Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 13:08:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716808.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_SRR9716808 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716808.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 13:08:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716808.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	999,823
Mapped reads	918,628 / 91.88%
Unmapped reads	81,195 / 8.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,855 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	28,091 / 2.81%
Duplication rate	2.26%
Clipped reads	919,015 / 91.92%

2.2. ACGT Content

Number/percentage of A's	13,498,348 / 25.31%
Number/percentage of C's	9,961,092 / 18.68%
Number/percentage of T's	17,209,092 / 32.27%
Number/percentage of G's	12,652,552 / 23.73%
Number/percentage of N's	1,069 / 0%
GC Percentage	42.41%

2.3. Coverage

Mean	0.0172

Standard Deviation	0.1812

2.4. Mapping Quality

Mean Mapping Quality	44.83

2.5. Mismatches and indels

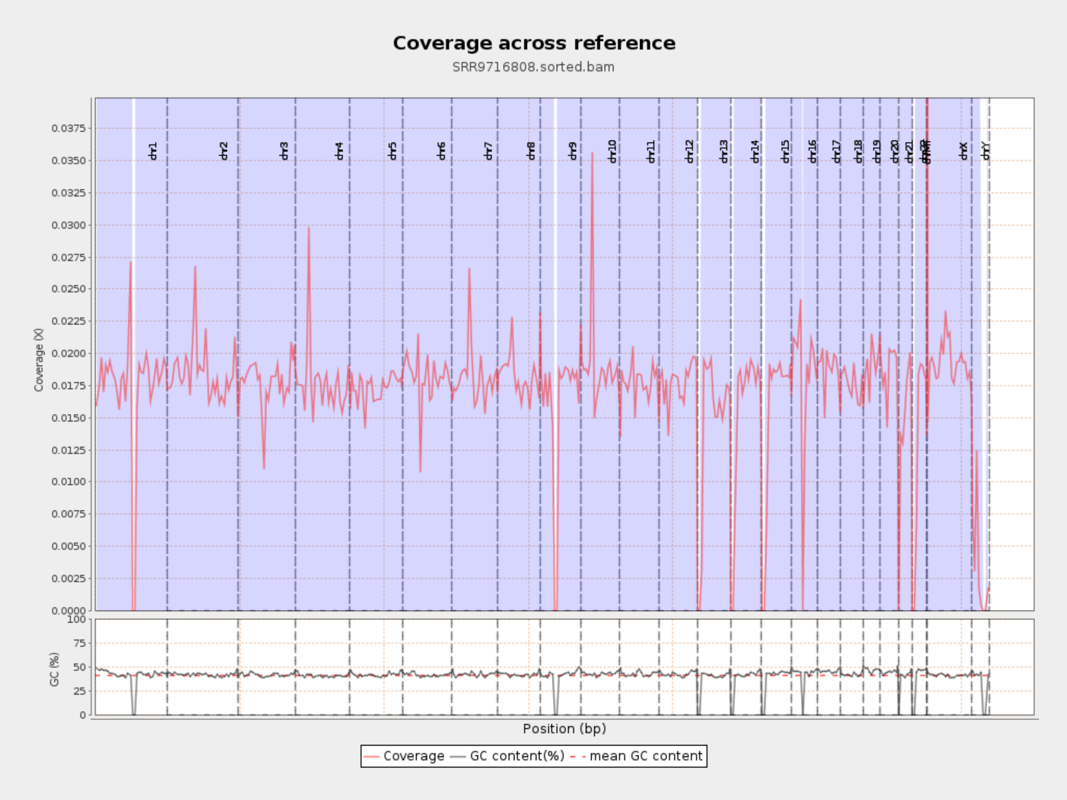
General error rate	0.52%
Mismatches	265,301
Insertions	4,493
Mapped reads with at least one insertion	0.49%
Deletions	10,210
Mapped reads with at least one deletion	1.1%
Homopolymer indels	41.79%

2.6. Chromosome stats

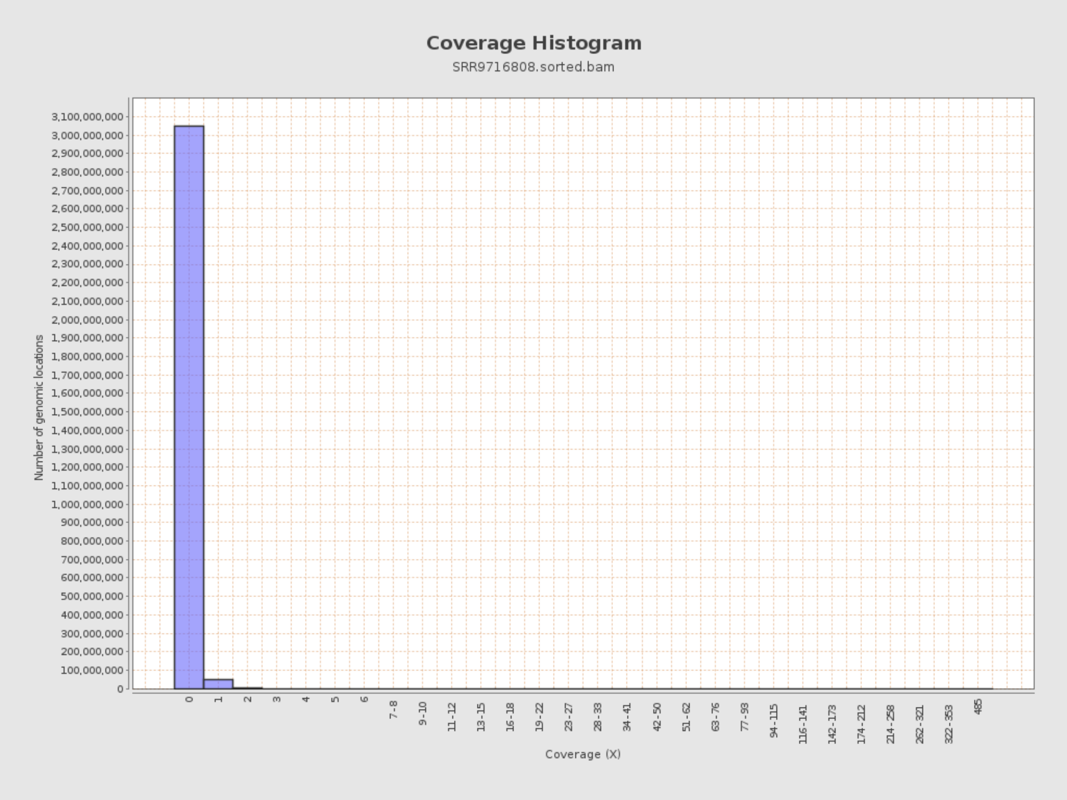
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4303745	0.0173	0.2694
chr2	243199373	4499406	0.0185	0.2505
chr3	198022430	3512250	0.0177	0.1416
chr4	191154276	3395787	0.0178	0.1575
chr5	180915260	3139223	0.0174	0.1395
chr6	171115067	3099601	0.0181	0.1584
chr7	159138663	2899137	0.0182	0.204

chr8	146364022	2670197	0.0182	0.2006
chr9	141213431	2236285	0.0158	0.1546
chr10	135534747	2600325	0.0192	0.1996
chr11	135006516	2407954	0.0178	0.1614
chr12	133851895	2379127	0.0178	0.1426
chr13	115169878	1651436	0.0143	0.1269
chr14	107349540	1632693	0.0152	0.1338
chr15	102531392	1537684	0.015	0.1292
chr16	90354753	1611301	0.0178	0.1469
chr17	81195210	1527022	0.0188	0.1508
chr18	78077248	1375222	0.0176	0.2394
chr19	59128983	1131510	0.0191	0.2084
chr20	63025520	1168939	0.0185	0.1482
chr21	48129895	703872	0.0146	0.1432
chr22	51304566	653944	0.0127	0.1204
chrMT	16571	12435	0.7504	0.9766
chrX	155270560	2998784	0.0193	0.1546
chrY	59373566	190470	0.0032	0.1321

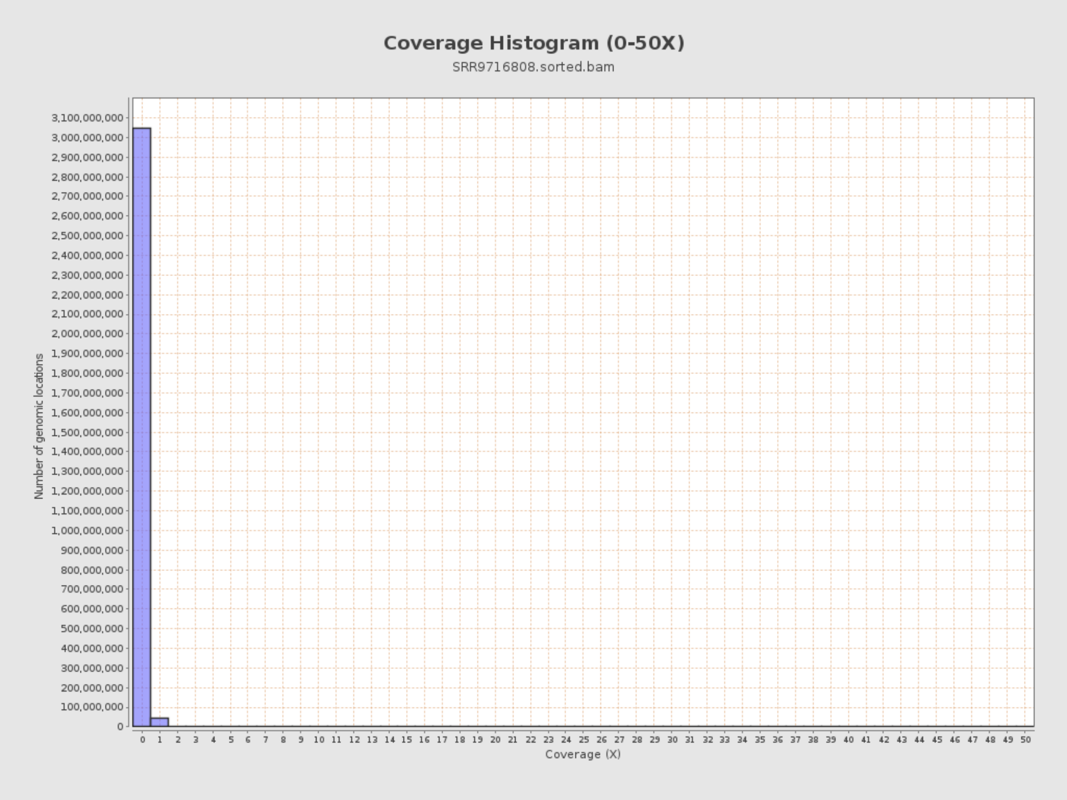
3. Results : Coverage across reference



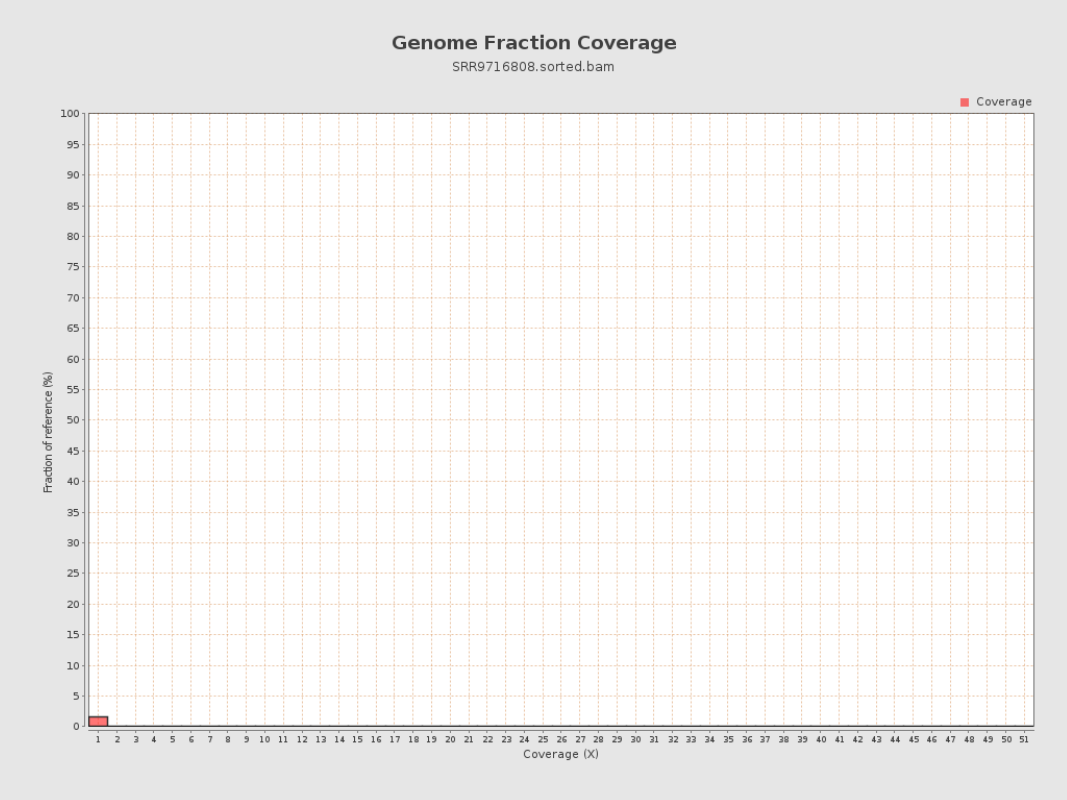
4. Results : Coverage Histogram



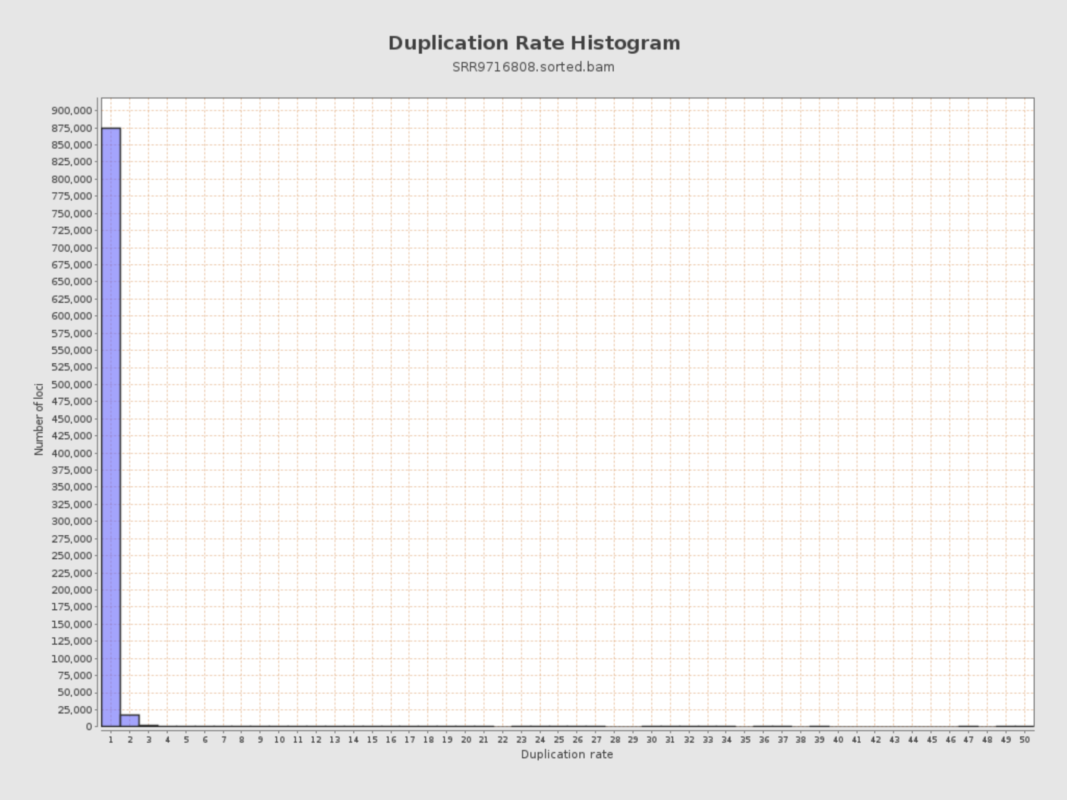
5. Results : Coverage Histogram (0-50X)



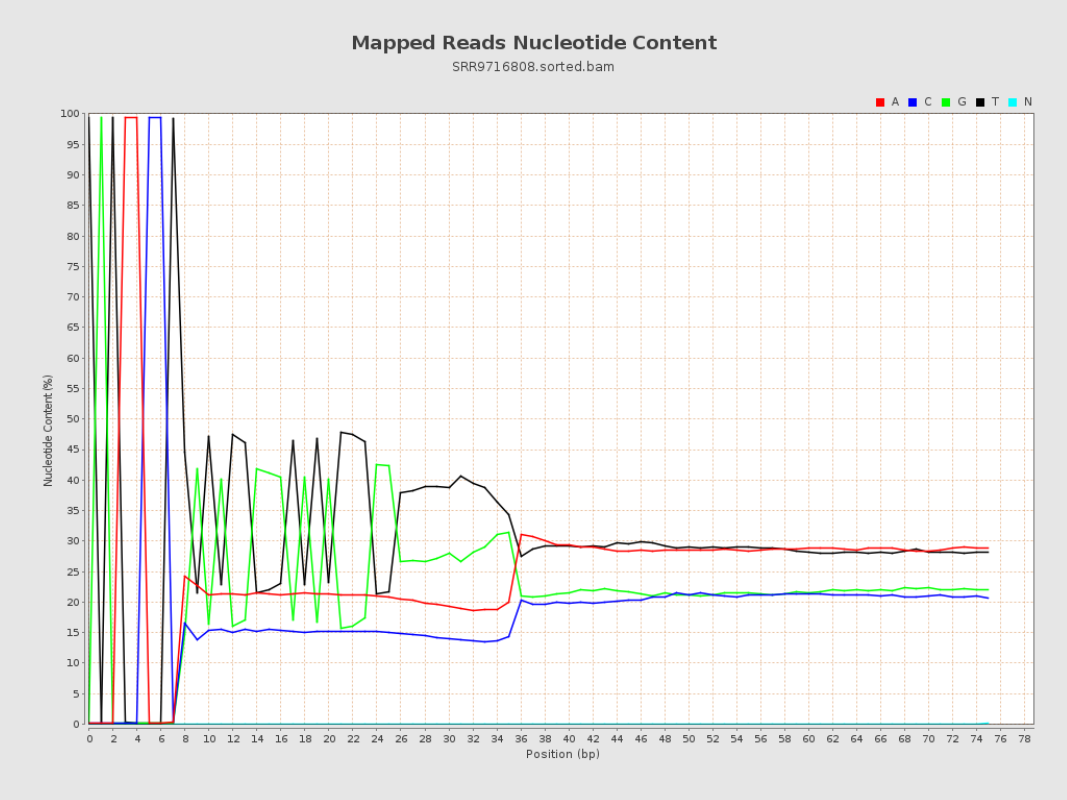
6. Results : Genome Fraction Coverage



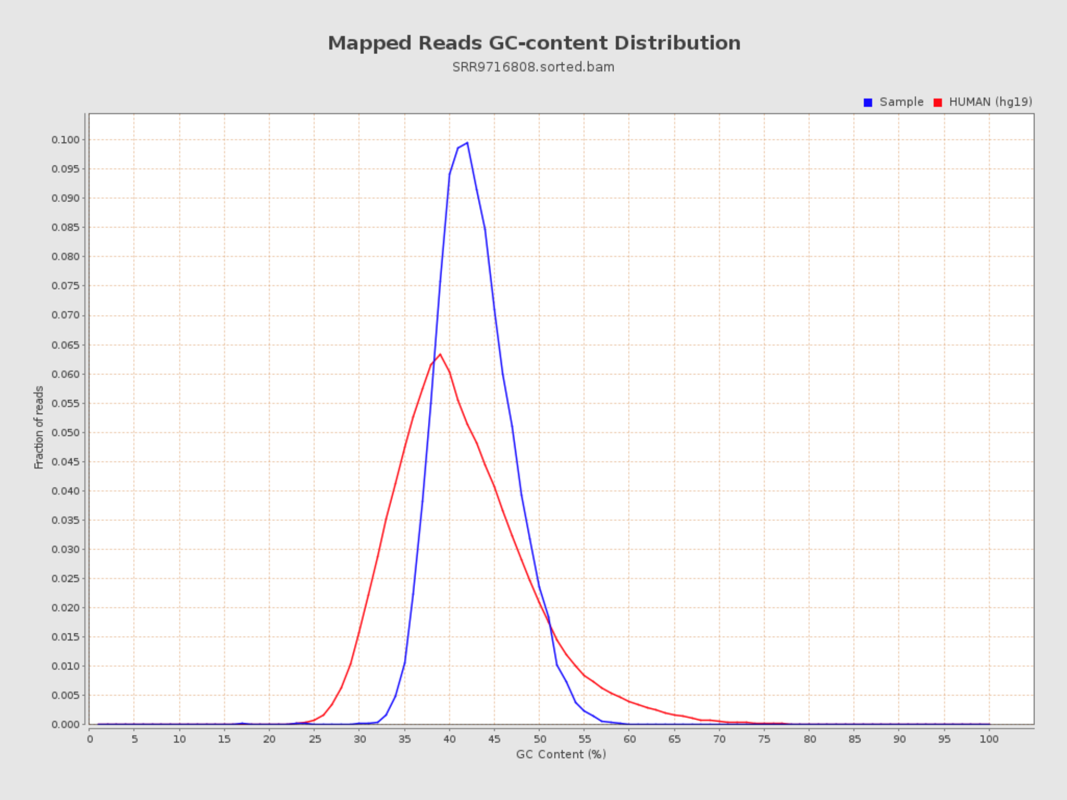
7. Results : Duplication Rate Histogram



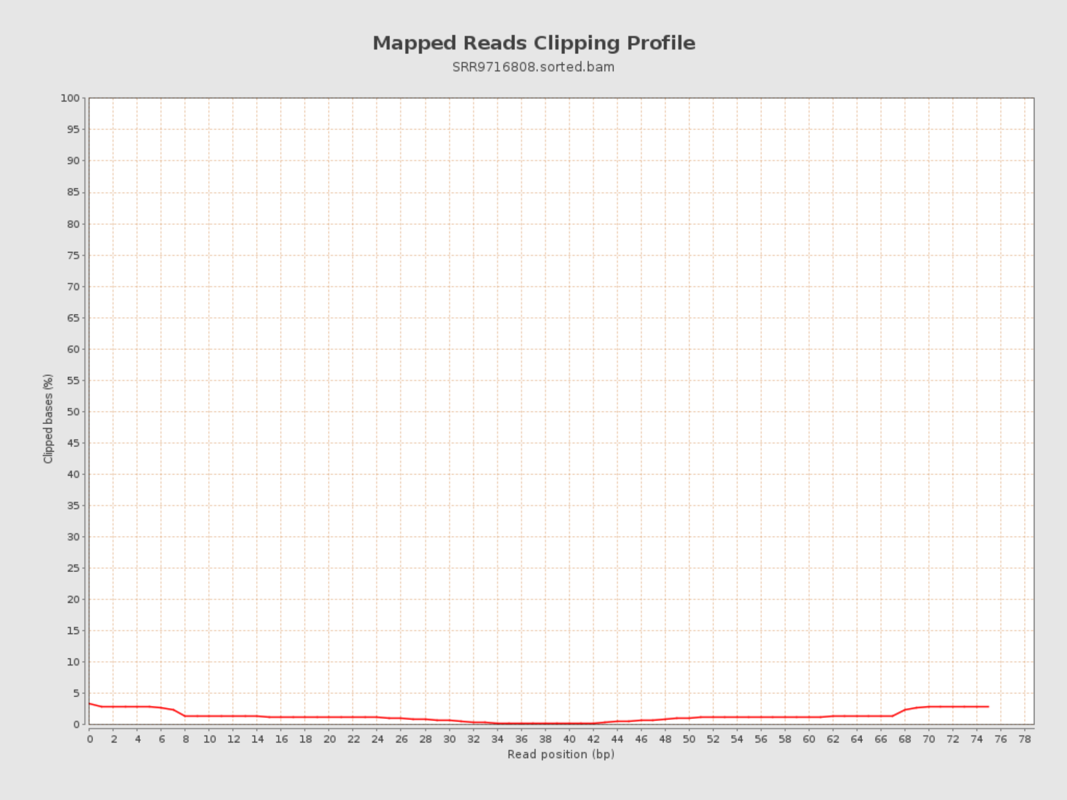
8. Results : Mapped Reads Nucleotide Content



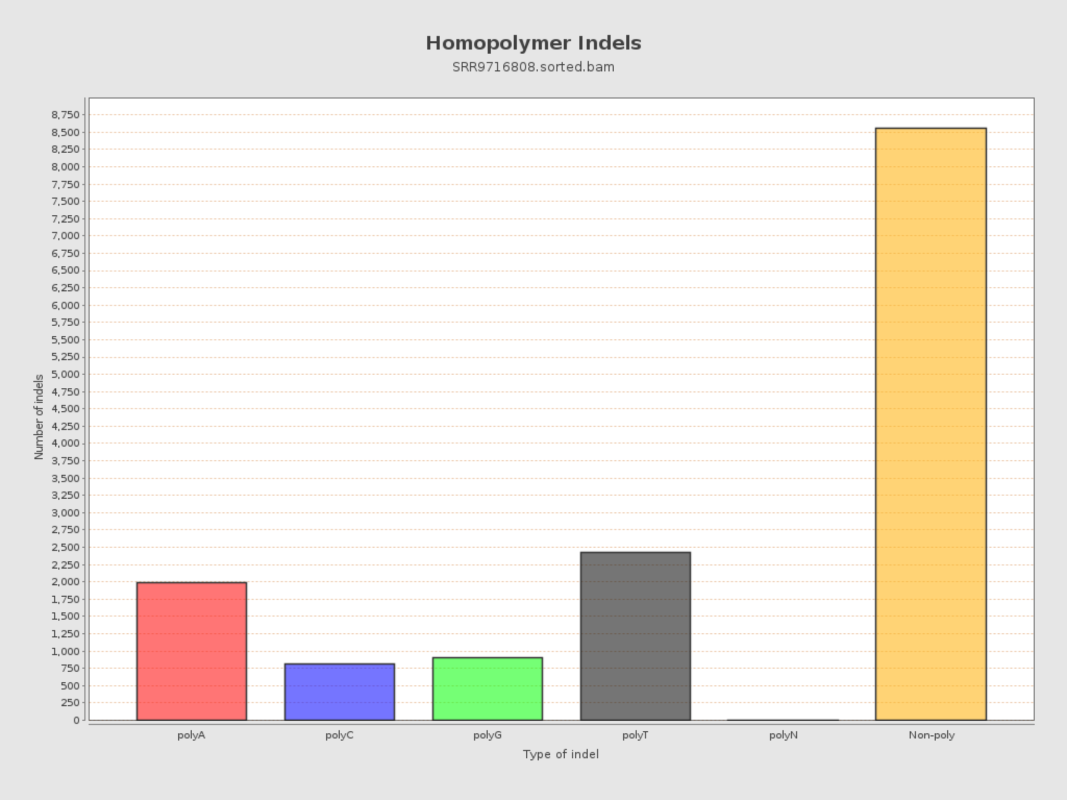
9. Results : Mapped Reads GC-content Distribution



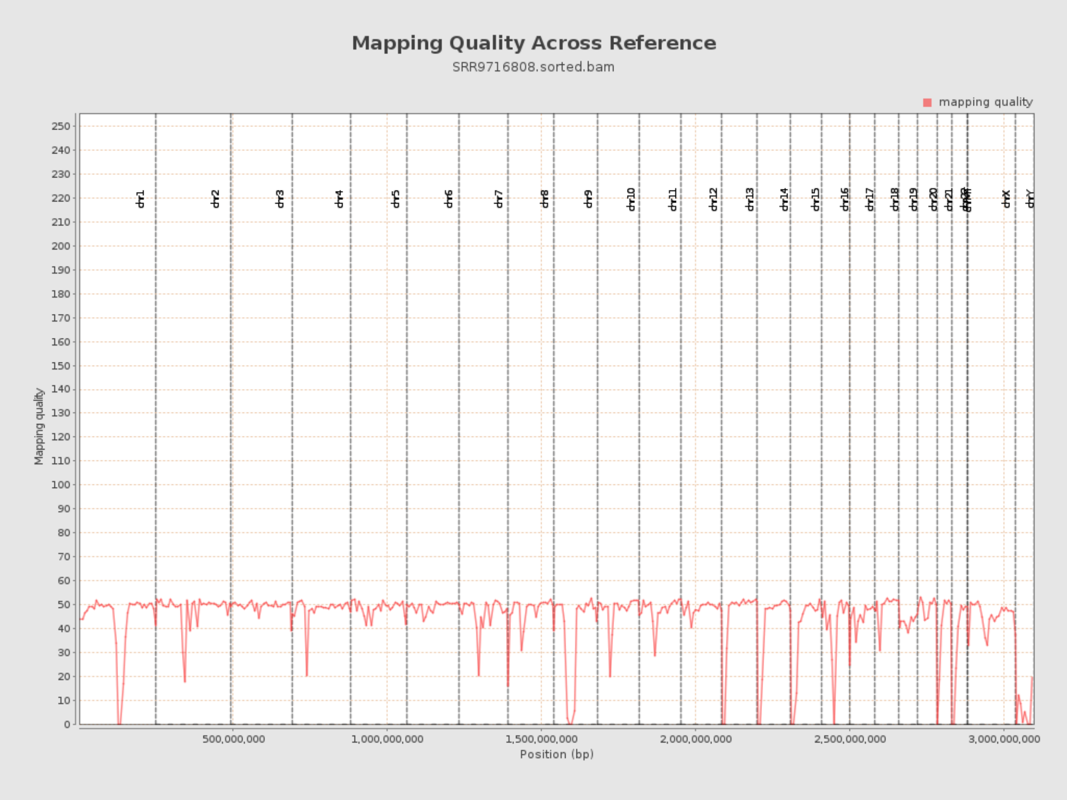
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram