Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 16:41:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084840.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_SRR3084840 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084840.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 16:41:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084840.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,872,231
Mapped reads	2,557,252 / 89.03%
Unmapped reads	314,979 / 10.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,073 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	150,862 / 5.25%
Duplication rate	4.9%
Clipped reads	943,504 / 32.85%

2.2. ACGT Content

Number/percentage of A's	50,501,805 / 28.81%
Number/percentage of C's	31,996,210 / 18.25%
Number/percentage of T's	56,272,312 / 32.1%
Number/percentage of G's	36,522,442 / 20.83%
Number/percentage of N's	27,310 / 0.02%
GC Percentage	39.08%

2.3. Coverage

Mean	0.0567

Standard Deviation	0.461

2.4. Mapping Quality

Mean Mapping Quality	47.92

2.5. Mismatches and indels

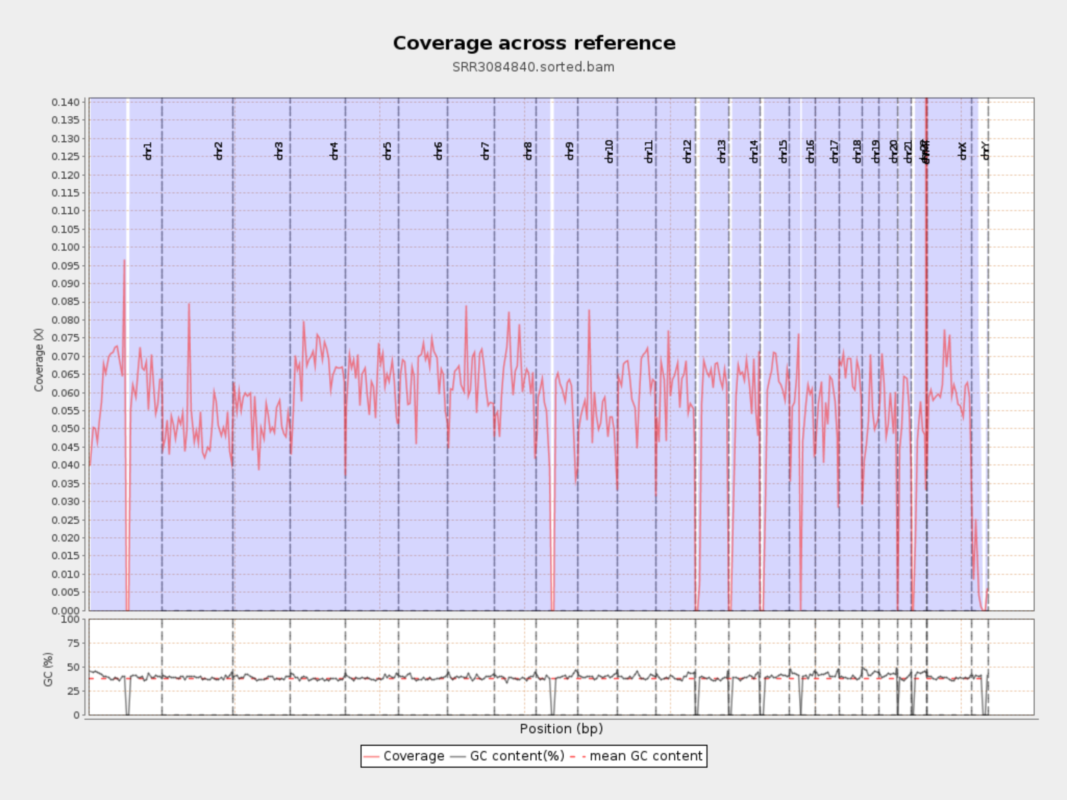
General error rate	0.84%
Mismatches	1,443,520
Insertions	14,602
Mapped reads with at least one insertion	0.57%
Deletions	37,443
Mapped reads with at least one deletion	1.45%
Homopolymer indels	48.69%

2.6. Chromosome stats

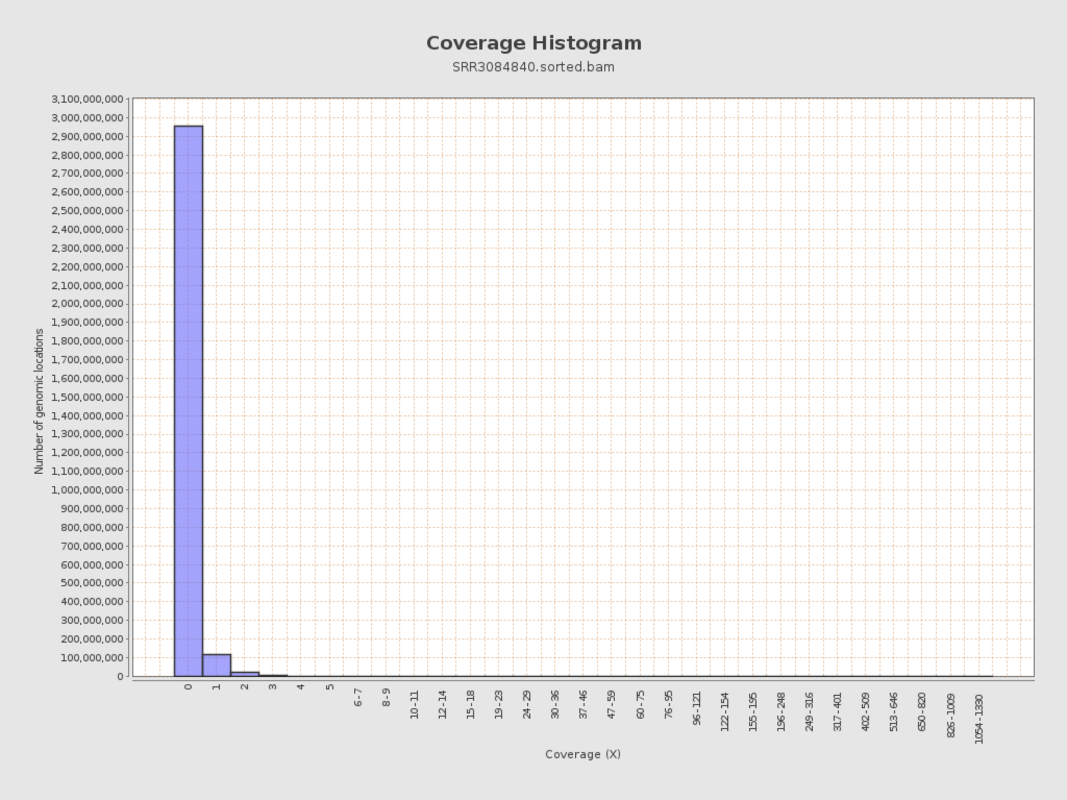
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14778334	0.0593	0.8761
chr2	243199373	12259226	0.0504	0.43
chr3	198022430	10561930	0.0533	0.2763
chr4	191154276	12865786	0.0673	0.3354
chr5	180915260	11469512	0.0634	0.3026
chr6	171115067	11095750	0.0648	0.3111
chr7	159138663	10135334	0.0637	0.4516

chr8	146364022	9259283	0.0633	0.8776
chr9	141213431	7199277	0.051	0.4015
chr10	135534747	7371218	0.0544	0.4088
chr11	135006516	8498746	0.063	0.3735
chr12	133851895	8093511	0.0605	0.2962
chr13	115169878	6105820	0.053	0.2761
chr14	107349540	5502316	0.0513	0.2793
chr15	102531392	5362006	0.0523	0.273
chr16	90354753	4698181	0.052	0.2931
chr17	81195210	4368705	0.0538	0.315
chr18	78077248	5159138	0.0661	0.7199
chr19	59128983	3036659	0.0514	0.5753
chr20	63025520	3536051	0.0561	0.2916
chr21	48129895	2357540	0.049	0.2924
chr22	51304566	1780199	0.0347	0.2194
chrMT	16571	68965	4.1618	2.7699
chrX	155270560	9387968	0.0605	0.3158
chrY	59373566	434931	0.0073	0.1799

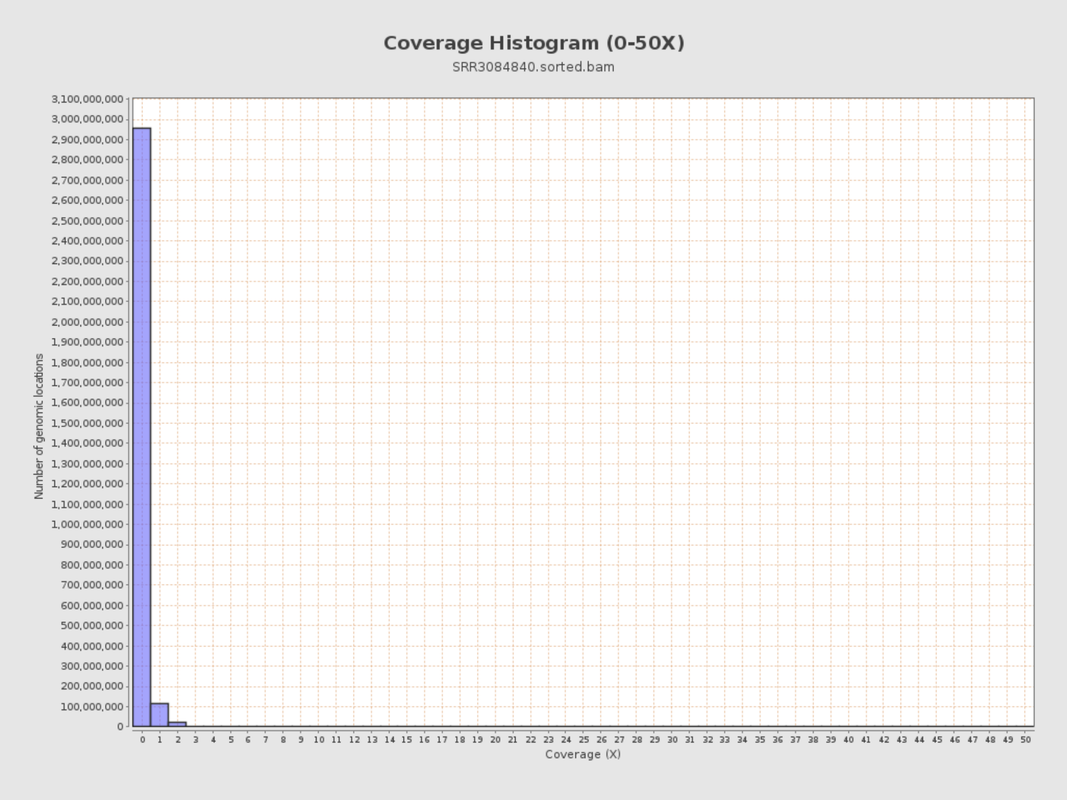
3. Results : Coverage across reference



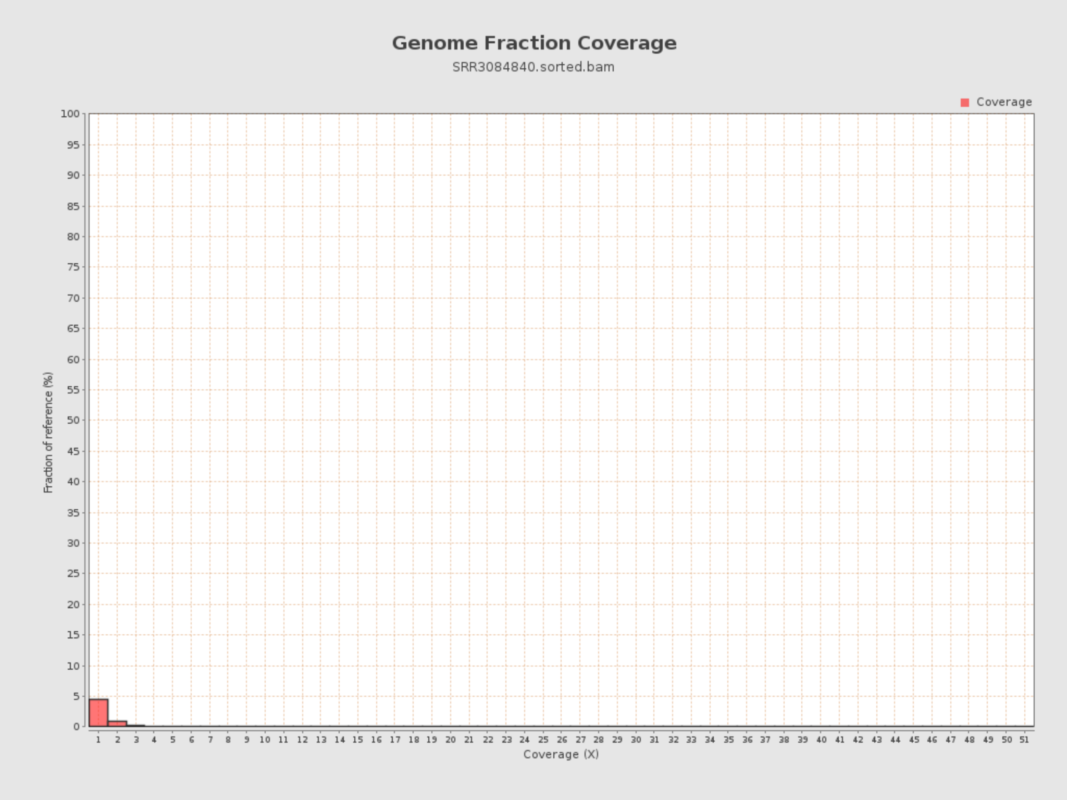
4. Results : Coverage Histogram



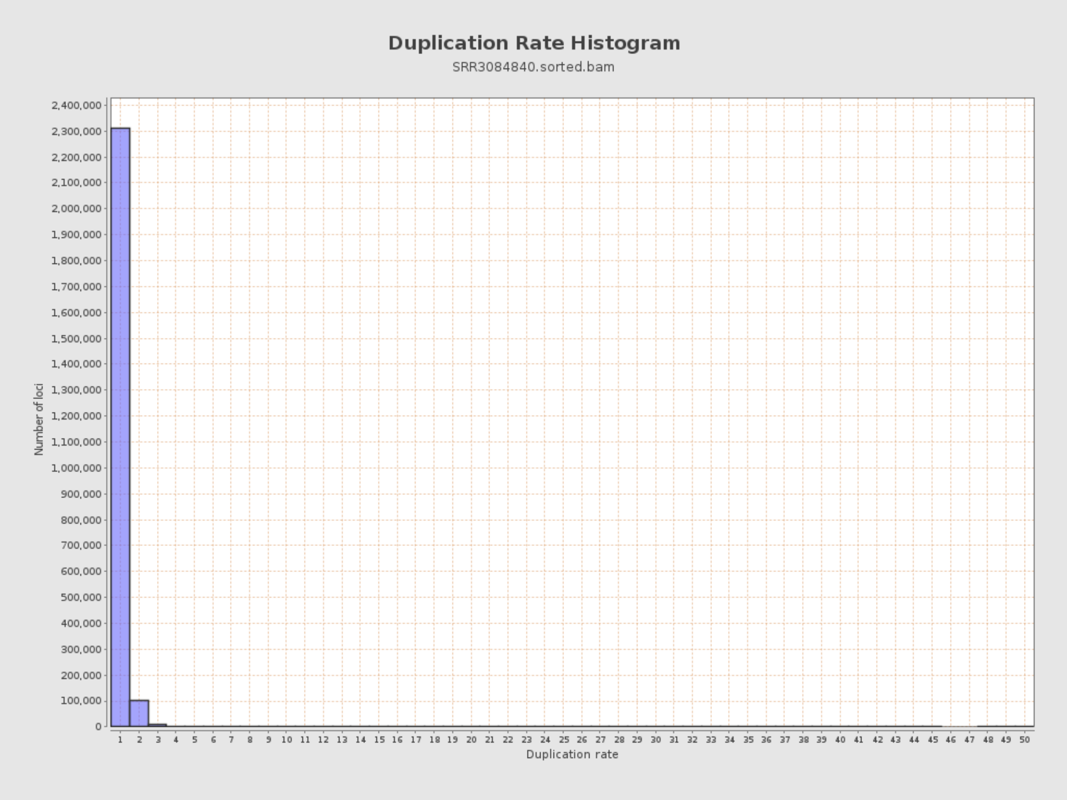
5. Results : Coverage Histogram (0-50X)



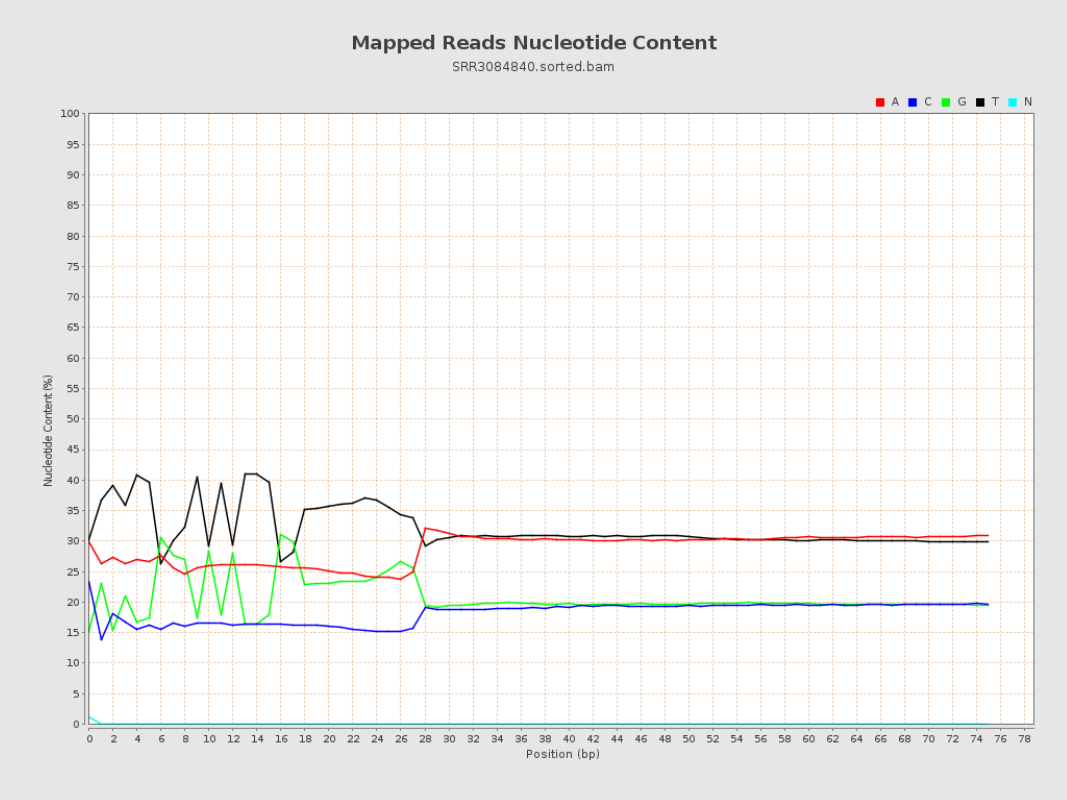
6. Results : Genome Fraction Coverage



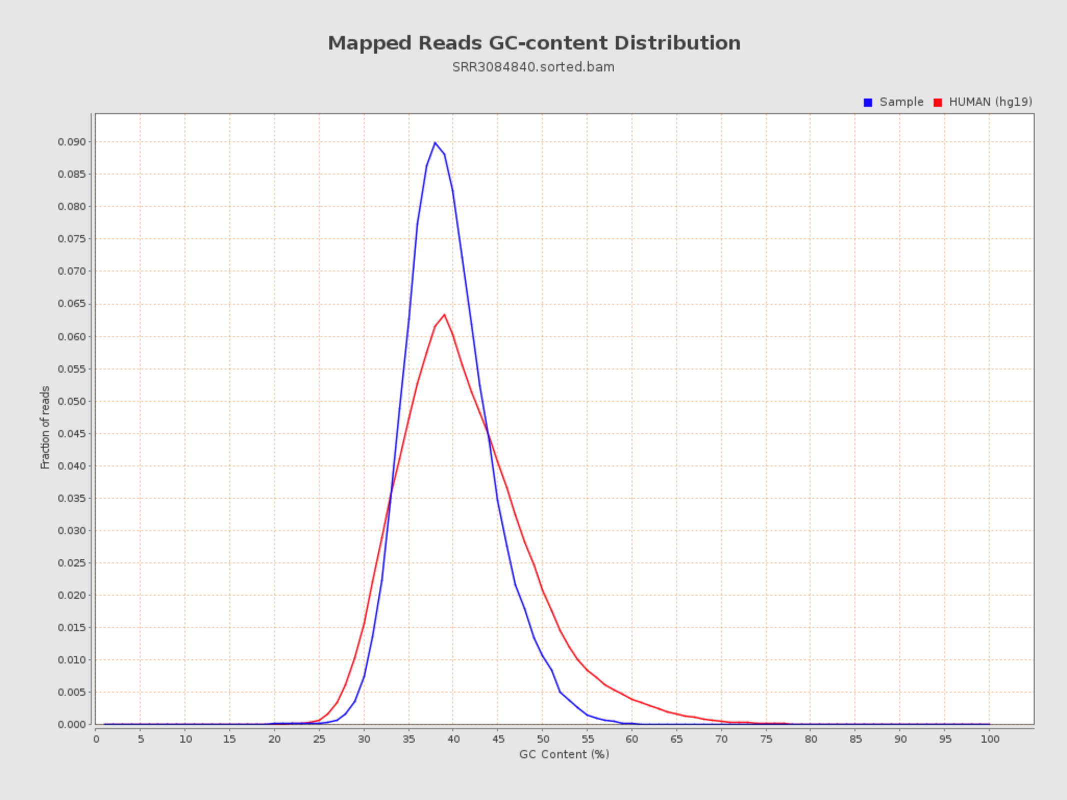
7. Results : Duplication Rate Histogram



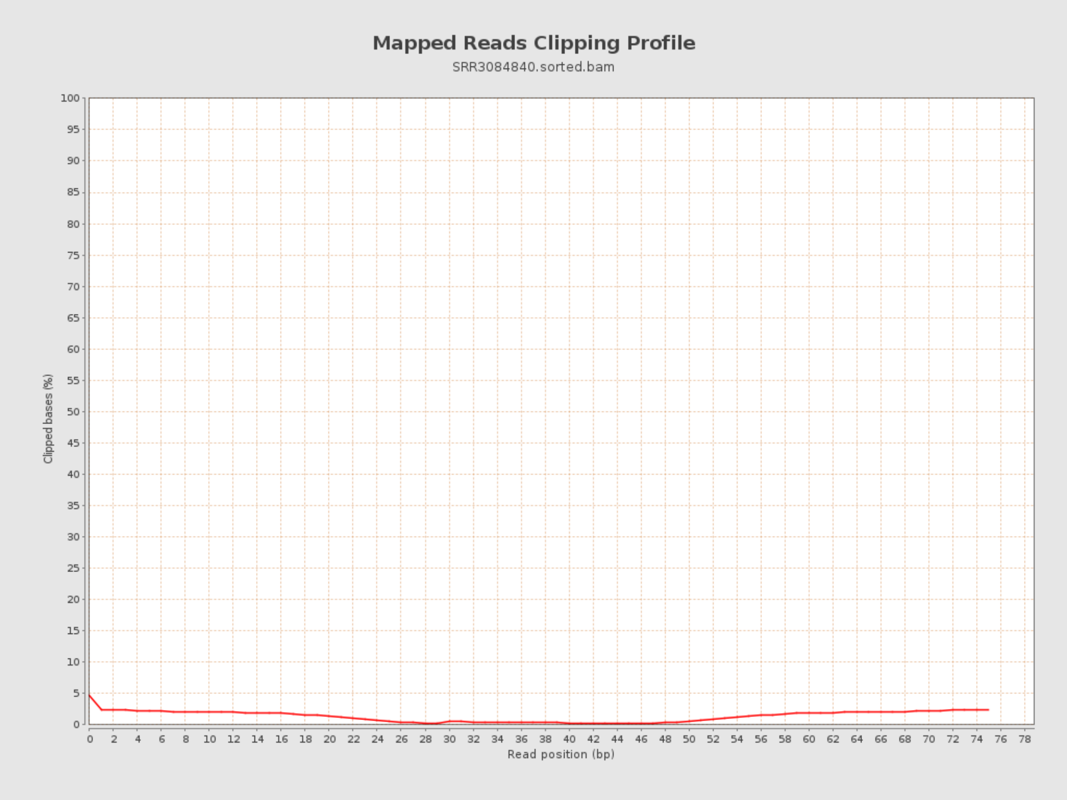
8. Results : Mapped Reads Nucleotide Content



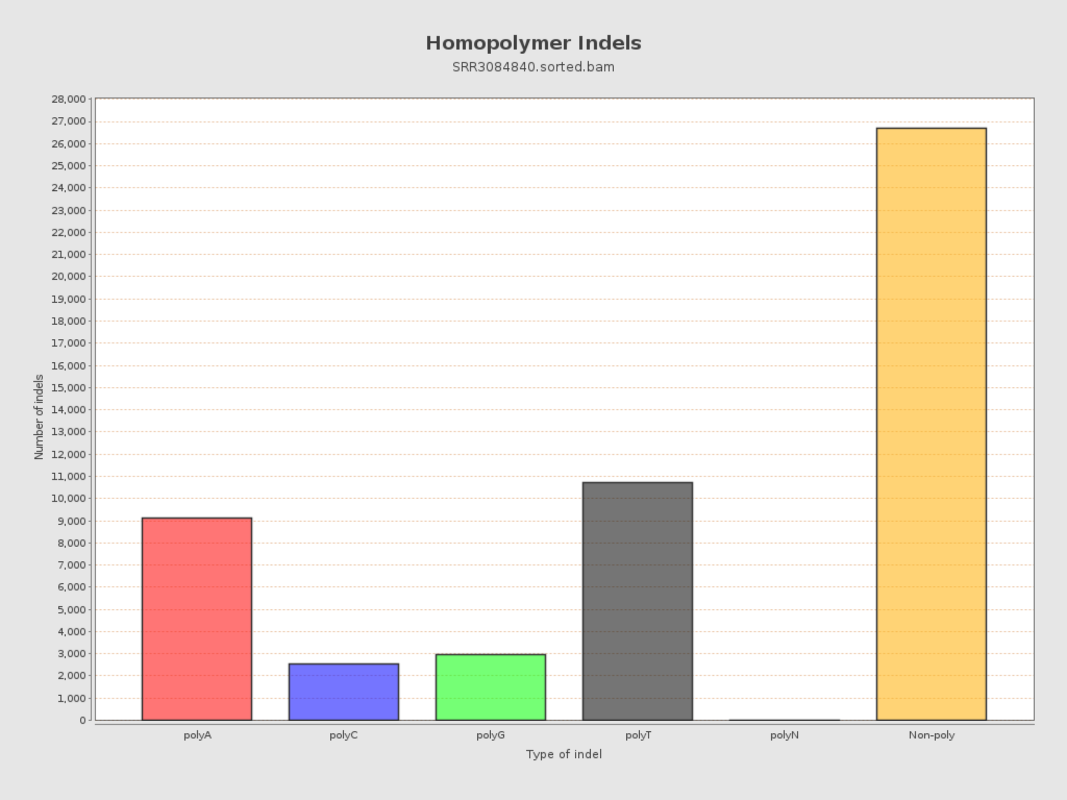
9. Results : Mapped Reads GC-content Distribution



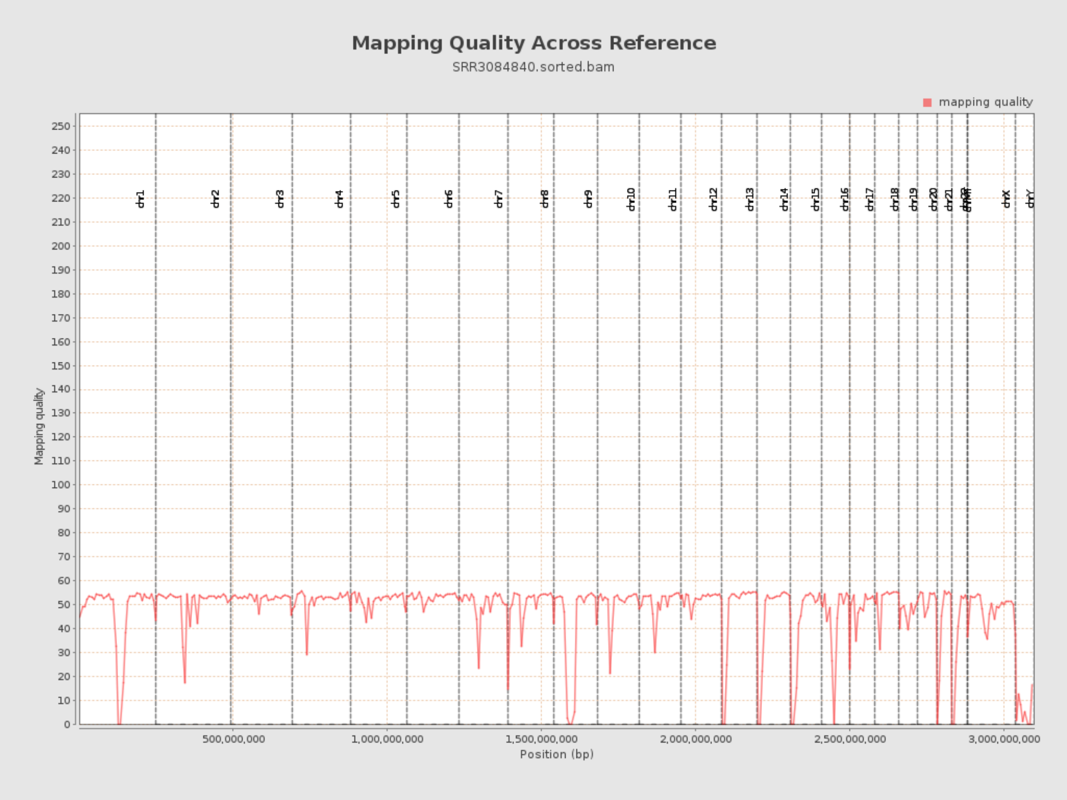
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram