Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 10:54:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084354.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_SRR3084354 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084354.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 10:54:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084354.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,330,844
Mapped reads	2,142,441 / 91.92%
Unmapped reads	188,403 / 8.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,890 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	70,143 / 3.01%
Duplication rate	2.73%
Clipped reads	933,488 / 40.05%

2.2. ACGT Content

Number/percentage of A's	40,122,222 / 27.83%
Number/percentage of C's	27,896,930 / 19.35%
Number/percentage of T's	44,178,393 / 30.65%
Number/percentage of G's	31,779,329 / 22.05%
Number/percentage of N's	178,199 / 0.12%
GC Percentage	41.4%

2.3. Coverage

Mean	0.0466

Standard Deviation	0.3164

2.4. Mapping Quality

Mean Mapping Quality	45.79

2.5. Mismatches and indels

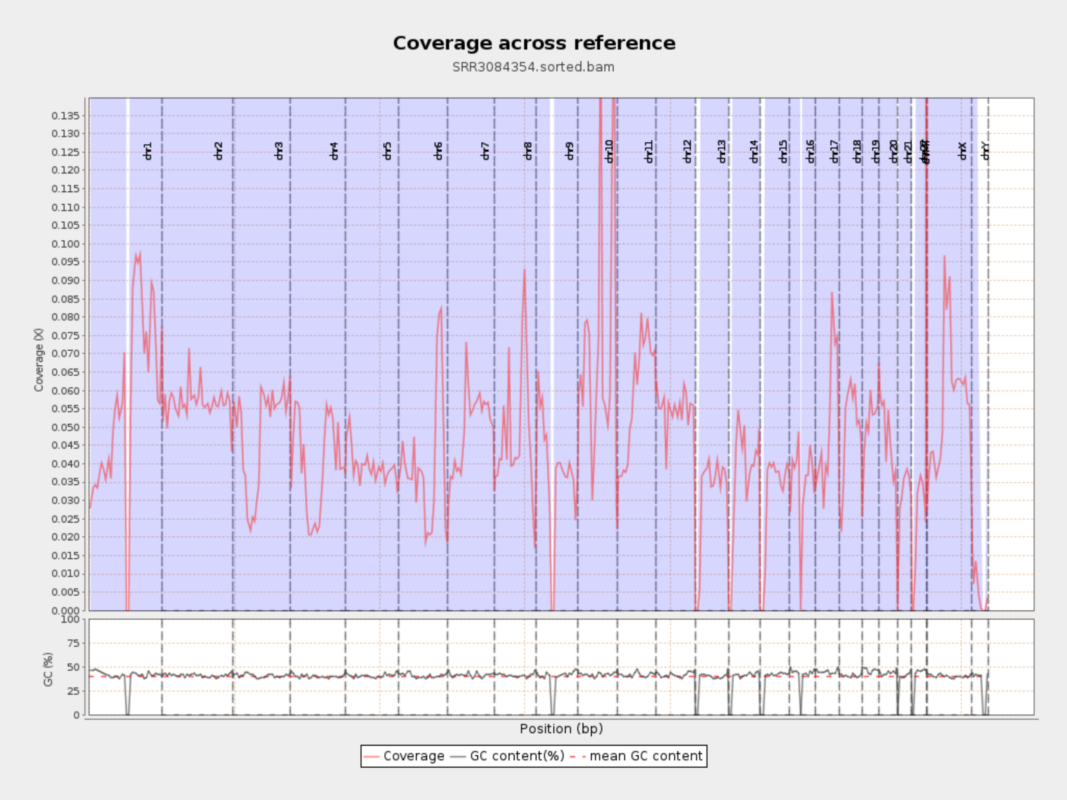
General error rate	0.97%
Mismatches	1,376,609
Insertions	9,892
Mapped reads with at least one insertion	0.46%
Deletions	28,153
Mapped reads with at least one deletion	1.3%
Homopolymer indels	46.45%

2.6. Chromosome stats

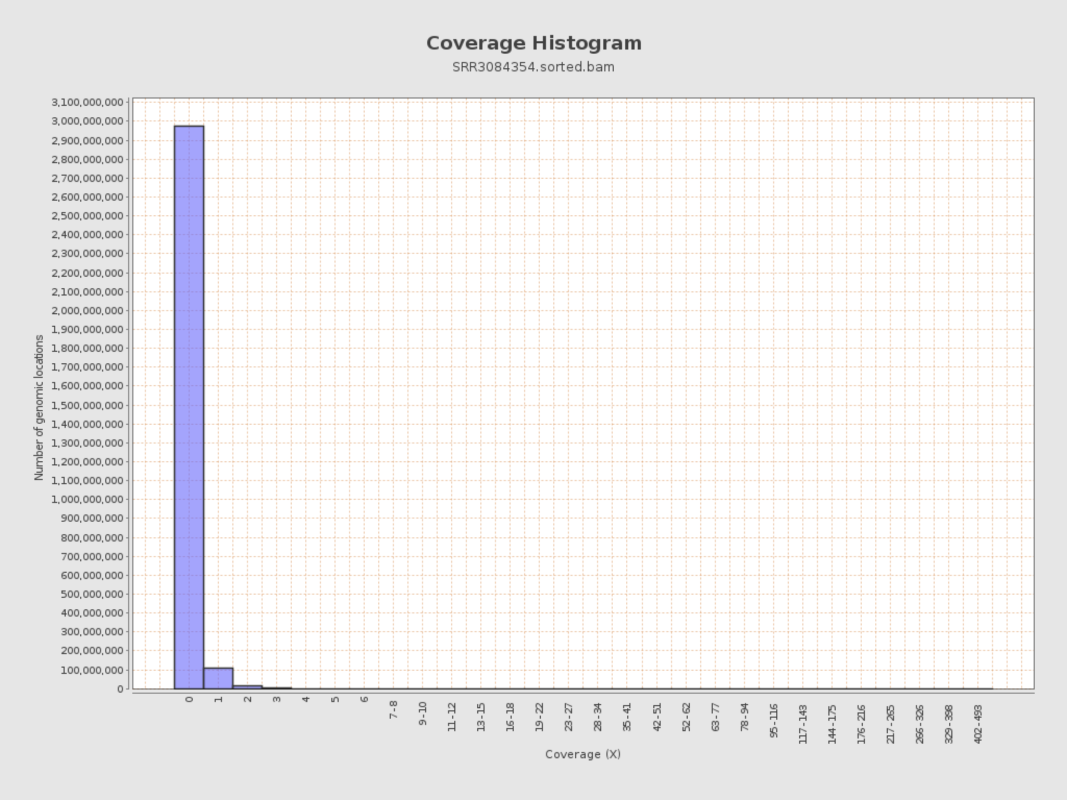
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13992368	0.0561	0.5015
chr2	243199373	13855560	0.057	0.3865
chr3	198022430	9572042	0.0483	0.2519
chr4	191154276	7634643	0.0399	0.2329
chr5	180915260	7145675	0.0395	0.2247
chr6	171115067	6810491	0.0398	0.2497
chr7	159138663	7995222	0.0502	0.4365

chr8	146364022	7049872	0.0482	0.3045
chr9	141213431	5285805	0.0374	0.2596
chr10	135534747	10152428	0.0749	0.4336
chr11	135006516	7908279	0.0586	0.325
chr12	133851895	7306618	0.0546	0.2658
chr13	115169878	3535265	0.0307	0.1977
chr14	107349540	3880625	0.0361	0.2225
chr15	102531392	3118611	0.0304	0.2002
chr16	90354753	3155260	0.0349	0.2274
chr17	81195210	4163332	0.0513	0.2709
chr18	78077248	3859139	0.0494	0.3793
chr19	59128983	3053438	0.0516	0.3686
chr20	63025520	2938564	0.0466	0.2483
chr21	48129895	1467613	0.0305	0.2065
chr22	51304566	1168830	0.0228	0.1699
chrMT	16571	11729	0.7078	1.0164
chrX	155270560	8838541	0.0569	0.2922
chrY	59373566	303776	0.0051	0.1036

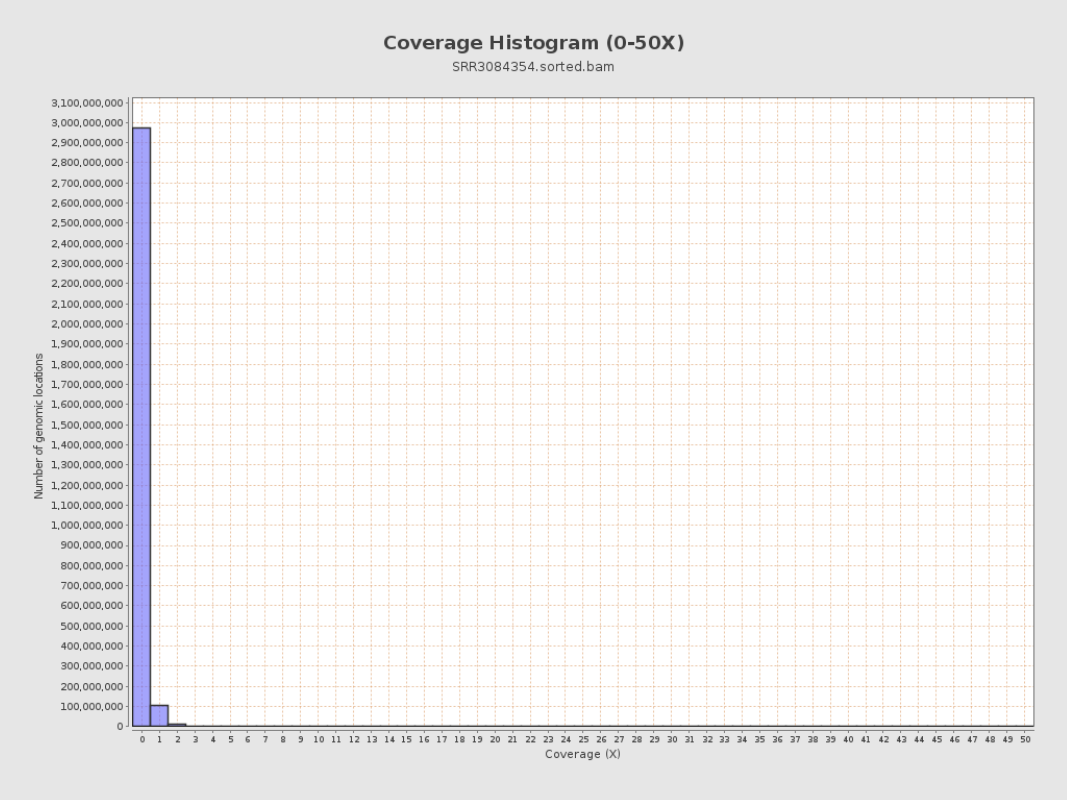
3. Results : Coverage across reference



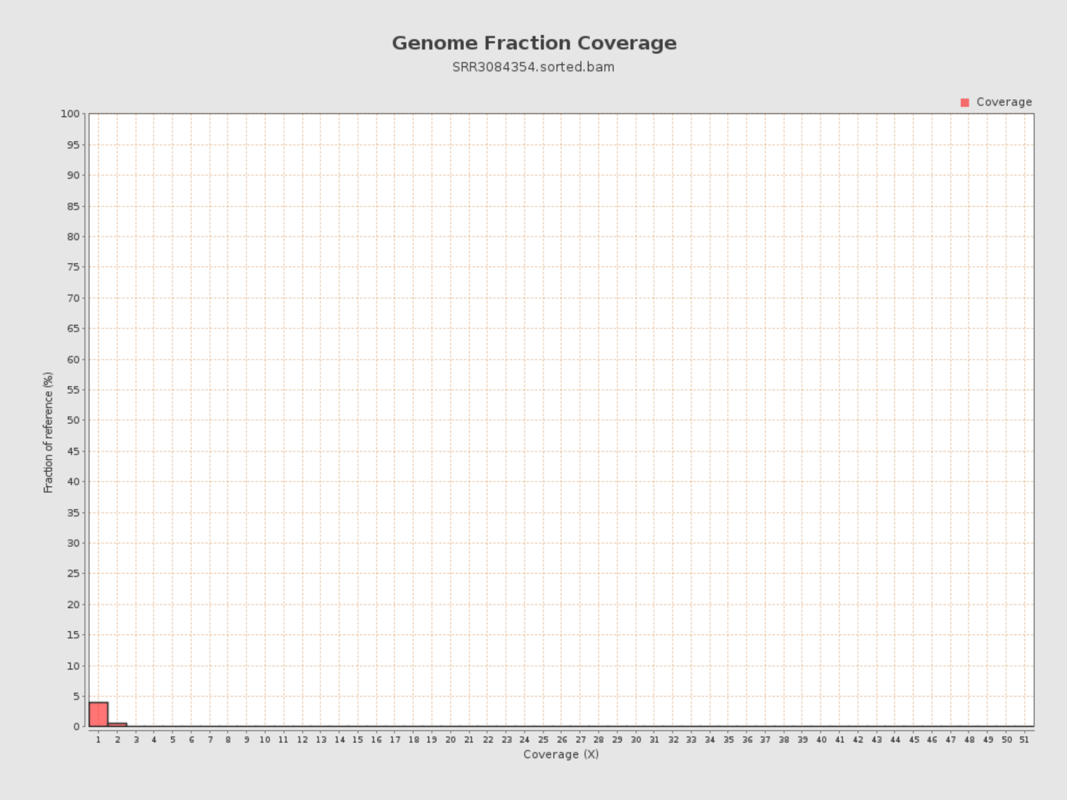
4. Results : Coverage Histogram



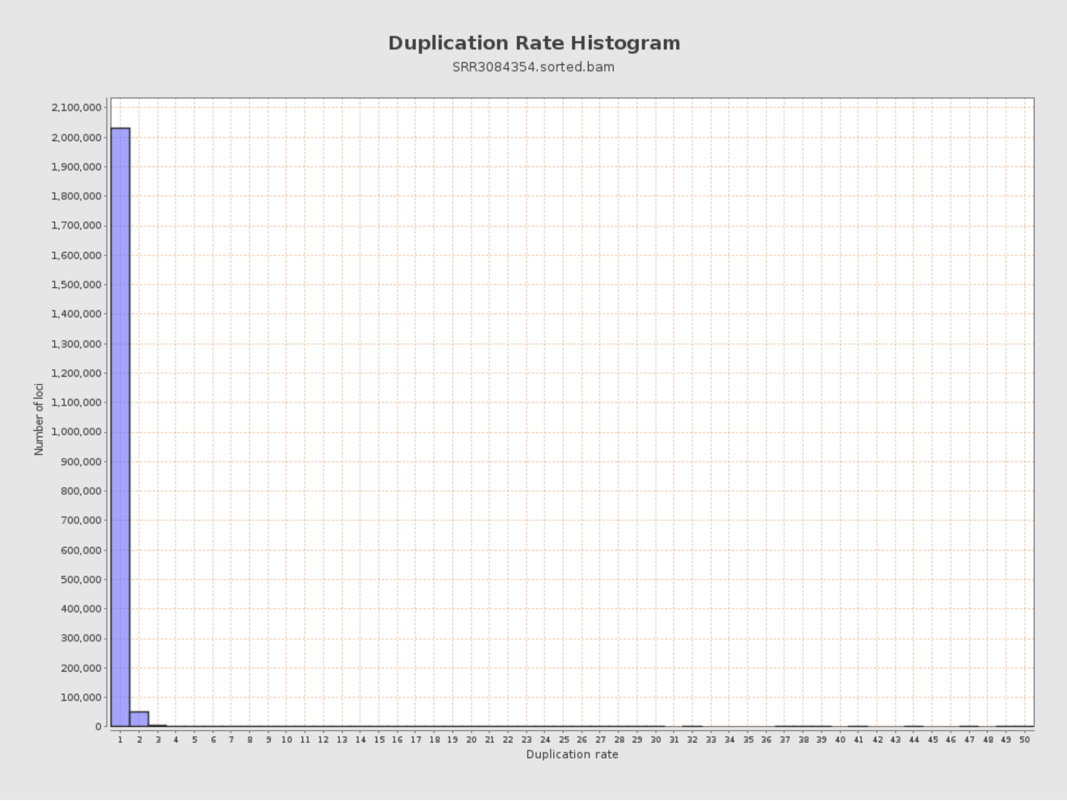
5. Results : Coverage Histogram (0-50X)



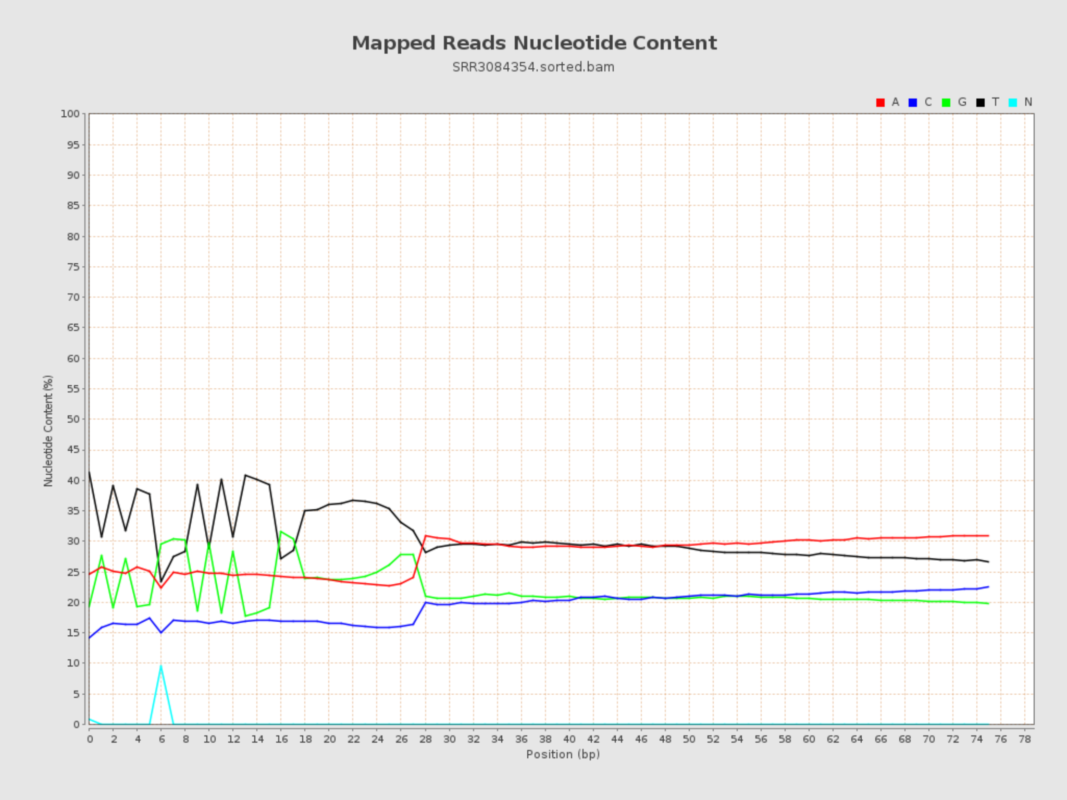
6. Results : Genome Fraction Coverage



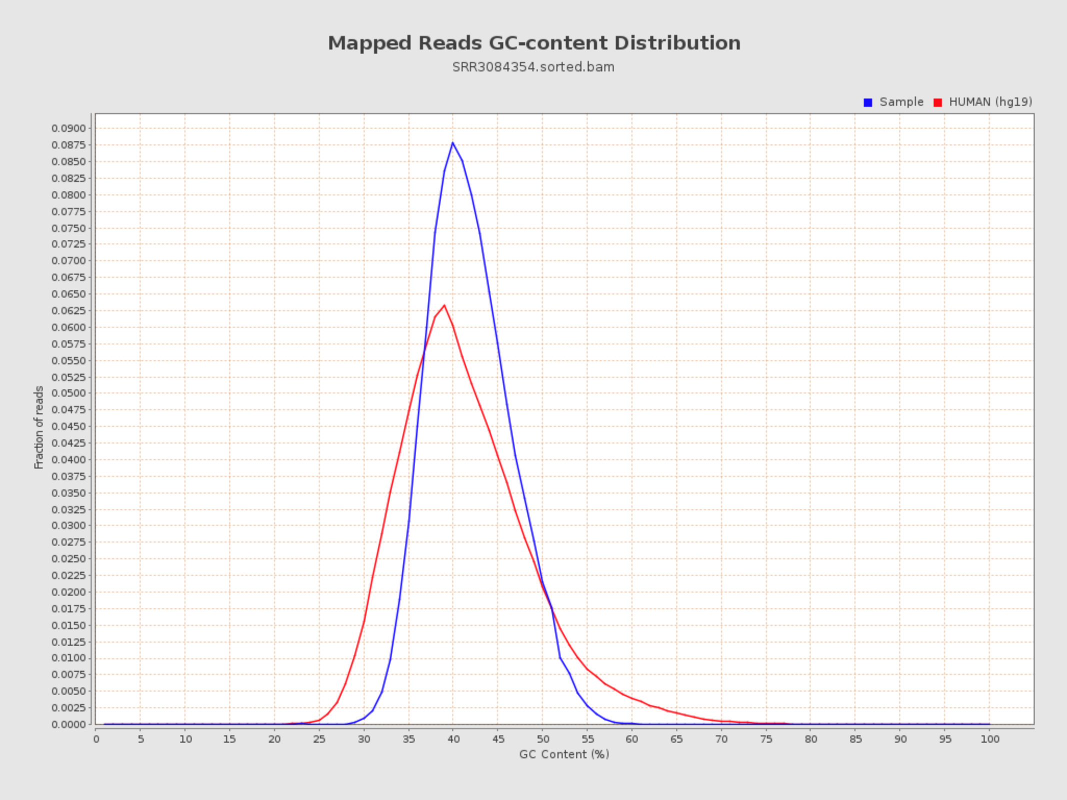
7. Results : Duplication Rate Histogram



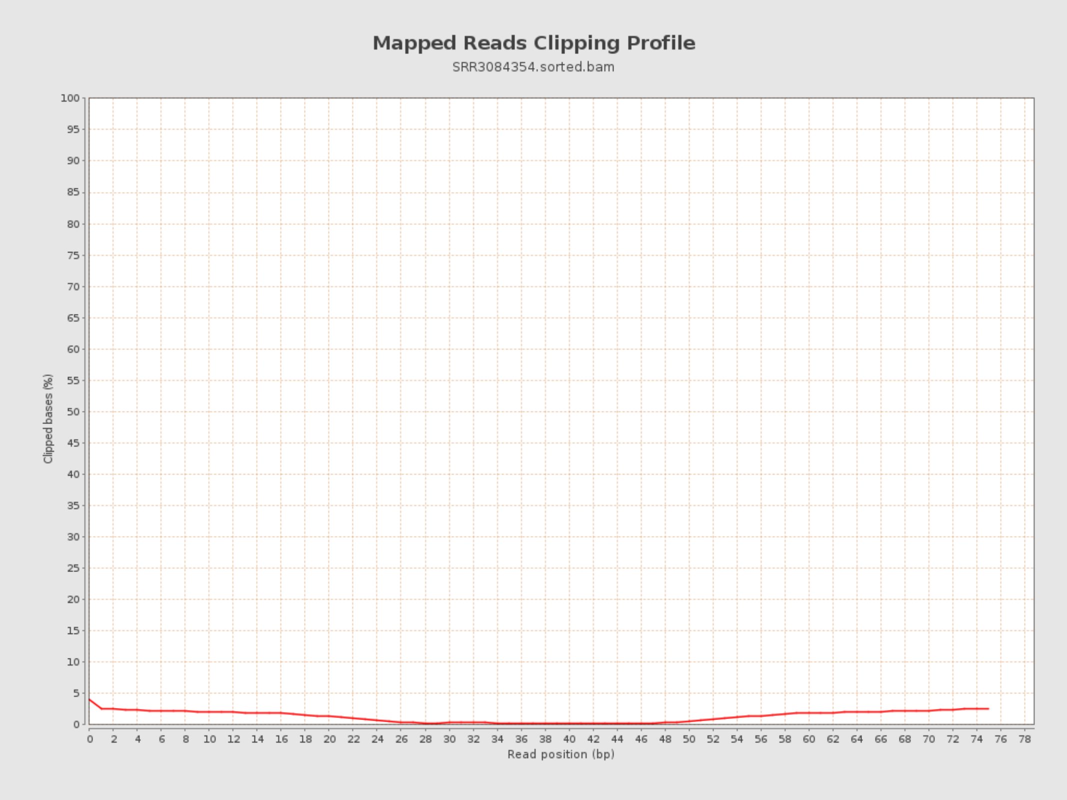
8. Results : Mapped Reads Nucleotide Content



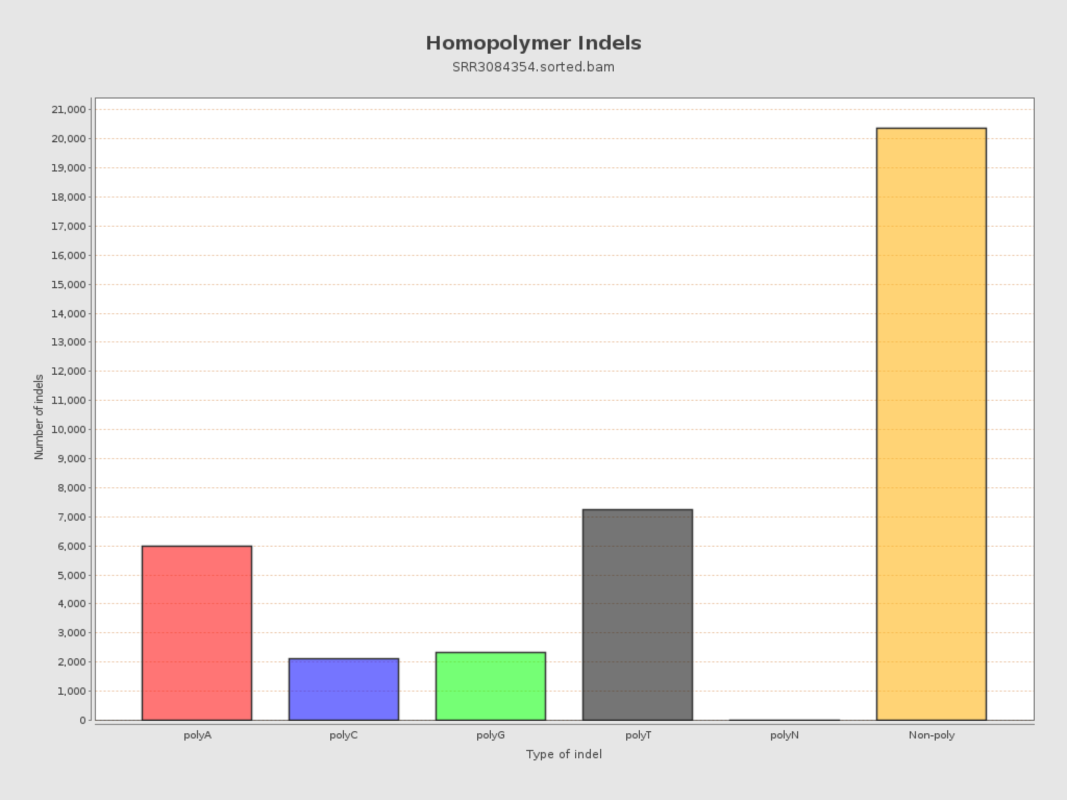
9. Results : Mapped Reads GC-content Distribution



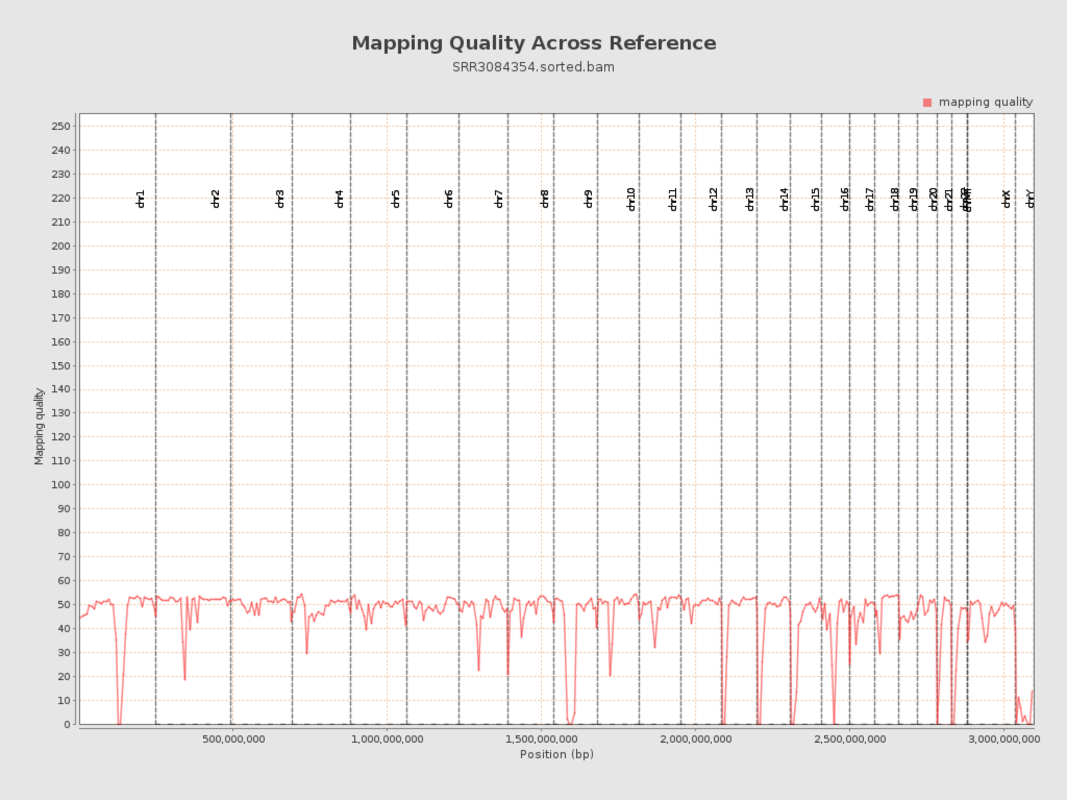
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram