

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 13:33:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238264.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_SRR6238264 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238264.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 13:33:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238264.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,935,416
Mapped reads	1,557,287 / 80.46%
Unmapped reads	378,129 / 19.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,496 / 0.9%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	192,368 / 9.94%
Duplication rate	9.56%
Clipped reads	888,727 / 45.92%

2.2. ACGT Content

Number/percentage of A's	27,887,389 / 27.94%
Number/percentage of C's	19,419,698 / 19.46%
Number/percentage of T's	30,541,838 / 30.6%
Number/percentage of G's	21,925,863 / 21.97%
Number/percentage of N's	30,447 / 0.03%
GC Percentage	41.43%

2.3. Coverage

Mean	0.0323

Standard Deviation	0.3542
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2.4. Mapping Quality

Mean Mapping Quality	45.17
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2.5. Mismatches and indels

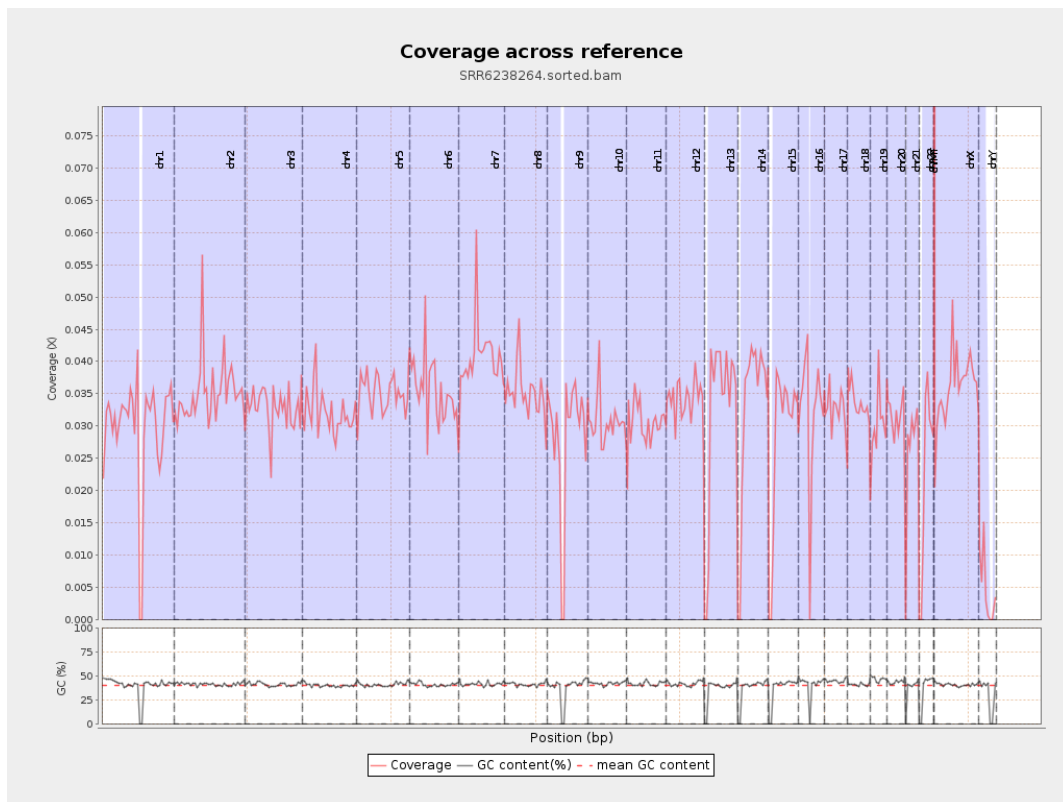
General error rate	1.05%
Mismatches	1,035,106
Insertions	8,412
Mapped reads with at least one insertion	0.54%
Deletions	39,629
Mapped reads with at least one deletion	2.51%
Homopolymer indels	46.25%

2.6. Chromosome stats

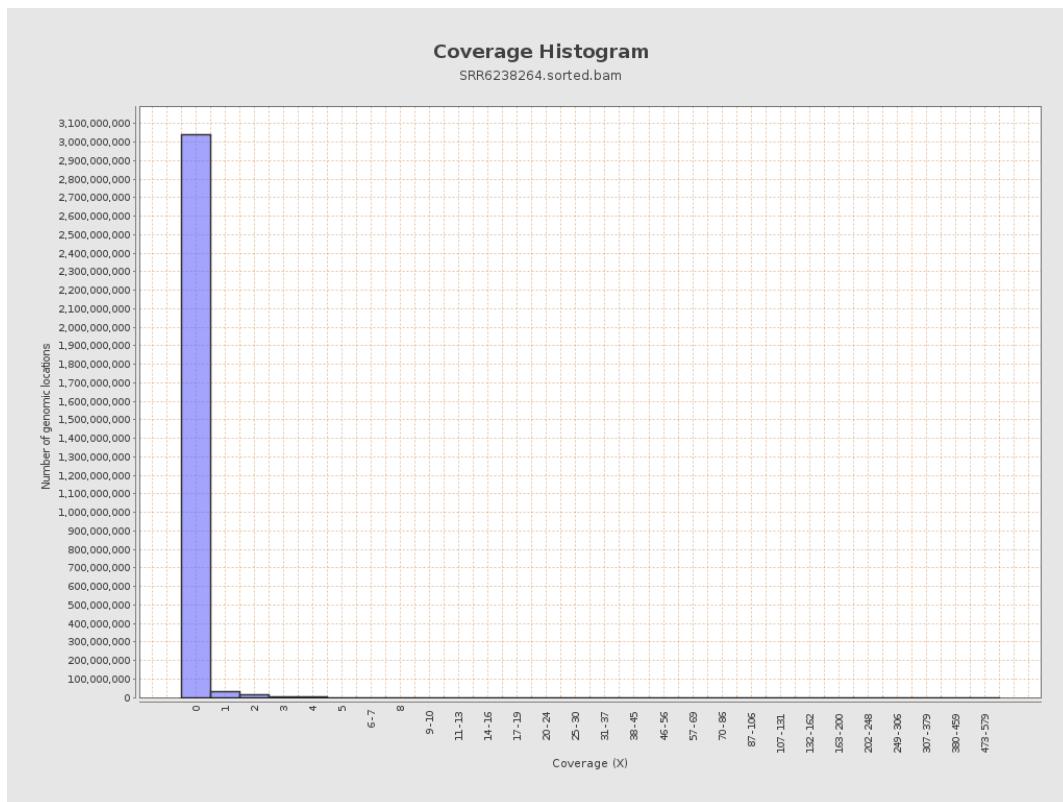
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7358015	0.0295	0.4588
chr2	243199373	8564342	0.0352	0.4417
chr3	198022430	6483442	0.0327	0.2843
chr4	191154276	6121658	0.032	0.2909
chr5	180915260	6373737	0.0352	0.2949
chr6	171115067	6060388	0.0354	0.345
chr7	159138663	6505535	0.0409	0.4806

chr8	146364022	5148364	0.0352	0.4495
chr9	141213431	3962227	0.0281	0.3189
chr10	135534747	4158296	0.0307	0.3154
chr11	135006516	4124163	0.0305	0.3042
chr12	133851895	4582493	0.0342	0.293
chr13	115169878	3695482	0.0321	0.2908
chr14	107349540	3528383	0.0329	0.3487
chr15	102531392	2893210	0.0282	0.3263
chr16	90354753	2862633	0.0317	0.2862
chr17	81195210	2630600	0.0324	0.2938
chr18	78077248	2628796	0.0337	0.4817
chr19	59128983	1802572	0.0305	0.37
chr20	63025520	1976234	0.0314	0.2775
chr21	48129895	1290295	0.0268	0.261
chr22	51304566	1196316	0.0233	0.2369
chrMT	16571	13830	0.8346	1.446
chrX	155270560	5635675	0.0363	0.3177
chrY	59373566	273582	0.0046	0.125

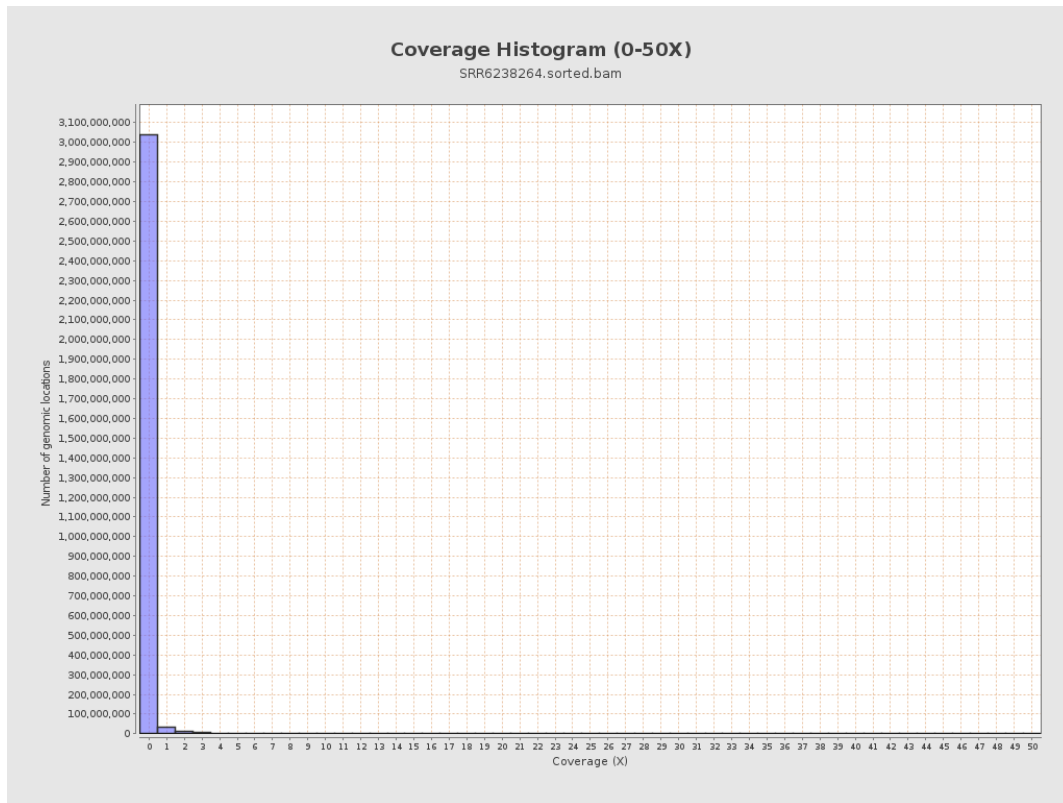
3. Results : Coverage across reference



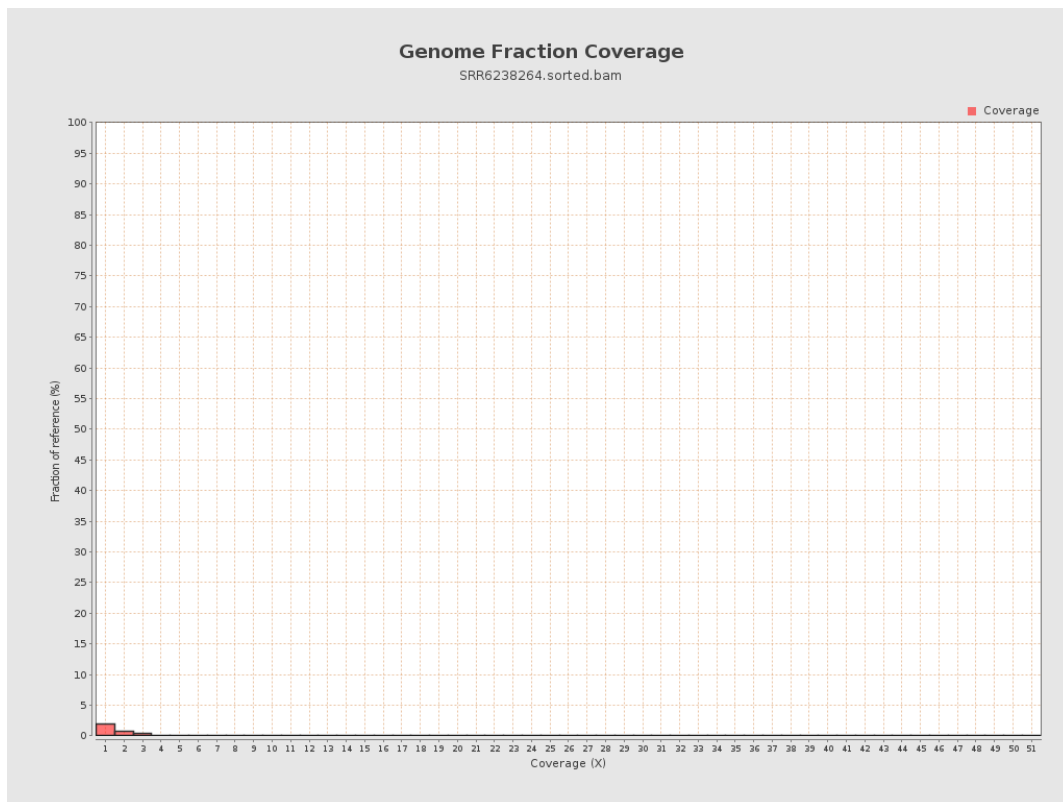
4. Results : Coverage Histogram



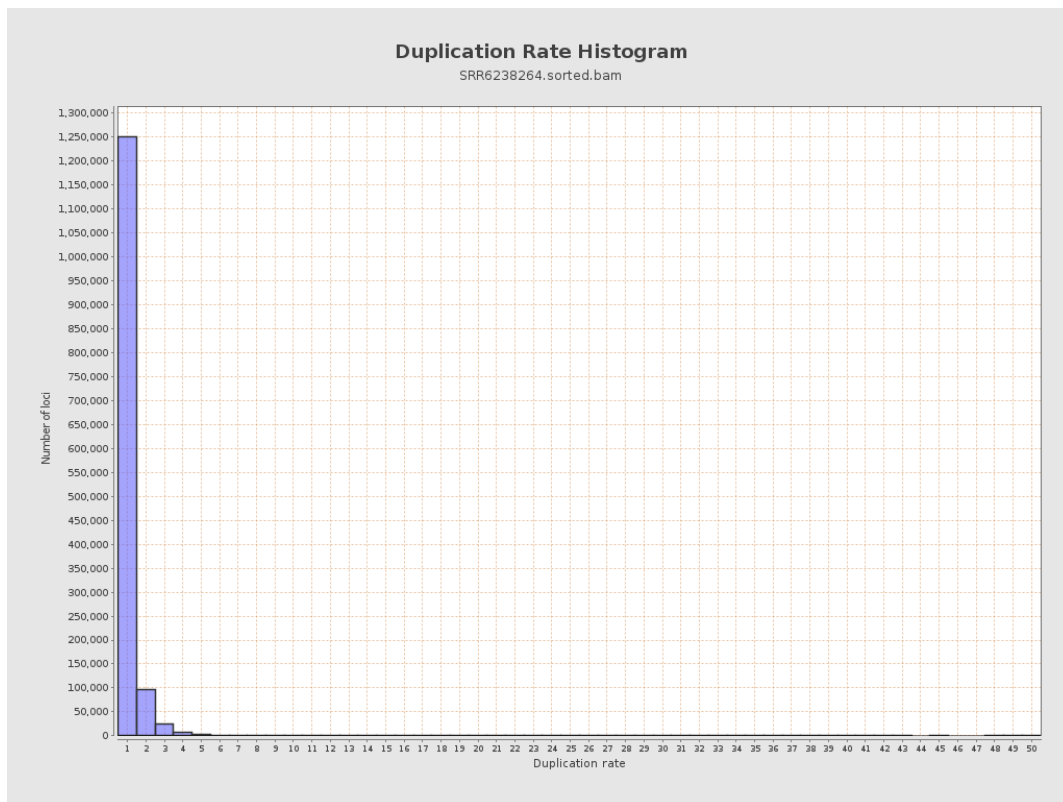
5. Results : Coverage Histogram (0-50X)



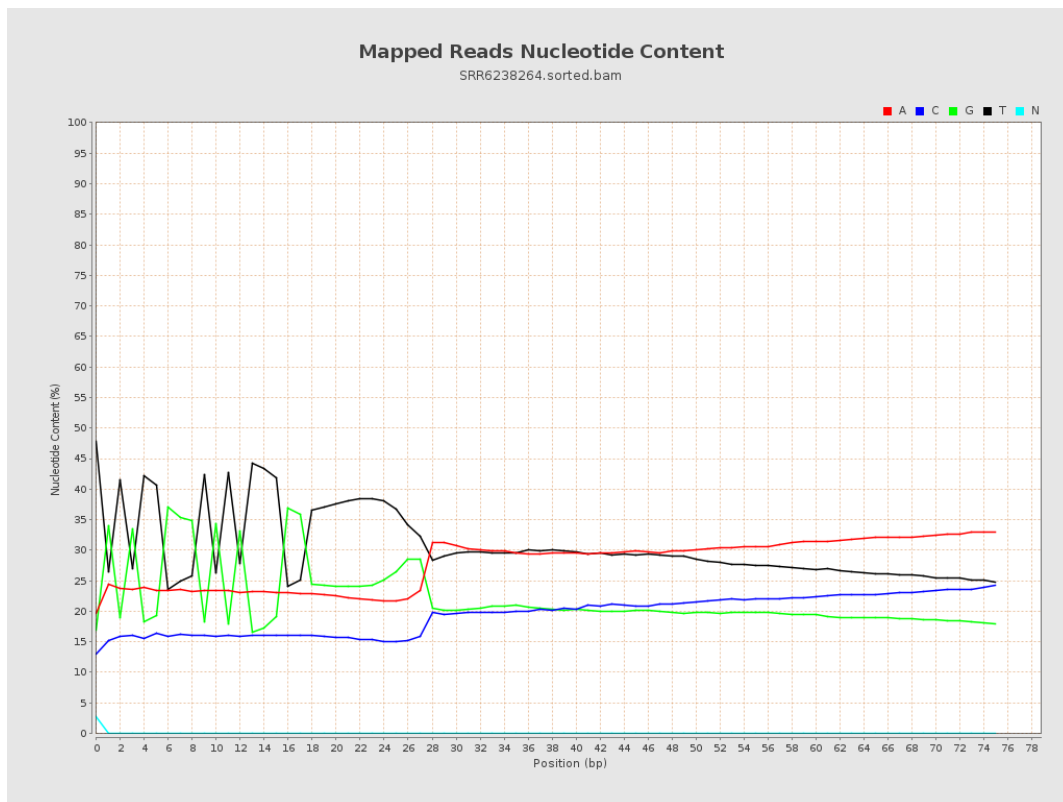
6. Results : Genome Fraction Coverage



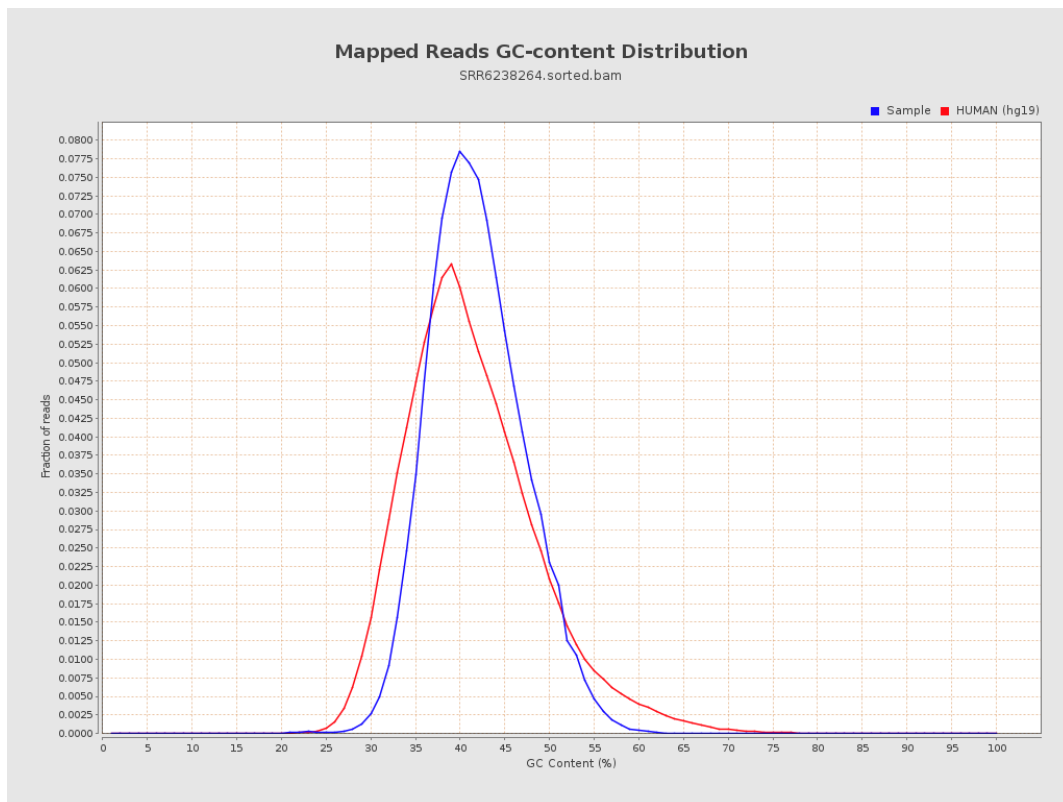
7. Results : Duplication Rate Histogram



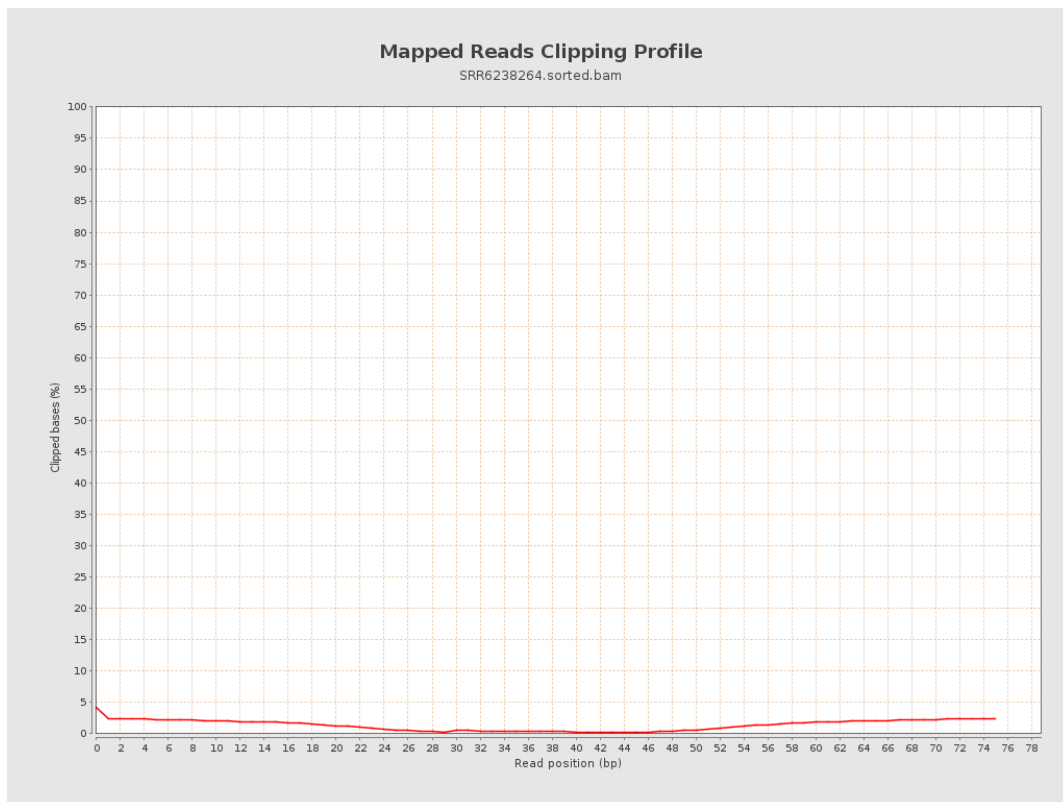
8. Results : Mapped Reads Nucleotide Content



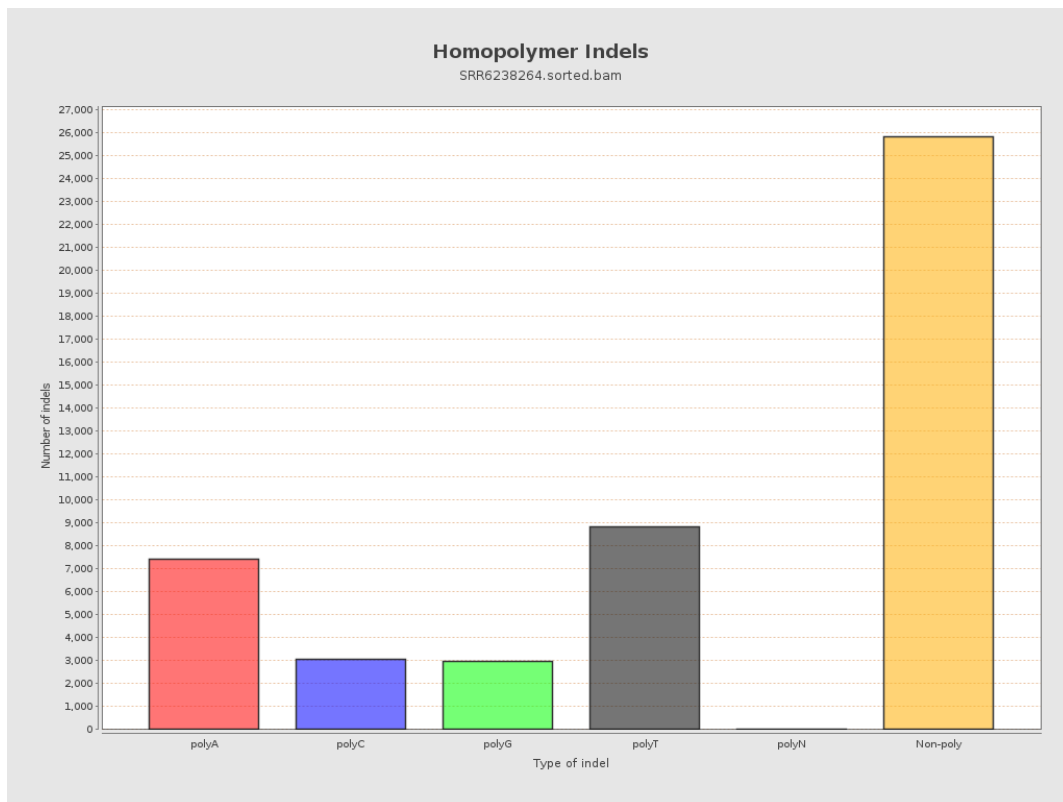
9. Results : Mapped Reads GC-content Distribution



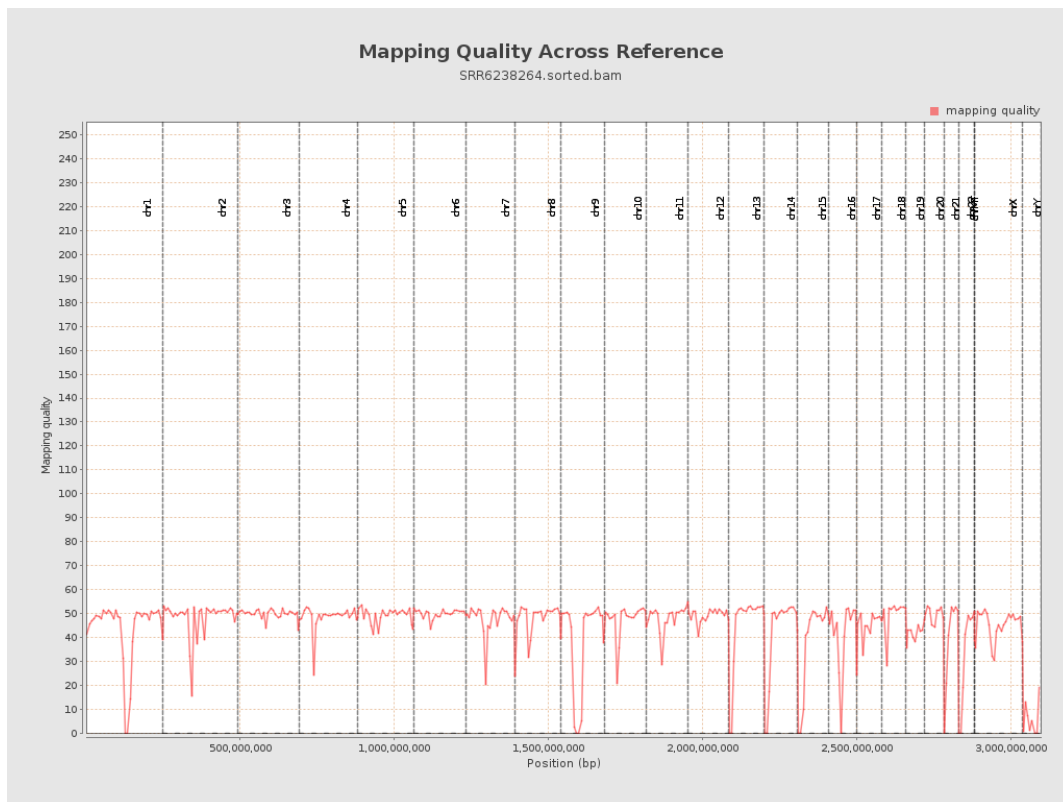
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

