SUPPLEMENTARY DATA

TRANSLOCATOR PROTEIN 2 IS INVOLVED IN CHOLESTEROL REDISTRIBUTION DURING ERYTHROPOIESIS

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SUPPLEMENTAL EXPERIMENTAL PROCEDURES

***Sequence selection and alignment* -** The TSPO homologous sequences were retrieved from the non-redundant GenBank database through BLAST searches (http://www.ncbi.nlm.nih.gov). The predicted protein sequence of human TSPO was used as the query sequence. The same sequence was also used to search other individual organism genomes. In addition, orthologous genes of TSPO, which are the representatives of each class of invertebrates, were also selected for comparison. Accession number of each gene used in following analysis is shown in supplementary Table 1. Protein and DNA sequences from GenBank (http://www.ncbi.nlm.nih.gov) were aligned using Clustal X (1). Codon-based alignment was made manually with the introduction of small internal deletions and/or gaps to optimize the alignment, or using PAL2NAL, a program that converts a multiple sequence alignment of proteins and the corresponding DNA (or mRNA) sequences into a codon alignment format (http://coot.embl.de/pal2nal) (2).

SUPPLEMENTAL RESULTS AND DISCUSSION

***Identification of new* Tspo *homologs by exploration of the non-redundant gene databases* -** To identify *Tspo* genes homologs, we used the predicted amino acid sequence of the human *Tspo* gene to search public databases using PSI-BLAST (http://www.ncbi.nlm.nih.gov). Sequence similarity indicated that *Tspo*-like genes are present in genomes spanning from birds to mammals. After excluding redundant sequences, *Tspo*-like genes from unique genomes were selected for comparison. Predicted protein sequences of each newly identified *Tspo*-like gene were aligned with previously characterized TSPO proteins (Figure S1). Basic sequence features, such as the five transmembrane domains with a high degree of amino acid conservation throughout different organisms and high sequence similarity (Tables S1 and S3), suggested that the identified *Tspo*-like genes are closely related *Tspo*-like sequences. Because of the recent nomenclature change of PBR to TSPO(3), we designated the PBR-like (*Pbrl1*) genes as *Tspo2* and the previous *Tspo* gene as *Tspo1*. These data also predict that TSPO2 is more hydrophobic than TSPO1. However, both likely share a similar secondary structure.

To define domain structures of the identified *Tspo2* members, the predicted amino acid sequence of each was used to search the Pfam database using HMMER set to the “global and local alignment separately” mode. Based on a raw score threshold, "gathering threshold" (GA cutoff), all of the TSPO2 proteins match with the TSPO/PBR family. Thus, the sequence alignments and database searches indicated that *Tspo2* genes are members of the *Tspo* gene family (Table S1).

Tspo2 *and* Tspo1 *involve distinct gene networks* - To investigate whether the *Tspo2* gene family is expressed, we searched the express sequence tags (ESTs) database using BLASTN (http://www.ncbi.nlm.nih.gov/dbEST). Almost all *Tspo2* genes detected in the dbEST database are listed in Table S3. Expression of human and mouse *Tspo2* seemed tissue-specific in erythroid cells. We then exploited the availability of an integrated protein interaction network database (4) and found that *TSPO2* (Gene ID no. 222642) has 703 interactions among 43 proteins, whereas *TSPO1* (Gene ID no.: 706) has 150 interactions among 40 proteins (Figure S2A). Many aspects of *Tspo1* biological functions appeared to be reflected in this gene network, such as mitochondrial localized proteins [VDAC1-3, voltage-dependent anion channel 1-3; translocase of outer mitochondrial membrane 20 homolog and 22 homolog (TOMM20 and 22); translocase of inner mitochondrial membrane 17 homolog B and 44 homolog (TIMM17B and 44)], lipid metabolism and cholesterol transport [lipase A (LIPA), lysosomal acid, cholesterol esterase; retinoid X receptor alpha (RXRA), acyl-CoA thioesterase 9 (ACATE2)], apoptosis, cell signaling, and cell proliferation [myeloid cell leukemia sequence 1 (MCL1); and PYCARD, PYD, and CARD domain containing proteins], as well as nuclear transport [nucleoporin 214 kDa (NUP214)] (Figure S2A). However, the gene network of *TSPO2* was indicative of an erythroid cell-related gene network (Fig. S2A), in which 27 of 43 proteins are erythrocyte-related, including EPB41, BSG, SPTA1, EIF2AK1, SLC22A4, and XPO7. These genes were confirmed to be erythroid cell-specific by two independent studies (5,6). Details of genes closely related to *Tspo1 and 2,* and involved in these two networks are available in Tables S4 and S5. Although the involvement of these genes should be experimentally tested, *TSPO2* is likely involved in erythrocyte differentiation and cholesterol transport and/or synthesis. Notably, 1 of the 43 genes within this gene network is oxysterol binding protein 2 (OSBP2), which regulates cellular metabolism, binding, and transport of cholesterol in mammals (7,8) and the synthesis of ergosterol, the yeast counterpart of cholesterol, in yeast (9-11).

Additionally, sequence alignments between a partial N-terminal peptide sequence of a TSPO1-like integral membrane protein, previously designated p18, from avian erythrocytes with TSPO2 and TSPO1 proteins showed that p18 is not the orthologous gene of *Tspo1* but the avian *Tspo2* protein (Figure S2B). In a previous report, we found that p18 is involved in a nuclear mutimeric complex with lamin-B receptor (LBR, p58), the nuclear lamins, and a LBR-specific kinase (12). These observations suggest that *Tspo2* has functions and cellular localization distinct from those of *Tspo1*.

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Table S1. Accession numbers of the genes used in this study

Table S2. Oligonucleotides used in this study

Table S3. Comparison of the characteristics of TSPO1 and TSPO2

Table S4. A list of genes involved in the human TSPO1 gene network.

Table S5. A list of genes involved in the human TSPO2 gene network.

Table S1. Accession numbers of the genes used in this study

Abbreviation[a]	Species	Accession No.	References
	Vertebrates		
TSPO1_humans	*Homo sapiens*	NM_000714	(13)
TSPO1_mouse	*Mus musculus*	P50637	(14)
TSPO1_rat	*Rattus norvegicus*	NP_036647	(15)
TSPO1_pig	*Sus scrofa*	NP_998918	(16)
TSPO1_dog	*Canis familiaris*	XP_531704	-
TSPO1_sheep	*Ovis aries*	NP_001009747	-
TSPO1_Monodelphis	*Monodelphis domestica*	XP_001369931	-
TSPO1_bovine	*Bos taurus*	NP_786970	(17)
TSPO1_Gallus	*Gallus gallus*	XP_416451	-
TSPO1_Xenopus	*Xenopus laevis*	AAH41505	-
TSPO1_Danio	*Danio rerio*	NP_001006032	-
TSPO1_Oncorhychus	*Oncorhynchus mykiss*	AAK31586	-
TSPO1_Tetraodon	*Tetraodon nigroviridis*	CAG06923	-
TSPO2_humans	*H. Sapiens*	NP_001010873	-
TSPO2_pig	*S. scrofa*	N166970	-
TSPO2_dog	*C. familiaris*	XP_538908	-
TSPO2_rat	*R. norvegicus*	XP_001063305	-
TSPO2_mouse	*M. Musculus*	NP_081568	-
TSPO2_Monodelphis	*M. domestica*	XP_001379628	-
TSPO2_Gallus	*G. gallus*	XP_418037	-
	Plants		
TSPO_Arabidopsis	*Arabidopsis thaliana*	NP_566110	(18)
TSPO_Solanum	*Solanum tuberosum*	CAH10765	(19)
	Nematoda		
TSPO_briggsae	*Caenorhabditis briggsae*	CAE56706	-
TSPO_elegans	*C. elegans*	NP_492528	-
	Insects		
TSPO_Anopheles	*Anopheles gambiae*	XP_310673	-
TSPO_Bombyx	*Bombyx mori*	NP_001040343	-
TSPO_Drosophila	*Drosophila melanogaster*	NP_608531	-
	Fungi		
TSPO_Cryptococcus	*Cryptococcus neoformans*	XP_568678	-
TSPO_Schizosaccharomyces	*Schizosaccharomyces pombe*	NP_595490	-
TSPO_Neurospora	*Neurospora crassa*	XP_964457	-
	Archaea		
TspO_Methanoculleus	*Methanoculleus marisnigri*	YP_001047813	-
TspO_Methanosaeta	*Methanosaeta thermophila*	YP_842785	-
	Bacteria		
TspO_Sphingopyxis	*Sphingopyxis alaskensis*	YP_615100	-
TspO_Acidiphilium	*Acidiphilium cryptum*	ZP_01146325	-
TspO_Francisella	*Francisella tularensis*	YP_170081	-

[a] TSPO1, translocator protein (18 kDa); TSPO2, TSPO-like protein; TspO, Tryptophan-Rich Sensory Protein; The letters after each abbreviation represent the name of the species from which the orthologous protein originates.

Table S2. Oligonucleotides used in this study

Primer	Sequence*	Purpose
GFP-mTSO2-R (HindIII)	GCGAAGCTTCAGCTTCAAGGACCTGTC	GFP-mTSPO2 cloning
GFP-mTSO2-F (BamHI)	GCGGGATCCCTAAGGCTGGTACGTTGGAC	GFP-mTSPO2 cloning
GFP-hTSO2-R (HindIII)	GCGAAGCTTCGGCTTCAAGGGGCTATC	GFP-hTSPO2 cloning
GFP-hTSO2-F (BamHI)	GCGGGATCCTCAGTCACTCTTCTCCGTG	GFP-hTSPO2 cloning
DsRed-hTSPO2-cracR (HindIII)	GCGAAGCTTCGCGGCTTCAAGGGGCTATC	DsRed-hTSPO2-crac cloning
DsRed-hTSPO2-cracF (BamHI)	GCGGGATCCTCAGAGCCAGGCTAGGTAGGGCAGC	DsRed-hTSPO2-crac cloning
DsRed-hTSPO2-wtR (HindIII)	GCGAAGCTTCGCGGCTTCAAGGGGCTATC	DsRed-hTSPO2-wt cloning
DsRed-hTSPO2-wtF (BamHI)	GCGGGATCCTCAGTCACTCTTCTCCGTG	DsRed-hTSPO2-wt cloning
mTSPO2-R(HindIII)	GCGAAGCTTAAAATGCAGCTTCAAGGACCTG	mTSPO2 cloning in yeast & Probe for *in situ* hybridization
mTSPO2-F(XhoI)	GCGCTCGAGAGGCTGGTACGTTGGACACAAGC	mTSPO2 cloning in yeast & Probe for *in situ* hybridization
hTSPO2-R(HindIII)	GCGAAGCTTAAAATGCGGCTTCAAGGGGCTATC	hTSPO2 cloning in yeast
hTSPO2-F(XhoI)	GCGCTCGAGGTCACTCTTCTCCGTGGGCTG	hTSPO2 cloning in yeast
mTSPO-R (HindIII)	GCGAAGCTTAAAATGCCTGAATCCTGGGTGCC	mTSPO1 cloning in yeast
mTSPO-F(XhoI)	GCGCTCGAGCTCTGGGAGCCGGGAGCC	mTSPO1 cloning in yeast
mTSPO2-RnoS(NdeI)	GCGCATATGTGTGAGGATGAGAGAAAGTTACC	mTSPO2 cloning in *E. coli*
mTSPO2-F*(XhoI)	GGCCTCGAGCTAAGGCTGGTACGTTGGACACAAGC	mTSPO2 cloning in *E. coli*
mTSPO-cracFSp(XhoI)	GCGCTCGAGTCACAGCCAGGCCAGGTAAGGGTACAGC	mTSPO2 cloning in *E. coli*
mTSPO2-RT-R	ATTGGGCAGACCAACCTGGATCTT	mTSPO2 RT-PCR
mTSPO2-RT-F	ACCGACTGGATGGCTGATGAATGA	mTSPO2 RT-PCR
mTSPO1-RT-R	TAGCTTGCAGAAACCCTCTTGGCA	mTSPO1 RT-PCR
mTSPO1-RT-F	TGTGAAACCTCCCAGCTCTTTCCA	mTSPO1 RT-PCR
mTubulin-RT-R	ACCGGCCTGTATGCTATCCAGAAA	mTubulin RT-PCR
mTubulin-RT-F	ATTTCAATGTGAGGCGGGTGGAAC	mTubulin RT-PCR
hTSPO2-RT-R	AGCTGGACTGTCCTGGTTCTCTTT	hTSPO2 RT-PCR
hTSPO2-RT-F	AACAGGGCAGCCAGTTTGTTGATG	hTSPO2 RT-PCR
hTSPO1-RT-R	TGGGCCTCTACACTGGGCA	hTSPO1 RT-PCR
hTSPO1-RT-F	ACCAGCAGGAGATCCACCAA	hTSPO1 RT-PCR
hHPRT-RT-R	CCTGGCGTCGTGATTAGTGATGAT	hHPRT RT-PCR
hHPRT-RT-F	AGCAAGACGTTCAGTCCTGTCCAT	hHPRT RT-PCR
hTSPO2-R(NheI)	GCGGCTAGCATGCGGCTTCAAGGGGCTATC	hTSPO2 overexpression
hTSPO2-F(XhoI)	GGCCTCGAGTCAGTCACTCTTCTCCGTGGGCTG	hTSPO2 overexpression

*Underlined characters indicate restriction enzyme sites introduced for the convenient cloning of the gene.

Table S3. Comparison of the characteristics of TSPO1 and TSPO2.

Properties	TSPO1	TSPO2
Length of predicted peptide	hTSPO1, 169 aa; about 158 aa conserved core region	hTSPO2, 170 aa; 39-47 % identical in this 158 aa conserved region to TSPO1
Molecular weight/theoretical pI	hTSPO2, 18.8 kDa/9.43	hTSPO2, 19.1 kDa/8.48
Genomic location	Chromosome: 22 (human) and 15 (mouse)	Chromosome: 6 (human) and 17 (mouse)
Structural signatures	Five transmembrane domains, with 10 conserved W residue (hTSPO: W5, 33, 42, 47, 68, 94, 96, 108, 144, 156). hTSPO is 81% identical to mTSPO1	Five transmembrane domains, but with only 6 conserved W residues, (hTSPO2: W38, 65, 91, 124, 141, 153). Relative to hTSPO1, the equivalents of W residues are all conserved. hTSPO2 is 35% identical to hTSPO1, and 65% identical to mTSPO2.
Tissue distribution	Almost every tissue in human and mouse, and likely in other organisms as well.	Most highly expressed in: **Human** fetal brain (DR001979), erythroid precursor cells (BU655765, BU657409), fetus (BX282068, AI052224; AI038082; R98203). **Mouse** liver (BY710385) and embryo or mixed whole body (AI326916, BY080031, BY138614, BY144851, BY339509, BY343020, BY447548, AA049790, W83846). **Pig** pooled (CN166970, CK453370, CK452313, DN133969). **Rat** mixed (AW921077). **Dog** Mixed (DR106737). **Chicken** limbs (BX931454); chondrocytes (CR353324); whole embryo (BX936041, BX934347); and EST: multi-tissues (BX261561, BX277681, BX261428, BX270576, CK987275, BX270575, BX261427); liver (BU241760); whole embryo (BU200250, CD764256, BU105064, BU214674); thymus (AM064061); Chondrocytes (BU483883, BU468730, BU424969, BU433040); limbs (BU258754); MDV infected splenic T cell (AW239804); cerebrum (BU363452); Somites associated with the neural tube (CD762456)
Ability to bind cholesterol (cholesterol recognition amino acid consensus sequence, CRAC)	Yes	Yes
Ability to bind benzodiazepine	Yes	-

Cellular protein complex	Mitochondrial complex: TSPO1, Star, PAP7, VDAC, etc.	Nuclear complex: TSPO2, LBR, lamin B, LBR-specific kinase (P34).
Phylogenetic distribution	From bacteria (except some such as *E. c*oli) to all eukaryotes (except some organisms, such as yeast *S. cerevisiae*)	Avians to mammalians

Table S4. A list of genes involved in the human TSPO1 gene network.

GeneID A	GeneID B	GeneA	GeneB	Score	PPI	Pheno type	GI	Gene Ontology	DDI	Micro array	Gene Context
29108	572	PYCARD	BAD	7.197	-	-	-	+	-	+	-
26056	572	RAB11FIP5	BAD	8.096	-	-	-	+	-	+	-
572	596	BAD	BCL2	7.785	-	-	-	+	-	+	-
2710	596	GK	BCL2	8.096	-	-	-	+	-	+	-
4170	596	MCL1	BCL2	8.14	-	-	-	+	+	+	-
5894	596	RAF1	BCL2	8.545	-	-	-	+	-	+	-
23597	706	ACATE2	**TSPO1**	7.406	-	-	-	+	-	+	-
572	706	BAD	**TSPO1**	8.545	-	-	-	+	-	+	-
596	706	BCL2	**TSPO1**	7.785	-	-	-	+	-	+	-
22918	706	C1QR1	**TSPO1**	8.256	-	-	-	+	-	+	-
2555	**706**	**GABRA2**	**TSPO1**	**10.12**	**-**	**-**	**-**	**+**	**-**	**+**	**-**
2710	706	GK	**TSPO1**	7.975	-	-	-	+	-	+	-
3267	706	HRB	**TSPO1**	7.406	-	-	-	+	-	+	-
11026	706	LILRA3	**TSPO1**	8.256	-	-	-	+	-	+	-
3988	**706**	**LIPA**	**TSPO1**	**7.406**	**-**	**-**	**-**	**+**	**-**	**+**	**-**
4170	706	MCL1	**TSPO1**	9.16	-	-	-	+	-	+	-
64747	*706*	*MFSD1*	***TSPO1***	*10.15*	-	-	-	+	-	+	-
64231	*706*	*MS4A6A*	***TSPO1***	*8.256*	-	-	-	+	-	+	-
4976	706	OPA1	**TSPO1**	8.031	-	-	-	+	-	+	-
5359	706	PLSCR1	**TSPO1**	9.485	-	-	-	+	-	+	-
5660	706	PSAP	**TSPO1**	10.9	-	-	-	+	-	+	-
5711	706	PSMD5	**TSPO1**	7.516	+	-	-	-	-	+	-
29108	706	PYCARD	**TSPO1**	8.256	-	-	-	+	-	+	-
26056	706	RAB11FIP5	**TSPO1**	8.096	-	-	-	+	-	+	-
5894	706	RAF1	**TSPO1**	9.835	-	-	-	+	-	+	-
5997	**706**	**RGS2**	**TSPO1**	**8.256**	**-**	**-**	**-**	**+**	**-**	**+**	**-**
6256	706	RXRA	**TSPO1**	8.739	-	-	-	+	-	+	-
11182	706	SLC2A6	**TSPO1**	7.406	-	-	-	+	-	+	-
58472	**706**	**SQRDL**	**TSPO1**	**8.256**	**-**	**-**	**-**	**+**	**-**	**+**	**-**
10245	*706*	*TIMM17B*	***TSPO1***	*11.02*	-	-	-	+	-	+	-
10469	*706*	*TIMM44*	***TSPO1***	*9.55*	-	-	-	+	-	+	-
10043	706	TOM1	**TSPO1**	7.406	-	-	-	+	-	+	-
56993	706	TOMM22	**TSPO1**	9.894	-	-	-	+	-	+	-
11026	22918	LILRA3	C1QR1	8.299	-	-	-	+	+	+	-
706	834	TSPO1	CASP1	8.256	-	-	-	+	-	+	-
4170	834	MCL1	CASP1	8.104	-	-	-	+	-	+	-
64231	834	MS4A6A	CASP1	9.626	-	-	-	+	-	+	-
29108	834	PYCARD	CASP1	17.07	-	-	-	+	+	+	-
5894	834	RAF1	CASP1	7.948	-	-	-	+	+	+	-
5997	834	RGS2	CASP1	11.07	-	-	-	+	+	+	-
7097	834	TLR2	CASP1	9.626	-	-	-	+	-	+	-
7305	834	TYROBP	CASP1	7.214	-	-	-	-	-	+	-
706	912	**TSPO1**	CD1D	8.256	-	-	-	+	-	+	-
22918	912	C1QR1	CD1D	8.256	-	-	-	+	-	+	-
834	912	CASP1	CD1D	7.214	-	-	-	-	-	+	-
11026	912	LILRA3	CD1D	9.626	-	-	-	+	-	+	-
4170	912	MCL1	CD1D	9.162	-	-	-	+	+	+	-
64231	912	MS4A6A	CD1D	9.626	-	-	-	+	-	+	-
7305	912	TYROBP	CD1D	8.256	-	-	-	+	-	+	-
706	9936	**TSPO1**	CD302	8.256	-	-	-	+	-	+	-
22918	9936	C1QR1	CD302	9.656	-	-	-	+	-	+	-
912	9936	CD1D	CD302	8.256	-	-	-	+	-	+	-

945	9936	CD33	CD302	9.656	-	-	-	+	-	+	-
11026	9936	LILRA3	CD302	8.256	-	-	-	+	-	+	-
64747	9936	MFSD1	CD302	7.214	-	-	-	-	-	+	-
64231	9936	MS4A6A	CD302	9.626	-	-	-	+	-	+	-
5997	9936	RGS2	CD302	7.214	-	-	-	-	-	+	-
7097	9936	TLR2	CD302	7.214	-	-	-	-	-	+	-
7305	9936	TYROBP	CD302	8.256	-	-	-	+	-	+	-
706	945	**TSPO1**	CD33	8.256	-	-	-	+	-	+	-
22918	945	C1QR1	CD33	9.668	-	-	-	+	+	+	-
834	945	CASP1	CD33	8.59	-	-	-	+	+	+	-
912	945	CD1D	CD33	9.626	-	-	-	+	-	+	-
11026	945	LILRA3	CD33	8.256	-	-	-	+	-	+	-
64231	945	MS4A6A	CD33	9.626	-	-	-	+	-	+	-
29108	945	PYCARD	CD33	8.299	-	-	-	+	+	+	-
5997	945	RGS2	CD33	8.299	-	-	-	+	+	+	-
7097	945	TLR2	CD33	9.961	-	-	-	+	+	+	-
7305	945	TYROBP	CD33	8.256	-	-	-	+	-	+	-
22918	3267	C1QR1	HRB	9.057	-	-	-	+	-	+	-
11182	3267	SLC2A6	HRB	7.406	-	-	-	+	-	+	-
10043	3988	TOM1	LIPA	7.485	-	-	-	+	-	+	-
2710	4170	GK	MCL1	9.055	-	-	-	+	-	+	-
26056	4170	RAB11FIP5	MCL1	8.204	-	-	-	+	-	+	-
3267	64747	HRB	MFSD1	7.406	-	-	-	+	-	+	-
5359	64747	PLSCR1	MFSD1	7.214	-	-	-	-	-	+	-
5660	64747	PSAP	MFSD1	10.15	-	-	-	+	-	+	-
29108	64747	PYCARD	MFSD1	7.214	-	-	-	-	-	+	-
11182	64747	SLC2A6	MFSD1	8.739	-	-	-	+	-	+	-
10043	64747	TOM1	MFSD1	7.406	-	-	-	+	-	+	-
22918	64231	C1QR1	MS4A6A	8.256	-	-	-	+	-	+	-
11026	64231	LILRA3	MS4A6A	9.626	-	-	-	+	-	+	-
29108	64231	PYCARD	MS4A6A	9.626	-	-	-	+	-	+	-
5997	64231	RGS2	MS4A6A	9.626	-	-	-	+	-	+	-
706	8021	**TSPO1**	NUP214	7.406	-	-	-	+	-	+	-
3267	8021	HRB	NUP214	9.835	-	-	-	+	-	+	-
64747	8021	MFSD1	NUP214	7.406	-	-	-	+	-	+	-
5660	8021	PSAP	NUP214	8.739	-	-	-	+	-	+	-
4170	4976	MCL1	OPA1	8.031	-	-	-	+	-	+	-
26056	4976	RAB11FIP5	OPA1	7.975	-	-	-	+	-	+	-
23597	5359	ACATE2	PLSCR1	7.406	-	-	-	+	-	+	-
22918	5359	C1QR1	PLSCR1	8.223	-	-	-	+	-	+	-
3988	5359	LIPA	PLSCR1	8.739	-	-	-	+	-	+	-
3988	5660	LIPA	PSAP	9.69	-	-	-	+	-	+	-
5359	5660	PLSCR1	PSAP	9.485	-	-	-	+	-	+	-
11182	5660	SLC2A6	PSAP	8.739	-	-	-	+	-	+	-
10043	5660	TOM1	PSAP	9.69	-	-	-	+	-	+	-
572	5894	BAD	RAF1	7.975	-	-	-	+	-	+	-
2710	5894	GK	RAF1	10.45	-	-	-	+	-	+	-
4170	5894	MCL1	RAF1	10.79	-	-	-	+	+	+	-
29108	5997	PYCARD	RGS2	9.626	-	-	-	+	-	+	-
5359	6256	PLSCR1	RXRA	7.406	-	-	-	+	-	+	-
5660	6256	PSAP	RXRA	8.797	-	-	-	+	+	+	-
10043	6256	TOM1	RXRA	7.174	-	-	-	+	-	+	-
706	**9997**	**TSPO1**	**SCO2**	**8.256**	**-**	**-**	**-**	**+**	**-**	**+**	**-**
10043	10245	TOM1	TIMM17 B	7.246	-	-	-	+	-	+	-
10245	10469	TIMM17B	TIMM44	10.46	-	-	-	+	-	+	-
706	7097	**TSPO1**	TLR2	8.256	-	-	-	+	-	+	-

22918	7097	C1QR1	TLR2	8.057	-	-	-	+	-	+	-
64231	7097	MS4A6A	TLR2	9.626	-	-	-	+	-	+	-
29108	7097	PYCARD	TLR2	8.256	-	-	-	+	-	+	-
5997	7097	RGS2	TLR2	9.626	-	-	-	+	-	+	-
706	*9804*	*TSPO1*	*TOMM20*	*9.894*	-	-	-	+	-	+	-
8021	9804	NUP214	TOMM20	7.975	-	-	-	+	-	+	-
10245	9804	TIMM17B	TOMM20	11.75	-	-	-	+	-	+	-
10469	9804	TIMM44	TOMM20	11.02	-	-	-	+	-	+	-
56993	9804	TOMM22	TOMM20	12.63	-	-	-	+	-	+	-
10245	56993	TIMM17B	TOMM22	11.75	-	-	-	+	-	+	-
10469	56993	TIMM44	TOMM22	11.02	-	-	-	+	-	+	-
706	7305	**TSPO1**	TYROBP	8.256	-	-	-	+	-	+	-
22918	7305	C1QR1	TYROBP	8.256	-	-	-	+	-	+	-
11026	7305	LILRA3	TYROBP	8.256	-	-	-	+	-	+	-
64231	7305	MS4A6A	TYROBP	9.626	-	-	-	+	-	+	-
5660	7305	PSAP	TYROBP	7.214	-	-	-	-	-	+	-
29108	7305	PYCARD	TYROBP	7.214	-	-	-	-	-	+	-
5894	7305	RAF1	TYROBP	9.835	-	-	-	+	-	+	-
5997	7305	RGS2	TYROBP	7.214	-	-	-	-	-	+	-
7097	7305	TLR2	TYROBP	7.214	-	-	-	-	-	+	-
572	7416	BAD	**VDAC1**	9.95	-	-	-	+	-	+	-
706	**7416**	**TSPO1**	**VDAC1**	**7.632**	**-**	**-**	**-**	**+**	**-**	**+**	**-**
4976	7416	OPA1	**VDAC1**	8.096	-	-	-	+	-	+	-
26056	7416	RAB11FIP5	**VDAC1**	9.16	-	-	-	+	-	+	-
5894	7416	RAF1	**VDAC1**	7.975	-	-	-	+	-	+	-
56993	7416	TOMM22	**VDAC1**	8.739	-	-	-	+	-	+	-
572	7417	BAD	**VDAC2**	9.104	-	-	-	+	-	+	-
706	7417	TSPO1	**VDAC2**	7.975	-	-	-	+	-	+	-
4170	7417	MCL1	**VDAC2**	7.728	-	-	-	+	-	+	-
4976	7417	OPA1	**VDAC2**	9.055	-	-	-	+	-	+	-
26056	7417	RAB11FIP5	**VDAC2**	8.204	-	-	-	+	-	+	-
5894	7417	RAF1	**VDAC2**	8.545	-	-	-	+	-	+	-
7416	7417	VDAC1	**VDAC2**	13.96	-	-	-	+	-	+	-
572	7419	BAD	**VDAC3**	7.975	-	-	-	+	-	+	-
706	7419	TSPO1	**VDAC3**	8.031	-	-	-	+	-	+	-
2710	7419	GK	**VDAC3**	7.975	-	-	-	+	-	+	-
4170	7419	MCL1	**VDAC3**	8.031	-	-	-	+	-	+	-
4976	7419	OPA1	**VDAC3**	9.055	-	-	-	+	-	+	-
26056	7419	RAB11FIP5	**VDAC3**	9.16	-	-	-	+	-	+	-
5894	7419	RAF1	**VDAC3**	9.104	-	-	-	+	-	+	-
7416	7419	VDAC1	**VDAC3**	12.63	-	-	-	+	-	+	-
7417	7419	VDAC2	**VDAC3**	11.75	-	-	-	+	-	+	-

Note: PPI, protein-protein interaction; GI, Genetic interactions ; DDI, Domain-domain interaction.

Table S5. A list of genes involved in the human TSPO2 gene network.

GeneID A	GeneID B	GeneA	GeneB	Score	PPI	Pheno type	GI	Gene Ontology	DDI	Micro array	Gene Context
210	220972	ALAD	March8	7.214	-	-	-	-	-	+	-
212	220972	ALAS2	March8	7.214	-	-	-	-	-	+	-
2035	220972	EPB41	March8	7.214	-	-	-	-	-	+	-
2038	220972	EPB42	March8	7.214	-	-	-	-	-	+	-
114625	220972	ERMAP	March8	7.214	-	-	-	-	-	+	-
10098	220972	TM4SF9	March8	7.214	-	-	-	-	-	+	-
10107	220972	TRIM10	March8	9.656	-	-	-	+	-	+	-
2038	210	EPB42	ALAD	7.214	-	-	-	-	-	+	-
114625	210	ERMAP	ALAD	7.214	-	-	-	-	-	+	-
210	212	ALAD	ALAS2	16.739	-	-	-	+	-	+	-
1193	212	CLIC2	ALAS2	7.214	-	-	-	-	-	+	-
2035	212	EPB41	ALAS2	7.549	-	-	-	-	+	+	-
2038	212	EPB42	ALAS2	7.933	-	-	-	-	+	+	-
114625	212	ERMAP	ALAS2	7.214	-	-	-	-	-	+	-
10098	212	TM4SF9	ALAS2	7.214	-	-	-	-	-	+	-
10107	212	TRIM10	ALAS2	7.214	-	-	-	-	-	+	-
220972	66008	March8	ALS2CR3	7.214	-	-	-	-	-	+	-
210	66008	ALAD	ALS2CR3	7.214	-	-	-	-	-	+	-
212	66008	ALAS2	ALS2CR3	7.214	-	-	-	-	-	+	-
286	66008	ANK1	ALS2CR3	11.027	-	-	-	+	-	+	-
222642	**66008**	**TSPO2**	**ALS2CR3**	**7.214**	**-**	**-**	**-**	**-**	**-**	**+**	**-**
1193	66008	CLIC2	ALS2CR3	7.214	-	-	-	-	-	+	-
27102	66008	EIF2AK1	ALS2CR3	7.214	-	-	-	-	-	+	-
2035	66008	EPB41	ALS2CR3	11.027	-	-	-	+	-	+	-
2038	66008	EPB42	ALS2CR3	11.027	-	-	-	+	-	+	-
51327	66008	ERAF	ALS2CR3	7.214	-	-	-	-	-	+	-
114625	66008	ERMAP	ALS2CR3	11.004	-	-	-	+	-	+	-
25793	66008	FBXO7	ALS2CR3	7.214	-	-	-	-	-	+	-
2235	66008	FECH	ALS2CR3	7.214	-	-	-	-	-	+	-
2993	66008	GYPA	ALS2CR3	11.027	-	-	-	+	-	+	-
2995	66008	GYPC	ALS2CR3	7.214	-	-	-	-	-	+	-
2996	66008	GYPE	ALS2CR3	7.214	-	-	-	-	-	+	-
3005	66008	H1F0	ALS2CR3	7.214	-	-	-	-	-	+	-
3049	66008	HBQ1	ALS2CR3	7.214	-	-	-	-	-	+	-
3145	66008	HMBS	ALS2CR3	7.214	-	-	-	-	-	+	-
4354	66008	MPP1	ALS2CR3	7.214	-	-	-	-	-	+	-
23762	66008	OSBP2	ALS2CR3	7.214	-	-	-	-	-	+	-
5498	66008	PPOX	ALS2CR3	7.214	-	-	-	-	-	+	-
5886	66008	RAD23A	ALS2CR3	7.214	-	-	-	-	-	+	-
57610	66008	RANBP10	ALS2CR3	7.214	-	-	-	-	-	+	-
6005	66008	RHAG	ALS2CR3	7.214	-	-	-	-	-	+	-
6006	66008	RHCE	ALS2CR3	7.214	-	-	-	-	-	+	-
6007	66008	RHD	ALS2CR3	7.214	-	-	-	-	-	+	-
6583	66008	SLC22A4	ALS2CR3	7.214	-	-	-	-	-	+	-
6521	66008	SLC4A1	ALS2CR3	7.214	-	-	-	-	-	+	-
10098	66008	TM4SF9	ALS2CR3	7.214	-	-	-	-	-	+	-

10107	66008	TRIM10	ALS2CR3	7.021	-	-	-	+	+	+	-
23039	66008	XPO7	ALS2CR3	9.626	-	-	-	+	-	+	-
220972	286	March8	ANK1	7.214	-	-	-	-	-	+	-
210	286	ALAD	ANK1	7.214	-	-	-	-	-	+	-
212	286	ALAS2	ANK1	7.214	-	-	-	-	-	+	-
222642	**286**	**TSPO2**	**ANK1**	**7.214**	**-**	**-**	**-**	**-**	**-**	**+**	**-**
2035	286	EPB41	ANK1	12.483	-	-	-	+	+	+	-
2038	286	EPB42	ANK1	12.47	-	-	-	+	-	+	-
114625	286	ERMAP	ANK1	7.214	-	-	-	-	-	+	-
25793	286	FBXO7	ANK1	7.214	-	-	-	-	-	+	-
2235	286	FECH	ANK1	7.214	-	-	-	-	-	+	-
23762	286	OSBP2	ANK1	7.214	-	-	-	-	-	+	-
10098	286	TM4SF9	ANK1	7.214	-	-	-	-	-	+	-
23039	286	XPO7	ANK1	7.214	-	-	-	-	-	+	-
220972	665	March8	BNIP3L	7.214	-	-	-	-	-	+	-
212	665	ALAS2	BNIP3L	8.057	-	-	-	+	-	+	-
66008	665	ALS2CR3	BNIP3L	7.214	-	-	-	-	-	+	-
222642	665	**TSPO2**	BNIP3L	7.214	-	-	-	-	-	+	-
27102	665	EIF2AK1	BNIP3L	7.214	-	-	-	-	-	+	-
2035	665	EPB41	BNIP3L	7.214	-	-	-	-	-	+	-
2038	665	EPB42	BNIP3L	7.214	-	-	-	-	-	+	-
114625	665	ERMAP	BNIP3L	7.214	-	-	-	-	-	+	-
25793	665	FBXO7	BNIP3L	7.214	-	-	-	-	-	+	-
2235	665	FECH	BNIP3L	8.057	-	-	-	+	-	+	-
2993	665	GYPA	BNIP3L	7.214	-	-	-	-	-	+	-
2996	665	GYPE	BNIP3L	7.214	-	-	-	-	-	+	-
3145	665	HMBS	BNIP3L	7.214	-	-	-	-	-	+	-
4354	665	MPP1	BNIP3L	7.214	-	-	-	-	-	+	-
4778	665	NFE2	BNIP3L	7.214	-	-	-	-	-	+	-
23762	665	OSBP2	BNIP3L	7.214	-	-	-	-	-	+	-
5498	665	PPOX	BNIP3L	8.057	-	-	-	+	-	+	-
5886	665	RAD23A	BNIP3L	7.214	-	-	-	-	-	+	-
6005	665	RHAG	BNIP3L	7.214	-	-	-	-	-	+	-
6006	665	RHCE	BNIP3L	7.214	-	-	-	-	-	+	-
6007	665	RHD	BNIP3L	7.214	-	-	-	-	-	+	-
6583	665	SLC22A4	BNIP3L	8.057	-	-	-	+	-	+	-
6521	665	SLC4A1	BNIP3L	7.214	-	-	-	-	-	+	-
23039	665	XPO7	BNIP3L	7.214	-	-	-	-	-	+	-
220972	682	March8	BSG	7.214	-	-	-	-	-	+	-
212	682	ALAS2	BSG	7.549	-	-	-	-	+	+	-
222642	**682**	**TSPO2**	**BSG**	**7.214**	**-**	**-**	**-**	**-**	**-**	**+**	**-**
1193	682	CLIC2	BSG	8.256	-	-	-	+	-	+	-
2035	682	EPB41	BSG	9.626	-	-	-	+	-	+	-
2038	682	EPB42	BSG	7.257	-	-	-	-	+	+	-
2235	682	FECH	BSG	7.214	-	-	-	-	-	+	-
2993	682	GYPA	BSG	9.626	-	-	-	+	-	+	-
3005	682	H1F0	BSG	7.226	-	-	-	-	+	+	-
4354	682	MPP1	BSG	8.268	-	-	-	+	+	+	-
23762	682	OSBP2	BSG	7.214	-	-	-	-	-	+	-
5886	682	RAD23A	BSG	7.549	-	-	-	-	+	+	-

6005	682	RHAG	BSG	9.626	-	-	-	+	-	+	-
6006	682	RHCE	BSG	9.626	-	-	-	+	-	+	-
6007	682	RHD	BSG	7.214	-	-	-	-	-	+	-
6521	682	SLC4A1	BSG	7.549	-	-	-	-	+	+	-
6708	682	SPTA1	BSG	9.626	-	-	-	+	-	+	-
23039	682	XPO7	BSG	7.549	-	-	-	-	+	+	-
220972	222642	March8	**TSPO2**	7.214	-	-	-	-	-	+	-
210	222642	ALAD	**TSPO2**	7.214	-	-	-	-	-	+	-
212	222642	ALAS2	**TSPO2**	7.214	-	-	-	-	-	+	-
1193	222642	CLIC2	**TSPO2**	7.214	-	-	-	-	-	+	-
2035	**222642**	**EPB41**	**TSPO2**	**7.214**	**-**	**-**	**-**	**-**	**-**	**+**	**-**
2038	**222642**	**EPB42**	**TSPO2**	**7.214**	**-**	**-**	**-**	**-**	**-**	**+**	**-**
114625	**222642**	**ERMAP**	**TSPO2**	**7.214**	**-**	**-**	**-**	**-**	**-**	**+**	**-**
10098	222642	TM4SF9	**TSPO2**	7.214	-	-	-	-	-	+	-
10107	222642	TRIM10	**TSPO2**	7.214	-	-	-	-	-	+	-
220972	760	March8	CA2	7.214	-	-	-	-	-	+	-
210	760	ALAD	CA2	12.322	-	-	-	+	-	+	-
212	760	ALAS2	CA2	7.214	-	-	-	-	-	+	-
66008	760	ALS2CR3	CA2	9.626	-	-	-	+	-	+	-
286	760	ANK1	CA2	7.214	-	-	-	-	-	+	-
222642	760	**TSPO2**	CA2	7.214	-	-	-	-	-	+	-
2035	760	EPB41	CA2	9.626	-	-	-	+	-	+	-
2038	760	EPB42	CA2	7.214	-	-	-	-	-	+	-
51327	760	ERAF	CA2	7.214	-	-	-	-	-	+	-
114625	760	ERMAP	CA2	7.214	-	-	-	-	-	+	-
25793	760	FBXO7	CA2	7.214	-	-	-	-	-	+	-
2235	760	FECH	CA2	12.322	-	-	-	+	-	+	-
2993	760	GYPA	CA2	7.214	-	-	-	-	-	+	-
2995	760	GYPC	CA2	7.214	-	-	-	-	-	+	-
2996	760	GYPE	CA2	7.214	-	-	-	-	-	+	-
3005	760	H1F0	CA2	7.214	-	-	-	-	-	+	-
3049	760	HBQ1	CA2	7.214	-	-	-	-	-	+	-
3145	760	HMBS	CA2	7.214	-	-	-	-	-	+	-
4354	760	MPP1	CA2	7.214	-	-	-	-	-	+	-
23762	760	OSBP2	CA2	7.214	-	-	-	-	-	+	-
5498	760	PPOX	CA2	7.214	-	-	-	-	-	+	-
57610	760	RANBP10	CA2	7.214	-	-	-	-	-	+	-
6005	760	RHAG	CA2	7.214	-	-	-	-	-	+	-
6006	760	RHCE	CA2	7.214	-	-	-	-	-	+	-
6007	760	RHD	CA2	7.214	-	-	-	-	-	+	-
6583	760	SLC22A4	CA2	7.214	-	-	-	-	-	+	-
6521	760	SLC4A1	CA2	7.214	-	-	-	-	-	+	-
6708	760	SPTA1	CA2	7.214	-	-	-	-	-	+	-
10098	760	TM4SF9	CA2	7.214	-	-	-	-	-	+	-
10107	760	TRIM10	CA2	9.633	-	-	-	+	-	+	-
23039	760	XPO7	CA2	9.626	-	-	-	+	-	+	-
222642	63893	**TSPO2**	E2-230K	7.214	-	-	-	-	-	+	-
2035	63893	EPB41	E2-230K	7.214	-	-	-	-	-	+	-
25793	63893	FBXO7	E2-230K	9.656	-	-	-	+	-	+	-
23039	63893	XPO7	E2-230K	7.214	-	-	-	-	-	+	-

220972	27102	March8	EIF2AK1	7.214	-	-	-	-	-	+	-
212	27102	ALAS2	EIF2AK1	8.057	-	-	-	+	-	+	-
222642	27102	**TSPO2**	EIF2AK1	7.214	-	-	-	-	-	+	-
2038	27102	EPB42	EIF2AK1	7.214	-	-	-	-	-	+	-
25793	27102	FBXO7	EIF2AK1	7.214	-	-	-	-	-	+	-
2235	27102	FECH	EIF2AK1	7.214	-	-	-	-	-	+	-
23039	27102	XPO7	EIF2AK1	7.214	-	-	-	-	-	+	-
1193	2035	CLIC2	EPB41	9.626	-	-	-	+	-	+	-
114625	2035	ERMAP	EPB41	7.214	-	-	-	-	-	+	-
10098	2035	TM4SF9	EPB41	7.214	-	-	-	-	-	+	-
10107	2035	TRIM10	EPB41	8.057	-	-	-	+	-	+	-
1193	2038	CLIC2	EPB42	7.214	-	-	-	-	-	+	-
2035	2038	EPB41	EPB42	13.189	-	-	-	+	+	+	-
114625	2038	ERMAP	EPB42	7.214	-	-	-	-	-	+	-
10098	2038	TM4SF9	EPB42	7.214	-	-	-	-	-	+	-
10107	2038	TRIM10	EPB42	7.214	-	-	-	-	-	+	-
220972	51327	March8	ERAF	7.214	-	-	-	-	-	+	-
210	51327	ALAD	ERAF	7.214	-	-	-	-	-	+	-
212	51327	ALAS2	ERAF	7.214	-	-	-	-	-	+	-
286	51327	ANK1	ERAF	7.214	-	-	-	-	-	+	-
222642	**51327**	**TSPO2**	**ERAF**	**7.214**	**-**	**-**	**-**	**-**	**-**	**+**	**-**
2038	51327	EPB42	ERAF	7.214	-	-	-	-	-	+	-
114625	51327	ERMAP	ERAF	7.214	-	-	-	-	-	+	-
25793	51327	FBXO7	ERAF	7.214	-	-	-	-	-	+	-
2235	51327	FECH	ERAF	7.214	-	-	-	-	-	+	-
2993	51327	GYPA	ERAF	7.214	-	-	-	-	-	+	-
2995	51327	GYPC	ERAF	7.214	-	-	-	-	-	+	-
2996	51327	GYPE	ERAF	7.214	-	-	-	-	-	+	-
3005	51327	H1F0	ERAF	7.214	-	-	-	-	-	+	-
3049	51327	HBQ1	ERAF	16.739	-	-	-	+	-	+	-
3145	51327	HMBS	ERAF	7.214	-	-	-	-	-	+	-
51312	51327	MSCP	ERAF	7.214	-	-	-	-	-	+	-
23762	51327	OSBP2	ERAF	7.214	-	-	-	-	-	+	-
10107	51327	TRIM10	ERAF	13.45	-	-	-	+	-	+	-
10098	114625	TM4SF9	ERMAP	7.214	-	-	-	-	-	+	-
220972	25793	March8	FBXO7	11.027	-	-	-	+	-	+	-
210	25793	ALAD	FBXO7	7.214	-	-	-	-	-	+	-
212	25793	ALAS2	FBXO7	7.214	-	-	-	-	-	+	-
222642	25793	**TSPO2**	FBXO7	7.214	-	-	-	-	-	+	-
2038	25793	EPB42	FBXO7	7.214	-	-	-	-	-	+	-
114625	25793	ERMAP	FBXO7	7.214	-	-	-	-	-	+	-
2235	25793	FECH	FBXO7	7.214	-	-	-	-	-	+	-
23762	25793	OSBP2	FBXO7	7.214	-	-	-	-	-	+	-
10107	25793	TRIM10	FBXO7	9.7	-	-	-	+	+	+	-
23039	25793	XPO7	FBXO7	7.214	-	-	-	-	-	+	-
220972	2235	March8	FECH	7.214	-	-	-	-	-	+	-
210	2235	ALAD	FECH	16.739	-	-	-	+	-	+	-
212	2235	ALAS2	FECH	16.739	-	-	-	+	-	+	-
222642	2235	**TSPO2**	FECH	7.214	-	-	-	-	-	+	-
1193	2235	CLIC2	FECH	7.214	-	-	-	-	-	+	-

2035	2235	EPB41	FECH	7.214	-	-	-	-	-	+	-
2038	2235	EPB42	FECH	7.214	-	-	-	-	-	+	-
114625	2235	ERMAP	FECH	7.214	-	-	-	-	-	+	-
10098	2235	TM4SF9	FECH	7.214	-	-	-	-	-	+	-
10107	2235	TRIM10	FECH	7.214	-	-	-	-	-	+	-
220972	2993	March8	GYPA	7.214	-	-	-	-	-	+	-
210	2993	ALAD	GYPA	7.214	-	-	-	-	-	+	-
212	2993	ALAS2	GYPA	7.214	-	-	-	-	-	+	-
286	2993	ANK1	GYPA	11.027	-	-	-	+	-	+	-
222642	**2993**	**TSPO2**	**GYPA**	**7.214**	**-**	**-**	**-**	**-**	**-**	**+**	**-**
1193	2993	CLIC2	GYPA	11.027	-	-	-	+	-	+	-
27102	2993	EIF2AK1	GYPA	7.214	-	-	-	-	-	+	-
2035	2993	EPB41	GYPA	11.027	-	-	-	+	-	+	-
2038	2993	EPB42	GYPA	11.027	-	-	-	+	-	+	-
114625	2993	ERMAP	GYPA	7.214	-	-	-	-	-	+	-
25793	2993	FBXO7	GYPA	7.214	-	-	-	-	-	+	-
2235	2993	FECH	GYPA	7.214	-	-	-	-	-	+	-
23762	2993	OSBP2	GYPA	7.214	-	-	-	-	-	+	-
10098	2993	TM4SF9	GYPA	7.214	-	-	-	-	-	+	-
10107	2993	TRIM10	GYPA	7.214	-	-	-	-	-	+	-
23039	2993	XPO7	GYPA	7.214	-	-	-	-	-	+	-
220972	2995	March8	GYPC	7.214	-	-	-	-	-	+	-
210	2995	ALAD	GYPC	7.214	-	-	-	-	-	+	-
212	2995	ALAS2	GYPC	7.214	-	-	-	-	-	+	-
286	2995	ANK1	GYPC	7.214	-	-	-	-	-	+	-
222642	**2995**	**TSPO2**	**GYPC**	**7.214**	**-**	**-**	**-**	**-**	**-**	**+**	**-**
2038	2995	EPB42	GYPC	7.214	-	-	-	-	-	+	-
114625	2995	ERMAP	GYPC	7.214	-	-	-	-	-	+	-
25793	2995	FBXO7	GYPC	7.214	-	-	-	-	-	+	-
2235	2995	FECH	GYPC	7.214	-	-	-	-	-	+	-
2993	2995	GYPA	GYPC	7.214	-	-	-	-	-	+	-
23039	2995	XPO7	GYPC	7.214	-	-	-	-	-	+	-
220972	2996	March8	GYPE	7.214	-	-	-	-	-	+	-
210	2996	ALAD	GYPE	7.214	-	-	-	-	-	+	-
212	2996	ALAS2	GYPE	7.214	-	-	-	-	-	+	-
286	2996	ANK1	GYPE	7.214	-	-	-	-	-	+	-
222642	2996	**TSPO2**	GYPE	7.214	-	-	-	-	-	+	-
1193	2996	CLIC2	GYPE	7.214	-	-	-	-	-	+	-
2035	2996	EPB41	GYPE	7.214	-	-	-	-	-	+	-
2038	2996	EPB42	GYPE	7.214	-	-	-	-	-	+	-
114625	2996	ERMAP	GYPE	7.214	-	-	-	-	-	+	-
25793	2996	FBXO7	GYPE	7.214	-	-	-	-	-	+	-
2235	2996	FECH	GYPE	7.214	-	-	-	-	-	+	-
2993	2996	GYPA	GYPE	7.214	-	-	-	-	-	+	-
2995	2996	GYPC	GYPE	9.626	-	-	-	+	-	+	-
23762	2996	OSBP2	GYPE	7.214	-	-	-	-	-	+	-
10098	2996	TM4SF9	GYPE	7.214	-	-	-	-	-	+	-
10107	2996	TRIM10	GYPE	7.214	-	-	-	-	-	+	-
23039	2996	XPO7	GYPE	7.214	-	-	-	-	-	+	-
220972	3005	March8	H1F0	7.214	-	-	-	-	-	+	-

212	3005	ALAS2	H1F0	7.214	-	-	-	-	-	+	-
286	3005	ANK1	H1F0	7.272	-	-	-	-	+	+	-
222642	3005	**TSPO2**	H1F0	7.214	-	-	-	-	-	+	-
2035	3005	EPB41	H1F0	7.272	-	-	-	-	+	+	-
2038	3005	EPB42	H1F0	7.214	-	-	-	-	-	+	-
114625	3005	ERMAP	H1F0	7.214	-	-	-	-	-	+	-
25793	3005	FBXO7	H1F0	7.214	-	-	-	-	-	+	-
2235	3005	FECH	H1F0	7.214	-	-	-	-	-	+	-
2993	3005	GYPA	H1F0	7.214	-	-	-	-	-	+	-
2995	3005	GYPC	H1F0	7.214	-	-	-	-	-	+	-
2996	3005	GYPE	H1F0	7.214	-	-	-	-	-	+	-
23762	3005	OSBP2	H1F0	7.214	-	-	-	-	-	+	-
10098	3005	TM4SF9	H1F0	7.214	-	-	-	-	-	+	-
23039	3005	XPO7	H1F0	7.214	-	-	-	-	-	+	-
220972	3049	March8	HBQ1	7.214	-	-	-	-	-	+	-
210	3049	ALAD	HBQ1	7.214	-	-	-	-	-	+	-
212	3049	ALAS2	HBQ1	7.214	-	-	-	-	-	+	-
286	3049	ANK1	HBQ1	7.214	-	-	-	-	-	+	-
222642	**3049**	**TSPO2**	**HBQ1**	**7.214**	**-**	**-**	**-**	**-**	**-**	**+**	**-**
27102	3049	EIF2AK1	HBQ1	13.45	-	-	-	+	-	+	-
2035	3049	EPB41	HBQ1	7.214	-	-	-	-	-	+	-
2038	3049	EPB42	HBQ1	7.214	-	-	-	-	-	+	-
114625	3049	ERMAP	HBQ1	7.214	-	-	-	-	-	+	-
25793	3049	FBXO7	HBQ1	7.214	-	-	-	-	-	+	-
2235	3049	FECH	HBQ1	7.214	-	-	-	-	-	+	-
2993	3049	GYPA	HBQ1	7.214	-	-	-	-	-	+	-
2995	3049	GYPC	HBQ1	7.214	-	-	-	-	-	+	-
2996	3049	GYPE	HBQ1	7.214	-	-	-	-	-	+	-
3005	3049	H1F0	HBQ1	7.214	-	-	-	-	-	+	-
23762	3049	OSBP2	HBQ1	8.057	-	-	-	+	-	+	-
10098	3049	TM4SF9	HBQ1	7.214	-	-	-	-	-	+	-
23039	3049	XPO7	HBQ1	8.057	-	-	-	+	-	+	-
220972	8364	March8	HIST1H4C	7.214	-	-	-	-	-	+	-
212	8364	ALAS2	HIST1H4C	7.214	-	-	-	-	-	+	-
66008	8364	ALS2CR3	HIST1H4C	7.83	-	-	-	-	+	+	-
286	8364	ANK1	HIST1H4C	7.214	-	-	-	-	-	+	-
665	8364	BNIP3L	HIST1H4C	7.214	-	-	-	-	-	+	-
222642	8364	**TSPO2**	HIST1H4C	7.214	-	-	-	-	-	+	-
760	8364	CA2	HIST1H4C	7.214	-	-	-	-	-	+	-
2035	8364	EPB41	HIST1H4C	7.214	-	-	-	-	-	+	-
2038	8364	EPB42	HIST1H4C	7.214	-	-	-	-	-	+	-
114625	8364	ERMAP	HIST1H4C	7.214	-	-	-	-	-	+	-
25793	8364	FBXO7	HIST1H4C	7.214	-	-	-	-	-	+	-
2235	8364	FECH	HIST1H4C	7.214	-	-	-	-	-	+	-
2993	8364	GYPA	HIST1H4C	7.214	-	-	-	-	-	+	-
2996	8364	GYPE	HIST1H4C	7.214	-	-	-	-	-	+	-
3005	8364	H1F0	HIST1H4C	7.214	-	-	-	-	-	+	-
3049	8364	HBQ1	HIST1H4C	7.214	-	-	-	-	-	+	-
3145	8364	HMBS	HIST1H4C	7.214	-	-	-	-	-	+	-
23762	8364	OSBP2	HIST1H4C	7.214	-	-	-	-	-	+	-

5498	8364	PPOX	HIST1H4C	7.214	-	-	-	-	-	+	-
5886	8364	RAD23A	HIST1H4C	7.214	-	-	-	-	-	+	-
57610	8364	RANBP10	HIST1H4C	7.214	-	-	-	-	-	+	-
6005	8364	RHAG	HIST1H4C	7.214	-	-	-	-	-	+	-
6006	8364	RHCE	HIST1H4C	7.214	-	-	-	-	-	+	-
6007	8364	RHD	HIST1H4C	7.214	-	-	-	-	-	+	-
6583	8364	SLC22A4	HIST1H4C	7.214	-	-	-	-	-	+	-
6521	8364	SLC4A1	HIST1H4C	7.214	-	-	-	-	-	+	-
6708	8364	SPTA1	HIST1H4C	7.83	-	-	-	-	+	+	-
10098	8364	TM4SF9	HIST1H4C	7.214	-	-	-	-	-	+	-
23039	8364	XPO7	HIST1H4C	7.214	-	-	-	-	-	+	-
220972	3145	March8	HMBS	7.214	-	-	-	-	-	+	-
210	3145	ALAD	HMBS	21.324	-	-	-	+	-	+	+
212	3145	ALAS2	HMBS	16.739	-	-	-	+	-	+	-
286	3145	ANK1	HMBS	7.214	-	-	-	-	-	+	-
222642	3145	**TSPO2**	HMBS	7.214	-	-	-	-	-	+	-
1193	3145	CLIC2	HMBS	7.214	-	-	-	-	-	+	-
27102	3145	EIF2AK1	HMBS	9.626	-	-	-	+	-	+	-
2035	3145	EPB41	HMBS	7.214	-	-	-	-	-	+	-
2038	3145	EPB42	HMBS	7.214	-	-	-	-	-	+	-
114625	3145	ERMAP	HMBS	7.214	-	-	-	-	-	+	-
25793	3145	FBXO7	HMBS	7.214	-	-	-	-	-	+	-
2235	3145	FECH	HMBS	16.739	-	-	-	+	-	+	-
2993	3145	GYPA	HMBS	7.214	-	-	-	-	-	+	-
2995	3145	GYPC	HMBS	7.214	-	-	-	-	-	+	-
2996	3145	GYPE	HMBS	7.214	-	-	-	-	-	+	-
3005	3145	H1F0	HMBS	7.214	-	-	-	-	-	+	-
3049	3145	HBQ1	HMBS	7.214	-	-	-	-	-	+	-
23762	3145	OSBP2	HMBS	7.214	-	-	-	-	-	+	-
10098	3145	TM4SF9	HMBS	7.214	-	-	-	-	-	+	-
23039	3145	XPO7	HMBS	7.214	-	-	-	-	-	+	-
220972	4354	March8	MPP1	7.214	-	-	-	-	-	+	-
212	4354	ALAS2	MPP1	7.549	-	-	-	-	+	+	-
286	4354	ANK1	MPP1	10.345	-	-	-	+	+	+	-
222642	4354	**TSPO2**	MPP1	7.214	-	-	-	-	-	+	-
1193	4354	CLIC2	MPP1	9.656	-	-	-	+	-	+	-
27102	4354	EIF2AK1	MPP1	7.214	-	-	-	-	-	+	-
2035	4354	EPB41	MPP1	8.59	-	-	-	+	+	+	-
2038	4354	EPB42	MPP1	7.549	-	-	-	-	+	+	-
114625	4354	ERMAP	MPP1	7.214	-	-	-	-	-	+	-
25793	4354	FBXO7	MPP1	7.214	-	-	-	-	-	+	-
2235	4354	FECH	MPP1	7.214	-	-	-	-	-	+	-
2993	4354	GYPA	MPP1	11.027	-	-	-	+	-	+	-
2995	4354	GYPC	MPP1	9.626	-	-	-	+	-	+	-
2996	4354	GYPE	MPP1	8.256	-	-	-	+	-	+	-
3049	4354	HBQ1	MPP1	7.214	-	-	-	-	-	+	-
3145	4354	HMBS	MPP1	7.214	-	-	-	-	-	+	-
23039	4354	XPO7	MPP1	7.549	-	-	-	-	+	+	-
220972	51312	March8	MSCP	7.214	-	-	-	-	-	+	-
212	51312	ALAS2	MSCP	9.626	-	-	-	+	-	+	-

222642	51312	TSPO2	MSCP	7.214	-	-	-	-	-	+	-
2035	51312	EPB41	MSCP	10.951	-	-	-	+	-	+	-
2038	51312	EPB42	MSCP	7.214	-	-	-	-	-	+	-
25793	51312	FBXO7	MSCP	7.214	-	-	-	-	-	+	-
2235	51312	FECH	MSCP	12.322	-	-	-	+	-	+	-
2993	51312	GYPA	MSCP	7.214	-	-	-	-	-	+	-
2995	51312	GYPC	MSCP	7.214	-	-	-	-	-	+	-
3049	51312	HBQ1	MSCP	8.256	-	-	-	+	-	+	-
3145	51312	HMBS	MSCP	7.214	-	-	-	-	-	+	-
4354	51312	MPP1	MSCP	7.214	-	-	-	-	-	+	-
23039	51312	XPO7	MSCP	10.149	-	-	-	+	-	+	-
220972	4778	March8	NFE2	7.214	-	-	-	-	-	+	-
212	4778	ALAS2	NFE2	7.214	-	-	-	-	-	+	-
222642	**4778**	**TSPO2**	**NFE2**	**7.214**	**-**	**-**	**-**	**-**	**-**	**+**	**-**
2035	4778	EPB41	NFE2	13.45	-	-	-	+	-	+	-
2038	4778	EPB42	NFE2	7.549	-	-	-	-	+	+	-
114625	4778	ERMAP	NFE2	7.214	-	-	-	-	-	+	-
2235	4778	FECH	NFE2	7.214	-	-	-	-	-	+	-
2993	4778	GYPA	NFE2	7.214	-	-	-	-	-	+	-
3145	4778	HMBS	NFE2	7.214	-	-	-	-	-	+	-
4354	4778	MPP1	NFE2	7.933	-	-	-	-	+	+	-
23039	4778	XPO7	NFE2	7.214	-	-	-	-	-	+	-
220972	23762	March8	OSBP2	7.214	-	-	-	-	-	+	-
212	23762	ALAS2	OSBP2	7.214	-	-	-	-	-	+	-
222642	**23762**	**TSPO2**	**OSBP2**	**7.214**	**-**	**-**	**-**	**-**	**-**	**+**	**-**
1193	23762	CLIC2	OSBP2	7.214	-	-	-	-	-	+	-
2035	23762	EPB41	OSBP2	7.549	-	-	-	-	+	+	-
2038	23762	EPB42	OSBP2	7.933	-	-	-	-	+	+	-
114625	23762	ERMAP	OSBP2	8.057	-	-	-	+	-	+	-
2235	23762	FECH	OSBP2	7.214	-	-	-	-	-	+	-
10098	23762	TM4SF9	OSBP2	7.214	-	-	-	-	-	+	-
10107	23762	TRIM10	OSBP2	7.549	-	-	-	-	+	+	-
23039	23762	XPO7	OSBP2	8.057	-	-	-	+	-	+	-
220972	5498	March8	PPOX	7.214	-	-	-	-	-	+	-
210	5498	ALAD	PPOX	16.739	-	-	-	+	-	+	-
212	5498	ALAS2	PPOX	16.739	-	-	-	+	-	+	-
286	5498	ANK1	PPOX	7.214	-	-	-	-	-	+	-
222642	5498	**TSPO2**	PPOX	7.214	-	-	-	-	-	+	-
1193	5498	CLIC2	PPOX	7.214	-	-	-	-	-	+	-
27102	5498	EIF2AK1	PPOX	7.214	-	-	-	-	-	+	-
2035	5498	EPB41	PPOX	7.214	-	-	-	-	-	+	-
2038	5498	EPB42	PPOX	7.214	-	-	-	-	-	+	-
51327	5498	ERAF	PPOX	7.214	-	-	-	-	-	+	-
114625	5498	ERMAP	PPOX	7.214	-	-	-	-	-	+	-
25793	5498	FBXO7	PPOX	7.214	-	-	-	-	-	+	-
2235	5498	FECH	PPOX	21.275	-	-	-	+	-	+	+
2993	5498	GYPA	PPOX	7.214	-	-	-	-	-	+	-
2995	5498	GYPC	PPOX	7.214	-	-	-	-	-	+	-
2996	5498	GYPE	PPOX	7.214	-	-	-	-	-	+	-
3005	5498	H1F0	PPOX	7.214	-	-	-	-	-	+	-

3049	5498	HBQ1	PPOX	7.214	-	-	-	-	-	+	-
3145	5498	HMBS	PPOX	16.739	-	-	-	+	-	+	-
4354	5498	MPP1	PPOX	7.214	-	-	-	-	-	+	-
51312	5498	MSCP	PPOX	9.626	-	-	-	+	-	+	-
4778	5498	NFE2	PPOX	7.214	-	-	-	-	-	+	-
23762	5498	OSBP2	PPOX	7.214	-	-	-	-	-	+	-
10098	5498	TM4SF9	PPOX	7.214	-	-	-	-	-	+	-
23039	5498	XPO7	PPOX	7.214	-	-	-	-	-	+	-
220972	5886	March8	RAD23A	7.214	-	-	-	-	-	+	-
212	5886	ALAS2	RAD23A	7.214	-	-	-	-	-	+	-
286	5886	ANK1	RAD23A	7.549	-	-	-	-	+	+	-
222642	5886	**TSPO2**	RAD23A	7.214	-	-	-	-	-	+	-
27102	5886	EIF2AK1	RAD23A	7.214	-	-	-	-	-	+	-
2035	5886	EPB41	RAD23A	7.549	-	-	-	-	+	+	-
2038	5886	EPB42	RAD23A	7.214	-	-	-	-	-	+	-
25793	5886	FBXO7	RAD23A	7.933	-	-	-	-	+	+	-
2235	5886	FECH	RAD23A	7.214	-	-	-	-	-	+	-
2993	5886	GYPA	RAD23A	7.214	-	-	-	-	-	+	-
3145	5886	HMBS	RAD23A	7.214	-	-	-	-	-	+	-
23762	5886	OSBP2	RAD23A	7.83	-	-	-	-	+	+	-
5498	5886	PPOX	RAD23A	7.214	-	-	-	-	-	+	-
57610	5886	RANBP10	RAD23A	7.214	-	-	-	-	-	+	-
23039	5886	XPO7	RAD23A	7.214	-	-	-	-	-	+	-
220972	57610	March8	RANBP10	7.214	-	-	-	-	-	+	-
212	57610	ALAS2	RANBP10	7.214	-	-	-	-	-	+	-
286	57610	ANK1	RANBP10	7.214	-	-	-	-	-	+	-
222642	57610	**TSPO2**	RANBP10	7.214	-	-	-	-	-	+	-
2035	57610	EPB41	RANBP10	7.214	-	-	-	-	-	+	-
2038	57610	EPB42	RANBP10	7.214	-	-	-	-	-	+	-
114625	57610	ERMAP	RANBP10	7.214	-	-	-	-	-	+	-
25793	57610	FBXO7	RANBP10	7.214	-	-	-	-	-	+	-
2235	57610	FECH	RANBP10	7.214	-	-	-	-	-	+	-
2993	57610	GYPA	RANBP10	7.214	-	-	-	-	-	+	-
2996	57610	GYPE	RANBP10	7.214	-	-	-	-	-	+	-
3005	57610	H1F0	RANBP10	7.214	-	-	-	-	-	+	-
3049	57610	HBQ1	RANBP10	7.214	-	-	-	-	-	+	-
3145	57610	HMBS	RANBP10	7.214	-	-	-	-	-	+	-
51312	57610	MSCP	RANBP10	10.149	-	-	-	+	-	+	-
23762	57610	OSBP2	RANBP10	7.214	-	-	-	-	-	+	-
5498	57610	PPOX	RANBP10	7.214	-	-	-	-	-	+	-
10098	57610	TM4SF9	RANBP10	7.214	-	-	-	-	-	+	-
23039	57610	XPO7	RANBP10	14.496	-	-	-	+	-	+	-
220972	6005	March8	RHAG	7.214	-	-	-	-	-	+	-
210	6005	ALAD	RHAG	7.214	-	-	-	-	-	+	-
212	6005	ALAS2	RHAG	7.214	-	-	-	-	-	+	-
286	6005	ANK1	RHAG	7.214	-	-	-	-	-	+	-
222642	6005	**TSPO2**	RHAG	7.214	-	-	-	-	-	+	-
1193	6005	CLIC2	RHAG	8.256	-	-	-	+	-	+	-
27102	6005	EIF2AK1	RHAG	7.214	-	-	-	-	-	+	-
2035	6005	EPB41	RHAG	14.82	-	-	-	+	-	+	-

2038	6005	EPB42	RHAG	7.214	-	-	-	-	-	+	-
51327	6005	ERAF	RHAG	7.214	-	-	-	-	-	+	-
114625	6005	ERMAP	RHAG	7.214	-	-	-	-	-	+	-
25793	6005	FBXO7	RHAG	7.214	-	-	-	-	-	+	-
2235	6005	FECH	RHAG	7.214	-	-	-	-	-	+	-
2993	6005	GYPA	RHAG	9.626	-	-	-	+	-	+	-
2995	6005	GYPC	RHAG	9.626	-	-	-	+	-	+	-
2996	6005	GYPE	RHAG	9.626	-	-	-	+	-	+	-
3005	6005	H1F0	RHAG	7.214	-	-	-	-	-	+	-
3049	6005	HBQ1	RHAG	8.057	-	-	-	+	-	+	-
3145	6005	HMBS	RHAG	7.214	-	-	-	-	-	+	-
4354	6005	MPP1	RHAG	9.626	-	-	-	+	-	+	-
51312	6005	MSCP	RHAG	8.057	-	-	-	+	-	+	-
4778	6005	NFE2	RHAG	13.45	-	-	-	+	-	+	-
23762	6005	OSBP2	RHAG	8.057	-	-	-	+	-	+	-
5498	6005	PPOX	RHAG	7.214	-	-	-	-	-	+	-
5886	6005	RAD23A	RHAG	7.214	-	-	-	-	-	+	-
57610	6005	RANBP10	RHAG	7.214	-	-	-	-	-	+	-
10098	6005	TM4SF9	RHAG	7.214	-	-	-	-	-	+	-
23039	6005	XPO7	RHAG	8.057	-	-	-	+	-	+	-
220972	6006	March8	RHCE	7.214	-	-	-	-	-	+	-
210	6006	ALAD	RHCE	7.214	-	-	-	-	-	+	-
212	6006	ALAS2	RHCE	7.214	-	-	-	-	-	+	-
286	6006	ANK1	RHCE	7.214	-	-	-	-	-	+	-
222642	6006	**TSPO2**	RHCE	7.214	-	-	-	-	-	+	-
1193	6006	CLIC2	RHCE	9.626	-	-	-	+	-	+	-
27102	6006	EIF2AK1	RHCE	7.214	-	-	-	-	-	+	-
2035	6006	EPB41	RHCE	9.626	-	-	-	+	-	+	-
2038	6006	EPB42	RHCE	7.214	-	-	-	-	-	+	-
51327	6006	ERAF	RHCE	7.214	-	-	-	-	-	+	-
114625	6006	ERMAP	RHCE	7.214	-	-	-	-	-	+	-
25793	6006	FBXO7	RHCE	7.214	-	-	-	-	-	+	-
2235	6006	FECH	RHCE	7.214	-	-	-	-	-	+	-
2993	6006	GYPA	RHCE	9.626	-	-	-	+	-	+	-
2995	6006	GYPC	RHCE	9.626	-	-	-	+	-	+	-
2996	6006	GYPE	RHCE	9.626	-	-	-	+	-	+	-
3005	6006	H1F0	RHCE	7.214	-	-	-	-	-	+	-
3049	6006	HBQ1	RHCE	9.626	-	-	-	+	-	+	-
3145	6006	HMBS	RHCE	7.214	-	-	-	-	-	+	-
4354	6006	MPP1	RHCE	9.626	-	-	-	+	-	+	-
51312	6006	MSCP	RHCE	9.626	-	-	-	+	-	+	-
4778	6006	NFE2	RHCE	7.214	-	-	-	-	-	+	-
23762	6006	OSBP2	RHCE	8.057	-	-	-	+	-	+	-
5498	6006	PPOX	RHCE	7.214	-	-	-	-	-	+	-
5886	6006	RAD23A	RHCE	7.214	-	-	-	-	-	+	-
57610	6006	RANBP10	RHCE	7.214	-	-	-	-	-	+	-
6005	6006	RHAG	RHCE	15.785	-	-	-	+	-	+	-
10098	6006	TM4SF9	RHCE	7.214	-	-	-	-	-	+	-
10107	6006	TRIM10	RHCE	7.214	-	-	-	-	-	+	-
23039	6006	XPO7	RHCE	8.057	-	-	-	+	-	+	-

220972	6007	March8	RHD	7.214	-	-	-	-	-	+	-
210	6007	ALAD	RHD	7.214	-	-	-	-	-	+	-
212	6007	ALAS2	RHD	7.214	-	-	-	-	-	+	-
286	6007	ANK1	RHD	7.214	-	-	-	-	-	+	-
222642	**6007**	**TSPO2**	**RHD**	**7.214**	**-**	**-**	**-**	**-**	**-**	**+**	**-**
1193	6007	CLIC2	RHD	7.214	-	-	-	-	-	+	-
27102	6007	EIF2AK1	RHD	7.214	-	-	-	-	-	+	-
2035	6007	EPB41	RHD	7.214	-	-	-	-	-	+	-
2038	6007	EPB42	RHD	7.214	-	-	-	-	-	+	-
51327	6007	ERAF	RHD	7.214	-	-	-	-	-	+	-
114625	6007	ERMAP	RHD	7.214	-	-	-	-	-	+	-
25793	6007	FBXO7	RHD	7.214	-	-	-	-	-	+	-
2235	6007	FECH	RHD	7.214	-	-	-	-	-	+	-
2993	6007	GYPA	RHD	7.214	-	-	-	-	-	+	-
2995	6007	GYPC	RHD	9.626	-	-	-	+	-	+	-
2996	6007	GYPE	RHD	9.626	-	-	-	+	-	+	-
3005	6007	H1F0	RHD	7.214	-	-	-	-	-	+	-
3049	6007	HBQ1	RHD	7.214	-	-	-	-	-	+	-
3145	6007	HMBS	RHD	7.214	-	-	-	-	-	+	-
4354	6007	MPP1	RHD	9.626	-	-	-	+	-	+	-
4778	6007	NFE2	RHD	7.214	-	-	-	-	-	+	-
23762	6007	OSBP2	RHD	7.214	-	-	-	-	-	+	-
5498	6007	PPOX	RHD	7.214	-	-	-	-	-	+	-
5886	6007	RAD23A	RHD	7.214	-	-	-	-	-	+	-
57610	6007	RANBP10	RHD	7.214	-	-	-	-	-	+	-
6005	6007	RHAG	RHD	9.626	-	-	-	+	-	+	-
6006	6007	RHCE	RHD	9.626	-	-	-	+	-	+	-
10098	6007	TM4SF9	RHD	7.214	-	-	-	-	-	+	-
23039	6007	XPO7	RHD	7.214	-	-	-	-	-	+	-
220972	8991	March8	SELENBP1	7.214	-	-	-	-	-	+	-
210	8991	ALAD	SELENBP1	7.214	-	-	-	-	-	+	-
212	8991	ALAS2	SELENBP1	7.214	-	-	-	-	-	+	-
66008	8991	ALS2CR3	SELENBP1	7.214	-	-	-	-	-	+	-
286	8991	ANK1	SELENBP1	7.214	-	-	-	-	-	+	-
665	8991	BNIP3L	SELENBP1	7.214	-	-	-	-	-	+	-
682	8991	BSG	SELENBP1	7.214	-	-	-	-	-	+	-
222642	8991	**TSPO2**	SELENBP1	7.214	-	-	-	-	-	+	-
760	8991	CA2	SELENBP1	7.214	-	-	-	-	-	+	-
1193	8991	CLIC2	SELENBP1	7.214	-	-	-	-	-	+	-
27102	8991	EIF2AK1	SELENBP1	7.214	-	-	-	-	-	+	-
2035	8991	EPB41	SELENBP1	7.214	-	-	-	-	-	+	-
2038	8991	EPB42	SELENBP1	7.214	-	-	-	-	-	+	-
51327	8991	ERAF	SELENBP1	7.214	-	-	-	-	-	+	-
114625	8991	ERMAP	SELENBP1	7.214	-	-	-	-	-	+	-
25793	8991	FBXO7	SELENBP1	7.214	-	-	-	-	-	+	-
2235	8991	FECH	SELENBP1	7.214	-	-	-	-	-	+	-
2993	8991	GYPA	SELENBP1	7.214	-	-	-	-	-	+	-
2995	8991	GYPC	SELENBP1	7.214	-	-	-	-	-	+	-
2996	8991	GYPE	SELENBP1	7.214	-	-	-	-	-	+	-
3005	8991	H1F0	SELENBP1	7.214	-	-	-	-	-	+	-

3049	8991	HBQ1	SELENBP1	7.214	-	-	-	-	-	+	-
8364	8991	HIST1H4C	SELENBP1	7.214	-	-	-	-	-	+	-
3145	8991	HMBS	SELENBP1	7.214	-	-	-	-	-	+	-
4354	8991	MPP1	SELENBP1	7.214	-	-	-	-	-	+	-
51312	8991	MSCP	SELENBP1	7.214	-	-	-	-	-	+	-
4778	8991	NFE2	SELENBP1	7.214	-	-	-	-	-	+	-
23762	8991	OSBP2	SELENBP1	7.214	-	-	-	-	-	+	-
5498	8991	PPOX	SELENBP1	7.214	-	-	-	-	-	+	-
5886	8991	RAD23A	SELENBP1	7.214	-	-	-	-	-	+	-
57610	8991	RANBP10	SELENBP1	7.214	-	-	-	-	-	+	-
6005	8991	RHAG	SELENBP1	7.214	-	-	-	-	-	+	-
6006	8991	RHCE	SELENBP1	7.214	-	-	-	-	-	+	-
6007	8991	RHD	SELENBP1	7.214	-	-	-	-	-	+	-
6583	8991	SLC22A4	SELENBP1	7.214	-	-	-	-	-	+	-
6521	8991	SLC4A1	SELENBP1	7.214	-	-	-	-	-	+	-
6708	8991	SPTA1	SELENBP1	7.214	-	-	-	-	-	+	-
10098	8991	TM4SF9	SELENBP1	7.214	-	-	-	-	-	+	-
10107	8991	TRIM10	SELENBP1	7.214	-	-	-	-	-	+	-
23039	8991	XPO7	SELENBP1	7.214	-	-	-	-	-	+	-
220972	6583	March8	SLC22A4	7.214	-	-	-	-	-	+	-
210	6583	ALAD	SLC22A4	7.214	-	-	-	-	-	+	-
212	6583	ALAS2	SLC22A4	8.057	-	-	-	+	-	+	-
286	6583	ANK1	SLC22A4	7.214	-	-	-	-	-	+	-
222642	**6583**	**TSPO2**	**SLC22A4**	**7.214**	**-**	**-**	**-**	**-**	**-**	**+**	**-**
1193	6583	CLIC2	SLC22A4	11.027	-	-	-	+	-	+	-
2035	6583	EPB41	SLC22A4	7.214	-	-	-	-	-	+	-
2038	6583	EPB42	SLC22A4	7.214	-	-	-	-	-	+	-
51327	6583	ERAF	SLC22A4	7.214	-	-	-	-	-	+	-
114625	6583	ERMAP	SLC22A4	7.214	-	-	-	-	-	+	-
25793	6583	FBXO7	SLC22A4	7.214	-	-	-	-	-	+	-
2235	6583	FECH	SLC22A4	8.057	-	-	-	+	-	+	-
2993	6583	GYPA	SLC22A4	7.214	-	-	-	-	-	+	-
2995	6583	GYPC	SLC22A4	7.214	-	-	-	-	-	+	-
2996	6583	GYPE	SLC22A4	7.214	-	-	-	-	-	+	-
3005	6583	H1F0	SLC22A4	7.214	-	-	-	-	-	+	-
3049	6583	HBQ1	SLC22A4	8.057	-	-	-	+	-	+	-
3145	6583	HMBS	SLC22A4	7.214	-	-	-	-	-	+	-
4354	6583	MPP1	SLC22A4	7.214	-	-	-	-	-	+	-
51312	6583	MSCP	SLC22A4	8.057	-	-	-	+	-	+	-
4778	6583	NFE2	SLC22A4	7.214	-	-	-	-	-	+	-
23762	6583	OSBP2	SLC22A4	8.057	-	-	-	+	-	+	-
5498	6583	PPOX	SLC22A4	8.057	-	-	-	+	-	+	-
57610	6583	RANBP10	SLC22A4	7.214	-	-	-	-	-	+	-
6005	6583	RHAG	SLC22A4	8.057	-	-	-	+	-	+	-
6006	6583	RHCE	SLC22A4	8.057	-	-	-	+	-	+	-
6007	6583	RHD	SLC22A4	7.214	-	-	-	-	-	+	-
6521	6583	SLC4A1	SLC22A4	8.057	-	-	-	+	-	+	-
10098	6583	TM4SF9	SLC22A4	7.214	-	-	-	-	-	+	-
23039	6583	XPO7	SLC22A4	8.057	-	-	-	+	-	+	-
220972	6521	March8	SLC4A1	7.214	-	-	-	-	-	+	-

210	6521	ALAD	SLC4A1	7.214	-	-	-	-	-	+	-
212	6521	ALAS2	SLC4A1	7.214	-	-	-	-	-	+	-
286	6521	ANK1	SLC4A1	7.214	-	-	-	-	-	+	-
222642	**6521**	**TSPO2**	**SLC4A1**	**7.214**	**-**	**-**	**-**	**-**	**-**	**+**	**-**
27102	6521	EIF2AK1	SLC4A1	7.214	-	-	-	-	-	+	-
2035	6521	EPB41	SLC4A1	7.549	-	-	-	-	+	+	-
2038	6521	EPB42	SLC4A1	7.214	-	-	-	-	-	+	-
51327	6521	ERAF	SLC4A1	7.214	-	-	-	-	-	+	-
114625	6521	ERMAP	SLC4A1	7.214	-	-	-	-	-	+	-
25793	6521	FBXO7	SLC4A1	7.214	-	-	-	-	-	+	-
2235	6521	FECH	SLC4A1	7.214	-	-	-	-	-	+	-
2993	6521	GYPA	SLC4A1	11.004	-	-	-	+	-	+	-
2995	6521	GYPC	SLC4A1	9.626	-	-	-	+	-	+	-
2996	6521	GYPE	SLC4A1	9.626	-	-	-	+	-	+	-
3005	6521	H1F0	SLC4A1	7.214	-	-	-	-	-	+	-
3049	6521	HBQ1	SLC4A1	8.057	-	-	-	+	-	+	-
3145	6521	HMBS	SLC4A1	7.214	-	-	-	-	-	+	-
4354	6521	MPP1	SLC4A1	9.626	-	-	-	+	-	+	-
51312	6521	MSCP	SLC4A1	8.057	-	-	-	+	-	+	-
4778	6521	NFE2	SLC4A1	7.214	-	-	-	-	-	+	-
23762	6521	OSBP2	SLC4A1	8.057	-	-	-	+	-	+	-
5498	6521	PPOX	SLC4A1	7.549	-	-	-	-	+	+	-
5886	6521	RAD23A	SLC4A1	7.214	-	-	-	-	-	+	-
57610	6521	RANBP10	SLC4A1	7.214	-	-	-	-	-	+	-
6005	6521	RHAG	SLC4A1	9.626	-	-	-	+	-	+	-
6006	6521	RHCE	SLC4A1	9.626	-	-	-	+	-	+	-
6007	6521	RHD	SLC4A1	9.626	-	-	-	+	-	+	-
10098	6521	TM4SF9	SLC4A1	7.214	-	-	-	-	-	+	-
10107	6521	TRIM10	SLC4A1	7.214	-	-	-	-	-	+	-
23039	6521	XPO7	SLC4A1	8.057	-	-	-	+	-	+	-
220972	6708	March8	SPTA1	7.214	-	-	-	-	-	+	-
210	6708	ALAD	SPTA1	7.214	-	-	-	-	-	+	-
212	6708	ALAS2	SPTA1	7.214	-	-	-	-	-	+	-
66008	6708	ALS2CR3	SPTA1	7.549	-	-	-	-	+	+	-
286	6708	ANK1	SPTA1	12.47	-	-	-	+	-	+	-
665	6708	BNIP3L	SPTA1	7.214	-	-	-	-	-	+	-
222642	**6708**	**TSPO2**	**SPTA1**	**7.214**	**-**	**-**	**-**	**-**	**-**	**+**	**-**
1193	6708	CLIC2	SPTA1	11.027	-	-	-	+	-	+	-
27102	6708	EIF2AK1	SPTA1	7.214	-	-	-	-	-	+	-
2035	6708	EPB41	SPTA1	16.739	-	-	-	+	-	+	-
2038	6708	EPB42	SPTA1	14.82	-	-	-	+	-	+	-
51327	6708	ERAF	SPTA1	7.214	-	-	-	-	-	+	-
114625	6708	ERMAP	SPTA1	7.214	-	-	-	-	-	+	-
25793	6708	FBXO7	SPTA1	7.214	-	-	-	-	-	+	-
2235	6708	FECH	SPTA1	7.214	-	-	-	-	-	+	-
2993	6708	GYPA	SPTA1	11.027	-	-	-	+	-	+	-
2995	6708	GYPC	SPTA1	7.214	-	-	-	-	-	+	-
2996	6708	GYPE	SPTA1	7.214	-	-	-	-	-	+	-
3005	6708	H1F0	SPTA1	7.214	-	-	-	-	-	+	-
3049	6708	HBQ1	SPTA1	7.214	-	-	-	-	-	+	-

3145	6708	HMBS	SPTA1	7.214	-	-	-	-	-	+	-
4354	6708	MPP1	SPTA1	11.027	-	-	-	+	-	+	-
51312	6708	MSCP	SPTA1	7.214	-	-	-	-	-	+	-
4778	6708	NFE2	SPTA1	7.214	-	-	-	-	-	+	-
23762	6708	OSBP2	SPTA1	7.214	-	-	-	-	-	+	-
5498	6708	PPOX	SPTA1	7.214	-	-	-	-	-	+	-
5886	6708	RAD23A	SPTA1	7.214	-	-	-	-	-	+	-
57610	6708	RANBP10	SPTA1	7.214	-	-	-	-	-	+	-
6005	6708	RHAG	SPTA1	9.626	-	-	-	+	-	+	-
6006	6708	RHCE	SPTA1	9.626	-	-	-	+	-	+	-
6007	6708	RHD	SPTA1	7.214	-	-	-	-	-	+	-
6583	6708	SLC22A4	SPTA1	7.214	-	-	-	-	-	+	-
6521	6708	SLC4A1	SPTA1	7.214	-	-	-	-	-	+	-
10098	6708	TM4SF9	SPTA1	7.214	-	-	-	-	-	+	-
10107	6708	TRIM10	SPTA1	7.214	-	-	-	-	-	+	-
23039	6708	XPO7	SPTA1	7.257	-	-	-	-	+	+	-
220972	9911	March8	TMCC2	7.214	-	-	-	-	-	+	-
212	9911	ALAS2	TMCC2	7.214	-	-	-	-	-	+	-
66008	9911	ALS2CR3	TMCC2	7.214	-	-	-	-	-	+	-
286	9911	ANK1	TMCC2	7.214	-	-	-	-	-	+	-
665	9911	BNIP3L	TMCC2	7.214	-	-	-	-	-	+	-
222642	9911	**TSPO2**	TMCC2	7.214	-	-	-	-	-	+	-
760	9911	CA2	TMCC2	7.214	-	-	-	-	-	+	-
63893	9911	E2-230K	TMCC2	7.214	-	-	-	-	-	+	-
2035	9911	EPB41	TMCC2	7.214	-	-	-	-	-	+	-
2038	9911	EPB42	TMCC2	7.214	-	-	-	-	-	+	-
114625	9911	ERMAP	TMCC2	7.214	-	-	-	-	-	+	-
25793	9911	FBXO7	TMCC2	7.214	-	-	-	-	-	+	-
2235	9911	FECH	TMCC2	7.214	-	-	-	-	-	+	-
2993	9911	GYPA	TMCC2	7.214	-	-	-	-	-	+	-
2996	9911	GYPE	TMCC2	7.214	-	-	-	-	-	+	-
3005	9911	H1F0	TMCC2	7.214	-	-	-	-	-	+	-
8364	9911	HIST1H4C	TMCC2	7.214	-	-	-	-	-	+	-
3145	9911	HMBS	TMCC2	7.214	-	-	-	-	-	+	-
23762	9911	OSBP2	TMCC2	7.214	-	-	-	-	-	+	-
5498	9911	PPOX	TMCC2	7.214	-	-	-	-	-	+	-
57610	9911	RANBP10	TMCC2	7.214	-	-	-	-	-	+	-
6005	9911	RHAG	TMCC2	7.214	-	-	-	-	-	+	-
6006	9911	RHCE	TMCC2	7.214	-	-	-	-	-	+	-
6007	9911	RHD	TMCC2	7.214	-	-	-	-	-	+	-
8991	9911	SELENBP1	TMCC2	7.214	-	-	-	-	-	+	-
6583	9911	SLC22A4	TMCC2	7.214	-	-	-	-	-	+	-
6521	9911	SLC4A1	TMCC2	7.214	-	-	-	-	-	+	-
6708	9911	SPTA1	TMCC2	7.214	-	-	-	-	-	+	-
10098	9911	TM4SF9	TMCC2	7.214	-	-	-	-	-	+	-
23039	9911	XPO7	TMCC2	7.214	-	-	-	-	-	+	-
220972	23039	March8	XPO7	7.214	-	-	-	-	-	+	-
210	23039	ALAD	XPO7	7.214	-	-	-	-	-	+	-
212	23039	ALAS2	XPO7	7.214	-	-	-	-	-	+	-
222642	**23039**	**TSPO2**	**XPO7**	**7.214**	**-**	**-**	**-**	**-**	**-**	**+**	**-**

1193	23039	CLIC2	XPO7	7.214	-	-	-	-	-	+	-
2035	23039	EPB41	XPO7	11.746	-	-	-	+	+	+	-
2038	23039	EPB42	XPO7	7.214	-	-	-	-	-	+	-
114625	23039	ERMAP	XPO7	7.214	-	-	-	-	-	+	-
2235	23039	FECH	XPO7	7.214	-	-	-	-	-	+	-
10098	23039	TM4SF9	XPO7	7.214	-	-	-	-	-	+	-
10107	23039	TRIM10	XPO7	8.057	-	-	-	+	-	+	-

Note: PPI, protein-protein interaction; GI, Genetic interactions ; DDI, Domain-domain interaction.

Figure S1. Alignment of the deduced amino acid sequence of TSPO and TSPO-like genes. The TSPO-like domains are indicated as follows: TM1-TM5, transmembrane domains. The red letters with black background indicate the potential PK11195 binding sites: R24, E29, L31, L37, P40, S41, W42, W107, and W161; E29, R32, K39, and V154 (in human) indicate the essential amino acid sites responsible for the benzodiazepine binding. E, R, and K indicate the essential amino acid sites responsible for the benzodiazepine binding. Upside-down arrowheads indicate the cholesterol binding sites, and conserved motif, L/I.Y….R, is indicated. The two conserved intron positions are indicated. Residues that show 100 percent conservation, 80 percent, or greater conservation, and 60 percent or greater conservation are highlighted in black, dark grey, and light grey, respectively. The top two conservation levels are also distinguished by either upper or lower case characters or numbers on the consensus line below the alignment. Similar amino acids are defined by Higgins (20) as being grouped in the same class as identity. Dashes indicate gaps introduced to facilitate alignment.

Figure S2. Different patterns of the transcription of *Tspo1*/*Tspo2*. ***A.*** Gene networks of human *Tspo1* and *Tspo2*. The gene networks were constructed through the IntNetDB server (http://hanlab.genetics.ac.cn/ IntNetDB.htm) using human *TSPO2* (Gene ID: 222642) and *TSPO1* (Gene ID: 706) as probes. ***B.*** Alignment of the N-terminal peptide sequence of the avian TSPO2 with the predicted amino acid sequences of TSPOs from avians, mouse, and human. Previously designated p18 was shown to be the avian *Tspo2*, which may be involved in a nuclear membrane complex and cholesterol synthesis (12). Erythrocyte-related genes in the TSPO2 network: aminolevulinate delta-synthase 2 (ALAS2); erythrocyte membrane protein band4.1 (EPB41); basigin (Ok blood group) (EPB41); tripartite motif-containing 10 (TRIM10); nuclear factor (erythroid-derived 2) (NFE2); glycophorin C (GYPC); hemoglobin theta 1 (HBQ1); Rh-associated glycoprotein (RHAG); erythroblast membrane-associated protein (ERMAP); erythrocyte membrane protein band 4.2 (EPB42); protoporphyrinogen oxidase (PPOX); erythroid associated factor (ERAF); hydroxymethylbilane synthase (HMBS); spectrin alpha erythrocytic 1 (SPTA1); solute carrier family 4 anion exchanger member 1 (SLC4A1); ferrochelatase (protoporphyria) (FECH); aminolevulinate delta-dehydratase (ALAD); Rh blood group CcEe antigens (RHCE); Rh blood group D antigen (RHD); ankyrin 1 erythrocytic (ANK1); glycophorin A (GYPA); F-box protein 7 (FBXO7); eukaryotic translation initiation factor 2-alpha kinase 1 (EIF2AK1); carbonic anhydrase II (CA2); solute carrier family 22 (SLC22A4); exportin 7 (XPO7); oxysterol binding protein 2 (OSBP2).

Figure S3. Colocalization of TSPO2 and TSPO1 and localization of TSPO2 onto ER (highlight from figure 2). ***A,*** Colocalization of mTSPO2 and mTSPO1 in NIH 3T3 cells. ***B,*** localization of mTSPO2 onto ER in NIH 3T3 cells. ***C,*** Colocalization of mTSPO2 and mTSPO1 in MA-10 cells. ***D,*** localization of mTSPO2 onto ER in MA-10 cells. ***E,*** Colocalization of hTSPO2 and mTSPO1 in HeLa cells. ***F,*** localization of hTSPO2 onto ER in HeLa cells. Green: TSPO2; Red, TSPO1; ER, Blue; Colocalization pixels, white.

Figure S4. Localization of TSPO2 onto ER. ***A,*** Colocalization of mTSPO2 and ER marker (RdFP2-with ER-retention tail) in NIH 3T3 cells. ***B,*** colocalization of mTSPO2 and ER marker (RdFP2-with ER-retention tail) in MA-10 cells; ***C,*** Colocalization of hTSPO2 and ER marker (RdFP-with ER-retention tail) in HeLa cells. Green, GFP-TSPO2; Red, RFP-ER marker; Green and red, merged image and Hoechst 33342 nuclear staining with blue.

Figure S5. Subcellular localization of mouse TSPO2 in cultured mouse and human cells. GFP-tagged mTSPO2 and hTPSO2 transfected into NIH 3T3 (***A-C***), MA-10 (***D-F***), HeLa (***G-I***) cells. The ER membrane was labeled with ER-tracker Blue-White DPX and then visualized by a multi-photon Zeiss 510 laser scanning microscope. ***A***, ***D***, ***G*** are GFP; ***B***, ***E***, ***H*** are ER-tracker Blue-White DPX; ***C***, ***F***, ***I*** are GFP and ER-tracker merged. Bars: 5 µm. *J, K and L*, Highlight of the localization of TSPO2 (green) on ER (grey) from NIH 3T3 (J), MA-10 (K) and HeLa (L) cells.

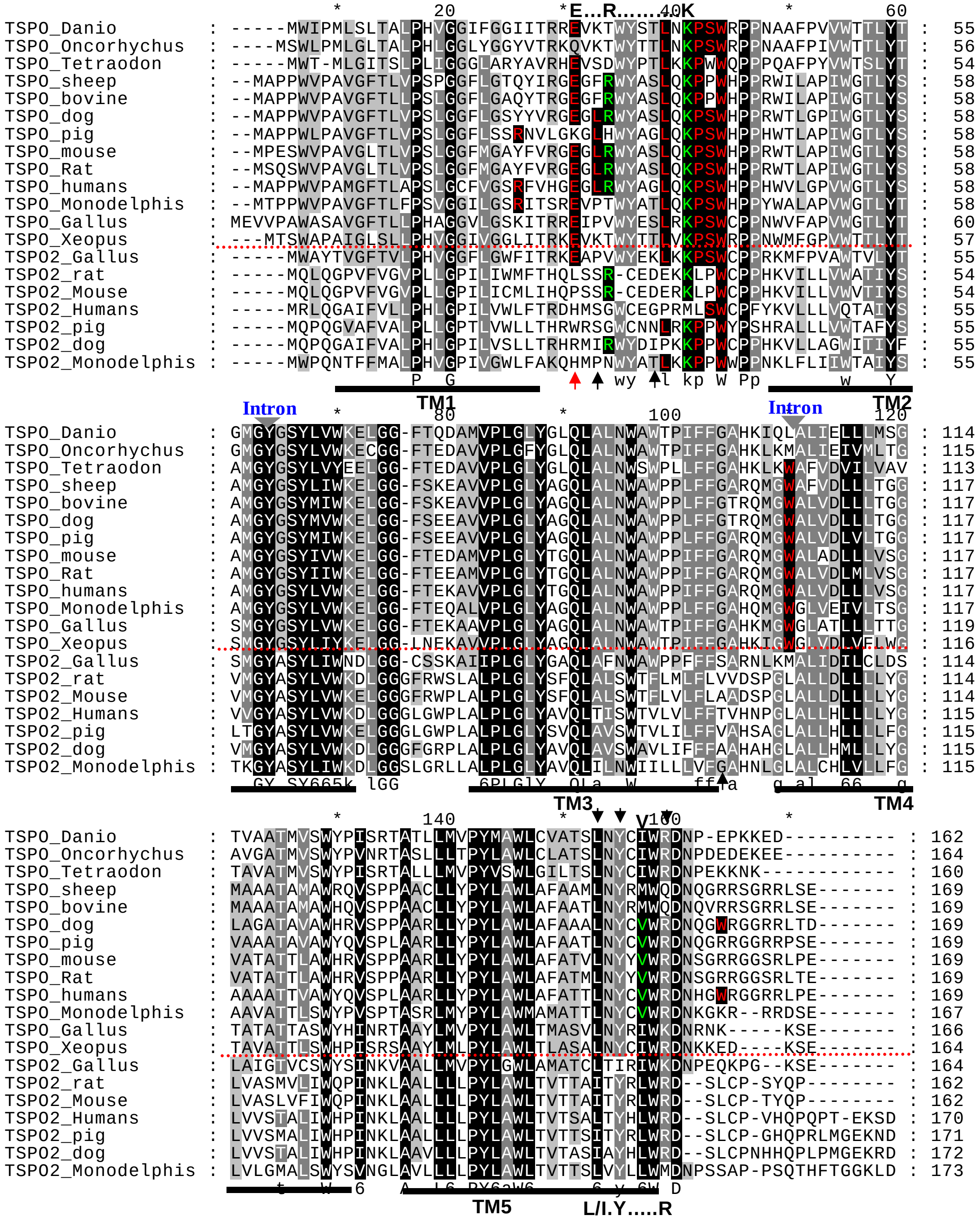
Figure S6. Schematic structure of human (***A***) and mouse (***B***) TSPO1/TSPO2 models. The primary sequence shown is that of human TSPO1 and TSPO2, and that of mouse TSPO and TSPO2 to illustrate the five transmembrane domains and cytoplasmic domains. The *lines* indicate the mitochondrial membrane. *c1* and *c2* refer to extramitochondrial cytoplasmic loops, *m1* and *m2* to intramitochondrial loops, n1 and n2, to intra-nuclear membrane loops, *Ct* and *Nt* to the carboxyl- and amino-terminal domains, respectively. The position of the unique sites under positive selection in the TSPO2 lineage are shown in red arrow. Dark arrowheads indicate potential important amino acid residues for binding benzodiazepine. Also noted as arrows are the conserved motif of L.Y….D, corresponding to the previous reported cholesterol recognition/interaction amino acid consensus (CRAC) domain (21). The open circles are the omitted amino acid positions. The snake-like diagram was constructed by using residue-based diagram editor RbDe (22).

Figure S7. NBD-cholesterol uptake assay (presenting the DIC images for the whole set shown in Fig. 3M to 3N). ***M,*** *S. cerevisiae* strains were induced with 2% galactose to overexpress mTSPO2 in the presence of NBD-cholesterol and under the aerobic conditions ($> O^2$; c and d). Vector alone cells were used as control (a and b). ***N,*** NBD-cholesterol uptake assay. *S. cerevisiae* strains were induced with 2% galactose to overexpress mTSPO2 in the presence of NBD-cholesterol and under the anaerobic conditions ($< O^2$; g and h). Vector alone was used as the control (e and f). Differential interference contrast (DIC) images of the cells were shown at the left (b, d, f, and h).

Figure S8. Expression profiling of *Tspo2* in 15 mouse and 7 human tissues using RT-PCR. Tspo2 was only detected weakly in E7, and strongly in the of E11, E15, and E17 stages. Among the 10 adult mouse and 7 human tissues tested, the only tissue where TSPO2 was expressed in both species was spleen. As controls, the mouse and human TSPO1, mouse tubulin, and human HPRT genes were detected in every tissue examined. ***A.*** *Tspo2* expression was detected in RT-PCR using gene-specific primers. ***B.*** *Tspo1* expression was detected in RT-PCR using gene-specific primers. ***C.*** As control is shown the results from a RT-PCR performed with the same cDNAs but with mouse tubulin-specific primers. The total RNAs from different tissues were from Mouse Total RNA Master Panel (Clontech, USA). Lane 1, brain; 2, E7; 3, E11; 4, E15; 5, E17; 6, eye;7, heart; 8, kidney; 9, liver; 10, lymph; 11, salivary gland; 12, spinal cord; 13, spleen; 14, stomach; 15, uterus. ***D.*** Expression profiling of hTSPO2 in thyroid tumor (lane 1) and normal thyroid (lane 2); lymphoma (lane 3) and normal lymphocytes (lane 4); fetal brain (lane 5); spleen (lane 6); and Jurkat cells (lane 7). hTSPO2 expression was detected in RT-PCR using gene-specific primers. As control is shown the results from a RT-PCR performed with the same cDNAs but with human TSPO1- and human HPRT-specific primers. The total RNAs from thyroid and lymphoma tissues were from Ambion and the total RNAs from human fetal brain and human spleen were from BioChain. The total RNA from jurkat cells were extracted using Trizon Reagent (Invitrogen) as described in materials and methods.

Figure S9. Effect of TSPO2 C-terminal CRAC-domain on intracellular cholesterol distribution. HeLa cells were transfected with plasmids containing mutant hTSPO2 with deletion of its C-terminal CRAC domain, wild-type hTSPO2, and pDsRed monomer C1 vector alone. The cells were then treated with NBD-cholesterol as described under Experimental Procedures. ***A-C***. Mutant DsRed-hTSPO2 with deletion of the CRAC domain; ***D-F***, Wild-type DsRed-hTSPO2; ***G-I***, pDsRed monomer C1 vector. ***A, D*** and ***G***. DsRed-fusion proteins (Red). ***B, E*** and ***H***. NBD-cholesterol (Green); ***C, F*** and ***I.*** Superimposed images with Hoechst 33342 (Nuclear staining; Blue). ***J-O***. Intensity surface plots of the images as shown in A-C and D-F. The non-evenly distributed cholesterol in HeLa cells transfected with the hTSPO2 CRAC mutant is highlighted in K.

Supplementary Figure 1.



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TSPO_Oncorhychus    : ----MSWLPMLGLTALPHLGGLYGGYVTRKQVKTWYTTLNKPSWRPPNAAFPIVWTTLYT :  56
TSPO_Tetraodon      : -----MWT-MLGITSLPLIGGGLARYAVRHEVSDWYPTLKKPWWQPPPQAFPYVWTSLYT :  54
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TSPO_dog            : --MAPPWVPAVGFTLVPSLGGFLGSYYVRGEGLRWYASLQKPSWHPPRWTLGPIWGTLYS :  58
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TSPO_mouse          : --MPESWVPAVGLTLVPSLGGFMGAYFVRGEGLRWYASLQKPSWHPPRWTLAPIWGTLYS :  58
TSPO_Rat            : --MSQSWVPAVGLTLVPSLGGFMGAYFVRGEGLRWYASLQKPSWHPPRWTLAPIWGTLYS :  58
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                                    TM1                                            TM2

                        Intron                                           Intron
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TSPO2_Humans        : VVGYASYLVWKDLGGGLGWPLALPLGLYAVQLTISWTVLVLFFTVHNPGLALLHLLLLYG : 115
TSPO2_pig           : LTGYASYLVWKELGGGLGWPLALPLGLYSVQLAVSWTVLILFFVAHSAGLALLHLLLLFG : 115
TSPO2_dog           : VMGYASYLVWKDLGGGFGRPLALPLGLYAVQLAVSWAVLIFFFAAHAHGLALLHMLLLYG : 115
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                                                 TM3                              TM4

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TSPO_bovine         : MAAATAMAWHQVSPPAACLLYPYLAWLAFAATLNYRMWQDNQVRRSGRRLSE------- : 169
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TSPO_pig            : VAAATAVAWYQVSPLAARLLYPYLAWLAFAATLNYCVWRDNQGRRGGRRPSE------- : 169
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TSPO_Xeopus         : TAVATTLSWHPISRSAAYLMLPYLAWLTLASALNYCIWRDNKKED----KSE------- : 164
TSPO2_Gallus        : LAIGTVCSWYSINKVAALLMVPYLGWLAMATCLTIRIWKDNPEQKPG--KSE------- : 164
TSPO2_rat           : LVASMVLIWQPINKLAALLLLPYLAWLTVTTAITYRLWRD--SLCP-SYQP-------- : 162
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TSPO2_Humans        : LVVSTALIWHPINKLAALLLLPYLAWLTVTSALTYHLWRD--SLCP-VHQPQPT-EKSD : 170
TSPO2_pig           : LVVSMALIWHPINKLAALLLLPYLAWLTVTTSITYRLWRD--SLCP-GHQPRLMGEKND : 171
TSPO2_dog           : LVVSTALIWHPINKLAAVLLLPYLAWLTVTASIAYHLWRD--SLCPNHHQPLPMGEKRD : 172
TSPO2_Monodelphis   : LVLGMALSWYSVNGLAVLLLLPYLAWLTVTTSLVYLLWMDNPSSAP-PSQTHFTGGKLD : 173
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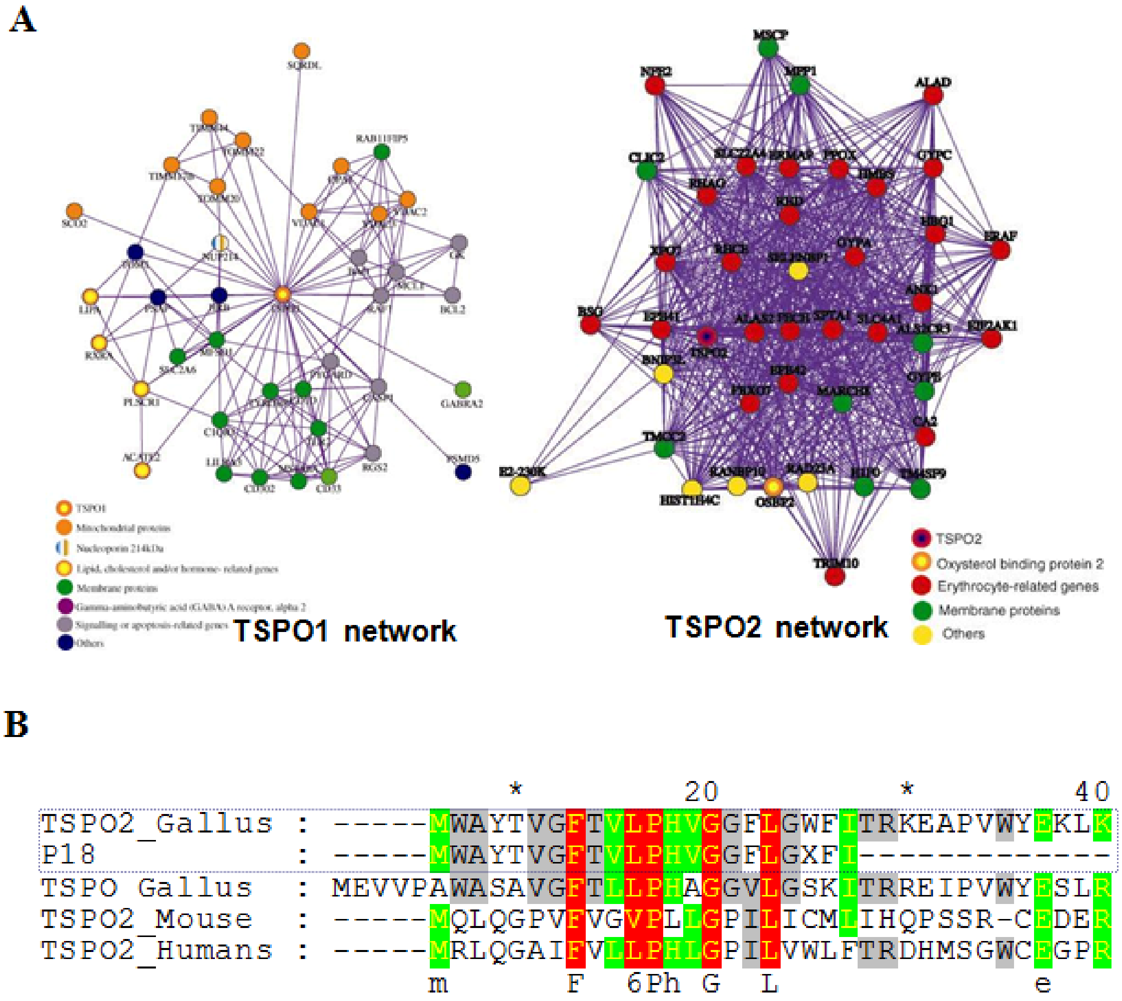
Supplementary Figure 2



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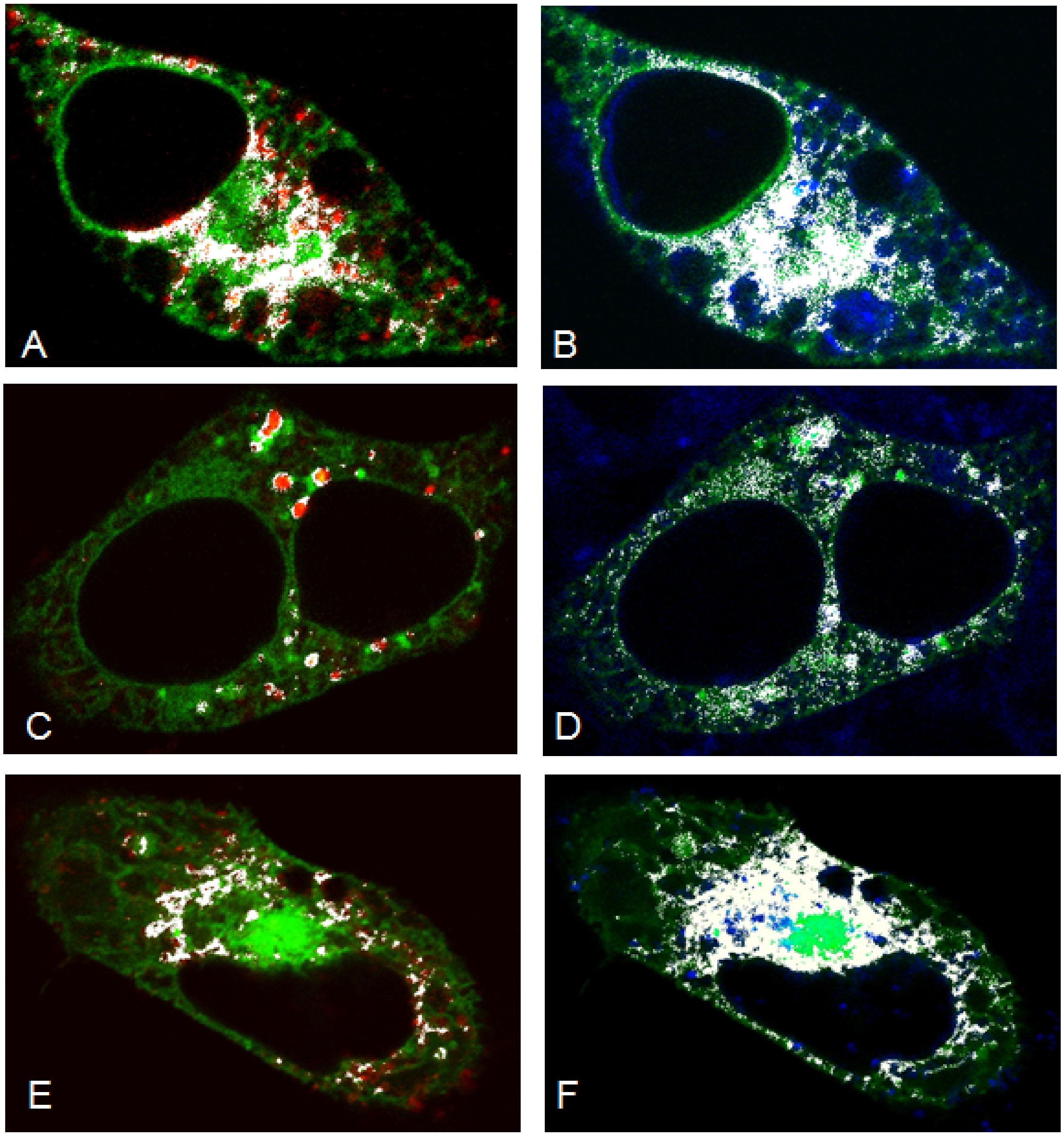
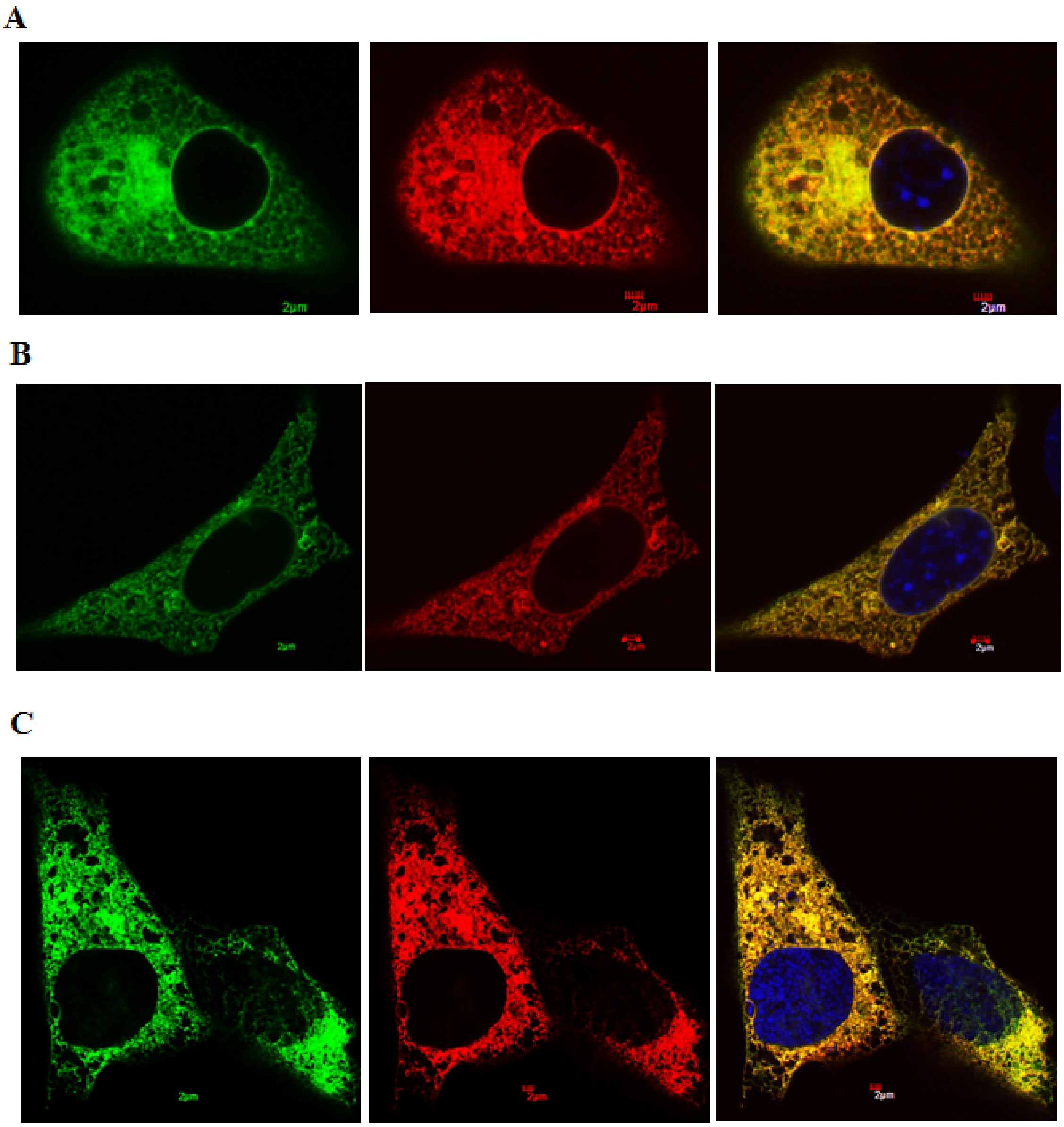
TSPO Gallus   : MEVVPAWASAVGFTLLPHAGGVLGSKITRREIPVWYESLR
TSPO2_Mouse   : -----MQLQGPVFVGVPLLGPILICMLIHQPSSR-CEDER
TSPO2_Humans  : -----MRLQGAIFVLLPHLGPILVWLFTRDHMSGWCEGPR
                     m      F  6Ph G  L              e
```

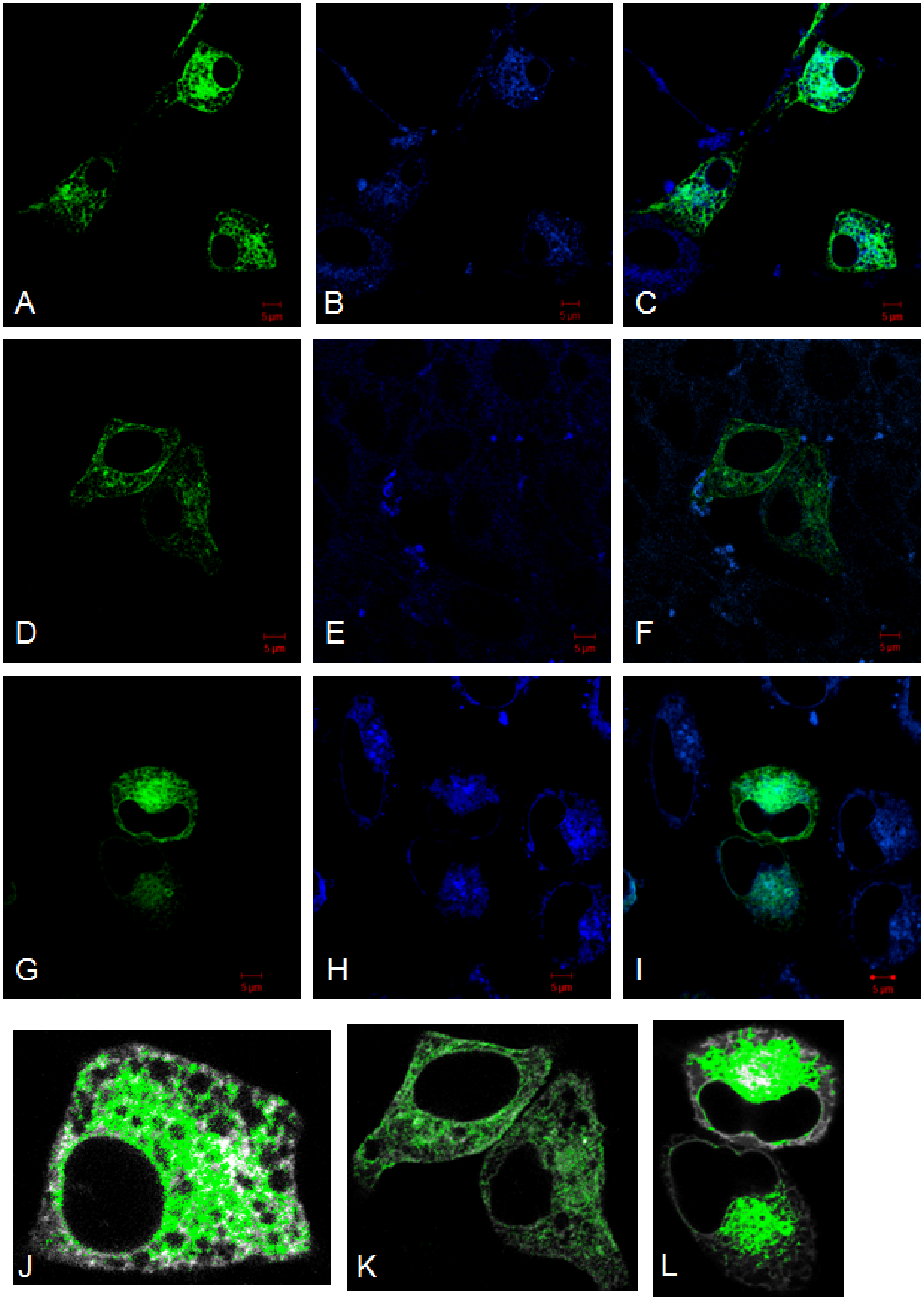
Supplementary Figure 3



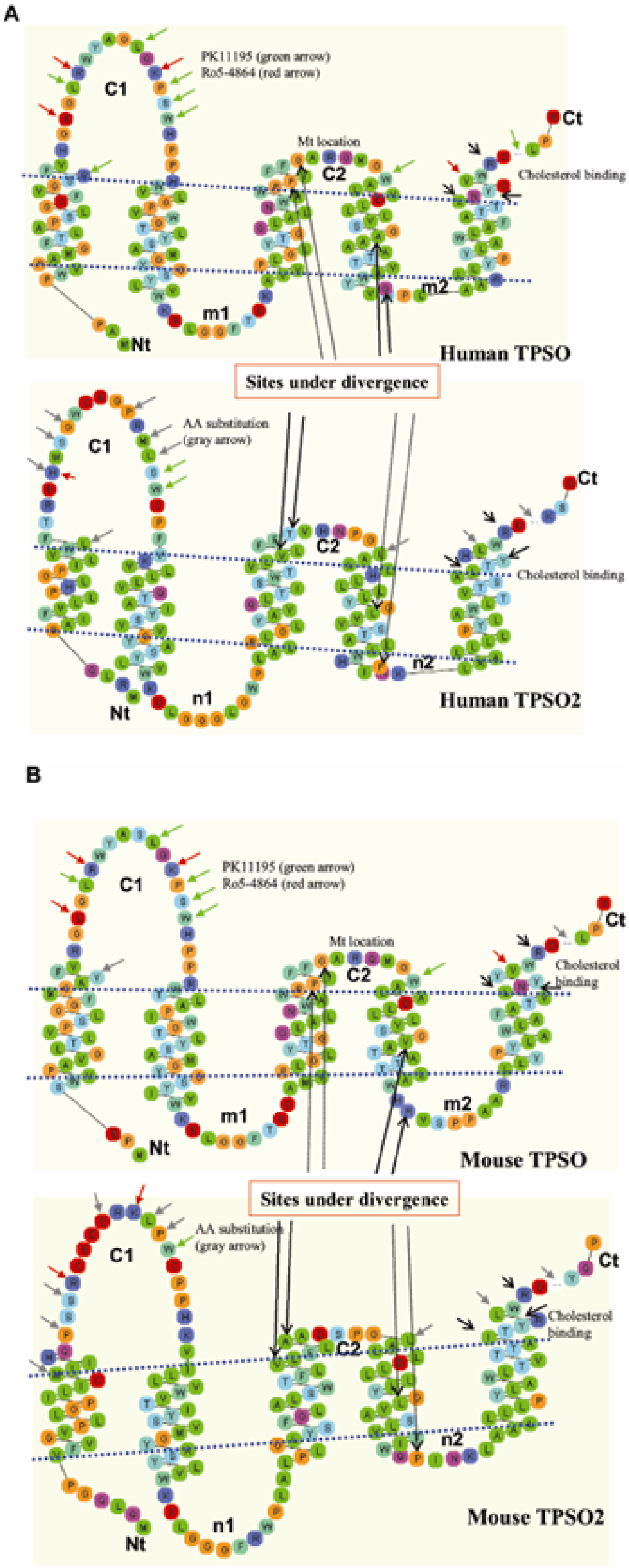
Supplementary Figure 4



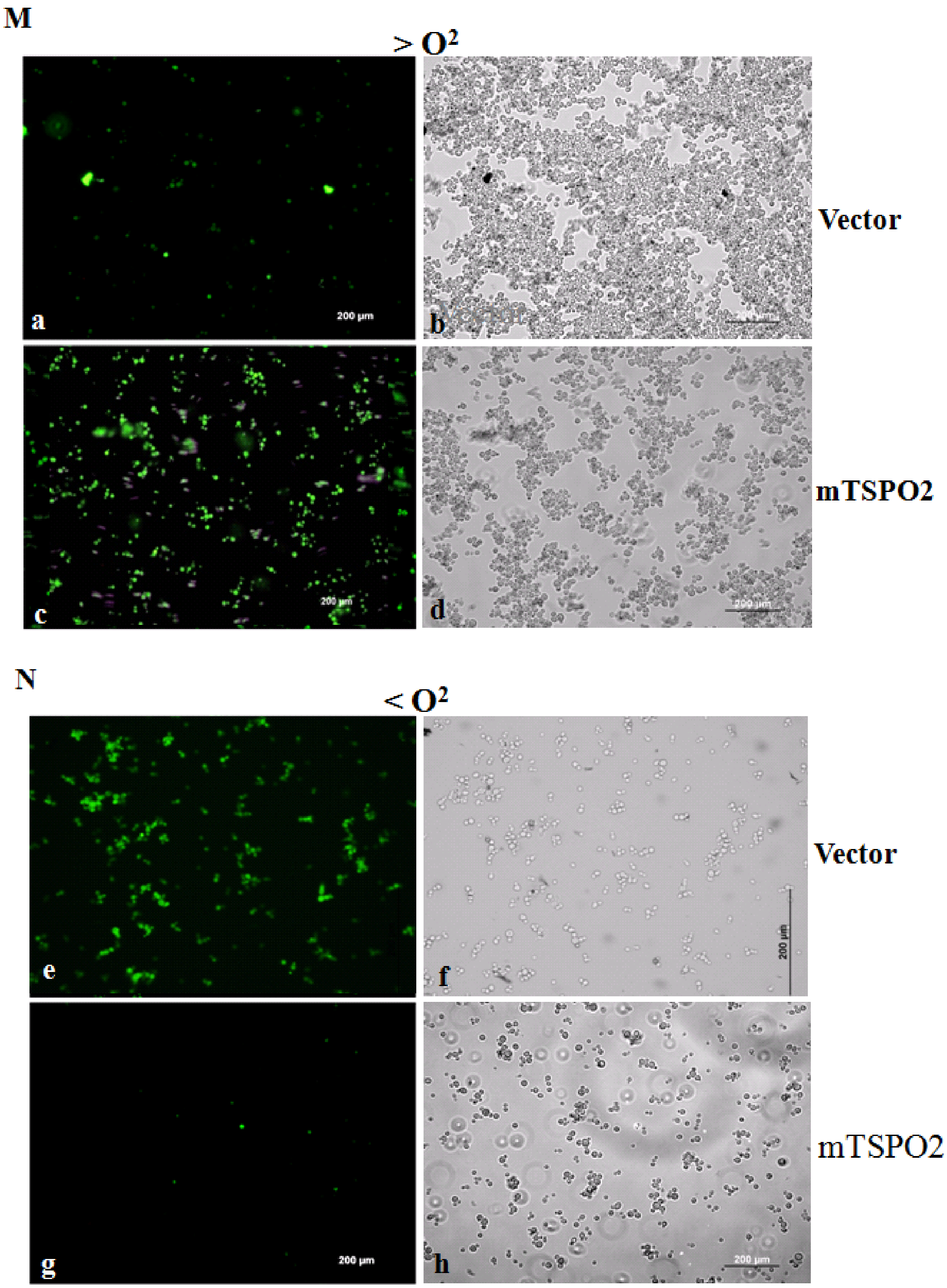
Supplementary Figure 5



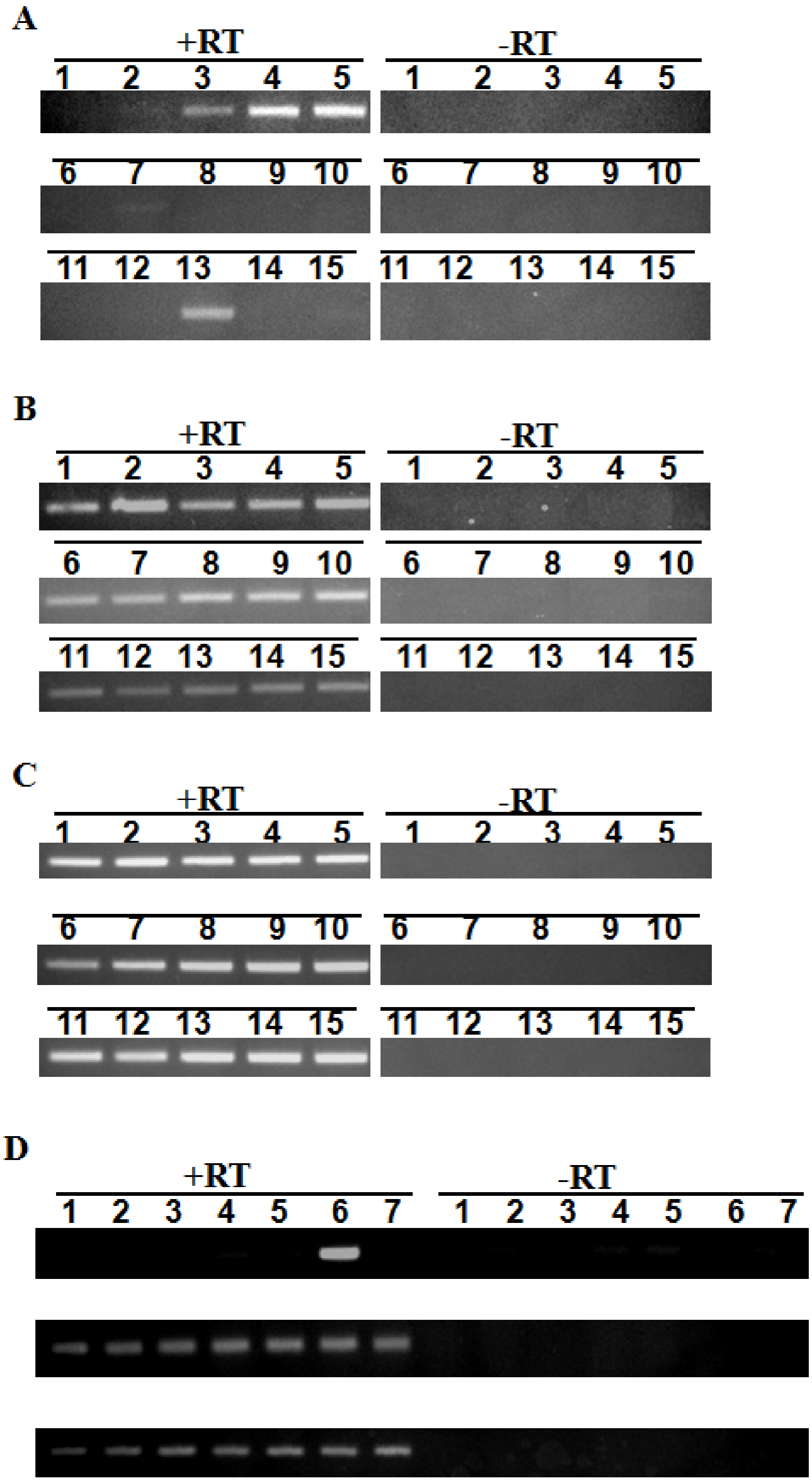
Supplementary Figure 6



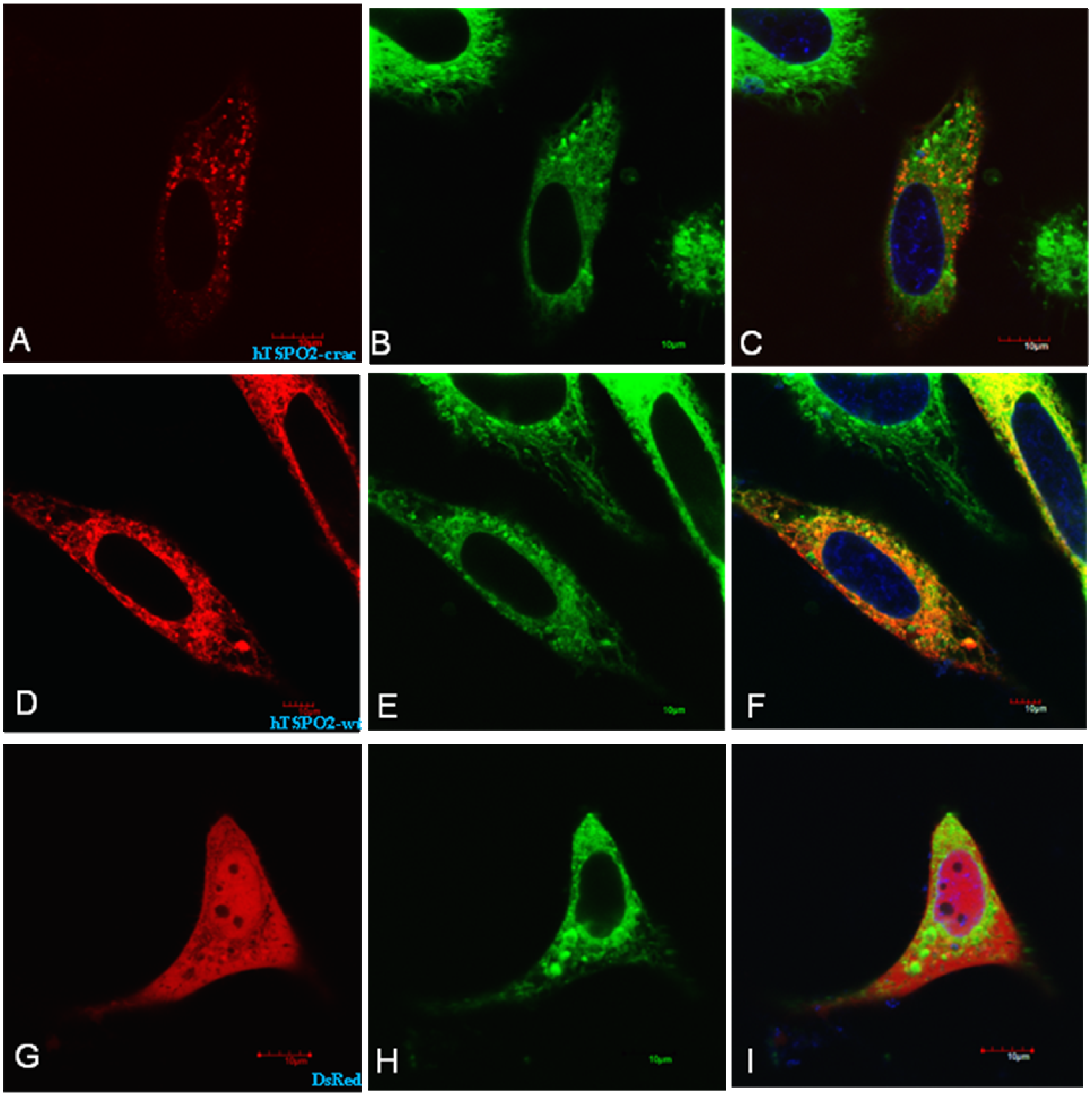
Supplementary Figure 7



Supplementary Figure 8



Supplementary Figure 9



Supplementary Figure 9
(cont.)