Table S2. Identification of the retromer interacting protein, TBC1D5								
Candidate (NCBInr accn#)	MALDI-MS data			Supporting tandem MS data				
	Peptide matches^{A}	Sequence coverage %	Mascot PMF Score^{B}	Peptide Ion mass/charge ratio [MH^{+}]		Amino Acid Residues	Sequence	Mascot Individual Ions Score^{B}
				Observed	Expected from Database Record			
1.TBC1D5 (gil15341918)	38/94	44	237/76	2139.068	2139.080	57 - 73	R.KEWEELFVNNNYLATIR.Q	23/45
				2010.976	2010.985	58 - 73	K.EWEELFVNNNYLATIR.Q	105/45
				1800.826	1800.830	170 - 183	R.TFPEMQFFQQENVR.K	89/45
				1272.727	1272.724	323 - 333	R.LEIAPQIYGLR.W	43/45
				1106.593	1106.588	457 - 466	K.VSNSLINFGR.K	78/45
				2101.999	2102.005	499 - 516	R.TSAEAPSHHLQQQQQQR.L	102/45
				1147.583	1147.578	729 - 739	R.GSFSGQAQPLR.T	56/45
2. Vacuolar protein sorting 35 (gil17999541)	54/105	59	338/76	1127.576	1127.555	45 - 54	K.HASNMLGELR.T	70/45
				1243.682	1243.659	227 - 237	R.LSQLEGVNVER.Y	62/45
				1852.006	1851.989	324 - 339	K.LFDIFSQQVATVIQSR.Q	64/45
				1886.841	1886.842	420 - 433	K.HFHPLFEYFDYESR.K	24/45
				1762.871	1762.853	500 - 514	R.SEDPDQQYLILNTAR.K	103/45
				943.467	943.442	516 - 524	K.HFGAGGNQR.I	58/45
				1616.946	1616.930	623 - 637	K.AQLAAITLIIGTFER.M	76/45
				2244.101	2244.092	750 - 768	K.IREDLPNLESSEETEQINK.H	55/45
				1303.675	1303.659	769 - 778	K.HFHNTLEHLR.L	76/45
3. VPS26B (gil30023568)	17/45	38	85/76	923.592	923.564	193 - 199	K.IYFLLVR.I	15/45
				1668.864	1668.841	270 - 282	R.YYLNLVLIDEEER.R	58/45
				1057.599	1057.572	287 - 294	K.QQEVVLWR.K	33/45
				1195.610	1195.588	314 - 324	R.FEGTTSLGEVR.T	65/45
4. VPS26A (gil3342000)	24/71	66	109/76	1313.816	1313.699	94 - 105	K.ELALPGELTQSR.S	58/45

				2688.487	2688.2213	106 - 127	R.SYDFEF(MetOx)QVEKPYESYIGANVR.L	44/45
				2332.388	2332.175	146 - 165	K.EYDLIVHQLATYPDVNNSIK.M	64/45
				923.648	923.564	195 - 201	K.IYFLLVR.I	15/45
				1891.116	1890.956	233 - 249	K.YEI(MetOx)DGAPVKGESIPIR.L	33/45
				1624.965	1624.814	272 - 284	R.YFLNLVLVDEEDR.S	80/45
				1085.702	1085.603	289 - 296	K.QQEIILWR.K	56/45
5. Hrs (gi|9506795)	31/66	39	220/76	1601.908	1601.888	108 - 120	K.ILYLIQAWAHAFR.N	41/45
				2839.483	2839.476	227 - 252	K.AASTTELPPEYLTSPLSQQSQLPPKR.D	93/45
				3663.822	3663.795	292 - 328	K.SEPAPLASSAPPAGSLYSSPVNSSAPLAEDIDPELAR.Y	47/45
				1319.722	1319.699	410 - 421	K.ALQNAVSTFVNR.M	92/45
				3110.649	3110.641	431 - 458	R.SITNDSAVLSLFQSINSTHPQLLELLNR.L	44/45
				1192.647	1192.625	520 - 528	K.KQEYLEVQR.Q	36/45
				1064.553	1064.530	521 - 528	K.QEYLEVQR.Q	31/45
6. signal transducing adaptor molecule (gi|4507249).	n/a	n/a	n/a	2786.561	2786.363	189 - 213	R.QQSTTLSTLYPSTSSLLTNHQHEGR.K	24/45
[A]number of mass matches/total number of masses searched [B]Scores are shown with associated threshold score for p(match)<0.05								