Table S1. Evidence of coordination in the proteomes analyzed

Using functional databases

Proteome/Stimulus	Number of categories	Number of changing categories	% Changing categories	Number of Q>C relations	Number of Q>C relations (without outliers)	Number of outlier relations	% Outlier relations
Yeast/- (Null Hypothesis)	2335	0	0.0%	61342	61333	9	0.0%
Yeast/H_2O_2	2676	104	3.9%	80193	78941	1252	1.6%
Pig heart/infarct	1139	119	10.4%	8853	8705	148	1.7%
Mouse fibroblasts/Zmpste24 KO	1383	55	4.0%	12288	12048	240	2.0%
Human secretome/HS vs CE	885	126	14.2%	4747	4412	335	7.1%
Mouse MAM/Caveolin-1 KO	3797	213	5.6%	34770	33483	1287	3.7%
Mouse lymphocytes/HDAC6 KO	4066	101	2.5%	123887	121360	2527	2.0%

Using randomized functional databases

Proteome/Stimulus	Number of categories	Number of changing categories	% Changing categories	Number of Q>R relations	Number of Q>R relations (without outliers)	Number of outlier relations	% Outlier relations
Yeast/- (Null Hypothesis)	2335	0	0.0%	61342	61333	9	0.0%
Yeast/H_2O_2	2676	19	0.7%	80193	79239	954	1.2%
Pig heart/infarct	1139	11	1.0%	8853	8701	152	1.7%
Mouse fibroblasts/Zmpste24 KO	1383	2	0.1%	12288	12108	180	1.5%
Human secretome/HS vs CE	885	28	3.2%	4747	4555	192	4.0%
Mouse MAM/Caveolin-1 KO	3797	44	1.2%	34770	33699	1071	3.1%
Mouse lymphocytes/HDAC6 KO	4066	18	0.4%	123887	121312	2575	2.1%