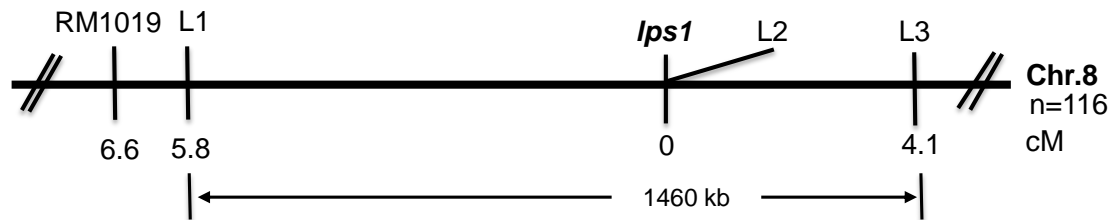


## Supplementary Material



**Figure S1** Preliminary mapping of the *lps1* locus.



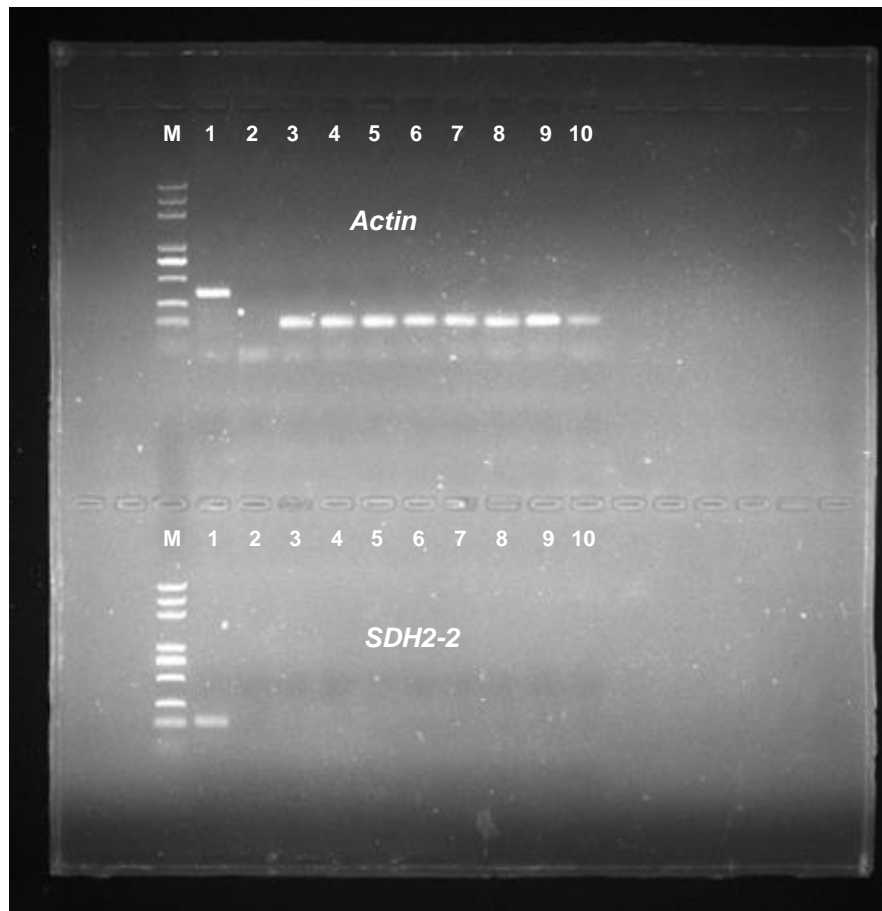
**Figure S2** Schematic representation of *LOC\_Os08g02640* gene, *RPS14* cDNA and *OsSDH2-1* cDNA. The substitution (C to T) happened at position 412 in genome sequence of *LOC\_Os08g02640* gene. Red box shows the common region of *OsSDH2-1* and *RPS14* cDNAs, in which yellow block indicates the sequence encoding mitochondrial signal peptide and blue block indicates the sequence encoding a peptide specifically belonged to functional SDH2.

OsSDH2-1	MAAAALRRSPAARALLSPALSSRLVASKPHSSSPAPP.PPP.SKA.....GANTKTFSTLYRWDPDSPSTKPHLKDVKVLDSDCGPMVLDLALKIK	89
TaSDH2	MAAAALRRSPAARALLSPALSSRLVASKPHSSSPAPP.PPS.SKP.....AS.TKTFSTLYRWDPDSPSTKPHLKDVKVLDSDCGPMVLDLALKIK	88
SbSDH2	MAAAALRRSSAARTLLSPALSSRLVASKPHSSSPAPP.PPPPAKA.....AANTKTFSTLYRWDPDSPSTKPHLKDVKVLDSDCGPMVLDLALKIK	91
ZmSDH2	MAAAALRRSPAARALLSPALSSRLVASKPHSSSPAPP.PPE.AKG.....ASSTKTFSTLYRWDPDSPSTKPHLKDVKVLDSDCGPMVLDLALKIK	89
AtSDH2-1	.MASGLIGR.LVGTKPSKLATAARLIPARWTSTGAEAEKASSGGGR.....GSNLKTFQYRWDPDPNG.KPELQYQVLDLKDCCGPMVLDLALKIK	89
AtSDH2-2	.MAFGLIGR.VVGTSSRLSTAARLIPARWTSTGSEAOQKASTGGG.....GASLKTFQYRWDPDPNG.KPELQYQVLDLKDCCGPMVLDLALKIK	88
NtSDH2	.MATGLIRR.AISRVHSS.PAAKLVARAHASEAKAH.QSESKQQ.....PNLKSFOYRWSPDPNG.KPELKEKIDLKECCGPMVLDLALKIK	84
SfSDH2-2	.MATSLIRR.AISRVQSSA.PAARLLVARAHASDQAO.QVESK.....PNLKSFOYRWDPDPNG.KPELKEKIDLKECCGPMVLDLALKIK	83
XaSDH2	.....MAEFTLPKNSTIGKGYHPAG.....AKNVRTFKIYRWDPD.DDSNERTDINEVDLDAACGPMVLDLALKIK	66
CrSDH2	MLPSLLTNARRGAQALQPGFLSAFISTTSSELNAAATATASKPAPSRPPLAKPPLYKEFOYRWDPD.SDEPKYASQVLDINNCGPMVLDLALKIK	97
ScSDH2	MLNVLRR.RK.....AFCLVTKKGMATATTAATH.....TPRLKTFKVIYRWDPDPSAKPHLQSYQVLDINNCGPMVLDLALKIK	74
OsSDH2-1	NEQDPSLTFRRSCREGICGSCAMINDGNGLAQLTKISSASS.ASTISPLPHMFVVKDLVDMTNFYNQKSVBWLKRRDPPPOGKFTPTKADRA	186
TaSDH2	NEQDPSLTFRRSCREGICGSCAMINDGNGLAQLTKISSAAGASTISPLPHMFVVKDLVDMTNFYNQKSVBWLKRRDPPSAGGKFTPTKADRA	186
SbSDH2	NEQDPSLTFRRSCREGICGSCAMINDGNGLAQLTKISSASS.ASTVSPHMFVVKDLVDMTNFYSYKSVBWLKRRDPPPOGKFTPTKADRA	188
ZmSDH2	NEQDPSLTFRRSCREGICGSCAMINDGNGLAQLTKISSASS.ASTVSPHMFVVKDLVDMTNFYNQKSVBWLKRRDPPPOGKFTPTKADRA	186
AtSDH2-1	NEQDPSLTFRRSCREGICGSCAMINDGNGLAQLTKIQDEAS.ETTITPLPHMFVVKDLVDMTNFYNQKSVBWLKRRTPASVPAKFTPTKADRA	186
AtSDH2-2	NEQDPSLTFRRSCREGICGSCAMINDGNGLAQLTKIESGSK.ETTITPLPHMFVVKDLVDMTNFYNQKSVBWLKRRNPASVPAKFTPTKADRA	185
NtSDH2	NEQDPSLTFRRSCREGICGSCAMINDGNGLAQLTKIDSGA..ESTITPLPHMFVVKDLVDMTNFYNQKSVBWLKRRTEPTTPGKFTPTKADRA	180
SfSDH2-2	NEQDPSLTFRRSCREGICGSCAMINDGNGLAQLTKISSDS..ESTITPLPHMFVVKDLVDMTNFYNQKSVBWLKRRTPAPTTPGKFTPTKADRA	179
XaSDH2	NEQDPSLTFRRSCREGICGSCAMINDGNTLACTKAIADCGKREVPYPLPHMFVVKDLVDMTNFYNQKSVBWLKRRTPAPTTPGKFTPTKADRA	163
CrSDH2	DEQDQTLTFRRSCREGICGSCAMINDGNTLACTCKVNRDPGHVGVKAPLPHMFVVKDLVDMTNFYNQKSVBWLKRRTPAPTTPGKFTPTKADRA	193
ScSDH2	DEQDSTLTFRRSCREGICGSCAMINDGNTLACTCKIDQNESKQLKIYPLPHMFVVKDLVDMTNFYNQKSVBWLKRRTPAPTTPGKFTPTKADRA	171
OsSDH2-1	KLDGMVECILCACCCSTSCPSYWWNPPEYLGPAALLHANRWIQDSRDQFTKBRLLDSINDEFKLYRCHITINCTHACPKGLNPAKQIDTIRKLOLEA..	281
TaSDH2	KLDGMVECILCACCCSTSCPSYWWNPPEYLGPAALLHANRWIQDSRDEFKBRLLDSINDEFKLYRCHITINCTHACPKGLNPAKQIDTIRKLOLEA..	281
SbSDH2	KLDGMVECILCACCCSTSCPSYWWNPPEYLGPAALLHANRWIQDSRDQFTKBRLLDSINDEFKLYRCHITINCTHACPKGLNPAKQIDTIRKLOLEA..	283
ZmSDH2	KLDGMVECILCACCCSTSCPSYWWNPPEYLGPAALLHANRWIQDSRDQFTKBRLLDAINDEFKLYRCHITINCTHACPKGLNPAKQIDTIRKLOLEA..	281
AtSDH2-1	KLDGMVECILCACCCSTSCPSYWWNPPEYLGPAALLHANRWIQDSRDEYTKBRLEAIDDEFKLYRCHITINCARACPKGLNPAKQIDTIRKLOLEA..	279
AtSDH2-2	KLDGMVECILCACCCSTSCPSYWWNPPEYLGPAALLHANRWIQDSRDEYTKBRLEAIDDEFKLYRCHITINCARACPKGLNPAKQIDTIRKLOLEA..	280
NtSDH2	KLDGMVECILCACCCSTSCPSYWWNPPEYLGPAALLHANRWIQDSRDEYTKBRLEAIDDEFKLYRCHITINCARACPKGLNPAKQIDTIRKLOLEA..	275
SfSDH2-2	KLDGMVECILCACCCSTSCPSYWWNPPEYLGPAALLHANRWIQDSRDEYTKBRLEAIDDEFKLYRCHITINCARACPKGLNPAKQIDTIRKLOLEA..	274
XaSDH2	KLDGMVECILCACCCSTSCPSYWWNPPEYLGPAALLHANRWIQDSRDEYTKBRLEAIDDEFKLYRCHITINCARACPKGLNPAKQIDTIRKLOLEA..	260
CrSDH2	KLDGMVECILCACCCSTSCPSYWWNPPEYLGPAALLHANRWIQDSRDEYTKBRLEAIDDEFKLYRCHITINCARACPKGLNPAKQIDTIRKLOLEA..	290
ScSDH2	KLDGMVECILCACCCSTSCPSYWWNPPEYLGPAALLHANRWIQDSRDEYTKBRLEAIDDEFKLYRCHITINCARACPKGLNPAKQIDTIRKLOLEA..	266

**Figure S3** Homolog sequences of OsSDH2-1. Black shades indicate the identical residues and gray shades indicate the similar residues ( $\geq 75\%$  identical). The red arrow indicates the mutation site of OsSDH2-1 in the *lps1* mutant, the blue lines indicate the cysteine clusters which were ligands to the iron-sulfur clusters, the red line indicates the mitochondrial signal peptide predicted from TargetP 1.1 Server. Accession numbers for the respective protein sequences are as Fig. 6.



**Figure S4** Detection of PCR amplification efficiency of *OsSDH2-1* and *RPS14* qRT-PCR specific primer in wild-type genomic DNA.



**Figure S5** Detection of *SDH2-2* expression in various organs of wild type. M: DL-5000 marker; 1: positive control (genomic DNA); 2: negative control; 3: seeds after 48-hours imbibition; 4-5: root and leaf at seedling stage; 6-10: root, stem, leaf, young panicle and leaf sheath at booting stage.

**Table S1** Primers used in the study.

Primers	Forward primer	Reverse primer	References
RM1019	GTTTGAACAGTAGGACTTGT	AGAACATCTCACACTTCTCT	[43]
L1	TGAAATCGGGATATGAG	TACTAGGAGCACGTTGC	
L2	CATTCCAACACTAGGCTCA	TCAATTCTTCGGTCCAC	
L3	CGCCATTAGTTCCTCCGTAT	GCAGCGAAAGCACTGGAA	
OsSDH2-1	CATGTACGAGTGCATCCT	TCCTTAGTGAACCTGGTCA	
OsSDH2-2	TCGTGCTCCATGTGCATC	CCTCACGACGTACATGTG	
RPS14	TCTGCGCCTGCTGCTCCA	GATGTGCATGAACATGTT	
Osh36	AACGCATTTGTGGTTGGCTC	TCAACTTTGGCCGGTGTCTT	[30]
Osl57	ACCCTAAAGTAAATGAAGTC	CCTGCTCTTGCTTGTTA	[30]
OsWRKY53	GAGCGACATCGACATCCT	TTGTGCTTGCCCTCGTAG	[44]
AOX1b	CCTGCTCAGTTCATCACCATCA	GCATAAAACGGAGTGACAATAGC	[30]
APX1	AGGTGCCACAAGGAAAGATCTGGT	TCAGCAGGGCTTTGTCCTAGGAA	[30]
SODB	TCCGCCGTATAAACTTGATGCCCT	TGGGTTGCCGTTGTTGTATGCTTC	[30]