

## Supplementary Material

NTLs	Groups	Subgroups	NAC proteins
NTL1	I	NAC2	ANAC013
NTL2	I	TIP	ANAC014
NTL3	I	NAC2	ANAC016
NTL4	I	NAC2	ANAC053
NTL5	I	OsNAC8	ANAC060
NTL6	I	TIP	ANAC062
NTL7	I	NAC2	ANAC017
NTL8	I	OsNAC8	ANAC040
NTL9	I	TIP	-
NTL10	II	ANAC001	ANAC001
NTL11	I	NAC2	ANAC078
NTL12	II	ANAC001	ANAC068
NTL13	II	ANAC001	ANAC069
OsNTL1	I	TIP	ONAC019
OsNTL2	I	TIP	ONAC037
OsNTL3	I	OsNAC8	ONAC074
OsNTL4	I	NAC2	ONAC051
OsNTL5	I	NAC2	ONAC040
OsNTL6	I	NAC2	ONAC070

**Figure S1.** Phylogenetic relationship of NTLs to the whole NAC family. The NAC proteins in *Arabidopsis* and rice have been classified into two major groups, I and II, that contain 14 and 4 subfamilies, respectively (S1). It is notable that the NTL proteins are mostly clustered in a few subfamilies of group I, such as NAC2, TIP, and OsNAC8. Only three of the 19 NTLs belong to group II. NTL9, which belongs to subgroup TIP of group I, has not been included in the original classification.

S1. Ooka,H., Satoh,K., Doi,K., Nagata,T., Otomo,Y., Murakami,K., Matsubara,K., Osato,N., Kawai,J., Carninci,P., Hayashizaki,Y., Suzuki,K., Kojima,K., Takahara,Y., Yamamoto,K. and Kikuchi,S. (2003) Comprehensive analysis of NAC family genes in *Oryza sativa* and *Arabidopsis thaliana*. *DNA Res.*, **10**, 239-247.

NTLs	cold	heat	drought	NaCl	H2O2	ABA	ACC	BL	IAA	GA	NPA	PAC
NTL1	<b>2.07</b>	<b>2.15</b>	0.91	<b>7.03</b>	1.02	<b>3.47</b>	1.11	0.8	1.08	1.4	1	0.69
NTL2	0.79	1.29	1.18	0.81	0.75	0.54	0.95	0.6	1.09	0.9	0.98	1.67
NTL3	0.39	0.97	0.5	1.63	0.62	0.48	0.61	1	0.98	0.6	0.76	0.97
NTL4	1.5	1.59	1.25	<b>2.35</b>	<b>3.13</b>	1.86	0.74	0.8	0.94	0.7	0.96	0.95
NTL5												
NTL6	<b>2.03</b>	1.22	0.86	<b>3.65</b>	<b>3.66</b>	1.15	0.96	1	1.23	1.1	0.77	0.69
NTL7	1.27	1.04	1.02	0.93	1.05	1.01	0.94	0.9	0.94	0.9	0.87	1.07
NTL8	1.23	1.15	1.08	<b>2.02</b>	1.31	0.73	1.14	0.4	0.95	0.9	0.83	1.13
NTL9	0.79	1.46	1.23	1.33	0.88	1.12	1.23	1.1	1.13	1.4	0.54	0.5
NTL10	1.49	0.83	1.29	<b>2.92</b>	0.99	0.97	1.54	0.5	1.47	1.1	0.9	1.06
NTL11	1.13	1.68	0.95	1.42	1.25	1.13	1.08	1	1.07	1	1.2	1.04

- Induced (bold) or repressed both in our and previous assays
- Induced (bold) or repressed in the previous assays but unaltered in our assays
- Unaltered in the previous assays but altered in our assays
- Unaltered both in our and previous assays

**Figure S2.** Comparison of *NTL* gene expression patterns to those in the transcriptome database GENEVESTIGATOR.

Effects of diverse stress conditions and growth hormones on the *NTL* expressions were compared to those in the GENEVESTIGATOR database (S2). Those induced by more than two-fold or repressed by more than 50% were considered here. Note that most of the up-regulated genes in the database were also induced by similar treatments in our assay system. The numbers denote fold changes in gene expressions and were extracted from the database.

S2. Zimmermann,P., Hirsch-Hoffmann,M., Hennig,L. and Gruissem,W. (2004) GENEVESTIGATOR. *Arabidopsis* microarray database and analysis toolbox. *Plant Physiol.*, **136**, 2621-2632.

Gene Loci	Chromosome No	AAs	Exons	Gene No
Os06g01230	6	683	6	<i>osNTL1</i>
Os08g06140	8	729	7	<i>osNTL2</i>
Os01g15640	1	489	4	<i>osNTL3</i>
Os09g32040	9	702	4	<i>osNTL4</i>
Os08g44820	8	656	5	<i>osNTL5</i>
Os02g57650	2	632	5	<i>osNTL6</i>

**Figure S3.** Rice *NTL* genes (*OsNTLs*).

They were predicted via the membrane protein database ARAMEMNON (S3). Those with hydrophobicity values of higher than 0.85 were listed.

S3. Schwacke,R., Schneider,A., van der Graaff,E., Fischer,K., Catoni,E., Desimone,M., Frommer,W.B., Flügge,U.-I. and Kunze,R. (2003) ARAMEMNON, a novel database for *Arabidopsis* integral membrane proteins. *Plant Physiol.*, **131**, 16-26.

<b>TF Family</b>	<b>Total Number</b>	<b>Predicted MTFs</b>
MYB	190	2
AP2/EREBP	144	1
bHLH	139	5
C2H2	105	4
HB	89	1
MADS box	82	4
bZIP	81	6
WRKY	72	1
C2C2	104	2
TCP	25	1
C3H	33	2
SBP	16	4
NAC	109	>13

**Figure S4.** Putative MTFs in *Arabidopsis* genome.

The *Arabidopsis* transcription factors were analyzed using the ARAMEMNON membrane protein database (S3) to identify putative MTFs. MTFs were identified from most of the major transcription factor (TF) families in *Arabidopsis*.