Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 19:45:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716947.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_SRR9716947 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716947.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 19:45:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716947.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,505,473
Mapped reads	3,236,425 / 92.32%
Unmapped reads	269,048 / 7.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,094 / 0.54%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	220,389 / 6.29%
Duplication rate	5.22%
Clipped reads	3,252,017 / 92.77%

2.2. ACGT Content

Number/percentage of A's	48,698,847 / 25.66%
Number/percentage of C's	39,781,534 / 20.96%
Number/percentage of T's	56,643,513 / 29.85%
Number/percentage of G's	44,654,921 / 23.53%
Number/percentage of N's	2,660 / 0%
GC Percentage	44.49%

2.3. Coverage

Mean	0.0613

Standard Deviation	0.5006

2.4. Mapping Quality

Mean Mapping Quality	44.81

2.5. Mismatches and indels

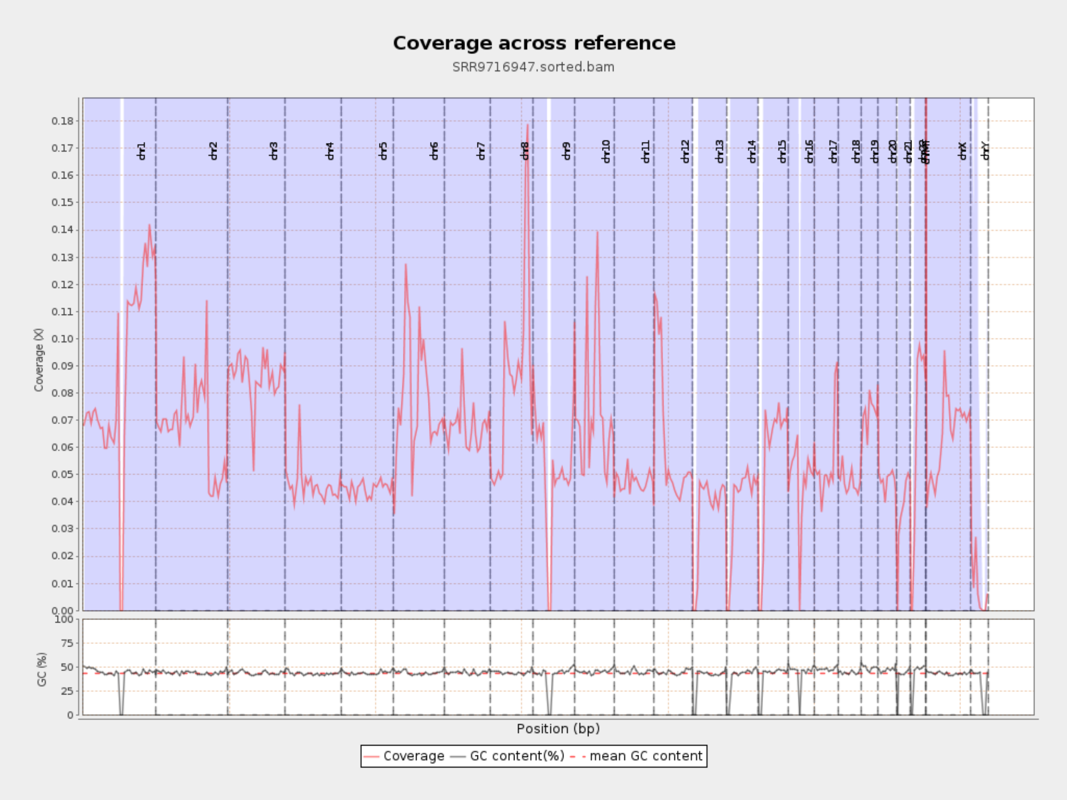
General error rate	0.5%
Mismatches	929,270
Insertions	10,829
Mapped reads with at least one insertion	0.33%
Deletions	35,693
Mapped reads with at least one deletion	1.09%
Homopolymer indels	44.45%

2.6. Chromosome stats

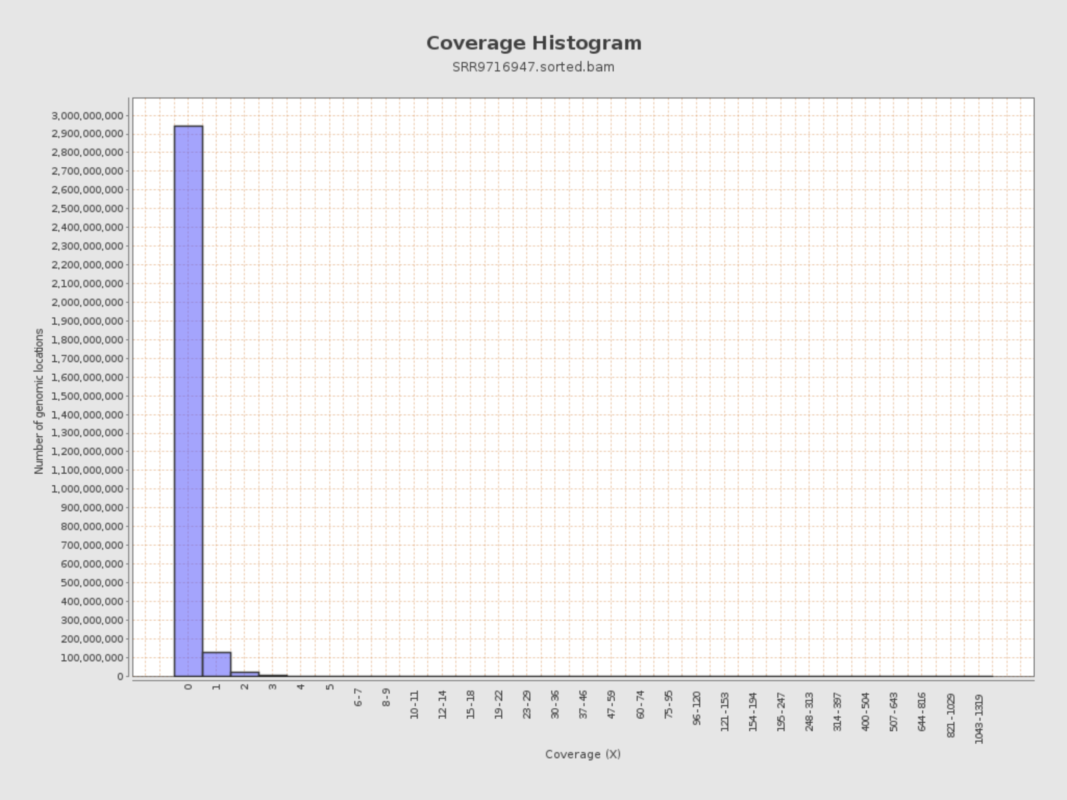
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21744855	0.0872	1.0457
chr2	243199373	16293280	0.067	0.5949
chr3	198022430	17002495	0.0859	0.3524
chr4	191154276	8870406	0.0464	0.3119
chr5	180915260	8146048	0.045	0.2607
chr6	171115067	13384008	0.0782	0.4818
chr7	159138663	10860329	0.0682	0.6313

chr8	146364022	12411273	0.0848	0.4354
chr9	141213431	7175213	0.0508	0.3859
chr10	135534747	9877160	0.0729	0.4668
chr11	135006516	6389421	0.0473	0.396
chr12	133851895	8409361	0.0628	0.3135
chr13	115169878	4170385	0.0362	0.2303
chr14	107349540	4203980	0.0392	0.2682
chr15	102531392	5711172	0.0557	0.2886
chr16	90354753	4220015	0.0467	0.2977
chr17	81195210	4398416	0.0542	0.3021
chr18	78077248	3694320	0.0473	0.7524
chr19	59128983	4285796	0.0725	0.6707
chr20	63025520	3016947	0.0479	0.2711
chr21	48129895	1788597	0.0372	0.2849
chr22	51304566	3278429	0.0639	0.3069
chrMT	16571	6437	0.3884	0.738
chrX	155270560	10010062	0.0645	0.3632
chrY	59373566	489614	0.0082	0.2059

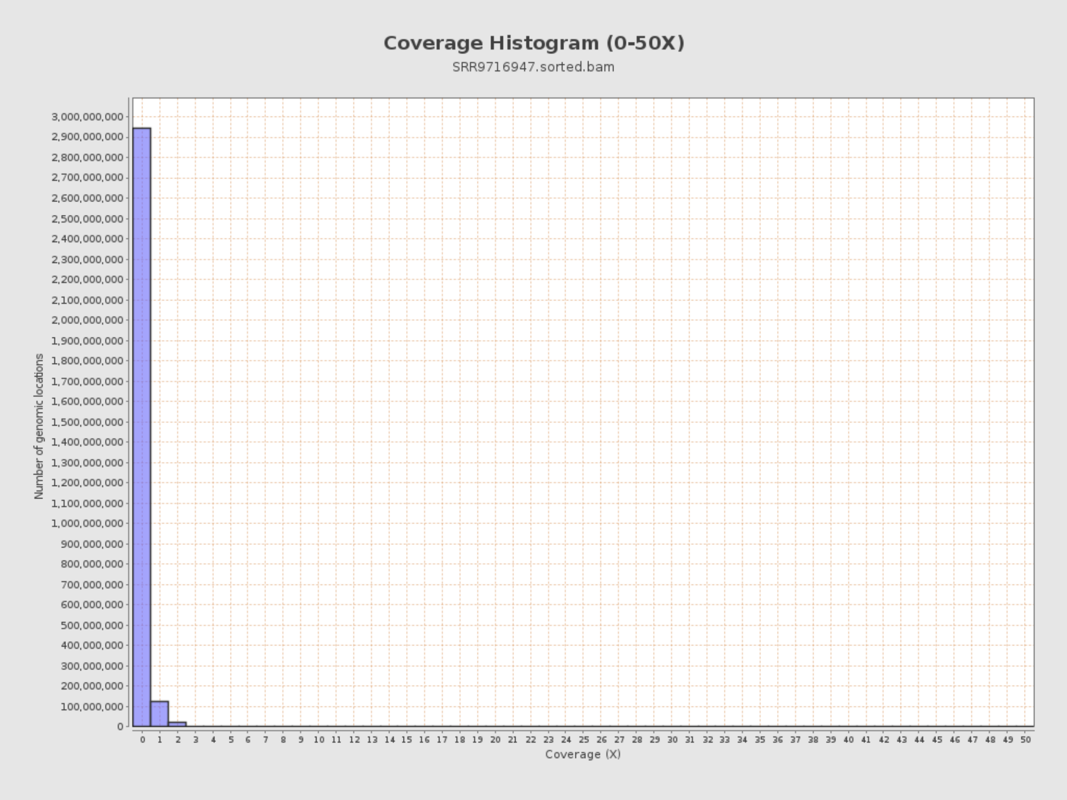
3. Results : Coverage across reference



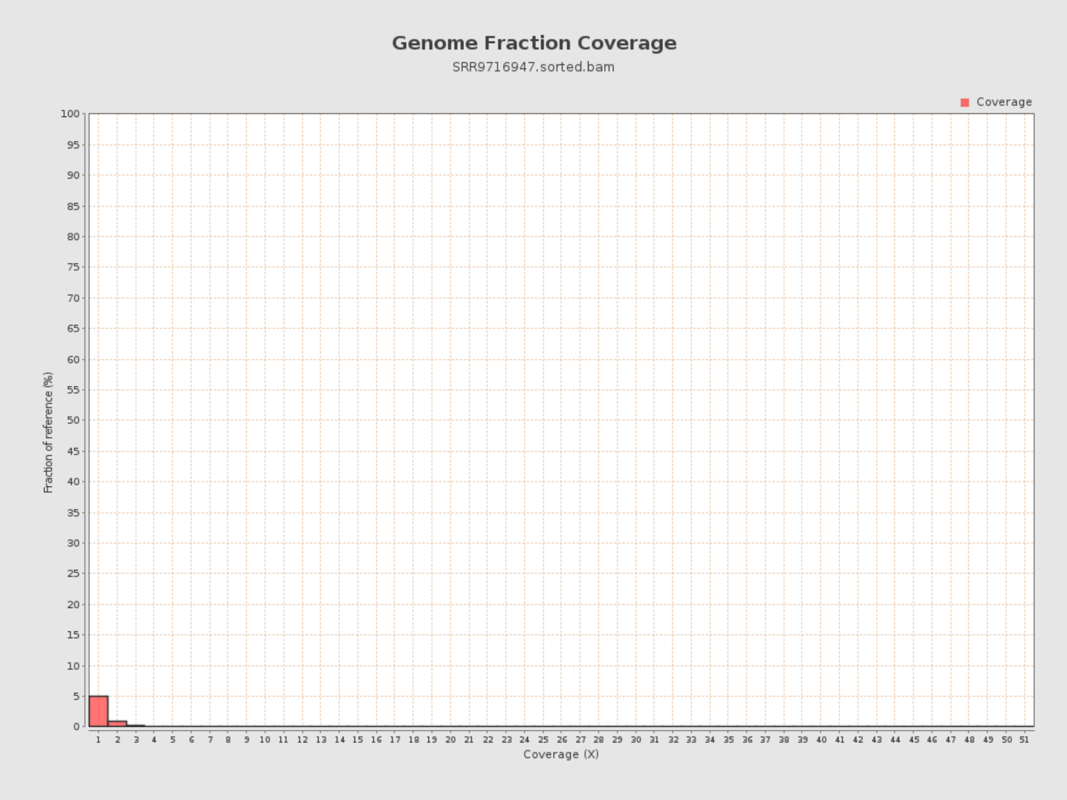
4. Results : Coverage Histogram



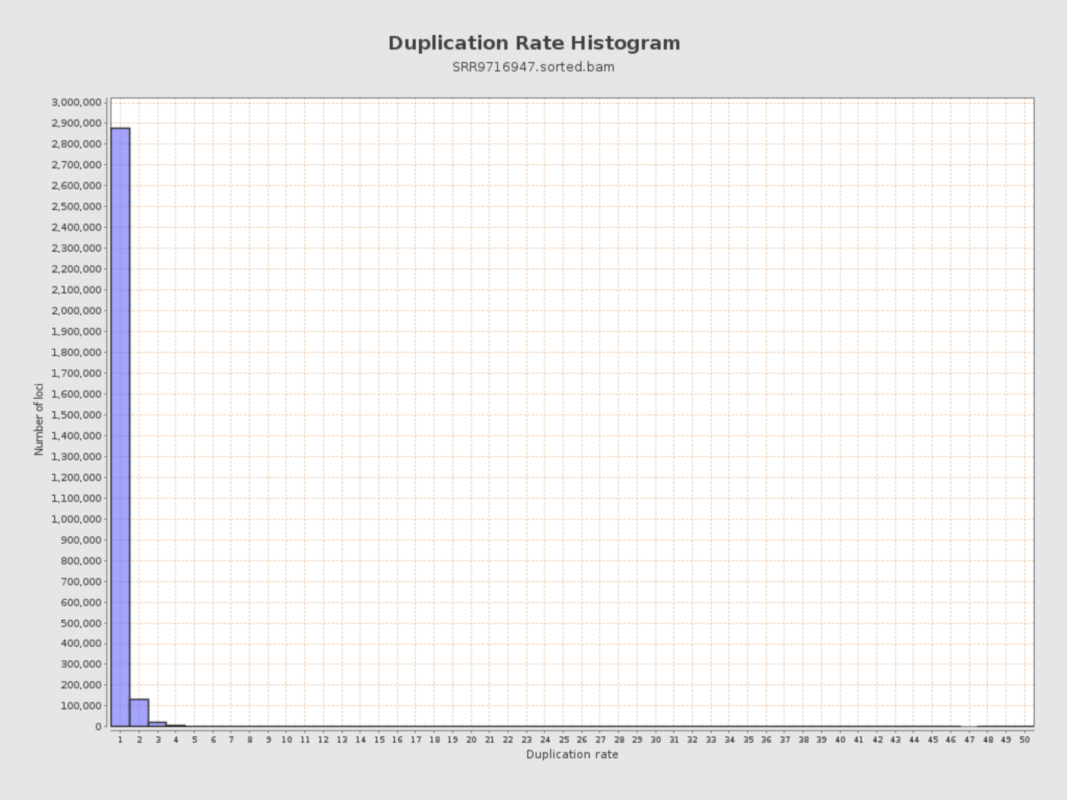
5. Results : Coverage Histogram (0-50X)



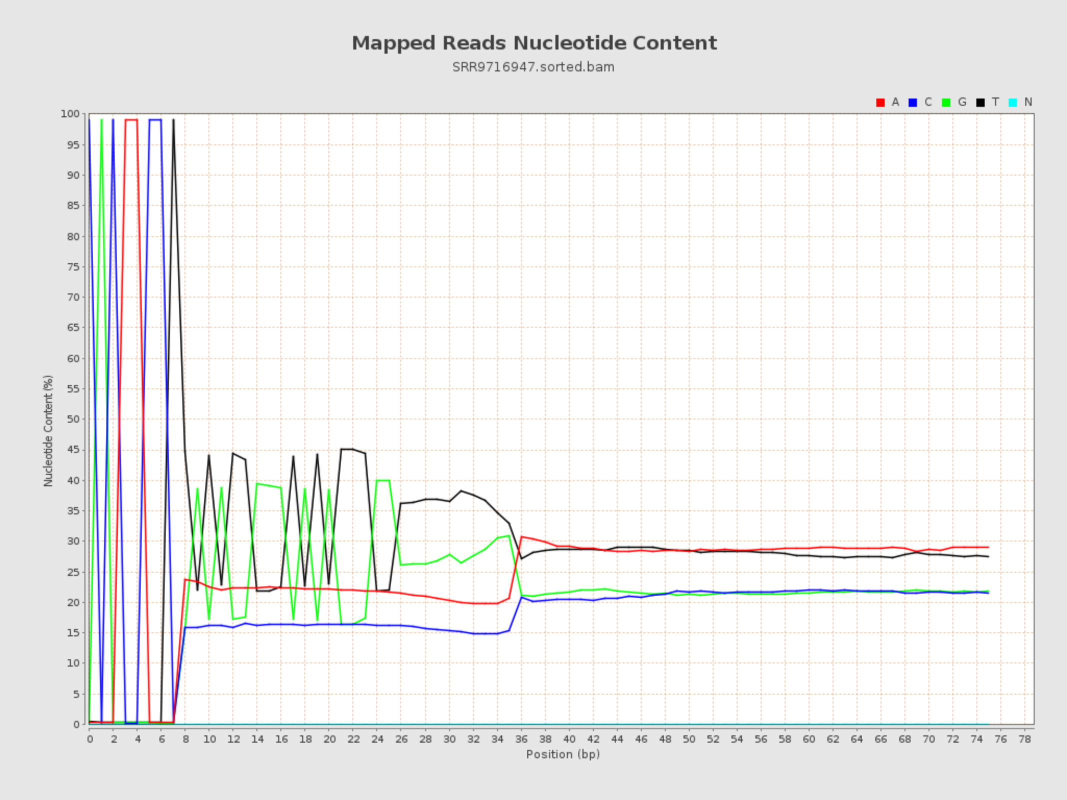
6. Results : Genome Fraction Coverage



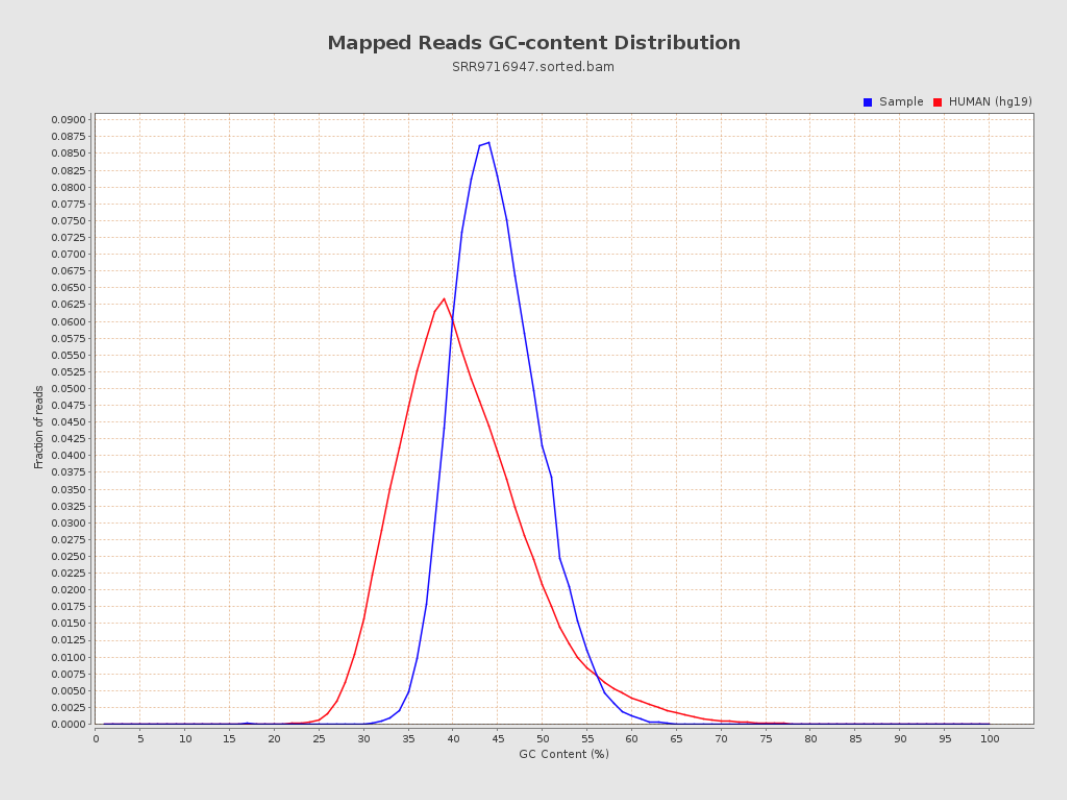
7. Results : Duplication Rate Histogram



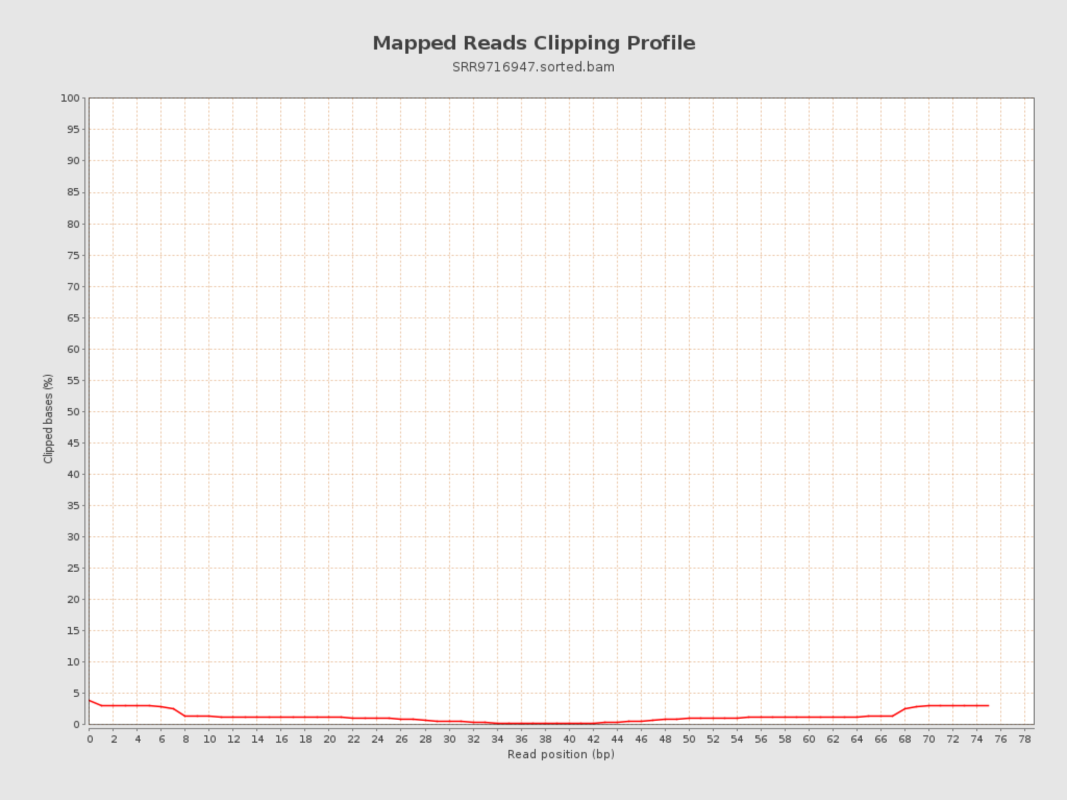
8. Results : Mapped Reads Nucleotide Content



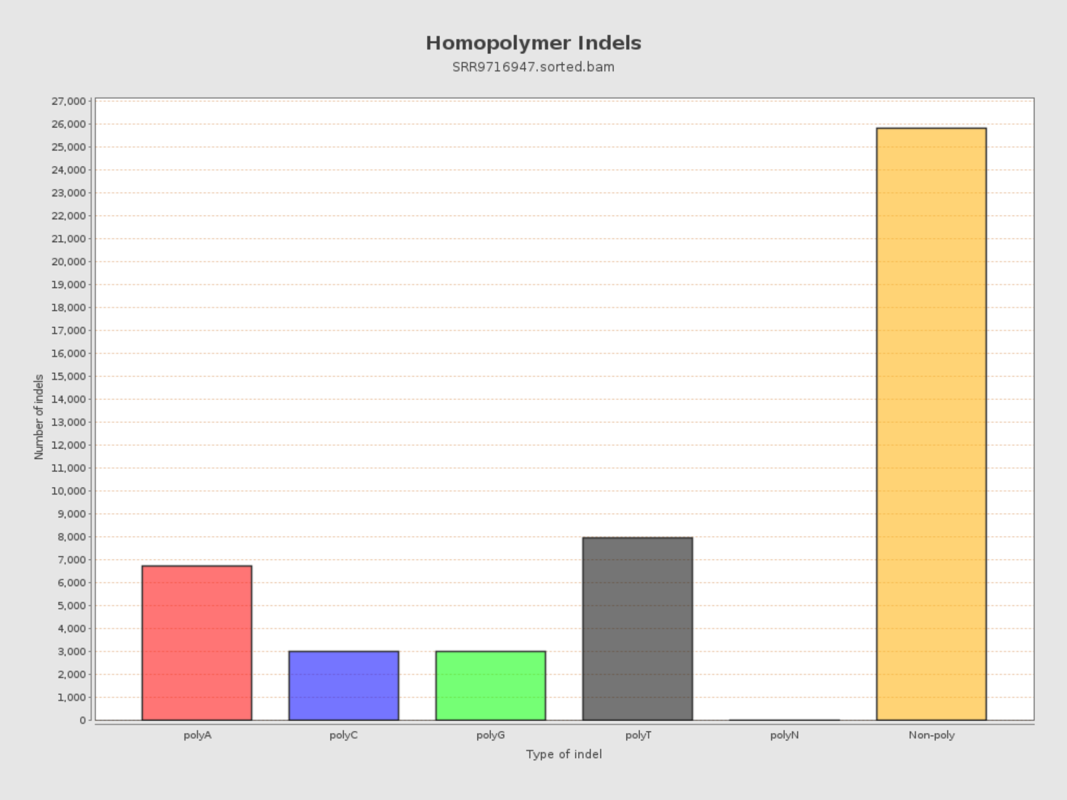
9. Results : Mapped Reads GC-content Distribution



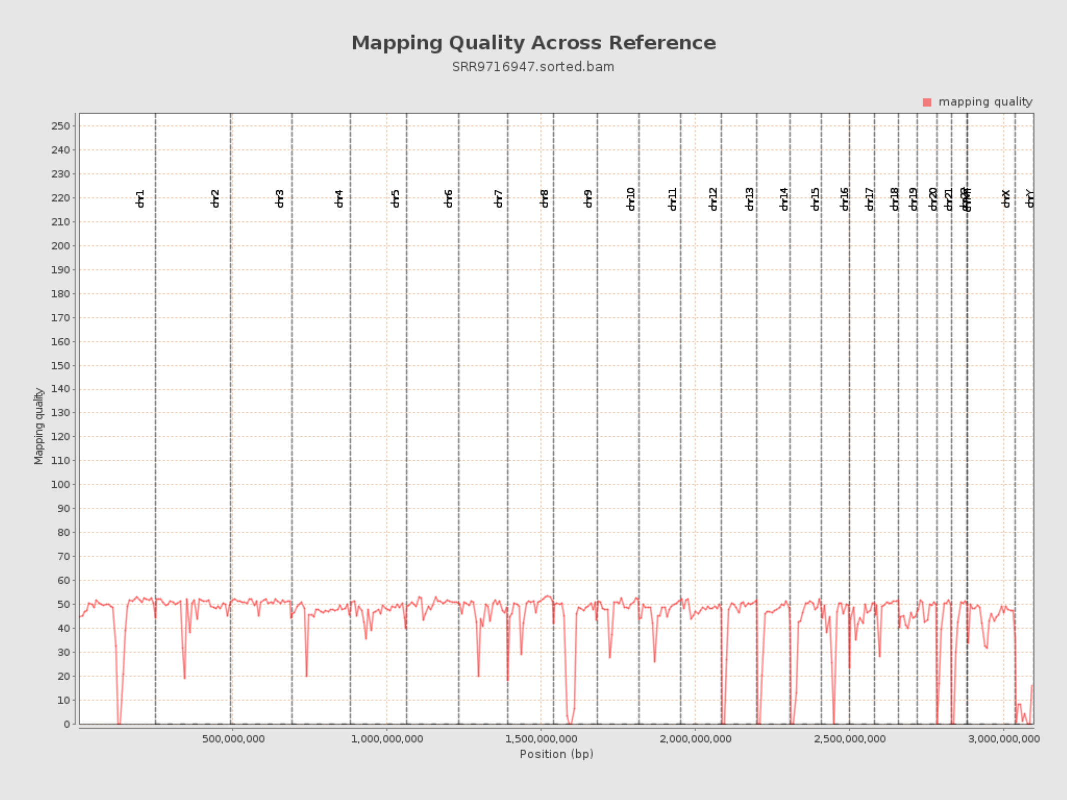
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram