

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 02:20:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238674.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_SRR6238674 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238674.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 02:20:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238674.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,345,499
Mapped reads	3,024,227 / 90.4%
Unmapped reads	321,272 / 9.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,027 / 0.96%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	681,003 / 20.36%
Duplication rate	17.63%
Clipped reads	1,920,707 / 57.41%

2.2. ACGT Content

Number/percentage of A's	47,776,279 / 25.53%
Number/percentage of C's	33,429,102 / 17.86%
Number/percentage of T's	62,120,195 / 33.19%
Number/percentage of G's	43,818,588 / 23.41%
Number/percentage of N's	9,480 / 0.01%
GC Percentage	41.28%

2.3. Coverage

Mean	0.0605

Standard Deviation	0.8923
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2.4. Mapping Quality

Mean Mapping Quality	39.46
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2.5. Mismatches and indels

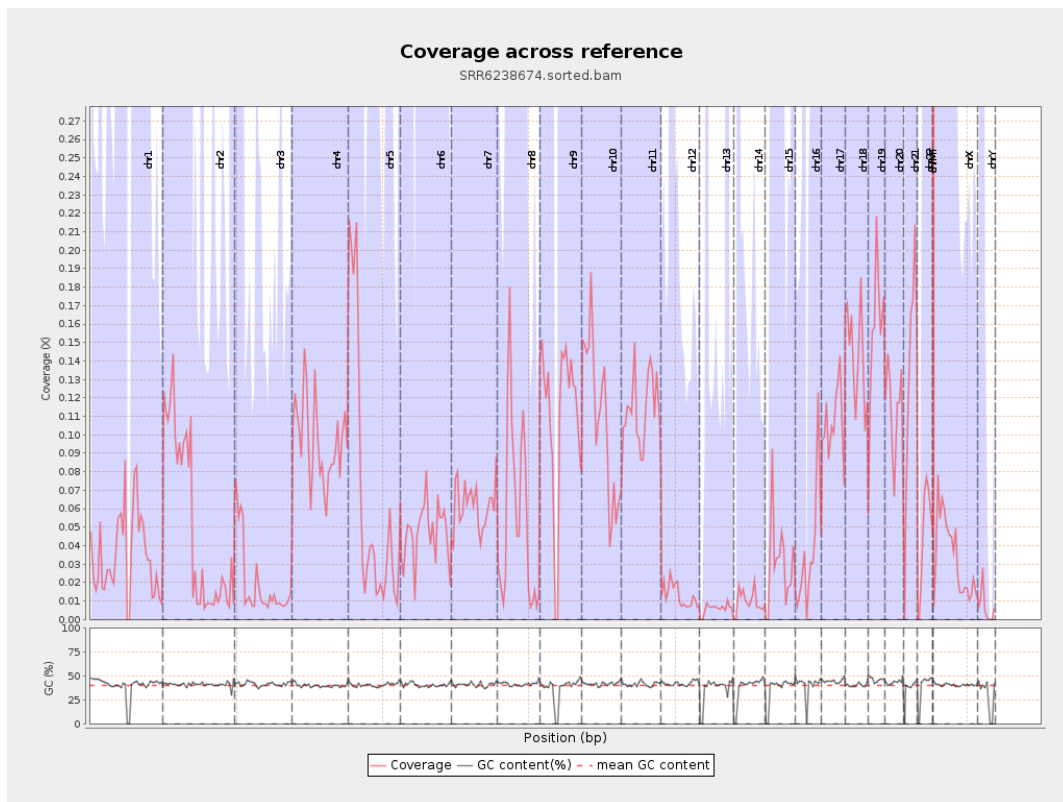
General error rate	0.64%
Mismatches	1,177,232
Insertions	13,409
Mapped reads with at least one insertion	0.44%
Deletions	56,247
Mapped reads with at least one deletion	1.84%
Homopolymer indels	41.3%

2.6. Chromosome stats

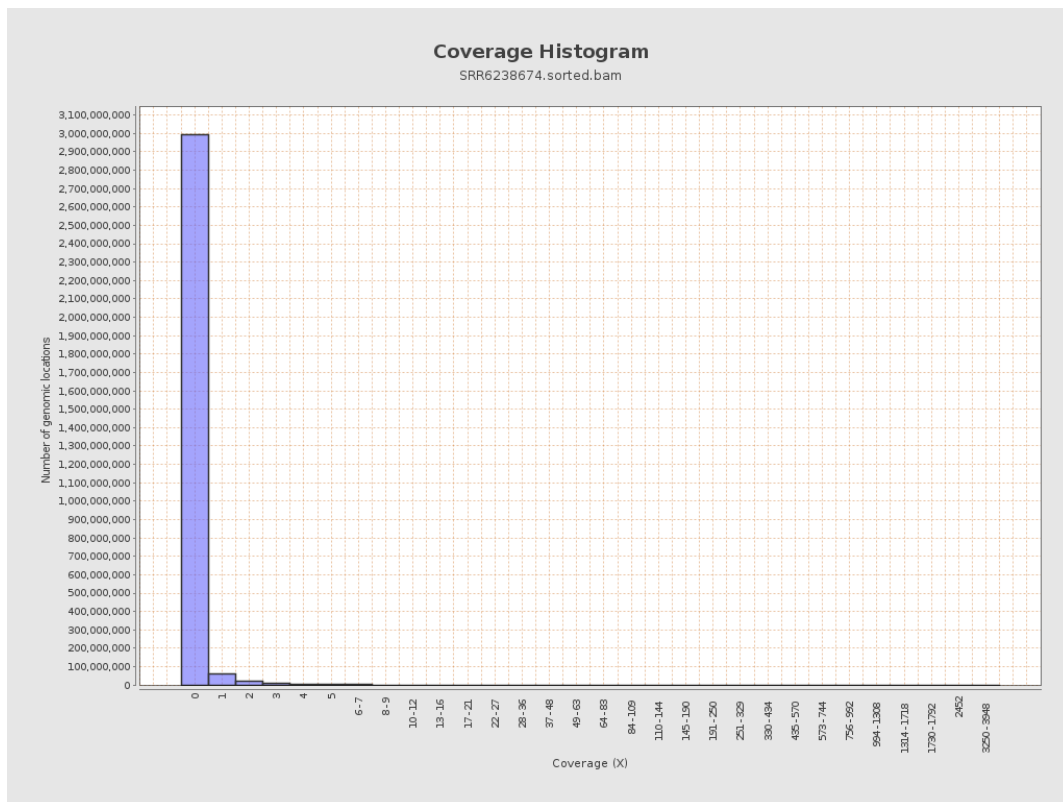
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8518216	0.0342	1.3869
chr2	243199373	12262052	0.0504	1.8431
chr3	198022430	3970707	0.0201	0.2537
chr4	191154276	18300908	0.0957	0.5167
chr5	180915260	11844237	0.0655	0.4419
chr6	171115067	8021199	0.0469	0.636
chr7	159138663	9783154	0.0615	0.5553

chr8	146364022	7865063	0.0537	1.1207
chr9	141213431	15592325	0.1104	0.8465
chr10	135534747	14547207	0.1073	0.6182
chr11	135006516	15363123	0.1138	0.6374
chr12	133851895	1713172	0.0128	0.2543
chr13	115169878	684037	0.0059	0.4111
chr14	107349540	1032625	0.0096	0.394
chr15	102531392	3182919	0.031	0.4322
chr16	90354753	3116819	0.0345	0.4432
chr17	81195210	8821379	0.1086	0.6004
chr18	78077248	11251211	0.1441	1.9273
chr19	59128983	9422382	0.1594	0.9307
chr20	63025520	7225017	0.1146	0.592
chr21	48129895	6216603	0.1292	0.6342
chr22	51304566	2395014	0.0467	0.3523
chrMT	16571	476411	28.7497	17.8774
chrX	155270560	5210585	0.0336	0.3636
chrY	59373566	432892	0.0073	0.3106

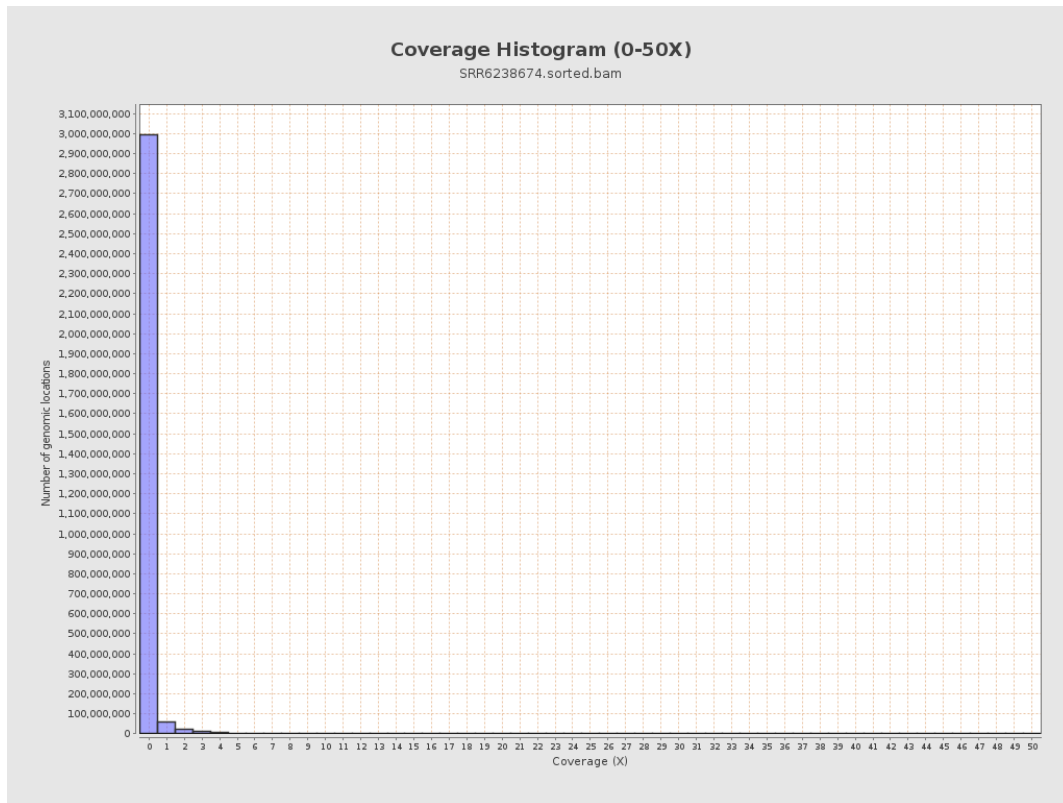
3. Results : Coverage across reference



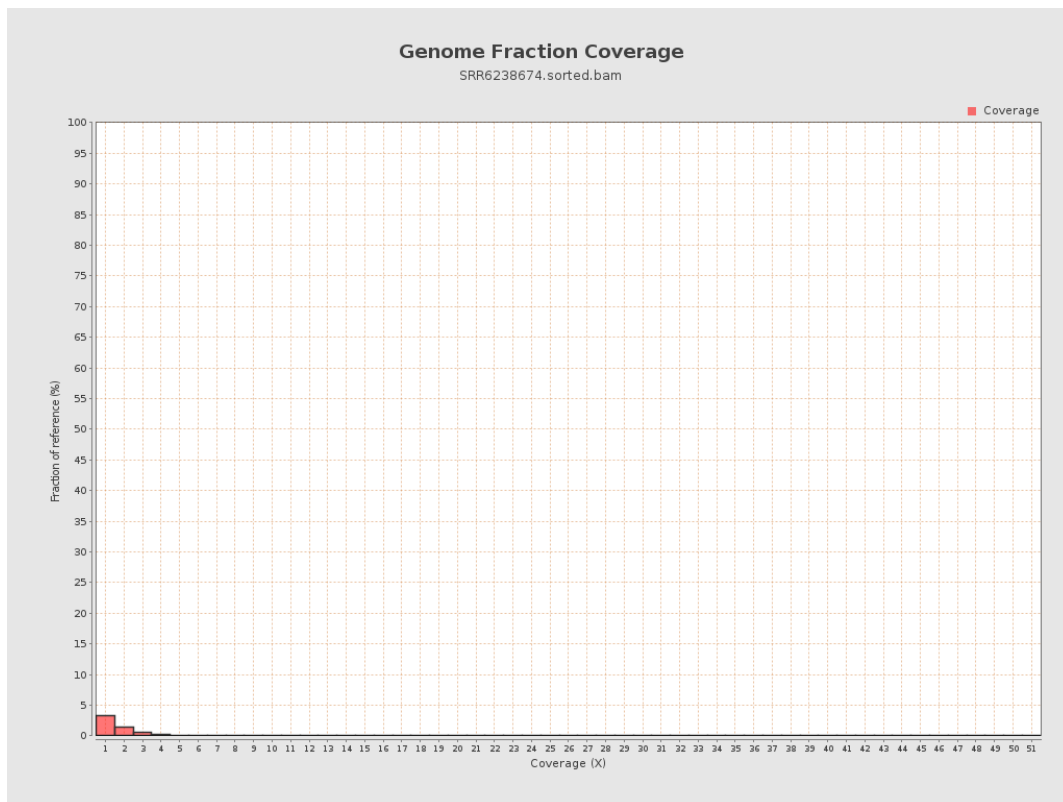
4. Results : Coverage Histogram



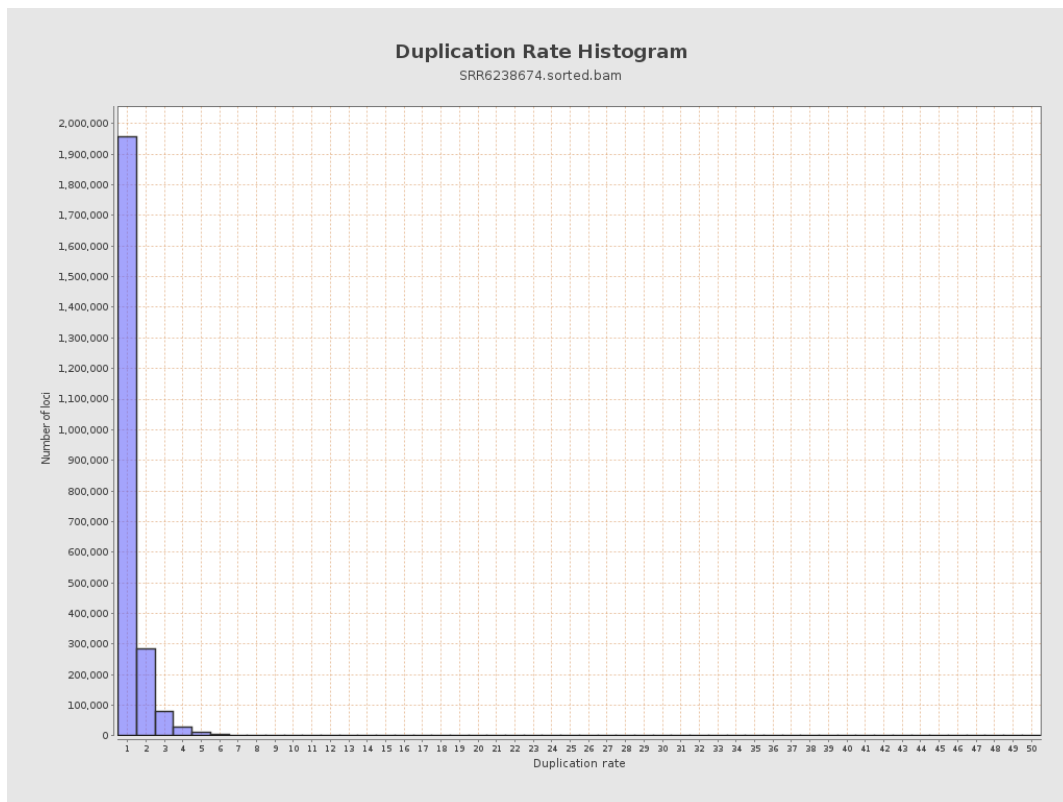
5. Results : Coverage Histogram (0-50X)



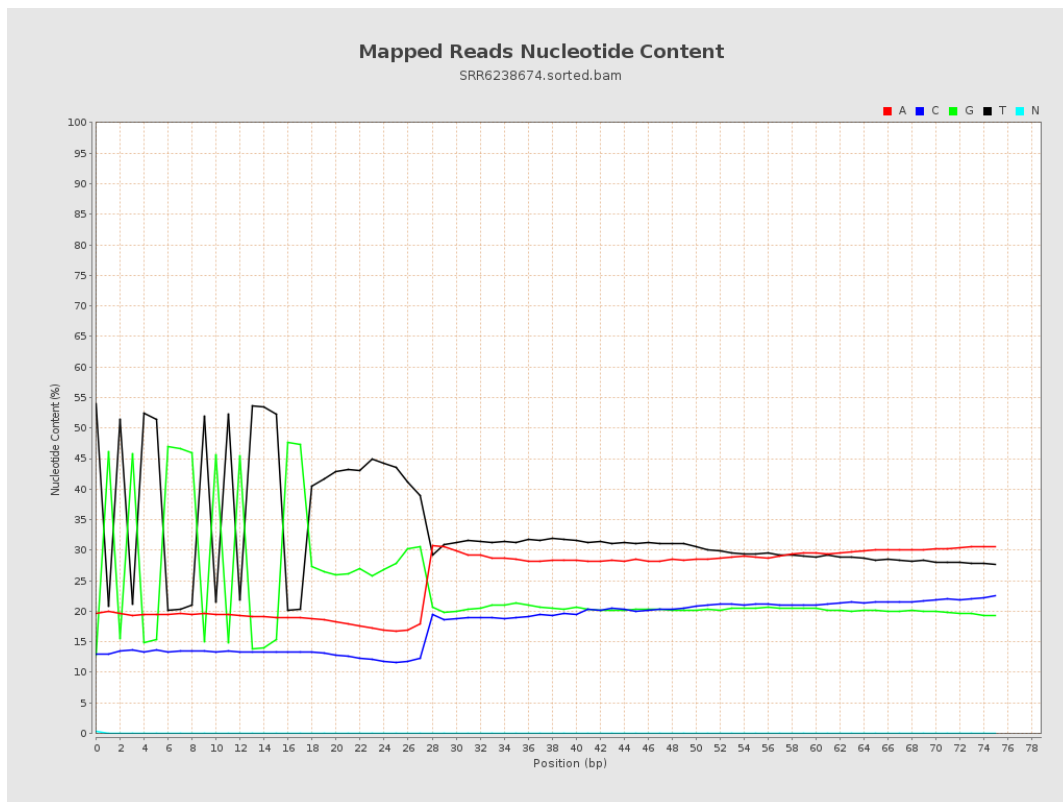
6. Results : Genome Fraction Coverage



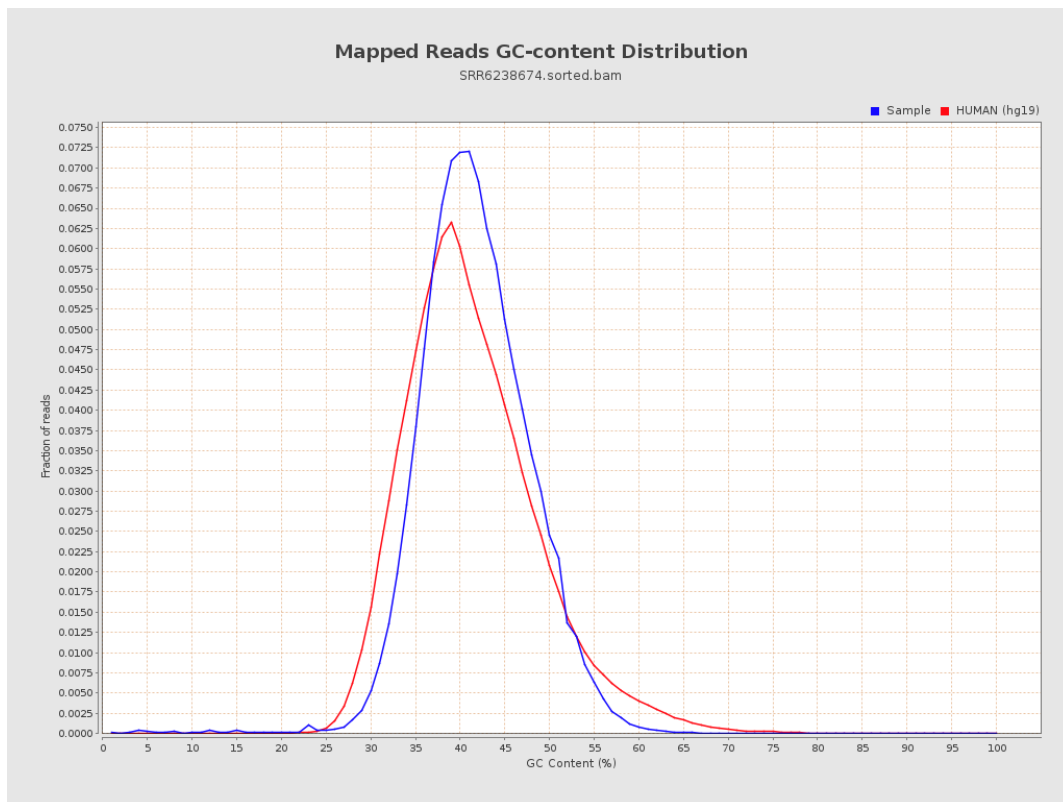
7. Results : Duplication Rate Histogram



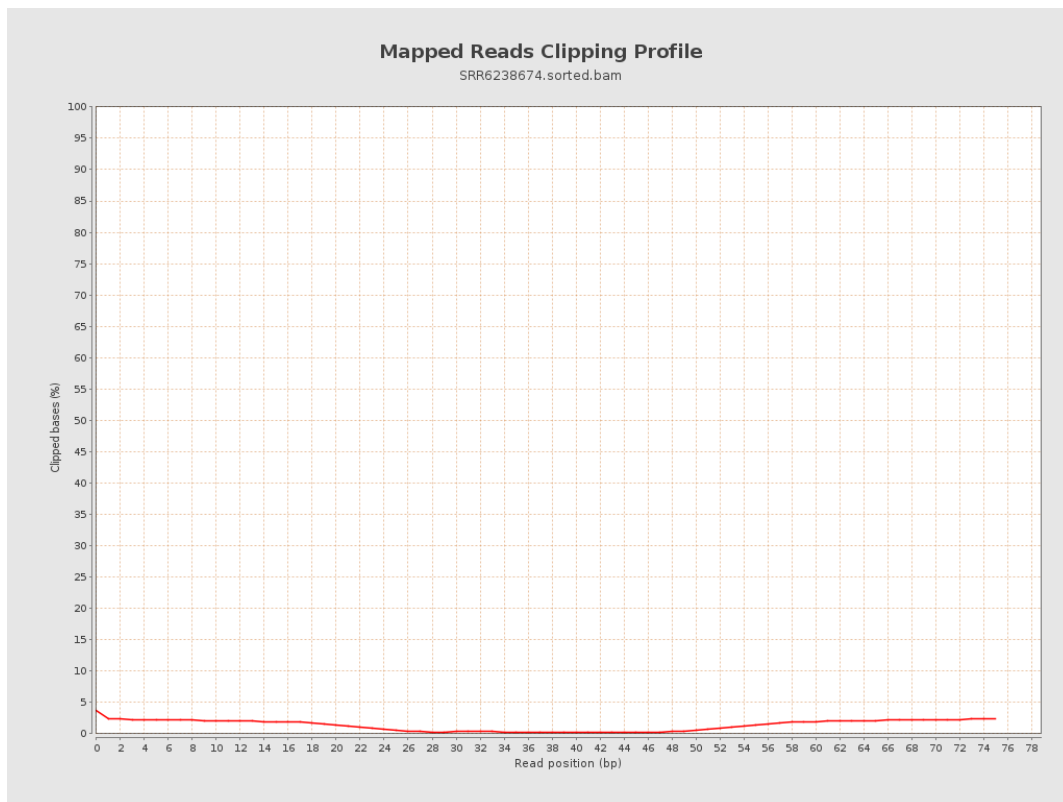
8. Results : Mapped Reads Nucleotide Content



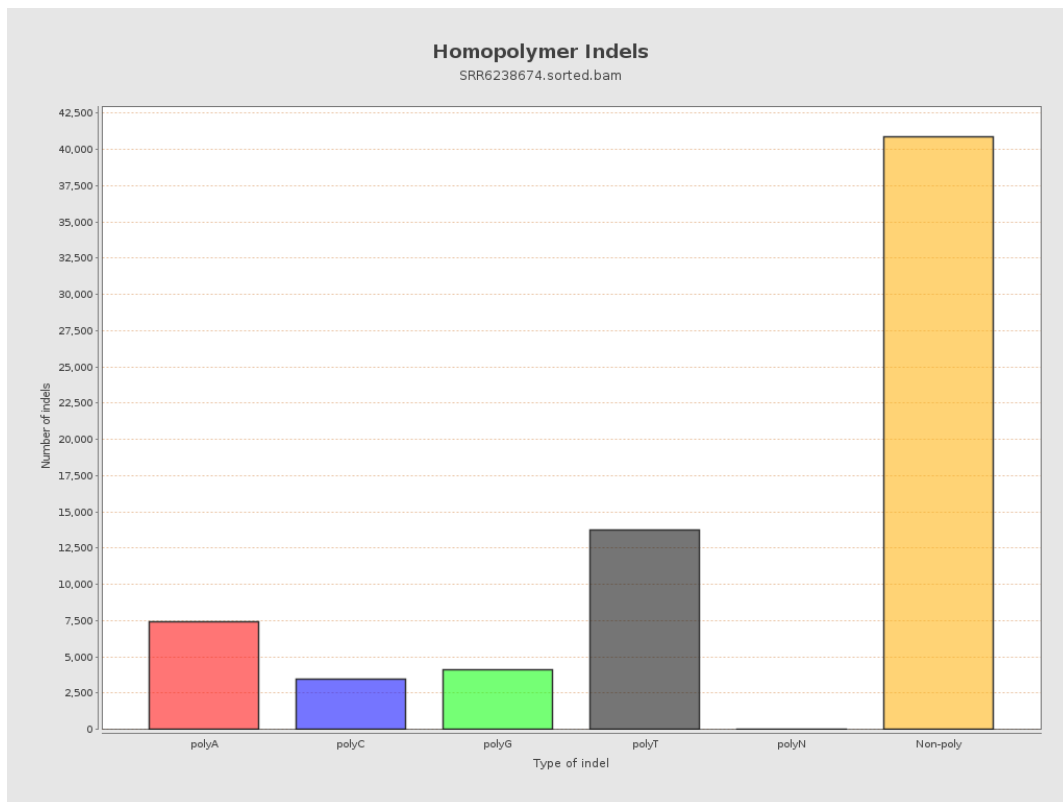
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

