Table S2: Comparative analysis of transcriptional regulatory networks

	Context-specific networks		Generic networks	
	Yu et al., 2012[a]	Le et al., 2013[b]	Liu et al., 2015[c]	This study
# of regulatory elements				
miRNAs	159	27	232	345
TFs	81	52	243	284
miRNAs+TFs	240	79	475	629
target genes	3178	834	3559	4624
# of regulatory interactions				
miRNA-gene	1625	1822	1426	1881
TF-gene	3413	724	6727	6071
TF-miRNA	98	118	492	670
Performance metrics				
Sensitivity	0.02	0.01	0.64	0.67
Specificity	0.99	0.99	0.98	0.95
F1 score	0.04	0.02	0.77	0.78

[a] A combinatorial network of transcriptional regulation and microRNA regulation in human cancer

[b] A three-component transcriptional regulation network reconstructed using heterogeneous data representing epithelial-to-mesenchymal transition in cancer

[c] A generic network, which was constructed using data in RegNetwork database using data from three independent resources: TF-gene interactions from TRED, miRNA-TF interactions from TransMir, and miRNA-gene interactions from miRecords databases