

Table S1. Number of statistically significant long non-coding RNA/pseudogene-mRNA-microRNA triplets in each cancer type (the ceRNA associations from GDCRNATools and both GDCRNATools and SPONGE-Sparse Partial correlation ON Gene Expression have been tabulated separately).

Cancer	Number of lncRNAs, mRNAs, and miRNAs in ceRNA network		Number of pseudogenes, mRNAs, and miRNAs in ceRNA network	
	GDCRNATools	GDCRNATools+SPONGE	GDCRNATools	GDCRNATools+SPONGE
<b>BRCA</b>	93, 432, 178	77, 364, 177	33, 764, 207	27, 571, 206
<b>COAD</b>	50,219, 168	28, 148, 160	57, 1044, 208	40, 521, 204
<b>PRAD</b>	86, 354, 178	61, 325, 178	42, 1339, 208	30, 1183, 206
<b>READ</b>	89, 353, 176	24, 155, 170	60, 1206, 207	28, 344, 203
<b>UCEC</b>	99, 359, 182	48, 163, 179	60, 654, 209	24, 207, 206
<b>Shared</b>	3, 12, 74	2, 9, 74	2, 3, 57	None

\*lncRNA, long non-coding ribonucleic acid; mRNA, messenger RNA; miRNA, microRNA; SPONGE, Sparse Partial correlation ON Gene Expression; BRCA, breast cancer; COAD, colon cancer; READ, rectal cancer; UCEC, endometrial cancer, Shared, common among BRCA, PRDA, (COAD/READ), and UCEC. GDCRNATools+SPONGE implies statistically significant ceRNA associations from both GDCRNATools and SPONGE.