Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 19:30:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082907.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_SRR3082907 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082907.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 19:30:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082907.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,907,499
Mapped reads	1,692,297 / 88.72%
Unmapped reads	215,202 / 11.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,079 / 1.11%
Read min/max/mean length	30 / 76 / 76.39
Duplicated reads (estimated)	83,437 / 4.37%
Duplication rate	4.23%
Clipped reads	781,529 / 40.97%

2.2. ACGT Content

Number/percentage of A's	30,476,238 / 27.15%
Number/percentage of C's	21,145,534 / 18.84%
Number/percentage of T's	35,175,185 / 31.34%
Number/percentage of G's	25,430,119 / 22.66%
Number/percentage of N's	4,916 / 0%
GC Percentage	41.5%

2.3. Coverage

Mean	0.0363

Standard Deviation	0.2895

2.4. Mapping Quality

Mean Mapping Quality	45.05

2.5. Mismatches and indels

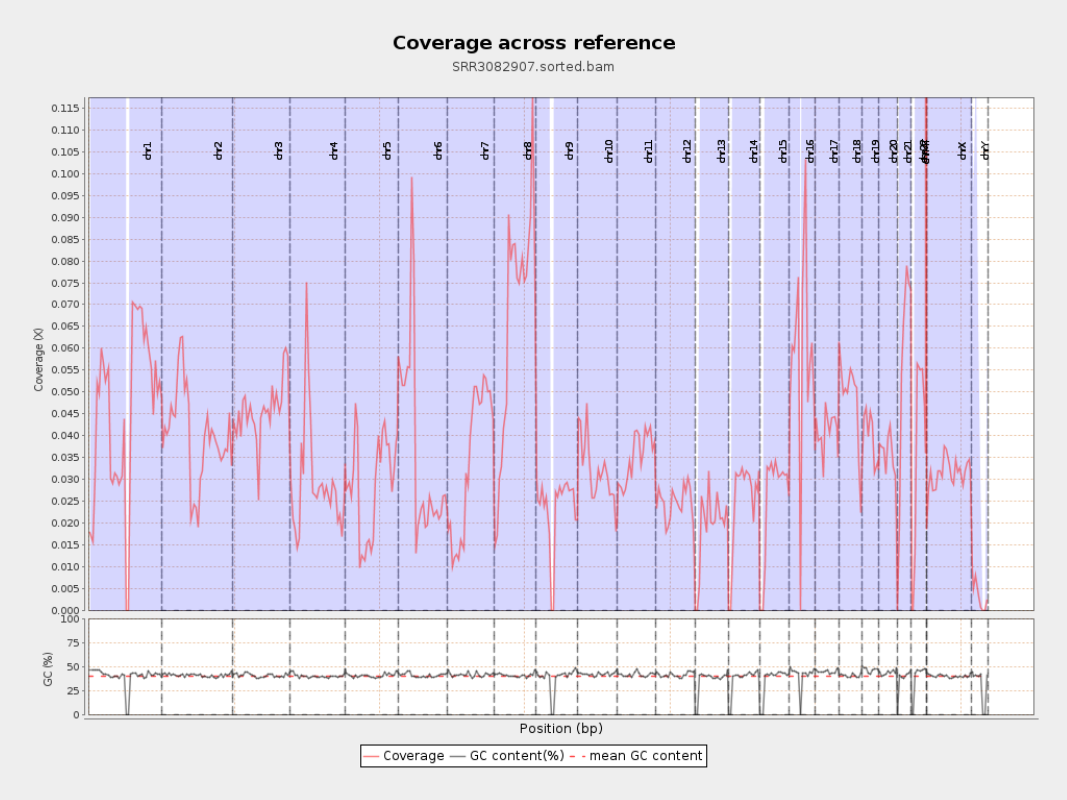
General error rate	0.73%
Mismatches	806,559
Insertions	8,766
Mapped reads with at least one insertion	0.51%
Deletions	25,056
Mapped reads with at least one deletion	1.46%
Homopolymer indels	47.77%

2.6. Chromosome stats

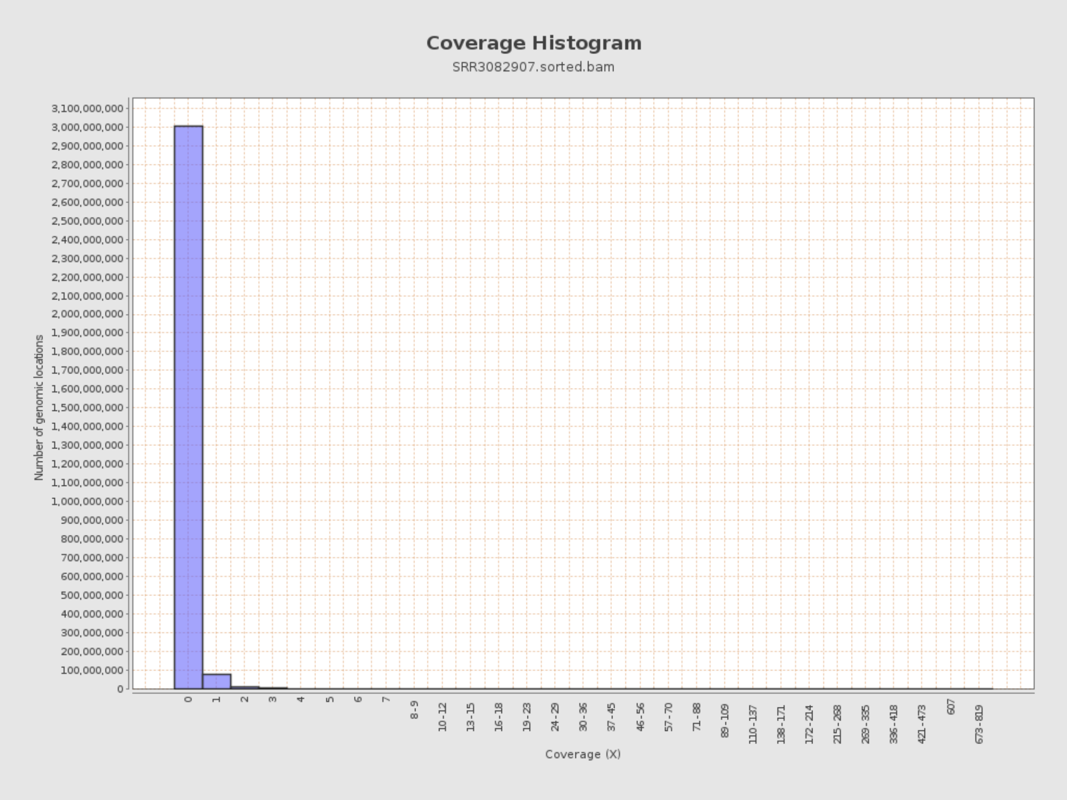
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11294979	0.0453	0.4748
chr2	243199373	9775475	0.0402	0.431
chr3	198022430	9065740	0.0458	0.2506
chr4	191154276	5536182	0.029	0.2005
chr5	180915260	5234392	0.0289	0.2007
chr6	171115067	6258511	0.0366	0.2554
chr7	159138663	5419405	0.0341	0.2373

chr8	146364022	9824868	0.0671	0.3444
chr9	141213431	3259740	0.0231	0.223
chr10	135534747	4367692	0.0322	0.2304
chr11	135006516	4697854	0.0348	0.2467
chr12	133851895	3274128	0.0245	0.1852
chr13	115169878	2195847	0.0191	0.1646
chr14	107349540	2637001	0.0246	0.1906
chr15	102531392	2627306	0.0256	0.1888
chr16	90354753	5313339	0.0588	0.2975
chr17	81195210	3345252	0.0412	0.2488
chr18	78077248	3822053	0.049	0.4296
chr19	59128983	2363987	0.04	0.3435
chr20	63025520	2230314	0.0354	0.2269
chr21	48129895	2635970	0.0548	0.2803
chr22	51304566	1835633	0.0358	0.2234
chrMT	16571	207048	12.4946	7.6504
chrX	155270560	4852889	0.0313	0.2167
chrY	59373566	197400	0.0033	0.0709

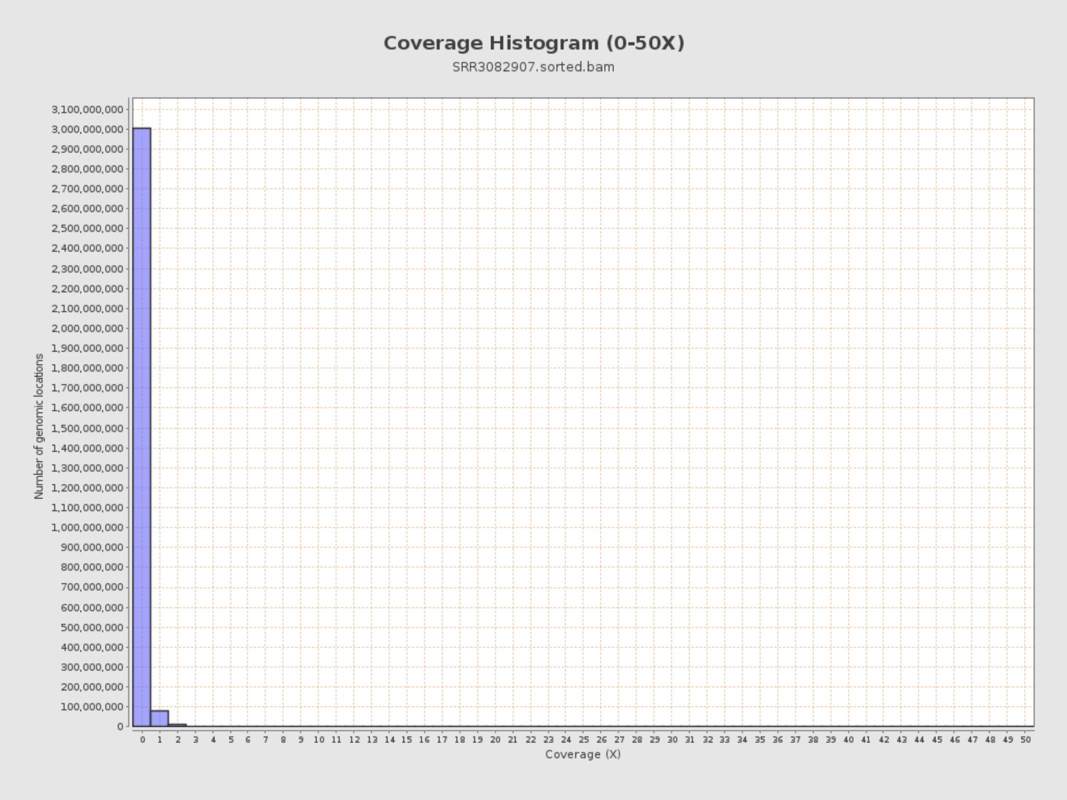
3. Results : Coverage across reference



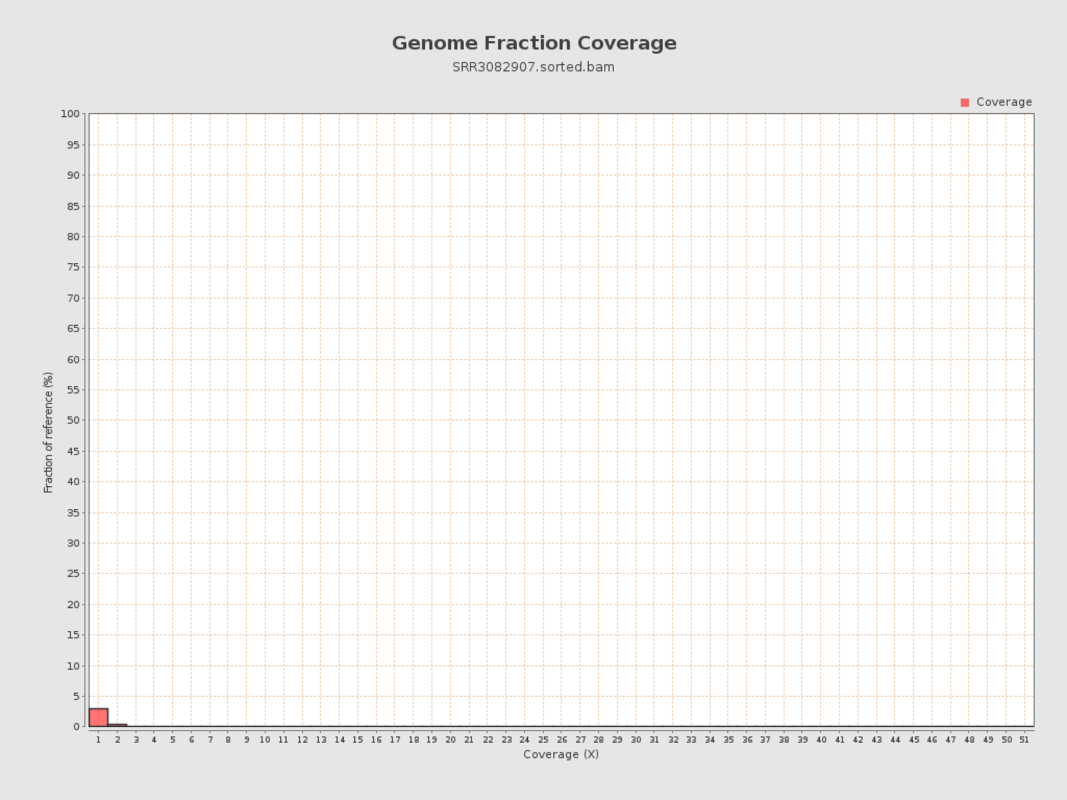
4. Results : Coverage Histogram



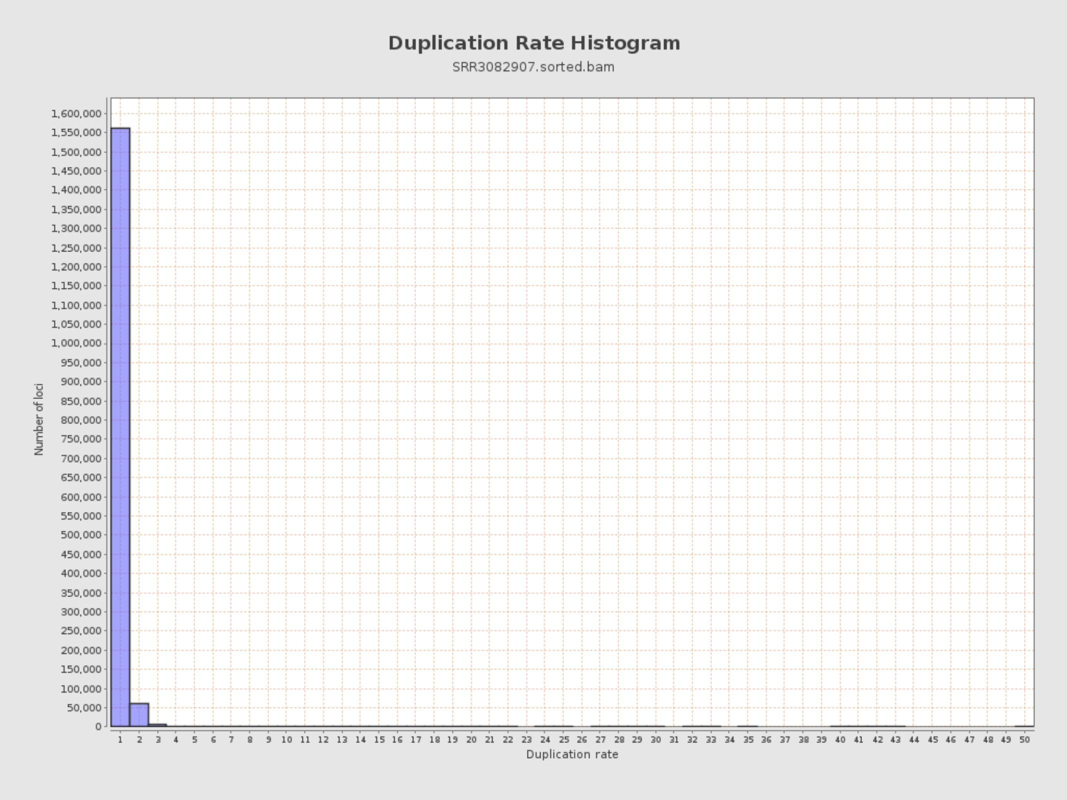
5. Results : Coverage Histogram (0-50X)



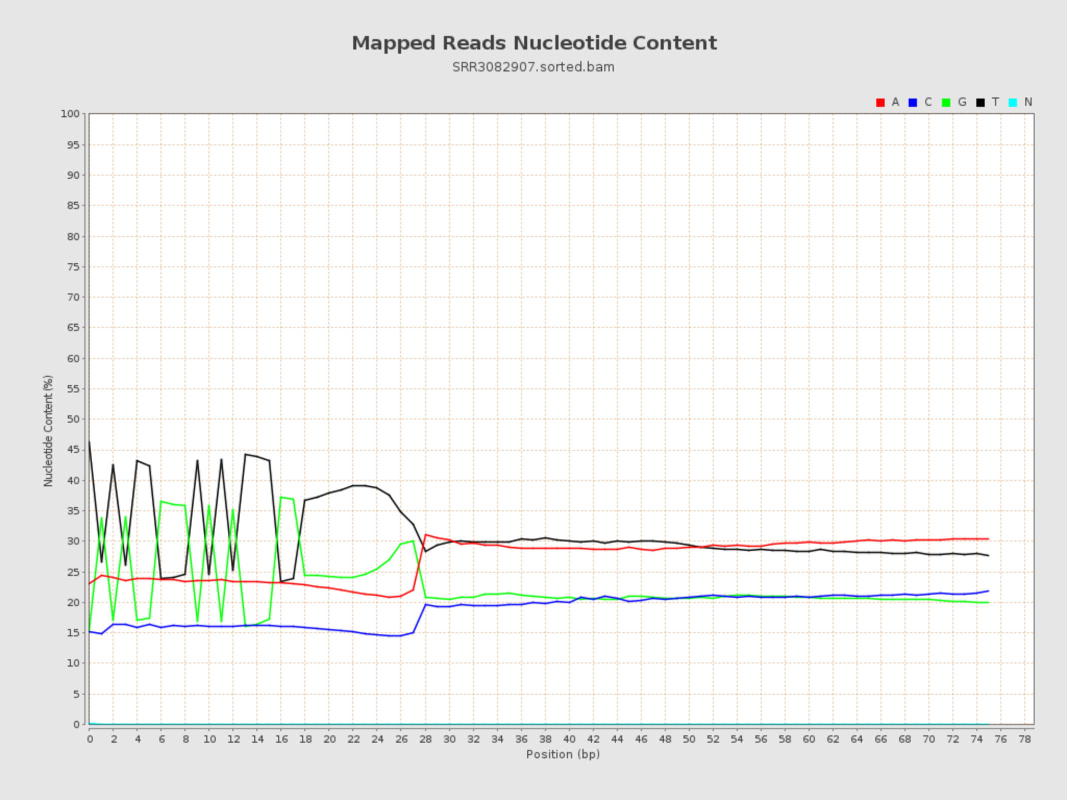
6. Results : Genome Fraction Coverage



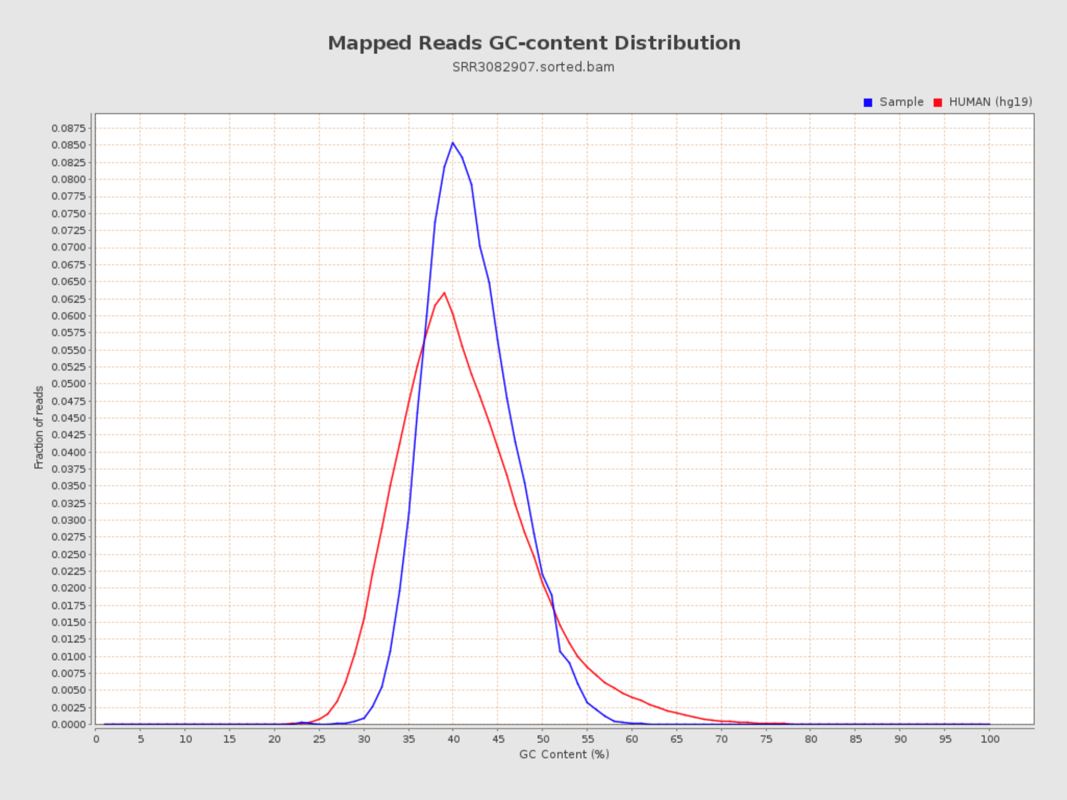
7. Results : Duplication Rate Histogram



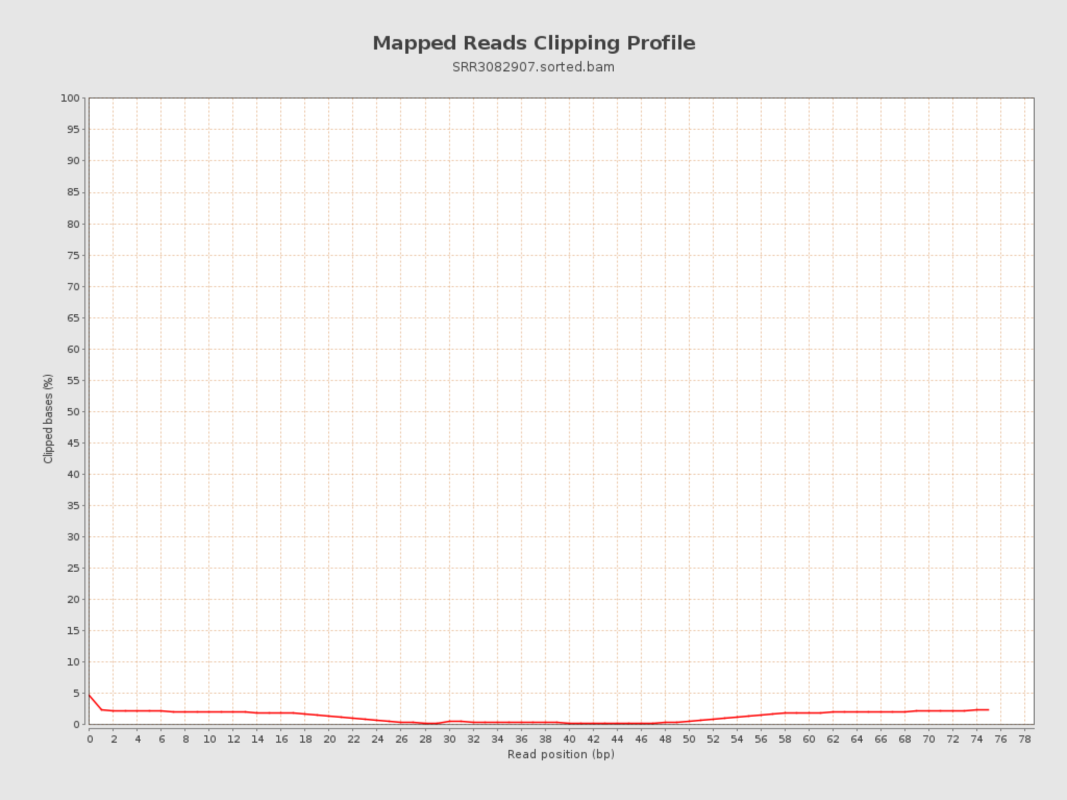
8. Results : Mapped Reads Nucleotide Content



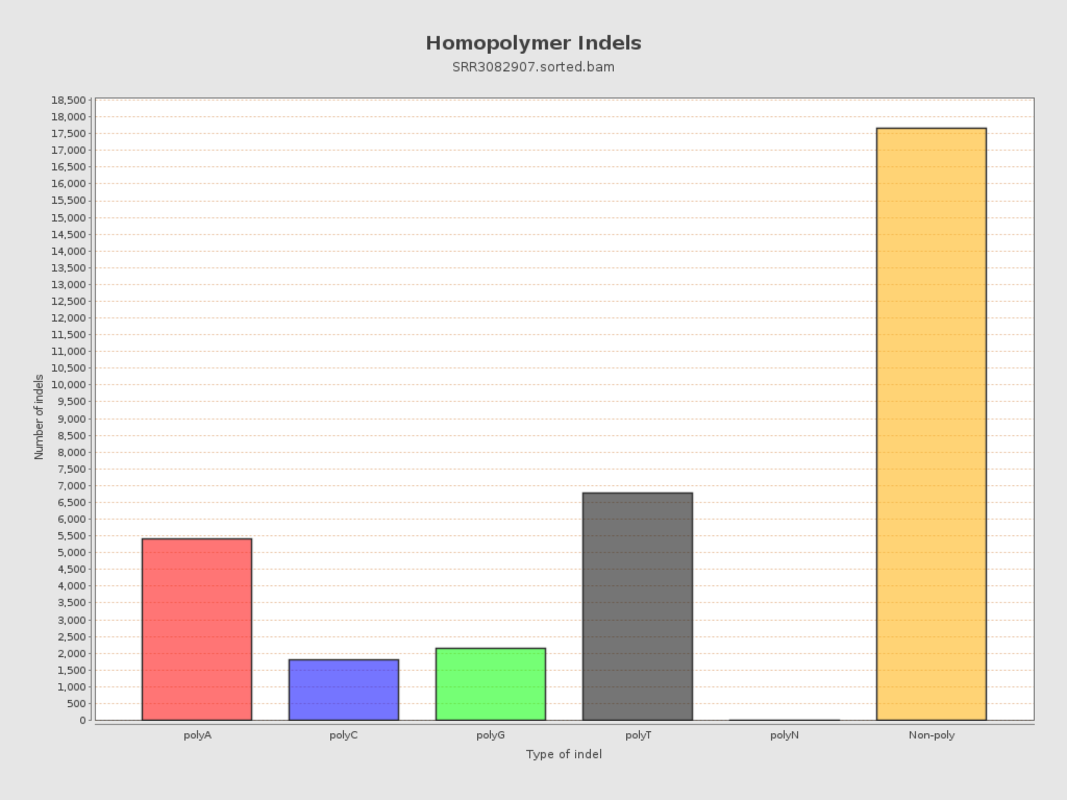
9. Results : Mapped Reads GC-content Distribution



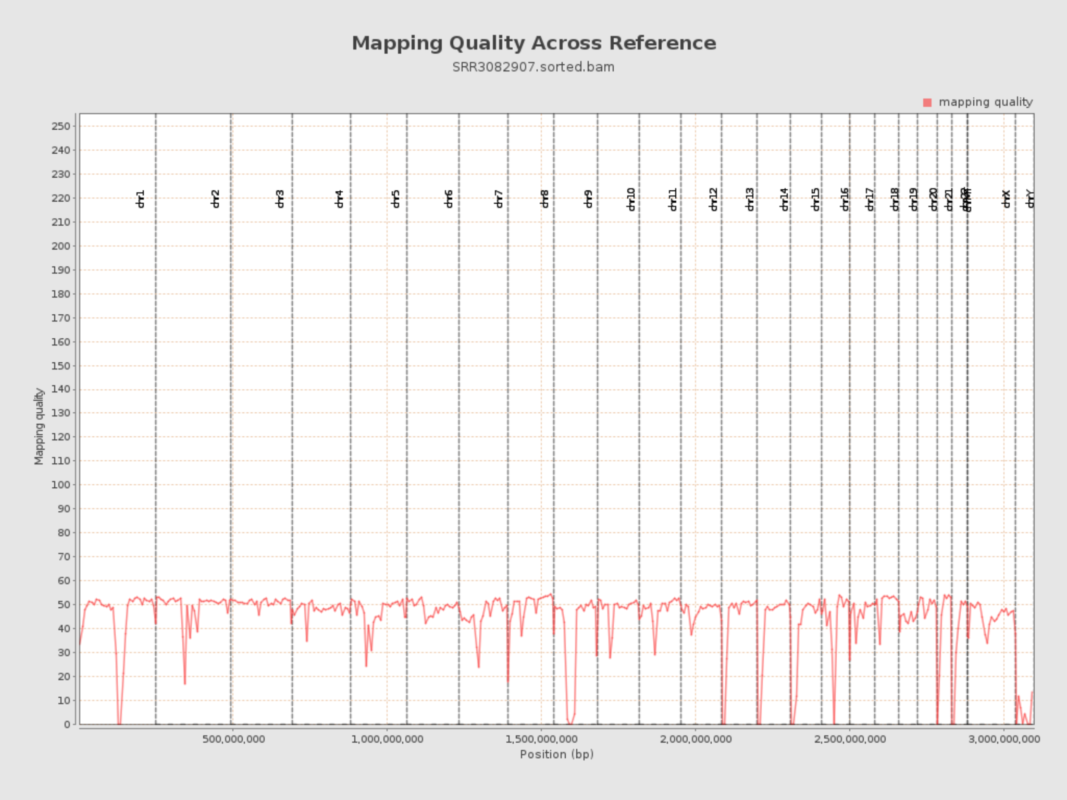
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram