Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 10:57:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084356.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_SRR3084356 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084356.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 10:57:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084356.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,083,964
Mapped reads	1,868,465 / 89.66%
Unmapped reads	215,499 / 10.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,309 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	57,943 / 2.78%
Duplication rate	2.55%
Clipped reads	903,633 / 43.36%

2.2. ACGT Content

Number/percentage of A's	34,371,679 / 27.83%
Number/percentage of C's	23,952,449 / 19.39%
Number/percentage of T's	37,566,650 / 30.42%
Number/percentage of G's	27,465,141 / 22.24%
Number/percentage of N's	152,293 / 0.12%
GC Percentage	41.63%

2.3. Coverage

Mean	0.0399

Standard Deviation	0.2921

2.4. Mapping Quality

Mean Mapping Quality	44.93

2.5. Mismatches and indels

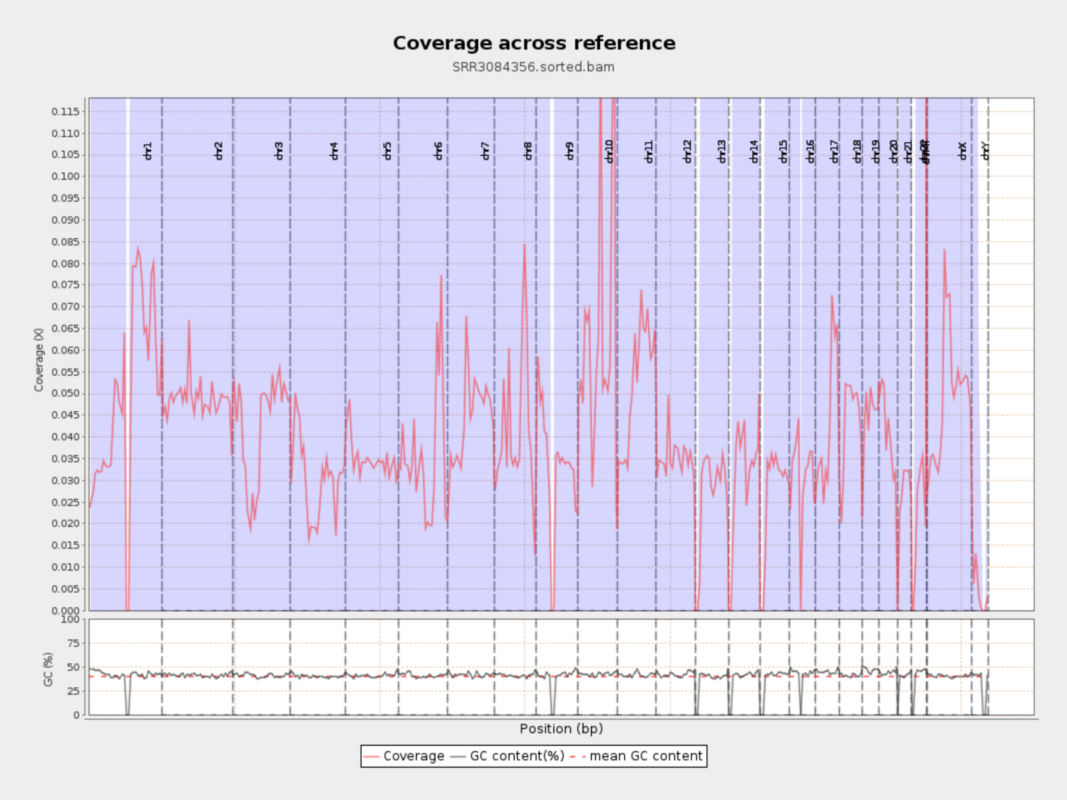
General error rate	0.98%
Mismatches	1,197,423
Insertions	8,667
Mapped reads with at least one insertion	0.46%
Deletions	24,705
Mapped reads with at least one deletion	1.31%
Homopolymer indels	46.15%

2.6. Chromosome stats

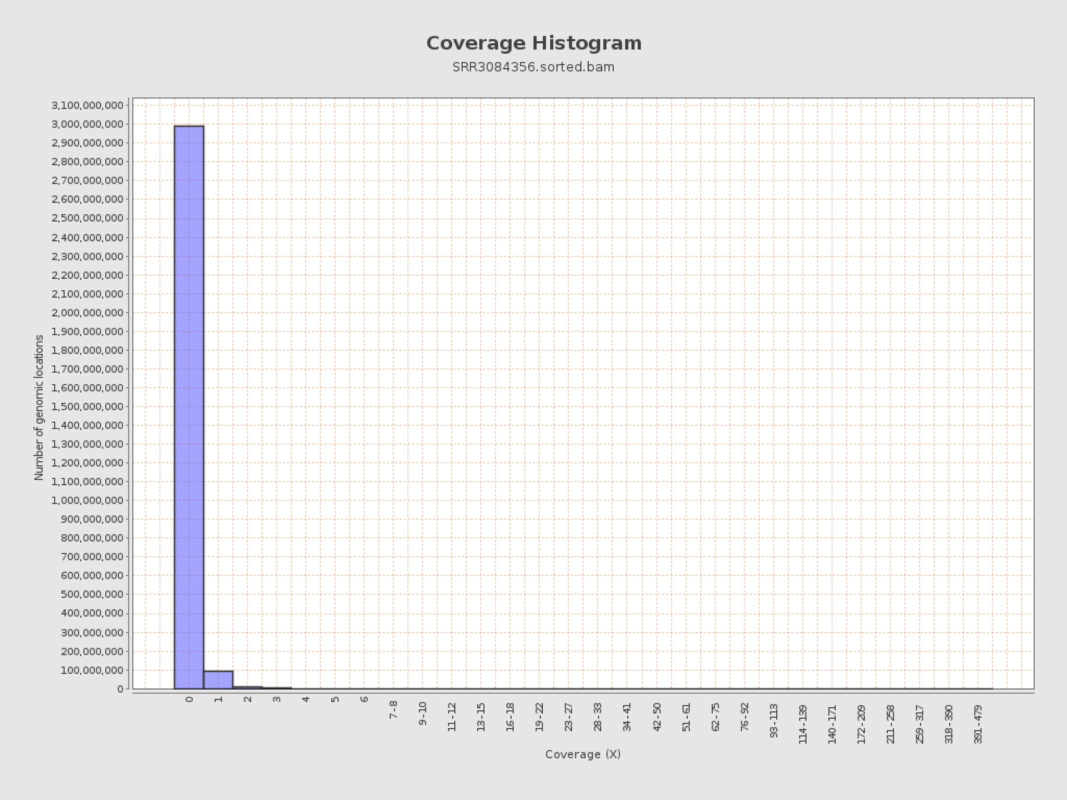
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12260185	0.0492	0.4593
chr2	243199373	11872022	0.0488	0.3356
chr3	198022430	8438643	0.0426	0.2325
chr4	191154276	5805726	0.0304	0.202
chr5	180915260	6323338	0.035	0.209
chr6	171115067	6057105	0.0354	0.2334
chr7	159138663	7140221	0.0449	0.4222

chr8	146364022	6104137	0.0417	0.2693
chr9	141213431	4693156	0.0332	0.2564
chr10	135534747	8897996	0.0657	0.4074
chr11	135006516	7038171	0.0521	0.3048
chr12	133851895	4700308	0.0351	0.2104
chr13	115169878	3030387	0.0263	0.1805
chr14	107349540	3292634	0.0307	0.2042
chr15	102531392	2738876	0.0267	0.1886
chr16	90354753	2796067	0.0309	0.2148
chr17	81195210	3508787	0.0432	0.2479
chr18	78077248	3414424	0.0437	0.4079
chr19	59128983	2689162	0.0455	0.3384
chr20	63025520	2562177	0.0407	0.2282
chr21	48129895	1254982	0.0261	0.1886
chr22	51304566	1059110	0.0206	0.1587
chrMT	16571	3851	0.2324	0.5605
chrX	155270560	7592714	0.0489	0.2669
chrY	59373566	276697	0.0047	0.1011

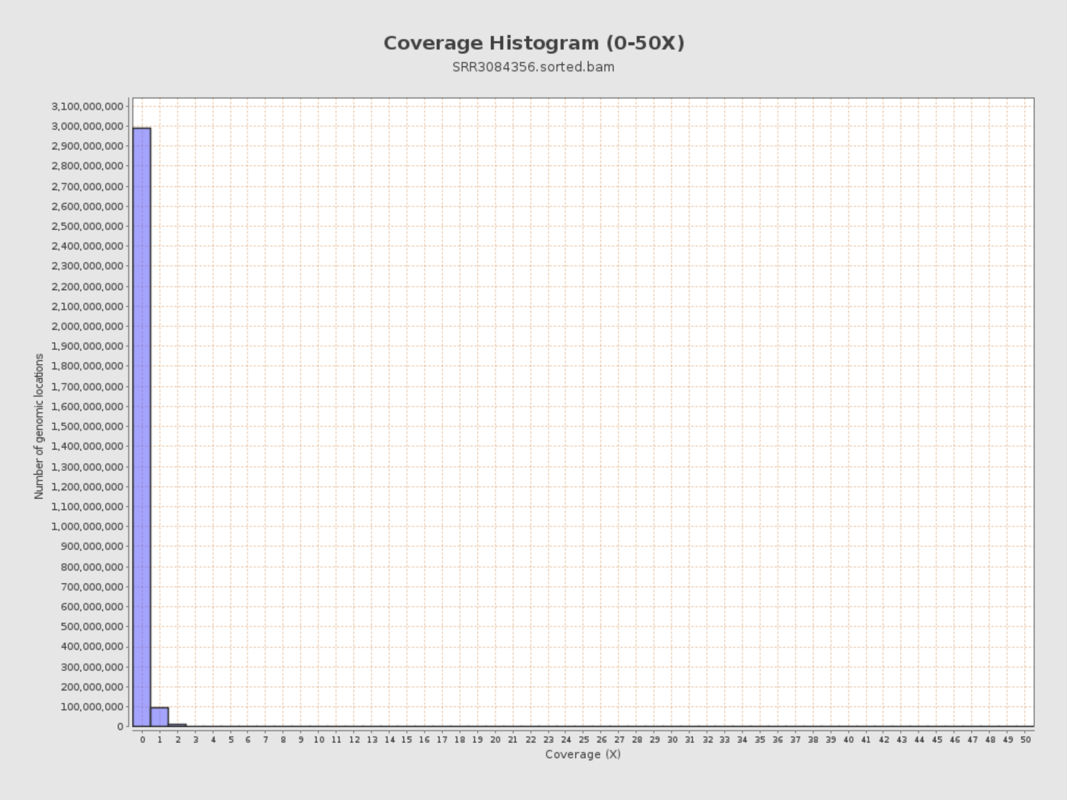
3. Results : Coverage across reference



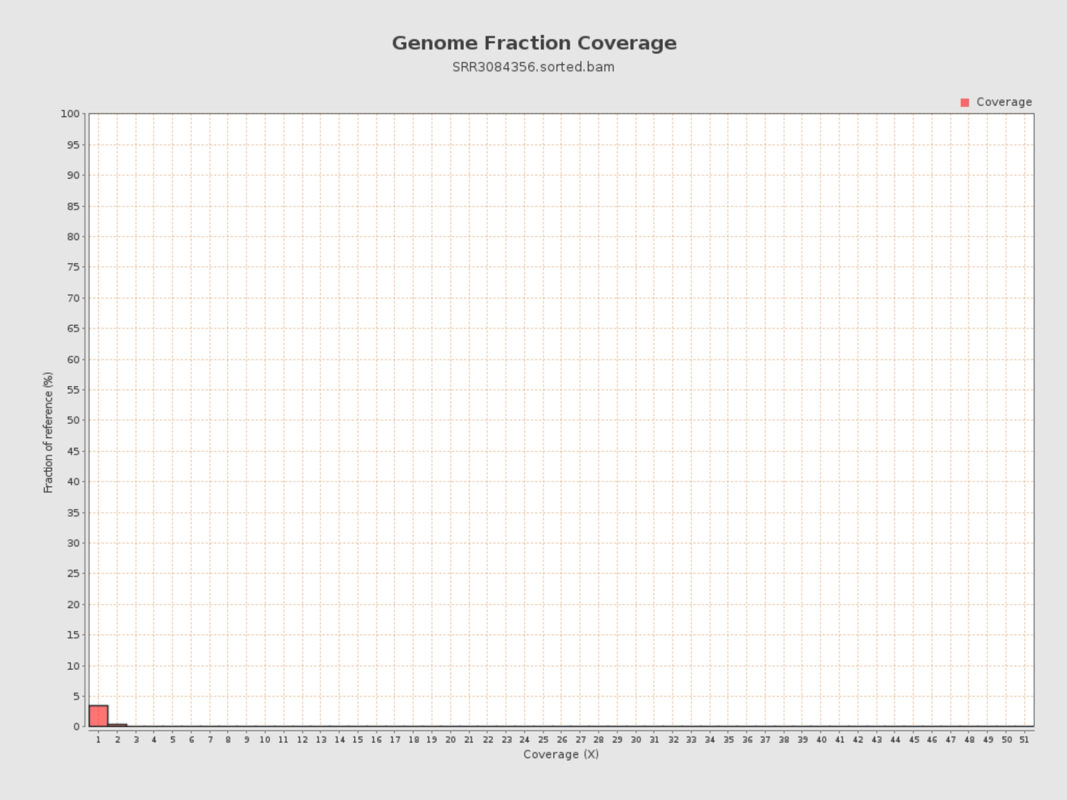
4. Results : Coverage Histogram



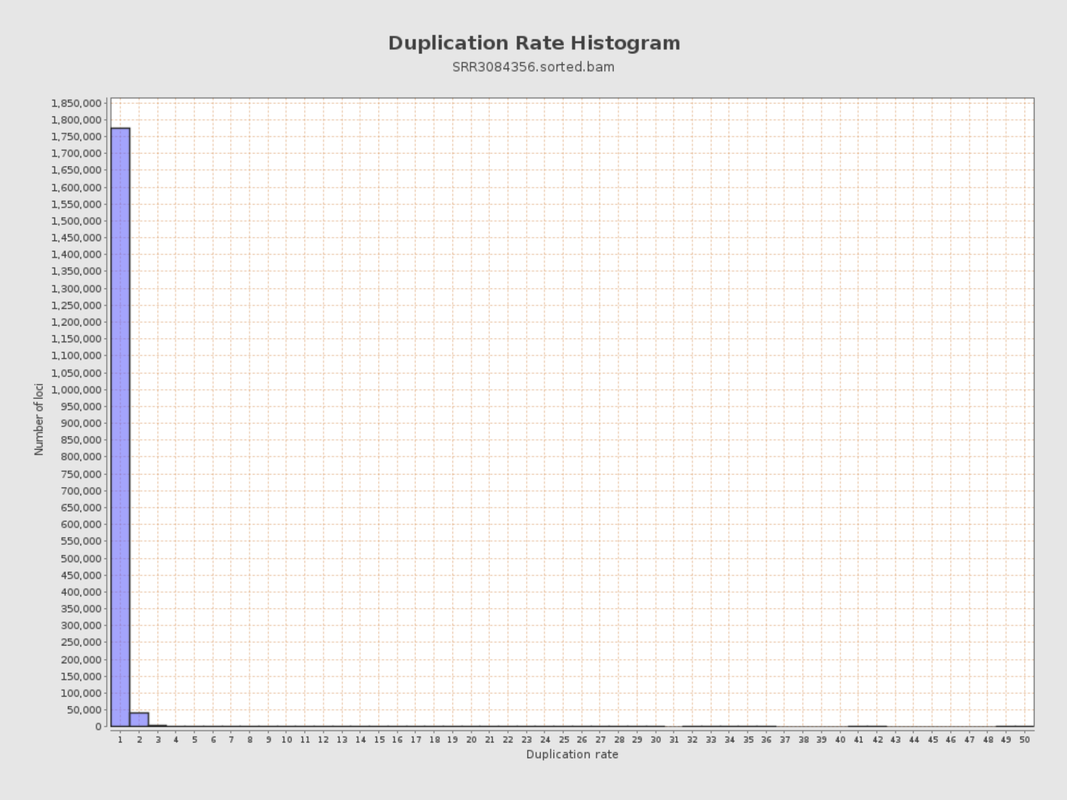
5. Results : Coverage Histogram (0-50X)



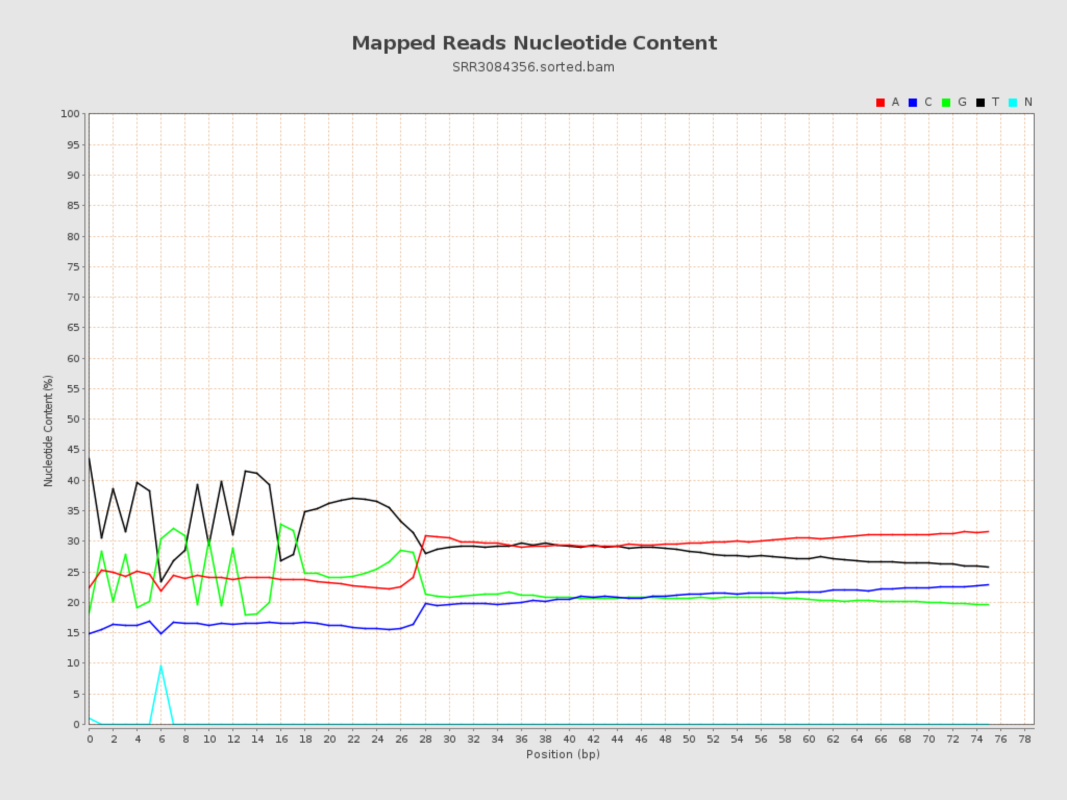
6. Results : Genome Fraction Coverage



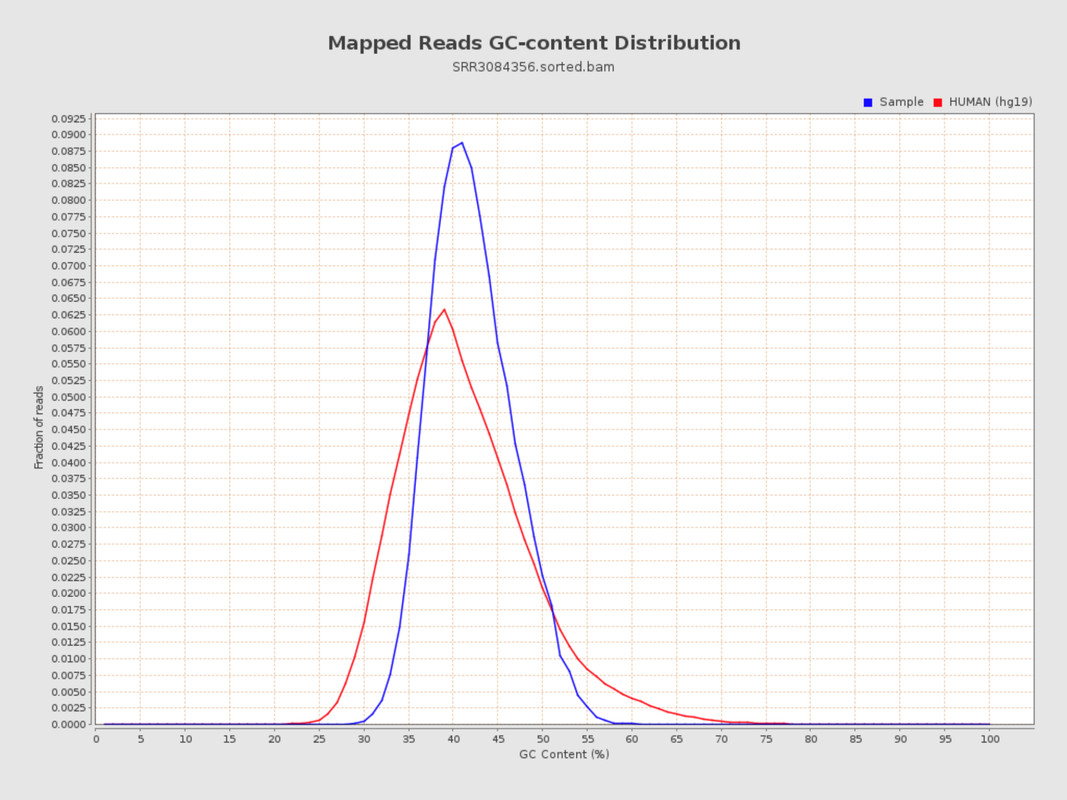
7. Results : Duplication Rate Histogram



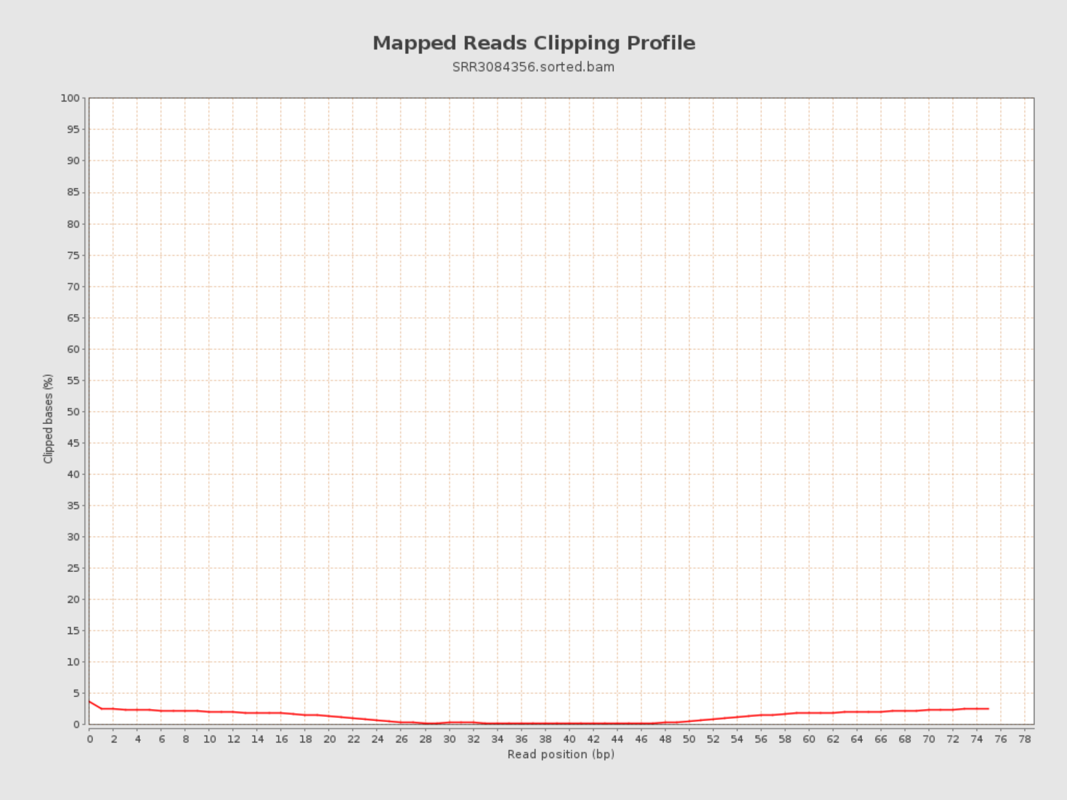
8. Results : Mapped Reads Nucleotide Content



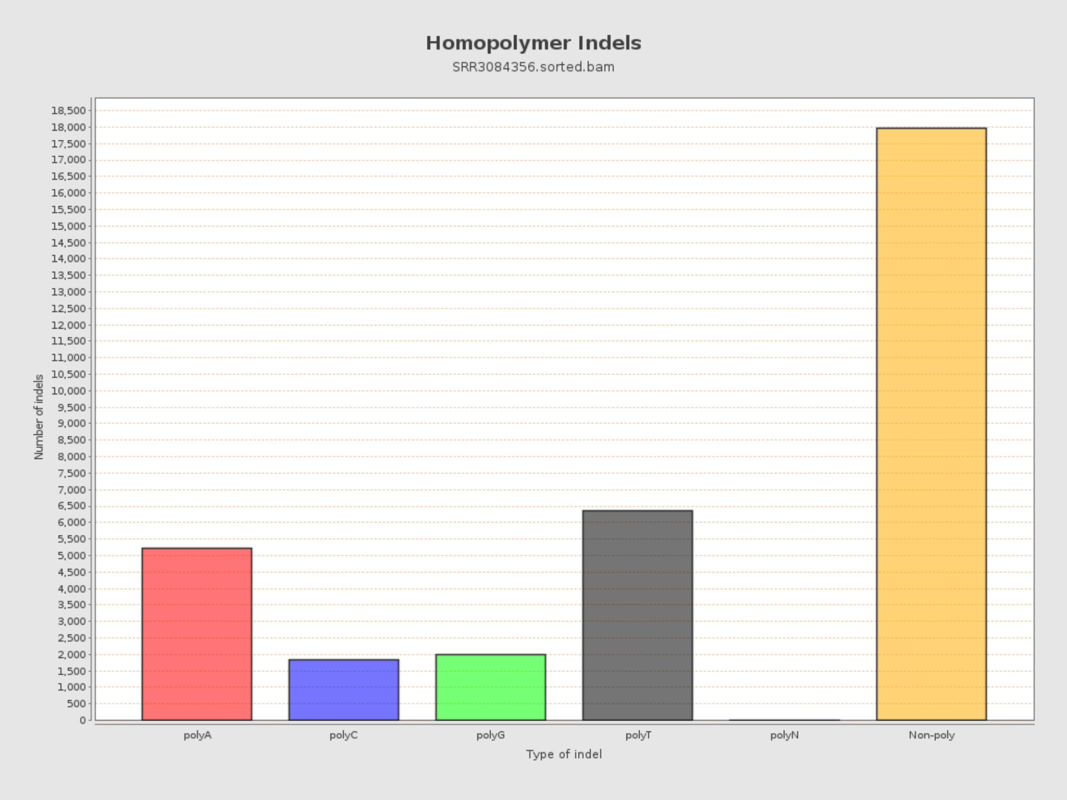
9. Results : Mapped Reads GC-content Distribution



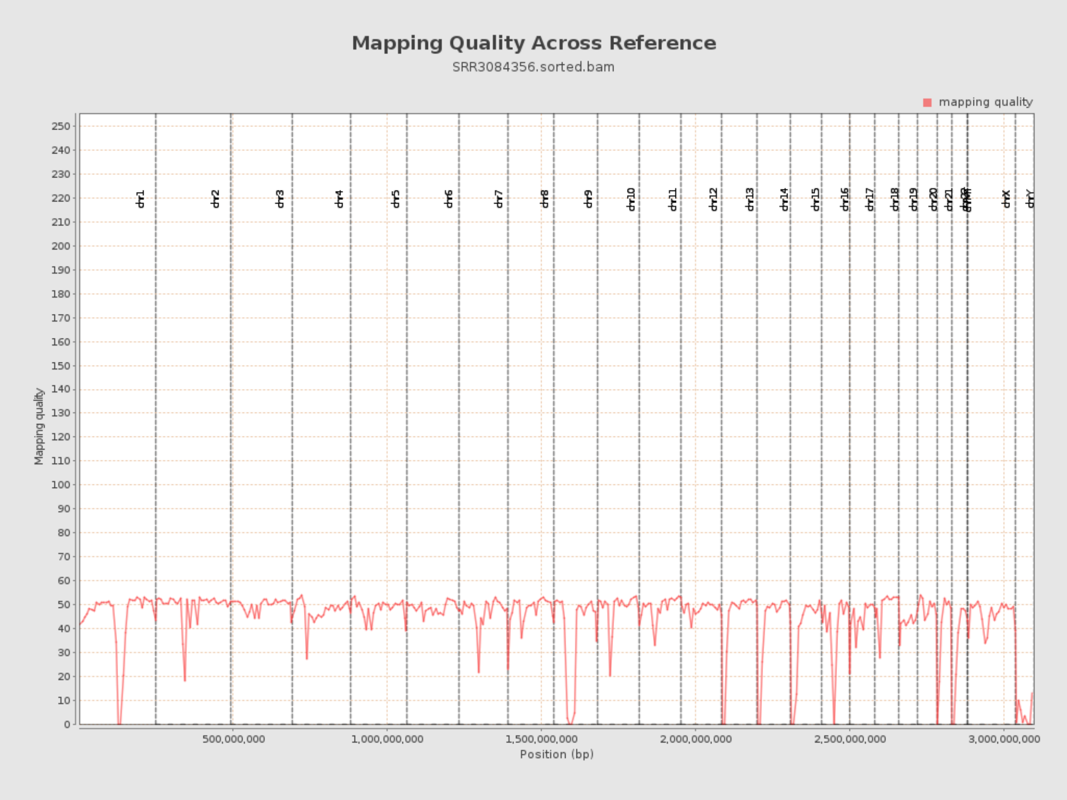
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram