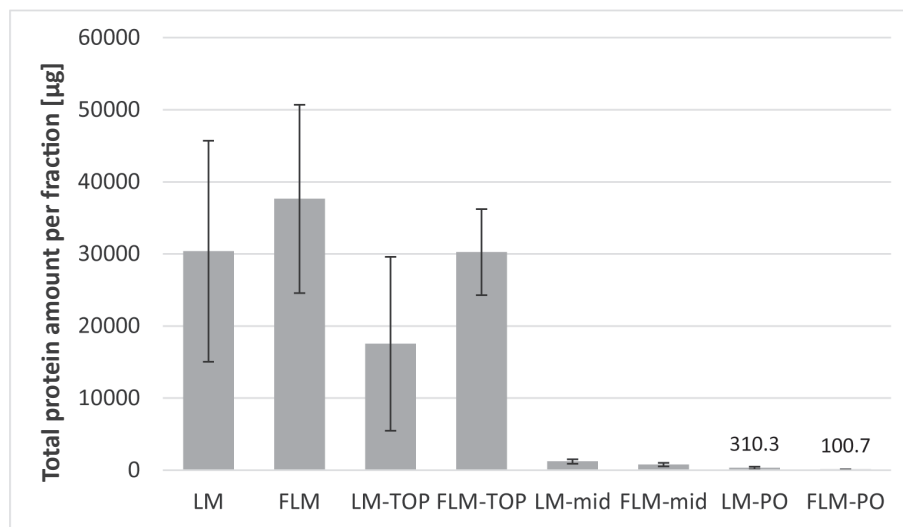


A



B

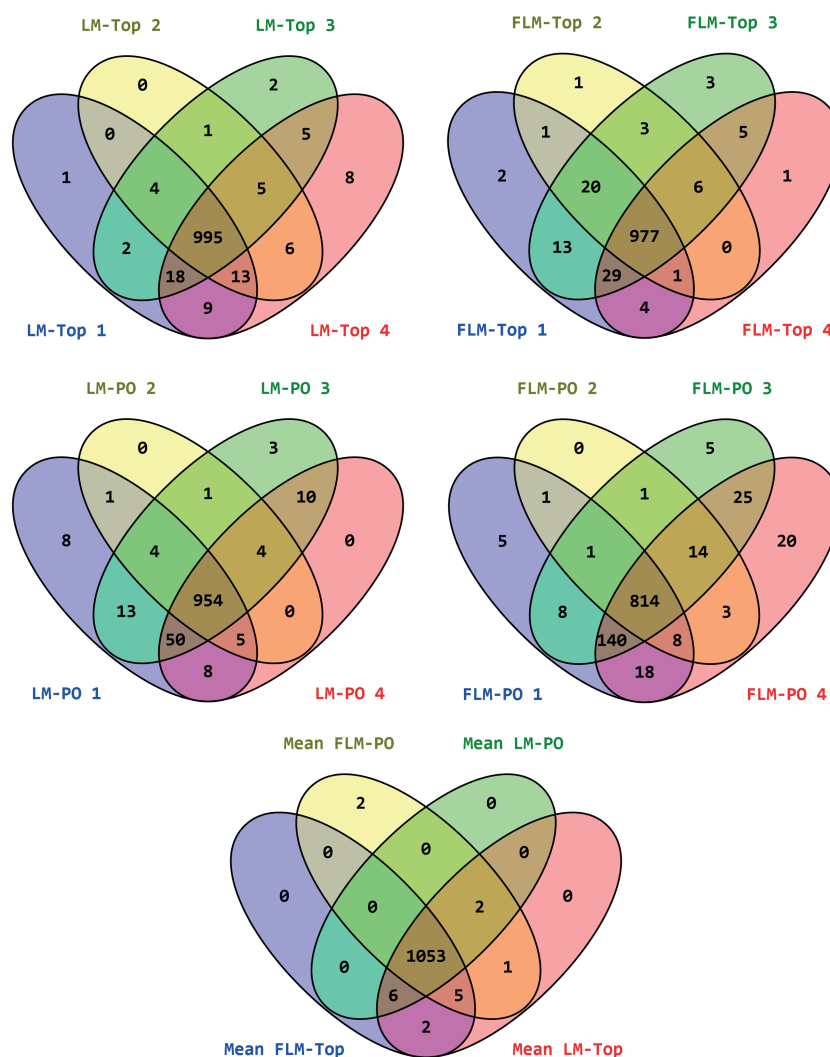


Fig. S1: (A) Average total protein amounts of the fractions subjected to MS. The graph compares prefractions subjected to density gradient centrifugation (LM, FLM) with the fractions eluted from the iodixanol gradients (LM-TOP, FLM-TOP, LM-PO, FLM-PO), which were analyzed via SWATH-MS. LM-mid/FLM-mid corresponds to the material, which was eluted in between the analyzed fractions.

(B) Overlap of quantified proteins among the replicate SWATH-MS runs and means of the 4 experimental groups, respectively. For $\geq 90\%$ of the proteins the quantification is based on at least 3 replicates (LM-TOP 96%, FLM-TOP 94%, LM-PO 94%, FLM-PO 90%).