

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 10:38:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238045.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_SRR6238045 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238045.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 10:38:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238045.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,791,264
Mapped reads	1,367,082 / 76.32%
Unmapped reads	424,182 / 23.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,437 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	136,159 / 7.6%
Duplication rate	7.93%
Clipped reads	760,347 / 42.45%

2.2. ACGT Content

Number/percentage of A's	23,212,306 / 26.76%
Number/percentage of C's	15,460,822 / 17.82%
Number/percentage of T's	27,870,508 / 32.13%
Number/percentage of G's	20,059,498 / 23.12%
Number/percentage of N's	149,899 / 0.17%
GC Percentage	40.94%

2.3. Coverage

Mean	0.028

Standard Deviation	0.4088
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2.4. Mapping Quality

Mean Mapping Quality	45.85
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2.5. Mismatches and indels

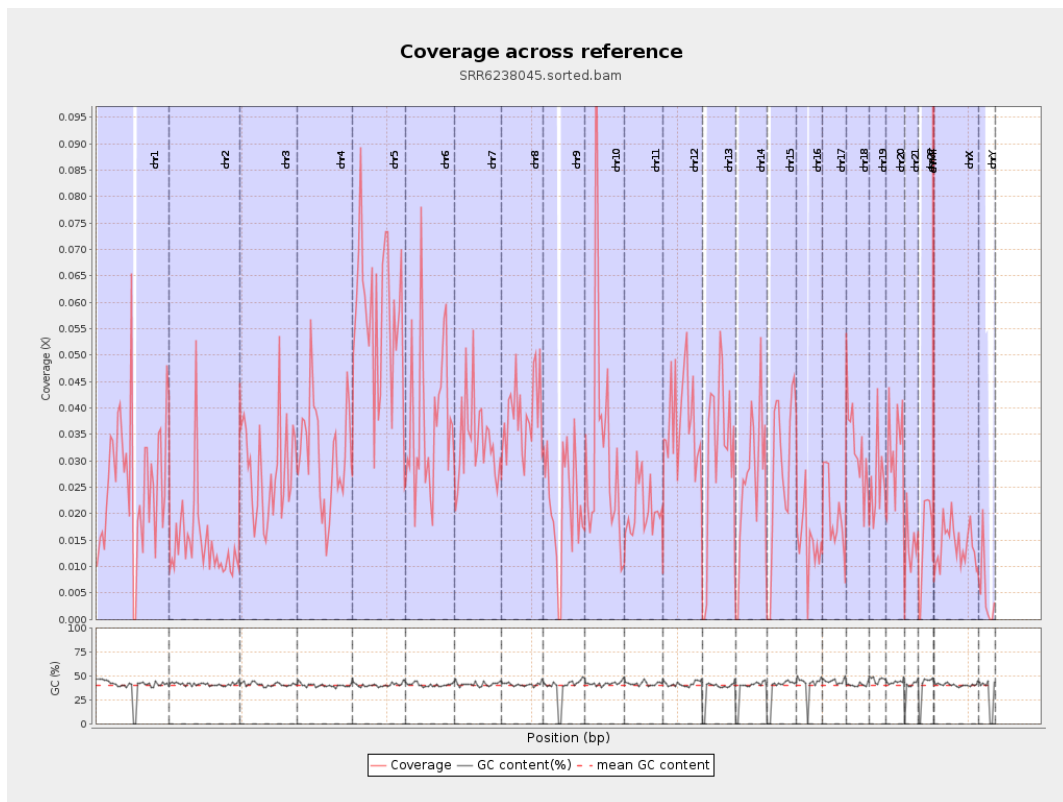
General error rate	0.92%
Mismatches	784,605
Insertions	6,949
Mapped reads with at least one insertion	0.5%
Deletions	29,960
Mapped reads with at least one deletion	2.16%
Homopolymer indels	45.12%

2.6. Chromosome stats

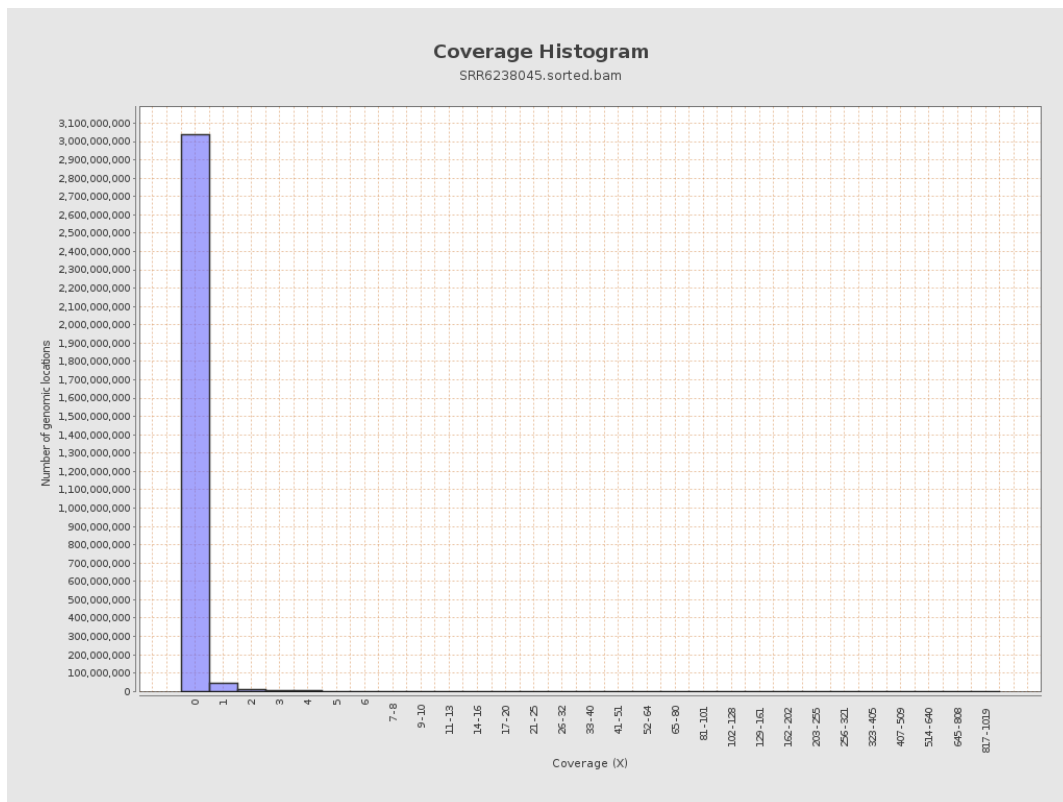
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6402086	0.0257	0.8808
chr2	243199373	3498666	0.0144	0.3324
chr3	198022430	5578171	0.0282	0.2583
chr4	191154276	5986944	0.0313	0.2614
chr5	180915260	10329571	0.0571	0.3332
chr6	171115067	6413881	0.0375	0.4551
chr7	159138663	5408523	0.034	0.3662

chr8	146364022	5657478	0.0387	0.354
chr9	141213431	3054635	0.0216	0.2909
chr10	135534747	4278482	0.0316	0.7137
chr11	135006516	2769312	0.0205	0.2462
chr12	133851895	5036852	0.0376	0.2742
chr13	115169878	3615260	0.0314	0.246
chr14	107349540	2893242	0.027	0.2337
chr15	102531392	2954558	0.0288	0.2367
chr16	90354753	1326559	0.0147	0.1857
chr17	81195210	1593679	0.0196	0.2249
chr18	78077248	2529646	0.0324	0.4761
chr19	59128983	1531522	0.0259	0.5665
chr20	63025520	2020006	0.0321	0.254
chr21	48129895	662490	0.0138	0.1746
chr22	51304566	780436	0.0152	0.1648
chrMT	16571	29378	1.7729	1.9348
chrX	155270560	2173142	0.014	0.1761
chrY	59373566	278479	0.0047	0.1679

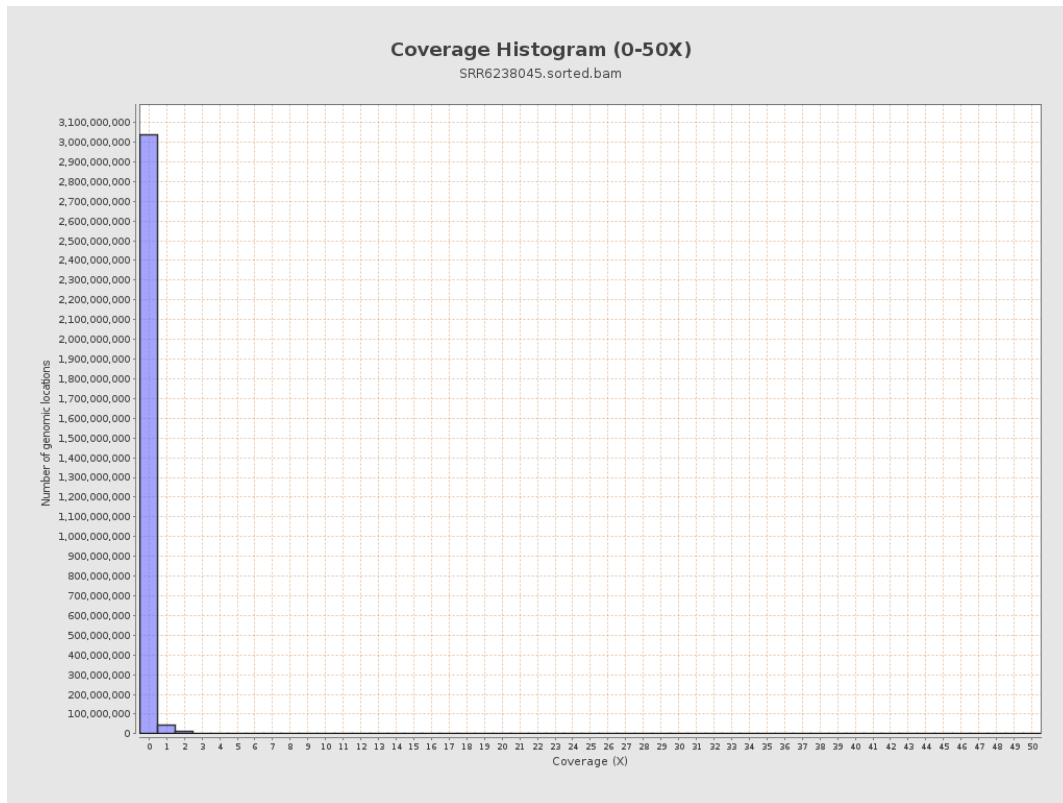
3. Results : Coverage across reference



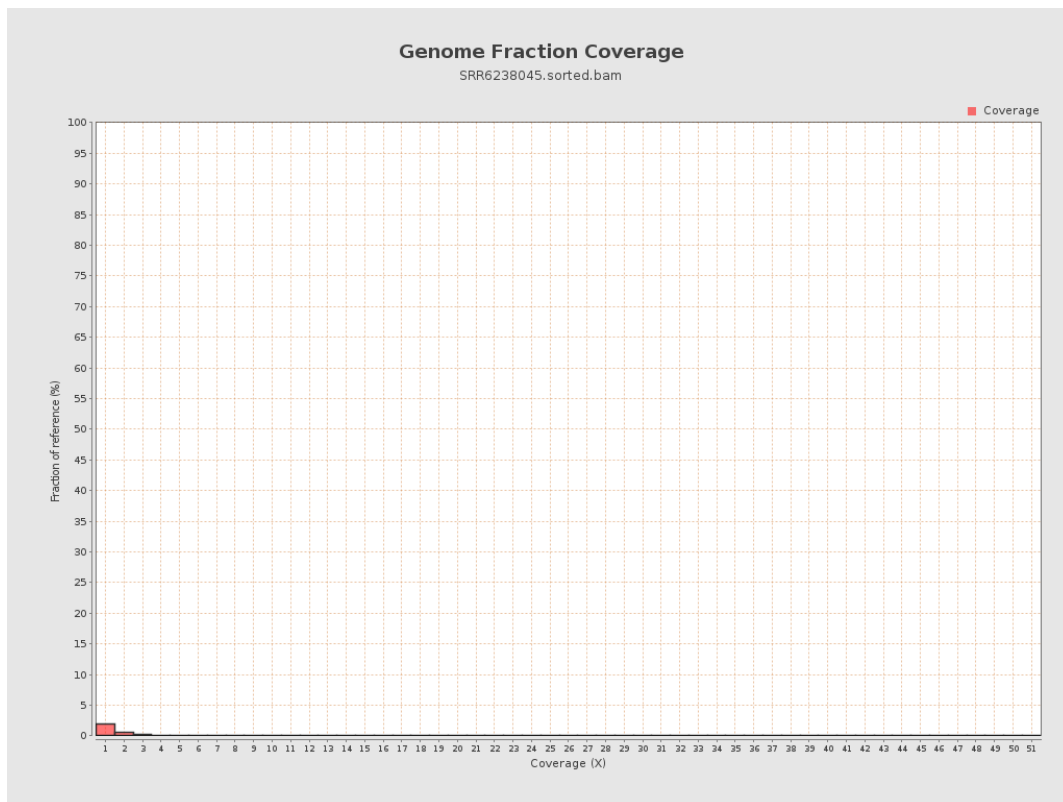
4. Results : Coverage Histogram



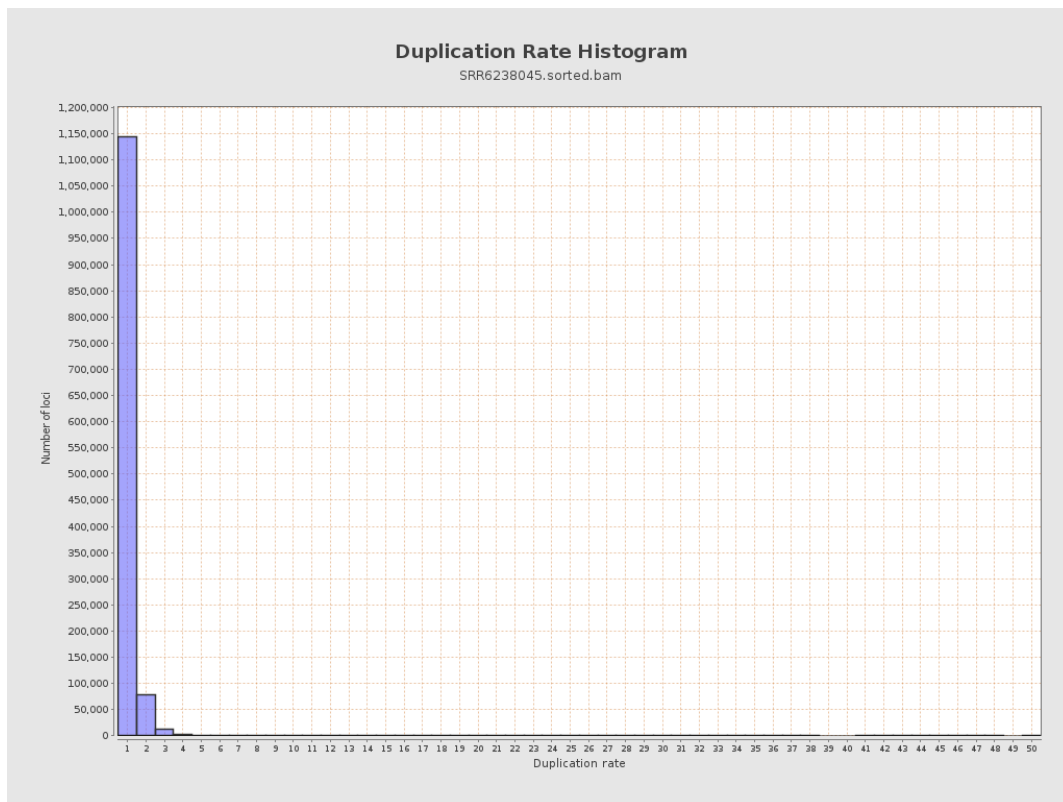
5. Results : Coverage Histogram (0-50X)



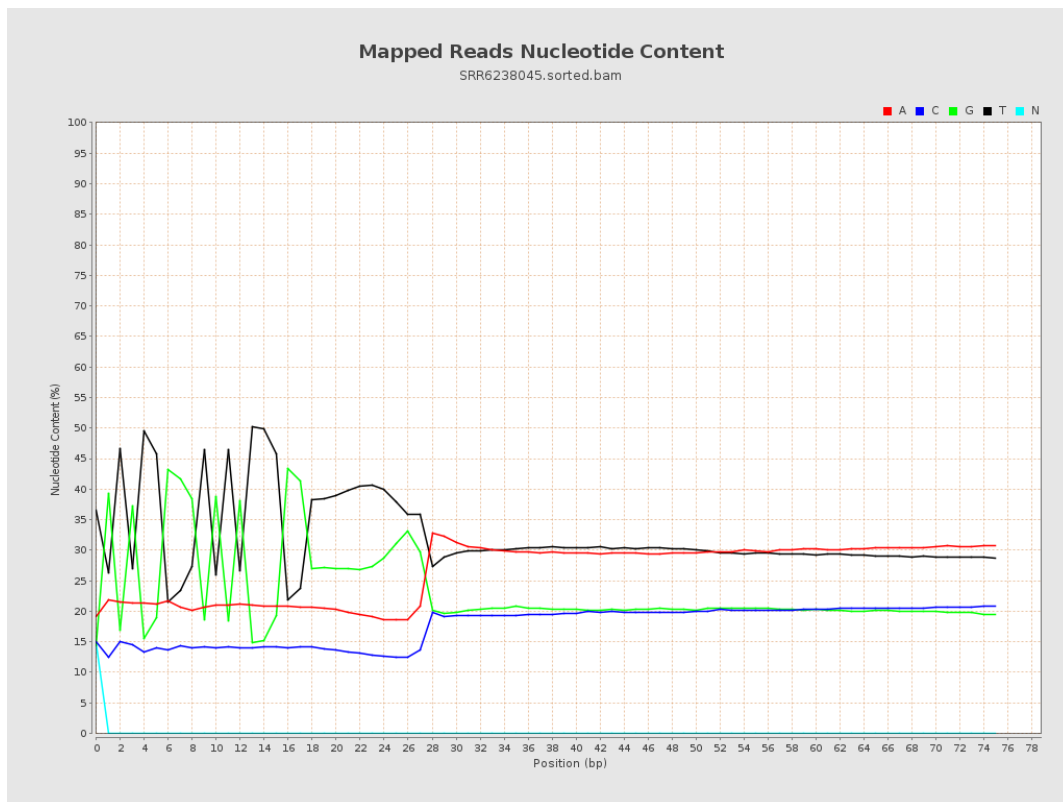
6. Results : Genome Fraction Coverage



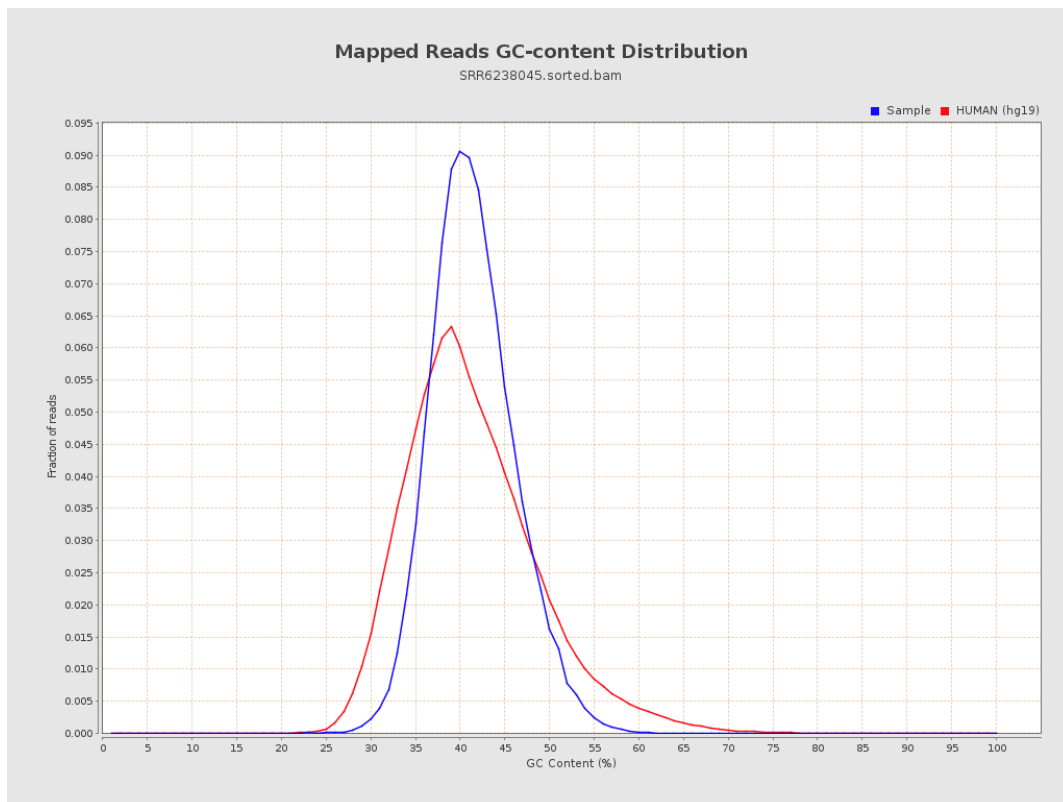
7. Results : Duplication Rate Histogram



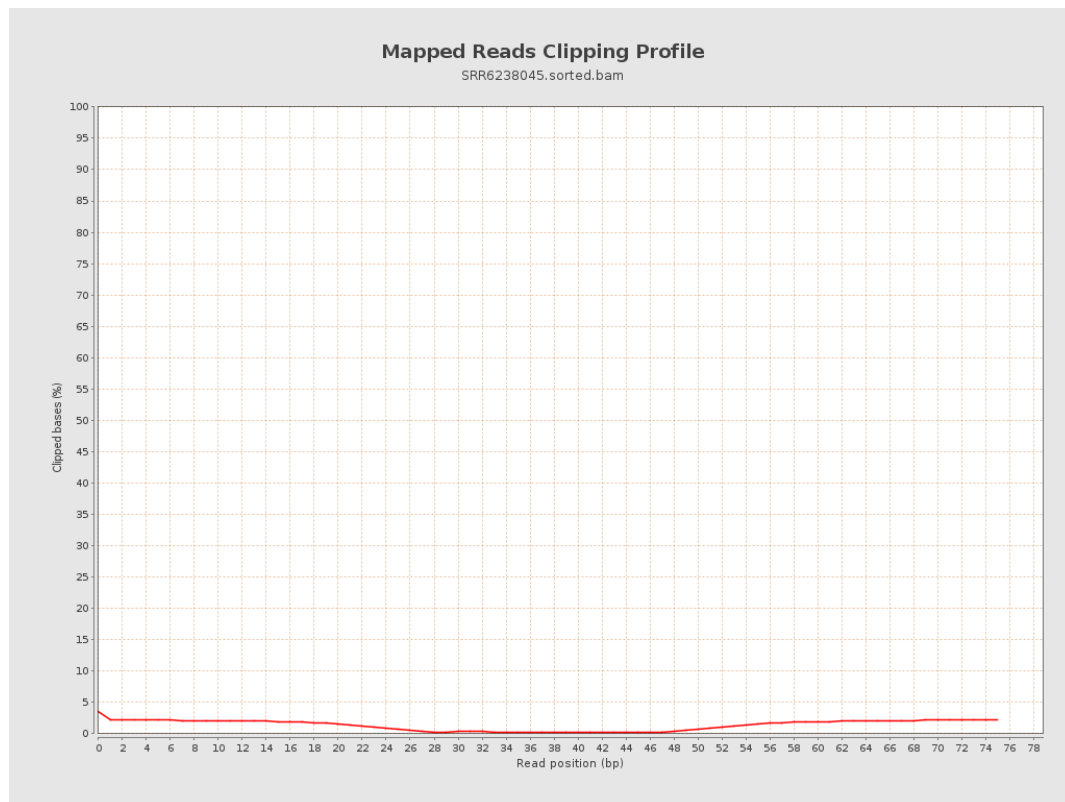
8. Results : Mapped Reads Nucleotide Content



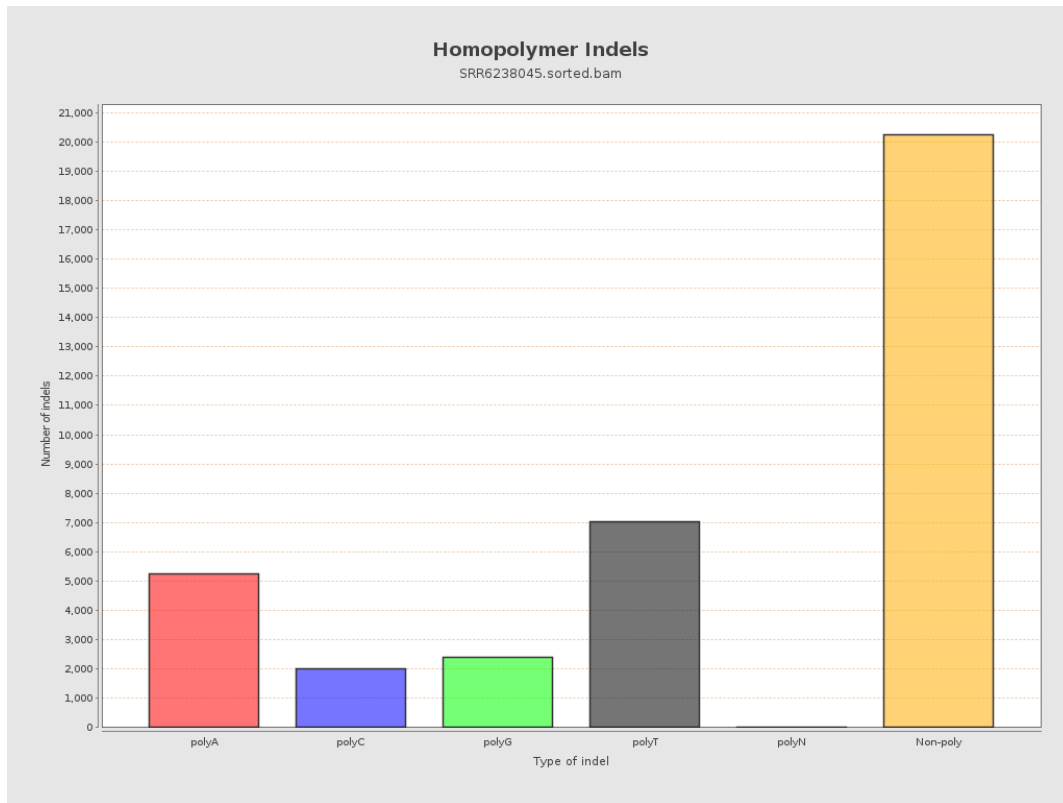
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

