

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 23:09:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708559.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_SRR1708559 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708559.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 23:09:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708559.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,454,817
Mapped reads	3,651,973 / 81.98%
Unmapped reads	802,844 / 18.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	83 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	17,548 / 0.39%
Duplication rate	0.48%
Clipped reads	49,982 / 1.12%

2.2. ACGT Content

Number/percentage of A's	56,506,622 / 31.03%
Number/percentage of C's	34,458,615 / 18.92%
Number/percentage of T's	56,387,656 / 30.96%
Number/percentage of G's	34,742,492 / 19.08%
Number/percentage of N's	7,517 / 0%
GC Percentage	38%

2.3. Coverage

Mean	0.0588

Standard Deviation	0.2511
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2.4. Mapping Quality

Mean Mapping Quality	46.34
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2.5. Mismatches and indels

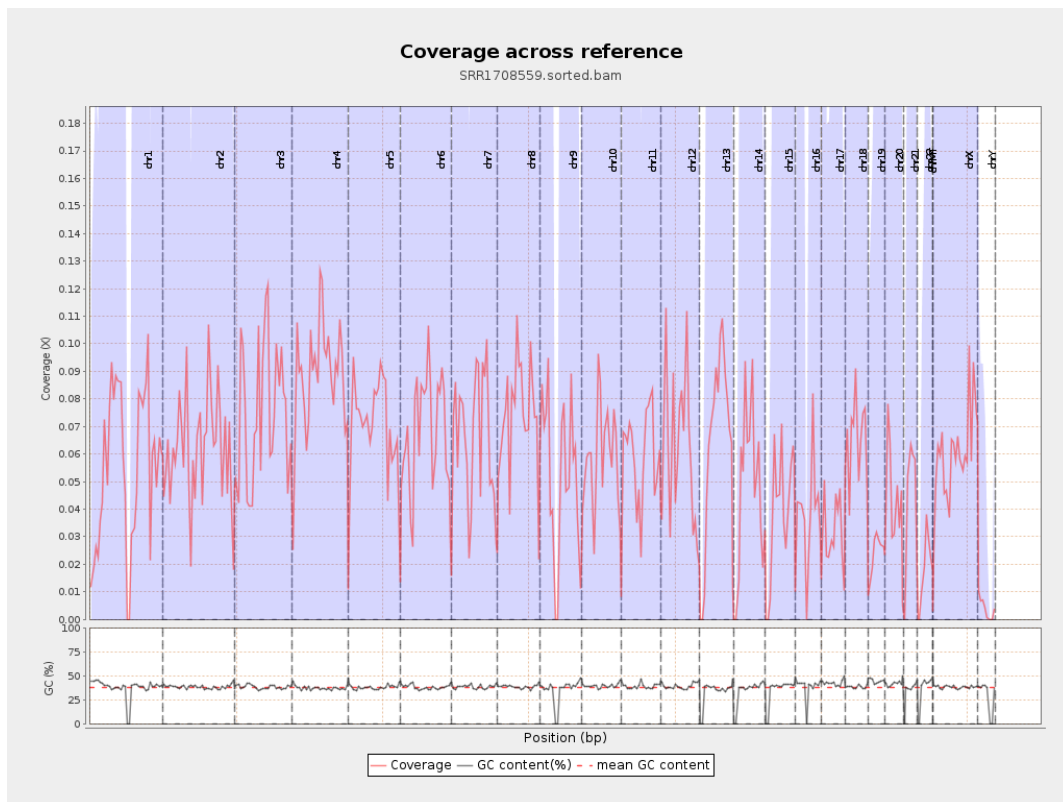
General error rate	0.17%
Mismatches	288,041
Insertions	12,387
Mapped reads with at least one insertion	0.34%
Deletions	9,632
Mapped reads with at least one deletion	0.26%
Homopolymer indels	47.4%

2.6. Chromosome stats

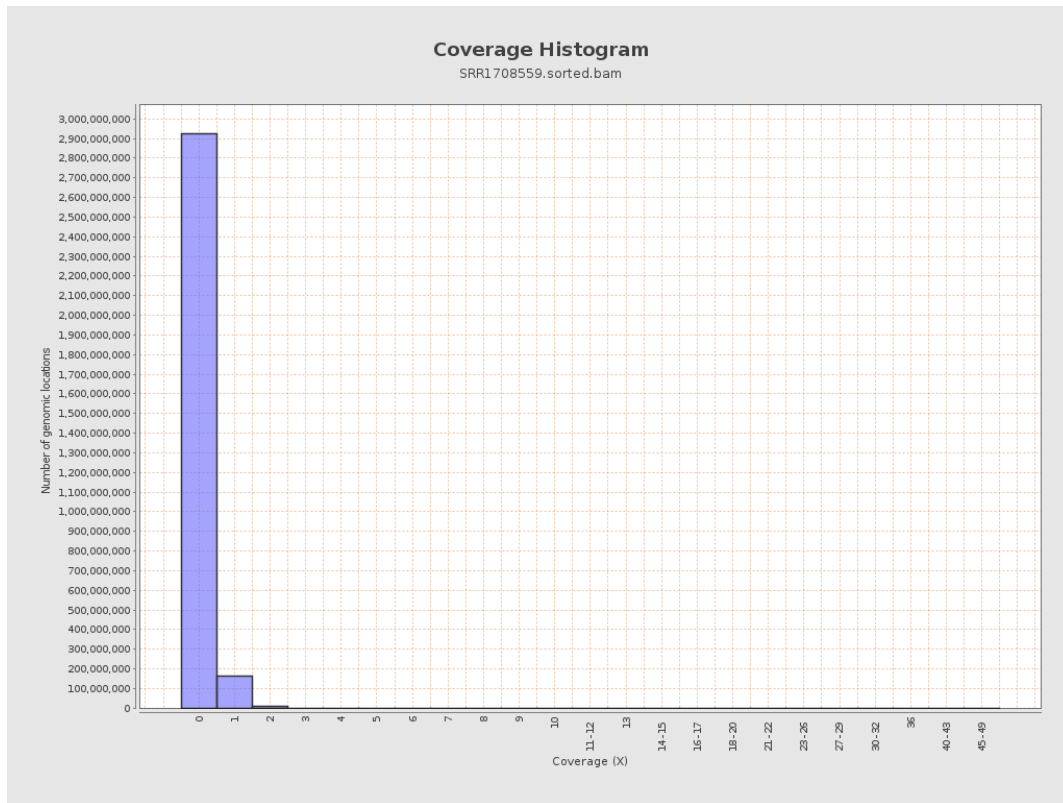
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13691398	0.0549	0.2438
chr2	243199373	15034281	0.0618	0.2562
chr3	198022430	14774792	0.0746	0.2822
chr4	191154276	16975788	0.0888	0.3072
chr5	180915260	12556910	0.0694	0.2714
chr6	171115067	11783143	0.0689	0.2708
chr7	159138663	10262483	0.0645	0.2625

chr8	146364022	10901447	0.0745	0.2815
chr9	141213431	7381300	0.0523	0.2366
chr10	135534747	8062726	0.0595	0.2516
chr11	135006516	7987644	0.0592	0.2521
chr12	133851895	8238174	0.0615	0.257
chr13	115169878	7388716	0.0642	0.2624
chr14	107349540	5148006	0.048	0.2268
chr15	102531392	3945423	0.0385	0.2035
chr16	90354753	3370344	0.0373	0.199
chr17	81195210	2639486	0.0325	0.1857
chr18	78077248	5136110	0.0658	0.2637
chr19	59128983	1434800	0.0243	0.1599
chr20	63025520	2798536	0.0444	0.2175
chr21	48129895	1993064	0.0414	0.2109
chr22	51304566	952558	0.0186	0.1405
chrMT	16571	50	0.003	0.0548
chrX	155270560	9434119	0.0608	0.2548
chrY	59373566	227732	0.0038	0.0648

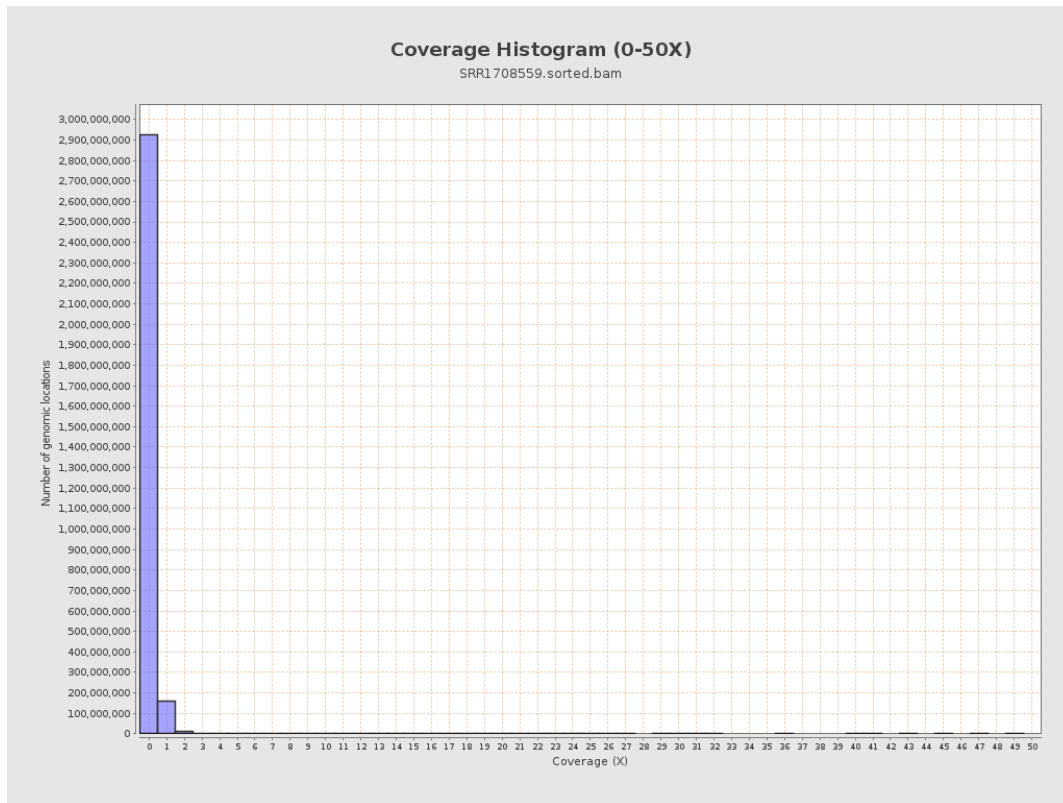
3. Results : Coverage across reference



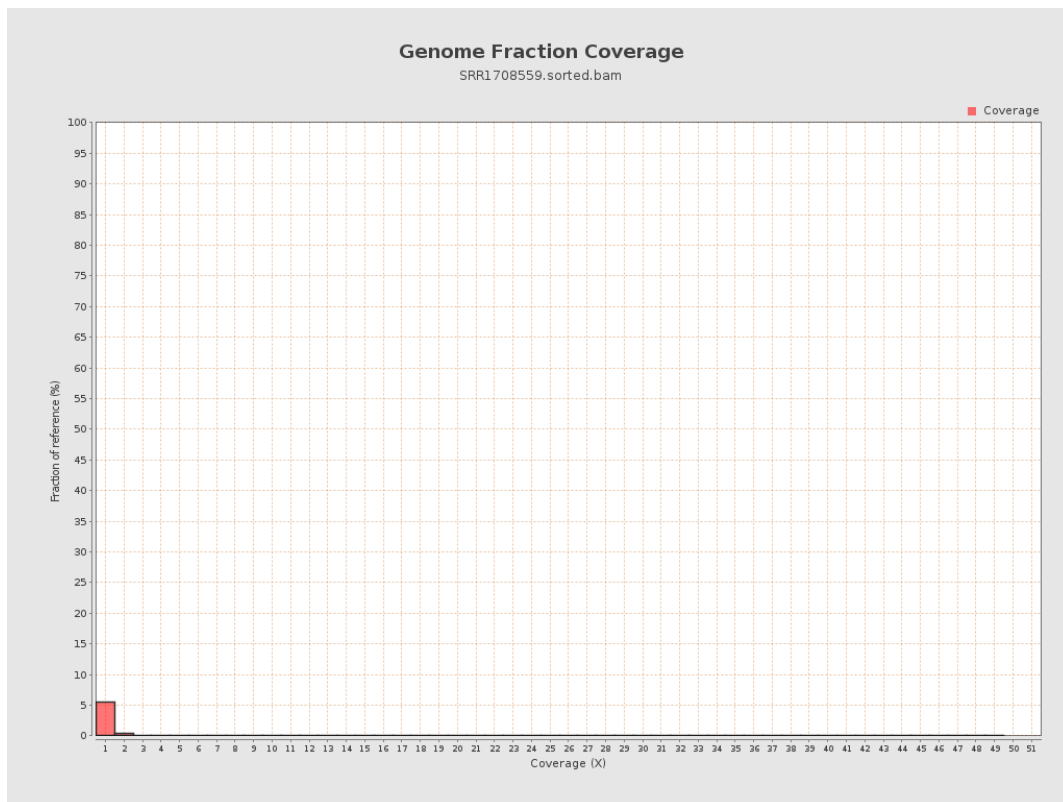
4. Results : Coverage Histogram



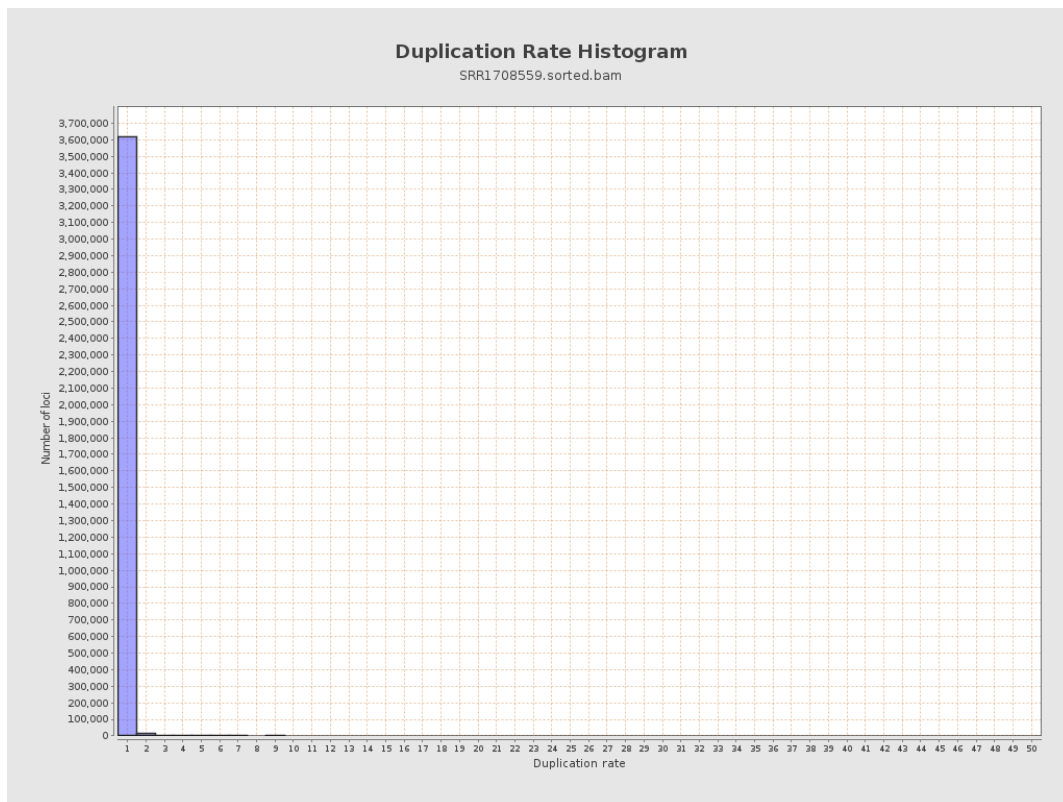
5. Results : Coverage Histogram (0-50X)



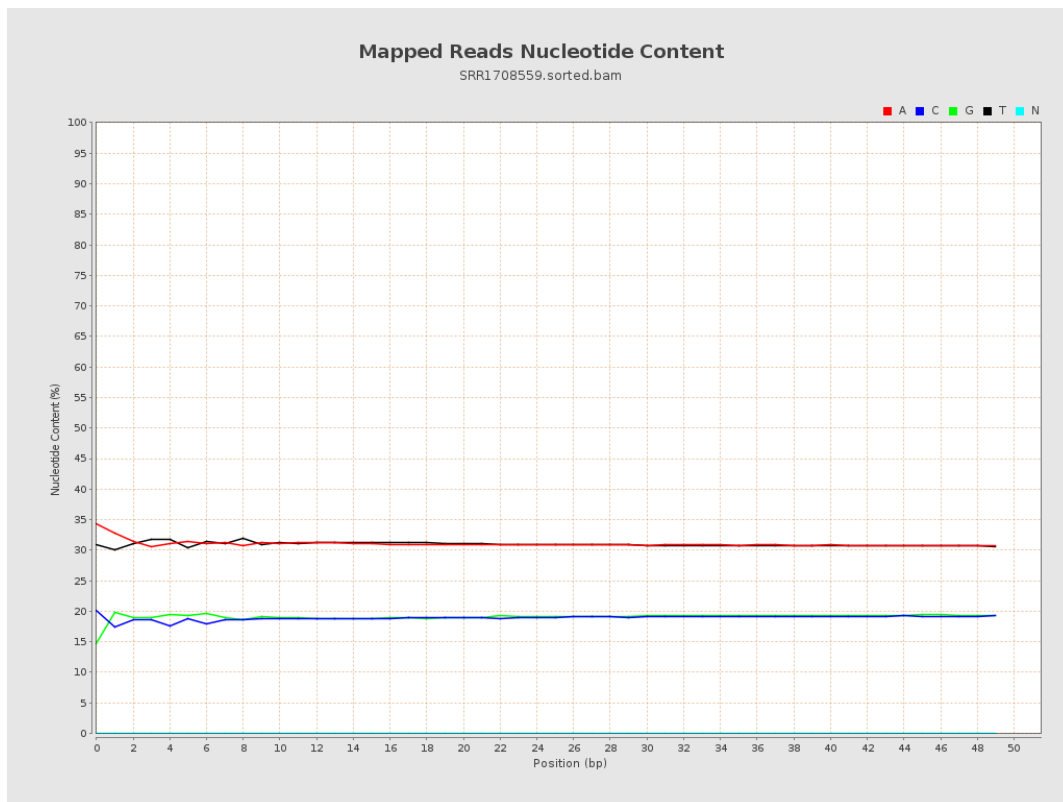
6. Results : Genome Fraction Coverage



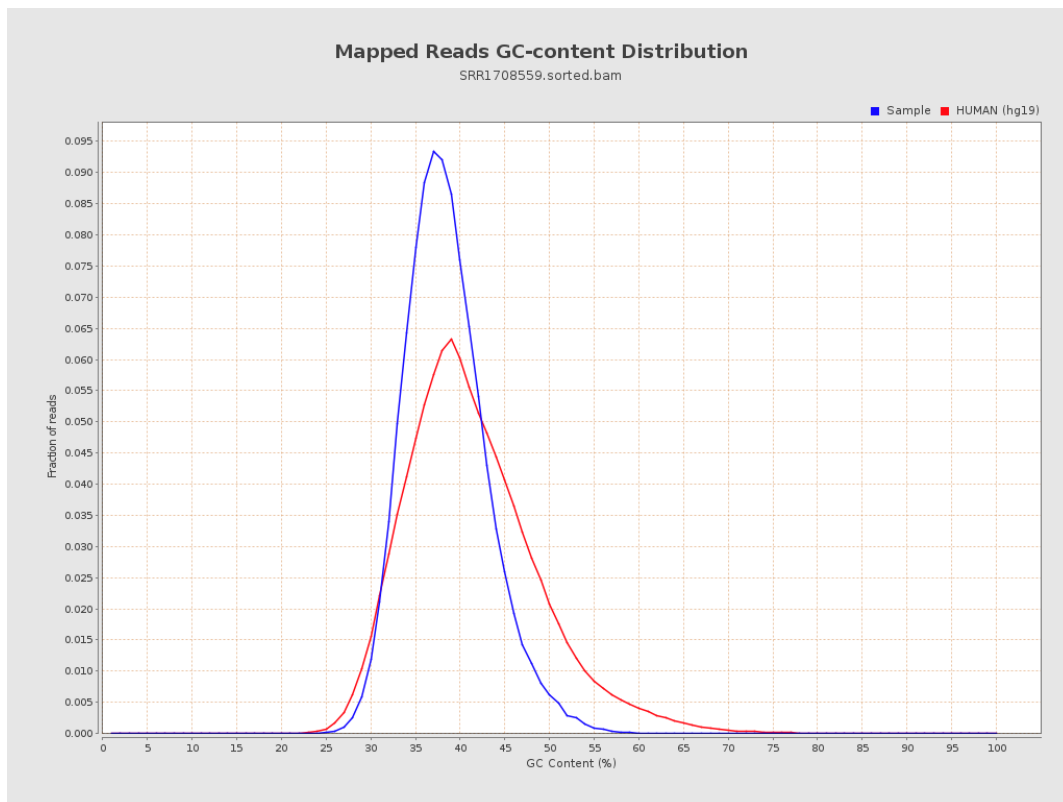
7. Results : Duplication Rate Histogram



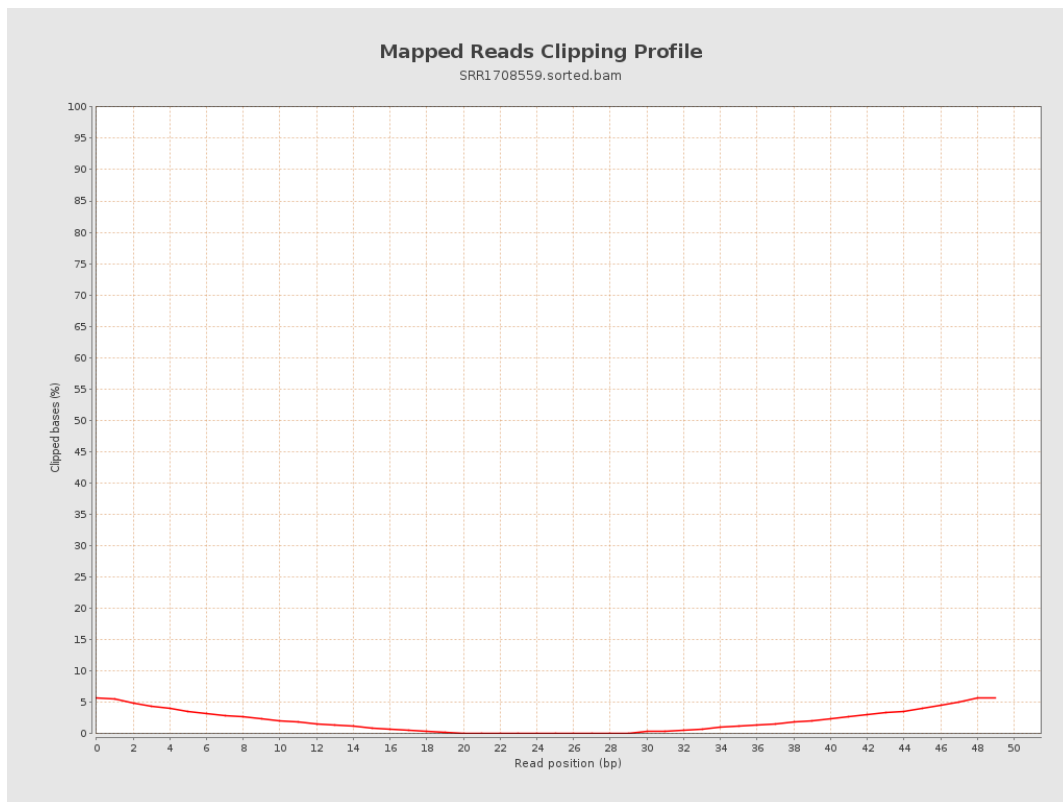
8. Results : Mapped Reads Nucleotide Content



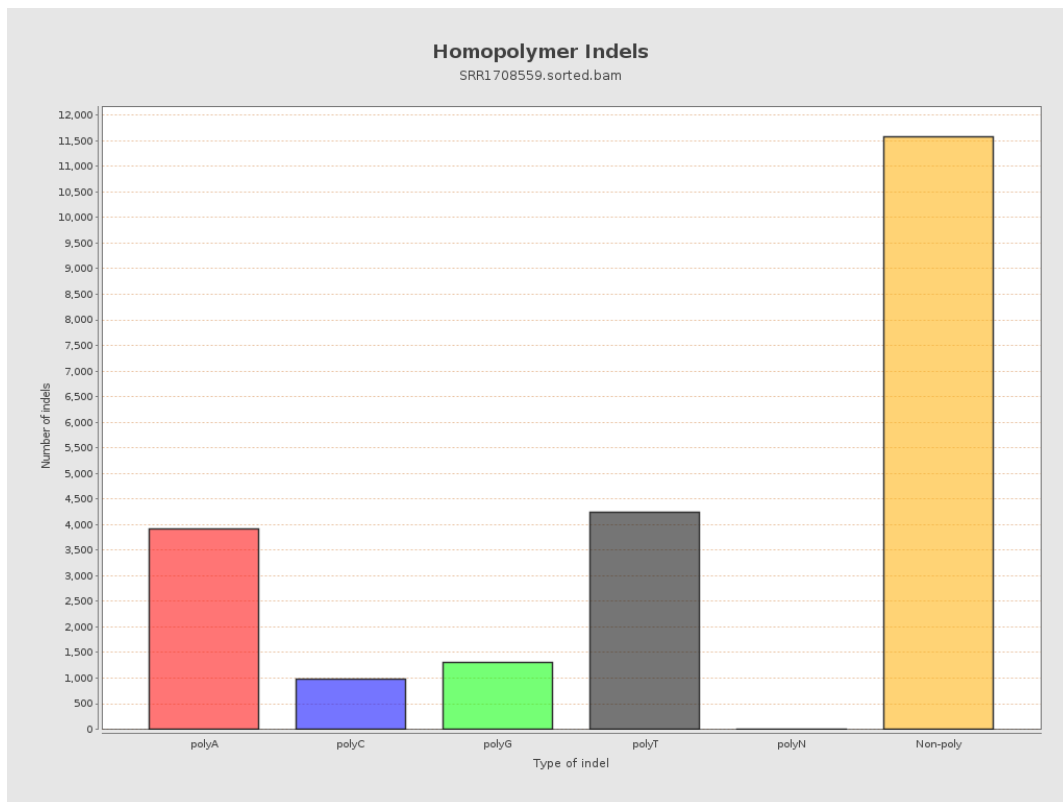
9. Results : Mapped Reads GC-content Distribution



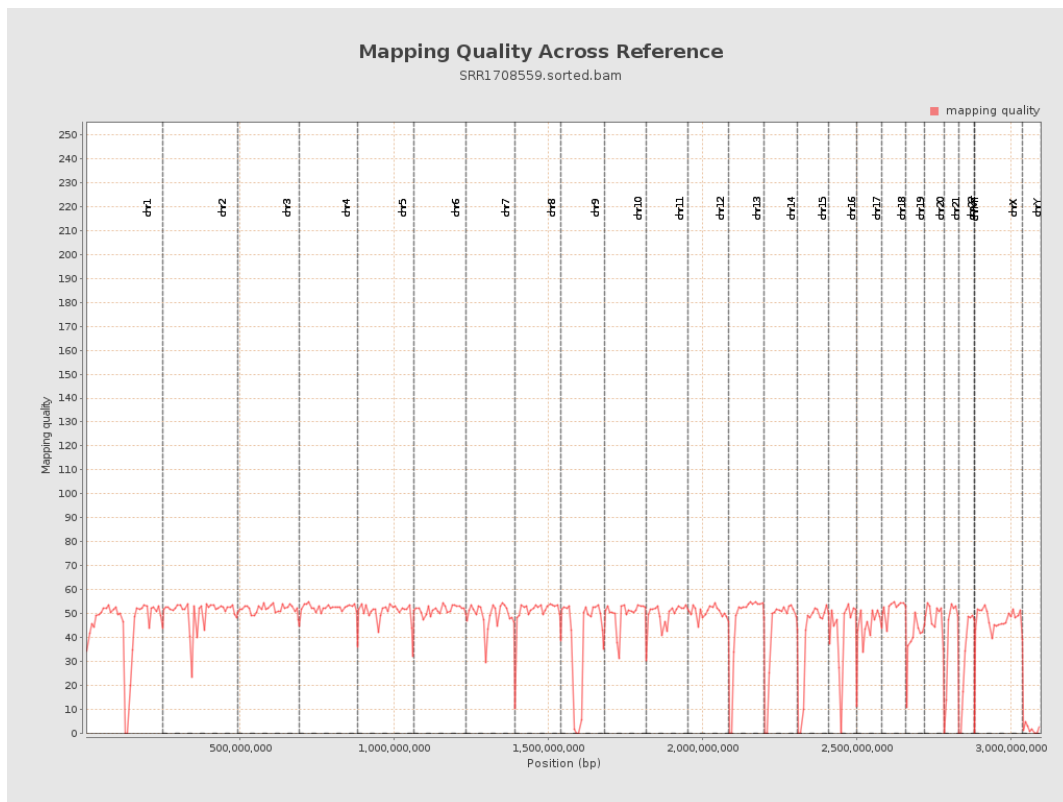
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

