

High-Reynolds Microfluidic Sorting of Large Yeast Populations

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Supporting Information

Figure S1. Proteomic analysis of three sample sets, young, adult and mix. **(A)** clustering analysis of all 932 proteins identified in this analysis. Clustering done on median LFQ intensity values using the Perseus software⁵². **(B)** Clustering analysis of significantly different proteins identified by the ANOVA test (P-value <0.05). The LFQ values were normalized using z-scoring ranging from -2 (low LFQ intensity) to 1.8 (high LFQ intensity).

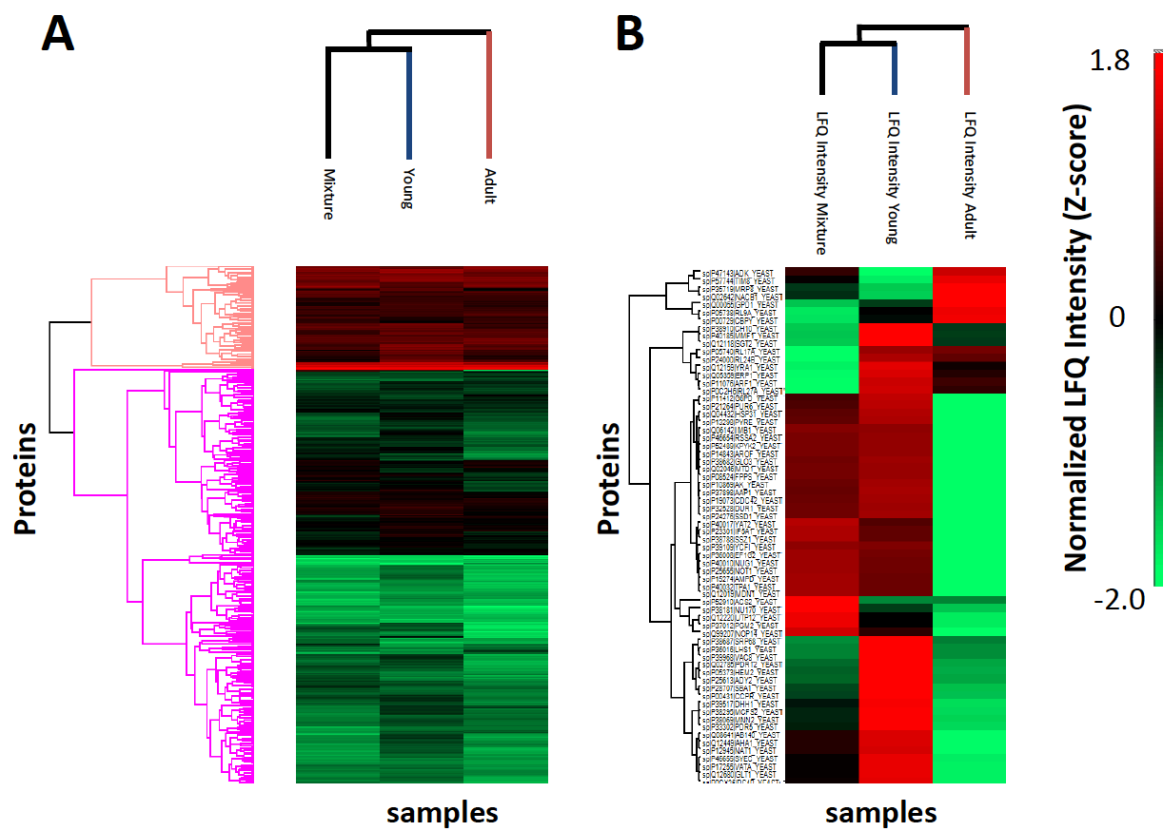


Table S1. Proteins which are present in all yeast groups: young (0-2 scars), adult (3-10 scars) and heterogeneous mixture.

Table S2. The cellular distribution of the proteins according to GO based cellular localization.

Table S3. ANOVA test which identifies a subset of 64 proteins showing significantly different expression levels between all three yeast groups: young (0-2 scars), adult (3-10 scars) and heterogeneous mixture.

Table S4. Distribution of biological functions within the group of significantly different proteins.