Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 13:50:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080672.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_SRR3080672 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080672.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 13:50:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080672.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,451,616
Mapped reads	1,289,492 / 88.83%
Unmapped reads	162,124 / 11.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,044 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	50,628 / 3.49%
Duplication rate	3.46%
Clipped reads	632,601 / 43.58%

2.2. ACGT Content

Number/percentage of A's	22,429,024 / 26.52%
Number/percentage of C's	15,882,185 / 18.78%
Number/percentage of T's	26,525,001 / 31.36%
Number/percentage of G's	19,735,022 / 23.33%
Number/percentage of N's	3,683 / 0%
GC Percentage	42.11%

2.3. Coverage

Mean	0.0273

Standard Deviation	0.2252

2.4. Mapping Quality

Mean Mapping Quality	45.04

2.5. Mismatches and indels

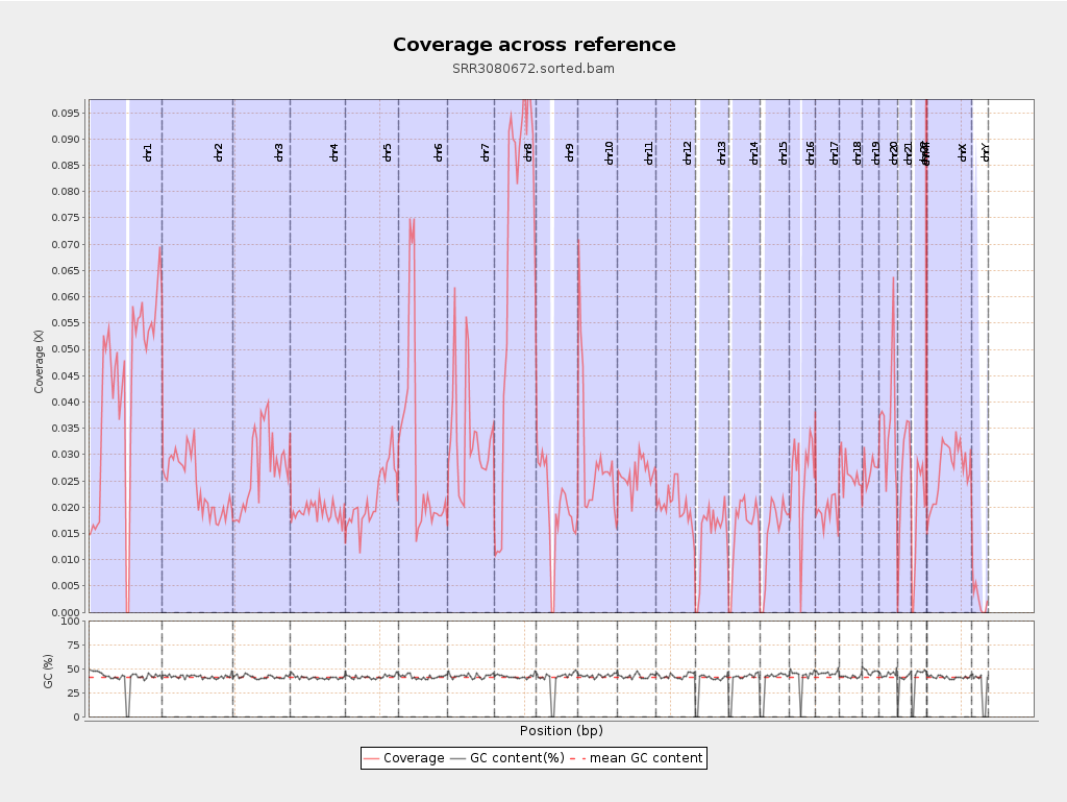
General error rate	0.7%
Mismatches	581,026
Insertions	6,177
Mapped reads with at least one insertion	0.48%
Deletions	19,005
Mapped reads with at least one deletion	1.46%
Homopolymer indels	47.09%

2.6. Chromosome stats

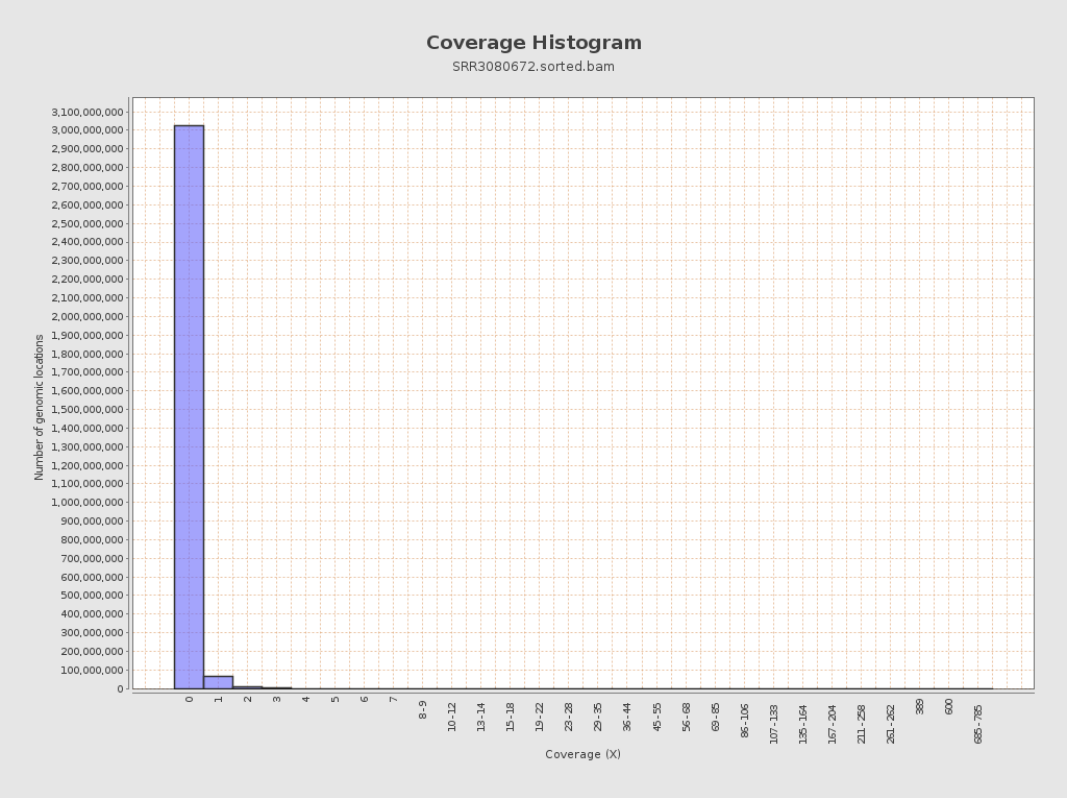
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10589757	0.0425	0.2589
chr2	243199373	5897266	0.0242	0.3699
chr3	198022430	5427913	0.0274	0.187
chr4	191154276	3655444	0.0191	0.1591
chr5	180915260	3974144	0.022	0.1678
chr6	171115067	5150579	0.0301	0.2356
chr7	159138663	5358769	0.0337	0.3347

chr8	146364022	10140937	0.0693	0.3194
chr9	141213431	2759088	0.0195	0.1685
chr10	135534747	4027719	0.0297	0.2028
chr11	135006516	3546571	0.0263	0.1896
chr12	133851895	2710691	0.0203	0.1604
chr13	115169878	1697243	0.0147	0.1381
chr14	107349540	1729638	0.0161	0.1447
chr15	102531392	1533850	0.015	0.1501
chr16	90354753	2355741	0.0261	0.1859
chr17	81195210	1543091	0.019	0.156
chr18	78077248	2065198	0.0265	0.2188
chr19	59128983	1597045	0.027	0.2
chr20	63025520	2292817	0.0364	0.2187
chr21	48129895	1269479	0.0264	0.186
chr22	51304566	919047	0.0179	0.1523
chrMT	16571	10240	0.6179	0.8741
chrX	155270560	4200541	0.0271	0.1896
chrY	59373566	153050	0.0026	0.0573

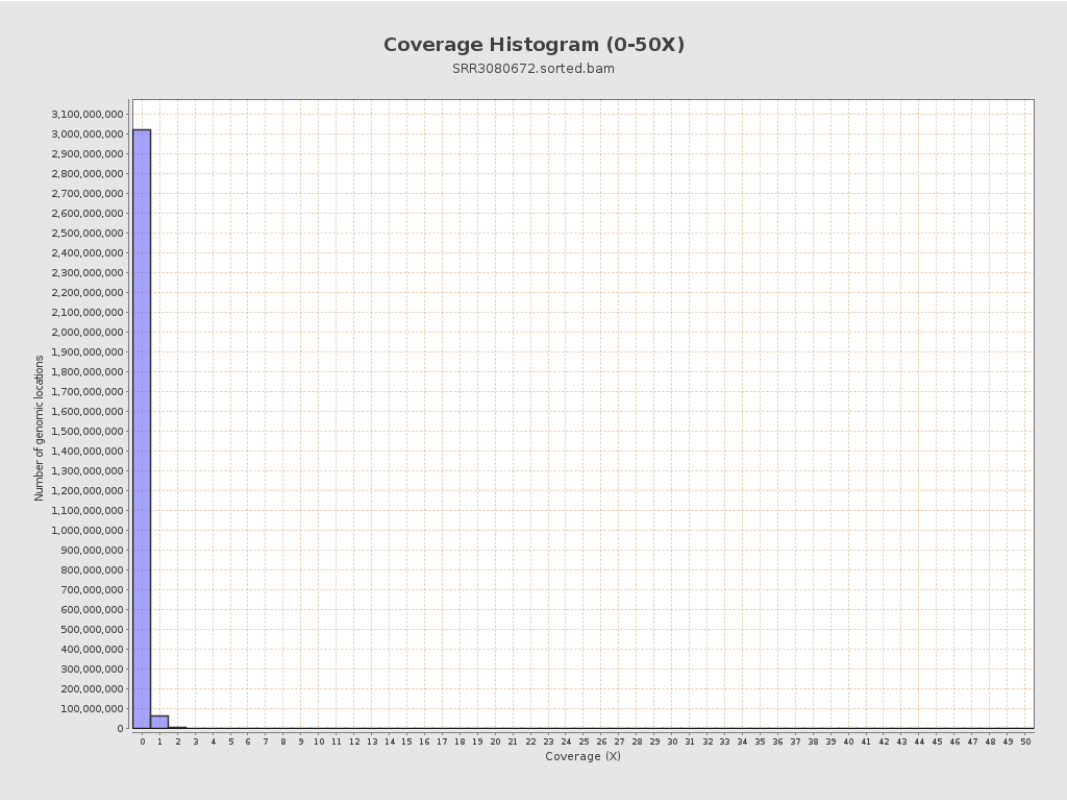
3. Results : Coverage across reference



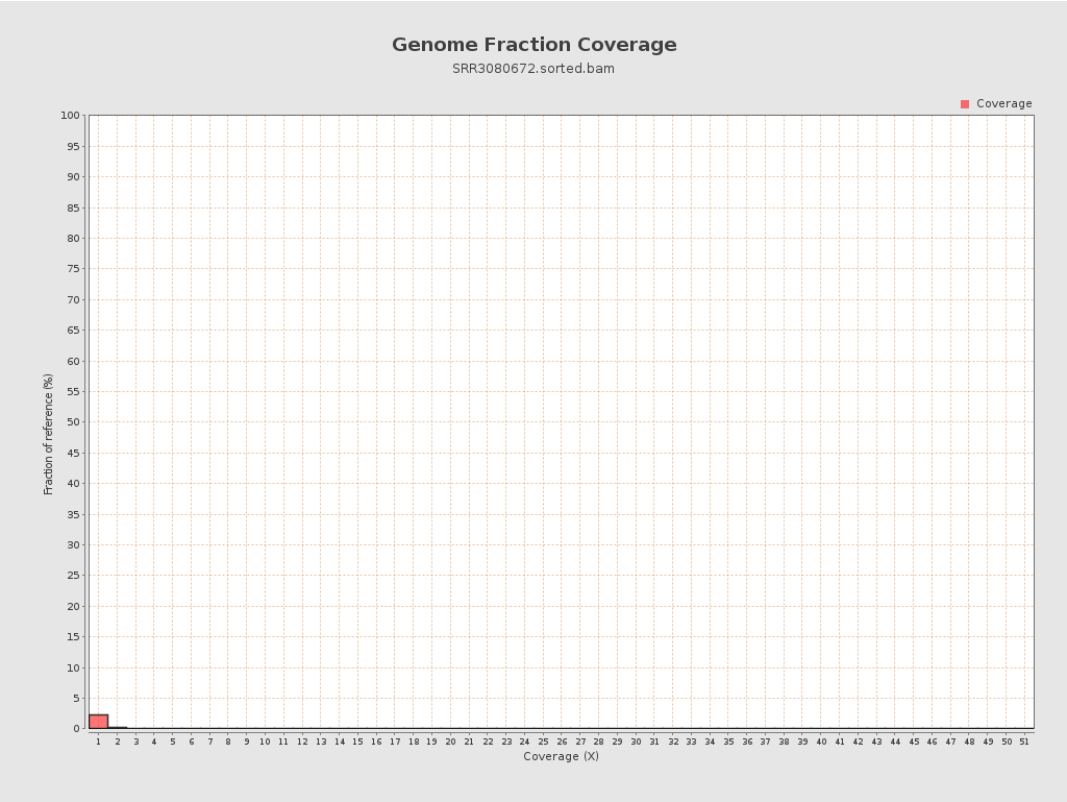
4. Results : Coverage Histogram



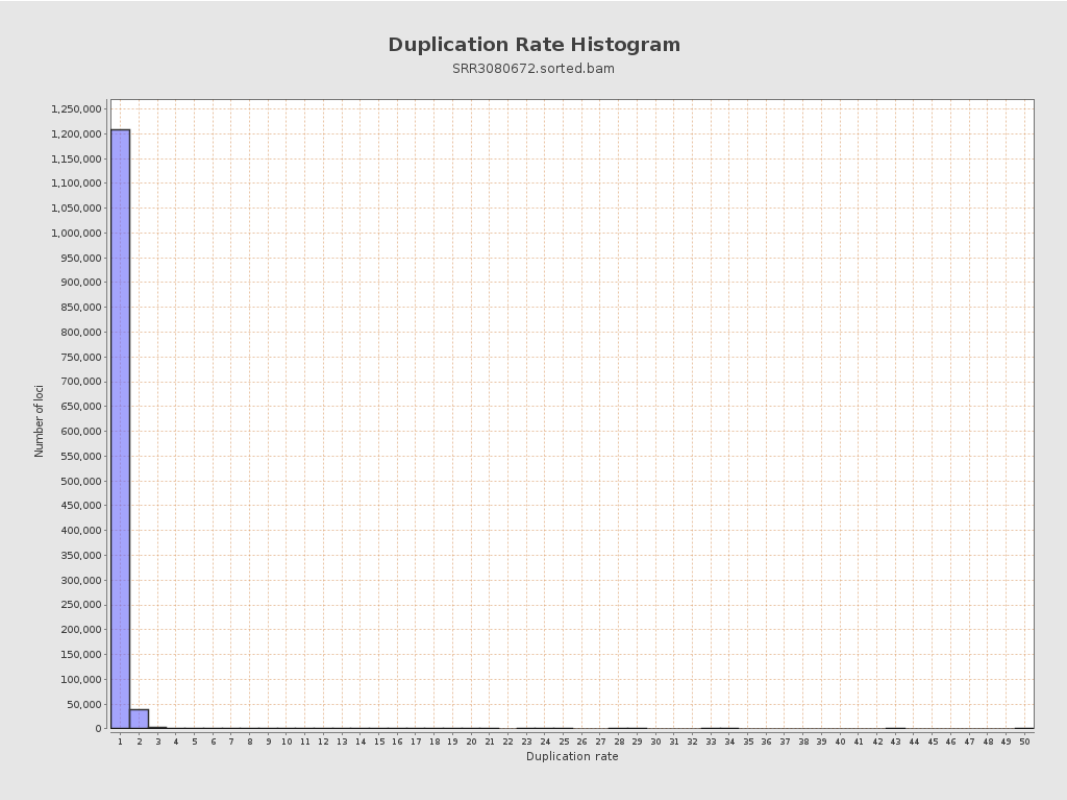
5. Results : Coverage Histogram (0-50X)



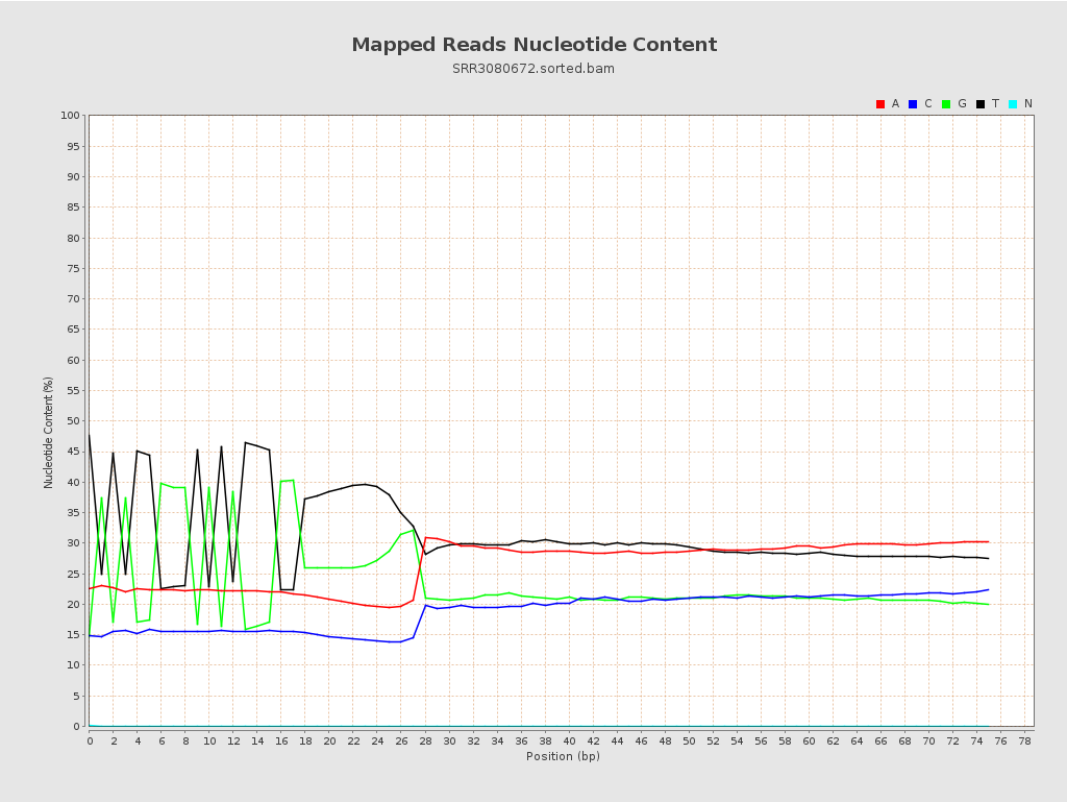
6. Results : Genome Fraction Coverage



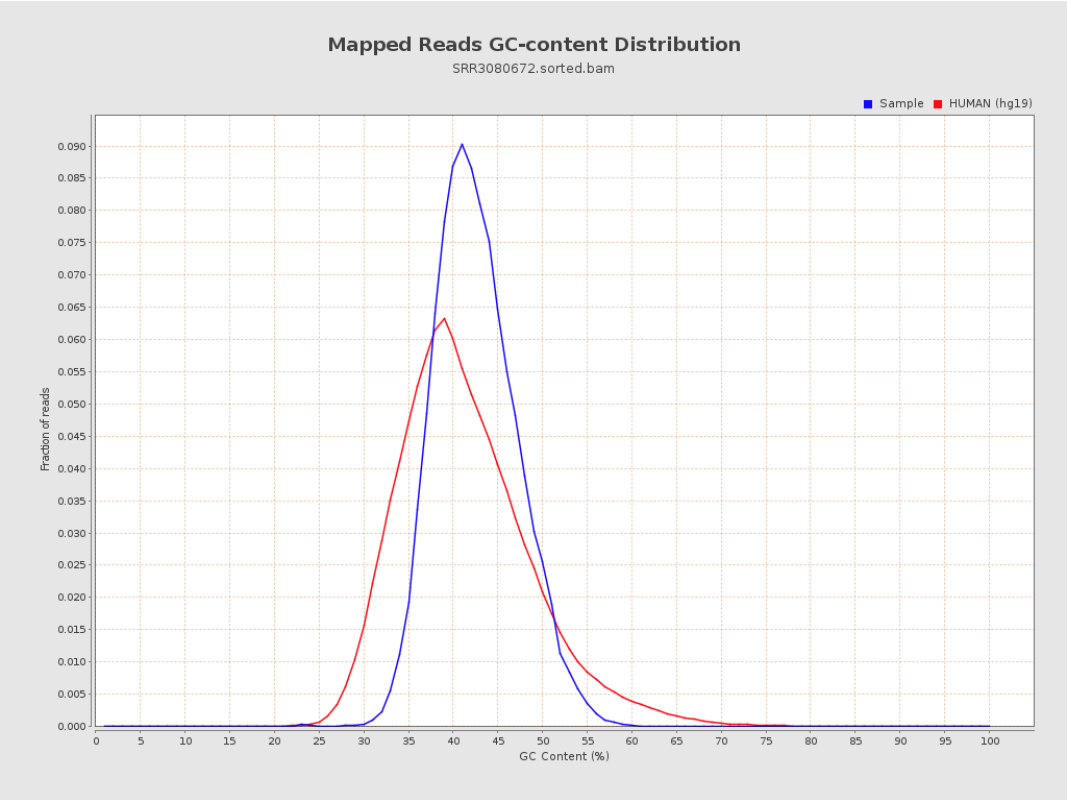
7. Results : Duplication Rate Histogram



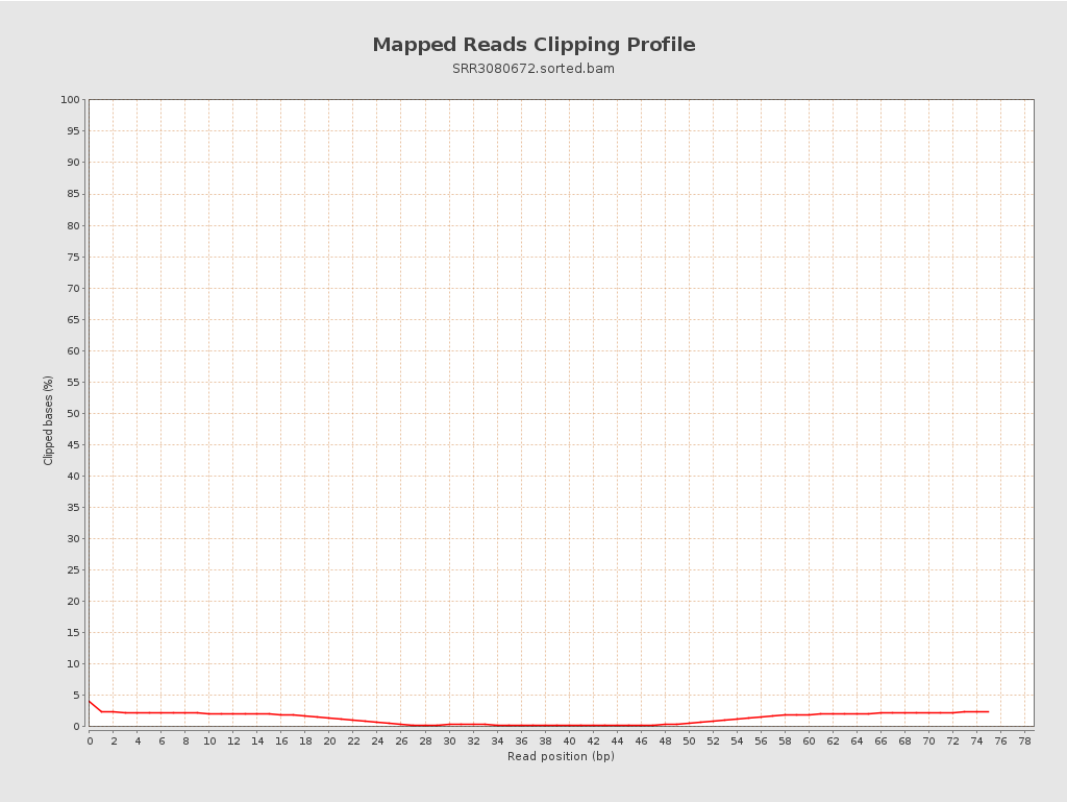
8. Results : Mapped Reads Nucleotide Content



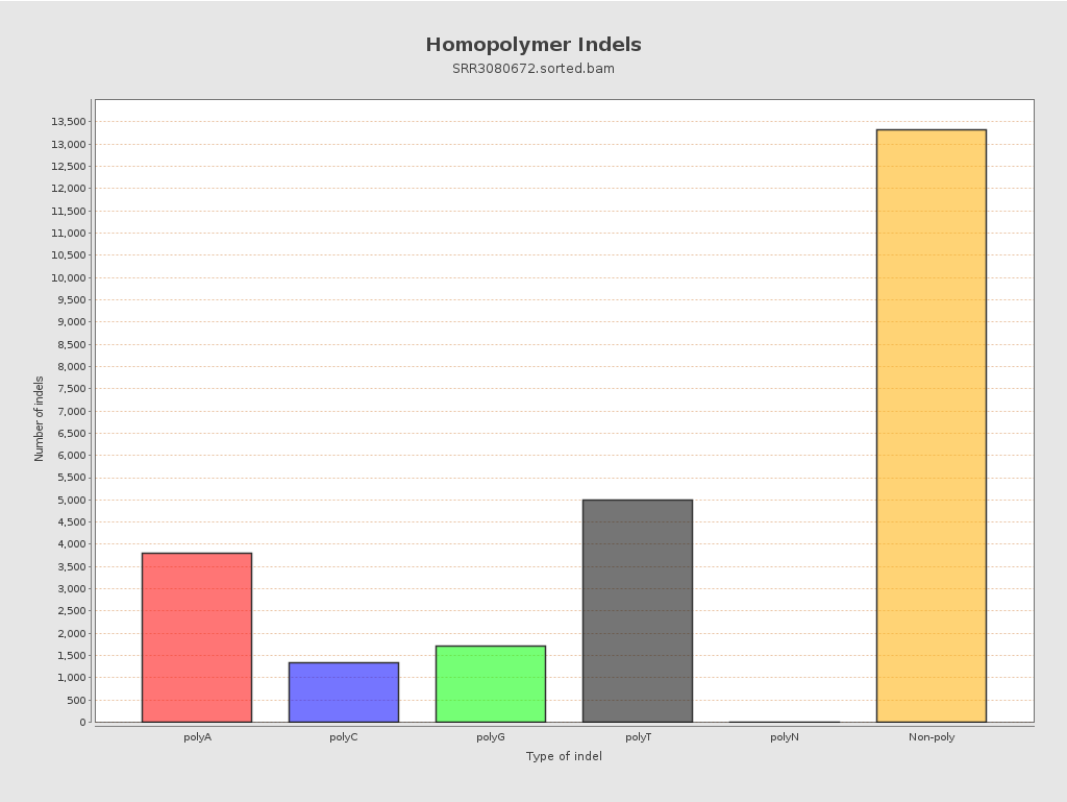
9. Results : Mapped Reads GC-content Distribution



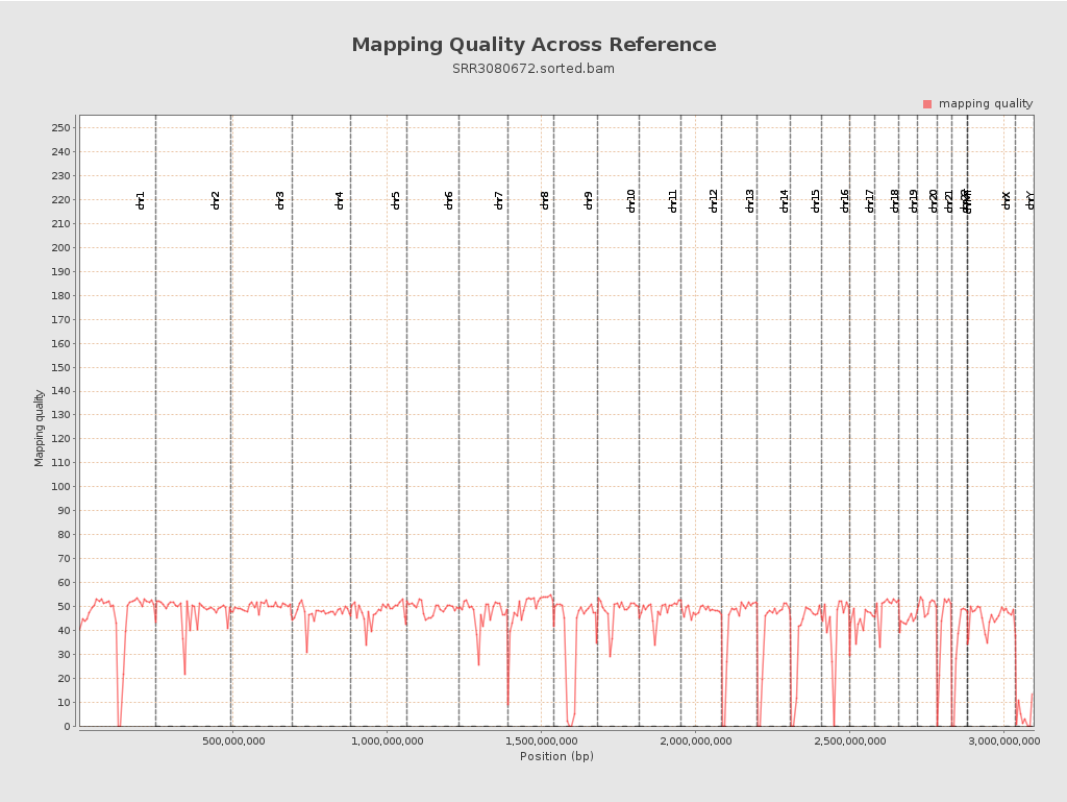
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram