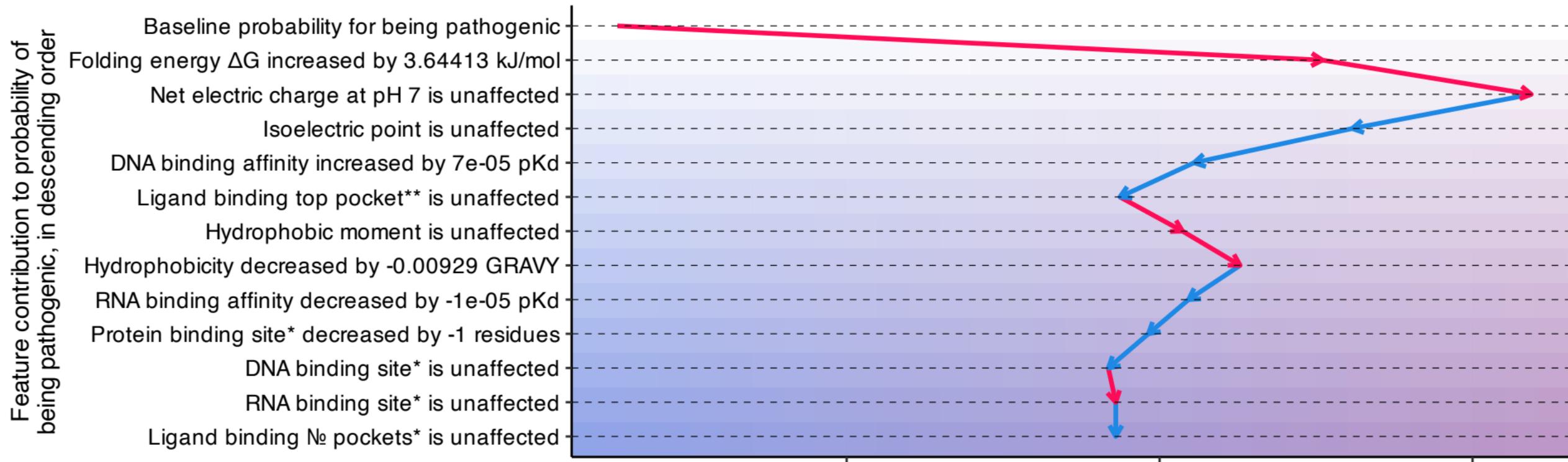


DAVE1 decision plot for AA302P in gene APOA5 (Q6Q788, ENST00000227665), GRCh38 11:116790325C>G

SHAP values do not correlate with feature values, but instead capture feature contributions based on the interactions among all features uniquely for this prediction



* = if any, one or more ** = if any

Cumulative probability heuristic for SHAP values
Final probability for being pathogenic is 0.386, variant is estimated to be pathogenic