

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 16:59:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238331.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_SRR6238331 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238331.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 16:59:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238331.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,564,440
Mapped reads	2,291,365 / 89.35%
Unmapped reads	273,075 / 10.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,799 / 1.24%
Read min/max/mean length	30 / 76 / 76.44
Duplicated reads (estimated)	153,014 / 5.97%
Duplication rate	5.13%
Clipped reads	1,101,260 / 42.94%

2.2. ACGT Content

Number/percentage of A's	42,865,751 / 28.08%
Number/percentage of C's	29,513,537 / 19.33%
Number/percentage of T's	46,932,009 / 30.74%
Number/percentage of G's	33,314,301 / 21.82%
Number/percentage of N's	36,255 / 0.02%
GC Percentage	41.15%

2.3. Coverage

Mean	0.0493

Standard Deviation	0.4682
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2.4. Mapping Quality

Mean Mapping Quality	46.05
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2.5. Mismatches and indels

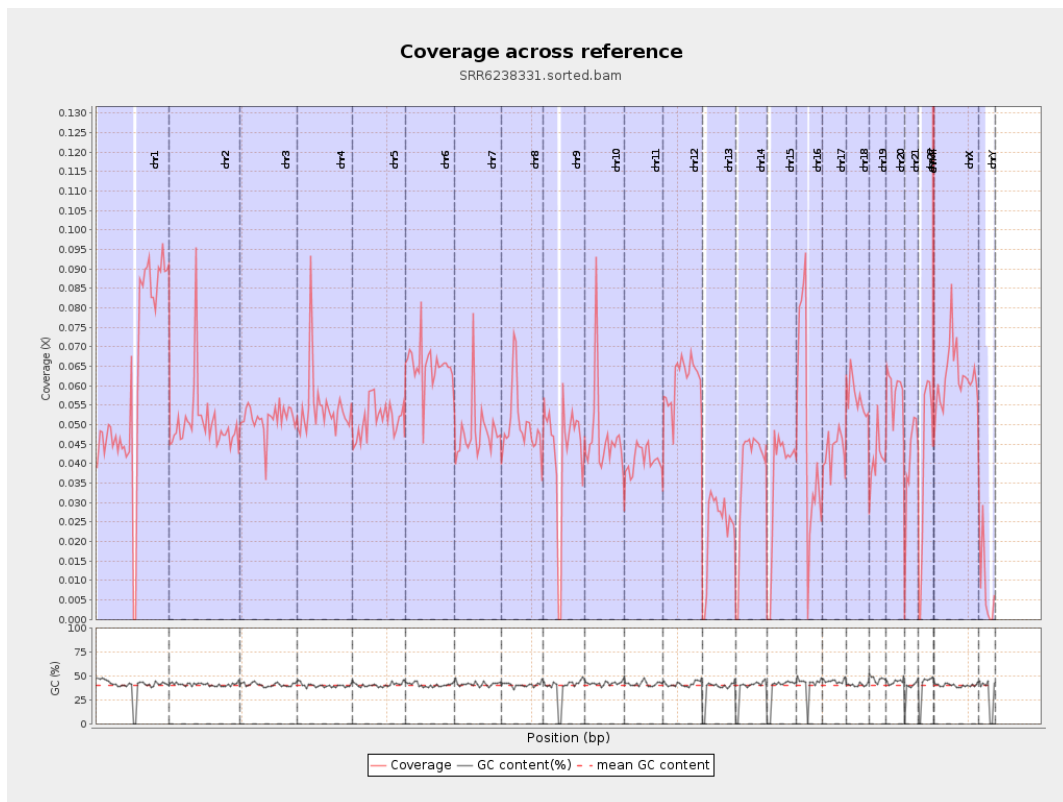
General error rate	0.87%
Mismatches	1,296,140
Insertions	12,786
Mapped reads with at least one insertion	0.55%
Deletions	39,405
Mapped reads with at least one deletion	1.7%
Homopolymer indels	46.59%

2.6. Chromosome stats

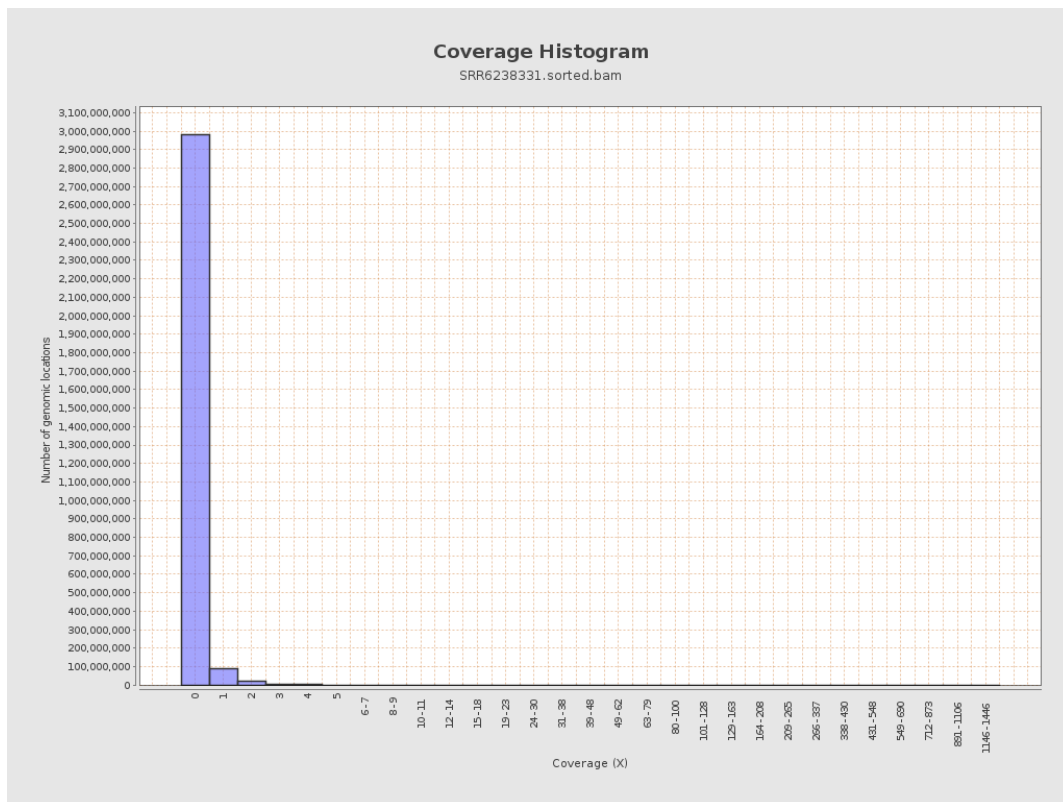
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15246505	0.0612	0.6419
chr2	243199373	12266352	0.0504	0.5942
chr3	198022430	10228478	0.0517	0.2859
chr4	191154276	10361593	0.0542	0.379
chr5	180915260	9313233	0.0515	0.2903
chr6	171115067	11114038	0.065	0.3974
chr7	159138663	7677875	0.0482	0.5323

chr8	146364022	7278965	0.0497	0.9096
chr9	141213431	6077671	0.043	0.4357
chr10	135534747	6360326	0.0469	0.5056
chr11	135006516	5489555	0.0407	0.4152
chr12	133851895	8216099	0.0614	0.3251
chr13	115169878	2681699	0.0233	0.1958
chr14	107349540	4030481	0.0375	0.2805
chr15	102531392	3688367	0.036	0.2436
chr16	90354753	4353945	0.0482	0.3091
chr17	81195210	3518231	0.0433	0.2995
chr18	78077248	4464829	0.0572	0.8024
chr19	59128983	2463151	0.0417	0.4827
chr20	63025520	3708888	0.0588	0.3209
chr21	48129895	1931425	0.0401	0.3109
chr22	51304566	2061444	0.0402	0.2512
chrMT	16571	42078	2.5393	2.9226
chrX	155270560	9671061	0.0623	0.3695
chrY	59373566	483907	0.0082	0.2625

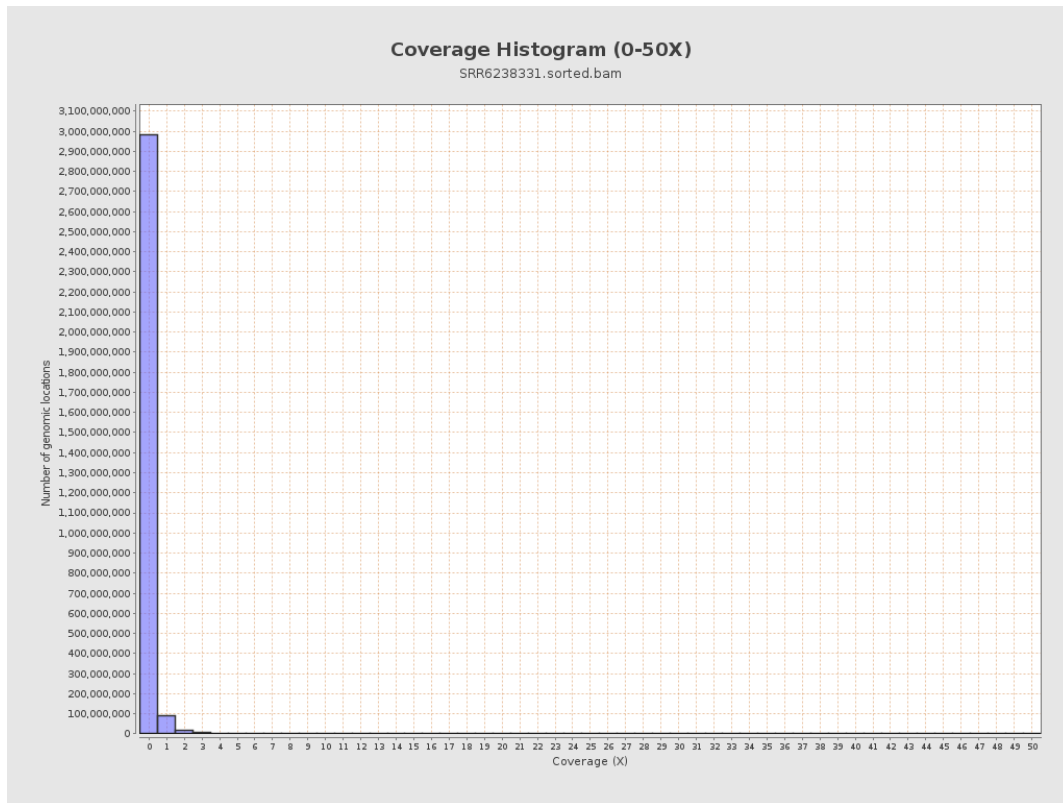
3. Results : Coverage across reference



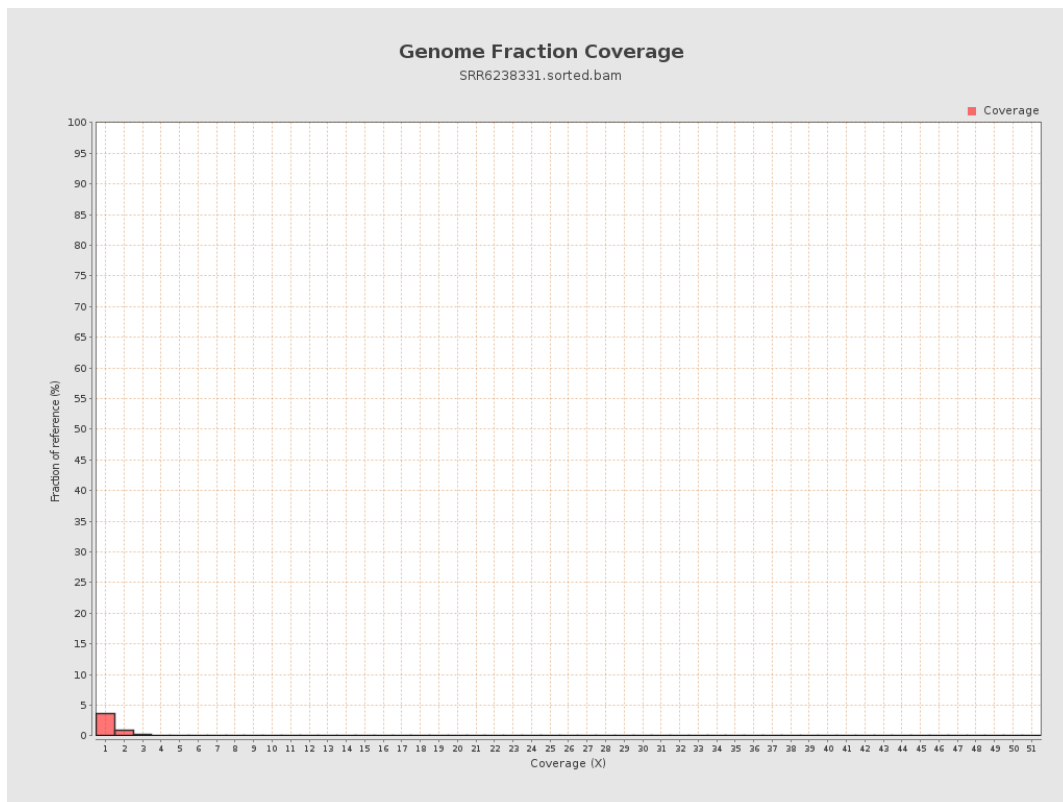
4. Results : Coverage Histogram



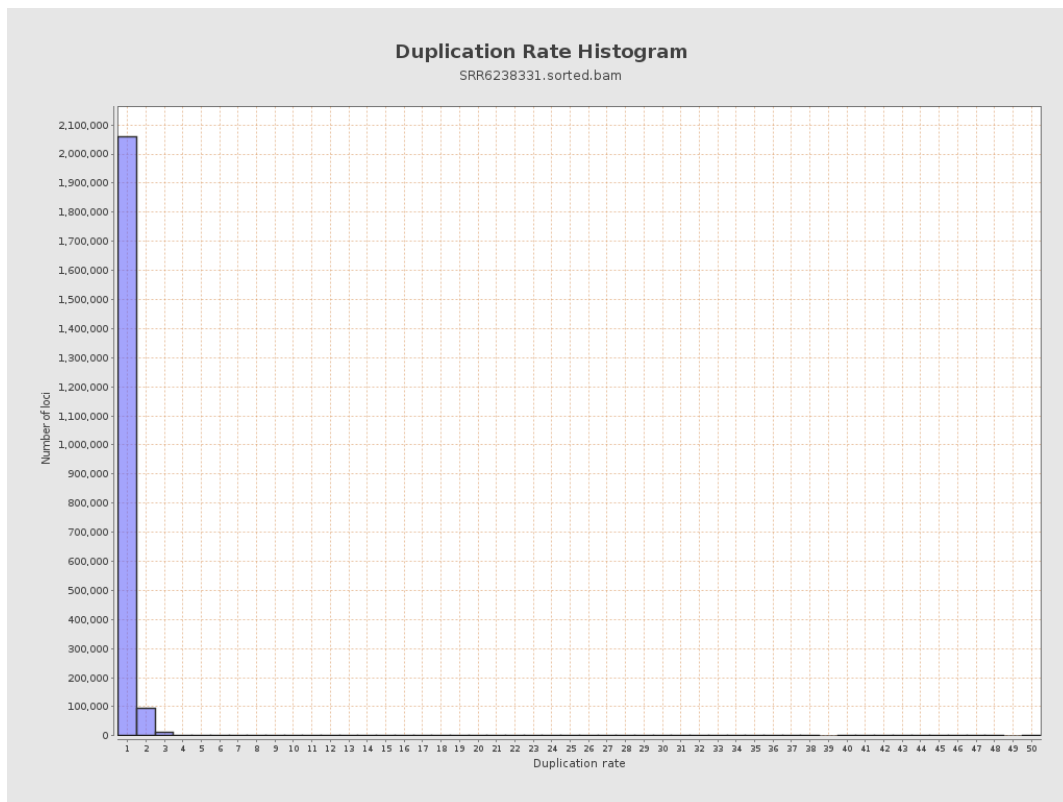
5. Results : Coverage Histogram (0-50X)



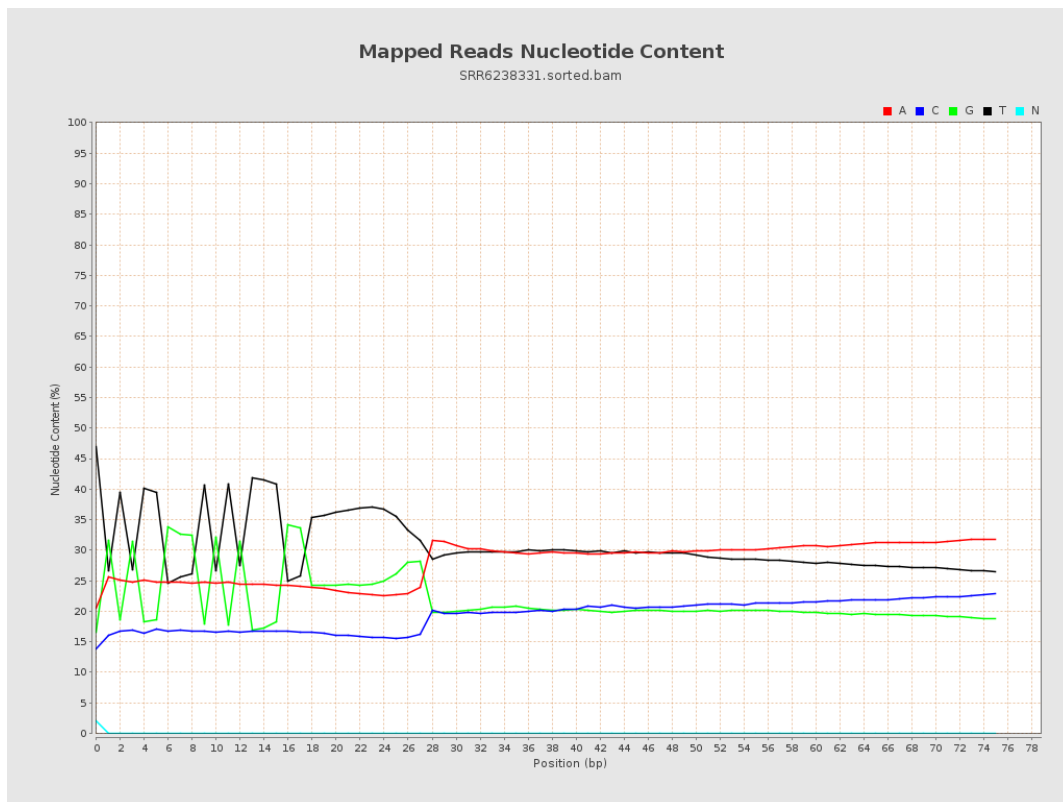
6. Results : Genome Fraction Coverage



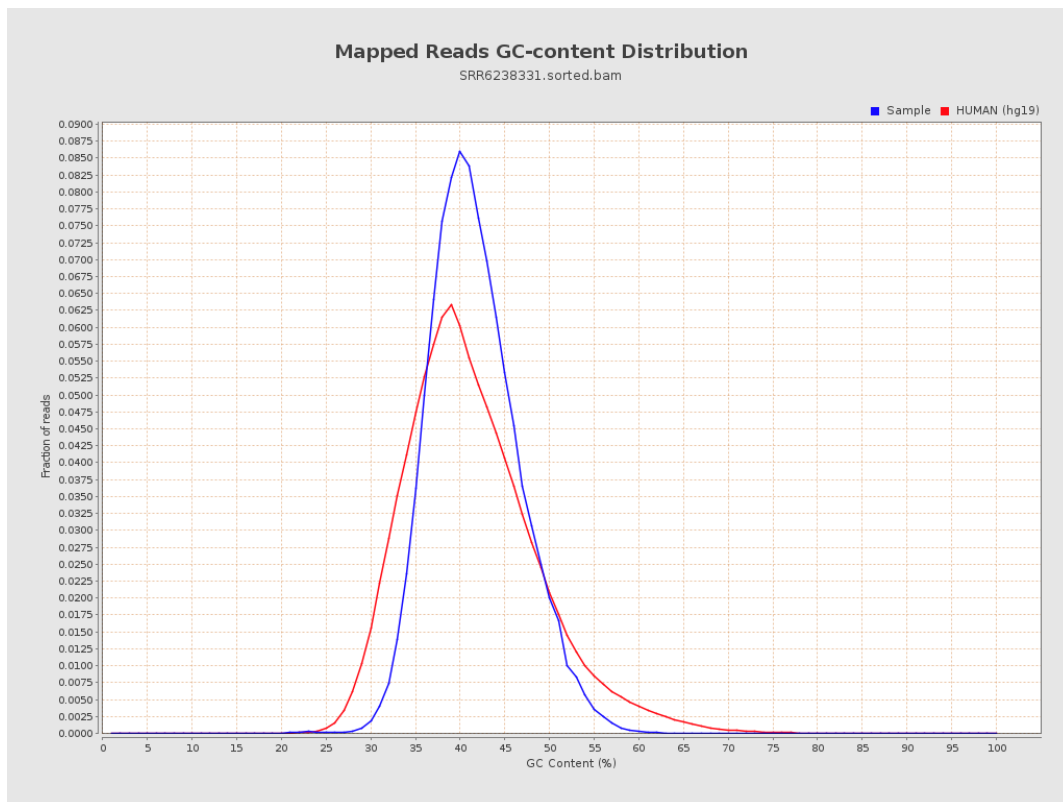
7. Results : Duplication Rate Histogram



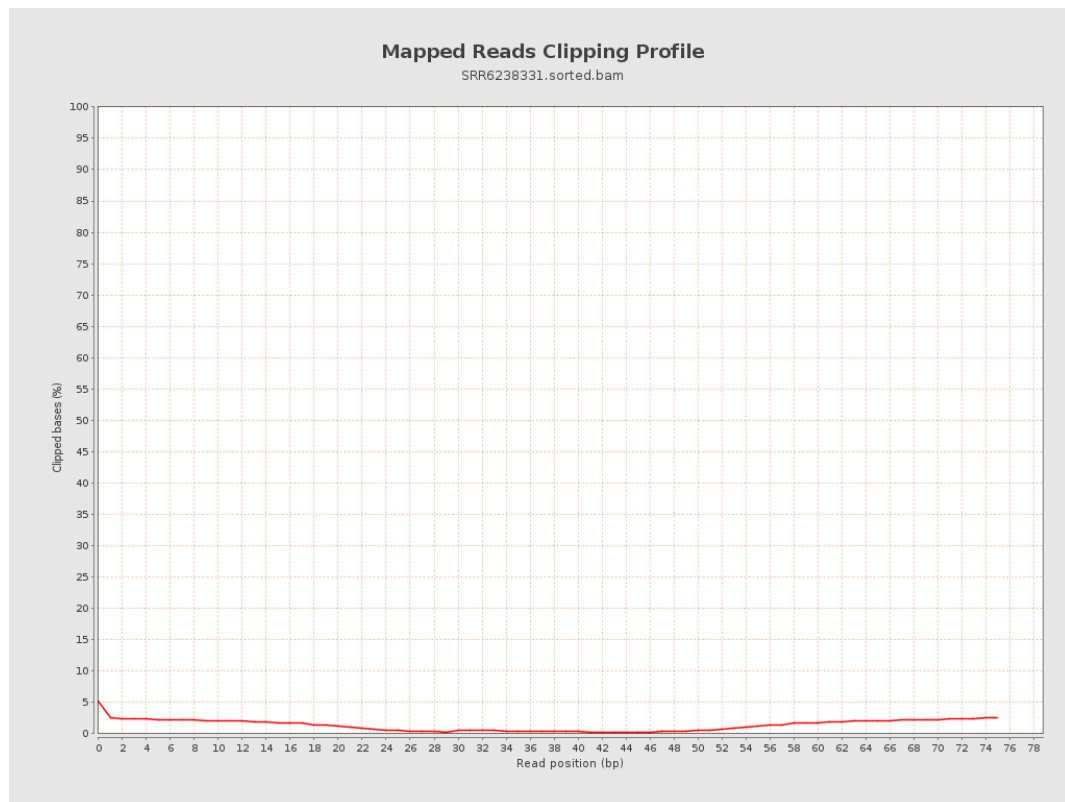
8. Results : Mapped Reads Nucleotide Content



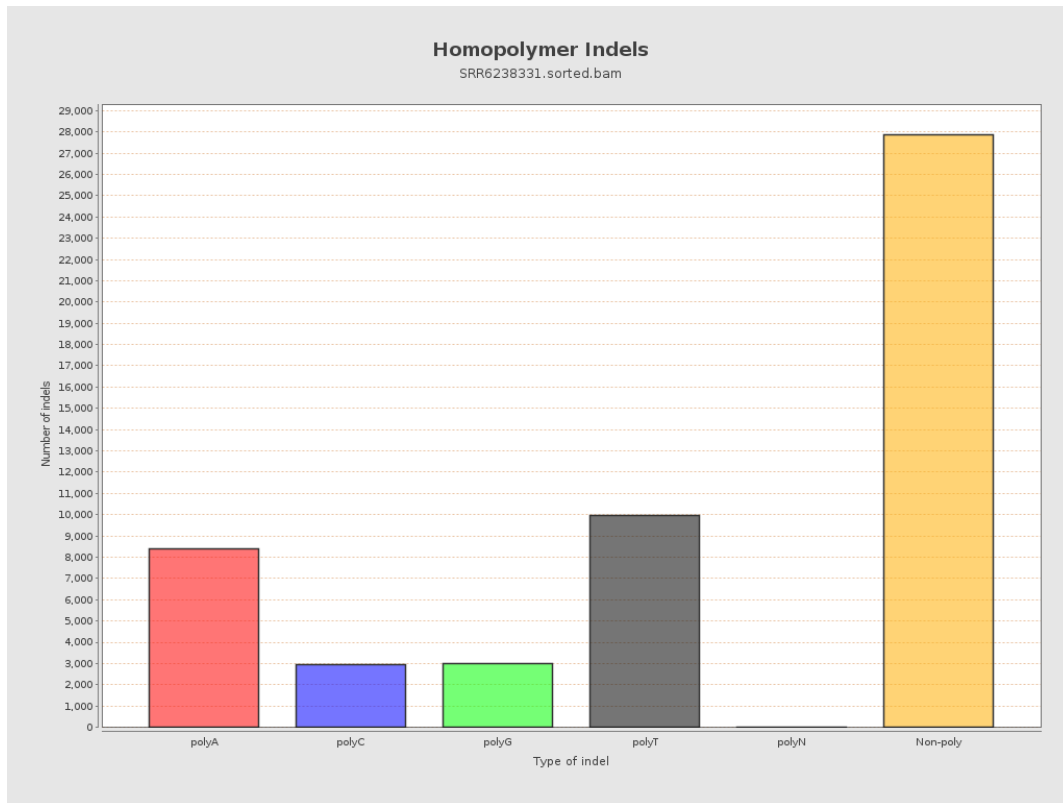
9. Results : Mapped Reads GC-content Distribution



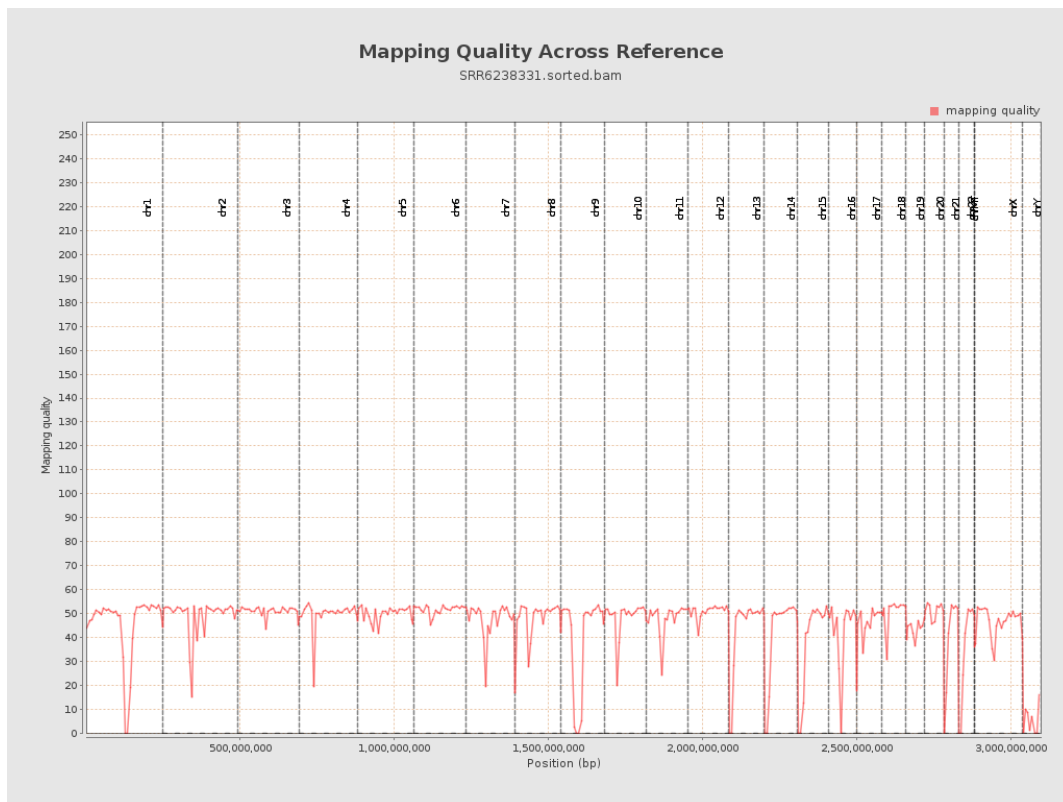
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

