Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/29 13:30:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779338.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_SRR1779338 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779338_1.fastq.gz SRR1779338_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 29 13:30:19 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779338.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	132,261,130
Mapped reads	126,674,809 / 95.78%
Unmapped reads	5,586,321 / 4.22%
Mapped paired reads	126,674,809 / 95.78%
Mapped reads, first in pair	64,024,028 / 48.41%
Mapped reads, second in pair	62,650,781 / 47.37%
Mapped reads, both in pair	124,414,210 / 94.07%
Mapped reads, singletons	2,260,599 / 1.71%
Secondary alignments	0
Supplementary alignments	458,681 / 0.35%
Read min/max/mean length	30 / 100 / 99.99
Duplicated reads (estimated)	7,577,368 / 5.73%
Duplication rate	5.66%
Clipped reads	6,722,905 / 5.08%

2.2. ACGT Content

Number/percentage of A's	3,737,878,682 / 29.8%
Number/percentage of C's	2,521,842,829 / 20.1%
Number/percentage of T's	3,719,724,122 / 29.65%
Number/percentage of G's	2,564,151,754 / 20.44%
Number/percentage of N's	660,294 / 0.01%

GC Percentage	40.54%

2.3. Coverage

Mean	4.0531
Standard Deviation	7.9954

2.4. Mapping Quality

Mean Mapping Quality	53.9

2.5. Insert size

Mean	53,372.08
Standard Deviation	2,302,924.6
P25/Median/P75	167 / 219 / 289

2.6. Mismatches and indels

General error rate	0.41%
Mismatches	49,523,573
Insertions	1,330,120
Mapped reads with at least one insertion	1.03%
Deletions	1,330,764
Mapped reads with at least one deletion	1.03%
Homopolymer indels	48.02%

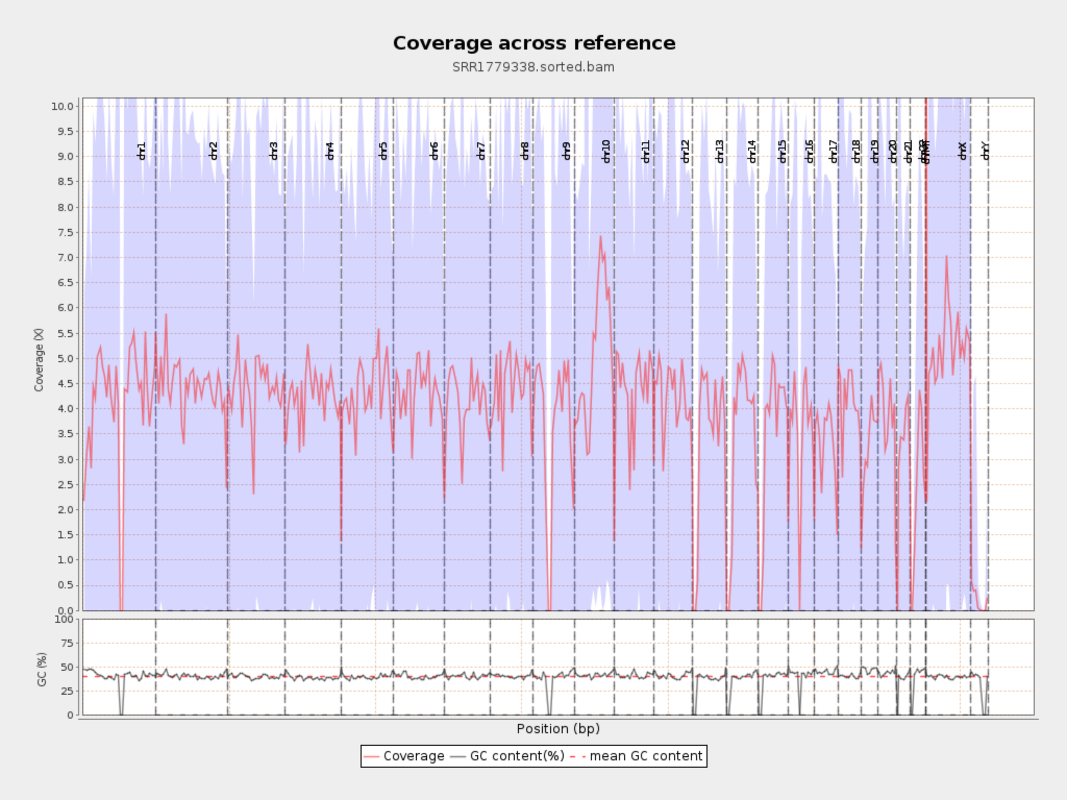
2.7. Chromosome stats

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

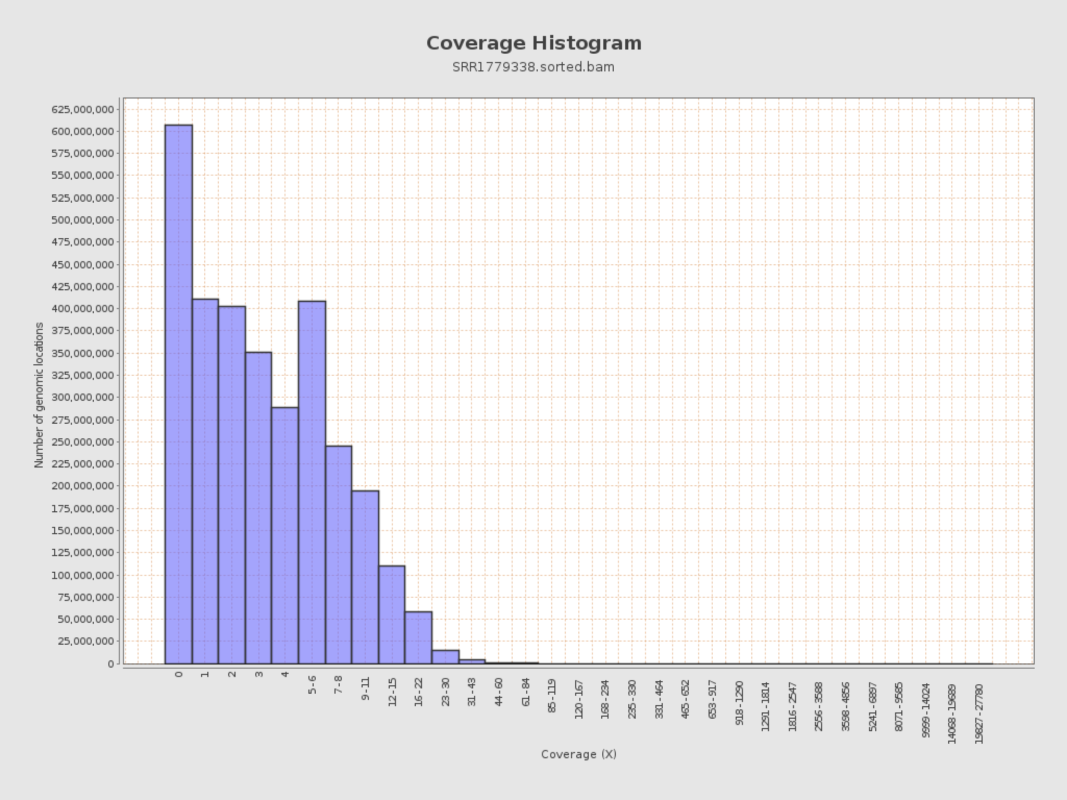
		bases	coverage	deviation
chr1	249250621	1025238833	4.1133	7.1797
chr2	243199373	1075633603	4.4228	22.2041
chr3	198022430	873561326	4.4114	4.5032
chr4	191154276	816021187	4.2689	4.8745
chr5	180915260	778525429	4.3033	4.3286
chr6	171115067	741405939	4.3328	4.7872
chr7	159138663	653306667	4.1053	4.8109
chr8	146364022	649987563	4.4409	4.5436
chr9	141213431	517049195	3.6615	5.4413
chr10	135534747	693070563	5.1136	7.314
chr11	135006516	589138606	4.3638	4.6922
chr12	133851895	573976416	4.2881	5.2991
chr13	115169878	391784757	3.4018	3.9942
chr14	107349540	371943172	3.4648	4.2624
chr15	102531392	350314938	3.4167	4.3831
chr16	90354753	312926500	3.4633	4.3144
chr17	81195210	276406700	3.4042	4.7428
chr18	78077248	323649559	4.1452	5.4832
chr19	59128983	194599725	3.2911	5.4497
chr20	63025520	248793803	3.9475	5.0551
chr21	48129895	152763487	3.174	6.747
chr22	51304566	121908128	2.3762	3.7739
chrMT	16571	890764	53.7544	15.0703
chrX	155270560	802834553	5.1706	5.2851

chrY	59373566	11470281	0.1932	2.3405

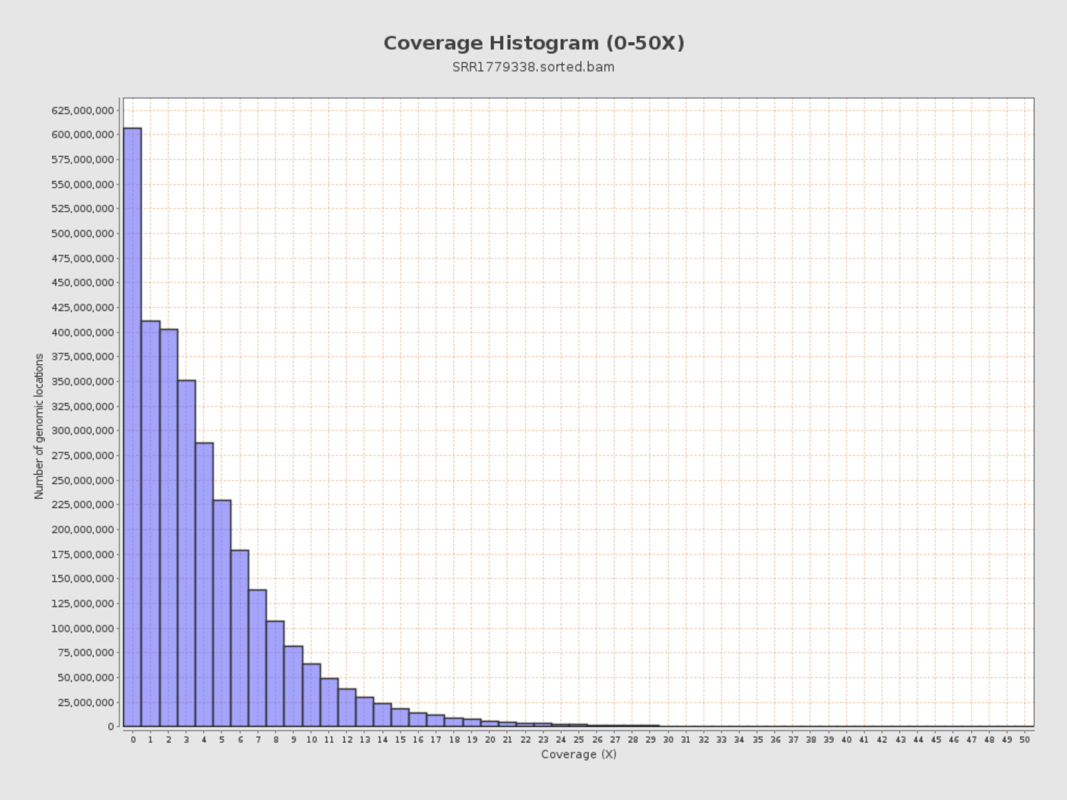
3. Results : Coverage across reference



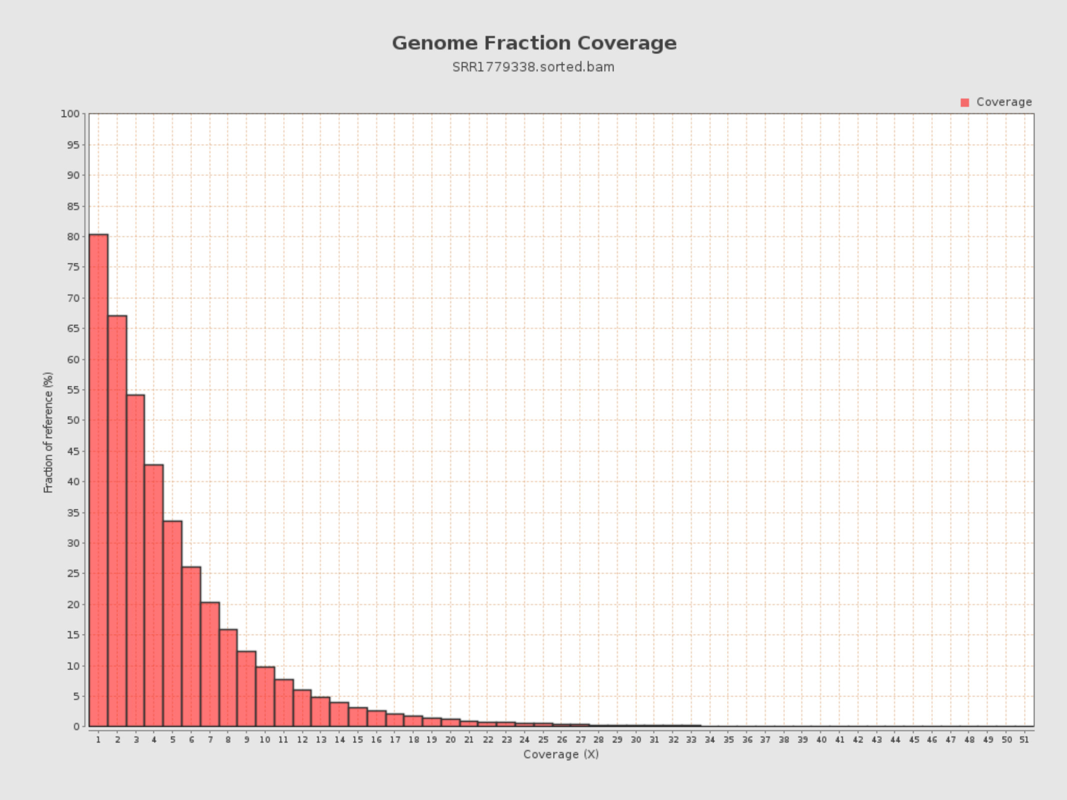
4. Results : Coverage Histogram



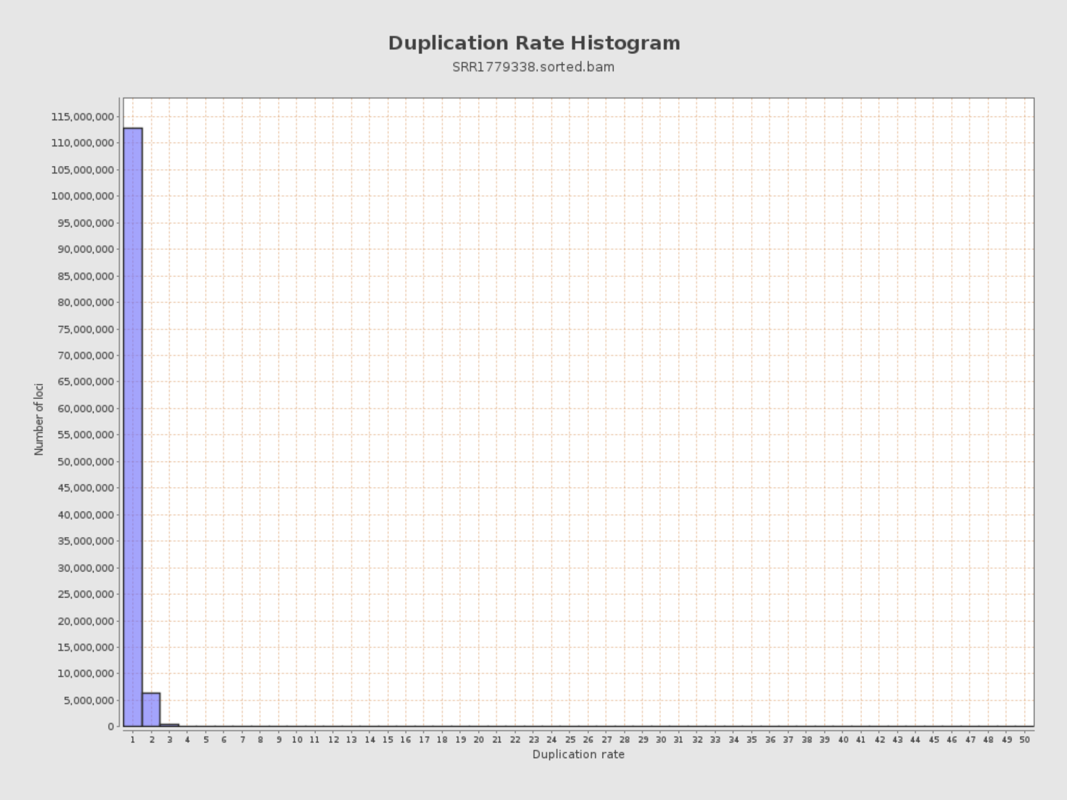
5. Results : Coverage Histogram (0-50X)



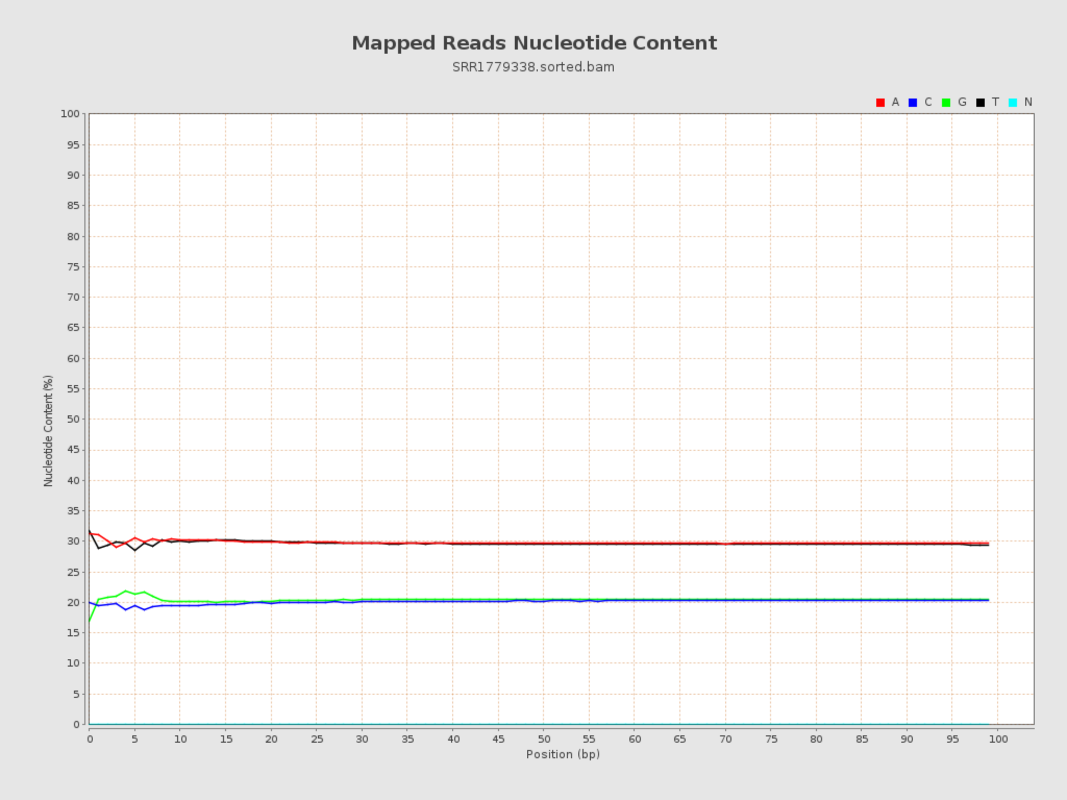
6. Results : Genome Fraction Coverage



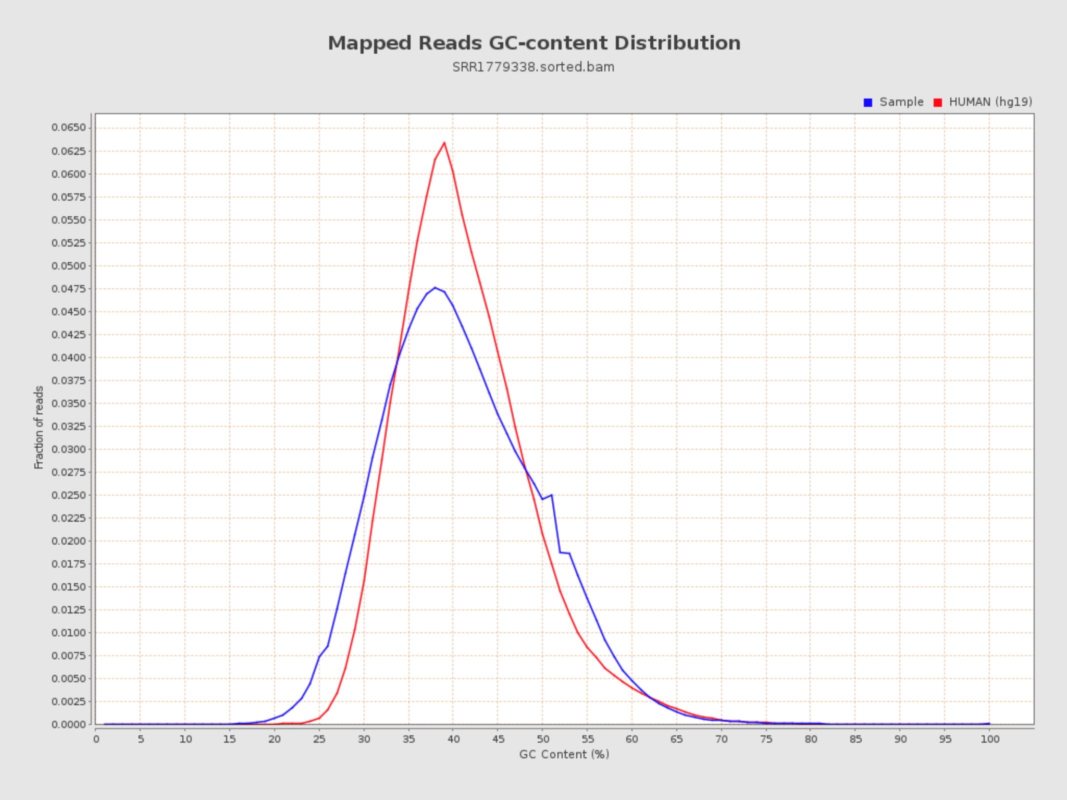
7. Results : Duplication Rate Histogram



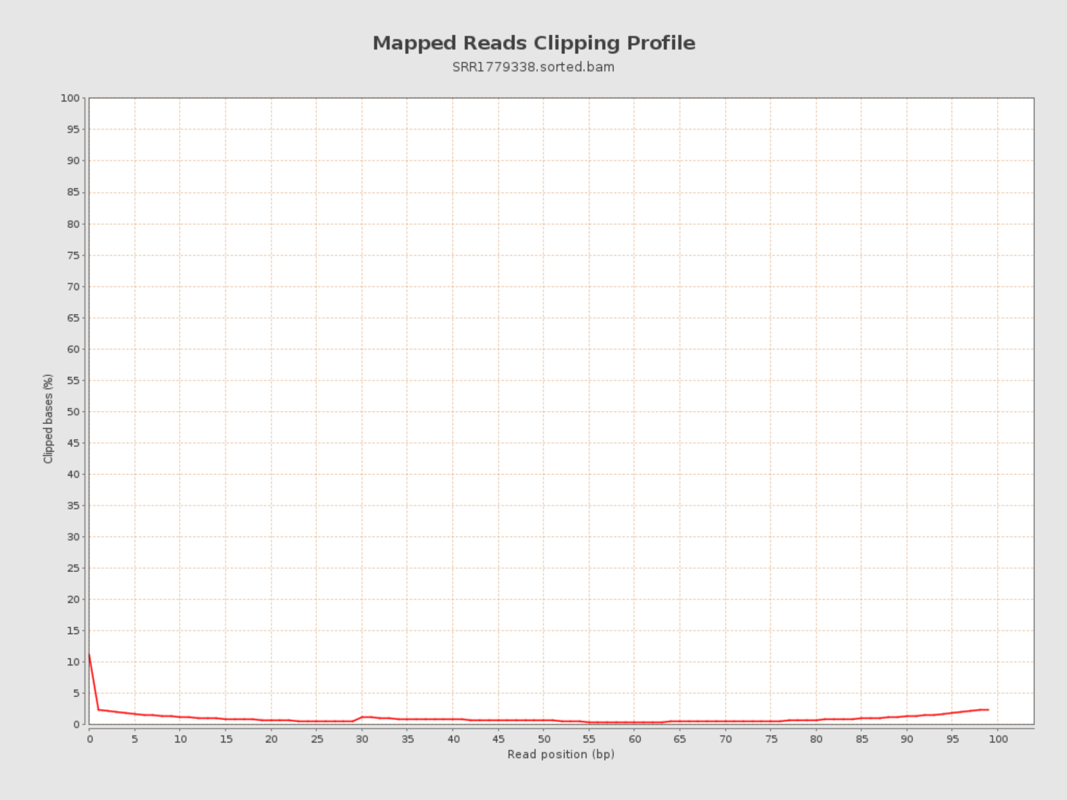
8. Results : Mapped Reads Nucleotide Content



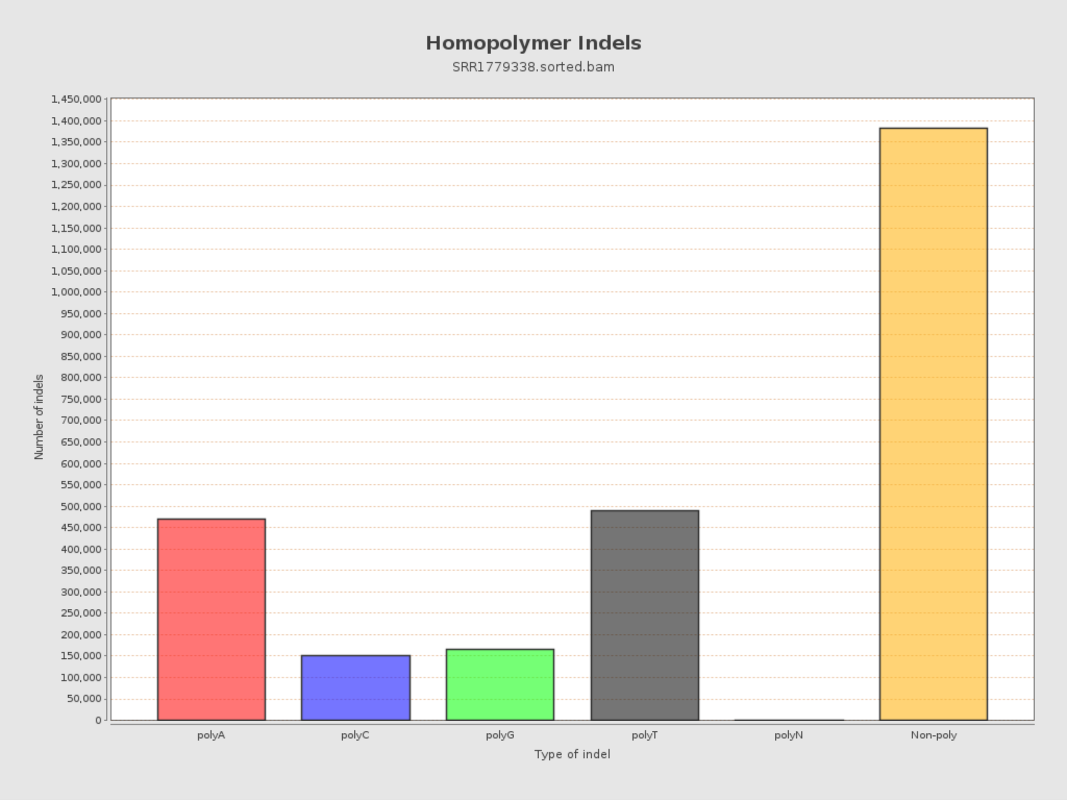
9. Results : Mapped Reads GC-content Distribution



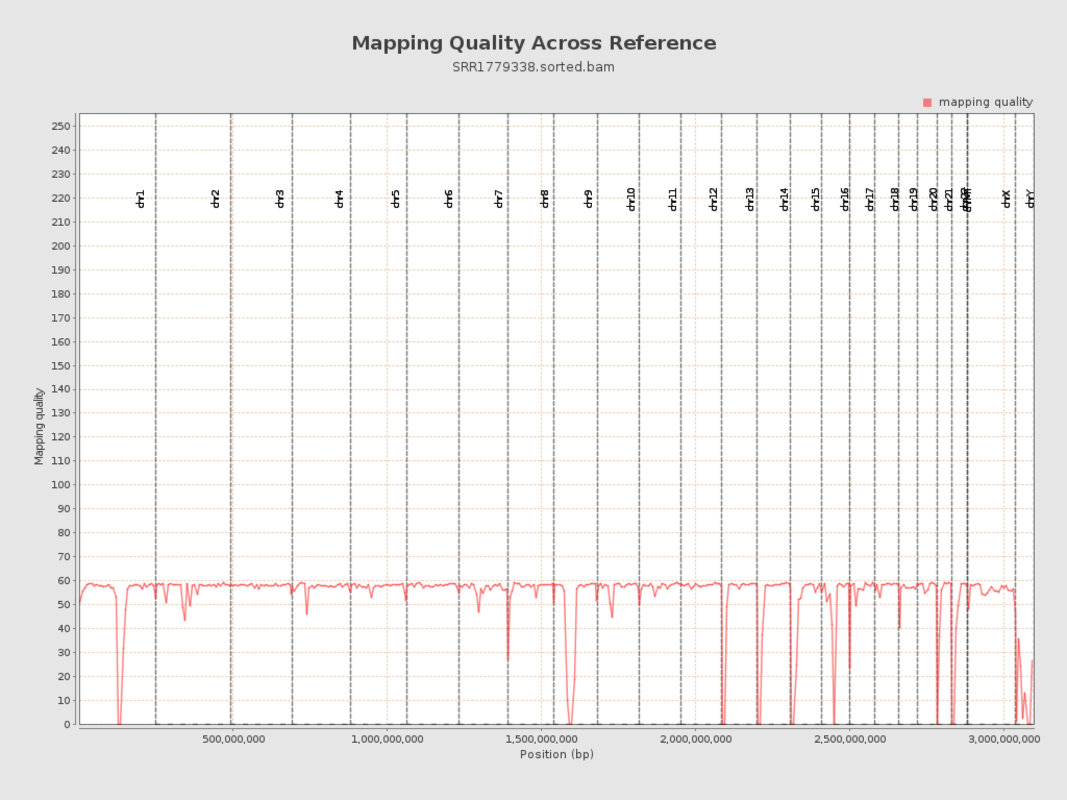
10. Results : Mapped Reads Clipping Profile



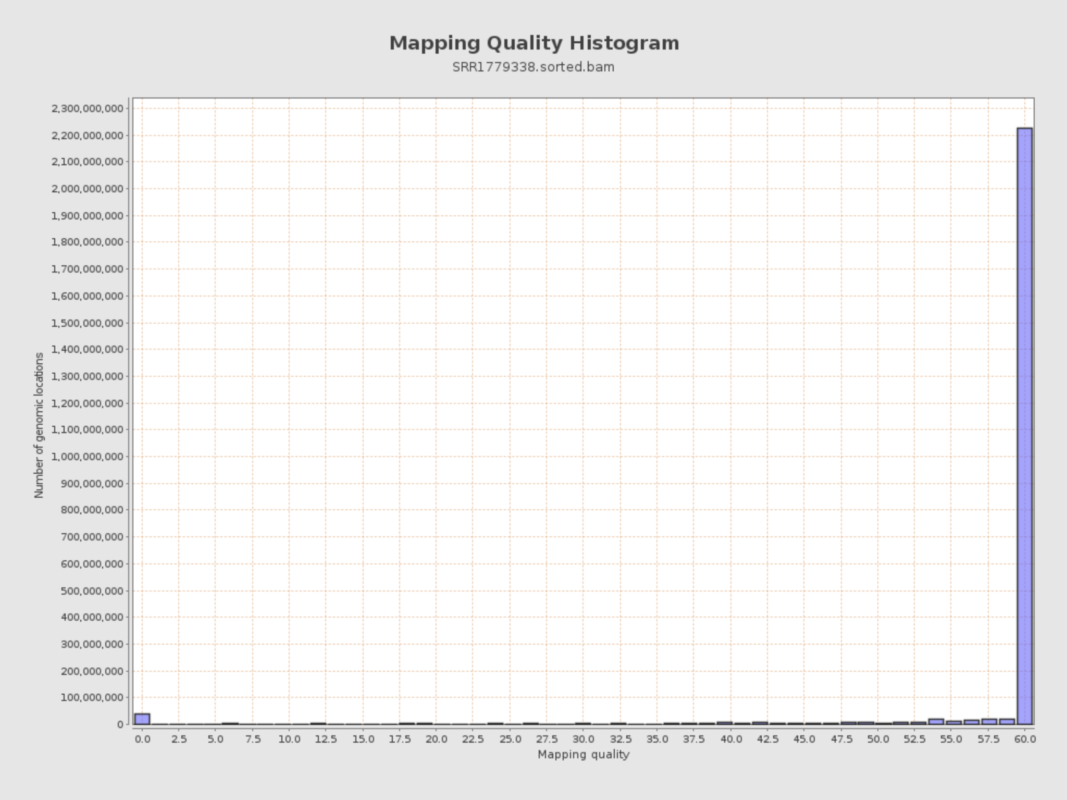
11. Results : Homopolymer Indels



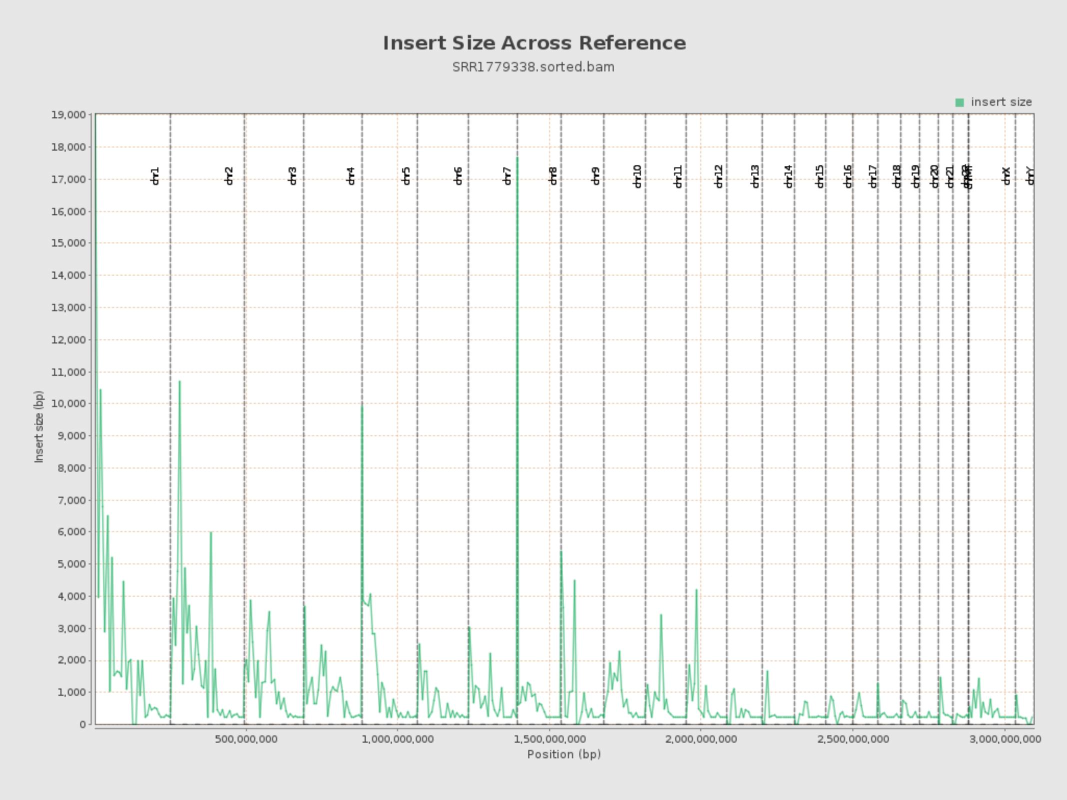
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram