Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 05:14:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716675.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_SRR9716675 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716675.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 05:14:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716675.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,001,486
Mapped reads	1,837,085 / 91.79%
Unmapped reads	164,401 / 8.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,857 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	75,974 / 3.8%
Duplication rate	3.19%
Clipped reads	1,841,657 / 92.01%

2.2. ACGT Content

Number/percentage of A's	25,780,194 / 24.05%
Number/percentage of C's	19,571,187 / 18.26%
Number/percentage of T's	34,831,841 / 32.49%
Number/percentage of G's	27,013,872 / 25.2%
Number/percentage of N's	657 / 0%
GC Percentage	43.46%

2.3. Coverage

Mean	0.0346

Standard Deviation	0.2974

2.4. Mapping Quality

Mean Mapping Quality	44.79

2.5. Mismatches and indels

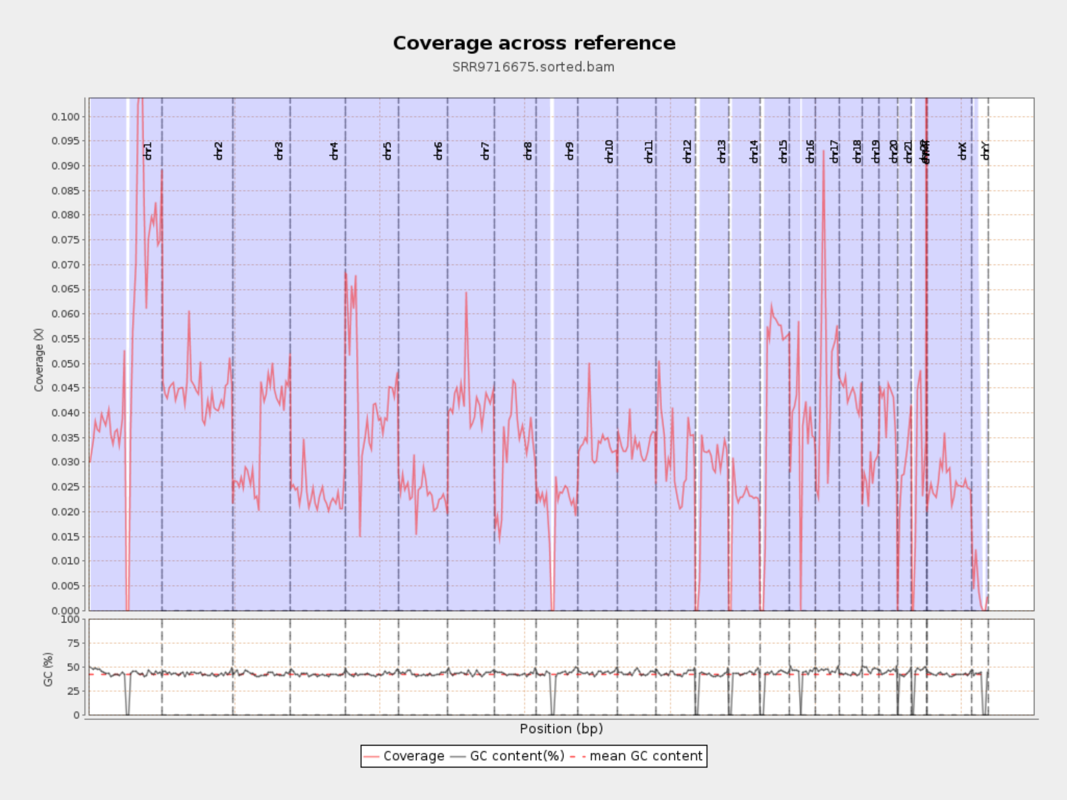
General error rate	0.51%
Mismatches	528,801
Insertions	7,366
Mapped reads with at least one insertion	0.4%
Deletions	18,317
Mapped reads with at least one deletion	0.99%
Homopolymer indels	41.28%

2.6. Chromosome stats

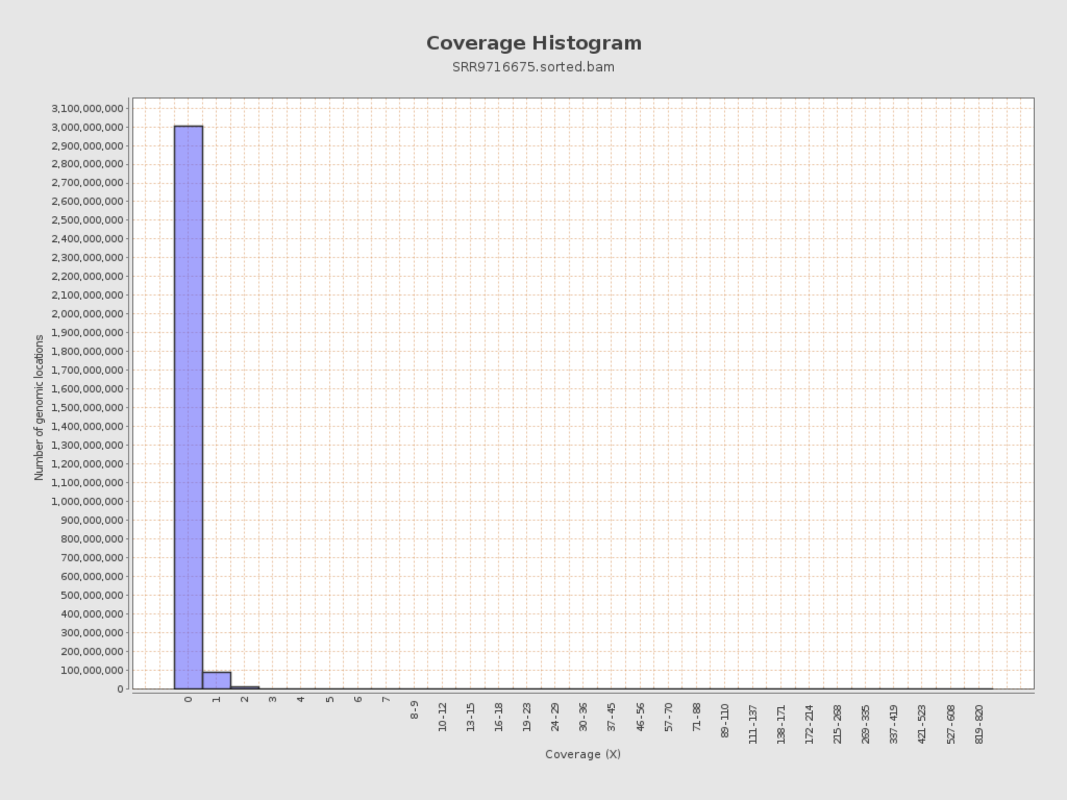
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13182564	0.0529	0.502
chr2	243199373	10811470	0.0445	0.4288
chr3	198022430	7039103	0.0355	0.209
chr4	191154276	4476118	0.0234	0.188
chr5	180915260	7891030	0.0436	0.232
chr6	171115067	4092116	0.0239	0.2009
chr7	159138663	6857761	0.0431	0.4371

chr8	146364022	4800806	0.0328	0.2671
chr9	141213431	2847410	0.0202	0.223
chr10	135534747	4614744	0.034	0.2517
chr11	135006516	4520140	0.0335	0.2737
chr12	133851895	4259214	0.0318	0.2002
chr13	115169878	3049125	0.0265	0.1823
chr14	107349540	2229858	0.0208	0.1683
chr15	102531392	4702897	0.0459	0.2384
chr16	90354753	3309981	0.0366	0.2258
chr17	81195210	3971927	0.0489	0.2644
chr18	78077248	3444994	0.0441	0.4794
chr19	59128983	1636549	0.0277	0.3564
chr20	63025520	2603373	0.0413	0.2287
chr21	48129895	1323460	0.0275	0.1903
chr22	51304566	1308618	0.0255	0.1773
chrMT	16571	5466	0.3299	0.6043
chrX	155270560	4009131	0.0258	0.2031
chrY	59373566	238400	0.004	0.0916

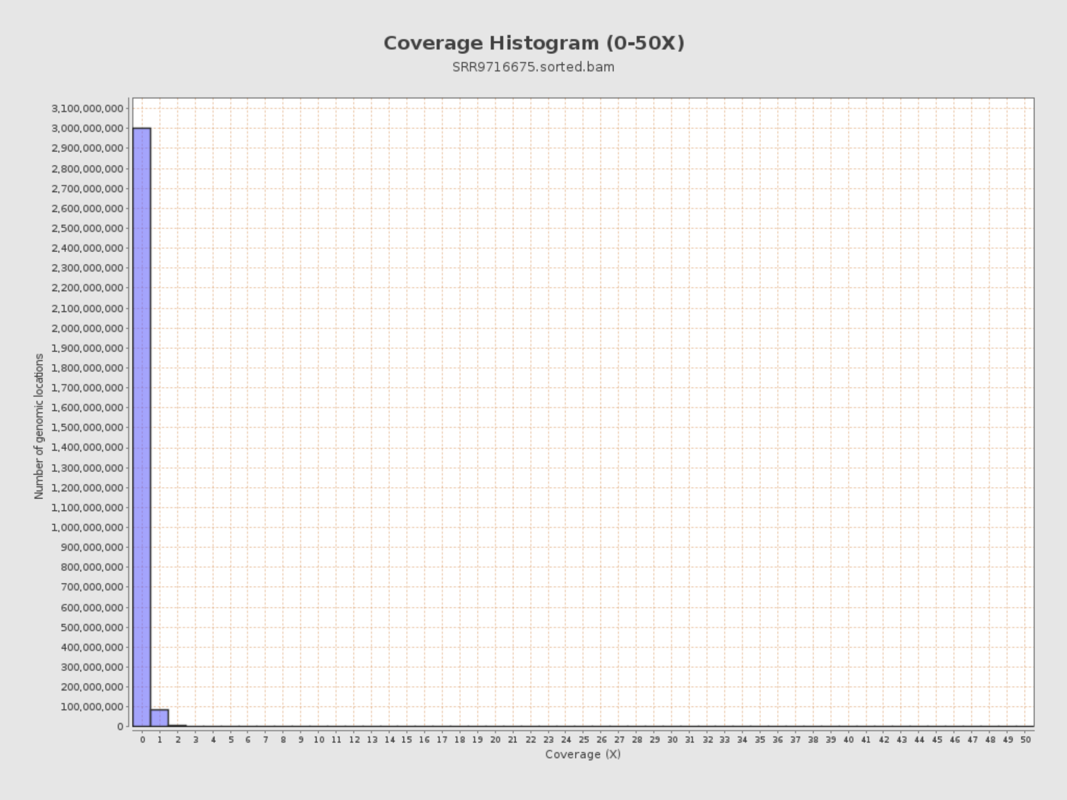
3. Results : Coverage across reference



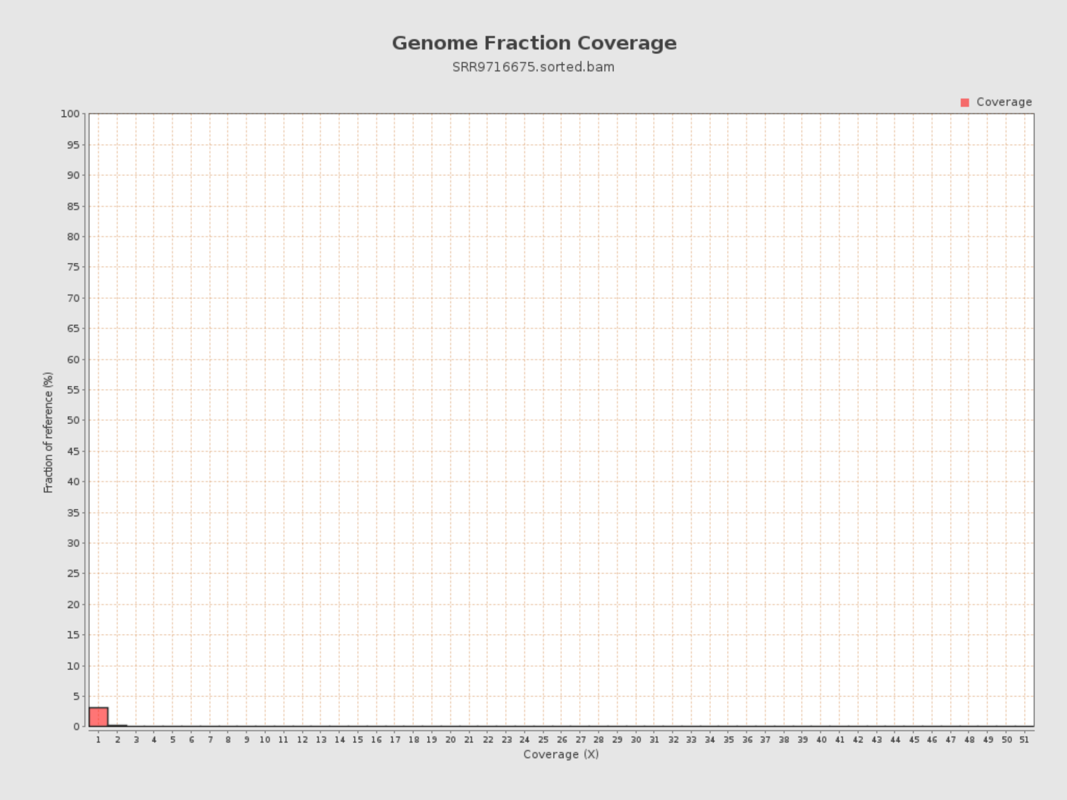
4. Results : Coverage Histogram



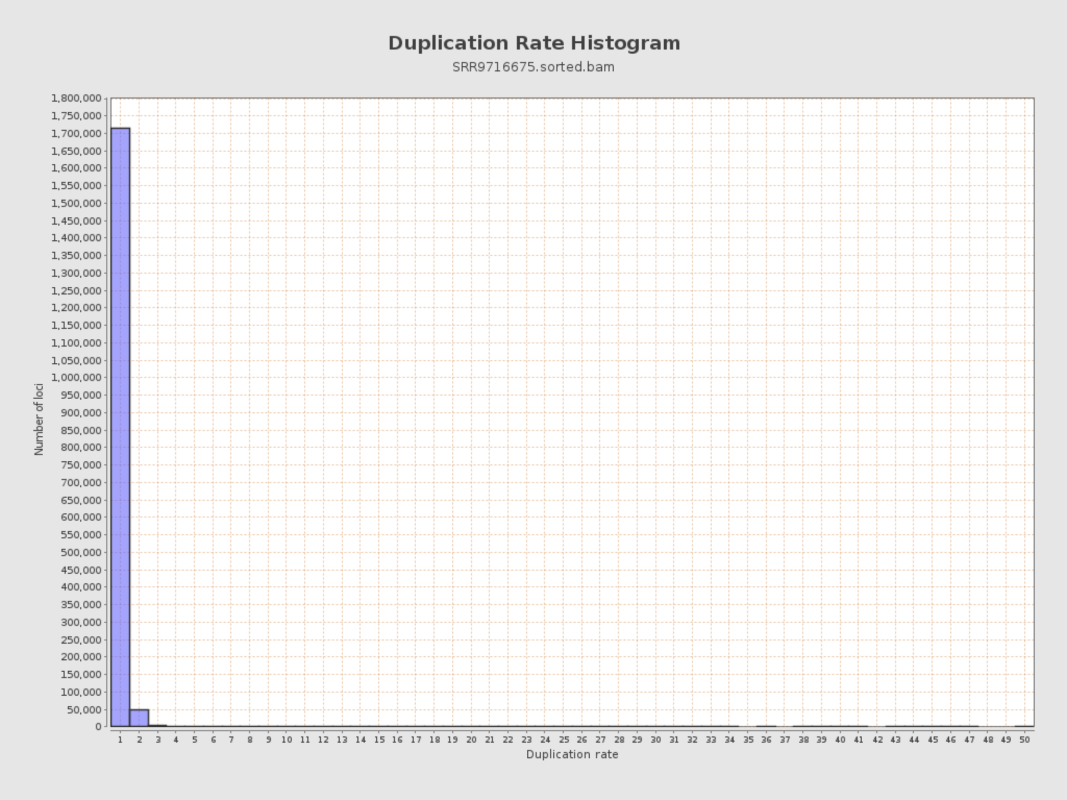
5. Results : Coverage Histogram (0-50X)



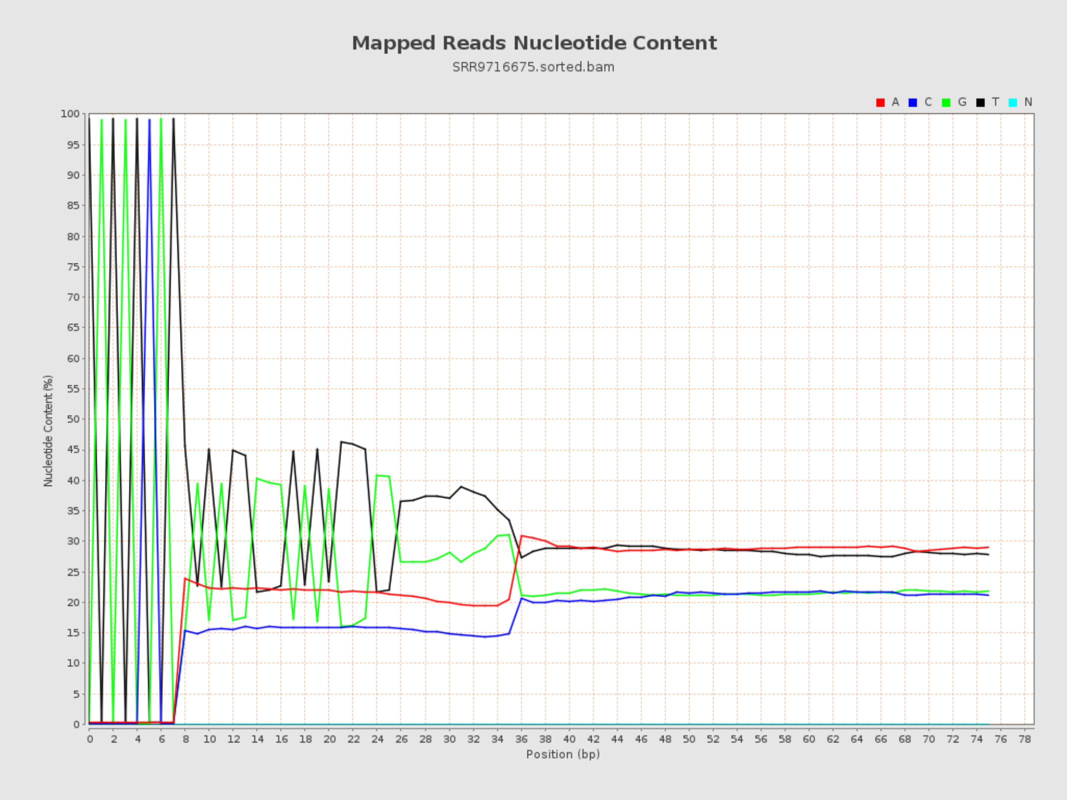
6. Results : Genome Fraction Coverage



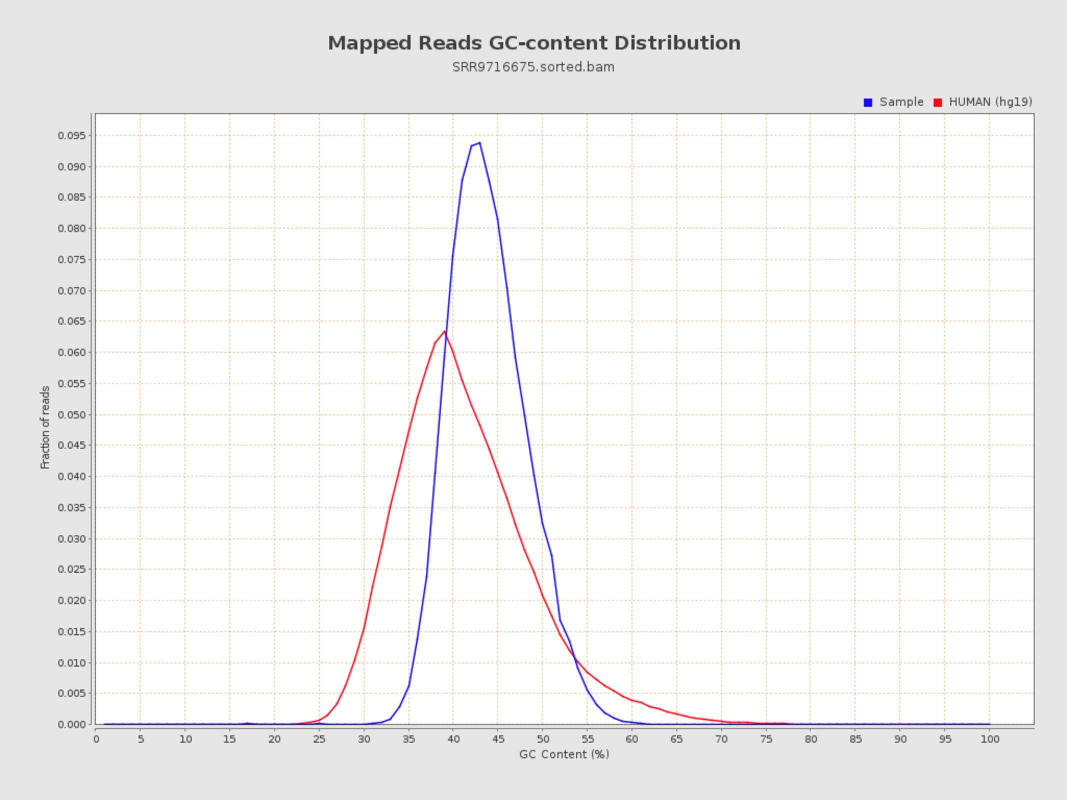
7. Results : Duplication Rate Histogram



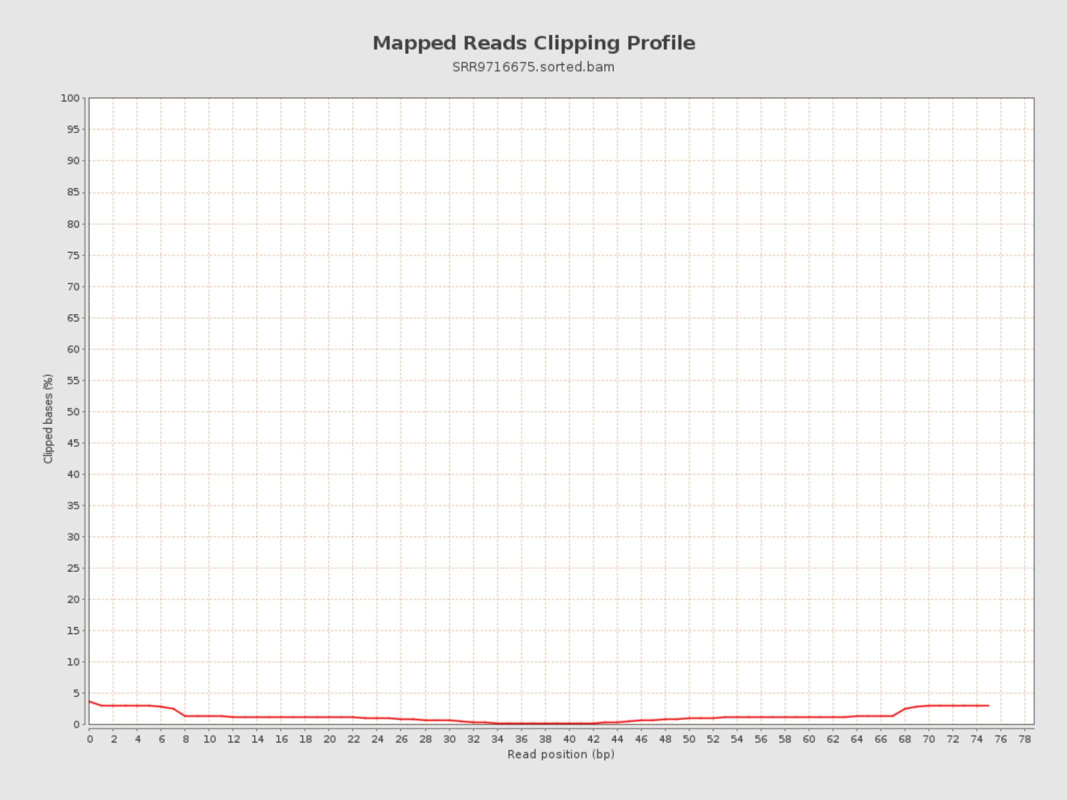
8. Results : Mapped Reads Nucleotide Content



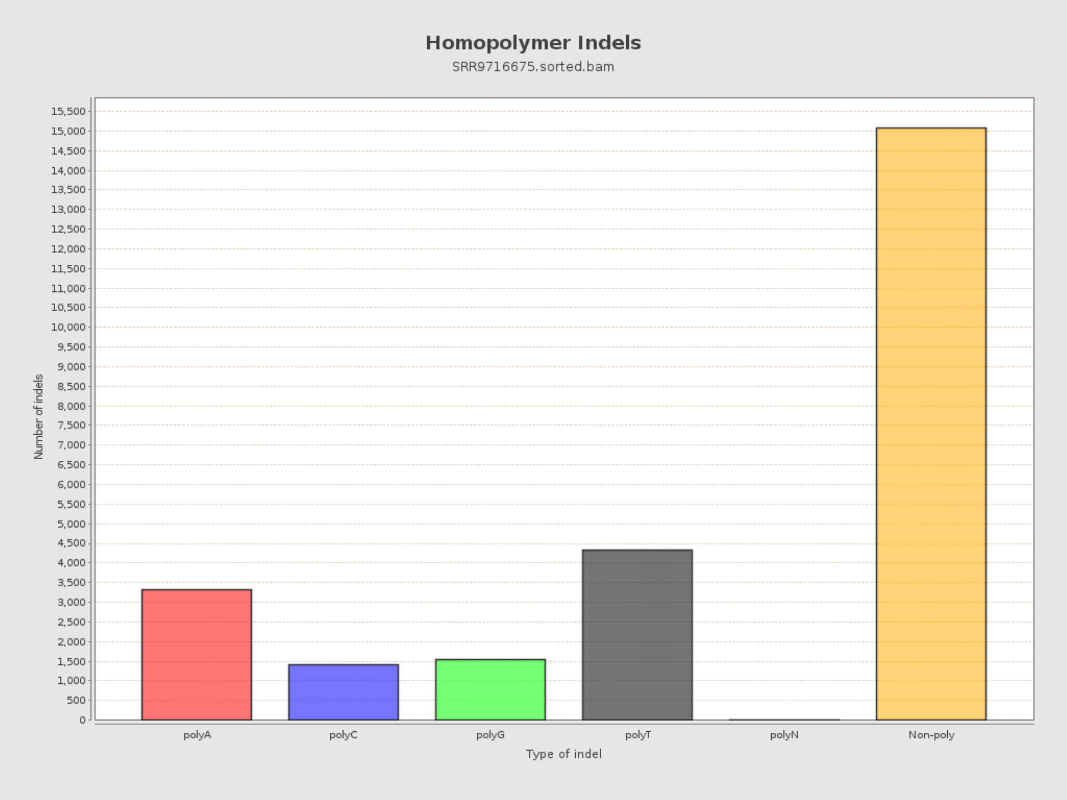
9. Results : Mapped Reads GC-content Distribution



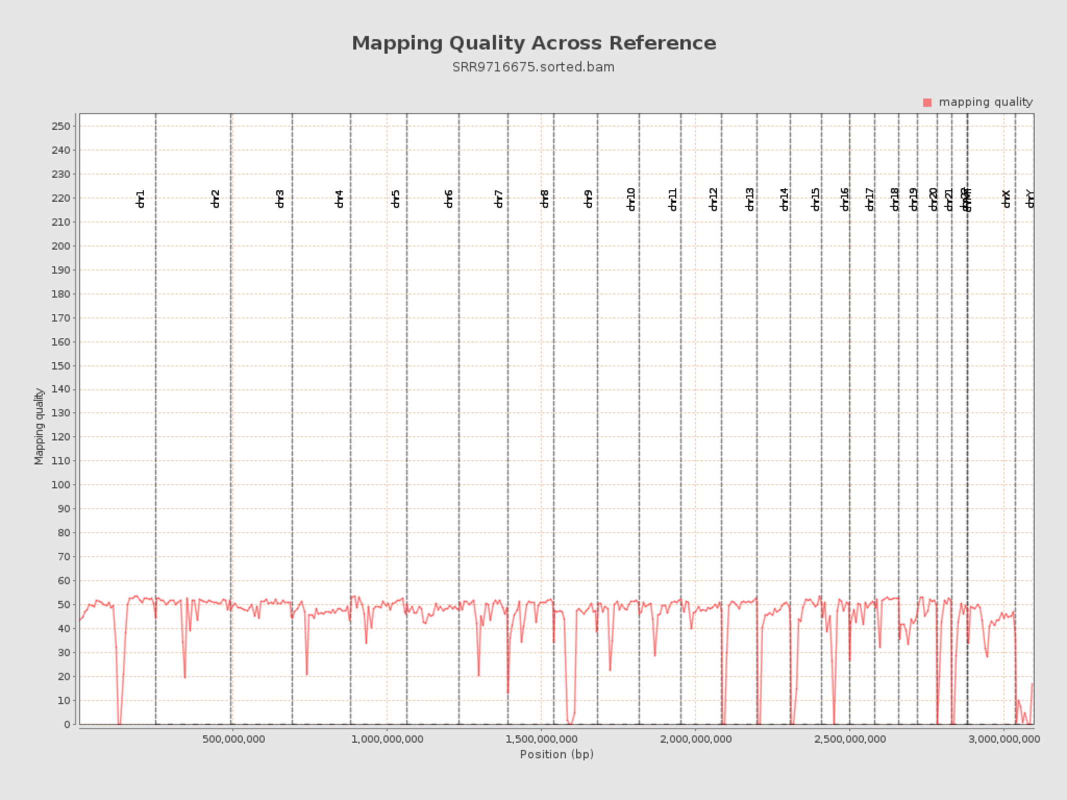
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram