Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 08:13:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008716.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_SRR6008716 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008716.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 08:13:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008716.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,918,921
Mapped reads	1,290,506 / 67.25%
Unmapped reads	628,415 / 32.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,128 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	41,313 / 2.15%
Duplication rate	2.43%
Clipped reads	685,207 / 35.71%

2.2. ACGT Content

Number/percentage of A's	25,246,350 / 30.22%
Number/percentage of C's	14,089,965 / 16.86%
Number/percentage of T's	24,970,399 / 29.89%
Number/percentage of G's	19,244,427 / 23.03%
Number/percentage of N's	2,040 / 0%
GC Percentage	39.9%

2.3. Coverage

Mean	0.027

Standard Deviation	0.2224

2.4. Mapping Quality

Mean Mapping Quality	46.75

2.5. Mismatches and indels

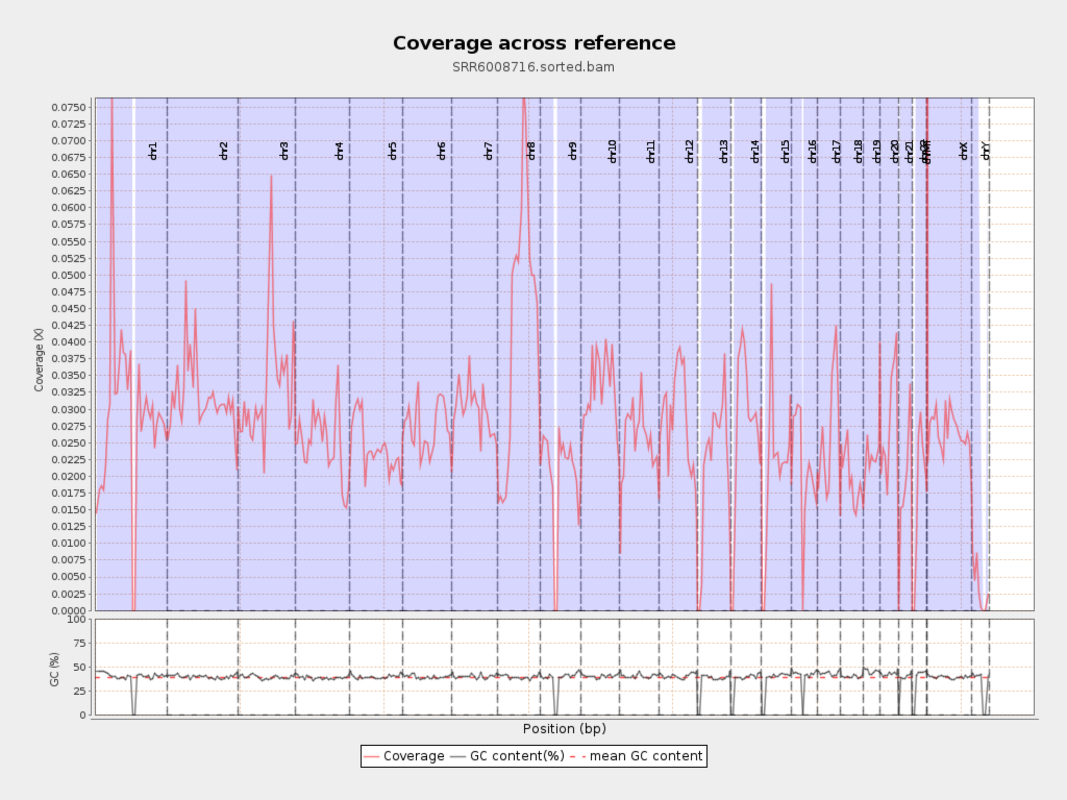
General error rate	0.98%
Mismatches	811,744
Insertions	6,521
Mapped reads with at least one insertion	0.5%
Deletions	26,742
Mapped reads with at least one deletion	2.05%
Homopolymer indels	48.7%

2.6. Chromosome stats

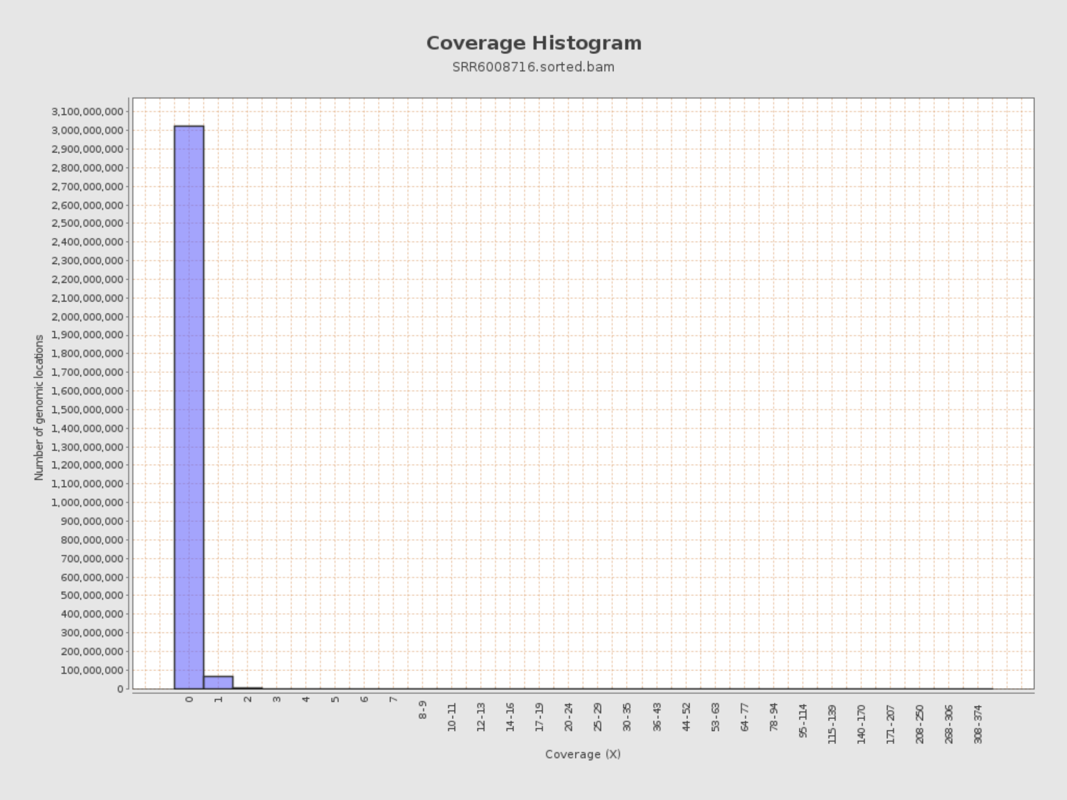
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7198990	0.0289	0.2786
chr2	243199373	7767659	0.0319	0.3019
chr3	198022430	6611526	0.0334	0.2062
chr4	191154276	4755246	0.0249	0.1789
chr5	180915260	4412326	0.0244	0.1745
chr6	171115067	4665871	0.0273	0.1989
chr7	159138663	4745388	0.0298	0.2721

chr8	146364022	6359229	0.0434	0.3293
chr9	141213431	2831023	0.02	0.1866
chr10	135534747	4444302	0.0328	0.2296
chr11	135006516	3456183	0.0256	0.2057
chr12	133851895	3854390	0.0288	0.1912
chr13	115169878	2524233	0.0219	0.1673
chr14	107349540	2910430	0.0271	0.1854
chr15	102531392	2154262	0.021	0.1657
chr16	90354753	1890811	0.0209	0.1694
chr17	81195210	2157152	0.0266	0.1927
chr18	78077248	1525238	0.0195	0.2788
chr19	59128983	1368091	0.0231	0.1979
chr20	63025520	1768291	0.0281	0.1893
chr21	48129895	927233	0.0193	0.1593
chr22	51304566	891036	0.0174	0.1457
chrMT	16571	21497	1.2973	1.478
chrX	155270560	4163466	0.0268	0.191
chrY	59373566	190614	0.0032	0.0723

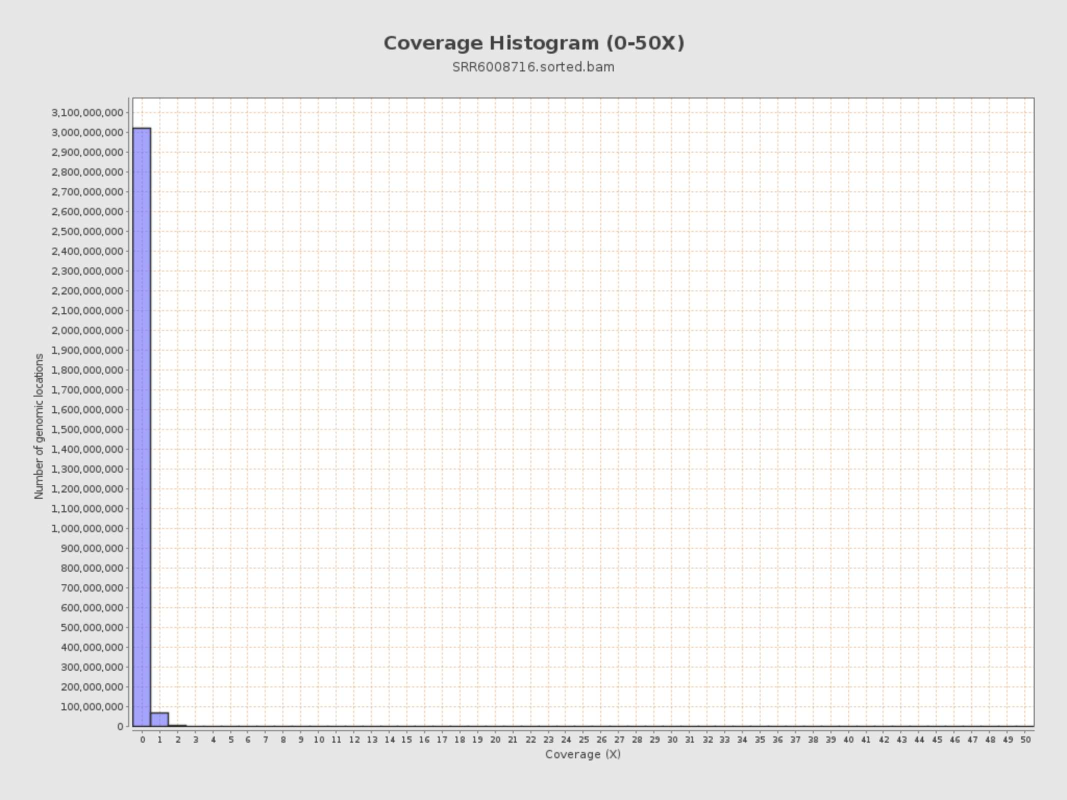
3. Results : Coverage across reference



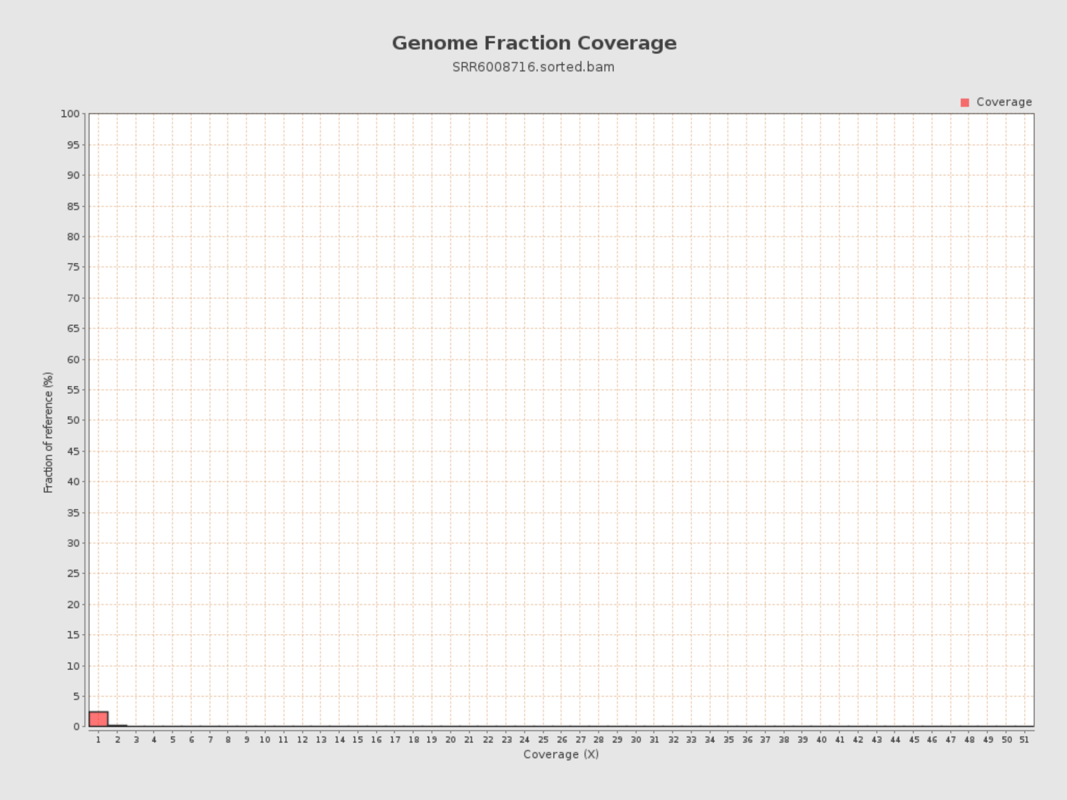
4. Results : Coverage Histogram



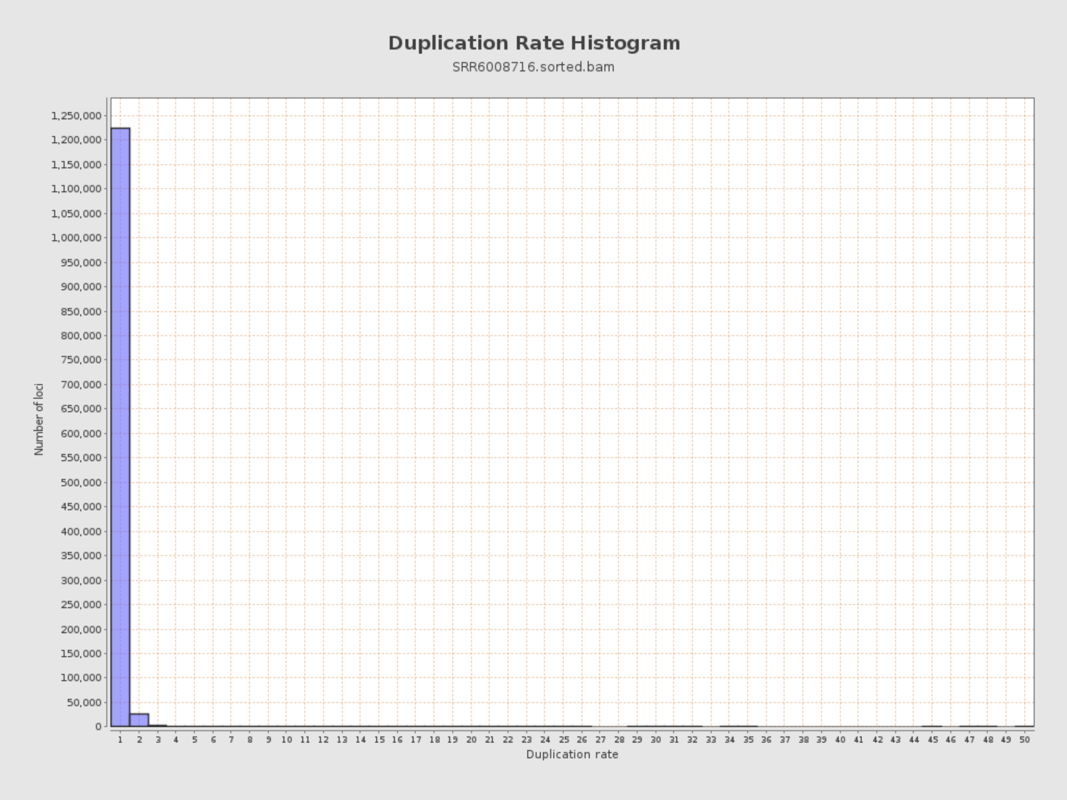
5. Results : Coverage Histogram (0-50X)



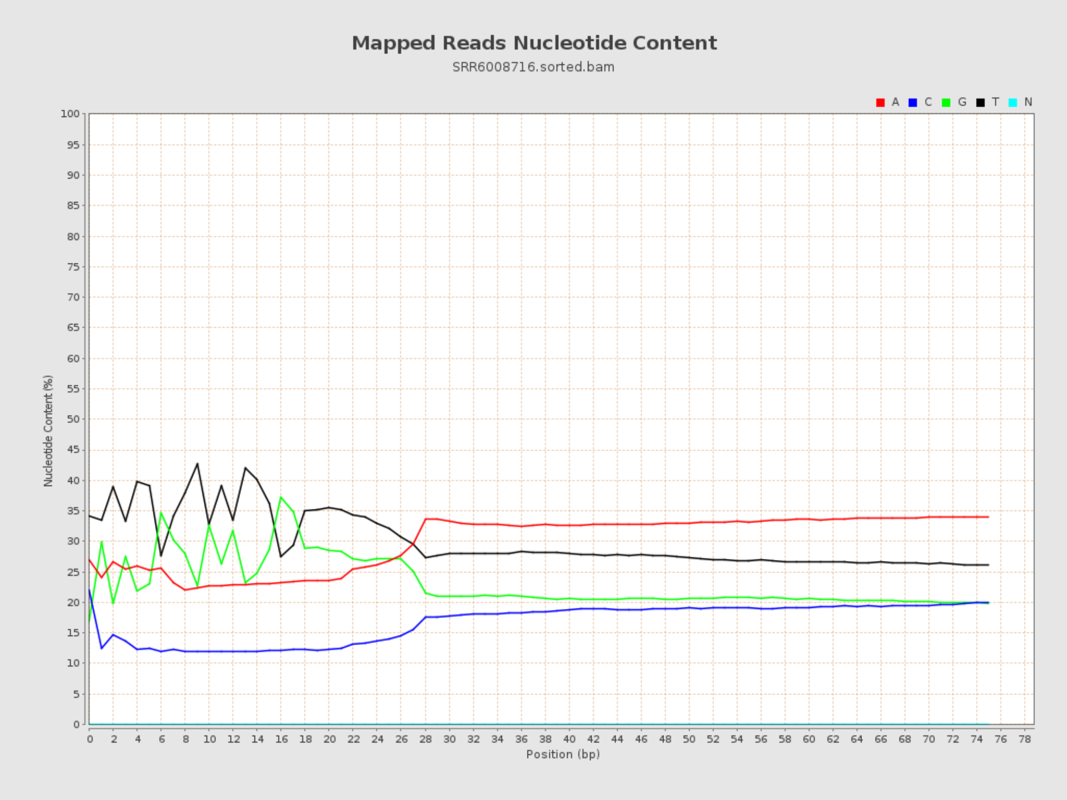
6. Results : Genome Fraction Coverage



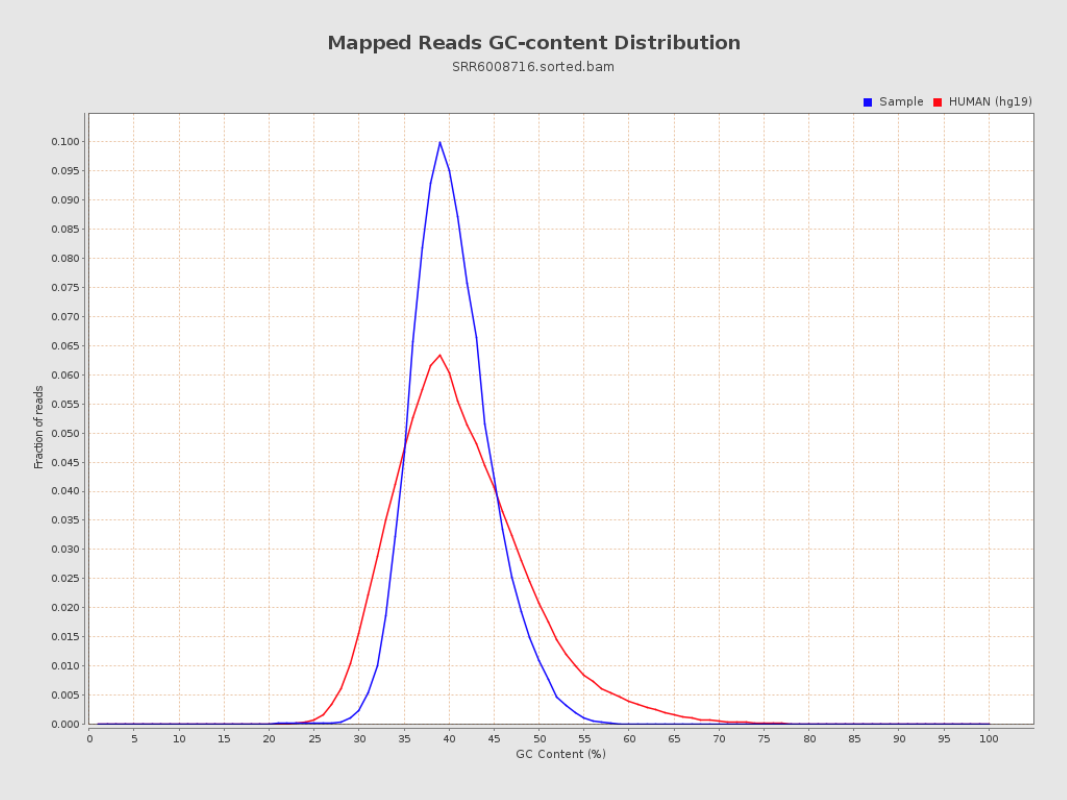
7. Results : Duplication Rate Histogram



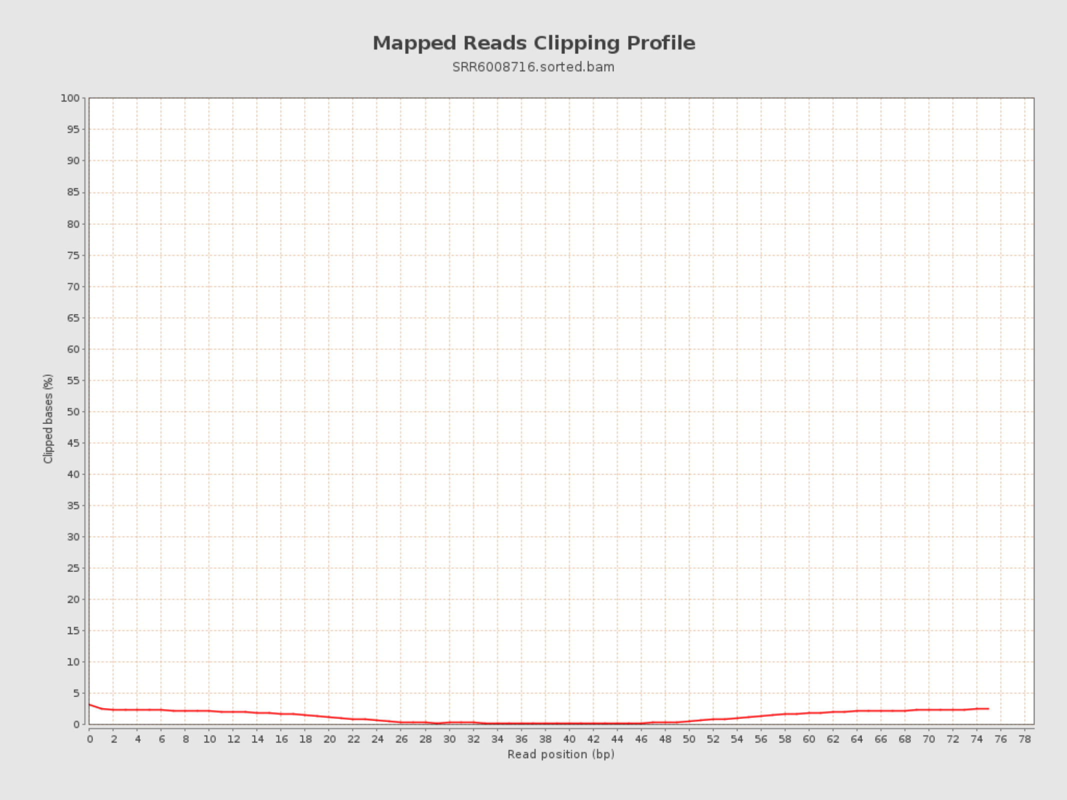
8. Results : Mapped Reads Nucleotide Content



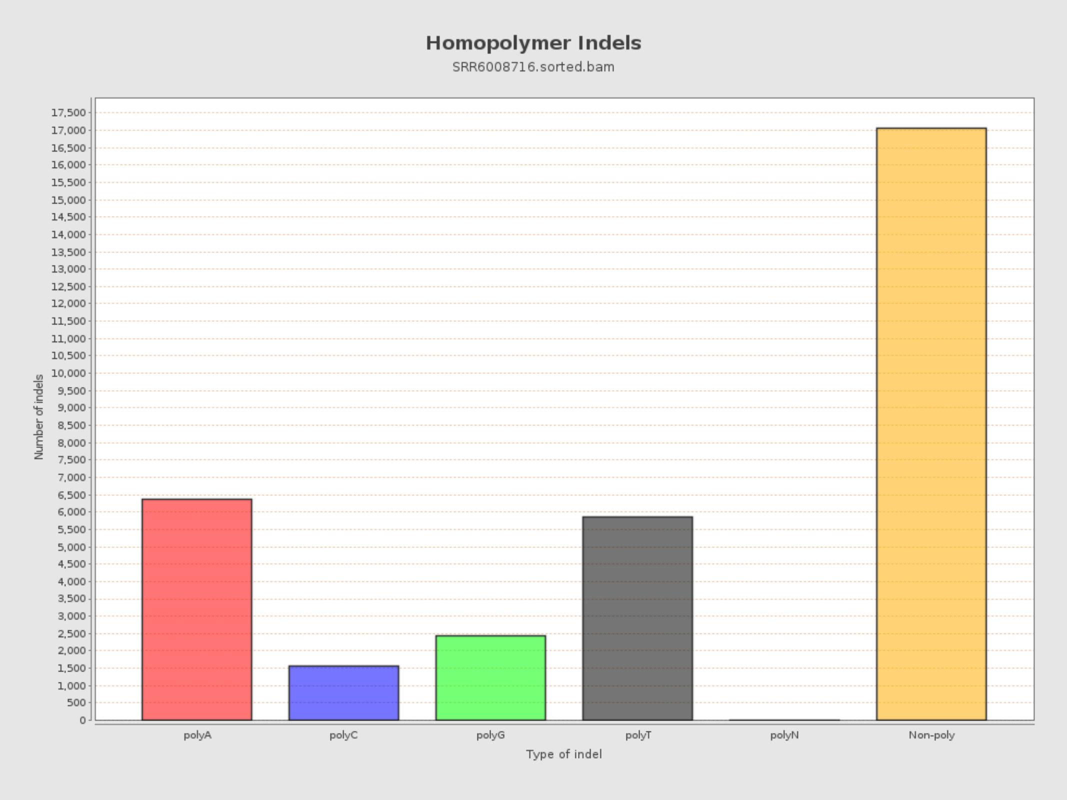
9. Results : Mapped Reads GC-content Distribution



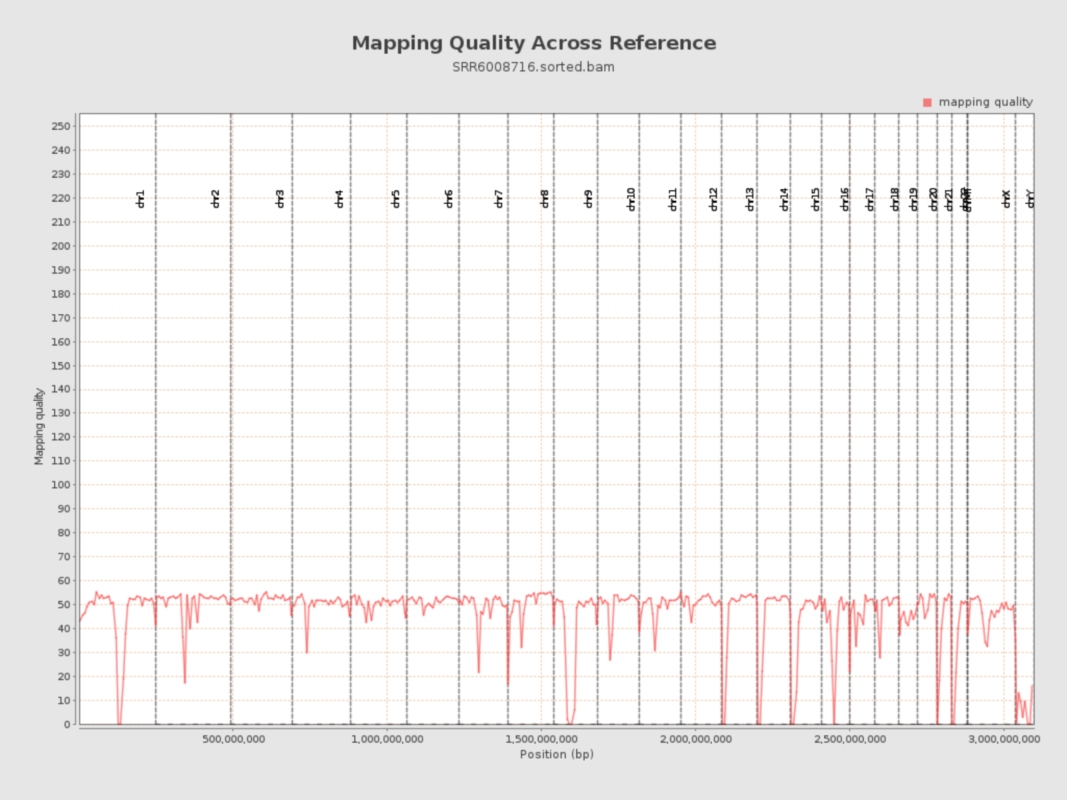
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram