Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 11:05:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084359.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_SRR3084359 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084359.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 11:05:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084359.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,458,781
Mapped reads	2,226,512 / 90.55%
Unmapped reads	232,269 / 9.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,851 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	81,697 / 3.32%
Duplication rate	3.08%
Clipped reads	976,015 / 39.7%

2.2. ACGT Content

Number/percentage of A's	41,447,081 / 27.75%
Number/percentage of C's	28,820,499 / 19.29%
Number/percentage of T's	45,837,284 / 30.69%
Number/percentage of G's	33,066,915 / 22.14%
Number/percentage of N's	201,207 / 0.13%
GC Percentage	41.43%

2.3. Coverage

Mean	0.0483

Standard Deviation	0.3366

2.4. Mapping Quality

Mean Mapping Quality	45.96

2.5. Mismatches and indels

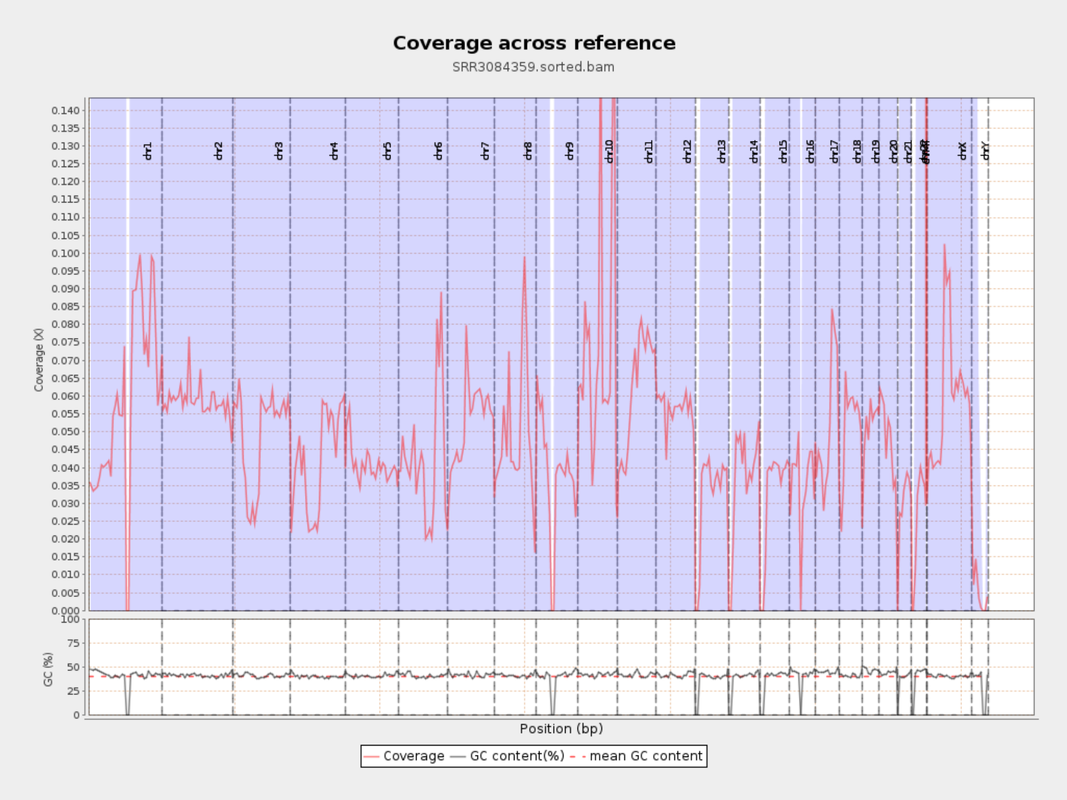
General error rate	1%
Mismatches	1,472,539
Insertions	10,342
Mapped reads with at least one insertion	0.46%
Deletions	28,776
Mapped reads with at least one deletion	1.28%
Homopolymer indels	46.29%

2.6. Chromosome stats

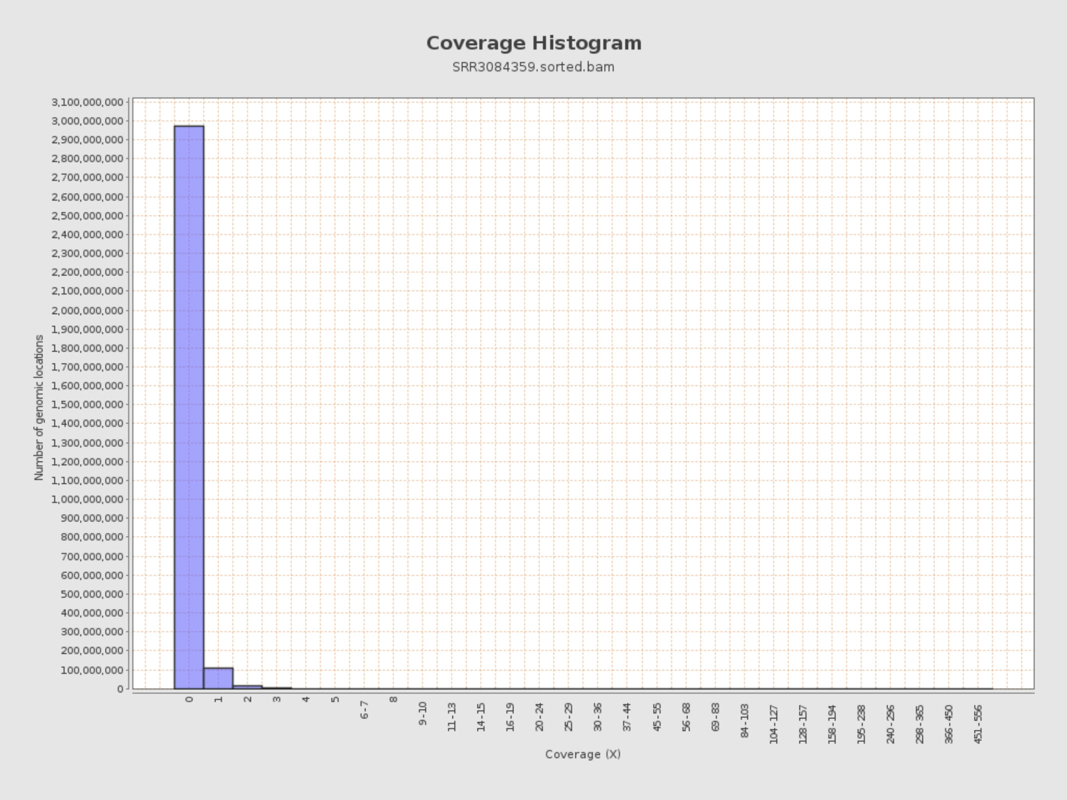
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14505262	0.0582	0.5437
chr2	243199373	14302631	0.0588	0.3718
chr3	198022430	9719422	0.0491	0.2563
chr4	191154276	8042490	0.0421	0.2423
chr5	180915260	7403995	0.0409	0.2325
chr6	171115067	7257866	0.0424	0.2628
chr7	159138663	8488341	0.0533	0.5252

chr8	146364022	7216965	0.0493	0.3131
chr9	141213431	5325896	0.0377	0.2709
chr10	135534747	10563656	0.0779	0.4334
chr11	135006516	8334404	0.0617	0.3474
chr12	133851895	7524950	0.0562	0.2729
chr13	115169878	3655807	0.0317	0.205
chr14	107349540	3901020	0.0363	0.2235
chr15	102531392	3290066	0.0321	0.2095
chr16	90354753	3203360	0.0355	0.2315
chr17	81195210	4184992	0.0515	0.2748
chr18	78077248	4001821	0.0513	0.4046
chr19	59128983	3061316	0.0518	0.3881
chr20	63025520	3015693	0.0478	0.2539
chr21	48129895	1415206	0.0294	0.2068
chr22	51304566	1260942	0.0246	0.1789
chrMT	16571	278657	16.8159	9.9652
chrX	155270560	9159561	0.059	0.3065
chrY	59373566	308719	0.0052	0.1099

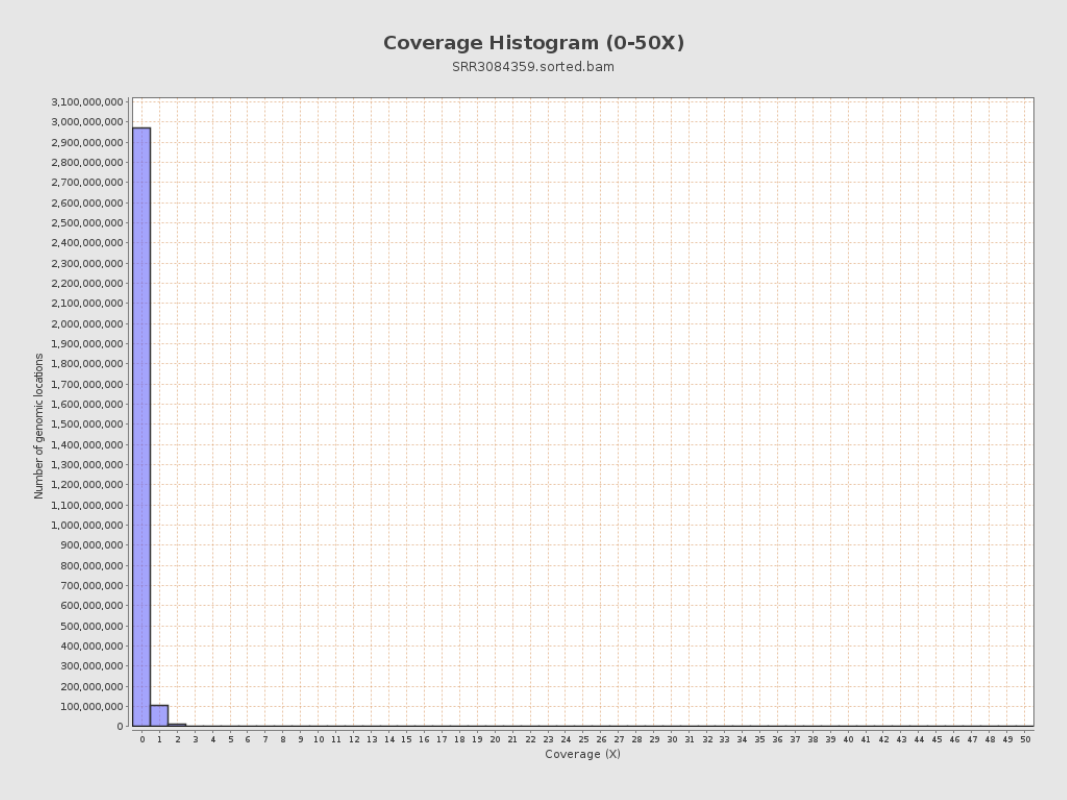
3. Results : Coverage across reference



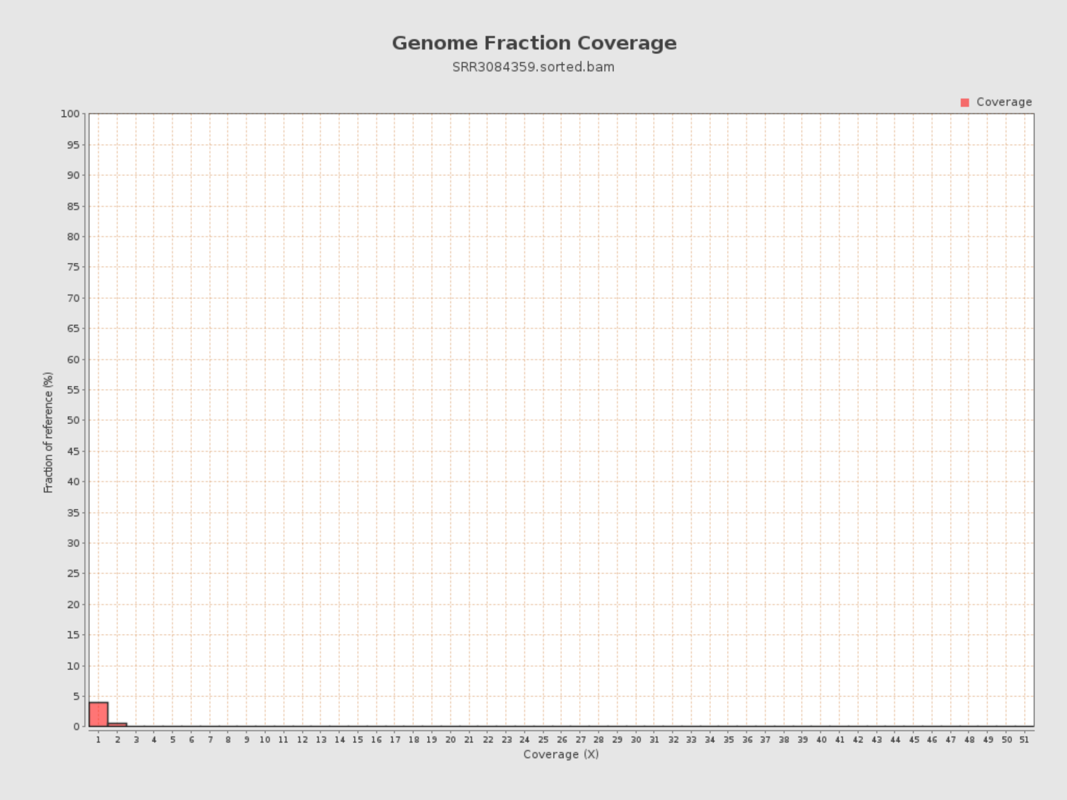
4. Results : Coverage Histogram



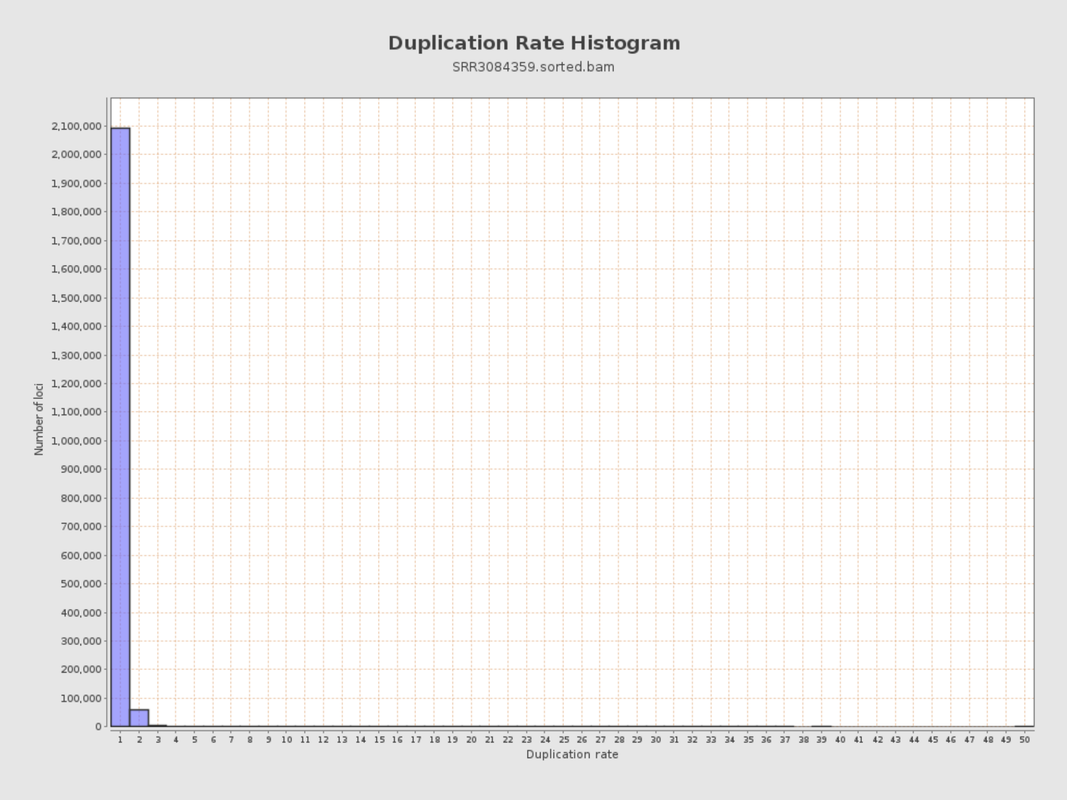
5. Results : Coverage Histogram (0-50X)



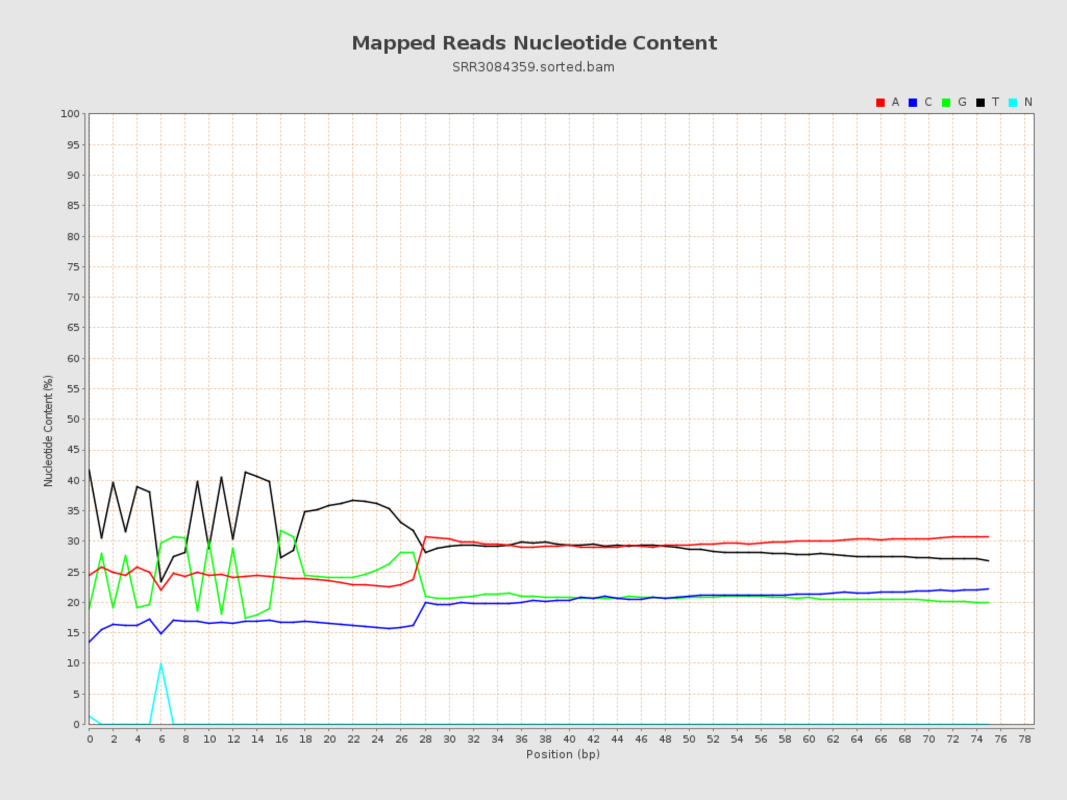
6. Results : Genome Fraction Coverage



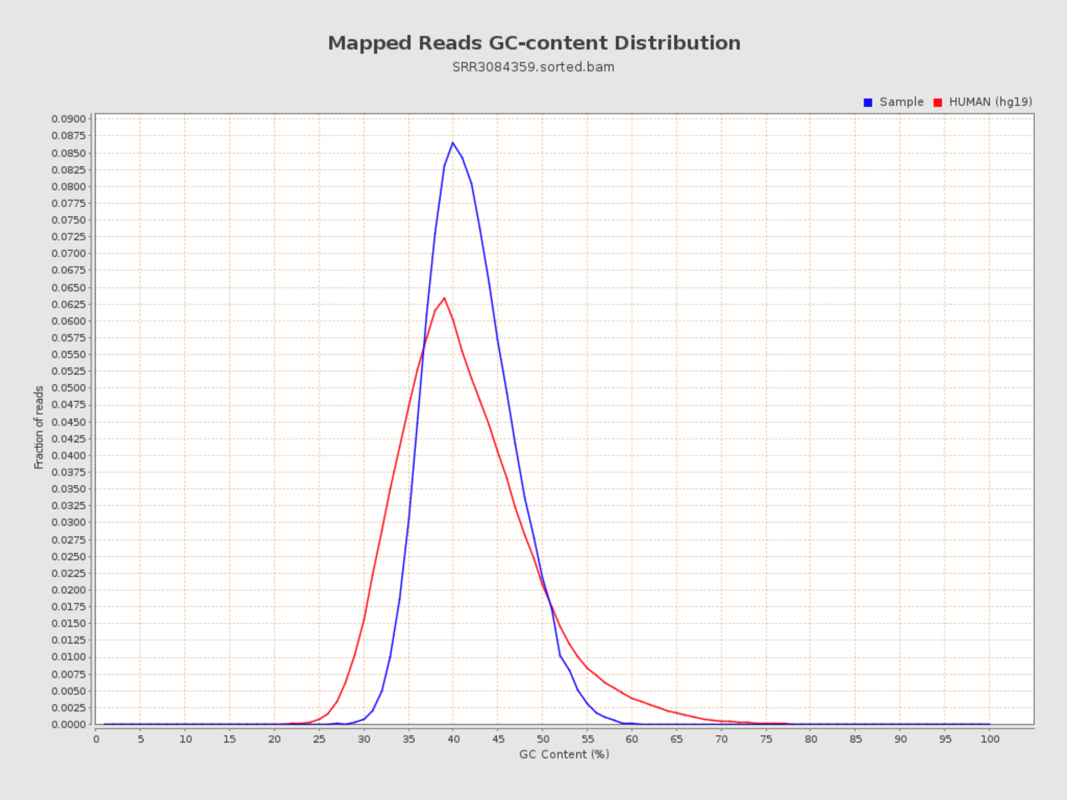
7. Results : Duplication Rate Histogram



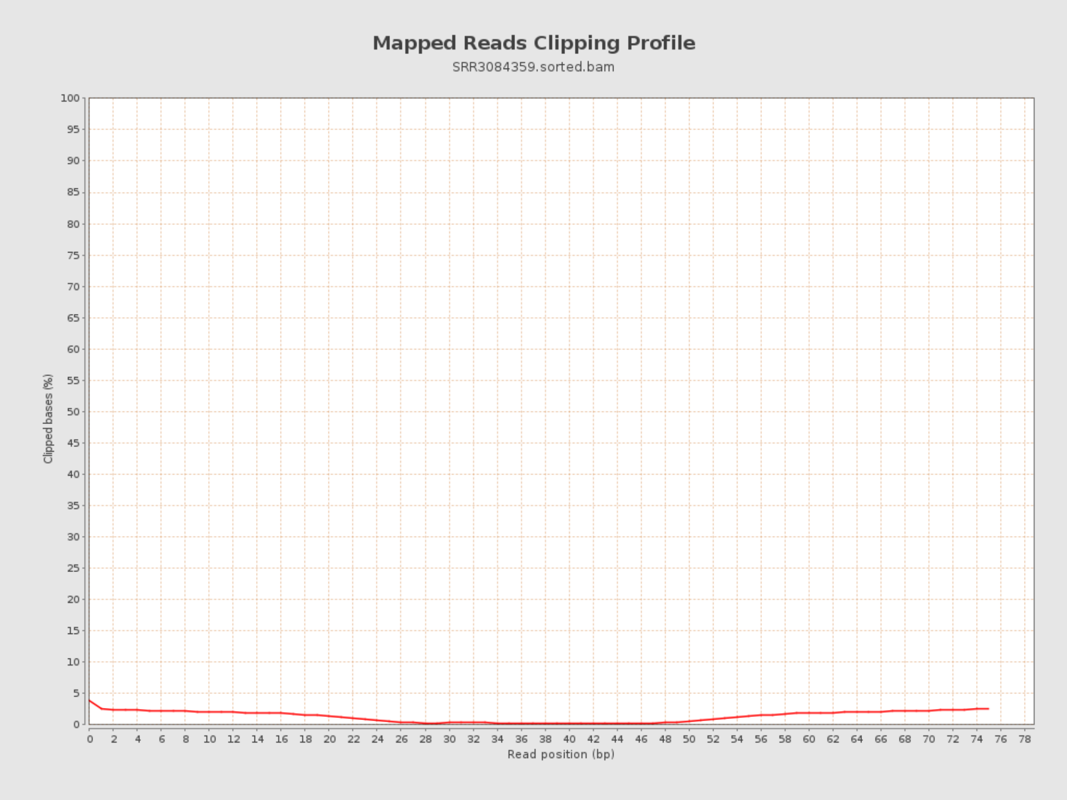
8. Results : Mapped Reads Nucleotide Content



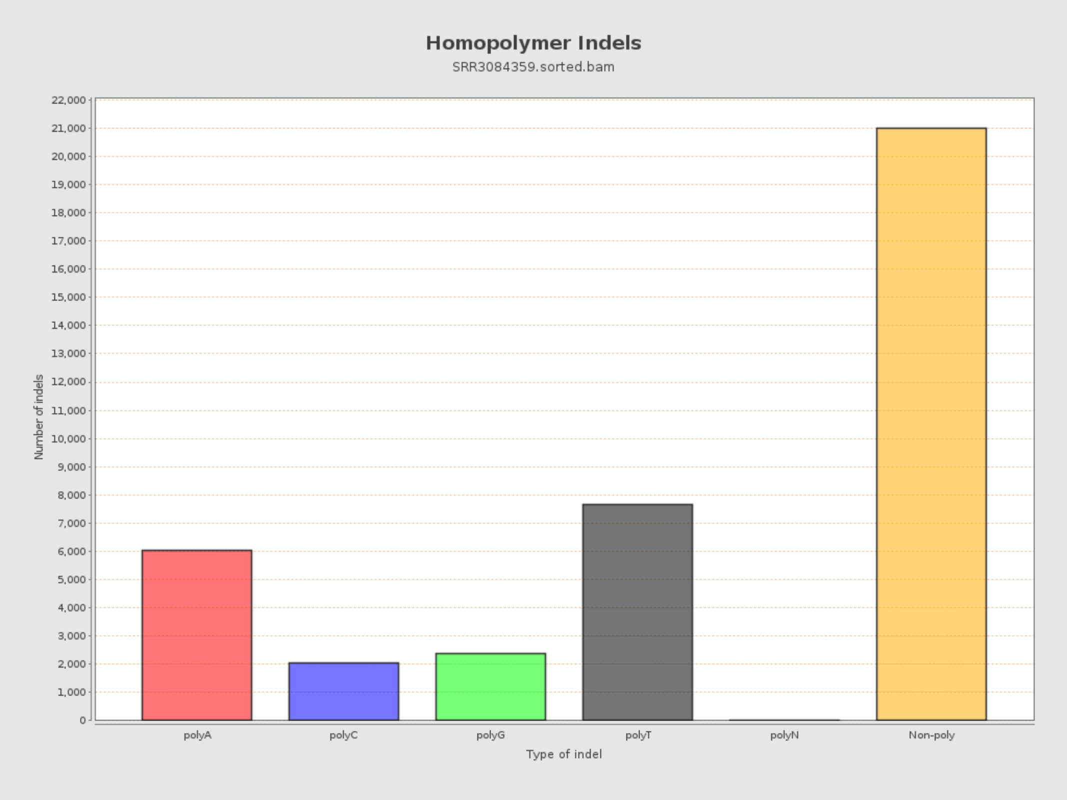
9. Results : Mapped Reads GC-content Distribution



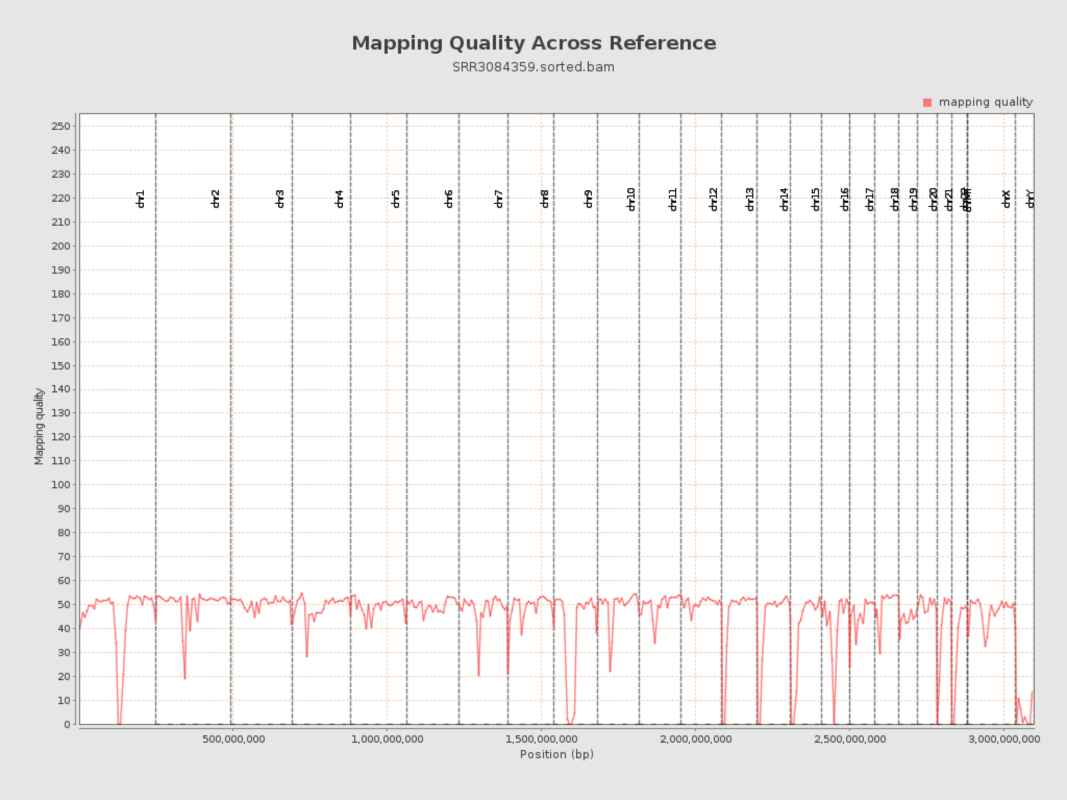
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram