



Fig. S6. Network analysis scheme depicting selected interactors of *PfSAMS*. A list of 1,114 query proteins was evaluated for potential interactions, using the String database. A network of the potential *PfSAMS* interactors was predicted with a confidence level of 0.009. A Markov Clustering (MCL) algorithm was used to describe possible clusters with an inflation parameter of 3. Based on the physical interaction among only the query proteins, different clusters of interactors were identified.