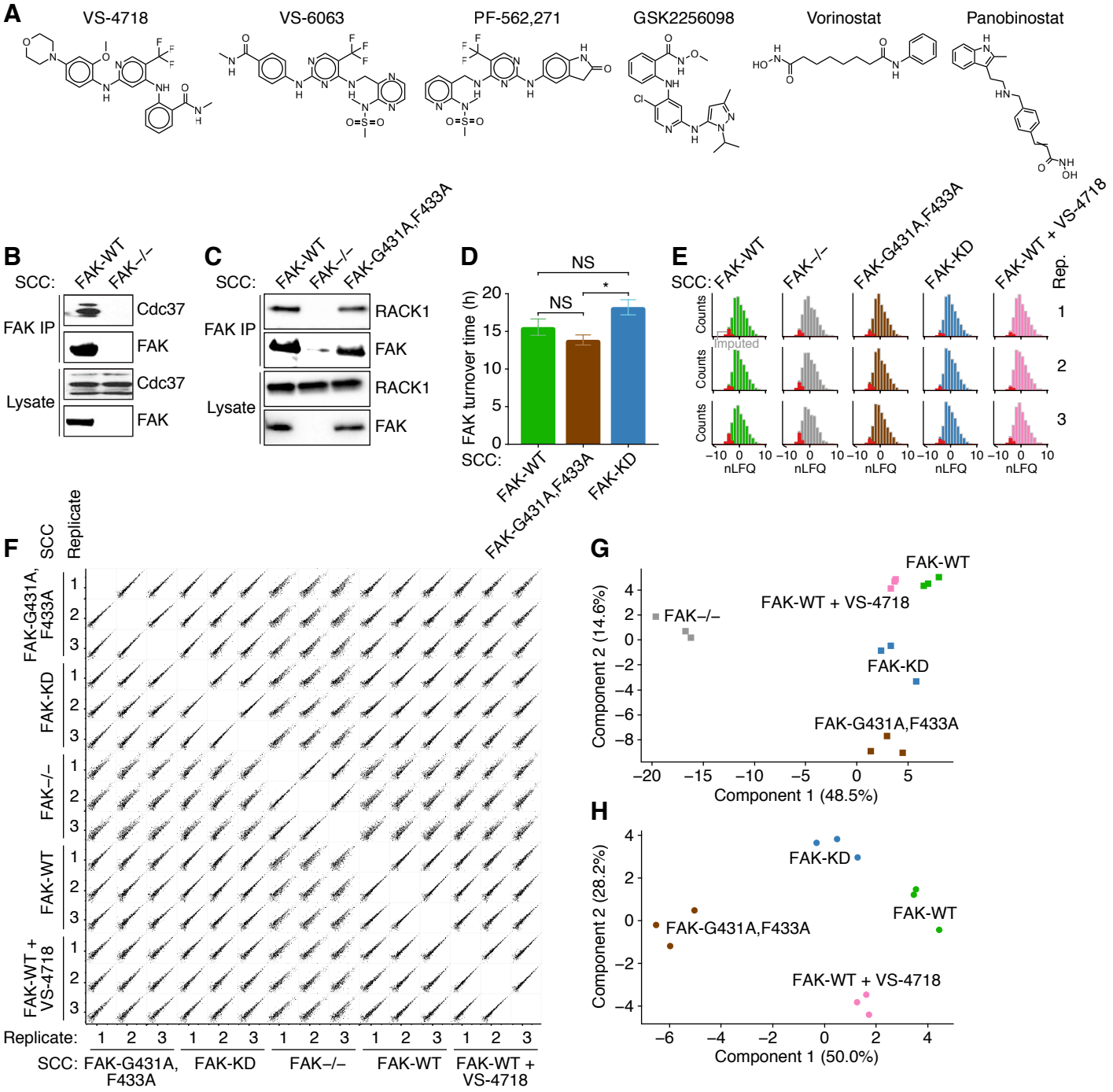

Supplementary Figure S1. Proteomic analysis of FAK protein complexes and turnover. **A**, Chemical structures of FAK kinase inhibitors (VS-4718, VS-6063, PF-562,271, and GSK2256098) and HDAC inhibitors (vorinostat and panobinostat) used in this study. **B**, Immunoprecipitation (IP) of FAK from SCC FAK-WT and FAK–/– cell lysates, immunoblotted for FAK and Cdc37. **C**, IP of FAK from SCC FAK-WT, FAK–/–, and FAK-G431A,F433A cell lysates, immunoblotted for FAK and RACK1. **D**, FAK 50% protein turnover times calculated from intersections of normalized SILAC ratio profiles for FAK synthesis and degradation determined by nonlinear regression. No curve best fits in any experiments were statistically significantly different as determined by extra sum-of-squares *F*-test ($\alpha = 0.0083$). Inferred FAK 50% turnover times are plotted as means ± SD ($n = 3$ independent experiments). *, $P < 0.05$; NS, not significant. Statistical significance of turnover times was determined by Kruskal–Wallis test with Dunn's post-hoc test ($\alpha = 0.05$, $H = 6.489$). **E**, Frequency distributions of normalized label-free quantification (nLFQ) values of proteins identified in IPs of FAK from indicated SCC cell lysates by mass spectrometry [false discovery rate (FDR) = 1%]. Missing values imputed from a width-compressed, down-shifted normal distribution are shown in red. **F**, Scatter plots of nLFQ values of proteins identified in IPs of FAK for all pair-wise sample combinations. Significantly differentially regulated proteins as determined by ANOVA (FDR = 5%) are shown in black. **G, H**, Principal component analyses of significantly differentially regulated proteins as determined by ANOVA (FDR = 5%) (**G**) and proteins significantly enriched over control IPs from SCC FAK–/– cell lysates as determined by Student's *t*-test (FDR = 5%) (**H**). The first two principal components account for 63.1% (**G**) and 78.2% (**H**) of the total variance of the respective datasets.