Quantification of non-coding RNA target localization diversity and its application in cancers

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Supplementary Figure S1 Localization coefficient distributions of proteins and the targets of IncRNAs. The four boxes from left to right indicate the LC distributions of all proteins, all IncRNAs, cancer IncRNA target proteins, and cancer IncRNAs, respectively. The target proteins of cancer IncRNAs (red box) have significantly higher LCs than the control set of proteins (gray box) with a P-value of 1.03e-02 using Mann-Whitney U test.
Supplementary Figure S2 (A) The Venn diagram of lncRNA-protein interactions between RAID v2.0 and NPInter v3.0. Only the interactions from high-throughput sequencing technologies were considered, including CLIP, HITS-CLIP, PAR-CLIP, and RIP. (B) TLC distributions of cancer and non-cancer lncRNAs. The cancer lncRNAs (red box) have significantly higher TLCs than the non-cancer ones (blue box) with a $P$-value of 3.25e-03 using Mann-Whitney U test.

Supplementary Figure S3 (A) Contour plot showing populations of the randomly selected practical lncRNA-protein interactions (red curves) and the simulated ones (blue curves), as a function of the ratios of nucleus and cytoplasm specific interactions. The sum of the ratios of interactions in nucleus and cytoplasm may be larger than one because an interaction may reside in more than one locations. (B) Interacting lncRNAs and proteins tend to reside in the same subcellular locations. Red arrow indicates the practical ratio of subcellular specific lncRNA-protein interactions, while the blue curve denotes the distribution of the ratios of the simulated subcellular specific interactions. (C) TLC distributions of cancer and non-cancer lncRNAs with more than one localization annotation. The $P$-value is calculated using MWU test.