Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 04:58:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717080.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_SRR9717080 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717080.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 04:58:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717080.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	887,540
Mapped reads	796,522 / 89.74%
Unmapped reads	91,018 / 10.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,816 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	18,008 / 2.03%
Duplication rate	1.74%
Clipped reads	795,481 / 89.63%

2.2. ACGT Content

Number/percentage of A's	11,150,830 / 24.3%
Number/percentage of C's	8,460,121 / 18.44%
Number/percentage of T's	14,919,333 / 32.51%
Number/percentage of G's	11,359,121 / 24.75%
Number/percentage of N's	525 / 0%
GC Percentage	43.19%

2.3. Coverage

Mean	0.0148

Standard Deviation	0.1538

2.4. Mapping Quality

Mean Mapping Quality	44.57

2.5. Mismatches and indels

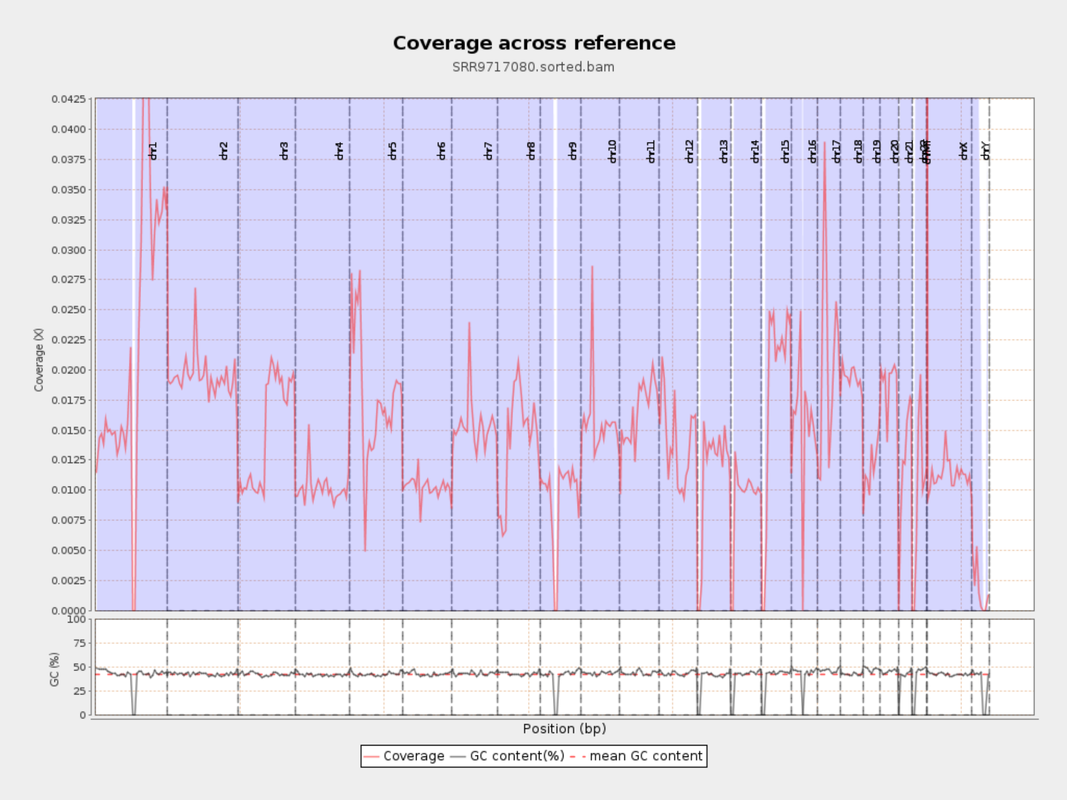
General error rate	0.5%
Mismatches	224,544
Insertions	3,458
Mapped reads with at least one insertion	0.43%
Deletions	9,030
Mapped reads with at least one deletion	1.12%
Homopolymer indels	41.94%

2.6. Chromosome stats

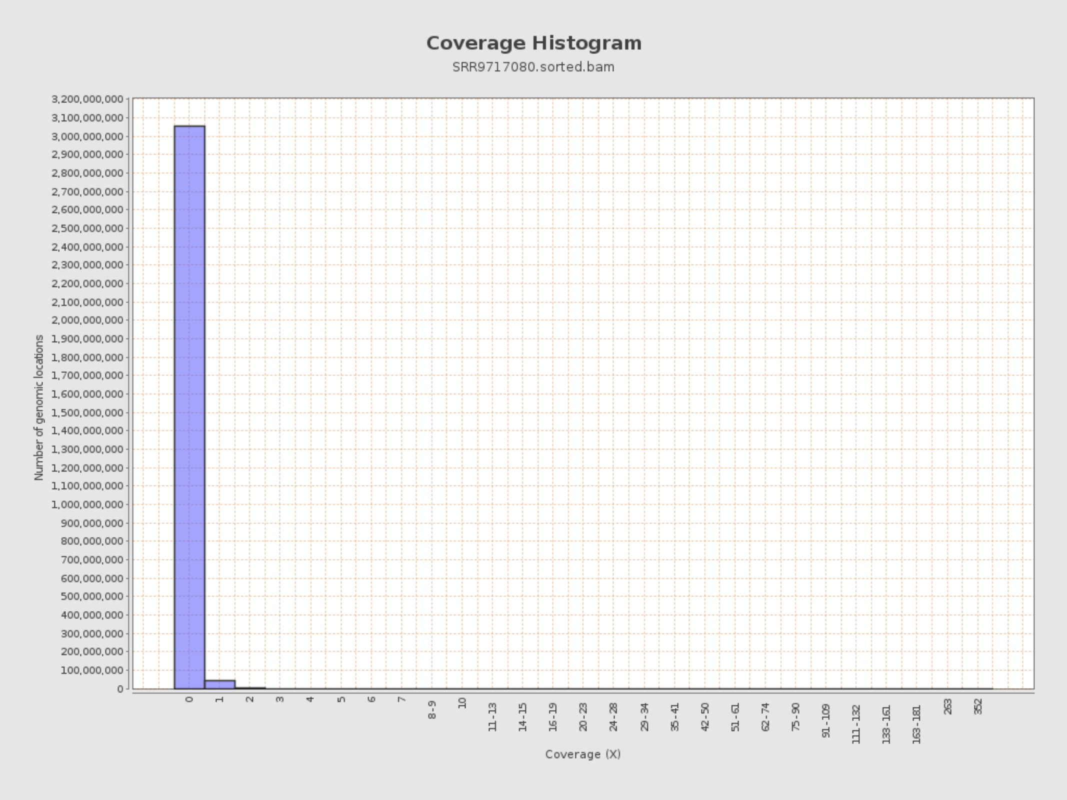
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5477656	0.022	0.2078
chr2	243199373	4741591	0.0195	0.2165
chr3	198022430	2944914	0.0149	0.1312
chr4	191154276	1949777	0.0102	0.1085
chr5	180915260	3231687	0.0179	0.1401
chr6	171115067	1753938	0.0103	0.1161
chr7	159138663	2457802	0.0154	0.1931

chr8	146364022	2099445	0.0143	0.1396
chr9	141213431	1316420	0.0093	0.1237
chr10	135534747	2137229	0.0158	0.1763
chr11	135006516	2245223	0.0166	0.1557
chr12	133851895	1866198	0.0139	0.1243
chr13	115169878	1308818	0.0114	0.1115
chr14	107349540	976458	0.0091	0.1023
chr15	102531392	1902963	0.0186	0.1434
chr16	90354753	1385440	0.0153	0.1383
chr17	81195210	1723369	0.0212	0.1591
chr18	78077248	1517165	0.0194	0.2259
chr19	59128983	713456	0.0121	0.1621
chr20	63025520	1183951	0.0188	0.1437
chr21	48129895	597231	0.0124	0.1189
chr22	51304566	508000	0.0099	0.104
chrMT	16571	3160	0.1907	0.4652
chrX	155270560	1756366	0.0113	0.1219
chrY	59373566	105761	0.0018	0.0528

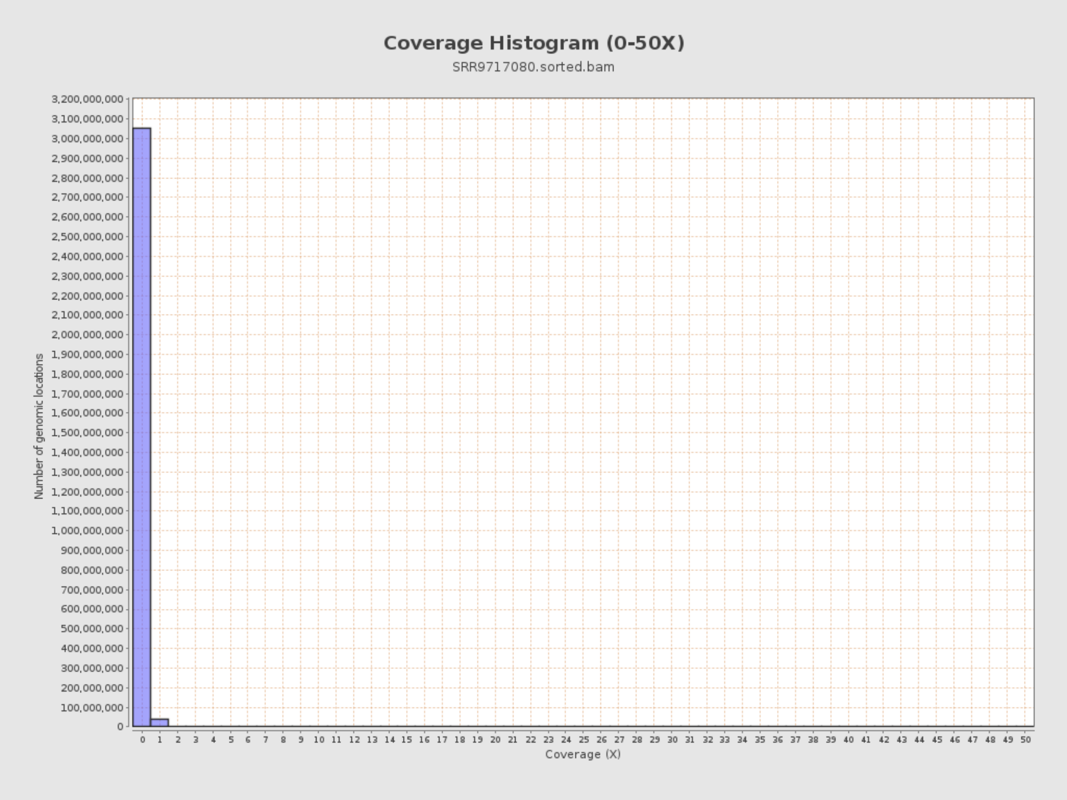
3. Results : Coverage across reference



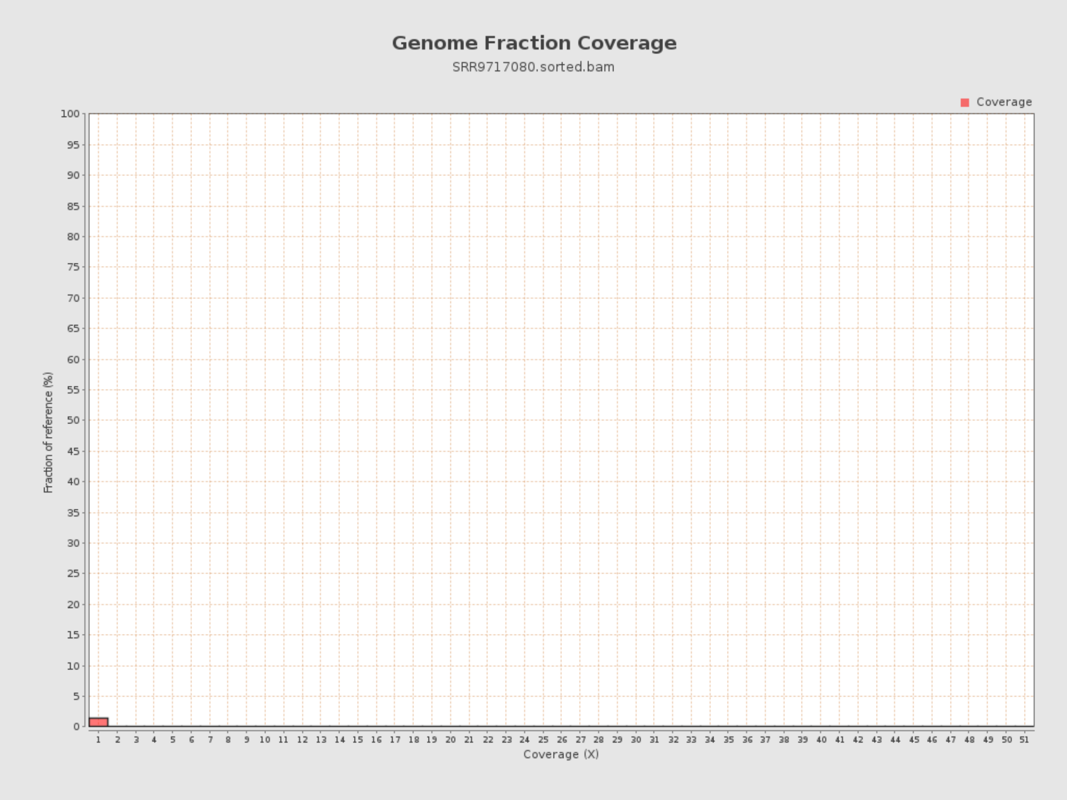
4. Results : Coverage Histogram



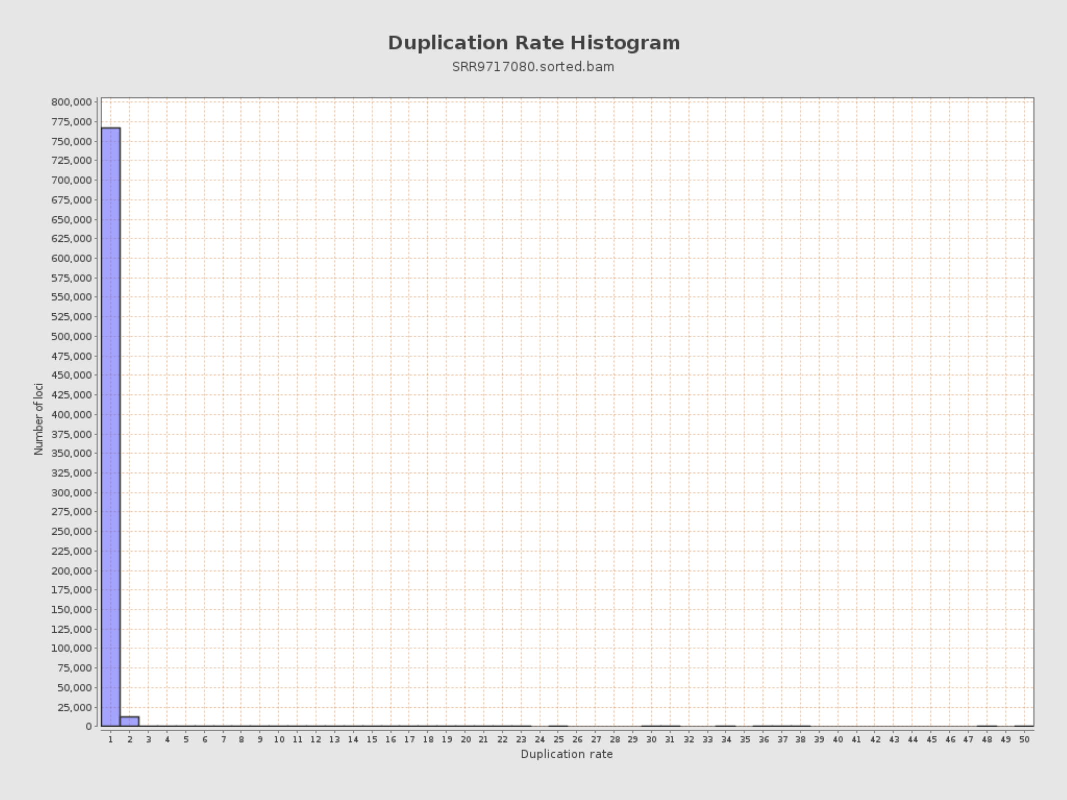
5. Results : Coverage Histogram (0-50X)



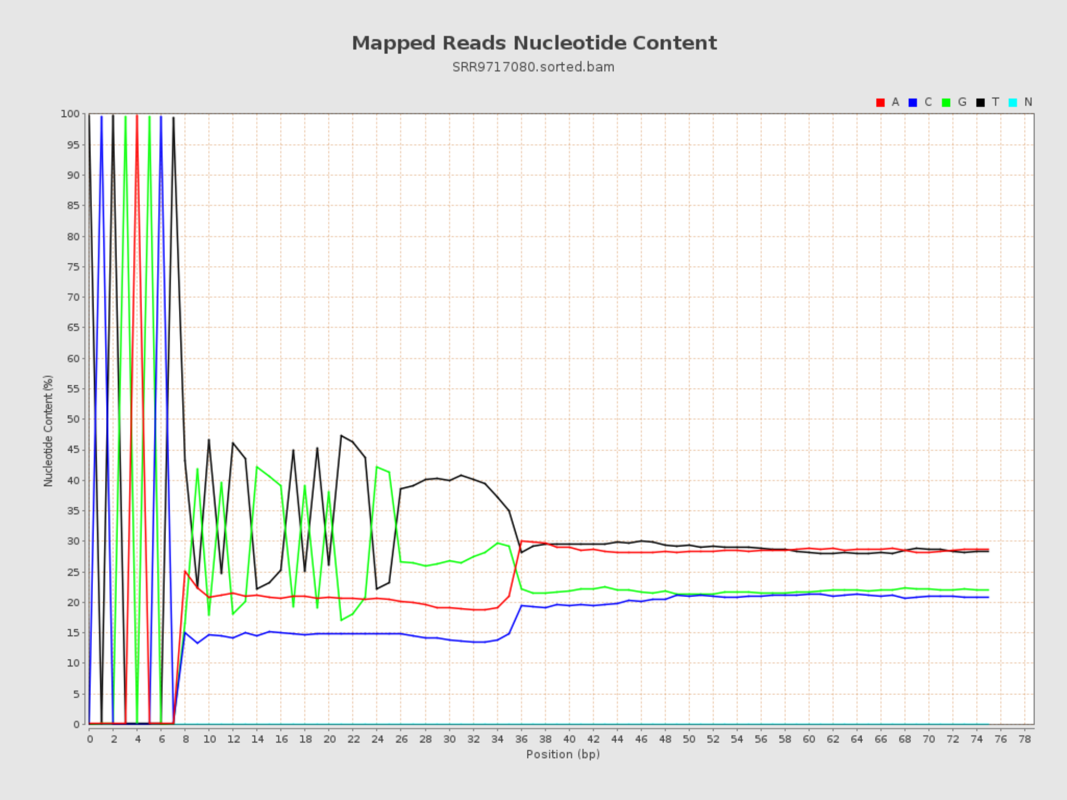
6. Results : Genome Fraction Coverage



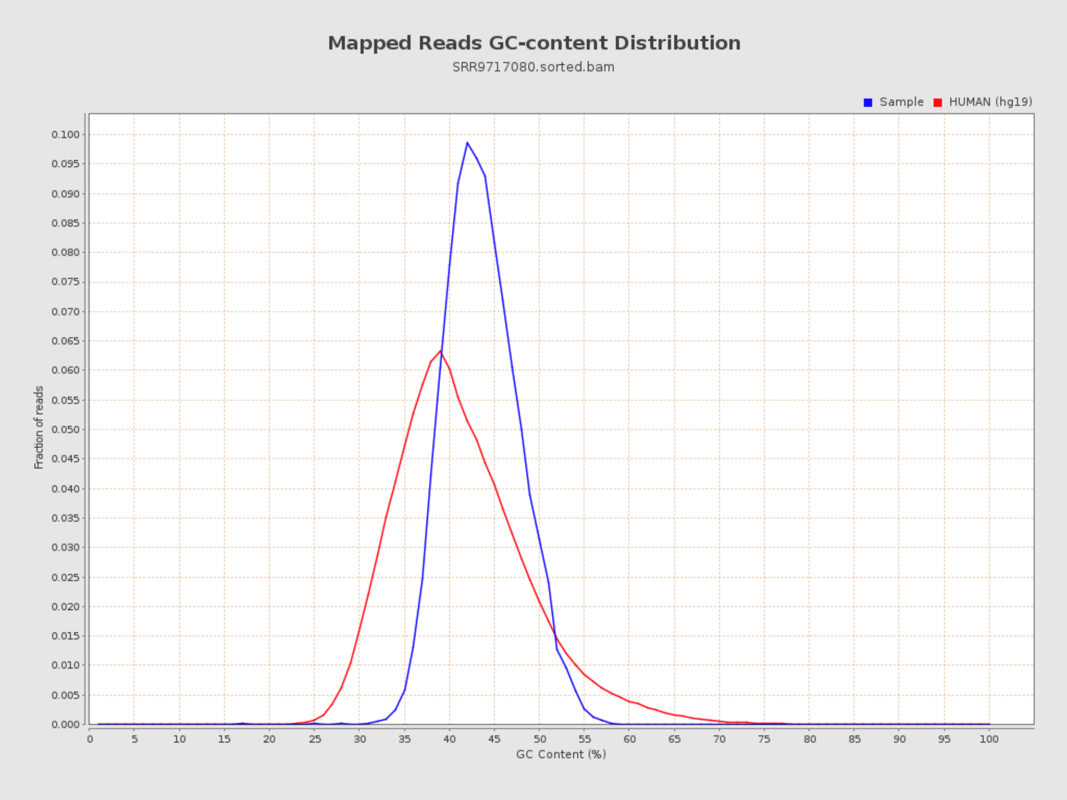
7. Results : Duplication Rate Histogram



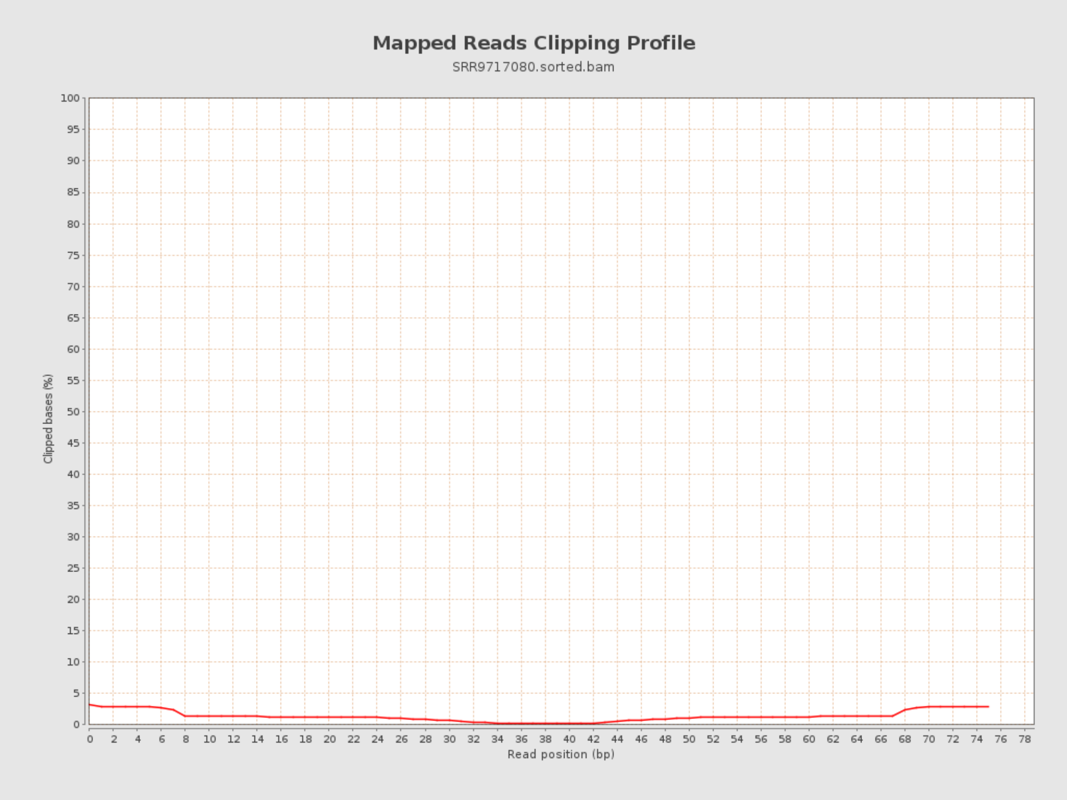
8. Results : Mapped Reads Nucleotide Content



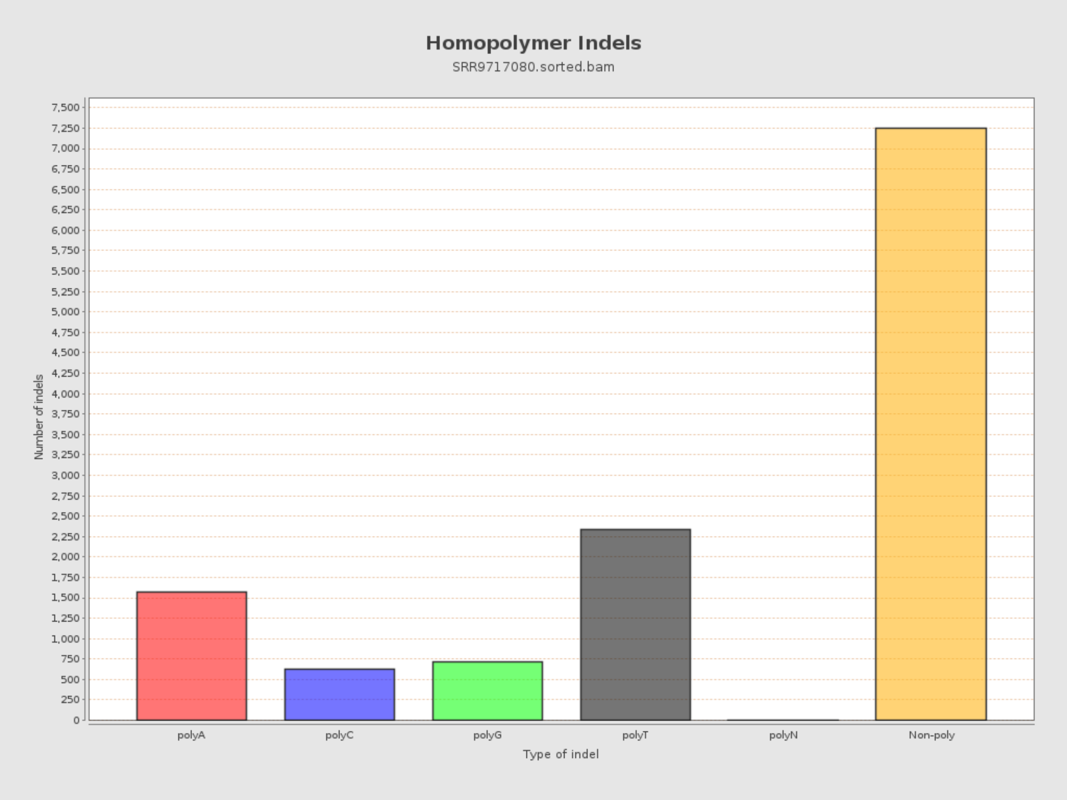
9. Results : Mapped Reads GC-content Distribution



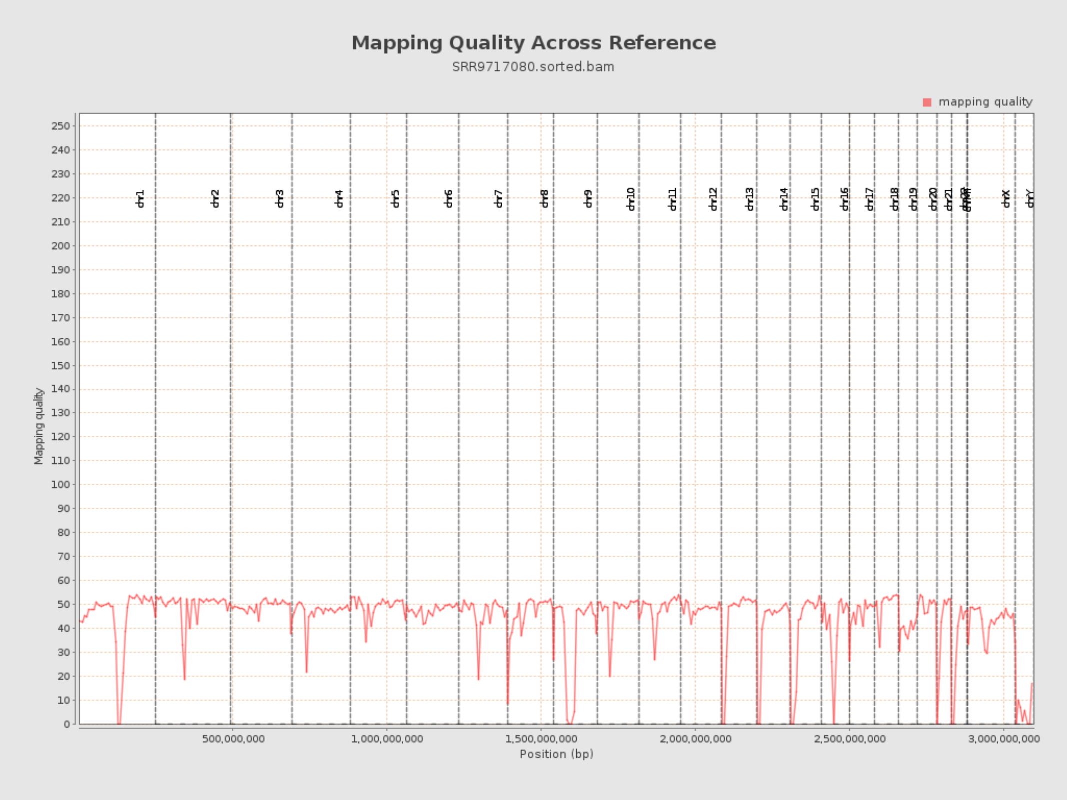
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram