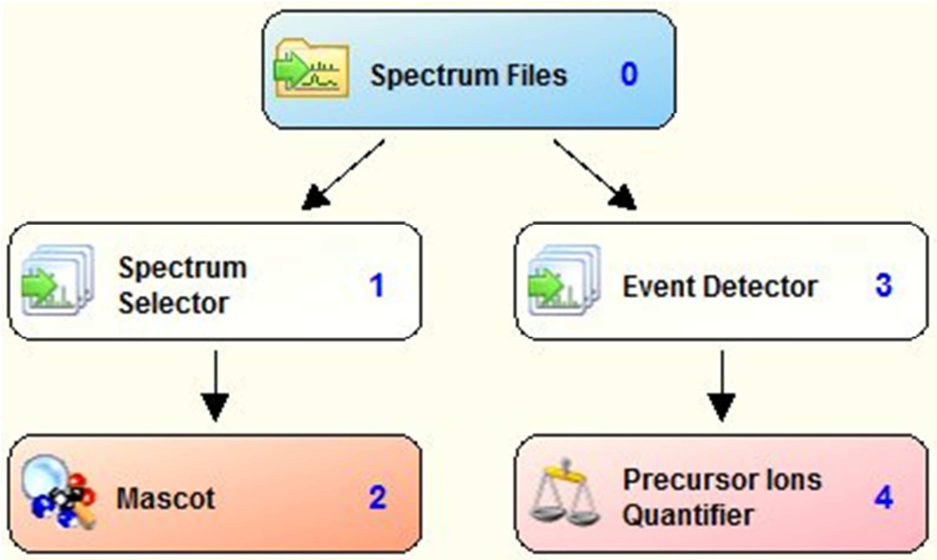
FIG. S1.



Processing node **0**: Spectrum Files		
Input data:	Technical replicates combined as MudPIT using Daemon 1.2	
Processing node **1**: Spectrum Selector		
	Min. Precursor Mass:	350 Da
	Max. Precursor Mass:	5000 Da
	Minimum Peak Count:	10
Processing node **2**: Mascot		
1. Input Data	Protein Database:	Sprot
	Enzyme Name:	Trypsin
	Max Missed Cleav. Sites:	2
	Instrument:	ESI-TRAP
	Taxonomy:	Homo sapiens (human)
1.1 Pep. Scoring Options:	Peptide Cut Off Score:	20
1.2 Prot. Scoring Options:	Use MudPIT Scoring:	True
	Prot. Relevance Thresh.:	20
	Prot. Relevance Factor:	1
3. Tolerances:	Prec. Mass Tolerance:	20 ppm
	Frag. Mass Tolerance:	0.5 Da
4. Dynamic Modifications:	1. Dynamic Modification:	Oxidation (M)
	2. Dynamic Modification:	Phospho (ST)
	3. Dynamic Modification:	Phospho (Y)
	4. Dynamic Modification:	Label:2H(4) (K)
	5. Dynamic Modification:	Label:13C(6)15N(2) (K)
	6. Dynamic Modification:	Label:13C(6) (R)
	7. Dynamic Modification:	Label:13C(6)15N(4) (R)
	8. Dynamic Modification:	Label:pY6 (Y)
	9. Dynamic Modification:	Label:pY10 (Y)
5. Static Modifications:	1. Static Modification:	Carbamidomethyl (C)
Processing node **3**: Event Detector		
1. General Settings:	Mass Precision:	2 ppm
	S/N Threshold:	1

FIG. S1. (cont.)

Processing node **4**: Precursor Ions Quantifier		
1. Quantification Method:	SILAC 5plex (Lys, Arg, Tyr)	
Quan Channel SM1:	None	
Quan Channel SM2:	Lys4: +4.025 Da; Arg6: +6.020 Da	
Quan Channel SM3:	Lys8: +8.014 Da; Arg10: +10.008 Da	
Quan Channel SM4:	Lys8: +8.014 Da; Arg10: +10.008 Da; Tyr6: +6.020 Da	
Quan Channel SM5:	Lys8: +8.014 Da; Arg10: +10.008 Da; Tyr10: +10.027 Da	
Ratio Calculation:	Minimum Quan Value Threshold:	1
	Replace Min Quan Value with Min Intensity:	True
	Use Single-Peak Quan Channels:	True
	Apply Quan Value Corrections:	True
	Reject All Quan Values If Not All Quan Channels Are Present:	False
	Maximum Allowed Fold Change:	100
	Use Ratios Above Maximum Allowed Fold Change for Quantification:	True
2. Isotope Pattern Ident.:	RT Tolerance of Isotope Pattern Mult.:	0.2 min
	Single-Peak/Missing Channels Allowed:	1

Fig. S1. **Proteome Discoverer peptide/protein identification and quantitation workflow.**
Selected parameters used for each of the following processing nodes: Spectrum Files (0), Spectrum Selector (1), Mascot (2), Event Detector (3), and Precursor Ions Quantifier (4). For each of the three biological replicates (BR1-3), four files, corresponding to technical replicates (2 LC-MS runs per either the PY99 or 4G10 anti-pTyr immuno-precipitate), were combined as a single MudPIT input file using Proteome Discoverer Daemon (version 1.2).