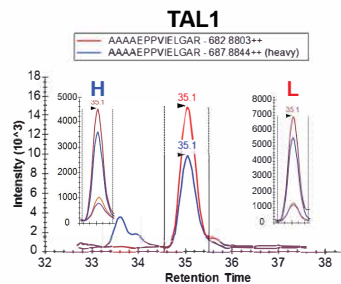
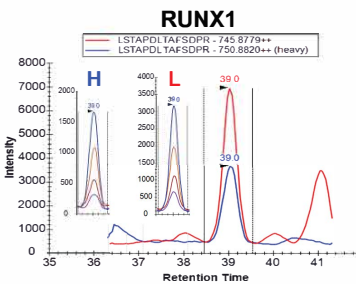
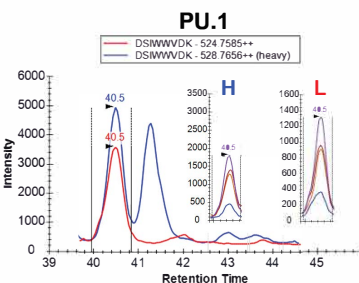
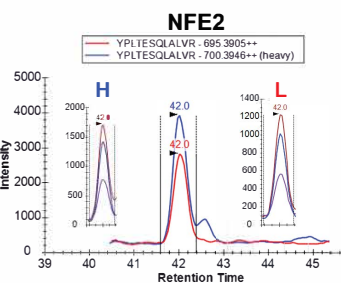
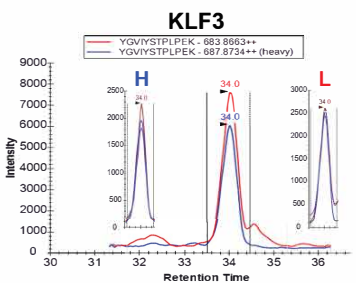
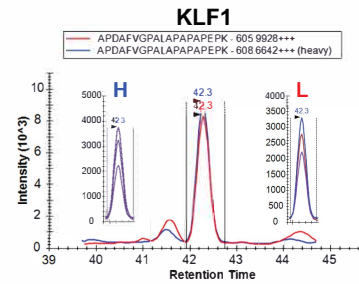
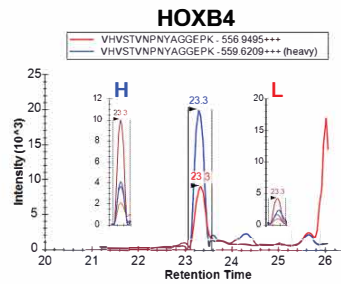
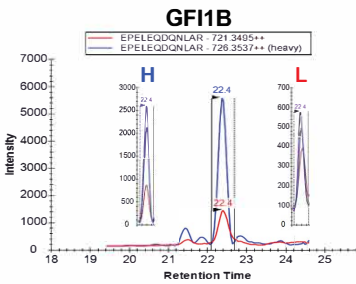
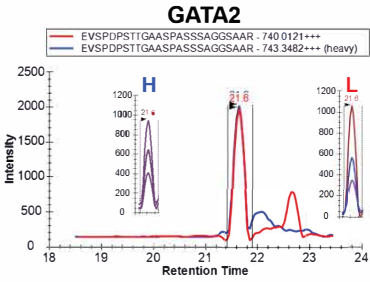
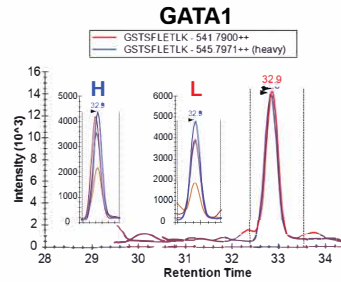
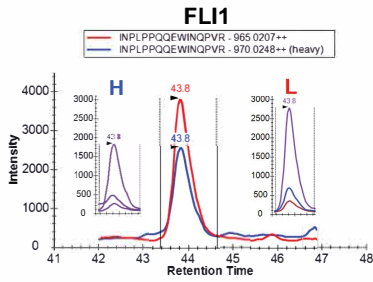
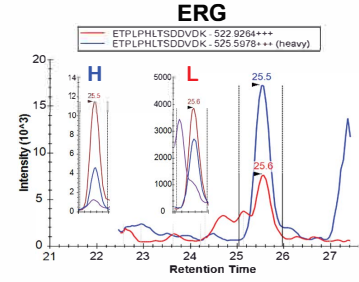
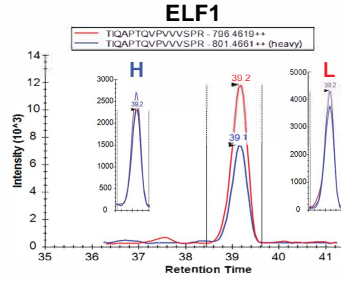
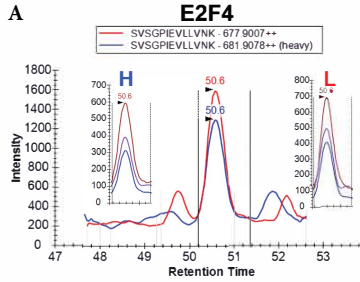
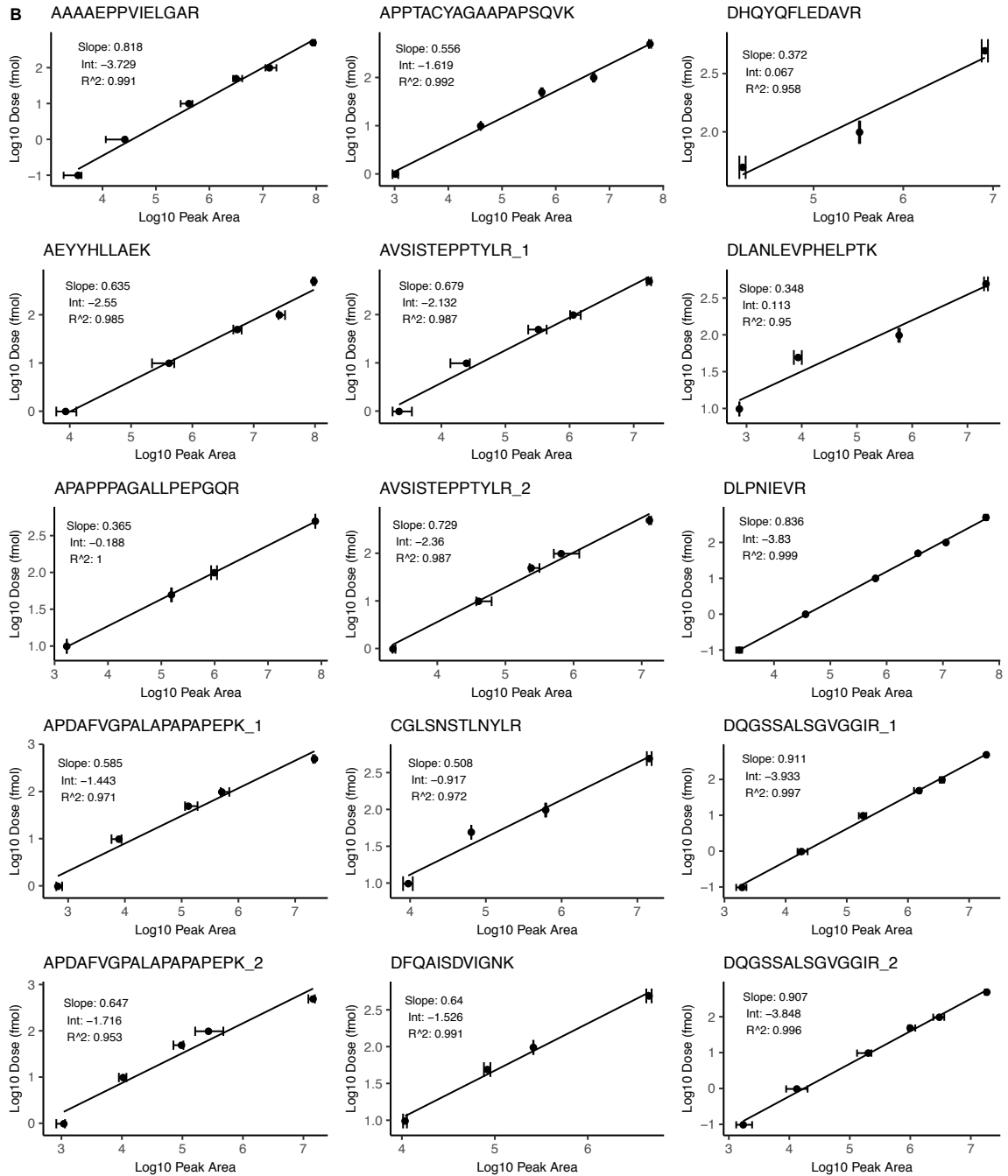
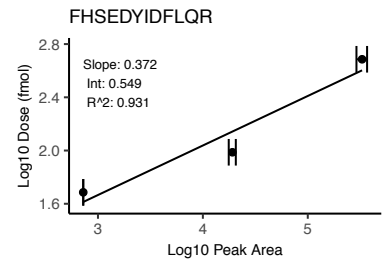
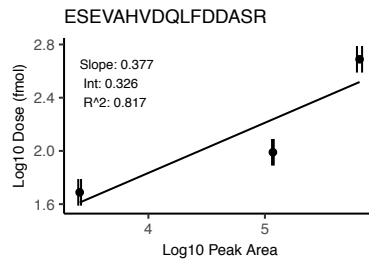
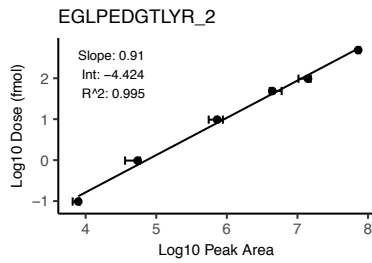
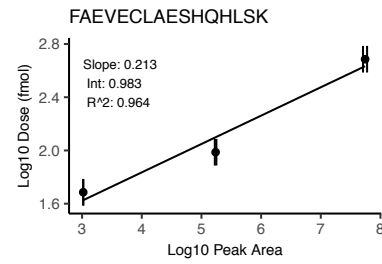
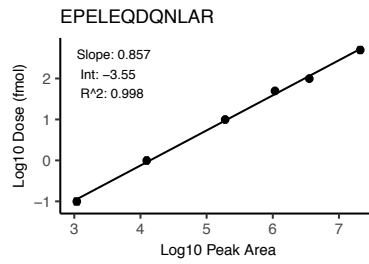
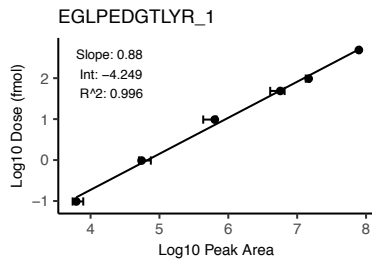
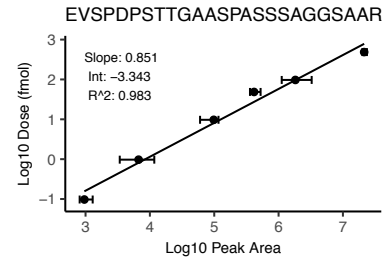
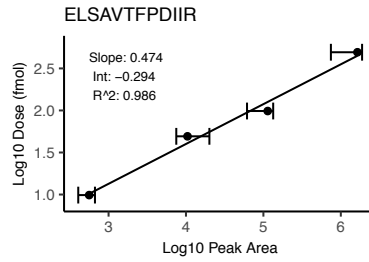
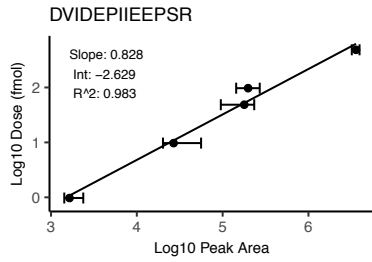
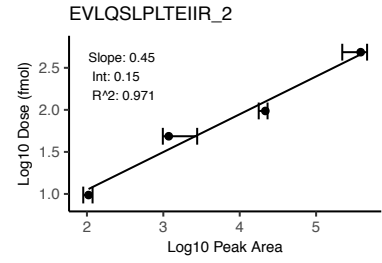
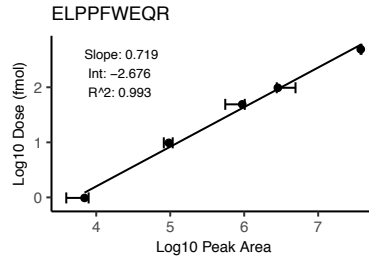
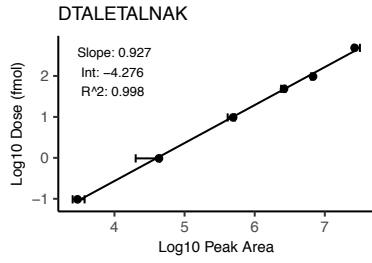
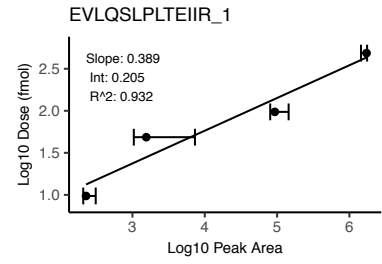
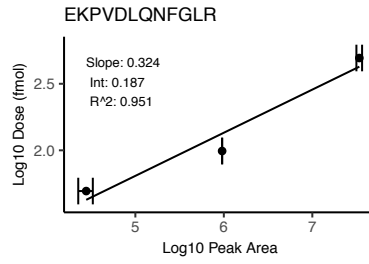
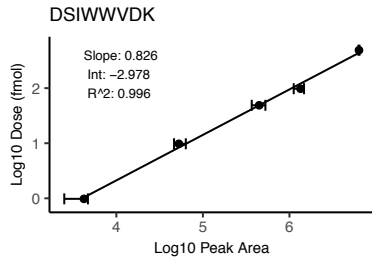
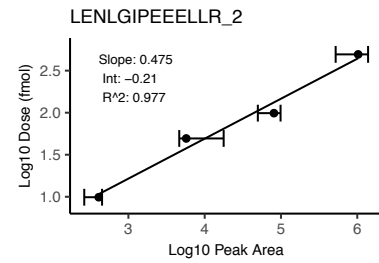
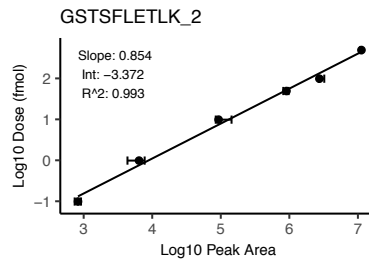
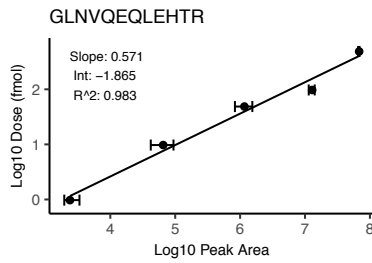
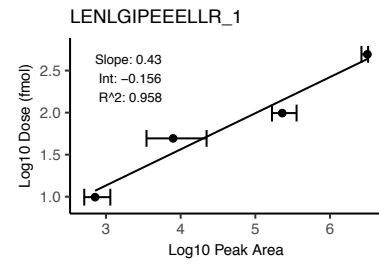
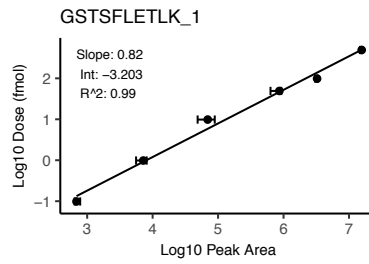
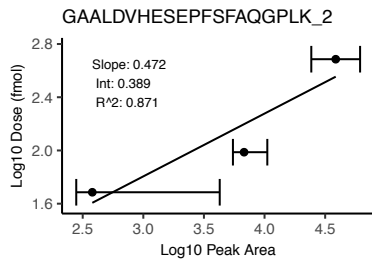
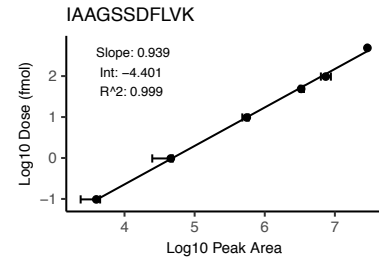
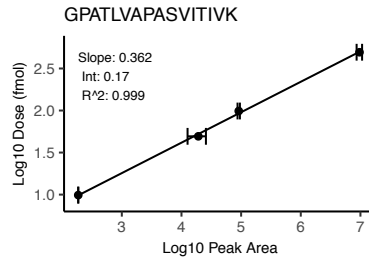
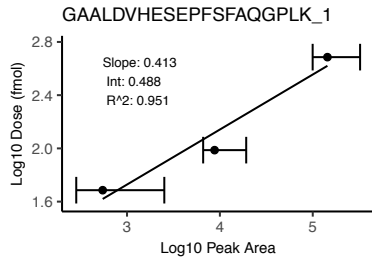
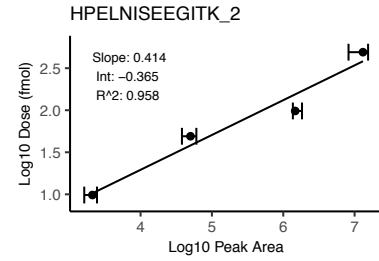
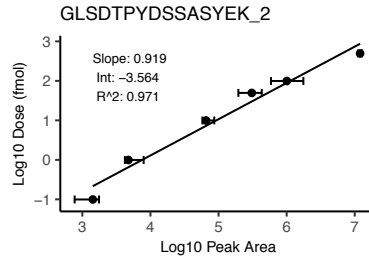
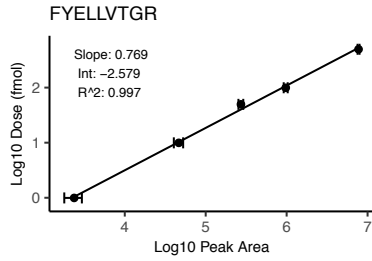
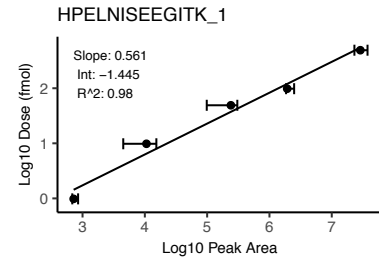
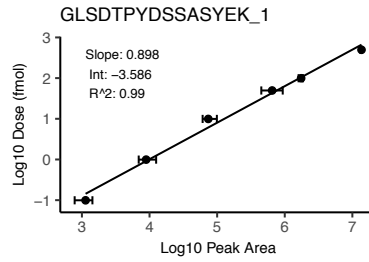
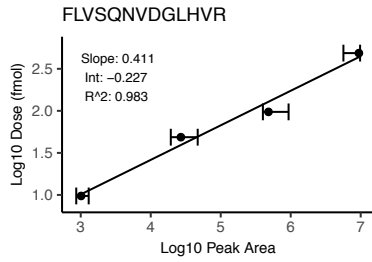
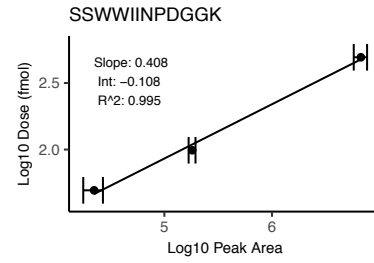
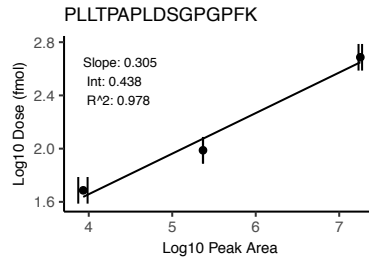
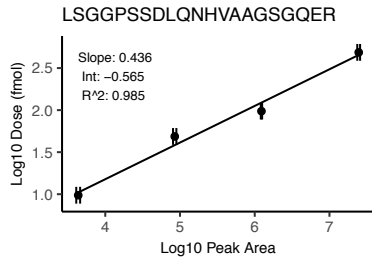
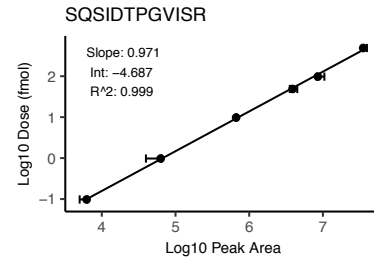
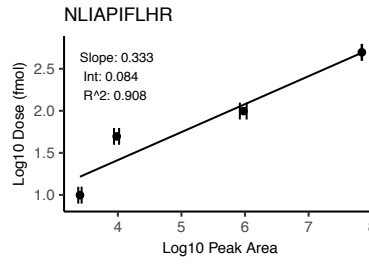
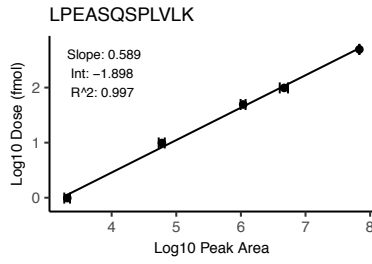
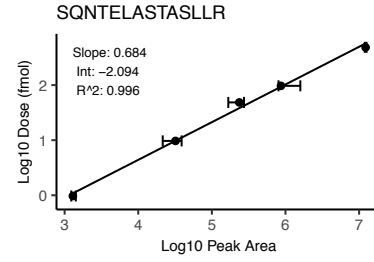
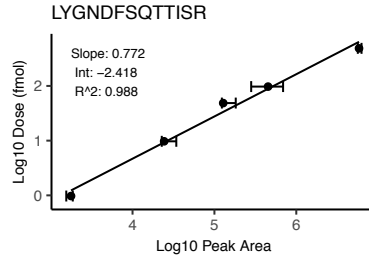
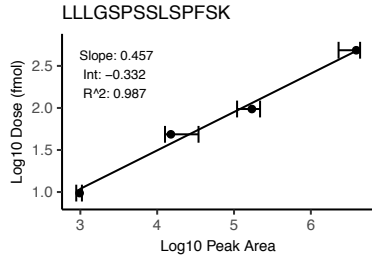
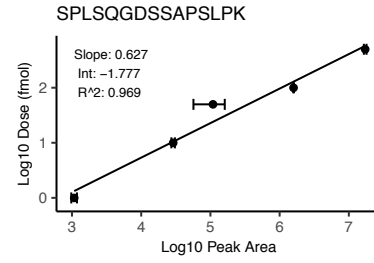
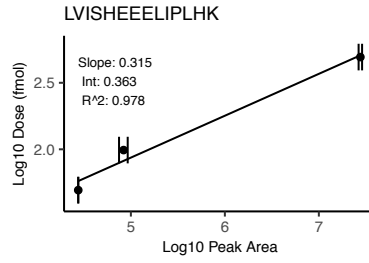
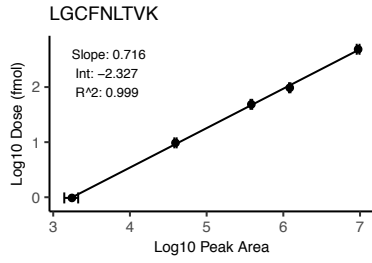
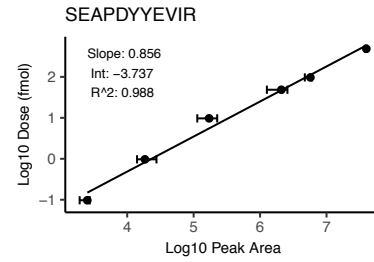
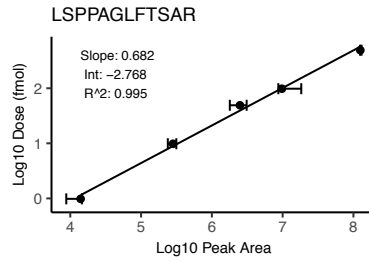
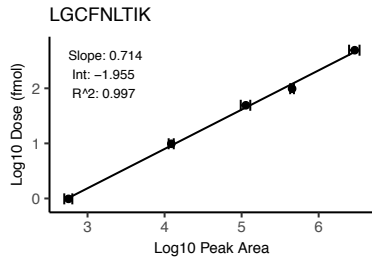


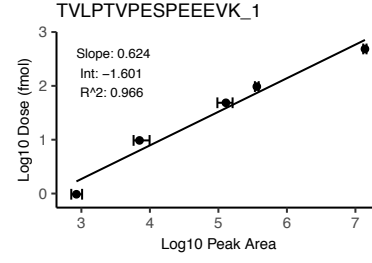
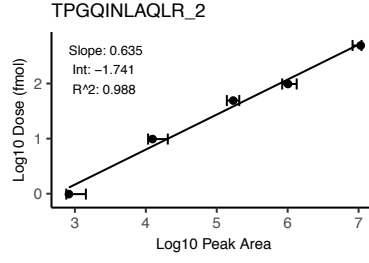
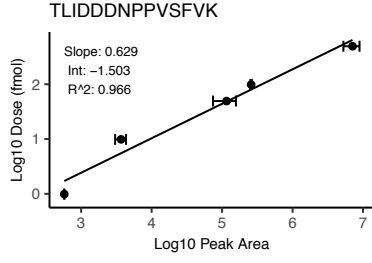
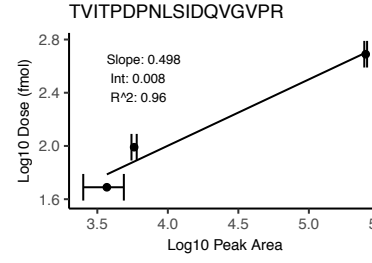
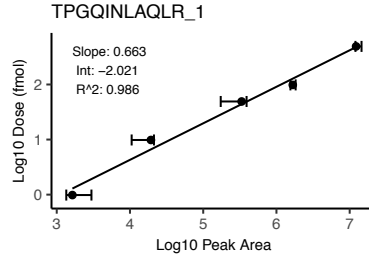
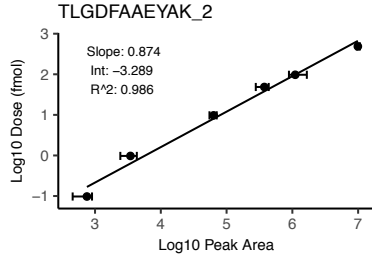
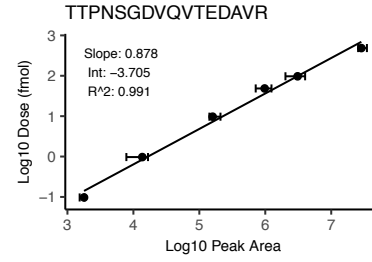
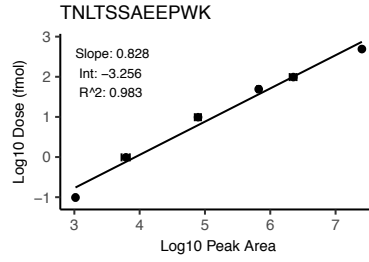
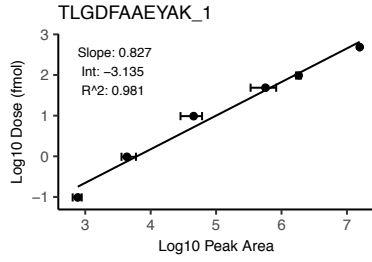
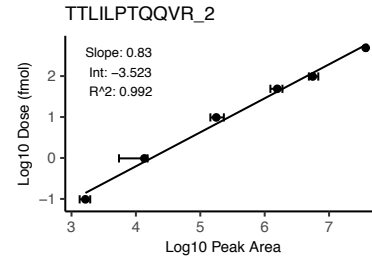
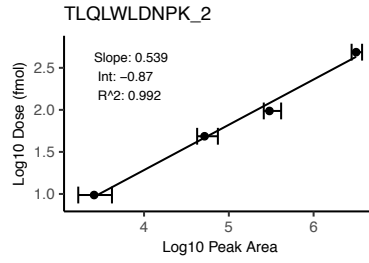
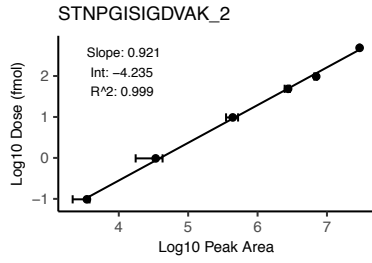
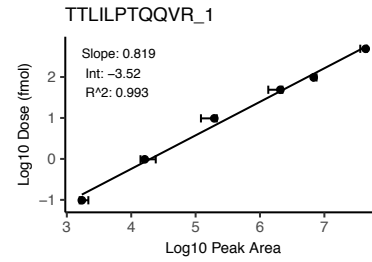
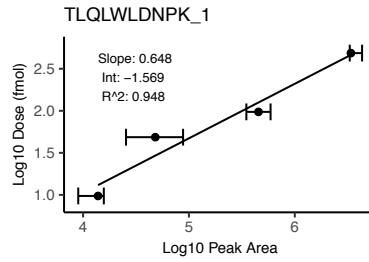
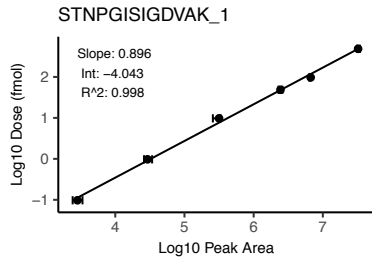
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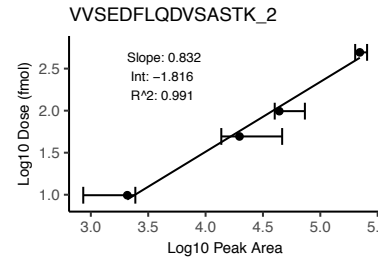
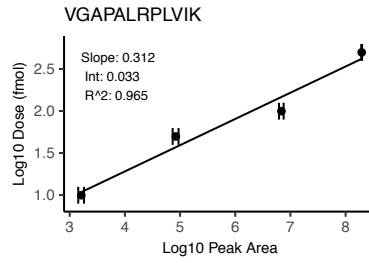
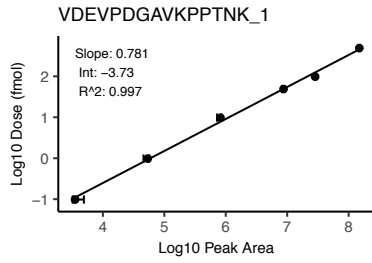
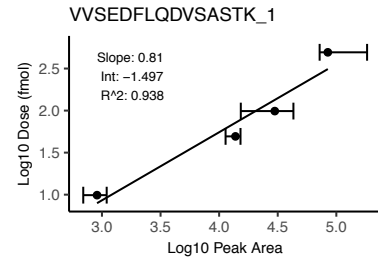
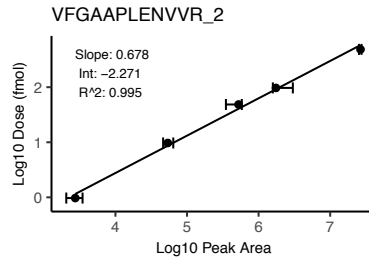
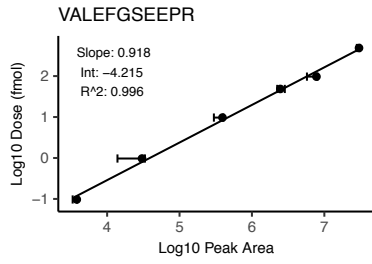
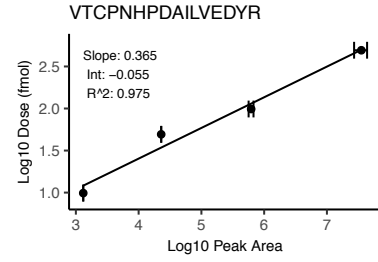
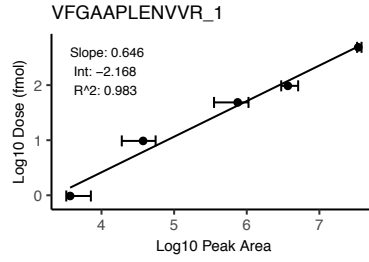
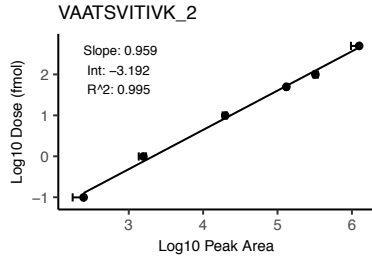
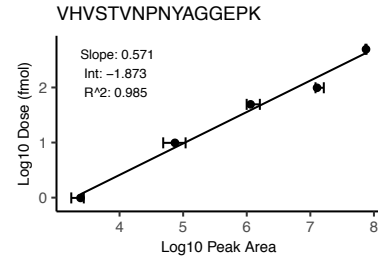
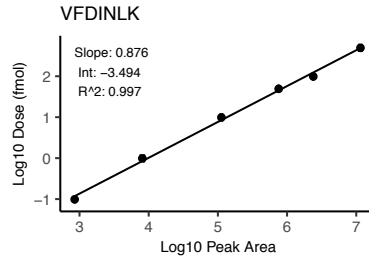
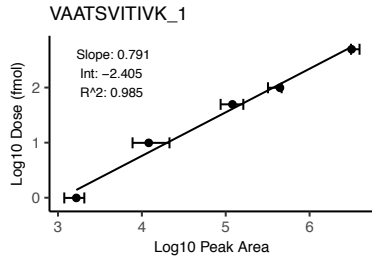
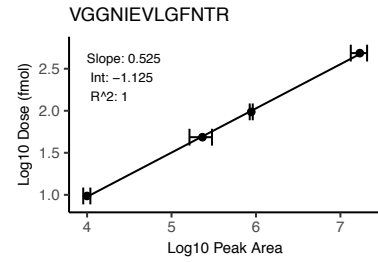
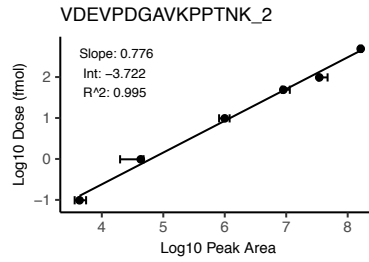
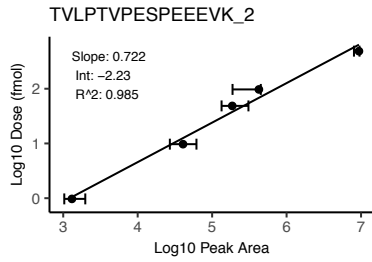


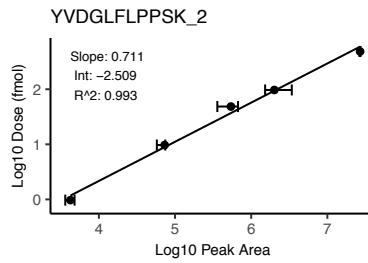
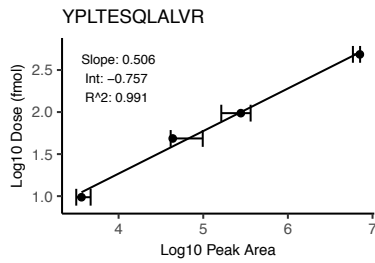
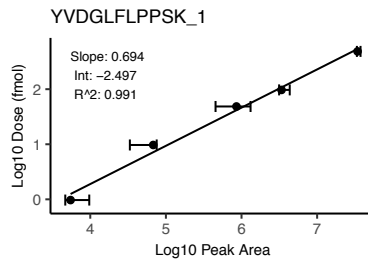
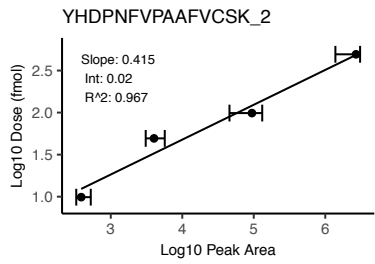
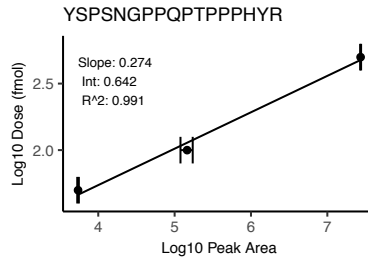
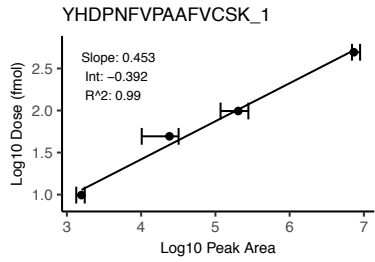
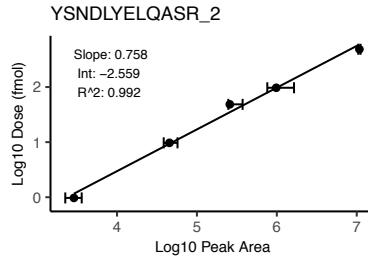
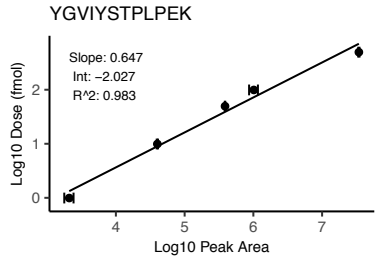
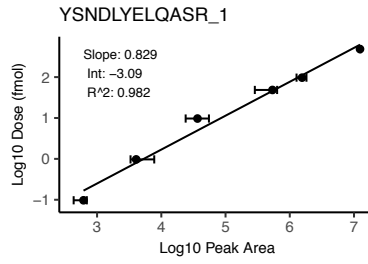
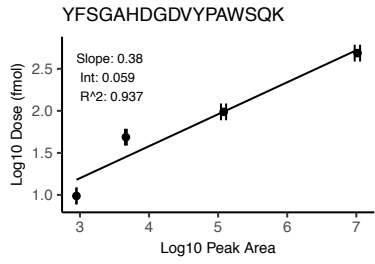


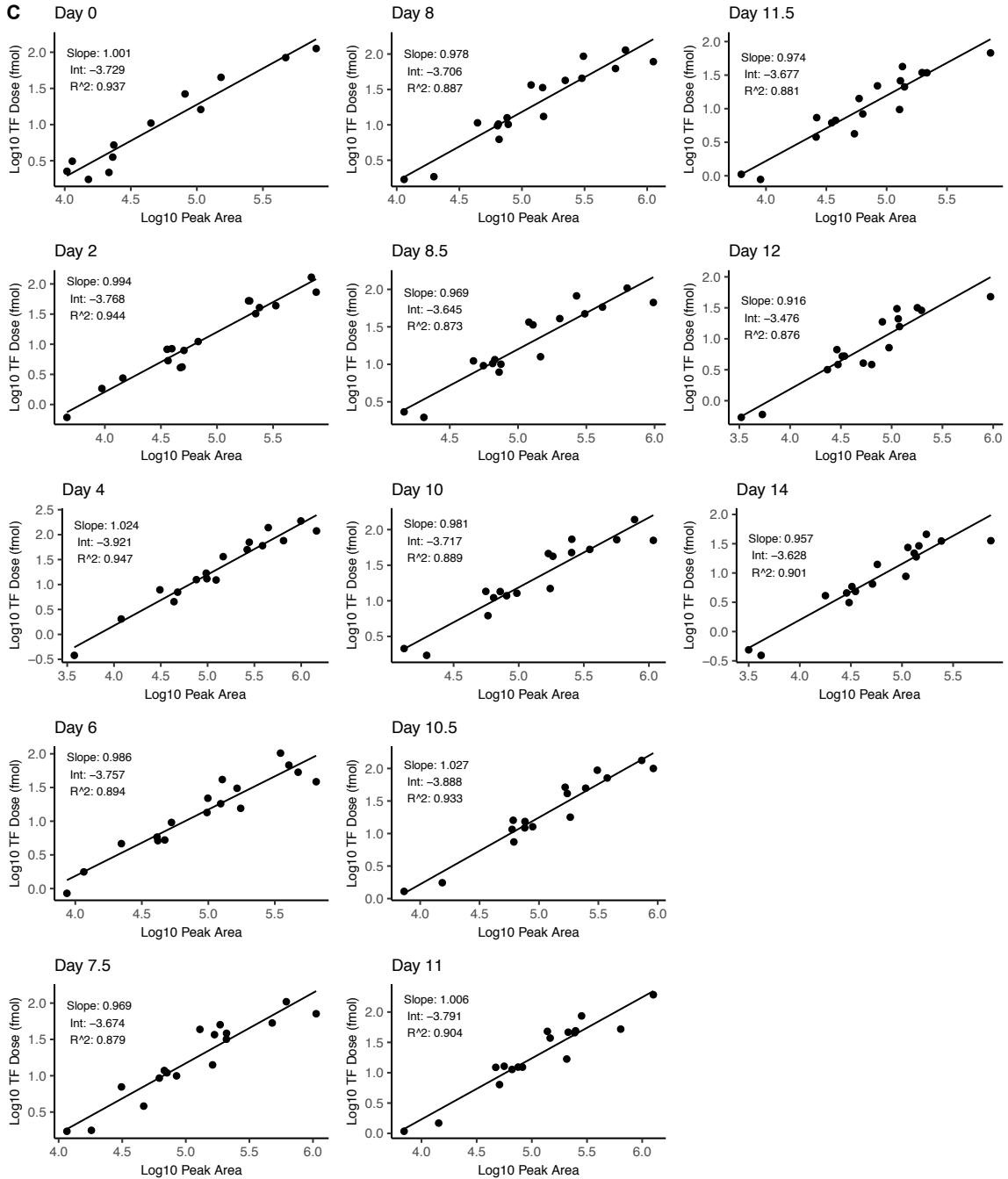


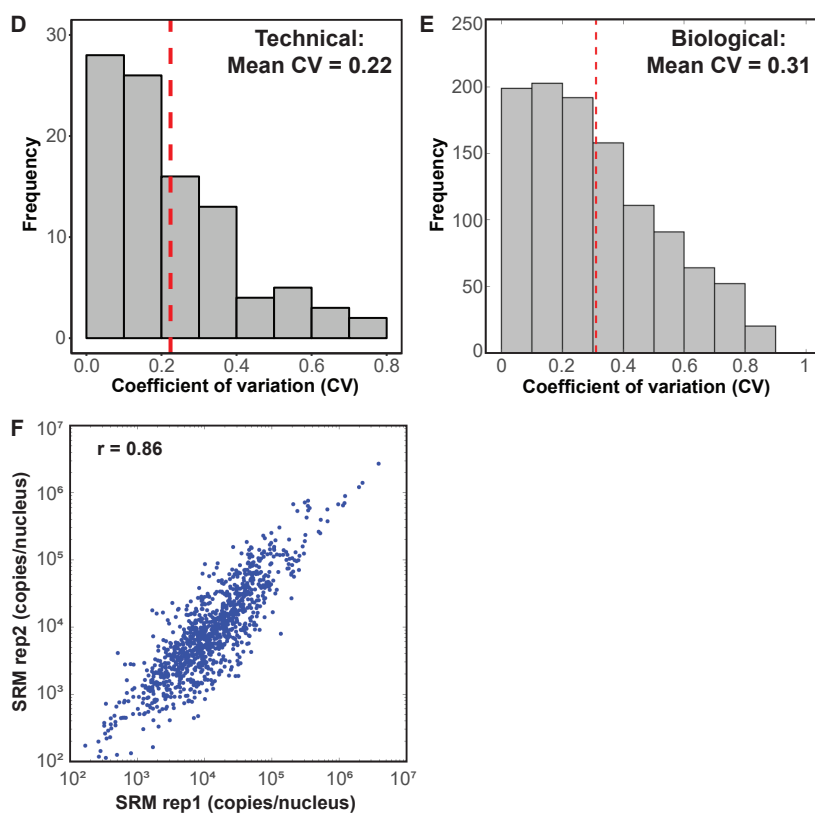












Data S1. (Related to Figure 1) SRM Related Plots

(A) Representative ion chromatograms of core network transcription factors measured by SRM. The main picture shows endogenous, isotopically light-labeled peptides (red) co-eluting with exogenous SIL peptides (blue). Inset pictures show specific transitions measured for each peptide isotope (H = heavy, L = light). Images were generated in Skyline and use Savitzky-Golay smoothing.

(B) Dose-response linear regression plots for all IS peptide standards (in solvent)

(C) Standard curves used for label free absolute quantification. Separate curves and regression parameters were generated for each time point of differentiation.

(D) Histogram of technical precision of replicate SIL peptide quantifications. Mean CV is denoted by red dashed line.

(E-F) Experimental precision of biological replicate protein concentrations shown by (E) histogram, and (F) scatter plot. Mean CV is denoted by red dashed line in (E).