Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 14:36:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006024.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_SRR1006024 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006024_1.fastq.gz SRR1006024_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 14:36:00 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006024.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,669,660
Mapped reads	5,887,474 / 67.91%
Unmapped reads	2,782,186 / 32.09%
Mapped paired reads	5,887,474 / 67.91%
Mapped reads, first in pair	2,982,558 / 34.4%
Mapped reads, second in pair	2,904,916 / 33.51%
Mapped reads, both in pair	5,077,518 / 58.57%
Mapped reads, singletons	809,956 / 9.34%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	143,416 / 1.65%
Duplication rate	1.93%
Clipped reads	496,495 / 5.73%

2.2. ACGT Content

Number/percentage of A's	67,326,832 / 29.62%
Number/percentage of C's	46,571,698 / 20.49%
Number/percentage of T's	66,120,138 / 29.09%
Number/percentage of G's	47,212,712 / 20.77%
Number/percentage of N's	83,135 / 0.04%
GC Percentage	41.26%

2.3. Coverage

Mean	0.0734
Standard Deviation	0.4237

2.4. Mapping Quality

Mean Mapping Quality	46.99

2.5. Insert size

Mean	73,457.82
Standard Deviation	2,622,854.96
P25/Median/P75	73 / 102 / 146

2.6. Mismatches and indels

General error rate	0.74%
Mismatches	1,672,365
Insertions	6,358
Mapped reads with at least one insertion	0.11%
Deletions	19,231
Mapped reads with at least one deletion	0.33%
Homopolymer indels	45.69%

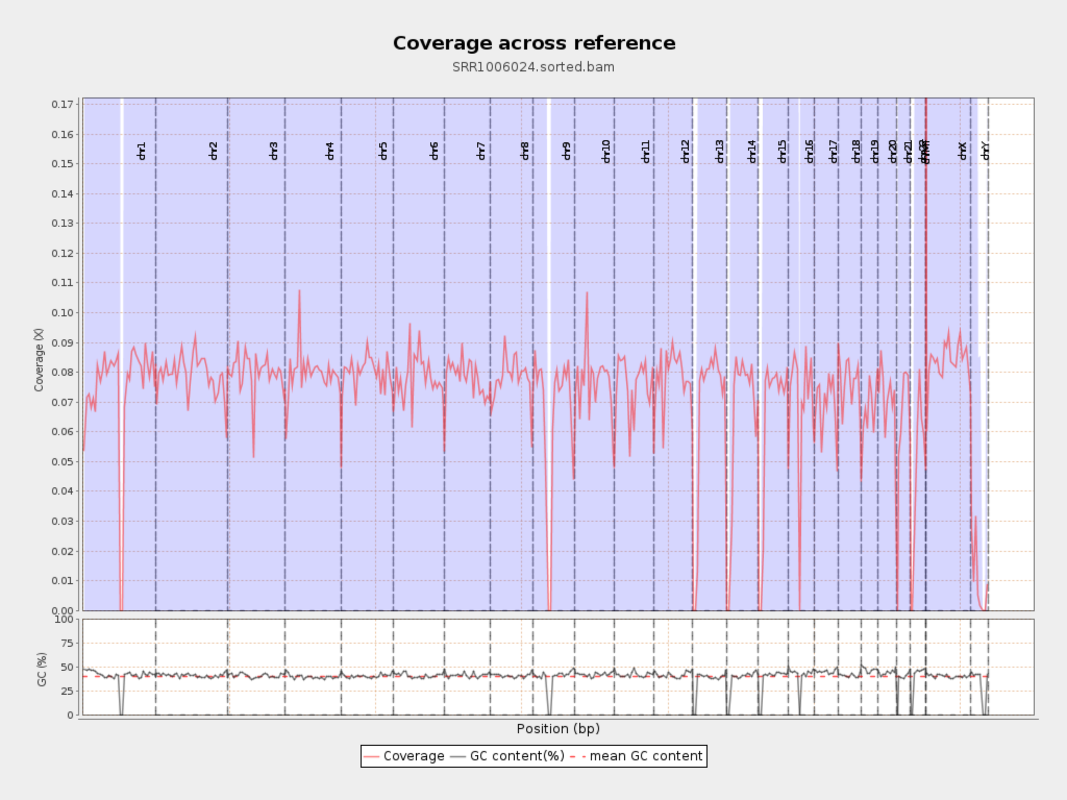
2.7. Chromosome stats

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

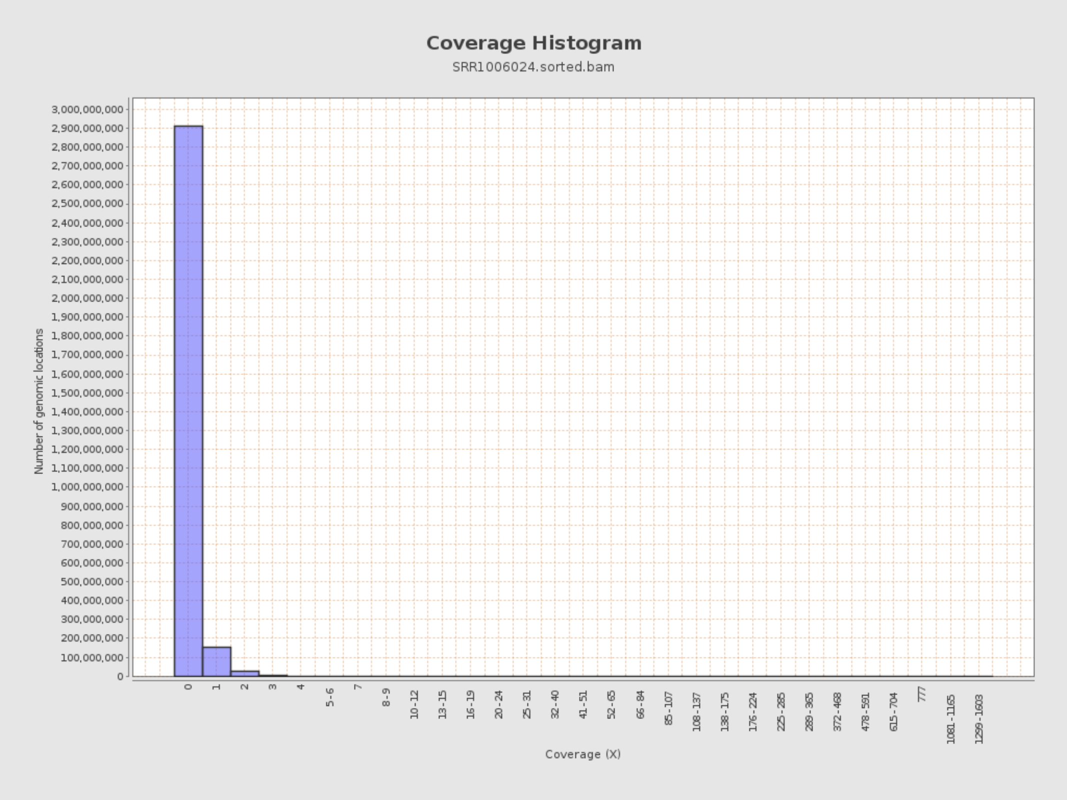
chr1	249250621	18475725	0.0741	0.5885
chr2	243199373	19272379	0.0792	0.3985
chr3	198022430	15825826	0.0799	0.3339
chr4	191154276	15235832	0.0797	0.3689
chr5	180915260	14454281	0.0799	0.3335
chr6	171115067	13455921	0.0786	0.4062
chr7	159138663	12402389	0.0779	0.461
chr8	146364022	11410984	0.078	0.8488
chr9	141213431	9226688	0.0653	0.3419
chr10	135534747	10498911	0.0775	0.4556
chr11	135006516	10236284	0.0758	0.3484
chr12	133851895	10567886	0.079	0.3325
chr13	115169878	7660782	0.0665	0.3039
chr14	107349540	6884378	0.0641	0.3152
chr15	102531392	6371390	0.0621	0.294
chr16	90354753	6196016	0.0686	0.3527
chr17	81195210	5661569	0.0697	0.3175
chr18	78077248	6007488	0.0769	0.4886
chr19	59128983	4007133	0.0678	0.4534
chr20	63025520	4521700	0.0717	0.3293
chr21	48129895	2997076	0.0623	0.3222
chr22	51304566	2350557	0.0458	0.2531
chrMT	16571	6402	0.3863	0.7941
chrX	155270560	13033427	0.0839	0.3643

chrY	59373566	578007	0.0097	0.2111

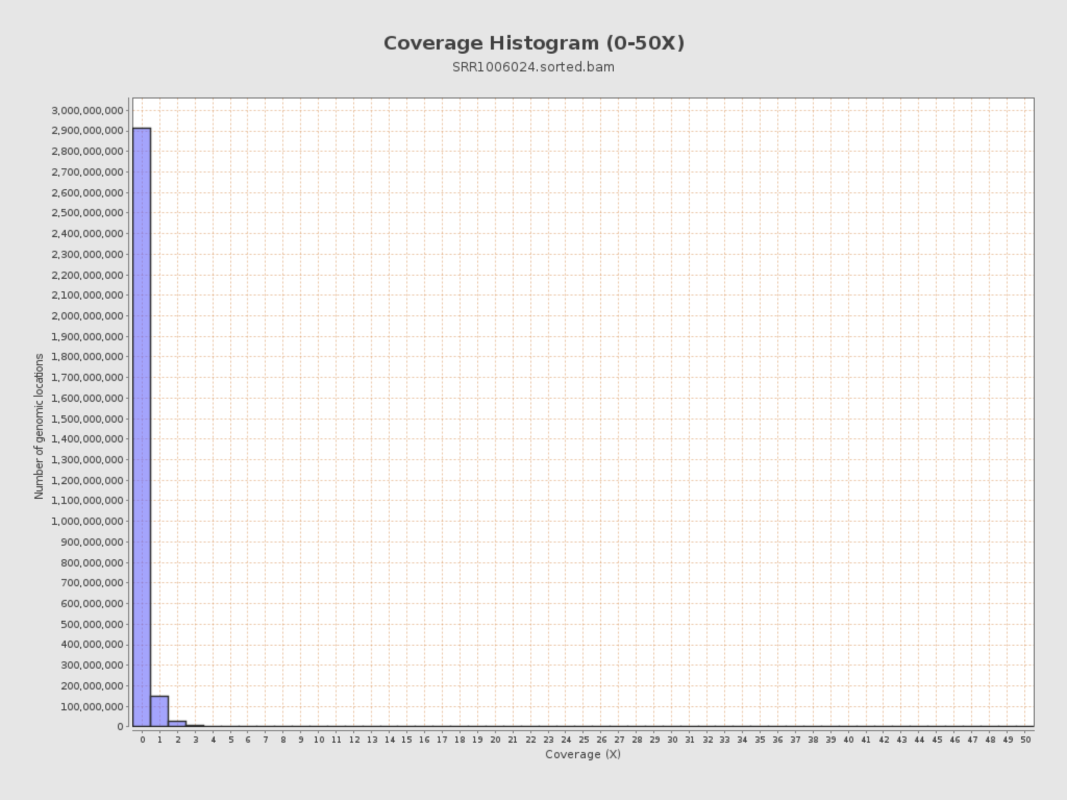
3. Results : Coverage across reference



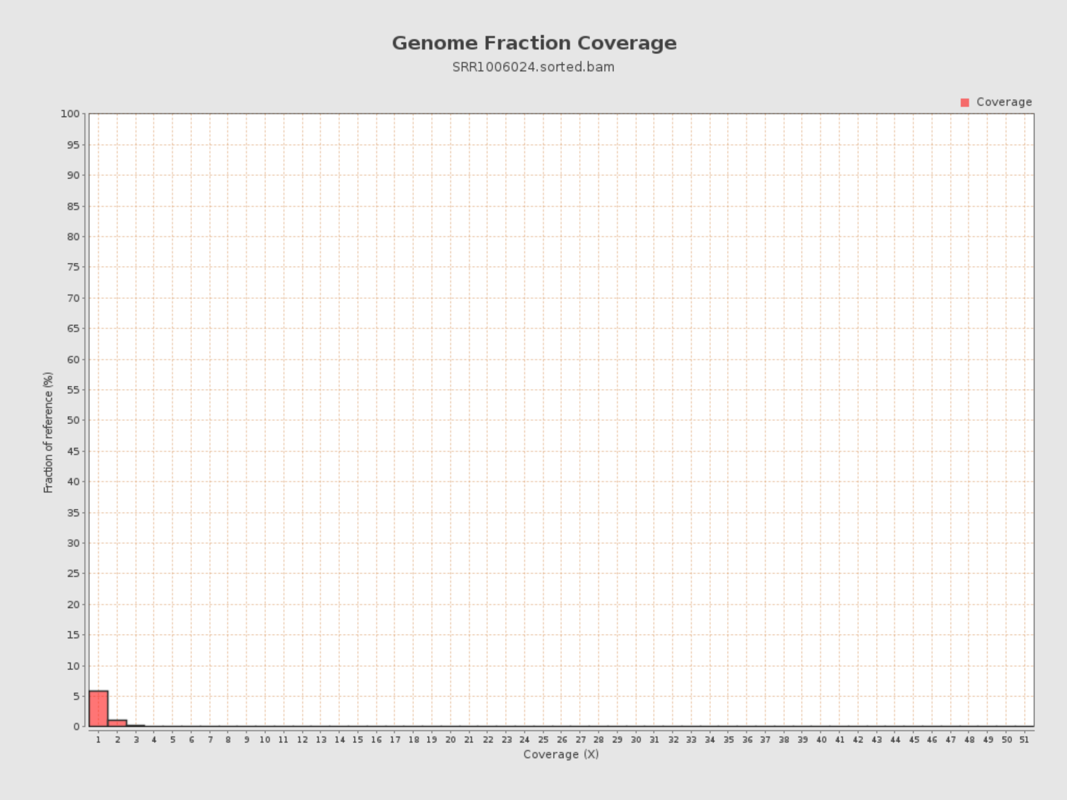
4. Results : Coverage Histogram



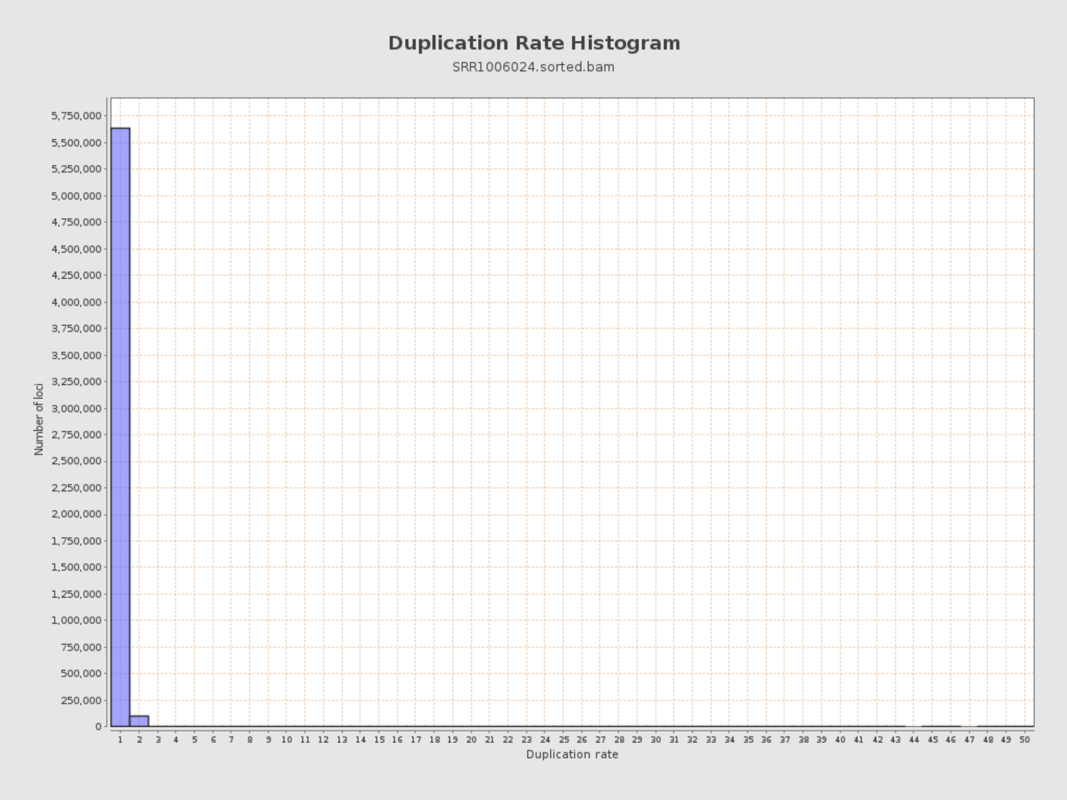
5. Results : Coverage Histogram (0-50X)



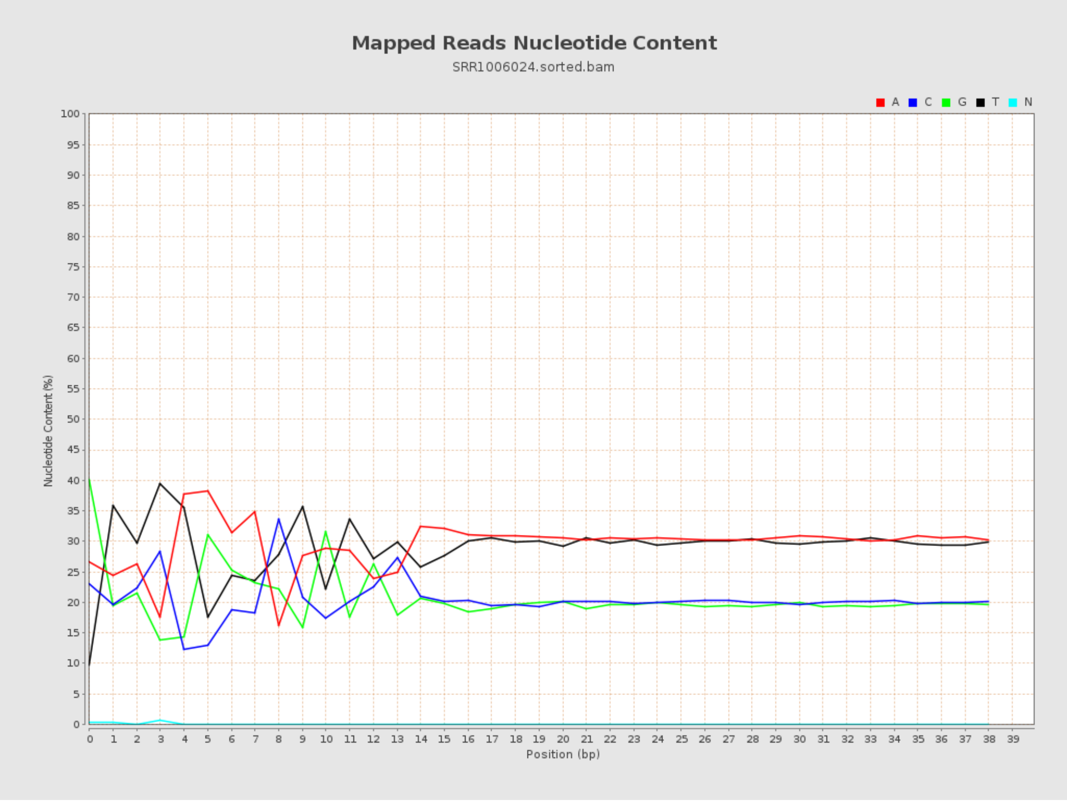
6. Results : Genome Fraction Coverage



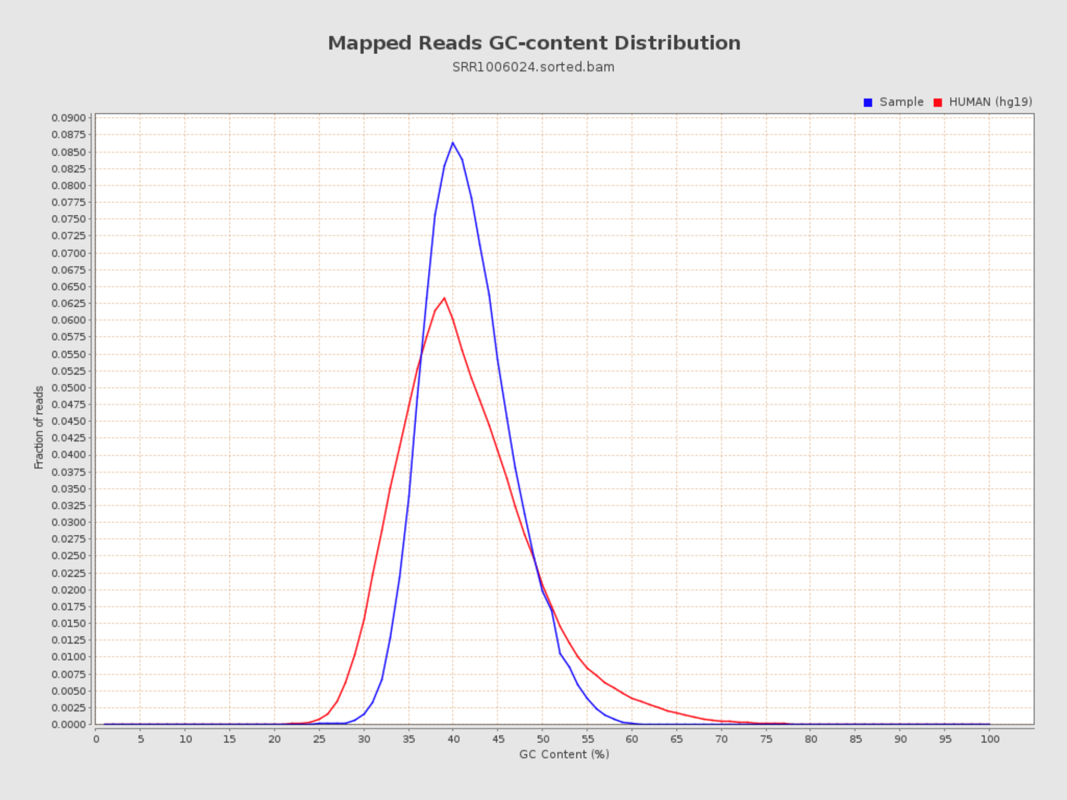
7. Results : Duplication Rate Histogram



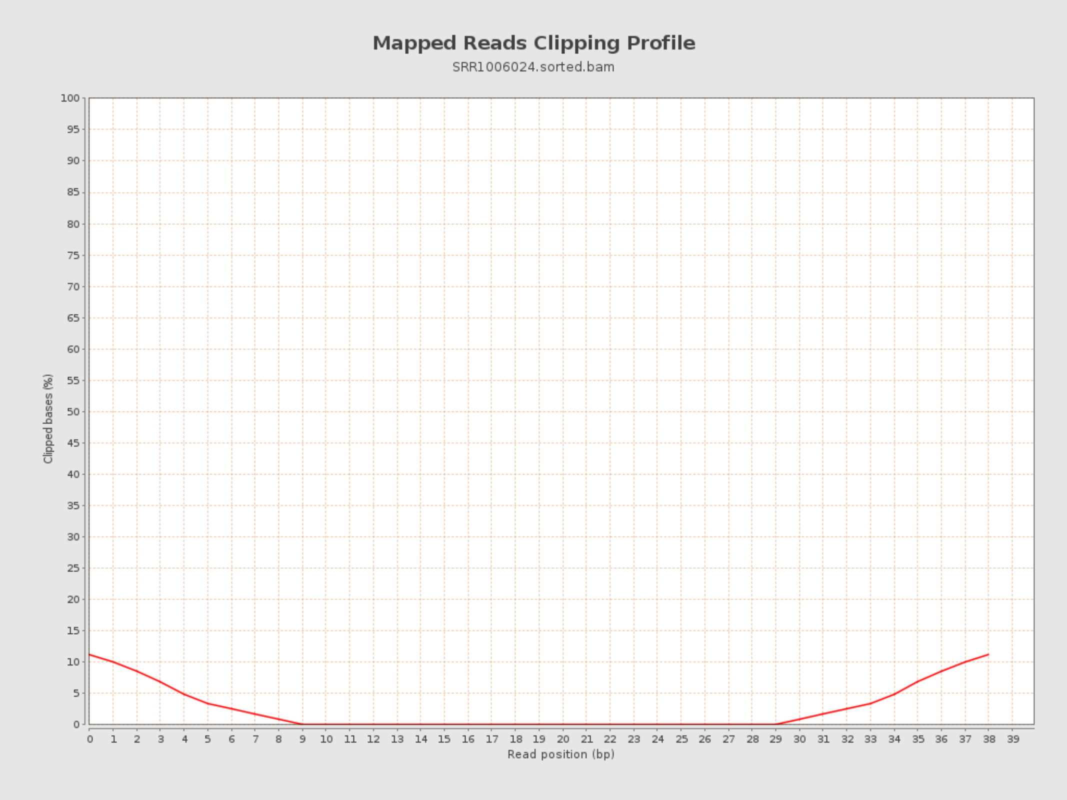
8. Results : Mapped Reads Nucleotide Content



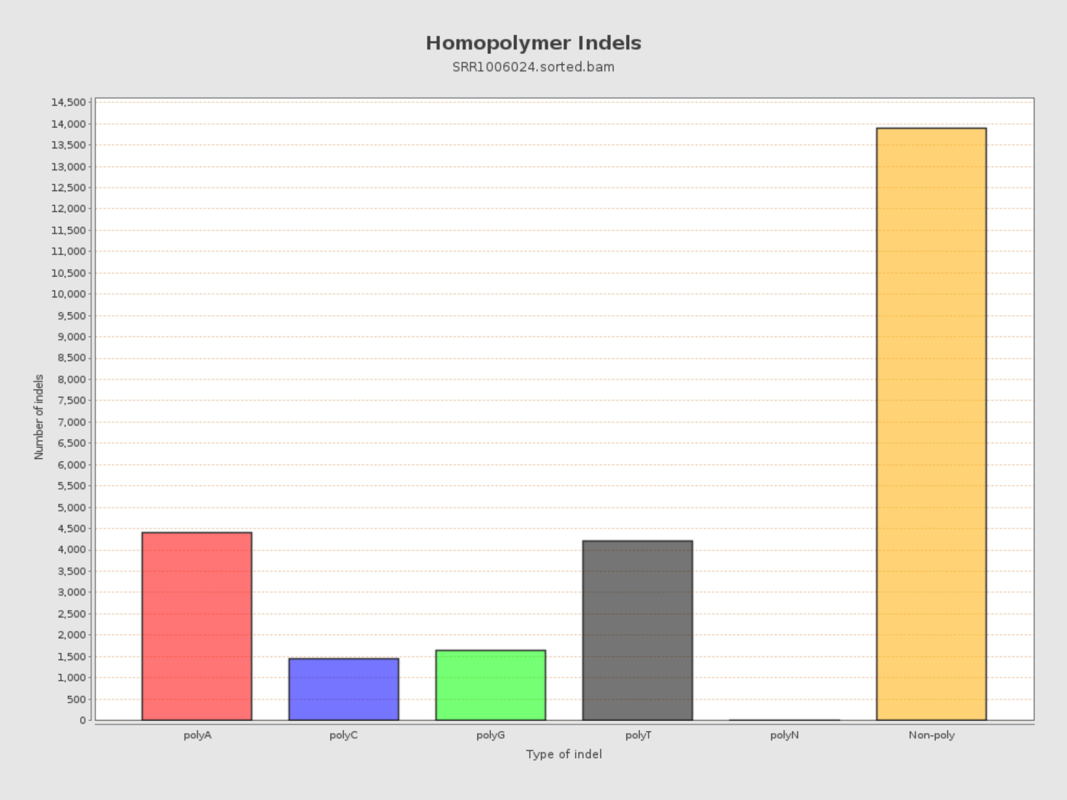
9. Results : Mapped Reads GC-content Distribution



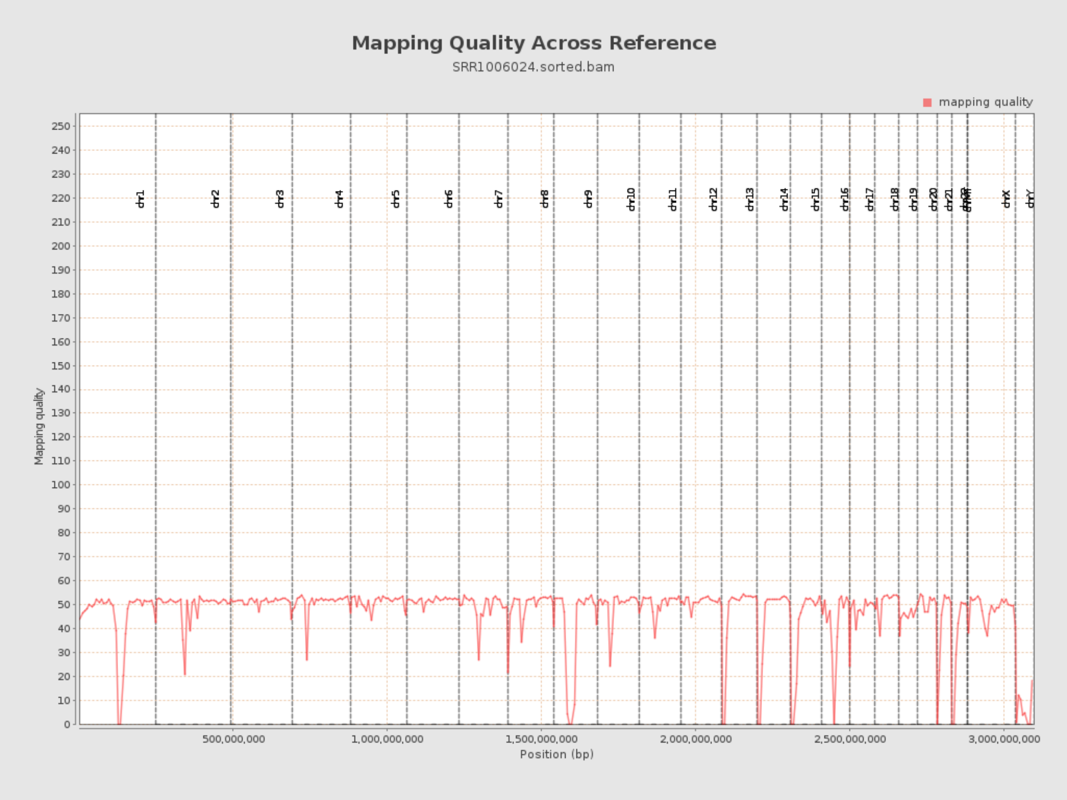
10. Results : Mapped Reads Clipping Profile



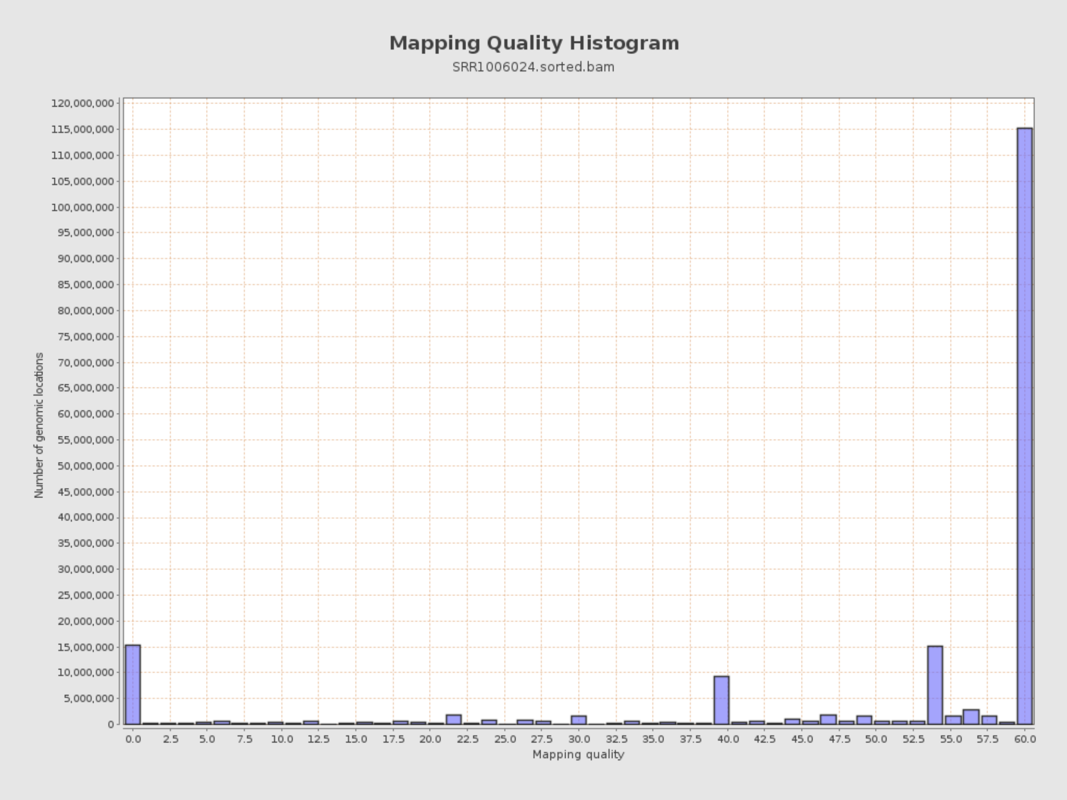
11. Results : Homopolymer Indels



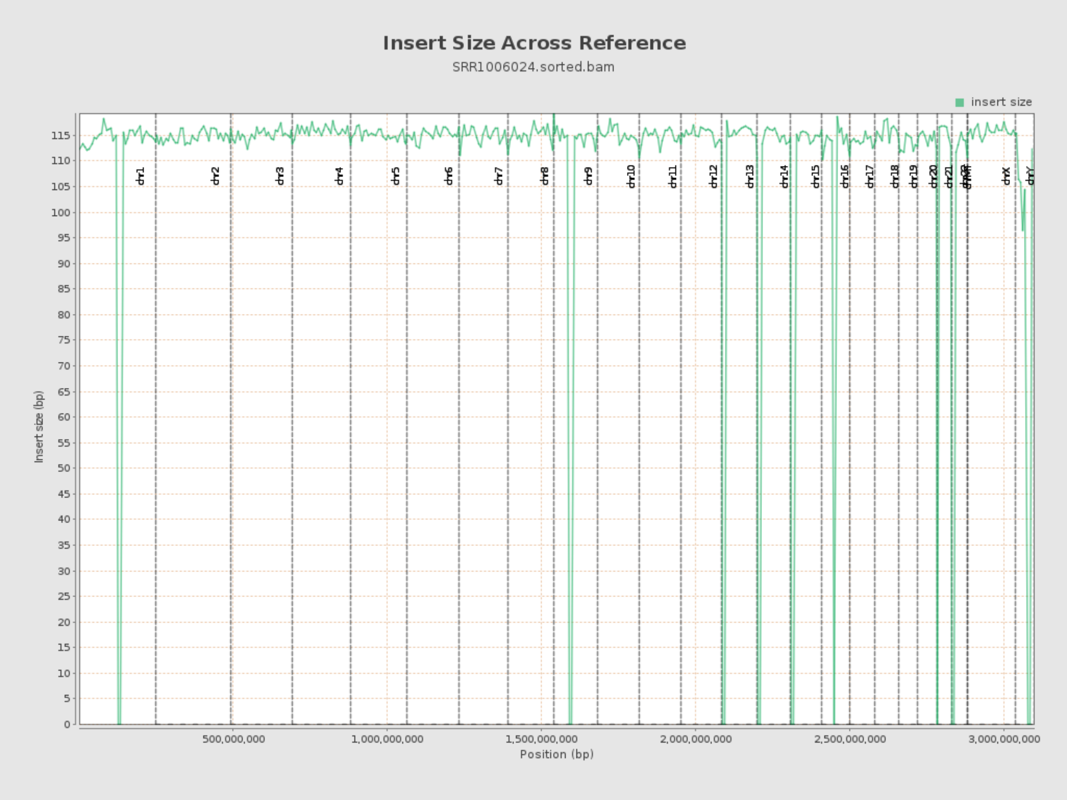
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram