Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 20:18:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716956.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_SRR9716956 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716956.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 20:18:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716956.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,427,563
Mapped reads	1,321,784 / 92.59%
Unmapped reads	105,779 / 7.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,761 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	46,286 / 3.24%
Duplication rate	2.52%
Clipped reads	1,325,736 / 92.87%

2.2. ACGT Content

Number/percentage of A's	19,172,508 / 24.71%
Number/percentage of C's	15,281,065 / 19.7%
Number/percentage of T's	24,231,860 / 31.23%
Number/percentage of G's	18,900,404 / 24.36%
Number/percentage of N's	1,538 / 0%
GC Percentage	44.06%

2.3. Coverage

Mean	0.0251

Standard Deviation	0.2469

2.4. Mapping Quality

Mean Mapping Quality	44.85

2.5. Mismatches and indels

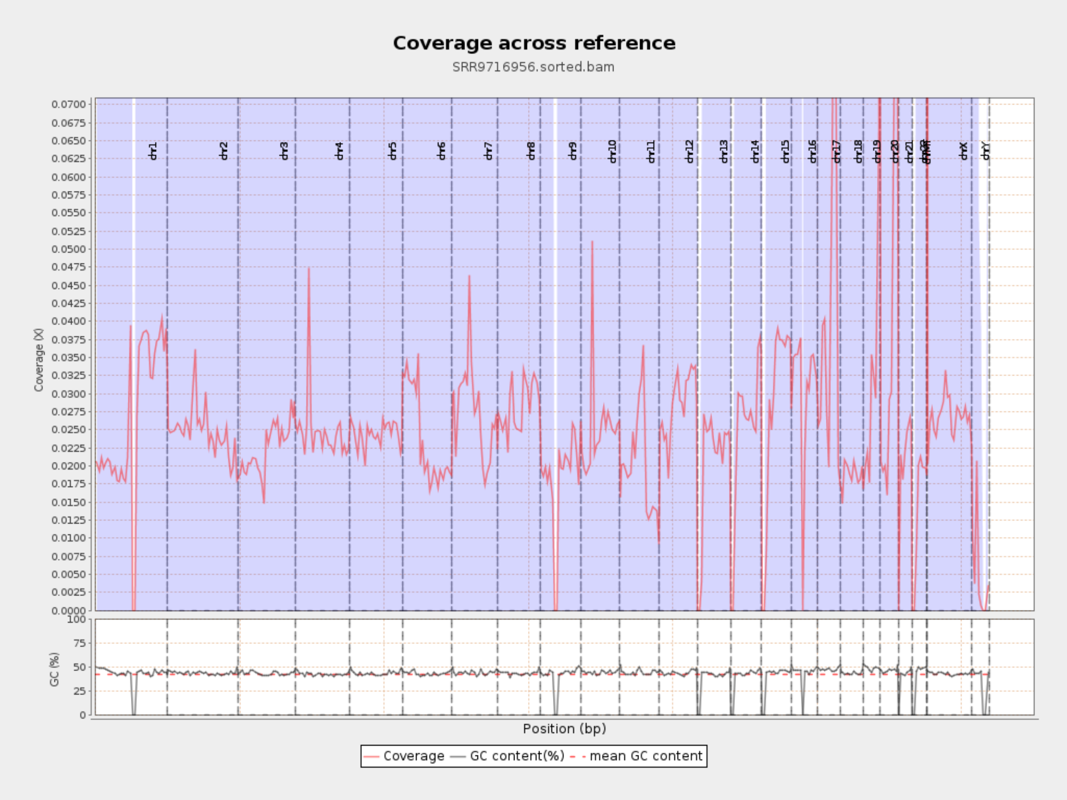
General error rate	0.51%
Mismatches	386,144
Insertions	4,756
Mapped reads with at least one insertion	0.36%
Deletions	14,862
Mapped reads with at least one deletion	1.12%
Homopolymer indels	43.93%

2.6. Chromosome stats

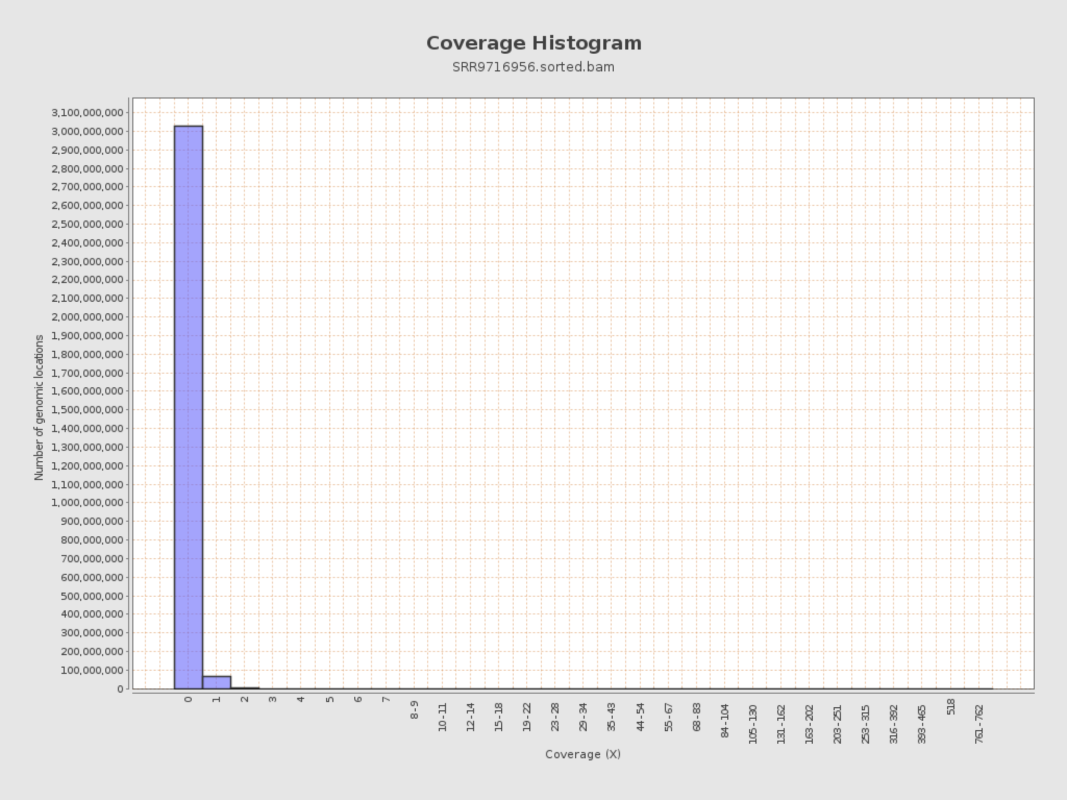
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6555896	0.0263	0.3748
chr2	243199373	6024576	0.0248	0.3529
chr3	198022430	4425435	0.0223	0.1613
chr4	191154276	4752771	0.0249	0.2039
chr5	180915260	4416310	0.0244	0.1676
chr6	171115067	4083334	0.0239	0.1919
chr7	159138663	4421567	0.0278	0.3191

chr8	146364022	4154673	0.0284	0.3272
chr9	141213431	2561376	0.0181	0.1761
chr10	135534747	3423316	0.0253	0.2617
chr11	135006516	2757694	0.0204	0.1958
chr12	133851895	3819912	0.0285	0.1839
chr13	115169878	2322586	0.0202	0.1531
chr14	107349540	2630310	0.0245	0.1706
chr15	102531392	2863182	0.0279	0.1806
chr16	90354753	2705405	0.0299	0.194
chr17	81195210	3345735	0.0412	0.2273
chr18	78077248	1460765	0.0187	0.2782
chr19	59128983	1997606	0.0338	0.3043
chr20	63025520	2584748	0.041	0.2257
chr21	48129895	999505	0.0208	0.1877
chr22	51304566	730230	0.0142	0.1289
chrMT	16571	107992	6.5169	4.461
chrX	155270560	4175018	0.0269	0.1869
chrY	59373566	291584	0.0049	0.2295

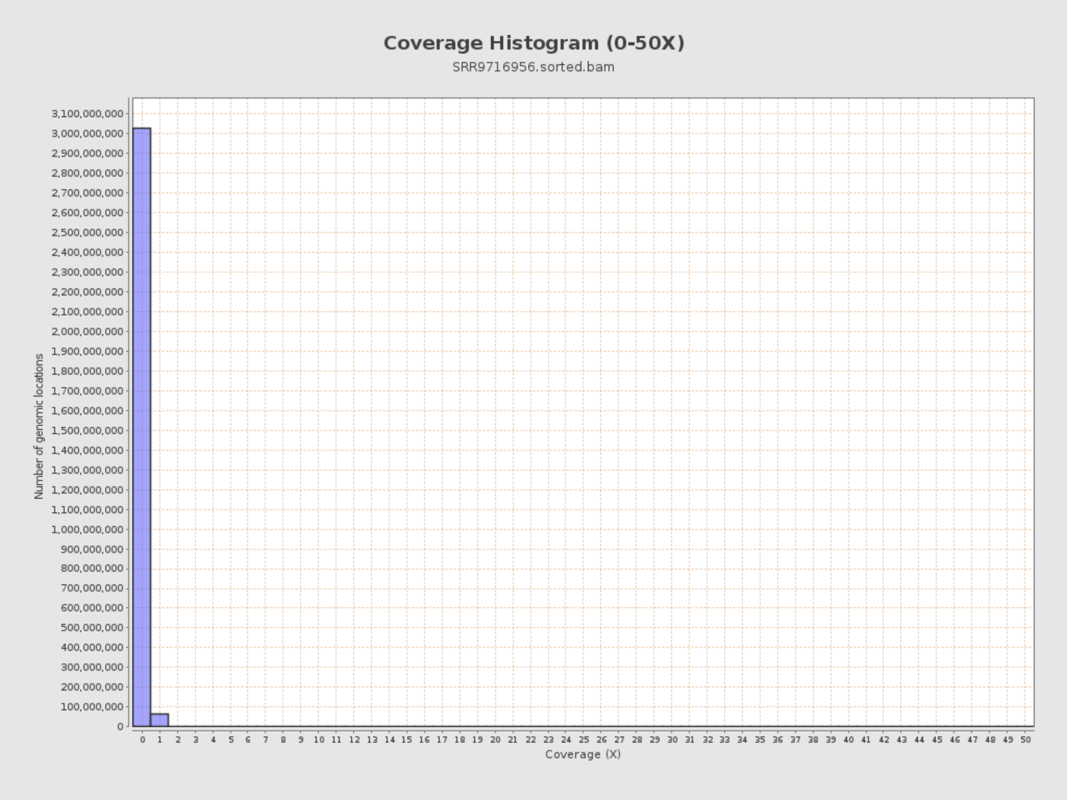
3. Results : Coverage across reference



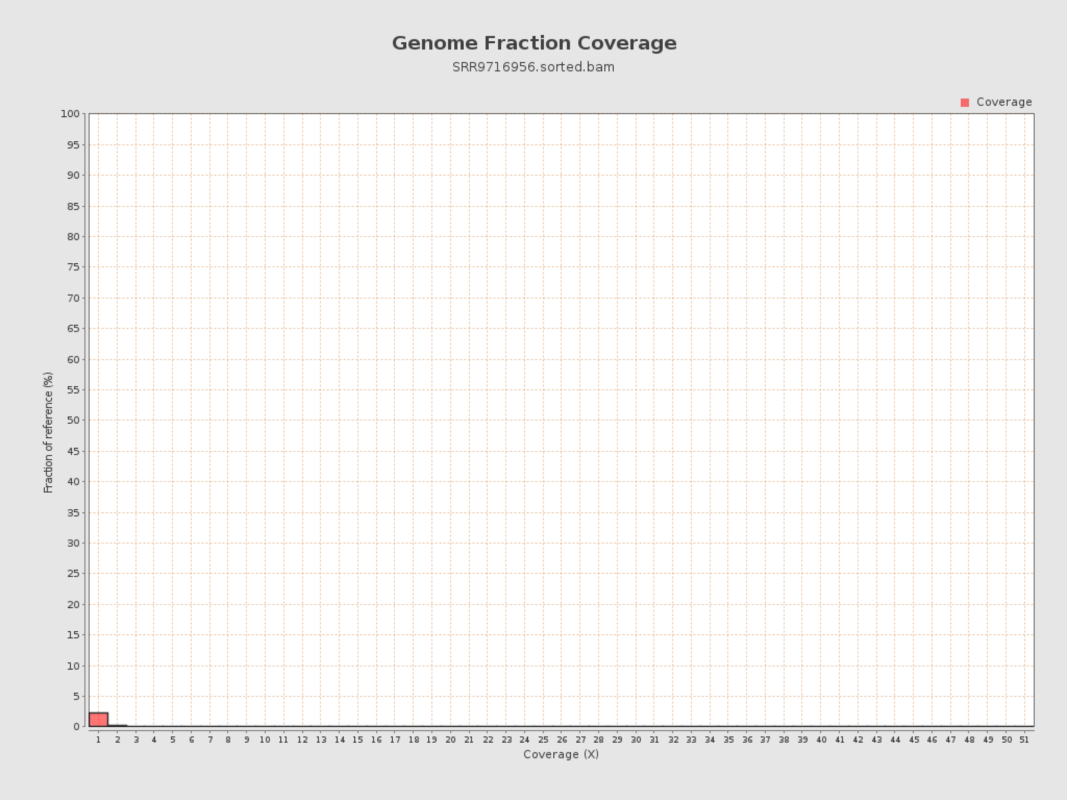
4. Results : Coverage Histogram



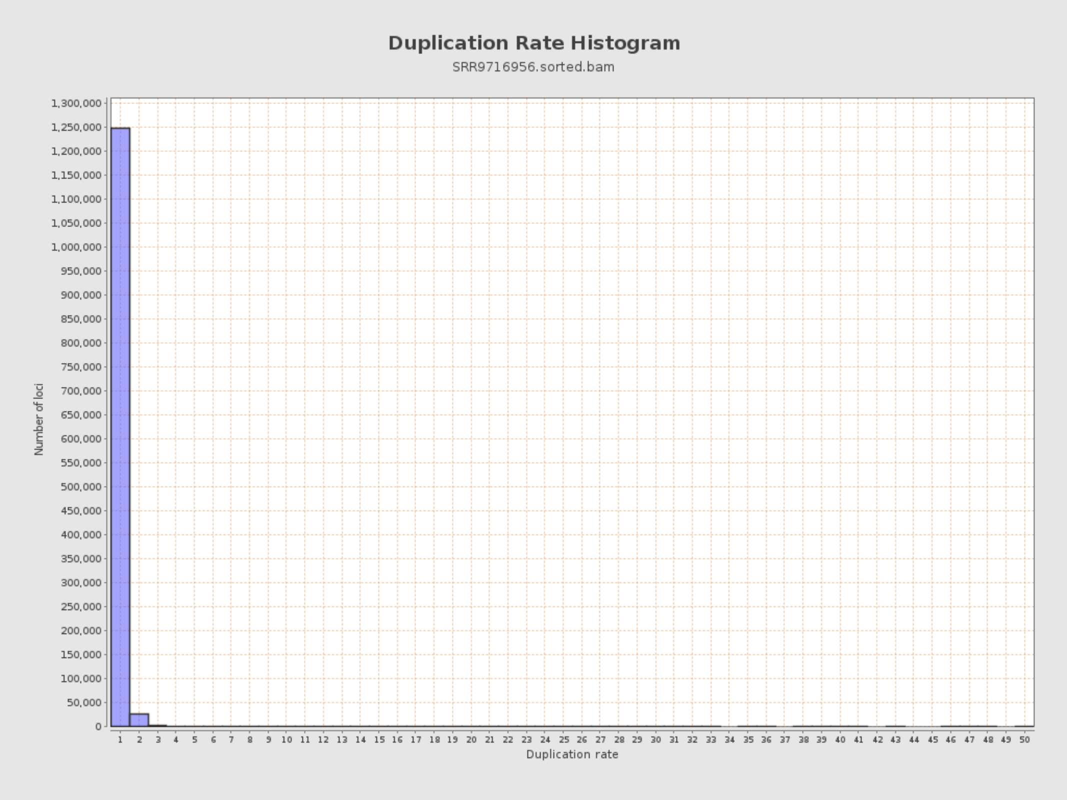
5. Results : Coverage Histogram (0-50X)



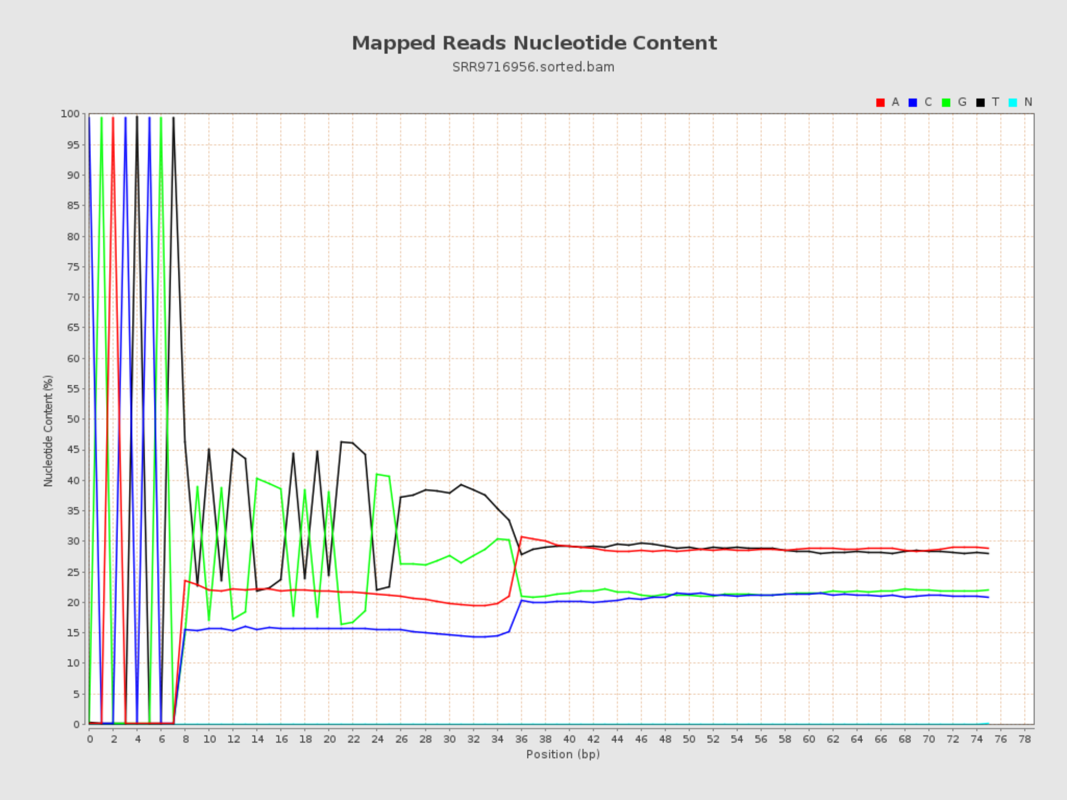
6. Results : Genome Fraction Coverage



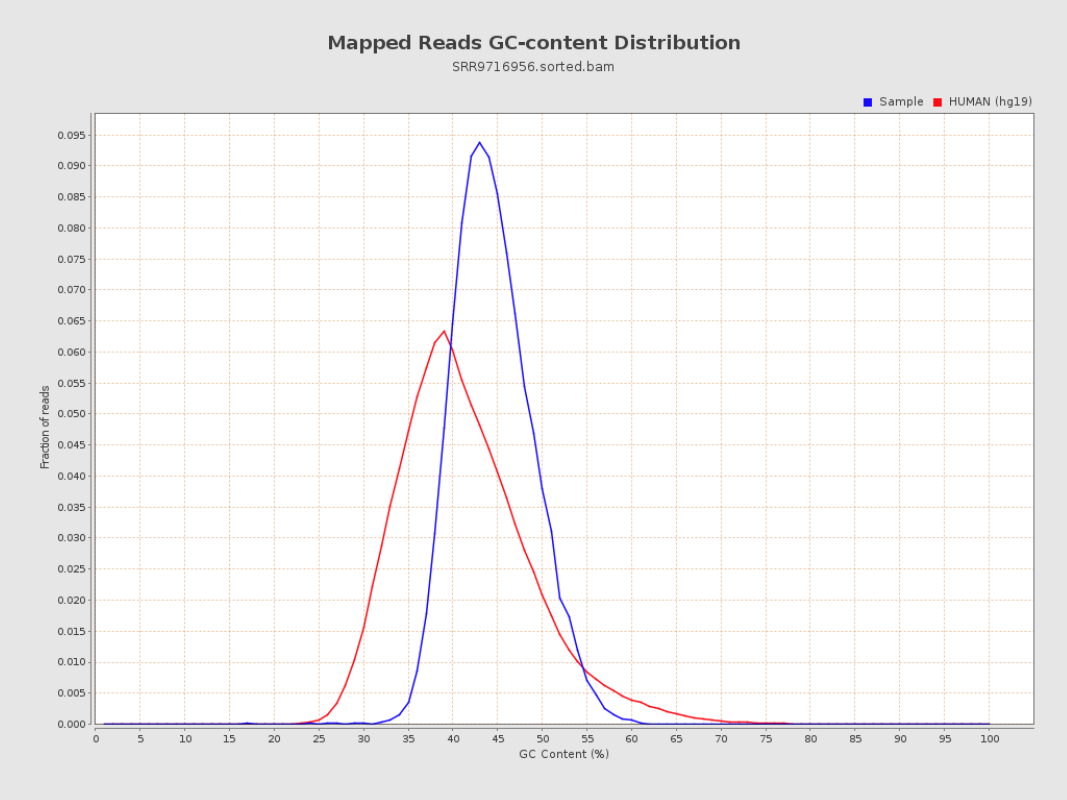
7. Results : Duplication Rate Histogram



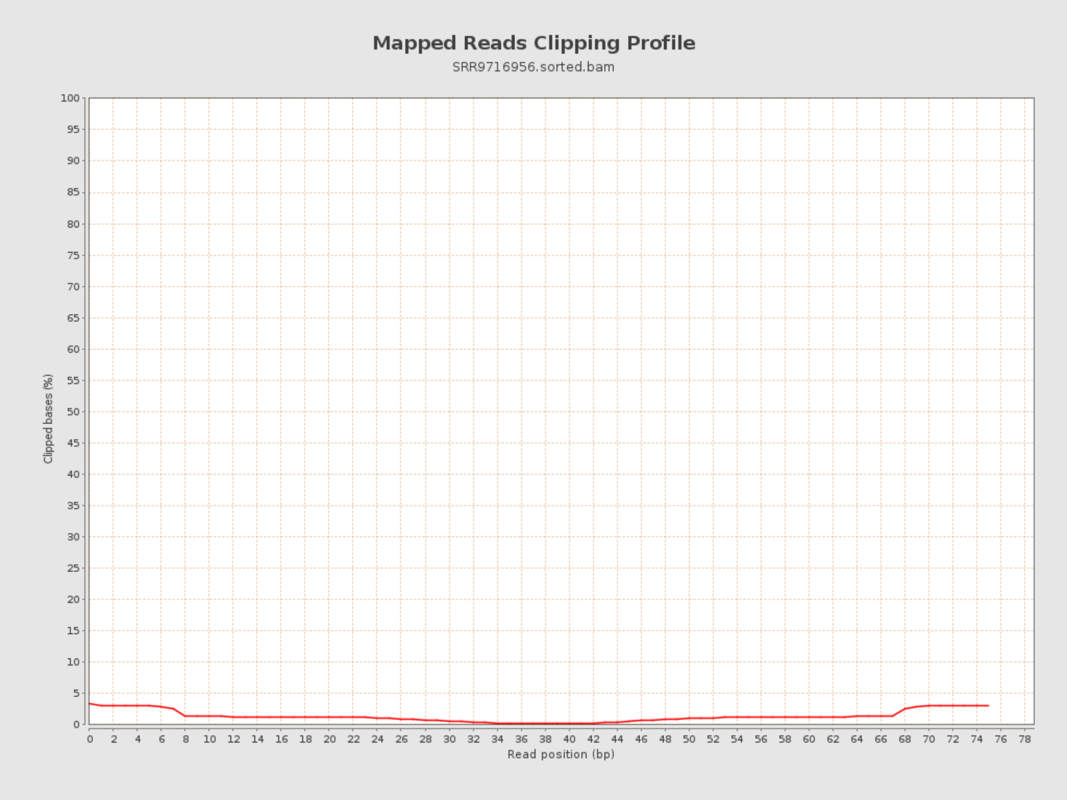
8. Results : Mapped Reads Nucleotide Content



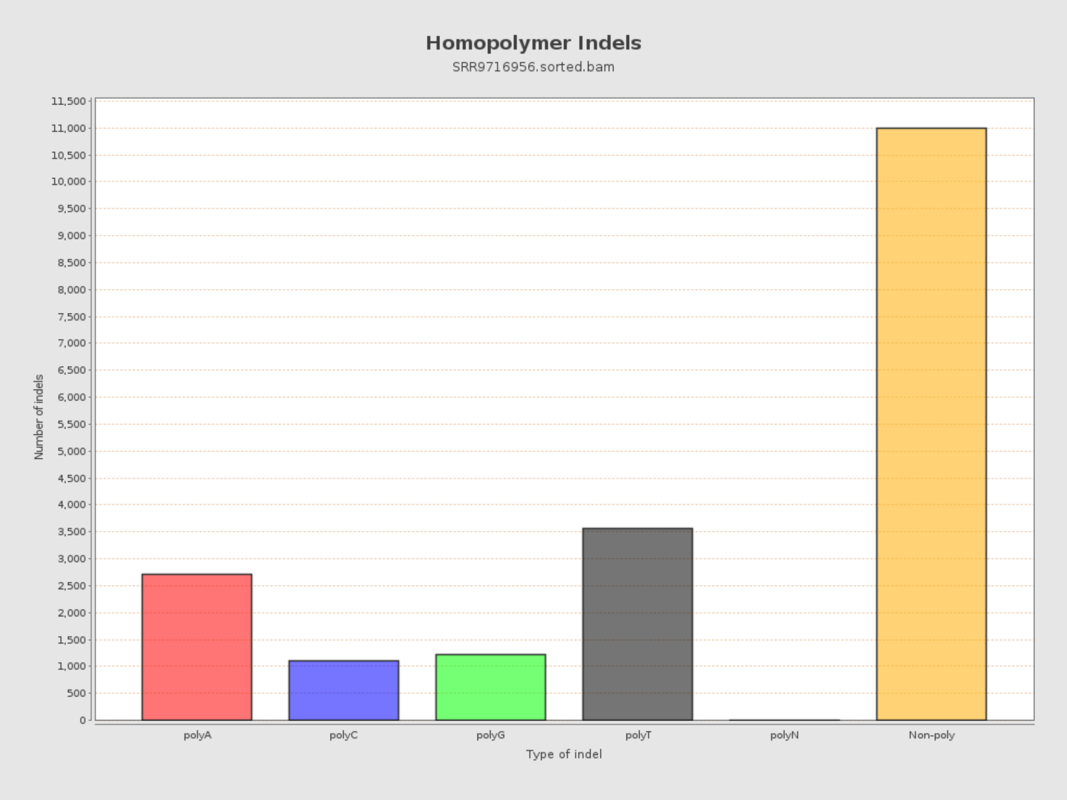
9. Results : Mapped Reads GC-content Distribution



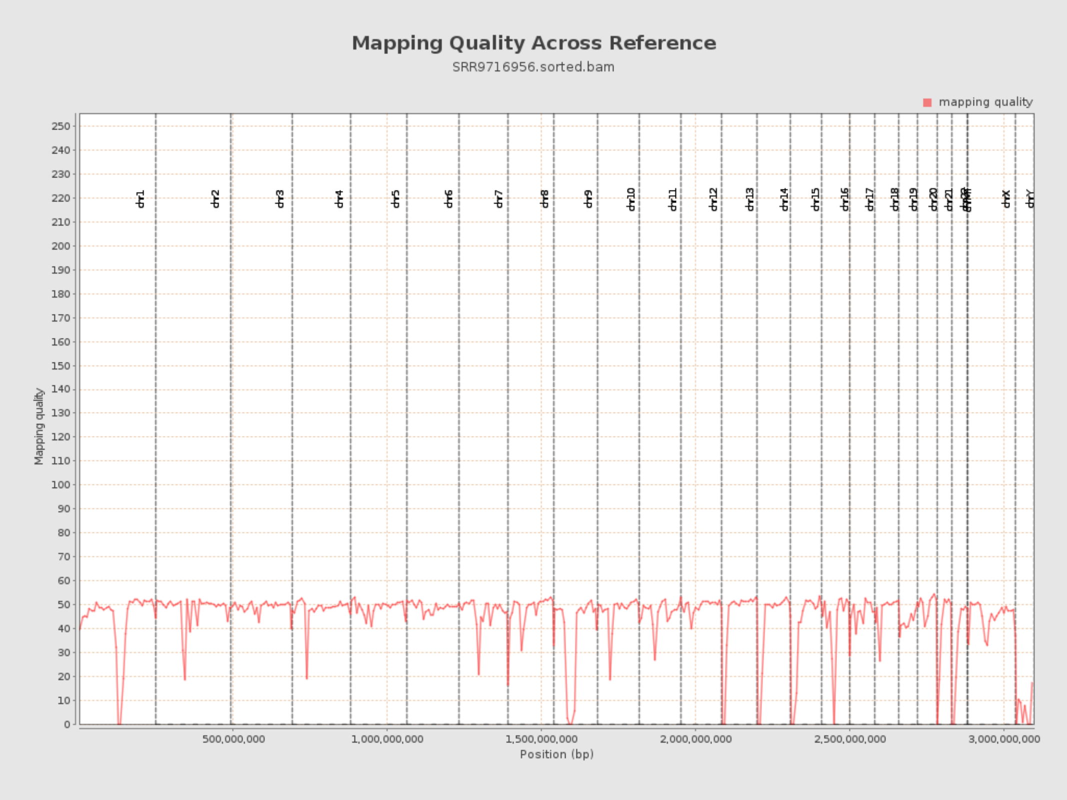
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram