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** |
| **BRCA** | 93, 432, 178 | 77, 364, 177 | 33, 764, 207 | 27, 571, 206 |
| **COAD** | 50,219, 168 | 28, 148, 160 | 57, 1044, 208 | 40, 521, 204 |
| **PRAD** | 86, 354, 178 | 61, 325, 178 | 42, 1339, 208 | 30, 1183, 206 |
| **READ** | 89, 353, 176 | 24, 155, 170 | 60, 1206, 207 | 28, 344, 203 |
| **UCEC** | 99, 359, 182 | 48, 163, 179 | 60, 654, 209 | 24, 207, 206 |
| **Shared** | 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.