Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 00:43:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716616.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_SRR9716616 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716616.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 00:43:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716616.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	541,249
Mapped reads	484,487 / 89.51%
Unmapped reads	56,762 / 10.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,407 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	9,819 / 1.81%
Duplication rate	1.6%
Clipped reads	484,438 / 89.5%

2.2. ACGT Content

Number/percentage of A's	6,381,505 / 23.11%
Number/percentage of C's	5,518,514 / 19.99%
Number/percentage of T's	9,039,474 / 32.74%
Number/percentage of G's	6,669,416 / 24.16%
Number/percentage of N's	309 / 0%
GC Percentage	44.14%

2.3. Coverage

Mean	0.0089

Standard Deviation	0.112

2.4. Mapping Quality

Mean Mapping Quality	44.79

2.5. Mismatches and indels

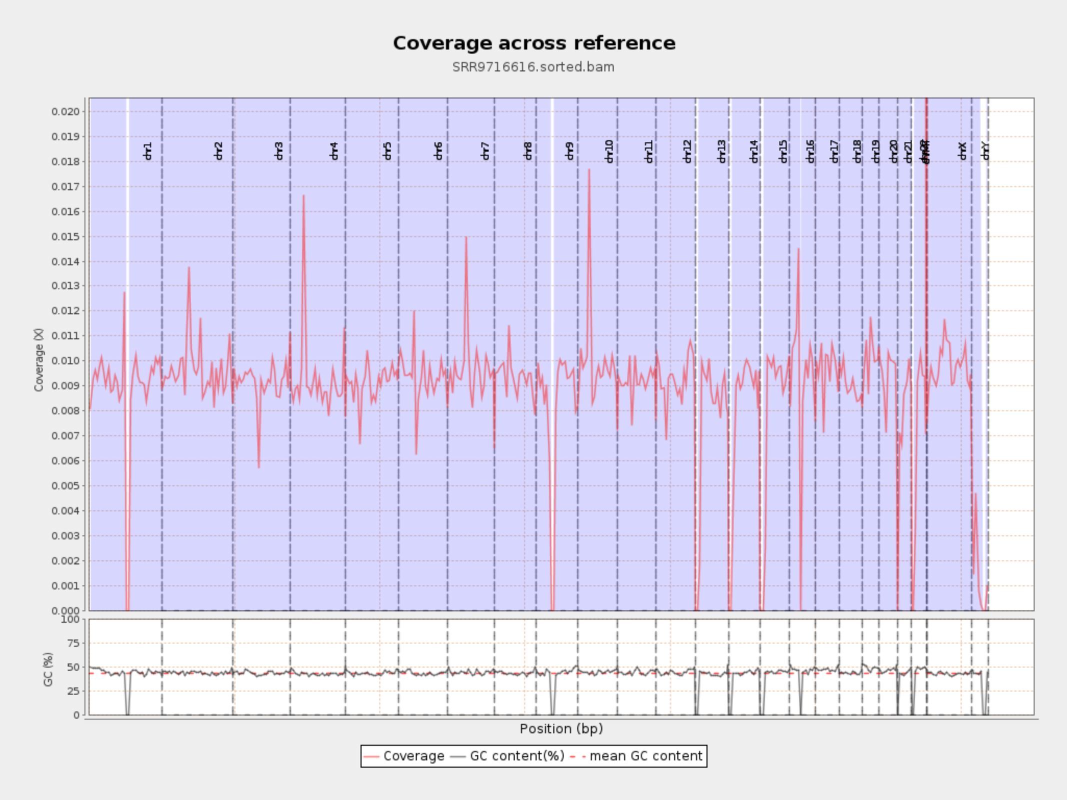
General error rate	0.52%
Mismatches	139,076
Insertions	1,941
Mapped reads with at least one insertion	0.4%
Deletions	5,564
Mapped reads with at least one deletion	1.14%
Homopolymer indels	43.38%

2.6. Chromosome stats

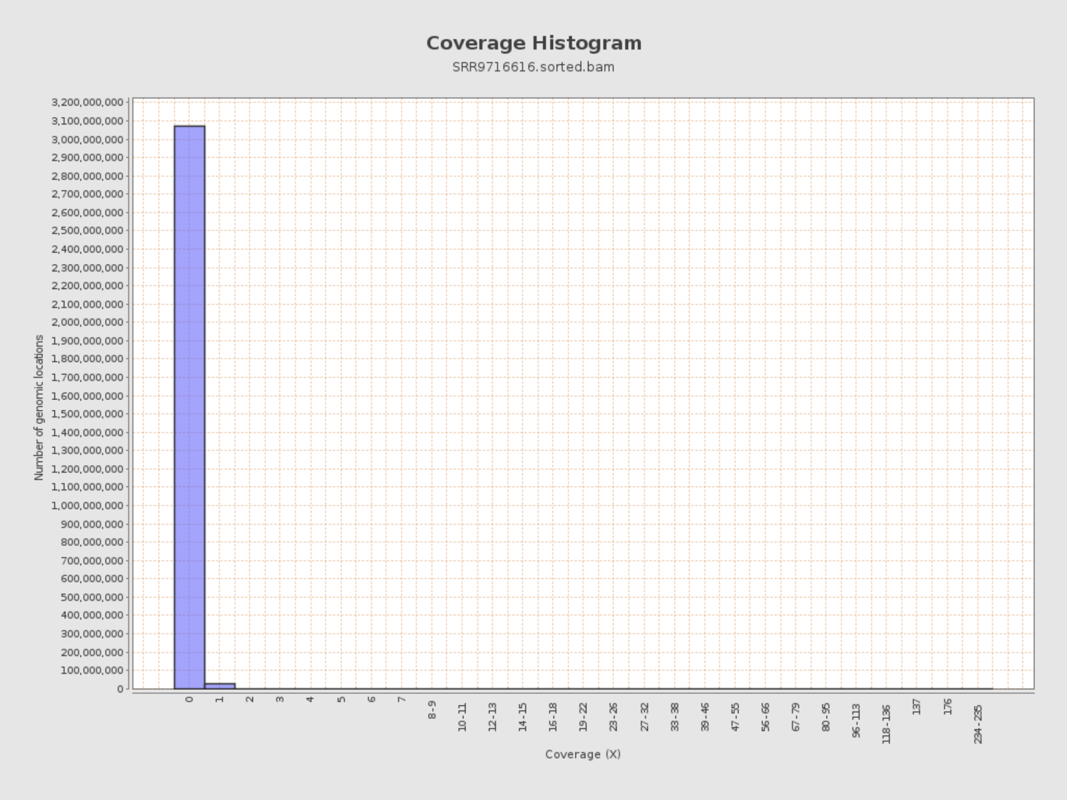
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2199733	0.0088	0.1362
chr2	243199373	2357675	0.0097	0.1453
chr3	198022430	1807214	0.0091	0.1001
chr4	191154276	1769778	0.0093	0.1039
chr5	180915260	1650082	0.0091	0.0987
chr6	171115067	1608140	0.0094	0.1078
chr7	159138663	1548656	0.0097	0.1366

chr8	146364022	1370990	0.0094	0.1068
chr9	141213431	1138140	0.0081	0.0986
chr10	135534747	1358258	0.01	0.1219
chr11	135006516	1241230	0.0092	0.1073
chr12	133851895	1243632	0.0093	0.1001
chr13	115169878	860376	0.0075	0.0898
chr14	107349540	830589	0.0077	0.092
chr15	102531392	793947	0.0077	0.0912
chr16	90354753	848290	0.0094	0.1047
chr17	81195210	783318	0.0096	0.1043
chr18	78077248	706643	0.0091	0.1409
chr19	59128983	601186	0.0102	0.1236
chr20	63025520	589816	0.0094	0.1007
chr21	48129895	367361	0.0076	0.0926
chr22	51304566	336112	0.0066	0.0839
chrMT	16571	8775	0.5295	0.768
chrX	155270560	1516710	0.0098	0.1058
chrY	59373566	81545	0.0014	0.0479

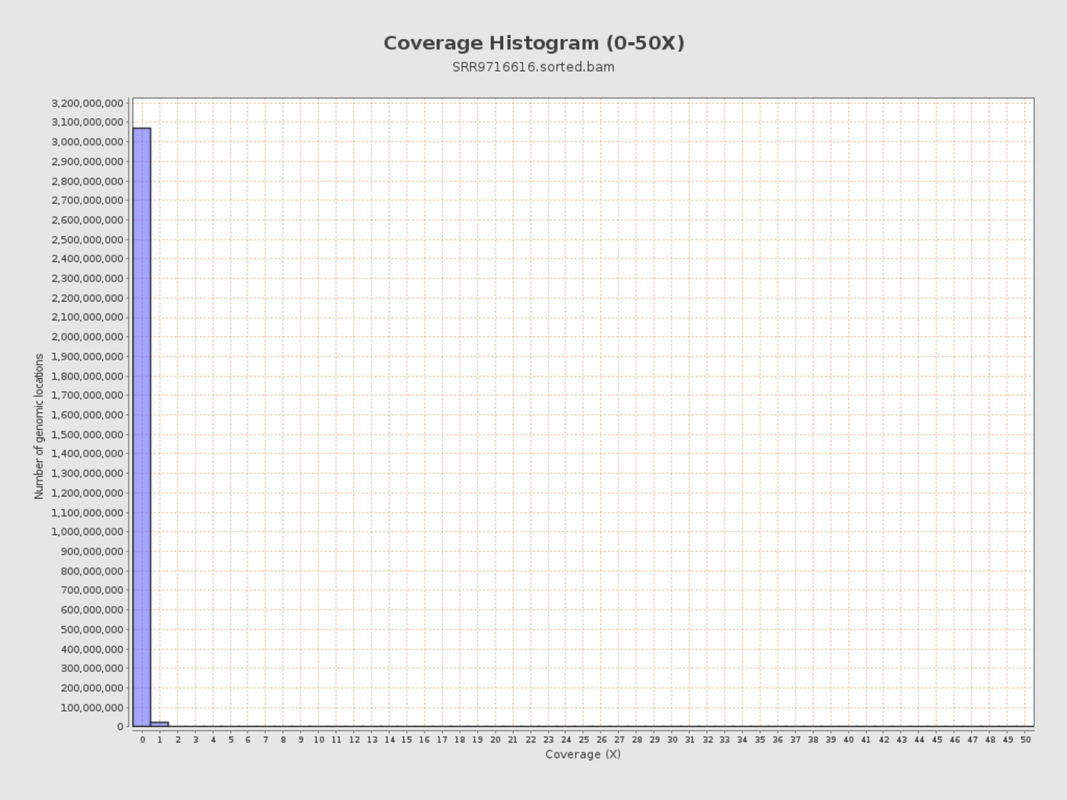
3. Results : Coverage across reference



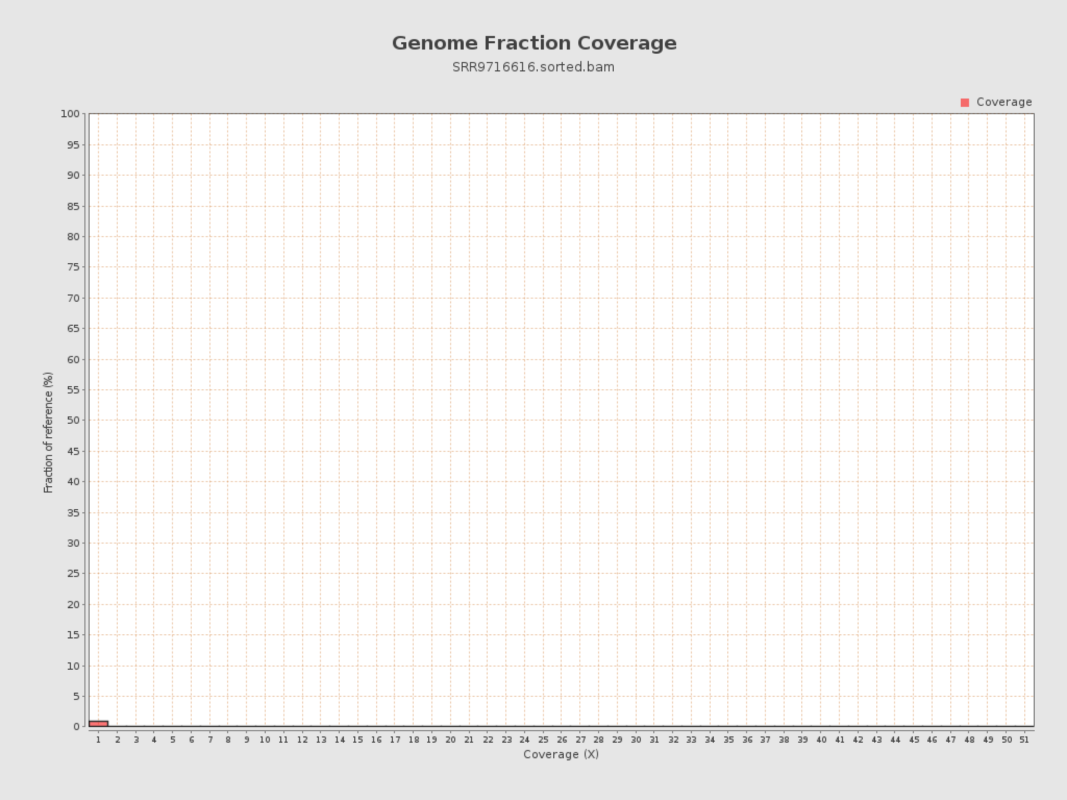
4. Results : Coverage Histogram



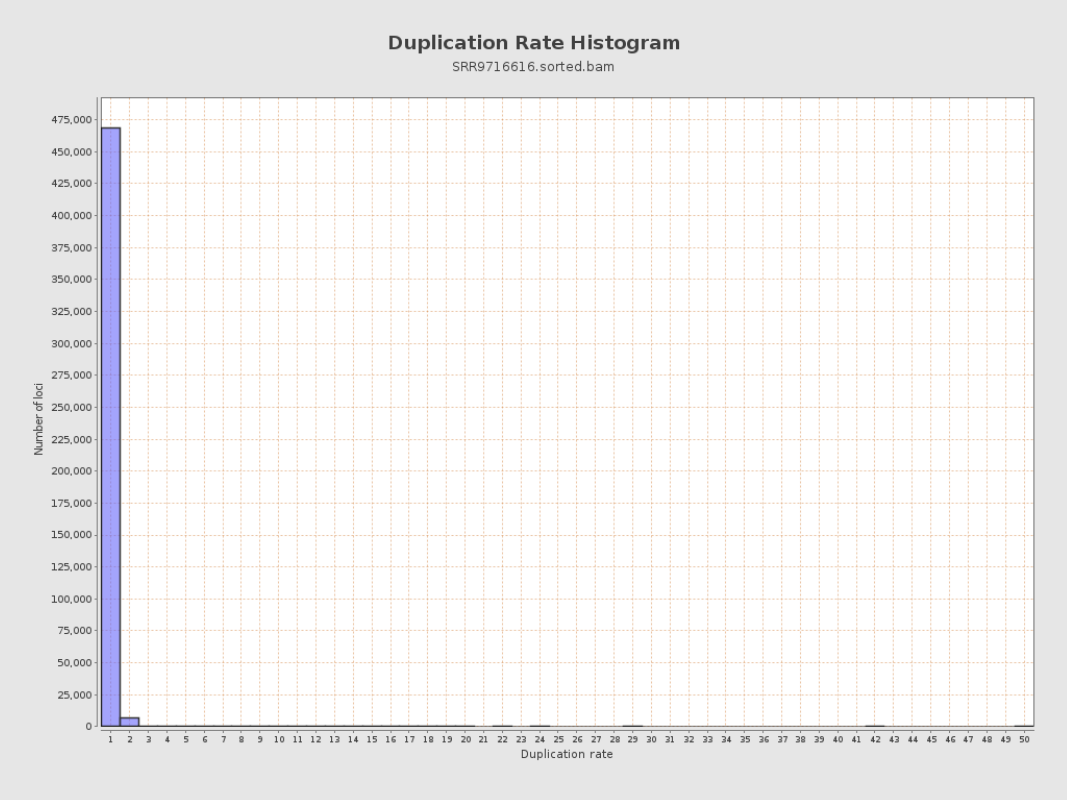
5. Results : Coverage Histogram (0-50X)



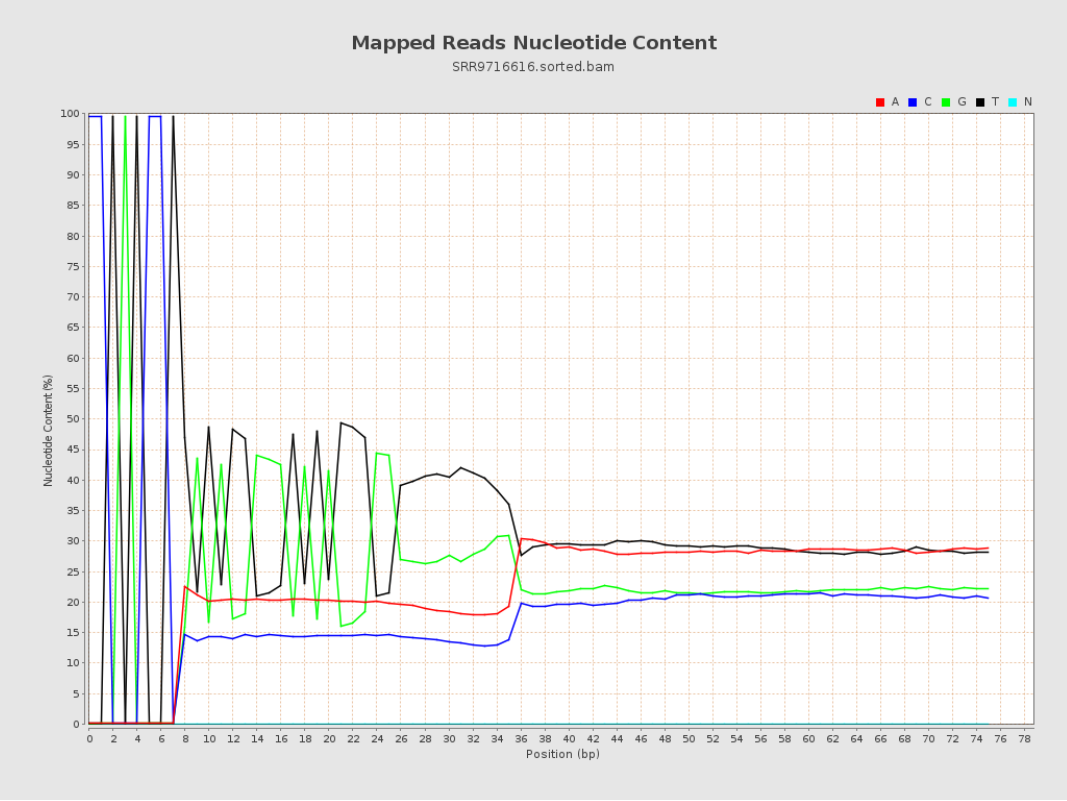
6. Results : Genome Fraction Coverage



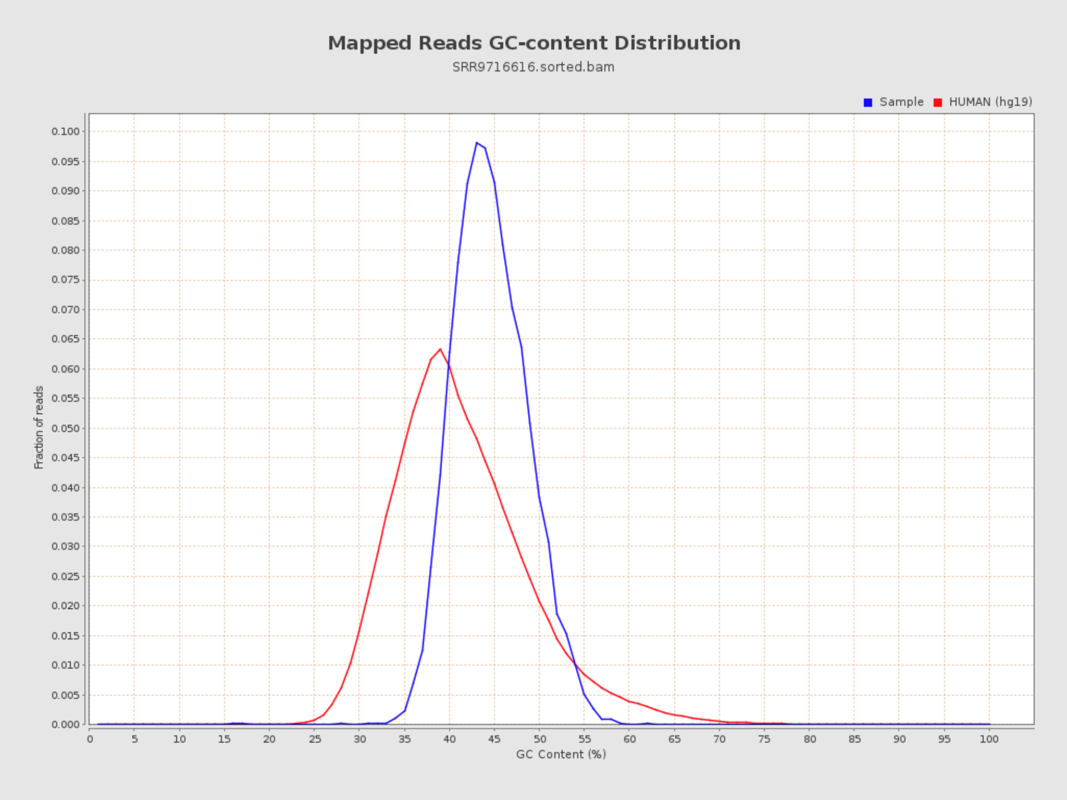
7. Results : Duplication Rate Histogram



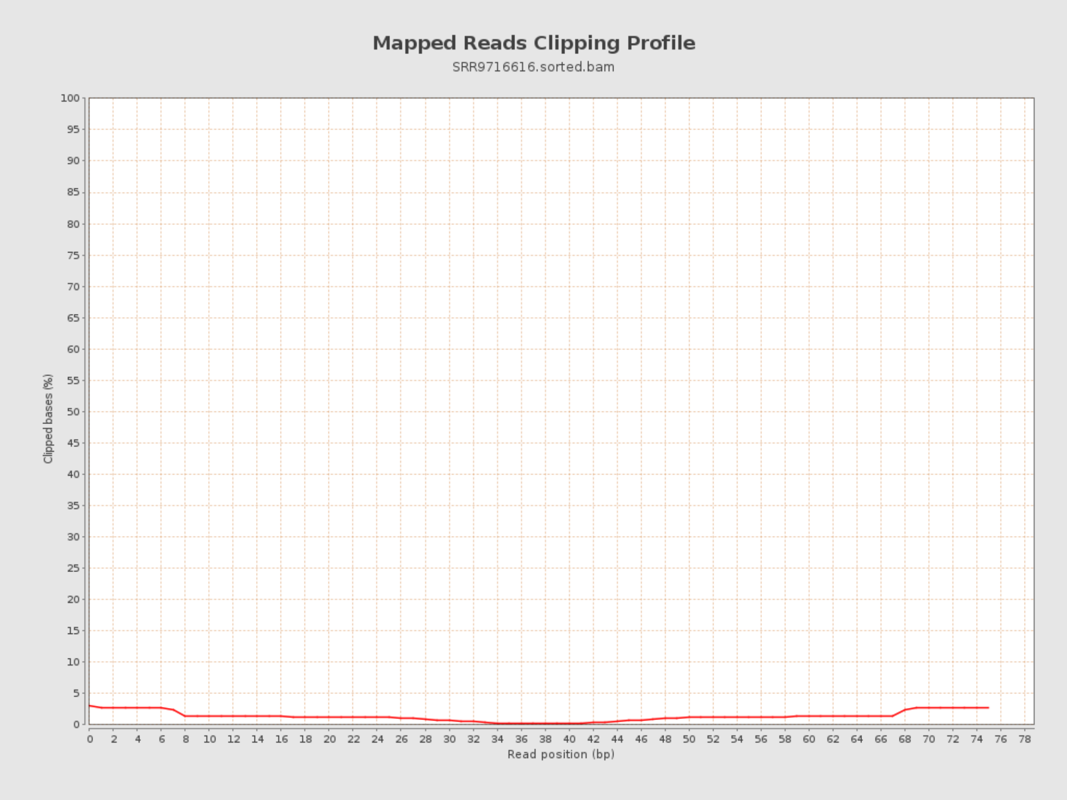
8. Results : Mapped Reads Nucleotide Content



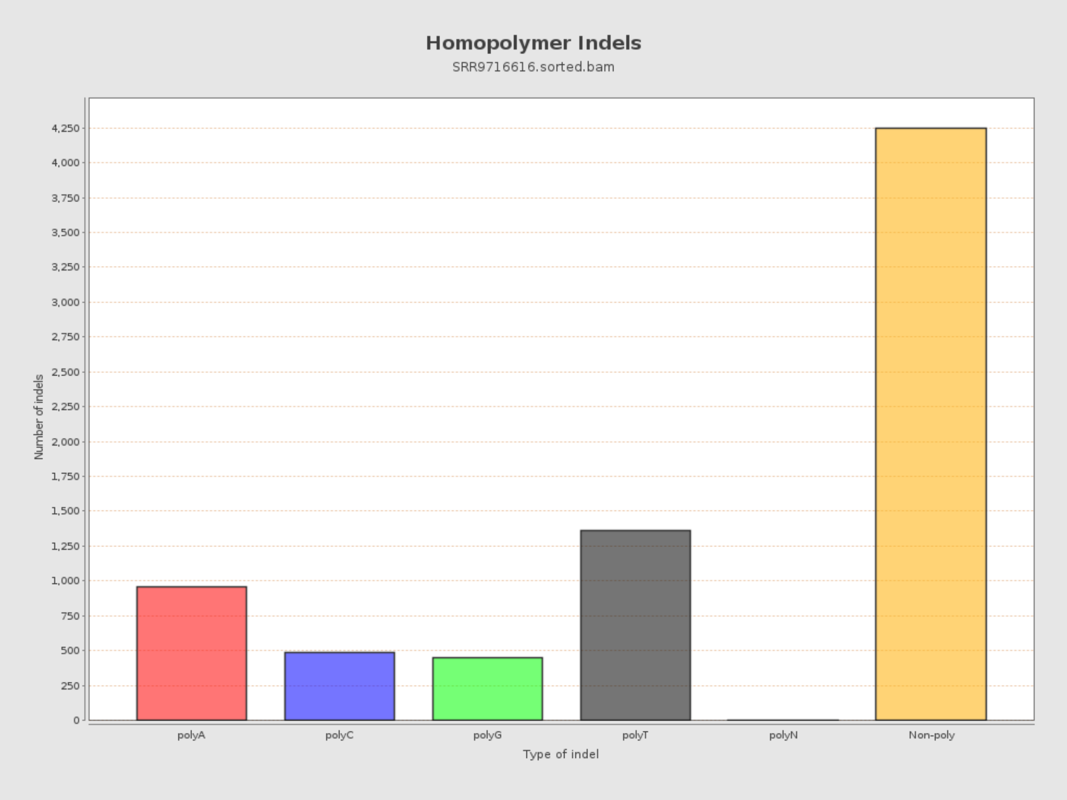
9. Results : Mapped Reads GC-content Distribution



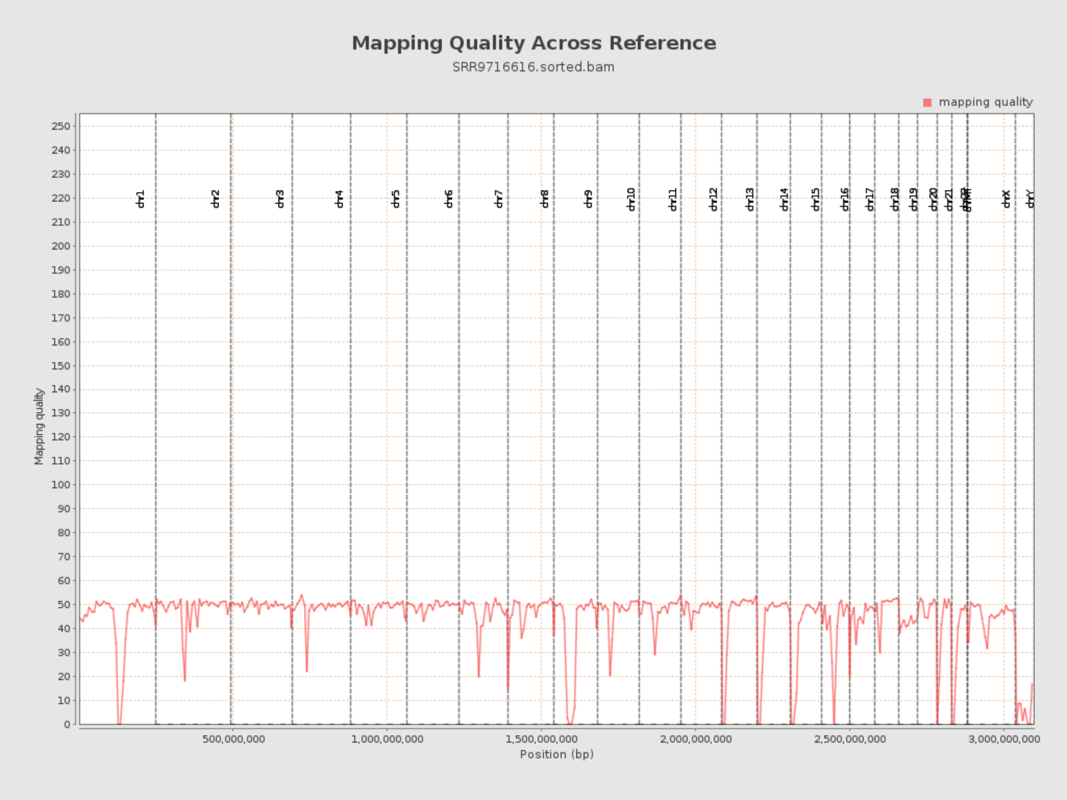
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram