Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 01:03:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716622.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_SRR9716622 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716622.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 01:03:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716622.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,004,250
Mapped reads	1,835,597 / 91.59%
Unmapped reads	168,653 / 8.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,042 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	64,497 / 3.22%
Duplication rate	2.73%
Clipped reads	1,838,153 / 91.71%

2.2. ACGT Content

Number/percentage of A's	26,534,323 / 25.18%
Number/percentage of C's	21,286,451 / 20.2%
Number/percentage of T's	32,199,366 / 30.55%
Number/percentage of G's	25,360,877 / 24.07%
Number/percentage of N's	2,276 / 0%
GC Percentage	44.26%

2.3. Coverage

Mean	0.0341

Standard Deviation	0.2654

2.4. Mapping Quality

Mean Mapping Quality	44.71

2.5. Mismatches and indels

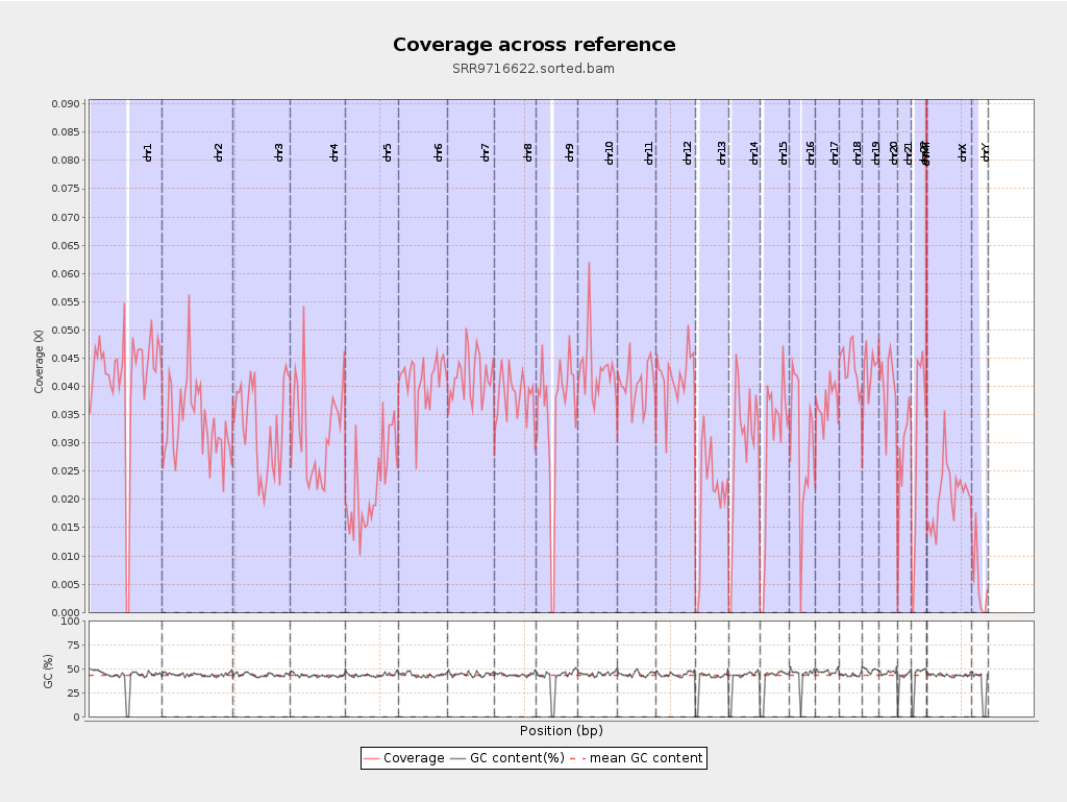
General error rate	0.49%
Mismatches	505,162
Insertions	7,616
Mapped reads with at least one insertion	0.41%
Deletions	15,333
Mapped reads with at least one deletion	0.83%
Homopolymer indels	39.75%

2.6. Chromosome stats

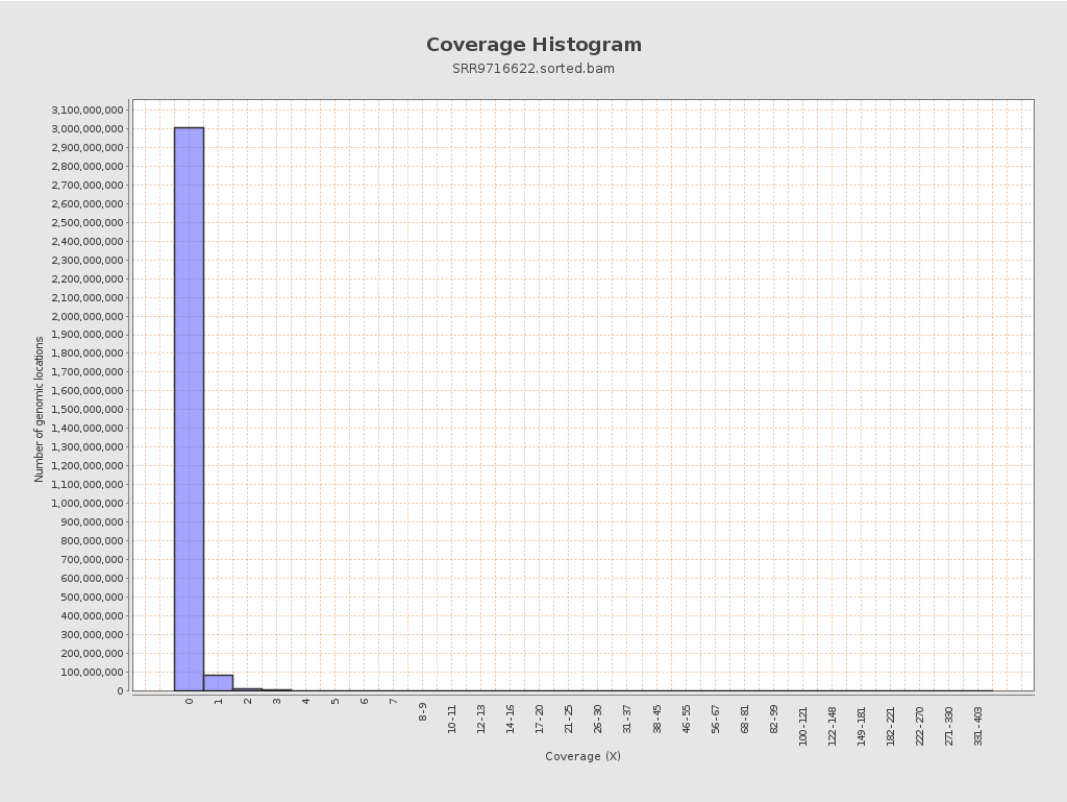
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10351295	0.0415	0.3955
chr2	243199373	8190372	0.0337	0.3069
chr3	198022430	6487212	0.0328	0.2024
chr4	191154276	6071632	0.0318	0.221
chr5	180915260	4068889	0.0225	0.1702
chr6	171115067	7038980	0.0411	0.2397
chr7	159138663	6639461	0.0417	0.3027

chr8	146364022	5606537	0.0383	0.25
chr9	141213431	4987041	0.0353	0.2857
chr10	135534747	5811132	0.0429	0.2904
chr11	135006516	5425243	0.0402	0.2892
chr12	133851895	5608477	0.0419	0.2308
chr13	115169878	2372637	0.0206	0.1586
chr14	107349540	3158502	0.0294	0.2053
chr15	102531392	3022402	0.0295	0.1914
chr16	90354753	2691892	0.0298	0.2095
chr17	81195210	3010551	0.0371	0.2266
chr18	78077248	3414110	0.0437	0.4972
chr19	59128983	2528152	0.0428	0.3021
chr20	63025520	2508774	0.0398	0.2308
chr21	48129895	1353439	0.0281	0.2129
chr22	51304566	1528733	0.0298	0.193
chrMT	16571	7039	0.4248	0.803
chrX	155270560	3241265	0.0209	0.1972
chrY	59373566	285687	0.0048	0.1197

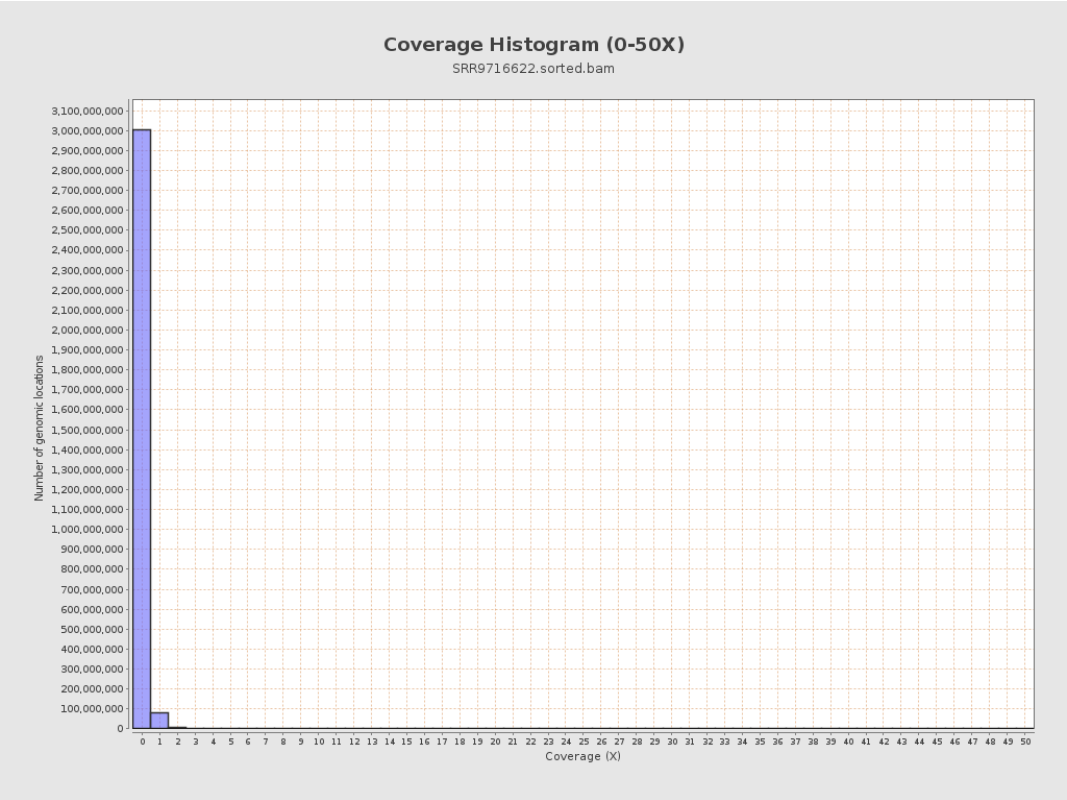
3. Results : Coverage across reference



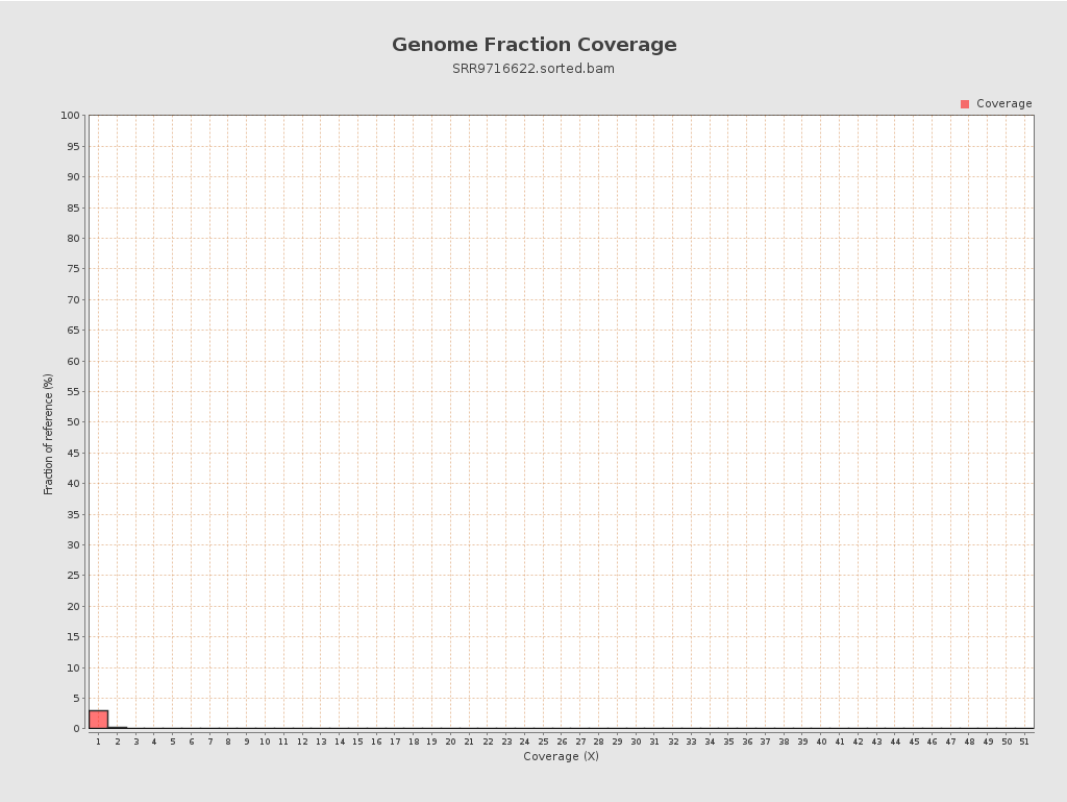
4. Results : Coverage Histogram



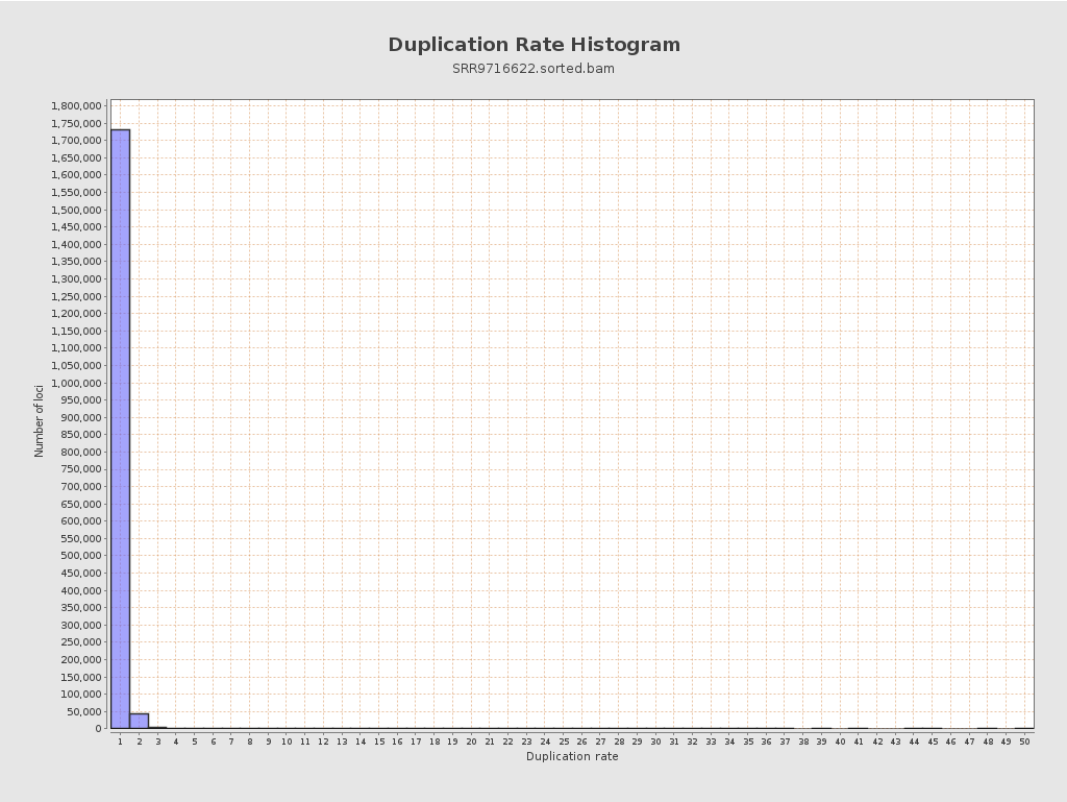
5. Results : Coverage Histogram (0-50X)



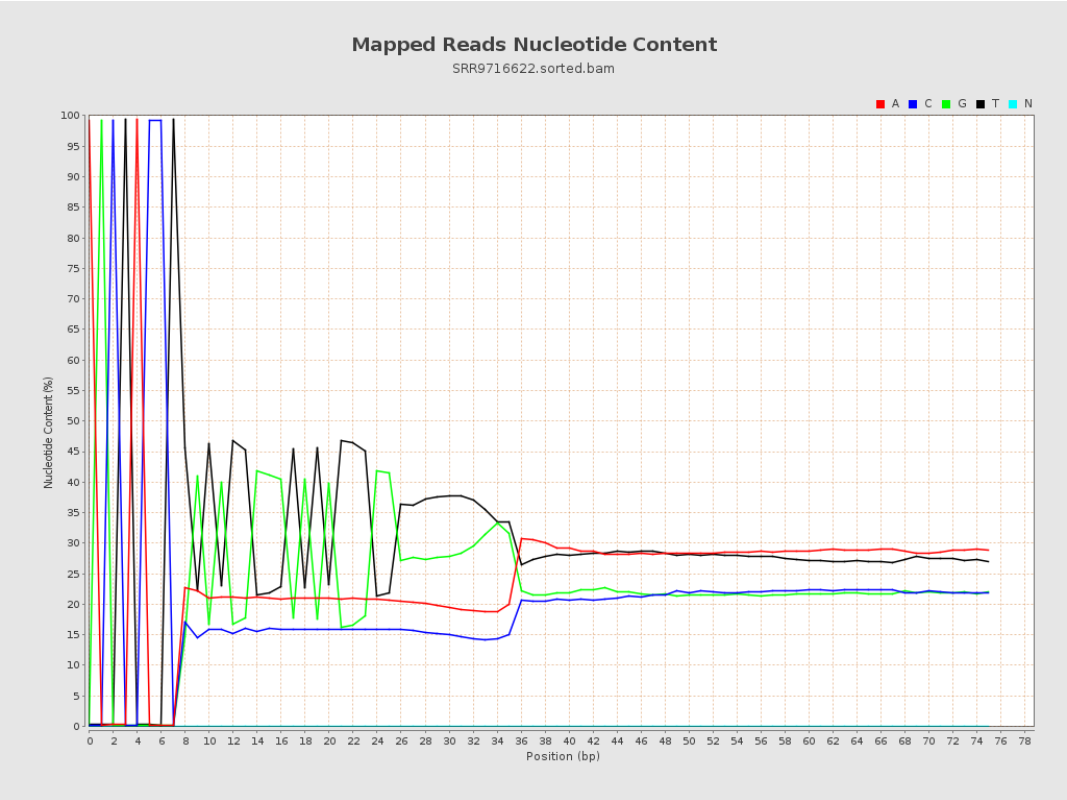
6. Results : Genome Fraction Coverage



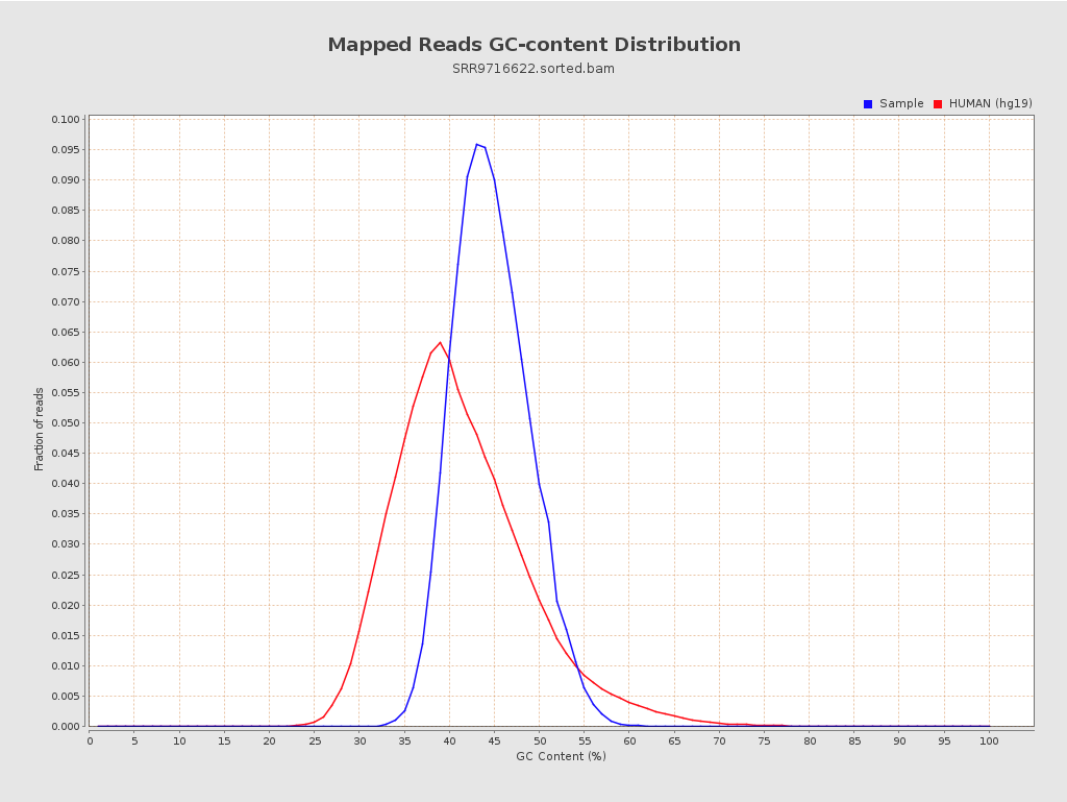
7. Results : Duplication Rate Histogram



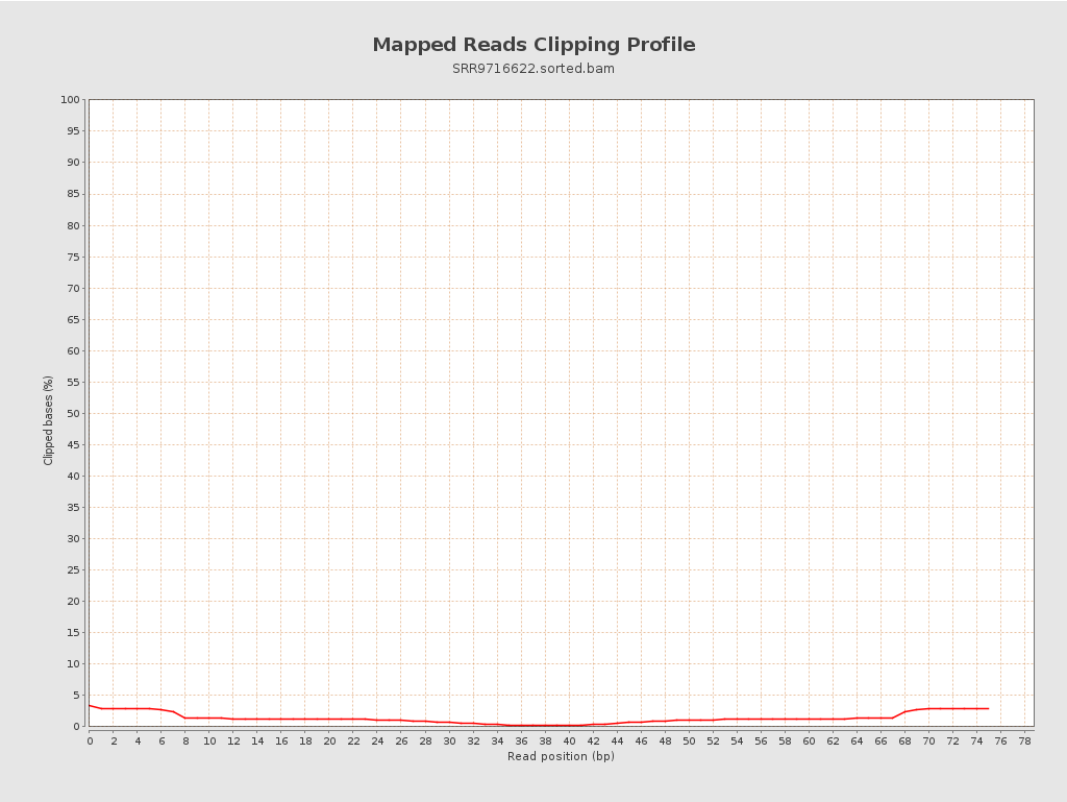
8. Results : Mapped Reads Nucleotide Content



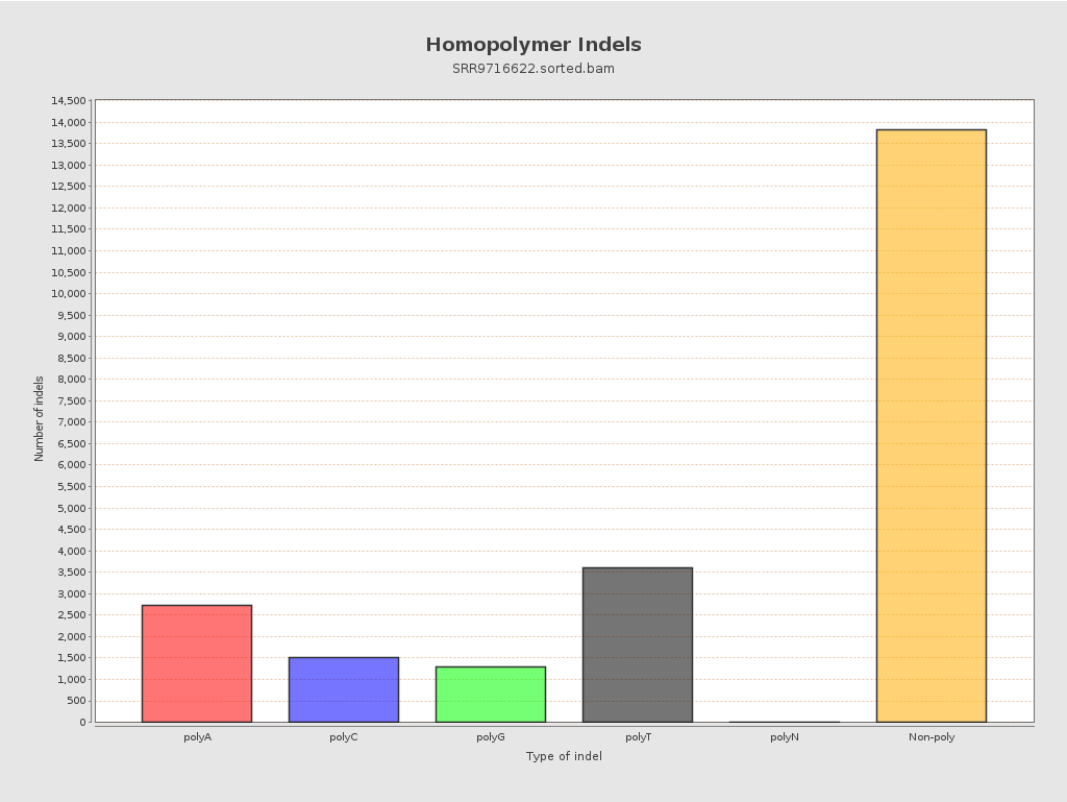
9. Results : Mapped Reads GC-content Distribution



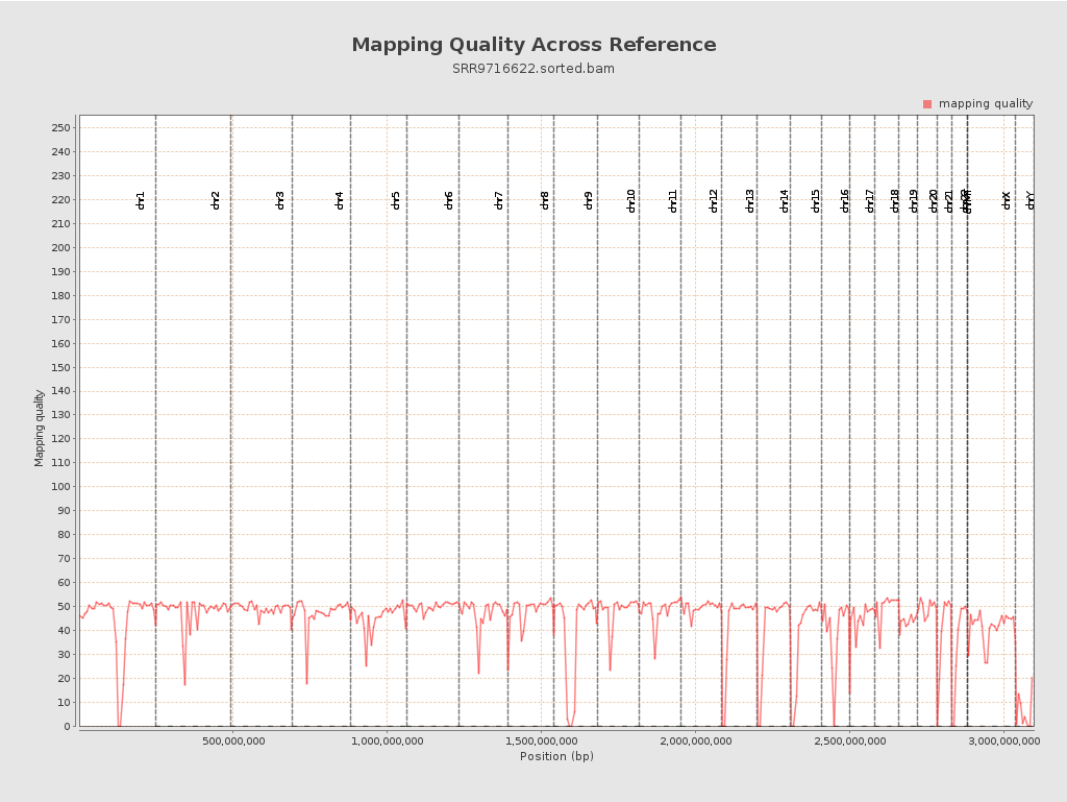
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram