Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 23:33:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716594.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_SRR9716594 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716594.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 23:33:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716594.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,603,767
Mapped reads	1,474,432 / 91.94%
Unmapped reads	129,335 / 8.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,529 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	52,939 / 3.3%
Duplication rate	2.77%
Clipped reads	1,475,083 / 91.98%

2.2. ACGT Content

Number/percentage of A's	20,946,344 / 24.52%
Number/percentage of C's	16,001,948 / 18.73%
Number/percentage of T's	27,475,887 / 32.16%
Number/percentage of G's	21,008,673 / 24.59%
Number/percentage of N's	776 / 0%
GC Percentage	43.32%

2.3. Coverage

Mean	0.0276

Standard Deviation	0.2404

2.4. Mapping Quality

Mean Mapping Quality	45.02

2.5. Mismatches and indels

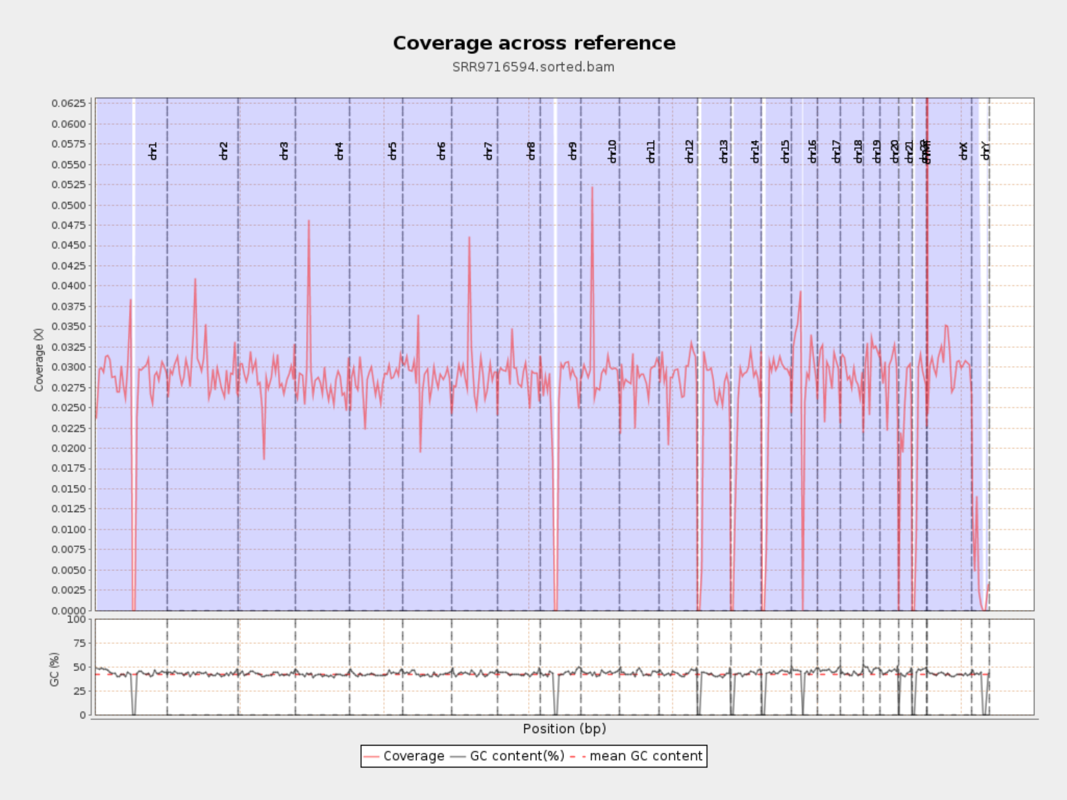
General error rate	0.5%
Mismatches	417,745
Insertions	6,371
Mapped reads with at least one insertion	0.43%
Deletions	16,470
Mapped reads with at least one deletion	1.11%
Homopolymer indels	42.79%

2.6. Chromosome stats

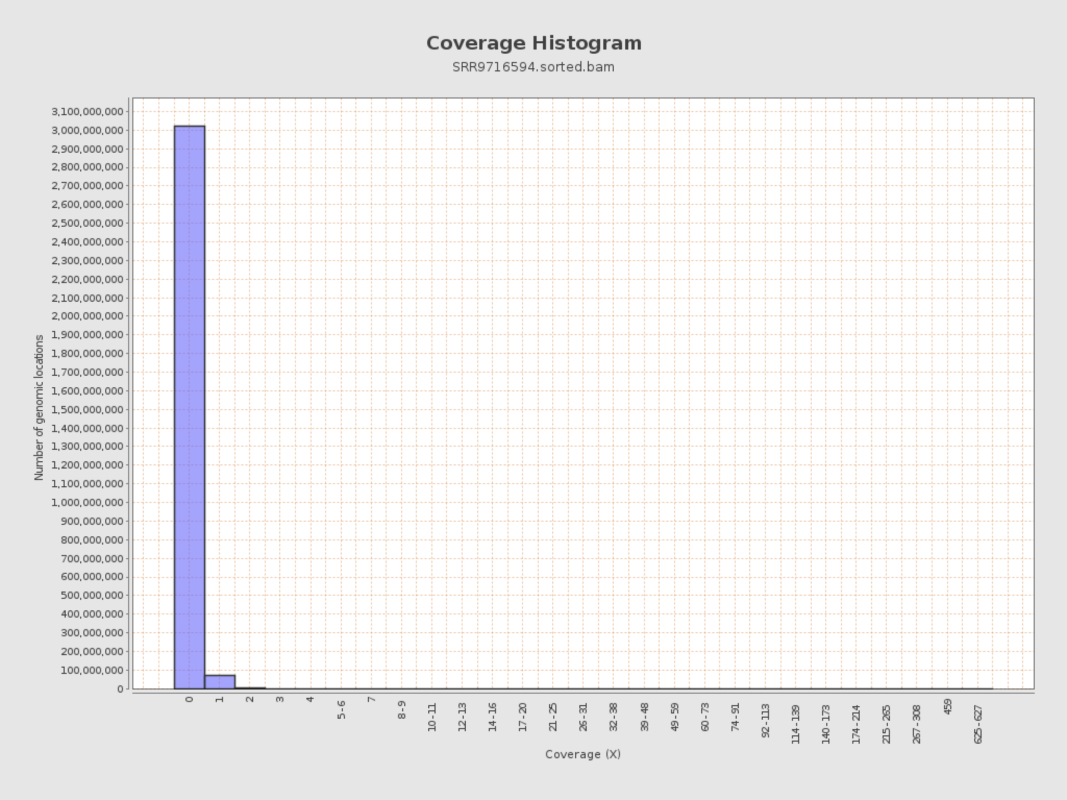
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6814774	0.0273	0.319
chr2	243199373	7235399	0.0298	0.3375
chr3	198022430	5664289	0.0286	0.1856
chr4	191154276	5469318	0.0286	0.2037
chr5	180915260	5165545	0.0286	0.1847
chr6	171115067	4930462	0.0288	0.218
chr7	159138663	4677547	0.0294	0.3421

chr8	146364022	4268866	0.0292	0.2406
chr9	141213431	3532089	0.025	0.2078
chr10	135534747	4118306	0.0304	0.2693
chr11	135006516	3866114	0.0286	0.225
chr12	133851895	3878186	0.029	0.1873
chr13	115169878	2702918	0.0235	0.1677
chr14	107349540	2593802	0.0242	0.1749
chr15	102531392	2477600	0.0242	0.1707
chr16	90354753	2596962	0.0287	0.2003
chr17	81195210	2395601	0.0295	0.2015
chr18	78077248	2266536	0.029	0.3339
chr19	59128983	1813770	0.0307	0.2733
chr20	63025520	1834185	0.0291	0.1916
chr21	48129895	1115915	0.0232	0.1822
chr22	51304566	1040528	0.0203	0.1557
chrMT	16571	15109	0.9118	1.0354
chrX	155270560	4729681	0.0305	0.2059
chrY	59373566	257101	0.0043	0.1242

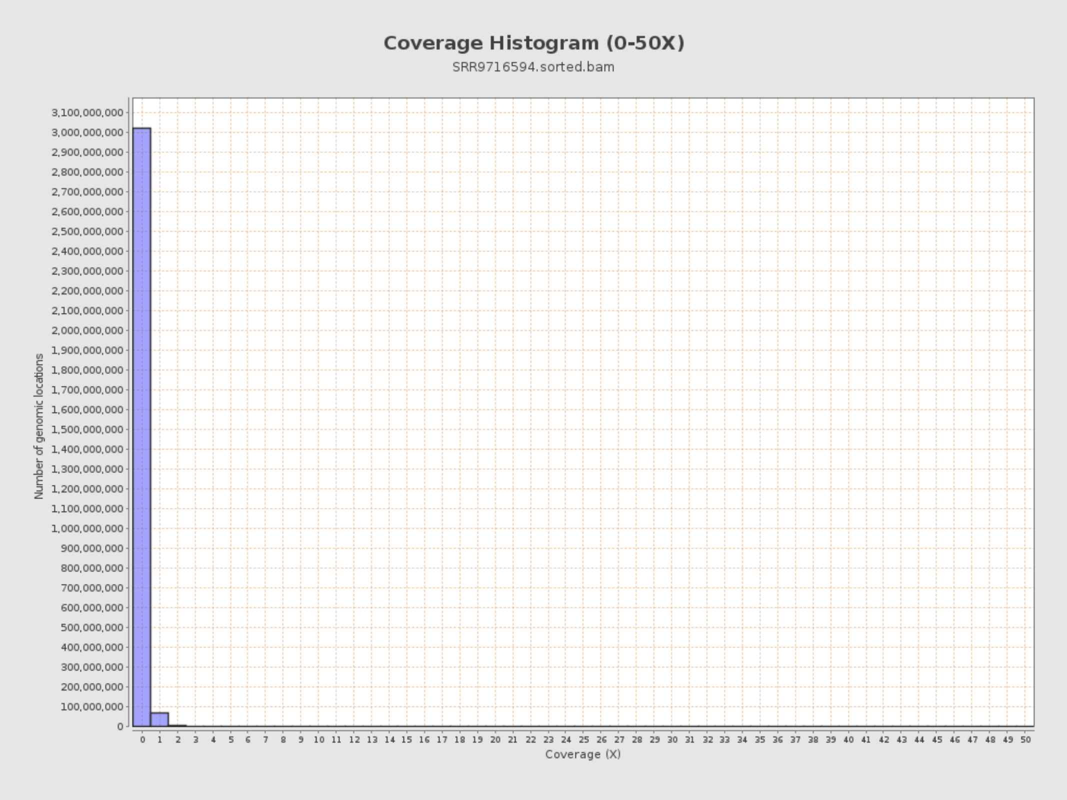
3. Results : Coverage across reference



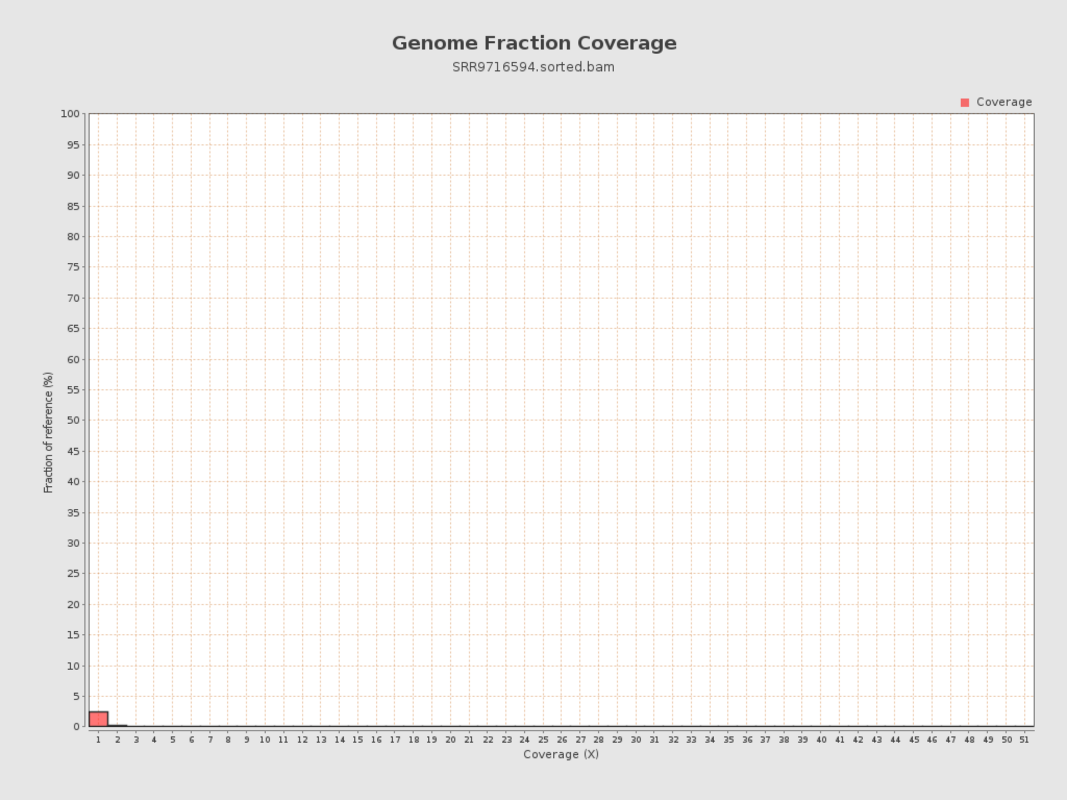
4. Results : Coverage Histogram



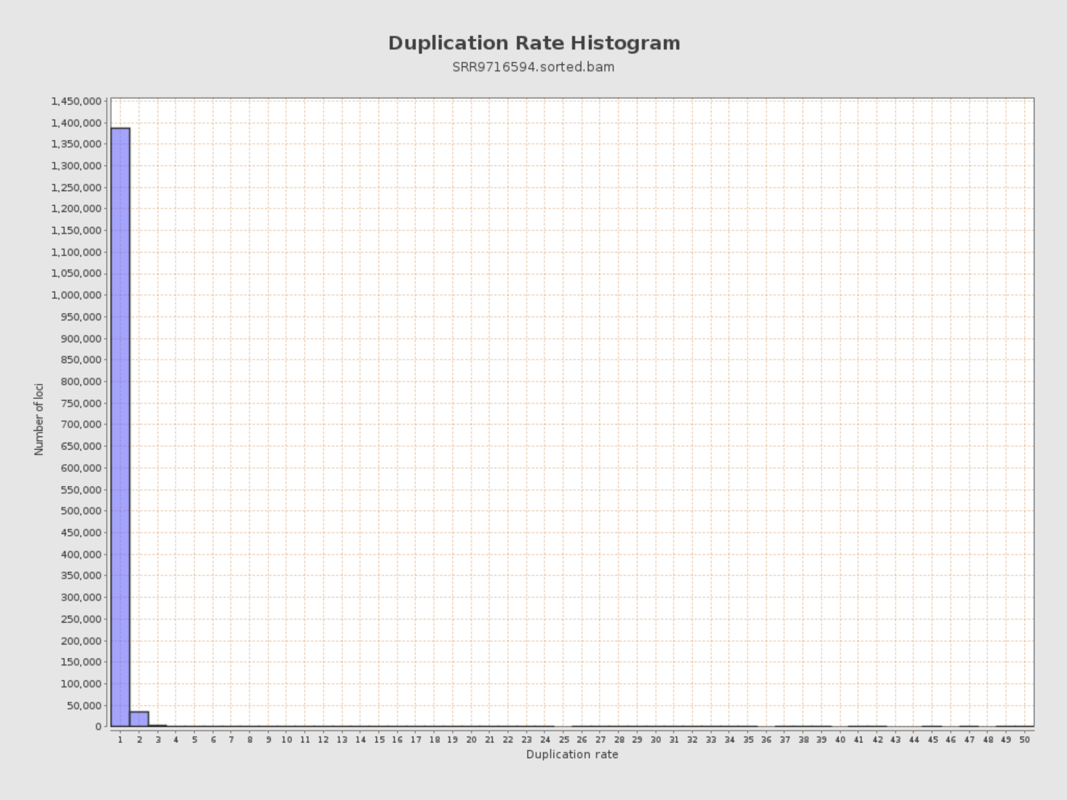
5. Results : Coverage Histogram (0-50X)



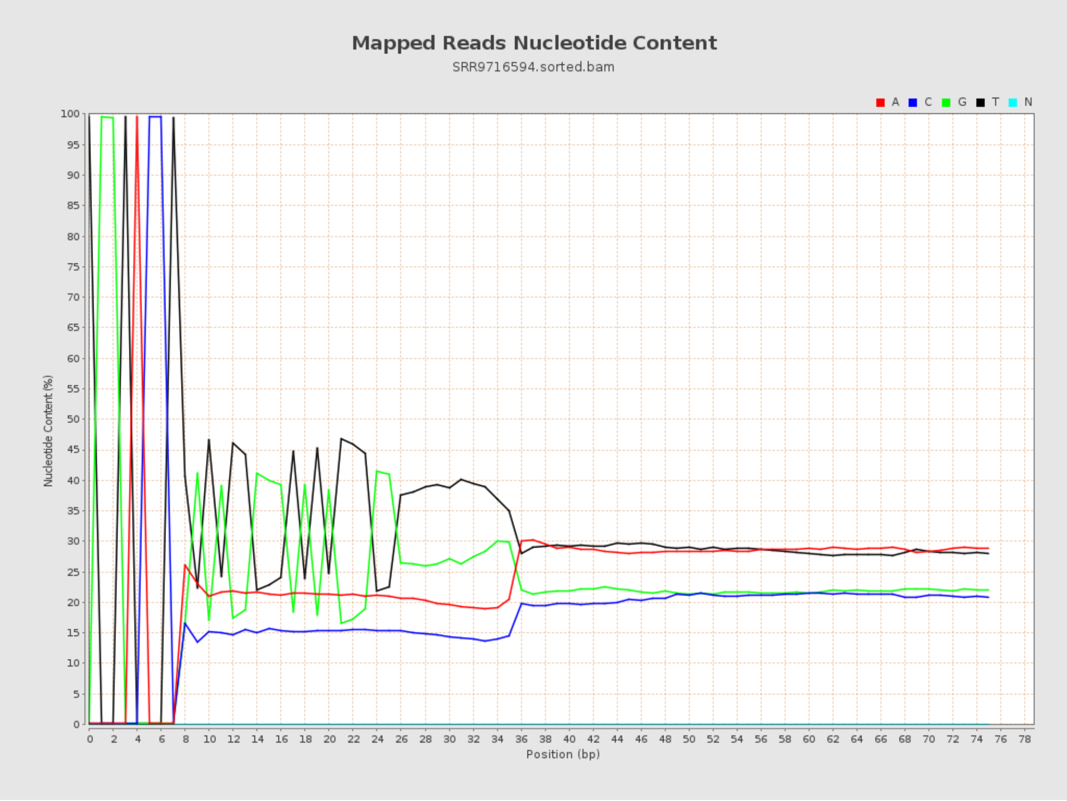
6. Results : Genome Fraction Coverage



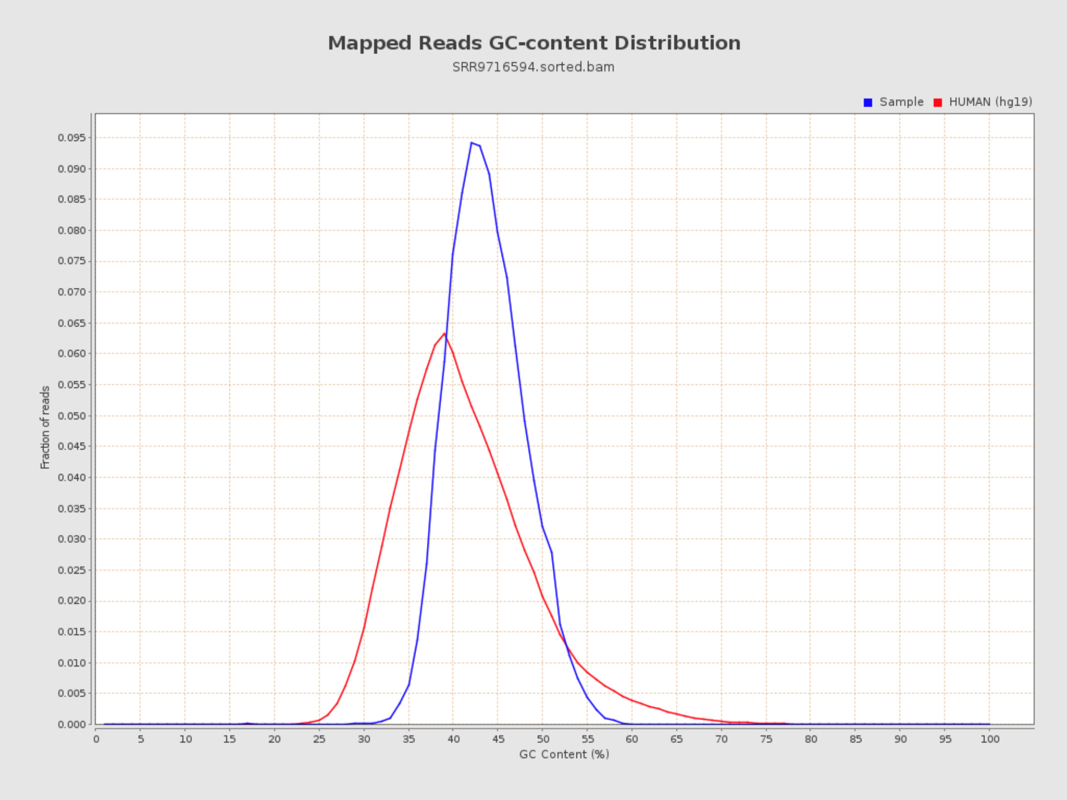
7. Results : Duplication Rate Histogram



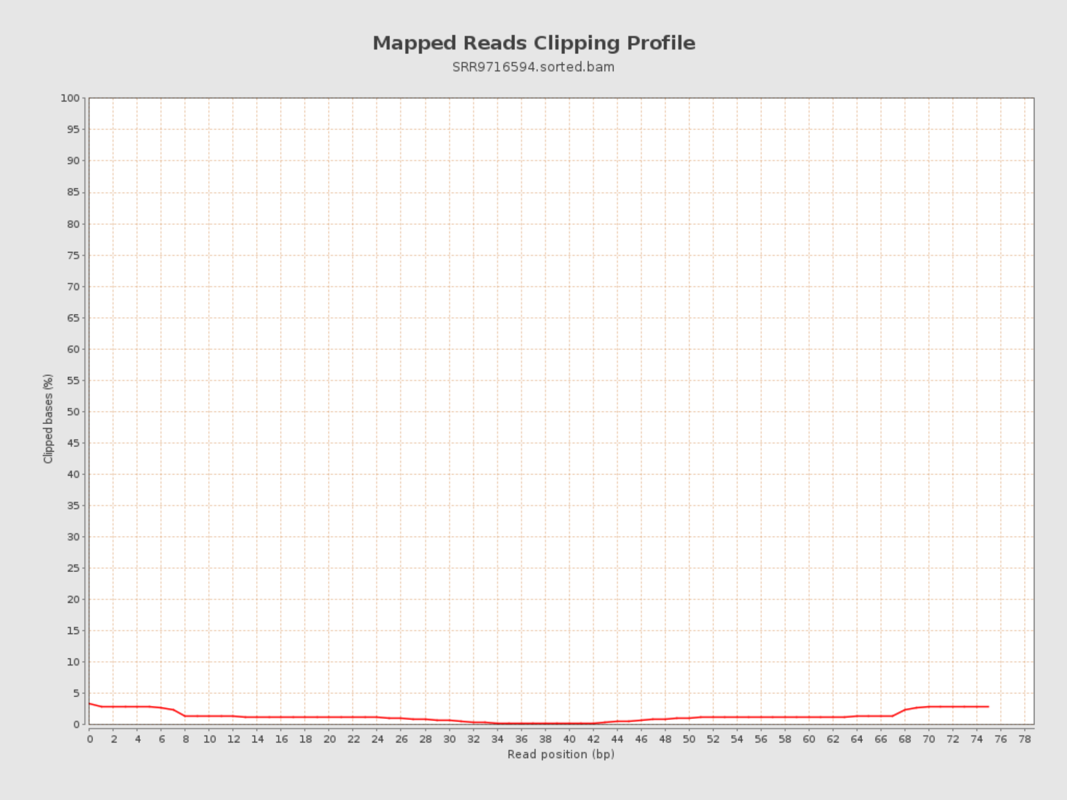
8. Results : Mapped Reads Nucleotide Content



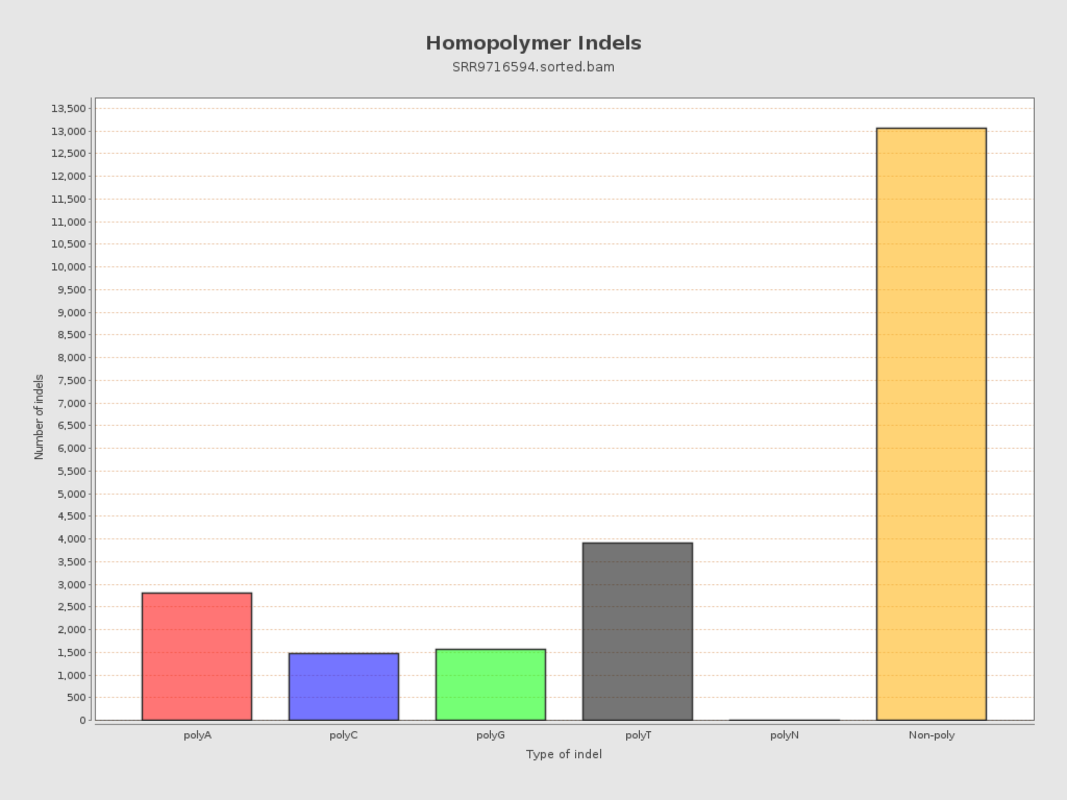
9. Results : Mapped Reads GC-content Distribution



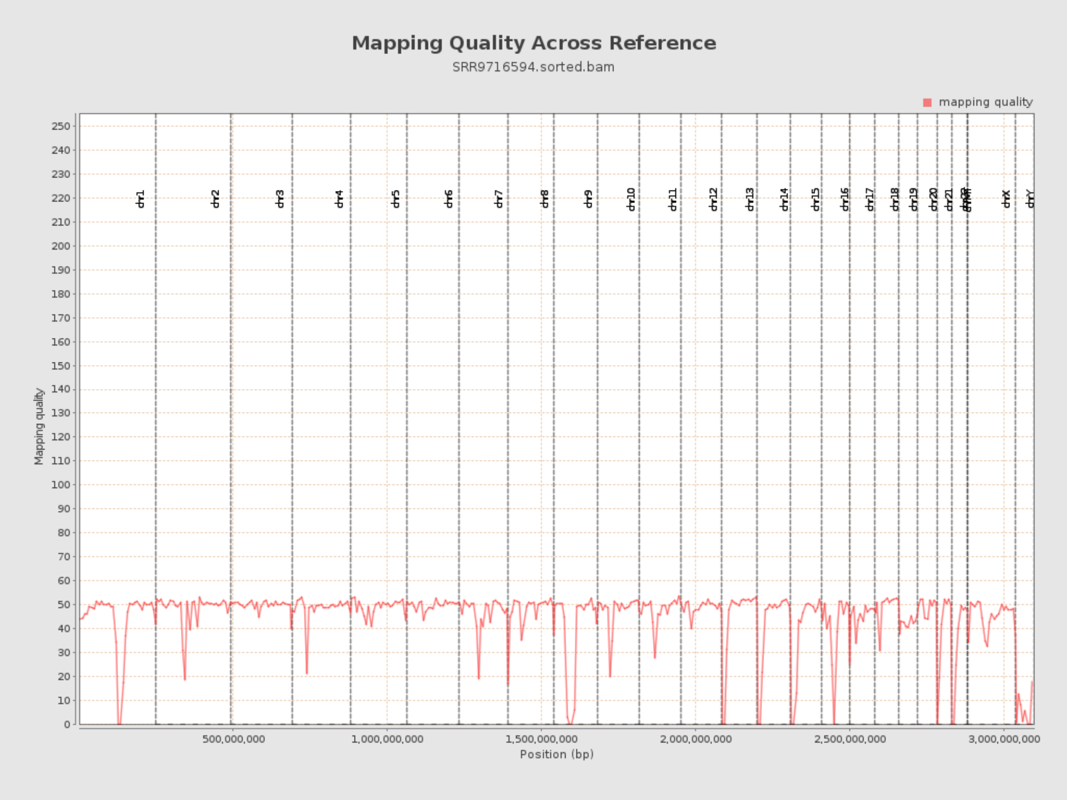
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram