Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 14:32:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082424.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_SRR3082424 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082424.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 14:32:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082424.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,997,463
Mapped reads	2,634,848 / 87.9%
Unmapped reads	362,615 / 12.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,563 / 0.79%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	112,191 / 3.74%
Duplication rate	3.1%
Clipped reads	1,178,673 / 39.32%

2.2. ACGT Content

Number/percentage of A's	49,032,353 / 27.76%
Number/percentage of C's	33,002,274 / 18.69%
Number/percentage of T's	55,274,596 / 31.3%
Number/percentage of G's	39,293,277 / 22.25%
Number/percentage of N's	3,770 / 0%
GC Percentage	40.94%

2.3. Coverage

Mean	0.0571

Standard Deviation	0.5135

2.4. Mapping Quality

Mean Mapping Quality	45.78

2.5. Mismatches and indels

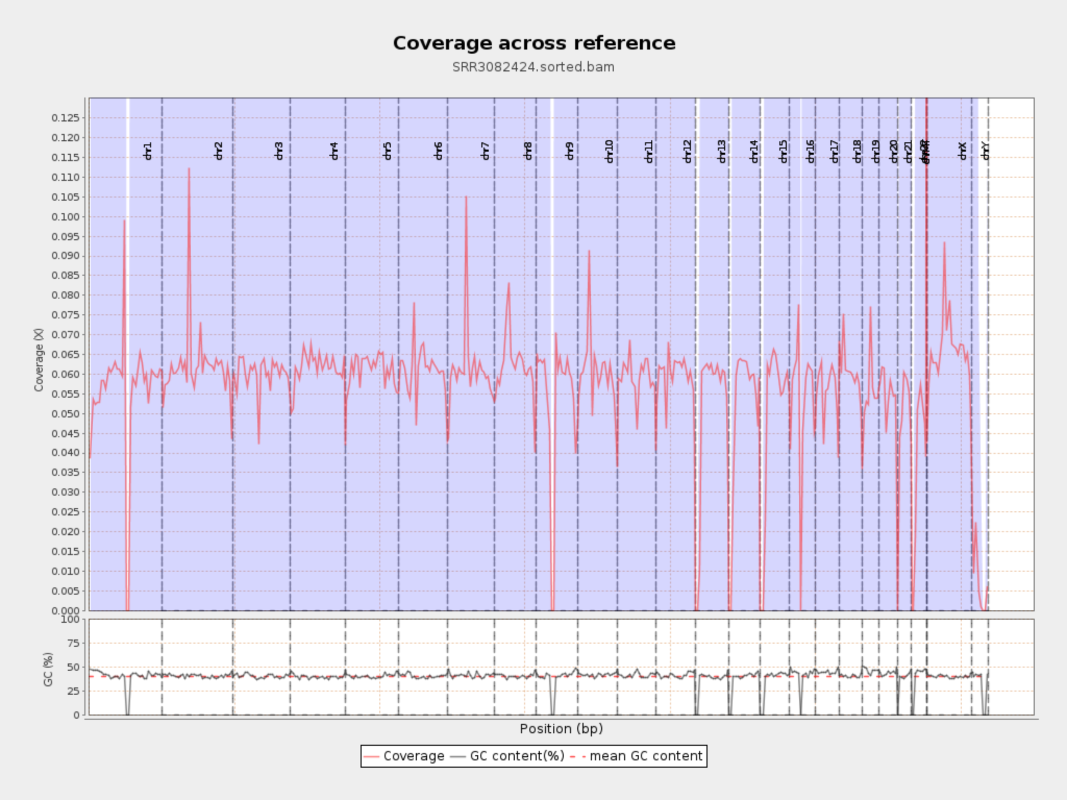
General error rate	0.87%
Mismatches	1,508,535
Insertions	14,489
Mapped reads with at least one insertion	0.54%
Deletions	40,287
Mapped reads with at least one deletion	1.51%
Homopolymer indels	46.87%

2.6. Chromosome stats

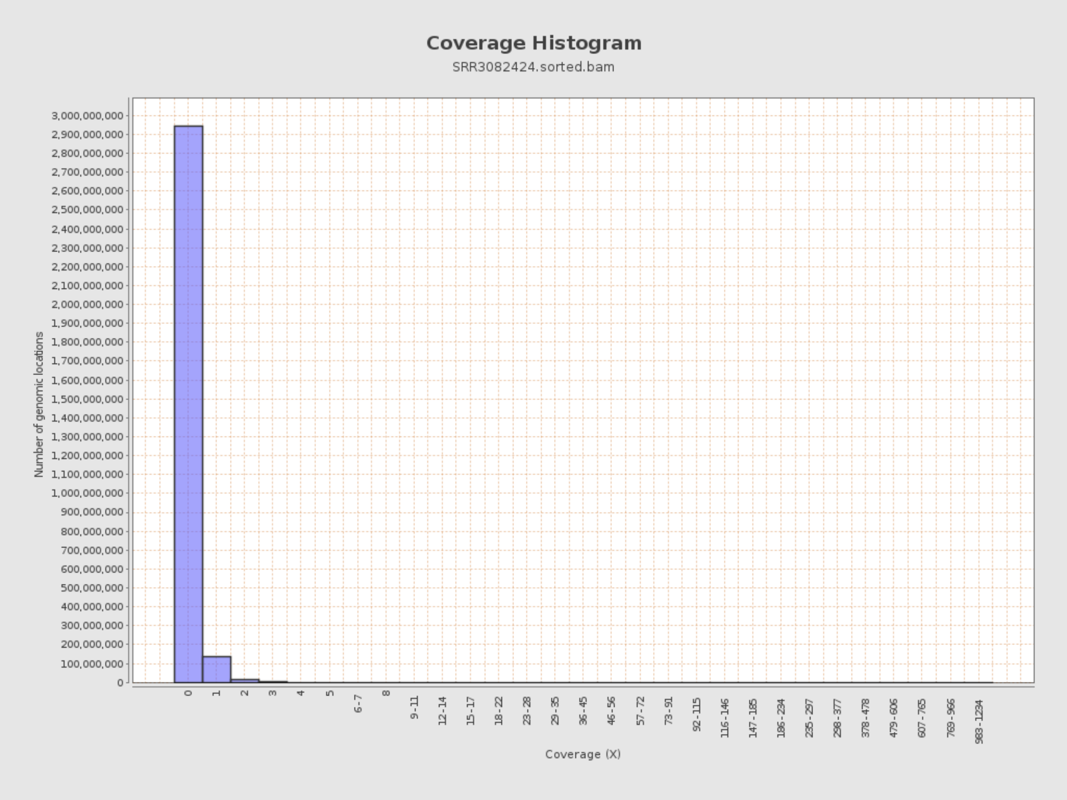
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13878922	0.0557	0.9513
chr2	243199373	15152661	0.0623	0.6479
chr3	198022430	11914243	0.0602	0.2727
chr4	191154276	11790499	0.0617	0.2951
chr5	180915260	11081799	0.0613	0.2801
chr6	171115067	10438346	0.061	0.3572
chr7	159138663	9844821	0.0619	0.6922

chr8	146364022	9094590	0.0621	0.8024
chr9	141213431	7452907	0.0528	0.4472
chr10	135534747	8260829	0.0609	0.4577
chr11	135006516	7962233	0.059	0.4256
chr12	133851895	8006789	0.0598	0.2821
chr13	115169878	5768468	0.0501	0.2492
chr14	107349540	5366081	0.05	0.2776
chr15	102531392	5023853	0.049	0.2593
chr16	90354753	4830983	0.0535	0.3032
chr17	81195210	4495562	0.0554	0.3016
chr18	78077248	4763854	0.061	0.8648
chr19	59128983	3293418	0.0557	0.7363
chr20	63025520	3435323	0.0545	0.272
chr21	48129895	2273276	0.0472	0.262
chr22	51304566	1834523	0.0358	0.2086
chrMT	16571	4595	0.2773	0.6174
chrX	155270560	10258069	0.0661	0.3448
chrY	59373566	444442	0.0075	0.1622

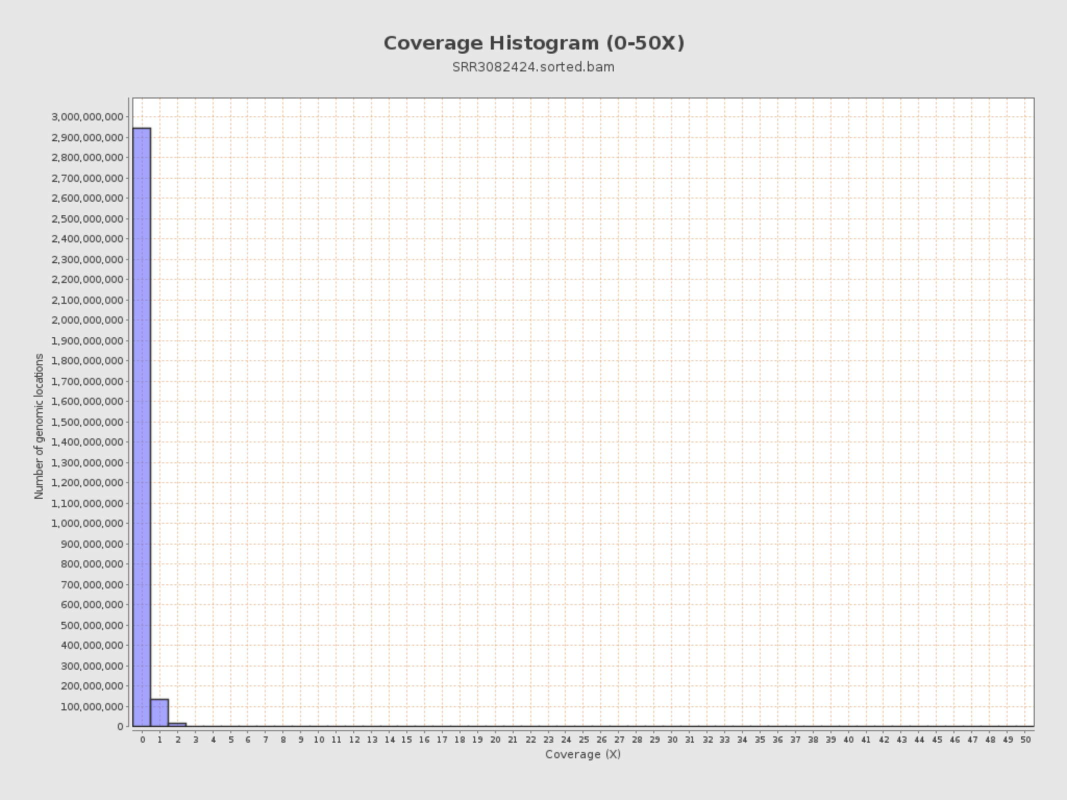
3. Results : Coverage across reference



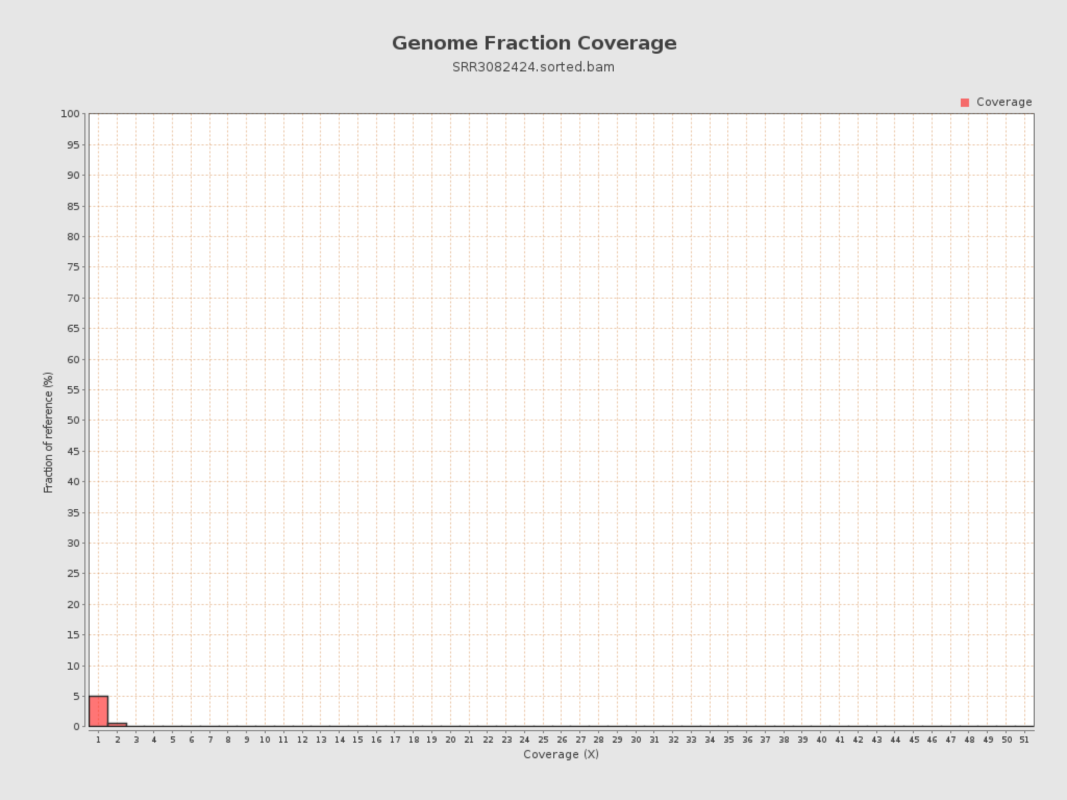
4. Results : Coverage Histogram



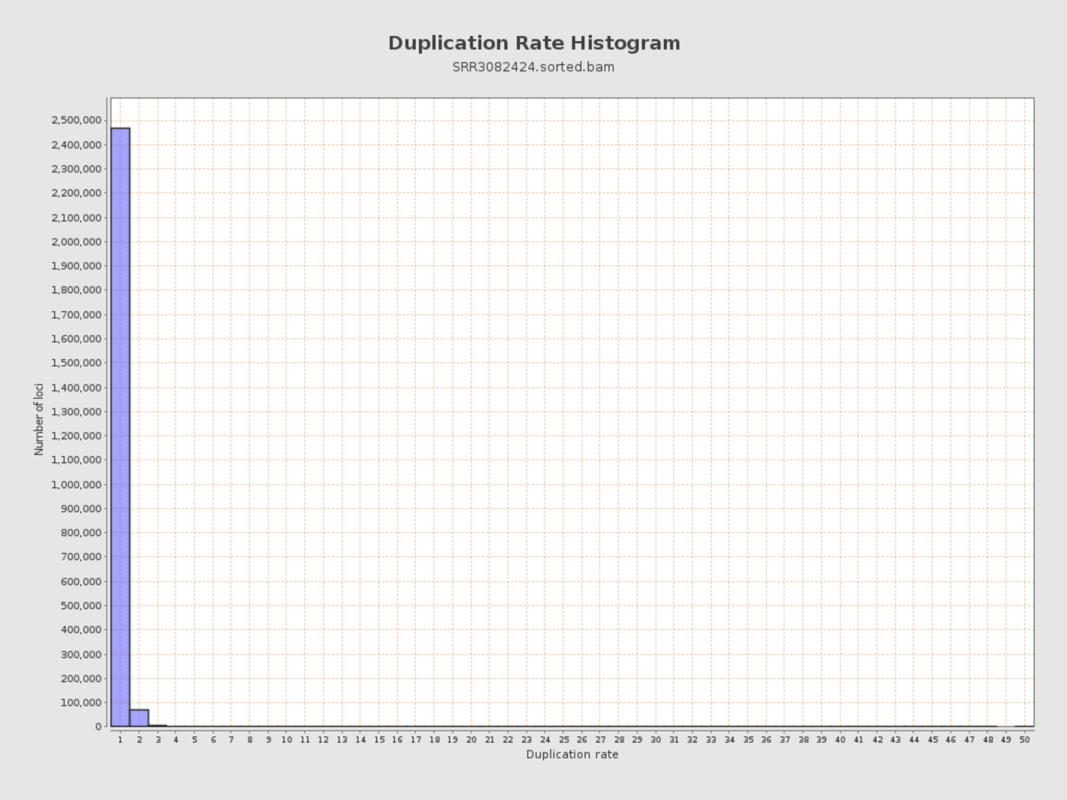
5. Results : Coverage Histogram (0-50X)



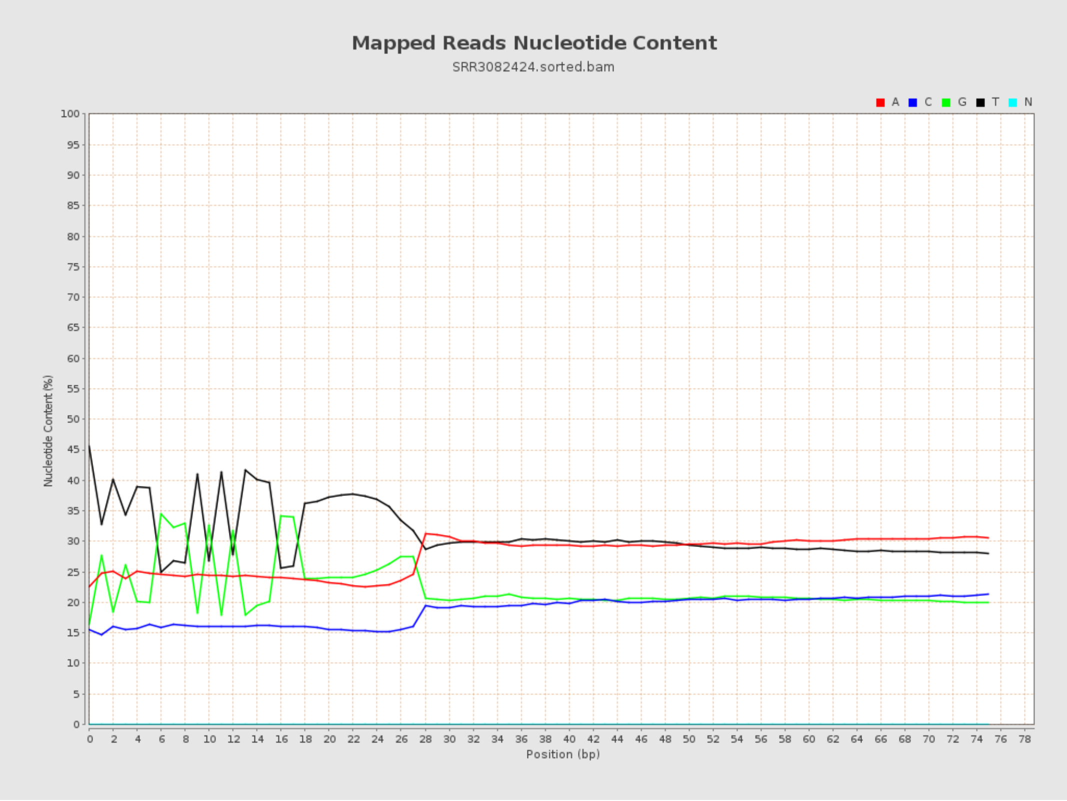
6. Results : Genome Fraction Coverage



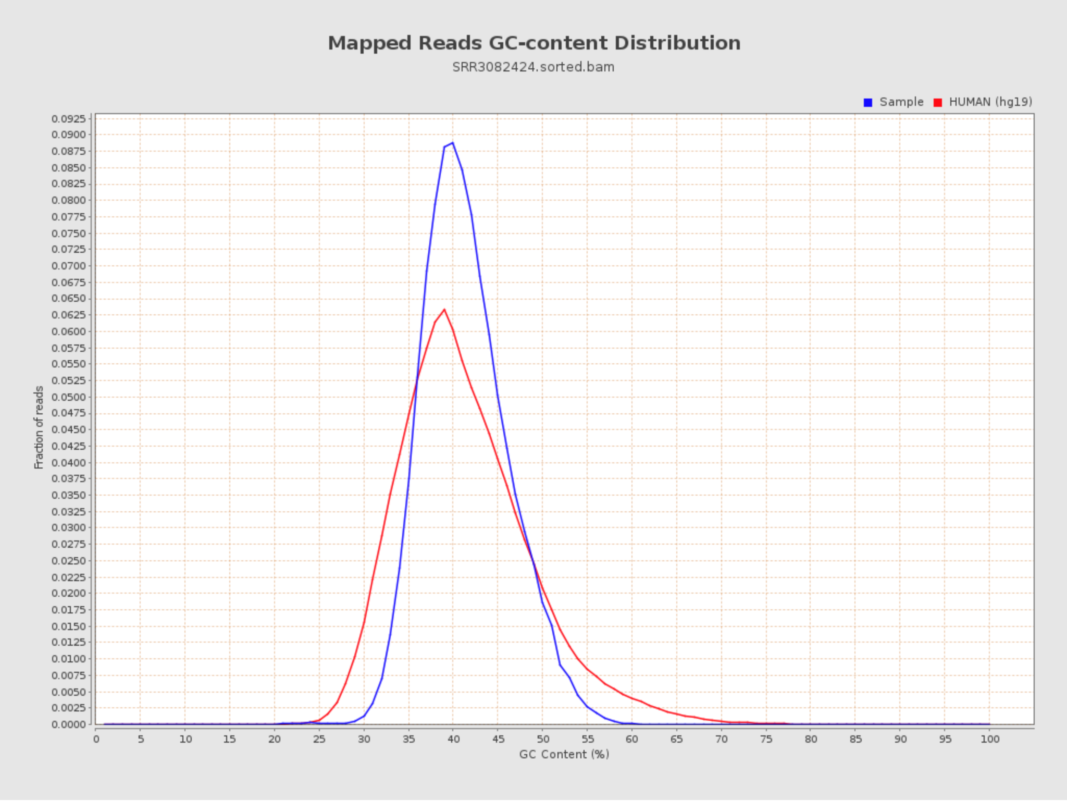
7. Results : Duplication Rate Histogram



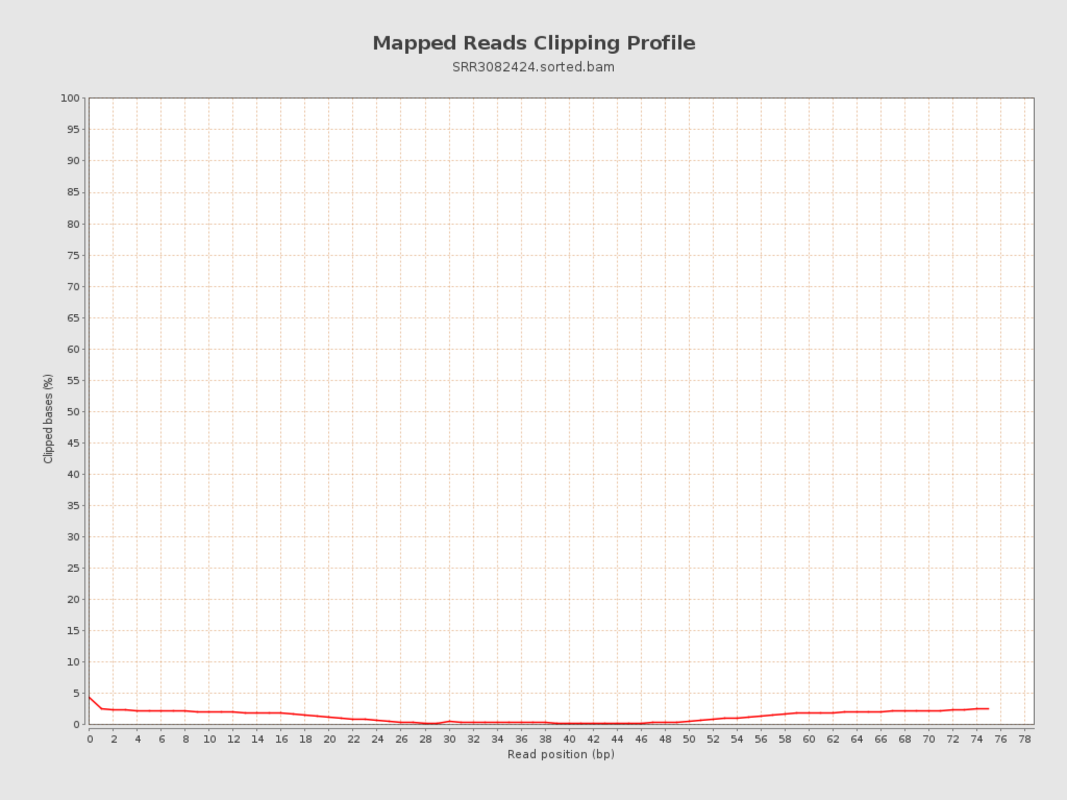
8. Results : Mapped Reads Nucleotide Content



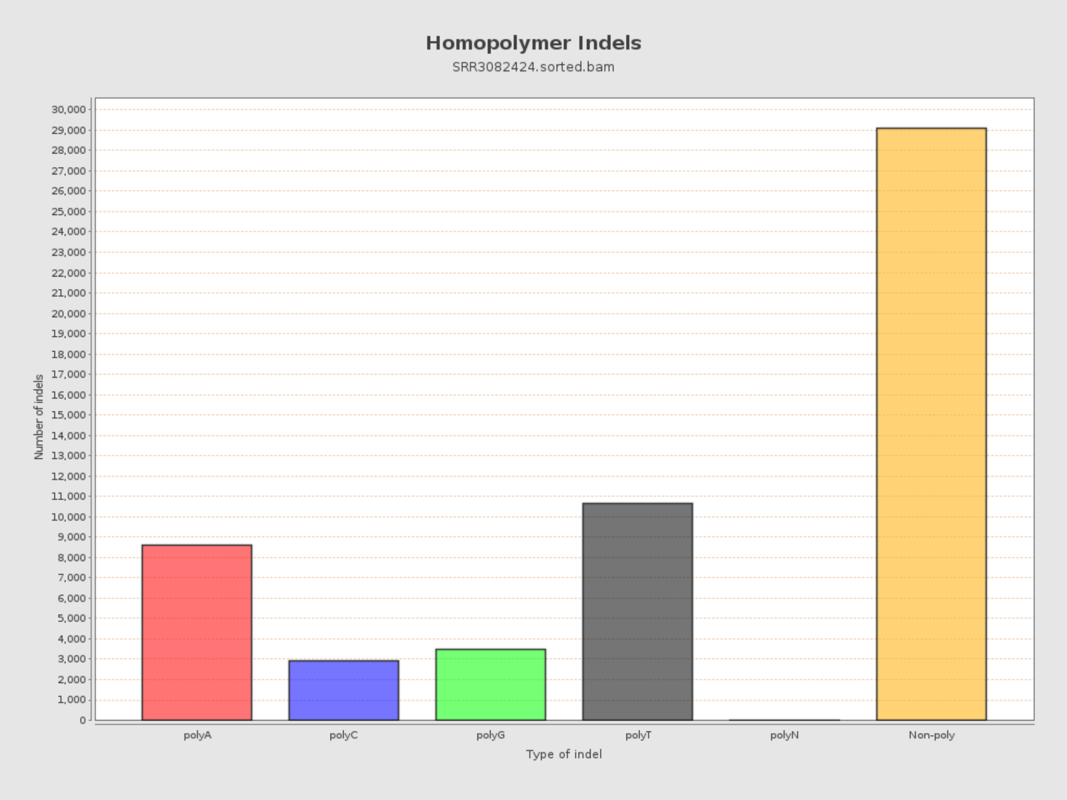
9. Results : Mapped Reads GC-content Distribution



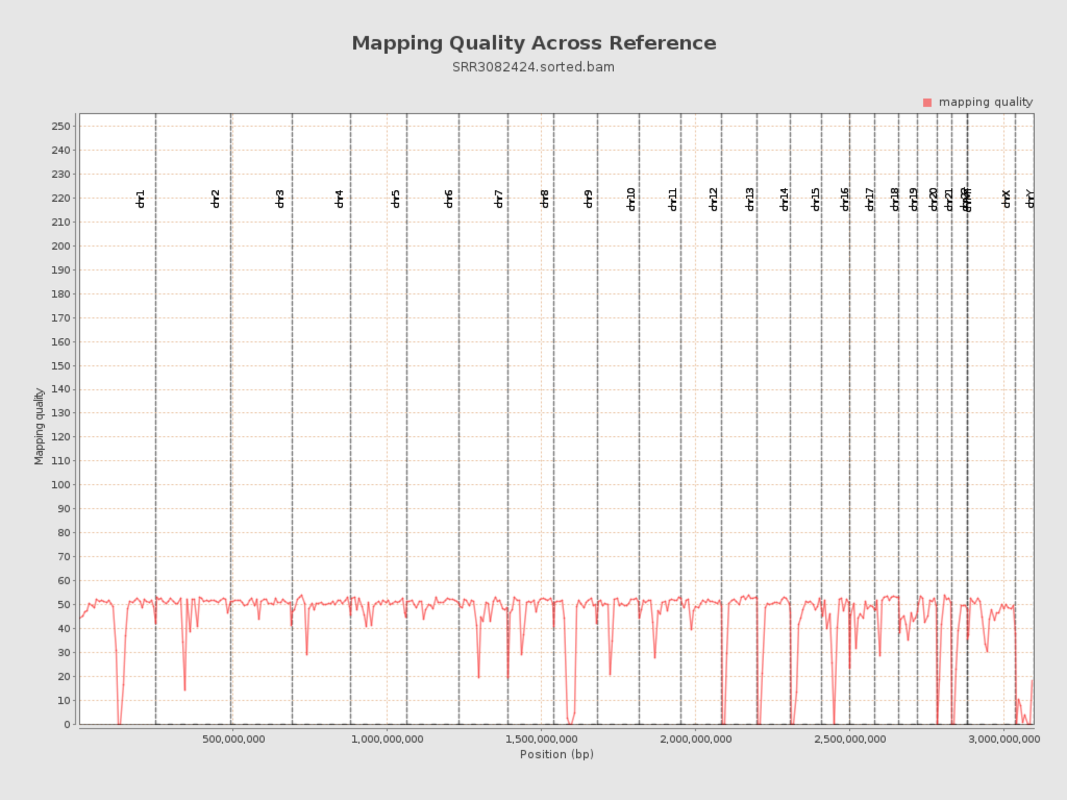
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram