Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 10:50:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084353.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_SRR3084353 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084353.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 10:50:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084353.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,172,154
Mapped reads	1,967,795 / 90.59%
Unmapped reads	204,359 / 9.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,394 / 0.62%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	70,761 / 3.26%
Duplication rate	2.79%
Clipped reads	881,636 / 40.59%

2.2. ACGT Content

Number/percentage of A's	36,736,399 / 27.88%
Number/percentage of C's	25,674,527 / 19.48%
Number/percentage of T's	40,234,830 / 30.53%
Number/percentage of G's	28,981,926 / 21.99%
Number/percentage of N's	158,874 / 0.12%
GC Percentage	41.47%

2.3. Coverage

Mean	0.0426

Standard Deviation	0.3485

2.4. Mapping Quality

Mean Mapping Quality	45.24

2.5. Mismatches and indels

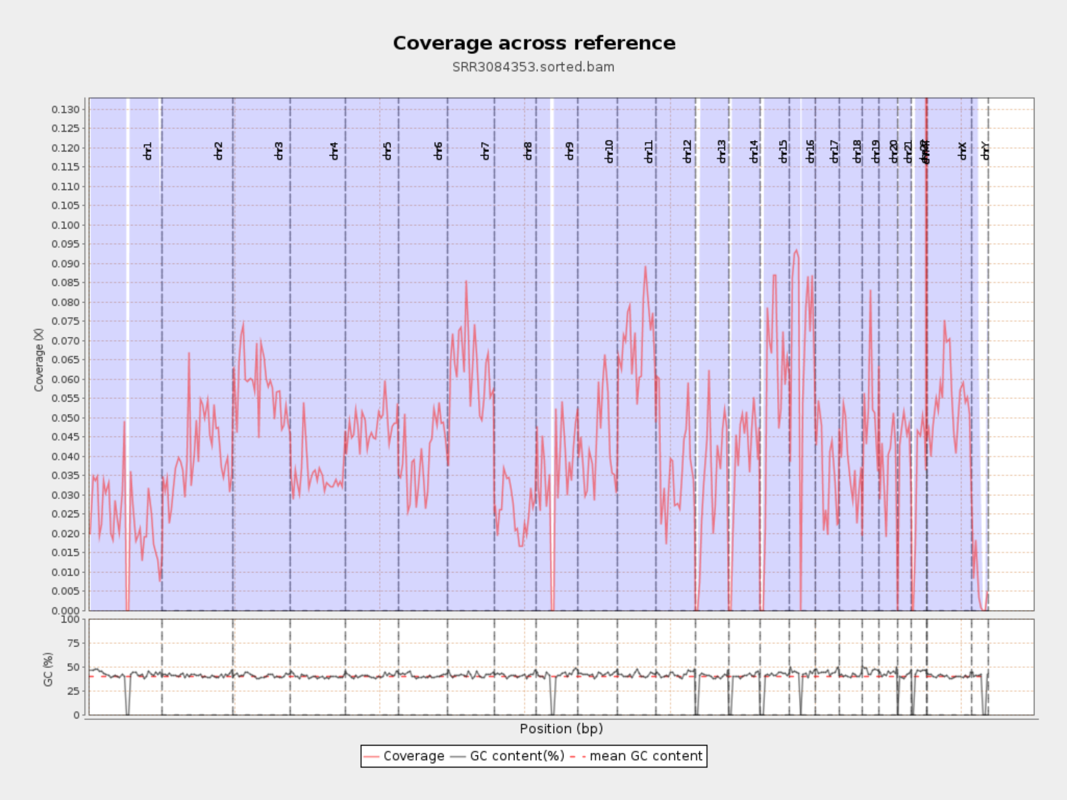
General error rate	1.01%
Mismatches	1,316,041
Insertions	9,788
Mapped reads with at least one insertion	0.49%
Deletions	26,587
Mapped reads with at least one deletion	1.34%
Homopolymer indels	46.2%

2.6. Chromosome stats

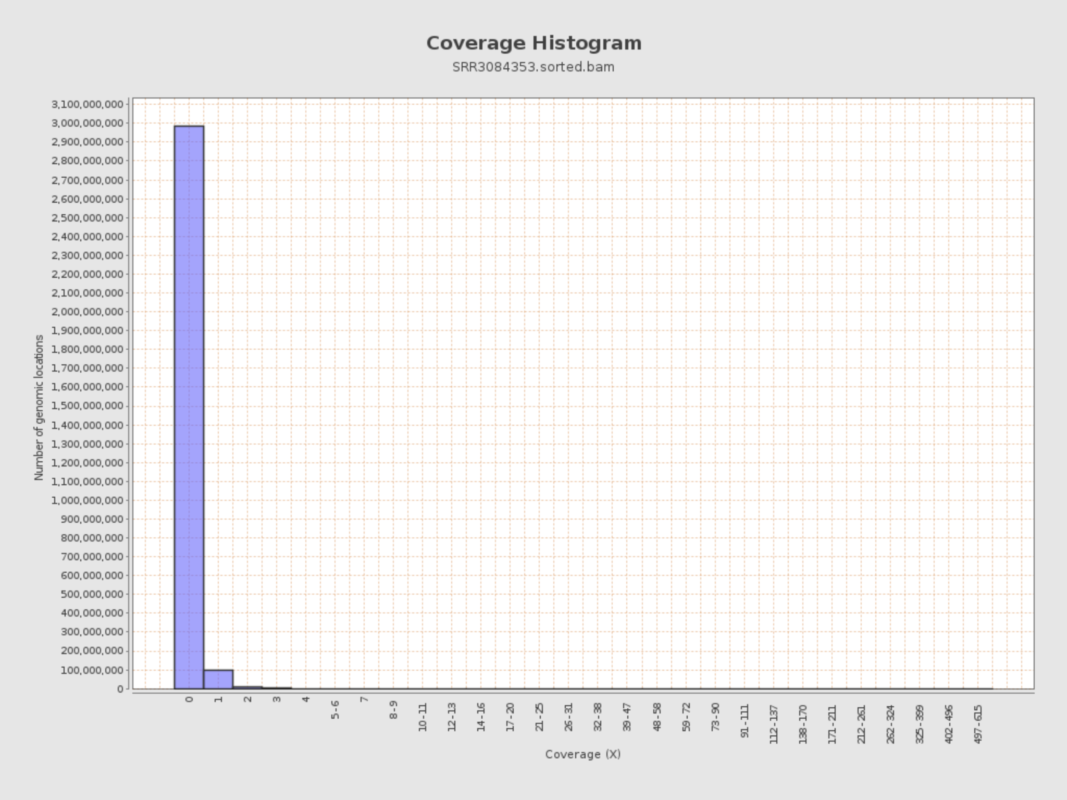
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5728415	0.023	0.5347
chr2	243199373	9842274	0.0405	0.3604
chr3	198022430	11527346	0.0582	0.2721
chr4	191154276	6678050	0.0349	0.2224
chr5	180915260	8634211	0.0477	0.2487
chr6	171115067	6752569	0.0395	0.2383
chr7	159138663	10073066	0.0633	0.5173

chr8	146364022	3797107	0.0259	0.3434
chr9	141213431	4863982	0.0344	0.3205
chr10	135534747	5796183	0.0428	0.2766
chr11	135006516	9431650	0.0699	0.4159
chr12	133851895	5002116	0.0374	0.2237
chr13	115169878	3770022	0.0327	0.2057
chr14	107349540	4112486	0.0383	0.2425
chr15	102531392	5644455	0.0551	0.2685
chr16	90354753	6454868	0.0714	0.3339
chr17	81195210	2806105	0.0346	0.2641
chr18	78077248	2952318	0.0378	0.726
chr19	59128983	3086943	0.0522	0.4666
chr20	63025520	2340377	0.0371	0.2308
chr21	48129895	1975166	0.041	0.2464
chr22	51304566	1659460	0.0323	0.2034
chrMT	16571	122260	7.3779	5.0242
chrX	155270560	8406364	0.0541	0.2952
chrY	59373566	375281	0.0063	0.1333

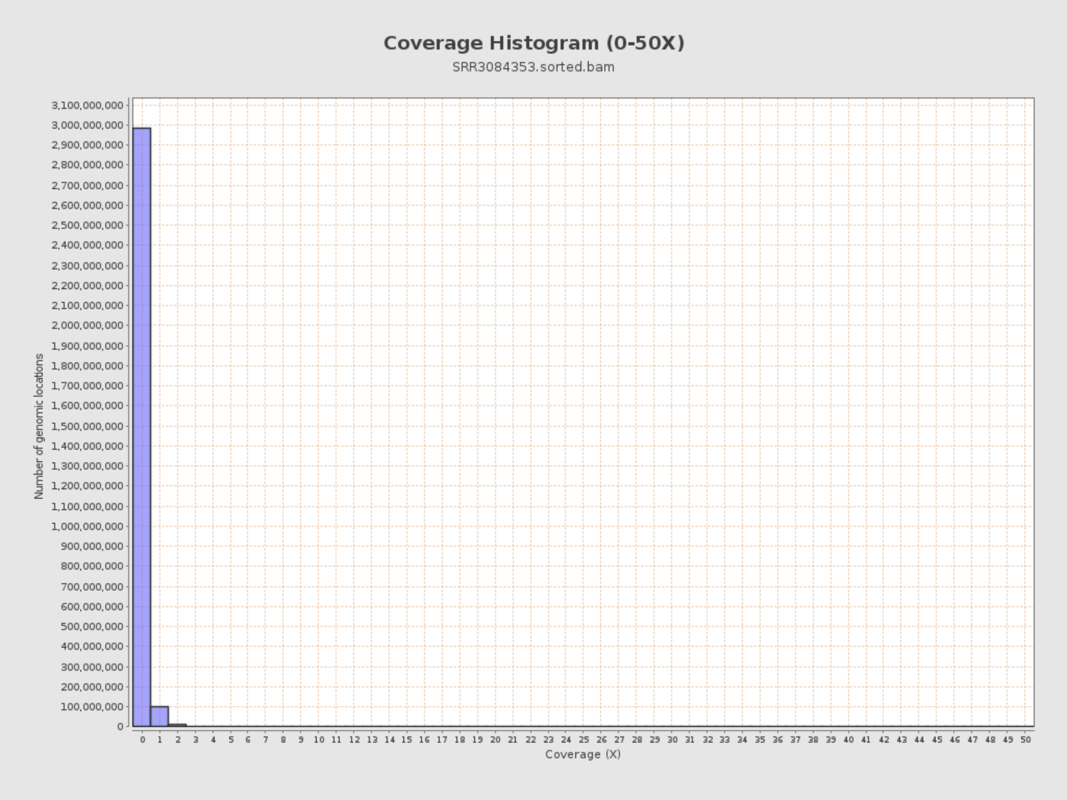
3. Results : Coverage across reference



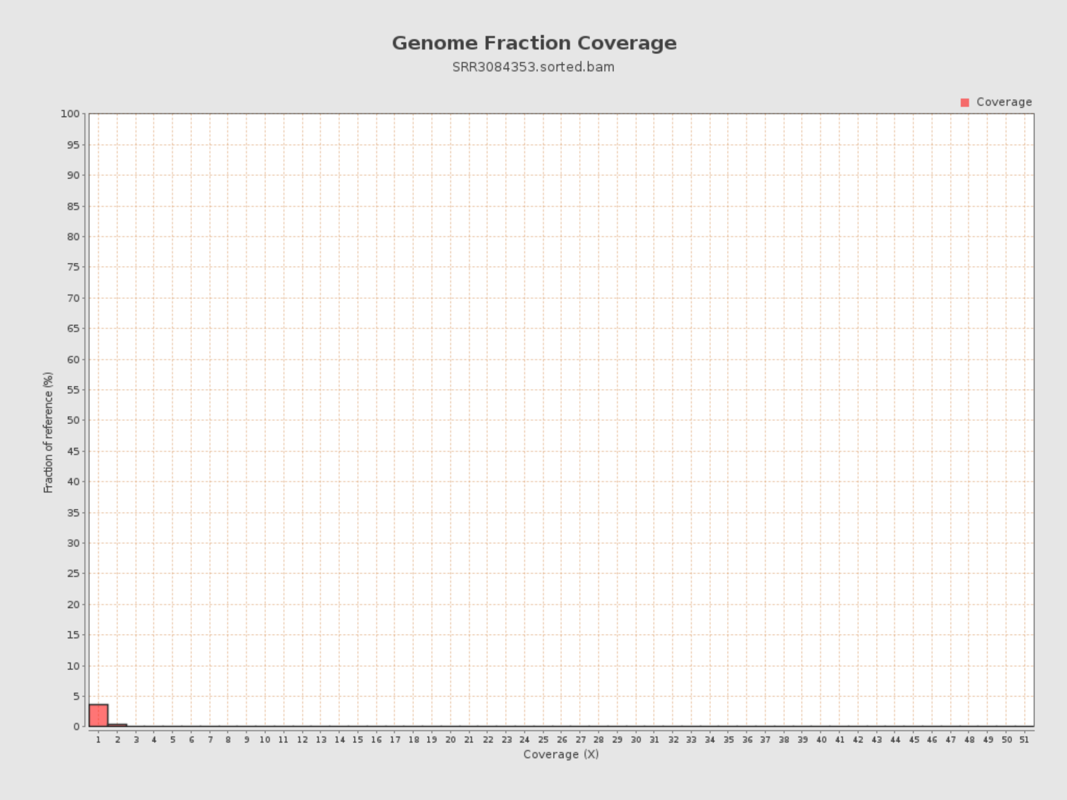
4. Results : Coverage Histogram



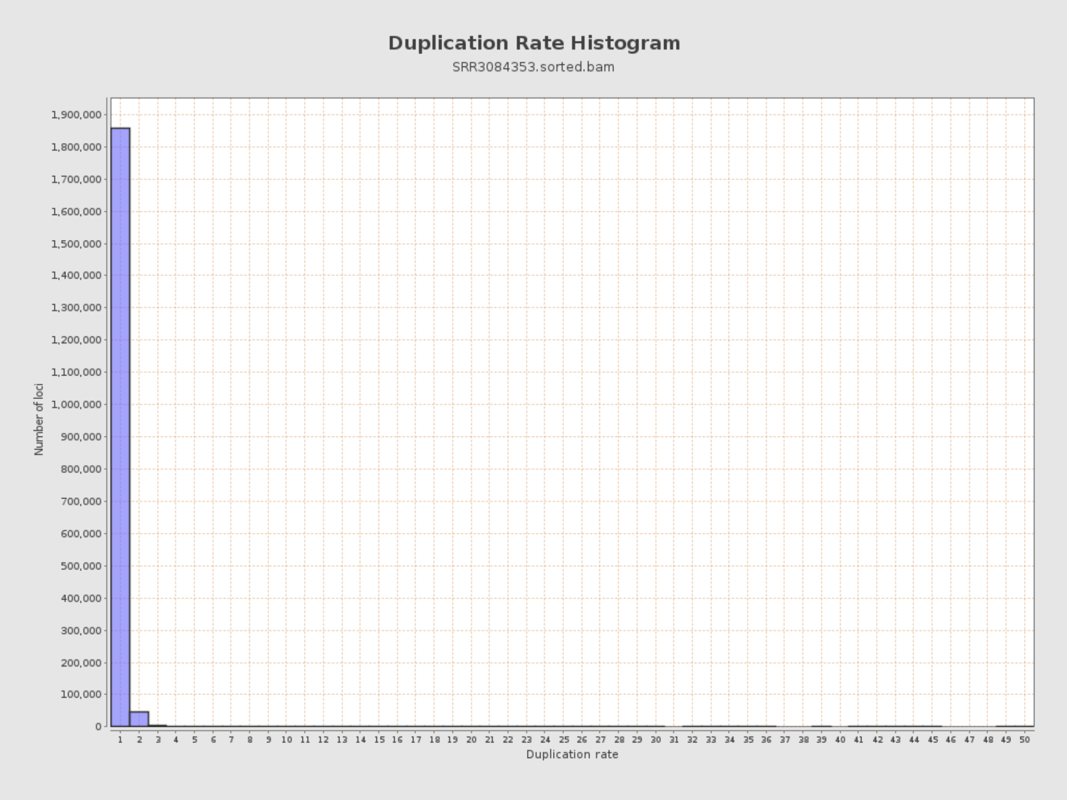
5. Results : Coverage Histogram (0-50X)



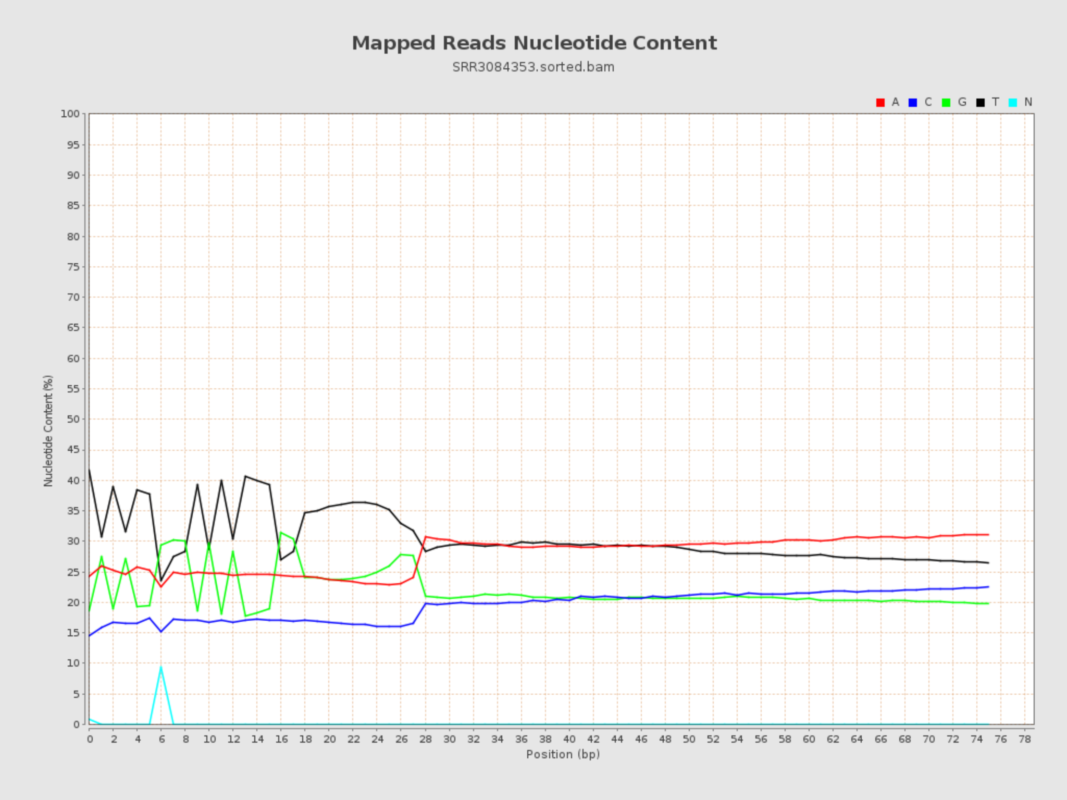
6. Results : Genome Fraction Coverage



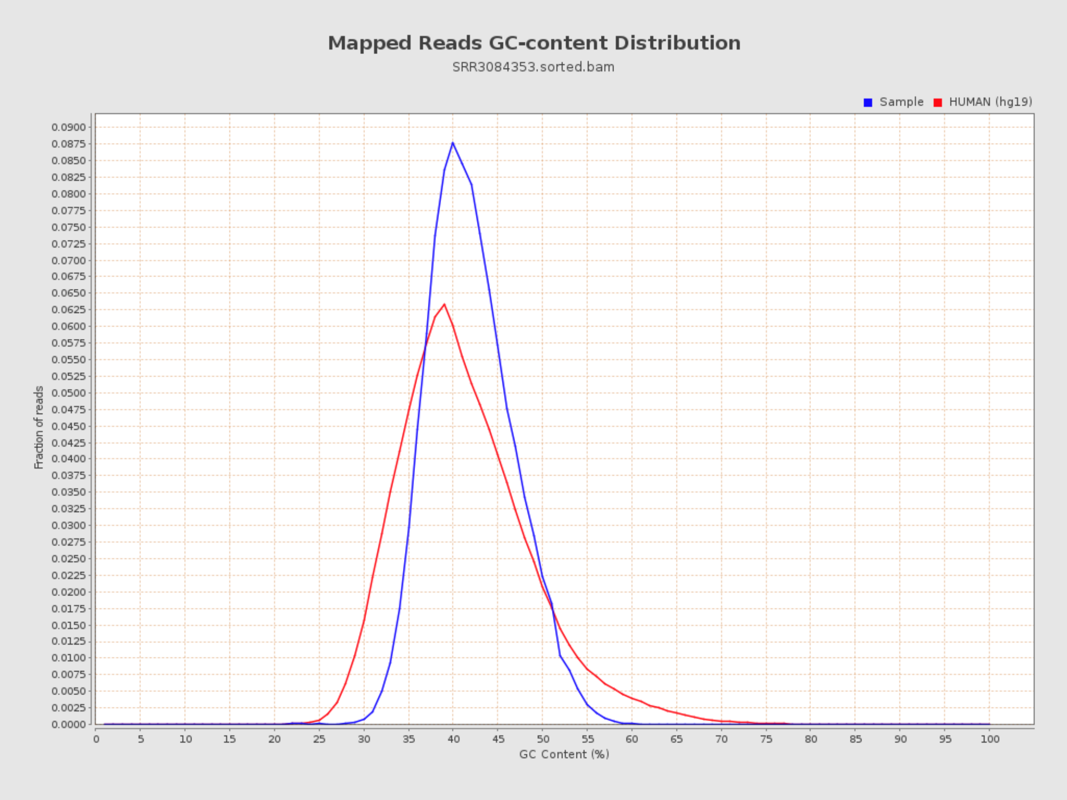
7. Results : Duplication Rate Histogram



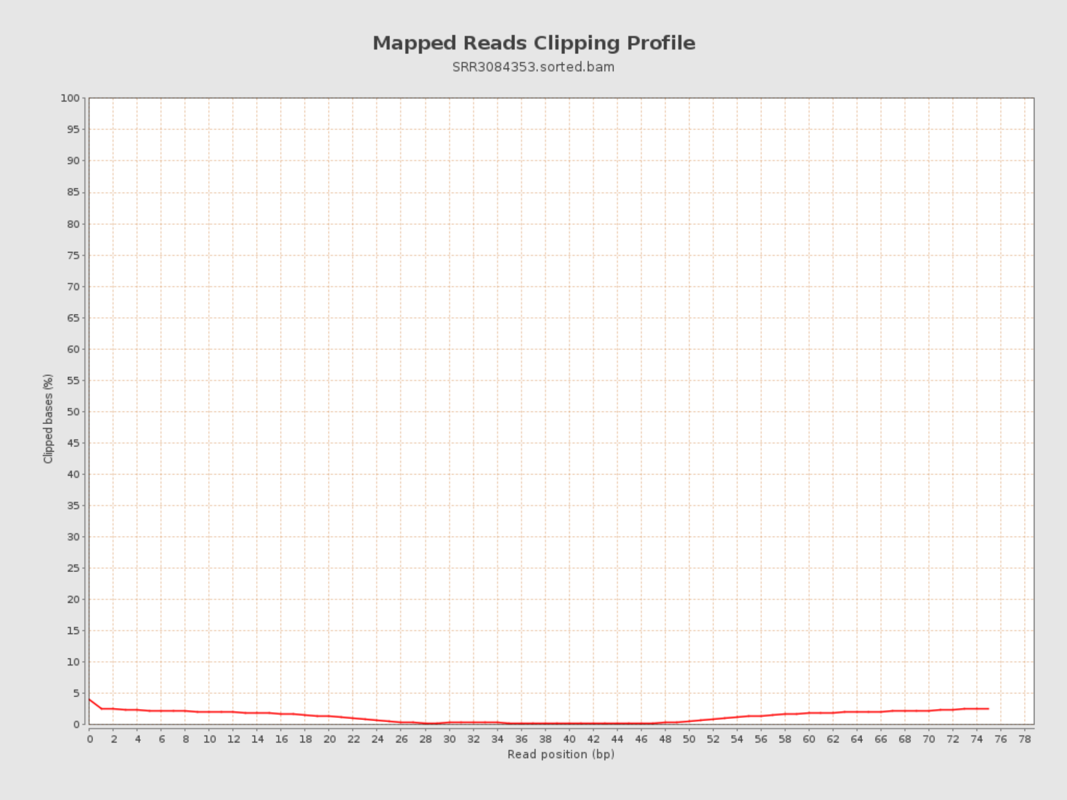
8. Results : Mapped Reads Nucleotide Content



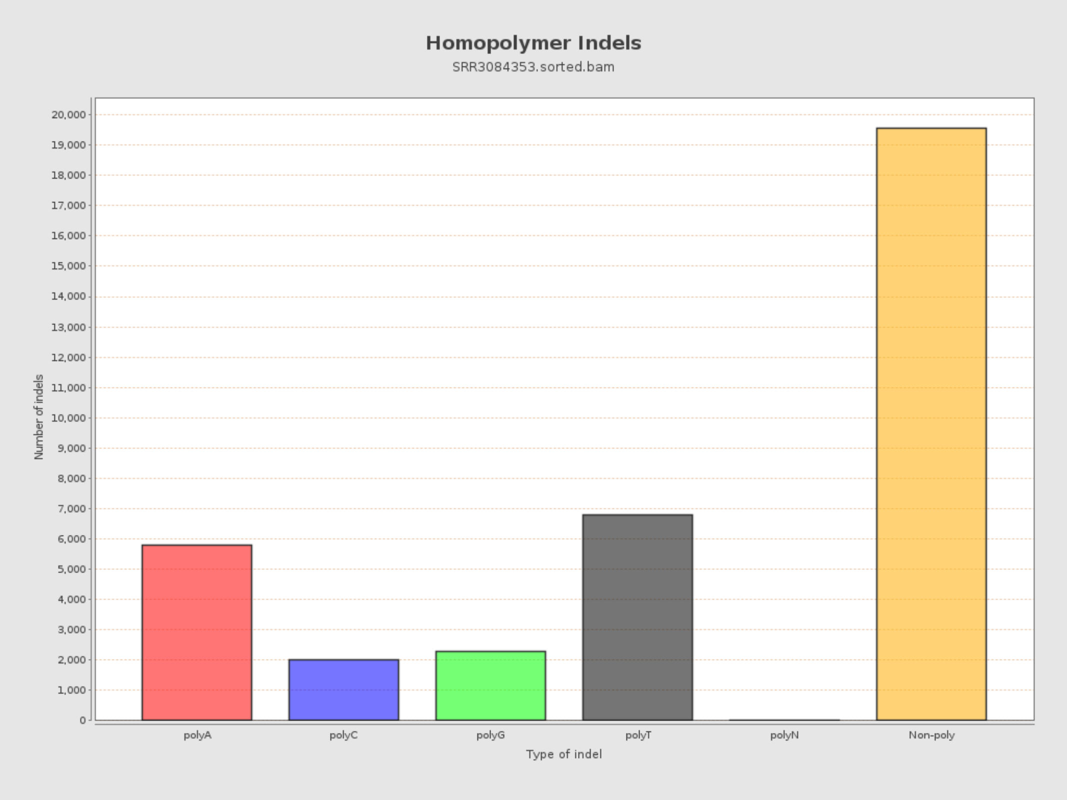
9. Results : Mapped Reads GC-content Distribution



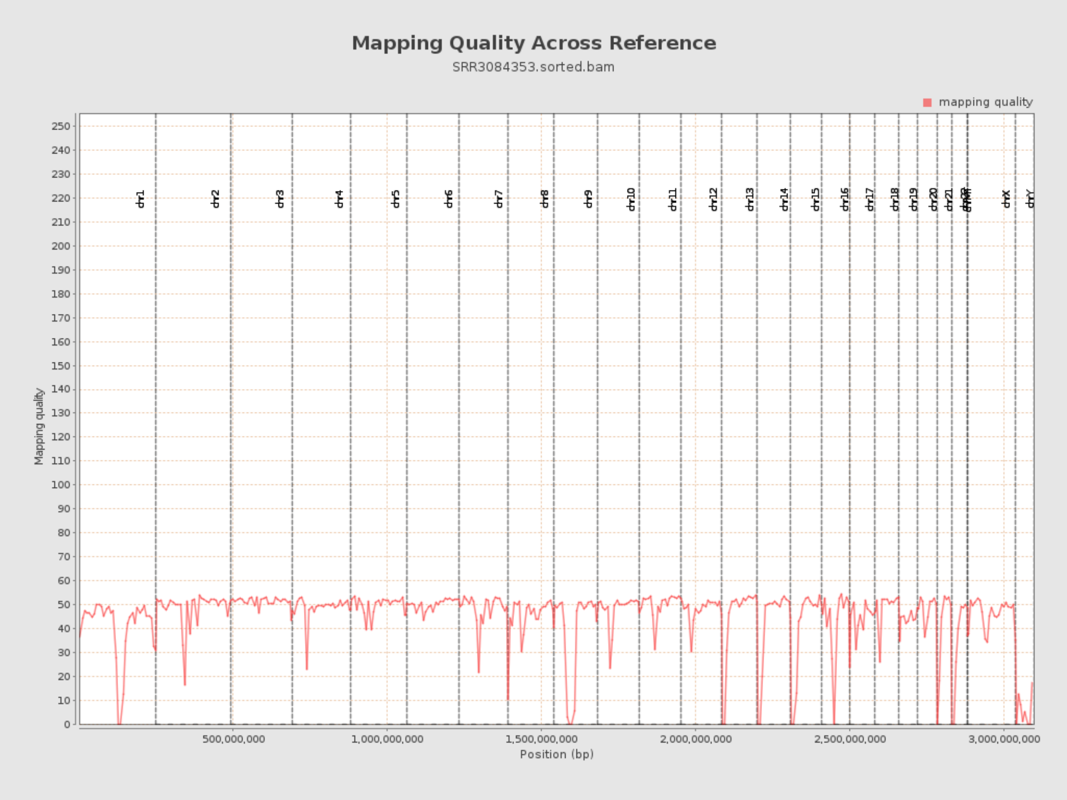
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram