Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 16:01:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084822.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_SRR3084822 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084822.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 16:01:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084822.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,343,891
Mapped reads	2,161,314 / 92.21%
Unmapped reads	182,577 / 7.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,223 / 0.95%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	112,636 / 4.81%
Duplication rate	4.56%
Clipped reads	889,927 / 37.97%

2.2. ACGT Content

Number/percentage of A's	40,670,510 / 27.91%
Number/percentage of C's	26,566,759 / 18.23%
Number/percentage of T's	46,731,277 / 32.07%
Number/percentage of G's	31,730,142 / 21.77%
Number/percentage of N's	21,179 / 0.01%
GC Percentage	40.01%

2.3. Coverage

Mean	0.0471

Standard Deviation	0.3066

2.4. Mapping Quality

Mean Mapping Quality	46.07

2.5. Mismatches and indels

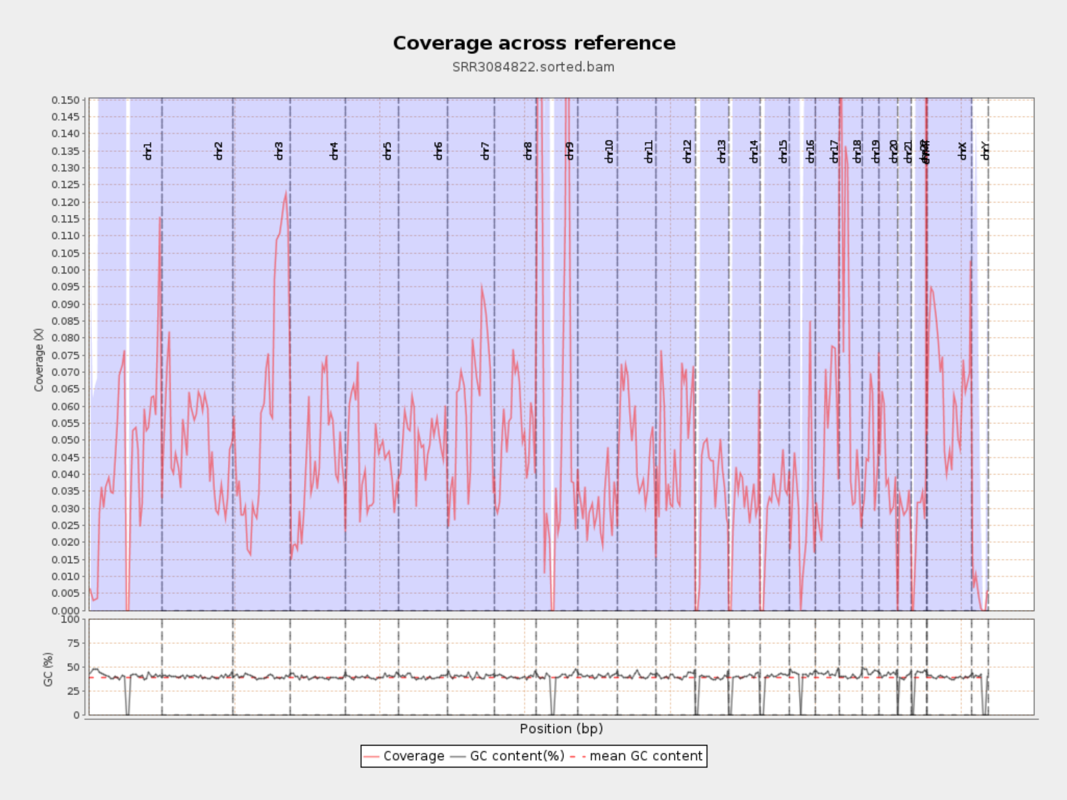
General error rate	0.77%
Mismatches	1,106,782
Insertions	11,818
Mapped reads with at least one insertion	0.54%
Deletions	34,396
Mapped reads with at least one deletion	1.58%
Homopolymer indels	49.07%

2.6. Chromosome stats

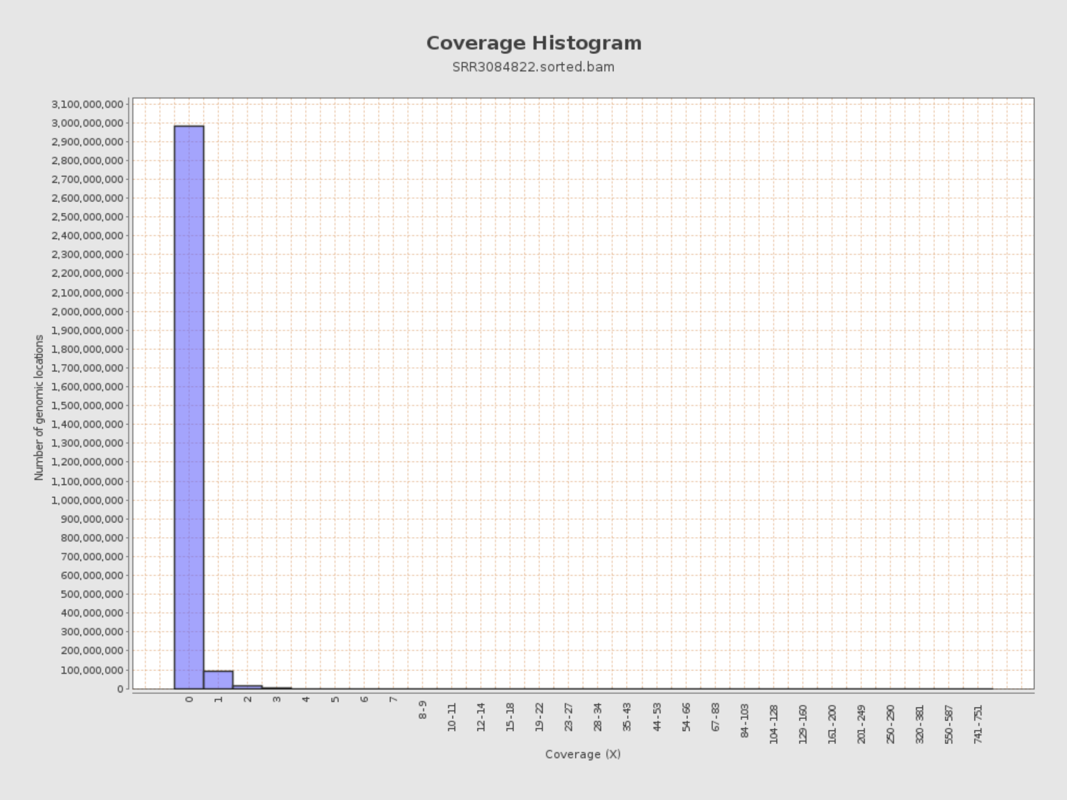
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10590793	0.0425	0.3352
chr2	243199373	11907178	0.049	0.433
chr3	198022430	12154307	0.0614	0.3037
chr4	191154276	8066600	0.0422	0.2537
chr5	180915260	8087521	0.0447	0.2557
chr6	171115067	8501910	0.0497	0.2854
chr7	159138663	9702416	0.061	0.3516

chr8	146364022	7605106	0.052	0.3537
chr9	141213431	10307374	0.073	0.3745
chr10	135534747	4079770	0.0301	0.2171
chr11	135006516	6613351	0.049	0.3317
chr12	133851895	6573919	0.0491	0.2696
chr13	115169878	3988454	0.0346	0.2246
chr14	107349540	3160293	0.0294	0.2095
chr15	102531392	3005938	0.0293	0.2149
chr16	90354753	2834047	0.0314	0.2175
chr17	81195210	4161852	0.0513	0.2823
chr18	78077248	5957954	0.0763	0.455
chr19	59128983	2775612	0.0469	0.2849
chr20	63025520	2624515	0.0416	0.2484
chr21	48129895	1313503	0.0273	0.2071
chr22	51304566	1160643	0.0226	0.1776
chrMT	16571	65957	3.9803	3.0018
chrX	155270560	10244264	0.066	0.3232
chrY	59373566	292400	0.0049	0.0873

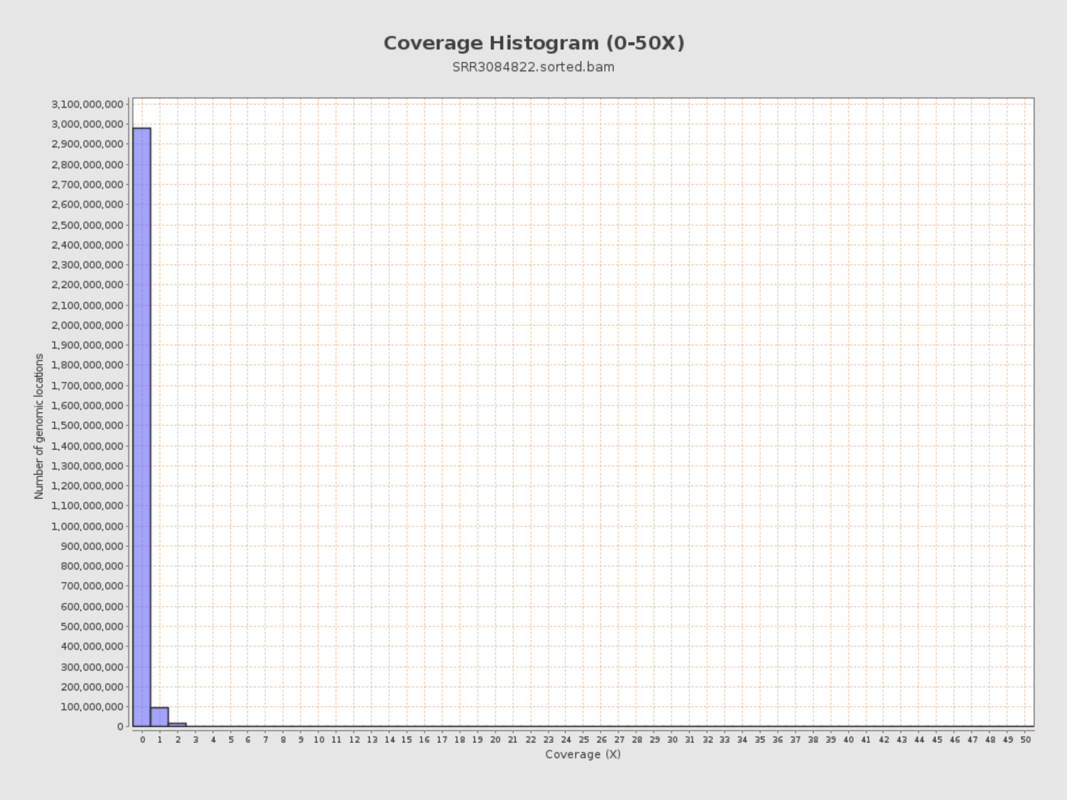
3. Results : Coverage across reference



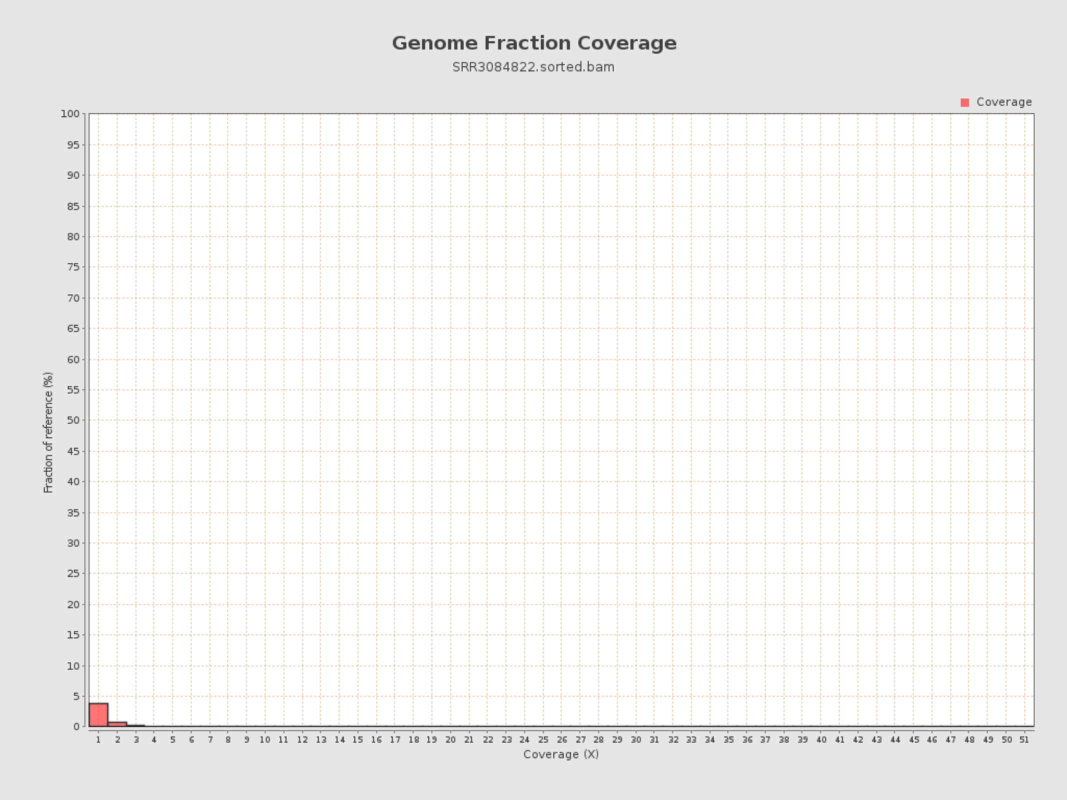
4. Results : Coverage Histogram



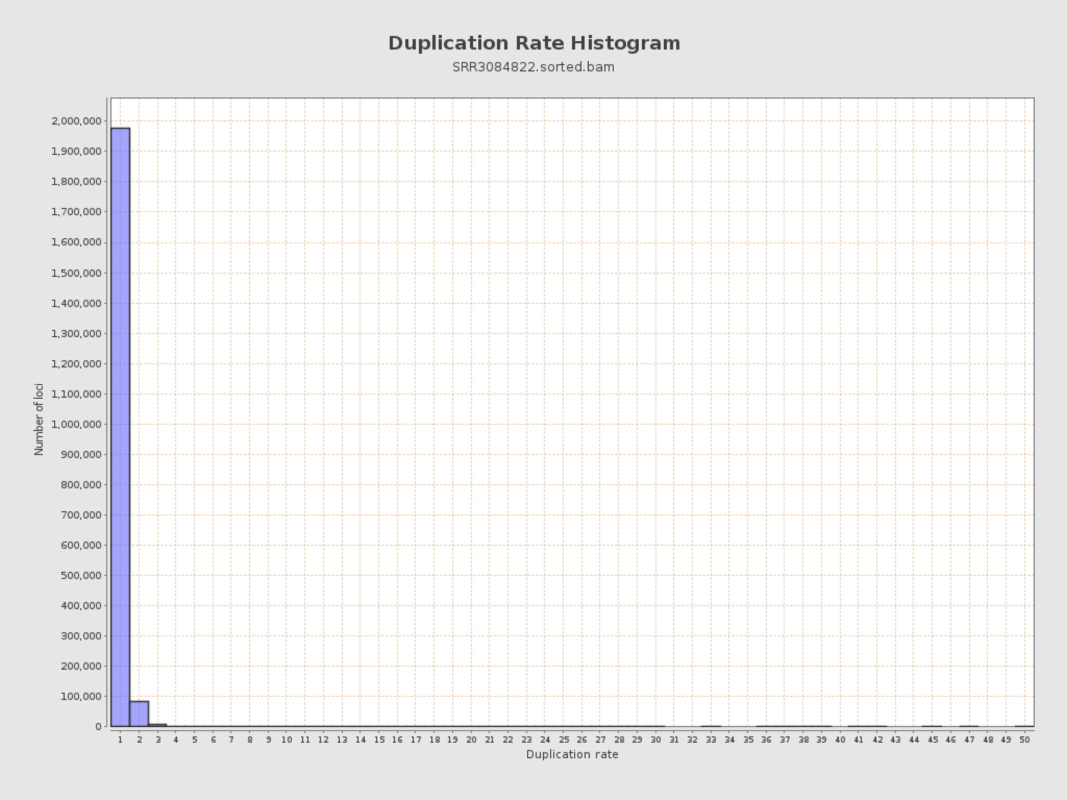
5. Results : Coverage Histogram (0-50X)



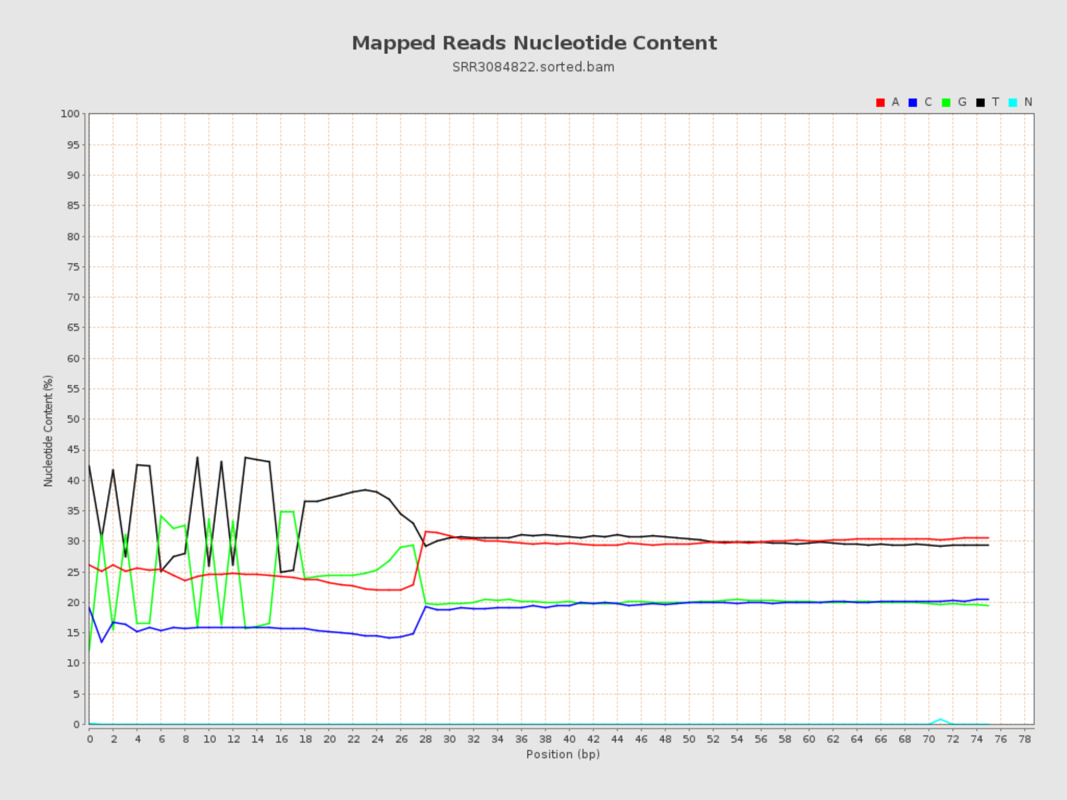
6. Results : Genome Fraction Coverage



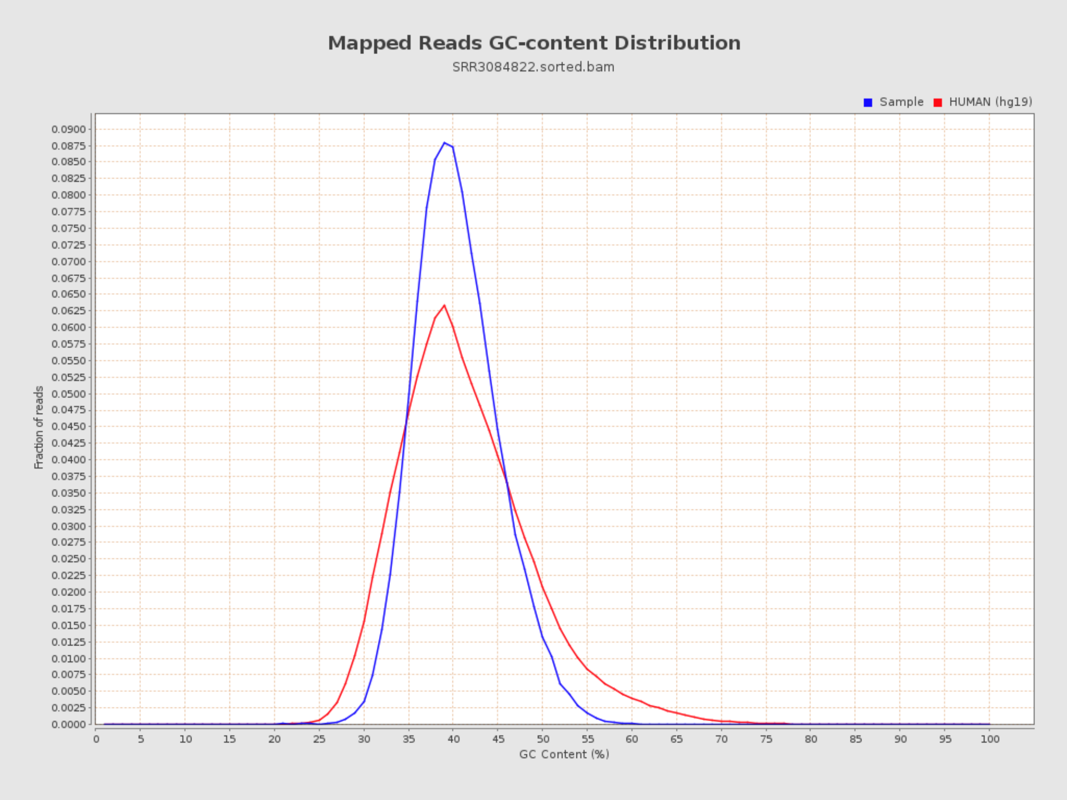
7. Results : Duplication Rate Histogram



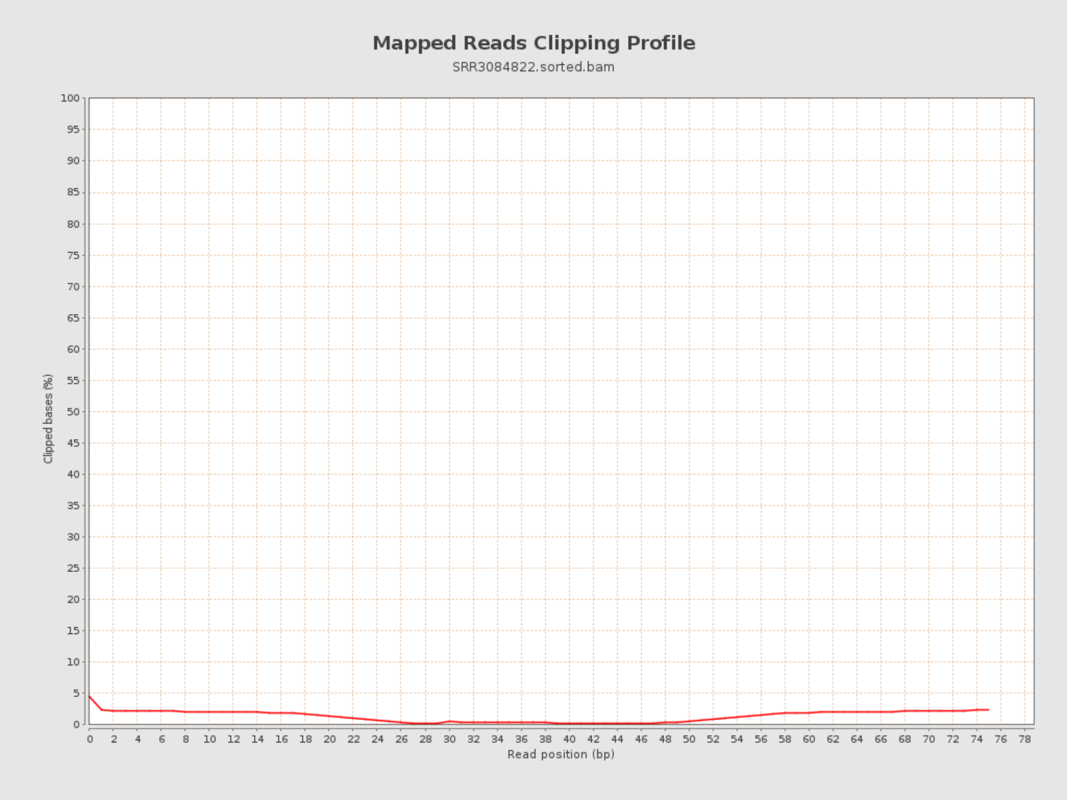
8. Results : Mapped Reads Nucleotide Content



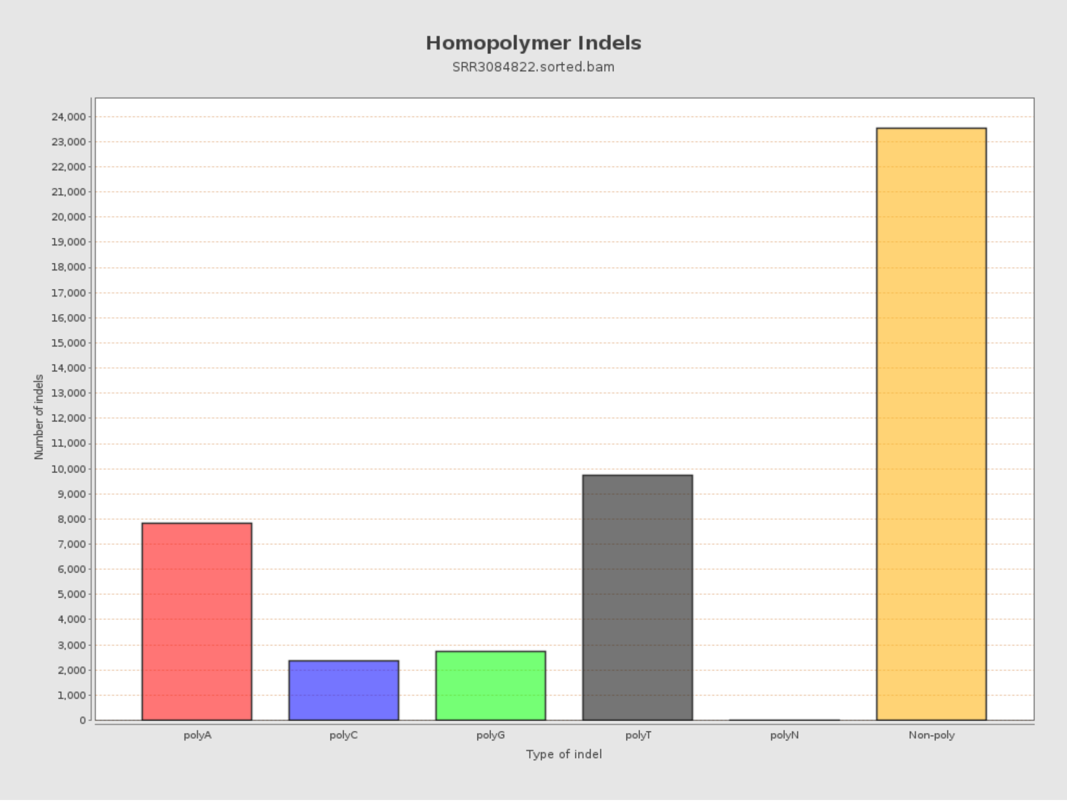
9. Results : Mapped Reads GC-content Distribution



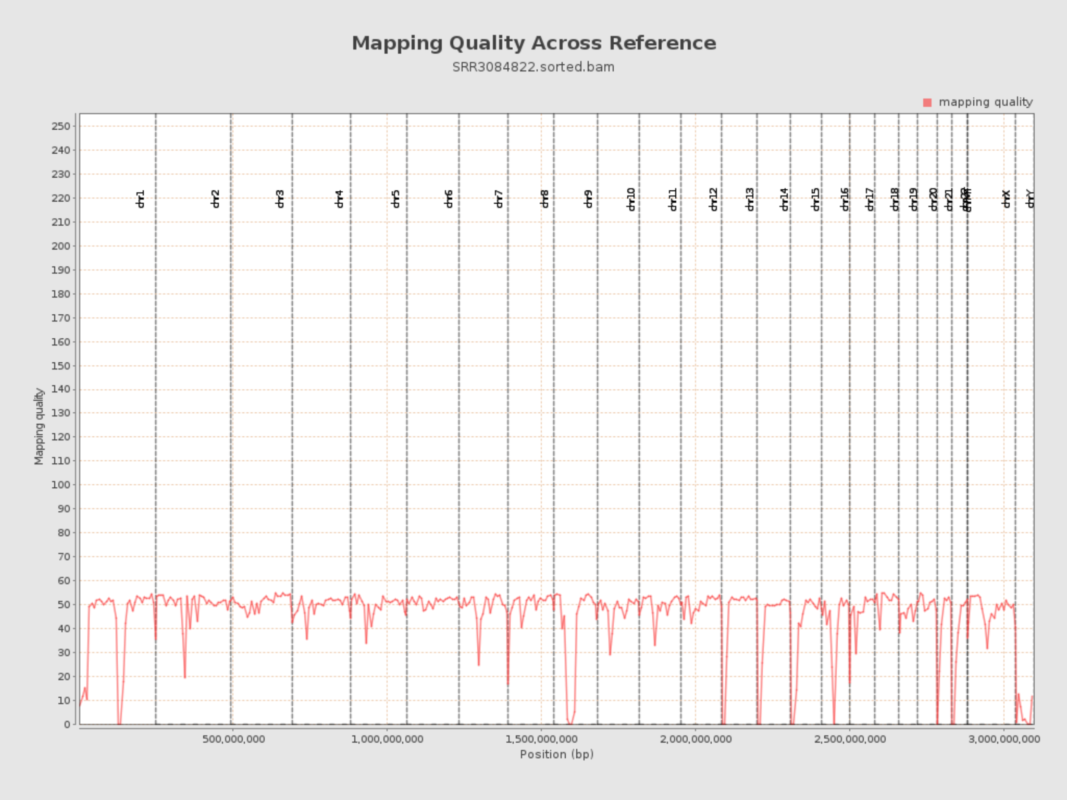
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram