Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 00:41:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006381.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_SRR1006381 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006381_1.fastq.gz SRR1006381_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 00:41:03 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006381.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,901,950
Mapped reads	6,159,492 / 89.24%
Unmapped reads	742,458 / 10.76%
Mapped paired reads	6,159,492 / 89.24%
Mapped reads, first in pair	3,122,807 / 45.25%
Mapped reads, second in pair	3,036,685 / 44%
Mapped reads, both in pair	5,678,024 / 82.27%
Mapped reads, singletons	481,468 / 6.98%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	243,732 / 3.53%
Duplication rate	3.47%
Clipped reads	324,200 / 4.7%

2.2. ACGT Content

Number/percentage of A's	66,561,741 / 27.9%
Number/percentage of C's	51,430,079 / 21.56%
Number/percentage of T's	67,477,771 / 28.29%
Number/percentage of G's	53,066,507 / 22.25%
Number/percentage of N's	10,157 / 0%
GC Percentage	43.81%

2.3. Coverage

Mean	0.0771
Standard Deviation	0.4086

2.4. Mapping Quality

Mean Mapping Quality	48.3

2.5. Insert size

Mean	75,659.69
Standard Deviation	2,633,839.72
P25/Median/P75	111 / 143 / 194

2.6. Mismatches and indels

General error rate	0.37%
Mismatches	877,284
Insertions	6,379
Mapped reads with at least one insertion	0.1%
Deletions	21,970
Mapped reads with at least one deletion	0.36%
Homopolymer indels	44.69%

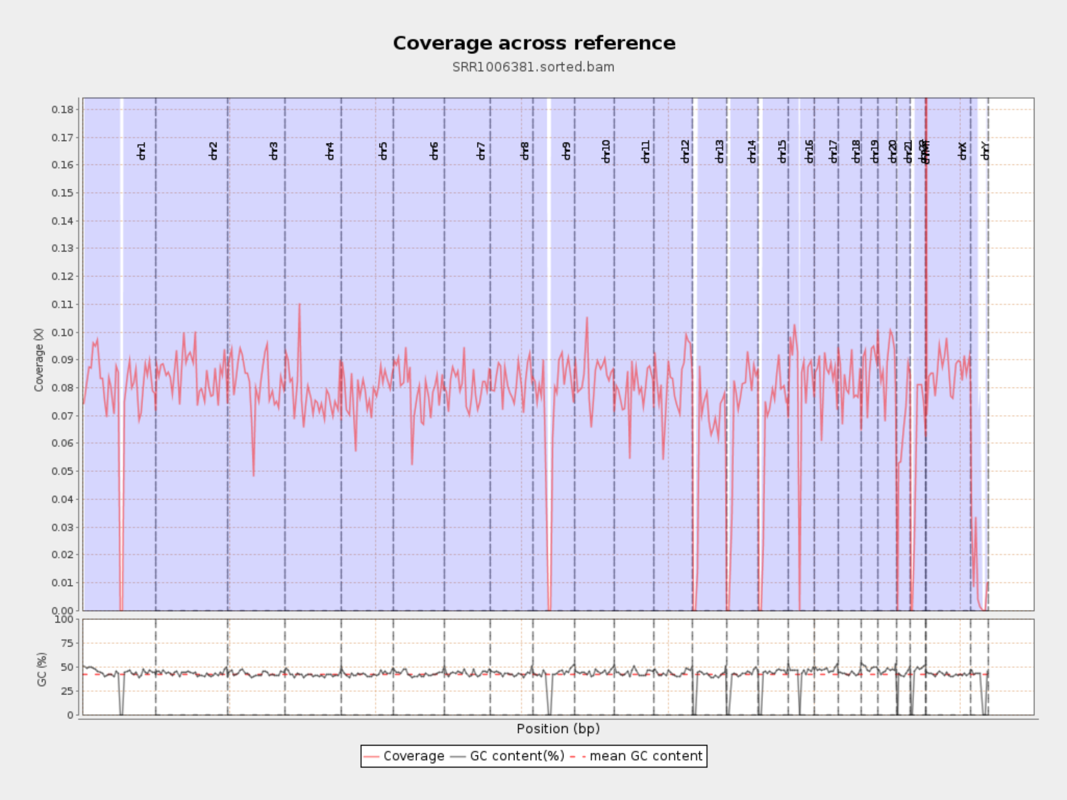
2.7. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**

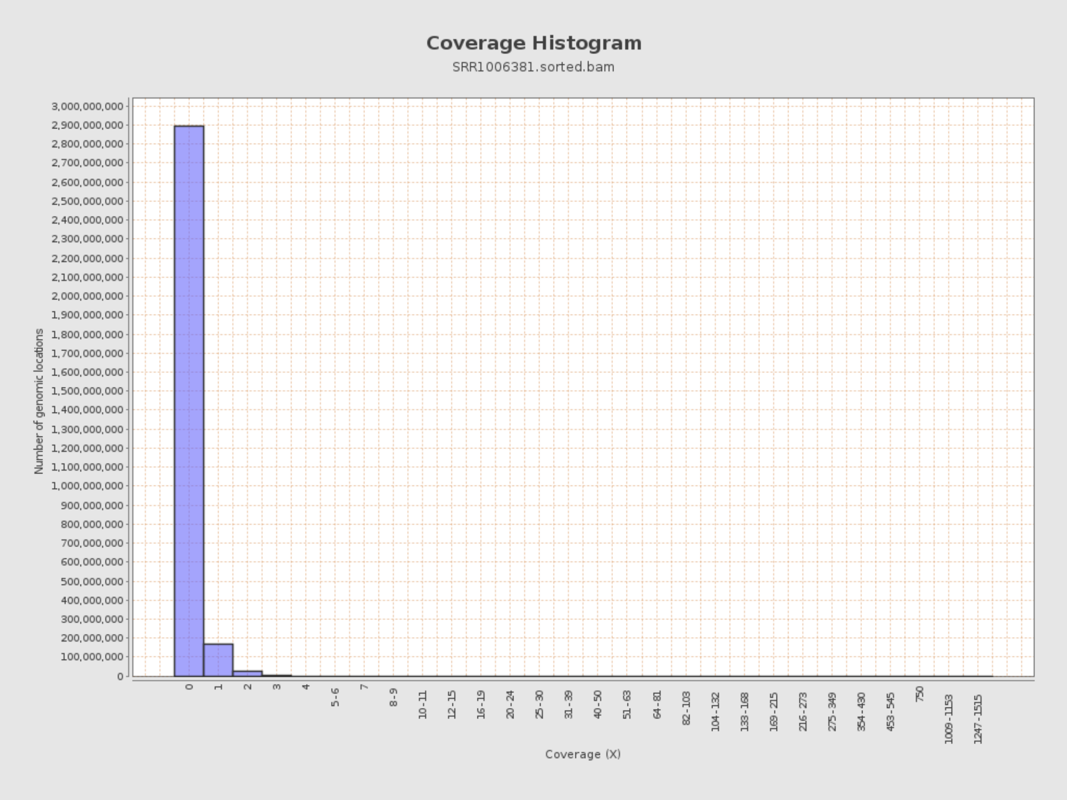
chr1	249250621	19293514	0.0774	0.4968
chr2	243199373	20690900	0.0851	0.4059
chr3	198022430	16157694	0.0816	0.326
chr4	191154276	14926989	0.0781	0.3551
chr5	180915260	14242769	0.0787	0.3194
chr6	171115067	13519240	0.079	0.3488
chr7	159138663	12777903	0.0803	0.4542
chr8	146364022	11995306	0.082	0.8116
chr9	141213431	10098044	0.0715	0.3456
chr10	135534747	11395296	0.0841	0.4433
chr11	135006516	10666059	0.079	0.3733
chr12	133851895	11075027	0.0827	0.332
chr13	115169878	6939704	0.0603	0.2816
chr14	107349540	7342327	0.0684	0.3131
chr15	102531392	6479519	0.0632	0.2874
chr16	90354753	7273038	0.0805	0.3804
chr17	81195210	6841825	0.0843	0.3463
chr18	78077248	6349255	0.0813	0.521
chr19	59128983	5177318	0.0876	0.4393
chr20	63025520	5567381	0.0883	0.3547
chr21	48129895	3006613	0.0625	0.3269
chr22	51304566	2765215	0.0539	0.272
chrMT	16571	24121	1.4556	1.6856
chrX	155270560	13356590	0.086	0.3567

chrY	59373566	613938	0.0103	0.2528

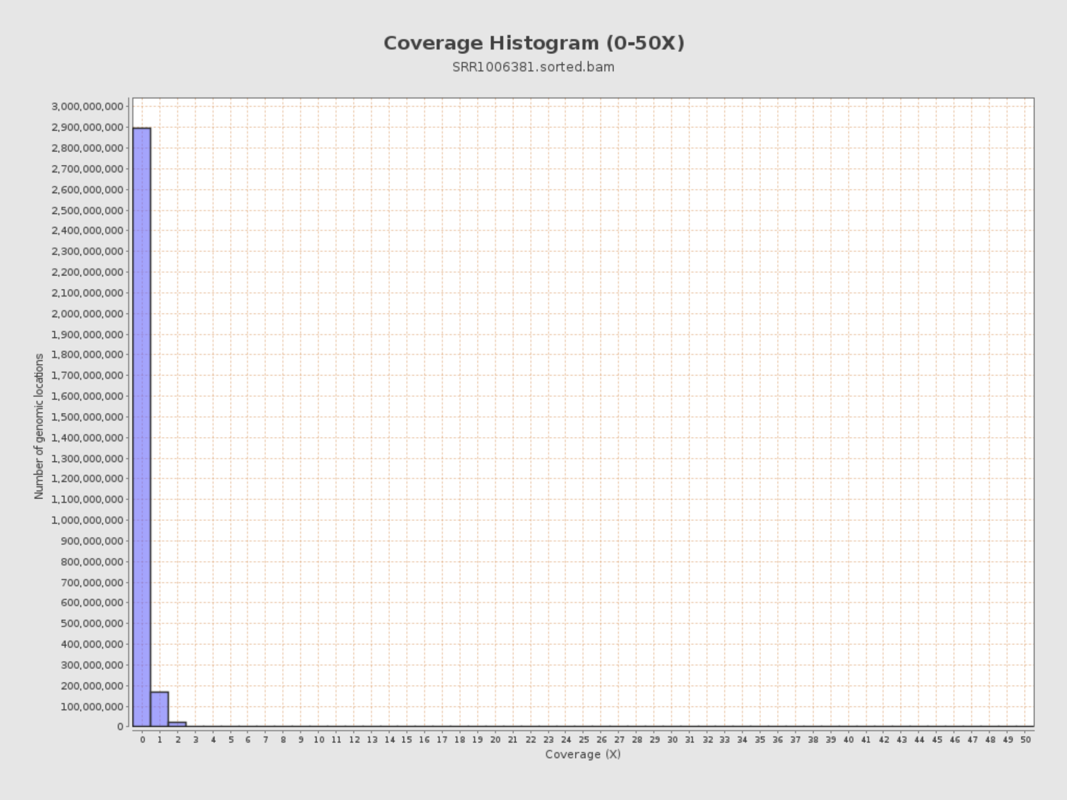
3. Results : Coverage across reference



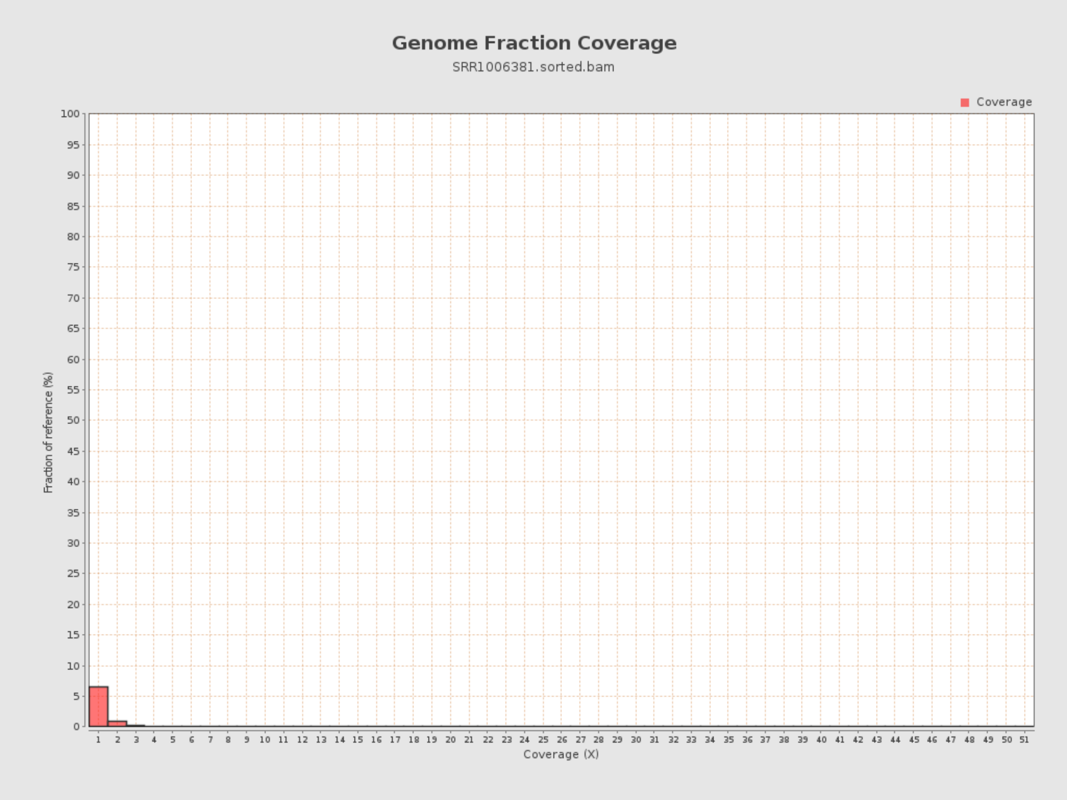
4. Results : Coverage Histogram



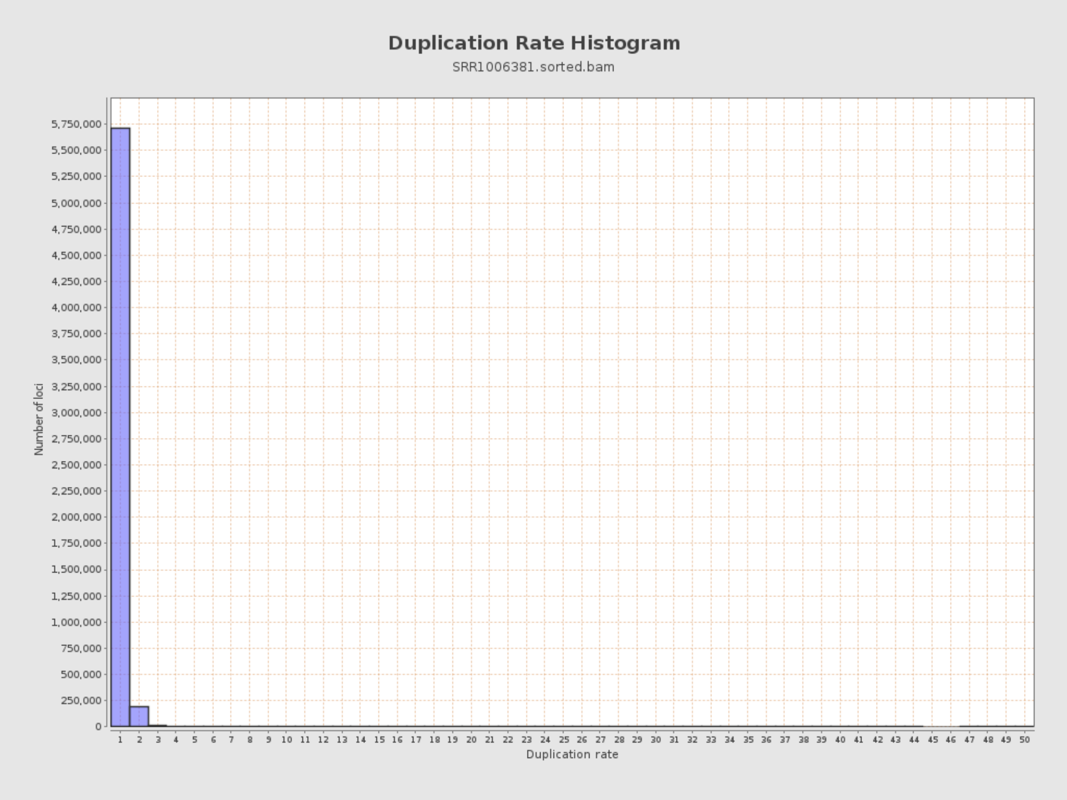
5. Results : Coverage Histogram (0-50X)



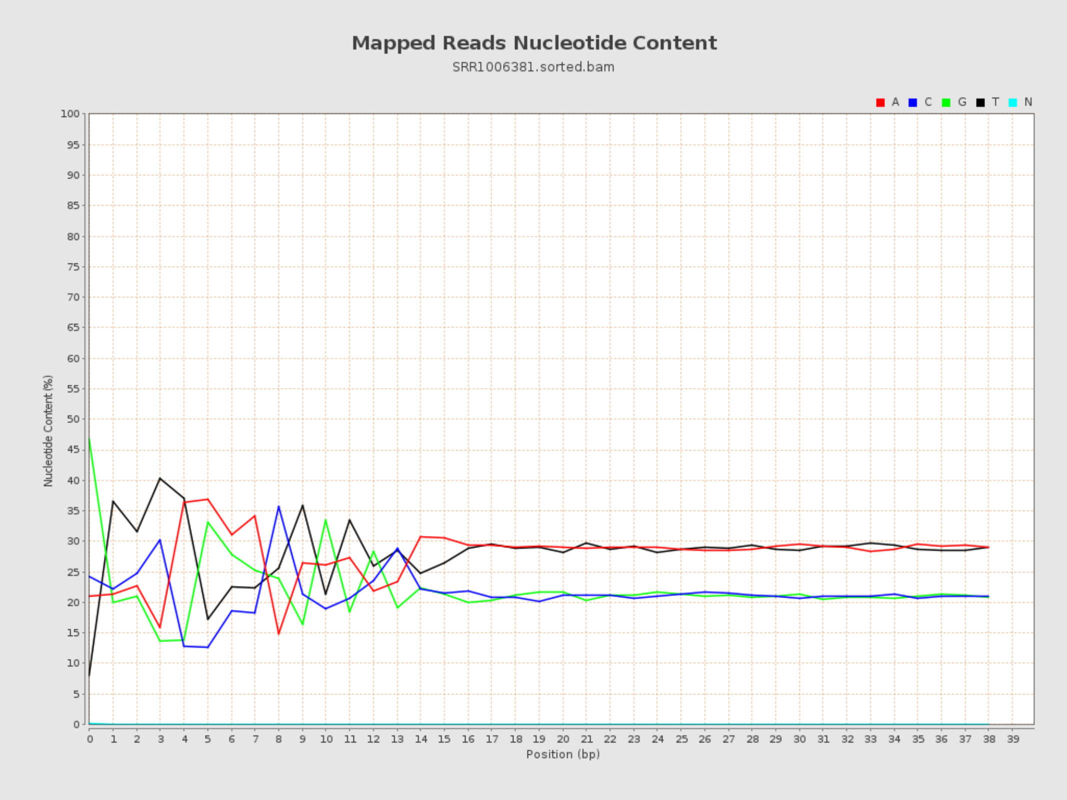
6. Results : Genome Fraction Coverage



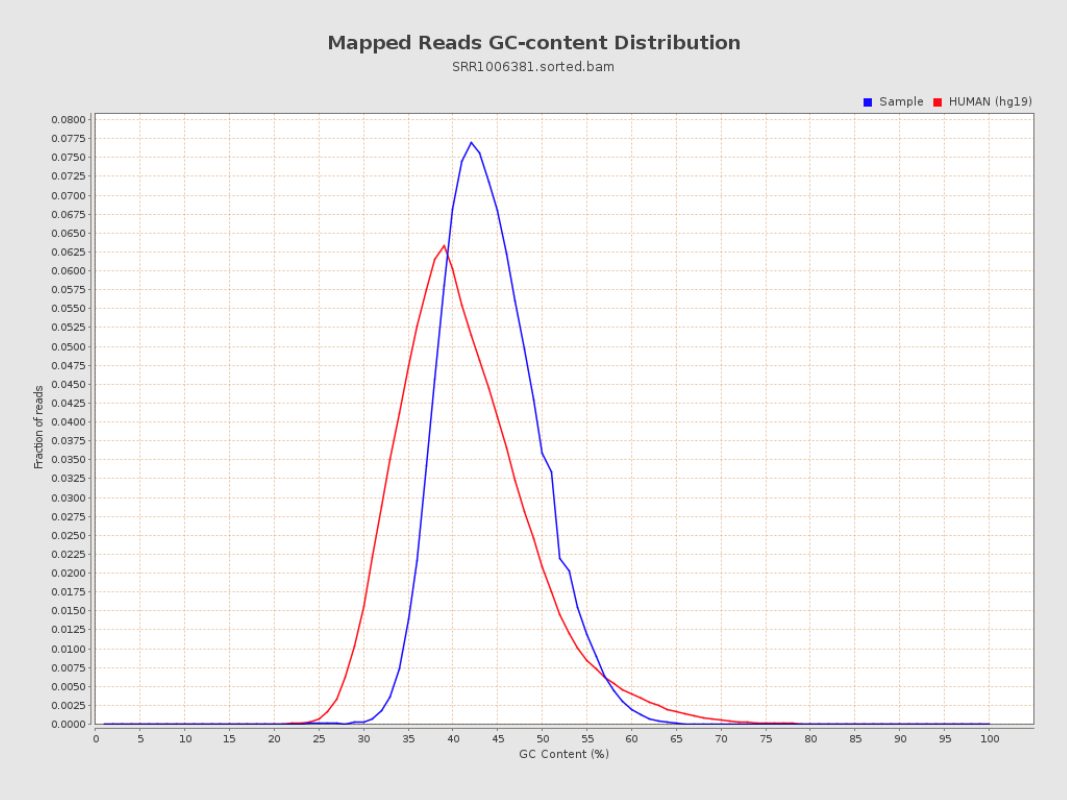
7. Results : Duplication Rate Histogram



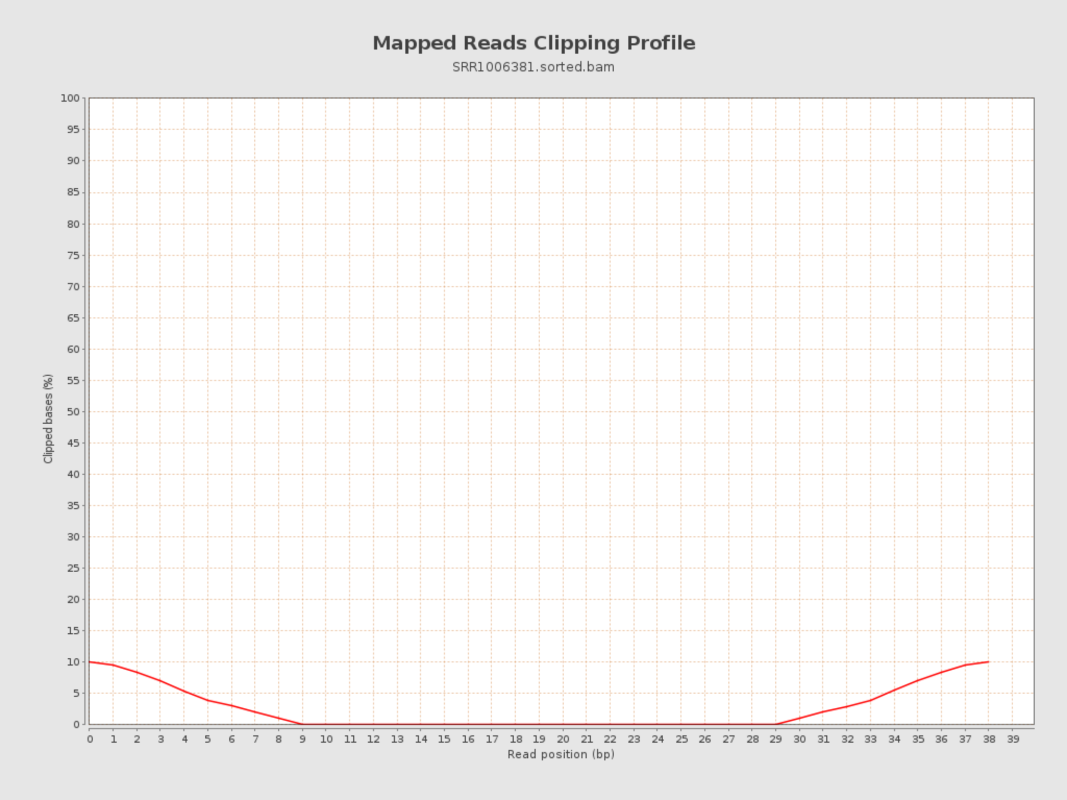
8. Results : Mapped Reads Nucleotide Content



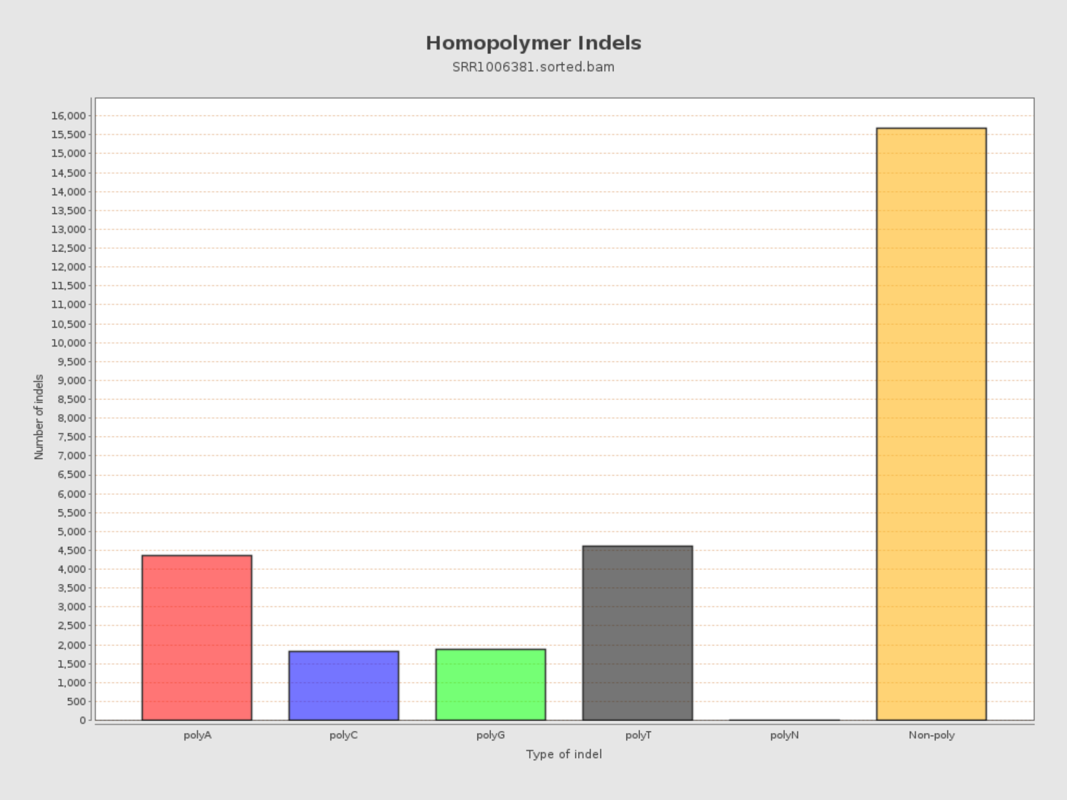
9. Results : Mapped Reads GC-content Distribution



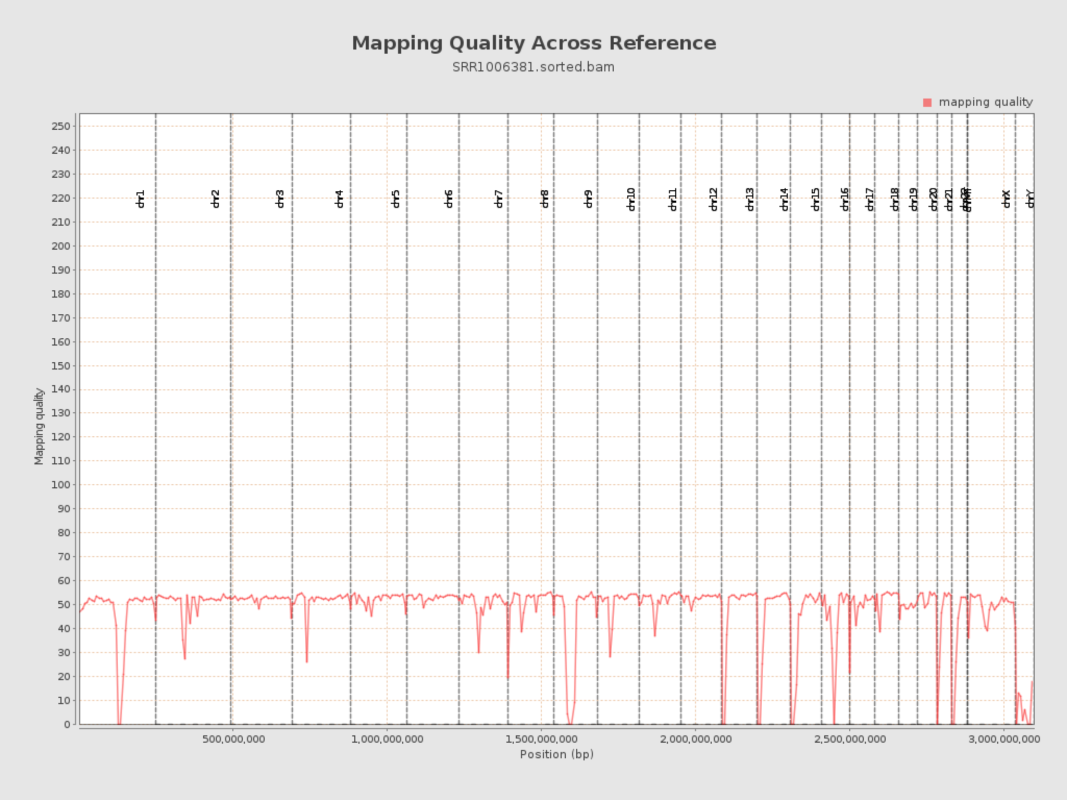
10. Results : Mapped Reads Clipping Profile



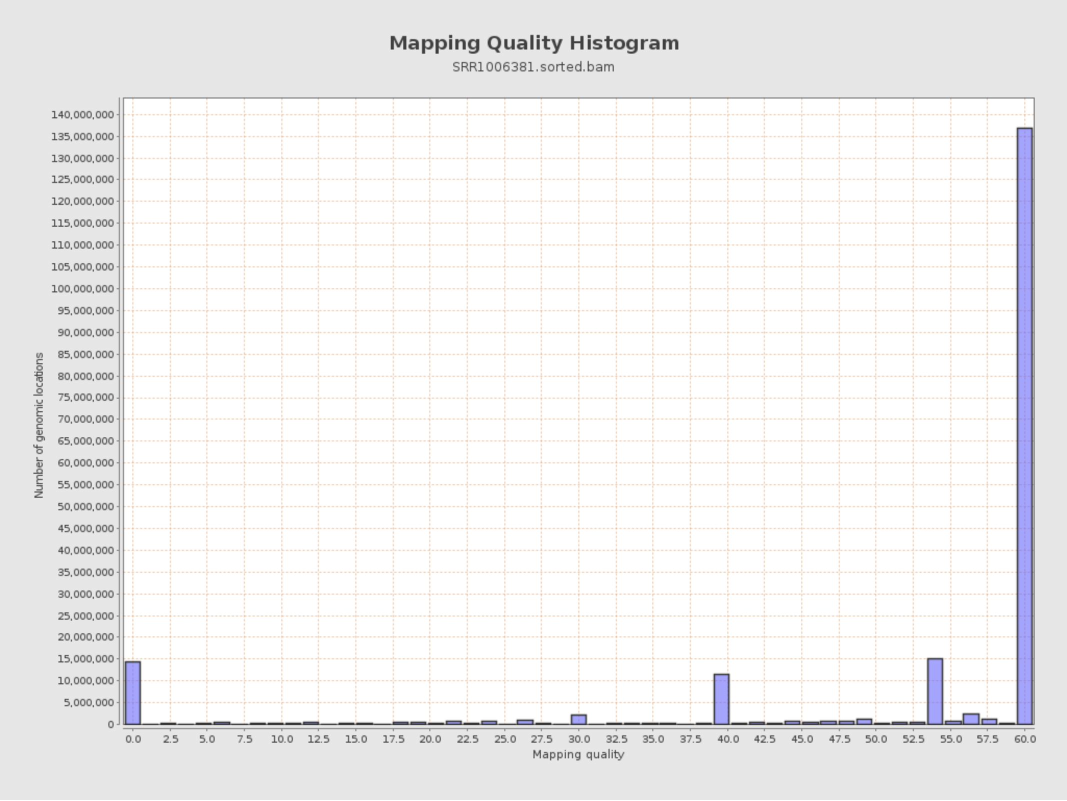
11. Results : Homopolymer Indels



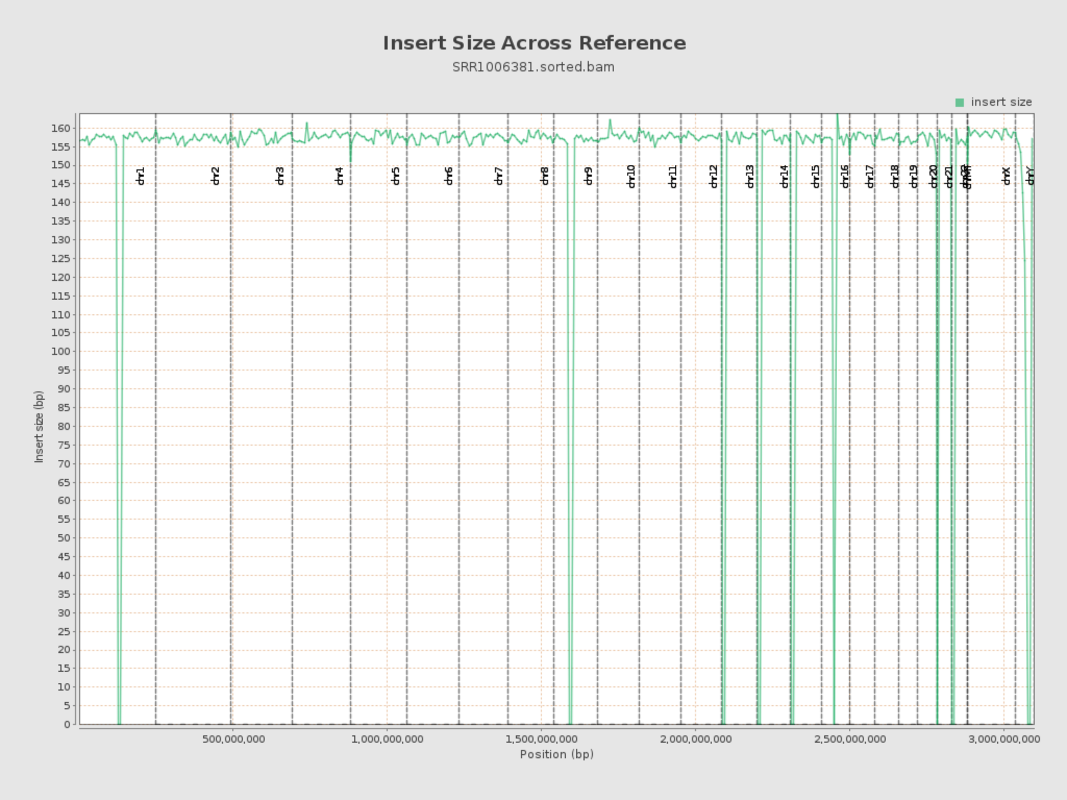
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram