Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 16:40:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779392.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_SRR1779392 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779392_1.fastq.gz SRR1779392_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 16:40:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779392.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,789,370
Mapped reads	5,649,031 / 83.2%
Unmapped reads	1,140,339 / 16.8%
Mapped paired reads	5,649,031 / 83.2%
Mapped reads, first in pair	2,855,224 / 42.05%
Mapped reads, second in pair	2,793,807 / 41.15%
Mapped reads, both in pair	5,553,074 / 81.79%
Mapped reads, singletons	95,957 / 1.41%
Secondary alignments	0
Supplementary alignments	19,311 / 0.28%
Read min/max/mean length	30 / 80 / 80.1
Duplicated reads (estimated)	100,747 / 1.48%
Duplication rate	1.52%
Clipped reads	283,469 / 4.18%

2.2. ACGT Content

Number/percentage of A's	136,272,711 / 30.39%
Number/percentage of C's	86,878,463 / 19.37%
Number/percentage of T's	133,288,684 / 29.72%
Number/percentage of G's	91,894,612 / 20.49%
Number/percentage of N's	97,472 / 0.02%

GC Percentage	39.87%

2.3. Coverage

Mean	0.1449
Standard Deviation	0.5642

2.4. Mapping Quality

Mean Mapping Quality	53.46

2.5. Insert size

Mean	42,687
Standard Deviation	1,964,258.44
P25/Median/P75	236 / 352 / 519

2.6. Mismatches and indels

General error rate	0.5%
Mismatches	2,155,314
Insertions	39,251
Mapped reads with at least one insertion	0.69%
Deletions	46,244
Mapped reads with at least one deletion	0.81%
Homopolymer indels	47.1%

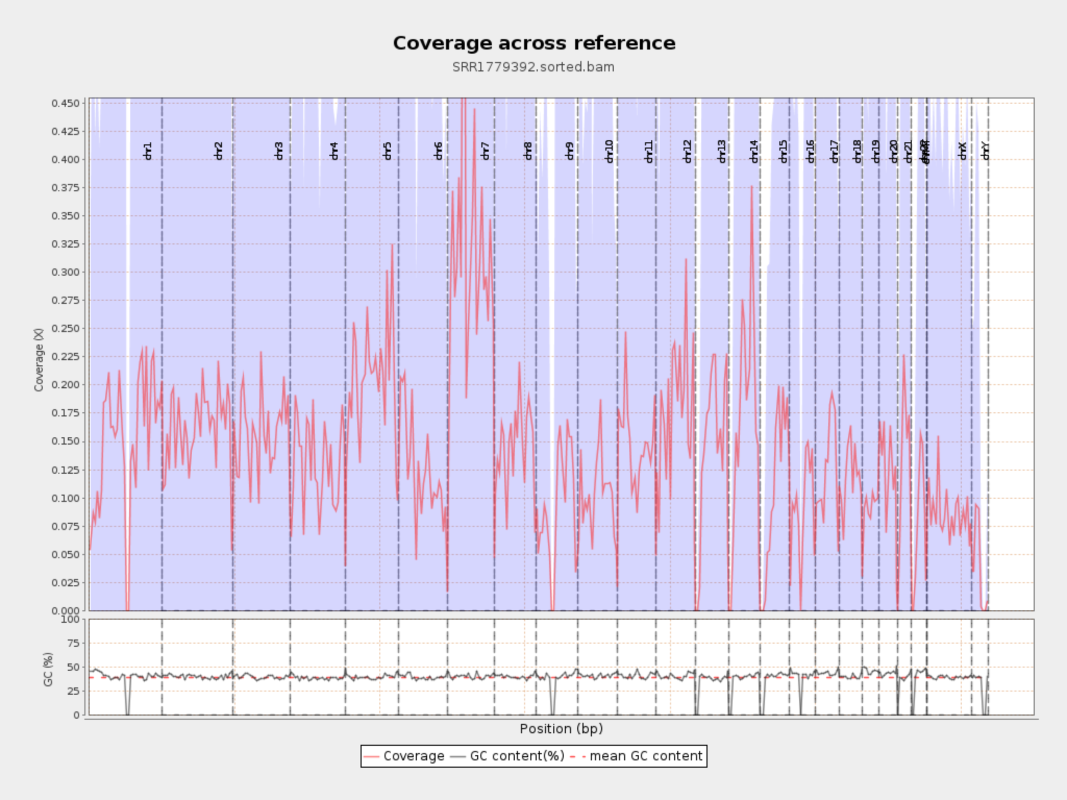
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

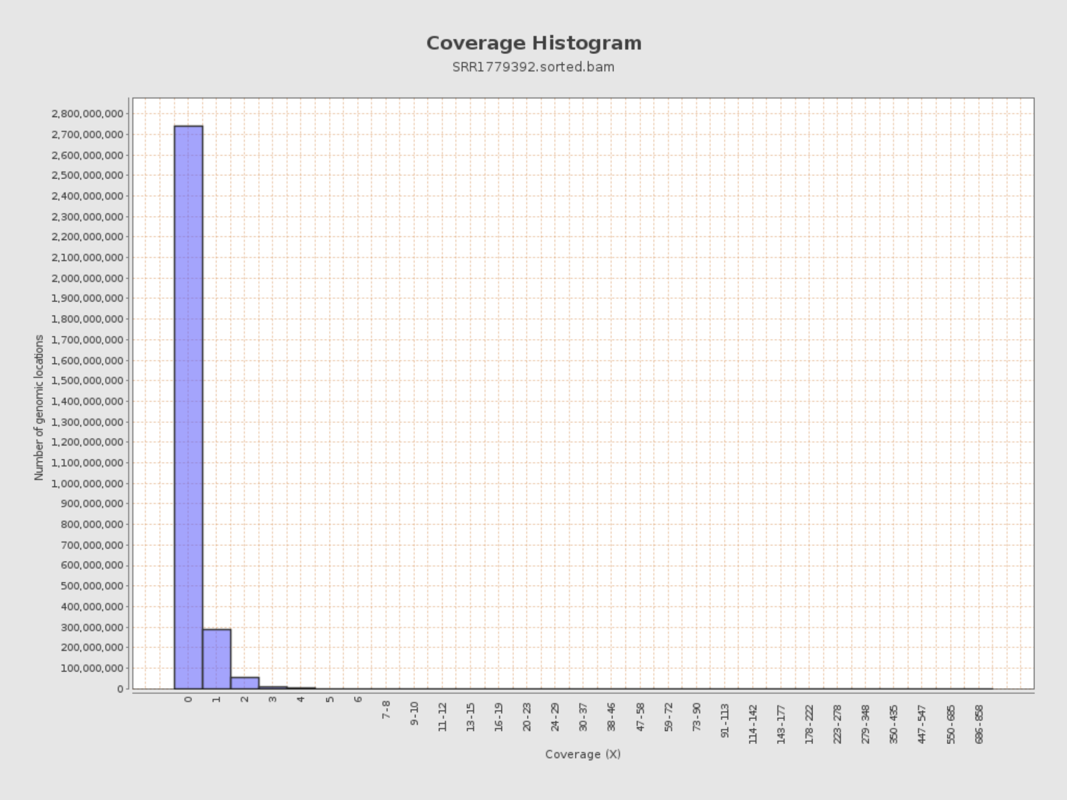
		bases	coverage	deviation
chr1	249250621	37353672	0.1499	0.9667
chr2	243199373	39472824	0.1623	0.5382
chr3	198022430	31105128	0.1571	0.4552
chr4	191154276	25224383	0.132	0.4185
chr5	180915260	37357070	0.2065	0.5196
chr6	171115067	21186547	0.1238	0.4175
chr7	159138663	51931959	0.3263	0.952
chr8	146364022	21351651	0.1459	0.4362
chr9	141213431	13017490	0.0922	0.3969
chr10	135534747	14225421	0.105	0.7373
chr11	135006516	19877107	0.1472	0.4623
chr12	133851895	23878249	0.1784	0.4962
chr13	115169878	16809616	0.146	0.4498
chr14	107349540	18735190	0.1745	0.5038
chr15	102531392	10725718	0.1046	0.3781
chr16	90354753	8150807	0.0902	0.3639
chr17	81195210	10040368	0.1237	0.4439
chr18	78077248	9269657	0.1187	0.4947
chr19	59128983	5507360	0.0931	0.7367
chr20	63025520	7892292	0.1252	0.4149
chr21	48129895	6077625	0.1263	0.4183
chr22	51304566	3899349	0.076	0.3299
chrMT	16571	983	0.0593	0.2857
chrX	155270560	13468636	0.0867	0.3399

chrY	59373566	1967767	0.0331	0.2088

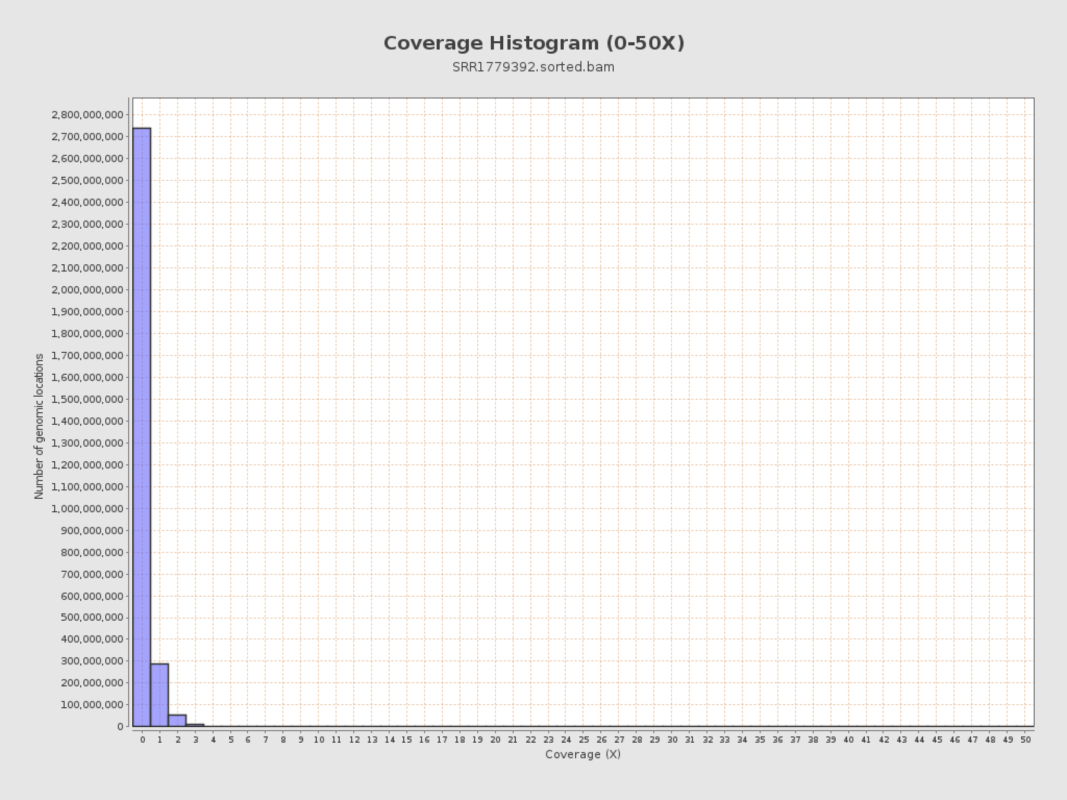
3. Results : Coverage across reference



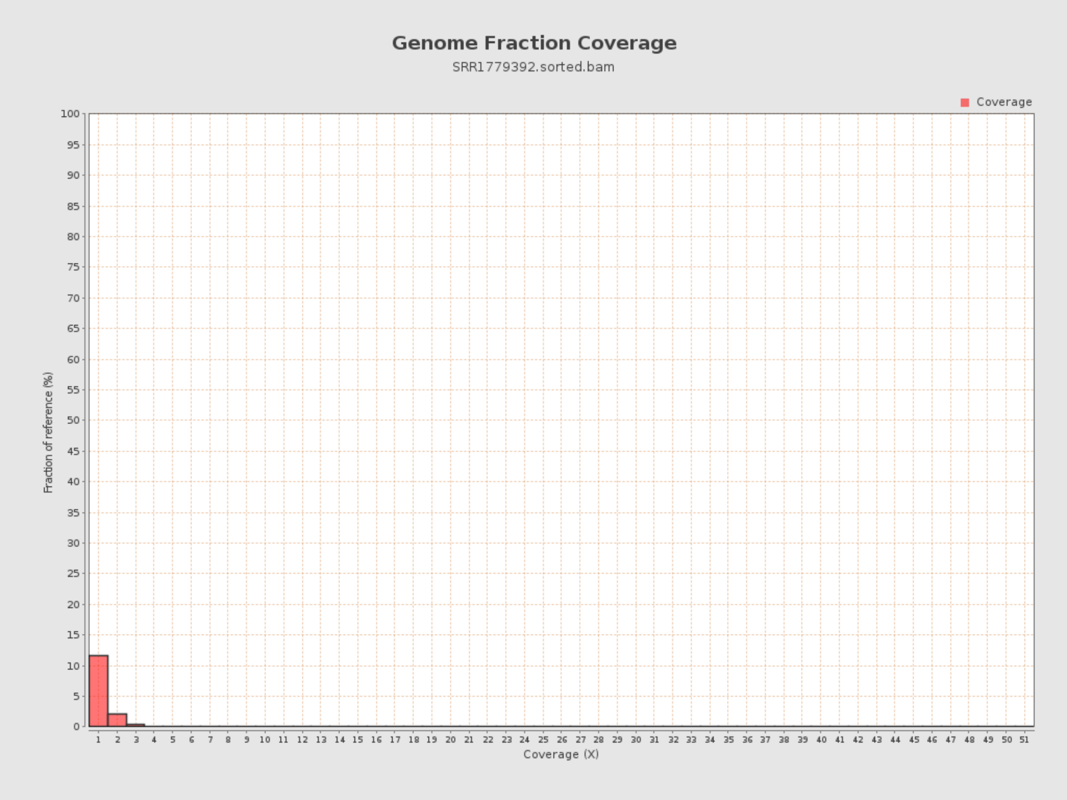
4. Results : Coverage Histogram



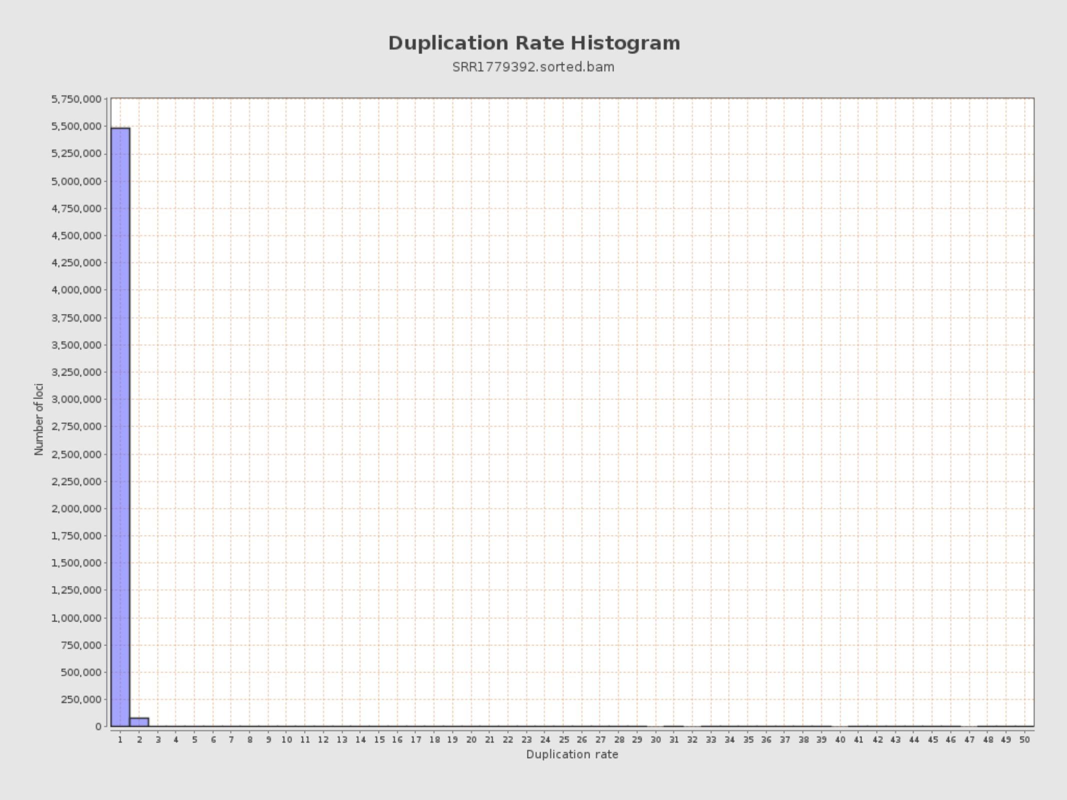
5. Results : Coverage Histogram (0-50X)



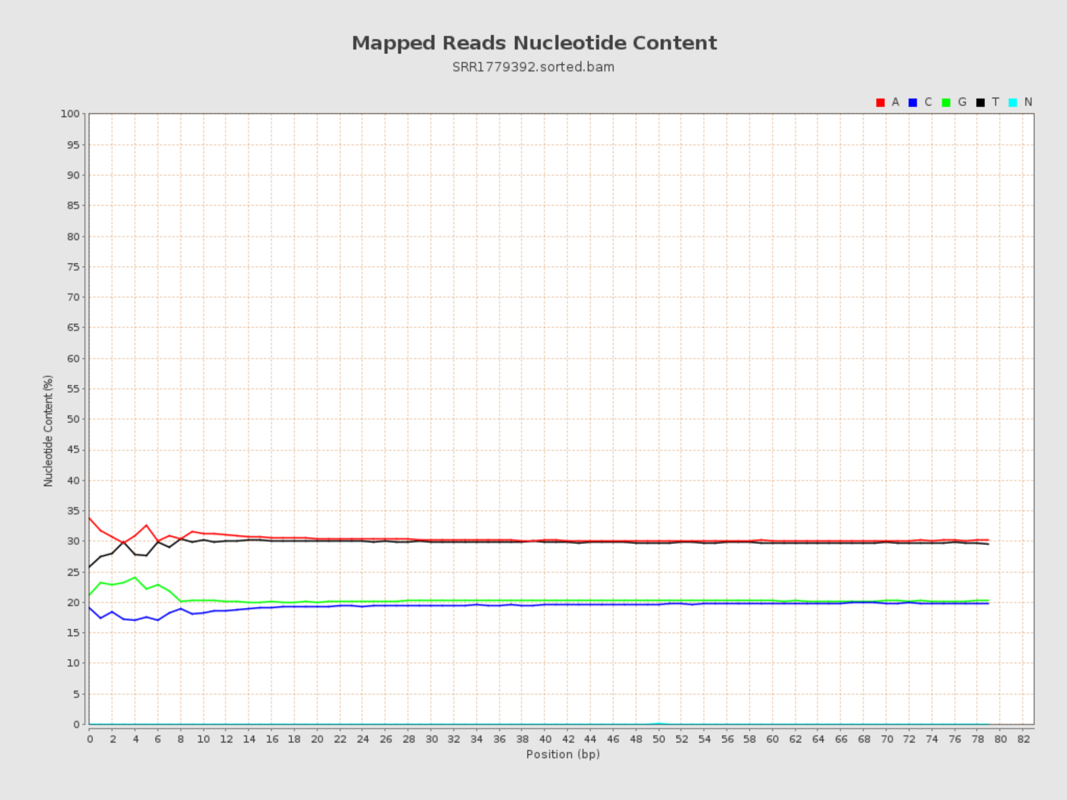
6. Results : Genome Fraction Coverage



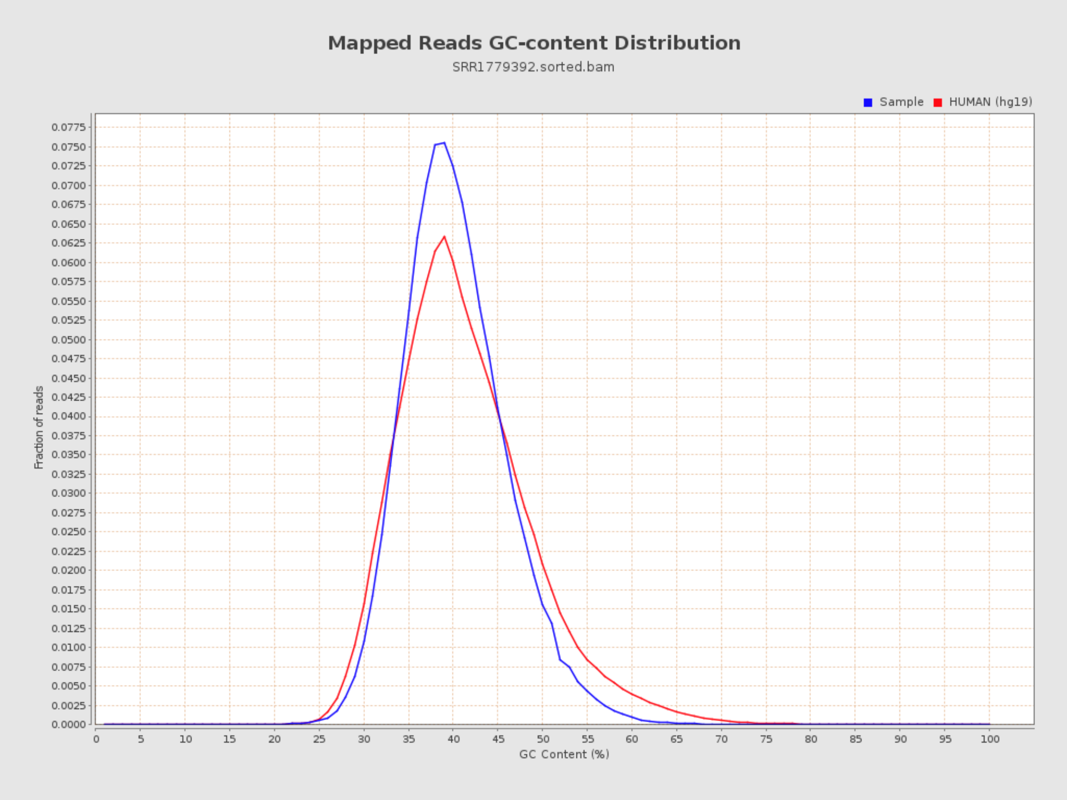
7. Results : Duplication Rate Histogram



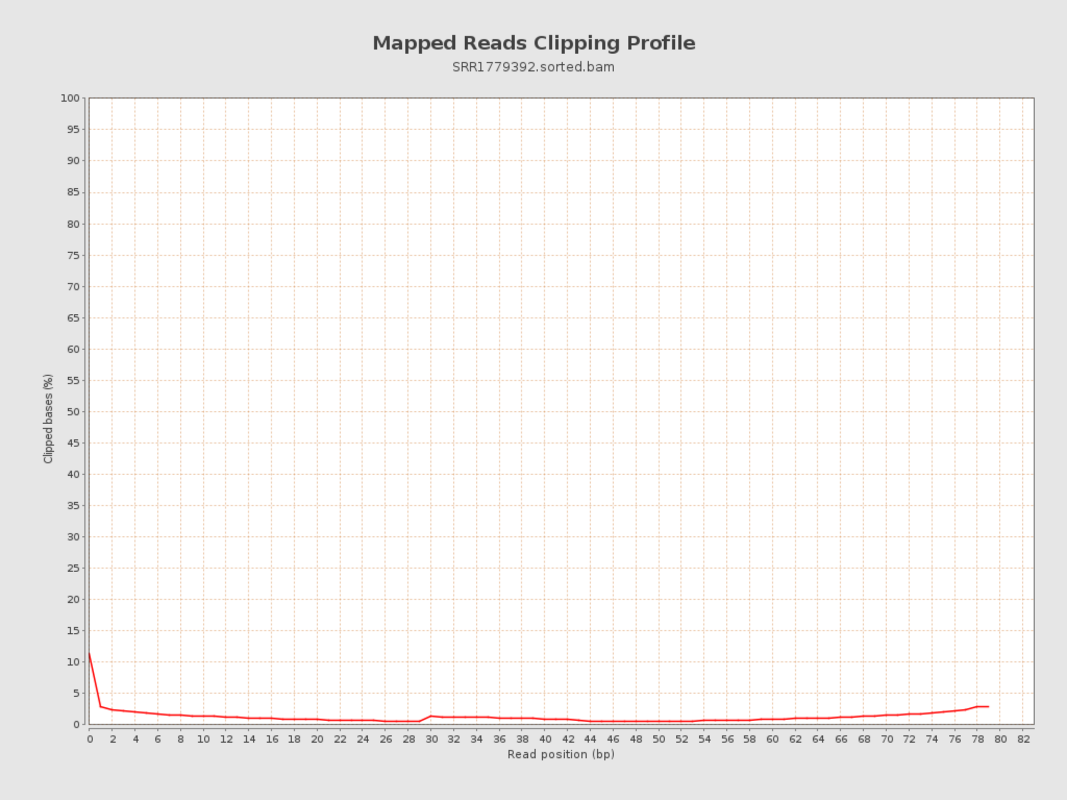
8. Results : Mapped Reads Nucleotide Content



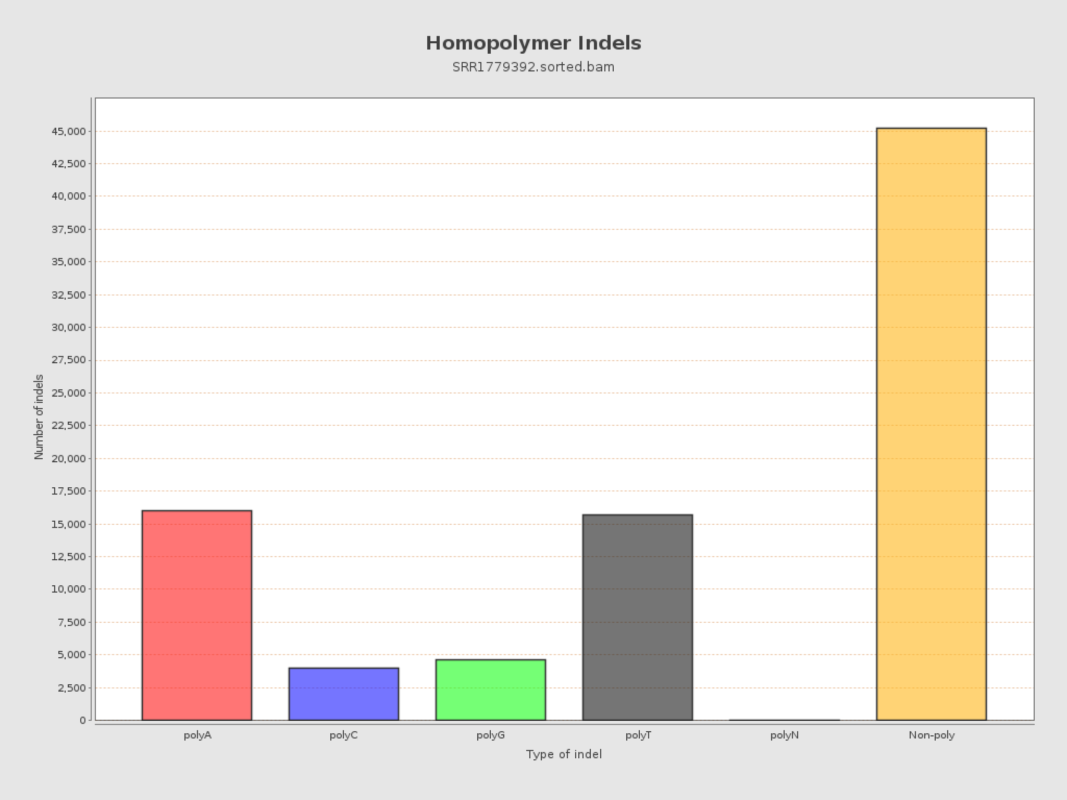
9. Results : Mapped Reads GC-content Distribution



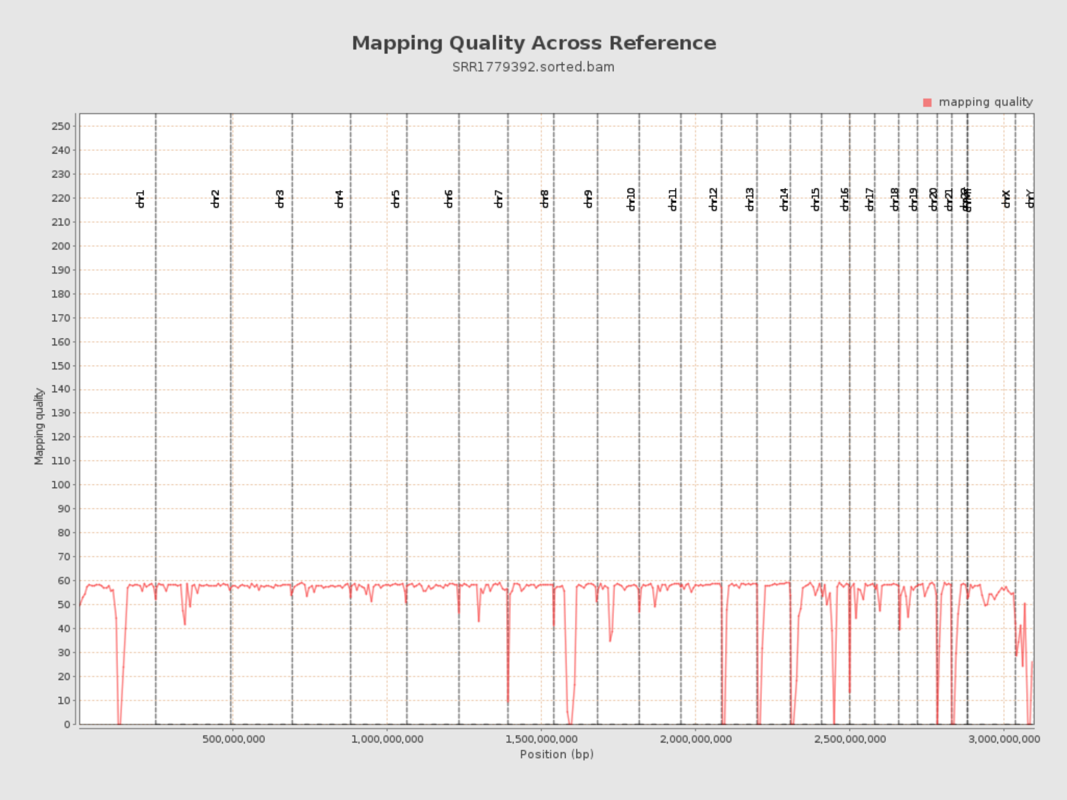
10. Results : Mapped Reads Clipping Profile



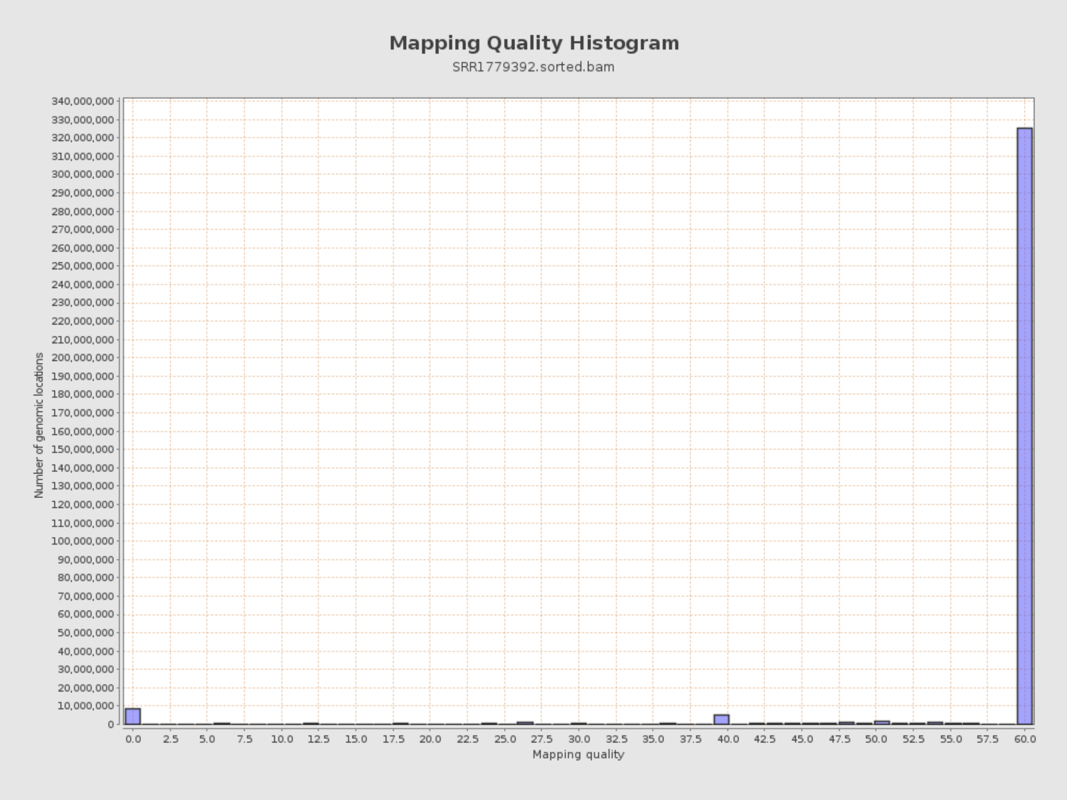
11. Results : Homopolymer Indels



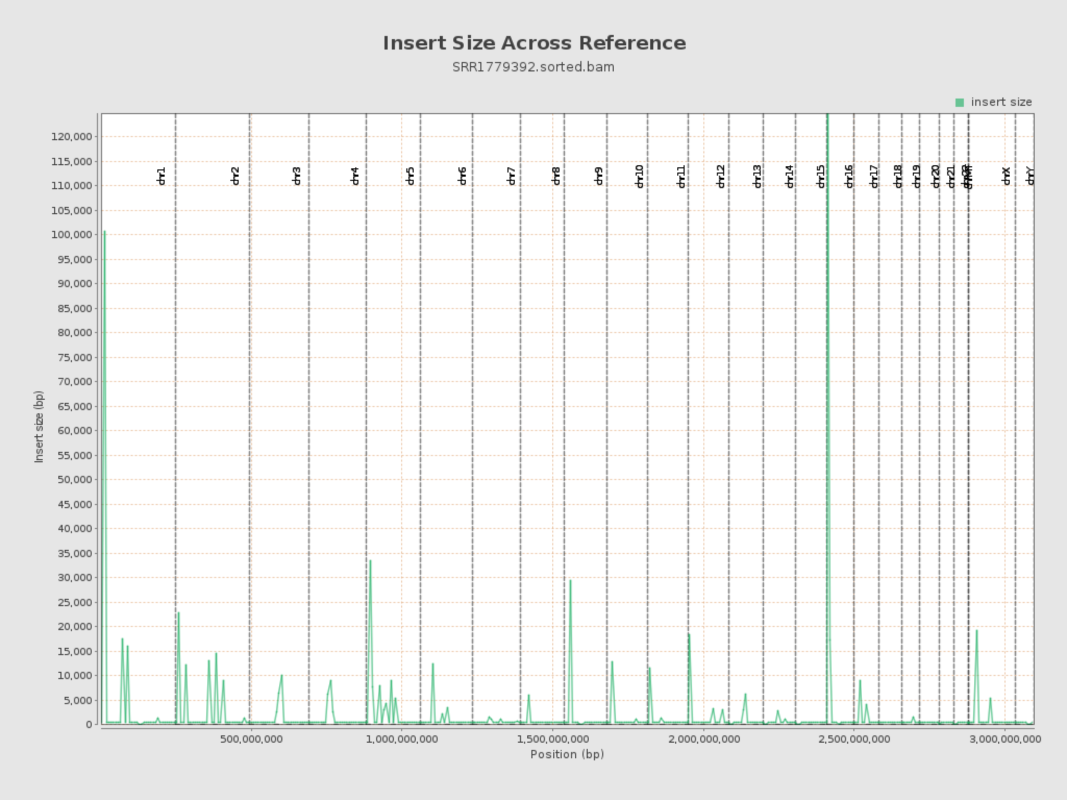
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram