Supplementary Figures

A Comprehensive Immunoreceptor Phosphotyrosine-based Signaling Network Revealed by Reciprocal Protein-Peptide Array Screening

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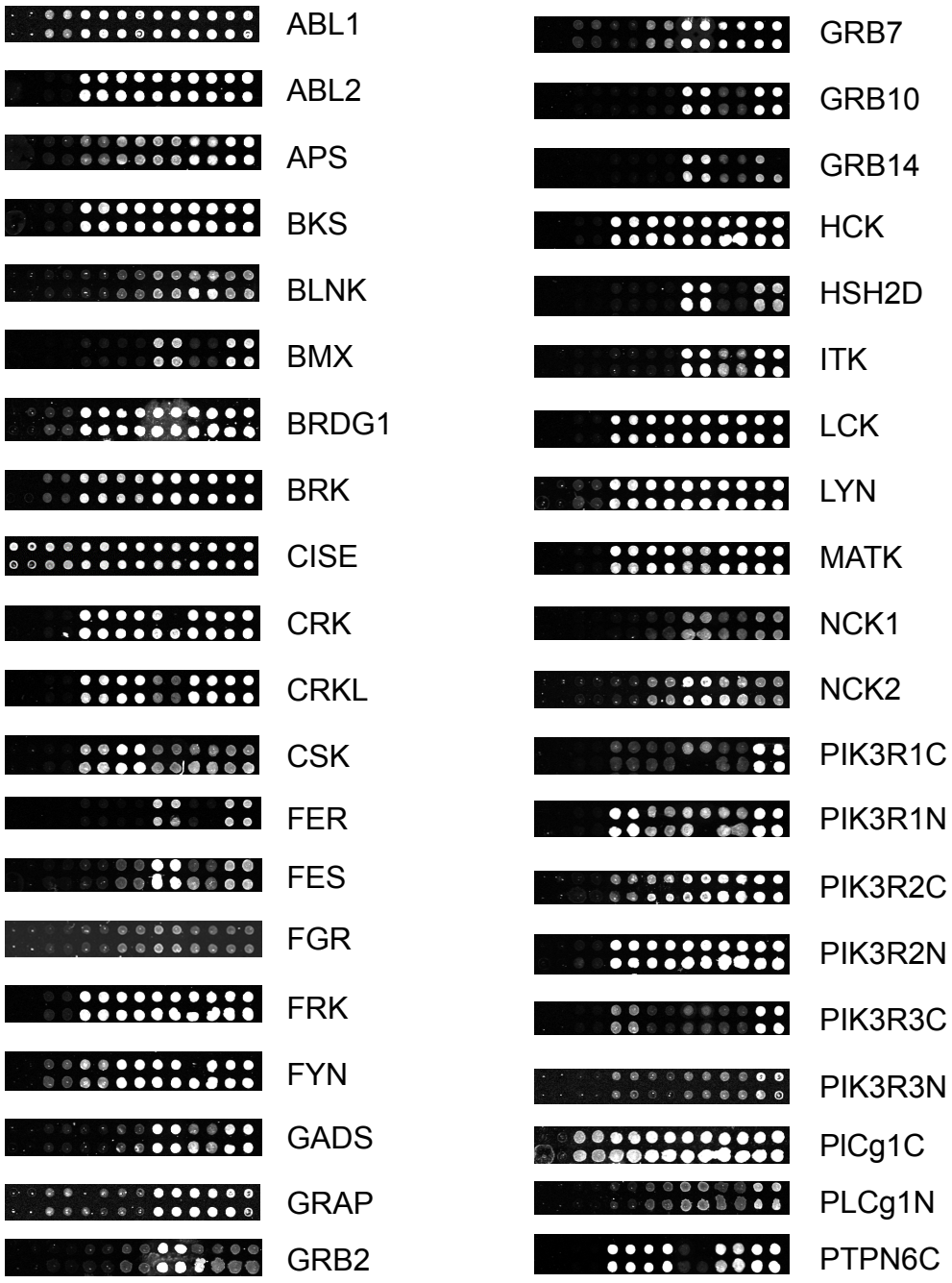
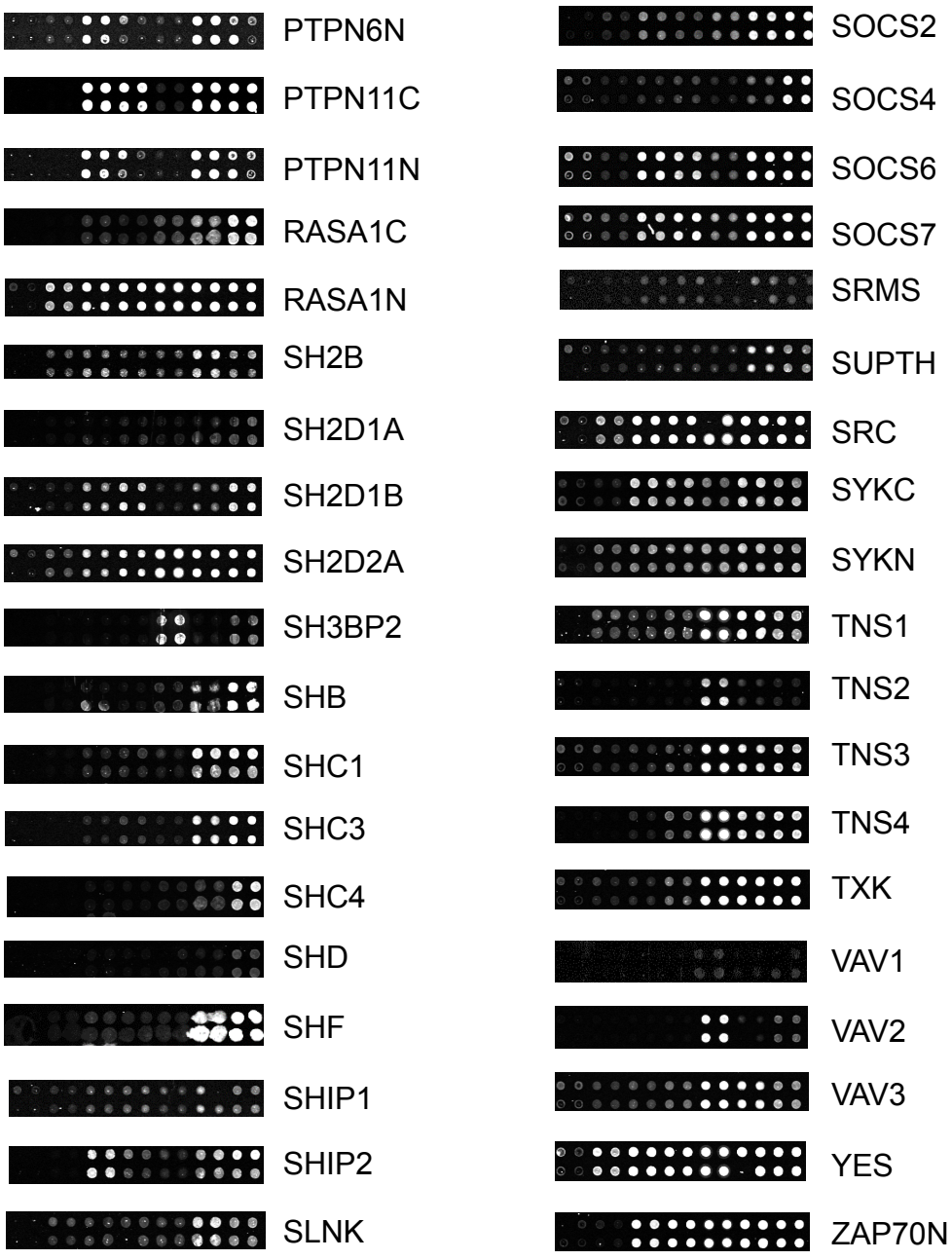
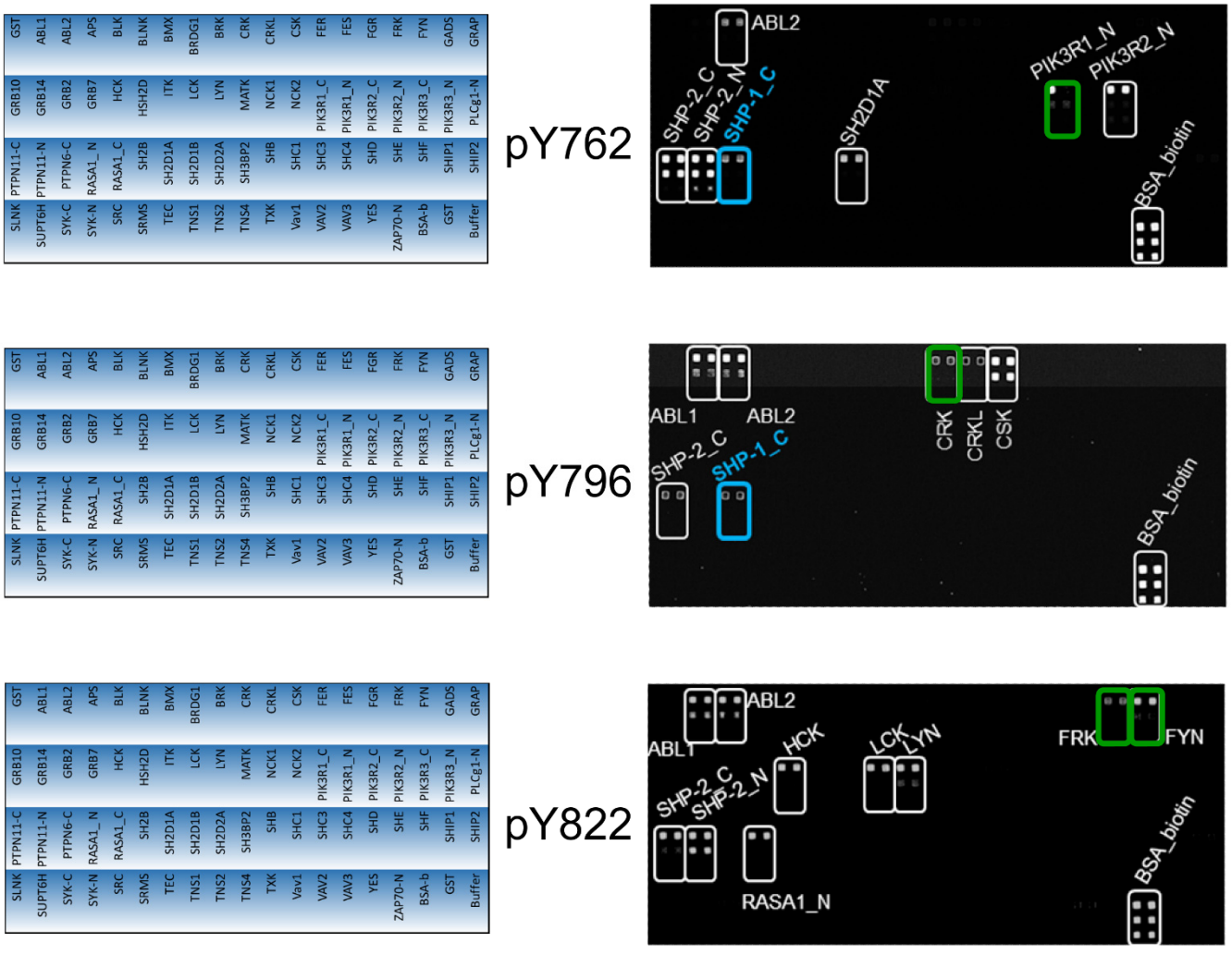


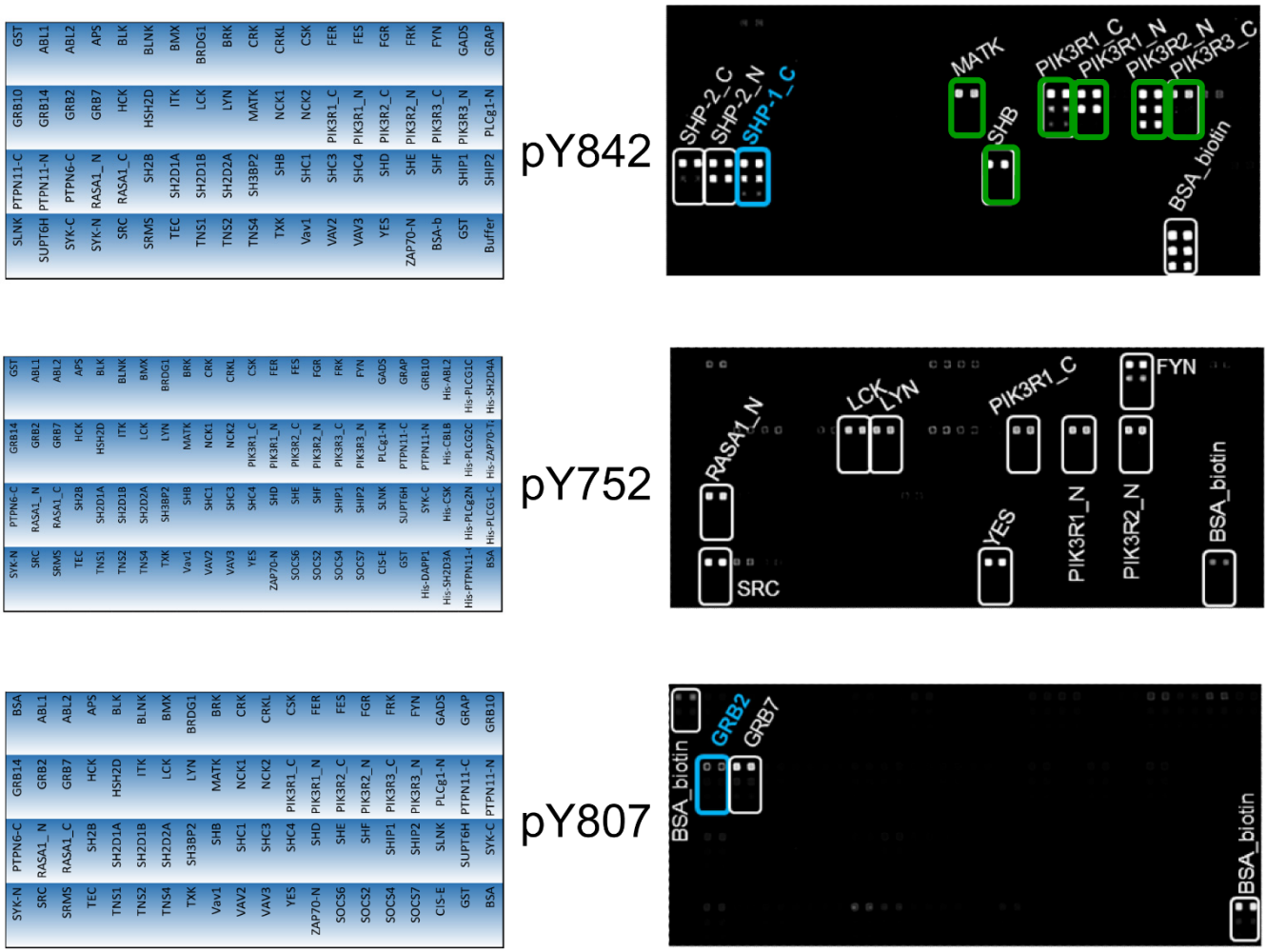
Supplementary Figure 1a. ***Binding profiles of different SH2 domains on a CD22-pY peptide array.*** The pY-containing peptide array representing the cytoplasmic Tyr phosphorylation sites in CD22 was probed for binding, respectively, to different human SH2 domains (in GST fusion). SH2 domains are identified on the right by the names of the corresponding proteins.



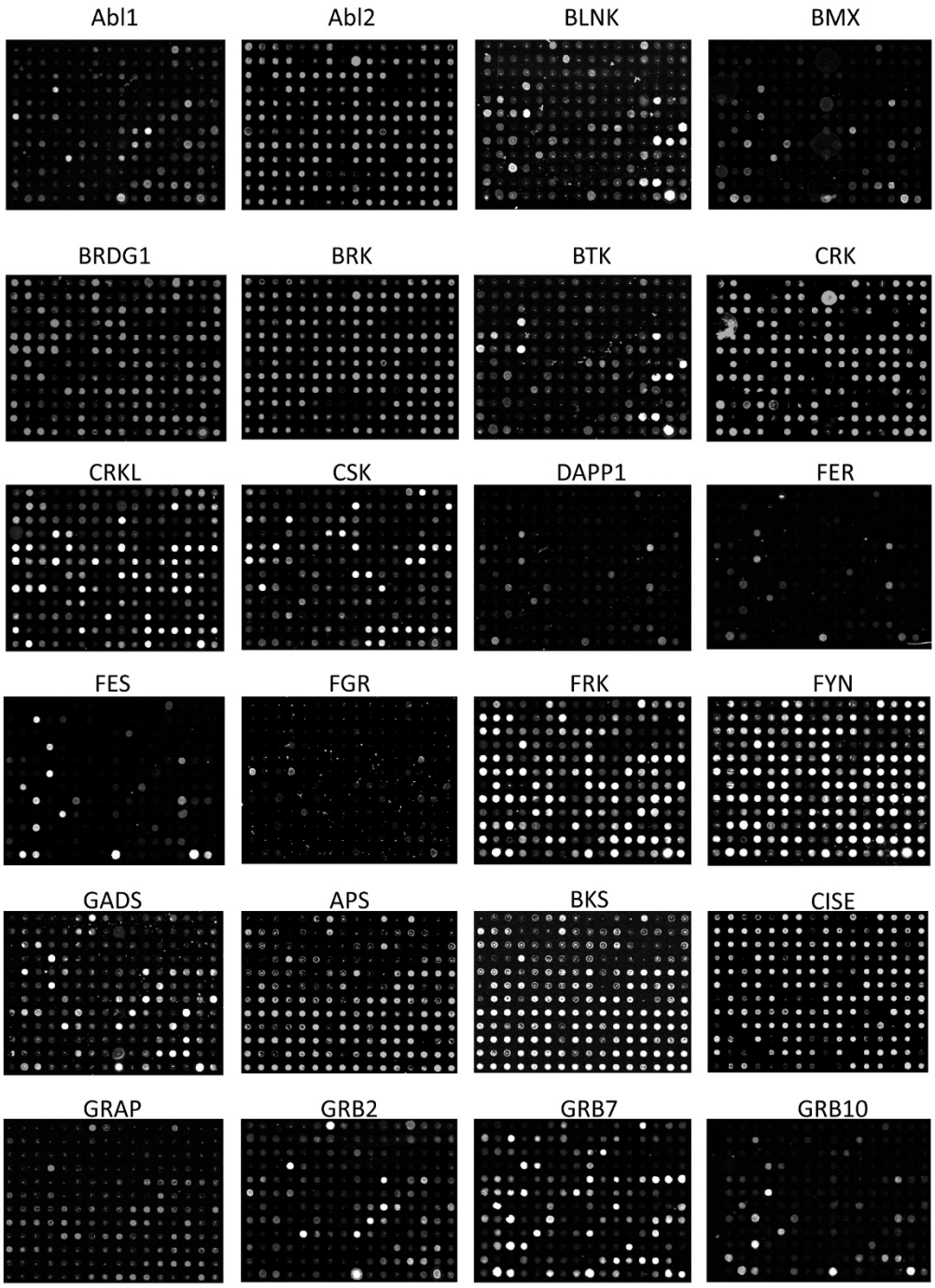
Supplementary Figure 1b. ***Binding profiles of different SH2 domains on a CD22-pY peptide array (cont'd).***



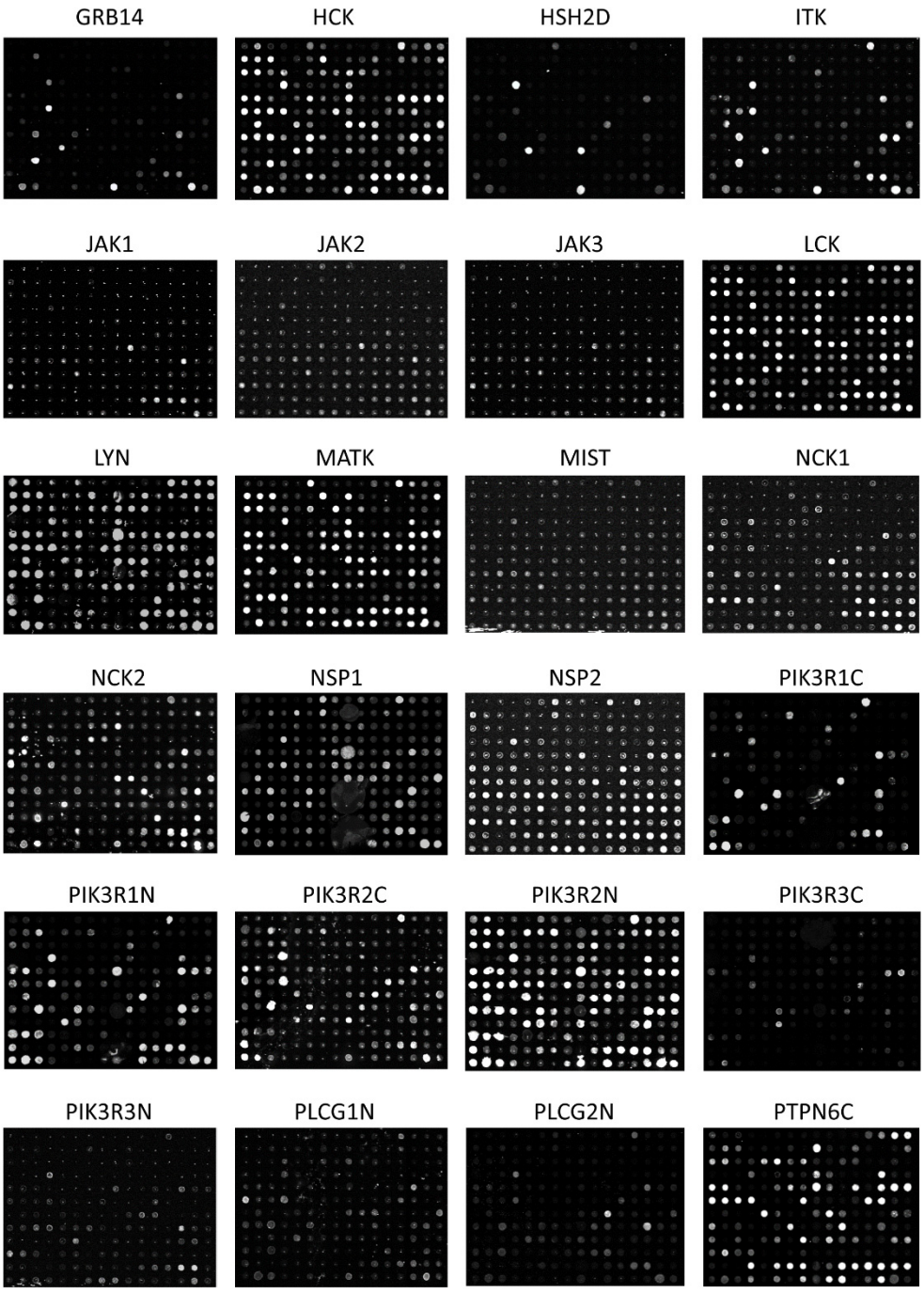
Supplementary Figure 2a. ***SH2 domain arrays probed by different CD22-pY peptides.*** This is a blown up version of data shown in Fig. 1 with the printing map shown on the left.



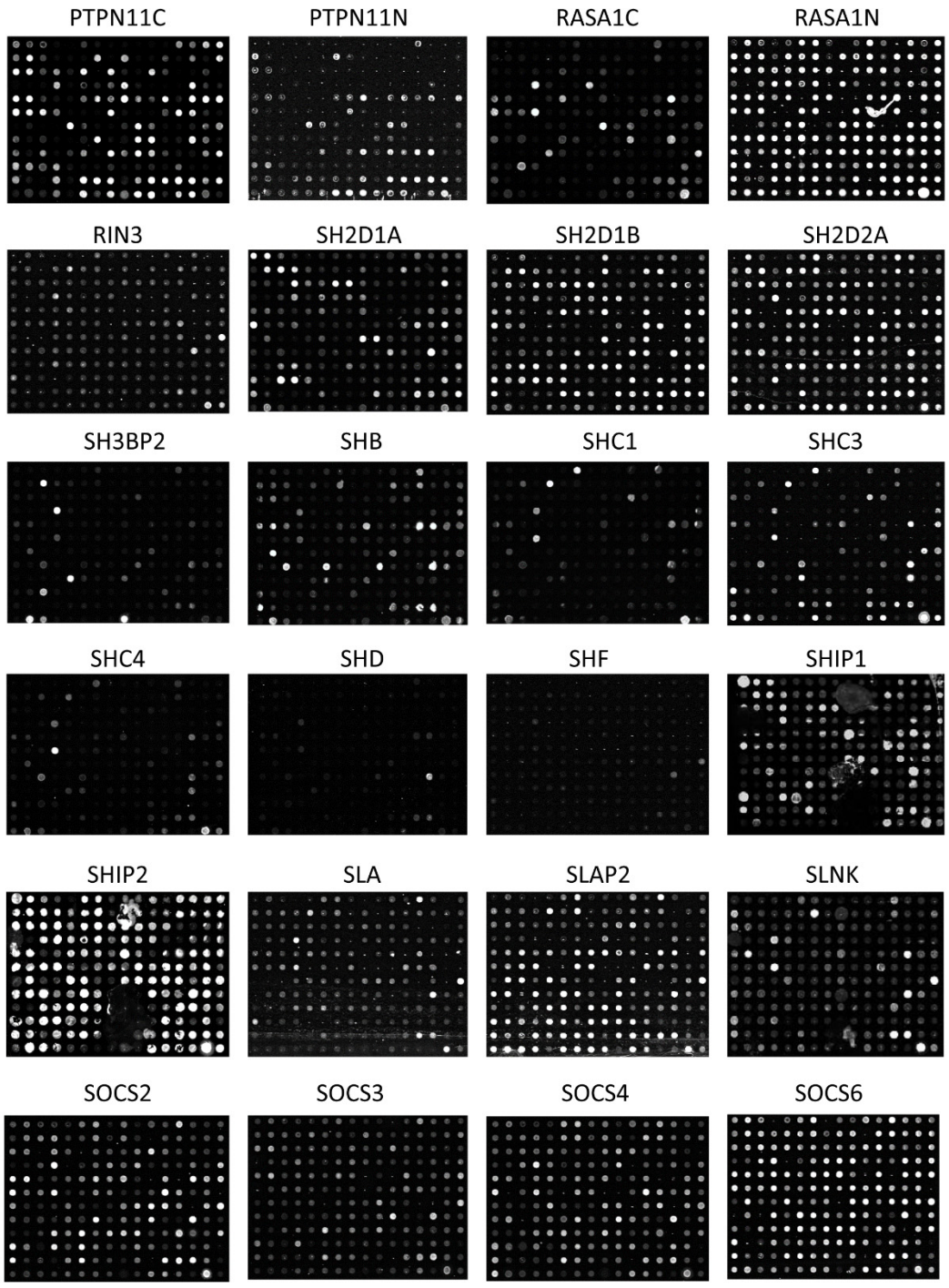
Supplementary Figure 2b. ***SH2 domain arrays probed by different CD22-pY peptides (cont'd).***



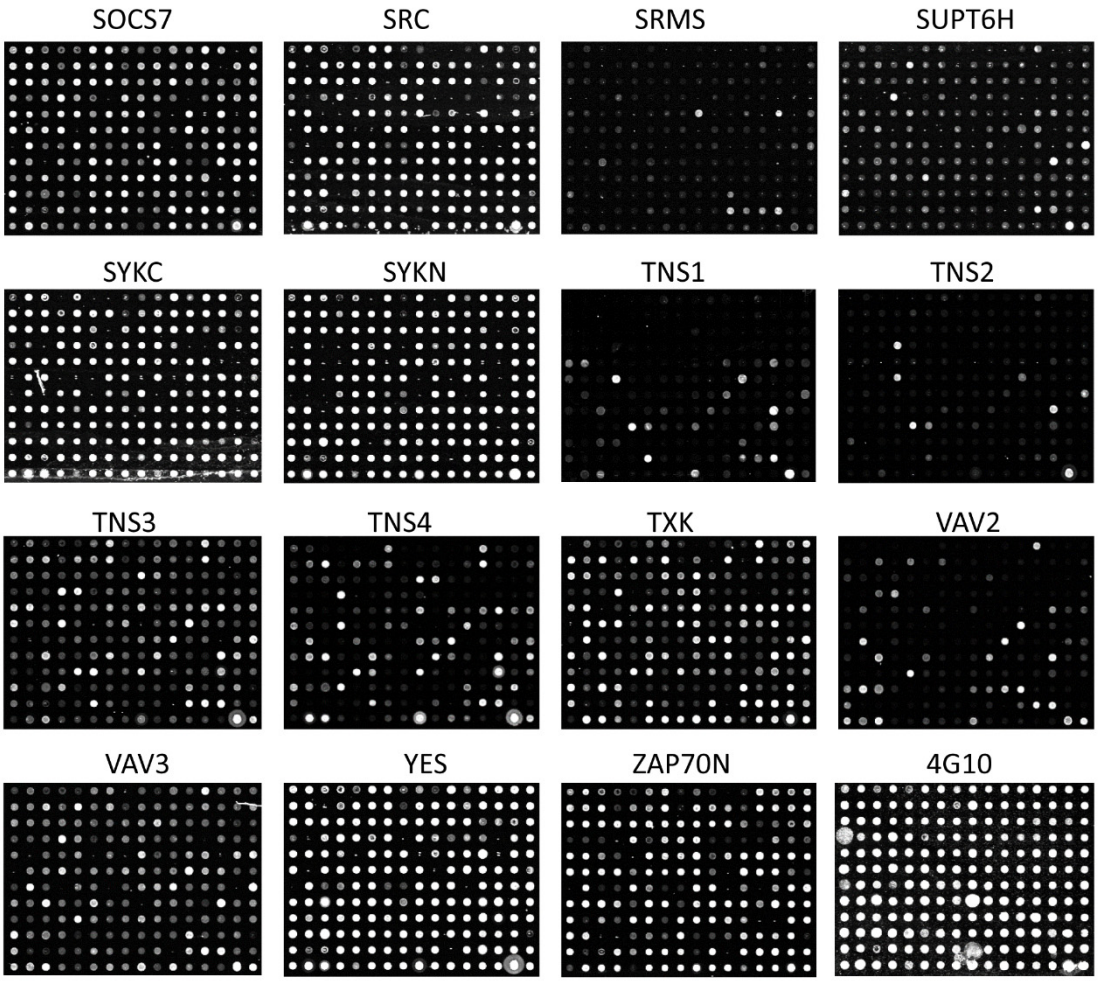
Supplementary Figure 3a. ***Binding profiles of different SH2 domains on an ITRM peptide array***.



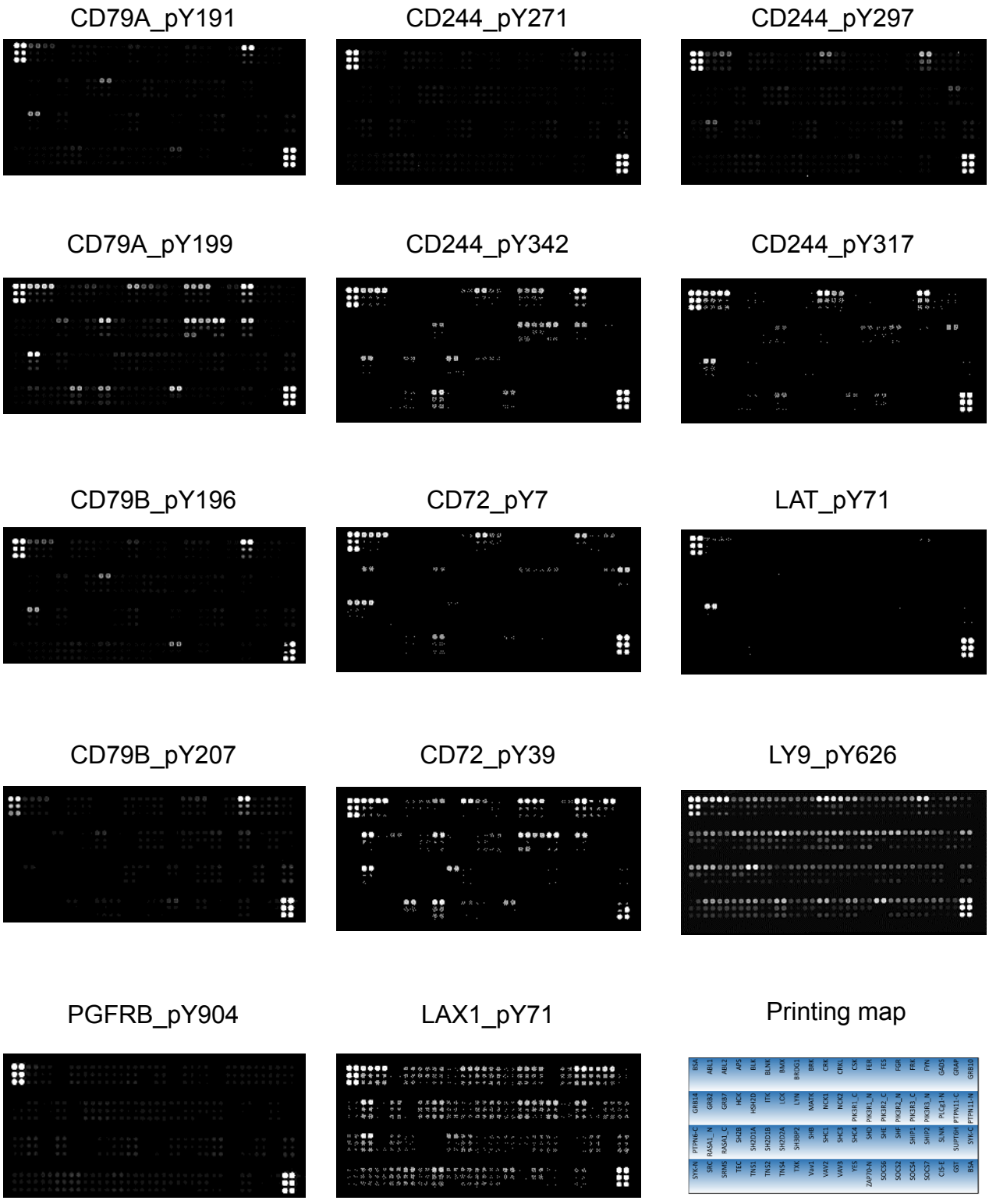
Supplementary Figure 3b. ***Binding profiles of different SH2 domains on an ITRM peptide array (cont'd)***.



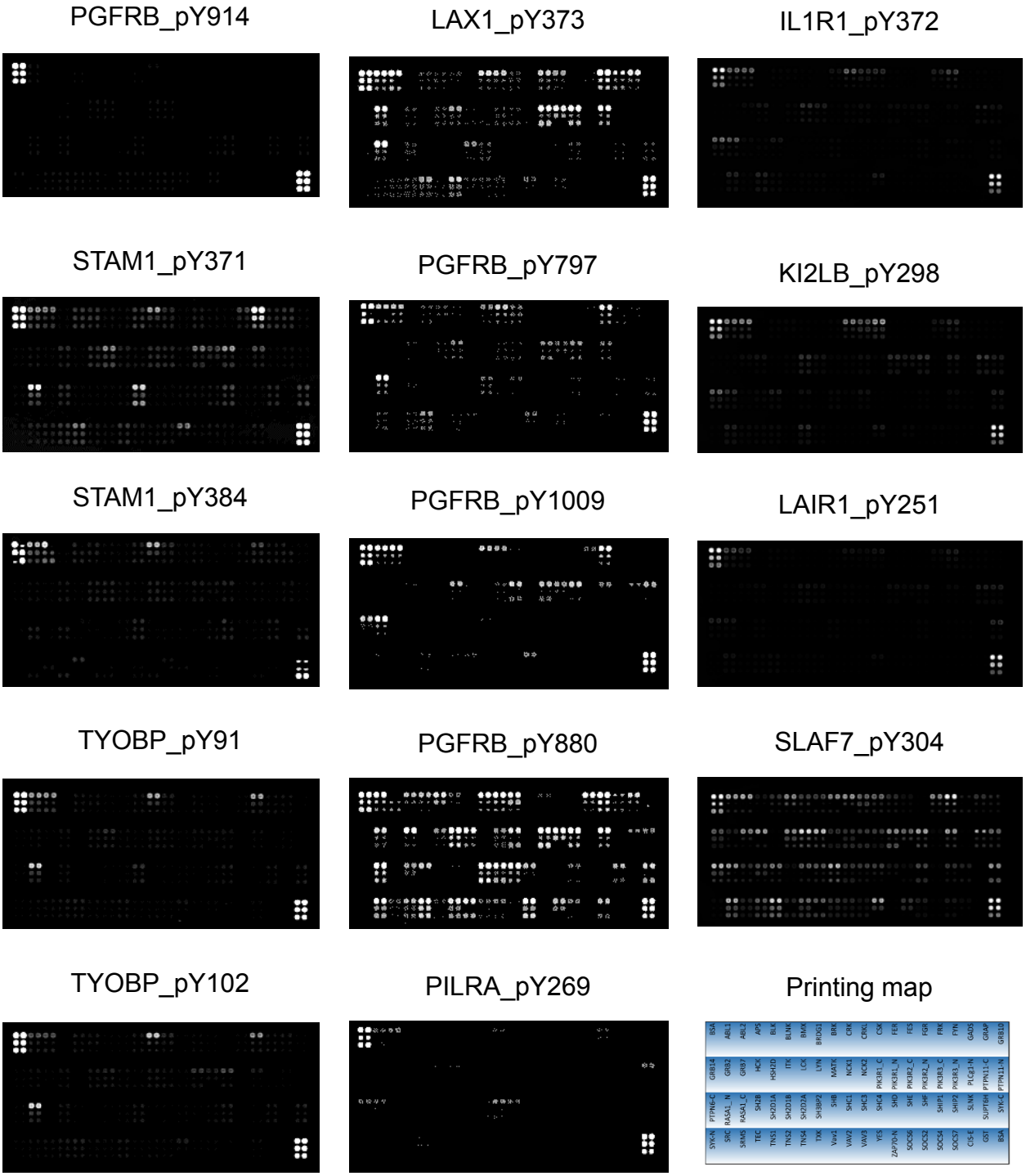
Supplementary Figure 3b. ***Binding profiles of different SH2 domains on an ITRM peptide array (cont'd)***.



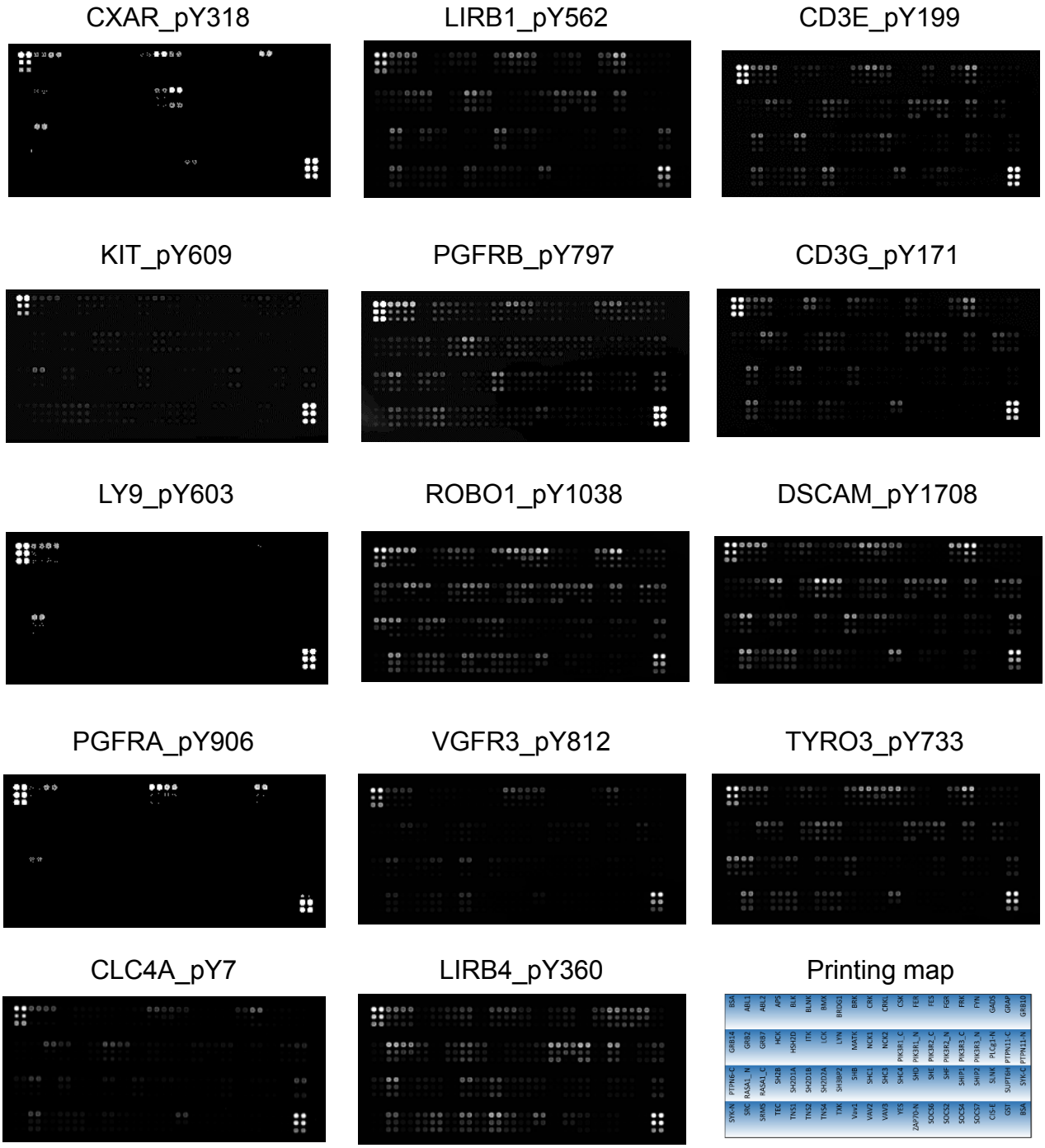
Supplementary Figure 3b. ***Binding profiles of different SH2 domains on an ITRM peptide array (cont'd)***.



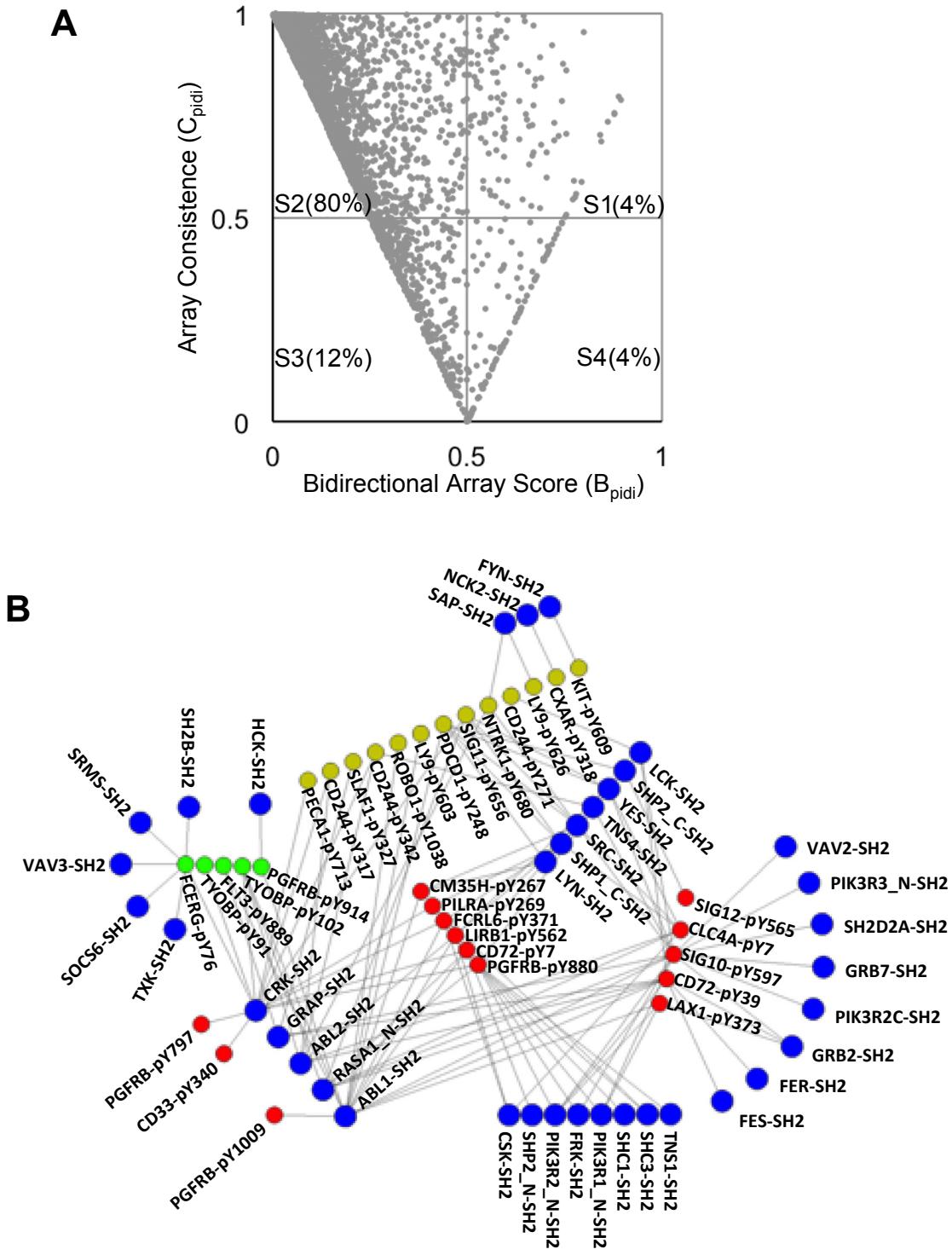
Supplementary Figure 4a. ***Binding profiles of different ITRM phosphopeptides on an SH2 domain array***.



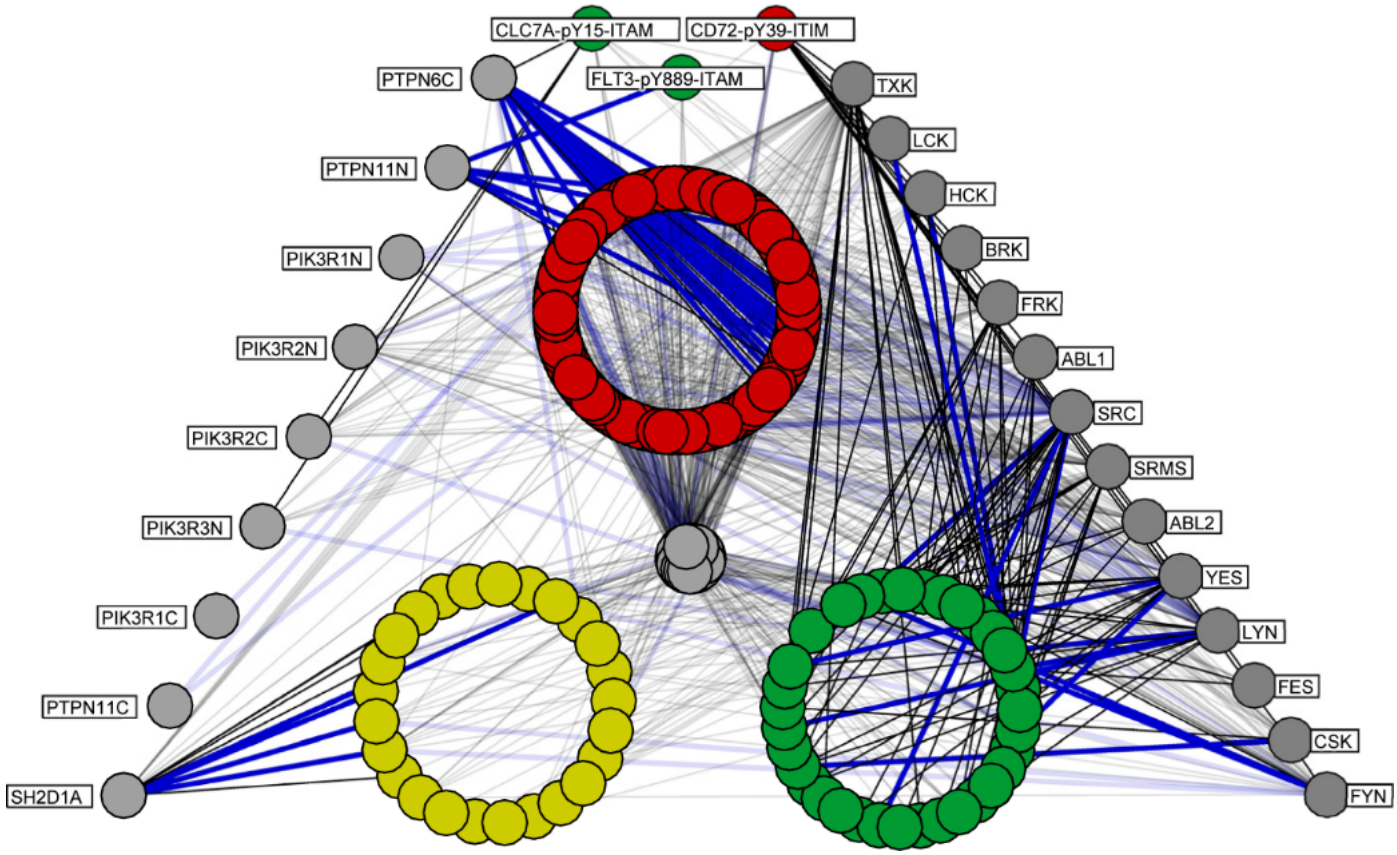
Supplementary Figure 3b. ***Binding profiles of different SH2 domains on an ITRM peptide array (cont'd)***.



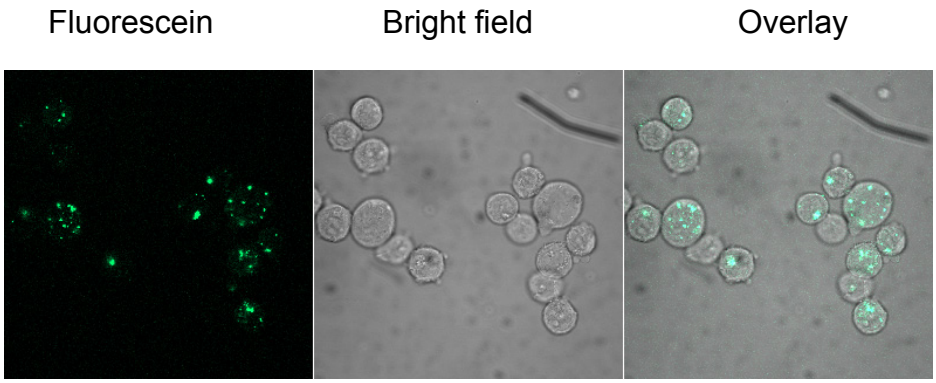
Supplementary Figure 3b. ***Binding profiles of different SH2 domains on an ITRM peptide array (cont'd)***.



Supplementary Figure 5. ***Analysis of data from bidirectional peptide-protein array screens.*** (**A**) Distribution of SH2-ITRM interactions in the bidirectional array plot. Interactions within each square are shown as percentage of the total interactions surveyed by the bidirectional array. (**B)** A high-confidence immunoreceptor-SH2 domain interactome derived from S1 in (A). ITIM motifs are shown in red, ITSM yellow, and ITAM green. SH2 domains were identified by the corresponding protein names and shown in blue. Proteins in the interactome are clustered using NAViGaTOR.



Supplementary Figure 6. ***Prediction of an immunoreceptor-SH2 domain signaling network based on data from bidirectional peptide-protein array screen.*** ITRM-SH2 pairs in S1 were used as gold standards to rescue true-positive interactions buried in S2-4 (see also Supplementary Figure 5A). The resultant interactome contains interactions located within S1 as well as those "rescued" by the scheme described in the paper. Interactions annotated in the STRING database are marked blue. ITIMs are shown in red, ITAMs in green, and ITSMs in yellow. Three peptides on the top were shown as examples.



Supplementary Figure 7. Microscopic images of cells transduced with fluorescein-labeled BSA- gold nanoparticles (AuNP) adducts. YT cells were incubated with 10 nM AuNP-FITC-BSA for 4h at 37° C. Shown are fluorescent (left) and bright-field (middle) images of the cells with the overlaid image shown on the right.