

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 09:18:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472832.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_SRR3472832 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472832.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 09:18:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472832.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,643,584
Mapped reads	2,277,604 / 86.16%
Unmapped reads	365,980 / 13.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,475 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	74,141 / 2.8%
Duplication rate	2.5%
Clipped reads	1,151,060 / 43.54%

2.2. ACGT Content

Number/percentage of A's	39,944,667 / 26.91%
Number/percentage of C's	29,100,750 / 19.61%
Number/percentage of T's	44,683,208 / 30.11%
Number/percentage of G's	34,682,454 / 23.37%
Number/percentage of N's	3,420 / 0%
GC Percentage	42.98%

2.3. Coverage

Mean	0.048

Standard Deviation	0.3418
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2.4. Mapping Quality

Mean Mapping Quality	44.61
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2.5. Mismatches and indels

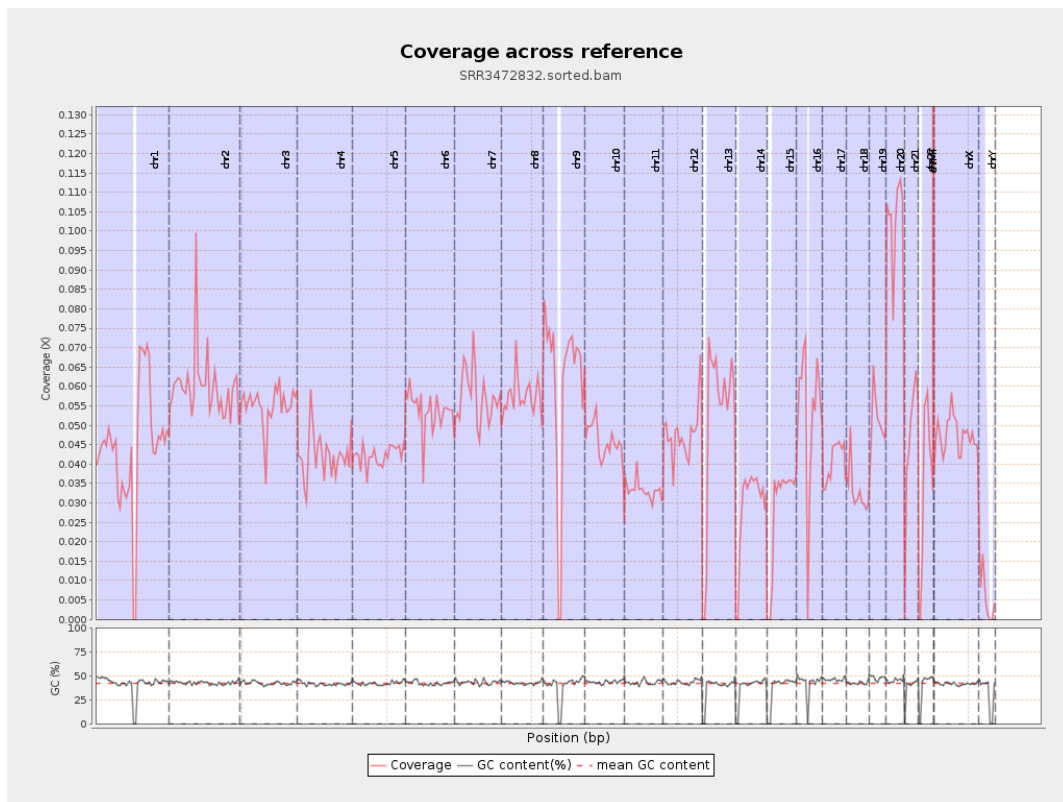
General error rate	0.88%
Mismatches	1,278,448
Insertions	11,614
Mapped reads with at least one insertion	0.5%
Deletions	34,896
Mapped reads with at least one deletion	1.52%
Homopolymer indels	45.41%

2.6. Chromosome stats

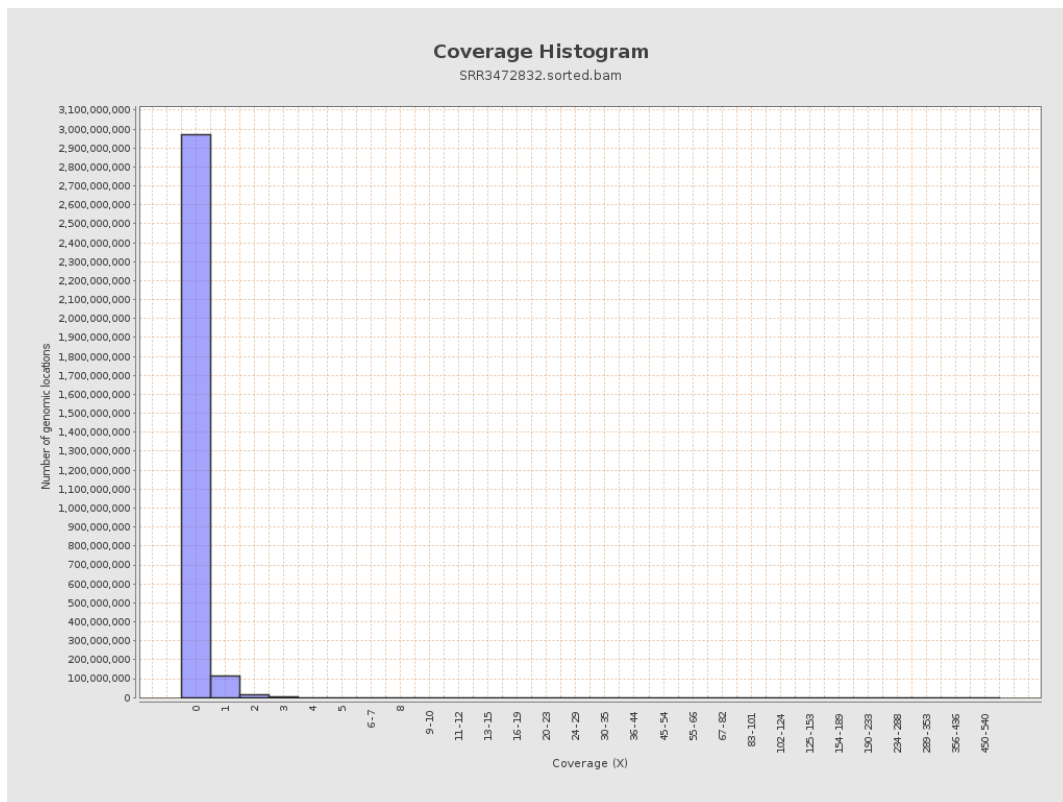
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11035504	0.0443	0.3821
chr2	243199373	14581980	0.06	0.4996
chr3	198022430	10872113	0.0549	0.2632
chr4	191154276	8035871	0.042	0.253
chr5	180915260	7631449	0.0422	0.2328
chr6	171115067	9200721	0.0538	0.2871
chr7	159138663	9142555	0.0575	0.4793

chr8	146364022	8401612	0.0574	0.3535
chr9	141213431	8544594	0.0605	0.4193
chr10	135534747	6217114	0.0459	0.2976
chr11	135006516	4471573	0.0331	0.3137
chr12	133851895	6402500	0.0478	0.2544
chr13	115169878	5957450	0.0517	0.2646
chr14	107349540	3087822	0.0288	0.2188
chr15	102531392	2892406	0.0282	0.2054
chr16	90354753	4825961	0.0534	0.2844
chr17	81195210	3318368	0.0409	0.2509
chr18	78077248	2592861	0.0332	0.6641
chr19	59128983	3041074	0.0514	0.3356
chr20	63025520	6399583	0.1015	0.3814
chr21	48129895	2257282	0.0469	0.2789
chr22	51304566	1724753	0.0336	0.2071
chrMT	16571	125556	7.5769	5.858
chrX	155270560	7356279	0.0474	0.2777
chrY	59373566	359122	0.006	0.1291

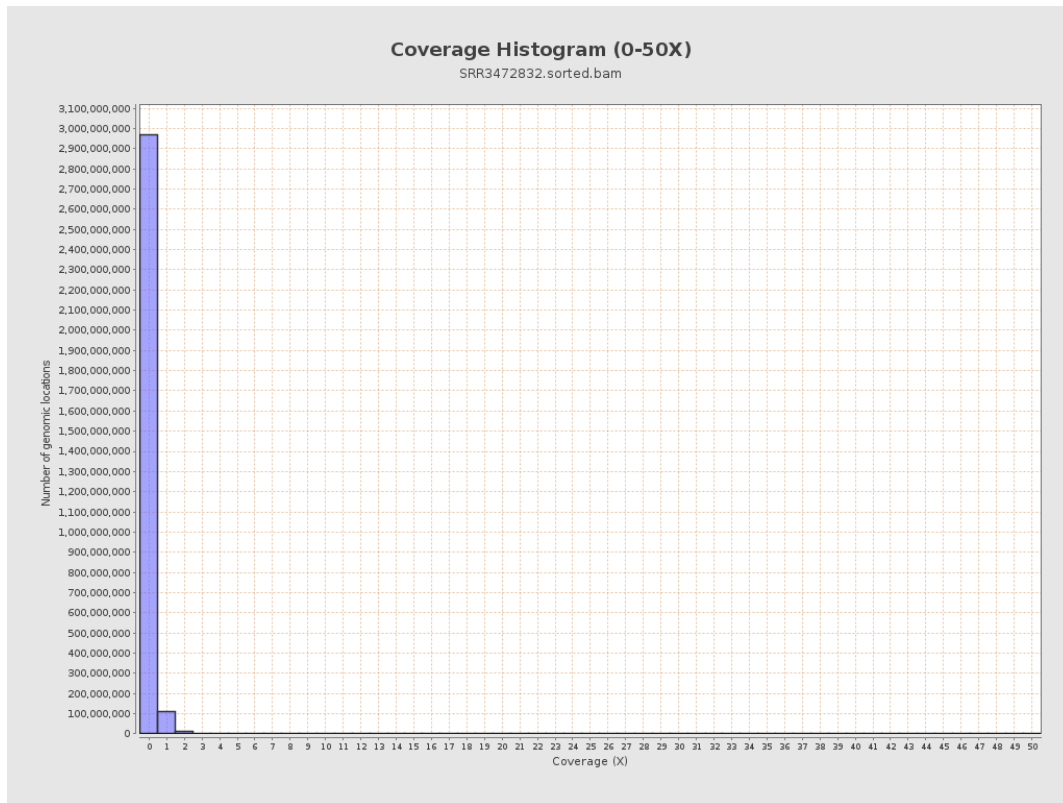
3. Results : Coverage across reference



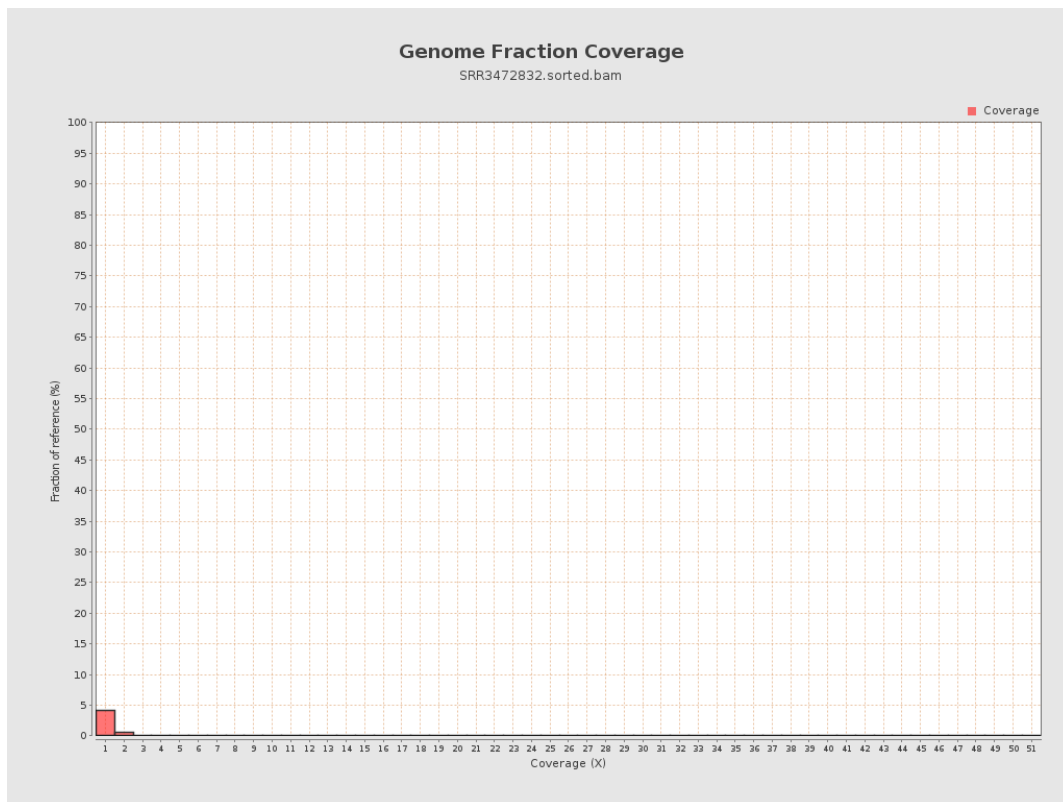
4. Results : Coverage Histogram



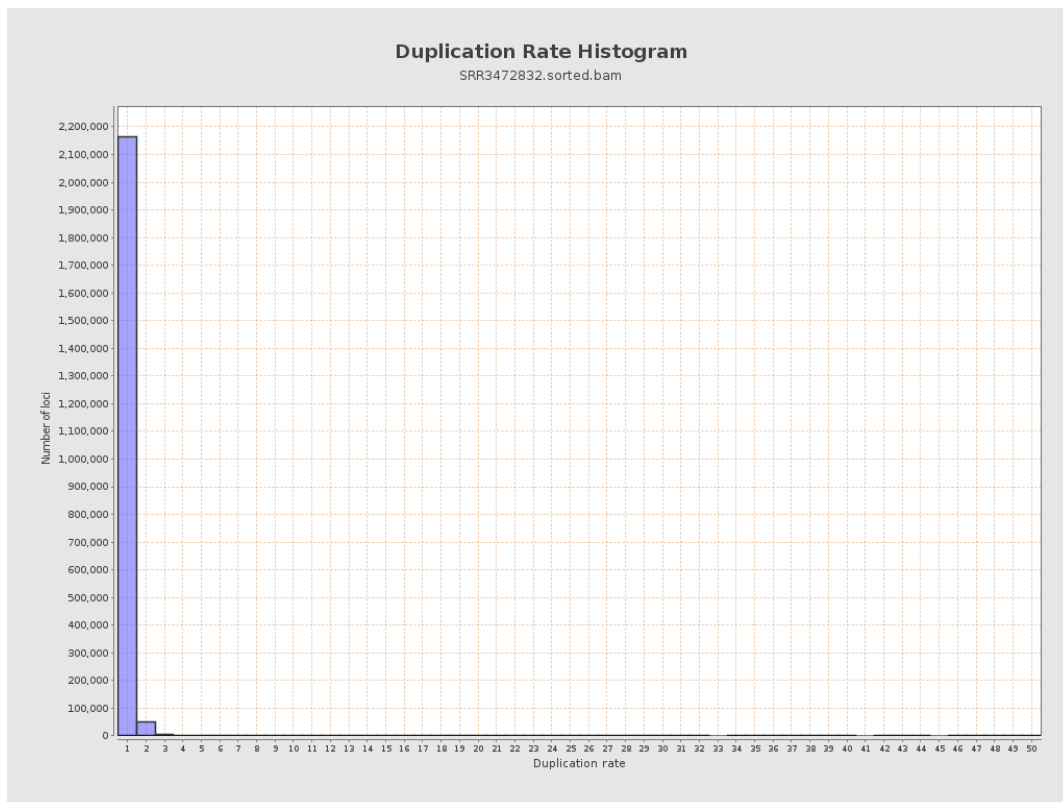
5. Results : Coverage Histogram (0-50X)



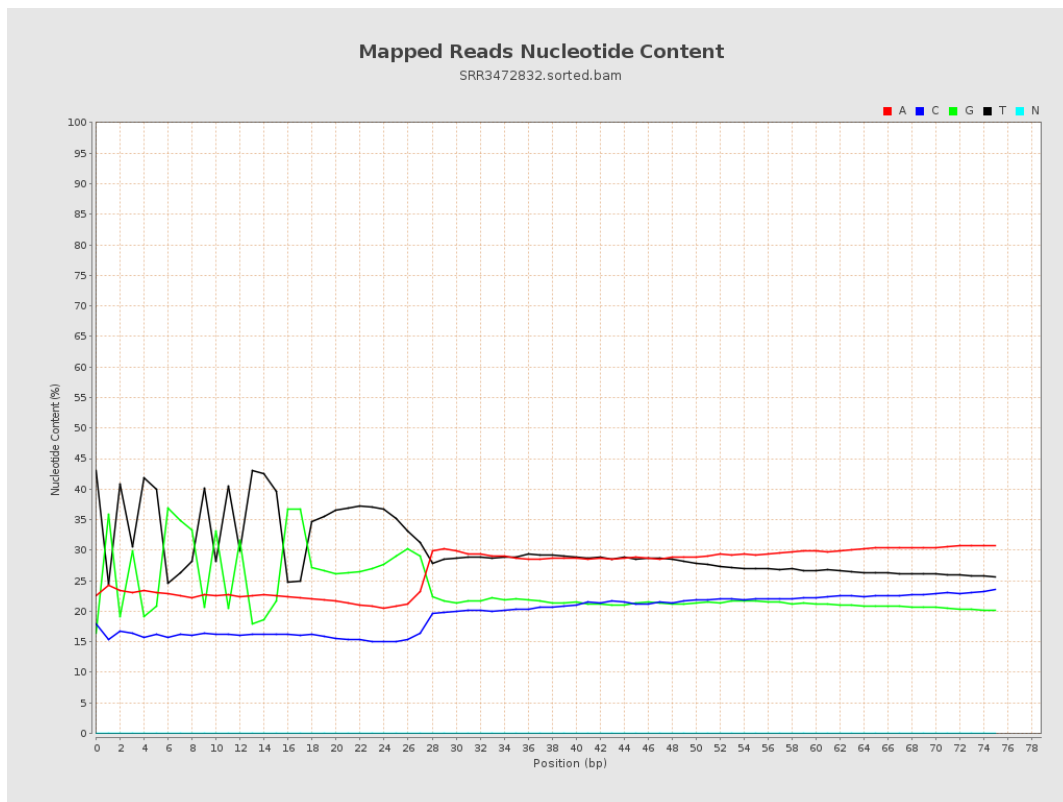
6. Results : Genome Fraction Coverage



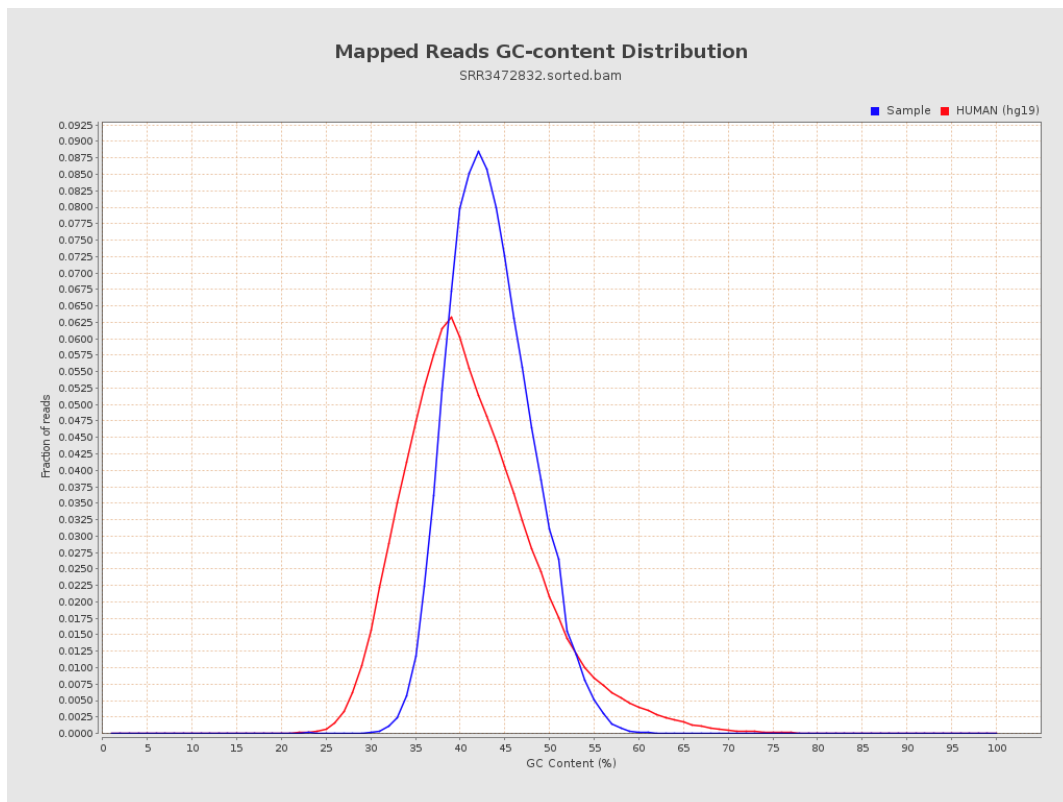
7. Results : Duplication Rate Histogram



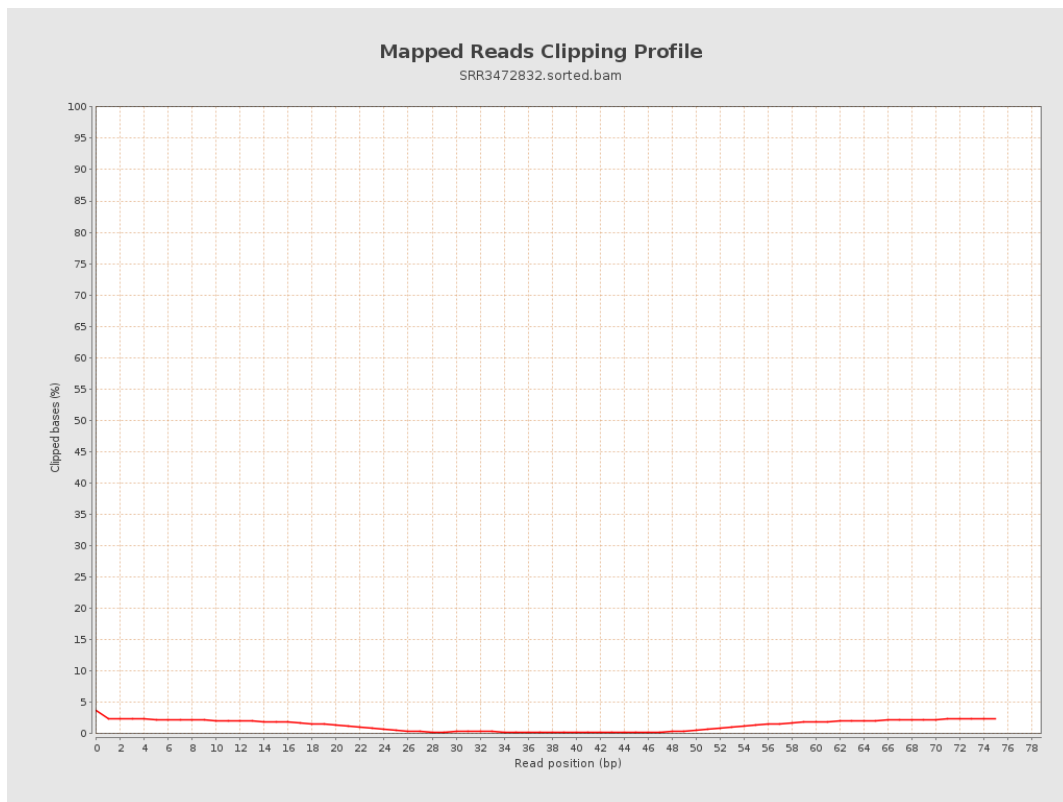
8. Results : Mapped Reads Nucleotide Content



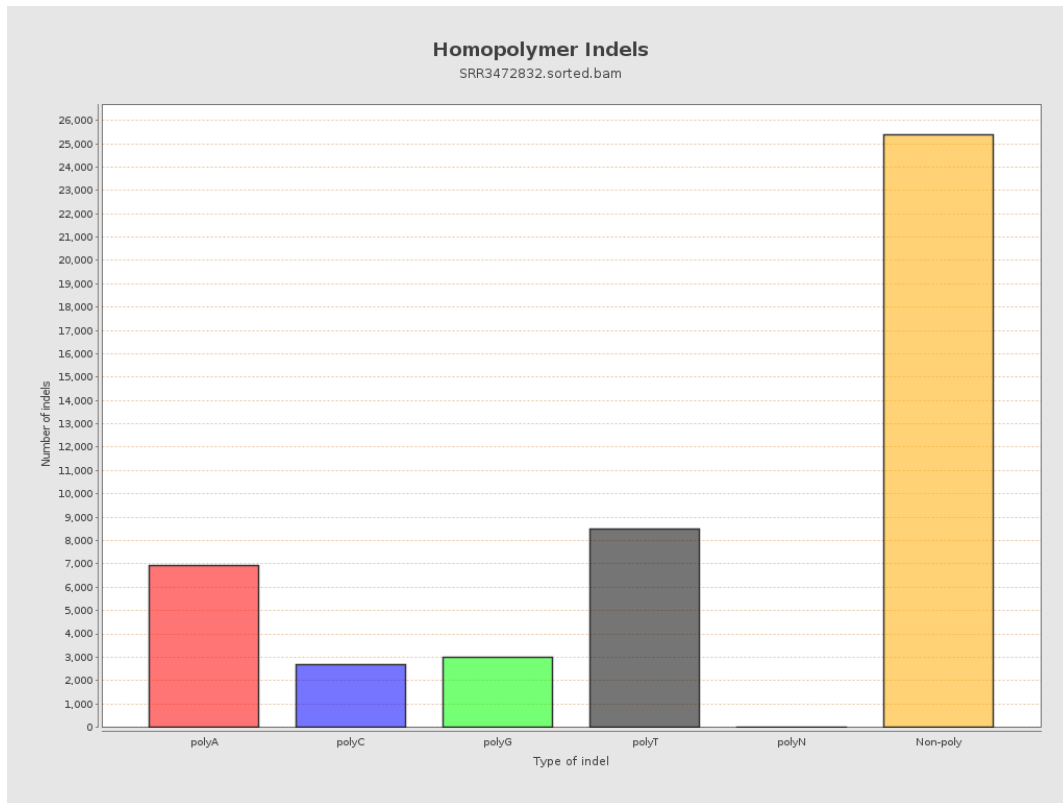
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

