Supplementary Table S2. Transmembrane Thioredoxin-Related Protein-Binding Proteins Identified by Mass Spectrometry

Sample	*Protein*
#1	Cps1: carbamoyl-phosphate synthetase 1
#2	Sf3b3: splicing factor 3b, subunit 3 Pcx: pyruvate carboxylase Nomo1: nodal modulator 1
#3	Mthfd1: methylenetetrahydrofolate dehydrogenase Snd1: staphylococcal nuclease and tudor domain-containing 1
#4	Hsp90aa1: heat shock protein 90, alpha (cytosolic), class A member 1 Immt: inner membrane protein, mitochondrial
#5	Ehhadh: enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase Hsd17b4: hydroxysteroid (17-beta) dehydrogenase 4
#6	Acsl5: acyl-CoA synthetase long-chain family member 5 Slc27a2: solute carrier family 27 (fatty acid transporter), member 2 Slc27a5: solute carrier family 27 (fatty acid transporter), member 5 Slc25a13: solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 13 Acadvl: acyl-Coenzyme A dehydrogenase, very long chain Rpn1: ribophorin I
#7	Aifm1: apoptosis-inducing factor, mitochondrion-associated 1 Abcd3: ATP-binding cassette, subfamily D (ALD), member 3
#8	Glud1: glutamate dehydrogenase 1 Atp5a1: ATP synthase, H+transporting, mitochondrial F1 complex, alpha subunit 1 Ugt1a10: UDP glycosyl transferase 1 family, polypeptide A10
#9	Slc25a5: solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 Slc25a4: solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 4
#10	Nipsnap1: 4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1 Dhrs4: dehydrogenase/reductase (SDR family) member 4 Hsd17b10: hydroxysteroid (17-beta) dehydrogenase 10 Dpm1: dolichol-phosphate (beta-D) mannosyl transferase 1
#11	Tmem33: transmembrane protein 33 Atp5f1: ATP synthase, H+transporting, mitochondrial F0 complex, subunit B1
#12	Derl1: Der1-like domain family, member 1

Because the luminal portion of TMX was used as bait, candidate TMX-binding proteins should be present in the endoplasmic reticulum at least at some stage during their biosynthesis. Several mitochondrial or peroxisomal proteins abundantly expressed in the liver were identified in the mass spectrometry analysis, but judging from their subcellular localization, the results appeared not to reflect the physiological binding.