## Supplementary Materials for "Incorporating topological information for predicting robust cancer subnetwork markers in human protein-protein interaction network"

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Figure S1: Discriminative power of subnetwork markers identified on NKI295 by different methods. We evaluated the discriminative power of the top K=10, 20, 30, 40, and 50 subnetwork markers identified on NKI295 by varied methods for the following PPI datasets: (a) Chuang, (b) HPRD, (c) GASOLINE, and (d) BioGRID.

10 9 8 7 6 5 4 3 2 1 0 12 Average absolute t-score Average absolute t-score 10 8 K = 10 K = 10 6 K = 20 K = 20 4 K = 30 K = 30 2 HUL HE POLITI K = 40 K = 40 0 isc. c. p. 0.251 AP-based . 13C 9 AP-based Greedy Y IN S Greedy **K** = 50 **K** = 50 (b) (a) 12 10 9 7 6 5 4 3 2 1 0 Average absolute t-score Average absolute t-score 10 8 K = 10 **K** = 10 6 K = 20 K = 20 4 ■ K = 30 ■ K = 30 2 K = 40 K = 40 0 AP-based Greedy AP-based Greedy isc full? isc fully **K** = 50 K = 50 (d) (c) Figure S2: Discriminative power of subnetwork markers across independent gene expression datasets. The markers were identified and sorted on NKI295 and their discriminative power

was evaluated on GSE2034. We repeated the cross-dataset discriminative power assessment for the following PPI datasets: (a) Chuang, (b) HPRD, (c) GASOLINE, and (d) BioGRID.

Page 2 of 2