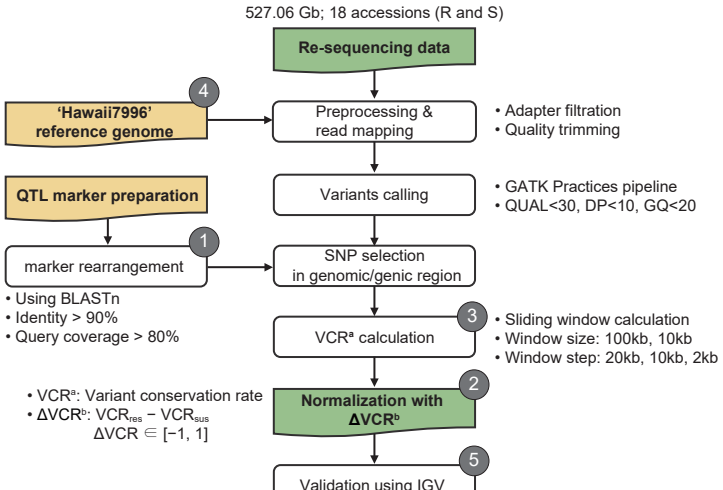
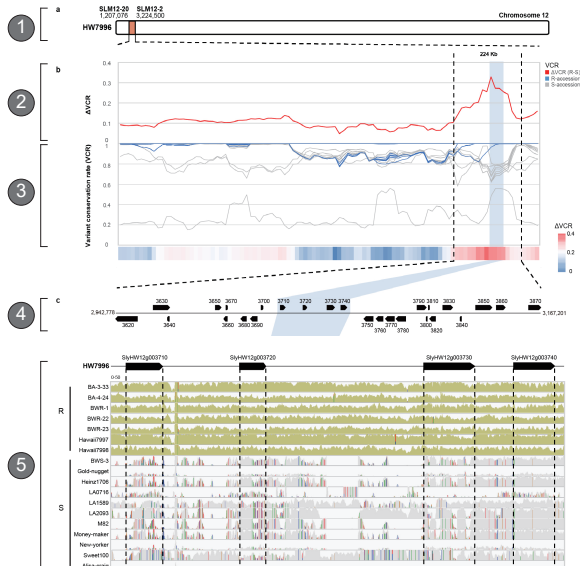

527.06 Gb; 18 accessions (R and S)
Re-sequencing data
4
'Hawaii7996' reference genome
Preprocessing & read mapping
• Adapter filtration
• Quality trimming
QTL marker preparation
Variants calling
• GATK Practices pipeline
• QUAL<30, DP<10, GQ<20
1
marker rearrangement
SNP selection in genomic/genic region
• Using BLASTn
• Identity > 90%
• Query coverage > 80%
3
VCRa calculation
• Sliding window calculation
• Window size: 100kb, 10kb
• Window step: 20kb, 10kb, 2kb
• VCRa: Variant conservation rate
• ΔVCRb: VCRres − VCRsus
ΔVCR ∈ [−1, 1]
2
Normalization with ΔVCRb
5
Validation using IGV


1
2
3
4
5
a
SLM12-20 1,207,076
SLM12-2 3,224,500
HW7996
Chromosome 12
224 Kb
b
ΔVCR
Variant conservation rate (VCR)
VCR
ΔVCR (R-S)
R-accession
S-accession
c
2,942,778
3,167,201
HW7996
SlyHW12g003710
SlyHW12g003720
SlyHW12g003730
SlyHW12g003740
R
S
BA-3-33
BA-4-24
BWR-1
BWR-22
BWR-23
Hawaii7997
Hawaii7998
BWS-3
Gold-nugget
Heinz1706
LA0716
LA1589
LA2093
M82
Money-maker
New-yorker
Sweet100
Alisa-craig