

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 11:29:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080659.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_SRR3080659 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080659.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 11:29:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080659.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,437,720
Mapped reads	1,278,660 / 88.94%
Unmapped reads	159,060 / 11.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,505 / 1.01%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	49,716 / 3.46%
Duplication rate	3.33%
Clipped reads	620,900 / 43.19%

2.2. ACGT Content

Number/percentage of A's	22,603,843 / 26.87%
Number/percentage of C's	15,466,731 / 18.39%
Number/percentage of T's	26,735,221 / 31.79%
Number/percentage of G's	19,302,510 / 22.95%
Number/percentage of N's	3,392 / 0%
GC Percentage	41.34%

2.3. Coverage

Mean	0.0272

Standard Deviation	0.2369
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2.4. Mapping Quality

Mean Mapping Quality	45.14
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2.5. Mismatches and indels

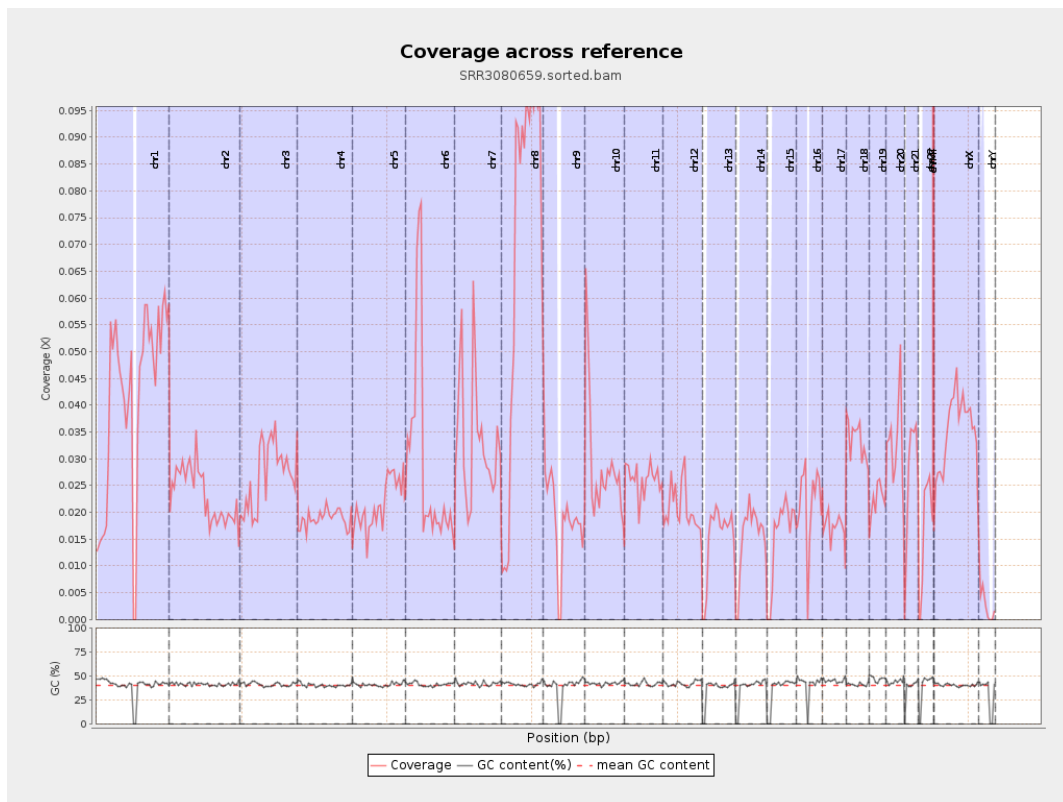
General error rate	0.71%
Mismatches	589,665
Insertions	6,206
Mapped reads with at least one insertion	0.48%
Deletions	19,312
Mapped reads with at least one deletion	1.5%
Homopolymer indels	47.66%

2.6. Chromosome stats

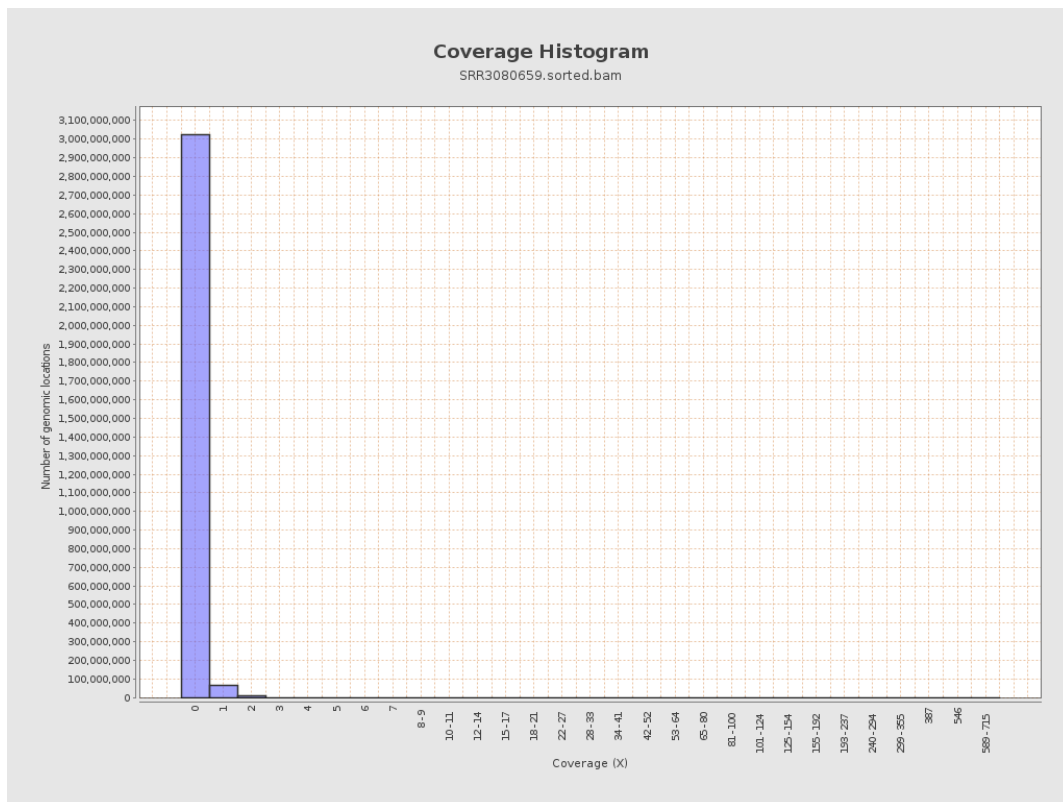
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10239356	0.0411	0.3054
chr2	243199373	5639515	0.0232	0.3436
chr3	198022430	5333720	0.0269	0.1823
chr4	191154276	3596849	0.0188	0.1564
chr5	180915260	3912598	0.0216	0.1631
chr6	171115067	4983450	0.0291	0.2345
chr7	159138663	5390450	0.0339	0.4426

chr8	146364022	10132191	0.0692	0.3231
chr9	141213431	2595325	0.0184	0.1747
chr10	135534747	3967634	0.0293	0.1996
chr11	135006516	3503797	0.026	0.1898
chr12	133851895	2756140	0.0206	0.1604
chr13	115169878	1739300	0.0151	0.1374
chr14	107349540	1642026	0.0153	0.14
chr15	102531392	1596320	0.0156	0.1441
chr16	90354753	1967366	0.0218	0.1676
chr17	81195210	1377171	0.017	0.1467
chr18	78077248	2608655	0.0334	0.2565
chr19	59128983	1332336	0.0225	0.2165
chr20	63025520	2064536	0.0328	0.2029
chr21	48129895	1291510	0.0268	0.1839
chr22	51304566	840217	0.0164	0.1405
chrMT	16571	33290	2.0089	1.9602
chrX	155270560	5432411	0.035	0.2151
chrY	59373566	166753	0.0028	0.0611

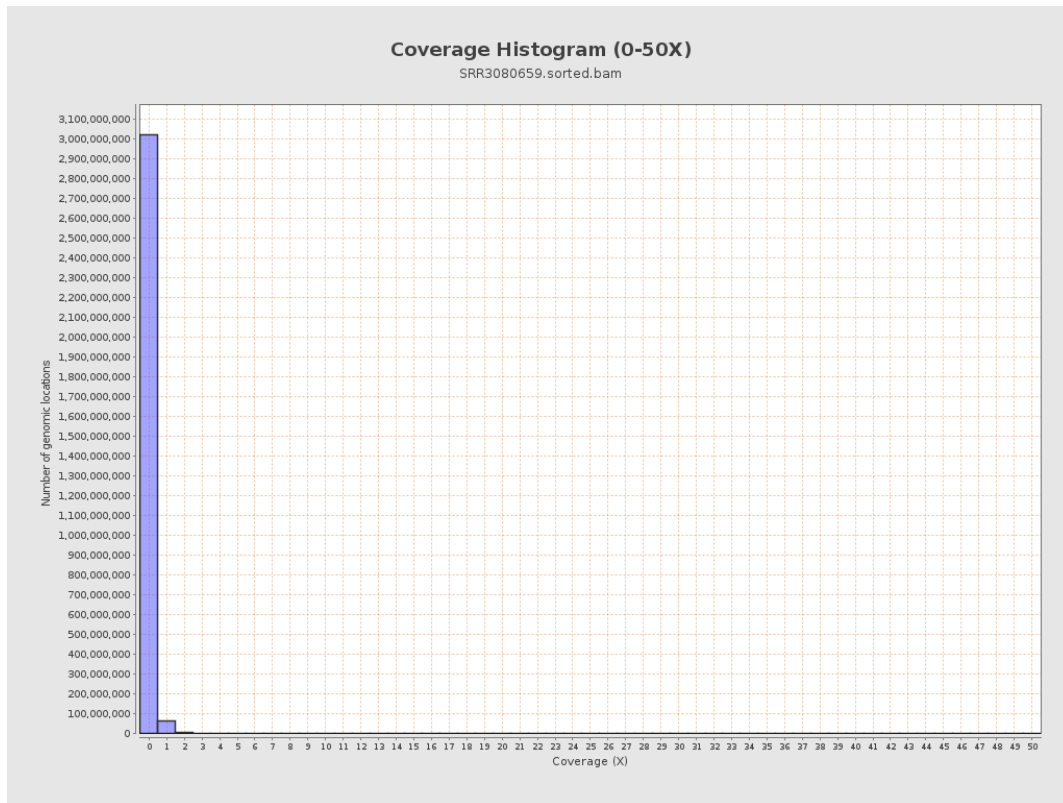
3. Results : Coverage across reference



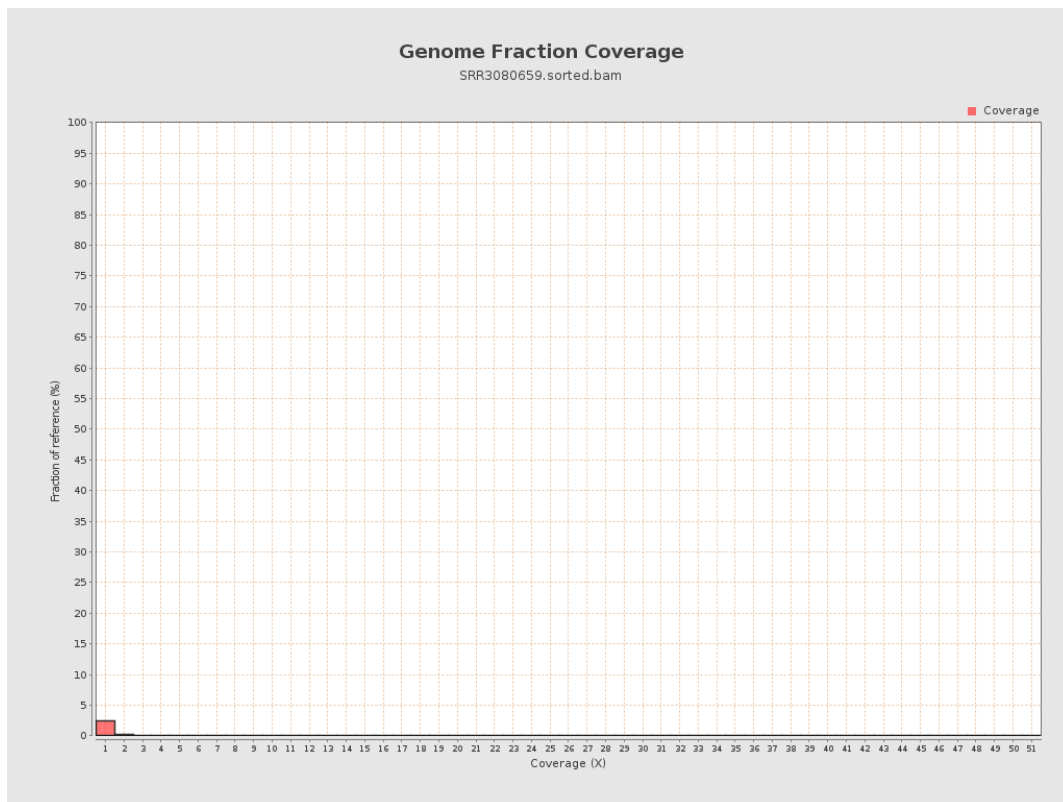
4. Results : Coverage Histogram



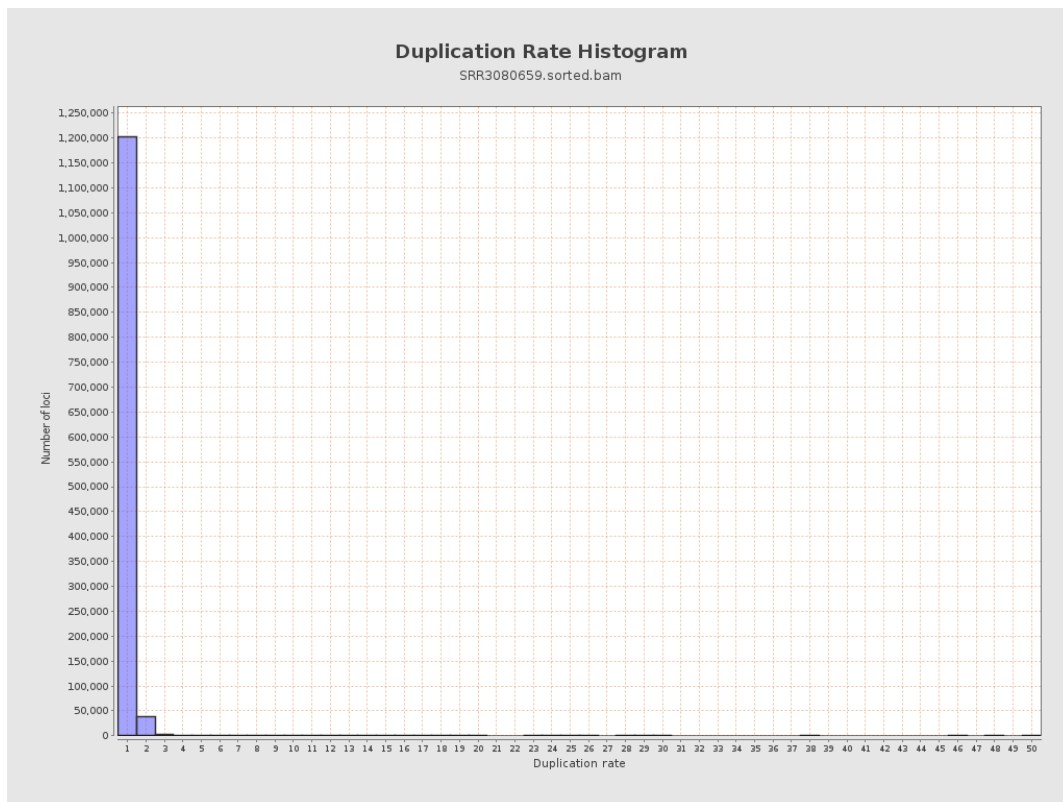
5. Results : Coverage Histogram (0-50X)



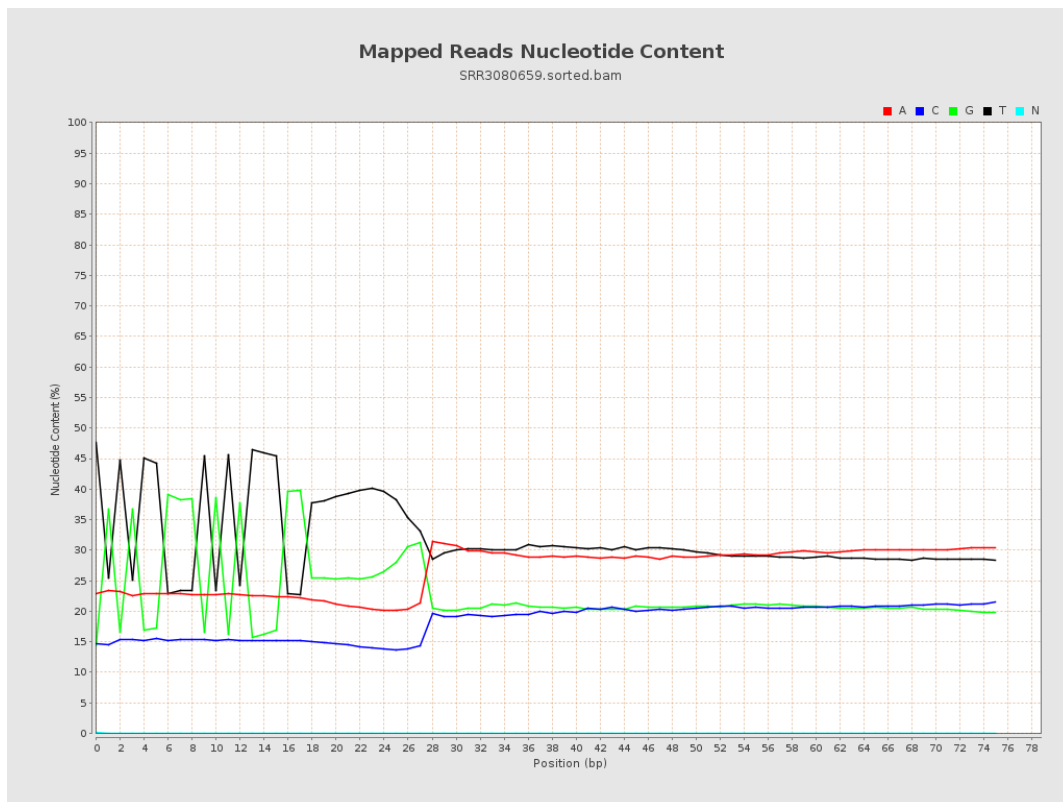
6. Results : Genome Fraction Coverage



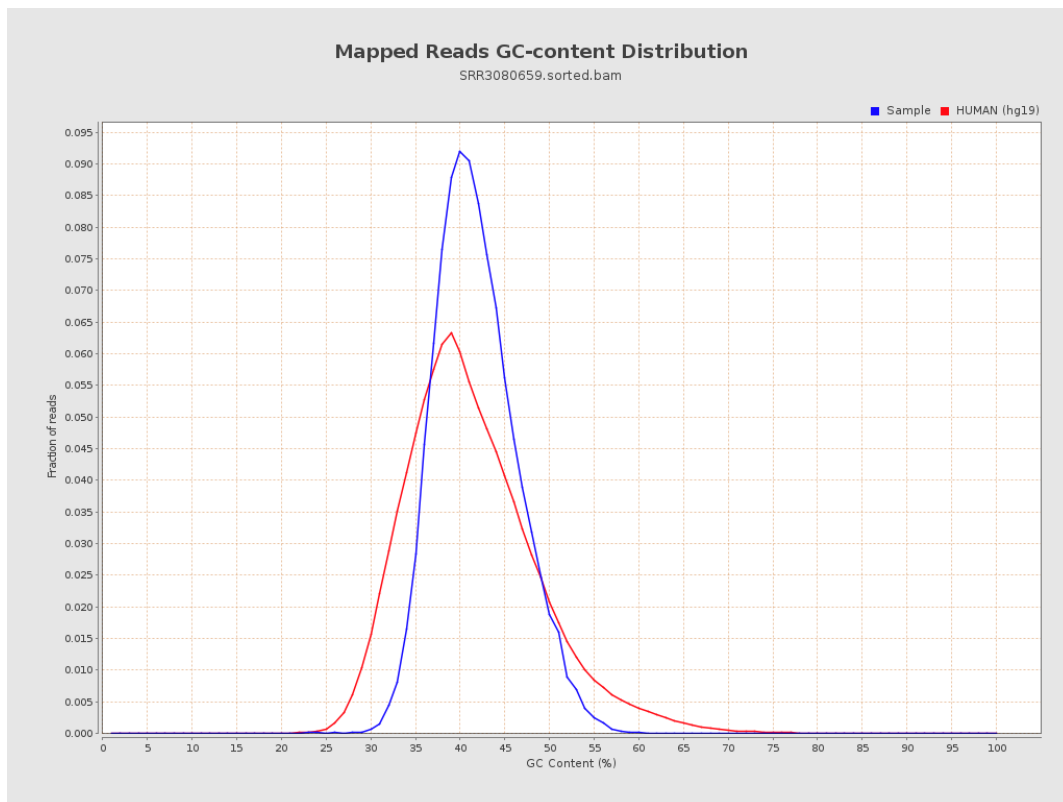
7. Results : Duplication Rate Histogram



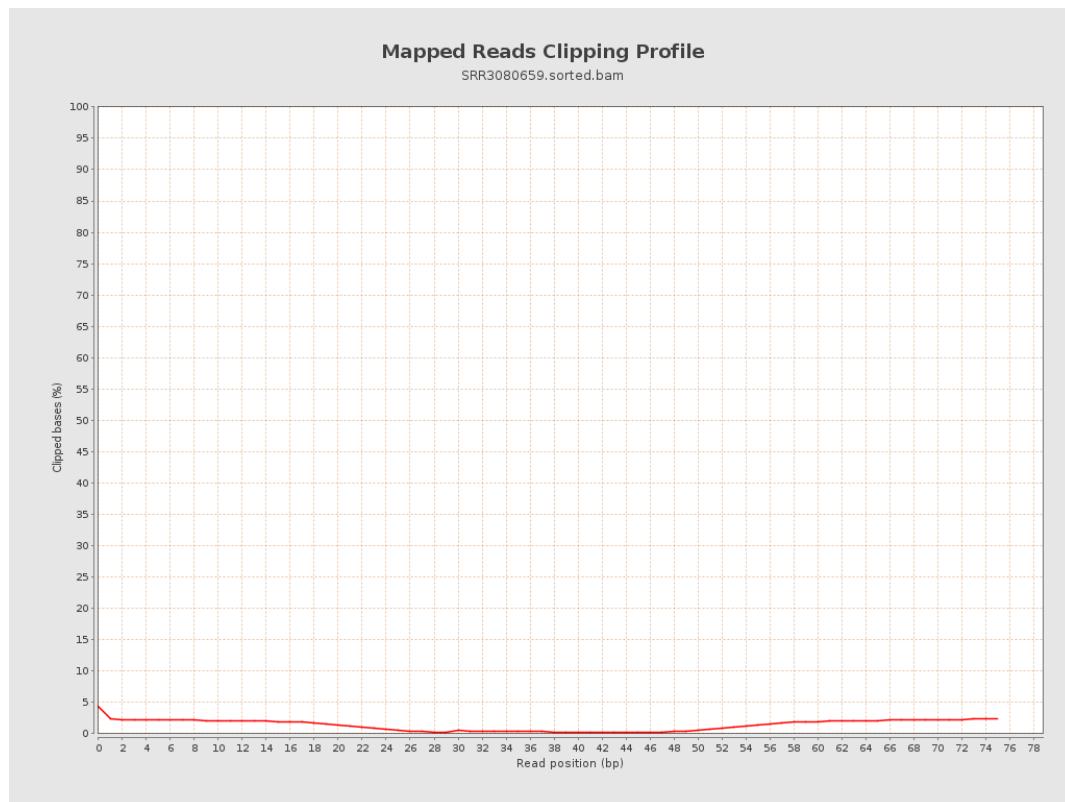
8. Results : Mapped Reads Nucleotide Content



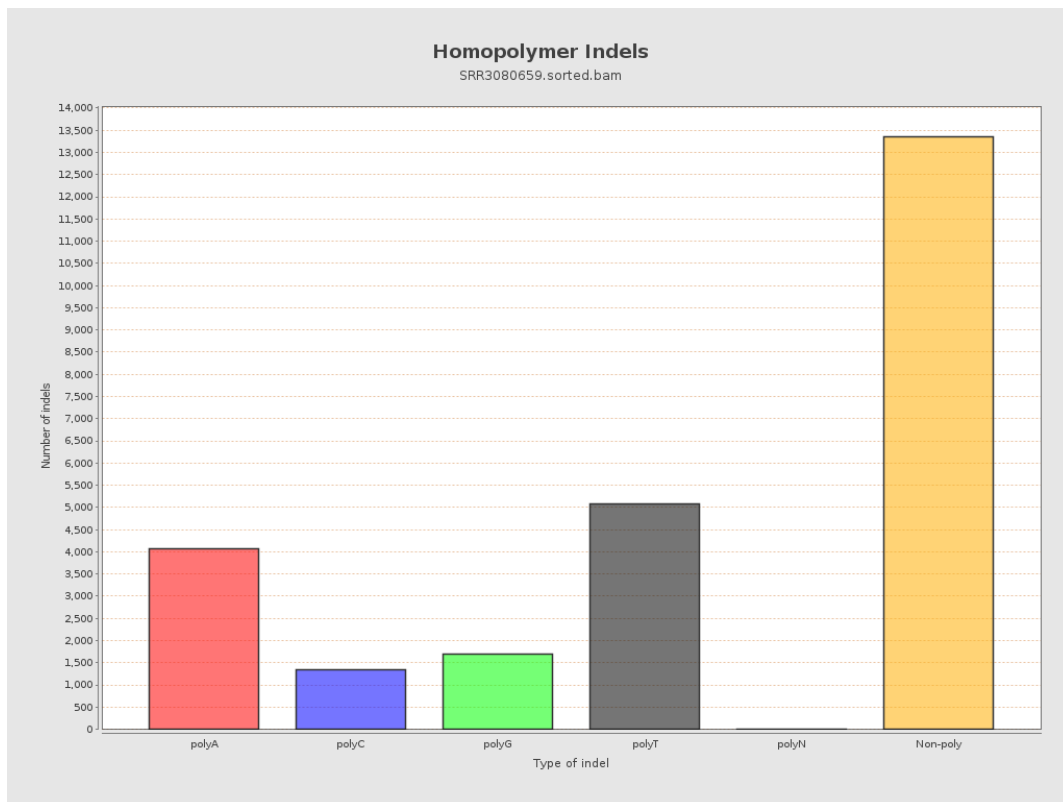
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

