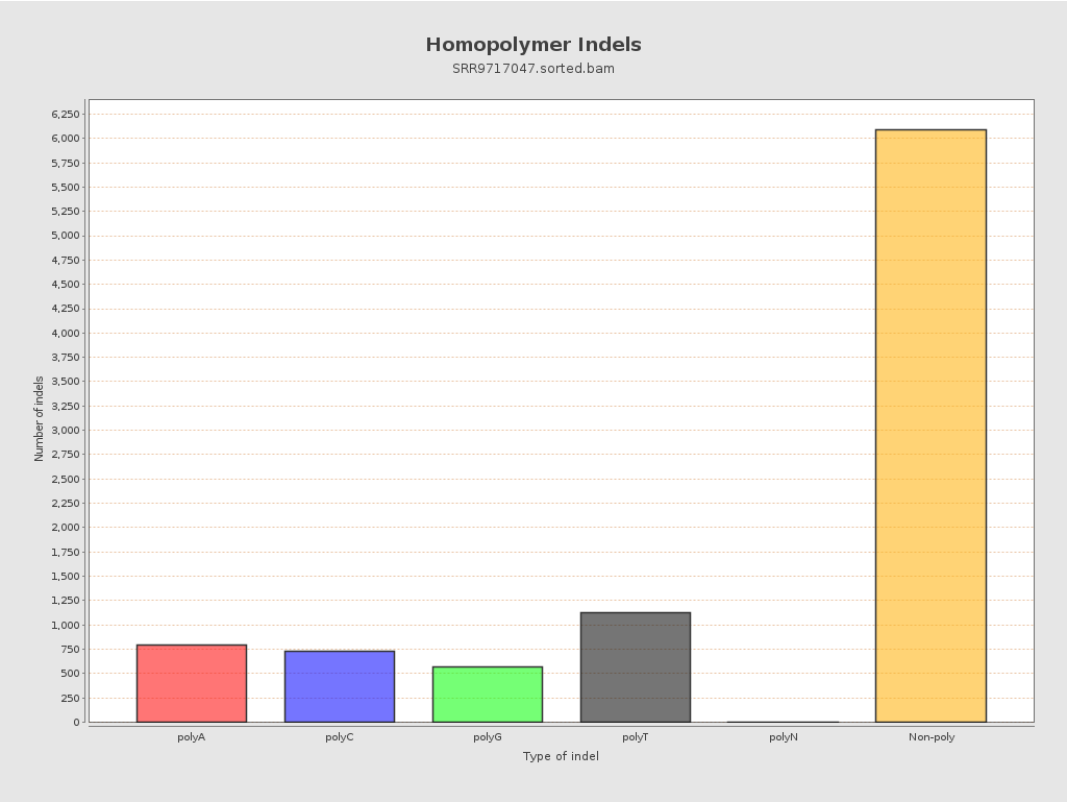
9. Results : Mapped Reads GC-content Distribution



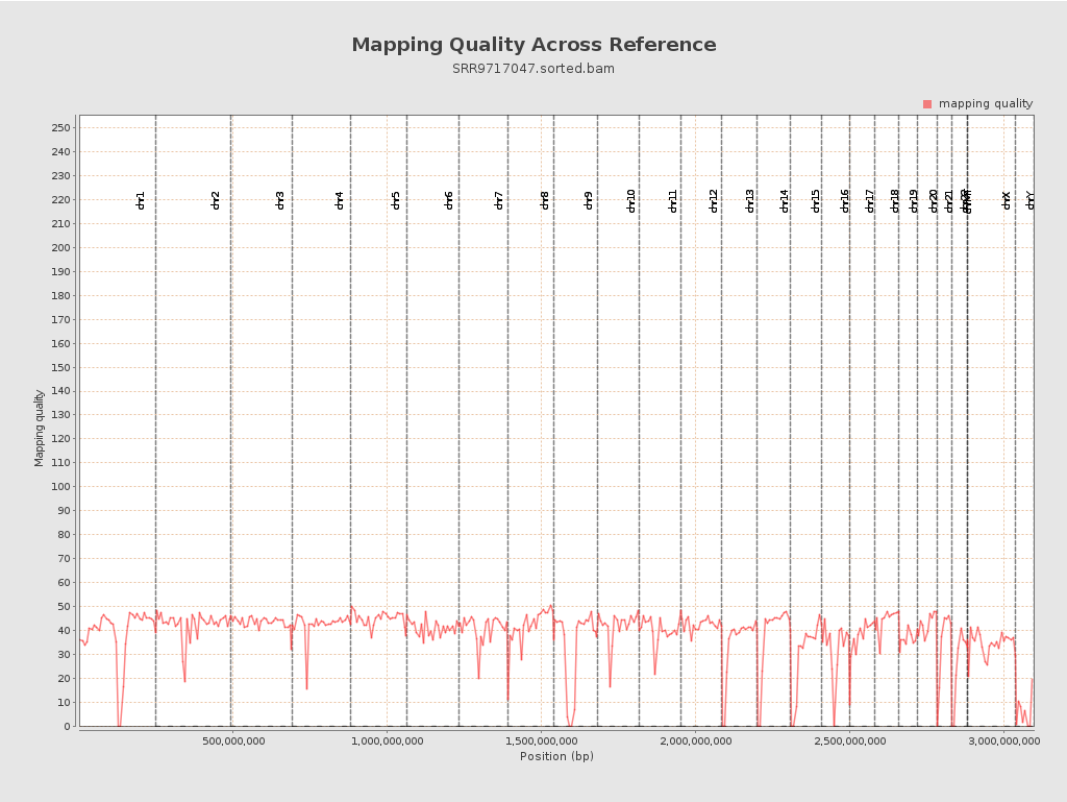
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram