

Table 1 Suppl. Gene-specific primer pairs used in RT-PCR and real-time PCR experiments.

Gene	Primers (5' to 3')
<i>OsPPR19</i>	Forward : ATACTAGAACTCTGCCGGCACA CTGA Reverse : ACATCTCGGTGGCCTTTCCAAGCAT Reverse : GAGATTAGTGGGTTTGGGTTGTGG
<i>rpl2</i>	Forward : GAAGGATGGAGCGTACAAAGTC
<i>rpl2 intron1</i>	Forward : TTCTTAGGAAGAGCCGTACGAGG
<i>rpl2</i>	Reverse : CCGAAGGTATGTATGAGCATT C
<i>rps3</i>	Forward : CCAATTTCCGTAAGACTTGATC
<i>rps3 intron1</i>	Forward : GTATGTAGTCTGCGCTGGTGA
<i>rps3</i>	Reverse : ATACACCTACCGAGACGAAAGC
<i>cox2</i>	Forward : TCATTGCTATACCATCGTTTGC
<i>cox2 intron1</i>	Forward : AATAAGAGTAGGCGTGGAGAGC
<i>cox2</i>	Reverse : GTGAGTGACTGTT CATCGGAAC
<i>ccb452</i>	Forward : CACATGGAGGAGTGTGCATC
<i>ccb452 intron1</i>	Reverse : CCCGGATCGAATCAGAGTT
<i>ccb452</i>	Reverse : GTGGGTCCATGTAAATGATCG
<i>nad1 exon1-2</i>	Forward : TTGCCATATCTTCGCTAGGTG
<i>nad1 intron1</i>	Forward : CGTGCTCGTACGGTTCATAG
<i>nad1 exon1-2</i>	Reverse : GACCAATAGAGACTTCATAAGGGACCA
<i>nad1 exon2-3</i>	Forward : TCTGCAGCTCAAATGGTCTC
<i>nad1 intron2</i>	Reverse : AACTTGCACGTGTGGTTCTGG
<i>nad1 exon2-3</i>	Reverse : TGCCTTTCTAGGAGCATTACG
<i>nad1 exon3-4</i>	Forward : AGGTCCCTGTAATTCGAGTGAG
<i>nad1 intron3</i>	Forward : CTGTCTGACTAGAGTTTGATG
<i>nad1 exon3-4</i>	Reverse : AAAAGAGCAGACCCCATTGA
<i>nad1 exon4-5</i>	Forward : TCTTCAATGGGCTCTGCTC
<i>nad1 intron4</i>	Forward : ACGGAGCTGCATCCCTACT
<i>nad1 exon4-5</i>	Reverse : GCCAAGTCCCATTAATTGATC
<i>nad2 exon1-2</i>	Forward : CAGAGATCTTTATCATTAAC
<i>nad2 intron1</i>	Forward : TCATGCTGGAGGTACTAACCAC
<i>nad2 exon1-2</i>	Reverse : TGGGCAATAGTTAGGAGAGG
<i>nad2 exon2-3</i>	Forward : TTAGGTGCATTCCCTCTGG
<i>nad2 intron2</i>	Reverse : ATACGTGTAGTGTGGTGGTTGG
<i>nad2 exon2-3</i>	Reverse : CTTGAATAGGAATCCTACAGCG
<i>nad2 exon3-4</i>	Forward : TACCCACTTCGATCAATTAGCC
<i>nad2 intron3</i>	Forward : AGCGGCGAATTAACA ACTTGT
<i>nad2 exon3-4</i>	Reverse : TAGGCGCAATAGAAAGGAATG
<i>nad2 exon4-5</i>	Forward : TGTTCATACGCAGGAATACC
<i>nad2 intron4</i>	Reverse : AGTGAAGTTGGTGAGCCGTATG
<i>nad2 exon4-5</i>	Reverse : AACGACTTGTACGATCCATTG
<i>nad4 exon1-2</i>	Forward : ATTCTATGTTTTTCCCGAAAGC
<i>nad4 intron1</i>	Forward : CCGTATGATGCGGAAGTCTC
<i>nad4 exon1-2</i>	Reverse : TGGGTTGGTCTGGTATGAGAAG
<i>nad4 exon2-3</i>	Forward : AATACCCATGTTTCCCGAAG
<i>nad4 intron2</i>	Forward : AAATGTCTGGAGGTTACCAGATC
<i>nad4 exon2-3</i>	Reverse : CCCAATTCCCTGTATGTT C
<i>nad4 exon3-4</i>	Forward : TCCCTTTGGCTATATAATCGTG
<i>nad4 intron3</i>	Forward : TCTAGCTTGGTTCGGAGAGC
<i>nad4 exon3-4</i>	Reverse : TGAAATTTGCCATGTTGCAC
<i>nad5 exon1-2</i>	Forward : CCATGGATCTCATCGGAAAT
<i>nad5 intron1</i>	Forward : GAGGTTCCACCACCACATCATTG
<i>nad5 exon1-2</i>	Reverse : ACATAAATCGAGGGCTATGCG
<i>nad5 exon2-3</i>	Forward : CTCCTTTTCGTTTACTATTT C
<i>nad5 intron2</i>	Forward : AACCTACGATCGCCGTCTC
<i>nad5 exon2-3</i>	Reverse : TACCTAAACCAATCATCATATC
<i>nad5 exon3-4</i>	Forward : GATATGATGATTGGTTTAGGTA
<i>nad5 intron3</i>	Forward : GCCGTGTAATAGGCGACCA
<i>nad5 exon3-4</i>	Reverse : AACTCGGATTCGGCAAGAA
<i>nad5 exon4-5</i>	Forward : GTTCCTGCGTTTCGGATAT
<i>nad5 intron4</i>	Forward : CCTGTAAACCCCATGATGT
<i>nad5 exon4-5</i>	Reverse : AACATTGCAAAGGCATAATGA

<i>nad7 exon1-2</i>	Forward : ACCTCAACATCCTGCTGCTC
<i>nad7 intron1</i>	Forward : GAGGTCGAGCAGTCTCAATTC
<i>nad7 exon1-2</i>	Reverse : AAGGTAAAGCTTGAAGATAAGTTTGT
<i>nad7 exon2-3</i>	Forward : GAGGGACTGAGAAATTAATC
<i>nad7 intron2</i>	Forward : AGTGGGAGAGCCGTGTTATG
<i>nad7 exon2-3</i>	Reverse : CCACATCCATAGCATGAGTAG
<i>nad7 exon3-4</i>	Forward : ACTGTCACGACAGCAAGC
<i>nad7 intron3</i>	Forward : AGAACCGTTGTTGCCTGATG
<i>nad7 exon3-4</i>	Reverse : CGCATCTCTTCGATACGGATAC
<i>nad7 exon4-5</i>	Forward : GATCAAAGCCGATGATCGTAA
<i>nad7 intron4</i>	Forward : ACCACGTTAGGTTTGGAGAGAG
<i>nad7 exon4-5</i>	Reverse : AGGTGCTTCAACTGCGGTAT
<i>UBQ</i>	Forward : CCCTGACTGGCAAGACCATCACAC
	Reverse : TTGACGAAGATCTGCATACCACCC

Fig. 1 Suppl. Alignment of the amino acid sequences of *Arabidopsis* PPR19 and rice PPR19 proteins which harbor PPR motifs. The alignment was conducted using the *ClustalW* program. Gaps in the sequences are indicated by dashes

AtPPR19	1	NGEACSSFLKLLARYRIFNETEDVLGNLRNENVKLTHEALSHVLHAYAESGSLSKAVEITY
OsPPR19	1	TPLAHSILLRLLARSRRFDAVDDTLQSMFLAGAAPTRACLGALVAAYADAGMLGKATEMC
AtPPR19	61	DYVVELYDSVPDVIACNSLLSLLVKSRRRLGDARKVYDEMCDRGDSVDNYSTCILVKGMCN
OsPPR19	61	ERVREQYGSLEPVTHCNRLKLLVEQRRWDDARKLYDEMLGKDSGADNYSTCVLVRGLCL
AtPPR19	121	EGKVEVGRKLIEGRWGKGCIPNTVFYNTTIGGYCKLGDIENTAYLVFKELKLKGFMPLET
OsPPR19	121	ERVVEEGLKLIEARWGAGCIPHVFYNVLLIDGYCRRGDMGRGLLLLGEMETNGFLPTLVT
AtPPR19	181	EGTMINGFCKEGDFVASDRLLSEVKERGLRVSVWFLNNIIDAKYRHGYKVDPAESIGWII
OsPPR19	181	VGSIINWLGGKGDLEKIGSLFLEMRKRGFSPNVQIYNSVIDALCNCRSATQAMVILKQMF
AtPPR19	241	ANDCKPDVATYNILINRLCKEGKKEVAVGFLDEASKKGLIPNNLSYAPLIQAYCKSKEYD
OsPPR19	241	ASGCDPDIITENTLITGLCHEGHVRKAHEHFLREAIRREINPNQLSYTPLIHGFCMRGELM
AtPPR19	301	LASKLLQMAERGCKPDIVTYGILIHGLVVSGHMDDAVNMKVKLIDRGVSPDAAIYNMLM
OsPPR19	301	VASDLLVEMMGRGHTPDVVTFGALIHGLVVGKVSSEALIVREKMTERRQVFPDVNIYNVLI
AtPPR19	361	SGLCKTGRFLPAKLLFSEMLDRNLLPDAYVYATLIDGFIRSGDFDEARKVFSLSVEKGVK
OsPPR19	361	SGLCKKRMLPAKNILEEMLEKNVQPDFVYATLIDGFIRSENLDARKIFEFEHKGVC
AtPPR19	421	VDLVHHNAMIKGFCRSGMLDEALACMNRMNNEHLVPDKFTYSTIIDGYVKQQDMATAIKI
OsPPR19	421	PDIVSCNAMIKGVCQFGMMSEAILCMSNMRKVGCIPEFTYTTVISGYAKQGNLNGALRW
AtPPR19	481	FRYMEKNCKKPNVVITYTSLINGFCCQGDFFKMAEETFKEMQLRDLVNPVVITYTTLIRSLAK
OsPPR19	481	LCDMIKRRCKKPNVVITYSSLINGYCKTGDTDSAEGLFANMQAEALSNPVVITYTILIGSLFK
AtPPR19	541	ESSTLEKAVYYELMMTNKCVNPEVTFNCLLQGFVKKTSVKVLAEPDGSNHGQ-SSLFSE
OsPPR19	541	KD-KVLEAGLYEETMLLNHCSPNDVTLHYLVNGLTSCTPCVINSICCNTSEVHGKDALLV
AtPPR19	600	FFHRMKSQGWSDHAAAYNSALVCLCVHGMVKTACMFQDKMVKKGFSPDPVSFAAILHGFC
OsPPR19	600	VFKKLVFDIGDPRNSAYNAIIFSLCRHNMLREALDFKNRMAKKGYVNPITFLSLLYGFC
AtPPR19	660	VVGNSKQWRNMDFCNLGEKGLEMAVRYSQVLEQHLPPQPVICEASTILHAMVEKADTKPEV
OsPPR19	660	SVGKSVNWRITLPNEFQQEEFELIFRYKFLFDQYATESVCEVSRVLQHLAGCKSLQERVE
AtPPR19	720	ESP---
OsPPR19	720	QKFANS

Fig. 2 Suppl. PPR codes in rice and *Arabidopsis* PPR19 proteins. The PPR codes in the PPR19 proteins and target RNA sequences were predicted as previously described (Barkan et al., 2014; Lee et al., 2017). *Red colors* and *light green* colors indicate predictable and not predictable target sequences, respectively.

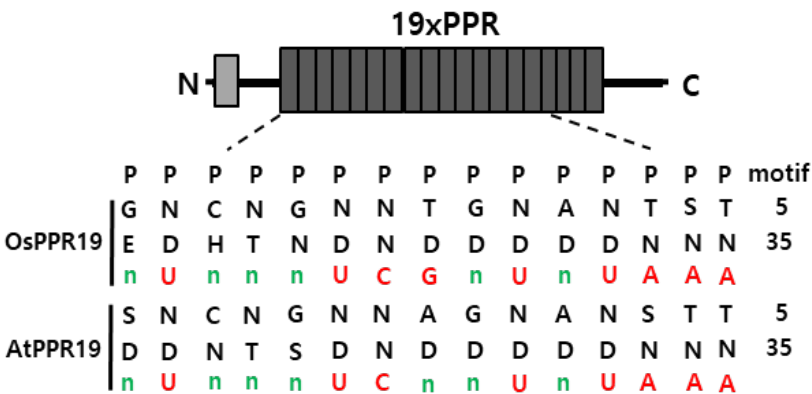


Fig. 3 Suppl. Phylogenetic tree of *Arabidopsis*, maize, and rice PPR19 orthologs. Phylogenetic tree rooted at midpoint was constructed using the neighbor-joining method with *MEGA11* program. Bootstrap value (percentages of 1 000 replications) was denoted at the branches and evolutionary distance was calculated using Poisson correction method. The Percentages (%) and the scale bar at bottom denote protein similarity between AtPPR19 and orthologous proteins and an evolutionary distance of 0.1 amino acid substitutions per position, respectively. AT - *Arabidopsis thaliana*, Os - *Oryza sativa*, GRMZM - *Zea mays*, POPRT - *Populus trichocarpa*.

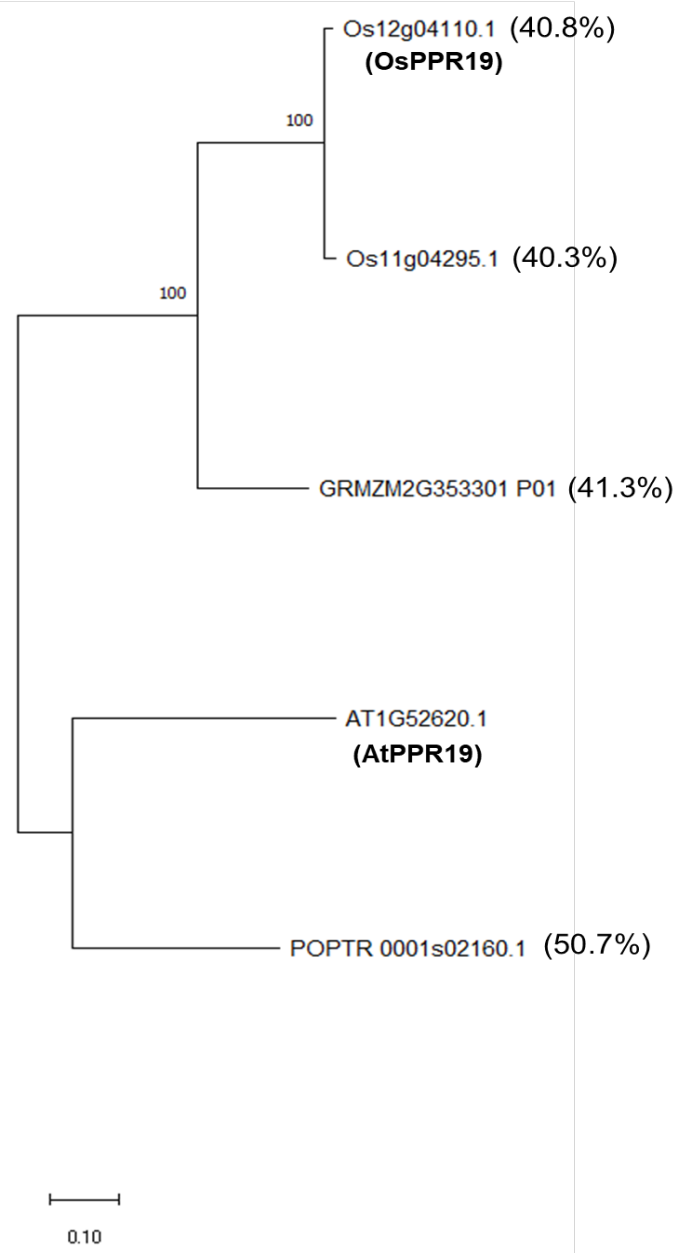


Fig. 4 Suppl. The structures of mitochondria in wild-type (WT) and *osprr19* mutants were analyzed using transmission electron micrographs (TEM).

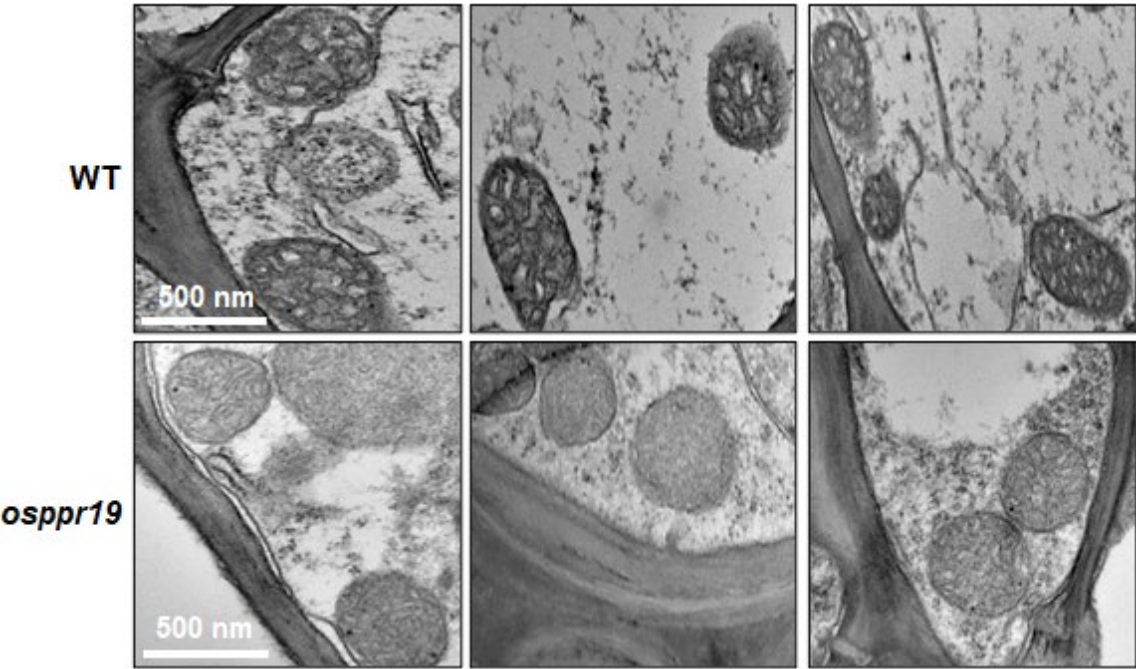


Fig. 5 Suppl. Subcellular localization of OsPPR19. *Green and red signals indicate mitochondria and mitotracker, respectively. Scale bar = 50 μ m*

