Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 20:07:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084906.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_SRR3084906 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084906.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 20:07:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084906.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,201,872
Mapped reads	1,980,187 / 89.93%
Unmapped reads	221,685 / 10.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,932 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	94,124 / 4.27%
Duplication rate	4.06%
Clipped reads	754,947 / 34.29%

2.2. ACGT Content

Number/percentage of A's	38,825,961 / 28.73%
Number/percentage of C's	24,548,229 / 18.17%
Number/percentage of T's	43,459,600 / 32.16%
Number/percentage of G's	28,283,889 / 20.93%
Number/percentage of N's	20,875 / 0.02%
GC Percentage	39.09%

2.3. Coverage

Mean	0.0437

Standard Deviation	0.3497

2.4. Mapping Quality

Mean Mapping Quality	47.33

2.5. Mismatches and indels

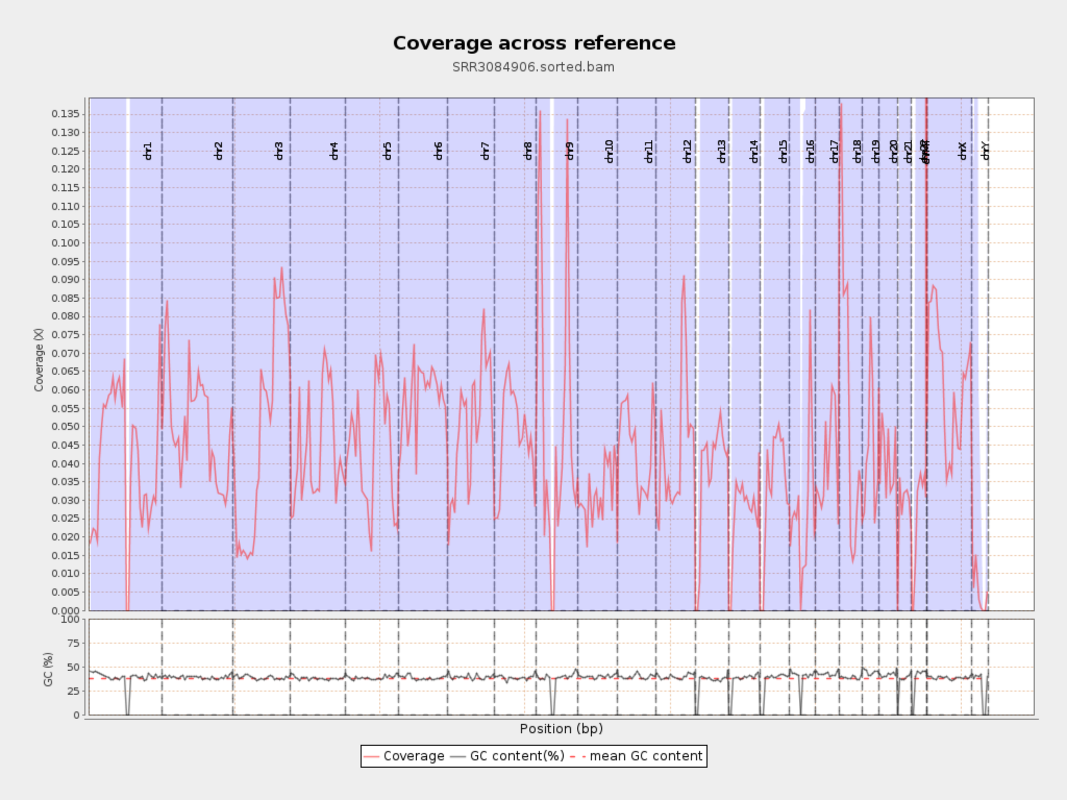
General error rate	0.83%
Mismatches	1,105,263
Insertions	10,231
Mapped reads with at least one insertion	0.51%
Deletions	29,031
Mapped reads with at least one deletion	1.45%
Homopolymer indels	48.36%

2.6. Chromosome stats

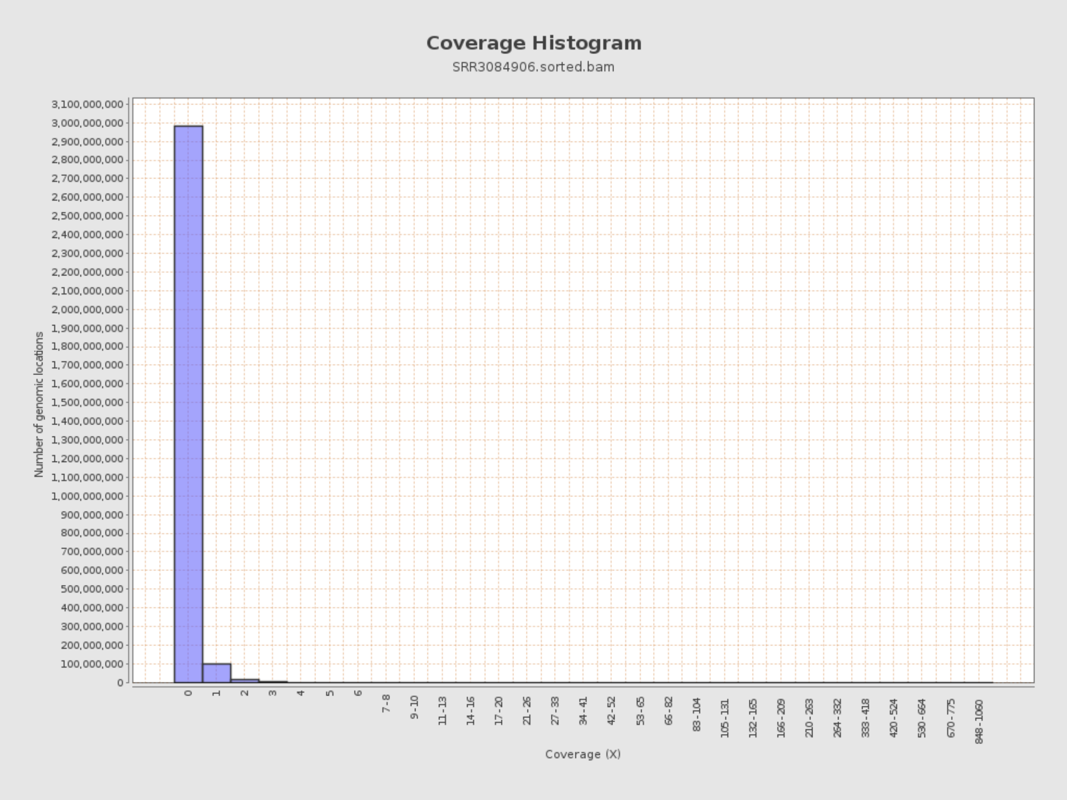
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10169738	0.0408	0.578
chr2	243199373	12169239	0.05	0.3711
chr3	198022430	9565378	0.0483	0.2507
chr4	191154276	8376523	0.0438	0.2406
chr5	180915260	7979496	0.0441	0.2432
chr6	171115067	9863500	0.0576	0.2875
chr7	159138663	8088171	0.0508	0.3228

chr8	146364022	6925338	0.0473	0.7152
chr9	141213431	7271824	0.0515	0.3487
chr10	135534747	4297953	0.0317	0.2439
chr11	135006516	5939575	0.044	0.2718
chr12	133851895	5948515	0.0444	0.2438
chr13	115169878	4234083	0.0368	0.2171
chr14	107349540	2731420	0.0254	0.1939
chr15	102531392	3439114	0.0335	0.2082
chr16	90354753	2530849	0.028	0.2091
chr17	81195210	3263101	0.0402	0.2317
chr18	78077248	4552335	0.0583	0.5637
chr19	59128983	2618732	0.0443	0.386
chr20	63025520	2587644	0.0411	0.2427
chr21	48129895	1323136	0.0275	0.1995
chr22	51304566	1252181	0.0244	0.1751
chrMT	16571	81781	4.9352	3.4458
chrX	155270560	9670955	0.0623	0.2986
chrY	59373566	309175	0.0052	0.1313

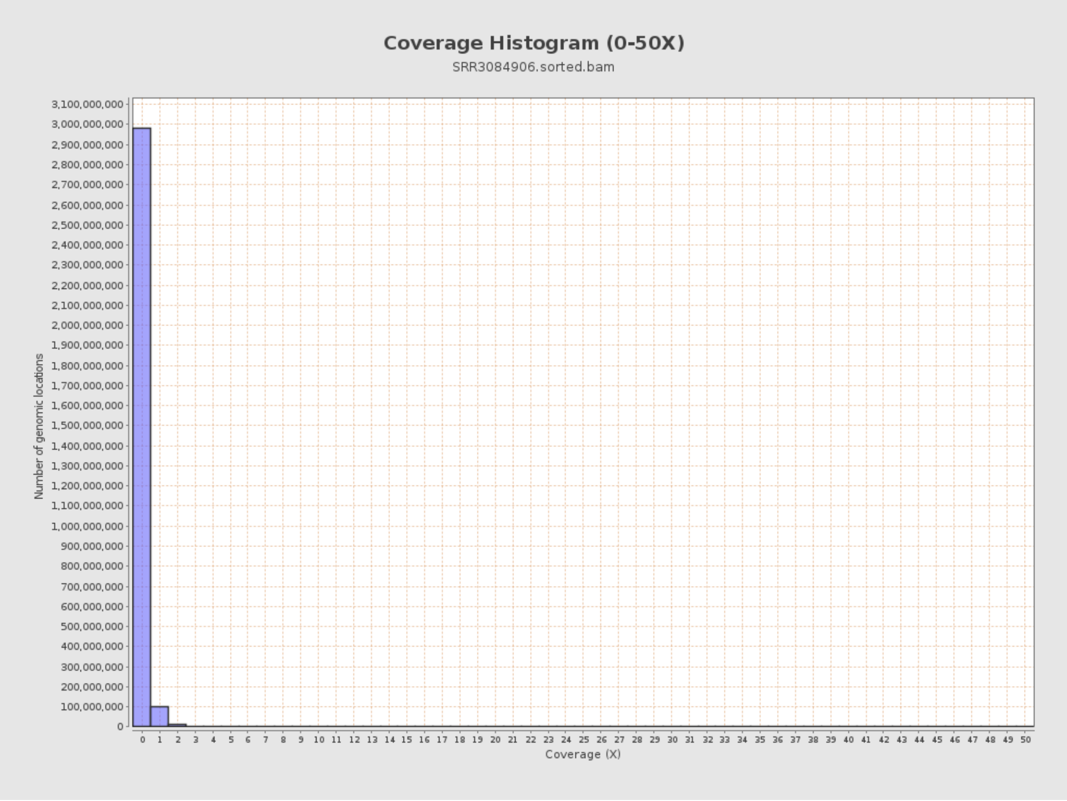
3. Results : Coverage across reference



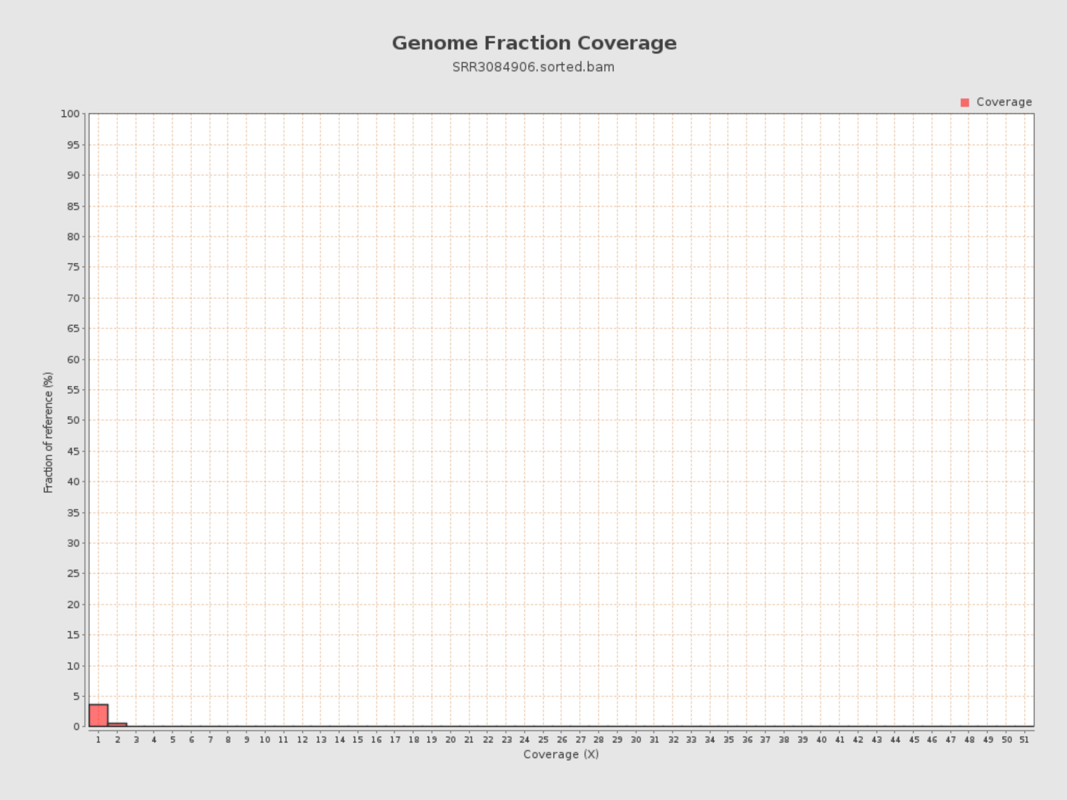
4. Results : Coverage Histogram



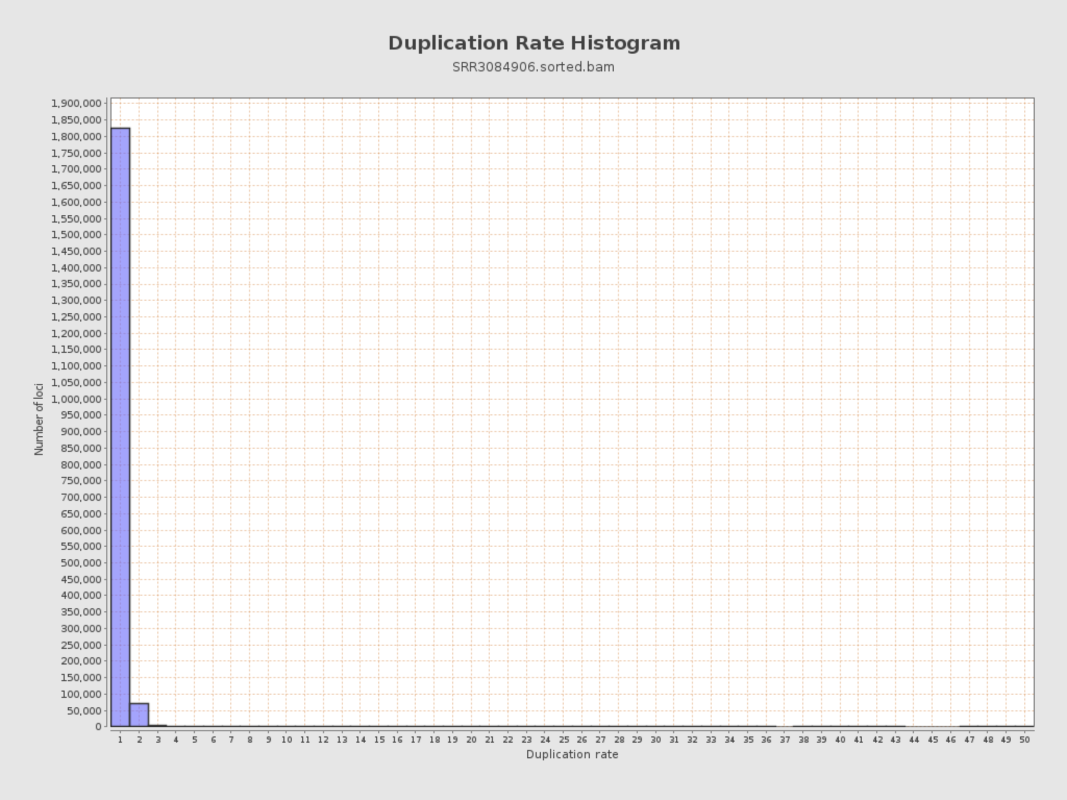
5. Results : Coverage Histogram (0-50X)



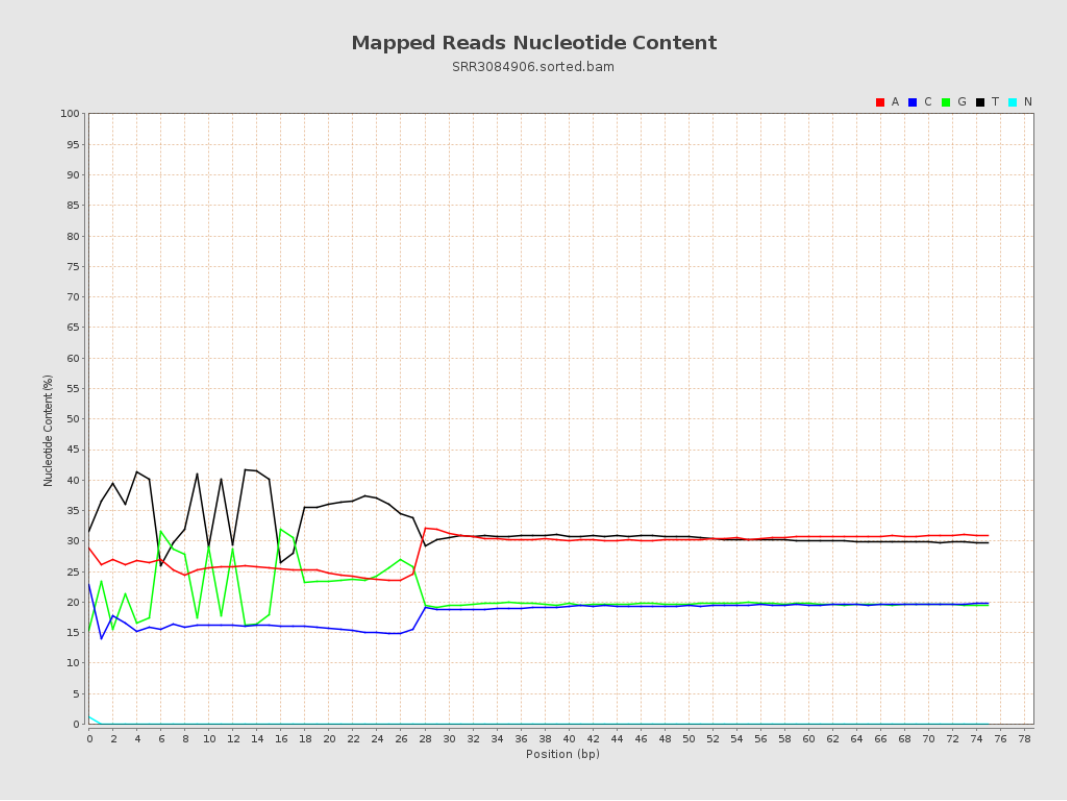
6. Results : Genome Fraction Coverage



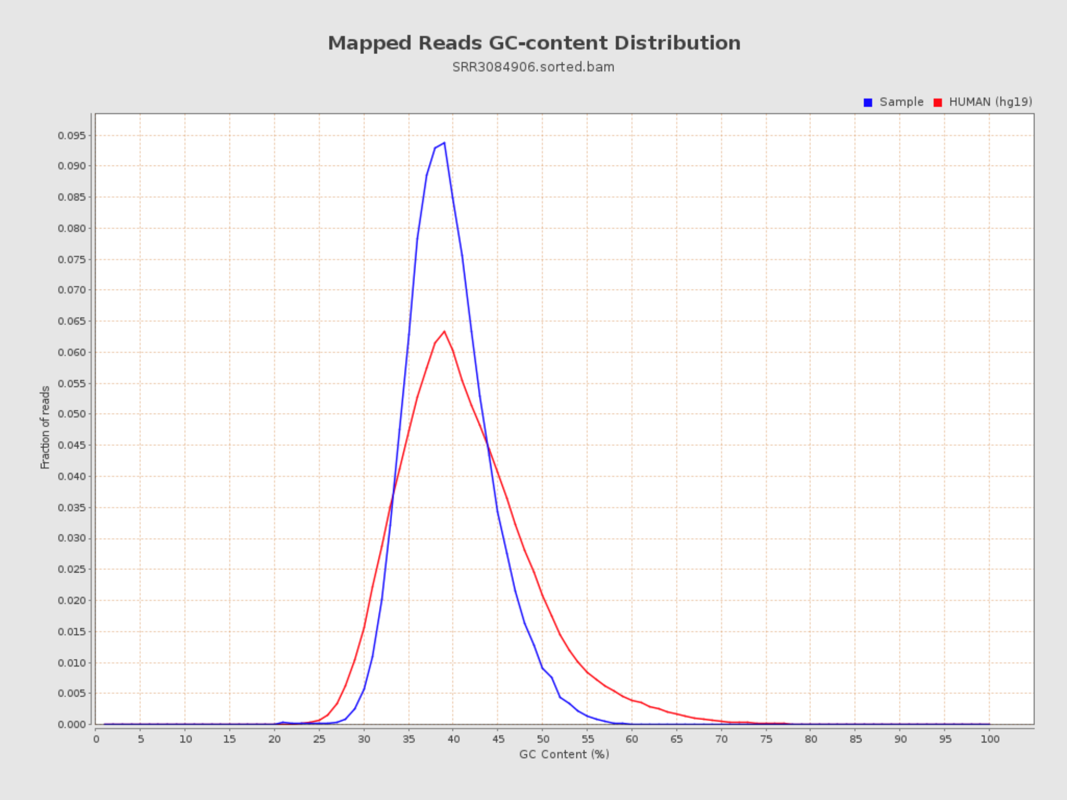
7. Results : Duplication Rate Histogram



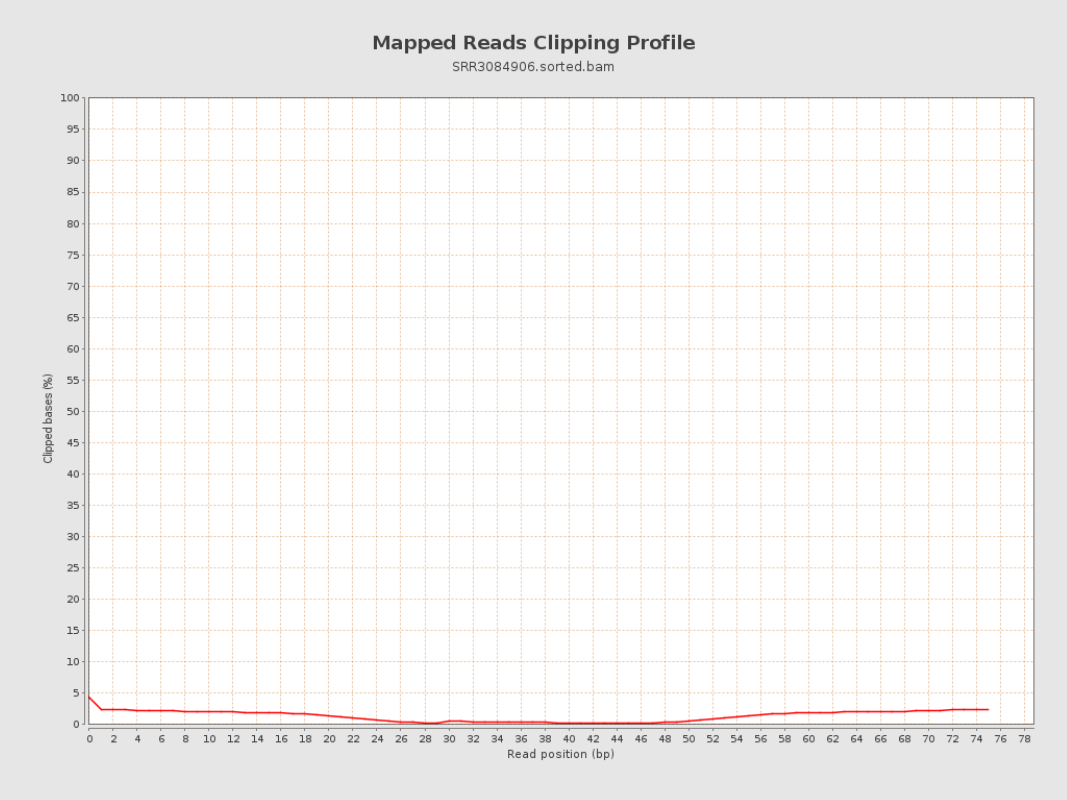
8. Results : Mapped Reads Nucleotide Content



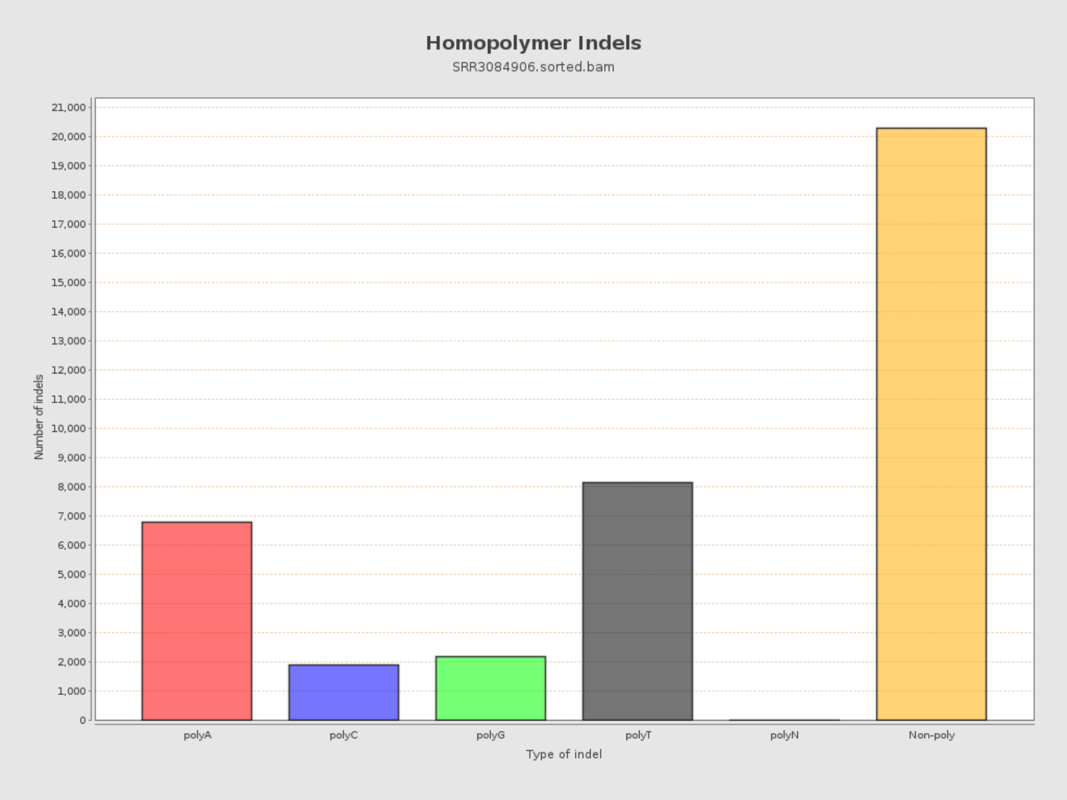
9. Results : Mapped Reads GC-content Distribution



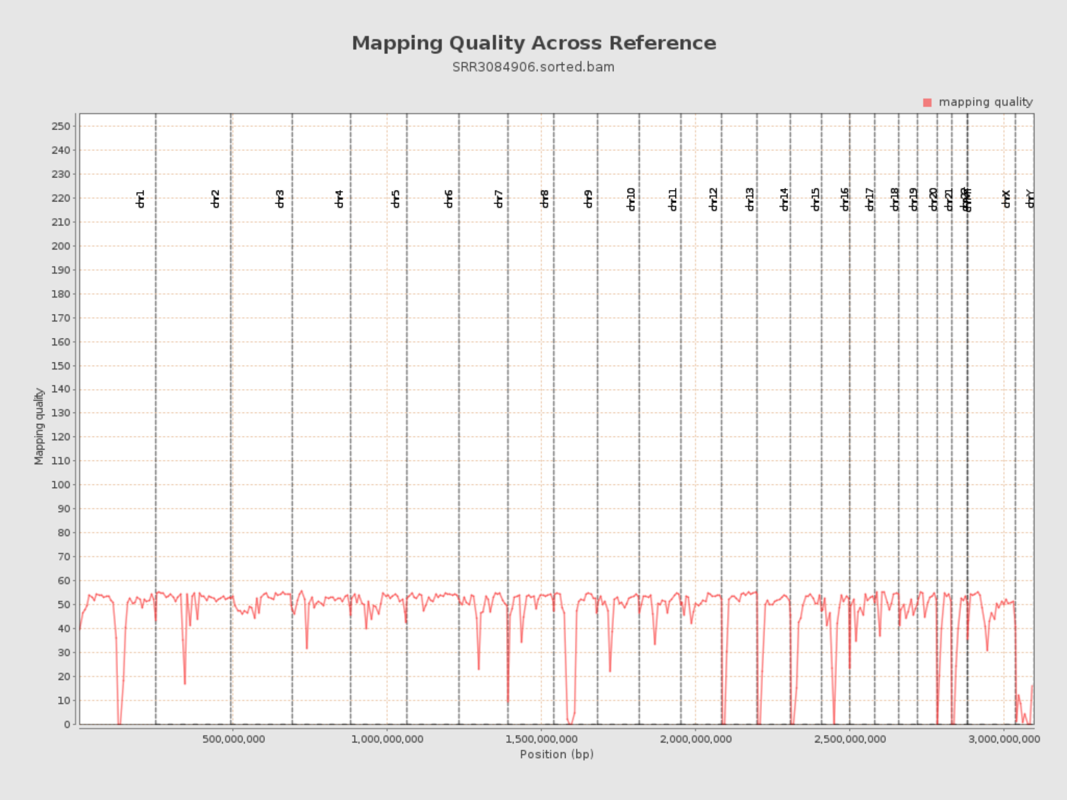
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram