

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 11:36:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234038.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_SRR6234038 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234038.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 11:36:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234038.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,246,459
Mapped reads	1,800,567 / 80.15%
Unmapped reads	445,892 / 19.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,439 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	89,551 / 3.99%
Duplication rate	3.93%
Clipped reads	742,469 / 33.05%

2.2. ACGT Content

Number/percentage of A's	34,698,859 / 28.72%
Number/percentage of C's	21,175,131 / 17.52%
Number/percentage of T's	39,693,522 / 32.85%
Number/percentage of G's	25,241,138 / 20.89%
Number/percentage of N's	25,566 / 0.02%
GC Percentage	38.41%

2.3. Coverage

Mean	0.0391

Standard Deviation	0.4272
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2.4. Mapping Quality

Mean Mapping Quality	46.27
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2.5. Mismatches and indels

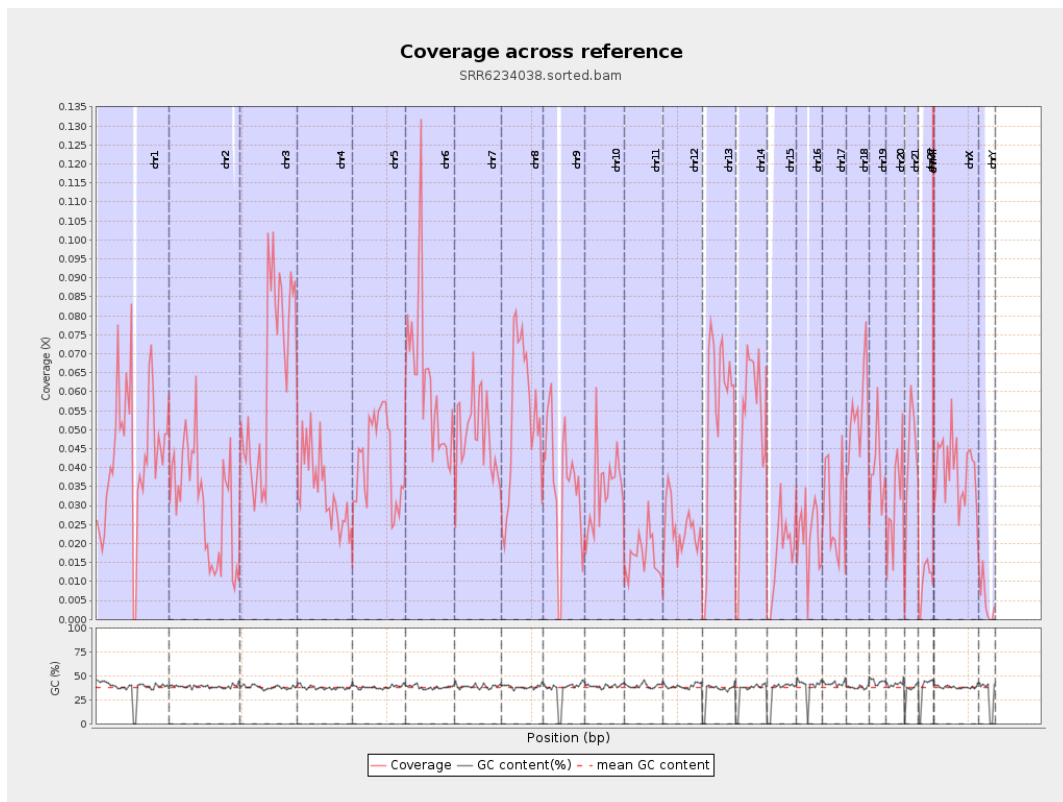
General error rate	0.86%
Mismatches	1,015,483
Insertions	9,673
Mapped reads with at least one insertion	0.53%
Deletions	45,628
Mapped reads with at least one deletion	2.49%
Homopolymer indels	44.74%

2.6. Chromosome stats

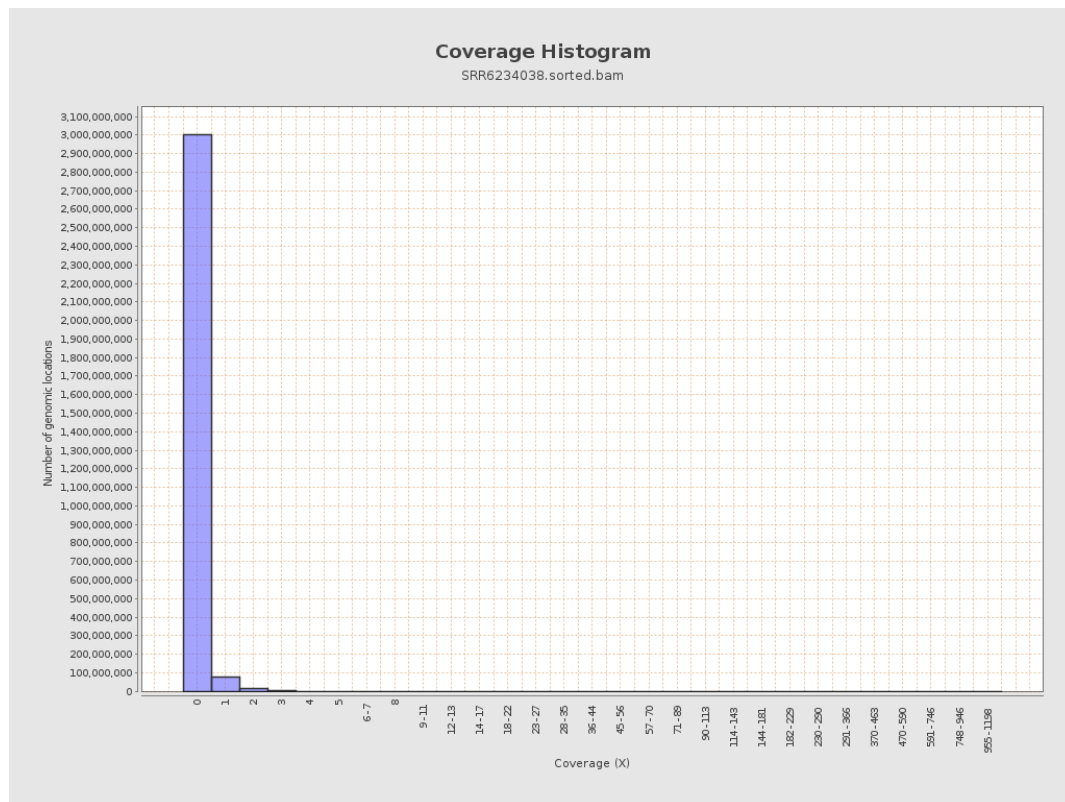
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10721822	0.043	0.9165
chr2	243199373	7374765	0.0303	0.3457
chr3	198022430	12470236	0.063	0.3112
chr4	191154276	6539201	0.0342	0.2394
chr5	180915260	7600973	0.042	0.2502
chr6	171115067	10600285	0.0619	0.4769
chr7	159138663	7730406	0.0486	0.4553

chr8	146364022	7763617	0.053	0.7949
chr9	141213431	5077448	0.036	0.2889
chr10	135534747	4599048	0.0339	0.3463
chr11	135006516	2259950	0.0167	0.1935
chr12	133851895	3204563	0.0239	0.1923
chr13	115169878	6204823	0.0539	0.2854
chr14	107349540	5368693	0.05	0.284
chr15	102531392	1772694	0.0173	0.16
chr16	90354753	1992086	0.022	0.208
chr17	81195210	2184877	0.0269	0.228
chr18	78077248	4253290	0.0545	0.5222
chr19	59128983	2376491	0.0402	0.4829
chr20	63025520	1941878	0.0308	0.2195
chr21	48129895	2015031	0.0419	0.2597
chr22	51304566	513285	0.01	0.1171
chrMT	16571	20974	1.2657	1.5317
chrX	155270560	6052381	0.039	0.2581
chrY	59373566	276030	0.0046	0.1194

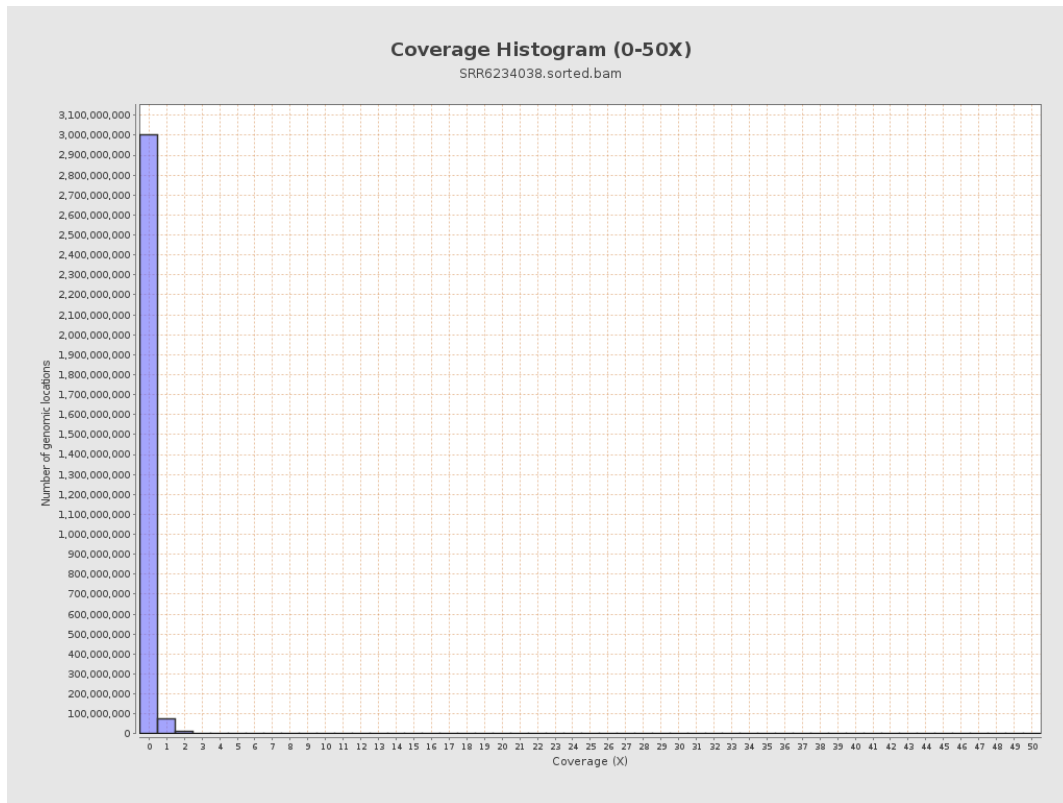
3. Results : Coverage across reference



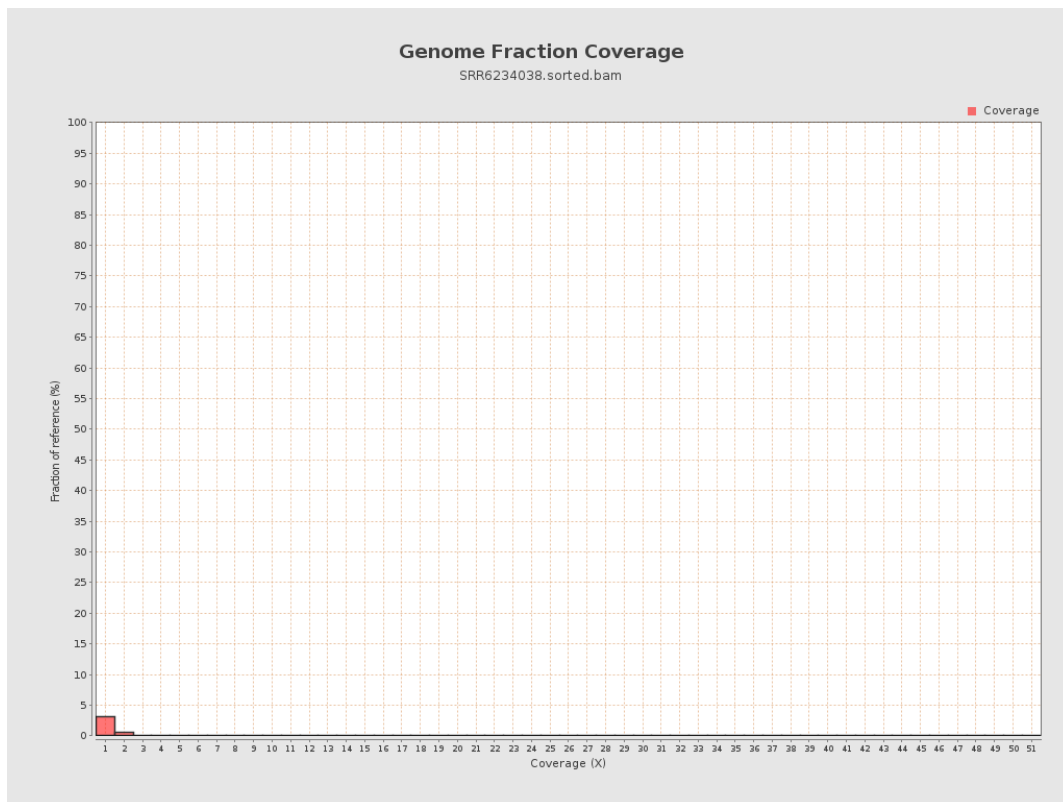
4. Results : Coverage Histogram



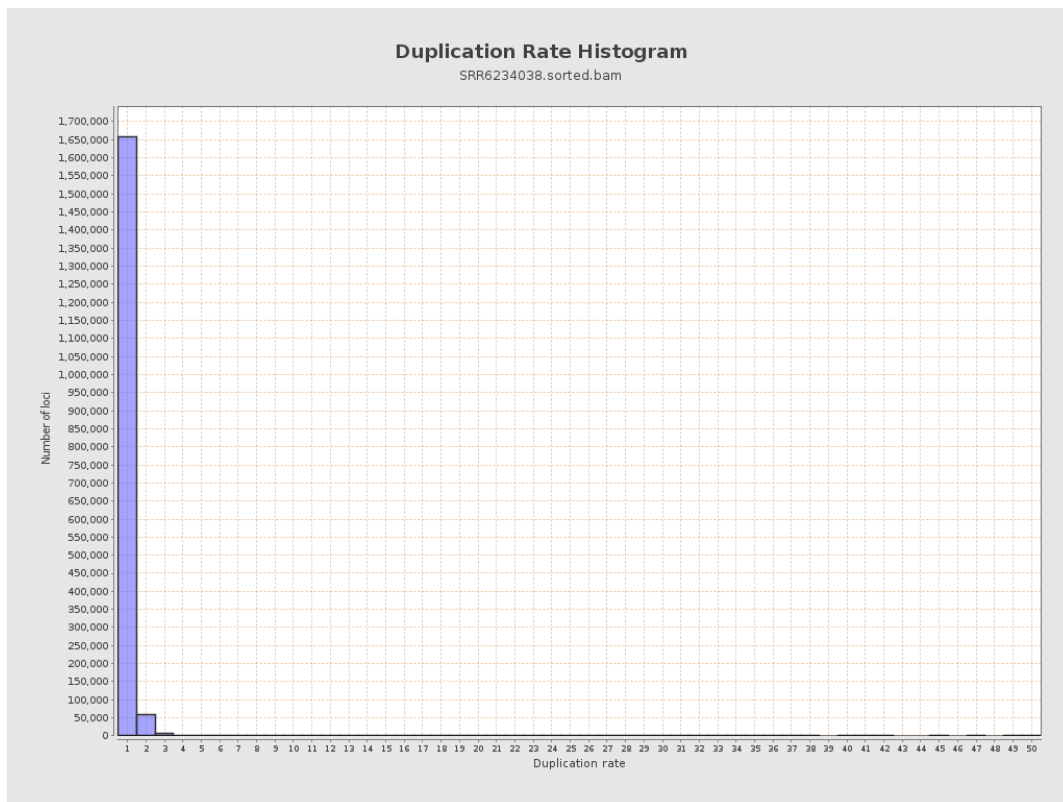
5. Results : Coverage Histogram (0-50X)



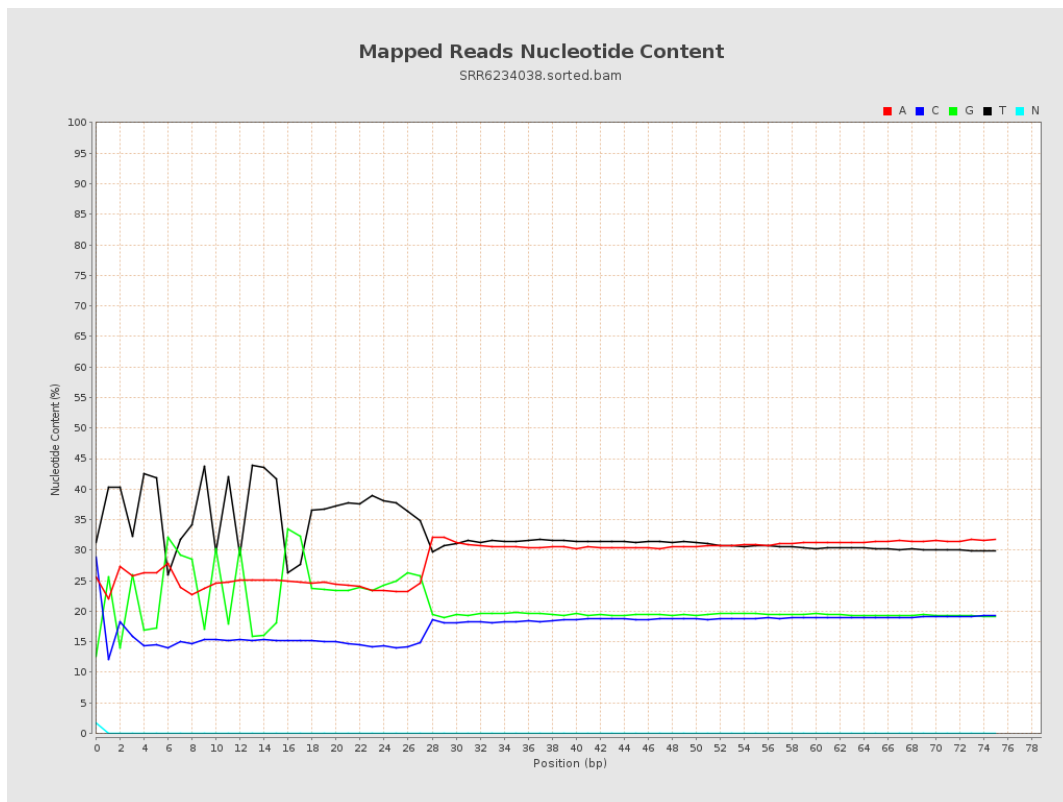
6. Results : Genome Fraction Coverage



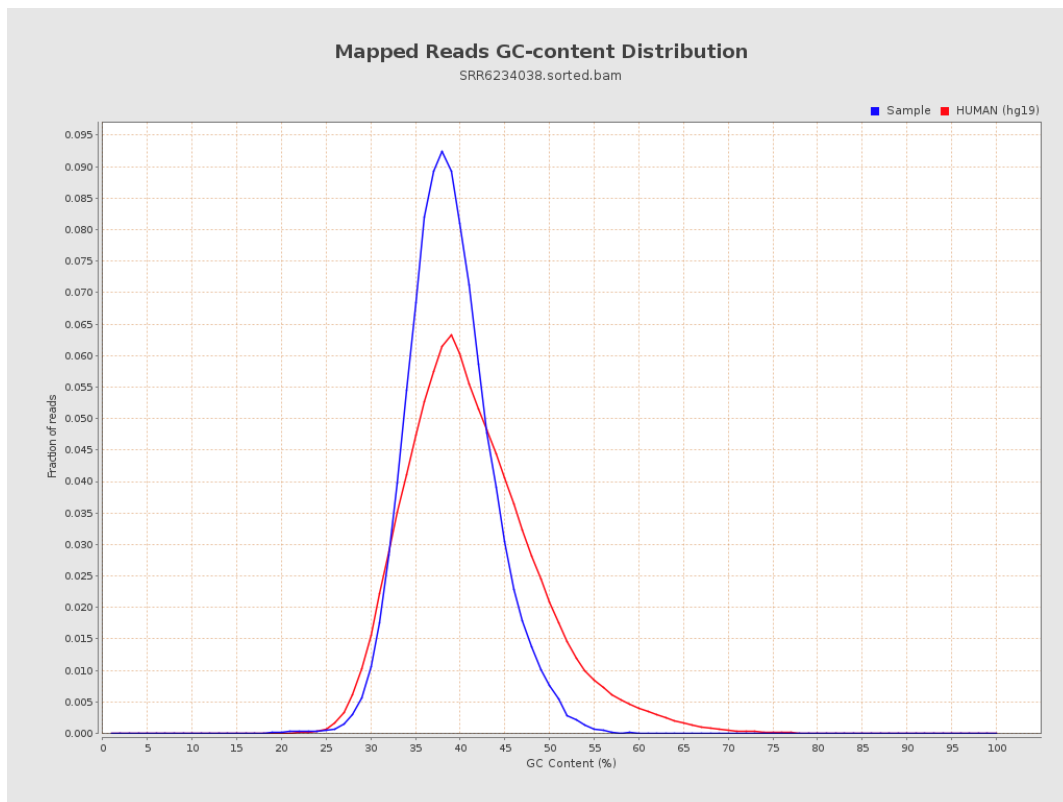
7. Results : Duplication Rate Histogram



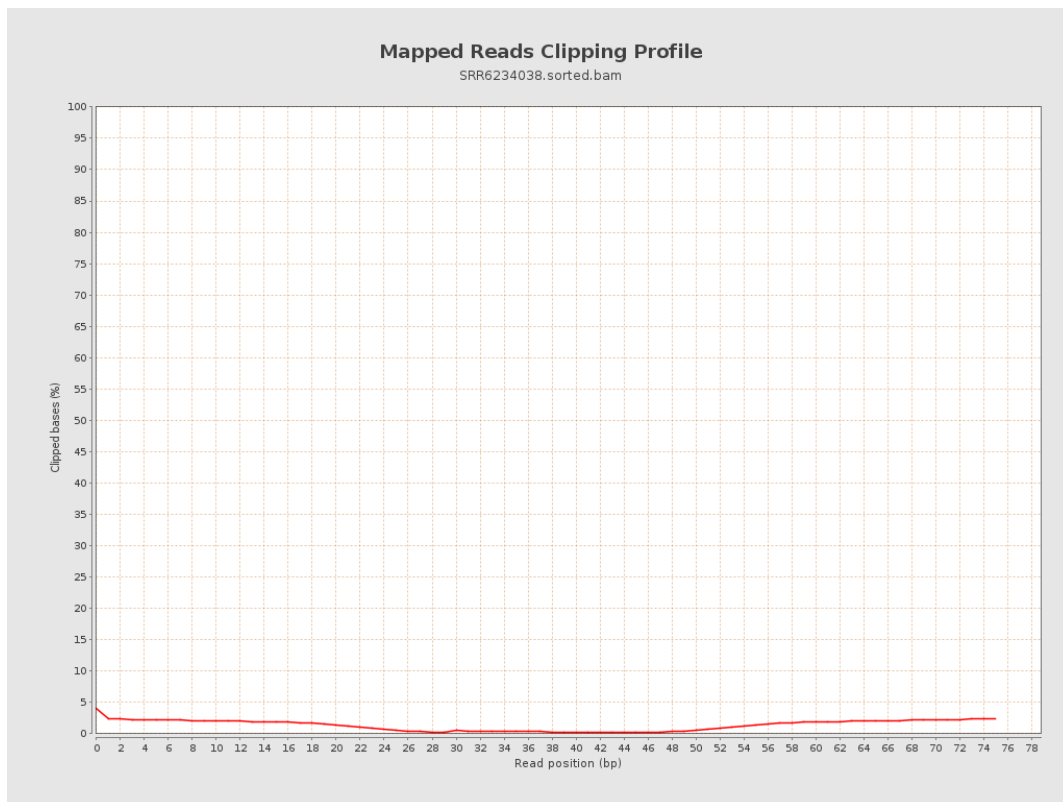
8. Results : Mapped Reads Nucleotide Content



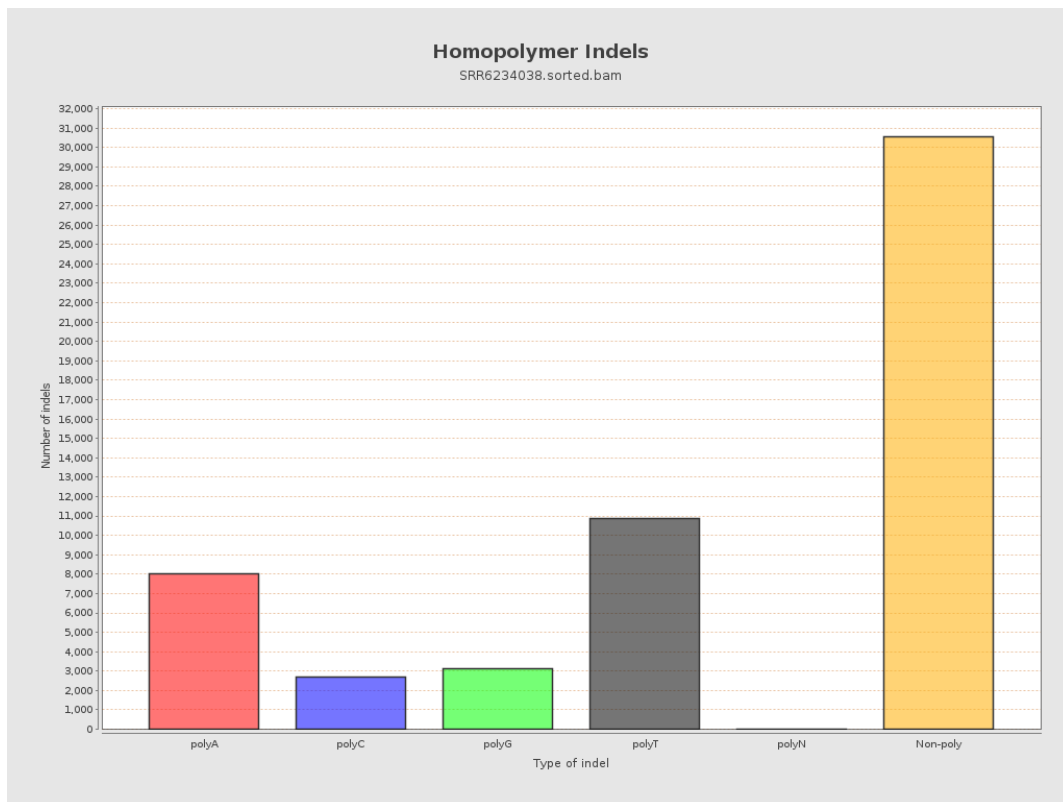
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

