

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 13:51:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251082.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_SRR10251082 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251082.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 13:51:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251082.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,091,860
Mapped reads	5,398,047 / 88.61%
Unmapped reads	693,813 / 11.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	54,878 / 0.9%
Read min/max/mean length	25 / 306 / 137.97
Duplicated reads (estimated)	3,903,568 / 64.08%
Duplication rate	38.58%
Clipped reads	5,449,644 / 89.46%

2.2. ACGT Content

Number/percentage of A's	155,005,914 / 27.88%
Number/percentage of C's	113,864,877 / 20.48%
Number/percentage of T's	165,124,757 / 29.7%
Number/percentage of G's	122,072,419 / 21.95%
Number/percentage of N's	0 / 0%
GC Percentage	42.43%

2.3. Coverage

Mean	0.1801

Standard Deviation	2.173
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2.4. Mapping Quality

Mean Mapping Quality	50.36
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2.5. Mismatches and indels

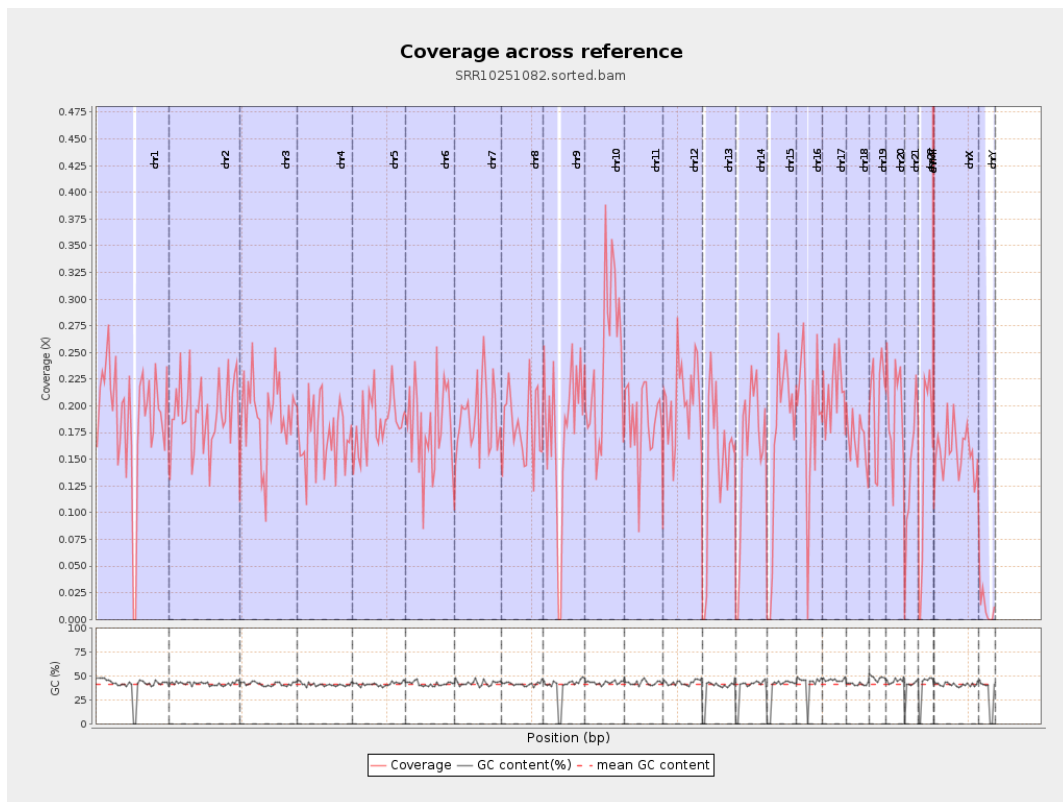
General error rate	1.04%
Mismatches	4,181,654
Insertions	1,448,996
Mapped reads with at least one insertion	19.07%
Deletions	1,126,899
Mapped reads with at least one deletion	17.05%
Homopolymer indels	40.55%

2.6. Chromosome stats

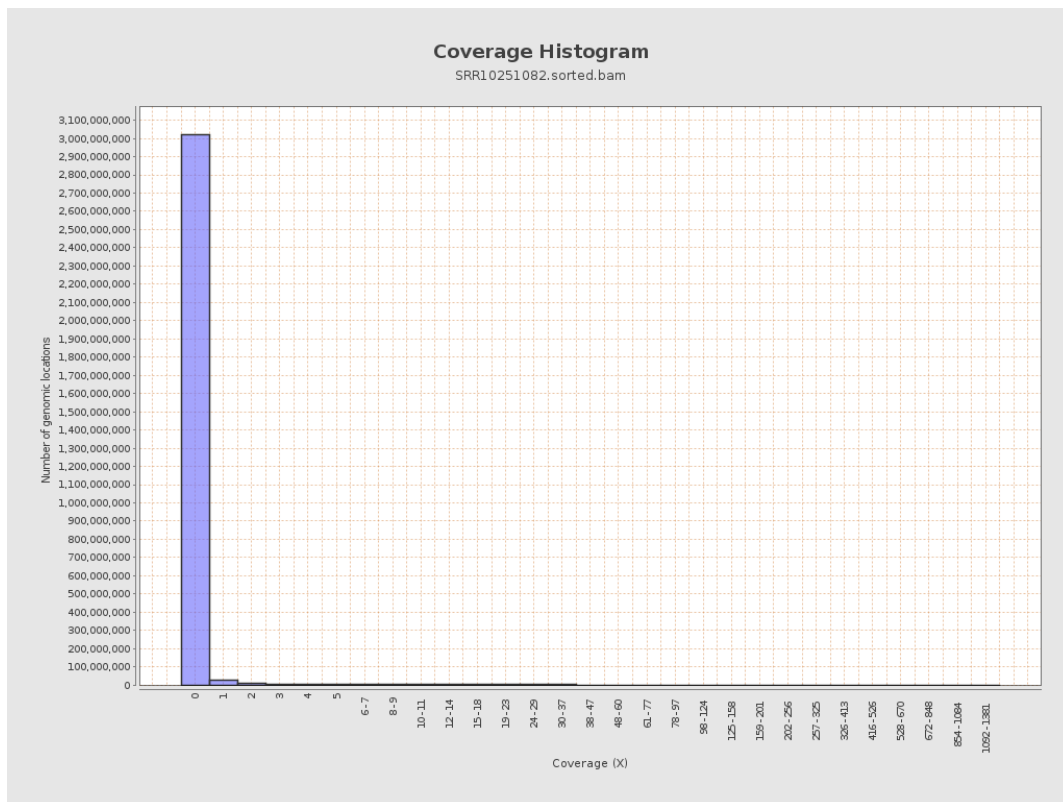
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	46901834	0.1882	2.2005
chr2	243199373	46972434	0.1931	2.2967
chr3	198022430	37761003	0.1907	2.1963
chr4	191154276	32723917	0.1712	2.0962
chr5	180915260	33332062	0.1842	2.2454
chr6	171115067	30643175	0.1791	2.1613
chr7	159138663	30325029	0.1906	2.2764

chr8	146364022	26424223	0.1805	2.2042
chr9	141213431	24474668	0.1733	2.1903
chr10	135534747	32688678	0.2412	2.481
chr11	135006516	25153779	0.1863	2.1254
chr12	133851895	27623534	0.2064	2.29
chr13	115169878	16422951	0.1426	1.8742
chr14	107349540	16889717	0.1573	1.9654
chr15	102531392	17117753	0.167	2.0327
chr16	90354753	17389328	0.1925	2.1426
chr17	81195210	17391376	0.2142	2.271
chr18	78077248	13109104	0.1679	2.082
chr19	59128983	12052814	0.2038	2.3564
chr20	63025520	12218891	0.1939	2.1971
chr21	48129895	6755749	0.1404	1.8701
chr22	51304566	7458726	0.1454	1.8733
chrMT	16571	653641	39.4449	116.9059
chrX	155270560	24188378	0.1558	1.9591
chrY	59373566	712493	0.012	0.4996

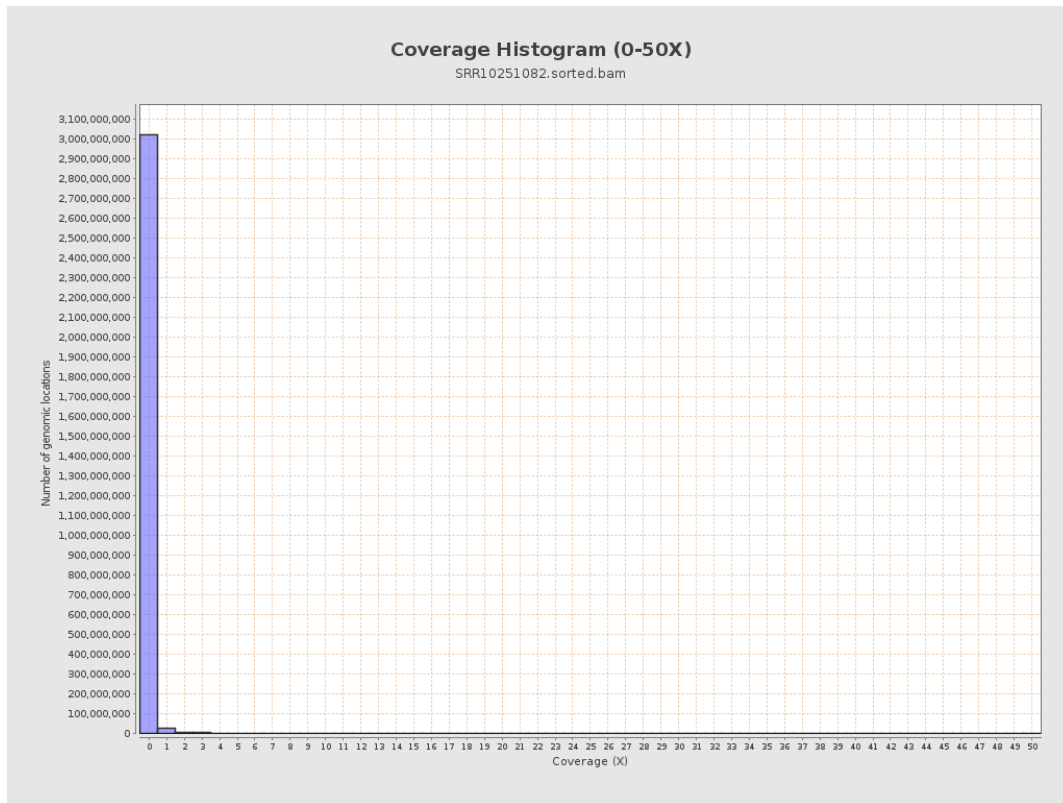
3. Results : Coverage across reference



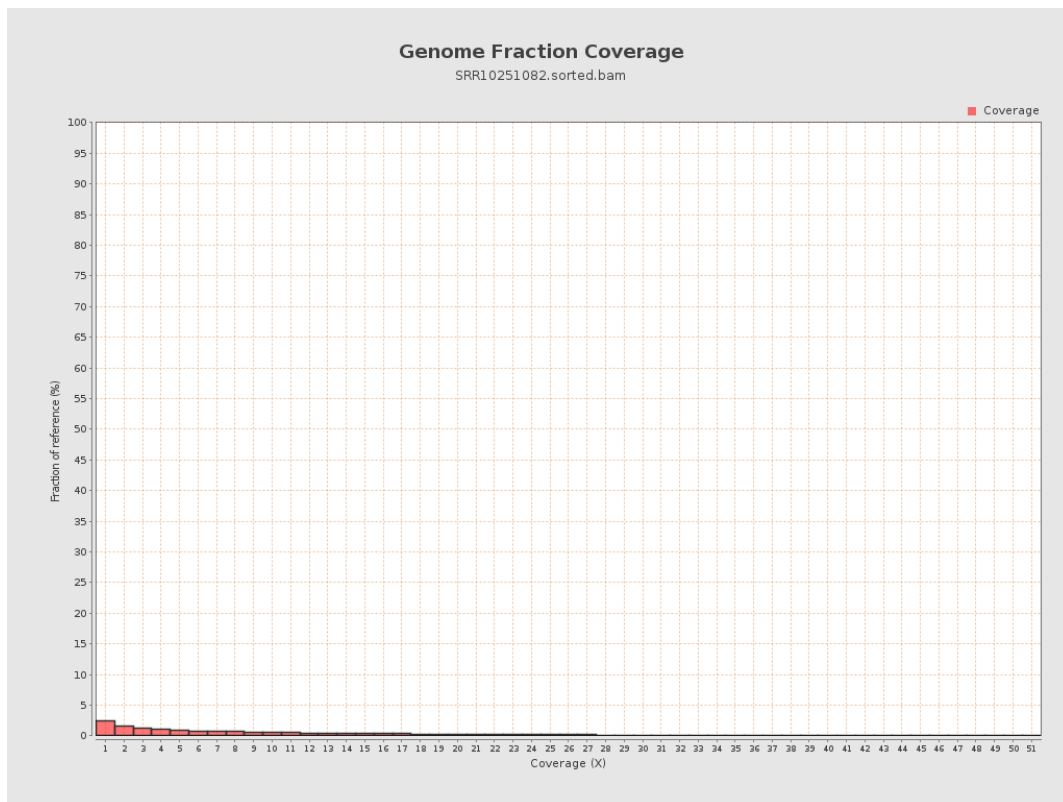
4. Results : Coverage Histogram



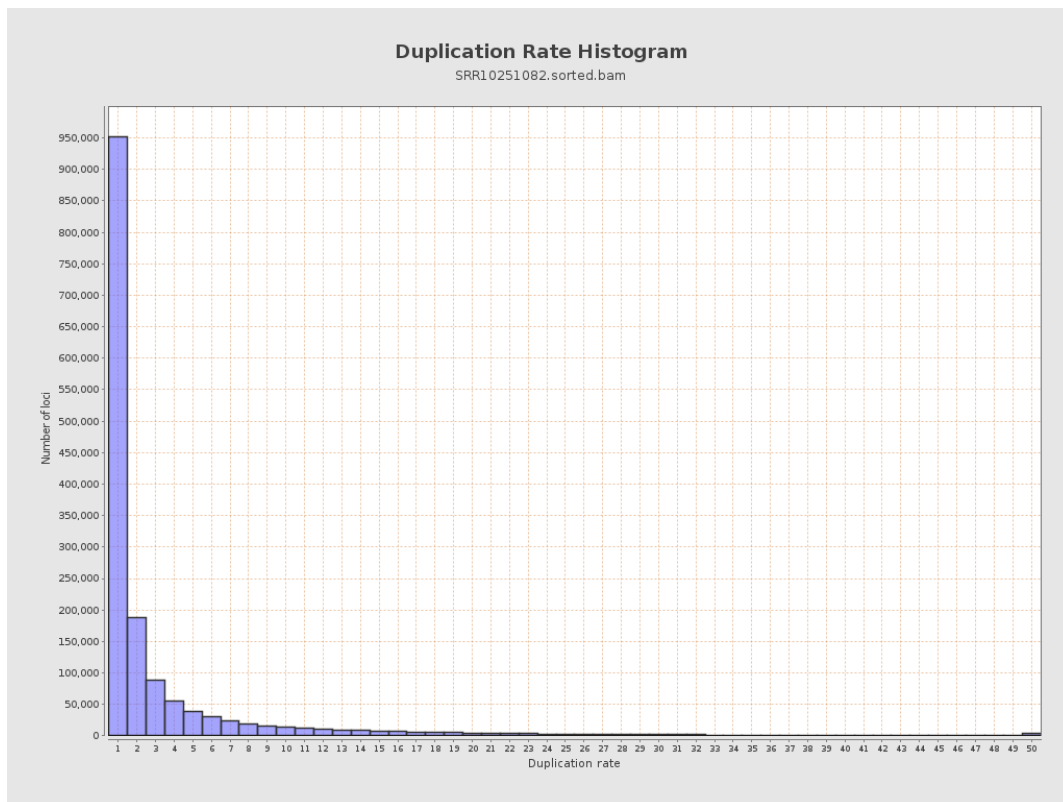
5. Results : Coverage Histogram (0-50X)



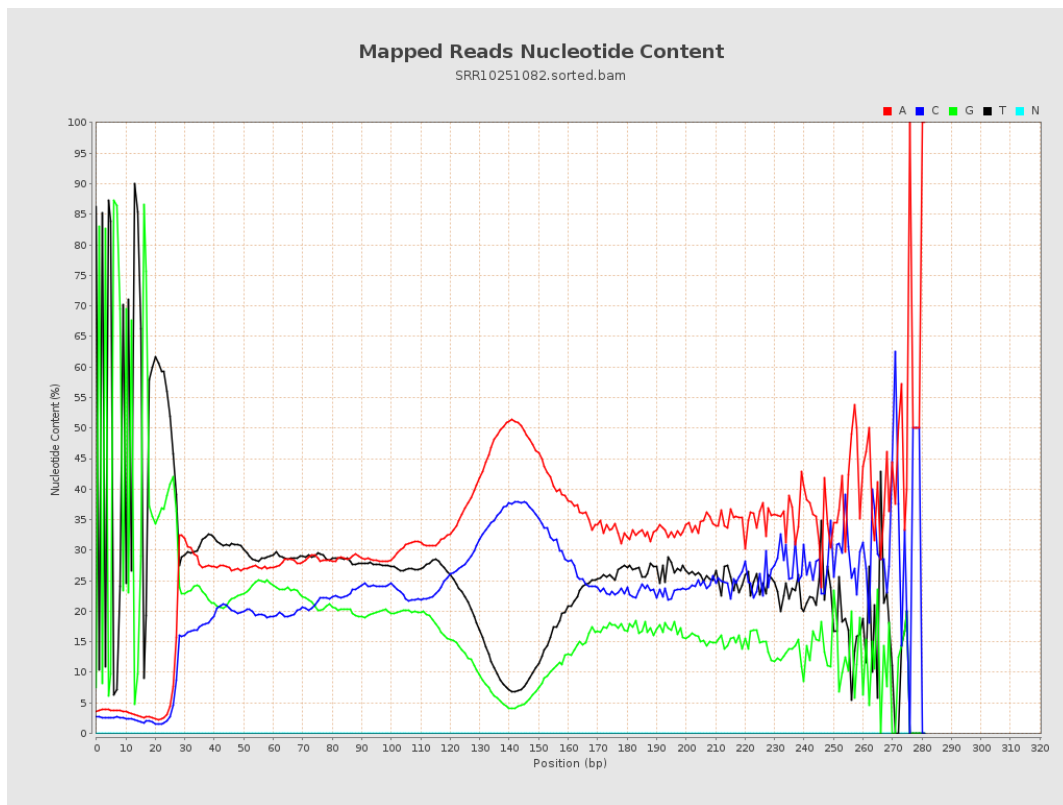
6. Results : Genome Fraction Coverage



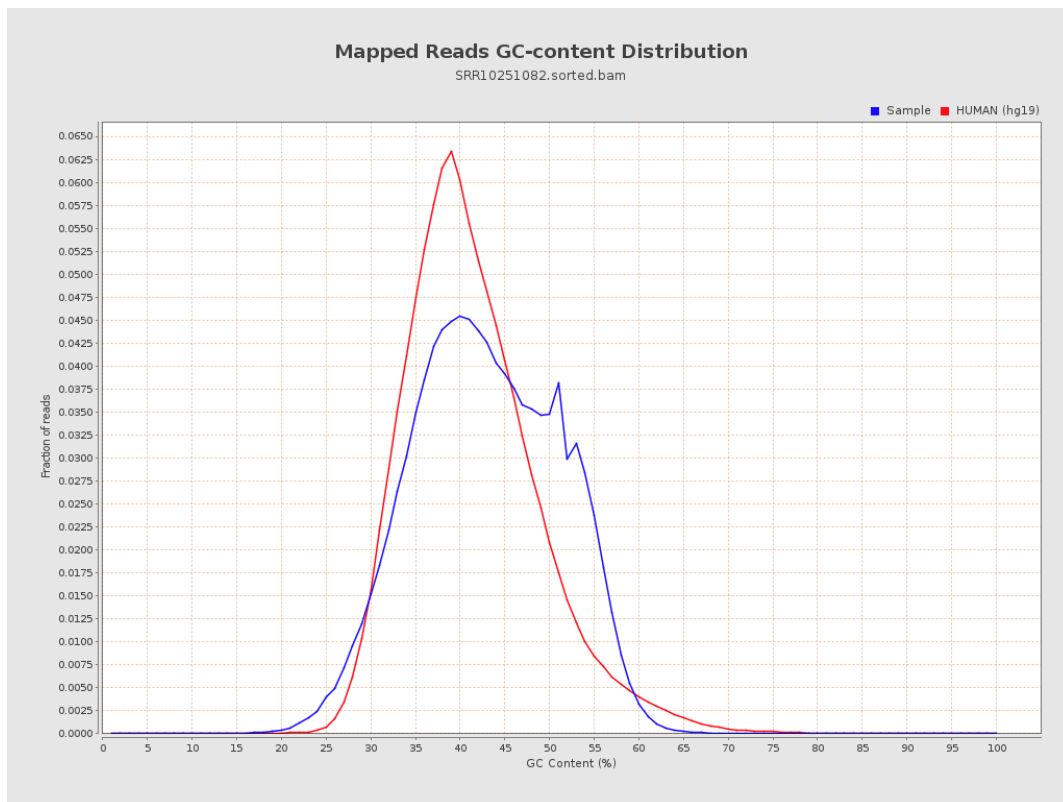
7. Results : Duplication Rate Histogram



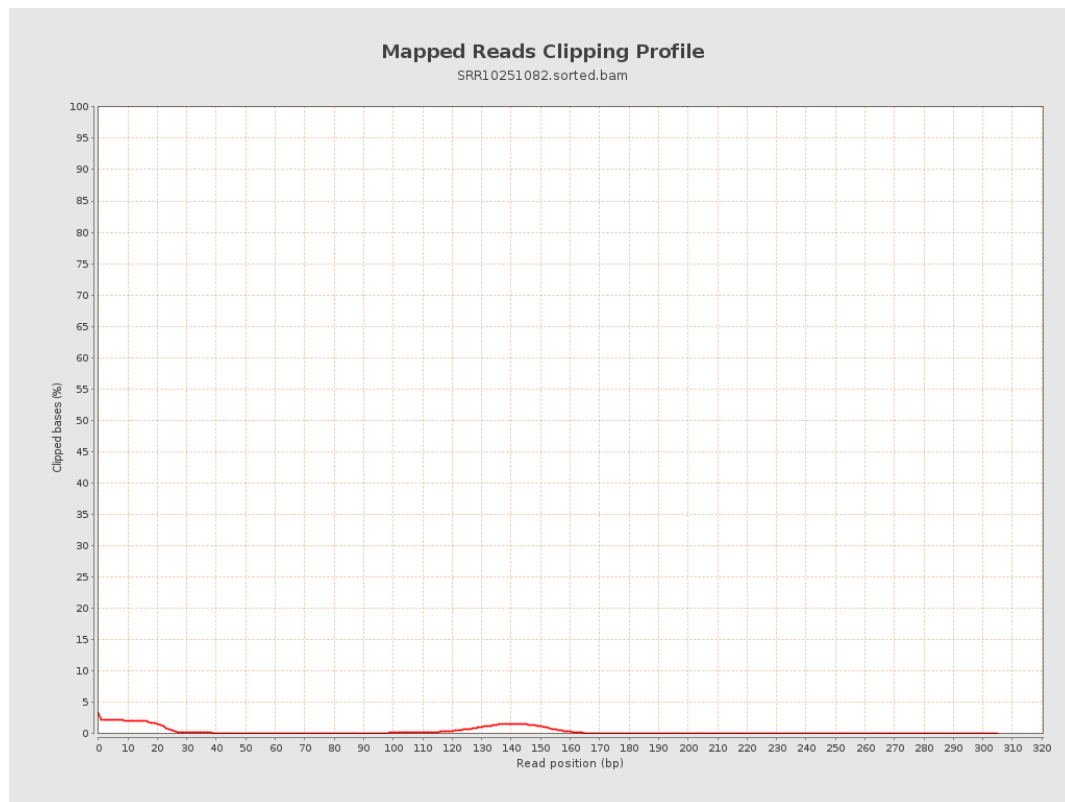
8. Results : Mapped Reads Nucleotide Content



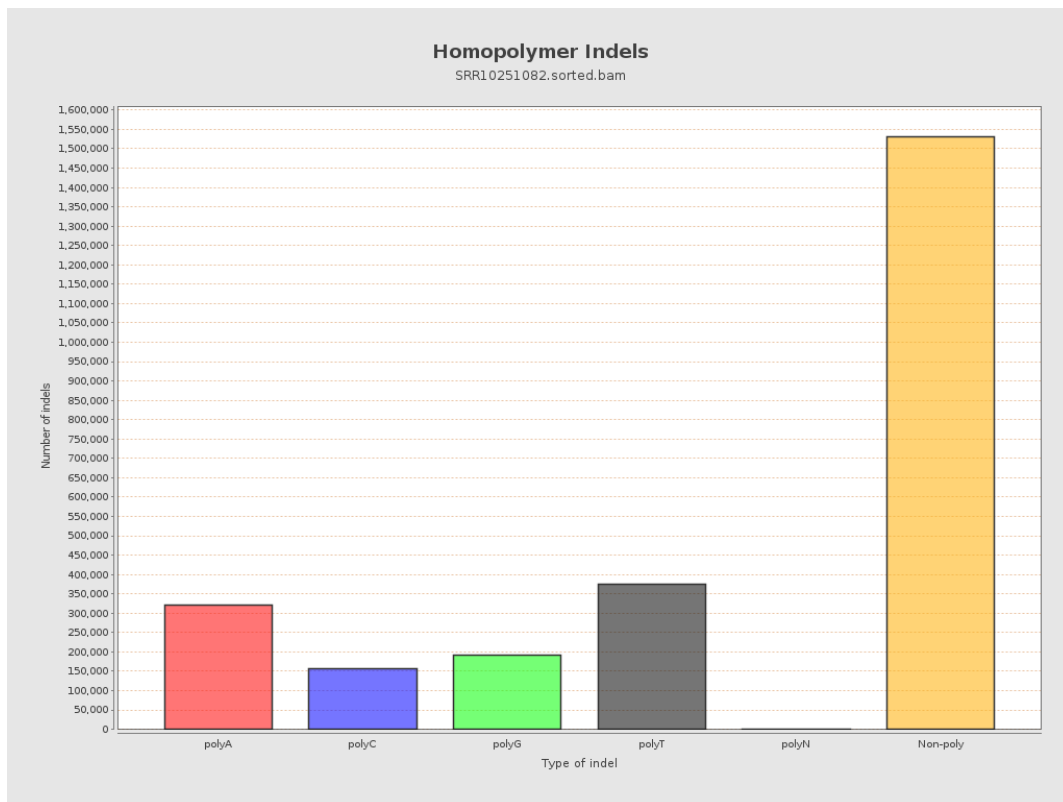
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

