



Figure S1

Interaction maps are probed for protein interaction sets (**A**): partners of proteins with multiple interactions are clustered together where there are no known sequence feature present (**B**). Domains and homologous regions are then identified (**B**) and removed prior to running exhaustive pattern discovery (**C**) to produce list of motifs ranked by their probabilities P (**D**). Hypothetical motifs are shown as coloured squares in **C** & **D**.

'Proteins' in **D** gives the set of proteins containing at least one copy of the motif.

I. Shows two separate cases of protein sets containing interactions partners for proteins X and Y that are pooled owing to the presence of a common domain to give a domain set shown in (**II**).