Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 17:56:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084856.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_SRR3084856 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084856.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 17:56:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084856.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,361,656
Mapped reads	2,089,805 / 88.49%
Unmapped reads	271,851 / 11.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,328 / 0.82%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	120,176 / 5.09%
Duplication rate	4.92%
Clipped reads	802,892 / 34%

2.2. ACGT Content

Number/percentage of A's	40,917,571 / 28.7%
Number/percentage of C's	25,780,213 / 18.09%
Number/percentage of T's	46,051,727 / 32.31%
Number/percentage of G's	29,775,384 / 20.89%
Number/percentage of N's	22,118 / 0.02%
GC Percentage	38.97%

2.3. Coverage

Mean	0.0461

Standard Deviation	0.3824

2.4. Mapping Quality

Mean Mapping Quality	47.87

2.5. Mismatches and indels

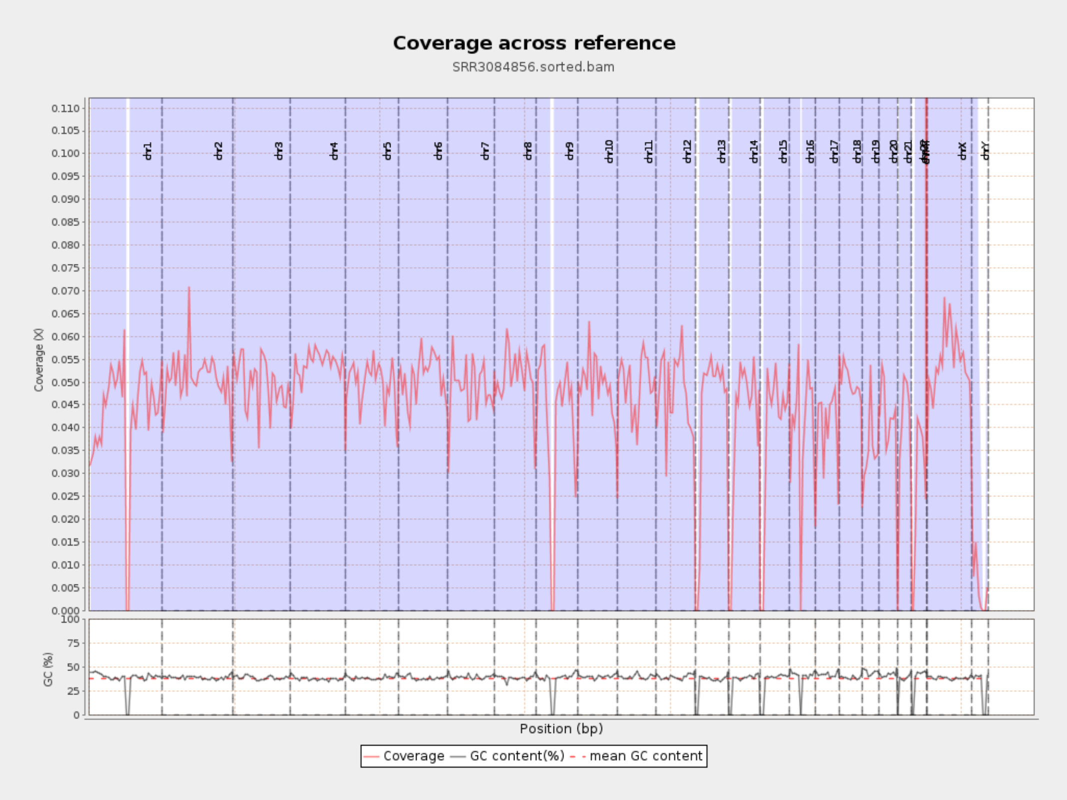
General error rate	0.83%
Mismatches	1,166,985
Insertions	11,225
Mapped reads with at least one insertion	0.53%
Deletions	30,157
Mapped reads with at least one deletion	1.43%
Homopolymer indels	48.13%

2.6. Chromosome stats

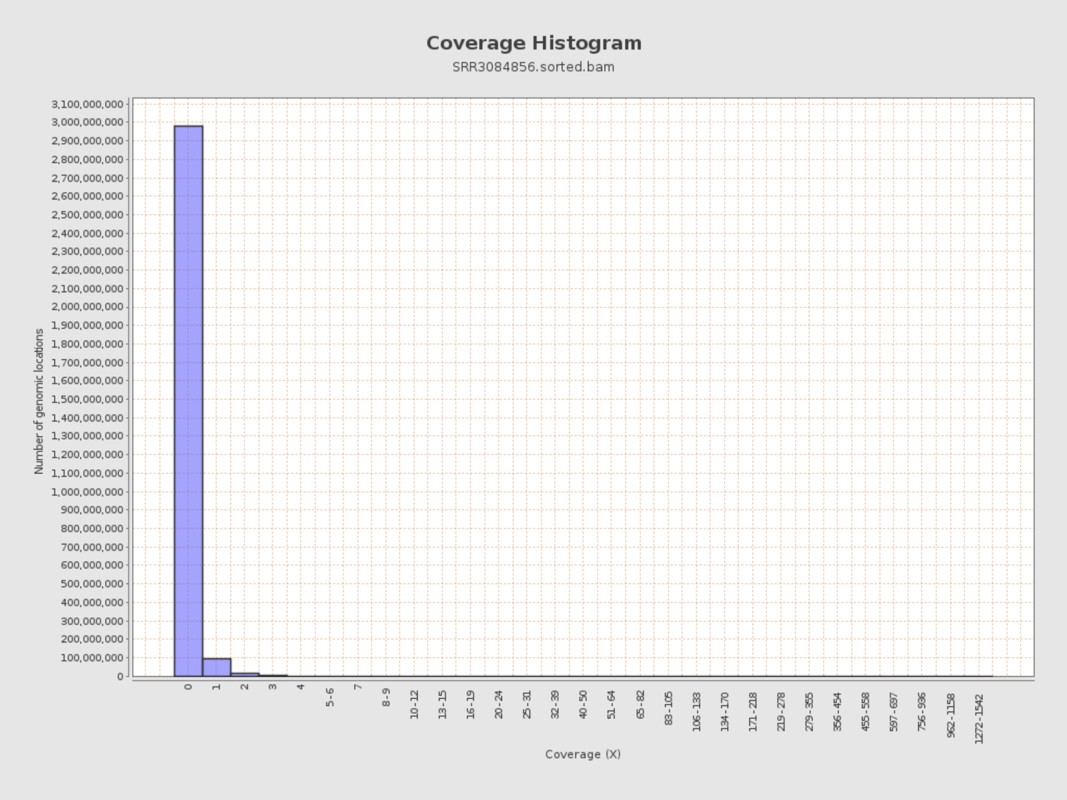
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10737581	0.0431	0.5003
chr2	243199373	12402185	0.051	0.3617
chr3	198022430	9855188	0.0498	0.2665
chr4	191154276	10248244	0.0536	0.2815
chr5	180915260	8999412	0.0497	0.2685
chr6	171115067	8760995	0.0512	0.2756
chr7	159138663	7782445	0.0489	0.3308

chr8	146364022	7465247	0.051	0.9838
chr9	141213431	5862862	0.0415	0.3171
chr10	135534747	6700355	0.0494	0.3381
chr11	135006516	6650925	0.0493	0.2849
chr12	133851895	6345750	0.0474	0.2625
chr13	115169878	4887630	0.0424	0.2466
chr14	107349540	4328435	0.0403	0.2516
chr15	102531392	3994042	0.039	0.2347
chr16	90354753	3609678	0.04	0.2535
chr17	81195210	3242633	0.0399	0.2496
chr18	78077248	3922069	0.0502	0.6419
chr19	59128983	2116690	0.0358	0.3648
chr20	63025520	2675526	0.0425	0.2609
chr21	48129895	1839459	0.0382	0.2422
chr22	51304566	1337568	0.0261	0.1897
chrMT	16571	79855	4.819	3.1083
chrX	155270560	8434394	0.0543	0.2946
chrY	59373566	320151	0.0054	0.1061

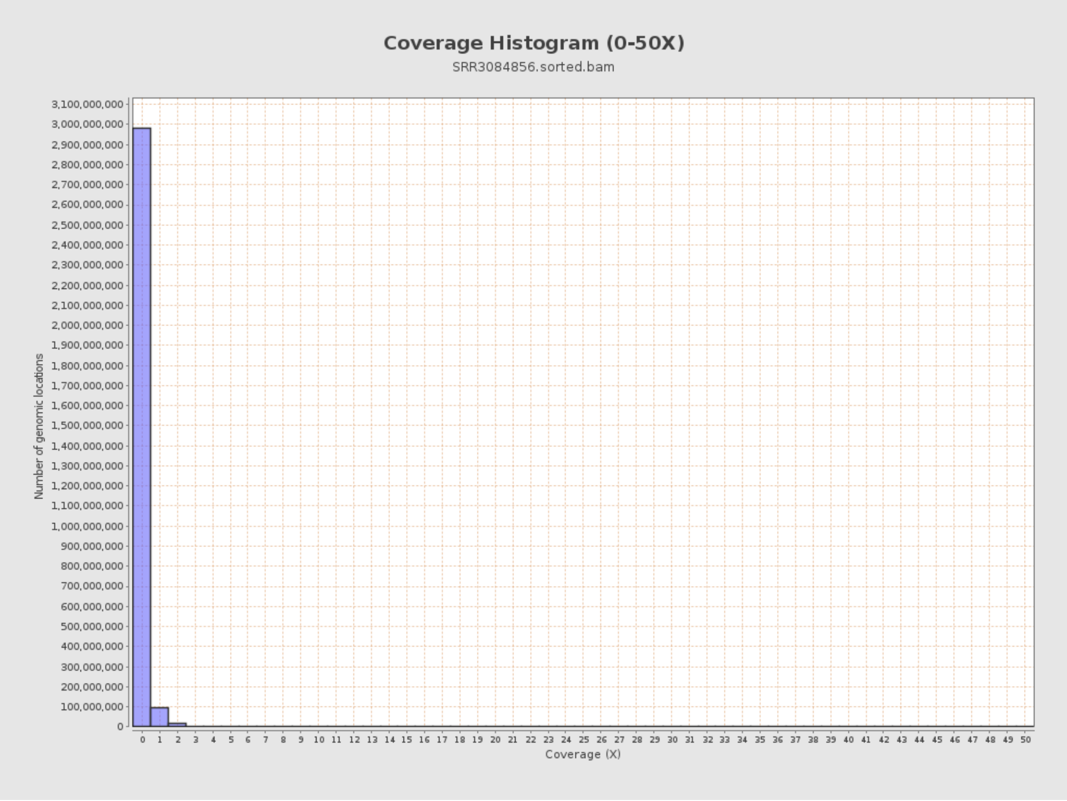
3. Results : Coverage across reference



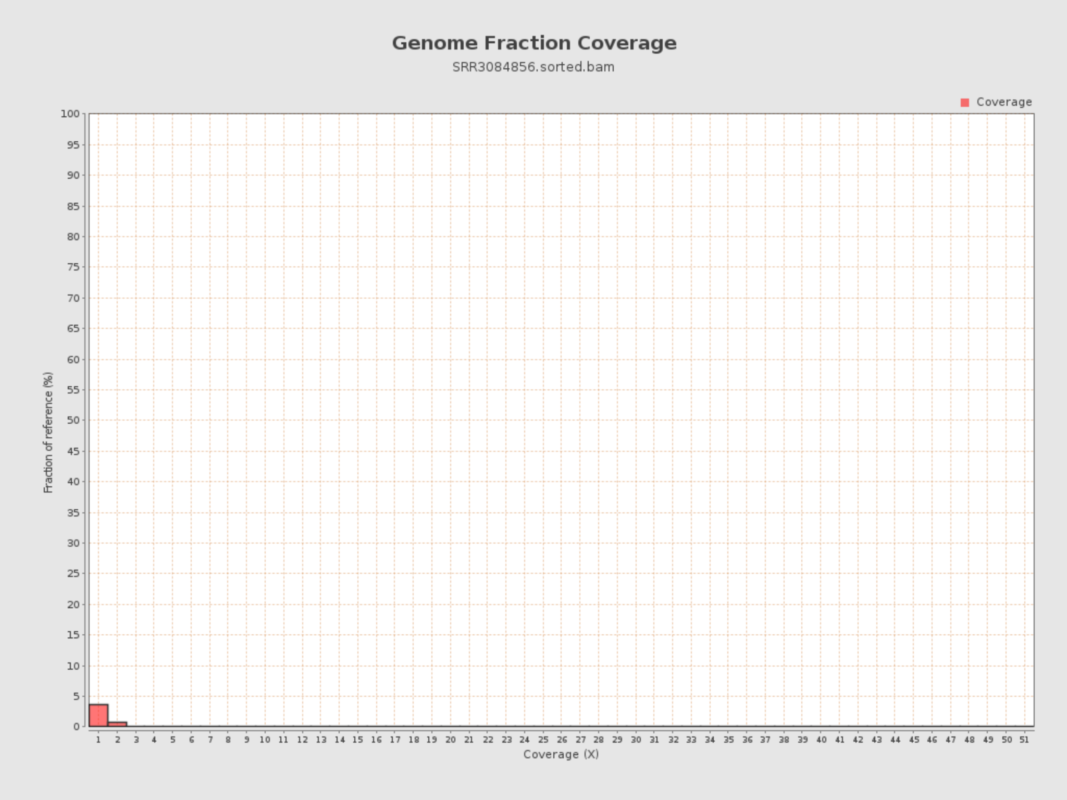
4. Results : Coverage Histogram



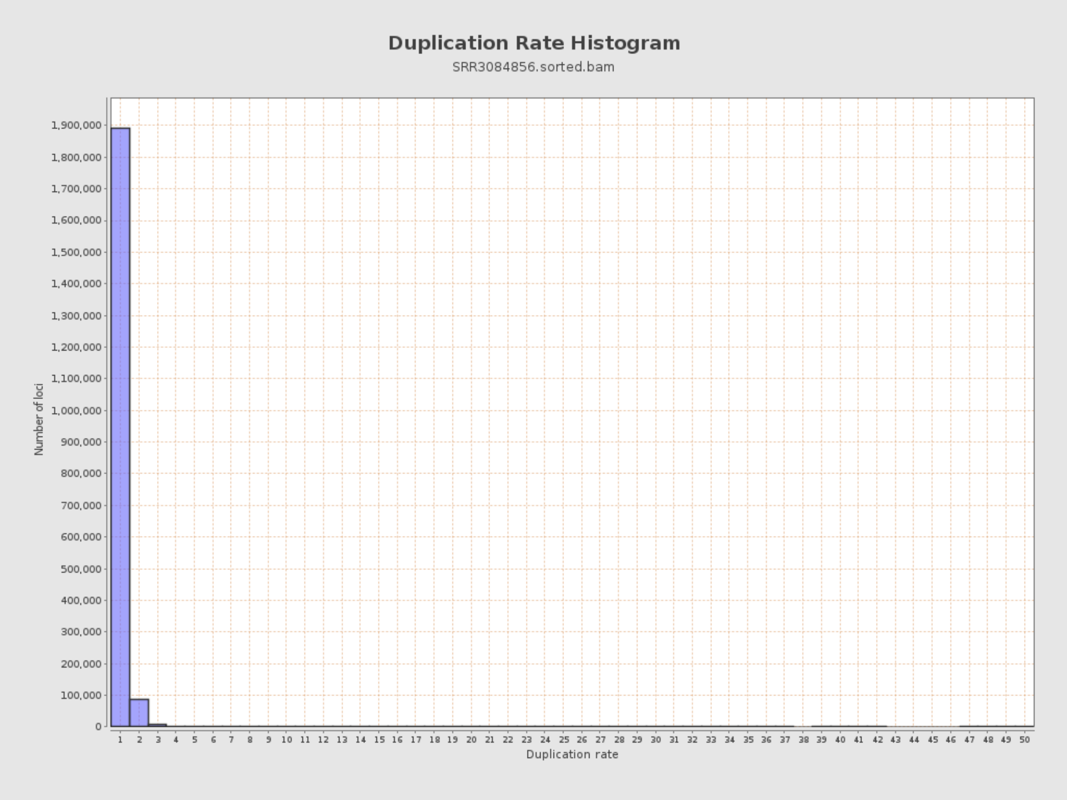
5. Results : Coverage Histogram (0-50X)



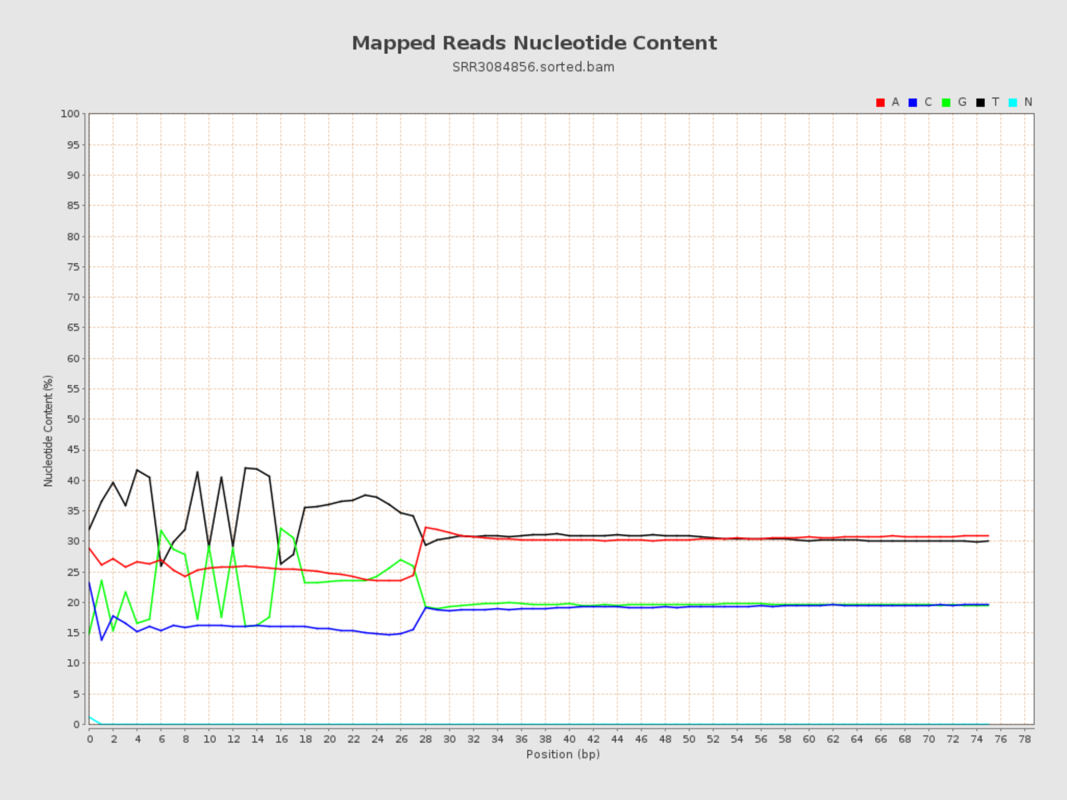
6. Results : Genome Fraction Coverage



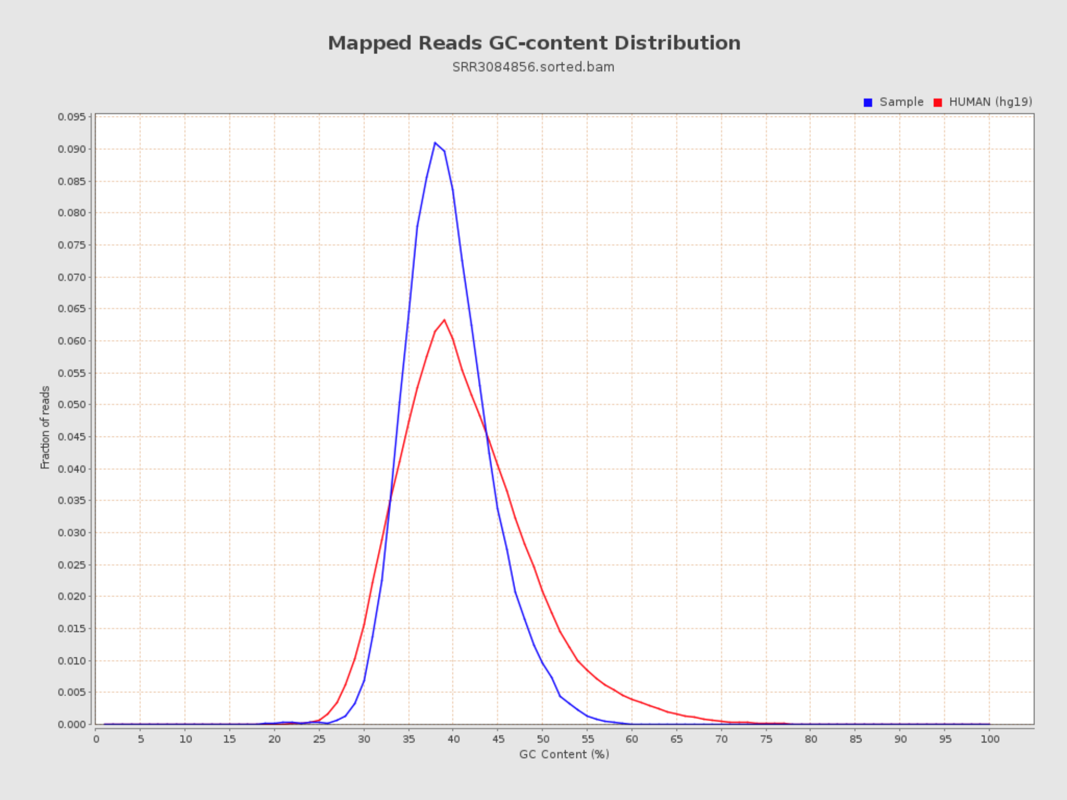
7. Results : Duplication Rate Histogram



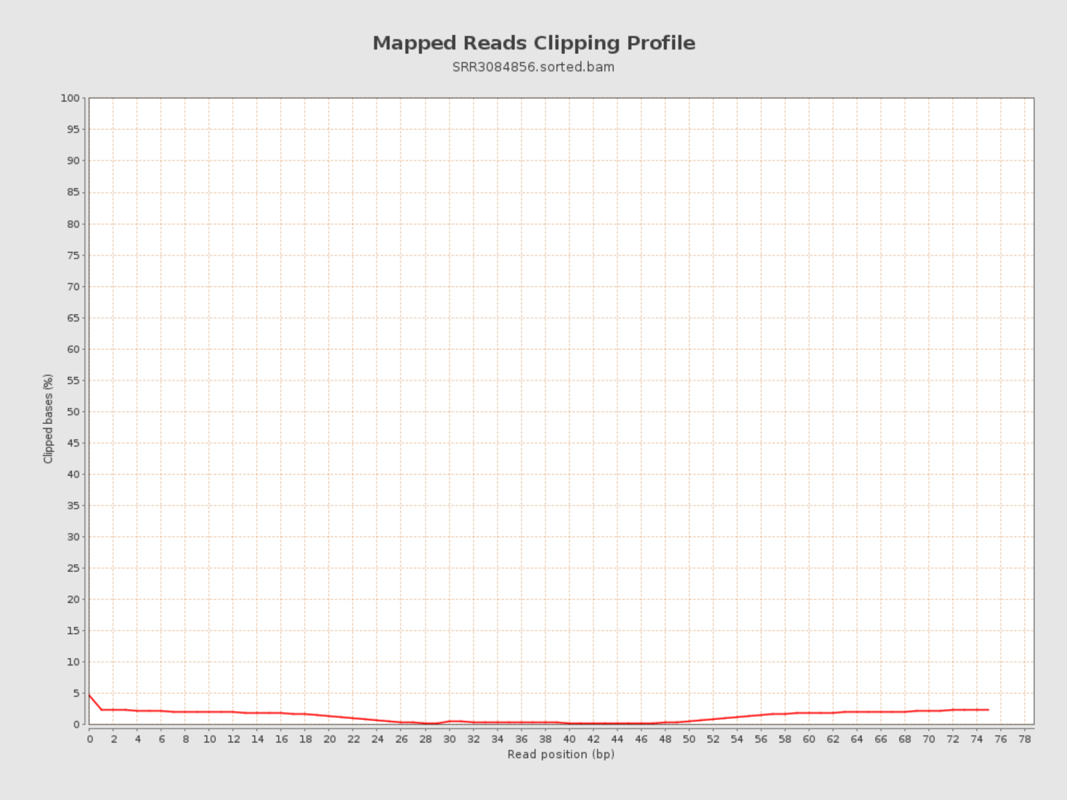
8. Results : Mapped Reads Nucleotide Content



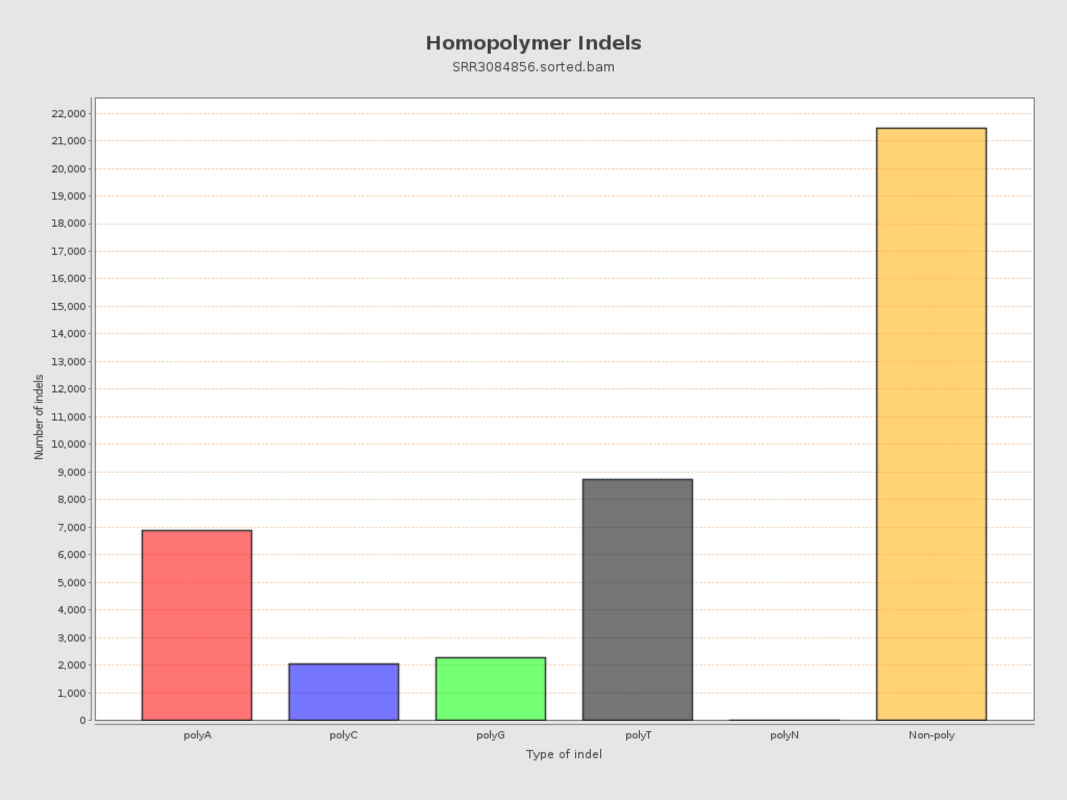
9. Results : Mapped Reads GC-content Distribution



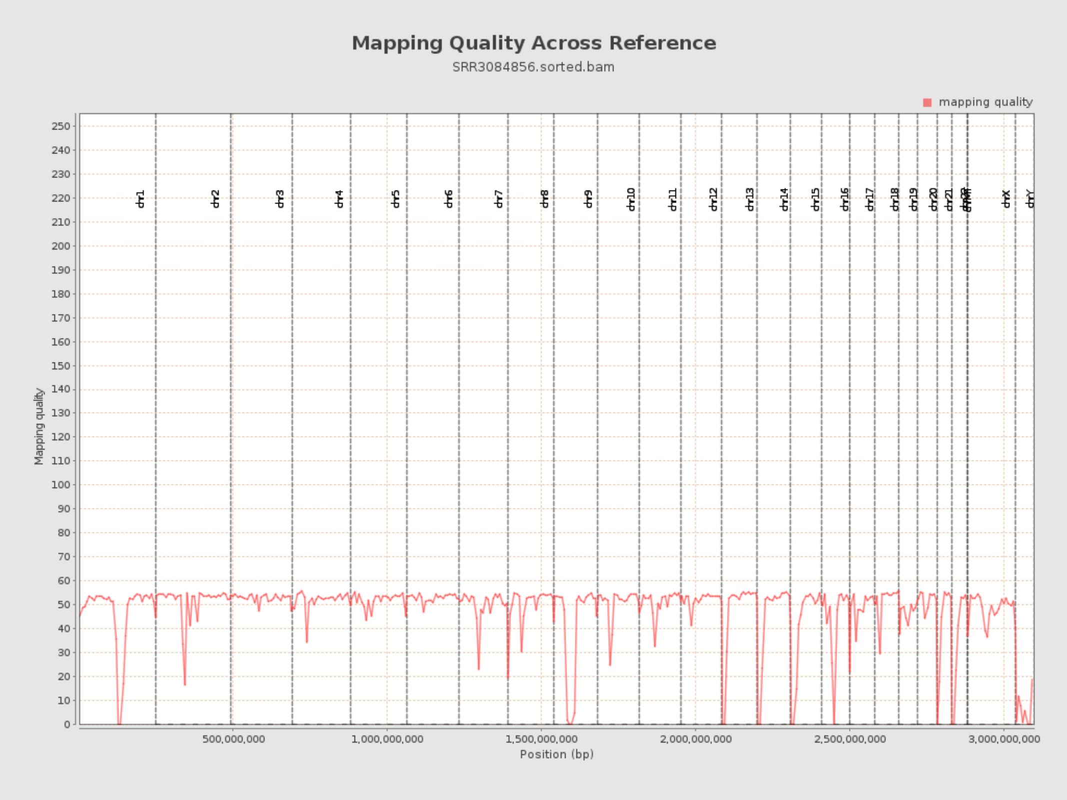
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram