Figure S1.

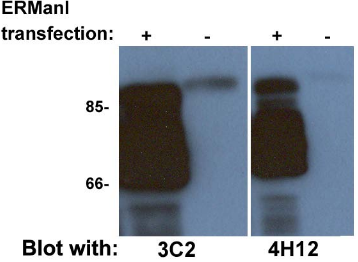


Figure S2.

Recovered peptide list of alpha 1,2-mannosidase (gi:770647) from 90kDa band

sequence	repeat number
ADSYYEYLLK	60
DKMESFFLGETLK	23
DVDVNLFESTIR	28
DVEVKPADR	1
FAWGHDELKPVSR	9
FQEAVEK	1
GPPHLQIRPPSQDLK	12
GVIDVFLHAWK	4
IPYSDVNIGTGVAHPPR	38
KFAWGHDELKPVSR	1
LTFVGELAHGR	37
LTGDKKFQEAVEK	1
MESFFLGETLK	4
MRPEIAGLKPANPPVLPAPQK	18
PANPPVLPAPQK	1
QETQLLEDYVEAIEGVR	1
QMETGLSPEIVHFNLYPQPGR	3
VPSGGYSSINNVQDPQKPEPR	18
VTQHIHGLSGK	10

MAACEGRRSGALGSSQSDFLTPPVGGAPWAVATTVVMYPPPPPPPHRDFISVTLSFGESYDNSKSWRRRSCWRKWK
QLSRLQRNMILFLLAFLLFCGLLFYINLADHWKALAFRLEEEQK**MRPEIAGLKPANPPVLPAPQK**ADTDPENLPEISSQK
TQRHIQR**GPPHLQIRPPSQDLK**DGTQEEATKRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTELPSRRAEVPTKPPLP
PARTQGTPVHLNYRQK**GVIDVFLHAWK**GYR**KFAWGHDELKPVSR**SFSEWFGLGLTLIDALDTMWILGLRKEFEEARK
WVSKKLHFEK**DVDVNLFESTIR**ILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFR**TPSKIPYSDVNIGTGVAHPPR**WTS
DSTVAEVTSIQLEFRELSR**LTGDKKFQEAVEKVTQHIHGLSGK**KDGLVPMFINTHSGLFTHLGVFTLGAR**ADSYYEYLLK**
QWIQGGK**QETQLLEDYVEAIEGVR**THLLRHSEPSK**LTFVGELAHGR**FSAKMDHLVCFLPGTLALGVYHGLPASHMELA
QELMETCYQMNR**QMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLLRPETVESLFYLYR**VTGDRKYQDWGWEILQ
SFSRFTR**VPSGGYSSINNVQDPQKPEPRDKMESFFLGETLK**YLFLLFSDDPNLLSLDAYVFNTEAHPLPIWTP

(A total 30.41 % of sequence was recovered)

Recovered peptide list of alpha 1,2-mannosidase (gi:770647) from 70kDa band

sequence	repeat number
DVDVNLFESTIR	2
IPYSDVNIGTGVAHPPR	2
LTFVGELAHGR	1
QMETGLSPEIVHFNLYPQPGR	1

MAACEGRRSGALGSSQSDFLTPPVGGAPWAVATTVVMYPPPPPPPHRDFISVTLSFGESYDNSKSWRRRSCWRKWK
QLSRLQRNMILFLLAFLLFCGLLFYINLADHWKALAFRLEEEQKMRPEIAGLKPANPPVLPAPQKADTDPENLPEISSQKT
QRHIQRGPPHLQIRPPSQDLKDGTQEEATKRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTELPSRRAEVPTKPPLPP
ARTQGTPVHLNYRQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWILGLRKEFEEARKW
VSKKLHFEK**DVDVNLFESTIR**ILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSK**IPYSDVNIGTGVAHPPR**WTSDS
TVAEVTSIQLEFRELSRLTGDKKFQEAVEKVTQHIHGLSGKKDGLVPMFINTHSGLFTHLGVFTLGARADSYYEYLLKQWI
QGGKQETQLLEDYVEAIEGVRTHLLRHSEPSK**LTFVGELAHGR**FSAKMDHLVCFLPGTLALGVYHGLPASHMELAQEL
METCYQMNR**QMETGLSPEIVHFNLYPQPGR**RDVEVKPADRHNLLRPETVESLFYLYRVTGDRKYQDWGWEILQSFSR
FTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLDAYVFNTEAHPLPIWTP

(A total 8.50 % of sequence was recovered)

Figure S3.

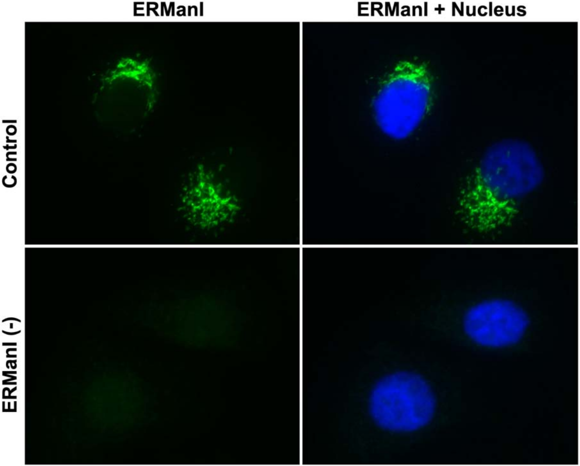
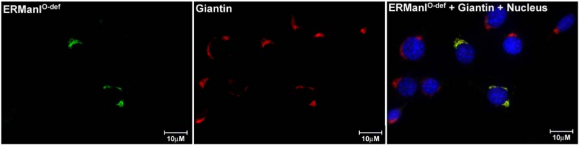
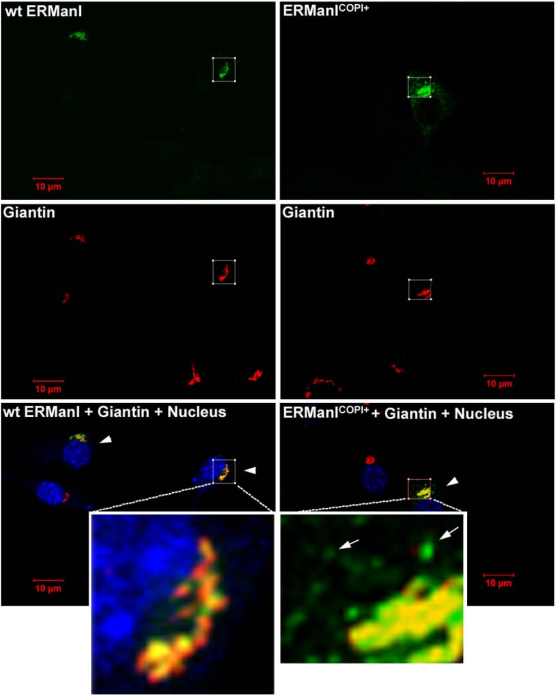


Figure S4



ERManI$^{O\text{-}def}$
10μM
Giantin
10μM
ERManI$^{O\text{-}def}$ + Giantin + Nucleus
10μM

Figure S5


wt ERManI
ERManI^{COPI+}
Giantin
Giantin
wt ERManI + Giantin + Nucleus
ERManI^{COPI+} + Giantin + Nucleus
10 µm
10 µm
10 µm
10 µm
10 µm
10 µm