

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 10:49:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238050.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_SRR6238050 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238050.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 10:49:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238050.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,978,083
Mapped reads	1,732,942 / 87.61%
Unmapped reads	245,141 / 12.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,473 / 1.09%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	121,972 / 6.17%
Duplication rate	5.6%
Clipped reads	798,717 / 40.38%

2.2. ACGT Content

Number/percentage of A's	31,682,085 / 27.6%
Number/percentage of C's	21,398,790 / 18.64%
Number/percentage of T's	36,239,843 / 31.57%
Number/percentage of G's	25,451,112 / 22.17%
Number/percentage of N's	15,816 / 0.01%
GC Percentage	40.81%

2.3. Coverage

Mean	0.0371

Standard Deviation	0.3658
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2.4. Mapping Quality

Mean Mapping Quality	41.4
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2.5. Mismatches and indels

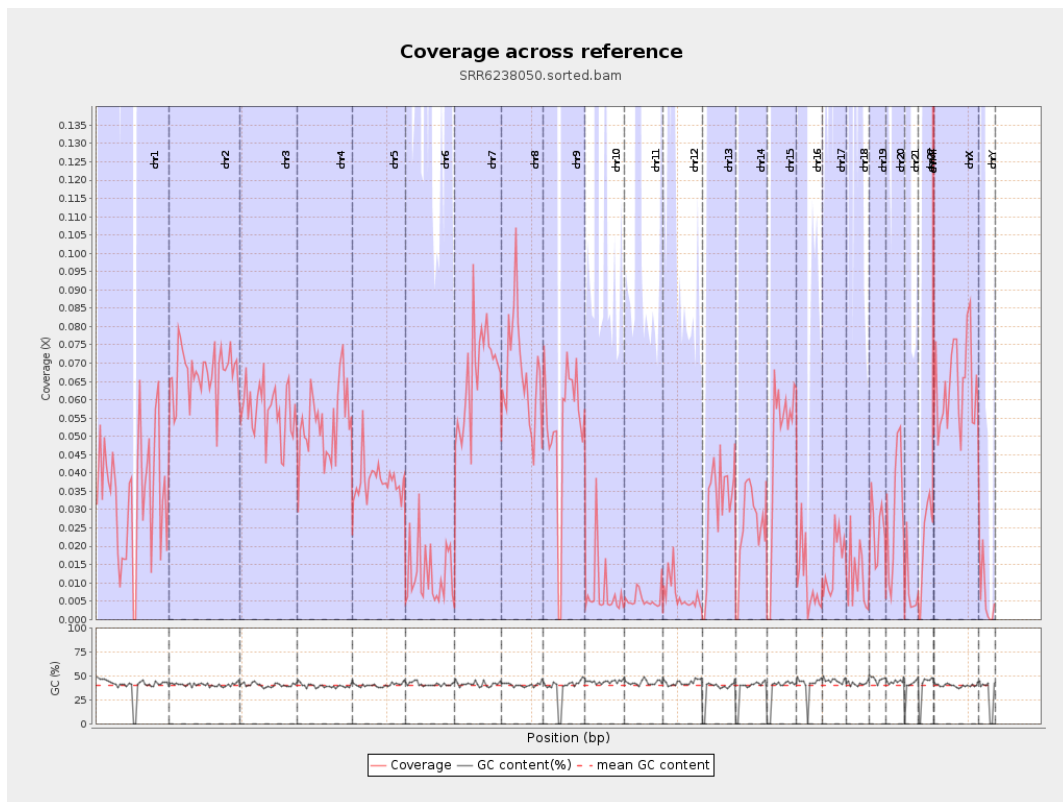
General error rate	0.79%
Mismatches	893,476
Insertions	8,344
Mapped reads with at least one insertion	0.48%
Deletions	32,092
Mapped reads with at least one deletion	1.83%
Homopolymer indels	45.74%

2.6. Chromosome stats

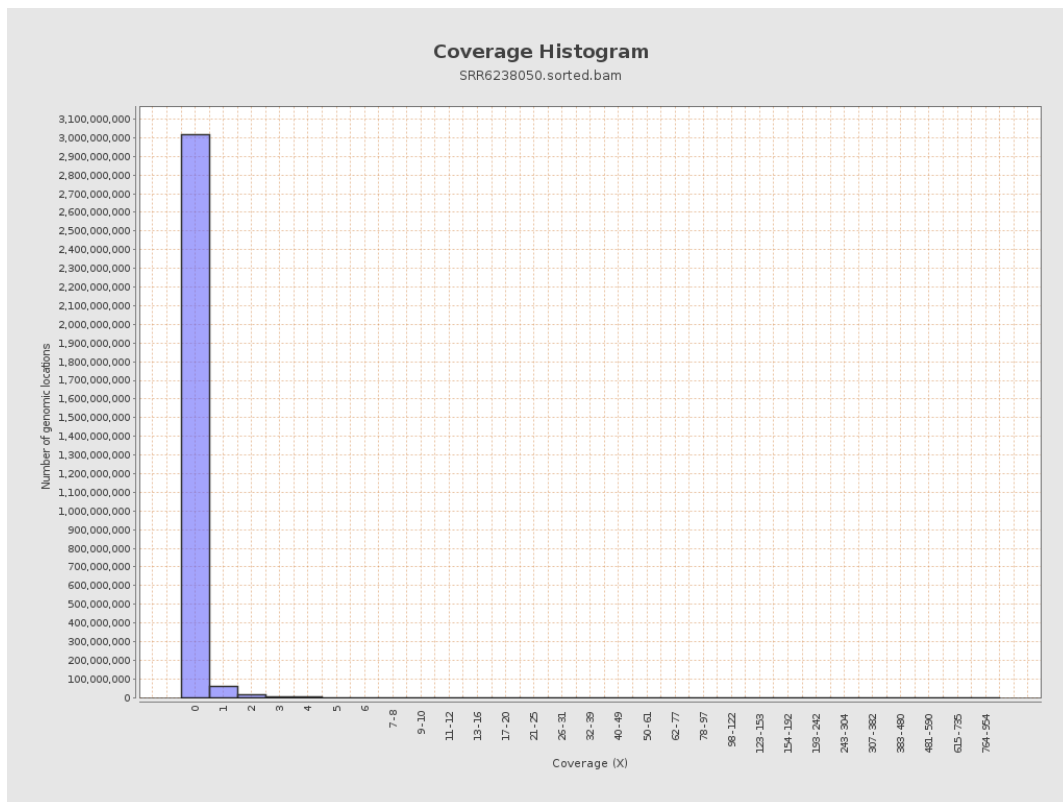
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8263978	0.0332	0.3038
chr2	243199373	16385689	0.0674	0.4637
chr3	198022430	11315941	0.0571	0.3186
chr4	191154276	10207022	0.0534	0.3419
chr5	180915260	6879023	0.038	0.2621
chr6	171115067	2104620	0.0123	0.16
chr7	159138663	10684588	0.0671	0.7062

chr8	146364022	9794152	0.0669	0.6554
chr9	141213431	7323408	0.0519	0.4148
chr10	135534747	986098	0.0073	0.2789
chr11	135006516	748630	0.0055	0.1499
chr12	133851895	910974	0.0068	0.1267
chr13	115169878	3503661	0.0304	0.2313
chr14	107349540	2726009	0.0254	0.2693
chr15	102531392	4922931	0.048	0.294
chr16	90354753	907524	0.01	0.1882
chr17	81195210	1277554	0.0157	0.1755
chr18	78077248	895145	0.0115	0.6388
chr19	59128983	1415813	0.0239	0.2858
chr20	63025520	1867159	0.0296	0.2385
chr21	48129895	379900	0.0079	0.2077
chr22	51304566	1101015	0.0215	0.1919
chrMT	16571	16711	1.0084	1.4797
chrX	155270560	9856714	0.0635	0.359
chrY	59373566	370170	0.0062	0.2237

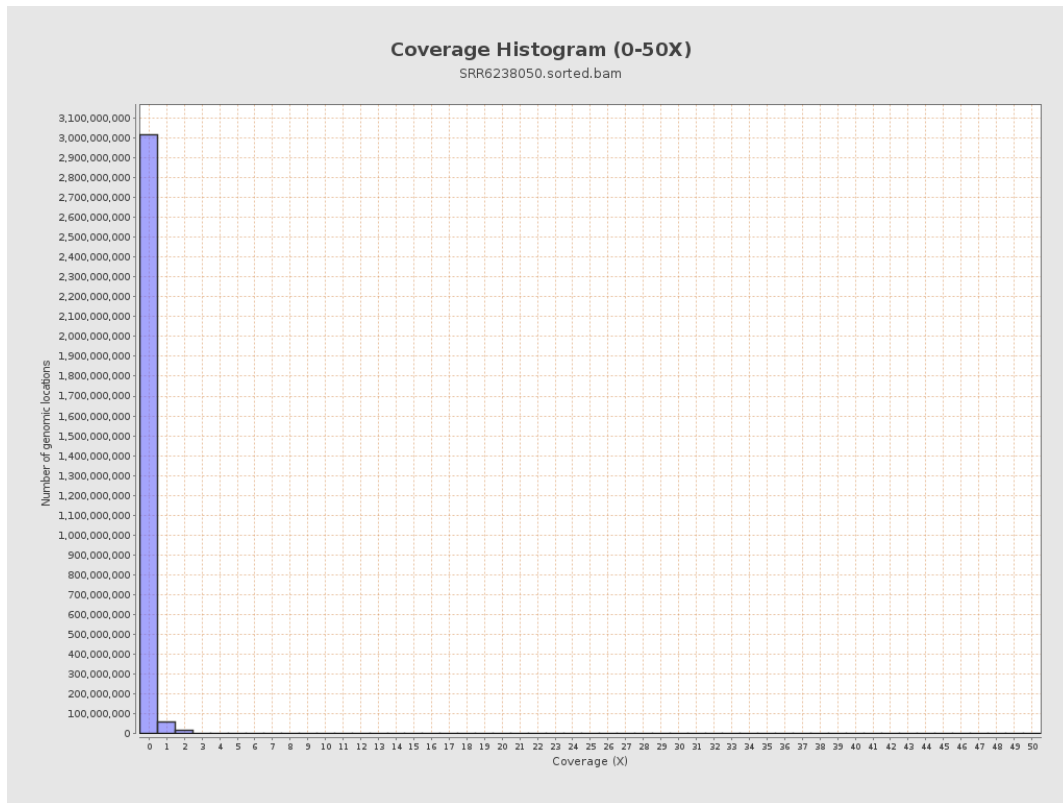
3. Results : Coverage across reference



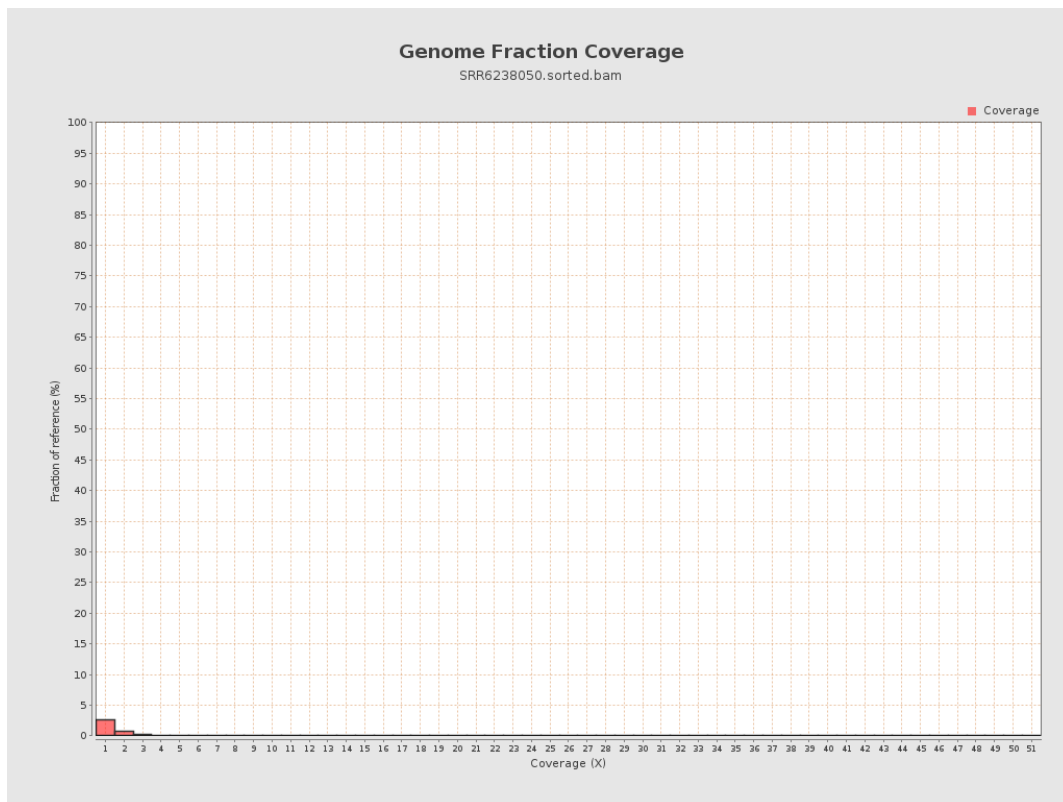
4. Results : Coverage Histogram



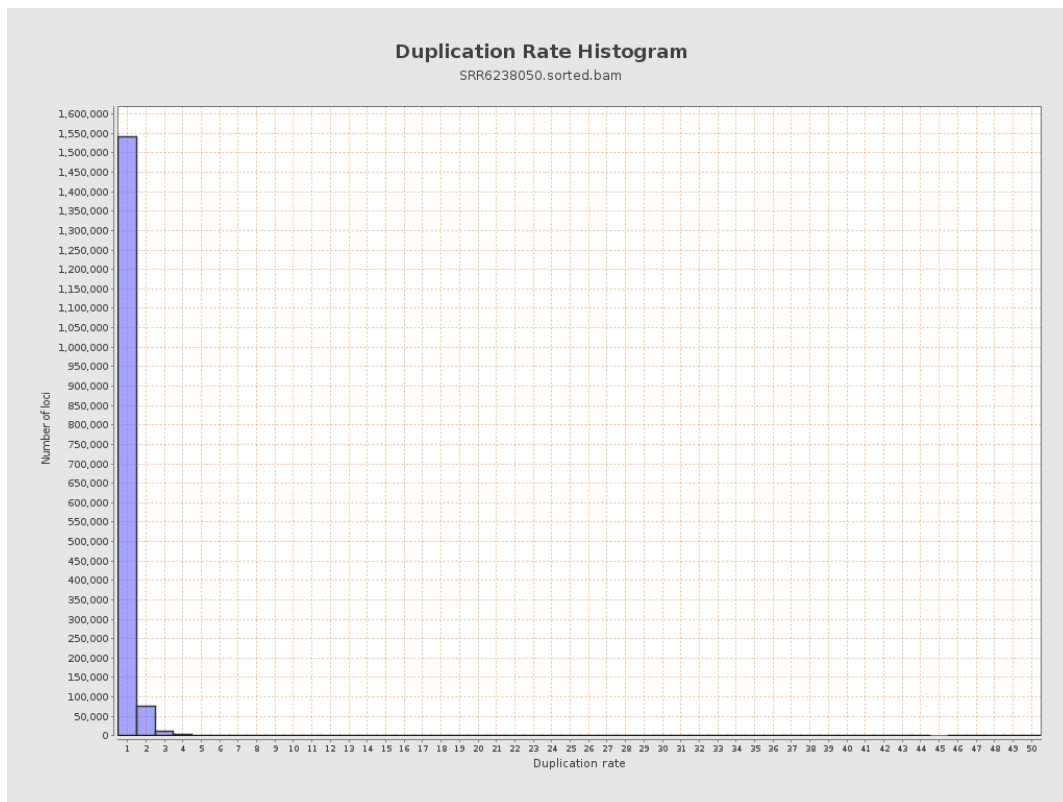
5. Results : Coverage Histogram (0-50X)



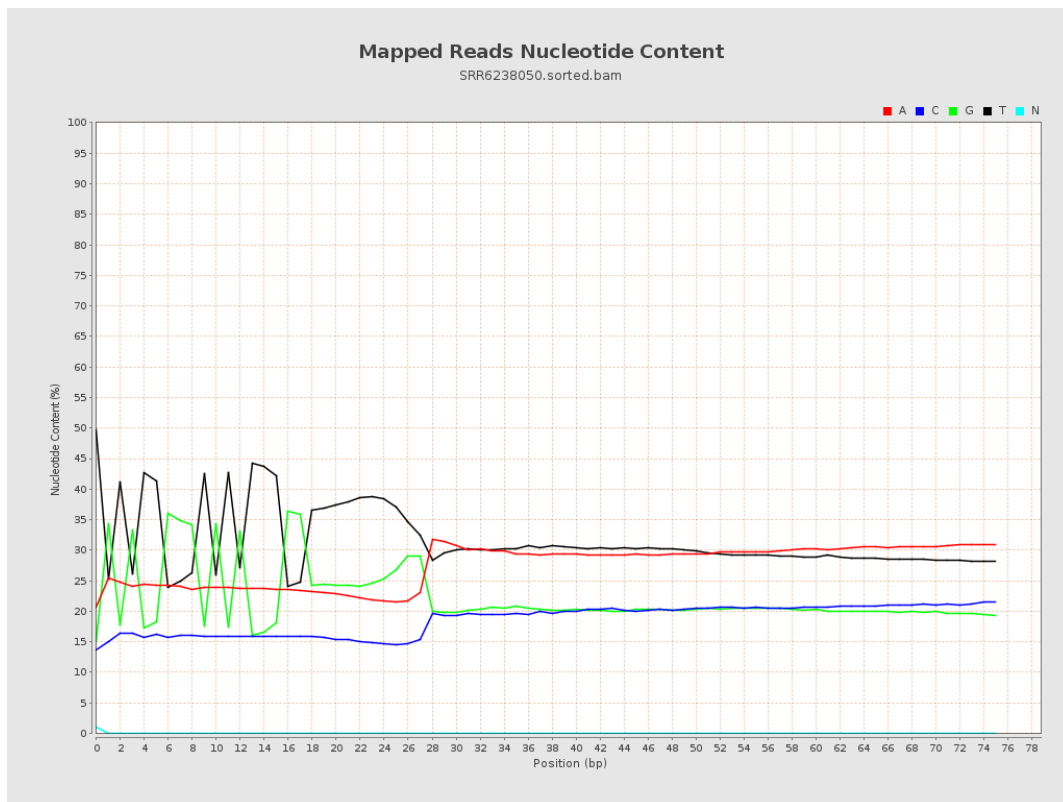
6. Results : Genome Fraction Coverage



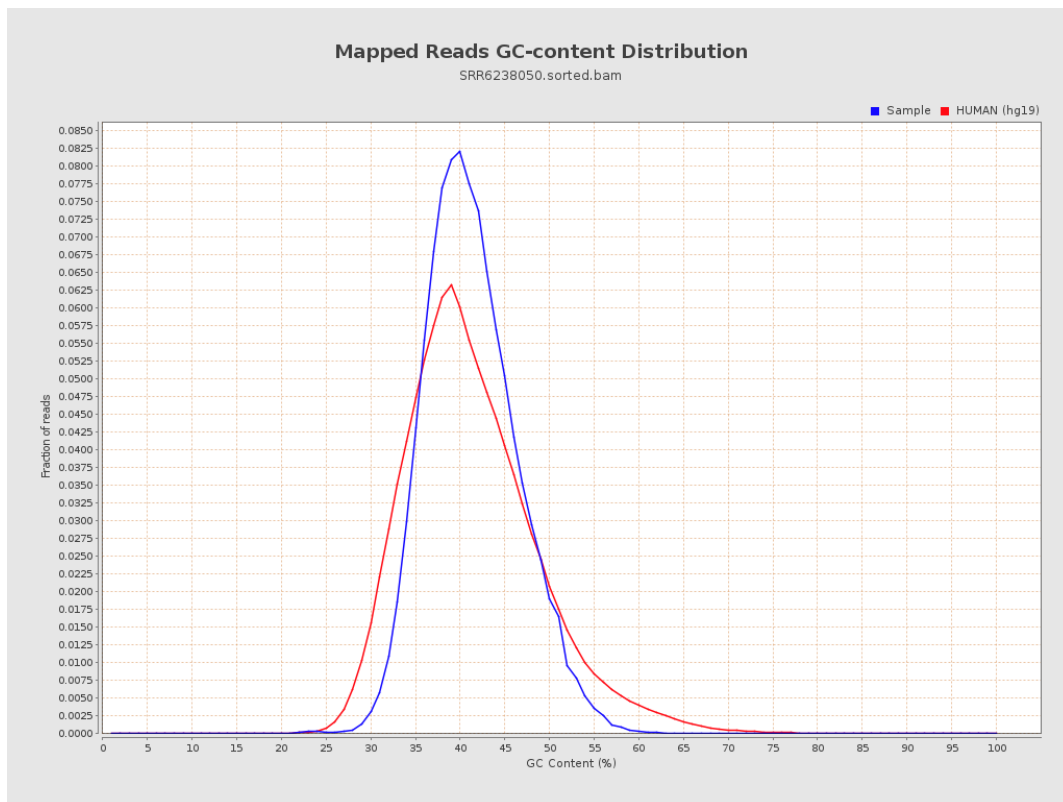
7. Results : Duplication Rate Histogram



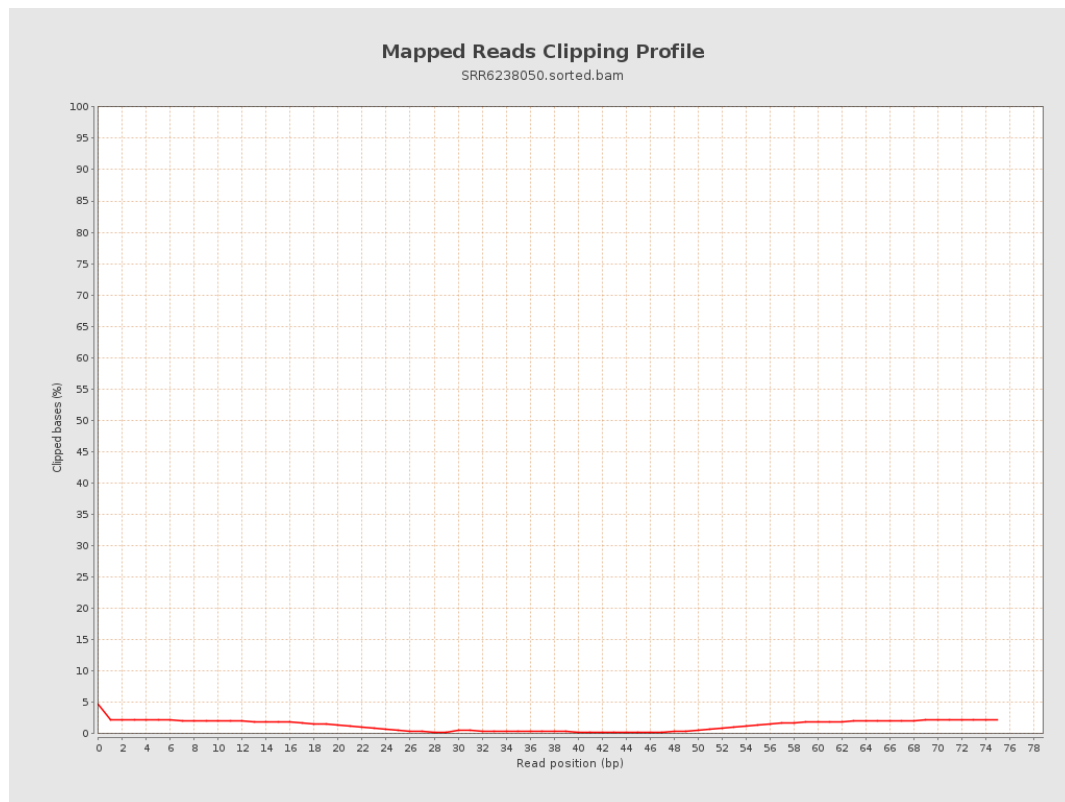
8. Results : Mapped Reads Nucleotide Content



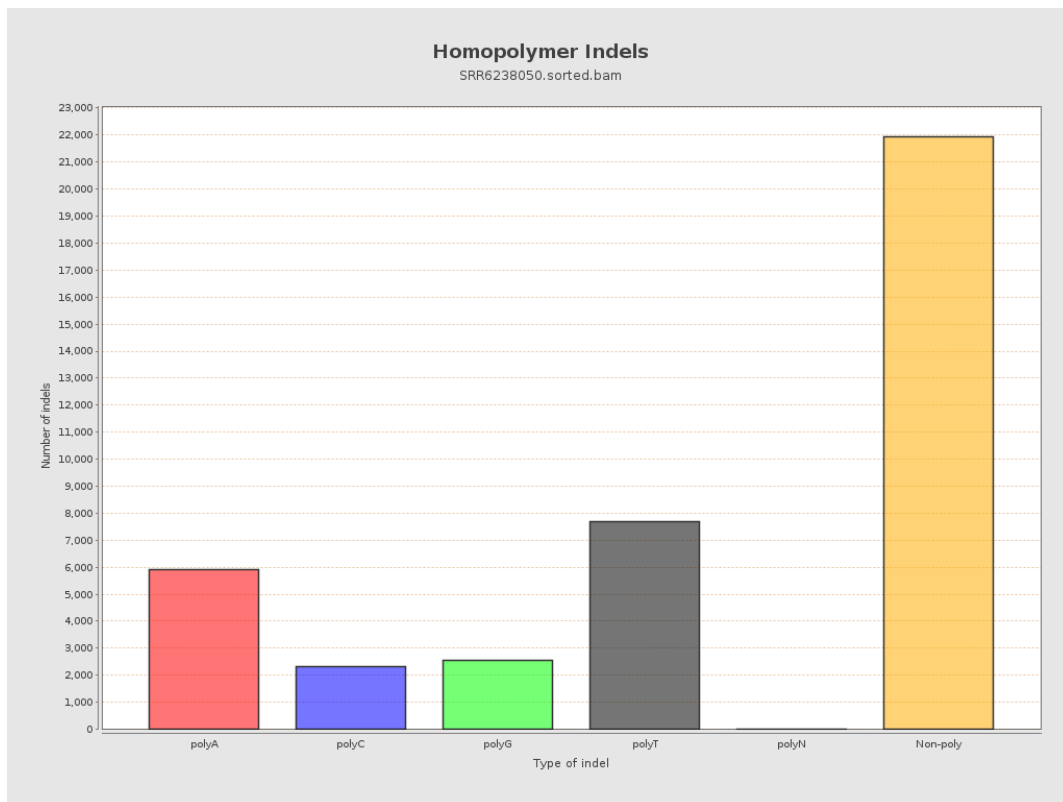
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

