Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 10:33:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084350.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_SRR3084350 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084350.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 10:33:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084350.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,098,144
Mapped reads	1,895,093 / 90.32%
Unmapped reads	203,051 / 9.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,731 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	63,205 / 3.01%
Duplication rate	2.77%
Clipped reads	857,244 / 40.86%

2.2. ACGT Content

Number/percentage of A's	35,034,127 / 27.69%
Number/percentage of C's	24,474,326 / 19.34%
Number/percentage of T's	38,710,799 / 30.6%
Number/percentage of G's	28,143,611 / 22.24%
Number/percentage of N's	154,751 / 0.12%
GC Percentage	41.59%

2.3. Coverage

Mean	0.0409

Standard Deviation	0.3001

2.4. Mapping Quality

Mean Mapping Quality	45.48

2.5. Mismatches and indels

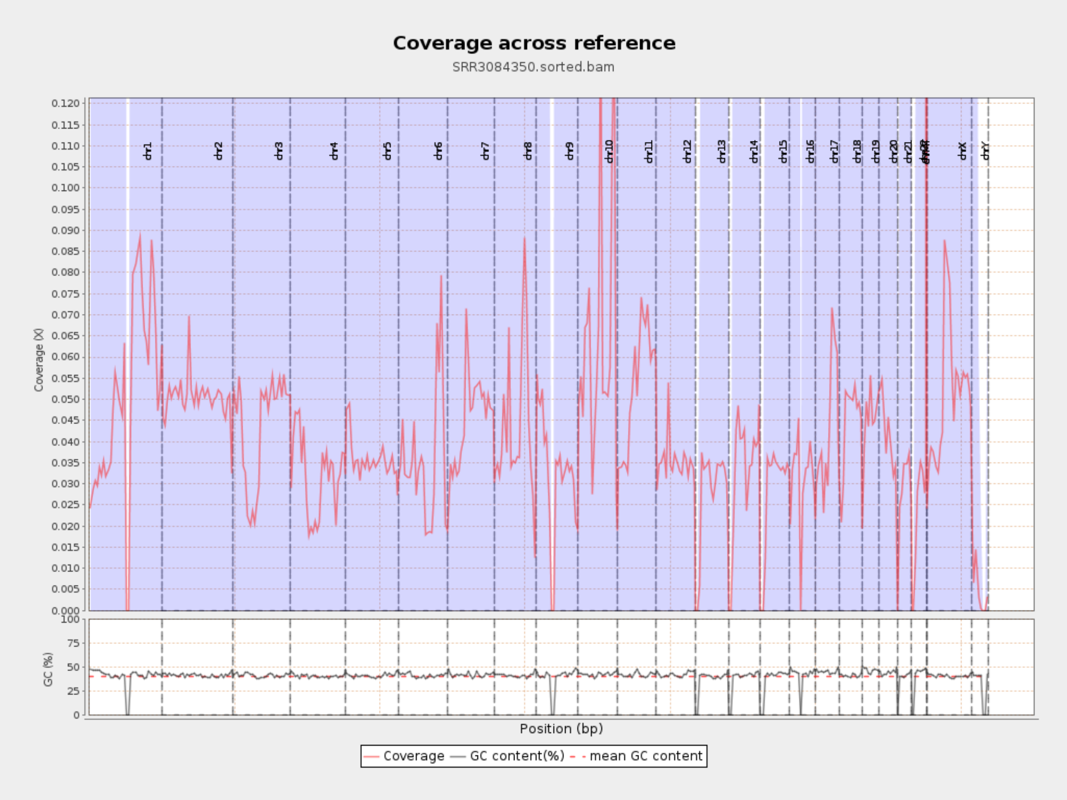
General error rate	0.98%
Mismatches	1,226,487
Insertions	8,770
Mapped reads with at least one insertion	0.46%
Deletions	24,229
Mapped reads with at least one deletion	1.27%
Homopolymer indels	46.83%

2.6. Chromosome stats

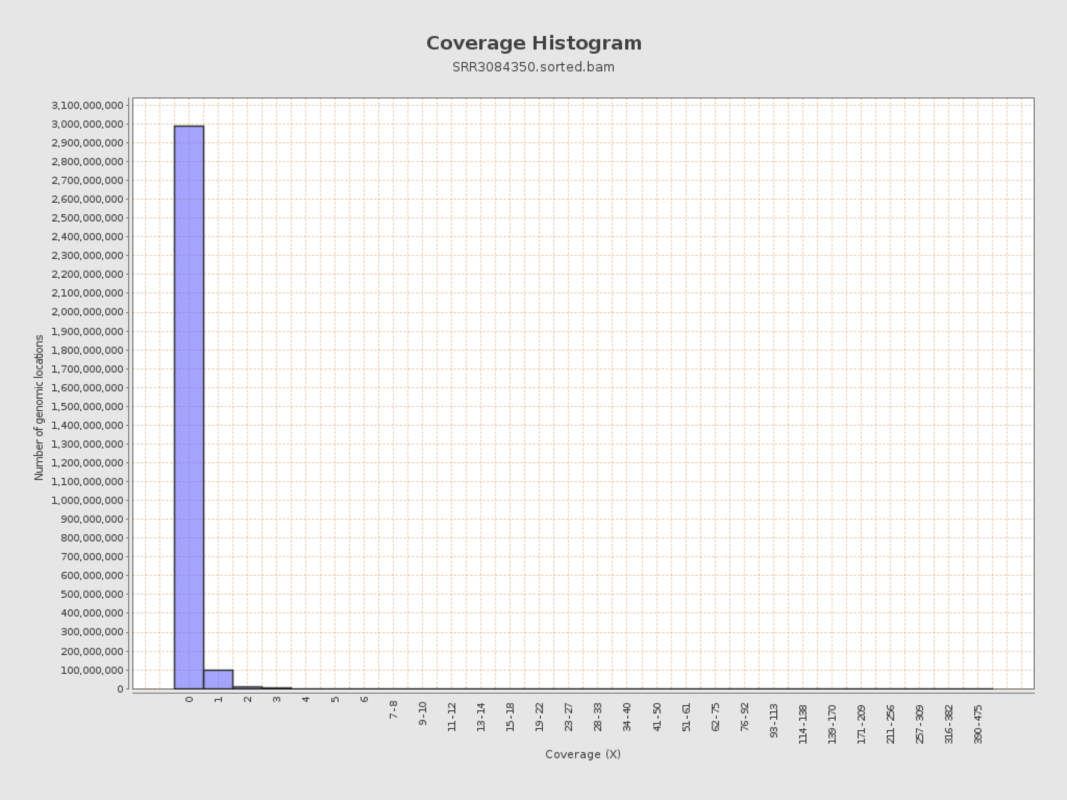
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12574137	0.0504	0.4829
chr2	243199373	12281445	0.0505	0.3449
chr3	198022430	8616977	0.0435	0.2365
chr4	191154276	6109392	0.032	0.2104
chr5	180915260	6491932	0.0359	0.2123
chr6	171115067	6115800	0.0357	0.2316
chr7	159138663	7265822	0.0457	0.4258

chr8	146364022	6341879	0.0433	0.2815
chr9	141213431	4571138	0.0324	0.2453
chr10	135534747	9025314	0.0666	0.4367
chr11	135006516	7124088	0.0528	0.3057
chr12	133851895	4711064	0.0352	0.2123
chr13	115169878	3137964	0.0272	0.1845
chr14	107349540	3489612	0.0325	0.2072
chr15	102531392	2865245	0.0279	0.1934
chr16	90354753	2825277	0.0313	0.215
chr17	81195210	3509851	0.0432	0.2464
chr18	78077248	3461252	0.0443	0.3848
chr19	59128983	2692233	0.0455	0.376
chr20	63025520	2595559	0.0412	0.23
chr21	48129895	1356418	0.0282	0.1991
chr22	51304566	1116145	0.0218	0.1647
chrMT	16571	41196	2.486	2.1765
chrX	155270560	7941612	0.0511	0.2783
chrY	59373566	298255	0.005	0.113

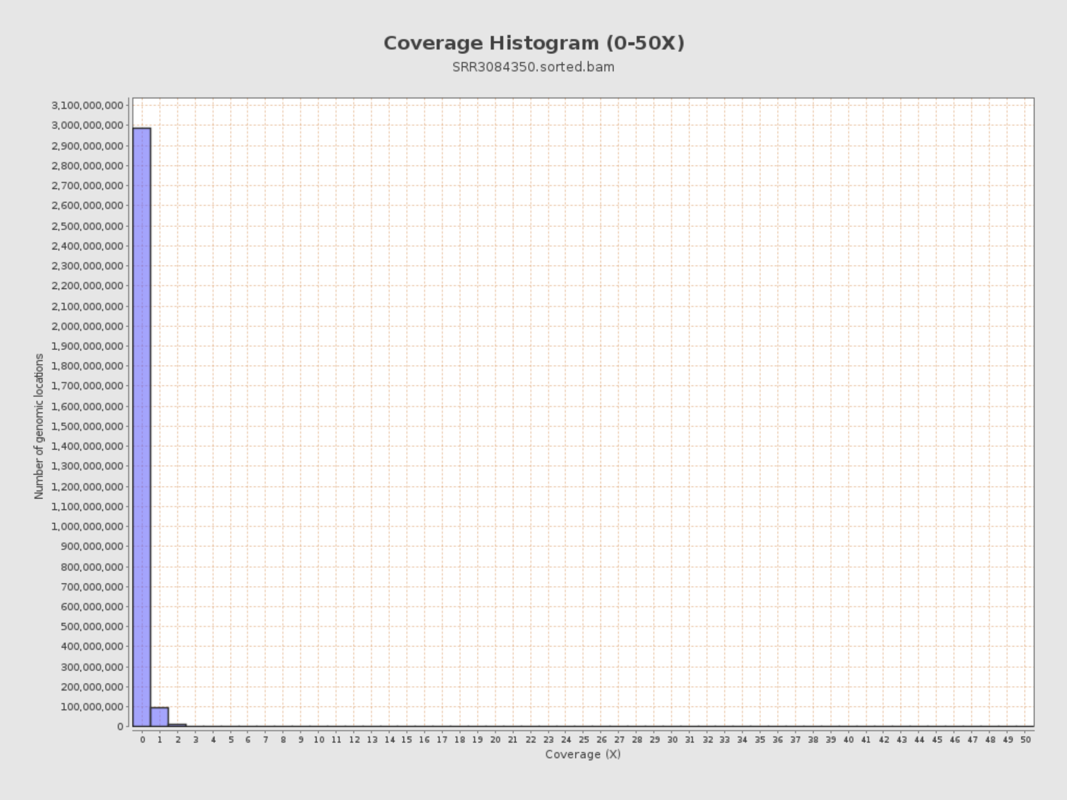
3. Results : Coverage across reference



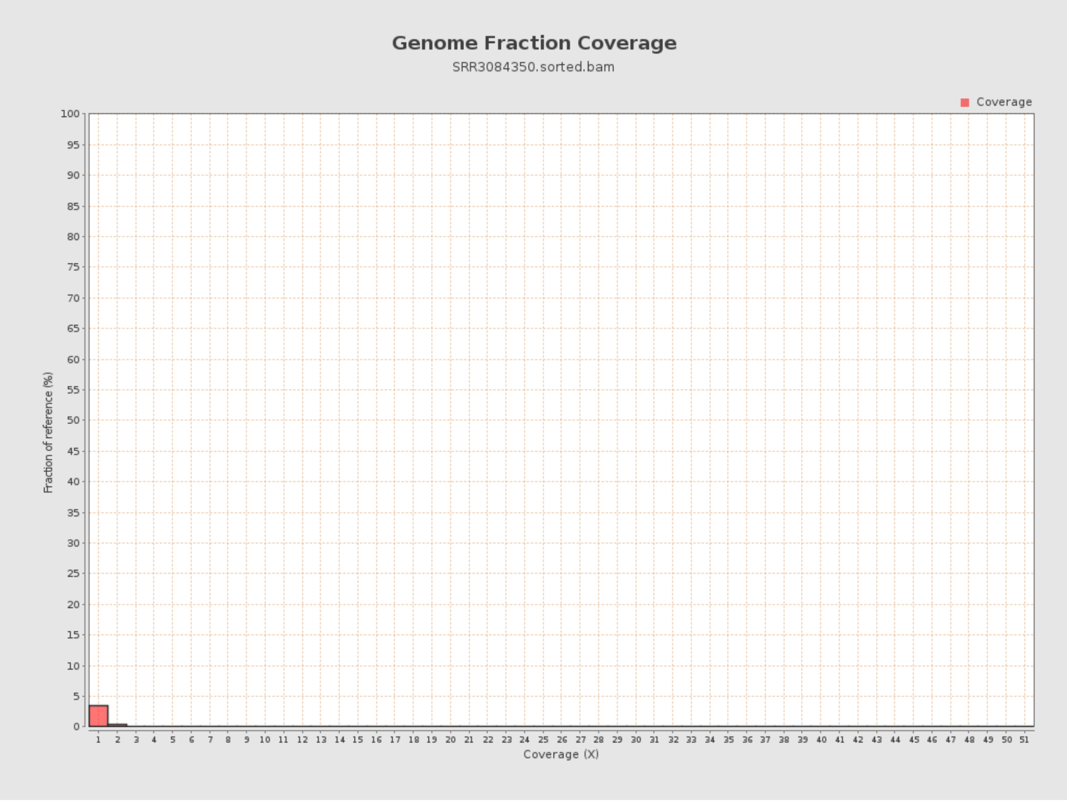
4. Results : Coverage Histogram



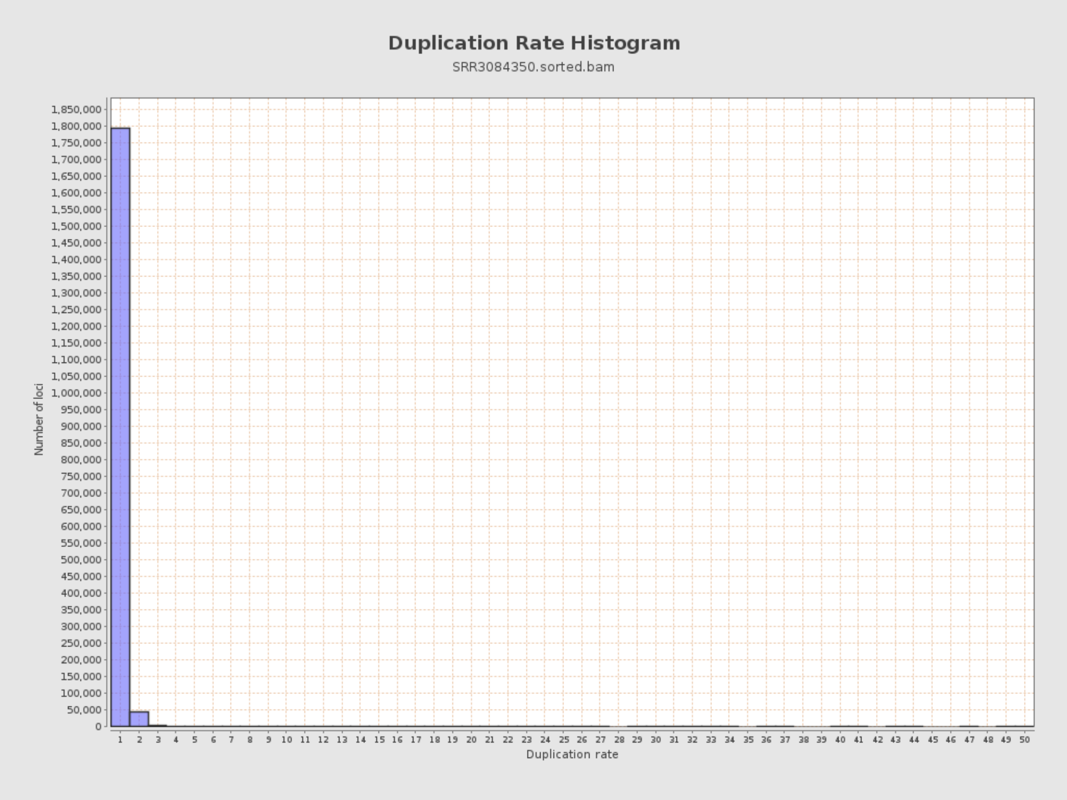
5. Results : Coverage Histogram (0-50X)



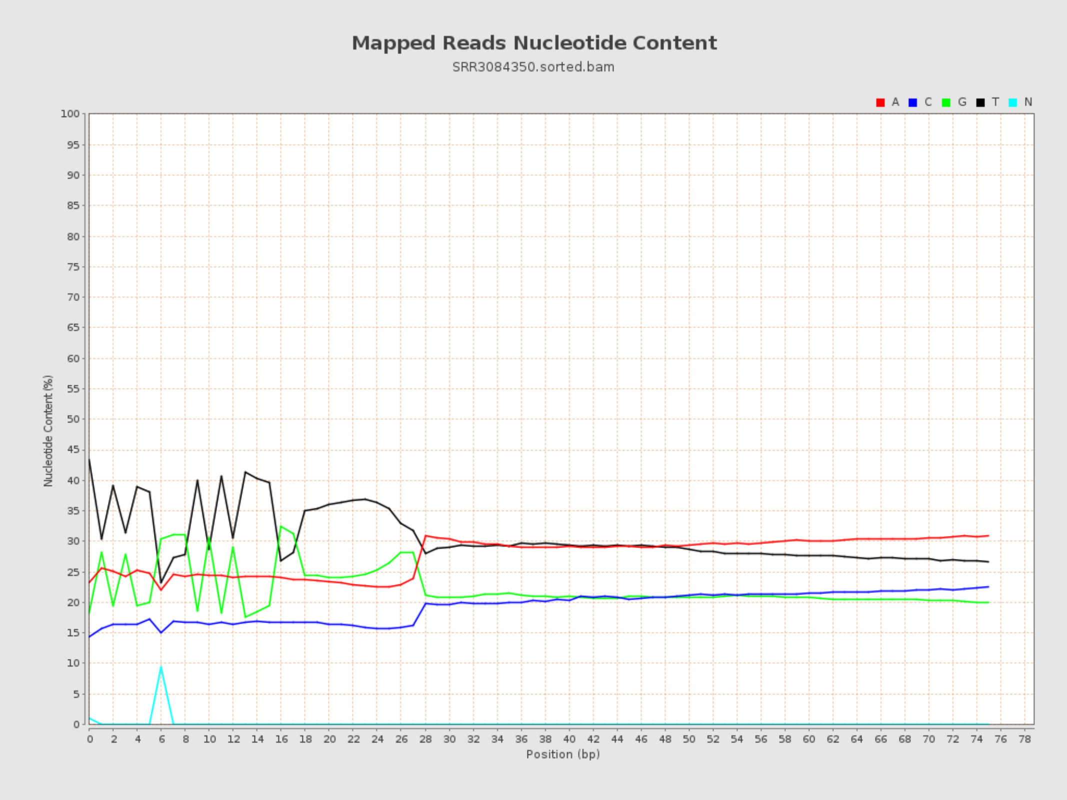
6. Results : Genome Fraction Coverage



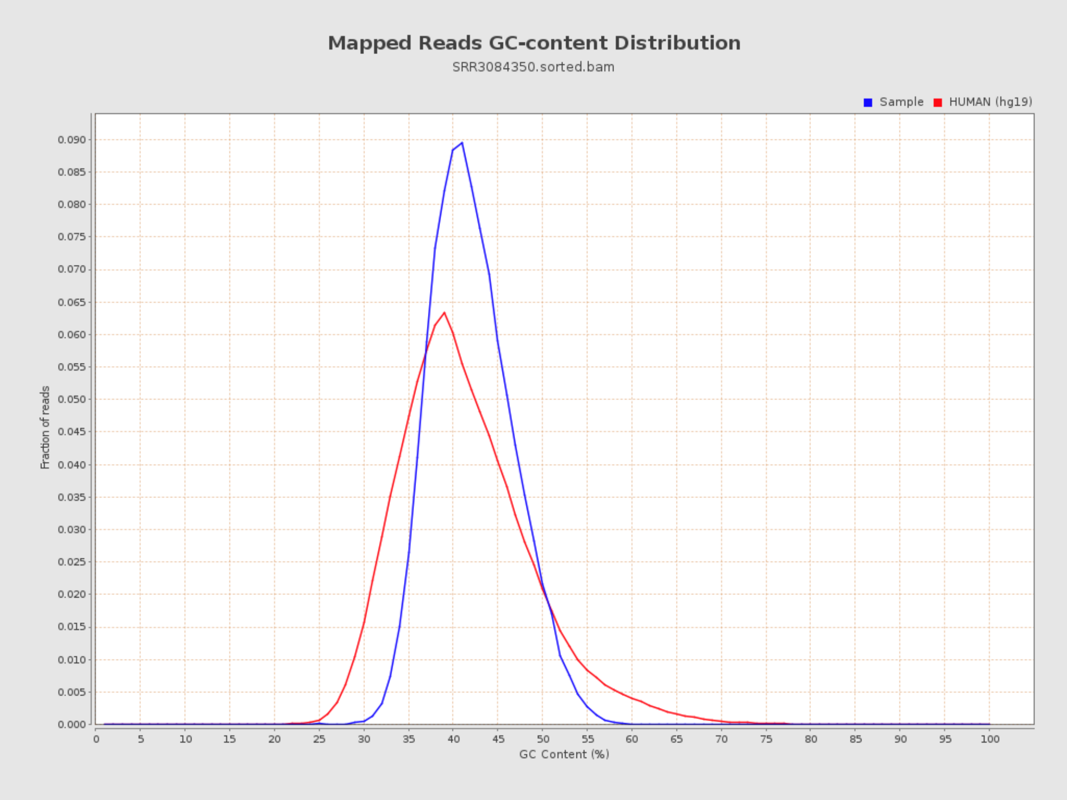
7. Results : Duplication Rate Histogram



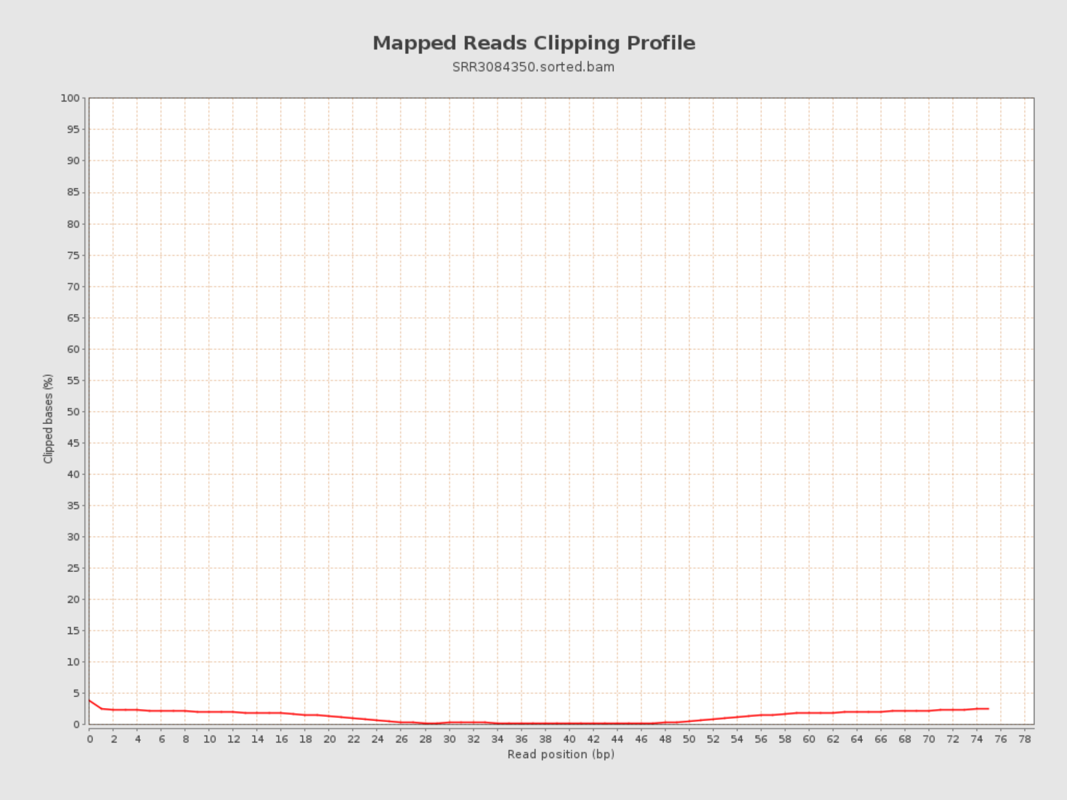
8. Results : Mapped Reads Nucleotide Content



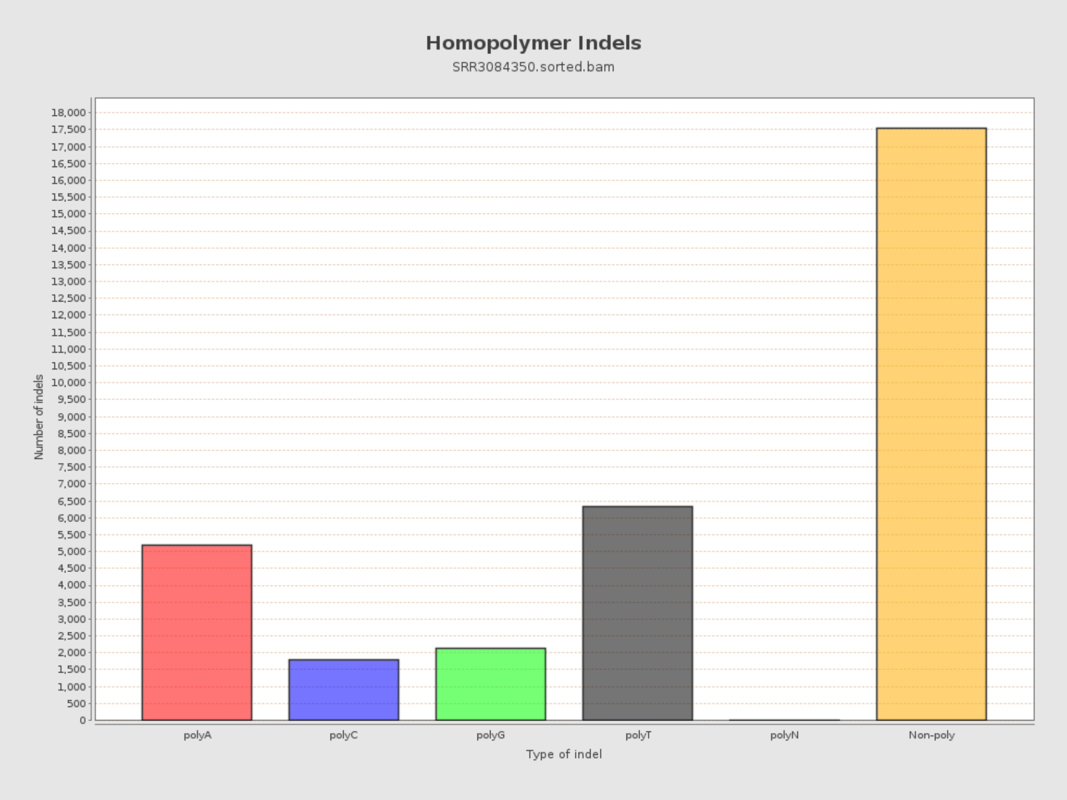
9. Results : Mapped Reads GC-content Distribution



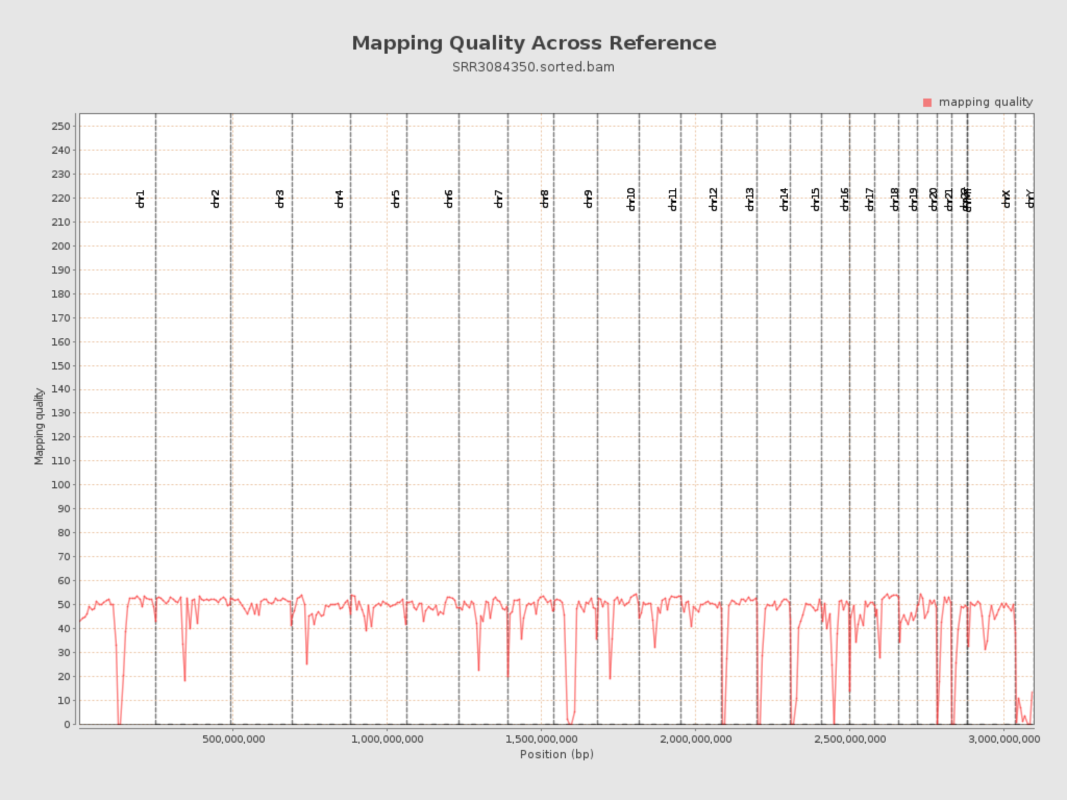
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram