Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 20:03:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716550.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_SRR9716550 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716550.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 20:03:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716550.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,742,521
Mapped reads	1,534,468 / 88.06%
Unmapped reads	208,053 / 11.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,583 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	37,796 / 2.17%
Duplication rate	1.69%
Clipped reads	1,538,361 / 88.28%

2.2. ACGT Content

Number/percentage of A's	20,616,513 / 23.73%
Number/percentage of C's	16,900,914 / 19.45%
Number/percentage of T's	27,335,809 / 31.46%
Number/percentage of G's	22,025,750 / 25.35%
Number/percentage of N's	699 / 0%
GC Percentage	44.81%

2.3. Coverage

Mean	0.0281

Standard Deviation	0.2412

2.4. Mapping Quality

Mean Mapping Quality	42.12

2.5. Mismatches and indels

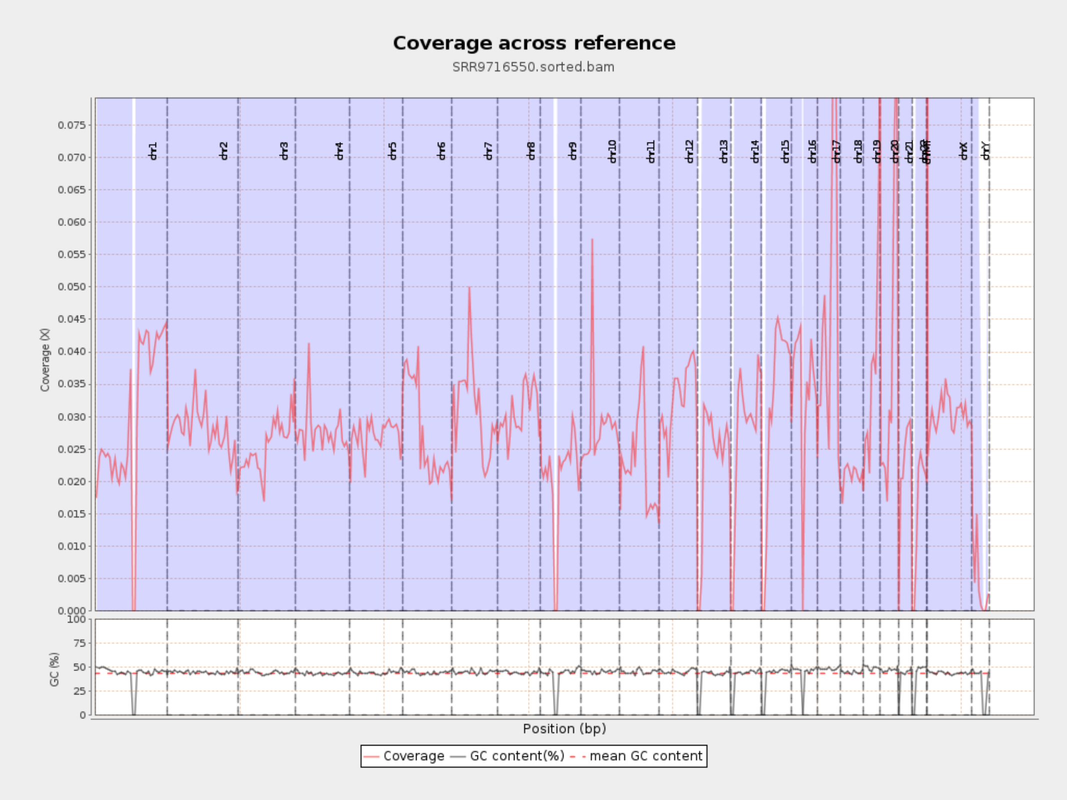
General error rate	0.55%
Mismatches	470,891
Insertions	5,248
Mapped reads with at least one insertion	0.34%
Deletions	16,328
Mapped reads with at least one deletion	1.06%
Homopolymer indels	40.82%

2.6. Chromosome stats

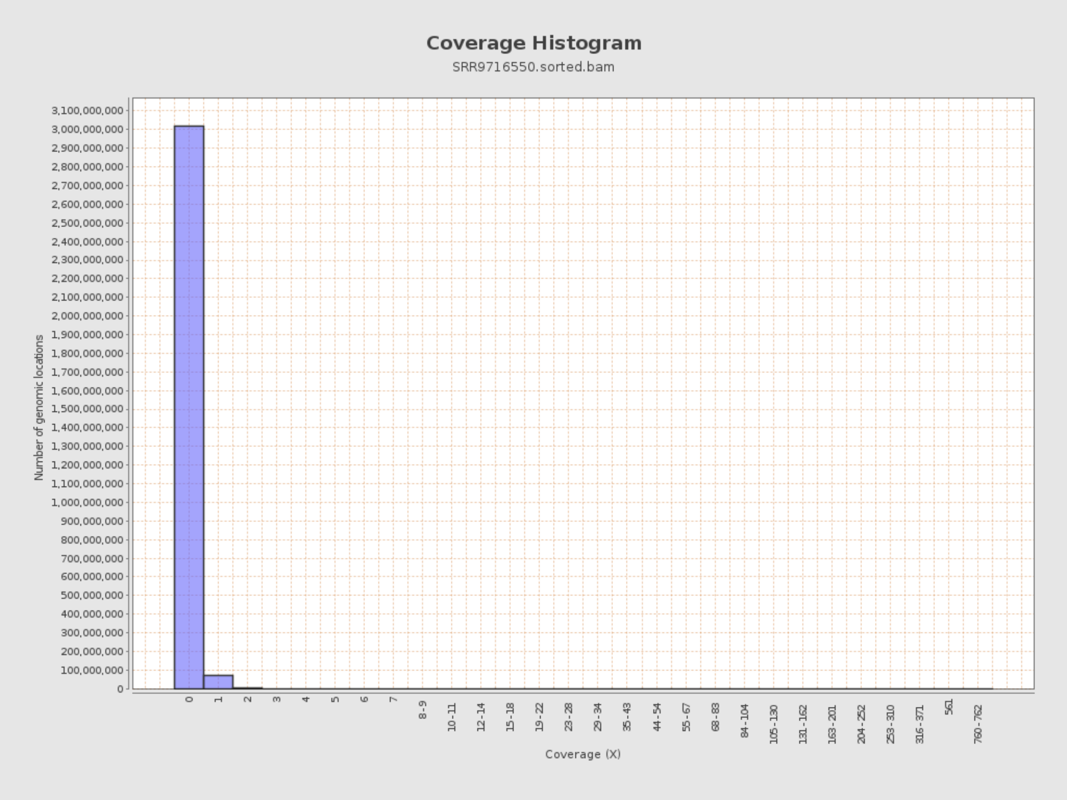
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7378694	0.0296	0.3182
chr2	243199373	6814909	0.028	0.356
chr3	198022430	5025447	0.0254	0.1739
chr4	191154276	5302807	0.0277	0.1925
chr5	180915260	4939626	0.0273	0.1772
chr6	171115067	4679305	0.0273	0.2119
chr7	159138663	4994375	0.0314	0.336

chr8	146364022	4489034	0.0307	0.2293
chr9	141213431	2898921	0.0205	0.1801
chr10	135534747	3874879	0.0286	0.3018
chr11	135006516	3110930	0.023	0.202
chr12	133851895	4382034	0.0327	0.1972
chr13	115169878	2628554	0.0228	0.1632
chr14	107349540	2919102	0.0272	0.1836
chr15	102531392	3225287	0.0315	0.1952
chr16	90354753	3041984	0.0337	0.2139
chr17	81195210	3920244	0.0483	0.2504
chr18	78077248	1621396	0.0208	0.275
chr19	59128983	2253802	0.0381	0.3035
chr20	63025520	2501562	0.0397	0.2249
chr21	48129895	1083605	0.0225	0.1756
chr22	51304566	810354	0.0158	0.1371
chrMT	16571	30983	1.8697	1.7613
chrX	155270560	4715021	0.0304	0.2014
chrY	59373566	263140	0.0044	0.1233

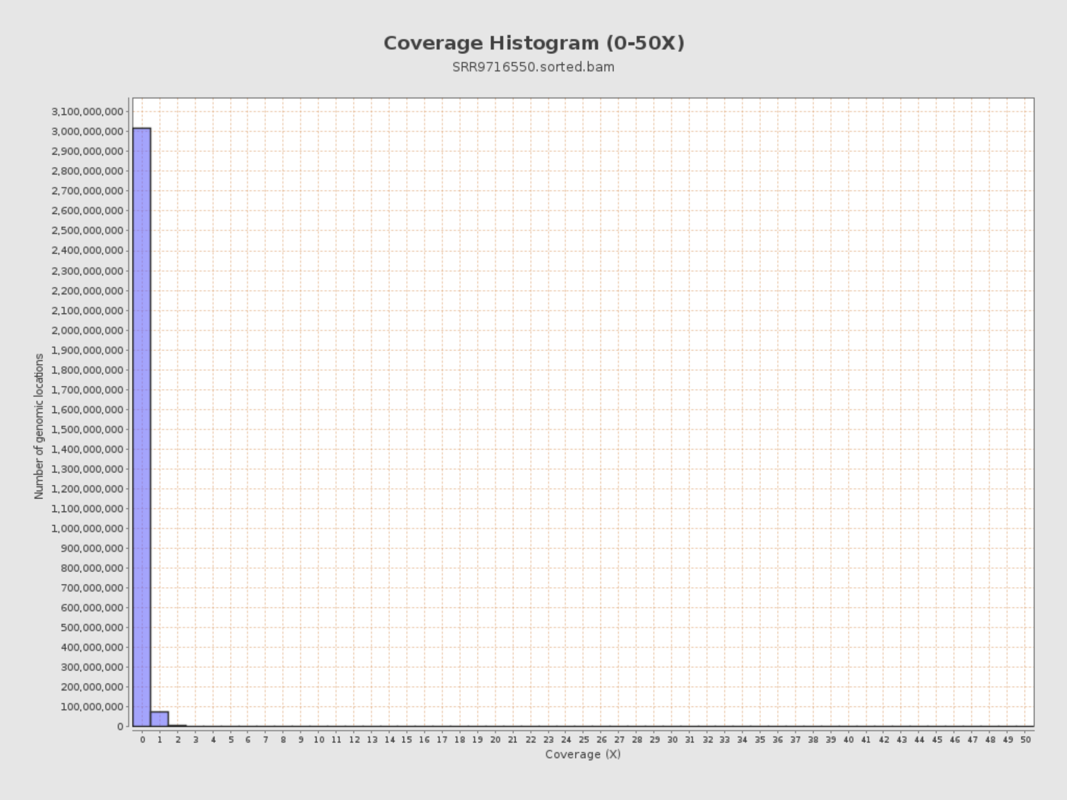
3. Results : Coverage across reference



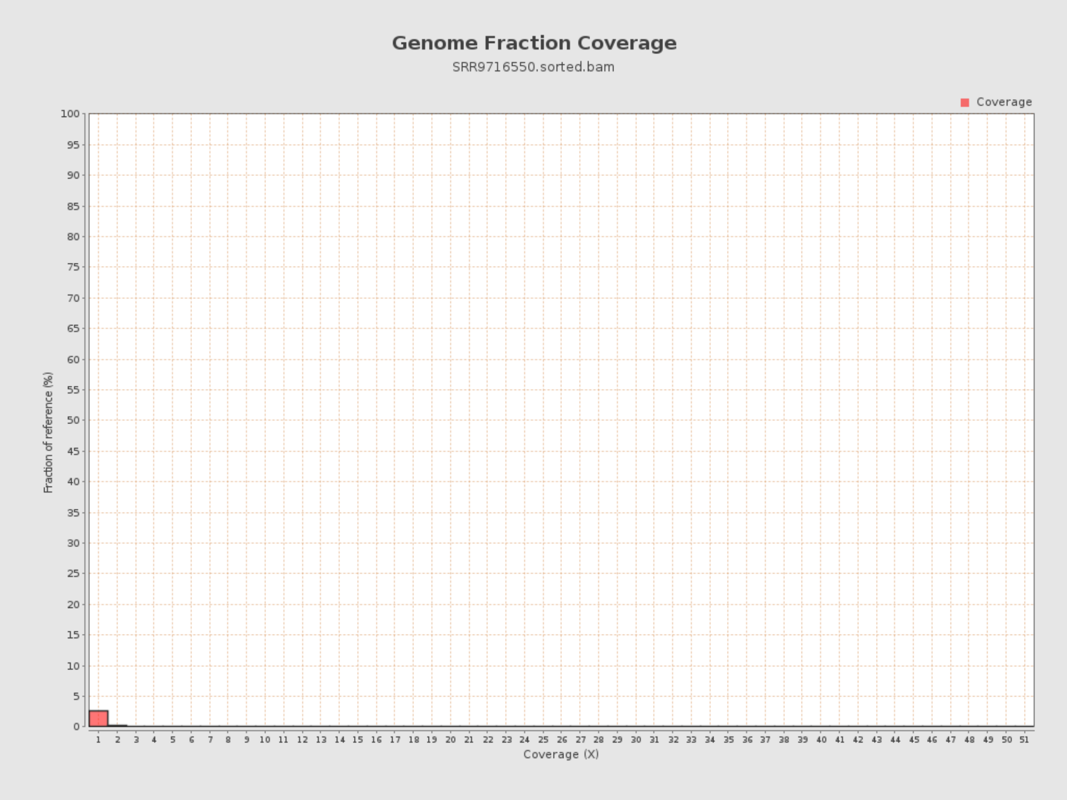
4. Results : Coverage Histogram



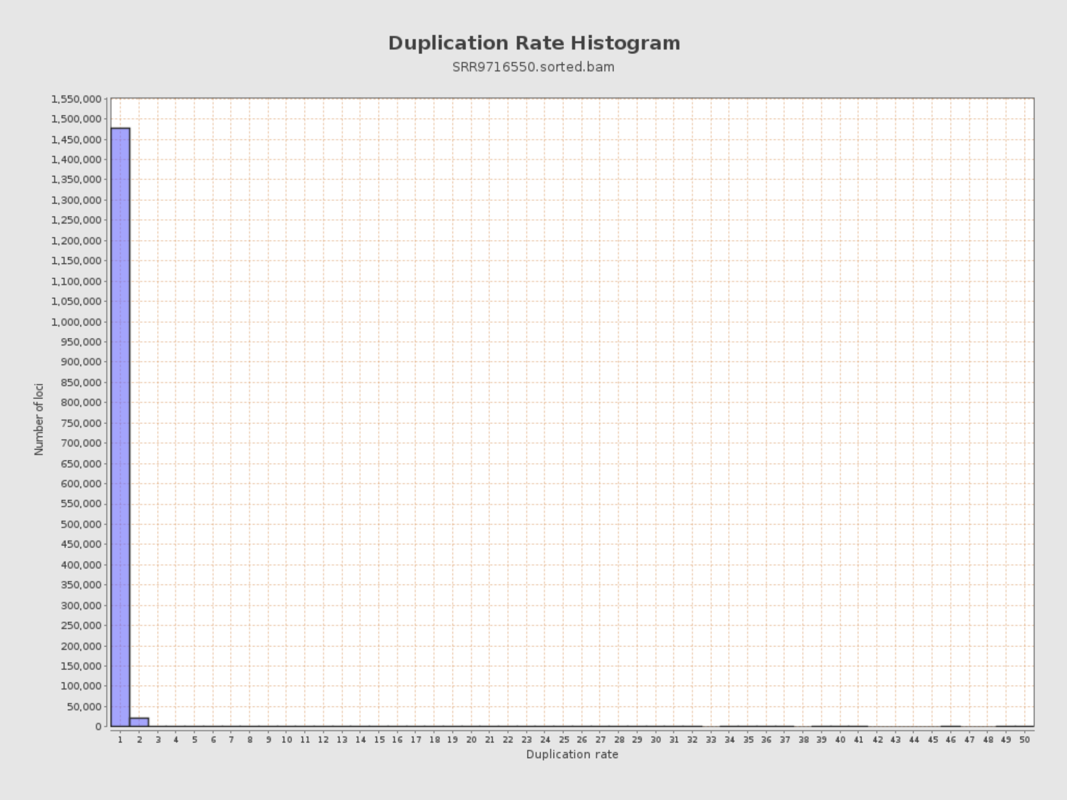
5. Results : Coverage Histogram (0-50X)



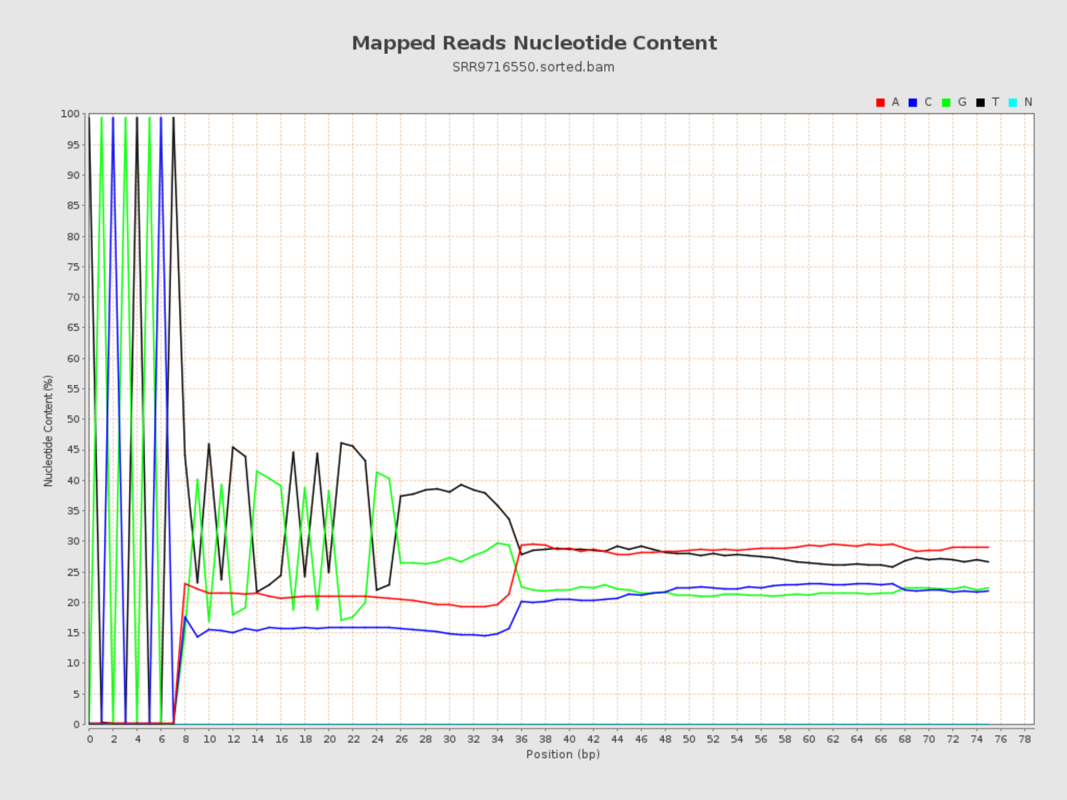
6. Results : Genome Fraction Coverage



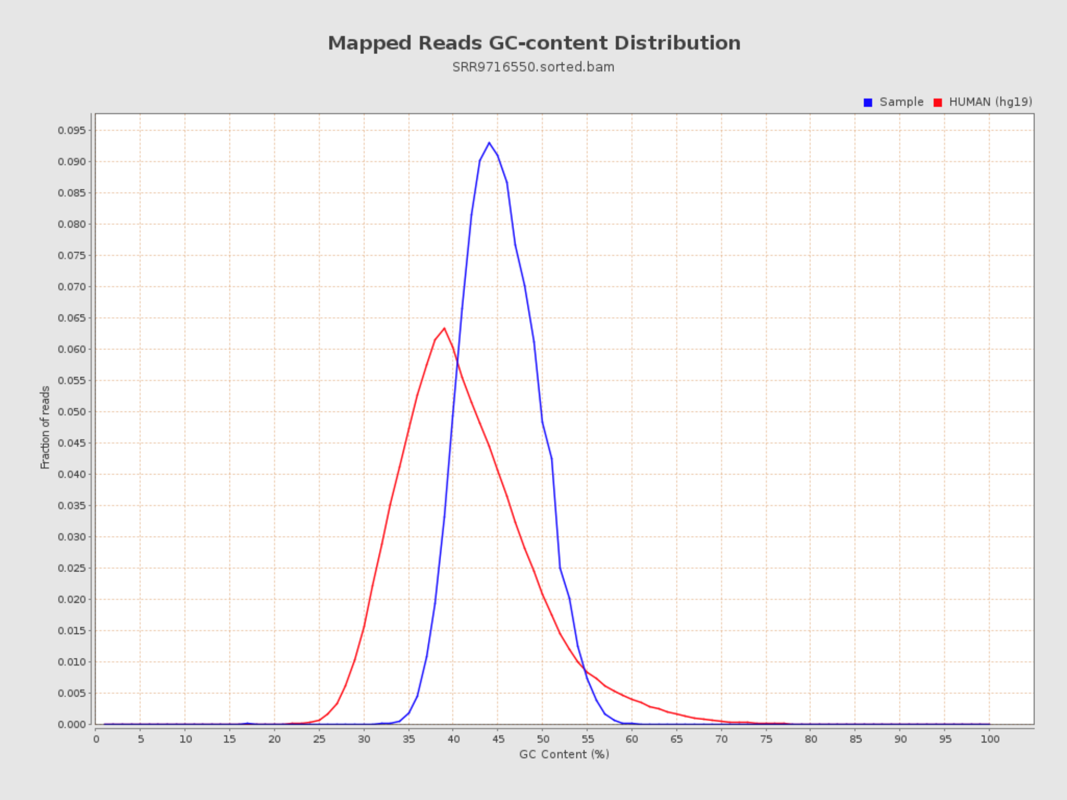
7. Results : Duplication Rate Histogram



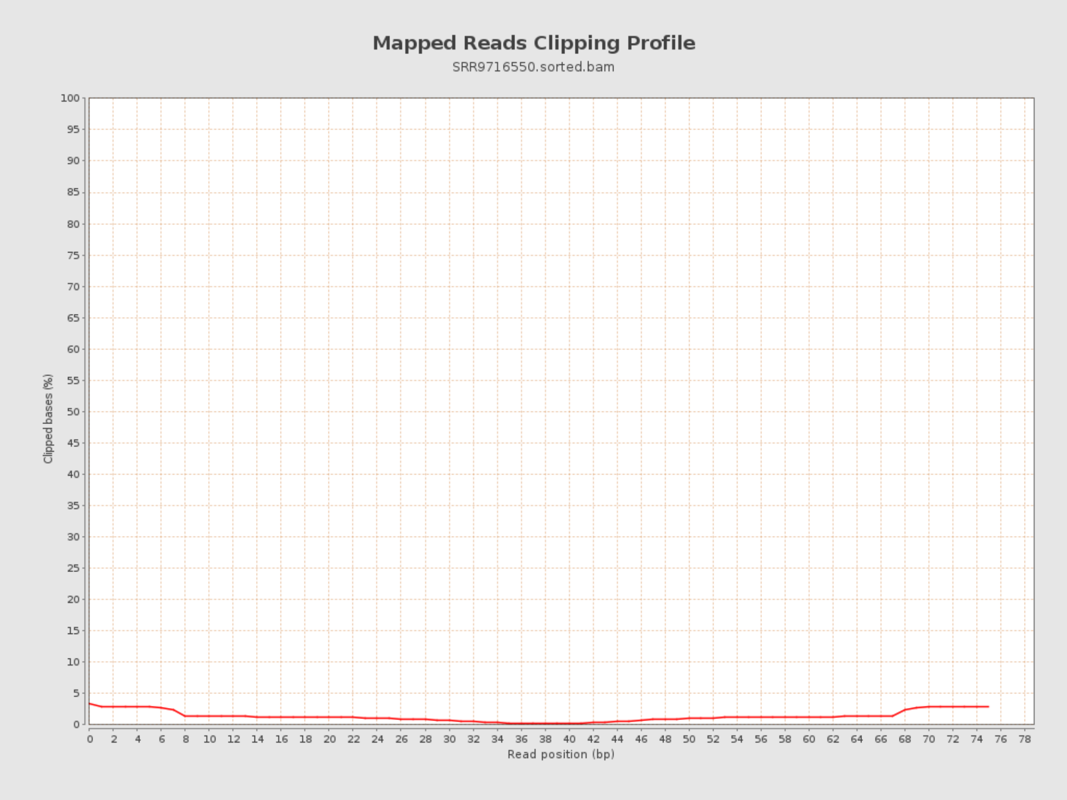
8. Results : Mapped Reads Nucleotide Content



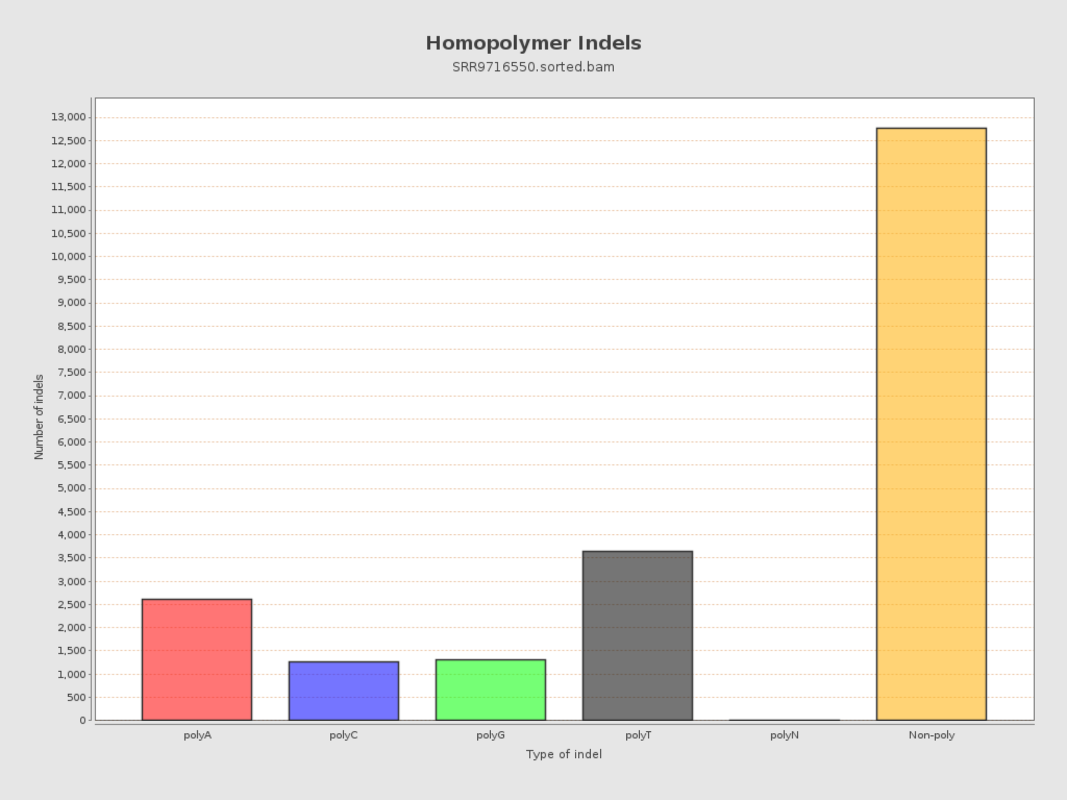
9. Results : Mapped Reads GC-content Distribution



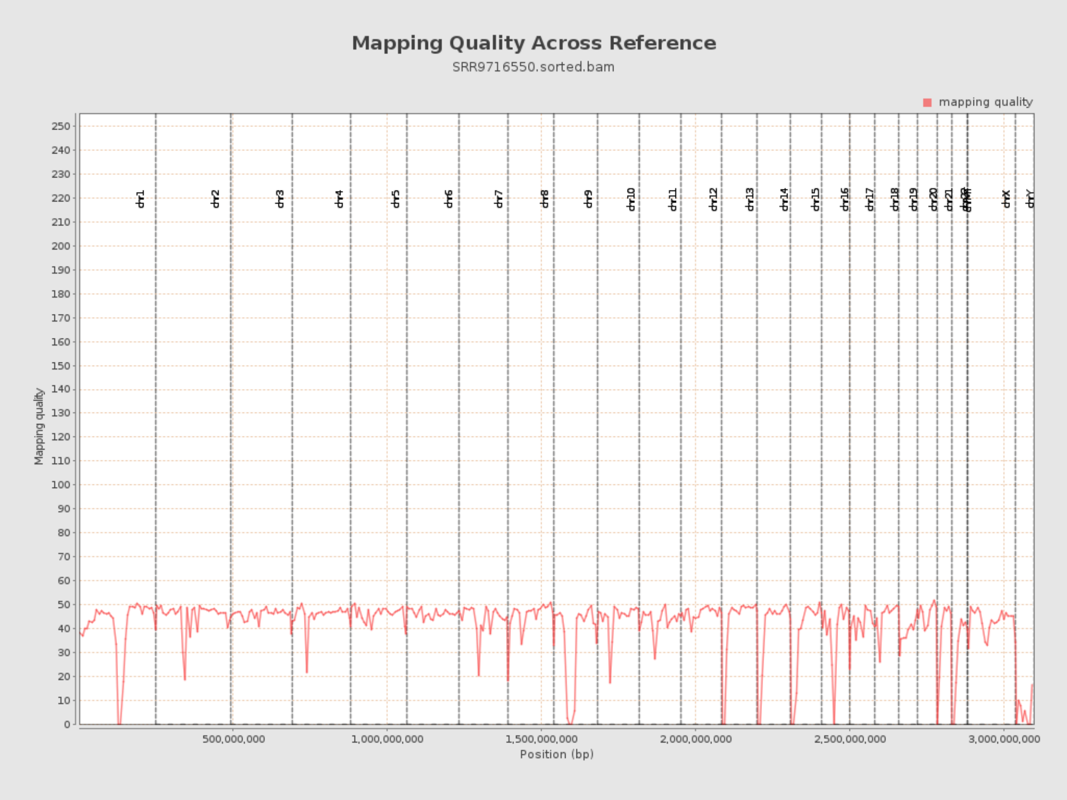
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram