

FIG. S2.

Bio Rep	Comment	Peptides				Proteins			
		Total	Forward	Reverse	%FDR	Total	Forward	Reverse	%FDR
1	Step 0: PSMs with Mascot Score ≥ 20	22373	20215	1079	4.82	2337	1359	489	20.92
	Step 1: Filter rank 1 peptides	16799	16453	173	1.03	1588	1358	115	7.24
	Step 2: Filter Y-containing peptides	5071	5005	33	0.65	642	592	25	3.89
	Step 3: Filter phospho-containing peptides	4404	4362	21	0.48	192	160	16	8.33
2	Step 0	20387	17719	1334	6.54	2176	1148	514	23.62
	Step 1	17811	17341	235	1.32	1466	1202	132	9.00
	Step 2	5857	5773	42	0.72	589	551	19	3.23
	Step 3	2999	2949	25	0.83	234	208	13	5.56
3	Step 0	19416	18092	662	3.41	1840	1268	286	15.54
	Step 1	14887	14615	136	0.91	1391	1233	79	5.68
	Step 2	5250	5208	21	0.40	670	648	11	1.64
	Step 3	1914	1882	16	0.84	182	166	8	4.40

Fig. S2. **False discovery rate (FDR) estimation at the peptide and protein level for each individual 5-plex SILAC biological replicate.**

The FDR were determined using Proteome Discoverer (version 1.2) connected to Mascot (version 2.3.2), and using a concatenated forward-decoy human UniProt/SwissProt database (release 2011_04, 20,232 protein sequences). The filter option in Proteome Discoverer was used to count the peptides and proteins reverse hits.