

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 09:51:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084338.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_SRR3084338 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084338.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 09:51:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084338.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,519,235
Mapped reads	1,565,189 / 62.13%
Unmapped reads	954,046 / 37.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,745 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	51,981 / 2.06%
Duplication rate	2.78%
Clipped reads	847,383 / 33.64%

2.2. ACGT Content

Number/percentage of A's	27,763,890 / 27.91%
Number/percentage of C's	18,805,197 / 18.9%
Number/percentage of T's	30,400,838 / 30.56%
Number/percentage of G's	22,514,733 / 22.63%
Number/percentage of N's	1,093 / 0%
GC Percentage	41.53%

2.3. Coverage

Mean	0.0321

Standard Deviation	0.2463
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2.4. Mapping Quality

Mean Mapping Quality	45.65
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2.5. Mismatches and indels

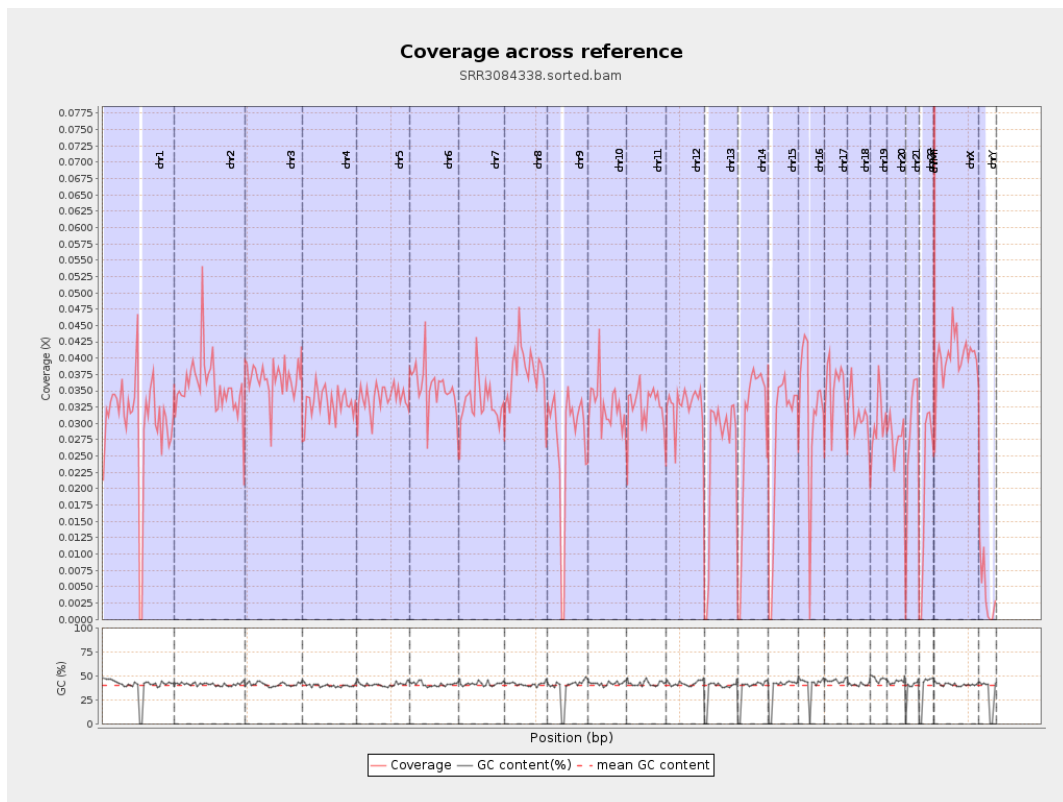
General error rate	0.84%
Mismatches	818,091
Insertions	7,412
Mapped reads with at least one insertion	0.47%
Deletions	20,622
Mapped reads with at least one deletion	1.31%
Homopolymer indels	46.15%

2.6. Chromosome stats

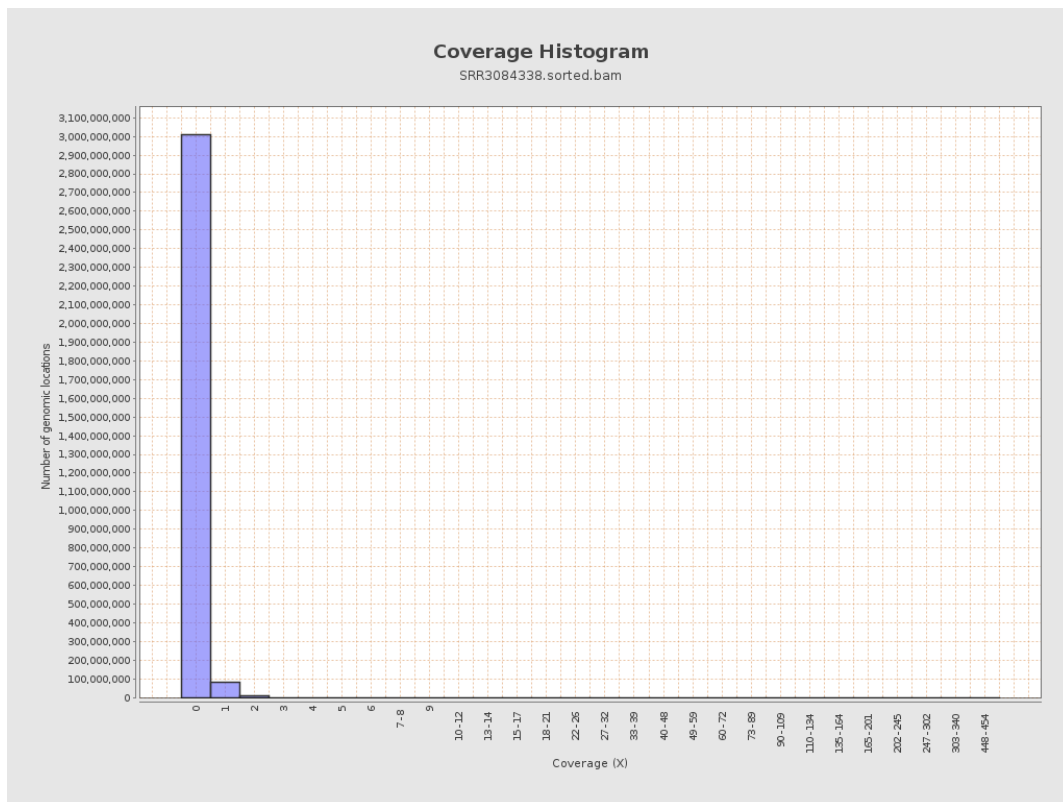
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7480375	0.03	0.3226
chr2	243199373	8680438	0.0357	0.3178
chr3	198022430	7291667	0.0368	0.2097
chr4	191154276	6297183	0.0329	0.2041
chr5	180915260	6158170	0.034	0.2022
chr6	171115067	6090827	0.0356	0.2348
chr7	159138663	5286956	0.0332	0.269

chr8	146364022	5544376	0.0379	0.2608
chr9	141213431	3885118	0.0275	0.2286
chr10	135534747	4431307	0.0327	0.2485
chr11	135006516	4437155	0.0329	0.2342
chr12	133851895	4381760	0.0327	0.1991
chr13	115169878	2907376	0.0252	0.1753
chr14	107349540	3113388	0.029	0.1929
chr15	102531392	2845987	0.0278	0.1878
chr16	90354753	2897343	0.0321	0.2091
chr17	81195210	2857341	0.0352	0.2298
chr18	78077248	2457500	0.0315	0.4453
chr19	59128983	1795163	0.0304	0.2843
chr20	63025520	1731595	0.0275	0.1851
chr21	48129895	1372864	0.0285	0.1919
chr22	51304566	1065240	0.0208	0.1578
chrMT	16571	17737	1.0704	1.2309
chrX	155270560	6250772	0.0403	0.2331
chrY	59373566	240835	0.0041	0.09

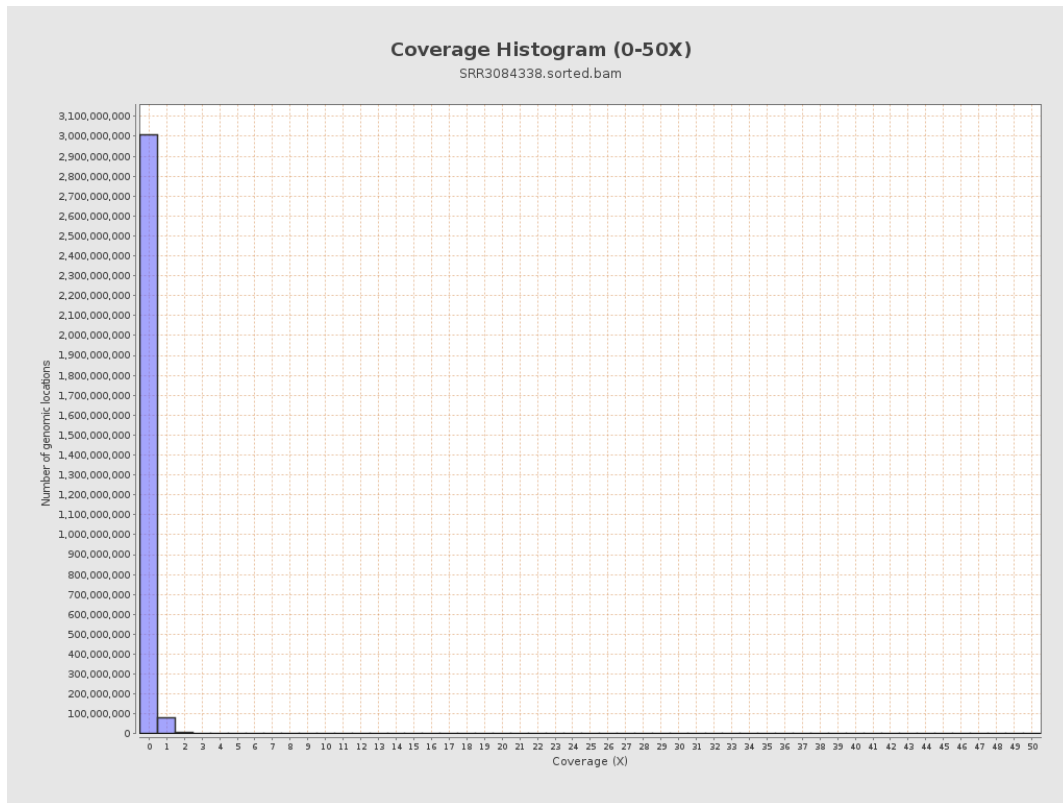
3. Results : Coverage across reference



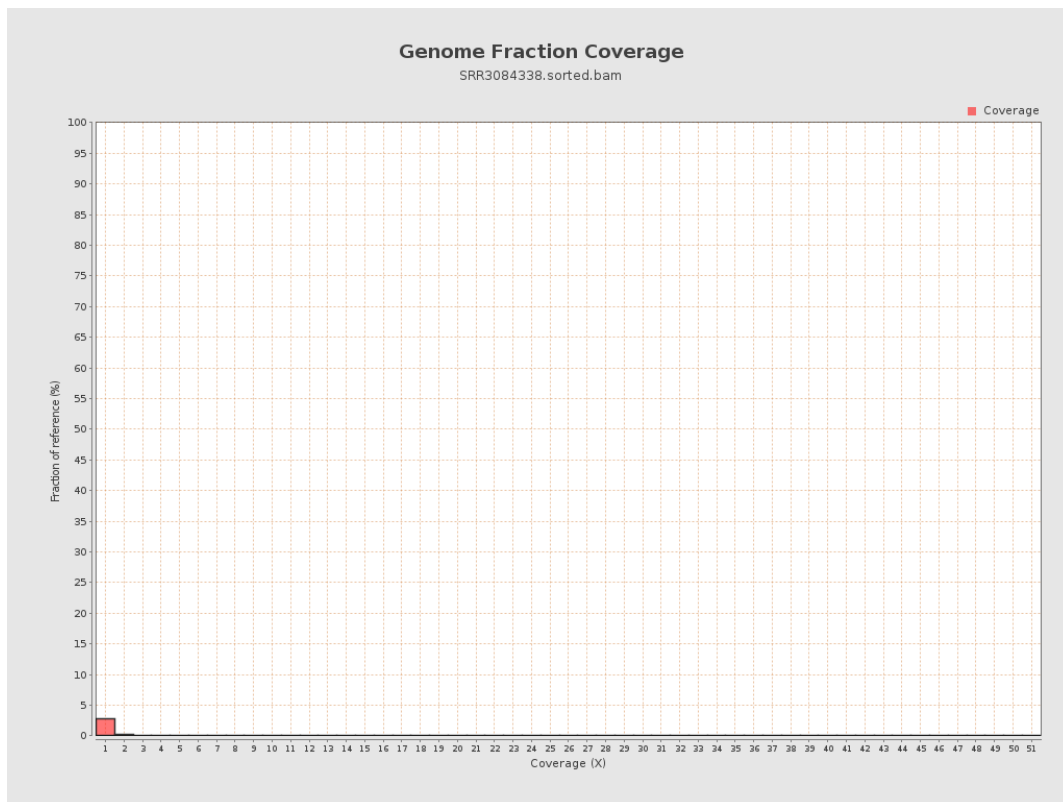
4. Results : Coverage Histogram



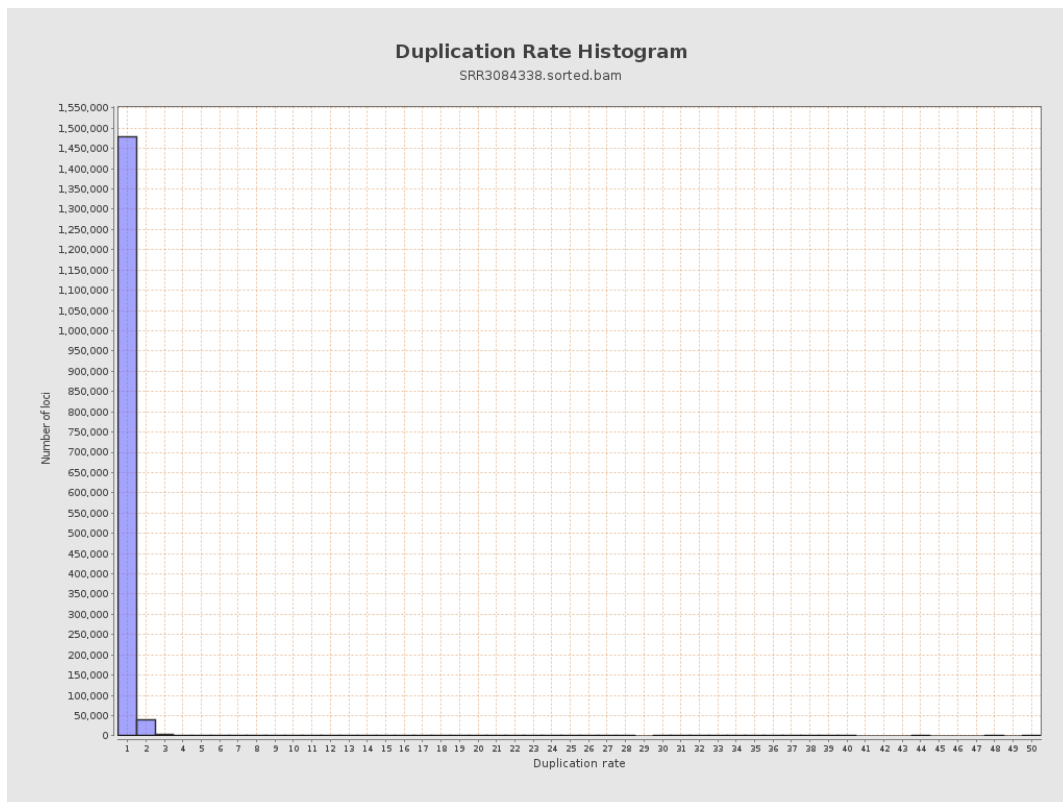
5. Results : Coverage Histogram (0-50X)



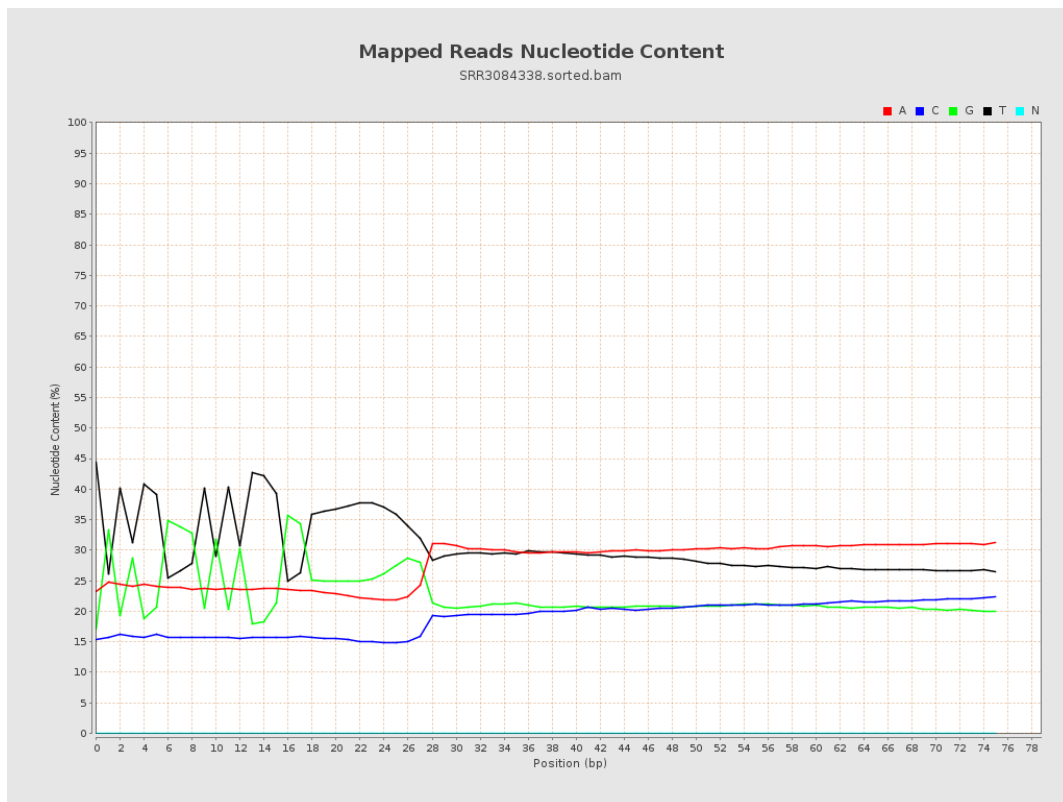
6. Results : Genome Fraction Coverage



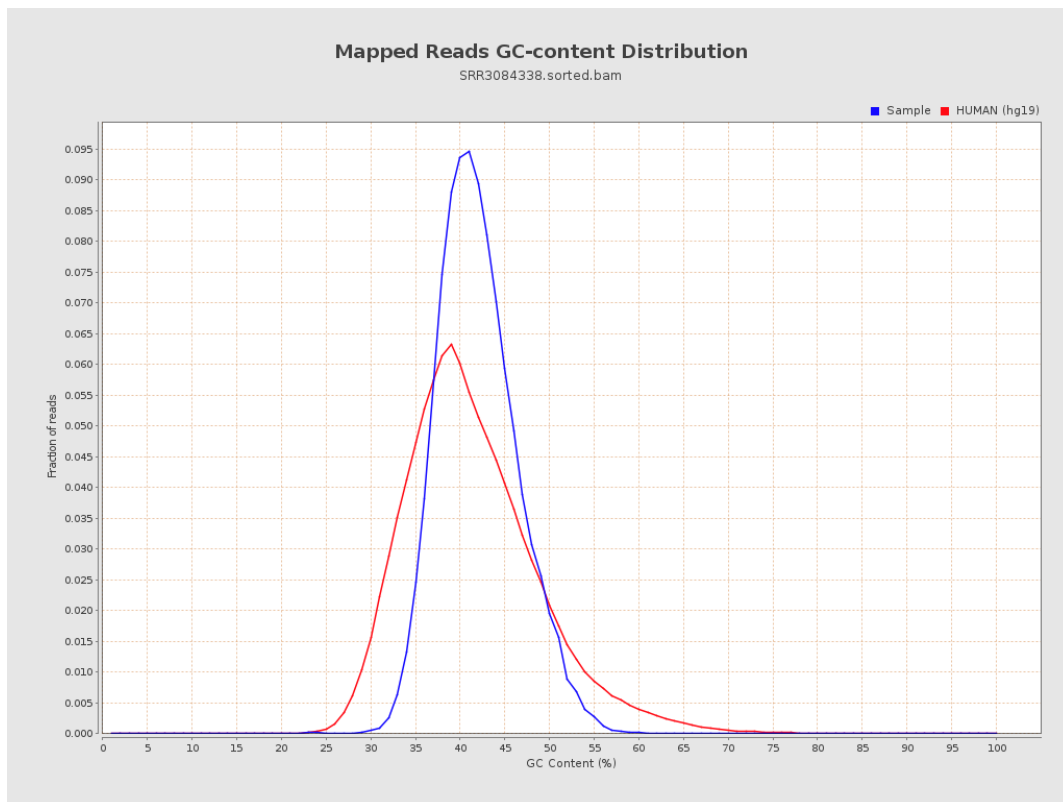
7. Results : Duplication Rate Histogram



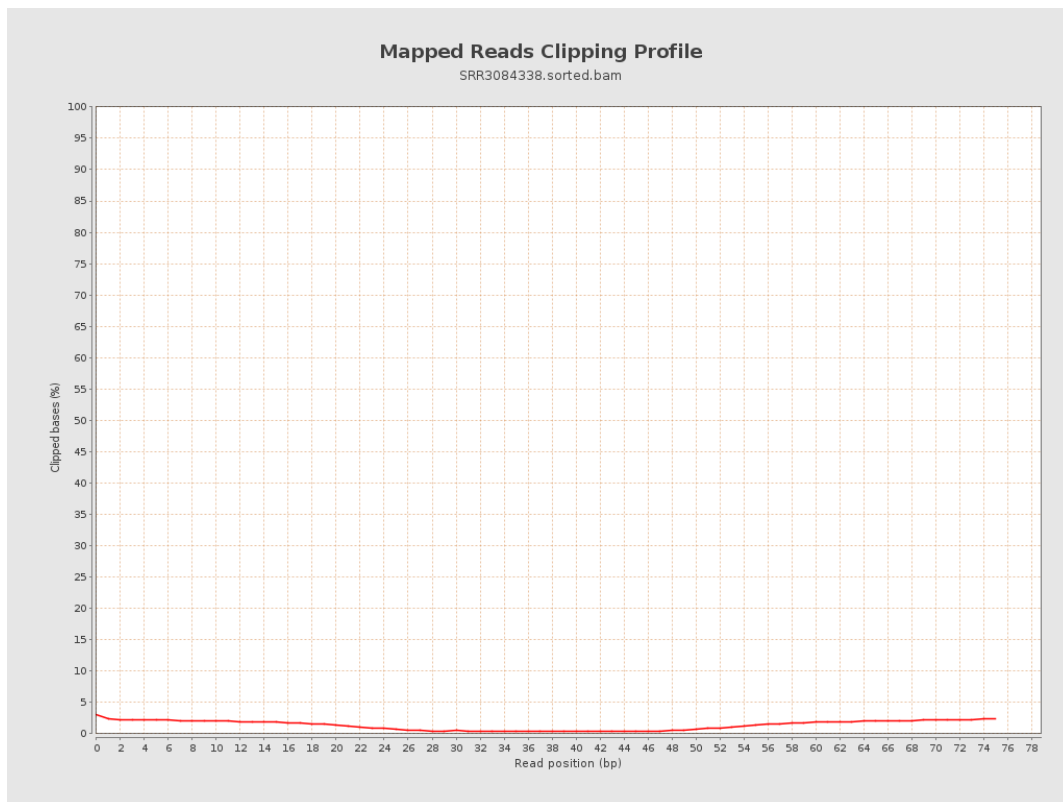
8. Results : Mapped Reads Nucleotide Content



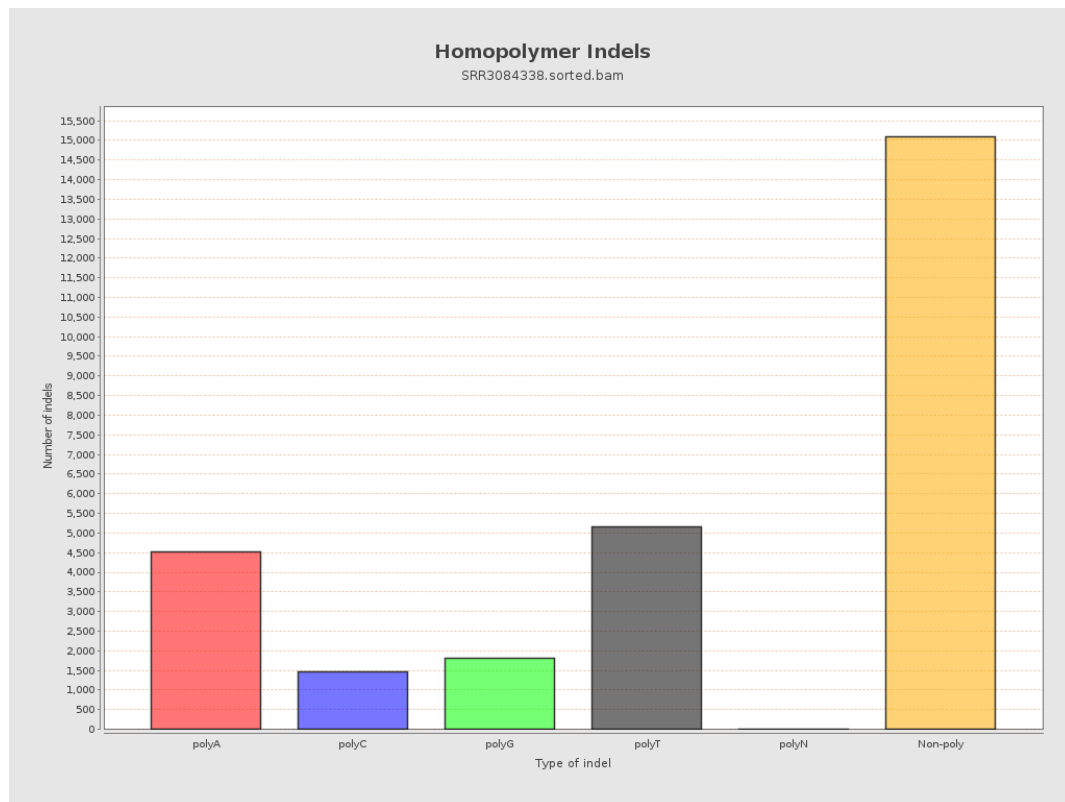
9. Results : Mapped Reads GC-content Distribution



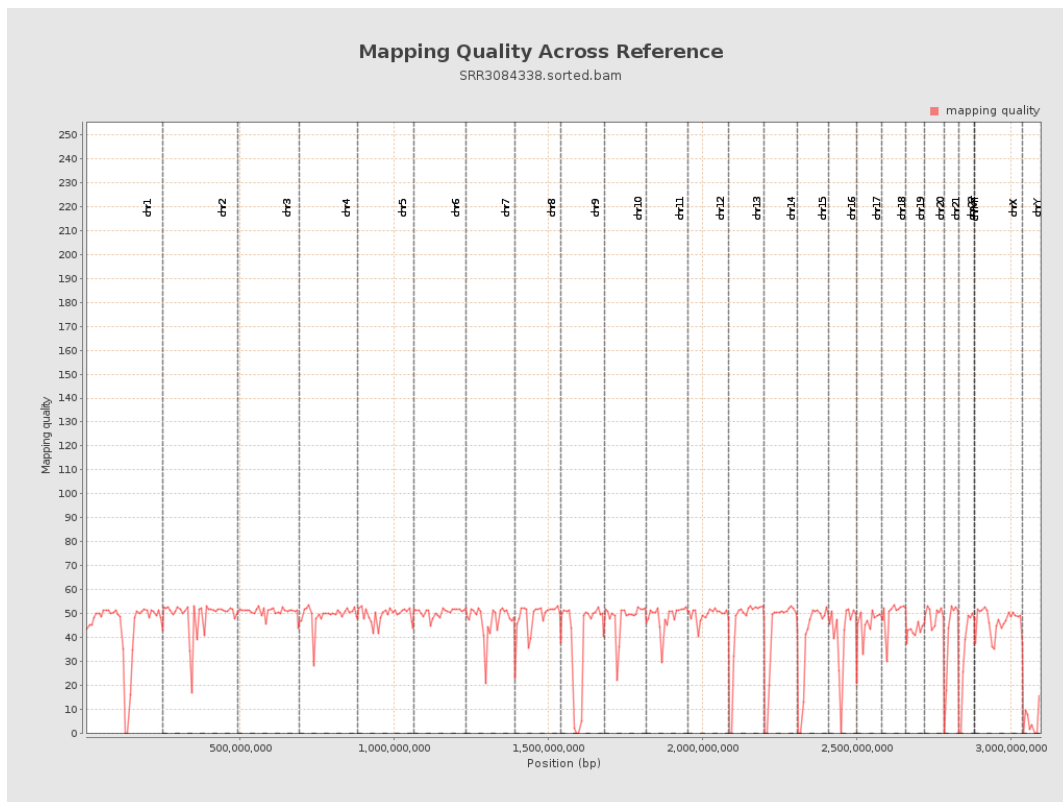
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

