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Supplemental Data

Allelic Expression Imbalance Promoting

a Mutant PEX6 Allele Causes

Zellweger Spectrum Disorder

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Supplemental data



Figure S1 – Severe import defect of peroxisomal matrix protein catalase in affected individuals.

Immunofluorescence microscopy assay to determine the subcellular localization of the peroxisomal matrix protein catalase (green signal) and the peroxisomal membrane protein ABDC3 (red signal) in affected individuals. Catalase colocalized with ABCD3 to peroxisomes in control cells, but was mislocalized to the cytosol in PEX6-deficient cells. Also in fibroblasts derived from the affected individuals catalase was mislocalized to the cytosol indicating a severe catalase import defect. In contrast, catalase was only in few fibroblasts derived from the mother of individual P2 mislocalized, indicating a very mild catalase import defect.

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PEX6	H. sapiens	842	V	F	V	Т	G	А	т	Ν	R	Ρ	D	L	L	D	Ρ	А	L	L	R	Ρ	G	R	F	D	к	L	V	F	V	870
PEX6	M. musculus	843	V	F	۷	Т	G	А	Т	Ν	R	Ρ	D	L	L	D	Ρ	А	L	L	R	Ρ	G	R	F	D	Κ	L	۷	F	V	871
PEX6	A. thaliana	797	L	F	Т	Т	G	А	S	Ν	R	Ρ	D	L	Т	D	Ρ	А	L	L	R	Ρ	G	R	F	D	Κ	L	L	Y	V	825
PEX6	D. melanogaster	758	Т	F	Т	L	А	А	Т	Ν	R	Ρ	D	L	Т	D	Ρ	А	L	L	R	Ρ	G	R	F	D	Κ	L	F	Y	V	786
PEX6	S. cerevisiae	871	V	F	۷	Т	G	А	Т	Ν	R	Ρ	D	L	L	D	Е	А	L	L	R	Ρ	G	R	F	D	Κ	L	L	Y	L	899
PEX6	C. elegans	866	V	Т	I	L	G	С	Т	s	R	Т	D	L	Т	D	D	А	L	L	R	Ρ	G	R	F	D	н	н	V	Y	С	894
p97	H. sapiens	617	V	F	Т	Т	G	А	т	Ν	R	Ρ	D	Т	Т	D	Ρ	А	Т	L	R	Ρ	G	R	L	D	Q	L	Т	Y	I.	645
p97	M. musculus	617	V	F	Т	Т	G	А	Т	Ν	R	Ρ	D	T	Т	D	Ρ	А	Т	L	R	Ρ	G	R	L	D	Q	L	Т	Y	1	645
NSF	H. sapiens	367	Ι	L	V	Т	G	М	Т	Ν	R	Ρ	D	L	Т	D	Е	А	L	L	R	Ρ	G	R	L	Е	V	к	М	Е	I.	395
SRH consensus sequence			۷	-	۷	Т	-	Α	т	Ν	R	Ρ	D	-	L	D	Ρ	Α	L	L	R	Р	G	R	-	D	R	-	Т	-	-	





Figure S2 – Arginine finger 2 in the SRH of AAA+ ATPases.

(A) Multiple sequence alignment of protein sequences of various AAA+ ATPases, including PEX6 of different organisms, human and mouse p97 and human NSF [prepared based on alignments created by UniProt (www.uniprot.org)]. The alignment demonstrates the high conservation of arginine finger 2, which is mutated in the affected individuals and indicated in red. The SRH consensus sequence, which is described in ¹, is indicated in grey. (B) 3D structure of an hexameric AAA+ ATPase complex, including the arginine finger 2 in the highly conserved SRH domain, which is located at the interface of two neighboring proteins in close vicinity to bound ADP (i.e. p.359Arg in the structure of p97of *M. musculus*, RCSB ID 1E32², prepared using Chimera Software³).



Figure S3 - The PEX6 variant p.Arg860Trp is pathogenic.

Functionality of PEX6-p.Arg860Trp variant. To determine whether PEX6-p.Arg860Trp can still support peroxisomal matrix import, we co-expressed the protein with a peroxisomal targeted GFP-SKL reporter in PEX6-deficient fibroblasts and determined the localization of GFP-SKL three days after transfection. Whereas co-expression of GFP-SKL with wild-type PEX6 results in restoration of peroxisomal matrix protein import in the majority of cells, we observed no complementation with PEX6-p.Arg860Trp, demonstrating that the mutant PEX6 protein is not functional. For this study, we determined the subcellular localization of GFP-SKL in 100-150 cells per condition in three to seven independent transfection experiments. Statistical analyses of the rescue efficiency of the co-transfected PEX6 variants versus non-transfected cells were performed using Mann-Whitney U test (*** $p \le 0.001$, *ns* not significant).



Figure S4 – PEX6 protein expression in affected individuals.

Immunoblot analyses on whole cell lysates of fibroblasts derived from the affected individuals, the mother of individual P2 or control individuals. Depicted are representative immunoblots using antibodies against PEX6 and against tubulin as a loading control which showed no marked changes in PEX6 protein expression in the affected individuals. To allow comparison of the PEX6 protein levels of samples run on different gels, we calculated the ratio PEX6:tubulin signal for each cell line and normalized these ratios per gel to the PEX6:tubulin ratio of the same control cell lysate run on each gel (set as 1.0).



Figure S5 – PEX1/6 complexes are correctly localized to peroxisomes in cells of affected individuals and in PEX6-deficient cells expressing PEX6-p.Arg860Trp.

Immunofluorescence microscopy assay to determine the subcellular localization of PEX1 (green signal) and the peroxisomal membrane protein ACBD3 (red signal) in affected individuals. Because the localization of PEX1 to peroxisomes is strictly dependent on its interaction with PEX6, which in turn interacts with the peroxisomal membrane protein PEX26, a colocalization of PEX1 with ACBD3 indicates the peroxisomal localization of the PEX1-PEX6 complex. Both in cells of control individuals and cells of individual P1, PEX1 was localized to peroxisomes, indicating the correct localization of PEX1-PEX6 complexes in the cells of individual P1. In cells of a PEX6-deficient individual, endogenous and overexpressed PEX1 is not localized at peroxisomes ("Mock", "+ PEX1"). Transfection of the PEX6-deficient cells with either wild-type or PEX6-p.Arg860Trp and PEX1 confirmed that PEX6-p.Arg860Trp is indeed able to interact with PEX1 and localize the PEX1-PEX6 complex to the peroxisomes. Note that we used PEX1 antibodies for these studies, because PEX6 antibodies suitable for immunofluorescence microscopy were not available. The images represent a cellular area of 25x25µm.



Figure S6 – PEX5 export defect in affected individuals.

Immunofluorescence microscopy assay to determine the subcellular localization of the peroxisomal matrix protein catalase (green signal) and the cytosolic protein receptor PEX5 (red signal) in affected individuals, including categories used in figure 1D. In control cells, catalase is localized in peroxisomes and PEX5 in the cytosol. In contrast, in cells of individual P2 catalase is mislocalized to the cytosol and PEX5 located at peroxisomes, indicative of the severe peroxisomal protein import defect. In cells of the mother of individual P2 PEX5 is partially peroxisomal. The images represent a cellular area of 25x25µm.



Figure S7 – Longer *PEX6-c.1_*462* mRNA is not less stable or more prone to nonsensemediated mRNA decay (NMD)

Allelic expression of PEX6 mRNA in cells treated with non-sense mediated mRNA decay-inhibitor emetine (A) or transcription inhibitor actinomycin D (B,C). (A) We treated fibroblasts of the affected individuals with the emetine, after which cDNA was prepared from RNA isolated from the cells. PEX6 cDNA was Sanger sequenced and the allele peak ratio of the mutant PEX6 allele c.2578T was determined as described in Figure 2B using in total 9 sequence reads from two independent experiments. The emetine-treated cells did not show an increase in the c.2578T peak ratio, which indicates that the long PEX6-c.*1_462 mRNA encoded by the lower expressed allele (c.2578C) is not degraded by nonsense-mediated mRNA decay. (B) and (C) We treated fibroblasts derived from the affected individuals, as well as other cell lines heterozygous for the c.*442_445delTAAA variant and displaying AEI, with the actinomycin D (ActD, 1µM), after which cDNA was prepared from RNA isolated from the cells. (B) The cDNA was Sanger sequenced and the allele peak ratio of the common heterozygous polymorphism c.2816C>A was determined as described in Figure 2B using sequence reads from two independent experiments. Actinomycin D treated cells did not show an increase in the c.2816A ratio, which indicates that the long PEX6-c.*1 462 encoded by the lower expressed allele (c.2816C) is not less stable. (C) We determined the ratio PEX6-c.*1_462 mRNA : total PEX6 mRNA using quantitative RT-PCR. We observed no decrease in the ratio, indicating that the longer PEX6-c.*1_462 mRNA is not less stable than other PEX6 mRNA. The ratio was normalized to the ratio of untreated cells in five independent experiments and is shown as mean with standard deviation.



microRNA hairpin inhibitors

Figure S8 – Inhibitors of miRNAs hsa-miR-33a-5p and hsa-miR-150-5p do not affect AEI of *PEX6* in affected individuals.

Allelic *PEX6* mRNA expression in cells treated with miRNA inhibitors. We transfected fibroblasts derived from the affected individuals with negative control inhibitors or inhibitors of miRNAs predicted to target exclusively the long *PEX6-c.* *1_462 for degradation (hsa-miR-33a-5p ("miR33"), hsa-miR-150-5p ("miR150")). (**A**) We analyzed whether the miRNA inhibition results in a decreased allele peak ratio of the variant c.2578C>T/C, as described in figure 2b. We observed no decrease of the ratio and thus no rescue of the AEI by miRNA inhibition, indicating that the decreased level of *PEX6-c.* *1_462 is not mediated by miRNAs hsa-miR-33a-5p or hsa-miR-150-5p. Data are shown as mean with standard deviation of one to three independent experiments. (**B**) We analyzed whether the miRNA inhibition results in increase of *PEX6-c.* *1_462 mRNA or total *PEX6* mRNA. The mRNA levels of the hsa-miR-33a-5p target gene *CPT1A* and the hsa-miR-150-5p target *p53* increased significantly, confirming the functionality of the miRNA inhibitors. mRNA levels were normalized to reference gene expression and the values of samples transfected with control mimics and are depicted as mean of two independent experiments.



Figure S9 – miRNAs hsa-miR-33a-5p, hsa-miR-33b-5p or hsa-miR-150-5p do not specifically affect the signal of NanoLuc with the long *PEX6-c.*1_462 3'*-UTR..

Reporter gene assay of Nanoluc constructs with different PEX6-3'-UTRs treated with miRNA mimics. We transfected HEK293-FlpIn cells stably expressing NanoLuc constructs with the long *PEX6-c*.*1_462 3'-UTR (light grey) or the short *PEX6-c*.*1_326 3'-UTR (dark grey, used as control) with mimics of the indicated miRNAs and subsequently measured NanoLuc luminescence in three independent experiments. None of the miRNA mimics resulted in a stronger decrease of the luminescence signal of NanoLuc with the long *PEX6-c*.*1_462 3'-UTR, indicating that the miRNAs do not cause a selective degradation of long *PEX6-c*.*1_462 mRNA. The measured luminescence values were normalized to values of cells transfected with negative control mimics and are shown as mean with standard deviation. The statistical analyses were performed using Mann-Whitney U tests versus values of cells transfected with negative control mimics (* p≤0.05, ** p≤0.01, *** p≤0.001, **** p≤0.0001, *ns* not significant).



Figure S10 – SV40 immortalized control cells overexpressing wild-type PEX6 do not show a peroxisome biogenesis defect.

Immunofluorescence microscopy assay in SV 40 cells over expressing wild-type PEX6.We stably overexpressed PEX6-p.Arg860Trp or wild-type PEX6 in SV40 immortalized control fibroblasts and confirmed PEX6 overexpression by quantitative RT-PCR of isolated RNA and immunoblot analysis of PEX6 protein in cell lysates (data not shown). Subsequently, we used immunofluorescence microscopy to determine the subcellular localization of catalase and ABCD3, or PEX5 and ABCD1 in cells overexpressing PEX6-p.Arg860Trp (shown in Figure 3A) or wild-type PEX6 (shown here). The microscopic images of cells overexpressing wild-type PEX6 demonstrate that PEX6 overexpression does not result in a PEX5 export defect or a catalase import deficiency, in contrast to PEX6-p.Arg860Trp overexpression.

Table S1 – PEX6 primers.

PEX8.c1218hw [-21M13]-CTGGGGCAGGAGTTCTTTG PEX8.c619rev [M13-Rev]-CAGCACATCTGGCACAAAACC PEX8.c667tw [-21M13]-TGACAGGGCAAGAAGCC PEX8.c60rev [M13-Rev]-CGGTGTCTGGTCAGAAGCG PEX8.c744rev [M13-Rev]-CGCTTGCAGCTGGAAACCCA PEX8.c744rev [M13-Rev]-AACAGTCGAAACCGAAAGCGA PEX8.c844rev [M13-Rev]-AACAGTCGAAACCGAAAGGAGCGCCCTGG PEX8.c844rev [M13-Rev]-AACCGCAAAGGAGGGCCCTGG PEX8.tarevII [M13-Rev]-AACCGCAAAGGAGGACCCC PEX8.tarevII [M13-Rev]-ATACGCACAAGGTAGGAGCACCG PEX8.tarevII [M13-Rev]-ATCAGACACGGAACGGGACCACAG PEX8.tarevII [M13-Rev]-ATTACAGACGTGAACCCAGG PEX8.tarevI [M13-Rev]-ATTACAGACGTGAACCCAGG PEX8.tarevI [M13-Rev]-ATTACAGACGTGAACGCAAGG PEX8.tarevI [M13-Rev]-ATTACAGACGTGAACGCAAGG PEX8.tarevI [M13-Rev]-ATTACAGACGTGAACGCAAGG PEX8.tarevI [M13-Rev]-CCCTGGCAGTTCATTAGG PEX8.tarevI [M13-Rev]-CTCTGGGCAGTTCATTAGG PEX8.tarevI [M13-Rev]-CCCCCAGGTTCATTAGG PEX8.tarevI [M13-Rev]-CCCCCAGGTTCATTAGG PEX8.tarev [M13-Rev]-CCCCCAGCTTGGTGTCTG		
PEX8_C-619rev [M13-Rev]-CAGCACATCTGGCACAAAACC PEX8_C-667fw [-21M13]-TGAACAGGGCAAGAAGAGC PEX8_C-687fw [-21M13]-TGAACAGGGCAAGAGAAGCG PEX8_C-860fw [-21M13]-TCACCACCTTGCATCTCCAG PEX8_C-860fw [-21M13]-TCACGAACTGGAAACCCA PEX6_C-744rev [M13-Rev]-AACAGTCGAACTGCGAACCGGCACCCG PEX6_C-844rev [M13-Rev]-AACAGTCGAAAGGGAACCCA PEX6_C-844rev [M13-Rev]-AAACGGAAAGGGAACCCG PEX6etb forw [-21M13]-TGGTGGCACATGCTTGG PEX6etb forw [-21M13]-TGGTTGGGCACAGGTTAGAG PEX6etb forw [-21M13]-TGTTCTTGGGAACTGCG PEX6exon2 forw [-21M13]-TGTTCTTGGGAACTGCG PEX6ex5 forw [-21M13]-TGTTCTTGGGCAGACTGCG PEX6ex5 forw [-21M13]-TGTTCTTGGGCAGACTGCG PEX6ex67 forw [-21M13]-TGTTCTTGGCCAGTTCATTAGG PEX6ex67 forw [-21M13]-TGTCTTGGCCAGTTCATTAGG PEX6ex67 forw [-21M13]-TGCCCGCCCCAGGTCACAGGAG PEX6ex67 forw [-21M13]-ACAAGGCAGTCACAGGAGC PEX6ex67 forw [-21M13]-ACAAGGCAGTCACAGGGAGC PEX6ex67 forw [-21M13]-ACAAGGCAGTCACAGGGAGC PEX6ex67 forw [-21M13]-ACAGGCAGTCACAGGGAGC	PEX6_c1218fw	[-21M13]-CTGGGGCAGGAGATTCTTTG
PEX6_c-667tw [-21M13]-TGAACAGGGCAAGAAGTCC PEX6_c-50rev [M13-Rev]-CGGTGTCTCGGTCGGAAAGG PEX6_c-607ev [M13-Rev]-CGTTGCCAGTCGCAAAGCG PEX6_c-860tw [-21M13]-TCCCCACTTGCAGTCCGAAACCCA PEX6_c-844rev [M13-Rev]-ACACGCGAACCGGAACCCGTG PEX6_c-860tw [-21M13]-TGCCGACACCGCACCCTGG PEX6ex-1arevII [M13-Rev]-AAACCGCAAAGCGGACCC PEX6ex011 [M13-Rev]-AACCGCAAAGCGGACCC PEX6ex02 [PEX6ex01] PEX6ex02 [M13-Rev]-AACCGCAAAGCGGACCC PEX6ex02 [PEX6ex01] PEX6ex02 [M13-Rev]-ATTACAGACGTGAGCCACAG PEX6ex02 [PEX6ex02 PEX6ex02 [W13-Rev]-ATTACAGACGTGAGCCACAG PEX6ex1ev [M13-Rev]-ATTACAGACGTGAGCCACAGG PEX6ex1ev [M13-Rev]-ATTACAGCACAGGATCACAGGAG PEX6ex1ev [M13-Rev]-ATCAGGGATCTCATGGGGGC PEX6ex1forw [-21M13]-TGTAGCAGCAGTCACAGGAG PEX6ex1forw [-21M13]-ACAAGGCAGTCACAGGAGC PEX6ex1forw [-21M13]-TCAAGGGAGTCACAGGAGC PEX6ex1forw [-21M13]-ACAAGGCAGTCACAGGAGC PEX6e10/11 row [-21M13]-ACAAGGCCTCACAGGAGC	PEX6_c619rev	[M13-Rev]-CAGCACATCTGGCACAAAACC
PEX8_c:50rev [M13-Rev]-CGGTGTCTCGGTCGGAAAGG PEX8_c:-860fw [-21M13]-TTCCCCACCTTGTCATCTCCAG PEX6_c:-744rev [M13-Rev]-ACAGTCGAAACCCA PEX8_c:-844rev [M13-Rev]-AACAGTCGAAACCGCAACCCA PEX8_c:-844rev [M13-Rev]-AACCGCAAGGGAACCGCACCC PEX6tin forw [-21M13]-TGACGGAAGCGCACTCCTGG PEX6tin forw [-21M13]-TGGTCGAGACCGCACGCTGG PEX6tin forw [-21M13]-TGCTGAGAGACGGAGTAGAG PEX6tin forw [-21M13]-TGTCCTTGGAGACACGGTAGAG PEX6exon2 forw [-21M13]-TGTTCCTTGGAGAACTGCG PEX6exon2 rev [M13-Rev]-ACTCATGCACCAGGTTAC PEX6exo1 forw [-21M13]-TGTTCCTTGGCAGTTACTGAGGACAGGTAC PEX6ex0 rev [M13-Rev]-ACTCAGGCAGTTCATTAGG PEX6ex1 forw [-21M13]-TGTTCCTTGGCCAGTTCATTAGG PEX6ex1 forw [-21M13]-TGCCCCAGCTTTGTGATTACTG PEX6ex6 frow [-21M13]-TGCCCCAGCTTTGAGAGAC PEX6ex7-rev [M13-Rev]-ACAGGGACGTCAAGGGAC PEX6ex8-rev [M13-Rev]-TACAAAGCCAGGGACC PEX6ex9-fw [-21M13]-TGCCCCAGCTTAGTGGCAC PEX6et0/11 forw [-21M13]-TGCCCGTCCTCTGTGAGAC PEX6et10/11 forw [M13-Rev]-TGTGGGAGTACCACAGGC <t< td=""><td>PEX6_c667fw</td><td>[-21M13]-TGAACAGGGCAAGAAGTCC</td></t<>	PEX6_c667fw	[-21M13]-TGAACAGGGCAAGAAGTCC
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PEX6in0 forw [-21M13]-TGACGGAAGCGGAAGCGGCCCTCG PEX6ex1arevil [M13-Rev]-AAACCGCAAAGGAGACACC PEX6etb forw [-21M13]-TAGTTGGCACTGCTTGG PEX6iN1 revil [M13-Rev]-TATGTTCAAAGTCCGGGATG PEX6exon2 forw [-21M13]-TGCTGAGAGACAGCTCACAG PEX8exon2 rev [M13-Rev]-ATTACAGACCTGAGCCACAG PEX8ex3-fw [-21M13]-TGTTCCTTGGAGAACTGCG PEX8ex3-fw [-21M13]-TGTTGTCCTCTGTGATTGAG PEX8ex3-fw [-21M13]-TGTTGTCCTCTGTGATTGAG PEX8ex3-fw [-21M13]-TGTTGTCCTCTGTGATTGAG PEX8ex4/5 rev [M13-Rev]-ACTCAGGCAGTTTATAGG PEX8ex5/rev [M13-Rev]-CCCCAGCTTTGAGAGGC PEX8ex6/r forw [-21M13]-TGACGGCAGTCACAGGAG PEX8ex8-rev [M13-Rev]-TATAACAAAGCCAGGGACC PEX8ex8-rev [M13-Rev]-TATACAAAGCCAGGGACC PEX8ex9-rev [M13-Rev]-TATGGCACTGATGGTGAG PEX8et0/11 forw [-21M13]-ATGGGACGTCAATGCAGGACC PEX8et12/13forw [-21M13]-TGCCGCCTCAAGGCACATAC PEX8et12/13forw [-21M13]-TGCAGCACTGAAGGCACCCCTAAGGCC PEX8et12/13forw [-21M13]-TGCATGCAACATGCAGGCC PEX8et12/13forw [-21M13]-TGCATGCAACATGCAGGCTACAAGC	PEX6_c844rev	[M13-Rev]-AACAGTCGACTTCCTGCGTG
PEX6ex1arevil [M13-Rev]-AAACCGCAAAGGAGGACACC PEX6e1b forw [-21M13]-TAGGTTGGCACTGCTGG PEX6e1b forw [-21M13]-TAGTTCAAAGTCCGGGATG PEX6exon2 forw [-21M13]-TGCTGAGAGACAGGTTAGAG PEX6exon2 rev [M13-Rev]-ATTACAGACGTGAGCCACAG PEX6exon2 rev [M13-Rev]-ATTACAGACGTGAGCCACAG PEX6ex3-rev [M13-Rev]-ACTCATGCACCCAGGTTAC PEX6ex3-rev [M13-Rev]-ACTCATGCACCCAGGTTAC PEX6ex3-rev [M13-Rev]-ACTCATGCCACCAGGTTAC PEX6ex3-rev [M13-Rev]-ACTCTGGCCAGTTCATTAGG PEX6ex4/5 rev [M13-Rev]-CCCCCAGCCTTGTGATAGG PEX6ex5/rev [M13-Rev]-CCCCCAGCTTTGAGAGGC PEX6ex6/rev [M13-Rev]-TATAACAAAGCCAGGGACC PEX6ex8-rev [M13-Rev]-TCCGCCTTGTGTGTCCT PEX6ex9-rev [M13-Rev]-TCTCGCCTTGTGTGCC PEX6ev10/11 forw [-21M13]-TGCGTGCAGTGGAGGCCC PEX6e12/13rev [M13-Rev]-TCTCTGGACTCTGACGGCC PEX6e14/15rev [M13-Rev]-TCTCTGGACTCTGAAGGC PEX6e16/17 forw [-21M13]-TGCATGCAACATGCAGGACG PEX6e16/17 forw [-21M13]-TGCATGCAACATGCAGGACG PEX6e16/17 forw [-21M13]-TGCCTGGCCTTCAAGGCC PEX6e	PEX6in0 forw	[-21M13]-TGACGGAAGCGGAAGCGGCCCTCG
PEX6e1b forw [-21M13]-TAGGTTGGGCACTGCTTGG PEX6IN1 revII [M13-Rev]-TATGTTCAAAGTCCGGGATG PEX6exon2 forw [-21M13]-TGCTGAGAGACAGGTTAGAG PEX6exon2 rev [M13-Rev]-ATTACAGACGTGAGCCACAG PEX6ex3-fev [M13-Rev]-ATTACAGACCGGAGCCACAG PEX6ex3-rev [M13-Rev]-ACTCATGCACCCAGGTTAC PEX6ex3-rev [M13-Rev]-ACTCATGCACCCAGGTTAC PEX6ex45 forw [-21M13]-TGTTGTCCTCTGGCATGGAT PEX6ex67-rev [M13-Rev]-ACTCAGGCAGTTCATTAGG PEX6ex67-rev [M13-Rev]-CCCCCAGGTTGAGAGGC PEX6ex7-rev [M13-Rev]-TCCAGGCAGTCCACAGGAG PEX6ex8-rev [M13-Rev]-TATAACAAAGCCAGGGACC PEX6ex9-rev [M13-Rev]-TATACAAAGCCAGGGAGC PEX6et0/11 forw [-21M13]-TGCCGCCTTTCTGGTGCC PEX6e10/11 forw [-21M13]-ATGGGACCGTGAGGTGAG PEX6e10/11 forw [-21M13]-TGTTGCATCTAGAGGCACCCCCTAGG PEX6e10/11 forw [-21M13]-TGTTGCATCTAGAGGCACCCCCCTAGG PEX6e11/15rev [M13-Rev]-TCCTGGACACAGGCACAAGGC PEX6e12/13rev [M13-Rev]-TCTTGGACCCCCAAGGCC PEX6e14/15rev [M13-Rev]-GCCCTAGACACACAGGCACAGGCACAGGCACCCCCCCCCAAG PEX6e14/15rev [M13-Rev]-GCCCTAGACACACAGC	PEX6ex1arevII	[M13-Rev]-AAACCGCAAAGGAGGACACC
PEX6IN1 revII [M13-Rev]-TATGTTCAAAGTCCGGGATG PEX6exon2 forw [-21M13]-TGCTGAGAGACAGGTTAGAG PEX6exon2 rev [M13-Rev]-ATTACAGACGTGAGCCACAG PEX6ex3-fw [-21M13]-TTGTTCTTGGAGAGACTGCG PEX6ex3-fw [-21M13]-TGTTCTTGGACCACAGGTTAC PEX6ex3-rev [M13-Rev]-ACTCATGCACCCAGGTTAC PEX6ex3-rev [M13-Rev]-ACTCATGCACCCAGGTTAG PEX6ex4/5 rev [M13-Rev]-ACTCATGCCCCAGGTTATAGG PEX6ex5-rev [M13-Rev]-ACTCAGGCAGTTCATTAGG PEX6ex6/rev [M13-Rev]-ACAAGGCAGTCCAAGGAG PEX6ex8-rev [M13-Rev]-TATAACAAAGCCAGGGACC PEX6ex8-rev [M13-Rev]-TATAACAAAGCCAGGGACC PEX6ex8-rev [M13-Rev]-TCCGCCTTCTGGTGCCT PEX6ex9-rev [M13-Rev]-TCCGCCTTCTGGAGCACATAC PEX6e10/11 forw [-21M13]-ATGGGACGCTGAAGGCACATAC PEX6e10/11 rev [M13-Rev]-TCTCGGACTCGAAGACTG PEX6e11/15rev [M13-Rev]-TCTCGGACTCGAAGACTG PEX6e12/13rev [M13-Rev]-TCTCGGACACATGCAGGATG PEX6e16/17 forw [-21M13]-TGCAGAGAGTACCACAGGC PEX6e16/17 forw [-21M13]-TGCCAGCACTGCAGAACAGCCAGGAGT PEX6e16/17 forw [-21M13]-TCCCACACTGTGCAACACGCAGGAGT	PEX6e1b forw	[-21M13]-TAGGTTGGGCACTGCTTGG
PEX6exon2 forw[-21M13]-TGCTGAGAGACAGGTTAGAGPEX6exon2 rev[M13-Rev]-ATTACAGACGTGAGCCACAGPEX6ex3-fw[-21M13]-TGTTCCTCTGGAGAACTGCGPEX6ex3-rev[M13-Rev]-ACTCATGCACCCAGGTTACPEX6ex/5 forw[-21M13]-TGTTGTCCTCTGTGATTGAGPEX6ex/5 rev[M13-Rev]-ACTCTGGCCAGTTCATTAGGPEX6ex/5 rev[M13-Rev]-ACTCAGGCAGTTCATGAGGGCPEX6ex/6 forw[-21M13]-TGCAGGCAGTCCACAGGAGPEX6ex/6 rev[M13-Rev]-CCCCCCAGCTTTGAGAGGCPEX6ex8-fw[-21M13]-ACAAGGCAGTCCACAGGAGPEX6ex8-rev[M13-Rev]-TATACAAAAGCCAGGAGCPEX6ex9-rev[M13-Rev]-TTCCGCCTTCTGGTGCCPEX6ex9-rev[M13-Rev]-TTCCGCCTTCTGGTGCCPEX6ex9-rev[M13-Rev]-TTCCGCCTCAGATGCACATACPEX6ex9-rev[M13-Rev]-TGTGCACCAGAGCACATACPEX6e12/13row[-21M13]-GTATGTGCATCTGACGGCTCPEX6e12/13rev[M13-Rev]-TGTTGCAGCACACAGGCPEX6e14/15rev[M13-Rev]-TGTTGCAGCACACAGGAGCPEX6e16/17 forw[-21M13]-TGCCCACACTGCACACAGGCPEX6e16/17 forw[-21M13]-TCCTCGTGGGCTATCAAGPEX6e16/17 rev[M13-Rev]-GCCTCTAGAGCAGACTACAGCPEX6_c.2807-21fw[-21M13]-TCCTCGTTGTGGTCCTGACPEX6_c.2807-21fw[-21M13]-TCCCGACAGAACCCCAAGGPEX6_c.295fw[-21M13]-TCCTCGTTGTGTCCTGTCPEX6_c.295fw[-21M13]-TCCTCGTGGGCTACAAGGPEX6_c.191fw[-21M13]-TCCTCCTCAGAGACTCCCTTCCPEX6_c.295fw[-21M13]-TCCTCGTGGAGATCACACCGPEX6_c.198frev[M13-Rev]-TCCTCCTCAGAGACACACACAGCACPEX6_c.198frev[M13-Rev]-TCCTCCTCCAGAGATGTGPEX6_c.230ffw[-21M13]-AAGGAGGAGAA	PEX6IN1 revII	[M13-Rev]-TATGTTCAAAGTCCGGGATG
PEX6exon2 rev [M13-Rev]-ATTACAGACGTGAGCCACAG PEX6ex3-fw [-21M13]-TTGTTCTTTGGAGAACTGCG PEX6ex3-rev [M13-Rev]-ACTCATGCACCCAGGTTAC PEX6ex4/5 forw [-21M13]-TGTTTGTCCTCTGTGATTGAG PEX6ex/5 rev [M13-Rev]-ACTCTGGCCAGTTCATTAGG PEX6ex/5 rev [M13-Rev]-ACTCTGGCCAGTTCATTAGG PEX6ex/7 rev [M13-Rev]-CCCCCAGCTTTGTGTTACTG PEX6ex7-rev [M13-Rev]-CCCCCAGCTTTGAGAGGC PEX6ex8-rev [M13-Rev]-TATAACAAAAGCCAGGGACC PEX6ex8-rev [M13-Rev]-TATAACAAAAGCCAGGGACC PEX6ex9-rev [M13-Rev]-TCCGCCTGTGTGTCT PEX6ex9-rev [M13-Rev]-TCCGCCTGCATGTGTGCC PEX6e10/11 forw [-21M13]-ATGGGACCGTGATGGTGAG PEX6e10/11 rev [M13-Rev]-TCTCGGCACAGACATAC PEX6e12/13rev [M13-Rev]-TCTCTGGACCTGAACATAC PEX6e12/13rev [M13-Rev]-TCTCTGTGGACTCAAGGC PEX6e14/15rev [M13-Rev]-TCTCTGTGGCACCCCAAGGC PEX6e14/15rev [M13-Rev]-TCTCTCTGTGGGCTATCAAG PEX6e16/17 rov [-21M13]-TAAGGAGAGGTACCACAGGC PEX6e16/17 rev [M13-Rev]-TCTCTCTGTGGGCCATCAGGC PEX6e16/17 rev [M13-Rev]-TCTCTCTGTGGGCTATCAAG	PEX6exon2 forw	[-21M13]-TGCTGAGAGACAGGTTAGAG
PEX6ex3-fw [-21M13]-TTGTTCCTTGGAGAACTGCG PEX6ex3-rev [M13-Rev]-ACTCATGCACCCAGGTTAC PEX6e4/5 forw [-21M13]-TGTTTGTCCTCTGTGATTGAG PEX6e4/5 forw [-21M13]-TCTAGGGCACCCAGGTTACTAGG PEX6e6/7 forw [-21M13]-TCTAGGGCAGTCTGTGTTACTG PEX6ee/7 forw [-21M13]-TCTAAGGGATCTTGTGTTACTG PEX6ex7-rev [M13-Rev]-CCCCCAGCTTTGAGAGGC PEX6ex8-fw [-21M13]-TCAAGGGCAGTCACAGGGAGC PEX6ex8-fw [-21M13]-TGCAGGGCAGTCACAGGGAGC PEX6ex9-fw [-21M13]-TGCGCCTGCTGTGTGTCT PEX6ex9-fw [-21M13]-TGCGGCCTGATGGTGAG PEX6e10/11 forw [-21M13]-ATGGGACCGTCAGATGCACATAC PEX6e10/11 forw [-21M13]-GTATGTGCATCTGACGGCTC PEX6e12/13forw [-21M13]-TAAGGAGGTACCACAGGC PEX6e12/13rev [M13-Rev]-TGTTGCATGCAACAGGCC PEX6e14/15rev [M13-Rev]-TGTTGCATGCACAGAGCTG PEX6e14/15rev [M13-Rev]-TCTCTGTGGGCTATCAAG PEX6e16/17 rev [M13-Rev]-TCTCTCTGTGGGCTATCAAG PEX6_c.2807-21fw [-21M13]-TCCCACACTGCAGAACCGCAAGGC PEX6_c.2807-21fw [-21M13]-TCCTGGTGGTGTCTGTC PEX6_c.2807-21fw [-21M13]-TCCTGGTGGGTATCAAGG	PEX6exon2 rev	[M13-Rev]-ATTACAGACGTGAGCCACAG
PEX6ex3-rev[M13-Rev]-ACTCATGCACCCAGGTTACPEX6e4/5 forw[-21M13]-TGTTTGTCCTCTGTGATTGAGPEX6e4/5 rev[M13-Rev]-ACTCTGGCCAGTTCATTAGGPEX6e4/5 rev[M13-Rev]-ACTCTGGCCAGTTCATTAGGPEX6e6/7 forw[-21M13]-TCTAAGGGATCTTGTGTTACTGPEX6ex7-rev[M13-Rev]-CCCCCAGCTTTGAGAGGCPEX6ex8-fw[-21M13]-ACAAGGCAGTCCACAGGAGPEX6ex8-rev[M13-Rev]-TATAACAAAAGCCAGGGACCPEX6ex9-fw[-21M13]-ACAGGCAGTCTCATGTGTCCTPEX6ex9-rev[M13-Rev]-TTCCGCCTTCTGGTGCCPEX6ex9-rev[M13-Rev]-TCCGCCTTCTGGTGAGPEX6e10/11 forw[-21M13]-ATGGGACGCTCAGATGCACATACPEX6e12/13rev[M13-Rev]-GAGCCGTCAGATGCACATACPEX6e12/13rev[M13-Rev]-TCTTGGACTCTGAAGACTGPEX6e14/15forw[-21M13]-TAAAGAAGAGTACCACAGGCPEX6e161/1 forw[-21M13]-TAAAGAAGAGTACCACAGGCPEX6e16/17 forw[-21M13]-TGCATGCAACATGCAGGATGPEX6e16/17 rev[M13-Rev]-TCTTCTGTGGGCTATCAAGPEX6_c.2807-21fw[-21M13]-TCCCACCACTTGCAGAGACTACAGCPEX6_c.265fw[-21M13]-TCCCCACCTTGTGCTGTCCTGTCPEX6_c.2491fw[-21M13]-TCCCCACCTTGCAGAGACTACAGCPEX6_c.2951fw[-21M13]-TGCAGAGAACACCCCAAGGPEX6_c.1951fw[-21M13]-TGCCAGAAGCCACAGTAGTGPEX6_c.1981rev[M13-Rev]-ATGGCAGAAACCCCACGPEX6_c.1981rev[M13-Rev]-ATGGCAGAAACCCCACGPEX6_c.1981rev[M13-Rev]-CCCACATGGAGACTTCCPEX6_c.239fw[-21M13]-ATGCAGAGAGACACACGCAAGGPEX6_c.230fw[-21M13]-ATGGAGAGACACACGCAGCPEX6_c.230fw[-21M13]-ACTGGGCAGAGAGTGCGGPEX6_c.230fw[-21M13]	PEX6ex3-fw	[-21M13]-TTGTTCCTTGGAGAACTGCG
PEX6e4/5 forw[-21M13]-TGTTTGTCCTCTGTGATTGAGPEX6e4/5 rev[M13-Rev]-ACTCTGGCCAGTTCATTAGGPEX6e4/5 rev[M13-Rev]-ACTCTGGCCAGTTCATTAGGPEX6e6/7 forw[-21M13]-TCTAAGGGATCTTGTGTTACTGPEX6ex7-rev[M13-Rev]-CCCCCAGCTTTGAGAGGCPEX6ex8-fw[-21M13]-ACAAGGCAGTCCACAGGAGPEX6ex8-rev[M13-Rev]-TATAACAAAAGCCAGGGACCPEX6ex9-fw[-21M13]-ACAGGACGCTGATGTGCCTPEX6ex9-fw[-21M13]-TGCCCTGCTCATGTGTCCTPEX6ex9-rev[M13-Rev]-TTCCGGCTTCTGGTGGCPEX6e10/11 forw[-21M13]-ATGGGACGCTCAGATGGAGGPEX6e10/11 rev[M13-Rev]-GAGCCGTCAGATGCACATACPEX6e12/13rev[M13-Rev]-TCTCTGGACTCTGAAGACTGPEX6e12/13rev[M13-Rev]-TCTTGGCATCCCAAGGCPEX6e14/15forw[-21M13]-TAAAGAGAGGTACCACAGGCPEX6e16/17 forw[-21M13]-TGCATGCAACATGCAGGAGGPEX6e16/17 rev[M13-Rev]-TCTCTCTGTGGGCTATCAAGPEX6_c.2807-21fw[-21M13]-TCCCCACCTTGCAGAGACTACAGCPEX6_c.25fw[-21M13]-TCCCCACCTTGCAGAGCCAAGGCPEX6_c.29fw[-21M13]-TCCCCACCTTGCAGAGACTACAGCPEX6_c.29fw[-21M13]-TCCTCGTGGTGTCCTGTCPEX6_c.39fw[-21M13]-TGCCAGAGAGTTACAAGGPEX6_c.1951fw[-21M13]-TGCCAGAGAGTTACAAGGCPEX6_c.198rev[M13-Rev]-ATGGCACAAGGCAAGCACACGAAGGPEX6_c.198rev[M13-Rev]-ATGGCACACAGCAGATGTGCPEX6_c.248fw[-21M13]-TGCCAGAAACCCCACAGTAGTGPEX6_c.239fw[-21M13]-TGCCAGAAACCACAGTAGCACPEX6_c.2339fw[-21M13]-ACTGGGCACAAGGAGACCACAGGAGPEX6_c.230fw[-21M13]-ACTGGGCTACCAAGGAGPEX6_c.230fw[-21M13	PEX6ex3-rev	[M13-Rev]-ACTCATGCACCCAGGTTAC
PEX6e4/5 rev [M13-Rev]-ACTCTGGCCAGTTCATTAGG PEX6e6/7 forw [-21M13]-TCTAAGGGATCTTGTGTTACTG PEX6ex7-rev [M13-Rev]-CCCCCAGCTTTGAGAGGC PEX6ex8-rev [-21M13]-ACAAGGCAGTCCACAGGAG PEX6ex8-rev [M13-Rev]-TATAACAAAAGCCAGGGACC PEX6ex8-rev [M13-Rev]-TATAACAAAAGCCAGGGACC PEX6ex9-rev [M13-Rev]-TATAACAAAAGCCAGGGAG PEX6e10/11 forw [-21M13]-TGGGACGCTGATGGTGAG PEX6e12/13forw [-21M13]-ATGGGACGCTGAAGAGCACATAC PEX6e12/13forw [-21M13]-GTATGTGCATCTGACGGCTC PEX6e12/13forw [-21M13]-GTATGTGCATCTGACGGCTC PEX6e14/15forw [-21M13]-TAAAGAGAGGTACCACAGGC PEX6e14/15forw [-21M13]-TGCATGCAACATGCCACAGGC PEX6e16/17 forw [-21M13]-TGCCATGCAACATGCCAGGATG PEX6e16/17 forw [-21M13]-TCCCAACTTGCAGGAGATCAAGG PEX6_c.2807-21fw [-21M13]-TCCCCACCTTGTCAAGGCAGCACACAGG PEX6_c.2807-21fw [-21M13]-TCCCAACATGCCAGAACCGCAAAGG PEX6_c.c325fw [-21M13]-TCCCGACTGTGTCCCAGG PEX6_c.c491fw [-21M13]-TCCCGACTGTGTCCCAGAGC PEX6_c.c491fw [-21M13]-TGCCAGACATACCACCCTTCC PEX6_c.c491fw [-21M13]-TGCCAGACACACCGC	PEX6e4/5 forw	[-21M13]-TGTTTGTCCTCTGTGATTGAG
PEX6e6/7 forw [-21M13]-TCTAAGGGATCTTGTGTTACTG PEX6ex7-rev [M13-Rev]-CCCCCAGCTTTGAGAGGC PEX6ex8-fw [-21M13]-ACAAGGCAGTCCACAGGAG PEX6ex8-rev [M13-Rev]-TATAACAAAAGCCAGGGACC PEX6ex8-rev [M13-Rev]-TATAACAAAAGCCAGGGACC PEX6ex9-fw [-21M13]-TGCCCTGCTCATGTGTCCT PEX6ex9-rev [M13-Rev]-TTCCGCCTTCTGGTGCC PEX6e10/11 forw [-21M13]-ATGGGACGCTGAGTGCACATAC PEX6e12/13forw [-21M13]-GTATGTGCATCTGACGACCACAGG PEX6e12/13rev [M13-Rev]-GTCTCTGGACTCTGAAGACTG PEX6e14/15rev [M13-Rev]-TCTCTGGACTCCCAAGGC PEX6e14/15rev [M13-Rev]-TGTTGCATGCATCCCCTAAG PEX6e16/17 forw [-21M13]-TCACAGCAACATGCAGGAGC PEX6e16/17 rev [M13-Rev]-TCTCTCTGTGGGGCTATCAAG PEX6_c.2807-21fw [-21M13]-TCCCCACCTTGCATCACAGC PEX6_c.2807-21fw [-21M13]-TCCCCGTCTGAGAGCACACAGC PEX6_c.c25fw [-21M13]-TCCCCGTTGGTGTCCTGTC PEX6_c.c22rev [M13-Rev]-GCCCTCAGAGACTCCCGCAAGGG PEX6_c.c1075rev [M13-Rev]-TGGCCAGAAGCCACAGGAGC PEX6_c.c191fw [-21M13]-TGCCAGAGAGTTACACATCG PEX6_c.1988rev [M13-Rev]-TCCTCCCAGAGGTTTGCAGCAC	PEX6e4/5 rev	[M13-Rev]-ACTCTGGCCAGTTCATTAGG
PEX6ex7-rev [M13-Rev]-CCCCCAGCTTTGAGAGGC PEX6ex8-fw [-21M13]-ACAAGGCAGTCCACAGGAG PEX6ex8-rev [M13-Rev]-TATAACAAAAGCCAGGGACC PEX6ex8-rev [M13-Rev]-TATAACAAAAGCCAGGGACC PEX6ex9-fw [-21M13]-TGCCCTGCTCATGTGCCT PEX6ex9-rev [M13-Rev]-TTCCGCCTTTCTGGTGCC PEX6e10/11 forw [-21M13]-ATGGGACGCTGATGGTGAG PEX6e10/11rev [M13-Rev]-GAGCCGTCAGATGCACATAC PEX6e12/13forw [-21M13]-GTATGTGCATCTGAAGGCCT PEX6e12/13rev [M13-Rev]-TCTCTGGACTCTGAAGACTG PEX6e14/15forw [-21M13]-TAAAGAGAGGTACCACAGGC PEX6e14/15forw [-21M13]-TGCATGCATGCACCACAGGC PEX6e16/17 forw [-21M13]-TGCATGCAACATGCAGGATG PEX6e16/17 rev [M13-Rev]-TCTCTGTGGGCTATCAAG PEX6_c.2807-21fw [-21M13]-TCCCCACCTTGCAGAGCACACAGC PEX6_c.2807-21fw [-21M13]-TCCTCGTTGGTGTCCTGTC PEX6_c.265fw [-21M13]-TCCTCGTTGGTGCCAGAGACTACAGC PEX6_c.2610/17 [M13-Rev]-GCCTCTAGAGCAGACTACAGC PEX6_c.2610/17 [M13-Rev]-GCCTCTAGAGCAGACTACAGC PEX6_c.2807-21fw [-21M13]-TCCCCGCTTGCAGAGCACAGC PEX6_c.2800/17 [M13-Rev]-GCCTCTAGAGCAGCCAGC	PEX6e6/7 forw	[-21M13]-TCTAAGGGATCTTGTGTTACTG
PEX6ex8-fw[-21M13]-ACAAGGCAGTCCACAGGAGPEX6ex8-rev[M13-Rev]-TATAACAAAAGCCAGGGACCPEX6ex9-rev[M13-Rev]-TATAACAAAAGCCAGGGACCPEX6e10/11 forw[-21M13]-TGCCCTGCTCATGTGTCCTPEX6e10/11 forw[-21M13]-ATGGGACGCTCAGATGCACATACPEX6e10/11rev[M13-Rev]-GAGCCGTCAGATGCACATACPEX6e12/13forw[-21M13]-GTATGTGCATCTGAAGGCTCPEX6e12/13rev[M13-Rev]-TCTCTGGACTCTGAAGACTGPEX6e14/15forw[-21M13]-TAAAGAGAGGTACCACAGGCPEX6e14/15rev[M13-Rev]-TGTTGCATGCATCCCCTAAGPEX6e16/17 forw[-21M13]-TGCATGCAACATGCACAGGAGTGPEX6e16/17 forw[-21M13]-TCCCCACCTTGTGGGGCTATCAAGPEX6e16/17 rev[M13-Rev]-TCTCTGTGGGGCTATCAAGPEX6_c.2807-21fw[-21M13]-TCCCCACCTTGCATCCCCAGPEX6_c.625fw[-21M13]-TCCCGACGAGAGCACAAGCPEX6_c.625fw[-21M13]-TCCCGAGAGAACCGCAAAGCPEX6_c.625fw[-21M13]-TCCTCGTTGGTGTCCTGTCPEX6_c.1075rev[M13-Rev]-GTGCCAGAAACCGCAAAGGPEX6_c.1075rev[M13-Rev]-ATGGCCTGCAGAAACCCCCTTCCPEX6_c.1422fw[-21M13]-TGCCAGAGAGCACCACAGTAGGTGPEX6_c.1422fw[-21M13]-TGCCCCCCTCCAGTAGAGCACPEX6_c.188erv[M13-Rev]-TCCTCCTCCAGTCAGCACGPEX6_c.188erv[M13-Rev]-TCCTCCTCCAGGAAATGTGCGGPEX6_c.239fw[-21M13]-ACTTGGGACAGCTACAAGCACPEX6_c.239fw[-21M13]-AAGTGAGGAAATGTGCGGPEX6_c.3004rev[M13-Rev]-TCTGTGGGGCTATCAAGGTACPEX6_c.330fw[-21M13]-AAGTGAGGAAGGAAGGAATGTGCGGPEX6_c.330fwATGTGGGCCAAAGTGAGGAG	PEX6ex7-rev	[M13-Rev]-CCCCCAGCTTTGAGAGGC
PEX6ex8-rev[M13-Rev]-TATAACAAAAGCCAGGGACCPEX6ex9-rev[-21M13]-TGCCCTGCTCATGTGTCCTPEX6ev9-rev[M13-Rev]-TTCCGCCTTTCTGGTGCCPEX6e10/11 forw[-21M13]-ATGGACGCTCAGATGCACATACPEX6e10/11 rev[M13-Rev]-GAGCCGTCAGATGCACATACPEX6e12/13forw[-21M13]-GTATGTGCATCTGACGGCTCPEX6e12/13rev[M13-Rev]-TCTCTGGACTCTGAAGACTGPEX6e14/15forw[-21M13]-GTATGTGCATCCACAGGCPEX6e14/15forw[-21M13]-TAAAAGAGAGGTACCACAGGCPEX6e14/15forw[-21M13]-TGCATGCAACATGCAGGATGPEX6e16/17 forw[-21M13]-TGCCTGCAGCACATGCAGGATGPEX6e16/17 forw[-21M13]-TCCCCACCTTGTGCAGGGATGPEX6_c.2807-21fw[-21M13]-TCCCCACCTTGTCATCCCAGPEX6_c.625fw[-21M13]-TCCCGTTGGTGTCCTGTCPEX6_c.625fw[-21M13]-TCCCGTGTGGTGCCAGAACCGCAAAGGPEX6_c.625fw[-21M13]-CCCAGACTGTGTCCAGAGTCPEX6_c.1075rev[M13-Rev]-GCCTGCAGAAACCGCAAAGGPEX6_c.191fw[-21M13]-TGCCAGAGAGTTACACATCGPEX6_c.1422fw[-21M13]-TGGCAGAGAGCCACAGTAGTGPEX6_c.1422fw[-21M13]-TGGCACAGCACAGTAGCACPEX6_c.1856fw[-21M13]-ACTTGGCACAGCTAGCACGPEX6_c.188fev[M13-Rev]-TCCTCCTCCAGTCAAGCCACPEX6_c.2488rev[M13-Rev]-TCCATCACTCCTCCAGAAACPEX6_c.2488rev[M13-Rev]-TCCTCTCCAGGCTATCAAGCACPEX6_c.239fw[-21M13]-AAGTGAGGAGAAATGTGCGGPEX6_c.3004rev[M13-Rev]-TCTGTGGGCTATCAAGGTACPEX6_c.330fwATGTGGGCCAAAGTGAGGAGPEX6_c.2330fwATGTGGGCCAAAGTGAGGAG	PEX6ex8-fw	[-21M13]-ACAAGGCAGTCCACAGGAG
PEX6ex9-fw[-21M13]-TGCCCTGCTCATGTGTCCTPEX6ex9-rev[M13-Rev]-TTCCGCCTTTCTGGTGCCPEX6e10/11 forw[-21M13]-ATGGGACGCTGAGATGGTGAGPEX6e10/11 rev[M13-Rev]-GAGCCGTCAGATGCACATACPEX6e12/13forw[-21M13]-GTATGTGCATCTGACGGCTCPEX6e12/13rev[M13-Rev]-TCTCGGACTCTGAAGACTGPEX6e14/15forw[-21M13]-TAAAGAGAGGTACCACAGGCPEX6e14/15rev[M13-Rev]-TCTTGGATGCATCCCCTAAGPEX6e16/17 forw[-21M13]-TGCATGCAACATGCAGGATGPEX6e16/17 rev[M13-Rev]-TCTCTCTGTGGGCTATCAAGPEX6_c.2807-21fw[-21M13]-TCCCCACCTTGTCATCCCAGPEX6_c.625fw[-21M13]-TCCTCGTTGGTGTCCTGTCPEX6_c.625fw[-21M13]-TCCTCGTTGGTGTCCTGTCPEX6_c.491fw[-21M13]-CCAGACTGGTGTCCAGAACGCAAAGGPEX6_c.1075rev[M13-Rev]-GTGCCAGAAACTCCCCTTCCPEX6_c.1541rev[M13-Rev]-CACATAGAACATCCCCTTCCPEX6_c.1422fw[-21M13]-TGGCAGAGAGTTACAACATCGPEX6_c.1422fw[-21M13]-TGGGAAGCCACAGTAGTGPEX6_c.1856fw[-21M13]-ACTTGGCACAGCAGCAGCACGPEX6_c.1856fw[-21M13]-ACTTGGCACAGCAGCACGPEX6_c.1856fw[-21M13]-ACTTGGCACAGCTAGCACGPEX6_c.2468rev[M13-Rev]-TCCTCCTCCAGAATGTGCGGPEX6_c.2339fw[-21M13]-AAGTGAGGAGAATGTGCGGPEX6_c.330fw[-21M13]-AAGTGAGGAGAGAAGTACCAAGGAACCACAGGAACCACAGGAACCACAGGAACCAAGGAACACAAGGAACACAAGGAACACACAGCACCAC	PEX6ex8-rev	[M13-Rev]-TATAACAAAAGCCAGGGACC
PEX8ex9-rev[M13-Rev]-TTCCGCCTTTCTGGTGCCPEX6e10/11 forw[-21M13]-ATGGGACGCTGATGGTGAGPEX6e10/11 rev[M13-Rev]-GAGCCGTCAGATGCACATACPEX6e12/13forw[-21M13]-GTATGTGCATCTGACGGCTCPEX6e12/13rev[M13-Rev]-TCTCTGGACTCTGAAGACTGPEX6e14/15forw[-21M13]-TAAAGAGAGGTACCACAGGCPEX6e14/15forw[-21M13]-TAAAGAGAGGTACCACAGGCPEX6e16/17 forw[-21M13]-TGCATGCATGCAACATGCAGGATGPEX6e16/17 rev[M13-Rev]-TGTTCTCTGTGGGCTATCAAGPEX6_c.2807-21fw[-21M13]-TCCCCACCTTGTCATCTCCAGPEX6_c.625fw[-21M13]-TCCTCGTTGGTGTCCTGTCPEX6_c.625fw[-21M13]-TCCTCGTTGGTGTCCTGTCPEX6_c.290rev[M13-Rev]-GCCTCTAGAACATCCCCTTCCPEX6_c.1075rev[M13-Rev]-CACATAGAACATCCCCTTCCPEX6_c.191fw[-21M13]-TGCCAGAGAGTTACACATCGPEX6_c.192fw[-21M13]-TGCCAGAGAGTTACACATCGPEX6_c.1988rev[M13-Rev]-ATGGCCTGCAGTTTGTCTCPEX6_c.1856fw[-21M13]-TGCGACAGACACACGCAAGCCACPEX6_c.2488rev[M13-Rev]-TCCTCCTCCAGAATGCACACPEX6_c.2339fw[-21M13]-AAGTGGAGAGAATGTGCGGPEX6_c.330fw[-21M13]-AAGTGAGGAGAATCCAAGGTACPEX6_c.2330fw[-21M13]-AAGTGAGGAGAATCCAAGGTACPEX6_c.2330fw[-21M13]-AAGTGAGGAGAAGACAACGGAAGTACPEX6_c.2330fw[-21M13]-AAGTGAGGAGAGAATGTGCGGPEX6_c.2330fw[-21M13]-AAGTGAGGAGAAGAGAAGACAACGGAAGTACPEX6_c.2330fw[-21M13]-AAGTGAGGAGAAGAAGTGCCGG	PEX6ex9-fw	[-21M13]-TGCCCTGCTCATGTGTCCT
PEX6e10/11 forw[-21M13]-ATGGGACGCTGATGGTGAGPEX6e10/11rev[M13-Rev]-GAGCCGTCAGATGCACATACPEX6e12/13forw[-21M13]-GTATGTGCATCTGACGGCTCPEX6e12/13rev[M13-Rev]-TCTCTGGACTCTGAAGACTGPEX6e14/15forw[-21M13]-TAAAGAGAGGGTACCACAGGCPEX6e14/15forw[-21M13]-TGCATGCATGCATCCCCTAAGPEX6e16/17 forw[-21M13]-TGCATGCAACATGCAGGATGPEX6e16/17 rev[M13-Rev]-TCTCTCTGTGGGCTATCAAGPEX6_c.2807-21fw[-21M13]-TCCCCACCTTGTCATCTCCAGPEX6_c.625fw[-21M13]-TCCCGTGGGGTCCTGTCPEX6_c.625fw[-21M13]-TCCCGTGGGGTCCTGTCPEX6_c.21075rev[M13-Rev]-GTGCCAGAAACCGCAAAGGPEX6_c.1951fw[-21M13]-TCCCCAGAGGAGTTACAACATCCPEX6_c.1422fw[M13-Rev]-ATGGCCTGCAGAGATGTGTCPEX6_c.1422fw[M13-Rev]-ATGGCCTGCAGTAGTGPEX6_c.1888rev[M13-Rev]-TCCTCCTCAGACAGCACCPEX6_c.2468rev[M13-Rev]-TCCTCCTCAGACAGCACCPEX6_c.2468rev[M13-Rev]-TCCTCACACTCCTCCAGAAACCPEX6_c.2339fw[-21M13]-ACTTGGGGCAAAGTGCGGPEX6_c.2330fwATGTGGGCCAAAGTGAGGAGPEX6_c.2330fw[-21M13]-AAGTGAGGAGAAGTGACGACACAGTACCPEX6_c.2330fw[-21M13]-AAGTGAGGAGAAGTGACGAGPEX6_c.2330fw[-21M13]-AAGTGAGGAGAAGTGACGAGPEX6_c.2330fw[-21M13]-AAGTGAGGAGAAGTGACGAGPEX6_c.2330fw[-21M13]-AAGTGAGGAGAAGTGACGAGPEX6_c.2330fw[-21M13]-AAGTGAGGAGAAGTGACGAGPEX6_c.2330fw[-21M13]-AAGTGAGGAGAAGTGACGAGGAGAAGTGCCACAGGAGAAGTGACGAGGAGAAGTGAGGAGAAGTGAGGAGAAGTGAGGAGAAGTGAGGAG	PEX6ex9-rev	[M13-Rev]-TTCCGCCTTTCTGGTGCC
PEX6e10/11rev[M13-Rev]-GAGCCGTCAGATGCACATACPEX6e12/13forw[-21M13]-GTATGTGCATCTGACGGCTCPEX6e12/13rev[M13-Rev]-TCTCTGGACTCTGAAGACTGPEX6e14/15forw[-21M13]-TAAAGAGAGGTACCACAGGCPEX6e14/15rev[M13-Rev]-TGTTGCATGCATCCCCTAAGPEX6e16/17 forw[-21M13]-TGCATGCAACATGCAGGATGPEX6e16/17 rev[M13-Rev]-TCTCTCTGTGGGCTATCAAGPEX6_c.2807-21fw[-21M13]-TCCCCACCTTGTCATCTCCAGPEX6_c.*541rev[M13-Rev]-GCCTCTAGAGCAGACTACAGCPEX6_c.*541rev[M13-Rev]-GCCCAGAAACCGCAAAGGPEX6_c22rev[M13-Rev]-GTGCCAGAAACCGCAAAGGPEX6_c.1075rev[M13-Rev]-CACATAGAACATCCCCTTCCPEX6_c.1075rev[M13-Rev]-ATGGCCTGCAGAGGTTACAACATCGPEX6_c.1422fw[-21M13]-TGCCAGAGAGTTACACATCGPEX6_c.1422fw[-21M13]-TGCCAGAGAGCACACAGTAGTGPEX6_c.1988rev[M13-Rev]-ATGGCCTGCAGCAGCACACGPEX6_c.1856fw[-21M13]-ACTTGGCACAGCAACCACCPEX6_c.2468rev[M13-Rev]-TCCTCCTCAGTCAAGCACCPEX6_c.2339fw[-21M13]-AAGTGAGGAGAAATGTGCGGPEX6_c.3004rev[M13-Rev]-TCTGTGGGCTATCAAGGTACPEX6_c.330fwATGTGGGCCAAAGTGAGGAGAPEX6_c.2330fwATGTGGGCCAAAGTGAGGAGA	PEX6e10/11 forw	[-21M13]-ATGGGACGCTGATGGTGAG
PEX6e12/13forw[-21M13]-GTATGTGCATCTGACGGCTCPEX6e12/13rev[M13-Rev]-TCTCTGGACTCTGAAGACTGPEX6e14/15forw[-21M13]-TAAAGAGAGGTACCACAGGCPEX6e14/15rev[M13-Rev]-TGTTGCATGCATGCACCCCTAAGPEX6e16/17 forw[-21M13]-TGCATGCAACATGCAGGATGPEX6e16/17 rev[M13-Rev]-TCTCTCTGTGGGGCTATCAAGPEX6_c.2807-21fw[-21M13]-TCCCCACCTTGTCATCTCCAGPEX6_c.2807-21fw[-21M13]-TCCCCACCTTGTCATCTCCAGPEX6_c.2807-21fw[-21M13]-TCCCCACCTTGTGTGTCCTGTCPEX6_c.2807-21fw[-21M13]-TCCCGTTGGTGTCCTGTCPEX6_c.625fw[-21M13]-TCCTCGTTGGTGTCCTGTCPEX6_c.625fw[-21M13]-TCCTCGTTGGTGTCCTGTCPEX6_c.921fw[-21M13]-CCAGACTGTGTCCAGAGGTCPEX6_c.1075rev[M13-Rev]-CACATAGAACATCCCCTTCCPEX6_c.1075rev[M13-Rev]-ATGGCCTGCAGTTACACATCGPEX6_c.1541rev[M13-Rev]-ATGGCCTGCAGTATCACATCGPEX6_c.1951fw[-21M13]-TGGGAAGACCACAGTAGTTGPEX6_c.1988rev[M13-Rev]-TCCTCCTCAGTCAAGCCACPEX6_c.1856fw[-21M13]-ACTTGGCACAGCTAGCACGPEX6_c.2468rev[M13-Rev]-TCCATCACTCCTCCAGAATCPEX6_c.2339fw[-21M13]-AAAGTGAGGAGAATGTGCGGPEX6_c.3004rev[M13-Rev]-TCTGTGGGCTATCAAGGTACPEx6_c.330fwATGTGGGCCAAAGTGAGGAGAG	PEX6e10/11rev	[M13-Rev]-GAGCCGTCAGATGCACATAC
PEX6e12/13rev[M13-Rev]-TCTCTGGACTCTGAAGACTGPEX6e14/15forw[-21M13]-TAAAGAGAGGTACCACAGGCPEX6e14/15rev[M13-Rev]-TGTTGCATGCATCCCCTAAGPEX6e16/17 forw[-21M13]-TGCATGCAACATGCAGGATGPEX6e16/17 rev[M13-Rev]-TCTCTCTGTGGGCTATCAAGPEX6_c.2807-21fw[-21M13]-TCCCCACCTTGTCATCTCCAGPEX6_c.2807-21fw[-21M13]-TCCCCACCTTGTCATCTCCAGPEX6_c.2807-21fw[-21M13]-TCCCCACCTTGTCATCTCCAGPEX6_c.2807-21fw[-21M13]-TCCCCACCTTGTCATCACAGCPEX6_c.2807-21fw[-21M13]-TCCCCACCTTGTCATCACAGCPEX6_c.625fw[-21M13]-TCCTCGTTGGTGTCCTGTCPEX6_c.625fw[-21M13]-CCCAGACTGTGTCCAGAGTCPEX6_c.1075rev[M13-Rev]-CACATAGAACATCCCCTTCCPEX6_c.1075rev[M13-Rev]-CACATAGAACATCCCCTTCCPEX6_c.1951fw[-21M13]-TGCCAGAGAGTTACACATCGPEX6_c.1541rev[M13-Rev]-ATGGCCTGCAGTTTTGTCTCPEX6_c.1422fw[-21M13]-TGCCAGAGACCACAGTAGTGGPEX6_c.1856fw[-21M13]-ACTTGGCACAGCTAGCACGPEX6_c.2468rev[M13-Rev]-TCCATCACTCCTCCAGAATCPEX6_c.2339fw[-21M13]-AAGTGAGGAGAATGTGCGGPEX6_c.3004rev[M13-Rev]-TCTGTGGGCTATCAAGGTACPEx6_c.330fwATGTGGGCCAAAGTGAGGAGAPEx6_c.330fwATGTGGGCCAAAGTGAGGAGA	PEX6e12/13forw	[-21M13]-GTATGTGCATCTGACGGCTC
PEX6e14/15forw[-21M13]-TAAAGAGAGGTACCACAGGCPEX6e14/15rev[M13-Rev]-TGTTGCATGCATCCCCTAAGPEX6e16/17 forw[-21M13]-TGCATGCAACATGCAGGATGPEX6e16/17 rev[M13-Rev]-TCTCTCTGTGGGCTATCAAGPEX6_c.2807-21fw[-21M13]-TCCCCACCTTGTCATCTCCAGPEX6_c.2807-21fw[-21M13]-TCCCCACCTTGTCATCTCCAGPEX6_c.2807-21fw[-21M13]-TCCCCACCTTGTCATCTCCAGPEX6_c.2807-21fw[-21M13]-TCCCCACCTTGTGTGTCCTGTCPEX6_c.625fw[-21M13]-TCCTCGTTGGTGTCCTGTCPEX6_c22rev[M13-Rev]-GTGCCAGAAACCGCAAAGGPEX6_c.191fw[-21M13]-CCAGACTGTGTCCAGAGTCPEX6_c.1075rev[M13-Rev]-CACATAGAACATCCCCTTCCPEX6_c.1951fw[-21M13]-TGCCAGAGAGTTACACATCGPEX6_c.1541rev[M13-Rev]-ATGGCCTGCAGTTTTGTCTCPEX6_c.1541rev[M13-Rev]-TCCTCCTCAGTCAGGCACGPEX6_c.1422fw[-21M13]-TGGGAAGACCACAGTAGTTGPEX6_c.1988rev[M13-Rev]-TCCTCCTCAGTCAAGCCACPEX6_c.2339fw[-21M13]-AAAGTGAGGAGAATGTGCGGPEX6_c.2339fw[-21M13]-AAAGTGAGGAGAGACCACAGGTACPEX6_c.3004rev[M13-Rev]-TCTGTGGGCTATCAAGGTACPex6_2330fwATGTGGGCCAAAGTGAGGAG	PEX6e12/13rev	[M13-Rev]-TCTCTGGACTCTGAAGACTG
PEX6e14/15rev[M13-Rev]-TGTTGCATGCATCCCCTAAGPEX6e16/17 forw[-21M13]-TGCATGCAACATGCAGGATGPEX6e16/17 rev[M13-Rev]-TCTCTCTGTGGGCTATCAAGPEX6_c.2807-21fw[-21M13]-TCCCCACCTTGTCATCTCCAGPEX6_c.541rev[M13-Rev]-GCCTCTAGAGCAGACTACAGCPEX6_c.625fw[-21M13]-TCCTCGTTGGTGTCCTGTCPEX6_c.625fw[-21M13]-TCCTCGTTGGTGTCCTGTCPEX6_c22rev[M13-Rev]-GTGCCAGAAACCGCAAAGGPEX6_c.491fw[-21M13]-CCAGACTGTGTCCAGAGTCPEX6_c.1075rev[M13-Rev]-CACATAGAACATCCCCTTCCPEX6_c.1951fw[-21M13]-TGCCAGAGAGTTACACATCGPEX6_c.1541rev[M13-Rev]-ATGGCCTGCAGTATTGTCTCPEX6_c.1422fw[-21M13]-TGGGAAGACCACAGTAGTTGPEX6_c.1422fw[-21M13]-TGGCACAGCTACAGCACPEX6_c.1856fw[-21M13]-ACTTGGCACAGCTAGCACGPEX6_c.2468rev[M13-Rev]-TCCATCACTCCTCCAGAATCPEX6_c.2339fw[-21M13]-AAAGTGAGGAGAATGTGCGGPEX6_c.3004rev[M13-Rev]-TCTGTGGGCTATCAAGGTACPex6_2330fwATGTGGGCCAAAGTGAGGAG	PEX6e14/15forw	[-21M13]-TAAAGAGAGGTACCACAGGC
PEX6e16/17 forw[-21M13]-TGCATGCAACATGCAGGATGPEX6e16/17 rev[M13-Rev]-TCTCTCTGTGGGCTATCAAGPEX6_c.2807-21fw[-21M13]-TCCCCACCTTGTCATCTCCAGPEX6_c.541rev[M13-Rev]-GCCTCTAGAGCAGACTACAGCPEX6_c.625fw[-21M13]-TCCTCGTTGGTGTCCTGTCPEX6_c22rev[M13-Rev]-GTGCCAGAAACCGCAAAGGPEX6_c.491fw[-21M13]-CCAGACTGTGTCCAGAGTCPEX6_c.1075rev[M13-Rev]-CACATAGAACATCCCCTTCCPEX6_c.951fw[-21M13]-TGCCAGAGAGTTACACATCGPEX6_c.1541rev[M13-Rev]-ATGGCCTGCAGTAGTTGTCCCPEX6_c.1422fw[-21M13]-TGGGAAGACCACAGTAGTTGPEX6_c.1888rev[M13-Rev]-TCCTCCTCAGTCAAGCCACPEX6_c.2468rev[M13-Rev]-TCCATCACTCCTCCAGAACCPEX6_c.2339fw[-21M13]-AAAGTGAGGAGAATGTGCGGPEX6_c.3004rev[M13-Rev]-TCTGTGGGCTATCAAGGTACPex6_2330fwATGTGGGGCCAAAGTGAGGAGA	PEX6e14/15rev	[M13-Rev]-TGTTGCATGCATCCCCTAAG
PEX6e16/17 rev[M13-Rev]-TCTCTCTGTGGGCTATCAAGPEX6_c.2807-21fw[-21M13]-TCCCCACCTTGTCATCTCCAGPEX6_c.*541rev[M13-Rev]-GCCTCTAGAGCAGACTACAGCPEX6_c.625fw[-21M13]-TCCTCGTTGGTGTCCTGTCPEX6_c22rev[M13-Rev]-GTGCCAGAAACCGCAAAGGPEX6_c.491fw[-21M13]-CCAGACTGTGTCCAGAGTCPEX6_c.1075rev[M13-Rev]-CACATAGAACATCCCCTTCCPEX6_c.951fw[-21M13]-TGCCAGAGAGTTACACATCGPEX6_c.1541rev[M13-Rev]-ATGGCCTGCAGTTTGTCTCPEX6_c.1422fw[-21M13]-TGCGAAGACCACAGTAGTTGPEX6_c.1988rev[M13-Rev]-TCCTCCTCAGTCAAGCCACPEX6_c.2468rev[M13-Rev]-TCCATCACTCCTCCAGAAACCPEX6_c.2339fw[-21M13]-AAAGTGAGGAGAATGTGCGGPEX6_c.3004rev[M13-Rev]-TCTGTGGGCTATCAAGGTACPex6_2330fwATGTGGGGCCAAAGTGAGGAG	PEX6e16/17 forw	[-21M13]-TGCATGCAACATGCAGGATG
PEX6_c.2807-21fw[-21M13]-TCCCCACCTTGTCATCTCCAGPEX6_c*541rev[M13-Rev]-GCCTCTAGAGCAGACTACAGCPEX6_c.625fw[-21M13]-TCCTCGTTGGTGTCCTGTCPEX6_c22rev[M13-Rev]-GTGCCAGAAACCGCAAAGGPEX6_c.491fw[-21M13]-CCAGACTGTGTCCAGAGTCPEX6_c.1075rev[M13-Rev]-CACATAGAACATCCCCTTCCPEX6_c.951fw[-21M13]-TGCCAGAGAGTTACACATCGPEX6_c.1541rev[M13-Rev]-ATGGCCTGCAGTTTTGTCTCPEX6_c.1422fw[-21M13]-TGGGAAGACCACAGTAGTTGPEX6_c.1988rev[M13-Rev]-TCCTCCTCAGTCAAGCCACPEX6_c.1856fw[-21M13]-ACTTGGCACAGCTAGCACGPEX6_c.2468rev[M13-Rev]-TCCATCACTCCTCCAGAATCPEX6_c.3004rev[M13-Rev]-TCTGTGGGCTATCAAGGTACPEx6_c.330fwATGTGGGCCAAAGTGAGGAG	PEX6e16/17 rev	[M13-Rev]-TCTCTCTGTGGGGCTATCAAG
PEX6_c*541rev[M13-Rev]-GCCTCTAGAGCAGACTACAGCPEX6_c.625fw[-21M13]-TCCTCGTTGGTGTCCTGTCPEX6_c.22rev[M13-Rev]-GTGCCAGAAACCGCAAAGGPEX6_c.491fw[-21M13]-CCAGACTGTGTCCAGAGTCPEX6_c.1075rev[M13-Rev]-CACATAGAACATCCCCTTCCPEX6_c.951fw[-21M13]-TGCCAGAGAGTTACACATCGPEX6_c.1541rev[M13-Rev]-ATGGCCTGCAGTTTTGTCTCPEX6_c.1422fw[-21M13]-TGGGAAGACCACAGTAGTTGPEX6_c.1988rev[M13-Rev]-TCCTCCTCAGTCAAGCCACPEX6_c.1856fw[-21M13]-ACTTGGCACAGCTAGCACGPEX6_c.2468rev[M13-Rev]-TCCATCACTCCTCCAGAATCPEX6_c.2339fw[-21M13]-AAAGTGAGGAGAATGTGCGGPEX6_c.3004rev[M13-Rev]-TCTGTGGGCTATCAAGGTACPex6_2330fwATGTGGGCCAAAGTGAGGAG	PEX6_c.2807-21fw	[-21M13]-TCCCCACCTTGTCATCTCCAG
PEX6_c.625fw[-21M13]-TCCTCGTTGGTGTCCTGTCPEX6_c22rev[M13-Rev]-GTGCCAGAAACCGCAAAGGPEX6_c.491fw[-21M13]-CCAGACTGTGTCCAGAGTCPEX6_c.1075rev[M13-Rev]-CACATAGAACATCCCCTTCCPEX6_c.951fw[-21M13]-TGCCAGAGAGTTACACATCGPEX6_c.1541rev[M13-Rev]-ATGGCCTGCAGTTTTGTCTCPEX6_c.1422fw[-21M13]-TGGGAAGACCACAGTAGTTGPEX6_c.1988rev[M13-Rev]-TCCTCCTCAGTCAAGCCACPEX6_c.1856fw[-21M13]-ACTTGGCACAGCTAGCACGPEX6_c.2468rev[M13-Rev]-TCCATCACTCCTCCAGAATCPEX6_c.3004rev[M13-Rev]-TCTGTGGGCTATCAAGGTACPEx6_c.330fwATGTGGGCCAAAGTGAGGAG	PEX6_c*541rev	[M13-Rev]-GCCTCTAGAGCAGACTACAGC
PEX6_c22rev[M13-Rev]-GTGCCAGAAACCGCAAAGGPEX6_c.491fw[-21M13]-CCAGACTGTGTCCAGAGTCPEX6_c.1075rev[M13-Rev]-CACATAGAACATCCCCTTCCPEX6_c.951fw[-21M13]-TGCCAGAGAGTTACACATCGPEX6_c.1541rev[M13-Rev]-ATGGCCTGCAGTTTTGTCTCPEX6_c.1422fw[-21M13]-TGGGAAGACCACAGTAGTTGPEX6_c.1988rev[M13-Rev]-TCCTCCTCAGTCAAGCCACPEX6_c.1856fw[-21M13]-ACTTGGCACAGCTAGCACGPEX6_c.2468rev[M13-Rev]-TCCATCACTCCTCCAGAATCPEX6_c.3004rev[M13-Rev]-TCTGTGGGCTATCAAGGTACPEx6_c.330fwATGTGGGCCAAAGTGAGGAG	PEX6_c.625fw	[-21M13]-TCCTCGTTGGTGTCCTGTC
PEX6_c.491fw[-21M13]-CCAGACTGTGTCCAGAGTCPEX6_c.1075rev[M13-Rev]-CACATAGAACATCCCCTTCCPEX6_c.951fw[-21M13]-TGCCAGAGAGTTACACATCGPEX6_c.1541rev[M13-Rev]-ATGGCCTGCAGTTTTGTCTCPEX6_c.1422fw[-21M13]-TGGGAAGACCACAGTAGTTGPEX6_c.1988rev[M13-Rev]-TCCTCCTCAGTCAAGCCACPEX6_c.1856fw[-21M13]-ACTTGGCACAGCTAGCACGPEX6_c.2468rev[M13-Rev]-TCCATCACTCCTCCAGAATCPEX6_c.2339fw[-21M13]-AAAGTGAGGAGAATGTGCGGPEX6_c.3004rev[M13-Rev]-TCTGTGGGCTATCAAGGTACPex6_2330fwATGTGGGCCAAAGTGAGGAG	PEX6_c22rev	[M13-Rev]-GTGCCAGAAACCGCAAAGG
PEX6_c.1075rev[M13-Rev]-CACATAGAACATCCCCTTCCPEX6_c.951fw[-21M13]-TGCCAGAGAGTTACACATCGPEX6_c.1541rev[M13-Rev]-ATGGCCTGCAGTTTTGTCTCPEX6_c.1422fw[-21M13]-TGGGAAGACCACAGTAGTTGPEX6_c.1988rev[M13-Rev]-TCCTCCTCAGTCAAGCCACPEX6_c.1856fw[-21M13]-ACTTGGCACAGCTAGCACGPEX6_c.2468rev[M13-Rev]-TCCATCACTCCTCCAGAATCPEX6_c.2339fw[-21M13]-AAAGTGAGGAGAATGTGCGGPEX6_c.3004rev[M13-Rev]-TCTGTGGGCTATCAAGGTACPex6_2330fwATGTGGGCCAAAGTGAGGAG	PEX6_c.491fw	[-21M13]-CCAGACTGTGTCCAGAGTC
PEX6_c.951fw[-21M13]-TGCCAGAGAGTTACACATCGPEX6_c.1541rev[M13-Rev]-ATGGCCTGCAGTTTTGTCTCPEX6_c.1422fw[-21M13]-TGGGAAGACCACAGTAGTTGPEX6_c.1988rev[M13-Rev]-TCCTCCTCAGTCAAGCCACPEX6_c.1856fw[-21M13]-ACTTGGCACAGCTAGCACGPEX6_c.2468rev[M13-Rev]-TCCATCACTCCTCCAGAATCPEX6_c.2339fw[-21M13]-AAAGTGAGGAGAATGTGCGGPEX6_c.3004rev[M13-Rev]-TCTGTGGGCTATCAAGGTACPex6_2330fwATGTGGGCCAAAGTGAGGAG	PEX6_c.1075rev	[M13-Rev]-CACATAGAACATCCCCTTCC
PEX6_c.1541rev [M13-Rev]-ATGGCCTGCAGTTTTGTCTC PEX6_c.1422fw [-21M13]-TGGGAAGACCACAGTAGTTG PEX6_c.1988rev [M13-Rev]-TCCTCCTCAGTCAAGCCAC PEX6_c.1856fw [-21M13]-ACTTGGCACAGCTAGCACG PEX6_c.2468rev [M13-Rev]-TCCATCACTCCTCCAGAATC PEX6_c.2339fw [-21M13]-AAAGTGAGGAGAATGTGCGG PEX6_c.3004rev [M13-Rev]-TCTGTGGGCTATCAAGGTAC Pex6_2330fw ATGTGGGCCAAAGTGAGGAG	PEX6_c.951fw	[-21M13]-TGCCAGAGAGTTACACATCG
PEX6_c.1422fw [-21M13]-TGGGAAGACCACAGTAGTTG PEX6_c.1988rev [M13-Rev]-TCCTCCTCAGTCAAGCCAC PEX6_c.1856fw [-21M13]-ACTTGGCACAGCTAGCACG PEX6_c.2468rev [M13-Rev]-TCCATCACTCCTCCAGAATC PEX6_c.2339fw [-21M13]-AAAGTGAGGAGAATGTGCGG PEX6_c.3004rev [M13-Rev]-TCTGTGGGCTATCAAGGTAC Pex6_2330fw ATGTGGGCCAAAGTGAGGAG	PEX6_c.1541rev	[M13-Rev]-ATGGCCTGCAGTTTTGTCTC
PEX6_c.1988rev [M13-Rev]-TCCTCCTCAGTCAAGCCAC PEX6_c.1856fw [-21M13]-ACTTGGCACAGCTAGCACG PEX6_c.2468rev [M13-Rev]-TCCATCACTCCTCCAGAATC PEX6_c.2339fw [-21M13]-AAAGTGAGGAGAATGTGCGG PEX6_c.3004rev [M13-Rev]-TCTGTGGGCTATCAAGGTAC Pex6_2330fw ATGTGGGCCAAAGTGAGGAG	PEX6_c.1422fw	[-21M13]-TGGGAAGACCACAGTAGTTG
PEX6_c.1856fw [-21M13]-ACTTGGCACAGCTAGCACG PEX6_c.2468rev [M13-Rev]-TCCATCACTCCTCCAGAATC PEX6_c.2339fw [-21M13]-AAAGTGAGGAGAATGTGCGG PEX6_c.3004rev [M13-Rev]-TCTGTGGGCTATCAAGGTAC Pex6_2330fw ATGTGGGCCAAAGTGAGGAG	PEX6_c.1988rev	[M13-Rev]-TCCTCCTCAGTCAAGCCAC
PEX6_c.2468rev [M13-Rev]-TCCATCACTCCTCCAGAATC PEX6_c.2339fw [-21M13]-AAAGTGAGGAGAATGTGCGG PEX6_c.3004rev [M13-Rev]-TCTGTGGGCTATCAAGGTAC Pex6_2330fw ATGTGGGCCAAAGTGAGGAG	PEX6_c.1856fw	[-21M13]-ACTTGGCACAGCTAGCACG
PEX6_c.2339fw [-21M13]-AAAGTGAGGAGAATGTGCGG PEX6_c.3004rev [M13-Rev]-TCTGTGGGCTATCAAGGTAC Pex6_2330fw ATGTGGGCCAAAGTGAGGAG	PEX6_c.2468rev	[M13-Rev]-TCCATCACTCCTCCAGAATC
PEX6_c.3004rev [M13-Rev]-TCTGTGGGCTATCAAGGTAC Pex6_2330fw ATGTGGGCCAAAGTGAGGAG	PEX6_c.2339fw	[-21M13]-AAAGTGAGGAGAATGTGCGG
Pex6_2330fw ATGTGGGCCAAAGTGAGGAG	PEX6_c.3004rev	[M13-Rev]-TCTGTGGGCTATCAAGGTAC
	Pex6_2330fw	ATGTGGGCCAAAGTGAGGAG

Pex6_c.2282fw	GTGCAGCCTTACCTTCCTCAG
PEX6attB2-rev	GGGGACCACTTTGTACAAGAAAGCTGGG
	TCCTAGCAGGCAGCAAACTTGC
PEX6-3end_mRNA_c2761fw	[-21M13]-GCTATGACAGCTGCCCTCAA
PEX6-3end_mRNA_c*459rev	[M13-Rev]-GCATGCATTGTGTTTATTTATGTCA
qPCR_PEX6_c.2466fw	GGACAGGGTGGTGTCTCAG
qPCR_PEX6_c.2566rev	GGTCCAGGAGATCTGGTCTG
qPCR_PEX6_c.*231fw	CATCTACTCAGGAAGAGGGCC
qPCR_PEX6_c.*375rev	CCACAACCCTGCTCTTTCTC

[M13-Rev], CAGGAAACAGCTATGACC; [-21M13], GTAAAACGACGGCCAGT

	individual P2		Half- P2 brother of P2		P3	P4	Father of P4	Р5	P6	P7		
	age at sampling	8 mo	9 уо	21 уо	n/a	7 уо	n/a	n/a	n/a	1 уо		
VLCFA	C22:0	0.457% (1.18 ± 0.61)	0.292% (1.18 ± 0.61)	1.002% (1.18 ± 0.61)	33.1µmol/l (55.1-11.43)	58µmol/l (28-76)	46µmol/l (16-76)	n/a	0.610% (1.18 ± 0.61)	18.62 µmol/l (40.3-103.7)		
concentration	C24:0	0.723% (0.78 ± 0.32)	0.668% (0.78 ± 0.32)	0.764% (0.78 ± 0.32)	47.9µmol/l (44.3-92.4)	65µmol/l (22-63)	40µmol/l (15-61)	n/a	0.818% (0.78 ± 0.32)	33.27 µmol/l (32.3-93.7)		
	C25:0	0.076% (0.03 ± 0.03)	0.058% (0.03 ± 0.03)	0.026% (0.03 ± 0.03)	n/a	1.8µmol/l (0-2)	1.1µmol/l (1-1.3)	n/a	0.061% (0.03 ± 0.03)	n/a		
	C26:0	0.093% (0.01 ± 0.01)	0.144% (0.01 ± 0.01)	0.008% (0.01 ± 0.01)	5.2µmol/l (0.220-0.880)	2.6µmol/l (0-0.8)	1.2µmol/l (0-0.74)	n/a	0.066% (0.01 ± 0.01)	6.29 µmol/l (0.35-1.36)		
		2.171µg/ml (0.33 ± 0.18)	1.937µg/ml (0.33 ± 0.18)	0.22µg/ml (0.33 ± 0.18)	n/a	n/a	n/a	n/a	1.42µg/ml (0.33 ± 0.18)	n/a		
	C26:1	n/a	0.432µg/ml (0.29 ± 0.19)	0.44µg/ml (0.29 ± 0.19)	n/a	n/a	n/a	n/a	0.42µg/ml (0.29 ± 0.19)	n/a		
VLCFA ratios	C24:0/C22:0	1.573 (0.84 ± 0.08)	2.287 (0.84 ± 0.08)	0.762 (0.84 ± 0.08)	1.40 (0.55-0.89)	1.11 (0-1.1)	0.96 (0-1.09)	1.225 (0.55-1.115)	1.341 (0.33 ± 0.18)	1.79 (0.69-1.08)		
	C26:0/C22:0	0.204 (0.01 ± 0.01)	0.492 (0.01 ± 0.01)	0.008 (0.01 ± 0.01)	0.157 (0.004-0.021)	0.045 (0-0.02)	0.028 (0-0.019)	0.194 (0- 0.035)	0.108 (0.01 ± 0.01)	0.338 (0.006-0.019)		
Phytanic acid		n/a	0.105 µg/ml (0-3)	n/a	2.8µg/ml (0-2.0)	5.2 μmol/l (0-5)	29.5µmol/l (0-5.9)	12 mg/100ml (0- 0.7)	10.5 μg/ml (0-3)	26.94 µmol/l (1.44-10.98)		
Pristanic acid		n/a	n/a	n/a	1.7µg/ml (0-1.0)	2.5 μmol/l (0-1)	16.6µmol/l (0-1.2)	n/a	n/a	10.32 µmol/l (0.06-1.42)		
Pipecolic acid		n/a	2.9 µmol/l (0.7-2.6)	n/a	n/a	n/a	n/a	n/a	8.8 µmol/l (0.7-2.6)	82 µmol/l (0-6)		

Table S2 – Peroxisomal parameters in blood of affected individuals & family members.

VLCFA, very long-chain fatty acids; mo, months old; yo, years old; *n/a*, not assessed; numbers between brackets indicate the reference range according to the laboratory in which the assays have been performed. Values measured in asymptomatic parents are depicted with a light grey background.

Supplemental references

- Karata K, Inagawa T, Wilkinson AJ, Tatsuta T, Ogura T. Dissecting the role of a conserved motif (the second region of homology) in the AAA family of ATPases. Site-directed mutagenesis of the ATPdependent protease FtsH. J Biol Chem 1999;274(37):26225–32.
- 2. Zhang X, Shaw A, Bates PA, et al. Structure of the AAA ATPase p97. 2000;6:1473–84.
- 3. Pettersen EF, Goddard TD, Huang CC, et al. UCSF Chimera A visualization system for exploratory research and analysis. J Comput Chem 2004;25(13):1605–12.