Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 00:17:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006229.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_SRR1006229 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006229_1.fastq.gz SRR1006229_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 00:17:07 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006229.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,492,084
Mapped reads	2,187,945 / 87.8%
Unmapped reads	304,139 / 12.2%
Mapped paired reads	2,187,945 / 87.8%
Mapped reads, first in pair	1,103,475 / 44.28%
Mapped reads, second in pair	1,084,470 / 43.52%
Mapped reads, both in pair	2,025,428 / 81.27%
Mapped reads, singletons	162,517 / 6.52%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	63,591 / 2.55%
Duplication rate	2.61%
Clipped reads	157,541 / 6.32%

2.2. ACGT Content

Number/percentage of A's	22,961,787 / 27.17%
Number/percentage of C's	18,818,067 / 22.26%
Number/percentage of T's	23,447,361 / 27.74%
Number/percentage of G's	19,292,712 / 22.83%
Number/percentage of N's	3,453 / 0%
GC Percentage	45.09%

2.3. Coverage

Mean	0.0273
Standard Deviation	0.2118

2.4. Mapping Quality

Mean Mapping Quality	47.44

2.5. Insert size

Mean	82,617.14
Standard Deviation	2,811,437.76
P25/Median/P75	81 / 132 / 172

2.6. Mismatches and indels

General error rate	0.41%
Mismatches	341,150
Insertions	2,534
Mapped reads with at least one insertion	0.12%
Deletions	7,518
Mapped reads with at least one deletion	0.34%
Homopolymer indels	40.97%

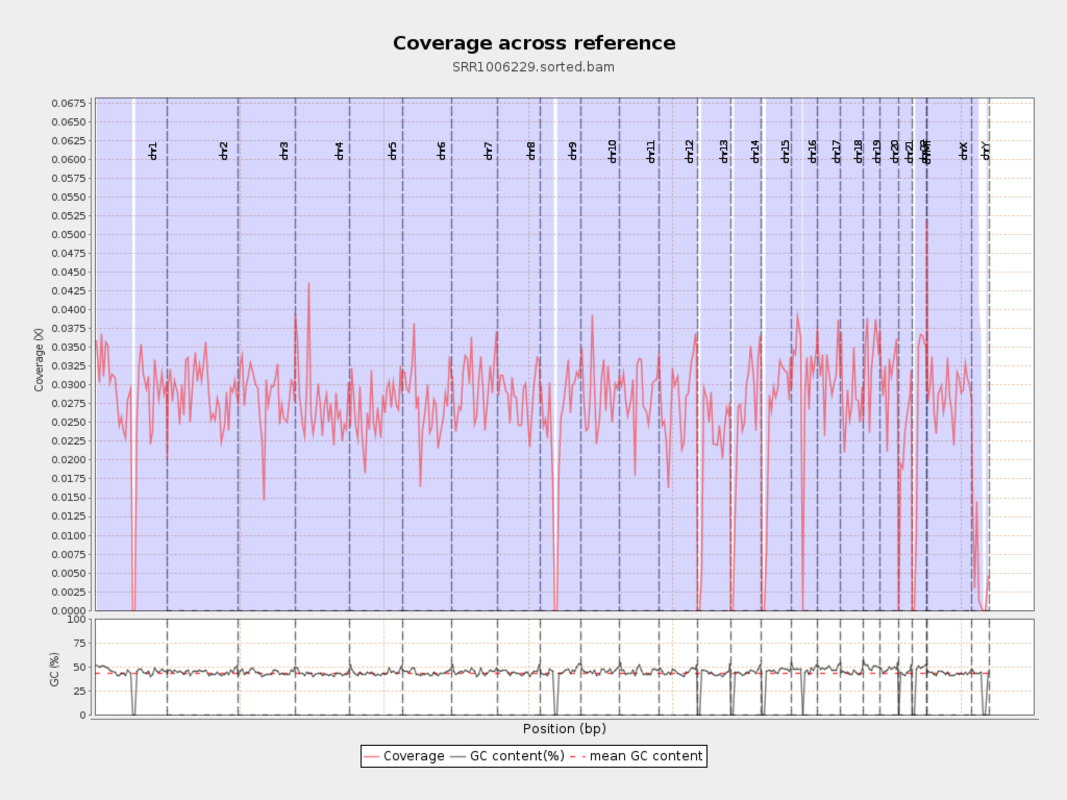
2.7. Chromosome stats

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

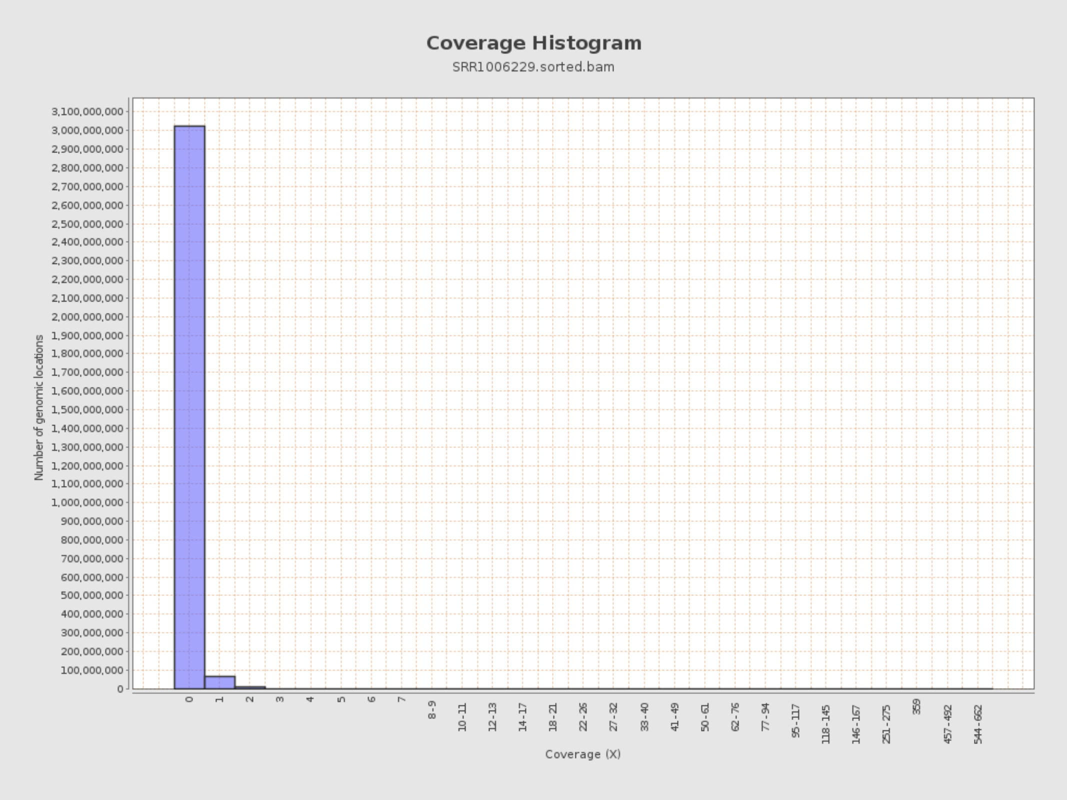
chr1	249250621	6957348	0.0279	0.2304
chr2	243199373	7059480	0.029	0.2078
chr3	198022430	5660725	0.0286	0.1884
chr4	191154276	5291777	0.0277	0.2013
chr5	180915260	4876382	0.027	0.1837
chr6	171115067	4729068	0.0276	0.1906
chr7	159138663	4770118	0.03	0.2266
chr8	146364022	4169035	0.0285	0.3733
chr9	141213431	3418459	0.0242	0.185
chr10	135534747	3943511	0.0291	0.2252
chr11	135006516	3891190	0.0288	0.1991
chr12	133851895	3708815	0.0277	0.1875
chr13	115169878	2417410	0.021	0.1622
chr14	107349540	2643194	0.0246	0.2042
chr15	102531392	2476399	0.0242	0.1734
chr16	90354753	2737684	0.0303	0.2093
chr17	81195210	2573997	0.0317	0.206
chr18	78077248	2189358	0.028	0.2244
chr19	59128983	1995163	0.0337	0.2274
chr20	63025520	1957654	0.0311	0.2064
chr21	48129895	1061779	0.0221	0.1802
chr22	51304566	1245774	0.0243	0.1829
chrMT	16571	858	0.0518	0.2521
chrX	155270560	4499030	0.029	0.193

chrY	59373566	259179	0.0044	0.1249

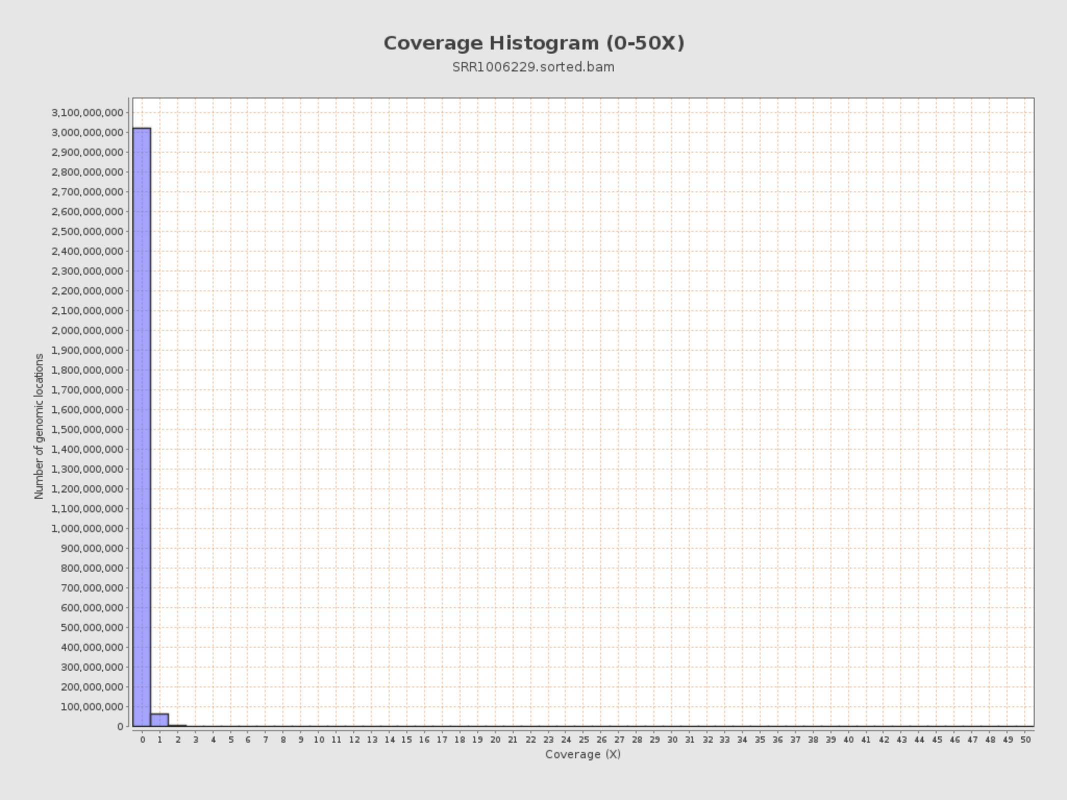
3. Results : Coverage across reference



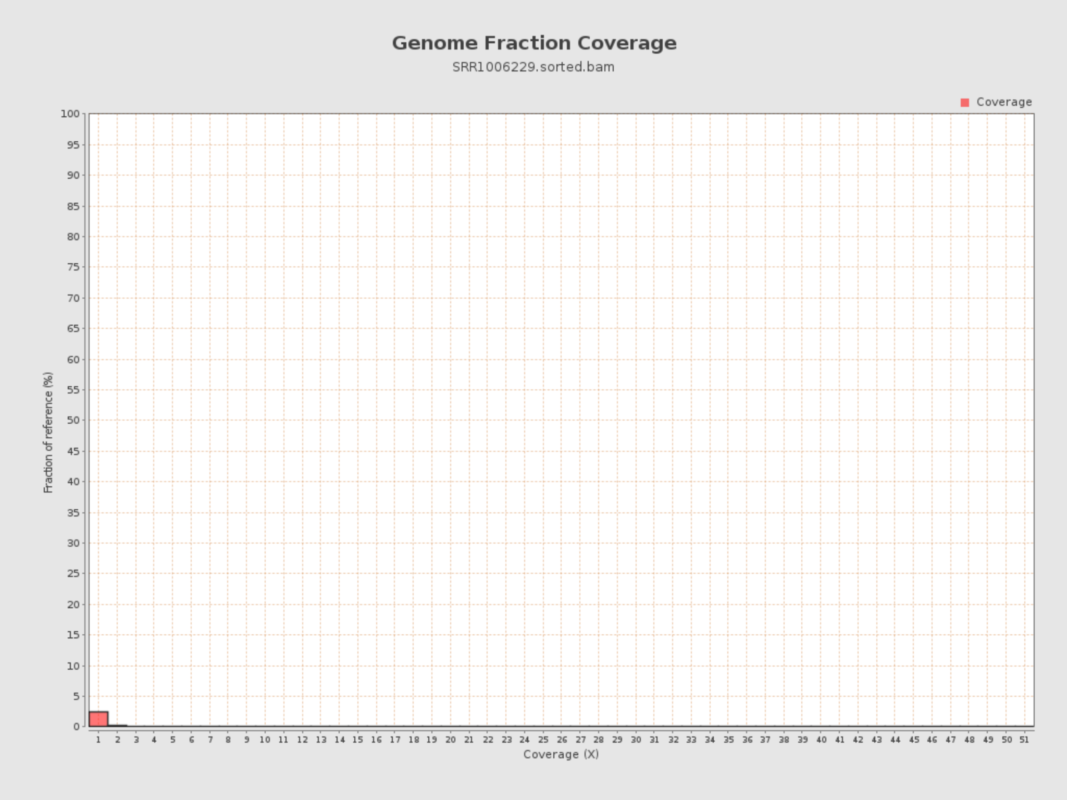
4. Results : Coverage Histogram



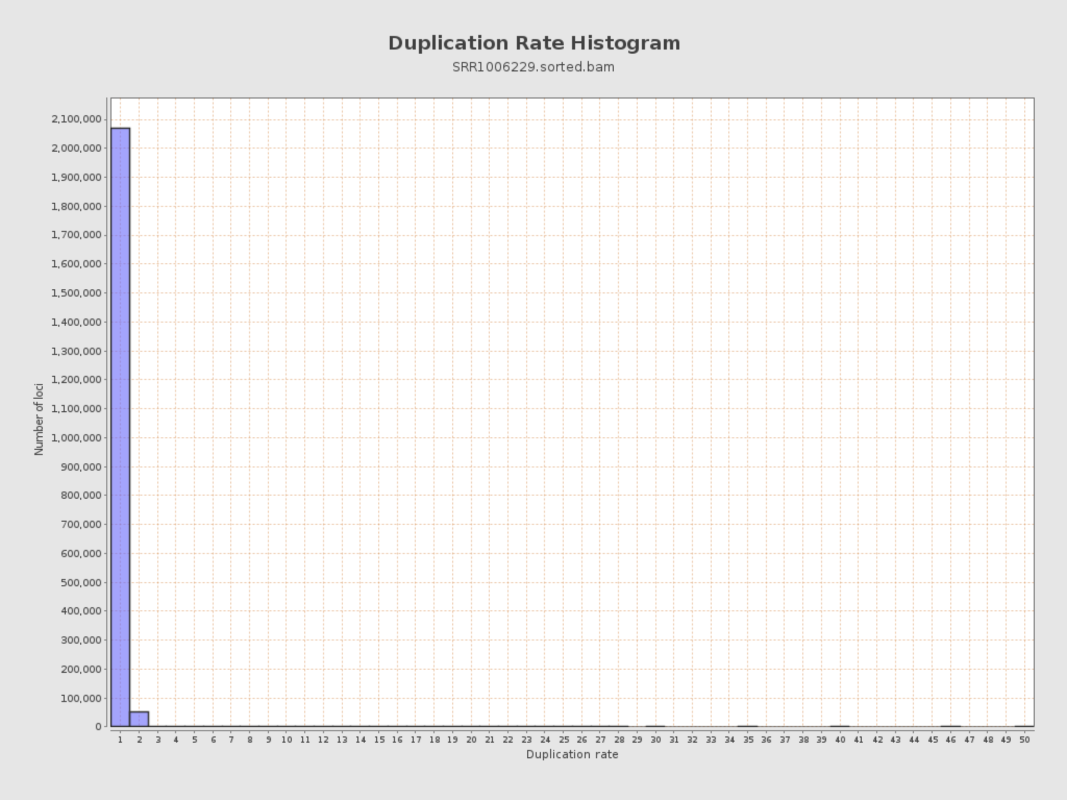
5. Results : Coverage Histogram (0-50X)



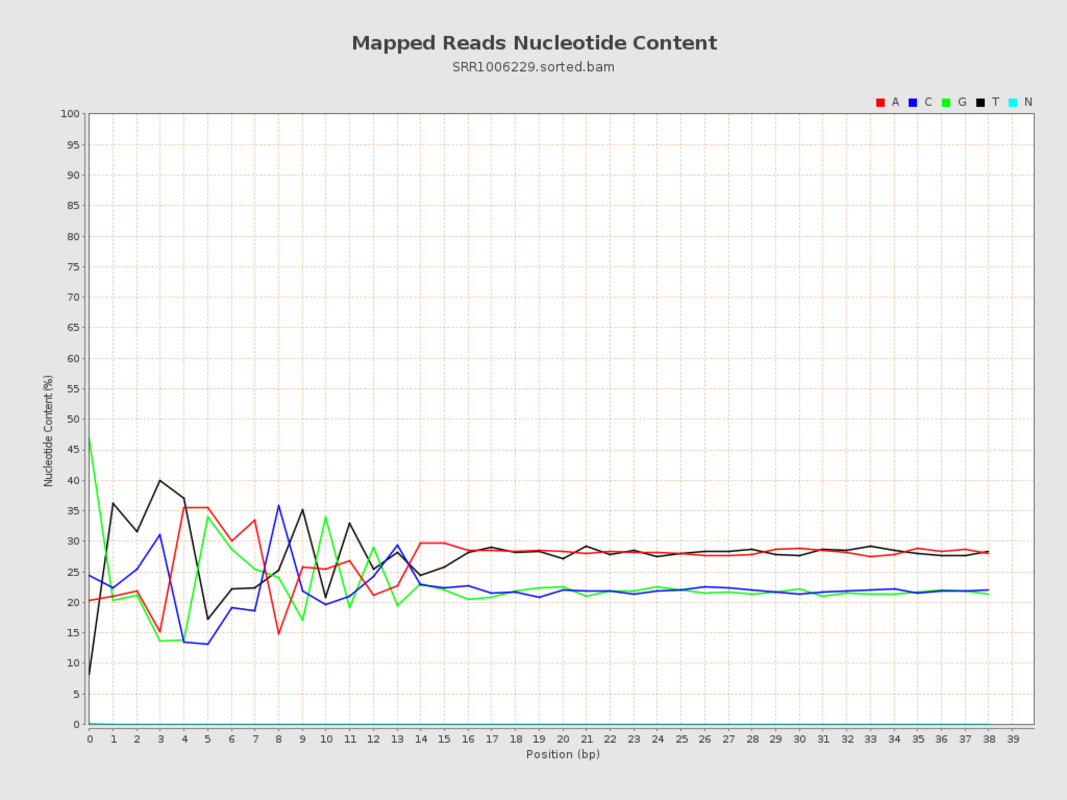
6. Results : Genome Fraction Coverage



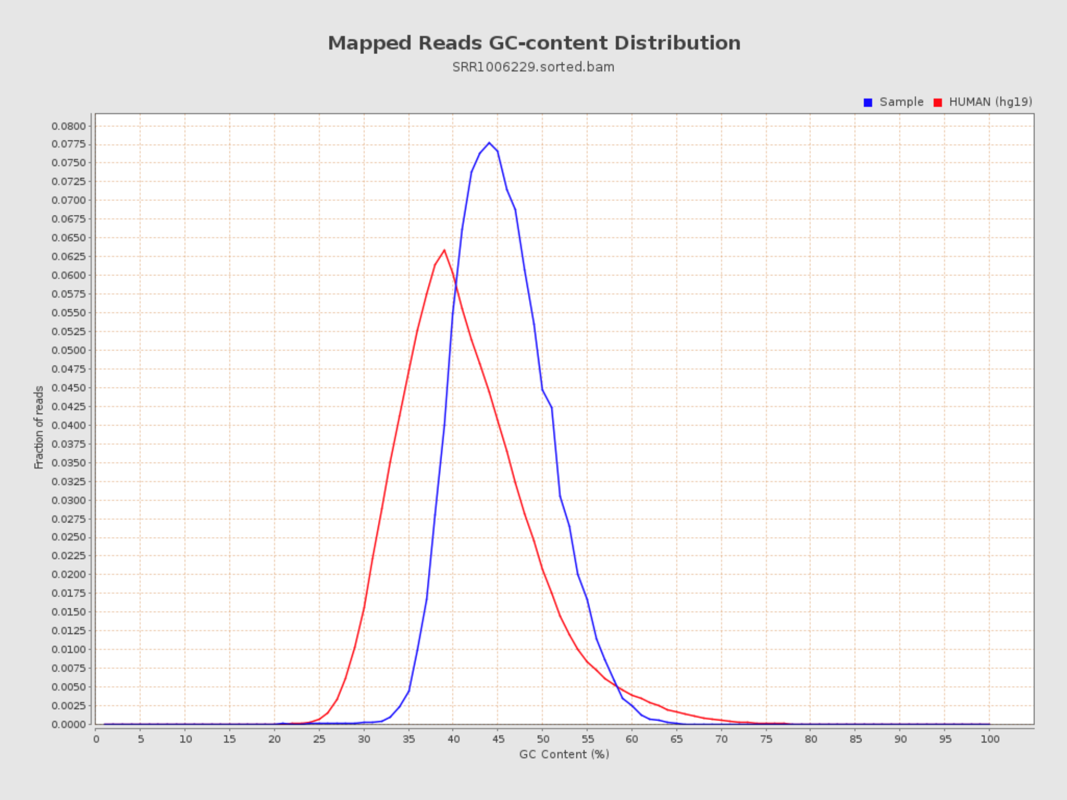
7. Results : Duplication Rate Histogram



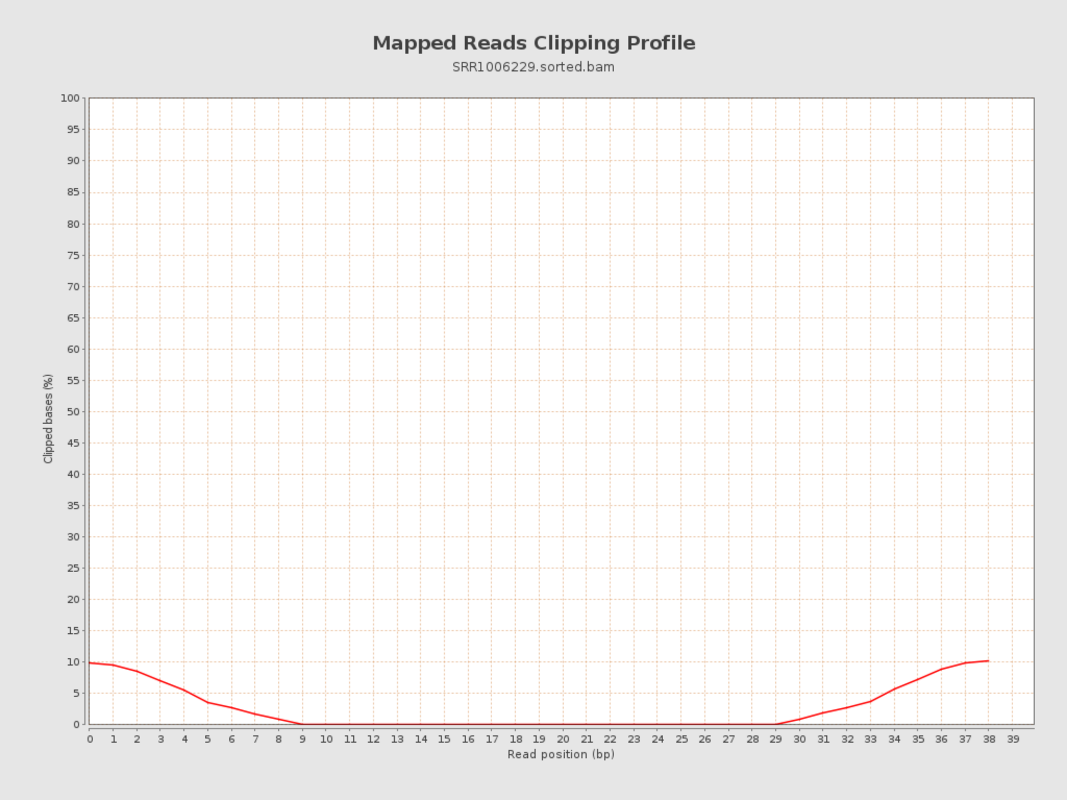
8. Results : Mapped Reads Nucleotide Content



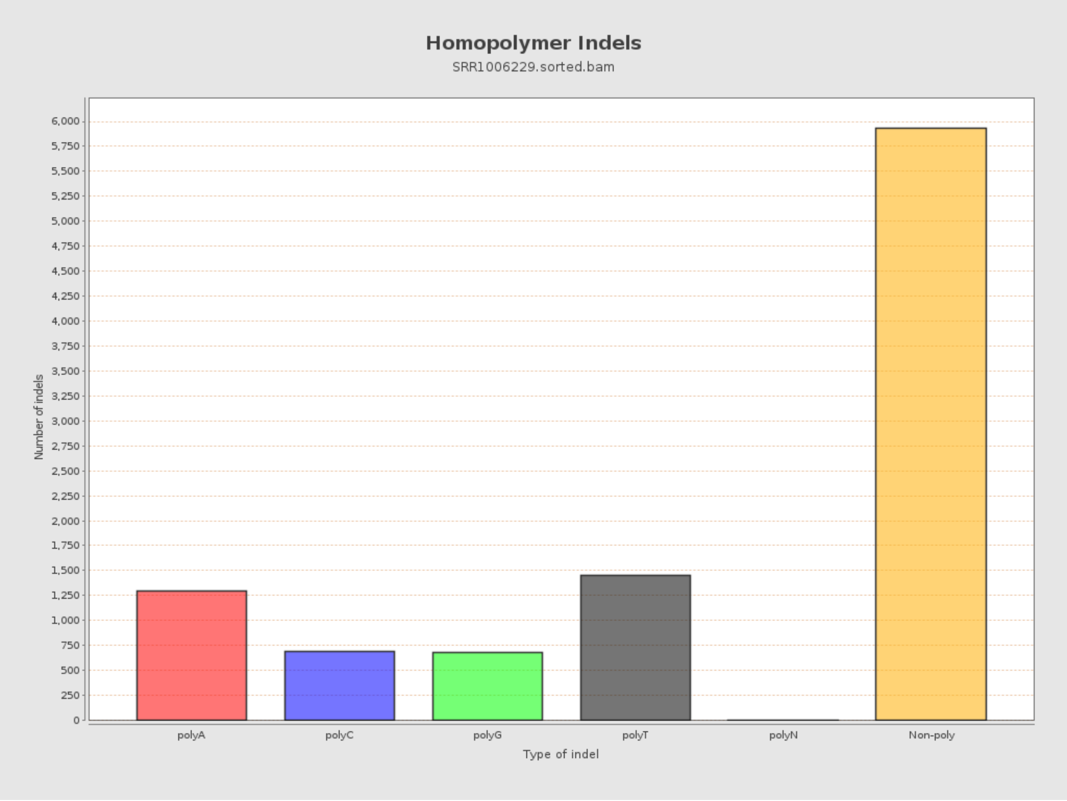
9. Results : Mapped Reads GC-content Distribution



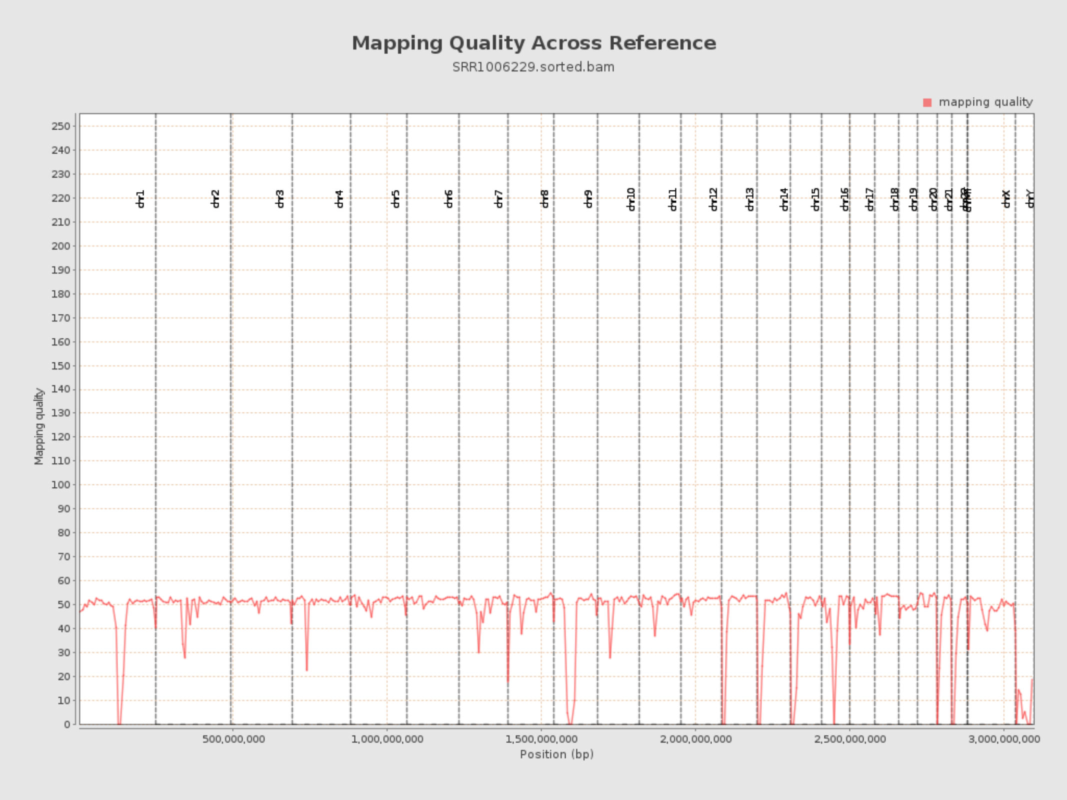
10. Results : Mapped Reads Clipping Profile



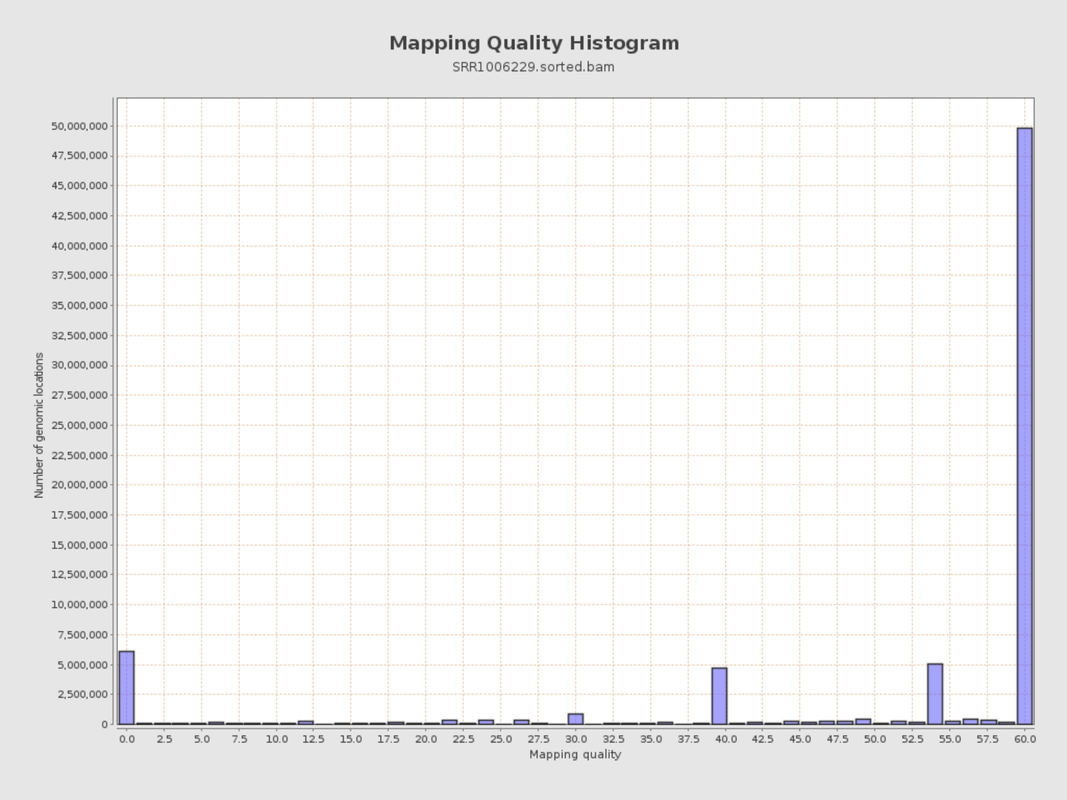
11. Results : Homopolymer Indels



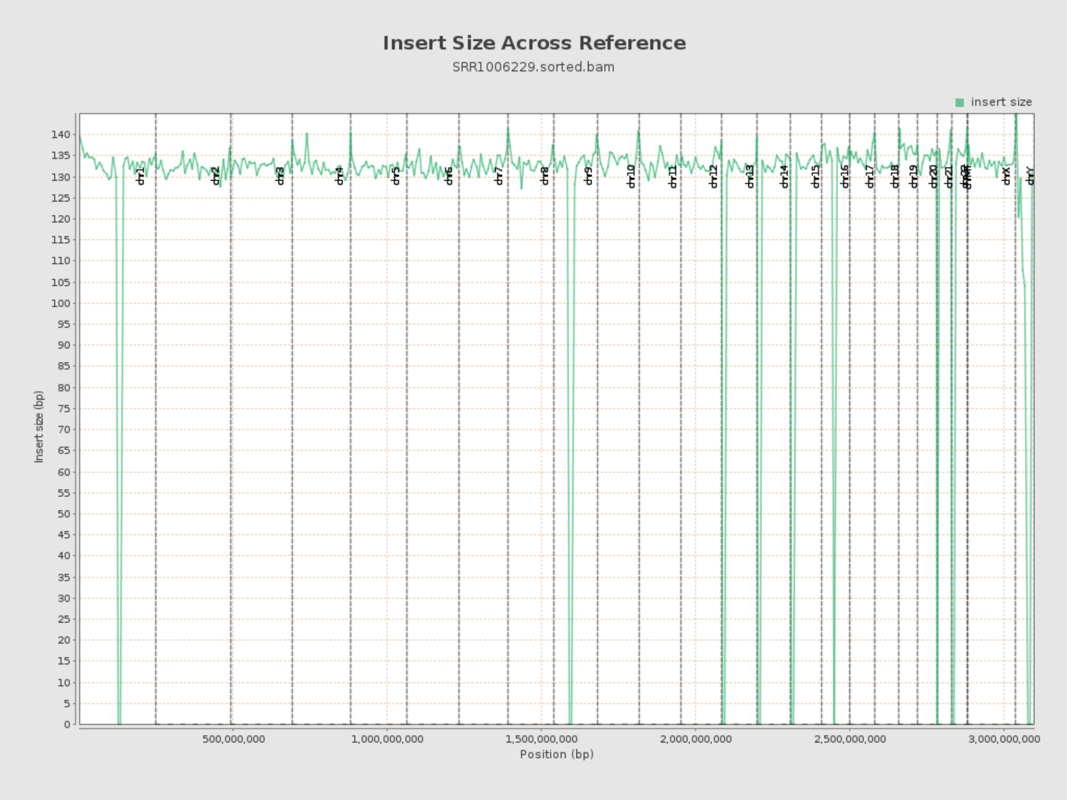
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram