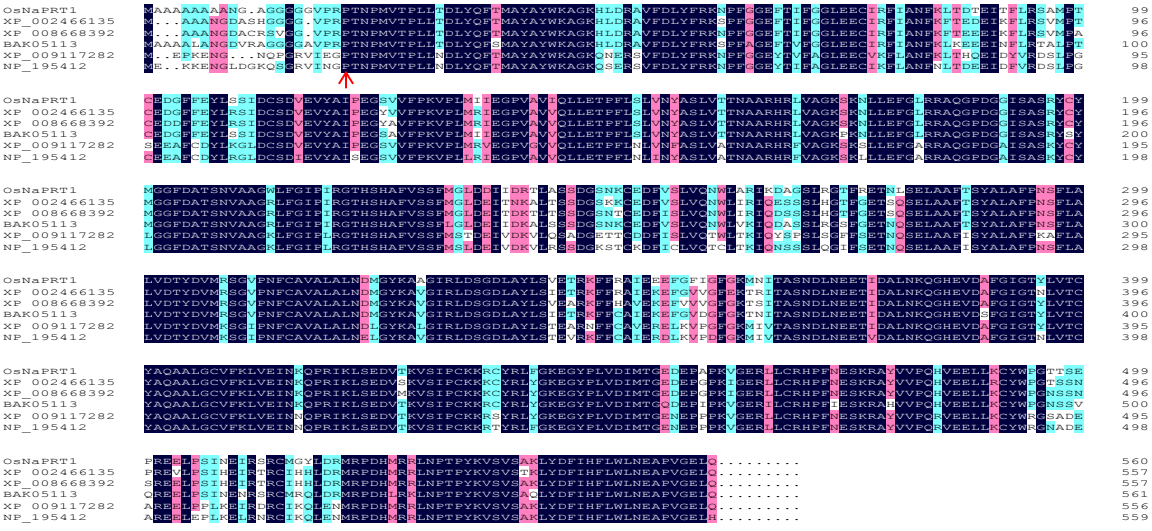
Supplemental Data



Supplemental Figure 1. Protein Sequence Alignment of OsNaPRT1 and Homologs.

Protein sequence alignment of OsNaPRT1 and homologs in sorghum, maize, barley, turnip, and *Arabidopsis thaliana* using Clustal W. Conserved amino acids are highlighted: white letters on a black background indicate amino acids conserved across all these samples (100% conservation). Arrowhead shows the mutant amino acid in *lts1*.

WT complementation OE

Supplemental Figure 2. The Phenotypes of Wild Type, Complementation and Overexpression Grains (top) and Brown Rice (bottom).

Bars=2 mm.

Supplemental Table 1. Functional Classification of Differentially Expressed Genes (DEGs) in *lts1* Mutant Compared to Wild Type Plants.

Gene Ontology Nos.	Gene Ontology Annotation	Down	Up
GO:0055114	oxidation reduction	36	75
GO:0006468	protein amino acid phosphorylation	21	73
GO:0045449	regulation of transcription	31	99
GO:0006508	proteolysis	10	22
GO:0016052	carbohydrate catabolic process	6	14
GO:0005976	polysaccharide metabolic process	2	15
GO:0009057	macromolecule catabolic process	5	13
GO:0019748	secondary metabolic process	2	14
GO:0006575	cellular amino acid derivative metabolic process	4	12
GO:0005996	monosaccharide metabolic process	5	9
GO:0009072	aromatic amino acid family metabolic process	2	10
GO:0006091	generation of precursor metabolites and energy	6	7
GO:0009698	phenylpropanoid metabolic process	0	11
GO:0046394	carboxylic acid biosynthetic process	4	13
GO:0051186	cofactor metabolic process	6	5
GO:0044271	nitrogen compound biosynthetic process	5	13
GO:0006811	ion transport	24	17
GO:0055085	transmembrane transport	5	6
GO:0007242	intracellular signaling cascade	3	10
GO:0006979	response to oxidative stress	2	11
GO:0010033	response to organic substance	4	8
GO:0009719	response to endogenous stimulus	3	8
GO:0006952	defense response	4	15
GO:0012501	cell death	1	8
Unknown	Unknown function	65	137
Total		256	625

Supplemental Table 2. Senescence-related Genes Identified by Affymetrix Microarray Analysis as Being Differentially Expressed in *lts1* Mutant Plants.

Locus	Annotation	Fold change
Up-regulated		Log2 ratio
LOC_Os09g35630	BAG domain-containing protein	2.15
LOC_Os12g36720	RGH1A	1.48
LOC_Os08g29854	RGH1A	1.17
LOC_Os06g41480	vrga1	1.17
LOC_Os02g35490	MLO domain containing protein	1.15
LOC_Os11g45930	NBS-LRR type disease resistance protein	1.10
LOC_Os11g13430	RGH1A	1.04
LOC_Os11g12330	disease resistance protein RPM1	1.01
Down-regulated		
LOC_Os11g31060	IQ calmodulin-binding and BAG domain containing protein	-1.27

Supplemental Table 3. PCR Primers Used in This Study.

Primer Name	Primer Sequence	Description
P1	AAGGAAAGAGTTGTCCGTAAAT	Fine mapping
	CCTGTAAGAAGATAGGGTCAAGAG	Fine mapping
P2	TGGTGGTAGTATTAGCCTTTGT	Fine mapping
	TTCTTTCAGGAGACTTGGGAAC	Fine mapping
P3	GGGTCCTAGTCCTTTCTTTCCG	Fine mapping
	AACTTTGCCTTTGCTTTGCCTC	Fine mapping
P4	TGCCAGCCTAGCGAGCCTAA	Fine mapping
	ATTGCAGCGAGCTACACG	Fine mapping
P5	ATGGCTTCAGACTTCAGAGT	Fine mapping
	CAAATTAACCTTCAGGCAAG	Fine mapping
ID-Na	TCCACTGTCCCTAAATCACC	Identification for osnaprt1
	TCCTTCTGCCTCGTCCAT	Identification for osnaprt1
ComNa1	CTGCAGGCAGGACATGCAGATGGAATGATGTCAGTG	Complementary construction
	GAGCTCACTTGATACCTGGCTGCCTCTAACACTAGG	Complementary construction
ComNa2	GAGCTCTATGGGAGGATTTGATGCAACAAGGTCTGG	Complementary construction
	GAGCTCCGCGCGGAGAGCTCCGGCGATGTCCTTGACGAGGAAGCG	Complementary construction
OE	GGATCCATGGCGGCGGCGGCGGCAGCGG	Overexpression construction
	CTGCAGTCATTGCAGTTCGCCTACCGGA	Overexpression construction
AntiNa	GGATCCATGGCGGCGGCGGCGGCAGCGG	Antibody of OsNaPRT1
	CTCGAGTTGCAGTTCGCCTACCGGAGCT	Antibody of OsNaPRT1
qACTIN	GACCCAGATCATGTTTGAGACCT	qRT-PCR Analysis
	CAGTGTGGCTGACACCATCAC	qRT-PCR Analysis
qNaPRT1	GCATACTTATCCGTTGAAACTCG	qRT-PCR Analysis
	GCATCTACCTCGTGACCCTG	qRT-PCR Analysis
EGFP	CGGGATCCATGGCGGCGGCGGCGGCA	Sub-cellular localization
	GCTCTAGATTGCAGTTCGCCTACCGGAGCTTCG	Sub-cellular localization
qNIC	GCCAGTCTTTGCGTTTCTTG	qRT-PCR Analysis
	CCTTTTCCAGCCACTCCAG	qRT-PCR Analysis
qSRT1	GAAGTTCTGGGAGCAAGATTTT	qRT-PCR Analysis
	TGAACCAACCACTAGAAGAGCA	qRT-PCR Analysis
qSRT2	ACTTTAGTGATGGTTGCGGCT	qRT-PCR Analysis
	CACGTGATCGATGCTCTGC	qRT-PCR Analysis
qOsh36	GCACGGAGGCGAACGA	qRT-PCR Analysis
	TTGAGCGGTAGCACCCATT	qRT-PCR Analysis
qOsI57	ACCCTAAAGTAAATGAAGTC	qRT-PCR Analysis
	CCTGCTCTTGTCTTGTTA	qRT-PCR Analysis
qOsh69	CCACAACACGGATAACTT	qRT-PCR Analysis
	GGTGAACACTATGGAACA	qRT-PCR Analysis
Ch-LOC_Os09g35630	GCCACTCCCTTCCCCAAT	ChIP-PCR Assay
	CGCAGCTAAAGCTCGCAA	ChIP-PCR Assay
Ch-LOC_Os12g36720	GCAGCTTAATTATTCAGATGTCGT	ChIP-PCR Assay
	TGAGCCTCTTGAGTTTATCAGTATG	ChIP-PCR Assay
Ch-LOC_Os08g29854	ATTCGTCTTCCCCCTCGG	ChIP-PCR Assay
	GAAATGGGGAATTGGGGAT	ChIP-PCR Assay
Ch-LOC_Os02g35490	TTCTCTCCCCGCACTCTCTAC	ChIP-PCR Assay
	GAGAATGTCAAACTCAAACTGGG	ChIP-PCR Assay
Ch-LOC_Os11g45930	CACTTACTTGTCTGATTTTGCACTC	ChIP-PCR Assay
	ATCCTCCAAGTCGTCTGCTAAG	ChIP-PCR Assay