Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:14:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081020.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_SRR3081020 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081020.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:14:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081020.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,880,881
Mapped reads	2,311,151 / 80.22%
Unmapped reads	569,730 / 19.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,709 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	76,810 / 2.67%
Duplication rate	2.52%
Clipped reads	1,445,777 / 50.19%

2.2. ACGT Content

Number/percentage of A's	40,508,297 / 28.44%
Number/percentage of C's	28,999,523 / 20.36%
Number/percentage of T's	40,991,850 / 28.78%
Number/percentage of G's	31,932,284 / 22.42%
Number/percentage of N's	1,841 / 0%
GC Percentage	42.78%

2.3. Coverage

Mean	0.046

Standard Deviation	0.3534

2.4. Mapping Quality

Mean Mapping Quality	44.76

2.5. Mismatches and indels

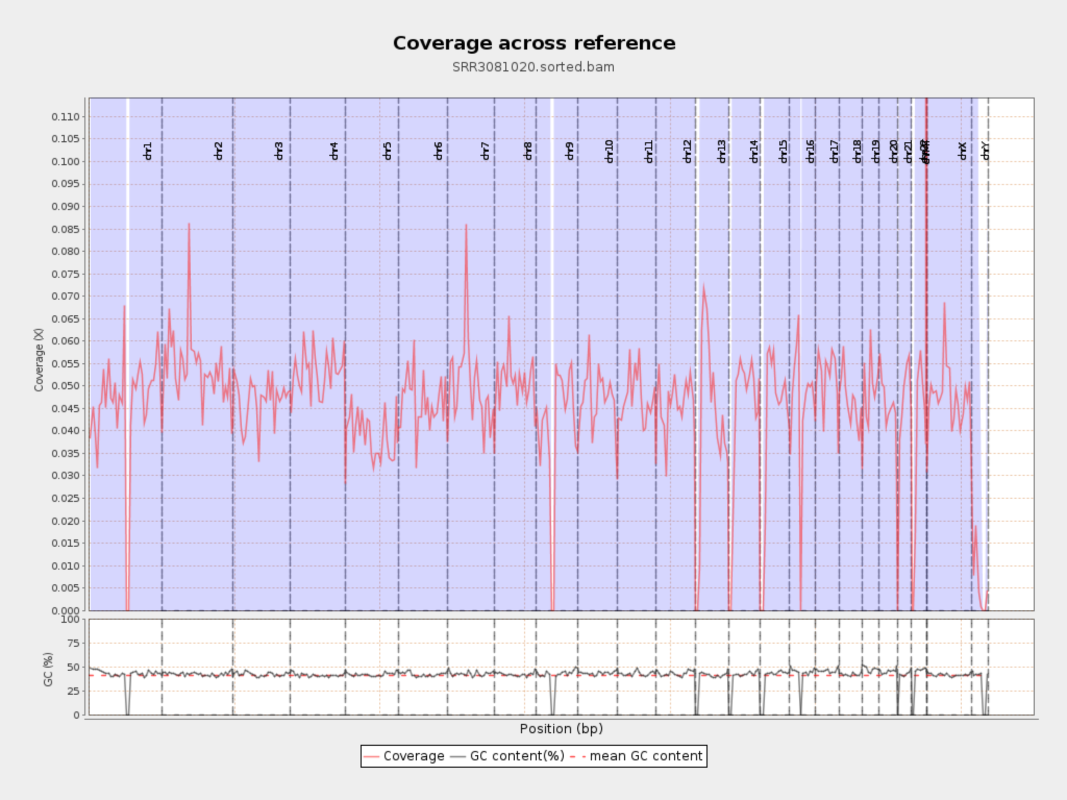
General error rate	0.75%
Mismatches	1,054,434
Insertions	9,861
Mapped reads with at least one insertion	0.42%
Deletions	28,156
Mapped reads with at least one deletion	1.21%
Homopolymer indels	45.22%

2.6. Chromosome stats

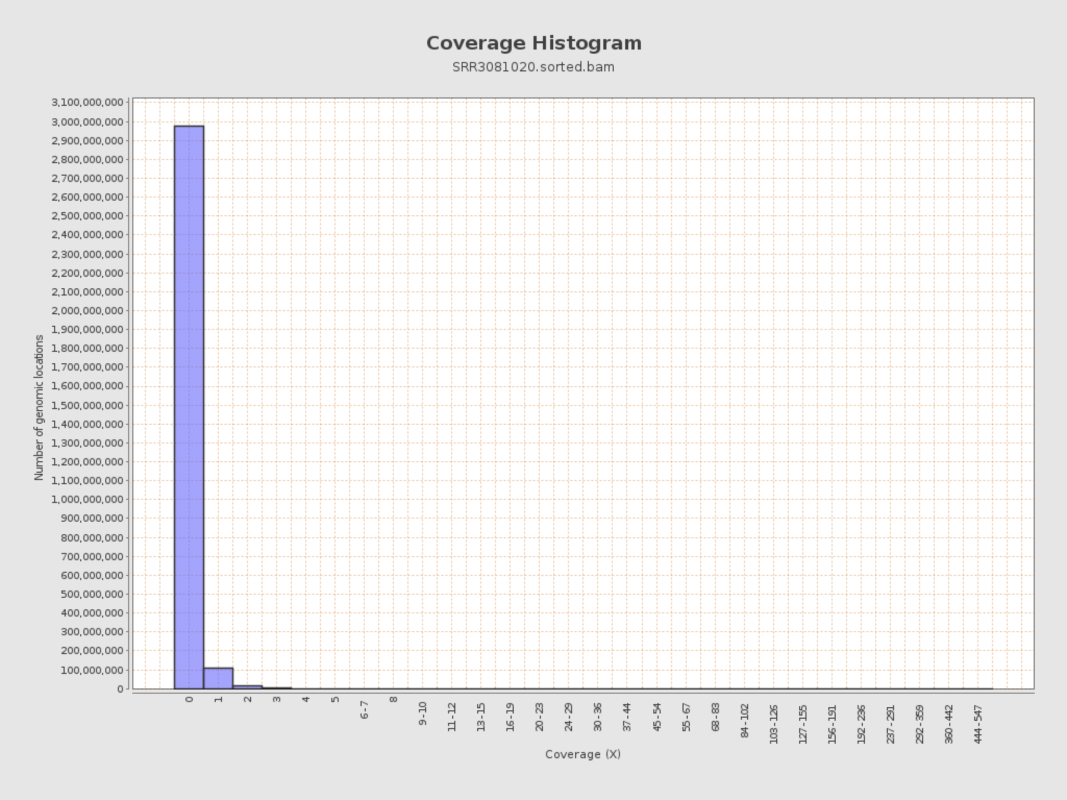
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11368229	0.0456	0.4788
chr2	243199373	13240510	0.0544	0.3978
chr3	198022430	9235043	0.0466	0.2432
chr4	191154276	10185074	0.0533	0.2755
chr5	180915260	7071883	0.0391	0.2252
chr6	171115067	7957177	0.0465	0.3152
chr7	159138663	8070617	0.0507	0.6151

chr8	146364022	7488967	0.0512	0.3516
chr9	141213431	5724225	0.0405	0.3544
chr10	135534747	6460387	0.0477	0.3057
chr11	135006516	6363915	0.0471	0.3527
chr12	133851895	6204648	0.0464	0.2486
chr13	115169878	4741142	0.0412	0.2308
chr14	107349540	4564093	0.0425	0.2535
chr15	102531392	4255341	0.0415	0.2434
chr16	90354753	4176308	0.0462	0.2744
chr17	81195210	4203419	0.0518	0.2938
chr18	78077248	3660214	0.0469	0.7081
chr19	59128983	2927092	0.0495	0.3976
chr20	63025520	2896200	0.046	0.2513
chr21	48129895	2099999	0.0436	0.2578
chr22	51304566	1790544	0.0349	0.2104
chrMT	16571	18000	1.0862	1.2472
chrX	155270560	7412531	0.0477	0.2857
chrY	59373566	367045	0.0062	0.1318

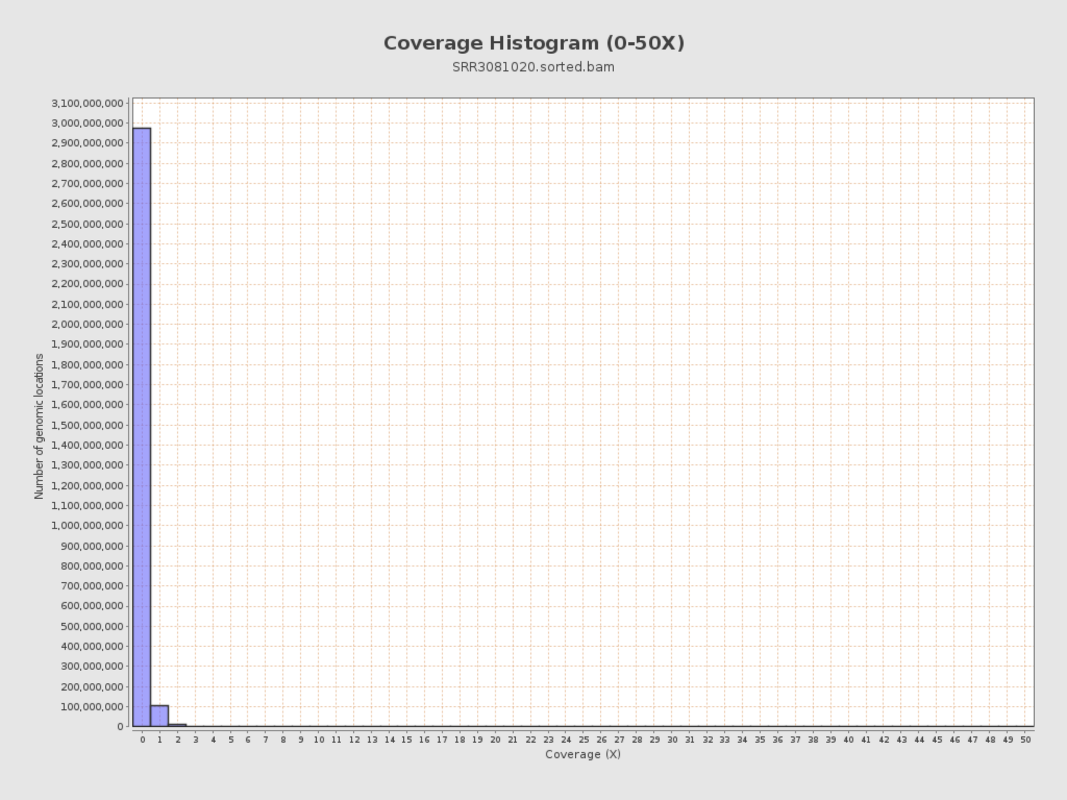
3. Results : Coverage across reference



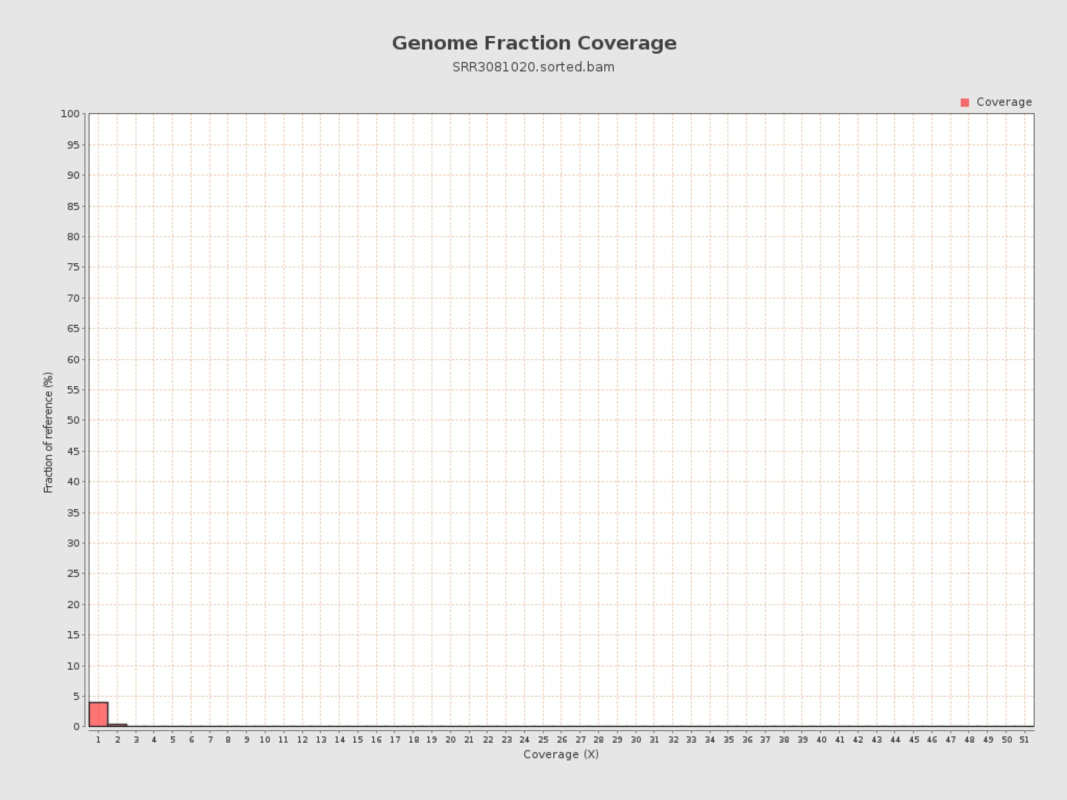
4. Results : Coverage Histogram



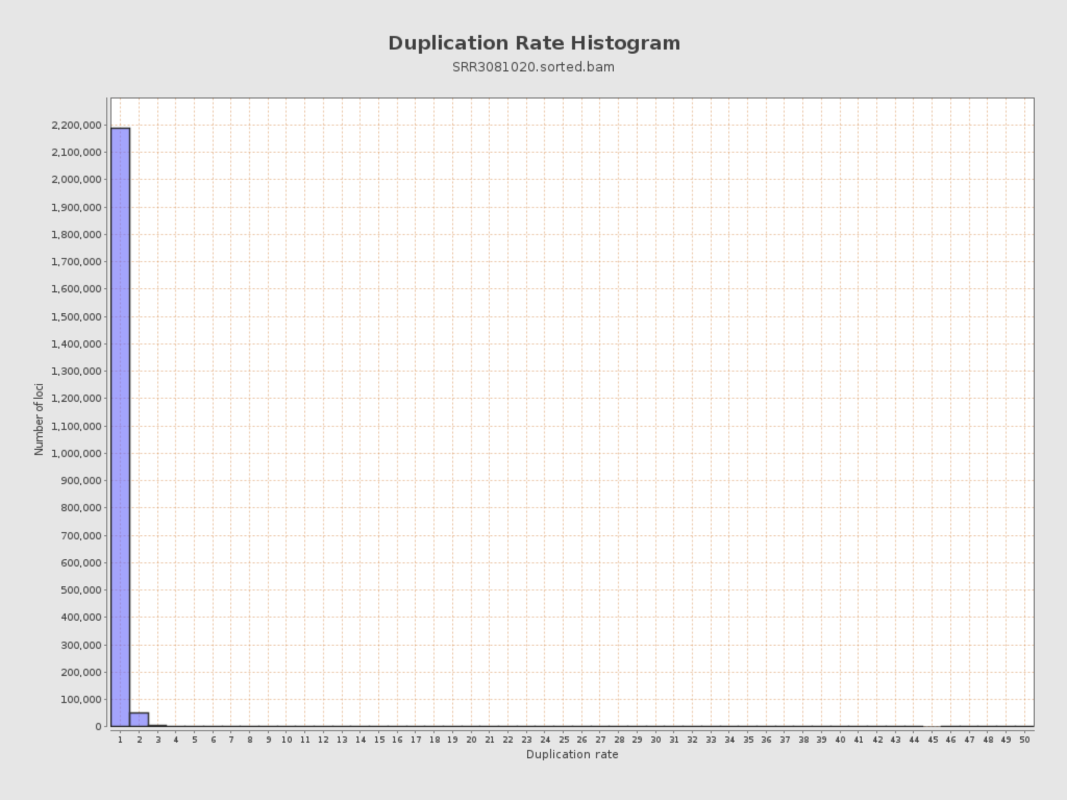
5. Results : Coverage Histogram (0-50X)



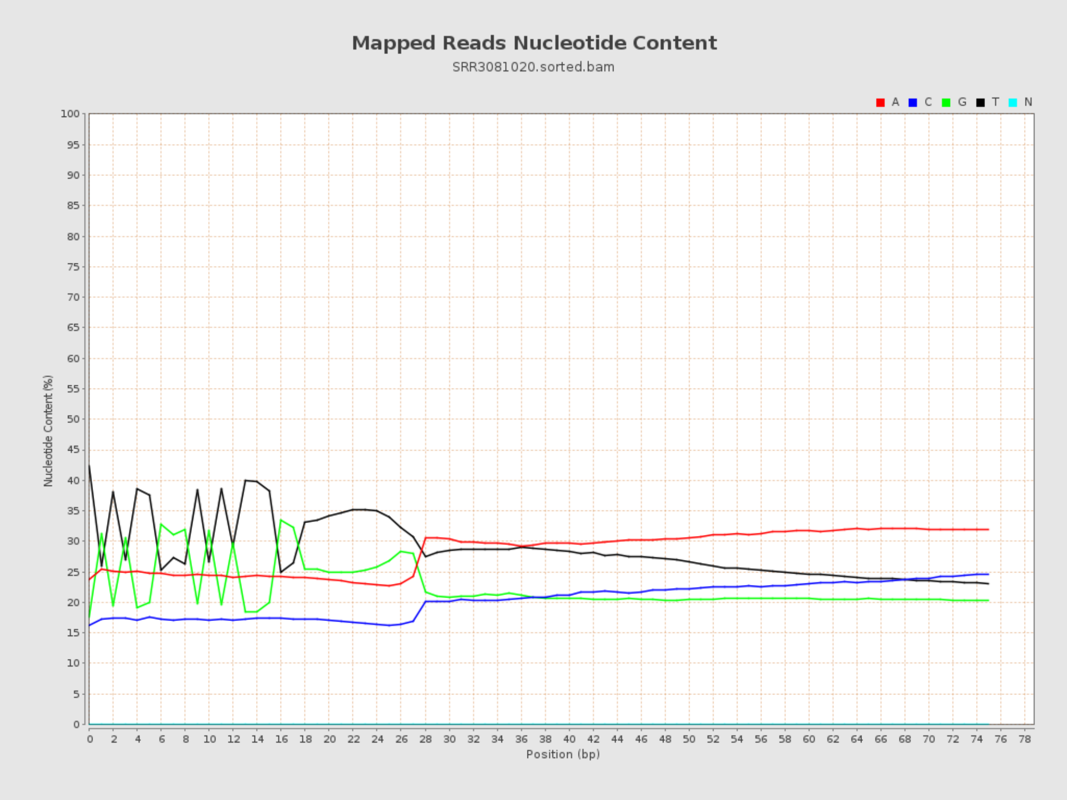
6. Results : Genome Fraction Coverage



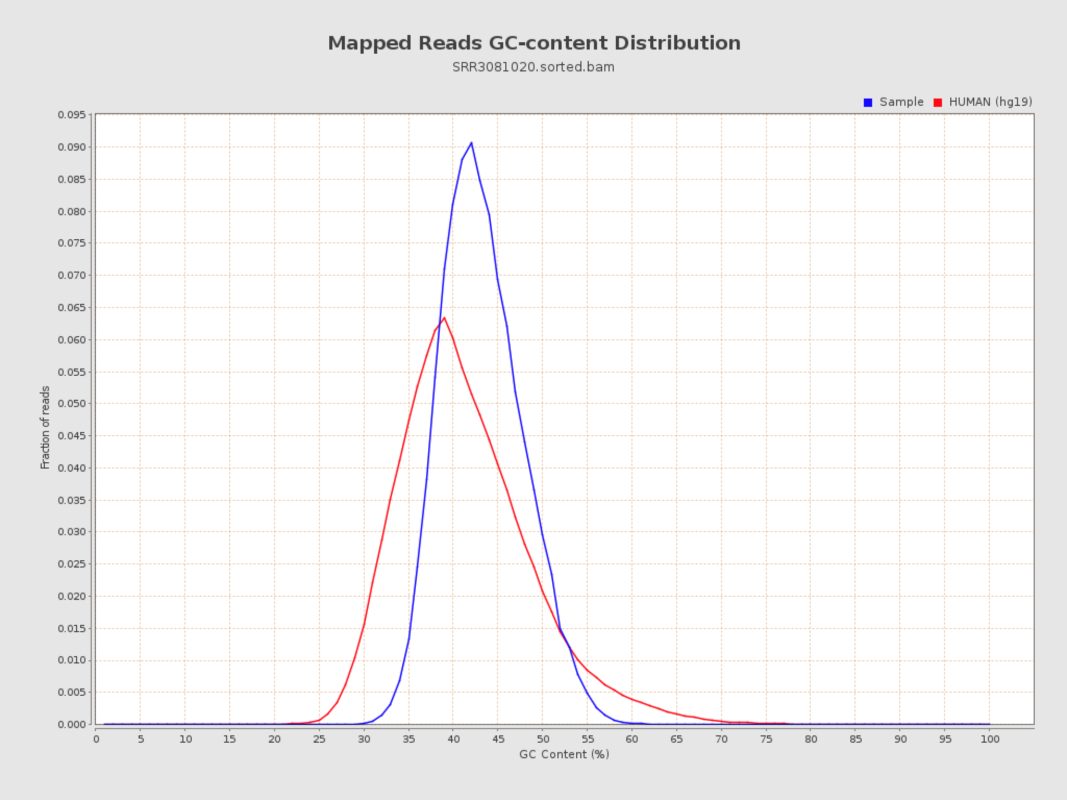
7. Results : Duplication Rate Histogram



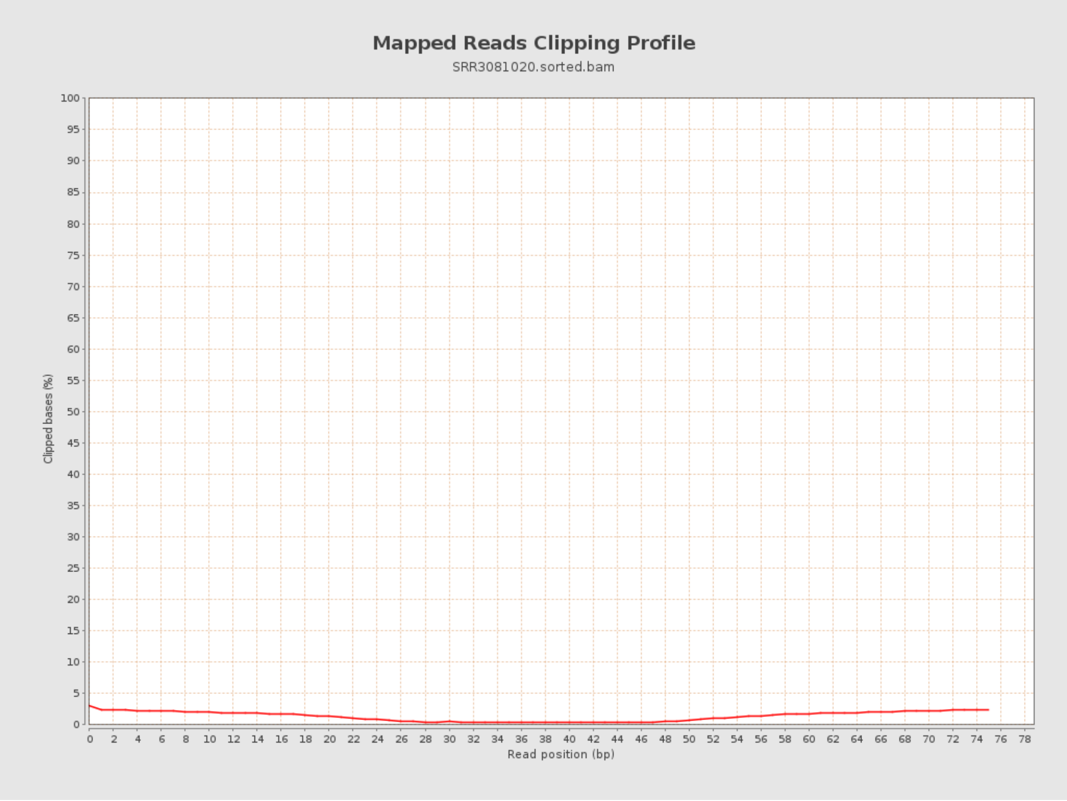
8. Results : Mapped Reads Nucleotide Content



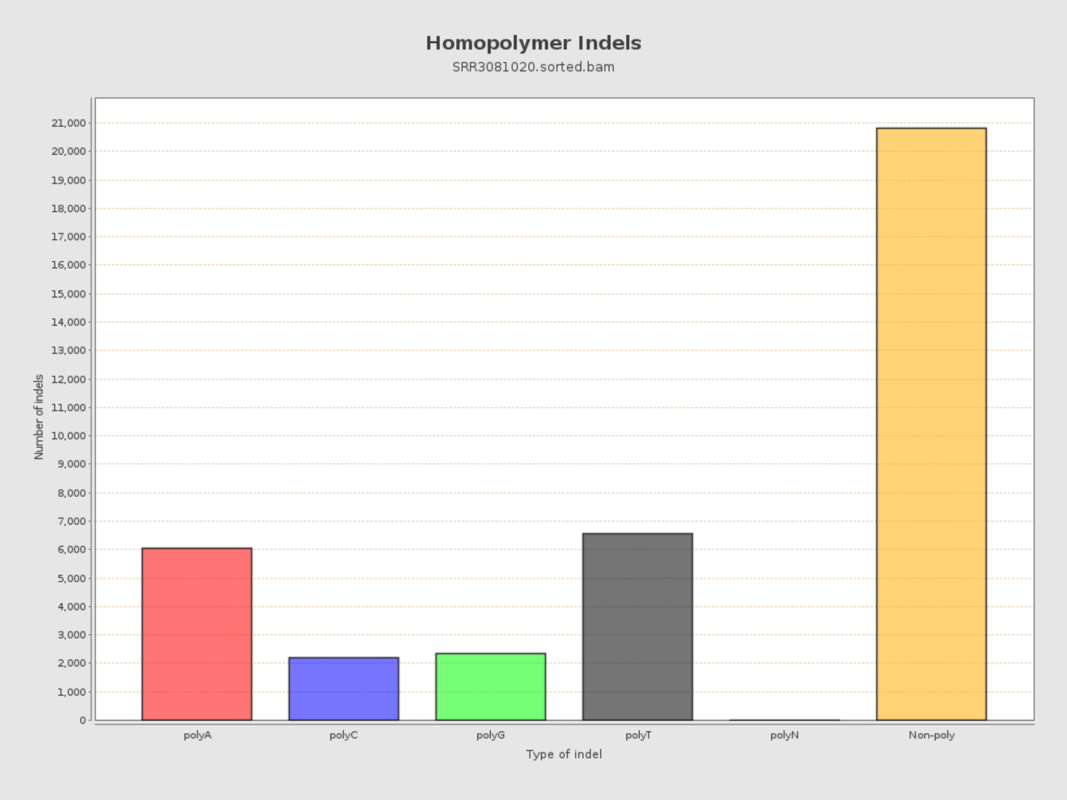
9. Results : Mapped Reads GC-content Distribution



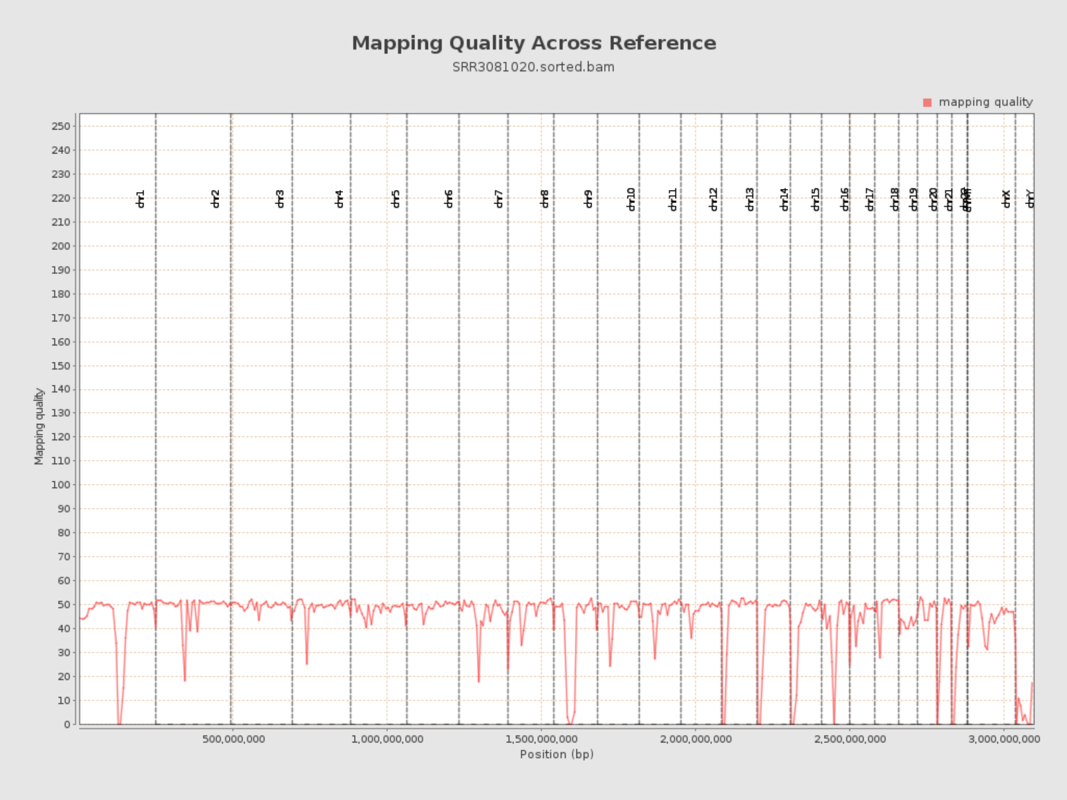
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram