Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 09:25:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716367.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_SRR9716367 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716367.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 09:25:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716367.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,848,352
Mapped reads	2,617,159 / 91.88%
Unmapped reads	231,193 / 8.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	57,547 / 2.02%
Read min/max/mean length	30 / 101 / 101.73
Duplicated reads (estimated)	129,423 / 4.54%
Duplication rate	3.5%
Clipped reads	2,668,373 / 93.68%

2.2. ACGT Content

Number/percentage of A's	54,173,311 / 26.28%
Number/percentage of C's	41,104,249 / 19.94%
Number/percentage of T's	62,687,904 / 30.41%
Number/percentage of G's	48,128,601 / 23.35%
Number/percentage of N's	15,207 / 0.01%
GC Percentage	43.29%

2.3. Coverage

Mean	0.0666

Standard Deviation	0.6162

2.4. Mapping Quality

Mean Mapping Quality	47.17

2.5. Mismatches and indels

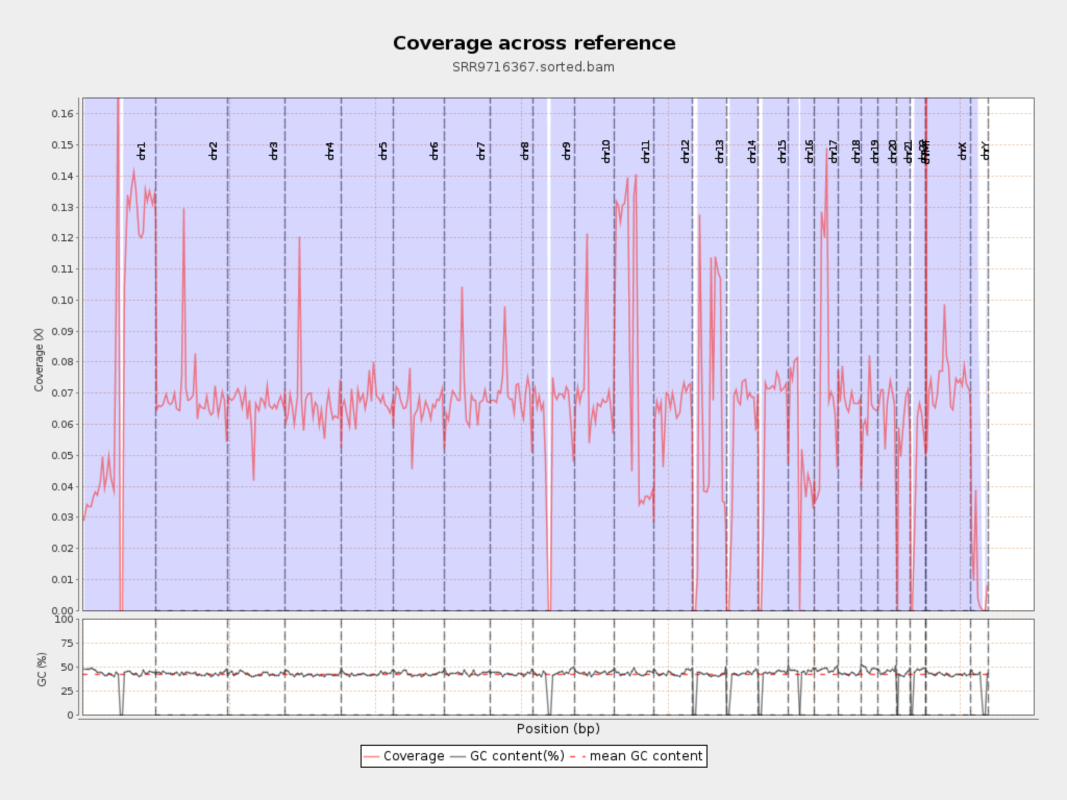
General error rate	0.68%
Mismatches	1,364,250
Insertions	18,558
Mapped reads with at least one insertion	0.7%
Deletions	49,199
Mapped reads with at least one deletion	1.85%
Homopolymer indels	42.67%

2.6. Chromosome stats

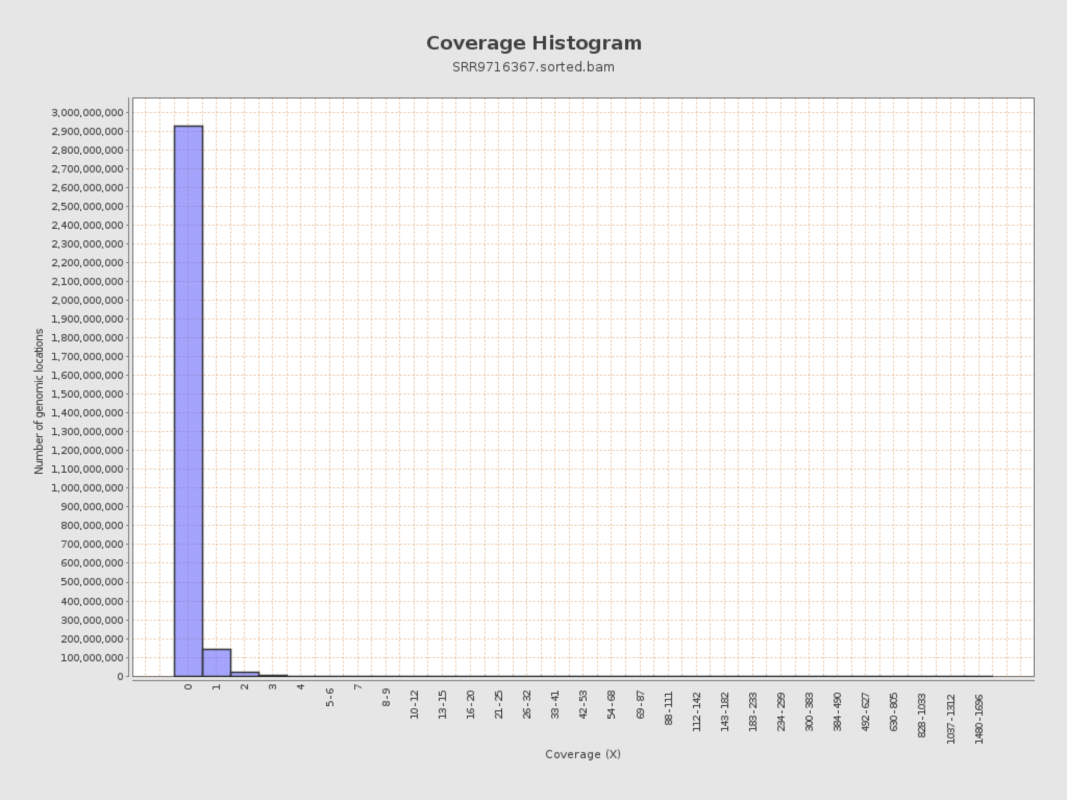
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20619590	0.0827	1.3979
chr2	243199373	16846027	0.0693	0.6606
chr3	198022430	13090423	0.0661	0.2973
chr4	191154276	12840392	0.0672	0.3973
chr5	180915260	12200744	0.0674	0.3052
chr6	171115067	11284599	0.0659	0.3427
chr7	159138663	10839718	0.0681	0.7331

chr8	146364022	10235105	0.0699	0.6712
chr9	141213431	8326745	0.059	0.4677
chr10	135534747	9346173	0.069	0.5734
chr11	135006516	11398106	0.0844	0.6623
chr12	133851895	8891145	0.0664	0.3036
chr13	115169878	7140405	0.062	0.2933
chr14	107349540	6155662	0.0573	0.3135
chr15	102531392	6016696	0.0587	0.2818
chr16	90354753	4611578	0.051	0.2928
chr17	81195210	6196382	0.0763	0.4161
chr18	78077248	5363398	0.0687	0.8357
chr19	59128983	3770462	0.0638	0.9036
chr20	63025520	4159190	0.066	0.3204
chr21	48129895	2685954	0.0558	0.3305
chr22	51304566	2201388	0.0429	0.2416
chrMT	16571	30027	1.812	1.8052
chrX	155270560	11359094	0.0732	0.3973
chrY	59373566	593368	0.01	0.3236

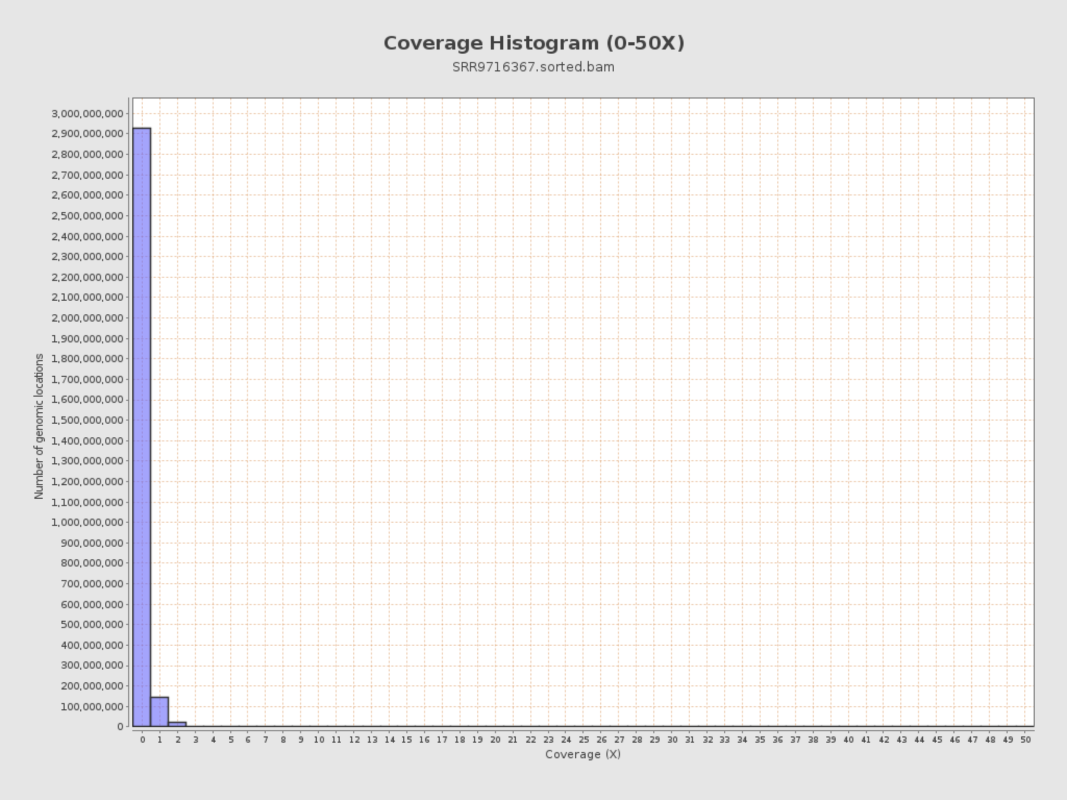
3. Results : Coverage across reference



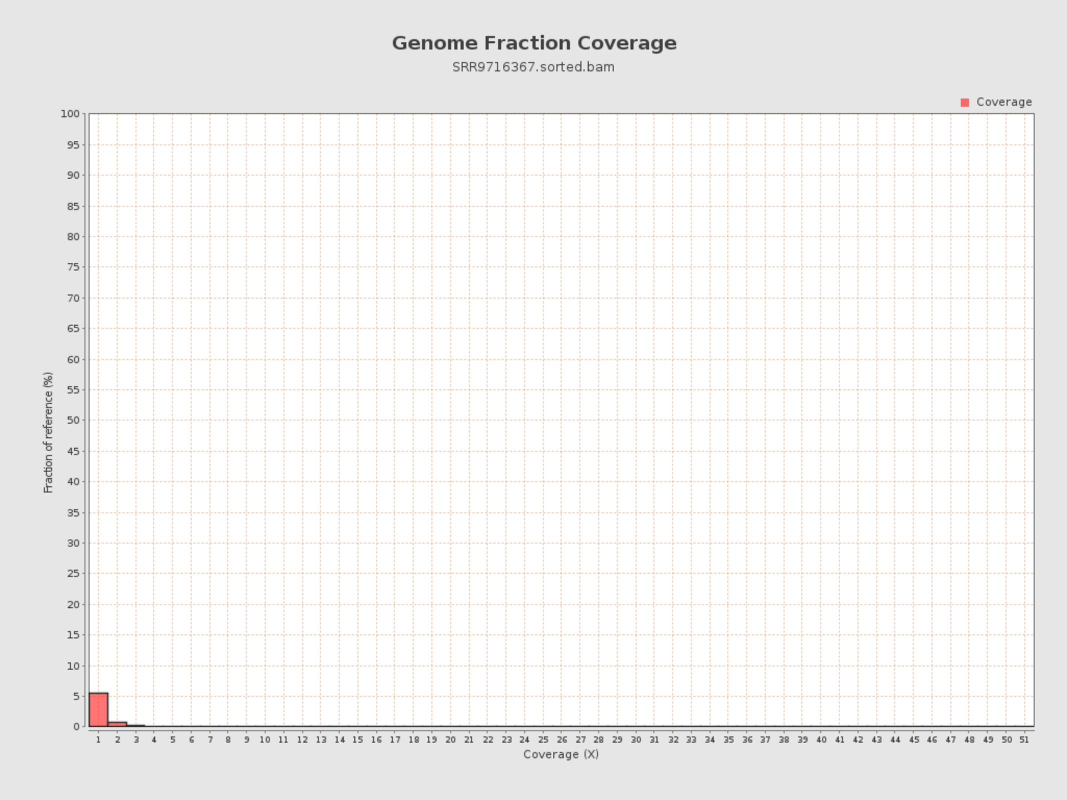
4. Results : Coverage Histogram



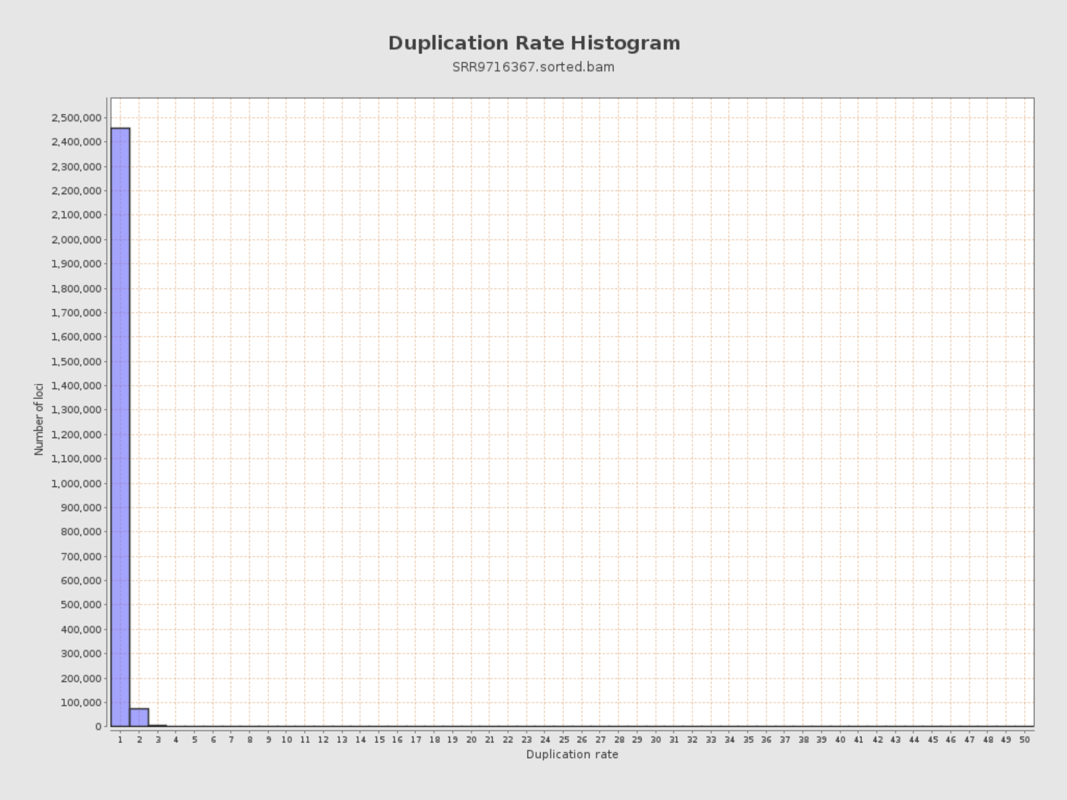
5. Results : Coverage Histogram (0-50X)



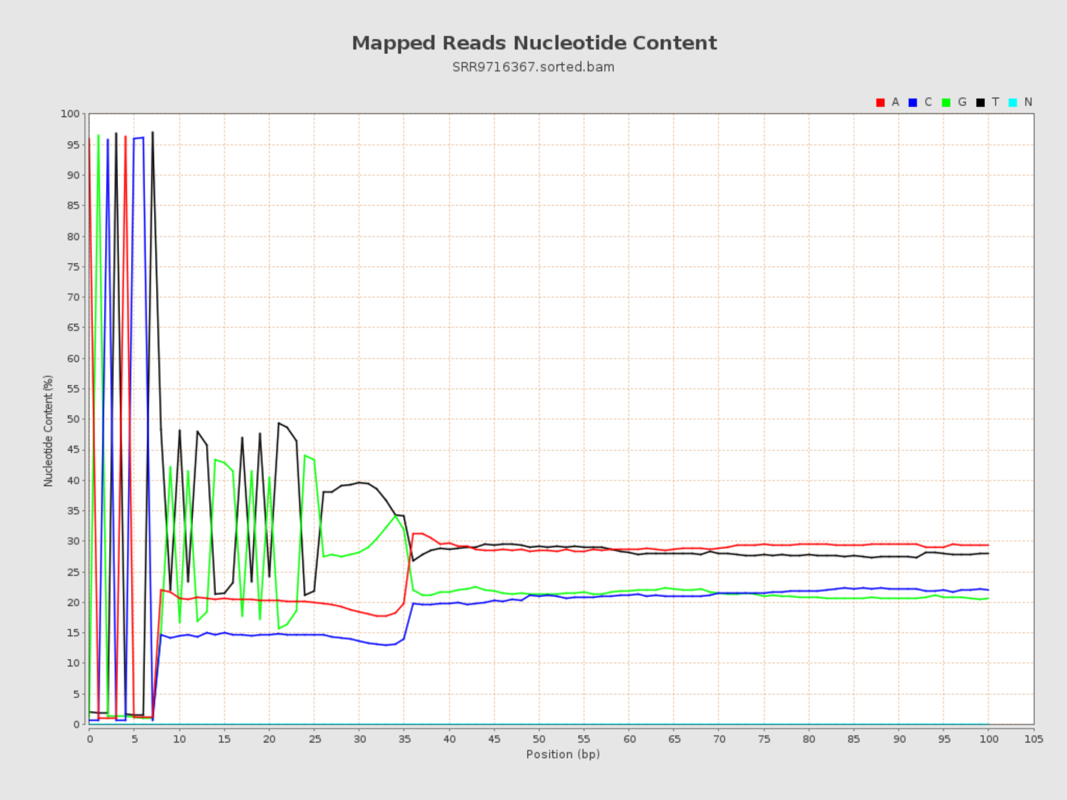
6. Results : Genome Fraction Coverage



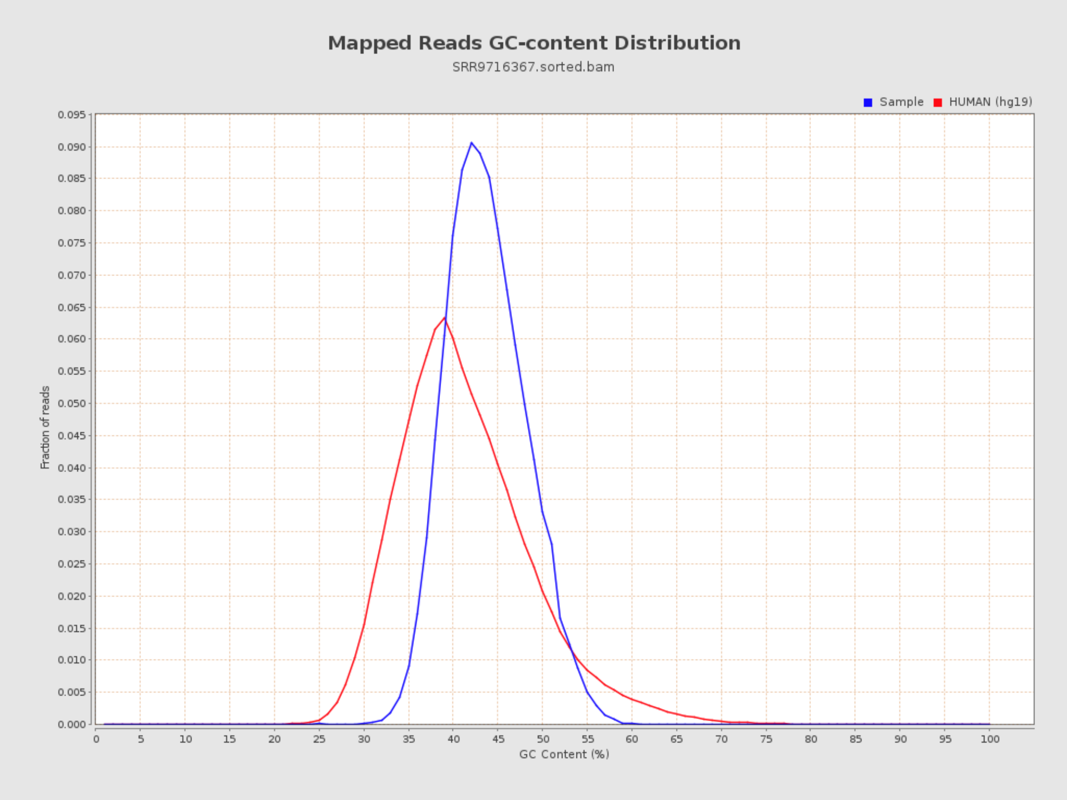
7. Results : Duplication Rate Histogram



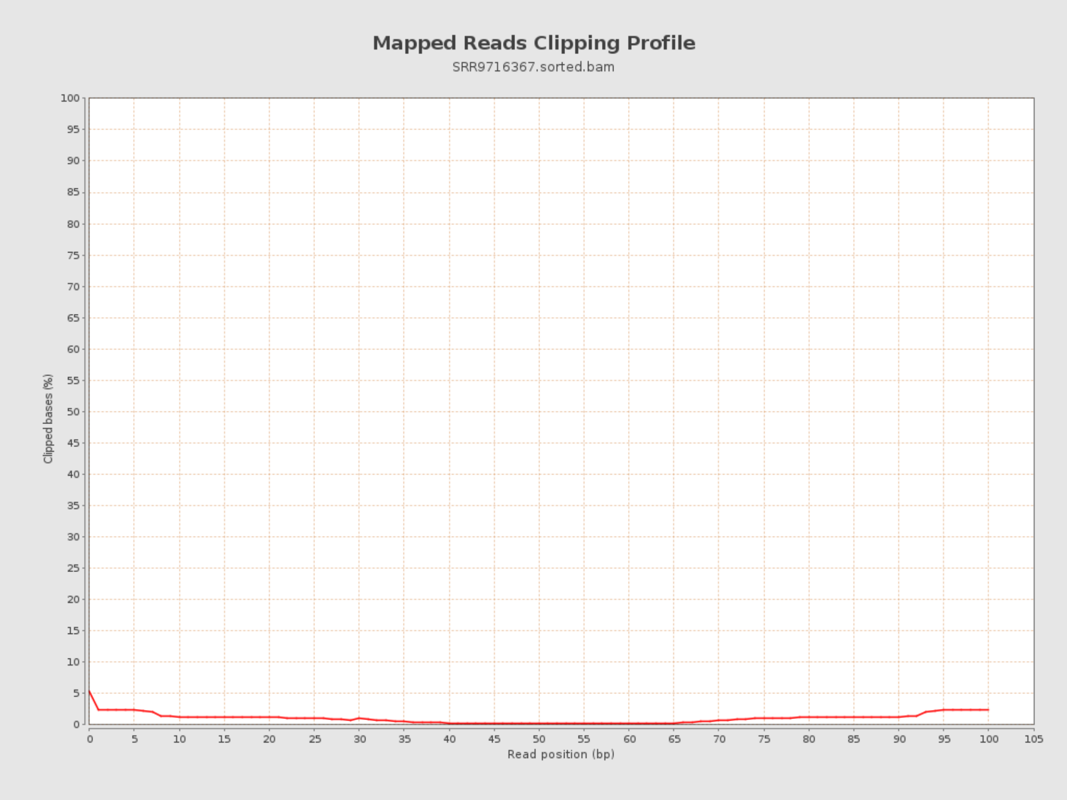
8. Results : Mapped Reads Nucleotide Content



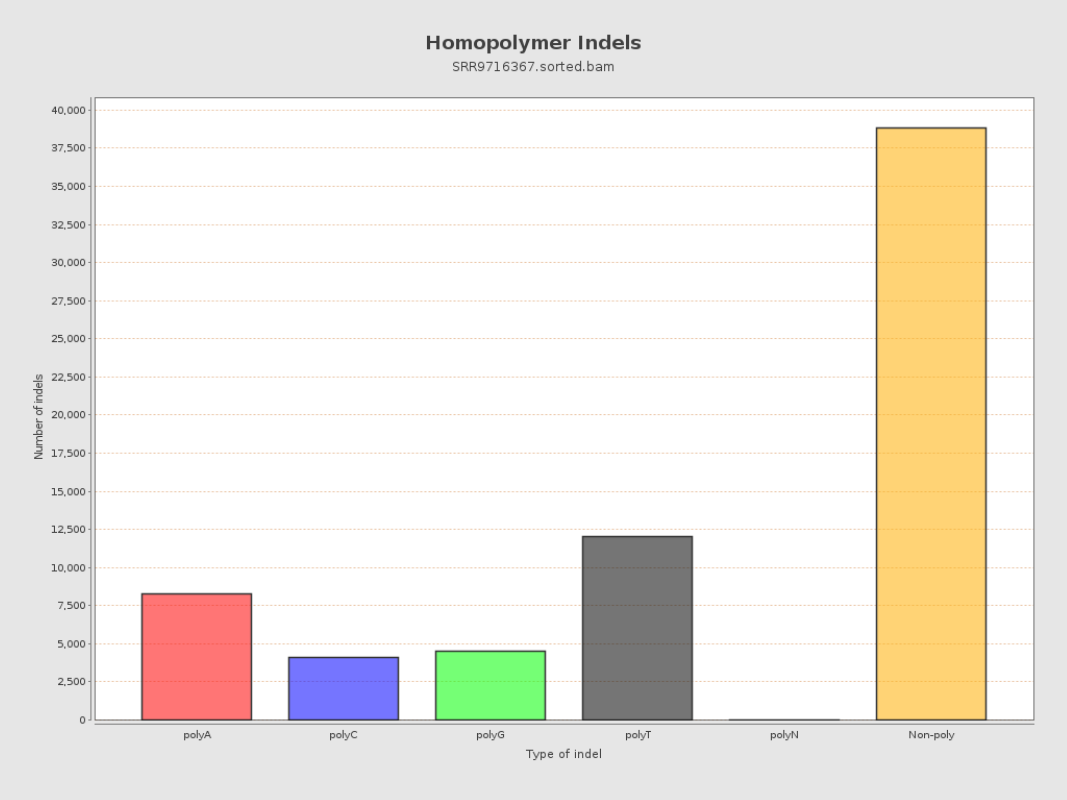
9. Results : Mapped Reads GC-content Distribution



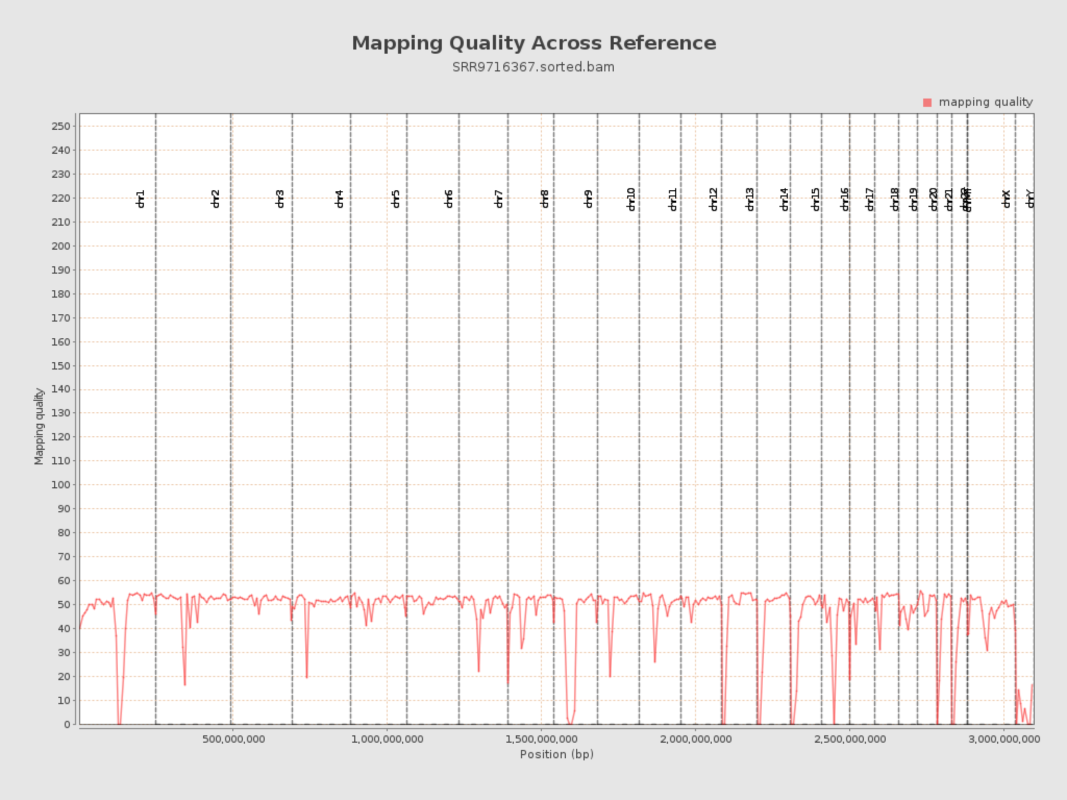
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram