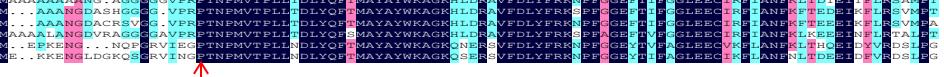
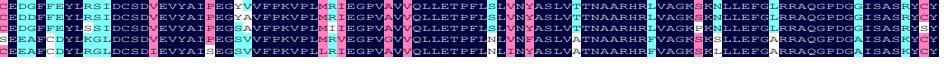
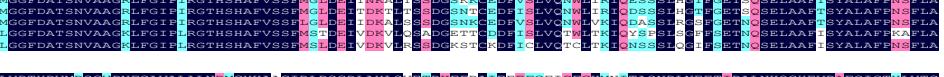


# Supplemental Data

OsNaPRT1		99
XP_002466135	.....AAAANGAGGCGVFRPTNFMVTFLLTDLYQPTMAYAYWKAGKHLDAVFDLYFRRNPFGGBFTFGGLEECIFIANPFXLTDTETTFLRSAMP	96
XP_008668392	.....AAAANGDASIGGGCGVFRPTNFMVTFLLTDLYQPTMAYAYWKAGKHLDAVFDLYFRRNPFGGBFTFGGLEECIFIANPFXLTDTETTFLRSAMP	96
BAK05113	.....AAANGDASIGGGCGVFRPTNFMVTFLLTDLYQPTMAYAYWKAGKHLDAVFDLYFRRNPFGGBFTFGGLEECIFIANPFXLTDTETTFLRSAMP	100
XP_009117282	.....EKEENG...NQPEGVINGPTNFMVTFLLTDLYQPTMAYAYWKAGKQNESVFDLYFRRNPFGGBFTFGGLEECIFIANPFXLTDTETTFLRSAMP	95
NF_195412	.....EKKNGIDGQGSRVINGPTNFMVTFLLTDLYQPTMAYAYWKAGKQSESVFDLYFRRNPFGGBFTFGGLEECIFIANPFXLTDTETTFLRSAMP	98
OsNaPRT1		199
XP_002466135	.....EDGFFYIYLBSIDCSFVEVVAIPEGSVVFFKVFPIIEGPVAVVQLLETFFISLNVASLVTTAARHRHVACKSNNLEFGCARRACQFPDGAIISAPYCY	196
XP_008668392	.....EDGFFYIYLRSIDCSFVEVVAIPEGSVVFFKVFPIIEGPVAVVQLLETFFISLNVASLVTTAARHRHVACKSNNLEFGCARRACQFPDGAIISAPYCY	196
BAK05113	.....EDGFFYIYLBSIDCSFVEVVAIPEGSVVFFKVFPIIEGPVAVVQLLETFFISLNVASLVTTAARHRHVACKSNNLEFGCARRACQFPDGAIISAPYCY	200
XP_009117282	.....EAEFCYIYLKGIDCSFVEVVAIPEGSVVFFKVFPIIEGPVAVVQLLETFFISLNVASLVTTAARHRHVACKSNNLEFGCARRACQFPDGAIISAPYCY	195
NF_195412	.....EAEFCYIYLRGIDCSFVEVVAIPEGSVVFFKVFPIIEGPVAVVQLLETFFISLNVASLVTTAARHRHVACKSNNLEFGCARRACQFPDGAIISAPYCY	198
OsNaPRT1		299
XP_002466135	.....GGFDATSNVAAAGLFGIIIRGTHSHAFVSSFMGLDIIIDRTIASDGSNKEDIVSVLVCNSWLAREHKDASLNLCTHRETNLSELAAFPNSFLA	296
XP_008668392	.....GGFDATSNVAAAGRLFGIIIRGTHSHAFVSSFMGLDIIITNAKATTSDDGSKRBDIVSVLVCNSWLAREHKDASLNLCTHRETNLSELAAFPNSFLA	296
BAK05113	.....GGFDATSNVAAAGLFGIIIRGTHSHAFVSSFMGLDIIITNAKATTSDDGSKRBDIVSVLVCNSWLAREHKDASLNLCTHRETNLSELAAFPNSFLA	300
XP_009117282	.....GGFDATSNVAAAGLFGIIIRGTHSHAFVSSFMGLDIIITNAKATTSDDGSKRBDIVSVLVCNSWLAREHKDASLNLCTHRETNLSELAAFPNSFLA	295
NF_195412	.....GGFDATSNVAAAGLFGIIIRGTHSHAFVSSFMGLDIIITNAKATTSDDGSKRBDIVSVLVCNSWLAREHKDASLNLCTHRETNLSELAAFPNSFLA	298
OsNaPRT1		399
XP_002466135	.....LVDTYDVMRSGVNFCAVALALNDGCKYKAVGIRLDSCDLAYLSDRKFCAIEKEFGVDCFGCTNTAASNDLNEETIDALNKQGHEVDSFGICITYLVTC	396
XP_008668392	.....LVDTYDVMRSGVNFCAVALALNDGCKYKAVGIRLDSCDLAYLSDRKFCAIEKEFGVDCFGCTNTAASNDLNEETIDALNKQGHEVDSFGICITYLVTC	396
BAK05113	.....LVDTYDVMRSGVNFCAVALALNDGCKYKAVGIRLDSCDLAYLSDRKFCAIEKEFGVDCFGCTNTAASNDLNEETIDALNKQGHEVDSFGICITYLVTC	400
XP_009117282	.....LVDTYDVMRSGVNFCAVALALNDGCKYKAVGIRLDSCDLAYLSDRKFCAIEKEFGVDCFGCTNTAASNDLNEETIDALNKQGHEVDSFGICITYLVTC	395
NF_195412	.....LVDTYDVMRSGVNFCAVALALNDGCKYKAVGIRLDSCDLAYLSDRKFCAIEKEFGVDCFGCTNTAASNDLNEETIDALNKQGHEVDSFGICITYLVTC	398
OsNaPRT1		499
XP_002466135	.....YAQAALGCVKLVEINHQPRIKLSEDVTVKSVIFPKKRCYVLSKEGYPLVDIMTDEDFPAFKVGERLCHRPNESKRAVVFCDVEELLCYWTSSN	496
XP_008668392	.....YAQAALGCVKLVEINHQPRIKLSEDVTVKSVIFPKKRCYVLSKEGYPLVDIMTDEDFPAFKVGERLCHRPNESKRAVVFCDVEELLCYWTSSN	496
BAK05113	.....YAQAALGCVKLVEINHQPRIKLSEDVTVKSVIFPKKRCYVLSKEGYPLVDIMTDEDFPAFKVGERLCHRPNESKRAVVFCDVEELLCYWTSSN	500
XP_009117282	.....YAQAALGCVKLVEINHQPRIKLSEDVTVKSVIFPKKRCYVLSKEGYPLVDIMTDEDFPAFKVGERLCHRPNESKRAVVFCDVEELLCYWTSSN	495
NF_195412	.....YAQAALGCVKLVEINHQPRIKLSEDVTVKSVIFPKKRCYVLSKEGYPLVDIMTDEDFPAFKVGERLCHRPNESKRAVVFCDVEELLCYWTSSN	498

**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*.



**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	AAGGAAAGAGTTGCCGTAAAT CCTGTAAGAAGATAGGTCAAGAG	Fine mapping
P2	TGGTGGTAGTATTAGCCTTGT TTCTTCAGGAGACTTGGGAAC	Fine mapping
P3	GGGTCTAGTCCTTCTTCCG AACTTGCCCTTGCTTGCCTC	Fine mapping
P4	TGCCAGCCTAGCGAGCCTAA ATTGCAGCGAGCTACACG	Fine mapping
P5	ATGGCTTCAGACTTCAGAGT CAAATTAACCTTCAGGCAAG	Fine mapping
ID-Na	TCCACTGTCCCTAAATCAC TCCTTCTGCCTCGTCCAT	Identification for osnaprt1 Identification for osnaprt1
ComNa1	CTGCAGGCAGGACATGCAGATGGAATGATGTCAGTG GAGCTCACTTGATACCTGGCTGCCTAACACTAGG	Complementary construction Complementary construction
ComNa2	GAGCTCTATGGGAGGATTGATGCAACAAGGTCTGG GAGCTCCGCGCGAGAGCTCCGGCGATGTCCTGACGAGGAAGCG	Complementary construction Complementary construction
OE	GGATCCATGGCGGCCGGCGGCCAGCGG CTGCAGTCATTGCAGTTGCCTACCGGA	Overexpression construction Overexpression construction
AntiNa	GGATCCATGGCGGCCGGCGGCCAGCGG CTCGAGTTGCAGTTGCCTACCGGAGCT	Antibody of OsNaPRT1 Antibody of OsNaPRT1
qACTIN	GACCCAGATCATGTTGAGACCT CAGTGTGGCTGACACCACATC	qRT-PCR Analysis qRT-PCR Analysis
qNaPRT1	GCATACTTATCCGTTGAAACTCG GCATCTACCTCGTGACCCCTG	qRT-PCR Analysis qRT-PCR Analysis
EGFP	CGGGATCCATGGCGGCCGGCGGCC GCTCTAGATTGCAGTTGCCTACCGGAGCTCG	Sub-cellular localization Sub-cellular localization
qNIC	GCCAGTCTTGCCTTCTTG CCTTTCCAGCCACTCCAG	qRT-PCR Analysis qRT-PCR Analysis
qSRT1	GAAGTTCTGGGAGCAAGATTT TGAACCAACCACTAGAAGAGCA	qRT-PCR Analysis qRT-PCR Analysis
qSRT2	ACTTTAGTGTGGTTGCGGCT CACGTGATCGATGCTCTGC	qRT-PCR Analysis qRT-PCR Analysis
qOsh36	GCACGGAGGCGAACGA TTGAGCGGTAGCACCCATT	qRT-PCR Analysis qRT-PCR Analysis
qOsI57	ACCCCTAAAGTAAATGAAGTC CCTGCTTGTCTTGT	qRT-PCR Analysis qRT-PCR Analysis
qOsh69	CCACAACACGGATAACTT GGTGAACACTATGGAACA	qRT-PCR Analysis qRT-PCR Analysis
Ch-LOC_Os09g35630	GCCACTCCCTCCCCAAT CGCAGCTAAAGCTCGCAA	ChIP-PCR Assay ChIP-PCR Assay
Ch-LOC_Os12g36720	GCAGCTTAAATTATTCA TGAGCCTTGTAGTTATCAGTATG	ChIP-PCR Assay ChIP-PCR Assay
Ch-LOC_Os08g29854	ATTCGTCTTCCCCCTCGG GAAATGGGAAATTGGGGAT	ChIP-PCR Assay ChIP-PCR Assay
Ch-LOC_Os02g35490	TTCTCTCCCGCACTCTAC GAGAATGTCAAACCAA CTGAGCTAAAGCTCGCAA	ChIP-PCR Assay ChIP-PCR Assay
Ch-LOC_Os11g45930	CACTTACTTGCTGATTTGCA ATCCTCCAAGTCGTCTGCTAAG	ChIP-PCR Assay ChIP-PCR Assay