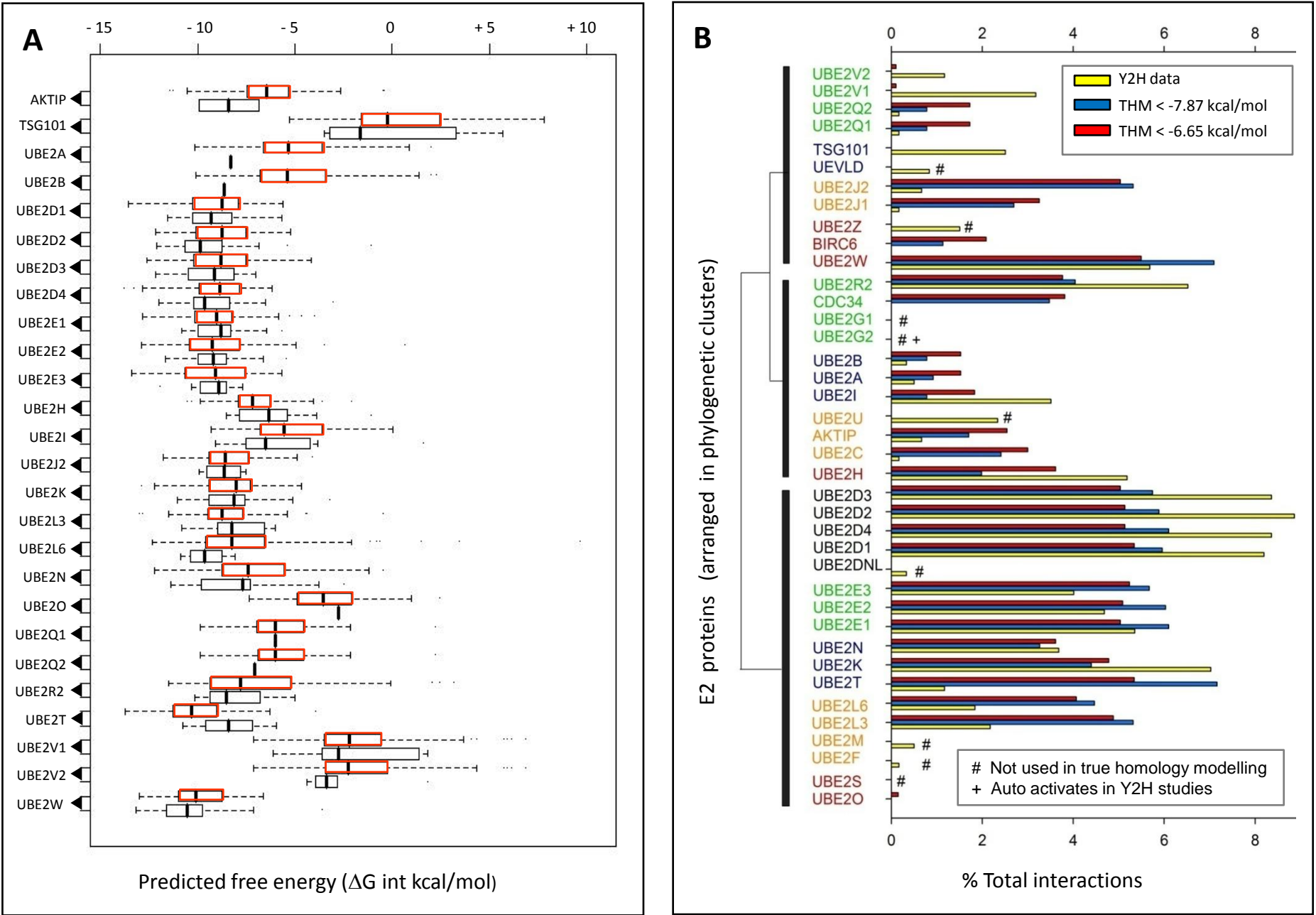


Supplementary File 9: Comparison of predicted free energy values and yeast two-hybrid data for individual E2 proteins



### Comparison of data from targeted Y2H studies and true homology modeling methods

(A) To assess the ability of true homology modelling methods to predict the probability of detecting E2/E3-RING complexes in Y2H assays, the predicted free energy values for 3150 E2/E3-RING complexes were compared to experimental profiles detected in Y2H studies. A binary score (1/0 = interaction was/was not observed) was assigned for each complex tested in Y2H assays. SigmaPlot 10.0 (Systat) was then used to fit the set of free energy/binary score data pairs to the logistic model:  $p(\text{Y2H interaction} \mid \text{free energy score} = x) = a / (1 + \exp(-(x + b)/c))$ , with values for the parameters a, b and c obtained by non-linear regression. The resulting regression curve is shown in black. Black vertical lines indicate the distribution of the predicted free energy values for interacting and non-interacting pairs on the upper and lower horizontal axes, respectively. Predicted free energy values were ordered and split into bins of 200 and the frequency of Y2H interactions within each bin is shown as a red horizontal bar (bar width indicates the free energy values covered by each bin). (B): Distribution of free energy values for: all predicted human E2/E3-RING complexes (OPEN bars); 'strong' Y2H interactions selected on - Ade and - His + 2.5mM 3AT plates (RED bars); 'weaker' Y2H interactions selected on - His + 2.5mM 3AT plates (YELLOW bars); interactions tested but not detected in Y2H studies (GREEN bars). Dashed line indicates the approximate predicted free energy values for the structurally defined UBE2L3/cCbl complex (-7.87 DG int kcal/mol).