Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 11:57:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084403.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_SRR3084403 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084403.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 11:57:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084403.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,851,656
Mapped reads	2,620,779 / 91.9%
Unmapped reads	230,877 / 8.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,759 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	96,847 / 3.4%
Duplication rate	3.08%
Clipped reads	1,118,022 / 39.21%

2.2. ACGT Content

Number/percentage of A's	50,416,340 / 28.51%
Number/percentage of C's	33,287,839 / 18.83%
Number/percentage of T's	55,266,610 / 31.26%
Number/percentage of G's	37,613,886 / 21.27%
Number/percentage of N's	234,660 / 0.13%
GC Percentage	40.1%

2.3. Coverage

Mean	0.0571

Standard Deviation	0.3733

2.4. Mapping Quality

Mean Mapping Quality	46.4

2.5. Mismatches and indels

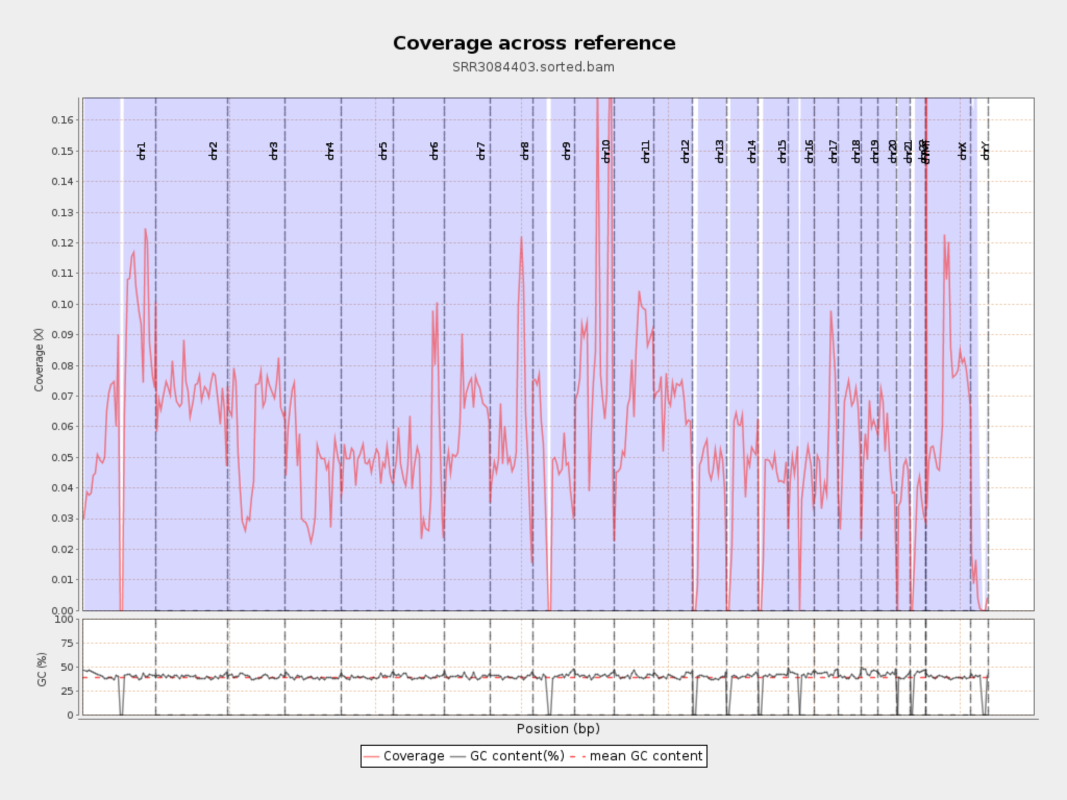
General error rate	1.01%
Mismatches	1,754,359
Insertions	12,769
Mapped reads with at least one insertion	0.48%
Deletions	35,881
Mapped reads with at least one deletion	1.35%
Homopolymer indels	47.31%

2.6. Chromosome stats

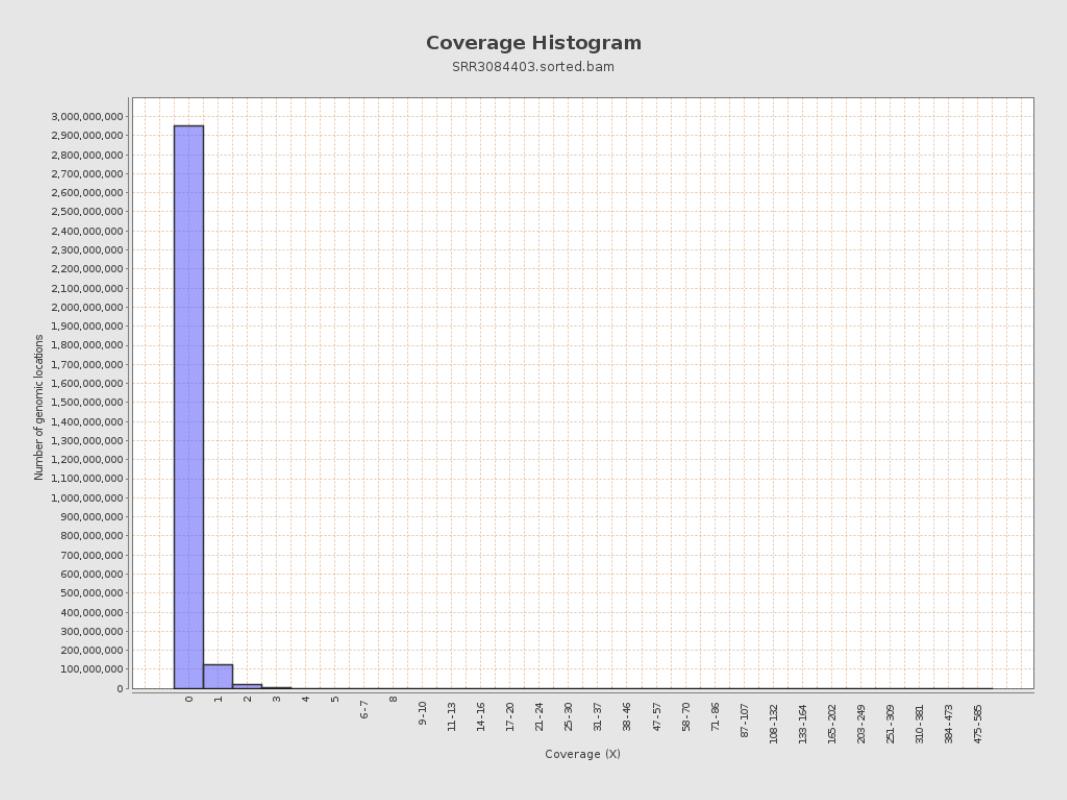
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17443731	0.07	0.596
chr2	243199373	17212265	0.0708	0.4222
chr3	198022430	11978256	0.0605	0.2905
chr4	191154276	8717796	0.0456	0.2554
chr5	180915260	8728864	0.0482	0.2534
chr6	171115067	8511707	0.0497	0.2902
chr7	159138663	10089331	0.0634	0.5313

chr8	146364022	8454932	0.0578	0.3937
chr9	141213431	6586621	0.0466	0.3115
chr10	135534747	12110137	0.0894	0.5072
chr11	135006516	9959885	0.0738	0.3841
chr12	133851895	9177087	0.0686	0.3058
chr13	115169878	4589946	0.0399	0.2304
chr14	107349540	4883417	0.0455	0.2562
chr15	102531392	3839260	0.0374	0.2295
chr16	90354753	3654044	0.0404	0.2548
chr17	81195210	4653518	0.0573	0.2971
chr18	78077248	4741862	0.0607	0.5645
chr19	59128983	3312545	0.056	0.4241
chr20	63025520	3357505	0.0533	0.2724
chr21	48129895	1786184	0.0371	0.2316
chr22	51304566	1345895	0.0262	0.1848
chrMT	16571	21055	1.2706	1.4909
chrX	155270560	11367023	0.0732	0.3399
chrY	59373566	358406	0.006	0.1205

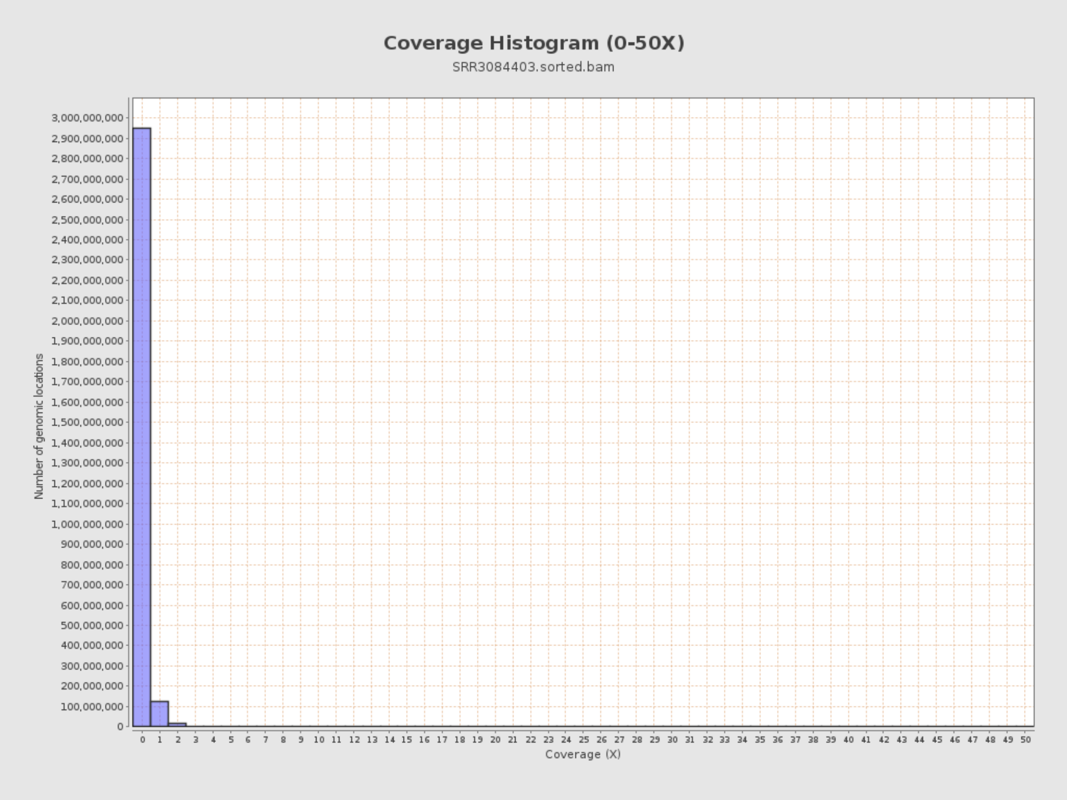
3. Results : Coverage across reference



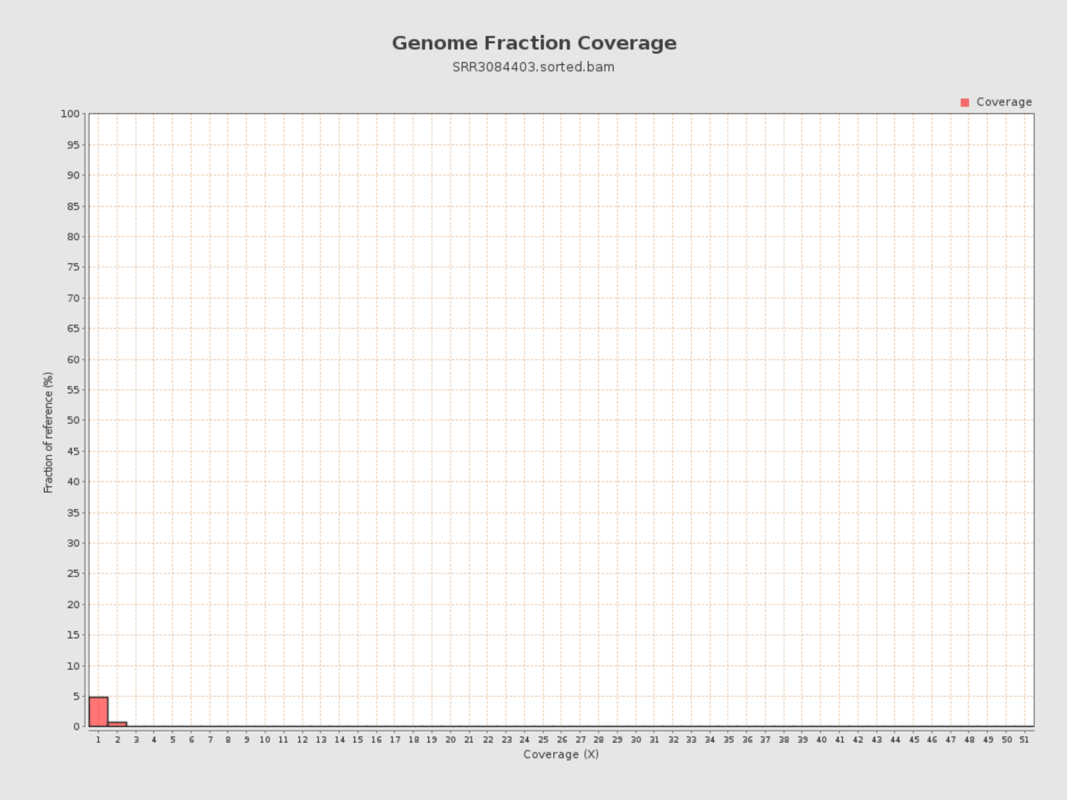
4. Results : Coverage Histogram



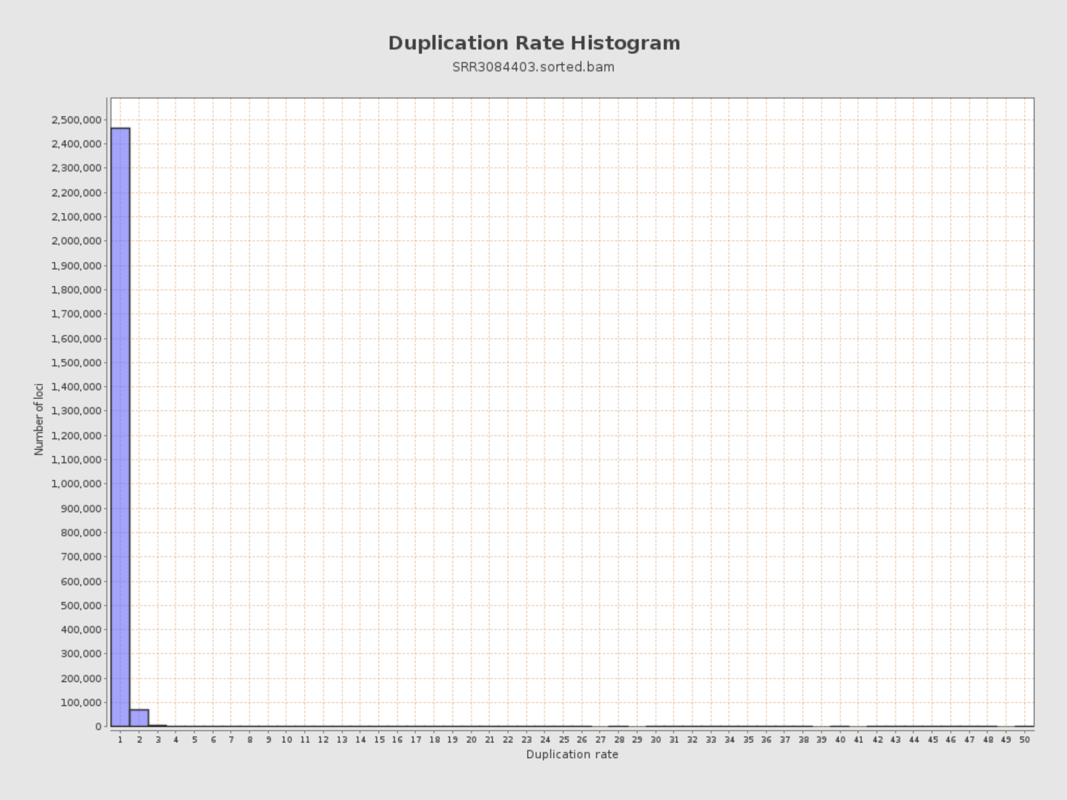
5. Results : Coverage Histogram (0-50X)



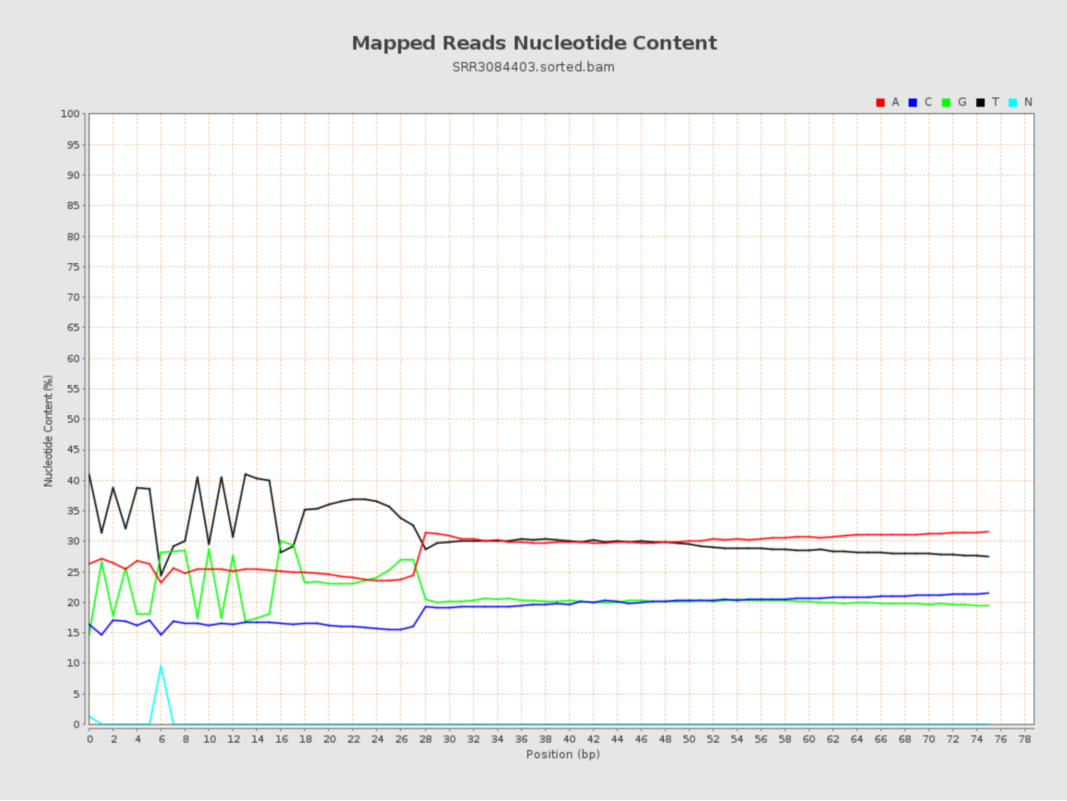
6. Results : Genome Fraction Coverage



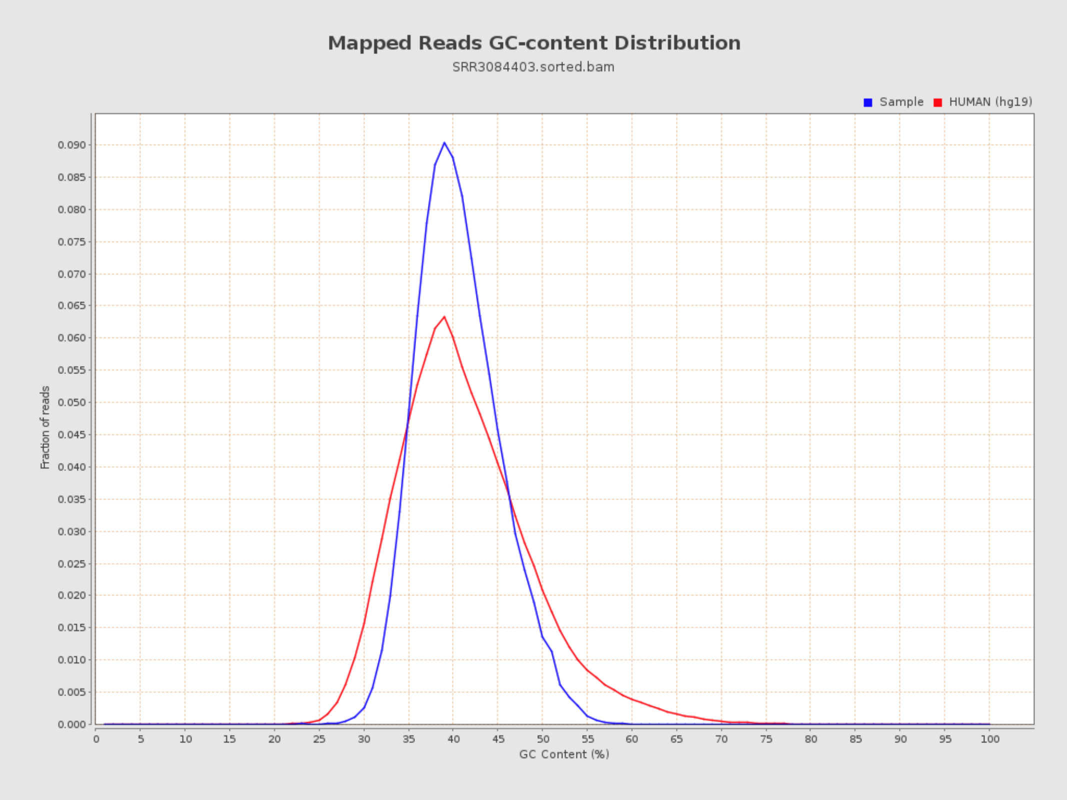
7. Results : Duplication Rate Histogram



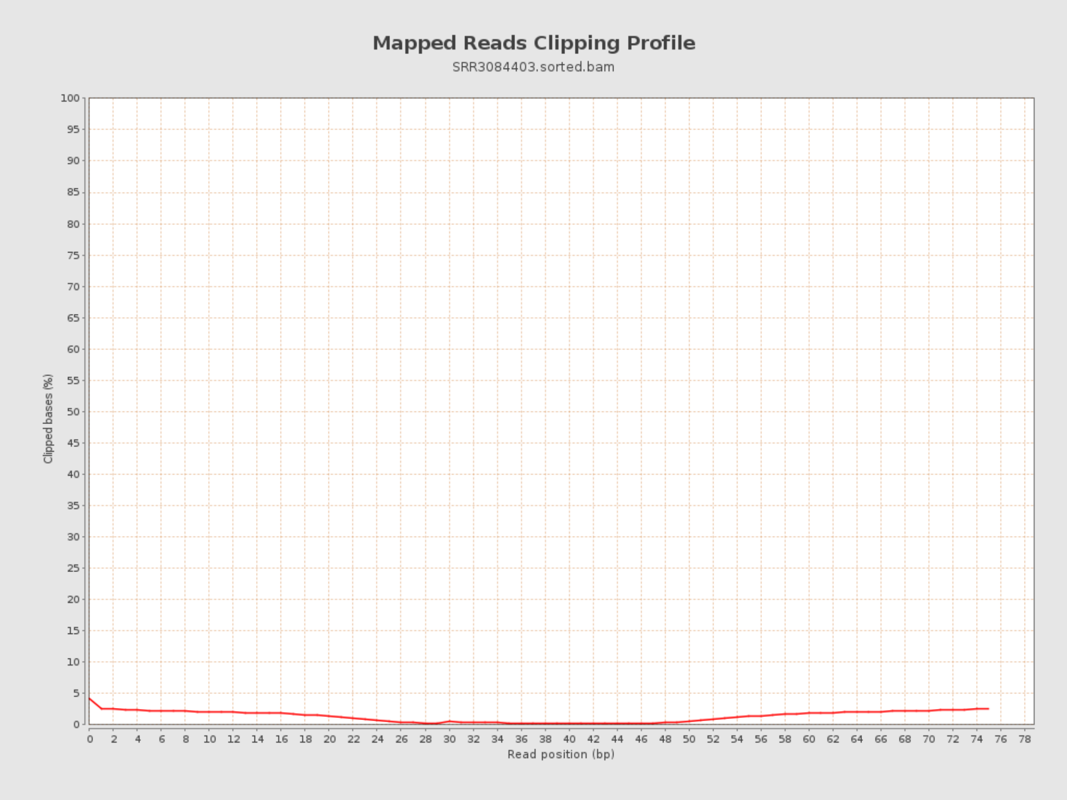
8. Results : Mapped Reads Nucleotide Content



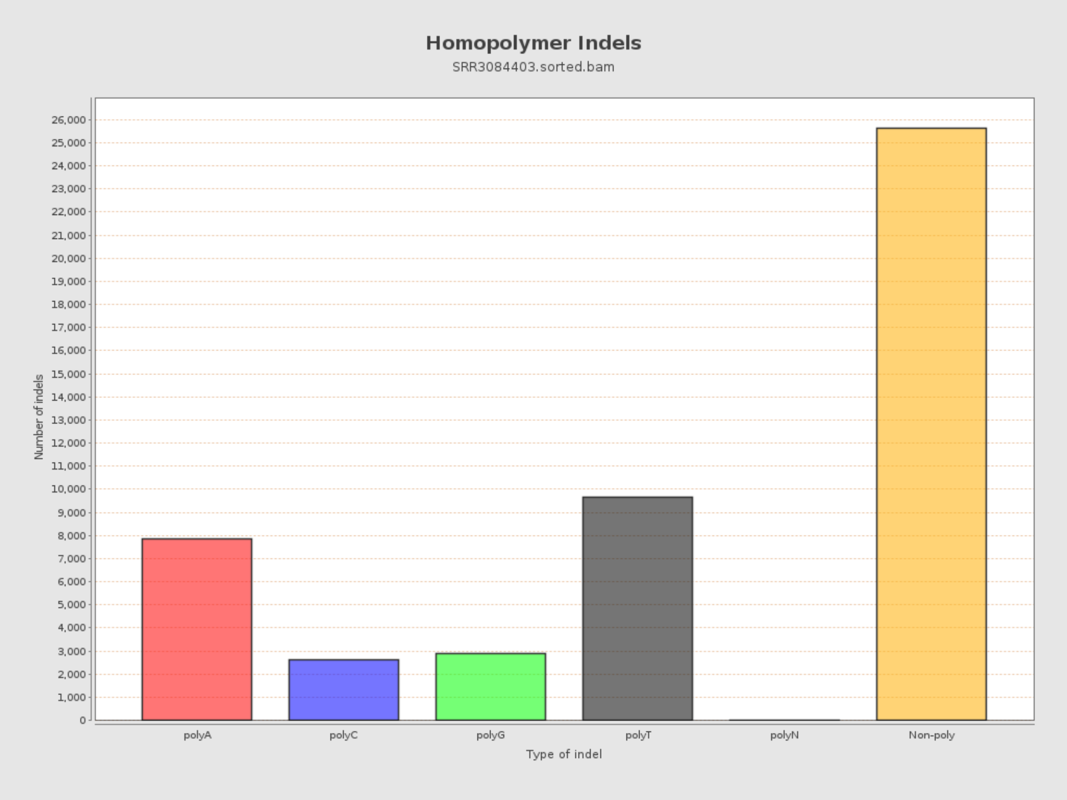
9. Results : Mapped Reads GC-content Distribution



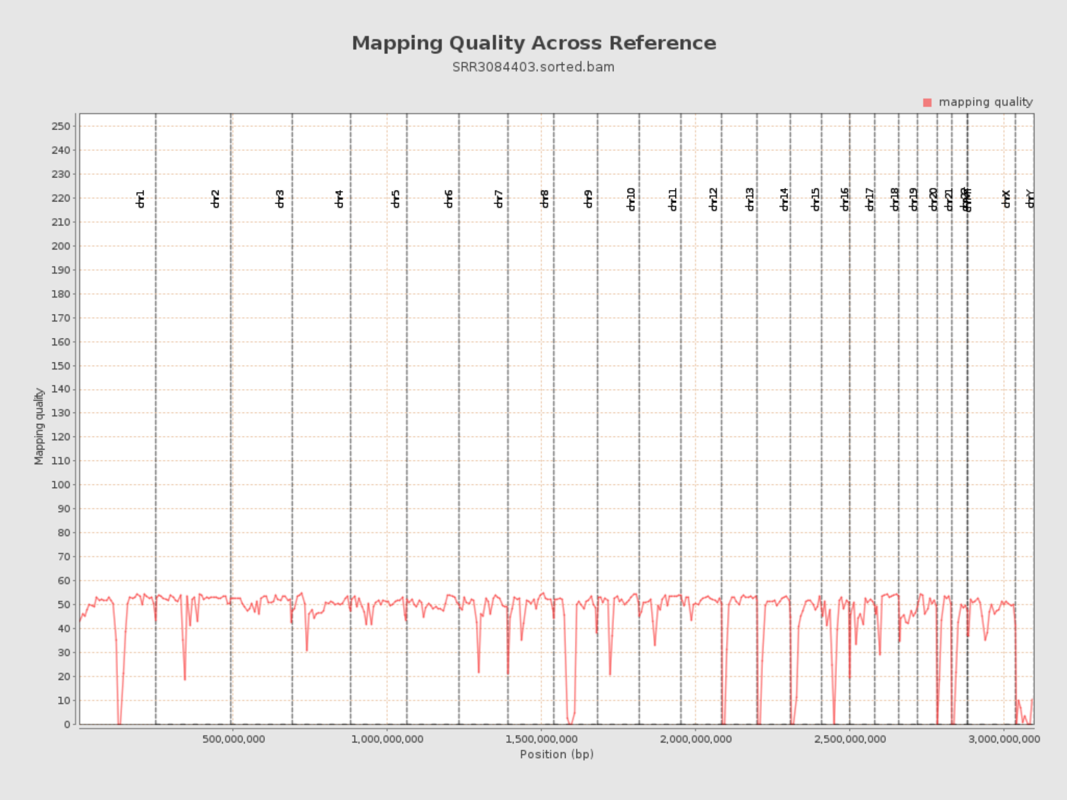
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram