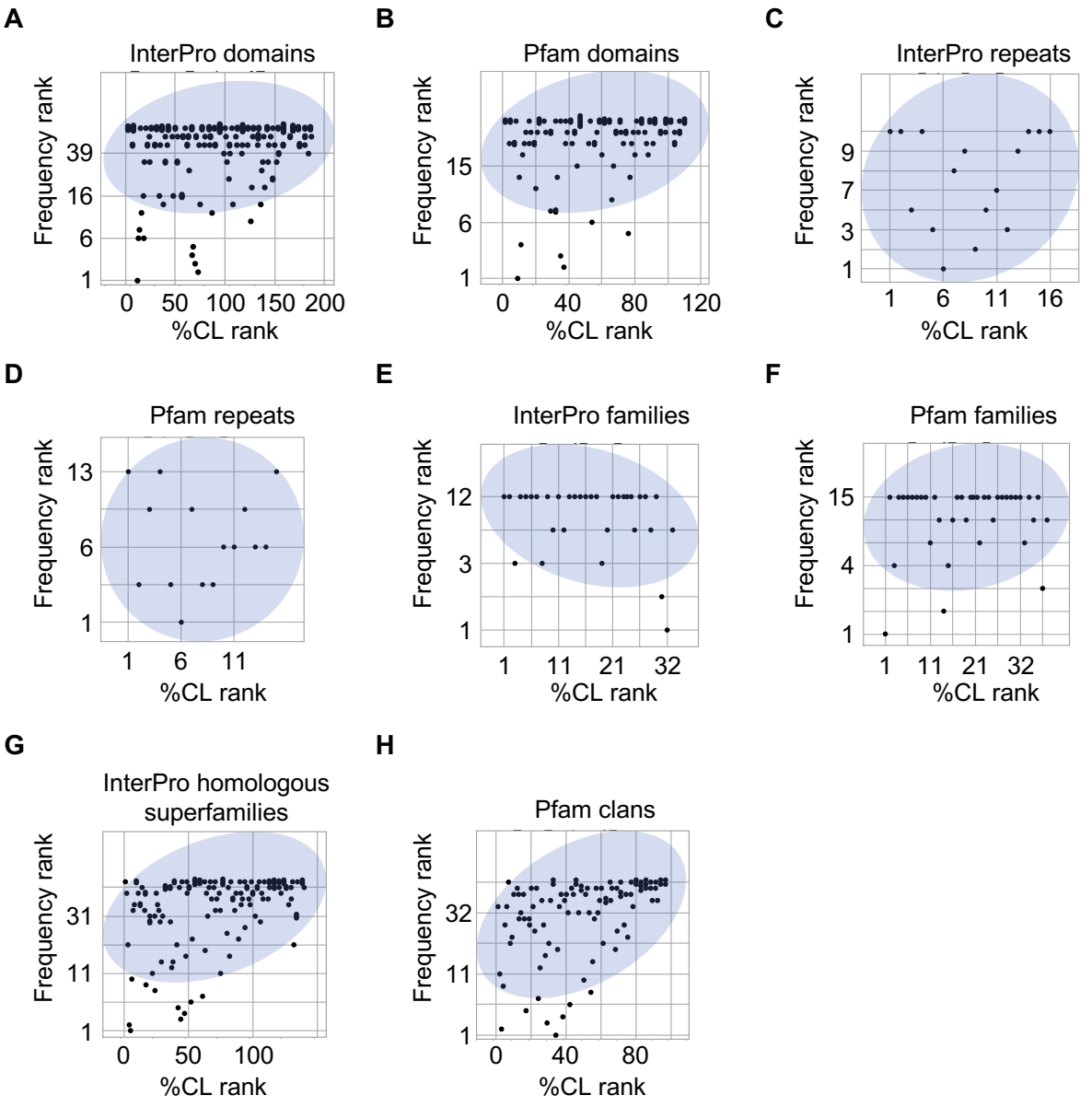

Figure S2. Frequency vs %CL ranking of InterPro and Pfam protein features and classifications. (*A*–*H*), Analytical summary: protein-specific UV-crosslinking efficiencies were estimated using protein abundances generated by LC-MS/MS analysis of input (total protein) and LEAP-RBP (clRNP) fractions isolated from DMSO-treated HeLa cells (n = 3 biologically independent replicates) and protein *S*/*N* ratios estimated by SILAC LC-MS/MS analysis of LEAP-RBP (clRNP) fractions isolated from pooled cellular samples containing UV-crosslinked and non-crosslinked HeLa cells [25]. InterPro and Pfam IDs were mapped to assigned UniProt IDs using the Retrieve/ID mapping tool feature on the UniProt website (Supplemental Table S2). InterPro domains (*A*), Pfam domains (*B*), InterPro repeats (*C*), Pfam repeats (*D*), InterPro families (*E*), Pfam families (*F*), InterPro homologous superfamilies (*G*), and Pfam clans (*H*) mapped to 3 or more candidate RBPs containing UV-crosslinking efficiencies were ranked according to frequency or the average %CL of candidate RBPs and analyzed by Spearman's rank correlation test. Summary of statistical test results included as part corresponding Source Data in the provided Source Data file. Complete list of %CL ranked InterPro and Pfam IDs, including those mapped to less than 3 candidate RBPs containing estimated UV-crosslinking efficiencies, were included as part of Supplemental Table S3.