



Supplementary Figure 3: Properties of *Botryllus schlosseri* DIA assay library (**A-D**) and corresponding DIA data (**E-I**). Numbers of protein groups (**A**) and unique peptides (**B**) represented in the DIA assay library are illustrated in dependence of the minimal number of peptides per protein. Red diamonds indicate the conditions selected for the final DIA assay library (min. 3 peptides per protein). The final number of peptides (red diamond in **B**) is lowered further after application of additional QC criteria described in the text. **C**) Numbers of transitions per precursor in the DIA assay library. **D**) Frequency distribution of transitions included in the DIA assay library. **E**) Mass error distribution of all peptides in the DIA assay library for all 44 samples. **F**) mProphet q values for all peaks of all samples indicating peak quality (lowest is best). **G**) Linear regression of predicted (based on iRT standards) and observed (average for all 44 samples) retention times. **H**) MSstats sample size calculation result based on DIA data for all 44 samples. **I**) MSstats QC plot illustrating the intensity distribution of all proteins across all 44 samples.