Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 11:24:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084365.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_SRR3084365 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084365.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 11:24:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084365.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,200,837
Mapped reads	1,979,071 / 89.92%
Unmapped reads	221,766 / 10.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,096 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	70,207 / 3.19%
Duplication rate	3.04%
Clipped reads	860,579 / 39.1%

2.2. ACGT Content

Number/percentage of A's	36,444,756 / 27.44%
Number/percentage of C's	25,689,735 / 19.34%
Number/percentage of T's	40,814,247 / 30.73%
Number/percentage of G's	29,700,609 / 22.36%
Number/percentage of N's	172,553 / 0.13%
GC Percentage	41.7%

2.3. Coverage

Mean	0.0429

Standard Deviation	0.2951

2.4. Mapping Quality

Mean Mapping Quality	46.1

2.5. Mismatches and indels

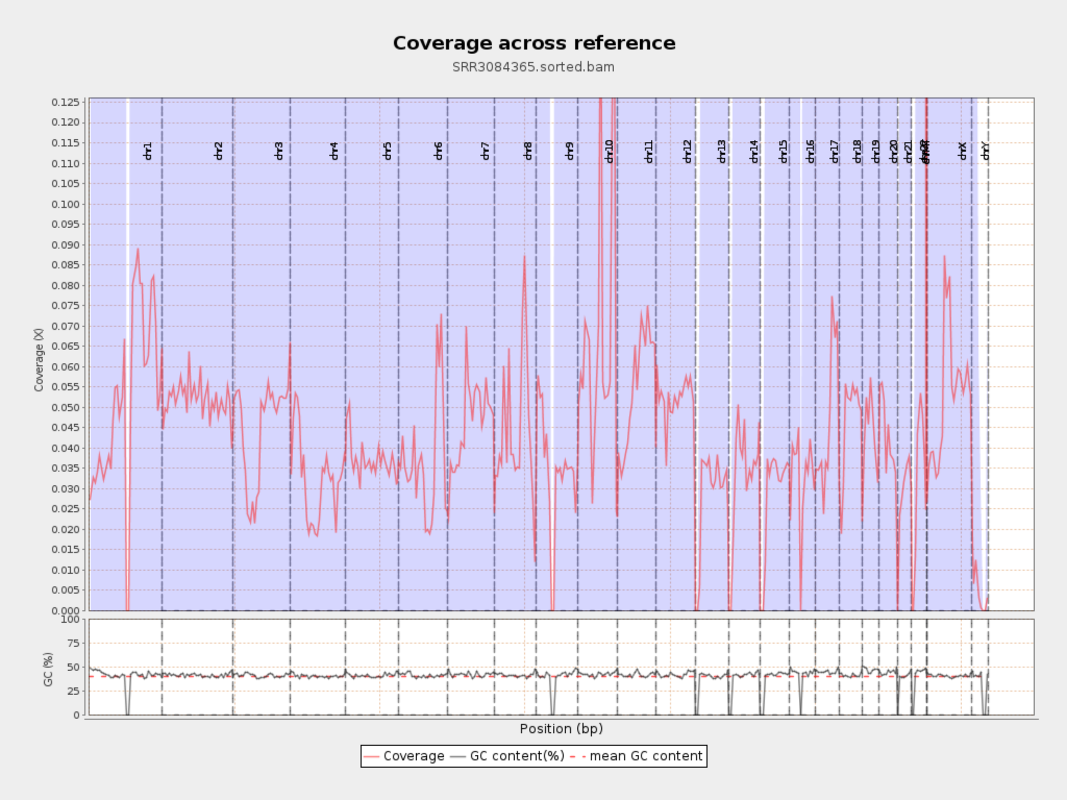
General error rate	1%
Mismatches	1,313,376
Insertions	8,997
Mapped reads with at least one insertion	0.45%
Deletions	24,927
Mapped reads with at least one deletion	1.25%
Homopolymer indels	46.87%

2.6. Chromosome stats

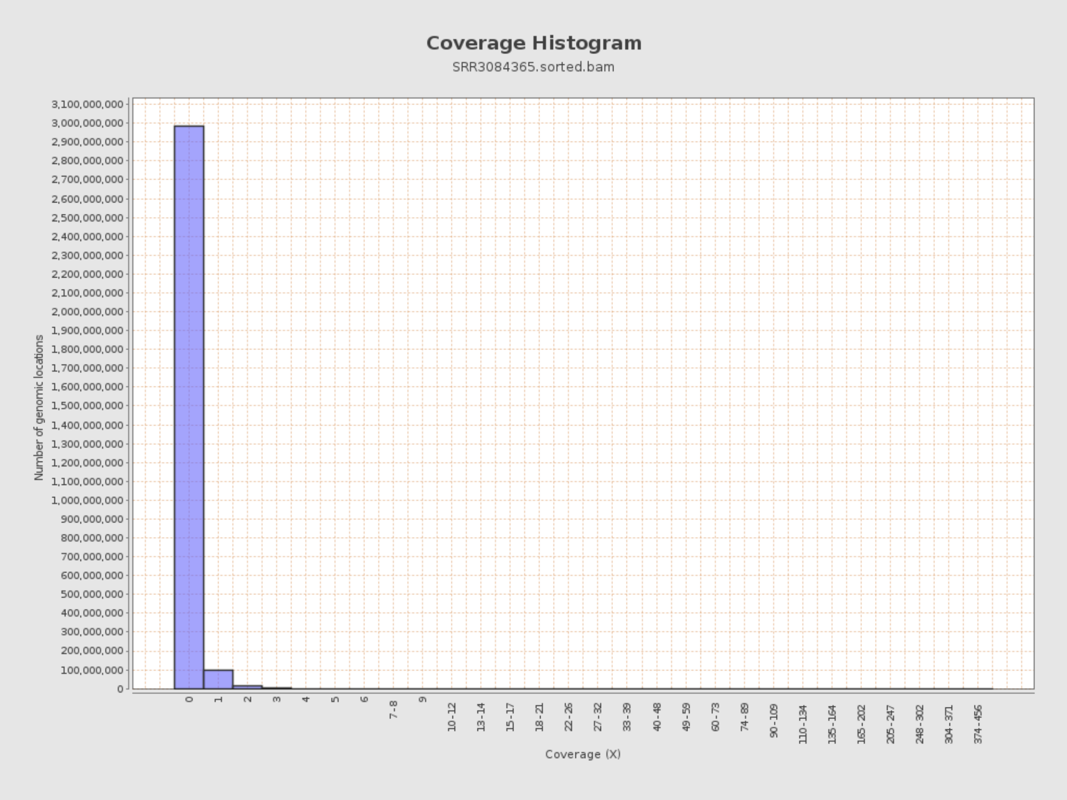
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12847013	0.0515	0.4527
chr2	243199373	12647688	0.052	0.3363
chr3	198022430	8846510	0.0447	0.2439
chr4	191154276	6191238	0.0324	0.2112
chr5	180915260	6696427	0.037	0.2183
chr6	171115067	6301765	0.0368	0.243
chr7	159138663	7403609	0.0465	0.4036

chr8	146364022	6485940	0.0443	0.2769
chr9	141213431	4789066	0.0339	0.2479
chr10	135534747	9598251	0.0708	0.4098
chr11	135006516	7418448	0.0549	0.3015
chr12	133851895	6951099	0.0519	0.2601
chr13	115169878	3240470	0.0281	0.1905
chr14	107349540	3458869	0.0322	0.2069
chr15	102531392	2900879	0.0283	0.1935
chr16	90354753	2961191	0.0328	0.2198
chr17	81195210	3812743	0.047	0.2596
chr18	78077248	3628234	0.0465	0.3893
chr19	59128983	2608483	0.0441	0.3366
chr20	63025520	2675791	0.0425	0.2368
chr21	48129895	1361324	0.0283	0.1962
chr22	51304566	1555623	0.0303	0.1978
chrMT	16571	71265	4.3006	3.2372
chrX	155270560	8133549	0.0524	0.281
chrY	59373566	279630	0.0047	0.0988

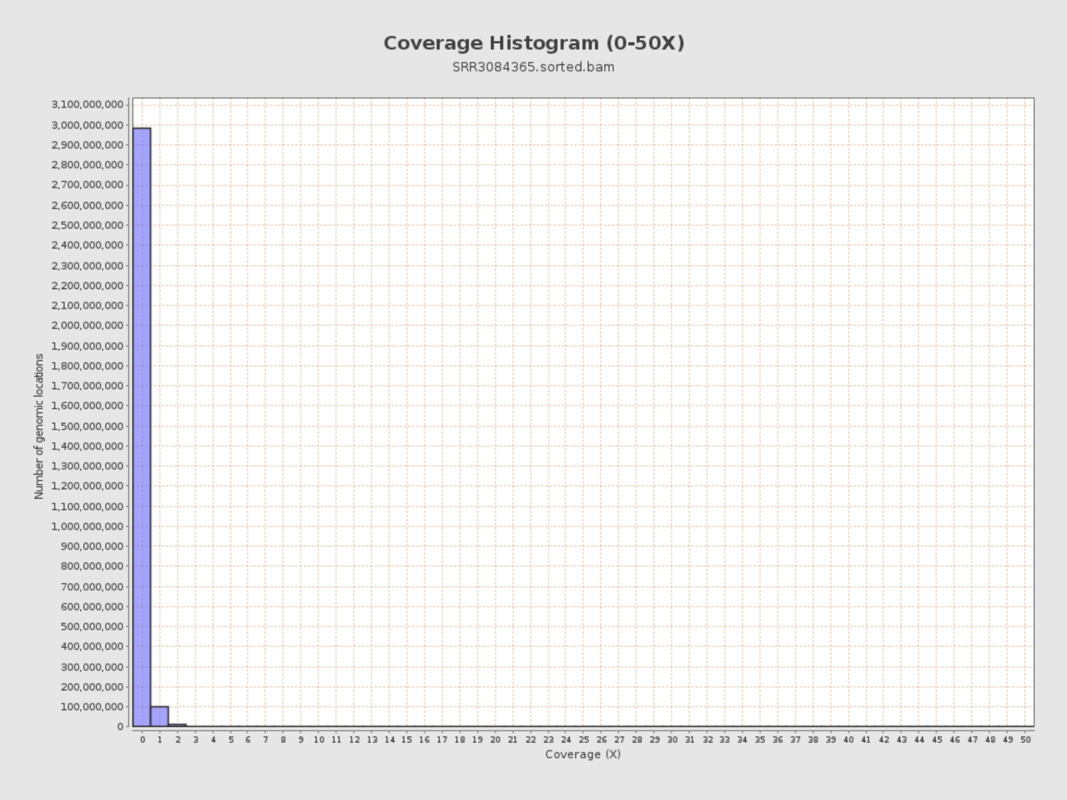
3. Results : Coverage across reference



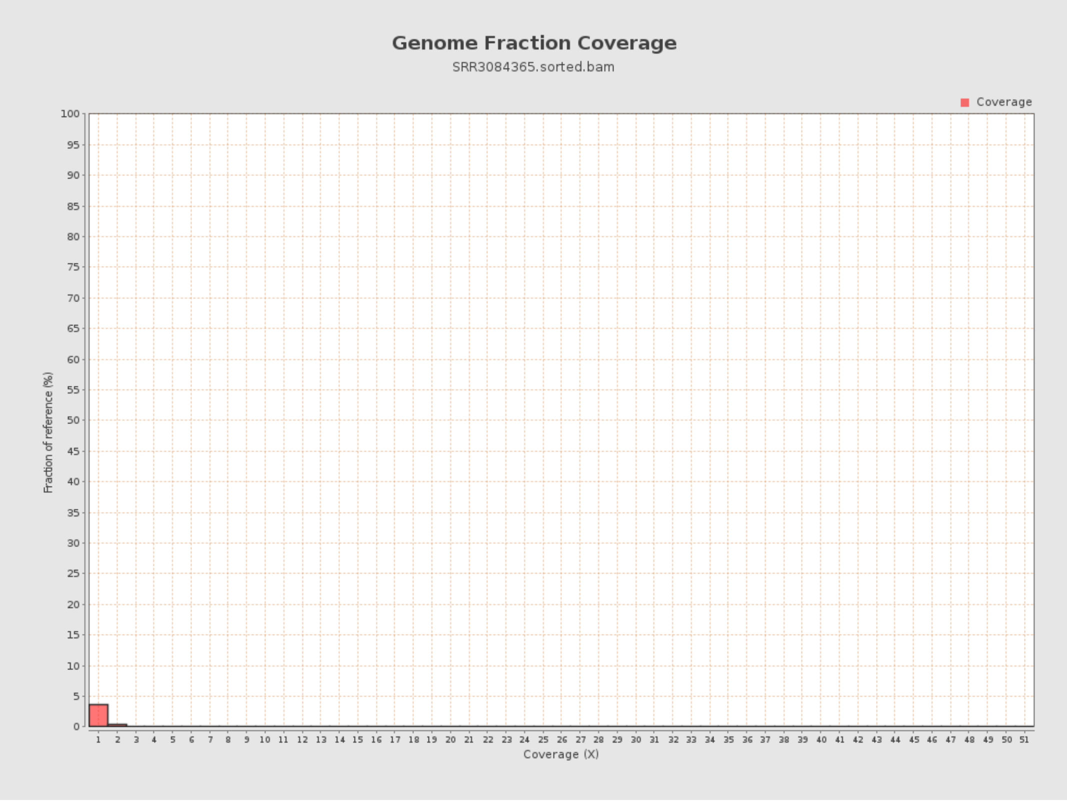
4. Results : Coverage Histogram



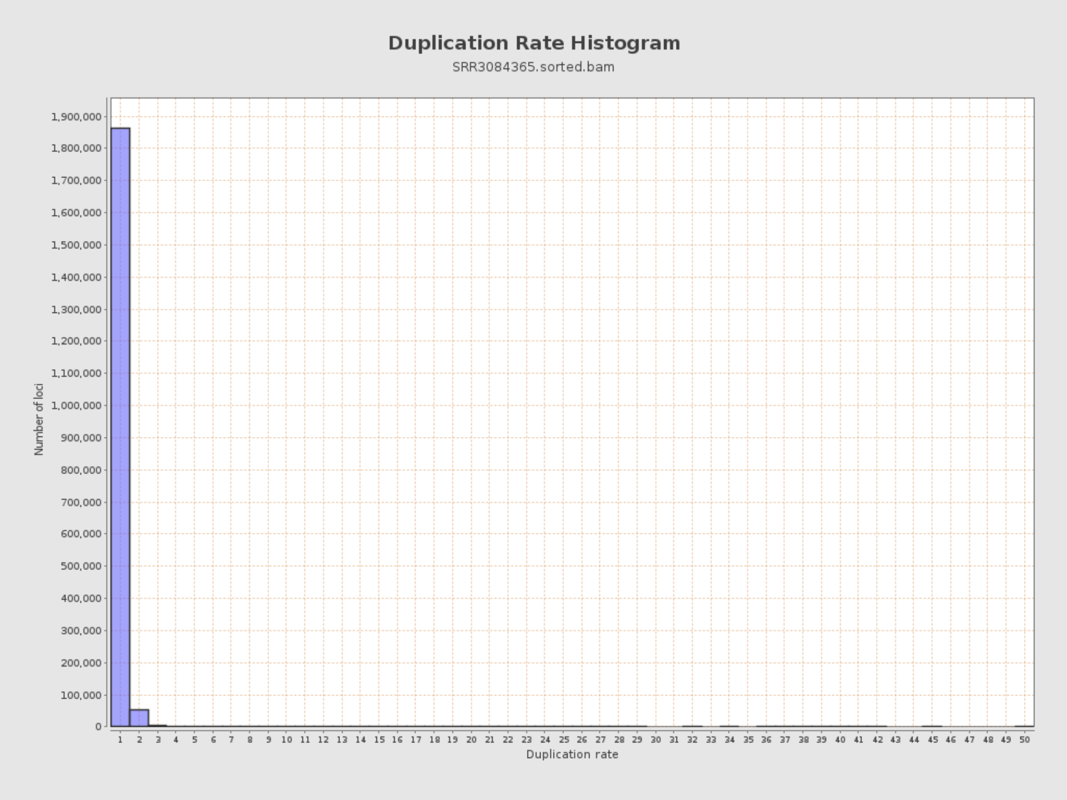
5. Results : Coverage Histogram (0-50X)



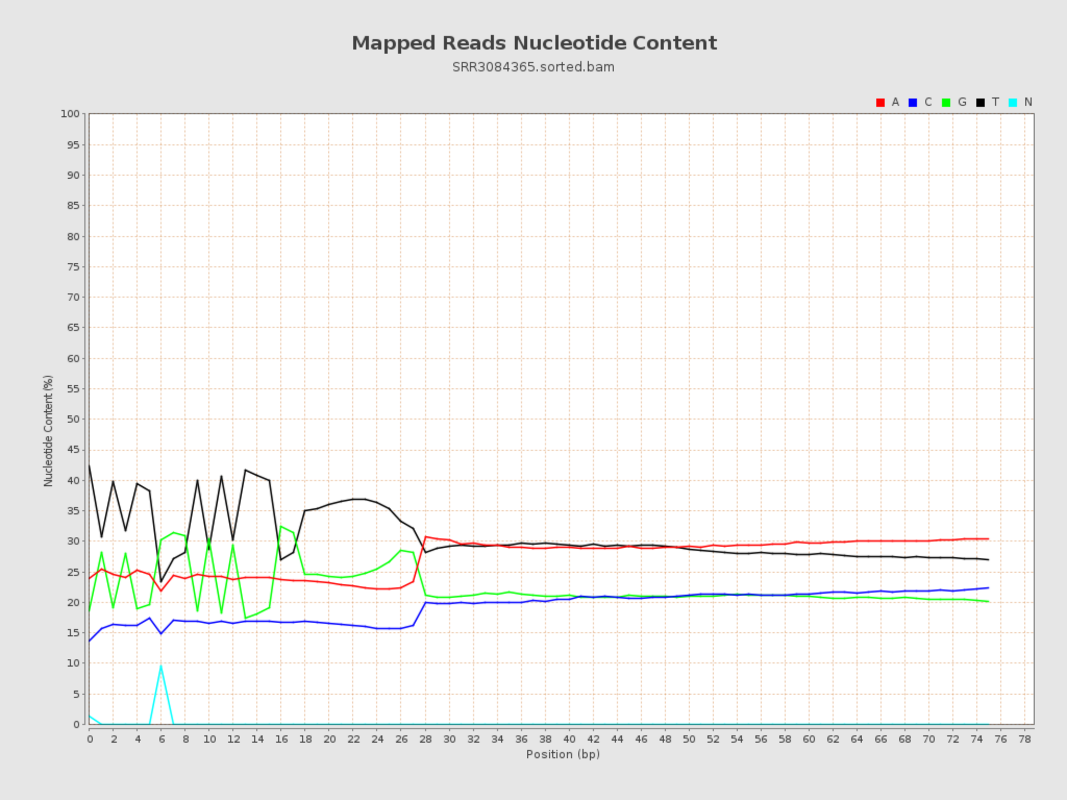
6. Results : Genome Fraction Coverage



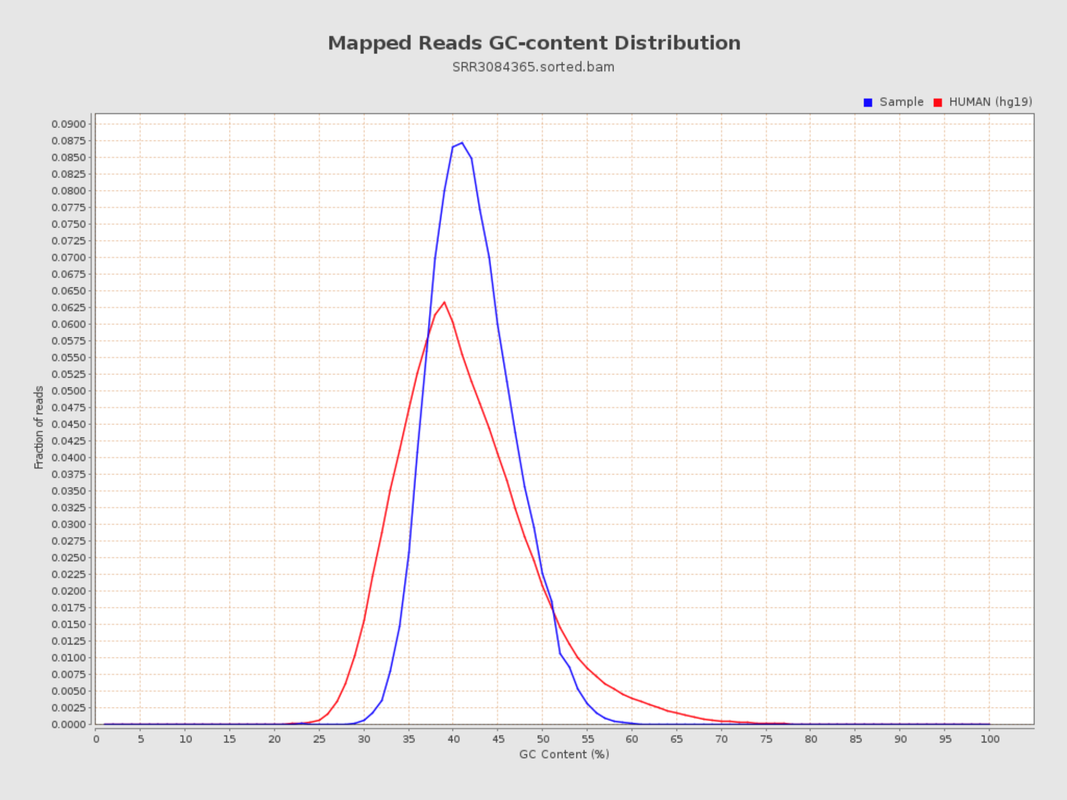
7. Results : Duplication Rate Histogram



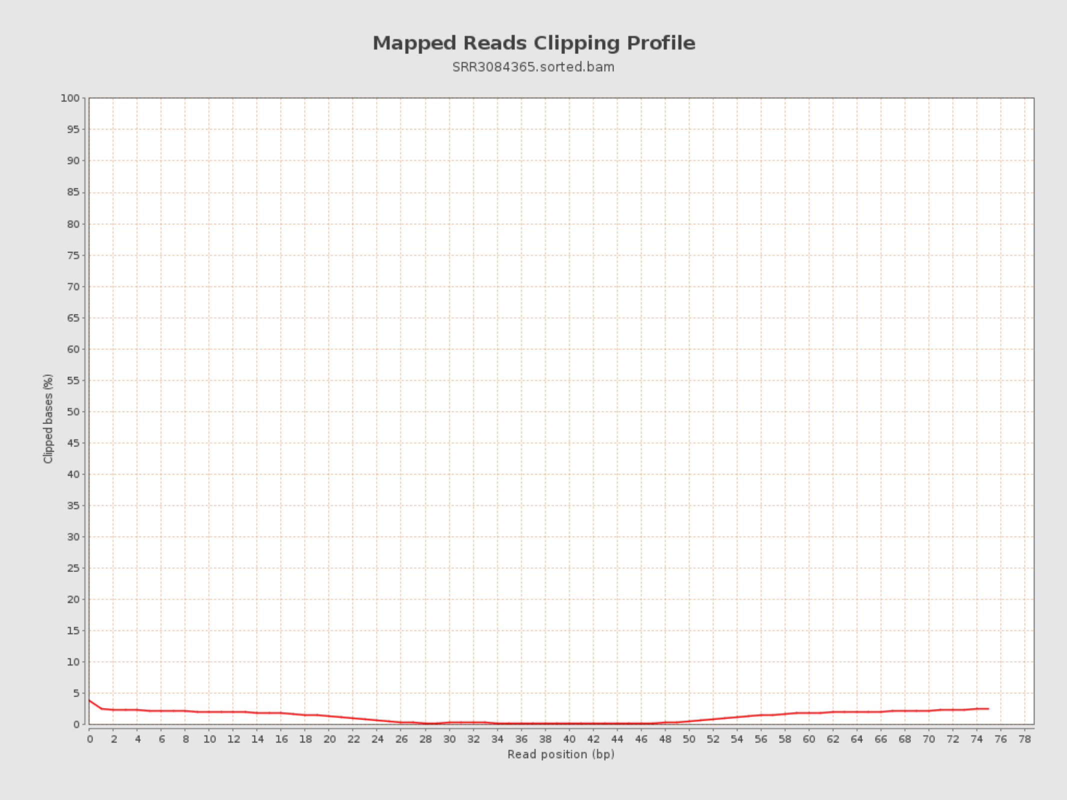
8. Results : Mapped Reads Nucleotide Content



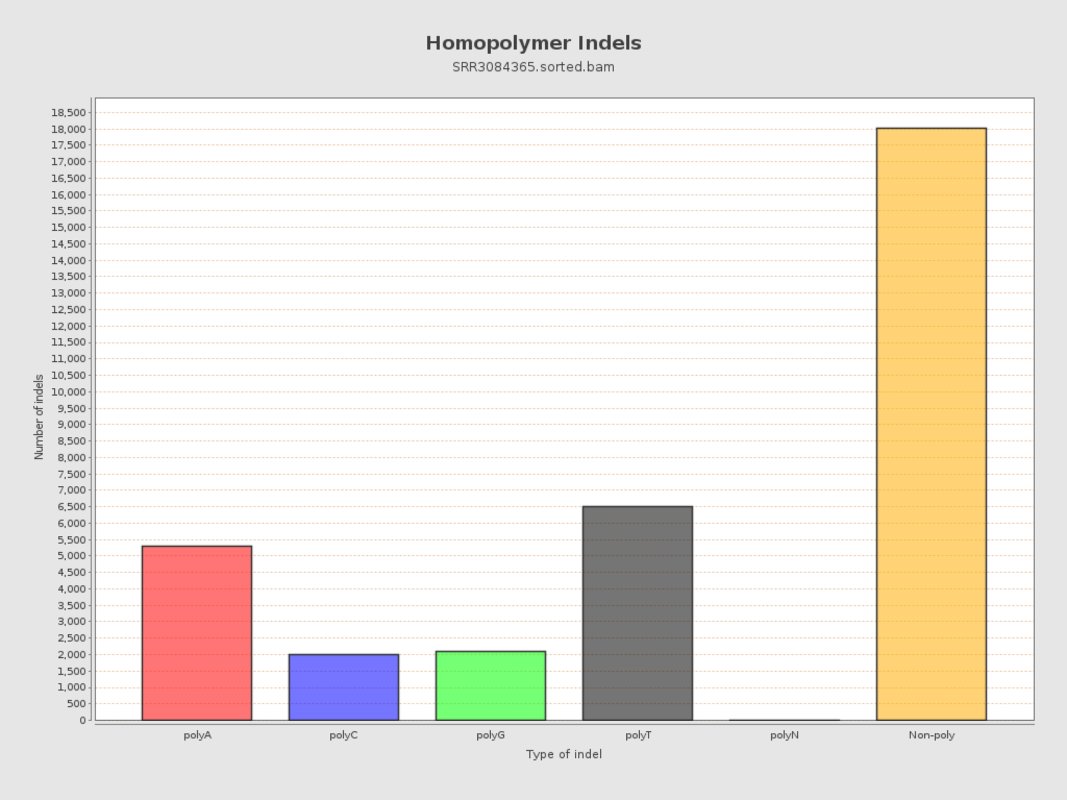
9. Results : Mapped Reads GC-content Distribution



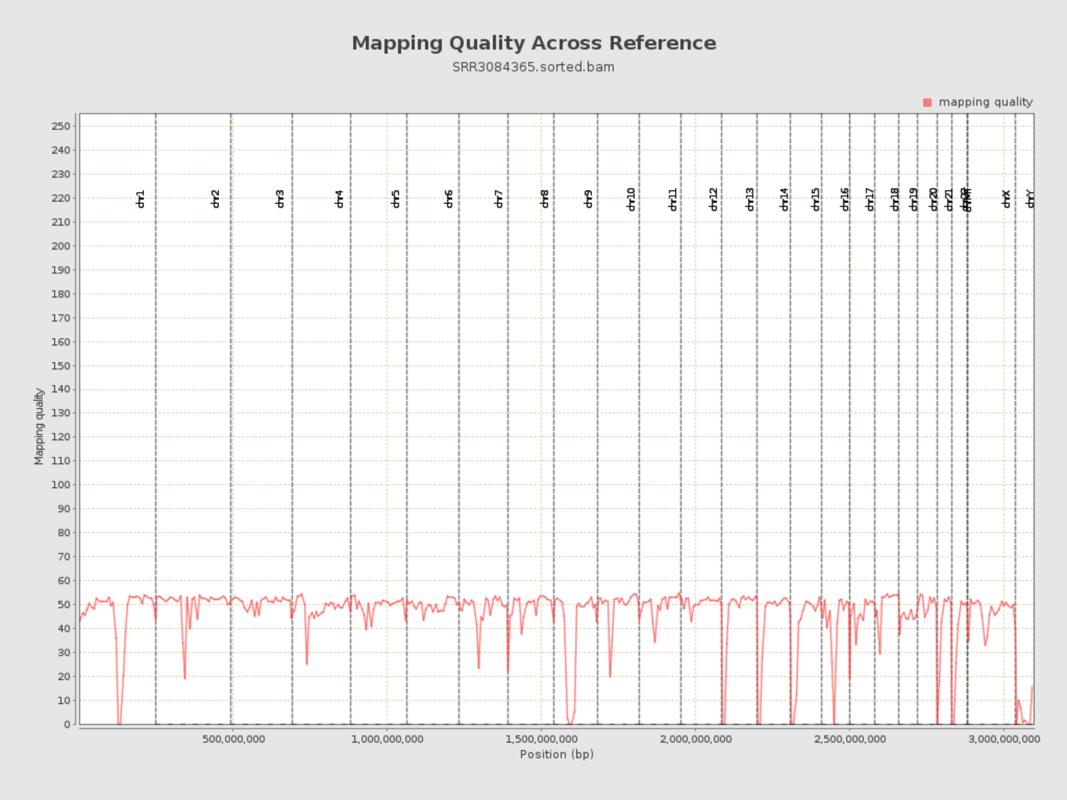
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram