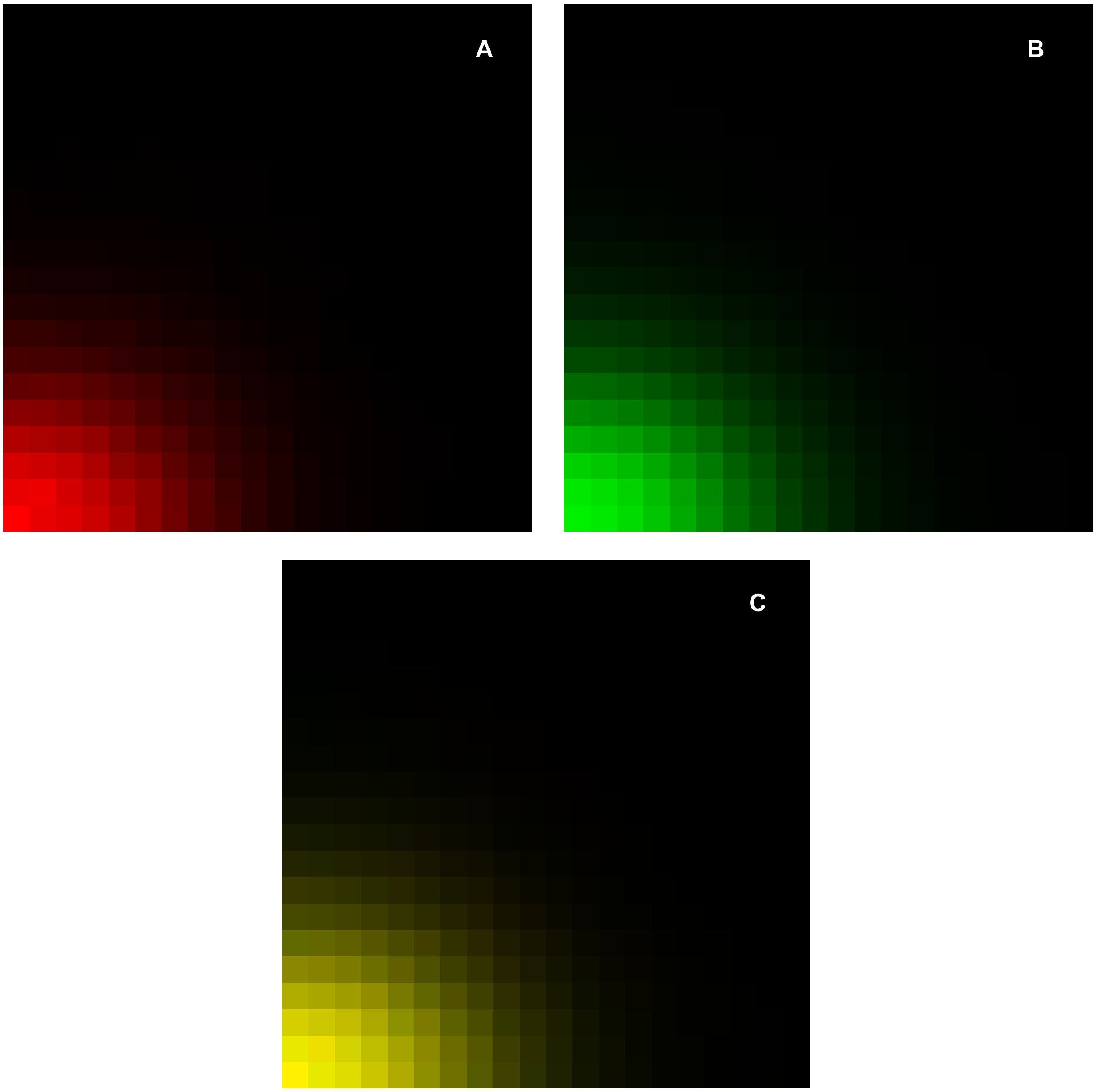

Figure S3 Comparison of naïve Bayesian network and fully connected Bayesian network in yeast gold standard negative set. In each panel, the horizontal axis shows *d*(TTT) and the vertical axis shows *d*(TTC). Color intensity represents the probability of a non-interacting pair of proteins having the respective *d*(TTT) and *d*(TTC) values, predicted by either fully connected Bayesian network (shown in red, panel **A**) or naïve Bayesian network (shown in green, panel **B**). Panel **C** shows the combination of panels **A** and **B** (yellow). The Naïve Bayesian network results in approximately the same distribution as the fully connected Bayesian network. The results are the same for almost all pairs of codons.