Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 22:41:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006182.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_SRR1006182 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006182_1.fastq.gz SRR1006182_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 22:41:26 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006182.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,558,948
Mapped reads	1,319,458 / 20.12%
Unmapped reads	5,239,490 / 79.88%
Mapped paired reads	1,319,458 / 20.12%
Mapped reads, first in pair	660,472 / 10.07%
Mapped reads, second in pair	658,986 / 10.05%
Mapped reads, both in pair	1,143,004 / 17.43%
Mapped reads, singletons	176,454 / 2.69%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	42,894 / 0.65%
Duplication rate	2.43%
Clipped reads	76,053 / 1.16%

2.2. ACGT Content

Number/percentage of A's	14,139,200 / 27.7%
Number/percentage of C's	11,107,787 / 21.76%
Number/percentage of T's	14,413,798 / 28.24%
Number/percentage of G's	11,382,151 / 22.3%
Number/percentage of N's	1,864 / 0%
GC Percentage	44.06%

2.3. Coverage

Mean	0.0165
Standard Deviation	0.3085

2.4. Mapping Quality

Mean Mapping Quality	47.43

2.5. Insert size

Mean	69,542.72
Standard Deviation	2,484,872.15
P25/Median/P75	105 / 141 / 191

2.6. Mismatches and indels

General error rate	0.29%
Mismatches	147,964
Insertions	1,833
Mapped reads with at least one insertion	0.14%
Deletions	5,777
Mapped reads with at least one deletion	0.44%
Homopolymer indels	40.66%

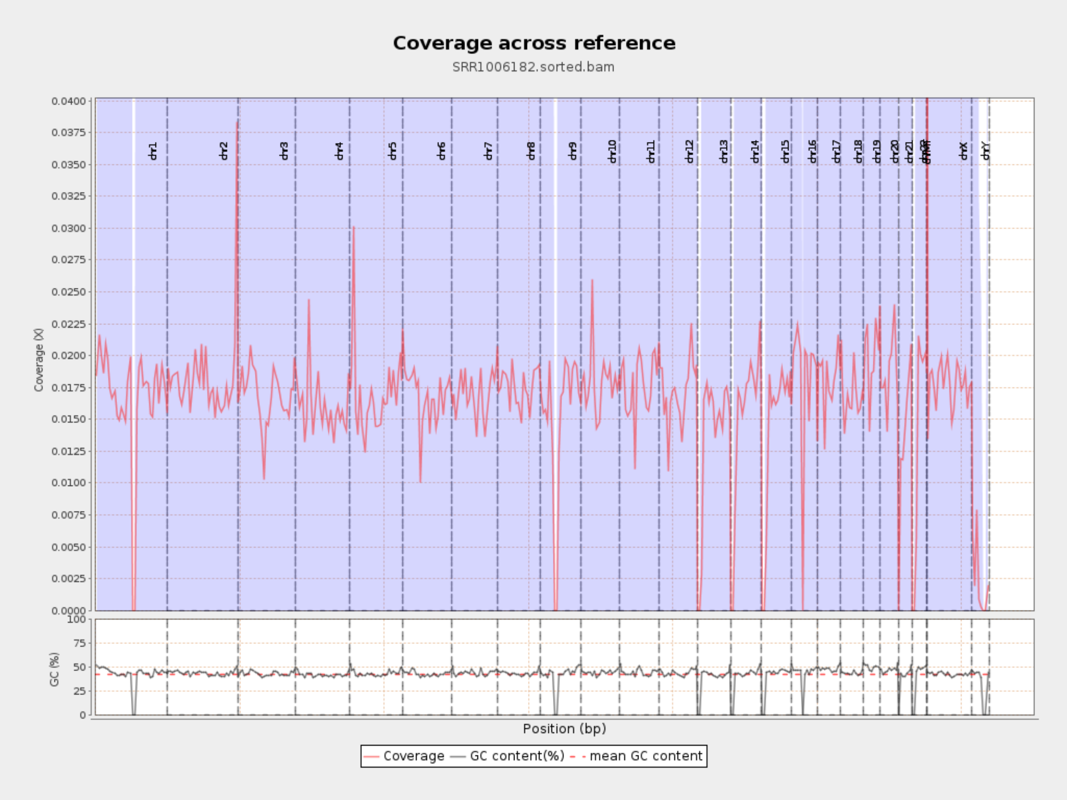
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

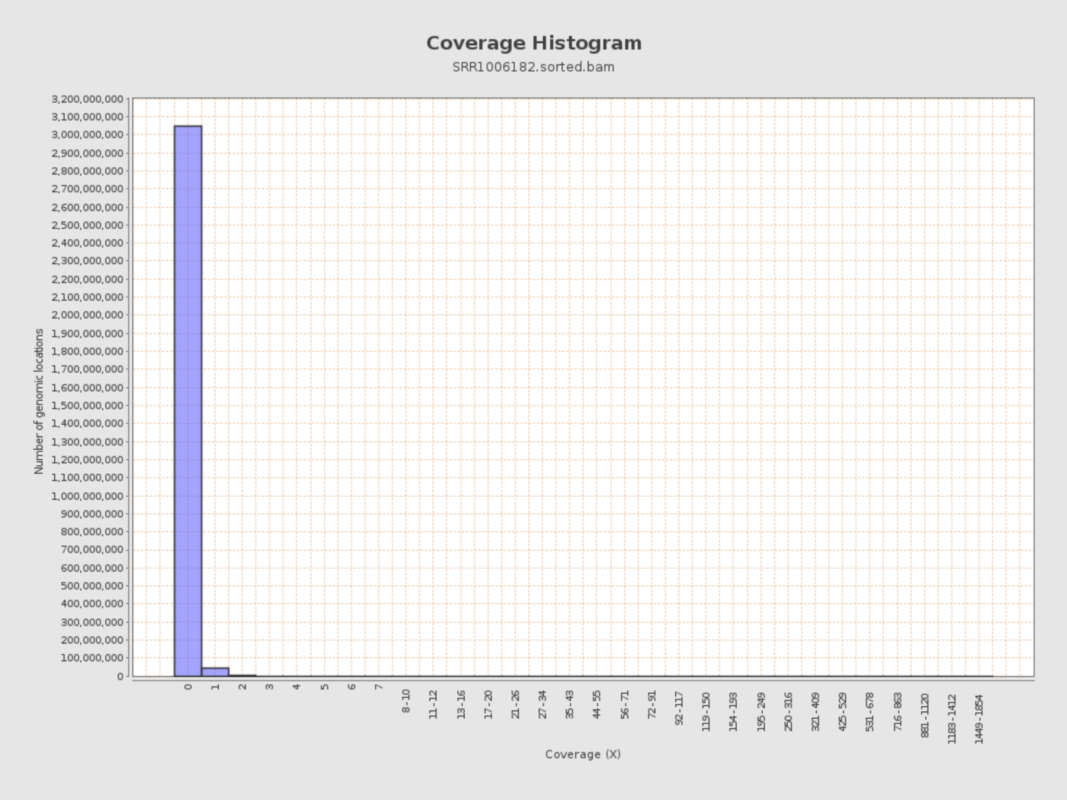
chr1	249250621	4140124	0.0166	0.2401
chr2	243199373	4407401	0.0181	0.6119
chr3	198022430	3338112	0.0169	0.1383
chr4	191154276	3073553	0.0161	0.1428
chr5	180915260	3077668	0.017	0.8149
chr6	171115067	2881051	0.0168	0.2616
chr7	159138663	2696439	0.0169	0.1551
chr8	146364022	2563091	0.0175	0.2261
chr9	141213431	2130702	0.0151	0.1361
chr10	135534747	2441015	0.018	0.1771
chr11	135006516	2386322	0.0177	0.1913
chr12	133851895	2277083	0.017	0.1395
chr13	115169878	1556700	0.0135	0.1243
chr14	107349540	1611126	0.015	0.1742
chr15	102531392	1431706	0.014	0.1257
chr16	90354753	1622177	0.018	0.1544
chr17	81195210	1488038	0.0183	0.1808
chr18	78077248	1314097	0.0168	0.1682
chr19	59128983	1169855	0.0198	0.1673
chr20	63025520	1172380	0.0186	0.1491
chr21	48129895	676094	0.014	0.2398
chr22	51304566	711608	0.0139	0.1272
chrMT	16571	3266	0.1971	0.4669
chrX	155270560	2751117	0.0177	0.1461

chrY	59373566	131953	0.0022	0.072

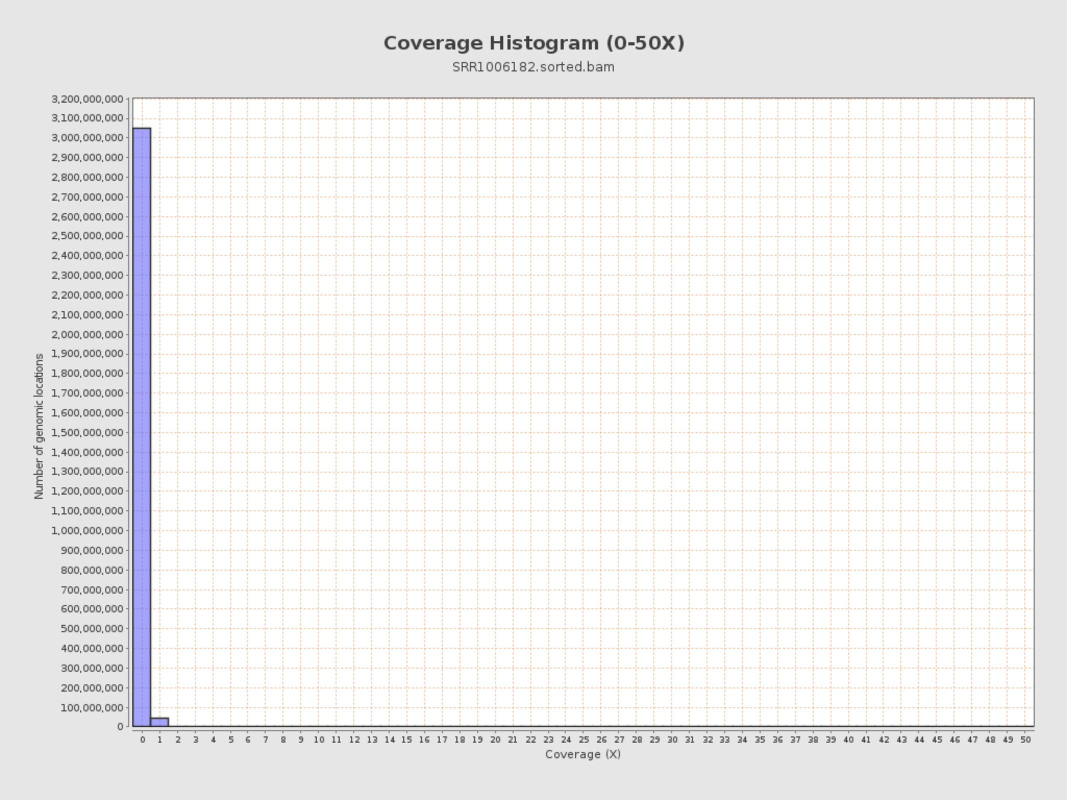
3. Results : Coverage across reference



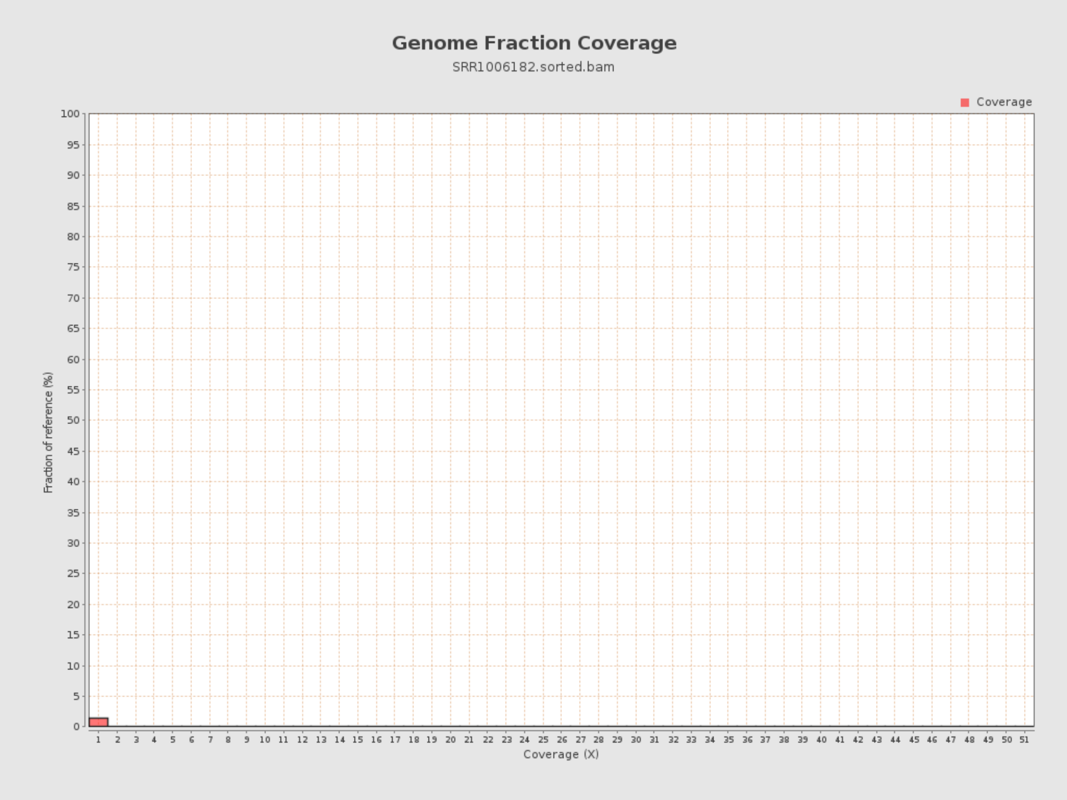
4. Results : Coverage Histogram



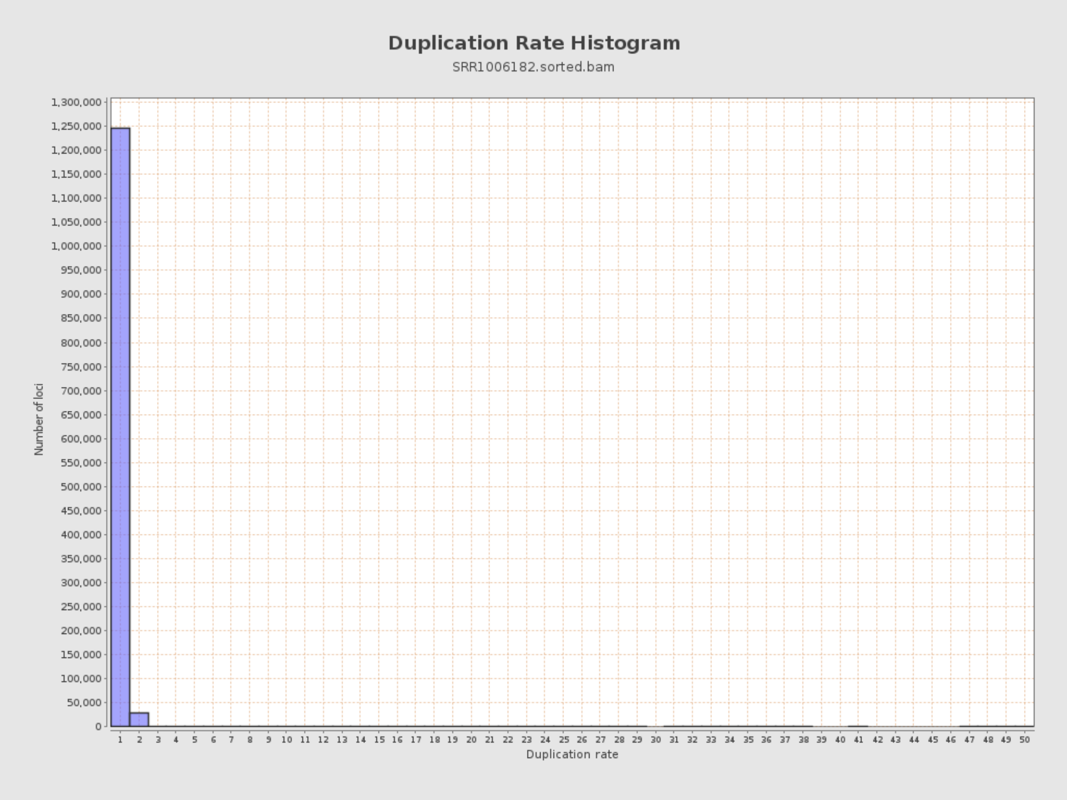
5. Results : Coverage Histogram (0-50X)



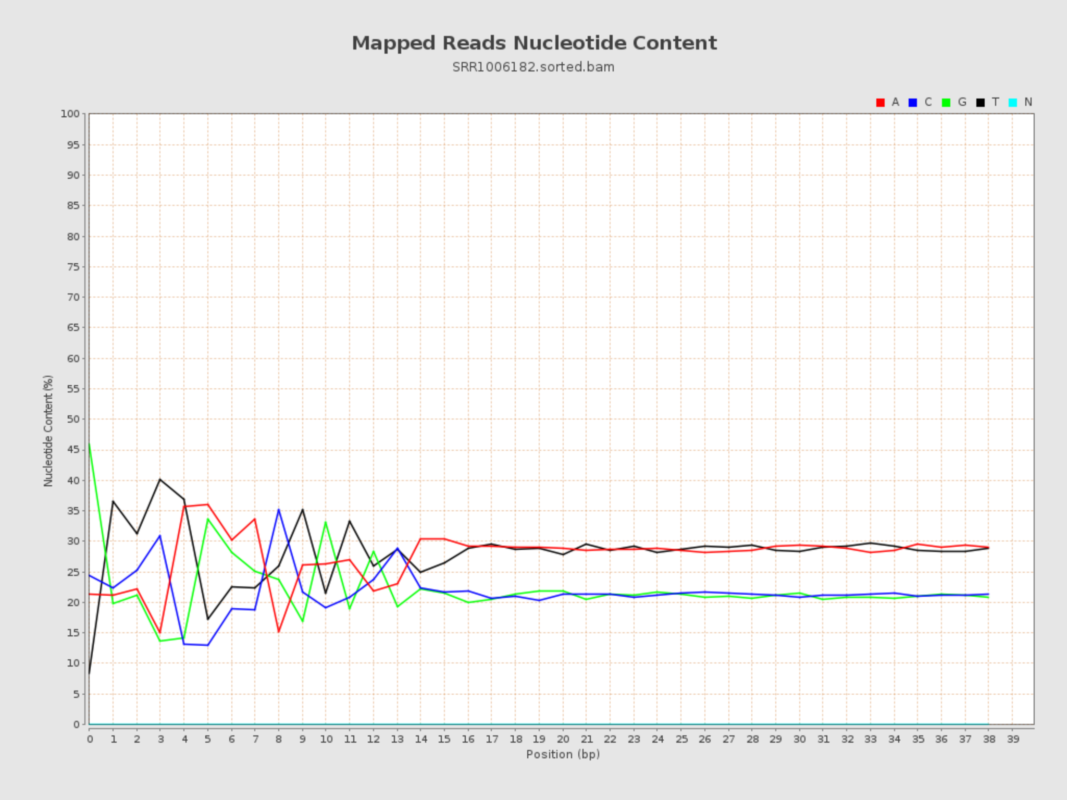
6. Results : Genome Fraction Coverage



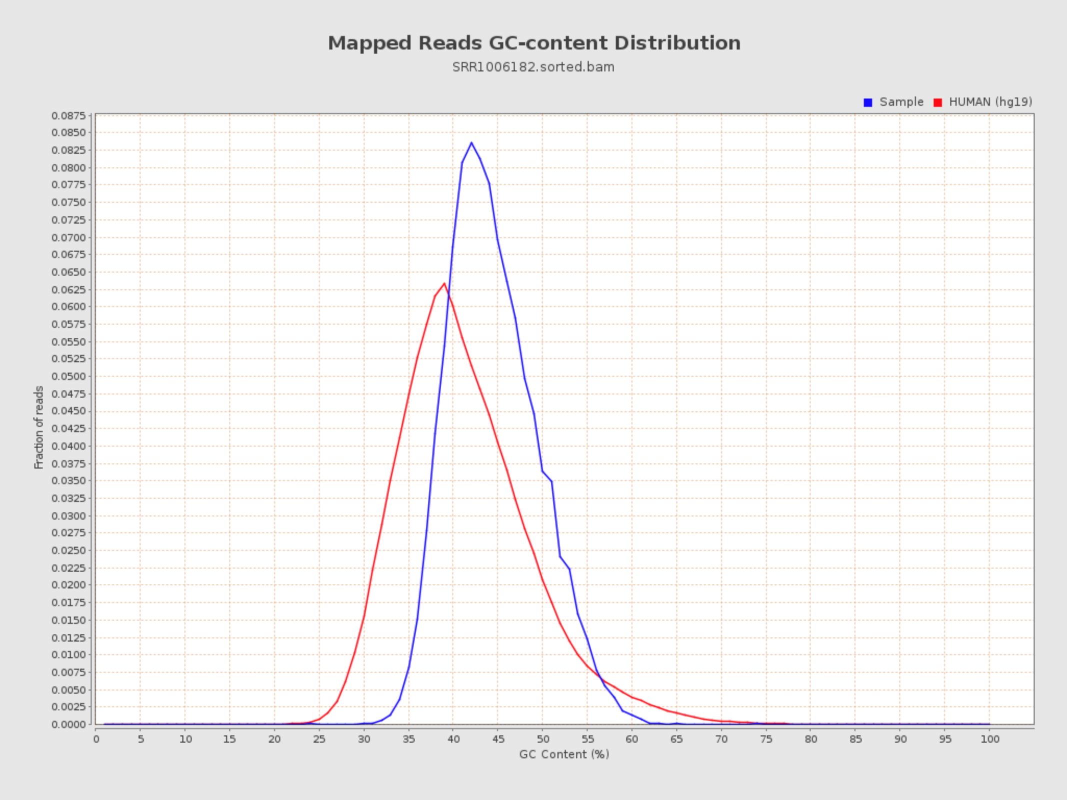
7. Results : Duplication Rate Histogram



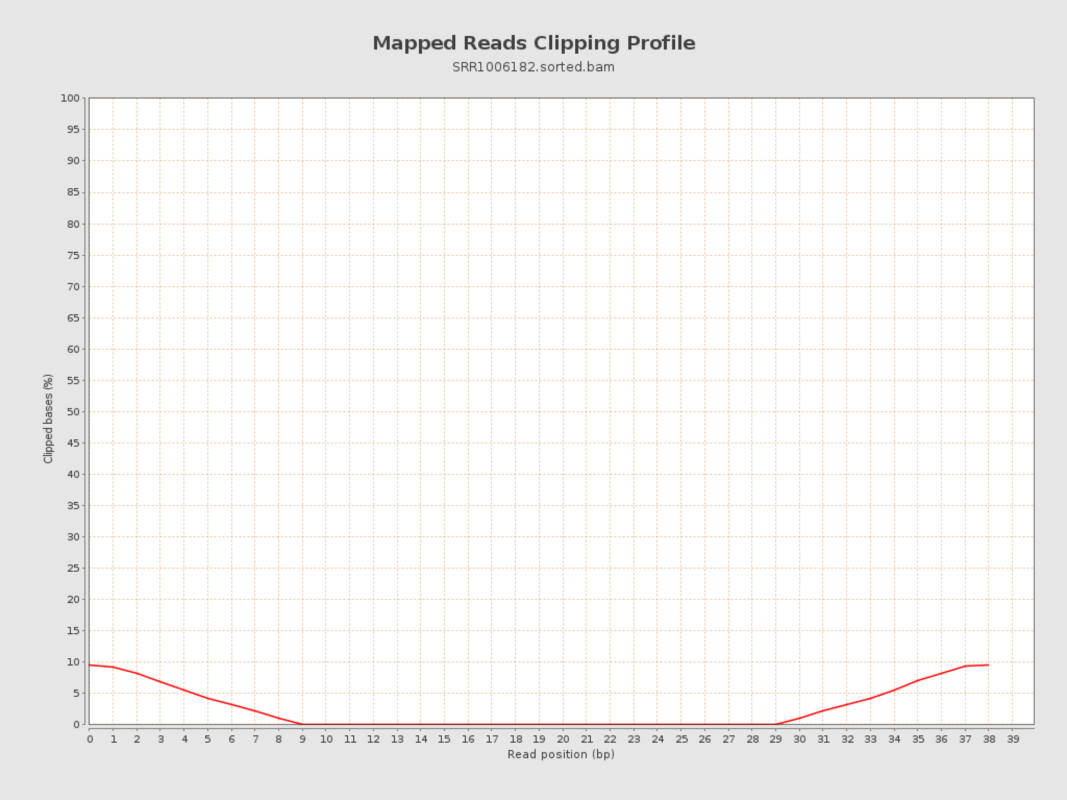
8. Results : Mapped Reads Nucleotide Content



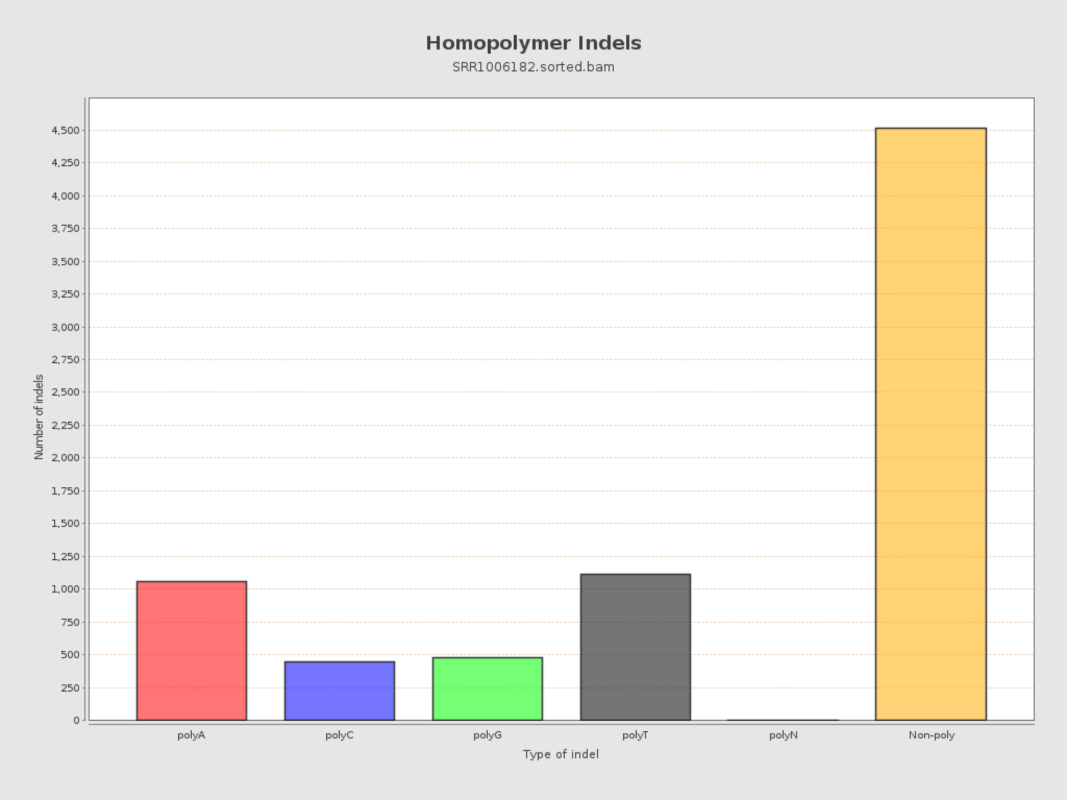
9. Results : Mapped Reads GC-content Distribution



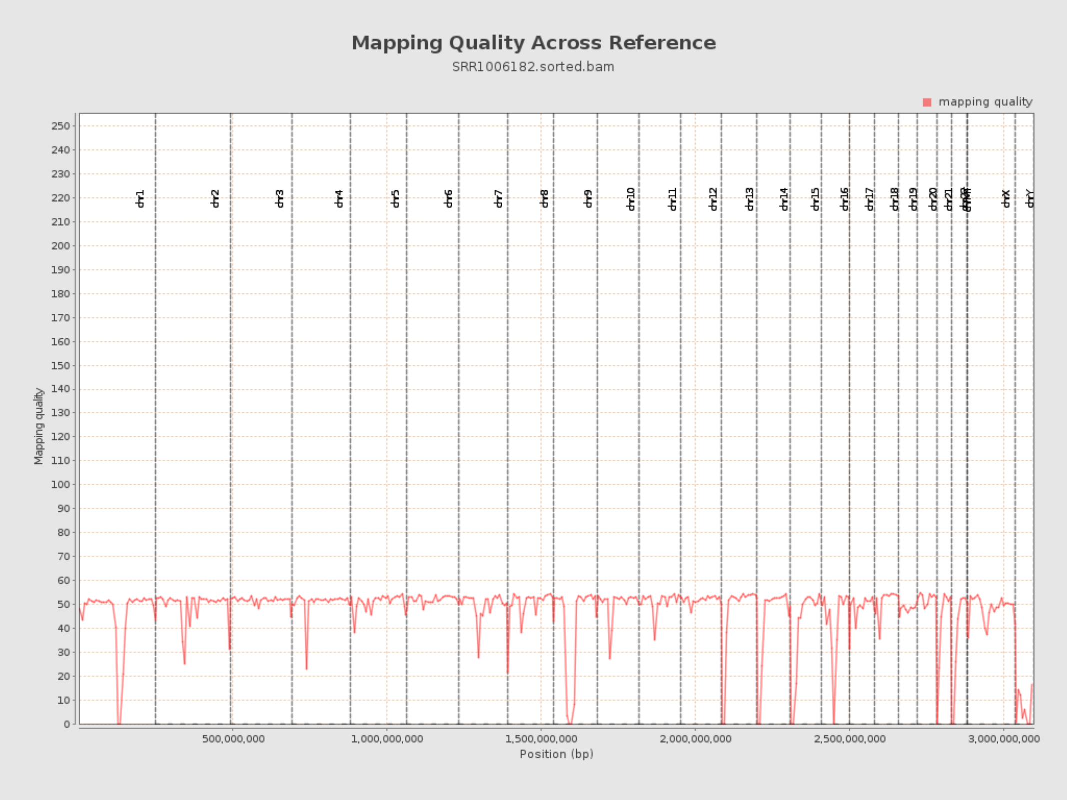
10. Results : Mapped Reads Clipping Profile



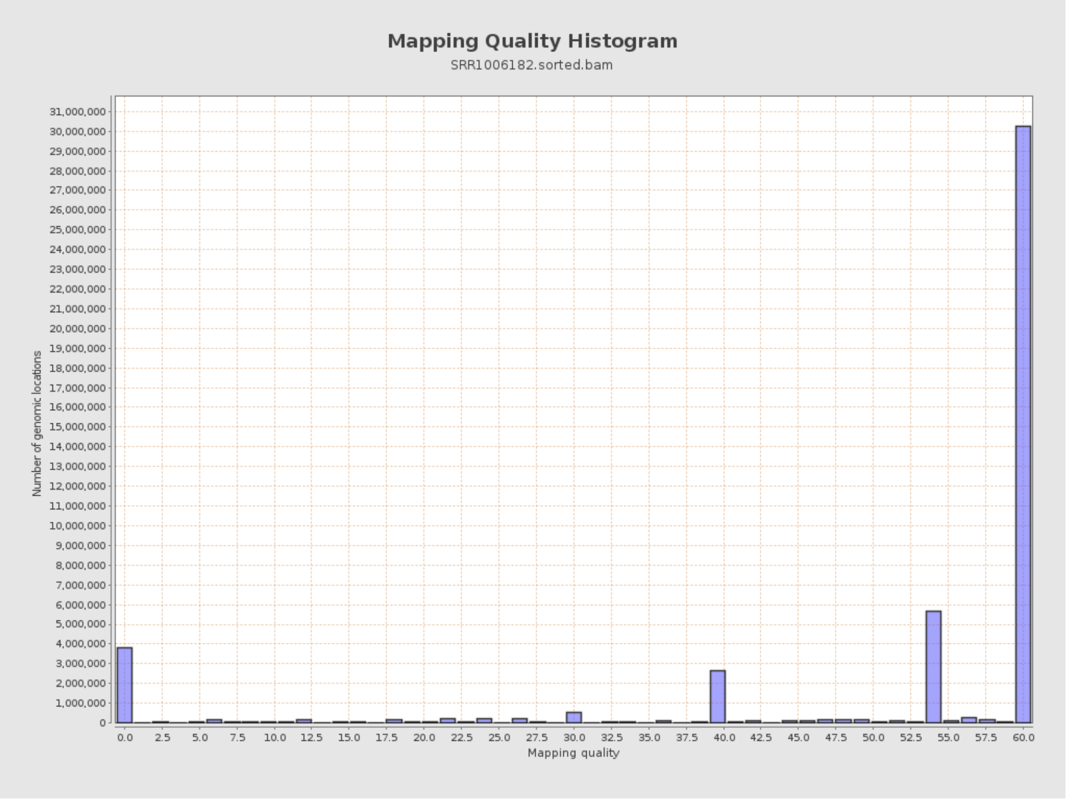
11. Results : Homopolymer Indels



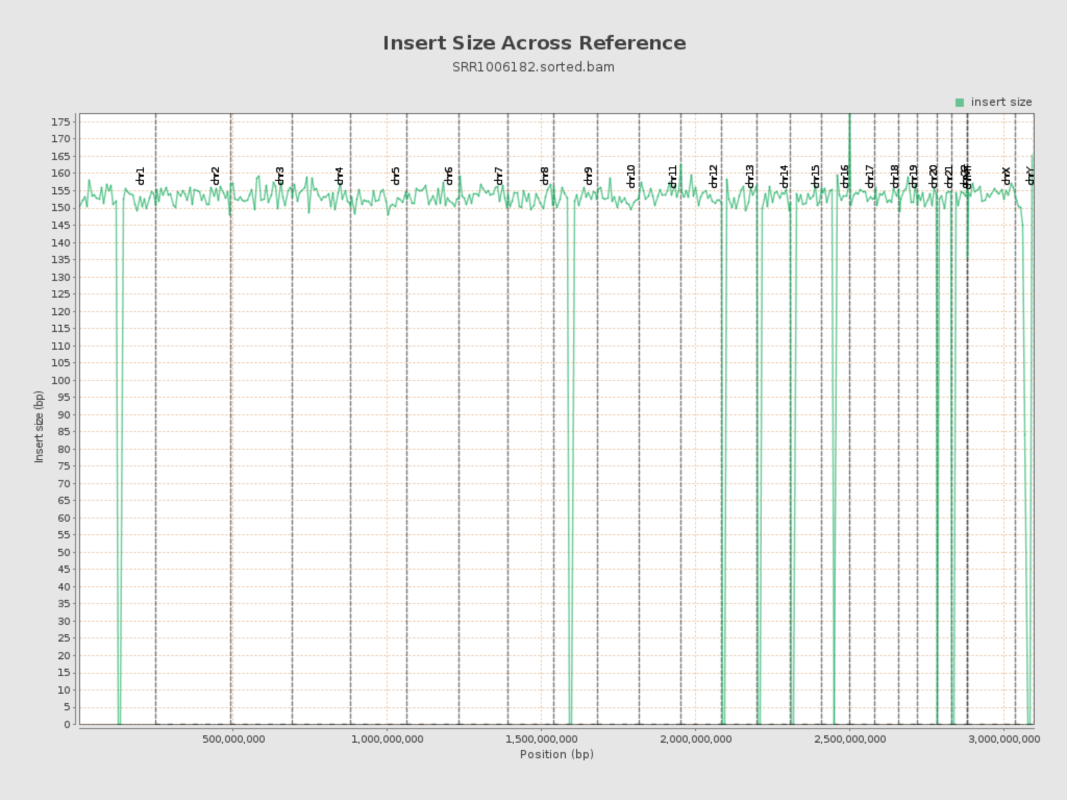
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram