SNX18

m/z Submitted	MH^+ Matched	Delta ppm	Start	End	Missed Cleavages	Sequence
728.4316	728.3978	46.5	232	237	0	(R) FSTFVK
784.3748	784.3988	-30.6	7	12	0	(R) ALYDFR
1107.5337	1107.5370	-3.02	315	322	0	(K) HFDWLYAR
1349.7282	1349.7576	-21.8	49	60	0	(R) GLFPASYVQVIR
1381.6365	1381.6971	-43.9	207	220	0	(R) GGSVPPQHHPSGPK
1398.5767	1398.6953	-84.8	313	322	1	(R) YKHFDWLYAR
1473.6985	1473.7081	-6.49	61	77	0	(R) APEPGPAGDGGPGAPAR
2507.3435	2507.3228	8.26	594	613	1	(K) SQMQHFLQQQIIFFQKVTQK

SNX30

m/z Submitted	MH^+ Matched	Delta ppm	Start	End	Missed Cleavages	Sequence
760.3342	760.3876	-70.2	248	253	0	(K) SYISYK
1042.5491	1042.5568	-7.35	378	386	1	(R) VDTFKAFSK
1095.6151	1095.5946	18.8	552	559	0	(R) QQILFYQR
1150.5877	1150.5429	39.0	269	276	0	(K) HFDWLYNR
1223.4630	1223.5691	-86.8	7	16	0	(R) ALYDFHSENK
1312.7345	1312.6579	58.3	182	191	1	(R) NLNRFSCFVR
1312.7345	1312.7008	25.6	254	265	0	(K) LTPTHAASPVYR
1366.6570	1366.6671	-7.37	208	219	0	(K) IAETYSIEMGPR
1366.6570	1366.7729	-84.8	281	292	0	(K) FTVISVPHLPEK
1637.8724	1637.8533	11.6	46	60	0	(R) GETGLFPASYVEIVR

Table S1. MALDI-TOF analysis of SNX18 and SNX30. Immunoprecipitated SNX18 and SNX30 were separated by SDS-PAGE (see Fig. 2A), and the major specific bands were trypsinized and subjected to MALDI-TOF analysis. Obtained peptide masses (Submitted) were compared with masses from a theoretical trypsin digest of the respective protein (Matched) by using MS-Fit (http://prospector.ucsf.edu/).