

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 11:50:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251069.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_SRR10251069 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251069.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 11:50:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251069.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,138,868
Mapped reads	3,920,198 / 94.72%
Unmapped reads	218,670 / 5.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,109 / 0.68%
Read min/max/mean length	30 / 80 / 80.24
Duplicated reads (estimated)	819,589 / 19.8%
Duplication rate	18.47%
Clipped reads	506,154 / 12.23%

2.2. ACGT Content

Number/percentage of A's	87,956,778 / 28.91%
Number/percentage of C's	60,956,673 / 20.03%
Number/percentage of T's	89,550,557 / 29.43%
Number/percentage of G's	65,821,035 / 21.63%
Number/percentage of N's	2,763 / 0%
GC Percentage	41.66%

2.3. Coverage

Mean	0.0984

Standard Deviation	1.0041
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2.4. Mapping Quality

Mean Mapping Quality	48.17
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2.5. Mismatches and indels

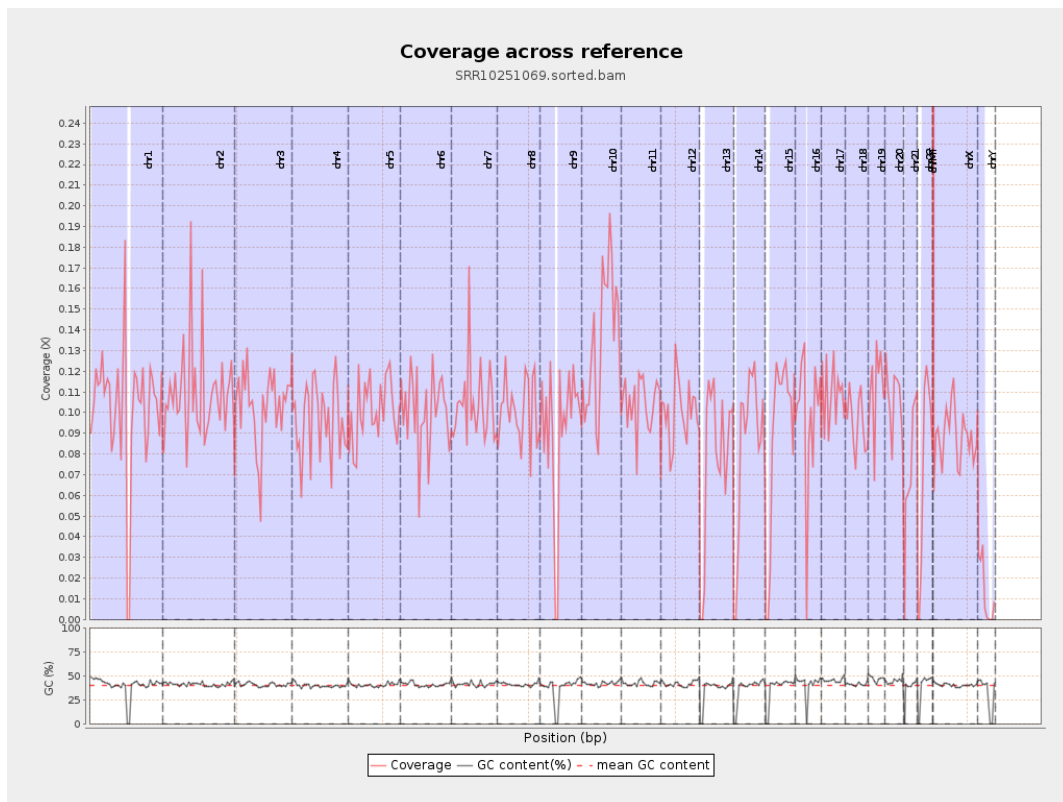
General error rate	0.59%
Mismatches	1,731,889
Insertions	36,099
Mapped reads with at least one insertion	0.9%
Deletions	105,545
Mapped reads with at least one deletion	2.65%
Homopolymer indels	45.19%

2.6. Chromosome stats

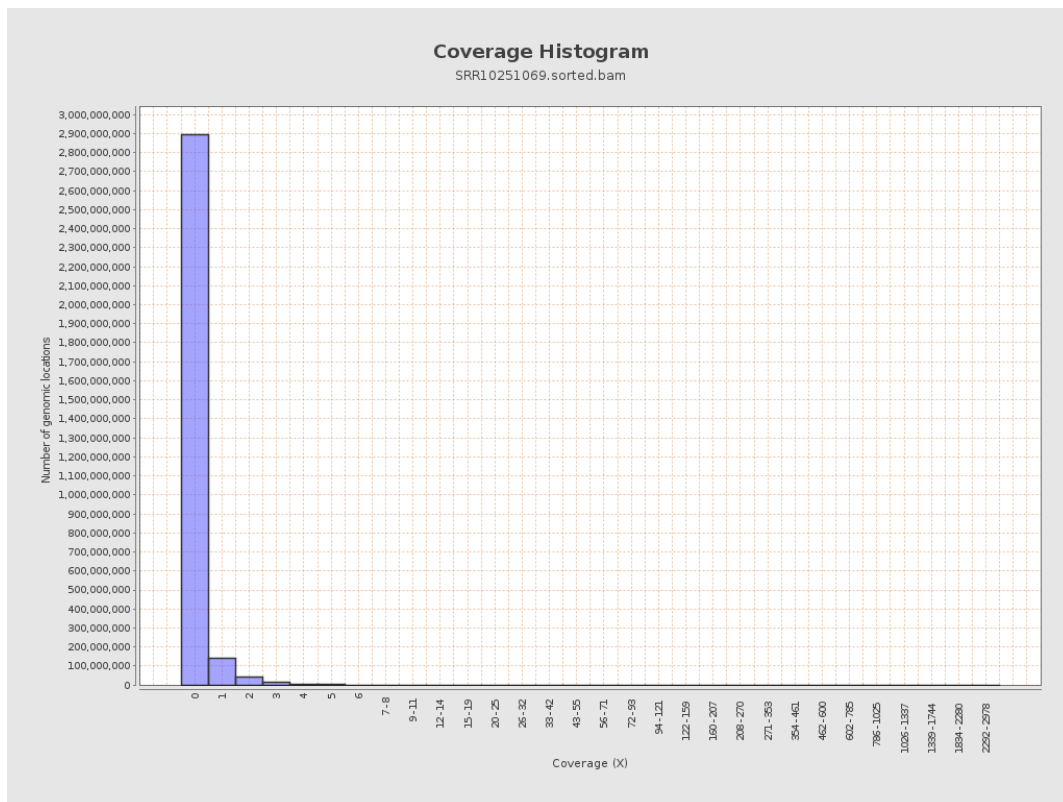
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	25526553	0.1024	2.109
chr2	243199373	26703617	0.1098	1.2414
chr3	198022430	20403523	0.103	0.4531
chr4	191154276	18419021	0.0964	0.5047
chr5	180915260	18334117	0.1013	0.4692
chr6	171115067	17193955	0.1005	0.5809
chr7	159138663	16505154	0.1037	1.5294

chr8	146364022	14723500	0.1006	0.6295
chr9	141213431	12953934	0.0917	1.0443
chr10	135534747	18282228	0.1349	1.0235
chr11	135006516	14088038	0.1044	0.6366
chr12	133851895	13615322	0.1017	0.468
chr13	115169878	8941860	0.0776	0.3876
chr14	107349540	9212451	0.0858	0.6394
chr15	102531392	8938963	0.0872	0.4131
chr16	90354753	8808183	0.0975	0.7949
chr17	81195210	8895313	0.1096	0.5675
chr18	78077248	7487066	0.0959	1.1781
chr19	59128983	6598158	0.1116	2.047
chr20	63025520	6658372	0.1056	0.4951
chr21	48129895	3576106	0.0743	0.4227
chr22	51304566	3862518	0.0753	0.4142
chrMT	16571	208463	12.58	8.3288
chrX	155270560	13766870	0.0887	0.4948
chrY	59373566	773914	0.013	0.8874

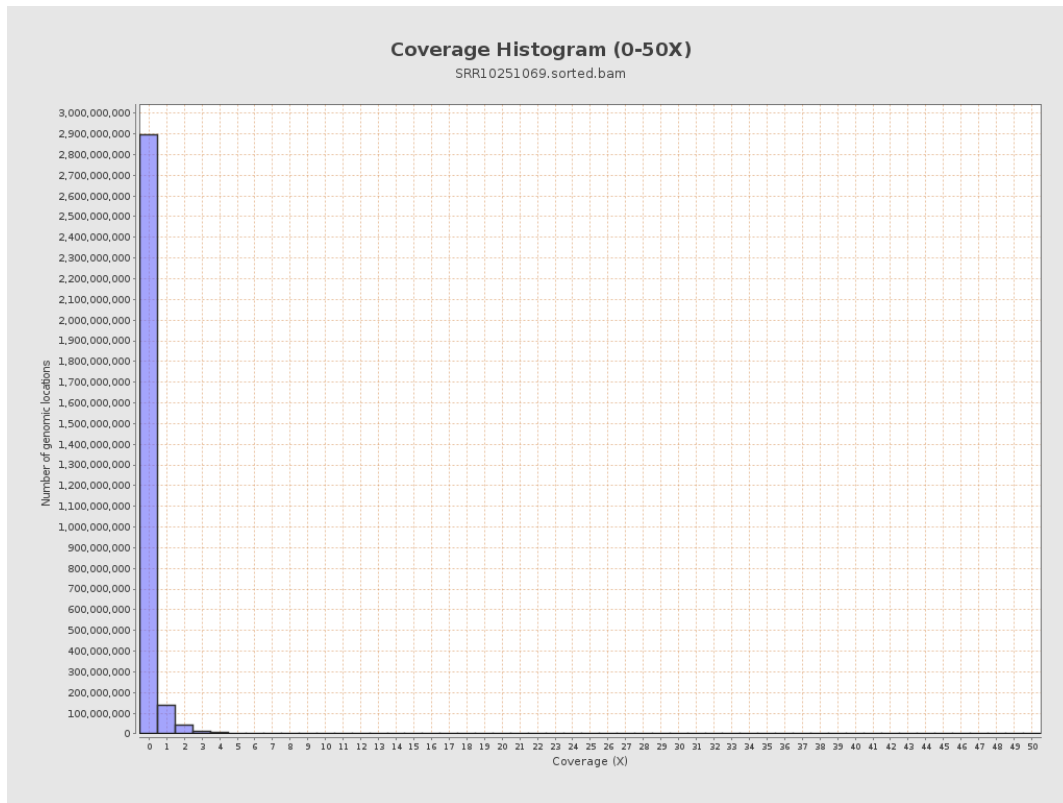
3. Results : Coverage across reference



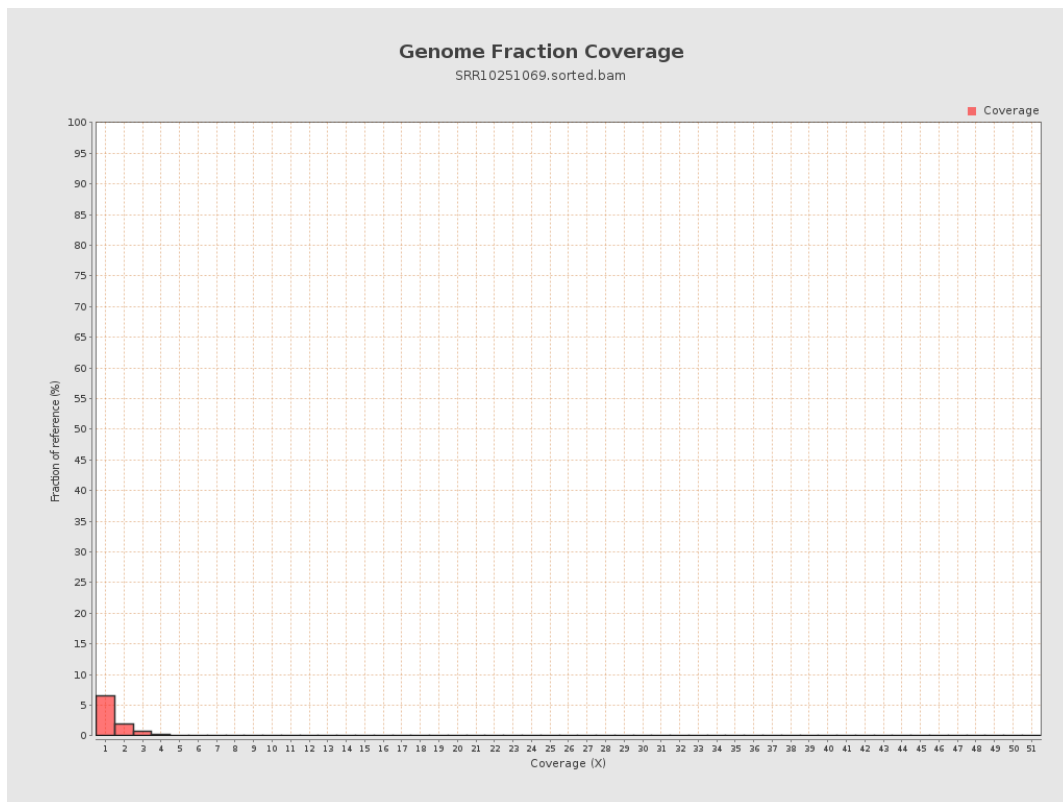
4. Results : Coverage Histogram



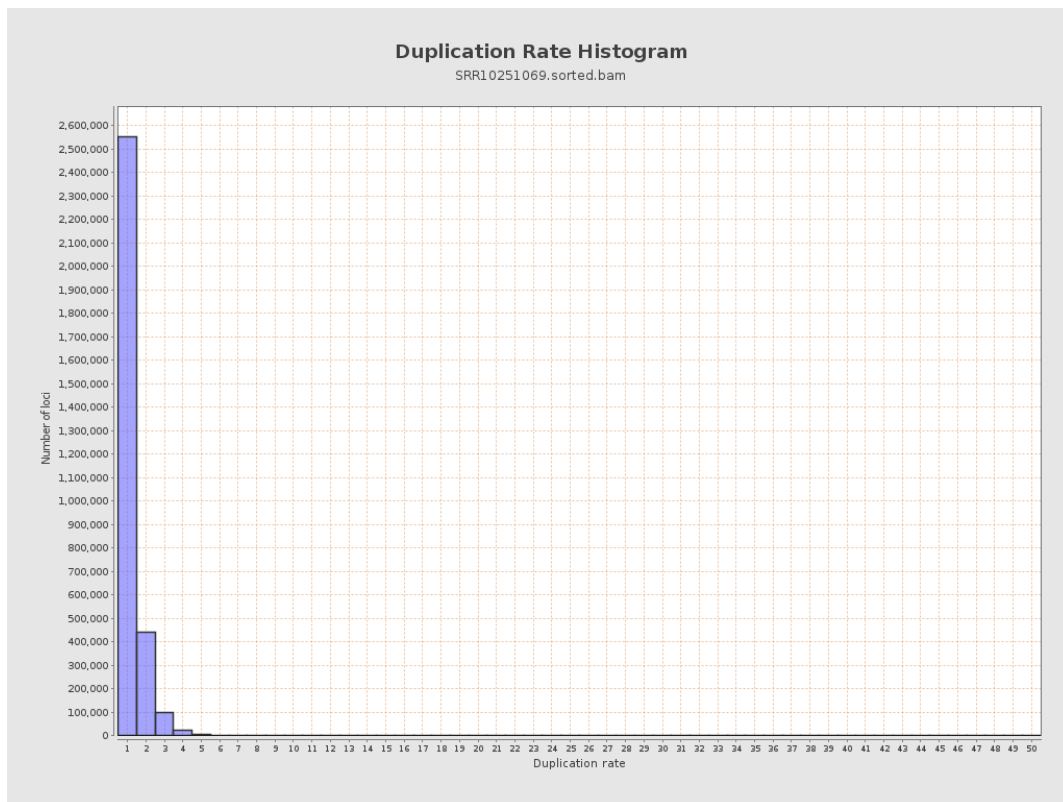
5. Results : Coverage Histogram (0-50X)



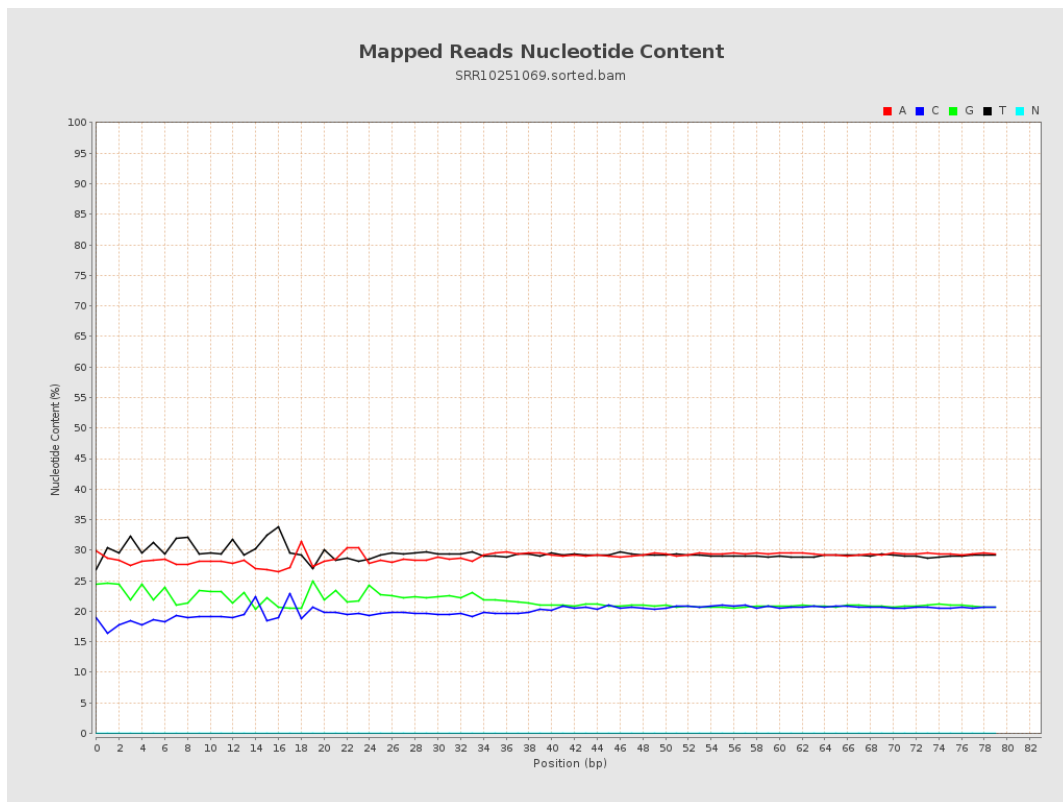
6. Results : Genome Fraction Coverage



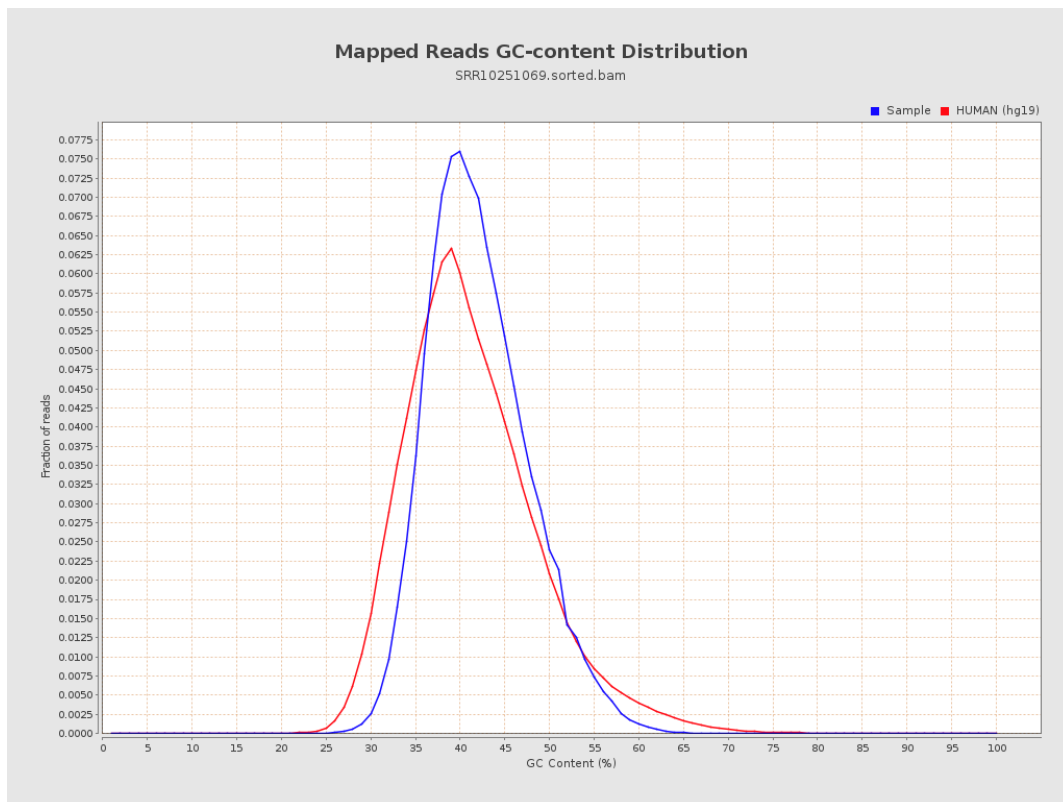
7. Results : Duplication Rate Histogram



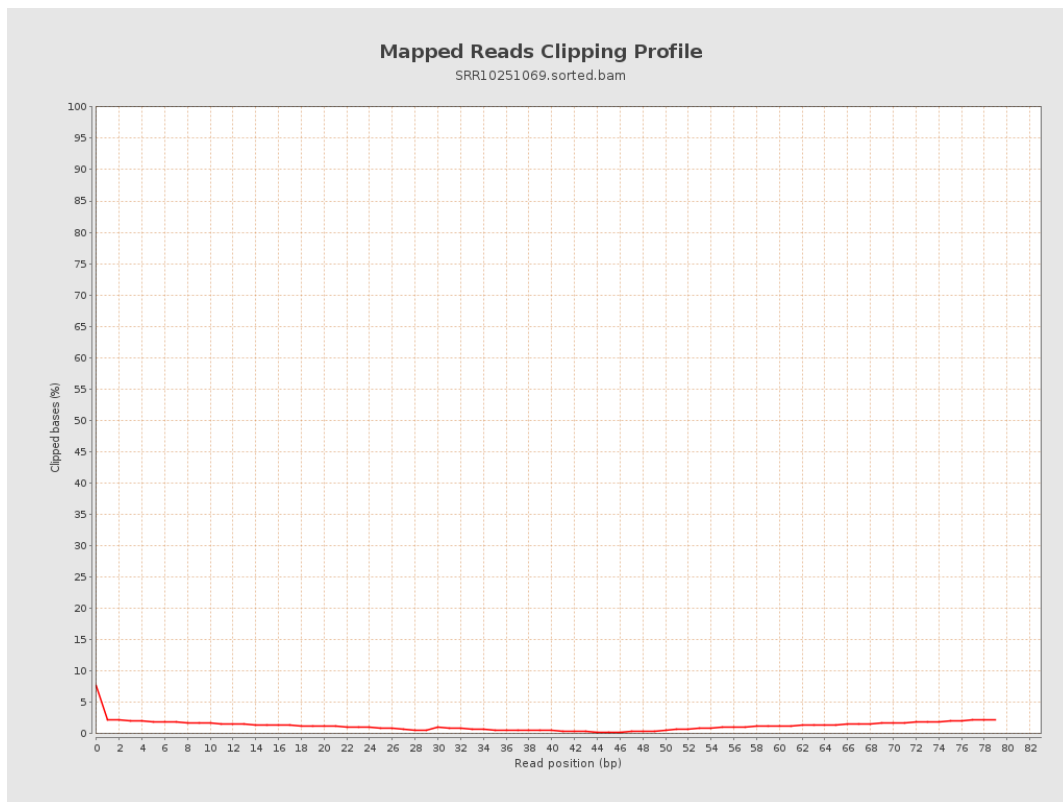
8. Results : Mapped Reads Nucleotide Content



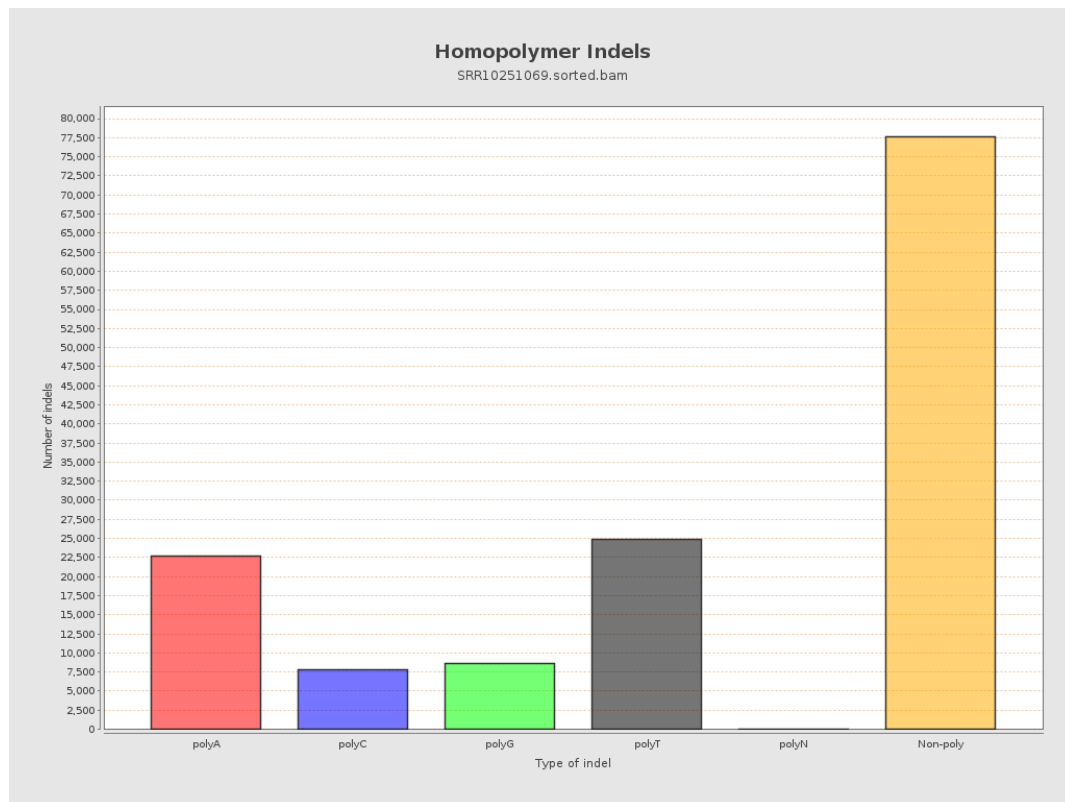
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

