Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 16:47:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084841.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_SRR3084841 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084841.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 16:47:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084841.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,589,902
Mapped reads	2,305,980 / 89.04%
Unmapped reads	283,922 / 10.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,656 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	131,053 / 5.06%
Duplication rate	4.77%
Clipped reads	782,276 / 30.2%

2.2. ACGT Content

Number/percentage of A's	46,516,750 / 29.12%
Number/percentage of C's	29,064,744 / 18.19%
Number/percentage of T's	51,687,336 / 32.35%
Number/percentage of G's	32,463,702 / 20.32%
Number/percentage of N's	25,308 / 0.02%
GC Percentage	38.51%

2.3. Coverage

Mean	0.0516

Standard Deviation	0.449

2.4. Mapping Quality

Mean Mapping Quality	48.24

2.5. Mismatches and indels

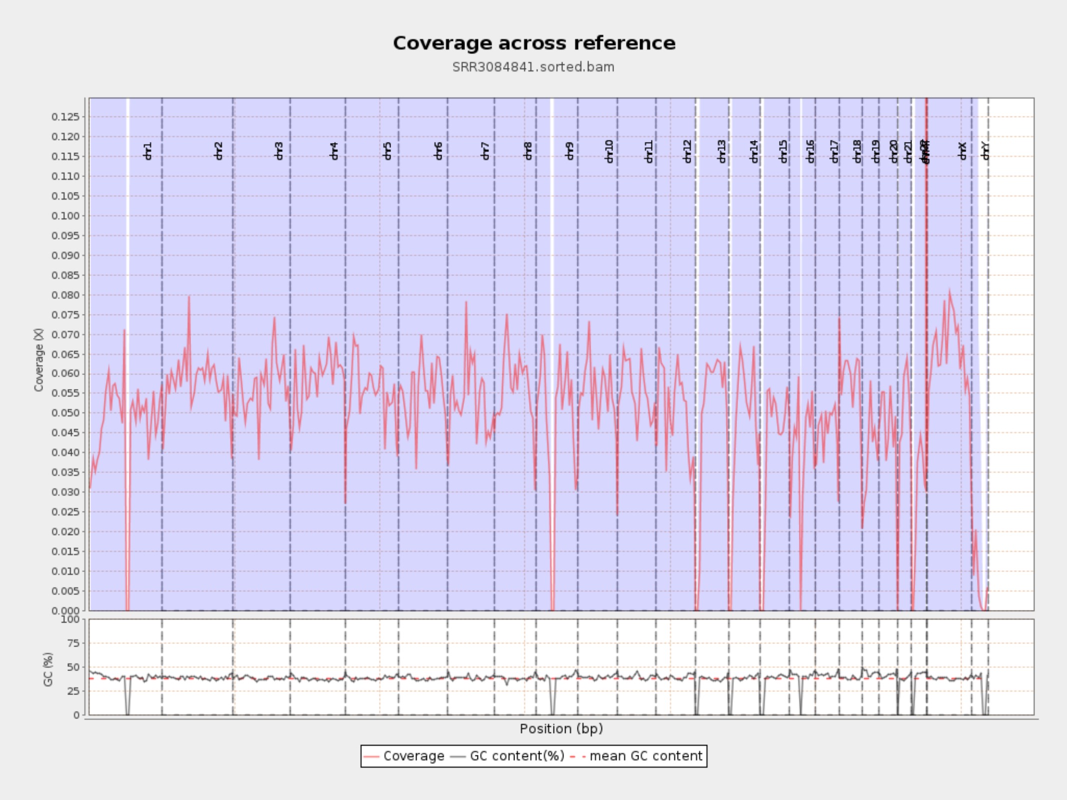
General error rate	0.83%
Mismatches	1,307,938
Insertions	13,231
Mapped reads with at least one insertion	0.57%
Deletions	35,281
Mapped reads with at least one deletion	1.51%
Homopolymer indels	48.79%

2.6. Chromosome stats

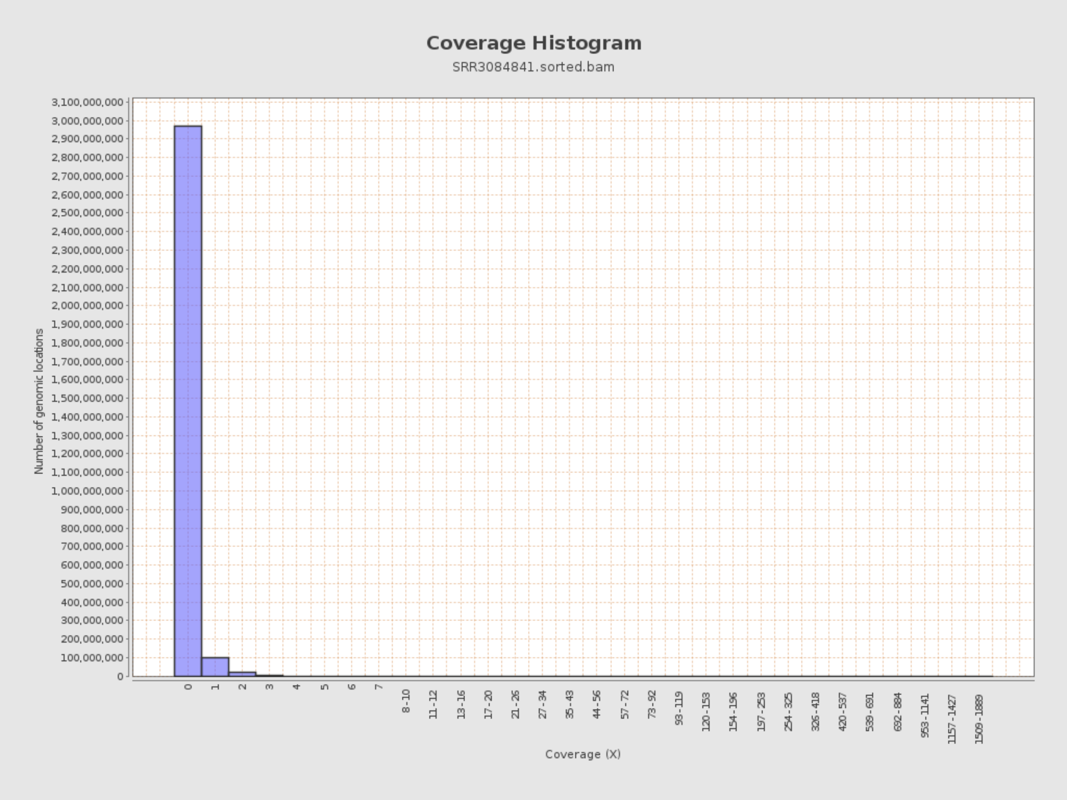
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11595573	0.0465	0.6431
chr2	243199373	14137116	0.0581	0.398
chr3	198022430	11238363	0.0568	0.2896
chr4	191154276	11219684	0.0587	0.3084
chr5	180915260	10063075	0.0556	0.2901
chr6	171115067	9473259	0.0554	0.2908
chr7	159138663	8631922	0.0542	0.4028

chr8	146364022	8261403	0.0564	1.2304
chr9	141213431	6806852	0.0482	0.351
chr10	135534747	7617821	0.0562	0.3499
chr11	135006516	7465286	0.0553	0.3411
chr12	133851895	6807468	0.0509	0.2766
chr13	115169878	5612408	0.0487	0.2701
chr14	107349540	4943475	0.0461	0.2689
chr15	102531392	4268737	0.0416	0.2471
chr16	90354753	3668327	0.0406	0.2603
chr17	81195210	3662425	0.0451	0.272
chr18	78077248	4644837	0.0595	0.6283
chr19	59128983	2377477	0.0402	0.4517
chr20	63025520	2979674	0.0473	0.2699
chr21	48129895	2246209	0.0467	0.278
chr22	51304566	1369416	0.0267	0.1941
chrMT	16571	256663	15.4887	7.4528
chrX	155270560	10068151	0.0648	0.328
chrY	59373566	405235	0.0068	0.1457

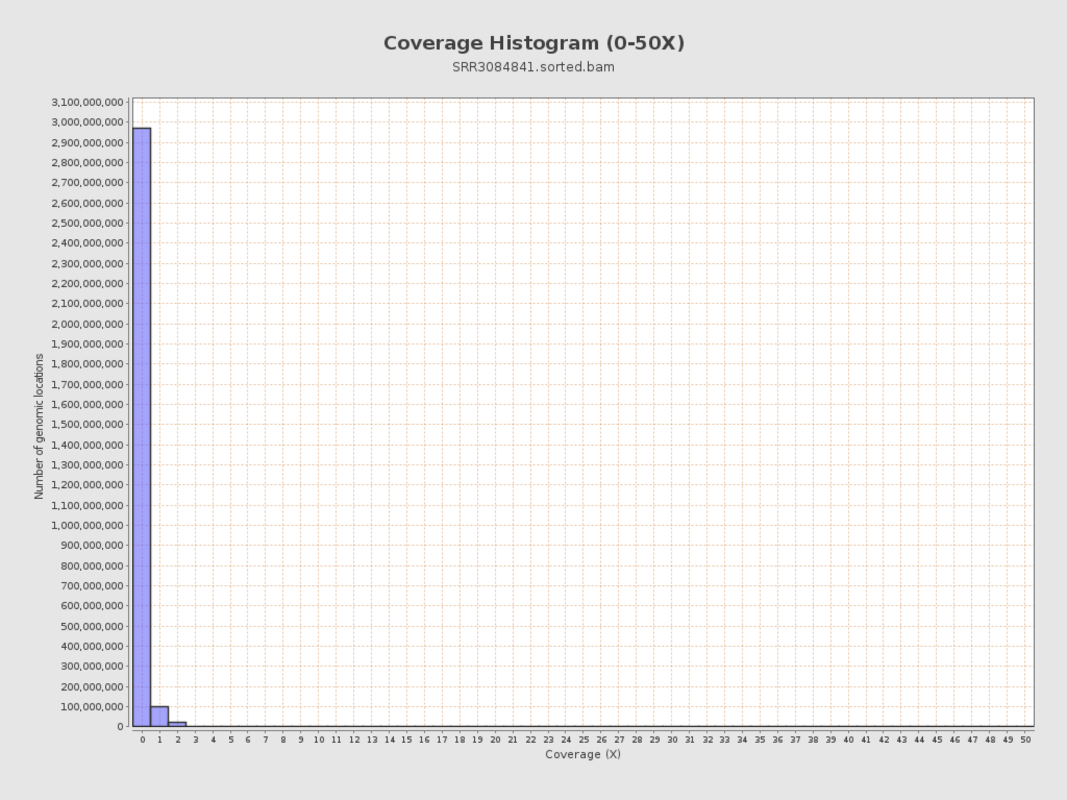
3. Results : Coverage across reference



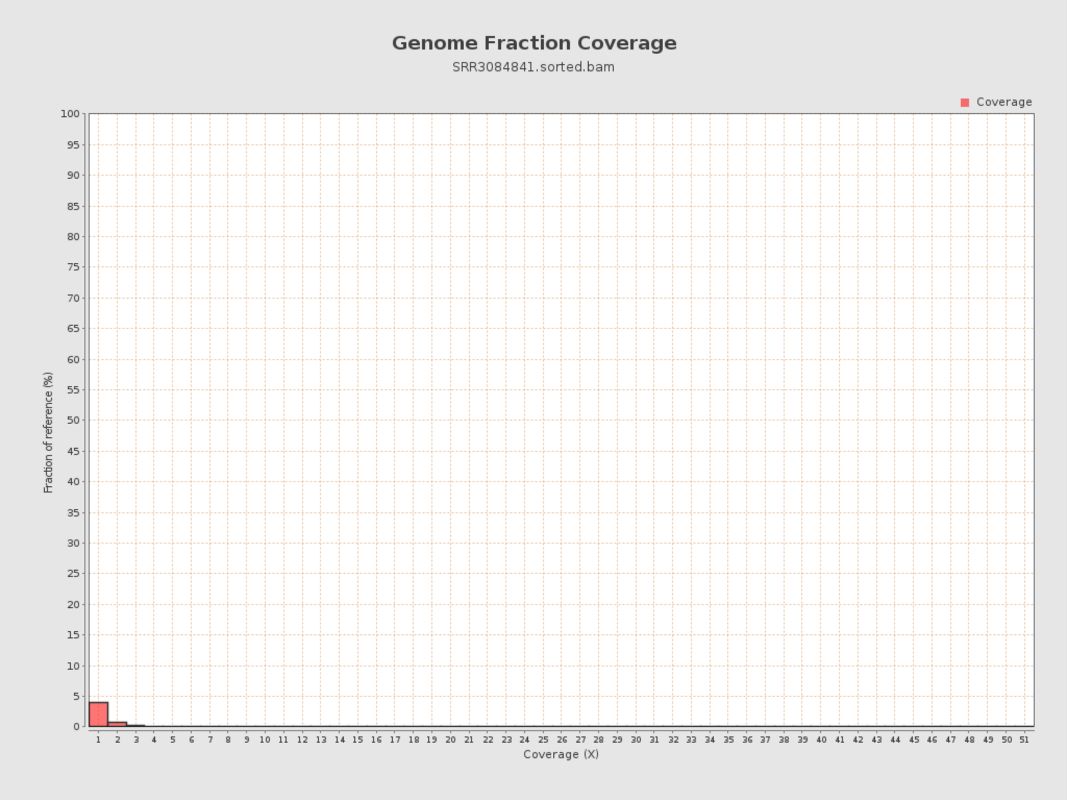
4. Results : Coverage Histogram



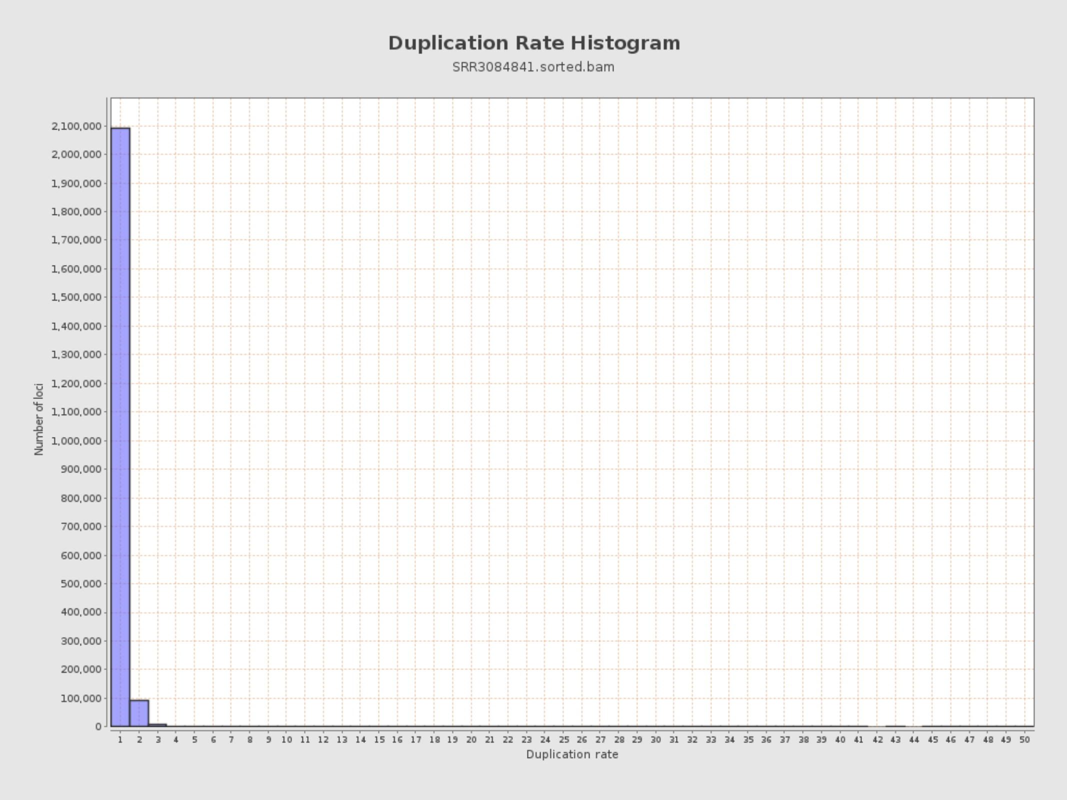
5. Results : Coverage Histogram (0-50X)



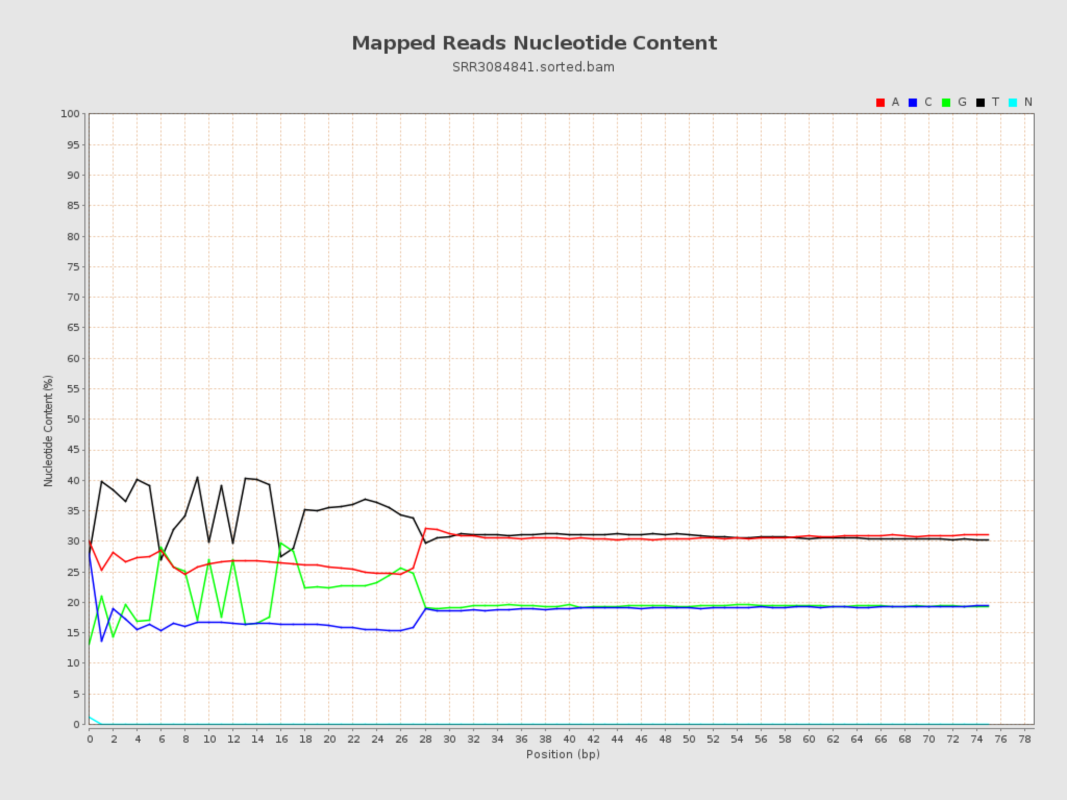
6. Results : Genome Fraction Coverage



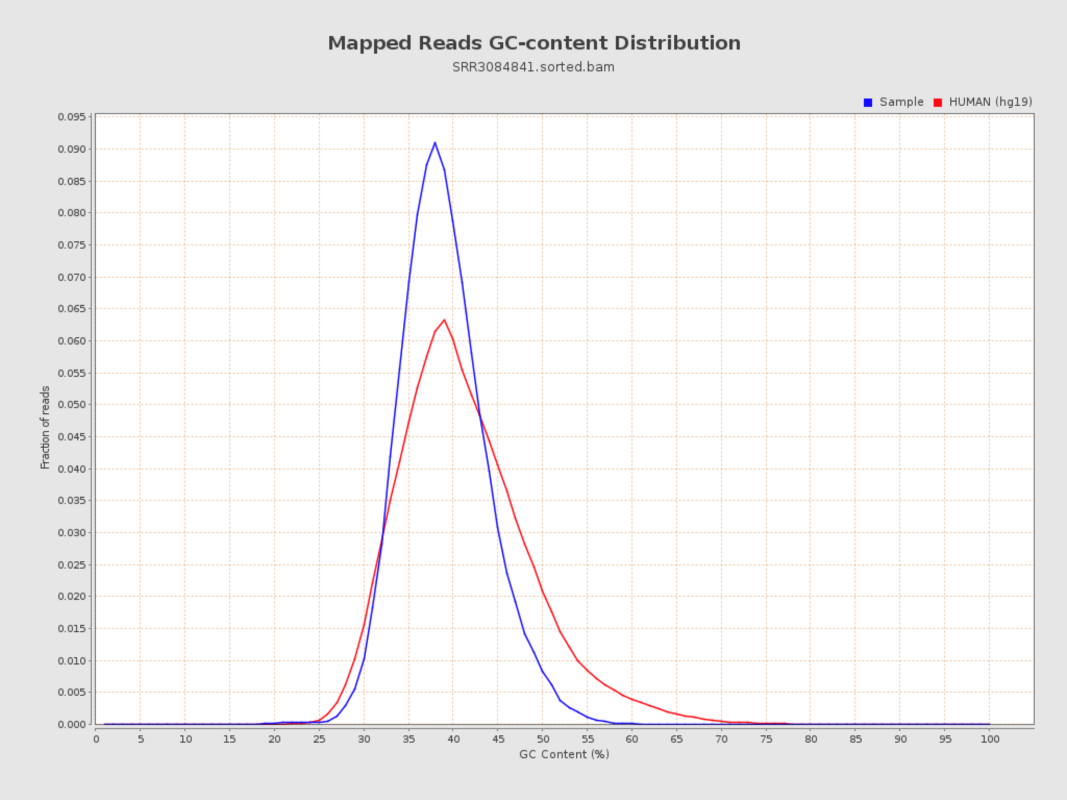
7. Results : Duplication Rate Histogram



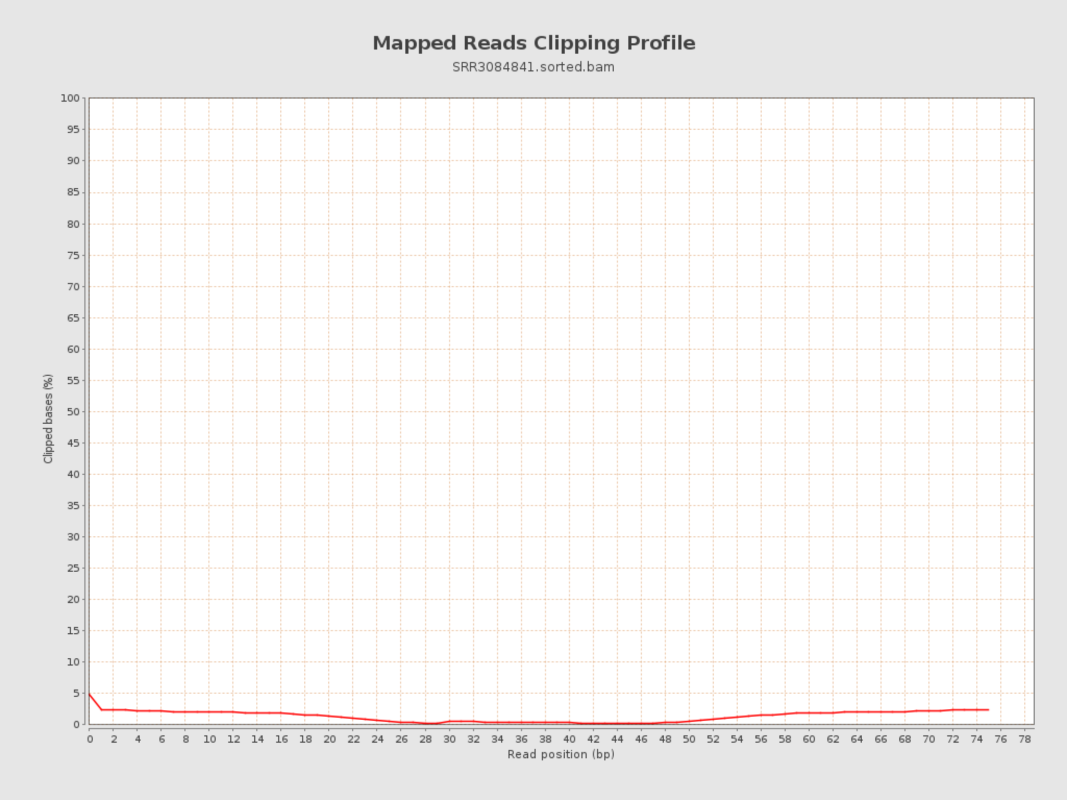
8. Results : Mapped Reads Nucleotide Content



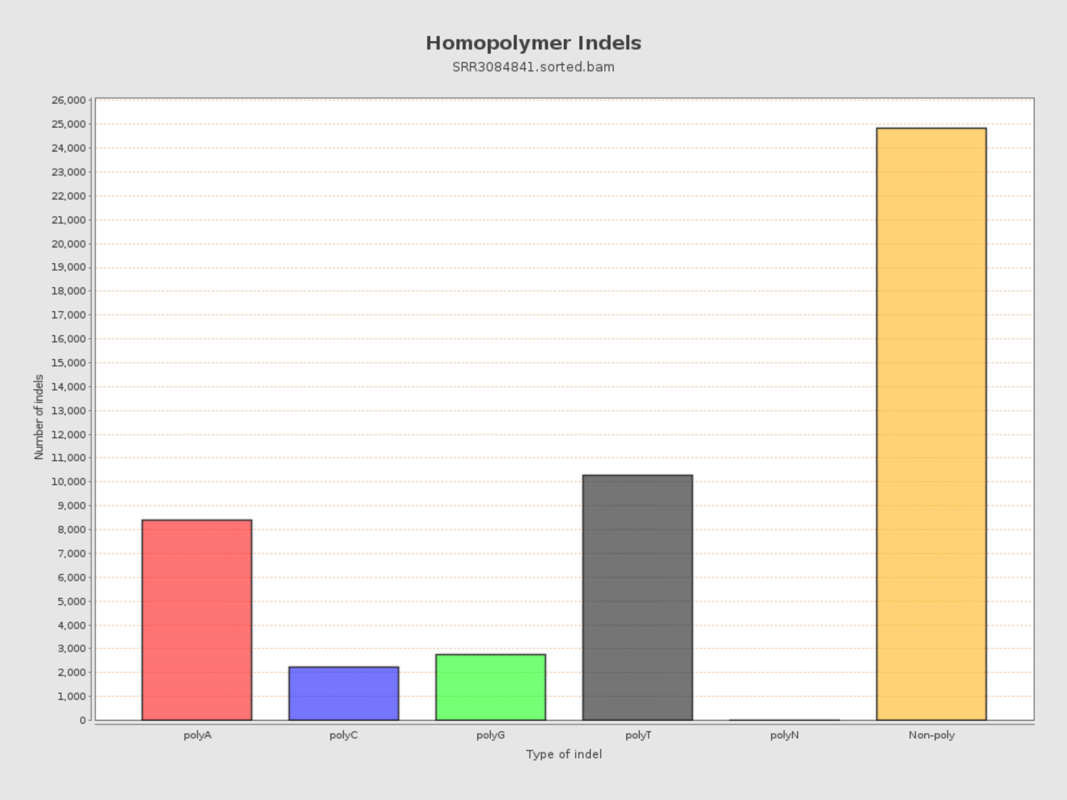
9. Results : Mapped Reads GC-content Distribution



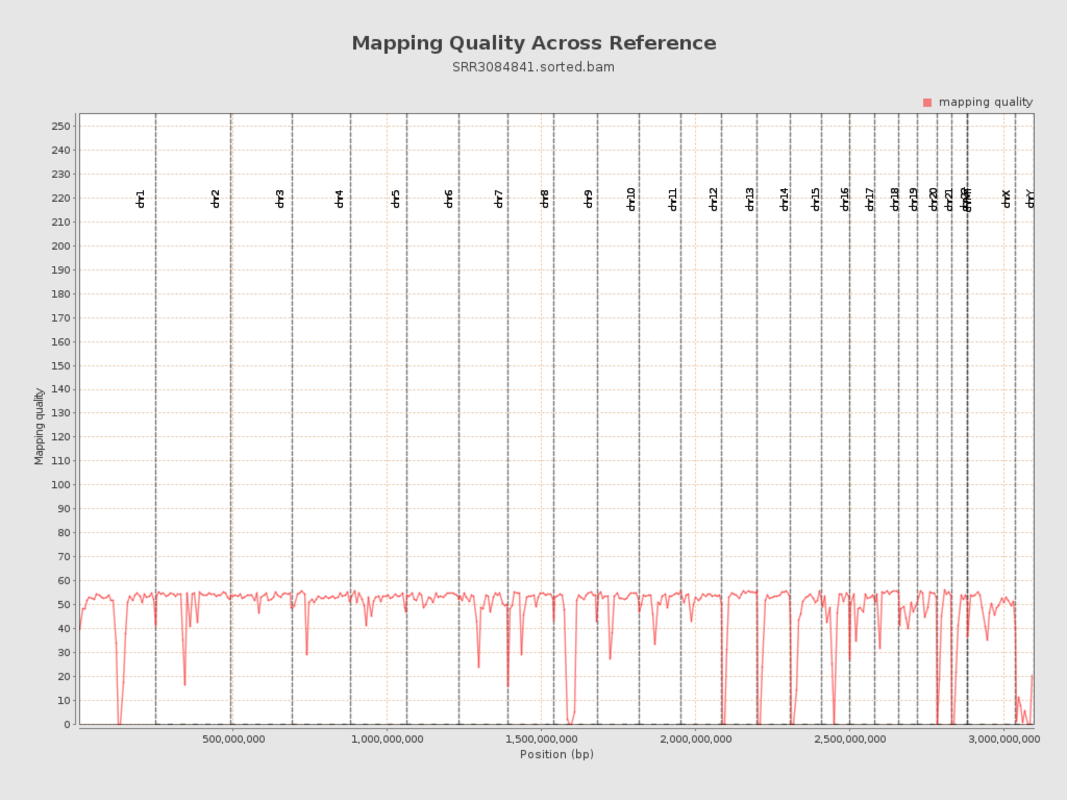
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram