Supplementary Information for

Dementia subtype prediction models constructed by penalized regression methods for multiclass classification using serum microRNA expression data

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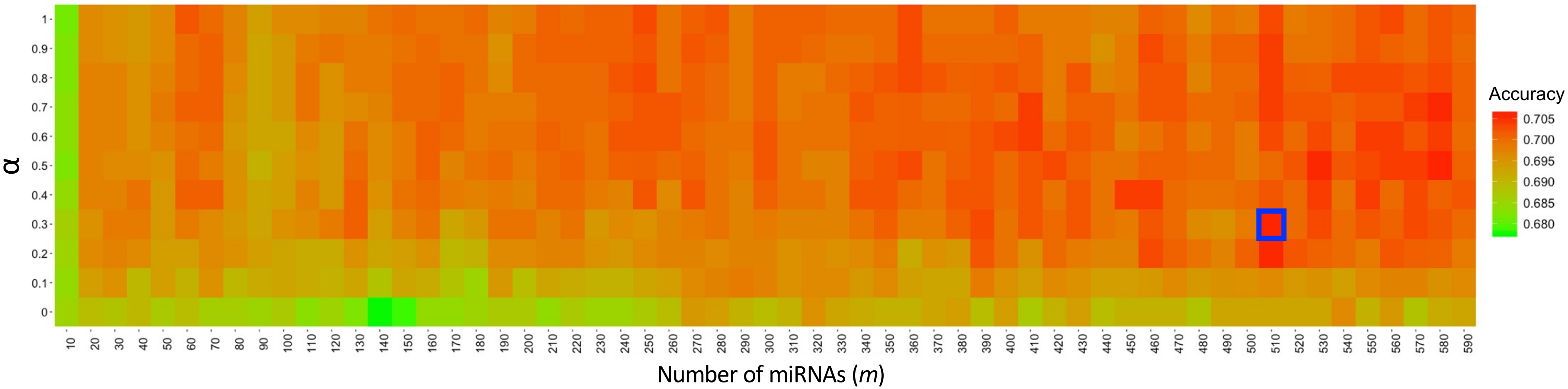
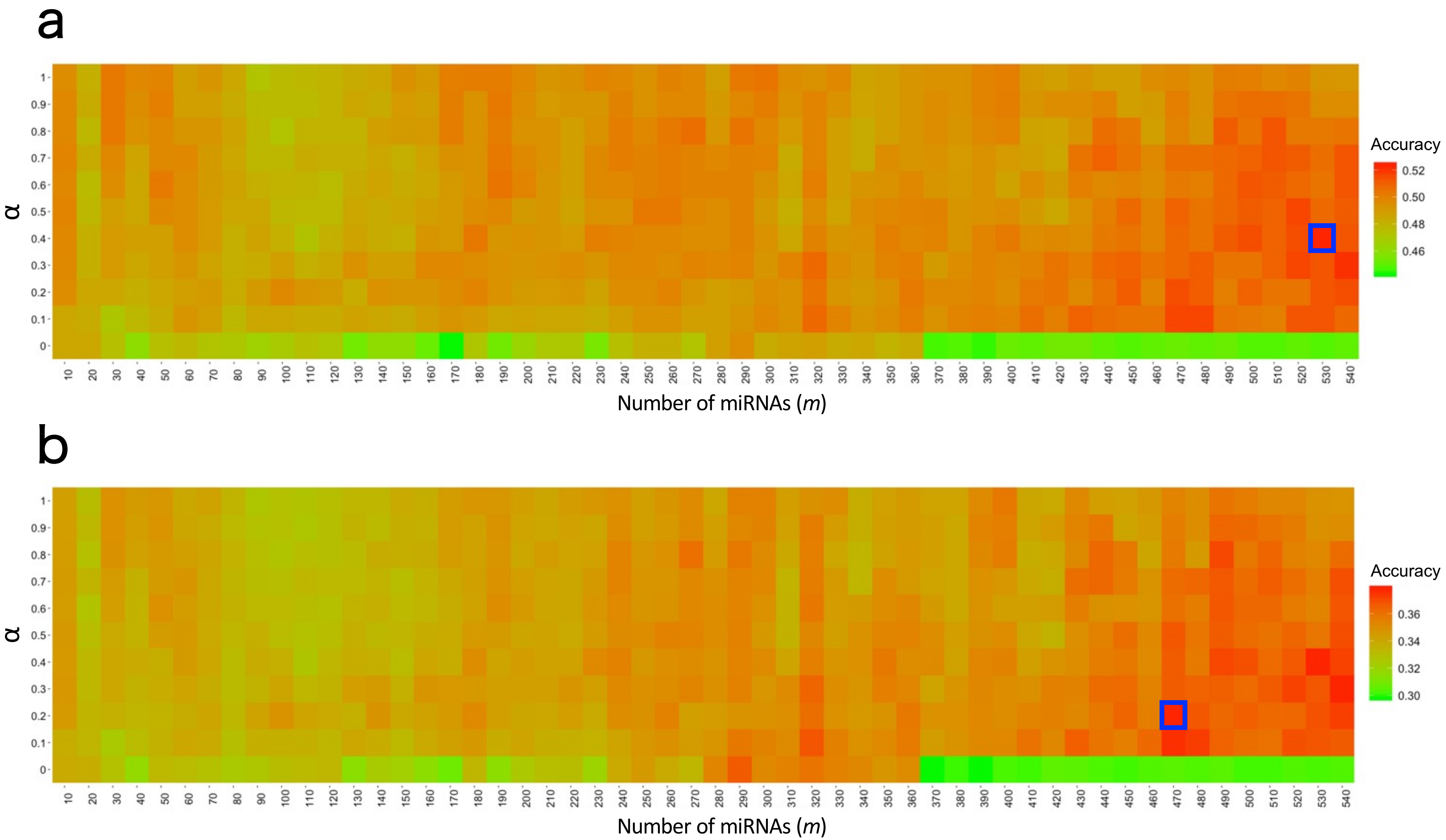
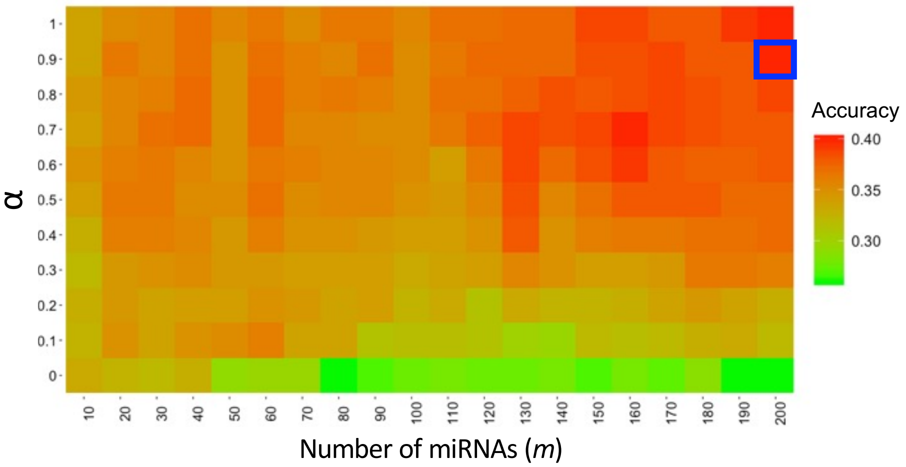


Supplementary Fig. S1. Five-fold cross-validation on a discovery set of Dataset 1.
The x-axis shows the number of miRNAs (m). The y-axis shows α, which is used for penalized regression methods. A combination of $(m, \alpha) = (510, 0.3)$ achieved the highest mean accuracy in the test set (blue rectangle).



Supplementary Fig. S2. Five-fold cross-validation on a discovery set of Dataset 2.
The x-axis shows the number of miRNAs (m). The y-axis shows α, which is used for penalized regression methods. a. A combination of $(m, \alpha) = (530, 0.4)$ achieved the highest mean accuracy in the test set (blue rectangle). b. A combination of $(m, \alpha) = (470, 0.2)$ achieved the highest mean of mean accuracies among subtypes in the test set (blue rectangle).



Supplementary Fig. S3. Five-fold cross-validation on a discovery set of Dataset 3.
The x-axis shows the number of miRNAs (m). The y-axis shows α, which is used for penalized regression methods. Combinations of $(m, \alpha) = (200, 0.9)$ and $(200, 1.0)$ achieved the same highest mean accuracy in the test set (blue rectangle).