Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 19:55:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716950.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_SRR9716950 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716950.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 19:55:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716950.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,612,873
Mapped reads	2,405,709 / 92.07%
Unmapped reads	207,164 / 7.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,086 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	112,262 / 4.3%
Duplication rate	3.53%
Clipped reads	2,413,417 / 92.37%

2.2. ACGT Content

Number/percentage of A's	34,712,427 / 24.8%
Number/percentage of C's	29,217,236 / 20.87%
Number/percentage of T's	41,930,882 / 29.96%
Number/percentage of G's	34,104,720 / 24.37%
Number/percentage of N's	1,898 / 0%
GC Percentage	45.24%

2.3. Coverage

Mean	0.0452

Standard Deviation	0.3602

2.4. Mapping Quality

Mean Mapping Quality	44.32

2.5. Mismatches and indels

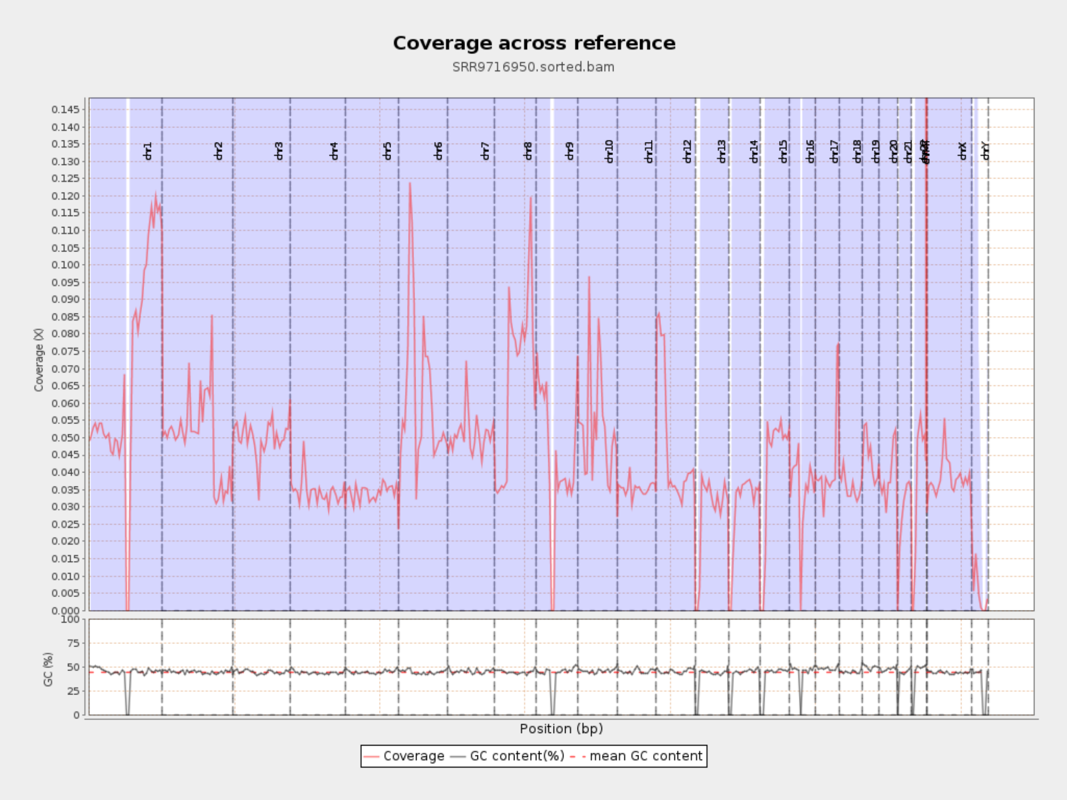
General error rate	0.51%
Mismatches	694,540
Insertions	9,600
Mapped reads with at least one insertion	0.4%
Deletions	24,438
Mapped reads with at least one deletion	1.01%
Homopolymer indels	42.01%

2.6. Chromosome stats

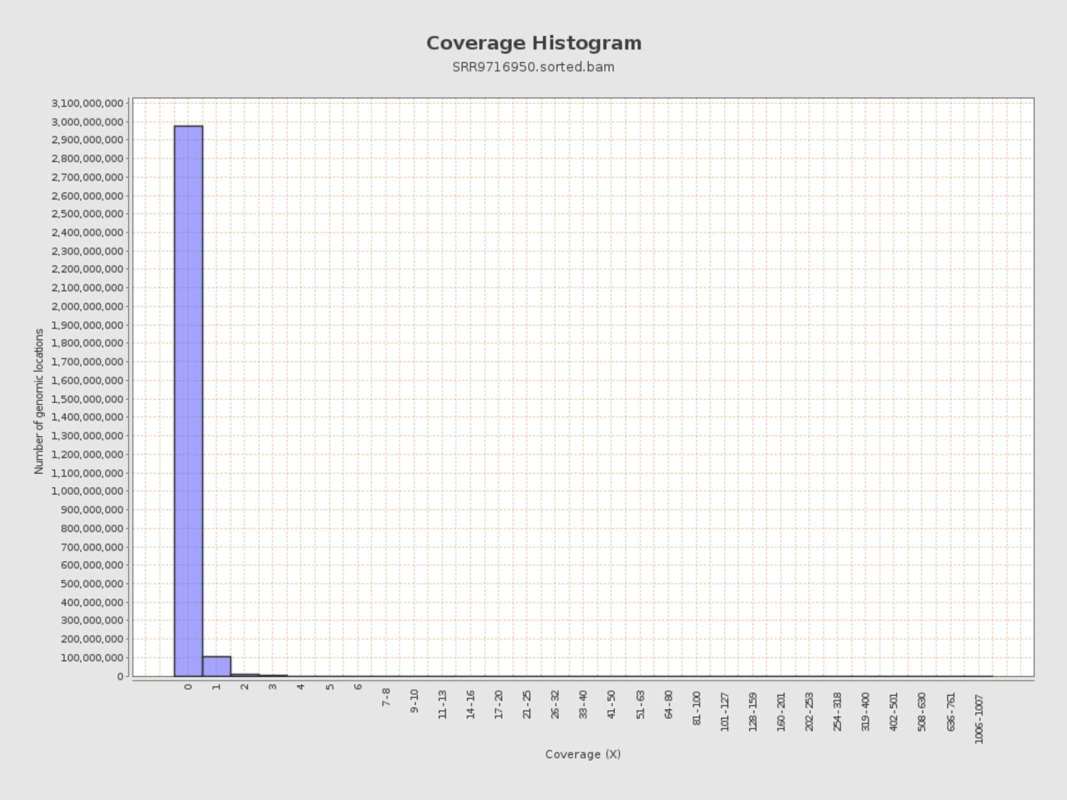
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17077007	0.0685	0.5773
chr2	243199373	12221617	0.0503	0.496
chr3	198022430	9897926	0.05	0.2597
chr4	191154276	6571566	0.0344	0.2319
chr5	180915260	6191477	0.0342	0.2144
chr6	171115067	10616267	0.062	0.3803
chr7	159138663	8158075	0.0513	0.4736

chr8	146364022	10000504	0.0683	0.3394
chr9	141213431	5964417	0.0422	0.3361
chr10	135534747	7309431	0.0539	0.405
chr11	135006516	4762237	0.0353	0.2984
chr12	133851895	6410048	0.0479	0.2598
chr13	115169878	3247170	0.0282	0.1915
chr14	107349540	3163138	0.0295	0.2484
chr15	102531392	4235182	0.0413	0.2358
chr16	90354753	3149819	0.0349	0.2517
chr17	81195210	3441878	0.0424	0.2502
chr18	78077248	2791418	0.0358	0.5701
chr19	59128983	2637357	0.0446	0.4335
chr20	63025520	2484567	0.0394	0.2314
chr21	48129895	1334503	0.0277	0.2197
chr22	51304566	1802484	0.0351	0.2172
chrMT	16571	254685	15.3693	9.2459
chrX	155270560	5970147	0.0384	0.2727
chrY	59373566	312536	0.0053	0.1238

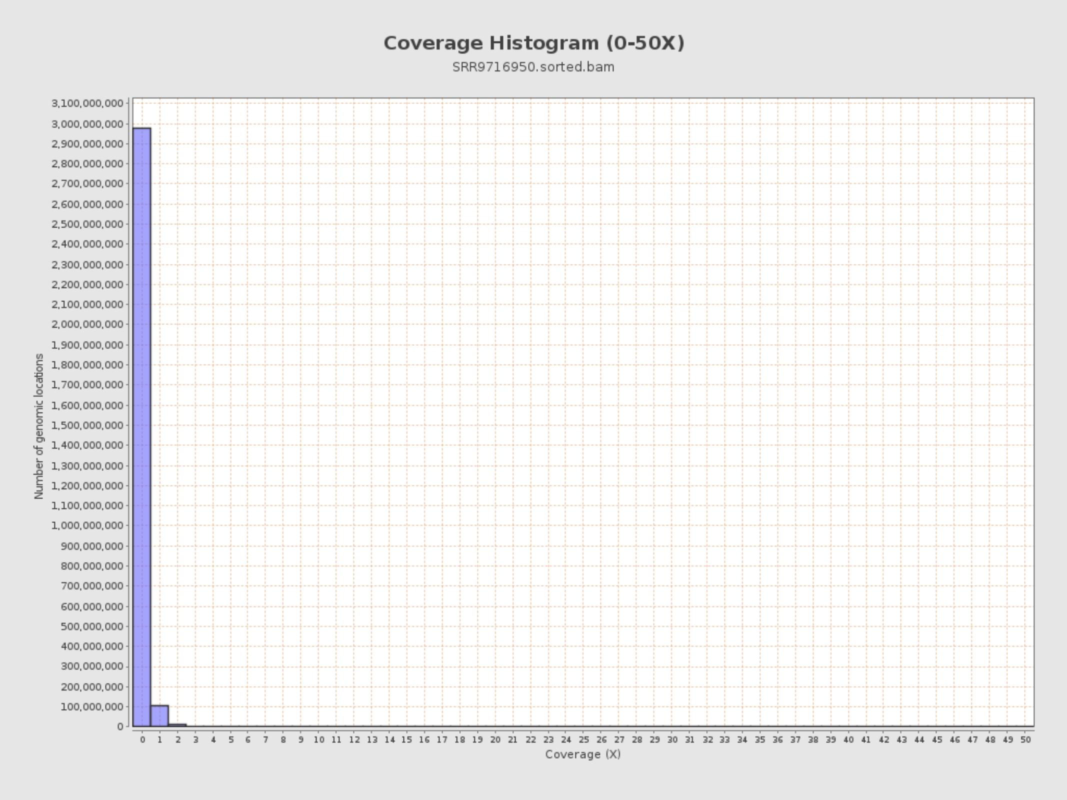
3. Results : Coverage across reference



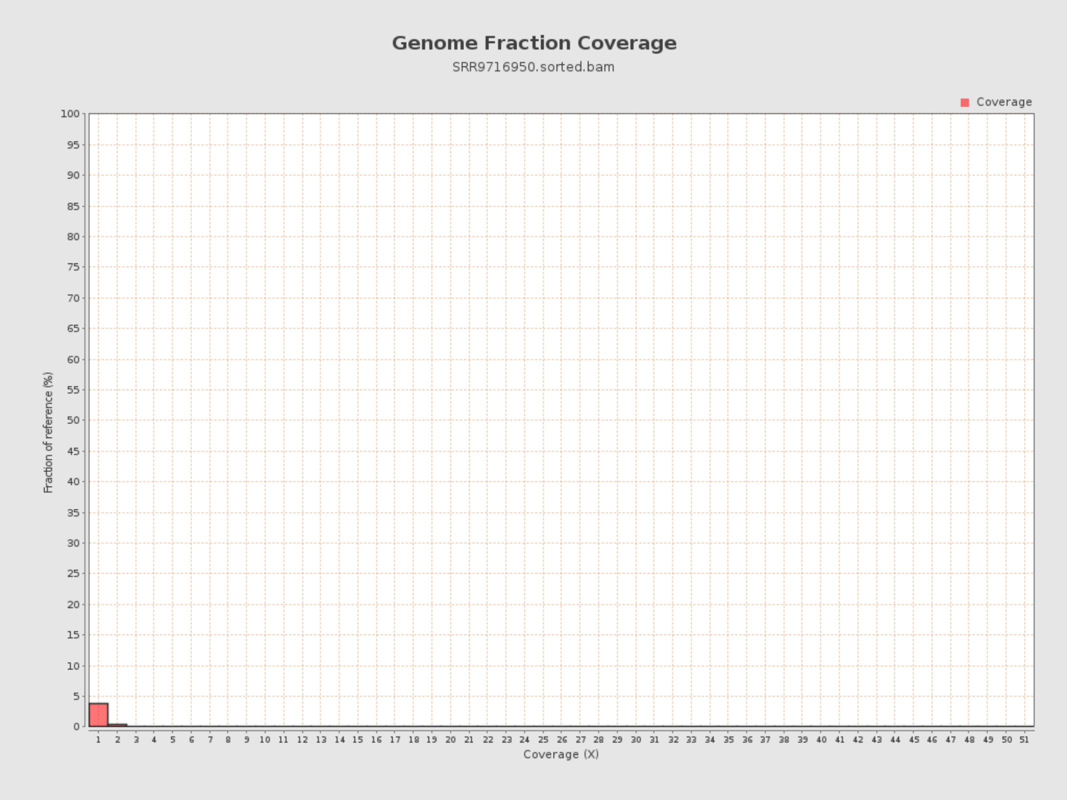
4. Results : Coverage Histogram



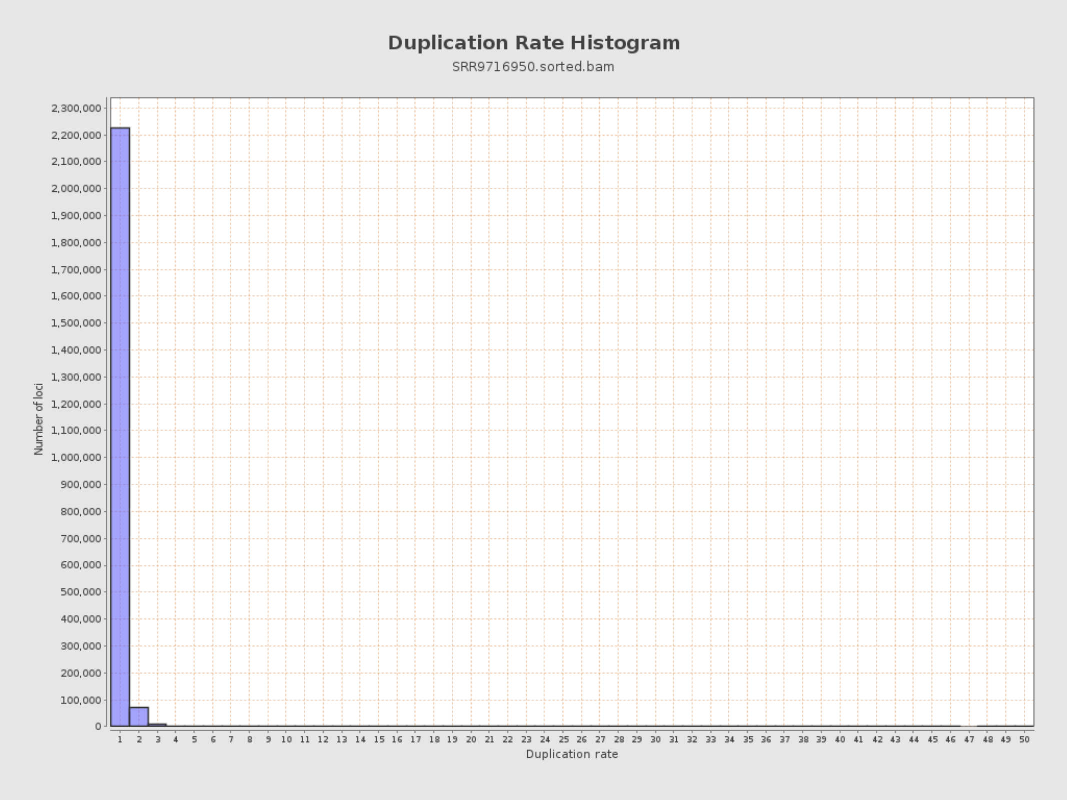
5. Results : Coverage Histogram (0-50X)



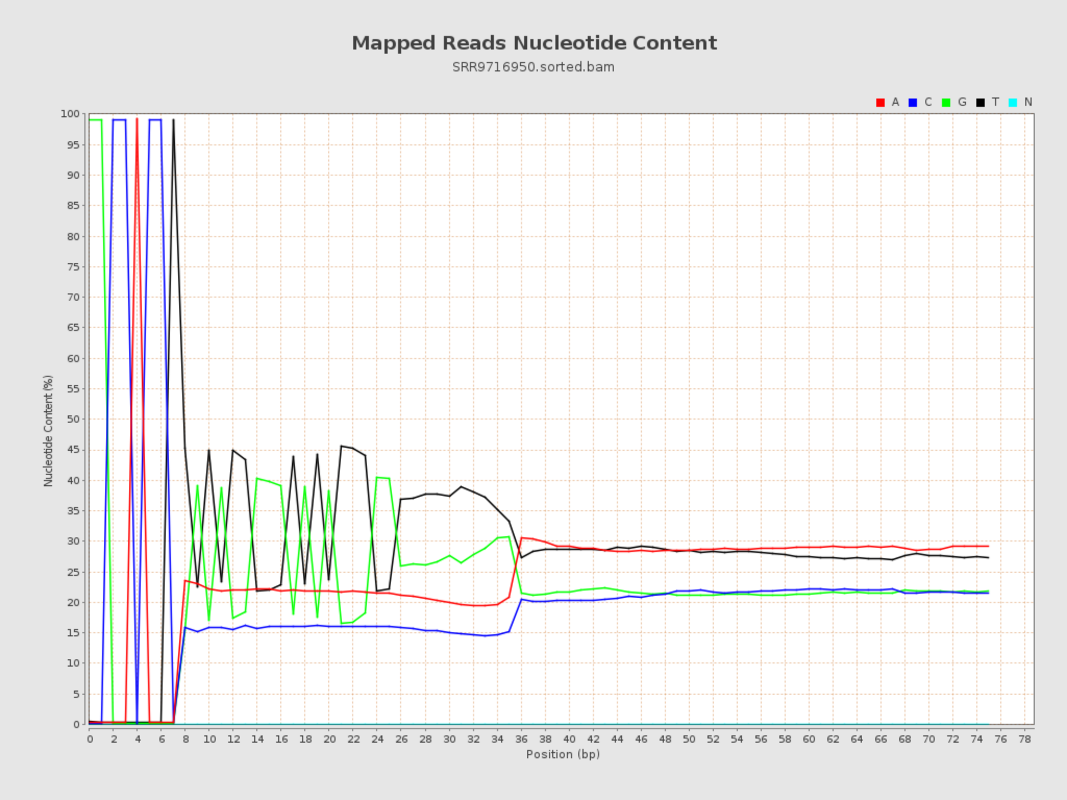
6. Results : Genome Fraction Coverage



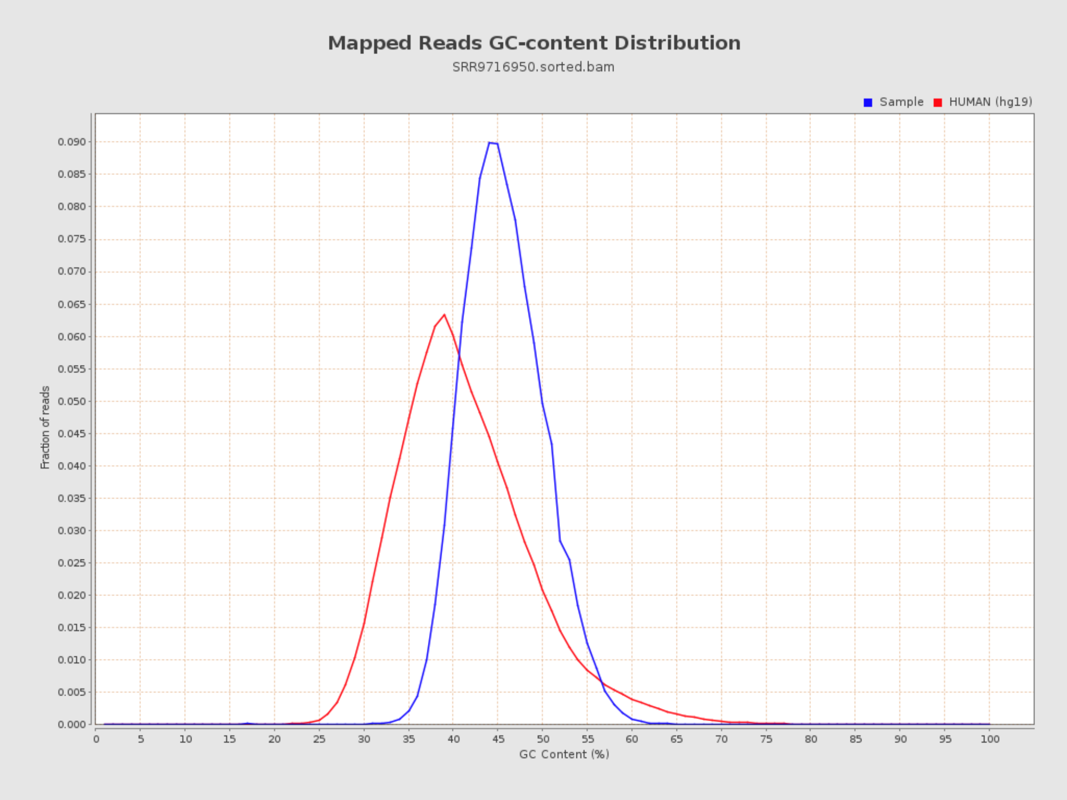
7. Results : Duplication Rate Histogram



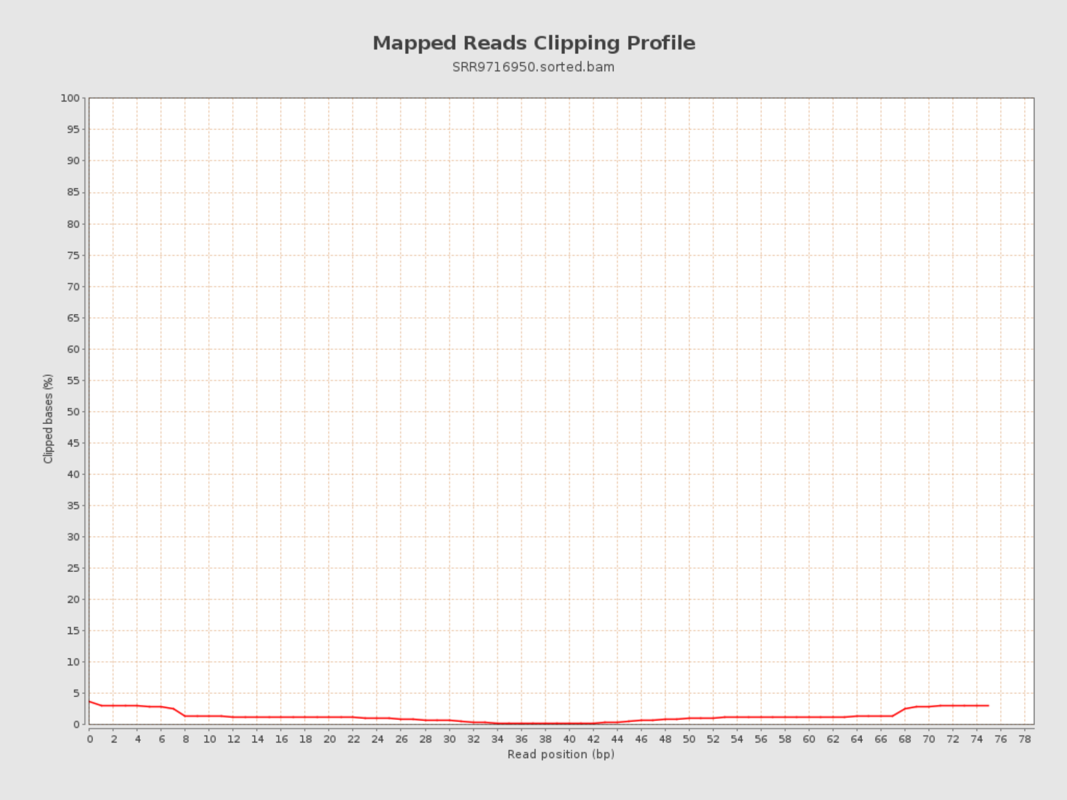
8. Results : Mapped Reads Nucleotide Content



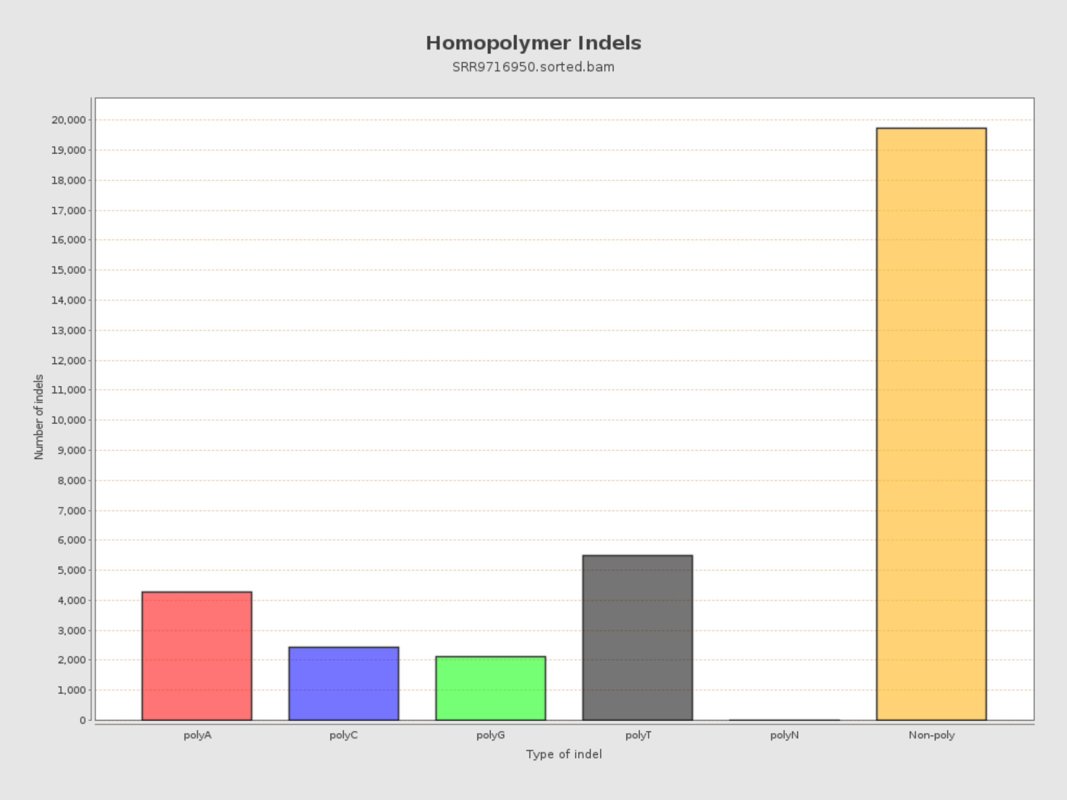
9. Results : Mapped Reads GC-content Distribution



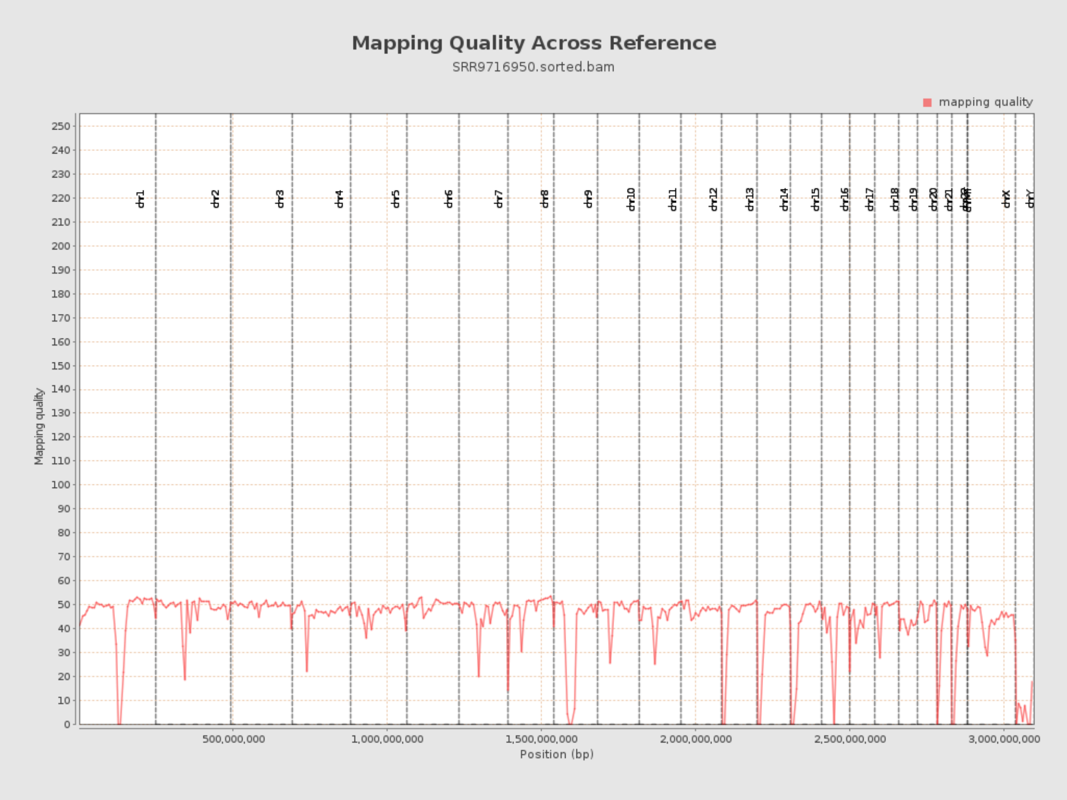
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram