Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 18:06:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084859.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_SRR3084859 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084859.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 18:06:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084859.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,400,888
Mapped reads	2,130,830 / 88.75%
Unmapped reads	270,058 / 11.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,608 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	111,894 / 4.66%
Duplication rate	4.27%
Clipped reads	805,960 / 33.57%

2.2. ACGT Content

Number/percentage of A's	41,524,968 / 28.58%
Number/percentage of C's	26,513,681 / 18.25%
Number/percentage of T's	46,554,093 / 32.04%
Number/percentage of G's	30,702,839 / 21.13%
Number/percentage of N's	22,131 / 0.02%
GC Percentage	39.37%

2.3. Coverage

Mean	0.047

Standard Deviation	0.4337

2.4. Mapping Quality

Mean Mapping Quality	47.62

2.5. Mismatches and indels

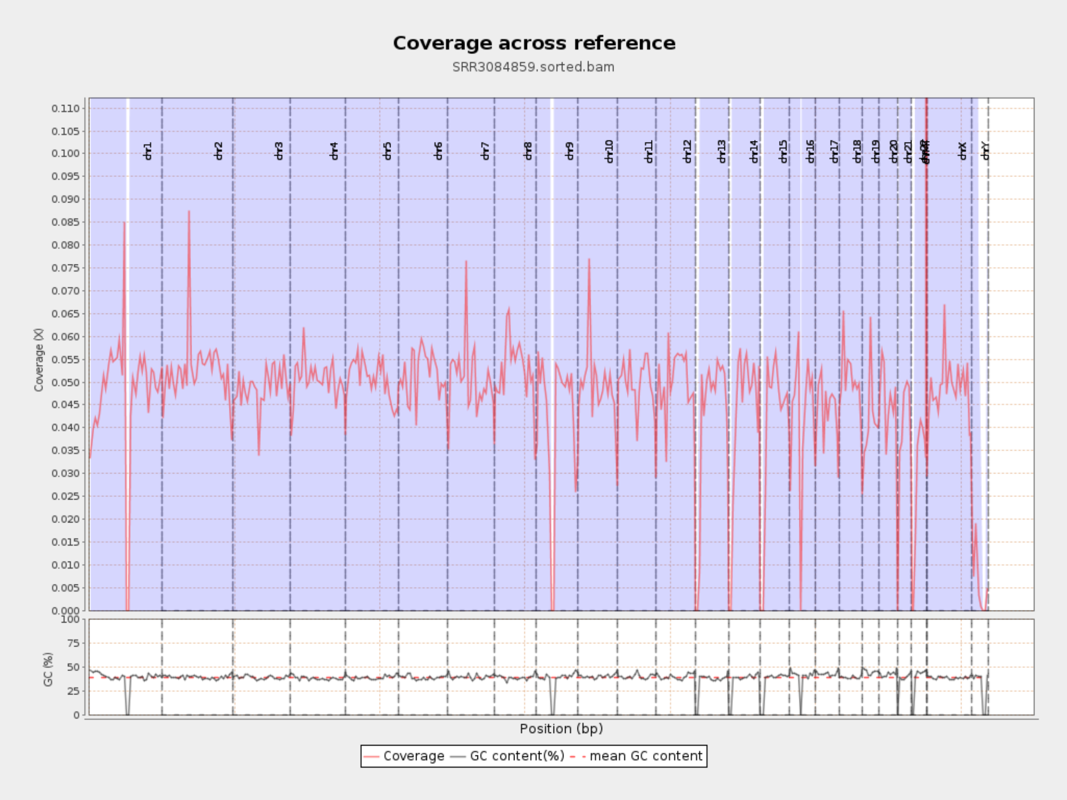
General error rate	0.87%
Mismatches	1,239,216
Insertions	11,662
Mapped reads with at least one insertion	0.54%
Deletions	34,136
Mapped reads with at least one deletion	1.58%
Homopolymer indels	47.59%

2.6. Chromosome stats

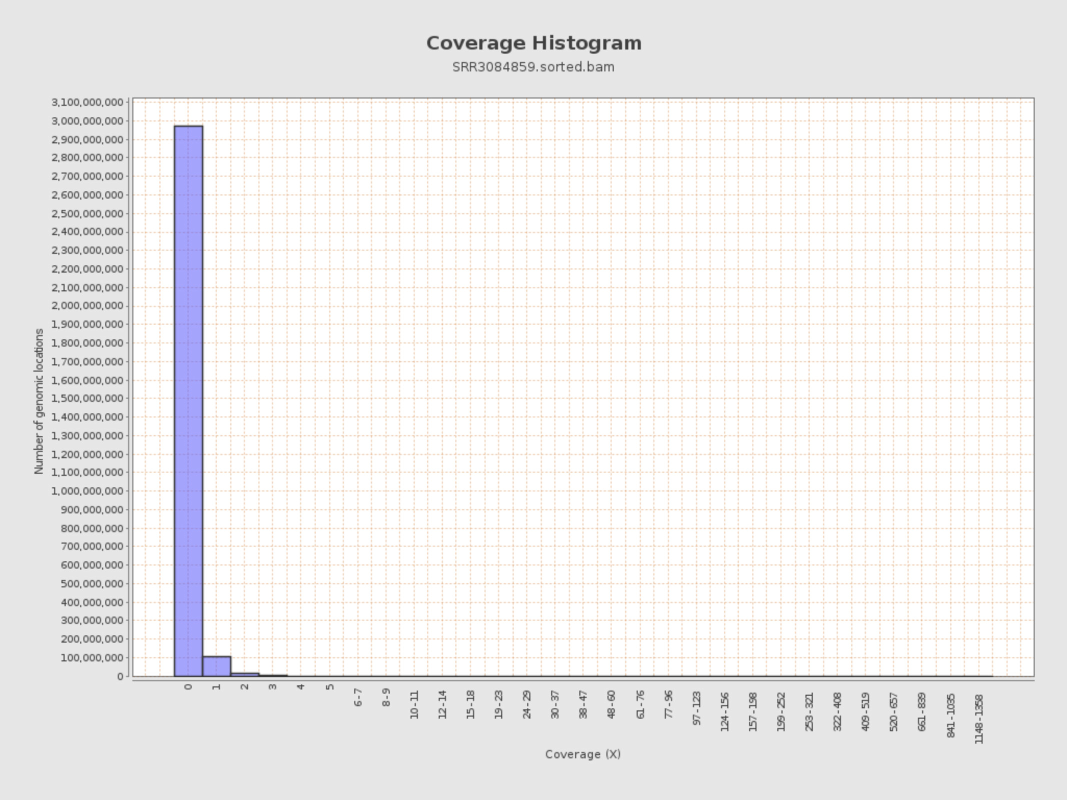
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11867285	0.0476	0.8032
chr2	243199373	12852735	0.0528	0.4025
chr3	198022430	9661961	0.0488	0.2513
chr4	191154276	9671059	0.0506	0.275
chr5	180915260	9186473	0.0508	0.2586
chr6	171115067	8843659	0.0517	0.2729
chr7	159138663	8148819	0.0512	0.4542

chr8	146364022	7742736	0.0529	0.8654
chr9	141213431	5977434	0.0423	0.3795
chr10	135534747	6754154	0.0498	0.3957
chr11	135006516	6671492	0.0494	0.3523
chr12	133851895	6706197	0.0501	0.2589
chr13	115169878	4769948	0.0414	0.2311
chr14	107349540	4489742	0.0418	0.2515
chr15	102531392	4124955	0.0402	0.227
chr16	90354753	3881583	0.043	0.2652
chr17	81195210	3540192	0.0436	0.2821
chr18	78077248	3970334	0.0509	0.7908
chr19	59128983	2475238	0.0419	0.5619
chr20	63025520	2898491	0.046	0.2606
chr21	48129895	1851355	0.0385	0.2422
chr22	51304566	1387224	0.027	0.1844
chrMT	16571	36608	2.2092	1.936
chrX	155270560	7523991	0.0485	0.2756
chrY	59373566	344368	0.0058	0.1414

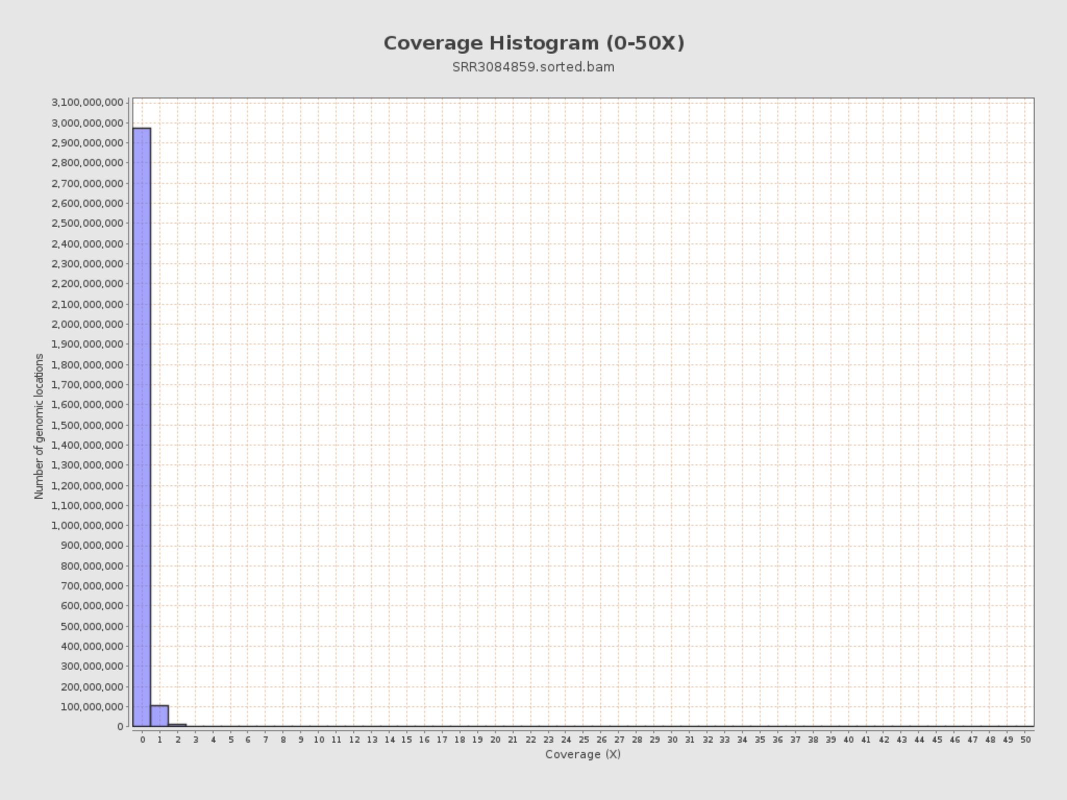
3. Results : Coverage across reference



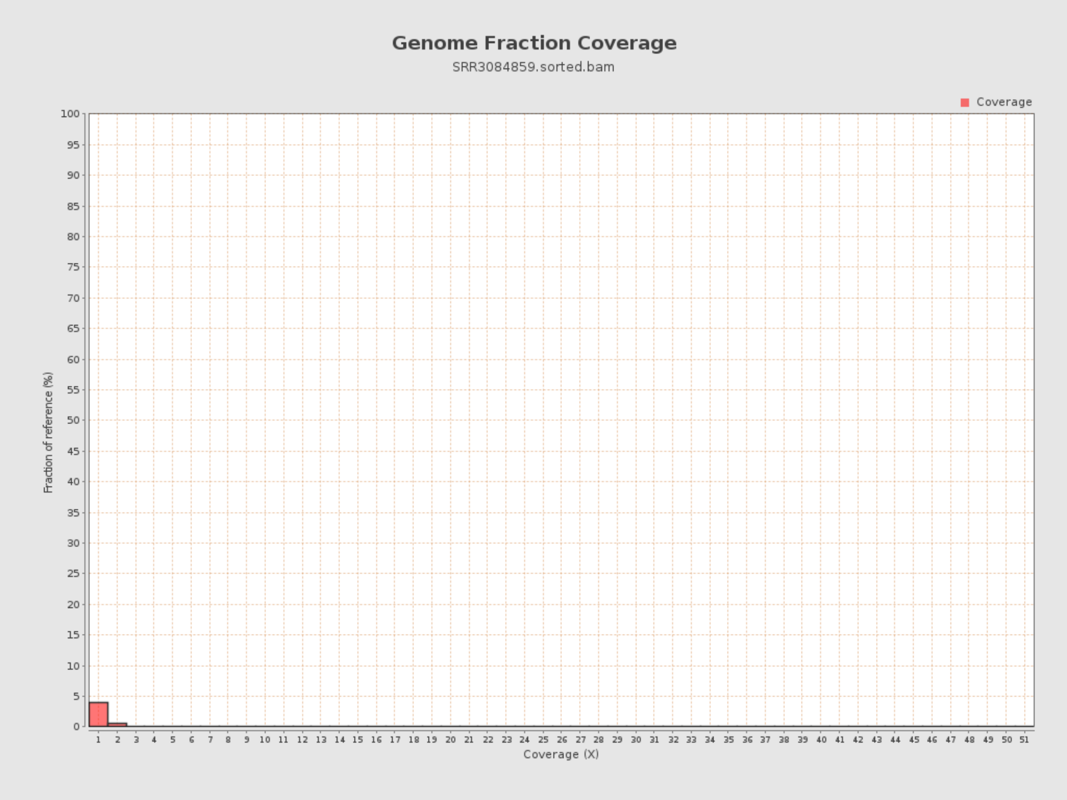
4. Results : Coverage Histogram



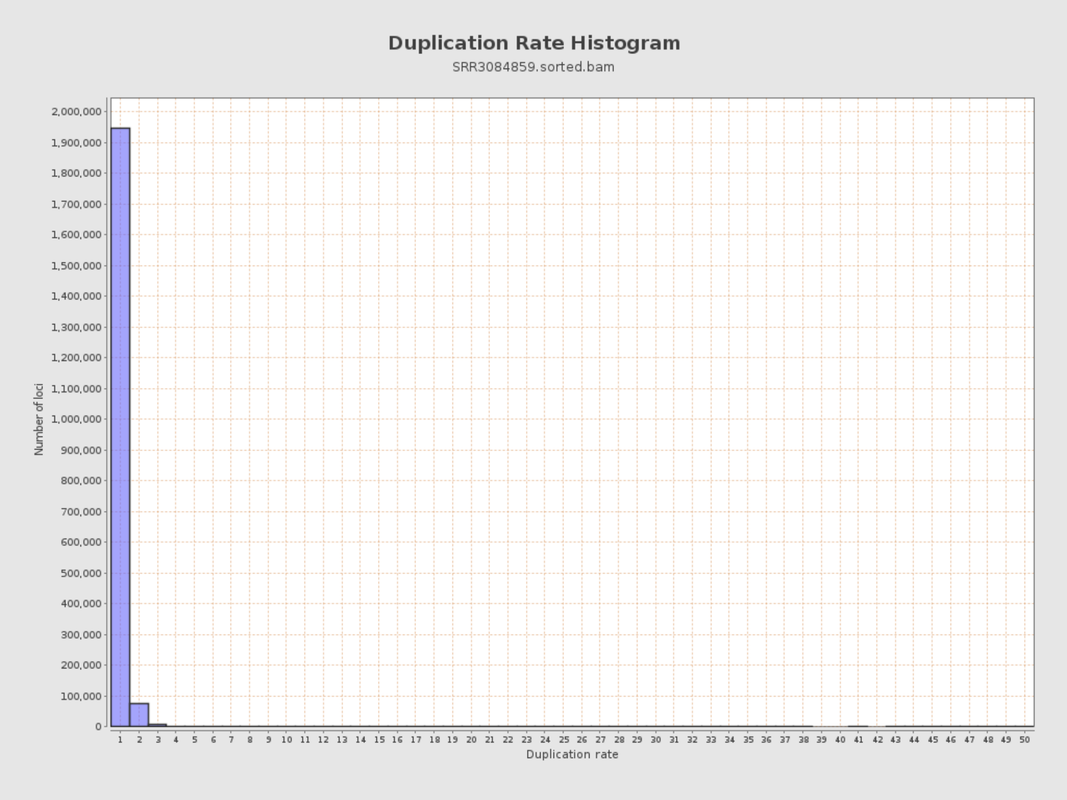
5. Results : Coverage Histogram (0-50X)



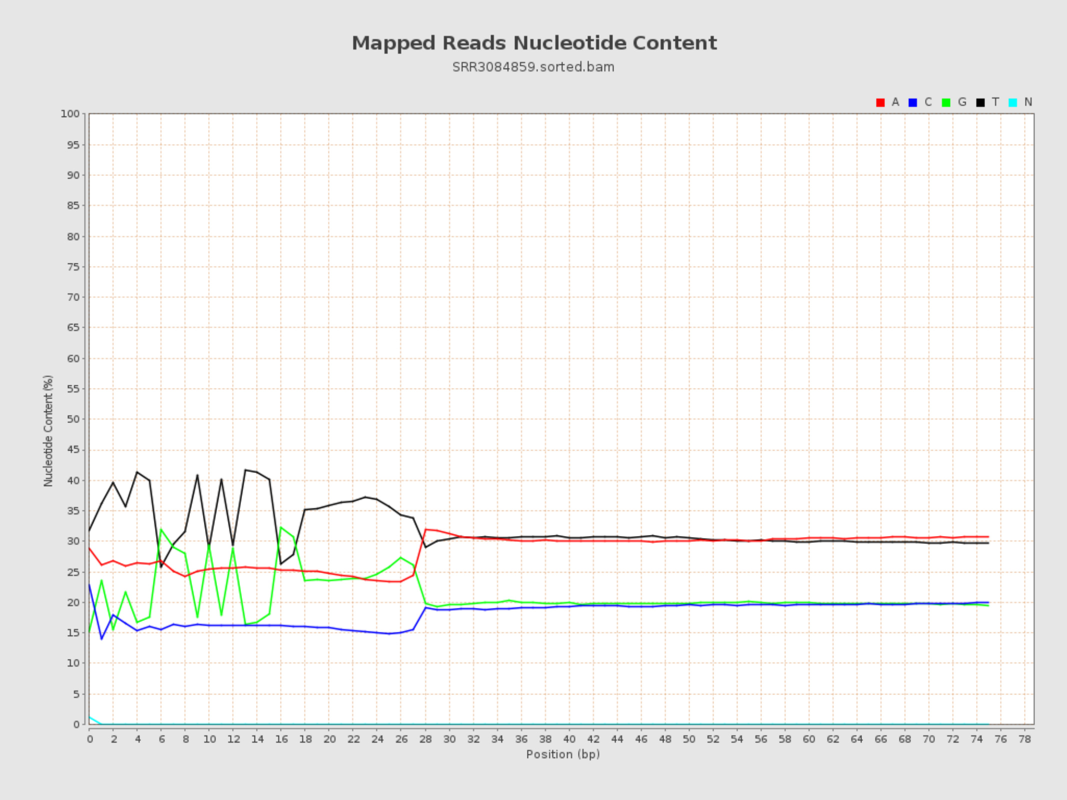
6. Results : Genome Fraction Coverage



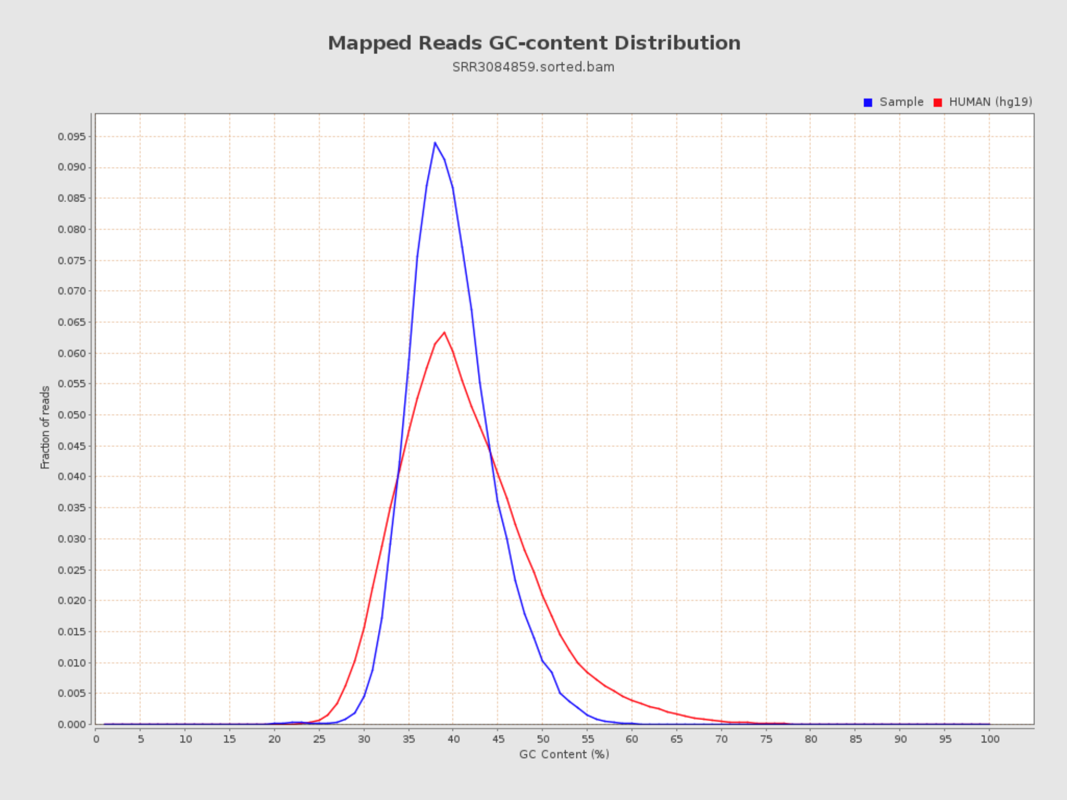
7. Results : Duplication Rate Histogram



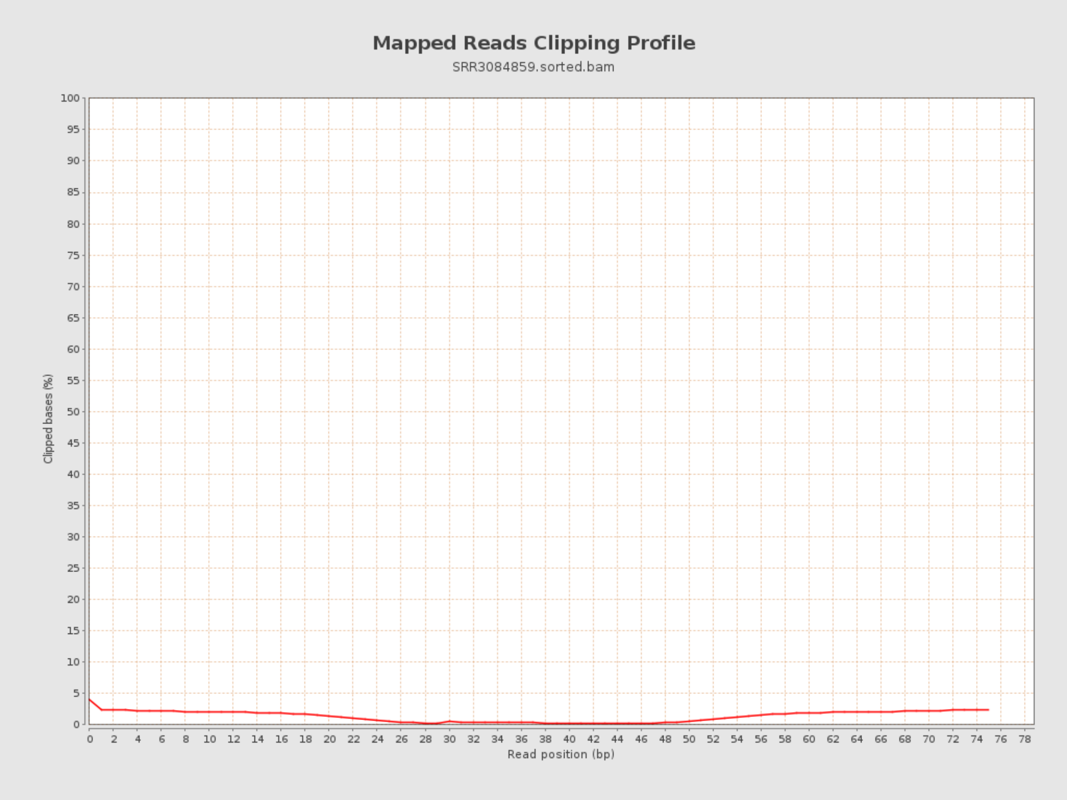
8. Results : Mapped Reads Nucleotide Content



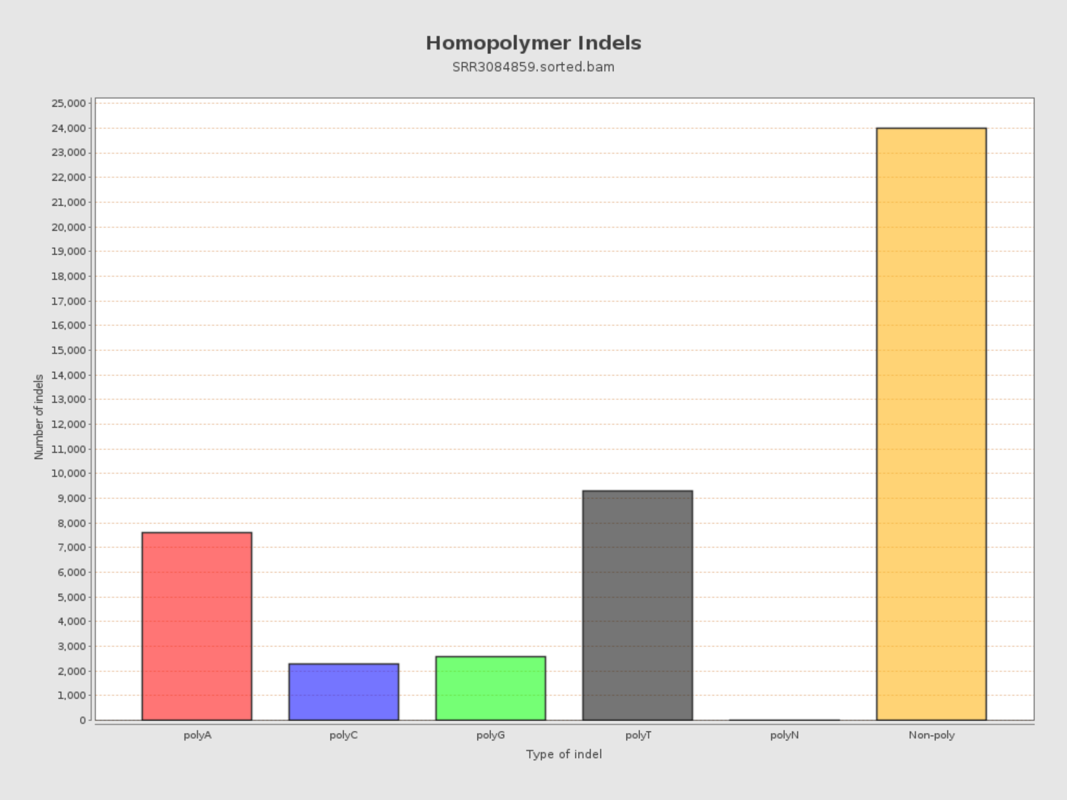
9. Results : Mapped Reads GC-content Distribution



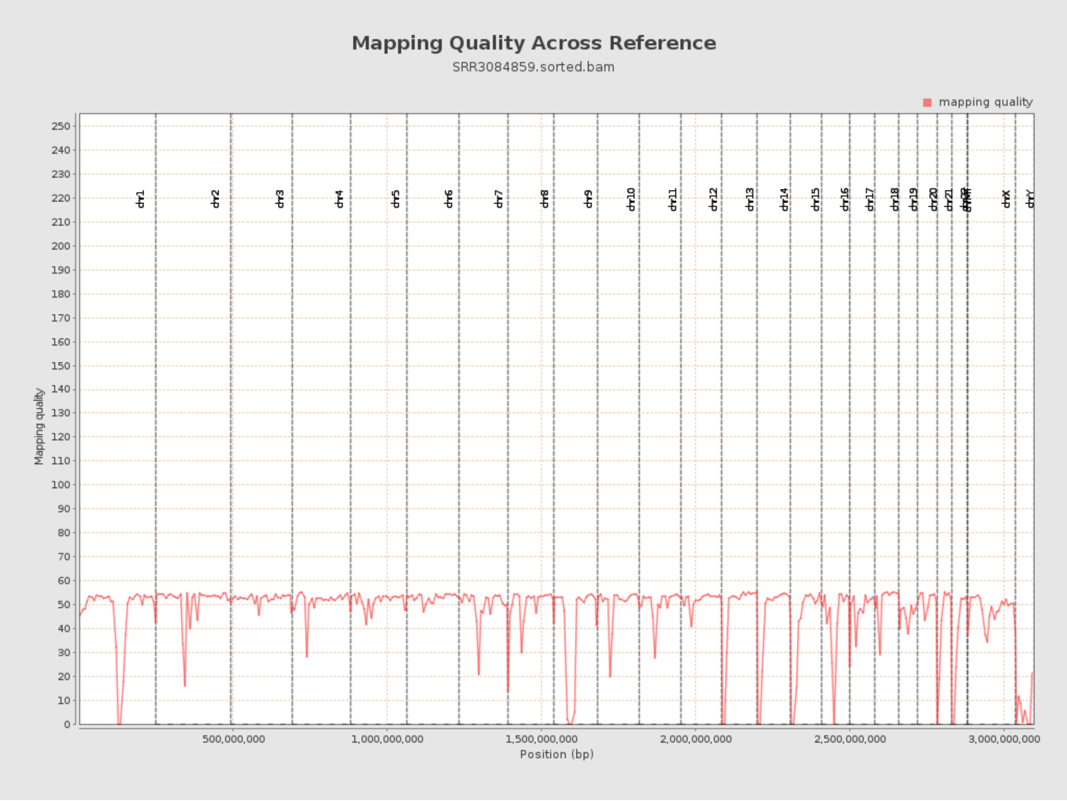
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram