Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 08:00:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084256.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_SRR3084256 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084256.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 08:00:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084256.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,909,774
Mapped reads	1,823,138 / 62.66%
Unmapped reads	1,086,636 / 37.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,441 / 0.39%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	69,042 / 2.37%
Duplication rate	3.22%
Clipped reads	1,034,034 / 35.54%

2.2. ACGT Content

Number/percentage of A's	32,363,476 / 28.08%
Number/percentage of C's	22,414,631 / 19.45%
Number/percentage of T's	34,811,552 / 30.21%
Number/percentage of G's	25,652,821 / 22.26%
Number/percentage of N's	1,288 / 0%
GC Percentage	41.71%

2.3. Coverage

Mean	0.0372

Standard Deviation	0.269

2.4. Mapping Quality

Mean Mapping Quality	45.65

2.5. Mismatches and indels

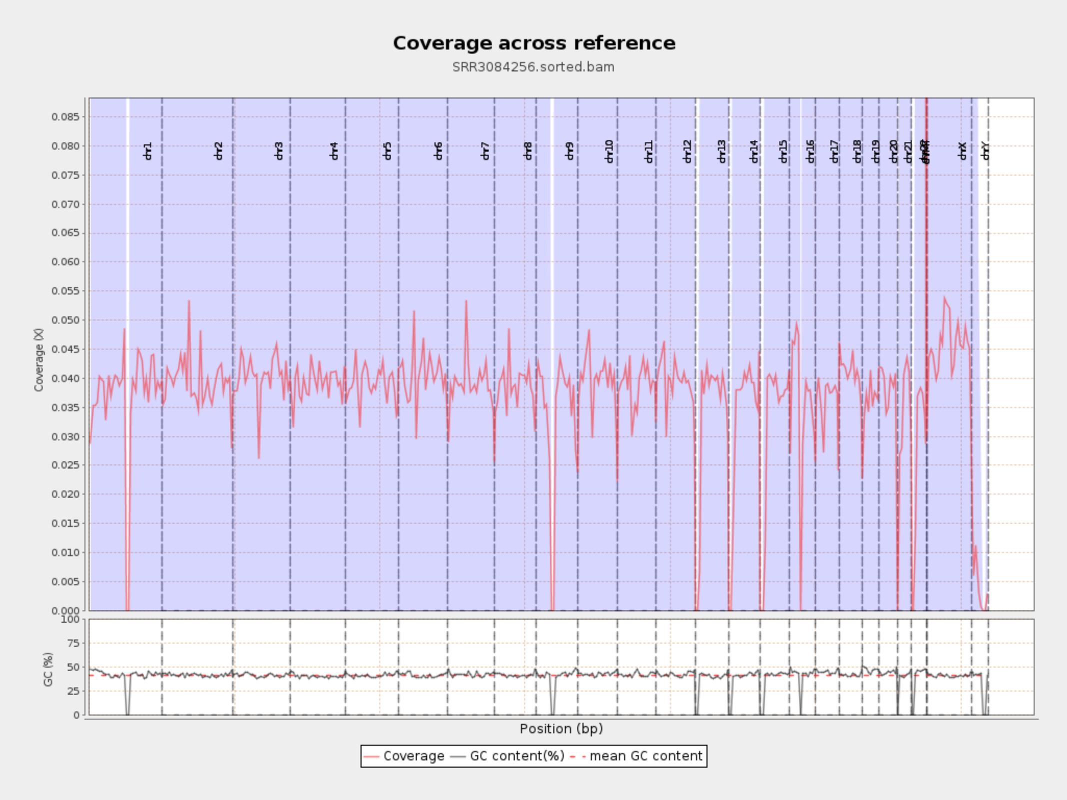
General error rate	0.84%
Mismatches	952,034
Insertions	8,459
Mapped reads with at least one insertion	0.46%
Deletions	23,906
Mapped reads with at least one deletion	1.3%
Homopolymer indels	45.87%

2.6. Chromosome stats

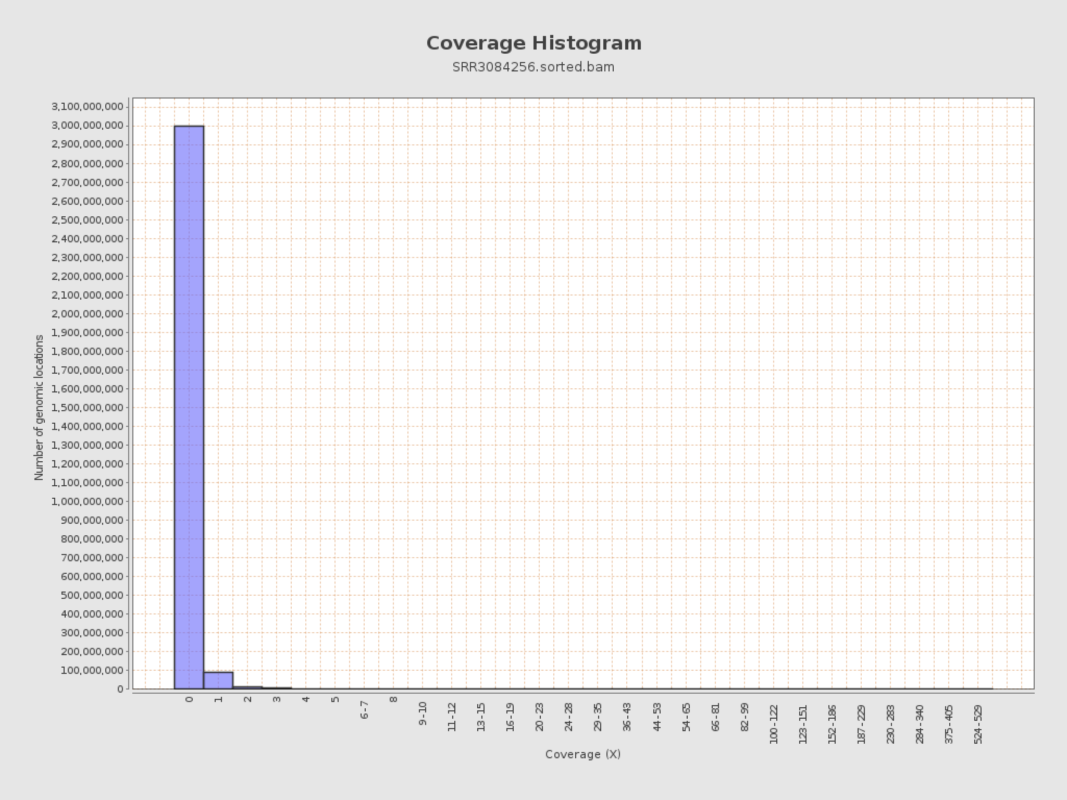
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9138869	0.0367	0.3571
chr2	243199373	9618563	0.0396	0.3544
chr3	198022430	7974583	0.0403	0.2246
chr4	191154276	7487971	0.0392	0.2255
chr5	180915260	7049950	0.039	0.221
chr6	171115067	6965706	0.0407	0.2719
chr7	159138663	6265587	0.0394	0.3199

chr8	146364022	5650657	0.0386	0.2787
chr9	141213431	4697874	0.0333	0.2489
chr10	135534747	5449443	0.0402	0.2674
chr11	135006516	5232705	0.0388	0.2449
chr12	133851895	5285507	0.0395	0.224
chr13	115169878	3756720	0.0326	0.2058
chr14	107349540	3436905	0.032	0.2083
chr15	102531392	3196761	0.0312	0.2017
chr16	90354753	3216169	0.0356	0.2232
chr17	81195210	2925844	0.036	0.2228
chr18	78077248	3225037	0.0413	0.4258
chr19	59128983	2131607	0.0361	0.3088
chr20	63025520	2392761	0.038	0.2214
chr21	48129895	1535575	0.0319	0.2067
chr22	51304566	1288187	0.0251	0.1774
chrMT	16571	58846	3.5511	3.0872
chrX	155270560	7045719	0.0454	0.2517
chrY	59373566	254226	0.0043	0.0865

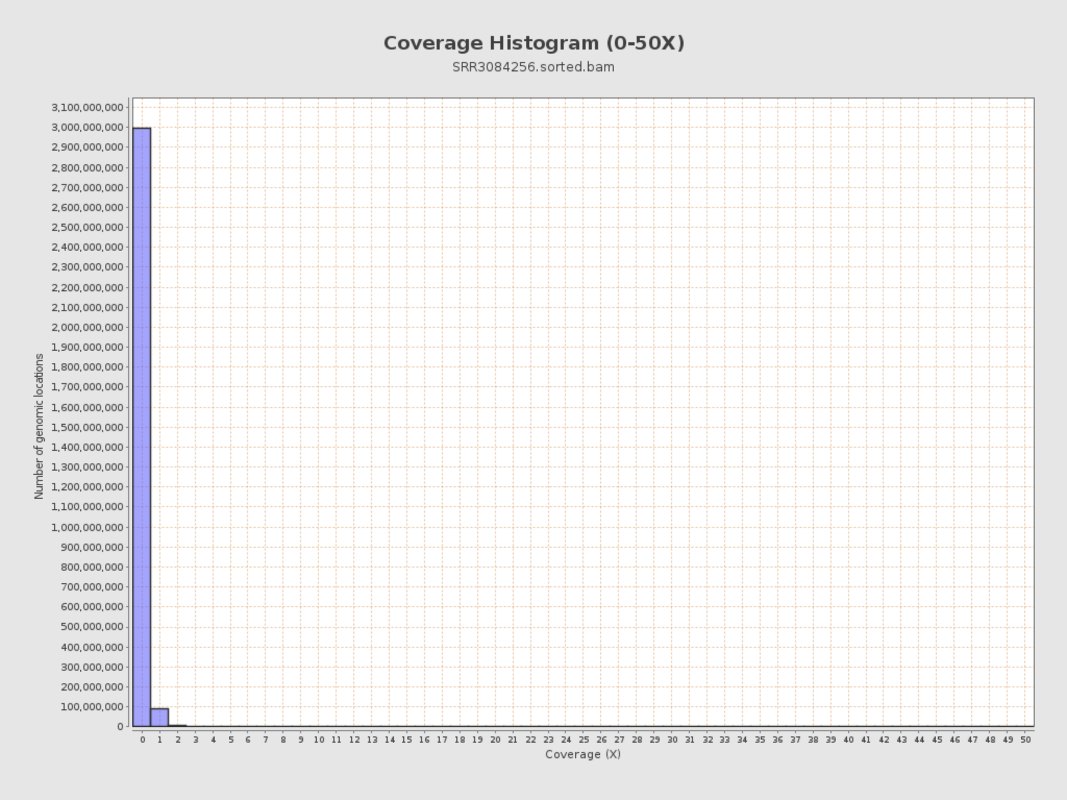
3. Results : Coverage across reference



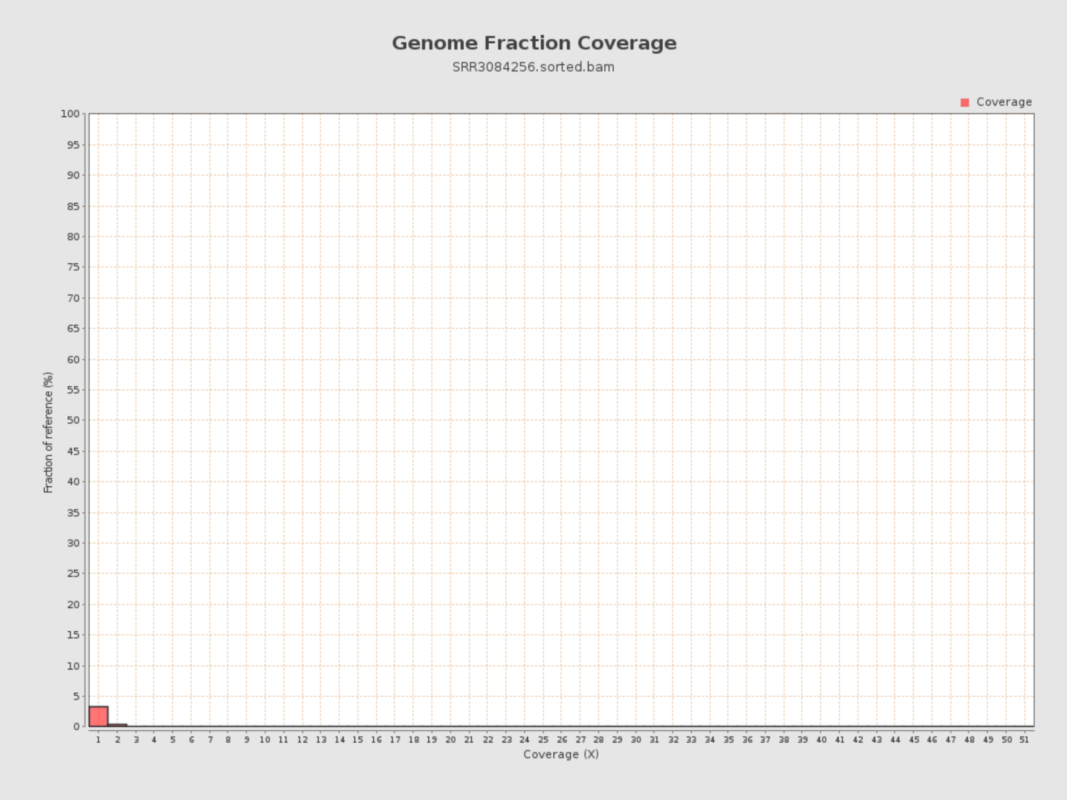
4. Results : Coverage Histogram



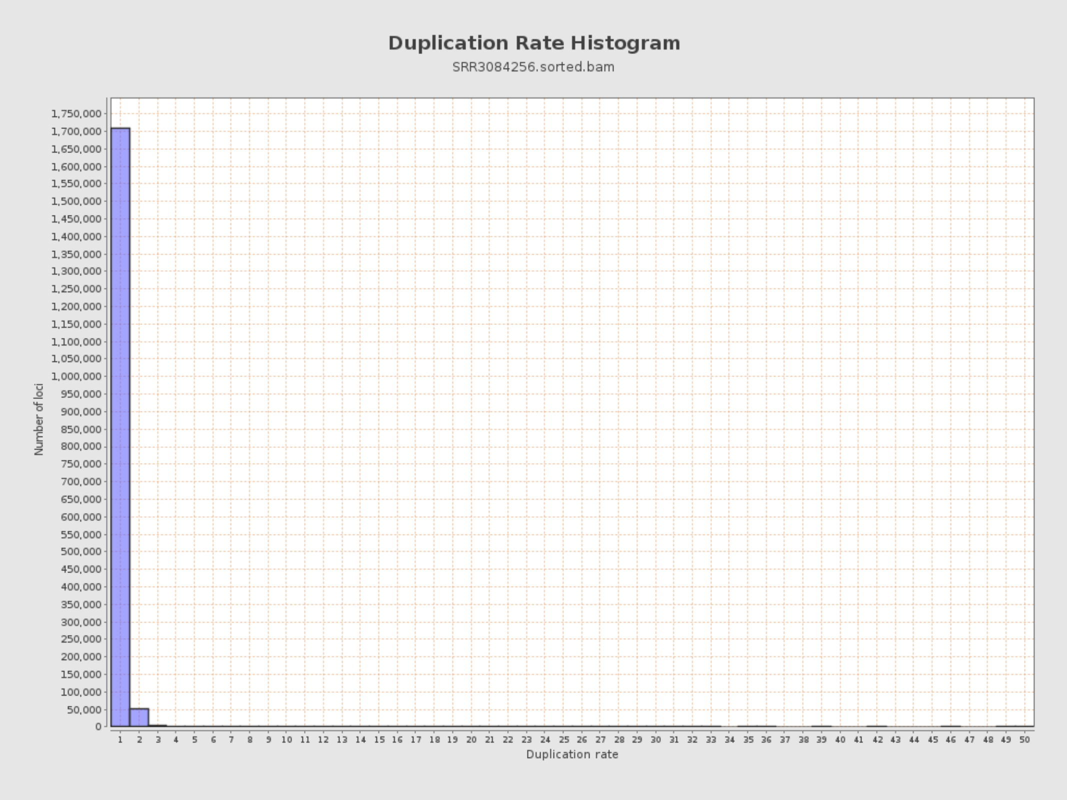
5. Results : Coverage Histogram (0-50X)



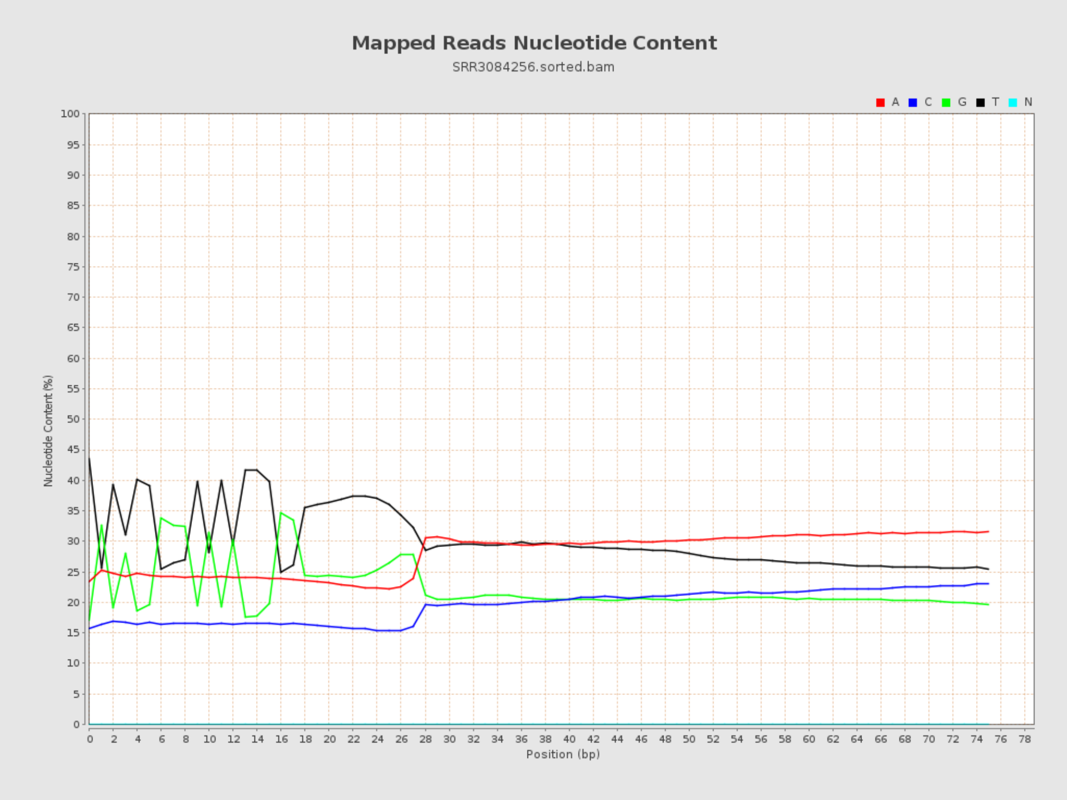
6. Results : Genome Fraction Coverage



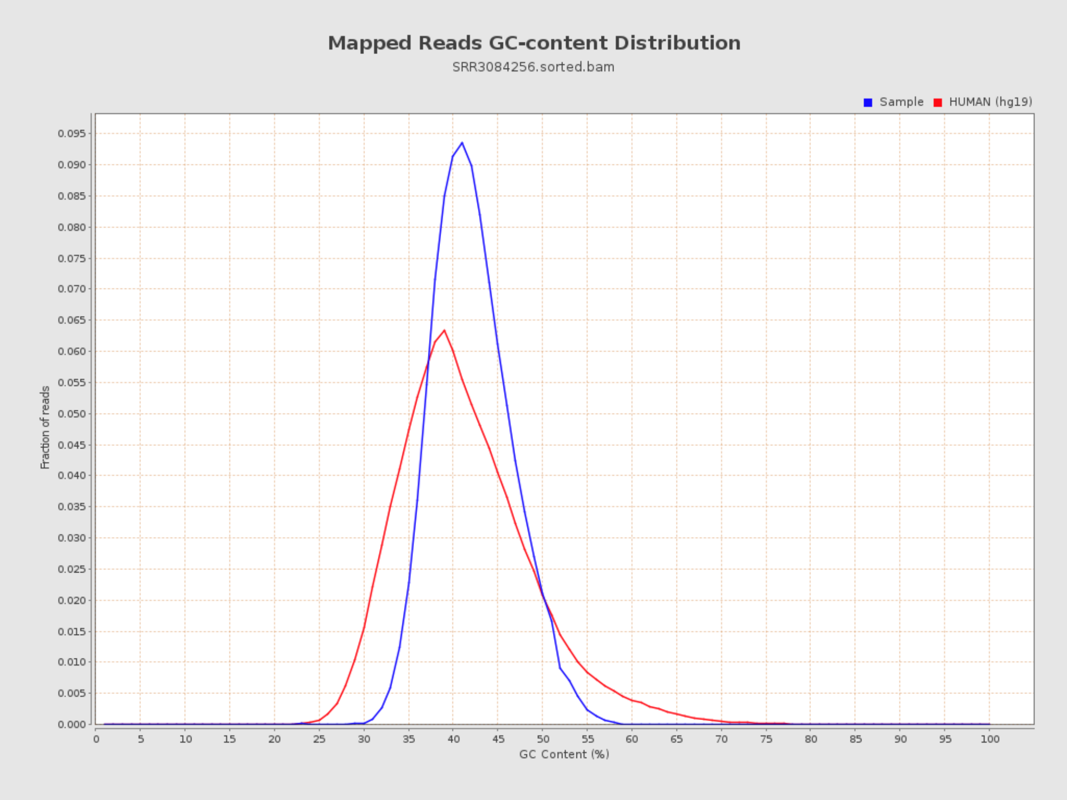
7. Results : Duplication Rate Histogram



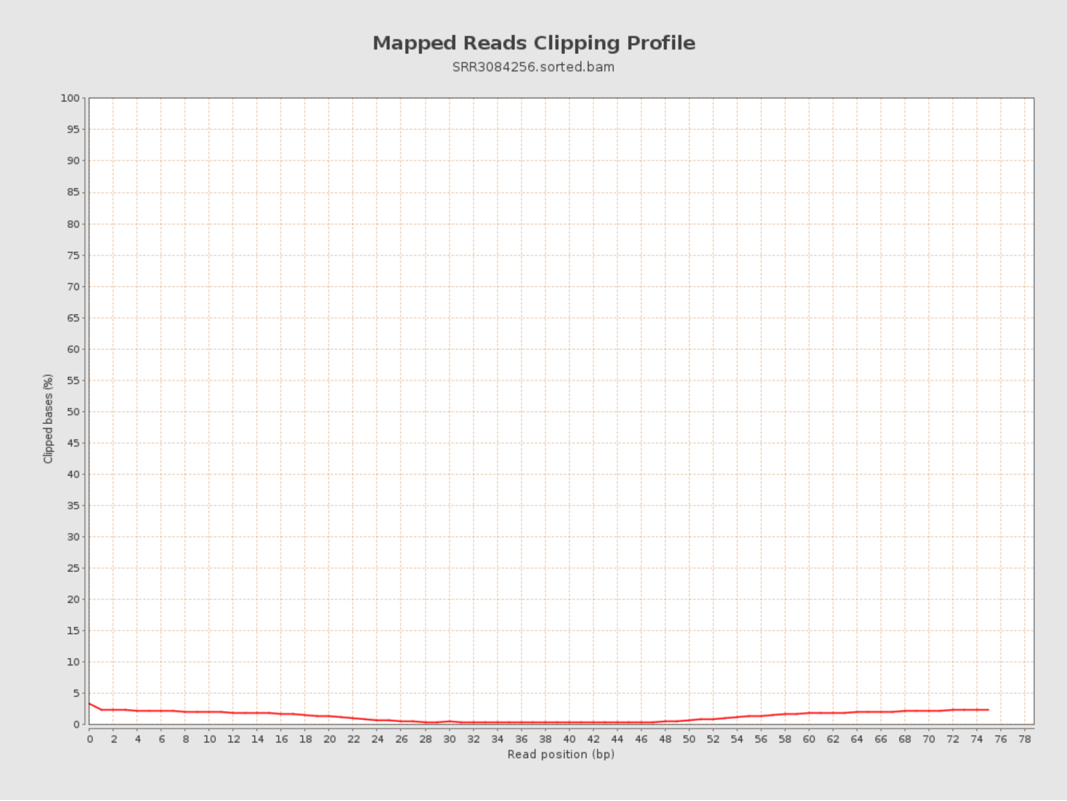
8. Results : Mapped Reads Nucleotide Content



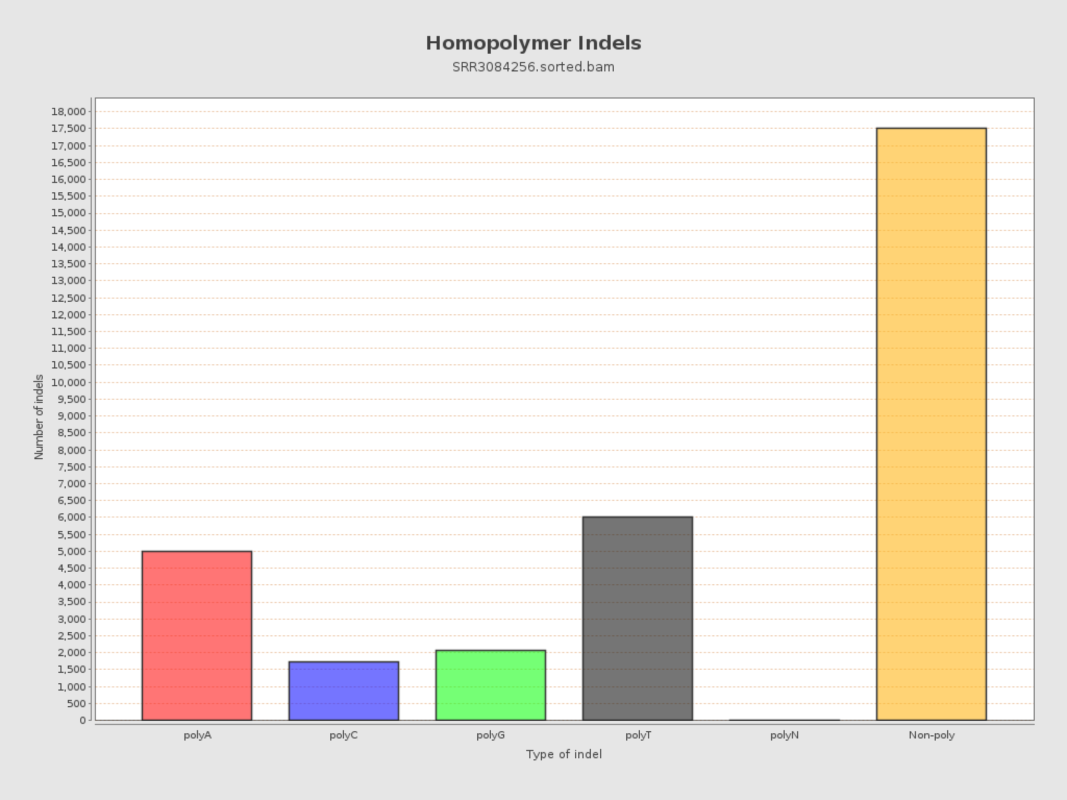
9. Results : Mapped Reads GC-content Distribution



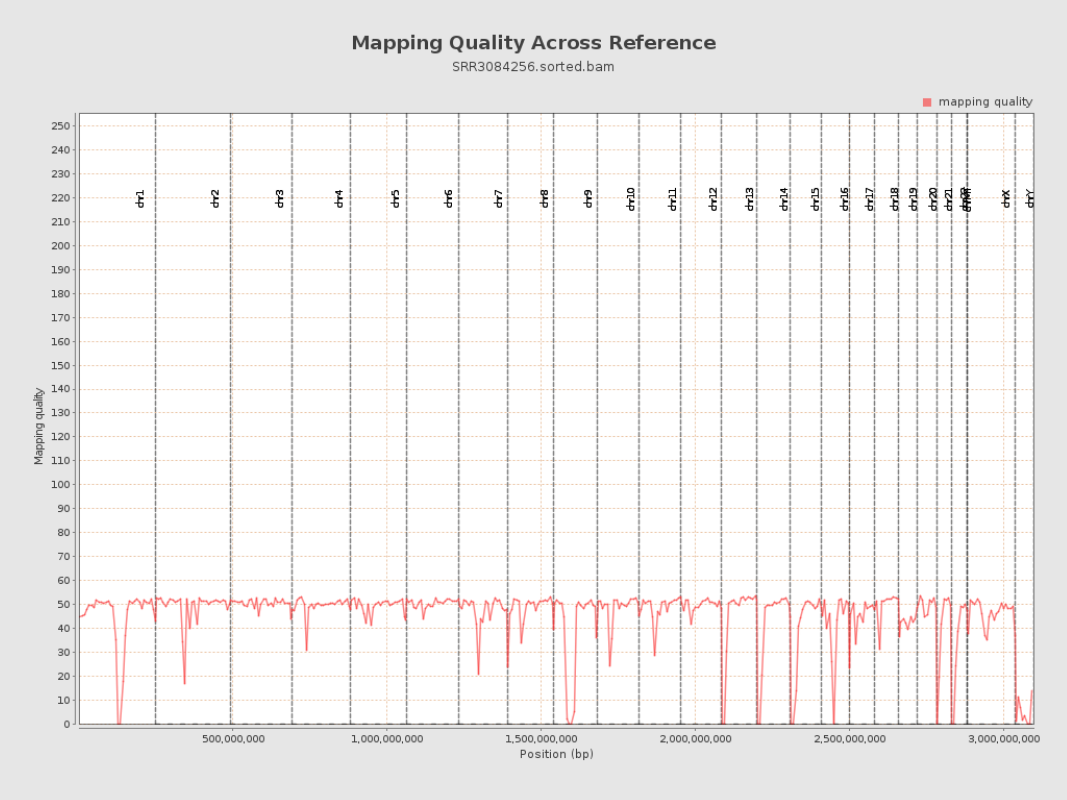
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram