Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 18:29:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084863.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_SRR3084863 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084863.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 18:29:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084863.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,511,090
Mapped reads	2,230,914 / 88.84%
Unmapped reads	280,176 / 11.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,080 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	101,465 / 4.04%
Duplication rate	3.74%
Clipped reads	757,024 / 30.15%

2.2. ACGT Content

Number/percentage of A's	44,969,107 / 29.11%
Number/percentage of C's	28,270,324 / 18.3%
Number/percentage of T's	49,562,054 / 32.08%
Number/percentage of G's	31,650,174 / 20.49%
Number/percentage of N's	24,216 / 0.02%
GC Percentage	38.79%

2.3. Coverage

Mean	0.0499

Standard Deviation	0.4413

2.4. Mapping Quality

Mean Mapping Quality	47.58

2.5. Mismatches and indels

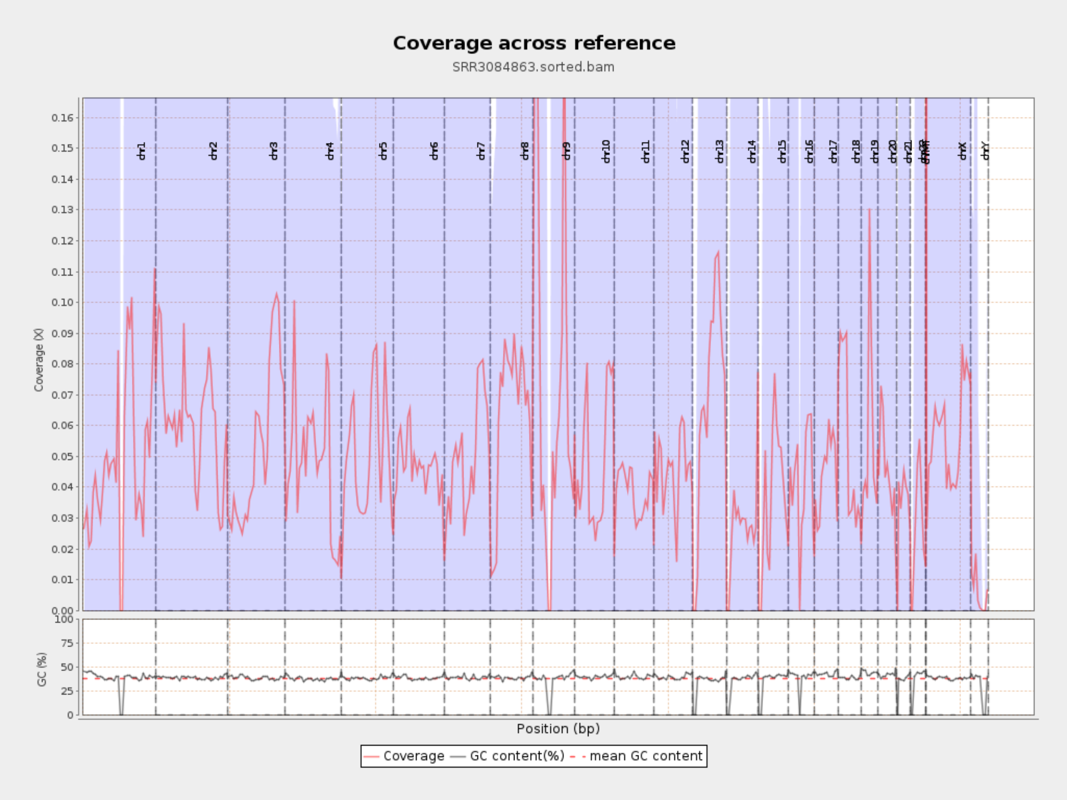
General error rate	0.84%
Mismatches	1,280,129
Insertions	12,419
Mapped reads with at least one insertion	0.55%
Deletions	33,056
Mapped reads with at least one deletion	1.47%
Homopolymer indels	48.13%

2.6. Chromosome stats

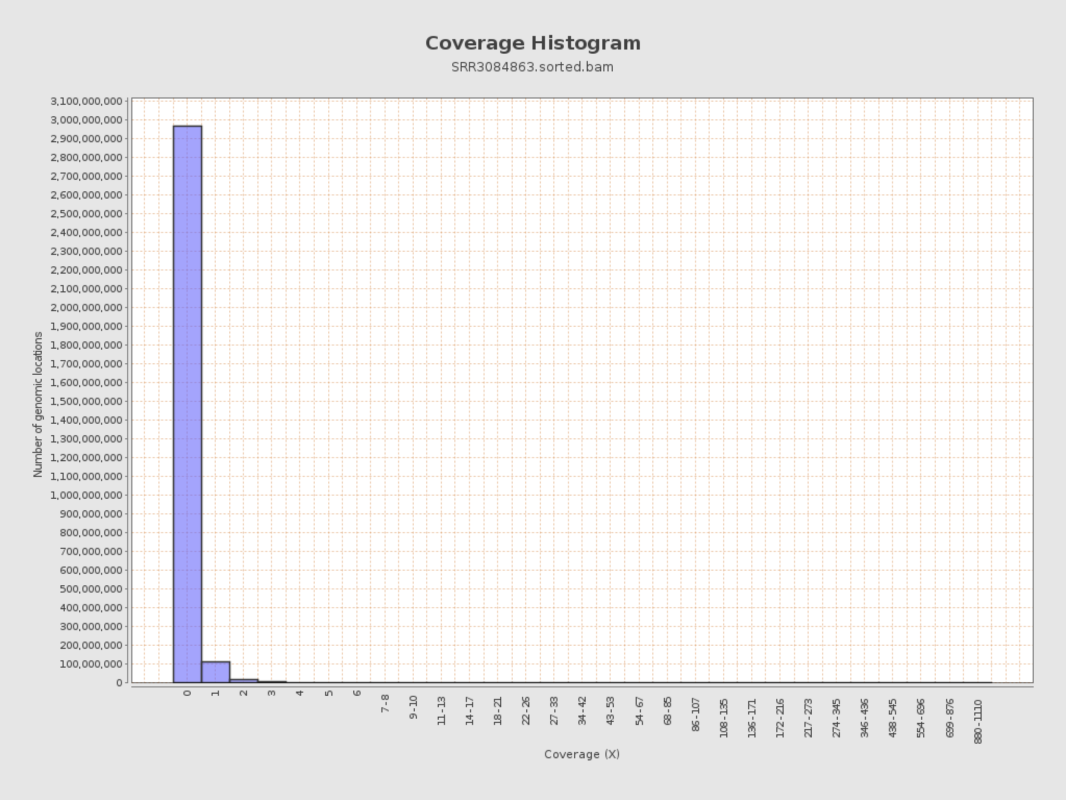
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12188893	0.0489	0.9706
chr2	243199373	15144459	0.0623	0.431
chr3	198022430	10588353	0.0535	0.2656
chr4	191154276	9195162	0.0481	0.2604
chr5	180915260	9047398	0.05	0.2683
chr6	171115067	8099015	0.0473	0.2538
chr7	159138663	7891514	0.0496	0.3264

chr8	146364022	9324502	0.0637	0.7517
chr9	141213431	10577959	0.0749	0.4247
chr10	135534747	6373814	0.047	0.3439
chr11	135006516	5206319	0.0386	0.2815
chr12	133851895	6171908	0.0461	0.2492
chr13	115169878	7938548	0.0689	0.3017
chr14	107349540	2724803	0.0254	0.201
chr15	102531392	3770688	0.0368	0.2176
chr16	90354753	3592867	0.0398	0.2579
chr17	81195210	3667896	0.0452	0.2515
chr18	78077248	4447514	0.057	0.7163
chr19	59128983	3331332	0.0563	0.5365
chr20	63025520	2926109	0.0464	0.2611
chr21	48129895	1665617	0.0346	0.2243
chr22	51304566	1407973	0.0274	0.1869
chrMT	16571	48193	2.9083	2.3456
chrX	155270560	8852491	0.057	0.2923
chrY	59373566	350878	0.0059	0.1478

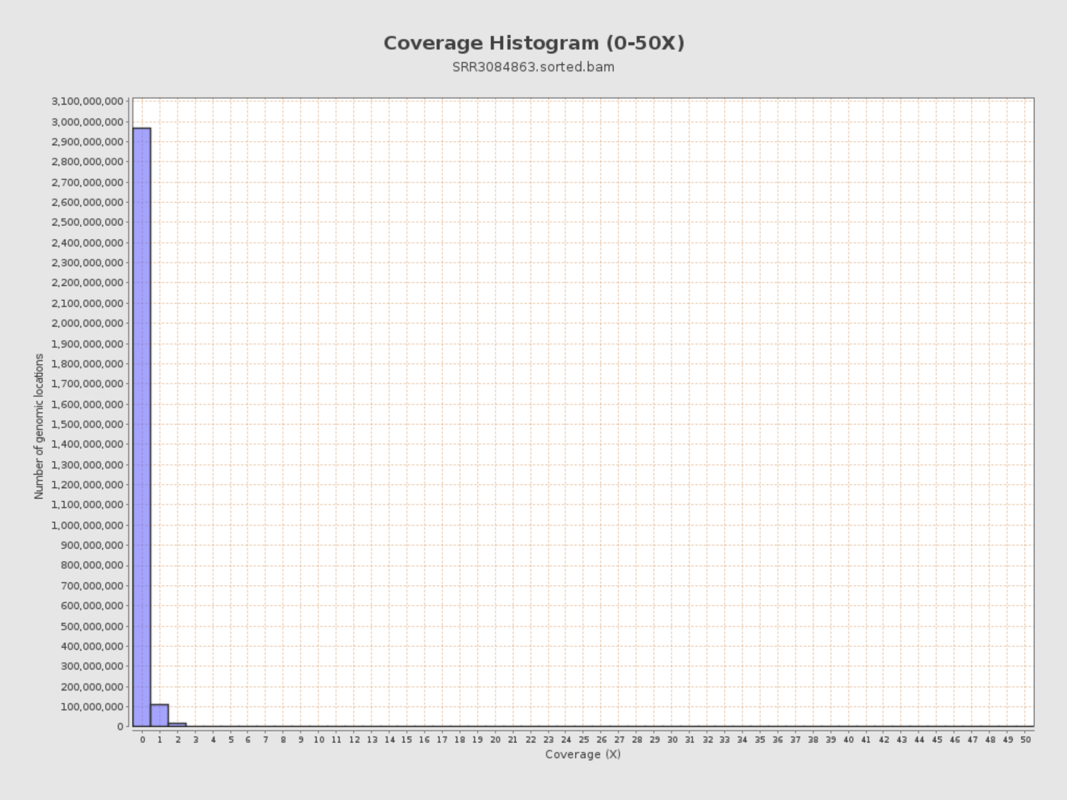
3. Results : Coverage across reference



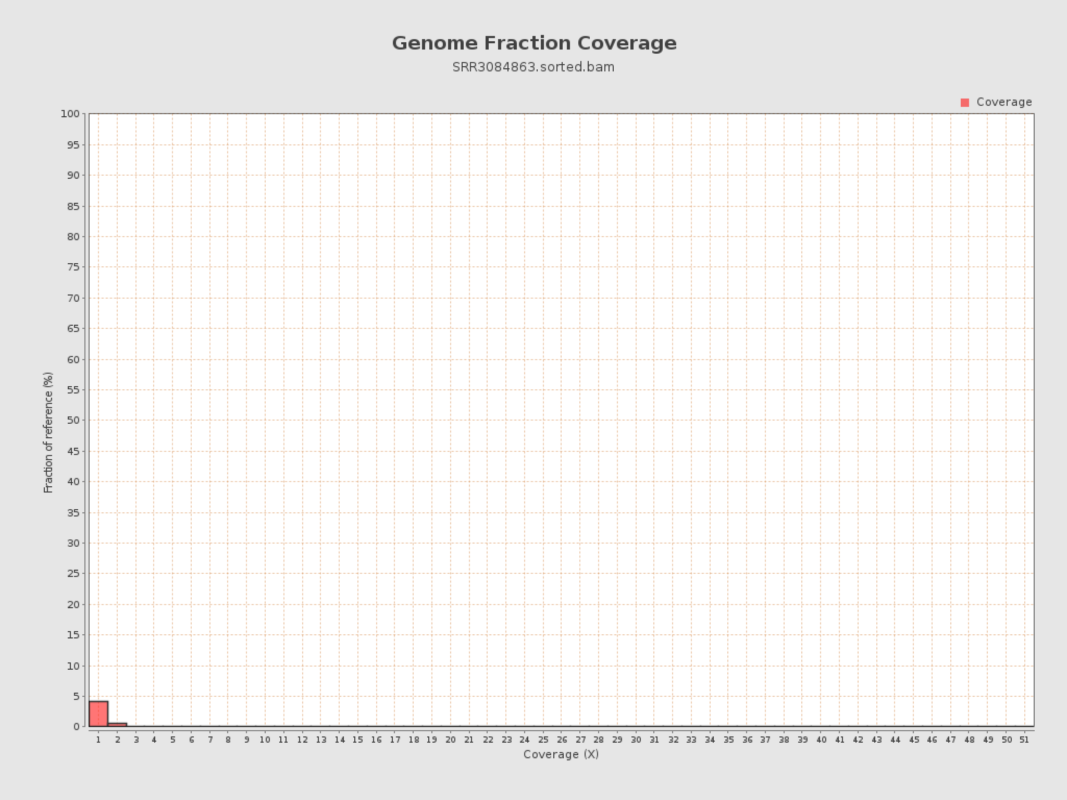
4. Results : Coverage Histogram



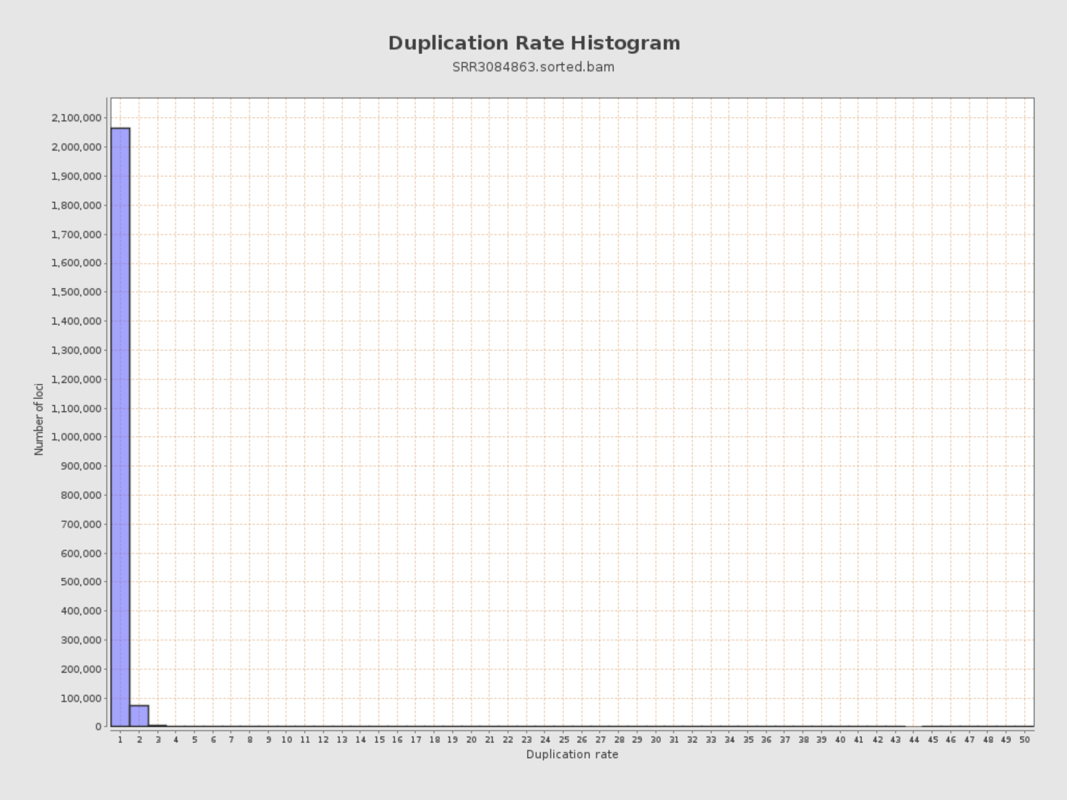
5. Results : Coverage Histogram (0-50X)



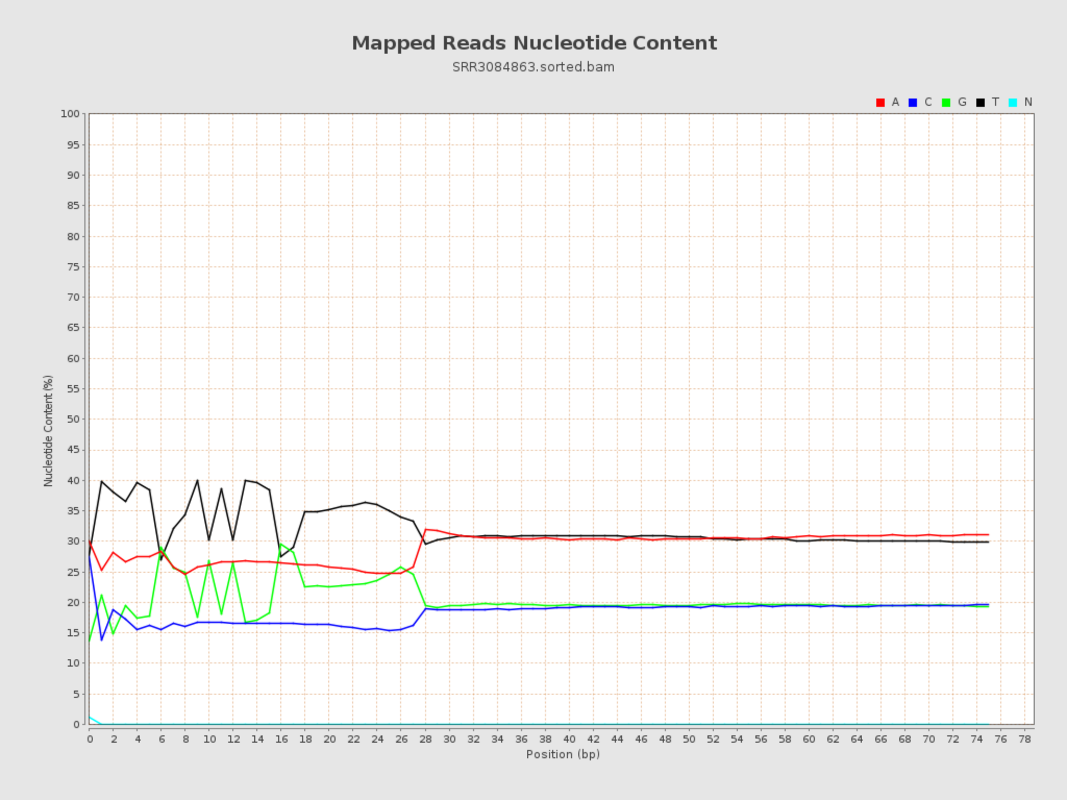
6. Results : Genome Fraction Coverage



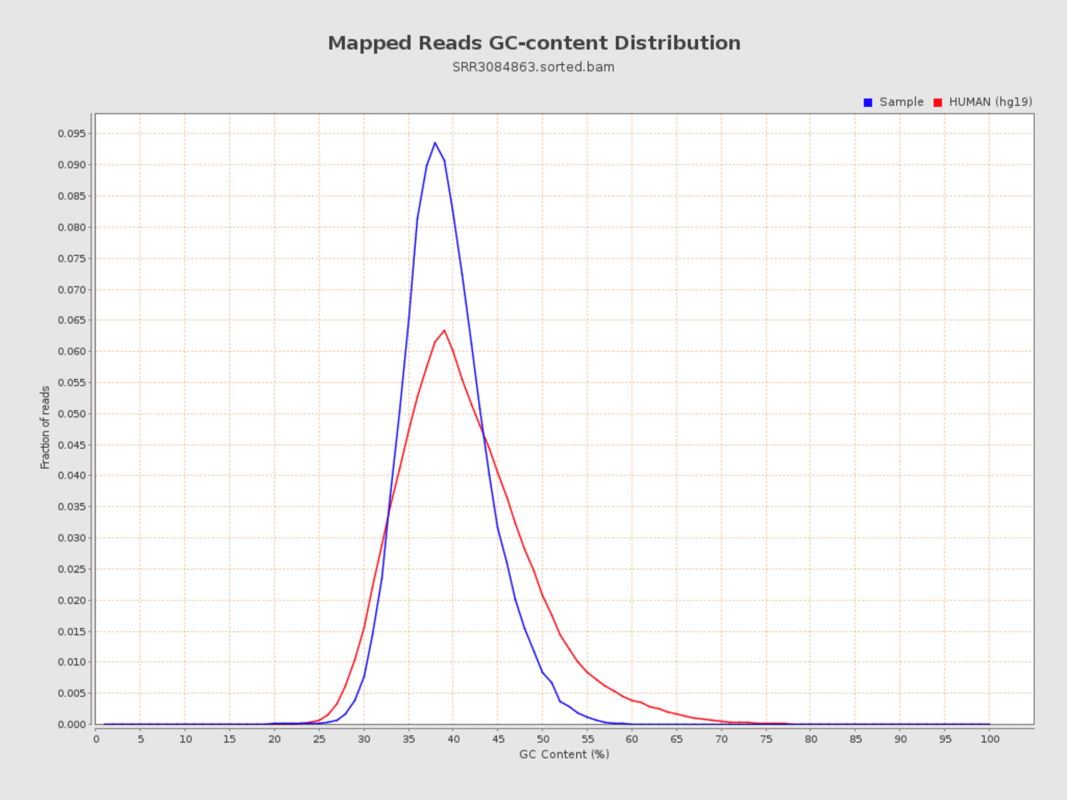
7. Results : Duplication Rate Histogram



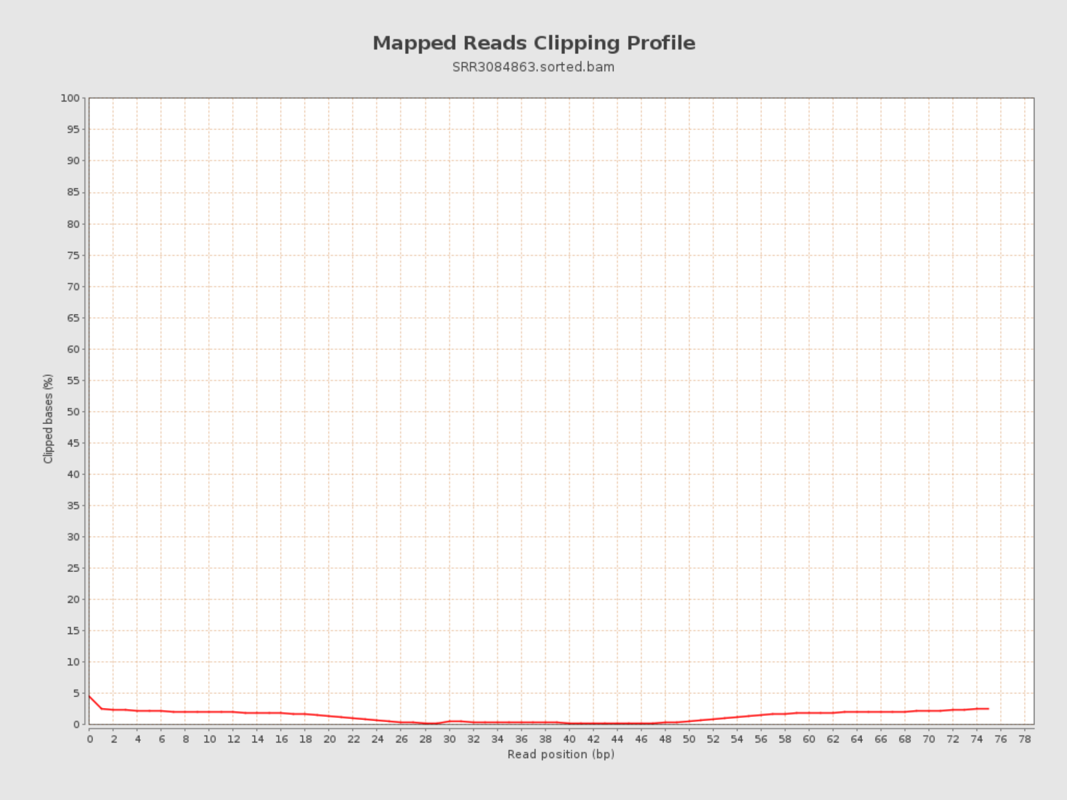
8. Results : Mapped Reads Nucleotide Content



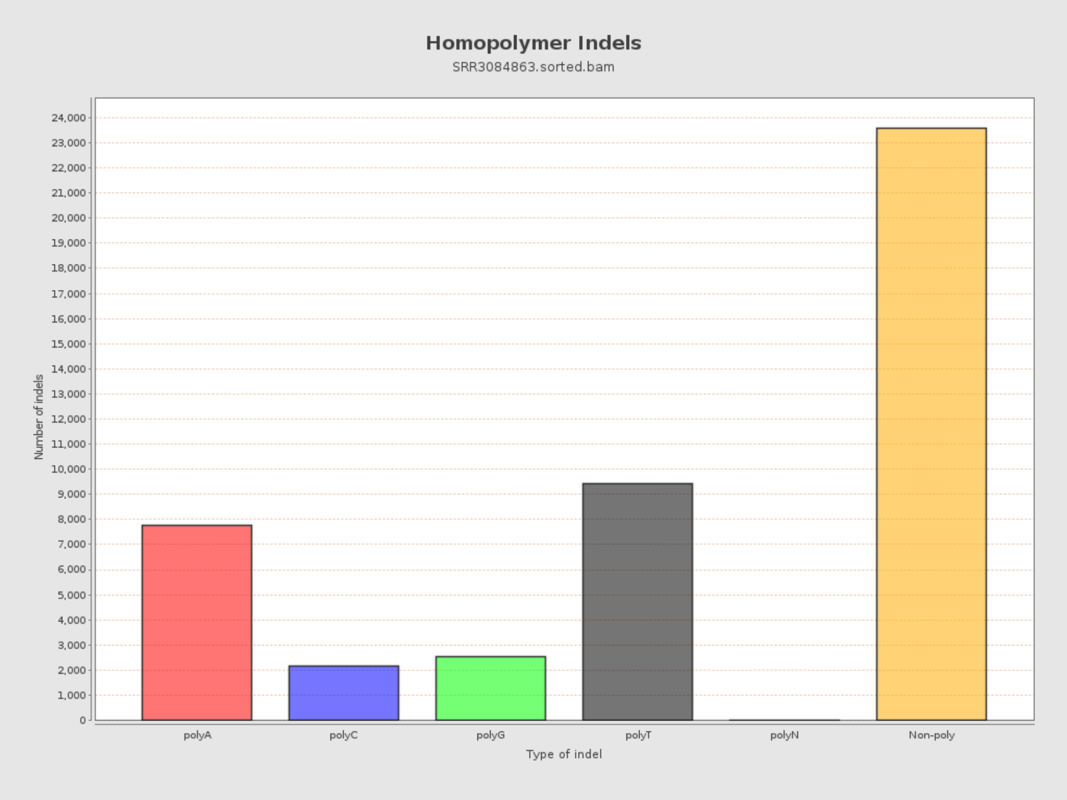
9. Results : Mapped Reads GC-content Distribution



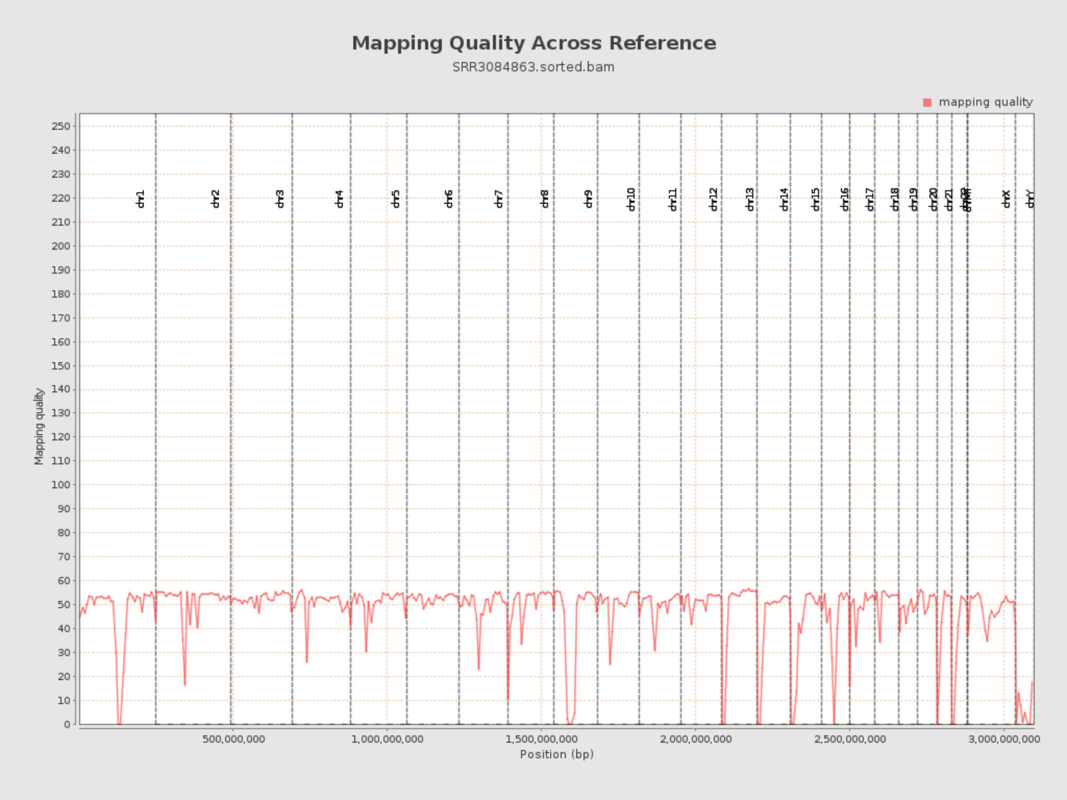
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram