

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 12:35:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708538.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_SRR1708538 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708538.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 12:35:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708538.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,168,003
Mapped reads	20,678,312 / 97.69%
Unmapped reads	489,691 / 2.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	565 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	218,907 / 1.03%
Duplication rate	1.05%
Clipped reads	288,244 / 1.36%

2.2. ACGT Content

Number/percentage of A's	321,055,435 / 31.13%
Number/percentage of C's	193,107,635 / 18.73%
Number/percentage of T's	319,450,802 / 30.98%
Number/percentage of G's	197,561,823 / 19.16%
Number/percentage of N's	36,664 / 0%
GC Percentage	37.88%

2.3. Coverage

Mean	0.3331

Standard Deviation	0.6637
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2.4. Mapping Quality

Mean Mapping Quality	46.67
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2.5. Mismatches and indels

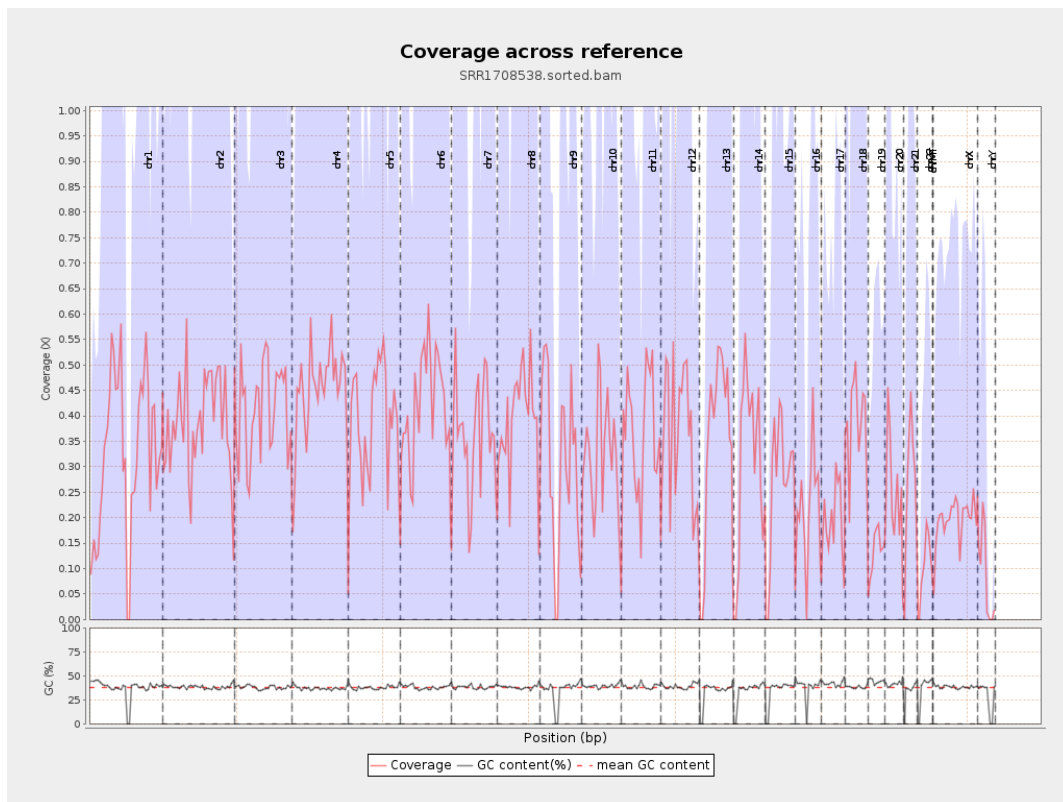
General error rate	0.21%
Mismatches	2,033,959
Insertions	62,376
Mapped reads with at least one insertion	0.3%
Deletions	56,828
Mapped reads with at least one deletion	0.27%
Homopolymer indels	49.24%

2.6. Chromosome stats

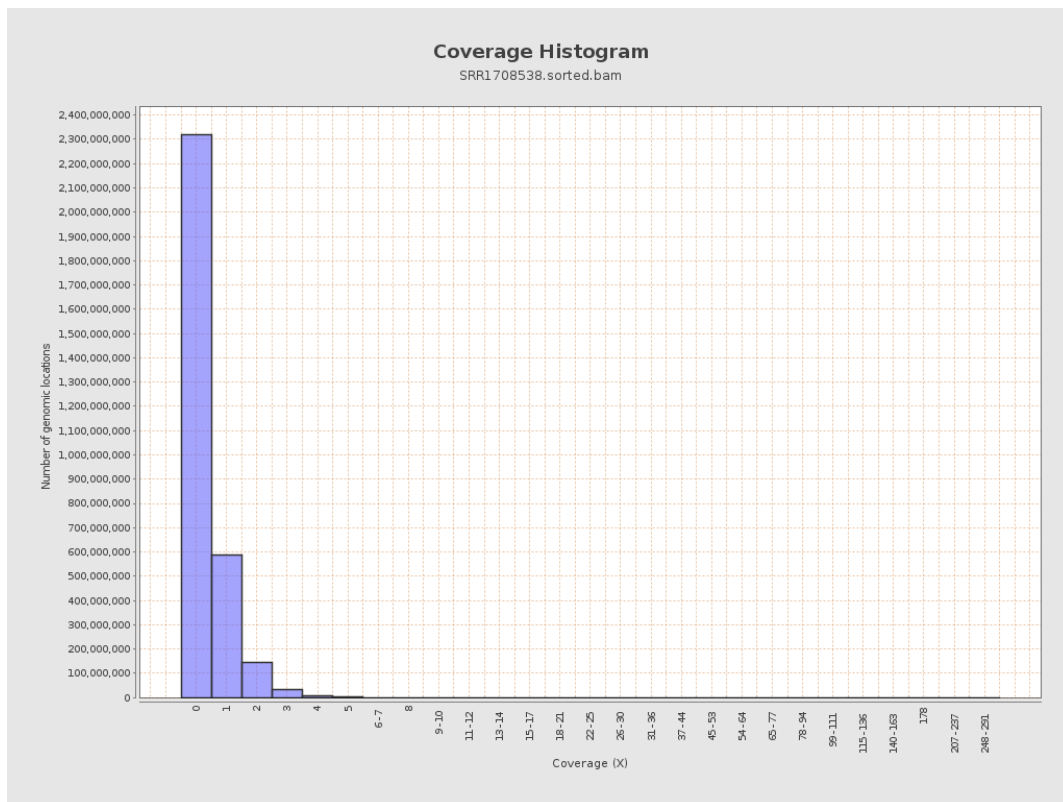
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	81201521	0.3258	0.6731
chr2	243199373	93650958	0.3851	0.7013
chr3	198022430	81933669	0.4138	0.7249
chr4	191154276	86106598	0.4505	0.7533
chr5	180915260	69880267	0.3863	0.7034
chr6	171115067	72864949	0.4258	0.7374
chr7	159138663	56943868	0.3578	0.6824

chr8	146364022	57785421	0.3948	0.7103
chr9	141213431	43935916	0.3111	0.6504
chr10	135534747	44122297	0.3255	0.6434
chr11	135006516	49384501	0.3658	0.6993
chr12	133851895	48167094	0.3599	0.6826
chr13	115169878	40881596	0.355	0.6828
chr14	107349540	33989419	0.3166	0.6549
chr15	102531392	27175087	0.265	0.5977
chr16	90354753	19220094	0.2127	0.5292
chr17	81195210	16114477	0.1985	0.5067
chr18	78077248	30279860	0.3878	0.7026
chr19	59128983	8129462	0.1375	0.4127
chr20	63025520	16161174	0.2564	0.5839
chr21	48129895	12243821	0.2544	0.5926
chr22	51304566	5337311	0.104	0.3634
chrMT	16571	1169	0.0705	0.2977
chrX	155270560	30663607	0.1975	0.4902
chrY	59373566	5133278	0.0865	0.3385

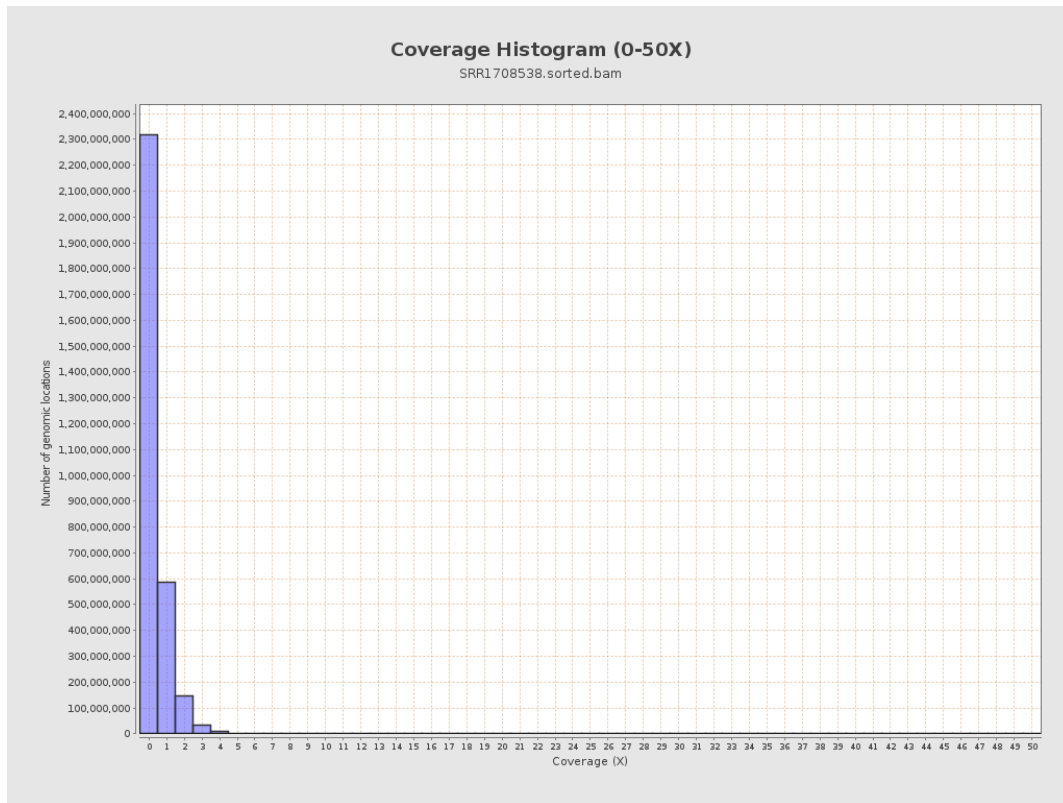
3. Results : Coverage across reference



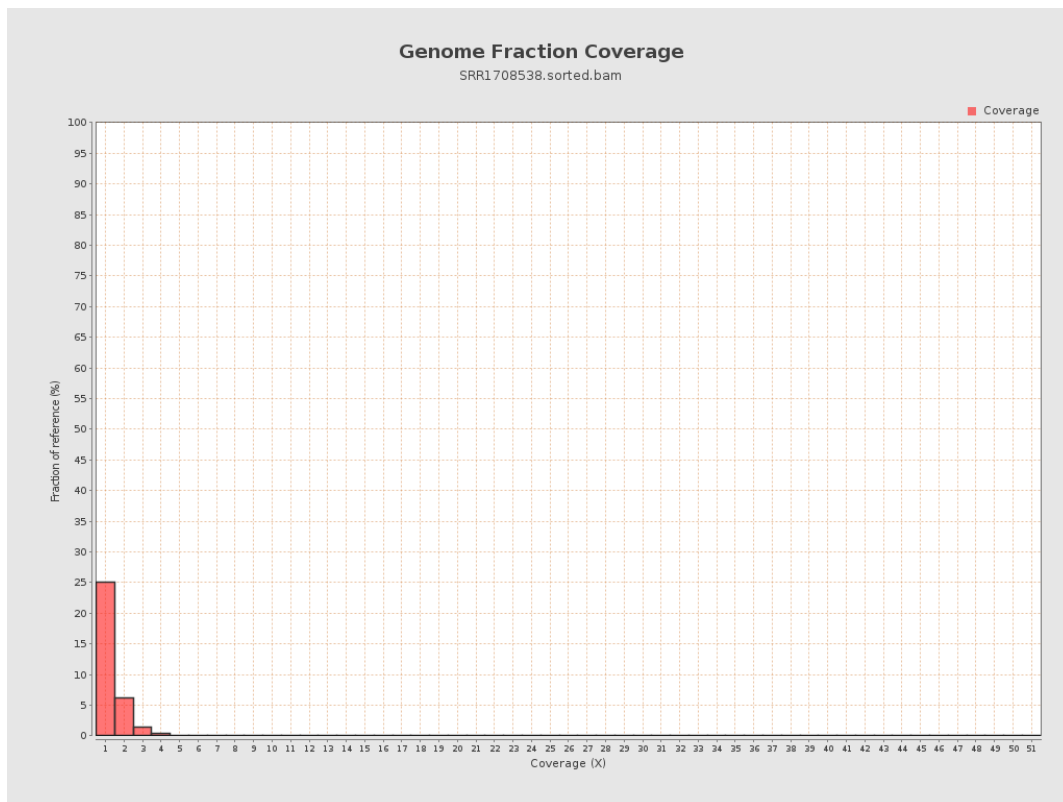
4. Results : Coverage Histogram



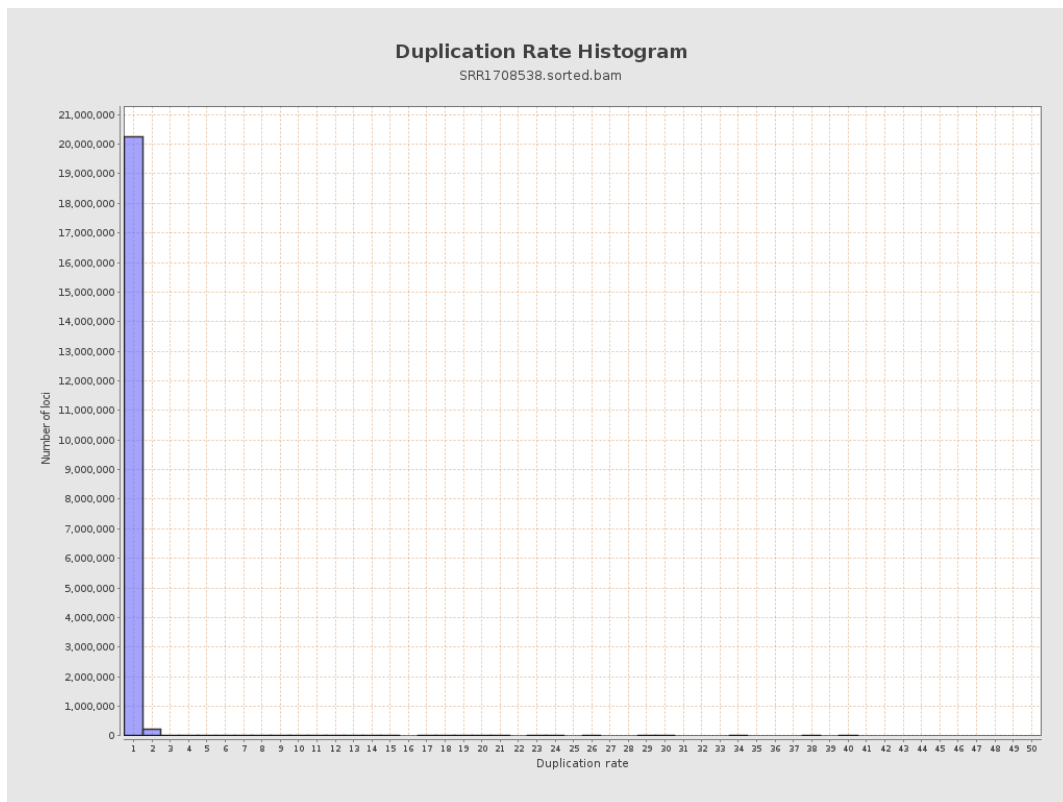
5. Results : Coverage Histogram (0-50X)



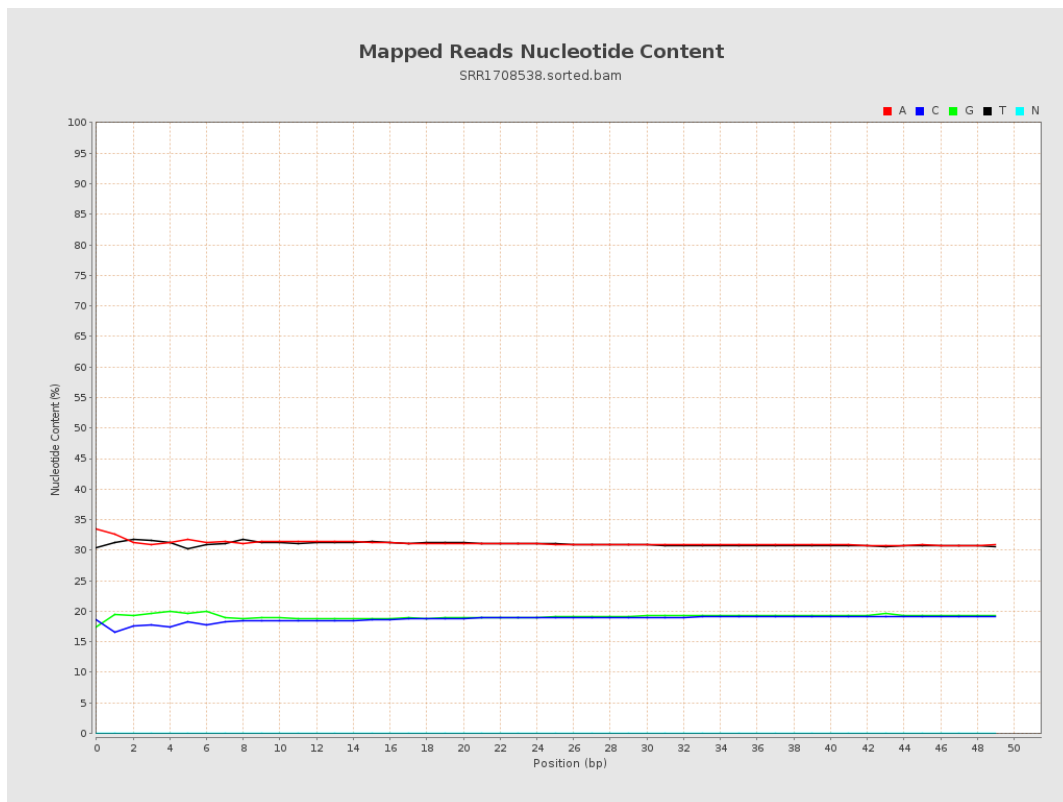
6. Results : Genome Fraction Coverage



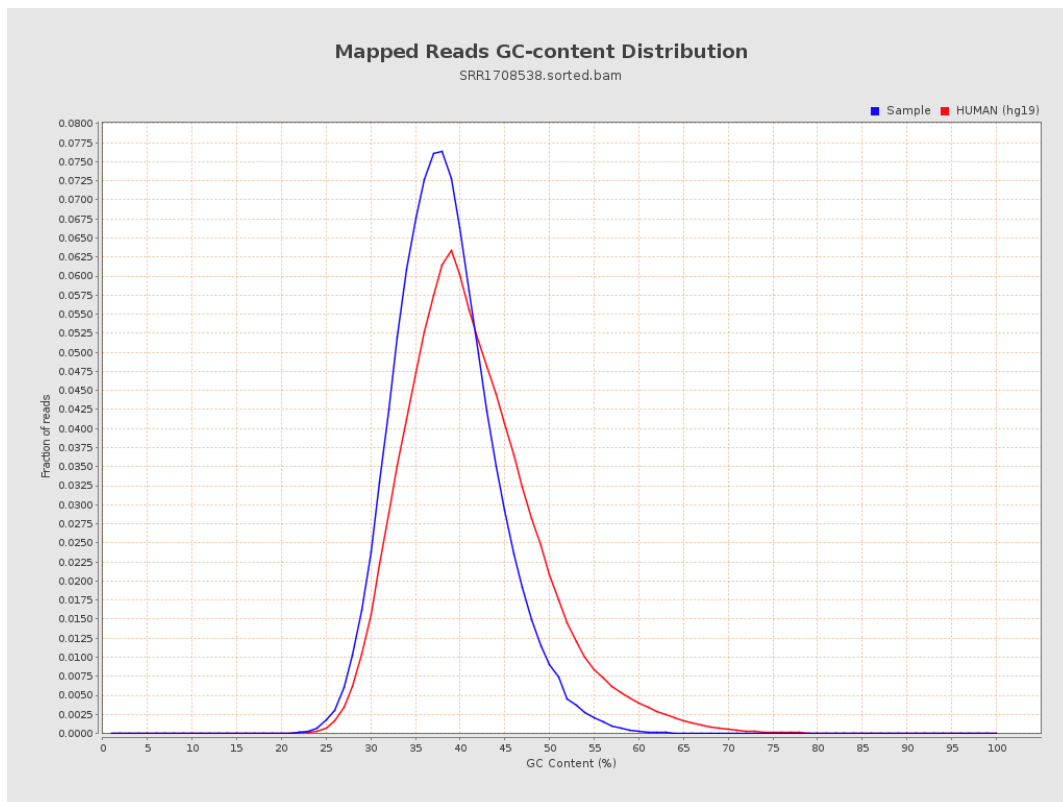
7. Results : Duplication Rate Histogram



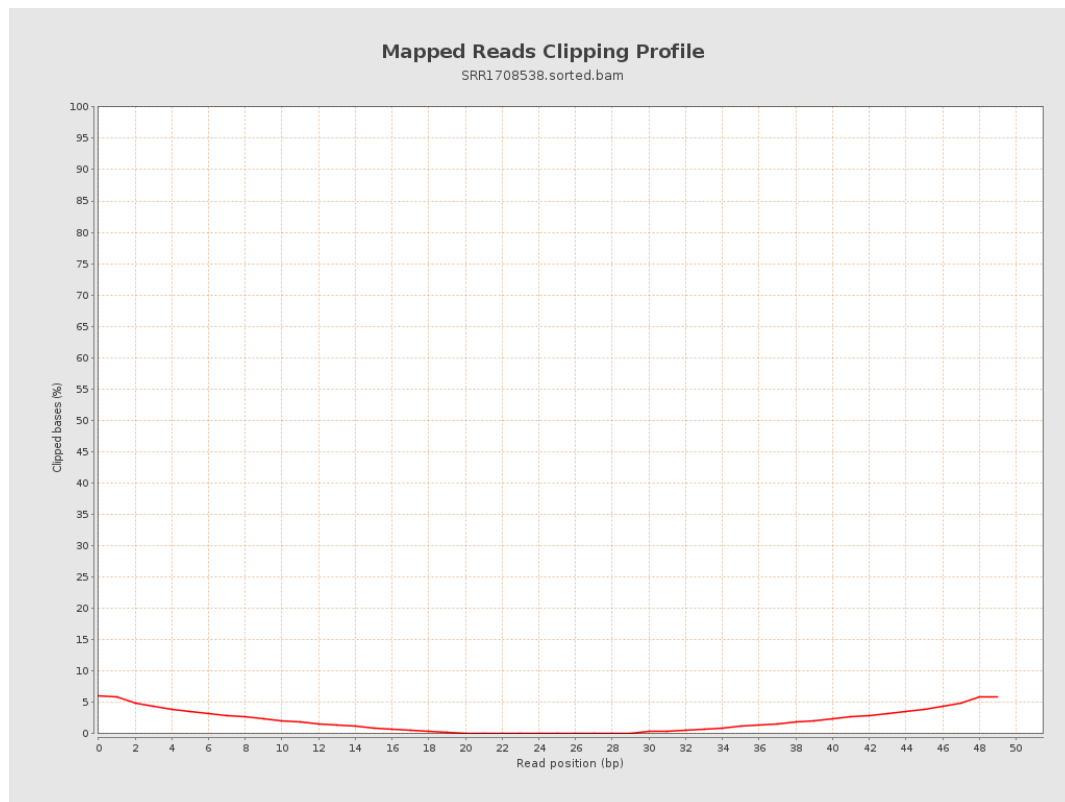
8. Results : Mapped Reads Nucleotide Content



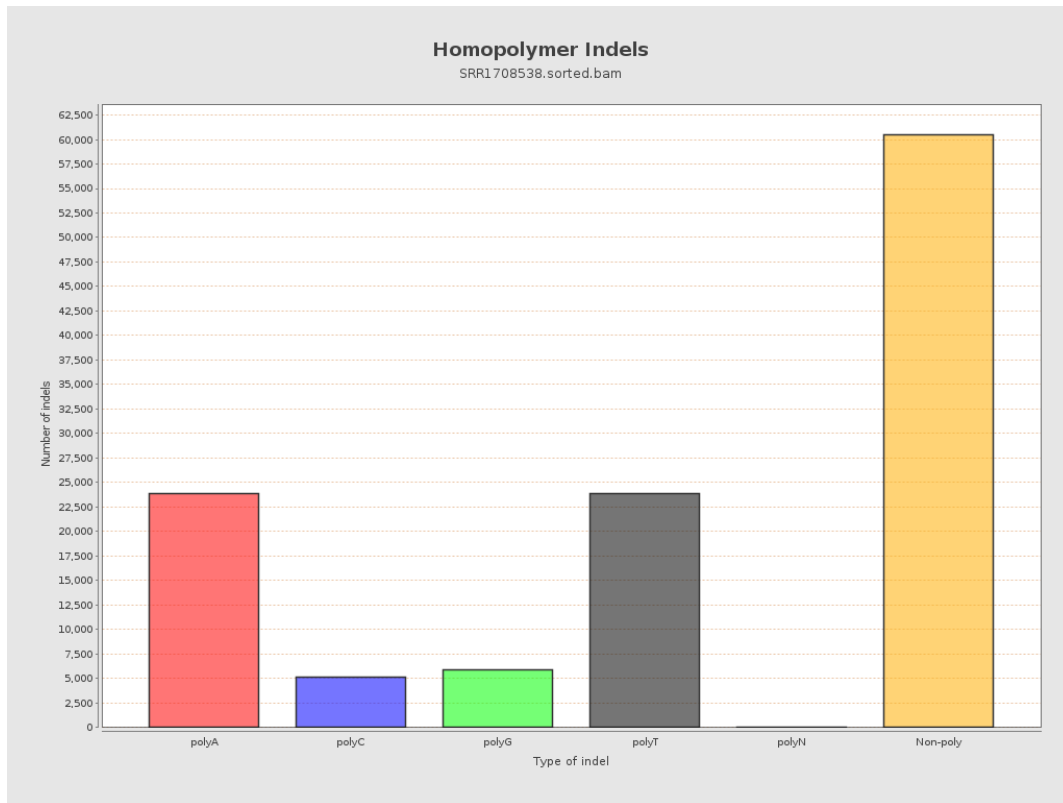
9. Results : Mapped Reads GC-content Distribution



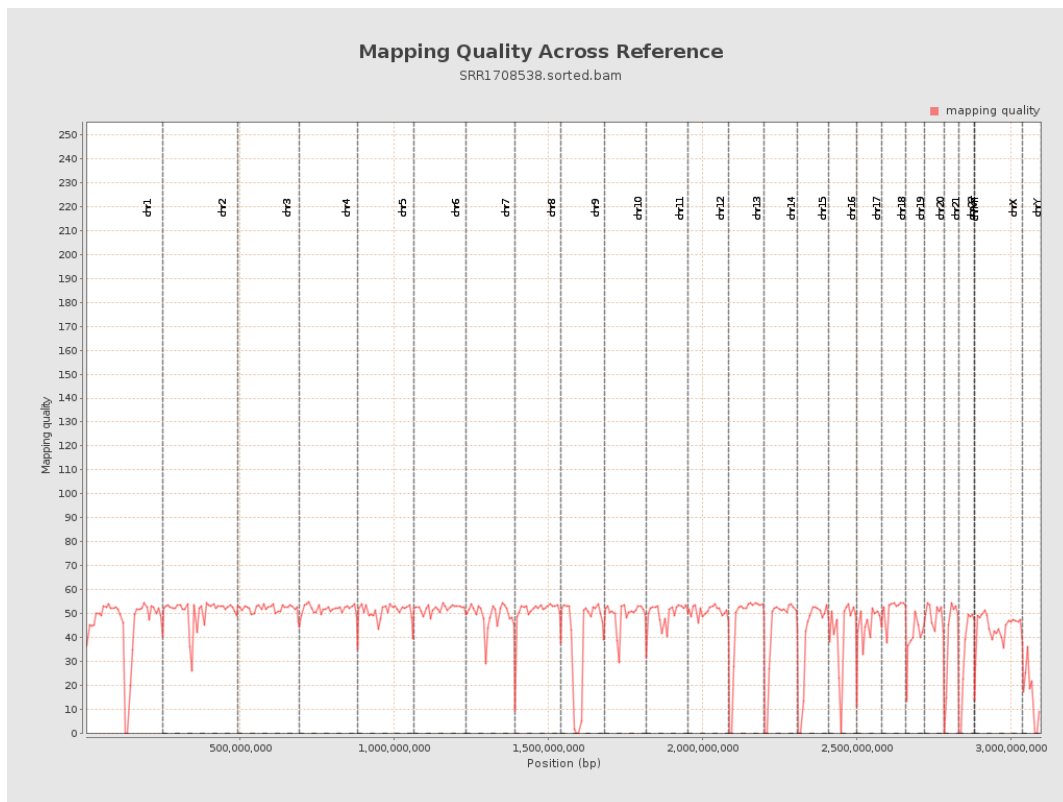
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

