



Fig. S1 Quality control of AP-MS samples. **A:** Overview of number of identified *P. berghei* proteins per sample. Samples LAP3/GFP rep 4 (non-crosslinked) and LAP3/GFP rep 4X (crosslinked) were removed from further analysis due to poor proteome coverage compared to other samples. **B:** Hierarchically clustered heat map representation of Pearson cross correlation table showing correlation coefficients of pairwise protein abundance (LOG2 LFK) comparisons between replicates with Pearson r values ranging between 0.5 and 1. Replicates constitute pulldown samples from LAP3/GFP ookinetes with crosslinking (rep 1X-3X) or without crosslinking (rep 1-3). This analysis demonstrates good correlation between replicates within the sample group without crosslinking (rep 1-3) and within the sample group with crosslinking (rep 1X-3X). Furthermore, the analysis shows that correlation between sample groups is much lower than within sample groups, demonstrating good reproducibility in protein abundance levels within the data set.