Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 00:21:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085059.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_SRR3085059 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085059.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 00:21:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085059.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,409,804
Mapped reads	1,137,399 / 80.68%
Unmapped reads	272,405 / 19.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,368 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	23,618 / 1.68%
Duplication rate	1.65%
Clipped reads	673,278 / 47.76%

2.2. ACGT Content

Number/percentage of A's	21,764,832 / 30.37%
Number/percentage of C's	13,560,863 / 18.92%
Number/percentage of T's	20,824,034 / 29.06%
Number/percentage of G's	15,515,342 / 21.65%
Number/percentage of N's	1,570 / 0%
GC Percentage	40.57%

2.3. Coverage

Mean	0.0232

Standard Deviation	0.2054

2.4. Mapping Quality

Mean Mapping Quality	46.02

2.5. Mismatches and indels

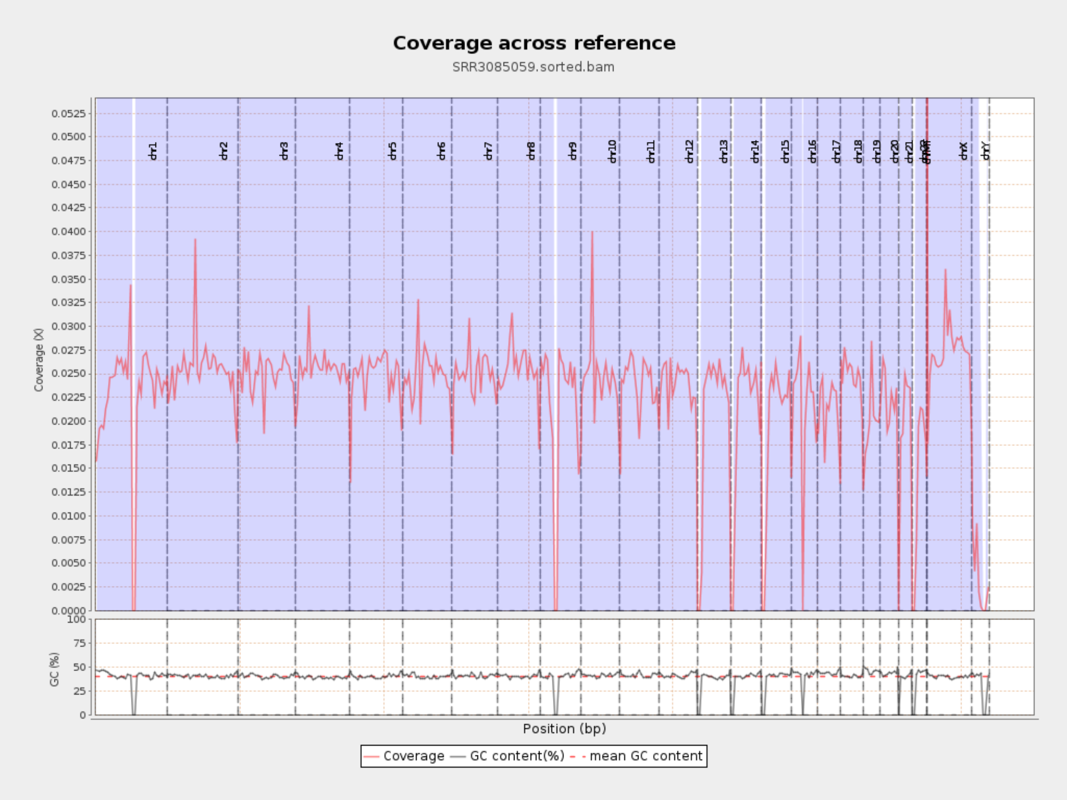
General error rate	0.92%
Mismatches	652,455
Insertions	5,517
Mapped reads with at least one insertion	0.48%
Deletions	14,363
Mapped reads with at least one deletion	1.25%
Homopolymer indels	46.03%

2.6. Chromosome stats

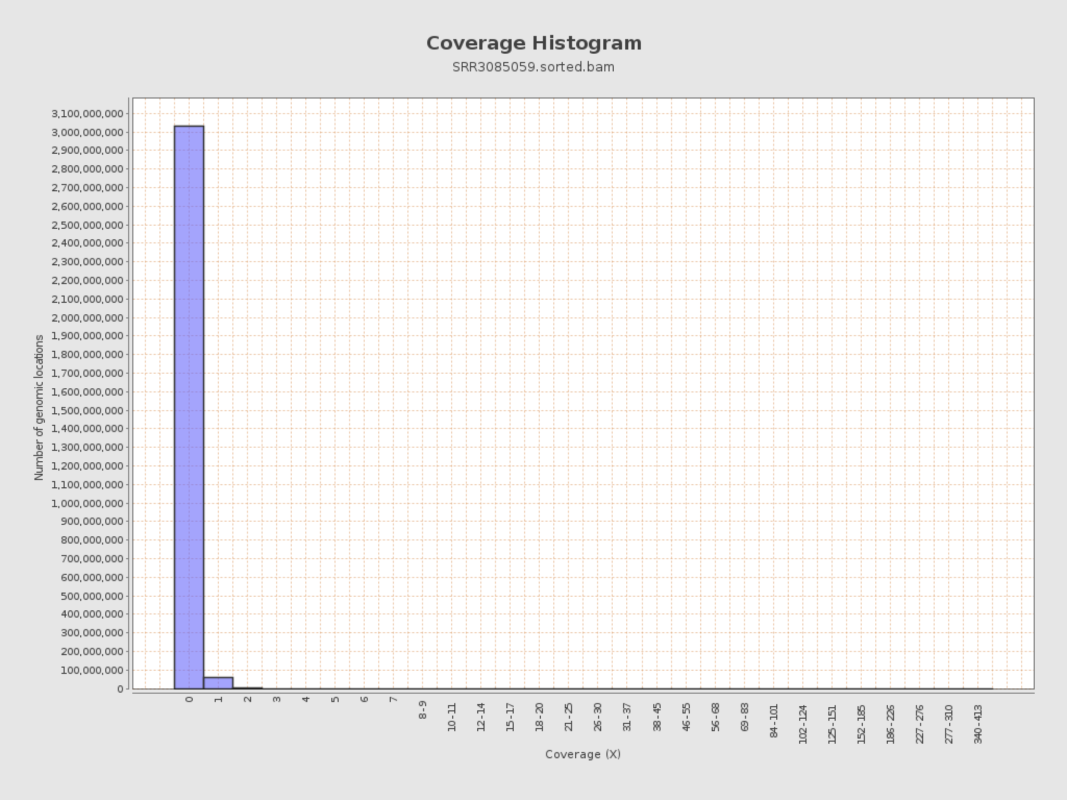
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5623281	0.0226	0.3013
chr2	243199373	6204370	0.0255	0.2179
chr3	198022430	4954488	0.025	0.1686
chr4	191154276	4880975	0.0255	0.1742
chr5	180915260	4526886	0.025	0.1683
chr6	171115067	4261188	0.0249	0.1882
chr7	159138663	3957166	0.0249	0.1987

chr8	146364022	3746432	0.0256	0.2942
chr9	141213431	3011445	0.0213	0.1961
chr10	135534747	3372299	0.0249	0.2221
chr11	135006516	3239752	0.024	0.2021
chr12	133851895	3215286	0.024	0.1656
chr13	115169878	2335976	0.0203	0.1508
chr14	107349540	2172097	0.0202	0.1568
chr15	102531392	1971229	0.0192	0.1468
chr16	90354753	1898913	0.021	0.1631
chr17	81195210	1714823	0.0211	0.1629
chr18	78077248	1944161	0.0249	0.342
chr19	59128983	1186387	0.0201	0.2223
chr20	63025520	1398127	0.0222	0.1609
chr21	48129895	921847	0.0192	0.1547
chr22	51304566	702182	0.0137	0.1242
chrMT	16571	2315	0.1397	0.3919
chrX	155270560	4262953	0.0275	0.1885
chrY	59373566	184861	0.0031	0.0741

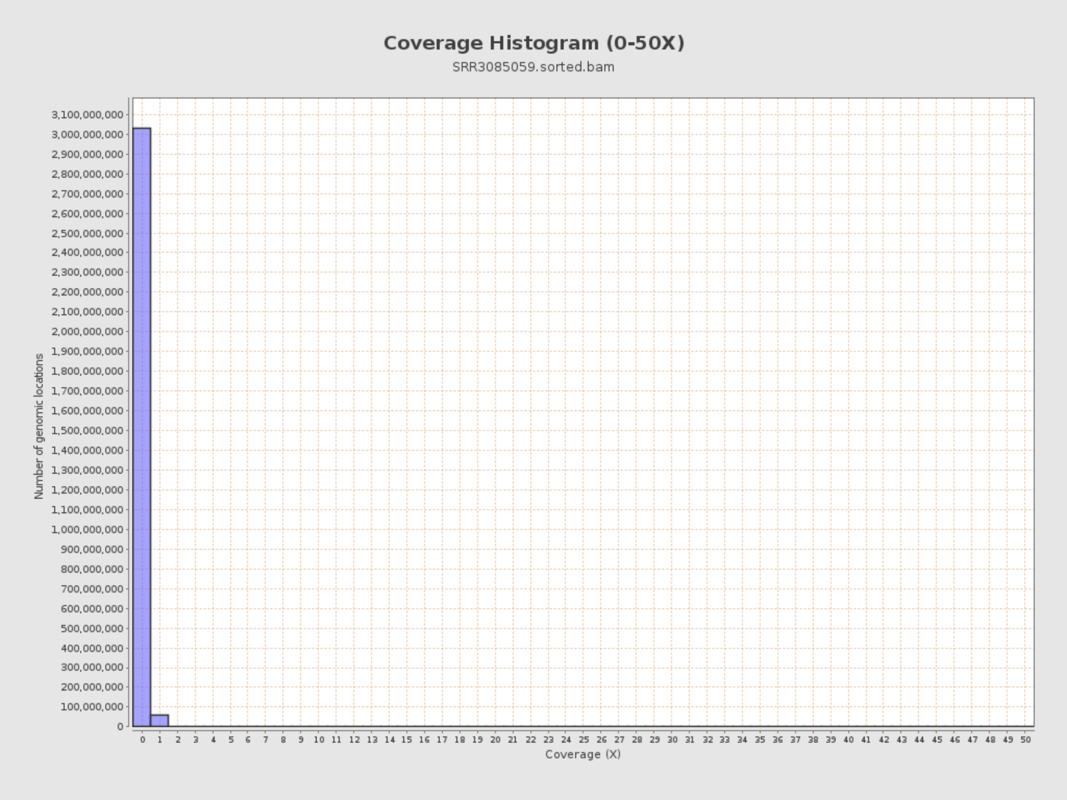
3. Results : Coverage across reference



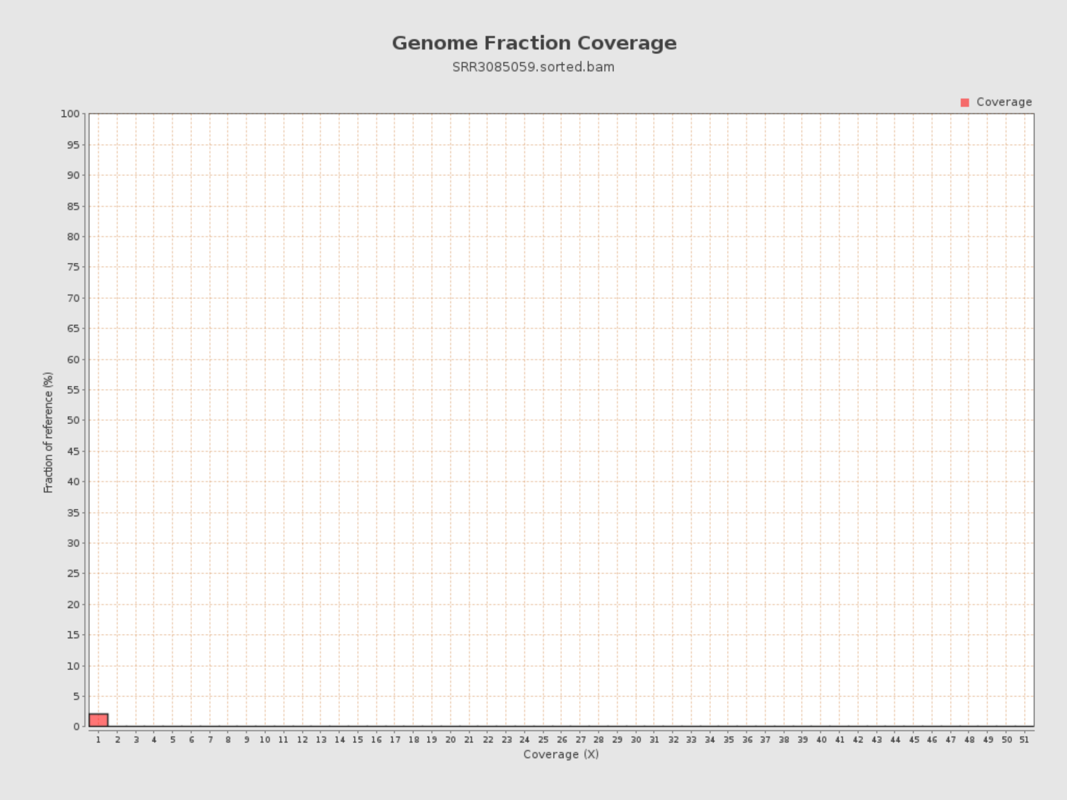
4. Results : Coverage Histogram



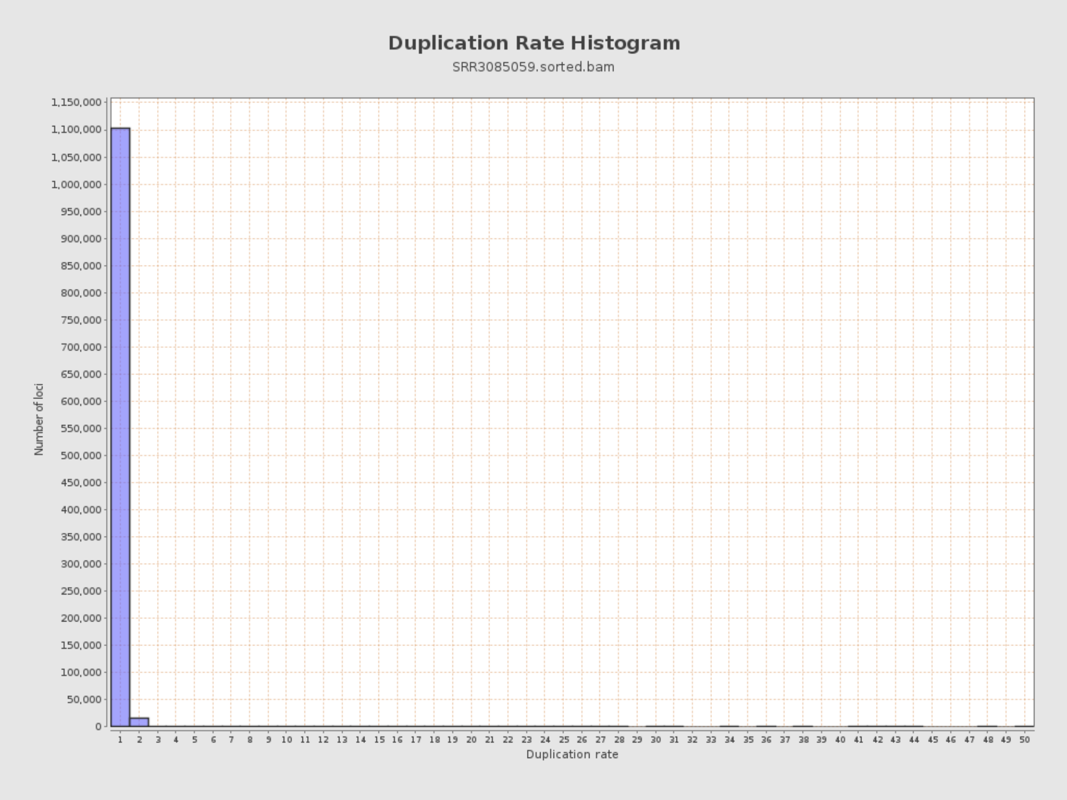
5. Results : Coverage Histogram (0-50X)



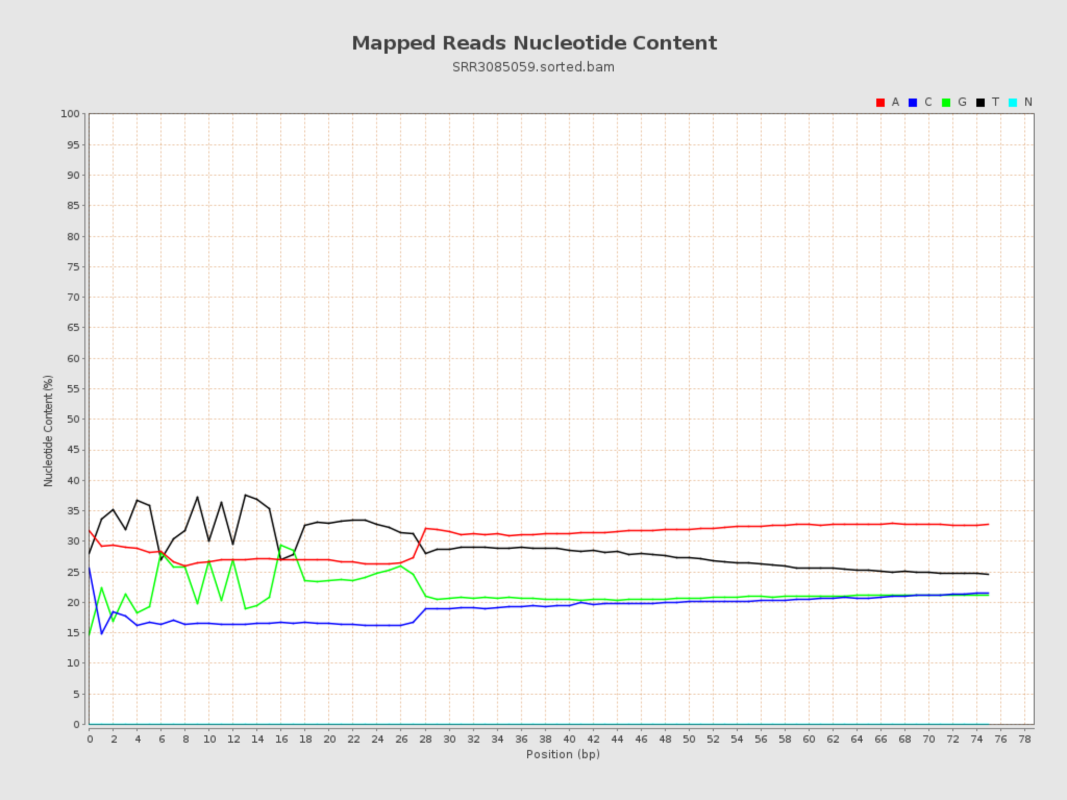
6. Results : Genome Fraction Coverage



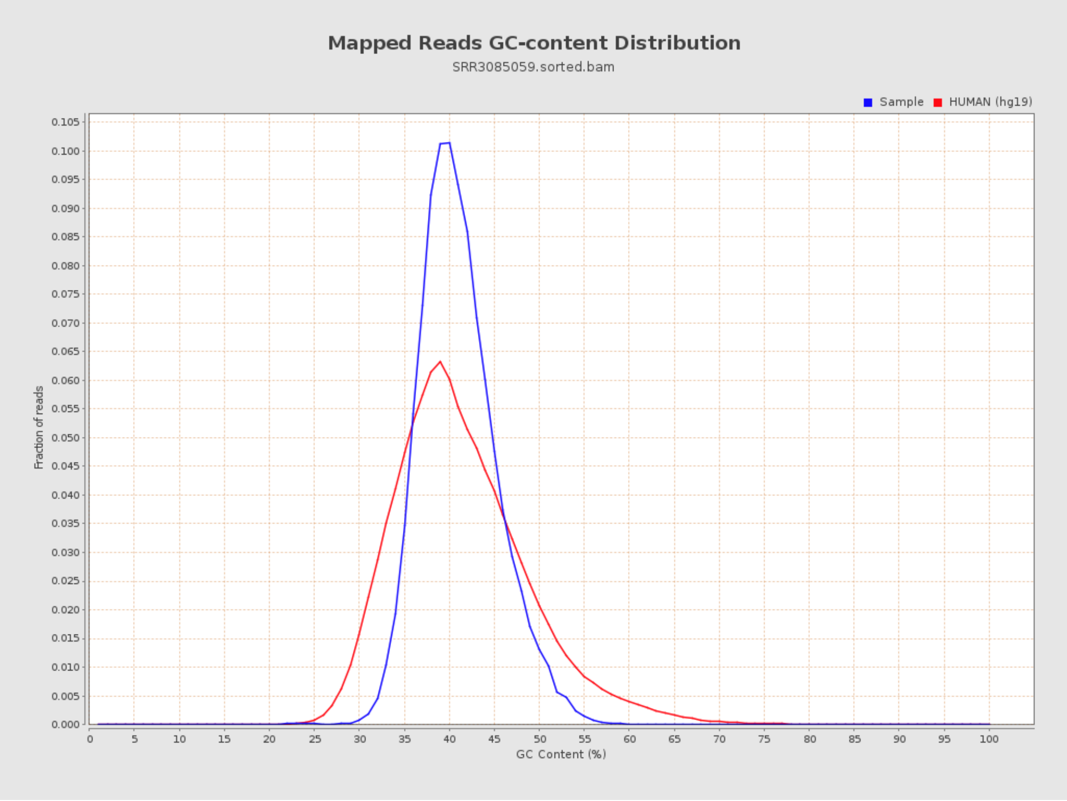
7. Results : Duplication Rate Histogram



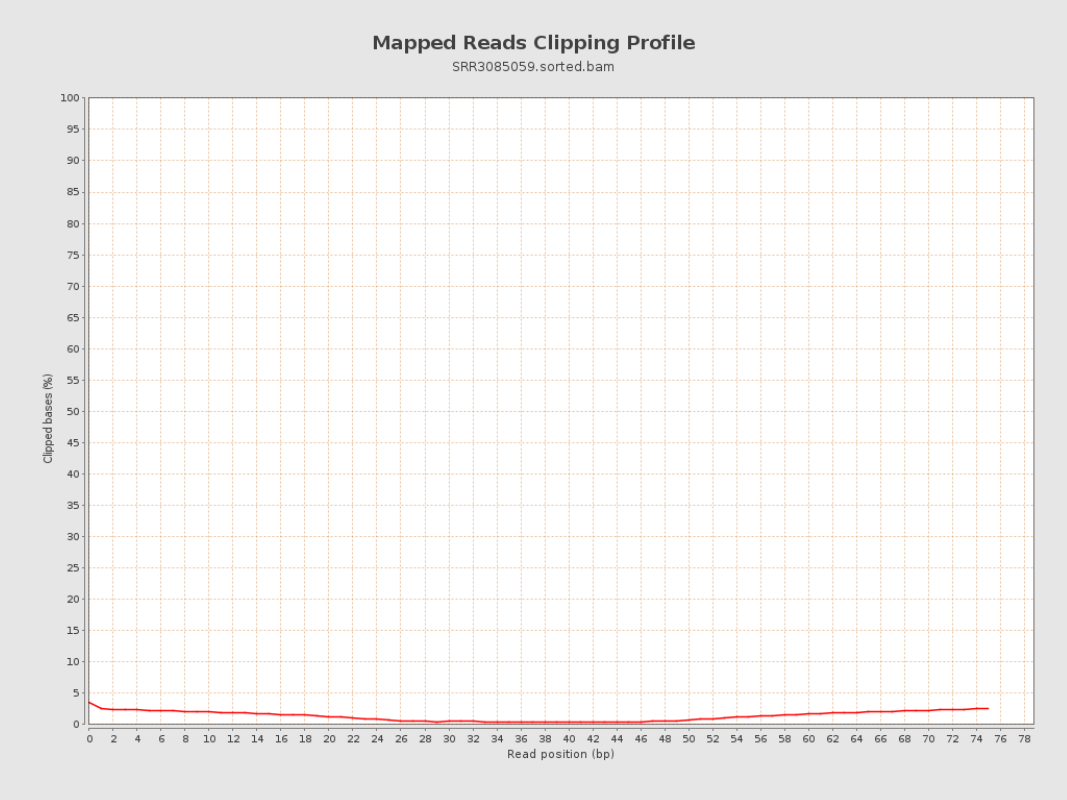
8. Results : Mapped Reads Nucleotide Content



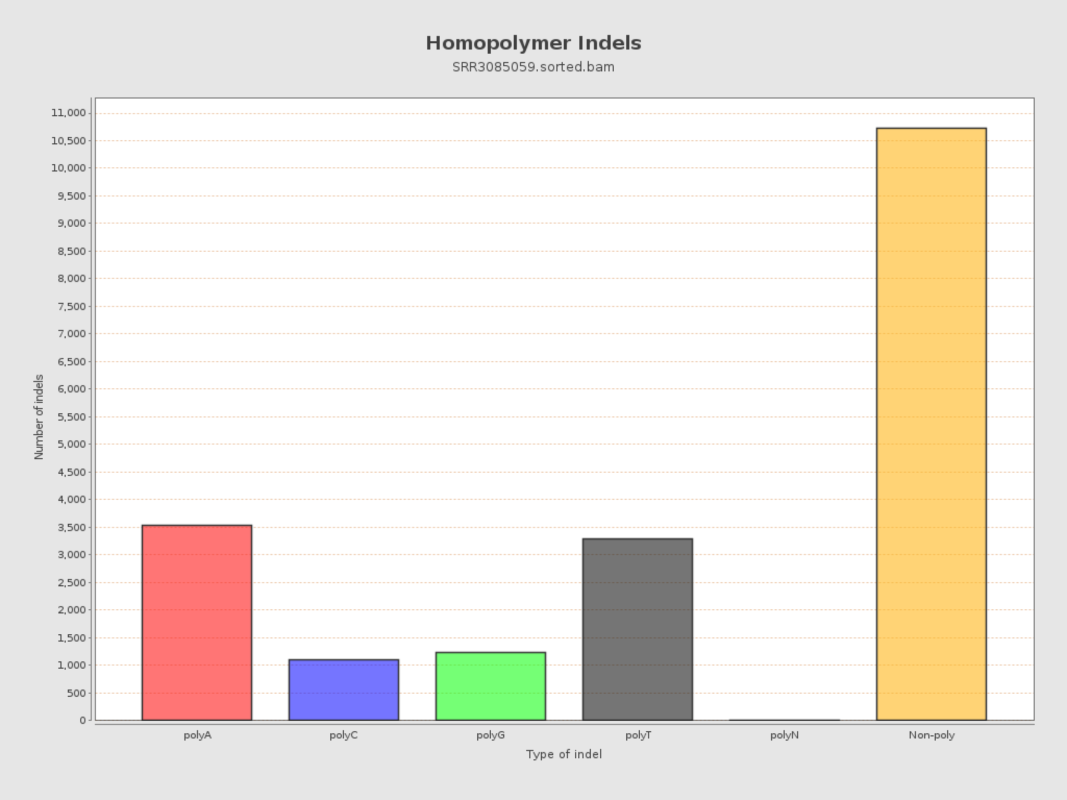
9. Results : Mapped Reads GC-content Distribution



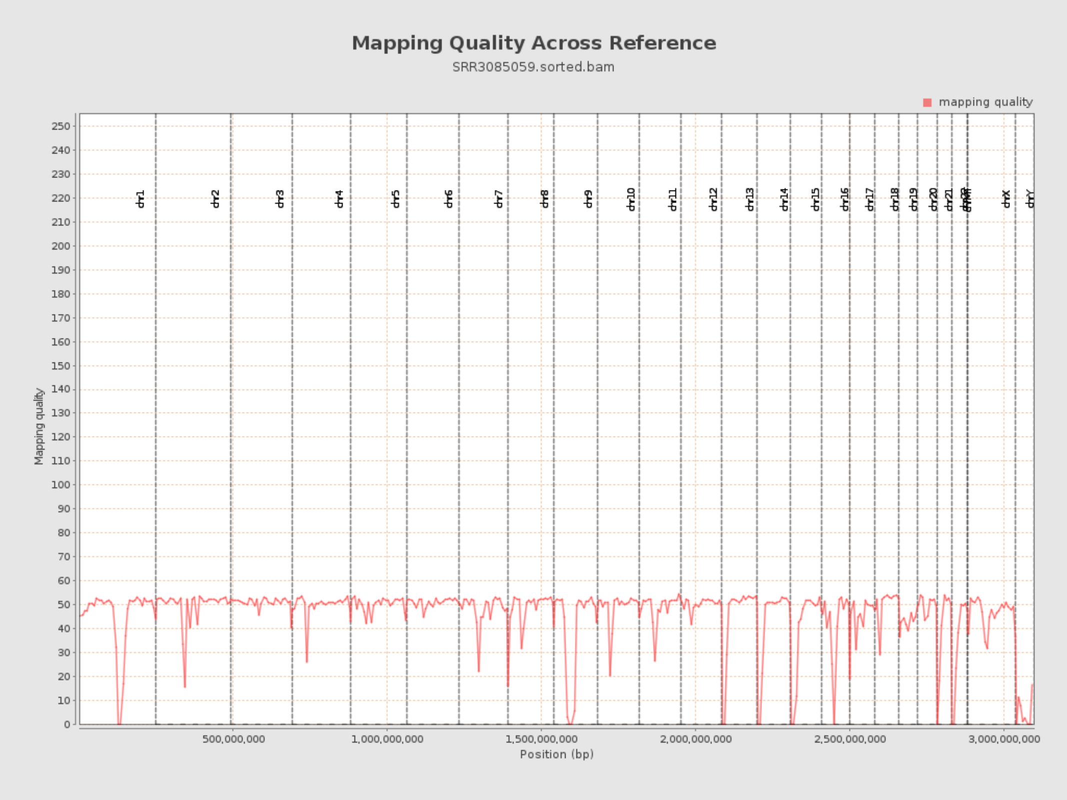
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram