Burkhart et al. Supplemental Data

	(pex2-2)	
At PEX2 Glycine max Oryza sativa Brachypodium Selaginella Physcomitrella Gallus gallus Danio rerio Homo sapiens PEX2 C. elegans PRX-2 S. cerevisiae Pex2p	MTPSTPADDAWIRSYQRLLP-ESQSLLASRRSVIPVATSRVNQFDAARLDVENSAMLKEQLVKVFTLMKPGMLFQYE MTLPSHDAWIHTSHTLLPRWKSLSLLSHQQSTLPISISRVNQVDAARLDVENSAMLKEQLVKVFLLMKPGMLFQYE MTDPETLPSPSASTDSSSPPPDAWAAEYRRLLPQWESMRDSSKIAIPISISRVNQFDAARLDVENSAMLKEQLVKVFSLVKPGULFQYE MIPISISRVNQFDAARLDVENSAMLKEQLVKVFSLVKPGULFQYE MAERAGAAAAAVMRPPSPEAWRQVWRDVLRS-QQLRKTIPSVAISRVNQFDAERLDFENTGMLRGQLLKIFSFVQPGLLSRYE MAEADVGGGGGVGAPP-ADAWLQAWRAIAPQWEQIRAKVKTVPDVPILRVNQTDAARLDVENTGMLKEQLSRVFSLSQPGLLLRYE MASSIGNEKSVNPVLRTSQLDALELNKALEQLVWSGFTSGFHGFKPGVLAHIE MAGAGGDKPFAKAGPSPLSRVLRISQLDALELNKALEQLVWSGFTQGFHGFKPGULARFE MASRKENAKSANRVLRISQLDALELNKALEQLVWSGFTQGFHGFKPGULARFE MACRCLRVDQLDAHVLDSEIRSIAQDSVDDVVNQMPLWVARIFEKLR MSRVAQUESIALDKELYGQFWSEFNAAFNTSEHKERWE	76 76 89 45 82 85 53 60 53 47 38
	K (pex2· 个	-1)
At PEX2 Glycine max Oryza sativa Brachypodium Selaginella Physcomitrella Gallus gallus Danio rerio Homo sapiens PEX2 C. elegans PRX-2 S. cerevisiae Pex2p	PELDAFLEFLIWRFS-IWVDKPTPGNALMNLRYRDERGVVAQHLGKVRTGLEGPGLTSPQKIWYQVASVGGQYLFSRLQSFSAFRRWGDSE AELDAFLEFLIWRFS-IWVDKPTPGNALMNLRYRDERAVEPRDKGKIRTGLEGPGLTVAQKLWYQVATVGGQYIWARLQSFSAFRRWGDTE PELDAFLEFLIWRFS-IWVDKPTPGNALMNLRYRDERAAPITGKEVRTGLEGPGLSVSQKVLYQISTVGGQYIWSRLQSFSAFRRWGDSE PELDAFLEFLIWRFS-IWVDKPTPGNALMNLRYRDERAAPIAGKEVRTGLEGPGLSVSQKVLYQISTVGGQYLLSRLQSFSAFRRWGDSE PELNAFLEFLIWRFS-IWVDKPTPGNALMNLRYRDERAPIAGKEVRTGLEGPGLSVSQKILYQISTVGGQYLLSRLQSFSAFRRWGDSE PELNAFLEFLIWRFS-IWVDKPTPGNALMNLRYRDEREFLKLPAS-QVRTGLEGPGLTALQKIFYQLALVGGRYGWARLQLVSAFQRWGDRD PELNAFLEFLIWRFS-IWVDKPTPGNALMNLRYRDERSFNTYLKFGK-AVRTGLEGAGLTKTQKILYQLLVVGGRYGWARLQLISAFQRWGDRD PELNAFLEFLWRFS-IWVDKPTPGNALMNLRYRNERSFNTYLKFGK-AVRTGLEGAGLTKTQKILYQLLVVGGRYGWARLQLISAFQRWGDRQ PEVKAFLWLLLWRFT-IYSKNATVGQAILNIQYKNNLSQTEKYQPLSKHQKLWYLIFTVGGRWLEE-RCYDLFSNRQ PELKALLQULLWRFT-IYSNSATVGQSULNIRYKNDFSPNLRYQPPSKNQKIWYAVCTIGGRWLEE-RCYDLFRNHH PEVKACUWFLWRFT-IYSKNATVGQSVLNIRYKNDFSPNLRYQPPSKNQKIWYAVCTIGGRWLEE-RCYDLFRNHH PELKVTLEAVLWTH-RFSRGASPGQEQMDIAYAGTLYVVTVLAGYWKKITHTIFNGPHOGNQMWLKLYKWVNLL	166 166 178 134 172 177 128 135 128 110 118
	predicted predicted transmembrane transmembrane	
At PEX2 Glycine max Oryza sativa Brachypodium Selaginella Physcomitrella Gallus gallus Danio rerio Homo sapiens PEX2 C. elegans PRX-2 S. cerevisiae Pex2p	QRPLARRINTUQRIEGIYRAAS FLNLL SFLYTGRYRNLIEKALKARLVYRSPHMRRSVSFEYMNRQLVWNEFSEMLLLLPLLNSSAVKNILS QRPLARRIWILIQRIEGIYRAAS FLNLL FLYCTGRYRNLIERALRARLVYGSPHMRRVSFEYMNRQLVWNEFSEMLLLLPLLNSSSVKNLLR QRPLARRAWGLVQHAEGLYRAAS FFNLLUFLYGARYKIIVERILKARLVYGSPHMRRVSFEYMNRQLVWNEFSEMLLLLPLLNSSSVKNLLR QRPLARRAWGLVQHAEGLYRAAS FFNLLUFLYGARYKIIVERILKARLVYGSPHMRRVSFEYMNRQLVWNEFSEMLLLLPLLNSSSVKNLLR QRPLARRAWGLVQHAEGLYRAAS FFNLLUFLYGARYKIIVERILKARLVYGSPHMRRVSFEYMNRQLVWNEFSEMLLLLPLLNSSSVKKLLR QRPLARRAWGLVQHAEGLYRAAS FFNLLUFLYGGRYKIIVERILKARLVYGSPHMRRVSFEYMNRQLVWNEFSEMLLLLPLLNSSSVKKLLL SRSWPRVWULLQRAESFYKVAYMINLIAFLRTGRYRNLVERILQTRLVYLRPNMSRAVSFEYMNRQLVWNEFSEMLLLLPLLNSSSVKKKLL LQS-VSKIKHYINFGAGLUKLCGLVNFIIFLYGGRYRTUFERILKARLVYGSPHMRRAVSFEYMNRQLVWNEFSEMLLLLPLLNVFSLKKVLP RTSWARRANLLLQKAESLYKIAGFANLVLFLHSGRYPSTVERLLGARLVYEKPDMRRAVSFEYMNRQLVWNEFSEMLLLLIPLLNVFSLKKVLP LQS-VSKIKHYINFGAGLUKLCGLVNFIIFLQKGTFATLTERILGIRSVFCKPQSVRQVGFEYMNRELUWHGFAEFLIFLLPLINVQKLKLKIC AESNARKARKVLSILLGUKAASLVNFILFLQRGFFATLTERILGIRSVFCKPQSVRQVGFEYMNRELUWHGFAEFLIFLLPLINVQKLKLKIC AESNARKARKVLSILLGUKAGSLVNFILFLQRGKFATLTERILGINSVFCKPQNRRGVGFEYMNRELUWHGFAEFLIFLLPLINVQKLKLKIC JSRMYSKIEAIYELGSLLHFLYFLRSGGHSTITESIFSLRNWNNHQPTISSINVDTQNRELWWHAFRDVILLTYPFIEKARQRIVKK YHGCDVTNFLRFLAAEGPNARAFLSPLYRAFNVHSTRLIRDGSAIASFYSNSVFAGLEYQNRQLWNALLELFSNTLLTKRGLLTFVK	260 260 272 228 266 271 221 229 221 198 207
	M (ted3) Salk_033081	
At PEX2 Glycine max Oryza sativa Brachypodium Selaginella Physcomitrella Gallus gallus Danio rerio Homo sapiens PEX2 C. elegans PRX-2	PFAKDKSSSTKEDTVTCPICQVDPA-IPFIALPCQ-RYCYYCIRTRCASAASFRCLRCNEPW-AIQREGVSSGK PFSKDKSSSSAEDGACPICQATPT-IPYVALPCQ-RYCYYCLRTRCAAAPSFRCSRCSEPW-AMQRLGGVPTE PFSKDKSASSSGDEACPICQSSSS-IPFFALPCQ-RYCYYCLQTRCAATNSYRCARCNEIW-AIQRQGSS SSLTGKETVKRTDEQGSS SSLTGKETVKRTDEQGSS SSLTGKETVKRTDEDACPICESPS-IPFVALPCQ-RYCYYCLSTRCIANSTYRCARCNSVTAMORYHPQVELGSSDQQNVKNKI FPFSTQAPASSLPEDACPICEACPIVTPYMALPCG-LYCYYCLSTRCIANSTYRCARCNSVTAMORYHPQVELGSSDQQNVKNKI SWCFPIANLPNSDKTLATHYKVCSLCGEWPTMPHTIGCS-VFCYYCIKSNYLFDMYFTCPKCGSEVHSLQP	333 342 298 352 356 304 312 305 273
S. cerevisiae Pex2p	KPPRSRSTTTY-KTVCFRCGGFPTN-FYQIACCRANYCYVCVVKALEWSMCDACGSSGRLTASPVY	271

## Supplemental Figure S1. Alignment of PEX2 proteins from various organisms.

*Arabidopsis* (*At*) PEX2 (At1g79810) was aligned with homologs from *Glycine max* (XP\_003530138.1), *Oryza sativa* (Os05g0275700), *Brachypodium distachyon* (XP\_003573500.1), *Selaginella moellendorffii* (XP\_002976539.1), *Physcomitrella patens* (XP\_001781834.1), *Gallus gallus* (NP\_001008454.1), *Danio rerio* (XP\_684073.2), *Homo sapiens* (NP\_000309.1), *Caenorhabditis elegans* (CAA92640.2), and *Saccharomyces cerevisiae* (NP\_012325.1). The alignment was generated using Lasergene MegAlign (DNASTAR, Madison, WI) with the Clustal W default settings and the Gonnet series protein weight matrix. Residues identical in at least six sequences are shaded in black or purple; chemically similar residues are shaded in gray. Transmembrane domains predicted using the ARAMEMNON database (Schwacke et al., 2003) are indicated in blue, metal-coordinating residues of the RING-finger domain are highlighted in purple, and positions of *Arabidopsis pex2* mutants are indicated in red.

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At PEX10 Glycine max Oryza sativa Brachypodium Physcomitrella Gallus gallus Danio rerio Homo sapiens PEX10 C. elegans PRX-10 S. cerevisiae Pex10p	MRLNGDSGPGQDEPGSSGFHGGIR <b>RFF</b> L MGWGHLGRHGSDSVDGAVAGPSTSATEPR <b>RFF</b> L MRGGGGGDAGTSSRGGSGGAPARPR <b>FFF</b> MPSAGAPASDAGPSSRGGTRGGAAARPR <b>FFT</b> MDIAESSSAASAGSGNGRSGSLPS-FF <b>FF</b> MPLVF MAPAA MNTYV MKNDNKLQKEALMRLSQL <b>RFF</b>	AAQPEIMRAAEKDDQYASFIHEA AAQPEIMRAAEKDDQYASFIYEA AAQPEIMRAAEKDDGYAAHVTEA AAQPEVMRAAEKDDGYAAHVTEA AAQPEVMRAAEKDDHYVASISDA AGPARLVRCGCKDEHYVASISDA AGPARLVRCGCKDEHYVASISDA ANOPQLIESCCKDEYYONNITNN. ASPPEVIRAACKDEYYONNITNN. ASPPEVIRAACKDEYYONNITNN. ASPPEVIRAACKDEYYONUITNN.	CRUAFRHLFGTRIALAYQKEMKLLCOM CRUAFRHLFGTRVAVAYQNETKLLGOM CRUAFRHLFGTRVAVAYQNETKLLGOS CRUAFRHLFGTRVAVAYQNETKLLGOS AHEAFRHALGTRLAVAYONETKLAC AGTALHGTACAKKWLEWRRETELLSDV ANELFHTFACSRRWLOWRKETELLSDV AGGALHSLACARKWLEWRKEVELLSDV LSRVSKELLCQRTWIRWFPYLKSIAST VTELCKLIKSQLFVNSPKELSIFAKL	78 83 80 82 79 55 55 55 55 72
	pex10-G93E D:	pex10-1) pex10-P126S		
At PEX10 Glycine max Oryza sativa Brachypodium Physcomitrella Gallus gallus Danio rerio Homo sapiens PEX10 C. elegans PRX-10 S. cerevisiae Pex10p	LYYVLTTGSGOOTLGEEYGDIIQVAGPYGLSPT LYYVLTTGSGOOTLGEEYGDIIQVAGPYGLPPT LYYVLTTGSGOOTLGEEYGDISQVATSHGLPPT LYYLLTTGSGOOTLGEEYGDISQVATSHGLPPT LYYLLTTGACUOTLGEEYGDISQVAVNSKLPAT AYFALTTLSGYOTLGEEYVNIVQVDSTKKRVP TYYILTTLSGYOTLGEEYVSIIQVDPSRIHVP LYYLTTLAGYGTLGEEYVSIIQVDPSRIHVP LYYTSTVVLGNOTLGEEYVLFESNGLERTVP LYYLFTGRRGRTLGEEYVDLTYNRKGTRLAG	PARRAL FILYQTAVPYIAERIST PARRAL FUVYQTATPYIAERISS PARRIL FILYQTTVPYLAERISS PARRIL FILYQTTVPYLAERISS PARRIL FILYQTTVPYLAERISS FARRATEVSLHTIVPYLLEKGLQ RIRRTALICEHTFVPYLLDKALL SISRRGVUTHAVLPYLLDKALL SISRISFVLHSAFFLISNYLIQ RIKMIVFAFAYPLCPYFITKLYK	AATQAVTFDESDEFFGDSHIH SIASRGIVLAD YESAEGFGENA-HRSH SIVARGIALED SQLDDHSESDSSSIGT MYSRGIYLDD SQLDYHHE RAAARGNALANAEELRGIGFTQEST HLEHELQIEDD GARTLQSNPA VIENELEAEAPQNTRRTWNP PLEQELQADPD SGRPLQGSLG KAESTLTHPS KIMKNNKESK	156 165 163 157 160 132 131 132 121 138
		predic transmer	cted mbrane	
At PEX10 Glycine max Oryza sativa Brachypodium Physcomitrella Gallus gallus Danio rerio Homo sapiens PEX10 C. elegans PRX-10 S. cerevisiae Pex10p	SPRMIDLPSSSQVETSTSVVSR NDRLMRSWHF SAQISGTSPSSSSGQSVTTLSR KGKMSAFWLF AAQPSPIRNSPSRSLSFSHLSR RGRVHTLWEV R RSRAHAFWLV SEIGGEDIVLSQRRSIIQIWQSWSQRMSQRYNA LGLSS-RTLIRNW QKQVRELTEQ PGGRG-CSGARRWMRHTATLTEQ TESF GIPIRKNQKA	RAIQRWFVLPVAREVLQLVLRAN ALVQRWFTMLPFVRELLQLVLRAN WLRKWPSNLPFAQDFIQLTURTN WVQRWPSNLPFAQDFIQLARTN VALQQWFTILPSVKEALLLVLRAH QQKKTILQVVYILKQSIPLLFRLH QRKSLIPLVFALQQGTLLYRLH QRRALLRAVFVLRQGTACLQRLH RQSFLDVFFWLRTKLFPQLQRAH - IEDTESVAAFCKGLUDFILDVH	LMLFYFEGFYYHISKRASGVRYVFIGK LMLFYFEGLYYHISKRAAGIRYVFIGK LMFFYEGLYYHISKRAAGIRYVFIGK LMFYFEGVYHLSKRAAGIRYVFIGK LMLFYFEGVYYHLAKRAAGIQYIFMGK LAVFYIIGTIYHISKRAAGVRYLRVG- VAUFYIIGTIYHIAKRAAGVRYLRVG- VAWFYIIGVFYHLAKRLIGIIYQALRP IALFYIIGAYYSIARRFIGIRELSAS- MILFYFKGAFYSISKRIFGMRYVFKHI	239 248 246 219 243 204 198 205 185 185
	predicted transmembrane	splicing (pe $ au$	x10-2) stop (pex10-W3	313*)
At PEX10 Glycine max Oryza sativa Brachypodium Physcomitrella Gallus gallus Danio rerio Homo sapiens PEX10 C. elegans PRX-10 S. cerevisiae Pex10p	QLNQRPRYQILGVFLLIQLGILAAEGLRRSN ASNQRPRYQILGVFLLIQLGITAAEGLRRN PLNQRPRYQILGIFLLIQLGILGAERLRRSN PMQRPRYQILGIFLLIQLGILGAERLRRSN PACQRPRYHMLGMFLLIQLSINGGDWLRRSV 	LSSTTSSIQQASIGSYQTSGGR- LTSTTGSVHQASFATHDRSACH- LSTTGSVHQASFATHDRSACH- LSTTASTINQISSGSYPSSTGR- LSSTATSINQISSGSYPSSTGR- LPALATSMRSRTRDPSAVSGGQ Q-STRSSYKFLGTISLFHLLTI P-RTSFSYRLLGGLSVLQLATTL L-RARVSYRLLGVTSLLHLVLSM I-PALKVYRFLGYTTLIQLAVSI VLTSTLGSWIYGRKRTNDSITRS	GLPVLN EEG-NLITSEAEKGNWS GLPVLN EEG-NLATPDIDKRSWV GVPVLN EDG-NIIS-DIRHGKTA SVPVLN EDG-NIIS-DIRHGKTA SVPVLN EDG-NIIS-DIRHGKAY GVQIYSFQQKQRARQEWRLHRNLA TLQFNLRQRQRARHEWRQHRNLA GLQLYGFRQRQRARKEWRLHRGLS GISLYSFLEQEKFNNKLKKEKKENNGG SVGLQERSEHESIEGIFKESQ-LTHIN	314 323 320 293 321 256 250 276 238 269
At PEX10 Glycine max Oryza sativa Brachypodium Physcomitrella Gallus gallus Danio rerio Homo sapiens PEX10 C. elegans PRX-10 S. cerevisiae Pex10p	TSDSTSTEAVGKCTLCLSTRQHPTATPCC SESSSSEYHATSGVSKCTLCLSTRQHPTATSC DLATSSEASSGKSKCTLCLSTRQNPTATTCC DLASGSEAPSSKSKCTLCLSTRQNPTATTCC TLAANTGDAEGGGRRKCELCLSPRQHPTATPCC LQKNTIKEGTTGRQSRCTLCLEERRATATPCC PSHQVSQSSSRTSRCTLCLEERRHPTATPCC SDRNLDENSLFHPTPCCSTCLEERRHPTATPCC LSDKNQLPFIPEASRKCTLCLENK-NPSALFCC LSDKNQLPFIPEASRKCTLCLENK-NPSALFCC	HVFCWSCIMEWCNEKQE HVFCWSCIMEWCNEKPE HVFCWSCIMEWCNEKPE HVFCWNCIMEWCNEKPE HVFCWNCIMEWCNEKPE HVFCWCITEWCNTRIE HVFCWECITEWCNTRIE HVFCWECITAWCSKAE HVFCWECITAWCSKAE HVFCWSCUMSWCKERPE	CPLCRTPNTHSSLVCLYHSDF CPLCRTPTTHSSLVCLYHSDF CPLCRTPTTHSSLTQLYHSDF CPLCRSPTHSSLTQLYHSDF CPLCRSPTHPQLVCLYHTDF CPLCREKFPQPKLTYLRYK CPLCREKFQPHRLYYLRSYK ARCPQCRLEFQPROVTPLNL CPLCRQHCQPQETLYLRQ	381 394 389 362 392 327 318 346 314 337

#### Supplemental Figure S2. Alignment of PEX10 proteins from various organisms.

Arabidopsis (At) PEX10 (At2g26350) was aligned with homologs from *Glycine max* (XP\_003544551.1), *Oryza sativa* (Os07g0608800), *Brachypodium distachyon* (XP\_003559973.1), *Physcomitrella patens* (XP\_001777562.1), *Gallus gallus* (NP\_001185583.1), *Danio rerio* (NP\_001005994.1), *Homo sapiens* (NP\_722540.1), *Caenorhabditis elegans* (NP\_001021200.2), and *Saccharomyces cerevisiae* (NP\_010551.1). The alignment was generated using Lasergene MegAlign (DNASTAR, Madison, WI) with the Clustal W default settings and the Gonnet series protein weight matrix. Residues identical in at least five sequences are shaded in black or purple; chemically similar residues are shaded in gray. Transmembrane domains predicted using the ARAMEMENON plant membrane protein database (Schwacke et al., 2003) are indicated in blue, metal-coordinating residues of the RING-finger domain are highlighted in purple, and positions of *Arabidopsis pex10* mutants are indicated in red.



**Supplemental Figure S3.** Membrane association of peroxisome matrix protein receptors in *pex2-1, pex10-2,* and *pex2-1 pex10-2.* 

Light-grown 8-d-old seedlings were homogenized and the resultant extracts were centrifuged to separate soluble proteins from proteins associated with organellar membranes. Homogenate (H), soluble (S), wash (W) and pellet (P) fractions were processed for immunoblotting and serially probed with the indicated antibodies. HSC70 and mitochondrial membrane complex V (mito ATP synthase) were used as cytosolic and organellar controls, respectively. Numbers above or below the bands indicate the relative level of the indicated protein in the S, W, or P fraction relative to the amount in the H fraction. This experiment was repeated three times with similar results.

	Nearest	Restriction	Fragment size (bp)		
Marker	gene	enzyme	Col-0	Ler	Primer sequences
LCS1127	At1g32130	TaqI	206	138, 68	CAAAATCCTGAAGTGGCTCTGTAG ATTTCGATTTCGTTTTTGTG
T14L22	At1g51913	Hinfl	~700	~450, ~250	GAAAAATTAAAGCCCAACC CACCCGCAAACACAACAACC
SNP10592	At1g69250	RsaI	115, 29	144	AGCGACGGCAACCTAAAAAAGTAAAG AGGTTCAAGCACATTGATGATACTCTGTA
SEC238	At2g18950	DdeI	145, 69	214	GAGTTCTGCGTTGTGATTCGAGTAAAGTTG GAAAACCTGTAAAACGCATCTAACGAGTC
SEC241	At2g20770	PvuII	177, 27	204	CAACTCAAACTTATTCACCATCAAACAACAA TATCTCTTCCTTGACATGGTCGACCCAGCT
SEC244	At2g25095	AvaII	197, 28	225	TAAAAATAGTAAACTTGTCCCGATAAA GTCGATAGATTCACGGACGTATTAGAAAGG
SEC245	At2g28360	RsaI	116, 28	144	CTGCAGCTTCGTTTCTAGGATATTTGGTCAT CTATAAGAATTGAAGAAAGGCGATGAAGTA
SEC246	At2g32340	RsaI	114, 27	141	TTTACCTGTTCCGCCAATCACTCCTC GAACCTGCGTCGCTATCTGCTTCCTCCGTA

Supplemental Table 1. Markers used in recombination mapping of pex2-1 and pex10-2

Gene/Accession #	Primer names	Primer sequences		
DEV2/4/1 700100	PEX2-12 and	CATGGATGAATCTCTGTGGGTGTGA		
PEX2/At1g/98100	PEX2-13	GAAAGAAAAAGAAGAGTAGCGGAAGTGAGAA		
	PEX2-14 and	TCGCTATGGTTGATTCTTTTTCTCCTT		
	PEX2-15	GCTGCTTGCCTTGGCTTTTTACACTTC		
DEV10/4/2-26250	PEX10-3 and	GACCACCTAACATCTCCAACTCTTTT		
PEX10/A12g20350	PEX10-4	ATGGCCACTCGACTGATCCCGCTCTAC		
	PEX10-5 and	AAGGAGTGGCCGTTGGGTGCTGAC		
	PEX10-6	TTCTTGGGGTTTTCCTTCTAATC		
	PEX10-7 and	CCTATAGAAGCCTGCTGAATGGAG		
	PEX10-8	TCAGGGCAACAAACTTTAGGAGAGGAAT		
	PEX10-9 and	TGGAACTGCGGTCTGGTACAATATGAACAAAG		
	PEX10-10	CTTTGAATTAAAAAAAAAATATCAAAGGC		

Supplemental Table 2. Primers used for amplification and sequencing of PEX2 and PEX10

			_	Product size (bp)	
Mutant	Primer names	Primer sequences	Restriction enzyme	Wt	Mutant
pfl36/pex2-1	PEX2-18	TGCGTTGCCTCCGTTGGTGGTCAG	D II	65, 18	02
	PEX2-DpnII <sup>1</sup>	CATACAGACCTGCTCAGAATCACCCGAT	Dpn11		93
pex2-2	PEX2-20	GCTTATTATATGTGGTCTTTGATGGCAGTC	N7 J - T	134	102
	PEX2-NdeI <sup>1</sup>	GAGTGAAAACCTTAACGAGCTGTTCCTTCCA	Nael		102
ted3	TED3-1	ATGCTTTTGTTGCTTCTCCCGCTGCTC	T 451	341, 99	440
	TED3-2	TCTAAGACACCGGAACGATGCTGCTG	<i>Tsp</i> 451		440
pf181/pex10-2	PEX10-11	CGTTGAAGTTGAATCGGAGGTAGAC	D-4	92, 28	120
	$PEX10-PstI^1$	AATATAGTTTTGGTATTGTTCCTGCA	PStl		
<i>pex10-P126S</i> <sup>2</sup>	PEX10-8	TCAGGGCAACAAACTTTAGGAGAGGAAT		229	220
	PEX10-TaqI	ACGAAACCTAATTCTCTCTGCGATATATC	-		229

# Supplemental Table 3. PCR-based markers for determining mutant genotypes

<sup>1</sup>dCAPS oligonucleotide (Michaels and Amasino, 1998; Neff et al., 1998); the underlined nucleotide differs from

wild-type sequence to create a restriction site in either the mutant or wild-type PCR amplicon.

 $^{2}pex10$ -P126S was amplified with the listed primers and sequenced with primer PEX10-8 to confirm genotype.

### Supplemental literature cited:

- Michaels SD, Amasino RM (1998) A robust method for detecting single-nucleotide changes as polymorphic markers by PCR. Plant J 14: 381-385
- **Neff MM, Neff JD, Chory J, Pepper AE** (1998) dCAPS, a simple technique for the genetic analysis of single nucleotide polymorphisms: experimental applications in *Arabidopsis thaliana* genetics. Plant J **14:** 387-392
- Schwacke R, Schneider A, van der Graaff E, Fischer K, Catoni E, Desimone M, Frommer WB, Flugge UI, Kunze R (2003) ARAMEMNON, a novel database for Arabidopsis integral membrane proteins. Plant Physiol 131: 16-26