

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 16:41:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238325.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_SRR6238325 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238325.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 16:41:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238325.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,854,301
Mapped reads	2,008,044 / 70.35%
Unmapped reads	846,257 / 29.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,237 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	161,754 / 5.67%
Duplication rate	6.31%
Clipped reads	1,089,415 / 38.17%

2.2. ACGT Content

Number/percentage of A's	36,750,538 / 28.22%
Number/percentage of C's	25,025,539 / 19.22%
Number/percentage of T's	40,175,643 / 30.85%
Number/percentage of G's	28,231,814 / 21.68%
Number/percentage of N's	39,823 / 0.03%
GC Percentage	40.9%

2.3. Coverage

Mean	0.0421

Standard Deviation	0.4702
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2.4. Mapping Quality

Mean Mapping Quality	44.93
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2.5. Mismatches and indels

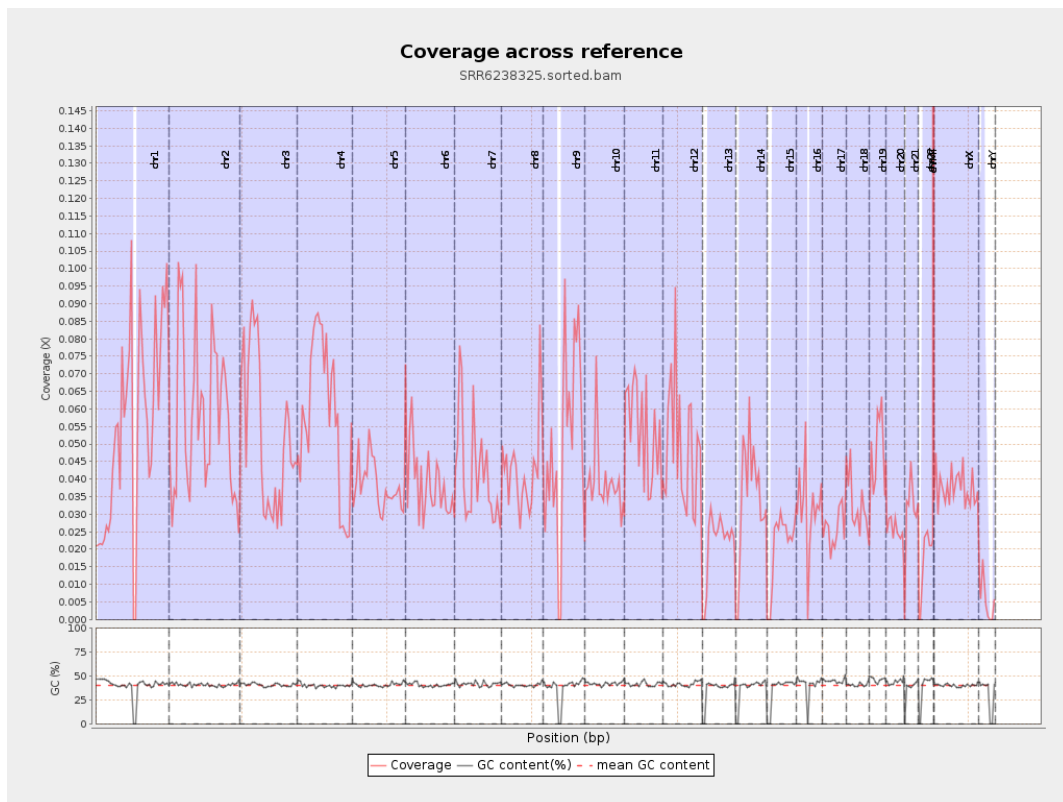
General error rate	0.88%
Mismatches	1,131,744
Insertions	9,437
Mapped reads with at least one insertion	0.47%
Deletions	34,371
Mapped reads with at least one deletion	1.69%
Homopolymer indels	46.32%

2.6. Chromosome stats

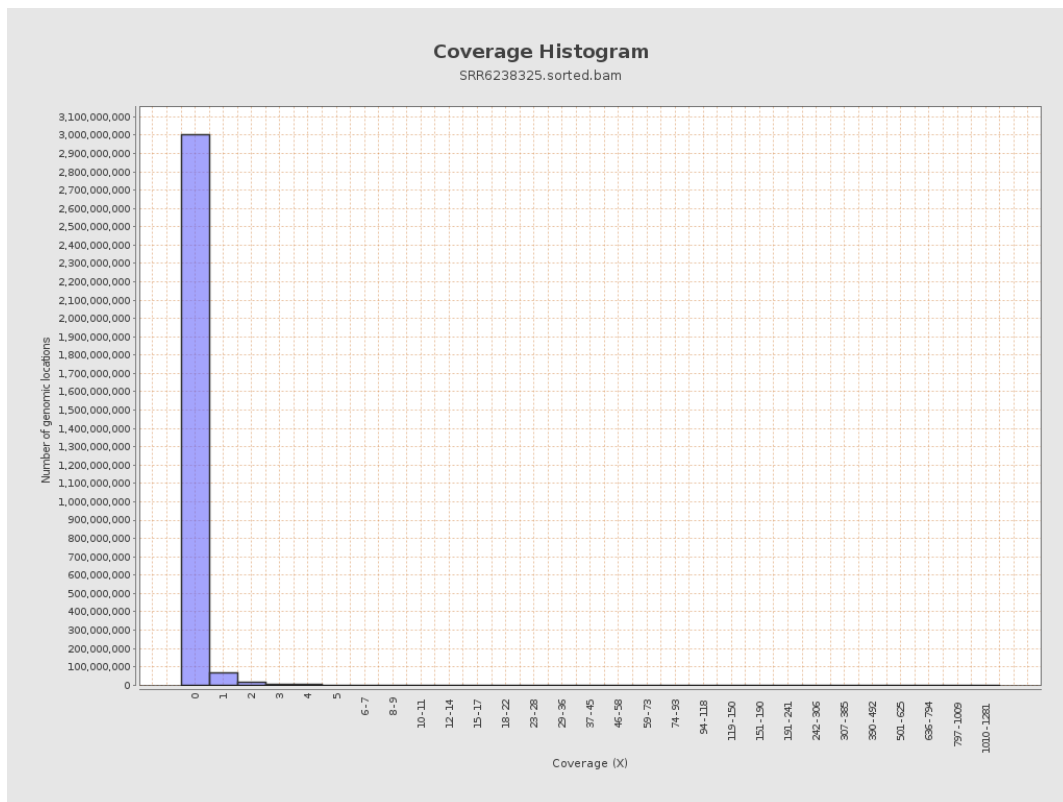
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13648835	0.0548	1.0628
chr2	243199373	13932954	0.0573	0.536
chr3	198022430	10279476	0.0519	0.3067
chr4	191154276	11103898	0.0581	0.3328
chr5	180915260	6853951	0.0379	0.2636
chr6	171115067	6670570	0.039	0.3047
chr7	159138663	6700650	0.0421	0.5667

chr8	146364022	6268301	0.0428	0.4556
chr9	141213431	7213155	0.0511	0.3976
chr10	135534747	5272965	0.0389	0.4055
chr11	135006516	7101413	0.0526	0.3642
chr12	133851895	6457764	0.0482	0.3033
chr13	115169878	2488507	0.0216	0.1985
chr14	107349540	3689019	0.0344	0.2757
chr15	102531392	2168716	0.0212	0.2012
chr16	90354753	2878574	0.0319	0.265
chr17	81195210	2080117	0.0256	0.2205
chr18	78077248	2551692	0.0327	0.6305
chr19	59128983	2799222	0.0473	0.6958
chr20	63025520	1605751	0.0255	0.2288
chr21	48129895	1492428	0.031	0.2447
chr22	51304566	834707	0.0163	0.1657
chrMT	16571	59009	3.561	3.2565
chrX	155270560	5817308	0.0375	0.2811
chrY	59373566	312479	0.0053	0.1138

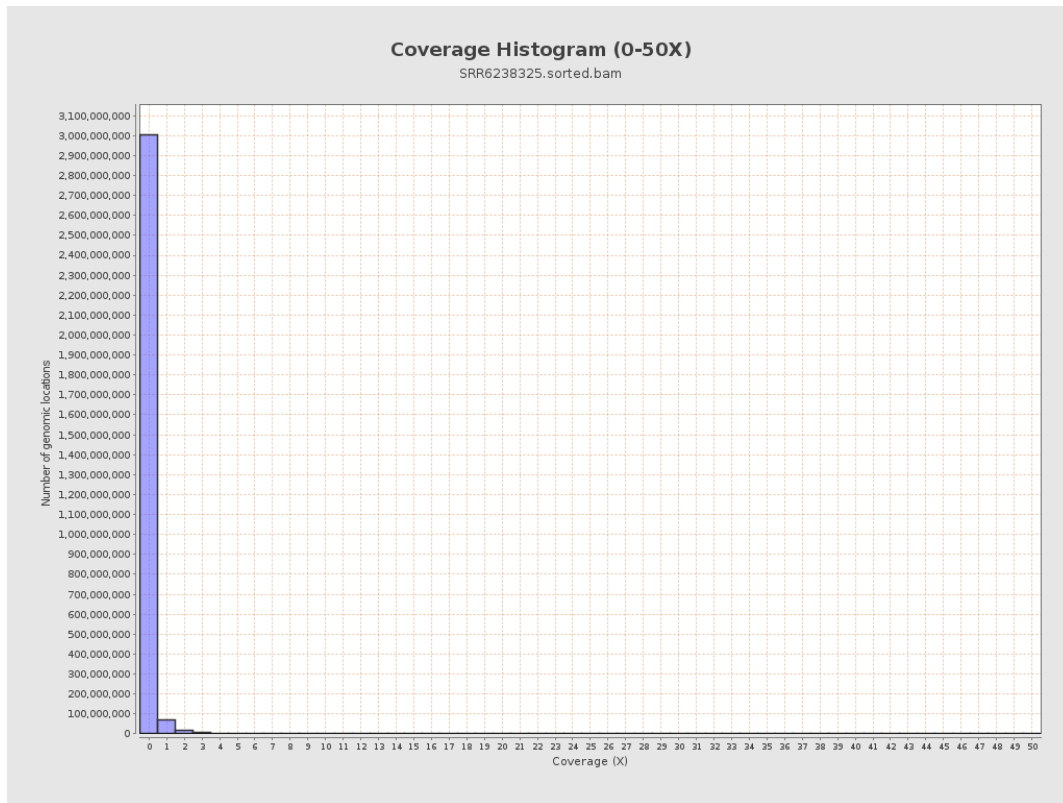
3. Results : Coverage across reference



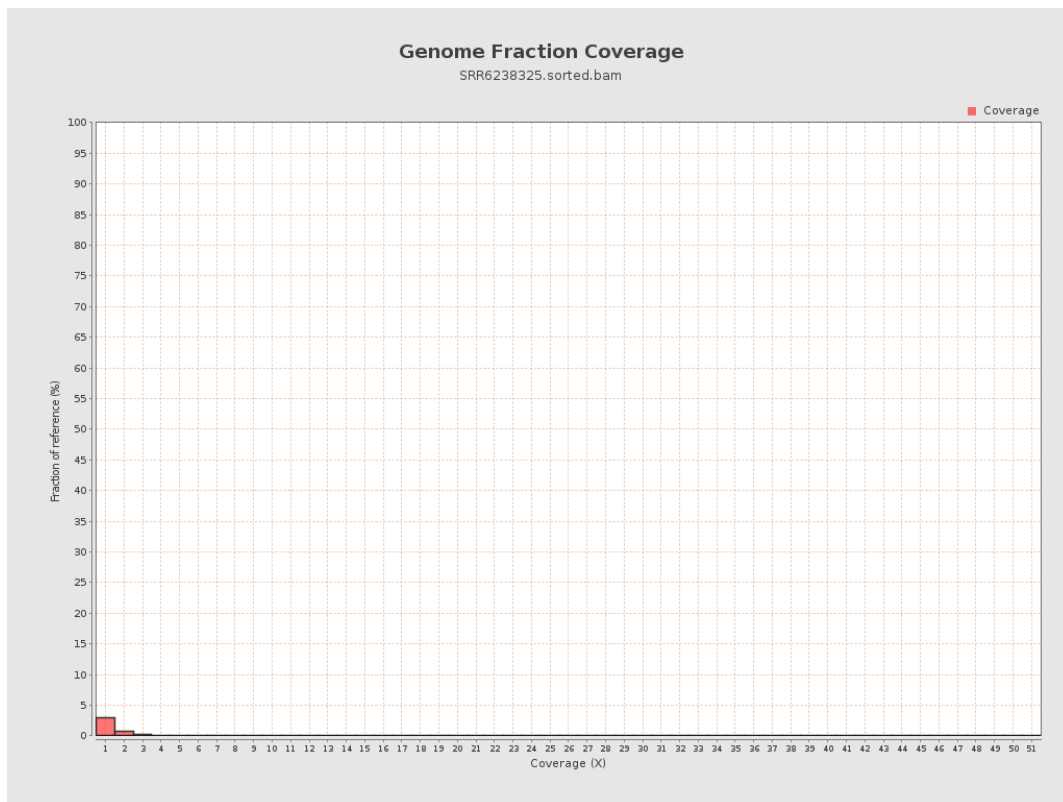
4. Results : Coverage Histogram



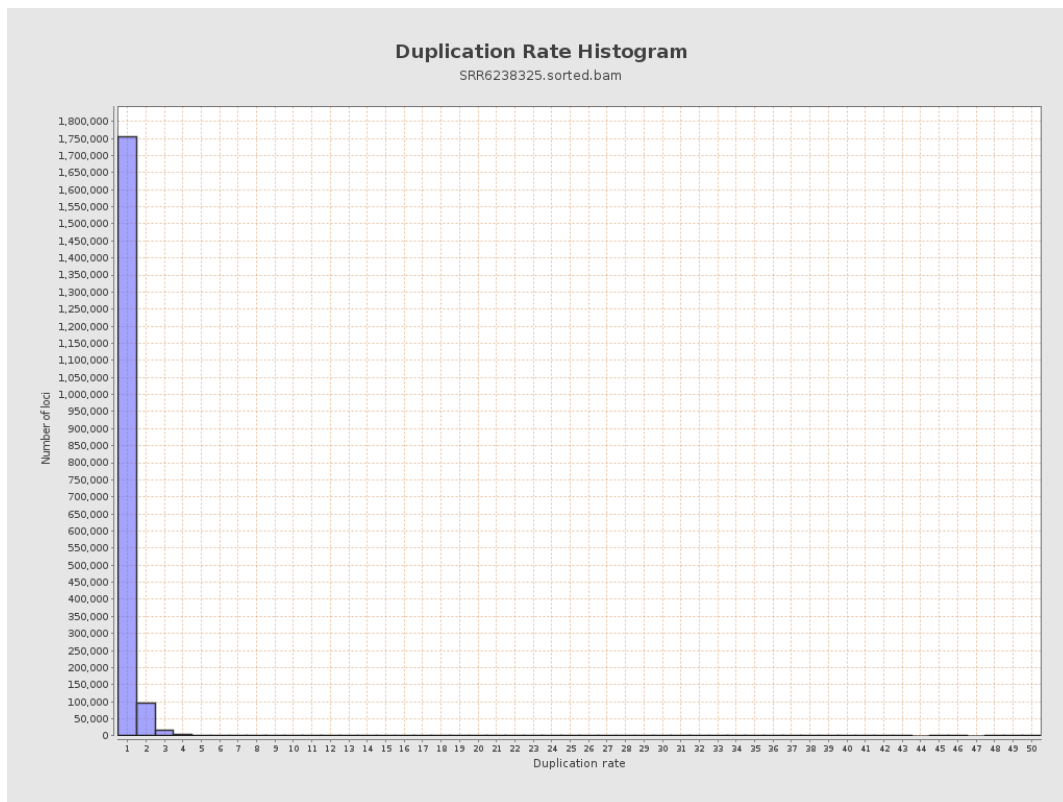
5. Results : Coverage Histogram (0-50X)



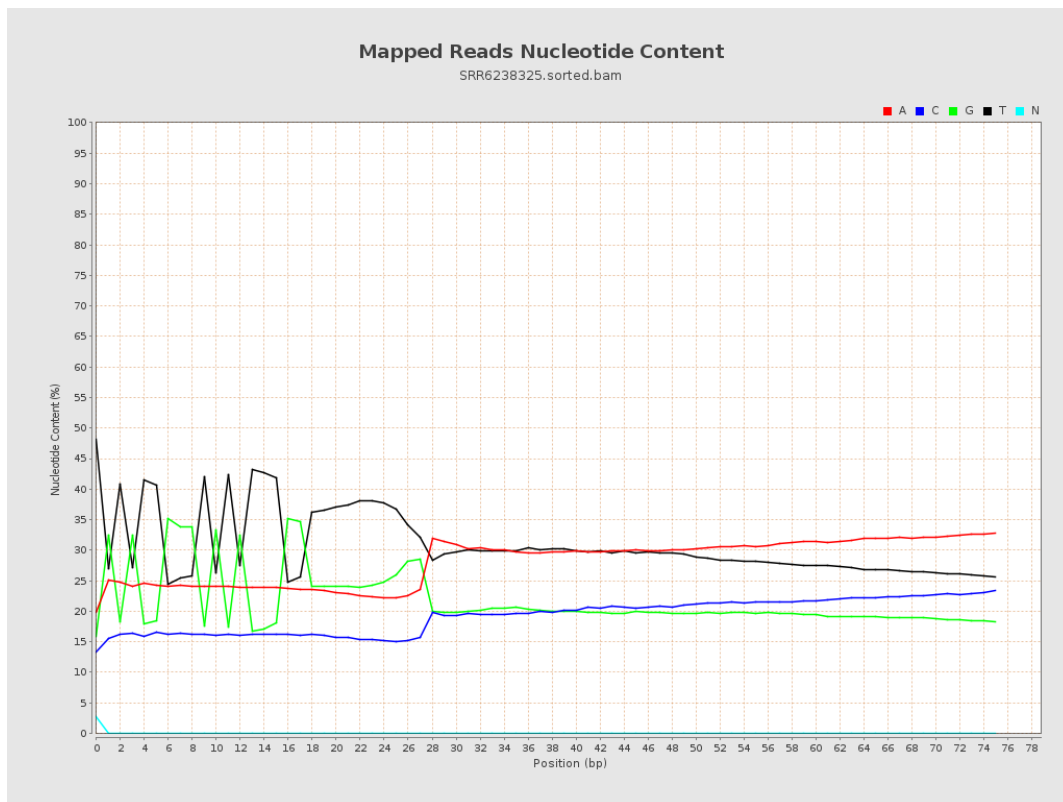
6. Results : Genome Fraction Coverage



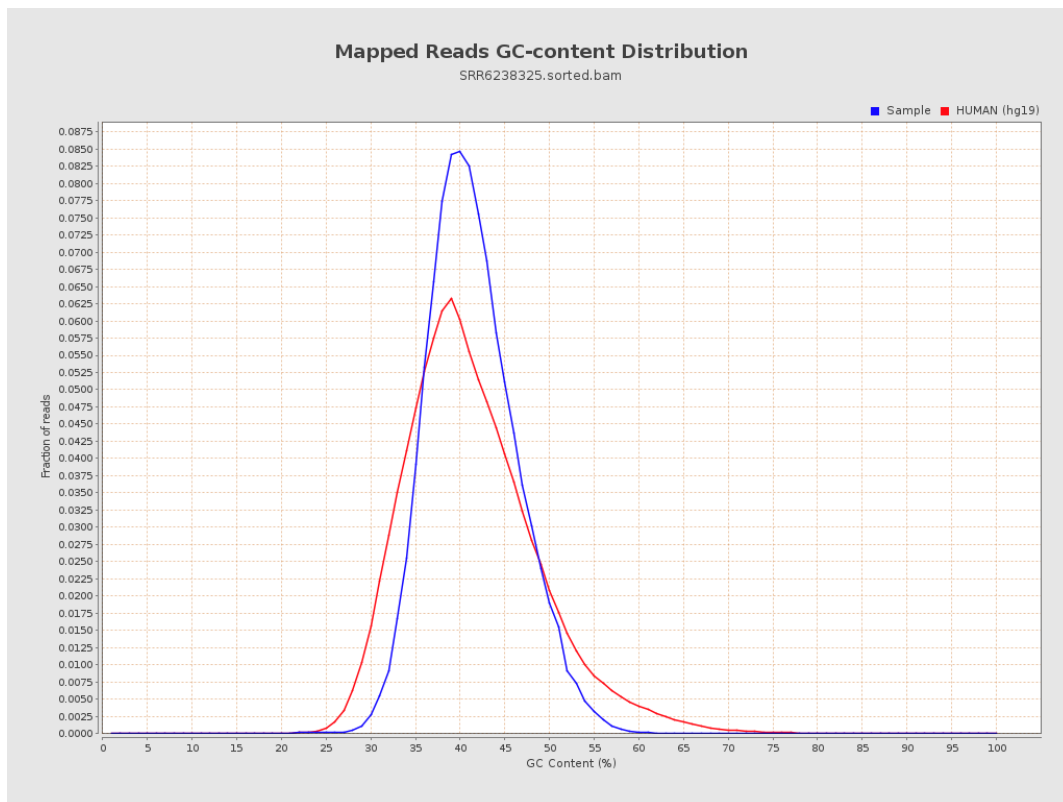
7. Results : Duplication Rate Histogram



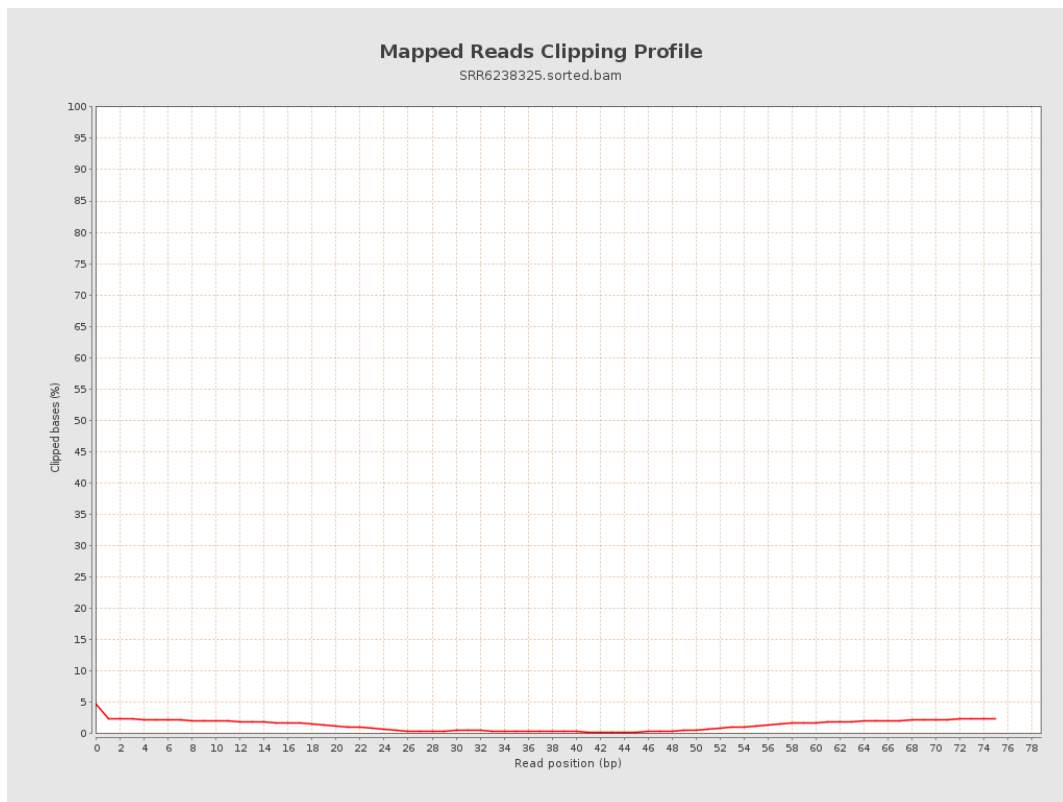
8. Results : Mapped Reads Nucleotide Content



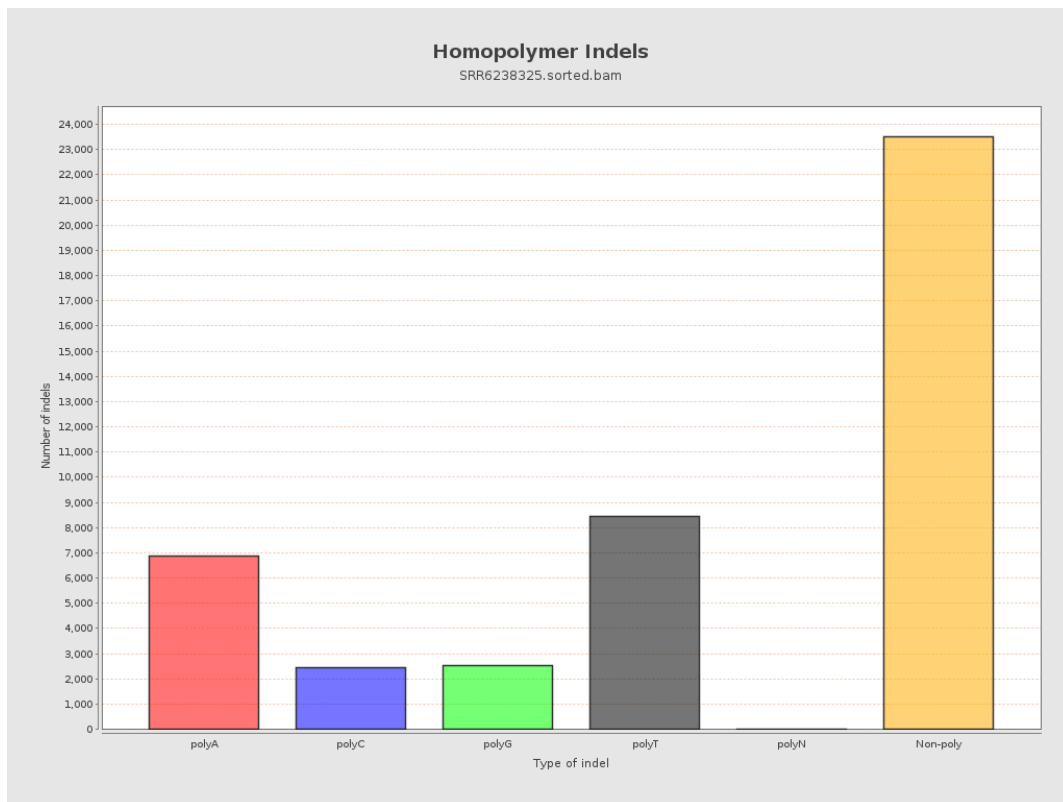
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

