Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 18:59:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084877.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_SRR3084877 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084877.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 18:59:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084877.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,605,057
Mapped reads	2,302,546 / 88.39%
Unmapped reads	302,511 / 11.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,552 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	107,242 / 4.12%
Duplication rate	3.92%
Clipped reads	784,528 / 30.12%

2.2. ACGT Content

Number/percentage of A's	46,340,824 / 29.1%
Number/percentage of C's	29,040,150 / 18.24%
Number/percentage of T's	51,188,032 / 32.15%
Number/percentage of G's	32,638,470 / 20.5%
Number/percentage of N's	24,921 / 0.02%
GC Percentage	38.73%

2.3. Coverage

Mean	0.0515

Standard Deviation	0.3879

2.4. Mapping Quality

Mean Mapping Quality	47.74

2.5. Mismatches and indels

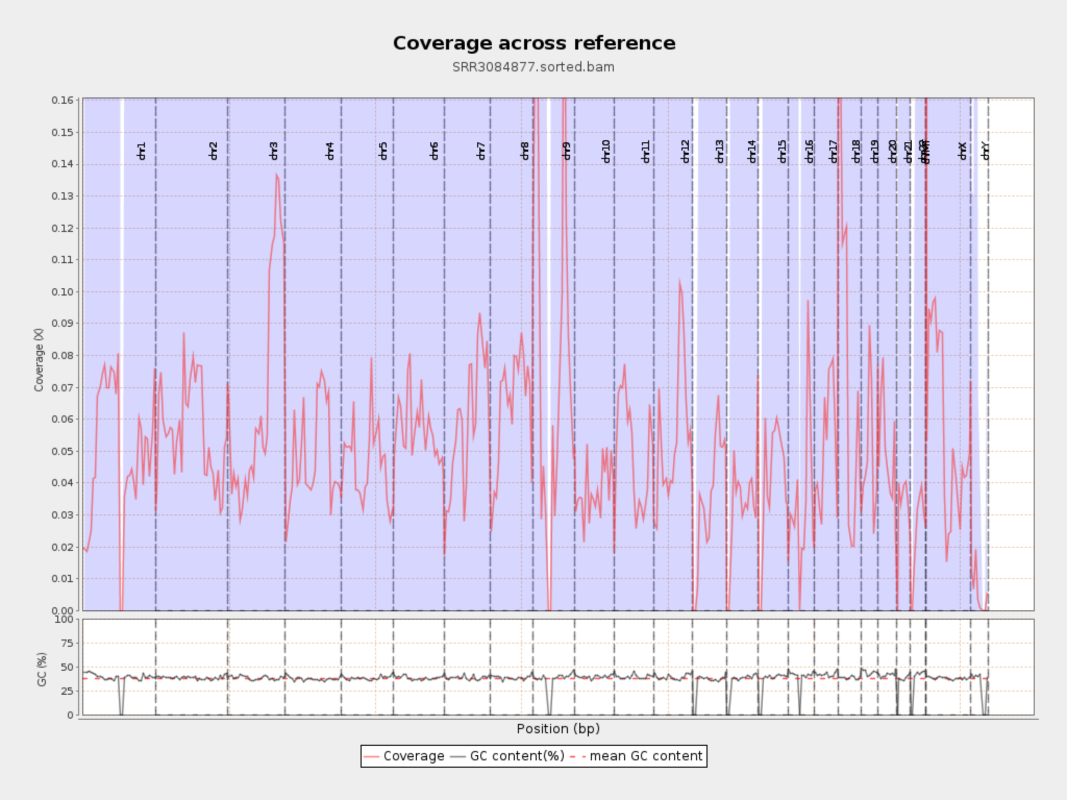
General error rate	0.83%
Mismatches	1,298,064
Insertions	12,651
Mapped reads with at least one insertion	0.55%
Deletions	33,948
Mapped reads with at least one deletion	1.46%
Homopolymer indels	48.72%

2.6. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12253572	0.0492	0.6325
chr2	243199373	13752355	0.0565	0.4168
chr3	198022430	13263657	0.067	0.303
chr4	191154276	9187262	0.0481	0.2575
chr5	180915260	8395694	0.0464	0.2551
chr6	171115067	9835238	0.0575	0.2861
chr7	159138663	9324049	0.0586	0.3696

chr8	146364022	9359251	0.0639	0.7208
chr9	141213431	11446732	0.0811	0.4464
chr10	135534747	5117523	0.0378	0.3043
chr11	135006516	6736998	0.0499	0.3345
chr12	133851895	7371087	0.0551	0.2794
chr13	115169878	4048262	0.0352	0.2165
chr14	107349540	3405601	0.0317	0.2327
chr15	102531392	4111022	0.0401	0.2316
chr16	90354753	2931563	0.0324	0.2402
chr17	81195210	4347192	0.0535	0.276
chr18	78077248	6264536	0.0802	0.7113
chr19	59128983	2976287	0.0503	0.414
chr20	63025520	3231417	0.0513	0.2712
chr21	48129895	1561187	0.0324	0.2321
chr22	51304566	1231366	0.024	0.1754
chrMT	16571	62350	3.7626	2.6111
chrX	155270560	8735523	0.0563	0.2979
chrY	59373566	342749	0.0058	0.1801

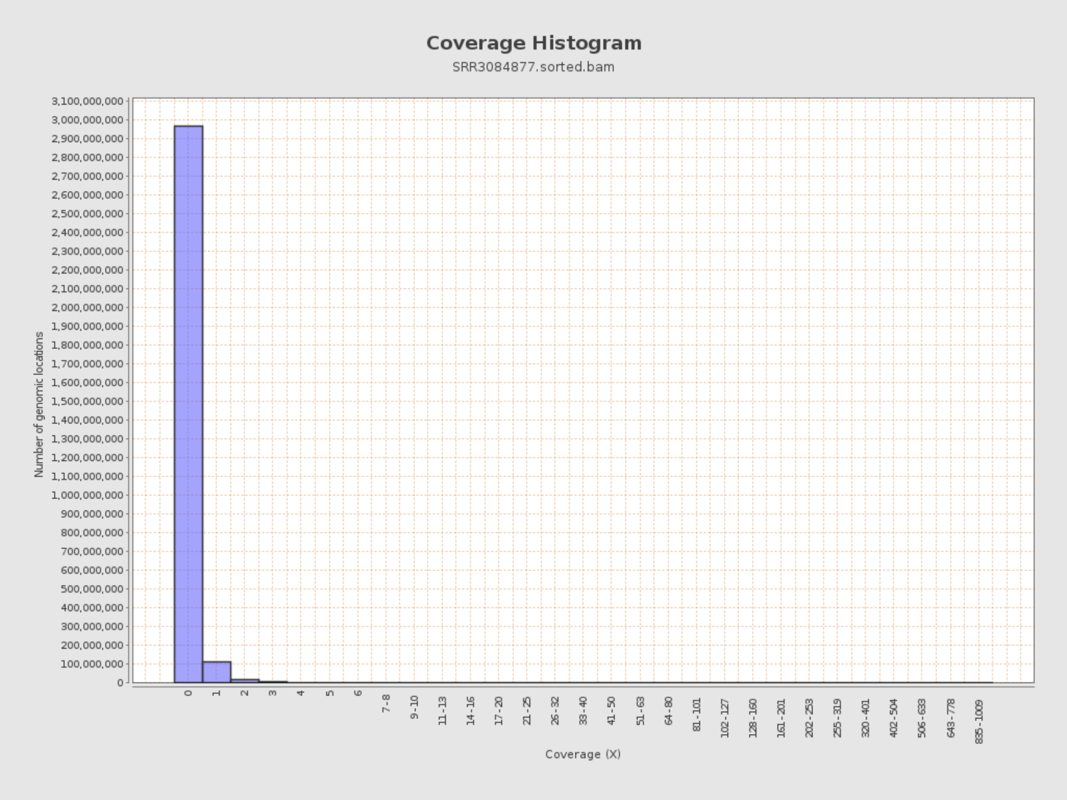
3. Results : Coverage across reference



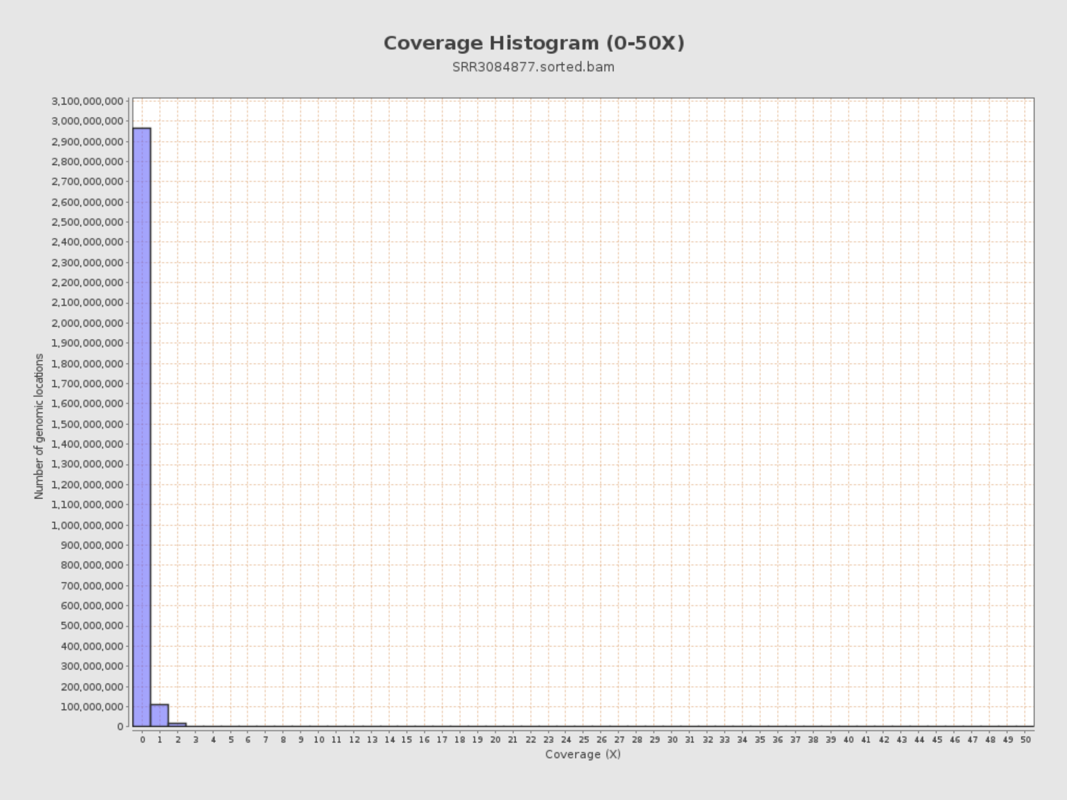
Coverage across reference

SRR3084877.sorted.bam

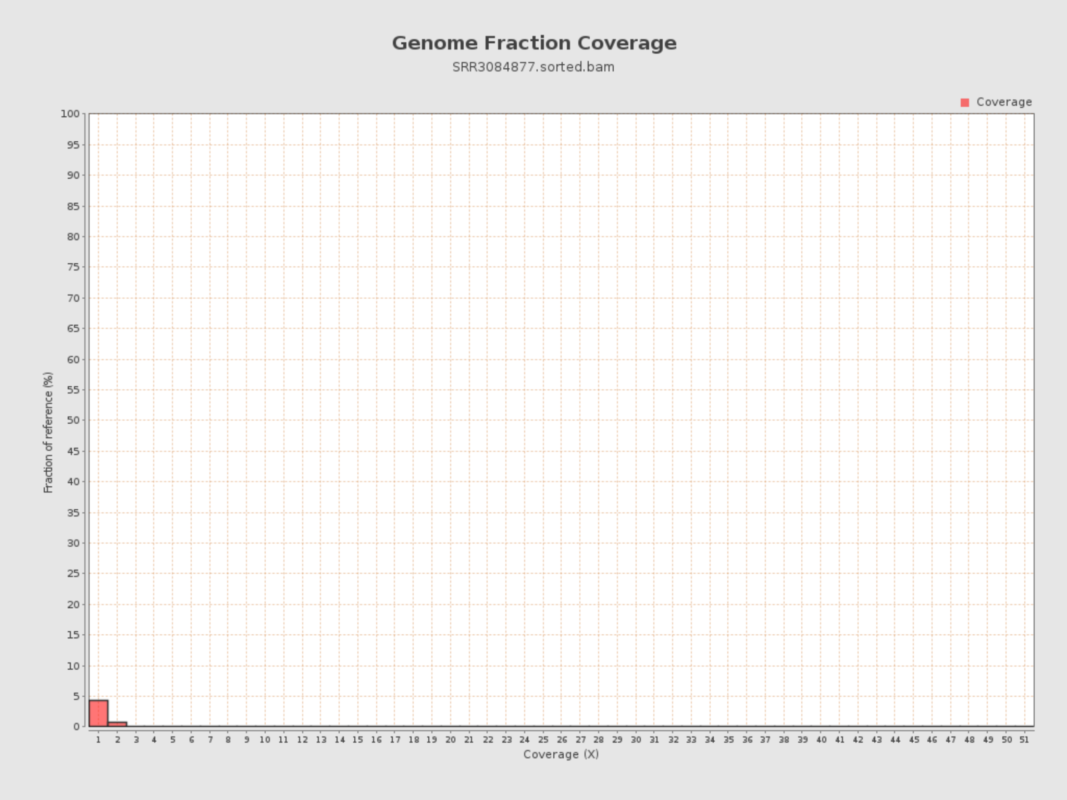
4. Results : Coverage Histogram



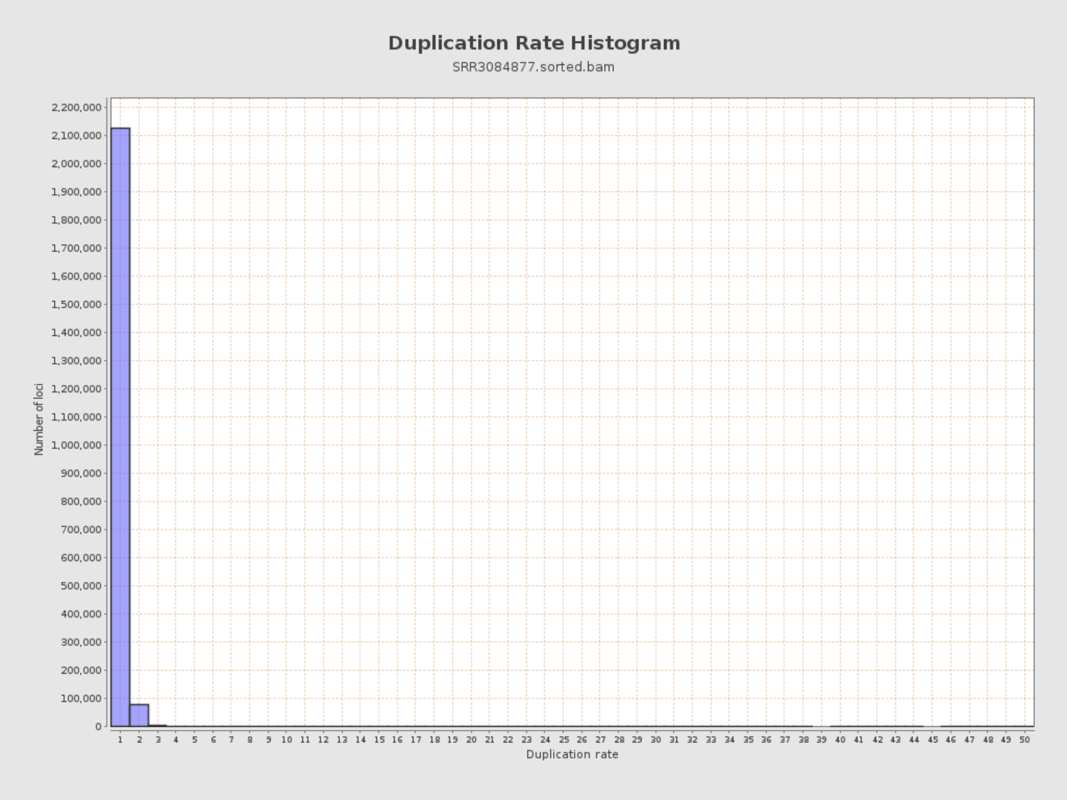
5. Results : Coverage Histogram (0-50X)



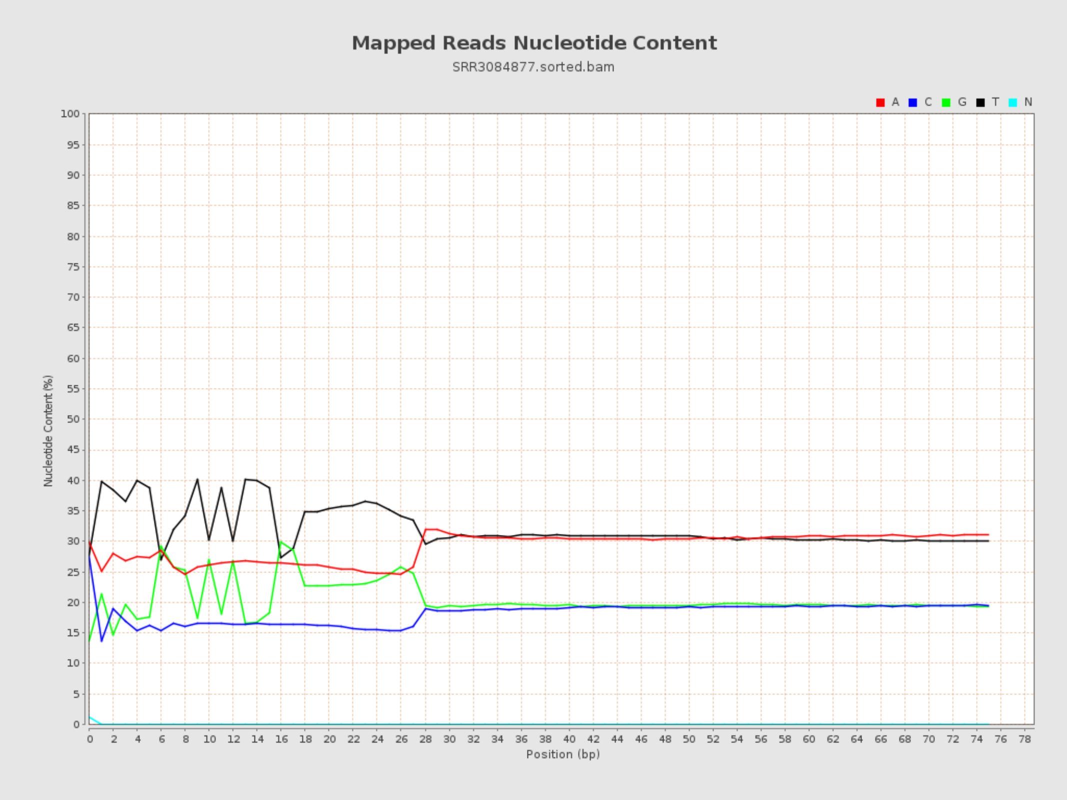
6. Results : Genome Fraction Coverage



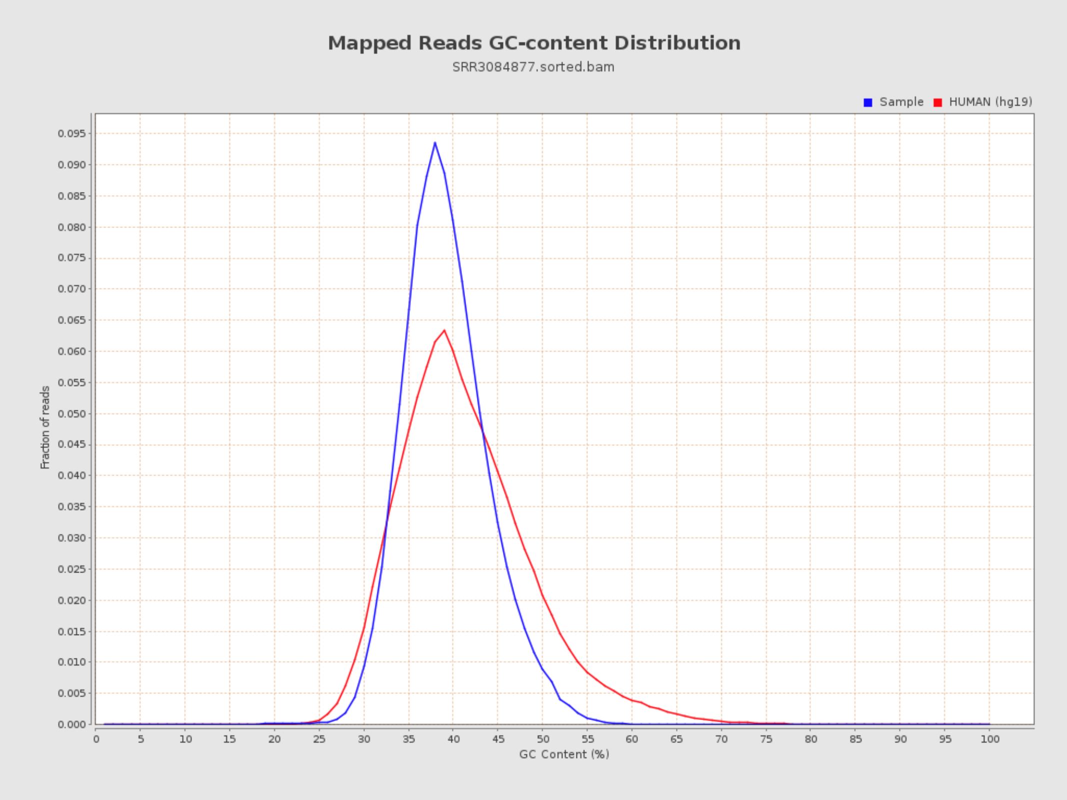
7. Results : Duplication Rate Histogram



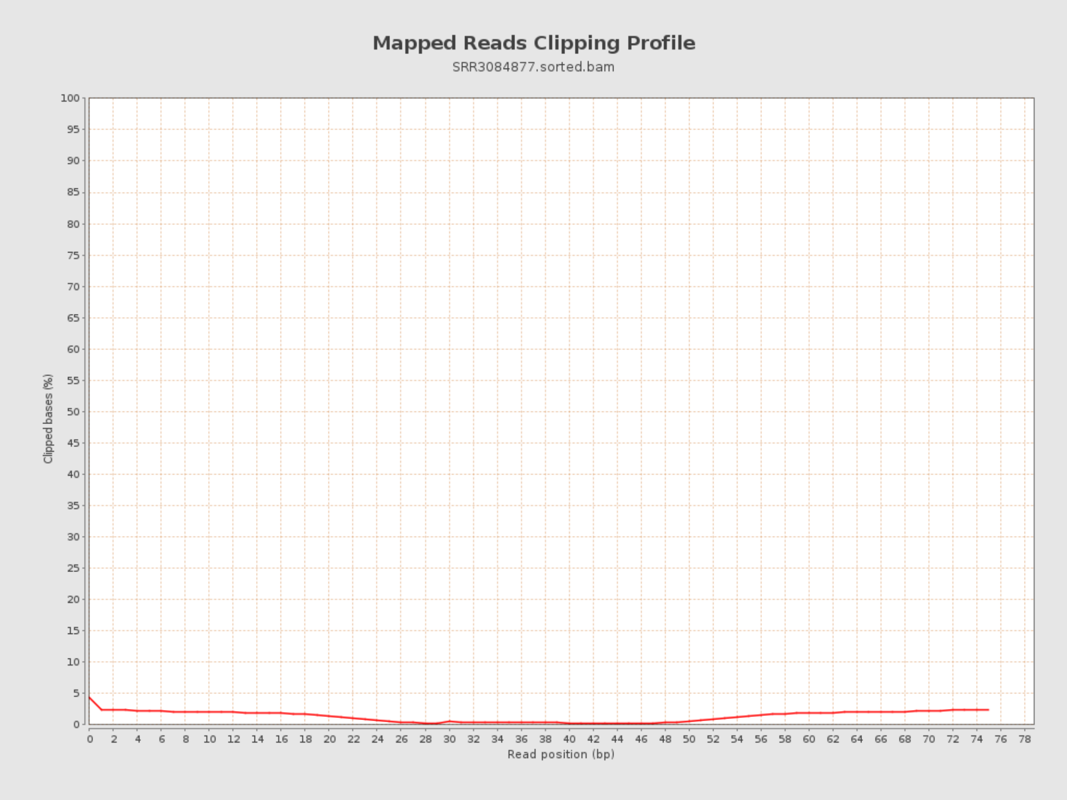
8. Results : Mapped Reads Nucleotide Content



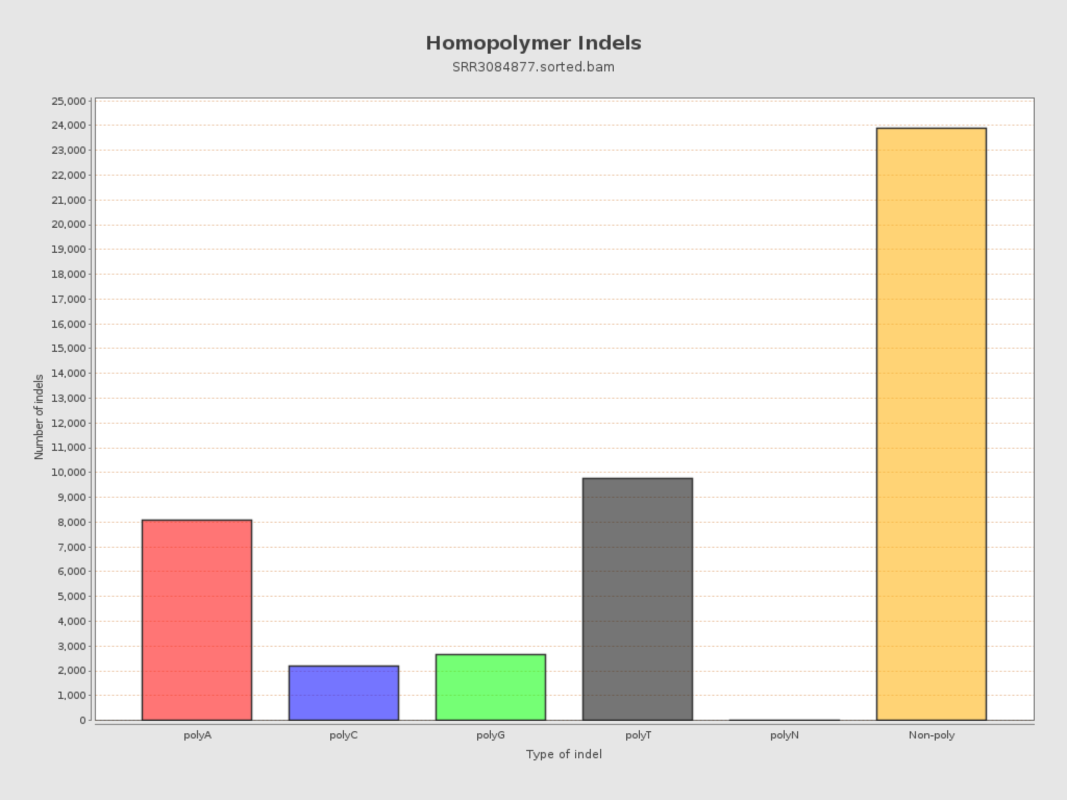
9. Results : Mapped Reads GC-content Distribution



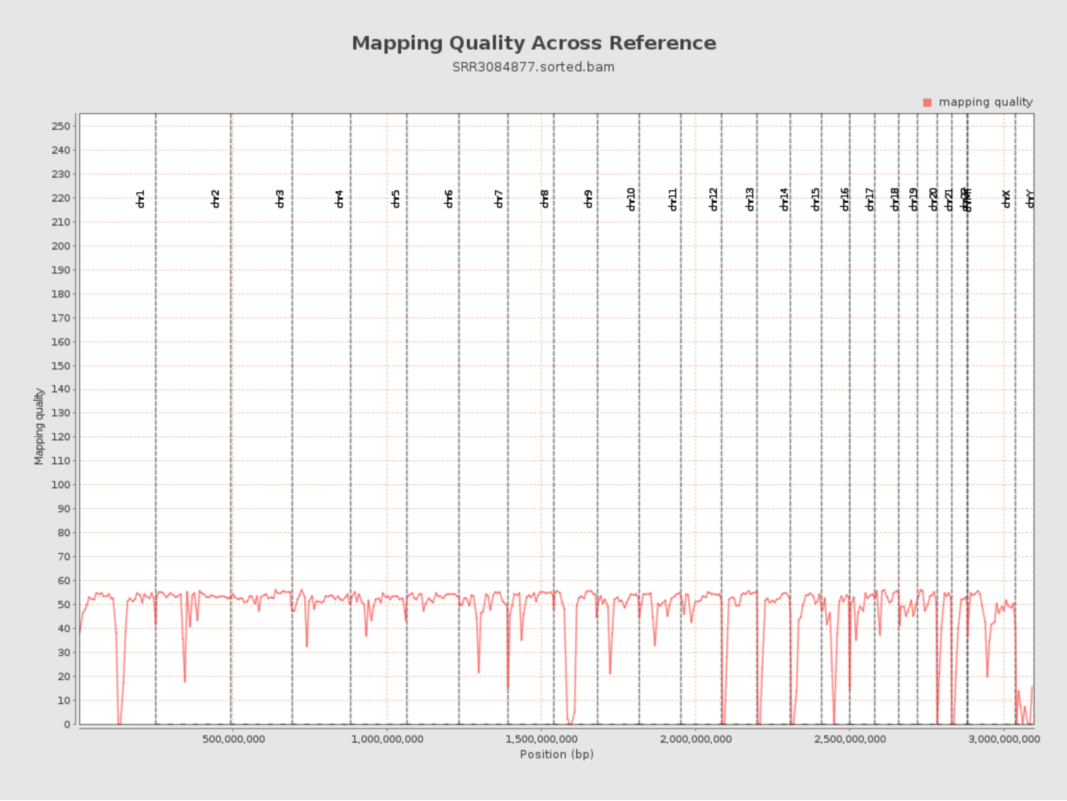
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram