Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 04:40:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716670.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_SRR9716670 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716670.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 04:40:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716670.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,691,016
Mapped reads	1,554,054 / 91.9%
Unmapped reads	136,962 / 8.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,749 / 0.52%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	65,242 / 3.86%
Duplication rate	3.25%
Clipped reads	1,558,038 / 92.14%

2.2. ACGT Content

Number/percentage of A's	22,009,572 / 24.16%
Number/percentage of C's	17,414,233 / 19.12%
Number/percentage of T's	28,769,062 / 31.58%
Number/percentage of G's	22,893,038 / 25.13%
Number/percentage of N's	687 / 0%
GC Percentage	44.25%

2.3. Coverage

Mean	0.0294

Standard Deviation	0.2656

2.4. Mapping Quality

Mean Mapping Quality	45.06

2.5. Mismatches and indels

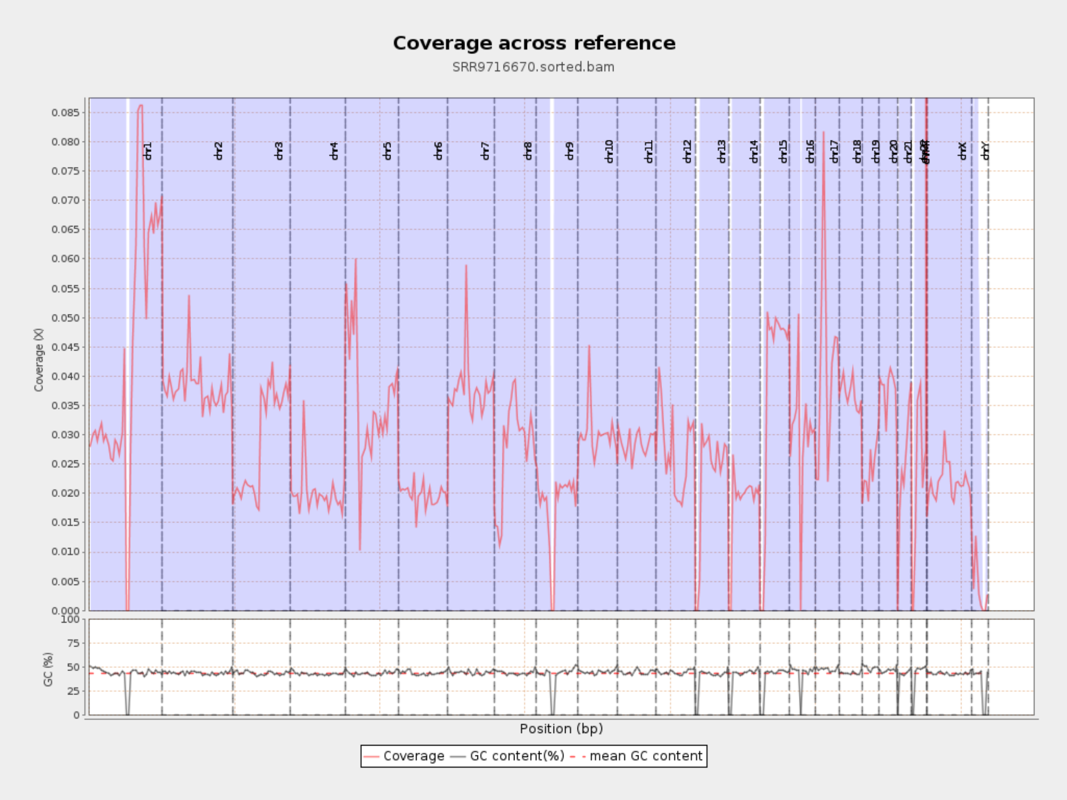
General error rate	0.51%
Mismatches	455,828
Insertions	6,224
Mapped reads with at least one insertion	0.4%
Deletions	16,225
Mapped reads with at least one deletion	1.04%
Homopolymer indels	43.61%

2.6. Chromosome stats

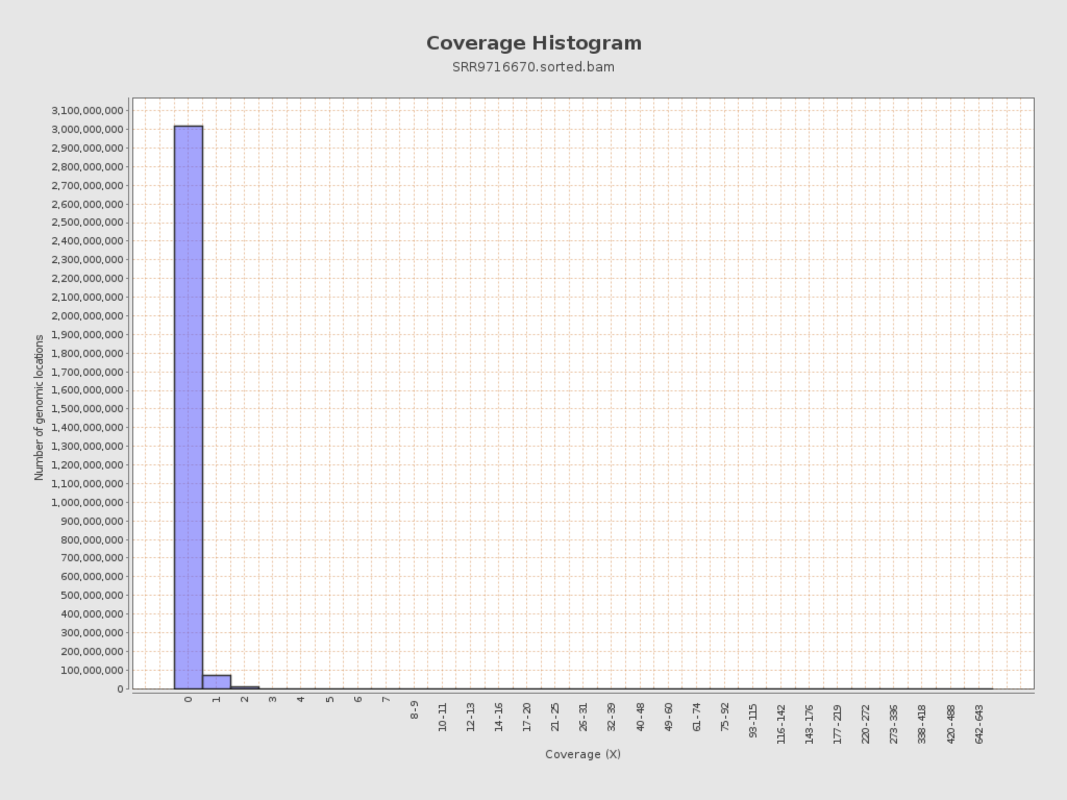
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10828916	0.0434	0.4275
chr2	243199373	9312138	0.0383	0.37
chr3	198022430	5729822	0.0289	0.1871
chr4	191154276	3804562	0.0199	0.1787
chr5	180915260	6509108	0.036	0.2097
chr6	171115067	3381690	0.0198	0.1743
chr7	159138663	6061071	0.0381	0.4022

chr8	146364022	4082321	0.0279	0.24
chr9	141213431	2495764	0.0177	0.1938
chr10	135534747	4101473	0.0303	0.2424
chr11	135006516	3853596	0.0285	0.2472
chr12	133851895	3631851	0.0271	0.1829
chr13	115169878	2618903	0.0227	0.1672
chr14	107349540	1937523	0.018	0.1562
chr15	102531392	3971626	0.0387	0.2184
chr16	90354753	2710067	0.03	0.2011
chr17	81195210	3453152	0.0425	0.2454
chr18	78077248	2898096	0.0371	0.4459
chr19	59128983	1428685	0.0242	0.3181
chr20	63025520	2380874	0.0378	0.2185
chr21	48129895	1179468	0.0245	0.1865
chr22	51304566	1090832	0.0213	0.1608
chrMT	16571	37557	2.2664	2.0667
chrX	155270560	3397052	0.0219	0.1839
chrY	59373566	216078	0.0036	0.1065

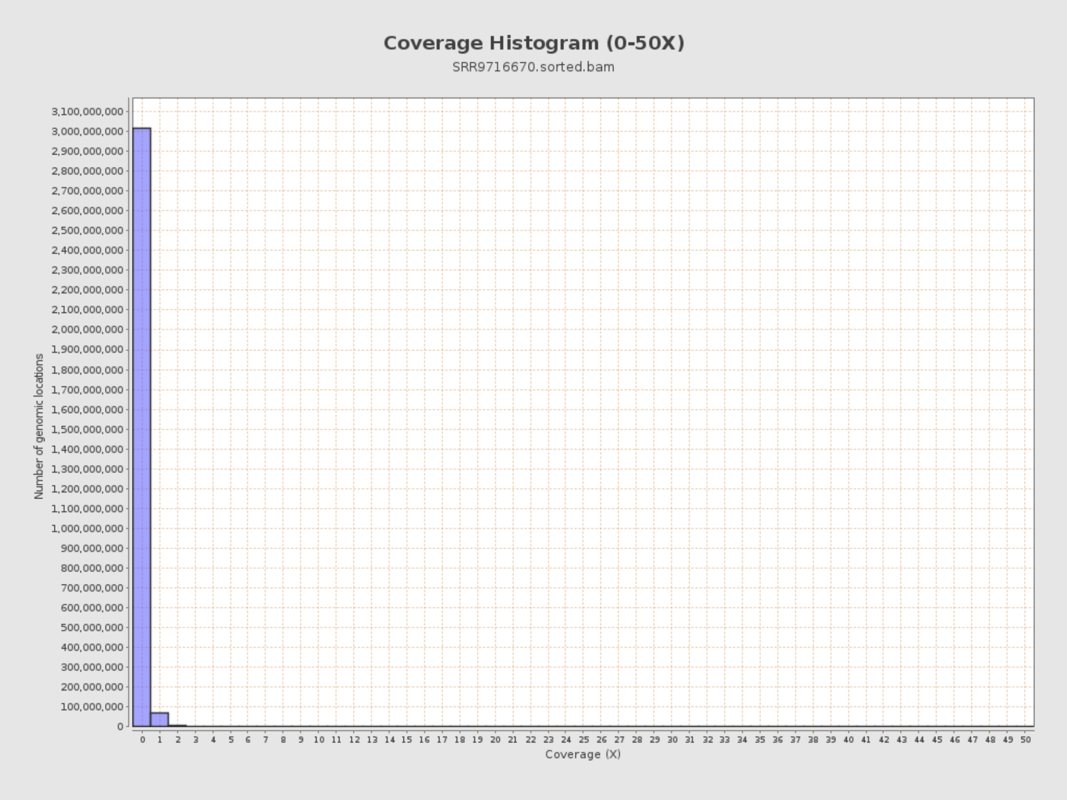
3. Results : Coverage across reference



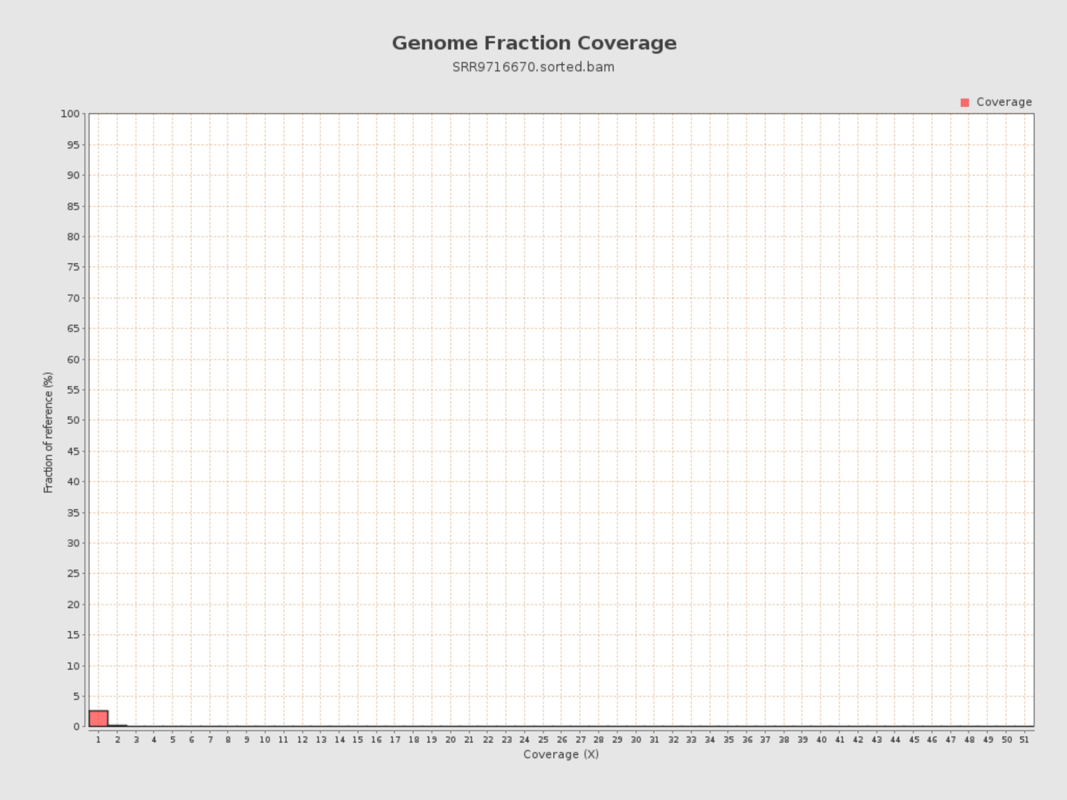
4. Results : Coverage Histogram



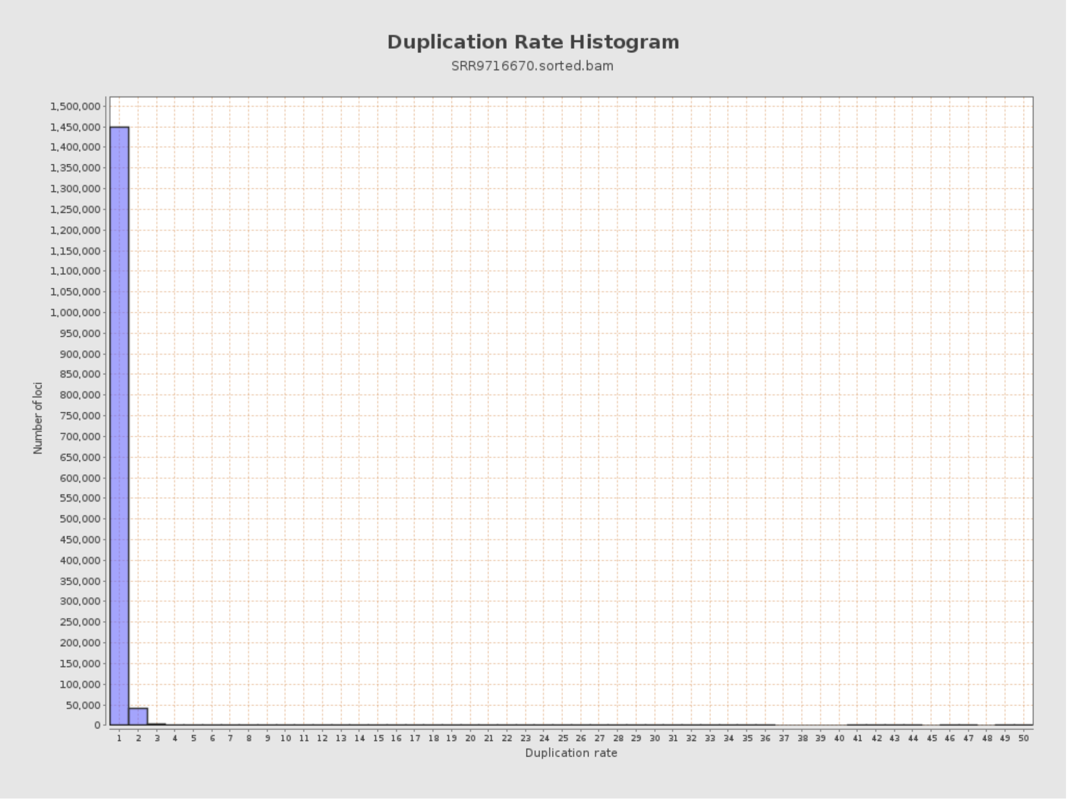
5. Results : Coverage Histogram (0-50X)



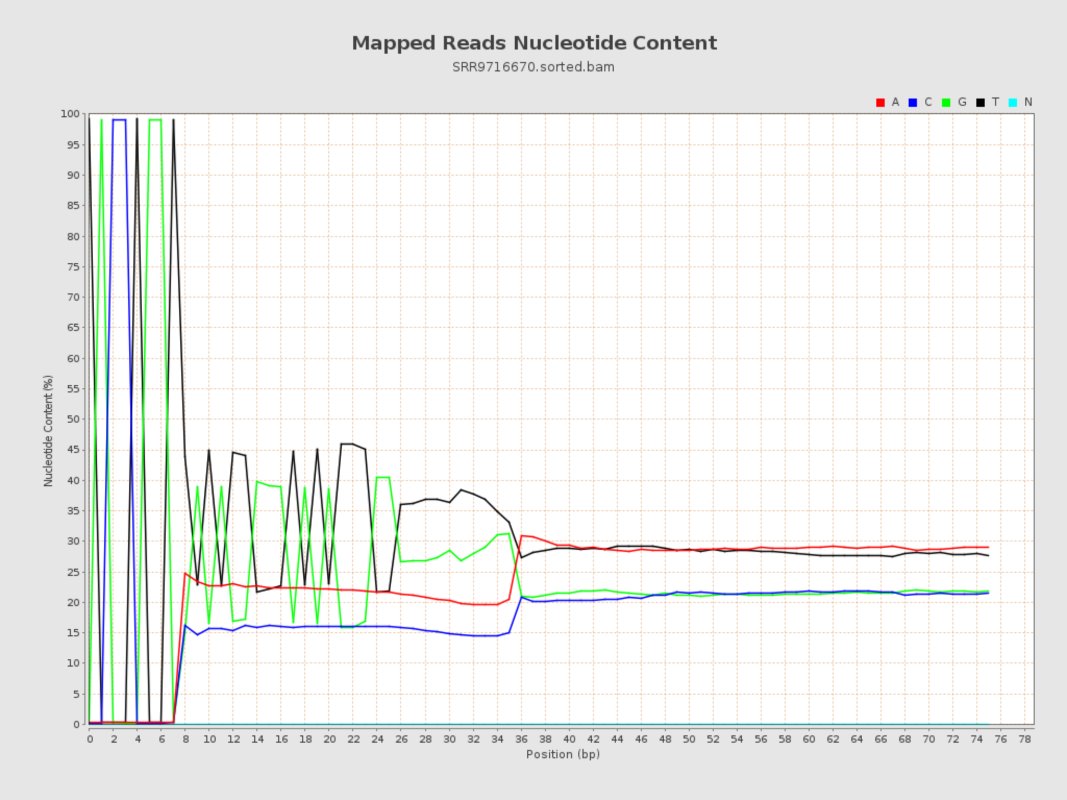
6. Results : Genome Fraction Coverage



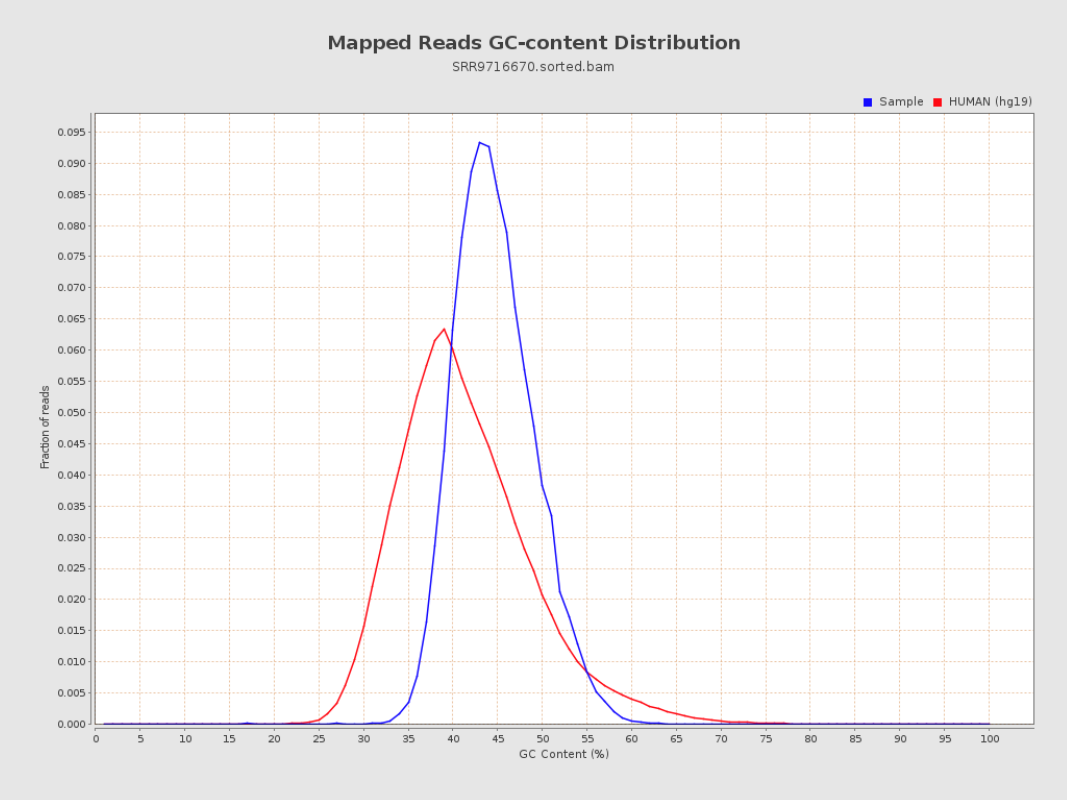
7. Results : Duplication Rate Histogram



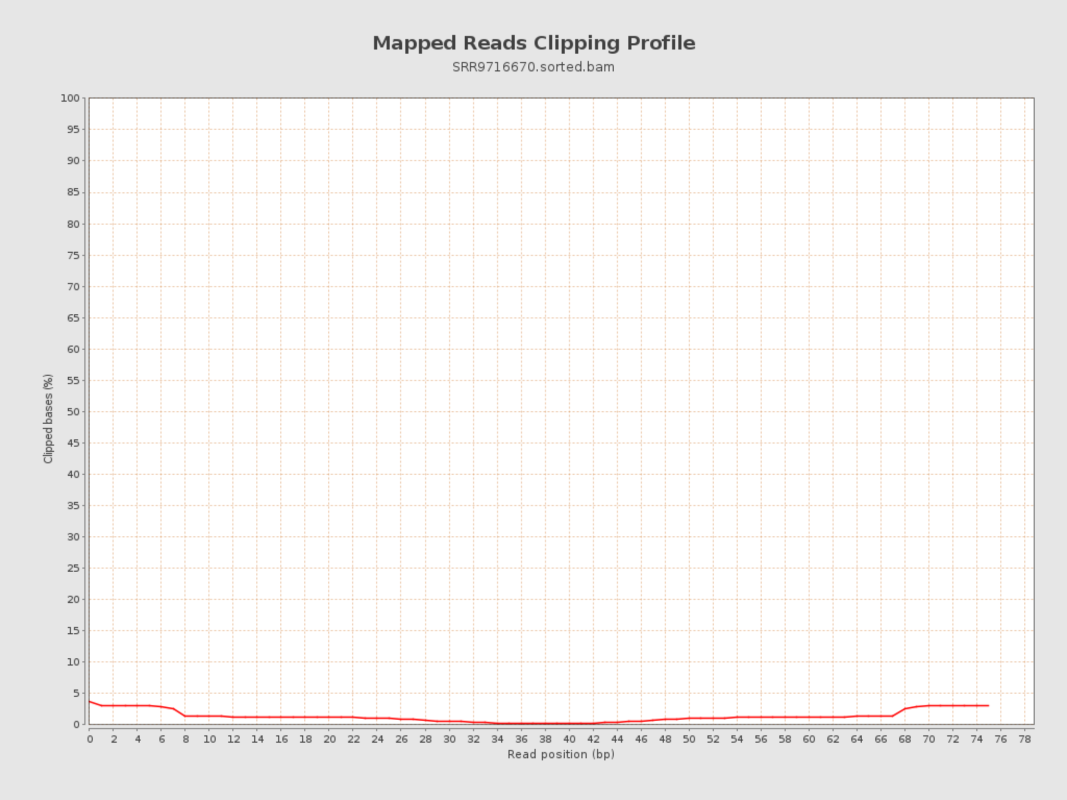
8. Results : Mapped Reads Nucleotide Content



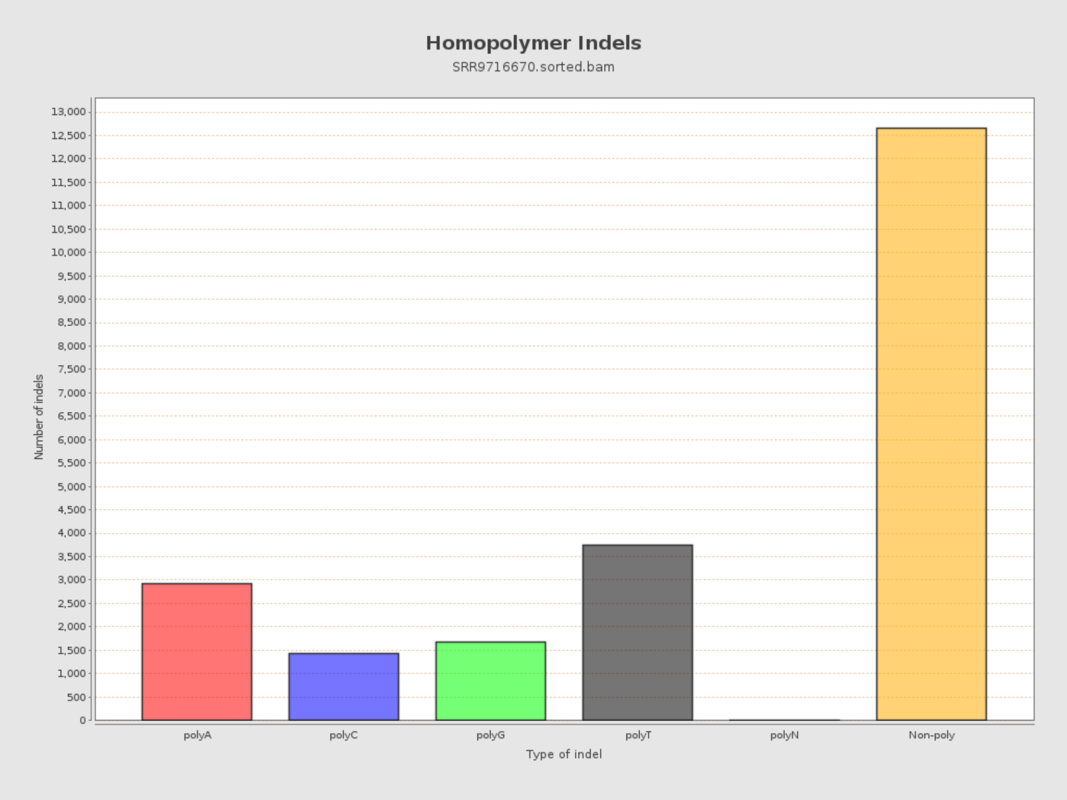
9. Results : Mapped Reads GC-content Distribution



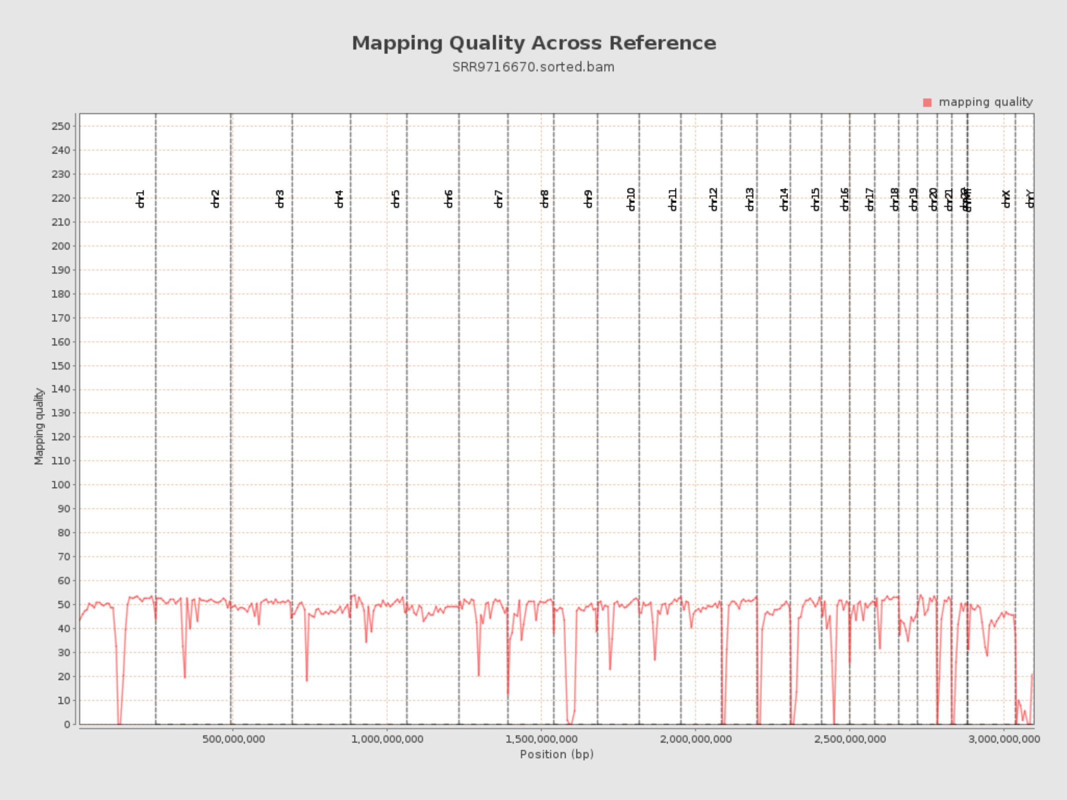
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram