Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 11:08:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084361.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_SRR3084361 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084361.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 11:08:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084361.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,486,386
Mapped reads	2,230,069 / 89.69%
Unmapped reads	256,317 / 10.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,640 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	76,777 / 3.09%
Duplication rate	2.82%
Clipped reads	1,006,240 / 40.47%

2.2. ACGT Content

Number/percentage of A's	41,198,491 / 27.66%
Number/percentage of C's	28,836,631 / 19.36%
Number/percentage of T's	45,422,066 / 30.5%
Number/percentage of G's	33,289,388 / 22.35%
Number/percentage of N's	191,526 / 0.13%
GC Percentage	41.71%

2.3. Coverage

Mean	0.0481

Standard Deviation	0.3415

2.4. Mapping Quality

Mean Mapping Quality	45.36

2.5. Mismatches and indels

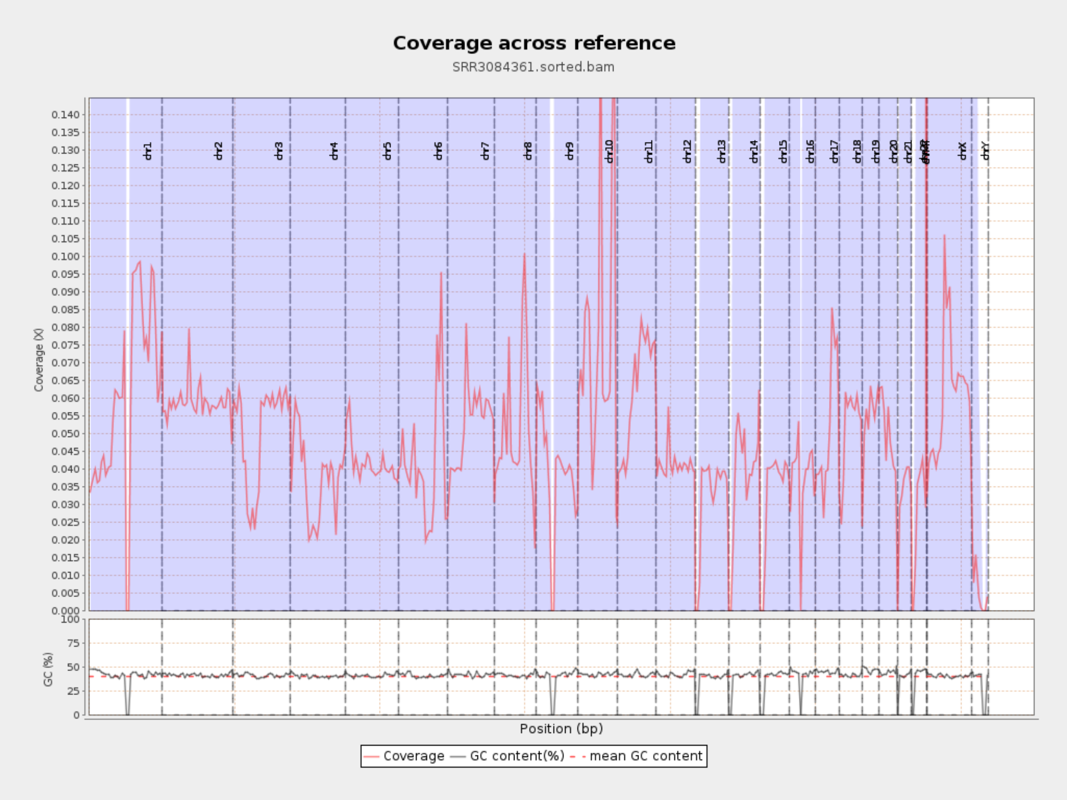
General error rate	1.02%
Mismatches	1,498,712
Insertions	10,546
Mapped reads with at least one insertion	0.47%
Deletions	28,910
Mapped reads with at least one deletion	1.29%
Homopolymer indels	46.2%

2.6. Chromosome stats

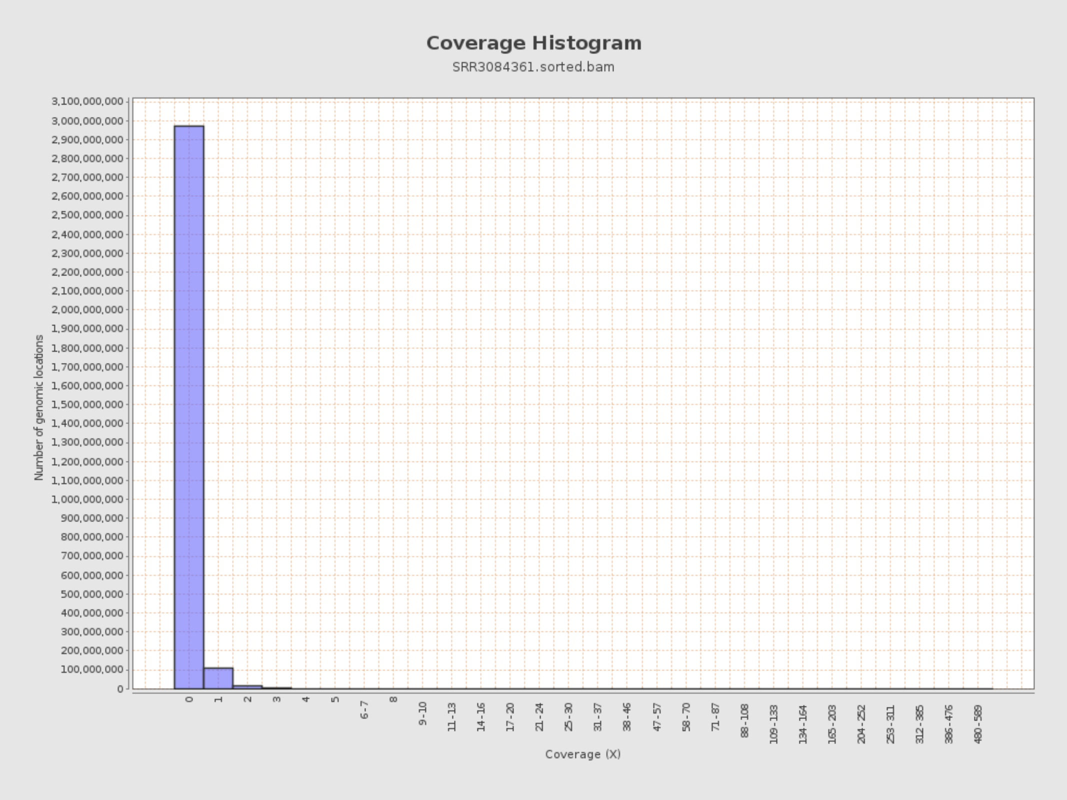
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14951533	0.06	0.5669
chr2	243199373	14340101	0.059	0.3825
chr3	198022430	10015616	0.0506	0.2588
chr4	191154276	7141628	0.0374	0.2302
chr5	180915260	7566881	0.0418	0.2307
chr6	171115067	7171663	0.0419	0.2575
chr7	159138663	8394861	0.0528	0.5149

chr8	146364022	7518303	0.0514	0.3166
chr9	141213431	5507144	0.039	0.2809
chr10	135534747	10856554	0.0801	0.482
chr11	135006516	8347846	0.0618	0.3519
chr12	133851895	5544197	0.0414	0.2314
chr13	115169878	3612378	0.0314	0.1999
chr14	107349540	3996536	0.0372	0.2258
chr15	102531392	3325488	0.0324	0.2113
chr16	90354753	3367078	0.0373	0.2373
chr17	81195210	4216319	0.0519	0.2757
chr18	78077248	4027793	0.0516	0.4613
chr19	59128983	3266706	0.0552	0.4163
chr20	63025520	3121749	0.0495	0.2546
chr21	48129895	1561057	0.0324	0.2177
chr22	51304566	1339640	0.0261	0.1805
chrMT	16571	43611	2.6318	2.4221
chrX	155270560	9419555	0.0607	0.3123
chrY	59373566	334460	0.0056	0.1198

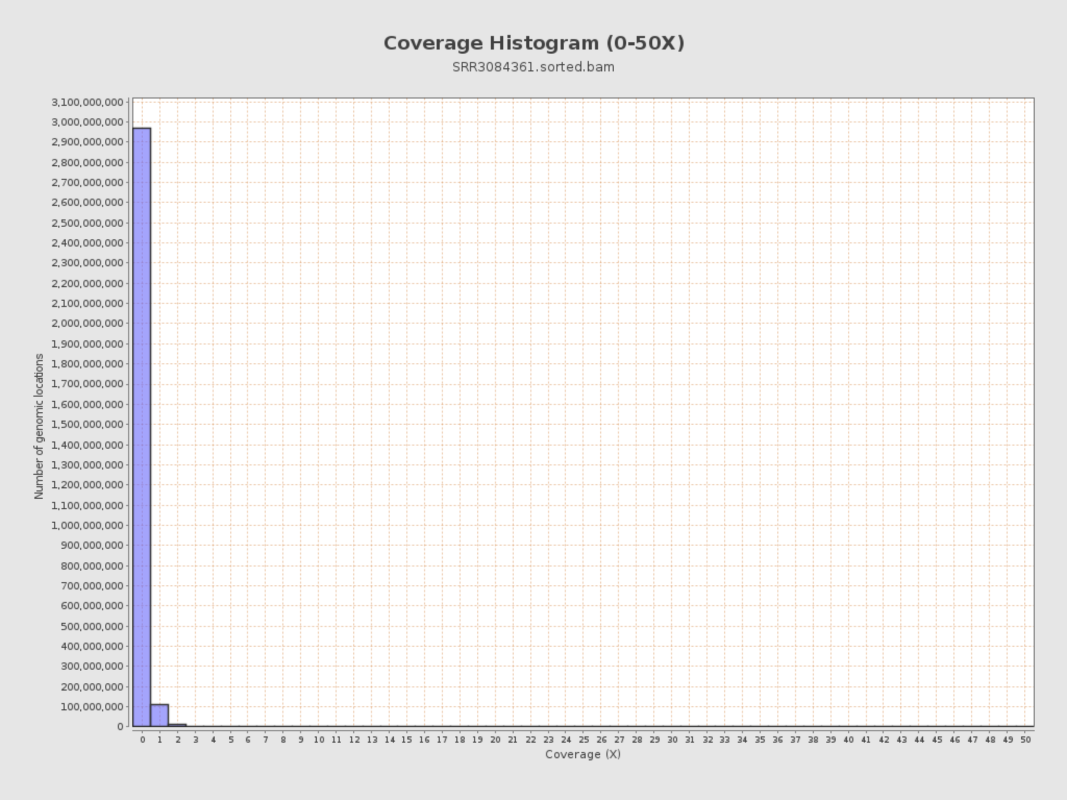
3. Results : Coverage across reference



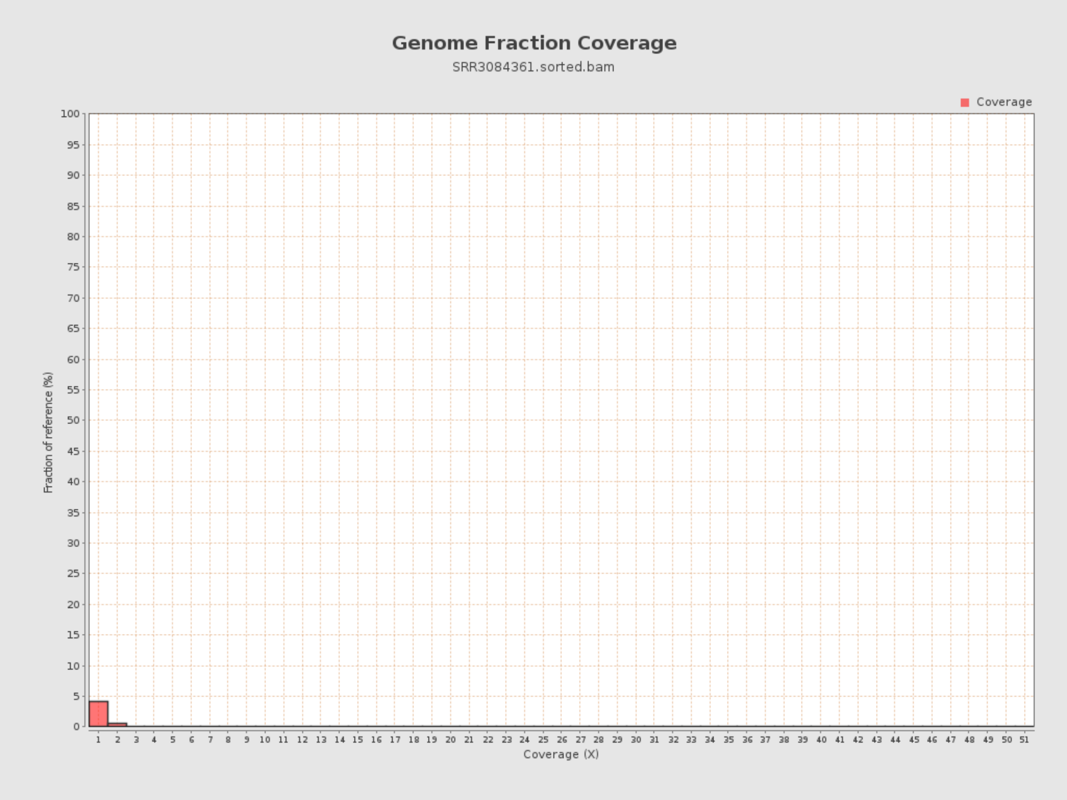
4. Results : Coverage Histogram



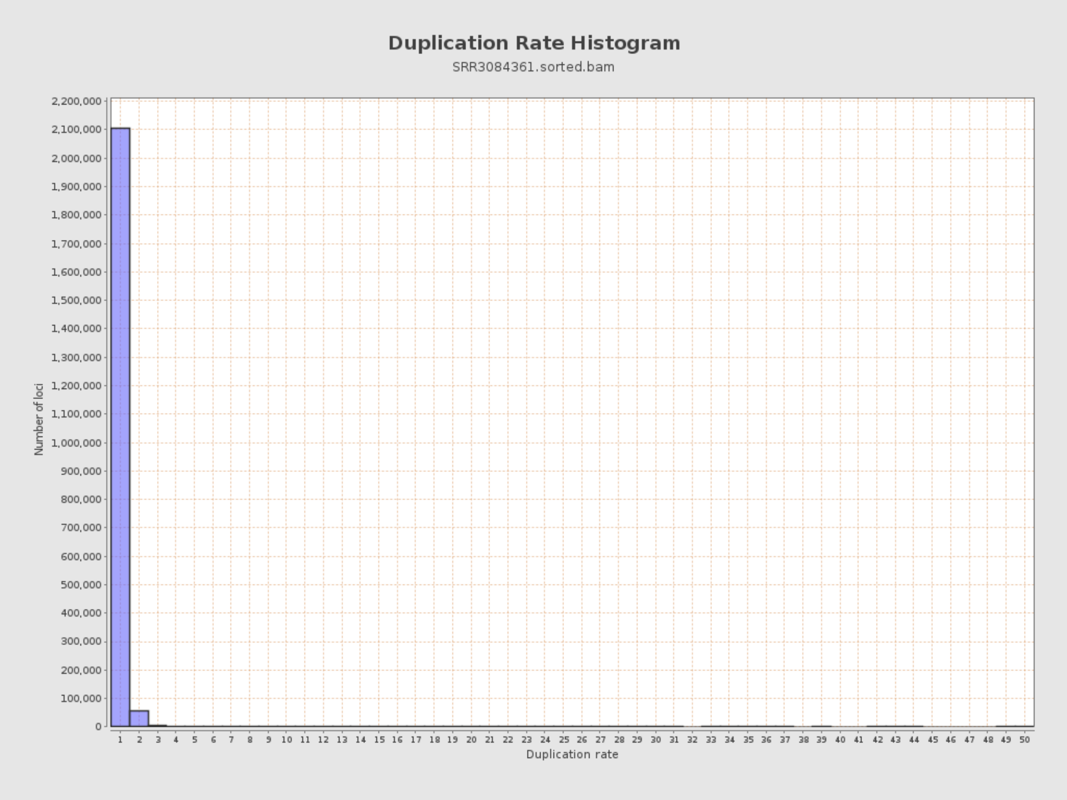
5. Results : Coverage Histogram (0-50X)



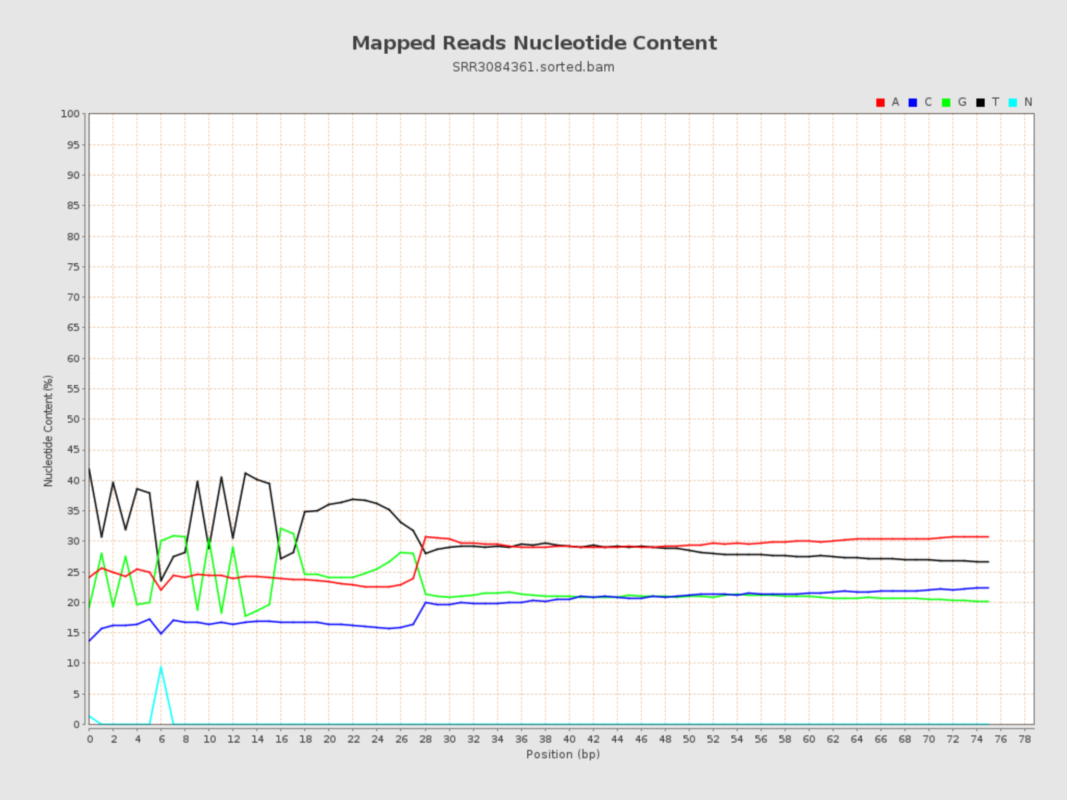
6. Results : Genome Fraction Coverage



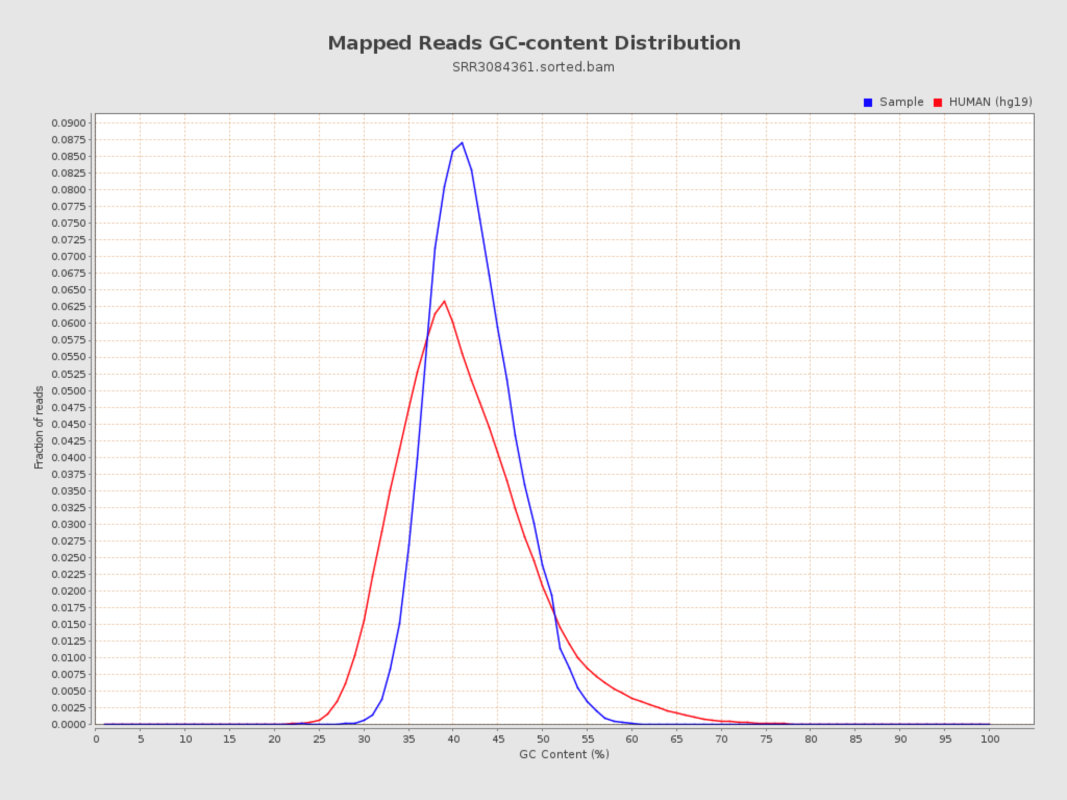
7. Results : Duplication Rate Histogram



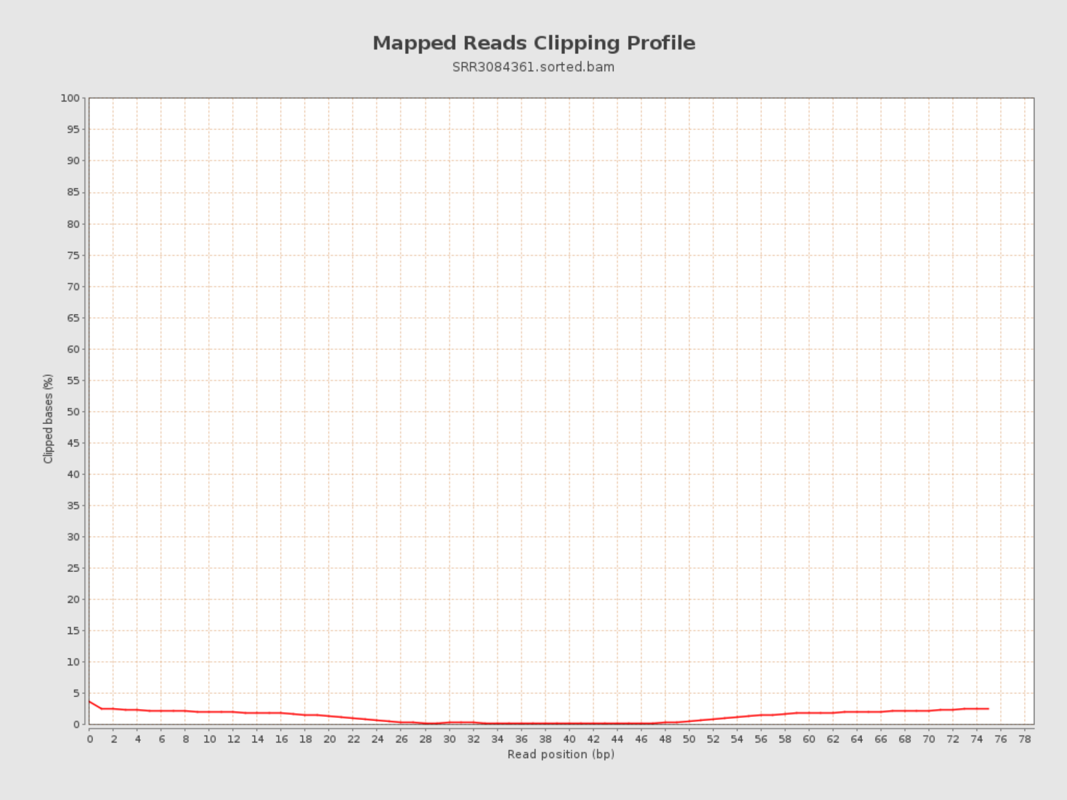
8. Results : Mapped Reads Nucleotide Content



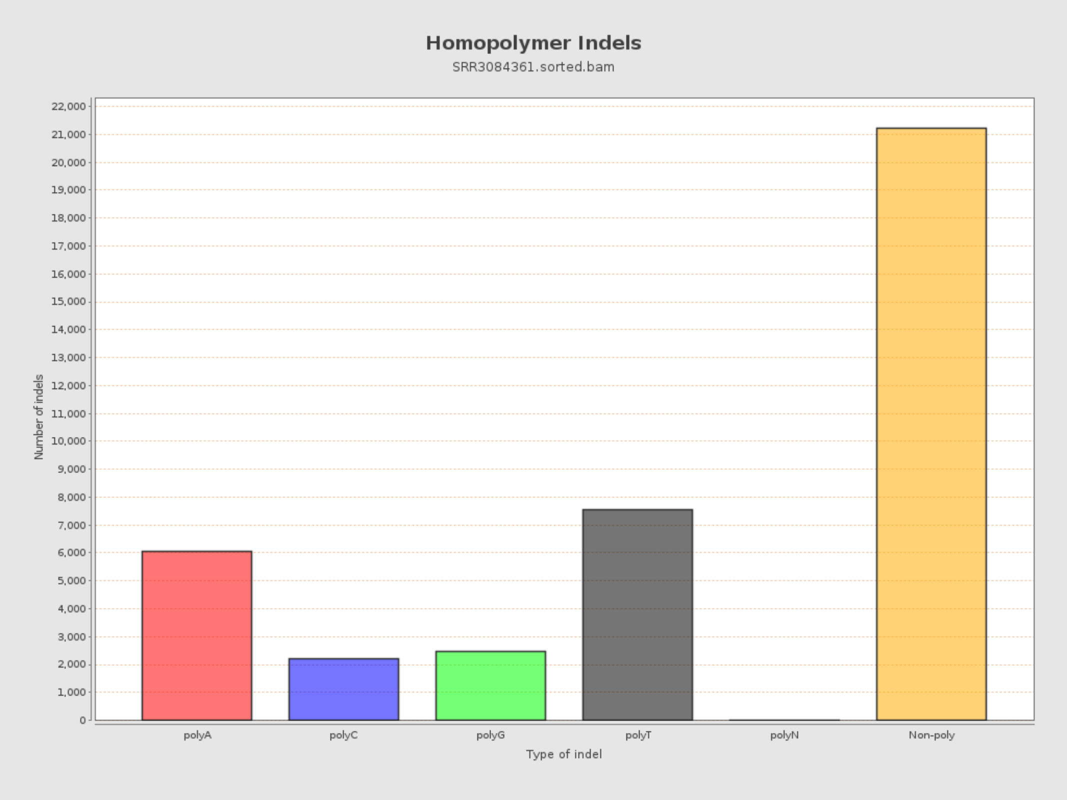
9. Results : Mapped Reads GC-content Distribution



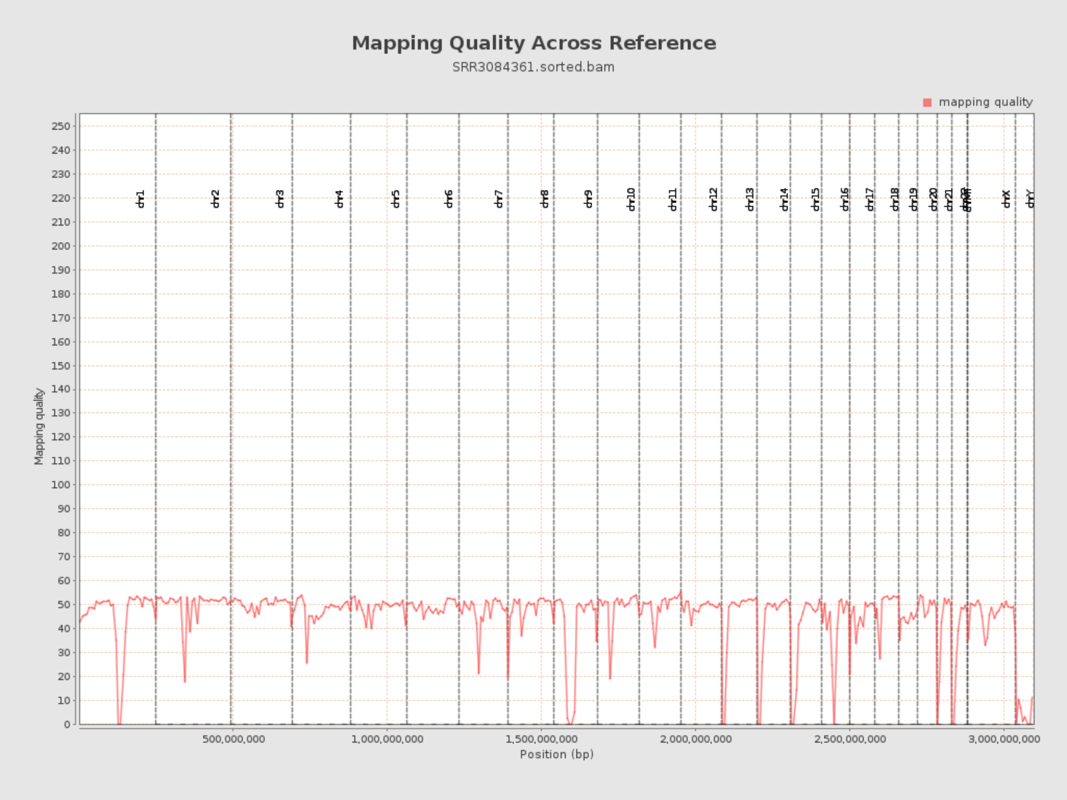
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram