Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 04:32:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716669.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_SRR9716669 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716669.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 04:32:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716669.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,714,545
Mapped reads	1,551,074 / 90.47%
Unmapped reads	163,471 / 9.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,711 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	53,101 / 3.1%
Duplication rate	2.55%
Clipped reads	1,557,090 / 90.82%

2.2. ACGT Content

Number/percentage of A's	22,139,619 / 24.65%
Number/percentage of C's	16,972,720 / 18.9%
Number/percentage of T's	28,656,028 / 31.91%
Number/percentage of G's	22,037,202 / 24.54%
Number/percentage of N's	631 / 0%
GC Percentage	43.44%

2.3. Coverage

Mean	0.029

Standard Deviation	0.2632

2.4. Mapping Quality

Mean Mapping Quality	44.49

2.5. Mismatches and indels

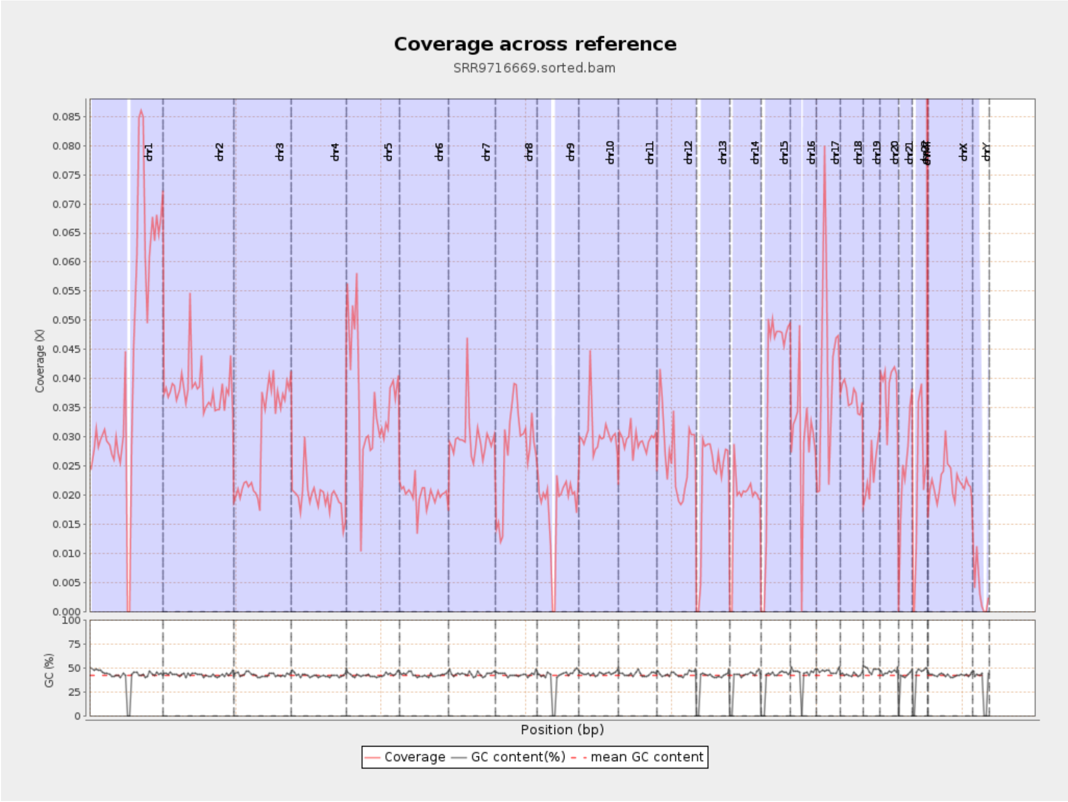
General error rate	0.51%
Mismatches	451,913
Insertions	5,003
Mapped reads with at least one insertion	0.32%
Deletions	16,216
Mapped reads with at least one deletion	1.04%
Homopolymer indels	42.6%

2.6. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10692982	0.0429	0.4367
chr2	243199373	9267764	0.0381	0.3952
chr3	198022430	5807480	0.0293	0.1863
chr4	191154276	3754202	0.0196	0.1653
chr5	180915260	6536515	0.0361	0.2069
chr6	171115067	3424990	0.02	0.1741
chr7	159138663	4734710	0.0298	0.3361

chr8	146364022	4067886	0.0278	0.2296
chr9	141213431	2505515	0.0177	0.2028
chr10	135534747	4123823	0.0304	0.2335
chr11	135006516	3948439	0.0292	0.2532
chr12	133851895	3605024	0.0269	0.1796
chr13	115169878	2576775	0.0224	0.162
chr14	107349540	1978911	0.0184	0.1557
chr15	102531392	3960594	0.0386	0.2166
chr16	90354753	2702292	0.0299	0.1993
chr17	81195210	3441647	0.0424	0.2434
chr18	78077248	2878584	0.0369	0.4389
chr19	59128983	1430303	0.0242	0.3225
chr20	63025520	2438117	0.0387	0.2136
chr21	48129895	1175928	0.0244	0.1778
chr22	51304566	1076544	0.021	0.1579
chrMT	16571	46706	2.8185	2.3456
chrX	155270560	3441067	0.0222	0.1877
chrY	59373566	215035	0.0036	0.0866

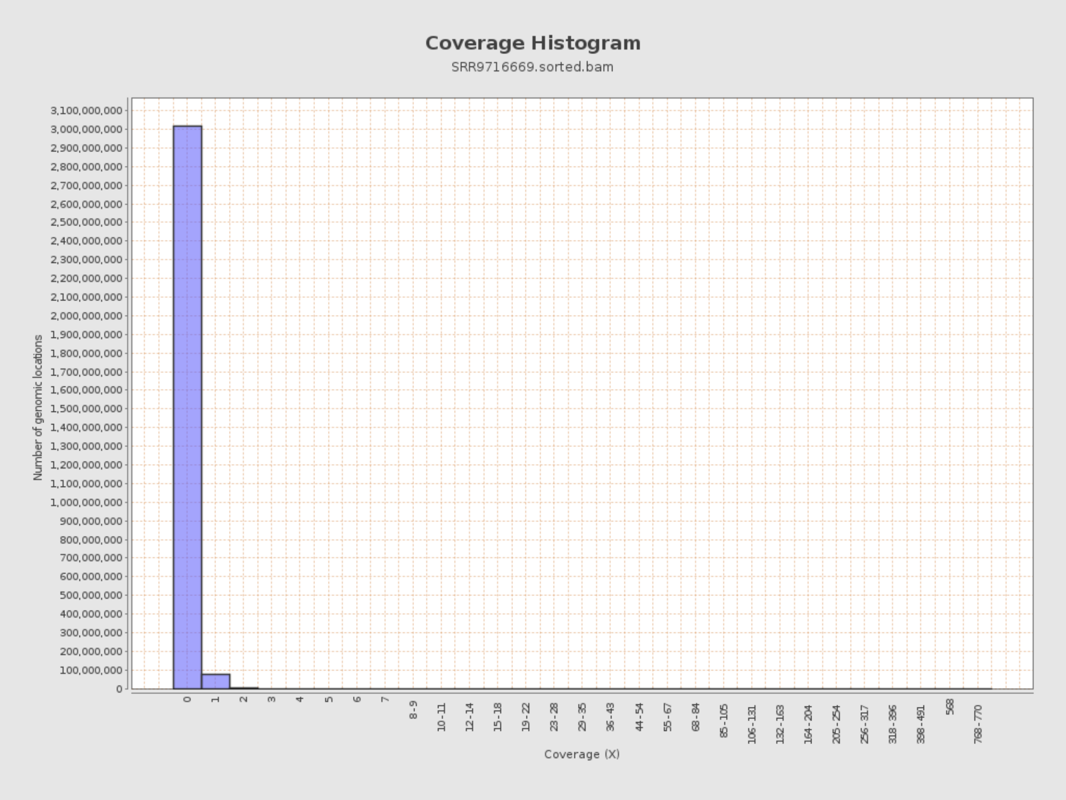
3. Results : Coverage across reference



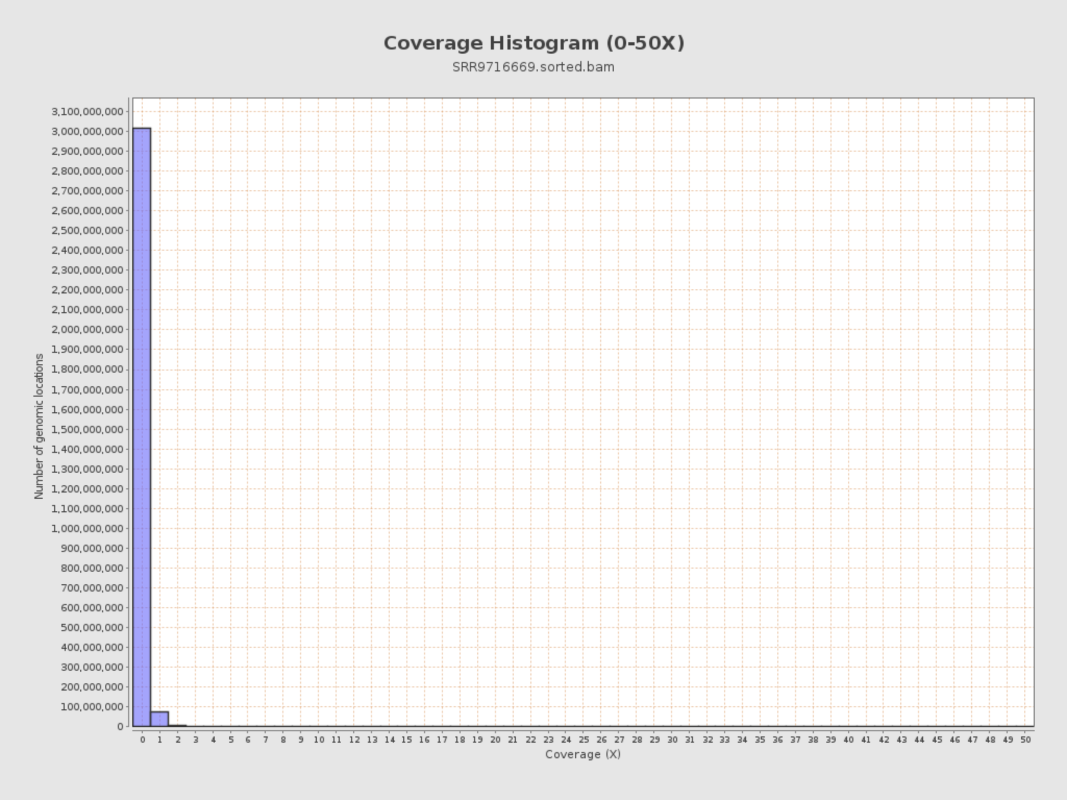
Coverage across reference

SRR9716669.sorted.bam

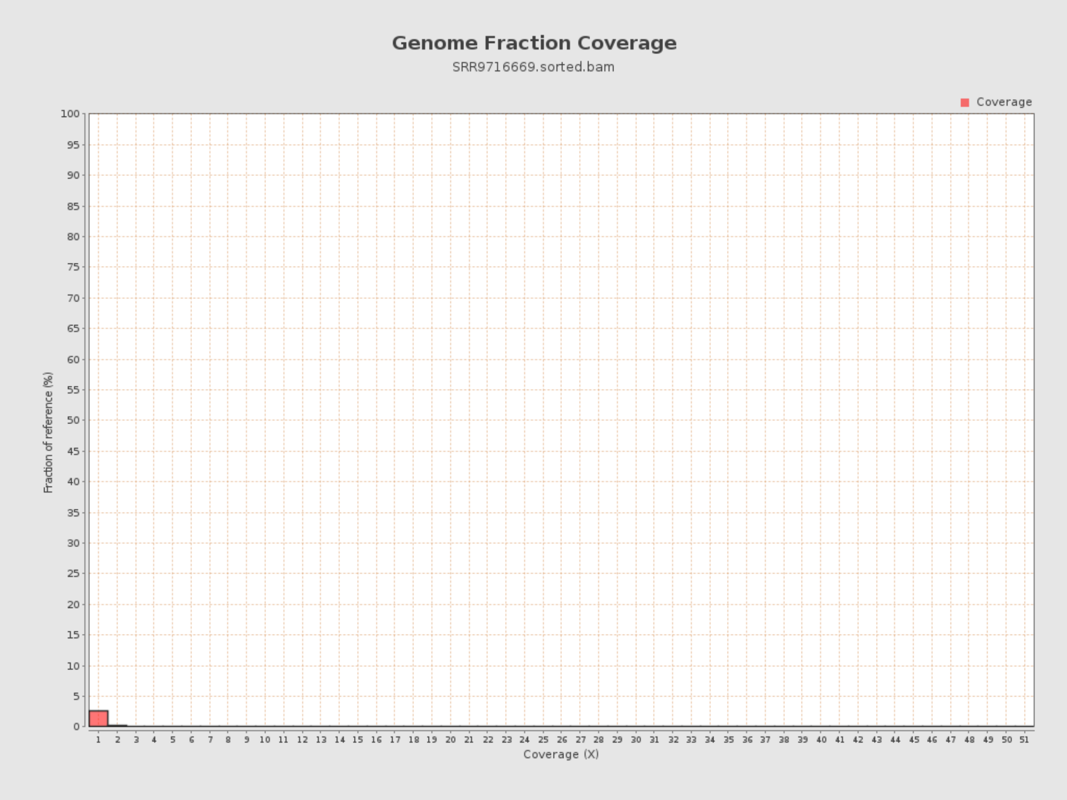
4. Results : Coverage Histogram



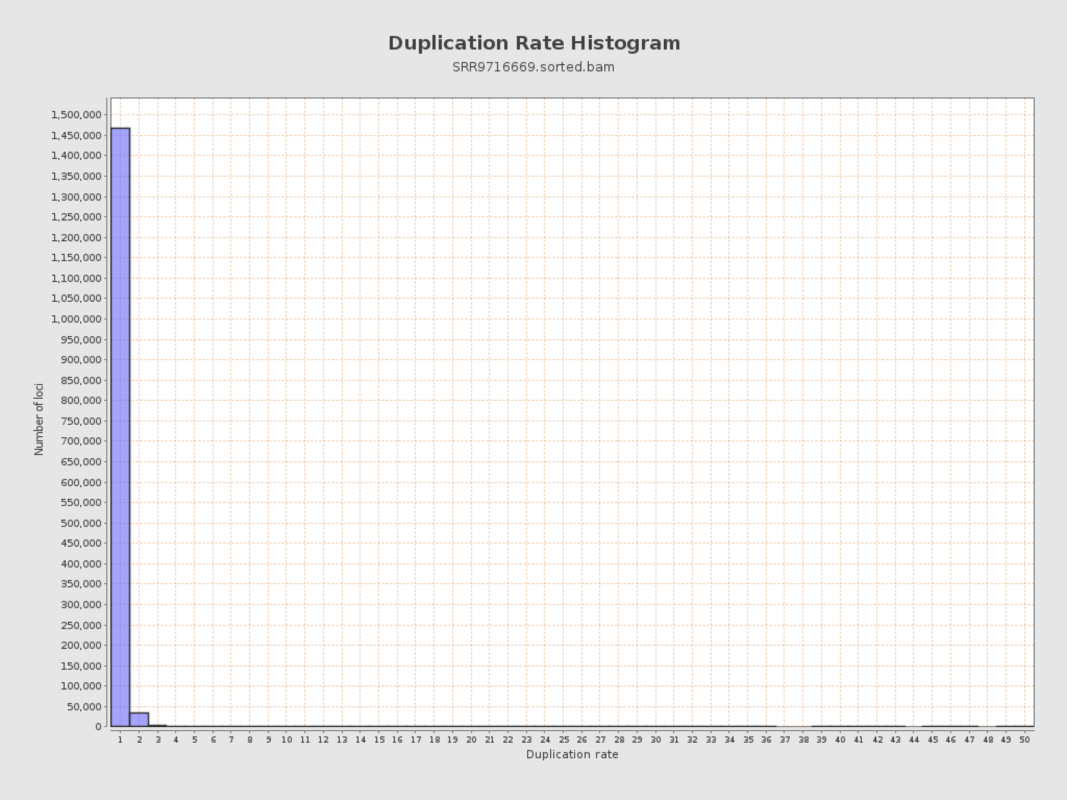
5. Results : Coverage Histogram (0-50X)



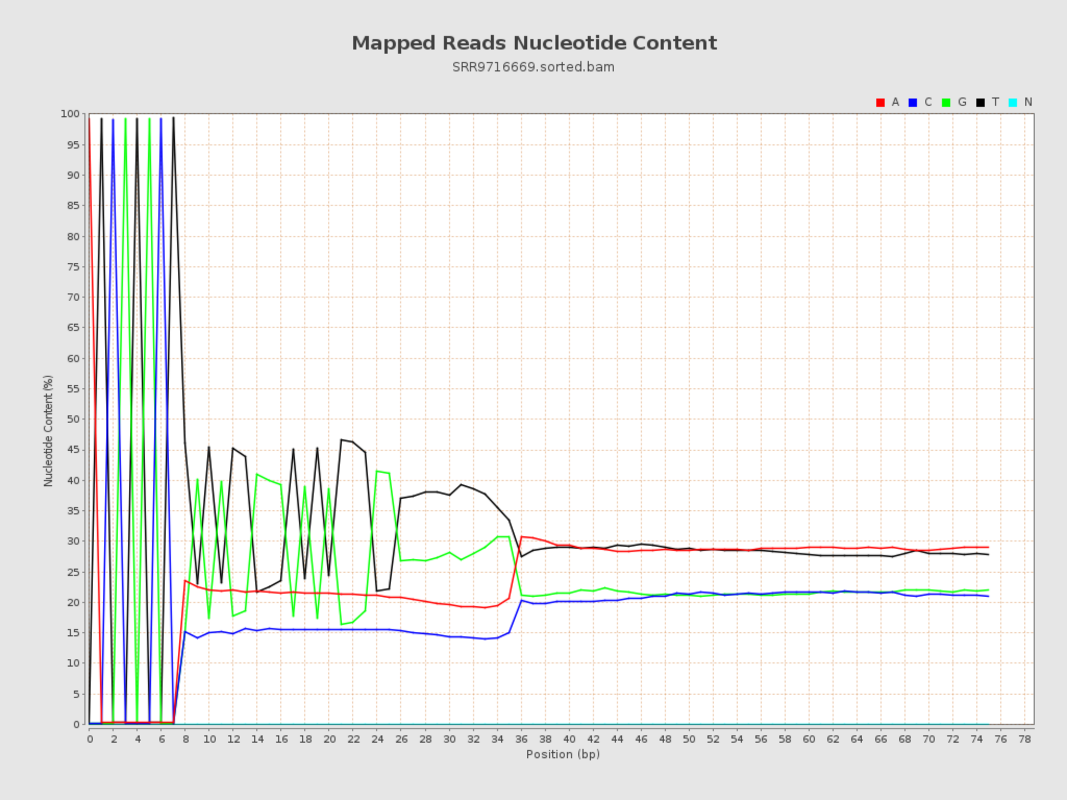
6. Results : Genome Fraction Coverage



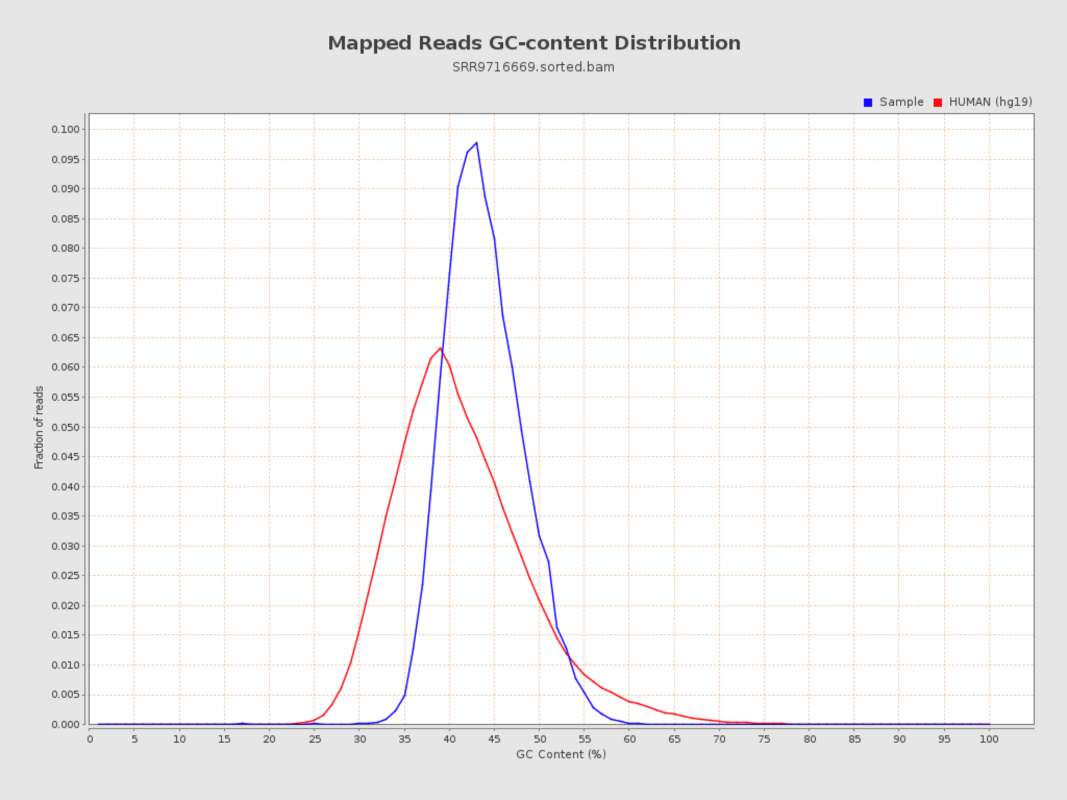
7. Results : Duplication Rate Histogram



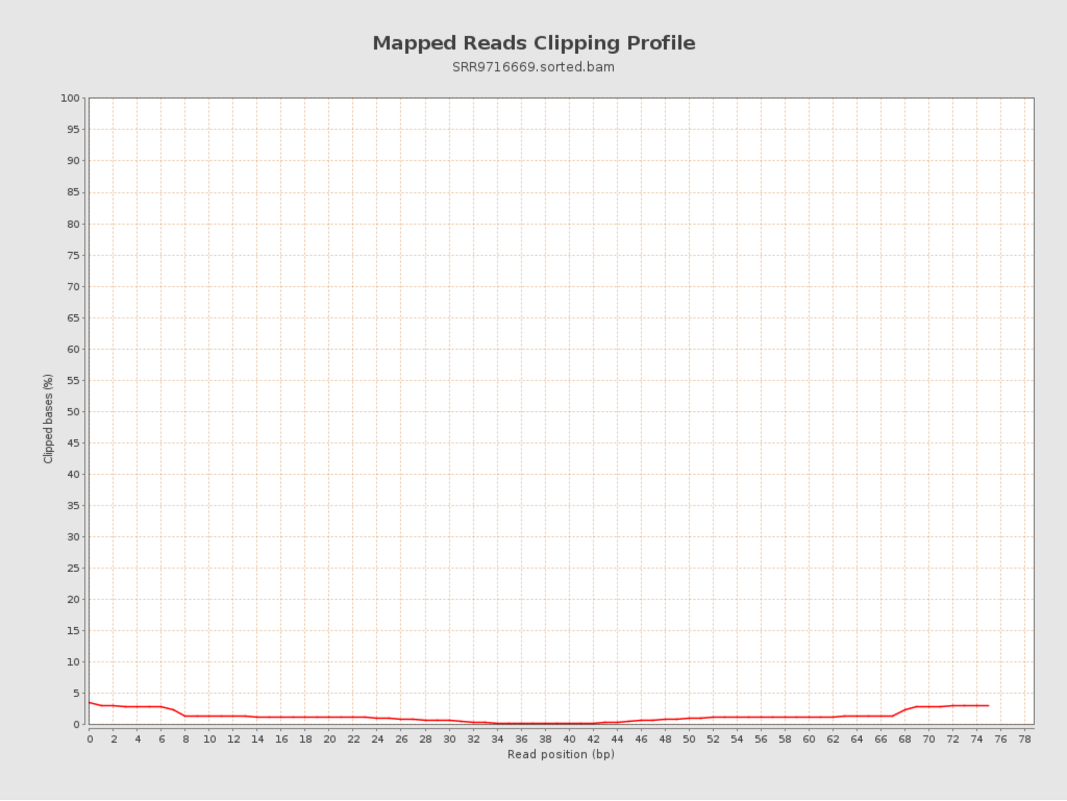
8. Results : Mapped Reads Nucleotide Content



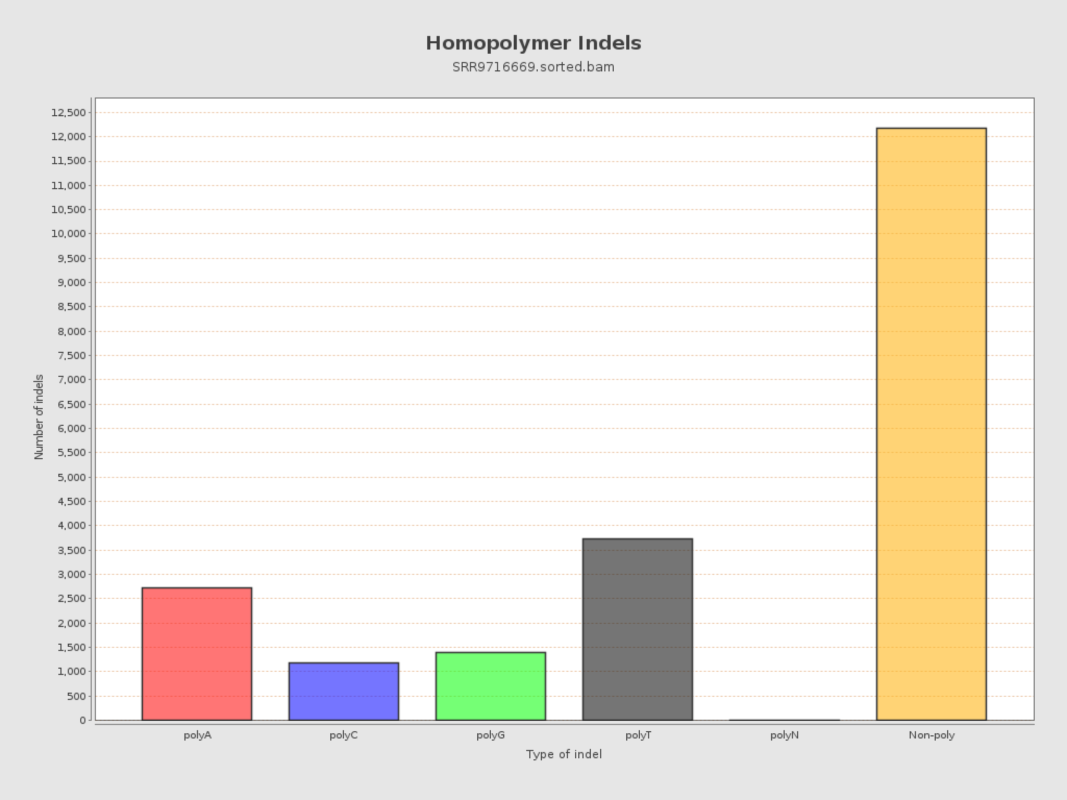
9. Results : Mapped Reads GC-content Distribution



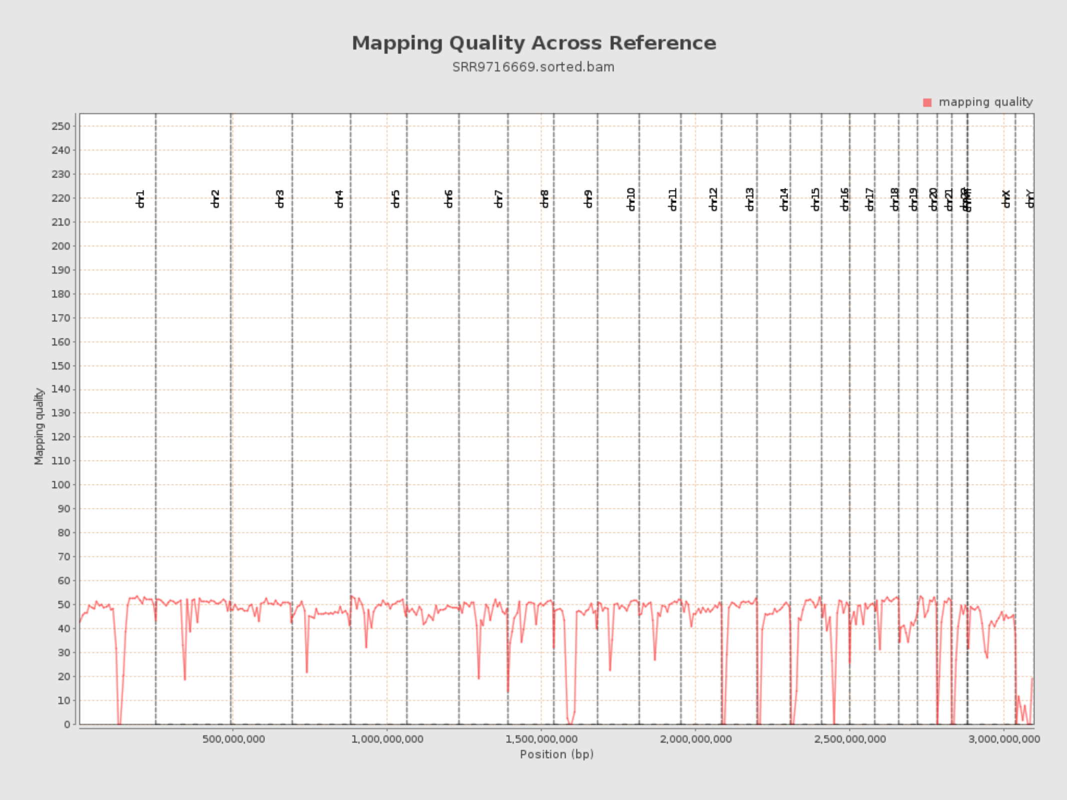
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram