

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 19:04:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081107.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_SRR3081107 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081107.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 19:04:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081107.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,325,418
Mapped reads	2,113,157 / 90.87%
Unmapped reads	212,261 / 9.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,330 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	90,594 / 3.9%
Duplication rate	3.41%
Clipped reads	913,446 / 39.28%

2.2. ACGT Content

Number/percentage of A's	39,429,910 / 27.72%
Number/percentage of C's	26,928,496 / 18.93%
Number/percentage of T's	44,269,871 / 31.12%
Number/percentage of G's	31,637,544 / 22.24%
Number/percentage of N's	1,556 / 0%
GC Percentage	41.17%

2.3. Coverage

Mean	0.046

Standard Deviation	0.3617
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2.4. Mapping Quality

Mean Mapping Quality	45.55
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2.5. Mismatches and indels

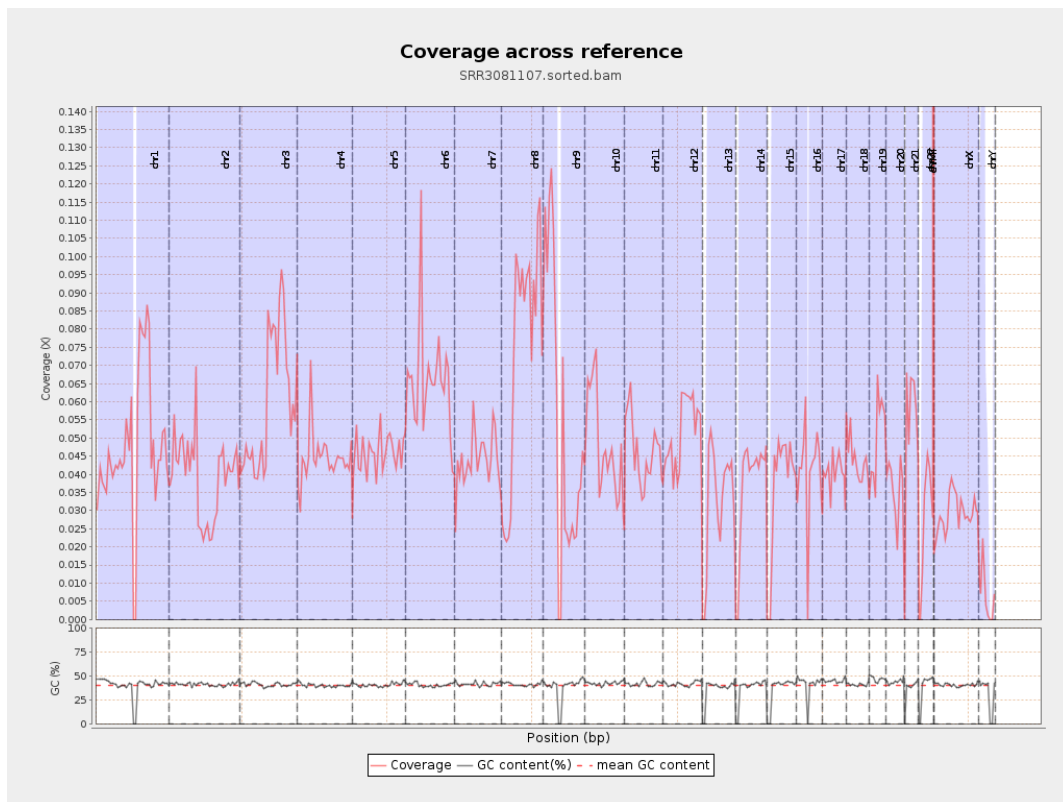
General error rate	0.9%
Mismatches	1,264,971
Insertions	11,407
Mapped reads with at least one insertion	0.53%
Deletions	31,212
Mapped reads with at least one deletion	1.46%
Homopolymer indels	46.68%

2.6. Chromosome stats

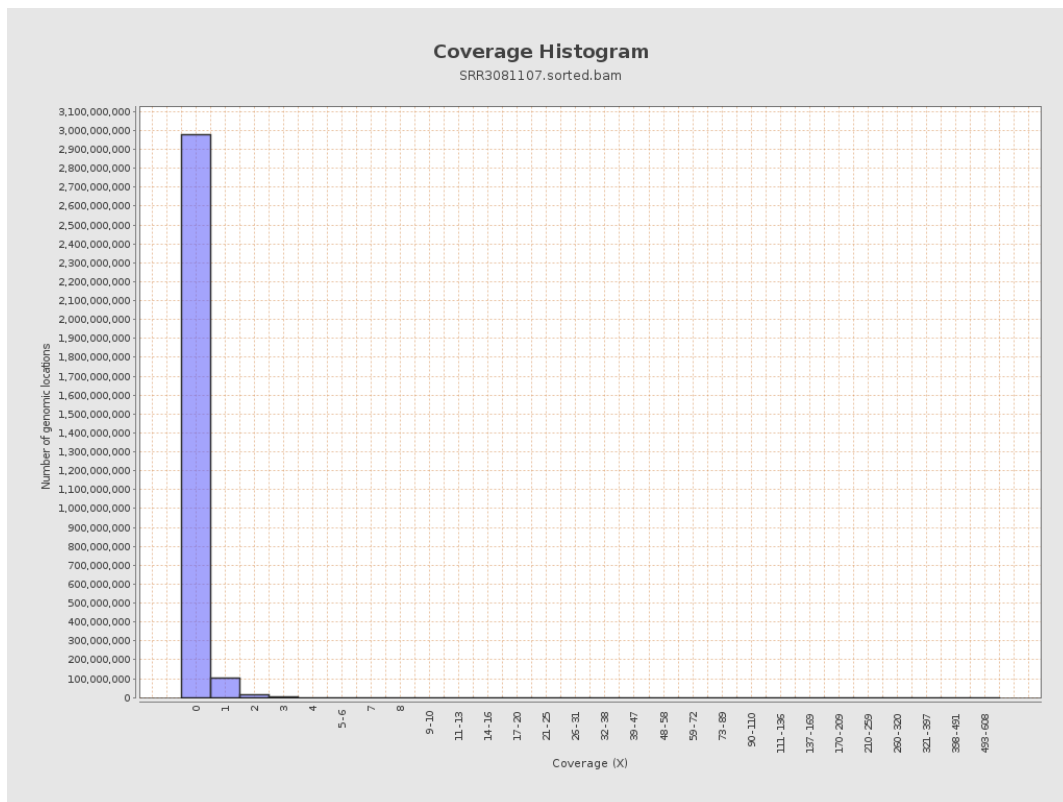
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11773480	0.0472	0.5128
chr2	243199373	9607809	0.0395	0.4283
chr3	198022430	11764169	0.0594	0.2799
chr4	191154276	8478635	0.0444	0.2637
chr5	180915260	8307423	0.0459	0.2467
chr6	171115067	11230410	0.0656	0.4322
chr7	159138663	7077902	0.0445	0.3214

chr8	146364022	10818952	0.0739	0.4288
chr9	141213431	7519382	0.0532	0.4226
chr10	135534747	6571257	0.0485	0.362
chr11	135006516	6204653	0.046	0.3079
chr12	133851895	6858870	0.0512	0.2731
chr13	115169878	3697490	0.0321	0.2051
chr14	107349540	3940666	0.0367	0.2811
chr15	102531392	3747952	0.0366	0.2185
chr16	90354753	3680227	0.0407	0.2924
chr17	81195210	3270000	0.0403	0.2359
chr18	78077248	3440327	0.0441	0.7631
chr19	59128983	2957333	0.05	0.4389
chr20	63025520	2245910	0.0356	0.2331
chr21	48129895	2590469	0.0538	0.3121
chr22	51304566	1354911	0.0264	0.1847
chrMT	16571	306438	18.4924	9.0917
chrX	155270560	4503981	0.029	0.2235
chrY	59373566	369556	0.0062	0.1599

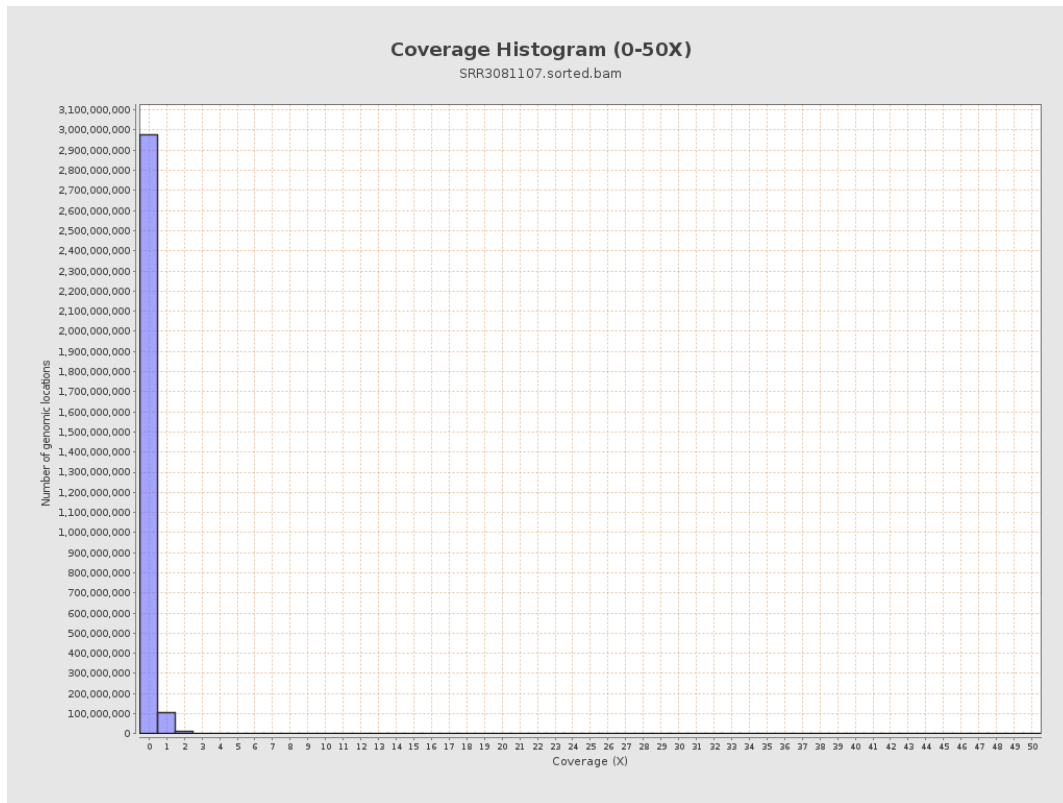
3. Results : Coverage across reference



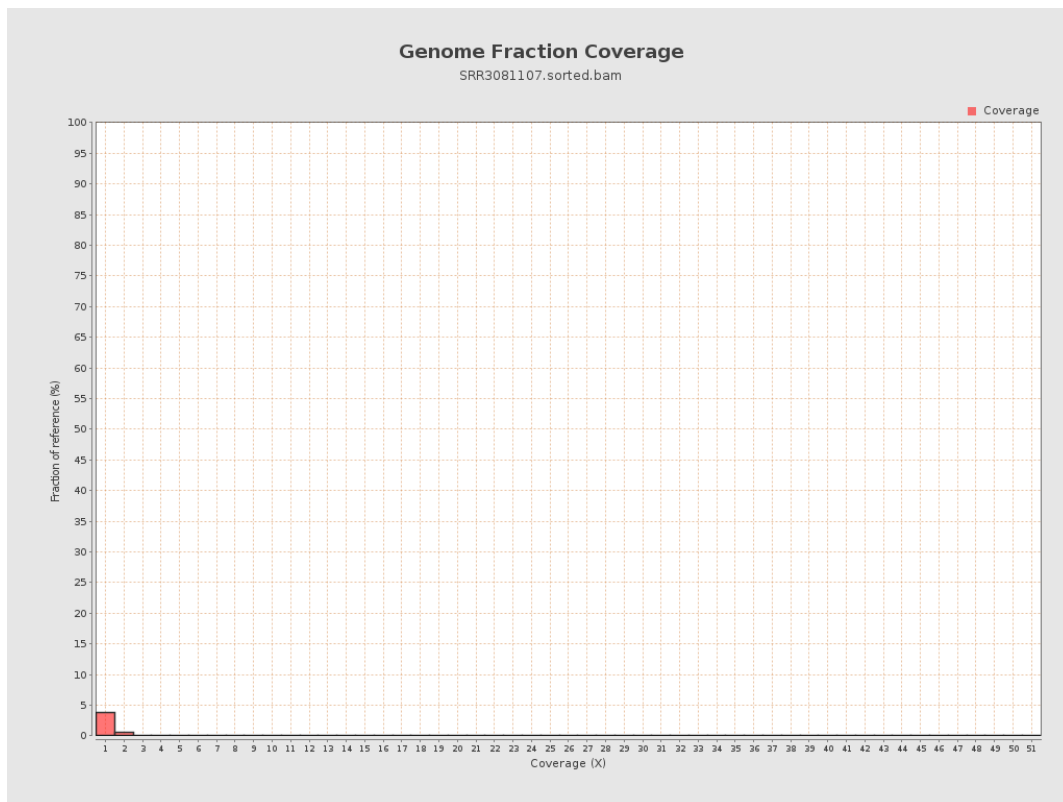
4. Results : Coverage Histogram



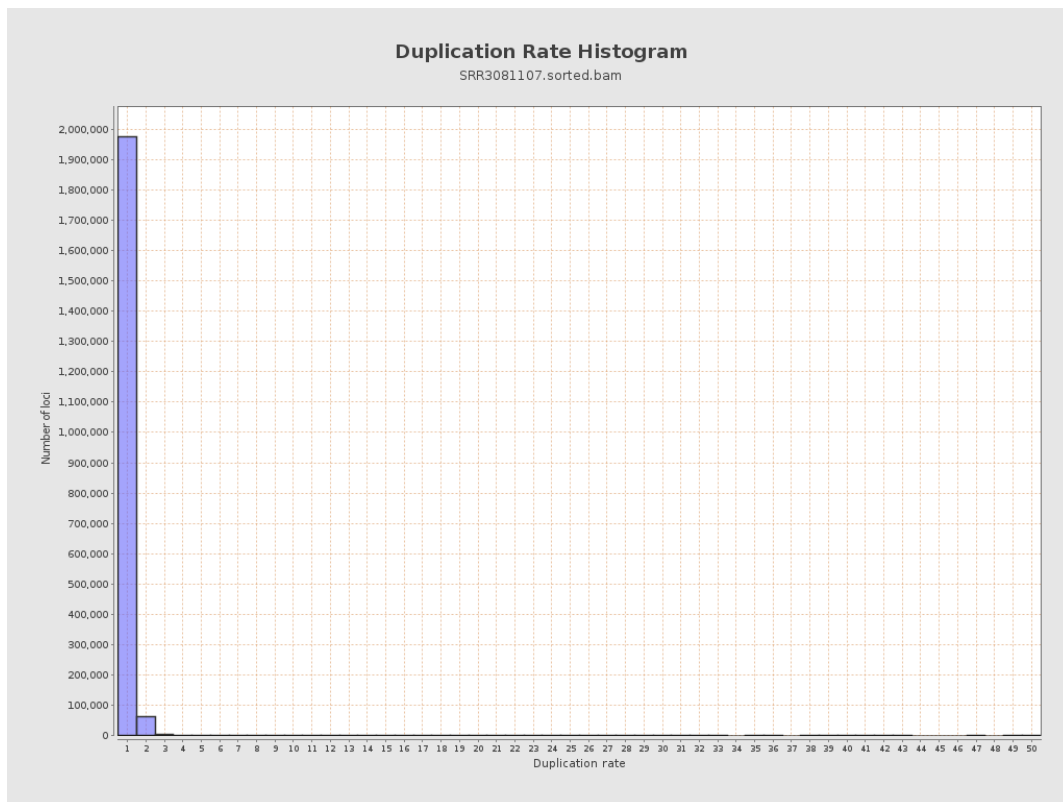
5. Results : Coverage Histogram (0-50X)



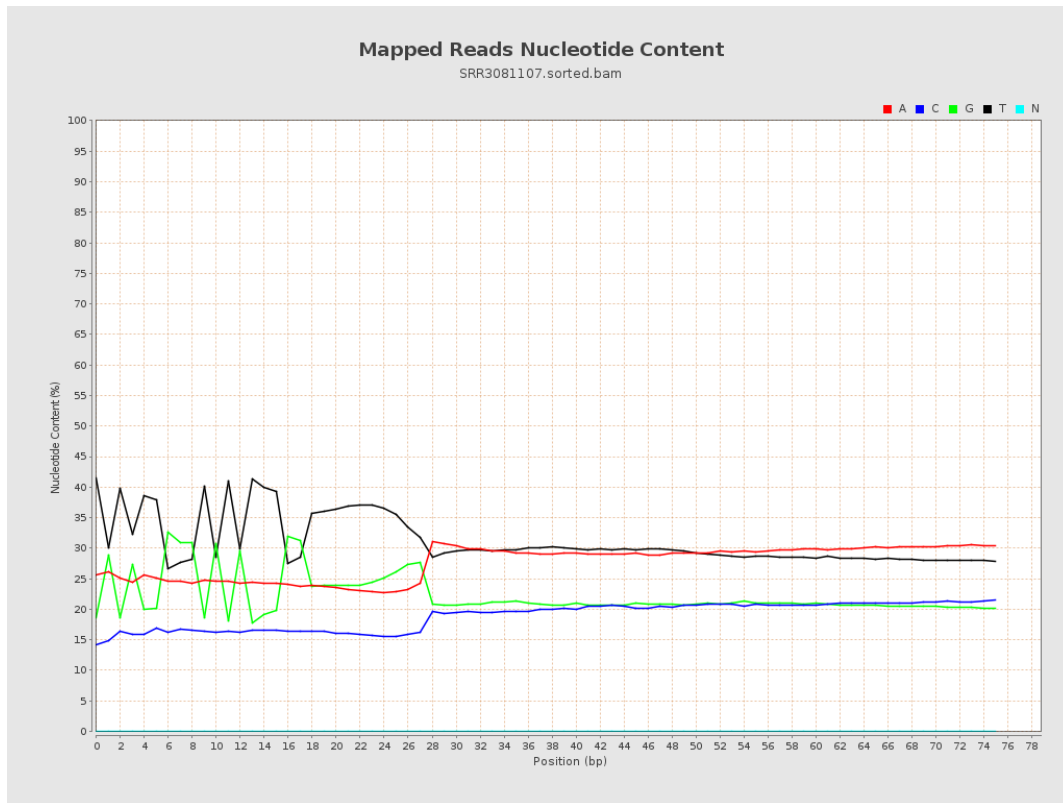
6. Results : Genome Fraction Coverage



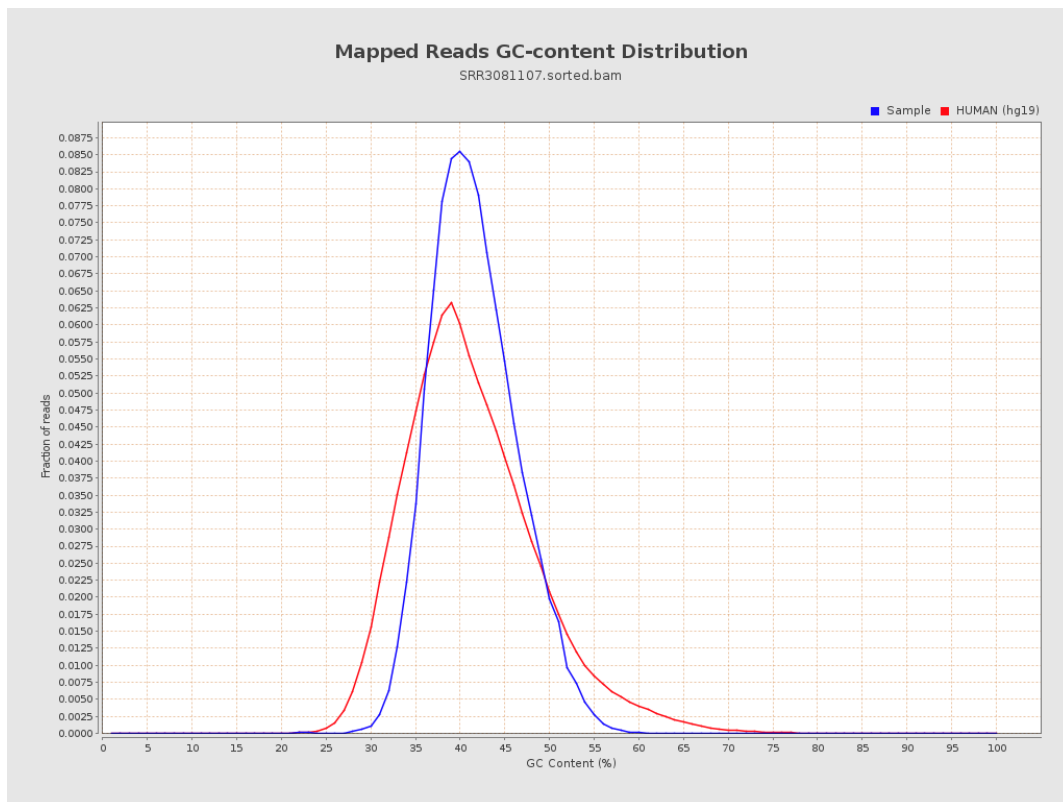
7. Results : Duplication Rate Histogram



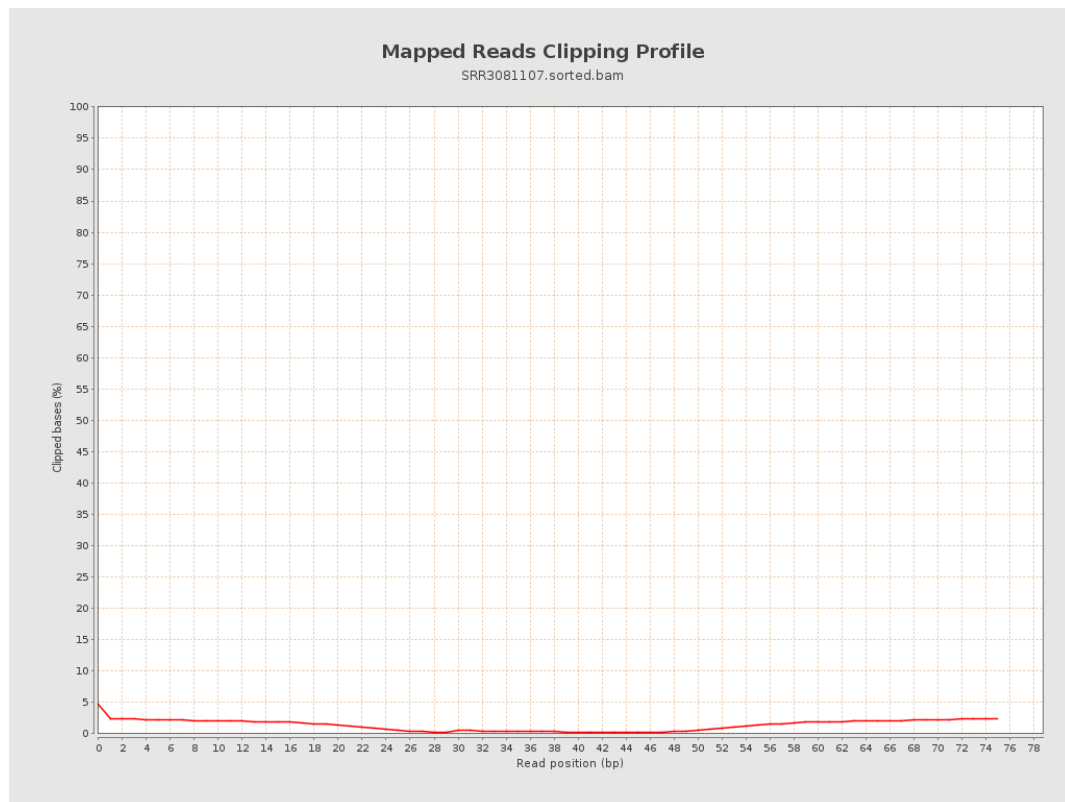
8. Results : Mapped Reads Nucleotide Content



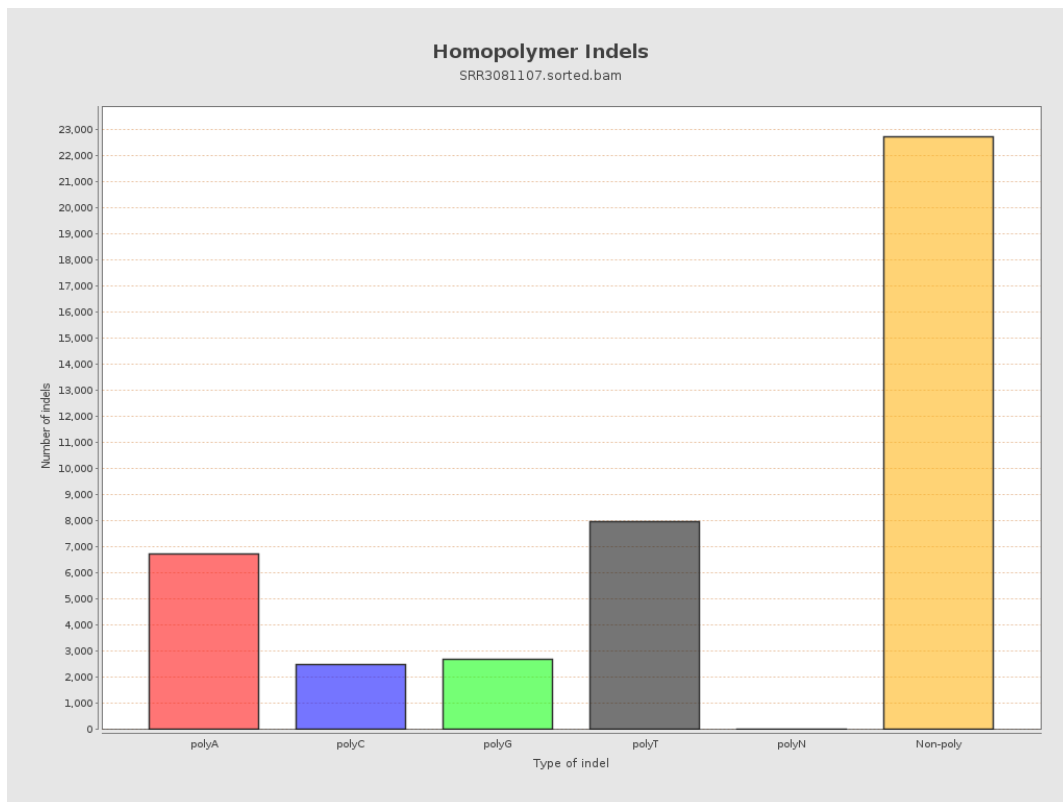
9. Results : Mapped Reads GC-content Distribution



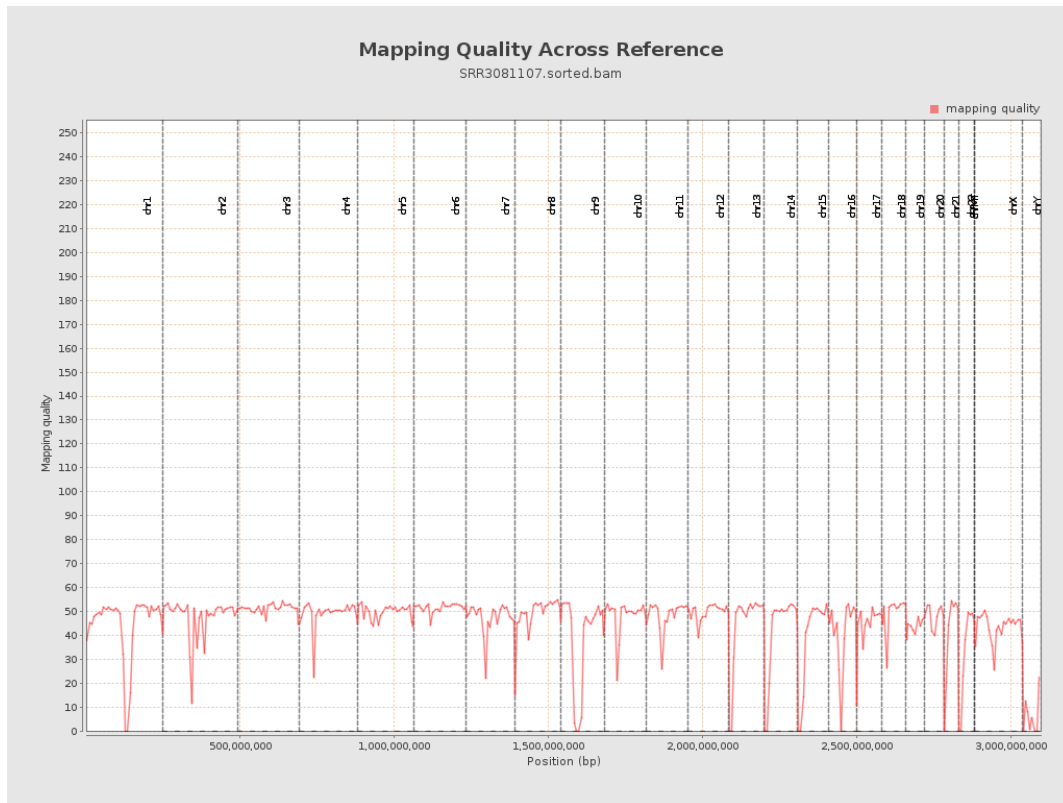
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

