

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 16:12:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238316.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_SRR6238316 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238316.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 16:12:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238316.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,466,559
Mapped reads	1,227,162 / 83.68%
Unmapped reads	239,397 / 16.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,146 / 0.96%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	98,339 / 6.71%
Duplication rate	6.5%
Clipped reads	629,023 / 42.89%

2.2. ACGT Content

Number/percentage of A's	22,178,891 / 27.61%
Number/percentage of C's	15,843,090 / 19.72%
Number/percentage of T's	24,249,929 / 30.19%
Number/percentage of G's	18,042,629 / 22.46%
Number/percentage of N's	16,183 / 0.02%
GC Percentage	42.18%

2.3. Coverage

Mean	0.026

Standard Deviation	0.2647
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2.4. Mapping Quality

Mean Mapping Quality	40.81
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2.5. Mismatches and indels

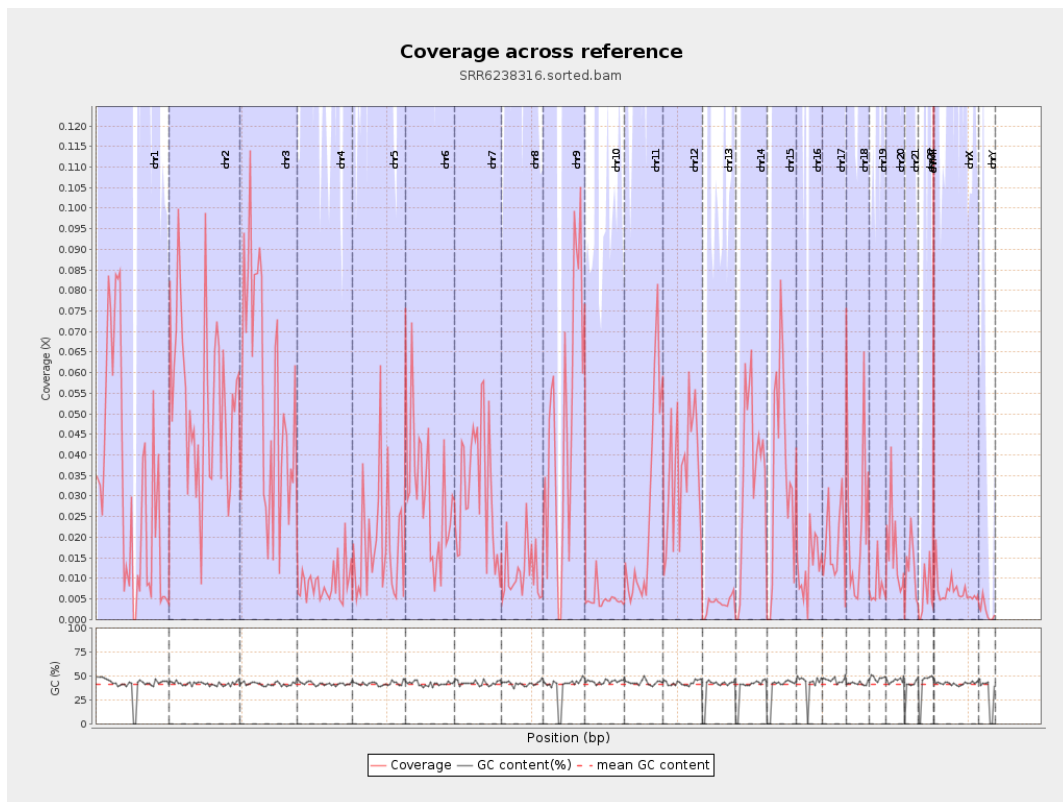
General error rate	0.78%
Mismatches	616,925
Insertions	5,537
Mapped reads with at least one insertion	0.45%
Deletions	17,854
Mapped reads with at least one deletion	1.44%
Homopolymer indels	47.36%

2.6. Chromosome stats

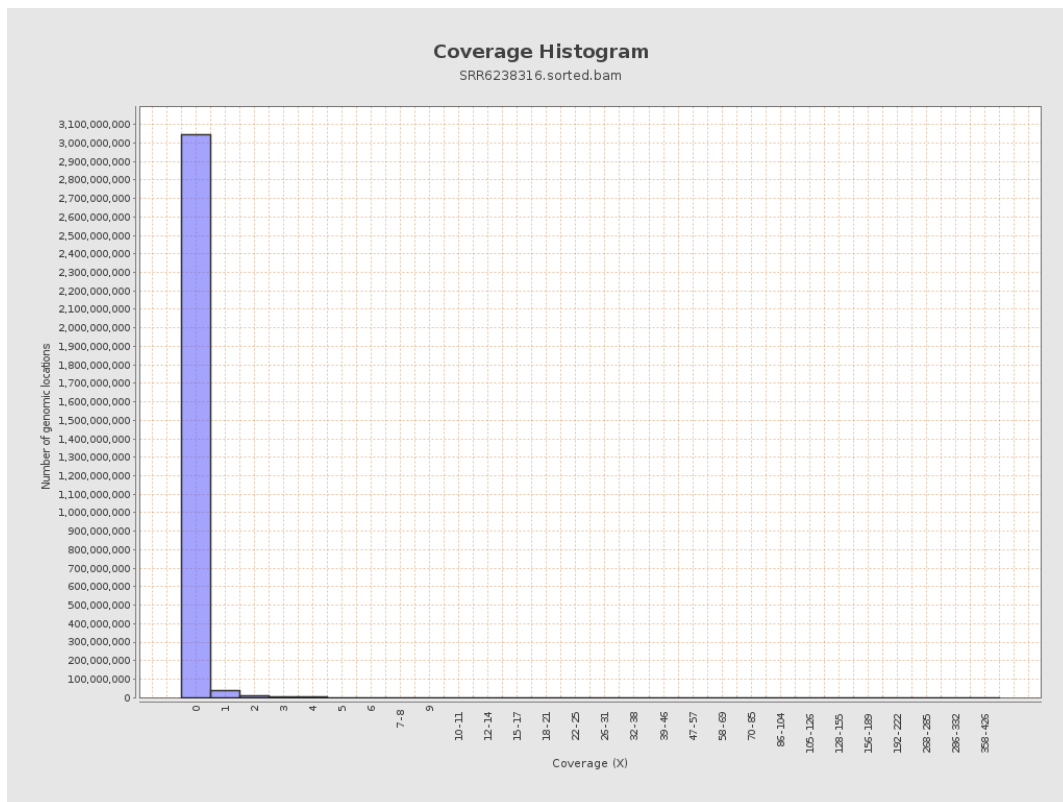
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7936924	0.0318	0.2901
chr2	243199373	13048083	0.0537	0.4078
chr3	198022430	10712929	0.0541	0.3427
chr4	191154276	1720585	0.009	0.152
chr5	180915260	3328334	0.0184	0.2051
chr6	171115067	5140128	0.03	0.2713
chr7	159138663	5083375	0.0319	0.3336

chr8	146364022	1642568	0.0112	0.1826
chr9	141213431	6897173	0.0488	0.329
chr10	135534747	659065	0.0049	0.1421
chr11	135006516	3346785	0.0248	0.2356
chr12	133851895	4804752	0.0359	0.2822
chr13	115169878	442509	0.0038	0.1157
chr14	107349540	3944893	0.0367	0.3563
chr15	102531392	3628984	0.0354	0.37
chr16	90354753	1155510	0.0128	0.1623
chr17	81195210	1422227	0.0175	0.2138
chr18	78077248	1843803	0.0236	0.224
chr19	59128983	449937	0.0076	0.1308
chr20	63025520	1082911	0.0172	0.1927
chr21	48129895	565851	0.0118	0.1524
chr22	51304566	318270	0.0062	0.1128
chrMT	16571	2893	0.1746	0.646
chrX	155270560	1073728	0.0069	0.1469
chrY	59373566	107490	0.0018	0.0622

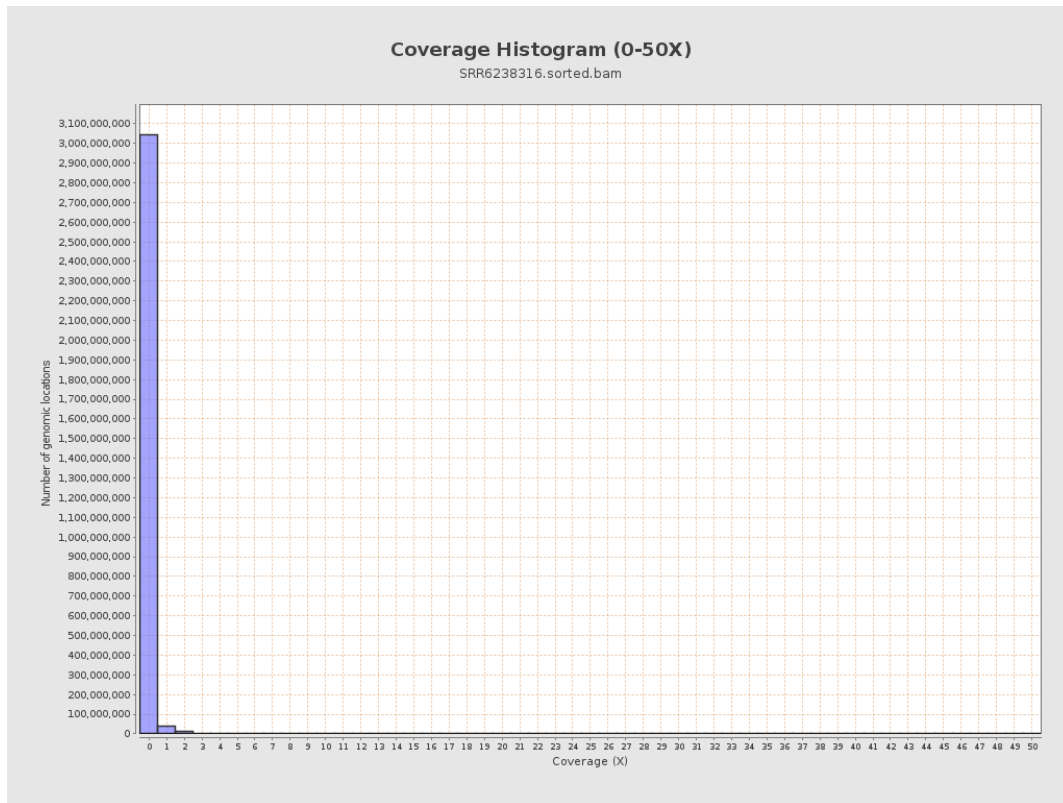
3. Results : Coverage across reference



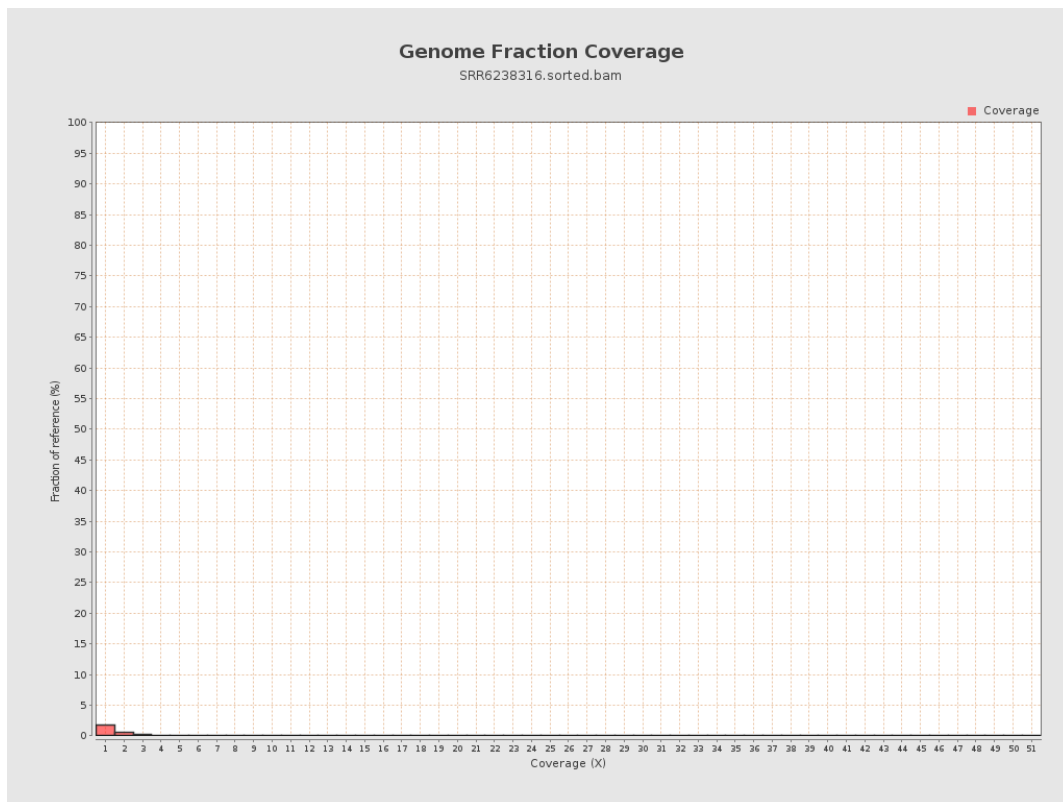
4. Results : Coverage Histogram



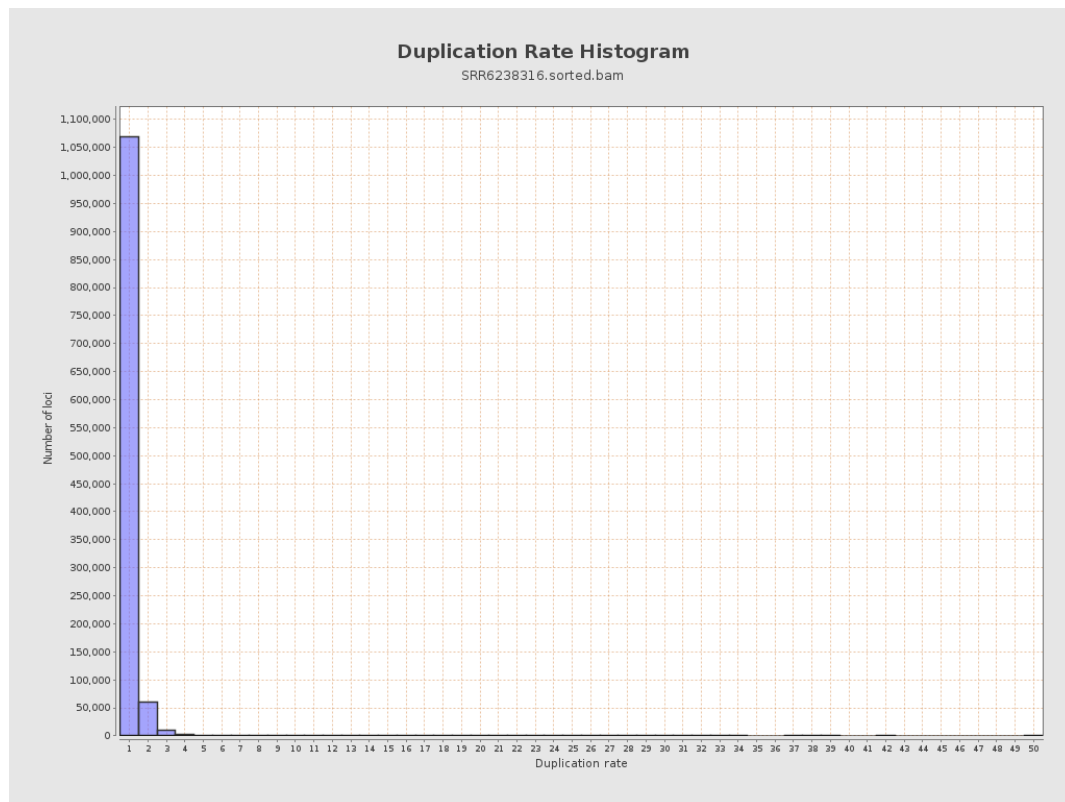
5. Results : Coverage Histogram (0-50X)



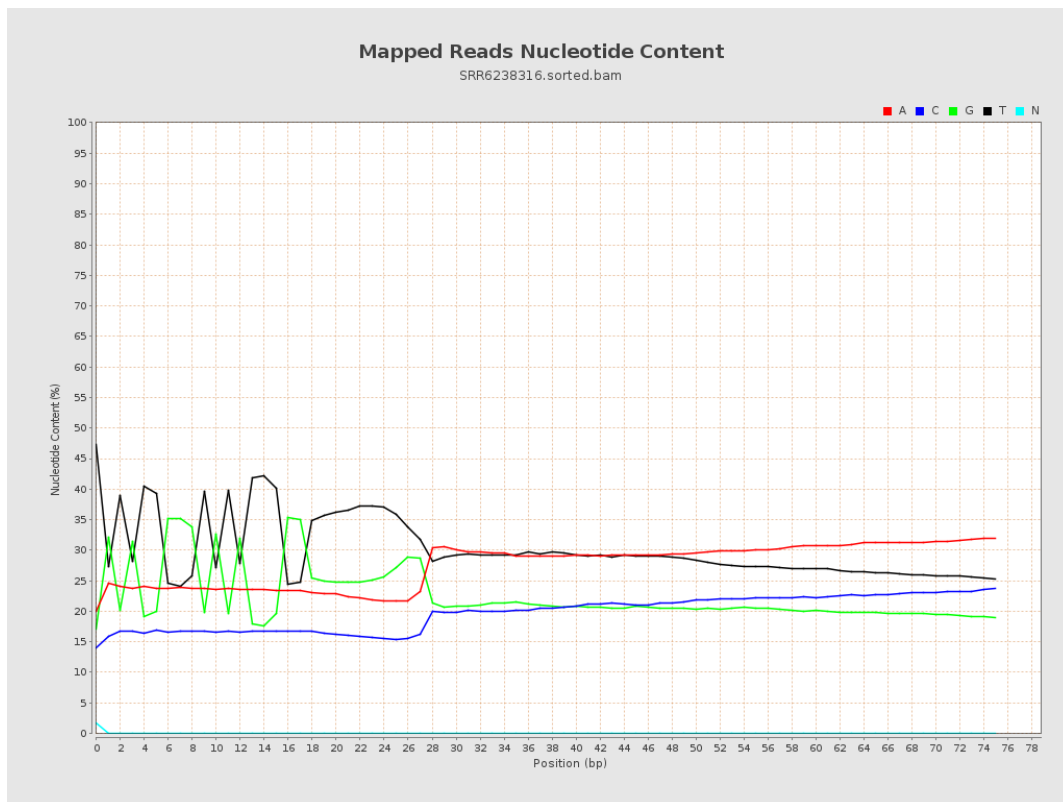
6. Results : Genome Fraction Coverage



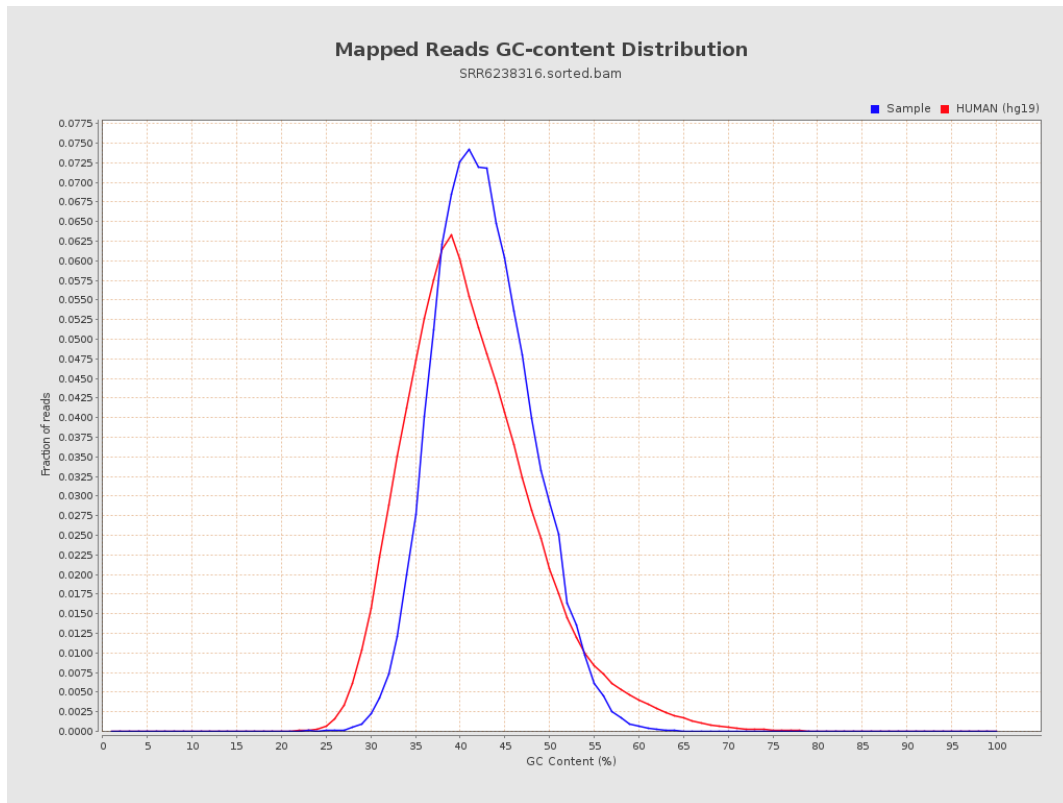
7. Results : Duplication Rate Histogram



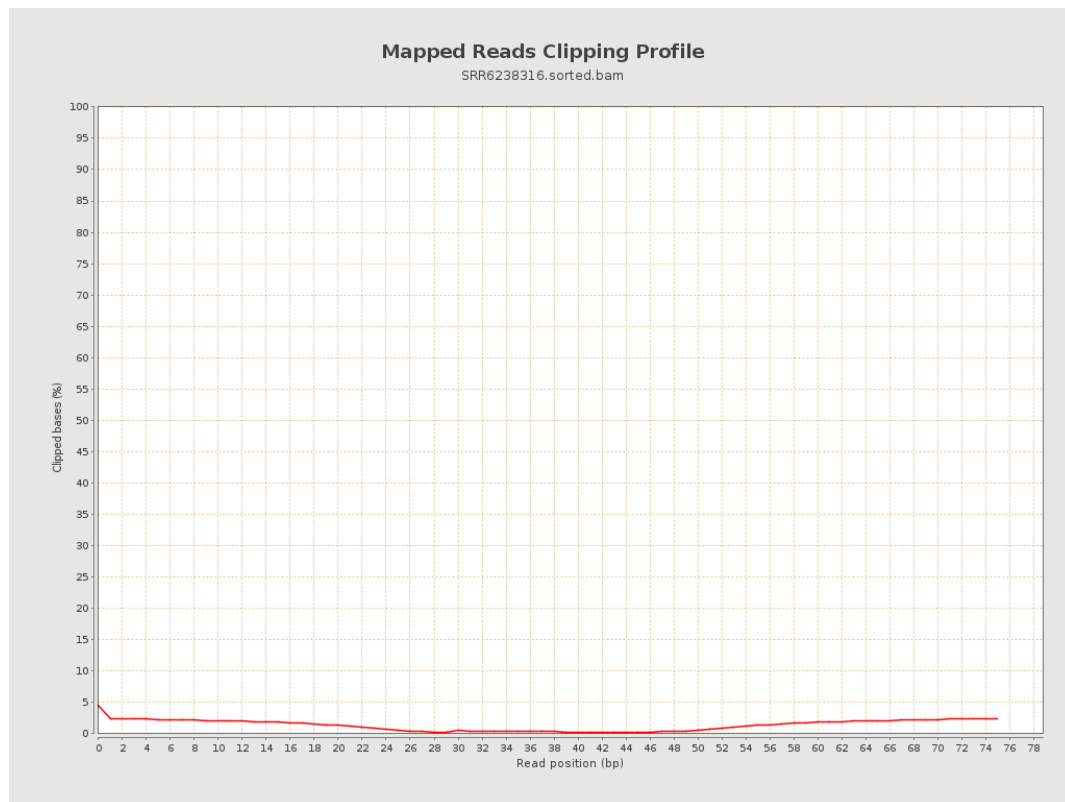
8. Results : Mapped Reads Nucleotide Content



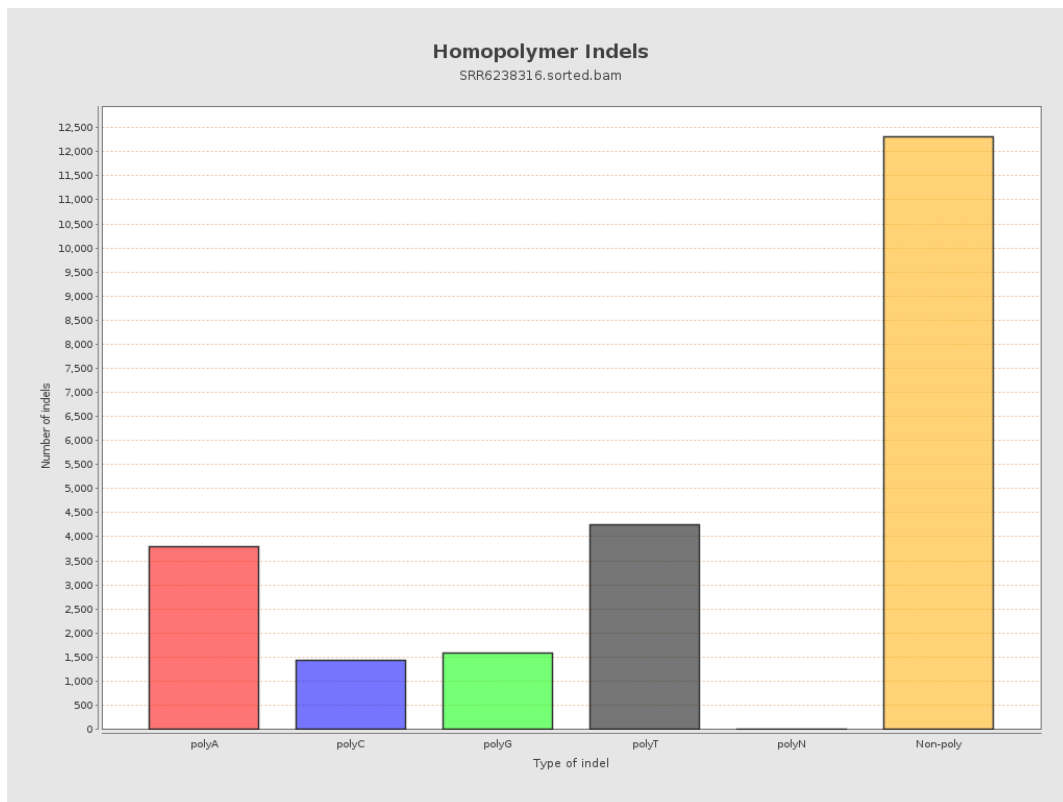
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

