Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 15:20:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084810.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_SRR3084810 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084810.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 15:20:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084810.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,215,821
Mapped reads	1,974,728 / 89.12%
Unmapped reads	241,093 / 10.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,418 / 0.97%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	107,446 / 4.85%
Duplication rate	4.73%
Clipped reads	893,226 / 40.31%

2.2. ACGT Content

Number/percentage of A's	35,534,095 / 27.03%
Number/percentage of C's	24,655,269 / 18.76%
Number/percentage of T's	41,249,607 / 31.38%
Number/percentage of G's	29,998,458 / 22.82%
Number/percentage of N's	18,466 / 0.01%
GC Percentage	41.58%

2.3. Coverage

Mean	0.0425

Standard Deviation	0.3021

2.4. Mapping Quality

Mean Mapping Quality	45.51

2.5. Mismatches and indels

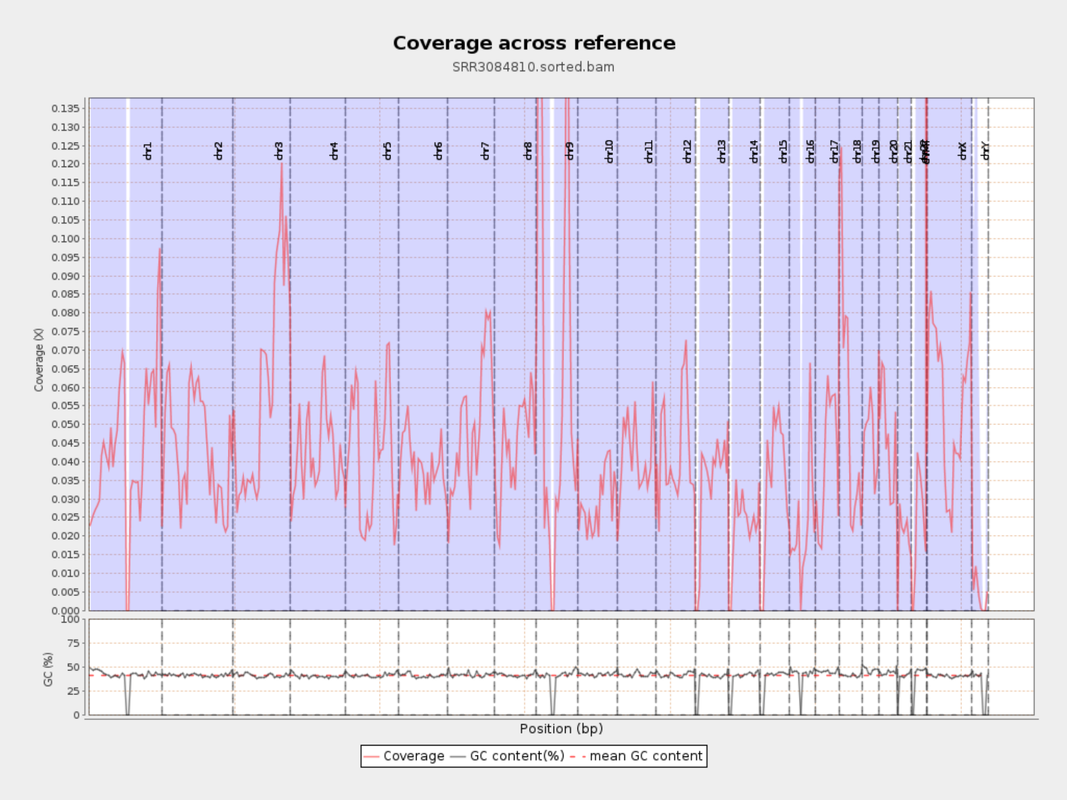
General error rate	0.79%
Mismatches	1,022,517
Insertions	10,204
Mapped reads with at least one insertion	0.51%
Deletions	29,985
Mapped reads with at least one deletion	1.5%
Homopolymer indels	47.8%

2.6. Chromosome stats

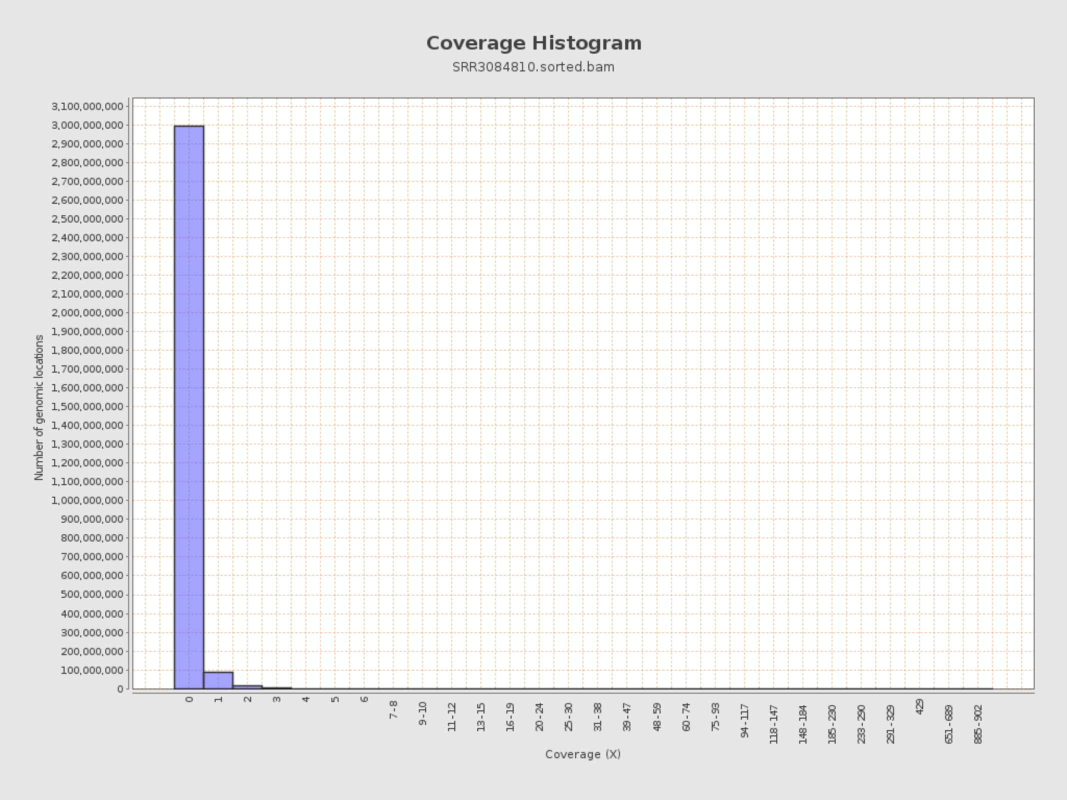
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10941971	0.0439	0.3742
chr2	243199373	10612065	0.0436	0.4687
chr3	198022430	11789519	0.0595	0.2975
chr4	191154276	8134425	0.0426	0.2523
chr5	180915260	7428791	0.0411	0.2482
chr6	171115067	6636767	0.0388	0.2595
chr7	159138663	7985699	0.0502	0.3321

chr8	146364022	6430698	0.0439	0.2882
chr9	141213431	9797964	0.0694	0.3738
chr10	135534747	3954217	0.0292	0.2157
chr11	135006516	5603292	0.0415	0.2838
chr12	133851895	5772722	0.0431	0.2524
chr13	115169878	3816571	0.0331	0.221
chr14	107349540	2353085	0.0219	0.1866
chr15	102531392	3583597	0.035	0.2344
chr16	90354753	2078629	0.023	0.1894
chr17	81195210	3371048	0.0415	0.2513
chr18	78077248	4342201	0.0556	0.4386
chr19	59128983	2817280	0.0476	0.318
chr20	63025520	2973286	0.0472	0.2678
chr21	48129895	954127	0.0198	0.1773
chr22	51304566	1109719	0.0216	0.1752
chrMT	16571	22629	1.3656	1.4368
chrX	155270560	8731226	0.0562	0.2959
chrY	59373566	263892	0.0044	0.0943

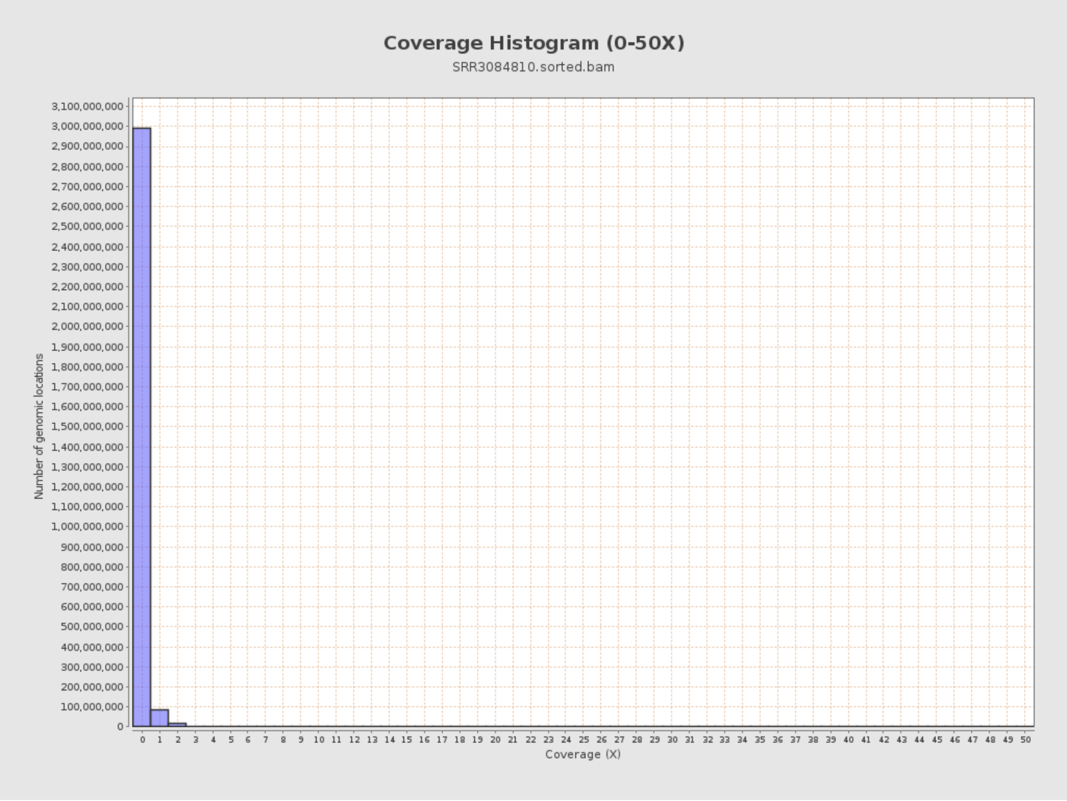
3. Results : Coverage across reference



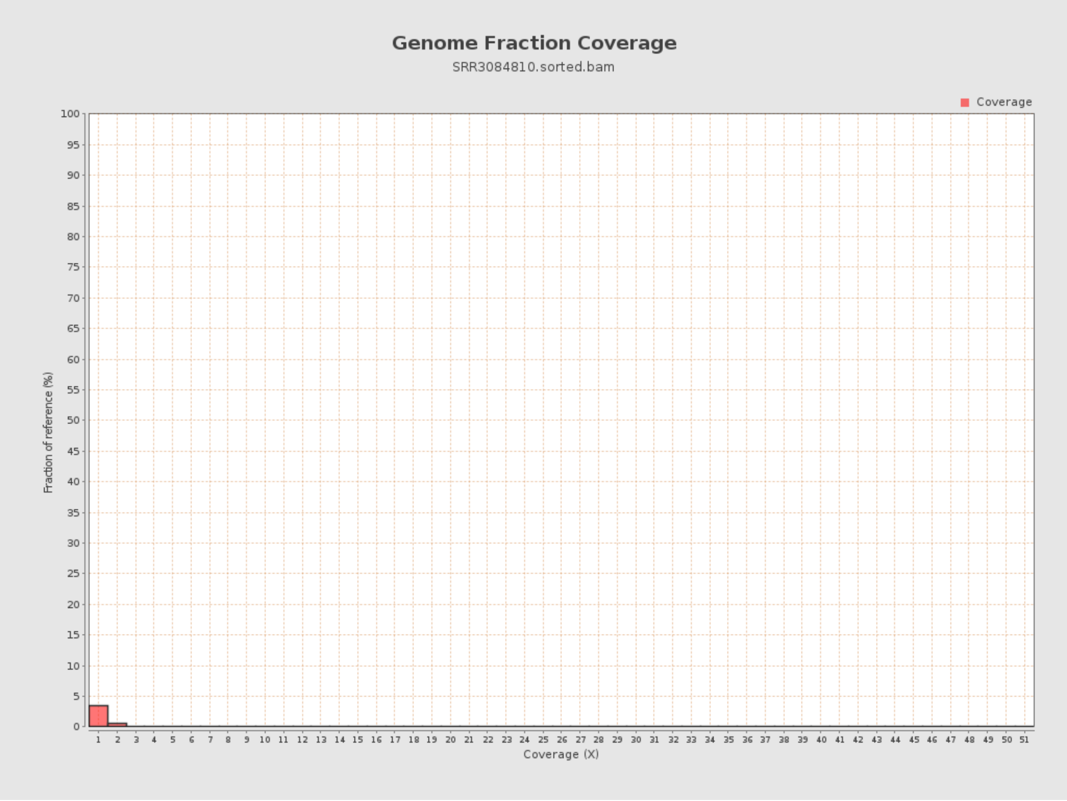
4. Results : Coverage Histogram



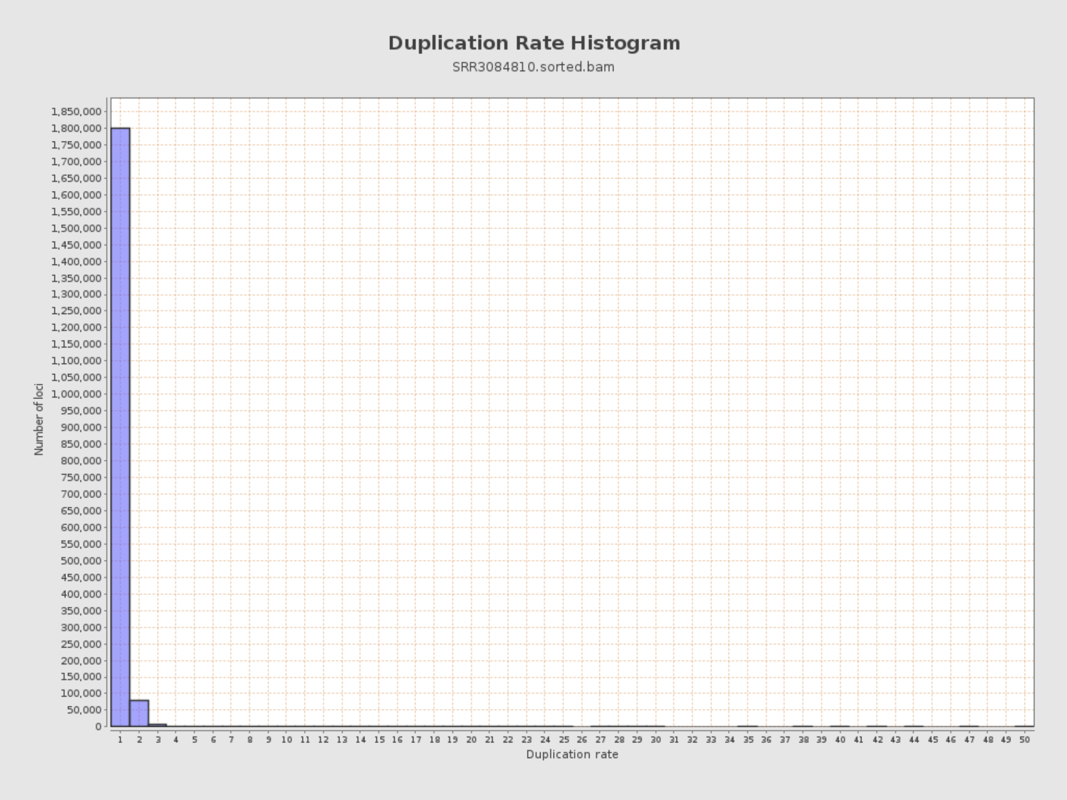
5. Results : Coverage Histogram (0-50X)



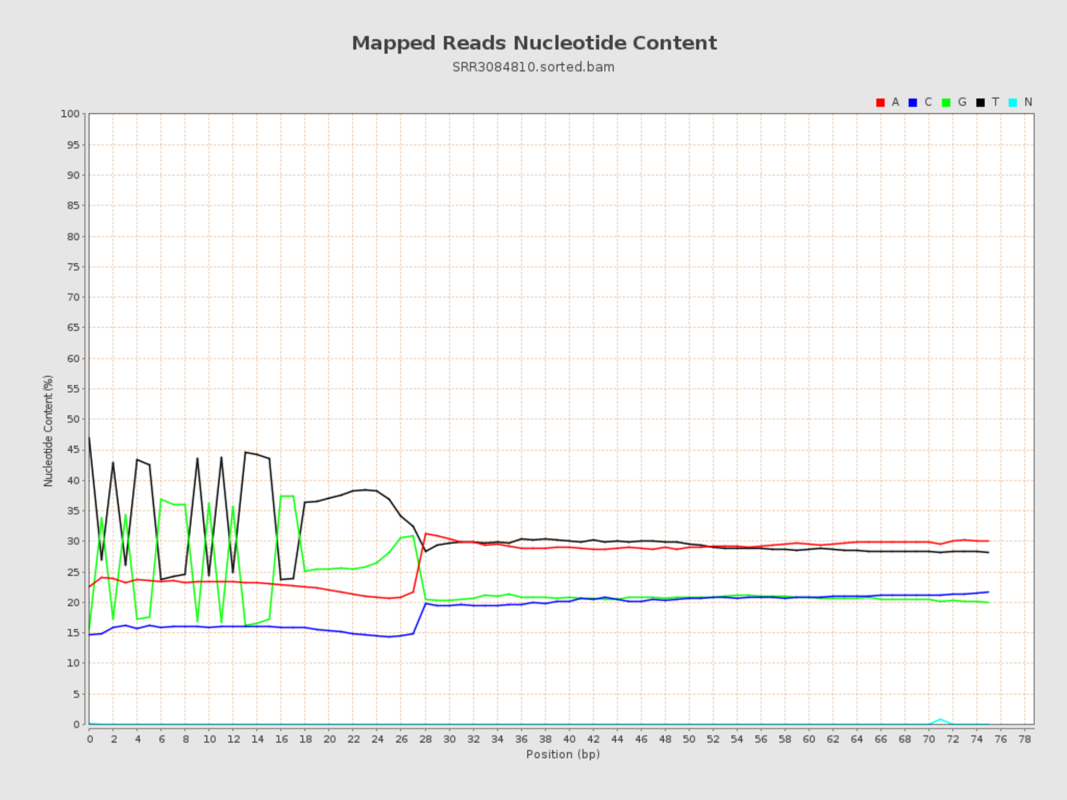
6. Results : Genome Fraction Coverage



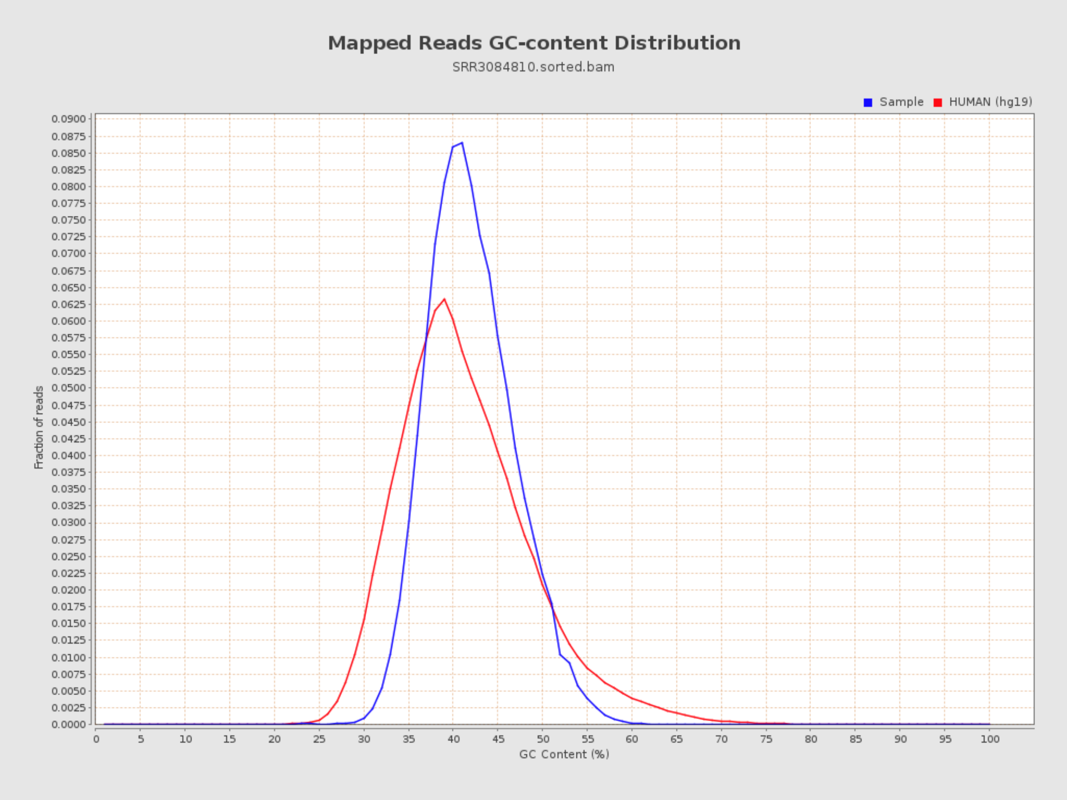
7. Results : Duplication Rate Histogram



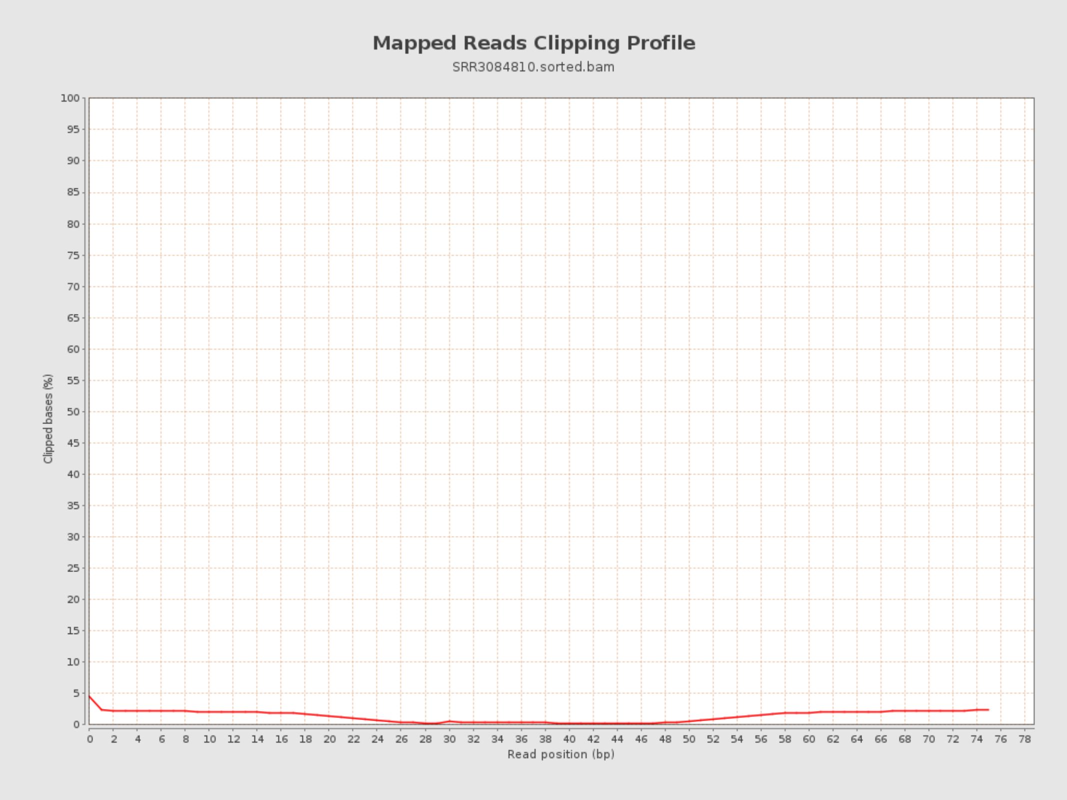
8. Results : Mapped Reads Nucleotide Content



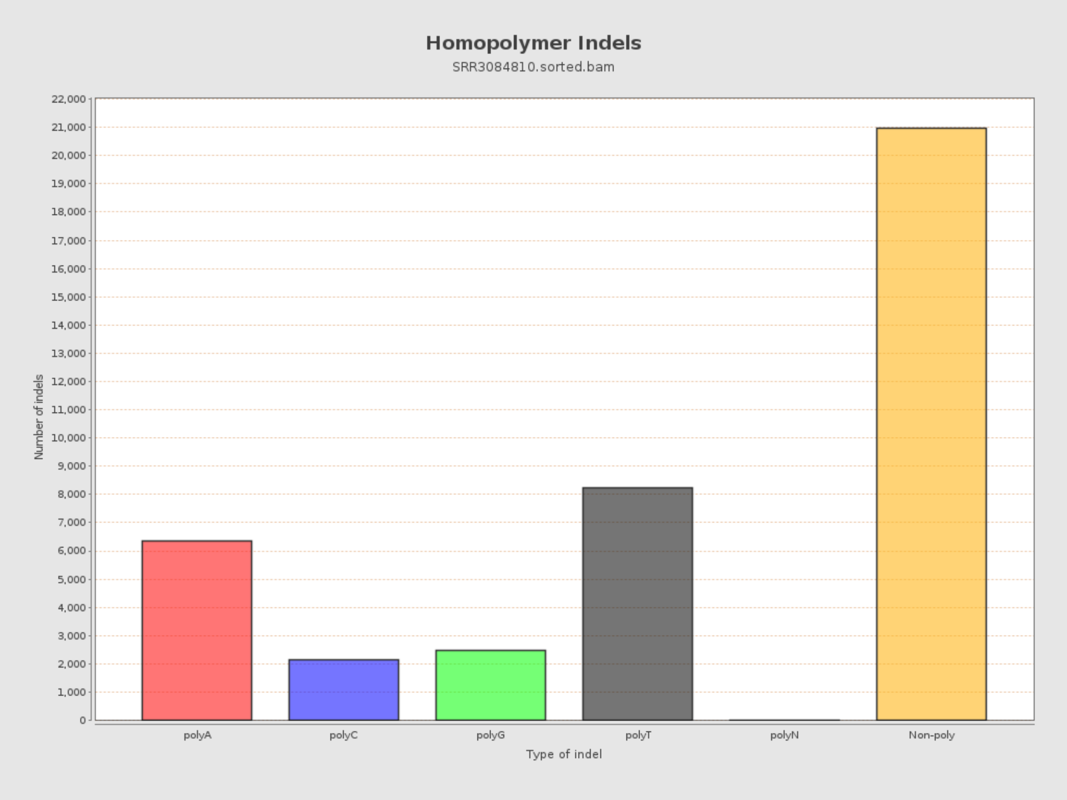
9. Results : Mapped Reads GC-content Distribution



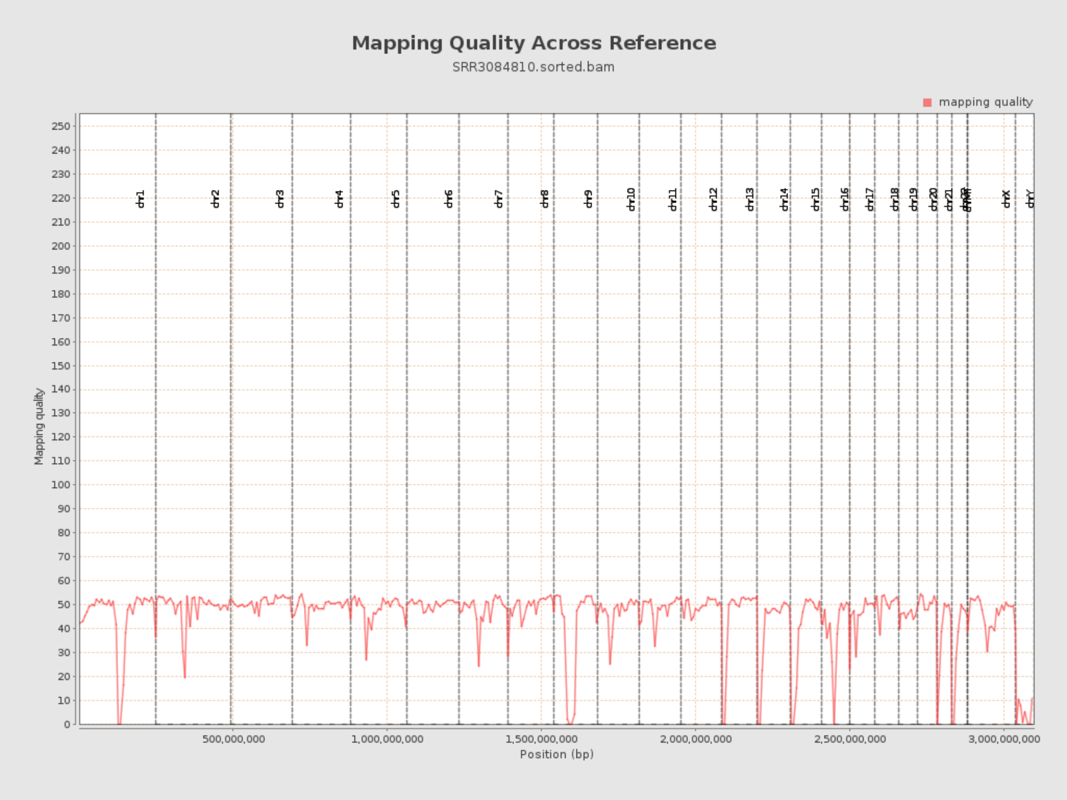
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram