Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 10:22:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080652.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_SRR3080652 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080652.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 10:22:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080652.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,454,243
Mapped reads	1,333,729 / 91.71%
Unmapped reads	120,514 / 8.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,439 / 0.79%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	48,197 / 3.31%
Duplication rate	3.2%
Clipped reads	570,410 / 39.22%

2.2. ACGT Content

Number/percentage of A's	24,665,263 / 27.6%
Number/percentage of C's	16,475,271 / 18.44%
Number/percentage of T's	28,334,604 / 31.71%
Number/percentage of G's	19,872,276 / 22.24%
Number/percentage of N's	3,893 / 0%
GC Percentage	40.68%

2.3. Coverage

Mean	0.0289

Standard Deviation	0.2252

2.4. Mapping Quality

Mean Mapping Quality	46

2.5. Mismatches and indels

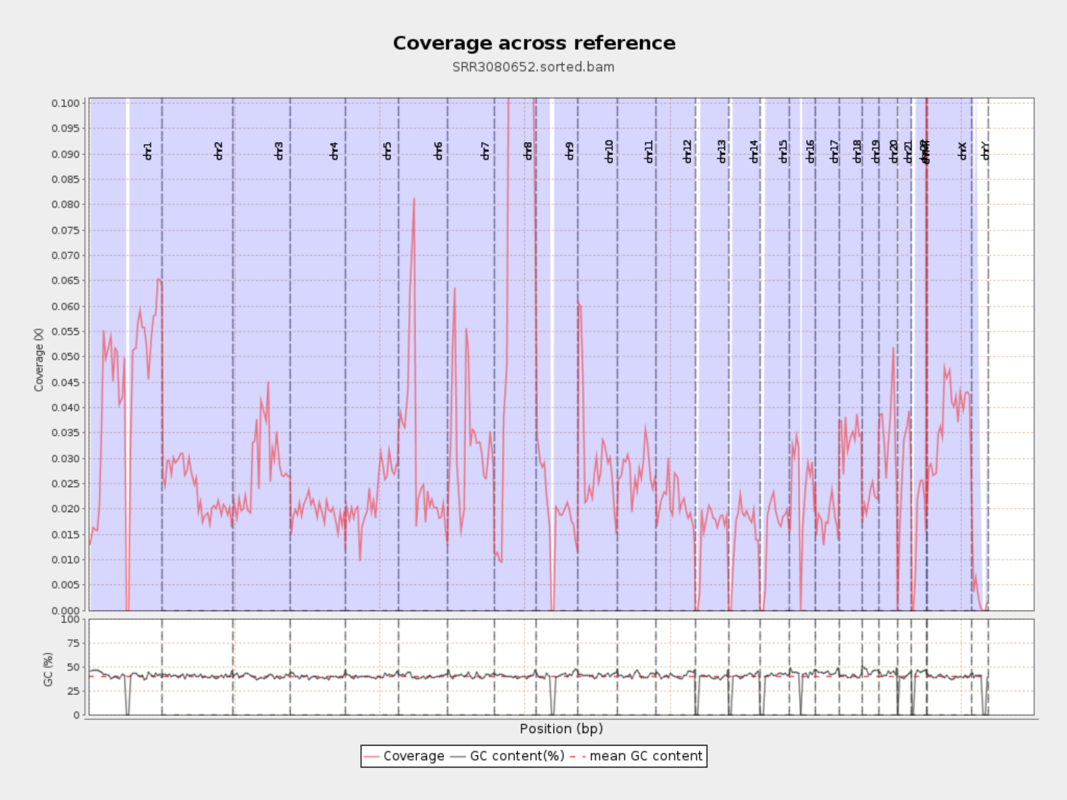
General error rate	0.68%
Mismatches	598,487
Insertions	6,907
Mapped reads with at least one insertion	0.51%
Deletions	20,768
Mapped reads with at least one deletion	1.54%
Homopolymer indels	49.02%

2.6. Chromosome stats

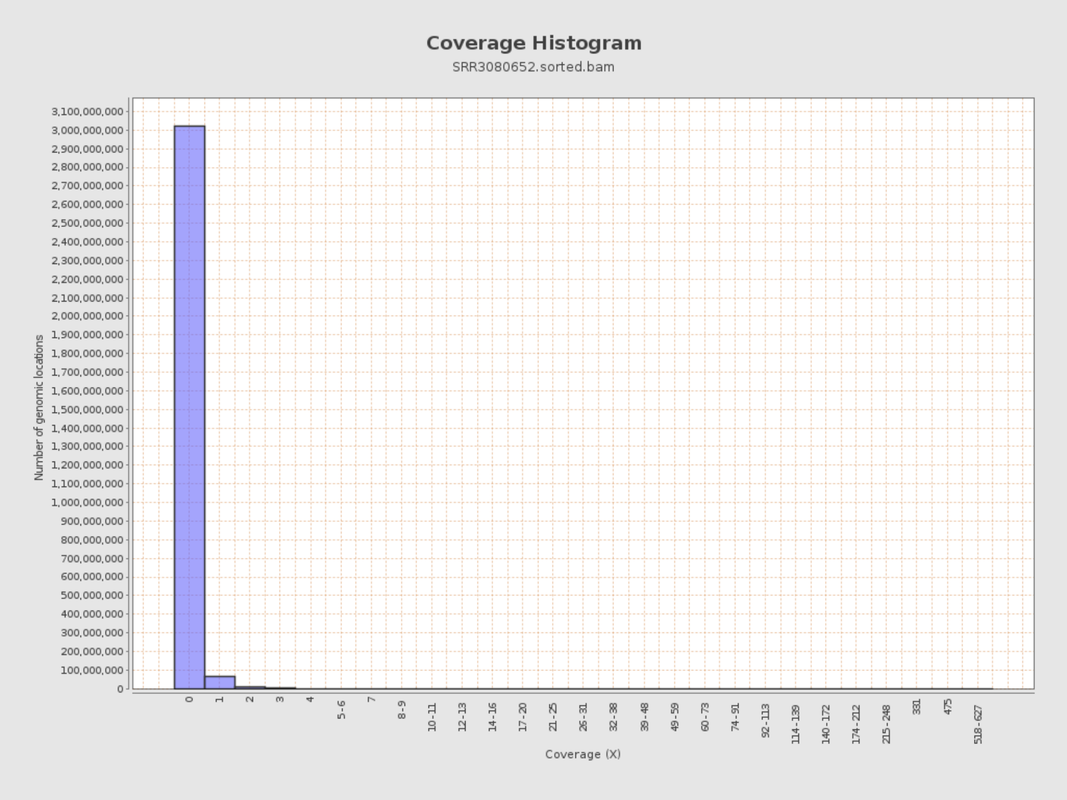
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10730844	0.0431	0.2571
chr2	243199373	5809916	0.0239	0.3142
chr3	198022430	5606758	0.0283	0.1898
chr4	191154276	3740713	0.0196	0.1596
chr5	180915260	4095447	0.0226	0.1696
chr6	171115067	5318907	0.0311	0.2265
chr7	159138663	5438710	0.0342	0.3546

chr8	146364022	12169720	0.0831	0.3632
chr9	141213431	2730143	0.0193	0.171
chr10	135534747	4180369	0.0308	0.2058
chr11	135006516	3695908	0.0274	0.196
chr12	133851895	2838399	0.0212	0.1647
chr13	115169878	1748551	0.0152	0.1399
chr14	107349540	1626361	0.0152	0.1414
chr15	102531392	1590398	0.0155	0.1454
chr16	90354753	2225155	0.0246	0.1801
chr17	81195210	1433025	0.0176	0.1518
chr18	78077248	2703828	0.0346	0.248
chr19	59128983	1325981	0.0224	0.1791
chr20	63025520	2243783	0.0356	0.2146
chr21	48129895	1297170	0.027	0.1882
chr22	51304566	820972	0.016	0.1421
chrMT	16571	5244	0.3165	0.6497
chrX	155270560	5835720	0.0376	0.2247
chrY	59373566	172669	0.0029	0.0618

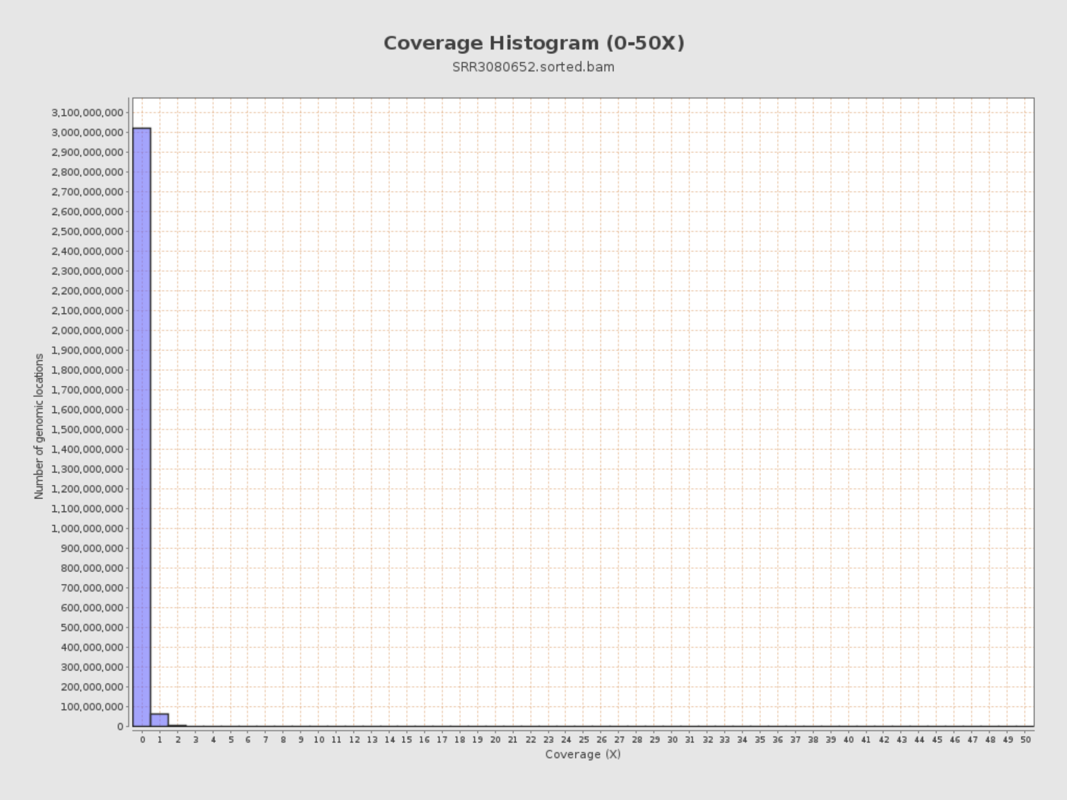
3. Results : Coverage across reference



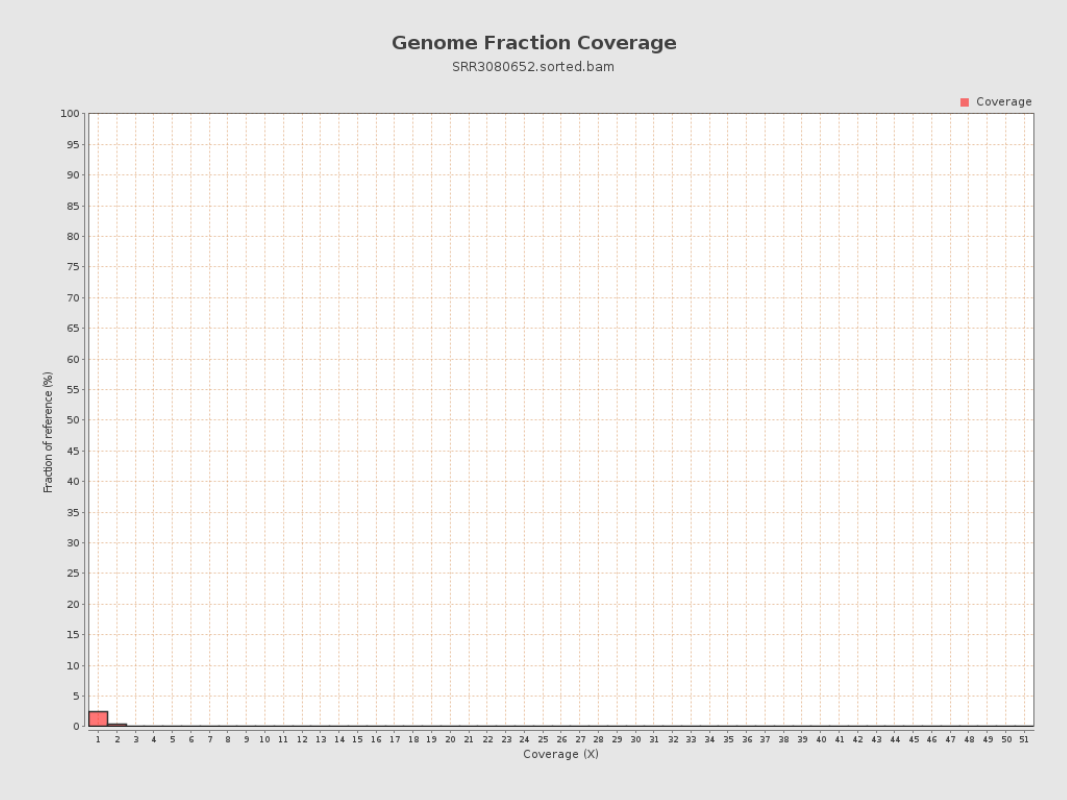
4. Results : Coverage Histogram



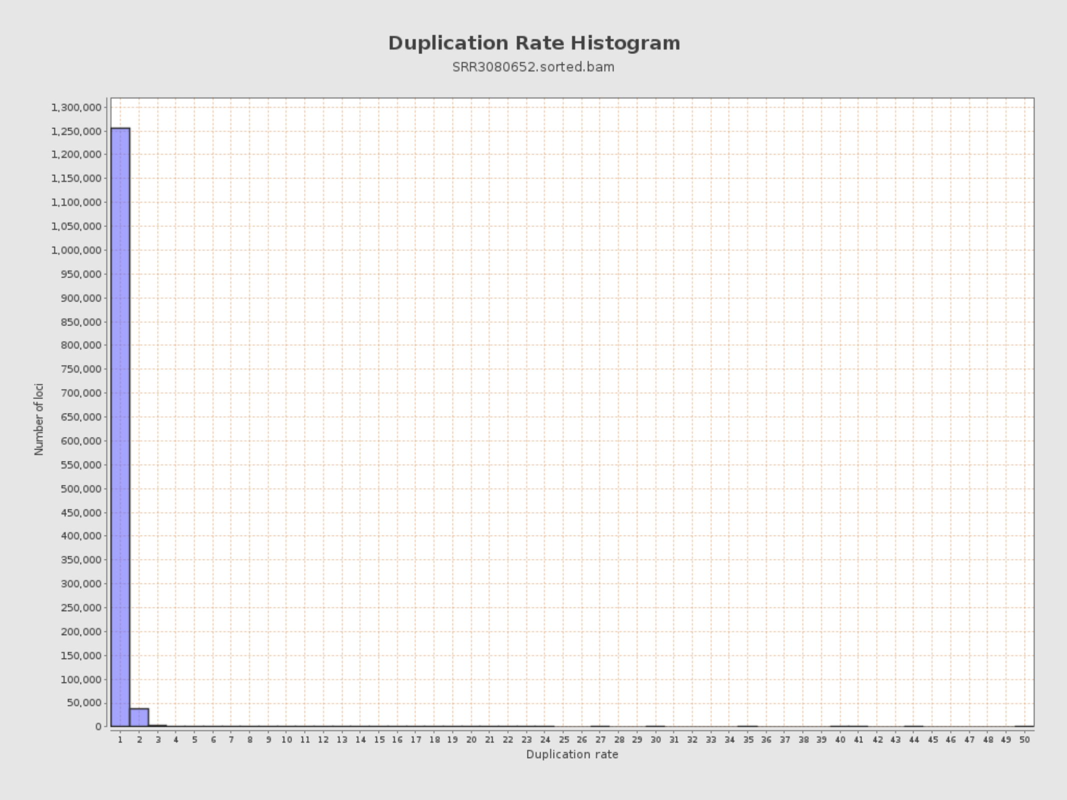
5. Results : Coverage Histogram (0-50X)



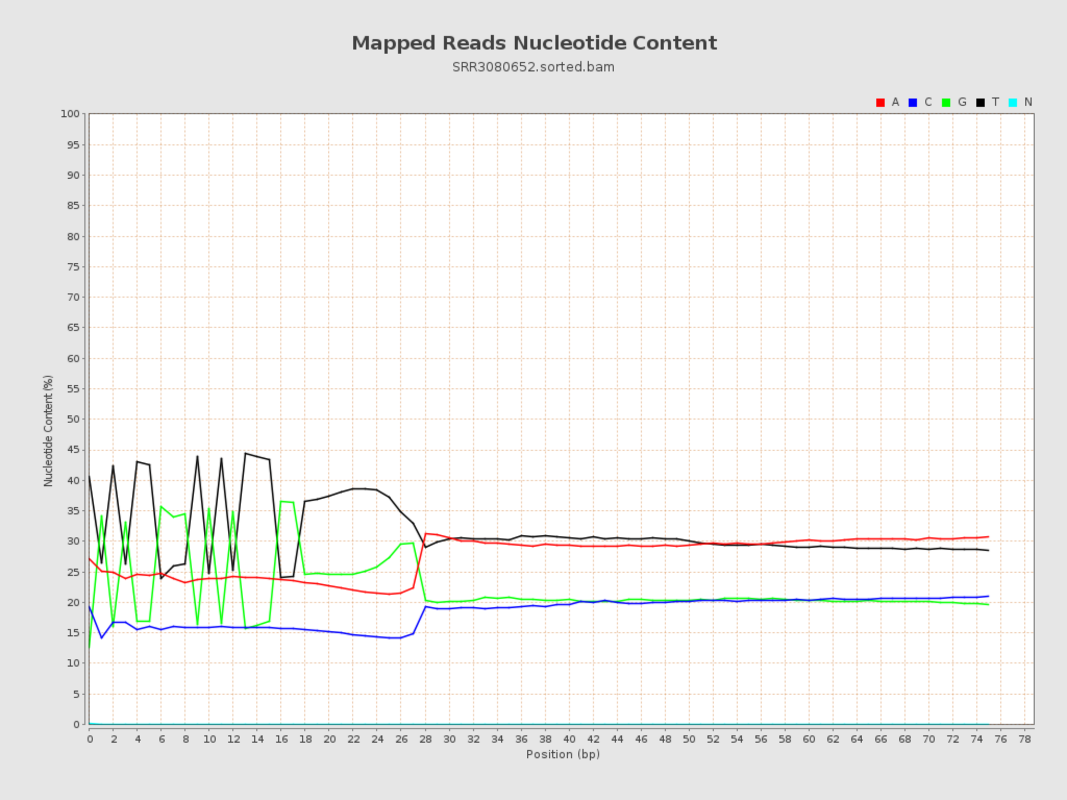
6. Results : Genome Fraction Coverage



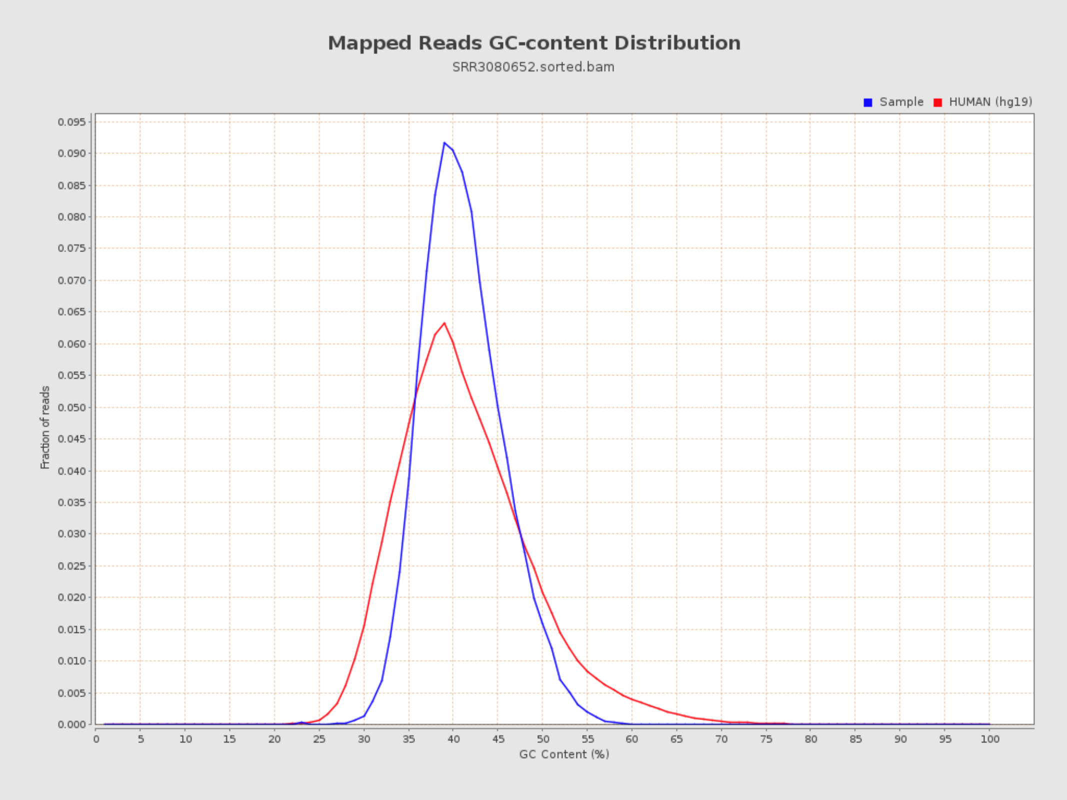
7. Results : Duplication Rate Histogram



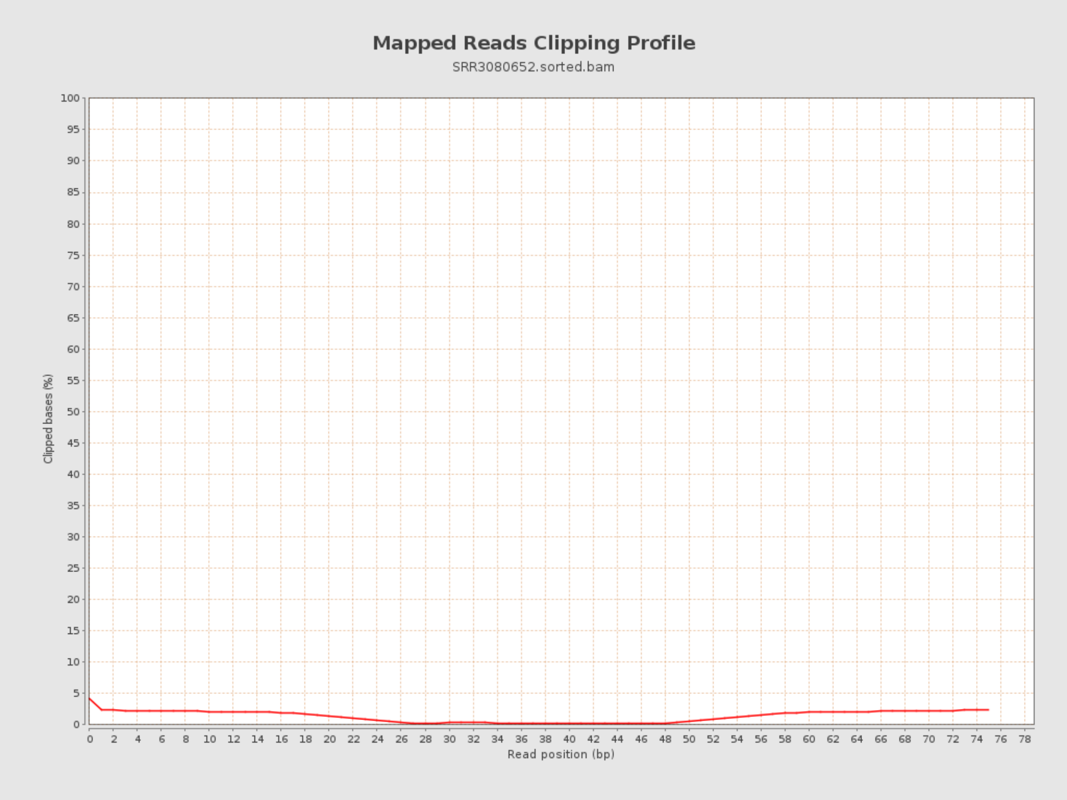
8. Results : Mapped Reads Nucleotide Content



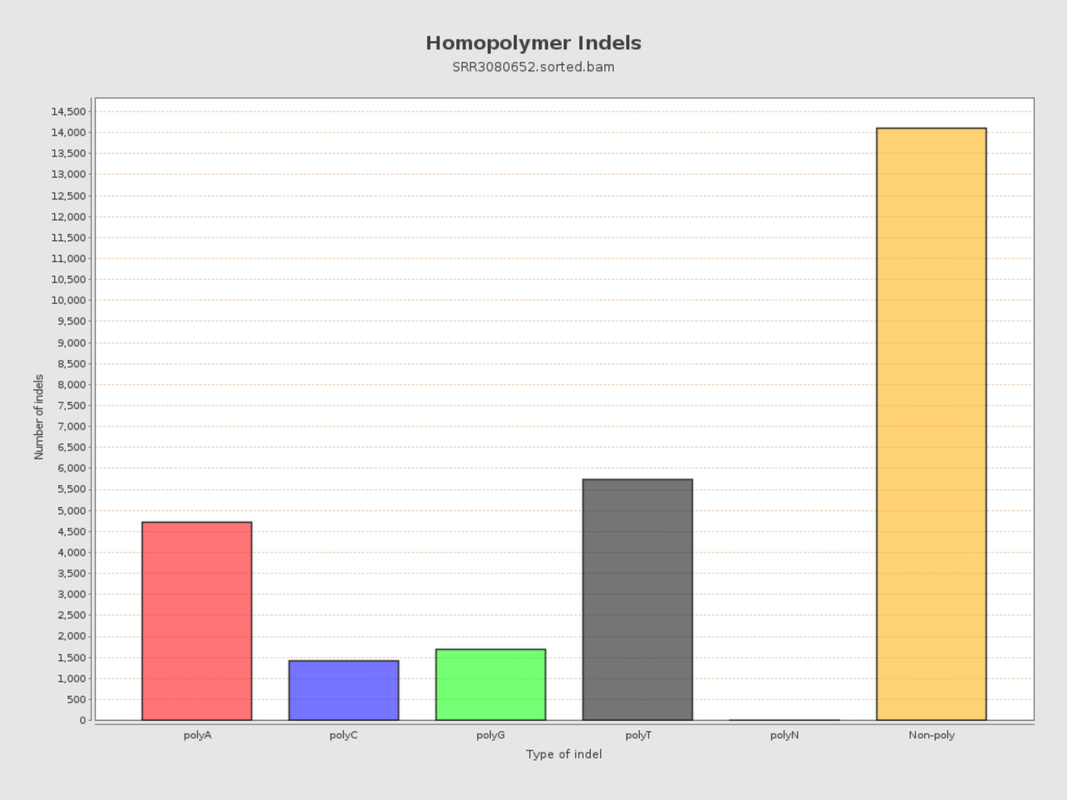
9. Results : Mapped Reads GC-content Distribution



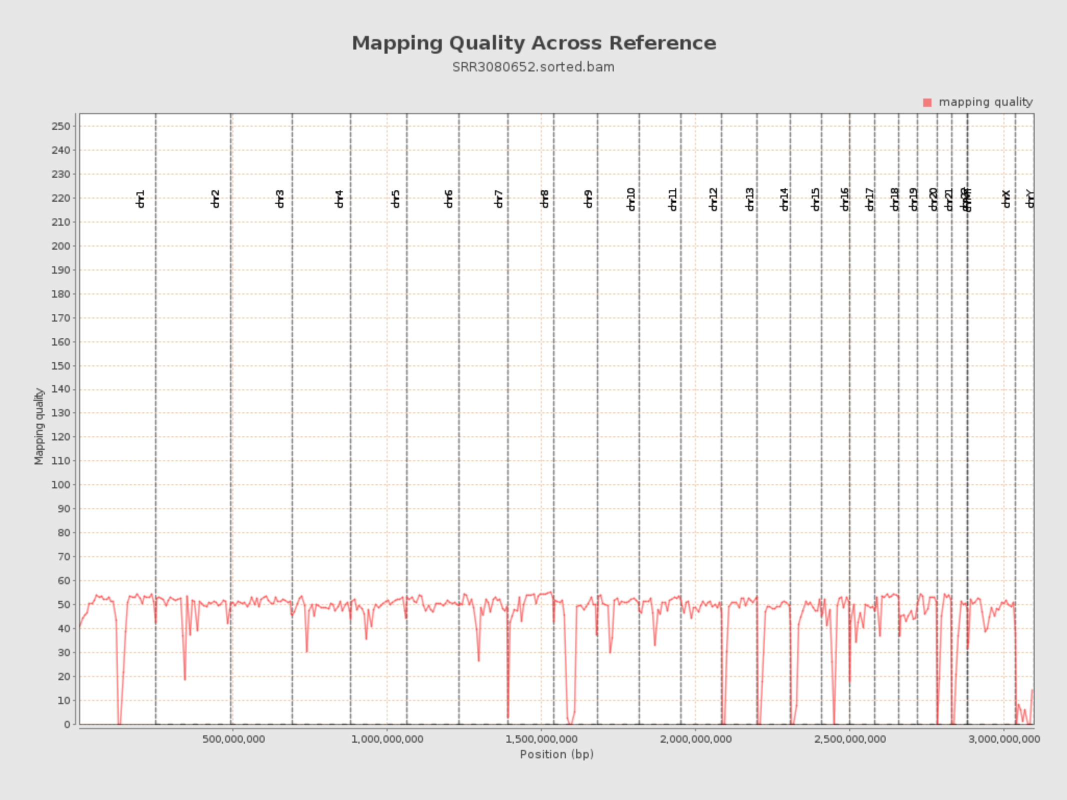
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram