Table S1. MS/MS database search parameters and the threshold scores

Parameters	Value
peaklist software	Spectrum Mill MS proteomics Workbench(Rev B.03.03.084)
Instrument	Agilent ESI ion trap
MH+	600-4000
Merge scans with same precursor m/z	± 15 sec ± 1.4 m/s
Digest	trypsin
Maximum # missed cleavages	2
Fixed Modifications	Carbamidomethylation
Variable Modifications	Oxidized methionine (M); Pyroglutamic acid (N-termQ)
Masses are	Monoisotopic
Precursor mass tolerance	± 2.5 Da
Product mass tolerance	±0.7
Database	Swissprot.human. Swissprot.human.reverse
Species	All
Search mode	Variable modifications
Precursor mass shift range	-18.0 to 177.0 Da
Autovalidate after search	Yes
Group proteins across all directories	Yes
Sort proteins by	Score
Filter by protein score	>11.0
Filter peptides by Score	>6
Filter peptides by %SPI	>60.0
PROTEINS >= 1 Peptide	>= 1 Peptide