SUPPLEMENTAL TABLE S4. Proteins involved in quality control and glycosylation.

Bold characters: higher sequence similarity to mammalian proteins.

A. niger	***S. cerevisiae***	**% Identity (E-value)**	***H. sapiens***	**% Identity (E-value)**	**Description**	**NSAF.10^4**	
						Sorbitol	**Xylose**
An05g00140	(Srp102)	46 (7e-12)	(SRPB)	41 (2e-04)	SRP receptor β subunit	25.6	11.6
An01g03820	Sbh2	68 (7e-22)	SEC61B	60 (6e-10)	Translocation to the ER (GEF)	25.6	7.8
An03g04340	**Sec61**	**79 (0.0)**	**SEC61A1**	**82 (0.0)**	**Targeting to ER**	**22.1**	**12.3**
An01g13070	Sec63	46 (5e-53)	SEC63	45 (5e-38)	Targeting and import to the ER	16.9	14.8
An02g01510	Sec62	55 (8e-31)	SEC62	48 (5e-18)	Targeting and import to the ER	14.3	9.1
An16g08830	(Sec66)	50 (2e-16)	no hits	no hits	Targeting and import to the ER	19.8	16.4
An17g00090	(Sec72)	41 (1e-05)	(LONRF3)	44 (4e-04)	Targeting and import to the ER	4.7	7.9
An16g07390	(Spc2)	47 (2e-11)	(SPC2)	43 (0.065)	Signal peptidase protein	11.8	9.1
An02g14800	Pdi1	56 (4e-90)	PDIA3	54 (2e-75)	Protein disulfide isomerase PdiA	75.6	59
An18g02020	**(Pdi1)**	**60 (2e-18)**	**(PDIA6)**	**53 (7e-40)**	**Protein disulfide isomerase TigA**	**33**	**25.9**
An01g04600	(Mpd1)	54 (5e-33)	(PDIA6)	58 (7e-24)	Protein disulfide isomerase PrpA	26.6	26.2
An02g05890	**(Mpd1)**	**58 (3e-14)**	**(TXNDC5)**	**45 (5e-29)**	**Protein disulfide isomerase**	**17.6**	**28.5**
An16g07620	(Ero1)	49 (2e-74)	(ERO1LB)	50 (1e-59)	Thiol-oxidase EroA	5	5.6
An04g02020	**Cpr1**	**79 (1e-59)**	**PPIB**	**79 (2e-67)**	**PPIase cyclophilin CypB**	**37.4**	**41.3**
An01g06670	**Fpr2**	**64 (4e-28)**	**FKBP2**	**60 (9e-29)**	**PPIase FK506 binding protein**	**4.8**	**4.7**
An11g04180	Kar2	84 (0.0)	HSPA5	83 (0.0)	DnaK chaperone ATPase BipA	71.8	52.7
An01g08420	**Cne1**	**48 (2e-56)**	**CANX**	**66 (3e-116)**	**Glycoprotein chaperone ClxA**	**42.4**	**46.4**
An12g10590	(Ecm10)	50 (0.030)	(HSPA5)	52 (0.39)	Unknown ER DnaK protein	2.4	2.4
An05g00880	Scj1	55 (2e-69)	DNAJA4	53 (8e-57)	ER DnaJ co-chaperone	9.1	7.6
An12g00580	(Scj1)	58 (3e-07)	(DNAJB5)	57 (3e-07)	ER DnaJ co-chaperone	6.8	3.2
An18g06470	(Erj5)	46 (5e-15)	(DNAJC1)	41 (1e-10)	DnaJ-domain protein	6.2	2.5
An01g13220	**(Lhs1)**	**52 (2e-50)**	**(HYOU1)**	**48 (2e-80)**	**Nucleotide exchange factor LhsA**	**20.2**	**22.1**
An04g07440	Shr3	49 (1e-17)	no hits	no hits	ER packaging chaperone	26.4	15.5
54765	**no hits**	**no hits**	**TTC35**	**55 (5e-19)**	**TTC35 protein**	**6.5**	**5.7**
An08g10400	**no hits**	**no hits**	**SLC35A3**	**59 (1e-45)**	**UDP-GlcNAc/UDP-Gal transporter**	**1**	**2.4**
An17g02140	Vrg4	74 (1e-102)	(SLC35D2)	44 (9e-11)	GDP-Mannose transporter	9.9	11.6
An14g03820	Gal10	72 (2e-122)	GALE	64 (6e-99)	UDP-Glc 4-epimerase	9.5	9.5
An08g04450	Gda1	67 (2e-126)	ENTPD6	47 (4e-45)	Guanosine-diphosphatase	9	13.3
An18g06820	Gfa1	78 (0.0)	GFPT2	72 (0.0)	Gln-Fru-6-P amidotransferase	12.9	7.4
An04g04990	Psa1	84 (7e-156)	GMPPB	79 (2e-130)	Mannose-1-P guanyltransferase	3.2	1.7
An18g05170	**Pcm1**	**57 (5e-39)**	**PGM3**	**63 (9e-53)**	**Phosphoglucomutase**	**3.1**	**2.8**
An12g00820	Ugp1	79 (0.0)	UGP2	70 (1e-147)	UGPase	23.2	26.5
An02g02980	Die2	42 (2e-36)	ALG10B	44 (6e-29)	α-1,2-Glucosyltransferase	3.9	2.1
An04g03130	**no hits**	**no hits**	**MPDU1**	**54 (1e-33)**	**Man-P-Dol utilization protein**	**2.2**	**4.5**
An16g04330	**Dpm1**	**50 (2e-24)**	**DPM1**	**80 (7e-92)**	**Dol-P β-D-mannosyltransferase**	**26**	**23.9**
An08g07020	**Alg9**	**50 (1e-83)**	**ALG9**	**52 (1e-89)**	**α-1,2-Mannosyltransferase**	**3.7**	**2.8**
An18g05910	**Alg11**	**56 (8e-68)**	**ALG11**	**59 (2e-94)**	**α-1,2-Mannosyltransferase**	**1.2**	**1.8**
An04g08820	Alg8	61 (2e-114)	ALG8	58 (7e-102)	α-1,3-Glucosyltransferase	0.7	1.7
An02g14560	**(Ost1)**	**48 (2e-45)**	**(RPN1)**	**47 (0.0)**	**OT α subunit OstA**	**41.1**	**35.7**
An07g04190	**(Wbp1)**	**49 (4e-47)**	**(DDOST)**	**52 (2e-50)**	**OT β subunit**	**42.3**	**38**
An02g14930	**(Ost3)**	**42 (4e-19)**	**(TUSC3)**	**46 (4e-21)**	**OT γ subunit**	**8.2**	**15.3**
An04g03495	**(Swp1)**	**47 (2e-11)**	**RPN2**	**52 (9e-14)**	**OT δ subunit**	**16.8**	**21.7**
An16g08570	Stt3	78 (0.0)	STT3B	71 (0.0)	OT catalytic subunit	11.4	15.7
An15g01420	Cwh41	55 (9e-146)	MOGS	46 (5e-107)	Processing α-glucosidase I	13.8	21
An09g05880	**Rot2**	**56 (0.0)**	**GANAB**	**56 (0.0)**	**Glucosidase II α subunit**	**27.6**	**28.9**
An13g00620	(Gtb1)	43 (7e-17)	(PRKCSH)	43 (2e-15)	Glucosidase II β subunit	16.7	12.9
An07g06430	**(Kre5)**	**40 (3e-26)**	**UGGT1**	**51 (0.0)**	**UDP-Glc glucosyltransferase**	**9.1**	**10**
An06g01510	(Ylr057w)	42 (4e-42)	MAN1B1	55 (1e-26)	α-1,2-Mannosidase	5.5	10.3
An18g06220	Mns1	59 (2e-119)	MAN1B1	60 (2e-103)	α-1,2-Mannosidase	2.9	3.4
An07g10350	Pmt2	67 (0.0)	(POMT2)	53 (2e-128)	O-Mannosyltransferase PmtA	9.3	12.5
An11g09890	Pmt1	60 (0.0)	(POMT2)	54 (1e-119)	O-Mannosyltransferase	7.6	4.9
An16g08490	Pmt4	64 (0.0)	(POMT1)	52 (3e-99)	O-Mannosyltransferase	4.9	6

An03g01090	(Hoc1)	42 (1e-15)	no hits	no hits	α-1,6-Mannosyltransferase	2.2	3.3
An05g02320	(Hoc1)	44 (9e-12)	no hits	no hits	α-1,6-Mannosyltransferase	1.6	5.6
An07g04940	Hoc1	55 (2e-64)	no hits	no hits	α-1,6-Mannosyltransferase	1.1	2.7
An12g07020	(Hoc1)	48 (3e-23)	no hits	no hits	α-1,6-Mannosyltransferase	2.2	4.9
An03g05010	Mnn9	64 (3e-98)	no hits	no hits	MTC complex subunit	4.3	4.8
An04g01260	Anp1	65 (2e-82)	no hits	no hits	MTC complex subunit	15.5	21.7
An15g06230	Anp1	69 (2e-136)	no hits	no hits	MTC complex subunit	3.4	4.2
An03g02990	(Gnt1)	58 (1e-17)	no hits	no hits	GlcNAc-transferase	1	2.4
An11g10260	Gnt1	60 (4e-25)	(GYG1)	46 (0.072)	GlcNAc-transferase	2.6	4.4
An18g02170	Ktr5	57 (8e-104)	no hits	no hits	α-1,2-Mannosyltransferase	8	16.4
An02g09940	Ktr1	64 (3e-85)	no hits	no hits	α-1,2-Mannosyltransferase	12.1	13.4
An14g03910	Ktr1	70 (2e-124)	no hits	no hits	α-1,2-Mannosyltransferase	11	11.7
An02g11720	Ams1	63 (0.0)	MAN2C1	60 (0.0)	α-Mannosidase Msd2/MsdB	1.1	1.2