Table S1. Mass spectrometry analysis of GFP-rab native IPs

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. RAB9, member RAS oncogene family (gi|9790227)	7/27	43	154/76	2447.108	2447.122	48 - 68	K.DLEVDGHFVTMQIWDTAGQER.F	119/46
				1479.846	1479.700	157 - 170	K.DSTNVAAAFEEAVR.R	20/46
				1635.922	1635.801	157 - 171	K.DSTNVAAAFEEAVRR.I	26/46
				1662.965	1662.849	179 - 192	R.SEHLIQTDTVNLHR.K	112/46
2. GDP dissociation inhibitor 2 (gi|30582575)	24/50	56	154/76	1402.741	1402.707	56 - 68	R.FKIPGSPPESMGR.G	15/46
				1125.627	1125.590	90 - 98	K.MLLYTEVTR.Y	16/46
				1916.838	1916.826	194 - 208	R.TDDYLDQP(PamC)YETINR.I	63/46
				2141.113	2141.099	222 - 240	K.SPYLYPLYGLGELPQGFAR.L	43/46
				2213.085	2213.065	310 - 328	K.NTNDANS(PamC)QIIIPQNQVNR.K	27/46
				1778.022	1777.999	365 - 379	K.EIRPALELLEPIEQK.F	21/46
				1365.724	1365.694	391 - 402	K.DLGTESQIFISR.T	74/46
3. VPS26A (gi|3342000)	n/a	n/a	n/a	1313.730	1313.699	94 - 105	K.ELALPGELTQSR.S	9/46
				923.569	923.564	195 - 201	K.IYFLLVR.I	2/46
				1624.866	1624.814	272 - 284	R.YFLNLVLVDEEDR.S	10/46
				1085.624	1085.603	289 - 296	K.QQEIILWR.K	10/46
4. GDP dissociation inhibitor 2 (gi|30582575)	25/47	64	175/76	1402.755	1402.707	56 - 68	R.FKIPGSPPESMGR.G	18/46
				1916.861	1916.826	194 - 208	R.TDDYLDQP(PamC)YETINR.I	38/46
				2213.075	2213.065	310 - 328	K.NTNDANS(PamC)QIIIPQNQVNR.K	16/46
				1778.052	1777.999	365 - 379	K.EIRPALELLEPIEQK.F	21/46
				1365.732	1365.694	391 - 402	K.DLGTESQIFISR.T	40/46
5. RAB7, member RAS oncogene family (gi|56269740)	17/35	76	152/76	1647.854	1647.809	56 - 69	R.LVTMQIWDTAGQER.F	83/46
				1187.641	1187.613	70 - 79	R.FQSLGVAFYR.G	62/46

				1934.001	1933.969	98 - 113	K.TLDSWRDEFLIQASPR.D	21/46
				1175.621	1175.598	104 - 113	R.DEFLIQASPR.D	86/46
				1475.777	1475.746	114 - 126	R.DPENFPFVVLGNK.I	52/46
				1589.865	1589.821	158 - 171	K.EAINVEQAFQTIAR.N	110/46
6. vacuolar sorting protein 35 (gi|9622850)	14/39	21	54/76	1762.894	1762.853	500 - 514	R.SEDPDQQYLILNTAR.K	28/46
7. choroideremia (Rab escort protein 1) (gi|9966761)	n/a	n/a	n/a	2474.214	2474.234	466 - 488	K.TDSDQQISILTVPAEEPGTFAVR.V	26/46
8. GDP dissociation inhibitor 2 (gi|30582575)	30/48	65	206/76	1402.726	1402.707	56 - 68	R.FKIPGSPPESMGR.G	46/46
				1312.707	1312.694	69 - 79	R.GRDWNVDLIPK.F	35/46
				1125.608	1125.590	90 - 98	K.MLLYTEVTR.Y	16/46
				1344.671	1344.676	143 - 153	K.FLVYVANFDEK.D	59/46
				1916.834	1916.826	194 - 208	R.TDDYLDQP(PamC)YETINR.I	80/46
				938.501	938.494	211 - 218	K.LYSESLAR.Y	21/46
				2141.113	2140.099	222 - 240	K.SPYLYPLYGLGELPQGFAR.L	107/46
				2213.080	2213.065	310 - 328	K.NTNDANS(PamC)QIIIPQNQVNR.K	47/46
				1778.009	1777.999	365 - 379	K.EIRPALELLEPIEQK.F	30/46
				1365.710	1365.694	391 - 402	K.DLGTESQIFISR.T	104/46
				1606.692	1606.680	424 - 436	R.MTGSEFDFEEMKR.K	59/46
9. Rab5c protein (gi|20988213)	13/47	78	79/76	1351.662	1351.620	72 - 82	K.FEIWDTAGQER.Y	77/46
				1300.644	1300.607	83 - 92	R.YHSLAPMYYR.G	57/46
				2026.037	2026.017	93 - 111	R.GAQAAIVVYDITNTDTFAR.A	142/46
				2678.155	2678.222	143 - 166	R.AVEFQEAQAYADDNSLLFMETSAK.T	76/46
				1552.814	1552.779	167 - 180	K.TAMNVNEIFMAIAK.K	72/46
				1181.584	1181.558	185 - 196	K.NEPQNAAGAPGR.T	68/46
10. GDP dissociation inhibitor 1 (gi|54696630)	17/31	48	123/76	1460.784	1460.713	56 - 68	R.FQLLEGPPESMGR.G	34/46
				1125.622	1125.590	90 - 98	K.MLLYTEVTR.Y	24/46
				1468.727	1468.666	157 - 169	K.TFEGVDPQTTSMR.D	18/46
				1852.885	1852.831	194 - 208	R.TDDYLDQP(PamC)LETVNR.I	81/46
				2213.082	2213.065	310 - 328	K.NTNDANS(PamC)QIIIPQNQVNR.K	18/46
				1361.633	1361.5791	424 - 435	R.MAGTAFDFENMK.R	66/46

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			
11. VPS26A (gil3342000)	6/20	21	59/77	nd[C]	nd	nd	nd	nd
12. RAB7, member RAS oncogene family (gil56269740)	6/16	33	72/76	1187.559	1187.613	70 - 79	R.FQSLGVAFYR.G	48/46
				1933.855	1933.969	98 - 113	K.TLDSWRDEFLIQASPR.D	21/46
				1175.550	1175.598	104 - 113	R.DEFLIQASPR.D	36/46
				1589.739	1589.821	158 - 171	K.EAINVEQAFQTIAR.N	82/46
				1632.753	1632.842	56 - 69	R.LVTMQIWDTAG[**L**]ER.F	bi[D]
13. RAB7, member RAS oncogene family (gil56269740)	12/30	63	128/76	1647.732	1647.809	56 - 69	R.LVTMQIWDTAG[**Q**]ER.F	55/46
				1663.716	1663.804	56 - 69	R.LVT(MetOx)QIWDTAG[**Q**]ER.F	17/46
				1187.554	1187.613	70 - 79	R.FQSLGVAFYR.G	68/46
				1933.883	1933.969	98 - 113	K.TLDSWRDEFLIQASPR.D	26/46
				1175.544	1175.598	104 - 113	R.DEFLIQASPR.D	38/46
				1589.742	1589.821	158 - 171	K.EAINVEQAFQTIAR.N	99/46
14. GDP dissociation inhibitor 1 (gil54696630)	22/30	48	256/76	1027.554	1027.539	104 - 112	K.VVEGSFVYK.G	19/46
				1654.747	1654.804	143 - 156	K.FLVFVANFDENDPK.T	64/46
				1852.784	1852.831	194 - 208	R.TDDYLDQP(PamC)LETVNR.I	48/46
				2141.095	2141.099	222 - 240	K.SPYLYPLYGLGELPQGFAR.L	27/46
				1722.842	1722.909	366 - 380	K.EVEPALELLEPIDQK.F	39/46
15. vacuolar sorting protein 35 (gil9622850)	9/19	14	73/76	nd[C]	nd	nd	nd	nd
16. vacuolar sorting protein 35 (gil9622850)	11/22	15	89/76	nd[C]	nd	nd	nd	nd