Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 14:31:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080676.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_SRR3080676 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080676.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 14:31:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080676.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,122,822
Mapped reads	1,043,514 / 92.94%
Unmapped reads	79,308 / 7.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,838 / 0.79%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	28,058 / 2.5%
Duplication rate	2.32%
Clipped reads	422,412 / 37.62%

2.2. ACGT Content

Number/percentage of A's	19,696,122 / 27.95%
Number/percentage of C's	12,878,244 / 18.28%
Number/percentage of T's	22,458,879 / 31.87%
Number/percentage of G's	15,431,057 / 21.9%
Number/percentage of N's	3,303 / 0%
GC Percentage	40.17%

2.3. Coverage

Mean	0.0228

Standard Deviation	0.1945

2.4. Mapping Quality

Mean Mapping Quality	46.24

2.5. Mismatches and indels

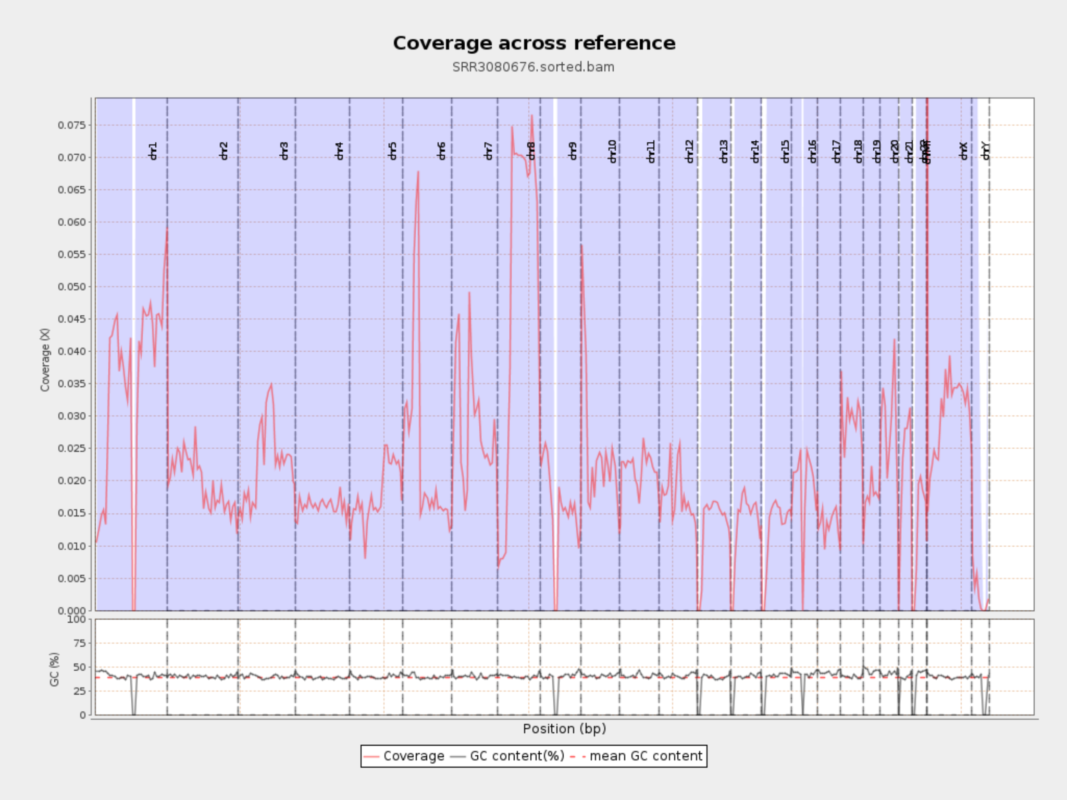
General error rate	0.7%
Mismatches	486,980
Insertions	5,490
Mapped reads with at least one insertion	0.52%
Deletions	16,534
Mapped reads with at least one deletion	1.57%
Homopolymer indels	49.05%

2.6. Chromosome stats

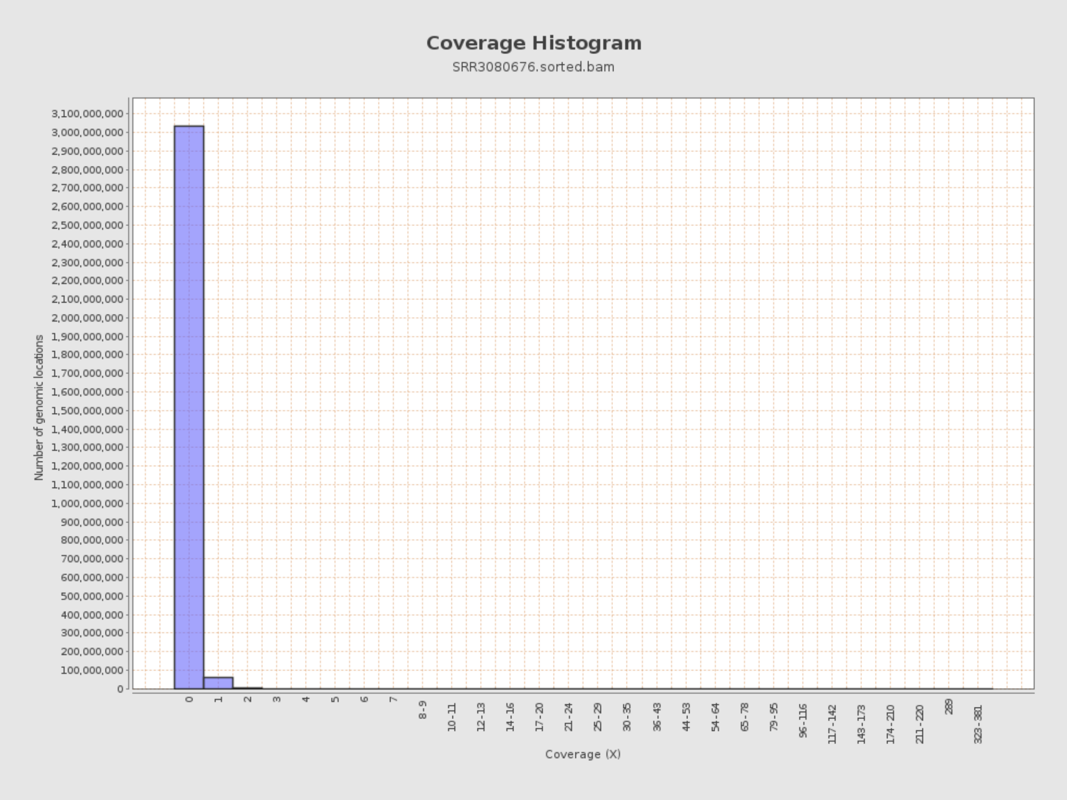
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8724233	0.035	0.2627
chr2	243199373	4804639	0.0198	0.2315
chr3	198022430	4551676	0.023	0.1629
chr4	191154276	3083980	0.0161	0.1379
chr5	180915260	3305758	0.0183	0.1448
chr6	171115067	4286541	0.0251	0.1994
chr7	159138663	4524094	0.0284	0.3298

chr8	146364022	7491368	0.0512	0.2764
chr9	141213431	2241478	0.0159	0.1545
chr10	135534747	3391383	0.025	0.1811
chr11	135006516	2961968	0.0219	0.1686
chr12	133851895	2355464	0.0176	0.1432
chr13	115169878	1486497	0.0129	0.1221
chr14	107349540	1422630	0.0133	0.125
chr15	102531392	1271028	0.0124	0.1232
chr16	90354753	1718546	0.019	0.1518
chr17	81195210	1086646	0.0134	0.1262
chr18	78077248	2322369	0.0297	0.2228
chr19	59128983	1056270	0.0179	0.1741
chr20	63025520	1823223	0.0289	0.1848
chr21	48129895	1067312	0.0222	0.1625
chr22	51304566	656594	0.0128	0.1213
chrMT	16571	9022	0.5444	0.757
chrX	155270560	4707491	0.0303	0.193
chrY	59373566	144197	0.0024	0.0574

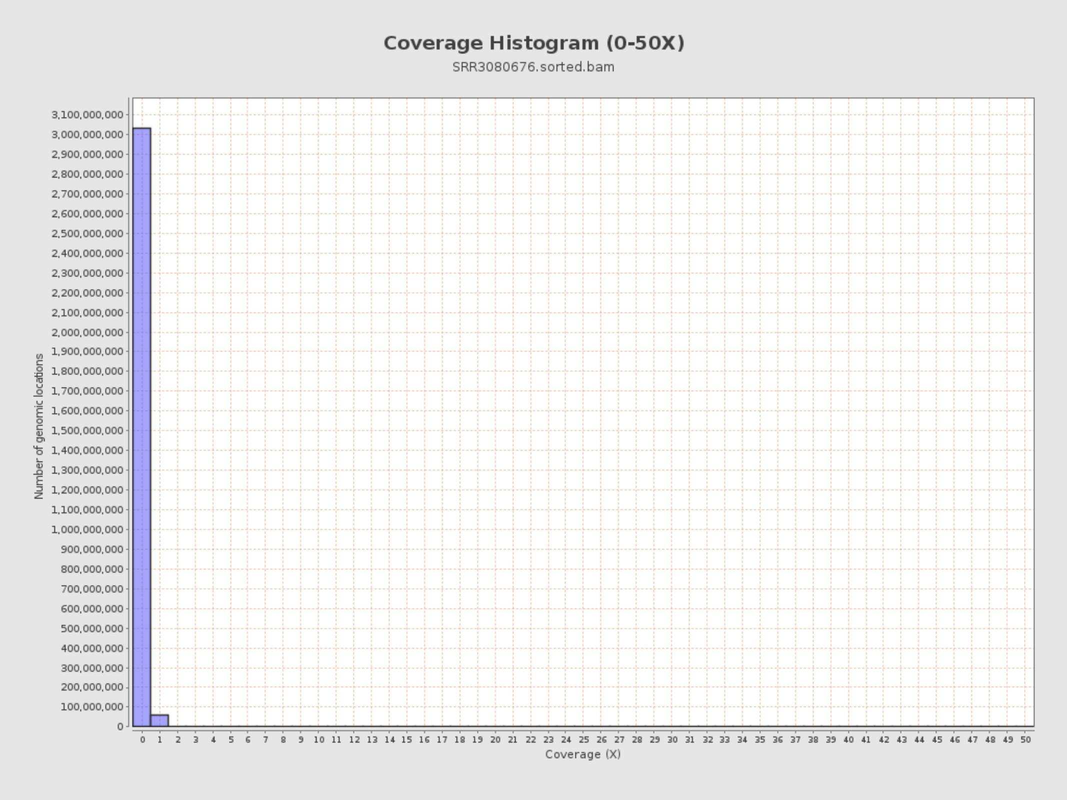
3. Results : Coverage across reference



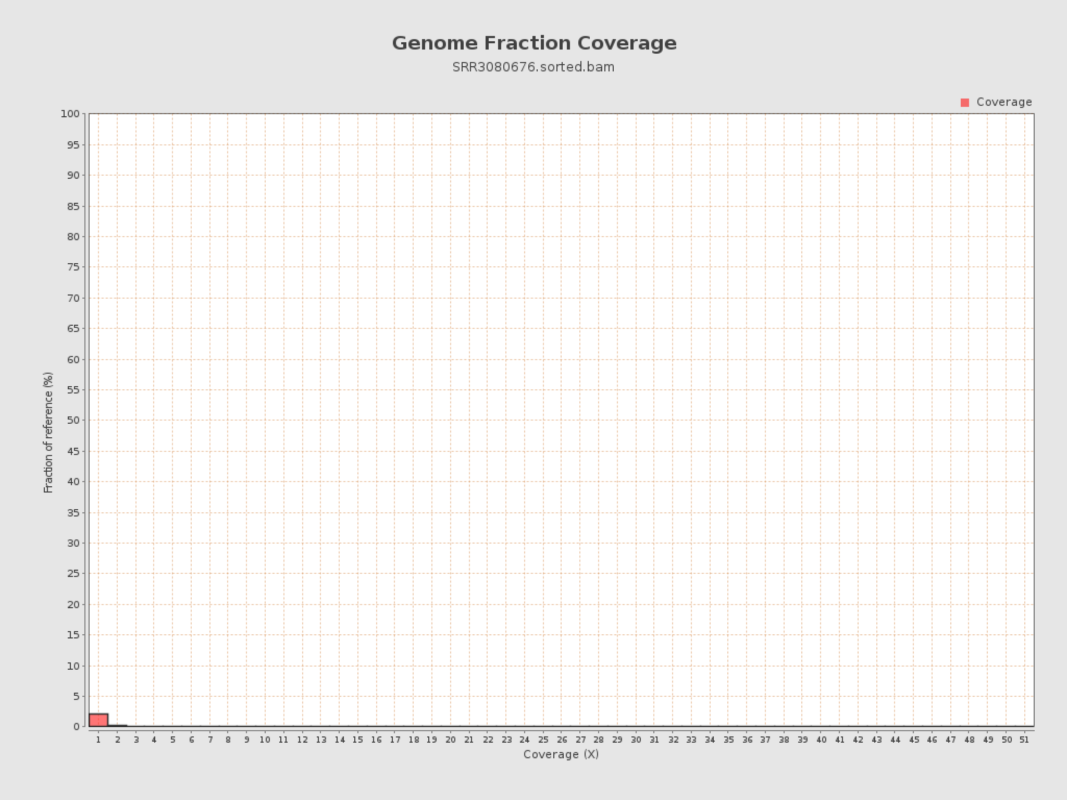
4. Results : Coverage Histogram



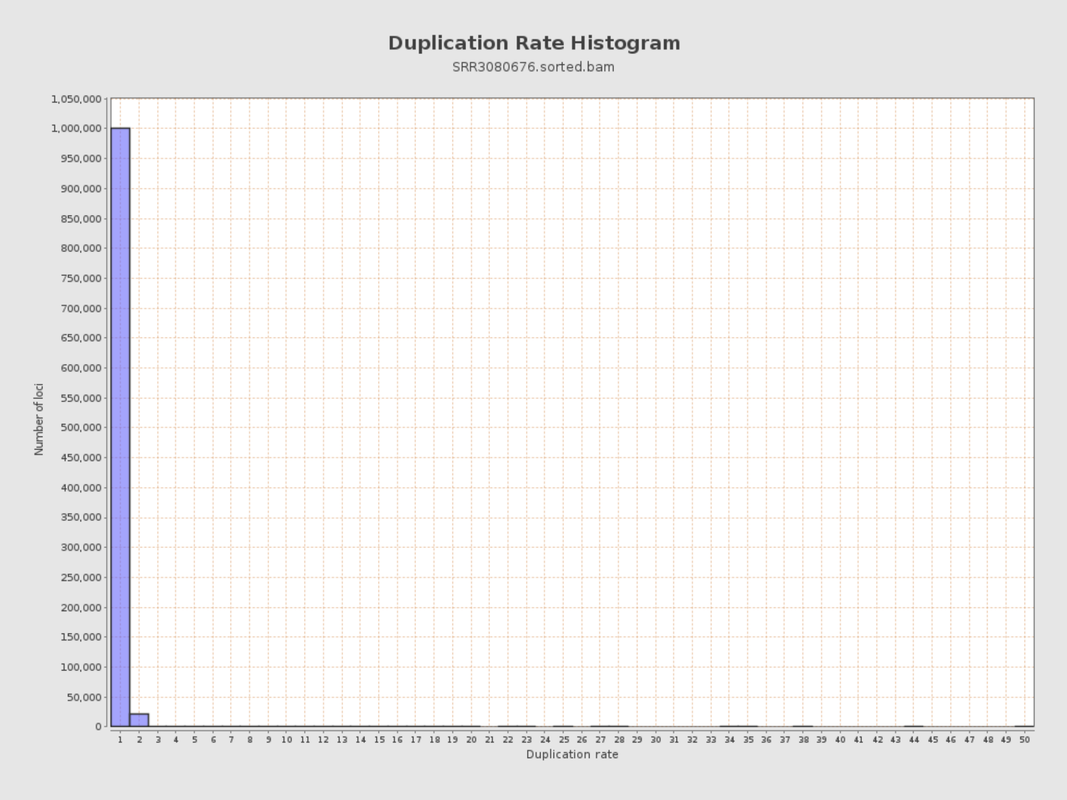
5. Results : Coverage Histogram (0-50X)



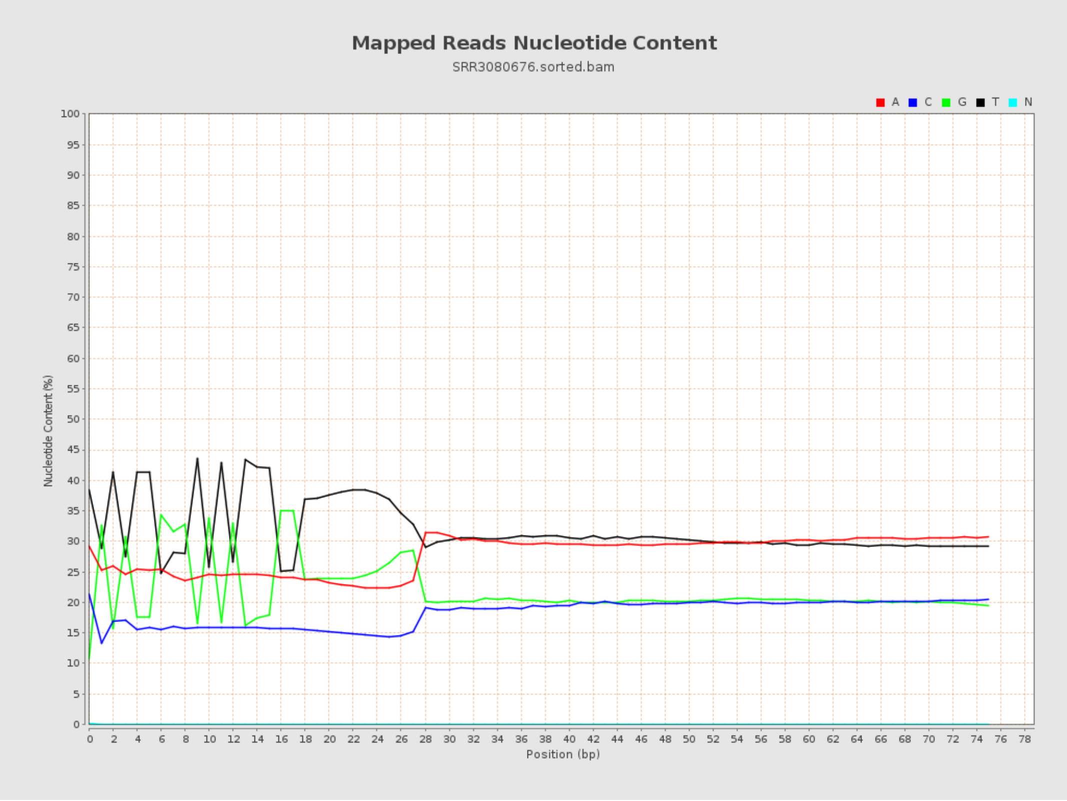
6. Results : Genome Fraction Coverage



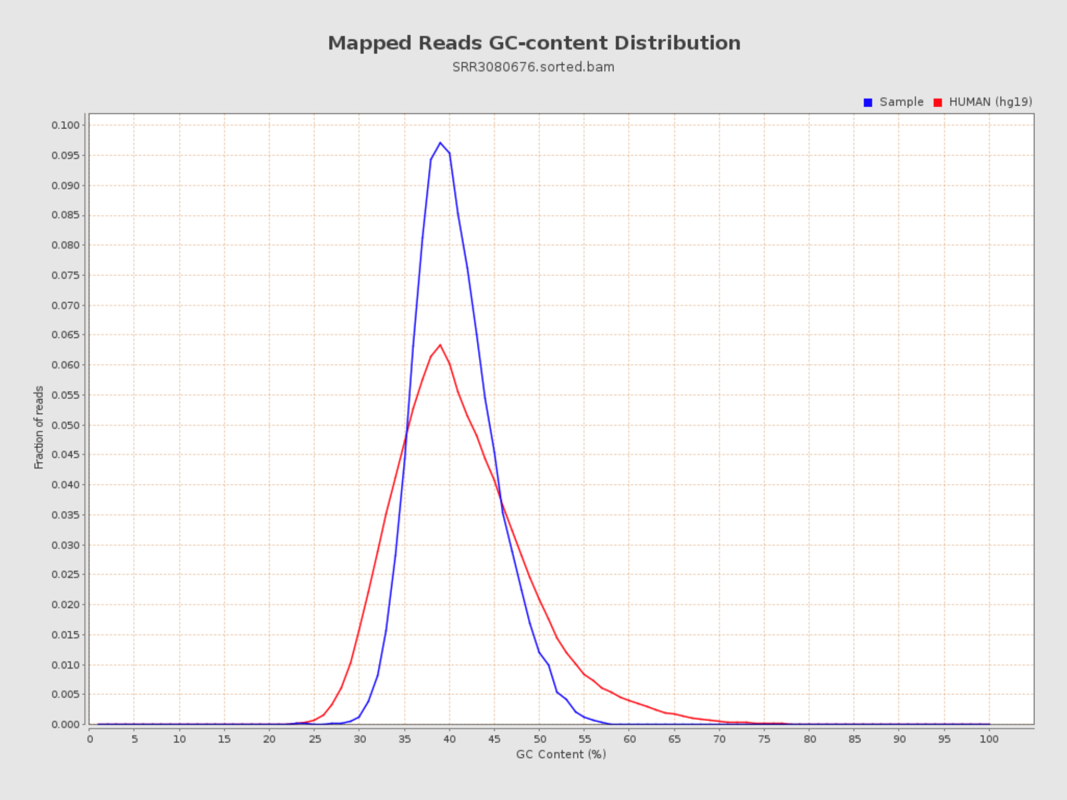
7. Results : Duplication Rate Histogram



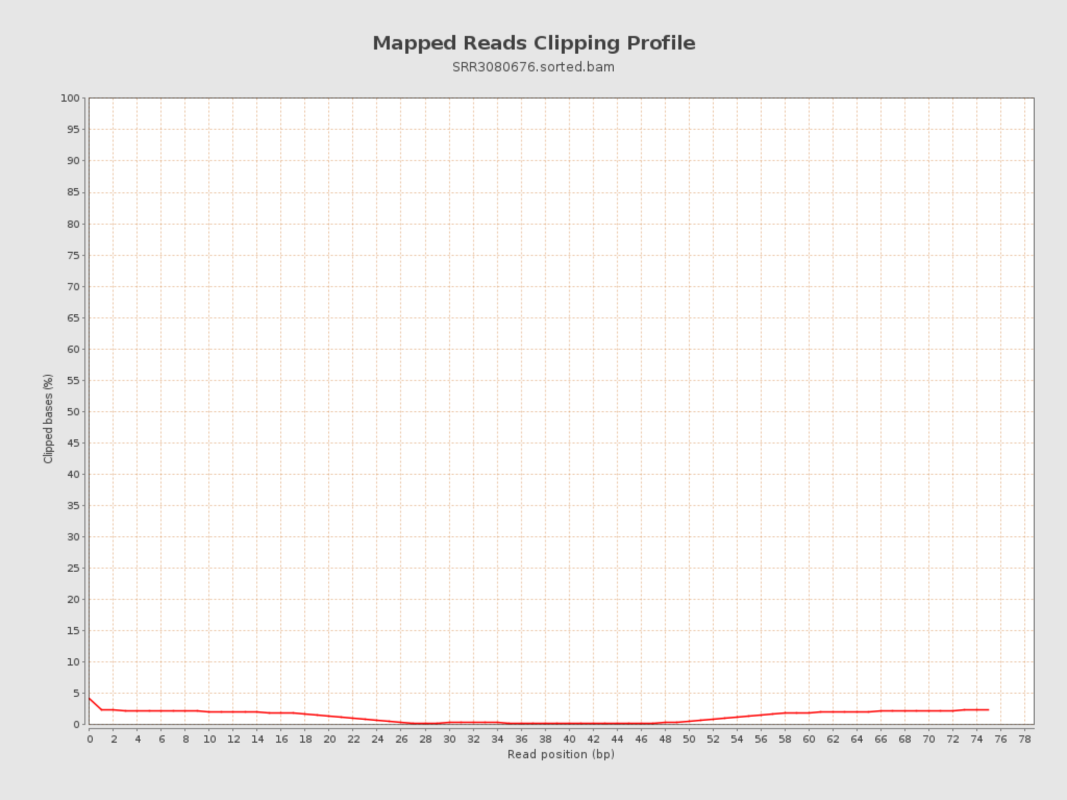
8. Results : Mapped Reads Nucleotide Content



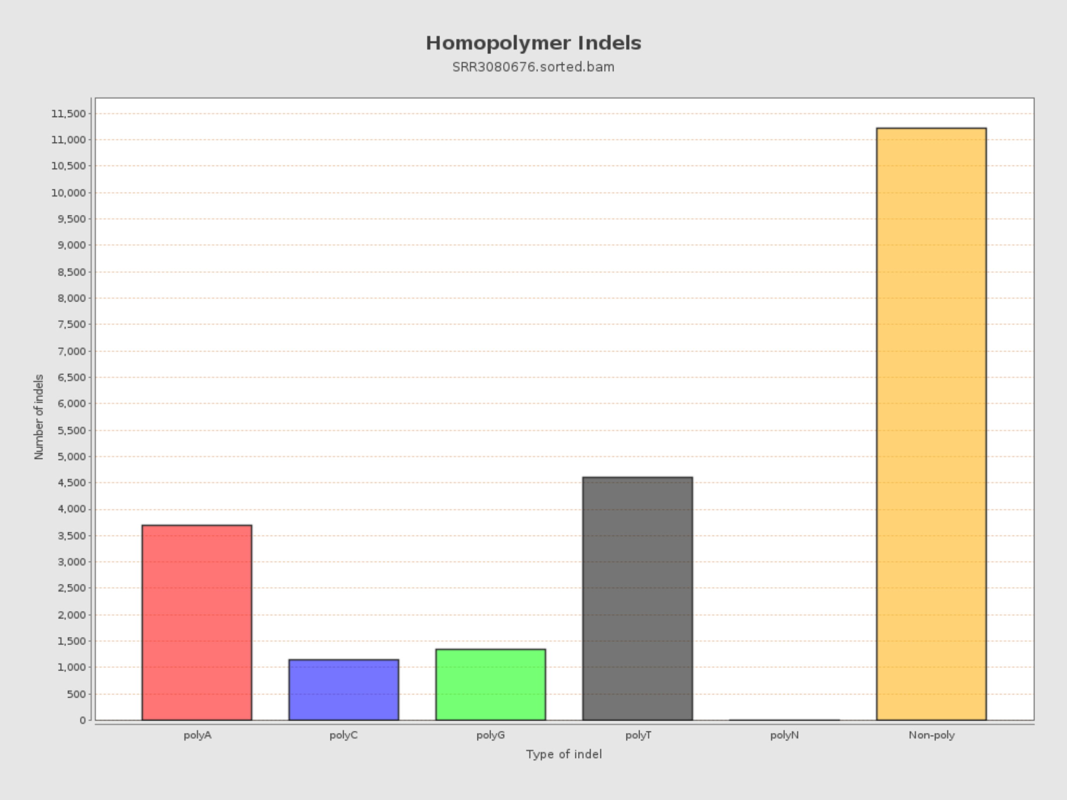
9. Results : Mapped Reads GC-content Distribution



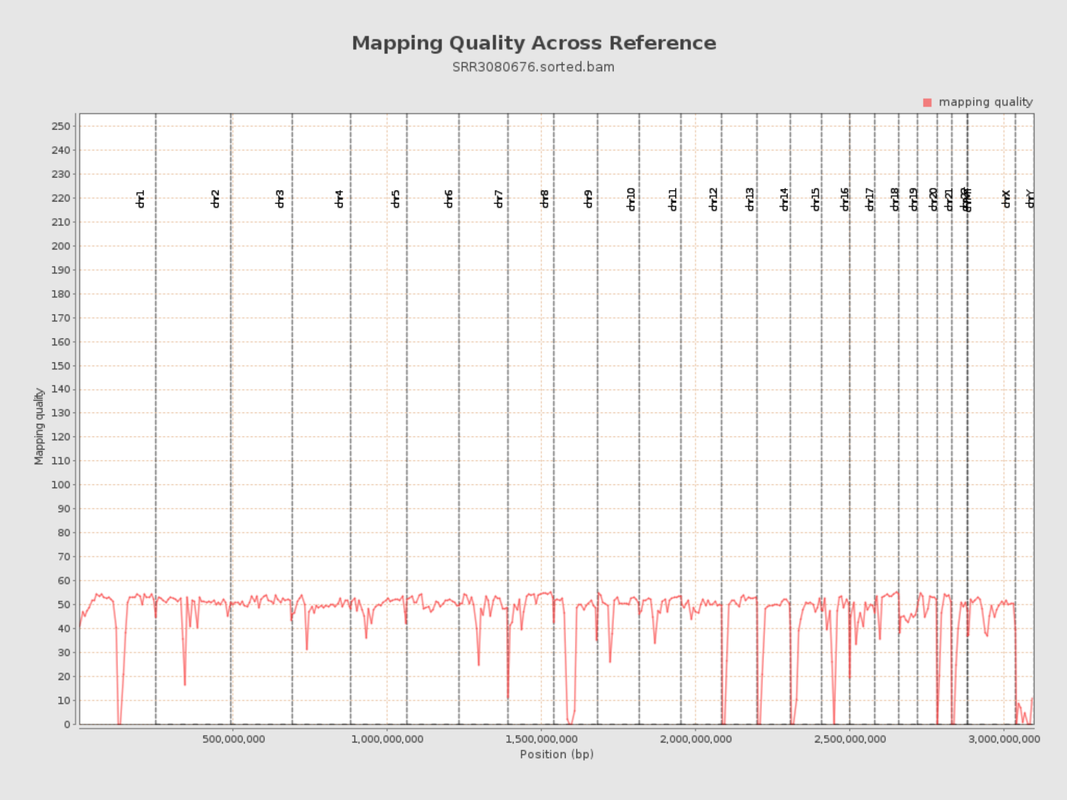
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram