Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 05:37:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716679.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_SRR9716679 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716679.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 05:37:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716679.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,927,964
Mapped reads	1,750,952 / 90.82%
Unmapped reads	177,012 / 9.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,663 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	77,824 / 4.04%
Duplication rate	3.41%
Clipped reads	1,757,224 / 91.14%

2.2. ACGT Content

Number/percentage of A's	24,561,995 / 24.05%
Number/percentage of C's	19,571,722 / 19.16%
Number/percentage of T's	32,221,198 / 31.55%
Number/percentage of G's	25,786,604 / 25.25%
Number/percentage of N's	702 / 0%
GC Percentage	44.41%

2.3. Coverage

Mean	0.033

Standard Deviation	0.2956

2.4. Mapping Quality

Mean Mapping Quality	44.53

2.5. Mismatches and indels

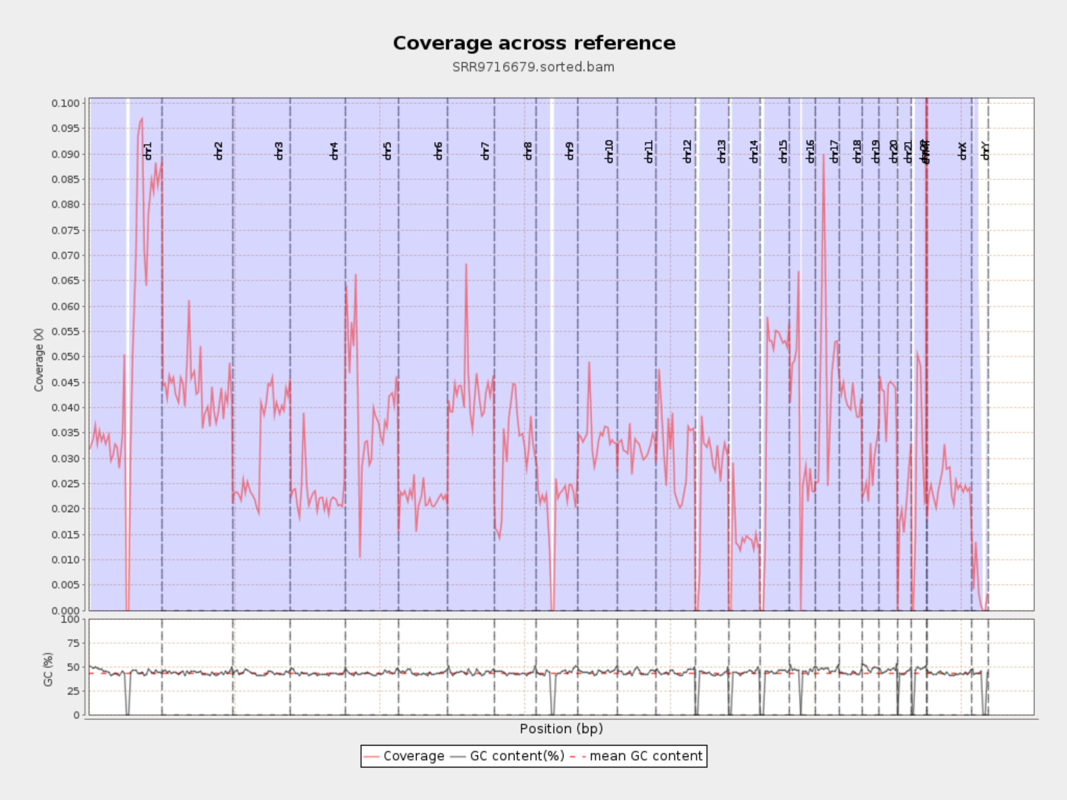
General error rate	0.52%
Mismatches	517,574
Insertions	6,585
Mapped reads with at least one insertion	0.37%
Deletions	18,485
Mapped reads with at least one deletion	1.05%
Homopolymer indels	43.39%

2.6. Chromosome stats

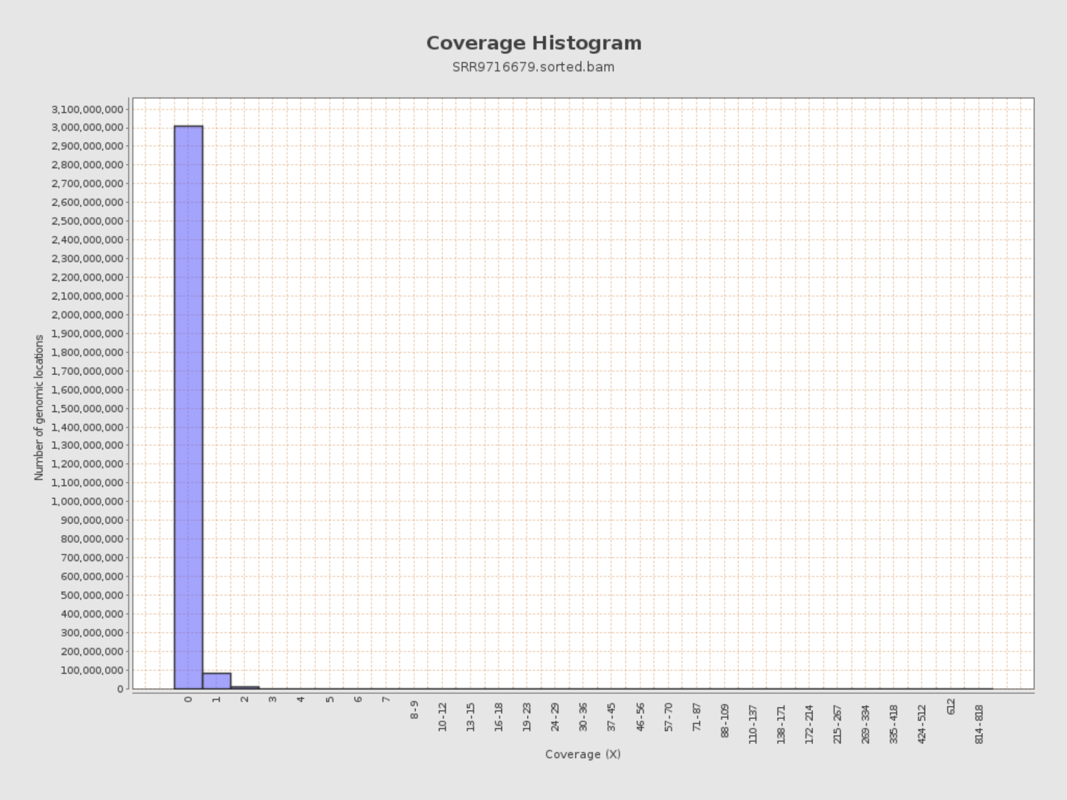
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12709359	0.051	0.4747
chr2	243199373	10562940	0.0434	0.4318
chr3	198022430	6426291	0.0325	0.2007
chr4	191154276	4319135	0.0226	0.1939
chr5	180915260	7261853	0.0401	0.2236
chr6	171115067	3753664	0.0219	0.1886
chr7	159138663	6892468	0.0433	0.4785

chr8	146364022	4611943	0.0315	0.2574
chr9	141213431	2831064	0.02	0.2191
chr10	135534747	4655734	0.0344	0.2576
chr11	135006516	4333022	0.0321	0.2793
chr12	133851895	4144901	0.031	0.1983
chr13	115169878	3039396	0.0264	0.1809
chr14	107349540	1387048	0.0129	0.1391
chr15	102531392	4425848	0.0432	0.2335
chr16	90354753	3037471	0.0336	0.2145
chr17	81195210	3879155	0.0478	0.2664
chr18	78077248	3241393	0.0415	0.4806
chr19	59128983	1636546	0.0277	0.3618
chr20	63025520	2682636	0.0426	0.2319
chr21	48129895	965493	0.0201	0.1744
chr22	51304566	1327888	0.0259	0.18
chrMT	16571	8881	0.5359	0.8557
chrX	155270560	3791902	0.0244	0.2017
chrY	59373566	245812	0.0041	0.1087

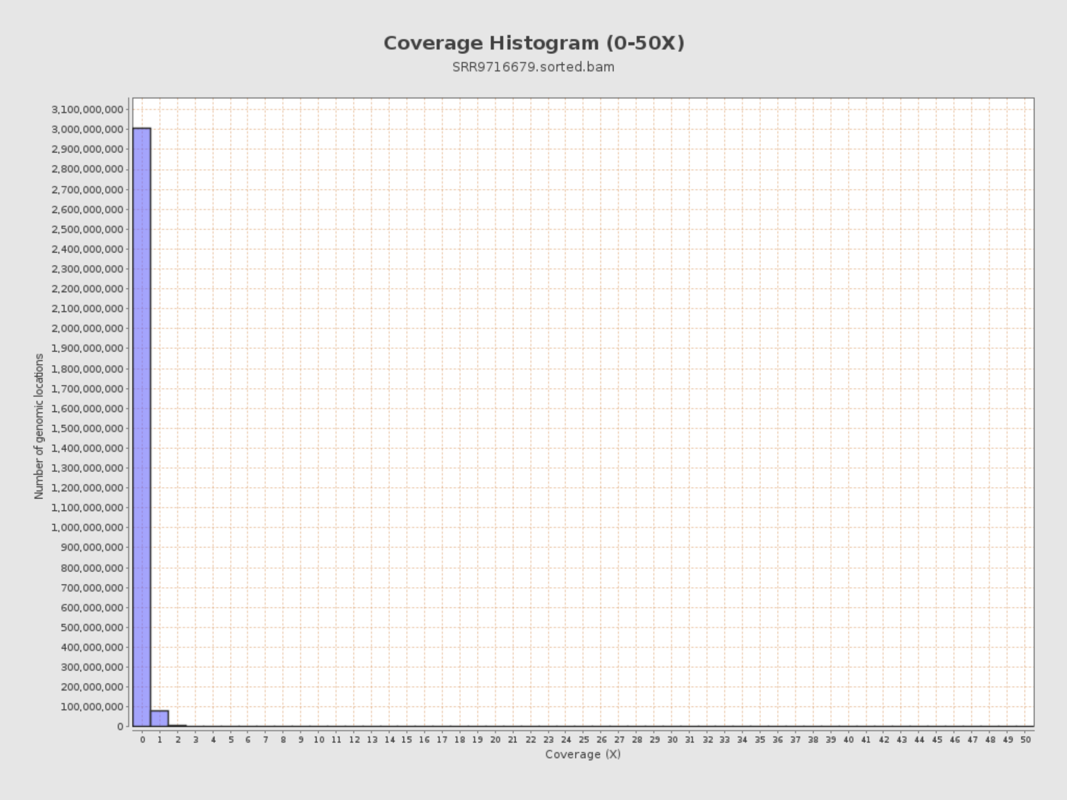
3. Results : Coverage across reference



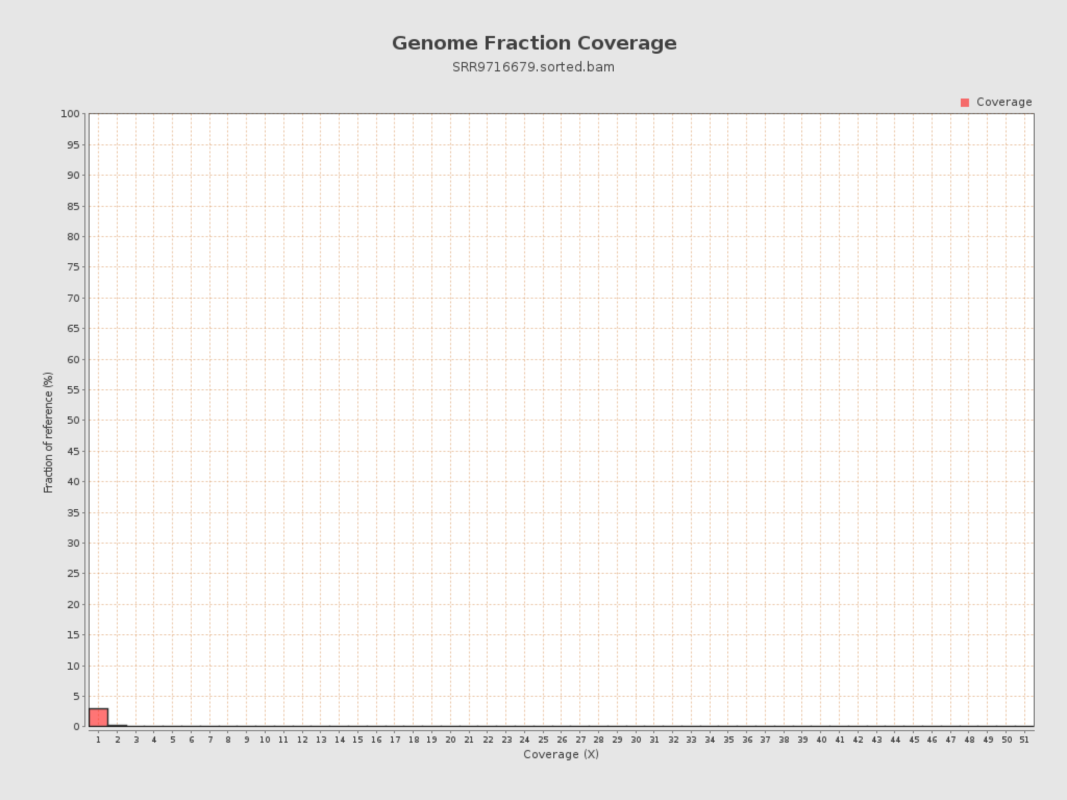
4. Results : Coverage Histogram



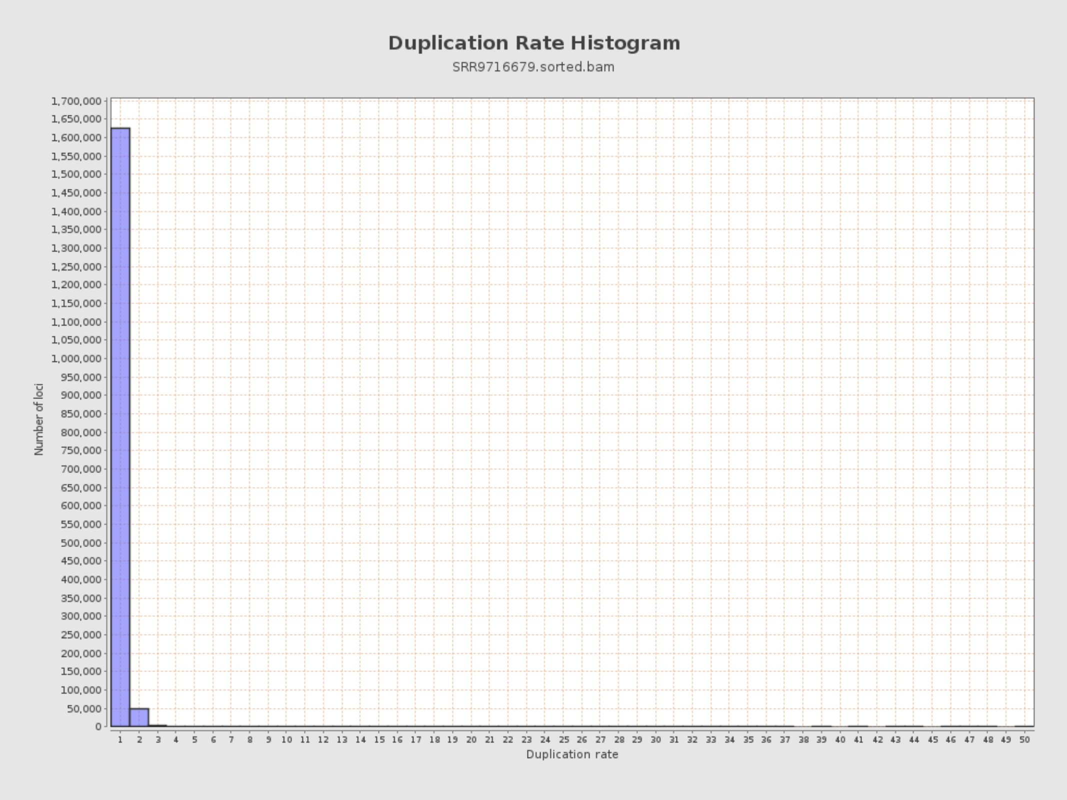
5. Results : Coverage Histogram (0-50X)



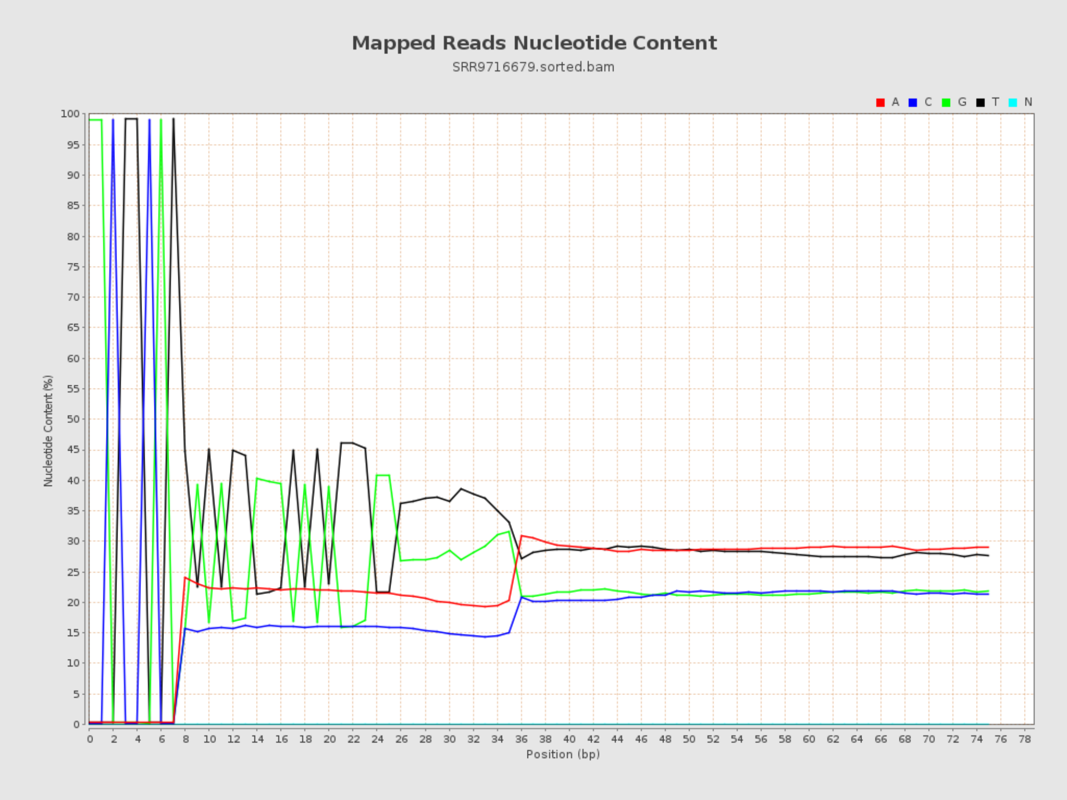
6. Results : Genome Fraction Coverage



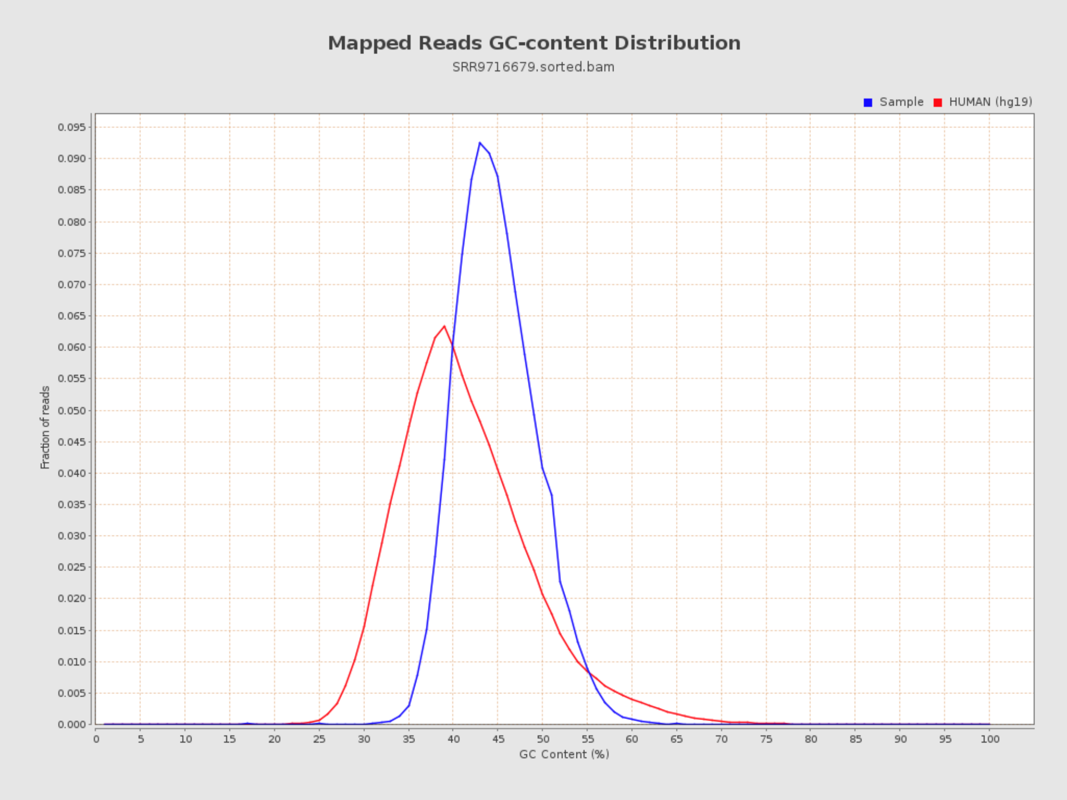
7. Results : Duplication Rate Histogram



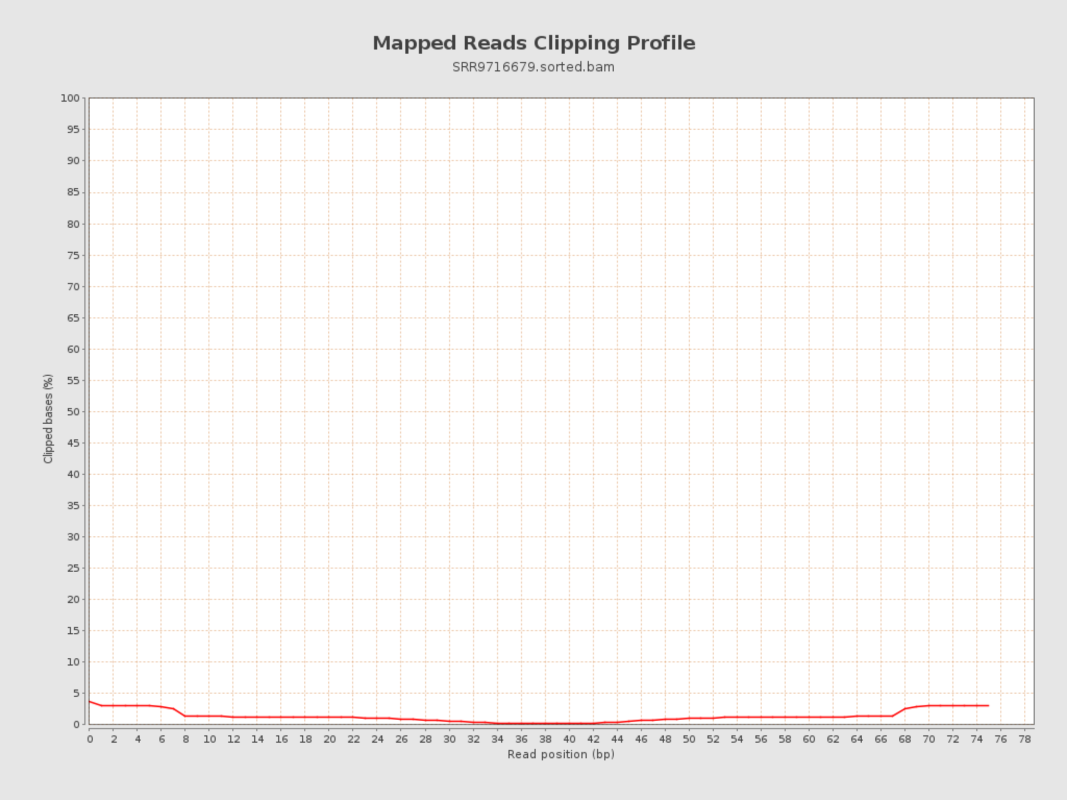
8. Results : Mapped Reads Nucleotide Content



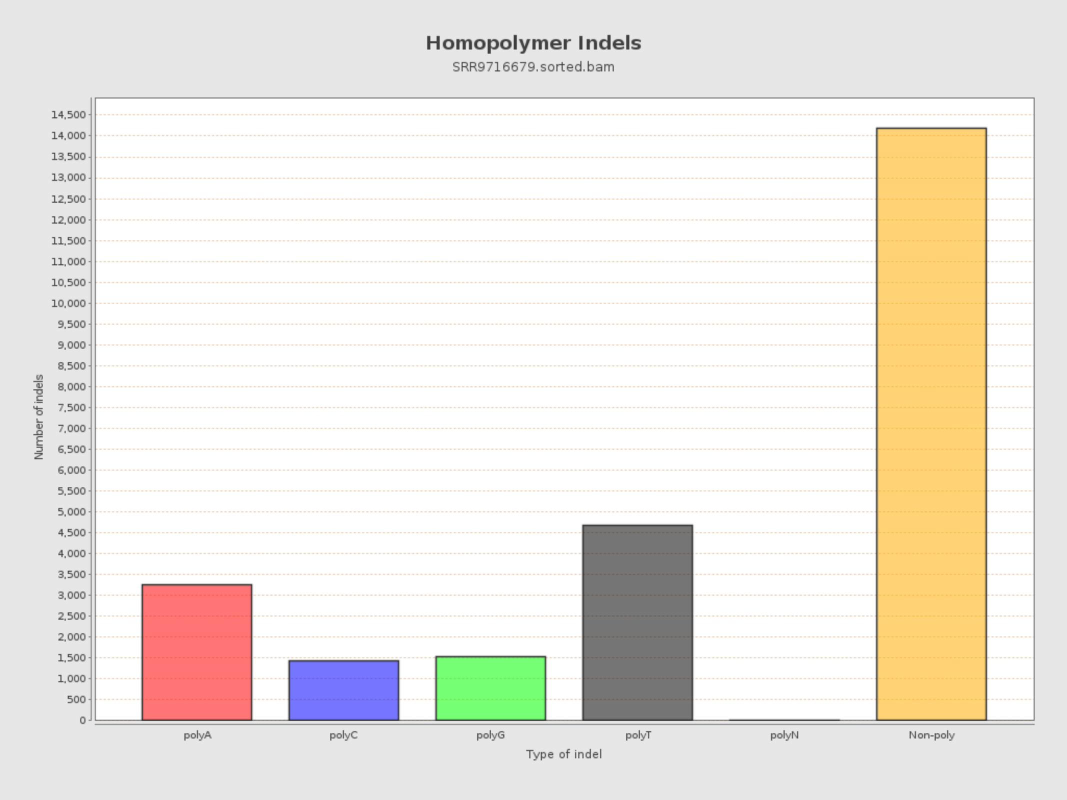
9. Results : Mapped Reads GC-content Distribution



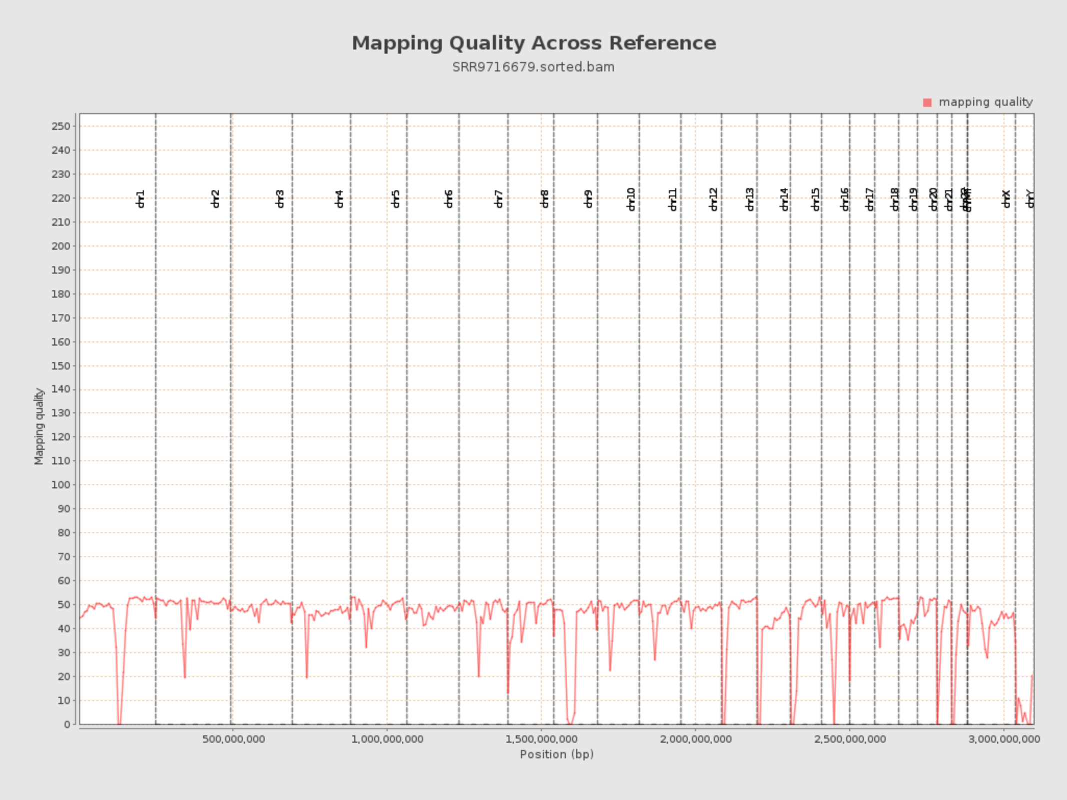
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram