

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 13:37:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251081.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_SRR10251081 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251081.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 13:37:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251081.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,704,596
Mapped reads	14,365,456 / 91.47%
Unmapped reads	1,339,140 / 8.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	186,562 / 1.19%
Read min/max/mean length	25 / 368 / 156.78
Duplicated reads (estimated)	10,526,768 / 67.03%
Duplication rate	37.27%
Clipped reads	14,542,390 / 92.6%

2.2. ACGT Content

Number/percentage of A's	500,031,835 / 28.84%
Number/percentage of C's	345,144,062 / 19.91%
Number/percentage of T's	524,054,937 / 30.23%
Number/percentage of G's	364,407,841 / 21.02%
Number/percentage of N's	0 / 0%
GC Percentage	40.93%

2.3. Coverage

Mean	0.5612

Standard Deviation	5.5394
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2.4. Mapping Quality

Mean Mapping Quality	51.19
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2.5. Mismatches and indels

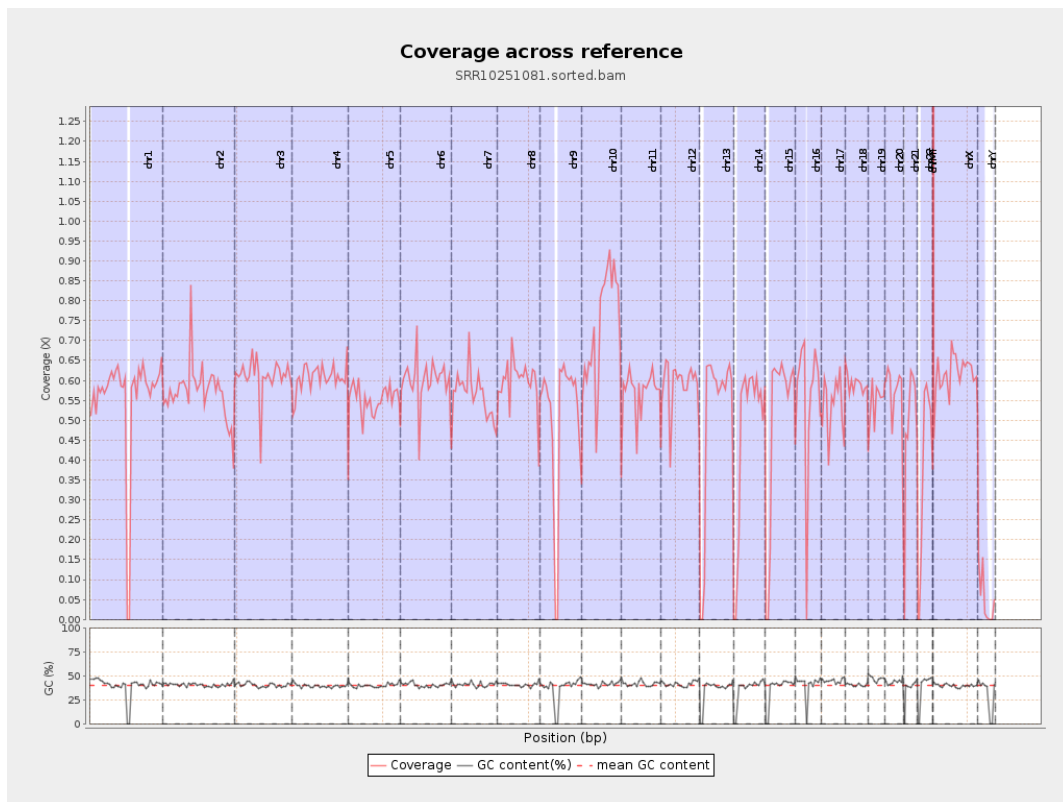
General error rate	1.32%
Mismatches	13,732,269
Insertions	8,292,297
Mapped reads with at least one insertion	34.3%
Deletions	3,030,229
Mapped reads with at least one deletion	17.24%
Homopolymer indels	36%

2.6. Chromosome stats

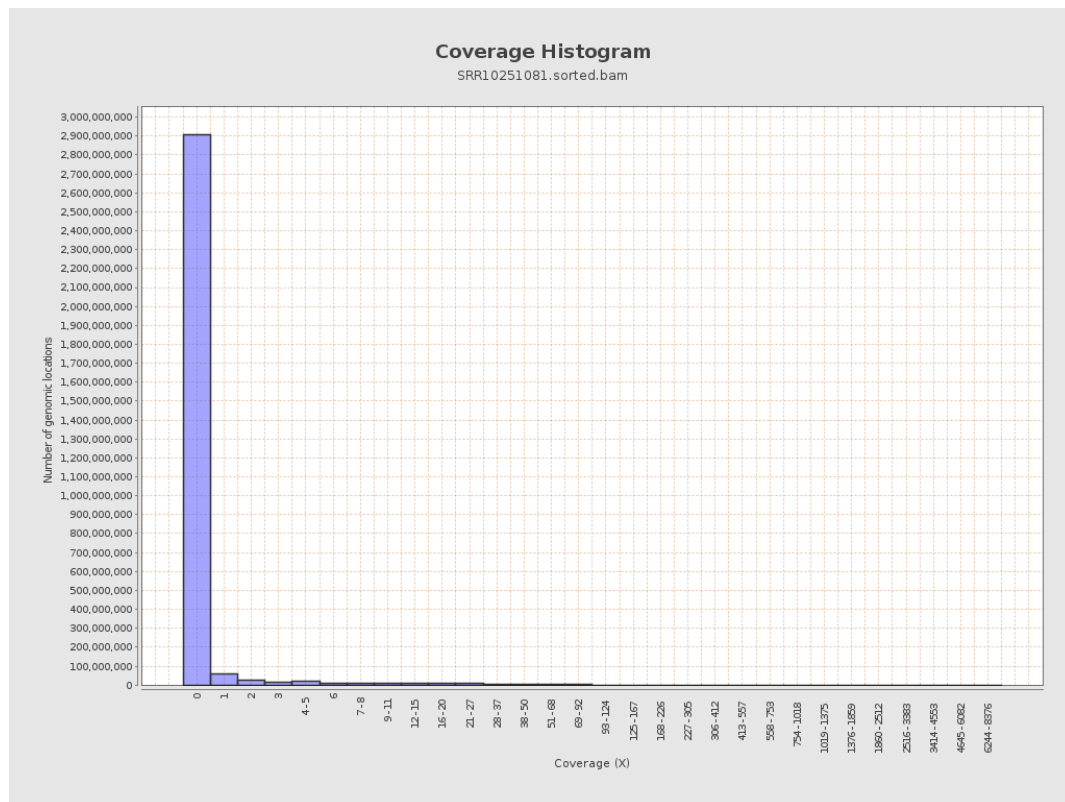
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	138478367	0.5556	5.6136
chr2	243199373	138983363	0.5715	6.0073
chr3	198022430	120720368	0.6096	4.7578
chr4	191154276	116090582	0.6073	4.9866
chr5	180915260	99840262	0.5519	4.5031
chr6	171115067	102880219	0.6012	5.4481
chr7	159138663	89528081	0.5626	6.6394

chr8	146364022	87406128	0.5972	5.2905
chr9	141213431	71655703	0.5074	5.0292
chr10	135534747	99775728	0.7362	6.7128
chr11	135006516	77375254	0.5731	4.6715
chr12	133851895	79382215	0.5931	4.541
chr13	115169878	58082974	0.5043	4.4062
chr14	107349540	51243638	0.4774	4.2249
chr15	102531392	50684899	0.4943	4.2042
chr16	90354753	49356518	0.5463	4.3813
chr17	81195210	43952592	0.5413	4.3373
chr18	78077248	46189062	0.5916	6.5274
chr19	59128983	32364890	0.5474	5.6809
chr20	63025520	36129676	0.5733	4.421
chr21	48129895	23454856	0.4873	4.2973
chr22	51304566	19496257	0.38	3.4897
chrMT	16571	5362797	323.6254	799.7362
chrX	155270560	95759424	0.6167	5.143
chrY	59373566	3002366	0.0506	1.9188

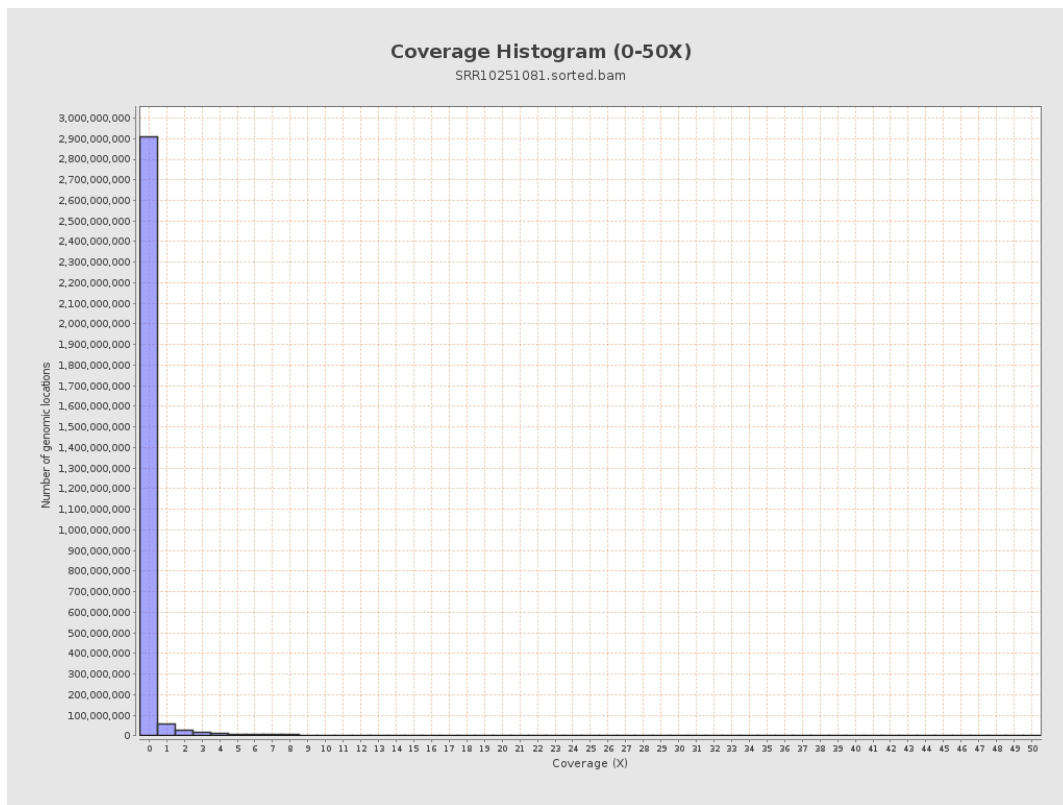
3. Results : Coverage across reference



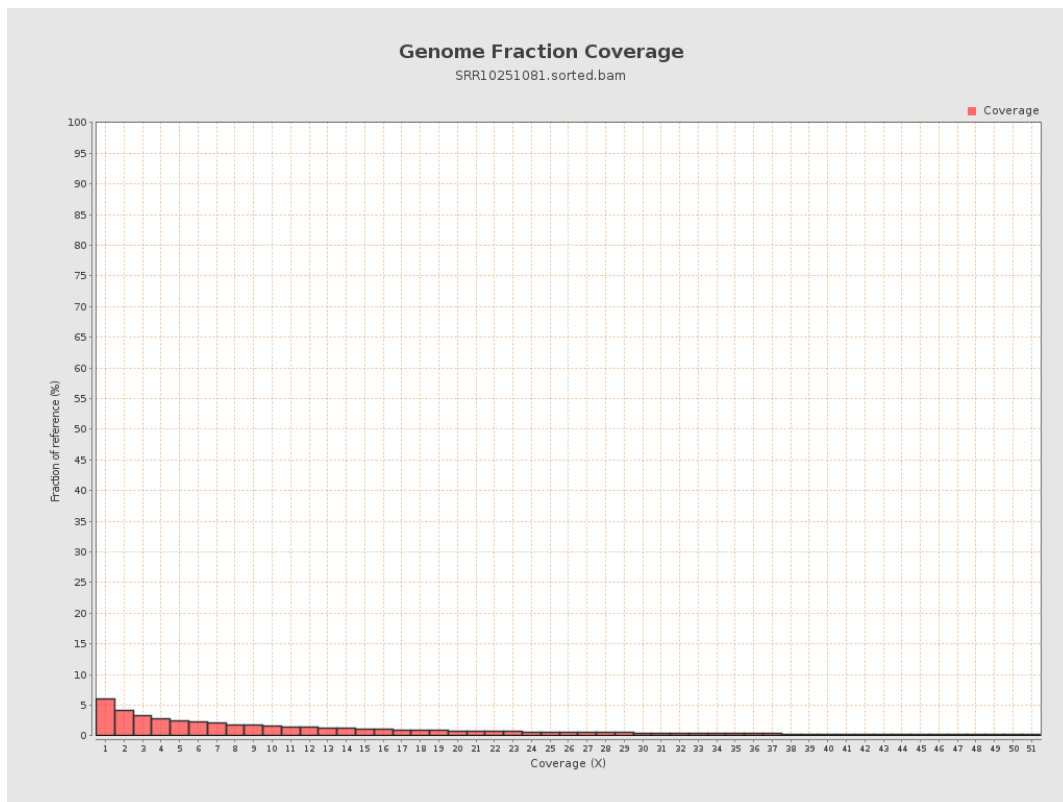
4. Results : Coverage Histogram



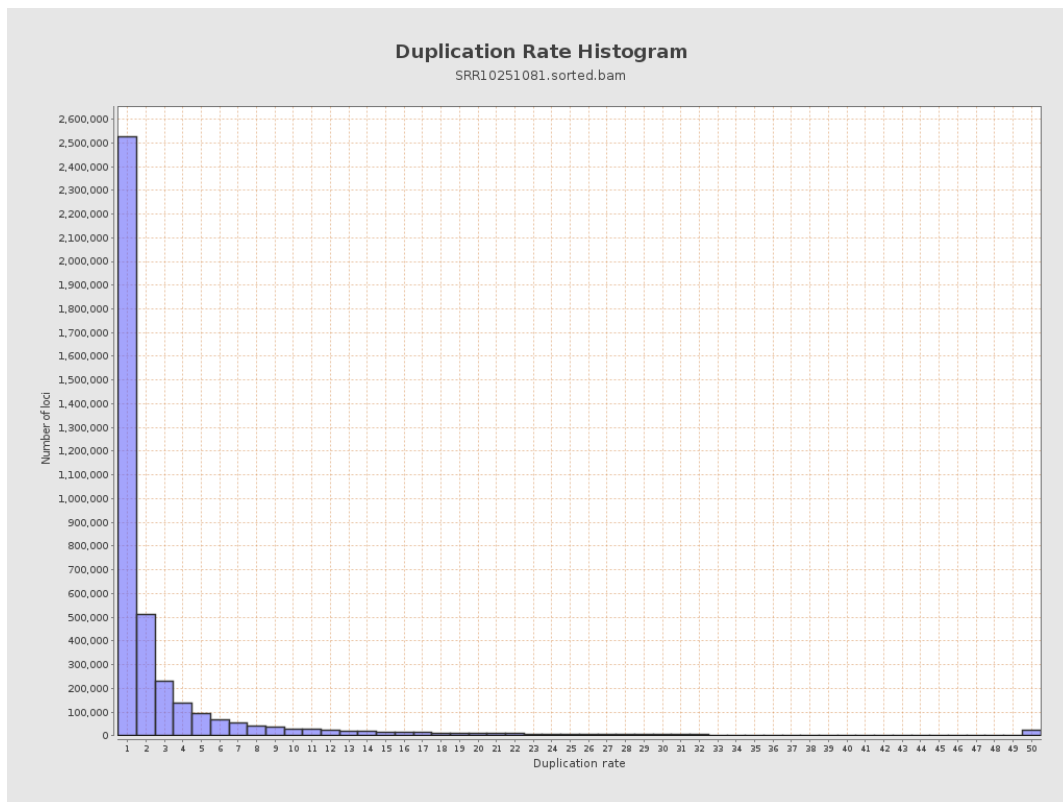
5. Results : Coverage Histogram (0-50X)



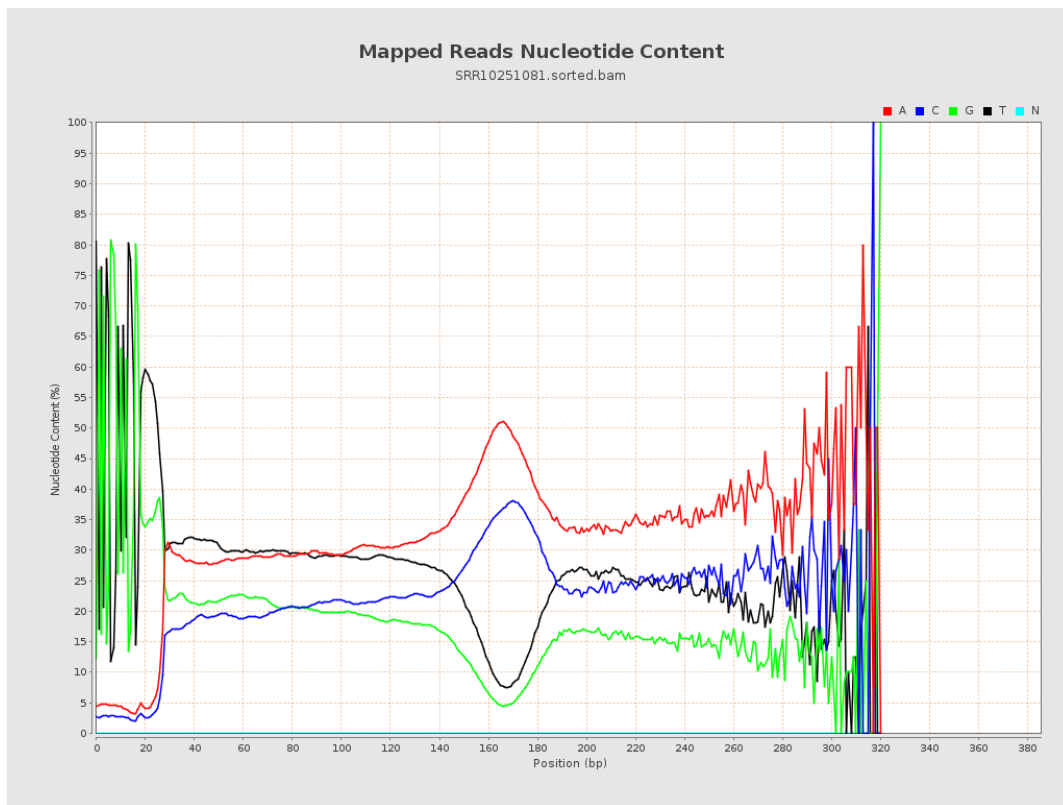
6. Results : Genome Fraction Coverage



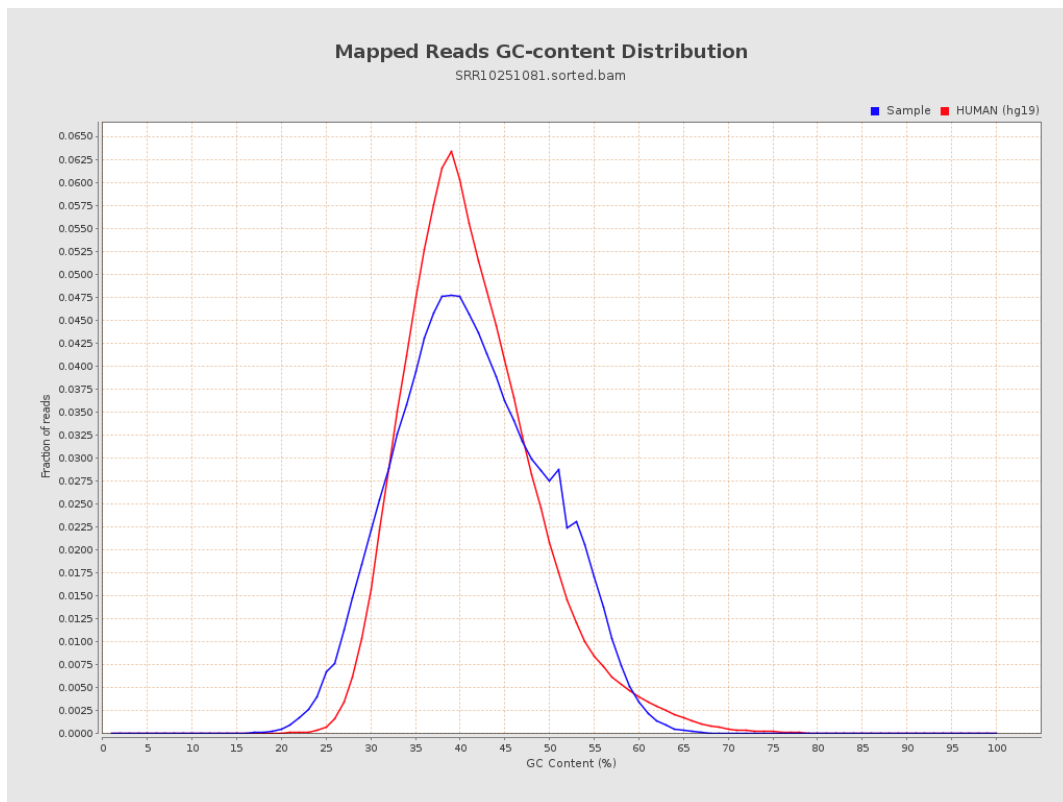
7. Results : Duplication Rate Histogram



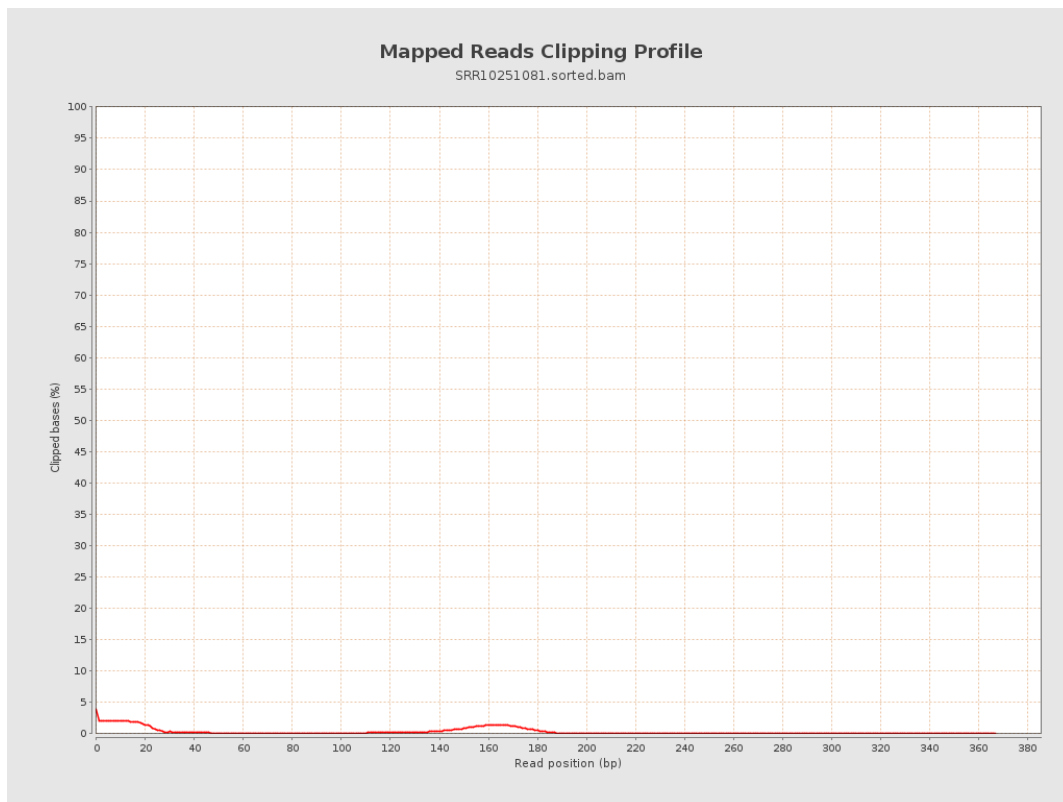
8. Results : Mapped Reads Nucleotide Content



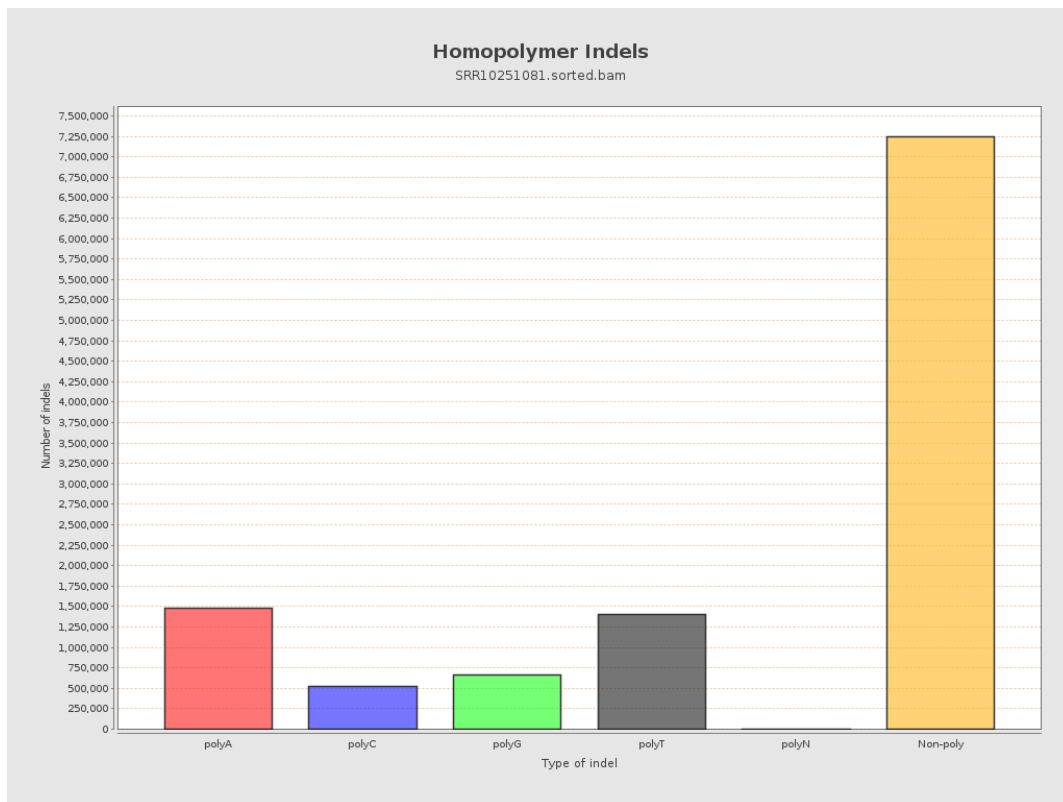
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

