

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 11:56:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708537.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_SRR1708537 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708537.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 11:56:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708537.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,326,306
Mapped reads	20,834,384 / 97.69%
Unmapped reads	491,922 / 2.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	541 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	221,055 / 1.04%
Duplication rate	1.05%
Clipped reads	285,053 / 1.34%

2.2. ACGT Content

Number/percentage of A's	320,356,001 / 30.83%
Number/percentage of C's	197,081,787 / 18.97%
Number/percentage of T's	320,639,035 / 30.86%
Number/percentage of G's	200,938,443 / 19.34%
Number/percentage of N's	36,680 / 0%
GC Percentage	38.31%

2.3. Coverage

Mean	0.3357

Standard Deviation	0.6678
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2.4. Mapping Quality

Mean Mapping Quality	46.66
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2.5. Mismatches and indels

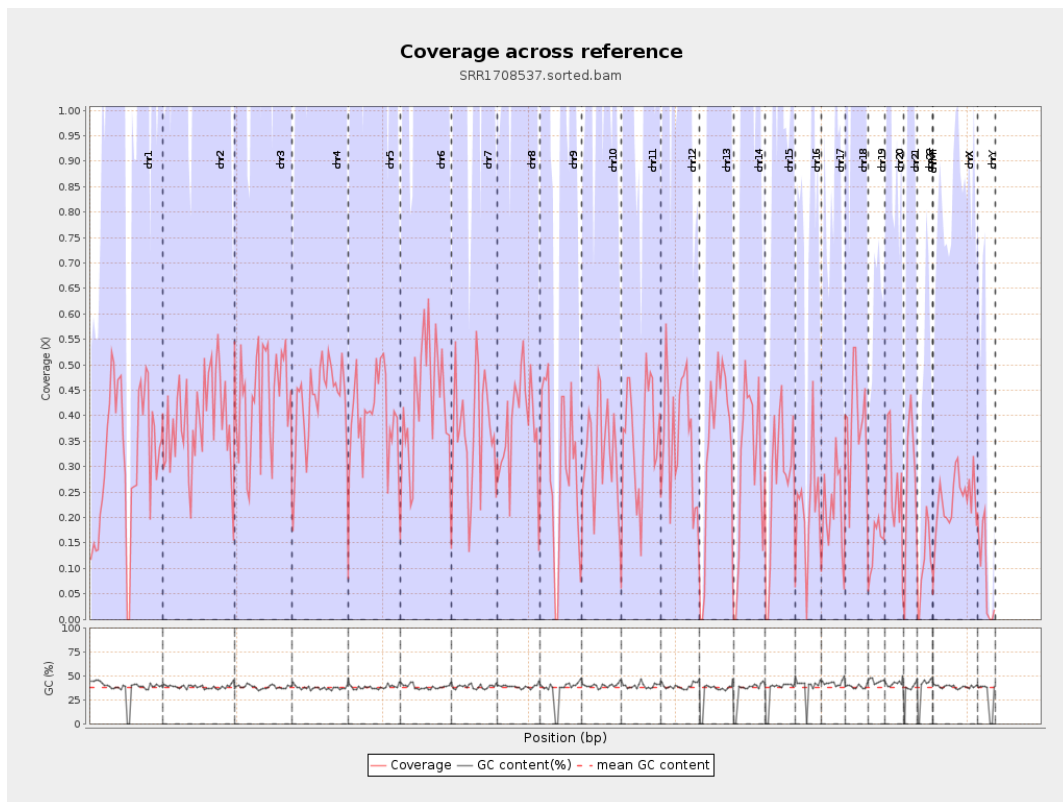
General error rate	0.2%
Mismatches	2,033,004
Insertions	61,038
Mapped reads with at least one insertion	0.29%
Deletions	55,180
Mapped reads with at least one deletion	0.26%
Homopolymer indels	49.37%

2.6. Chromosome stats

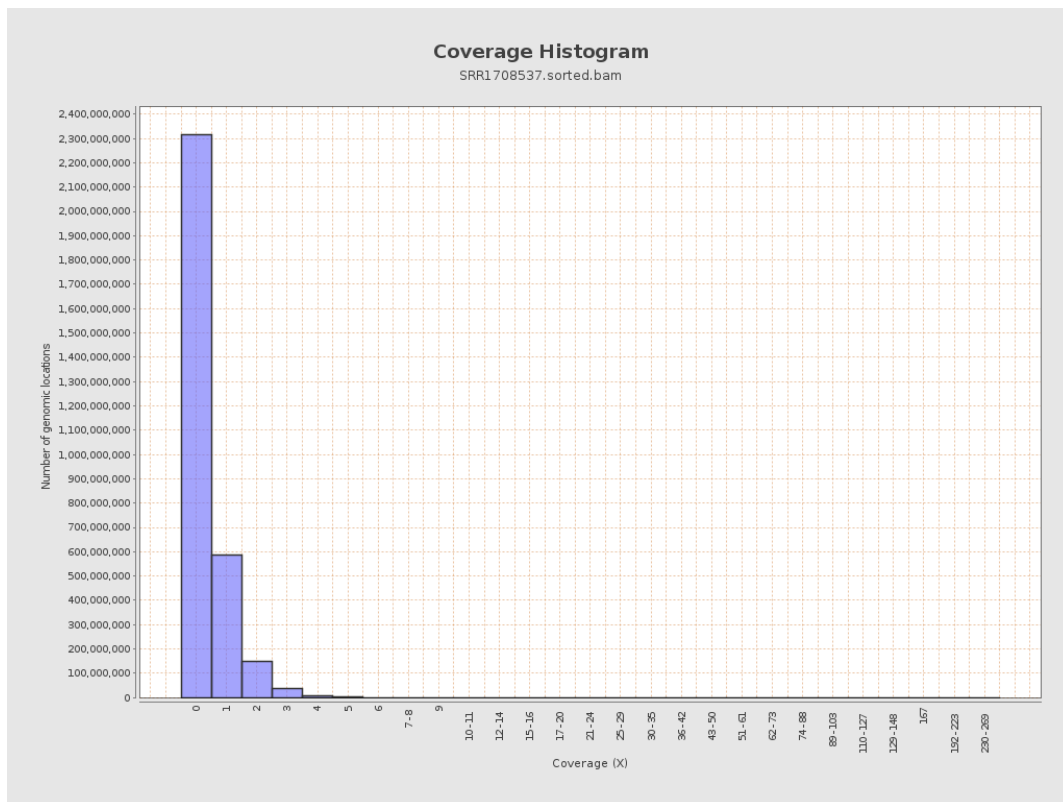
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	78980407	0.3169	0.6617
chr2	243199373	94002355	0.3865	0.7046
chr3	198022430	86697320	0.4378	0.7543
chr4	191154276	82147542	0.4297	0.7389
chr5	180915260	71467510	0.395	0.7103
chr6	171115067	73983618	0.4324	0.752
chr7	159138663	58202123	0.3657	0.6933

chr8	146364022	56144899	0.3836	0.6984
chr9	141213431	42788366	0.303	0.6427
chr10	135534747	44615930	0.3292	0.6478
chr11	135006516	48706874	0.3608	0.6957
chr12	133851895	47771224	0.3569	0.6864
chr13	115169878	39603886	0.3439	0.6754
chr14	107349540	32392229	0.3017	0.6367
chr15	102531392	27804468	0.2712	0.6089
chr16	90354753	19545032	0.2163	0.5326
chr17	81195210	17798950	0.2192	0.5348
chr18	78077248	30391572	0.3893	0.7064
chr19	59128983	8953325	0.1514	0.4374
chr20	63025520	16916780	0.2684	0.5962
chr21	48129895	12939838	0.2689	0.615
chr22	51304566	5787944	0.1128	0.3835
chrMT	16571	797	0.0481	0.229
chrX	155270560	36416839	0.2345	0.5365
chrY	59373566	5083080	0.0856	0.3403

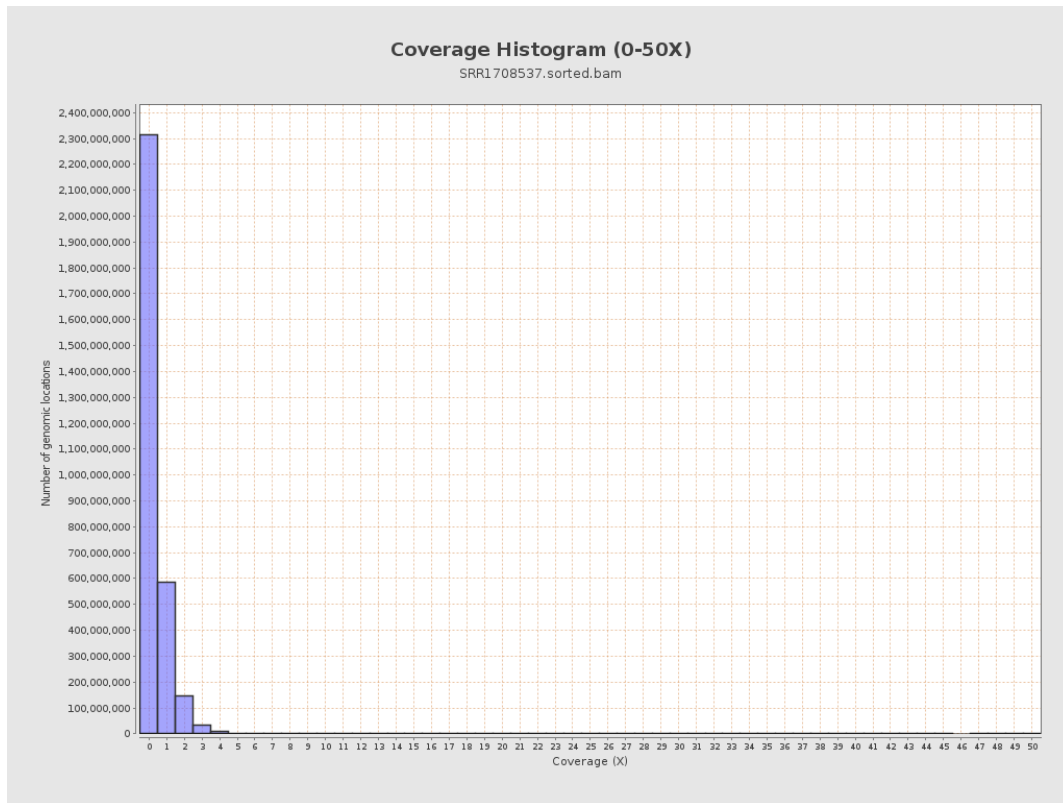
3. Results : Coverage across reference



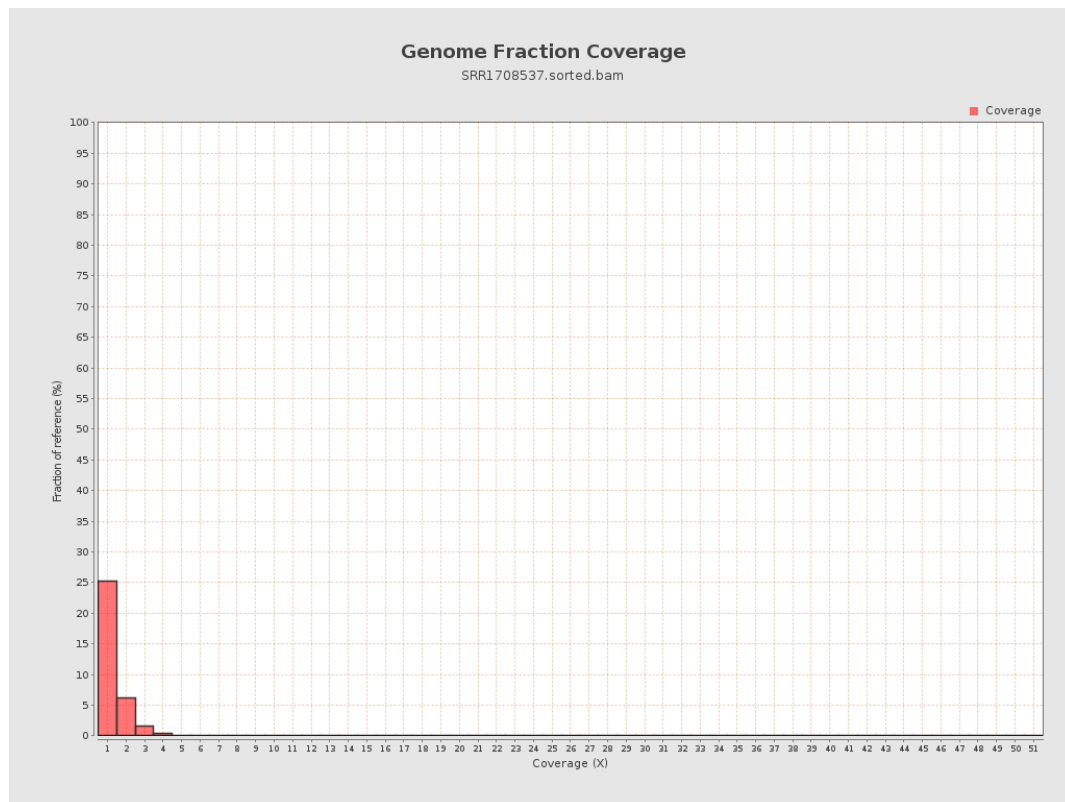
4. Results : Coverage Histogram



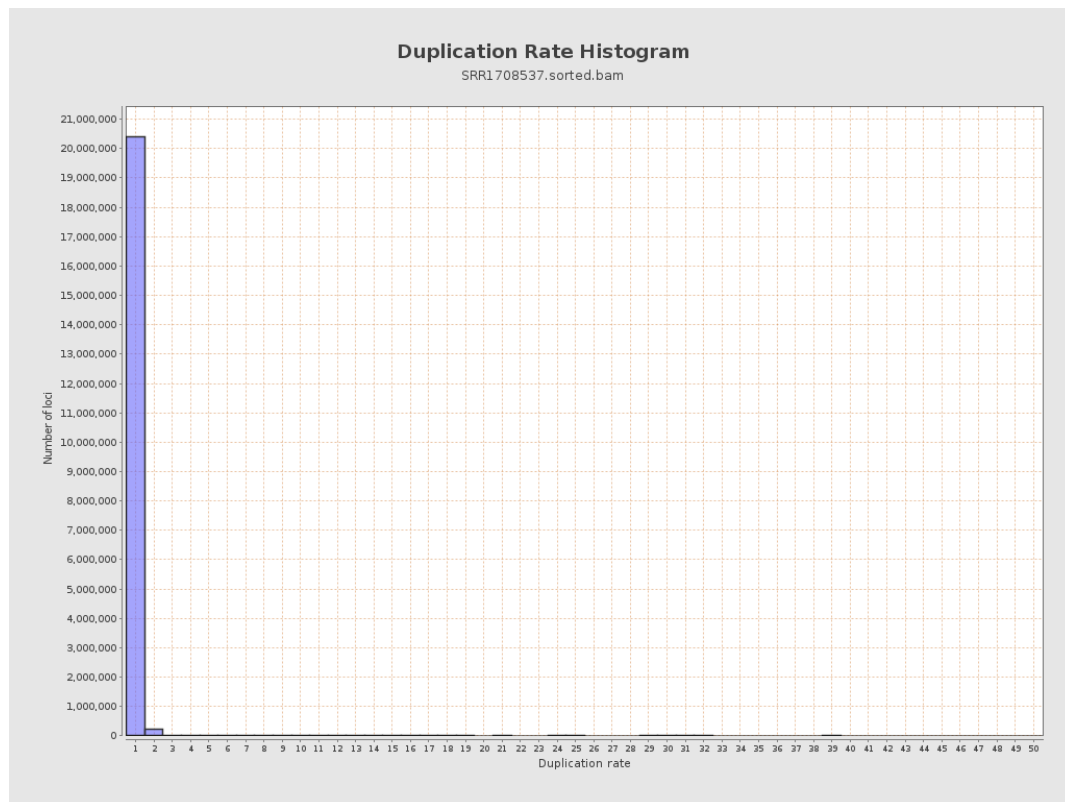
5. Results : Coverage Histogram (0-50X)



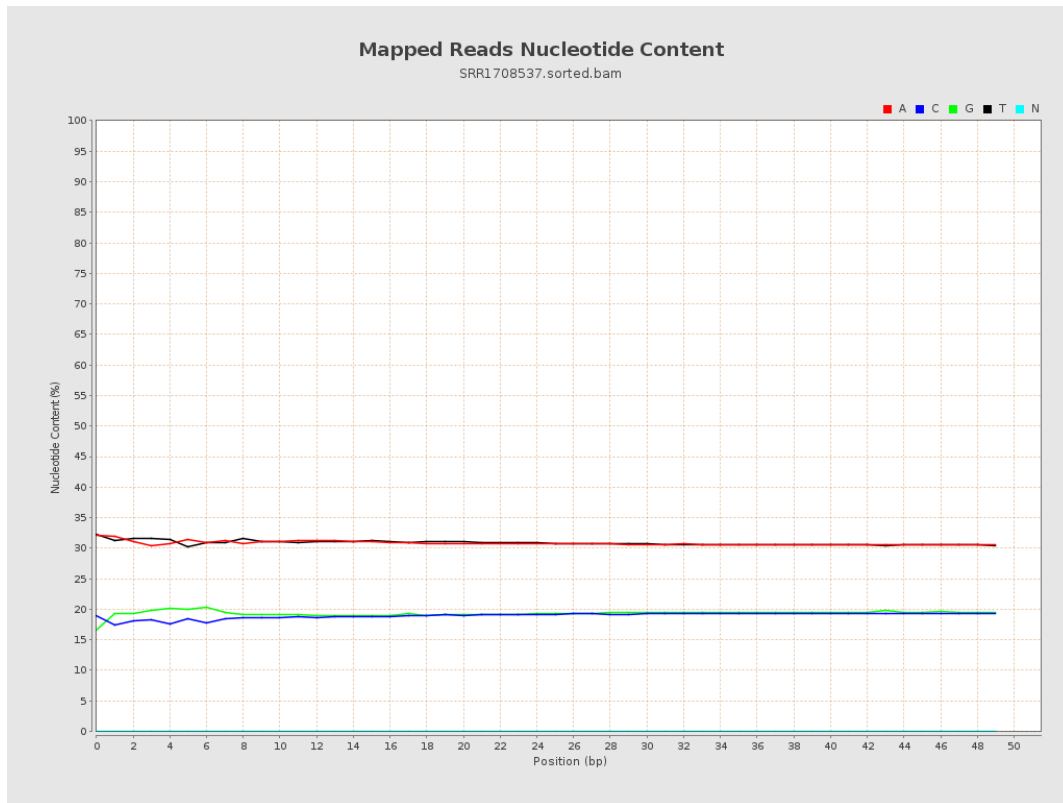
6. Results : Genome Fraction Coverage



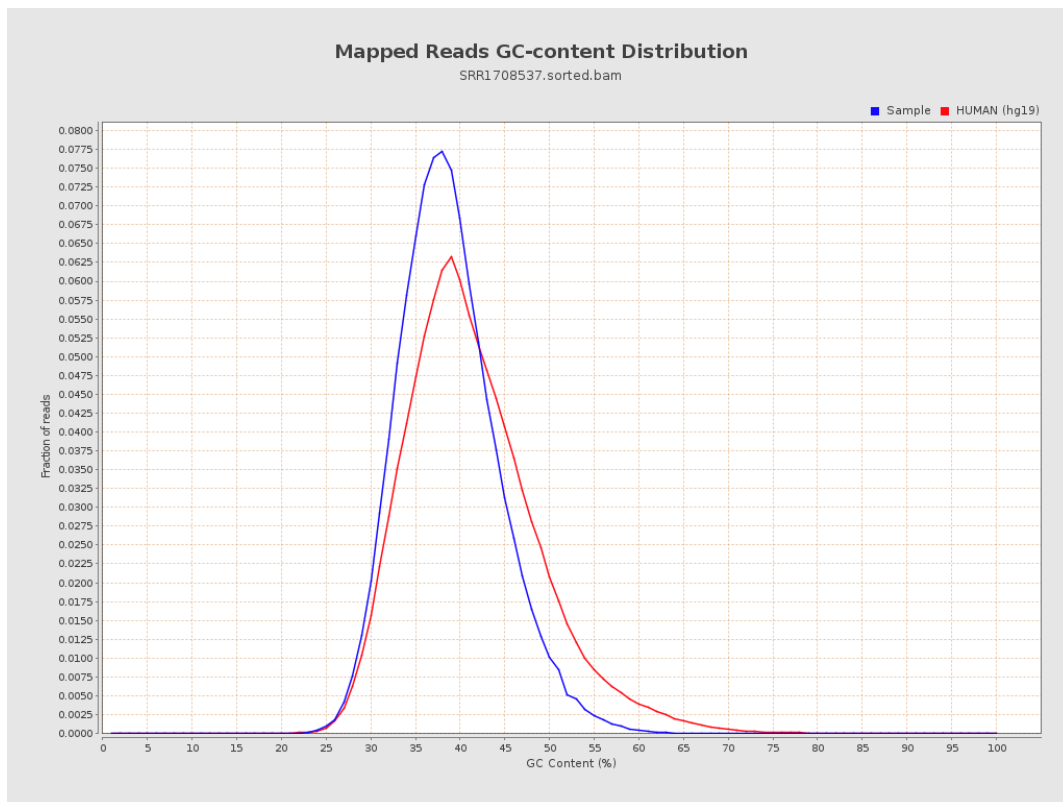
7. Results : Duplication Rate Histogram



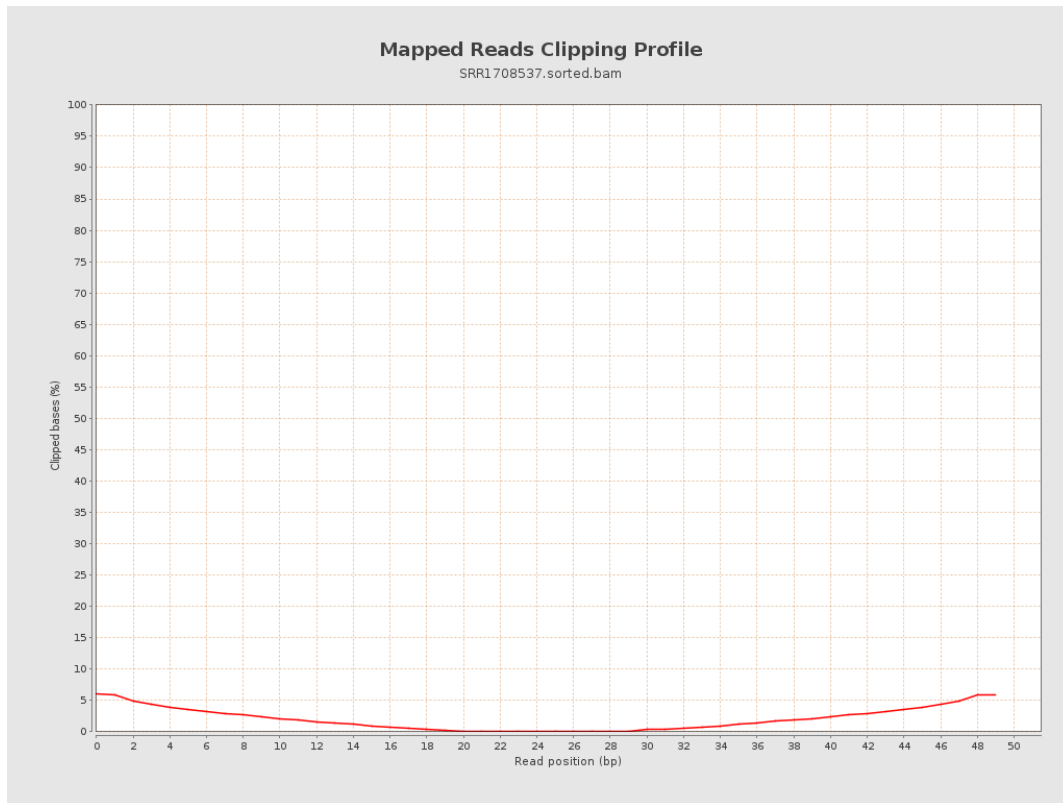
8. Results : Mapped Reads Nucleotide Content



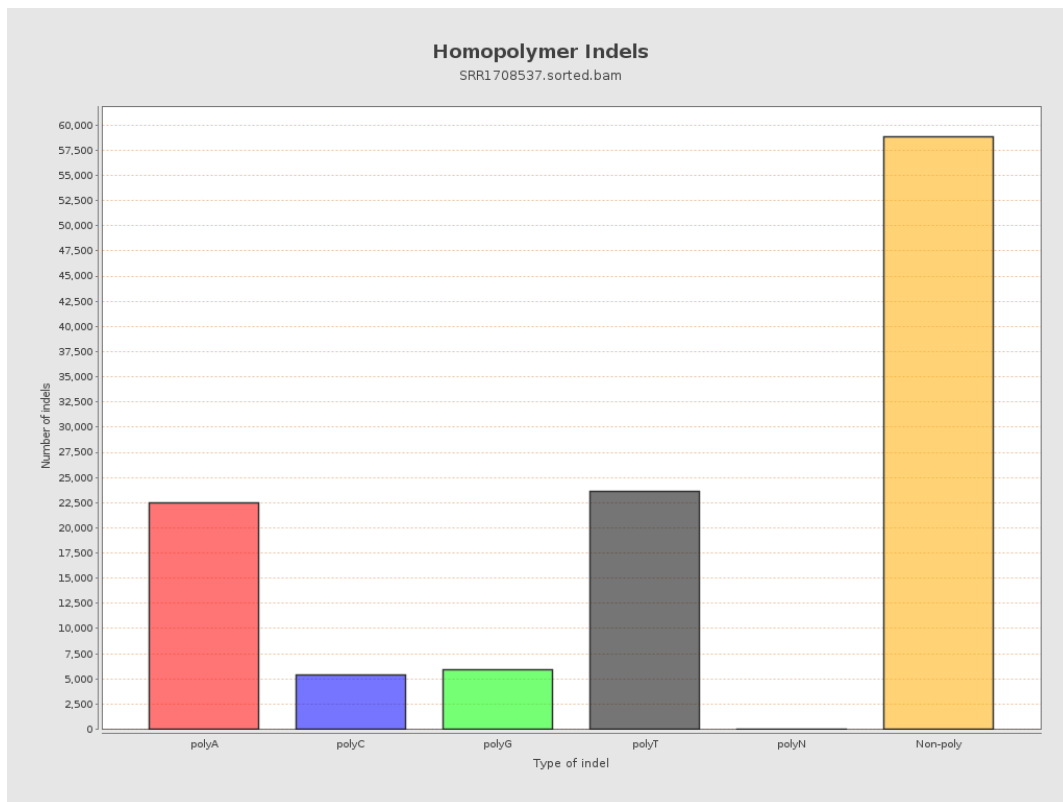
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

