

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 12:21:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251076.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_SRR10251076 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251076.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 12:21:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251076.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,301,594
Mapped reads	3,195,548 / 96.79%
Unmapped reads	106,046 / 3.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,546 / 0.86%
Read min/max/mean length	30 / 80 / 80.31
Duplicated reads (estimated)	579,358 / 17.55%
Duplication rate	16.04%
Clipped reads	442,167 / 13.39%

2.2. ACGT Content

Number/percentage of A's	72,590,377 / 29.26%
Number/percentage of C's	49,448,597 / 19.93%
Number/percentage of T's	73,473,178 / 29.61%
Number/percentage of G's	52,568,614 / 21.19%
Number/percentage of N's	19,556 / 0.01%
GC Percentage	41.12%

2.3. Coverage

Mean	0.0802

Standard Deviation	0.8022
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2.4. Mapping Quality

Mean Mapping Quality	48.15
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2.5. Mismatches and indels

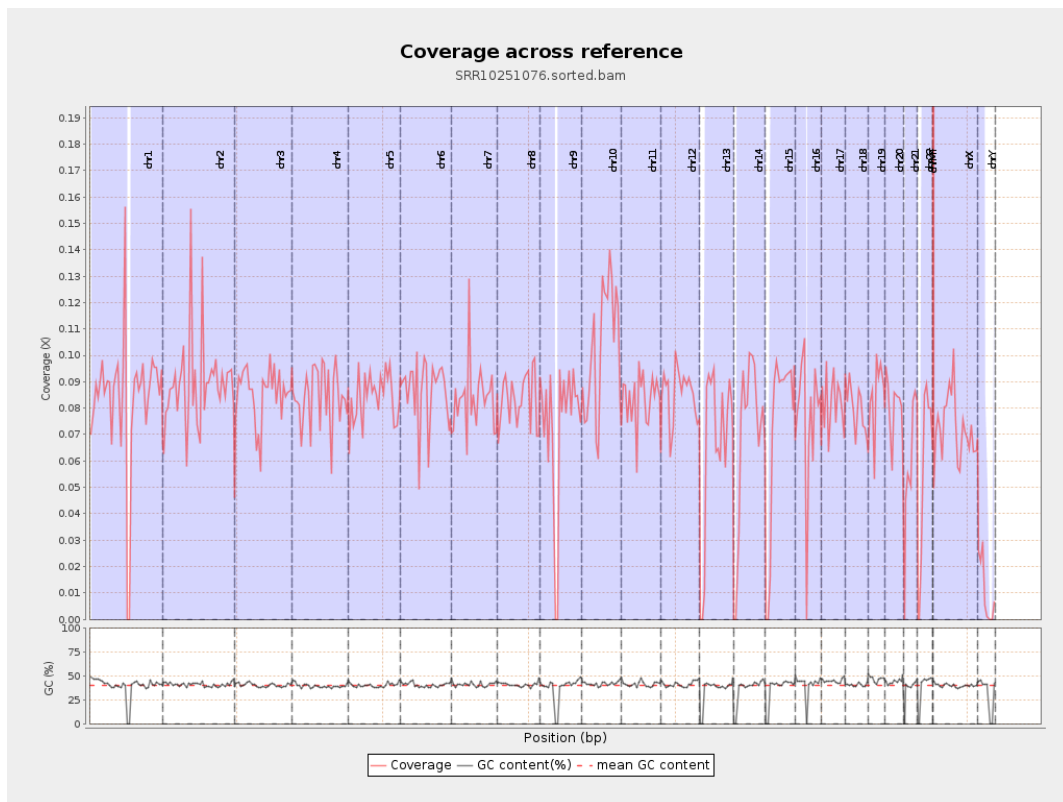
General error rate	0.59%
Mismatches	1,402,285
Insertions	30,112
Mapped reads with at least one insertion	0.92%
Deletions	84,903
Mapped reads with at least one deletion	2.62%
Homopolymer indels	45.51%

2.6. Chromosome stats

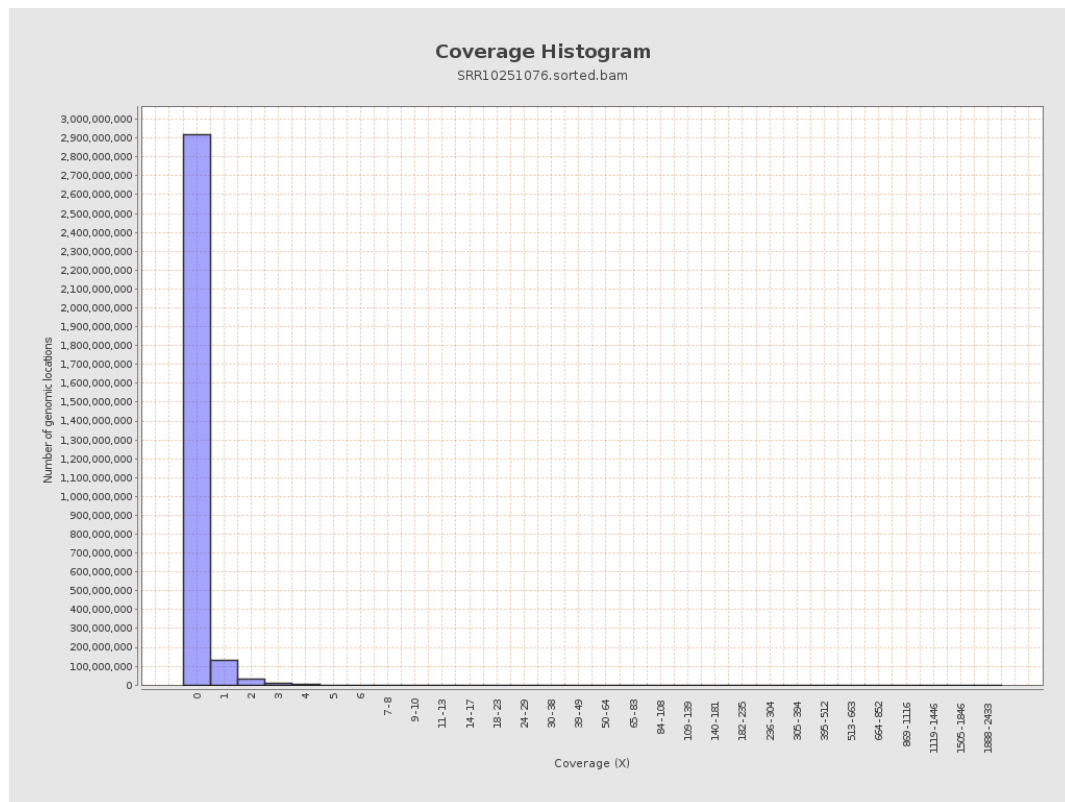
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	20883665	0.0838	1.6753
chr2	243199373	21806229	0.0897	1.0577
chr3	198022430	16836757	0.085	0.3847
chr4	191154276	16124325	0.0844	0.4421
chr5	180915260	15222555	0.0841	0.397
chr6	171115067	14746543	0.0862	0.4655
chr7	159138663	13286203	0.0835	1.0985

chr8	146364022	12164166	0.0831	0.5371
chr9	141213431	10338190	0.0732	0.7786
chr10	135534747	13932811	0.1028	0.81
chr11	135006516	11261288	0.0834	0.5214
chr12	133851895	11520365	0.0861	0.3969
chr13	115169878	7583054	0.0658	0.335
chr14	107349540	7534870	0.0702	0.5056
chr15	102531392	7296124	0.0712	0.3501
chr16	90354753	6831059	0.0756	0.6424
chr17	81195210	6699137	0.0825	0.4659
chr18	78077248	6261753	0.0802	0.9975
chr19	59128983	4998278	0.0845	1.6032
chr20	63025520	5046977	0.0801	0.4069
chr21	48129895	2883669	0.0599	0.3528
chr22	51304566	2899277	0.0565	0.3351
chrMT	16571	249548	15.0593	9.0485
chrX	155270560	11208173	0.0722	0.4145
chrY	59373566	635545	0.0107	0.7089

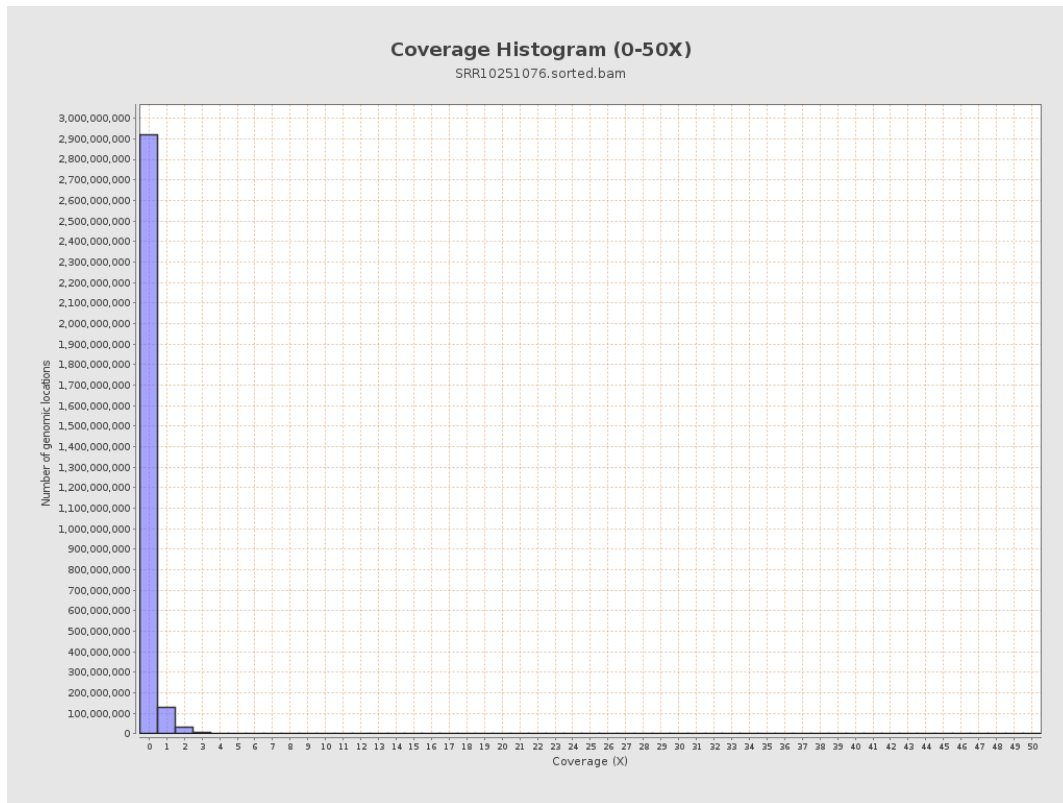
3. Results : Coverage across reference



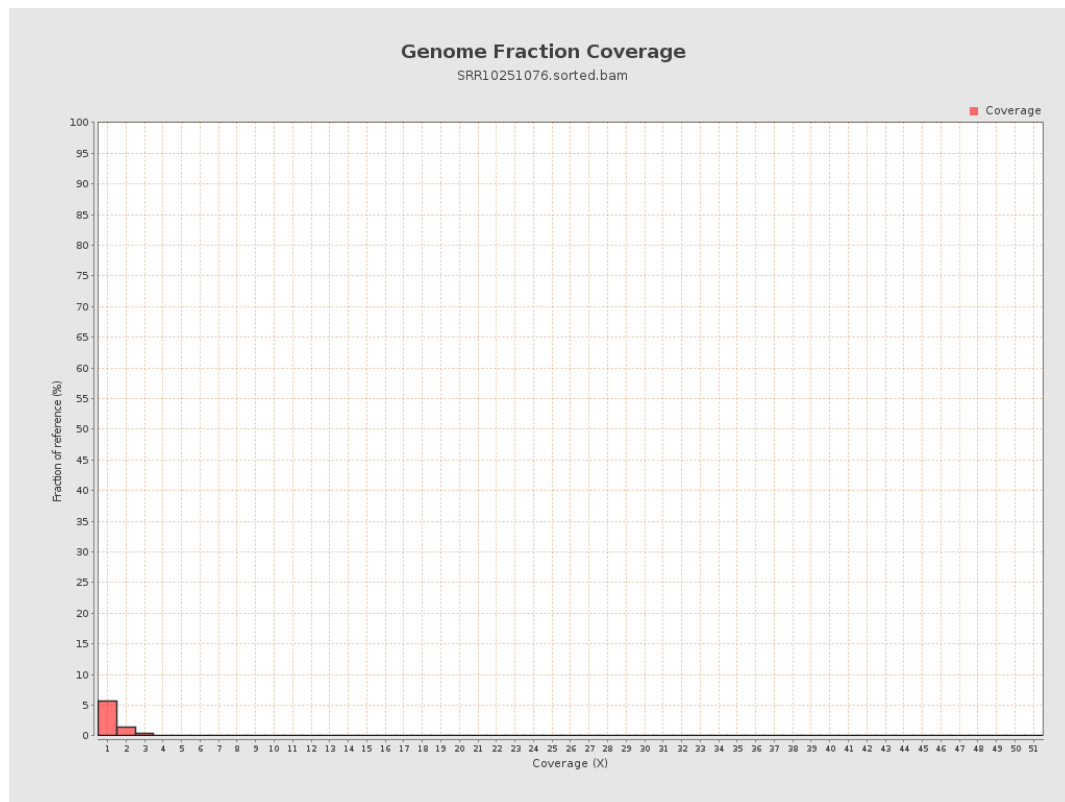
4. Results : Coverage Histogram



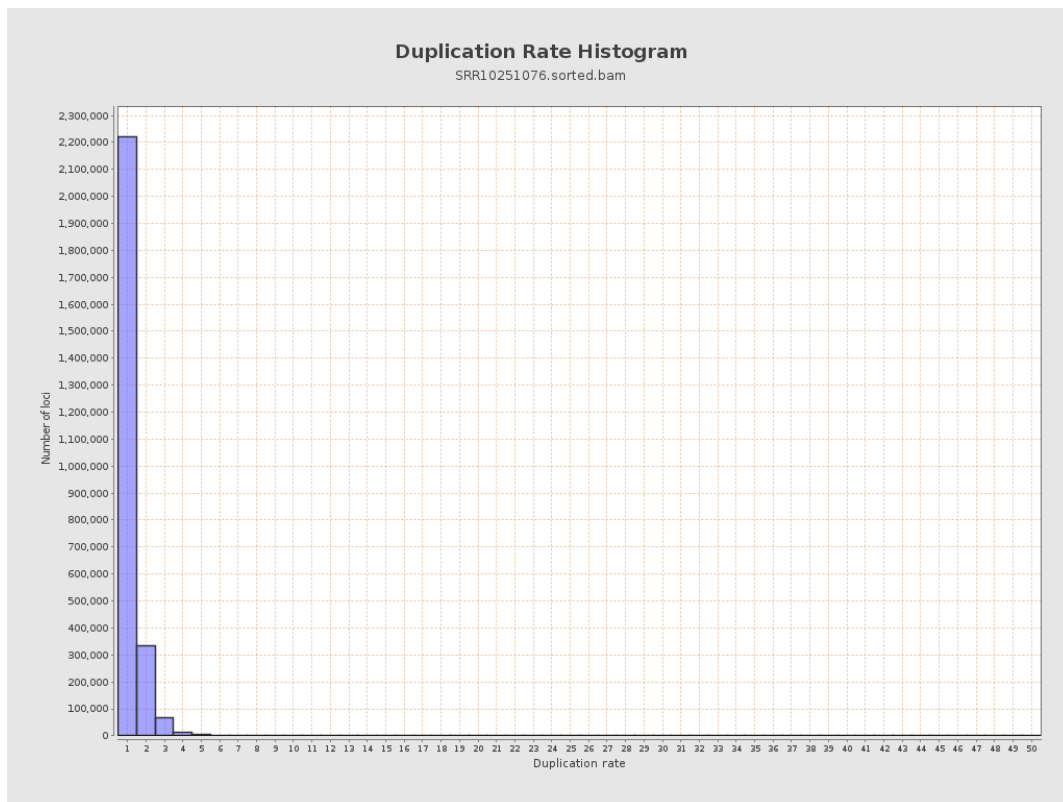
5. Results : Coverage Histogram (0-50X)



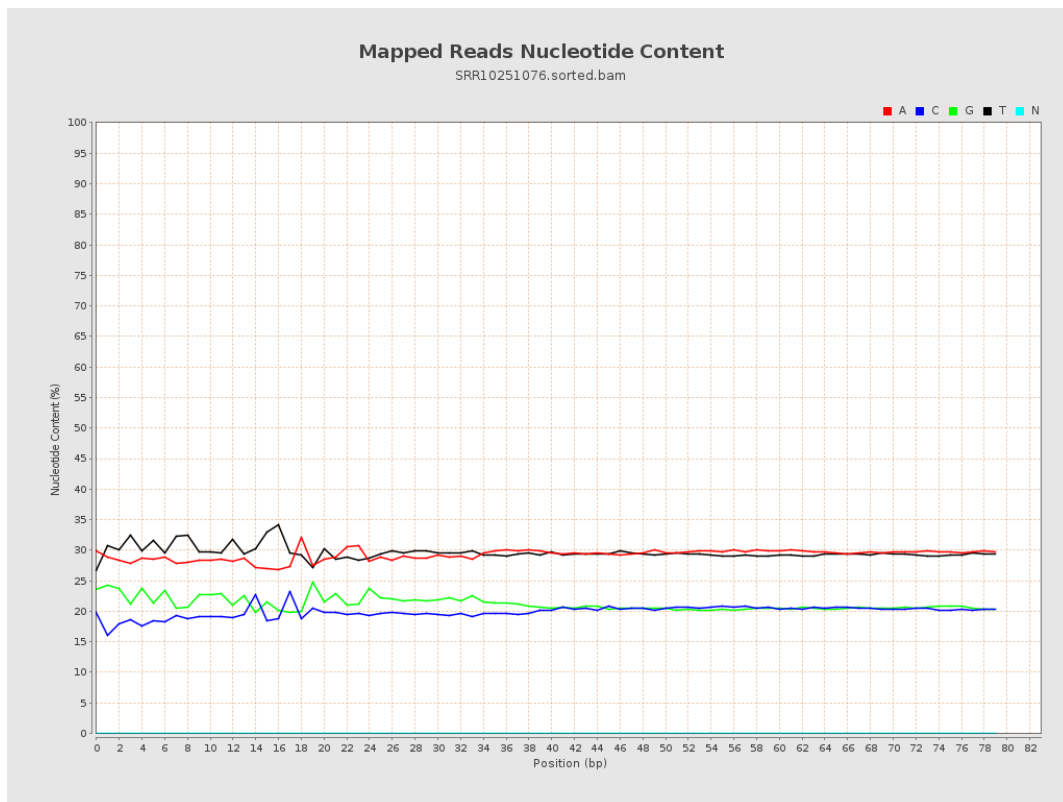
6. Results : Genome Fraction Coverage



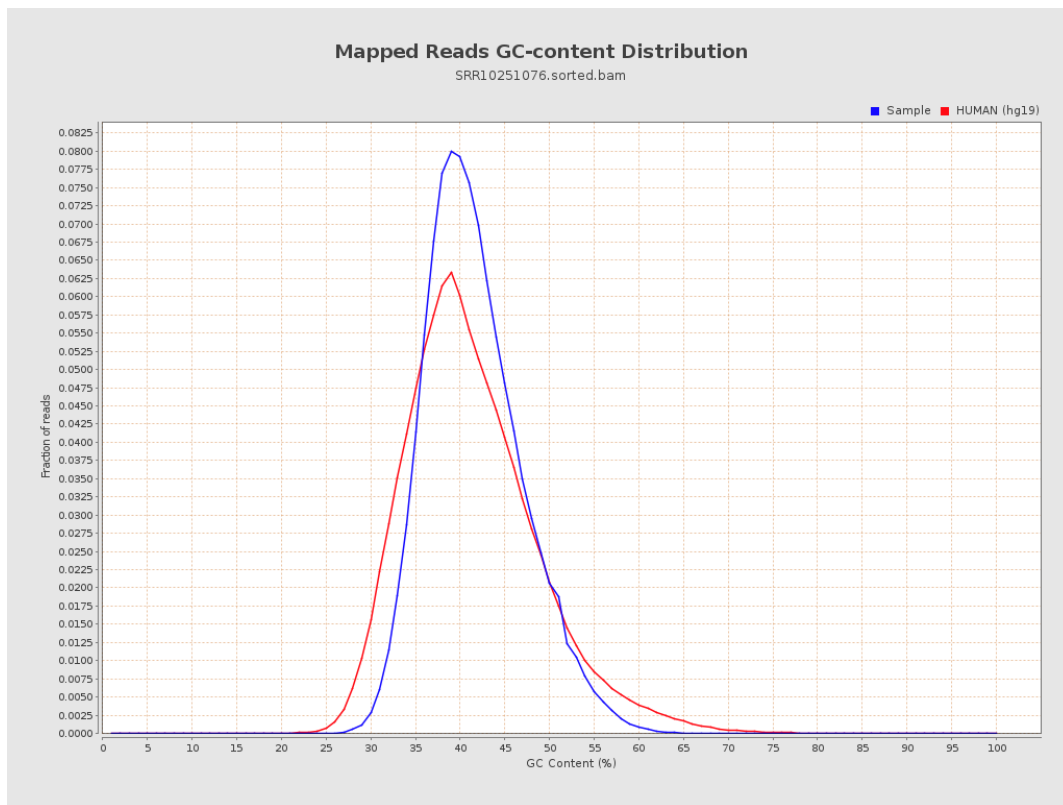
7. Results : Duplication Rate Histogram



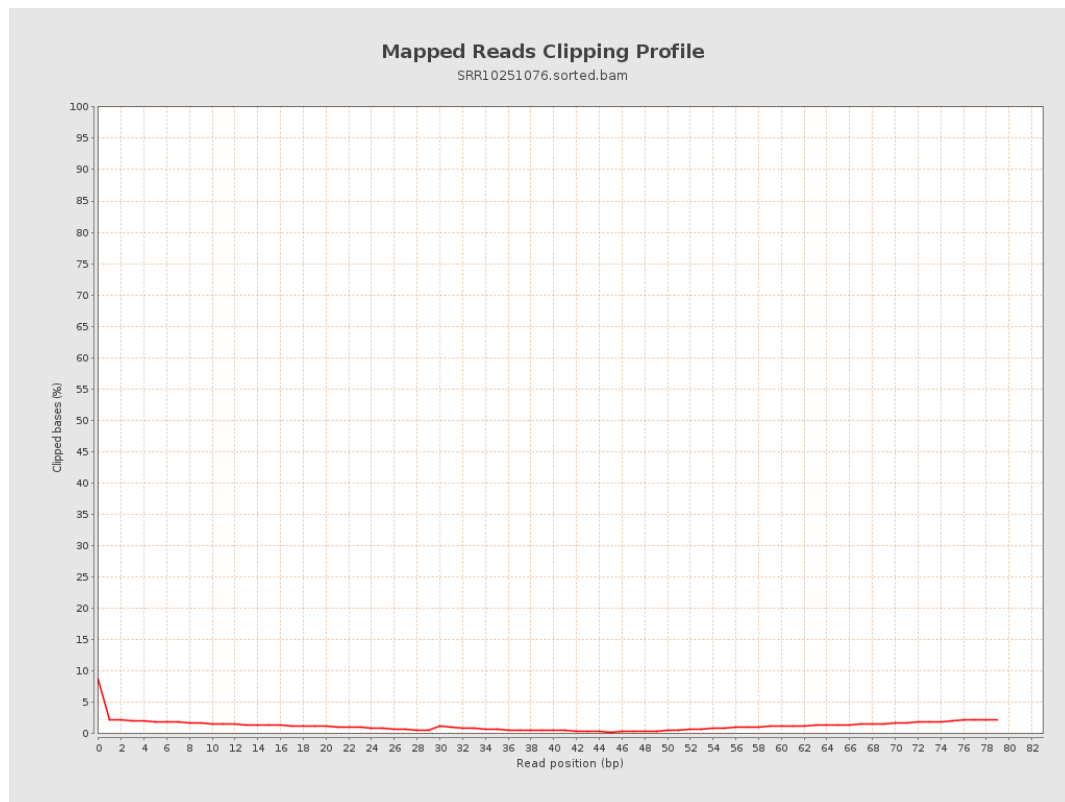
8. Results : Mapped Reads Nucleotide Content



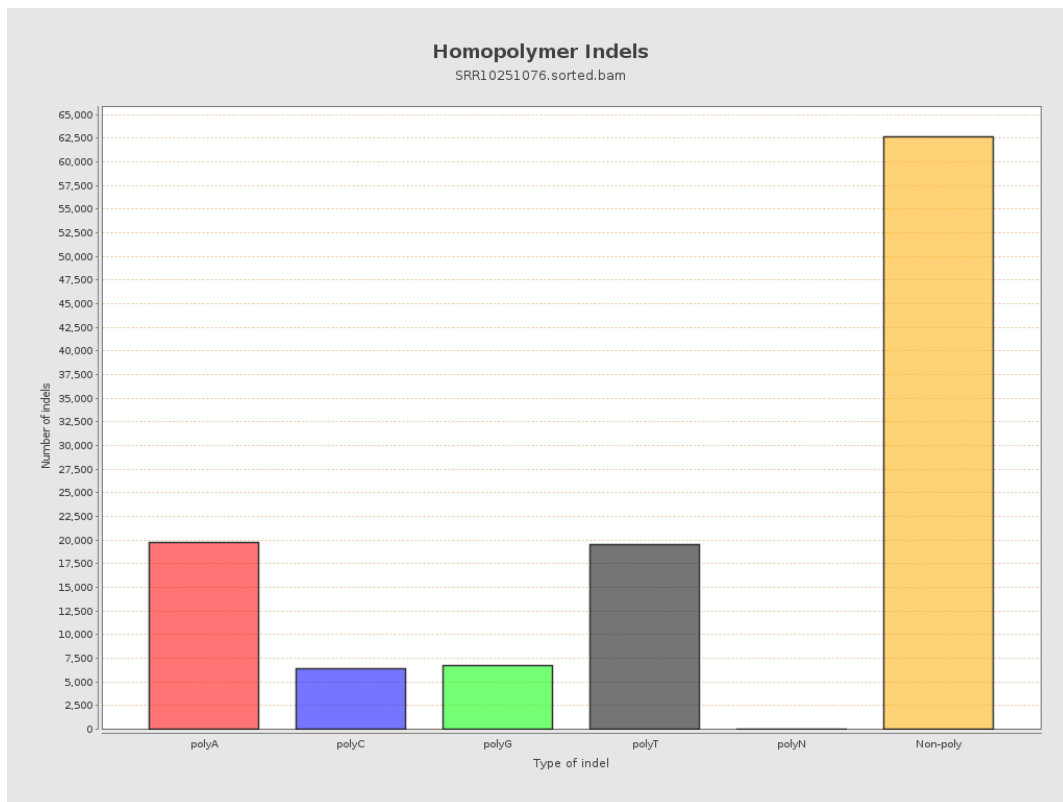
9. Results : Mapped Reads GC-content Distribution



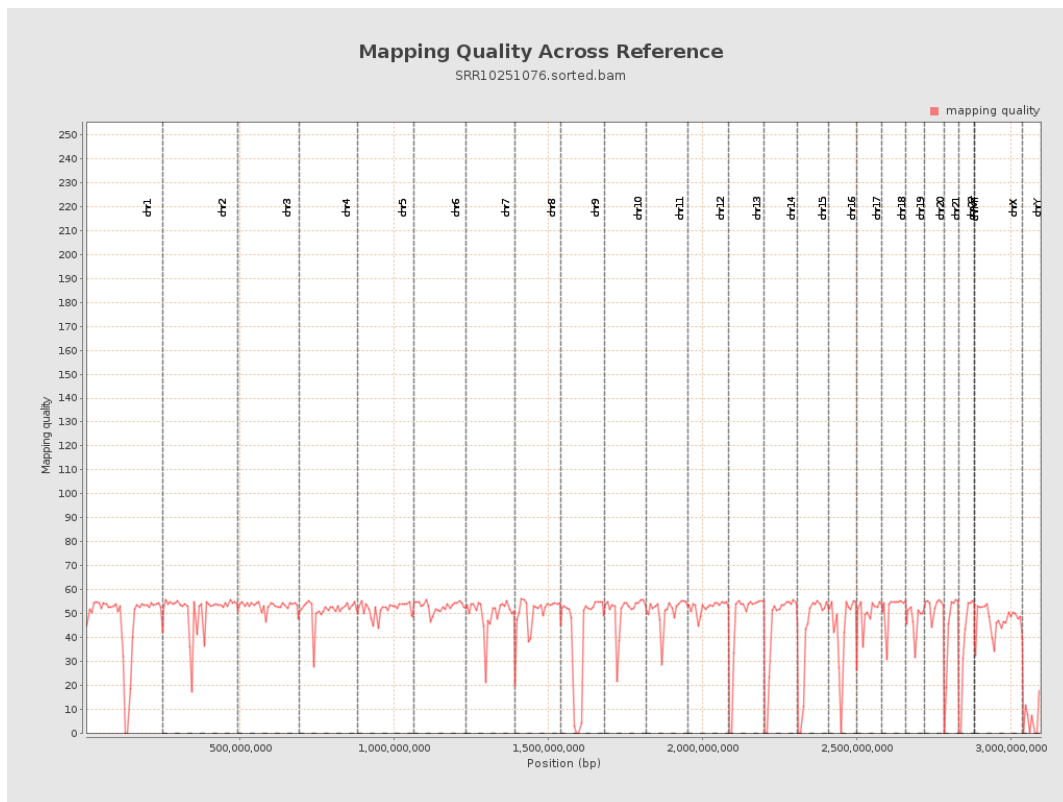
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

