Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 10:13:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084346.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_SRR3084346 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084346.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 10:13:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084346.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,268,312
Mapped reads	2,038,091 / 89.85%
Unmapped reads	230,221 / 10.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,700 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	65,325 / 2.88%
Duplication rate	2.7%
Clipped reads	942,647 / 41.56%

2.2. ACGT Content

Number/percentage of A's	37,526,413 / 27.69%
Number/percentage of C's	26,441,533 / 19.51%
Number/percentage of T's	41,261,912 / 30.44%
Number/percentage of G's	30,132,072 / 22.23%
Number/percentage of N's	176,642 / 0.13%
GC Percentage	41.74%

2.3. Coverage

Mean	0.0438

Standard Deviation	0.2977

2.4. Mapping Quality

Mean Mapping Quality	45.65

2.5. Mismatches and indels

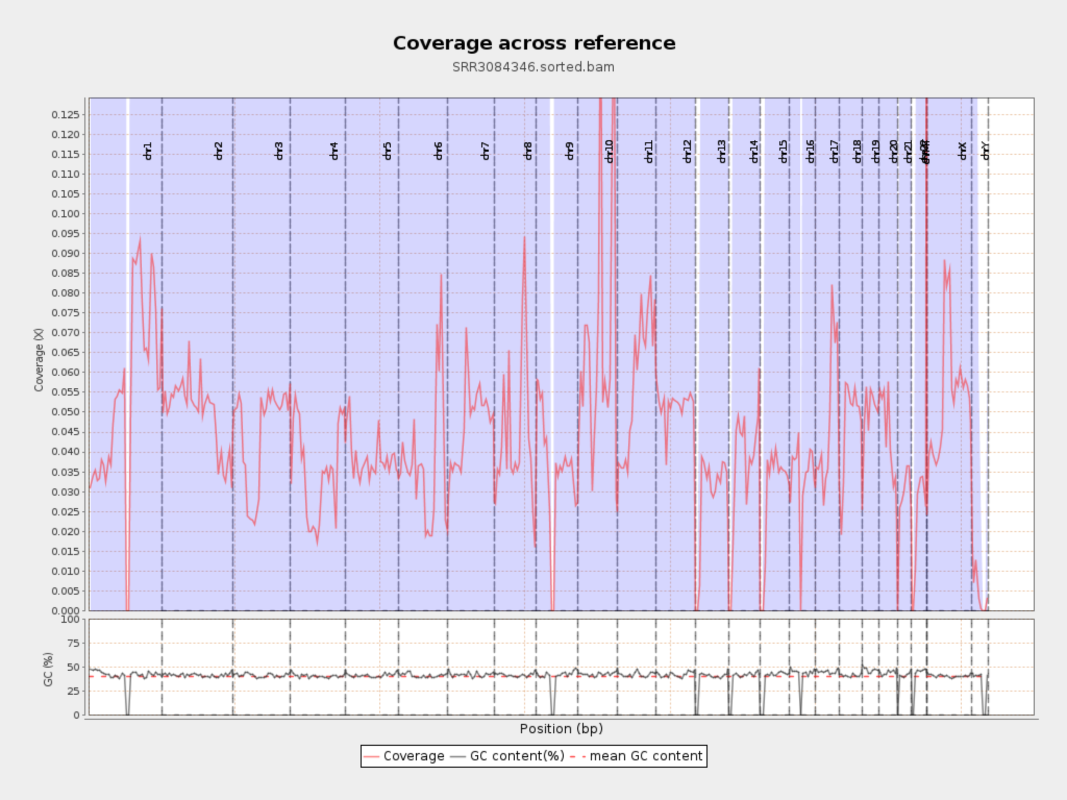
General error rate	1.02%
Mismatches	1,364,406
Insertions	9,348
Mapped reads with at least one insertion	0.45%
Deletions	27,382
Mapped reads with at least one deletion	1.33%
Homopolymer indels	46.92%

2.6. Chromosome stats

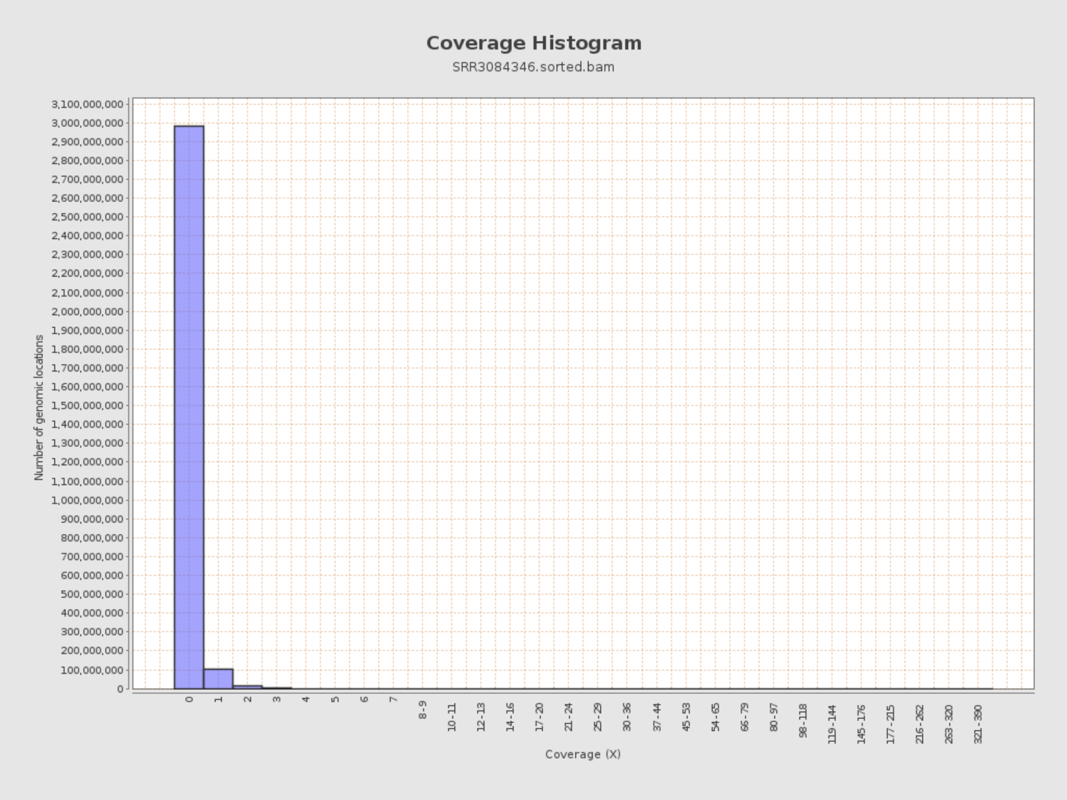
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13473322	0.0541	0.4401
chr2	243199373	12156965	0.05	0.336
chr3	198022430	8831882	0.0446	0.2403
chr4	191154276	6792406	0.0355	0.2204
chr5	180915260	6923338	0.0383	0.2204
chr6	171115067	6444904	0.0377	0.2461
chr7	159138663	7581179	0.0476	0.4291

chr8	146364022	6527420	0.0446	0.2823
chr9	141213431	4946969	0.035	0.2593
chr10	135534747	9636470	0.0711	0.396
chr11	135006516	7800859	0.0578	0.3235
chr12	133851895	6895693	0.0515	0.2578
chr13	115169878	3271846	0.0284	0.1898
chr14	107349540	3804841	0.0354	0.2174
chr15	102531392	3005186	0.0293	0.2007
chr16	90354753	3030460	0.0335	0.2227
chr17	81195210	3917993	0.0483	0.2681
chr18	78077248	3664513	0.0469	0.4031
chr19	59128983	2978763	0.0504	0.3368
chr20	63025520	2813272	0.0446	0.2423
chr21	48129895	1334734	0.0277	0.1966
chr22	51304566	1108216	0.0216	0.1646
chrMT	16571	4819	0.2908	0.6283
chrX	155270560	8361846	0.0539	0.2883
chrY	59373566	278070	0.0047	0.1019

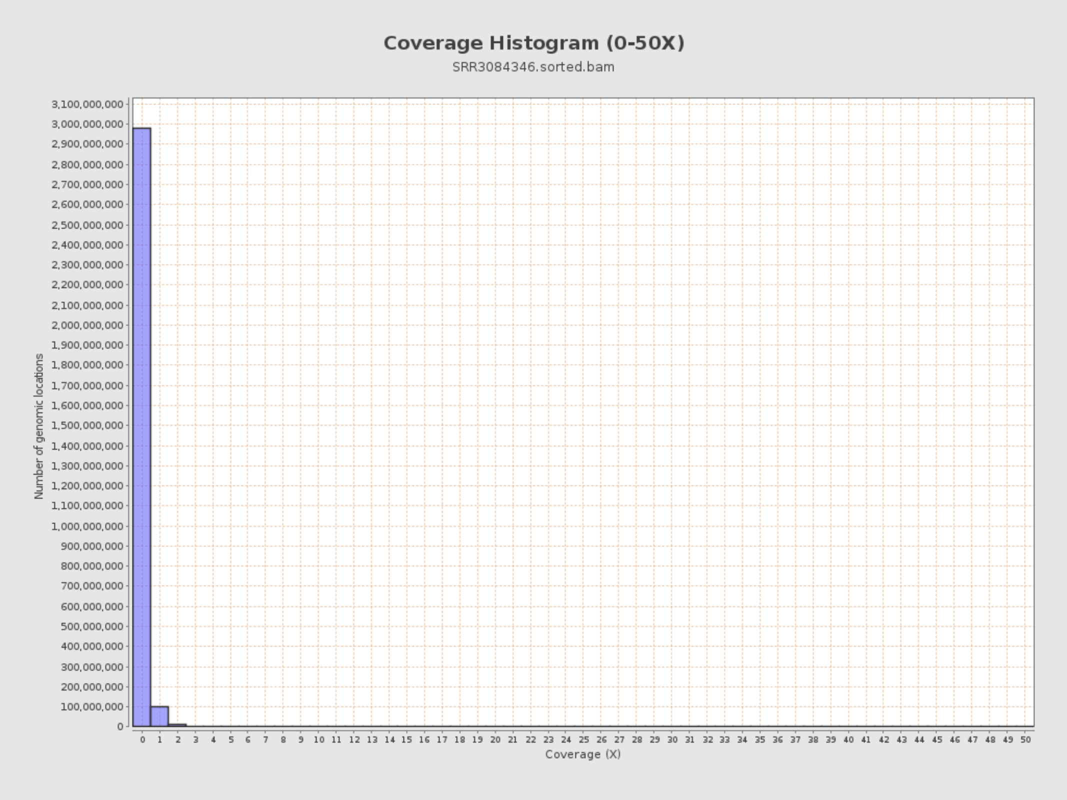
3. Results : Coverage across reference



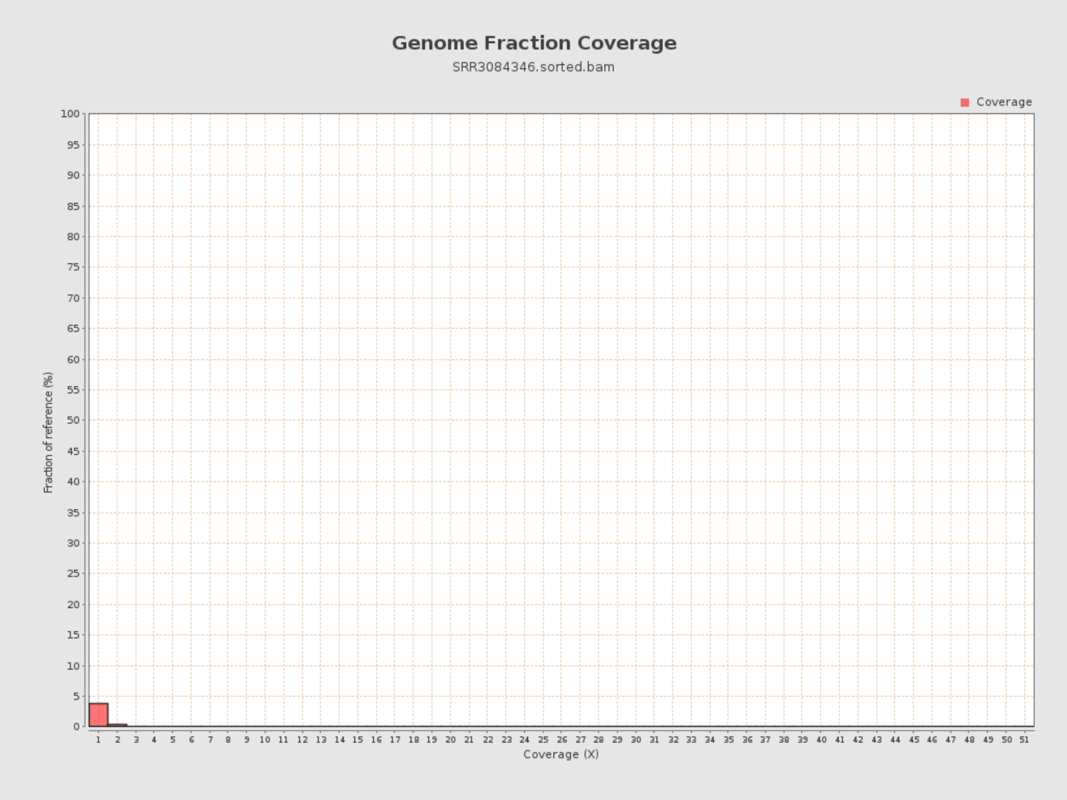
4. Results : Coverage Histogram



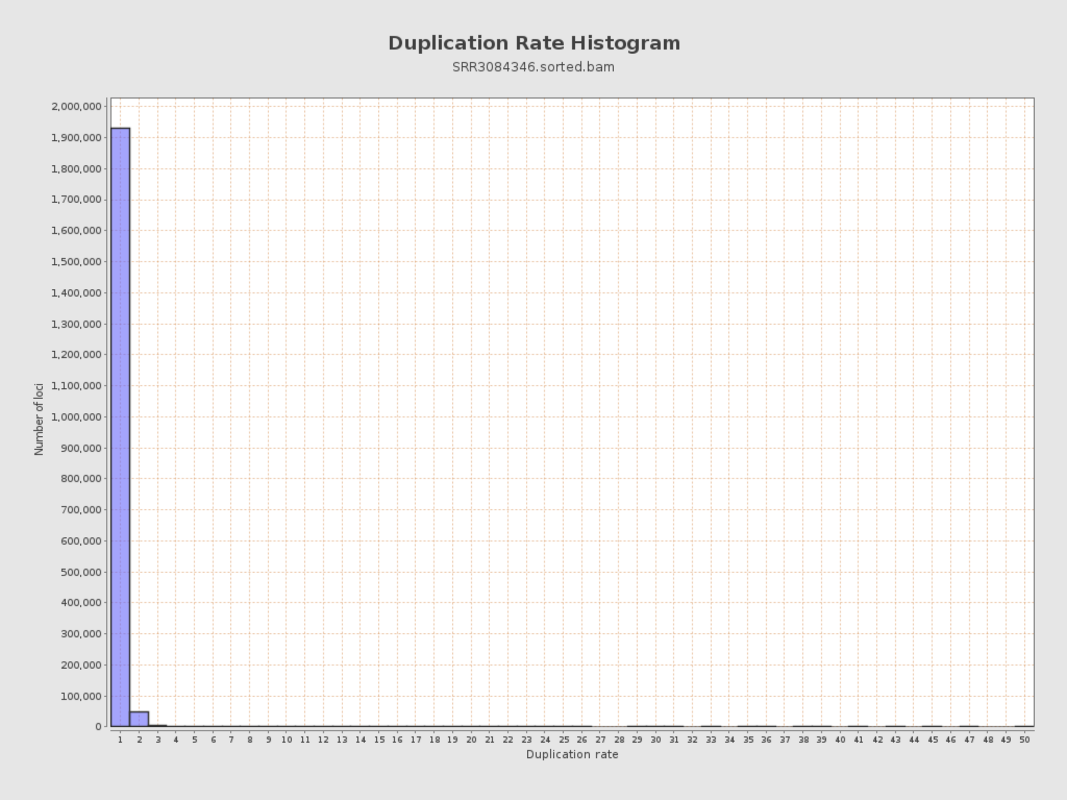
5. Results : Coverage Histogram (0-50X)



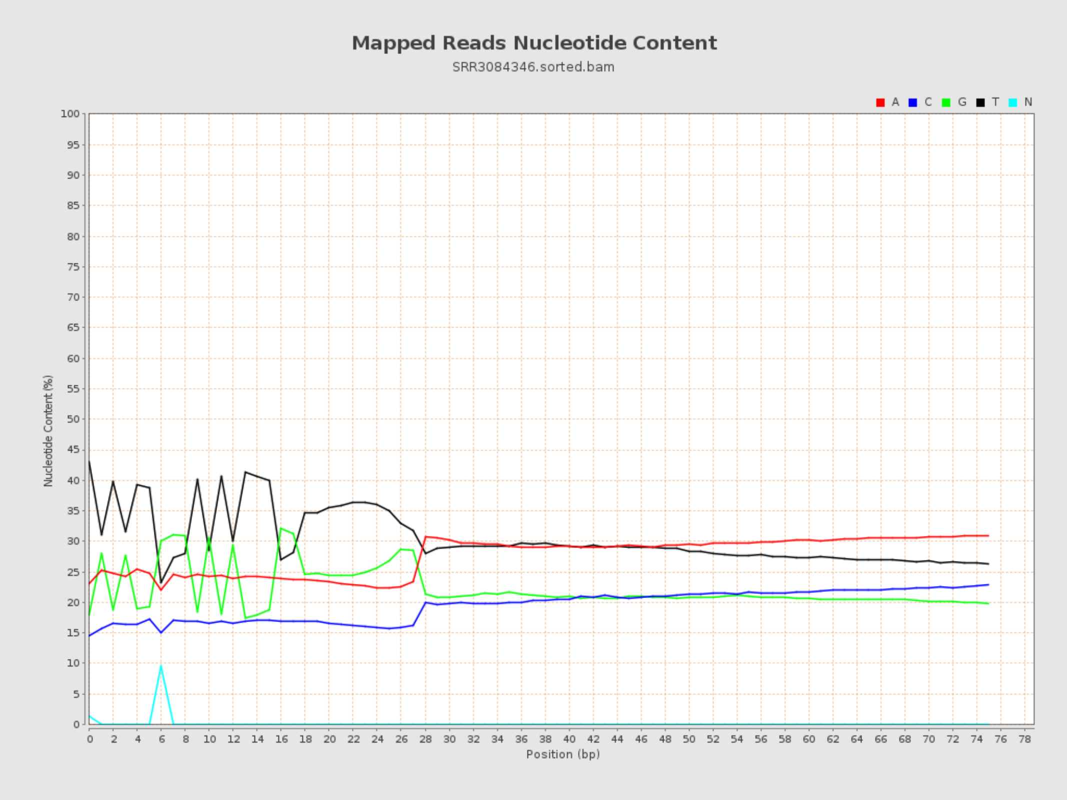
6. Results : Genome Fraction Coverage



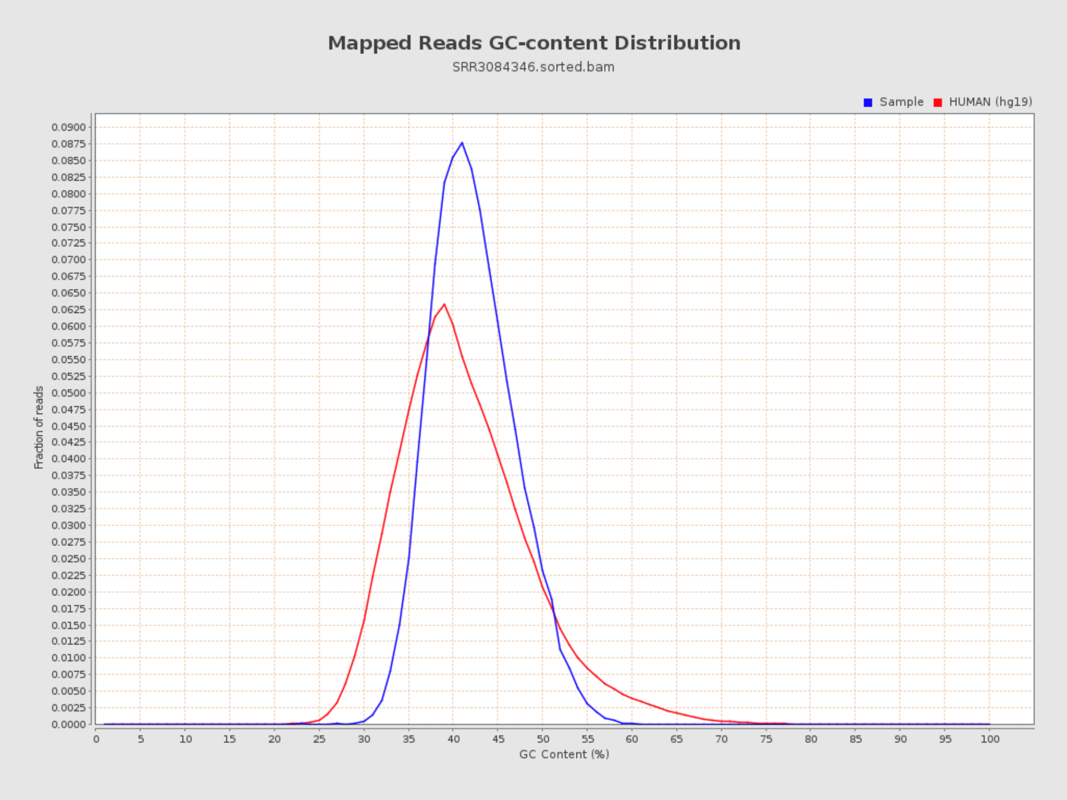
7. Results : Duplication Rate Histogram



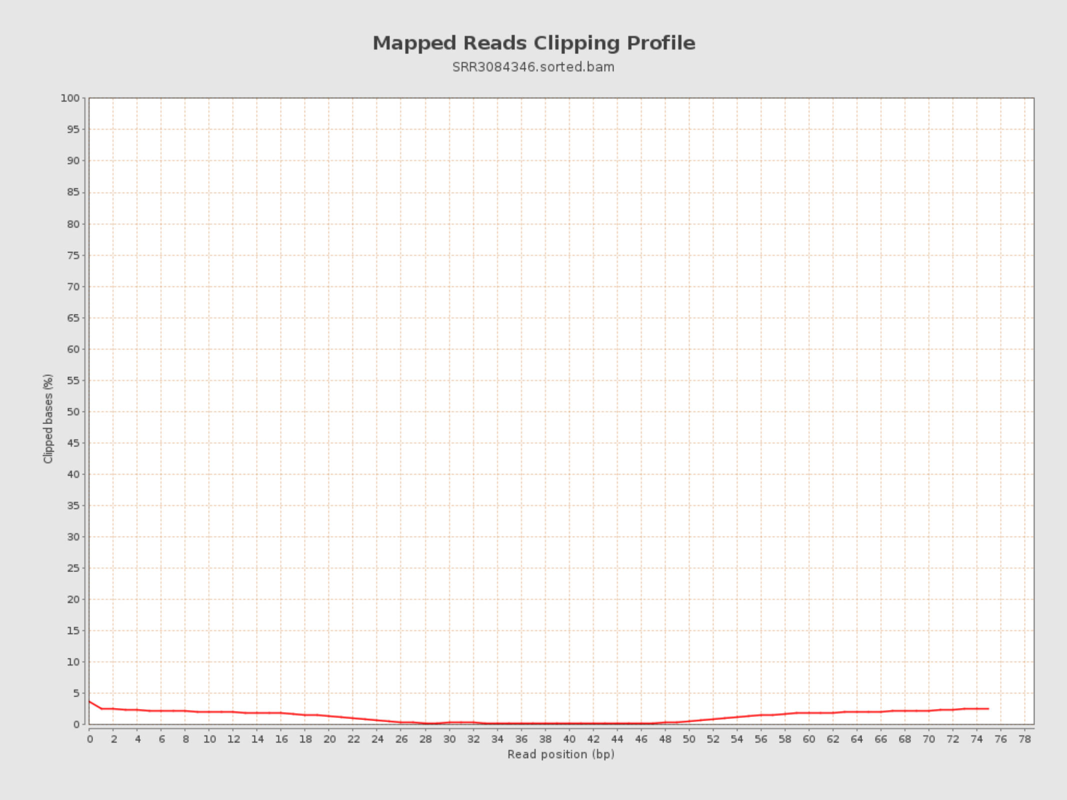
8. Results : Mapped Reads Nucleotide Content



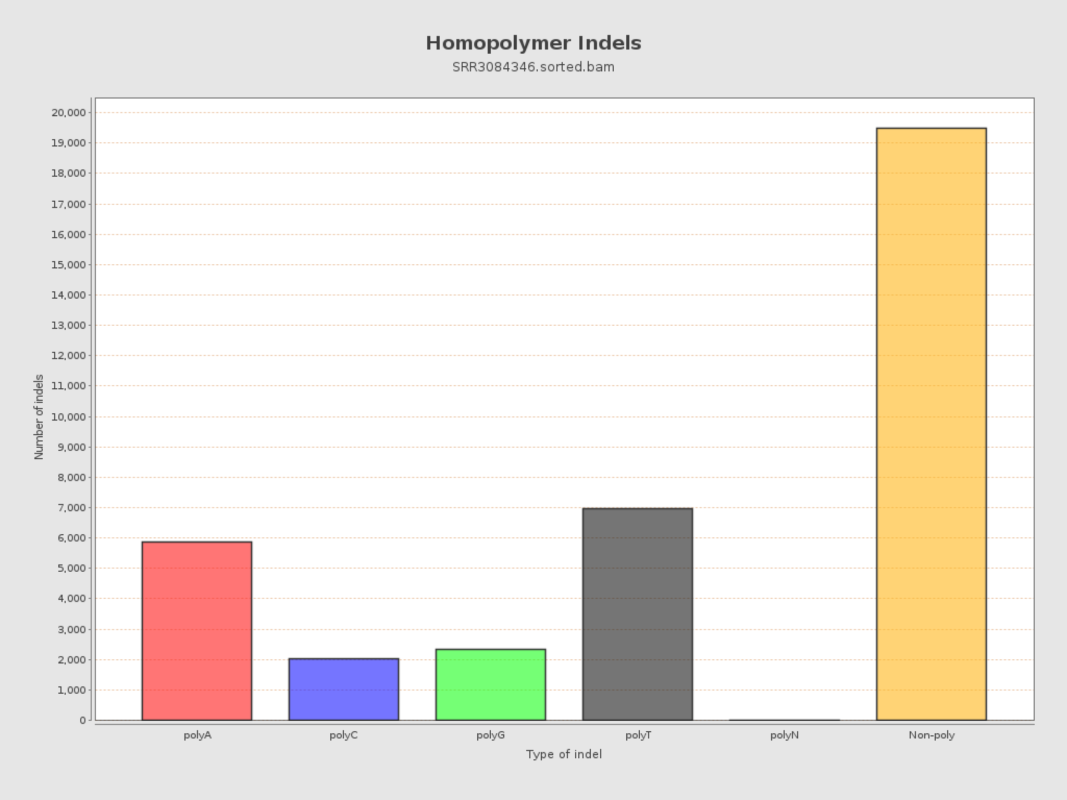
9. Results : Mapped Reads GC-content Distribution



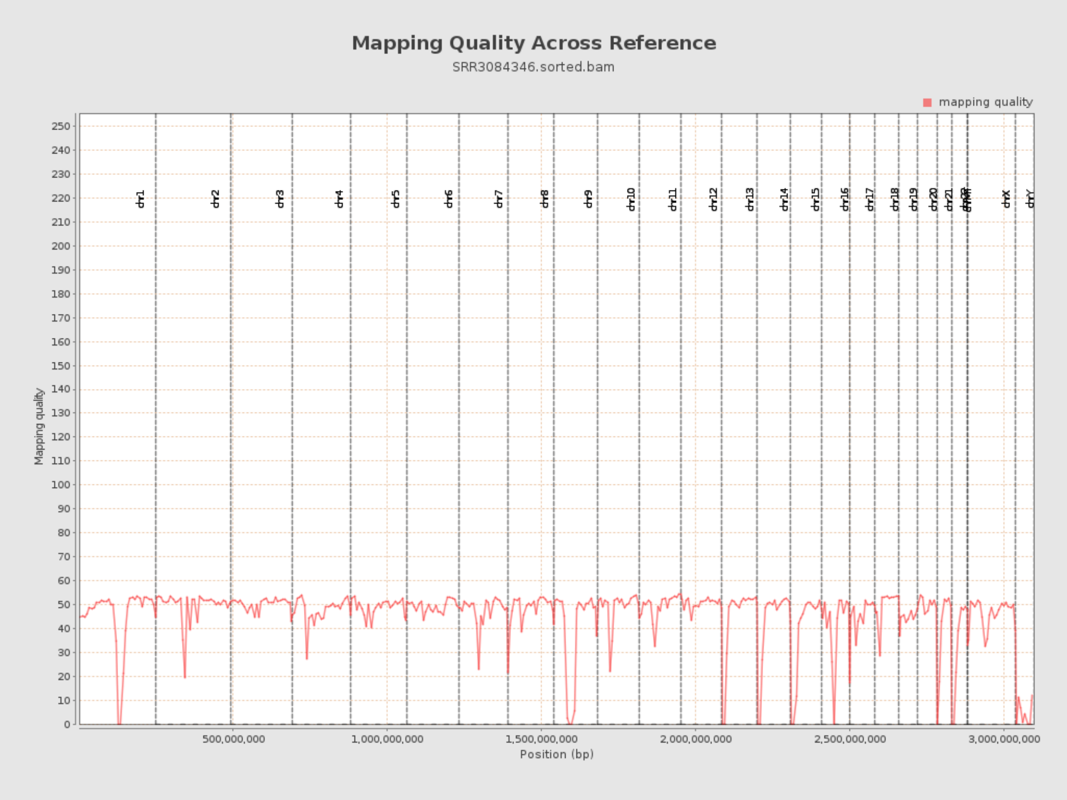
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram