Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 16:13:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084826.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_SRR3084826 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084826.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 16:13:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084826.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,784,754
Mapped reads	1,649,423 / 92.42%
Unmapped reads	135,331 / 7.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,249 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	66,199 / 3.71%
Duplication rate	3.54%
Clipped reads	651,749 / 36.52%

2.2. ACGT Content

Number/percentage of A's	31,312,018 / 28.03%
Number/percentage of C's	20,339,228 / 18.21%
Number/percentage of T's	35,878,779 / 32.12%
Number/percentage of G's	24,160,290 / 21.63%
Number/percentage of N's	15,975 / 0.01%
GC Percentage	39.84%

2.3. Coverage

Mean	0.0361

Standard Deviation	0.2547

2.4. Mapping Quality

Mean Mapping Quality	46.77

2.5. Mismatches and indels

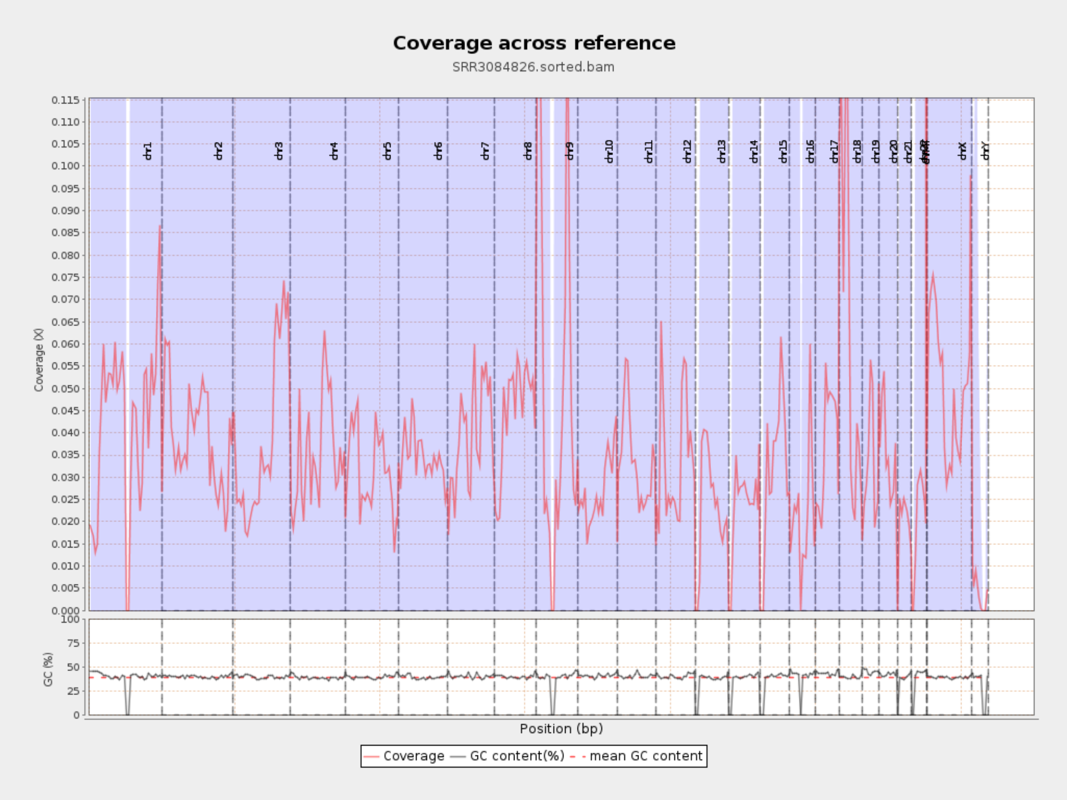
General error rate	0.78%
Mismatches	850,633
Insertions	9,002
Mapped reads with at least one insertion	0.54%
Deletions	26,366
Mapped reads with at least one deletion	1.58%
Homopolymer indels	49.37%

2.6. Chromosome stats

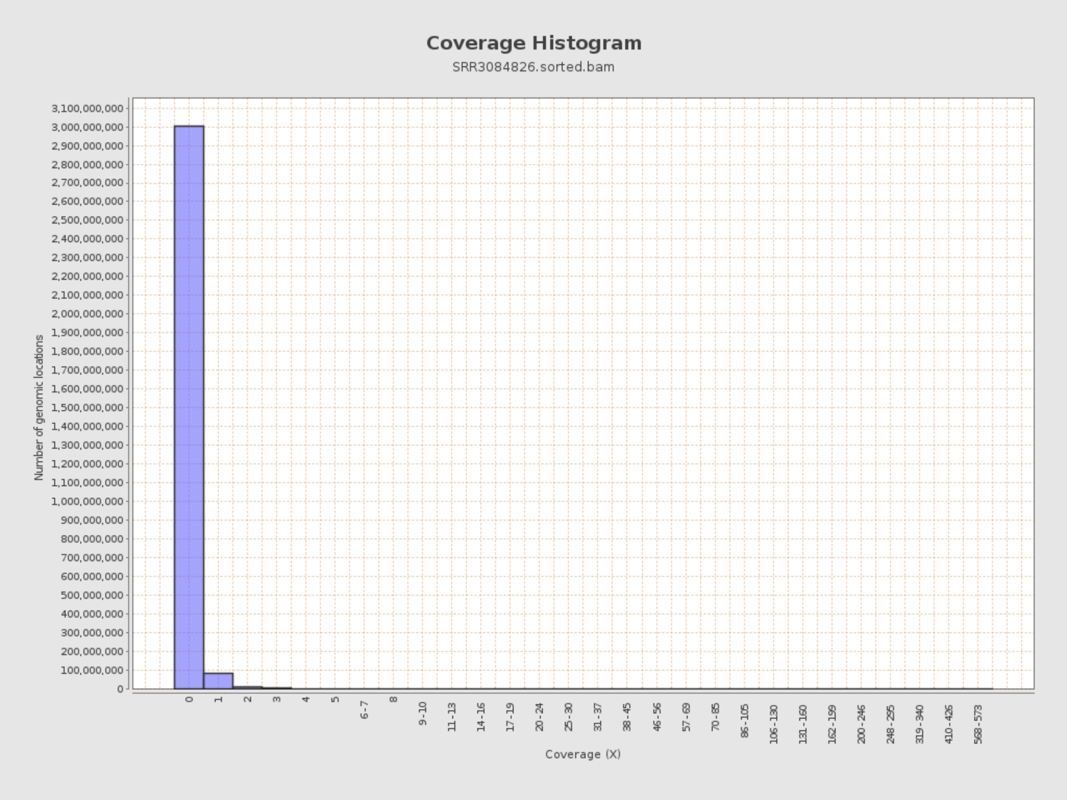
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10508392	0.0422	0.2972
chr2	243199373	9510787	0.0391	0.3531
chr3	198022430	7681200	0.0388	0.2277
chr4	191154276	6812353	0.0356	0.2188
chr5	180915260	5705492	0.0315	0.2045
chr6	171115067	5897477	0.0345	0.2244
chr7	159138663	6345080	0.0399	0.2786

chr8	146364022	6514401	0.0445	0.3283
chr9	141213431	7240454	0.0513	0.2996
chr10	135534747	3640215	0.0269	0.194
chr11	135006516	4570709	0.0339	0.2299
chr12	133851895	4551975	0.034	0.2125
chr13	115169878	2649411	0.023	0.174
chr14	107349540	2463944	0.023	0.1779
chr15	102531392	3289685	0.0321	0.2115
chr16	90354753	1988446	0.022	0.1765
chr17	81195210	3087046	0.038	0.2279
chr18	78077248	4997663	0.064	0.4316
chr19	59128983	2002855	0.0339	0.2369
chr20	63025520	2250057	0.0357	0.2208
chr21	48129895	947404	0.0197	0.1644
chr22	51304566	998821	0.0195	0.1577
chrMT	16571	35075	2.1166	1.8011
chrX	155270560	7837482	0.0505	0.2653
chrY	59373566	223210	0.0038	0.0796

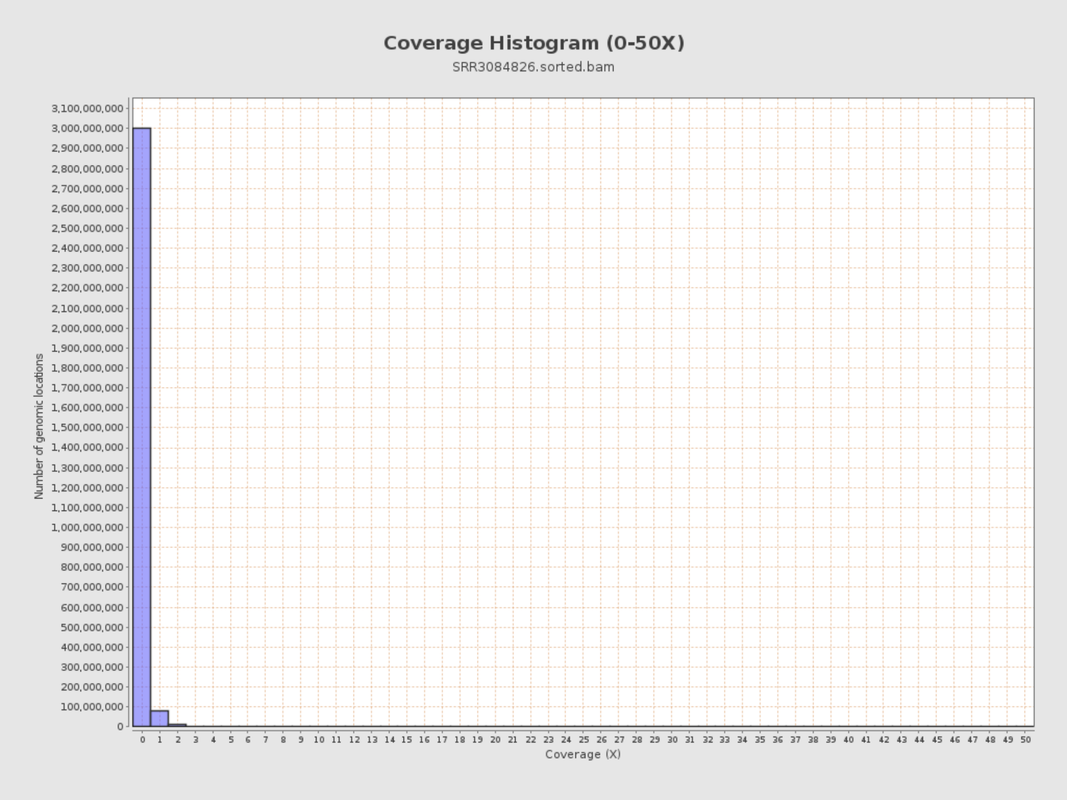
3. Results : Coverage across reference



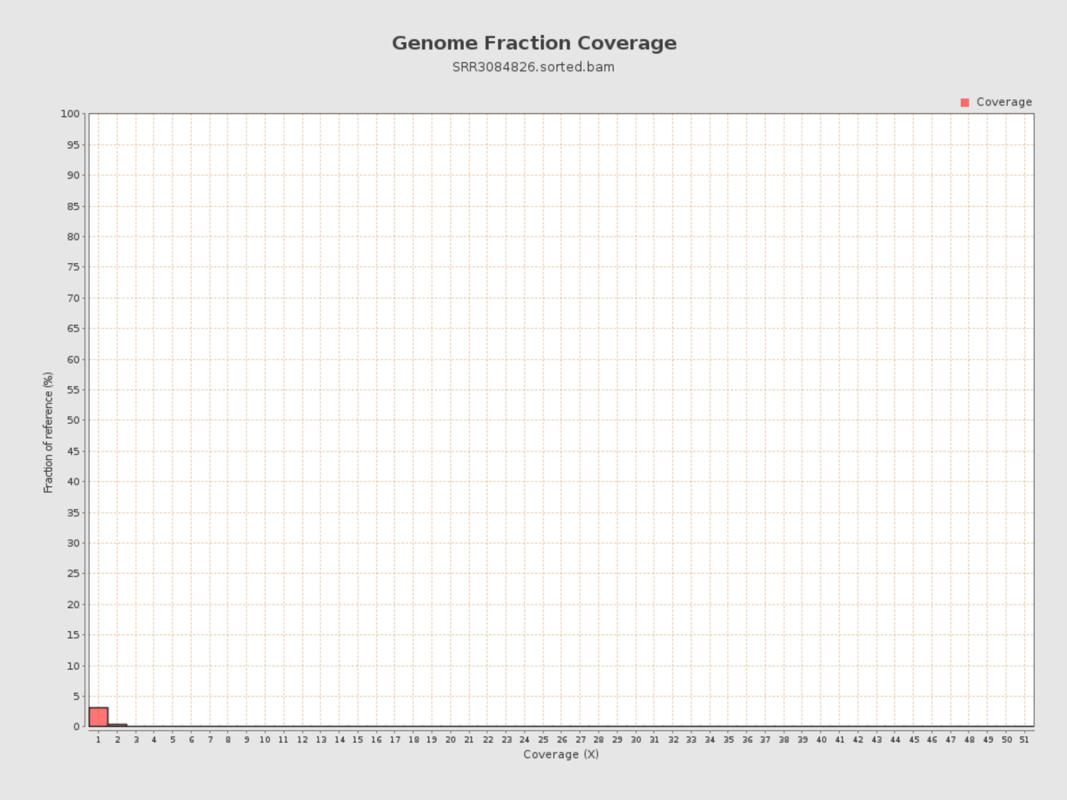
4. Results : Coverage Histogram



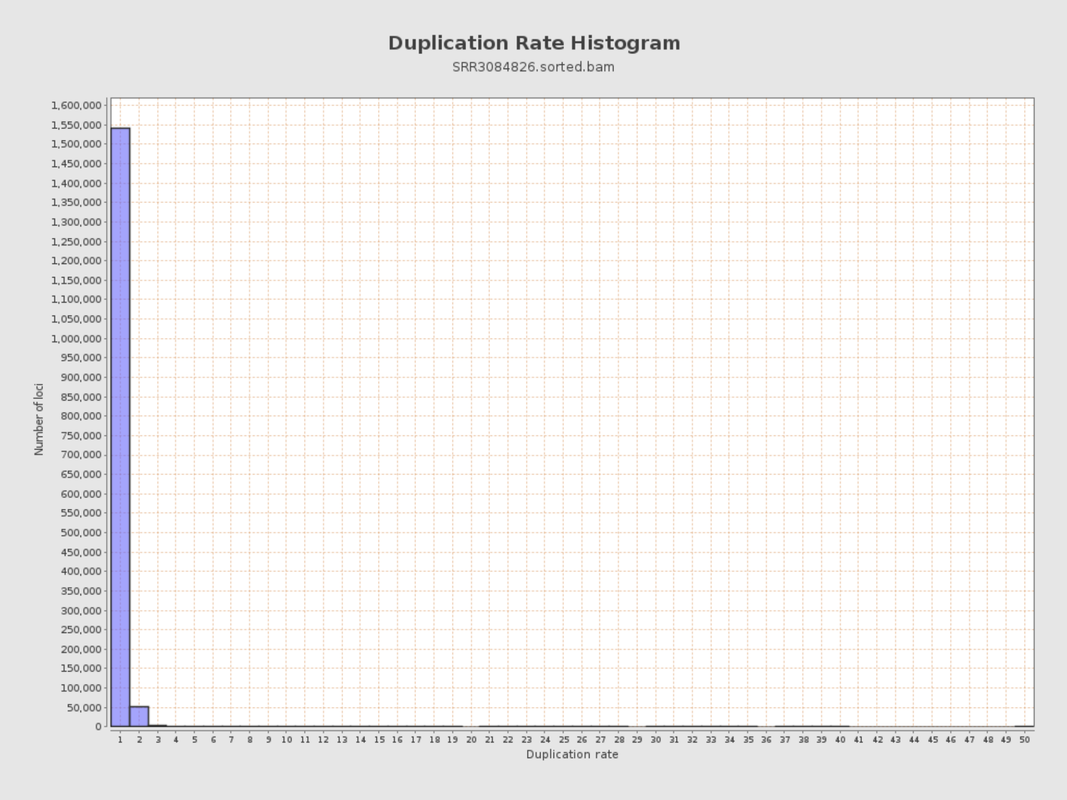
5. Results : Coverage Histogram (0-50X)



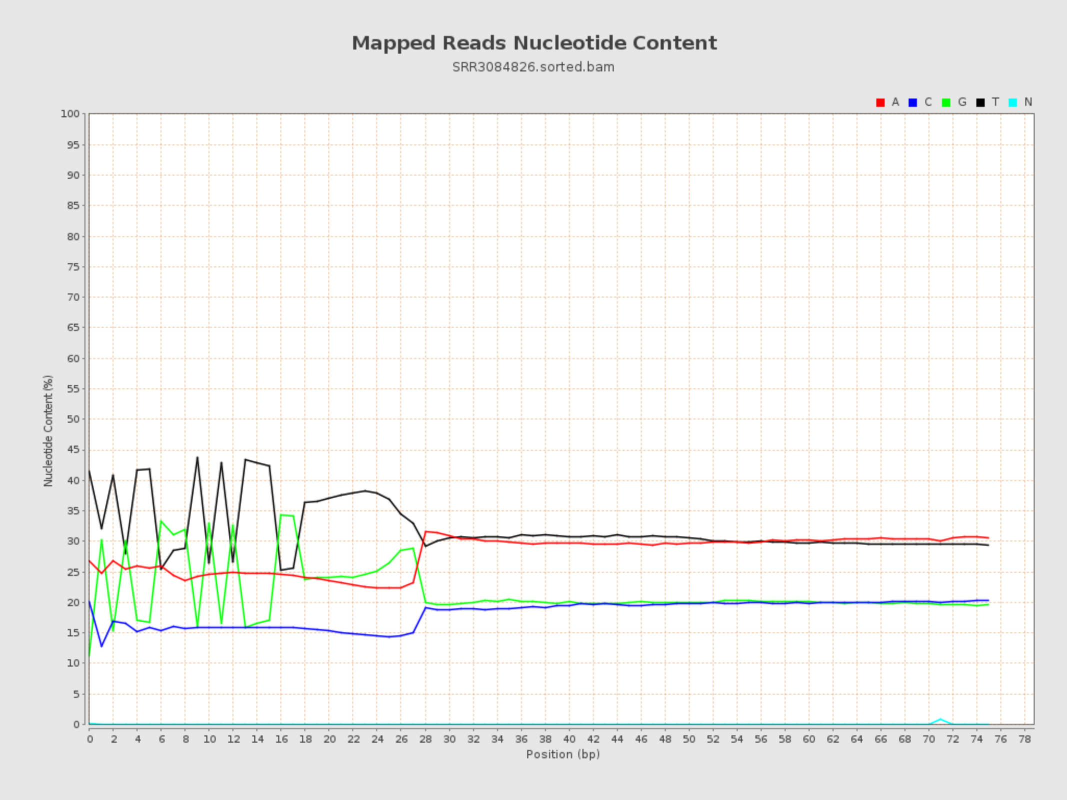
6. Results : Genome Fraction Coverage



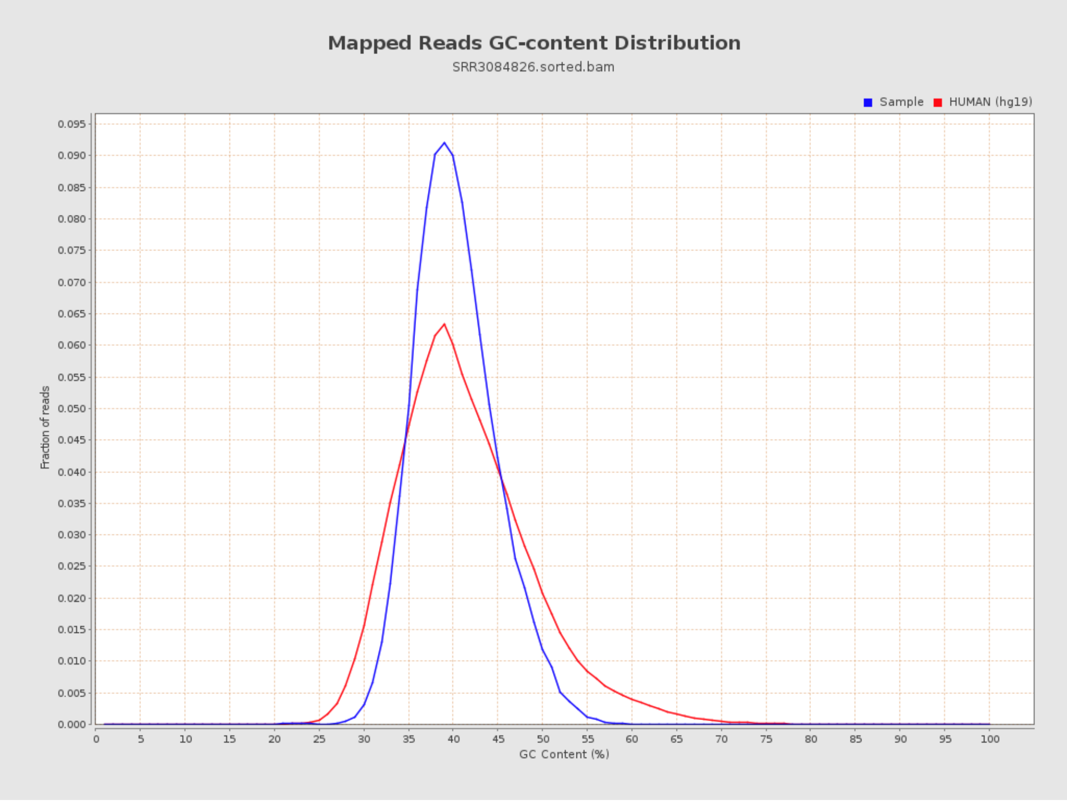
7. Results : Duplication Rate Histogram



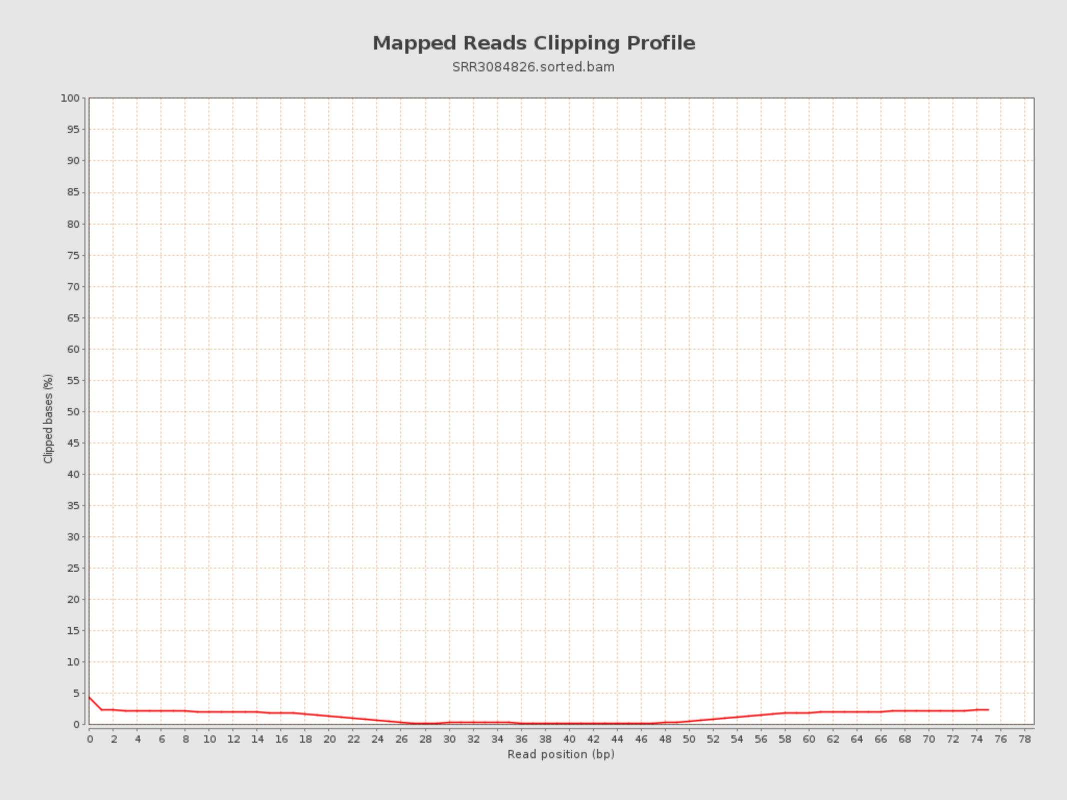
8. Results : Mapped Reads Nucleotide Content



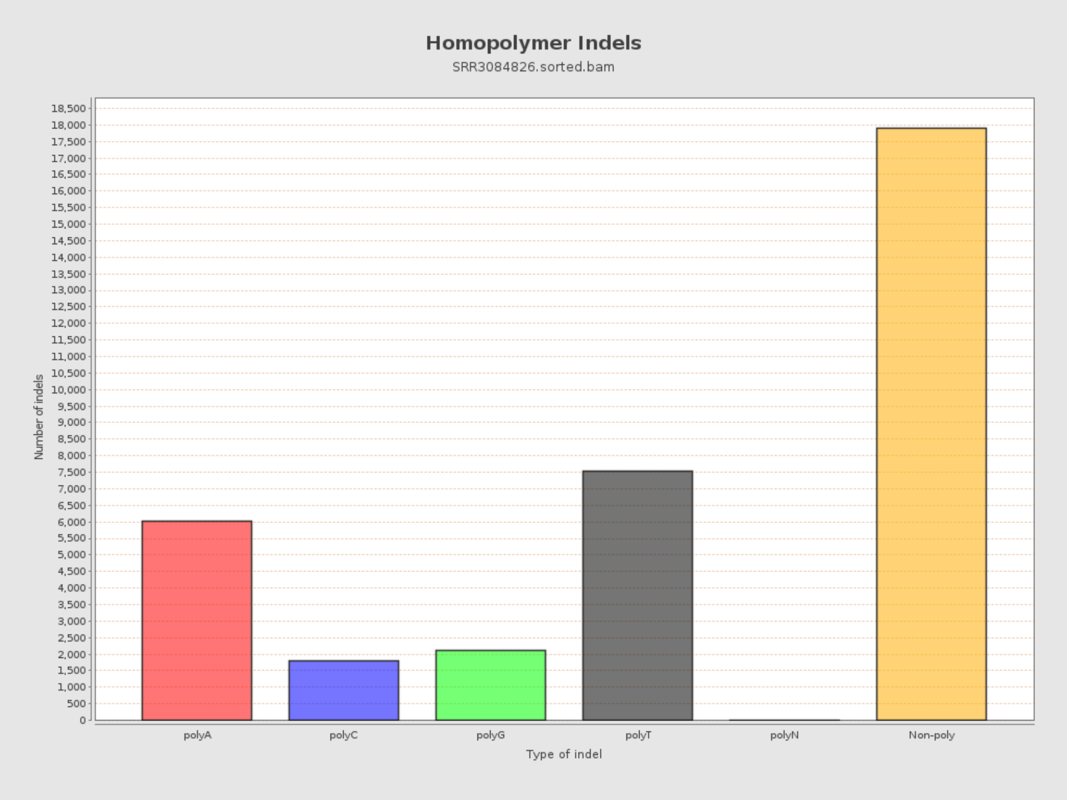
9. Results : Mapped Reads GC-content Distribution



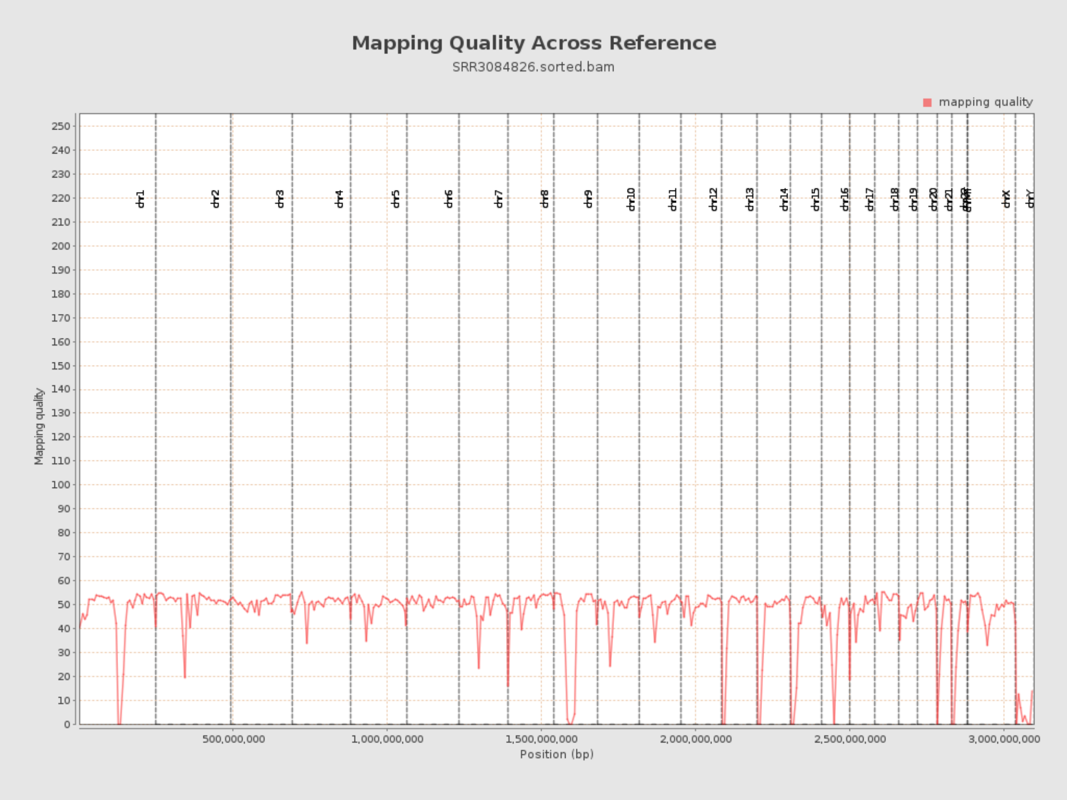
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram