Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 10:24:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084349.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_SRR3084349 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084349.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 10:24:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084349.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,356,025
Mapped reads	2,105,975 / 89.39%
Unmapped reads	250,050 / 10.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,279 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	71,799 / 3.05%
Duplication rate	2.84%
Clipped reads	976,777 / 41.46%

2.2. ACGT Content

Number/percentage of A's	38,933,673 / 27.78%
Number/percentage of C's	27,037,620 / 19.29%
Number/percentage of T's	43,005,855 / 30.69%
Number/percentage of G's	30,985,776 / 22.11%
Number/percentage of N's	169,269 / 0.12%
GC Percentage	41.41%

2.3. Coverage

Mean	0.0453

Standard Deviation	0.3191

2.4. Mapping Quality

Mean Mapping Quality	45.56

2.5. Mismatches and indels

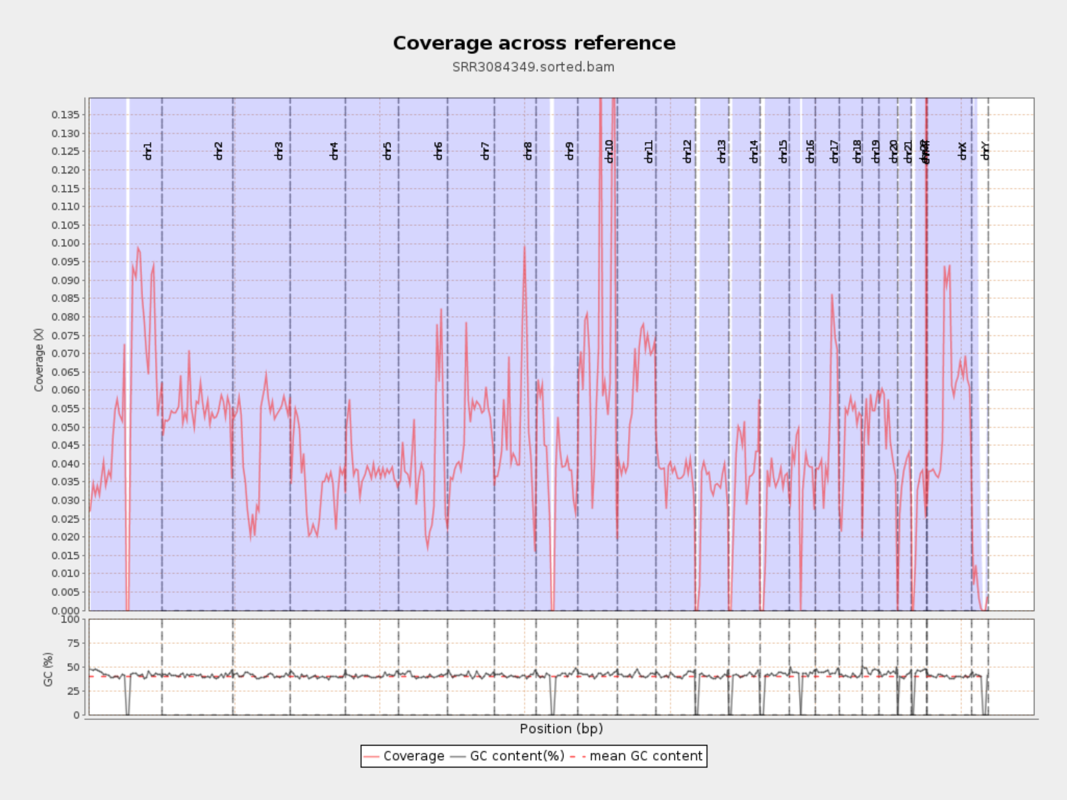
General error rate	1%
Mismatches	1,385,124
Insertions	10,199
Mapped reads with at least one insertion	0.48%
Deletions	28,451
Mapped reads with at least one deletion	1.34%
Homopolymer indels	46.72%

2.6. Chromosome stats

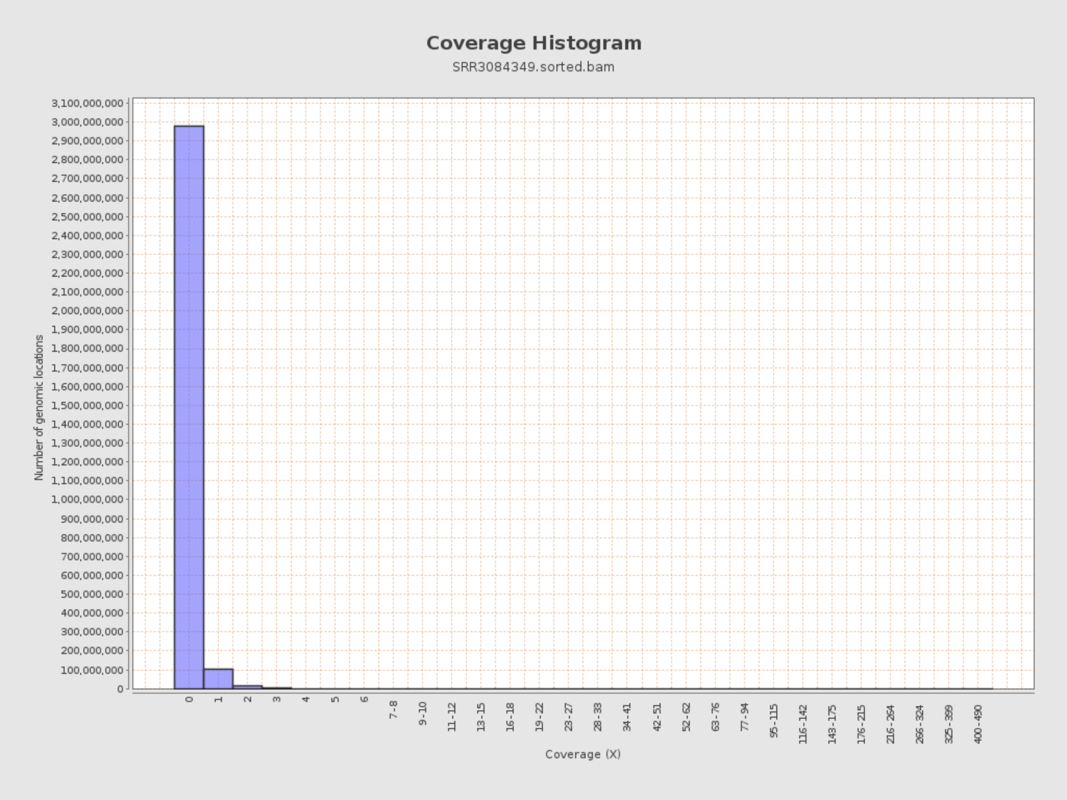
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13889197	0.0557	0.4998
chr2	243199373	13307297	0.0547	0.3727
chr3	198022430	9351596	0.0472	0.2483
chr4	191154276	6595229	0.0345	0.2168
chr5	180915260	7024772	0.0388	0.2231
chr6	171115067	6758349	0.0395	0.2492
chr7	159138663	7910250	0.0497	0.4815

chr8	146364022	7141335	0.0488	0.3244
chr9	141213431	5406196	0.0383	0.2729
chr10	135534747	10242260	0.0756	0.4267
chr11	135006516	7965571	0.059	0.3249
chr12	133851895	5026748	0.0376	0.2197
chr13	115169878	3425947	0.0297	0.1956
chr14	107349540	3793058	0.0353	0.2205
chr15	102531392	3021052	0.0295	0.1994
chr16	90354753	3267662	0.0362	0.2308
chr17	81195210	4106369	0.0506	0.2725
chr18	78077248	3758850	0.0481	0.4205
chr19	59128983	3106336	0.0525	0.392
chr20	63025520	3039148	0.0482	0.2528
chr21	48129895	1566165	0.0325	0.2125
chr22	51304566	1219812	0.0238	0.1742
chrMT	16571	14249	0.8599	1.2212
chrX	155270560	8946450	0.0576	0.2991
chrY	59373566	297095	0.005	0.0974

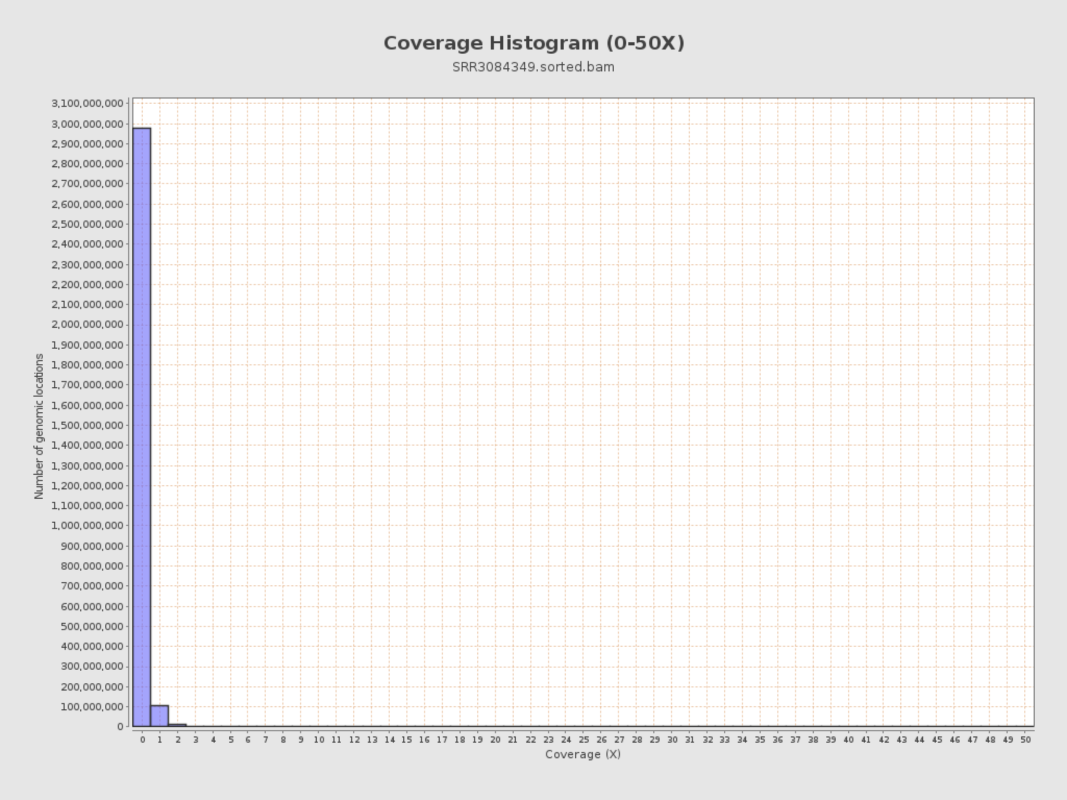
3. Results : Coverage across reference



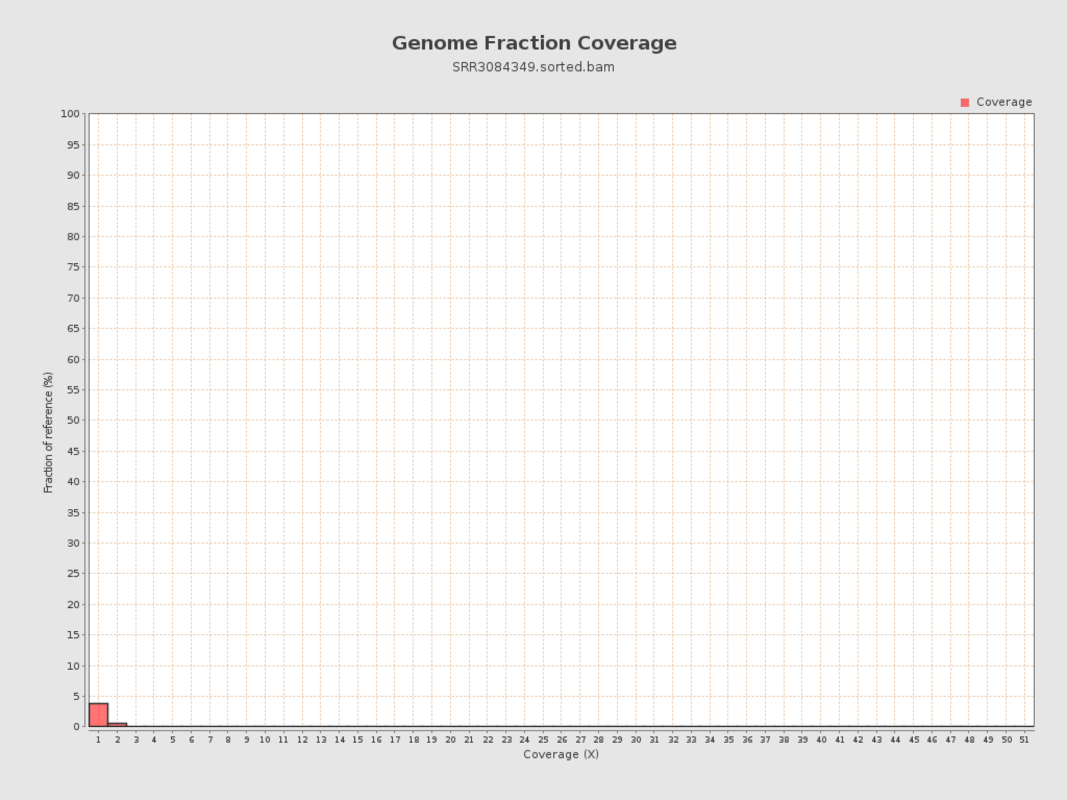
4. Results : Coverage Histogram



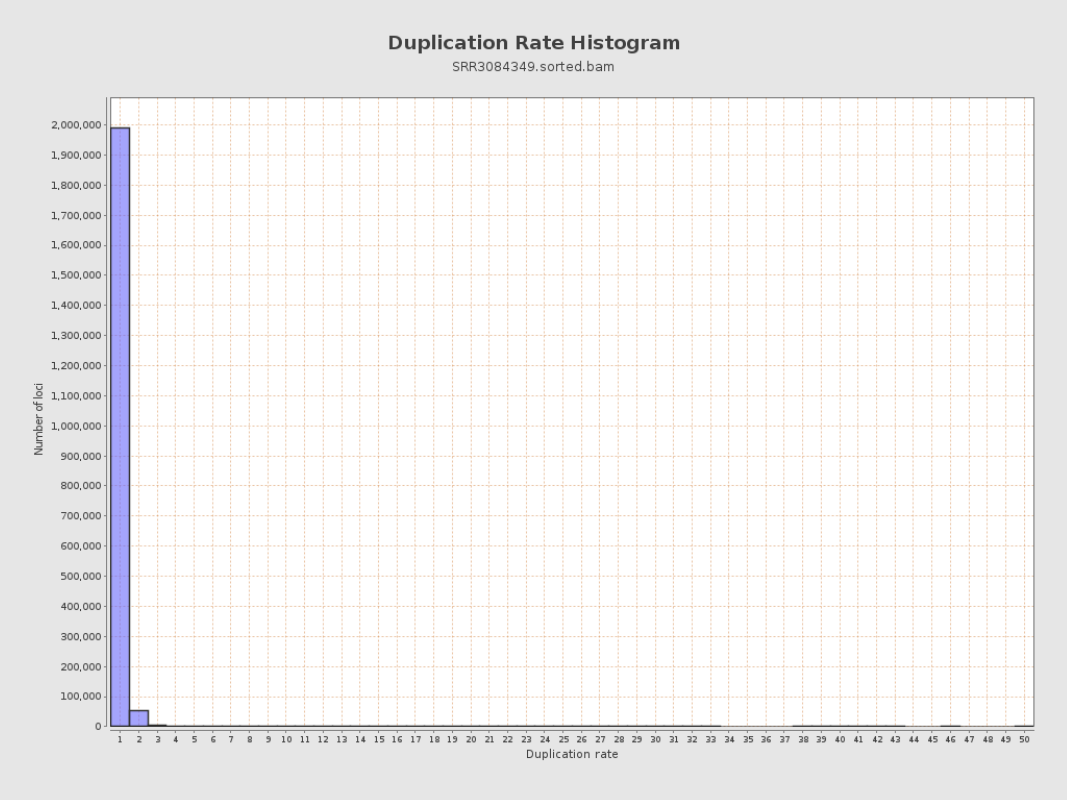
5. Results : Coverage Histogram (0-50X)



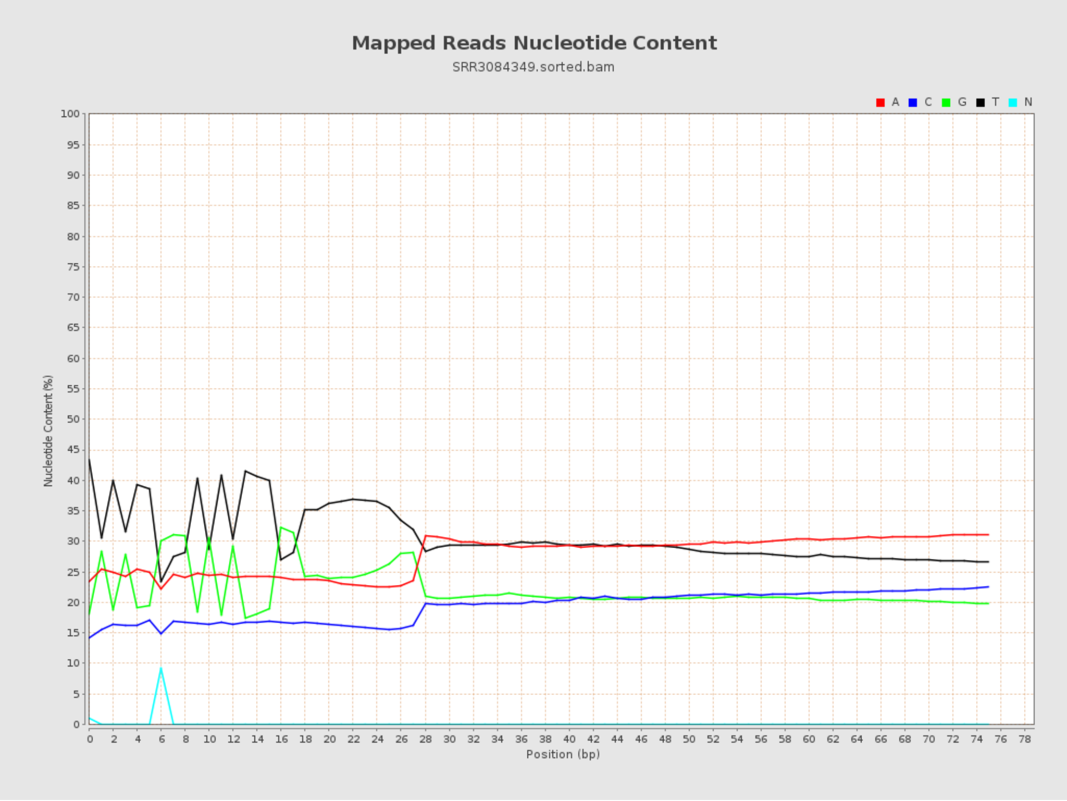
6. Results : Genome Fraction Coverage



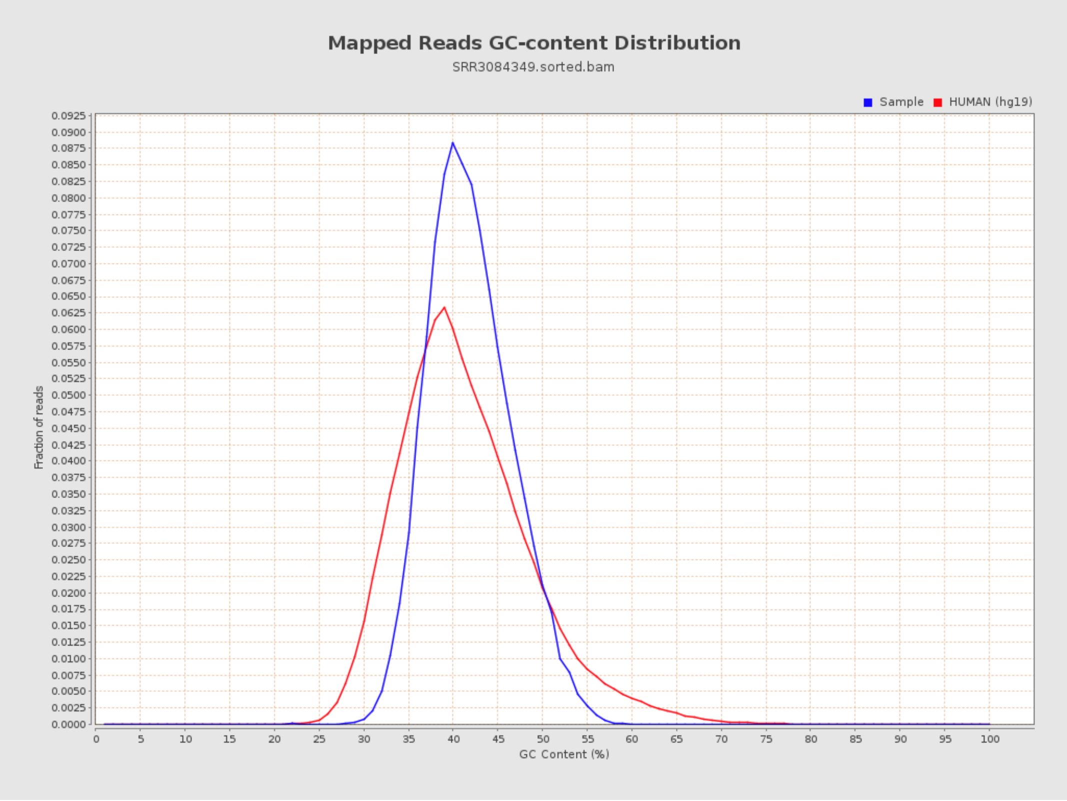
7. Results : Duplication Rate Histogram



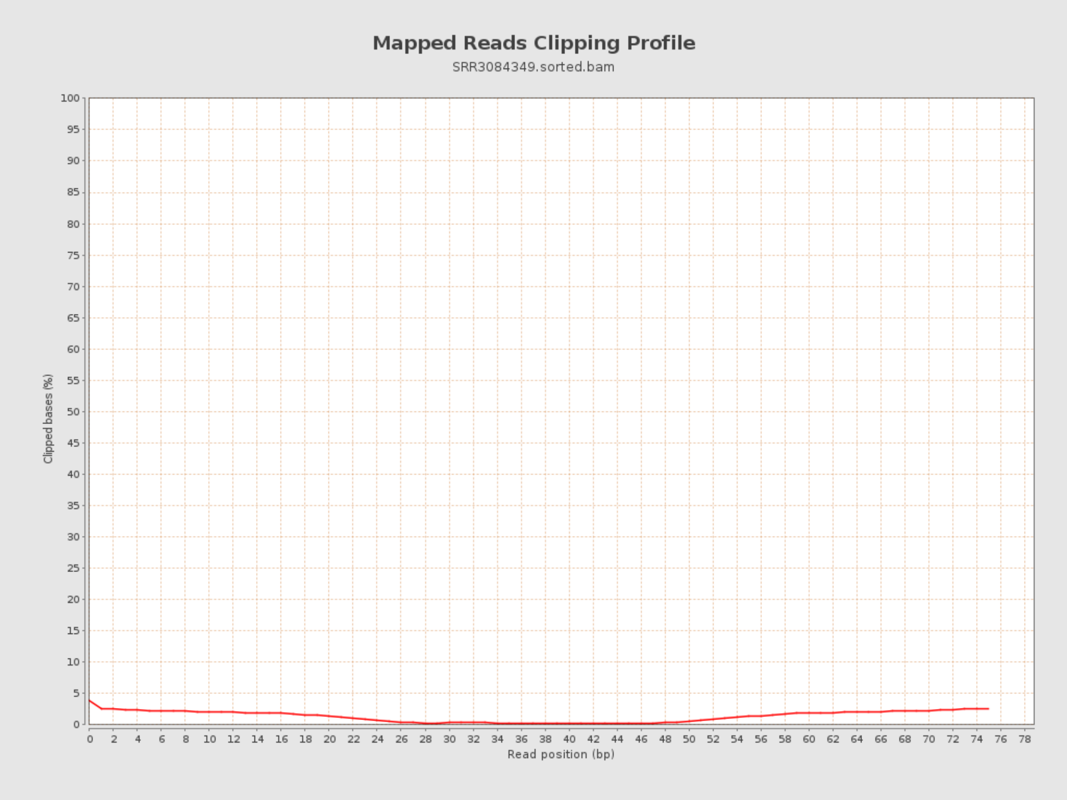
8. Results : Mapped Reads Nucleotide Content



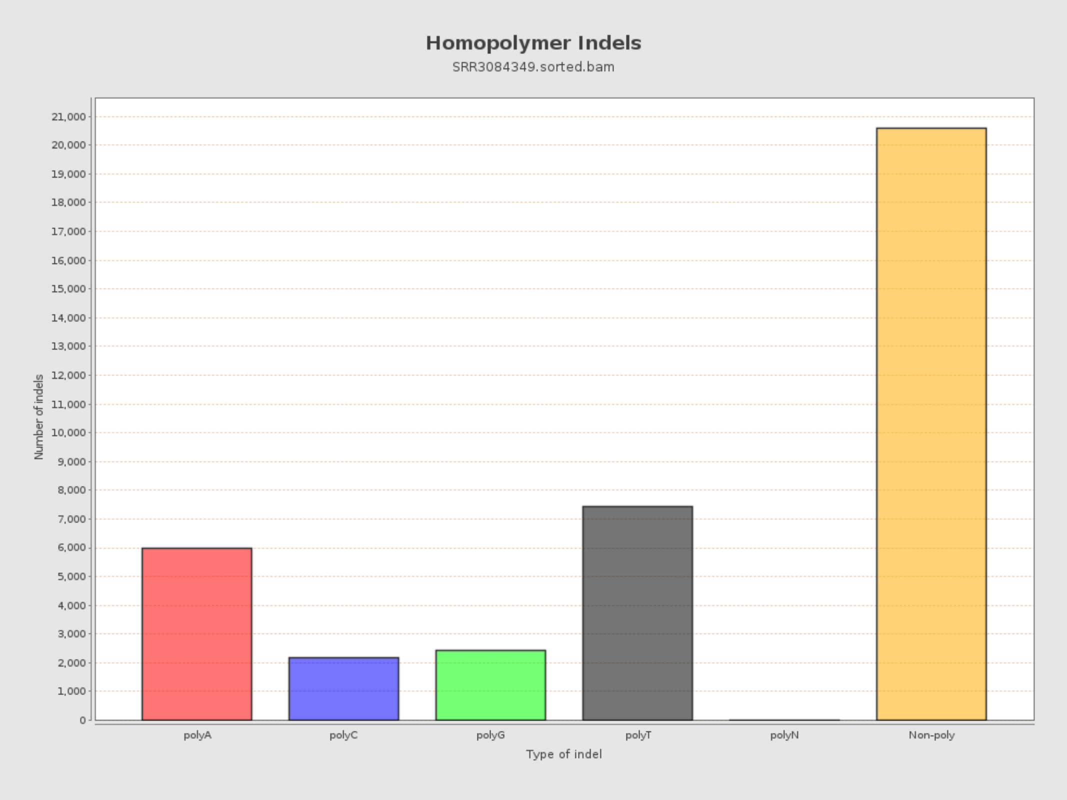
9. Results : Mapped Reads GC-content Distribution



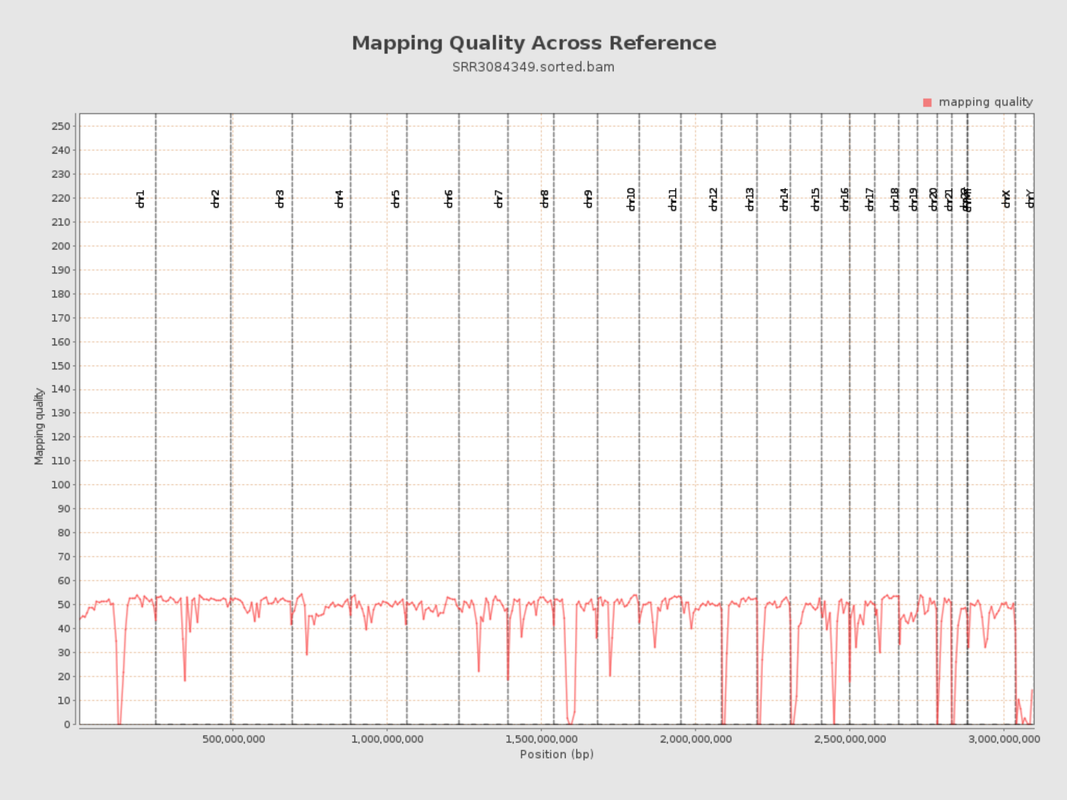
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram