Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 09:50:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173941.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_SRR10173941 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173941_1.fastq.gz SRR10173941_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 09:50:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173941.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,225,956
Mapped reads	3,150,844 / 97.67%
Unmapped reads	75,112 / 2.33%
Mapped paired reads	3,150,844 / 97.67%
Mapped reads, first in pair	1,578,202 / 48.92%
Mapped reads, second in pair	1,572,642 / 48.75%
Mapped reads, both in pair	3,106,112 / 96.29%
Mapped reads, singletons	44,732 / 1.39%
Secondary alignments	0
Supplementary alignments	421,169 / 13.06%
Read min/max/mean length	30 / 133 / 124.26
Duplicated reads (estimated)	2,461,223 / 76.29%
Duplication rate	61.52%
Clipped reads	1,764,928 / 54.71%

2.2. ACGT Content

Number/percentage of A's	105,041,055 / 29.96%
Number/percentage of C's	69,388,172 / 19.79%
Number/percentage of T's	104,115,891 / 29.7%
Number/percentage of G's	72,045,759 / 20.55%
Number/percentage of N's	2,997 / 0%

GC Percentage	40.34%

2.3. Coverage

Mean	0.1133
Standard Deviation	2.2646

2.4. Mapping Quality

Mean Mapping Quality	52.54

2.5. Insert size

Mean	1,016,235.1
Standard Deviation	9,597,519.23
P25/Median/P75	98 / 140 / 211

2.6. Mismatches and indels

General error rate	0.89%
Mismatches	3,017,504
Insertions	40,444
Mapped reads with at least one insertion	1.23%
Deletions	107,128
Mapped reads with at least one deletion	3.32%
Homopolymer indels	40.57%

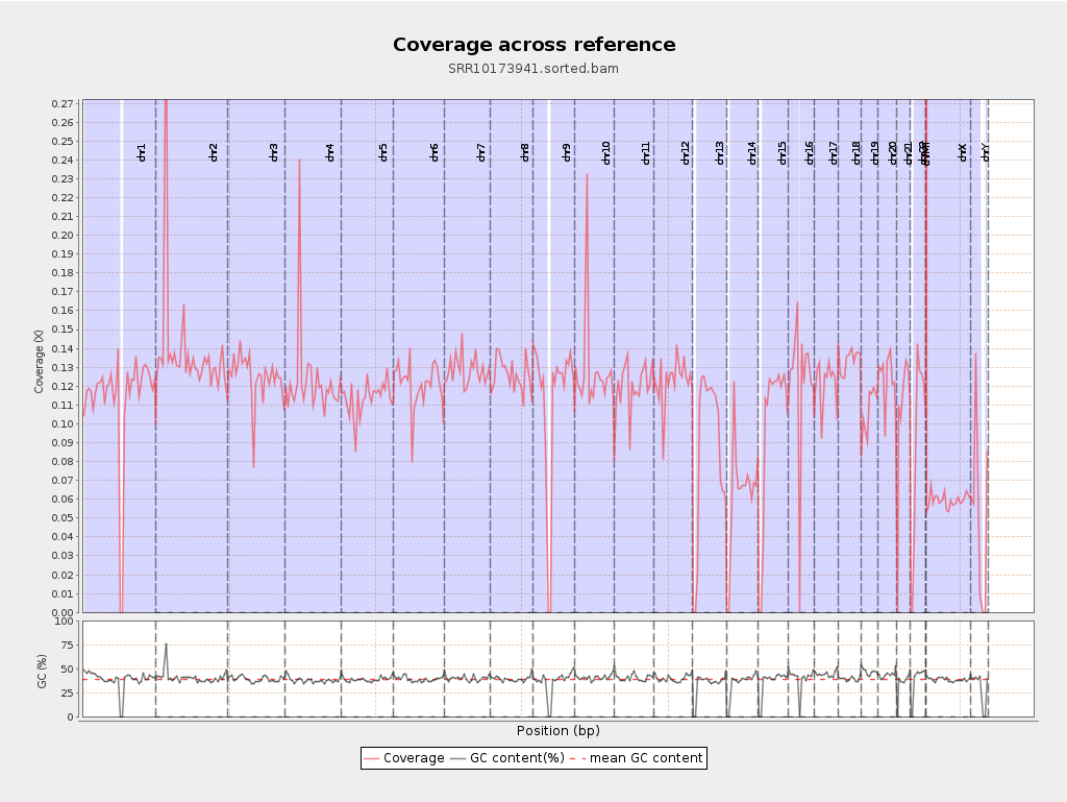
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard

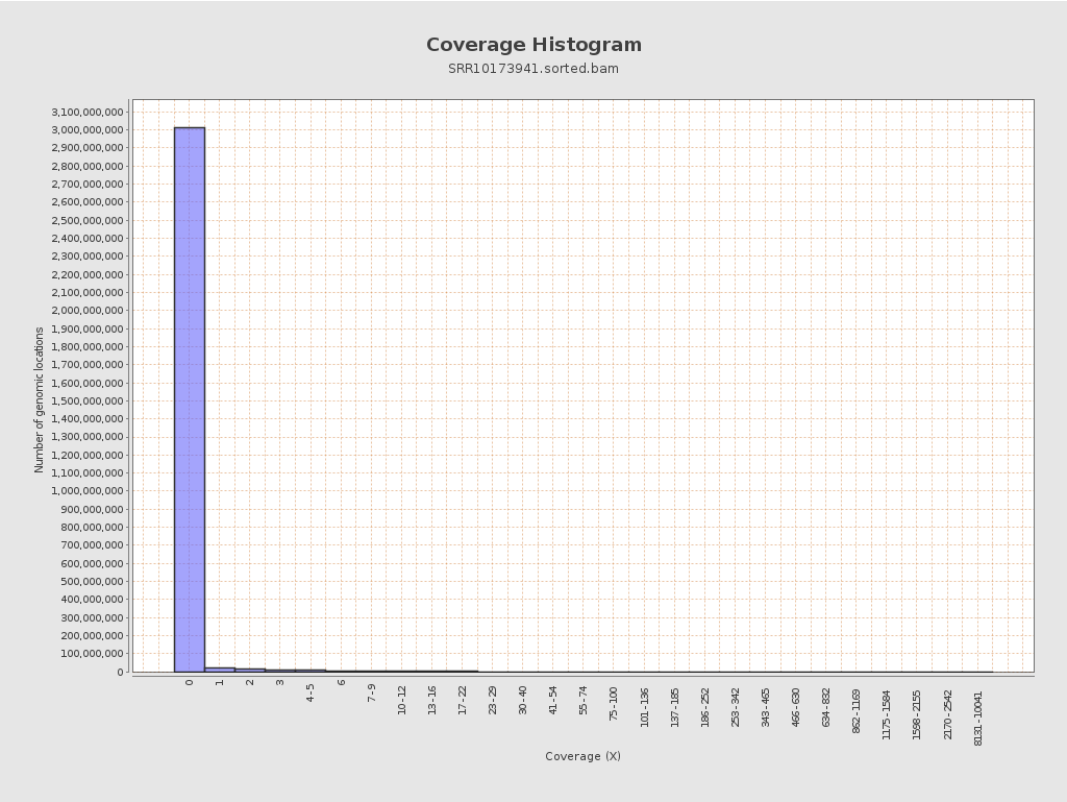
		bases	coverage	deviation
chr1	249250621	28184568	0.1131	1.2574
chr2	243199373	33655009	0.1384	7.0647
chr3	198022430	24651295	0.1245	1.0642
chr4	191154276	23520809	0.123	1.3254
chr5	180915260	20570533	0.1137	1.0015
chr6	171115067	20731396	0.1212	1.084
chr7	159138663	20447638	0.1285	1.2765
chr8	146364022	18471875	0.1262	1.5287
chr9	141213431	15822364	0.112	1.1261
chr10	135534747	17297336	0.1276	1.456
chr11	135006516	16237177	0.1203	1.0521
chr12	133851895	16487276	0.1232	1.0686
chr13	115169878	9995523	0.0868	0.8768
chr14	107349540	6767811	0.063	0.7552
chr15	102531392	9905295	0.0966	0.9225
chr16	90354753	10961350	0.1213	1.1324
chr17	81195210	9919506	0.1222	1.0515
chr18	78077248	10428041	0.1336	1.4275
chr19	59128983	6345667	0.1073	1.0548
chr20	63025520	7796519	0.1237	1.1166
chr21	48129895	5193523	0.1079	1.115
chr22	51304566	4557113	0.0888	0.9921
chrMT	16571	555746	33.5373	29.9251
chrX	155270560	9240531	0.0595	0.7195

chrY	59373566	3099859	0.0522	1.0017

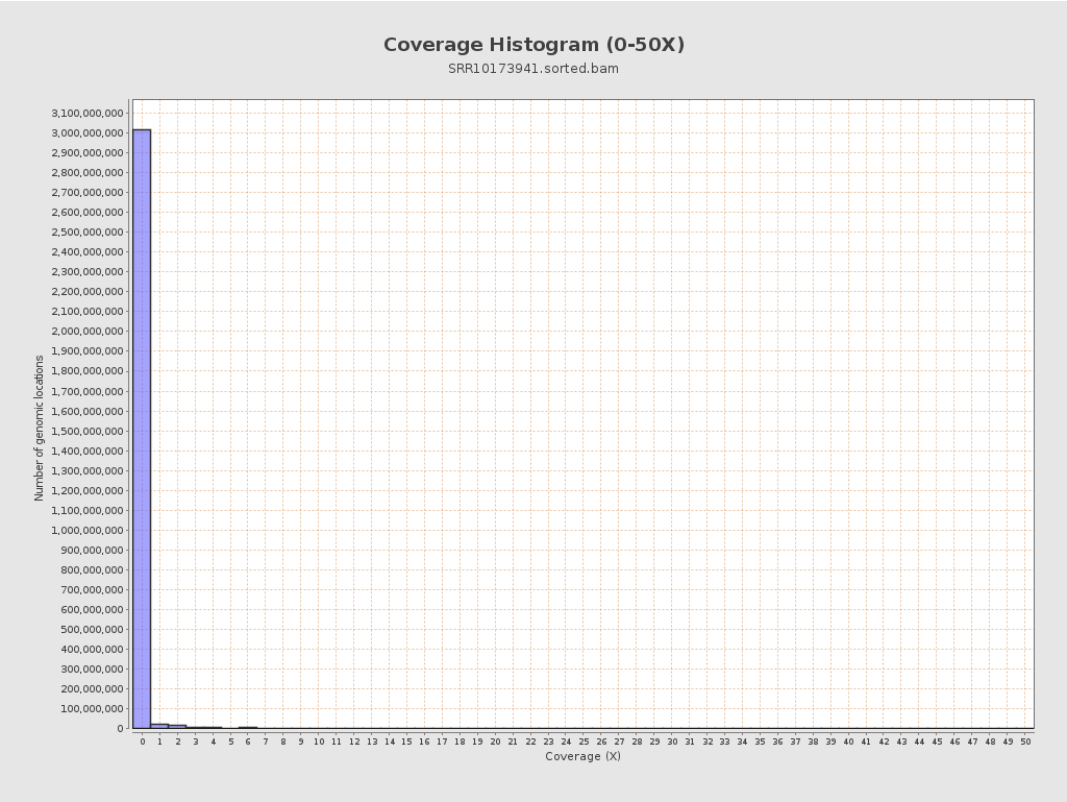
3. Results : Coverage across reference



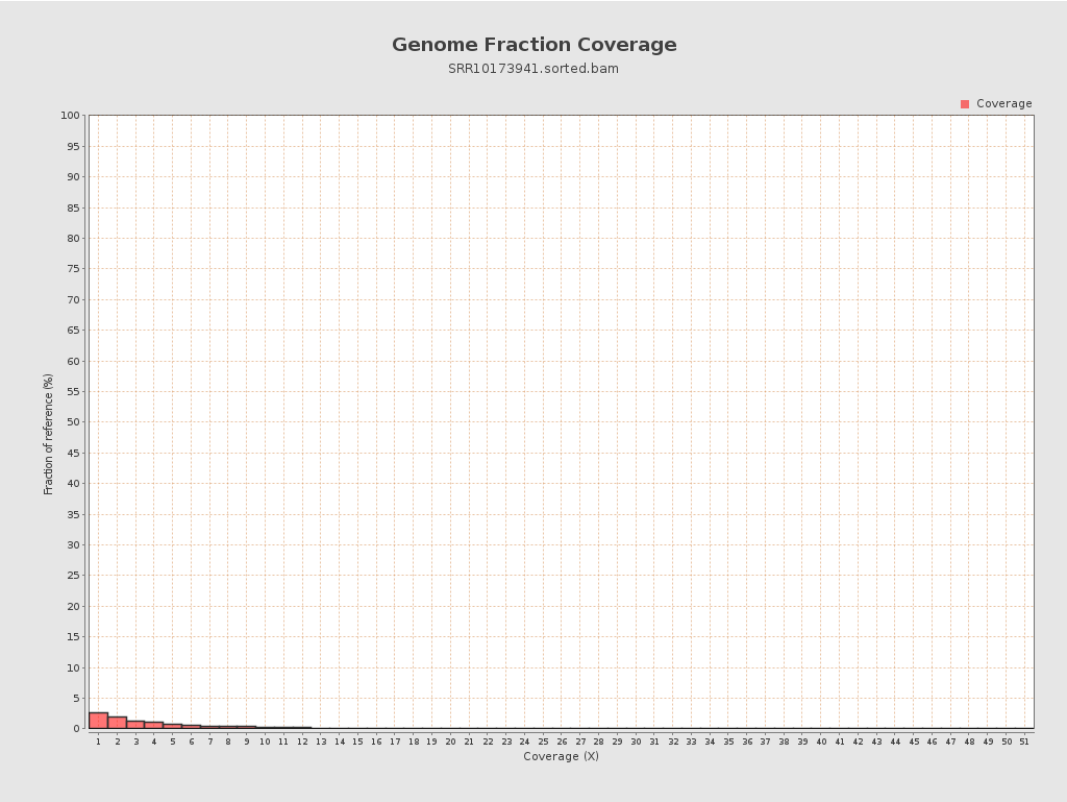
4. Results : Coverage Histogram



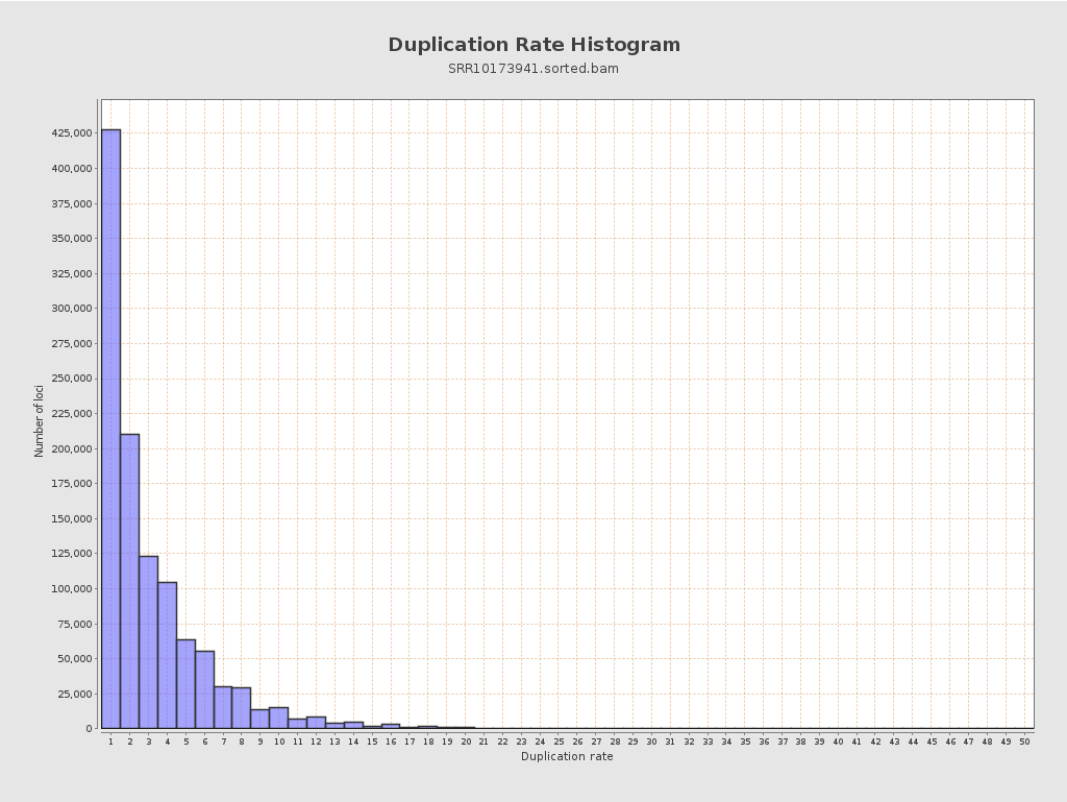
5. Results : Coverage Histogram (0-50X)



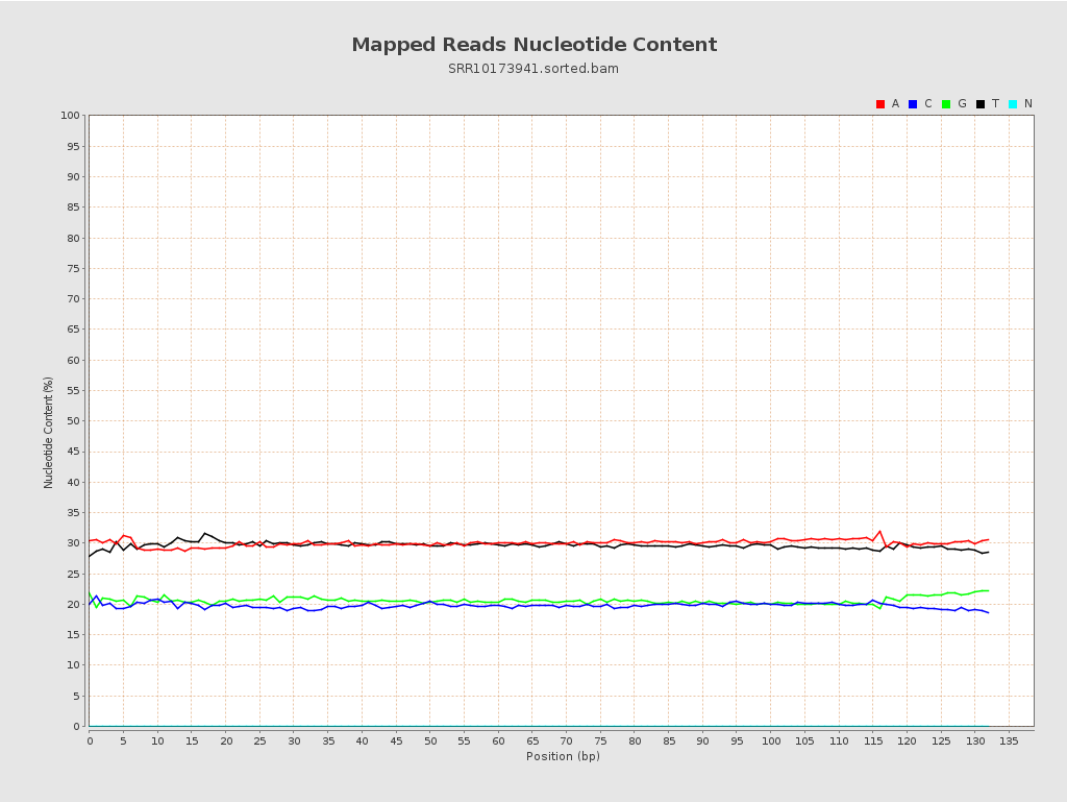
6. Results : Genome Fraction Coverage



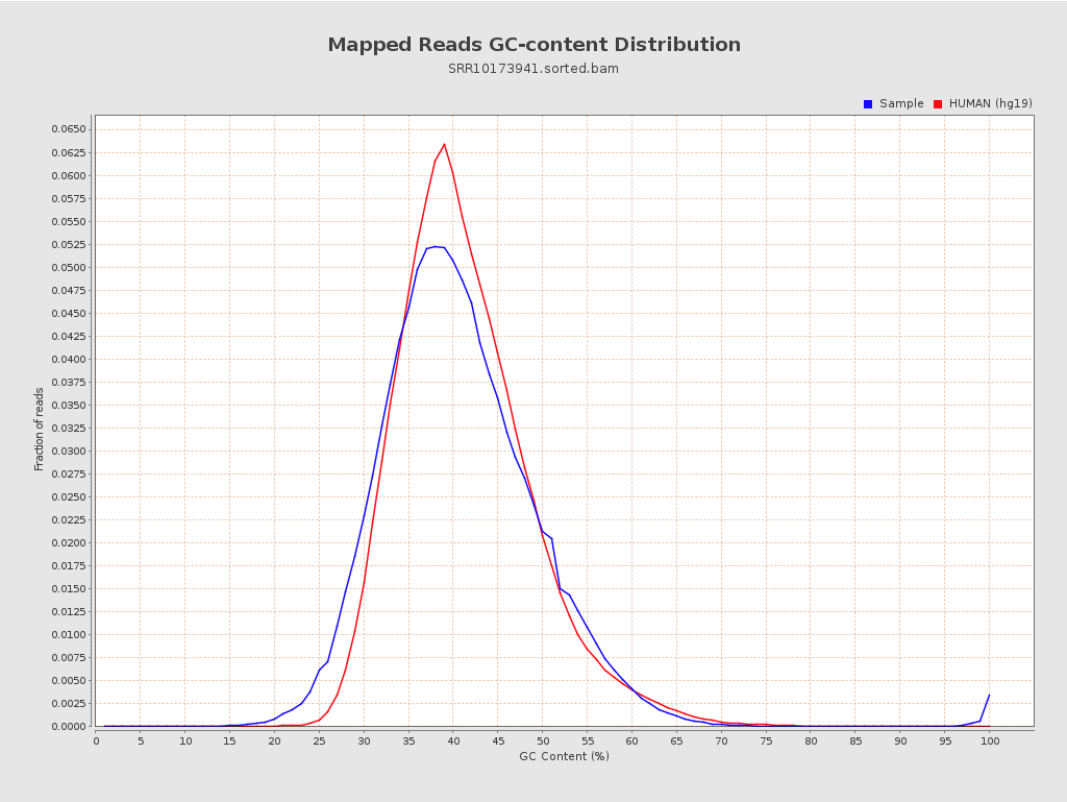
7. Results : Duplication Rate Histogram



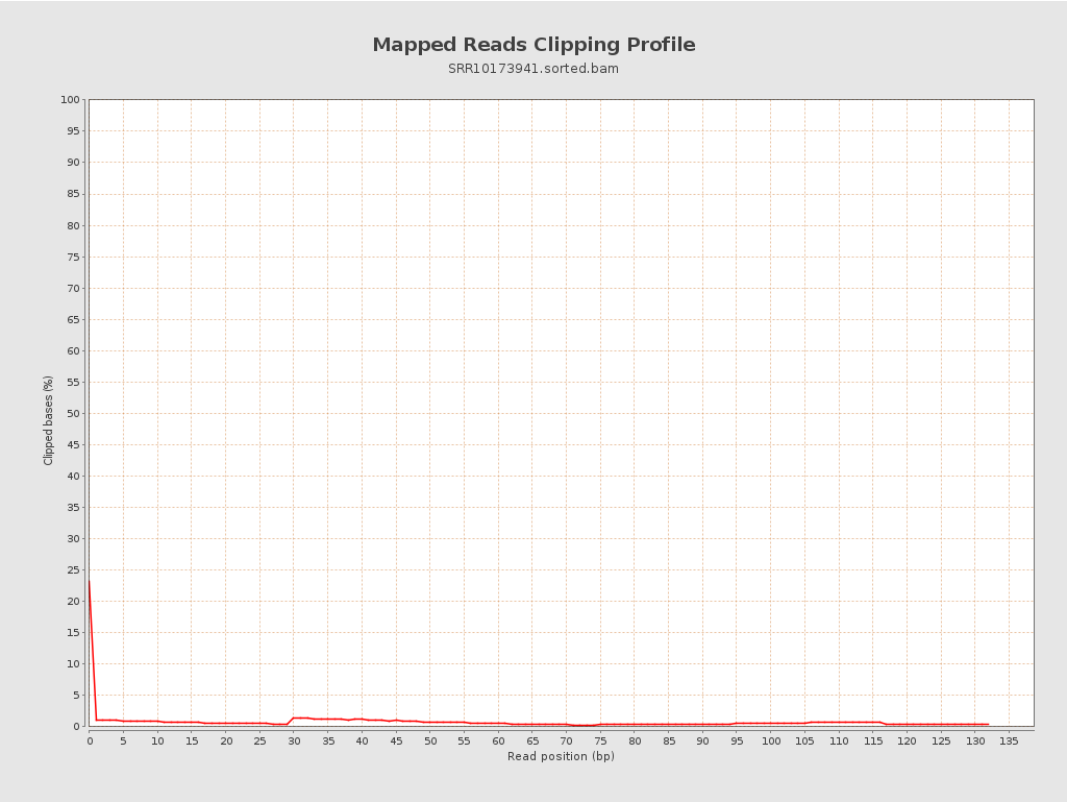
8. Results : Mapped Reads Nucleotide Content



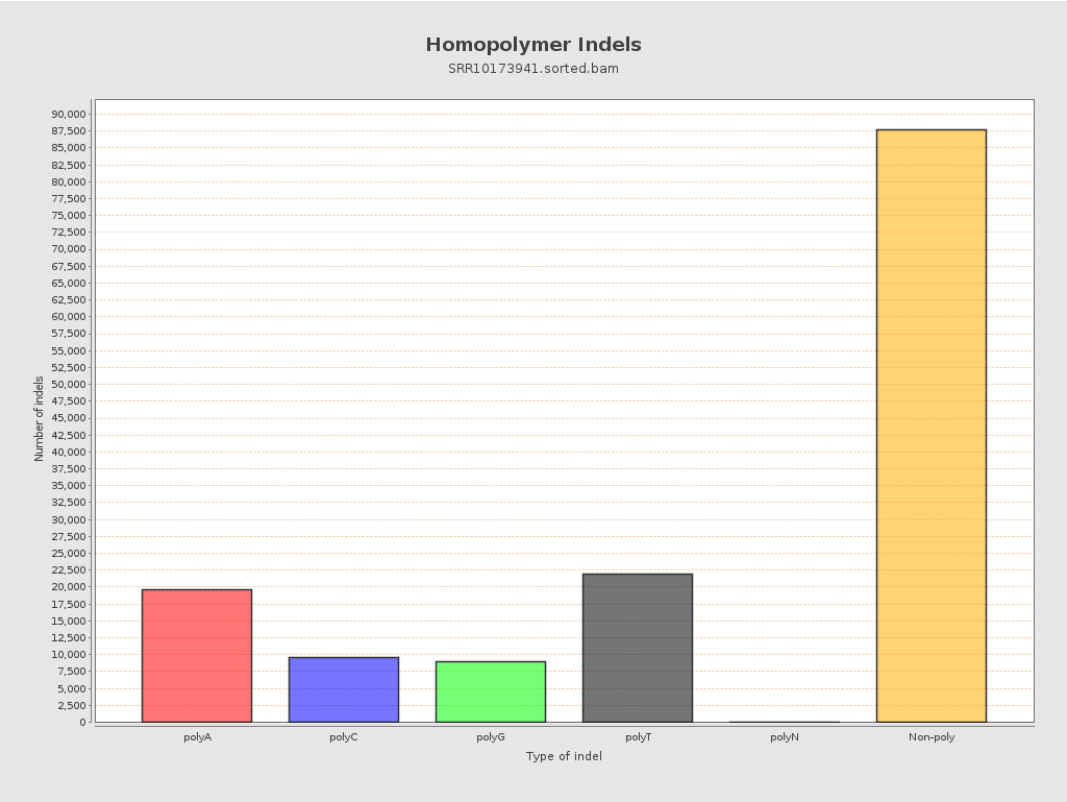
9. Results : Mapped Reads GC-content Distribution



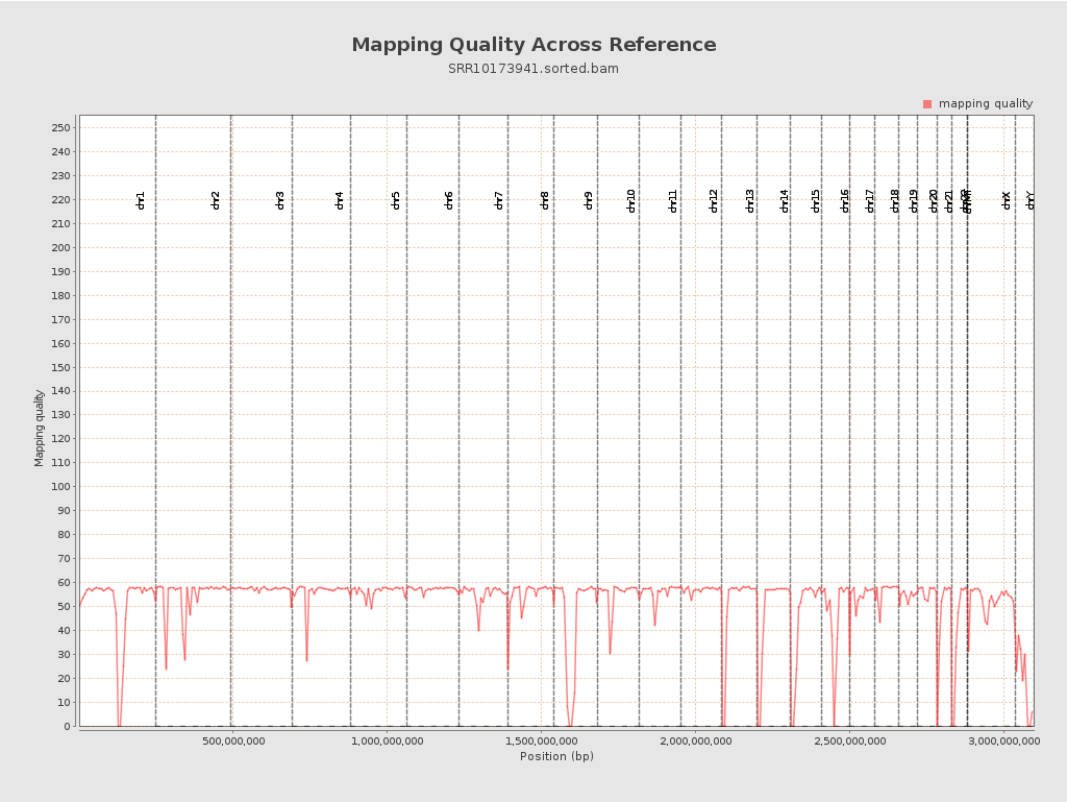
10. Results : Mapped Reads Clipping Profile



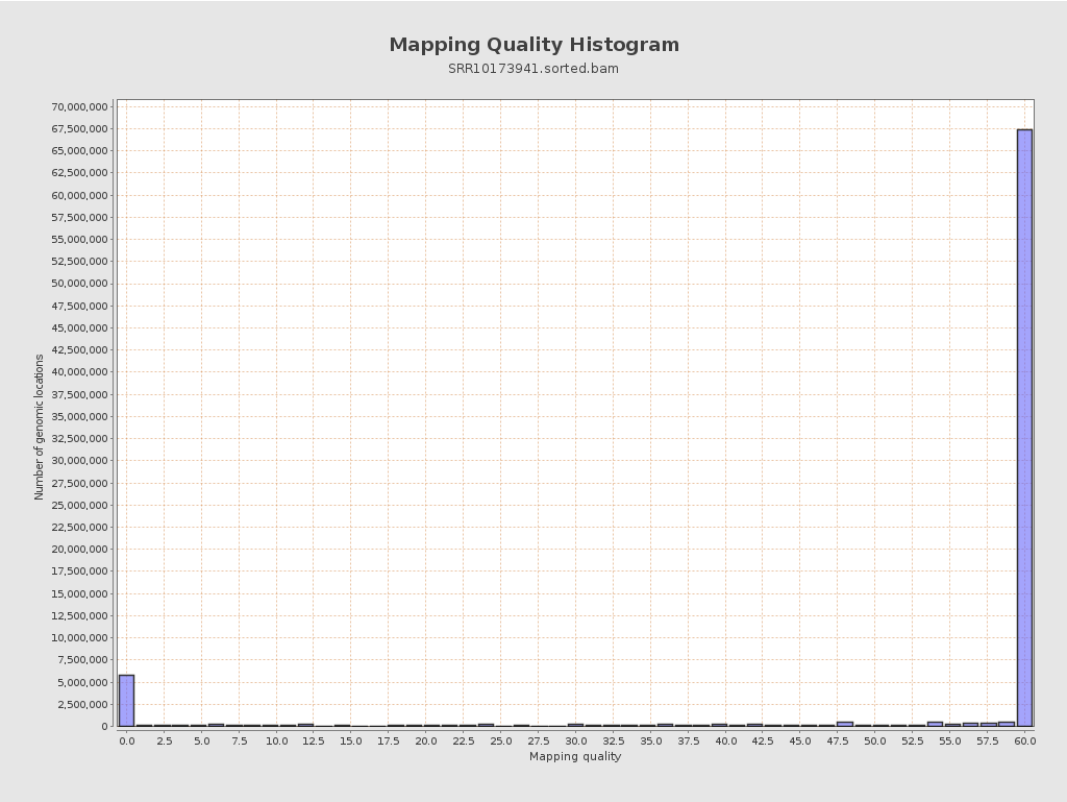
11. Results : Homopolymer Indels



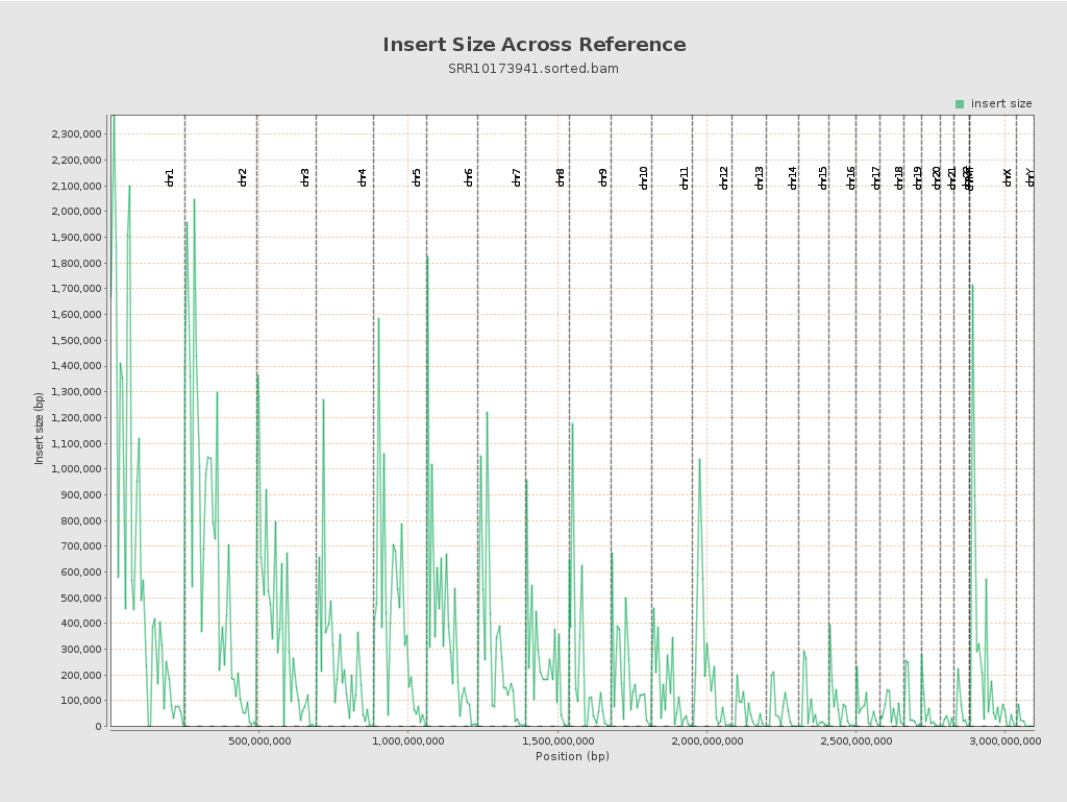
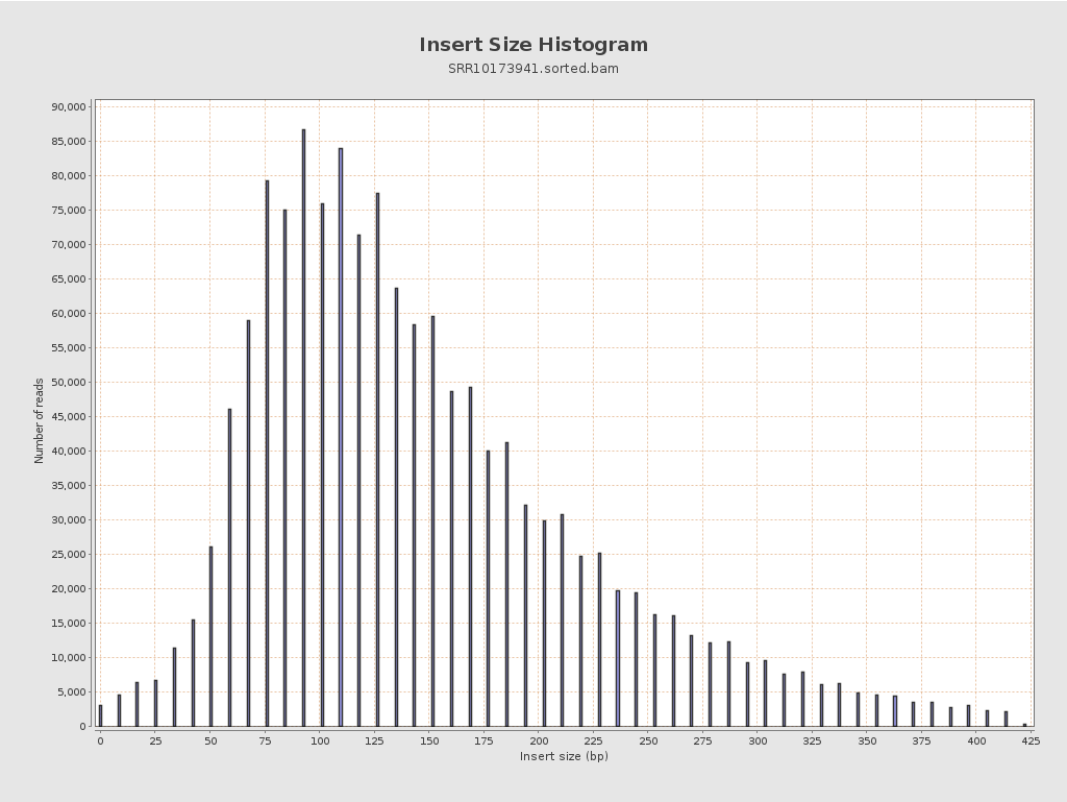
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram