



Figure S2. Performance depends on the number of aligned sequences. Performance was measured by the area under the curve (AUC) of sensitivity versus specificity (lines) and 95% confidence intervals were obtained from 2,000 bootstraps (shaded areas). The number of ungapped sequences at the amino acid position of interest was obtained from BAD_Mutations alignments of proteins from 42 plant genomes. AUC was calculated for four groups binned by the number of aligned sequences.