

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 09:12:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472831.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_SRR3472831 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472831.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 09:12:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472831.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,285,779
Mapped reads	2,832,700 / 86.21%
Unmapped reads	453,079 / 13.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,528 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	96,454 / 2.94%
Duplication rate	2.52%
Clipped reads	1,443,919 / 43.94%

2.2. ACGT Content

Number/percentage of A's	49,958,028 / 27.1%
Number/percentage of C's	36,618,125 / 19.87%
Number/percentage of T's	54,953,706 / 29.81%
Number/percentage of G's	42,787,835 / 23.21%
Number/percentage of N's	3,692 / 0%
GC Percentage	43.08%

2.3. Coverage

Mean	0.0596

Standard Deviation	0.4176
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2.4. Mapping Quality

Mean Mapping Quality	44.51
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2.5. Mismatches and indels

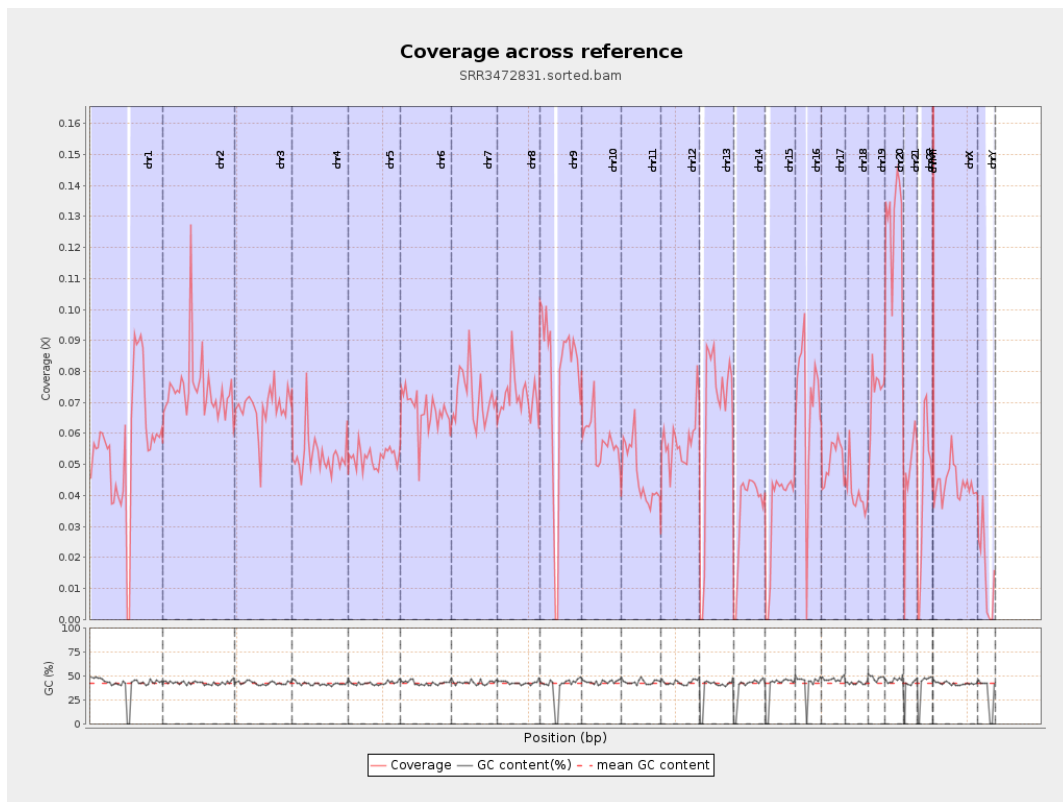
General error rate	0.86%
Mismatches	1,551,856
Insertions	14,276
Mapped reads with at least one insertion	0.5%
Deletions	41,259
Mapped reads with at least one deletion	1.44%
Homopolymer indels	44.99%

2.6. Chromosome stats

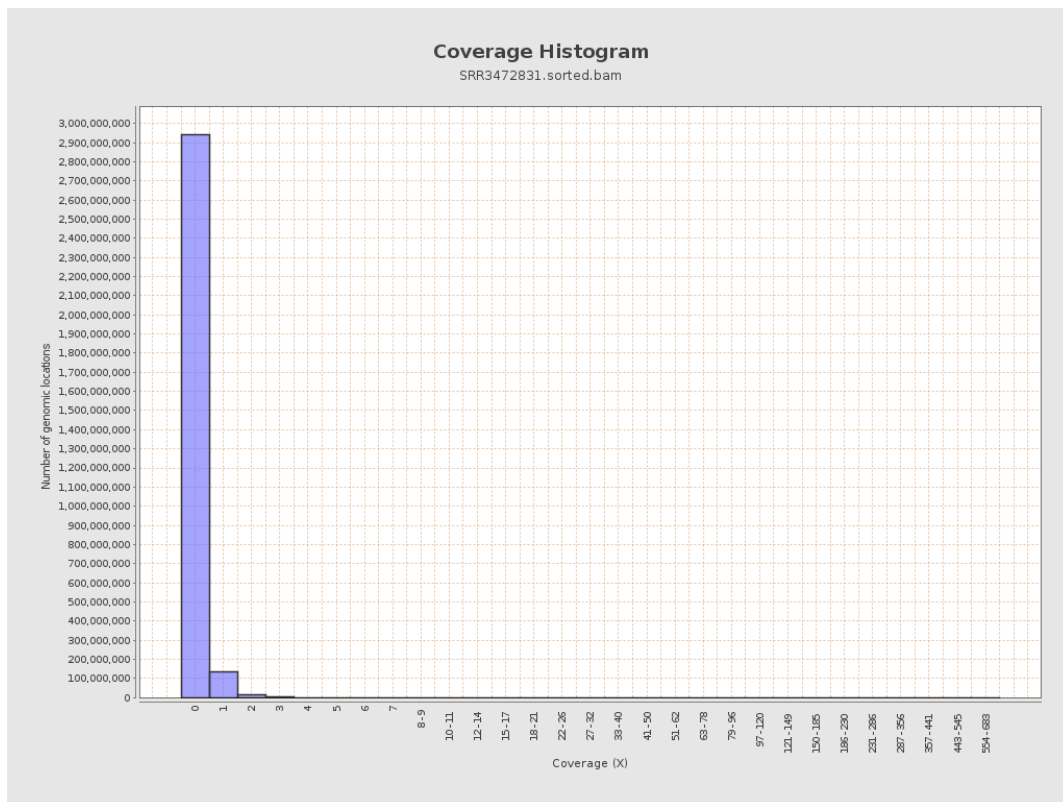
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13905632	0.0558	0.5584
chr2	243199373	18047466	0.0742	0.6266
chr3	198022430	13480978	0.0681	0.2964
chr4	191154276	10180770	0.0533	0.2939
chr5	180915260	9469781	0.0523	0.2604
chr6	171115067	11509164	0.0673	0.3277
chr7	159138663	11425742	0.0718	0.542

chr8	146364022	10503911	0.0718	0.4246
chr9	141213431	10854491	0.0769	0.5152
chr10	135534747	7838172	0.0578	0.3717
chr11	135006516	6276572	0.0465	0.4009
chr12	133851895	7722780	0.0577	0.2863
chr13	115169878	7556453	0.0656	0.3063
chr14	107349540	3807288	0.0355	0.2581
chr15	102531392	3543504	0.0346	0.2345
chr16	90354753	6249421	0.0692	0.3386
chr17	81195210	4176731	0.0514	0.2884
chr18	78077248	3191446	0.0409	0.8207
chr19	59128983	4327240	0.0732	0.4451
chr20	63025520	8125928	0.1289	0.4344
chr21	48129895	2307345	0.0479	0.3019
chr22	51304566	2169806	0.0423	0.247
chrMT	16571	16146	0.9744	1.1788
chrX	155270560	6797483	0.0438	0.2816
chrY	59373566	910171	0.0153	0.2006

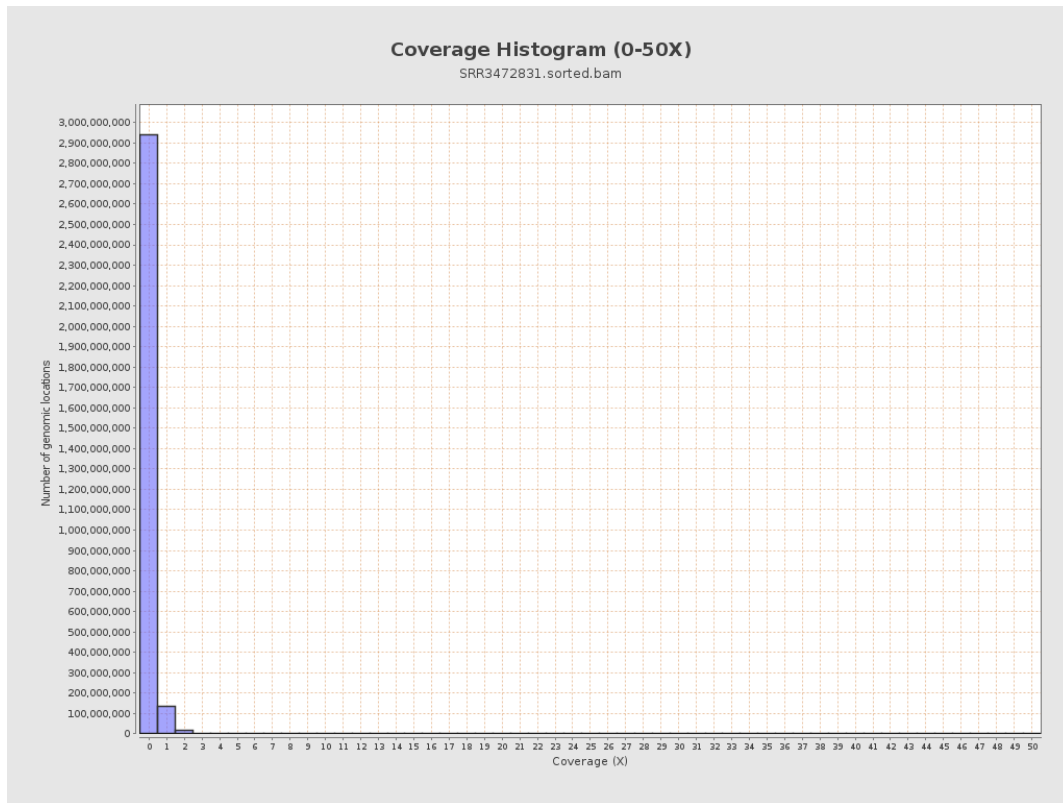
3. Results : Coverage across reference



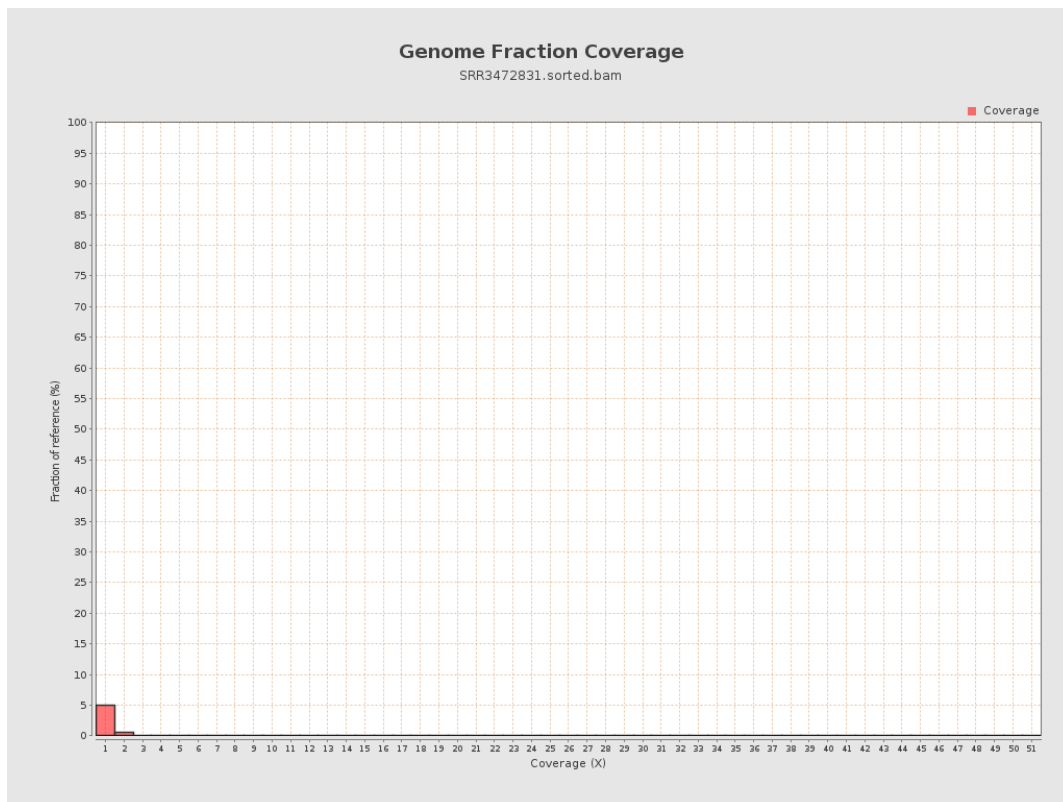
4. Results : Coverage Histogram



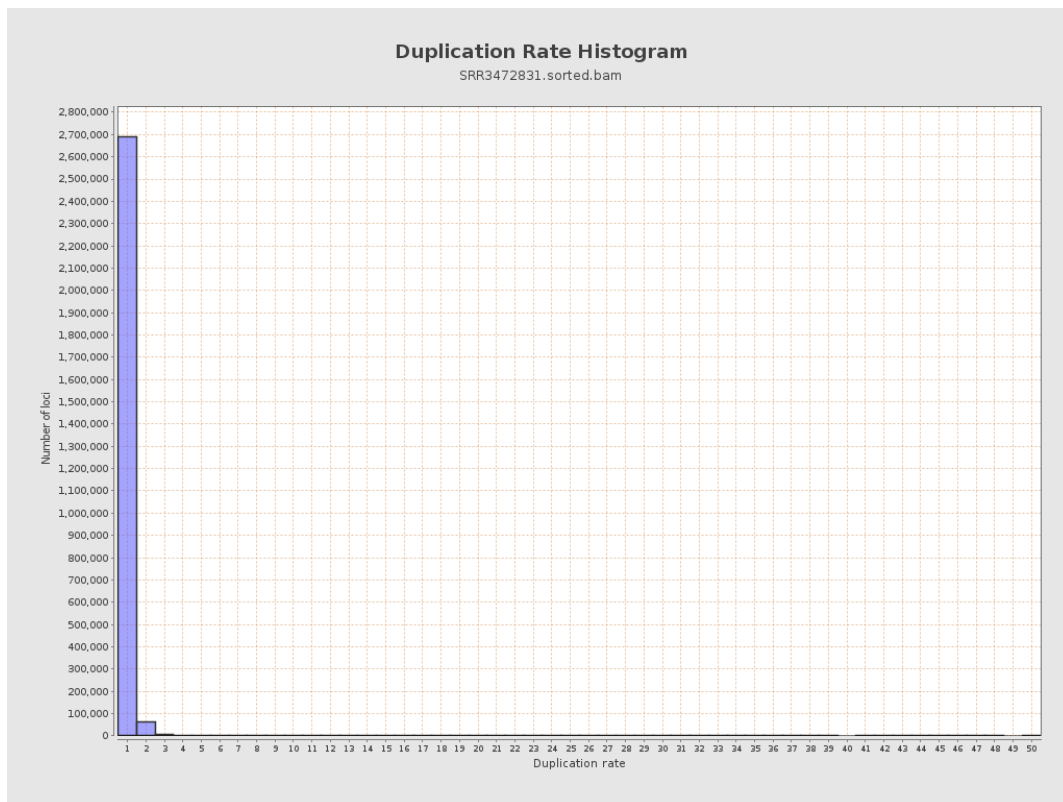
5. Results : Coverage Histogram (0-50X)



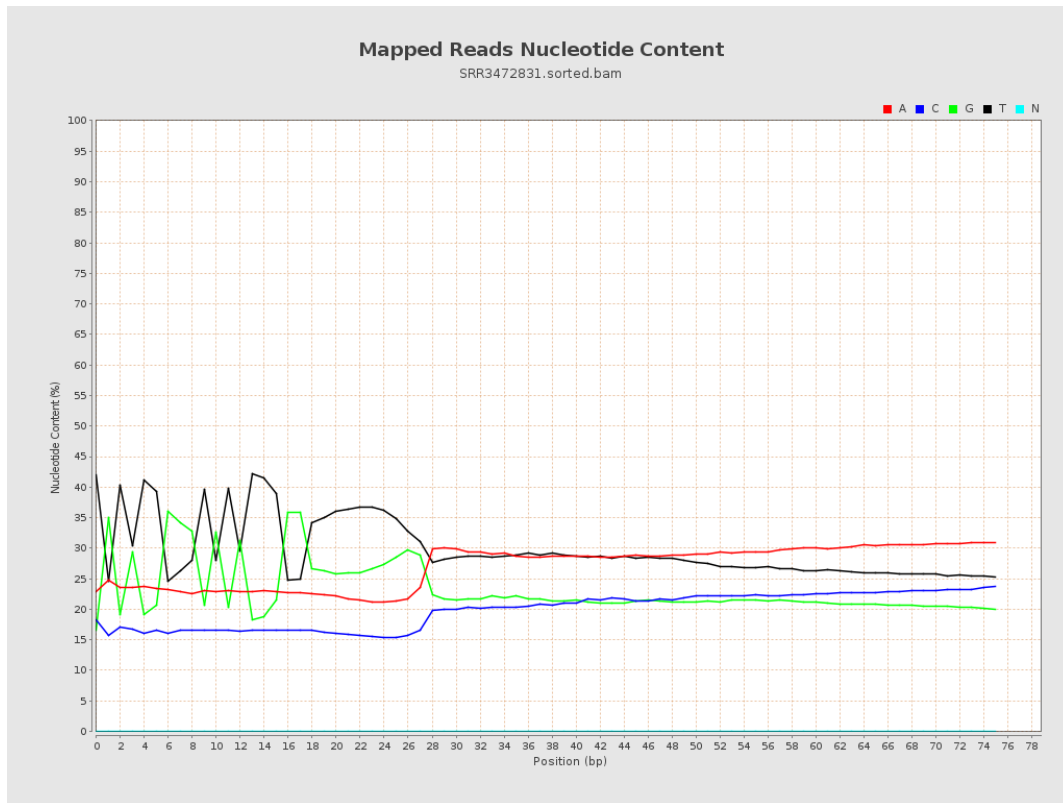
6. Results : Genome Fraction Coverage



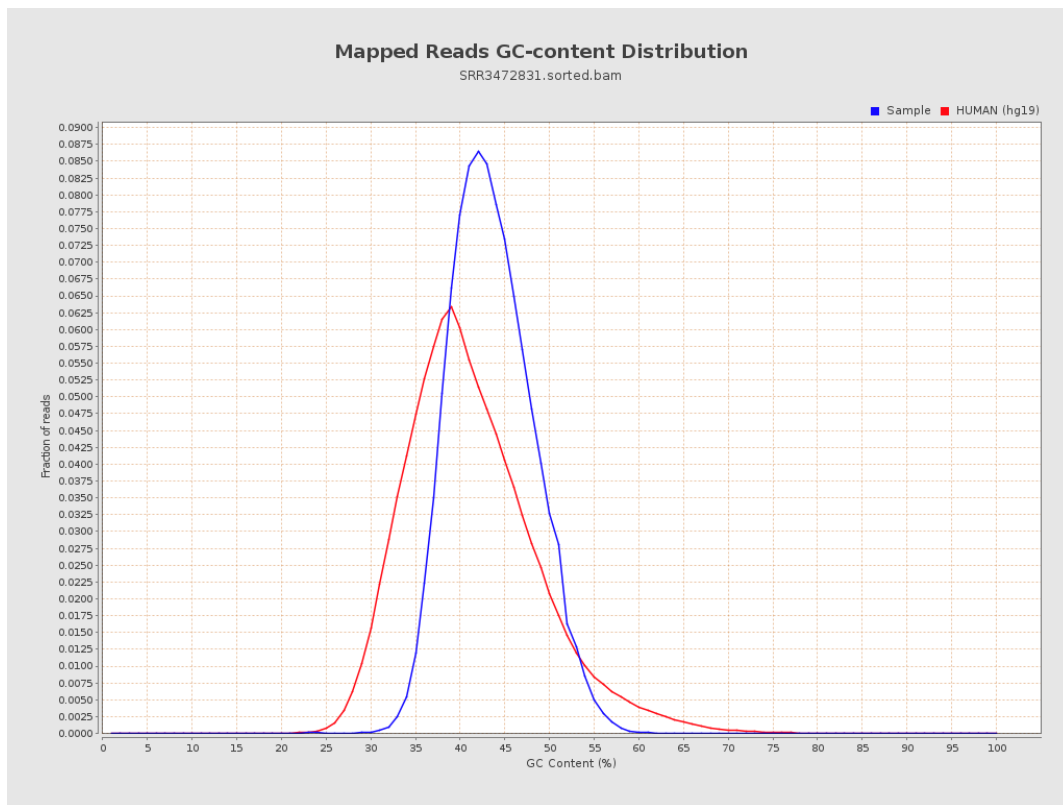
7. Results : Duplication Rate Histogram



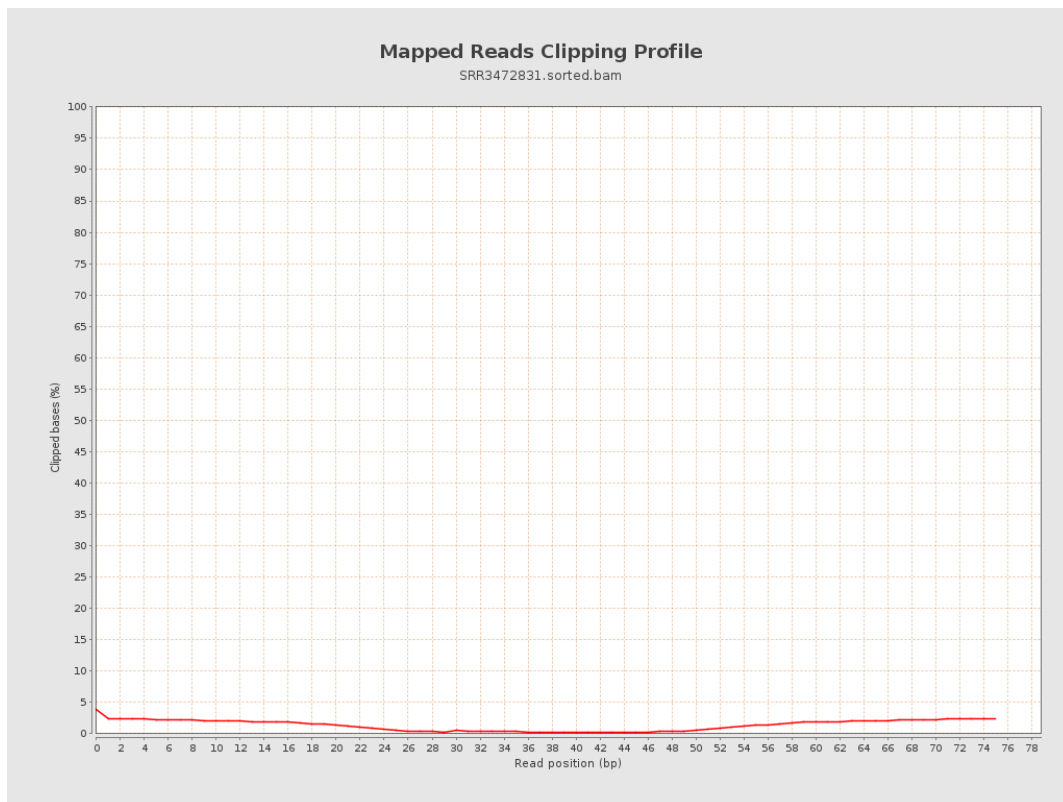
8. Results : Mapped Reads Nucleotide Content



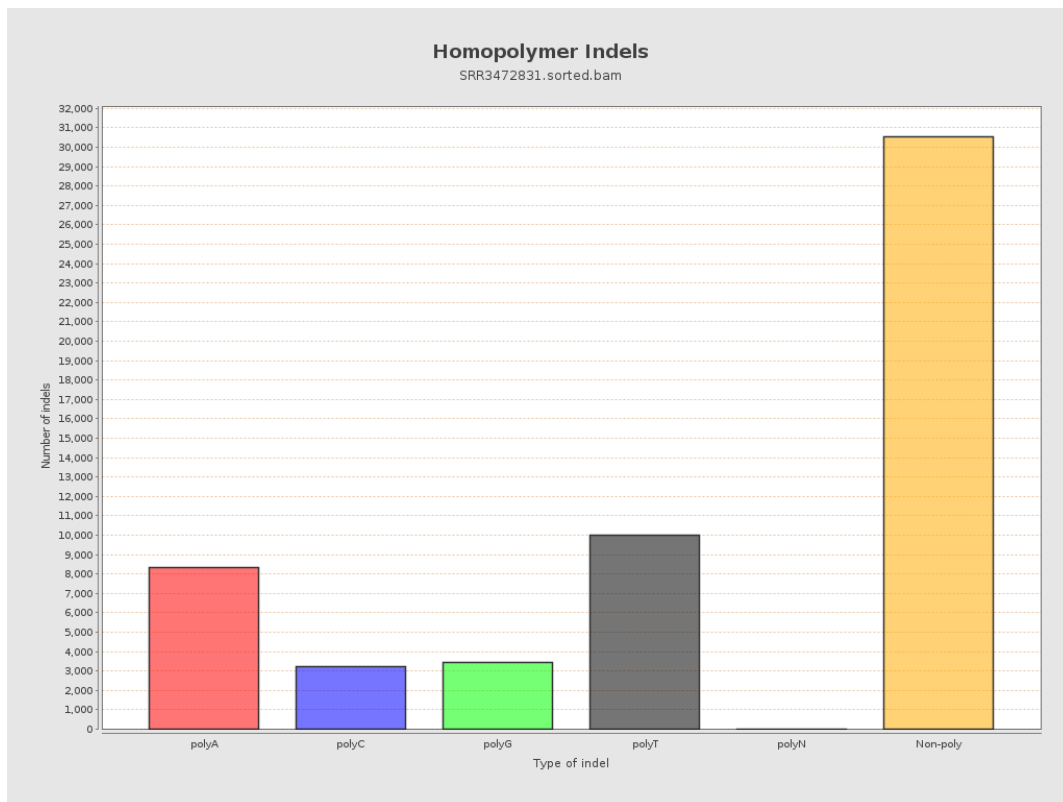
9. Results : Mapped Reads GC-content Distribution



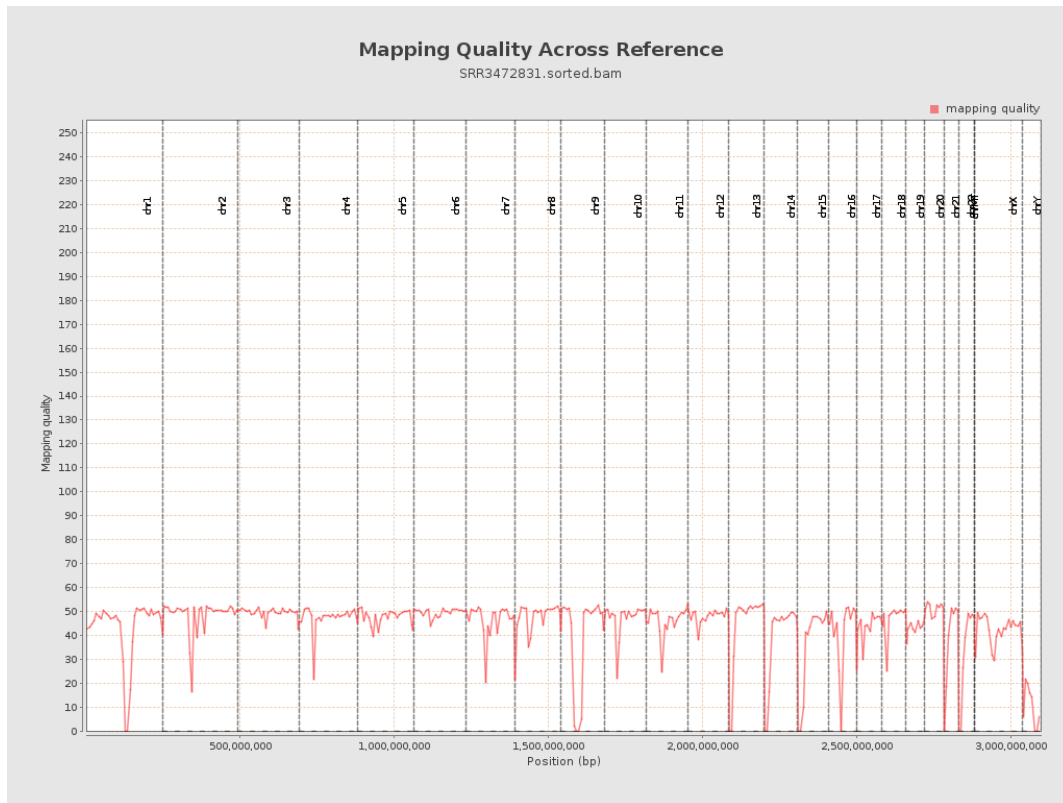
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

