



Figure S7. Distribution of *PfSAMS* interactors according to log₂ ratio and functional prediction. The 1,114 identified interaction partners were plotted based on the peptide count and the log₂ ratio. (A) Dotplot graph depicting the interactors aggregating in two distinct groups based on their log₂ ratio and peptide count. Selected proteins representing each group are labeled with their PlasmoDB gene IDs. (B) Dotplot graph depicting the subcellular localization of the interactors of both groups. The GO categories “Nucleus” (GO:0005634) and “Cytoplasm” (GO:0005737) were considered. (C) Dotplot graph comparing the clusters A-F, as identified by STRING analysis, based on the log₂ ratio. The six clusters are defined in Fig. 6. The red diamond (B, C) represents the median of each group.