Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 03:09:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717056.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_SRR9717056 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717056.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 03:09:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717056.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	829,549
Mapped reads	713,369 / 85.99%
Unmapped reads	116,180 / 14.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,950 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	11,600 / 1.4%
Duplication rate	1.18%
Clipped reads	715,304 / 86.23%

2.2. ACGT Content

Number/percentage of A's	9,350,846 / 23.24%
Number/percentage of C's	8,528,620 / 21.2%
Number/percentage of T's	11,288,185 / 28.06%
Number/percentage of G's	11,059,821 / 27.49%
Number/percentage of N's	1,065 / 0%
GC Percentage	48.69%

2.3. Coverage

Mean	0.013

Standard Deviation	0.1358

2.4. Mapping Quality

Mean Mapping Quality	39.3

2.5. Mismatches and indels

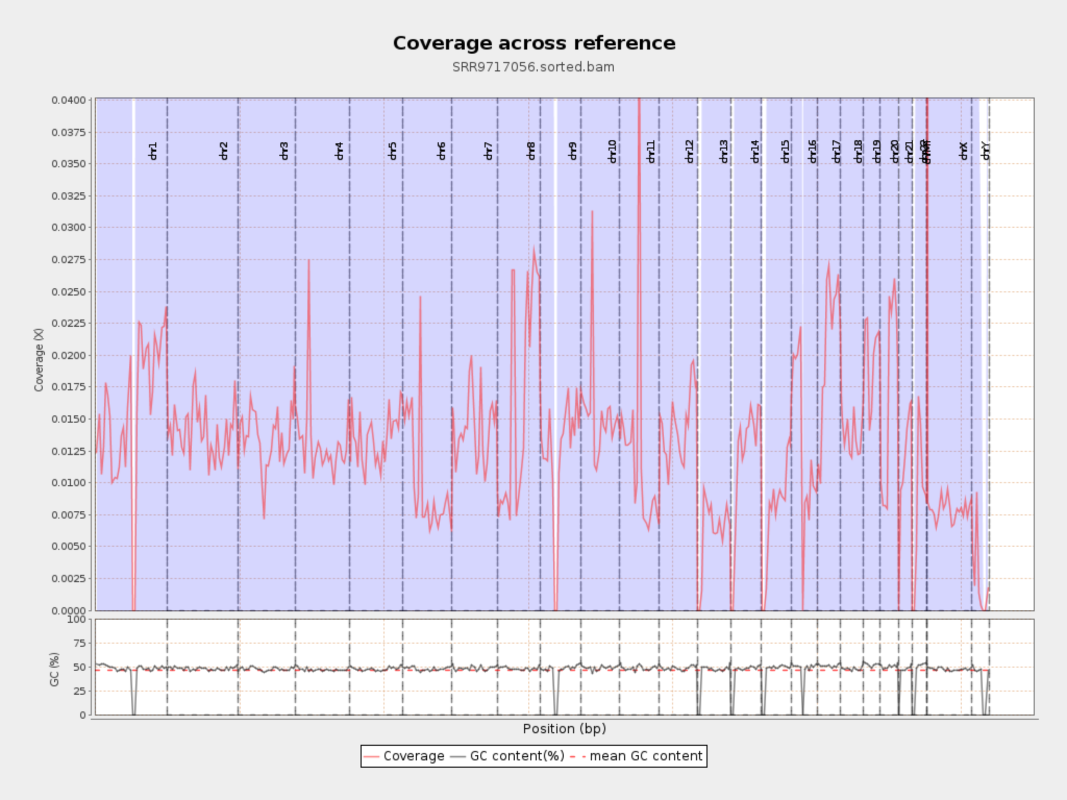
General error rate	0.55%
Mismatches	215,287
Insertions	2,785
Mapped reads with at least one insertion	0.39%
Deletions	6,796
Mapped reads with at least one deletion	0.94%
Homopolymer indels	36.74%

2.6. Chromosome stats

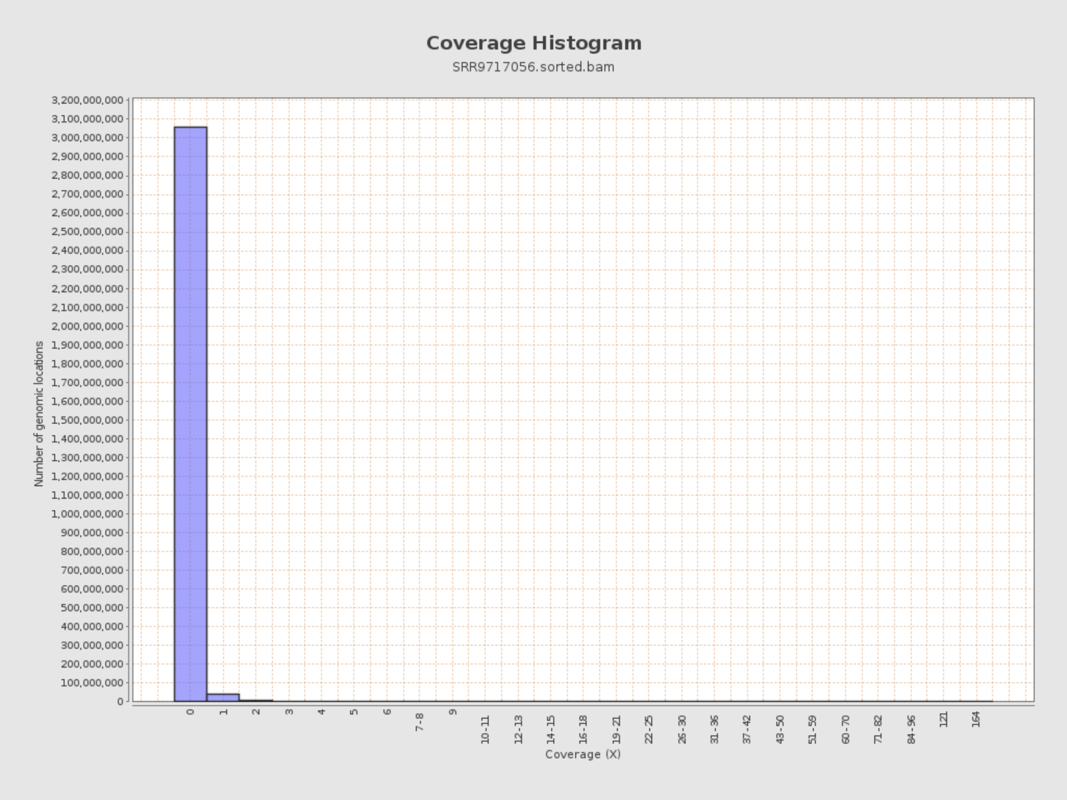
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3914150	0.0157	0.155
chr2	243199373	3405382	0.014	0.1587
chr3	198022430	2657900	0.0134	0.1255
chr4	191154276	2543206	0.0133	0.1367
chr5	180915260	2463160	0.0136	0.1259
chr6	171115067	1754799	0.0103	0.109
chr7	159138663	2292604	0.0144	0.1501

chr8	146364022	2440973	0.0167	0.1423
chr9	141213431	1730444	0.0123	0.1255
chr10	135534747	2107750	0.0156	0.1925
chr11	135006516	1709970	0.0127	0.137
chr12	133851895	1934121	0.0144	0.1292
chr13	115169878	701699	0.0061	0.0835
chr14	107349540	1262919	0.0118	0.1171
chr15	102531392	789662	0.0077	0.0942
chr16	90354753	1149419	0.0127	0.1281
chr17	81195210	1692010	0.0208	0.1603
chr18	78077248	1068769	0.0137	0.1474
chr19	59128983	1163278	0.0197	0.1707
chr20	63025520	1059404	0.0168	0.1438
chr21	48129895	560047	0.0116	0.1231
chr22	51304566	440873	0.0086	0.0992
chrMT	16571	32180	1.9419	2.068
chrX	155270560	1226205	0.0079	0.0983
chrY	59373566	139140	0.0023	0.0843

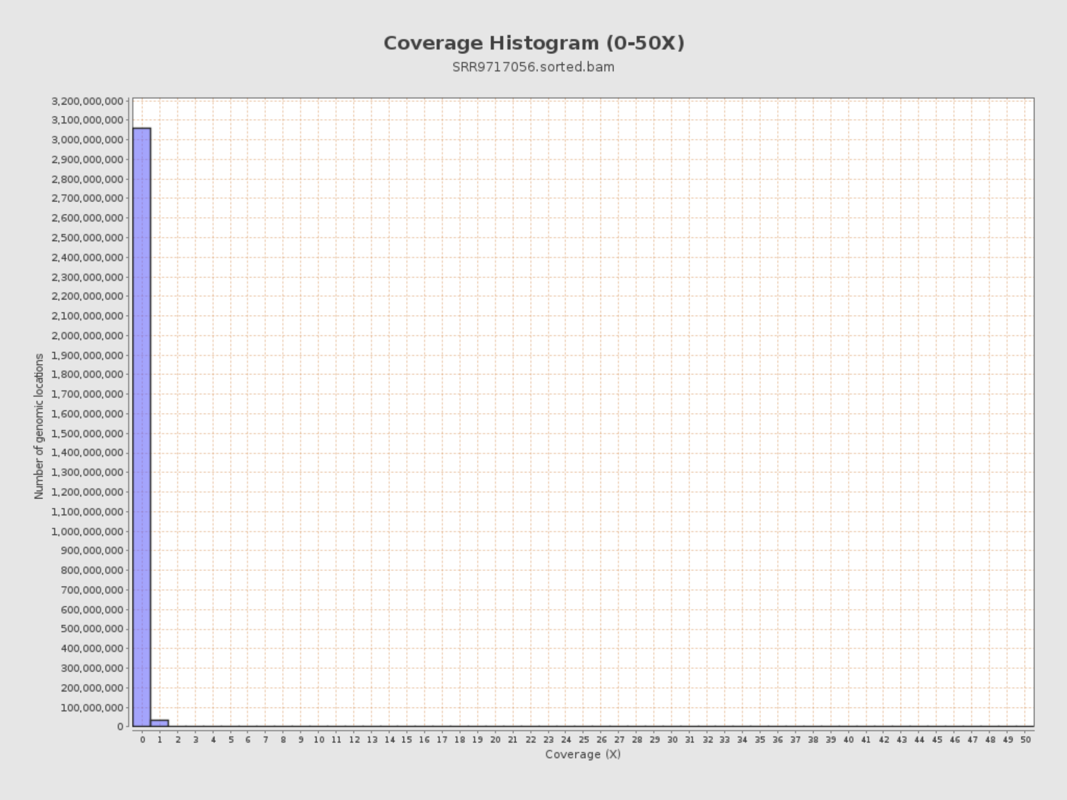
3. Results : Coverage across reference



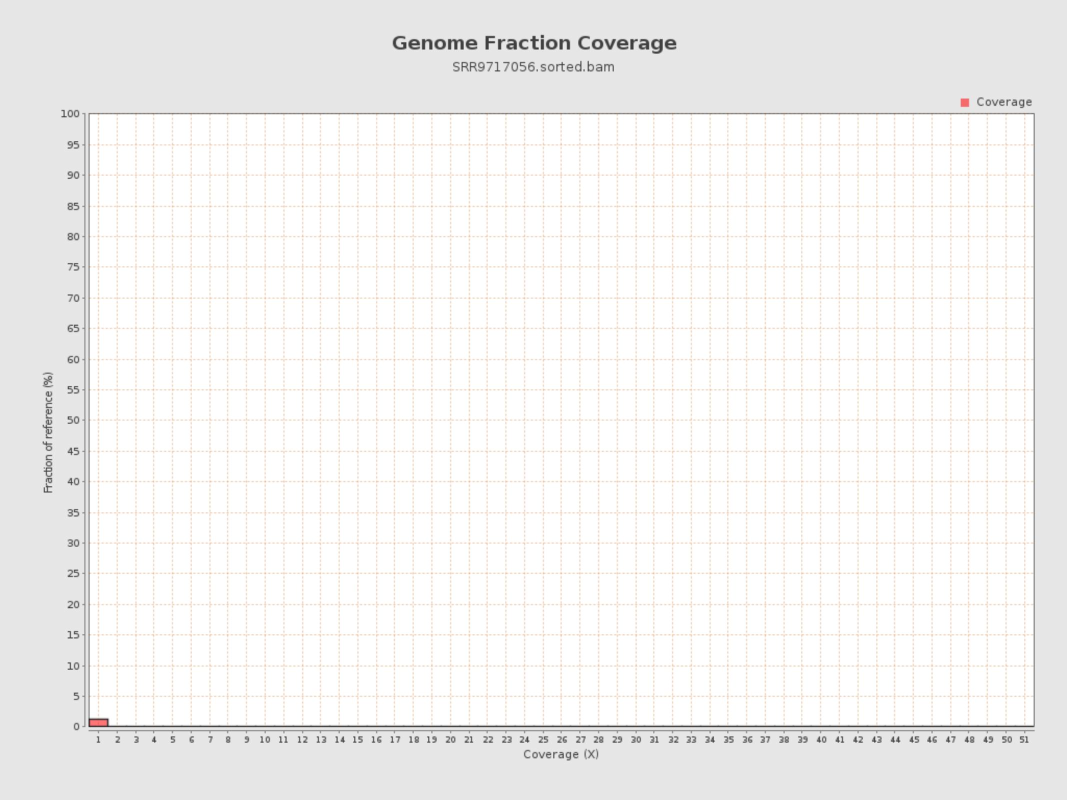
4. Results : Coverage Histogram



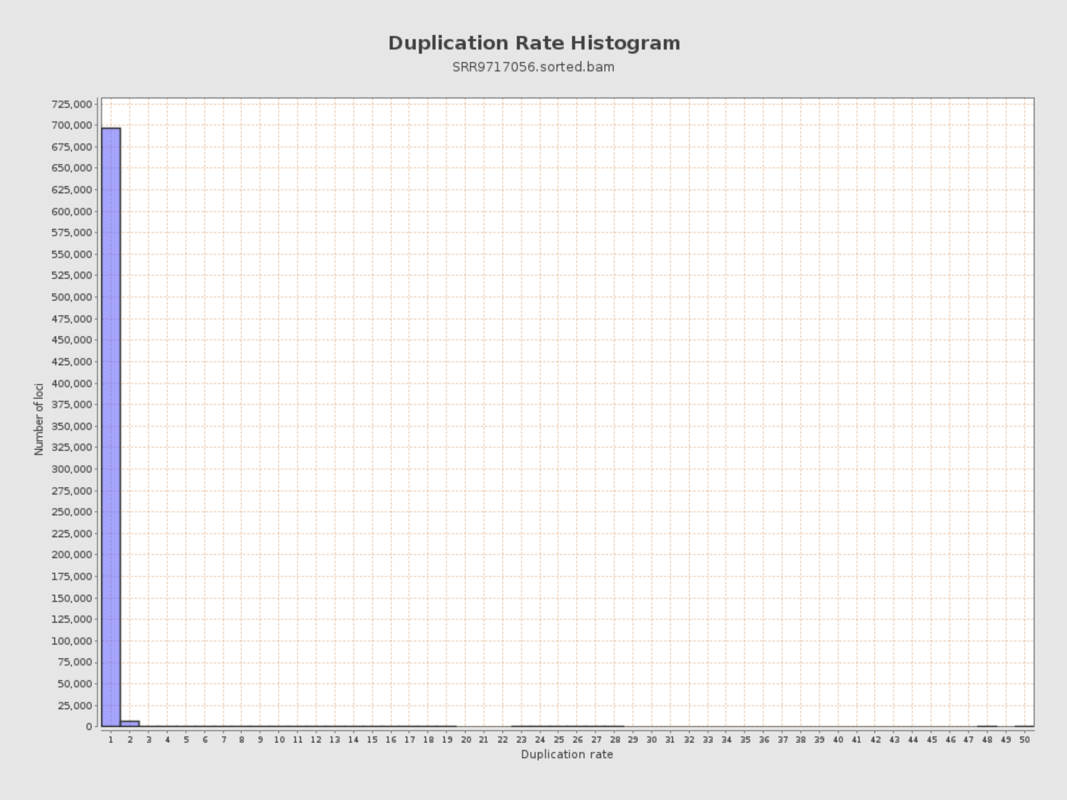
5. Results : Coverage Histogram (0-50X)



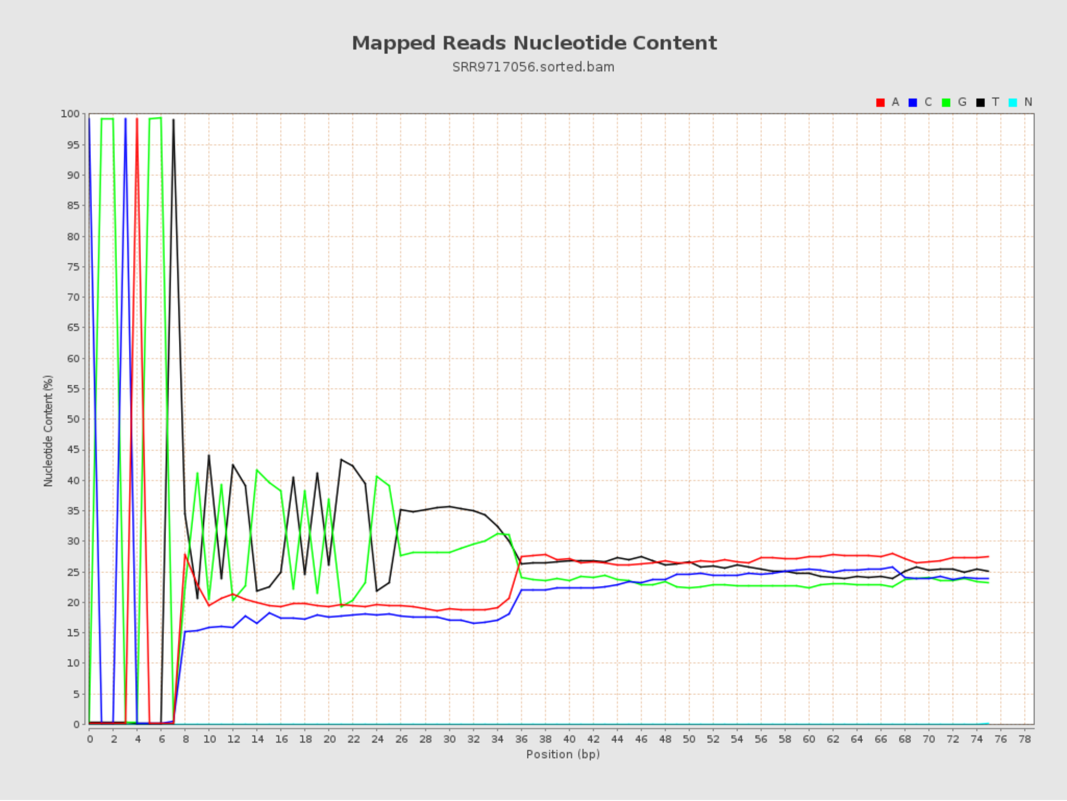
6. Results : Genome Fraction Coverage



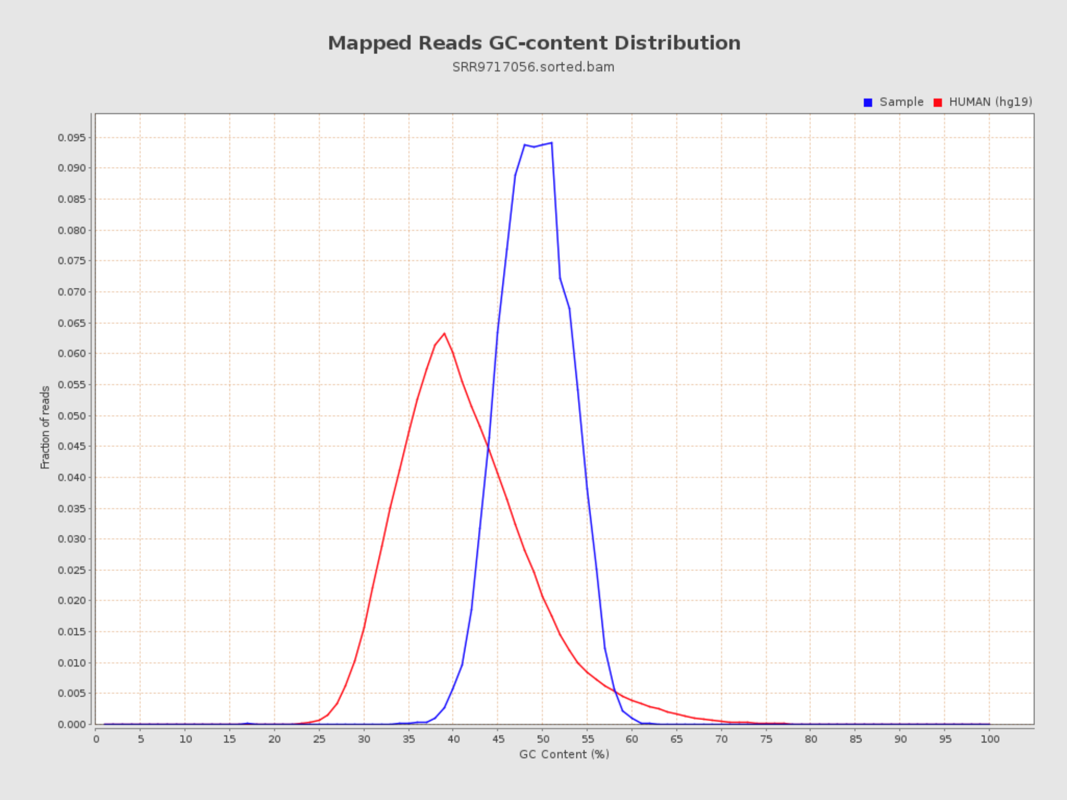
7. Results : Duplication Rate Histogram



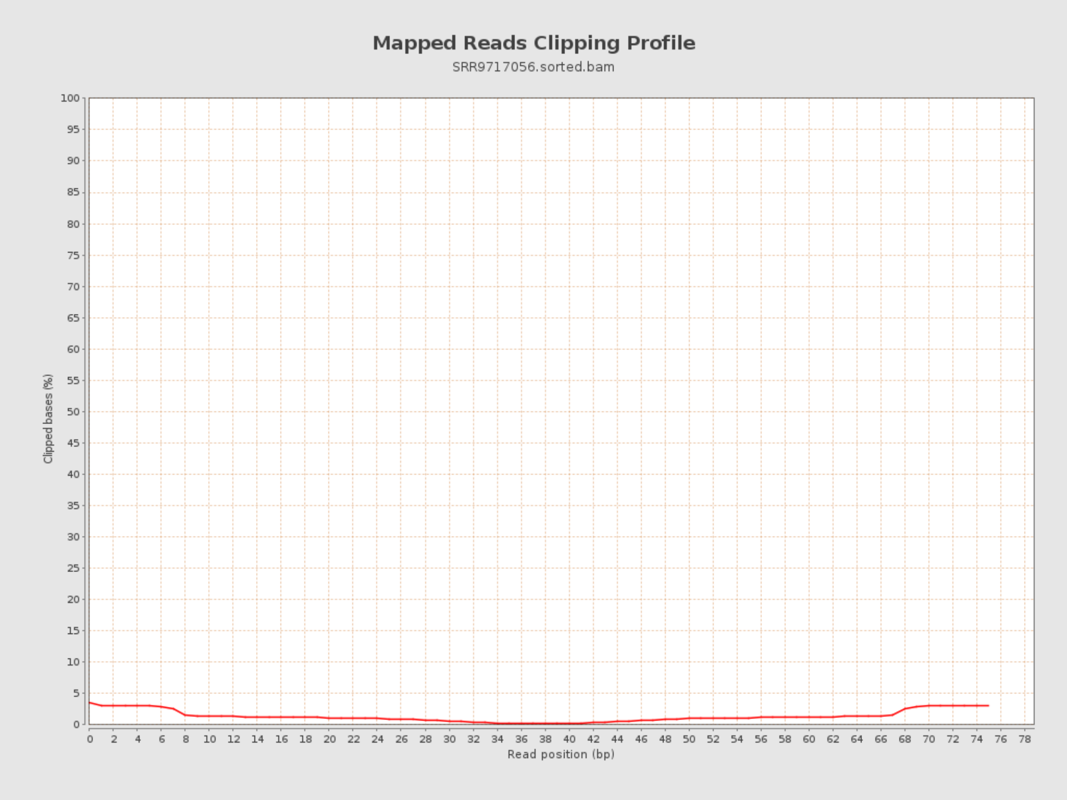
8. Results : Mapped Reads Nucleotide Content



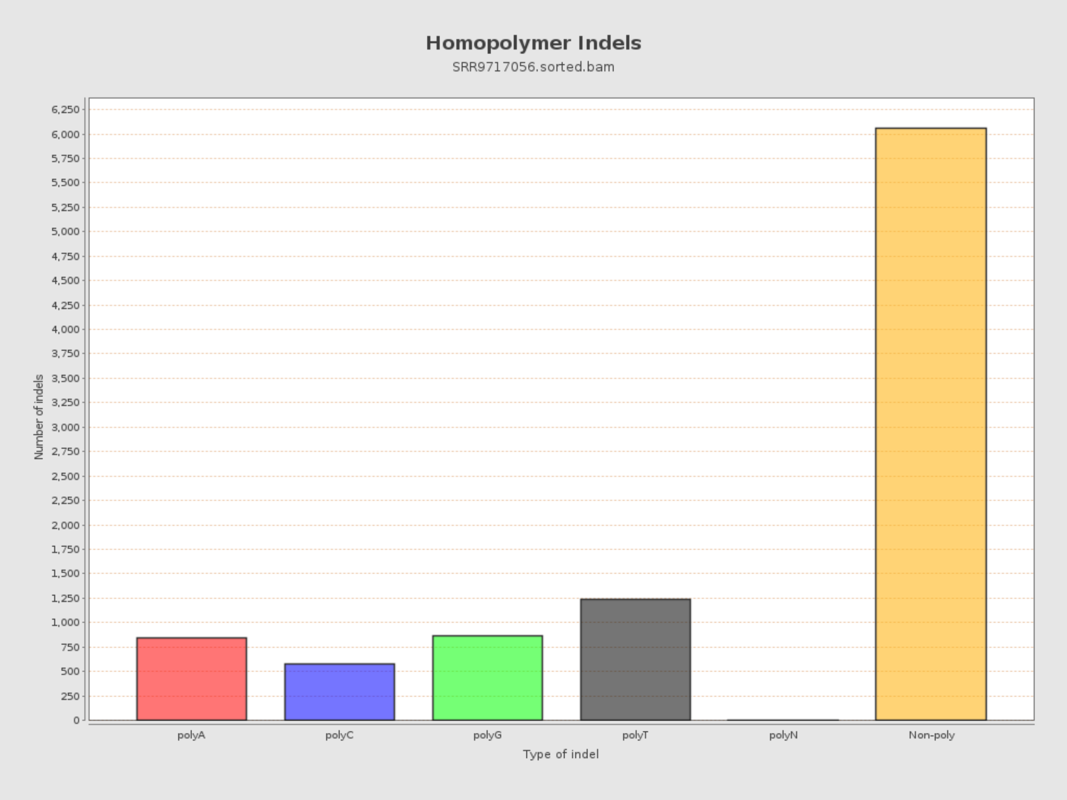
9. Results : Mapped Reads GC-content Distribution



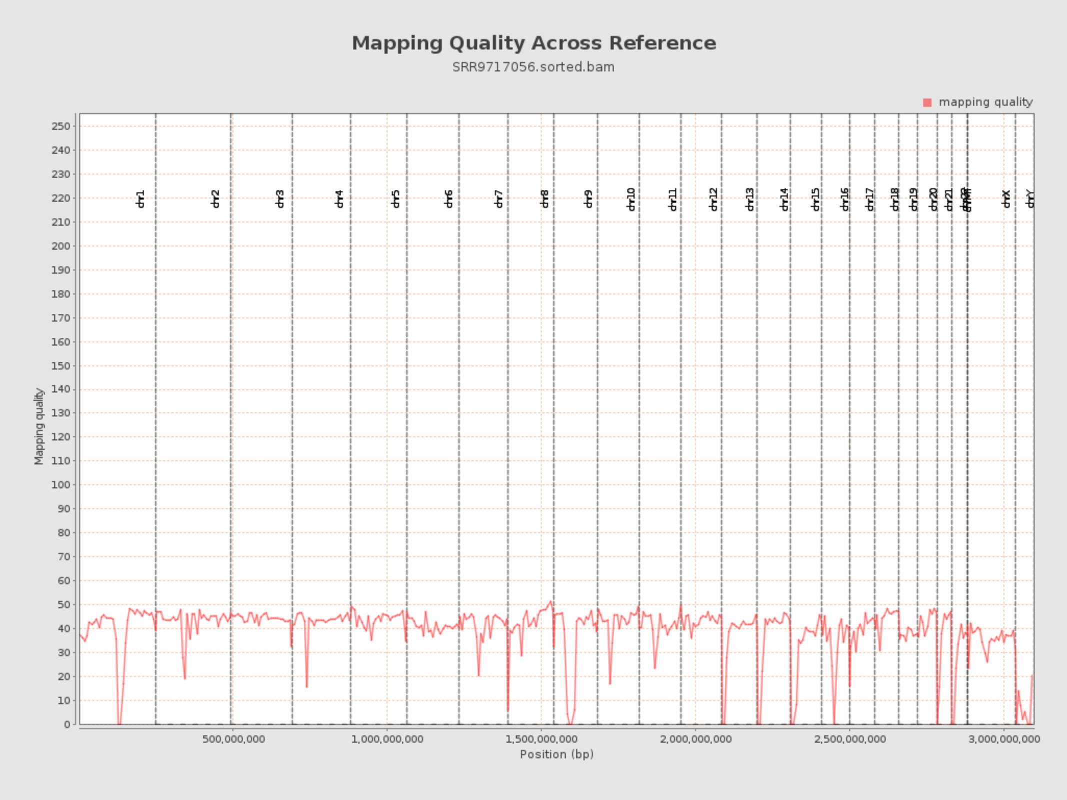
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram