S13 Fig. Interaction prediction accuracies increase when assessing biological pathways. A density histogram showing the distribution of prediction accuracies for individual genes (red), KEGG pathways (green), and PID pathways (blue). Interaction prediction accuracies are highest for human cancer-specific pathways from PID. The genes (red) exhibit a double peak distribution due to the relatively high accuracy achieved when predicting the presence of LoF mutations in KMT2C (80%).