Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 20:54:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084971.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_SRR3084971 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084971.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 20:54:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084971.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,493,471
Mapped reads	2,298,896 / 92.2%
Unmapped reads	194,575 / 7.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,407 / 0.82%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	80,833 / 3.24%
Duplication rate	2.55%
Clipped reads	802,496 / 32.18%

2.2. ACGT Content

Number/percentage of A's	46,484,532 / 29.22%
Number/percentage of C's	29,526,423 / 18.56%
Number/percentage of T's	49,802,287 / 31.31%
Number/percentage of G's	33,244,343 / 20.9%
Number/percentage of N's	22,620 / 0.01%
GC Percentage	39.46%

2.3. Coverage

Mean	0.0514

Standard Deviation	0.469

2.4. Mapping Quality

Mean Mapping Quality	47.06

2.5. Mismatches and indels

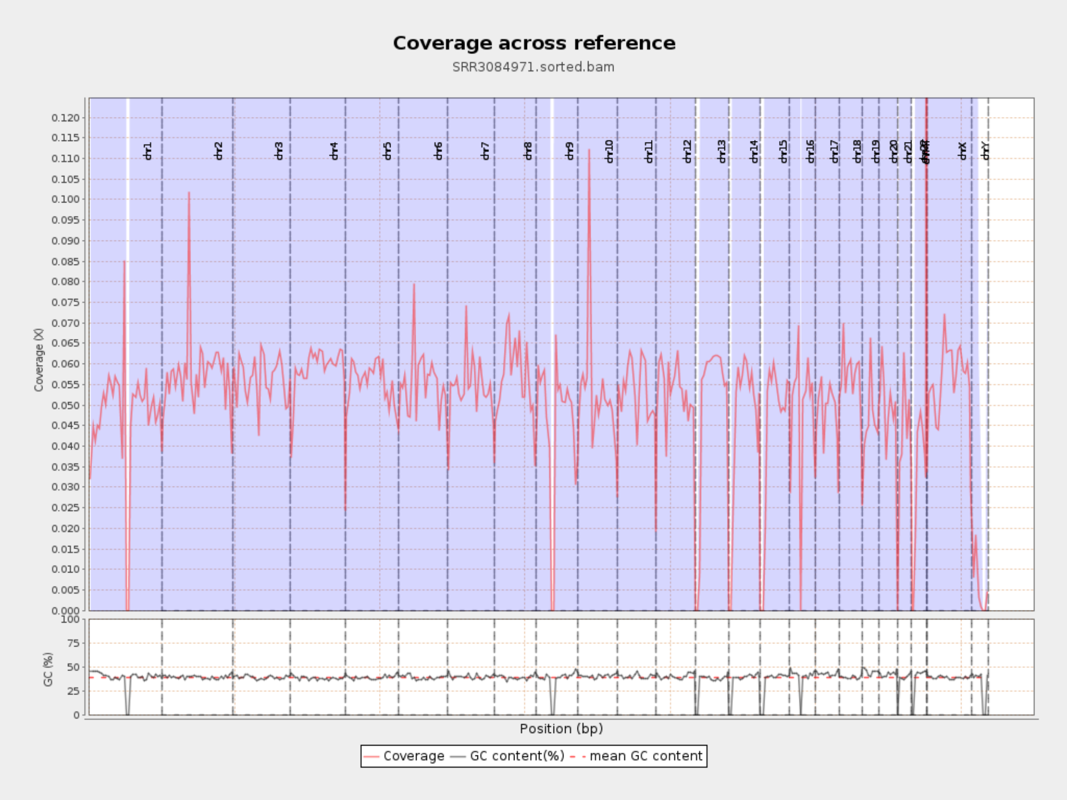
General error rate	0.85%
Mismatches	1,325,670
Insertions	13,258
Mapped reads with at least one insertion	0.57%
Deletions	38,979
Mapped reads with at least one deletion	1.68%
Homopolymer indels	47.98%

2.6. Chromosome stats

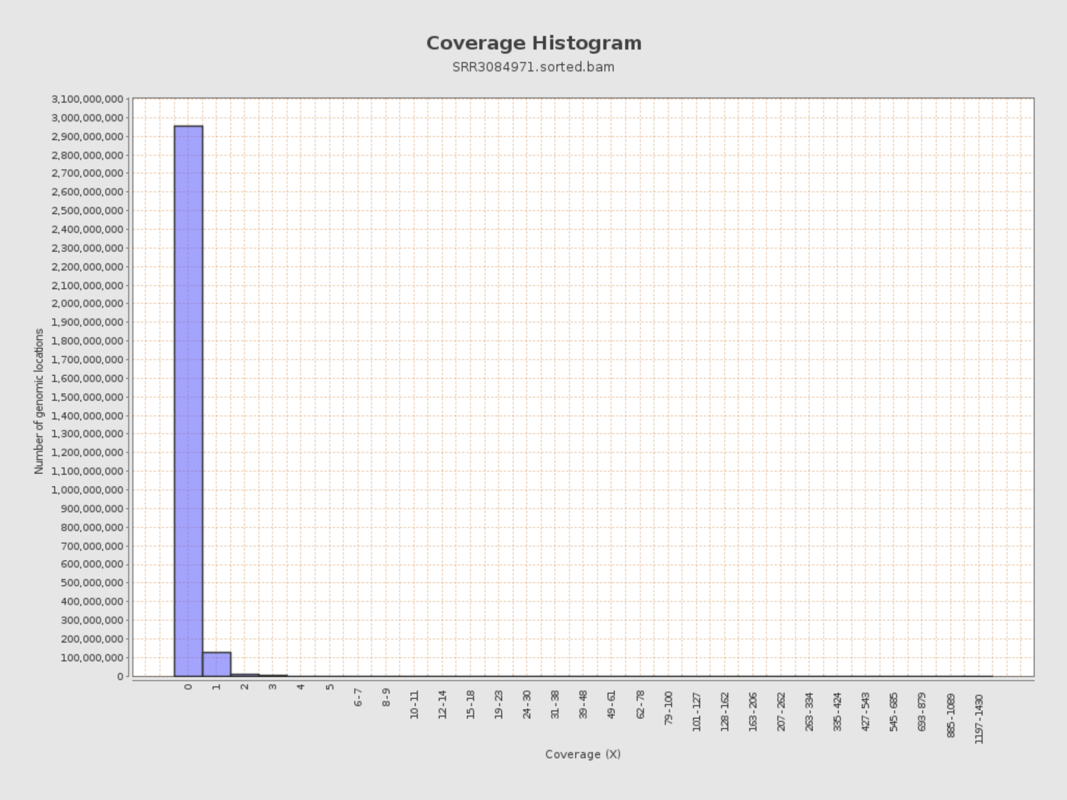
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11862725	0.0476	0.8769
chr2	243199373	14104219	0.058	0.4772
chr3	198022430	11145054	0.0563	0.2723
chr4	191154276	11279507	0.059	0.2748
chr5	180915260	10055357	0.0556	0.2595
chr6	171115067	9448099	0.0552	0.3485
chr7	159138663	8723116	0.0548	0.3684

chr8	146364022	8283030	0.0566	0.8963
chr9	141213431	6476894	0.0459	0.4189
chr10	135534747	7254682	0.0535	0.594
chr11	135006516	7204139	0.0534	0.3912
chr12	133851895	7080062	0.0529	0.2579
chr13	115169878	5631476	0.0489	0.2403
chr14	107349540	4870389	0.0454	0.2543
chr15	102531392	4482267	0.0437	0.228
chr16	90354753	4382377	0.0485	0.2993
chr17	81195210	3916602	0.0482	0.2812
chr18	78077248	4492714	0.0575	0.8256
chr19	59128983	2754094	0.0466	0.5886
chr20	63025520	3095814	0.0491	0.2532
chr21	48129895	1956533	0.0407	0.2403
chr22	51304566	1544453	0.0301	0.1878
chrMT	16571	12083	0.7292	0.9245
chrX	155270560	8734465	0.0563	0.2951
chrY	59373566	354251	0.006	0.1309

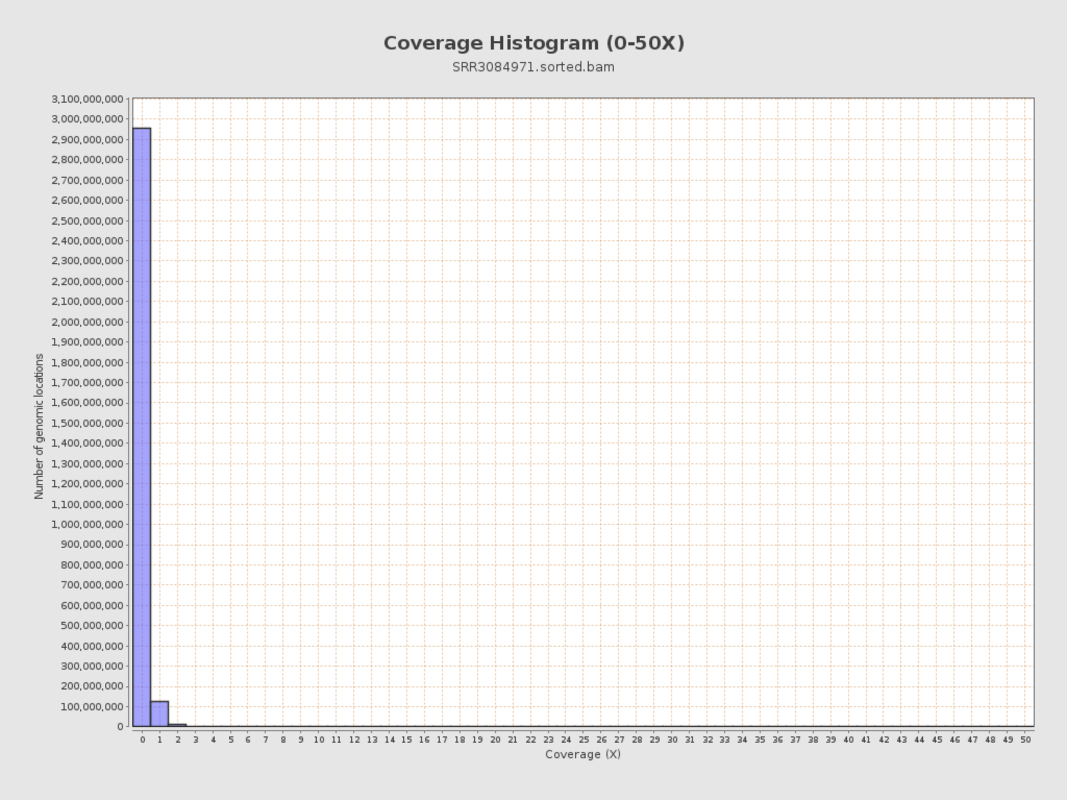
3. Results : Coverage across reference



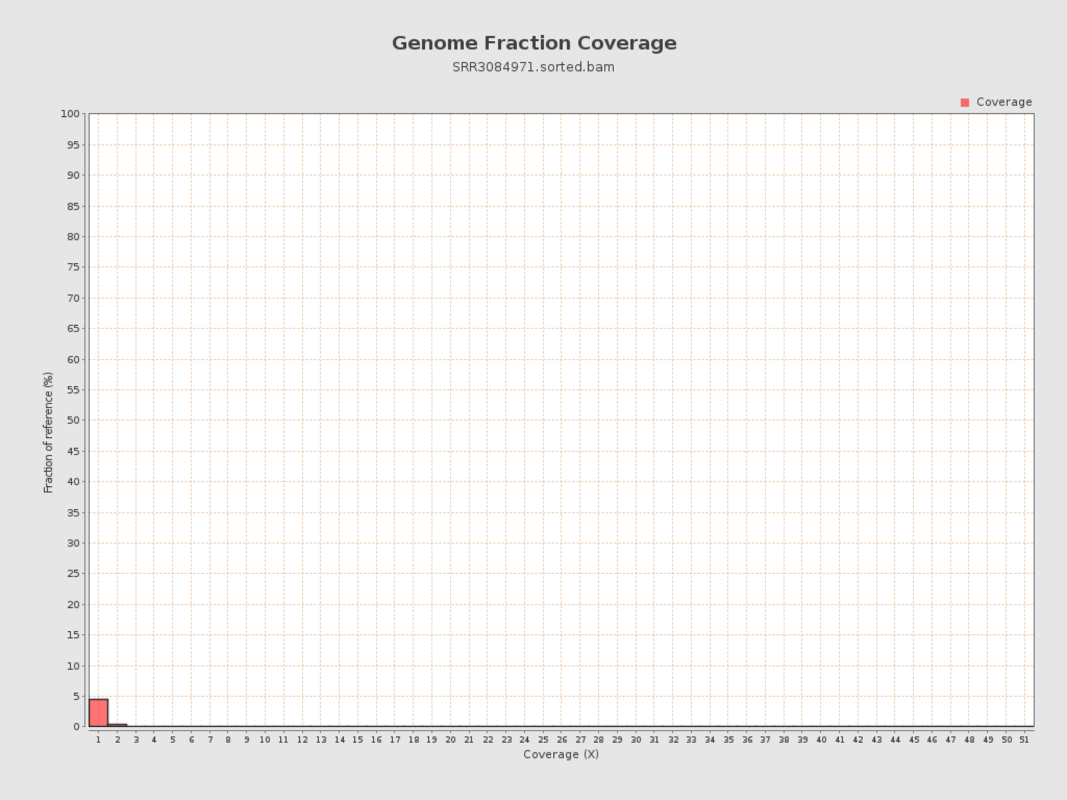
4. Results : Coverage Histogram



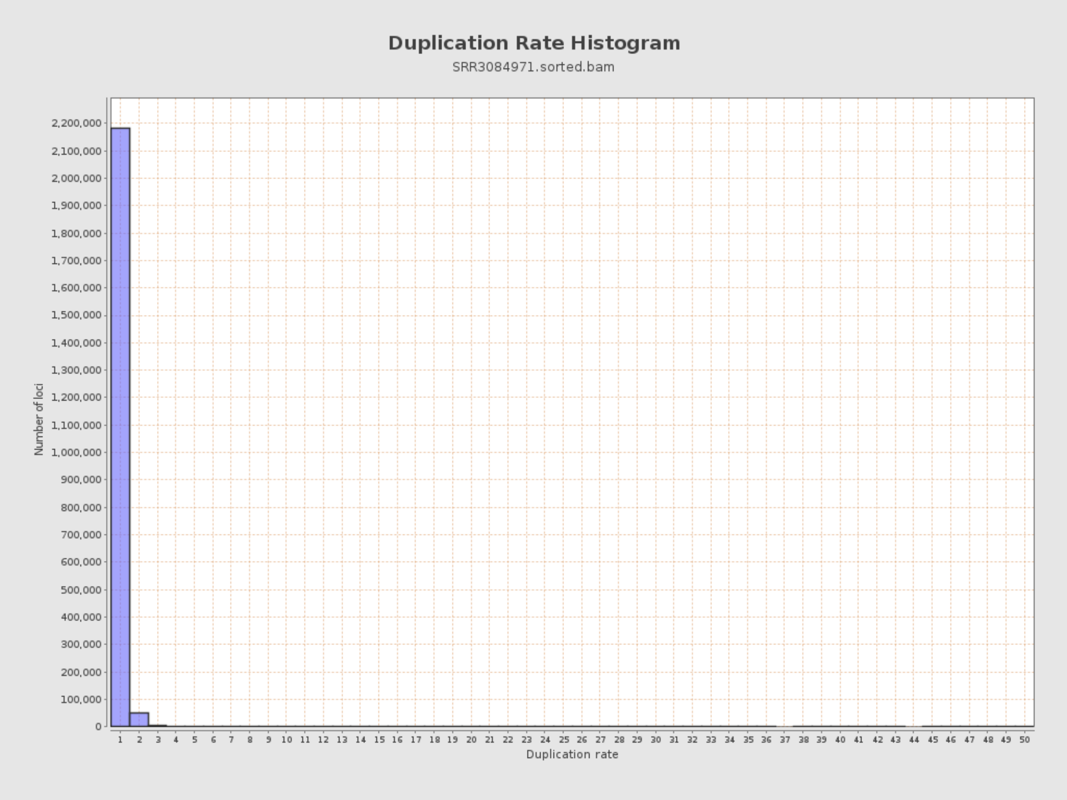
5. Results : Coverage Histogram (0-50X)



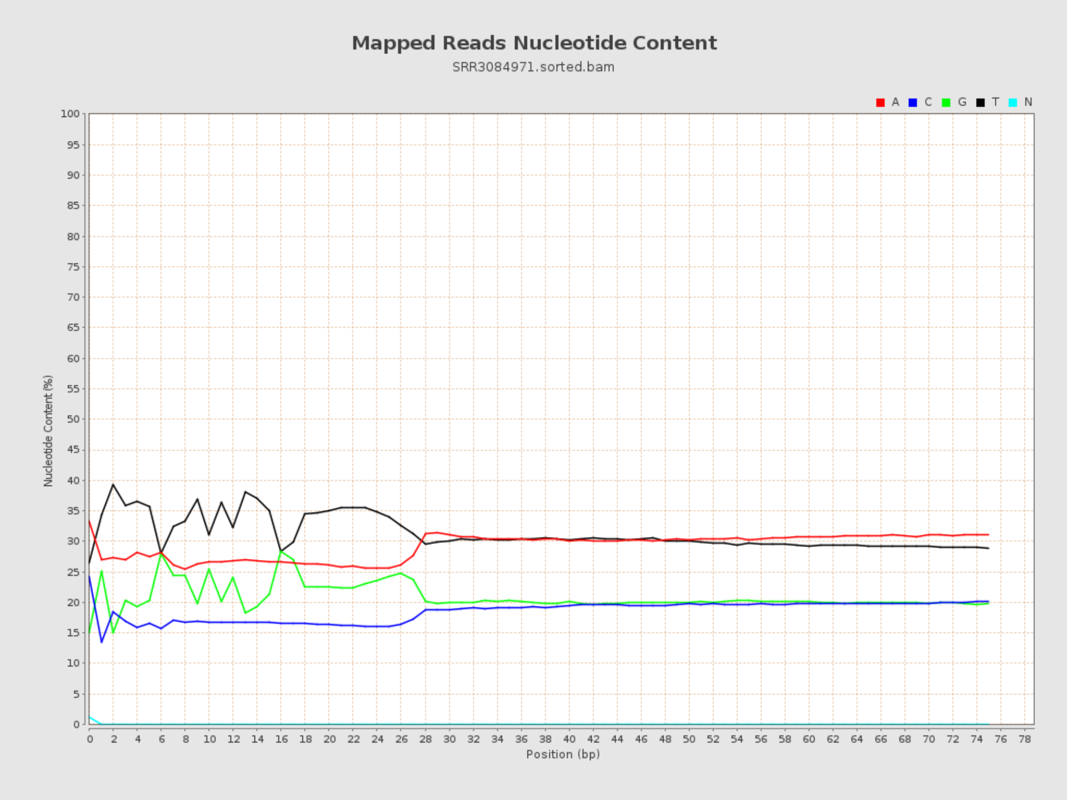
6. Results : Genome Fraction Coverage



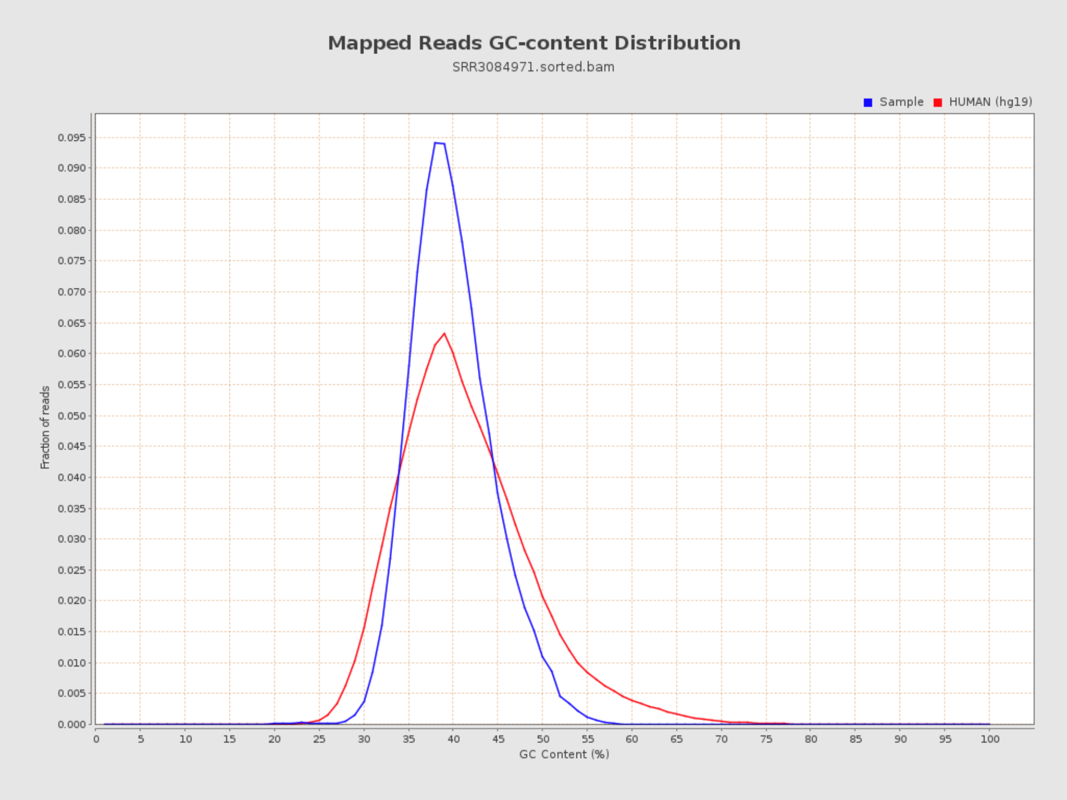
7. Results : Duplication Rate Histogram



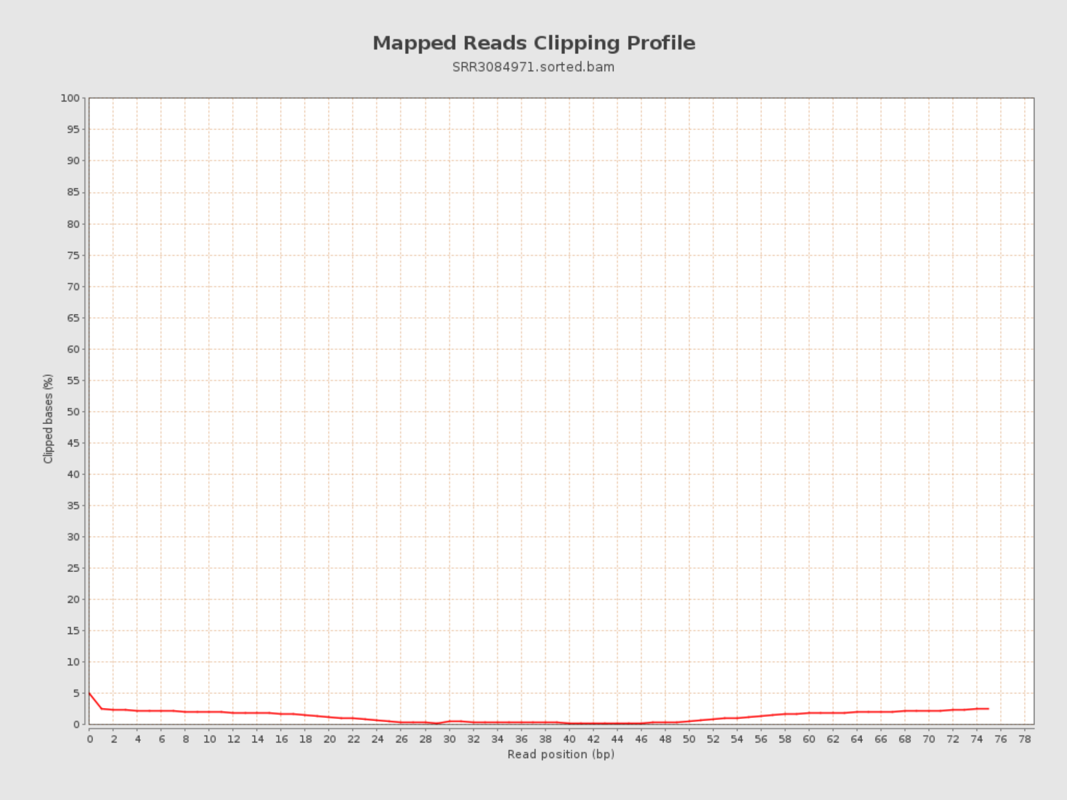
8. Results : Mapped Reads Nucleotide Content



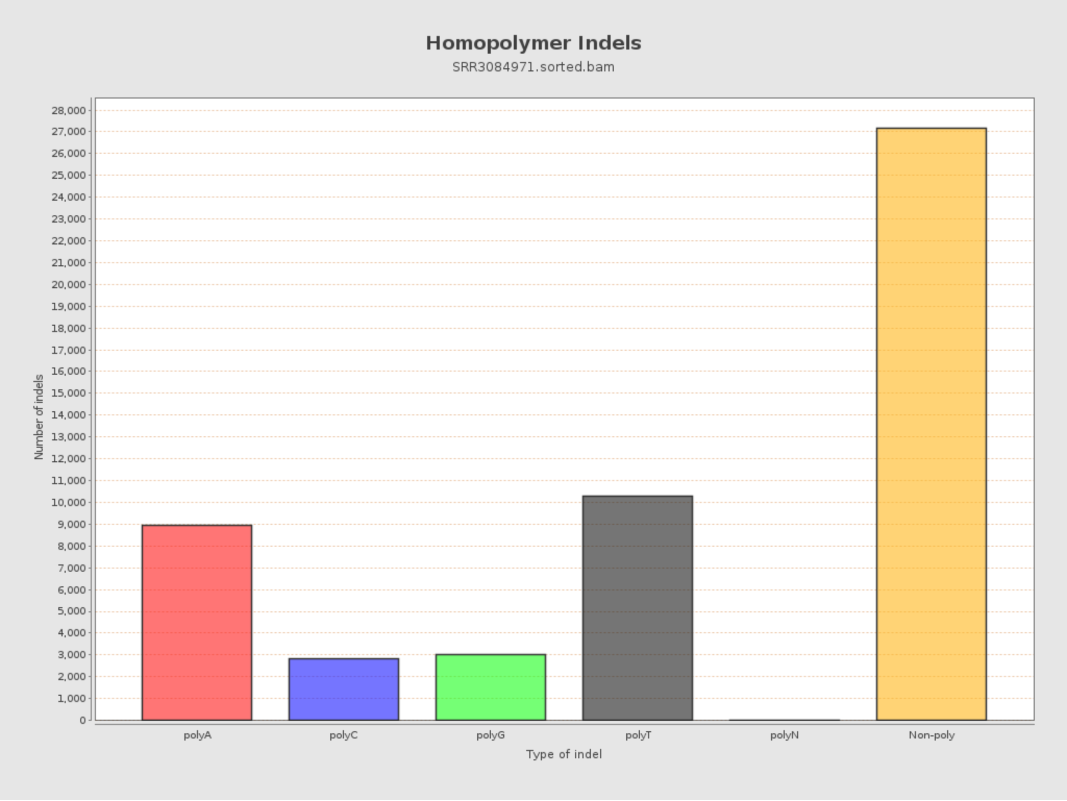
9. Results : Mapped Reads GC-content Distribution



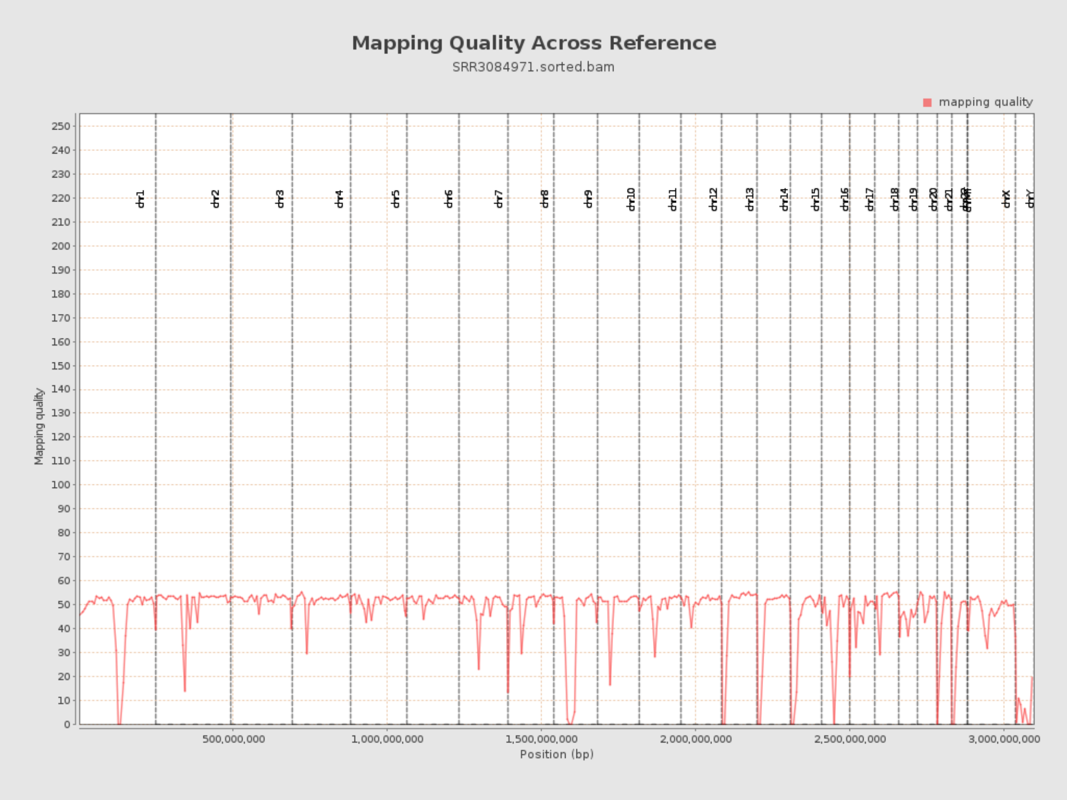
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram