

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 10:03:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238033.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_SRR6238033 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238033.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 10:03:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238033.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,610,163
Mapped reads	1,234,404 / 76.66%
Unmapped reads	375,759 / 23.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,764 / 0.79%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	96,319 / 5.98%
Duplication rate	6.25%
Clipped reads	557,529 / 34.63%

2.2. ACGT Content

Number/percentage of A's	22,274,115 / 27.25%
Number/percentage of C's	15,372,446 / 18.81%
Number/percentage of T's	25,691,168 / 31.43%
Number/percentage of G's	18,382,463 / 22.49%
Number/percentage of N's	10,738 / 0.01%
GC Percentage	41.3%

2.3. Coverage

Mean	0.0264

Standard Deviation	0.2998
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2.4. Mapping Quality

Mean Mapping Quality	45.64
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2.5. Mismatches and indels

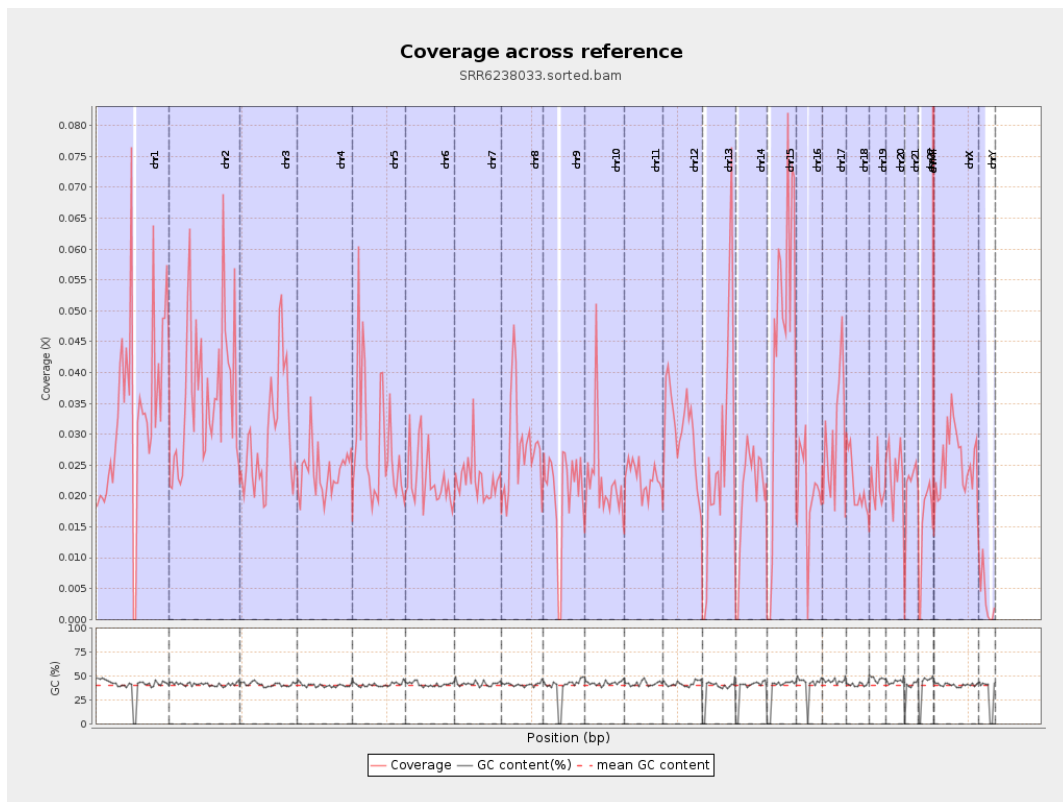
General error rate	0.78%
Mismatches	628,488
Insertions	5,644
Mapped reads with at least one insertion	0.45%
Deletions	19,221
Mapped reads with at least one deletion	1.54%
Homopolymer indels	47.22%

2.6. Chromosome stats

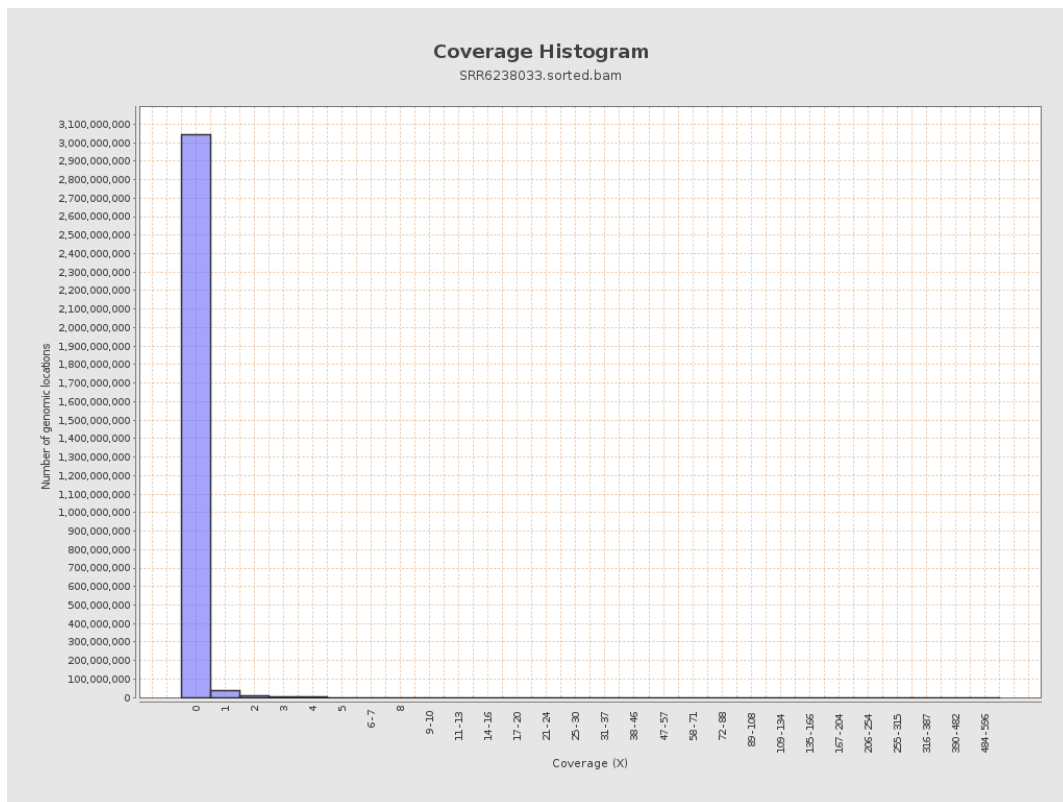
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8230815	0.033	0.5518
chr2	243199373	8793360	0.0362	0.3369
chr3	198022430	5824768	0.0294	0.2425
chr4	191154276	4561227	0.0239	0.2215
chr5	180915260	5150372	0.0285	0.2371
chr6	171115067	3867866	0.0226	0.2323
chr7	159138663	3619565	0.0227	0.2814

chr8	146364022	4036473	0.0276	0.322
chr9	141213431	2905739	0.0206	0.261
chr10	135534747	3021447	0.0223	0.3053
chr11	135006516	3064980	0.0227	0.2499
chr12	133851895	4084717	0.0305	0.2486
chr13	115169878	3082803	0.0268	0.2302
chr14	107349540	2200395	0.0205	0.2114
chr15	102531392	4595776	0.0448	0.3016
chr16	90354753	1903303	0.0211	0.2158
chr17	81195210	2371802	0.0292	0.2471
chr18	78077248	1698923	0.0218	0.4278
chr19	59128983	1275945	0.0216	0.3713
chr20	63025520	1497927	0.0238	0.2212
chr21	48129895	1014345	0.0211	0.2116
chr22	51304566	777778	0.0152	0.1712
chrMT	16571	30709	1.8532	2.0459
chrX	155270560	3955078	0.0255	0.2317
chrY	59373566	199240	0.0034	0.0917

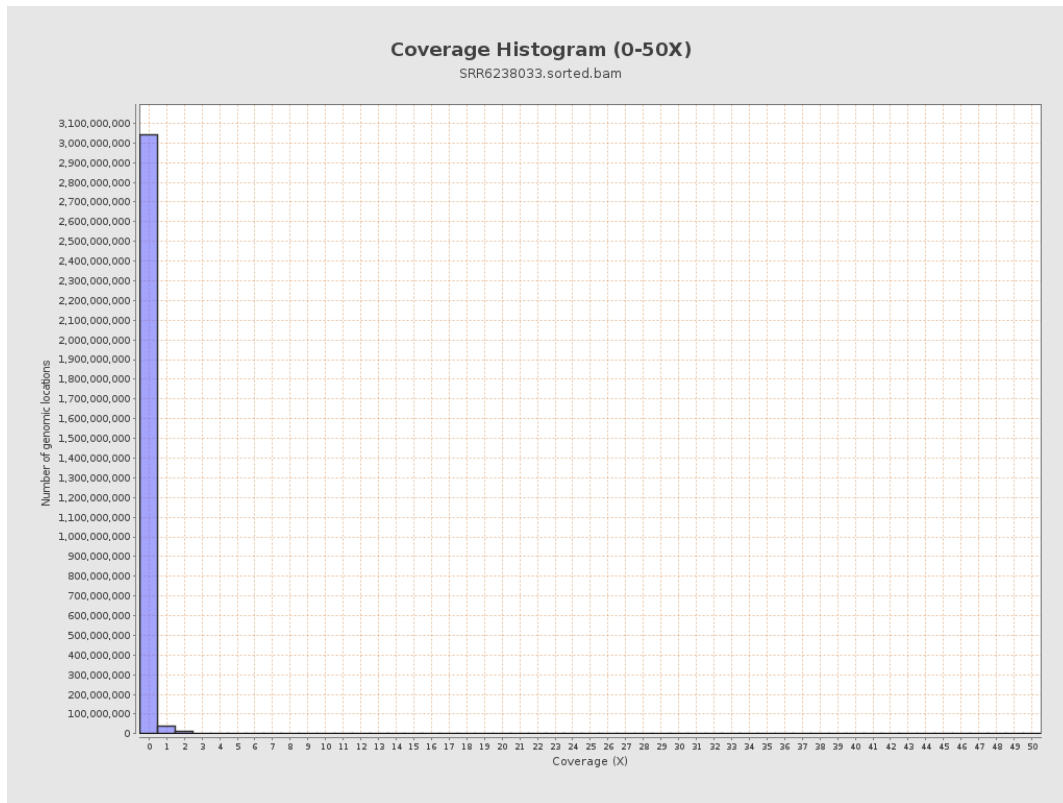
3. Results : Coverage across reference



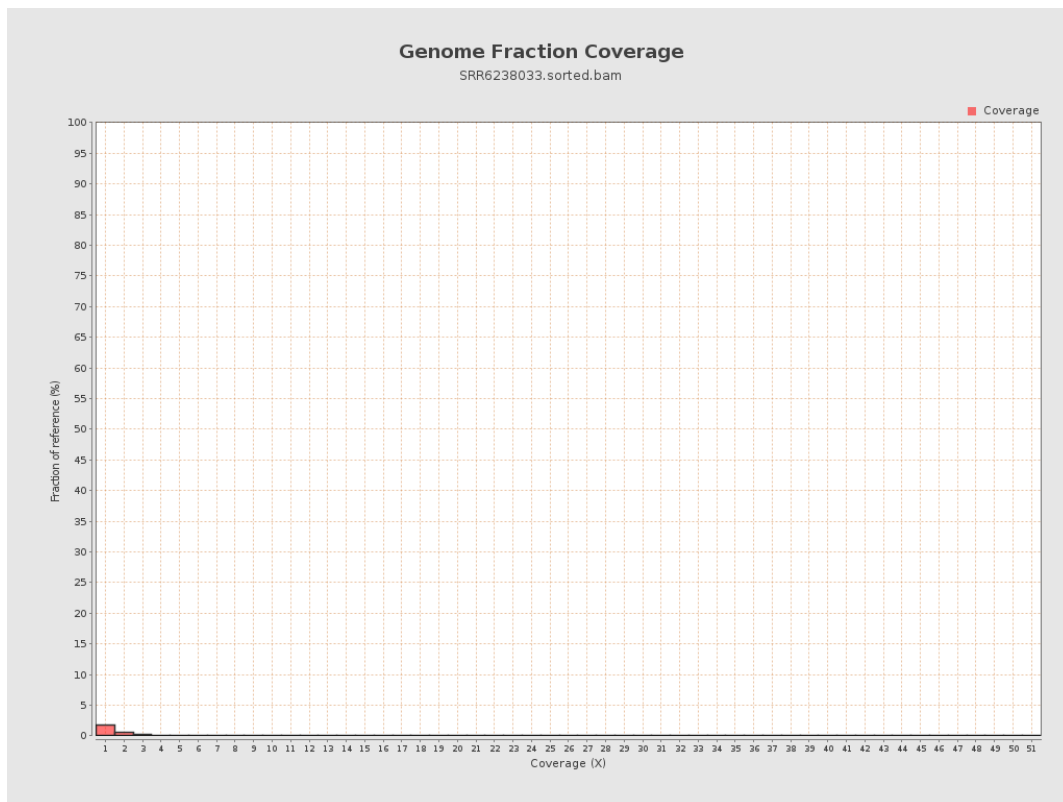
4. Results : Coverage Histogram



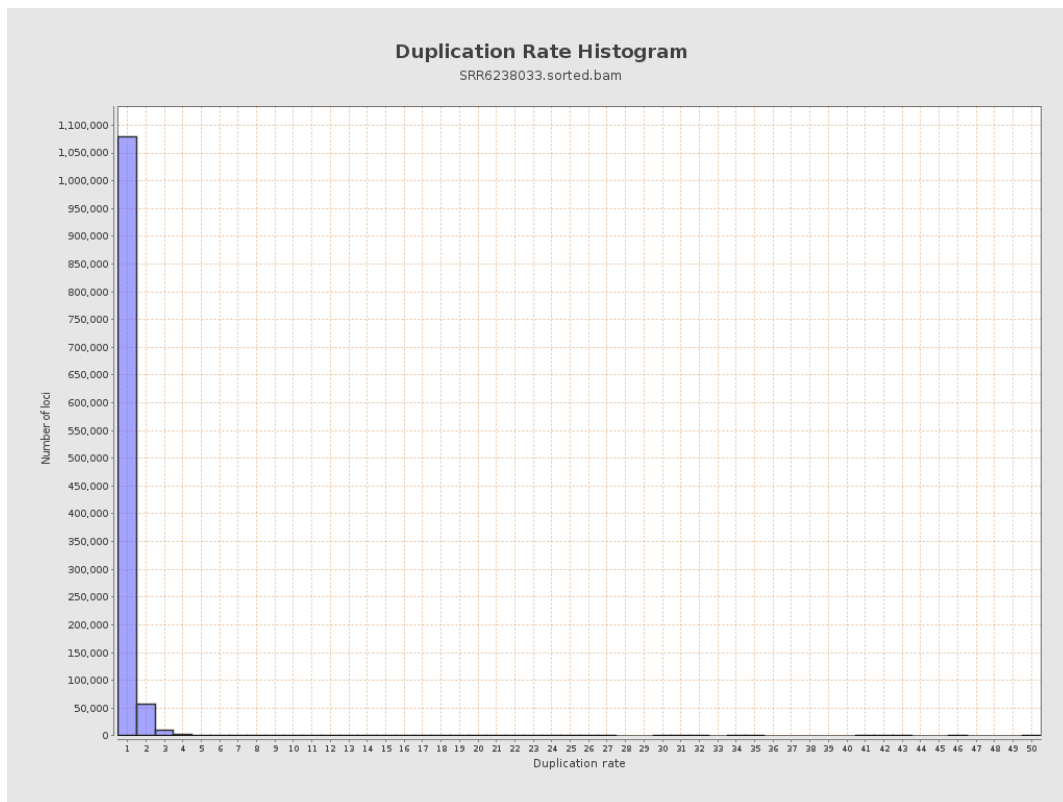
5. Results : Coverage Histogram (0-50X)



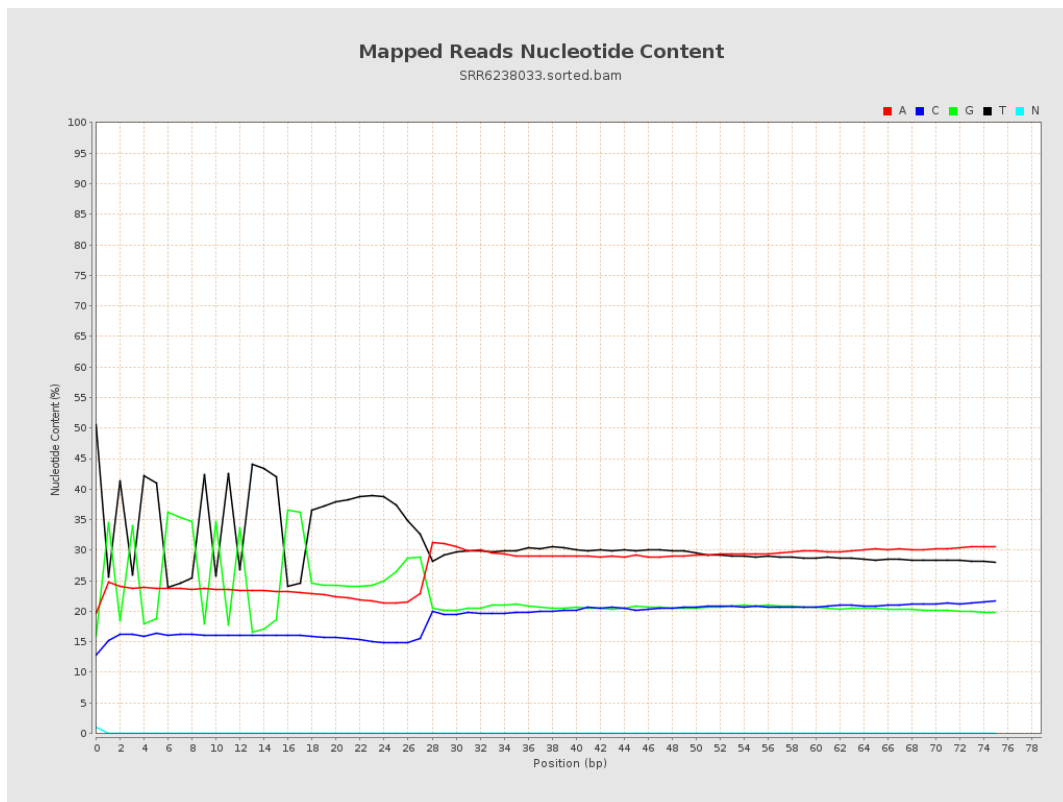
6. Results : Genome Fraction Coverage



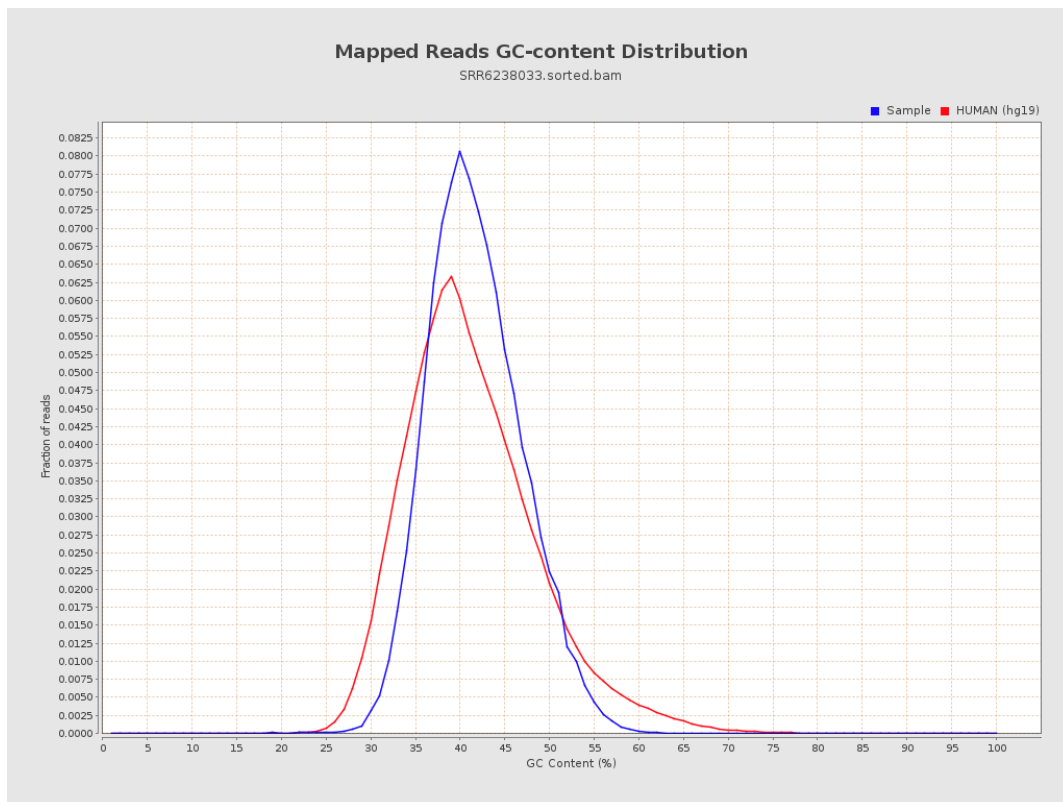
7. Results : Duplication Rate Histogram



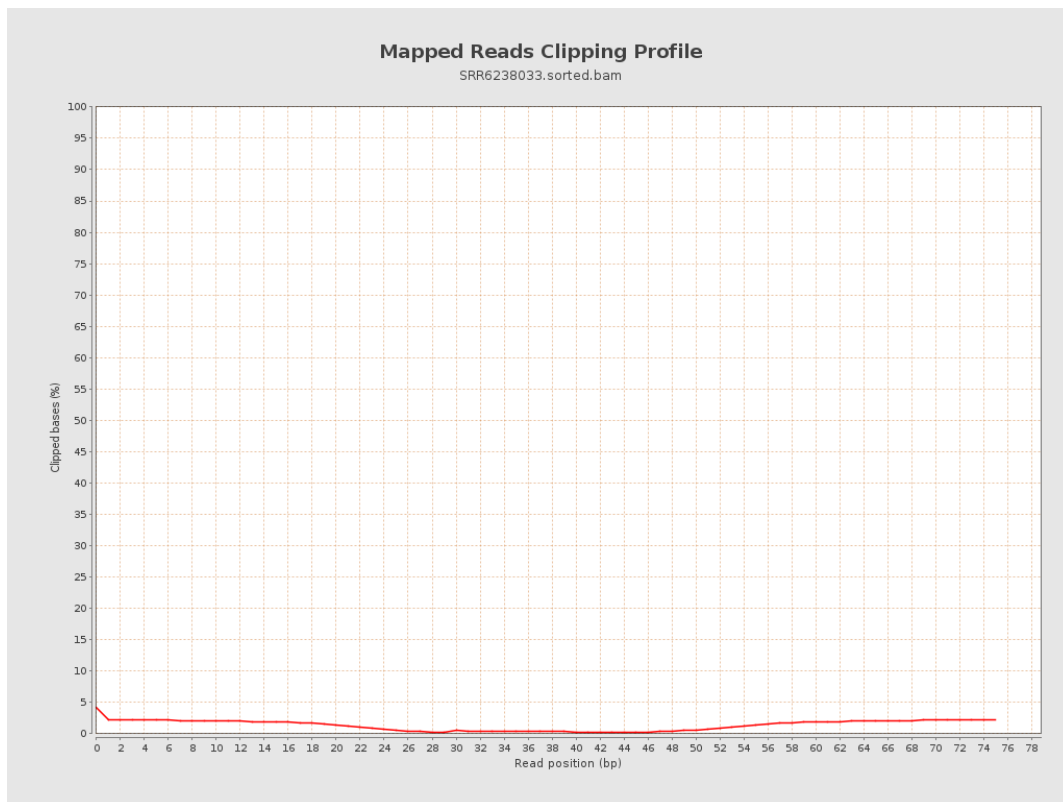
8. Results : Mapped Reads Nucleotide Content



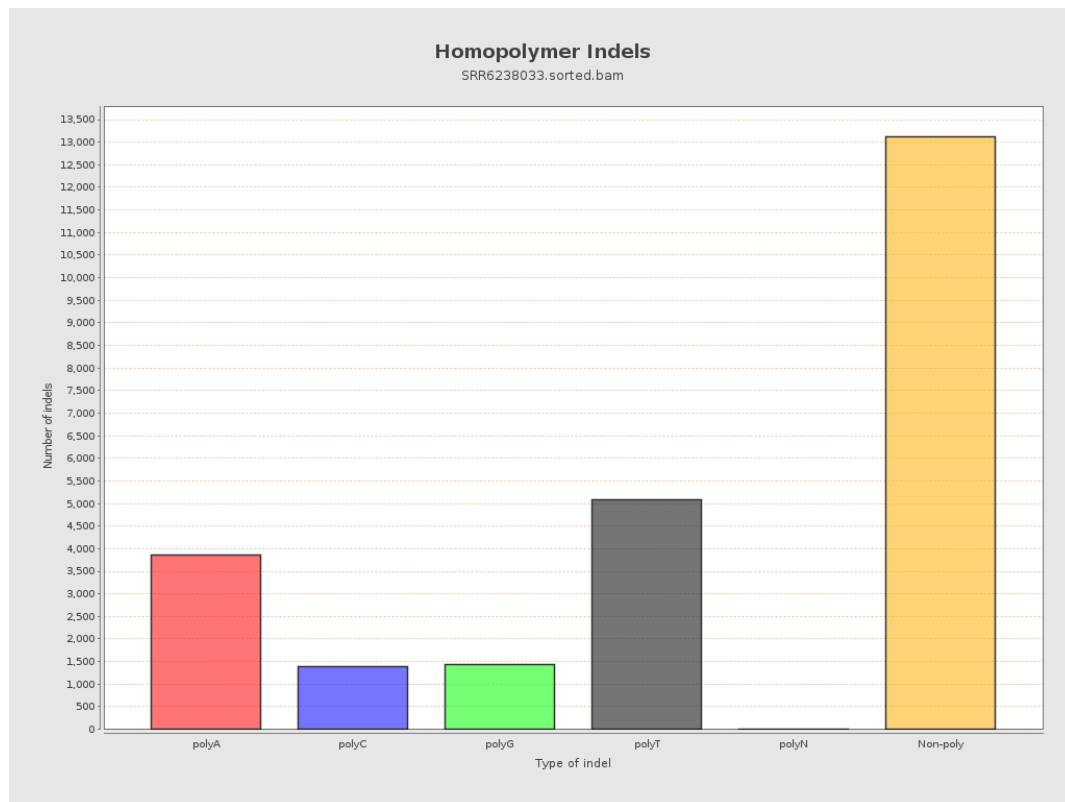
9. Results : Mapped Reads GC-content Distribution



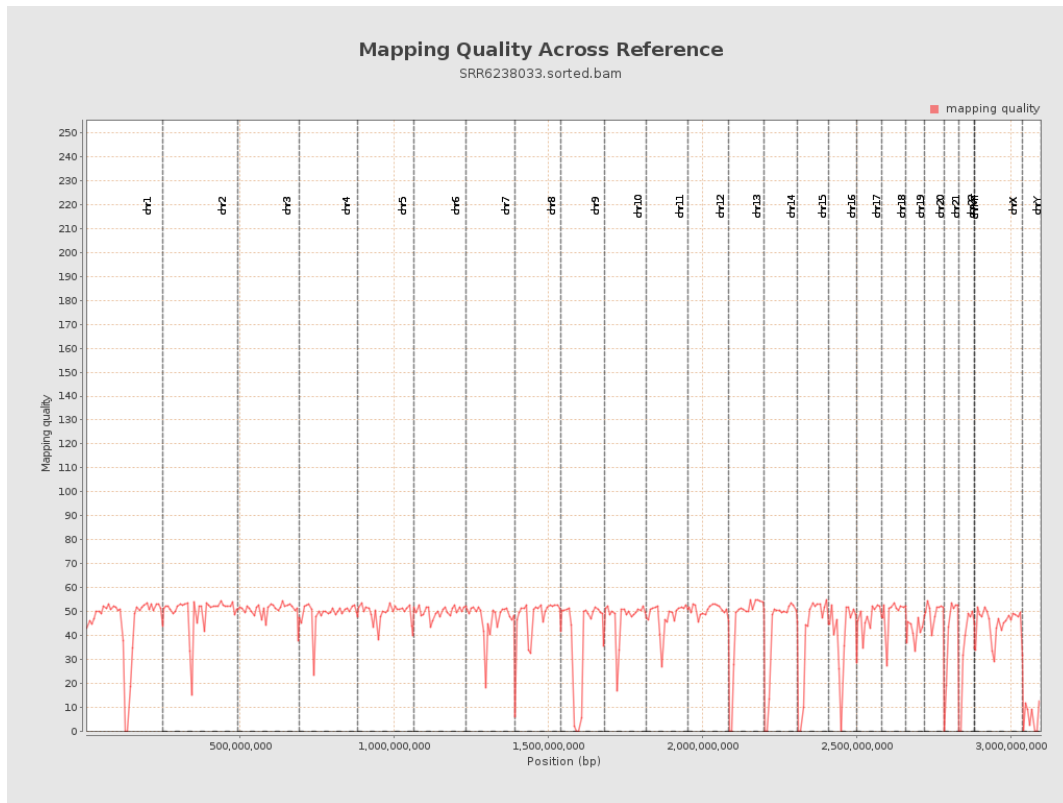
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

