Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 01:20:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006398.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_SRR1006398 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006398_1.fastq.gz SRR1006398_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 01:20:53 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006398.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,384,526
Mapped reads	3,728,825 / 85.05%
Unmapped reads	655,701 / 14.95%
Mapped paired reads	3,728,825 / 85.05%
Mapped reads, first in pair	1,876,643 / 42.8%
Mapped reads, second in pair	1,852,182 / 42.24%
Mapped reads, both in pair	3,435,374 / 78.35%
Mapped reads, singletons	293,451 / 6.69%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	95,883 / 2.19%
Duplication rate	2.15%
Clipped reads	216,980 / 4.95%

2.2. ACGT Content

Number/percentage of A's	39,331,661 / 27.26%
Number/percentage of C's	31,808,478 / 22.05%
Number/percentage of T's	40,155,193 / 27.83%
Number/percentage of G's	32,974,653 / 22.86%
Number/percentage of N's	6,341 / 0%
GC Percentage	44.9%

2.3. Coverage

Mean	0.0466
Standard Deviation	0.2944

2.4. Mapping Quality

Mean Mapping Quality	47.78

2.5. Insert size

Mean	83,327.62
Standard Deviation	2,790,973.09
P25/Median/P75	90 / 125 / 174

2.6. Mismatches and indels

General error rate	0.31%
Mismatches	441,770
Insertions	4,028
Mapped reads with at least one insertion	0.11%
Deletions	13,521
Mapped reads with at least one deletion	0.36%
Homopolymer indels	44.13%

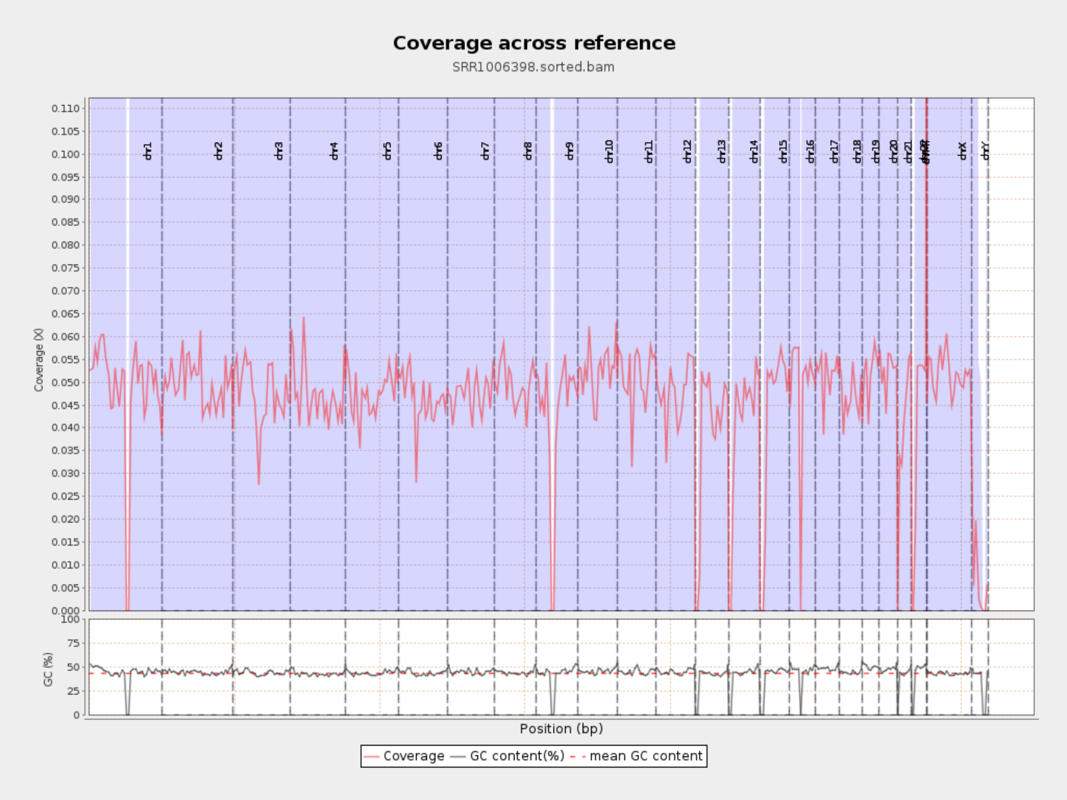
2.7. Chromosome stats

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

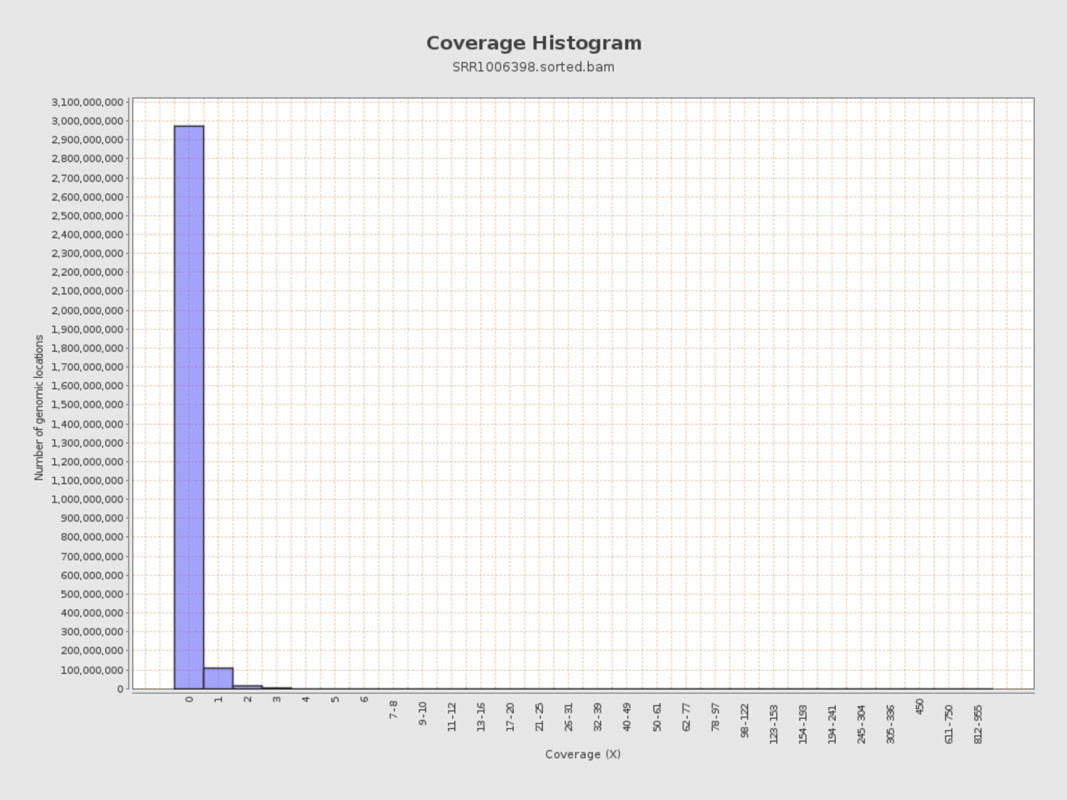
chr1	249250621	12038318	0.0483	0.3571
chr2	243199373	12154087	0.05	0.2874
chr3	198022430	9381732	0.0474	0.2432
chr4	191154276	9039490	0.0473	0.2623
chr5	180915260	8590574	0.0475	0.2445
chr6	171115067	7953933	0.0465	0.2565
chr7	159138663	7544232	0.0474	0.3284
chr8	146364022	7242423	0.0495	0.5302
chr9	141213431	5943949	0.0421	0.252
chr10	135534747	7074942	0.0522	0.3019
chr11	135006516	6932992	0.0514	0.2841
chr12	133851895	6395784	0.0478	0.2459
chr13	115169878	4420842	0.0384	0.2196
chr14	107349540	4303103	0.0401	0.2889
chr15	102531392	4330516	0.0422	0.2307
chr16	90354753	4434555	0.0491	0.2725
chr17	81195210	4202278	0.0518	0.2648
chr18	78077248	3672303	0.047	0.3588
chr19	59128983	3074230	0.052	0.3059
chr20	63025520	3318474	0.0527	0.2658
chr21	48129895	1915465	0.0398	0.2543
chr22	51304566	1904673	0.0371	0.2265
chrMT	16571	4188	0.2527	0.5913
chrX	155270560	8055395	0.0519	0.2671

chrY	59373566	365892	0.0062	0.1552

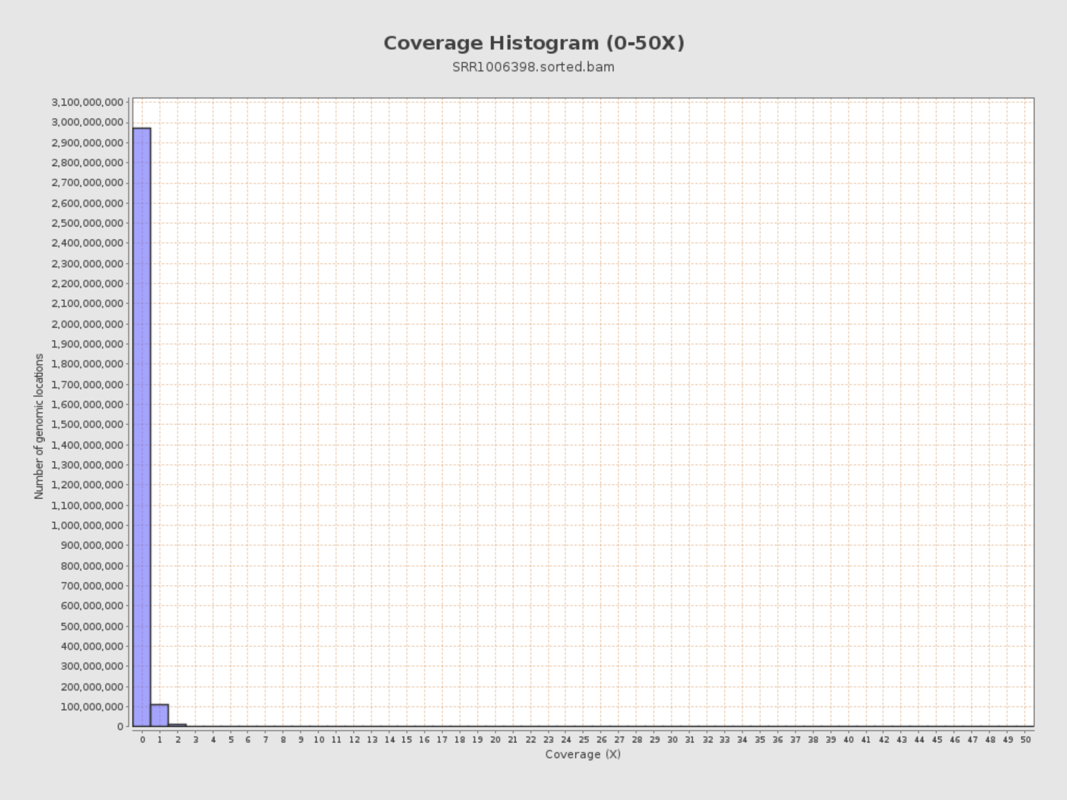
3. Results : Coverage across reference



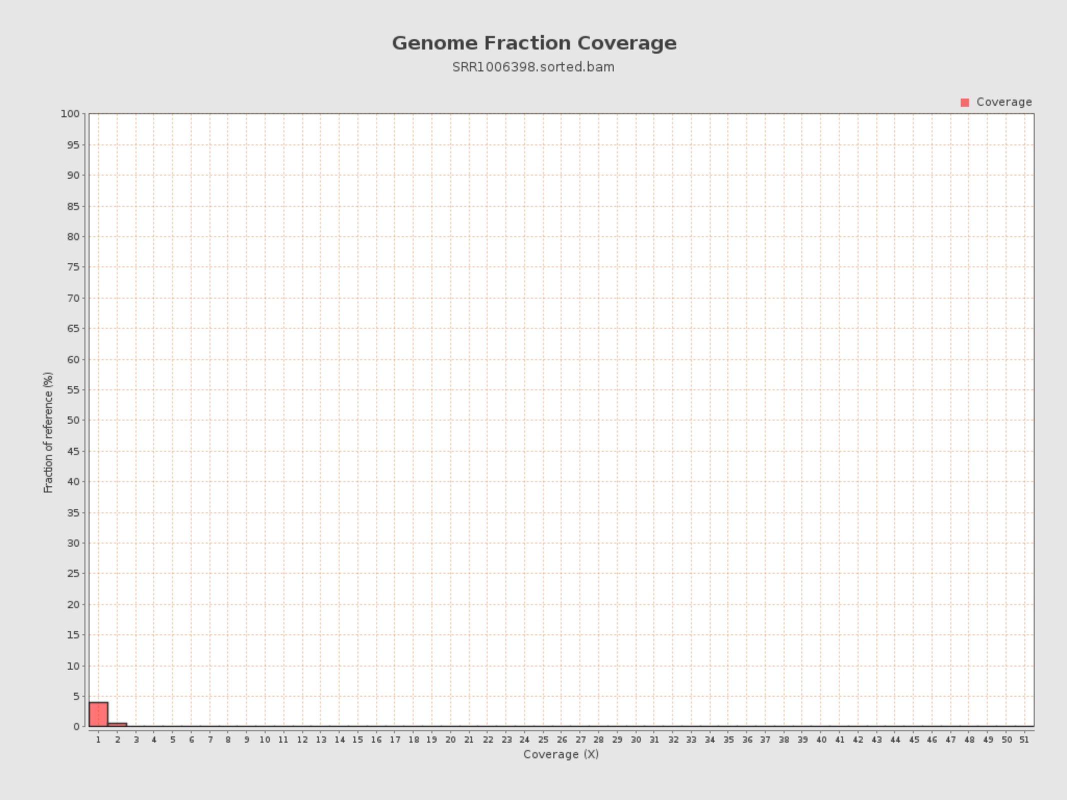
4. Results : Coverage Histogram



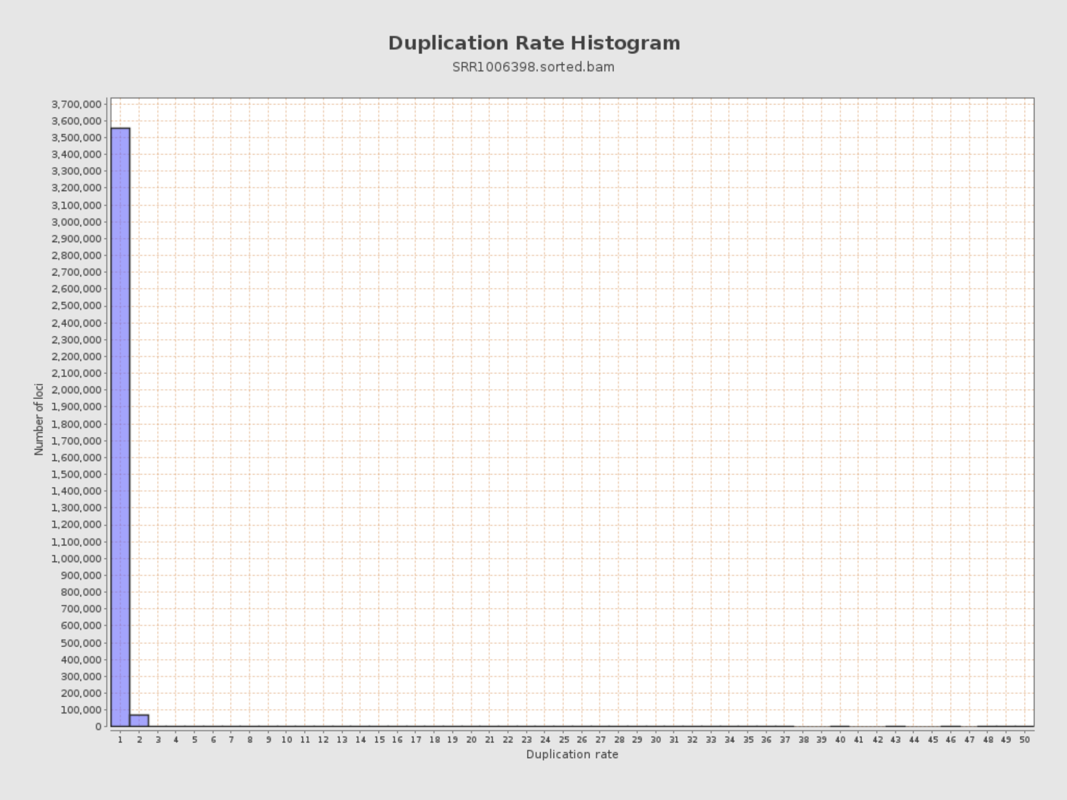
5. Results : Coverage Histogram (0-50X)



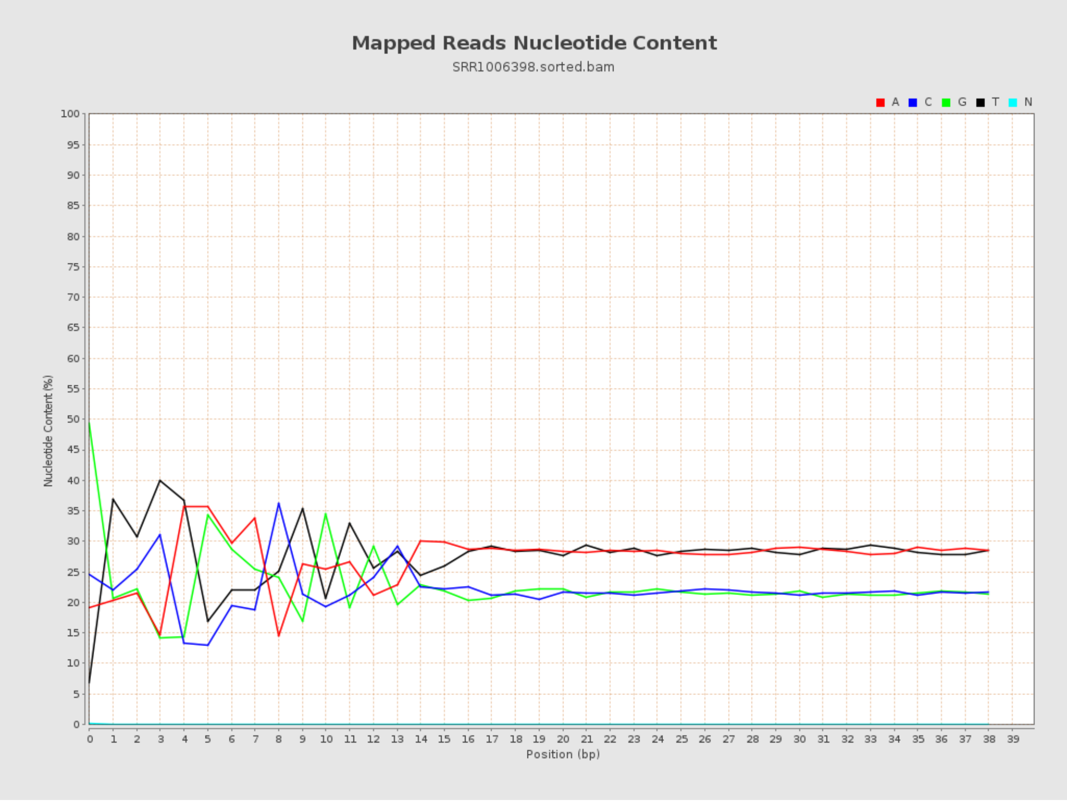
6. Results : Genome Fraction Coverage



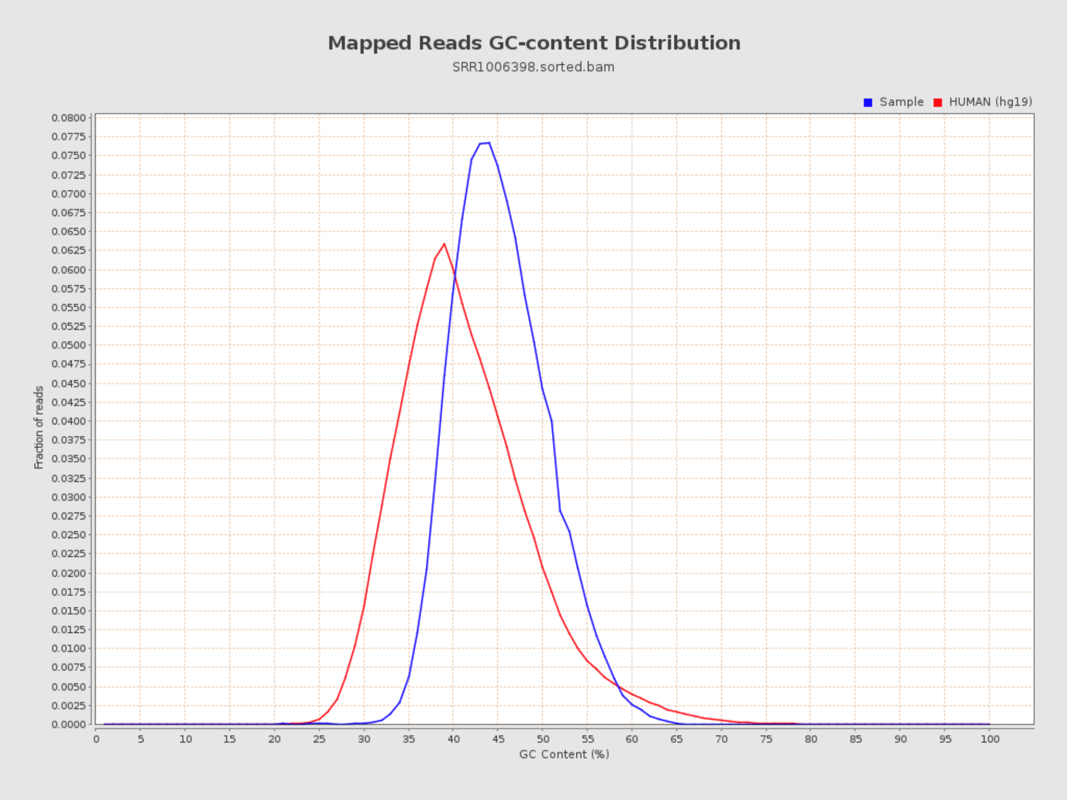
7. Results : Duplication Rate Histogram



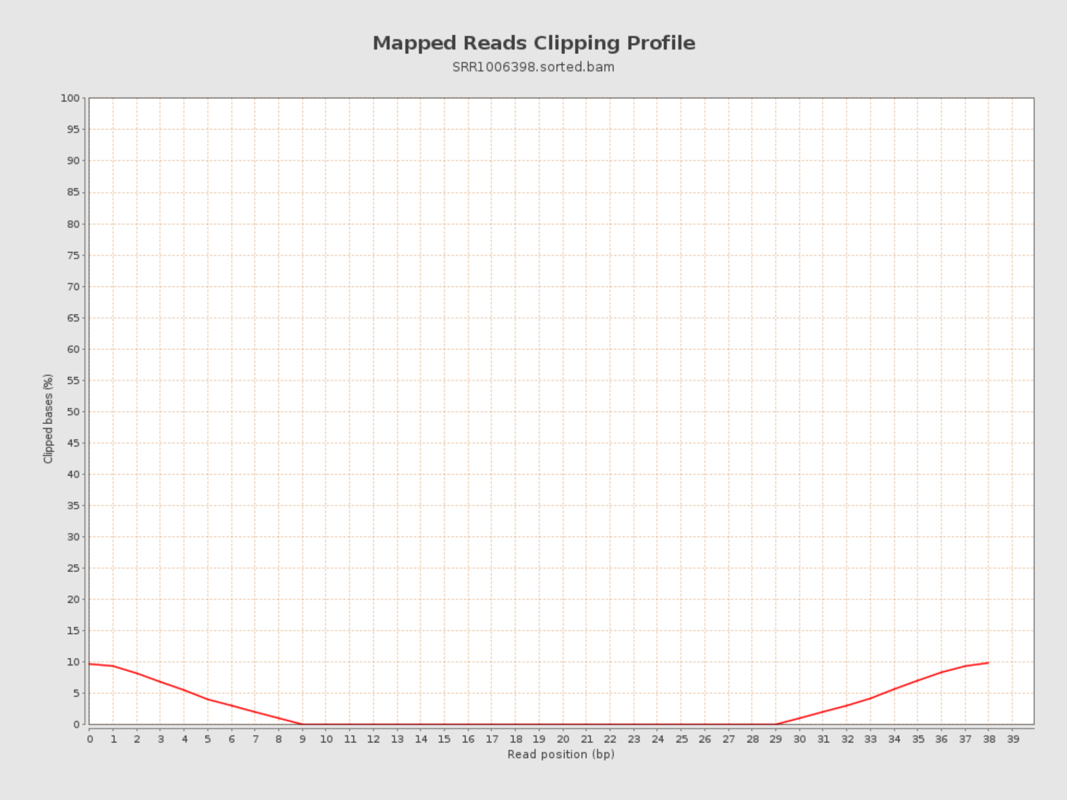
8. Results : Mapped Reads Nucleotide Content



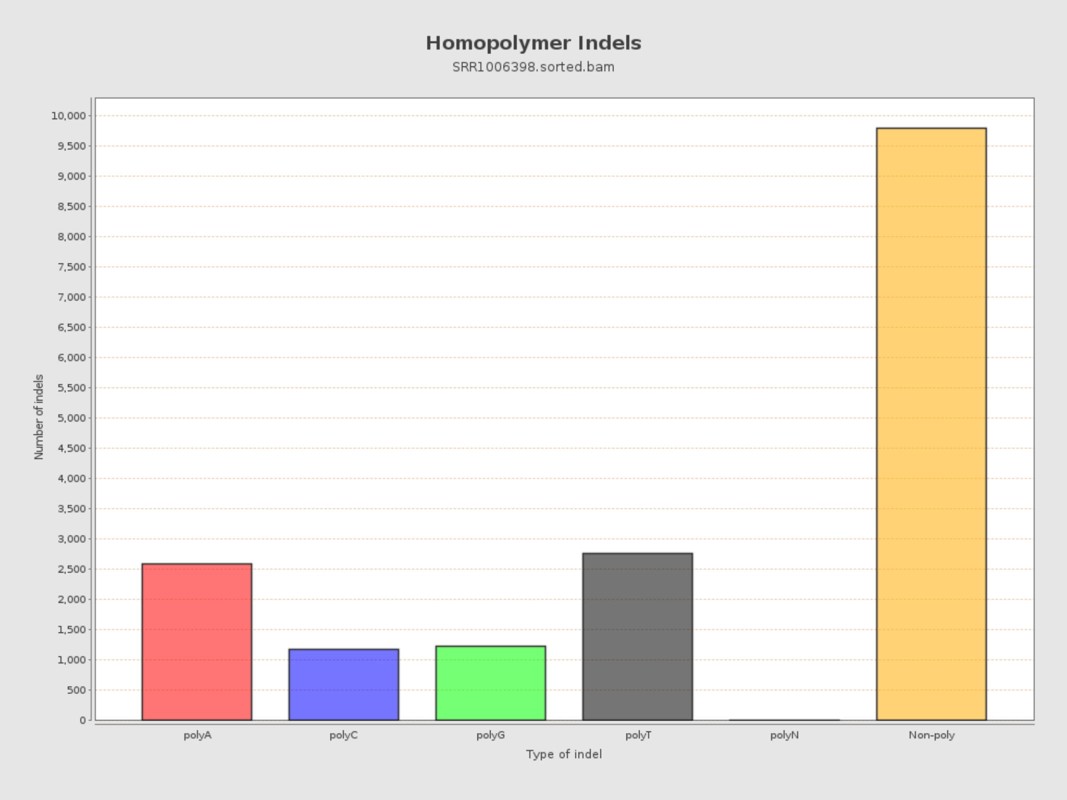
9. Results : Mapped Reads GC-content Distribution



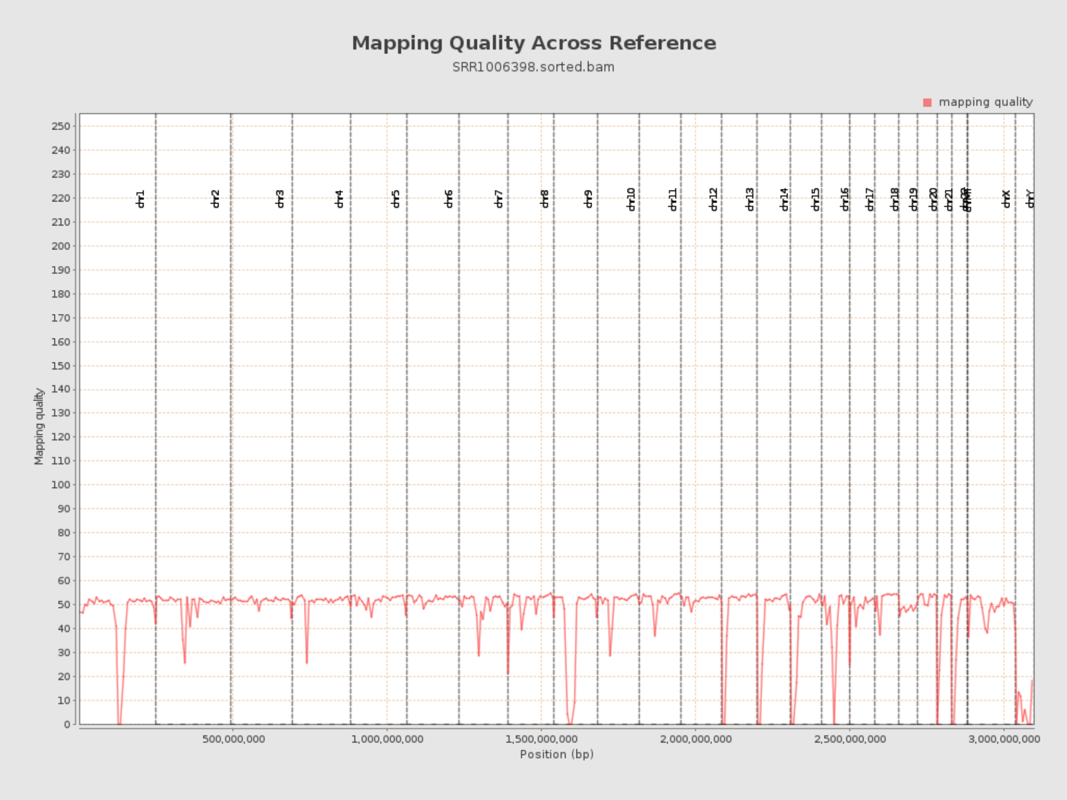
10. Results : Mapped Reads Clipping Profile



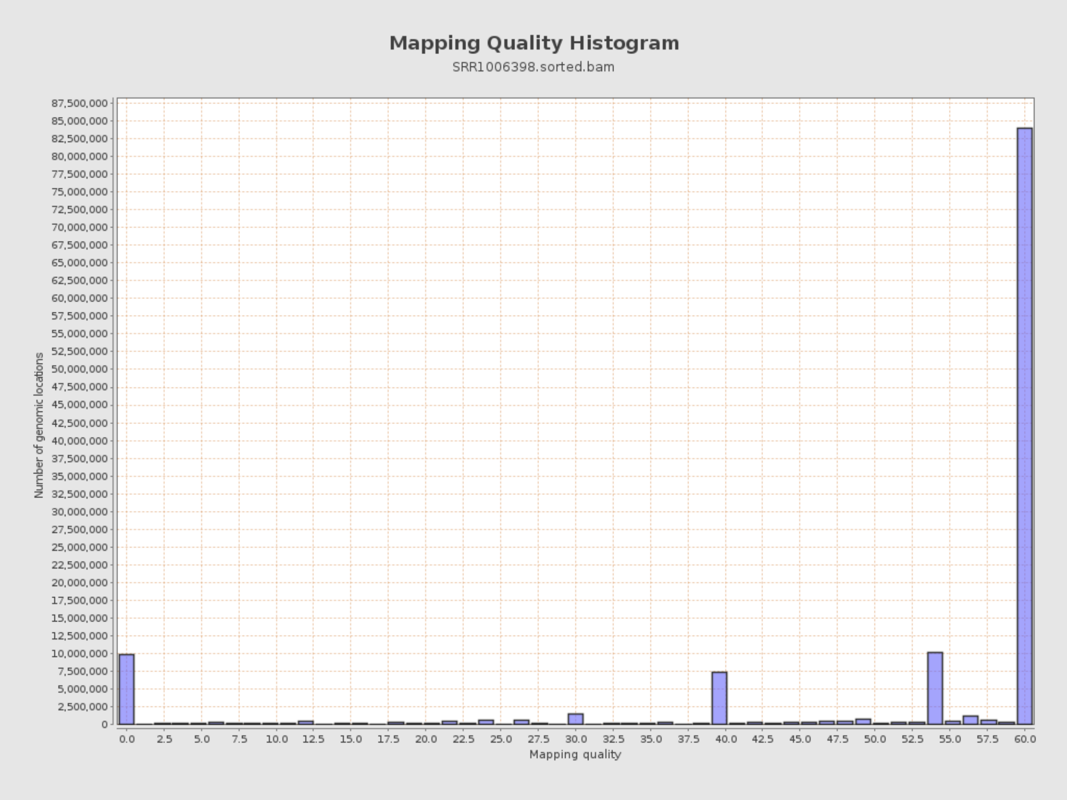
11. Results : Homopolymer Indels



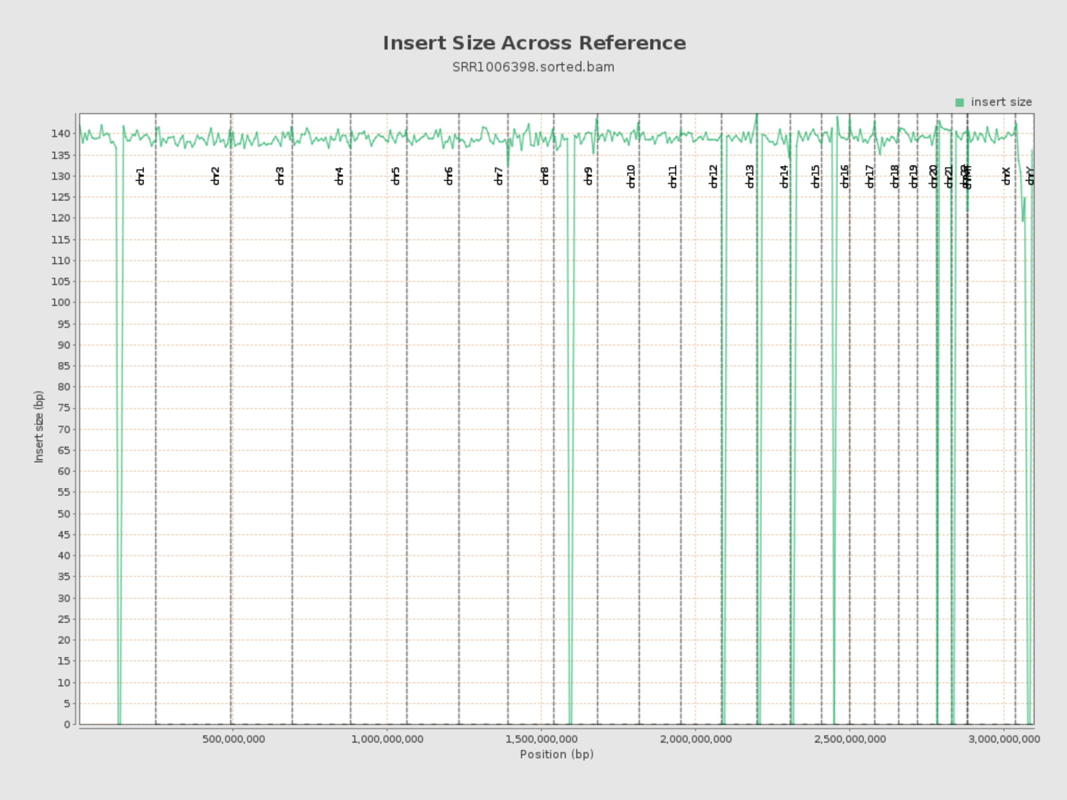
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram