Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 15:05:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716458.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_SRR9716458 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716458.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 15:05:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716458.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,621,028
Mapped reads	2,350,967 / 89.7%
Unmapped reads	270,061 / 10.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,902 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	98,488 / 3.76%
Duplication rate	3.12%
Clipped reads	2,353,335 / 89.79%

2.2. ACGT Content

Number/percentage of A's	33,531,015 / 24.71%
Number/percentage of C's	27,312,475 / 20.13%
Number/percentage of T's	41,674,636 / 30.72%
Number/percentage of G's	33,161,198 / 24.44%
Number/percentage of N's	1,168 / 0%
GC Percentage	44.57%

2.3. Coverage

Mean	0.0438

Standard Deviation	0.3361

2.4. Mapping Quality

Mean Mapping Quality	44.01

2.5. Mismatches and indels

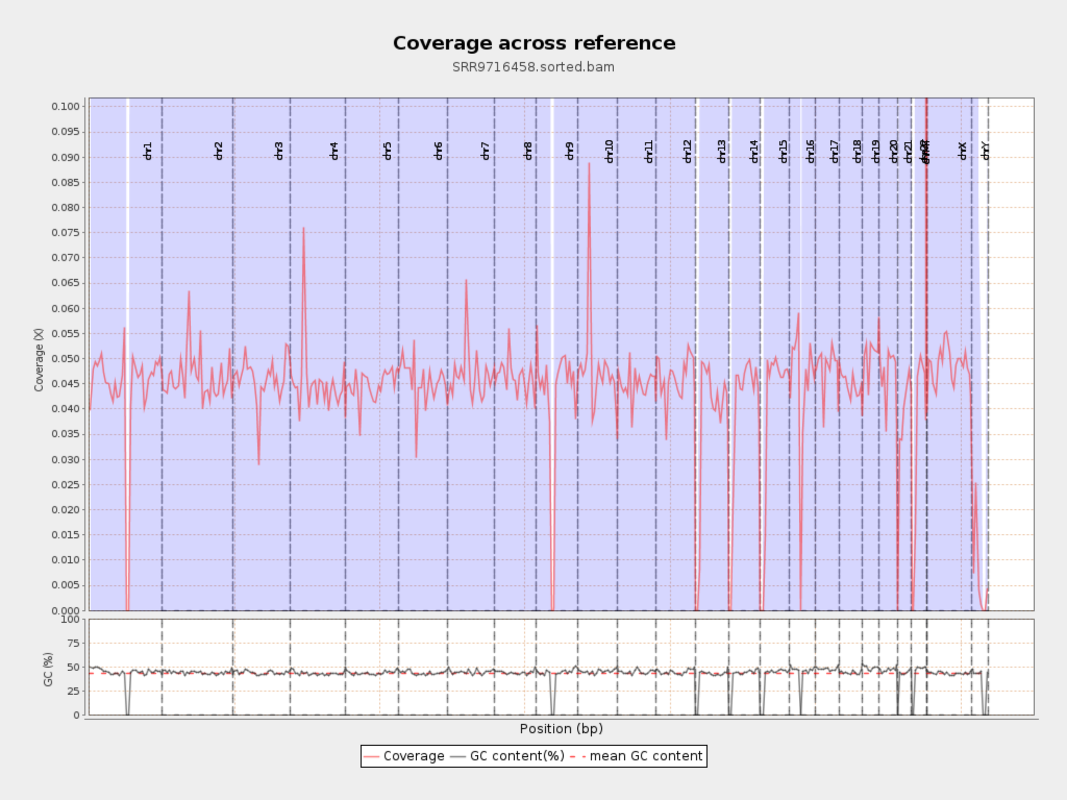
General error rate	0.54%
Mismatches	713,475
Insertions	10,825
Mapped reads with at least one insertion	0.46%
Deletions	26,156
Mapped reads with at least one deletion	1.1%
Homopolymer indels	39.52%

2.6. Chromosome stats

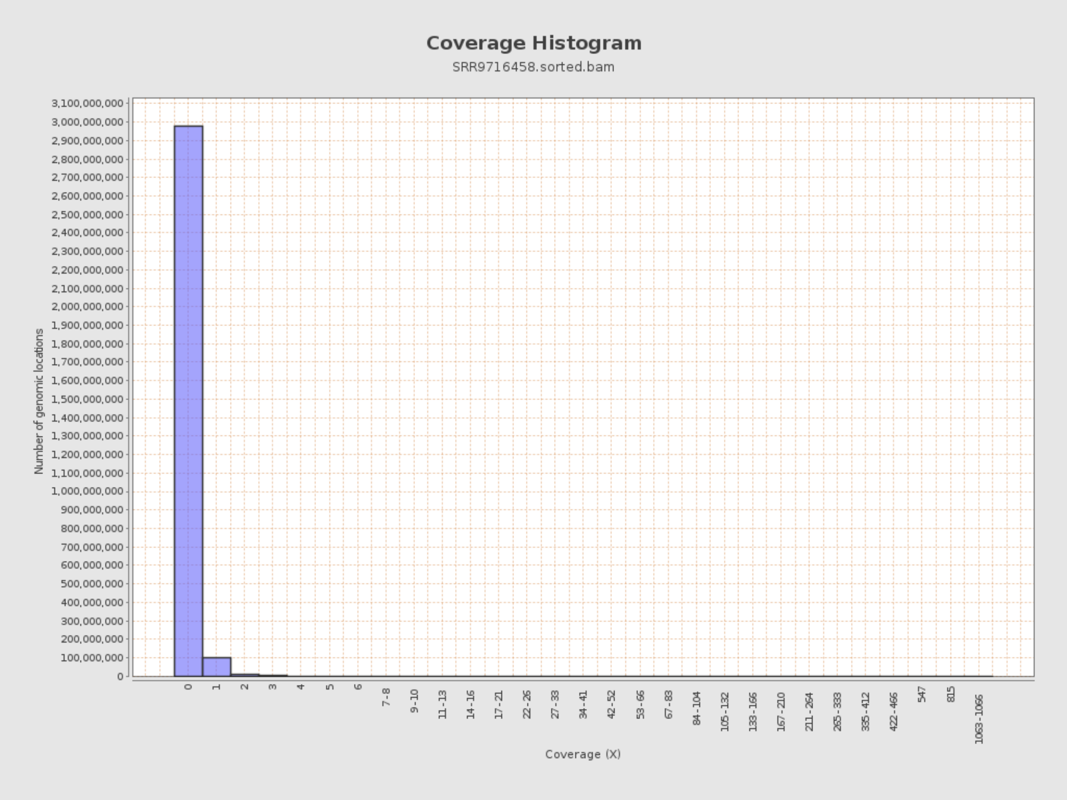
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10854414	0.0435	0.4425
chr2	243199373	11272836	0.0464	0.5294
chr3	198022430	9103167	0.046	0.2488
chr4	191154276	8642644	0.0452	0.2841
chr5	180915260	8088962	0.0447	0.2407
chr6	171115067	7785886	0.0455	0.2857
chr7	159138663	7451854	0.0468	0.4232

chr8	146364022	6774569	0.0463	0.3332
chr9	141213431	5772701	0.0409	0.2884
chr10	135534747	6559669	0.0484	0.4199
chr11	135006516	6032869	0.0447	0.3075
chr12	133851895	6200182	0.0463	0.2485
chr13	115169878	4209666	0.0366	0.2186
chr14	107349540	4142723	0.0386	0.2394
chr15	102531392	3962845	0.0387	0.2283
chr16	90354753	4033934	0.0446	0.2671
chr17	81195210	3895758	0.048	0.267
chr18	78077248	3505918	0.0449	0.4534
chr19	59128983	2978580	0.0504	0.4005
chr20	63025520	2955749	0.0469	0.2563
chr21	48129895	1771450	0.0368	0.2553
chr22	51304566	1686507	0.0329	0.21
chrMT	16571	50999	3.0776	2.6274
chrX	155270560	7557534	0.0487	0.2759
chrY	59373566	430700	0.0073	0.209

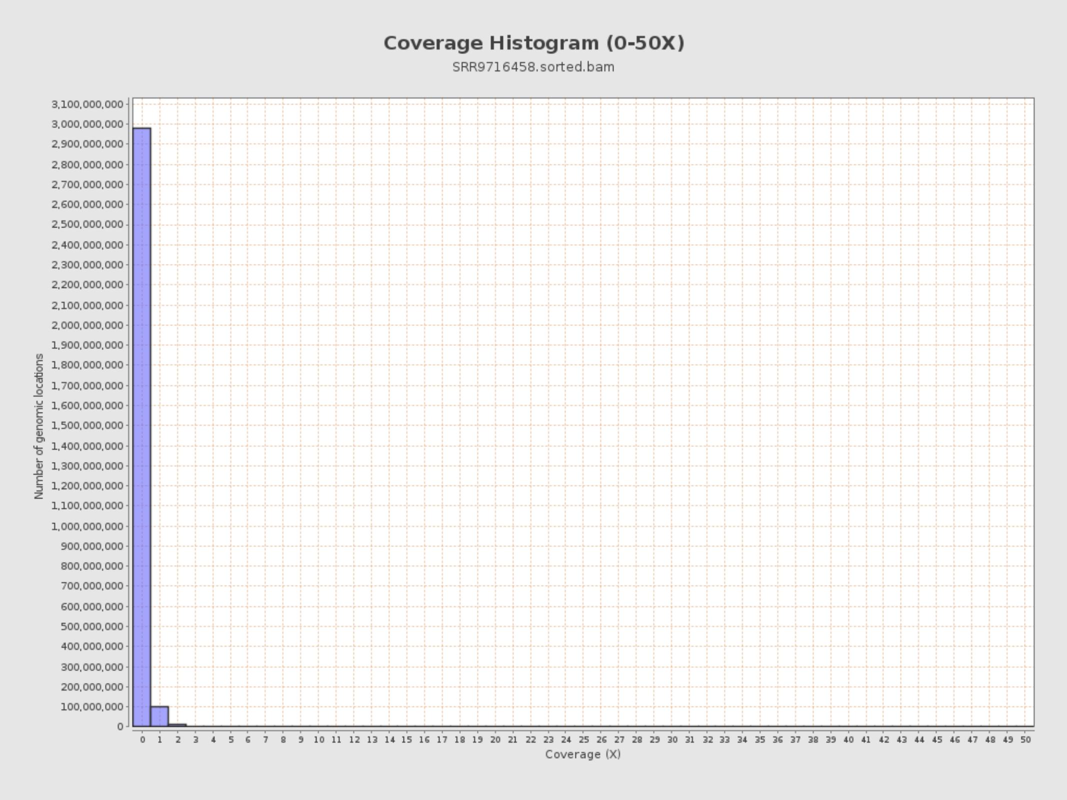
3. Results : Coverage across reference



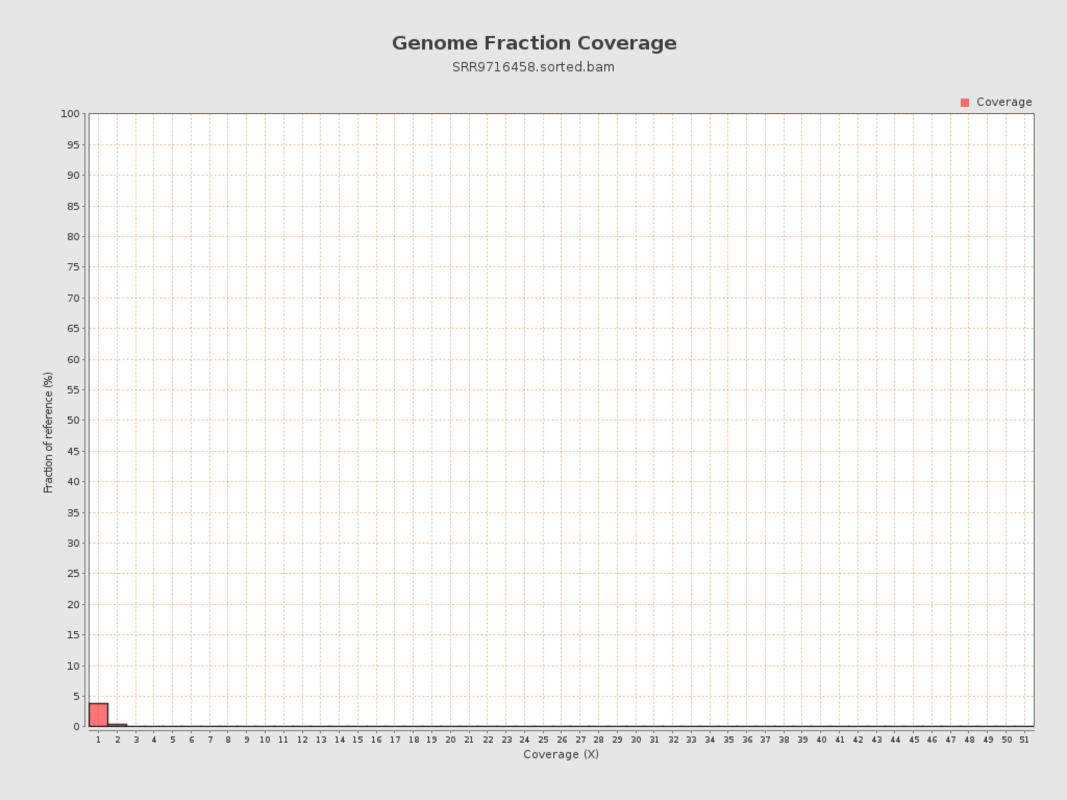
4. Results : Coverage Histogram



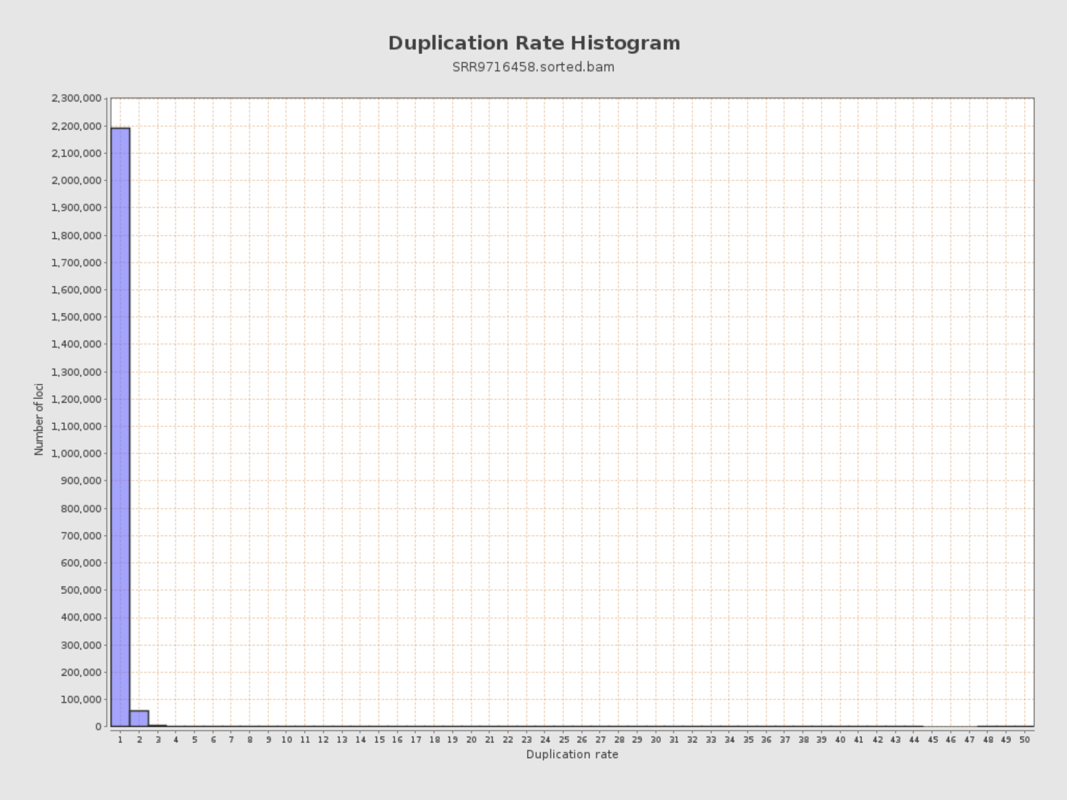
5. Results : Coverage Histogram (0-50X)



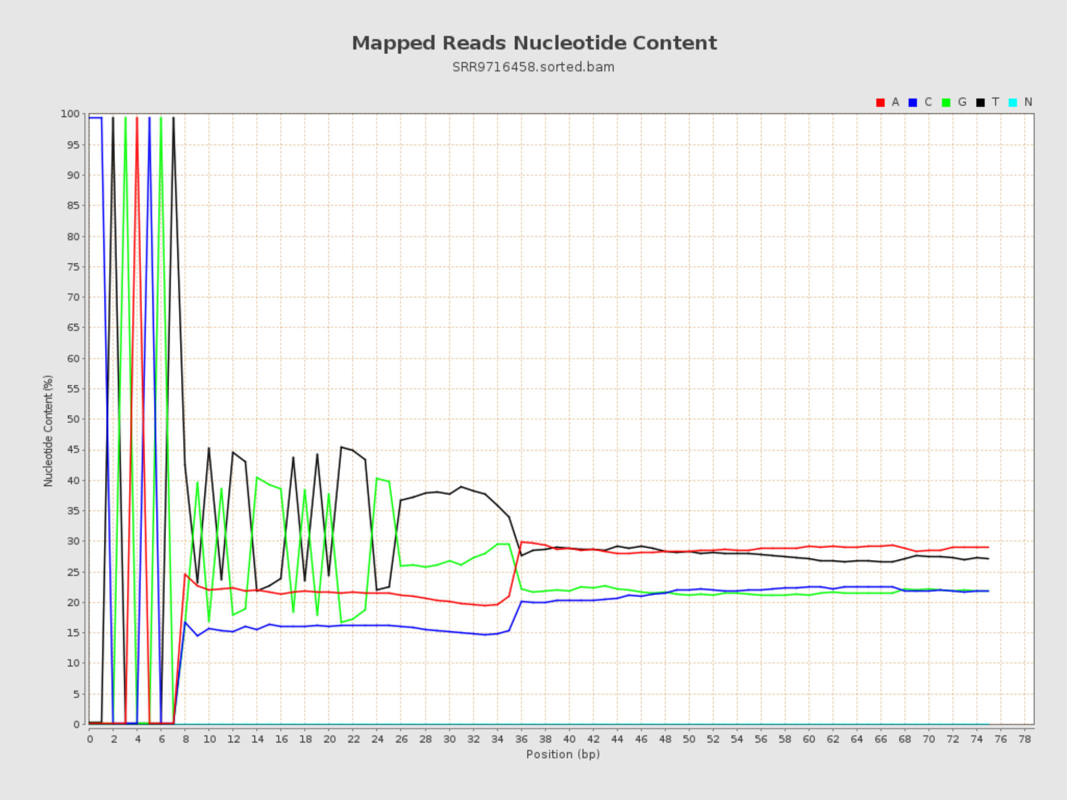
6. Results : Genome Fraction Coverage



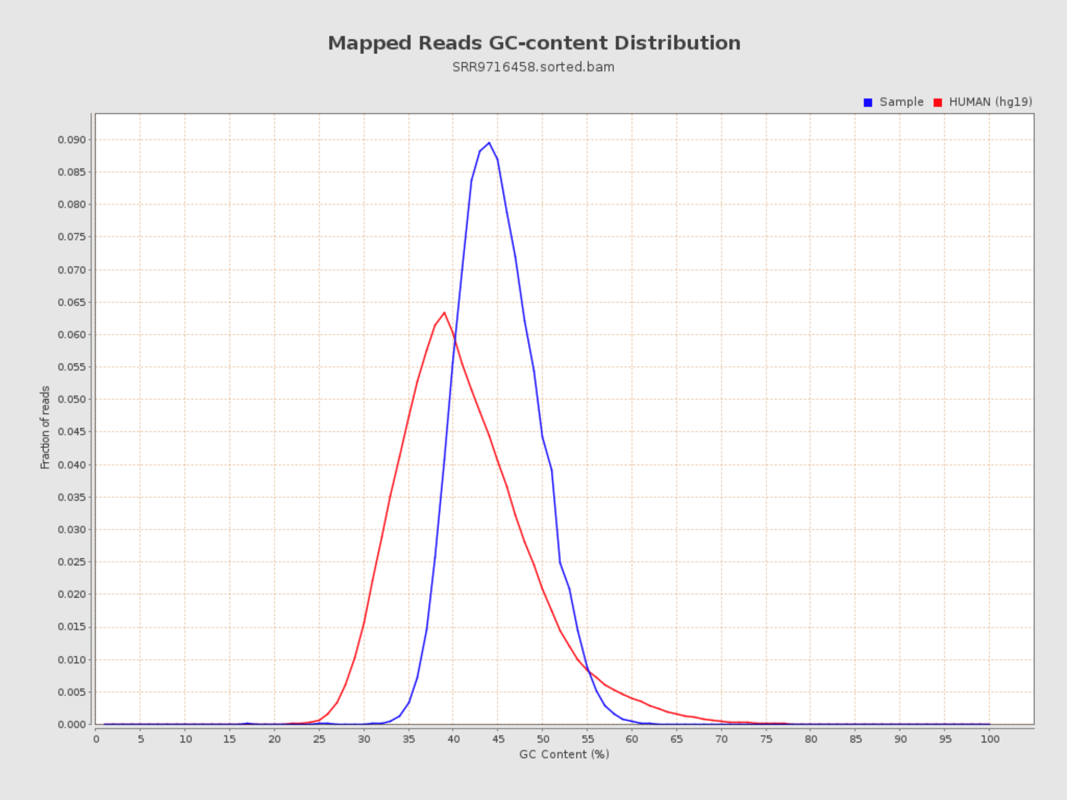
7. Results : Duplication Rate Histogram



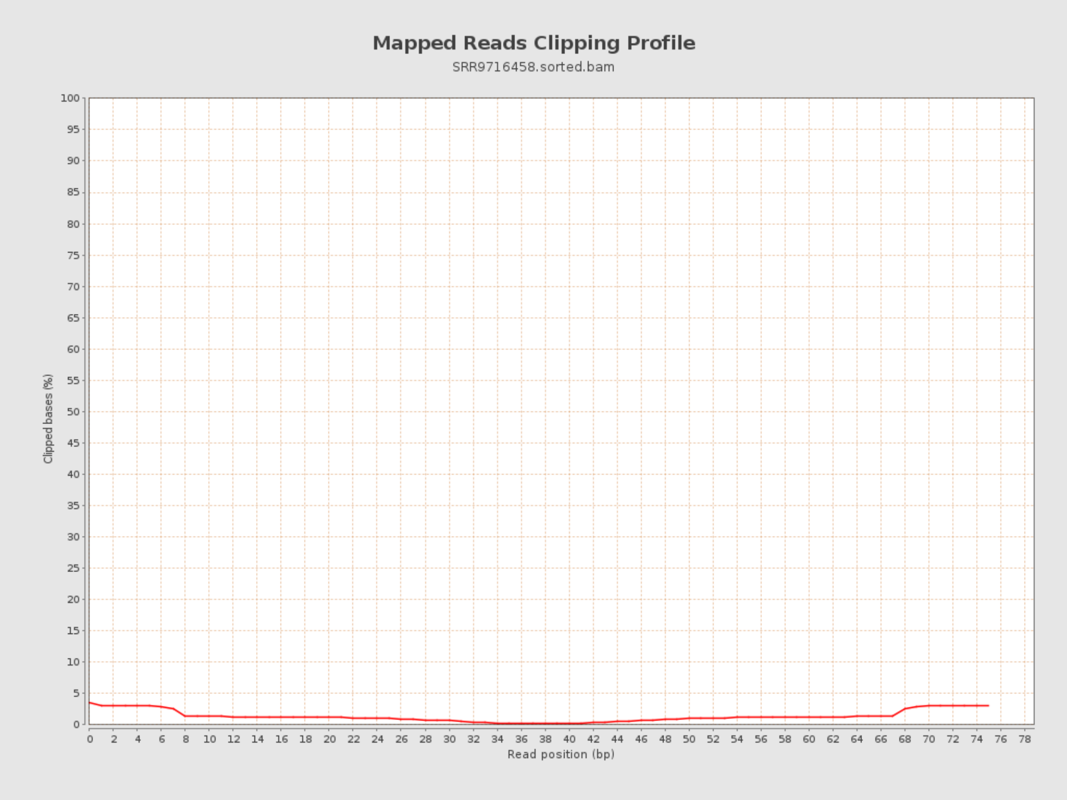
8. Results : Mapped Reads Nucleotide Content



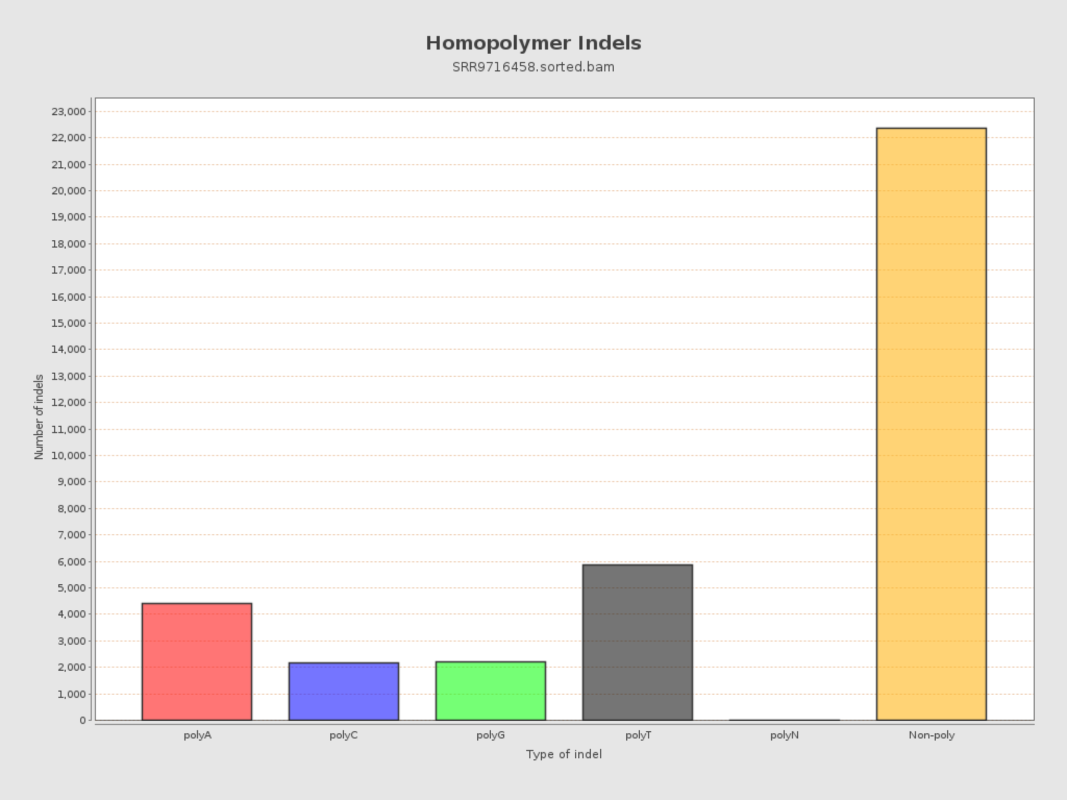
9. Results : Mapped Reads GC-content Distribution



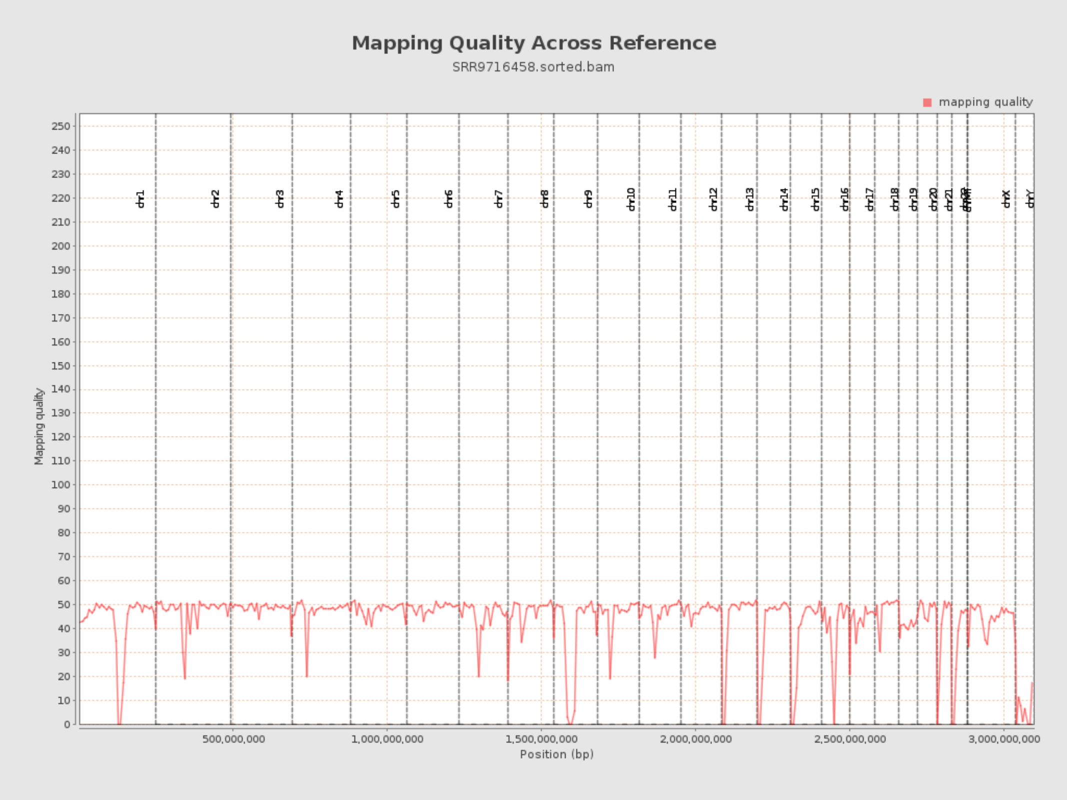
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram