Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 15:50:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716867.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_SRR9716867 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716867.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 15:49:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716867.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,854,240
Mapped reads	1,559,069 / 84.08%
Unmapped reads	295,171 / 15.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,407 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	47,039 / 2.54%
Duplication rate	2.22%
Clipped reads	1,560,148 / 84.14%

2.2. ACGT Content

Number/percentage of A's	21,838,517 / 24.54%
Number/percentage of C's	17,729,291 / 19.92%
Number/percentage of T's	27,548,313 / 30.95%
Number/percentage of G's	21,885,959 / 24.59%
Number/percentage of N's	1,317 / 0%
GC Percentage	44.51%

2.3. Coverage

Mean	0.0288

Standard Deviation	0.2438

2.4. Mapping Quality

Mean Mapping Quality	43.34

2.5. Mismatches and indels

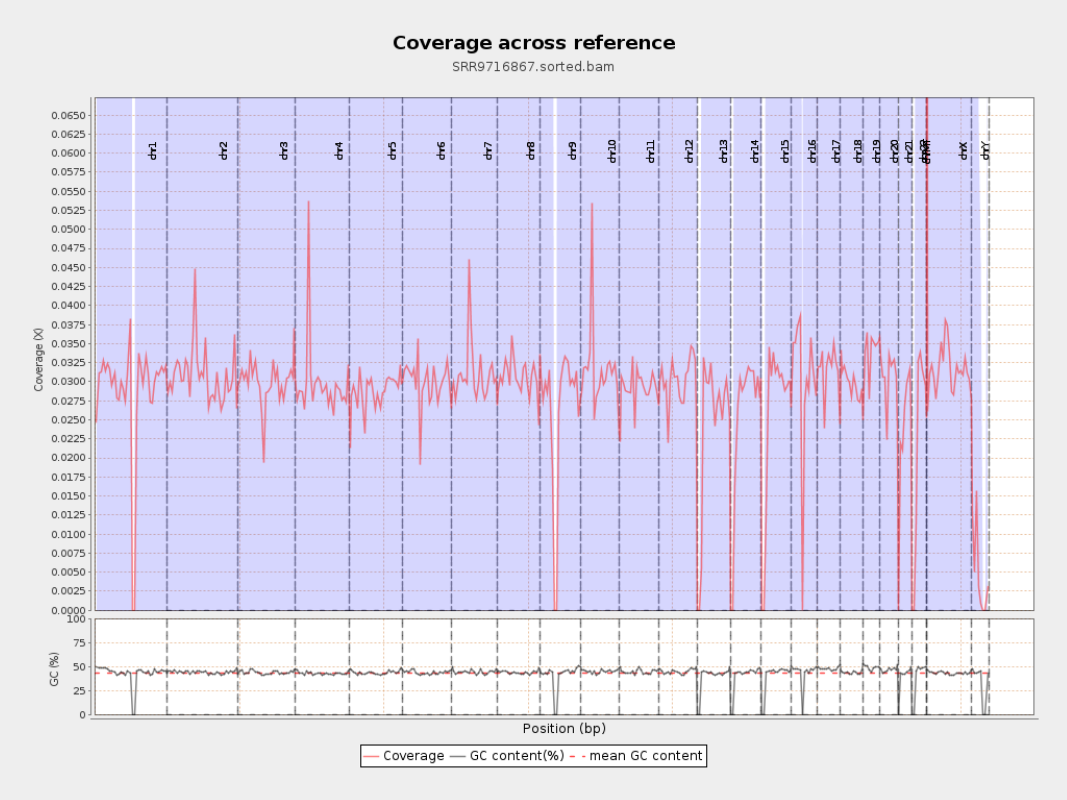
General error rate	0.54%
Mismatches	466,832
Insertions	7,539
Mapped reads with at least one insertion	0.48%
Deletions	17,520
Mapped reads with at least one deletion	1.11%
Homopolymer indels	38.98%

2.6. Chromosome stats

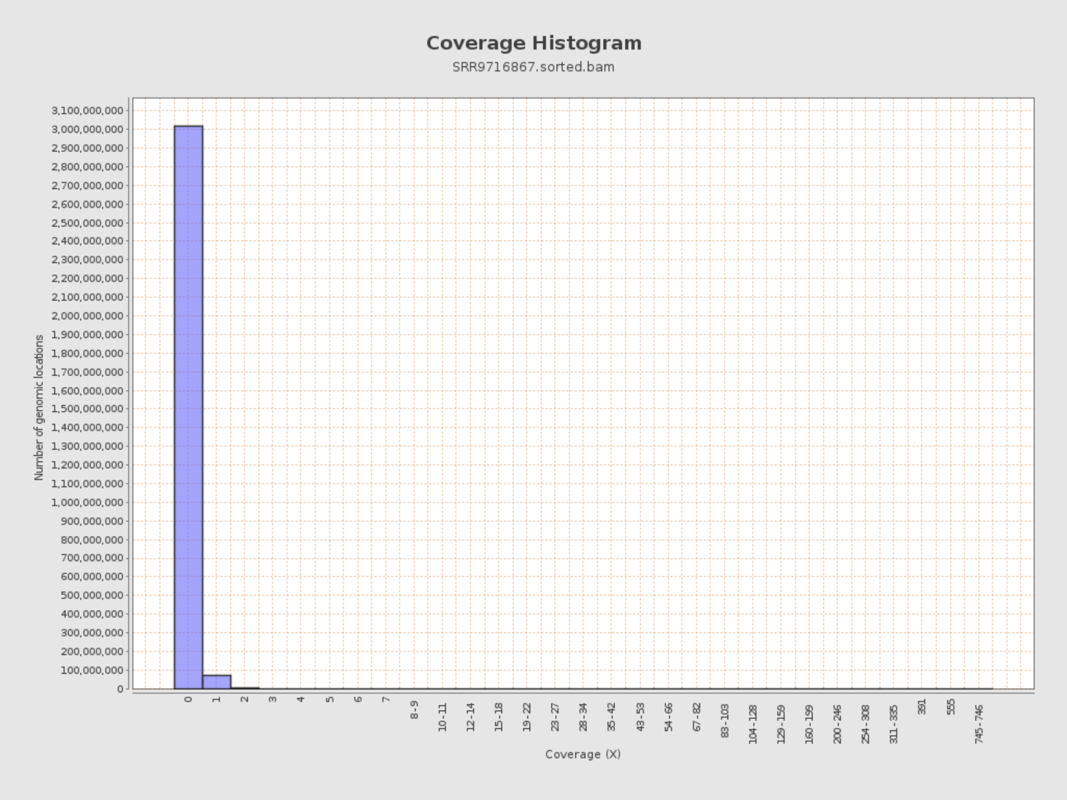
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7130361	0.0286	0.3125
chr2	243199373	7501476	0.0308	0.3786
chr3	198022430	5912770	0.0299	0.1899
chr4	191154276	5701079	0.0298	0.2132
chr5	180915260	5243588	0.029	0.1851
chr6	171115067	5121602	0.0299	0.2122
chr7	159138663	4947450	0.0311	0.3152

chr8	146364022	4481016	0.0306	0.2267
chr9	141213431	3679441	0.0261	0.2074
chr10	135534747	4287868	0.0316	0.281
chr11	135006516	3971218	0.0294	0.2202
chr12	133851895	4038574	0.0302	0.1916
chr13	115169878	2762873	0.024	0.169
chr14	107349540	2696014	0.0251	0.1784
chr15	102531392	2599485	0.0254	0.1782
chr16	90354753	2679837	0.0297	0.2019
chr17	81195210	2557479	0.0315	0.2046
chr18	78077248	2329908	0.0298	0.3268
chr19	59128983	1999133	0.0338	0.2841
chr20	63025520	1914382	0.0304	0.1949
chr21	48129895	1143596	0.0238	0.1889
chr22	51304566	1127667	0.022	0.164
chrMT	16571	7518	0.4537	0.7409
chrX	155270560	4916036	0.0317	0.2116
chrY	59373566	281127	0.0047	0.1231

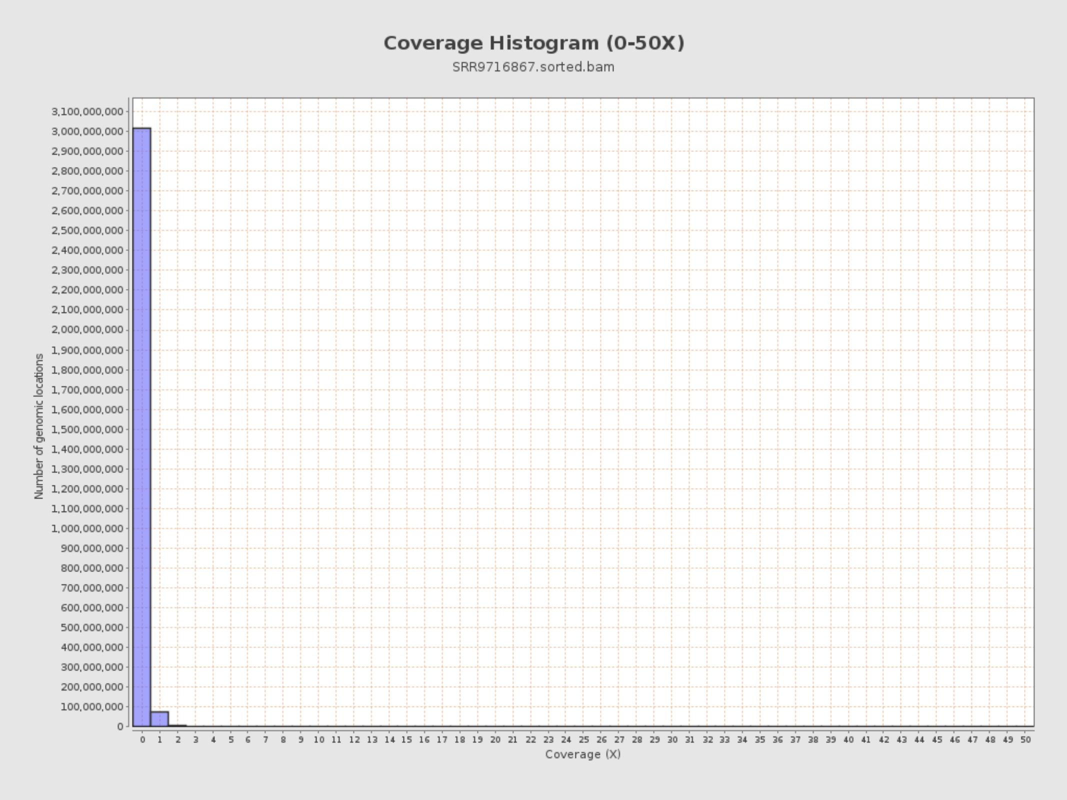
3. Results : Coverage across reference



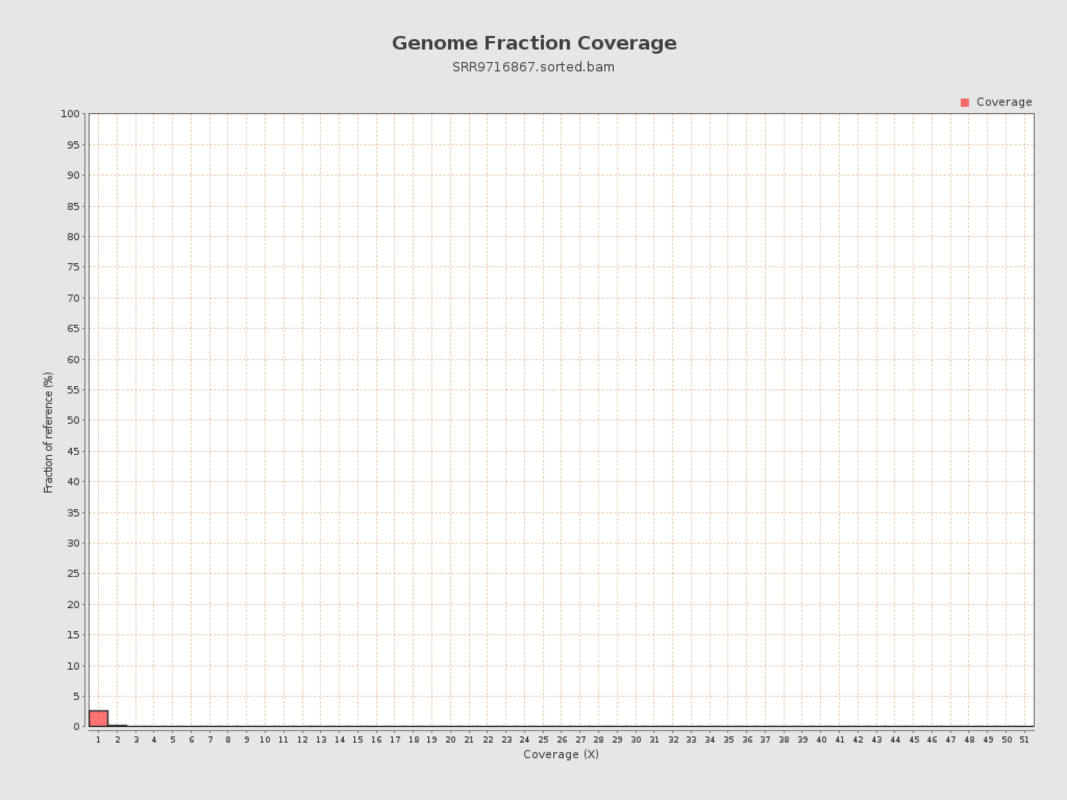
4. Results : Coverage Histogram



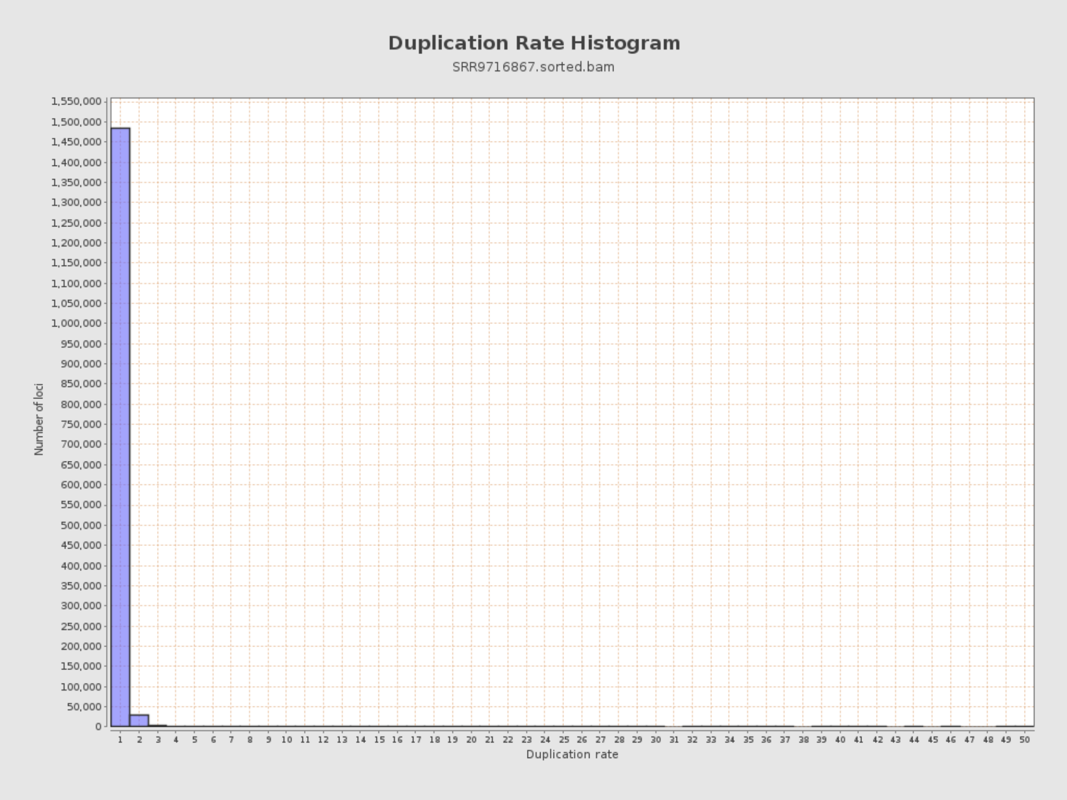
5. Results : Coverage Histogram (0-50X)



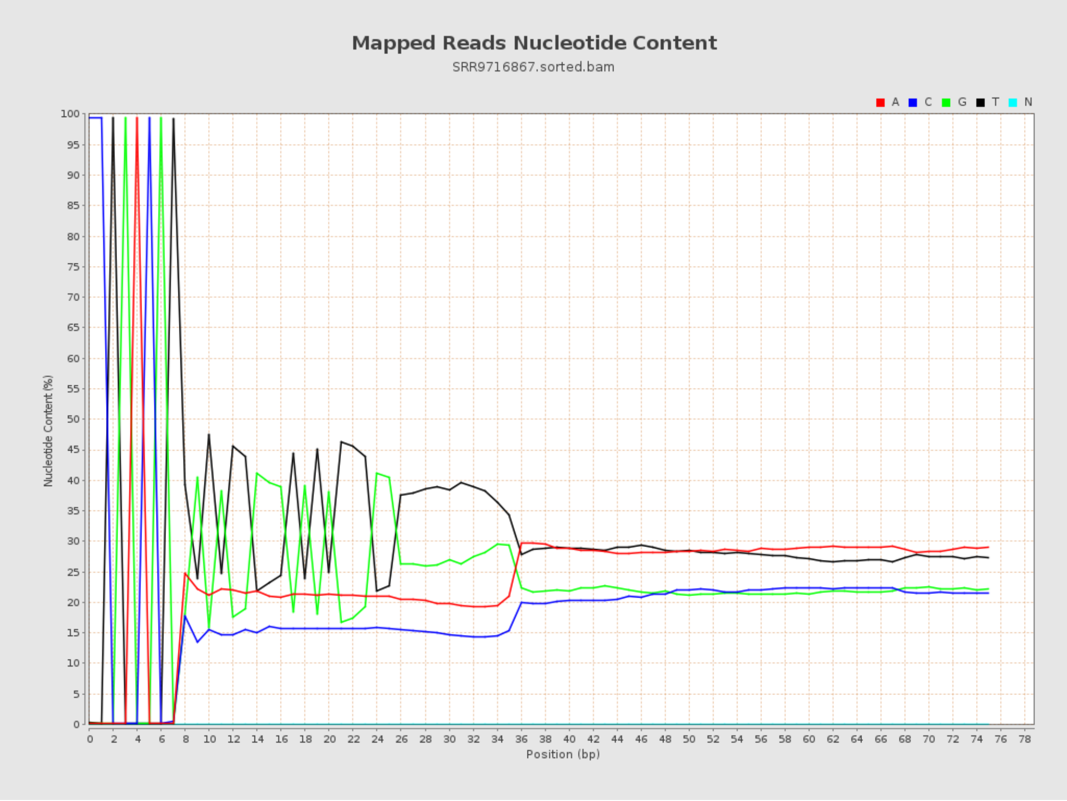
6. Results : Genome Fraction Coverage



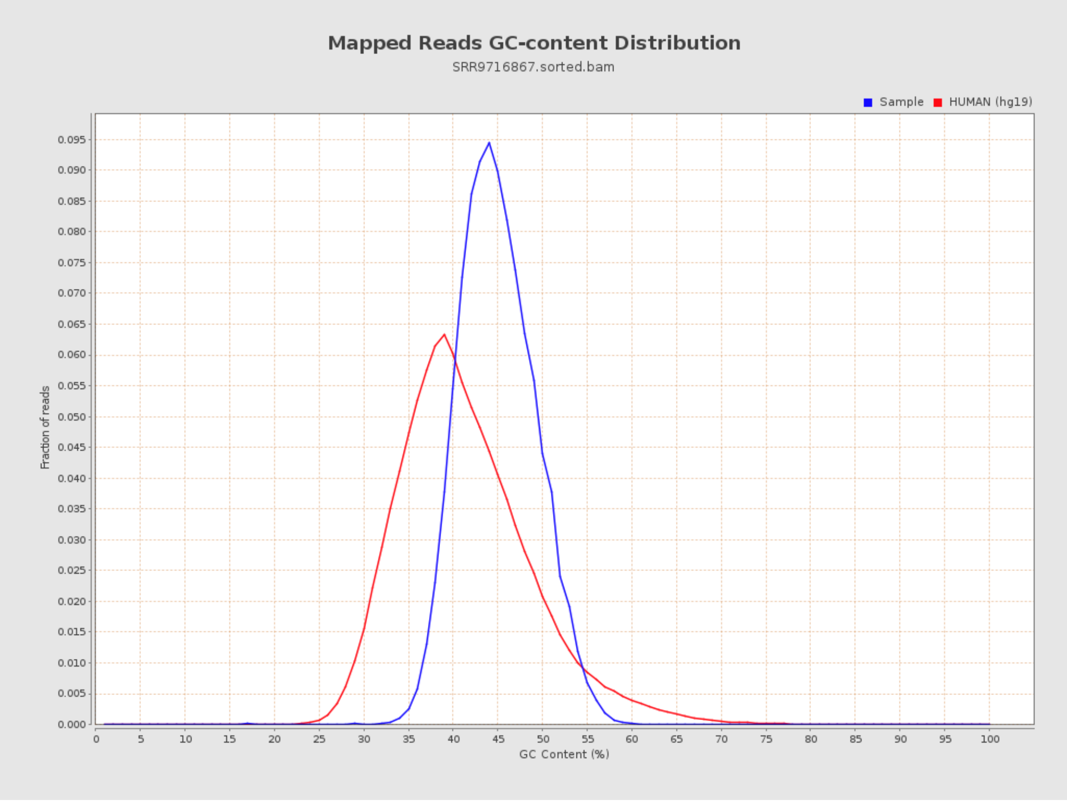
7. Results : Duplication Rate Histogram



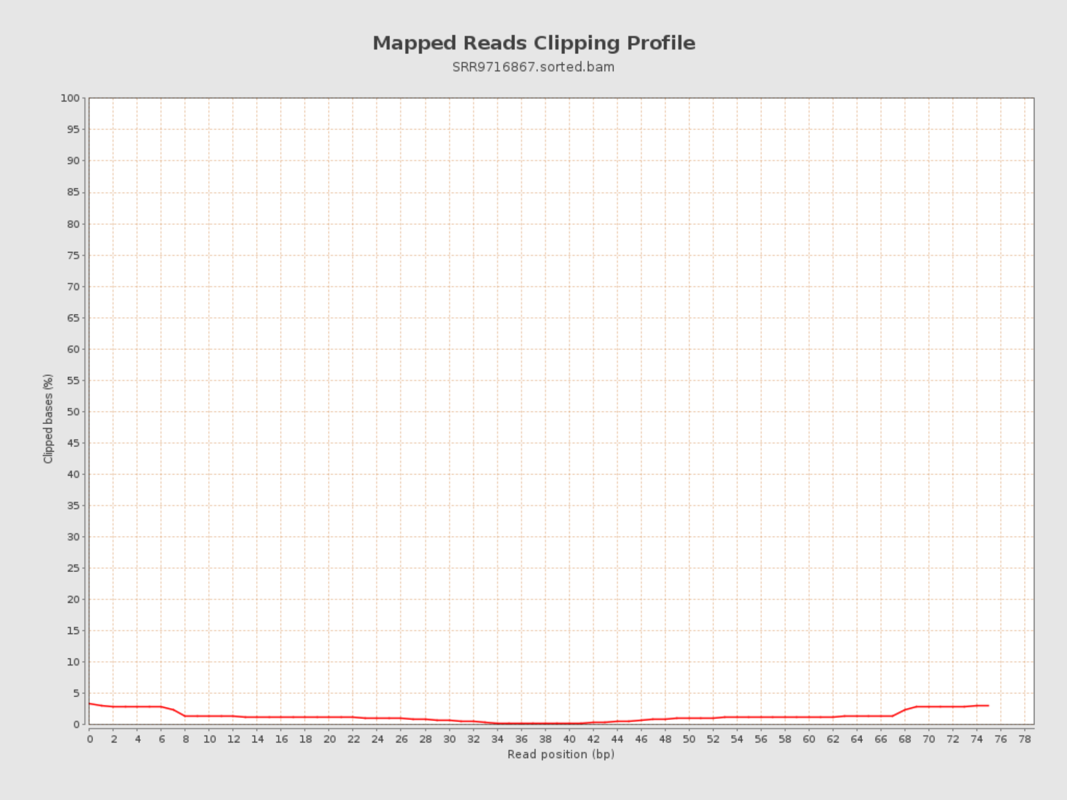
8. Results : Mapped Reads Nucleotide Content



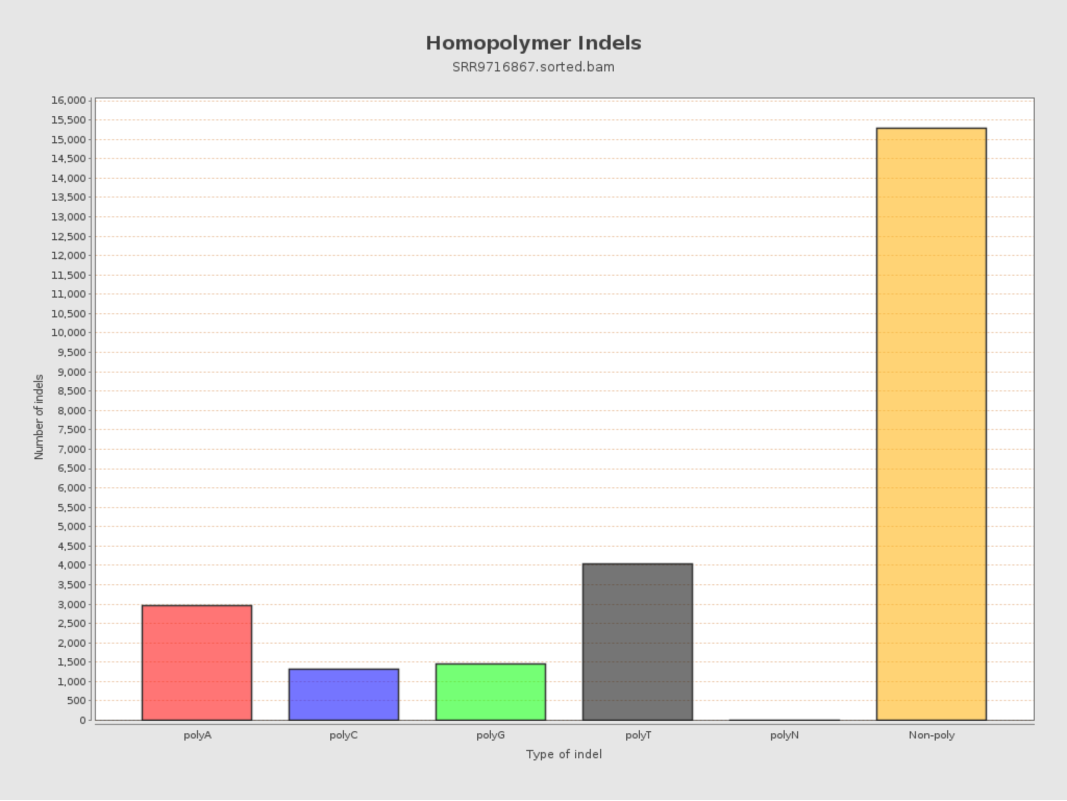
9. Results : Mapped Reads GC-content Distribution



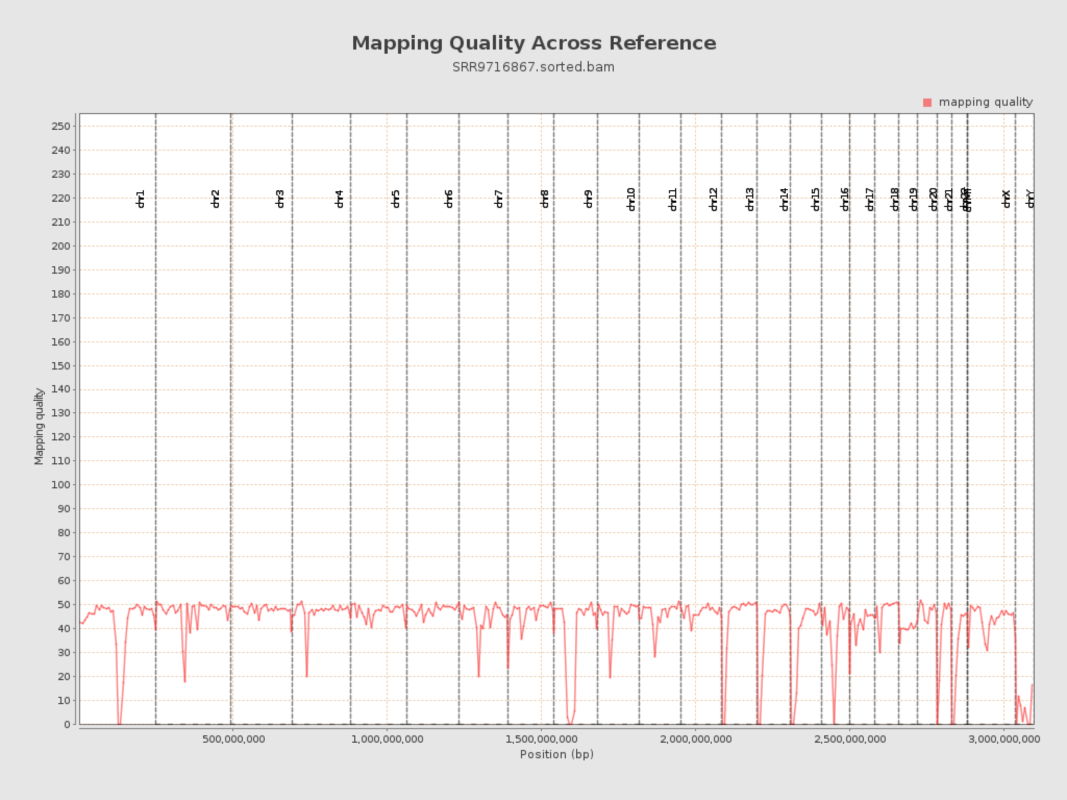
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram