Figure S1. Pan-cancer distribution of AS classes in TCGA. Among the 33 TCGA cancer types analyzed, only those where at least one clinical feature was associated with >50 significant ASEs (PCT ≥75%; ≥20 samples per arm; |ΔPSI| >0.1; FDR <0.05) were retained for visualization, resulting in 24 cancer types. Percentages represent the proportion of AS events assigned to each AS class across the displayed cancer types. Data are derived from bulk tumor RNA-sequencing; therefore, the reported frequencies reflect composite signals from malignant and stromal/immune cells and are not exclusively tumor-cell intrinsic. AS, alternative splicing; TCGA, The Cancer Genome Atlas.