

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 12:00:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238075.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_SRR6238075 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238075.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 12:00:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238075.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,550,435
Mapped reads	2,311,773 / 90.64%
Unmapped reads	238,662 / 9.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,354 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	96,436 / 3.78%
Duplication rate	3.16%
Clipped reads	950,187 / 37.26%

2.2. ACGT Content

Number/percentage of A's	42,576,587 / 27.42%
Number/percentage of C's	29,487,547 / 18.99%
Number/percentage of T's	48,450,266 / 31.2%
Number/percentage of G's	34,757,795 / 22.38%
Number/percentage of N's	21,995 / 0.01%
GC Percentage	41.37%

2.3. Coverage

Mean	0.0502

Standard Deviation	0.406
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2.4. Mapping Quality

Mean Mapping Quality	45.64
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2.5. Mismatches and indels

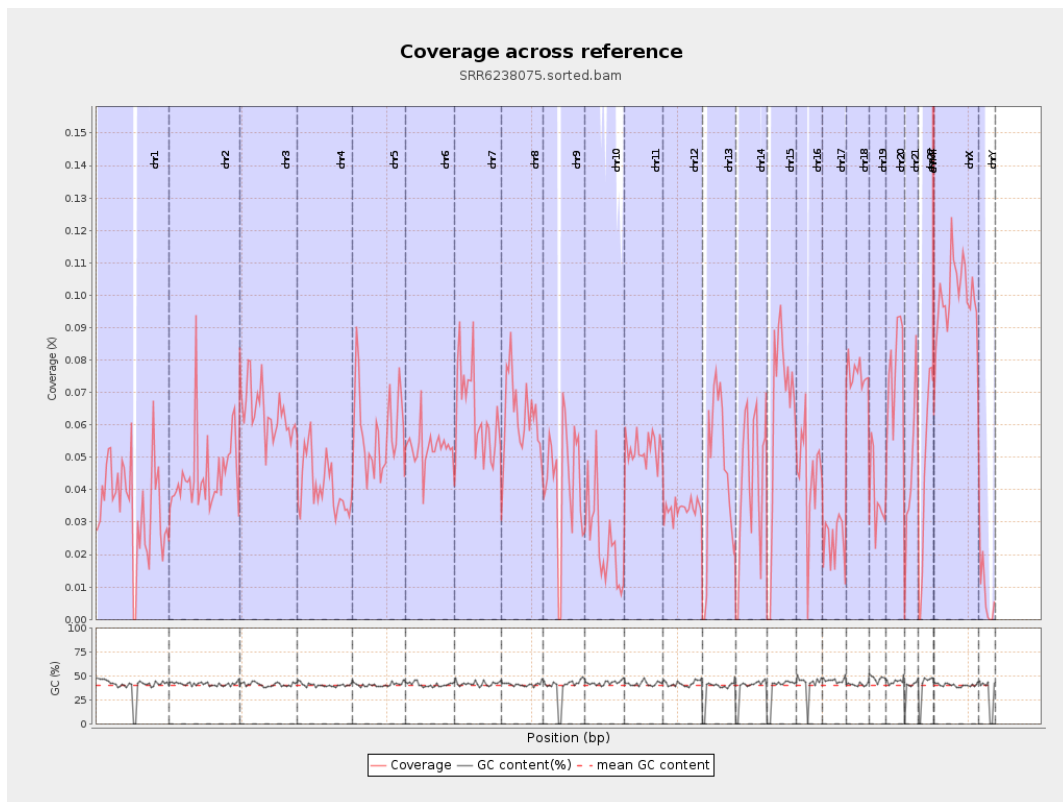
General error rate	0.75%
Mismatches	1,145,252
Insertions	10,471
Mapped reads with at least one insertion	0.45%
Deletions	40,534
Mapped reads with at least one deletion	1.73%
Homopolymer indels	45.89%

2.6. Chromosome stats

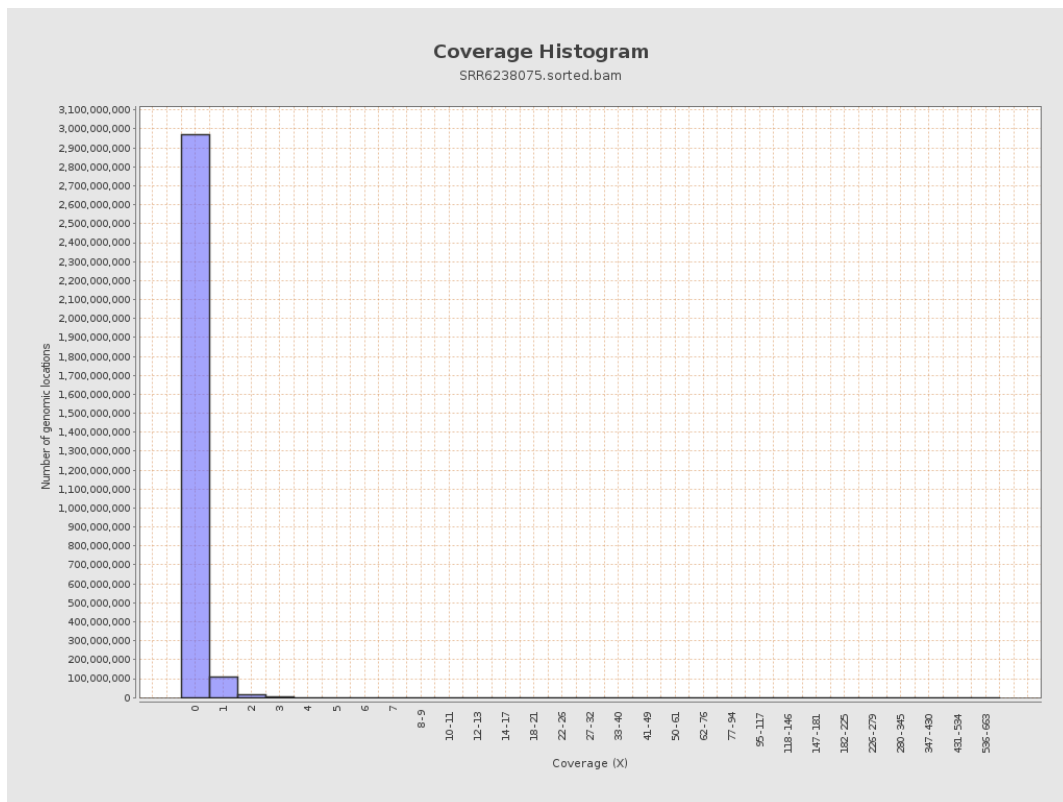
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8714580	0.035	0.5784
chr2	243199373	10919232	0.0449	0.5286
chr3	198022430	12683227	0.064	0.2939
chr4	191154276	7853360	0.0411	0.256
chr5	180915260	10435147	0.0577	0.2825
chr6	171115067	9058523	0.0529	0.3493
chr7	159138663	10131540	0.0637	0.6402

chr8	146364022	9099732	0.0622	0.4573
chr9	141213431	6070234	0.043	0.4311
chr10	135534747	3217219	0.0237	0.3248
chr11	135006516	7059747	0.0523	0.3667
chr12	133851895	4548855	0.034	0.2229
chr13	115169878	5088989	0.0442	0.2439
chr14	107349540	4457043	0.0415	0.2695
chr15	102531392	6557089	0.064	0.2982
chr16	90354753	4056447	0.0449	0.2894
chr17	81195210	1925937	0.0237	0.2122
chr18	78077248	5913706	0.0757	0.7134
chr19	59128983	2235971	0.0378	0.4885
chr20	63025520	4862781	0.0772	0.3282
chr21	48129895	2225935	0.0462	0.2827
chr22	51304566	2312312	0.0451	0.2495
chrMT	16571	28773	1.7363	1.9567
chrX	155270560	15432662	0.0994	0.4172
chrY	59373566	476929	0.008	0.1851

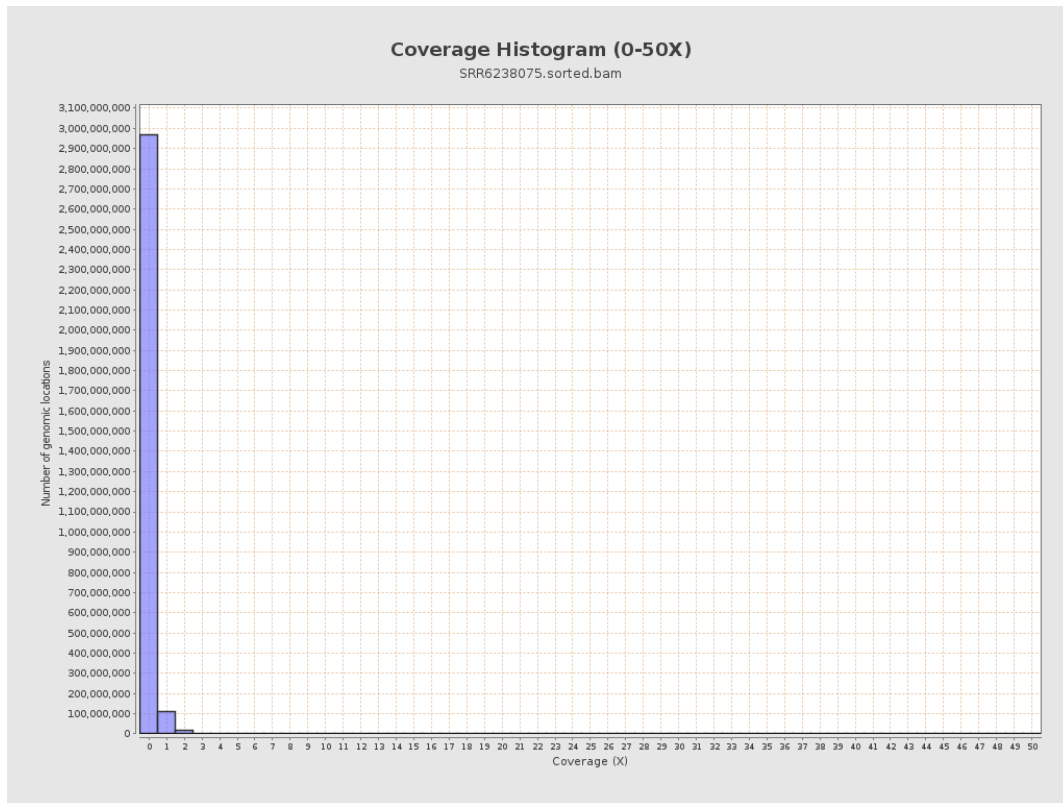
3. Results : Coverage across reference



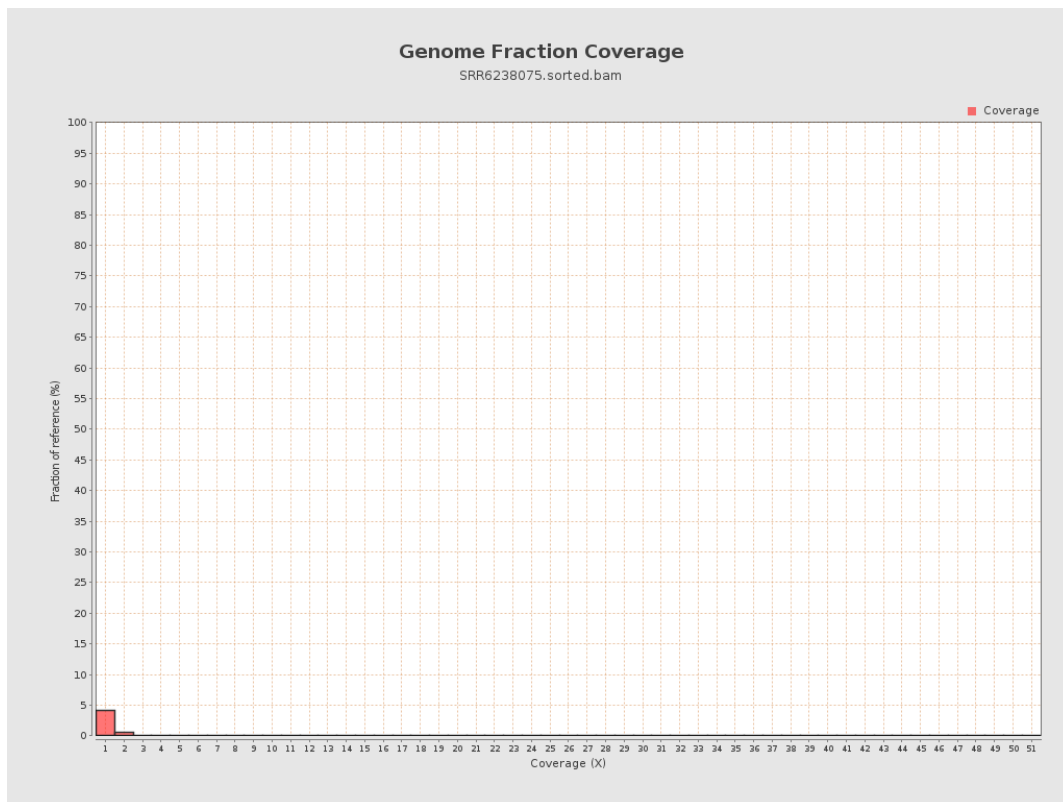
4. Results : Coverage Histogram



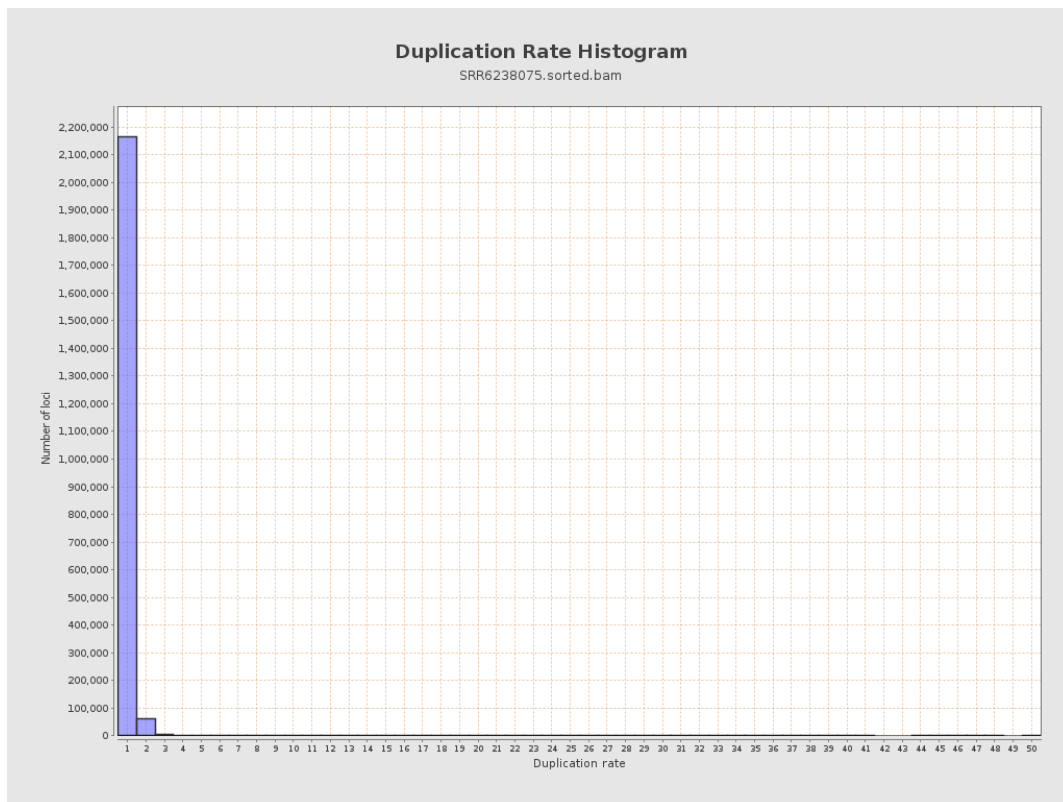
5. Results : Coverage Histogram (0-50X)



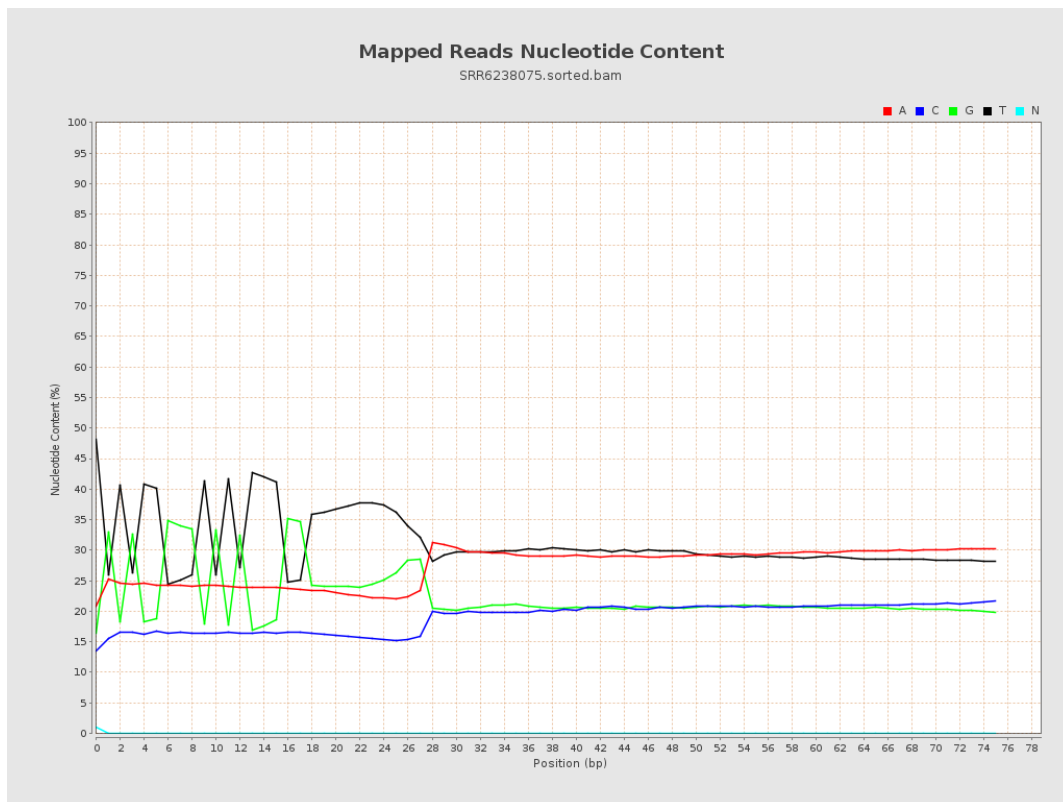
6. Results : Genome Fraction Coverage



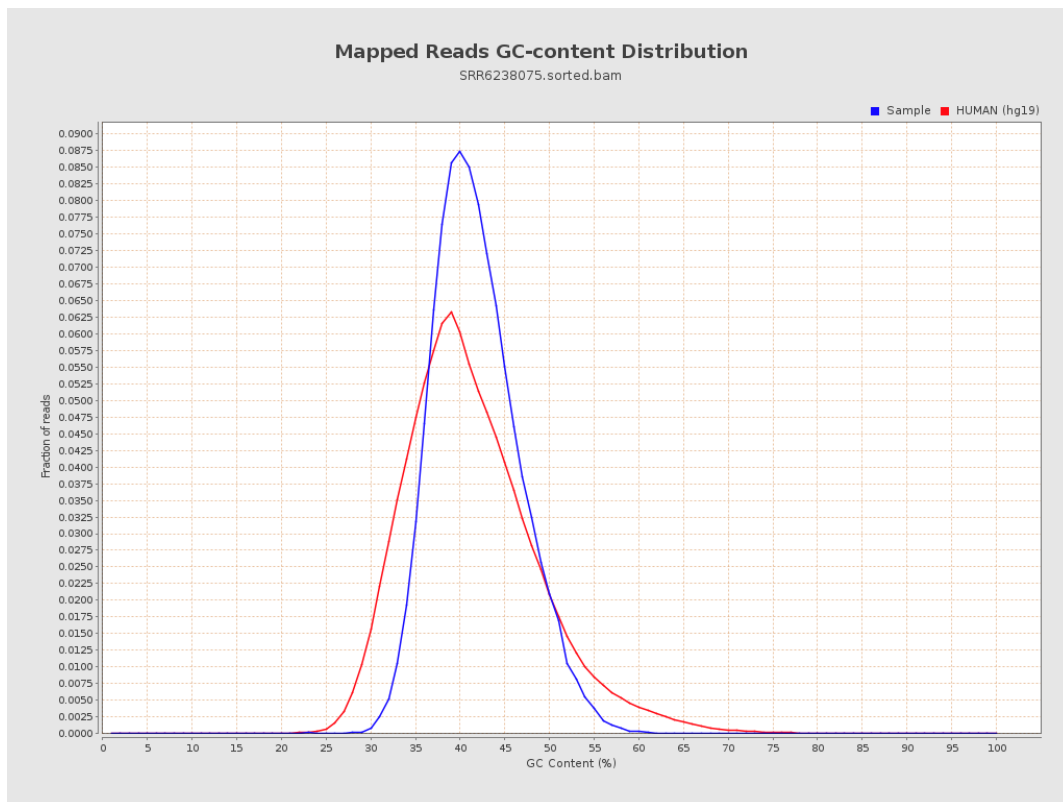
7. Results : Duplication Rate Histogram



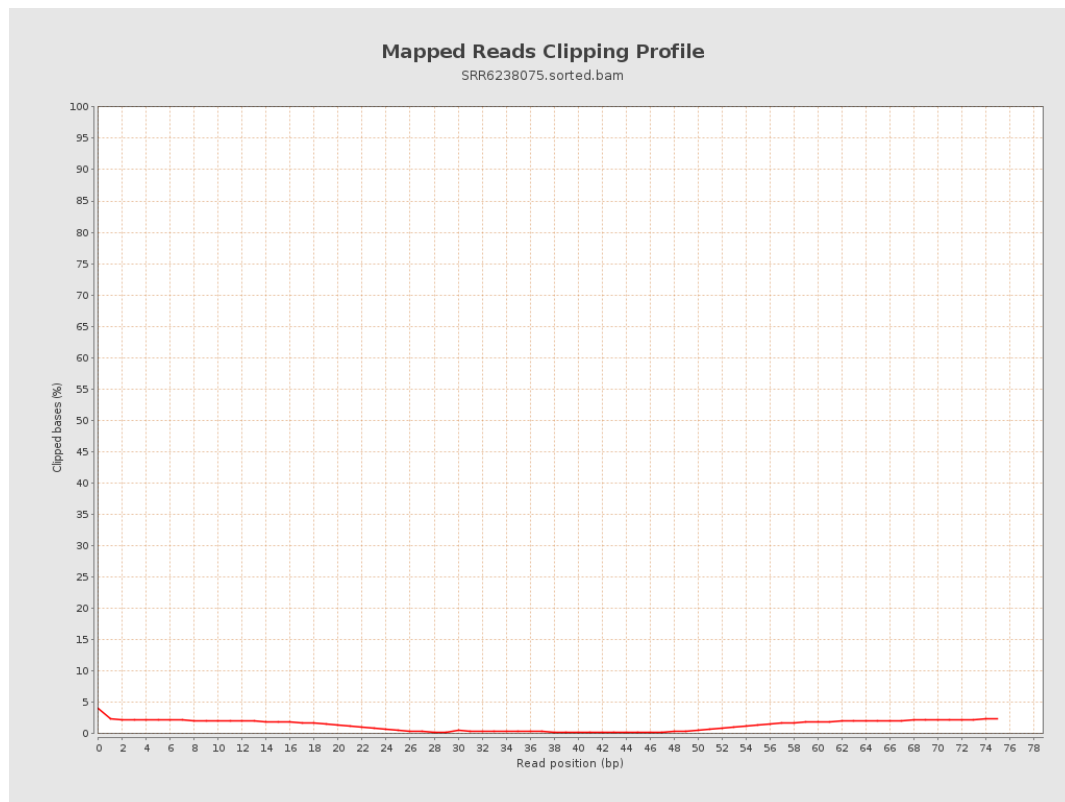
8. Results : Mapped Reads Nucleotide Content



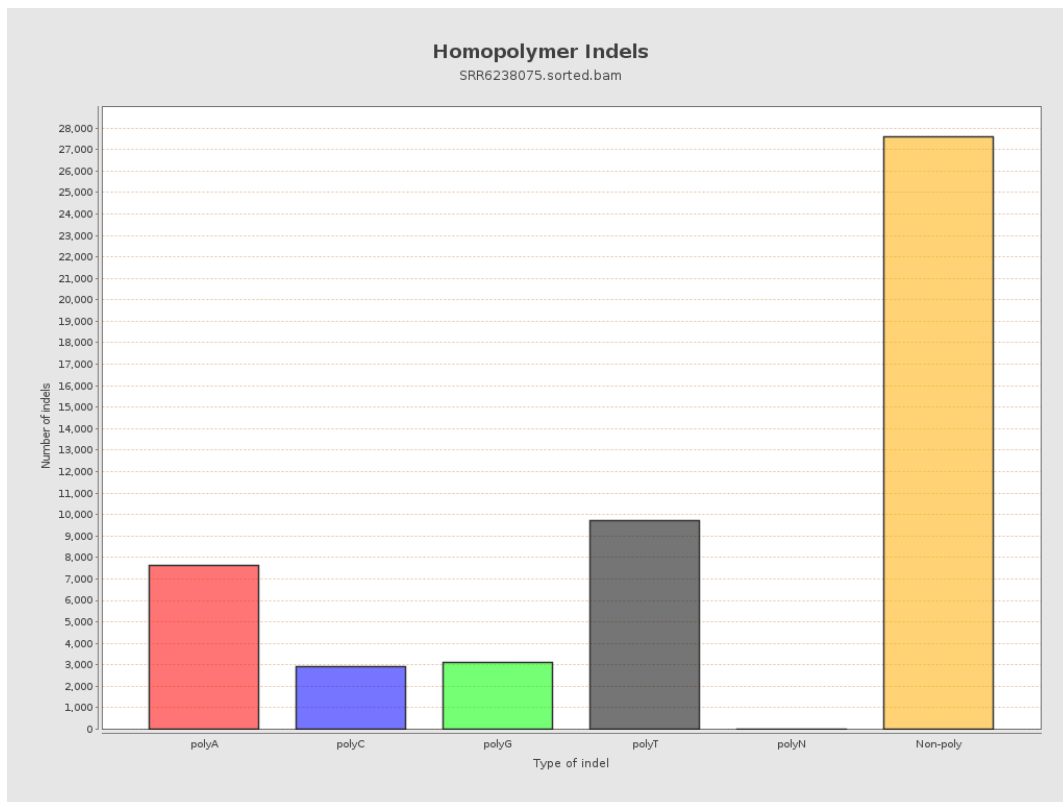
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

