



Figure 5 - Figure Supplement 2: Significantly differing proteins in two out of three analyses with accession numbers

All proteins that significantly differ in two out of three of the analysis methods (frequentist, empirical Bayes and random forest classification with SHAP values). From left to right, accession numbers, proportion of samples in which the protein was identified in colony samples and single individual samples, average iBAQ abundance across all samples calculated without zero values, log<sub>2</sub> of the fold change in abundance between types for a given comparison, the comparisons for which the protein was significant in two out of three methods are marked with yellow dots, annotation terms.