Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 10:53:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777294.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_SRR1777294 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777294_1.fastq.gz SRR1777294_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 10:53:55 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777294.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	86,550,558
Mapped reads	85,289,432 / 98.54%
Unmapped reads	1,261,126 / 1.46%
Mapped paired reads	85,289,432 / 98.54%
Mapped reads, first in pair	42,736,292 / 49.38%
Mapped reads, second in pair	42,553,140 / 49.17%
Mapped reads, both in pair	84,922,740 / 98.12%
Mapped reads, singletons	366,692 / 0.42%
Secondary alignments	0
Supplementary alignments	3,169,814 / 3.66%
Read min/max/mean length	30 / 101 / 102.52
Duplicated reads (estimated)	15,764,311 / 18.21%
Duplication rate	13.1%
Clipped reads	24,971,420 / 28.85%

2.2. ACGT Content

Number/percentage of A's	2,389,436,476 / 29.02%
Number/percentage of C's	1,727,554,102 / 20.98%
Number/percentage of T's	2,333,957,304 / 28.34%
Number/percentage of G's	1,783,622,237 / 21.66%
Number/percentage of N's	136,728 / 0%

GC Percentage	42.64%

2.3. Coverage

Mean	2.661
Standard Deviation	28.2904

2.4. Mapping Quality

Mean Mapping Quality	53.12

2.5. Insert size

Mean	122,790.62
Standard Deviation	3,367,526.02
P25/Median/P75	111 / 153 / 208

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	50,306,556
Insertions	1,785,450
Mapped reads with at least one insertion	2.04%
Deletions	1,087,499
Mapped reads with at least one deletion	1.23%
Homopolymer indels	44.98%

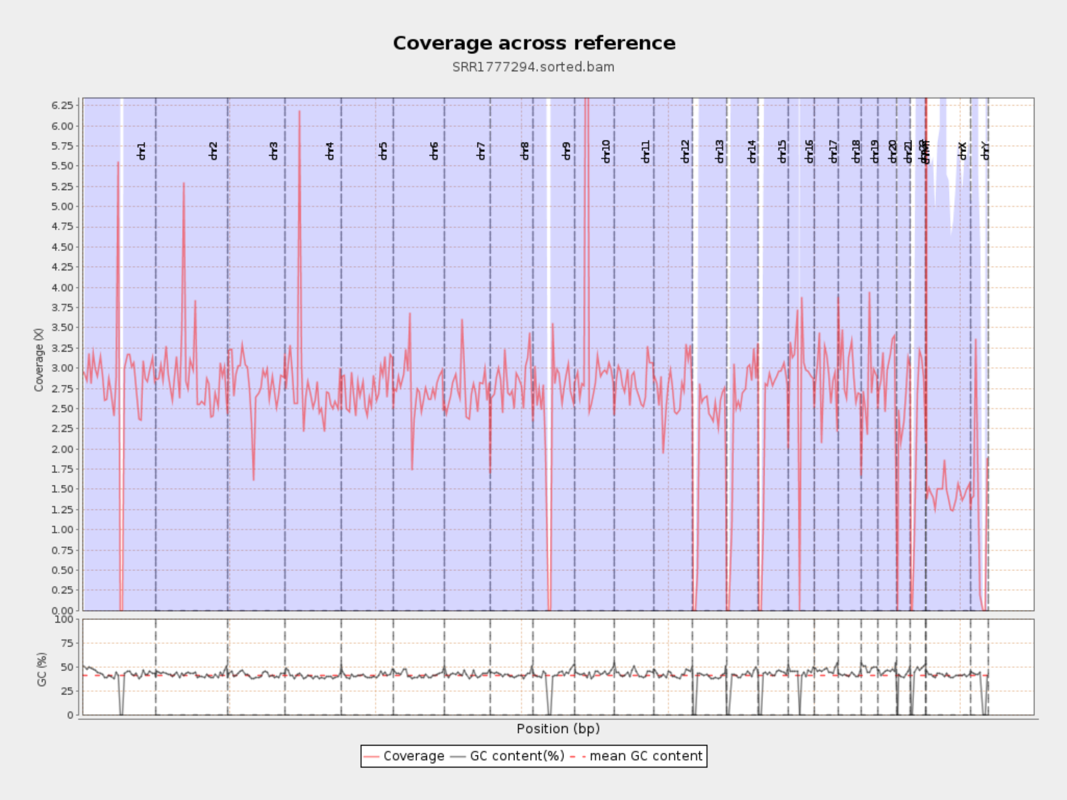
2.7. Chromosome stats

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

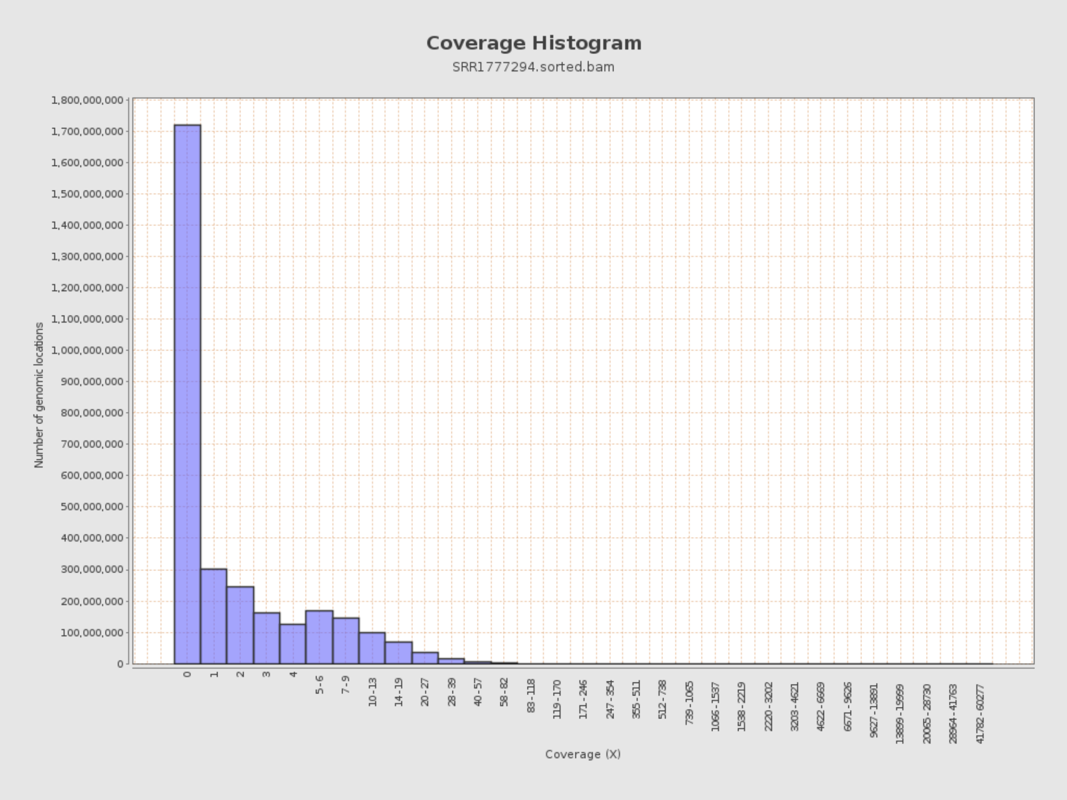
		bases	coverage	deviation
chr1	249250621	695090564	2.7887	59.1776
chr2	243199373	712323121	2.929	19.7784
chr3	198022430	556249378	2.809	9.5837
chr4	191154276	537741257	2.8131	23.4219
chr5	180915260	498176861	2.7536	6.0721
chr6	171115067	470940568	2.7522	14.557
chr7	159138663	435595862	2.7372	20.9881
chr8	146364022	413095152	2.8224	10.8181
chr9	141213431	349149513	2.4725	25.3822
chr10	135534747	450907840	3.3269	75.9581
chr11	135006516	382089968	2.8302	12.9315
chr12	133851895	367867161	2.7483	5.8793
chr13	115169878	245280922	2.1297	5.0306
chr14	107349540	252230143	2.3496	5.8352
chr15	102531392	240024334	2.341	5.3432
chr16	90354753	258414096	2.86	13.659
chr17	81195210	233033665	2.87	13.031
chr18	78077248	231425054	2.9641	33.7415
chr19	59128983	164217823	2.7773	33.2369
chr20	63025520	187648348	2.9773	8.5338
chr21	48129895	113224657	2.3525	12.1195
chr22	51304566	102980821	2.0072	5.3613
chrMT	16571	41639658	2,512.803	534.3444
chrX	155270560	224798861	1.4478	6.7356

chrY	59373566	73350445	1.2354	23.2332

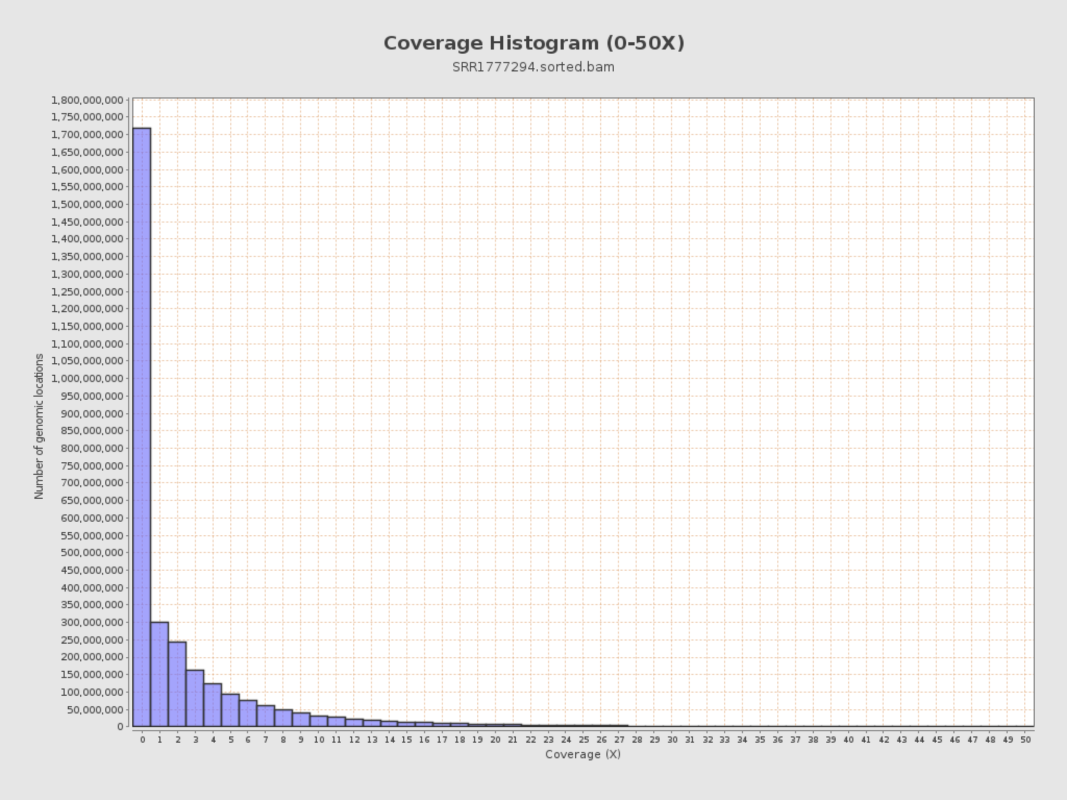
3. Results : Coverage across reference



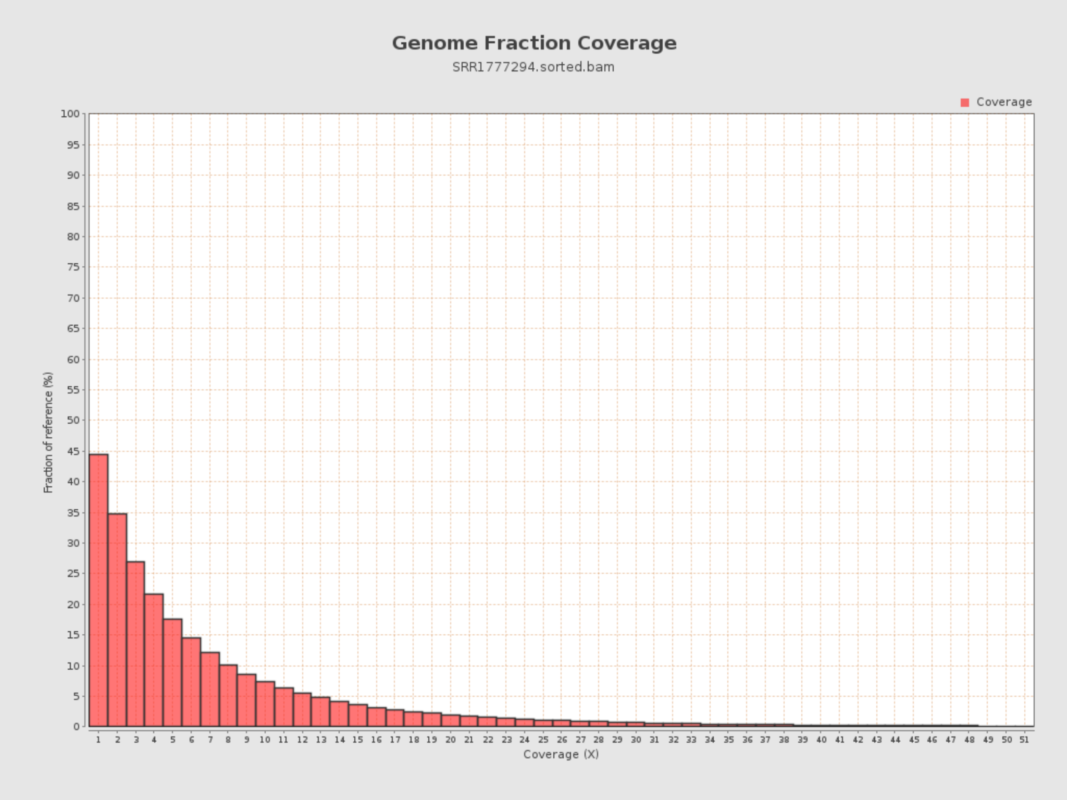
4. Results : Coverage Histogram



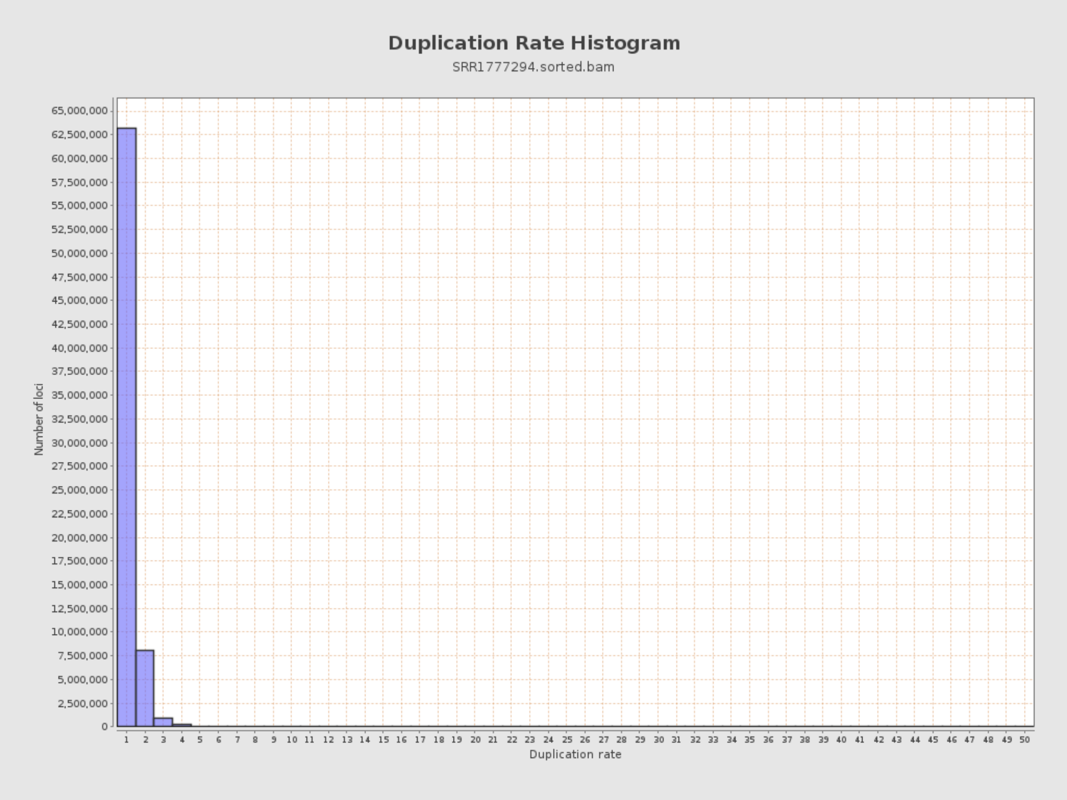
5. Results : Coverage Histogram (0-50X)



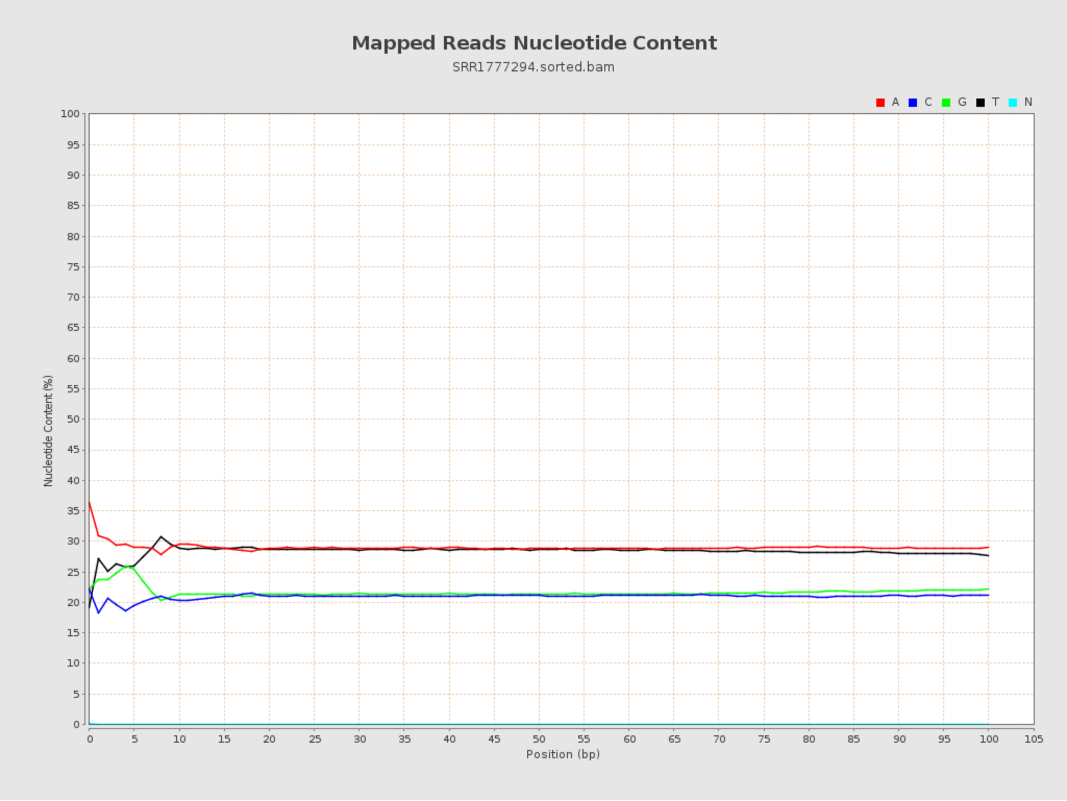
6. Results : Genome Fraction Coverage



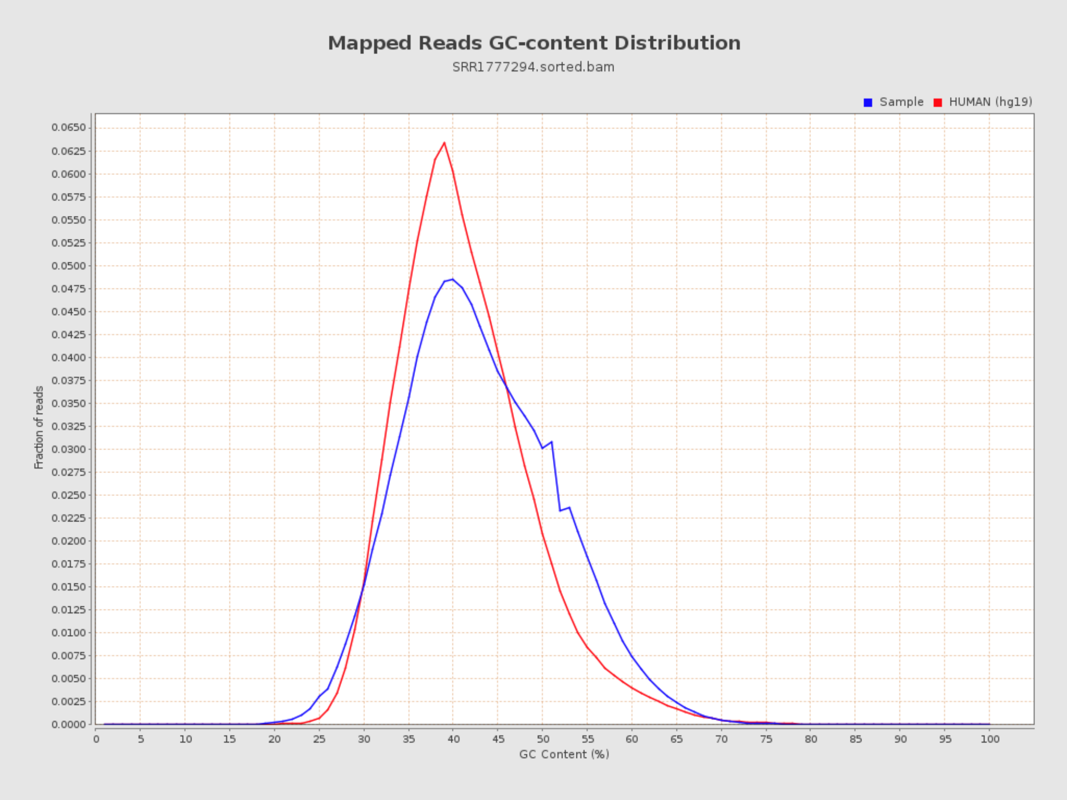
7. Results : Duplication Rate Histogram



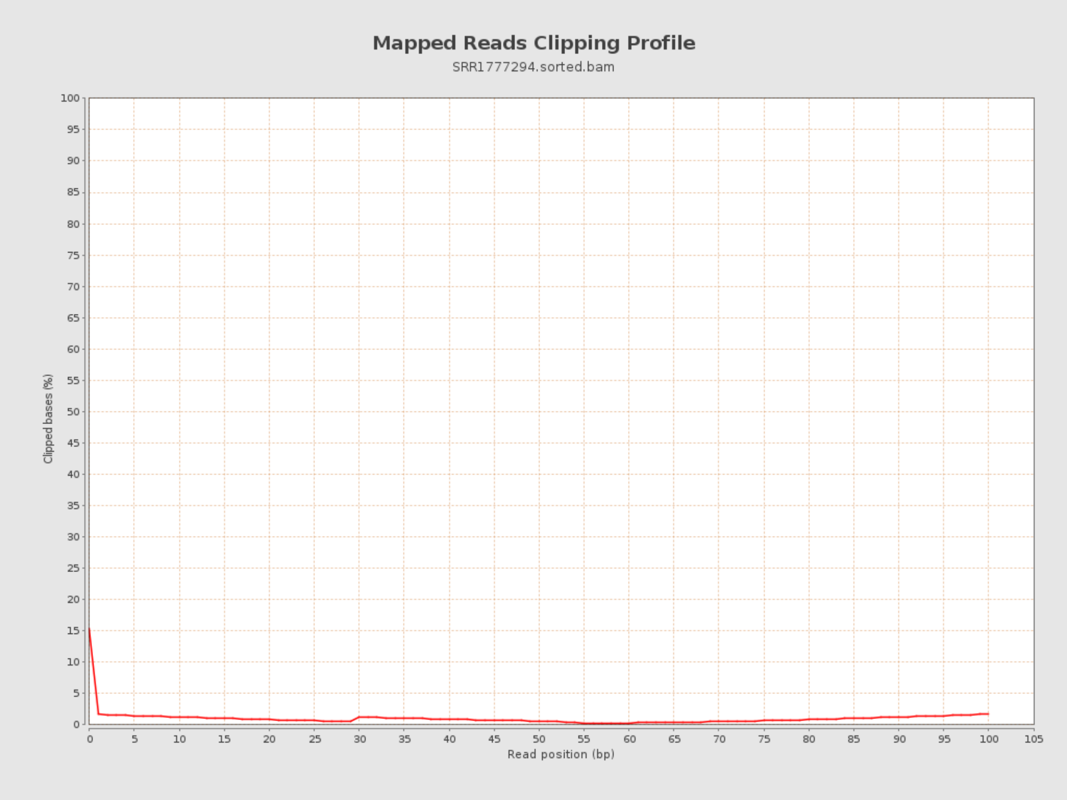
8. Results : Mapped Reads Nucleotide Content



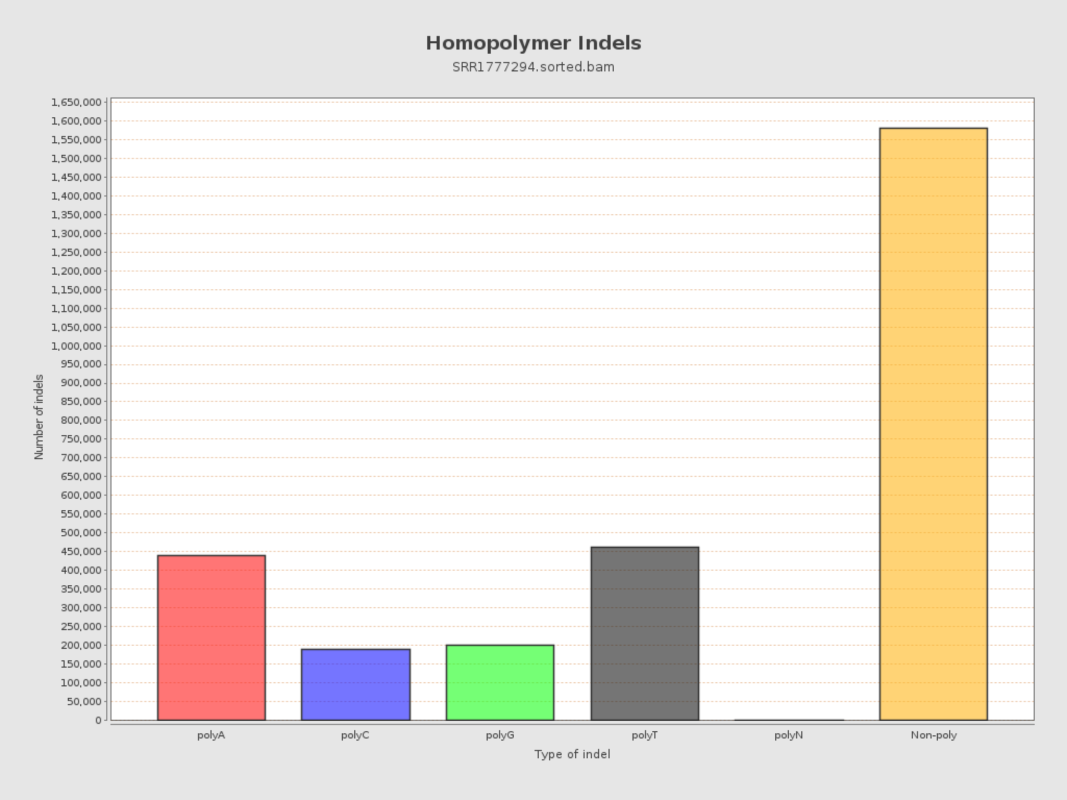
9. Results : Mapped Reads GC-content Distribution



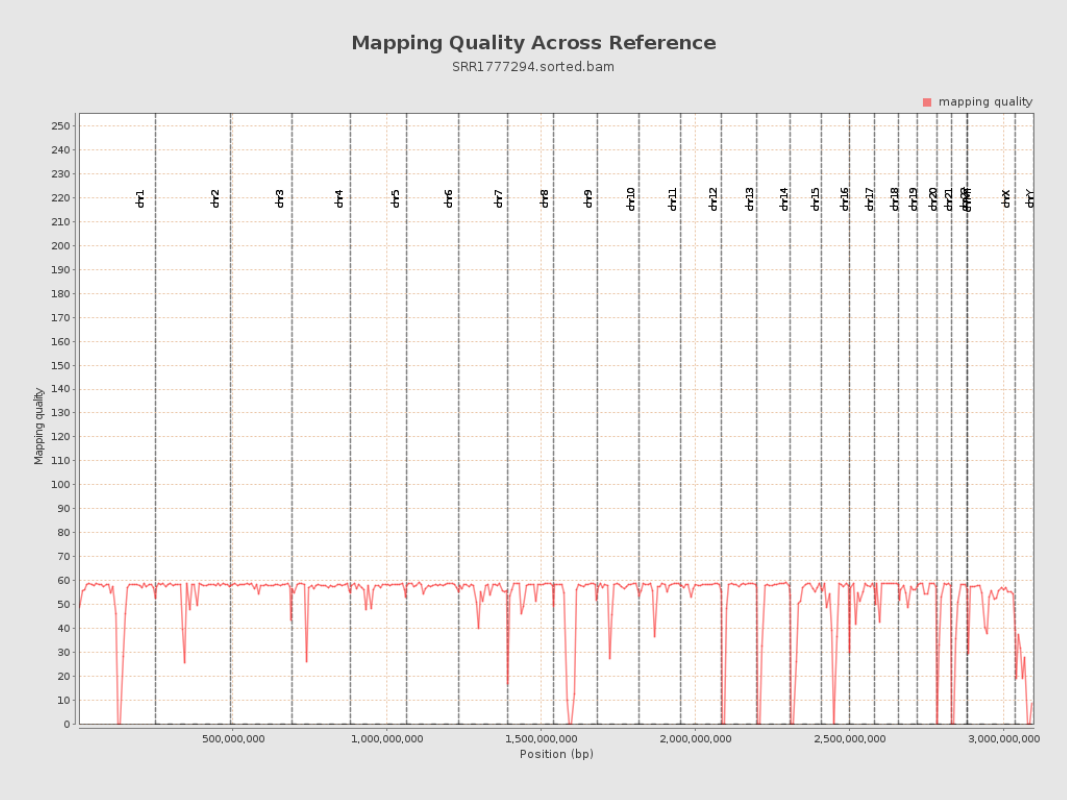
10. Results : Mapped Reads Clipping Profile



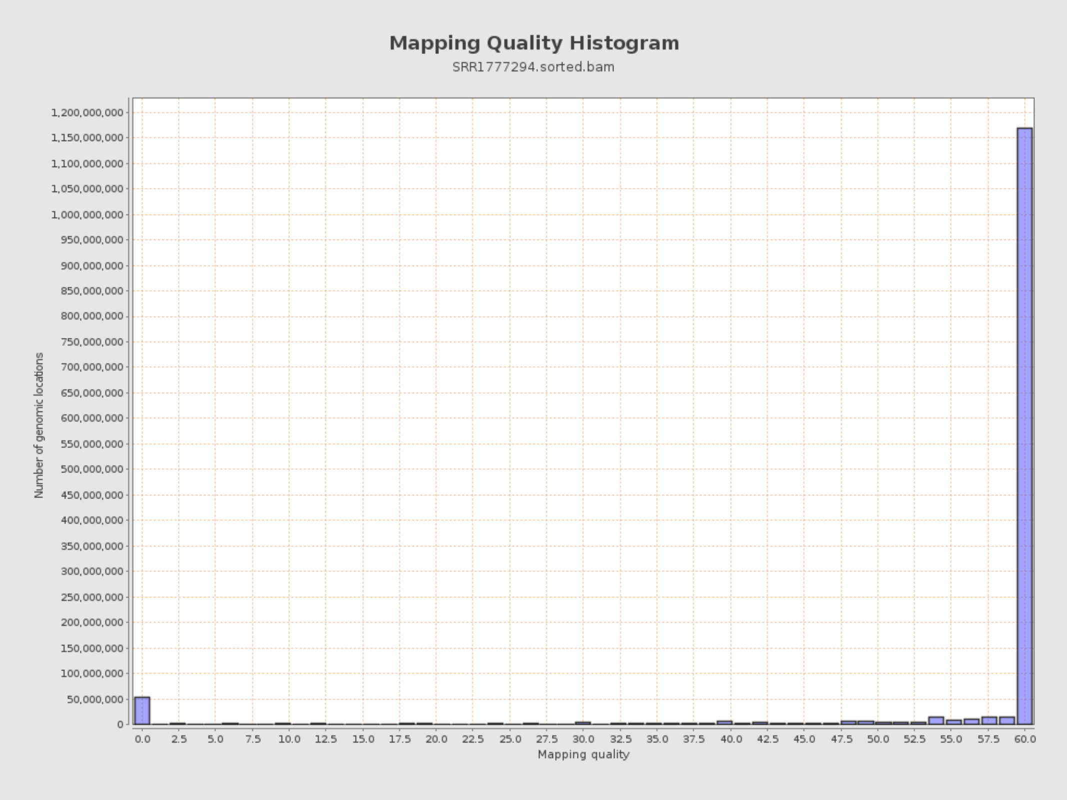
11. Results : Homopolymer Indels



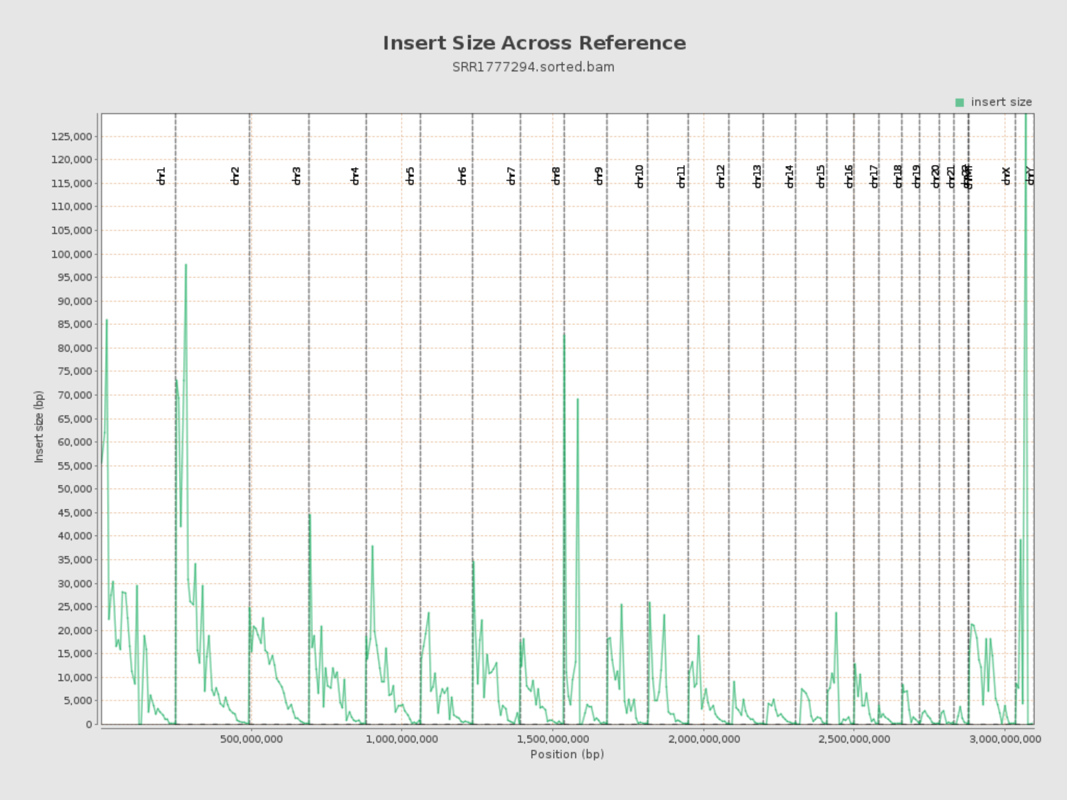
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram