Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 09:53:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080649.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_SRR3080649 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080649.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 09:53:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080649.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,228,774
Mapped reads	1,082,618 / 88.11%
Unmapped reads	146,156 / 11.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,649 / 0.87%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	44,869 / 3.65%
Duplication rate	3.37%
Clipped reads	545,273 / 44.38%

2.2. ACGT Content

Number/percentage of A's	18,870,650 / 26.71%
Number/percentage of C's	13,134,219 / 18.59%
Number/percentage of T's	22,254,577 / 31.5%
Number/percentage of G's	16,382,641 / 23.19%
Number/percentage of N's	3,010 / 0%
GC Percentage	41.78%

2.3. Coverage

Mean	0.0228

Standard Deviation	0.245

2.4. Mapping Quality

Mean Mapping Quality	44.61

2.5. Mismatches and indels

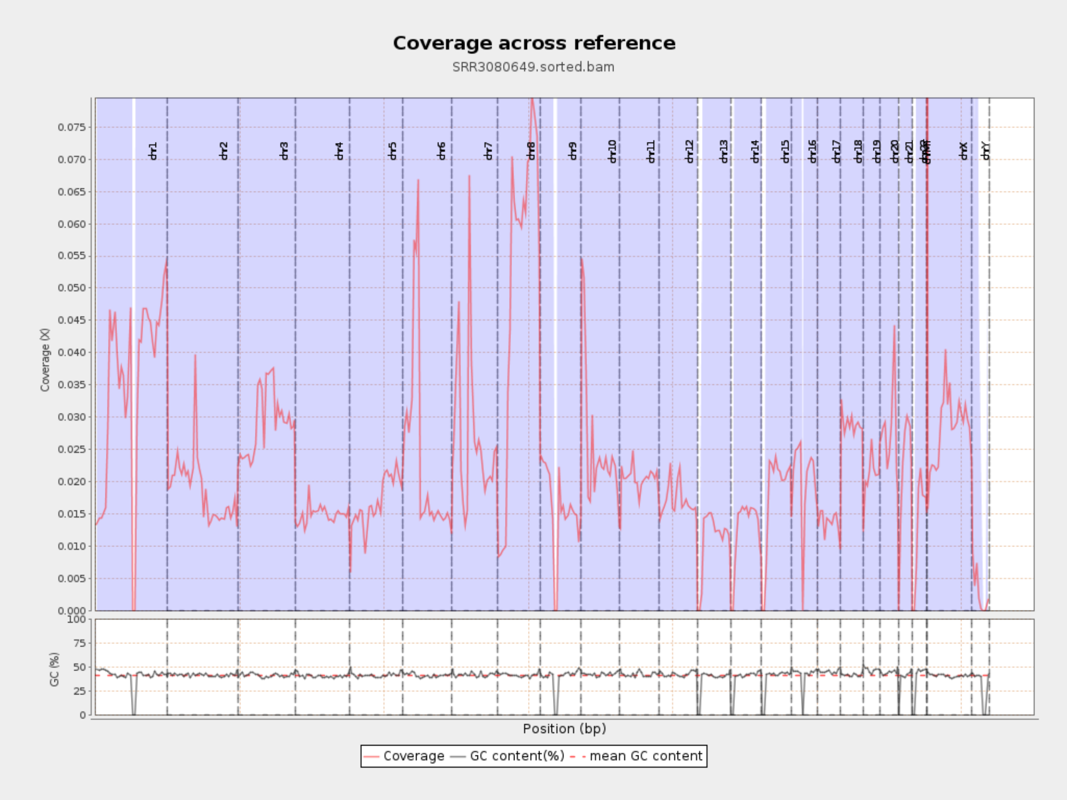
General error rate	0.78%
Mismatches	541,808
Insertions	5,375
Mapped reads with at least one insertion	0.49%
Deletions	21,435
Mapped reads with at least one deletion	1.96%
Homopolymer indels	45.51%

2.6. Chromosome stats

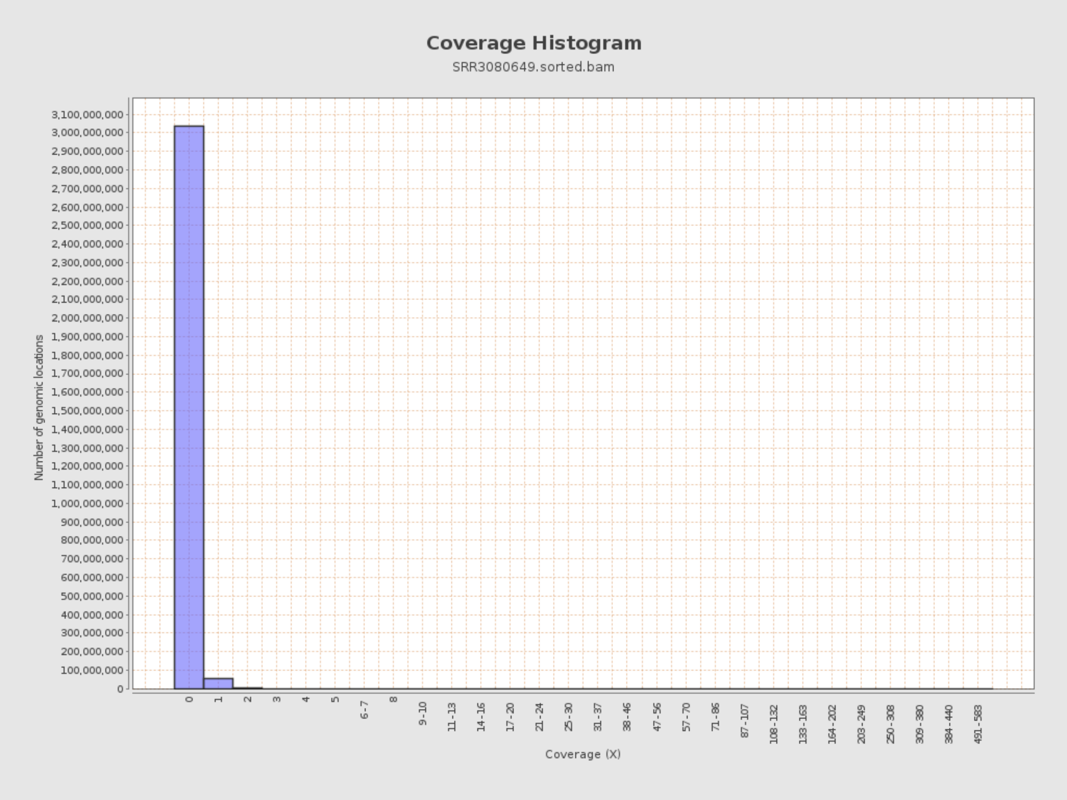
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8703532	0.0349	0.3309
chr2	243199373	4572698	0.0188	0.3156
chr3	198022430	5814533	0.0294	0.1909
chr4	191154276	2851545	0.0149	0.1415
chr5	180915260	3083258	0.017	0.1448
chr6	171115067	4096471	0.0239	0.2261
chr7	159138663	4246292	0.0267	0.5554

chr8	146364022	7545764	0.0516	0.3019
chr9	141213431	2224972	0.0158	0.1848
chr10	135534747	3476907	0.0257	0.2106
chr11	135006516	2775019	0.0206	0.1904
chr12	133851895	2294527	0.0171	0.1473
chr13	115169878	1263485	0.011	0.1162
chr14	107349540	1336550	0.0125	0.1309
chr15	102531392	1817957	0.0177	0.1539
chr16	90354753	1801372	0.0199	0.163
chr17	81195210	1113306	0.0137	0.1354
chr18	78077248	2270046	0.0291	0.2652
chr19	59128983	1264361	0.0214	0.2202
chr20	63025520	1746345	0.0277	0.1873
chr21	48129895	1073064	0.0223	0.1716
chr22	51304566	674465	0.0131	0.1261
chrMT	16571	61735	3.7255	2.7819
chrX	155270560	4406613	0.0284	0.1994
chrY	59373566	165747	0.0028	0.0685

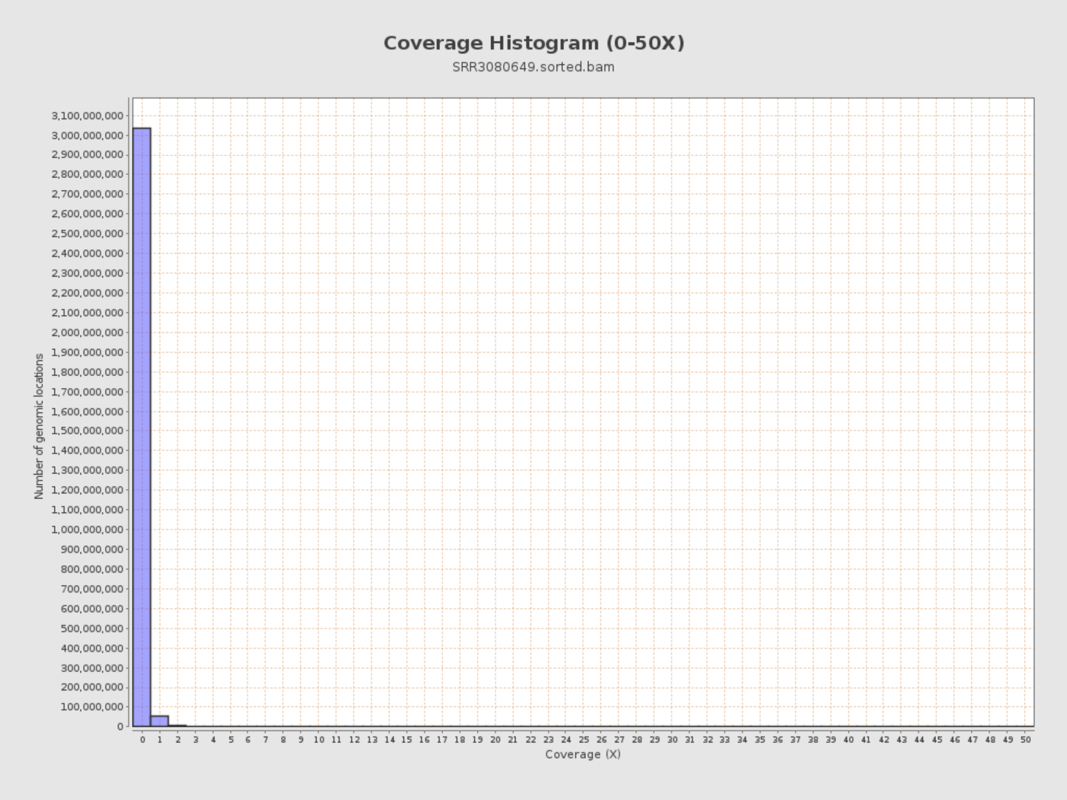
3. Results : Coverage across reference



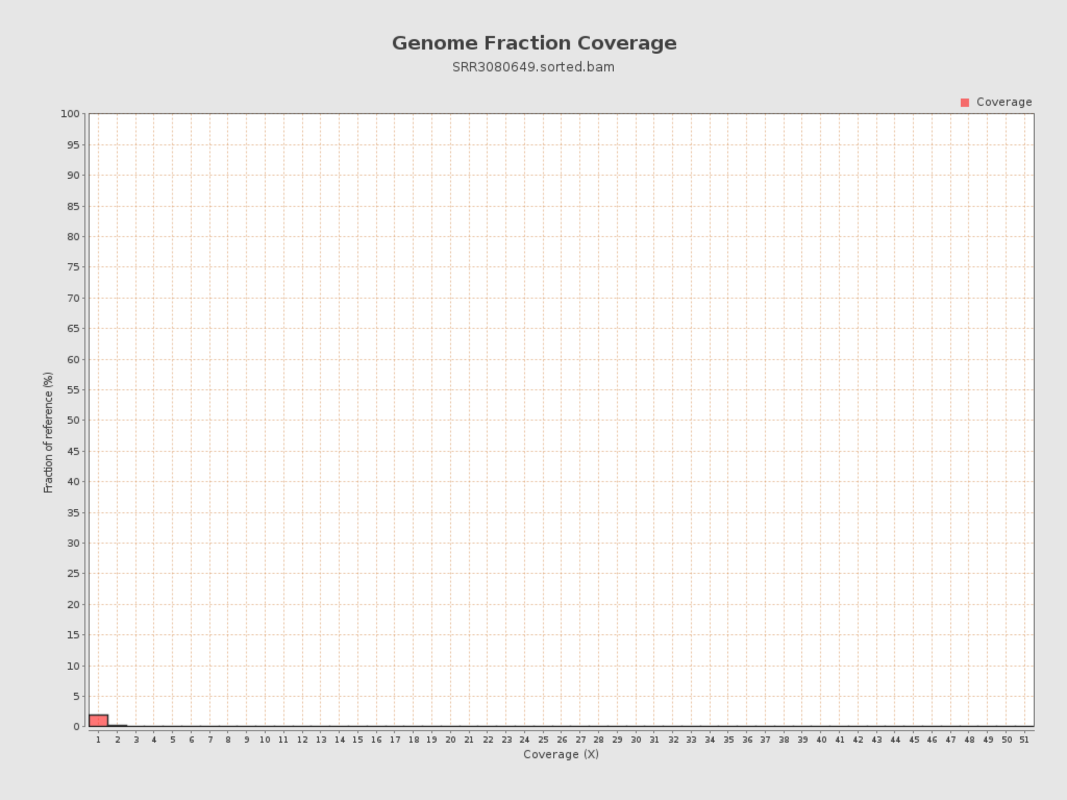
4. Results : Coverage Histogram



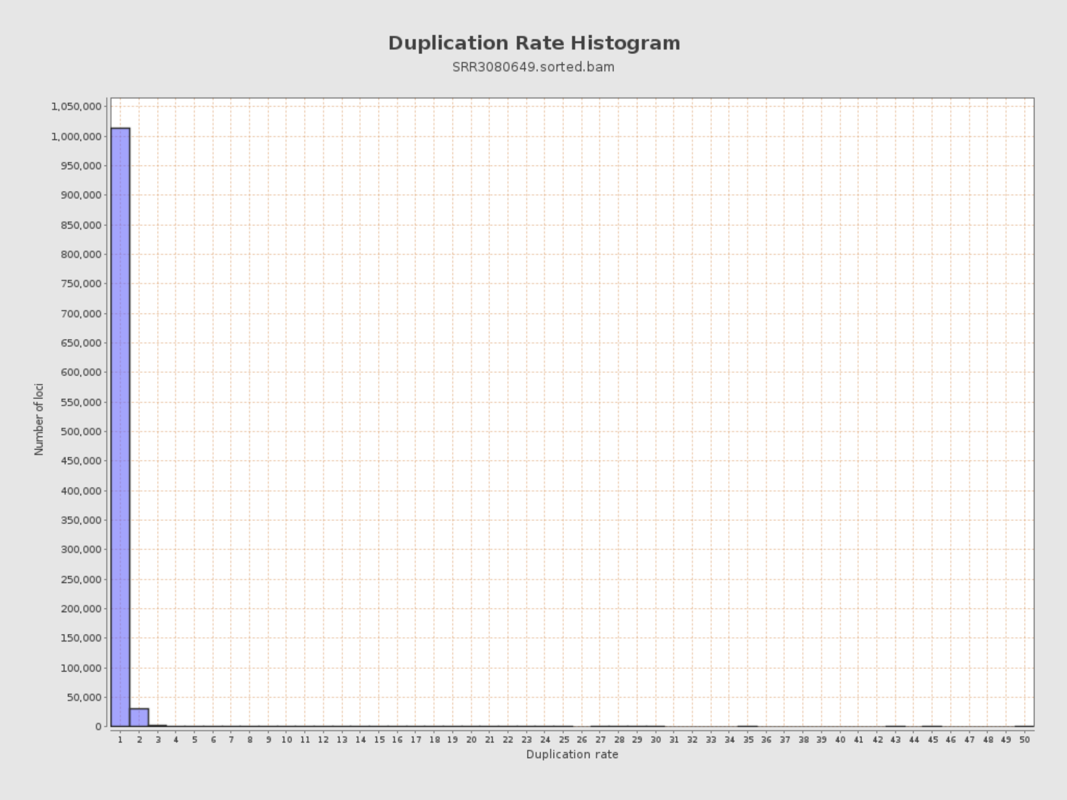
5. Results : Coverage Histogram (0-50X)



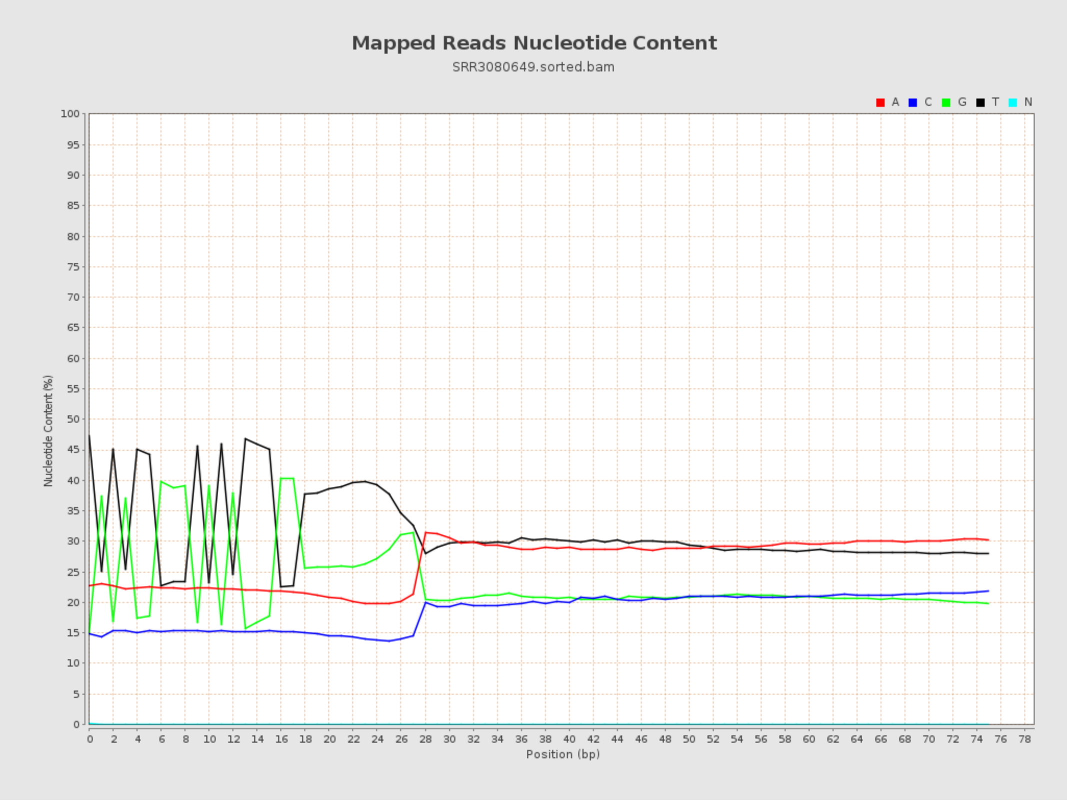
6. Results : Genome Fraction Coverage



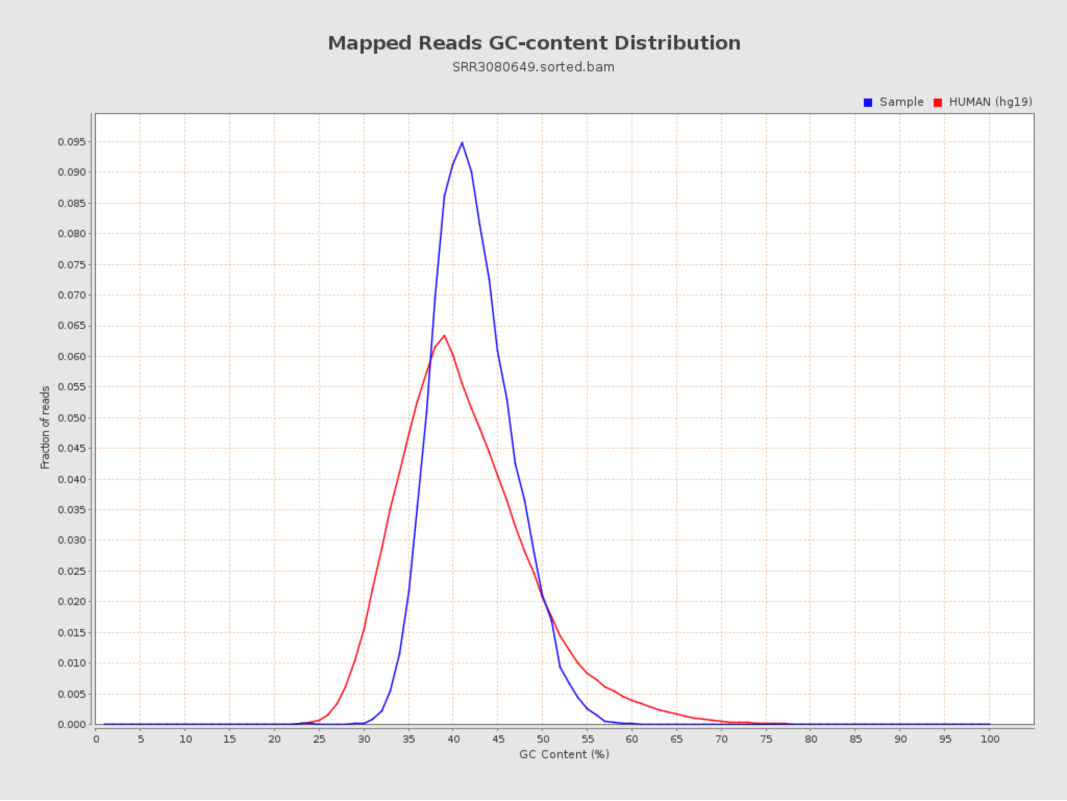
7. Results : Duplication Rate Histogram



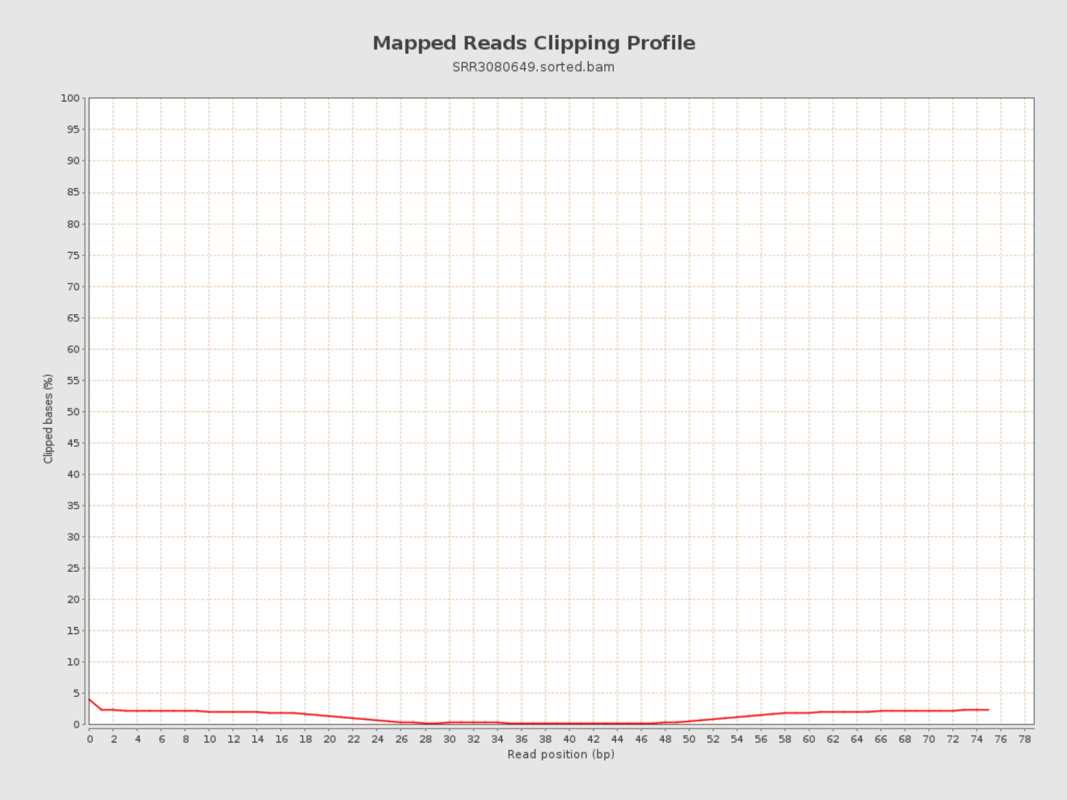
8. Results : Mapped Reads Nucleotide Content



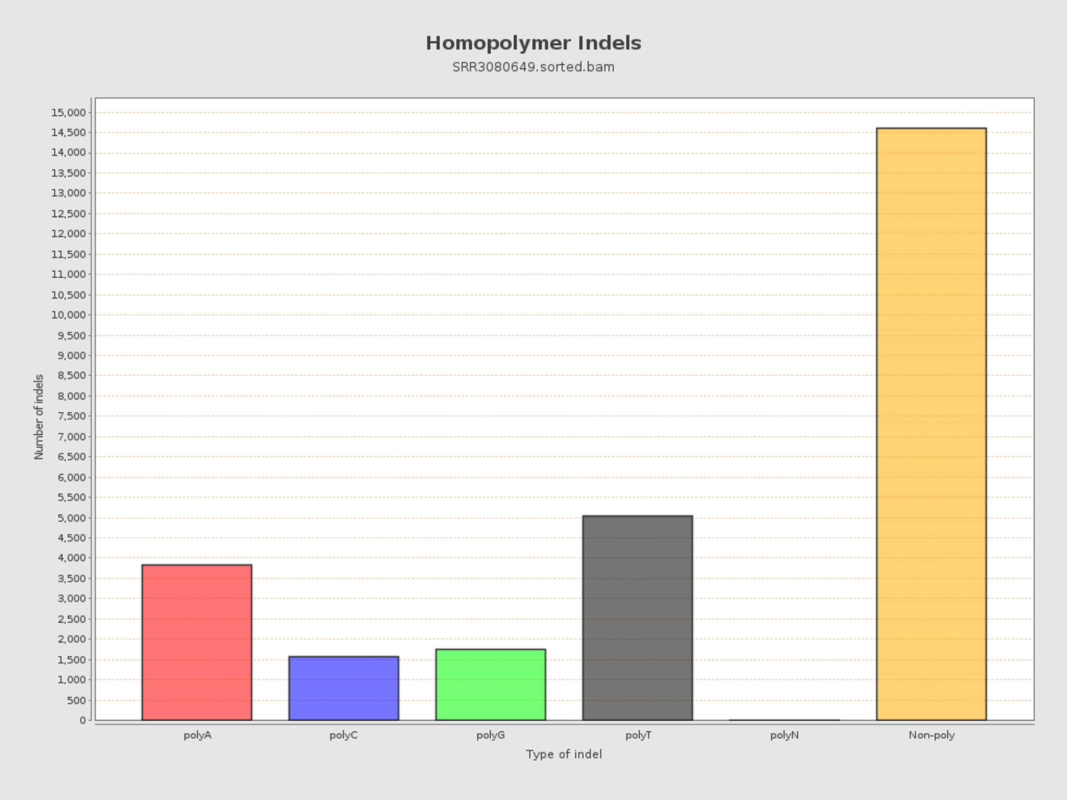
9. Results : Mapped Reads GC-content Distribution



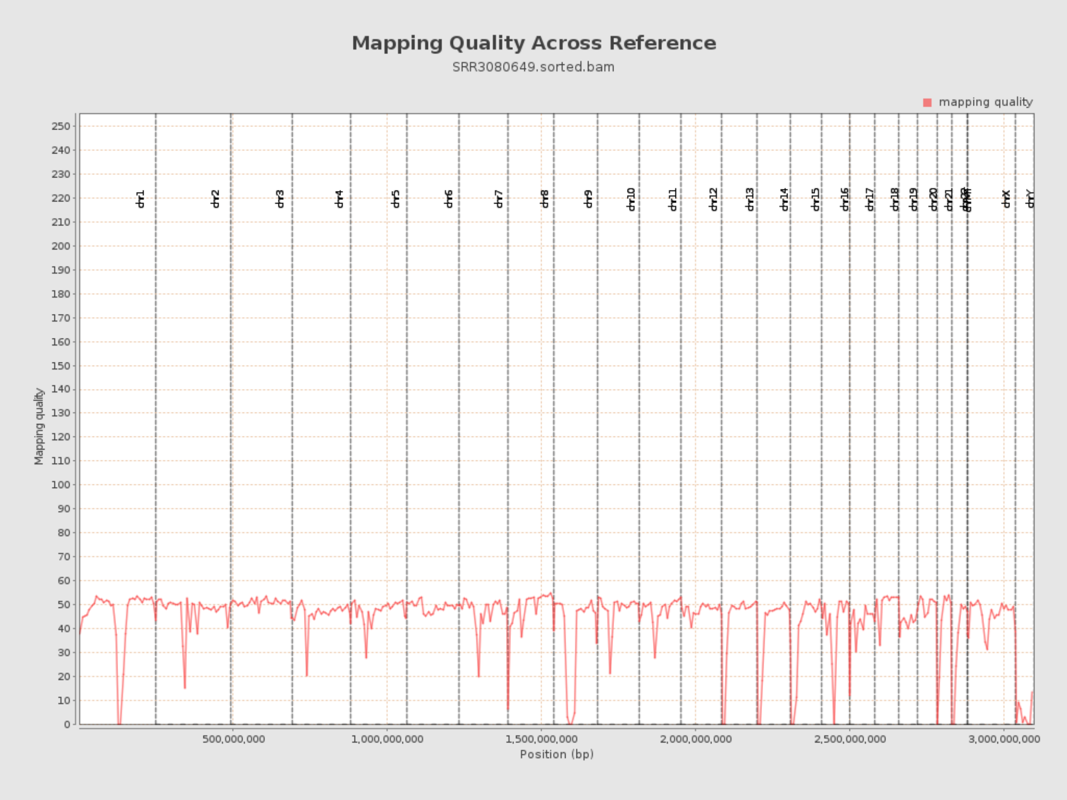
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram