

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 08:43:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708533.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_SRR1708533 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708533.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 08:43:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708533.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,993,248
Mapped reads	20,519,507 / 97.74%
Unmapped reads	473,741 / 2.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	553 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	216,344 / 1.03%
Duplication rate	1.04%
Clipped reads	258,602 / 1.23%

2.2. ACGT Content

Number/percentage of A's	315,248,597 / 30.8%
Number/percentage of C's	194,988,537 / 19.05%
Number/percentage of T's	315,241,977 / 30.8%
Number/percentage of G's	197,959,306 / 19.34%
Number/percentage of N's	35,691 / 0%
GC Percentage	38.39%

2.3. Coverage

Mean	0.3306

Standard Deviation	0.6785
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2.4. Mapping Quality

Mean Mapping Quality	46.4
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2.5. Mismatches and indels

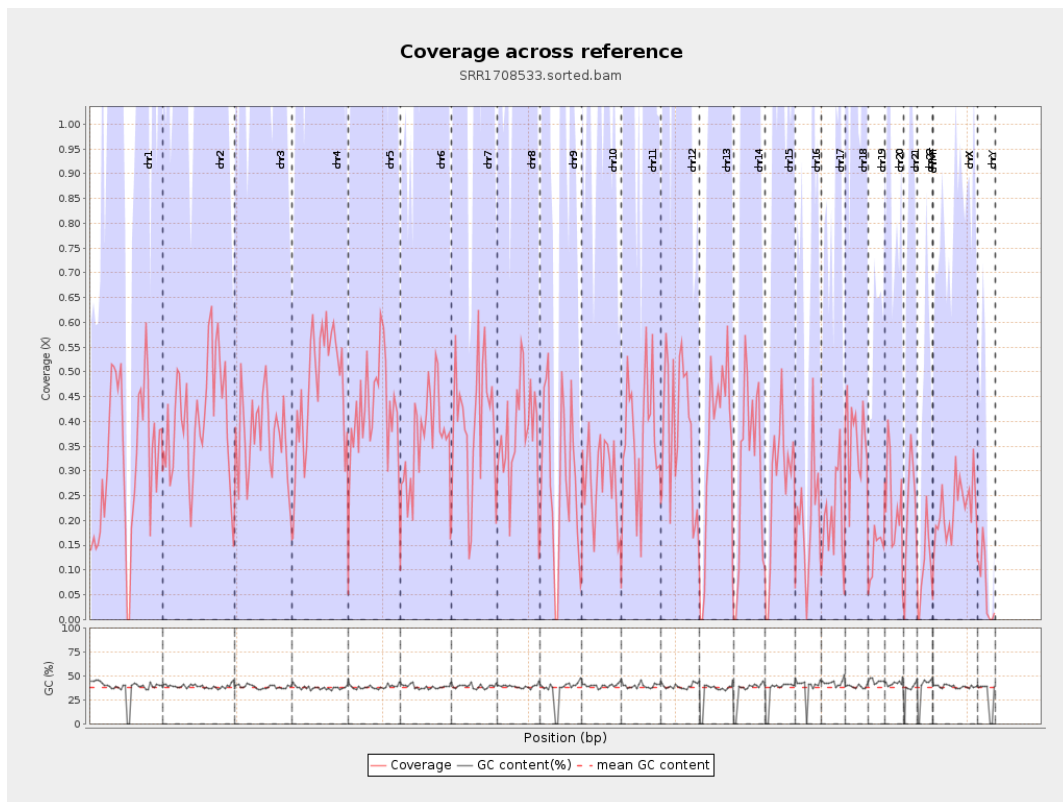
General error rate	0.2%
Mismatches	1,930,073
Insertions	58,521
Mapped reads with at least one insertion	0.28%
Deletions	53,534
Mapped reads with at least one deletion	0.26%
Homopolymer indels	48.78%

2.6. Chromosome stats

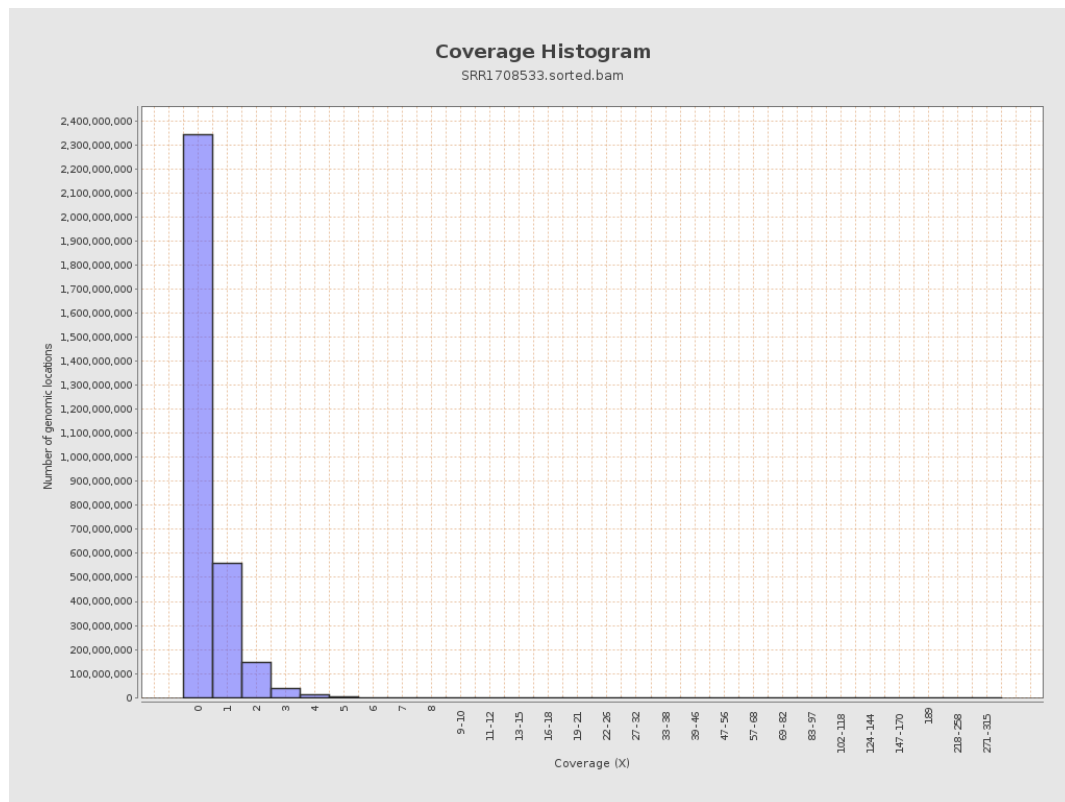
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	79231730	0.3179	0.6777
chr2	243199373	98286838	0.4041	0.7414
chr3	198022430	72731525	0.3673	0.6983
chr4	191154276	90663235	0.4743	0.7993
chr5	180915260	75588131	0.4178	0.7481
chr6	171115067	62681000	0.3663	0.7082
chr7	159138663	63017681	0.396	0.7412

chr8	146364022	55416147	0.3786	0.7097
chr9	141213431	41392931	0.2931	0.6452
chr10	135534747	38785638	0.2862	0.6135
chr11	135006516	49981910	0.3702	0.7185
chr12	133851895	51201259	0.3825	0.7305
chr13	115169878	41016163	0.3561	0.7014
chr14	107349540	33583086	0.3128	0.6632
chr15	102531392	28376258	0.2768	0.629
chr16	90354753	17783021	0.1968	0.5178
chr17	81195210	17175185	0.2115	0.5444
chr18	78077248	28537092	0.3655	0.6963
chr19	59128983	8384875	0.1418	0.4313
chr20	63025520	14887551	0.2362	0.5647
chr21	48129895	10553903	0.2193	0.5549
chr22	51304566	5632455	0.1098	0.382
chrMT	16571	1242	0.075	0.3112
chrX	155270560	34674549	0.2233	0.5423
chrY	59373566	3979905	0.067	0.3027

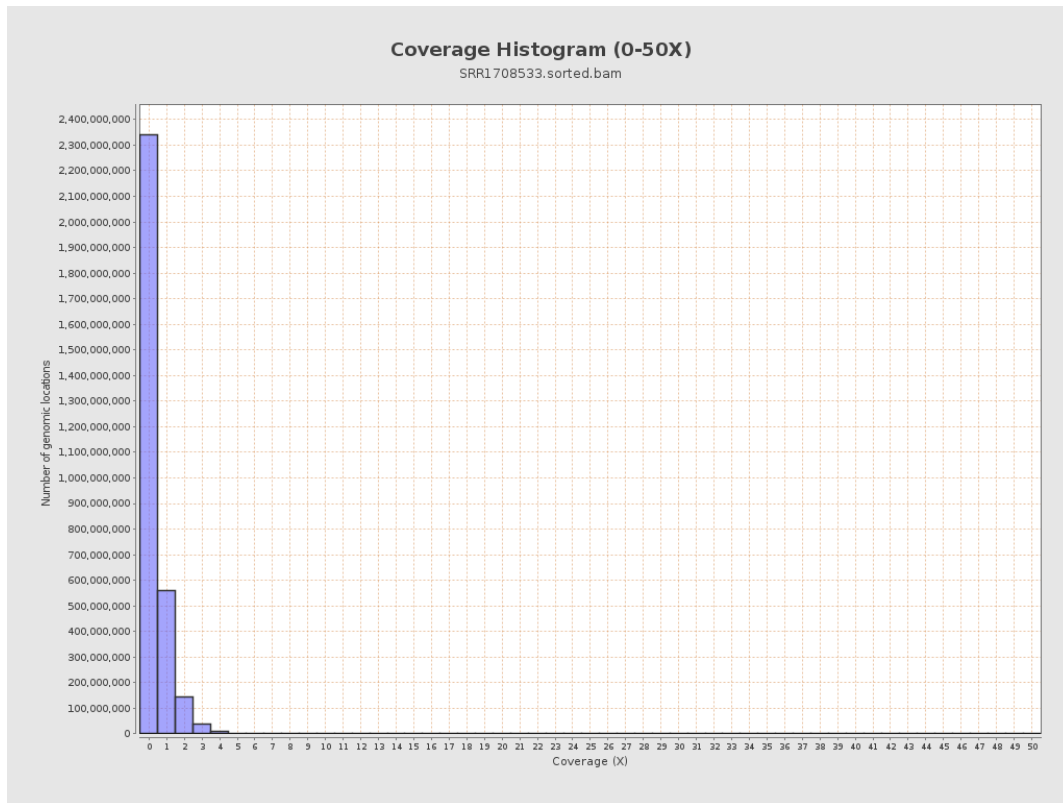
3. Results : Coverage across reference



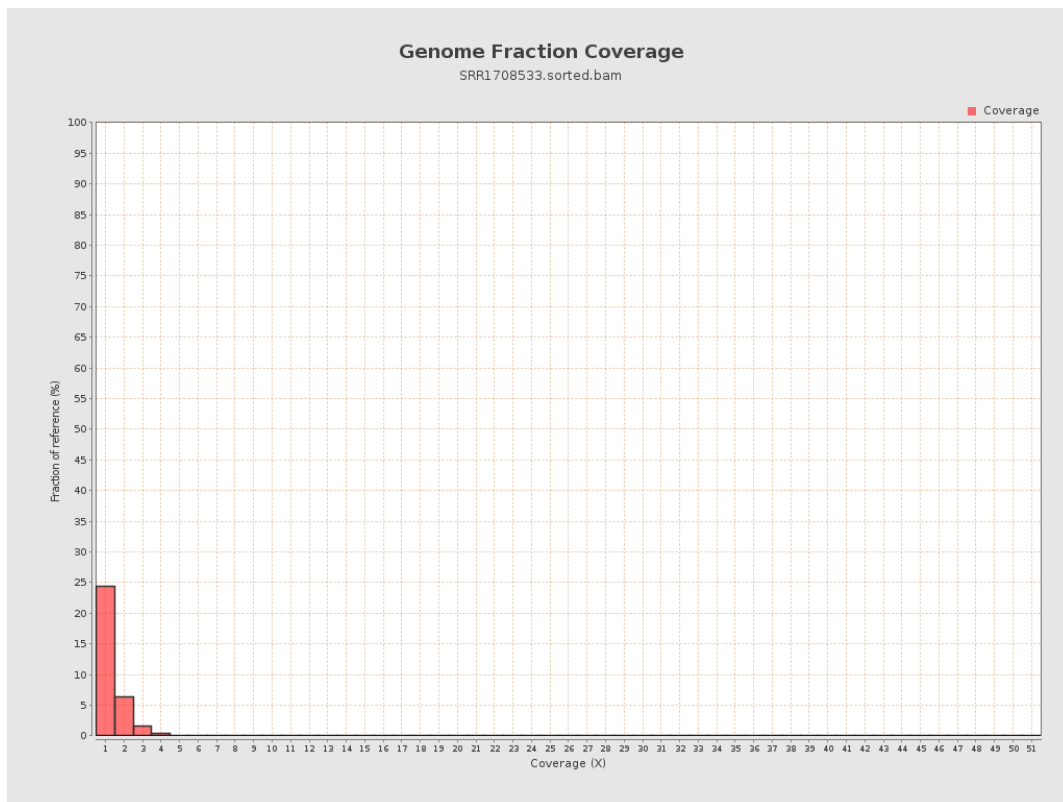
4. Results : Coverage Histogram



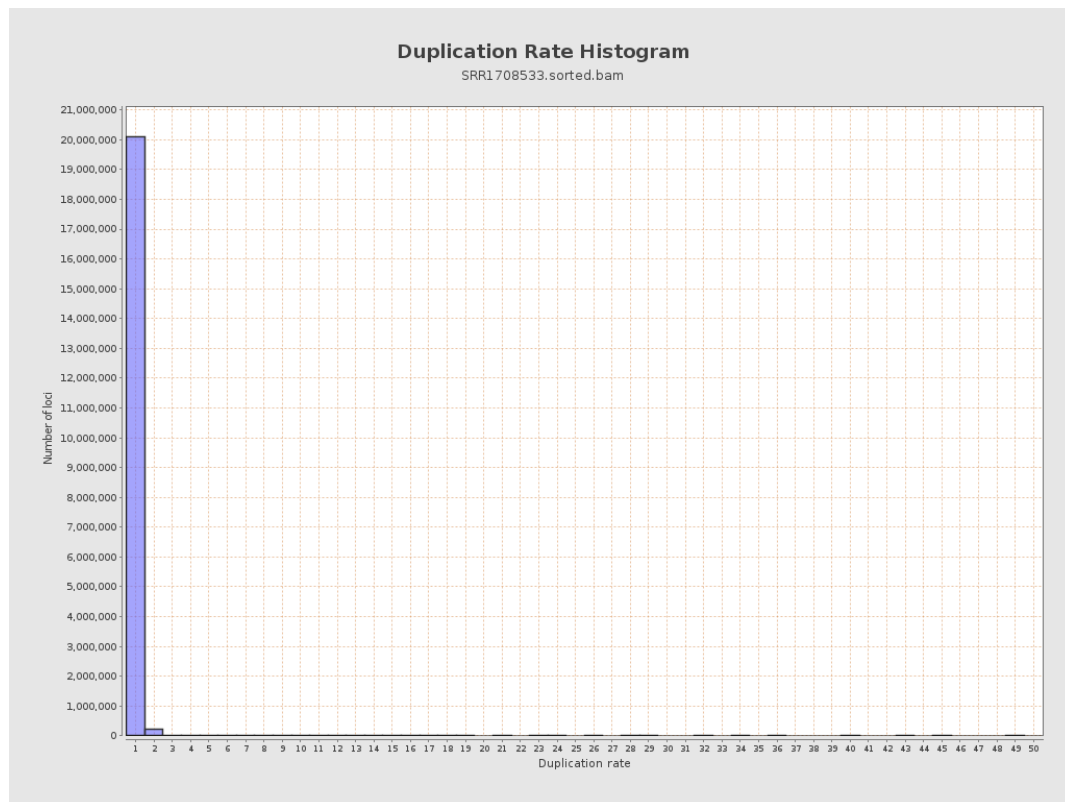
5. Results : Coverage Histogram (0-50X)



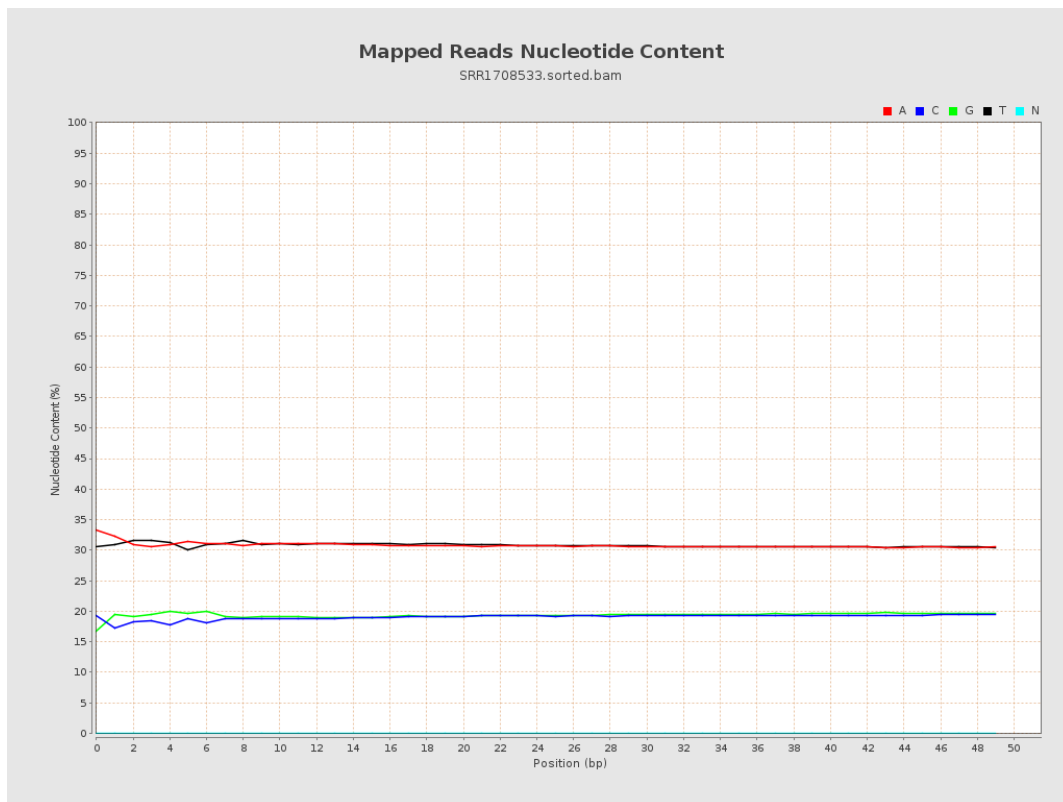
6. Results : Genome Fraction Coverage



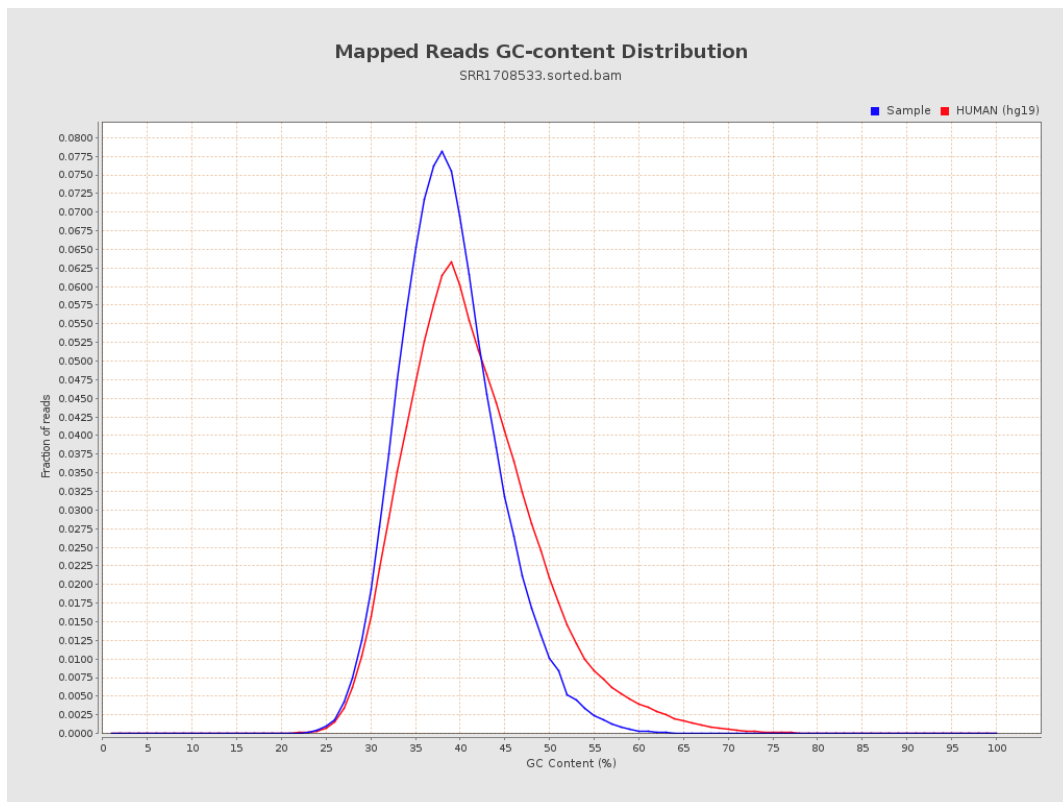
7. Results : Duplication Rate Histogram



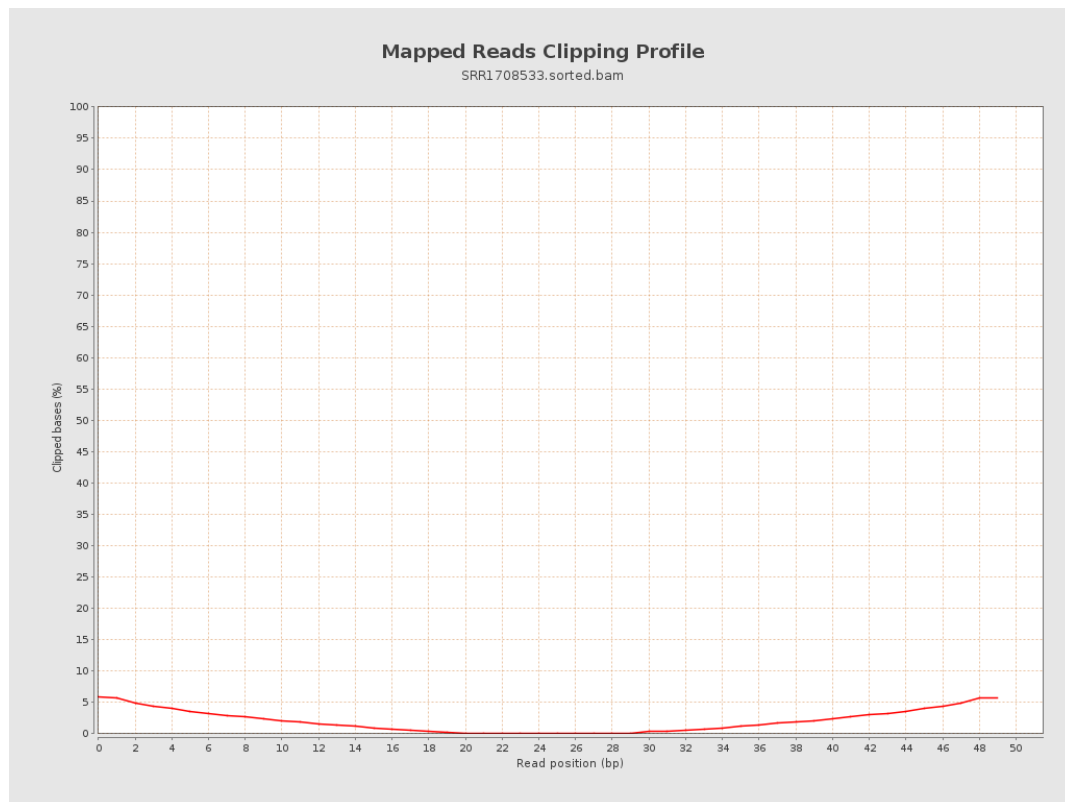
8. Results : Mapped Reads Nucleotide Content



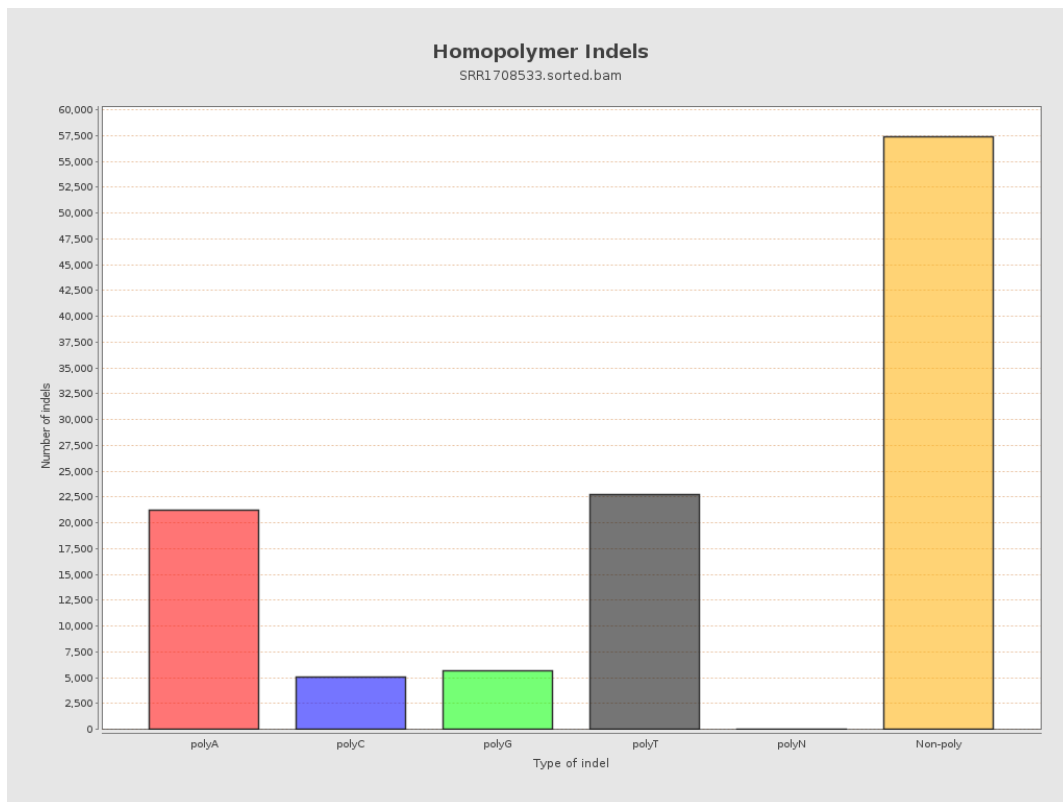
9. Results : Mapped Reads GC-content Distribution



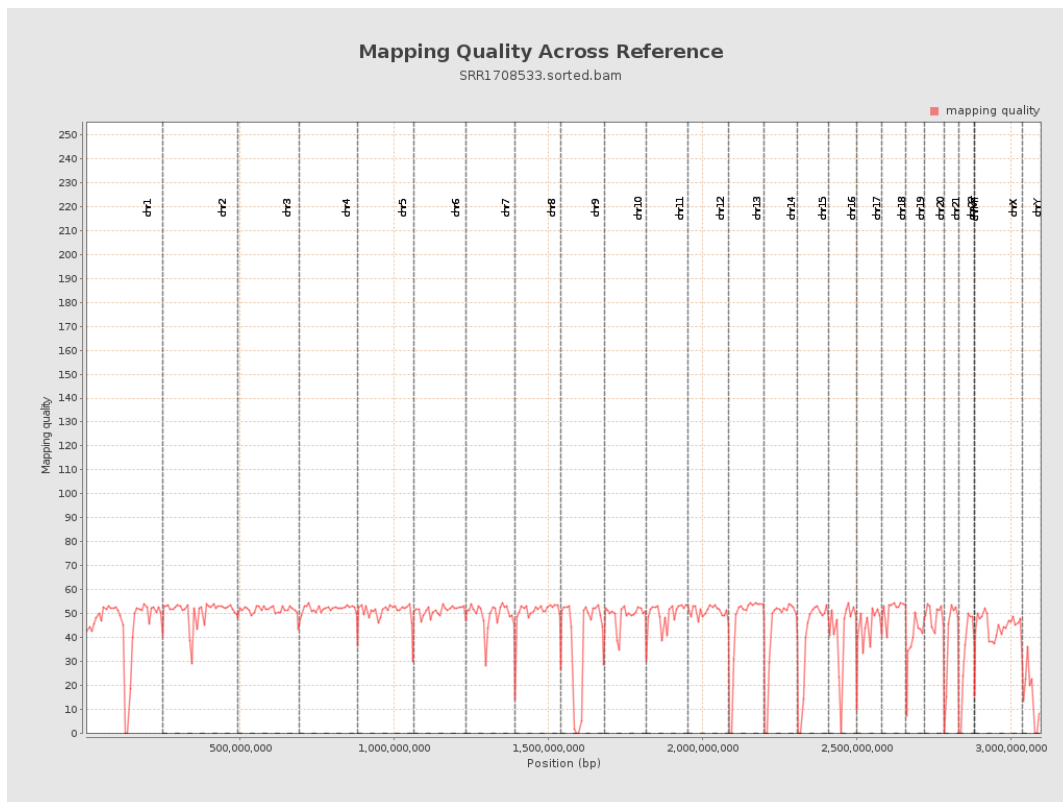
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

