Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 02:25:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717042.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_SRR9717042 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717042.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 02:25:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717042.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,384,847
Mapped reads	7,833,136 / 93.42%
Unmapped reads	551,711 / 6.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	172,103 / 2.05%
Read min/max/mean length	30 / 101 / 101.74
Duplicated reads (estimated)	692,758 / 8.26%
Duplication rate	6.42%
Clipped reads	7,996,269 / 95.37%

2.2. ACGT Content

Number/percentage of A's	153,523,345 / 26.18%
Number/percentage of C's	122,524,327 / 20.9%
Number/percentage of T's	173,280,369 / 29.55%
Number/percentage of G's	136,941,090 / 23.36%
Number/percentage of N's	70,506 / 0.01%
GC Percentage	44.25%

2.3. Coverage

Mean	0.1895

Standard Deviation	1.3524

2.4. Mapping Quality

Mean Mapping Quality	45.96

2.5. Mismatches and indels

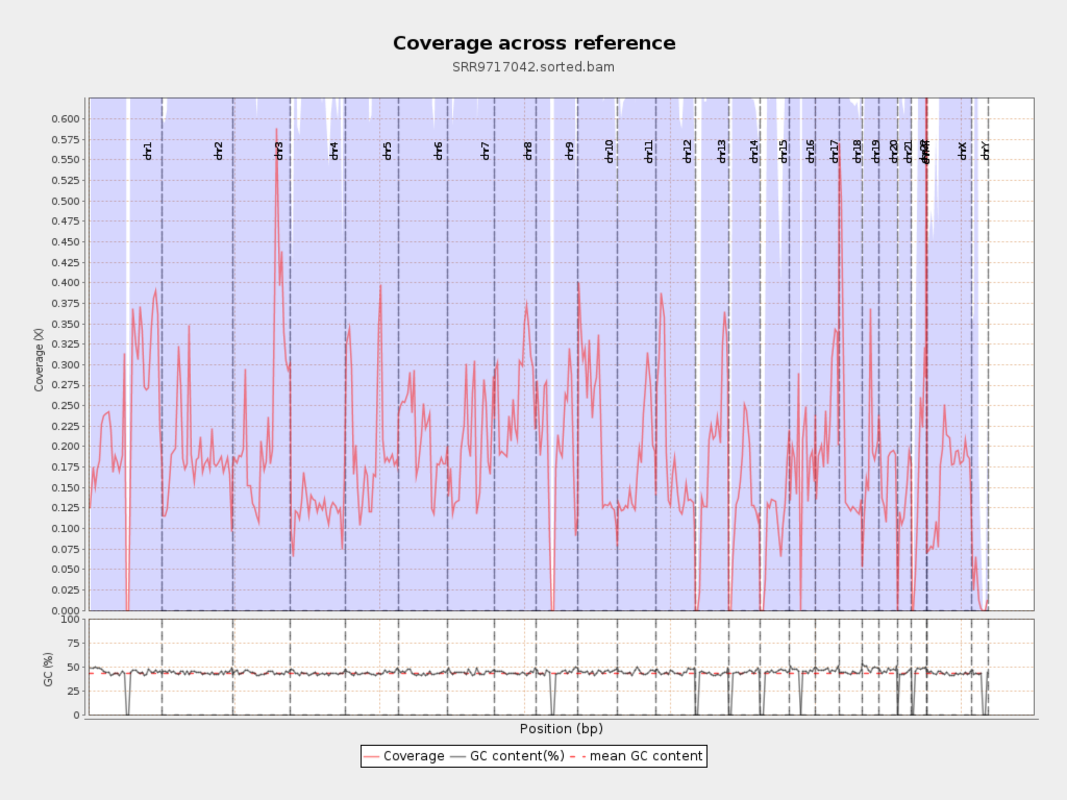
General error rate	0.75%
Mismatches	4,309,593
Insertions	44,995
Mapped reads with at least one insertion	0.57%
Deletions	121,094
Mapped reads with at least one deletion	1.53%
Homopolymer indels	40.7%

2.6. Chromosome stats

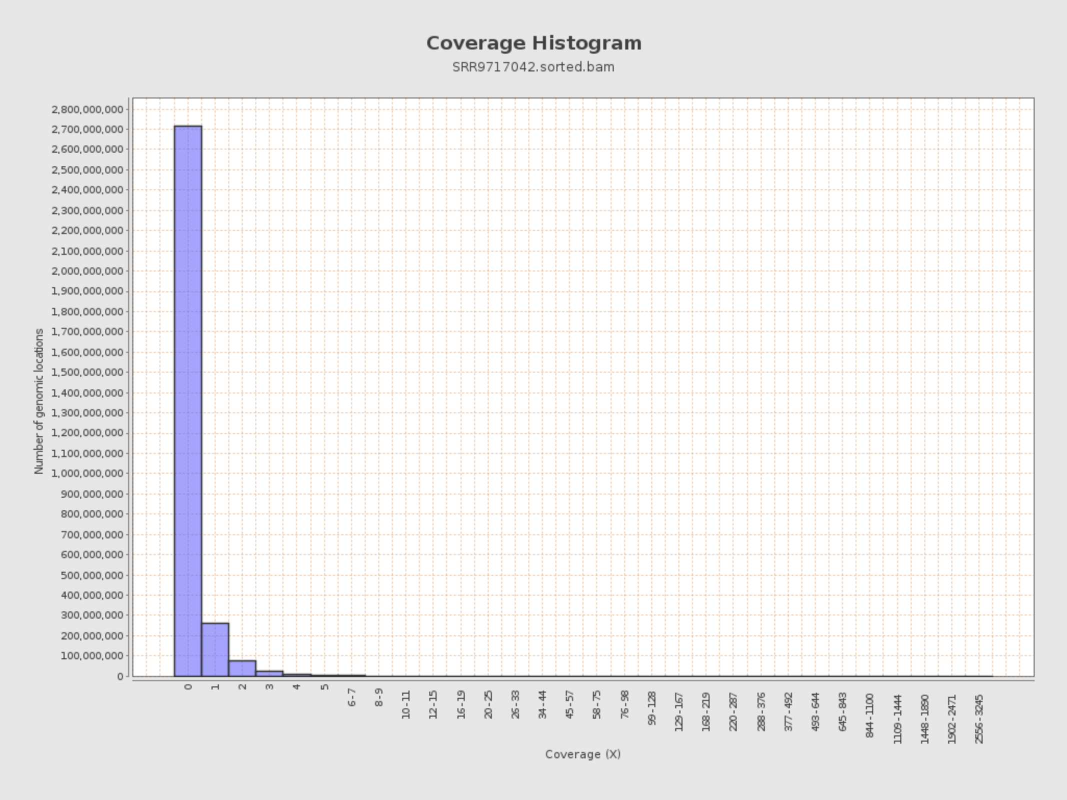
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	59129621	0.2372	2.4066
chr2	243199373	45624431	0.1876	2.176
chr3	198022430	46868885	0.2367	0.7215
chr4	191154276	23539398	0.1231	0.5999
chr5	180915260	36707364	0.2029	0.6571
chr6	171115067	36705153	0.2145	0.955
chr7	159138663	31740262	0.1995	2.1828

chr8	146364022	38515517	0.2631	1.6598
chr9	141213431	27269101	0.1931	1.1949
chr10	135534747	31804481	0.2347	1.3184
chr11	135006516	24093684	0.1785	1.0678
chr12	133851895	24912274	0.1861	0.6444
chr13	115169878	21747448	0.1888	0.6344
chr14	107349540	14561910	0.1356	0.6197
chr15	102531392	10527155	0.1027	0.4674
chr16	90354753	15814467	0.175	0.6779
chr17	81195210	18924695	0.2331	0.8804
chr18	78077248	15713253	0.2013	1.6232
chr19	59128983	11289195	0.1909	2.0633
chr20	63025520	10400649	0.165	0.6161
chr21	48129895	6184302	0.1285	0.5725
chr22	51304566	8005862	0.156	0.6003
chrMT	16571	35283	2.1292	4.3545
chrX	155270560	25223519	0.1624	0.787
chrY	59373566	1206221	0.0203	0.5751

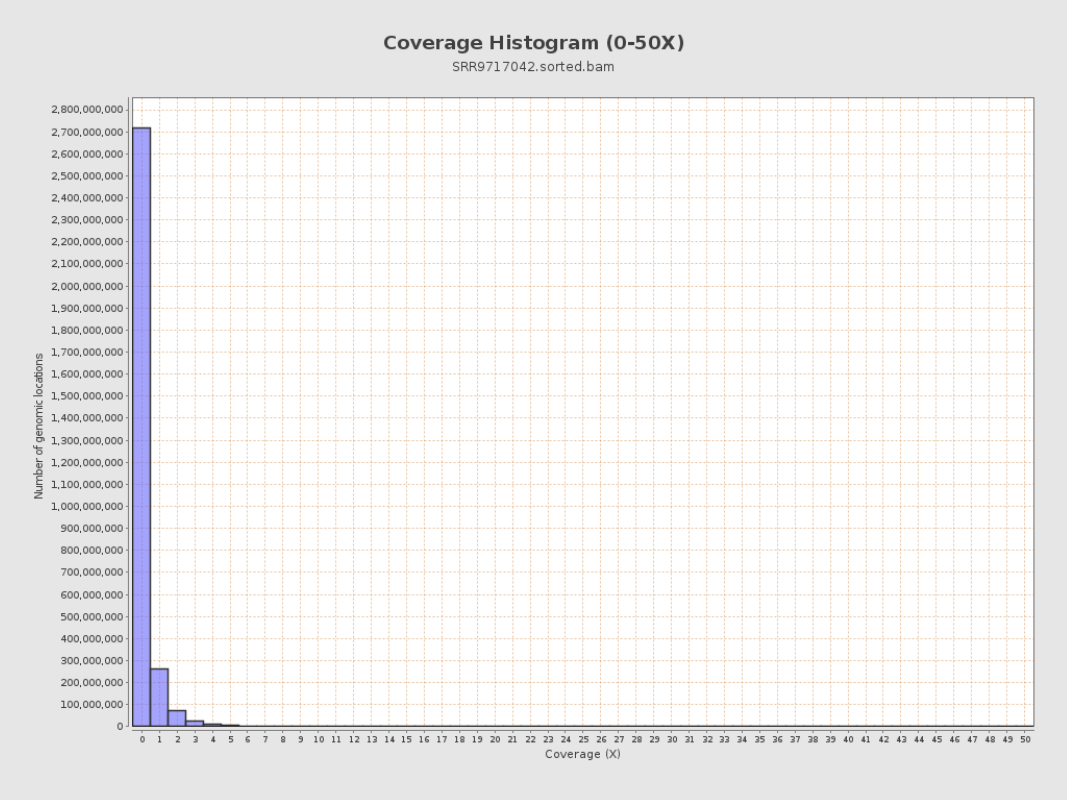
3. Results : Coverage across reference



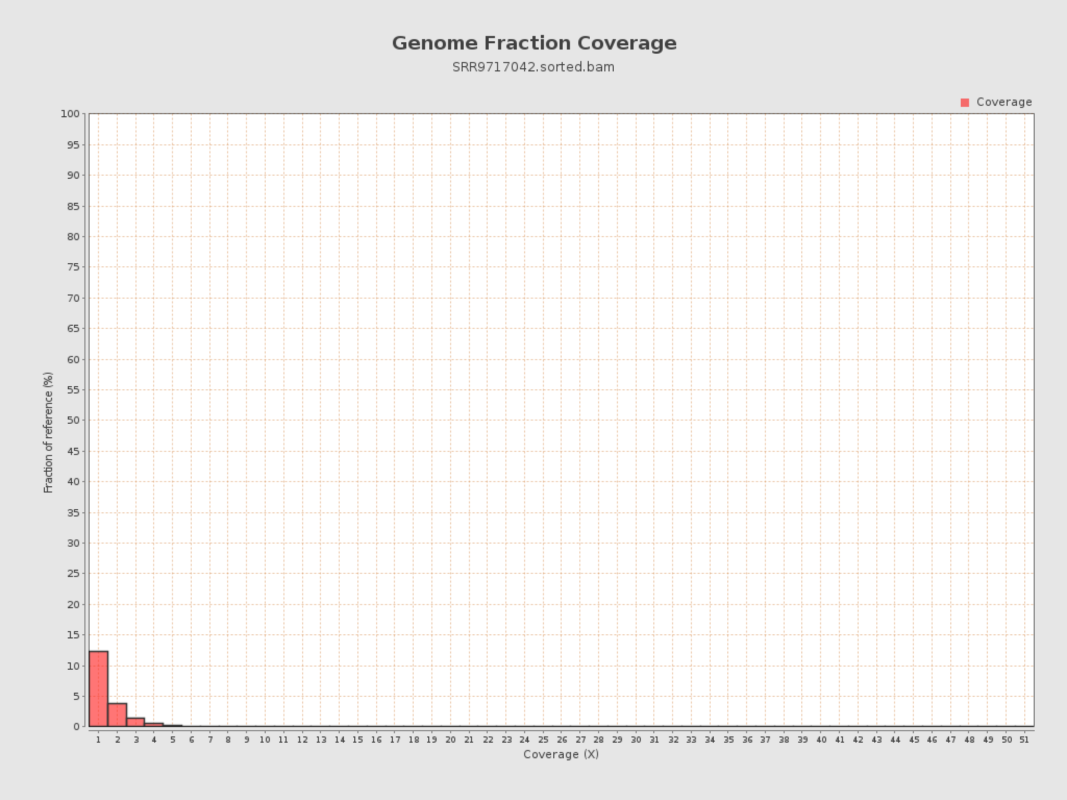
4. Results : Coverage Histogram



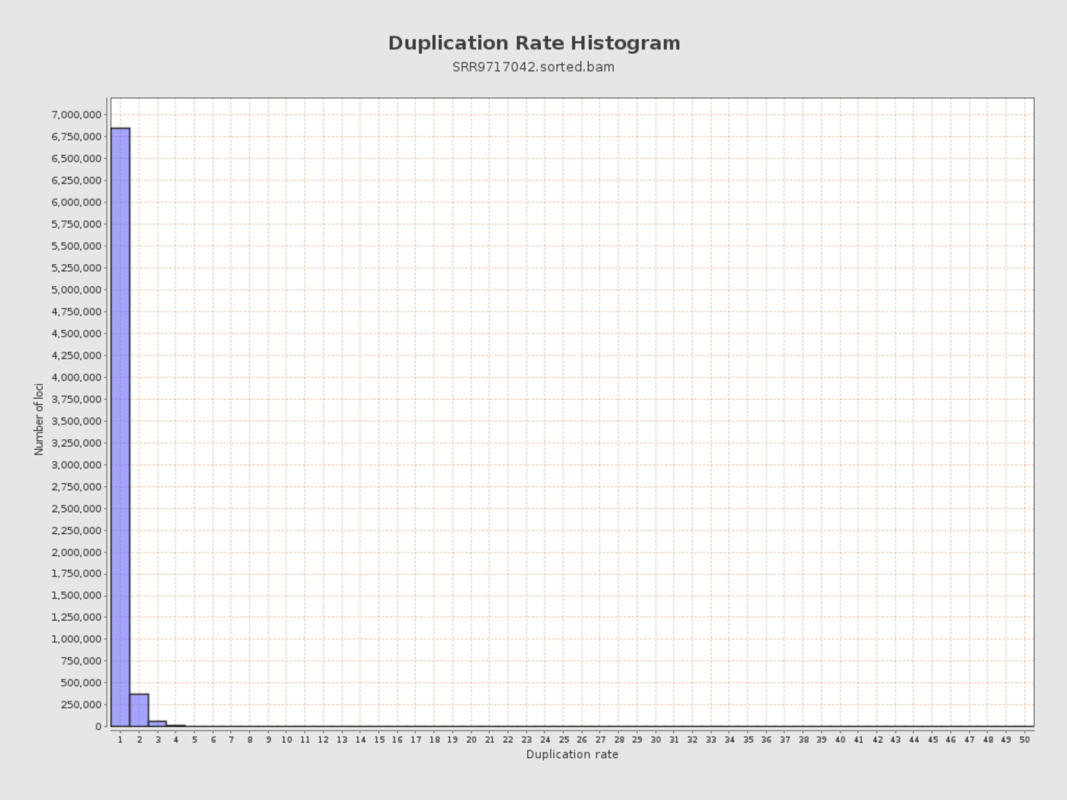
5. Results : Coverage Histogram (0-50X)



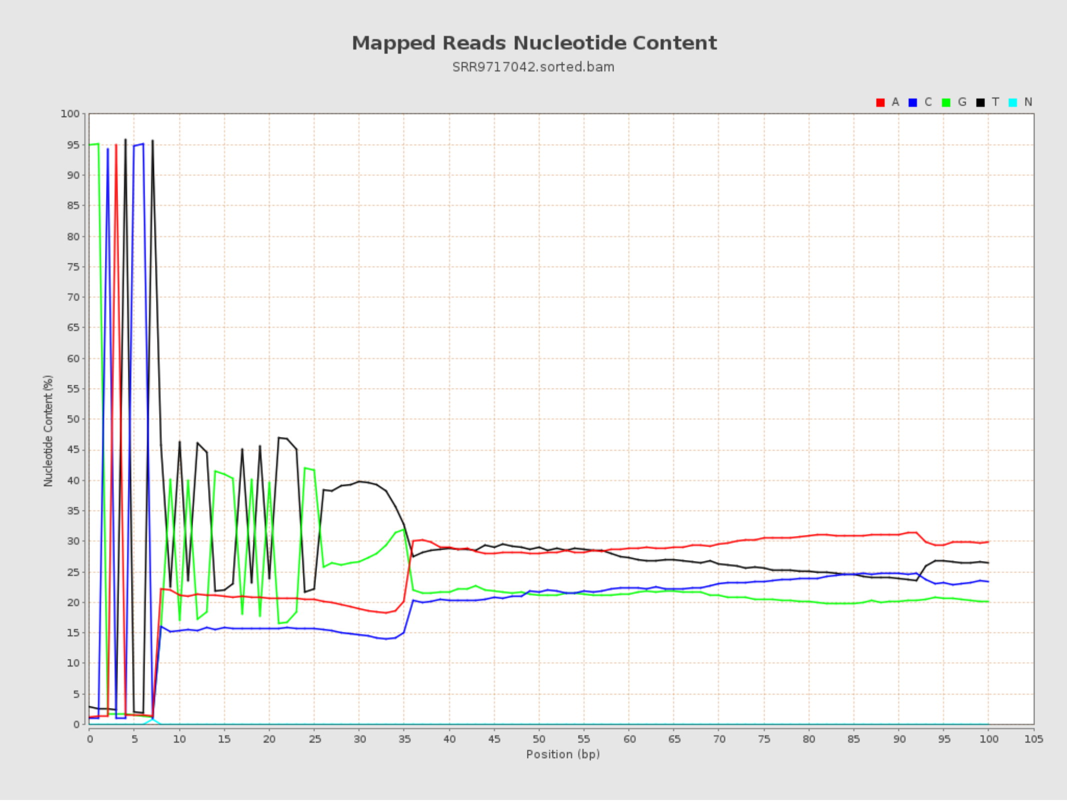
6. Results : Genome Fraction Coverage



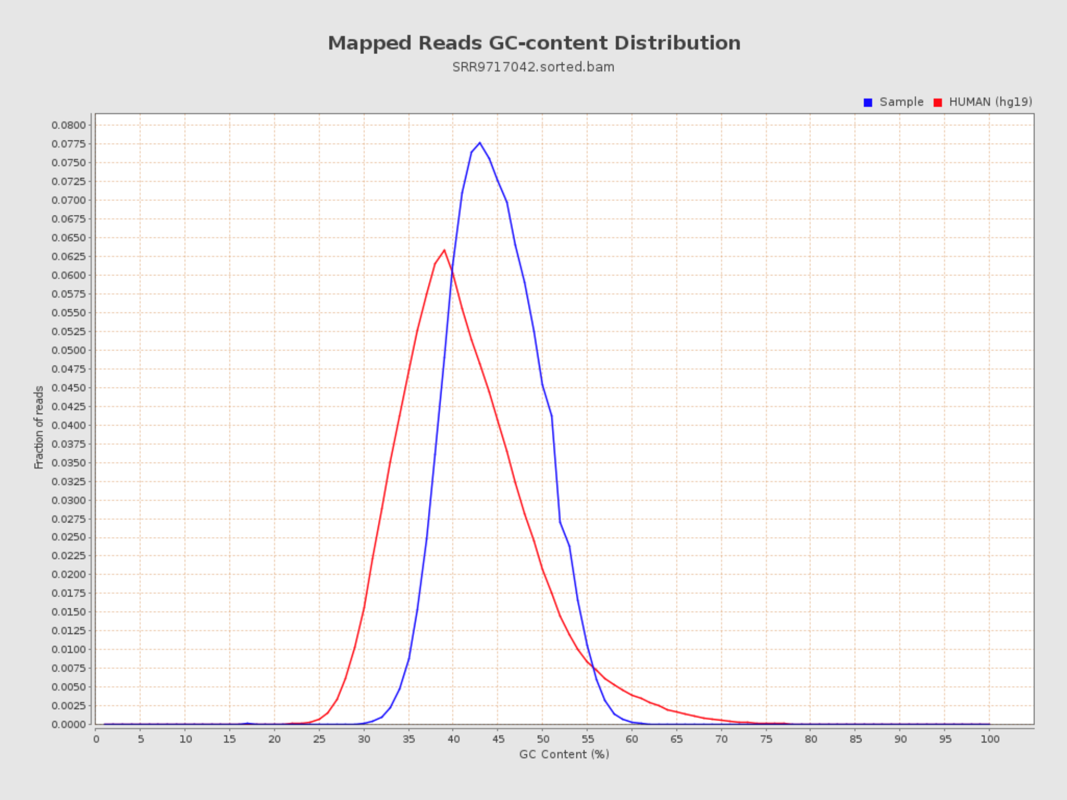
7. Results : Duplication Rate Histogram



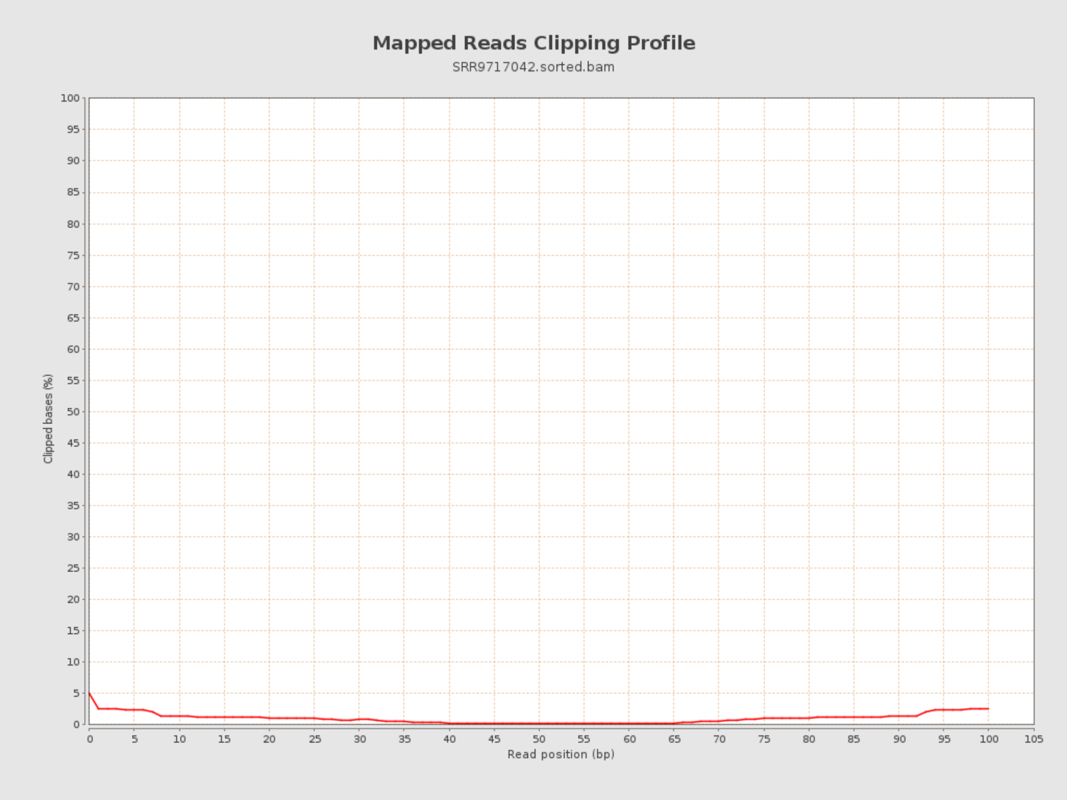
8. Results : Mapped Reads Nucleotide Content



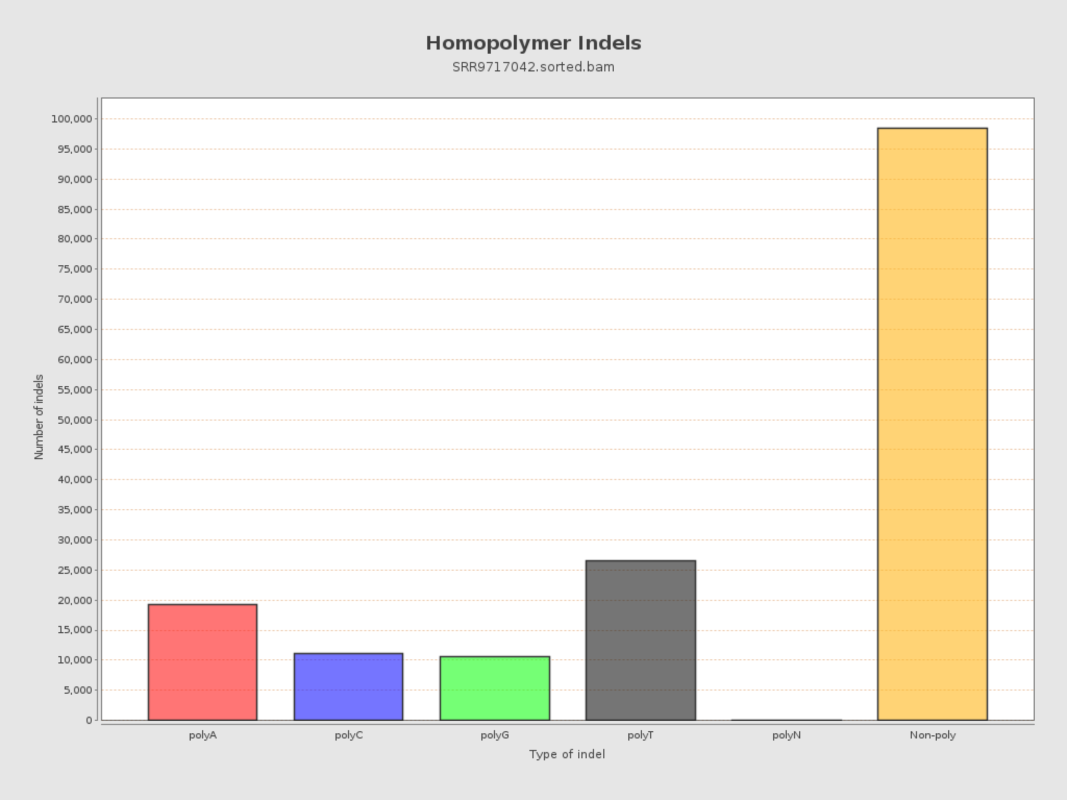
9. Results : Mapped Reads GC-content Distribution



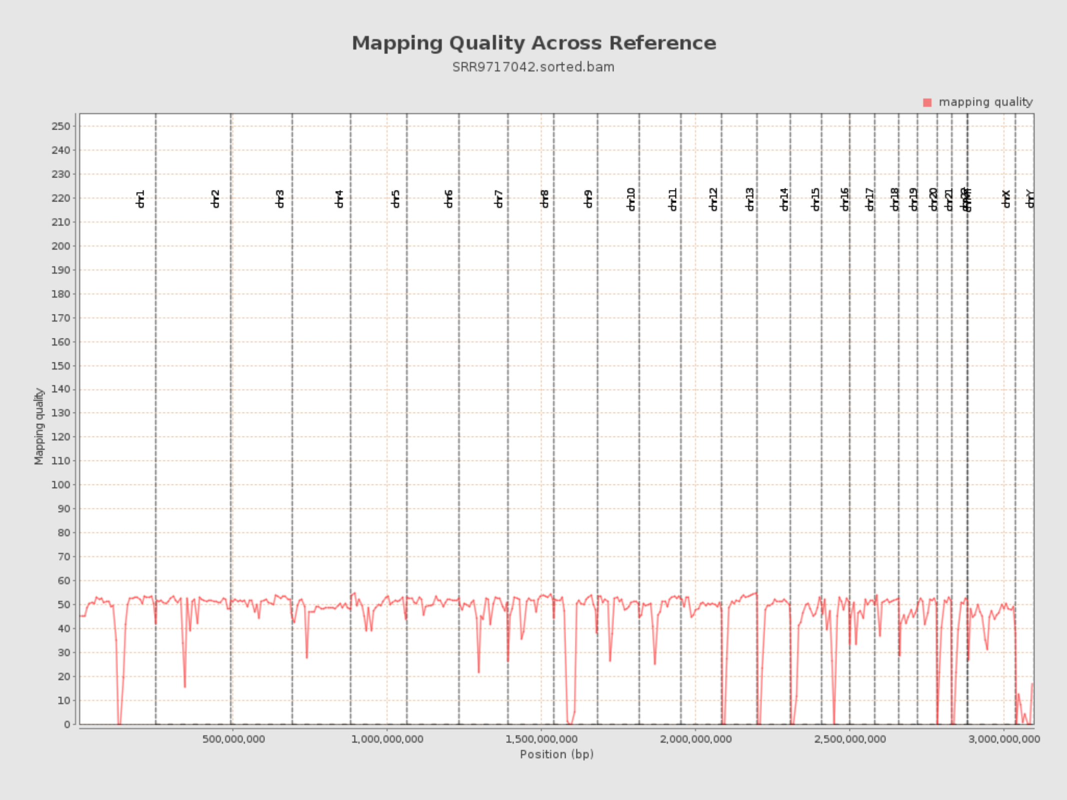
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram