Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 12:12:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084409.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_SRR3084409 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084409.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 12:12:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084409.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,404,164
Mapped reads	2,222,373 / 92.44%
Unmapped reads	181,791 / 7.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,748 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	76,574 / 3.19%
Duplication rate	2.87%
Clipped reads	961,432 / 39.99%

2.2. ACGT Content

Number/percentage of A's	42,565,962 / 28.43%
Number/percentage of C's	28,479,437 / 19.02%
Number/percentage of T's	46,446,880 / 31.02%
Number/percentage of G's	32,046,336 / 21.4%
Number/percentage of N's	193,451 / 0.13%
GC Percentage	40.42%

2.3. Coverage

Mean	0.0484

Standard Deviation	0.3335

2.4. Mapping Quality

Mean Mapping Quality	46.2

2.5. Mismatches and indels

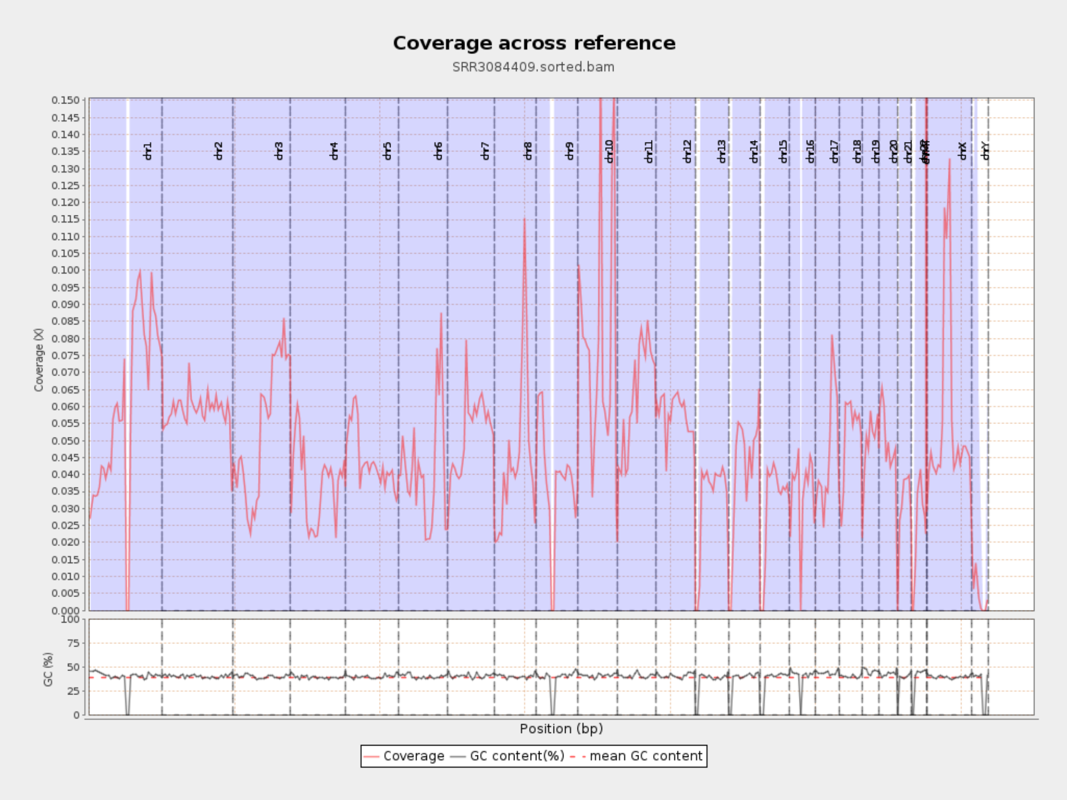
General error rate	1%
Mismatches	1,485,414
Insertions	10,685
Mapped reads with at least one insertion	0.48%
Deletions	29,897
Mapped reads with at least one deletion	1.33%
Homopolymer indels	46.56%

2.6. Chromosome stats

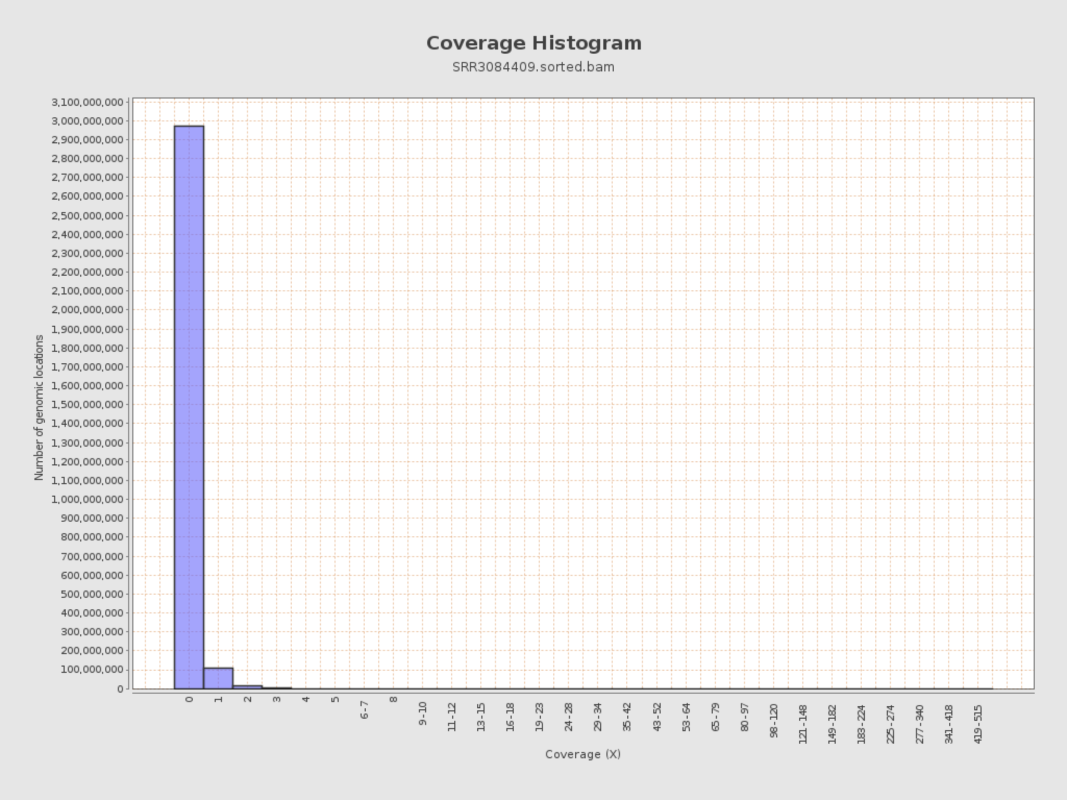
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14942954	0.06	0.531
chr2	243199373	14302358	0.0588	0.3727
chr3	198022430	10558645	0.0533	0.2676
chr4	191154276	7156672	0.0374	0.2283
chr5	180915260	8027501	0.0444	0.2406
chr6	171115067	7125391	0.0416	0.2619
chr7	159138663	8381057	0.0527	0.4753

chr8	146364022	6617479	0.0452	0.3453
chr9	141213431	5441891	0.0385	0.273
chr10	135534747	11042397	0.0815	0.4562
chr11	135006516	8498572	0.0629	0.3464
chr12	133851895	7716397	0.0576	0.2763
chr13	115169878	3711618	0.0322	0.2055
chr14	107349540	4354905	0.0406	0.2387
chr15	102531392	3174736	0.031	0.2033
chr16	90354753	3157656	0.0349	0.227
chr17	81195210	3779614	0.0465	0.2596
chr18	78077248	4001337	0.0512	0.458
chr19	59128983	2936652	0.0497	0.4023
chr20	63025520	3145466	0.0499	0.259
chr21	48129895	1478326	0.0307	0.2089
chr22	51304566	1190501	0.0232	0.1716
chrMT	16571	55128	3.3268	2.983
chrX	155270560	8707726	0.0561	0.3071
chrY	59373566	278217	0.0047	0.1005

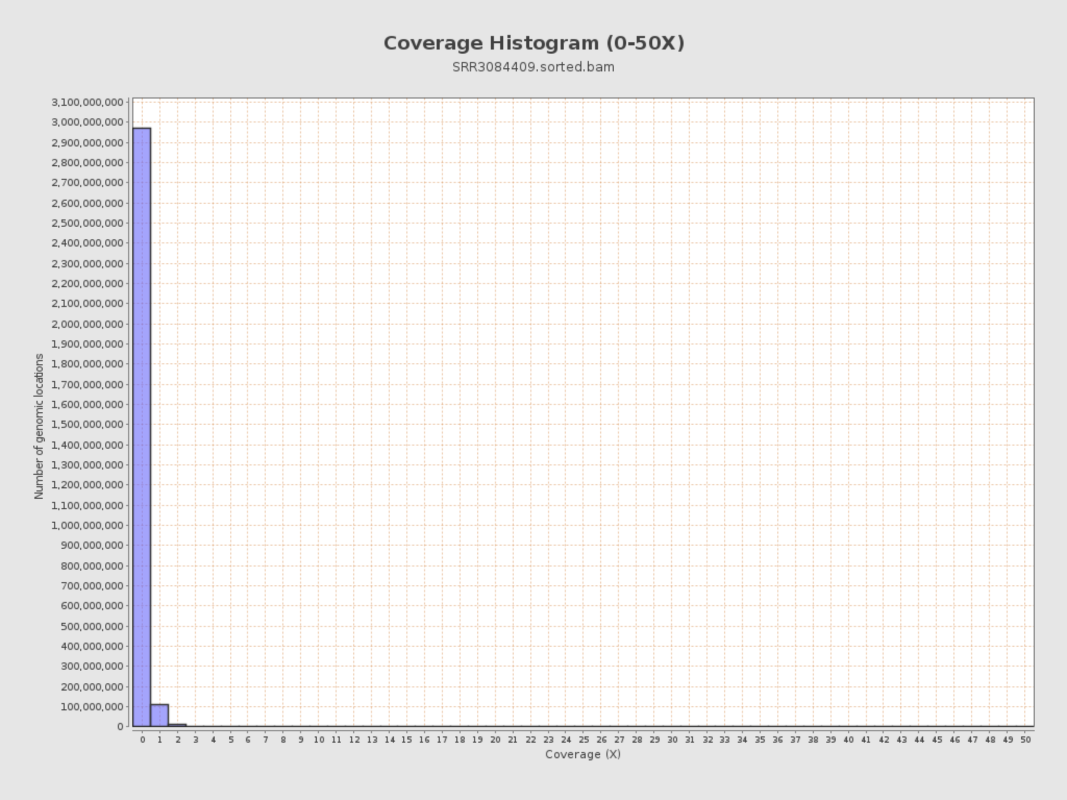
3. Results : Coverage across reference



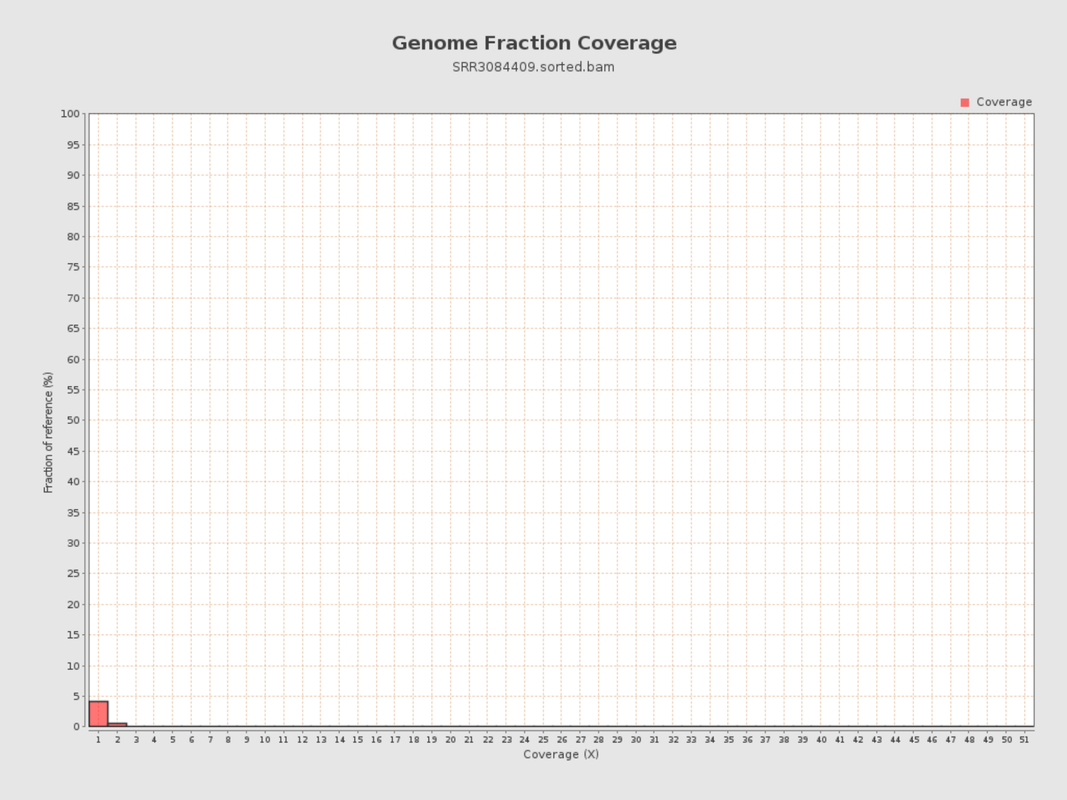
4. Results : Coverage Histogram



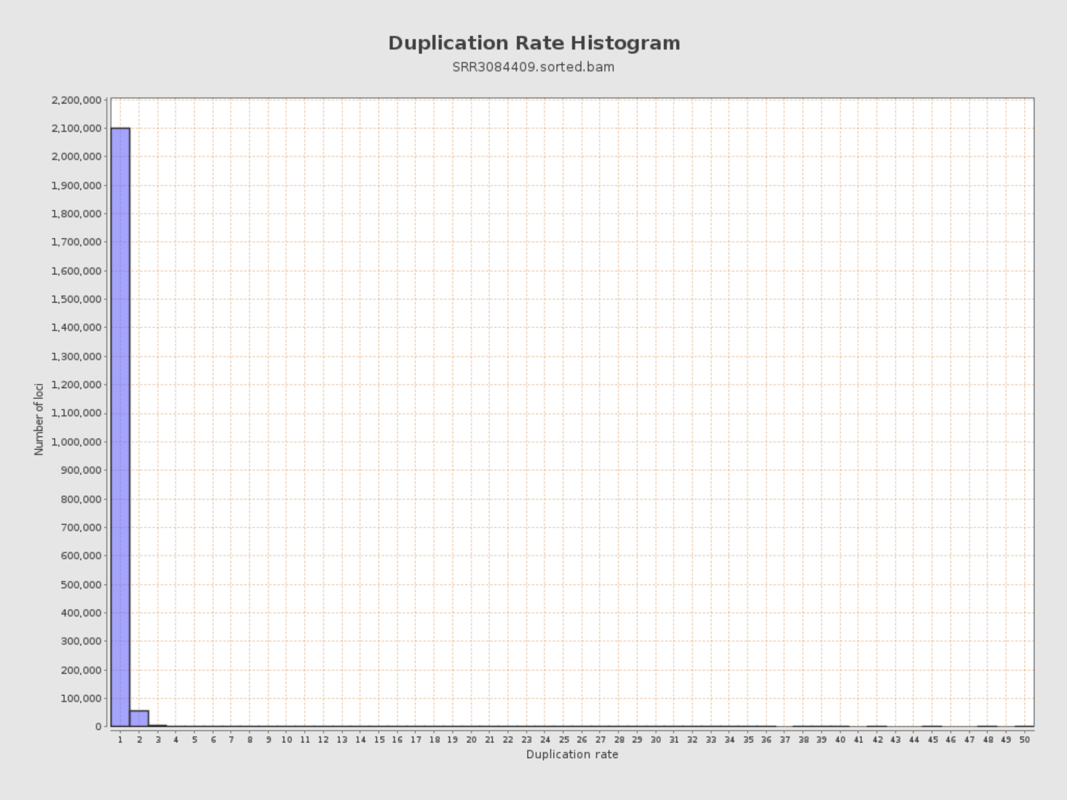
5. Results : Coverage Histogram (0-50X)



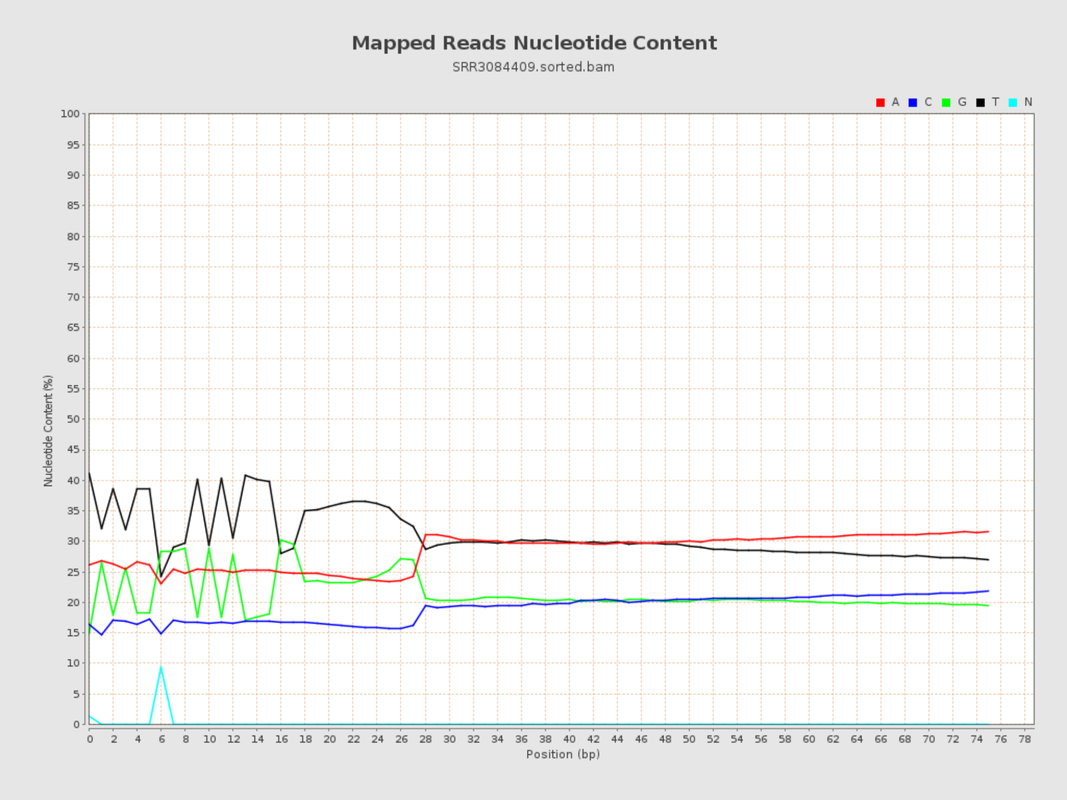
6. Results : Genome Fraction Coverage



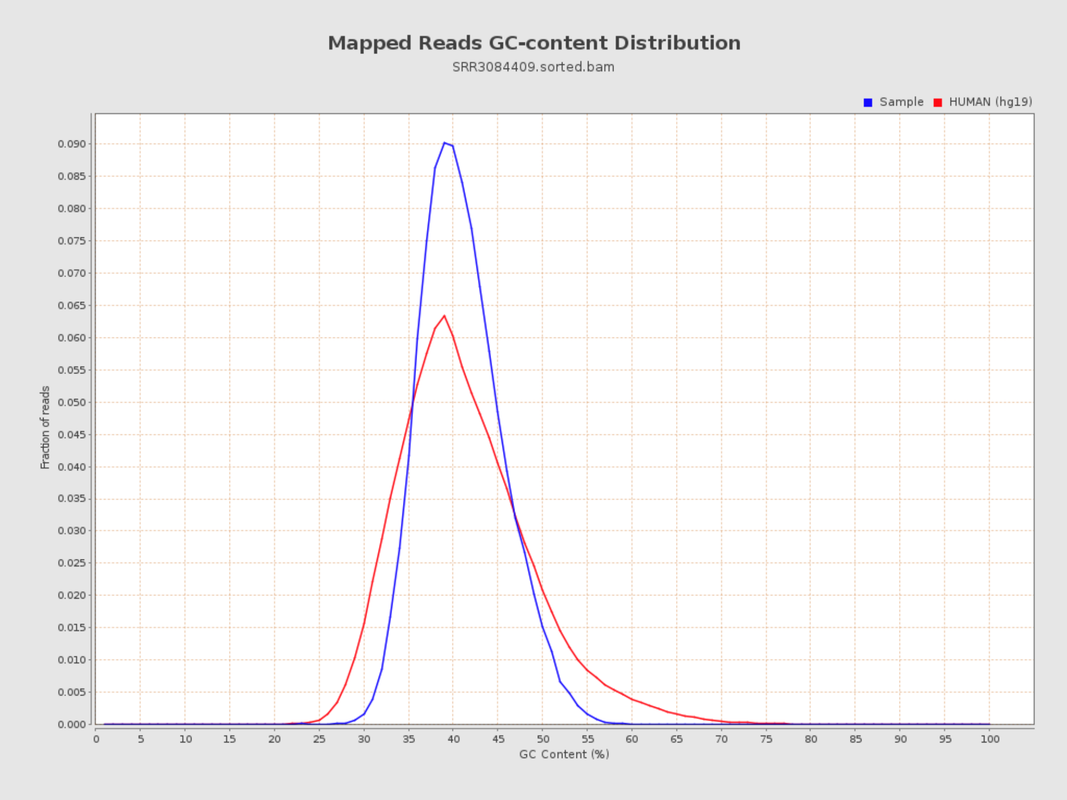
7. Results : Duplication Rate Histogram



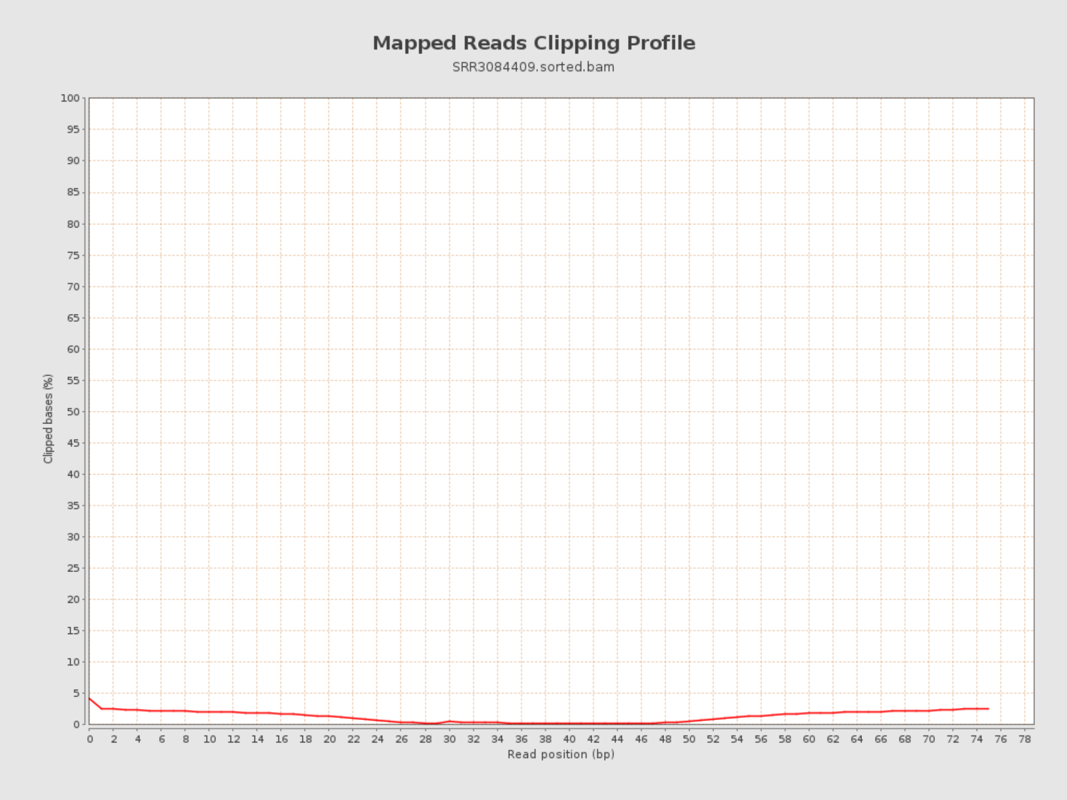
8. Results : Mapped Reads Nucleotide Content



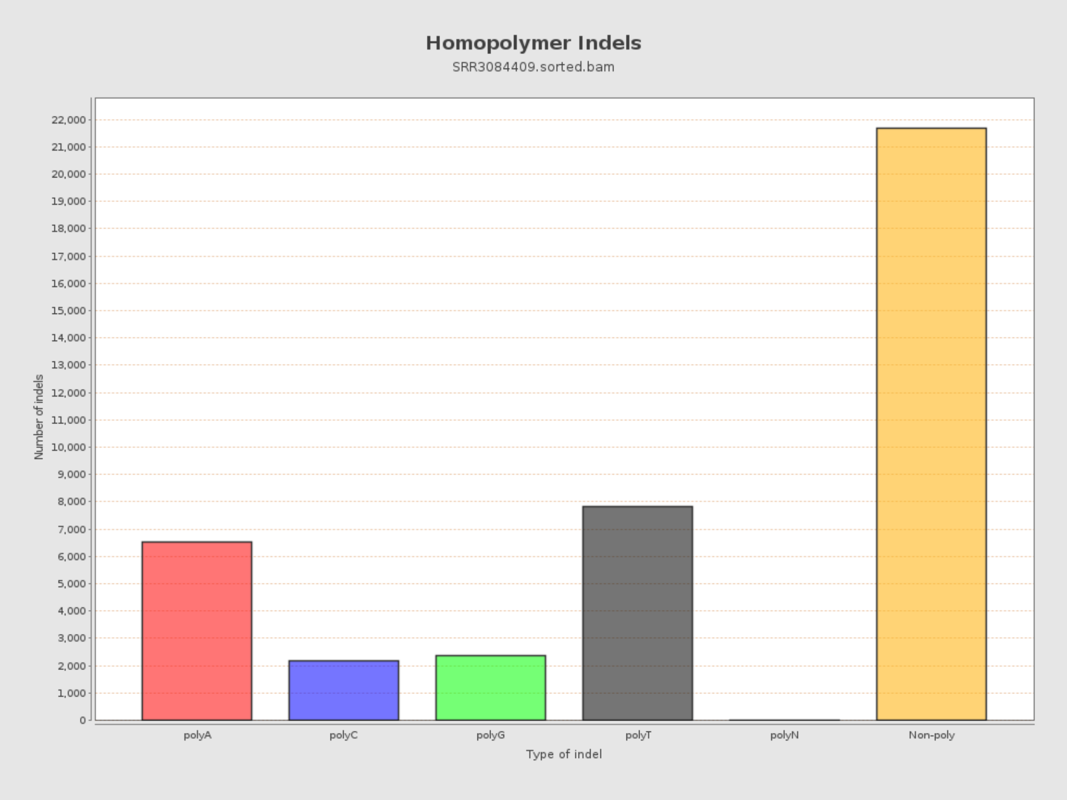
9. Results : Mapped Reads GC-content Distribution



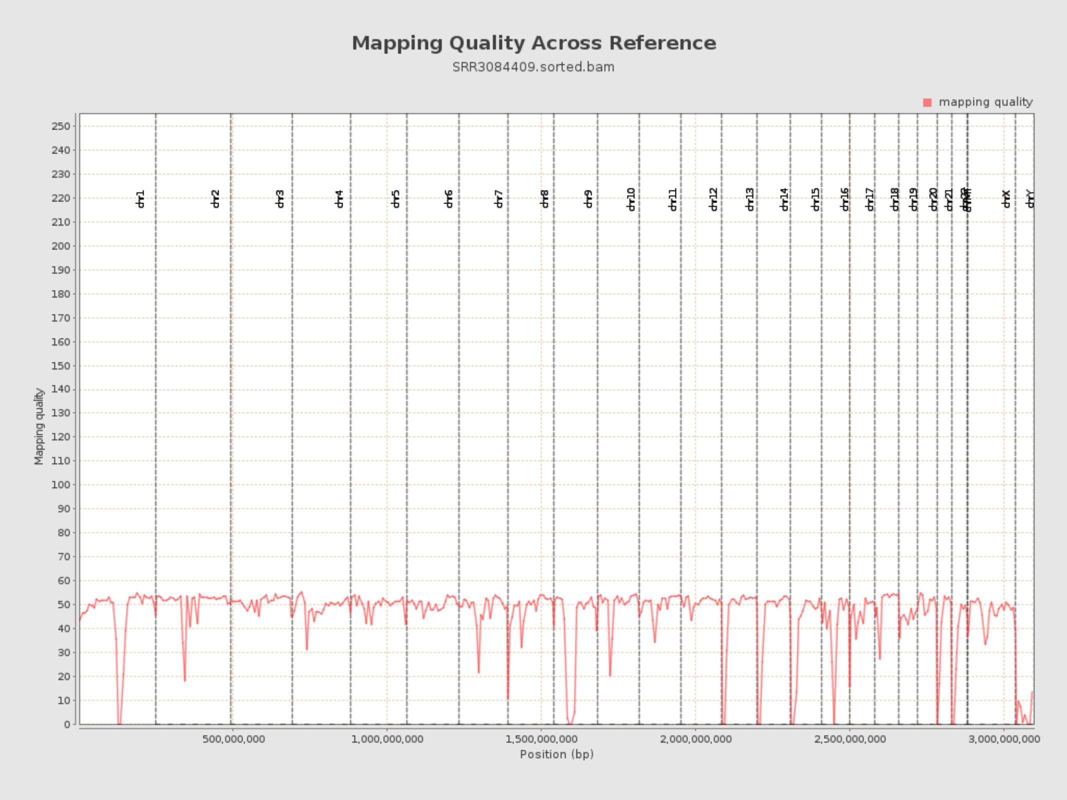
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram