Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 12:40:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716796.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_SRR9716796 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716796.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 12:40:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716796.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	743,966
Mapped reads	557,431 / 74.93%
Unmapped reads	186,535 / 25.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	646 / 0.09%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	30,695 / 4.13%
Duplication rate	4.87%
Clipped reads	557,239 / 74.9%

2.2. ACGT Content

Number/percentage of A's	6,286,737 / 21.49%
Number/percentage of C's	5,411,597 / 18.5%
Number/percentage of T's	9,499,999 / 32.48%
Number/percentage of G's	8,048,910 / 27.52%
Number/percentage of N's	524 / 0%
GC Percentage	46.02%

2.3. Coverage

Mean	0.0095

Standard Deviation	0.1174

2.4. Mapping Quality

Mean Mapping Quality	42.36

2.5. Mismatches and indels

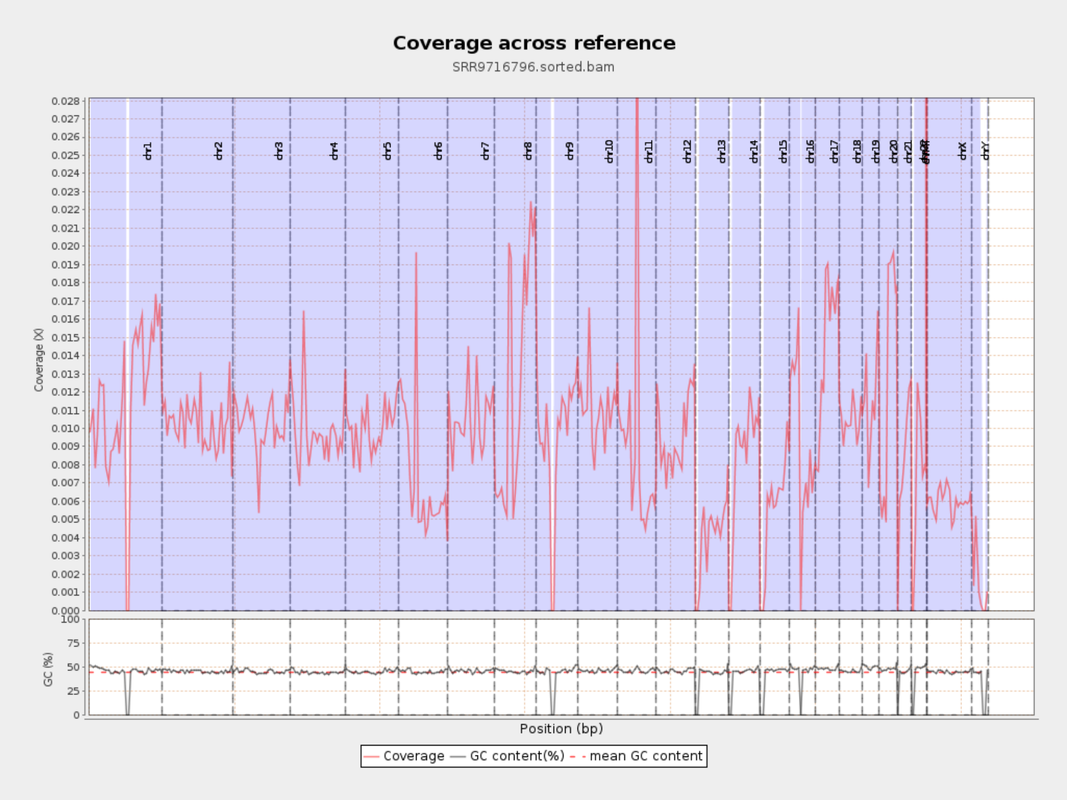
General error rate	0.68%
Mismatches	196,534
Insertions	1,818
Mapped reads with at least one insertion	0.33%
Deletions	4,513
Mapped reads with at least one deletion	0.8%
Homopolymer indels	39.2%

2.6. Chromosome stats

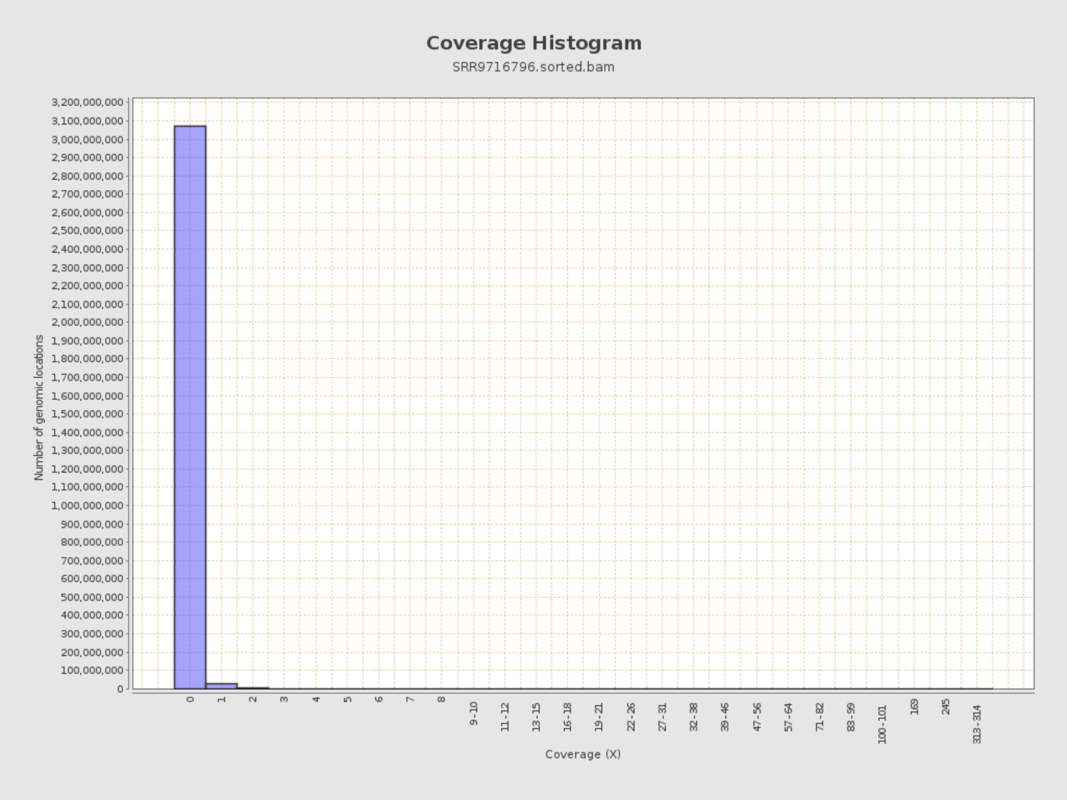
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2868264	0.0115	0.1343
chr2	243199373	2495916	0.0103	0.1661
chr3	198022430	2021794	0.0102	0.1111
chr4	191154276	1861832	0.0097	0.1112
chr5	180915260	1805127	0.01	0.1096
chr6	171115067	1276502	0.0075	0.1062
chr7	159138663	1672529	0.0105	0.1192

chr8	146364022	1868667	0.0128	0.1275
chr9	141213431	1305690	0.0092	0.1098
chr10	135534747	1493702	0.011	0.126
chr11	135006516	1271161	0.0094	0.1167
chr12	133851895	1292166	0.0097	0.1087
chr13	115169878	465791	0.004	0.0718
chr14	107349540	888037	0.0083	0.1005
chr15	102531392	568084	0.0055	0.0818
chr16	90354753	827492	0.0092	0.1094
chr17	81195210	1201174	0.0148	0.1379
chr18	78077248	815012	0.0104	0.1208
chr19	59128983	680707	0.0115	0.1417
chr20	63025520	802650	0.0127	0.1271
chr21	48129895	399972	0.0083	0.1035
chr22	51304566	343909	0.0067	0.0942
chrMT	16571	8357	0.5043	0.8369
chrX	155270560	931671	0.006	0.0861
chrY	59373566	89280	0.0015	0.0529

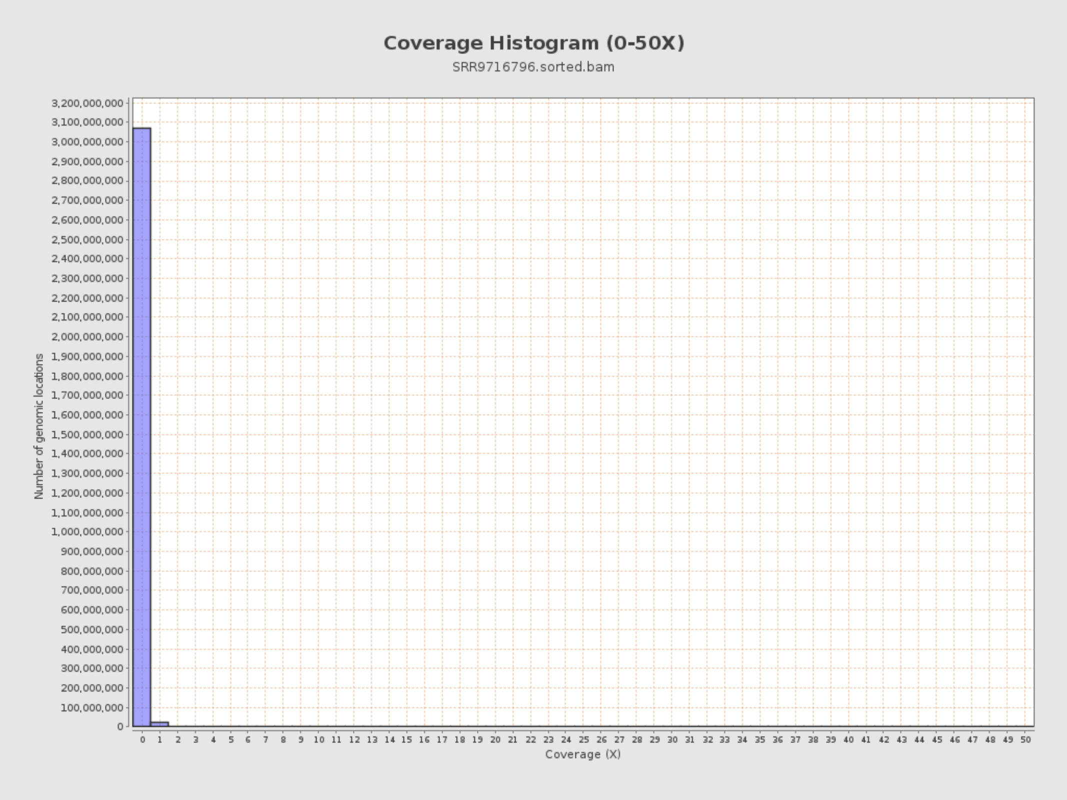
3. Results : Coverage across reference



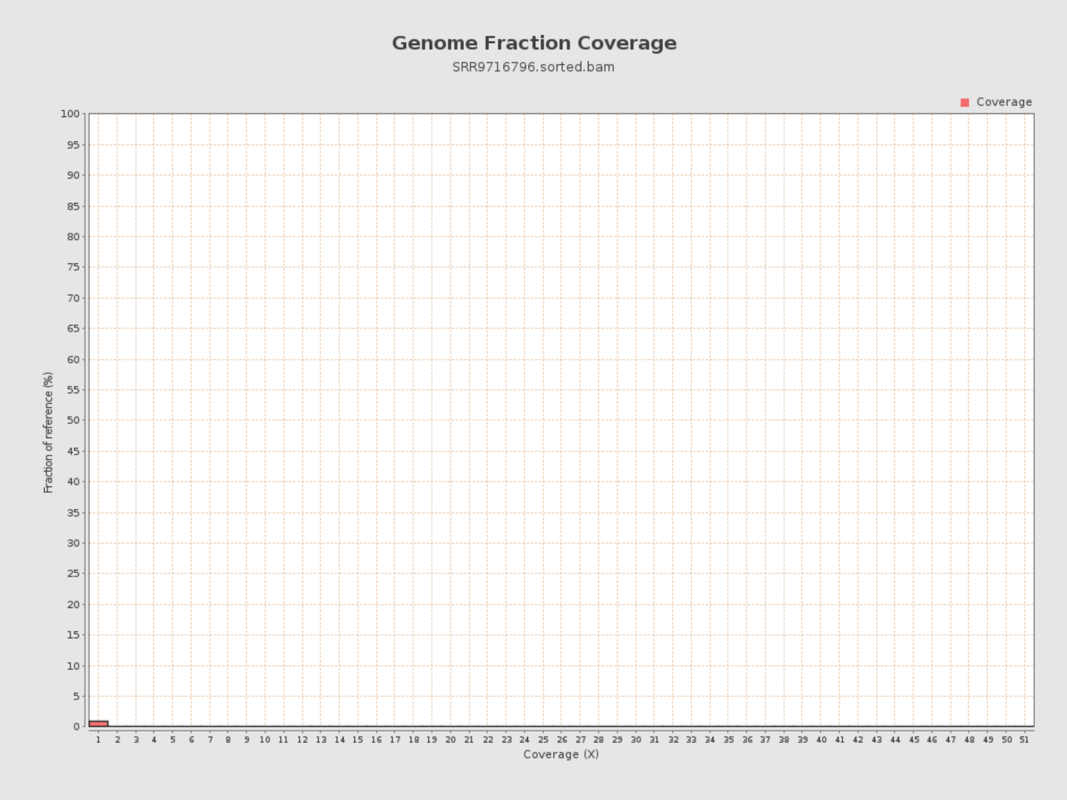
4. Results : Coverage Histogram



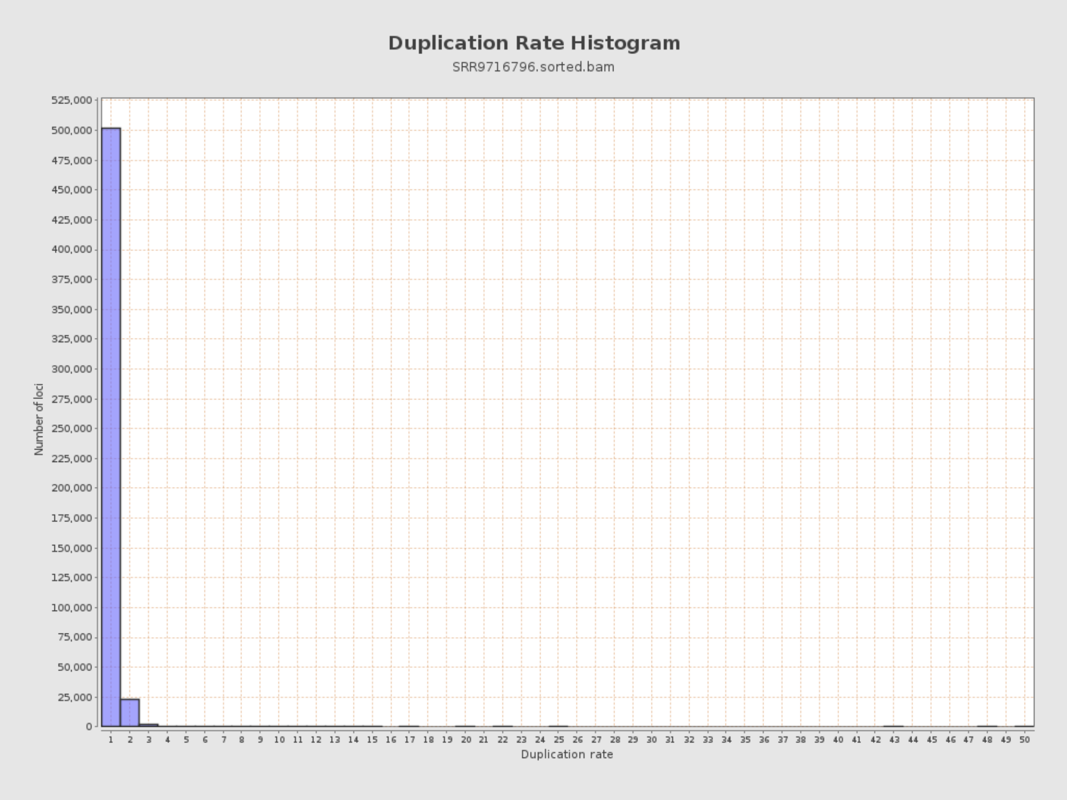
5. Results : Coverage Histogram (0-50X)



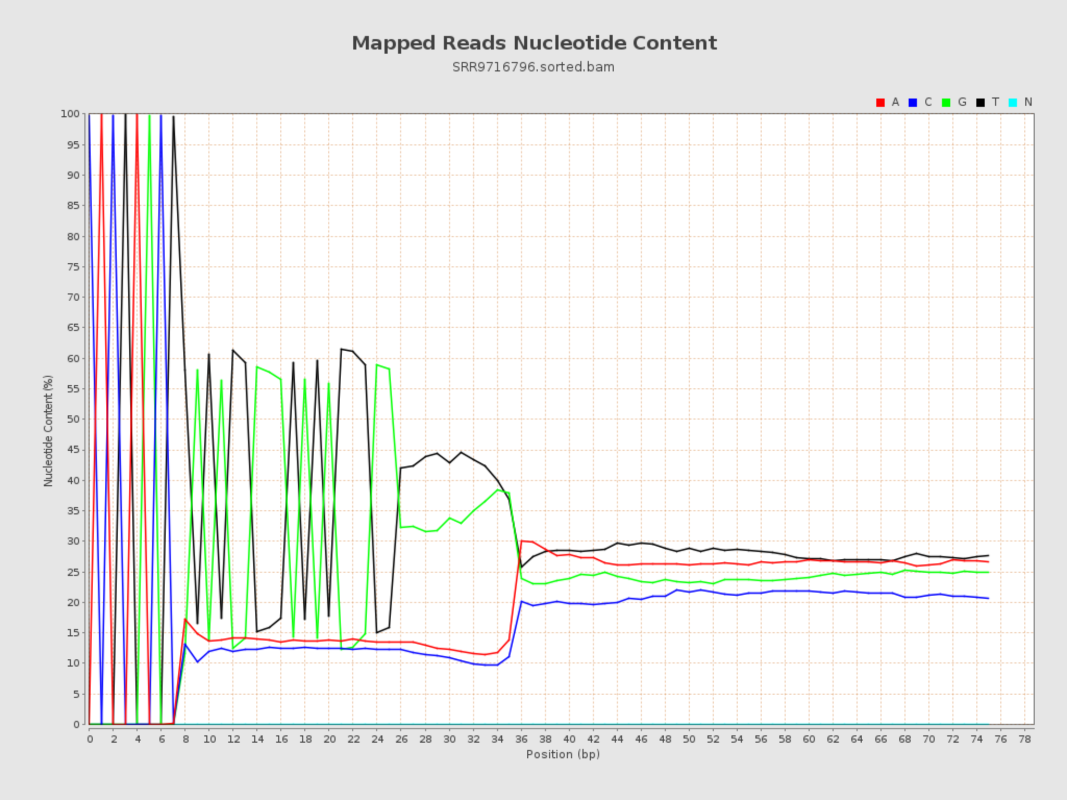
6. Results : Genome Fraction Coverage



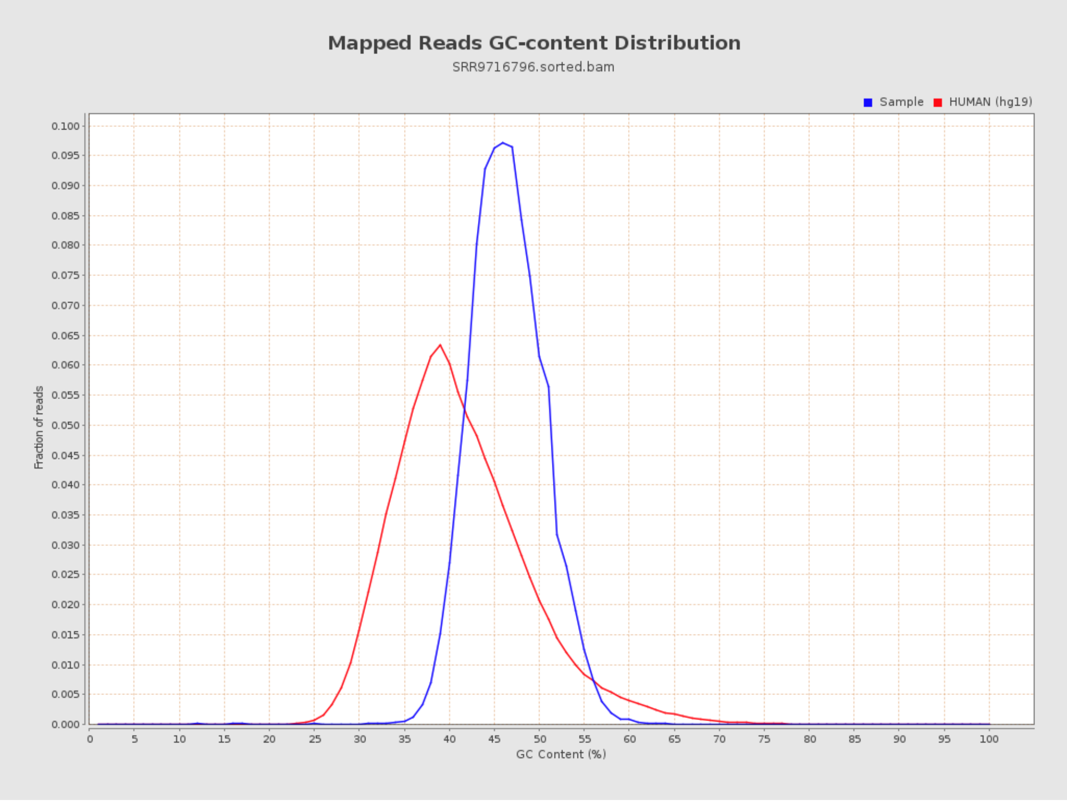
7. Results : Duplication Rate Histogram



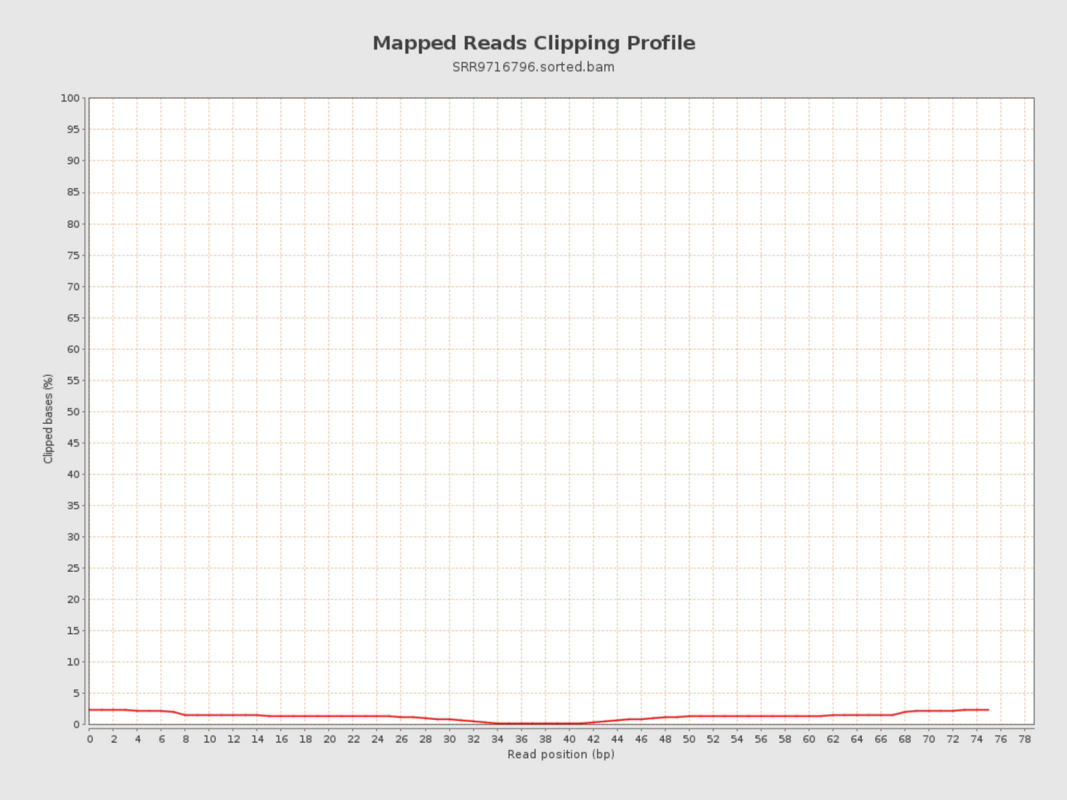
8. Results : Mapped Reads Nucleotide Content



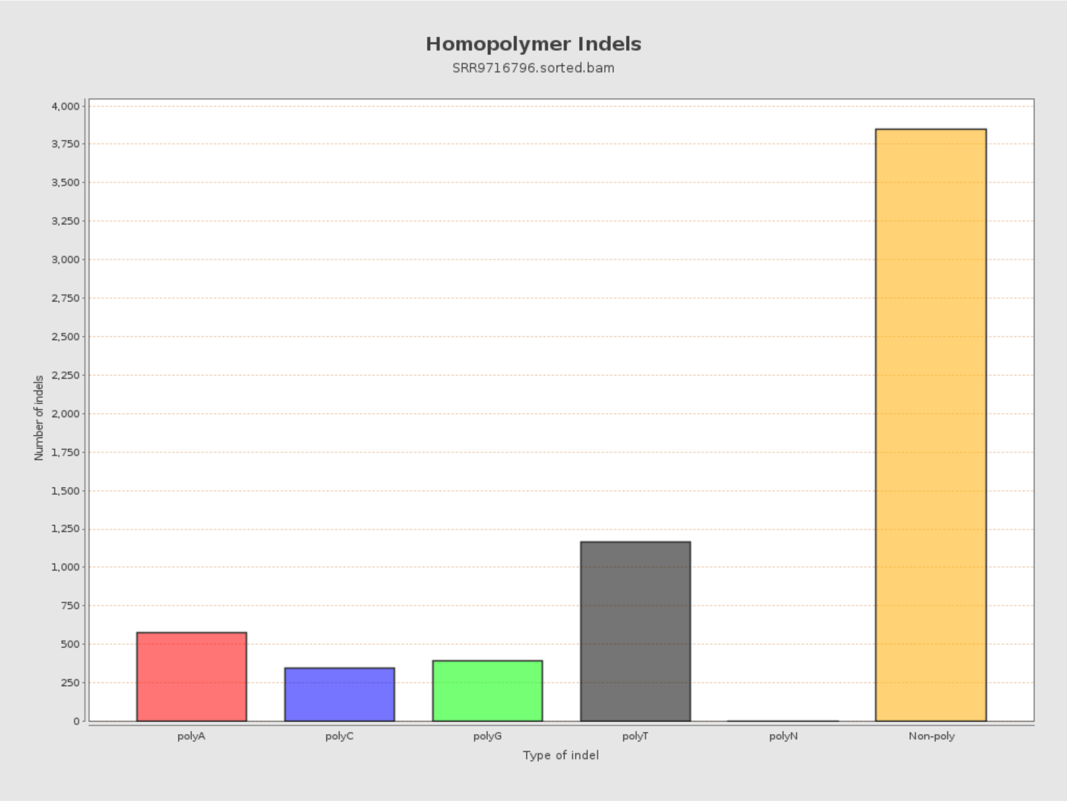
9. Results : Mapped Reads GC-content Distribution



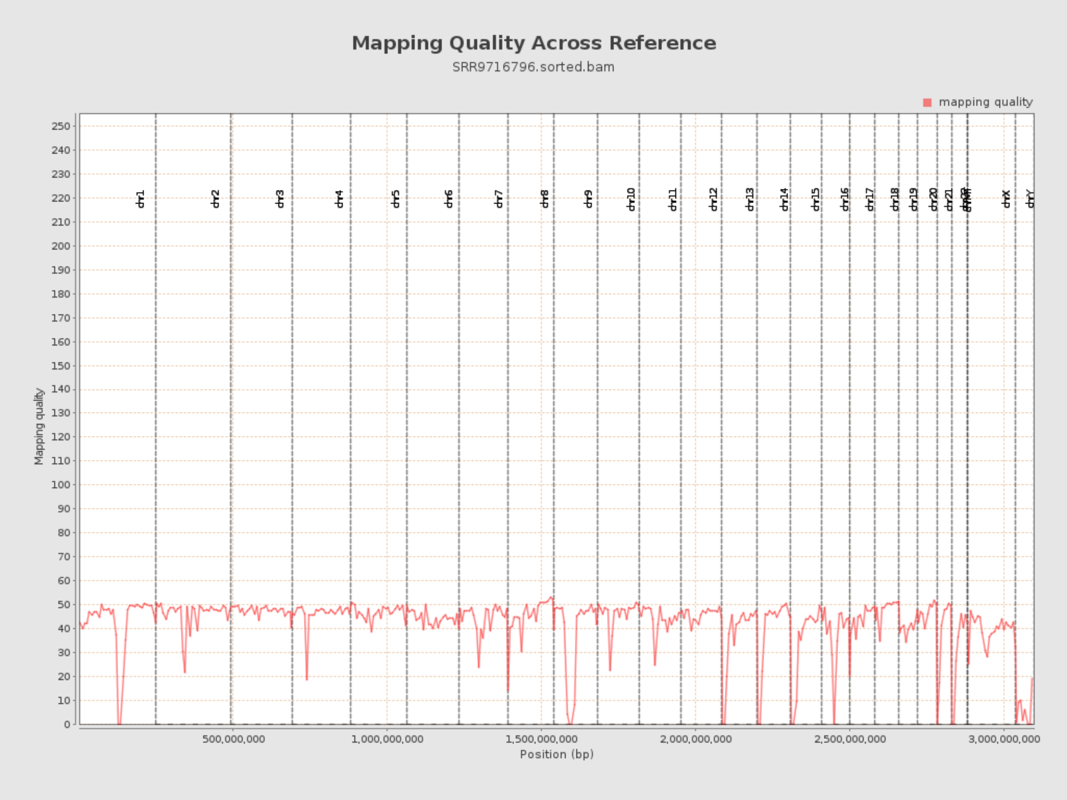
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram