Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 19:53:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080705.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_SRR3080705 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080705.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 19:53:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080705.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,981,303
Mapped reads	1,686,150 / 85.1%
Unmapped reads	295,153 / 14.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,170 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	102,454 / 5.17%
Duplication rate	5.21%
Clipped reads	662,485 / 33.44%

2.2. ACGT Content

Number/percentage of A's	33,796,616 / 29.4%
Number/percentage of C's	21,061,092 / 18.32%
Number/percentage of T's	36,023,751 / 31.34%
Number/percentage of G's	24,056,096 / 20.93%
Number/percentage of N's	1,621 / 0%
GC Percentage	39.25%

2.3. Coverage

Mean	0.0371

Standard Deviation	0.3187

2.4. Mapping Quality

Mean Mapping Quality	47.18

2.5. Mismatches and indels

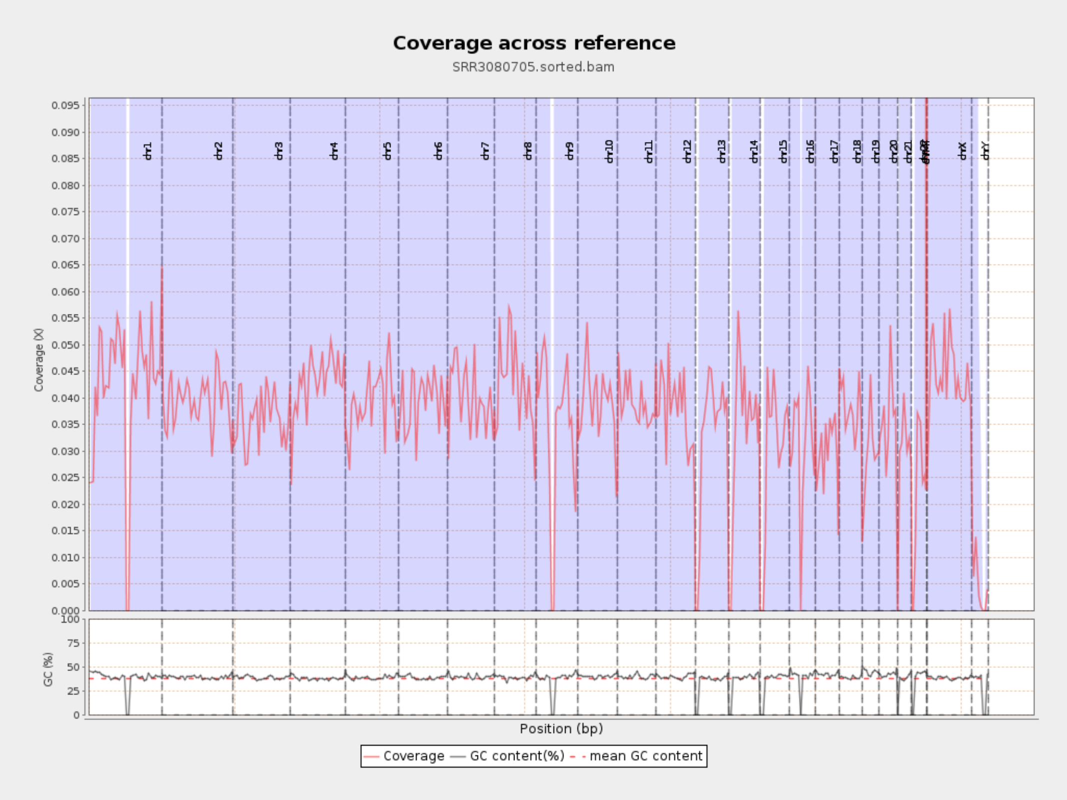
General error rate	0.83%
Mismatches	937,949
Insertions	8,666
Mapped reads with at least one insertion	0.51%
Deletions	23,894
Mapped reads with at least one deletion	1.4%
Homopolymer indels	47.45%

2.6. Chromosome stats

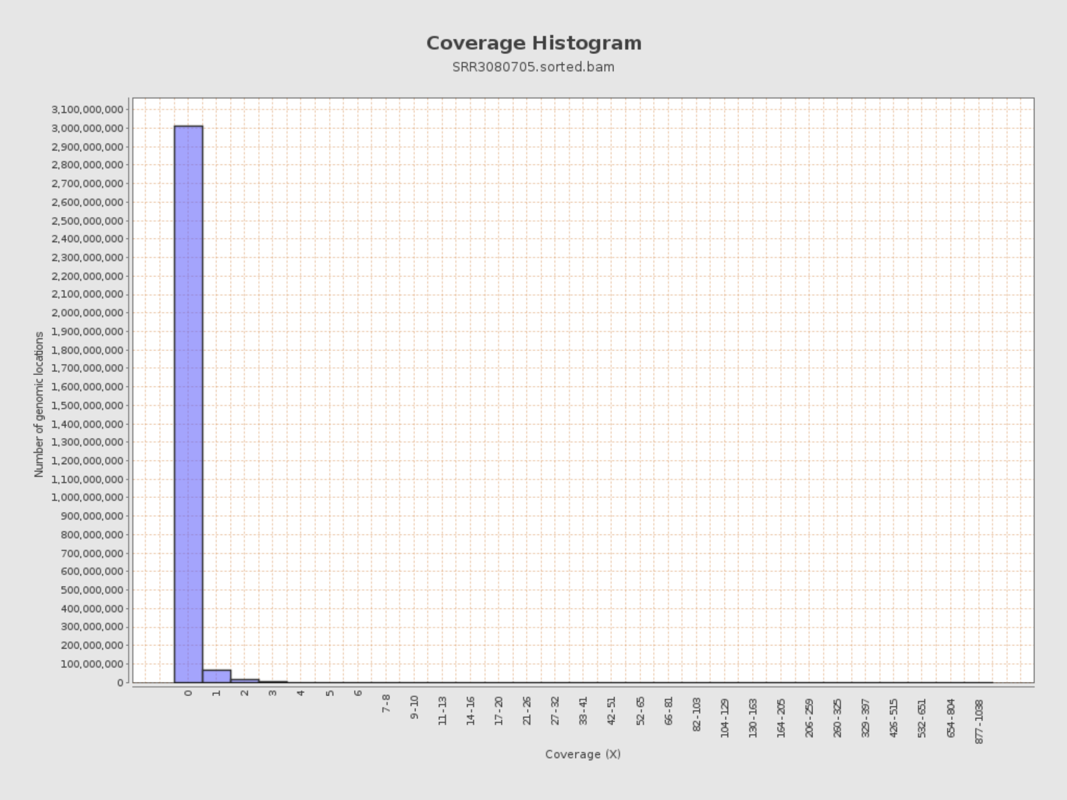
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10547938	0.0423	0.3964
chr2	243199373	9583008	0.0394	0.3313
chr3	198022430	7152008	0.0361	0.2449
chr4	191154276	8265976	0.0432	0.2761
chr5	180915260	7095380	0.0392	0.2563
chr6	171115067	6735070	0.0394	0.268
chr7	159138663	6428401	0.0404	0.3453

chr8	146364022	6225995	0.0425	0.6643
chr9	141213431	4856564	0.0344	0.2881
chr10	135534747	5365401	0.0396	0.2806
chr11	135006516	5232921	0.0388	0.2784
chr12	133851895	5039125	0.0376	0.2533
chr13	115169878	3780446	0.0328	0.2352
chr14	107349540	3611872	0.0336	0.2506
chr15	102531392	3026622	0.0295	0.2222
chr16	90354753	2847628	0.0315	0.2374
chr17	81195210	2390398	0.0294	0.2238
chr18	78077248	2978455	0.0381	0.4333
chr19	59128983	1762921	0.0298	0.3008
chr20	63025520	2250692	0.0357	0.2467
chr21	48129895	1410948	0.0293	0.2291
chr22	51304566	1083222	0.0211	0.1834
chrMT	16571	239535	14.4551	8.4724
chrX	155270560	6800627	0.0438	0.278
chrY	59373566	270153	0.0046	0.1054

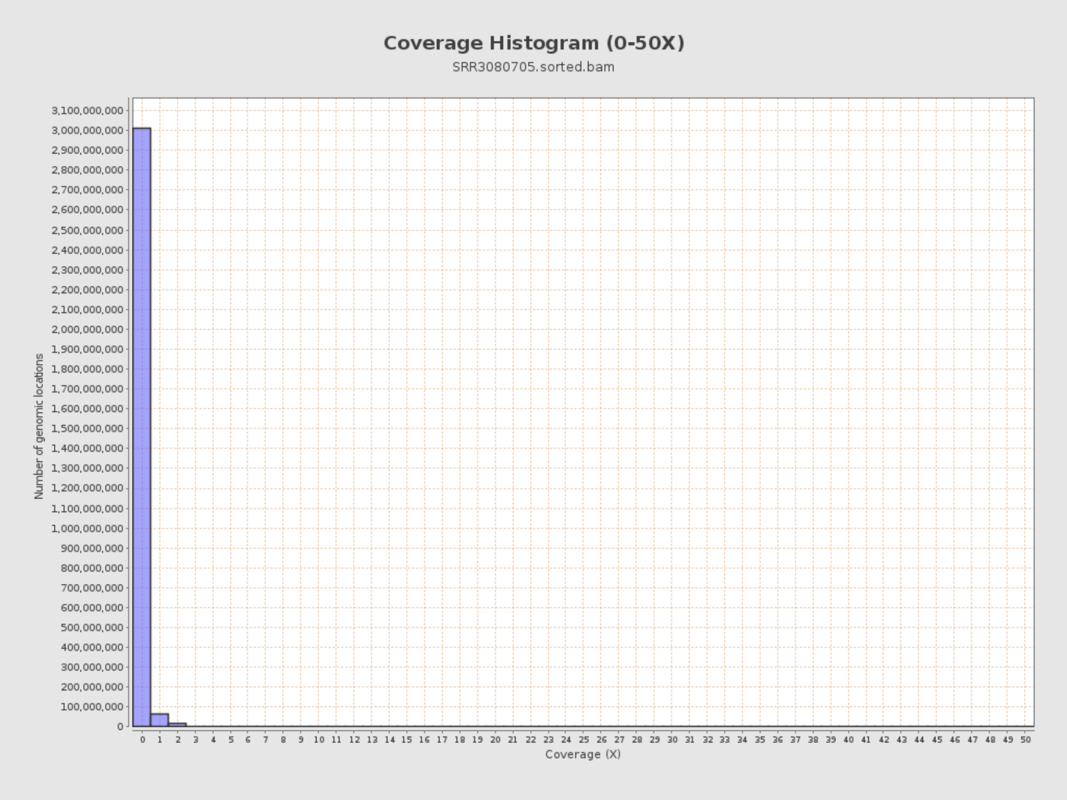
3. Results : Coverage across reference



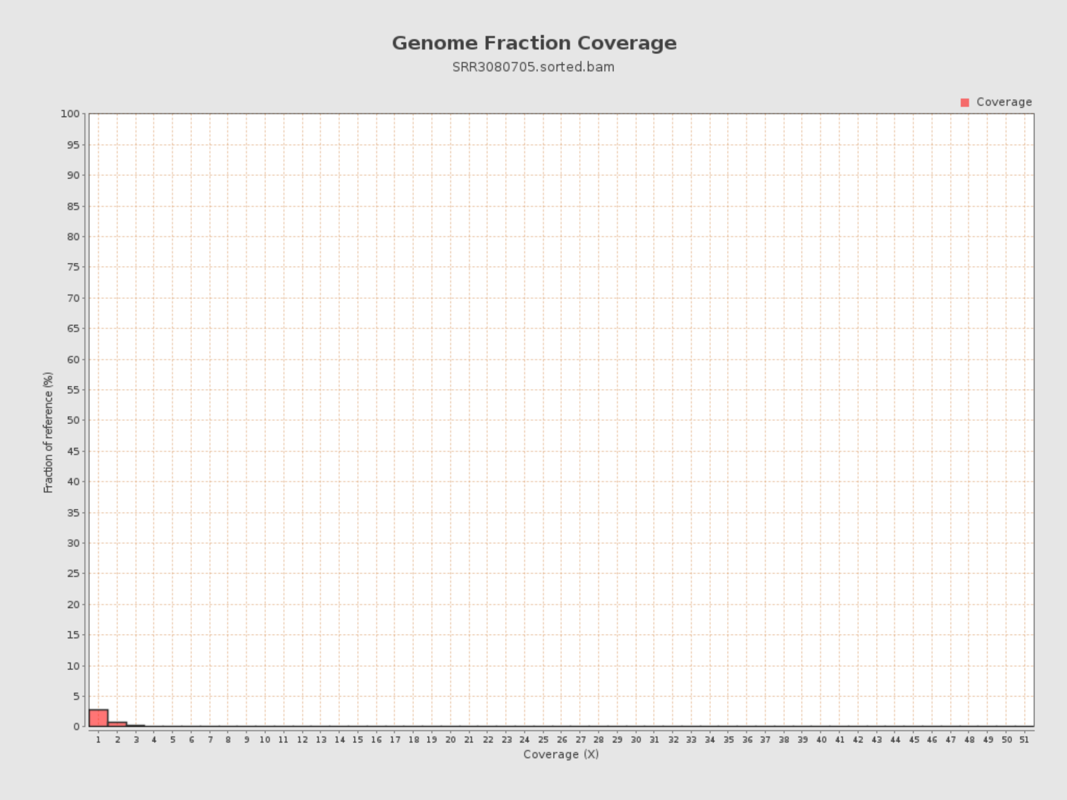
4. Results : Coverage Histogram



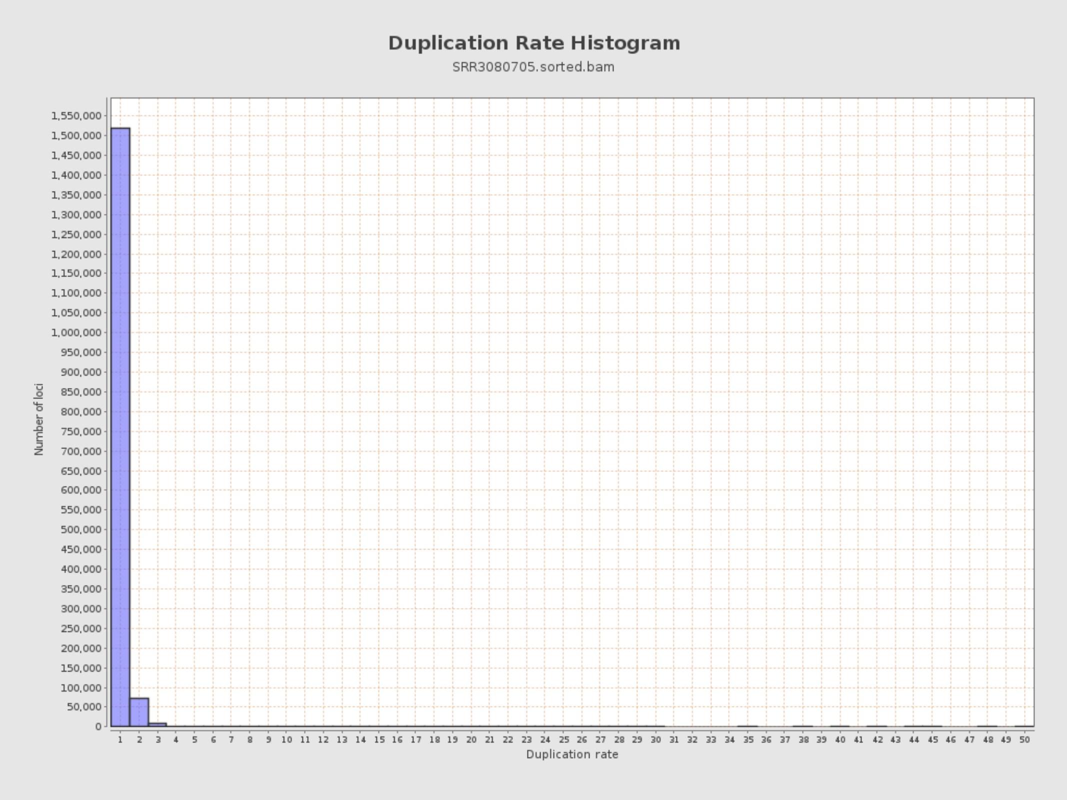
5. Results : Coverage Histogram (0-50X)



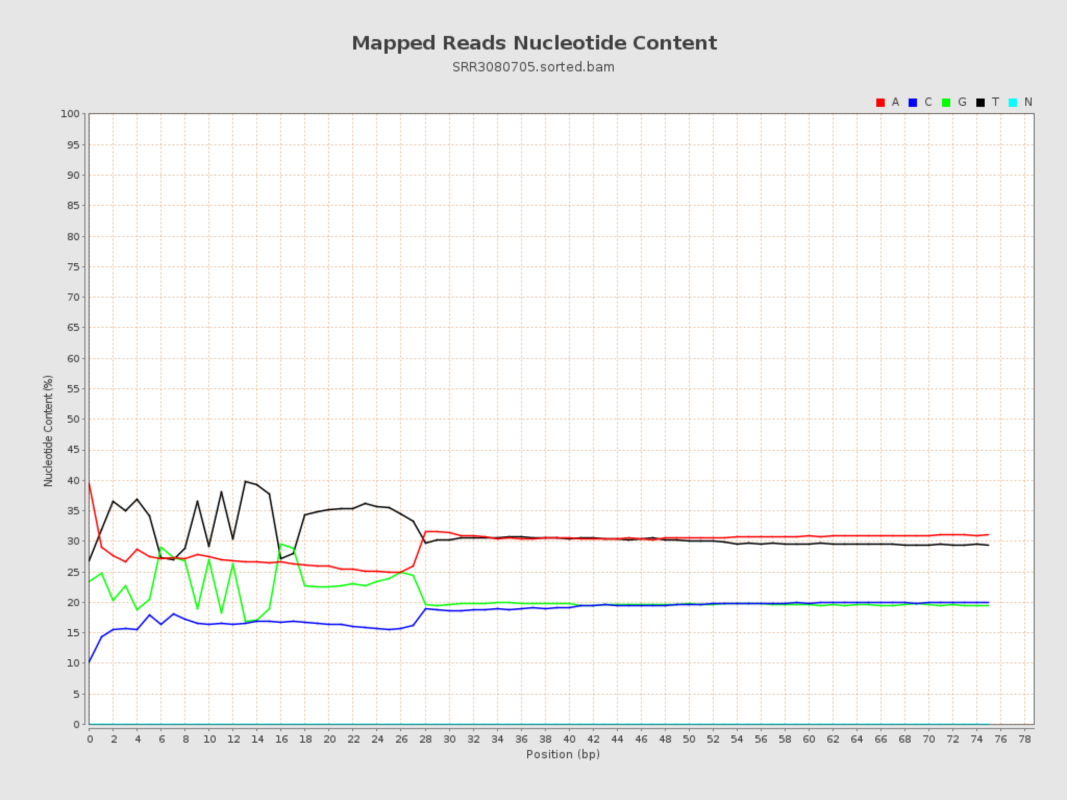
6. Results : Genome Fraction Coverage



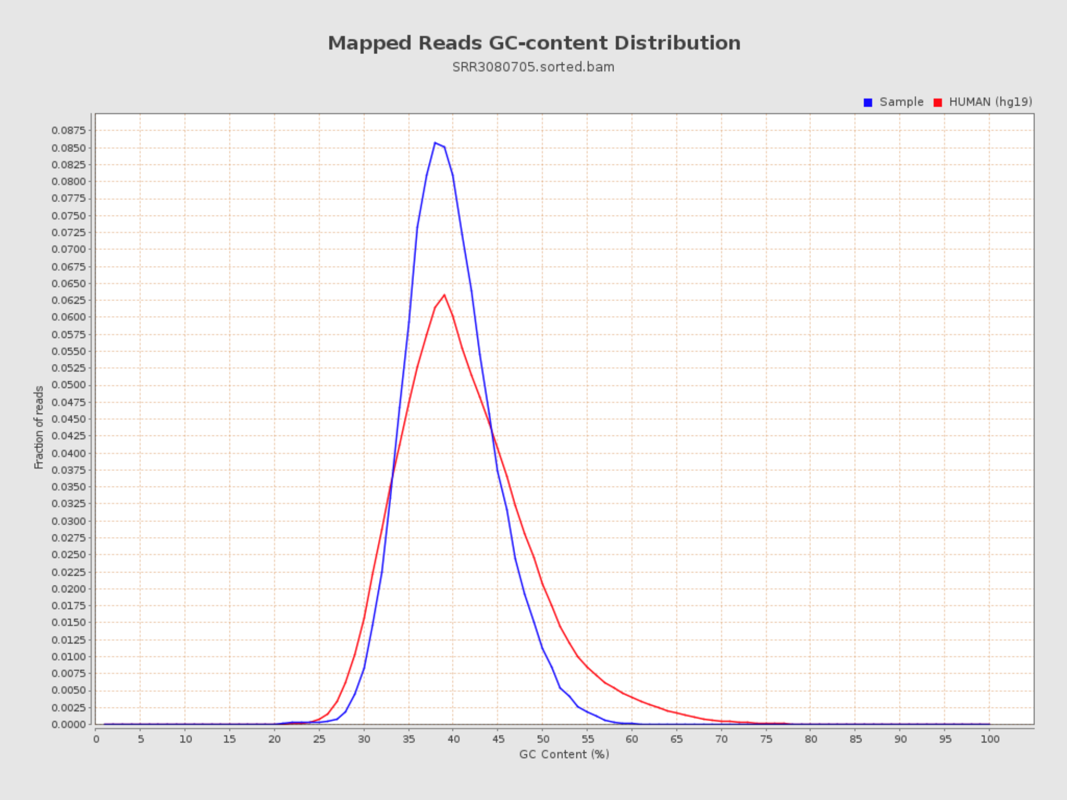
7. Results : Duplication Rate Histogram



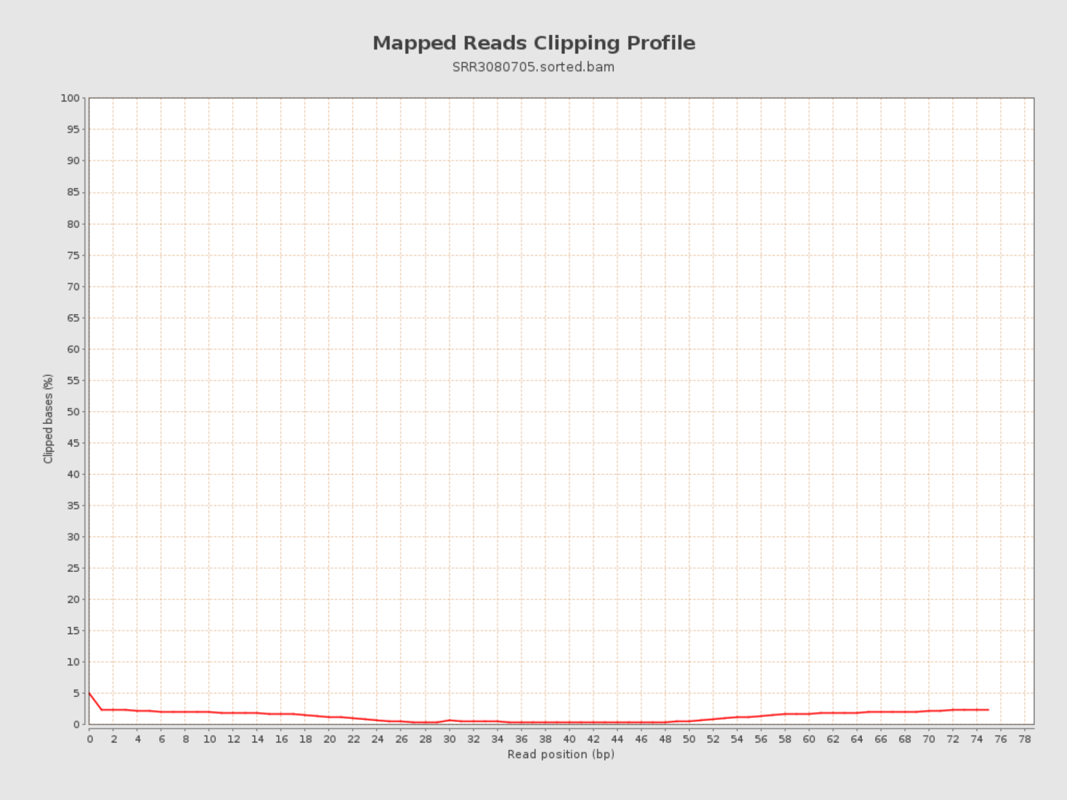
8. Results : Mapped Reads Nucleotide Content



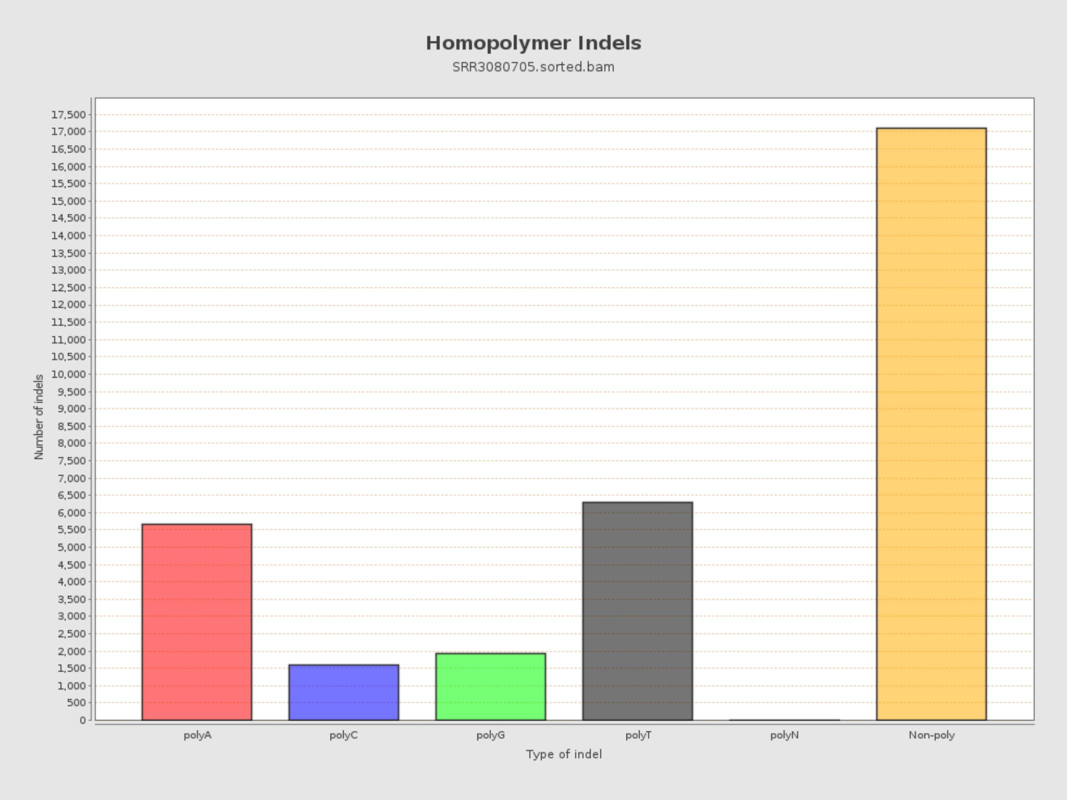
9. Results : Mapped Reads GC-content Distribution



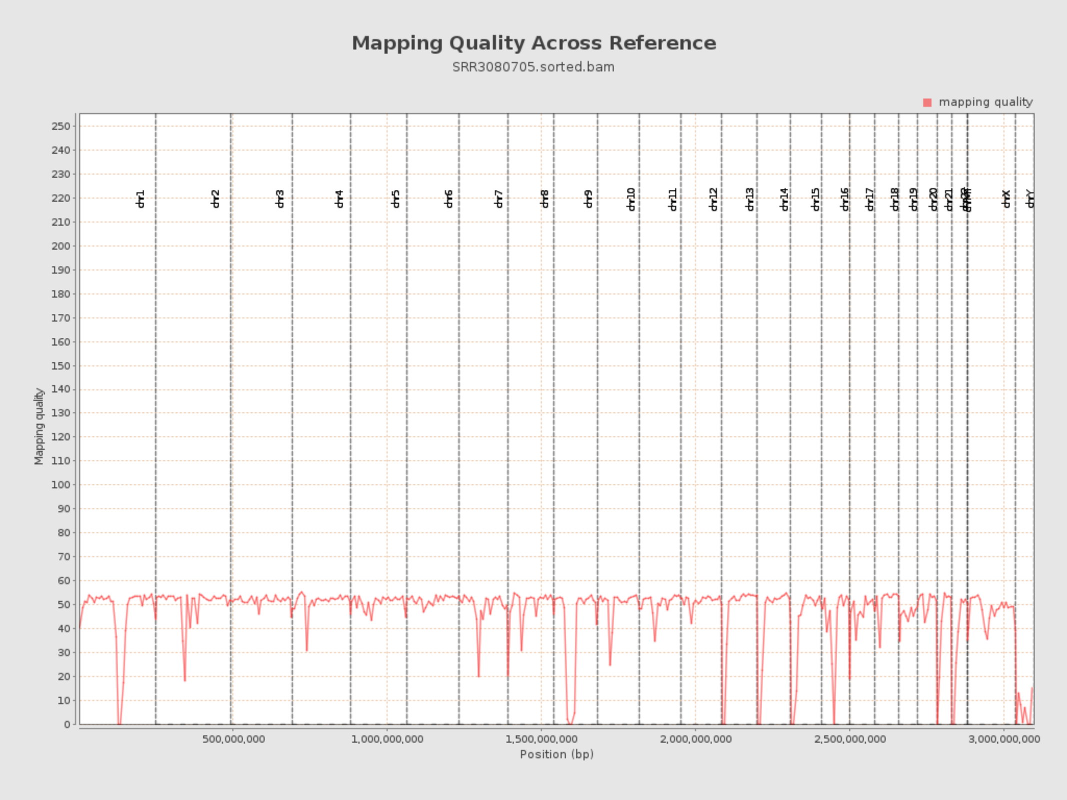
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram