

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 09:15:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008738.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_SRR6008738 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008738.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 09:15:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008738.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,144,773
Mapped reads	864,400 / 75.51%
Unmapped reads	280,373 / 24.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,848 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	21,107 / 1.84%
Duplication rate	1.86%
Clipped reads	409,037 / 35.73%

2.2. ACGT Content

Number/percentage of A's	16,352,599 / 28.69%
Number/percentage of C's	10,200,250 / 17.9%
Number/percentage of T's	17,128,884 / 30.05%
Number/percentage of G's	13,310,732 / 23.35%
Number/percentage of N's	3,116 / 0.01%
GC Percentage	41.25%

2.3. Coverage

Mean	0.0184

Standard Deviation	0.1832
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2.4. Mapping Quality

Mean Mapping Quality	44.75
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2.5. Mismatches and indels

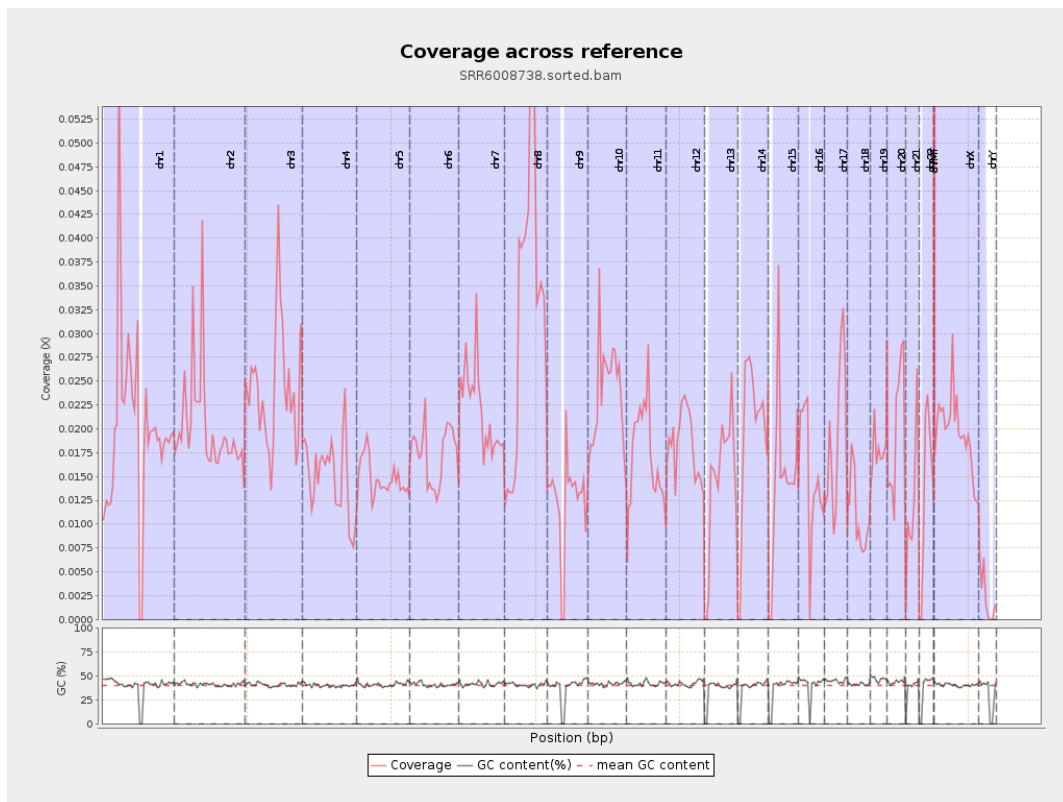
General error rate	0.86%
Mismatches	484,045
Insertions	4,614
Mapped reads with at least one insertion	0.53%
Deletions	17,448
Mapped reads with at least one deletion	2%
Homopolymer indels	47.07%

2.6. Chromosome stats

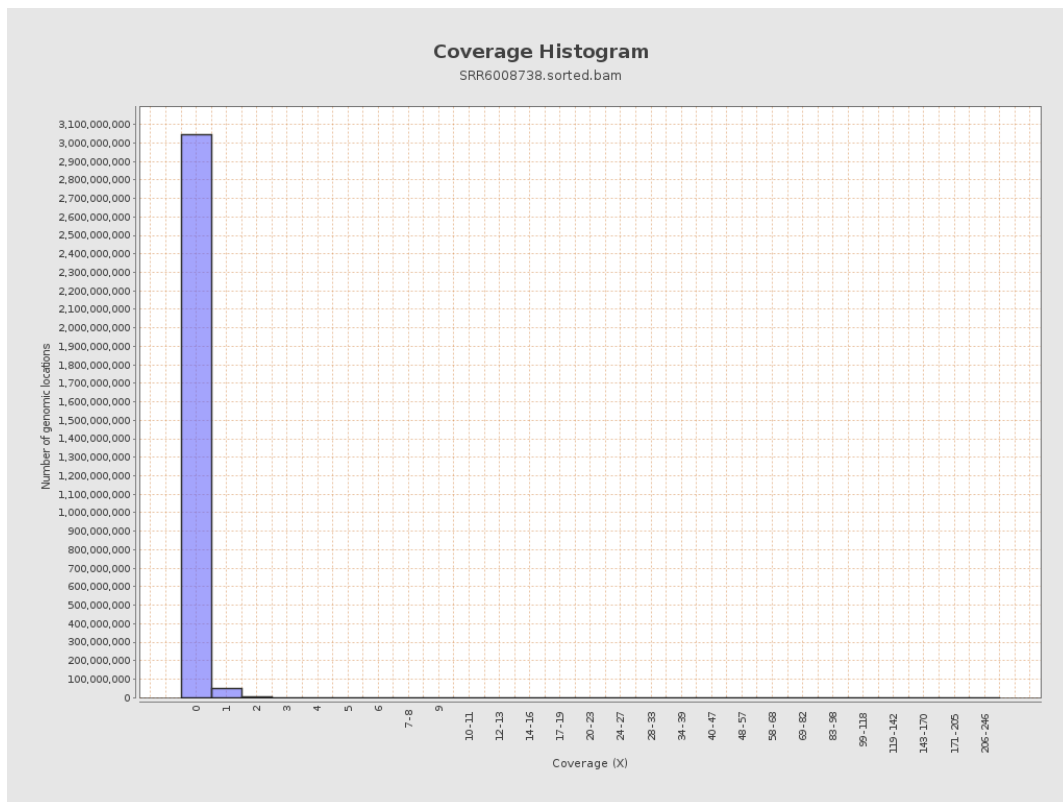
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4938152	0.0198	0.2491
chr2	243199373	4911728	0.0202	0.2309
chr3	198022430	4779037	0.0241	0.164
chr4	191154276	2869178	0.015	0.1311
chr5	180915260	2691733	0.0149	0.127
chr6	171115067	2966090	0.0173	0.1536
chr7	159138663	3500208	0.022	0.2481

chr8	146364022	4799264	0.0328	0.2283
chr9	141213431	1751065	0.0124	0.1738
chr10	135534747	3187830	0.0235	0.2101
chr11	135006516	2356706	0.0175	0.184
chr12	133851895	2457748	0.0184	0.1432
chr13	115169878	1677201	0.0146	0.1262
chr14	107349540	2111164	0.0197	0.1507
chr15	102531392	1494759	0.0146	0.1272
chr16	90354753	1345259	0.0149	0.1368
chr17	81195210	1549988	0.0191	0.1644
chr18	78077248	834493	0.0107	0.2763
chr19	59128983	1061601	0.018	0.1786
chr20	63025520	1244470	0.0197	0.1496
chr21	48129895	595667	0.0124	0.1215
chr22	51304566	705757	0.0138	0.1226
chrMT	16571	9424	0.5687	0.8609
chrX	155270560	3045012	0.0196	0.162
chrY	59373566	139580	0.0024	0.0642

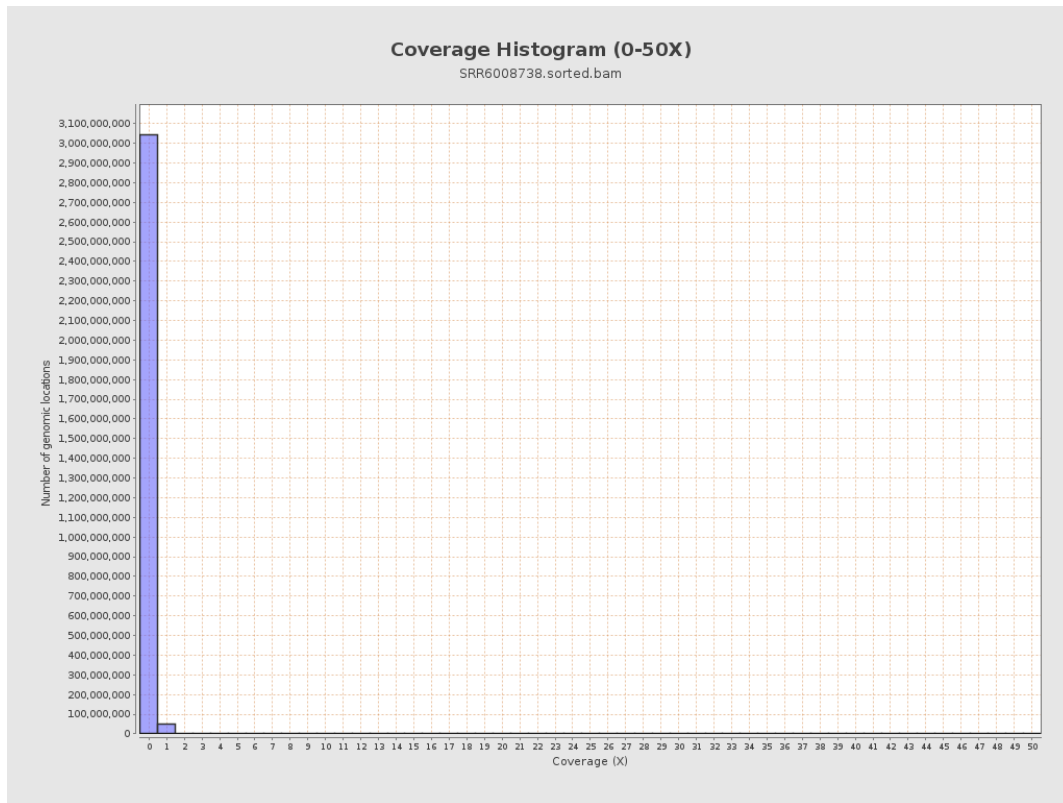
3. Results : Coverage across reference



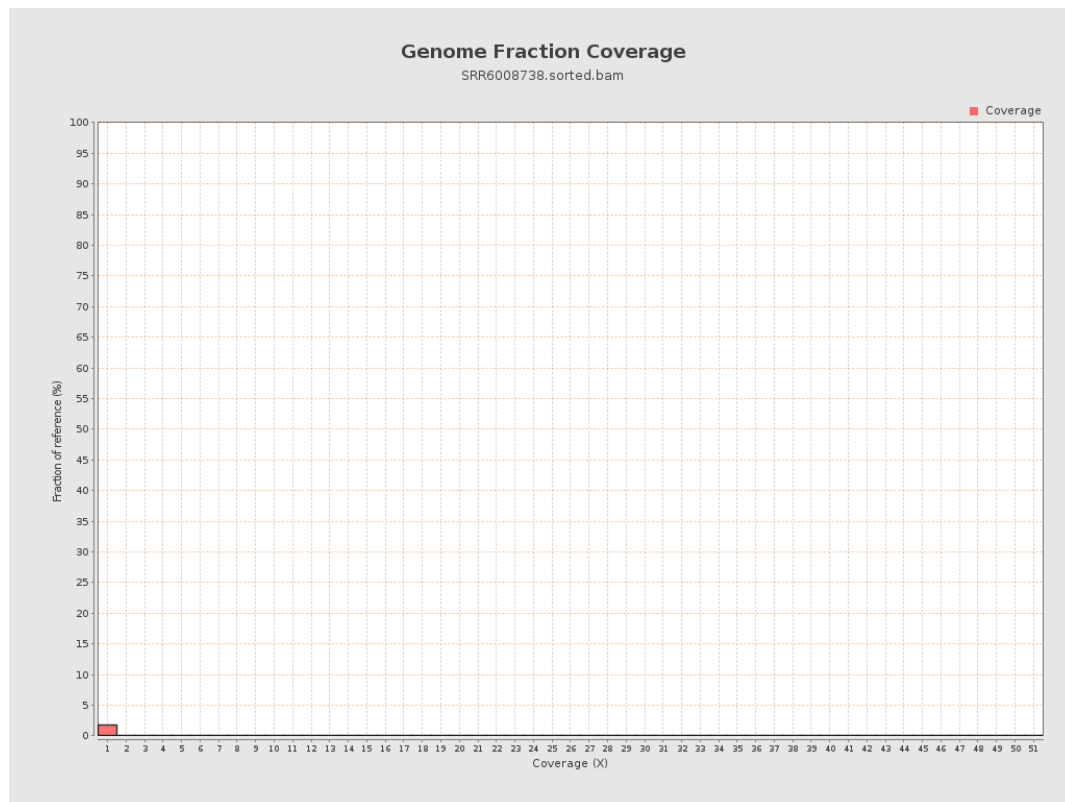
4. Results : Coverage Histogram



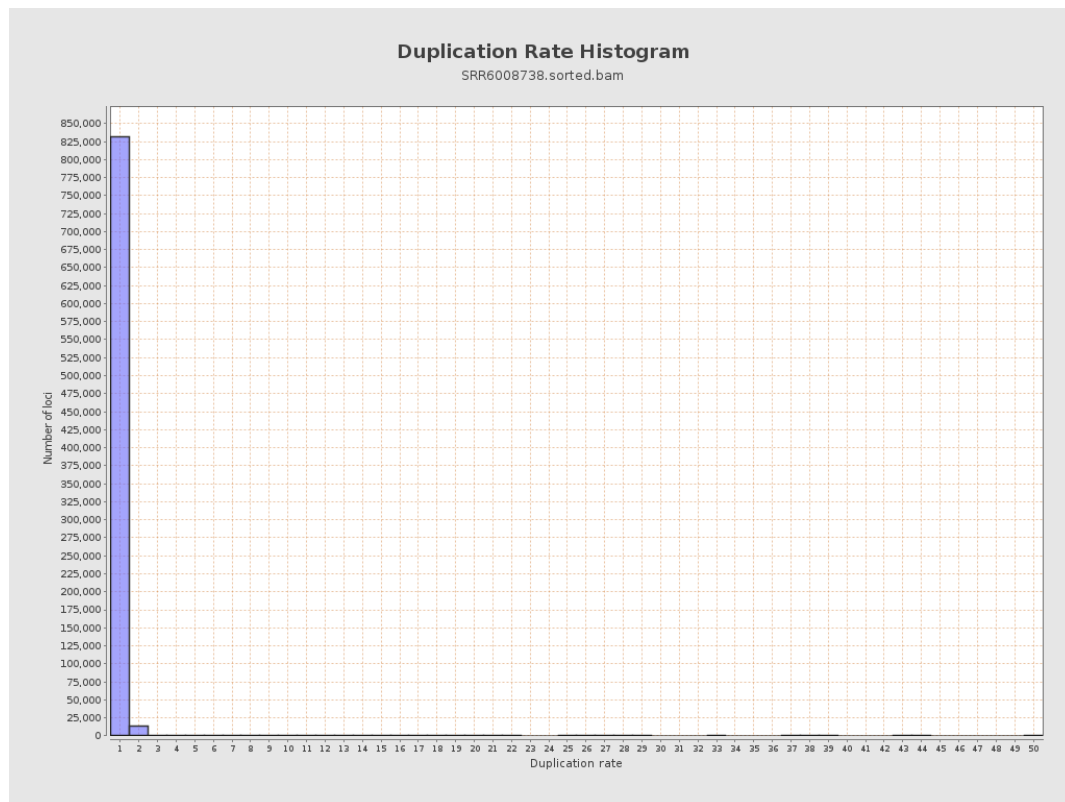
5. Results : Coverage Histogram (0-50X)



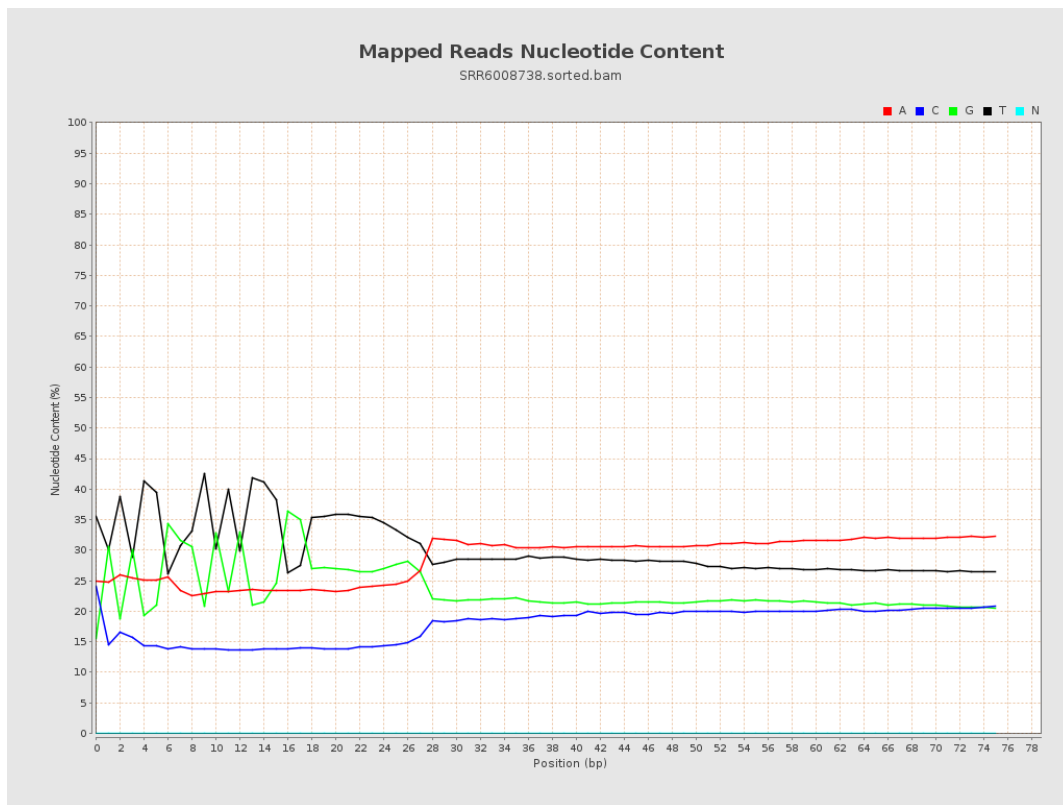
6. Results : Genome Fraction Coverage



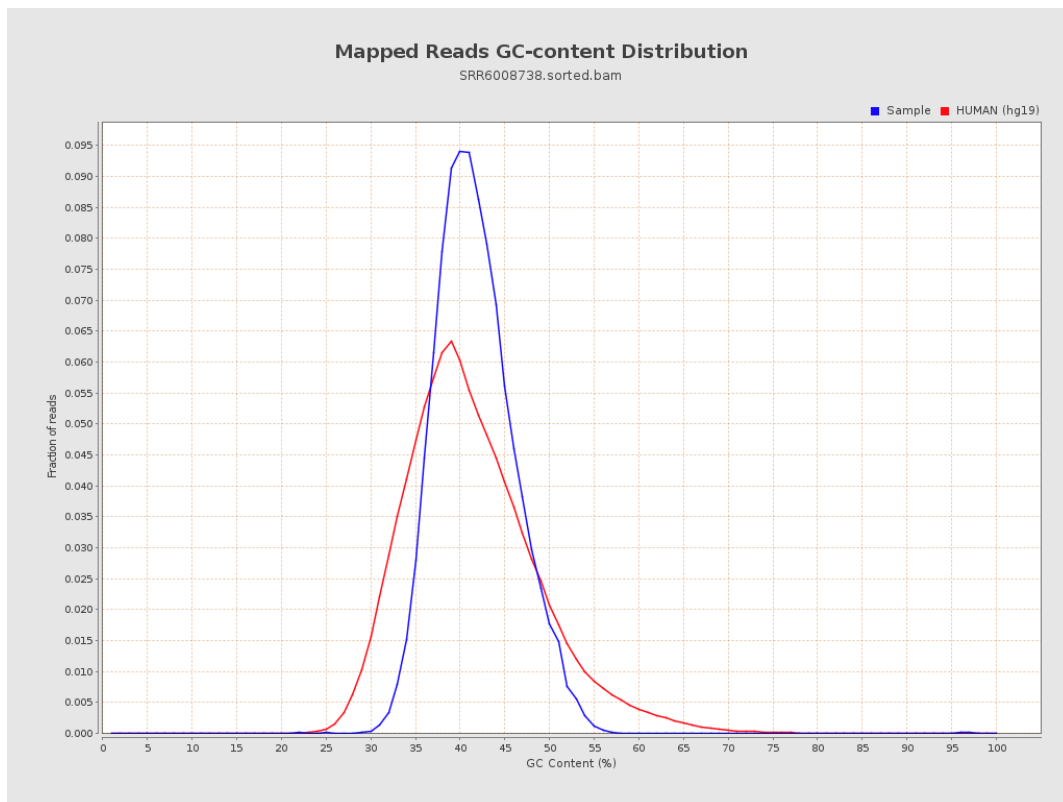
7. Results : Duplication Rate Histogram



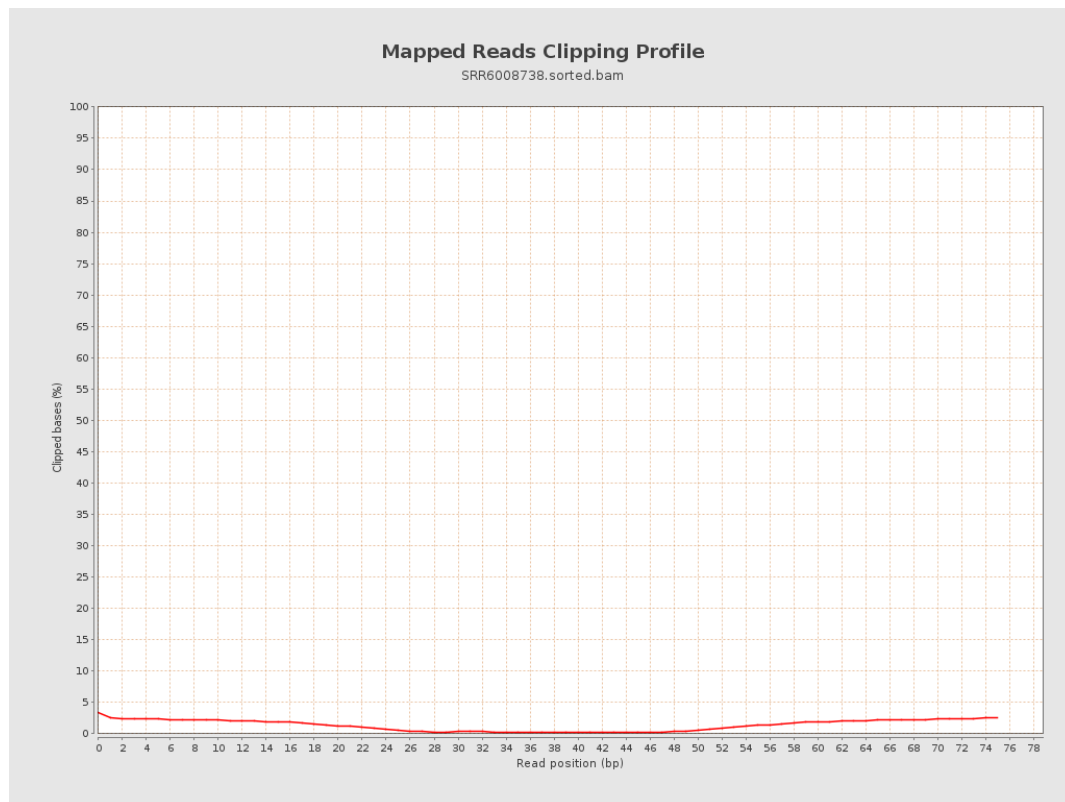
8. Results : Mapped Reads Nucleotide Content



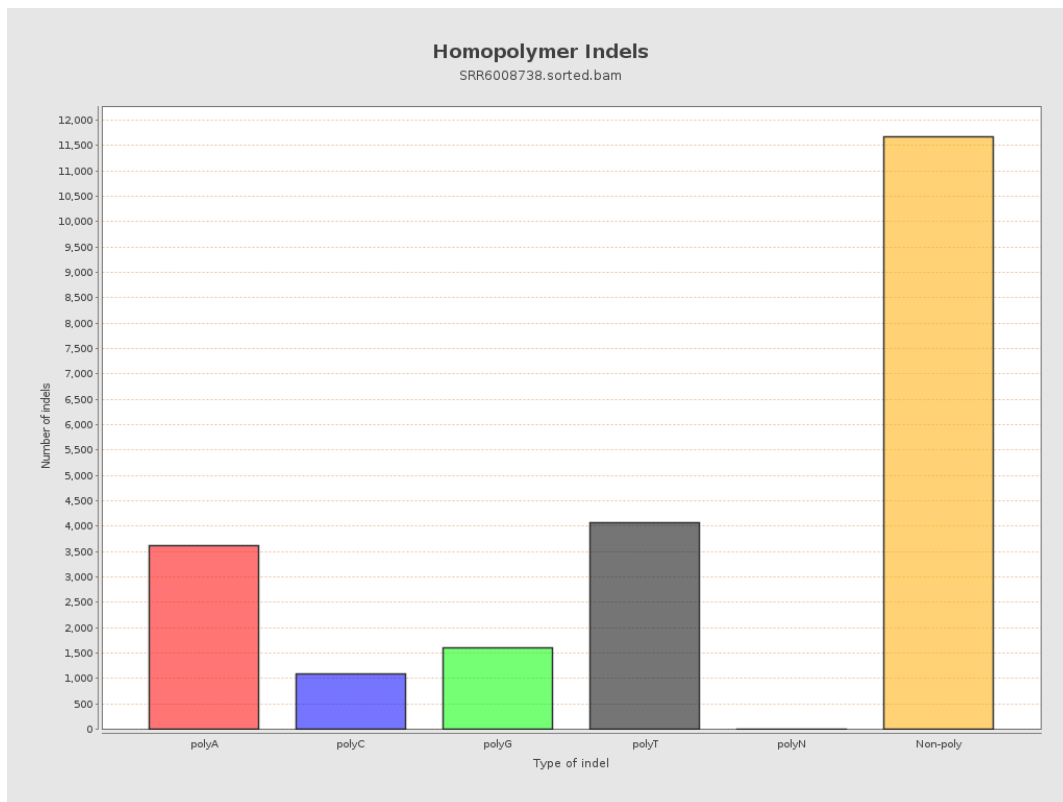
9. Results : Mapped Reads GC-content Distribution



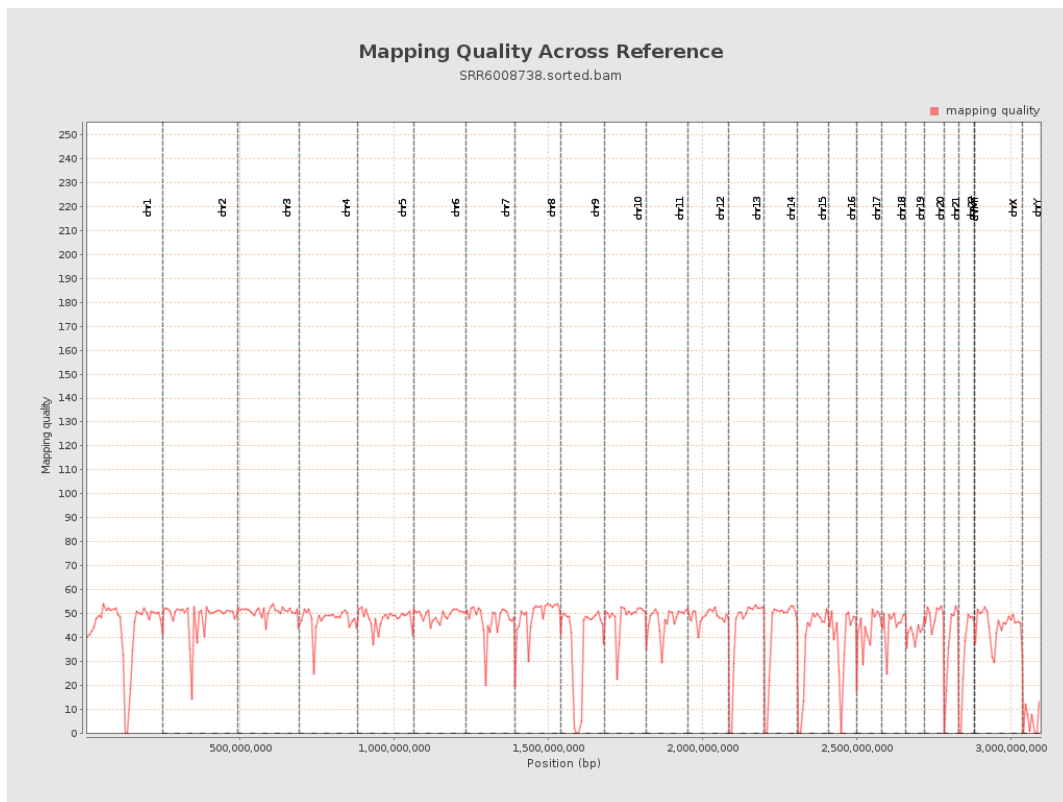
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

