Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 11:01:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084358.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_SRR3084358 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084358.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 11:01:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084358.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,203,424
Mapped reads	2,931,561 / 91.51%
Unmapped reads	271,863 / 8.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,968 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	103,023 / 3.22%
Duplication rate	2.58%
Clipped reads	1,123,390 / 35.07%

2.2. ACGT Content

Number/percentage of A's	55,993,219 / 27.85%
Number/percentage of C's	39,885,939 / 19.84%
Number/percentage of T's	59,820,904 / 29.75%
Number/percentage of G's	45,087,185 / 22.43%
Number/percentage of N's	264,890 / 0.13%
GC Percentage	42.26%

2.3. Coverage

Mean	0.065

Standard Deviation	0.5082

2.4. Mapping Quality

Mean Mapping Quality	44.57

2.5. Mismatches and indels

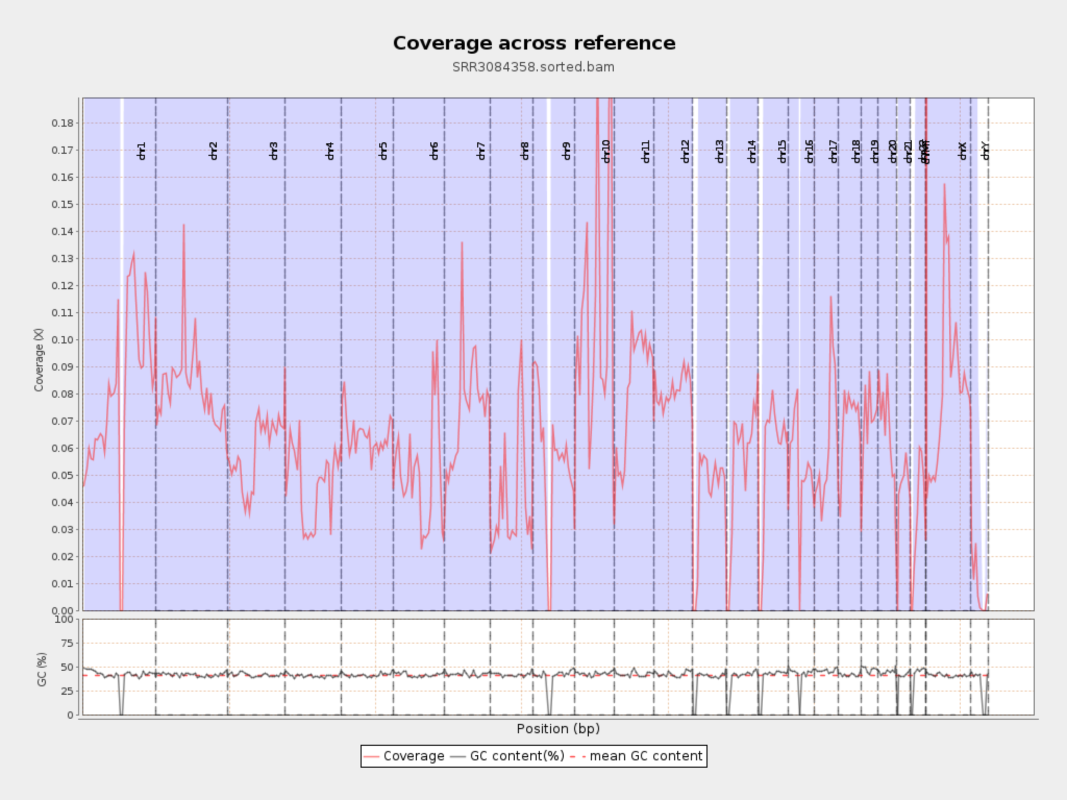
General error rate	1.05%
Mismatches	2,082,221
Insertions	14,996
Mapped reads with at least one insertion	0.51%
Deletions	42,823
Mapped reads with at least one deletion	1.45%
Homopolymer indels	47.1%

2.6. Chromosome stats

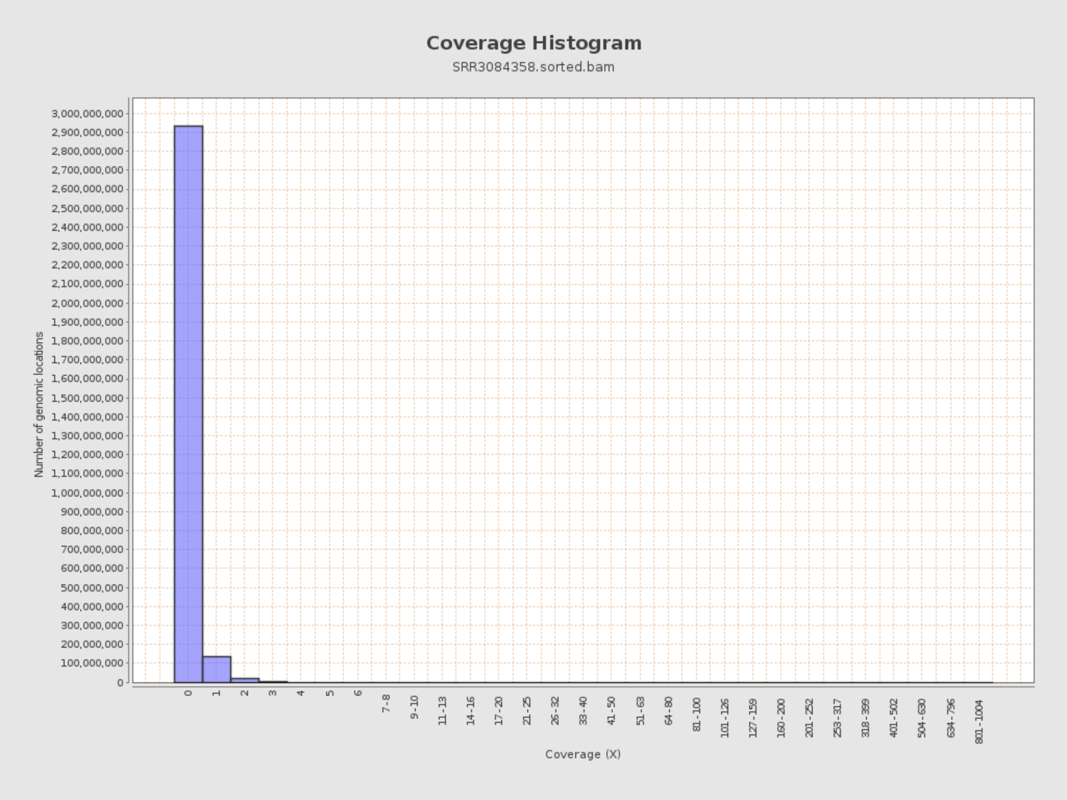
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20086206	0.0806	0.8877
chr2	243199373	20139149	0.0828	0.5718
chr3	198022430	11587037	0.0585	0.2956
chr4	191154276	8874217	0.0464	0.2801
chr5	180915260	11710296	0.0647	0.3001
chr6	171115067	8775517	0.0513	0.2985
chr7	159138663	11897752	0.0748	0.9164

chr8	146364022	5959568	0.0407	0.3348
chr9	141213431	7842238	0.0555	0.4519
chr10	135534747	15026132	0.1109	0.7361
chr11	135006516	11113286	0.0823	0.4872
chr12	133851895	10943129	0.0818	0.3403
chr13	115169878	4901571	0.0426	0.2391
chr14	107349540	5840437	0.0544	0.3018
chr15	102531392	5636021	0.055	0.2774
chr16	90354753	4641275	0.0514	0.321
chr17	81195210	5139806	0.0633	0.3354
chr18	78077248	5357514	0.0686	0.7931
chr19	59128983	4171189	0.0705	0.6451
chr20	63025520	4173411	0.0662	0.3153
chr21	48129895	2111854	0.0439	0.2818
chr22	51304566	1760725	0.0343	0.2165
chrMT	16571	53750	3.2436	2.7275
chrX	155270560	12885615	0.083	0.4213
chrY	59373566	500700	0.0084	0.185

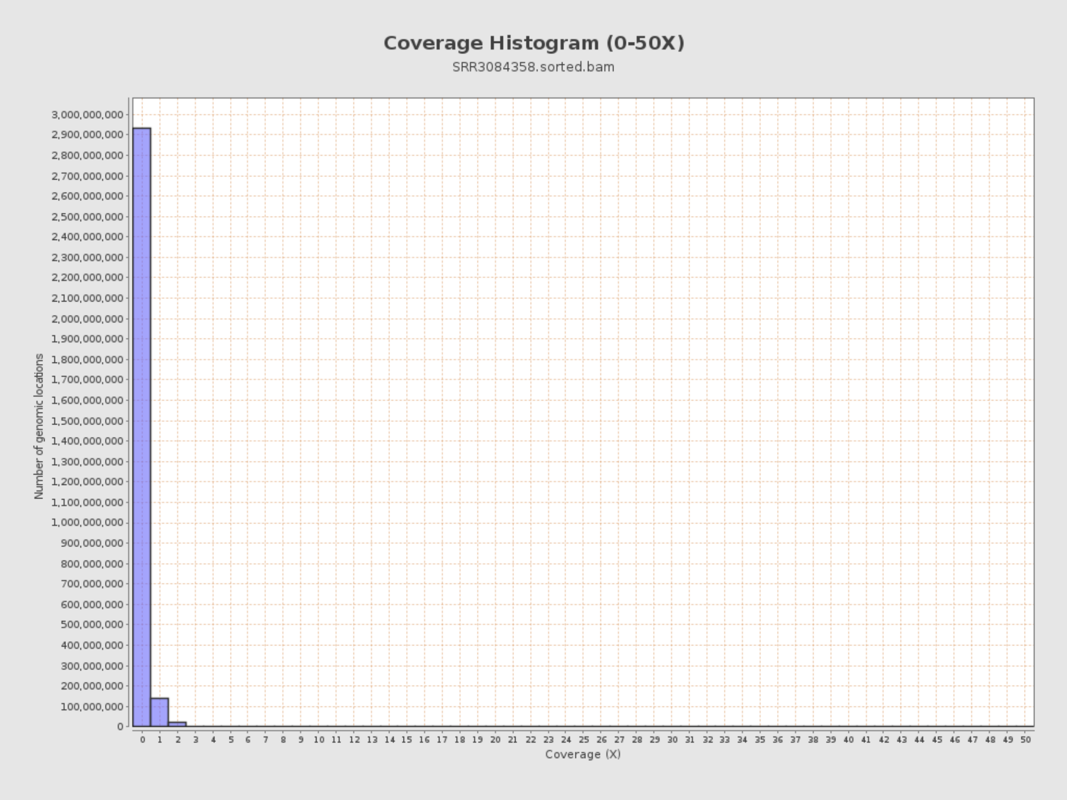
3. Results : Coverage across reference



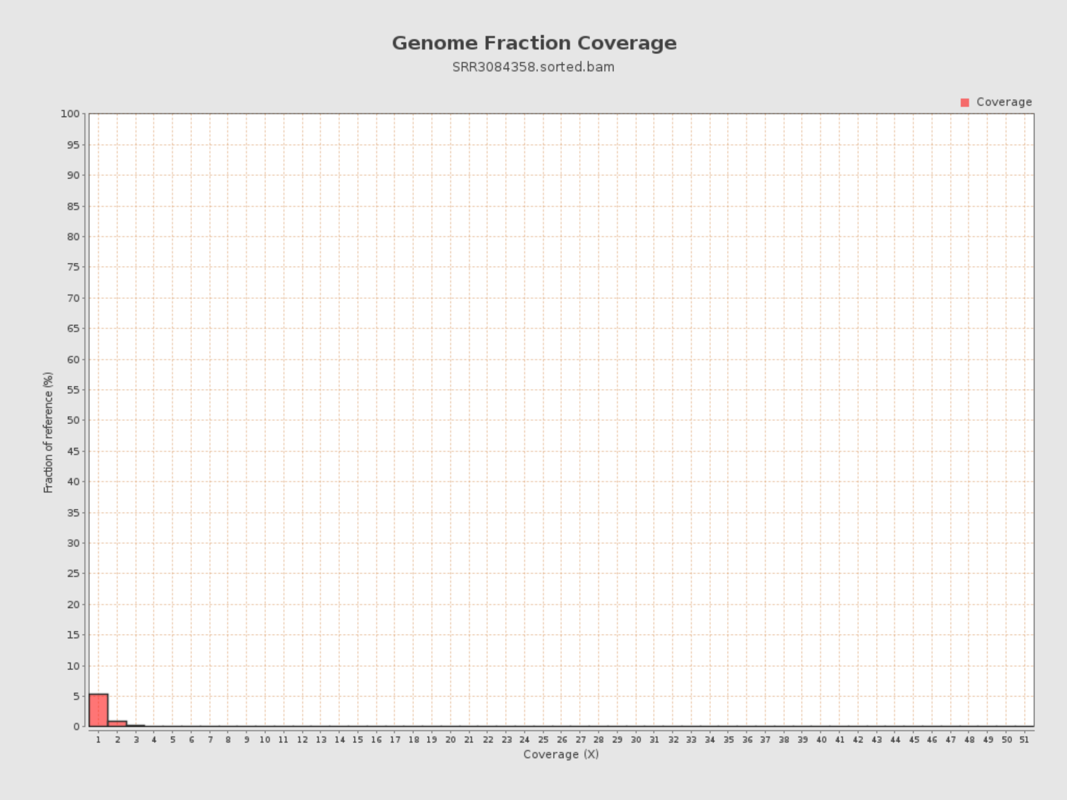
4. Results : Coverage Histogram



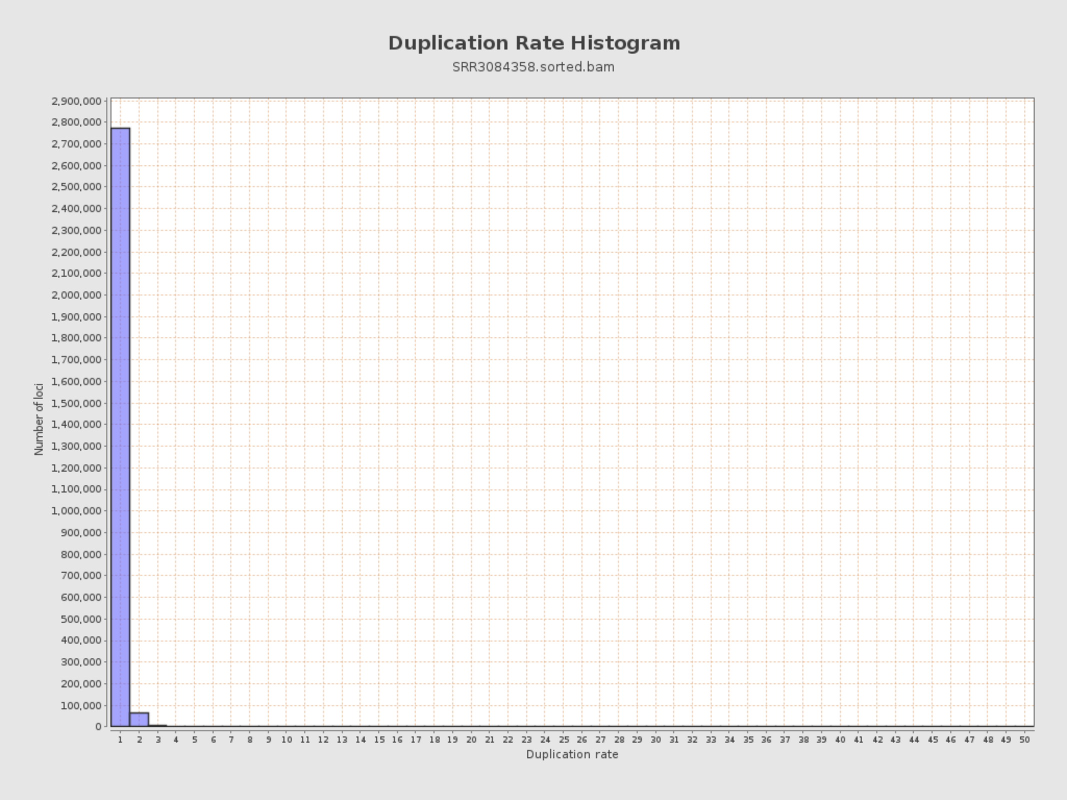
5. Results : Coverage Histogram (0-50X)



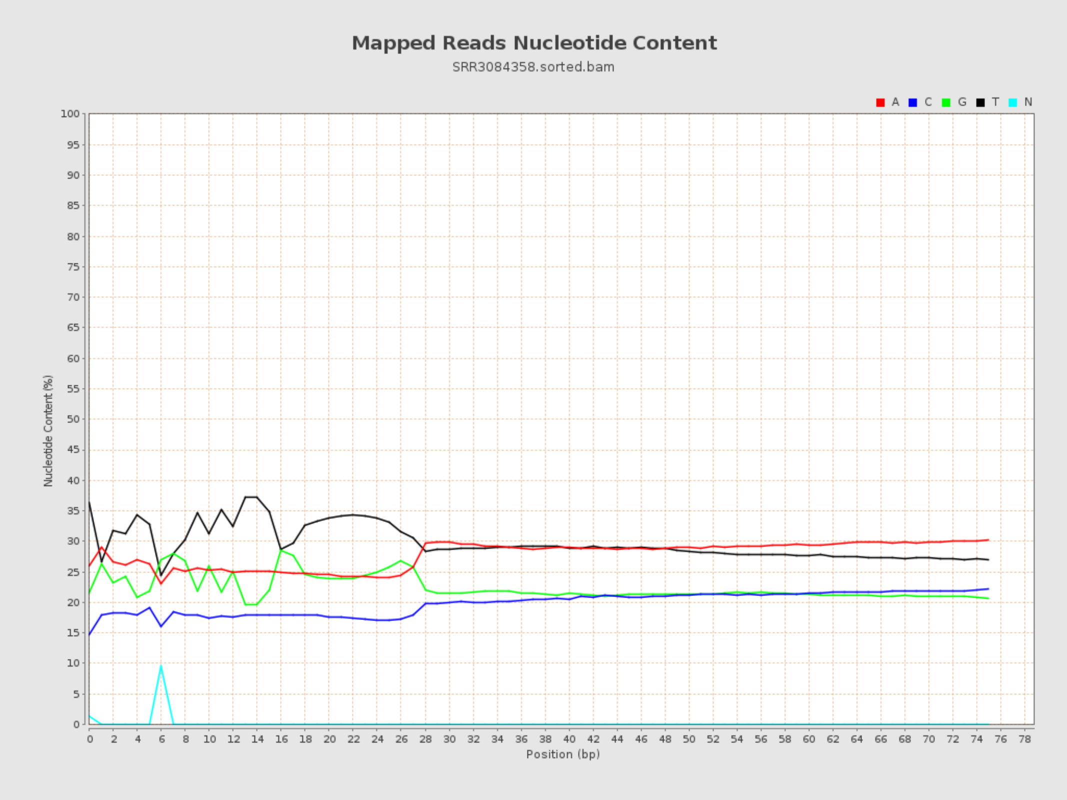
6. Results : Genome Fraction Coverage



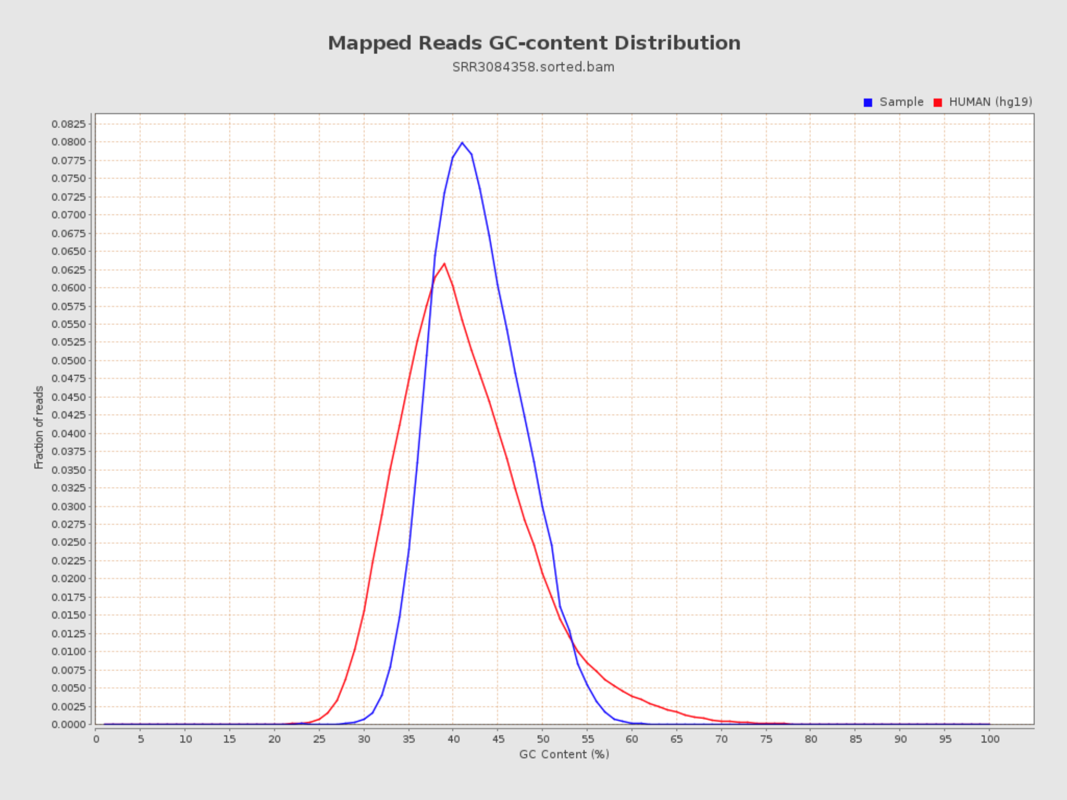
7. Results : Duplication Rate Histogram



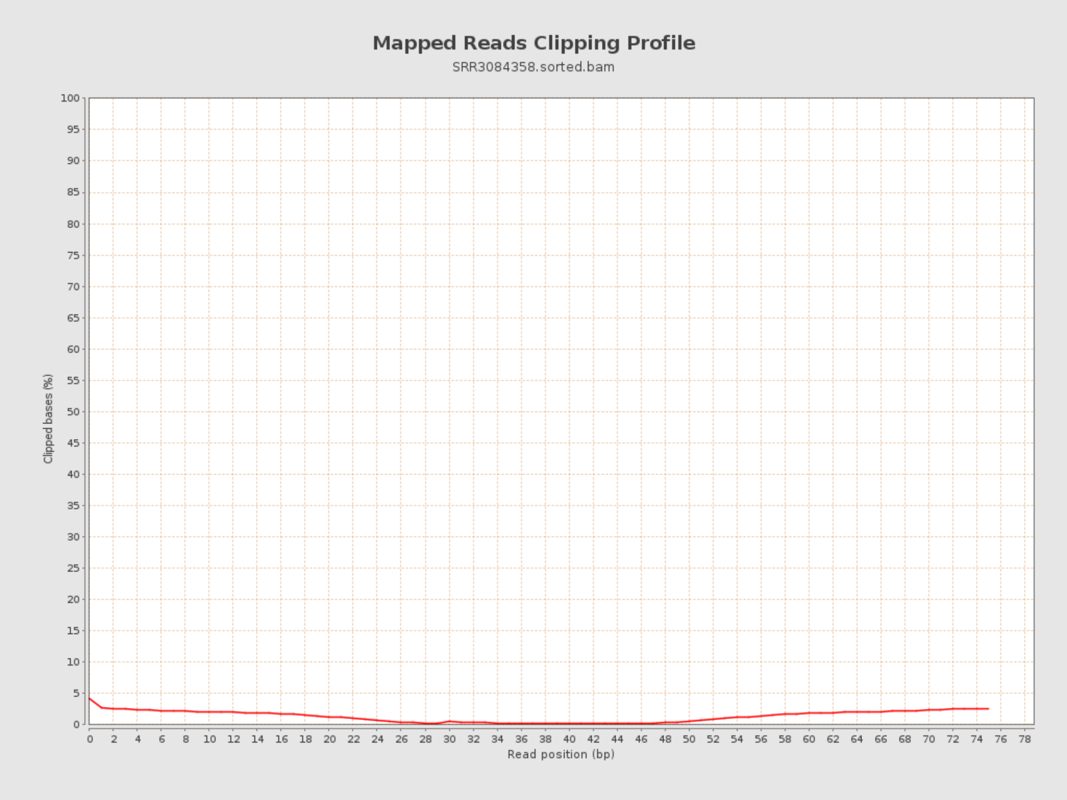
8. Results : Mapped Reads Nucleotide Content



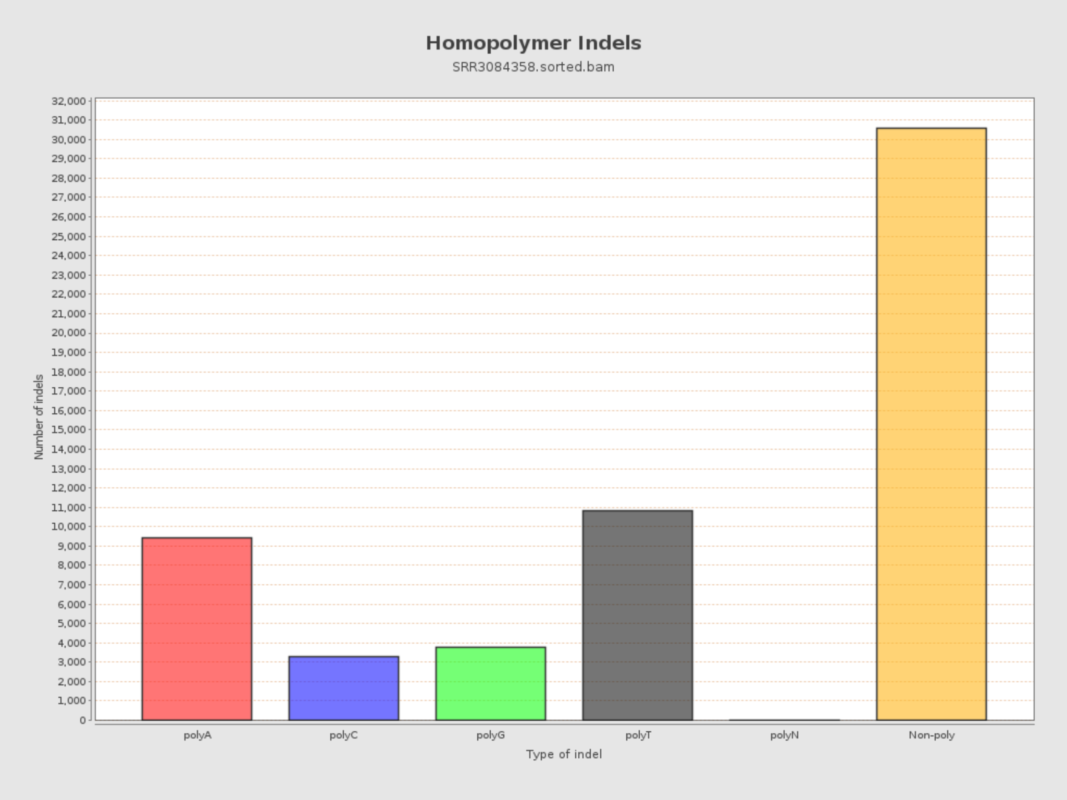
9. Results : Mapped Reads GC-content Distribution



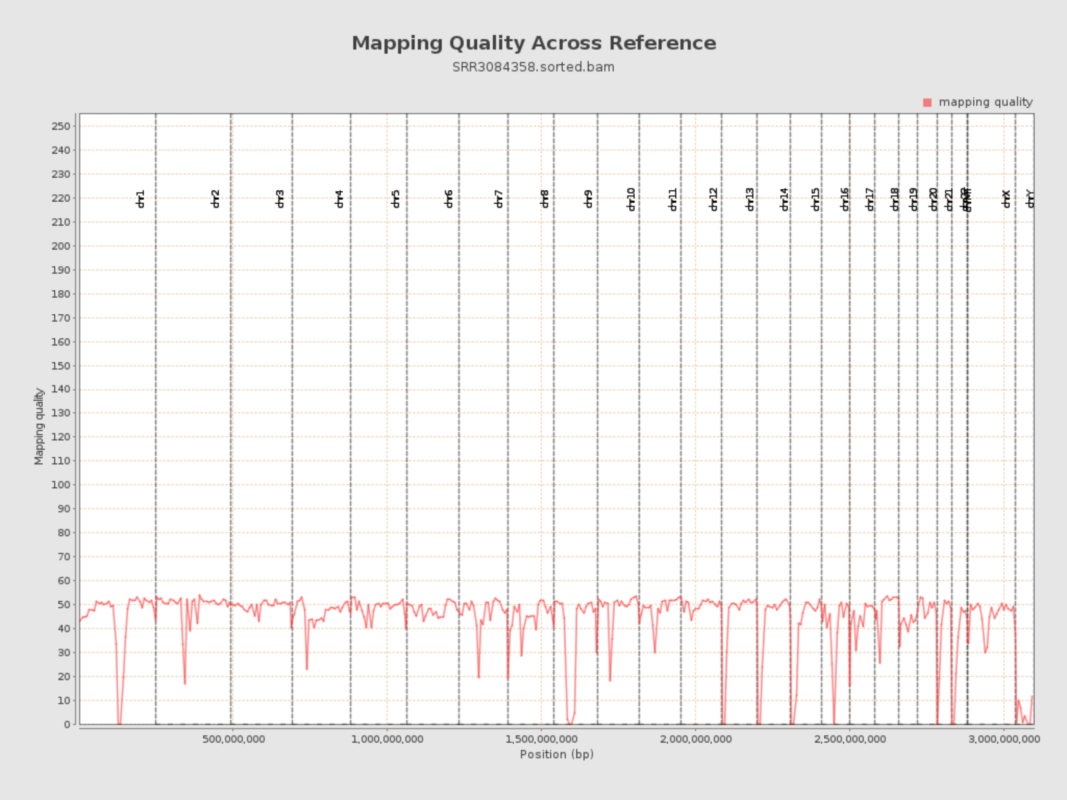
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram