Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 00:34:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006380.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_SRR1006380 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006380_1.fastq.gz SRR1006380_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 00:34:23 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006380.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,962,470
Mapped reads	6,186,962 / 88.86%
Unmapped reads	775,508 / 11.14%
Mapped paired reads	6,186,962 / 88.86%
Mapped reads, first in pair	3,135,891 / 45.04%
Mapped reads, second in pair	3,051,071 / 43.82%
Mapped reads, both in pair	5,689,088 / 81.71%
Mapped reads, singletons	497,874 / 7.15%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	209,016 / 3%
Duplication rate	2.85%
Clipped reads	325,452 / 4.67%

2.2. ACGT Content

Number/percentage of A's	67,494,591 / 28.17%
Number/percentage of C's	51,040,774 / 21.3%
Number/percentage of T's	68,291,378 / 28.5%
Number/percentage of G's	52,778,832 / 22.03%
Number/percentage of N's	10,201 / 0%
GC Percentage	43.33%

2.3. Coverage

Mean	0.0774
Standard Deviation	0.4199

2.4. Mapping Quality

Mean Mapping Quality	48.42

2.5. Insert size

Mean	67,557.14
Standard Deviation	2,471,912.07
P25/Median/P75	114 / 148 / 199

2.6. Mismatches and indels

General error rate	0.37%
Mismatches	881,294
Insertions	6,380
Mapped reads with at least one insertion	0.1%
Deletions	22,225
Mapped reads with at least one deletion	0.36%
Homopolymer indels	44.85%

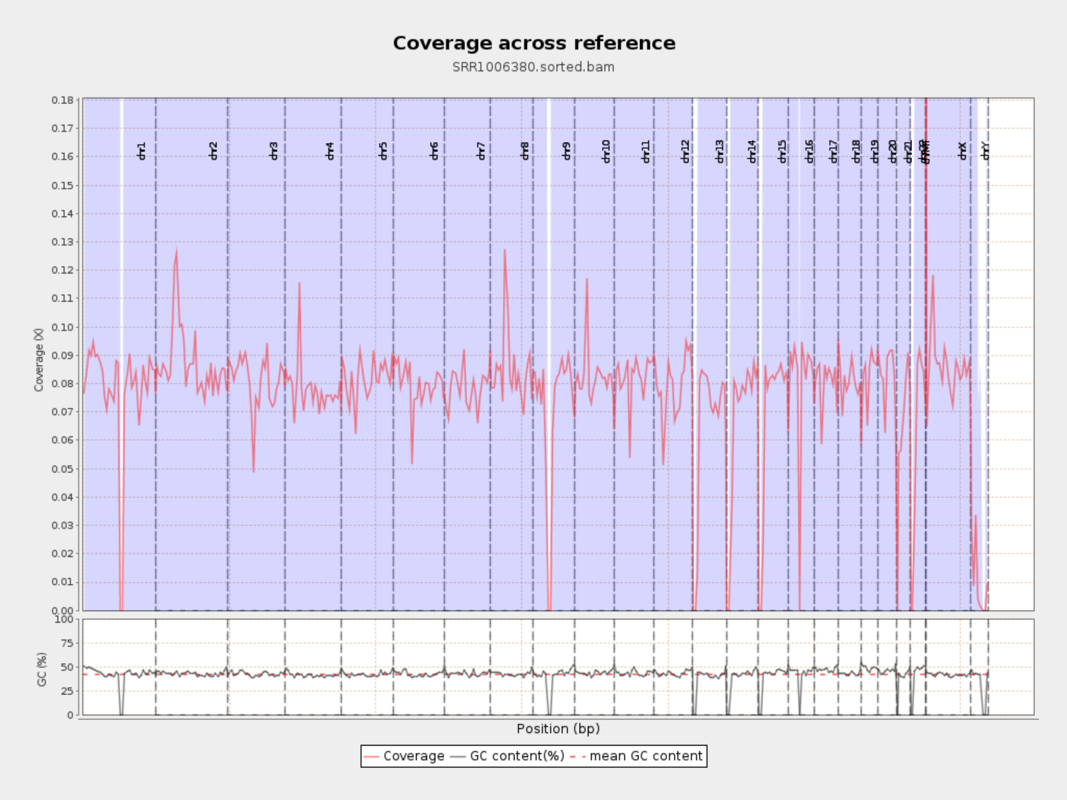
2.7. Chromosome stats

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

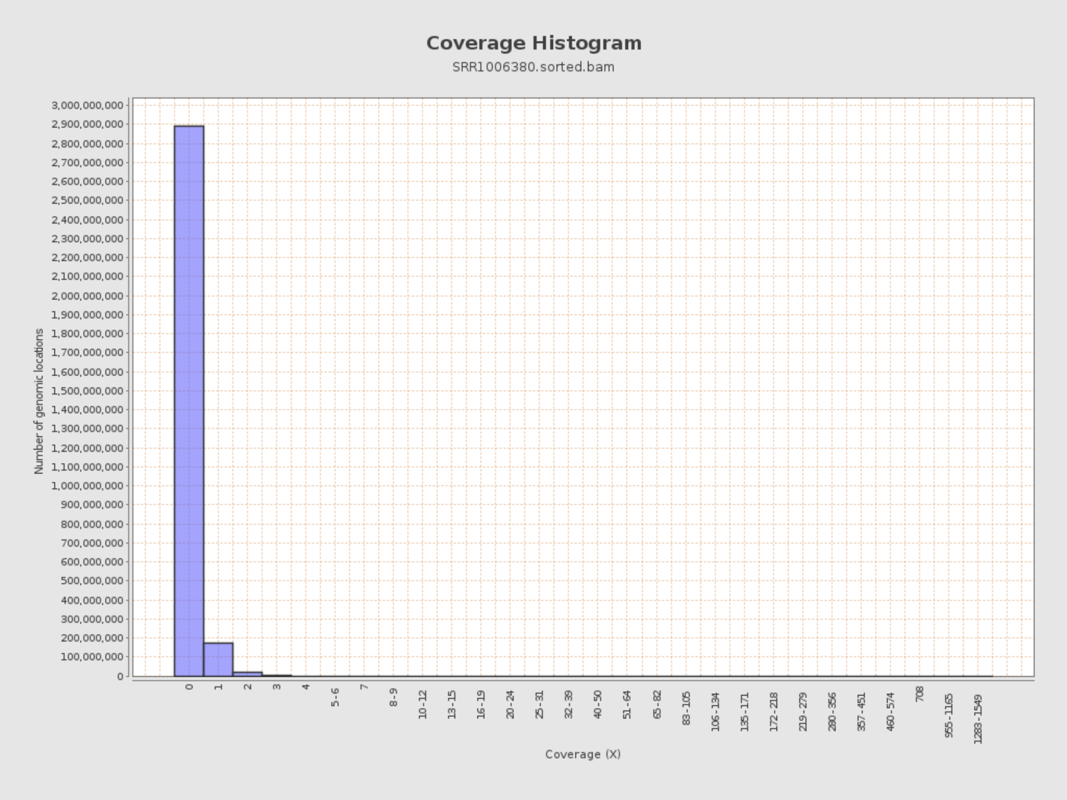
chr1	249250621	19311838	0.0775	0.5531
chr2	243199373	21284835	0.0875	0.4104
chr3	198022430	16028219	0.0809	0.3201
chr4	191154276	14982600	0.0784	0.3598
chr5	180915260	14794079	0.0818	0.3223
chr6	171115067	13627766	0.0796	0.3472
chr7	159138663	12460087	0.0783	0.4721
chr8	146364022	12427234	0.0849	0.8276
chr9	141213431	9970447	0.0706	0.3482
chr10	135534747	11191853	0.0826	0.4733
chr11	135006516	11056940	0.0819	0.3815
chr12	133851895	10661031	0.0796	0.3212
chr13	115169878	7433826	0.0645	0.2861
chr14	107349540	7180270	0.0669	0.3165
chr15	102531392	6865776	0.067	0.2947
chr16	90354753	7161817	0.0793	0.3859
chr17	81195210	6569474	0.0809	0.3371
chr18	78077248	6309327	0.0808	0.5409
chr19	59128983	4911530	0.0831	0.4582
chr20	63025520	5221653	0.0828	0.3351
chr21	48129895	3136620	0.0652	0.3384
chr22	51304566	3071774	0.0599	0.2827
chrMT	16571	11518	0.6951	0.9725
chrX	155270560	13381981	0.0862	0.3568

chrY	59373566	592850	0.01	0.2447

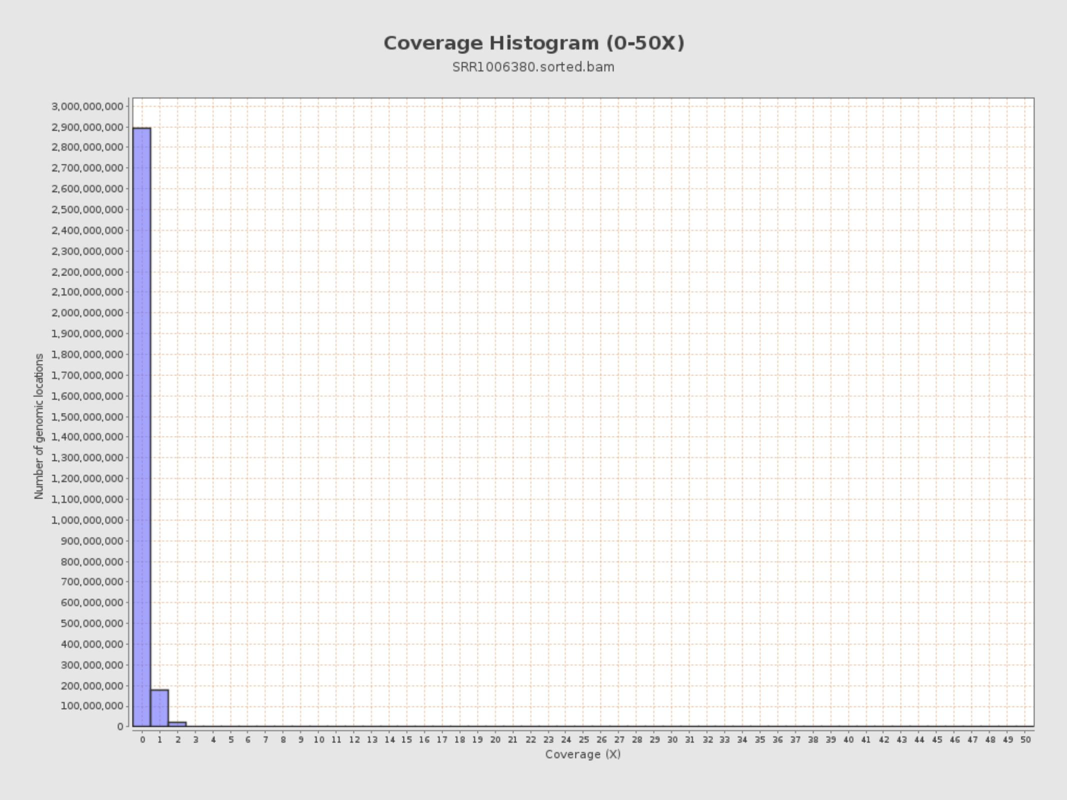
3. Results : Coverage across reference



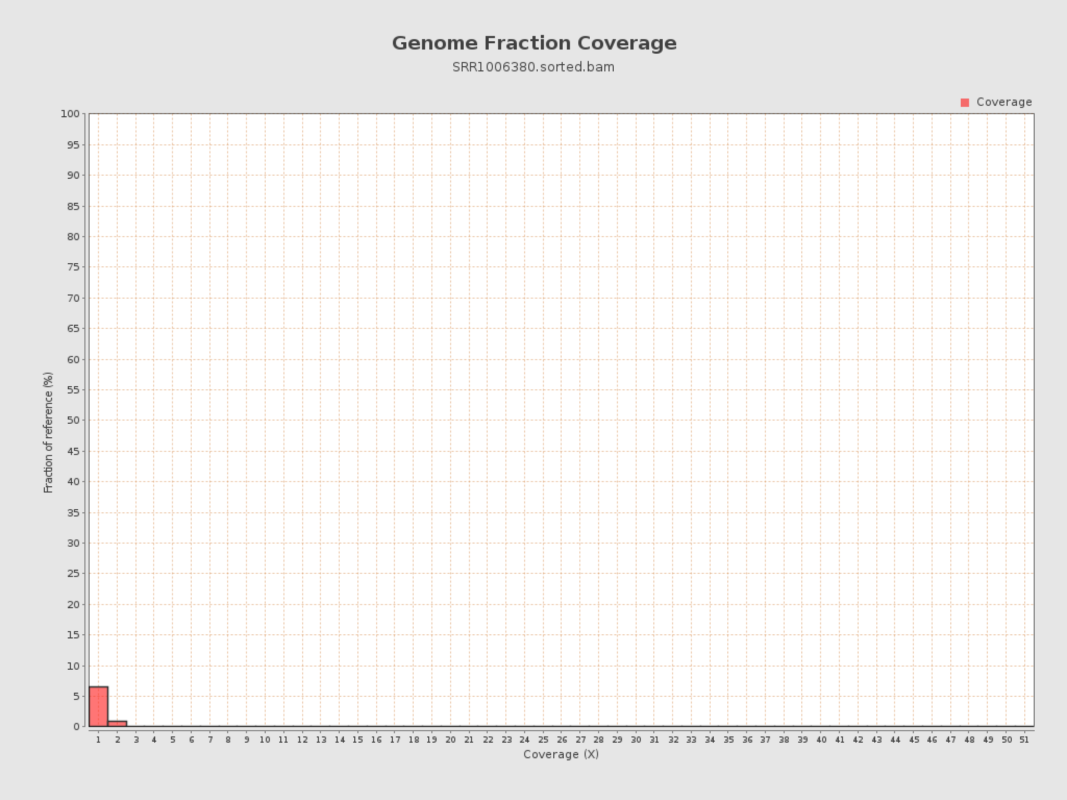
4. Results : Coverage Histogram



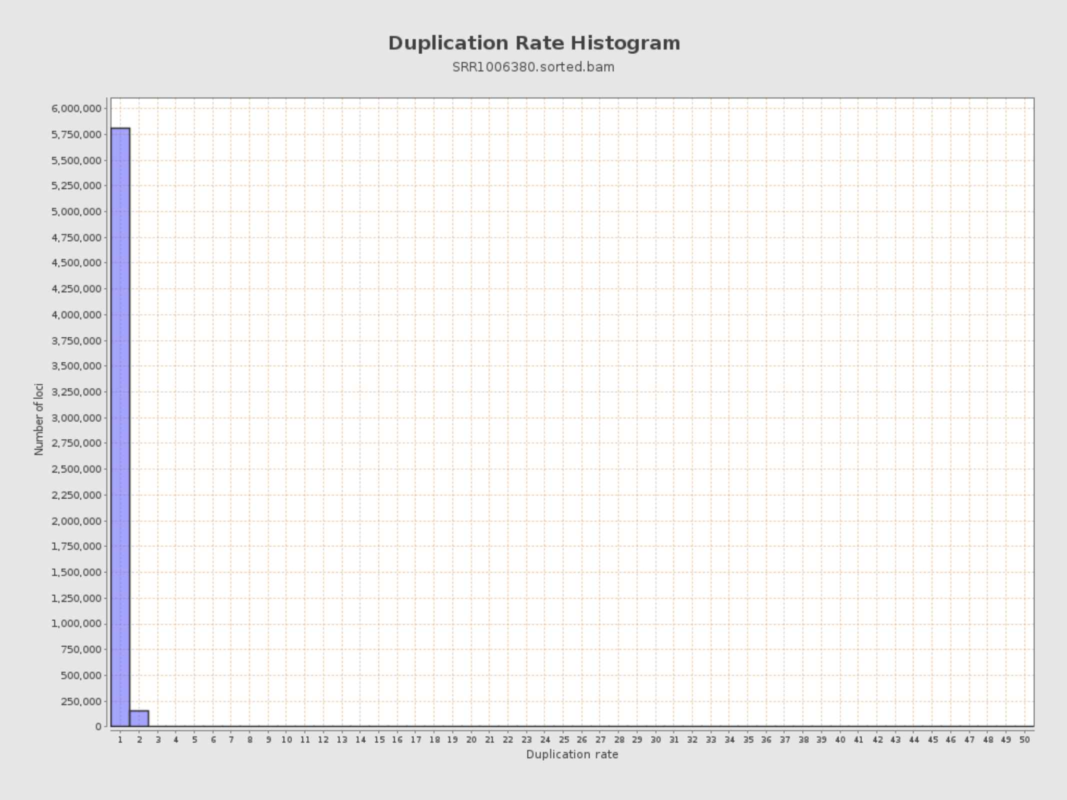
5. Results : Coverage Histogram (0-50X)



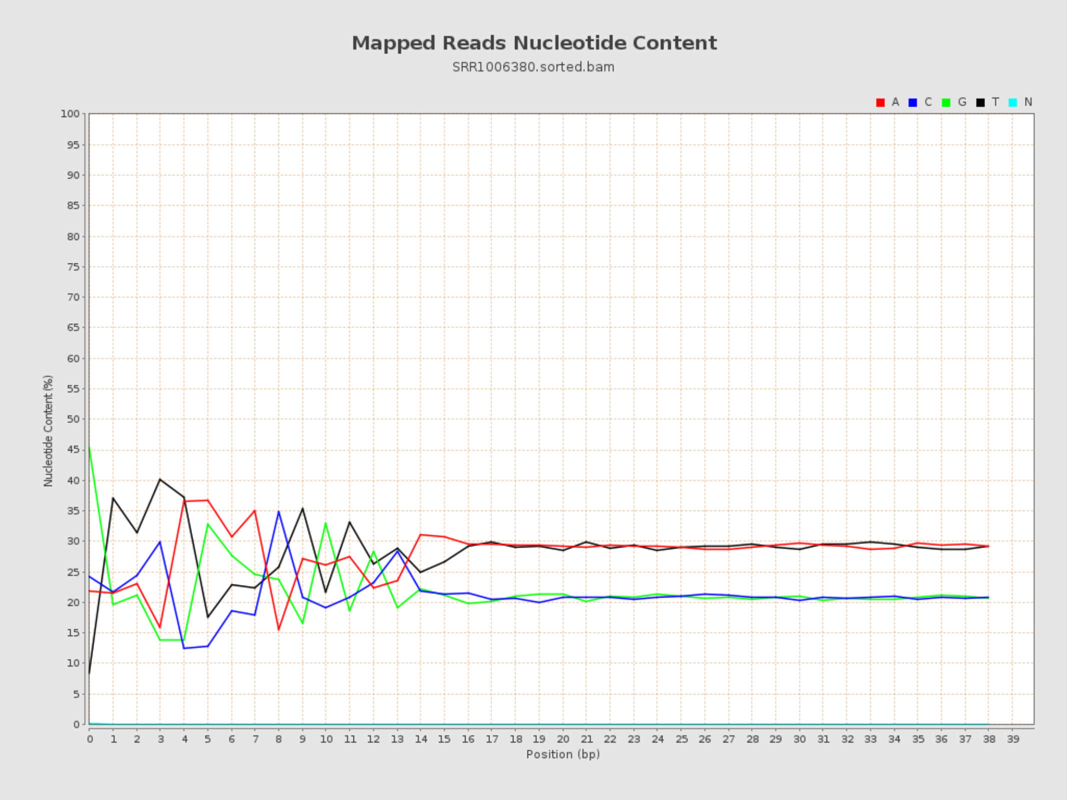
6. Results : Genome Fraction Coverage



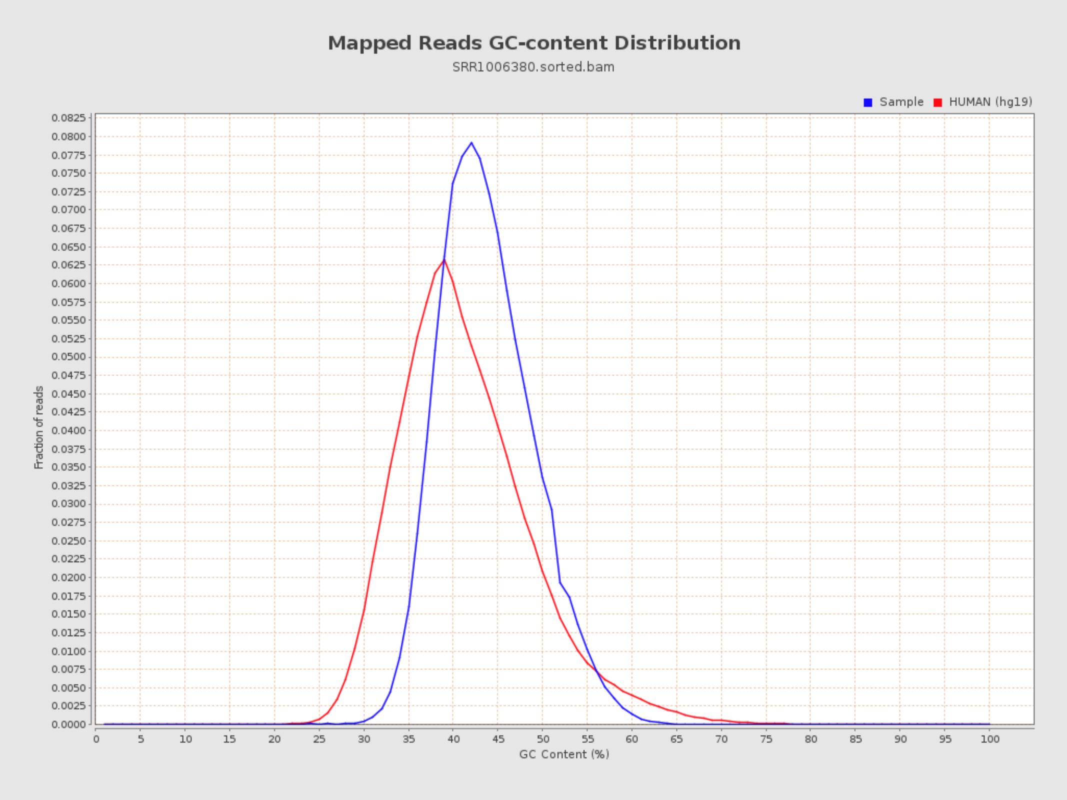
7. Results : Duplication Rate Histogram



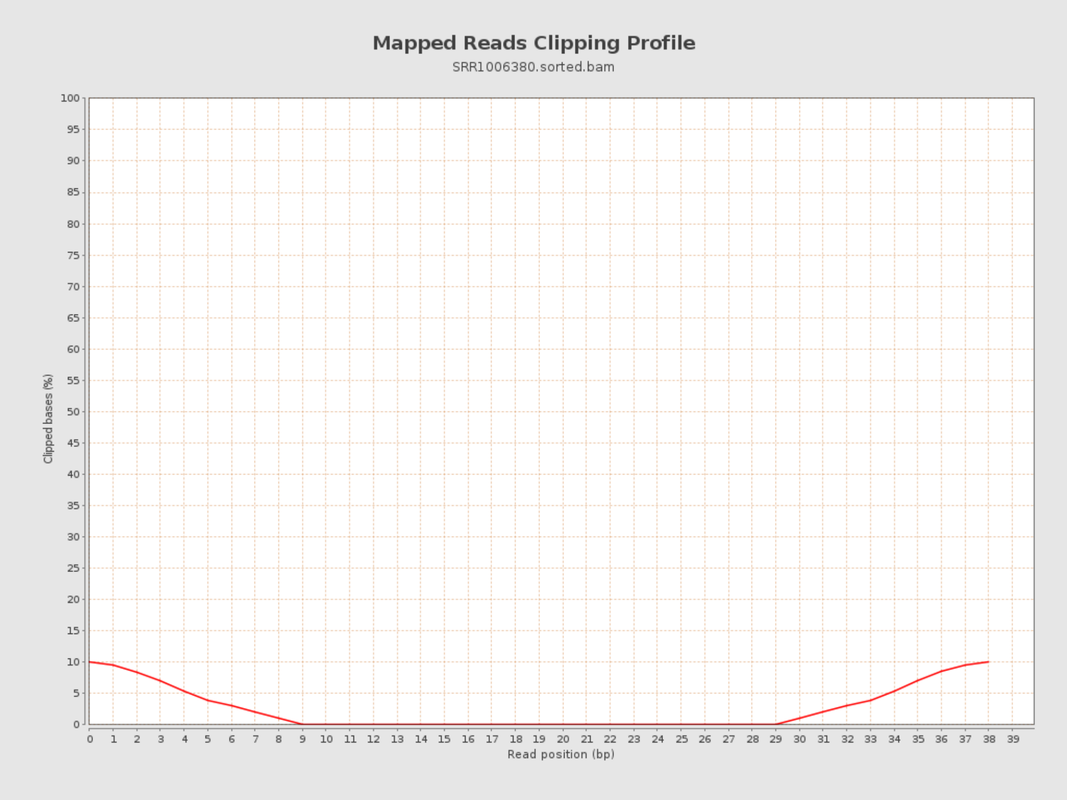
8. Results : Mapped Reads Nucleotide Content



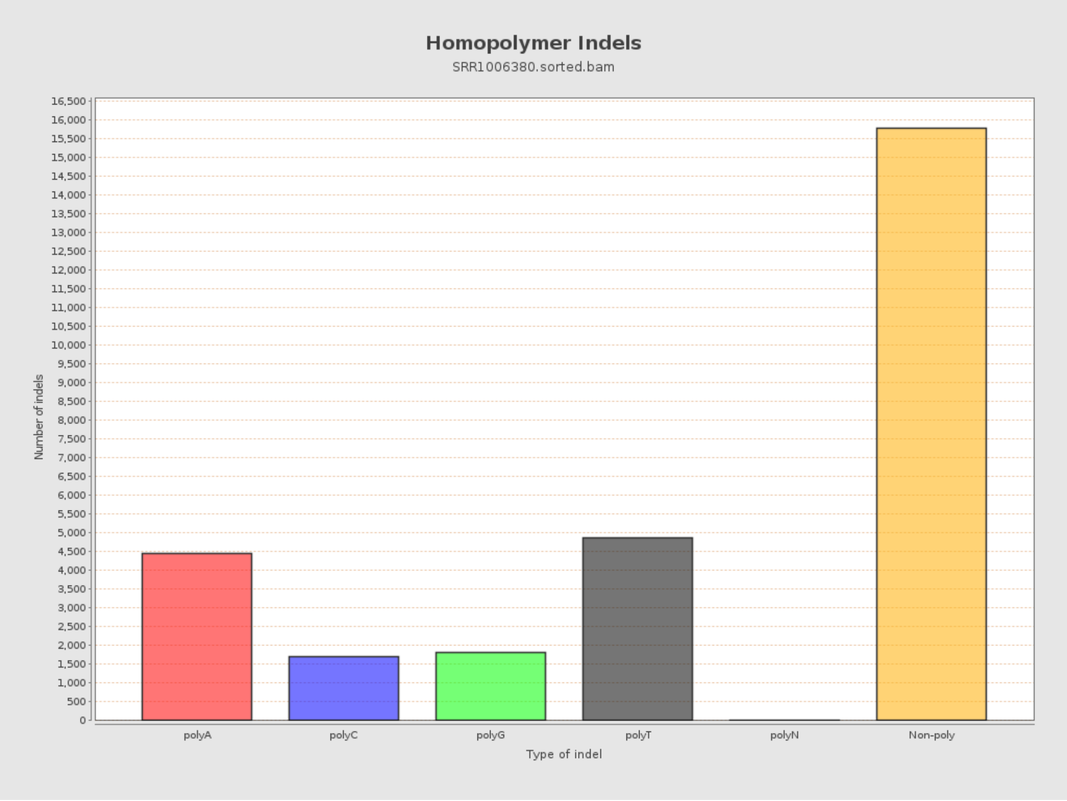
9. Results : Mapped Reads GC-content Distribution



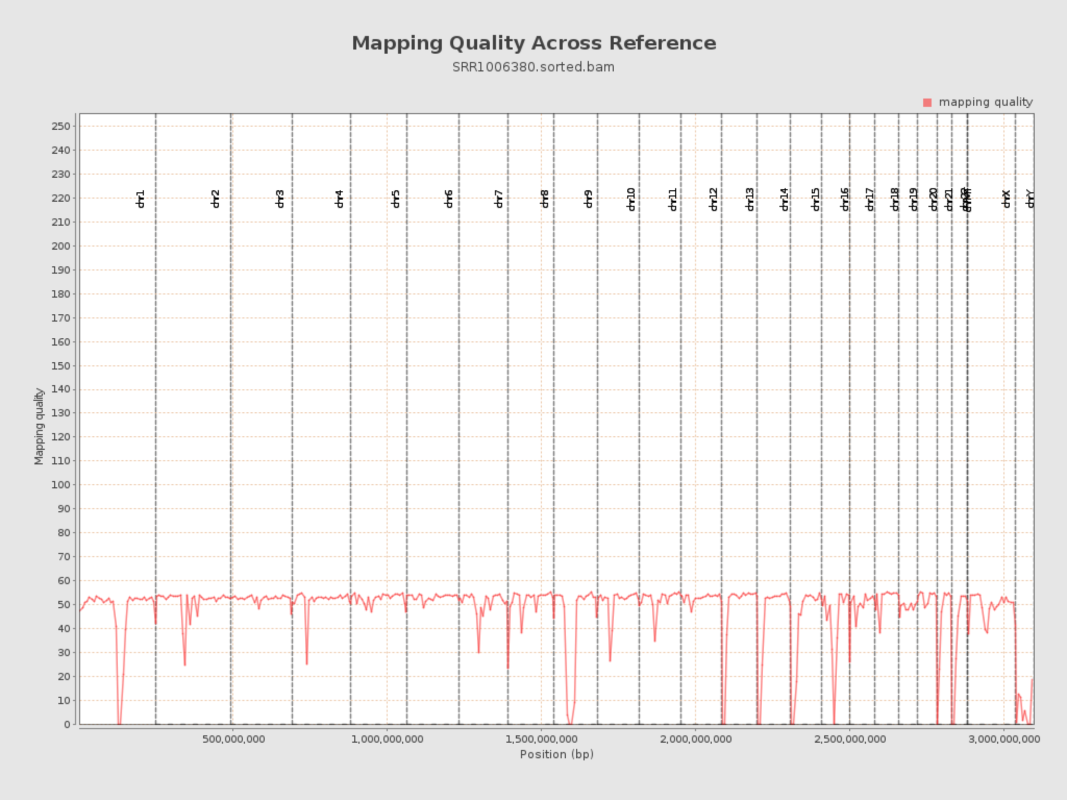
10. Results : Mapped Reads Clipping Profile



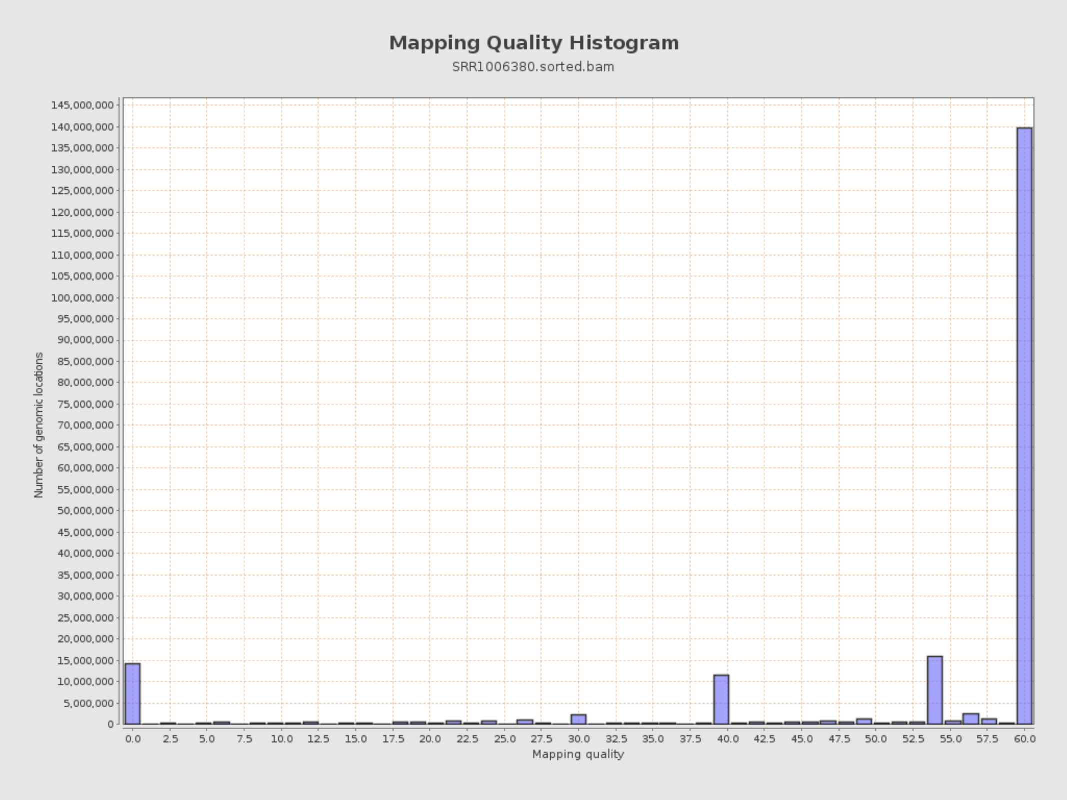
11. Results : Homopolymer Indels



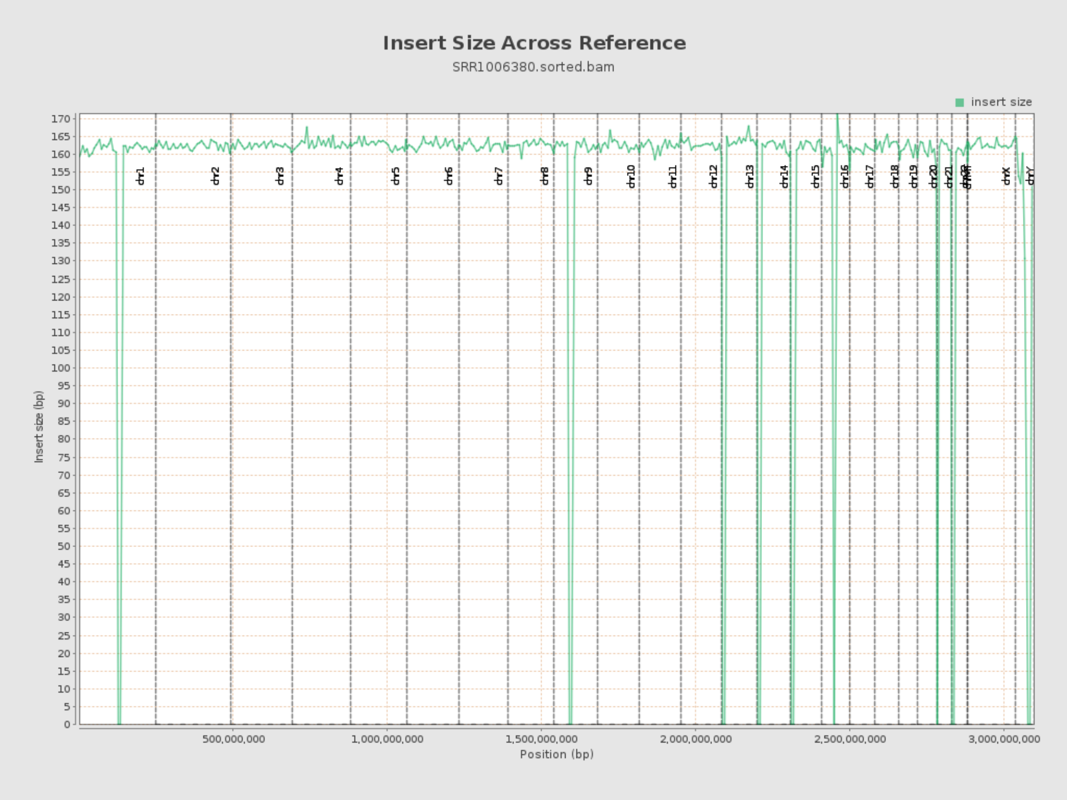
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram