Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 17:10:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084846.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_SRR3084846 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084846.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 17:10:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084846.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,511,864
Mapped reads	2,193,726 / 87.33%
Unmapped reads	318,138 / 12.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,593 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	109,357 / 4.35%
Duplication rate	4.16%
Clipped reads	745,386 / 29.67%

2.2. ACGT Content

Number/percentage of A's	44,456,275 / 29.25%
Number/percentage of C's	27,953,876 / 18.39%
Number/percentage of T's	48,741,900 / 32.07%
Number/percentage of G's	30,819,011 / 20.28%
Number/percentage of N's	24,506 / 0.02%
GC Percentage	38.67%

2.3. Coverage

Mean	0.0491

Standard Deviation	0.4226

2.4. Mapping Quality

Mean Mapping Quality	48.07

2.5. Mismatches and indels

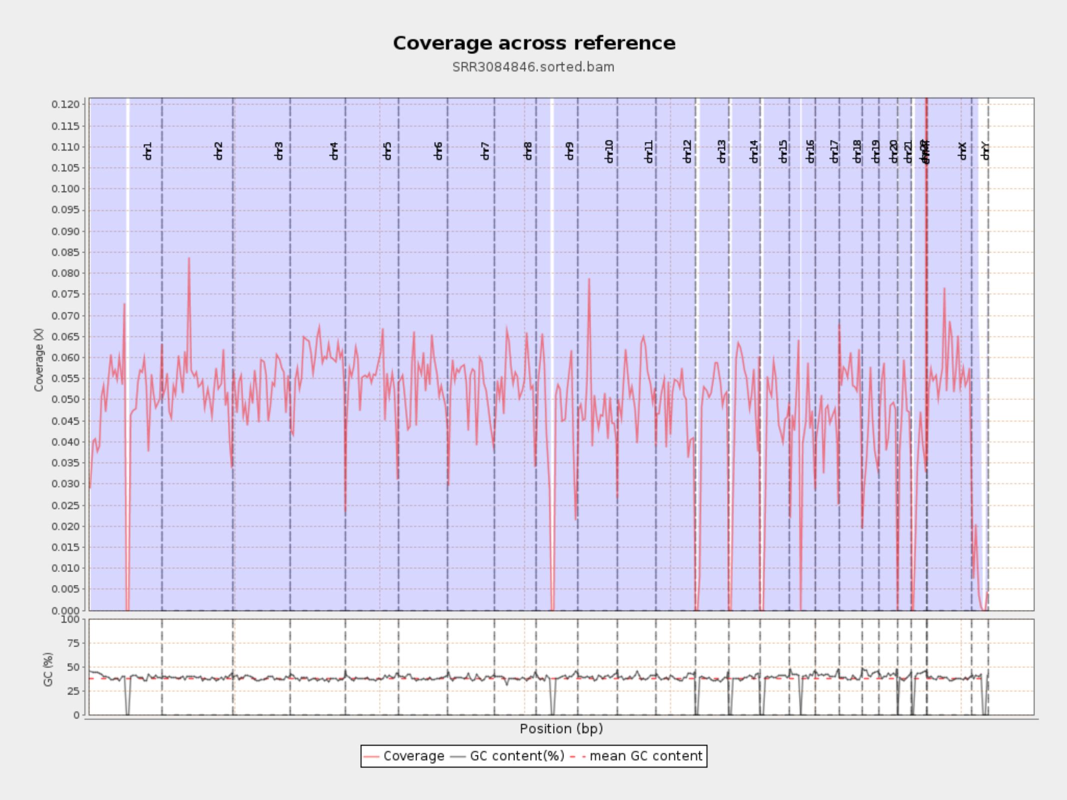
General error rate	0.84%
Mismatches	1,256,559
Insertions	12,831
Mapped reads with at least one insertion	0.58%
Deletions	33,495
Mapped reads with at least one deletion	1.51%
Homopolymer indels	47.86%

2.6. Chromosome stats

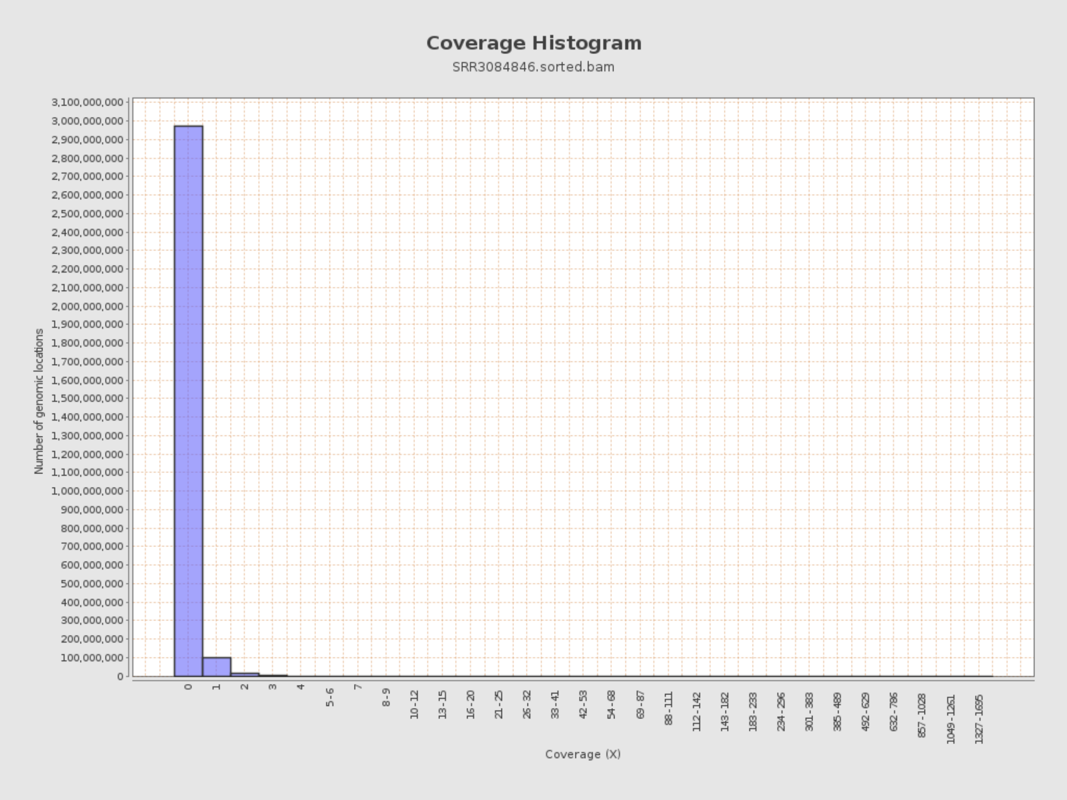
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11897308	0.0477	0.6212
chr2	243199373	13036246	0.0536	0.389
chr3	198022430	10453763	0.0528	0.2733
chr4	191154276	11233786	0.0588	0.304
chr5	180915260	9858701	0.0545	0.2794
chr6	171115067	9276620	0.0542	0.2903
chr7	159138663	8332957	0.0524	0.3313

chr8	146364022	7939117	0.0542	1.1044
chr9	141213431	6163828	0.0436	0.3431
chr10	135534747	6535190	0.0482	0.386
chr11	135006516	7168950	0.0531	0.3438
chr12	133851895	6418608	0.048	0.2623
chr13	115169878	5040316	0.0438	0.2487
chr14	107349540	4890222	0.0456	0.2615
chr15	102531392	4136517	0.0403	0.2378
chr16	90354753	3777105	0.0418	0.2655
chr17	81195210	3521060	0.0434	0.2833
chr18	78077248	4356216	0.0558	0.6259
chr19	59128983	2325520	0.0393	0.4036
chr20	63025520	2964651	0.047	0.2639
chr21	48129895	2008433	0.0417	0.2609
chr22	51304566	1404603	0.0274	0.1928
chrMT	16571	162972	9.8348	5.3806
chrX	155270560	8789274	0.0566	0.3048
chrY	59373566	364006	0.0061	0.1524

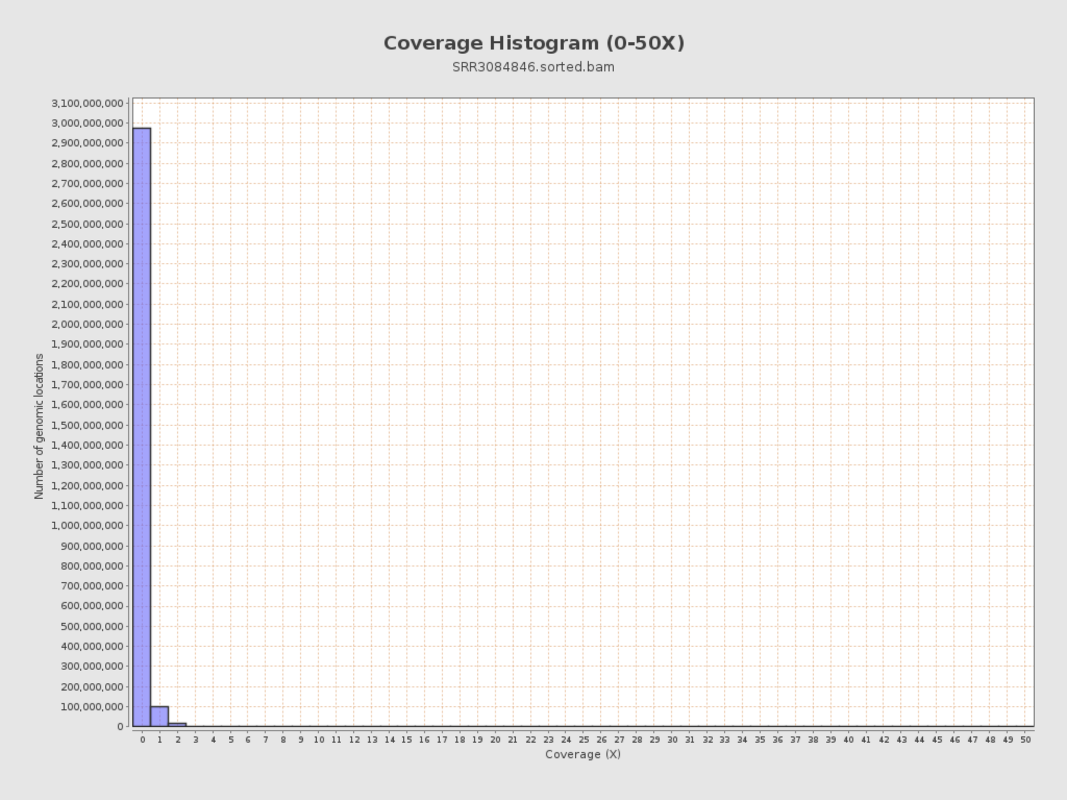
3. Results : Coverage across reference



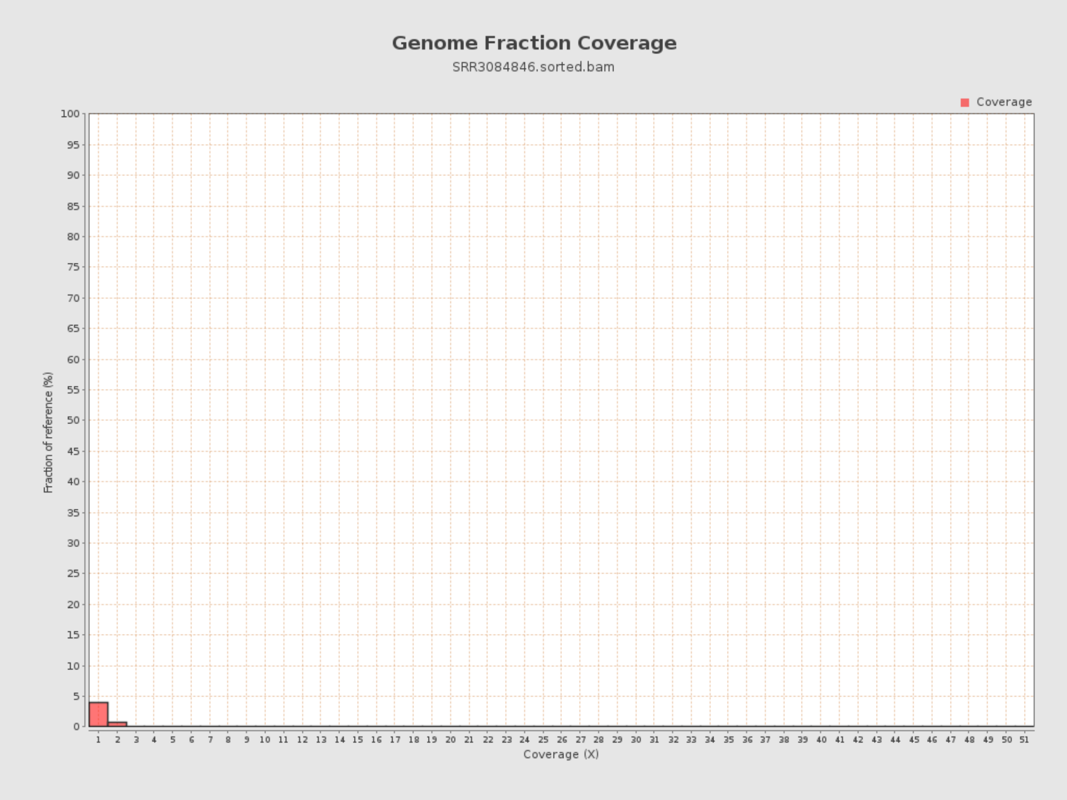
4. Results : Coverage Histogram



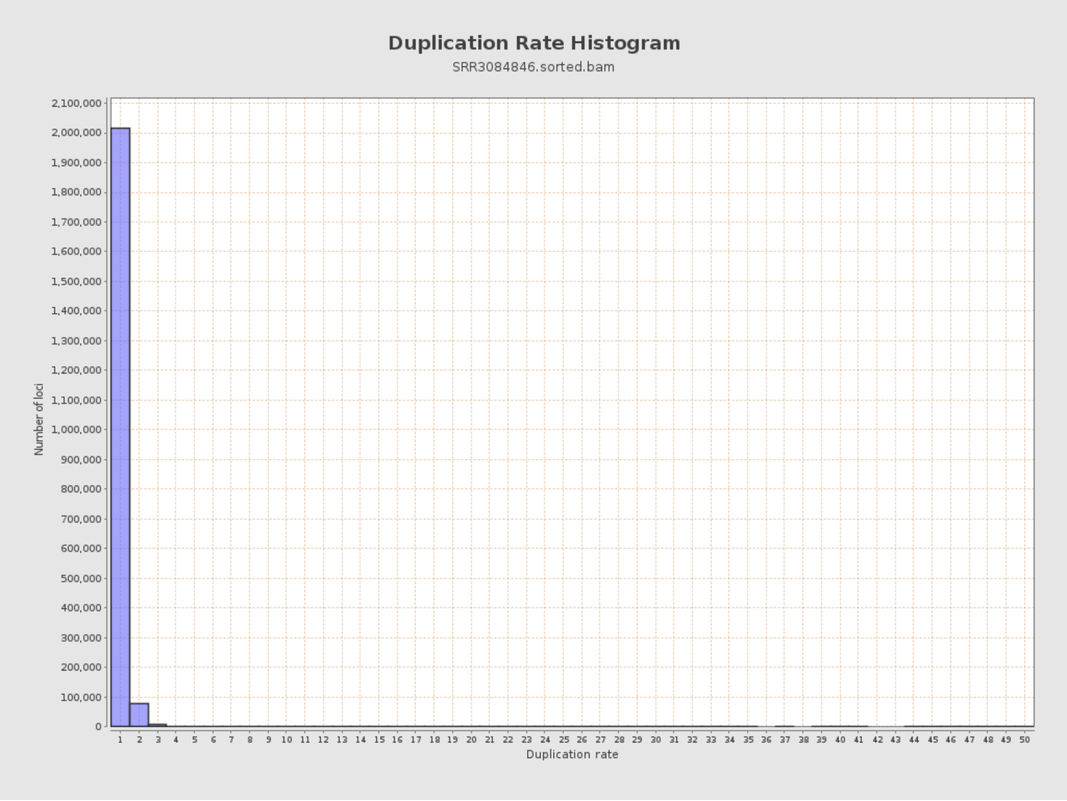
5. Results : Coverage Histogram (0-50X)



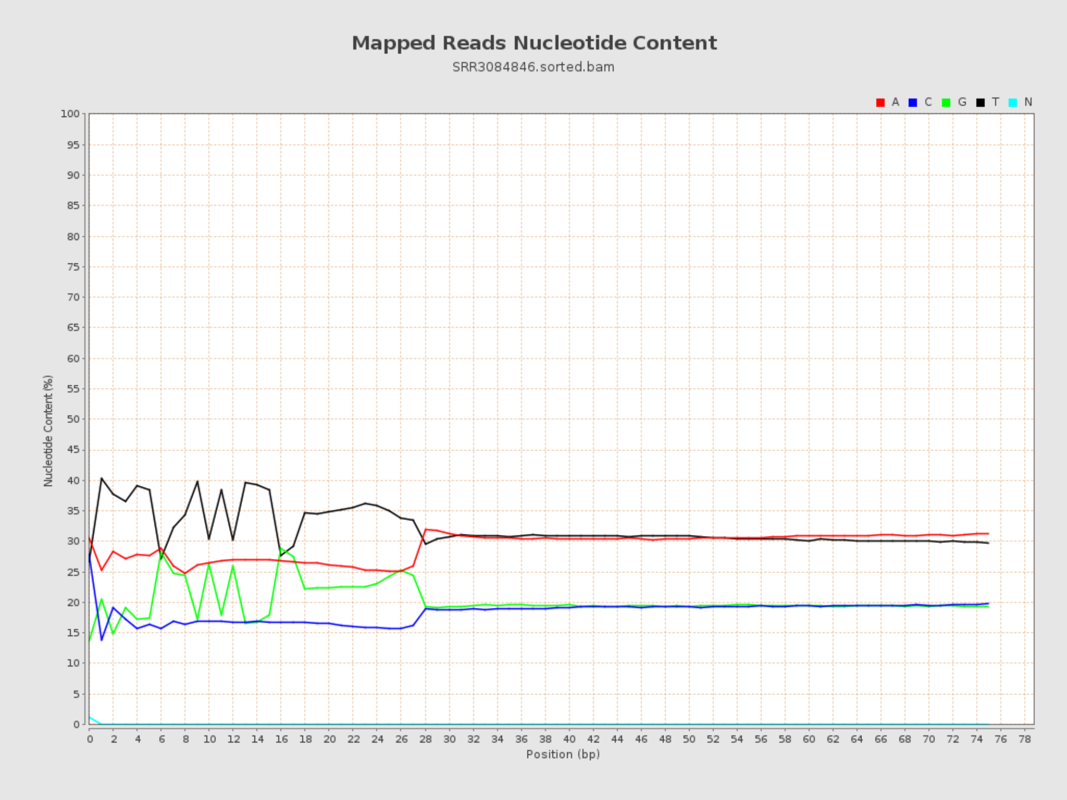
6. Results : Genome Fraction Coverage



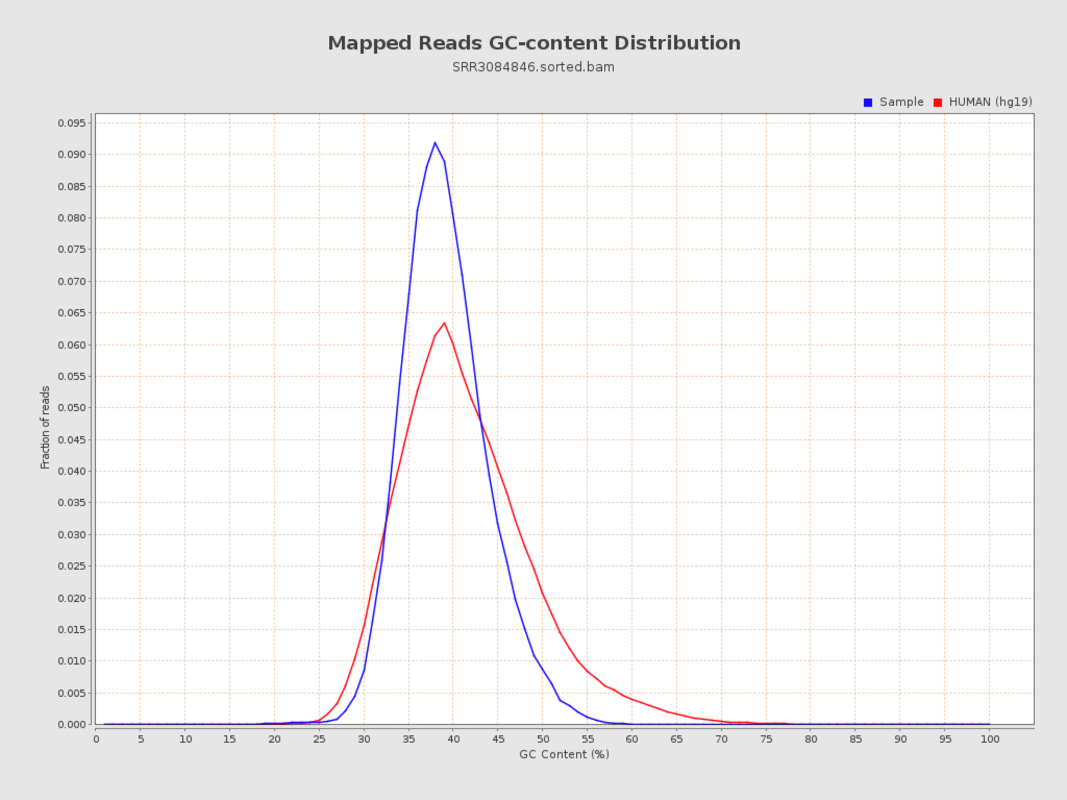
7. Results : Duplication Rate Histogram



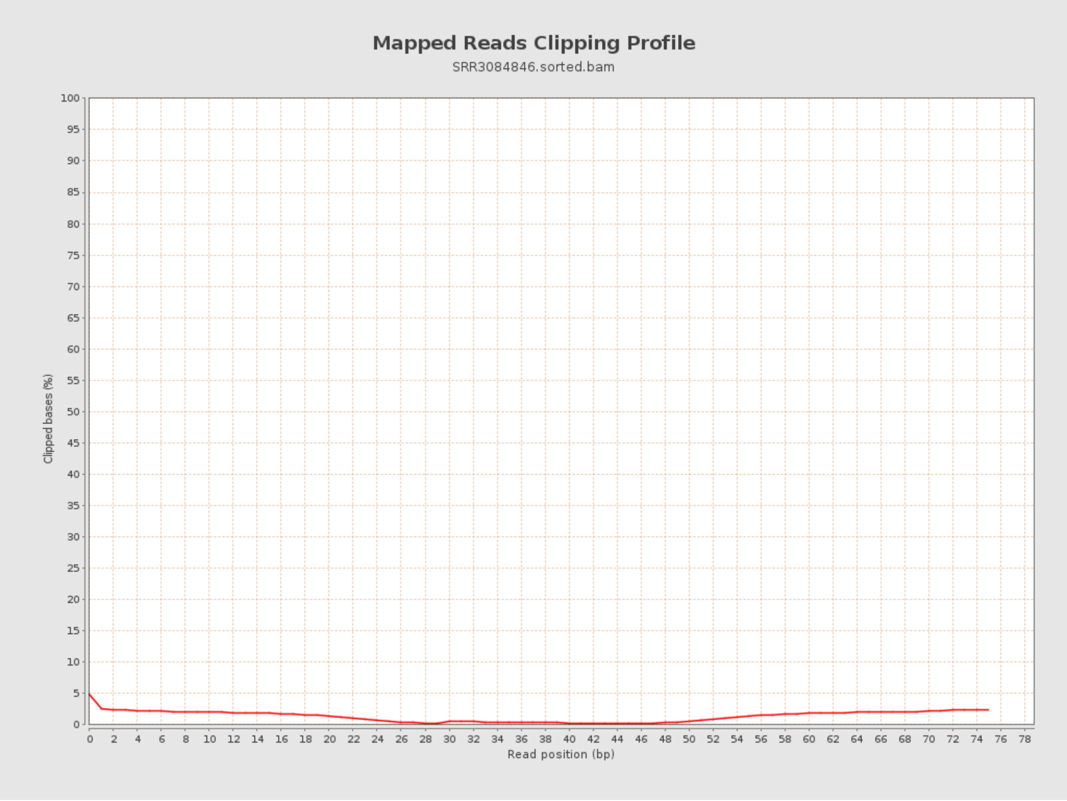
8. Results : Mapped Reads Nucleotide Content



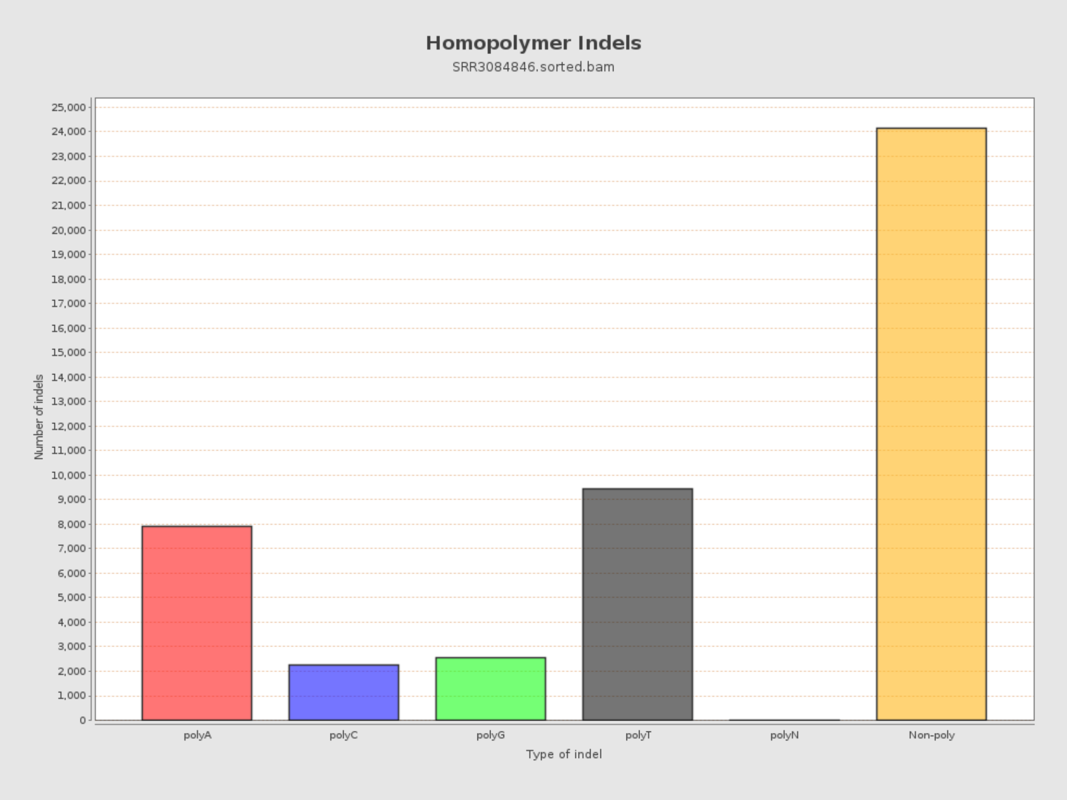
9. Results : Mapped Reads GC-content Distribution



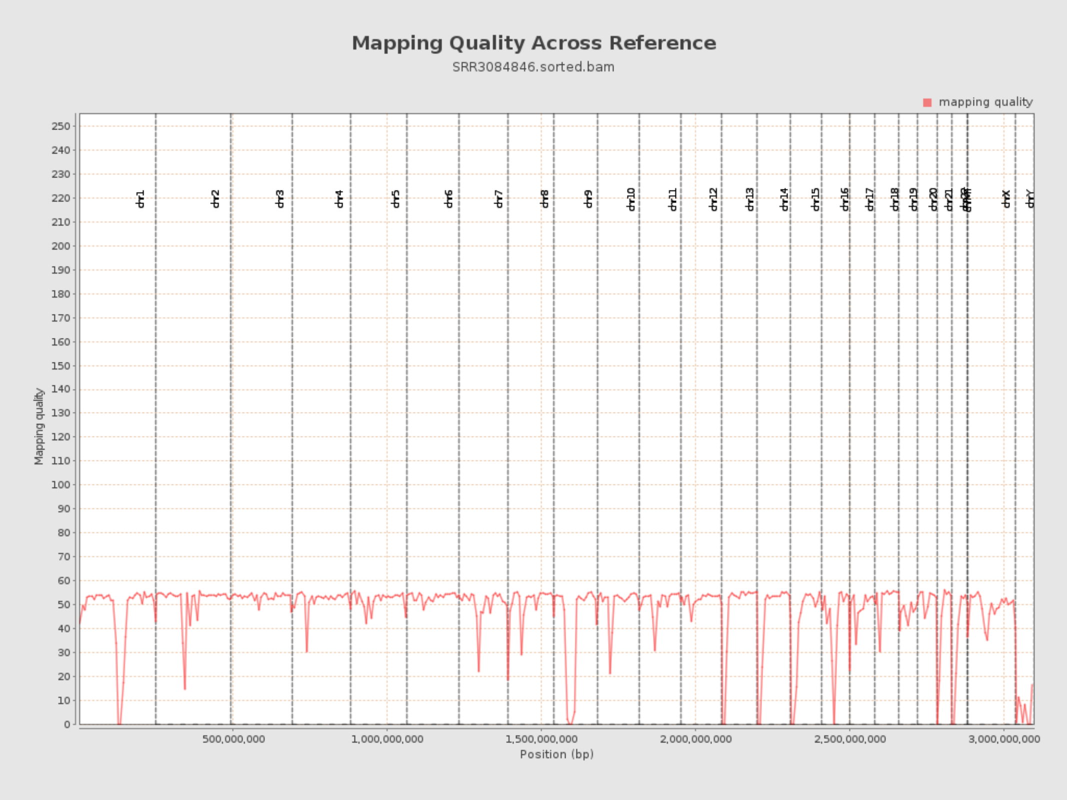
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram