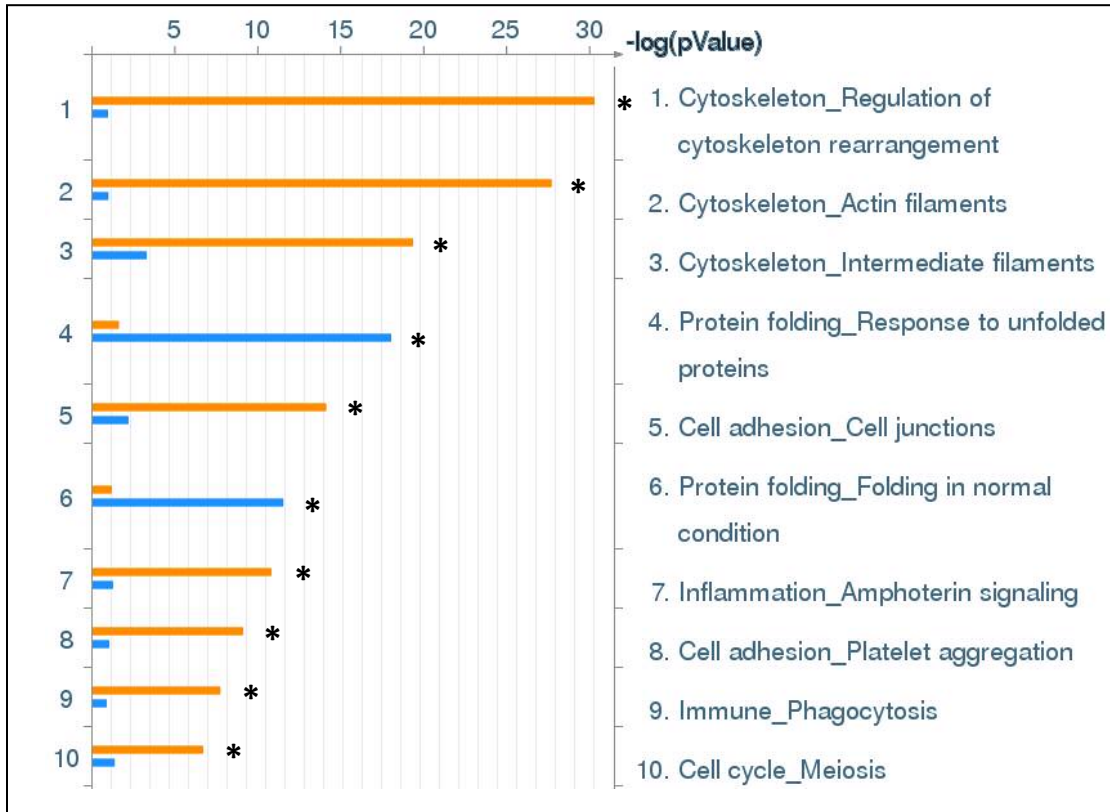


SUPPLEMENTARY RESULTS:

Supplementary Figure 1: Analysis of enrichment of GeneGo categories for all proteins differentially expressed proteins.



Supplementary Figure 1: Enrichment analysis of differentially expressed proteins for cellular processes. All differentially regulated proteins were subjected to enrichment analysis for cellular processes using Metacore pathway mapping tool from GeneGo. Orange bars represent up regulated proteins and blue bars represent down regulated proteins. Bars with asterisk indicate significant enrichment with $< 1\%$ false discovery rate.

SUPPLEMENTARY MATERIALS AND METHODS:

S1. Correction of each reporter ion for its isotopic abundance: The “Certificate Of Analysis”

(COA) essentially consists of a matrix C shown in the following table, which gives the fraction of each iTRAQ reporter group resulting in each type of ion.

	114 Da reporter	115 Da reporter	116 Da reporter	117 Da reporter
112 Da ion	0	0	0	0
113 Da ion	0.010	0	0	0
114 Da ion	0.925	0.020	0	0
115 Da ion	0.063	0.919	0.030	0.001
116 Da ion	0.002	0.060	0.920	0.040
117 Da ion	0	0.001	0.049	0.920
118 Da ion	0	0	0.001	0.038
119 Da ion	0	0	0	0.001

We let the vector $A = [A_1 \ A_2 \ A_3 \ A_4]^T$ be the unknown reporter abundances for reports of 114 through 117 Da, and let the vector $O = [O_1 \ O_2 \ O_3 \ O_4 \ O_5 \ O_6 \ O_7 \ O_8]^T$ be the observed abundances of ions 112 through 119 Da, where superscript T indicates the transpose of a matrix. The matrix C from the COA relates A and O, by $O = CA$. We used just $O_t = [O_3 \ O_4 \ O_5 \ O_6]^T$, and that 4 by 4 part of the matrix C giving the fraction of each reporter resulting in ions of 114 to 117 Da (in bold in above table), which we denote C_t . This allowed us to simply use $\hat{A} = C_t^{-1}O_t$ as our estimate of A. Our estimate is unbiased, as is the least-squares estimator using all of the ions ($\hat{A} = (C^T C)^{-1} C^T O$), but ours ignores data from the 112, 113, 118 and 119 ions, which give smaller peaks, less reliable information, and alter the estimate only slightly.

S2. Tranche hyperlinks for the data presented in Keshamouni et al.,:

The data associated with this manuscript may be downloaded from the [ProteomeCommons.org](https://proteomecommons.org) [Tranche](#) system using the following hash.

Password to access: “timecourse”

vuiWSWyTFsTEkYFwh1YHAbZ3XUoxFnP5hKfz4sVBUwi7jWLQx5e+Gpb+z4Td7GA47427
rWlpq0iQDYKTjvddTKS4yo8AAAAAAAAAOOA==

or using [this hyperlink](#).

Alternatively, individual components of the data associated with this manuscript can be downloaded by using hyperlinks below.

