Additional file 3. PCR-based markers for genotyping mutants.

Genotype	Primers	Restriction enzyme	Product size (bp)	
			Wild type	Mutant
atg7-3	LB1-SAIL (GCCTTTTCAGAAATGGATAAATAGCCTTGCTTCC) ATG7-5 (GTTGCCATGTCTAATCCAGTCAGG)	-	none	350
ATG7	ATG7-5 (GTTGCCATGTCTAATCCAGTCAGG) ATG7-23 (GTTGCCATGTCTAATCCAGTCAGG)	-	281	none
pex4-1	PEX4-A (TGCATCTCTTTTTATAACAACCTTCTCC) PEX4-B (GAACTAGAACCGAACGGGAACCAAACC)	*Mnl*I	201, 91	292
pex4-2	PEX4-16 (ATTCGGGTTGCTTCAGTTCG) PEX4-dCAPS-RsaI (CTTAGAAGATTCCCTTTTTTCCATAGCAAG)	*Rsa*I	139	108, 31
pex5-1	PEX5-B (TCATCAATAATAAGTTCACCACGGCTCATCT) PEX5-32 (GTTGGACGACATATCTCTTTTCTGG)	*Eco*RI	77, 59,117	77, 176
pex5-10	LB1-SALK (CAAACCAGCGTGGACCGCTTGCTGCAACTC) PEX5-21 (GATATCAAATGCGACTCAAACACTGATGAC)	-	none	405
PEX5	PEX5-3 (GTCGTTGGCTGAATATTTTGTTCGGC) PEX5-21 (GATATCAAATGCGACTCAAACACTGATGAC)	-	541	none
35S:PEX5	PEX5-38 (TGAAGACCAACAGATAAGG) PEX5-39 (CCCATTGGAGGCATAGG)	-	264	264, 168
35S:PEX7	35S-F (GGATGACGCACAATCCCACTATCCTTCG) PEX7-22 (AGGCGTGACTCGTAGAATGGACTG)	-	none	158

pex4-1 carries a C-to-T mutation at the 533rd nucleotide that destroys an *Mnl*I restriction enzyme cut site.

pex4-2 carries an intronic G-to-A mutation at the 1085th nucleotide (18 bp 5′ of the fourth exon of *PEX4*). We used the dCAPS website [http://helix.wustl.edu/dcaps/dcaps.html, 73] to design a genotyping marker for *pex4-2*.

pex5-1 carries a C-to-T mutation at the 2910th nucleotide that destroys an *Eco*RI restriction enzyme cut site [3].

pex5-10 has a T-DNA inserted in exon 5 and results the reduced and truncated pex5-10 protein [13].

The *35S:PEX5* construct expresses a *PEX5* cDNA [17]; for *35S:PEX5* genotyping, *PEX5* primers spanning introns were used to amplify larger genomic *PEX5* or the smaller *PEX5* cDNA products.

PEX7 lacks introns, so a primer from the *35S* promoter and a reverse *PEX7* primer were used to genotype *35S:PEX7* lines.