

SUPPLEMENTAL TABLE S5. Proteins involved in protein sorting, vesicular transport and membrane fusion. Bold characters: higher sequence similarity to mammalian proteins.

<i>A. niger</i>	<i>S. cerevisiae</i>	% Identity (E-value)	<i>H. sapiens</i>	% Identity (E-value)	Description	NSAF 10 ⁴	
						Sorbitol	Xylose
An14g00900	Mcd4	60 (0.0)	PIGN	57 (0.0)	GPI anchor assembly	4.1	2.1
An05g02300	(Gpi12)	46 (2e-17)	(PIGL)	45 (6e-24)	GPI anchor assembly	2.2	14
An17g00780	(Pbn1)	44 (3e-11)	no hits	no hits	GPI Man-transferase subunit	1.8	2.3
An10g00480	(Gpi11)	38 (0.002)	no hits	no hits	Man-EthNH P-transferase	2.5	2.4
An01g13530	Gpi8	82 (4e-116)	PIGK	75 (1e-95)	GPI-transamidase complex	2.3	0.7
An07g09270	(Gpi17)	43 (3e-34)	(PIGS)	42 (9e-32)	GPI-transamidase complex	1.1	1.4
An11g06770	Gpi16	59 (9e-114)	PIGT	46 (3e-77)	GPI-transamidase complex	2	1.7
An18g05180	(Per1)	50 (2e-42)	(PGAP3)	51 (2e-33)	Assists GPI-phospholipase	1.7	2.7
An16g03370	Cwh43	60 (0.0)	CWH43	46 (5e-84)	Addition of ceramides to GPI	9.6	8.4
An04g02500	Nmt1	67 (2e-121)	NMT2	64 (8e-109)	N-myristoyl transferase	2.4	2.4
An05g00200	(Akr1)	49 (1e-93)	(ZDHHC17)	46 (1e-52)	Palmitoyl transferase	4.8	7.5
An03g03570	(Tor2)	52 (0.017)	no hits	no hits	C-methylation of prenylCys.	0.3	2.6
An02g08450	Sec18	71 (0.0)	NSF	69 (0.0)	NsfA for release of Sec17	3.4	4.3
An02g01580	Sec17	60 (4e-44)	NAPB	62 (4e-43)	SNAP for NSF binding	6.6	15.6
An12g04710	Vtc4	65 (0.0)	(XPR1)	47 (2e-08)	VTC subunit	7.9	6.8
An07g09800	Vtc3	52 (5e-133)	(XPR1)	42 (3e-05)	VTC subunit	10.3	9.2
An09g04170	Sly1	57 (1e-126)	SCFD1	55 (6e-119)	SM protein, binds Sed5	1.3	2.2
An02g12980	Sed5	54 (3e-49)	STX5	53 (2e-47)	Qa.II type SNARE	2.7	0.8
An08g01410	Sft2	60 (3e-37)	SFT2D3	53 (9e-05)	Qa type SNARE (putative)	4.2	2.1
An04g07020	Tlg2	52 (4e-34)	STX16	51 (63-33)	Qa.III.a type SNARE	3.1	3.6
An04g01530	(Pep12)	49 (2e-20)	(STX12)	54 (2e-20)	Qa.III.b type SNARE	14.8	16.8
An12g01190	(Sso2)	50 (5e-20)	(STX2)	51 (3e-10)	Qa.IV type SNARE	2.1	7.9
An07g02170	(Bos1)	47 (2e-14)	(GOSR2)	59 (2e-10)	Qb.II type SNARE	4.8	5.5
An04g05980	Vti1	59 (2e-26)	VTI1A	56 (5e-26)	Qb.III.b type SNARE	18	19.7
An08g02460	Gos1	58 (1e-33)	GOSR1	51 (1e-24)	Qb.II type SNARE	4	2
An12g07570	Snc2	72 (3E-28)	VAMP4	68 (5e-11)	R.IV type SNARE	6.7	7.3
An08g07470	(Nyv1)	60 (1e-11)	(VAMP7)	50 (2e-20)	R.III type SNARE	2.4	6.4
An04g08480	Ykt6	72 (9e-60)	YKT6	66 (2e-45)	R.II tye SNARE	8.6	9.7
An12g00800	Tcb1	50 (8e-157)	no hits	no hits	Tricalbin	6.9	9.3
An03g04940	(Erv41)	47 (4e-36)	(PTX1)	44 (4e-33)	Erv41/46 complex	7.5	11.1
An01g04320	Erv46	56 (5e-79)	ERGIC3	56 (3e-76)	Erv41/46 complex	12.5	14.9
An15g01680	(Yif1)	47 (1e-30)	(YIF1A)	54 (2e-34)	COPII/Golgi fusion	1.8	2.8
An01g04730	Sec23	69 (0.0)	SEC23A	71 (0.0)	Activator of GTPase	9	4.1
An08g10650	Sec24	60 (0.0)	SEC24B	59 (1e-150)	Sec23/24 complex	6.4	6.6
225665	Sed4	37 (0.062)	no hits	no hits	Regulator of SarA	8.6	8
An02g01690	Sec31	46 (9e-152)	SEC31A	51 (1e-116)	COPII coat	0.7	1.5
An08g03960	Erv29	67 (5e-55)	SURF4	61 (3e-44)	vesicle transport	9.7	12.4
An04g08830	(Emp47)	52 (1e-17)	(LMAN1L)	40 (2e-09)	vesicle transport	17.9	19.8
An01g08870	Erv25	69 (2e-53)	TMED10	59 (1e-28)	Erv25 p24 family	16.7	22.7
An04g01780	Erp1	60 (1e-44)	TMED9	56 (1e-33)	Erp1 p24 family	10.7	13.6
An09g05490	Erp3	52 (7e-26)	TMED2	50 (4e-21)	p24 family	6	12.5
An08g03590	Emp24	62 (6e-47)	TMED2	55 (4e-29)	Erv25/Erp1/Emp24	12.2	17.3
An07g07830	(Ted1)	42 (1e-50)	no hits	no hits	Cargo exit from ER	0.7	1.1
An16g03320	Sfb3	48 (7e-111)	SEC24C	53 (3e-130)	Sorting of PmaA	2.2	1.5
An07g07340	Erd2	55 (2e-28)	KDEL3	59 (4e-31)	(K/H)DEL binding	2.7	4
An04g00670	(Get1)	46 (3e-05)	(WRB)	51 (4e-08)	GET subunit	6	4.1
An02g07090	Get3	70 (1e-93)	ASNA1	72 (1e-95)	GET subunit	3.4	3.4
An02g04250	(Uip5)	43 (5e-11)	LMAN2L	56 (1e-40)	ER export receptor	18.1	19.2
An02g02830	Rer1	70 (1e-50)	RER1	79 (1e-57)	Retrieves ER membrane proteins	18.6	13.8
An07g06080	Hrr25	87 (2e-134)	CSNK1E	78 (3e-143)	Ser/Thr kinase	3.2	3.7
An01g02500	Trx1	34 (1e-23)	TXN	57 (1e-17)	Thioredoxin	22.9	9.2
An16g02460	Cop1	69 (0.0)	COPA	67 (0.0)	COPI α subunit	9.8	6.1

An08g03270	Sec26	69 (0.0)	COPB1	69 (0.0)	COPI β subunit	6.9	4.3
An02g05870	Sec27	72 (0.0)	COPB2	75 (0.0)	COPI β' subunit	4	5.7
An07g06030	Sec21	63 (0.0)	COPG2	61 (0.0)	COPI γ subunit protein	9.2	3.1
An01g14250	Ret2	56 (5e-78)	ARCN1	57 (1e-96)	COPI δ subunit	2.8	2.3
An08g06330	(Sec28)	43 (3e-05)	(COPE)	51 (2e-28)	COPI ϵ subunit	3.6	4.7
An01g04040	Sar1	82 (1e-76)	SAR1A	75 (1e-66)	ARF GTPase SarA	39.2	26.2
An08g03690	Arf2	89 (3e-81)	ARF1	90 (2e-84)	ARF GTPase	5	7.4
An08g04480	Sey1	53 (5e-127)	no hits	no hits	Dynamamin GTPase	20.2	19.9
An03g06950	Dnm1	69 (0.0)	DNM1	61 (0.0)	Dynamamin GTPase	10.3	6.9
An02g10450	Vps1	77 (0.0)	DNM1L	64 (3e-167)	Dynamamin GTPase	9.5	13.6
An11g00010	(Vps1)	44 (2e-19)	(MX2)	48 (3e-29)	Dynamamin GTPase	6.3	4.6
An14g00010	Sec4	81 (7e-65)	RAB8A	79 (6e-72)	Rab8 GTPase SrgA	0.6	6.6
An01g06060	Ypt31	85 (7e-74)	RAB11A	84 (1e-89)	Rab11 GTPase	21.6	24.4
An09g06790	Ypt1	82 (1e-82)	RAB1A	87 (2e-92)	Rab1 GTPase SrgB	24	21.1
An15g05740	Ypt6	75 (7e-66)	RAB6A	85 (2e-87)	Rab6 GTPase SrgC	20.5	15.1
An04g02470	Vps21	69 (2e-58)	RAB5C	73 (6e-67)	Rab5 GTPase	0.6	7
An02g06400	Vps21	62 (8e-67)	RAB5B	59 (1e-53)	Rab5 GTPase	2.5	5.9
An06g02180	no hits	no hits	(C8orf80)	48 (0.001)	Ras GTPase	1.1	0.6
An01g02320	Ras2	82 (2e-65)	KRAS	81 (6e-59)	Ras GTPase RasA	5.5	12.3
An18g05980	Rho1	90 (6e-85)	RHOA	81 (8e-79)	Ras GTPase RhoA	33	61.2
An18g02490	(Gea2)	49 (1e-149)	GBF1	54 (5e-74)	GEF for ARFs	2.3	0.4
An07g02190	Sec7	57 (0.0)	ARGEF2	52 (0.0)	GEF HypB for ARFs	0.2	0.6
An18g06440	Yip3	73 (4e-43)	RABAC1	54 (6e-13)	Interacts with Rab GTPases	12.8	16.2
An04g09250	Mvp1	54 (2e-58)	SNX8	49 (3e-29)	PtdIns-3-P binding protein	2.6	7.6
An03g06880	Pep1	51 (7e-175)	no hits	no hits	Sorting receptor vacuolar hydrolases	2.6	7.9
An18g03490	(Mr11)	53 (2e-18)	(M6PR)	42 (3e-09)	Sorting receptor vacuolar hydrolases	2	2.5
An18g03980	Vps70	49 (3e-104)	FOLH1	52 (1e-95)	Vacuolar protein sorting	1.5	1.8
An14g05020	Vac8	79 (0.0)	no hits	no hits	Cytoplasm to vacuole targeting	3.4	2.3
An16g04270	Vps35	76 (5e-90)	VPS35	59 (3e-92)	Retromer coat	11.3	9.5
An01g07320	Pep8	55 (1e-76)	VPS26B	75 (4e-109)	Retromer coat	9.2	4.4
An08g01030	Vps29	61 (4e-31)	VPS29	64 (2e-46)	Retromer coat	10	5.1
An01g08400	Vps5	51 (1e-65)	SNX1	54 (2e-58)	Retromer coat	2.5	0.5
An12g04500	Drs2	71 (0.0)	ATP8A1	66 (0.0)	Flippase	0.1	0.7
An15g01510	Neo1	67 (2e-96)	OSBPL9	45 (1e-36)	Flippase	0.5	1.7
An02g07570	Kes1	72 (0.0)	ATP9B	66 (0.0)	Oxysterol binding protein	4.1	2
An04g02070	Chc1	73 (0.0)	CLTC	75 (0.0)	Clathrin heavy chain	31.4	15
An16g02490	Apl2	58 (1e-146)	AP2B1	69 (0.0)	β -Adaptin: AP-1 complex	2.6	0.8
An01g02600	Apl4	54 (4e-113)	AP1G1	63 (0.0)	γ -Adaptin: AP-1 complex	2.6	1.4
An07g03200	Apm1	72 (6e-154)	AP1M1	83 (5e-176)	μ -Like subunit: AP-1 complex	2.8	1.5
An07g08220	Ent3	75 (4e-61)	CLINT1	68 (8E-41)	Epsin-like domain protein	2.2	0.5
An02g08820	(Bud7)	46 (5e-69)	no hits	no hits	Golgi cargo export	5.7	1.7
An02g03120	Gdi1	75 (2e-154)	GDI1	70 (8e-132)	GDP dissociation inhibitor	1.4	3.7
An01g08590	(Tvp38)	57 (1e-29)	(TMEM64)	45 (8e-08)	Asymmetric localization of Kar9	2.7	3.4
An17g01420	Yop1	56 (7e-27)	REEP5	55 (2e-21)	ER tubular morphology	56.2	40
An08g08600	No Hits	no hits	no hits	no hits	Reticulon-like protein	11.6	9.7
An08g01610	Ola1	80 (6e-154)	OLA1	67 (6e-108)	P-loop ATPase	14.2	8
An02g05210	no hits	no hits	(ANXA7)	50 (1e-48)	Annexin AnxC3.1	1.4	1.4
An01g12810	(Yet3)	52 (4e-19)	no hits	no hits	Invertase secretion in yeast	34.6	20.7
An01g13390	(Atg27)	46 (0.087)	no hits	no hits	Autophagy	0.3	3.1
An09g06580	(Bre5)	45 (1e-08)	(G3BP1)	42 (3e-23)	Ras-GTPase-activating protein	3.6	2.2
An14g00900	Mcd4	60 (0.0)	PIGN	57 (0.0)	GPI anchor assembly	4.1	2.1
An05g02300	(Gpi12)	46 (2e-17)	(PIGL)	45 (6e-24)	GPI anchor assembly	2.2	14
An17g00780	(Pbn1)	44 (3e-11)	no hits	no hits	GPI Man-transferase subunit	1.8	2.3
An10g00480	(Gpi11)	38 (0.002)	no hits	no hits	Man-EthNH P-transferase	2.5	2.4