

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 00:55:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238653.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_SRR6238653 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238653.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 00:55:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238653.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,476,150
Mapped reads	3,800,564 / 84.91%
Unmapped reads	675,586 / 15.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,048 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	1,163,287 / 25.99%
Duplication rate	21.17%
Clipped reads	2,398,457 / 53.58%

2.2. ACGT Content

Number/percentage of A's	58,680,851 / 25.05%
Number/percentage of C's	41,430,865 / 17.68%
Number/percentage of T's	78,338,743 / 33.44%
Number/percentage of G's	55,834,568 / 23.83%
Number/percentage of N's	5,272 / 0%
GC Percentage	41.51%

2.3. Coverage

Mean	0.0757

Standard Deviation	1.118
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2.4. Mapping Quality

Mean Mapping Quality	43.8
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2.5. Mismatches and indels

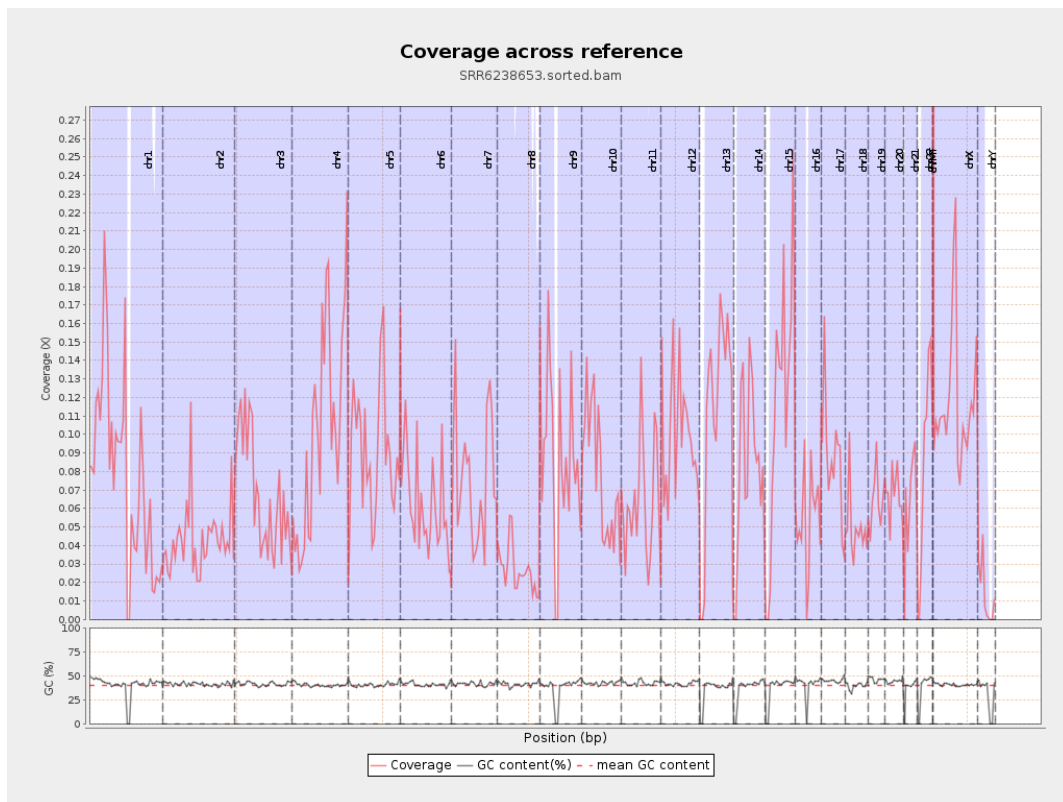
General error rate	0.59%
Mismatches	1,350,843
Insertions	15,896
Mapped reads with at least one insertion	0.41%
Deletions	59,906
Mapped reads with at least one deletion	1.56%
Homopolymer indels	41.56%

2.6. Chromosome stats

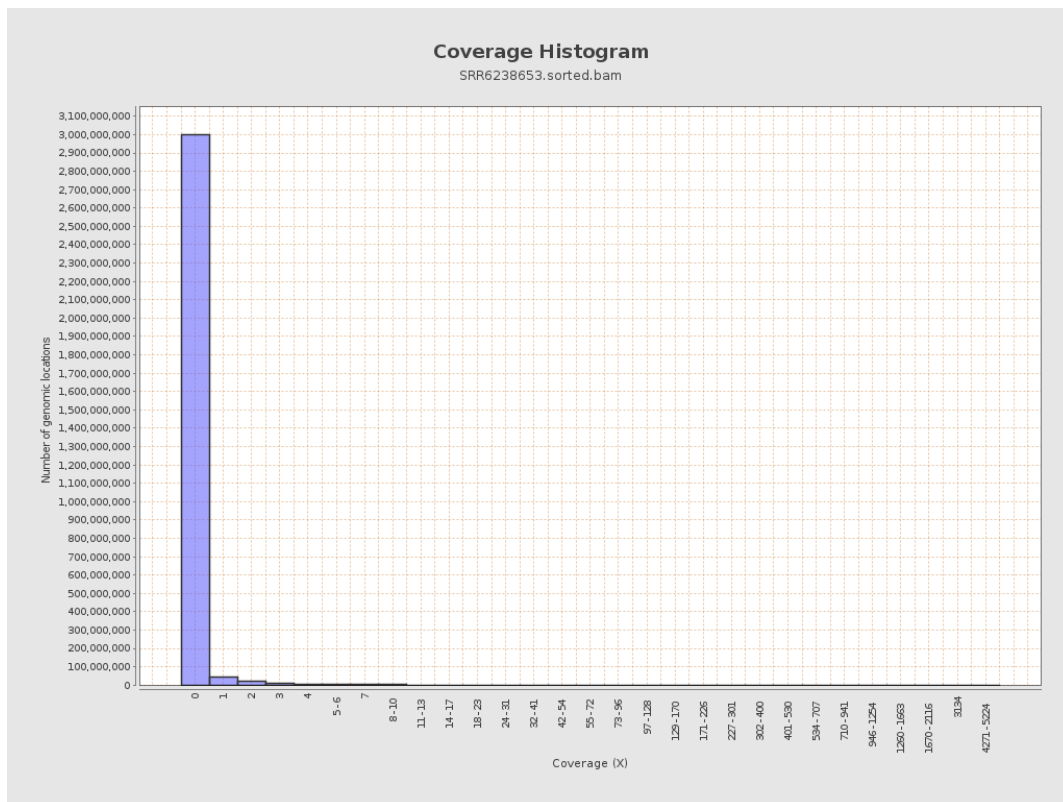
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19152558	0.0768	1.4371
chr2	243199373	10582676	0.0435	2.3408
chr3	198022430	13292337	0.0671	0.5781
chr4	191154276	19540784	0.1022	0.7025
chr5	180915260	16426000	0.0908	0.6539
chr6	171115067	10585626	0.0619	0.9637
chr7	159138663	11831749	0.0743	0.7644

chr8	146364022	3864307	0.0264	0.7753
chr9	141213431	12241601	0.0867	0.8647
chr10	135534747	10535916	0.0777	0.7889
chr11	135006516	8537383	0.0632	0.6899
chr12	133851895	13324268	0.0995	0.6814
chr13	115169878	12923512	0.1122	0.8642
chr14	107349540	8991156	0.0838	0.6622
chr15	102531392	11782916	0.1149	0.8172
chr16	90354753	4856062	0.0537	0.6003
chr17	81195210	7221791	0.0889	0.6583
chr18	78077248	3869705	0.0496	2.846
chr19	59128983	3847108	0.0651	1.0314
chr20	63025520	4204909	0.0667	0.5478
chr21	48129895	3074263	0.0639	0.569
chr22	51304566	4414425	0.086	0.6123
chrMT	16571	30176	1.821	2.7267
chrX	155270560	18443001	0.1188	0.7758
chrY	59373566	819145	0.0138	0.4836

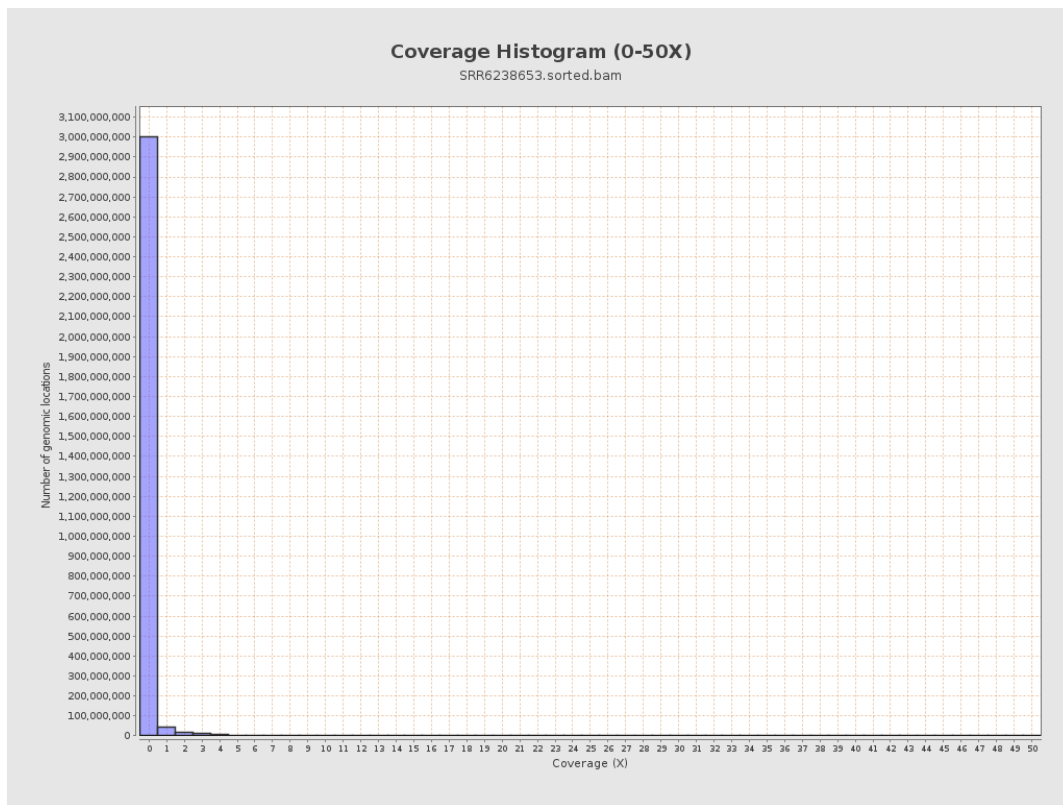
3. Results : Coverage across reference



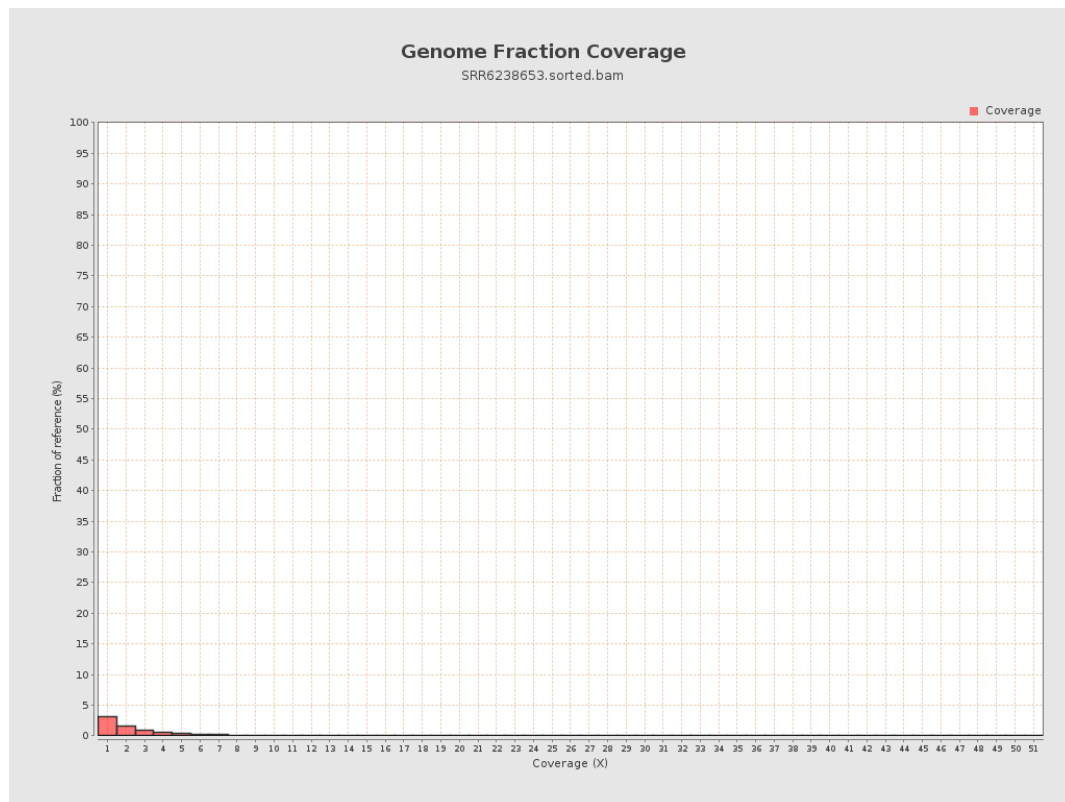
4. Results : Coverage Histogram



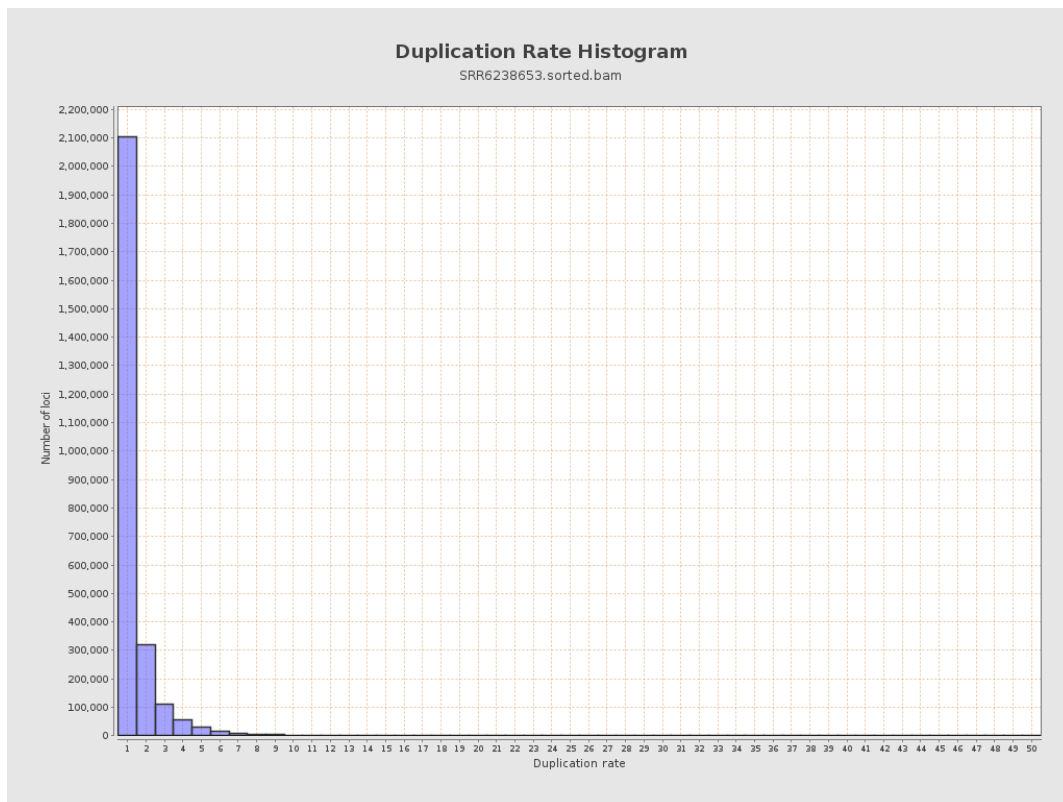
5. Results : Coverage Histogram (0-50X)



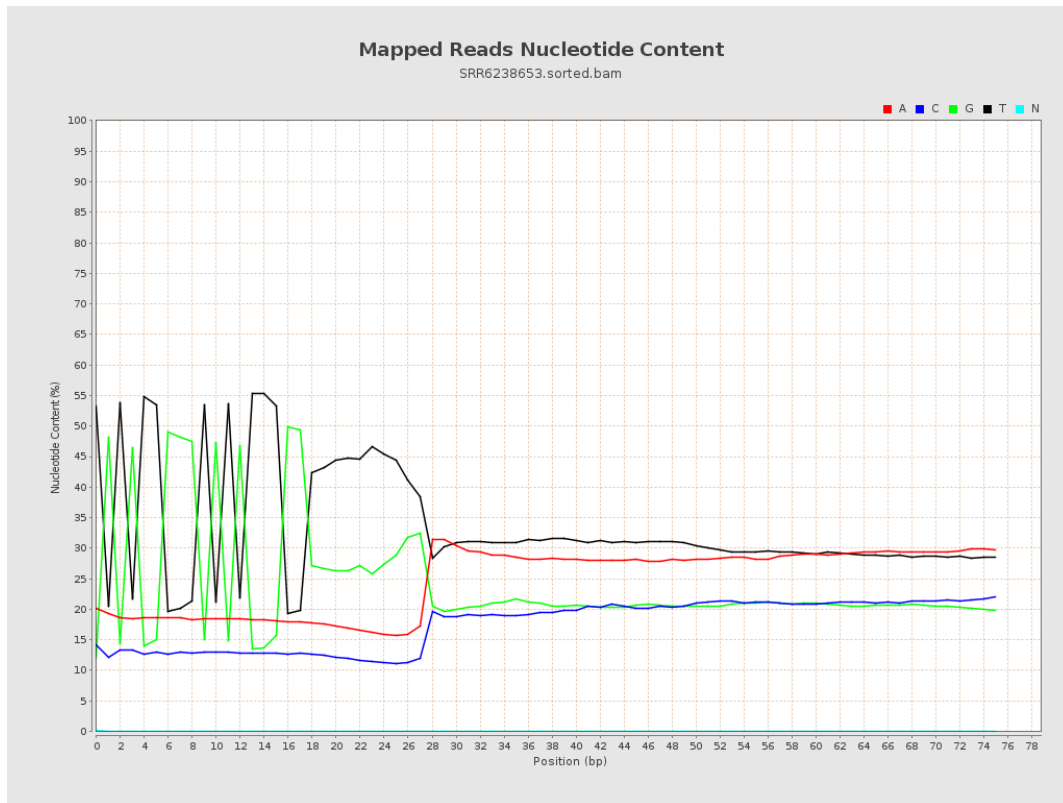
6. Results : Genome Fraction Coverage



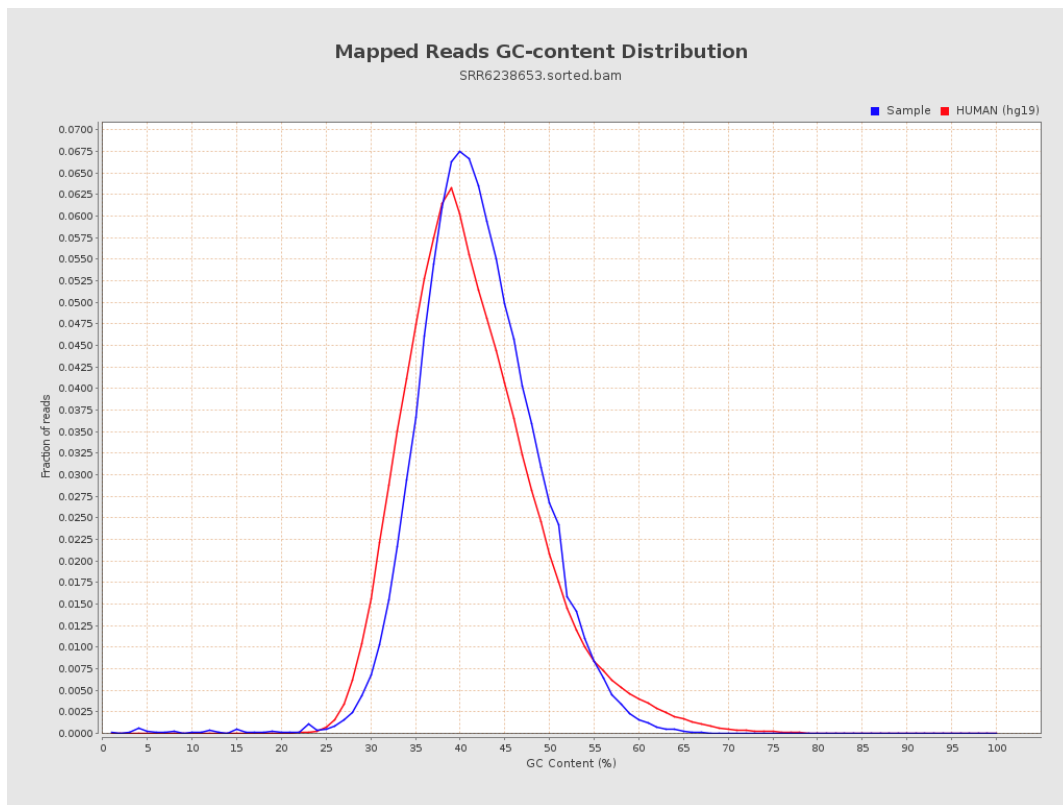
7. Results : Duplication Rate Histogram



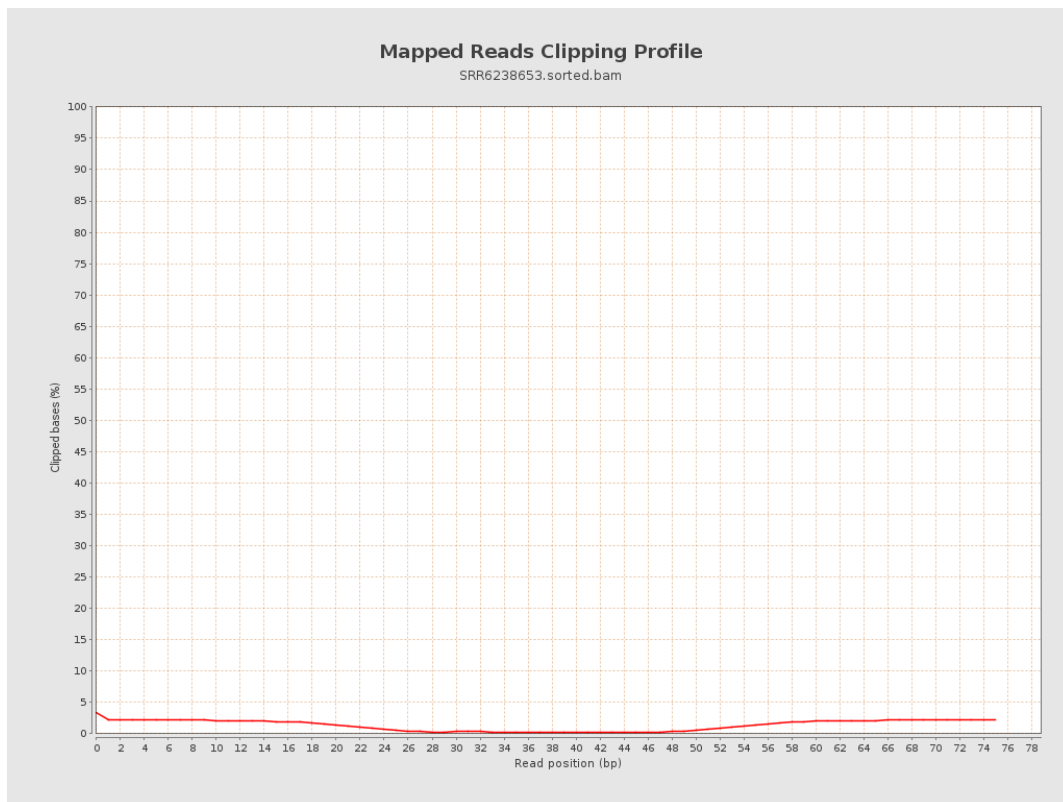
8. Results : Mapped Reads Nucleotide Content



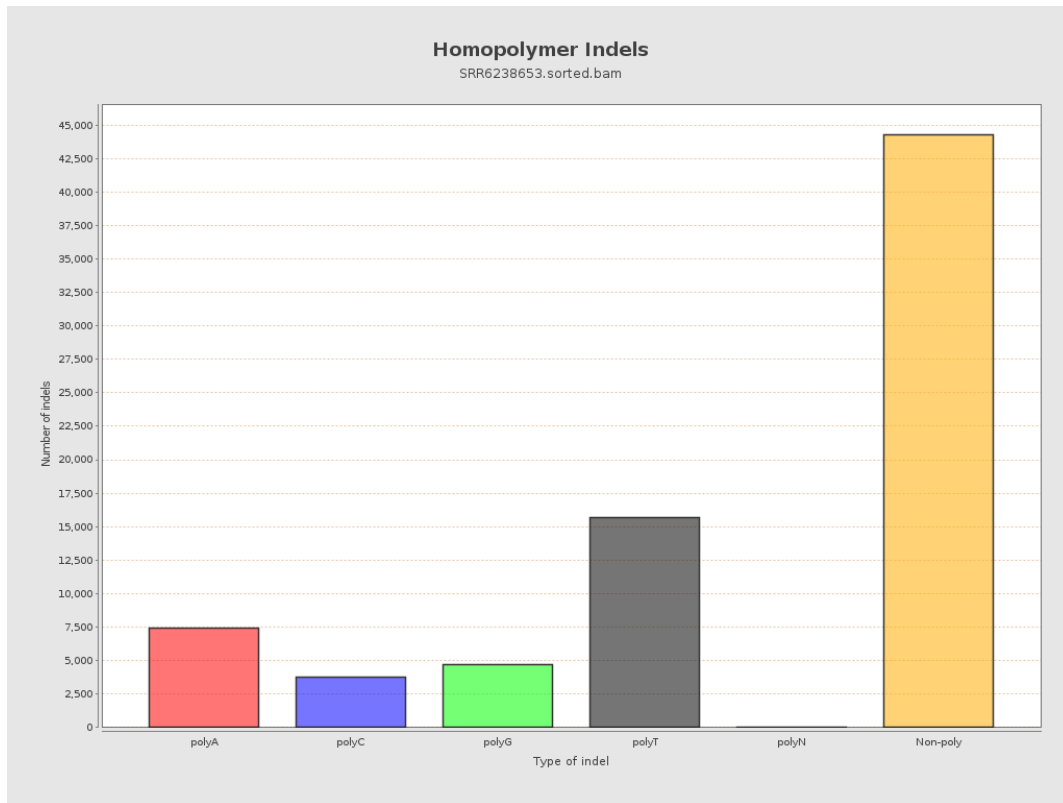
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

