Table 1 Suppl. Primer list (based on Vighi *et al.* 2017).

Gene	Accession number	Sense /antisense	Primer sequence	Amplicon size [bp]
OsSOD Cu/Zn	AK120348.1	F	5'-GCTCTATTGCGTTGTATGCCA-3'	138
		R	5'-GCTTGACTCCCAAATGGTGAC-3'	
*OsSOD*3 *Cu/Zn*	AK243377.1	F	5'-GGTGTTGCTAATGTCAATGTCTC-3'	100
		R	5'-ATCATCAGGATCAGCATGGAC-3'	
*OsSOD*4 *Cu/Zn*	AK059841.1	F	5'-GCACCAGAAGATGAAGTCCGT-3'	136
		R	5'-CGAATGCTCTCCCAACAACAG-3'	
*OsCAT*A	AK065094.1	F	5'-GTGAAGATTGCGAATAGGCTC-3'	114
		R	5'-TCTGGCCTTATTTGGTTGGT-3'	
*OsCAT*B	AK100019.1	F	5'-GACAAGGAGAACAATTTCCAACAG-3'	146
		R	5'-AGTAGGAGATCCAGATGCCAC-3'	
*OsCAT*C	AK066378.1	F	5'-GTGATTGCCAAGGAGAACAAC-3'	103
		R	5'-GAGTGCGTCGATCCATCTCT-3'	
*OsUBQ*10	AK101547.1	F	5'-TGGTCAGTAATCAGCCAGTTTGG-3'	381
		R	5'-GCACCACAAATACTTGACGAACAG-3'	

Table 2 Suppl. *BLAST* results of RT-qPCR amplified fragment of the respective gene.

Gene	Hit sequence description	Query cover	E-value	Identity	Accession number	Query sequence
OsSOD Cu/Zn	*Oryza sativa* var. *japonica* group cDNA clone:J013064M11, full insert sequence	100 %	7.00E-41	97.98 %	AK120348.1	GCTCTATTGCTTTGTATGCCACTGAGGACAGATCAGATCCTGGCATTGCAGCTGCCGTGATTGCAAGAAGCGCTGGGGTGGCGAGAACTACAAGAAGC
*OsSOD*3 *Cu/Zn*	*Oryza sativa* var. *Japonica* group cDNA, clone: J100063A11, full insert sequence	100 %	1.00E-10	100 %	AK243377.1	CTTGCTCTCTCATGAACATATGTGCTGACCTTTTTCTTATCATTTCCTCTTAAGACAGTTAATTTGACATCGGTAACATTCTTTGAACGGCAGATCCCCCTTACTGGAGCACACTCCATCATTGGCCG
*OsSOD*4 *Cu/Zn*	*Oryza sativa* var. *japonica* group cDNA clone:006-206-D10, full insert sequence	100 %	2.00E-08	90.70 %	AK059841.1	TGCGCCAAAAGATCAAGTCCGTCATGCGGGTGGCCTGGGAAAC
*OsCAT*A	*Oryza sativa* var. *japonica* group cDNA clone:J013001M08, full insert sequence	100 %	5.00E-20	98.33 %	AK065094.1	TGAAGATTGCGAATAGGCTCAAACGTGAAGCCAAGCATGTGAAGAAACTAAGGCACAAGA
*OsCAT*B	*Oryza sativa* var. *japonica* group cDNA clone:J013145C05, full insert sequence	100 %	1.00E-31	100 %	AK100019.1	ATCGTTTTCTCCAGCGGTGGGTTGATGCTCTCTCAGATCCTCGTATTACACATGAACTCCGTGGCATCTGGATCT
*OsCAT*C	*Oryza sativa* var. *japonica* group cDNA clone:J013060B21, full insert sequence	100 %	6.00E-18	100 %	AK066378.1	TCATGGGATCCGGCAAGGCAAGACCGGTTCATCAAGAGATGGATCGACGCA
*OsUBQ*10	*Oryza sativa* var. *japonica* group cDNA clone:J033048M20, full insert sequence	100 %	8.00E-09	95 %	AK101547.1	GGTCTCCCGAGCCTCTGTTCGTCAAGTATTTGTGGGTGC

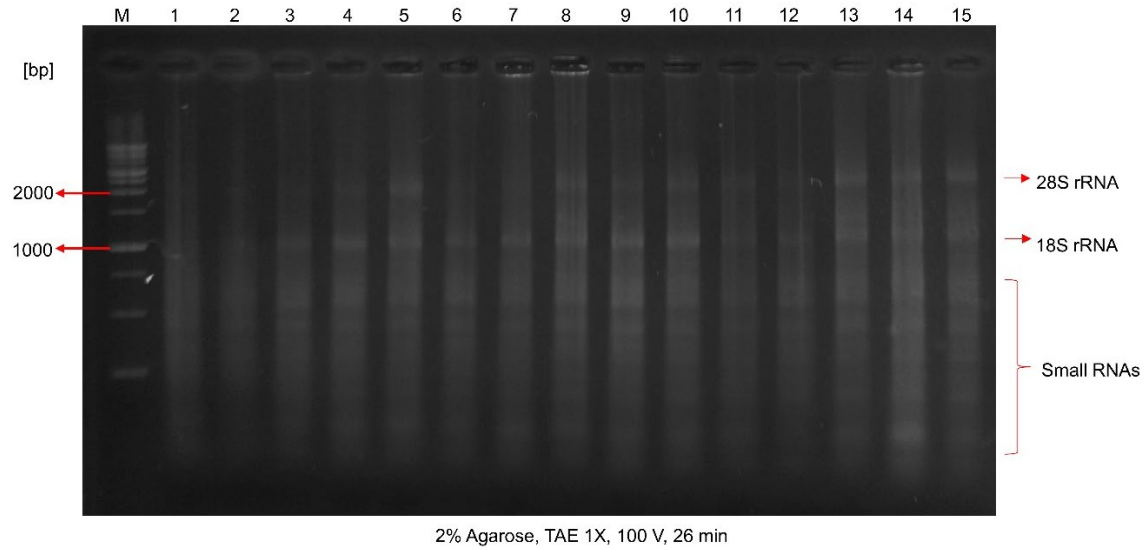

Fig. 1 Suppl. Agarose gel electrophoresis [2 % (m/v) agarose, TAE 1 ×, 100 V, 26 min] of RNA extracts. Each lane contains extracted RNA originated from the roots of 20 individual seedlings treated by 0 (lane 1-5), 75 (lane 6-10), and 150 (11-15) µg cm^{-3} of esDNA. These were then used for the subsequent qRT-PCR analysis.

Fig. 2 Suppl. Superoxide ($O_2^{\cdot-}$) and hydrogen peroxide (H_2O_2) histochemical staining of 5 d-old rice seedlings. The unstained roots, immersed in the phosphate buffer without NBT ($O_2^{\cdot-}$ staining) or DAB (H_2O_2 staining), represent as negative control of ROS histochemical staining. The observed brown color indicates the presence of hydrogen peroxide, while blue color indicates the presence of superoxide. The samples used in this image were not treated by esDNA to show the basal ROS production in rice roots. The images of root tips in higher magnification are also displayed to better show color changes in root tips after staining with NBT or DAB.