Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 15:04:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084808.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_SRR3084808 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084808.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 15:04:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084808.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,705,742
Mapped reads	1,532,661 / 89.85%
Unmapped reads	173,081 / 10.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,146 / 1.12%
Read min/max/mean length	30 / 76 / 76.39
Duplicated reads (estimated)	67,035 / 3.93%
Duplication rate	3.83%
Clipped reads	688,148 / 40.34%

2.2. ACGT Content

Number/percentage of A's	28,111,359 / 27.45%
Number/percentage of C's	19,339,657 / 18.89%
Number/percentage of T's	31,932,136 / 31.18%
Number/percentage of G's	23,002,670 / 22.46%
Number/percentage of N's	14,544 / 0.01%
GC Percentage	41.35%

2.3. Coverage

Mean	0.0331

Standard Deviation	0.2484

2.4. Mapping Quality

Mean Mapping Quality	45.41

2.5. Mismatches and indels

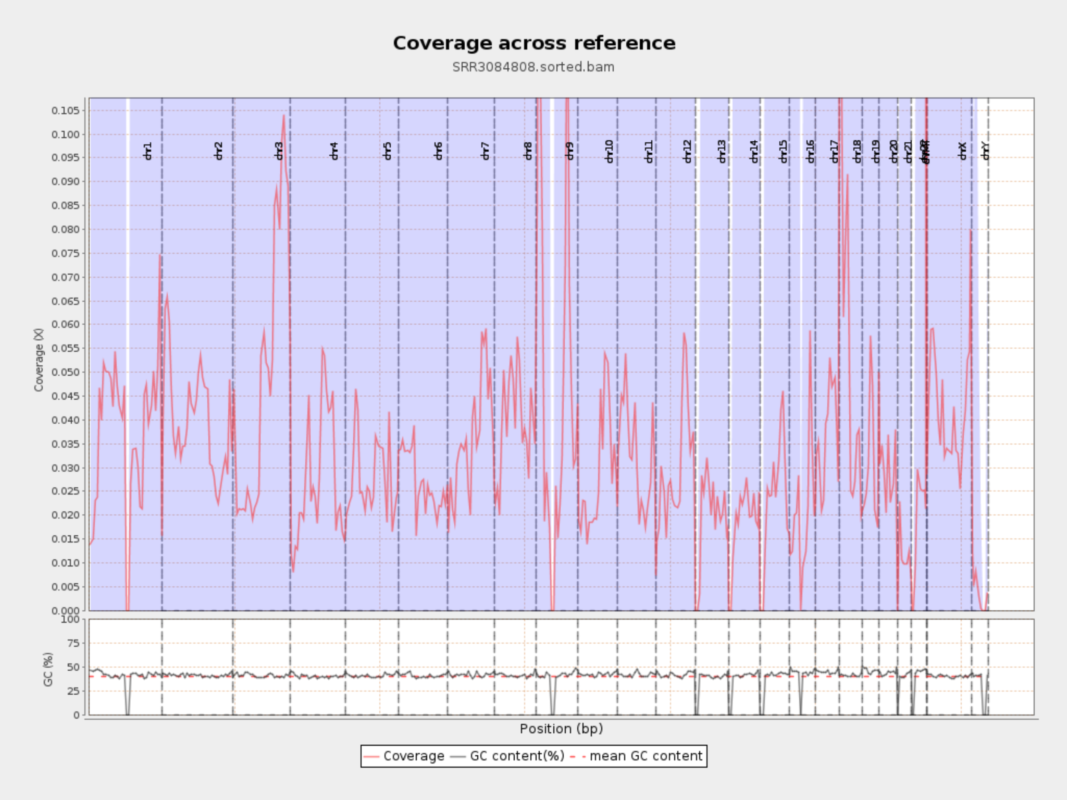
General error rate	0.78%
Mismatches	781,441
Insertions	7,974
Mapped reads with at least one insertion	0.52%
Deletions	23,410
Mapped reads with at least one deletion	1.51%
Homopolymer indels	47.75%

2.6. Chromosome stats

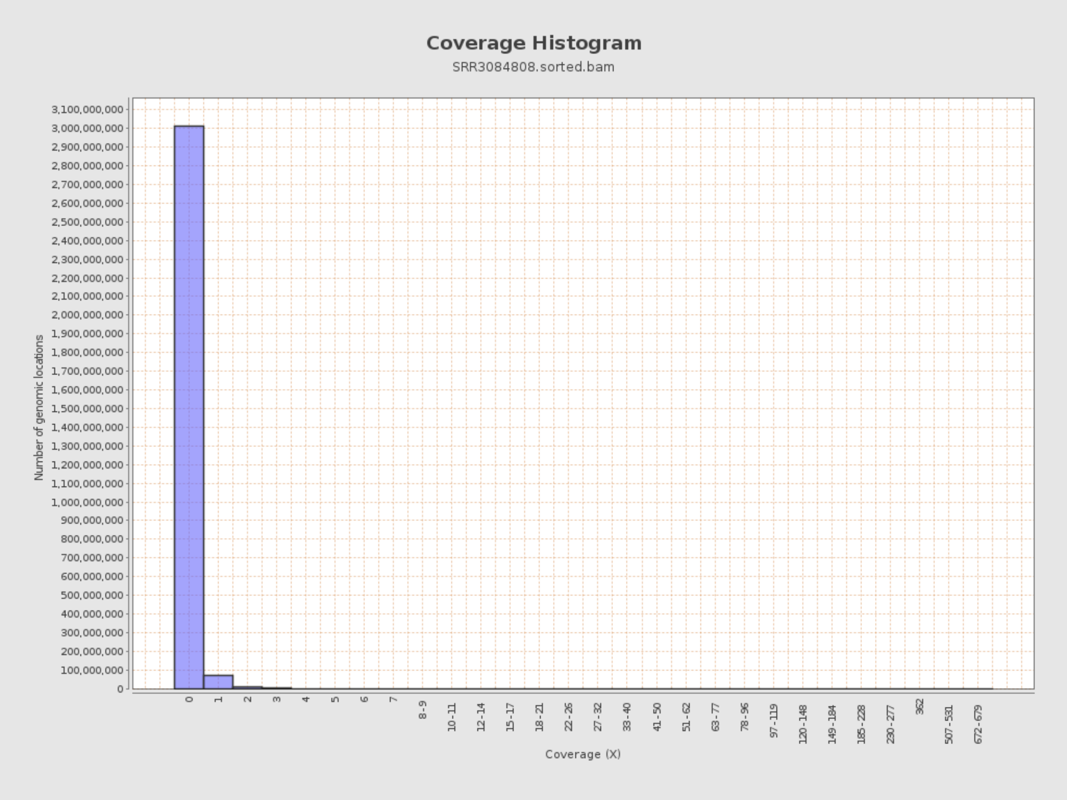
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9313684	0.0374	0.3231
chr2	243199373	9766839	0.0402	0.38
chr3	198022430	9782628	0.0494	0.2639
chr4	191154276	5235560	0.0274	0.1952
chr5	180915260	5050743	0.0279	0.1958
chr6	171115067	4644836	0.0271	0.2032
chr7	159138663	5819739	0.0366	0.2512

chr8	146364022	5785652	0.0395	0.2713
chr9	141213431	6884393	0.0488	0.2859
chr10	135534747	3869710	0.0286	0.2058
chr11	135006516	4372117	0.0324	0.2404
chr12	133851895	4058844	0.0303	0.2039
chr13	115169878	2226292	0.0193	0.1625
chr14	107349540	1950249	0.0182	0.1589
chr15	102531392	2451528	0.0239	0.1871
chr16	90354753	1905734	0.0211	0.172
chr17	81195210	3023780	0.0372	0.2316
chr18	78077248	4368759	0.056	0.3315
chr19	59128983	1877494	0.0318	0.2488
chr20	63025520	1846996	0.0293	0.2024
chr21	48129895	540384	0.0112	0.1264
chr22	51304566	932081	0.0182	0.1557
chrMT	16571	23499	1.4181	1.5409
chrX	155270560	6487176	0.0418	0.2447
chrY	59373566	219809	0.0037	0.0791

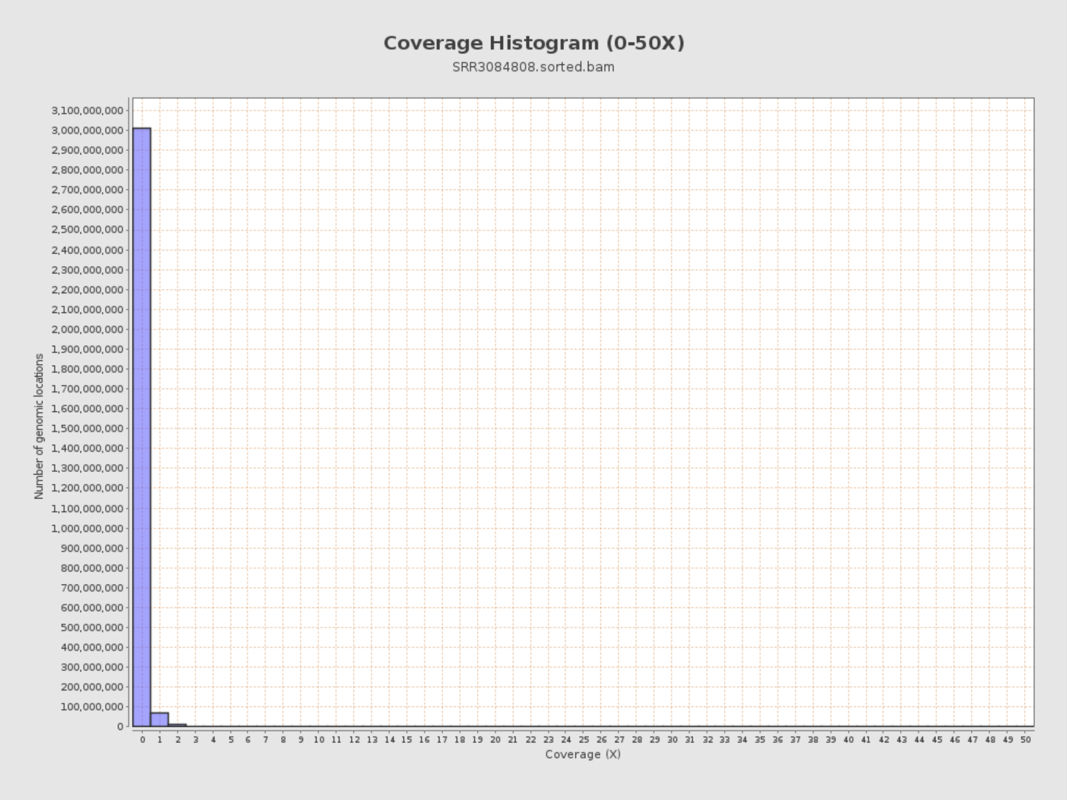
3. Results : Coverage across reference



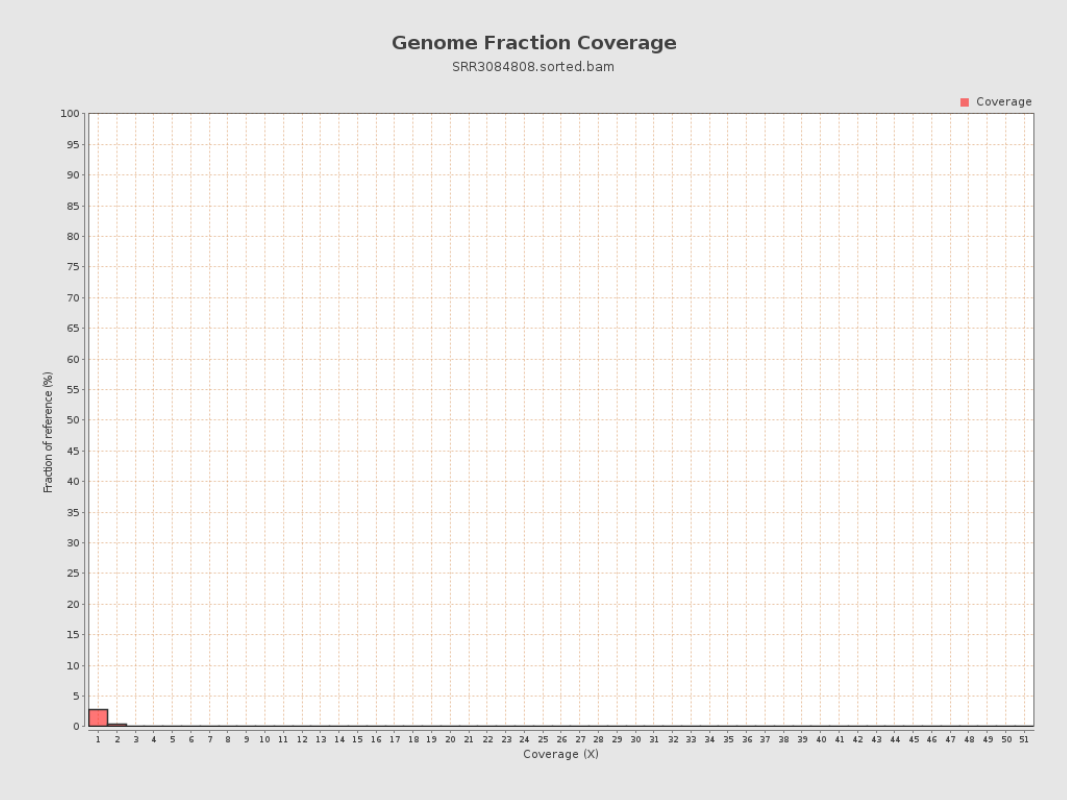
4. Results : Coverage Histogram



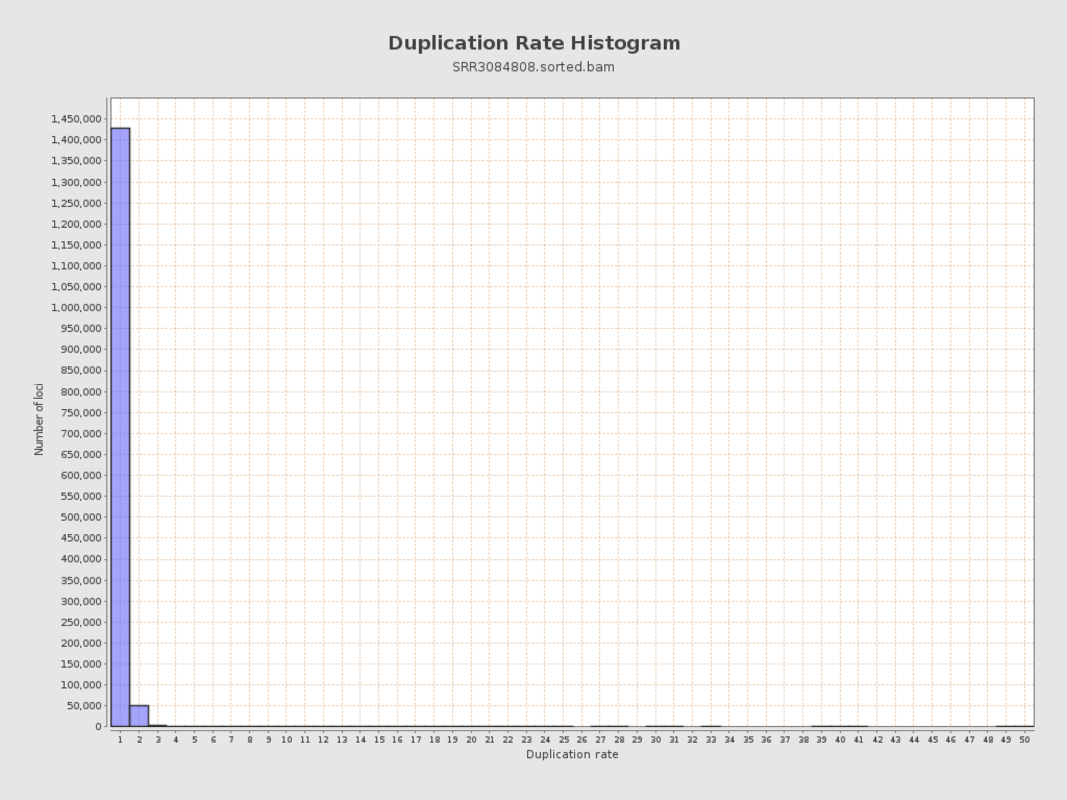
5. Results : Coverage Histogram (0-50X)



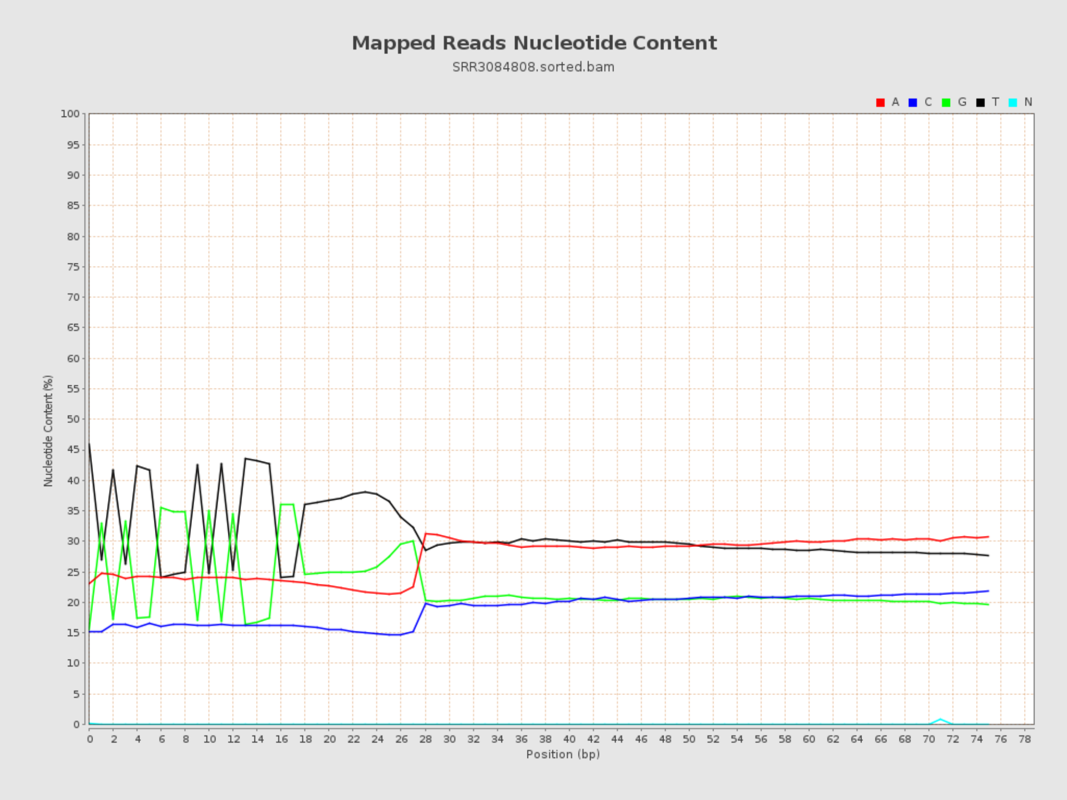
6. Results : Genome Fraction Coverage



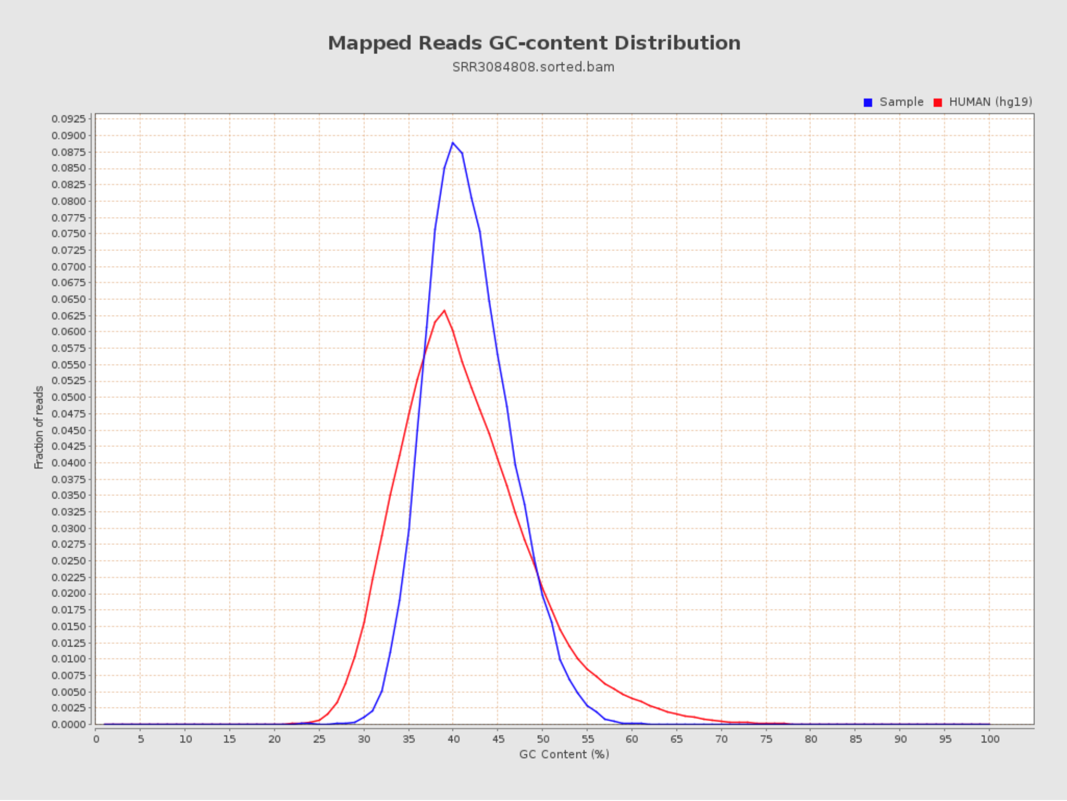
7. Results : Duplication Rate Histogram



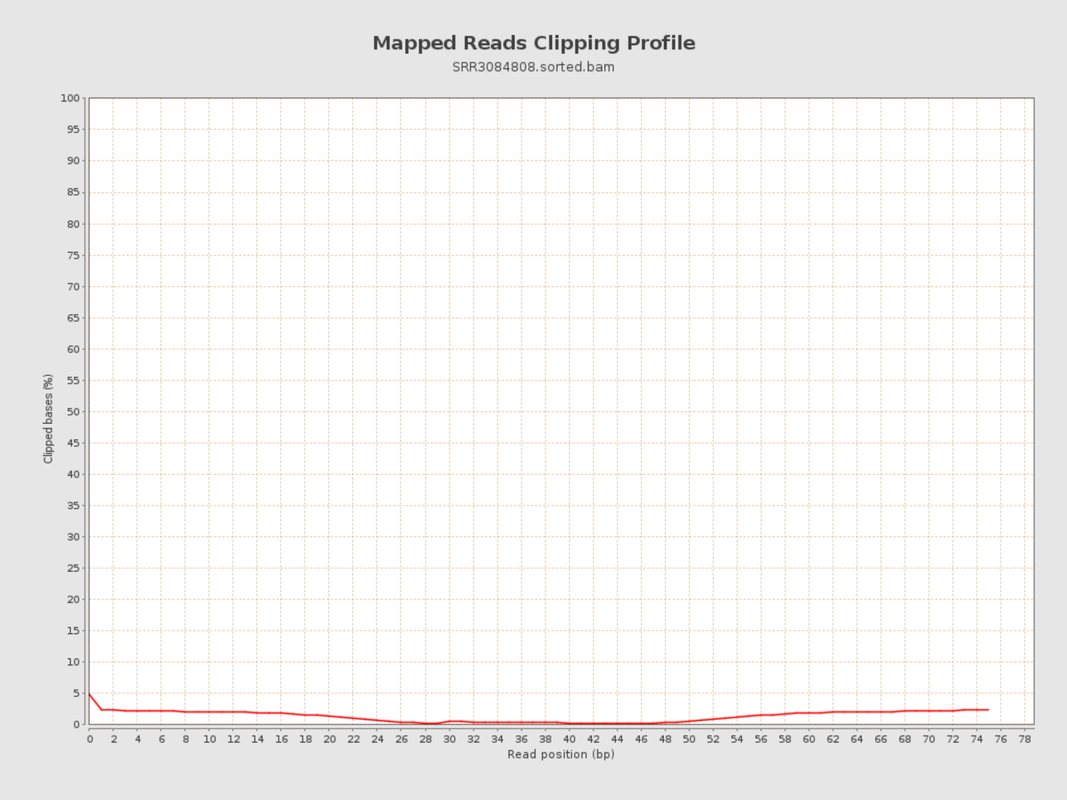
8. Results : Mapped Reads Nucleotide Content



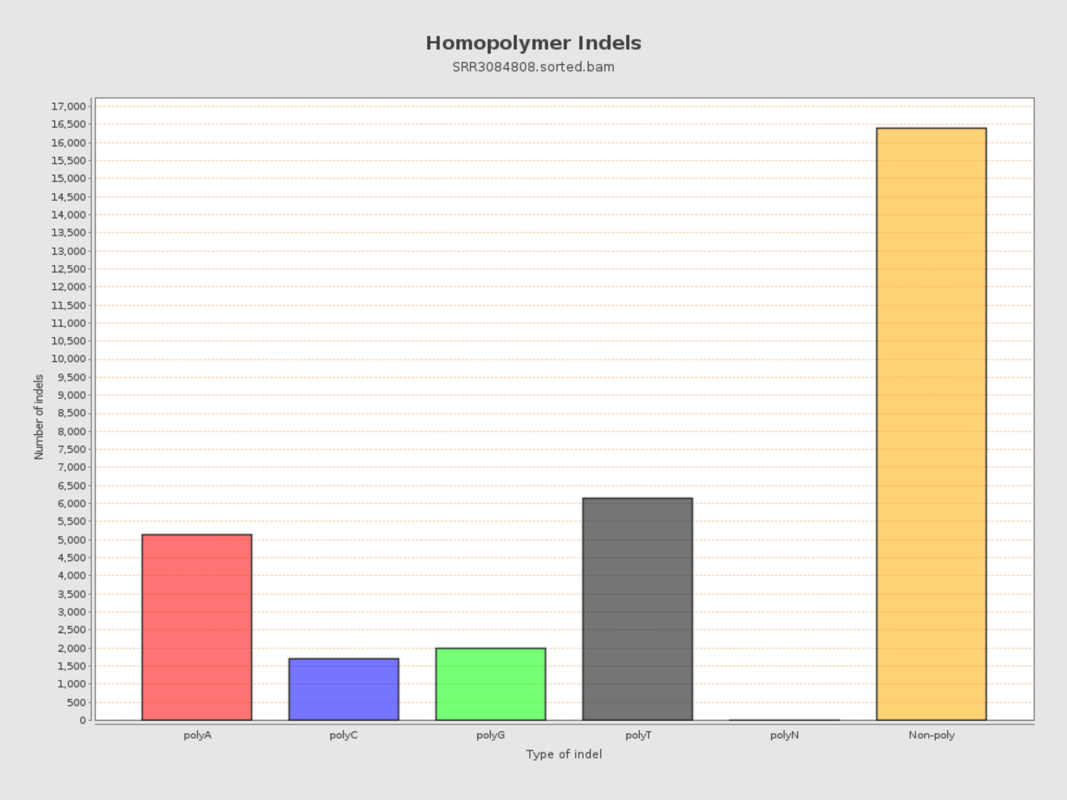
9. Results : Mapped Reads GC-content Distribution



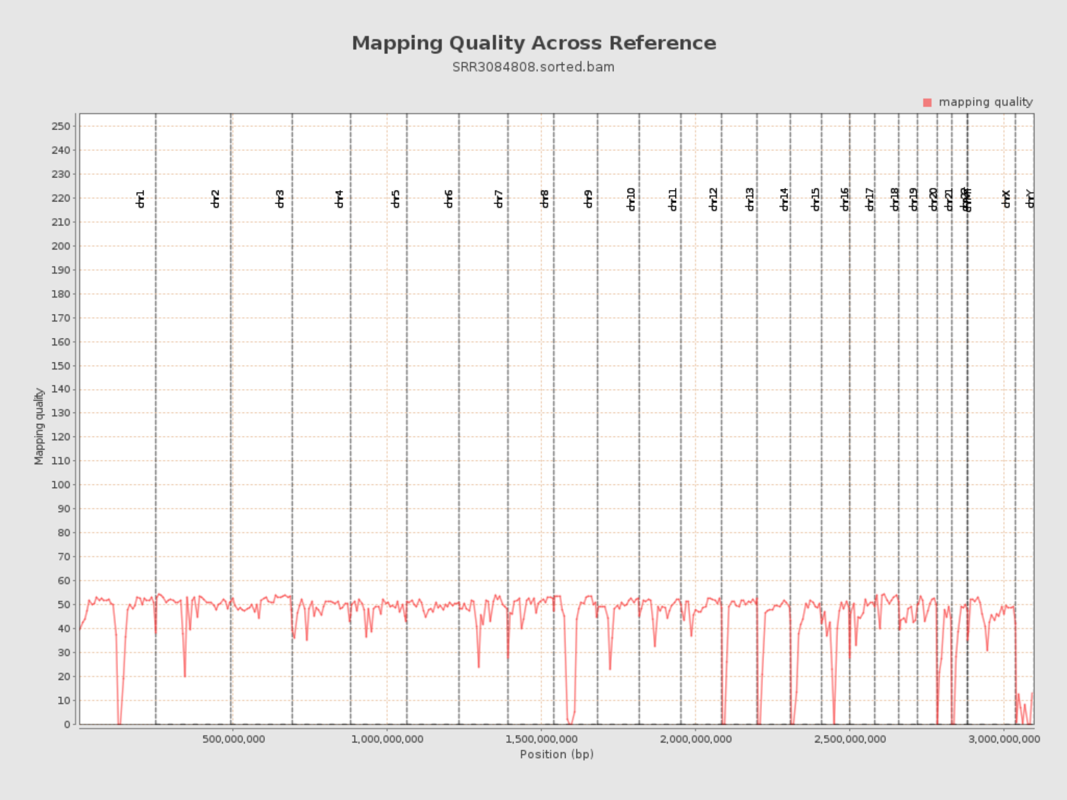
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram