Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 14:24:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006022.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_SRR1006022 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006022_1.fastq.gz SRR1006022_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 14:24:55 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006022.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,799,268
Mapped reads	16,905,843 / 71.04%
Unmapped reads	6,893,425 / 28.96%
Mapped paired reads	16,905,843 / 71.04%
Mapped reads, first in pair	8,528,584 / 35.84%
Mapped reads, second in pair	8,377,259 / 35.2%
Mapped reads, both in pair	15,035,856 / 63.18%
Mapped reads, singletons	1,869,987 / 7.86%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	899,767 / 3.78%
Duplication rate	4.41%
Clipped reads	1,284,668 / 5.4%

2.2. ACGT Content

Number/percentage of A's	190,592,237 / 29.18%
Number/percentage of C's	134,792,849 / 20.63%
Number/percentage of T's	191,032,002 / 29.24%
Number/percentage of G's	136,727,722 / 20.93%
Number/percentage of N's	79,634 / 0.01%
GC Percentage	41.57%

2.3. Coverage

Mean	0.211
Standard Deviation	1.0658

2.4. Mapping Quality

Mean Mapping Quality	47.27

2.5. Insert size

Mean	64,719.46
Standard Deviation	2,445,876.12
P25/Median/P75	65 / 92 / 134

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	3,874,363
Insertions	19,375
Mapped reads with at least one insertion	0.11%
Deletions	58,089
Mapped reads with at least one deletion	0.34%
Homopolymer indels	45.66%

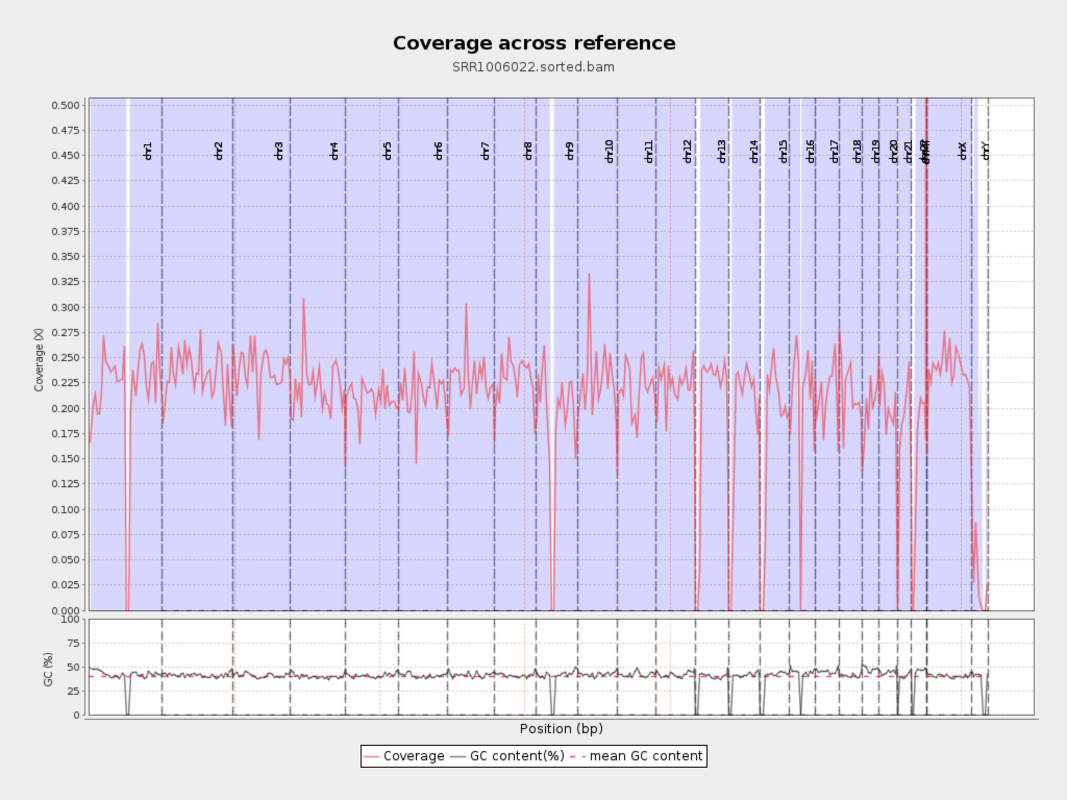
2.7. Chromosome stats

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

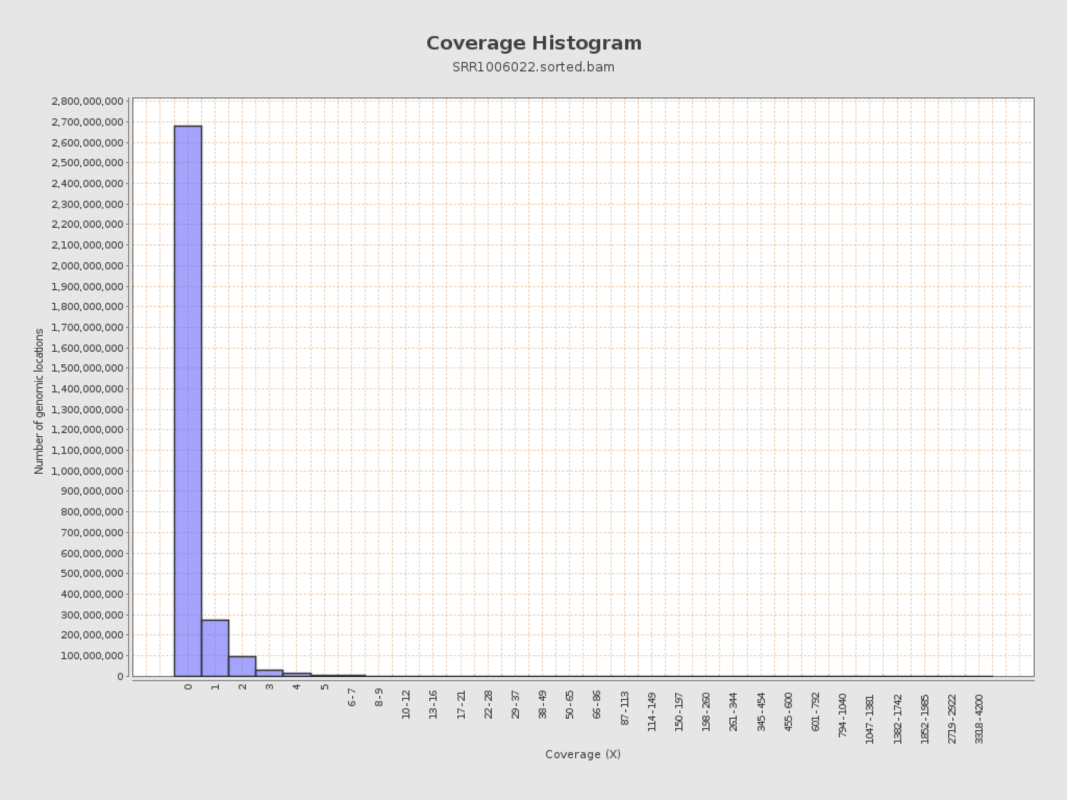
chr1	249250621	53869269	0.2161	1.6696
chr2	243199373	56581929	0.2327	0.9621
chr3	198022430	47254761	0.2386	0.6892
chr4	191154276	42242153	0.221	0.7909
chr5	180915260	38099101	0.2106	0.6529
chr6	171115067	36887202	0.2156	0.9678
chr7	159138663	36666341	0.2304	1.4843
chr8	146364022	33776581	0.2308	2.2072
chr9	141213431	25850452	0.1831	0.8139
chr10	135534747	31164560	0.2299	1.1945
chr11	135006516	29565602	0.219	0.8395
chr12	133851895	29878851	0.2232	0.6775
chr13	115169878	22538037	0.1957	0.6245
chr14	107349540	19690600	0.1834	0.672
chr15	102531392	17887143	0.1745	0.5887
chr16	90354753	18848340	0.2086	0.82
chr17	81195210	17107965	0.2107	0.7293
chr18	78077248	16898568	0.2164	1.1891
chr19	59128983	11922406	0.2016	1.3203
chr20	63025520	12553607	0.1992	0.6668
chr21	48129895	8413861	0.1748	0.7102
chr22	51304566	7117411	0.1387	0.5371
chrMT	16571	41073	2.4786	2.5386
chrX	155270560	36843061	0.2373	0.8199

chrY	59373566	1599314	0.0269	0.5336

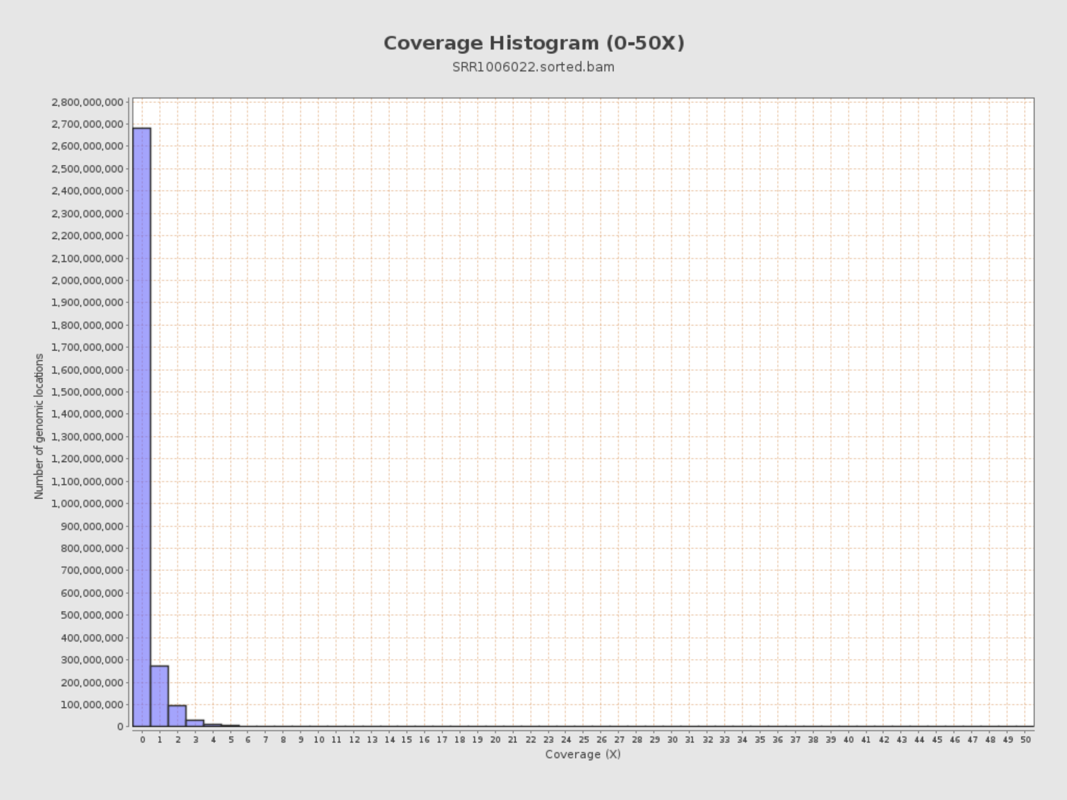
3. Results : Coverage across reference



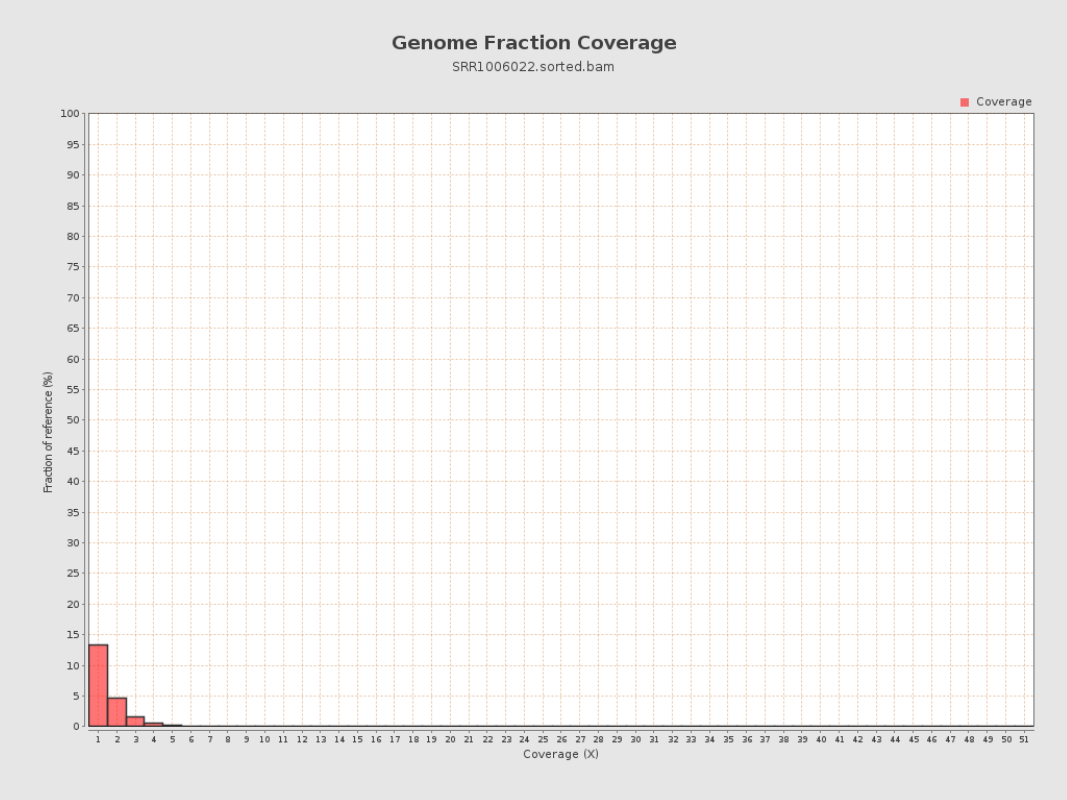
4. Results : Coverage Histogram



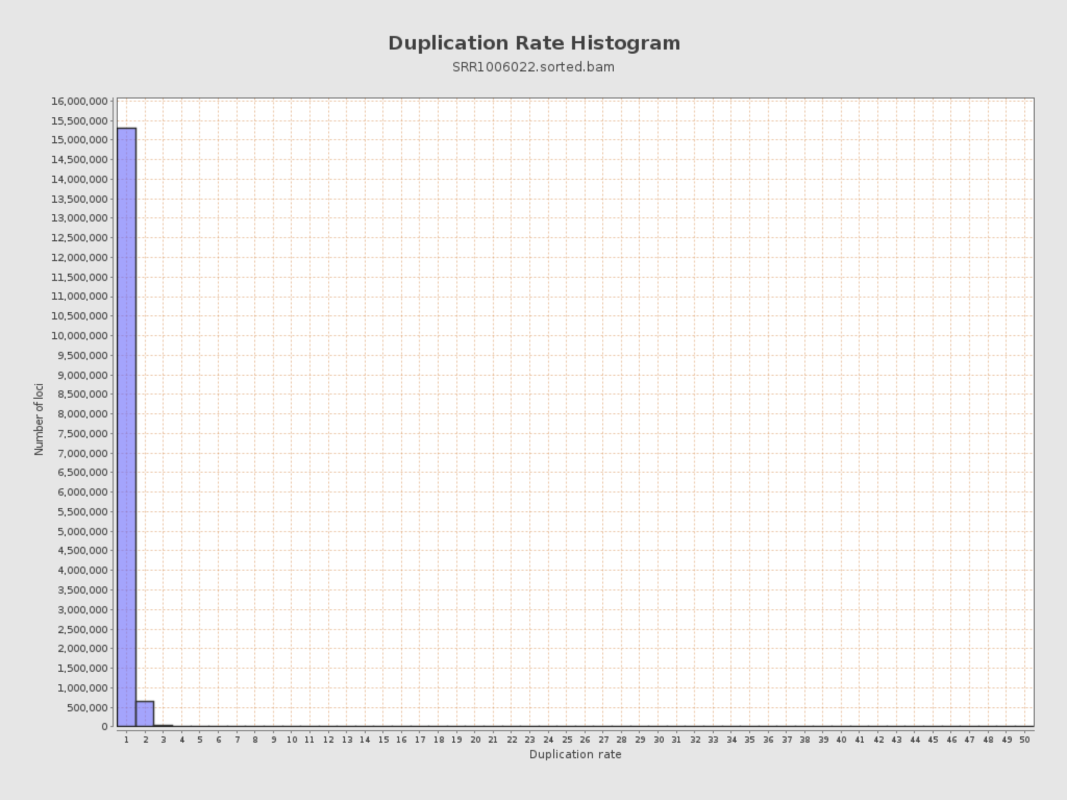
5. Results : Coverage Histogram (0-50X)



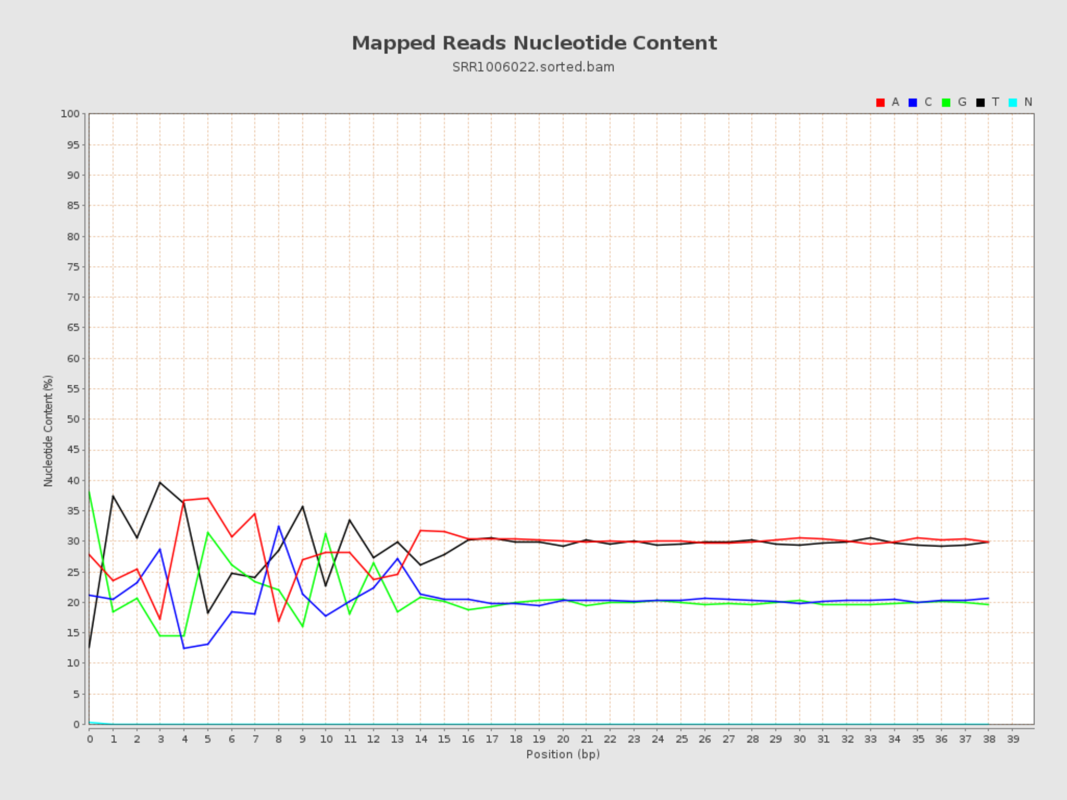
6. Results : Genome Fraction Coverage



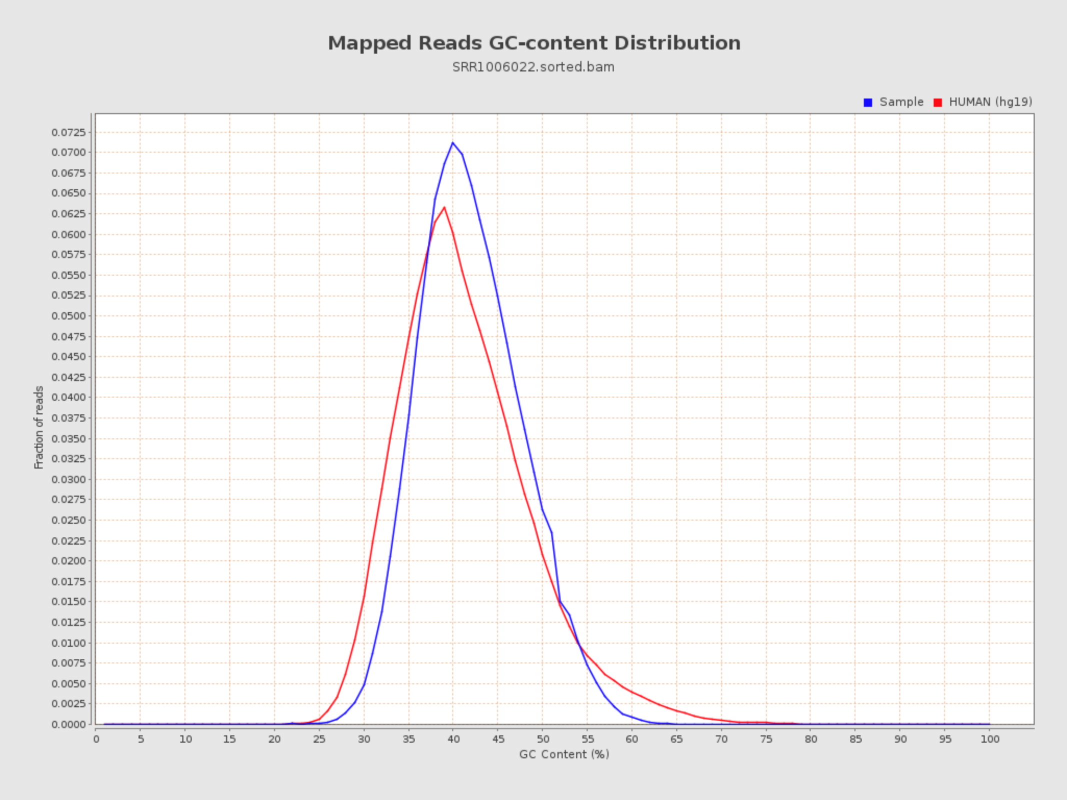
7. Results : Duplication Rate Histogram



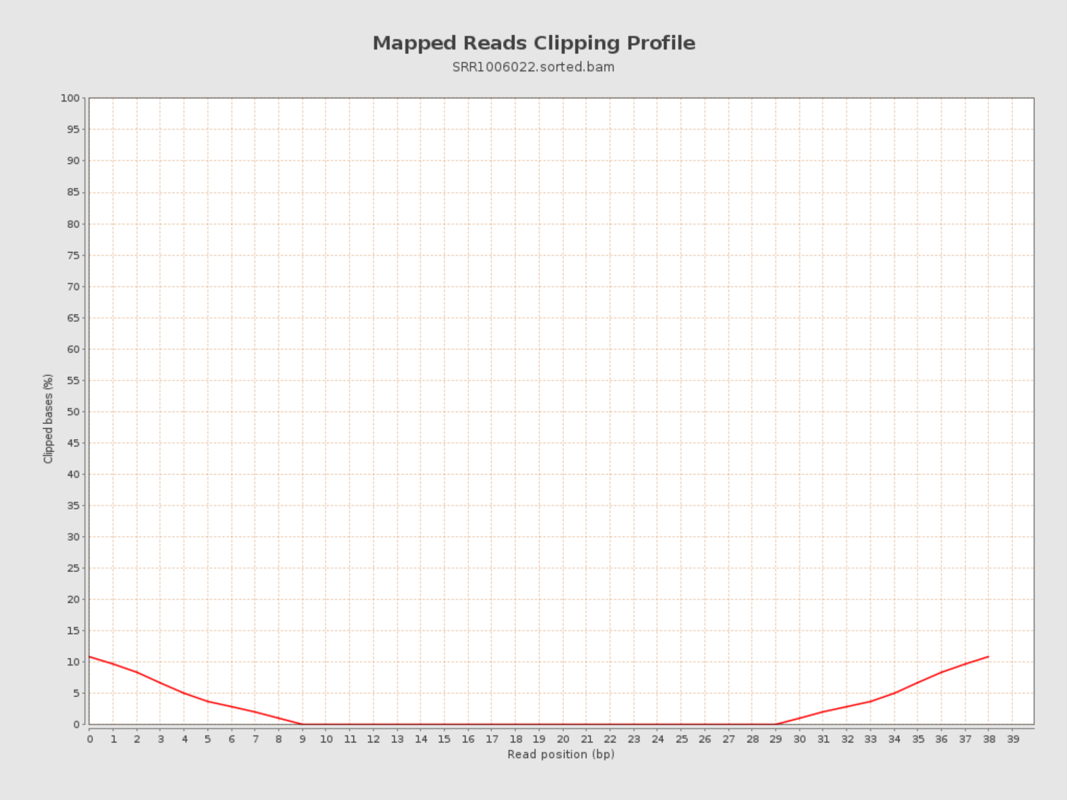
8. Results : Mapped Reads Nucleotide Content



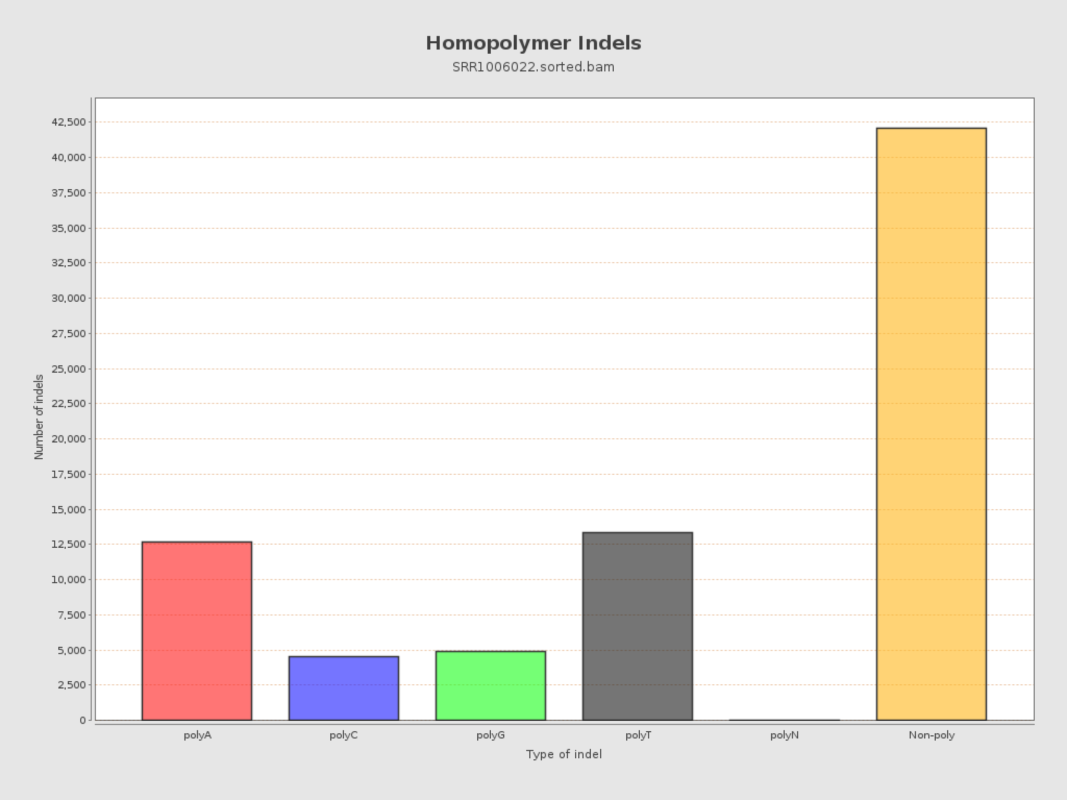
9. Results : Mapped Reads GC-content Distribution



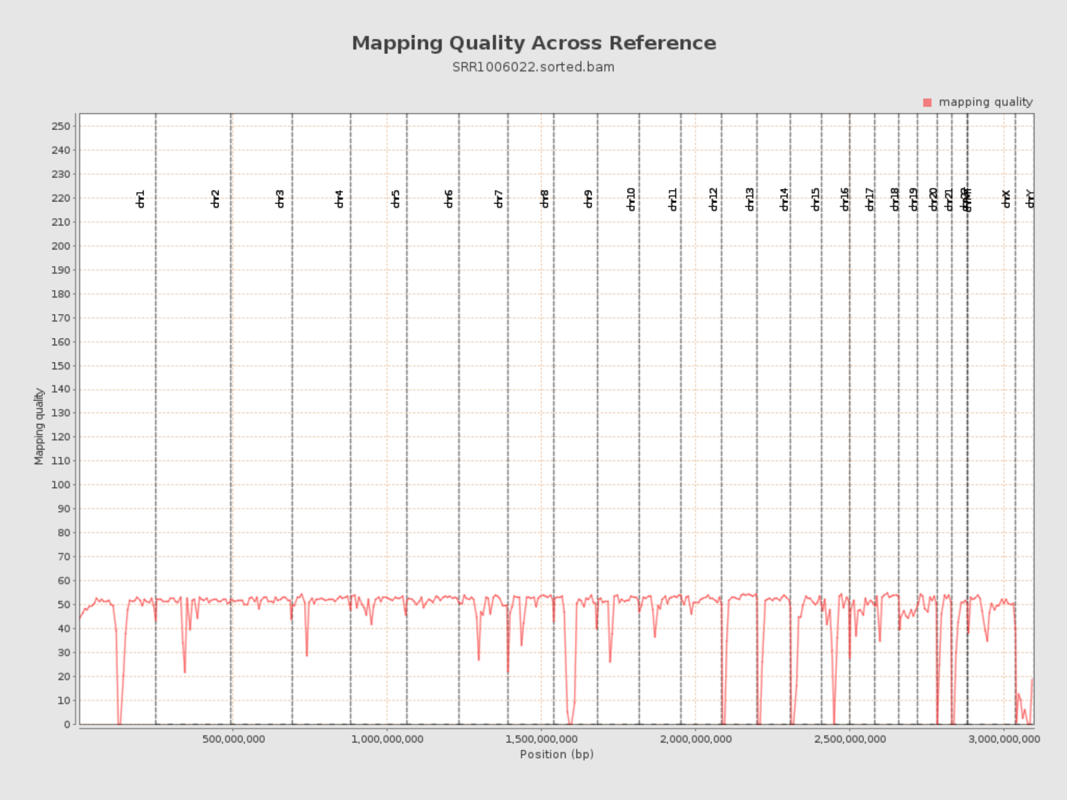
10. Results : Mapped Reads Clipping Profile



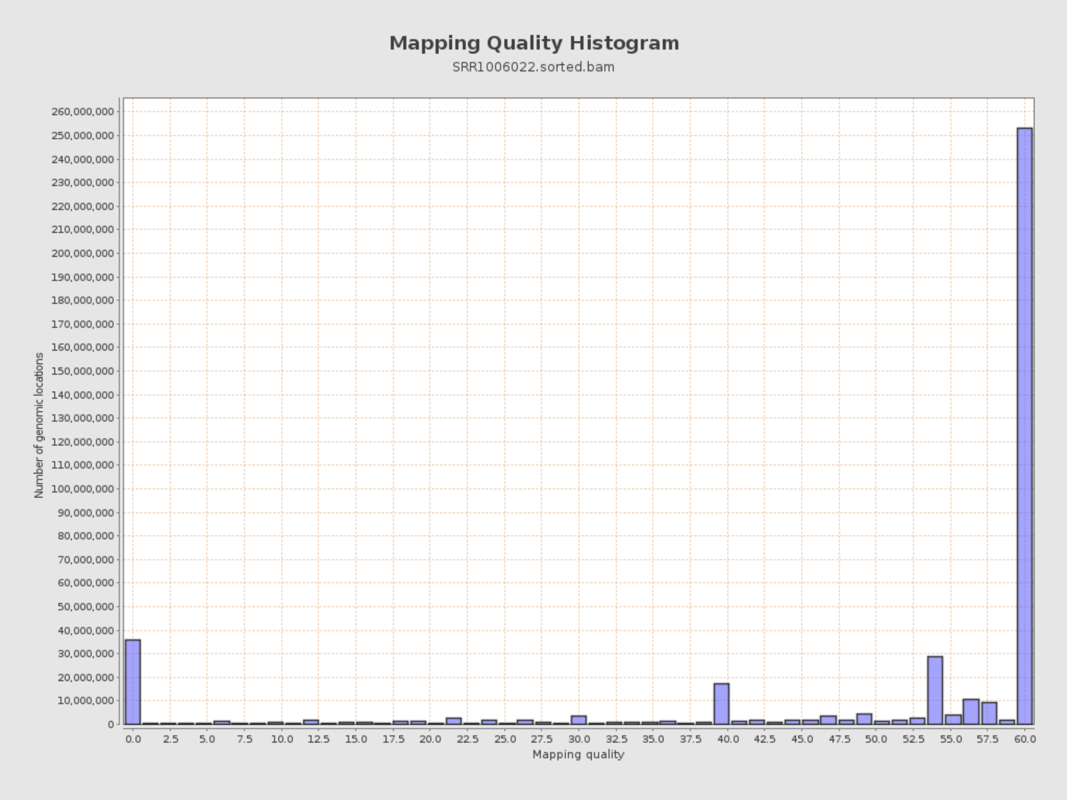
11. Results : Homopolymer Indels



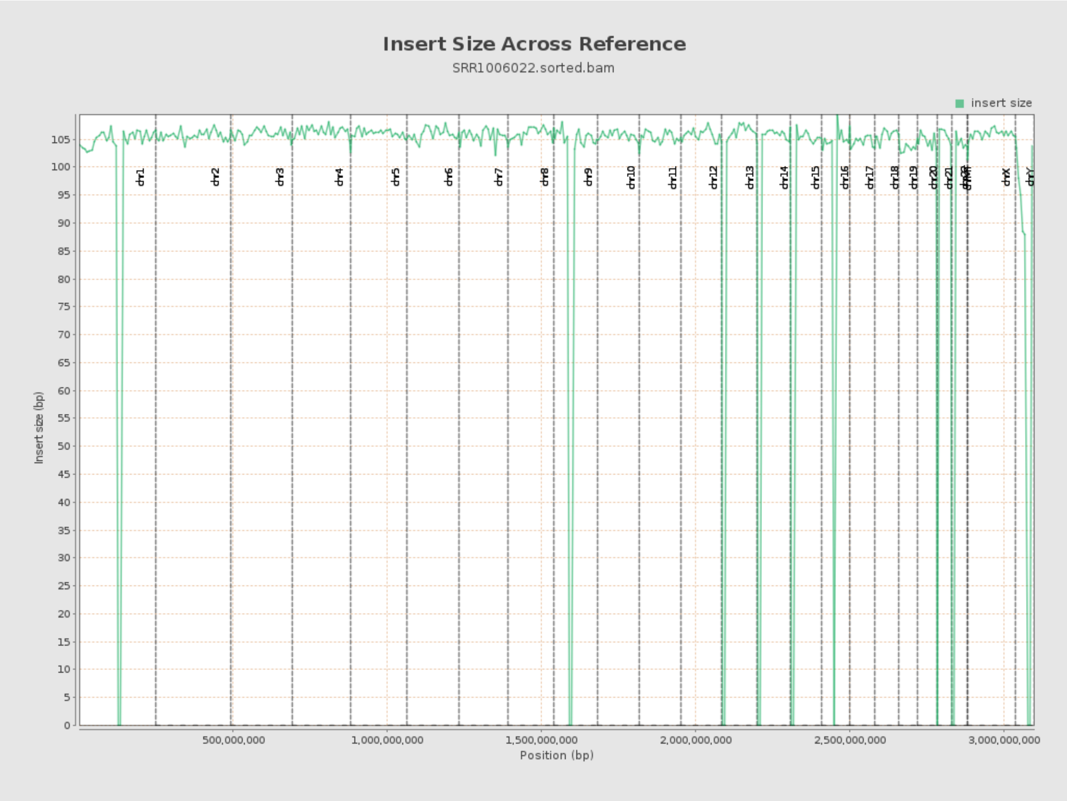
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram