Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 22:12:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716171.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_SRR9716171 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716171.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 22:12:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716171.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	681,553
Mapped reads	635,951 / 93.31%
Unmapped reads	45,602 / 6.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,546 / 1.84%
Read min/max/mean length	30 / 101 / 101.66
Duplicated reads (estimated)	13,589 / 1.99%
Duplication rate	1.53%
Clipped reads	647,064 / 94.94%

2.2. ACGT Content

Number/percentage of A's	12,841,004 / 25.56%
Number/percentage of C's	10,043,405 / 19.99%
Number/percentage of T's	15,222,962 / 30.31%
Number/percentage of G's	12,120,258 / 24.13%
Number/percentage of N's	3,726 / 0.01%
GC Percentage	44.12%

2.3. Coverage

Mean	0.0162

Standard Deviation	0.1702

2.4. Mapping Quality

Mean Mapping Quality	47.61

2.5. Mismatches and indels

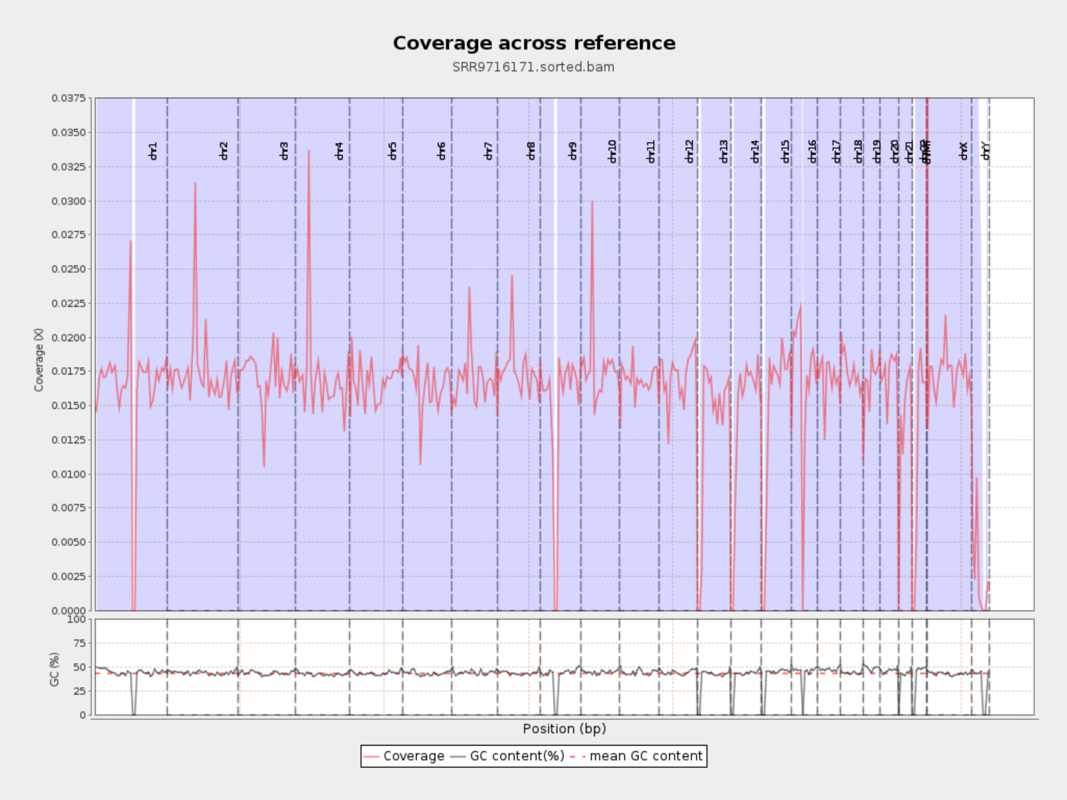
General error rate	0.67%
Mismatches	326,862
Insertions	4,735
Mapped reads with at least one insertion	0.73%
Deletions	11,899
Mapped reads with at least one deletion	1.84%
Homopolymer indels	41.87%

2.6. Chromosome stats

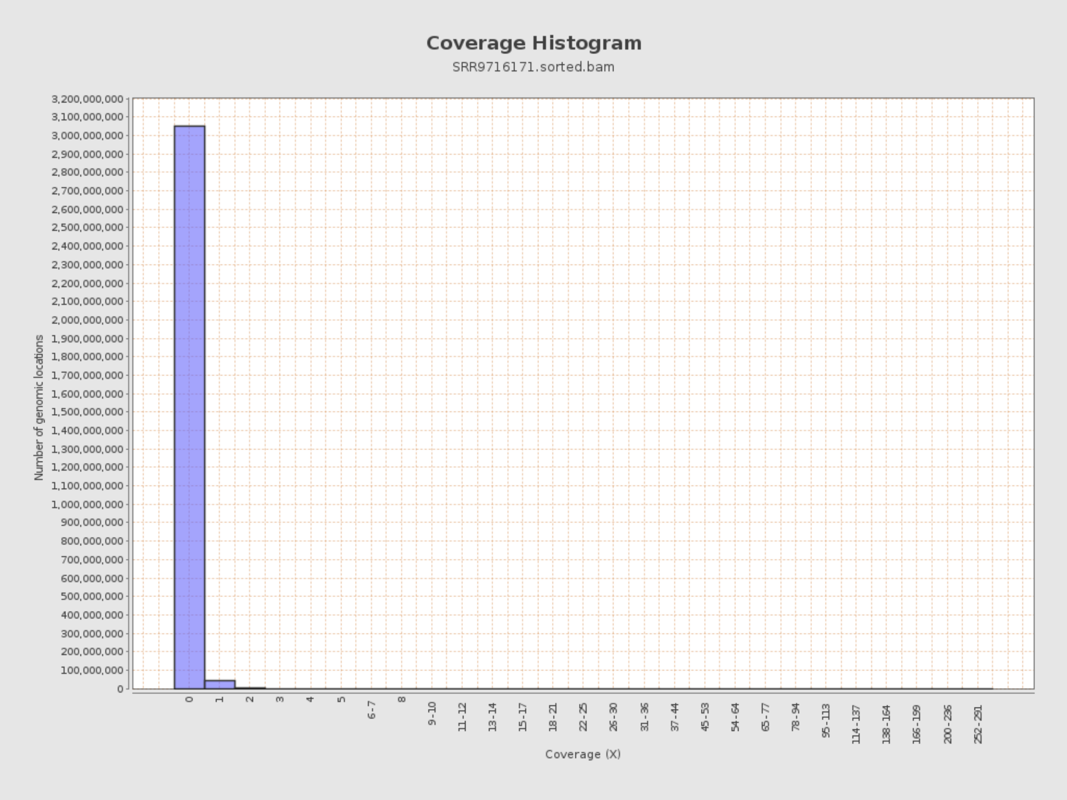
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4043289	0.0162	0.2643
chr2	243199373	4257283	0.0175	0.1922
chr3	198022430	3388743	0.0171	0.1369
chr4	191154276	3275248	0.0171	0.1566
chr5	180915260	3054677	0.0169	0.1367
chr6	171115067	2849158	0.0167	0.1412
chr7	159138663	2714104	0.0171	0.2001

chr8	146364022	2580144	0.0176	0.2016
chr9	141213431	2085704	0.0148	0.1591
chr10	135534747	2427351	0.0179	0.1859
chr11	135006516	2291551	0.017	0.1673
chr12	133851895	2296473	0.0172	0.1377
chr13	115169878	1536727	0.0133	0.1206
chr14	107349540	1508114	0.014	0.1265
chr15	102531392	1488107	0.0145	0.126
chr16	90354753	1501533	0.0166	0.1397
chr17	81195210	1372867	0.0169	0.1442
chr18	78077248	1366521	0.0175	0.2158
chr19	59128983	1003488	0.017	0.1964
chr20	63025520	1088686	0.0173	0.1411
chr21	48129895	661170	0.0137	0.1329
chr22	51304566	611681	0.0119	0.1147
chrMT	16571	4293	0.2591	0.6016
chrX	155270560	2697070	0.0174	0.1477
chrY	59373566	150360	0.0025	0.0972

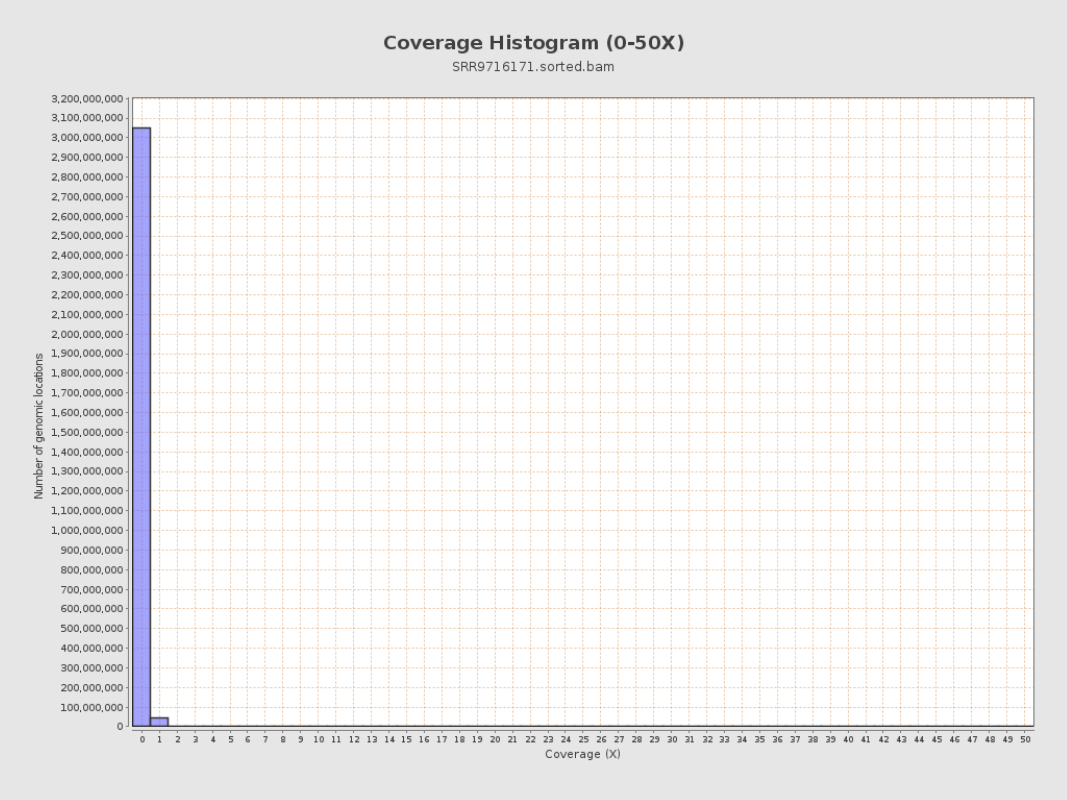
3. Results : Coverage across reference



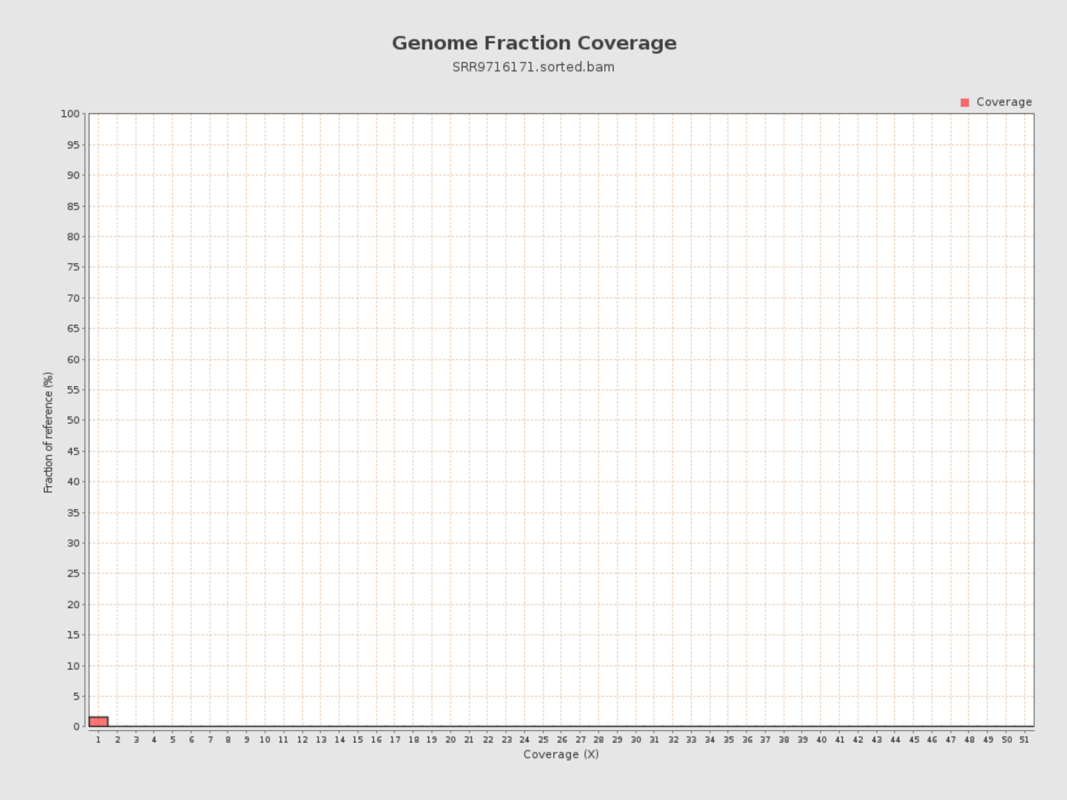
4. Results : Coverage Histogram



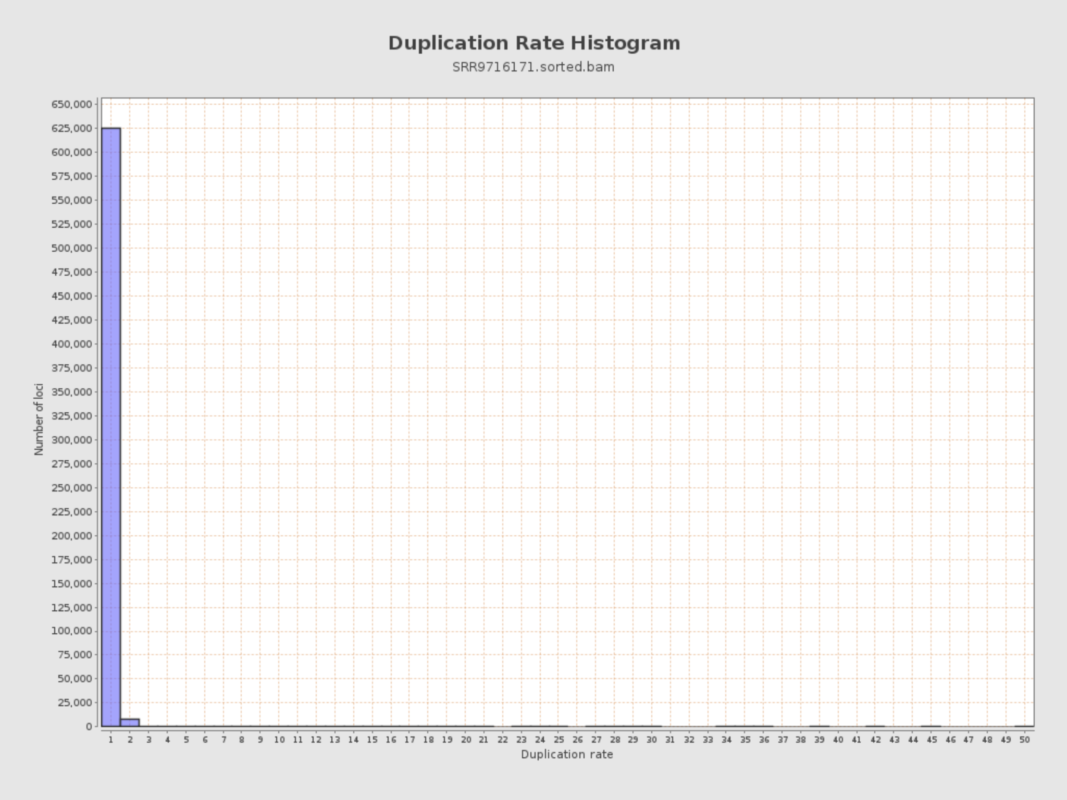
5. Results : Coverage Histogram (0-50X)



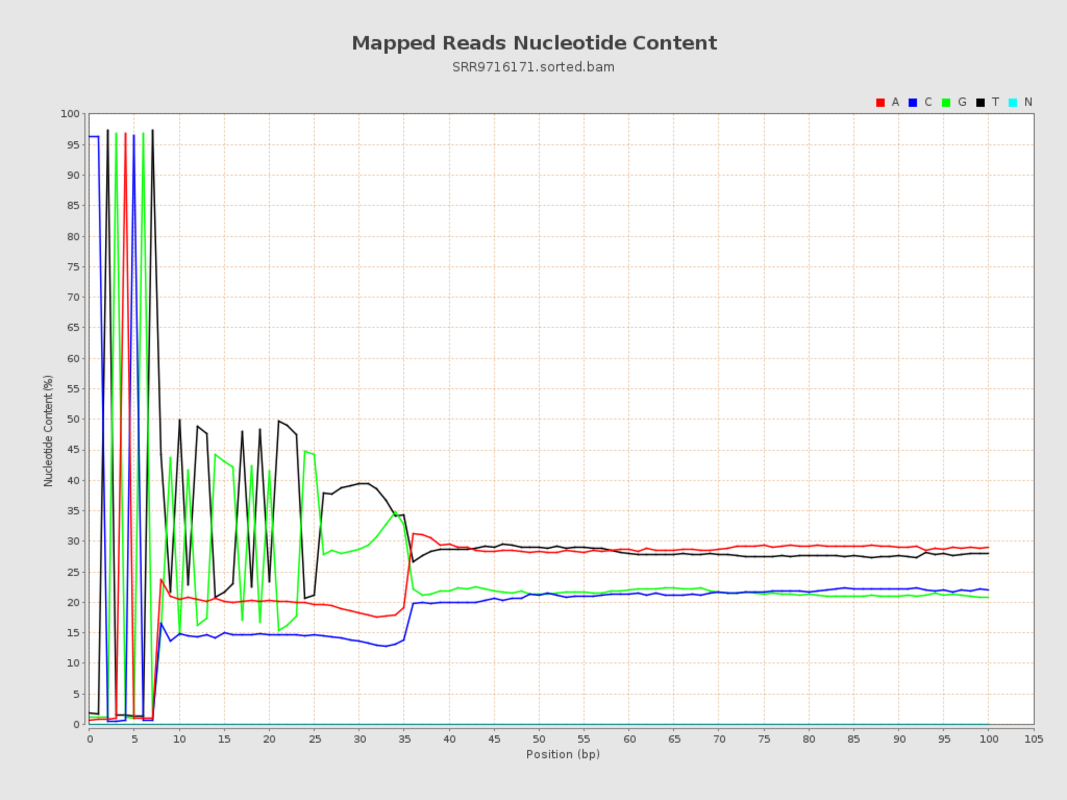
6. Results : Genome Fraction Coverage



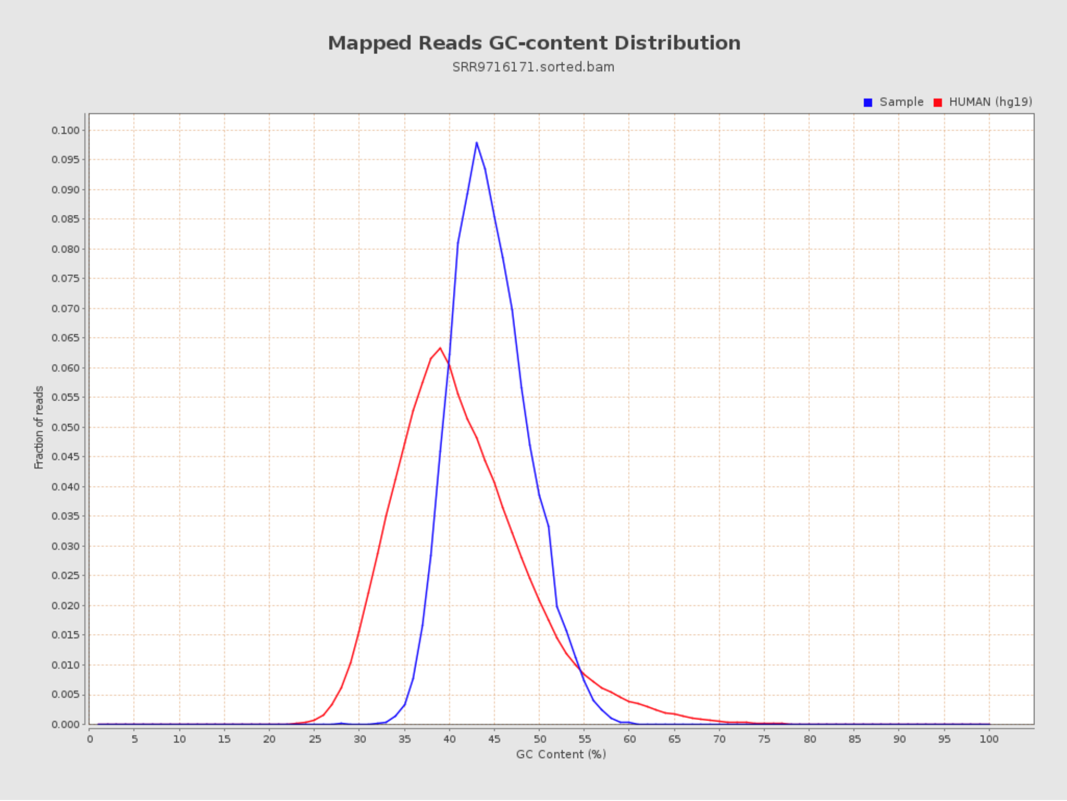
7. Results : Duplication Rate Histogram



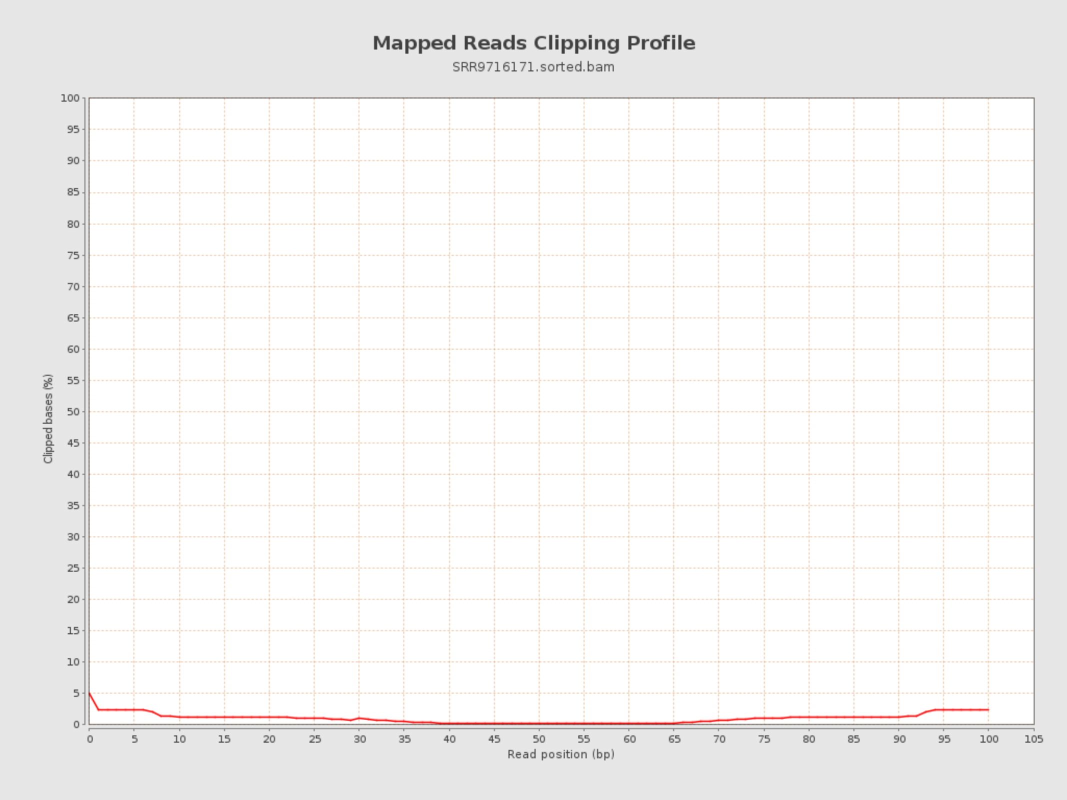
8. Results : Mapped Reads Nucleotide Content



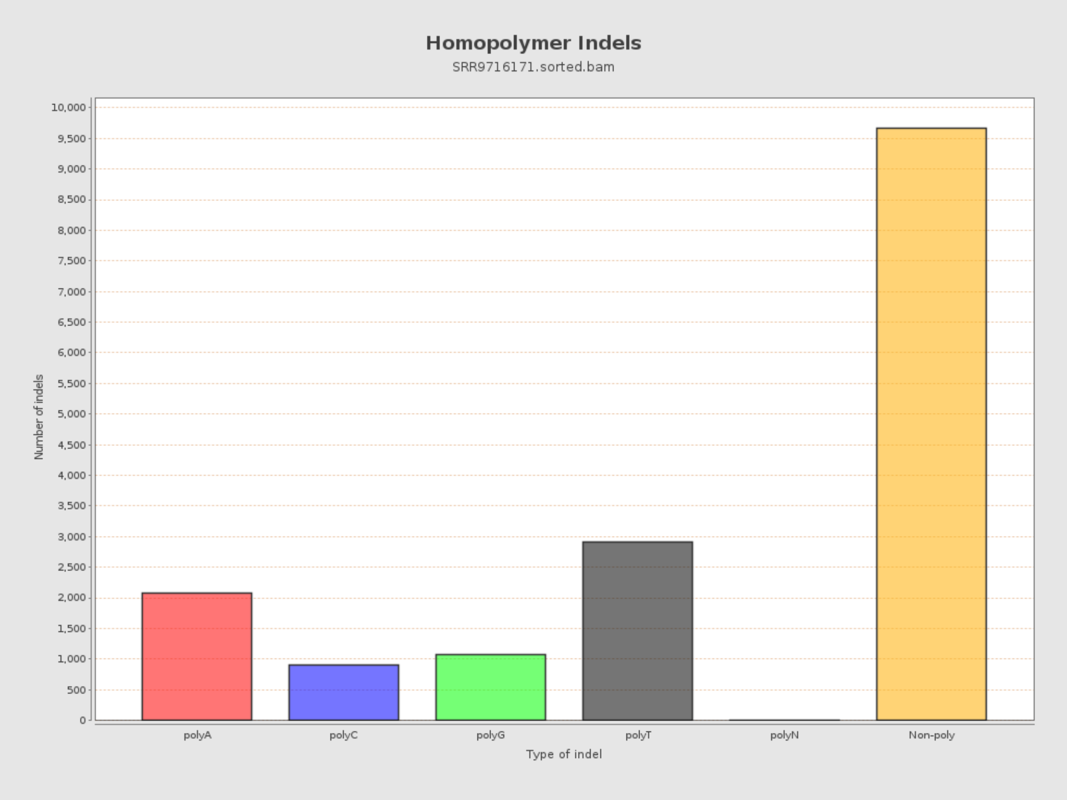
9. Results : Mapped Reads GC-content Distribution



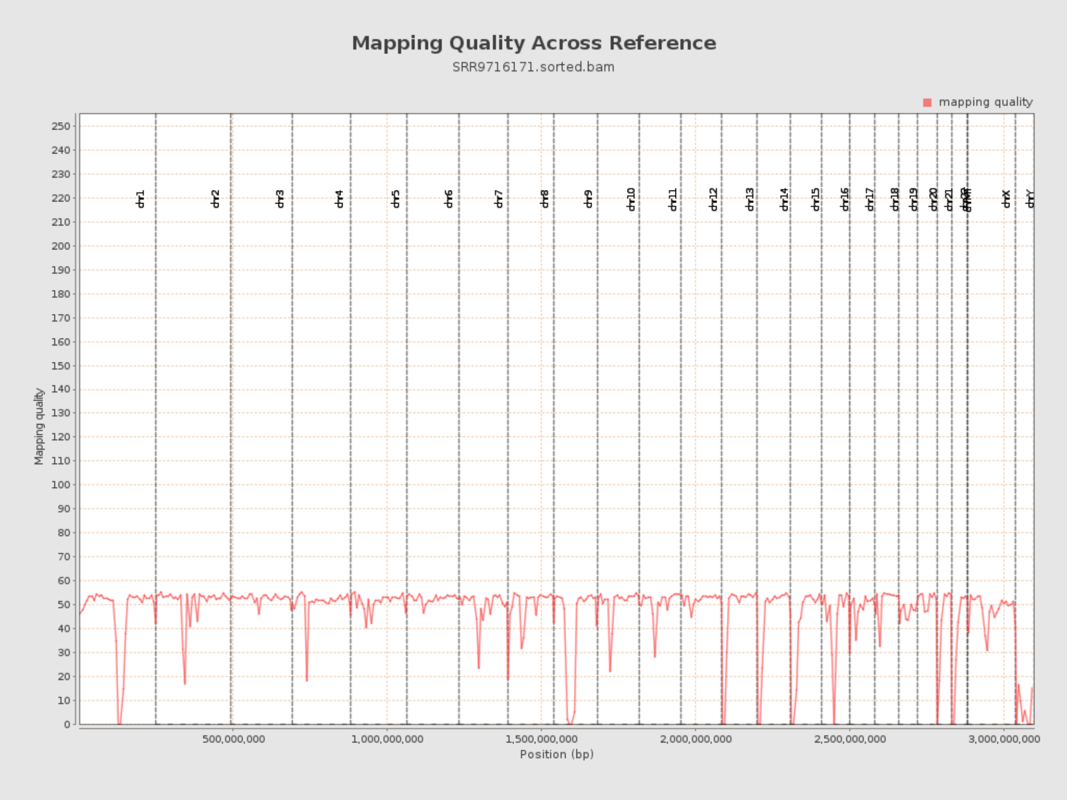
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram