Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 07:48:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716326.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_SRR9716326 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716326.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 07:48:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716326.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,711,230
Mapped reads	1,548,129 / 90.47%
Unmapped reads	163,101 / 9.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,973 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	49,021 / 2.86%
Duplication rate	2.3%
Clipped reads	1,552,716 / 90.74%

2.2. ACGT Content

Number/percentage of A's	23,408,394 / 26%
Number/percentage of C's	16,735,665 / 18.59%
Number/percentage of T's	27,621,484 / 30.68%
Number/percentage of G's	22,276,721 / 24.74%
Number/percentage of N's	2,542 / 0%
GC Percentage	43.33%

2.3. Coverage

Mean	0.0291

Standard Deviation	0.2689

2.4. Mapping Quality

Mean Mapping Quality	44.12

2.5. Mismatches and indels

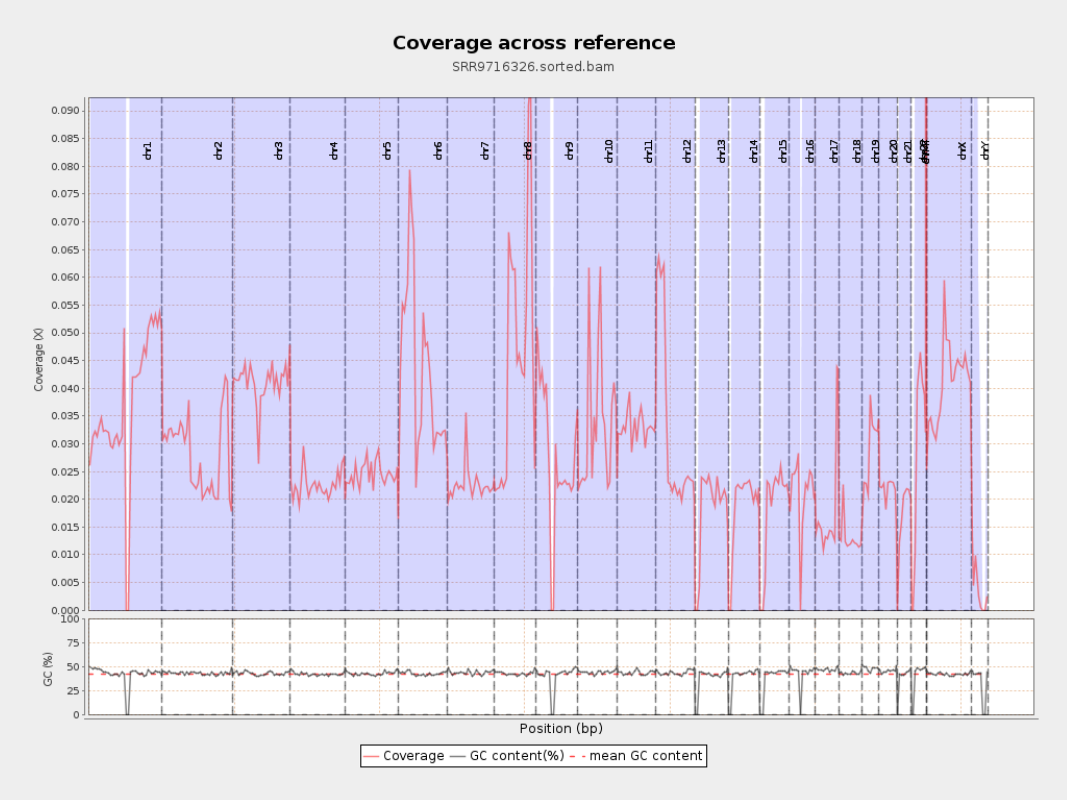
General error rate	0.52%
Mismatches	454,482
Insertions	6,127
Mapped reads with at least one insertion	0.39%
Deletions	16,066
Mapped reads with at least one deletion	1.03%
Homopolymer indels	40.81%

2.6. Chromosome stats

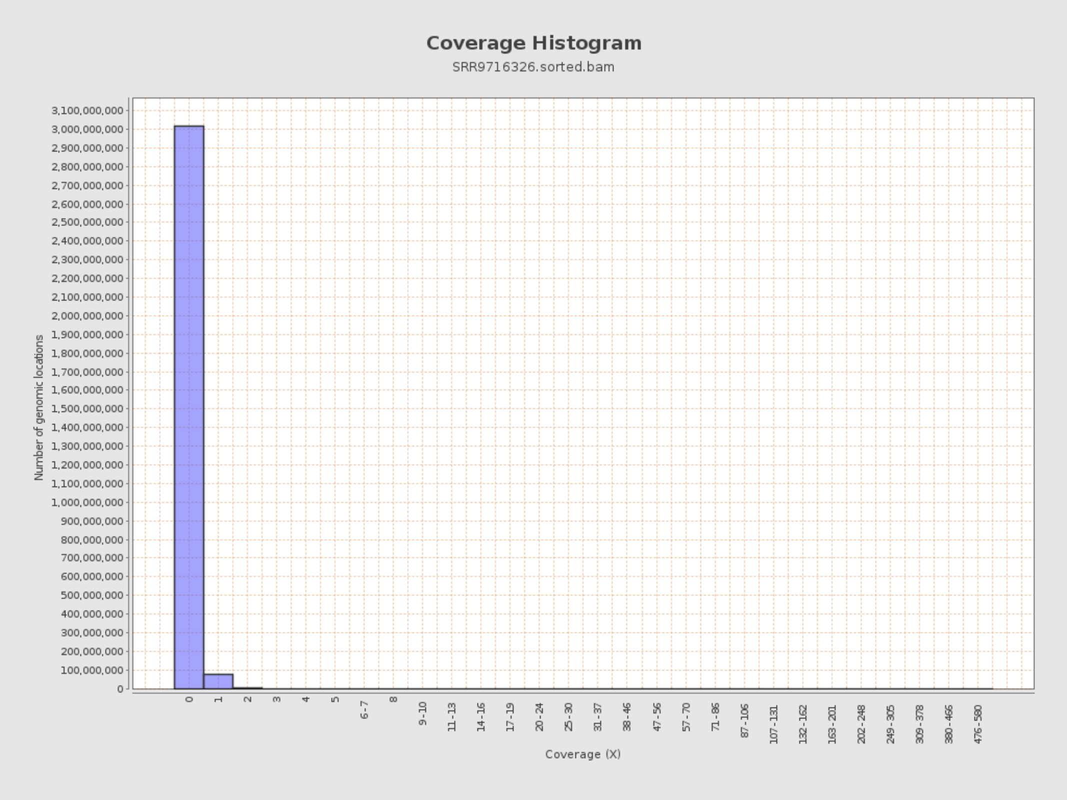
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9108014	0.0365	0.4739
chr2	243199373	6879338	0.0283	0.2964
chr3	198022430	8105703	0.0409	0.2217
chr4	191154276	4330626	0.0227	0.1737
chr5	180915260	4436546	0.0245	0.174
chr6	171115067	7416031	0.0433	0.3238
chr7	159138663	3615695	0.0227	0.256

chr8	146364022	6804014	0.0465	0.2613
chr9	141213431	3784134	0.0268	0.2569
chr10	135534747	4586299	0.0338	0.2987
chr11	135006516	4457057	0.033	0.2696
chr12	133851895	4313884	0.0322	0.2028
chr13	115169878	2091608	0.0182	0.1466
chr14	107349540	1964334	0.0183	0.1882
chr15	102531392	1857043	0.0181	0.1517
chr16	90354753	1901775	0.021	0.1815
chr17	81195210	1466308	0.0181	0.1565
chr18	78077248	1025199	0.0131	0.4228
chr19	59128983	1692626	0.0286	0.3498
chr20	63025520	1366868	0.0217	0.1606
chr21	48129895	815505	0.0169	0.1677
chr22	51304566	1429817	0.0279	0.1809
chrMT	16571	39046	2.3563	1.8888
chrX	155270560	6359120	0.041	0.2551
chrY	59373566	223174	0.0038	0.0858

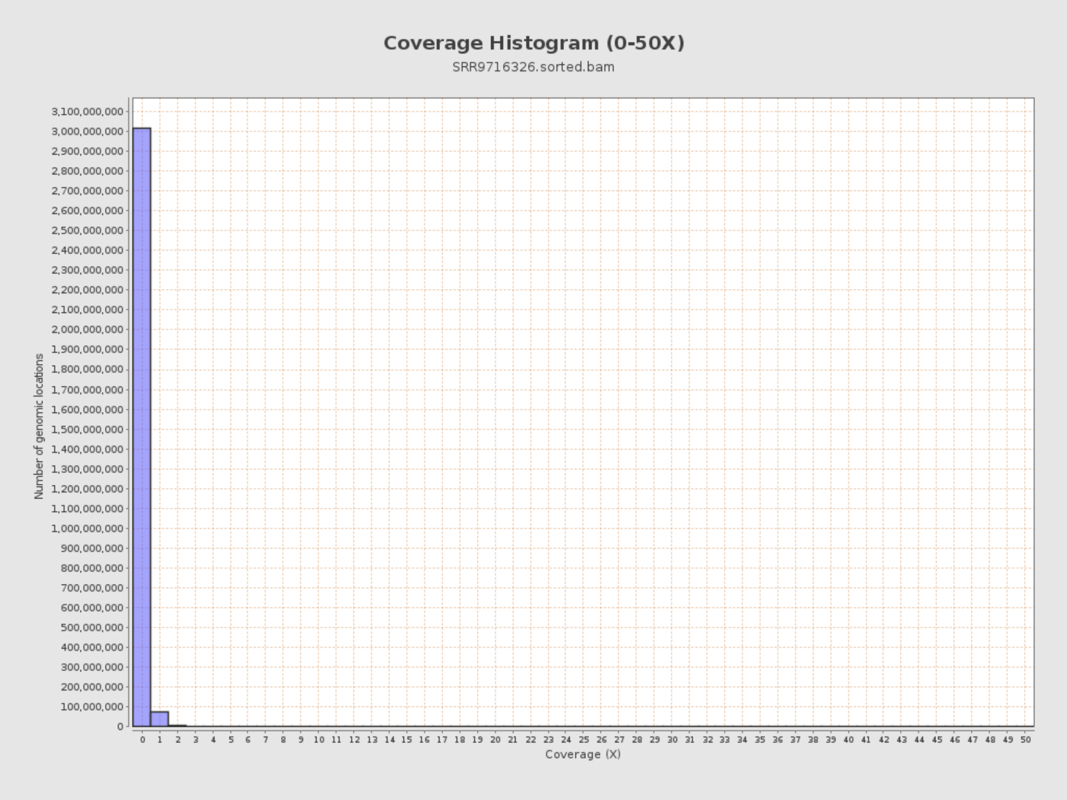
3. Results : Coverage across reference



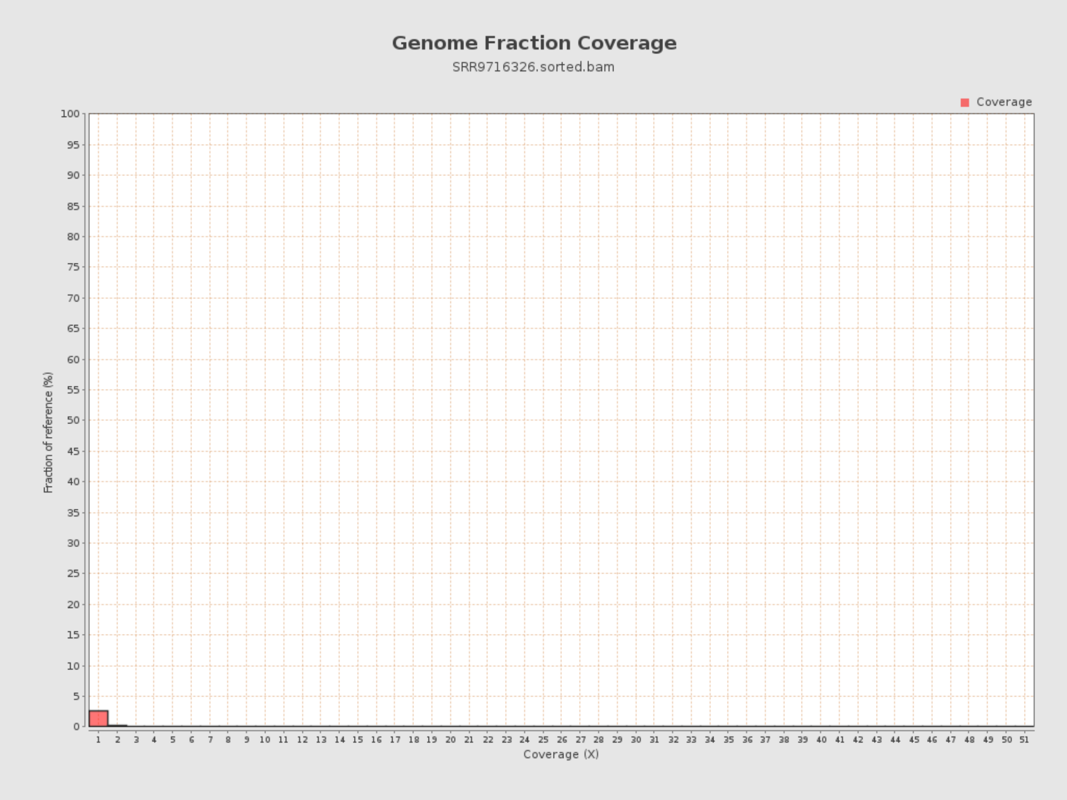
4. Results : Coverage Histogram



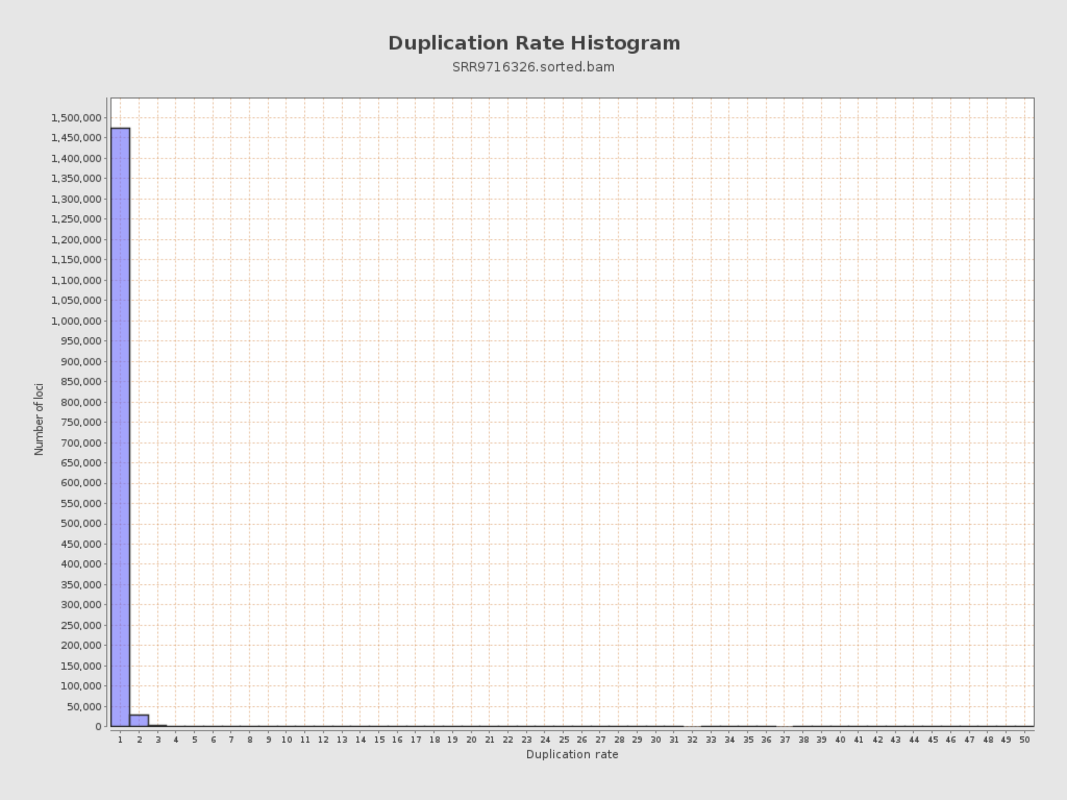
5. Results : Coverage Histogram (0-50X)



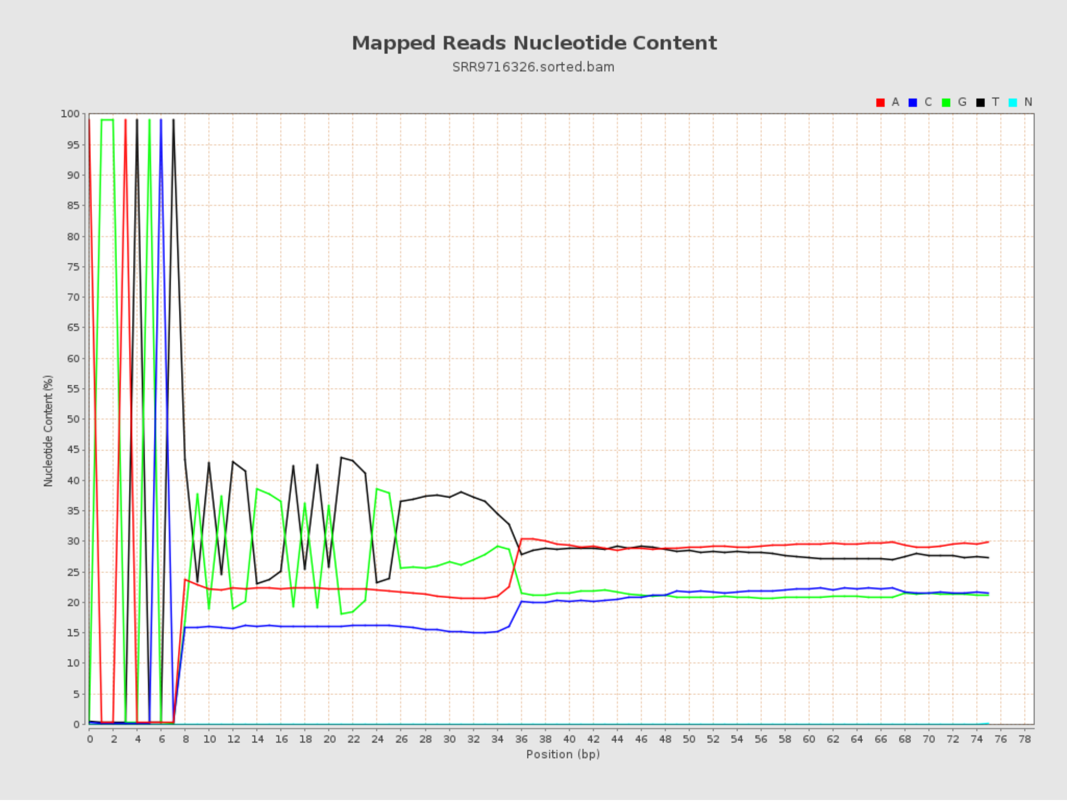
6. Results : Genome Fraction Coverage



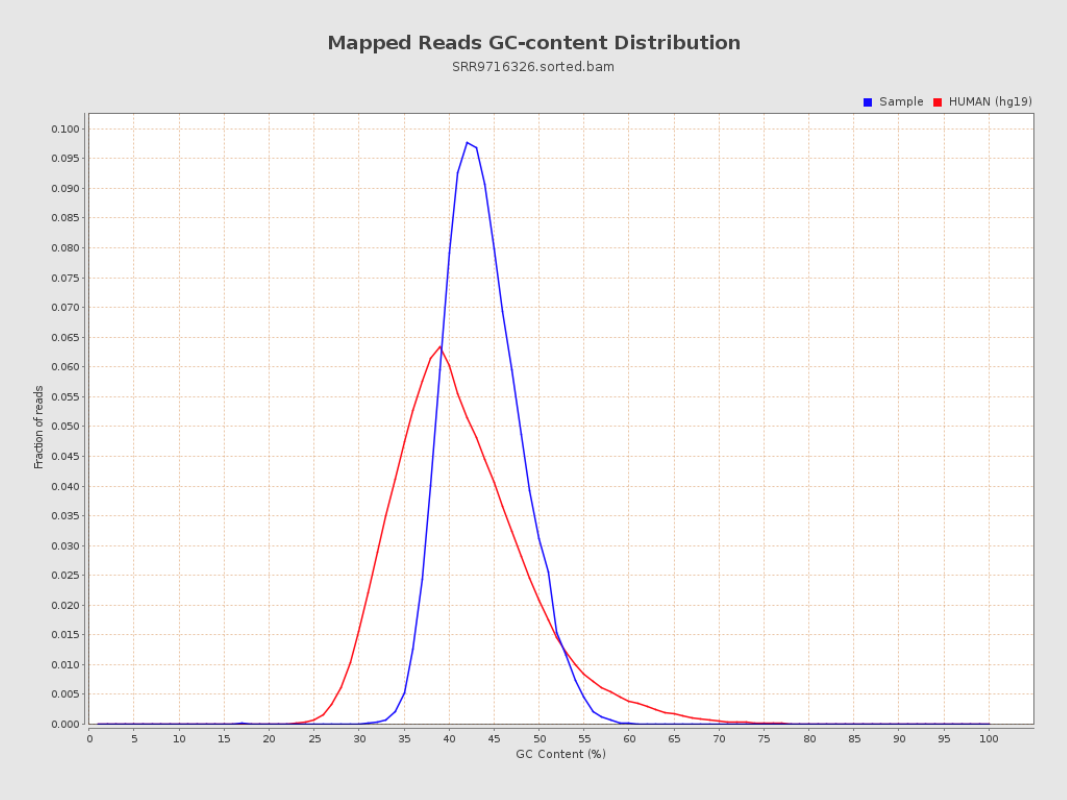
7. Results : Duplication Rate Histogram



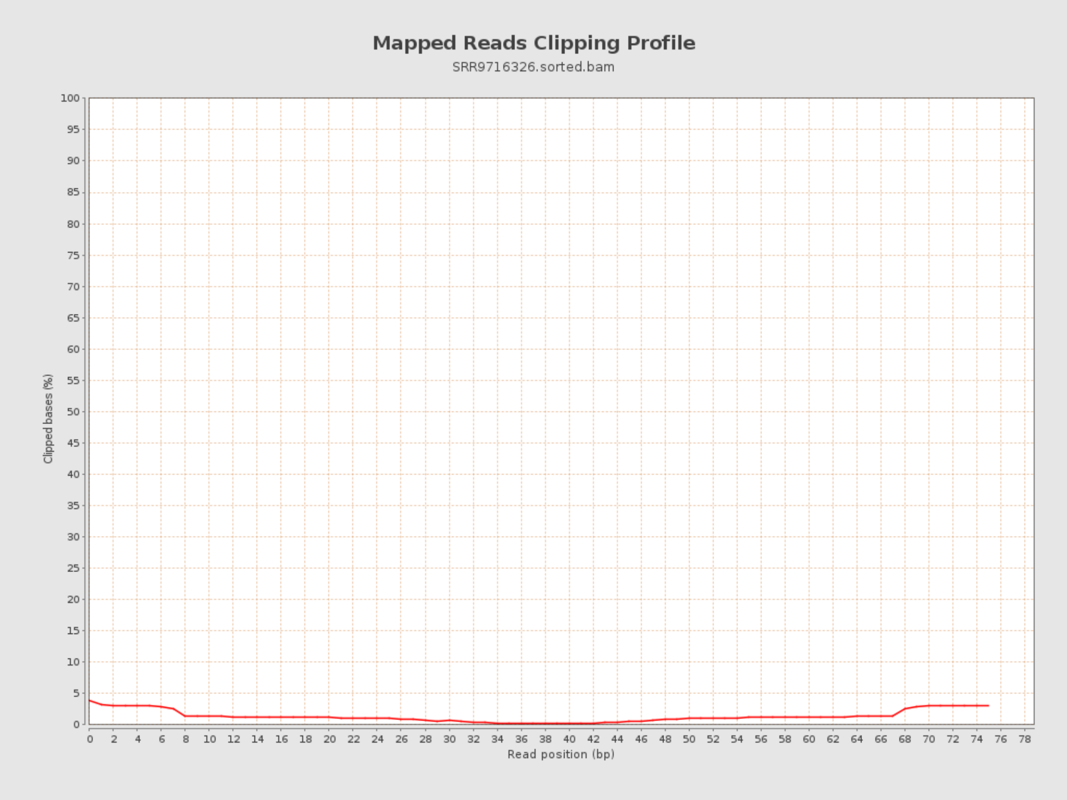
8. Results : Mapped Reads Nucleotide Content



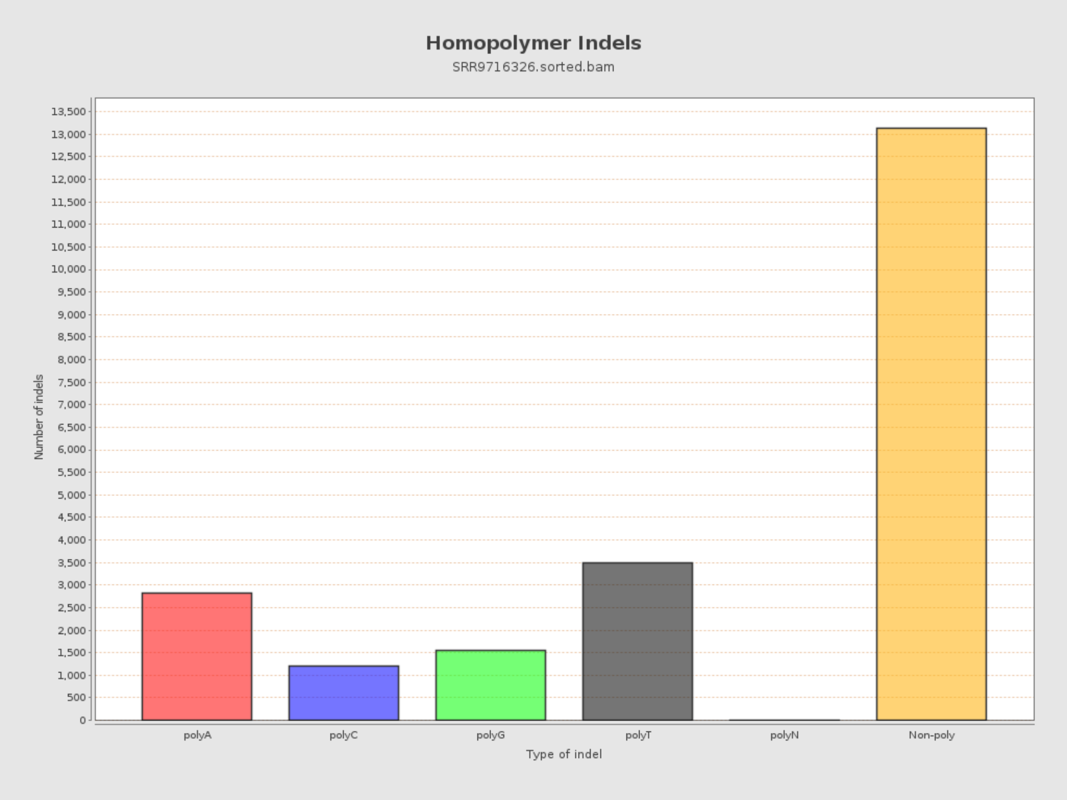
9. Results : Mapped Reads GC-content Distribution



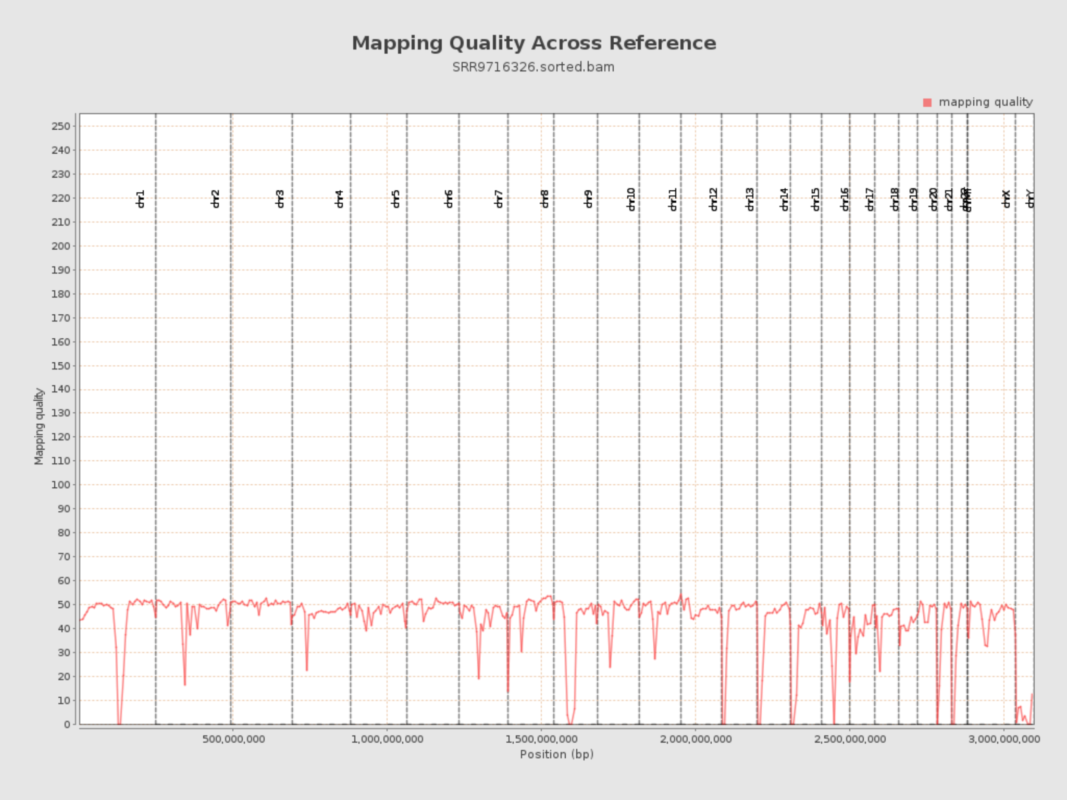
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram