Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 15:57:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084820.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_SRR3084820 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084820.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 15:57:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084820.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,367,204
Mapped reads	2,186,187 / 92.35%
Unmapped reads	181,017 / 7.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,767 / 1.05%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	105,191 / 4.44%
Duplication rate	4.11%
Clipped reads	890,183 / 37.6%

2.2. ACGT Content

Number/percentage of A's	41,569,776 / 28.08%
Number/percentage of C's	27,092,919 / 18.3%
Number/percentage of T's	47,397,101 / 32.01%
Number/percentage of G's	31,977,054 / 21.6%
Number/percentage of N's	20,922 / 0.01%
GC Percentage	39.9%

2.3. Coverage

Mean	0.0478

Standard Deviation	0.3303

2.4. Mapping Quality

Mean Mapping Quality	46.45

2.5. Mismatches and indels

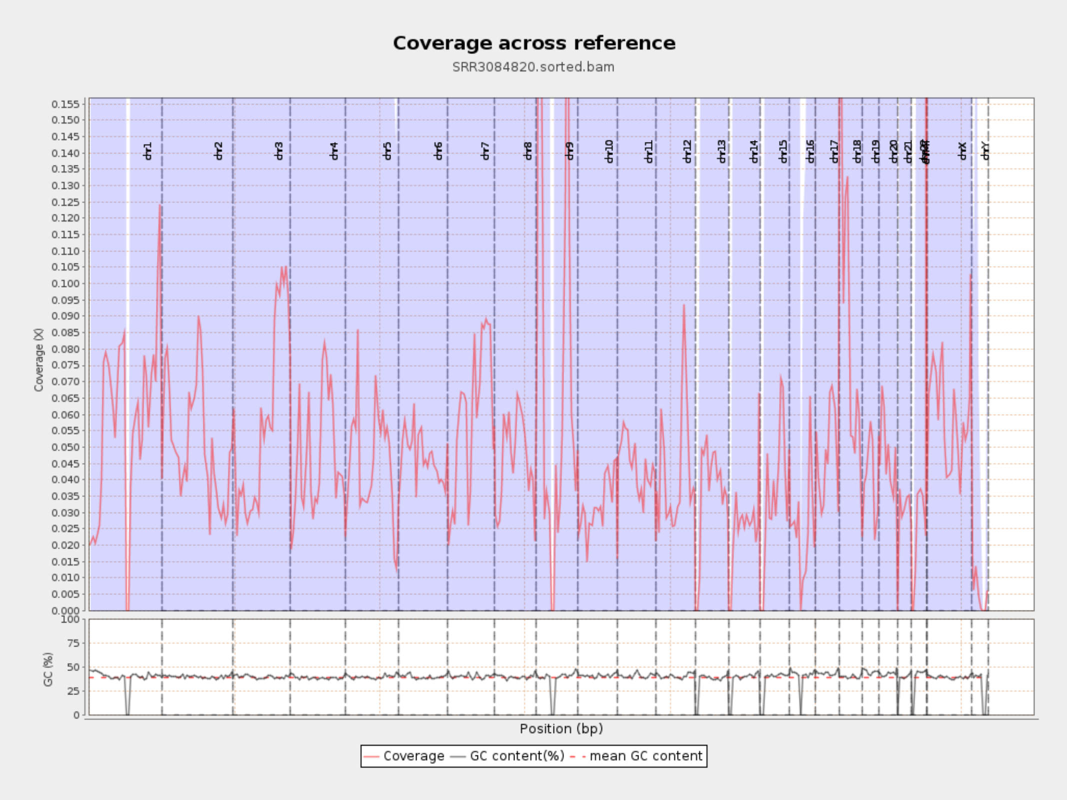
General error rate	0.79%
Mismatches	1,152,275
Insertions	12,192
Mapped reads with at least one insertion	0.55%
Deletions	34,680
Mapped reads with at least one deletion	1.57%
Homopolymer indels	48.72%

2.6. Chromosome stats

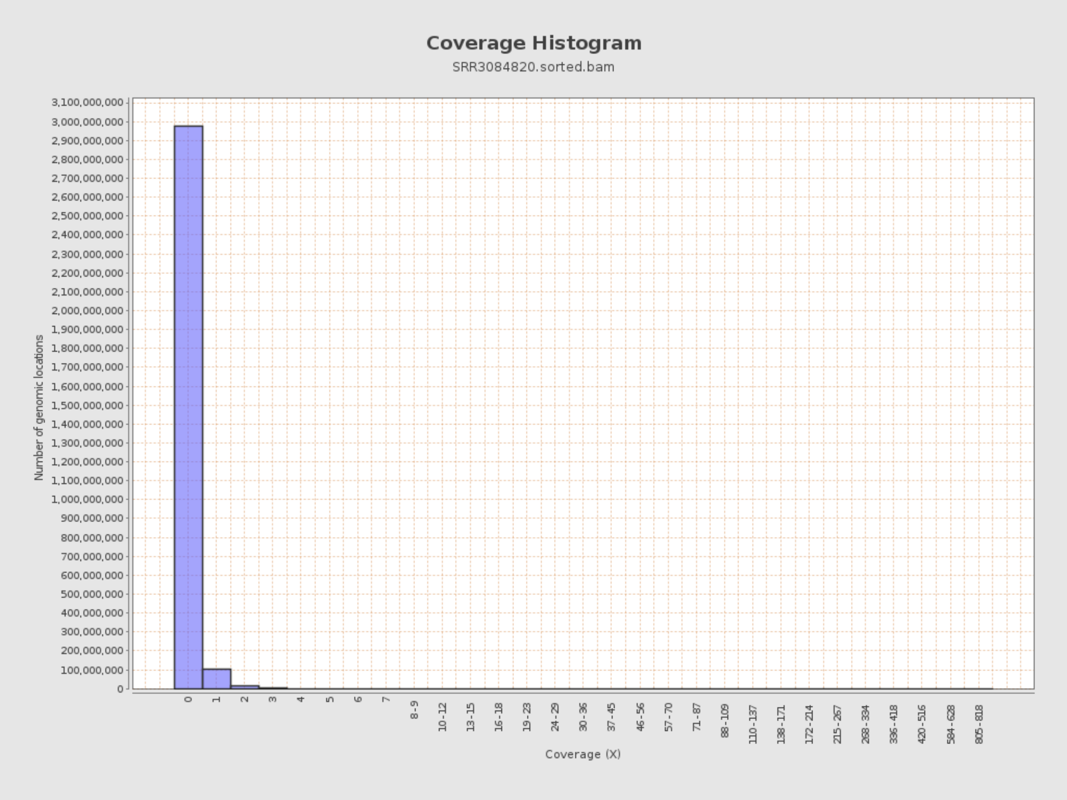
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14406085	0.0578	0.4517
chr2	243199373	12494852	0.0514	0.4717
chr3	198022430	11487701	0.058	0.2835
chr4	191154276	9068271	0.0474	0.2676
chr5	180915260	8213101	0.0454	0.2514
chr6	171115067	7965008	0.0465	0.2693
chr7	159138663	9530329	0.0599	0.3663

chr8	146364022	6712102	0.0459	0.4753
chr9	141213431	11075428	0.0784	0.3916
chr10	135534747	4351308	0.0321	0.2223
chr11	135006516	5934846	0.044	0.2843
chr12	133851895	5791067	0.0433	0.245
chr13	115169878	4127448	0.0358	0.2227
chr14	107349540	2554133	0.0238	0.189
chr15	102531392	3626169	0.0354	0.23
chr16	90354753	2274813	0.0252	0.2017
chr17	81195210	3912662	0.0482	0.266
chr18	78077248	6959399	0.0891	0.5584
chr19	59128983	2440881	0.0413	0.2998
chr20	63025520	3039756	0.0482	0.26
chr21	48129895	1418850	0.0295	0.2086
chr22	51304566	1194677	0.0233	0.1753
chrMT	16571	67668	4.0835	3.1094
chrX	155270560	9159064	0.059	0.2991
chrY	59373566	309065	0.0052	0.1016

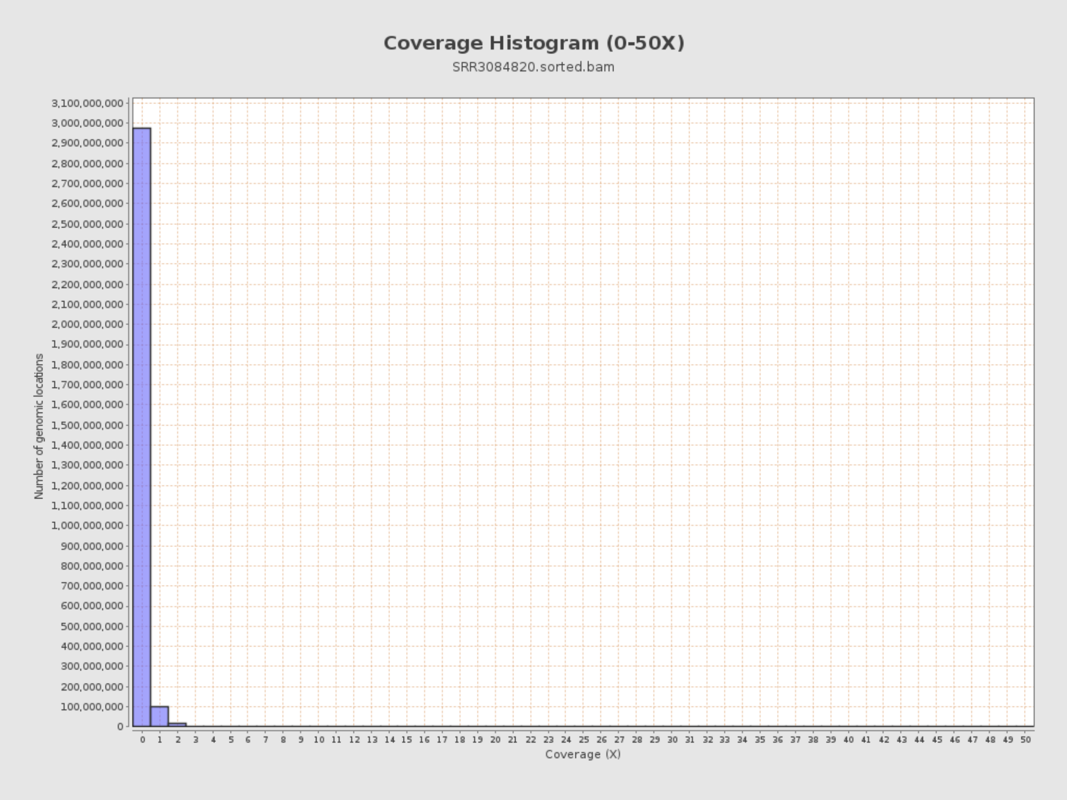
3. Results : Coverage across reference



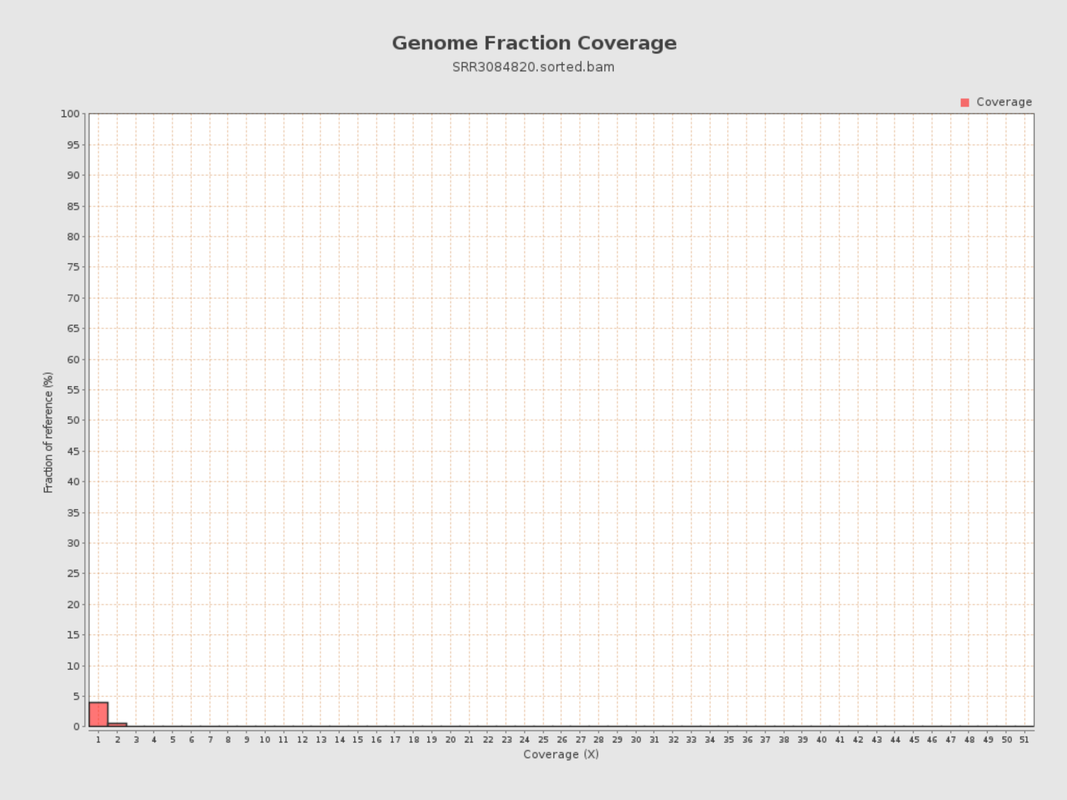
4. Results : Coverage Histogram



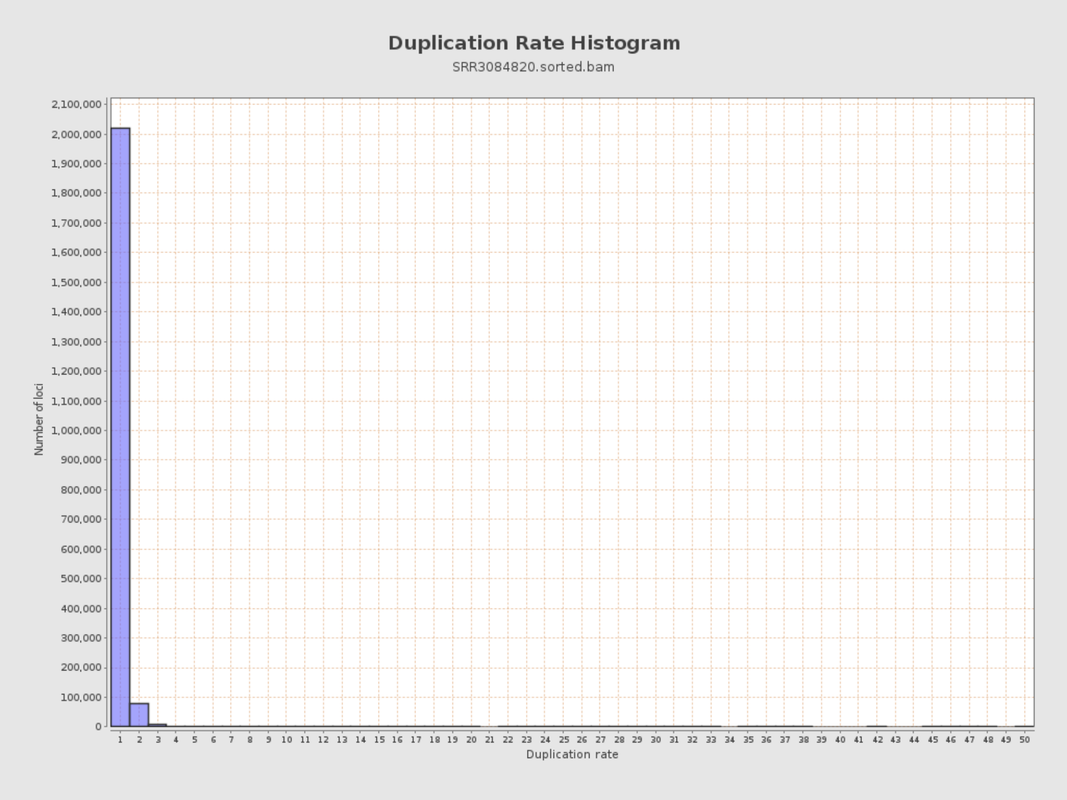
5. Results : Coverage Histogram (0-50X)



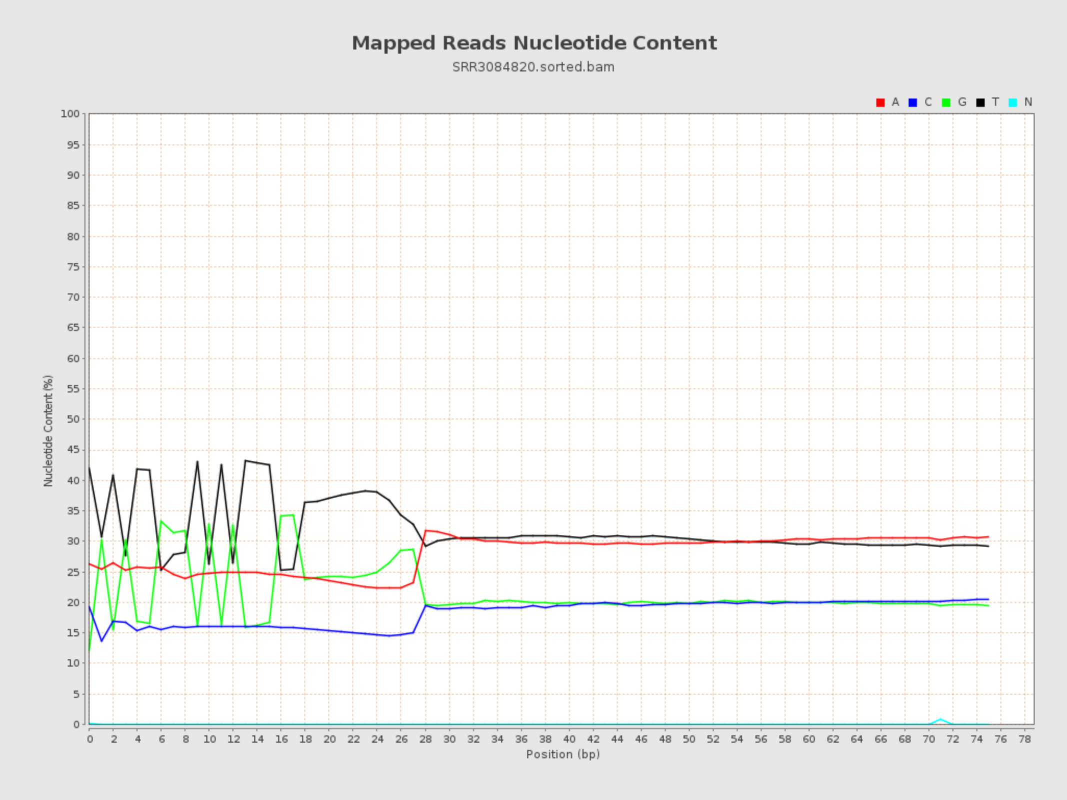
6. Results : Genome Fraction Coverage



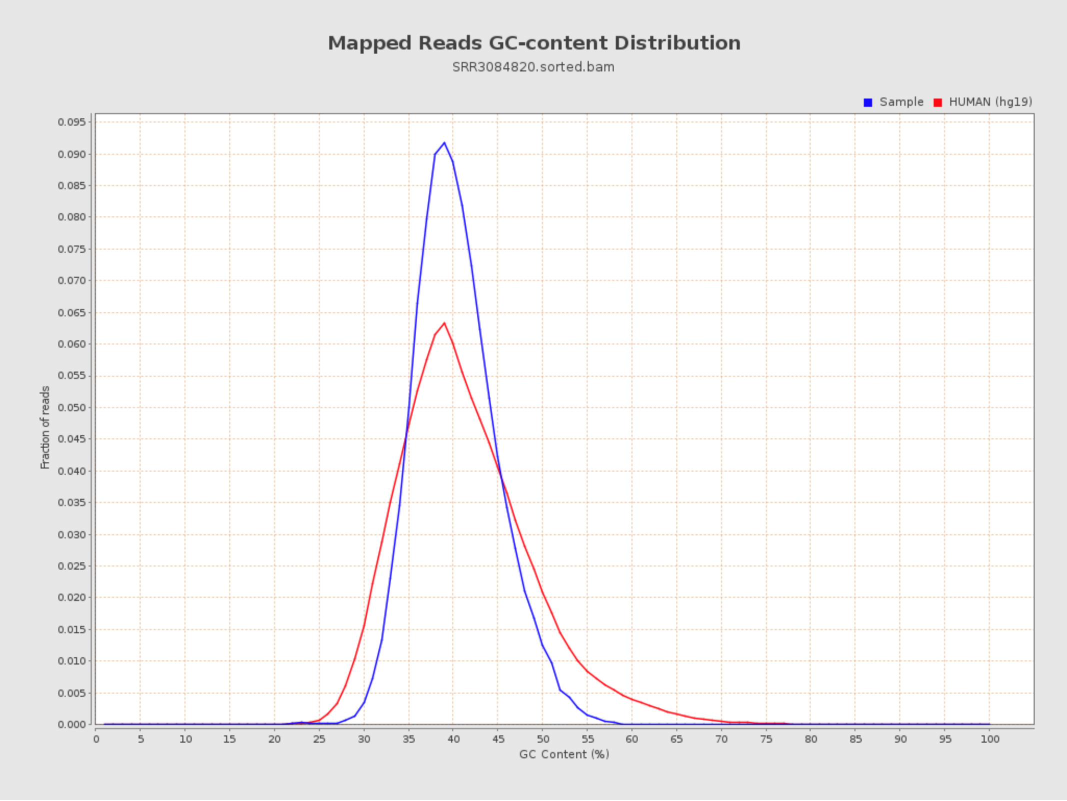
7. Results : Duplication Rate Histogram



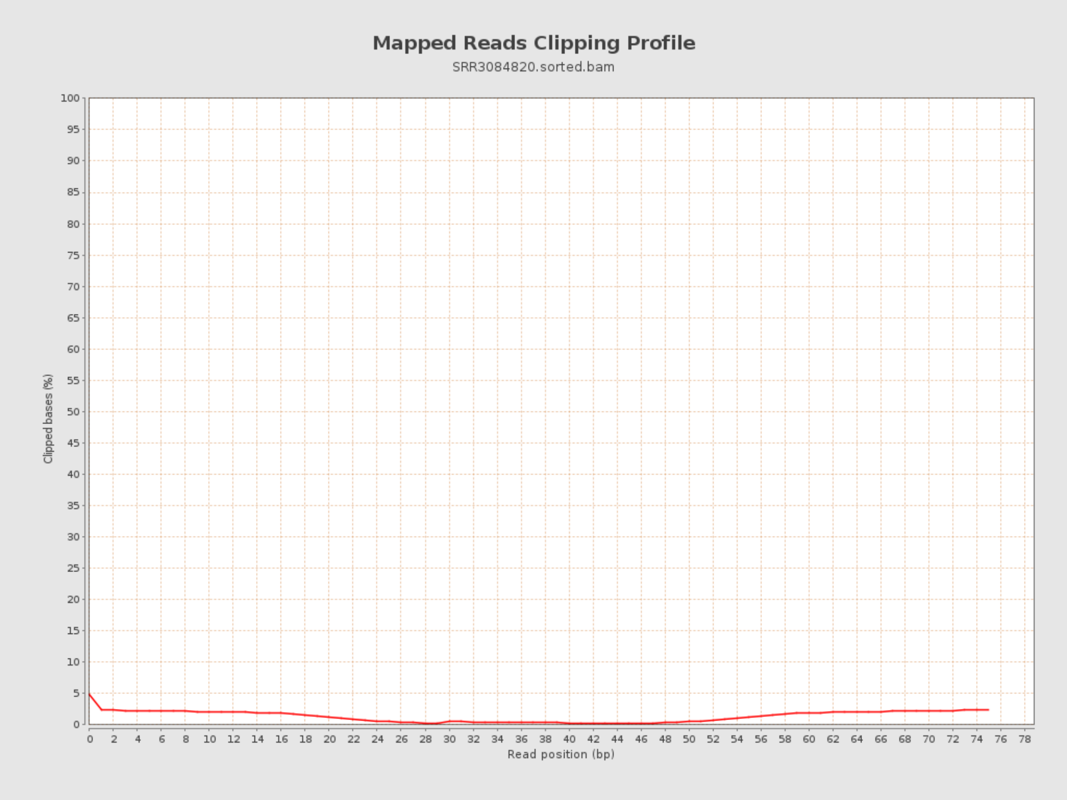
8. Results : Mapped Reads Nucleotide Content



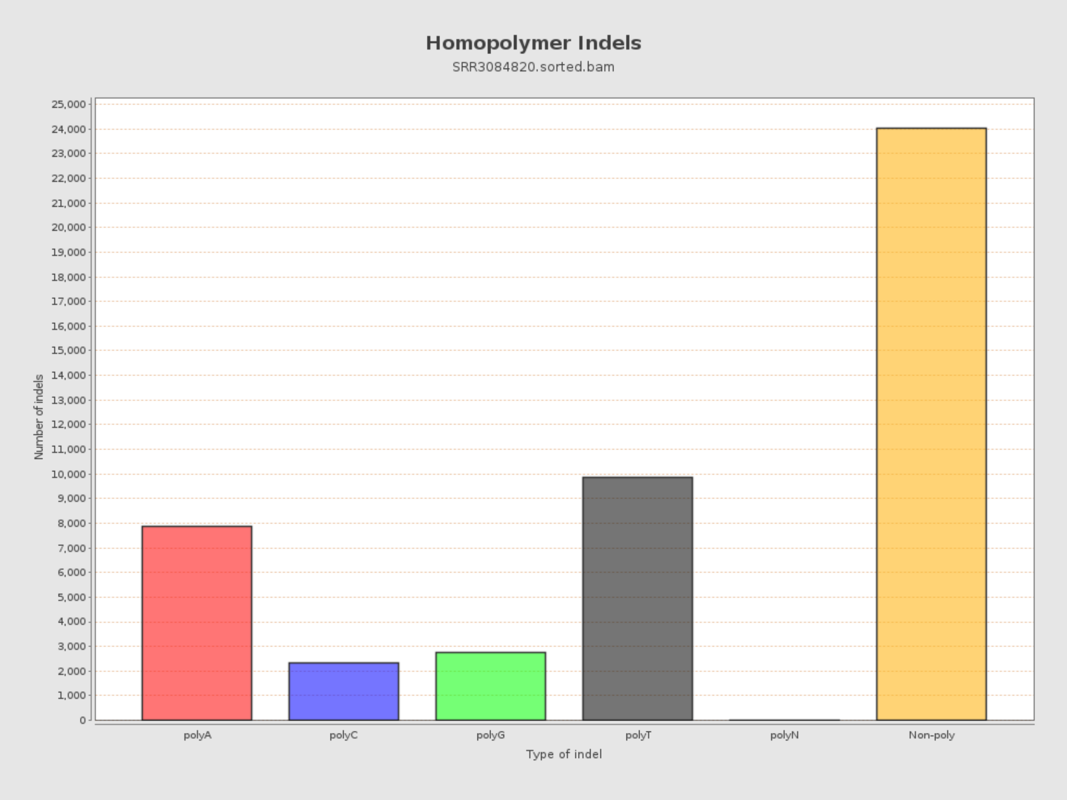
9. Results : Mapped Reads GC-content Distribution



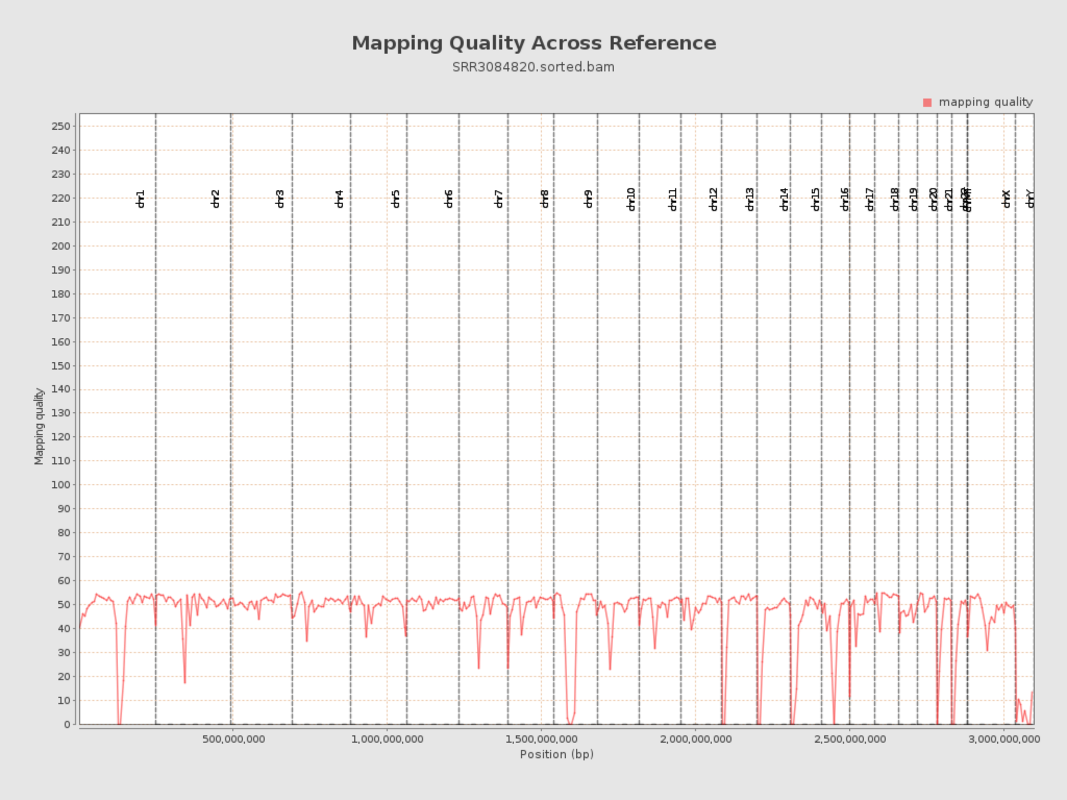
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram