Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 00:50:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006384.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_SRR1006384 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006384_1.fastq.gz SRR1006384_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 00:50:03 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006384.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,988,012
Mapped reads	875,167 / 17.55%
Unmapped reads	4,112,845 / 82.45%
Mapped paired reads	875,167 / 17.55%
Mapped reads, first in pair	444,423 / 8.91%
Mapped reads, second in pair	430,744 / 8.64%
Mapped reads, both in pair	770,806 / 15.45%
Mapped reads, singletons	104,361 / 2.09%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	25,553 / 0.51%
Duplication rate	2.41%
Clipped reads	53,674 / 1.08%

2.2. ACGT Content

Number/percentage of A's	9,426,344 / 27.85%
Number/percentage of C's	7,311,678 / 21.6%
Number/percentage of T's	9,563,494 / 28.25%
Number/percentage of G's	7,544,733 / 22.29%
Number/percentage of N's	1,379 / 0%
GC Percentage	43.89%

2.3. Coverage

Mean	0.0109
Standard Deviation	0.1622

2.4. Mapping Quality

Mean Mapping Quality	47.73

2.5. Insert size

Mean	74,491.85
Standard Deviation	2,590,690.21
P25/Median/P75	129 / 170 / 227

2.6. Mismatches and indels

General error rate	0.38%
Mismatches	127,904
Insertions	1,105
Mapped reads with at least one insertion	0.13%
Deletions	3,345
Mapped reads with at least one deletion	0.38%
Homopolymer indels	40.67%

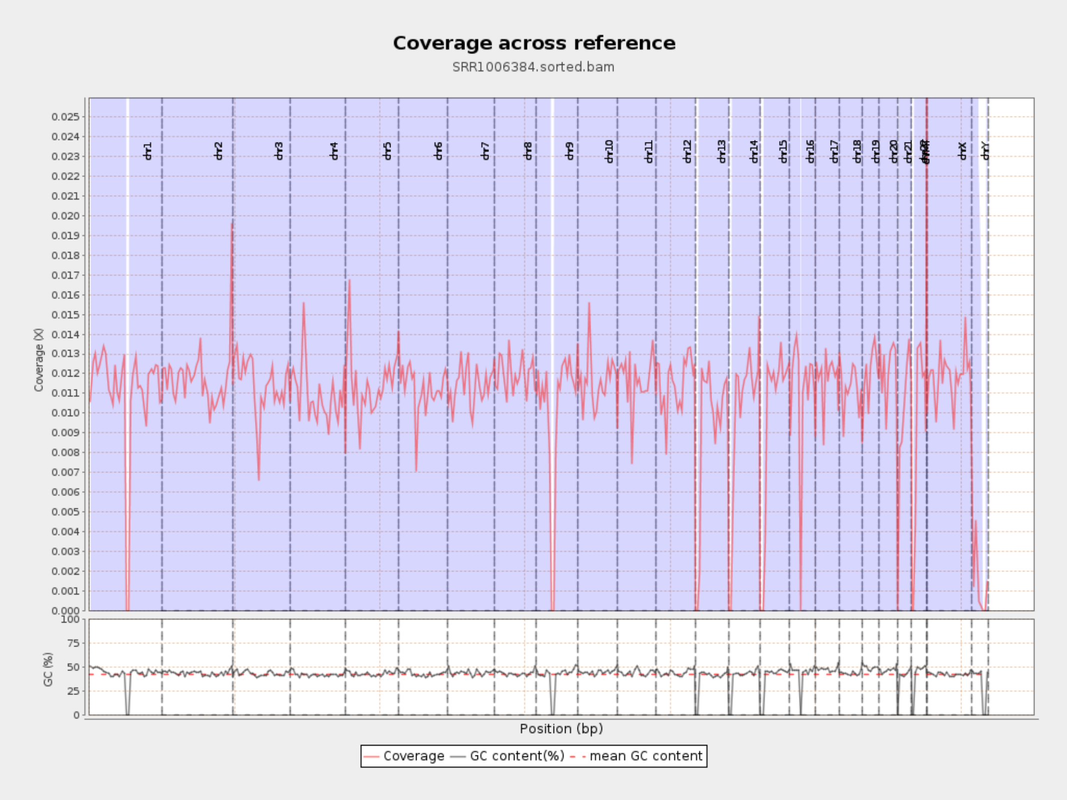
2.7. Chromosome stats

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

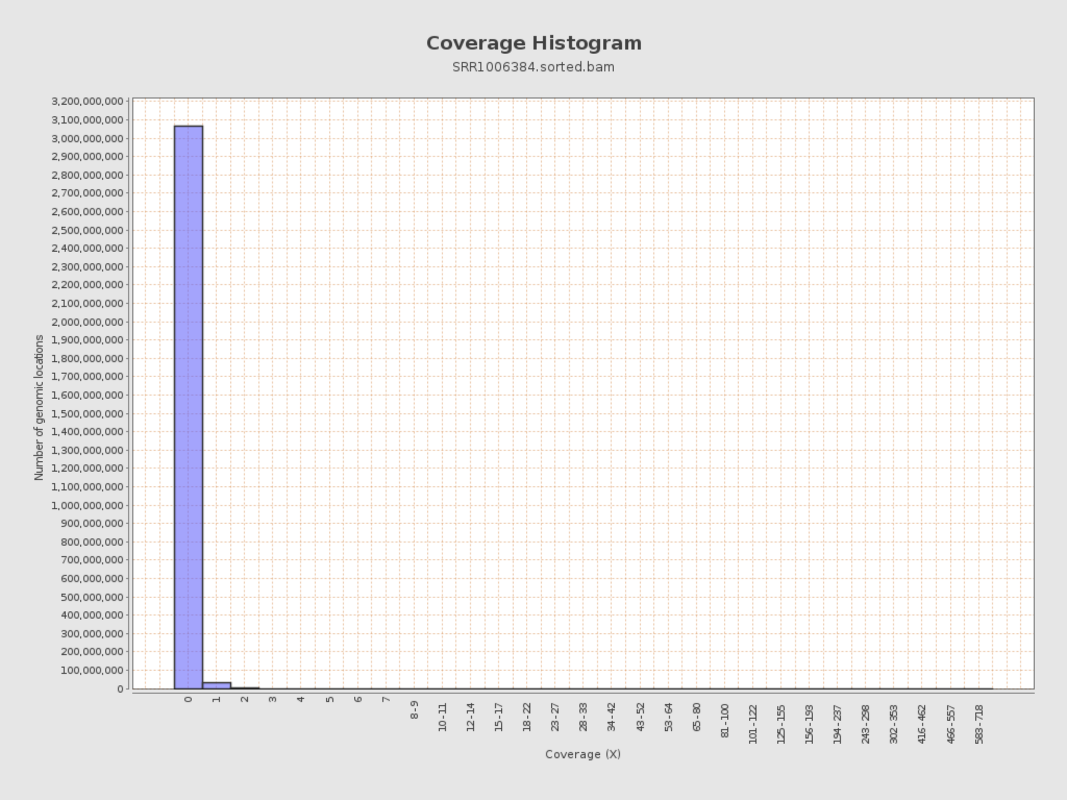
chr1	249250621	2742215	0.011	0.1697
chr2	243199373	2856888	0.0117	0.2619
chr3	198022430	2258893	0.0114	0.1124
chr4	191154276	2086993	0.0109	0.1133
chr5	180915260	2066788	0.0114	0.3248
chr6	171115067	1933167	0.0113	0.175
chr7	159138663	1803894	0.0113	0.1224
chr8	146364022	1752046	0.012	0.1831
chr9	141213431	1417049	0.01	0.1075
chr10	135534747	1571397	0.0116	0.1251
chr11	135006516	1574556	0.0117	0.1448
chr12	133851895	1544049	0.0115	0.1135
chr13	115169878	1046757	0.0091	0.1002
chr14	107349540	1048051	0.0098	0.1089
chr15	102531392	1000473	0.0098	0.1038
chr16	90354753	993443	0.011	0.1146
chr17	81195210	958273	0.0118	0.1199
chr18	78077248	879093	0.0113	0.1259
chr19	59128983	710324	0.012	0.1229
chr20	63025520	766856	0.0122	0.1171
chr21	48129895	469624	0.0098	0.1466
chr22	51304566	444193	0.0087	0.0992
chrMT	16571	466	0.0281	0.1783
chrX	155270560	1842730	0.0119	0.1168

chrY	59373566	83890	0.0014	0.0495

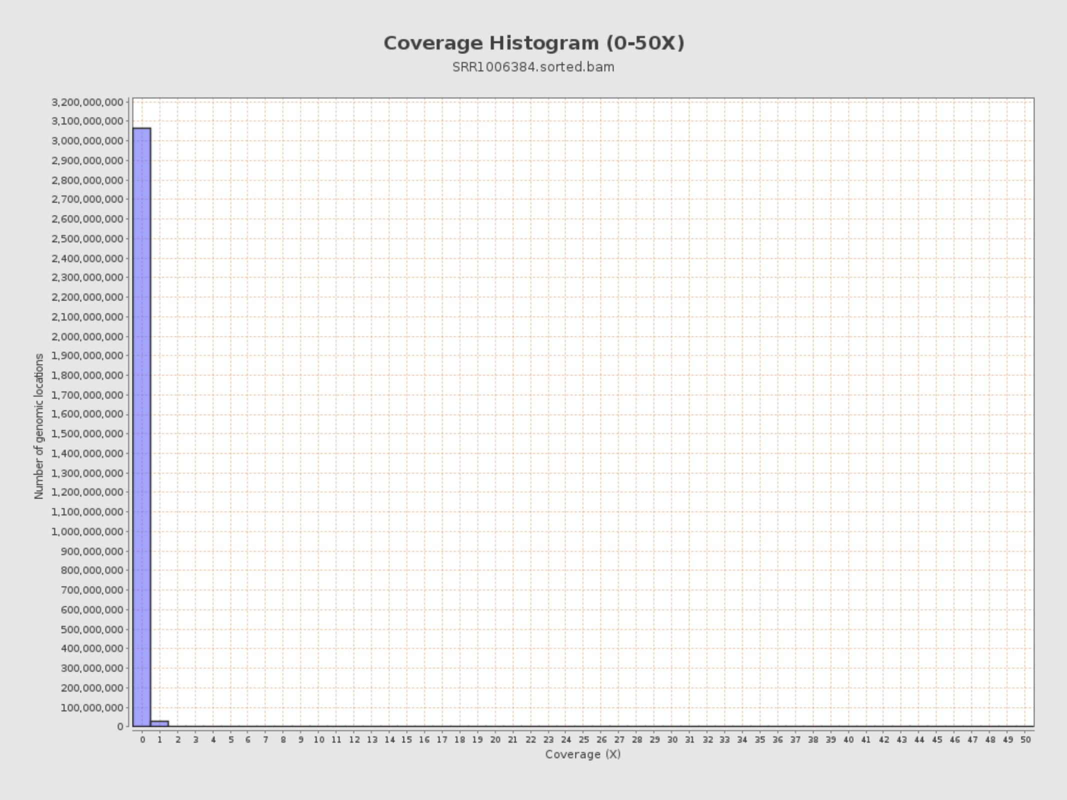
3. Results : Coverage across reference



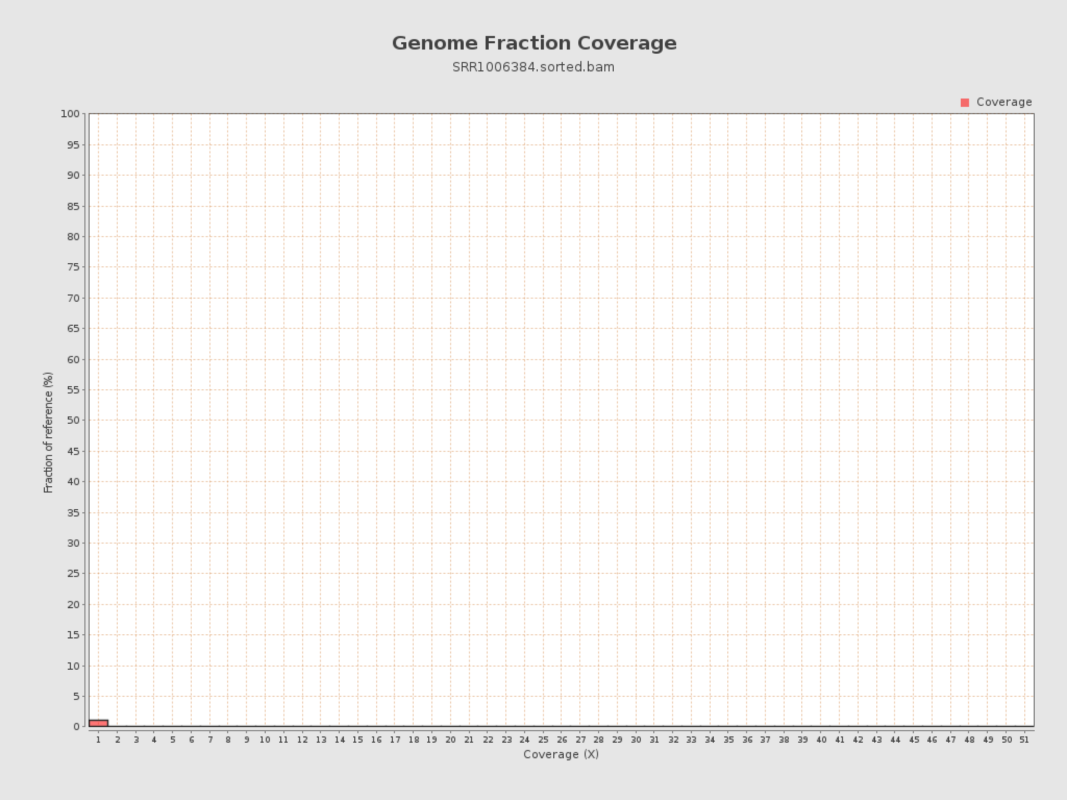
4. Results : Coverage Histogram



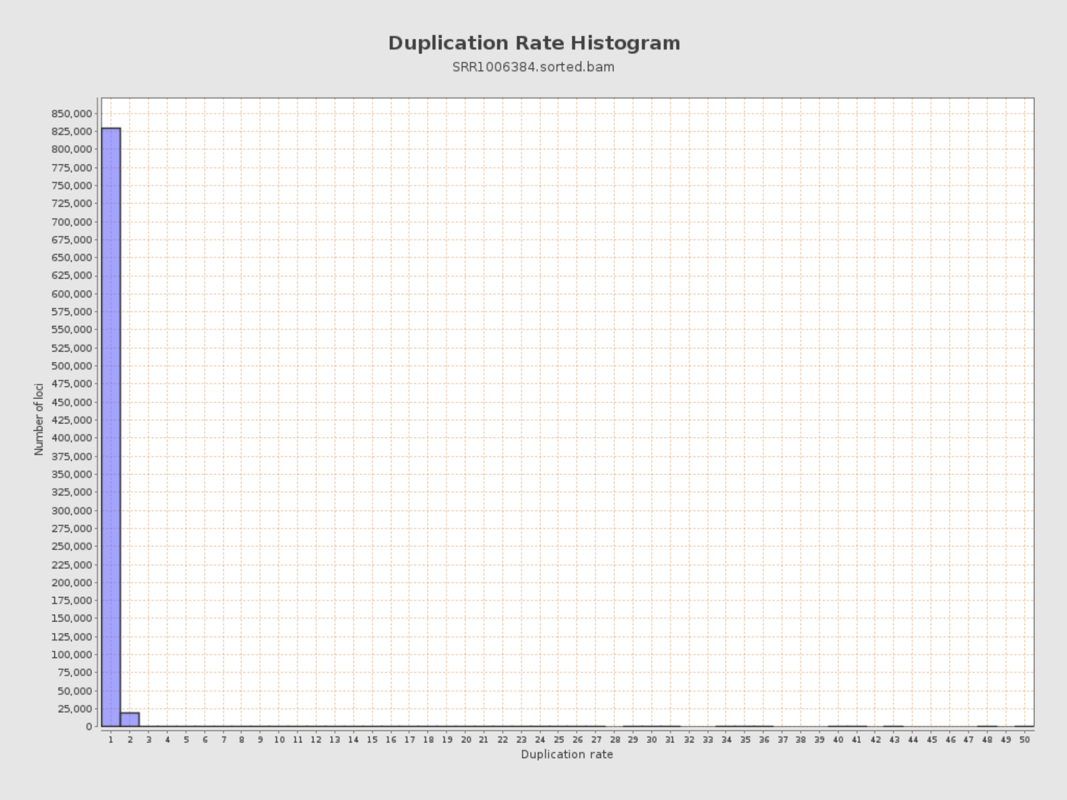
5. Results : Coverage Histogram (0-50X)



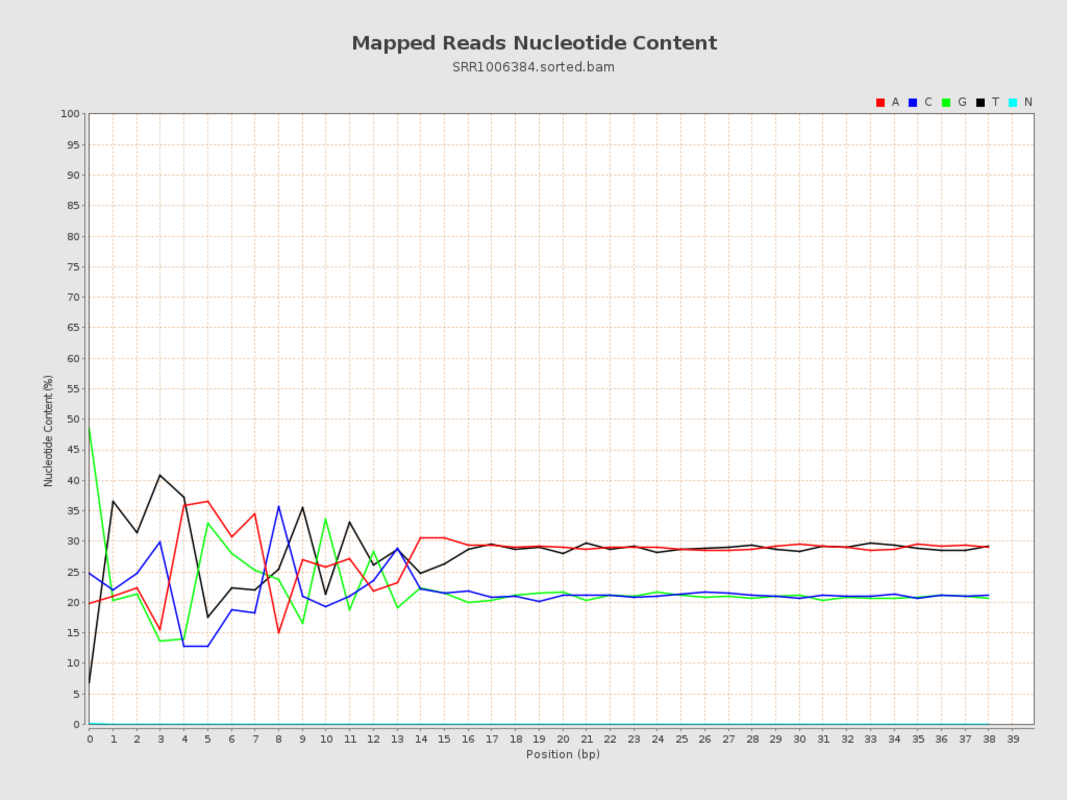
6. Results : Genome Fraction Coverage



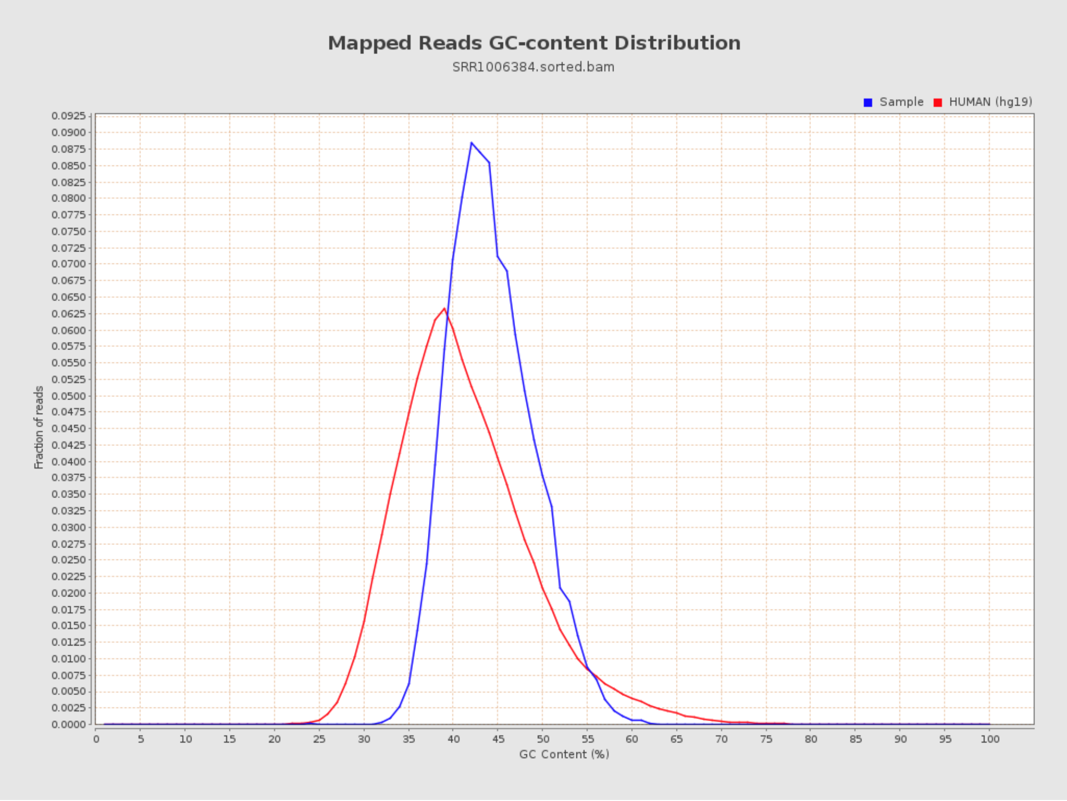
7. Results : Duplication Rate Histogram



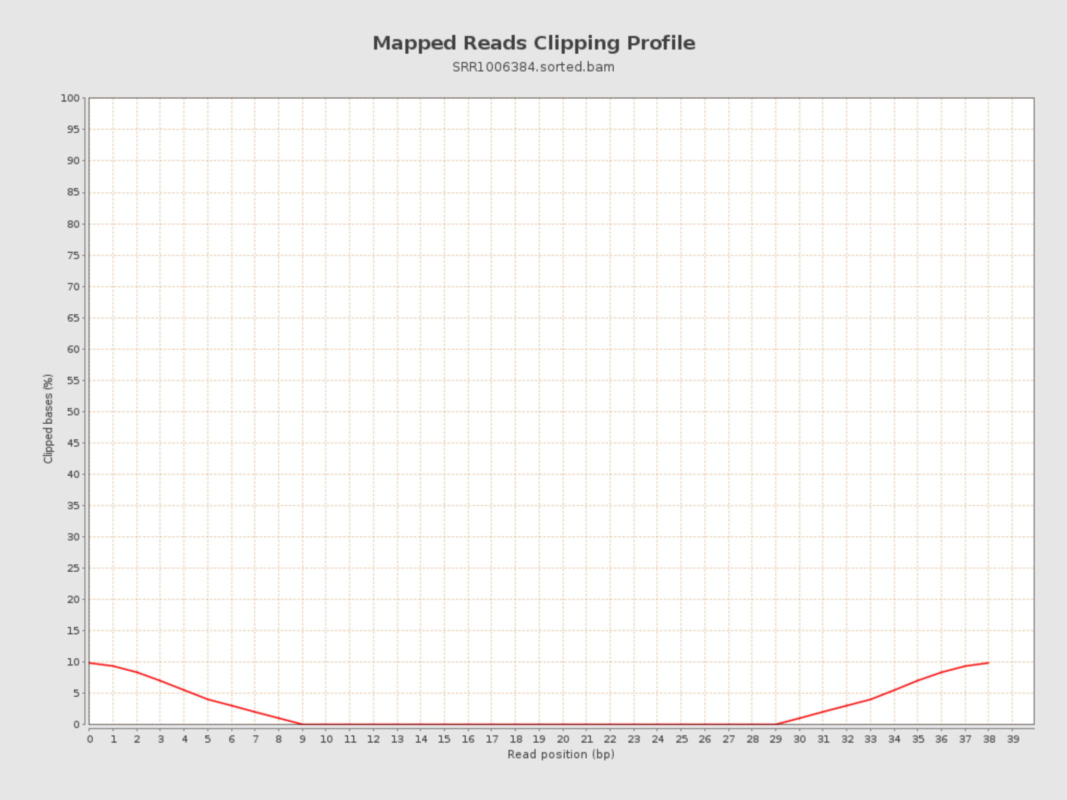
8. Results : Mapped Reads Nucleotide Content



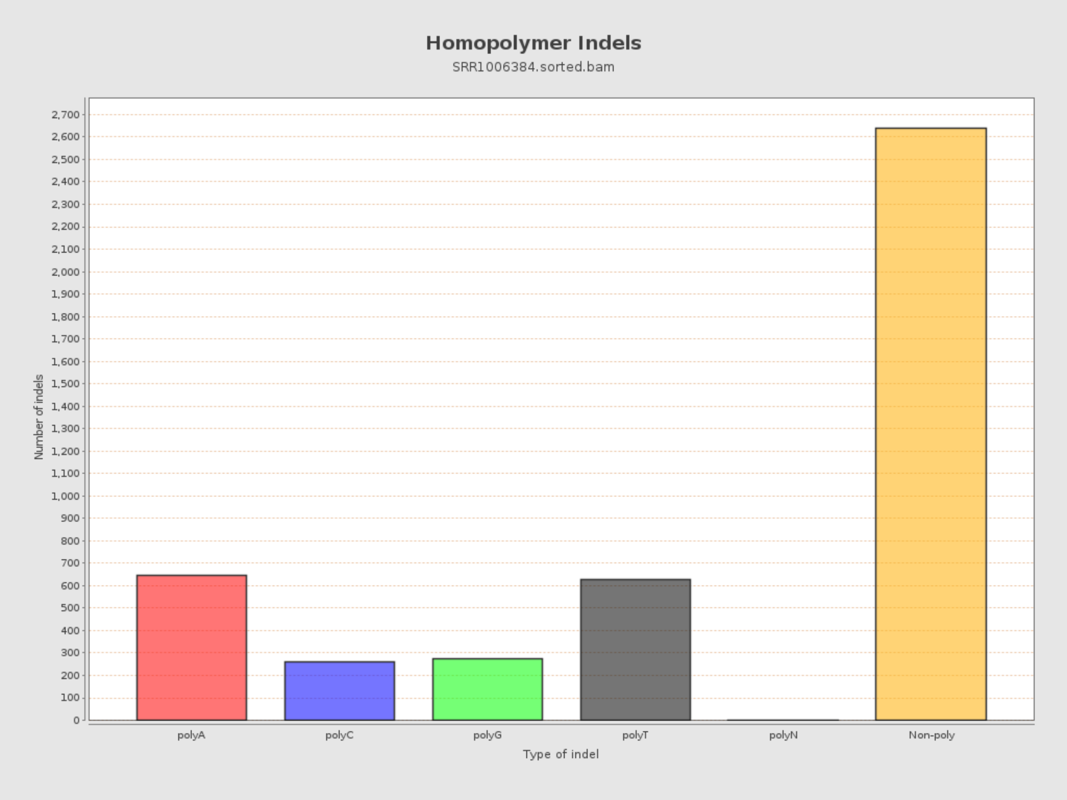
9. Results : Mapped Reads GC-content Distribution



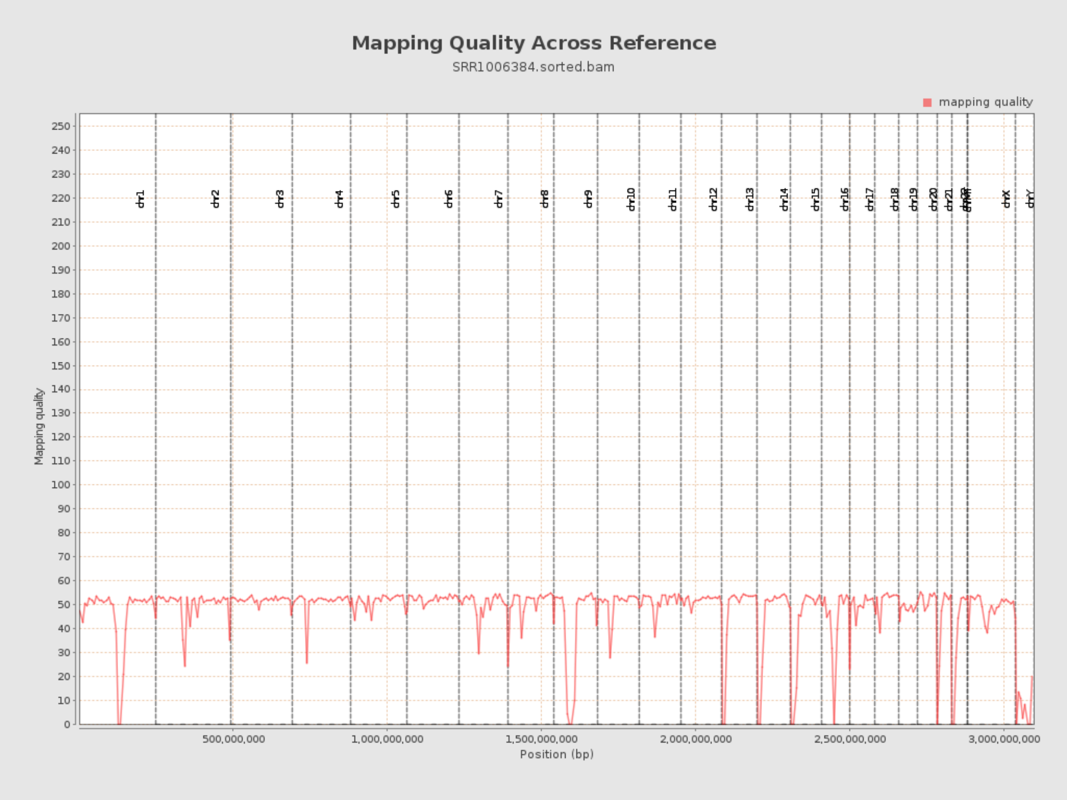
10. Results : Mapped Reads Clipping Profile



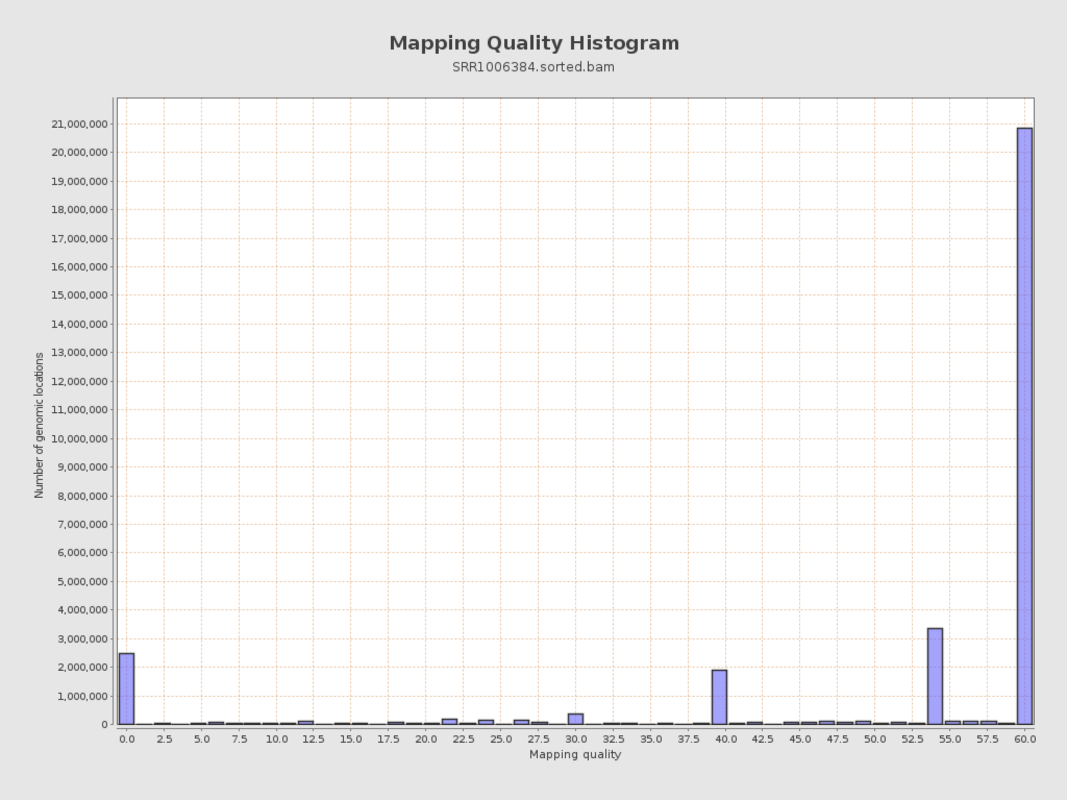
11. Results : Homopolymer Indels



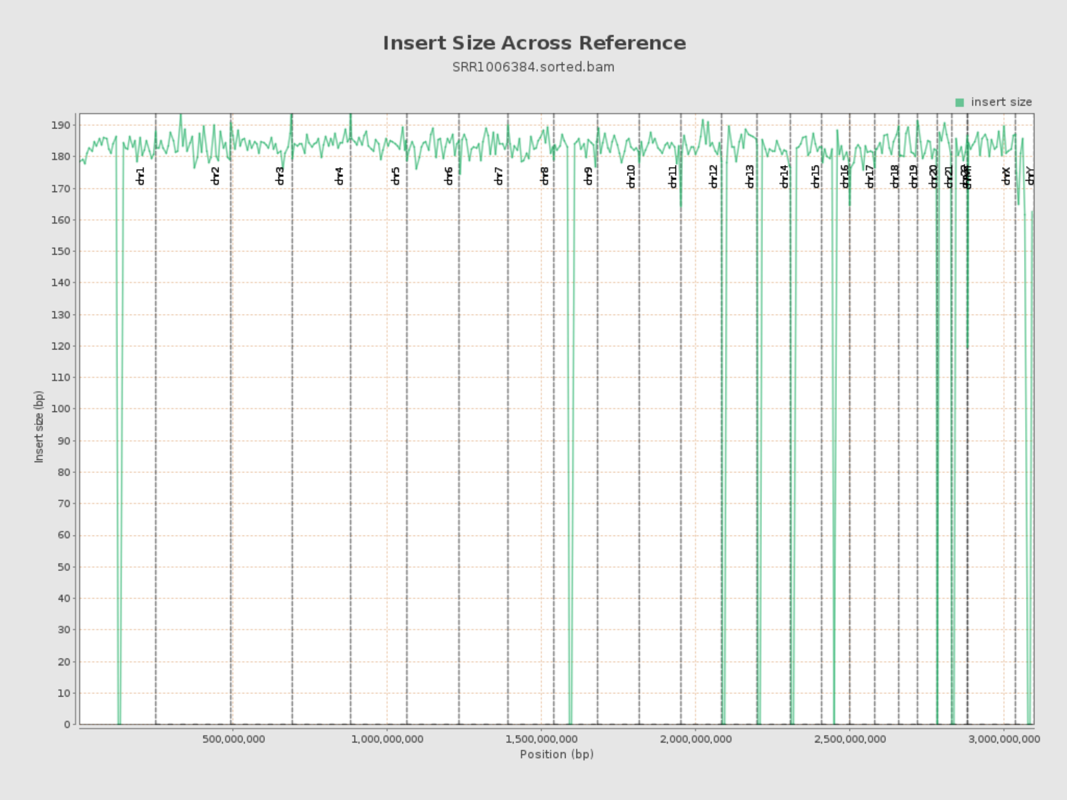
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram