Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 19:07:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716930.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_SRR9716930 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716930.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 19:07:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716930.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,639,988
Mapped reads	1,302,200 / 79.4%
Unmapped reads	337,788 / 20.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,972 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	34,218 / 2.09%
Duplication rate	1.78%
Clipped reads	1,306,127 / 79.64%

2.2. ACGT Content

Number/percentage of A's	18,674,424 / 25.44%
Number/percentage of C's	13,952,092 / 19.01%
Number/percentage of T's	23,379,831 / 31.85%
Number/percentage of G's	17,390,347 / 23.69%
Number/percentage of N's	1,062 / 0%
GC Percentage	42.7%

2.3. Coverage

Mean	0.0237

Standard Deviation	0.2416

2.4. Mapping Quality

Mean Mapping Quality	43.1

2.5. Mismatches and indels

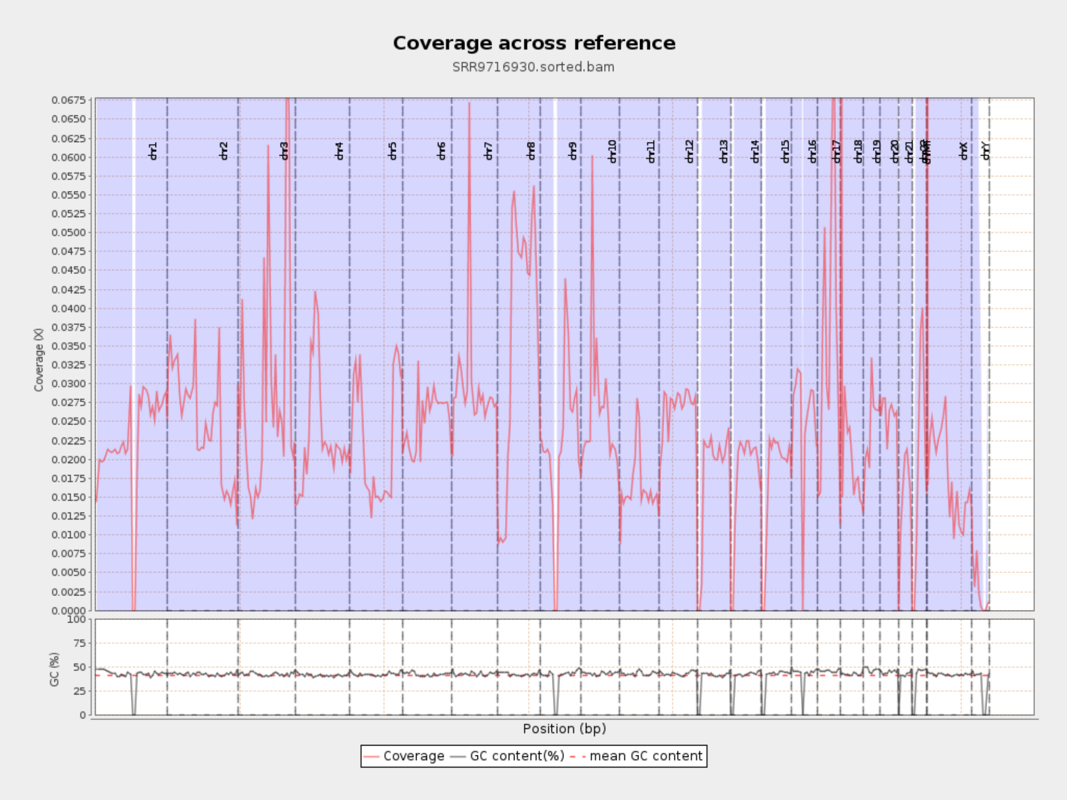
General error rate	0.53%
Mismatches	373,945
Insertions	5,924
Mapped reads with at least one insertion	0.45%
Deletions	14,022
Mapped reads with at least one deletion	1.07%
Homopolymer indels	38.74%

2.6. Chromosome stats

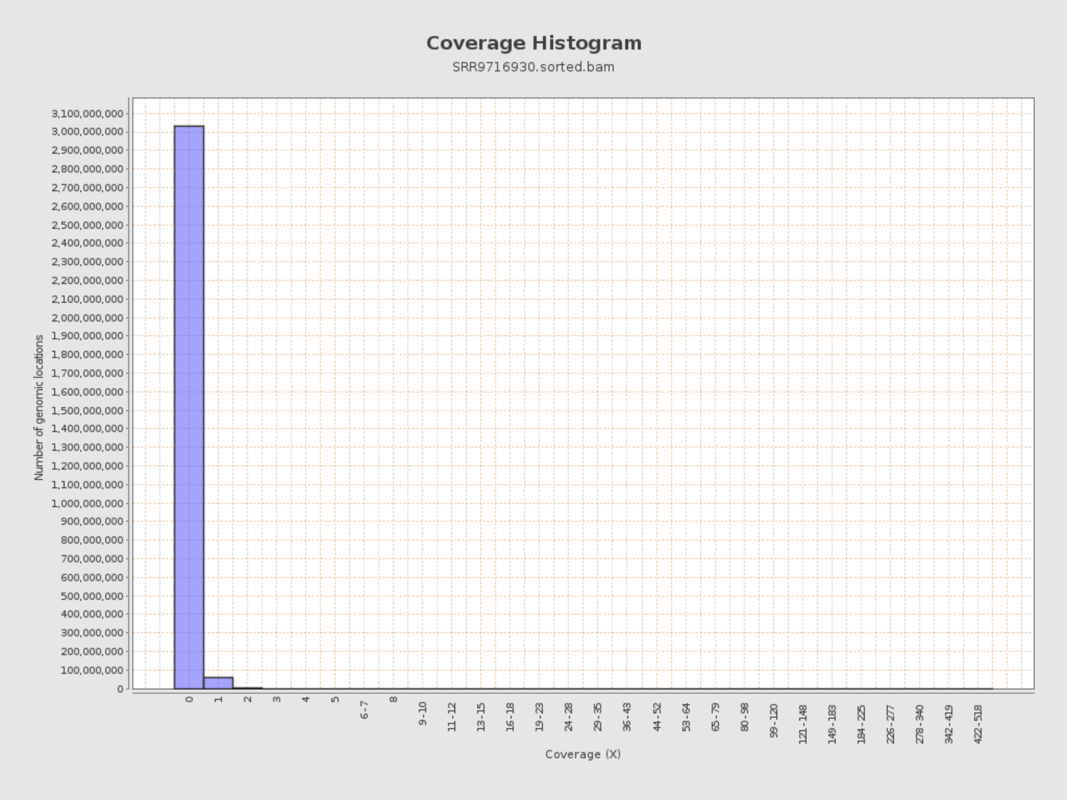
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5573112	0.0224	0.2675
chr2	243199373	6097950	0.0251	0.2864
chr3	198022430	5745347	0.029	0.1933
chr4	191154276	4403113	0.023	0.1672
chr5	180915260	4022589	0.0222	0.1592
chr6	171115067	4339126	0.0254	0.1867
chr7	159138663	4778753	0.03	0.5739

chr8	146364022	5407970	0.0369	0.2459
chr9	141213431	3107964	0.022	0.1813
chr10	135534747	3572943	0.0264	0.3075
chr11	135006516	2255839	0.0167	0.1703
chr12	133851895	3575577	0.0267	0.1856
chr13	115169878	2059816	0.0179	0.1428
chr14	107349540	1897317	0.0177	0.146
chr15	102531392	1787073	0.0174	0.1449
chr16	90354753	2247693	0.0249	0.1787
chr17	81195210	3002276	0.037	0.2131
chr18	78077248	1802329	0.0231	0.2688
chr19	59128983	1441271	0.0244	0.2809
chr20	63025520	1618180	0.0257	0.1776
chr21	48129895	712227	0.0148	0.1326
chr22	51304566	1006332	0.0196	0.1519
chrMT	16571	28304	1.708	1.7065
chrX	155270560	2781542	0.0179	0.1647
chrY	59373566	155418	0.0026	0.0704

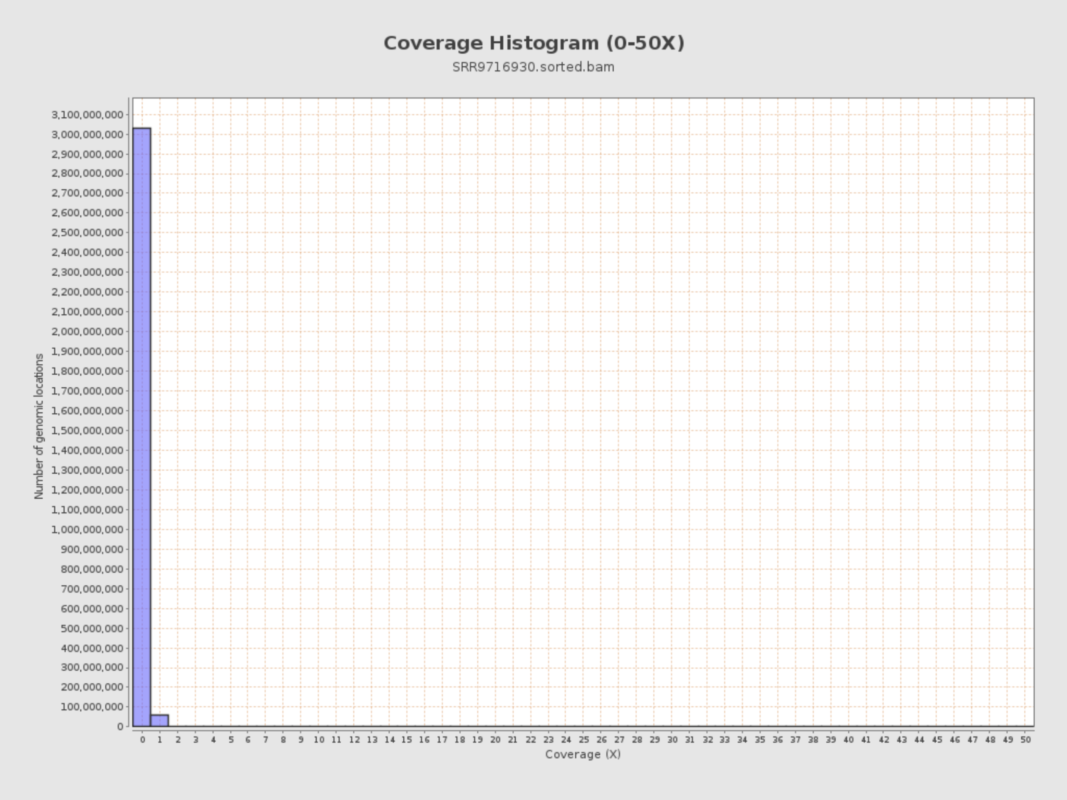
3. Results : Coverage across reference



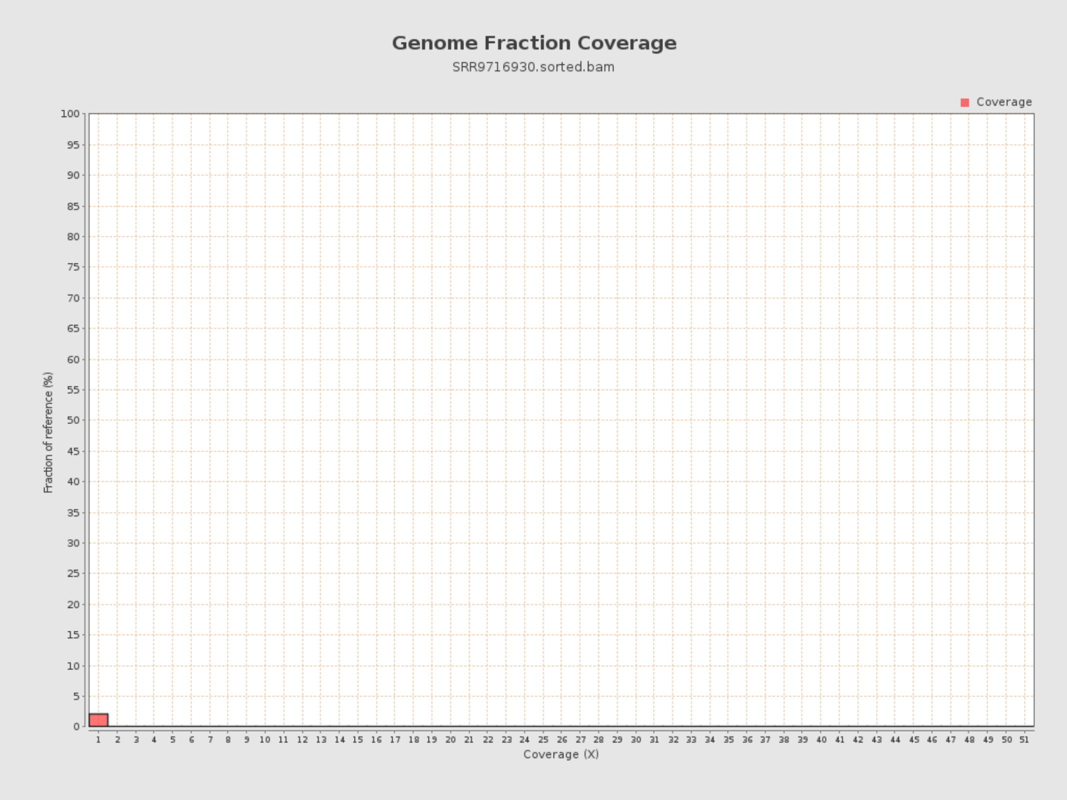
4. Results : Coverage Histogram



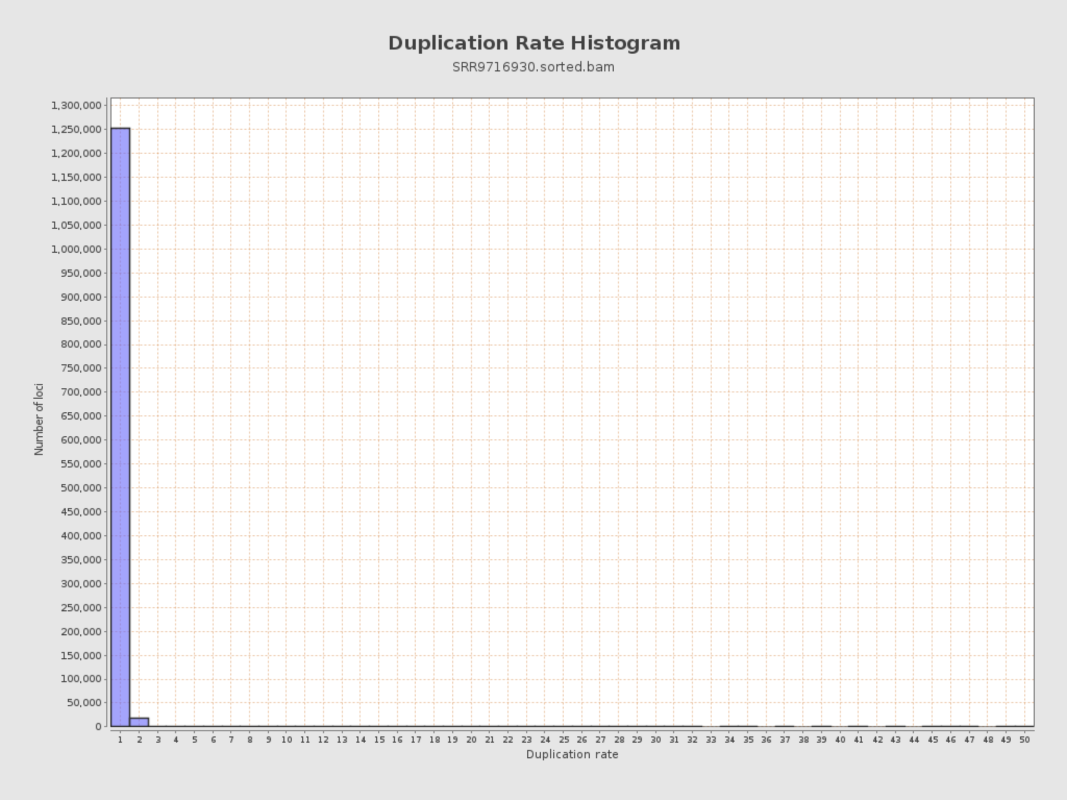
5. Results : Coverage Histogram (0-50X)



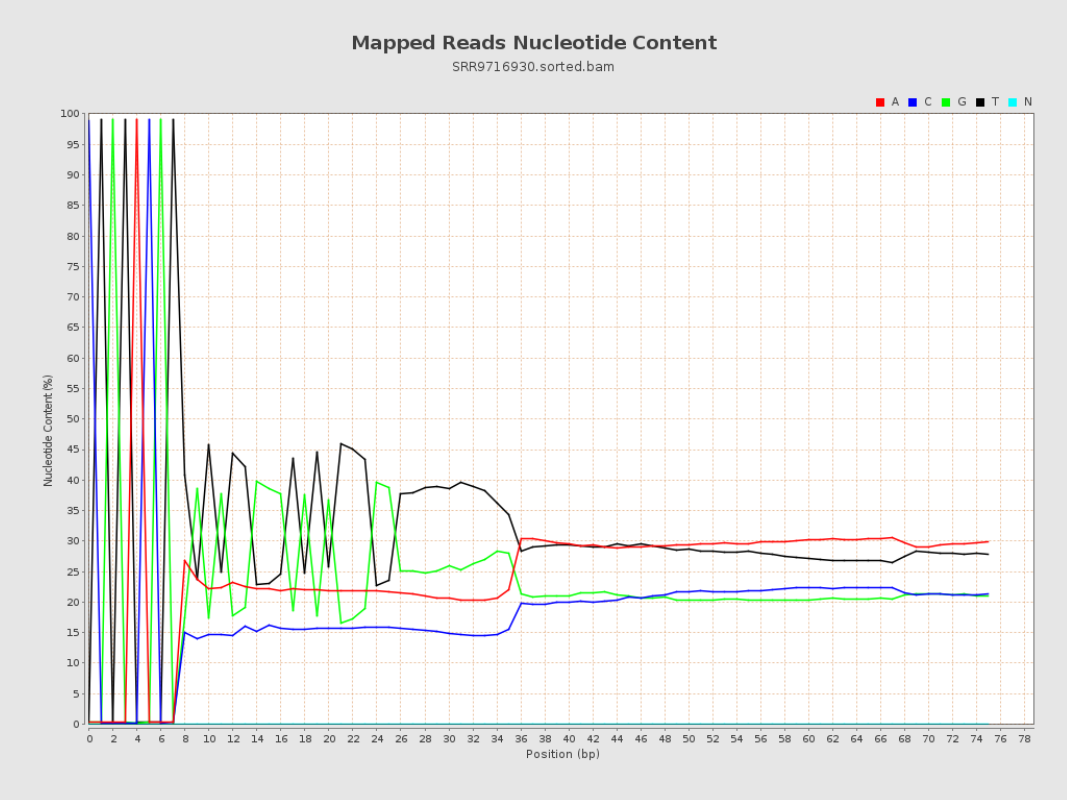
6. Results : Genome Fraction Coverage



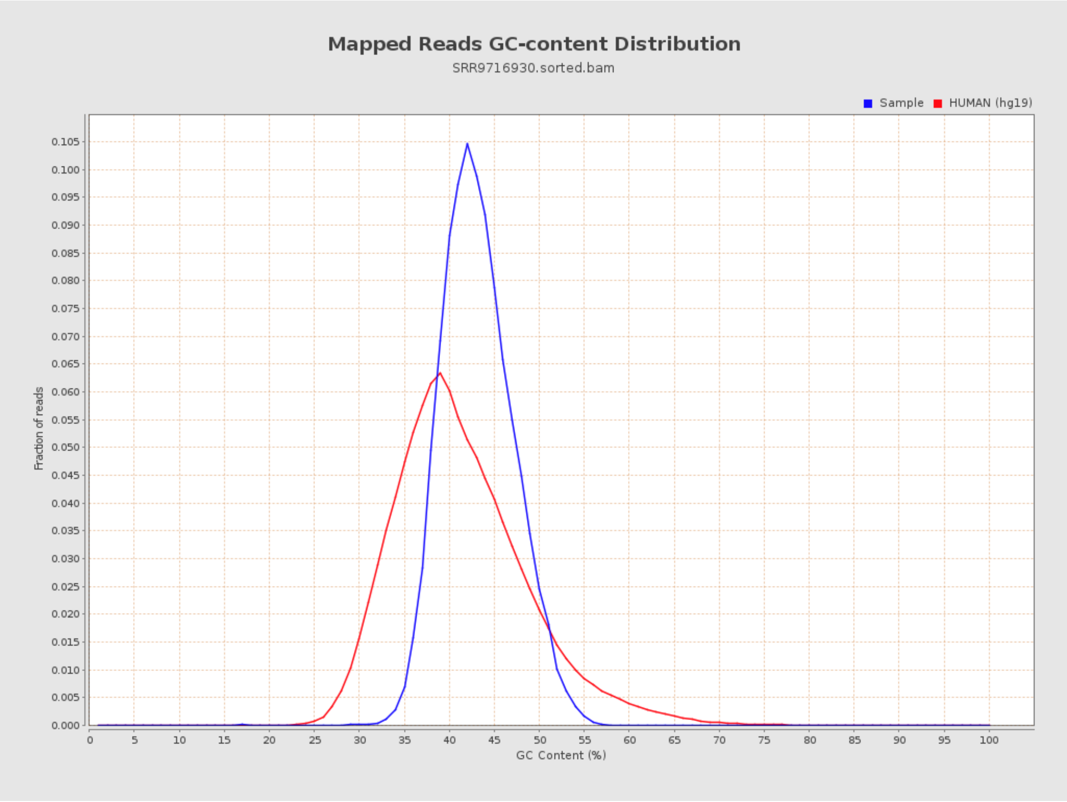
7. Results : Duplication Rate Histogram



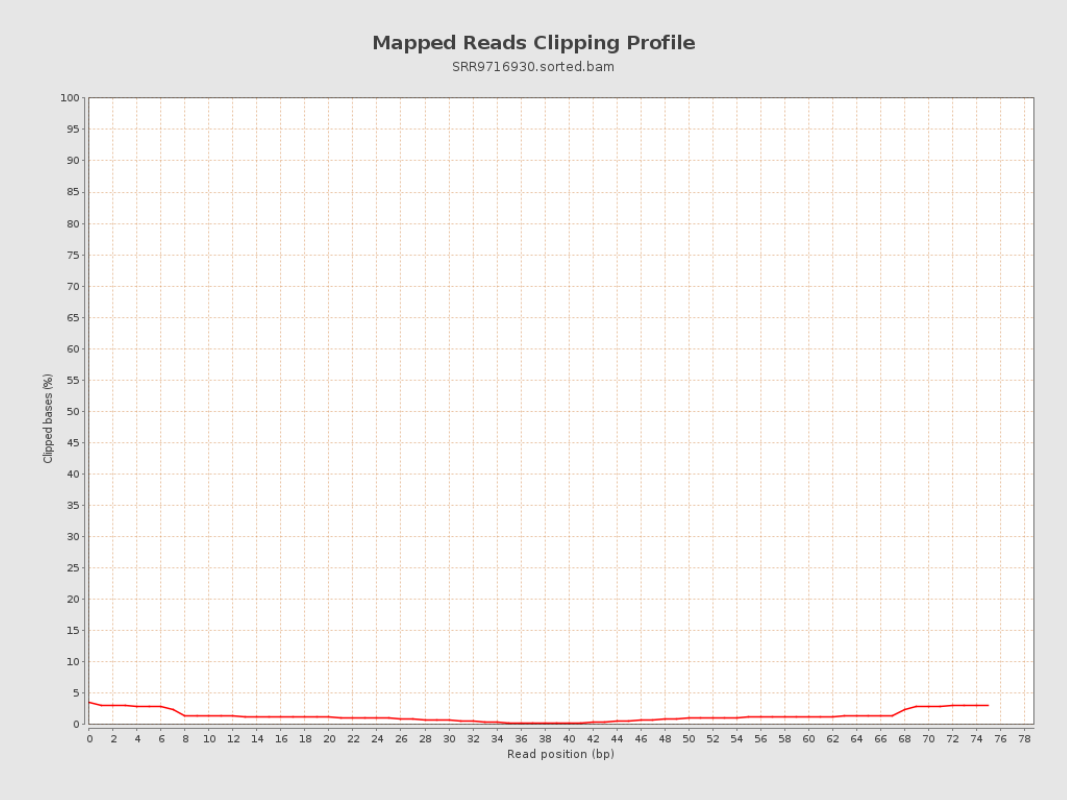
8. Results : Mapped Reads Nucleotide Content



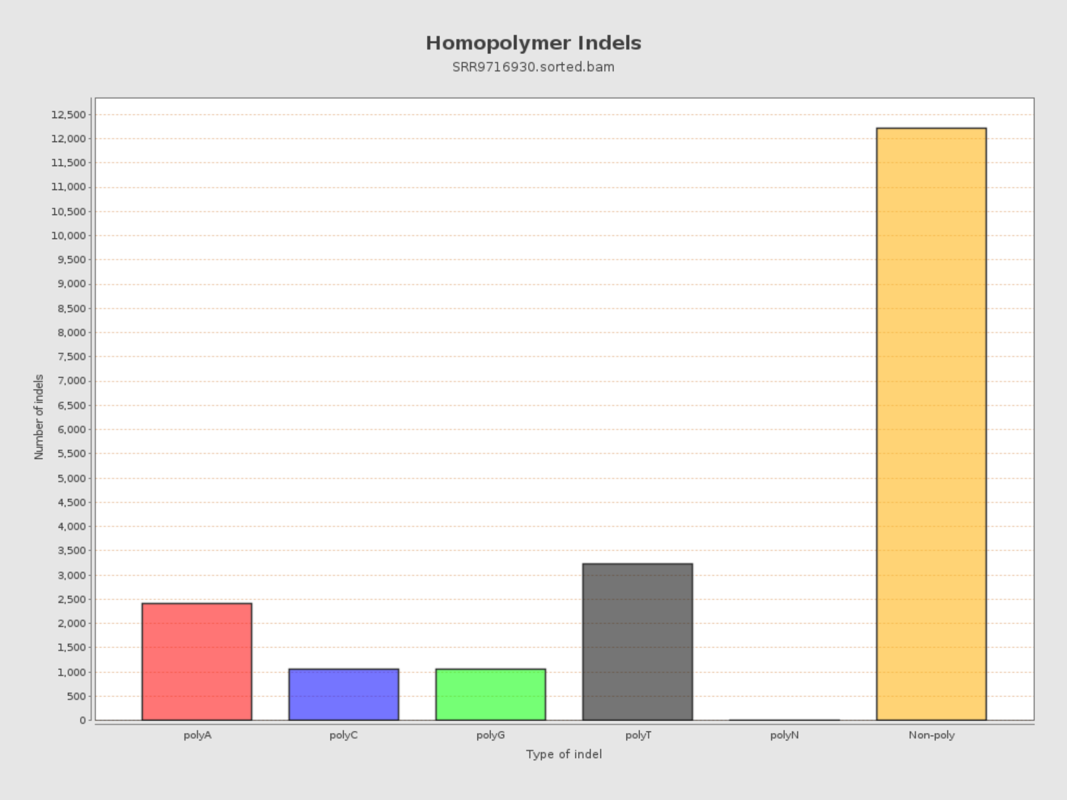
9. Results : Mapped Reads GC-content Distribution



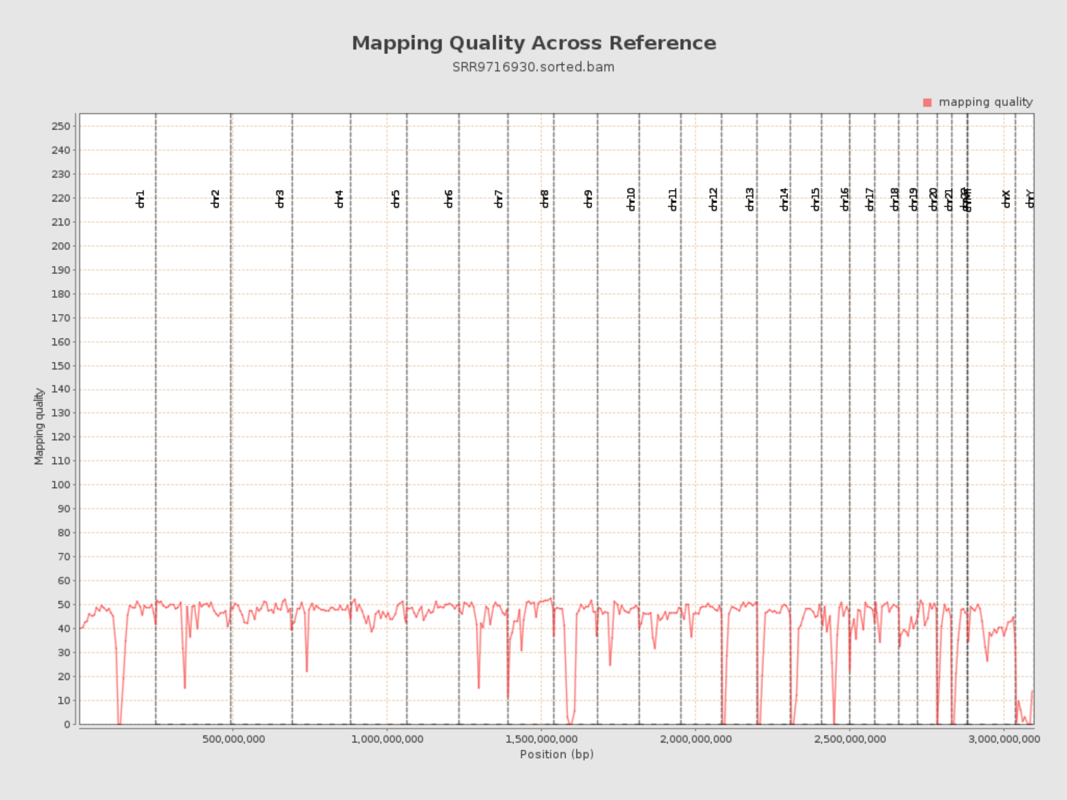
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram