

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 11:55:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251070.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_SRR10251070 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251070.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 11:55:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251070.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,040,658
Mapped reads	3,748,946 / 92.78%
Unmapped reads	291,712 / 7.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,667 / 0.68%
Read min/max/mean length	30 / 80 / 80.25
Duplicated reads (estimated)	792,429 / 19.61%
Duplication rate	18.55%
Clipped reads	493,607 / 12.22%

2.2. ACGT Content

Number/percentage of A's	84,181,900 / 28.95%
Number/percentage of C's	58,133,194 / 20%
Number/percentage of T's	85,757,768 / 29.5%
Number/percentage of G's	62,660,366 / 21.55%
Number/percentage of N's	2,706 / 0%
GC Percentage	41.55%

2.3. Coverage

Mean	0.094

Standard Deviation	1.005
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2.4. Mapping Quality

Mean Mapping Quality	48.25
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2.5. Mismatches and indels

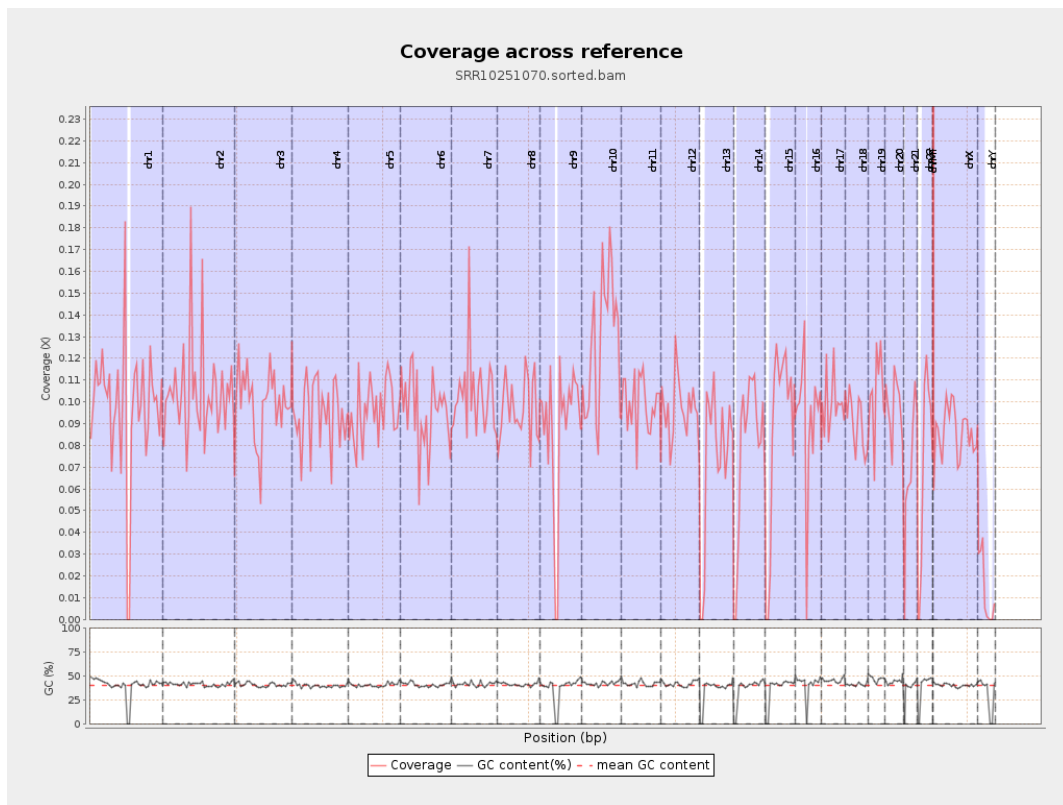
General error rate	0.6%
Mismatches	1,671,288
Insertions	35,549
Mapped reads with at least one insertion	0.93%
Deletions	101,145
Mapped reads with at least one deletion	2.65%
Homopolymer indels	44.59%

2.6. Chromosome stats

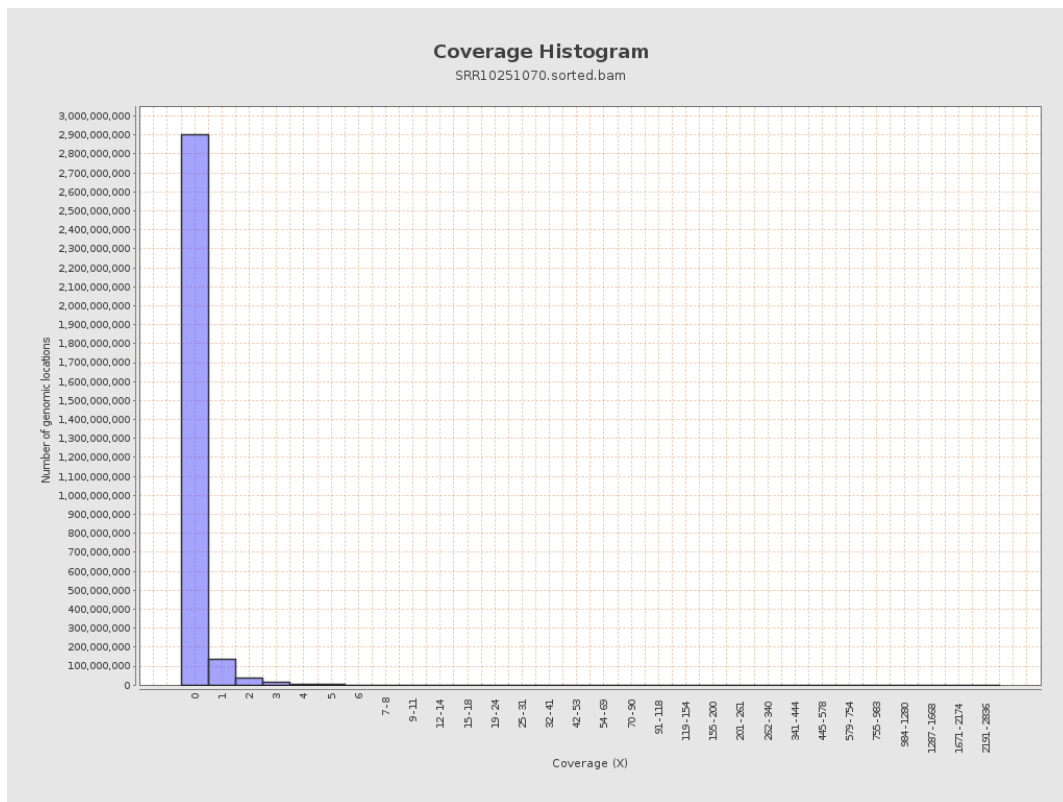
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24318057	0.0976	2.0265
chr2	243199373	25440148	0.1046	1.4333
chr3	198022430	19627629	0.0991	0.4411
chr4	191154276	18112439	0.0948	0.518
chr5	180915260	17411678	0.0962	0.4656
chr6	171115067	16291725	0.0952	0.5427
chr7	159138663	16381589	0.1029	1.4908

chr8	146364022	14175638	0.0969	0.6392
chr9	141213431	12436591	0.0881	0.9954
chr10	135534747	17302625	0.1277	1.0462
chr11	135006516	13368732	0.099	0.6322
chr12	133851895	13116292	0.098	0.4589
chr13	115169878	8446865	0.0733	0.3752
chr14	107349540	8629215	0.0804	0.6872
chr15	102531392	8814089	0.086	0.4103
chr16	90354753	8273844	0.0916	0.8571
chr17	81195210	8107722	0.0999	0.5699
chr18	78077248	7027887	0.09	1.1367
chr19	59128983	6135947	0.1038	1.9663
chr20	63025520	6098151	0.0968	0.4966
chr21	48129895	3397823	0.0706	0.4125
chr22	51304566	3687408	0.0719	0.4163
chrMT	16571	146285	8.8278	5.8346
chrX	155270560	13370845	0.0861	0.5045
chrY	59373566	798344	0.0134	1.0005

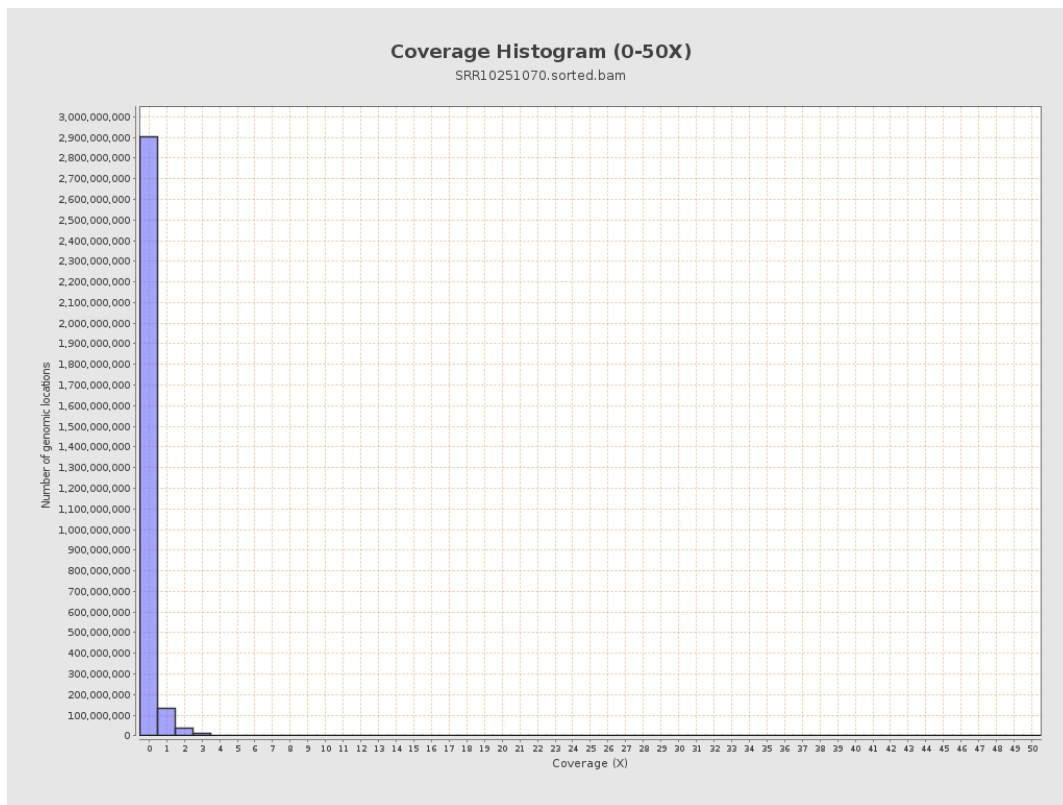
3. Results : Coverage across reference



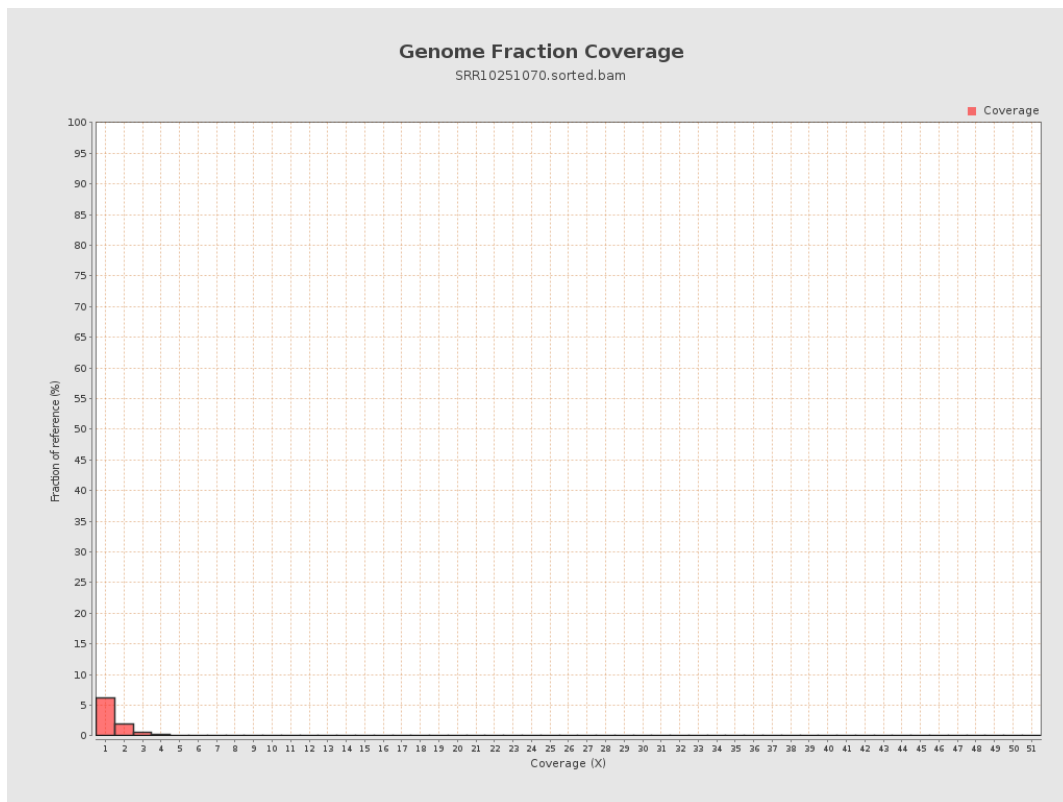
4. Results : Coverage Histogram



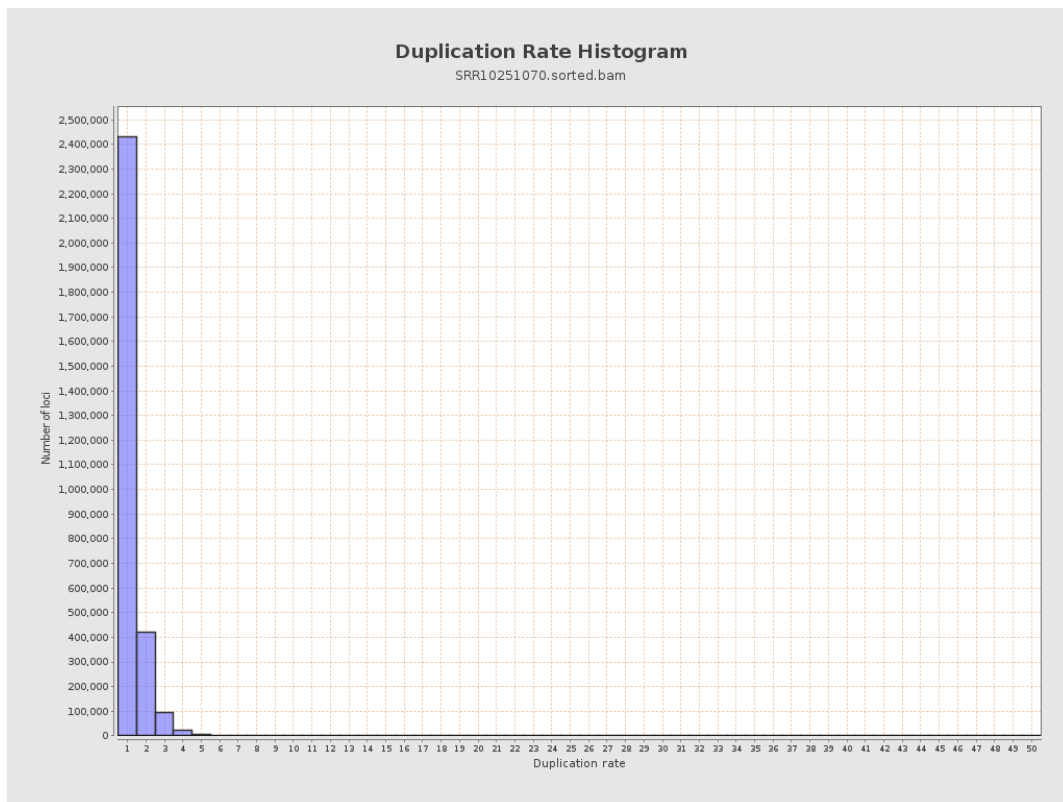
5. Results : Coverage Histogram (0-50X)



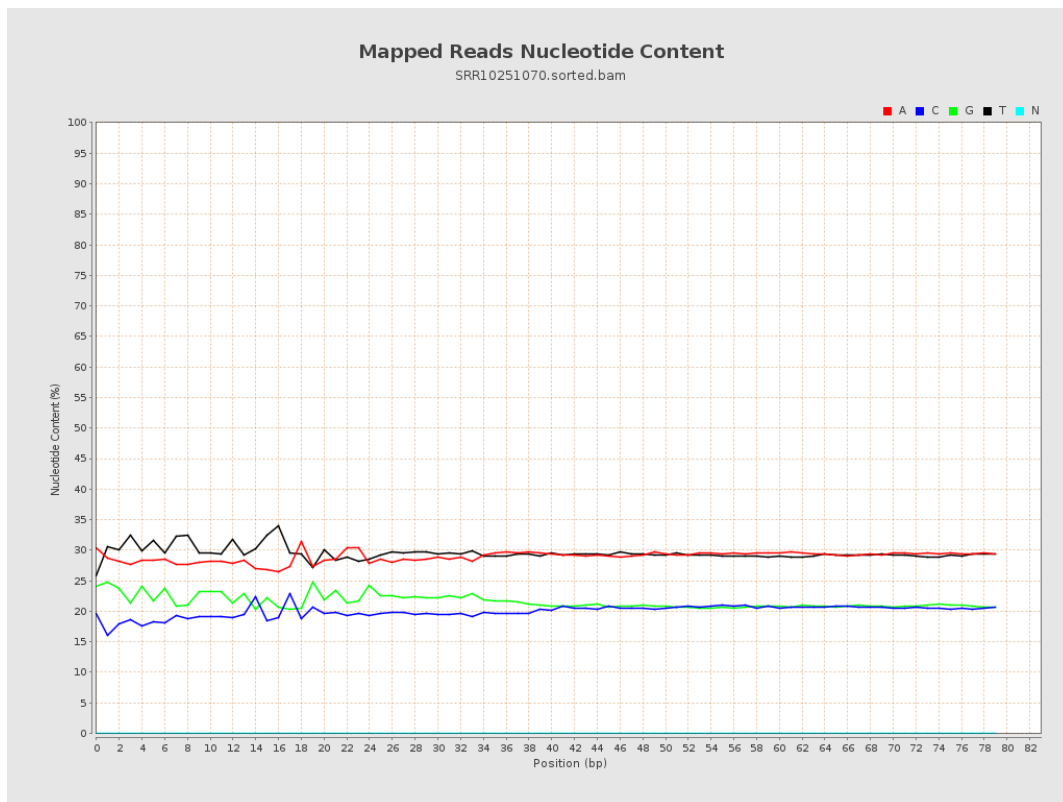
6. Results : Genome Fraction Coverage



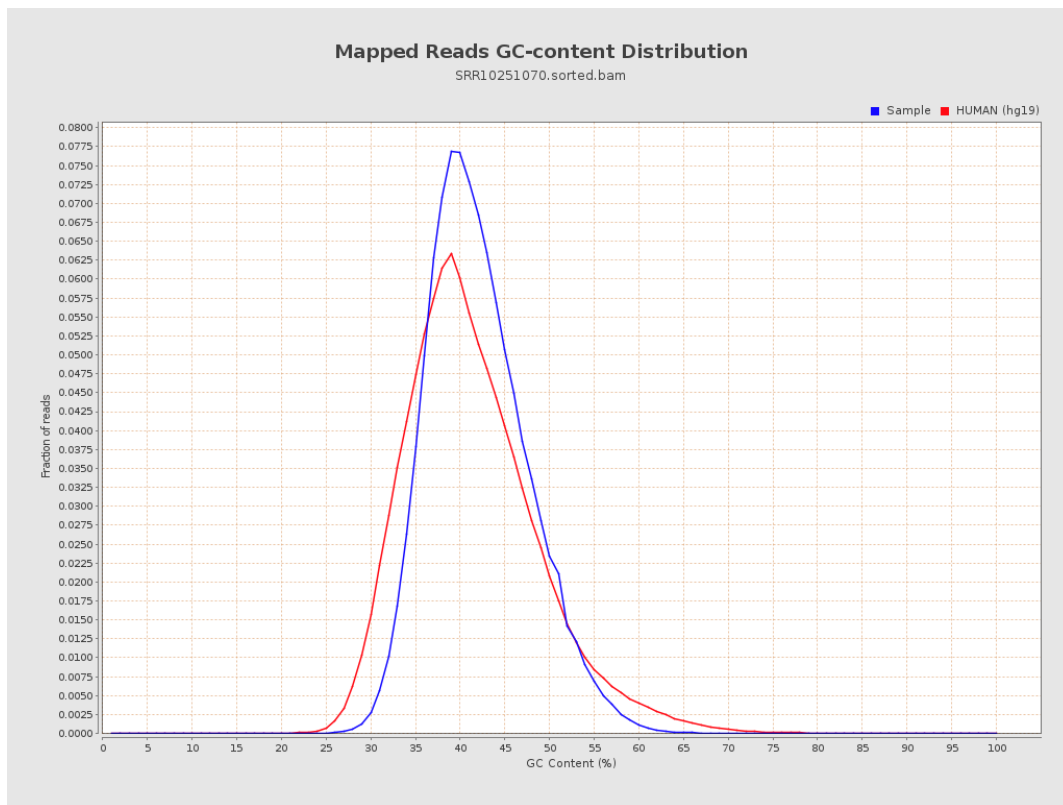
7. Results : Duplication Rate Histogram



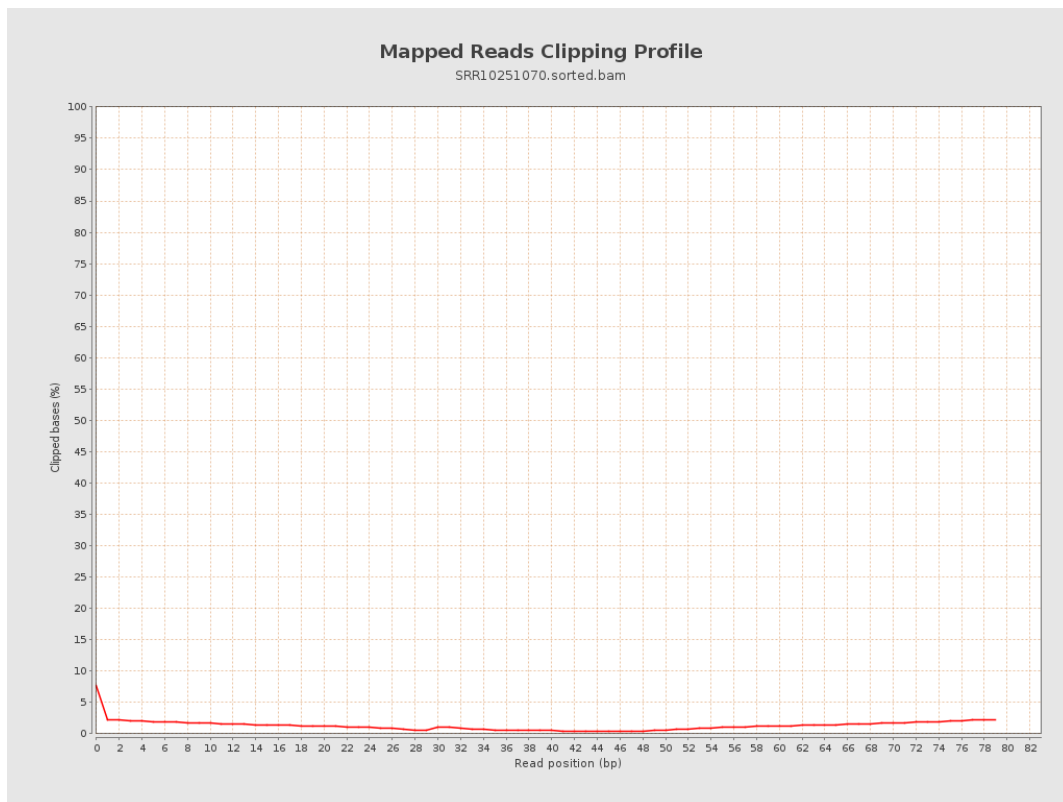
8. Results : Mapped Reads Nucleotide Content



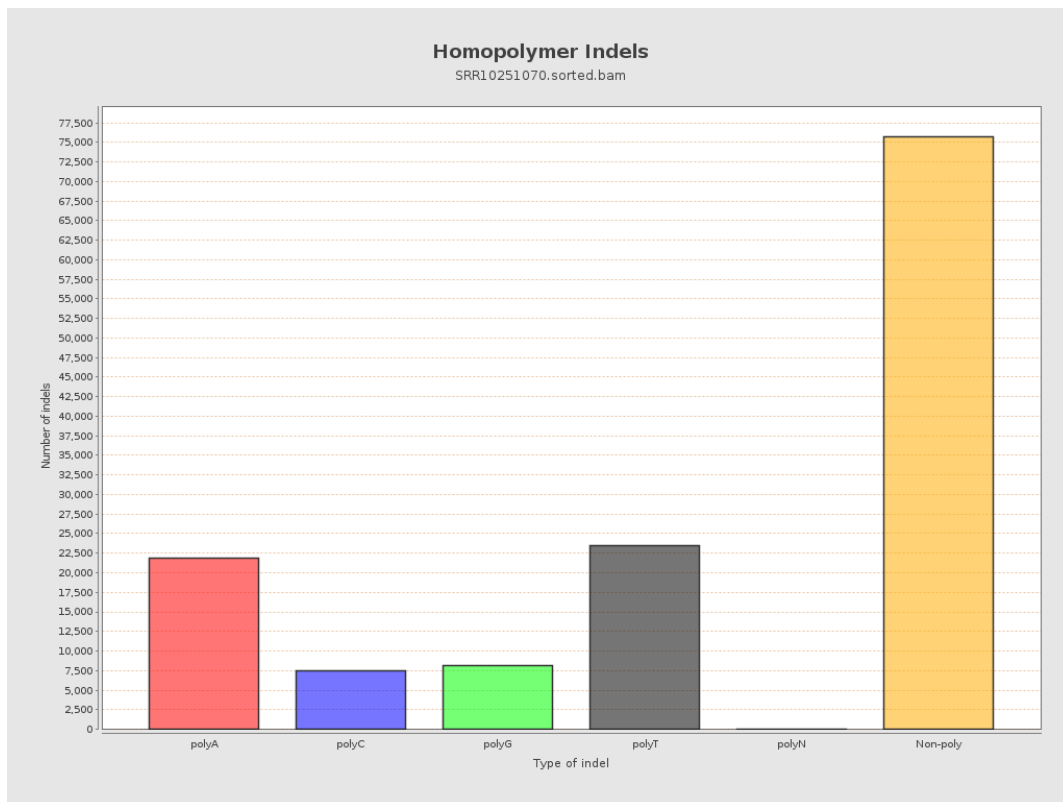
9. Results : Mapped Reads GC-content Distribution



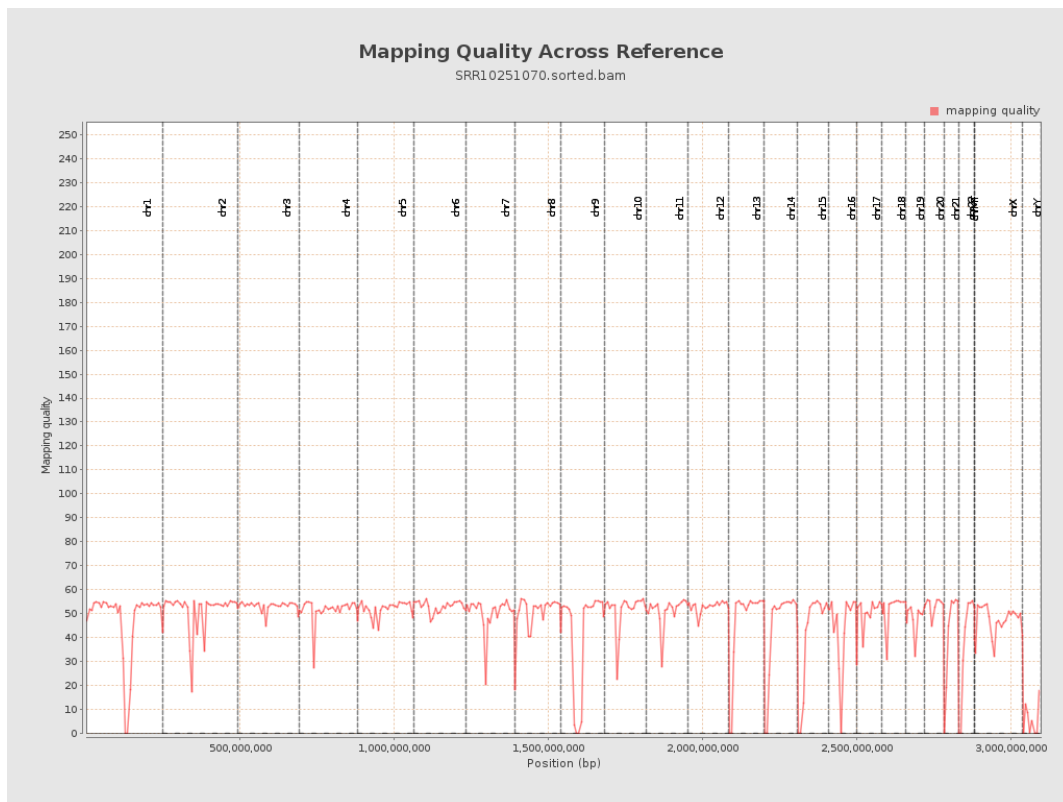
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

