Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 20:06:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006140.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_SRR1006140 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006140_1.fastq.gz SRR1006140_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 20:06:37 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006140.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,642,640
Mapped reads	13,532,011 / 86.51%
Unmapped reads	2,110,629 / 13.49%
Mapped paired reads	13,532,011 / 86.51%
Mapped reads, first in pair	6,886,148 / 44.02%
Mapped reads, second in pair	6,645,863 / 42.49%
Mapped reads, both in pair	12,317,208 / 78.74%
Mapped reads, singletons	1,214,803 / 7.77%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	1,210,295 / 7.74%
Duplication rate	8.11%
Clipped reads	1,163,604 / 7.44%

2.2. ACGT Content

Number/percentage of A's	142,156,394 / 27.23%
Number/percentage of C's	113,439,753 / 21.73%
Number/percentage of T's	147,069,092 / 28.17%
Number/percentage of G's	119,384,710 / 22.87%
Number/percentage of N's	23,016 / 0%
GC Percentage	44.6%

2.3. Coverage

Mean	0.1687
Standard Deviation	0.8514

2.4. Mapping Quality

Mean Mapping Quality	46.84

2.5. Insert size

Mean	63,295.59
Standard Deviation	2,479,515.9
P25/Median/P75	64 / 92 / 134

2.6. Mismatches and indels

General error rate	0.5%
Mismatches	2,586,277
Insertions	17,736
Mapped reads with at least one insertion	0.13%
Deletions	46,182
Mapped reads with at least one deletion	0.34%
Homopolymer indels	45.8%

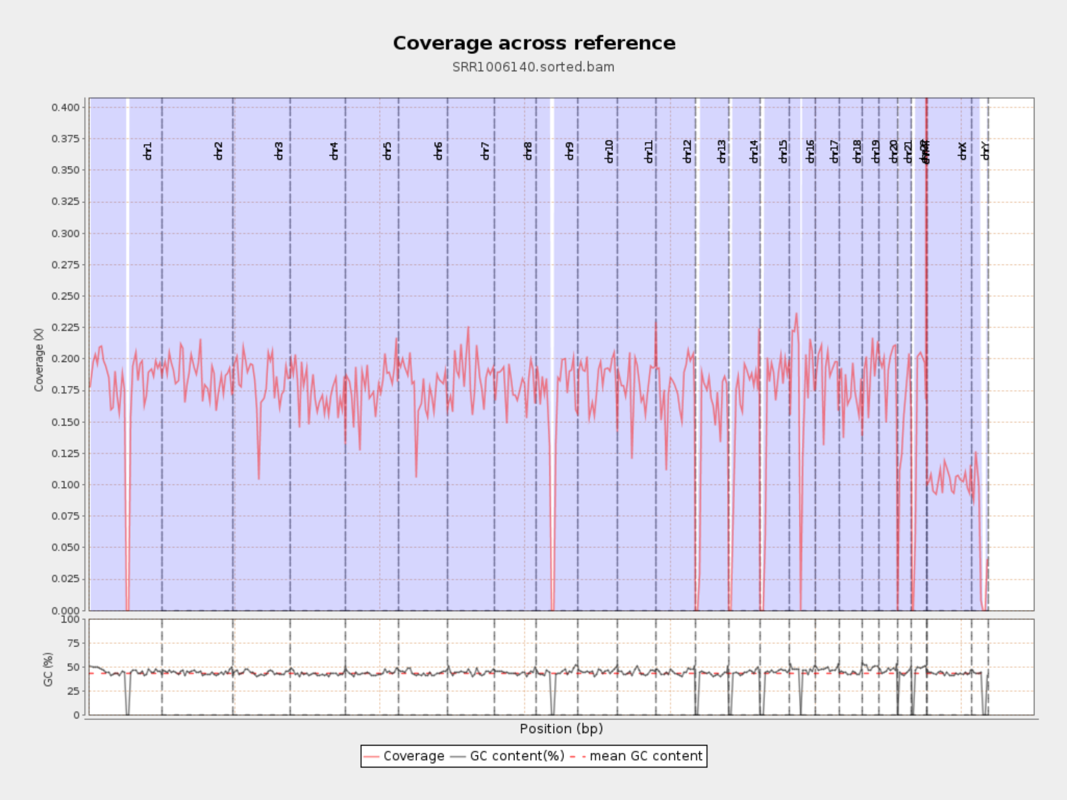
2.7. Chromosome stats

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

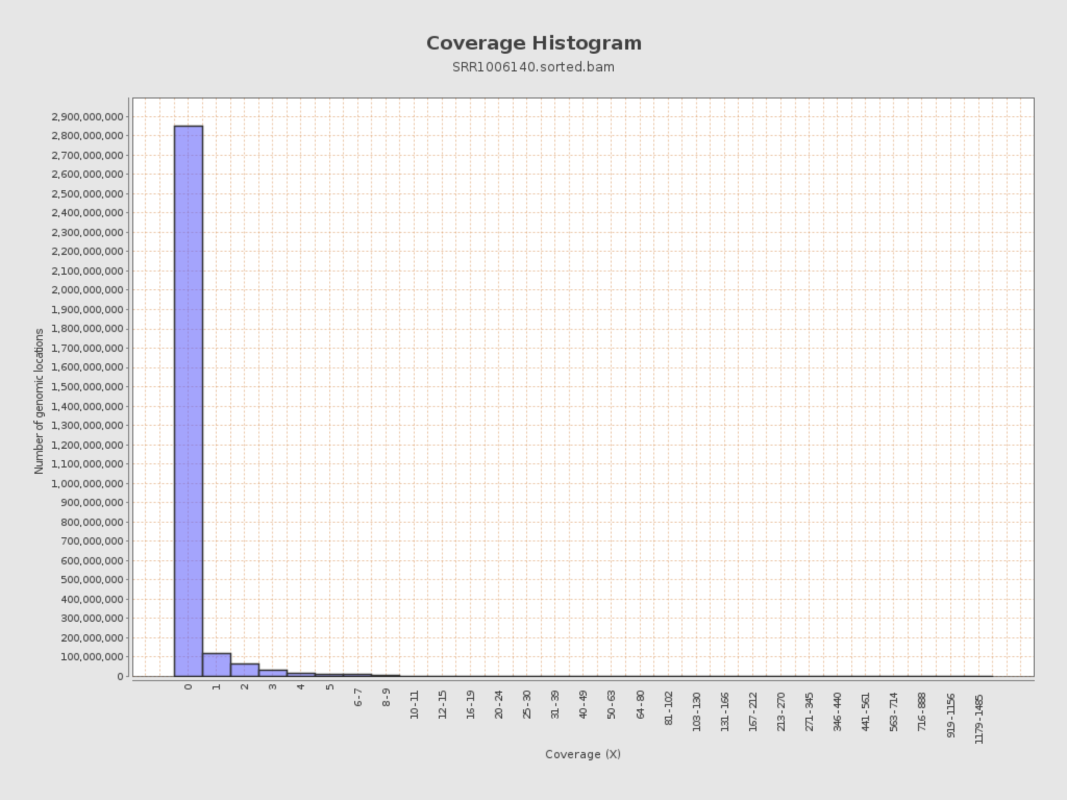
chr1	249250621	43627872	0.175	0.9046
chr2	243199373	45555339	0.1873	0.9323
chr3	198022430	36052718	0.1821	0.7628
chr4	191154276	33133814	0.1733	0.7759
chr5	180915260	32290260	0.1785	0.7571
chr6	171115067	30218648	0.1766	0.8711
chr7	159138663	29566534	0.1858	1.2101
chr8	146364022	26223914	0.1792	0.9069
chr9	141213431	22348622	0.1583	0.79
chr10	135534747	25176829	0.1858	0.808
chr11	135006516	24164071	0.179	1.1157
chr12	133851895	23743919	0.1774	0.7594
chr13	115169878	16501270	0.1433	0.6834
chr14	107349540	16156187	0.1505	0.72
chr15	102531392	15739811	0.1535	0.7166
chr16	90354753	16196882	0.1793	0.8363
chr17	81195210	15353032	0.1891	0.8597
chr18	78077248	13483482	0.1727	0.9875
chr19	59128983	11313595	0.1913	0.9935
chr20	63025520	12135465	0.1925	0.806
chr21	48129895	6824990	0.1418	0.7657
chr22	51304566	7019943	0.1368	0.7506
chrMT	16571	25865	1.5609	2.7777
chrX	155270560	15999773	0.103	0.6041

chrY	59373566	3278367	0.0552	0.4597

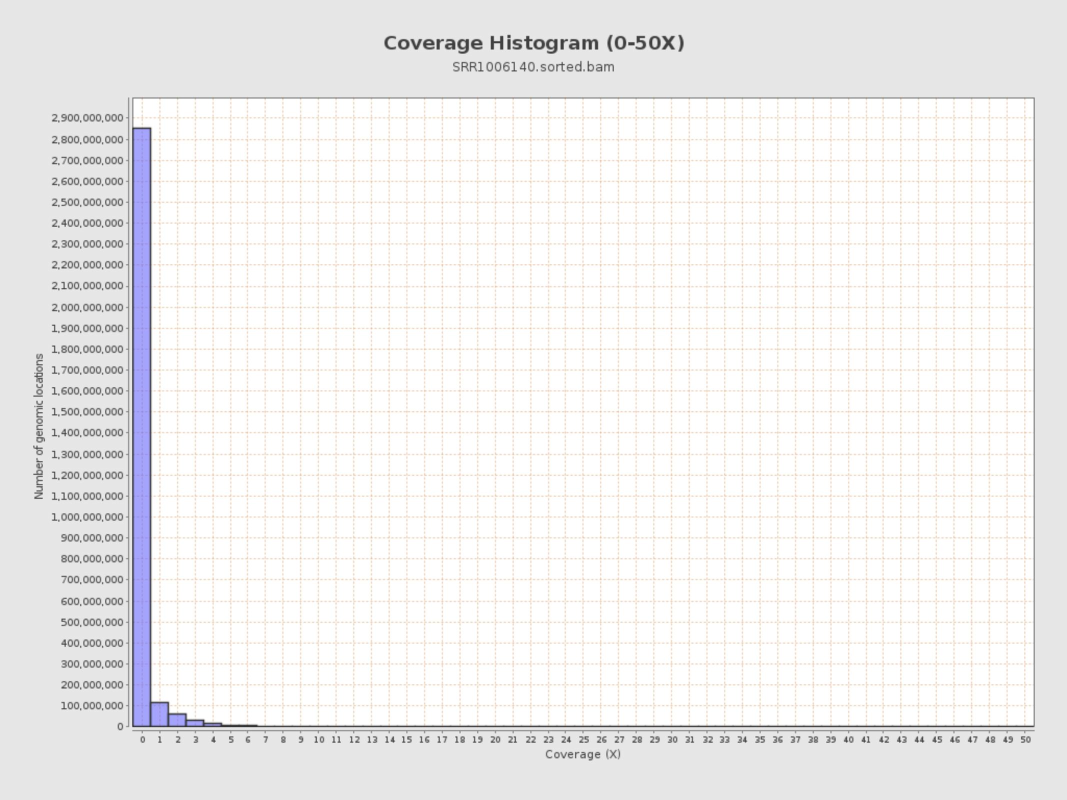
3. Results : Coverage across reference



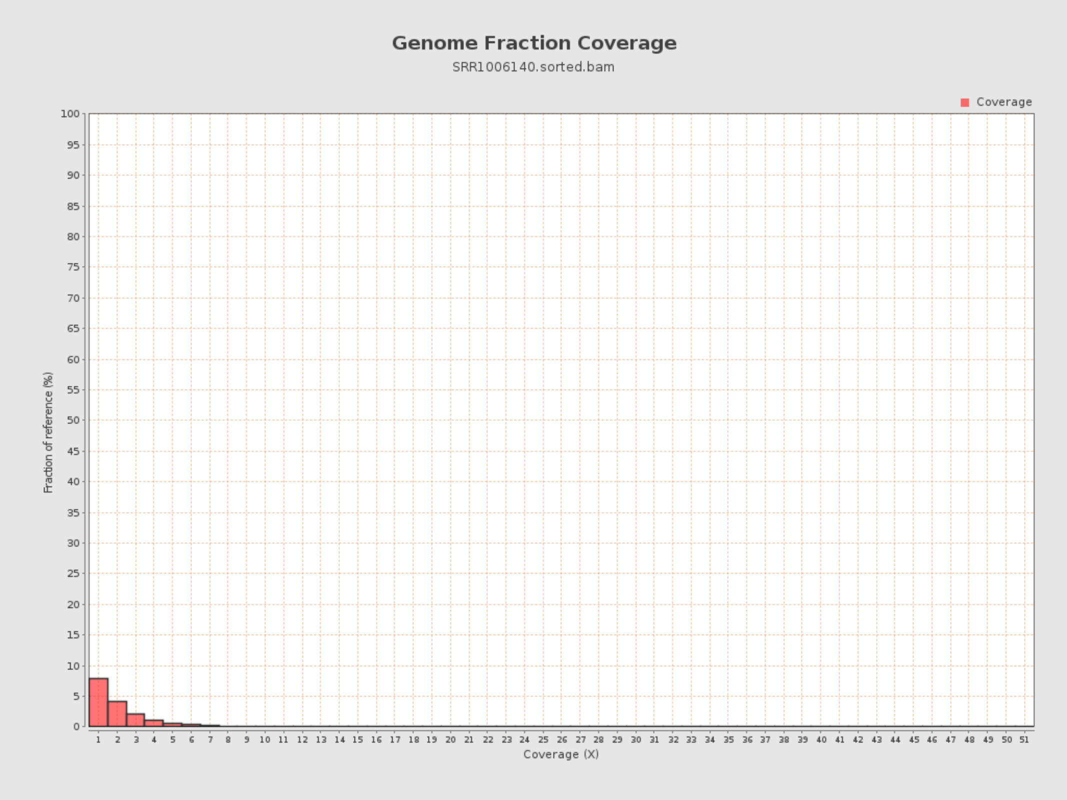
4. Results : Coverage Histogram



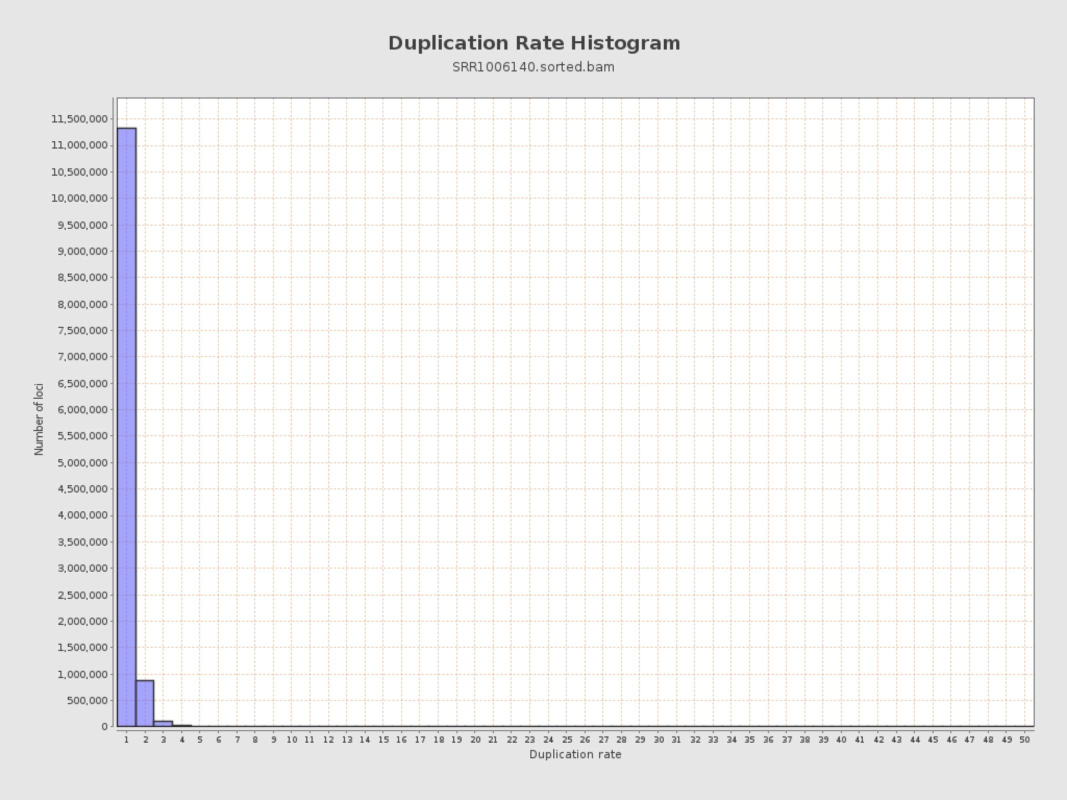
5. Results : Coverage Histogram (0-50X)



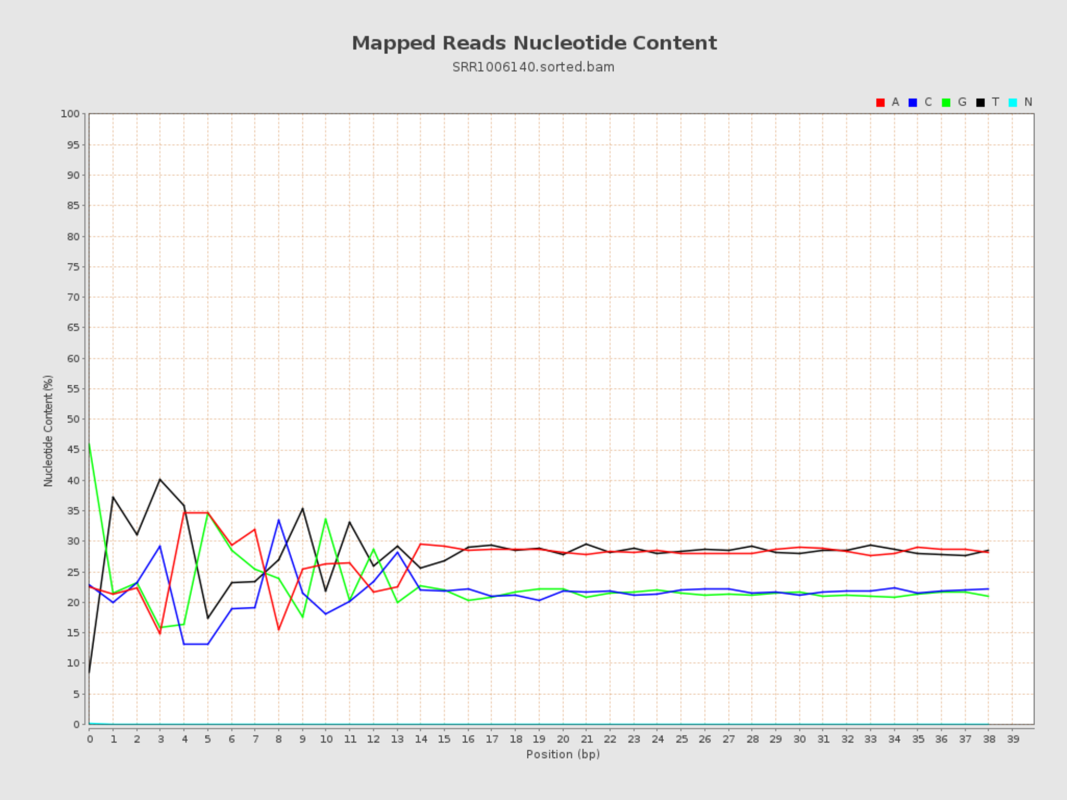
6. Results : Genome Fraction Coverage



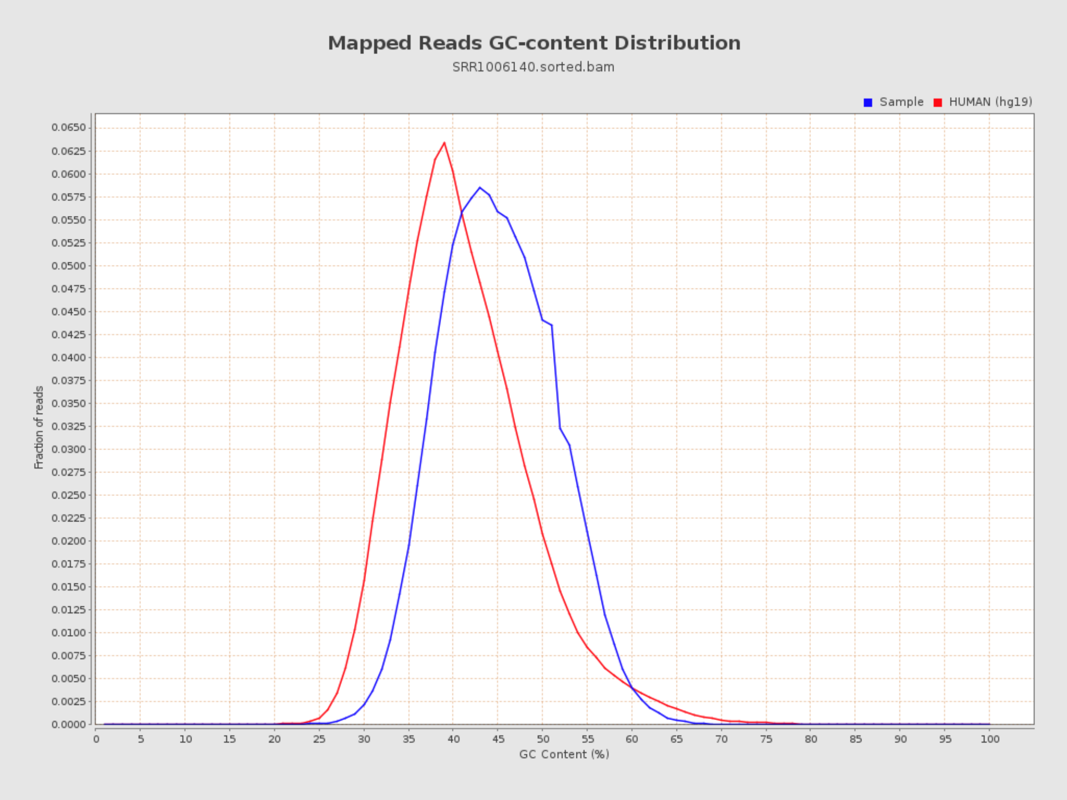
7. Results : Duplication Rate Histogram



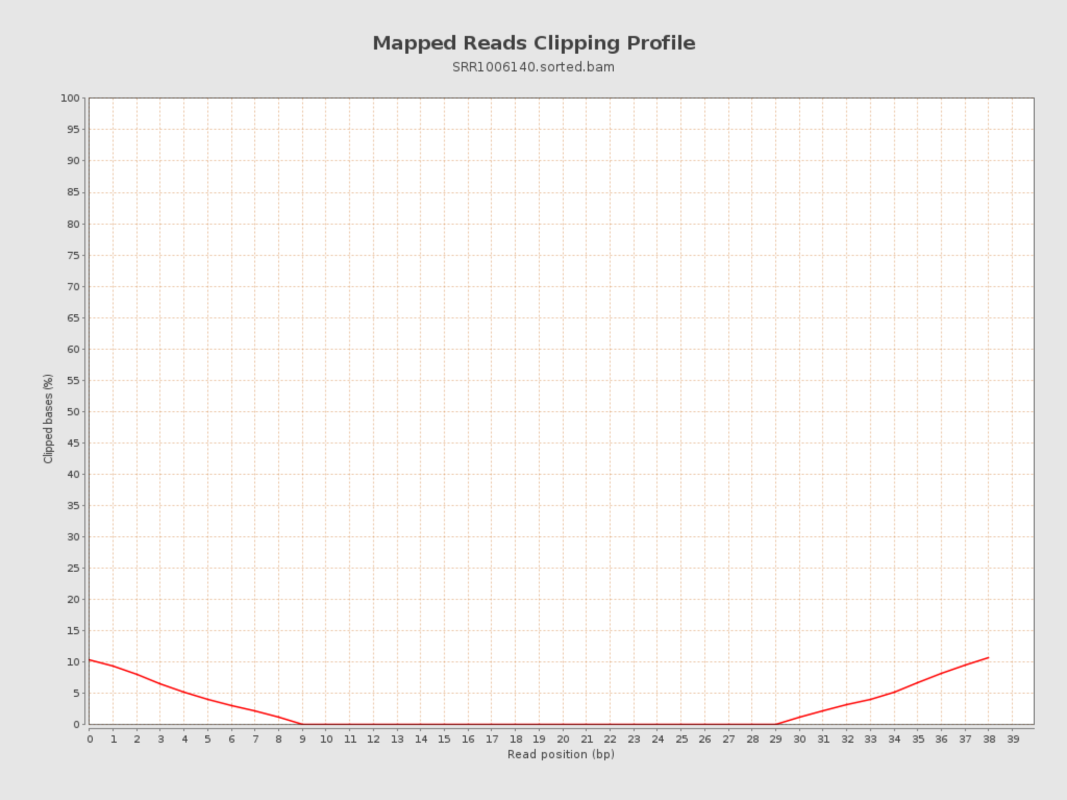
8. Results : Mapped Reads Nucleotide Content



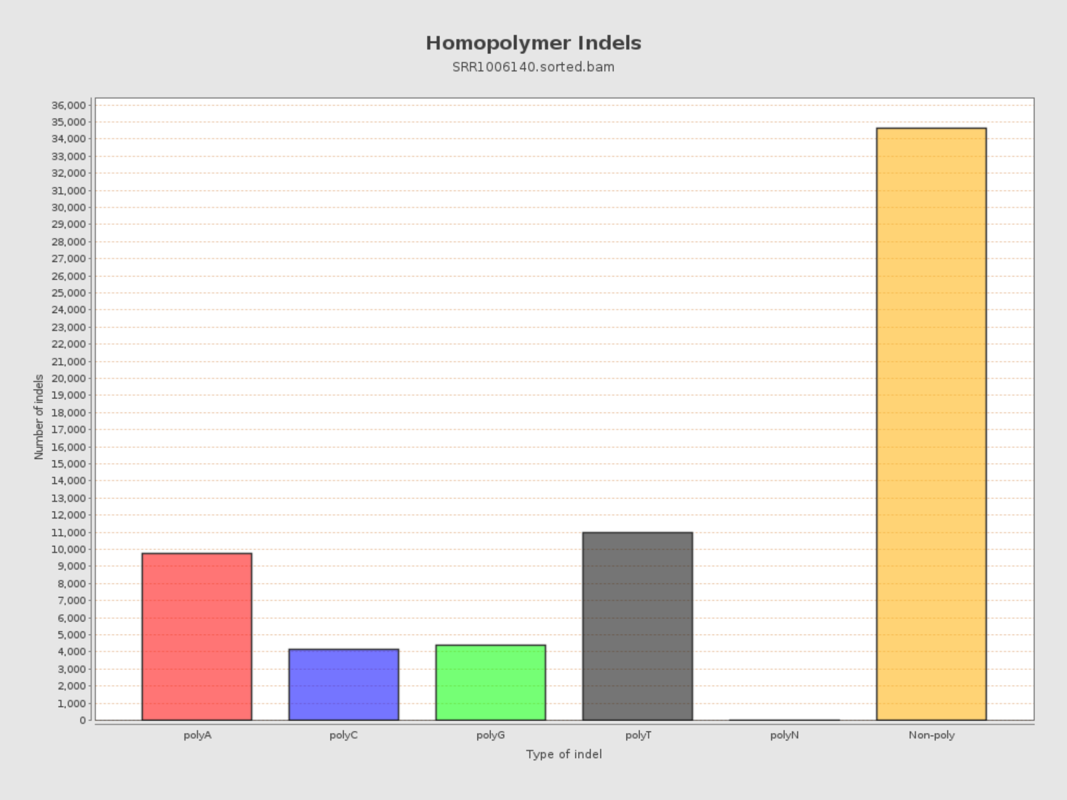
9. Results : Mapped Reads GC-content Distribution



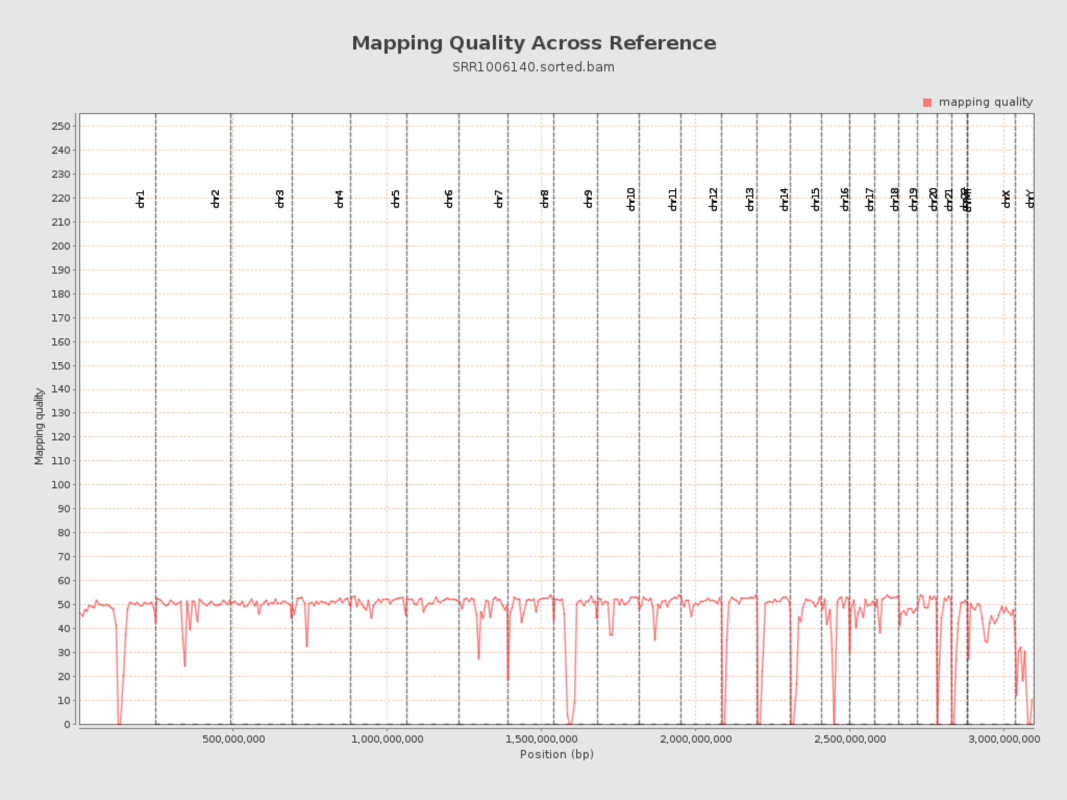
10. Results : Mapped Reads Clipping Profile



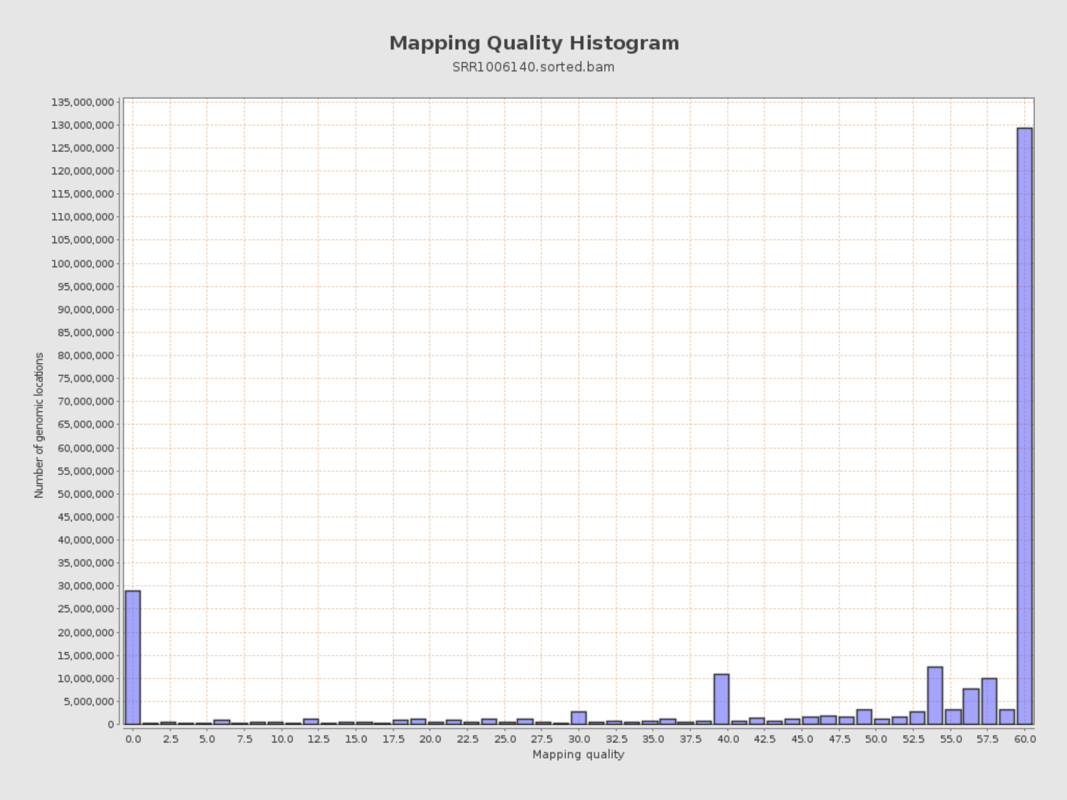
11. Results : Homopolymer Indels



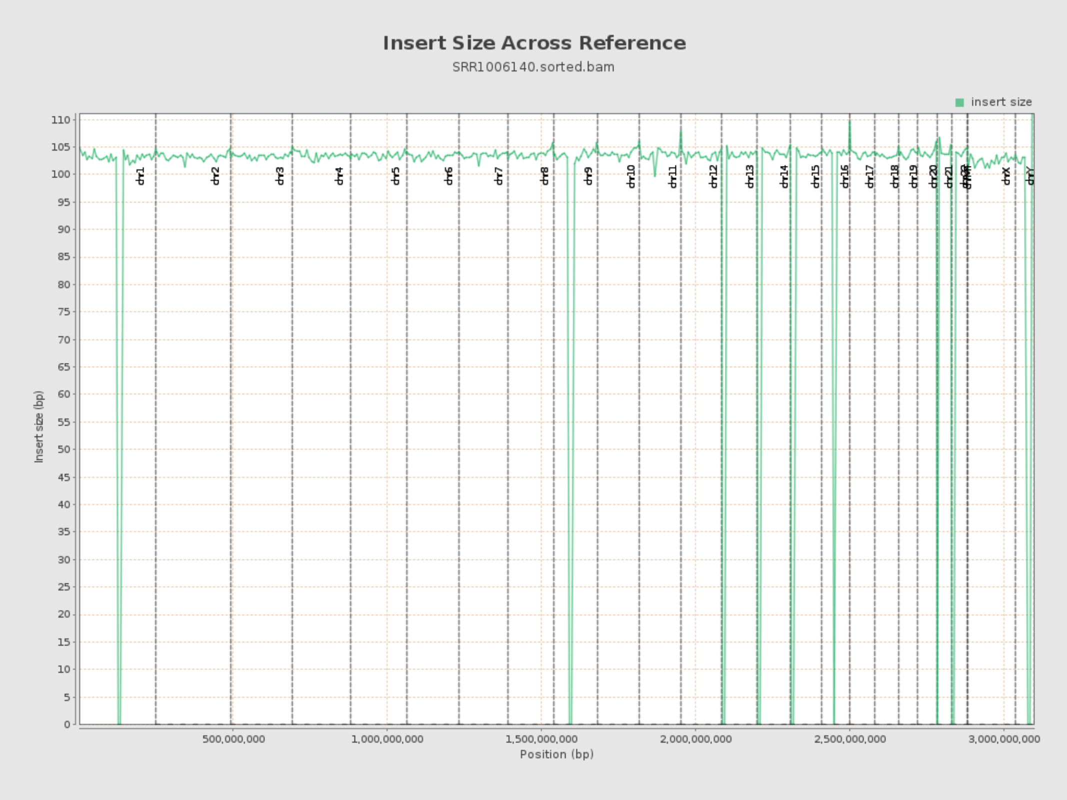
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram