Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 23:12:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716194.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_SRR9716194 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716194.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 23:12:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716194.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	514,401
Mapped reads	479,567 / 93.23%
Unmapped reads	34,834 / 6.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,011 / 1.95%
Read min/max/mean length	30 / 101 / 101.7
Duplicated reads (estimated)	11,441 / 2.22%
Duplication rate	1.86%
Clipped reads	488,580 / 94.98%

2.2. ACGT Content

Number/percentage of A's	9,127,279 / 24.77%
Number/percentage of C's	7,449,545 / 20.22%
Number/percentage of T's	11,120,753 / 30.18%
Number/percentage of G's	9,147,250 / 24.83%
Number/percentage of N's	1,314 / 0%
GC Percentage	45.04%

2.3. Coverage

Mean	0.0119

Standard Deviation	0.1397

2.4. Mapping Quality

Mean Mapping Quality	46.09

2.5. Mismatches and indels

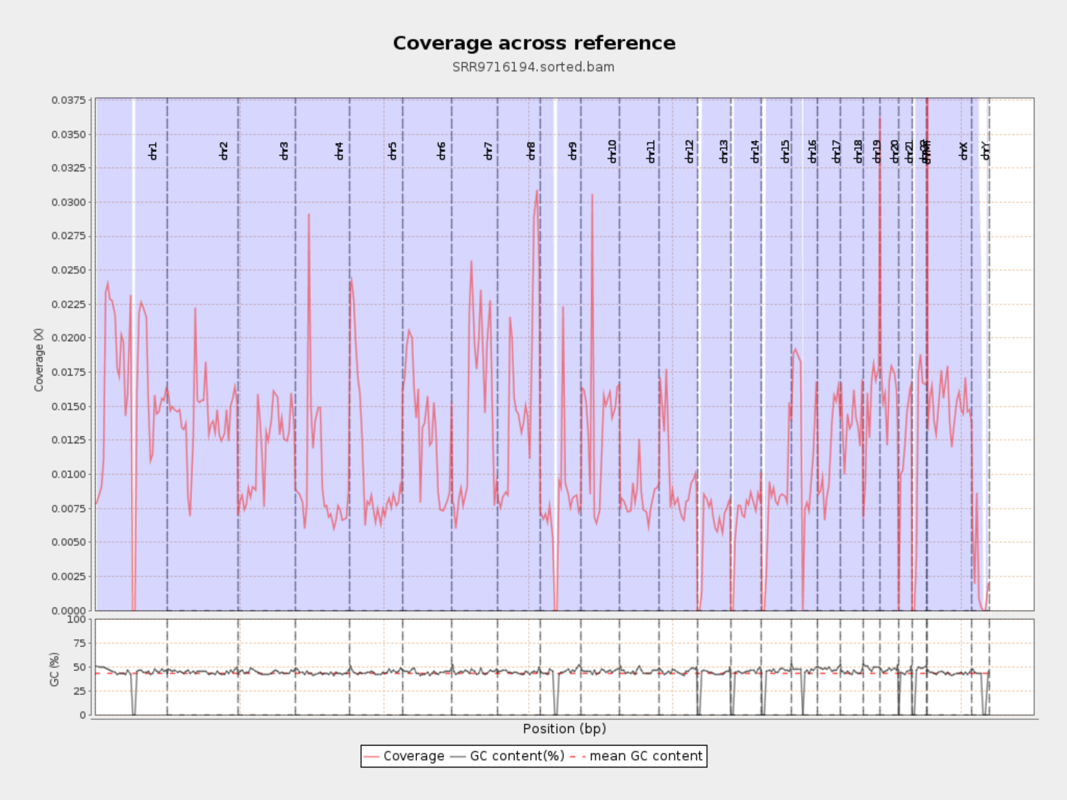
General error rate	0.69%
Mismatches	243,658
Insertions	3,679
Mapped reads with at least one insertion	0.75%
Deletions	6,830
Mapped reads with at least one deletion	1.4%
Homopolymer indels	38.5%

2.6. Chromosome stats

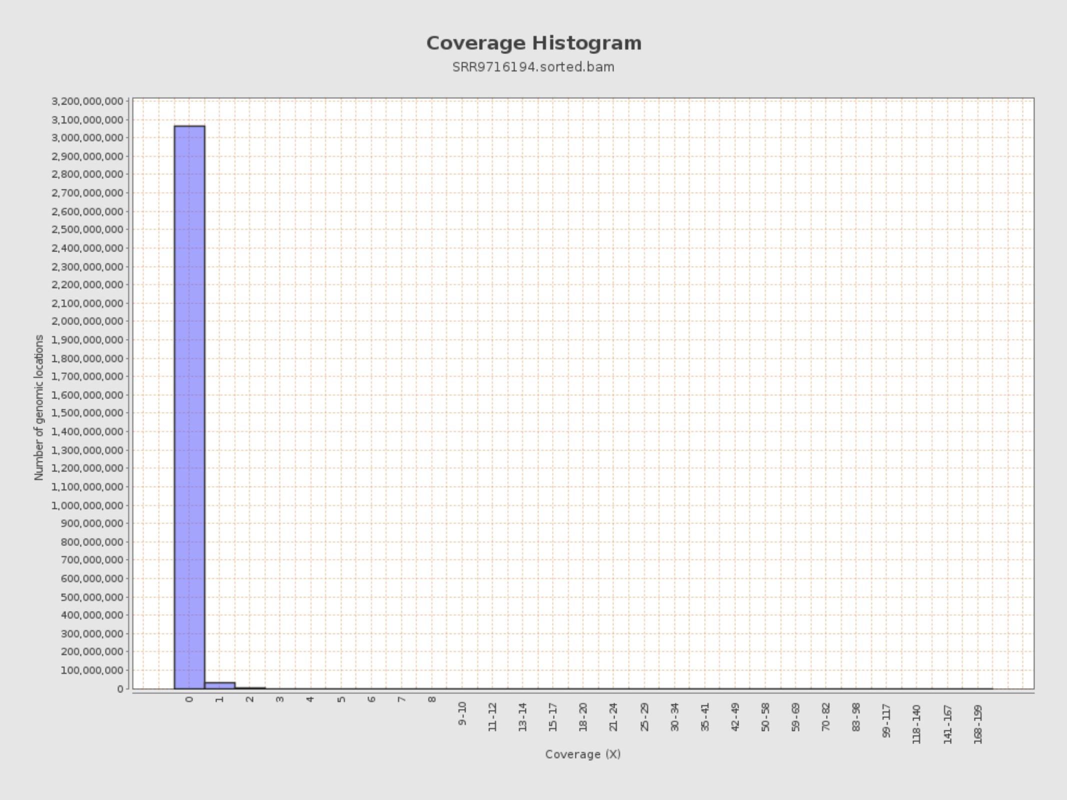
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4004184	0.0161	0.2219
chr2	243199373	3464302	0.0142	0.1523
chr3	198022430	2356361	0.0119	0.1156
chr4	191154276	1854866	0.0097	0.1288
chr5	180915260	1911918	0.0106	0.1085
chr6	171115067	2269203	0.0133	0.1244
chr7	159138663	2299836	0.0145	0.1703

chr8	146364022	2291405	0.0157	0.1519
chr9	141213431	1093262	0.0077	0.1067
chr10	135534747	1925296	0.0142	0.1867
chr11	135006516	1115608	0.0083	0.11
chr12	133851895	1365343	0.0102	0.1064
chr13	115169878	695389	0.006	0.0813
chr14	107349540	714294	0.0067	0.0865
chr15	102531392	769746	0.0075	0.0912
chr16	90354753	1121898	0.0124	0.1223
chr17	81195210	927951	0.0114	0.1166
chr18	78077248	1080661	0.0138	0.1522
chr19	59128983	928410	0.0157	0.1739
chr20	63025520	1011570	0.0161	0.1383
chr21	48129895	571344	0.0119	0.1278
chr22	51304566	602499	0.0117	0.116
chrMT	16571	6485	0.3913	0.6837
chrX	155270560	2341756	0.0151	0.1326
chrY	59373566	137340	0.0023	0.0967

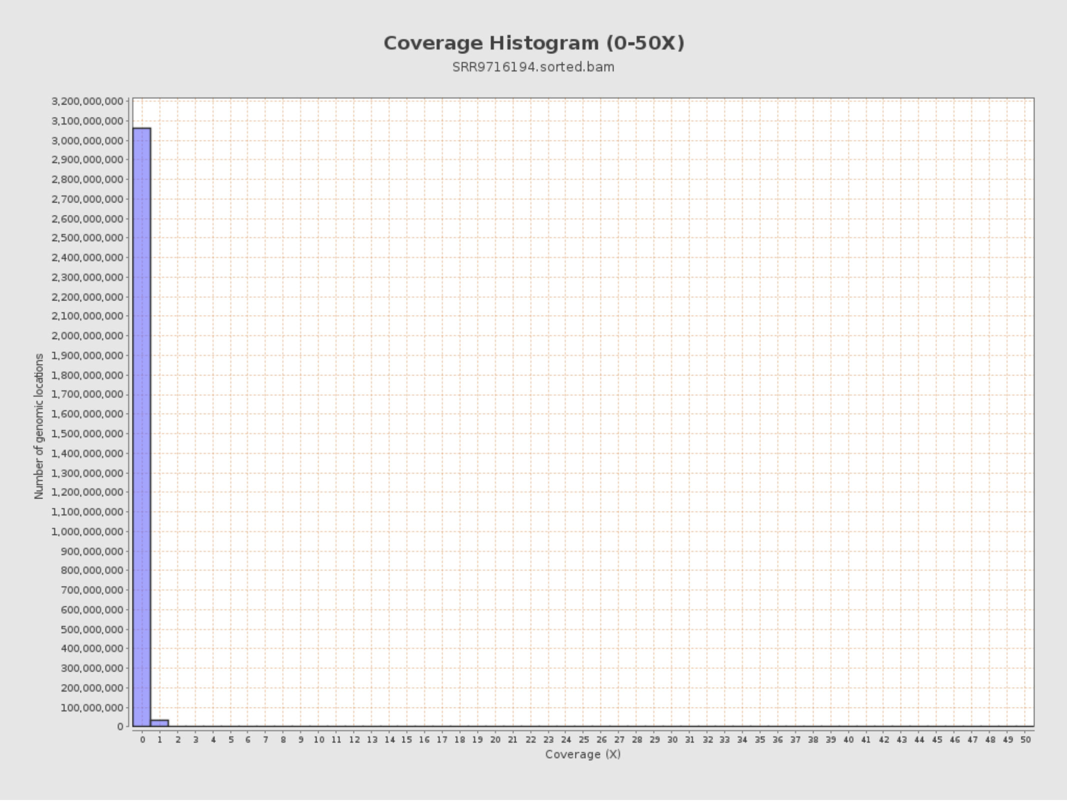
3. Results : Coverage across reference



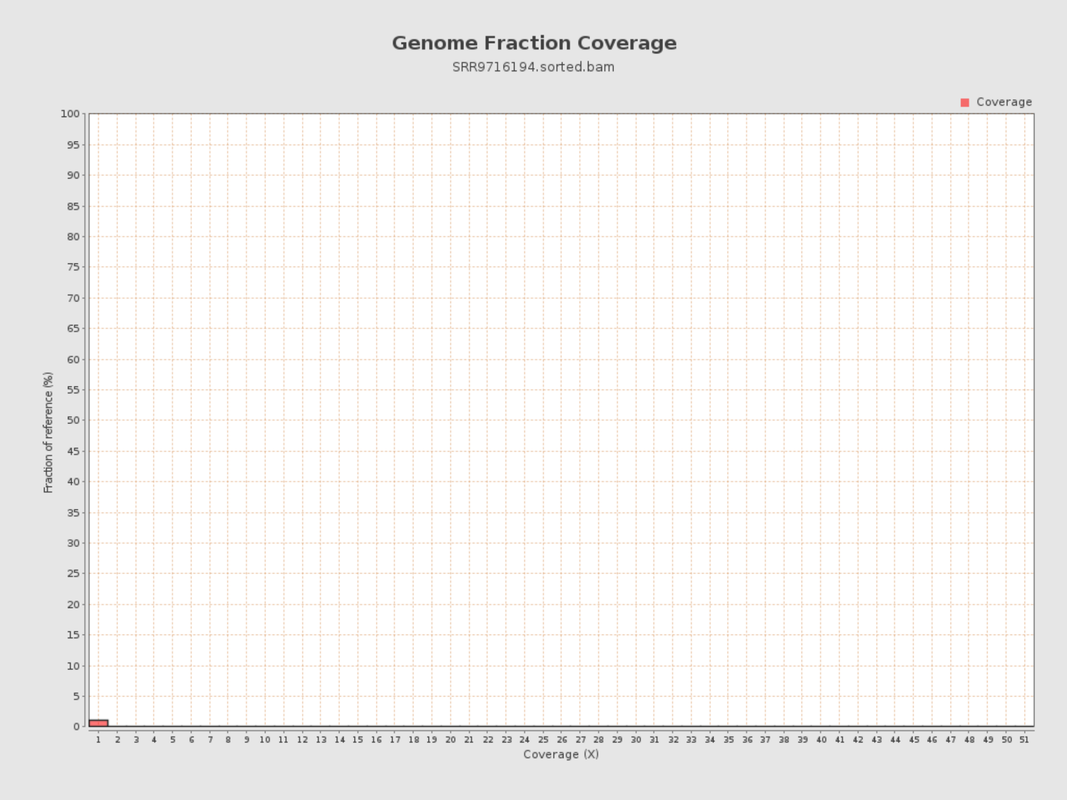
4. Results : Coverage Histogram



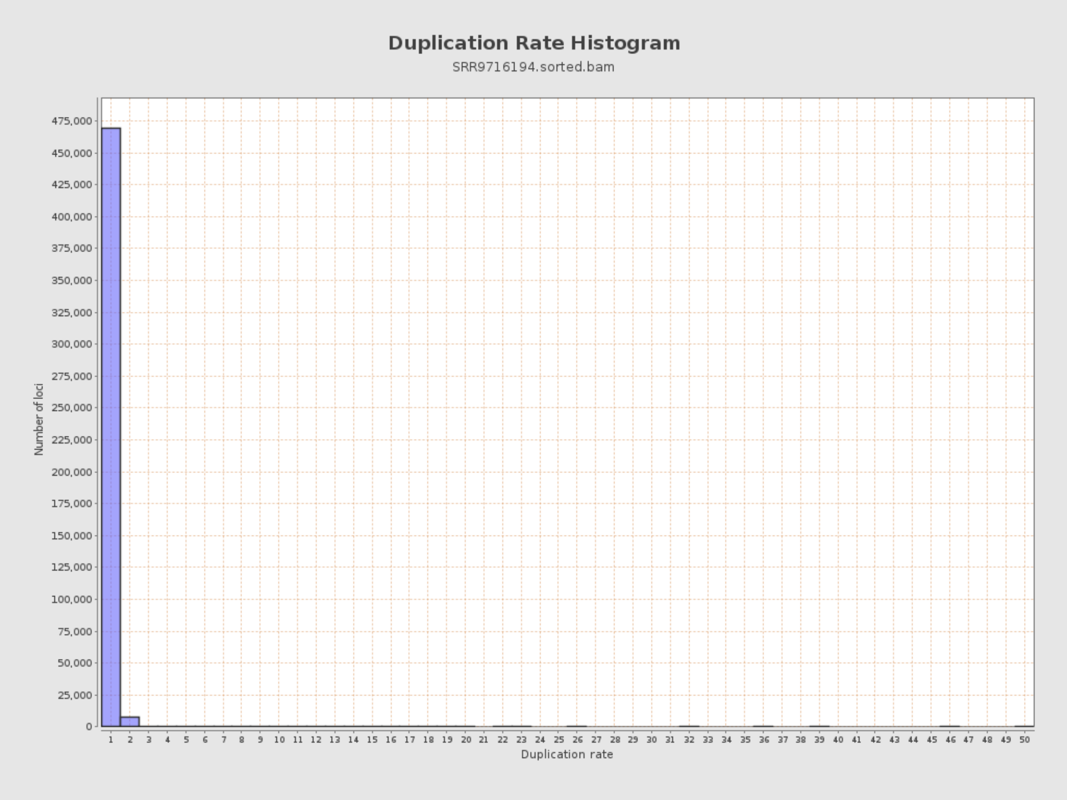
5. Results : Coverage Histogram (0-50X)



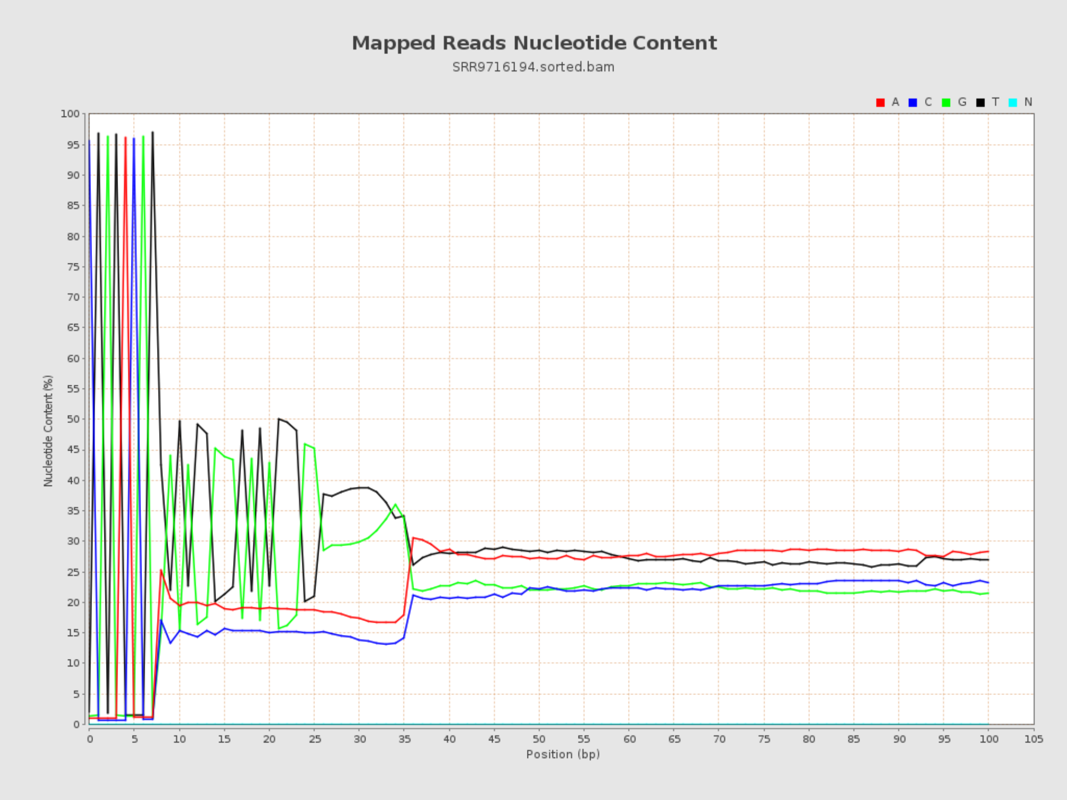
6. Results : Genome Fraction Coverage



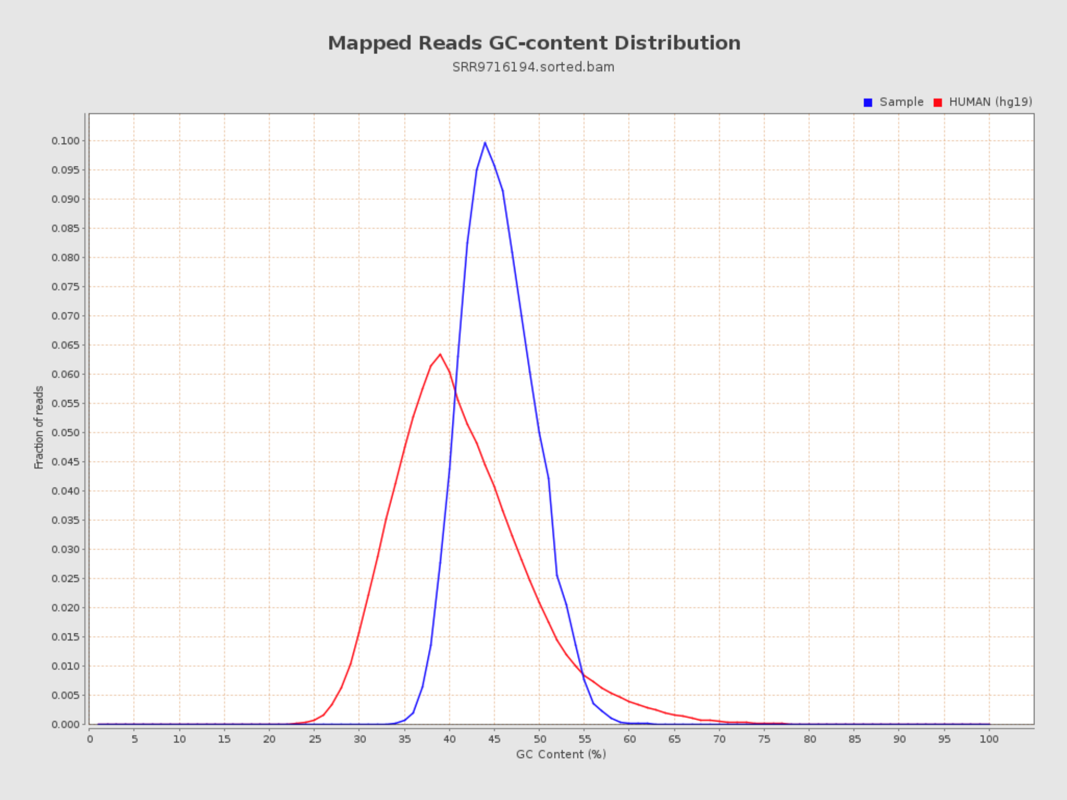
7. Results : Duplication Rate Histogram



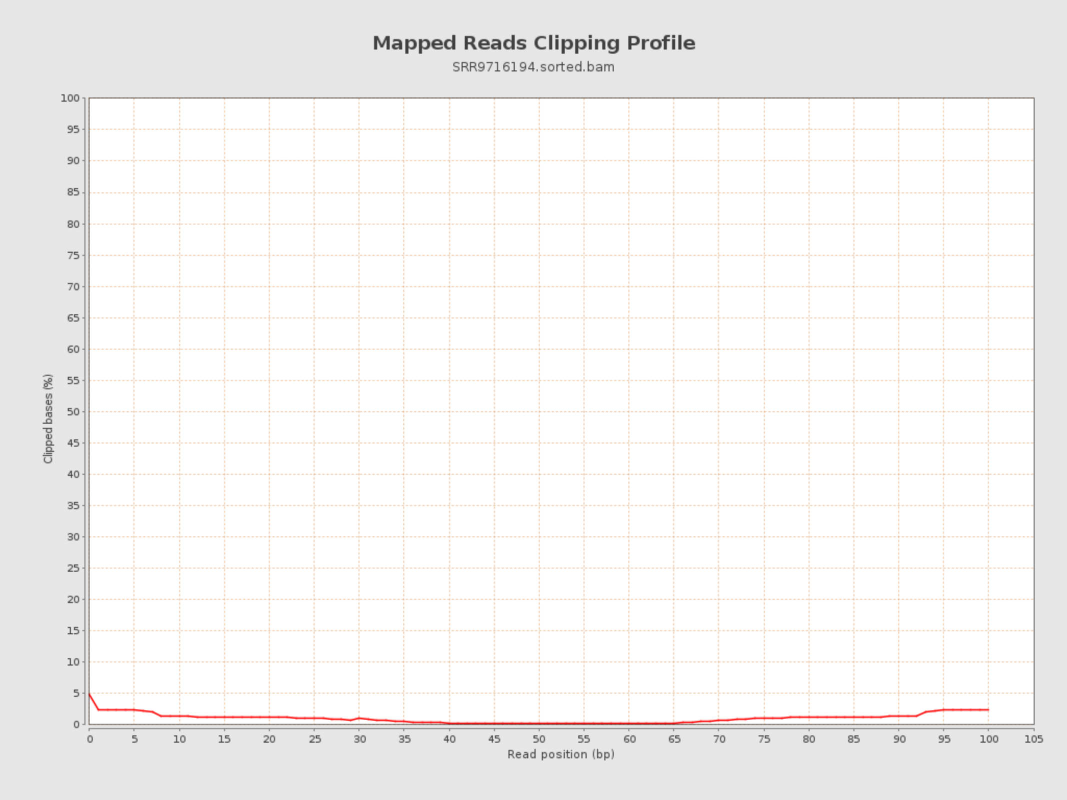
8. Results : Mapped Reads Nucleotide Content



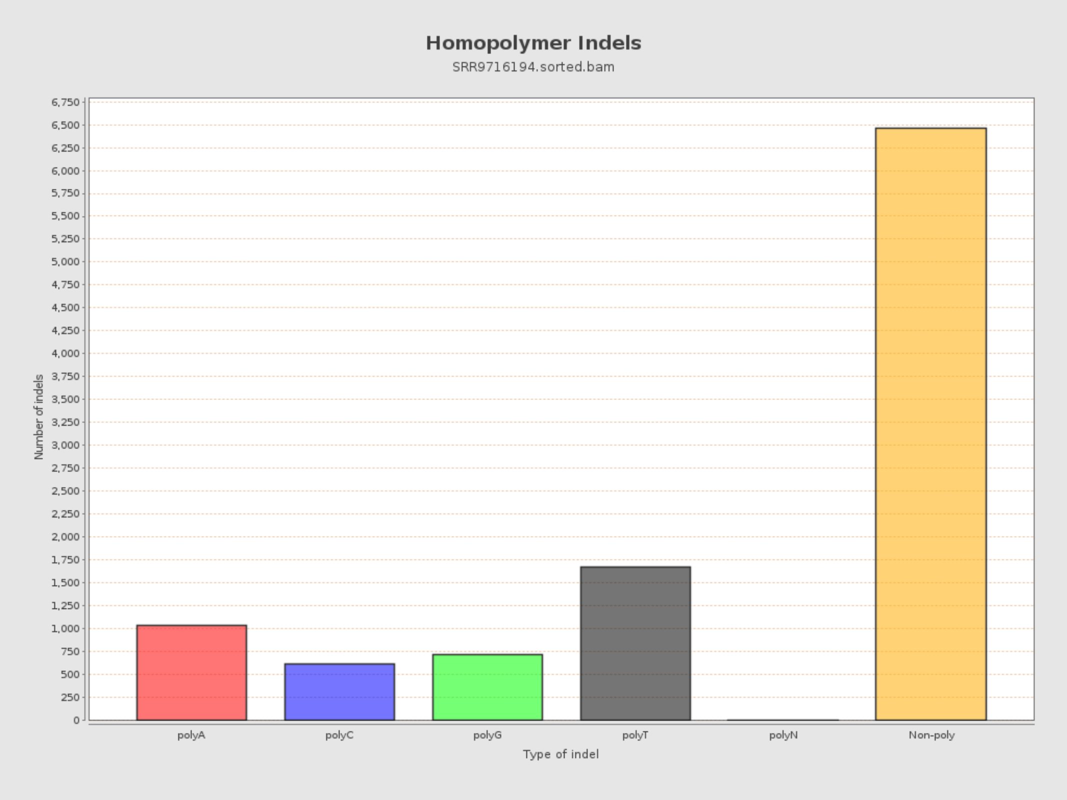
9. Results : Mapped Reads GC-content Distribution



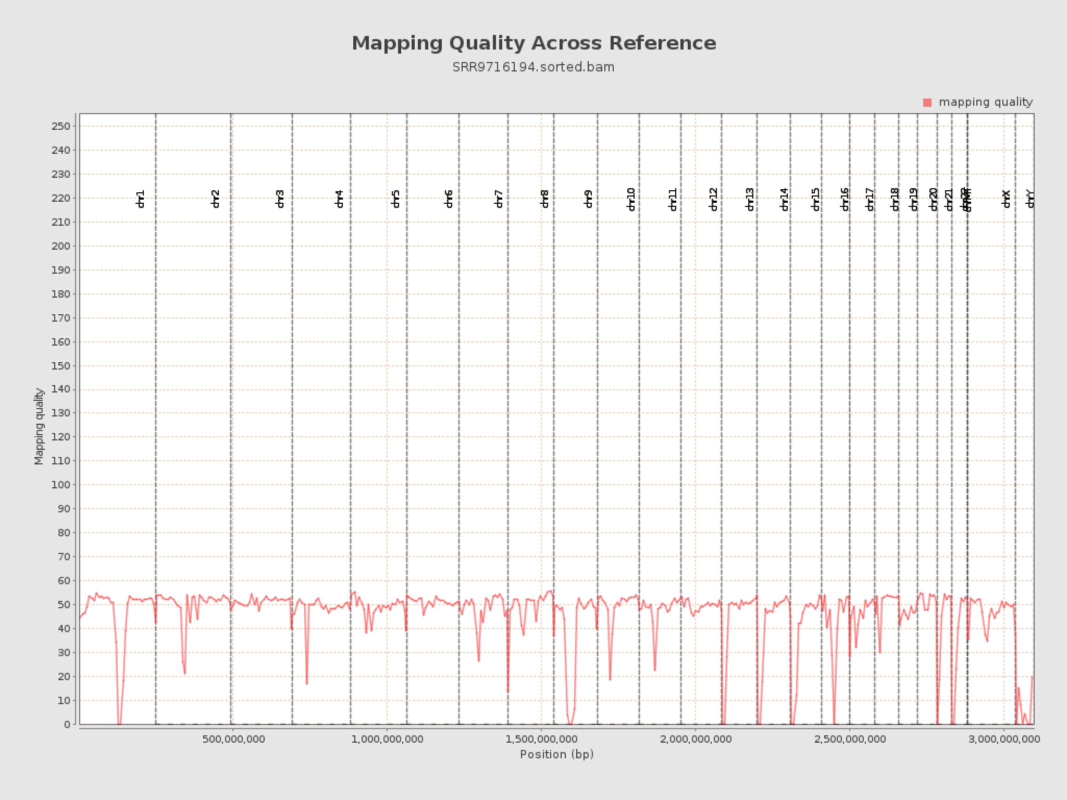
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram