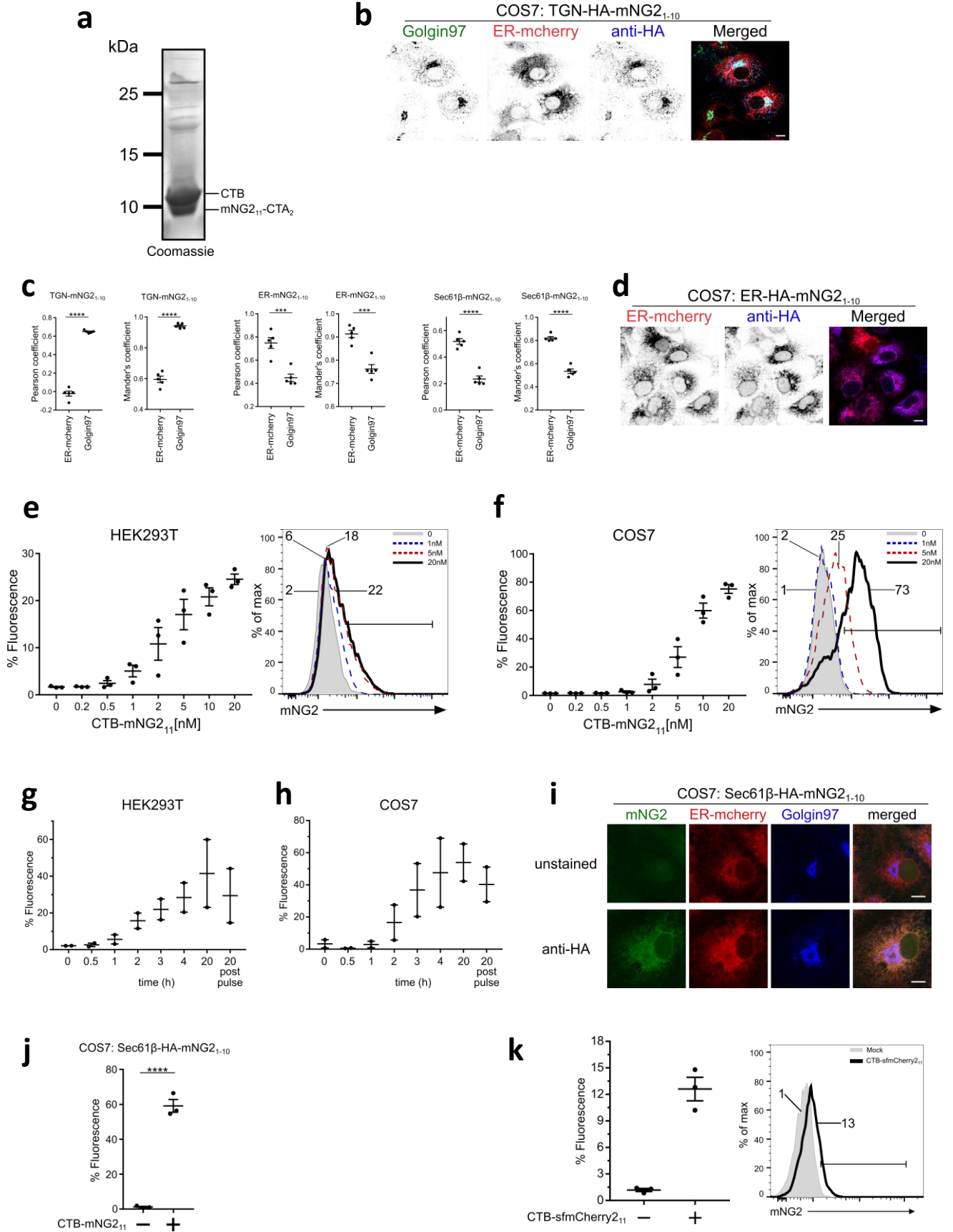


Supplemental Materials

Molecular Biology of the Cell

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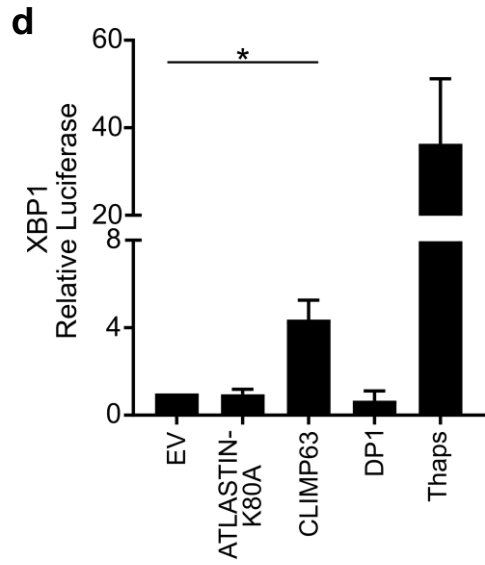
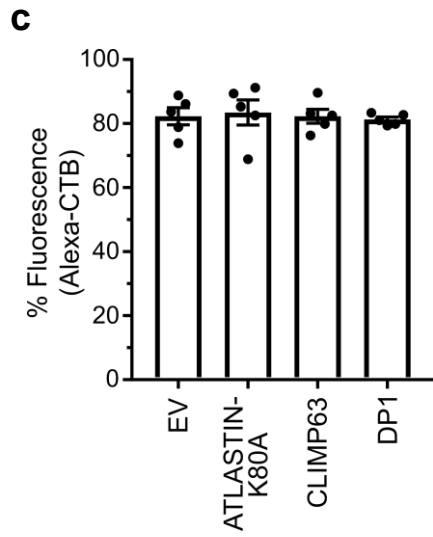
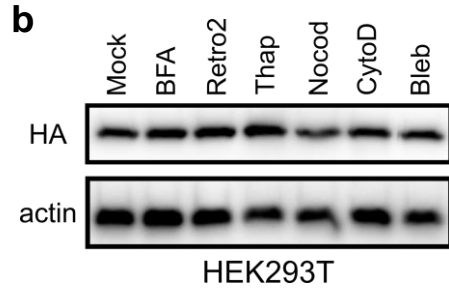
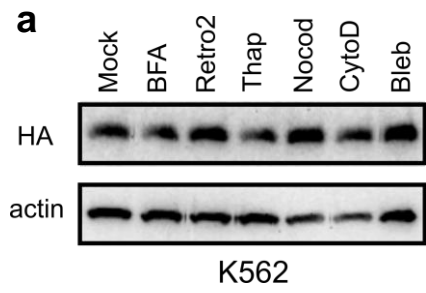
Supplementary Figure 1



Supplementary Figure 1.

Retrograde trafficking of CTB-mNG2₁₁ from the plasma membrane to the ER. **a** Coomassie stained gel of recombinant purified CTB-mNG2₁₁. **b** Confocal microscopy of HA-tagged split neon green 2 (HA-mNG2₁₋₁₀) to trans-Golgi (TGN-HA-mNG2₁₋₁₀) in COS7. TGN is marked by immunocytochemistry of Golgin97 and ER is marked by expression of luminal ER-mCherry. Anti-HA detects the split HA-mNG2₁₋₁₀ constructs. **c** Pearson's and Mander's coefficient calculations for TGN-HA-mNG2₁₋₁₀, ER-HA-mNG2₁₋₁₀ and Sec61 β -HA-mNG2₁₋₁₀ with ER-mcherry and Golgin97. n=5 individual images. **d** Confocal performed as in **b** but with ER-HA-mNG2₁₋₁₀. **e, f** Retrograde trafficking in HEK293T and COS7 cells expressing ER-HA-mNG2₁₋₁₀. Cells were treated with indicated concentrations of CTB-mNG2₁₁ for 4 hours at 37°C. Representative flow cytometry graph is displayed highlighting CTB-mNG2₁₁ concentrations at 0, 1nM, 5nM and 20nM. n=3 independent experiments each performed with 3 biologic replicates and mean marked as one point for each dose. **g, h** Flow cytometry time course of retrograde trafficking into the ER in HEK293T and COS7 cells with CTB-mNG2₁₁, respectively. Cells were treated with 10nM CTB-mNG2₁₁ continuously at 0, 0.5, 1, 2, 4, 20-hour and a condition where cells were treated with a 2-hour toxin pulse and chase for a total of 20 hours. n=2 independent experiments with 3 biological replicates per experiment. CT-1XmNG2₁₁ CT-2X mNG2₁₁ CT-5XmNG2₁₁. **i** Confocal images as in **b** but with Sec61 β -HA-mNG2₁₋₁₀. **j** PM-ER retrograde trafficking in COS7 cells stably expressing Sec61 β -HA-mNG2₁₋₁₀ incubated for 5 hours with 20nM CTB-mNG2₁₁. n=3 independent experiments. **k** Retrograde trafficking of CTB-sfmCherry2₁₁ in K562 cells stably expressing trans-Golgi localized sfmCherry2₁₋₁₀. Cells were incubated with 20nM CTB-sfmCherry2₁₁ for 5 hours at 37°C. n=3 independent experiments. Error bars indicate \pm SEM. Scale bars are 10 μ m.

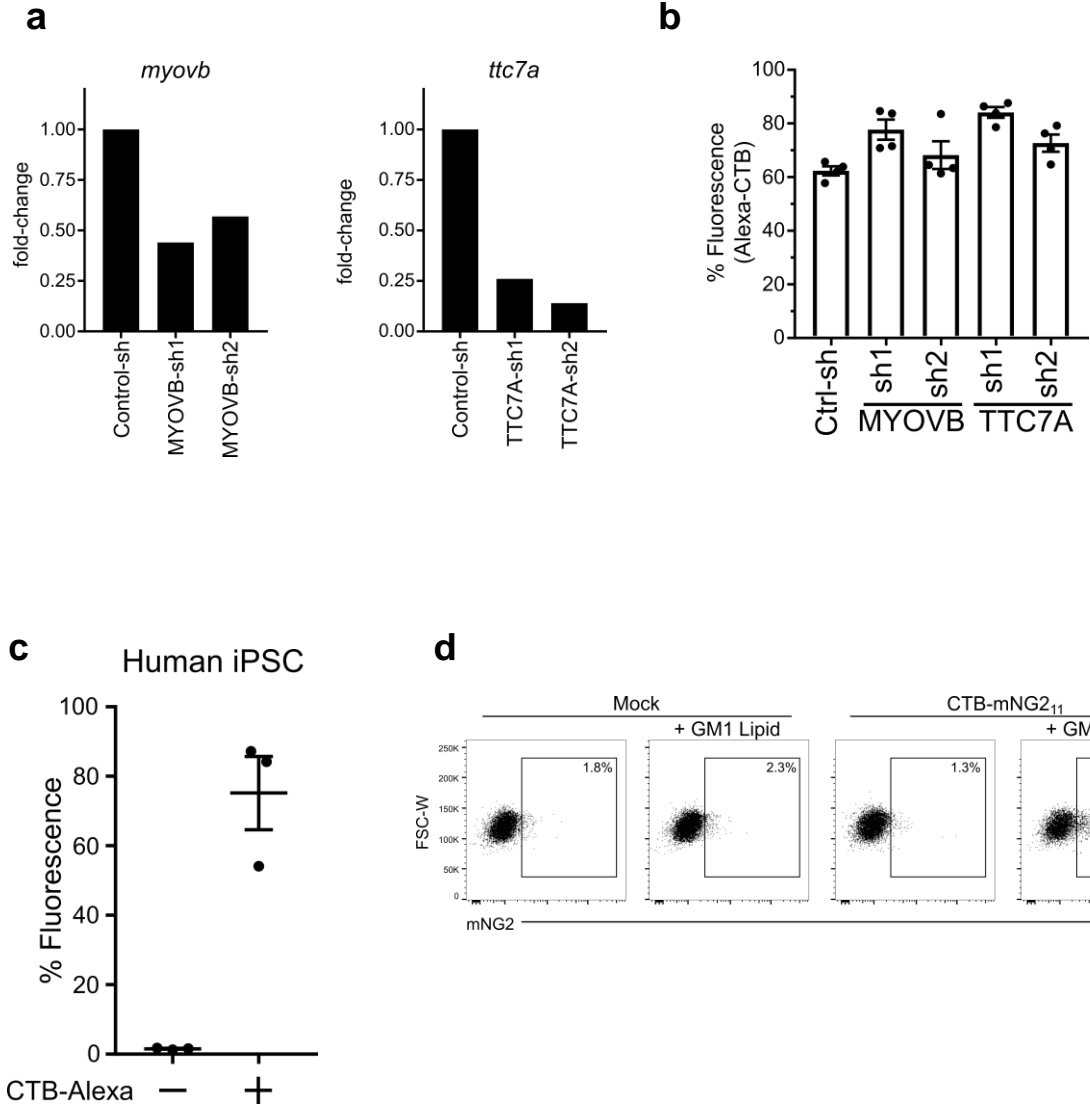
Supplementary Figure 2



Supplementary Figure 2.

Toxin binding and XBP1 stress response to ER shape gene expression. **a, b** Immunoblots for ER-HA-mNG2₁₋₁₀ in K562 (a) and HEK293T (b) cells treated or not with the indicated compounds used as above. Immunoblots for β -actin provide loading controls. **c** Binding control experiment displays equal loading of CTB-Alexa Fluor 488 in HEK293T cells expressing empty vector (EV), and ER shape genes ATLASTIN1-K80A, CLIMP63 and DP1. Cells were incubated with 2nM CTB-Alexa Fluor 488 for 5 hours 37°C, and then harvested and assayed by flow cytometry. n=5 independent experiments. **d** XBP1 luciferase reporter assay in cells expressing vector (EV), and ER shape genes ATLASTIN1-K80A, CLIMP63 and DP1. Cells were treated with thapsigargin (Thaps) at 300nM for 4 hours as positive control to induce ER stress. Graph displays average of n=3 independent experiments. Error bars indicate \pm SEM, *p<0.05.

Supplementary Figure 3



Supplementary Figure 3.

mRNA expression and toxin binding CTB-Alexa Fluor 488 in cells with knockdown of monogenic disease genes. **a** Relative mRNA expression to control by qPCR of MYOVB and TTC7A in HEK293T cells expressing shRNA against indicated gene. Actin is used as expression control. **b** Binding control experiment displays equal loading of CTB-Alexa Fluor 488 in HEK293T expressing control shRNA or shRNA targeting MYOVB or TTC7A. Cells were incubated with 2nM CTB-Alexa Fluor 488 for 5 hours 37°C, and then harvested and assayed by flow cytometry. **c** CTB-Alexa Fluor 488 binding controls for human iPSCs loaded with GM1 C12:0 lipid, Incubation conditions same as above. n=3 independent experiments. **d** Representative flow cytometry graph from Fig 3e. Error bars indicate \pm SEM.

Supplementary Table 1 :	Sequence of split-FP constructs
CTA2-sfmcherry211	TACACCATCGTGGAGCAGTACGAGAGAGCCGAGGCCAGACACAGCACCCGGAGG TGGAGGTTCCCTCGATGAGTAATACTTGGCGATGAAAAACCCAAAGTCTAGGTGTA AAATTCCTTGACGAATACCAATCTAAAGTTAAAAGACAAATATTTTCAGGCTATCA ATCTGATATTGATACACATAATAGAATTAAGGATGAATTA
CTA2-mNG2 11	ACCGAGCTCAACTTCAAGGAGTGGCAAAAGGCCCTTTACCGATATGATGGGAGGT GGAGGTTCCCTCGATGAGTAATACTTGGCGATGAAAAACCCAAAGTCTAGGTGTAA AATTCCTTGACGAATACCAATCTAAAGTTAAAAGACAAATATTTTCAGGCTATCAAT CTGATATTGATACACATAATAGAATTAAGGATGAATTA
ER-HA-mNG2 1-10	ATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGCCGCGCAC TCCGGAGAACAGAAGCTGATCTCAGAGGAGGACCTGGGAGGTATGGTGAGCAA GGGTGAGGAGGATAACATGGCCTCTCTCCCAGCGACTCATGAGTTACACATCTTT GGCTCCATCAACGGTGTGGACTTTGACATGGTGGGTCAGGGTACCGGCAATCCA AATGATGGTTATGAGGAGTTAAACCTGAAGTCCACCAAGGGTGACCTCCAGTTCT CCCCCTGGATTCTGGTCCCTCATATCGGGTATGGCTTCCATCAGTACCTGCCCTA CCCTGACGGGATGTCGCCTTTCCAGGCCGCCATGGTAGATGGCTCCGGATACCA AGTCCATCGCACAATGCAGTTTGAAGATGGTGCCTCCCTTACTGTAACTACCGC TACACCTACGAGGGAAGCCACATCAAAGGAGAGGCCAGGTGATGGGGACTGG TTTCCCTGCTGACGGTCTGTGATGACCAACACGCTGACCGCTGCGGACTGGTG CATGTCGAAGAAGACTTACCCCAACGACAAAACCATCATCAGTACCTTTAAGTGG AGTTACACCACTGTAAATGGCAAACGCTACCGGAGCACTGCGCGGACCACCTAC ACCTTTGCCAAGCCAATGGCGGCTAACTATCTGAAGAACCAGCCGATGTACGTGT TCCGTAAGACGGAGCTCAAGCACTCCATGGGAGAGAAGGATGAACTG
TGN-HA-mNG2 1-10	ATGAGGCTTCGGGAGCCGCTCCTGAGCGGCAGCGCCGCGATGCCAGGCCGCGT CCTACAGCGGGCCTGCCGCTGCTCGTGGCCGCTGCGCTCTGCACCTTGGCG TCACCCTCGTTTACTACCTGGCTGGCCGCGACCTGAGCCGCCTGCCCAACTGG TCGGAGTCTCCACACCGCTGCAGGGCGGCTCGAACAGTGCCGCGGCCATCGGG CAGTCCCTCCGGGGAGCTCCGGACCGGAGGGGCCAAGGATCCACCGGTGCGCCAC CTACCCATACGATGTTCCAGATTACGCTGGAGGTATGGTGAGCAAGGGTGAGGA GGATAACATGGCCTCTCTCCCAGCGACTCATGAGTTACACATCTTTGGCTCCATC AACGGTGTGGACTTTGACATGGTGGGTCAGGGTACCGGCAATCCAATGATGGT TATGAGGAGTTAAACCTGAAGTCCACCAAGGGTGACCTCCAGTTCTCCCCCTGG ATTCTGGTCCCTCATATCGGGTATGGCTTCCATCAGTACCTGCCCTACCCTGACG GGATGTCGCCTTTCCAGGCCGCCATGGTAGATGGCTCCGGATACCAAGTCCATC GCACAATGCAGTTTGAAGATGGTGCCTCCCTTACTGTAACTACCGCTACACCTA CGAGGGAAGCCACATCAAAGGAGAGGCCAGGTGATGGGGACTGGTTTTCCCTG CTGACGGTCTGTGATGACCAACACGCTGACCGCTGCGGACTGGTGCATGTGCA AGAAGACTTACCCCAACGACAAAACCATCATCAGTACCTTTAAGTGGAGTTACAC CACTGTAAATGGCAAACGCTACCGGAGCACTGCGCGGACCACCTACACCTTTGC CAAGCCAATGGCGGCTAACTATCTGAAGAACCAGCCGATGTACGTGTTCCGTAA GACGGAGCTCAAGCACTCCATG
Sec61 β -HA-mNG2 1-10	ATGCCTGGTCCGACCCCAAGTGGCACTAACGTGGGATCCTCAGGGCGCTCTCCC AGCAAAGCAGTGGCCGCCCGGGCGGGGATCCACTGTCCGGCAGAGGAAAA TGCCAGCTGTGGGACAAGGAGTGCAGGCCGCACAACCTCGGCAGGCACCGGGG GGATGTGGCGATTCTACACAGAAGATTCACCTGGGCTCAAAGTTGGCCCTGTTC

	<p>CAGTATTGGTTATGAGTCTTCTGTTTCATCGCTTCTGTATTTATGTTGCACATTTGG GGCAAGTACACTCGTTCGGGAGGAGGATACCCATACGATGTTCCAGATTACGCT ATGGTGAGCAAGGGTGAGGAGGATAACATGGCCTCTCTCCCAGCGACTCATGAG TTACACATCTTTGGCTCCATCAACGGTGTGGACTTTGACATGGTGGGTCAGGGTA CCGGCAATCCAAATGATGGTTATGAGGAGTTAAACCTGAAGTCCACCAAGGGTG ACCTCCAGTTCTCCCCCTGGATTCTGGTCCCTCATATCGGGTATGGCTTCCATCA GTACCTGCCCTACCCTGACGGGATGTCGCCTTTCCAGGCCGCCATGGTAGATGG CTCCGGATACCAAGTCCATCGCACAATGCAGTTTGAAGATGGTGCCTCCCTTACT GTTAACTACCGCTACACCTACGAGGGAAGCCACATCAAAGGAGAGGCCAGGTG ATGGGGACTGGTTTCCCTGCTGACGGTCTGTGATGACCAACACGCTGACCGCT GCGGACTGGTGCATGTGGAAGAAGACTTACCCCAACGACAAAACCATCATCAGT ACCTTTAAGTGGAGTTACACCACTGTAAATGGCAAACGCTACCGGAGCACTGCG CGGACCACCTACACCTTTGCCAAGCCAATGGCGGCTAACTATCTGAAGAACCAG CCGATGTACGTGTTCCGTAAGACGGAGCTCAAGCACTCCATG</p>
<p>TGN- FLAG- sfmche rry21- 10</p>	<p>ATGCGCCTTAGAGAGCCATTGCTTTCAGGCTCAGCTGCCATGCCGGGTGCATCC TTGCAACGGGCTTGTGCTTGTGGTGCAGTGTGCGCACTGCATCTTGGTGTG ACGCTCGTATATACTTGGCCGGGCGCGACTTGAGTCGACTGCCACAGTTGGTA GGGGTAAGCACCCATTGCAGGGCGGGTCTAATTCAGCGGCTGCGATTGGCCA GTCTTCAGGGGAAGTGAAGACGGGAGGTGCTGATTATAAAGATGACGATGACAA AATGGAAGAAGACAATATGGCCATAATCAAGGAGTTCATGAGGTTCAAGGTTTCA ATGGAAGGTAGTGTGAACGGGCATGAGTTTGAATCGAGGGAGAGGGCGAGGG GCACCCTTATGAGGGTACCCAGACGGCCAAATTGAAGGTAACAAAAGGGGGGCC ACTTCCCTTTCGCATGGGATATACTCAGCCCCCAGTTTATGTATGGTTCTAAGGCTT ATGTAAAACATCCGGCTGACATACCCGATTATCTCAAGCTCTCATTCCCCGAGGG CTTTACTTGGGAGCGGGTGTGAATTTGAAGATGGAGGAGTGGTTACGGTTAC GCAGGACAGTTCTTCAAGACGGGCAATTCATTTACAAAGTTAACTCCTCGGG ATAAACTTCCCTAGTGTATGGCCCTGTCATGCAGAAGAAGACTATGGGGTGGGAA GCCAGCACGGAGAGGATGTATCCGGAGGATGGTGCCTTGAAAGGTGAGATCAAC CAACGCCTCAAGCTCAAAGATGGTGGACACTATGATGCCGAGGTTAAGACCACC TATAAAGCCAAGAAACCGGTCCAGCTCCCCGGTGCATACAACGTTGATATAAAGC TCGATATAACATCTCACAATGAGGAC</p>
<p>CTA1- (EE/D D)- 1XmN G2</p>	<p>AATGATGATAAGTTATATCGGGCAGATTCTAGACCTCCTGATGAAATAAAGCAGT CAGGTGGTCTTATGCCAAGAGGACAGAGTGAGTACTTTGACCGAGGTACTIONCAA GAATATCAACCTTTATGATCATGCAAGAGGAACTCAGACGGGATTTGTTAGGCAC GATGATGGATATGTTTCCACCTCAATTAGTTTGAAGTGGCCACTTAGTGGGTC AACTATATTGTCTGGTCACTTACTTATTATATATATGTTATAGCCACTGCACCCA ACATGTTTAAACGTTAATGATGTATTAGGGGCATACAGTCCTCATCCAGATGACCAA GACGTTTCTGCTTTAGGTGGGATTCCATACTCCCAAATATATGGATGGTATCGAG TTCATTTTGGGGTGCCTTATGAACAATTACATCGTAATAGGGGCTACAGAGATAG ATATTACAGTAACTTAGATATTGCTCCAGCTGCAGATGGTTATGGATTGGCAGGTT TCCCTCCGGAGCATAGAGCTTGGAGGGAAGAGCCGTGGATTATCATGCACCGC CGGGTTGTGGGAATGCTGGTGGAGGAGGTGGAACCGAGCTCAACTTCAAGGAG TGGCAAAGGCCTTTACCGATATGATG</p>
<p>CTA1- (EE/D D)- 2XmN G2</p>	<p>AATGATGATAAGTTATATCGGGCAGATTCTAGACCTCCTGATGAAATAAAGCAGT CAGGTGGTCTTATGCCAAGAGGACAGAGTGAGTACTTTGACCGAGGTACTIONCAA GAATATCAACCTTTATGATCATGCAAGAGGAACTCAGACGGGATTTGTTAGGCAC GATGATGGATATGTTTCCACCTCAATTAGTTTGAAGTGGCCACTTAGTGGGTC AACTATATTGTCTGGTCACTTACTTATTATATATATGTTATAGCCACTGCACCCA ACATGTTTAAACGTTAATGATGTATTAGGGGCATACAGTCCTCATCCAGATGACCAA GACGTTTCTGCTTTAGGTGGGATTCCATACTCCCAAATATATGGATGGTATCGAG</p>

	TTCATTTTGGGGTGCTTGATGAACAATTACATCGTAATAGGGGCTACAGAGATAG ATATTACAGTAACTTAGATATTGCTCCAGCTGCAGATGGTTATGGATTGGCAGGTT TCCCTCCGGAGCATAGAGCTTGGAGGGAAGAGCCGTGGATTTCATCATGCACCGC CGGGTTGTGGGAATGCTGGTGGTTCTGGAGGAACCGAGCTCAACTTCAAGGAGT GGCAAAGGCCTTTACCGATATGATGGGCAGCGCAGGAGGGACTGAATTAATT TTAAGAATGGCAGAAAGCATTCACTGACATGATG
CTA1- (EE/D D)- 5XmN G2	AATGATGATAAGTTATATCGGGCAGATTCTAGACCTCCTGATGAAATAAAGCAGT CAGGTGGTCTTATGCCAAGAGGACAGAGTGAGTACTTTGACCGAGGTTACTCAAAT GAATATCAACCTTTATGATCATGCAAGAGGAACTCAGACGGGATTTGTTAGGCAC GATGATGGATATGTTTCCACCTCAATTAGTTTGAGAAGTGCCCACTTAGTGGGTC AACTATATTGTCTGGTCATTCTACTTATTATATATATGTTATAGCCACTGCACCCA ACATGTTTAAACGTTAATGATGTATTAGGGGCATACAGTCCTCATCCAGATGACCAA GACGTTTCTGCTTTAGGTGGGATTCCATACTCCCAAATATATGGATGGTATCGAG TTCATTTTGGGGTGCTTGATGAACAATTACATCGTAATAGGGGCTACAGAGATAG ATATTACAGTAACTTAGATATTGCTCCAGCTGCAGATGGTTATGGATTGGCAGGTT TCCCTCCGGAGCATAGAGCTTGGAGGGAAGAGCCGTGGATTTCATCATGCACCGC CGGGTTGTGGGAATGCTGGTGGTtctGGAGGAACCGAGCTCAACTTCAAGGAGTG GCAAAGGCCTTTACCGATATGATGGGCtctggaAGCGGGACTGAATTAATTTTAA AGAATGGCAGAAAGCATTCACTGACATGATGGGagcaggtggatcaACaGAGCTaAAC TTAAGGAaTGGCAAAGGCtTTTACaGATATGATGggtgggtctgcaggaACgGAGCTgA AtTTCAAaGAGTGGCAgAAGGCCTTTACgGAcATGATG

Supplementary Table2:	shRNA and qPCR oligo sequences
MYOVB shRNA-1 Forward	TTTgcggtgttacagccgatgatTTCAAGAGAtcatcggctgtaacacgcTTTTTA
MYOVB shRNA-1 Reverse	AGCTTAAAAAgcggtgttacagccgatgatTCTCTTGAAatcatcggctgtaacacg
MYOVB shRNA-2 Forward	TTTgatgggtgattcctgtagtataTTCAAGAGAtatactacaggaatcacatcTTTTTA
MYOVB shRNA-2 Reverse	AGCTTAAAAAgatgggtgattcctgtagtataTCTCTTGAAatactacaggaatcacat
TTC7A shRNA- 1 Forward	TTTgcaagatgaattgcaccggAATTCAAGAGATTcgggtgcaattcatcttgcTTTTTA
TTC7A shRNA- 1 Reverse	AGCTTAAAAAgcaagatgaattgcaccggAATCTCTTGAATTcgggtgcaattcatcttg
TTC7A shRNA- 2 Forward	TTTgcgtttgagaatttcaccttTTCAAGAGAAaggtgaaattctcaaacgcTTTTTA
TTC7A shRNA- 2 Reverse	AGCTTAAAAAgcgtttgagaatttcaccttTCTCTTGAAaaggtgaaattctcaaacg
TTC7A qPCR Primer Forward	CATCTATGACCTCCTGAGCATC
TTC7A qPCR	CTGACTTCCCACAAGCCA

Primer Reverse	
MYOVB qPCR Primer Forward	TGCTGAGTGACCTTTCCATTC
MYOVB qPCR Primer Reverse	CCAGATAGACCCTGAATGCTC