Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 00:03:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006222.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_SRR1006222 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006222_1.fastq.gz SRR1006222_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 00:03:57 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006222.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,197,444
Mapped reads	1,492,562 / 20.74%
Unmapped reads	5,704,882 / 79.26%
Mapped paired reads	1,492,562 / 20.74%
Mapped reads, first in pair	752,874 / 10.46%
Mapped reads, second in pair	739,688 / 10.28%
Mapped reads, both in pair	1,331,564 / 18.5%
Mapped reads, singletons	160,998 / 2.24%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	51,876 / 0.72%
Duplication rate	2.75%
Clipped reads	102,529 / 1.42%

2.2. ACGT Content

Number/percentage of A's	16,131,740 / 27.97%
Number/percentage of C's	12,409,828 / 21.52%
Number/percentage of T's	16,431,779 / 28.49%
Number/percentage of G's	12,695,001 / 22.01%
Number/percentage of N's	2,442 / 0%
GC Percentage	43.53%

2.3. Coverage

Mean	0.0186
Standard Deviation	0.2996

2.4. Mapping Quality

Mean Mapping Quality	47.62

2.5. Insert size

Mean	69,074.77
Standard Deviation	2,487,013.77
P25/Median/P75	97 / 129 / 176

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	228,386
Insertions	1,946
Mapped reads with at least one insertion	0.13%
Deletions	6,052
Mapped reads with at least one deletion	0.4%
Homopolymer indels	42.02%

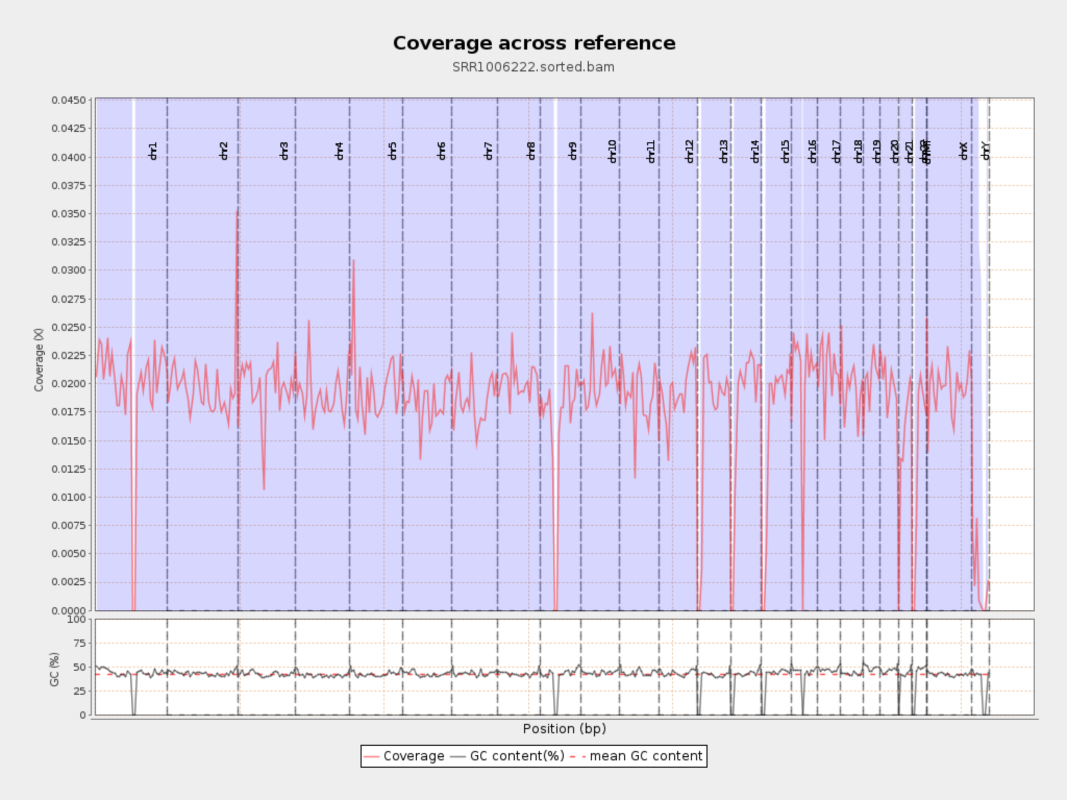
2.7. Chromosome stats

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

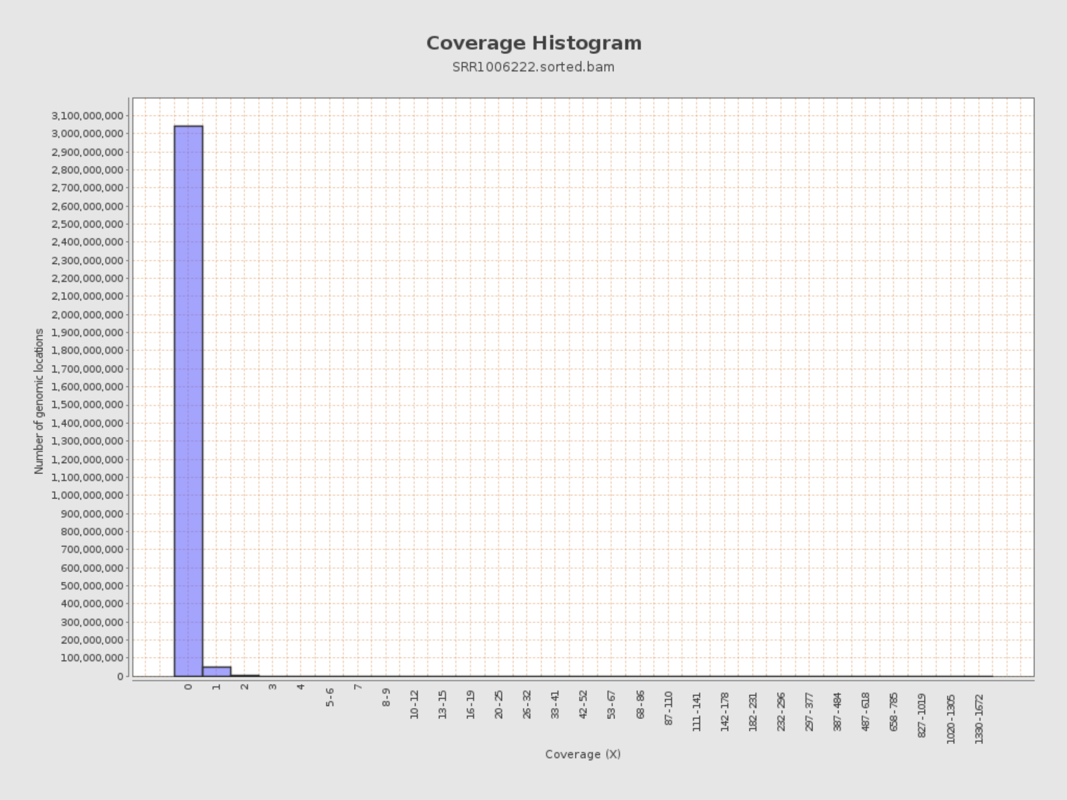
chr1	249250621	4904053	0.0197	0.2504
chr2	243199373	4764043	0.0196	0.5029
chr3	198022430	3901913	0.0197	0.1513
chr4	191154276	3652700	0.0191	0.1528
chr5	180915260	3582318	0.0198	0.7236
chr6	171115067	3160919	0.0185	0.2545
chr7	159138663	2914537	0.0183	0.1627
chr8	146364022	2946306	0.0201	0.2318
chr9	141213431	2315381	0.0164	0.1441
chr10	135534747	2771053	0.0204	0.1745
chr11	135006516	2576162	0.0191	0.1866
chr12	133851895	2579854	0.0193	0.1502
chr13	115169878	1897669	0.0165	0.16
chr14	107349540	1895443	0.0177	0.1744
chr15	102531392	1665623	0.0162	0.1369
chr16	90354753	1818366	0.0201	0.1609
chr17	81195210	1715224	0.0211	0.6613
chr18	78077248	1530521	0.0196	0.1999
chr19	59128983	1220716	0.0206	0.1781
chr20	63025520	1241465	0.0197	0.1534
chr21	48129895	730771	0.0152	0.1864
chr22	51304566	691371	0.0135	0.1259
chrMT	16571	429	0.0259	0.1588
chrX	155270560	3057547	0.0197	0.1558

chrY	59373566	144552	0.0024	0.0743

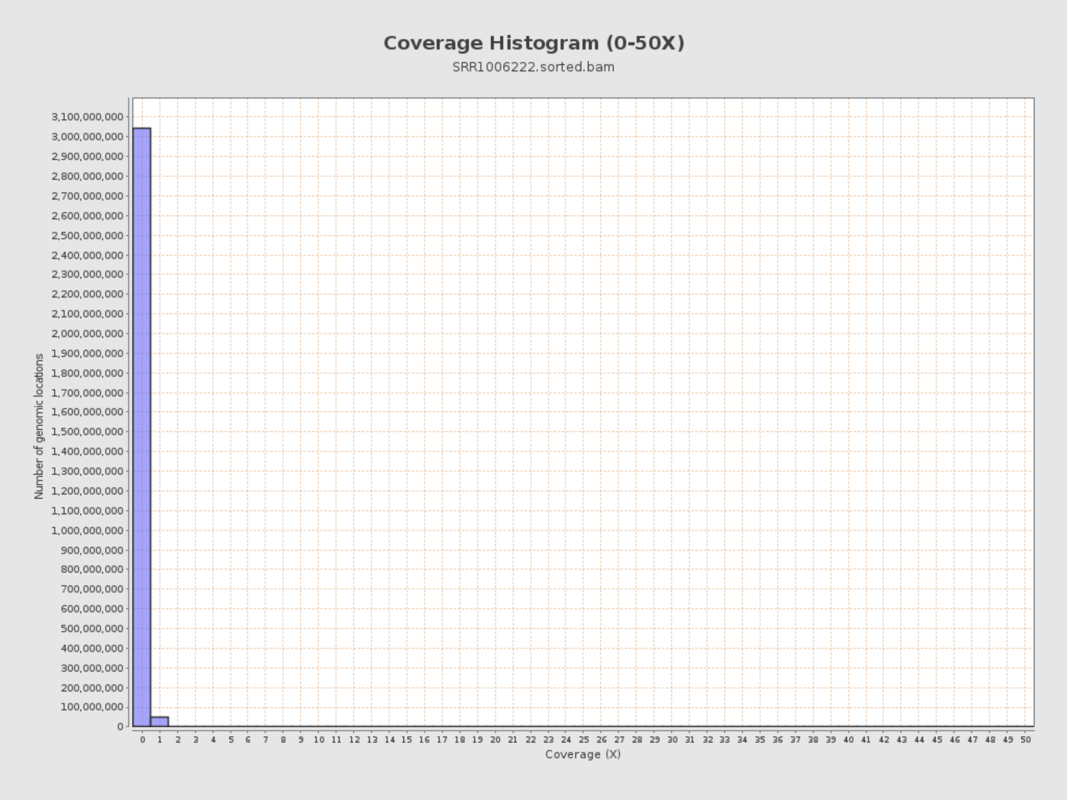
3. Results : Coverage across reference



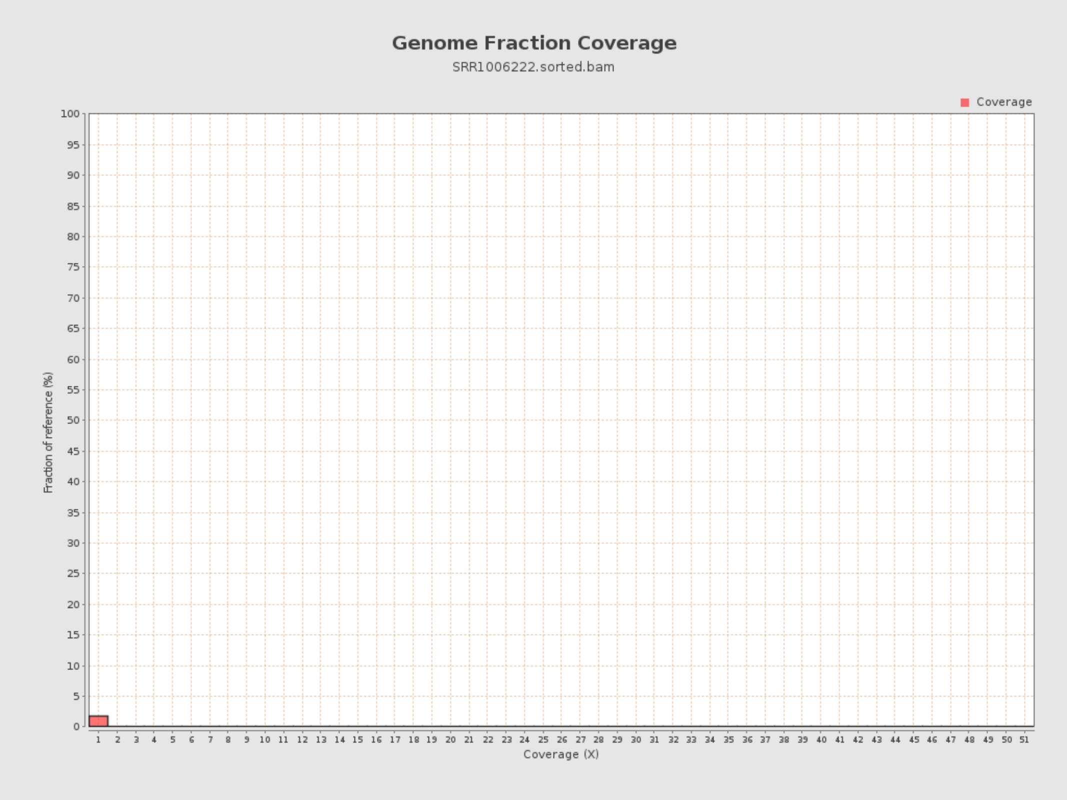
4. Results : Coverage Histogram



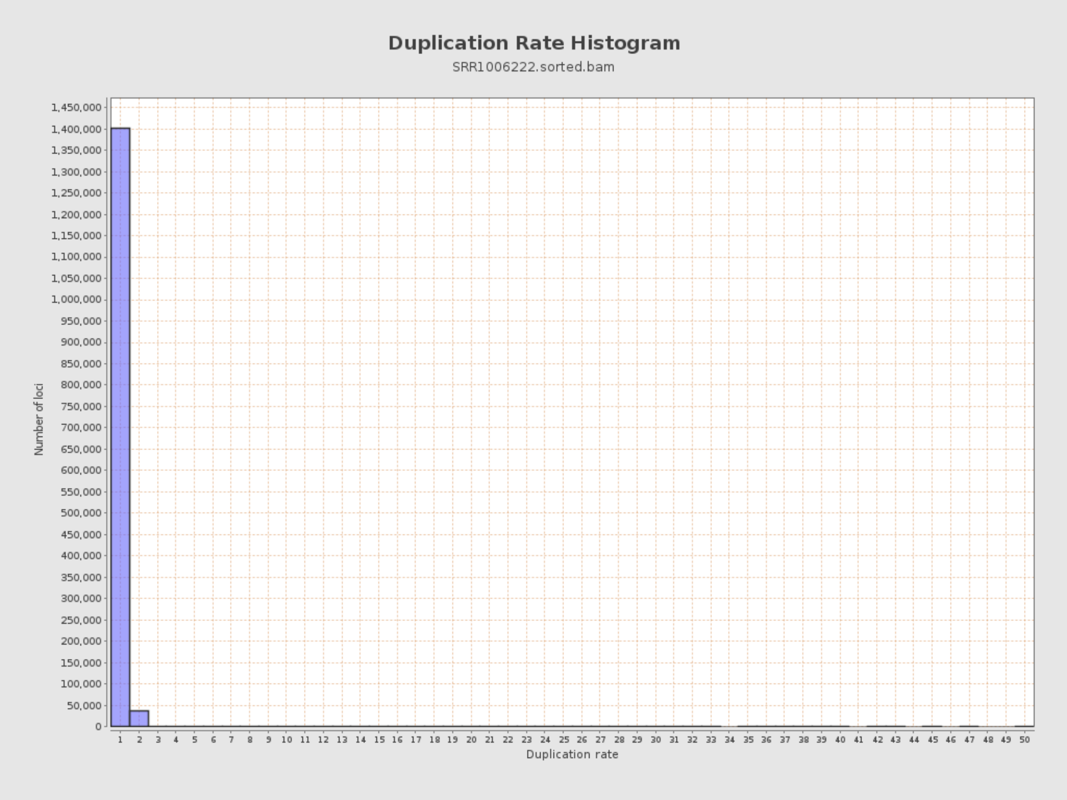
5. Results : Coverage Histogram (0-50X)



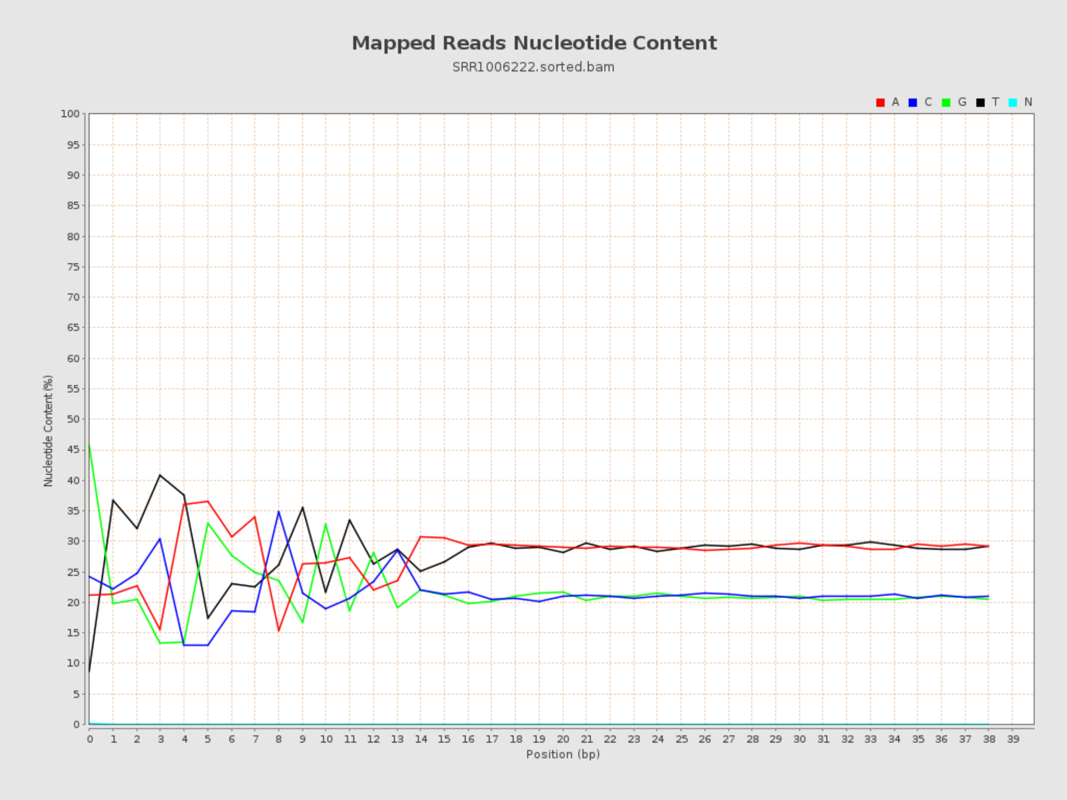
6. Results : Genome Fraction Coverage



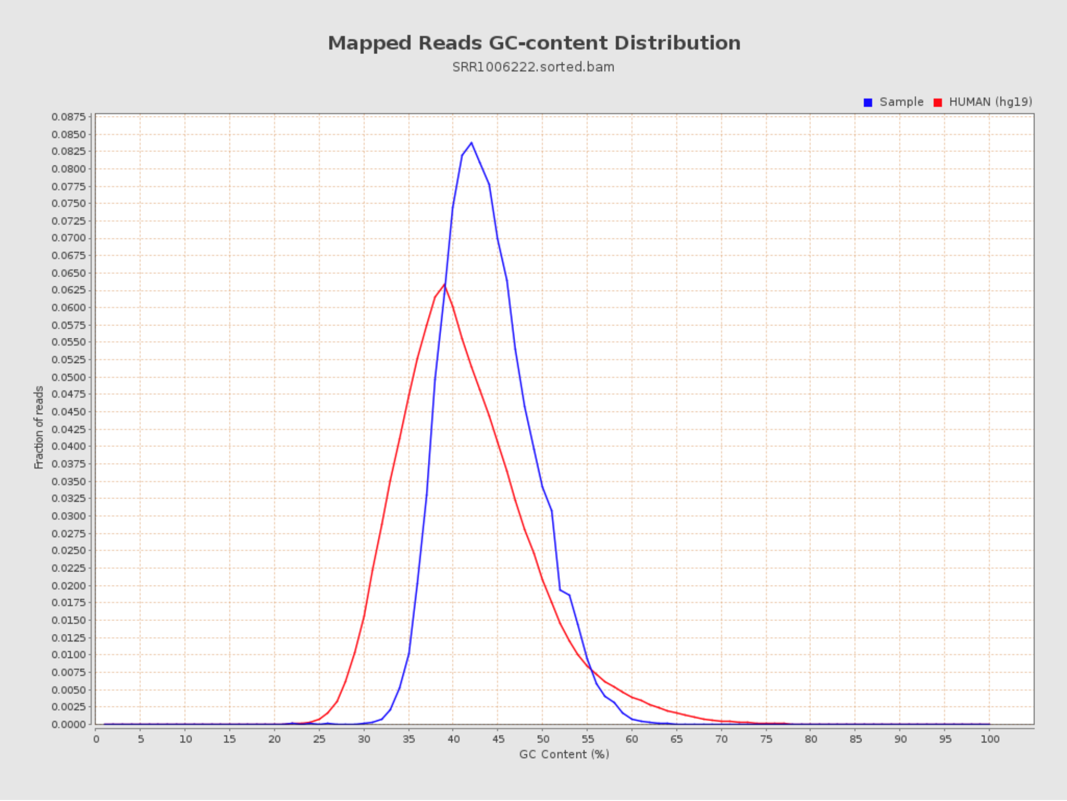
7. Results : Duplication Rate Histogram



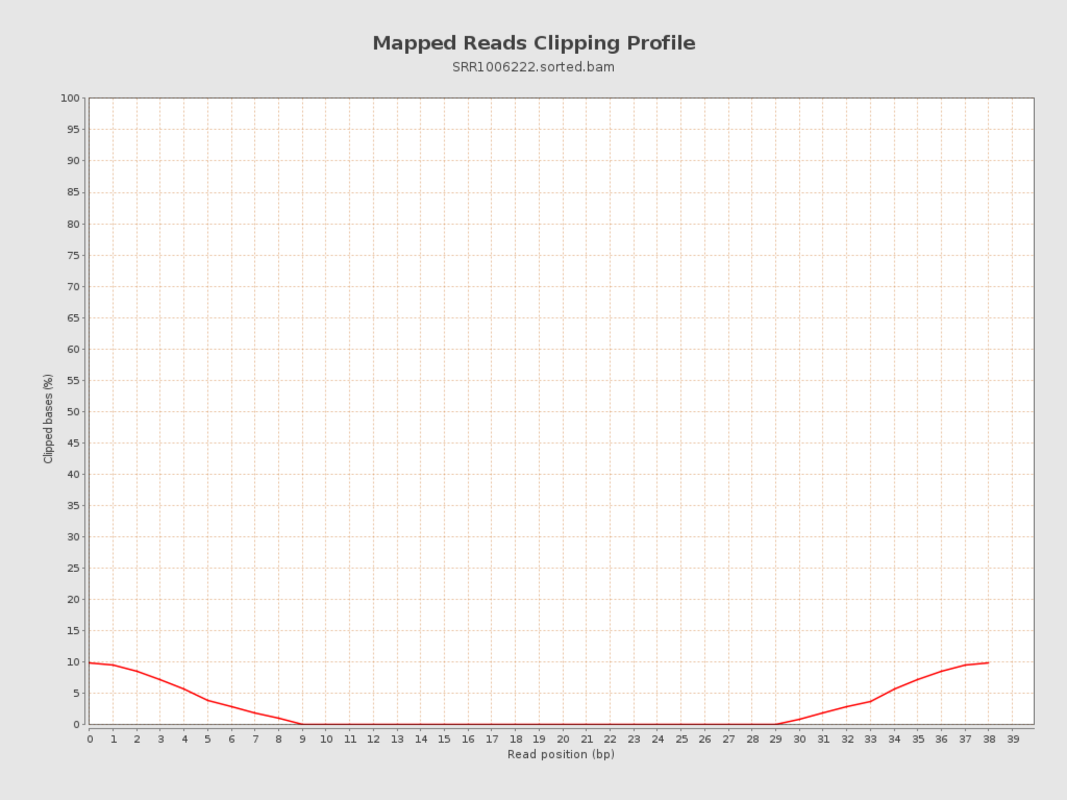
8. Results : Mapped Reads Nucleotide Content



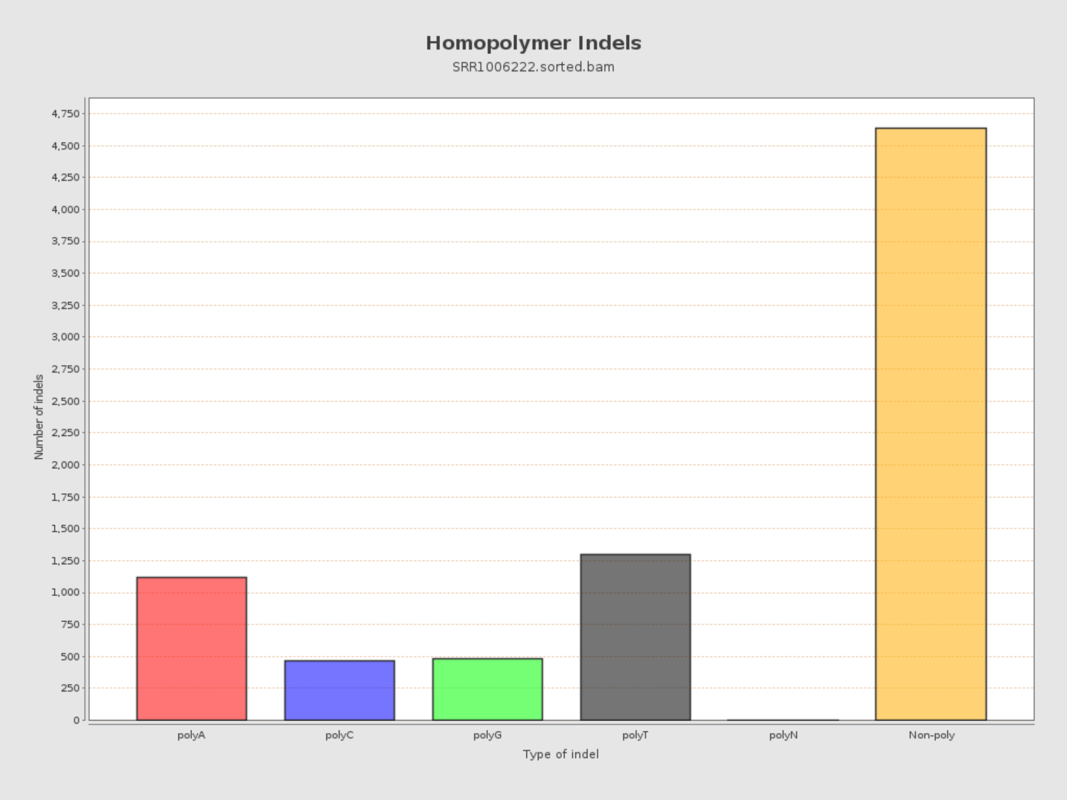
9. Results : Mapped Reads GC-content Distribution



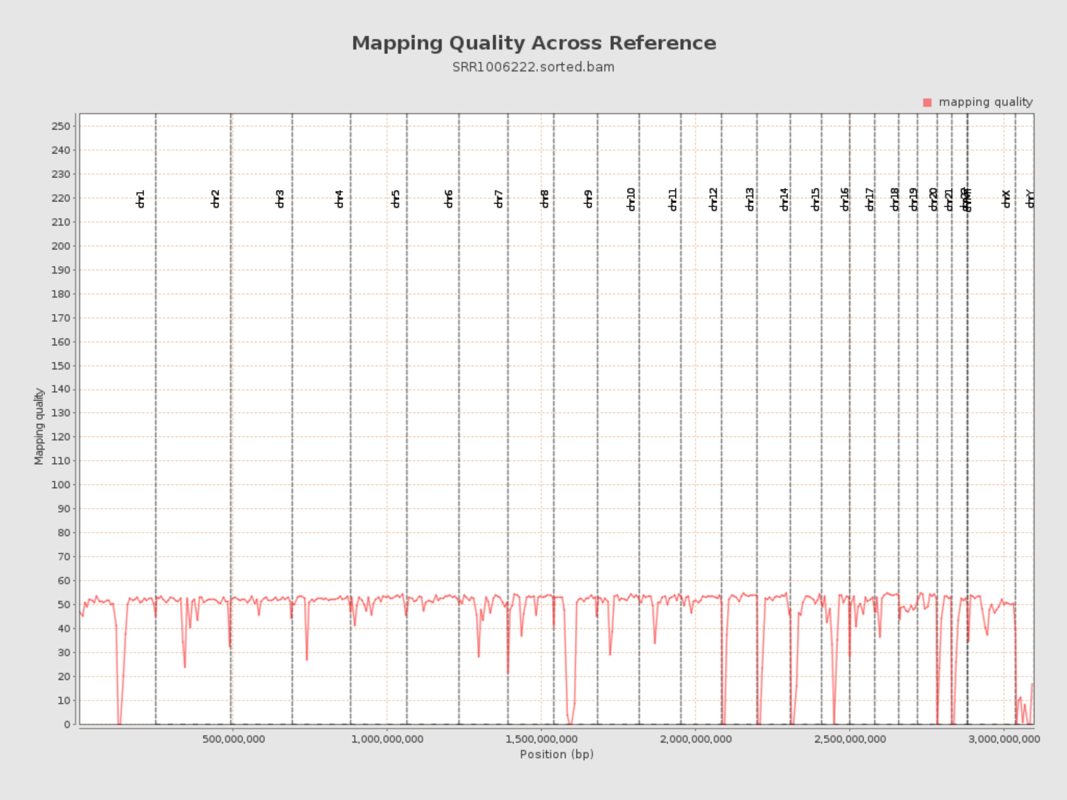
10. Results : Mapped Reads Clipping Profile



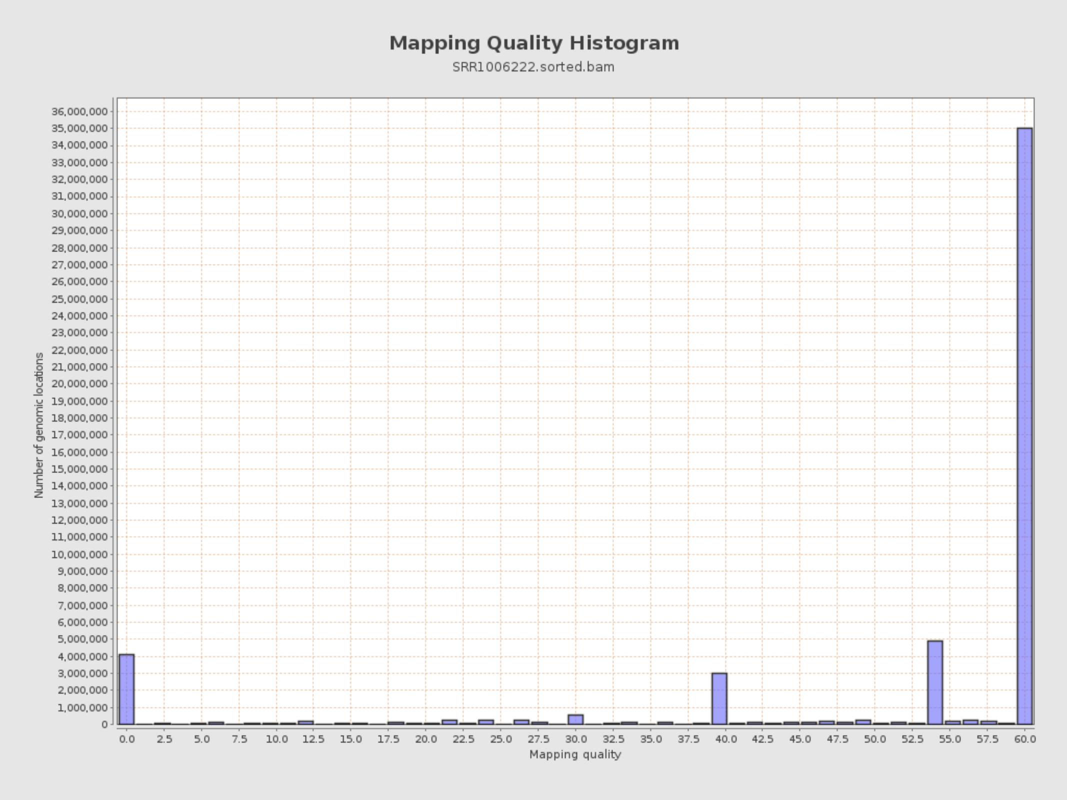
11. Results : Homopolymer Indels



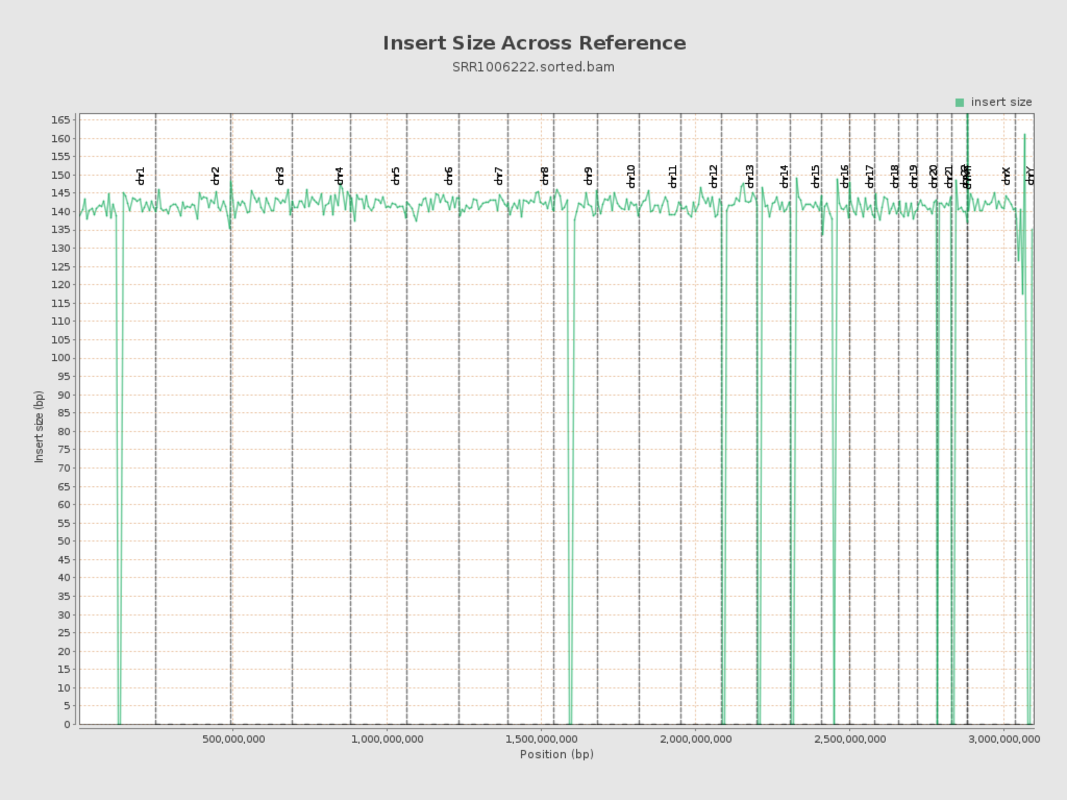
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram