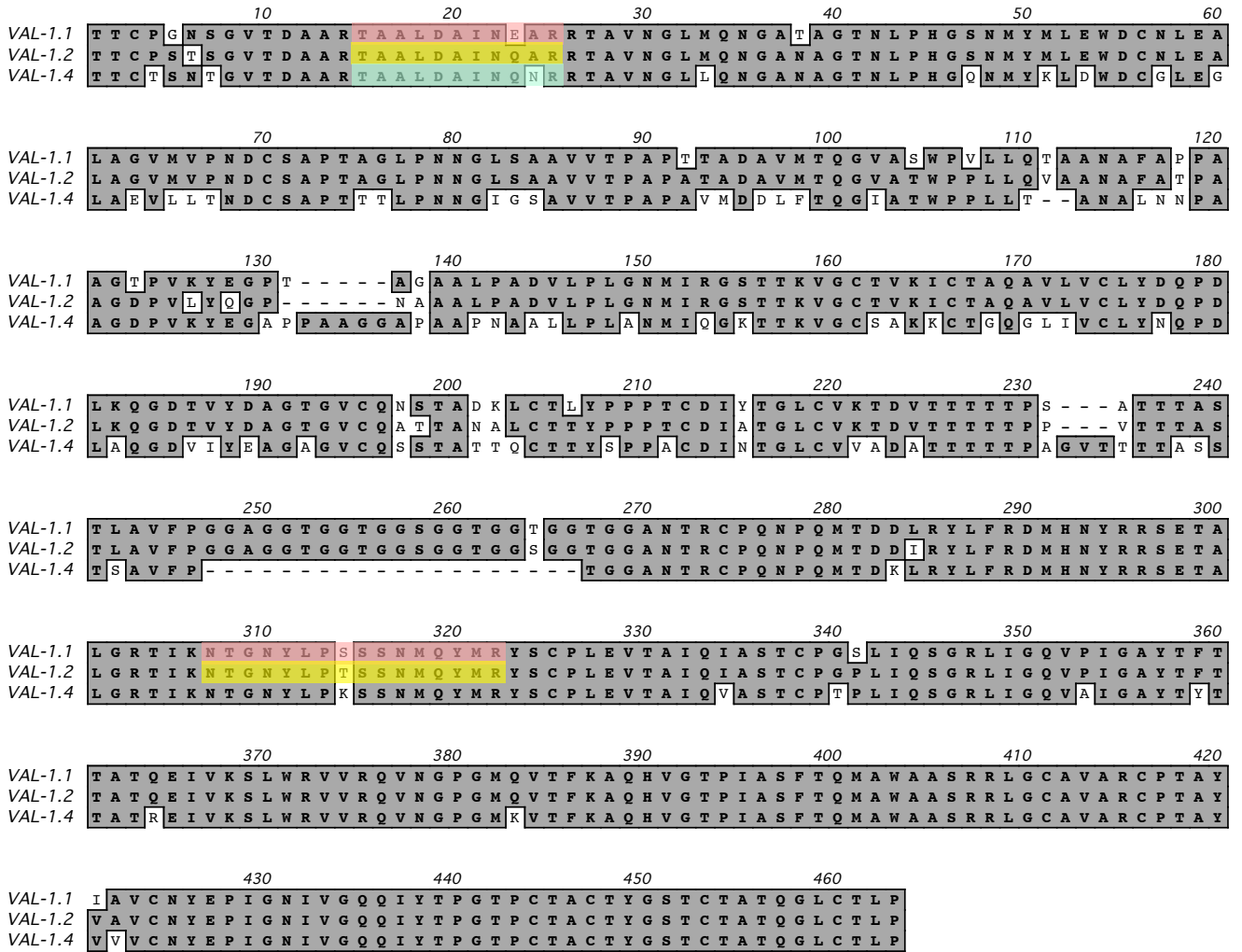
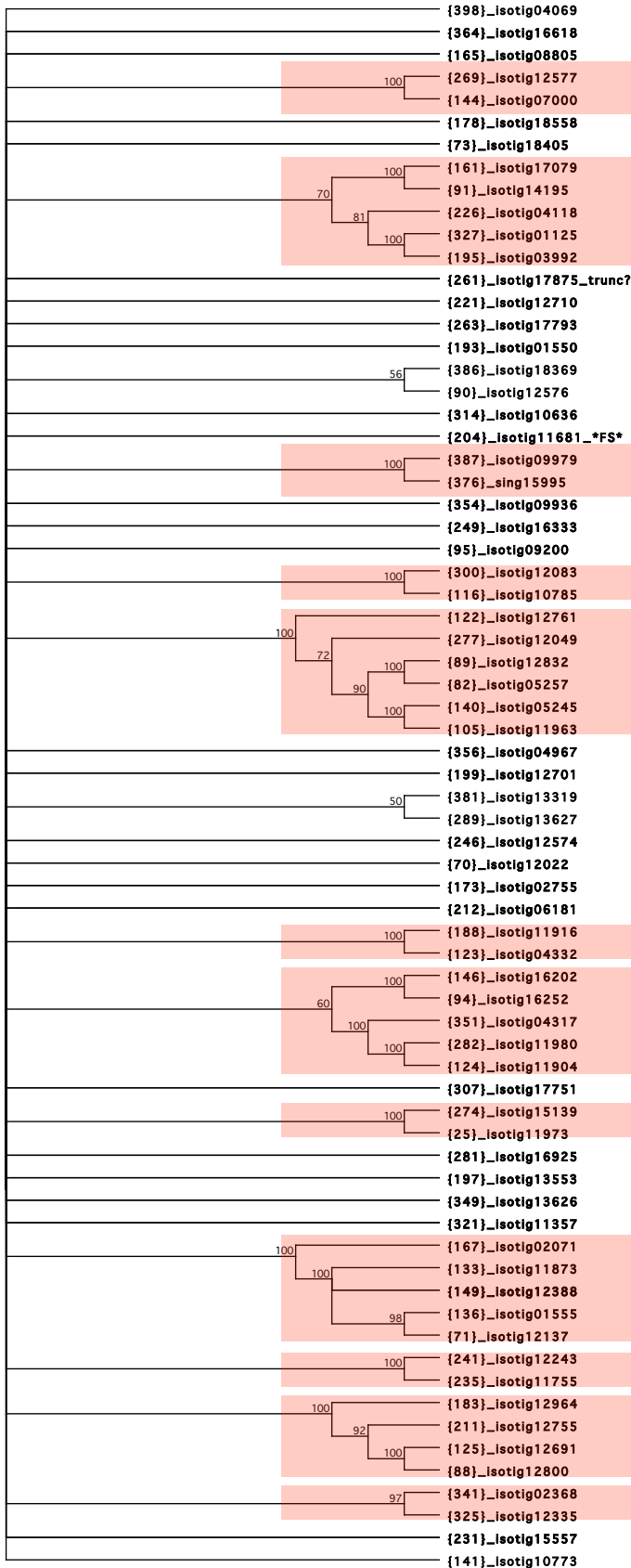


Hewitson et al., Supplementary Figure 1

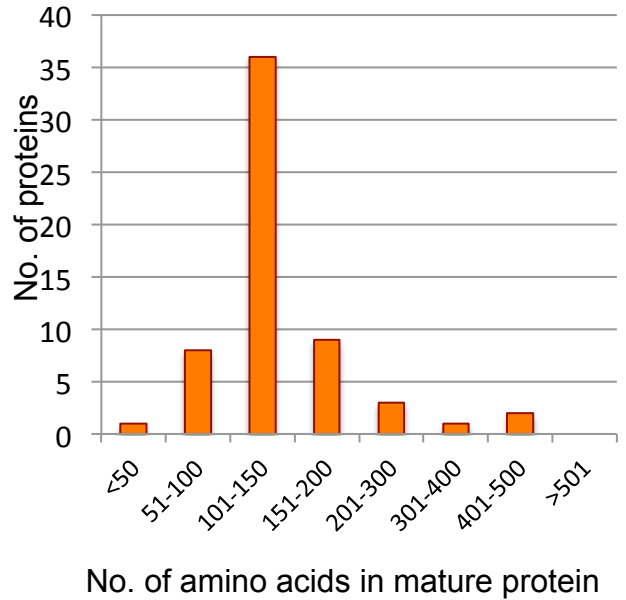


Hewitson et al., Supplementary Figure 2

Method: Neighbor Joining; Bootstrap (1000 reps); tie breaking = Systematic
 Distance: Uncorrected ("p")
 Gaps distributed proportionally



Replace tree with table detailing Mw / pI / related sequences in HES



Hewitson et al.,
Supplementary Figure 3

