Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 13:06:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084778.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_SRR3084778 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084778.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 13:06:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084778.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,430,148
Mapped reads	2,161,992 / 88.97%
Unmapped reads	268,156 / 11.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,307 / 0.96%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	98,619 / 4.06%
Duplication rate	3.82%
Clipped reads	947,193 / 38.98%

2.2. ACGT Content

Number/percentage of A's	40,680,073 / 28.06%
Number/percentage of C's	26,759,928 / 18.46%
Number/percentage of T's	45,803,482 / 31.59%
Number/percentage of G's	31,678,251 / 21.85%
Number/percentage of N's	56,481 / 0.04%
GC Percentage	40.31%

2.3. Coverage

Mean	0.0468

Standard Deviation	0.335

2.4. Mapping Quality

Mean Mapping Quality	47

2.5. Mismatches and indels

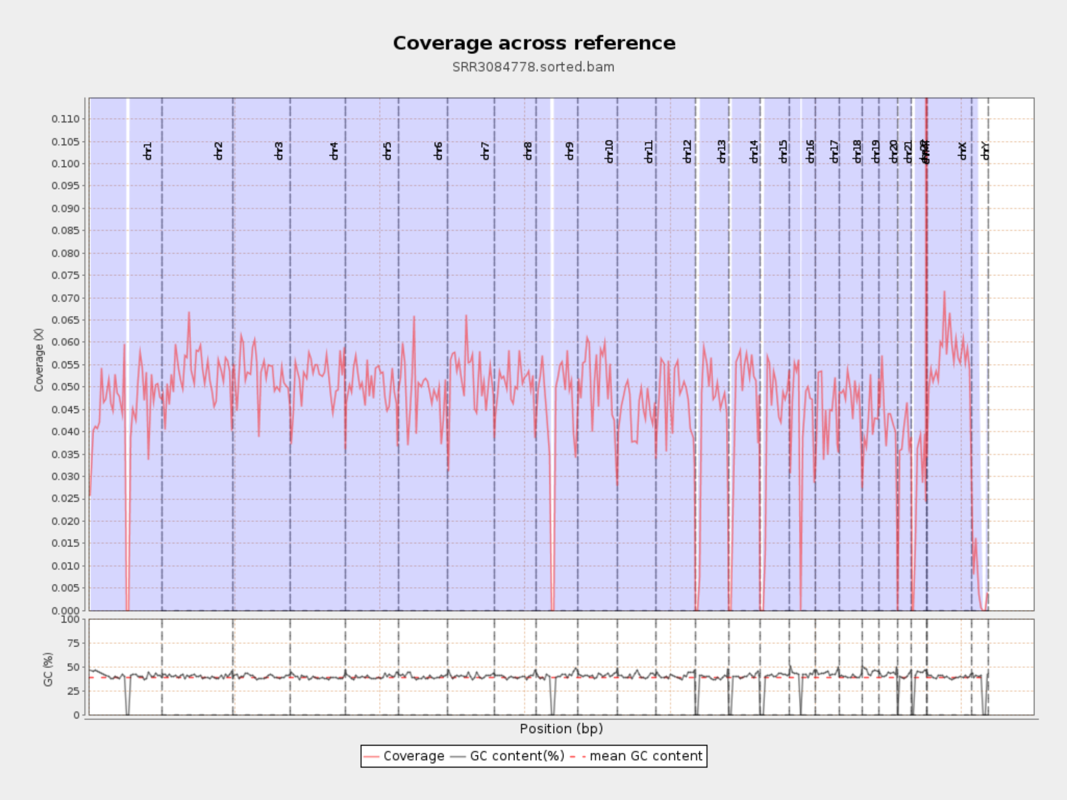
General error rate	0.87%
Mismatches	1,247,454
Insertions	10,971
Mapped reads with at least one insertion	0.5%
Deletions	33,154
Mapped reads with at least one deletion	1.52%
Homopolymer indels	47.96%

2.6. Chromosome stats

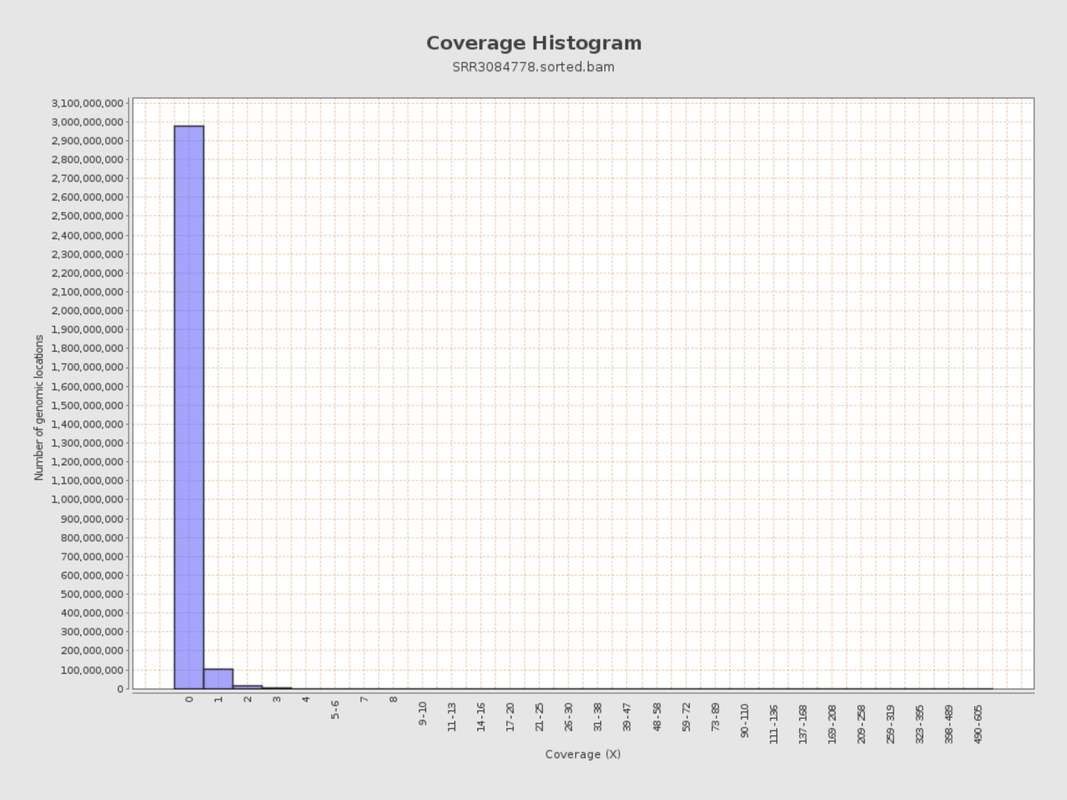
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10970454	0.044	0.4986
chr2	243199373	12846840	0.0528	0.4066
chr3	198022430	10486862	0.053	0.2668
chr4	191154276	9964775	0.0521	0.2763
chr5	180915260	9123771	0.0504	0.2612
chr6	171115067	8406961	0.0491	0.3067
chr7	159138663	8339289	0.0524	0.3935

chr8	146364022	7395639	0.0505	0.4405
chr9	141213431	6155657	0.0436	0.3189
chr10	135534747	6997586	0.0516	0.3223
chr11	135006516	6012898	0.0445	0.2859
chr12	133851895	6361588	0.0475	0.256
chr13	115169878	4763994	0.0414	0.2405
chr14	107349540	4739783	0.0442	0.2544
chr15	102531392	4082159	0.0398	0.2373
chr16	90354753	3821712	0.0423	0.2524
chr17	81195210	3516234	0.0433	0.2767
chr18	78077248	3754882	0.0481	0.5613
chr19	59128983	2481835	0.042	0.3778
chr20	63025520	2724864	0.0432	0.2485
chr21	48129895	1704279	0.0354	0.226
chr22	51304566	1276094	0.0249	0.1801
chrMT	16571	14985	0.9043	1.057
chrX	155270560	8750516	0.0564	0.2948
chrY	59373566	337682	0.0057	0.1095

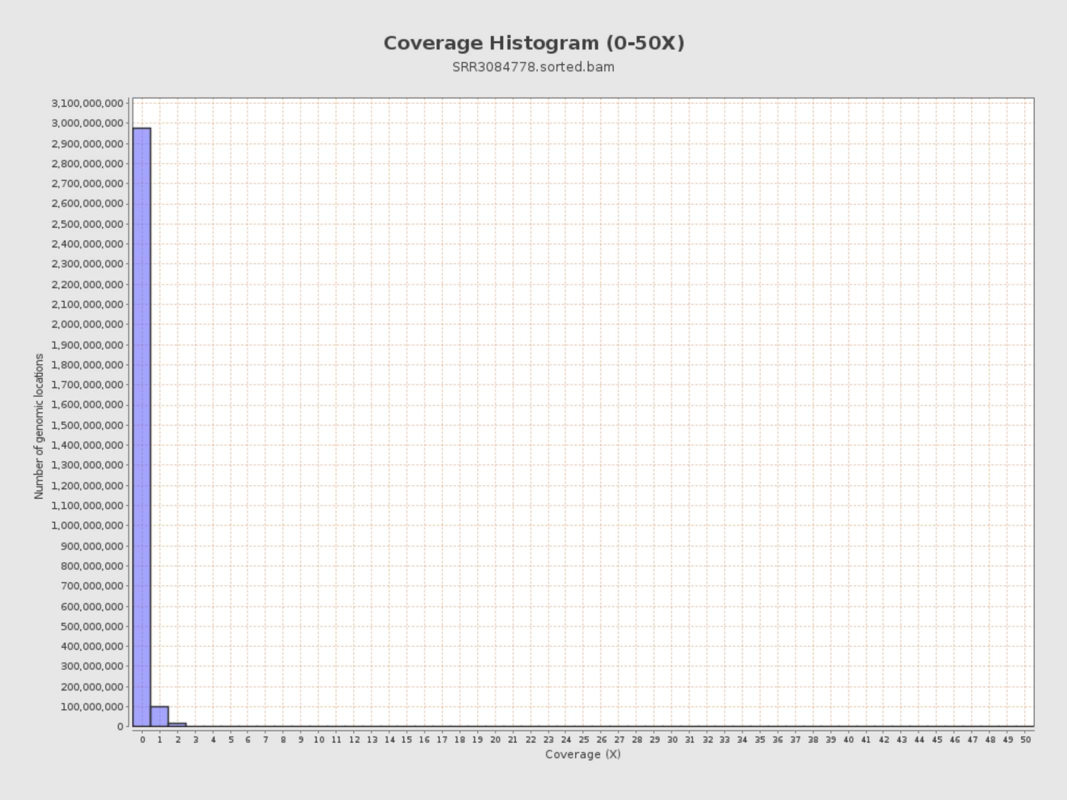
3. Results : Coverage across reference



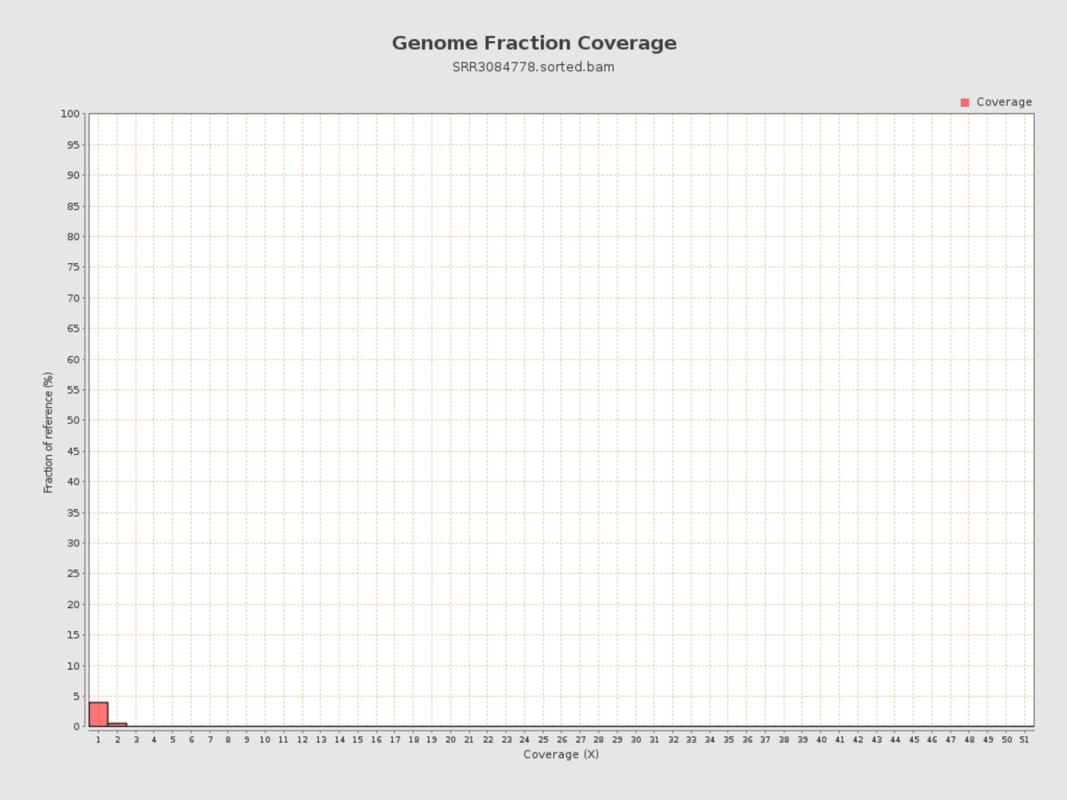
4. Results : Coverage Histogram



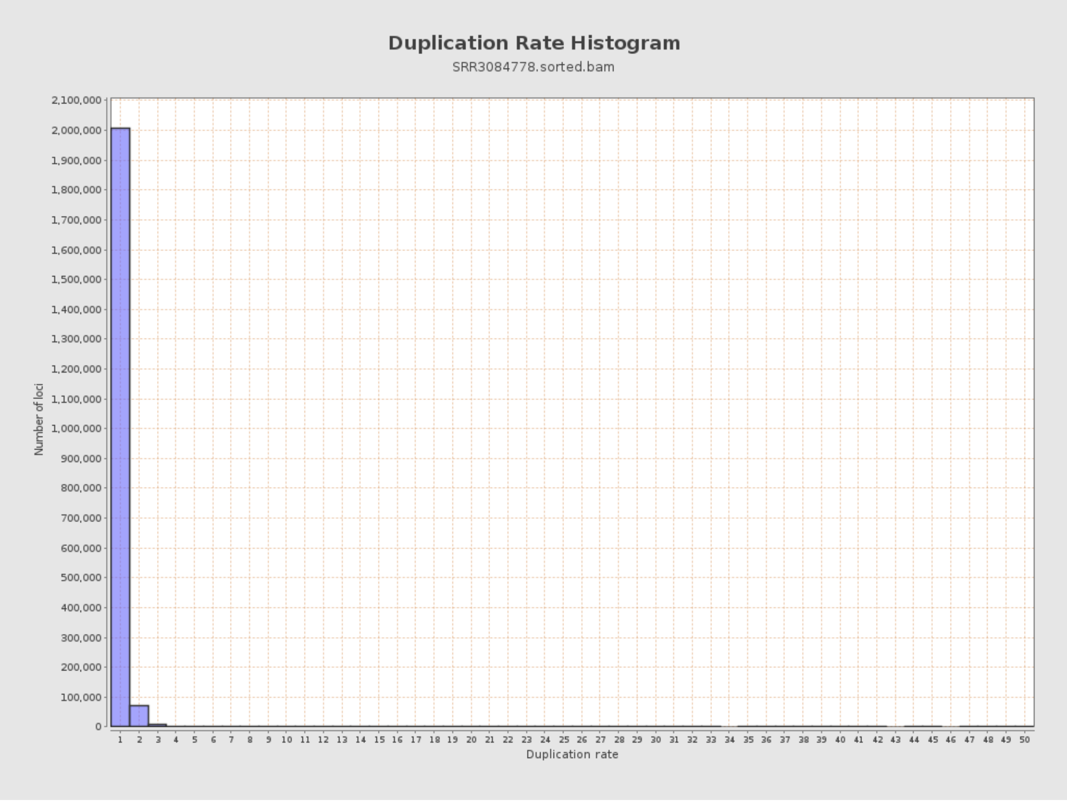
5. Results : Coverage Histogram (0-50X)



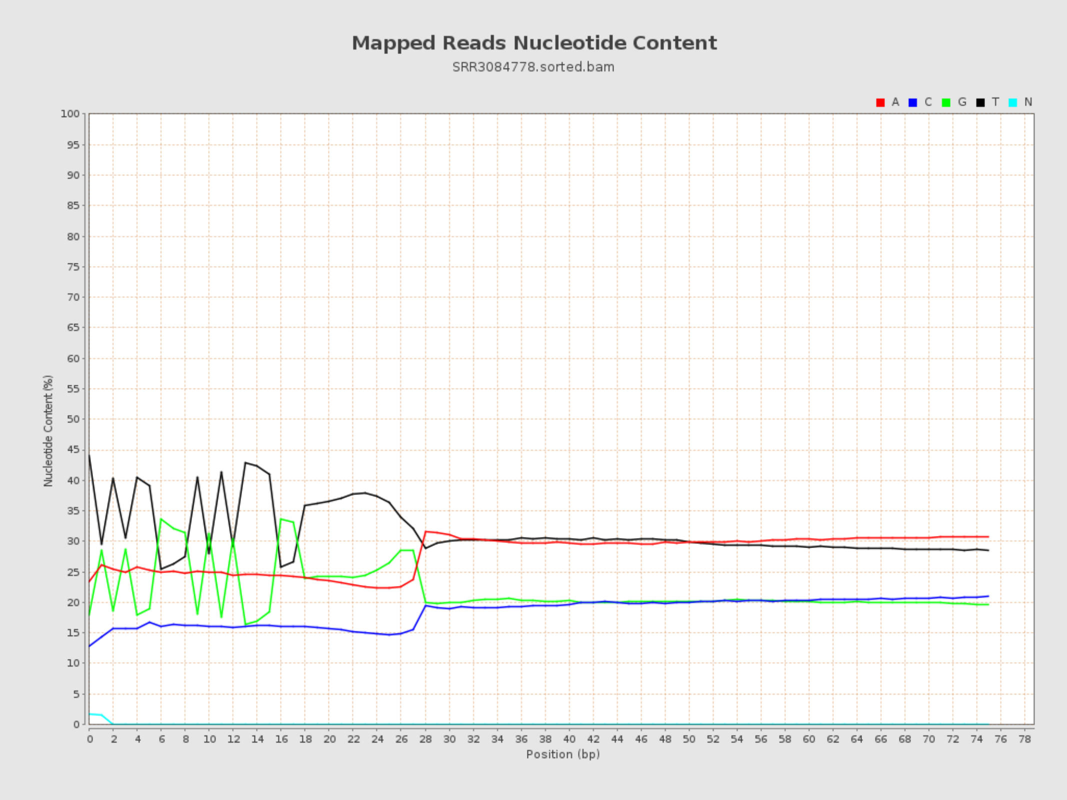
6. Results : Genome Fraction Coverage



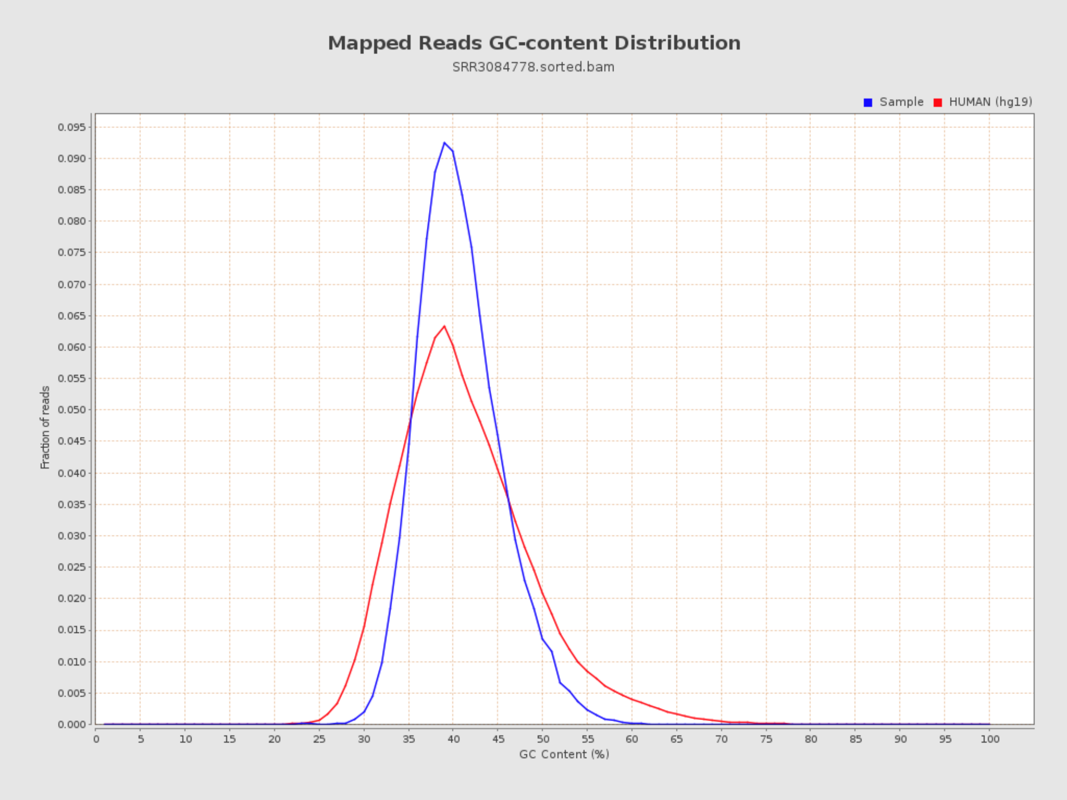
7. Results : Duplication Rate Histogram



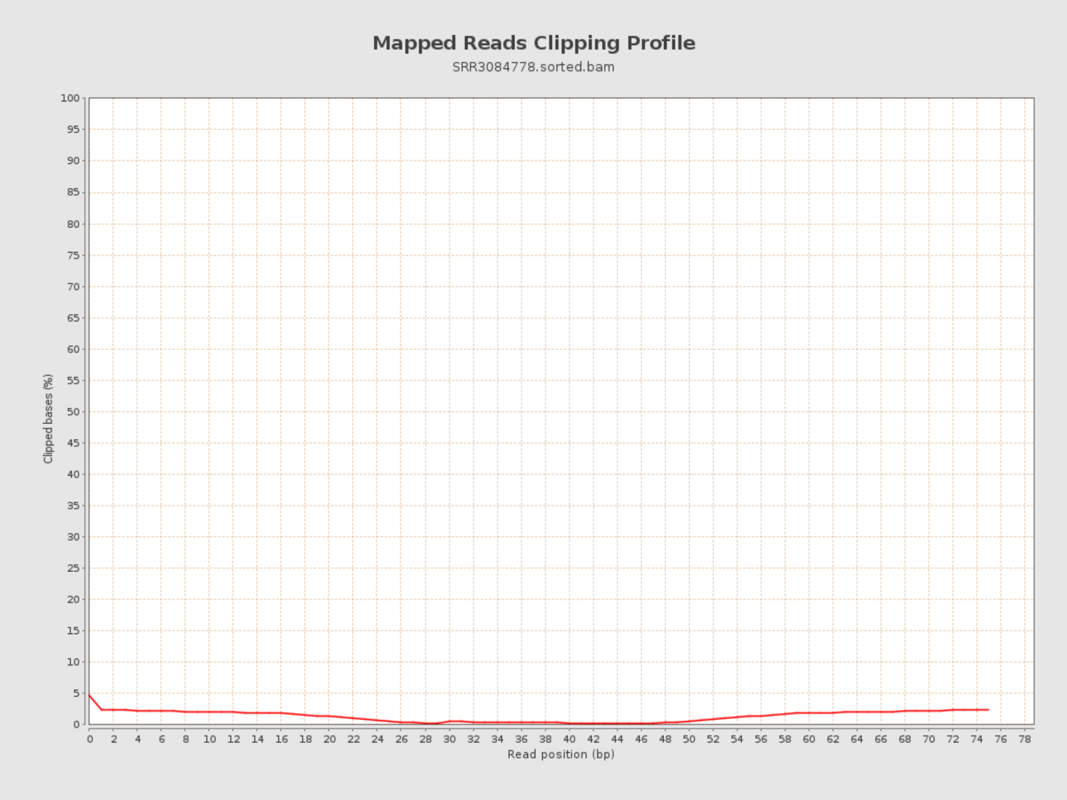
8. Results : Mapped Reads Nucleotide Content



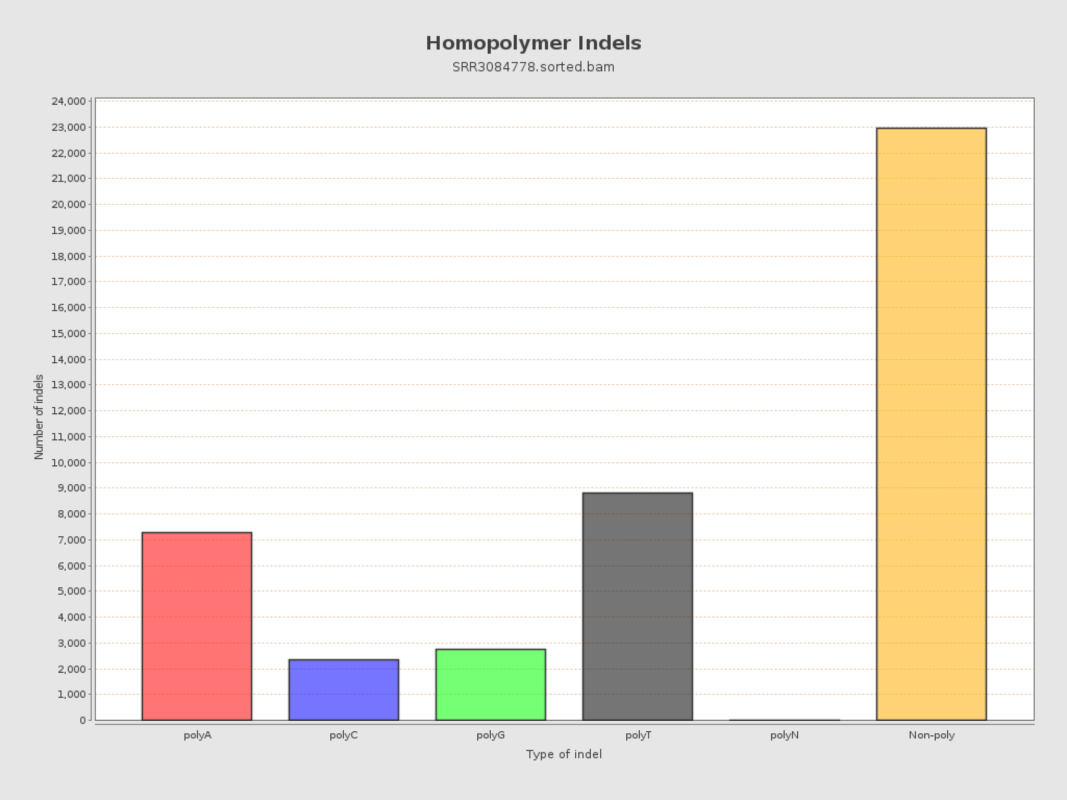
9. Results : Mapped Reads GC-content Distribution



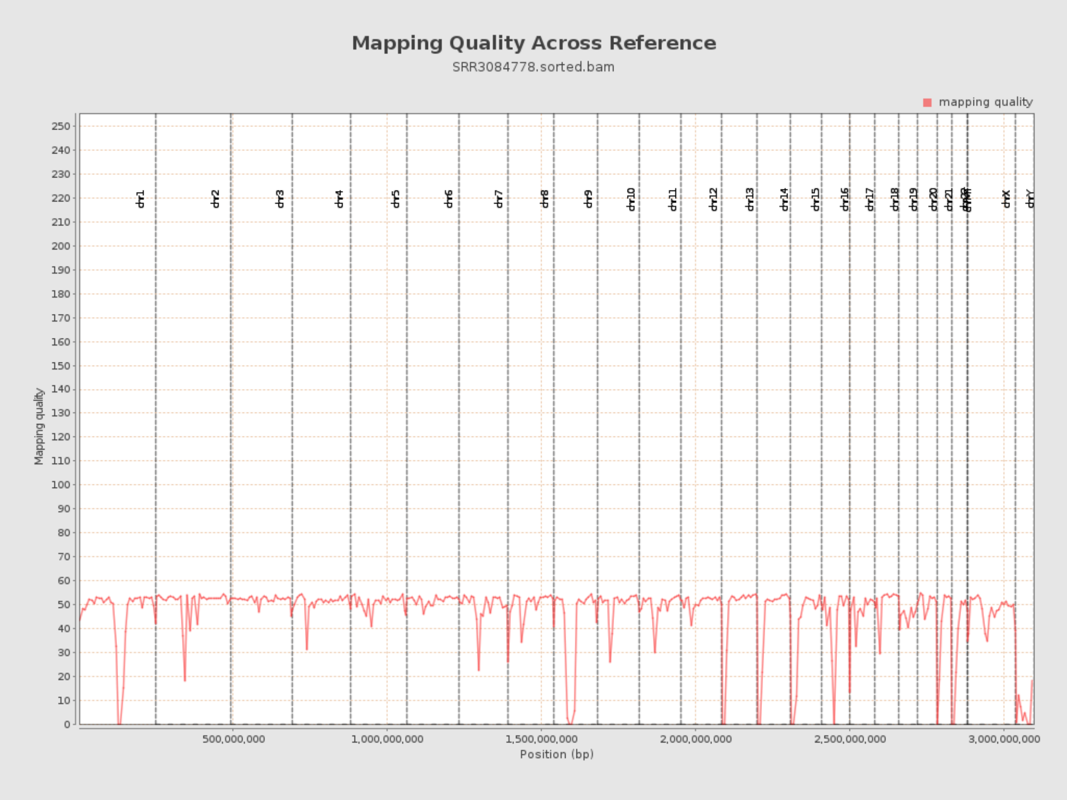
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram