

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 02:45:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006438.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_SRR1006438 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006438.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 02:45:59 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006438.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,140,433
Mapped reads	2,028,910 / 94.79%
Unmapped reads	111,523 / 5.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,972 / 0.37%
Read min/max/mean length	30 / 59 / 57.88
Duplicated reads (estimated)	82,527 / 3.86%
Duplication rate	3.43%
Clipped reads	290,707 / 13.58%

2.2. ACGT Content

Number/percentage of A's	32,259,485 / 28.28%
Number/percentage of C's	23,804,747 / 20.87%
Number/percentage of T's	33,258,809 / 29.15%
Number/percentage of G's	24,752,728 / 21.7%
Number/percentage of N's	2,593 / 0%
GC Percentage	42.57%

2.3. Coverage

Mean	0.0369

Standard Deviation	0.3633
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2.4. Mapping Quality

Mean Mapping Quality	45.98
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2.5. Mismatches and indels

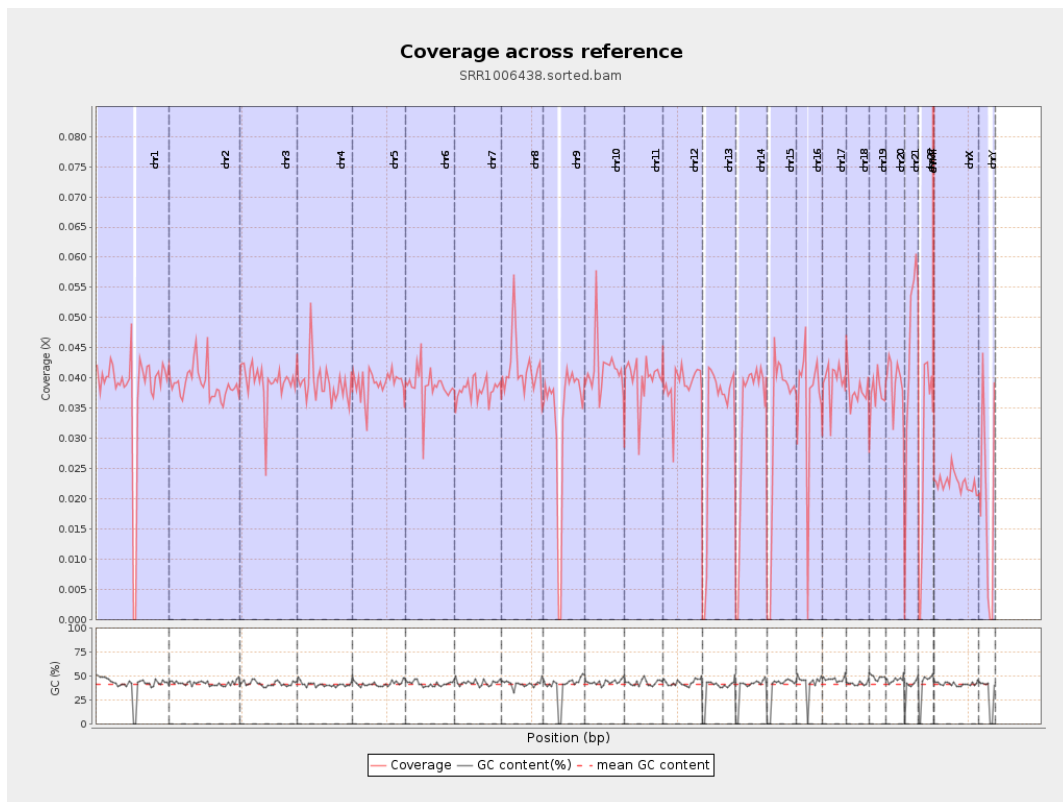
General error rate	0.42%
Mismatches	470,383
Insertions	7,566
Mapped reads with at least one insertion	0.37%
Deletions	24,725
Mapped reads with at least one deletion	1.21%
Homopolymer indels	41.57%

2.6. Chromosome stats

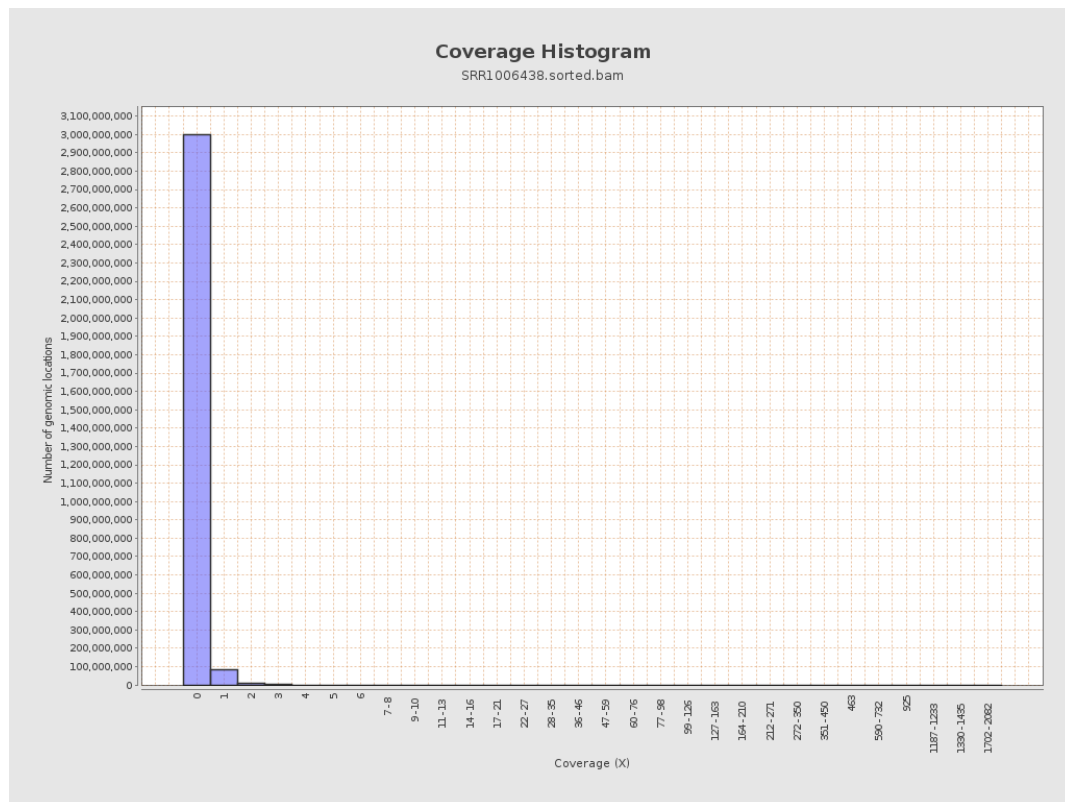
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9434505	0.0379	0.3883
chr2	243199373	9498220	0.0391	0.2619
chr3	198022430	7789973	0.0393	0.2268
chr4	191154276	7454873	0.039	0.2413
chr5	180915260	7065142	0.0391	0.2295
chr6	171115067	6623764	0.0387	0.2341
chr7	159138663	6058427	0.0381	0.2702

chr8	146364022	6055455	0.0414	1.1923
chr9	141213431	4751204	0.0336	0.2315
chr10	135534747	5622842	0.0415	0.2996
chr11	135006516	5369278	0.0398	0.2484
chr12	133851895	5197249	0.0388	0.2279
chr13	115169878	3729051	0.0324	0.2074
chr14	107349540	3539056	0.033	0.2115
chr15	102531392	3392214	0.0331	0.2082
chr16	90354753	3298675	0.0365	0.2415
chr17	81195210	3207771	0.0395	0.2432
chr18	78077248	2965434	0.038	0.3186
chr19	59128983	2225808	0.0376	0.3237
chr20	63025520	2471669	0.0392	0.2296
chr21	48129895	2140450	0.0445	0.2627
chr22	51304566	1432720	0.0279	0.2115
chrMT	16571	204115	12.3176	7.0272
chrX	155270560	3511382	0.0226	0.1772
chrY	59373566	1082241	0.0182	0.2546

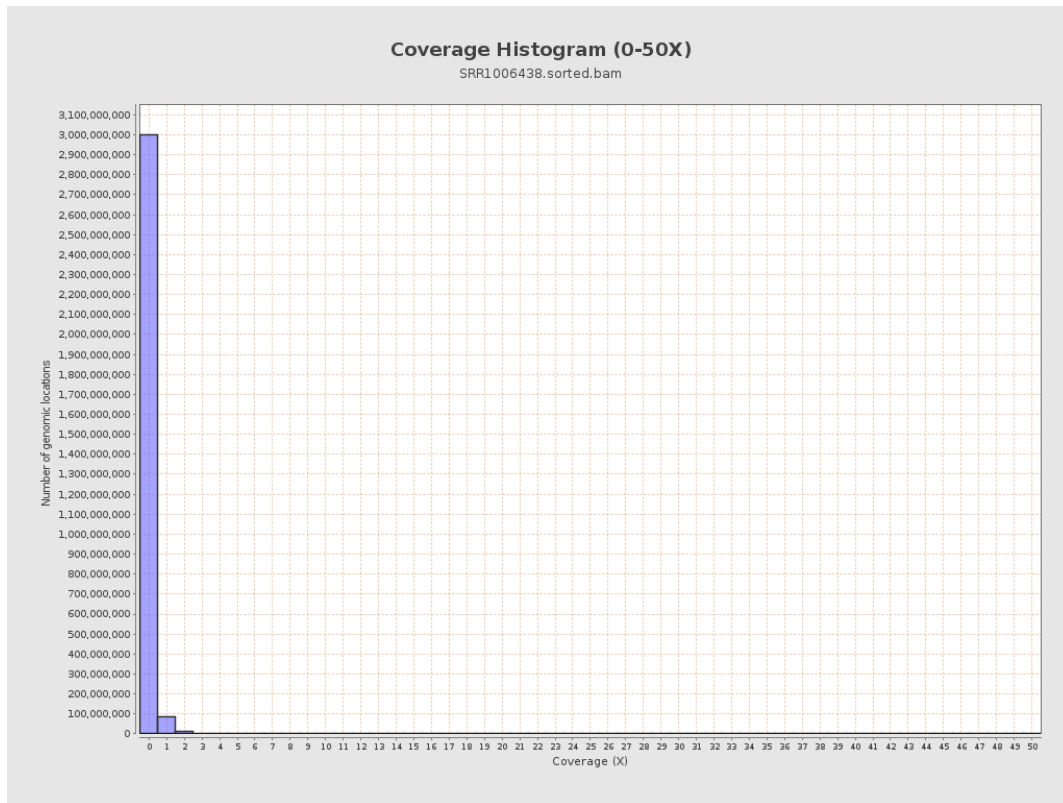
3. Results : Coverage across reference



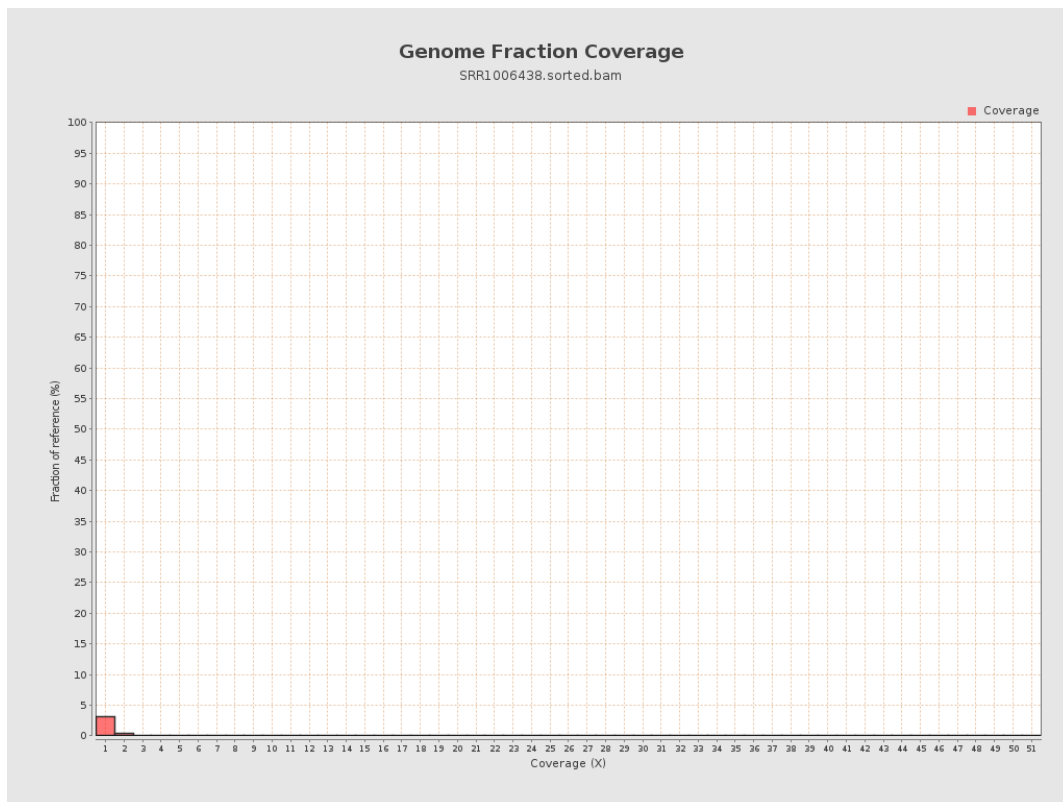
4. Results : Coverage Histogram



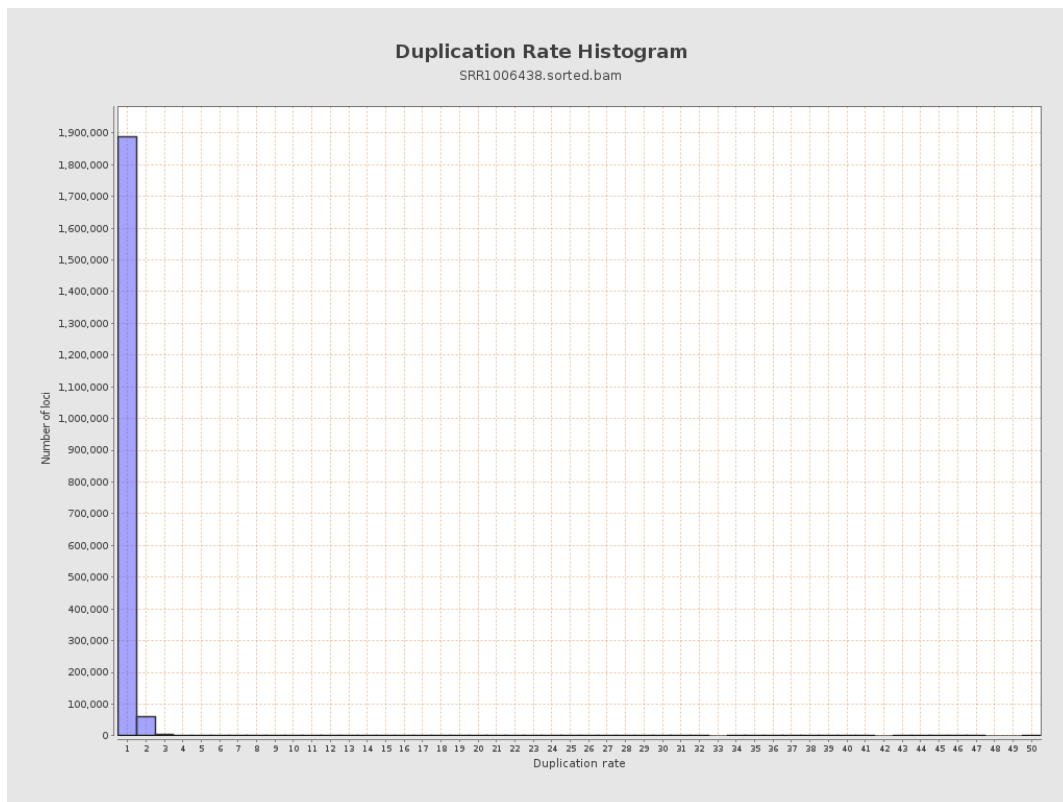
5. Results : Coverage Histogram (0-50X)



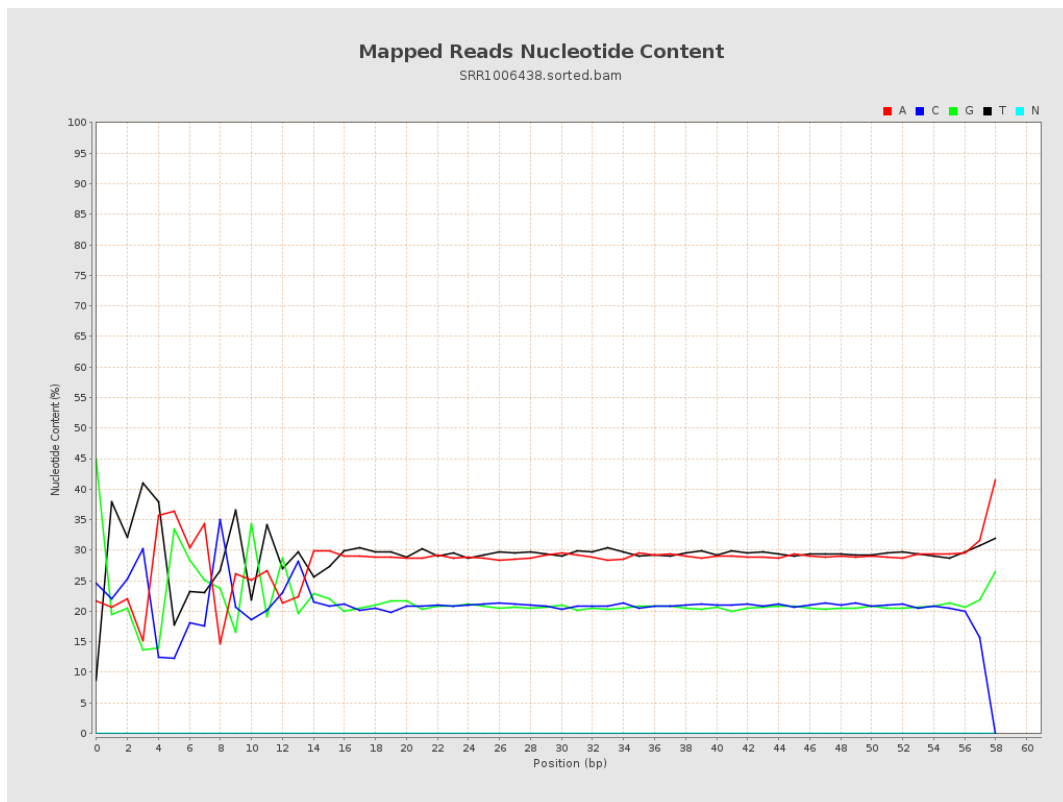
6. Results : Genome Fraction Coverage



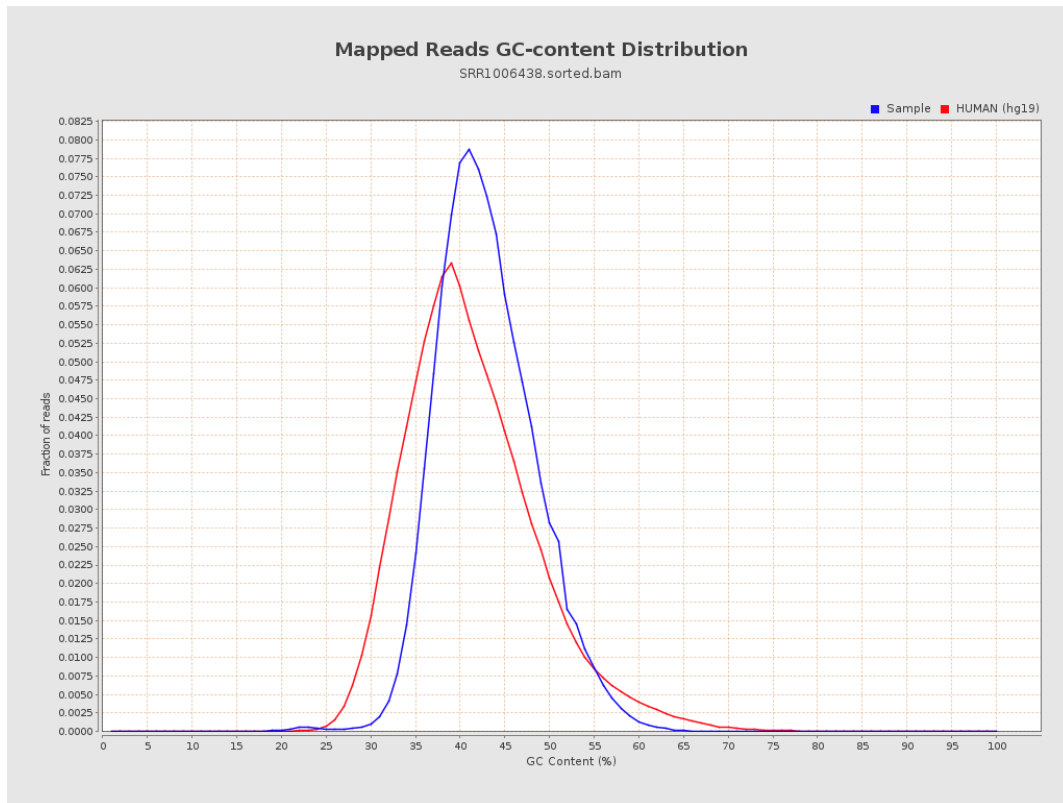
7. Results : Duplication Rate Histogram



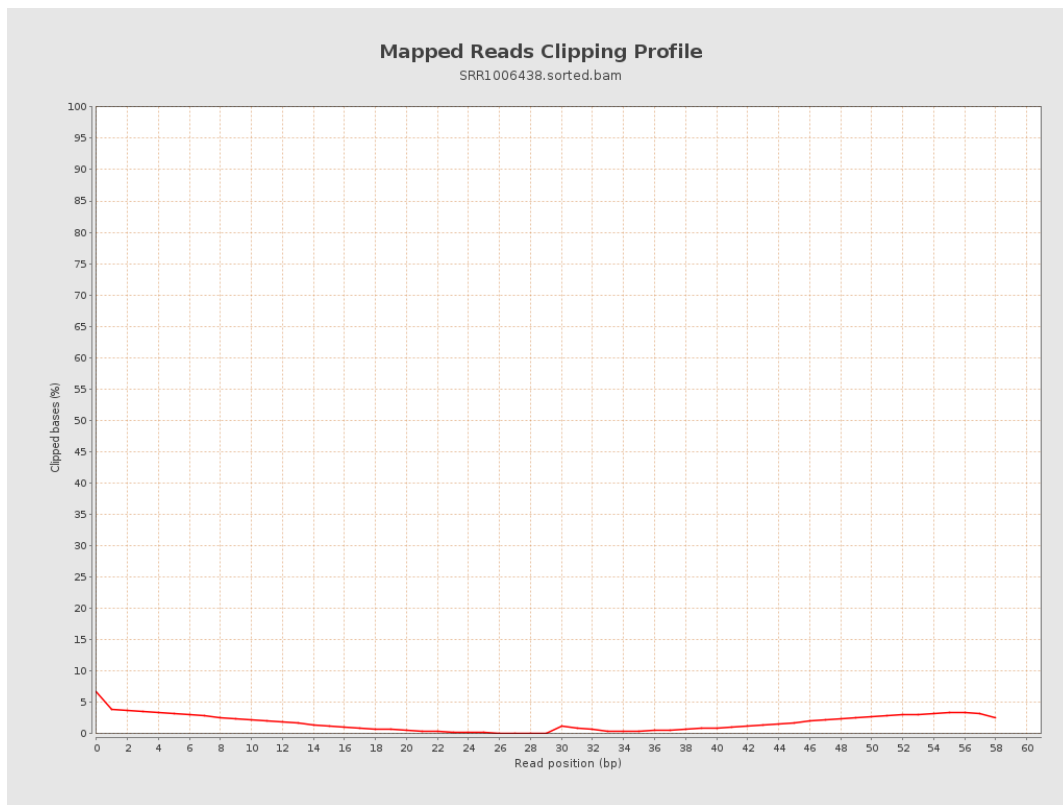
8. Results : Mapped Reads Nucleotide Content



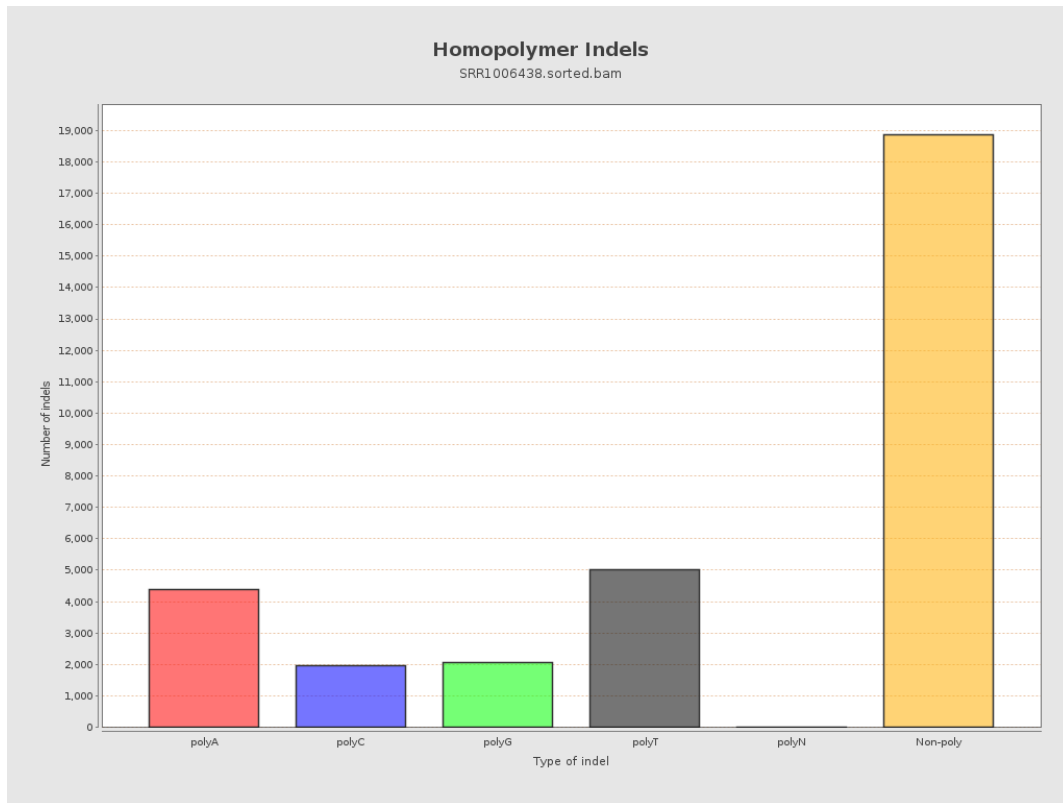
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

