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(54) **Titre : COMPOSITIONS ET PROCEDES POUR AMELIORER LA TOLERANCE AU STRESS ABIOTIQUE**

(54) **Title: COMPOSITIONS AND METHODS FOR IMPROVING ABIOTIC STRESS TOLERANCE**

(57) **Abrégé/Abstract:**

The present invention relates to compositions and methods for improving the abiotic stress tolerance of plants. Plants and plant parts identified, selected and/or produced using compositions and methods of the present invention are also provided.



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(54) Title: COMPOSITIONS AND METHODS FOR IMPROVING ABIOTIC STRESS TOLERANCE

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# COMPOSITIONS AND METHODS FOR IMPROVING ABIOTIC STRESS TOLERANCE

## RELATED APPLICATIONS

5 This application claims priority to Chinese Provisional Patent Application Nos. 201310322634.4, filed July 29, 2013, and 201310322316.8, filed July 29, 2013, the disclosure of each of which is hereby incorporated by reference in its entirety.

## FIELD OF THE INVENTION

10 The present invention relates to compositions and methods for improving the abiotic stress tolerances of plants.

## BACKGROUND OF THE INVENTION

15 Abiotic stress is a major factor affecting the normal growth and development of plants and limiting crop yields. At present, the impact of drought stress on crop yields around the world ranks first among abiotic stress factors; the damage caused by drought is equivalent to the damage caused by all natural disasters combined and has become the predominant obstruction to agricultural development in many areas.

20 Identifying genes that enhance the drought tolerance of plants could lead to more efficient crop production by allowing for the identification, selection and production of plants with enhanced drought tolerance.

## SUMMARY OF THE INVENTION

25 The present invention provides abiotic stress tolerant plants and plant parts, as well as methods and compositions for identifying, selecting and/or producing abiotic stress tolerant plants and plant parts.

30 In some embodiments, the present invention provides a nonnaturally occurring plant or plant part that expresses one or more exogenous COBL4 proteins and/or one or more exogenous ERF62 proteins. For example, in some embodiments, the present invention provides a plant or plant part having within its genome one or more exogenous nucleic acids comprising, consisting essentially of or consisting of the nucleotide sequence set forth in any one of SEQ ID NOs: 1–27, a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 28–44, a nucleotide sequence that is at least 95% identical to the nucleotide sequence set forth in any one of SEQ ID NOs: 1–27, a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence that is at least 95% identical to the amino acid

35

sequence of any one of SEQ ID NOs: 28–44, a nucleotide sequence that is complementary to any one of the aforementioned nucleotide sequences and/or a nucleotide sequence that specifically hybridizes to any one of the aforementioned nucleotide sequences under stringent hybridization conditions.

5 In some embodiments, the present invention provides a nonnaturally occurring nucleic acid that comprises, consists essentially of or consists of a nucleotide sequence encoding one or more COBL4 proteins and/or one or more ERF62 proteins. For example, in some embodiments, the present invention provides a nucleic acid comprising, consisting essentially of or consisting of the nucleotide sequence set forth in any one of SEQ ID NOs: 1–27, a nucleotide sequence that  
10 encodes a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 28–44, a nucleotide sequence that is at least 95% identical to the nucleotide sequence set forth in any one of SEQ ID NOs: 1–27, a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence that is at least 95% identical to the amino acid sequence of any one of SEQ ID NOs: 28–44, a nucleotide sequence that is complementary to any one of the aforementioned  
15 nucleotide sequences and/or a nucleotide sequence that specifically hybridizes to any one of the aforementioned nucleotide sequences under stringent hybridization conditions.

In some embodiments, the present invention provides a nonnaturally occurring virus or bacterium that expresses one or more exogenous COBL4 proteins and/or one or more exogenous ERF62 proteins. For example, in some embodiments, the present invention provides a  
20 recombinant virus or bacterium that expresses a nonnaturally occurring nucleic acid of the present invention.

In some embodiments, the present invention provides a nonnaturally occurring COBL4 protein. For example, in some embodiments, the present invention provides a protein comprising, consisting essentially of or consisting of the amino acid sequence of any one of SEQ ID NOs:  
25 28–35. In some embodiments, the protein has an amino acid sequence that is at least 95% identical to one or more of SEQ ID NOs: 28–35.

In some embodiments, the present invention provides a nonnaturally occurring ERF62 protein. For example, in some embodiments, the present invention provides a protein comprising, consisting essentially of or consisting of the amino acid sequence of any one of SEQ ID NOs:  
30 36–44. In some embodiments, the protein has an amino acid sequence that is at least 95% identical to one or more of SEQ ID NOs: 36–44.

In some embodiments, the present invention provides uses for nucleic acids, expression cassettes, vectors, recombinant virus, recombinant bacteria and proteins of the present invention for enhancing abiotic stress tolerance in a plant or plant part.

In some embodiments, the present invention provides uses for nucleic acids, expression cassettes, vectors, recombinant virus, recombinant bacteria and proteins of the present invention for producing an abiotic stress tolerant in a plant or plant part.

5 In some embodiments, the present invention provides a method of increasing the abiotic stress tolerance of a plant or plant part, the method comprising increasing the expression and/or activity of one or more COBL4 proteins and/or of one or more ERF62 proteins in the plant or plant part.

10 In some embodiments, the present invention provides a method of increasing the expression and/or activity of one or more COBL4 proteins in a plant or plant part, the method comprising increasing the expression of one or more nucleic acids encoding the COBL4 protein(s) in the plant or plant part. In some such embodiments, increasing the expression of one or more nucleic acids encoding the COBL4 protein(s) in the plant or plant part comprises expressing one or more exogenous nucleic acids encoding the COBL4 protein(s) in the plant or plant part. In some such  
15 protein(s) in the plant or plant part further comprises introducing one or more exogenous nucleic acids encoding the COBL4 protein(s) into the plant or plant part. Such methods may be useful for producing plants and plant parts having enhanced abiotic stress tolerance.

In some embodiments, the present invention provides a method of increasing the expression and/or activity of one or more ERF62 proteins in a plant or plant part, the method comprising: (a)  
20 increasing the expression of one or more nucleic acids encoding the ERF62 protein(s) in the plant or plant part. In some such embodiments, increasing the expression of one or more nucleic acids encoding the ERF62 protein(s) in the plant or plant part comprises expressing one or more exogenous nucleic acids encoding the ERF62 protein(s) in the plant or plant part. In some such  
25 protein(s) in the plant or plant part further comprises introducing one or more exogenous nucleic acids encoding the ERF62 protein(s) into the plant or plant part. Such methods may be useful for producing plants and plant parts having enhanced abiotic stress tolerance.

In some embodiments, the present invention provides a method of identifying a plant or plant part having enhanced abiotic stress tolerance, the method comprising detecting, in a plant  
30 or plant part, one or more nucleic acids that comprises, consists essentially of or consists of the nucleotide sequence set forth in any one of SEQ ID NOs: 1–27, a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 28–44, a nucleotide sequence that is at least 95% identical to the nucleotide sequence set forth in any one of SEQ ID NOs: 1–27, a nucleotide sequence that encodes a polypeptide comprising an amino  
35 acid sequence that is at least 95% identical to the amino acid sequence of any one of SEQ ID

NOs: 28–44, a nucleotide sequence that is complementary to any one of the aforementioned nucleotide sequences and/or a nucleotide sequence that specifically hybridizes to any one of the aforementioned nucleotide sequences under stringent hybridization conditions.

5 In some embodiments, the present invention provides a method of producing a plant having enhanced abiotic stress tolerance, the method comprising detecting, in a plant part, one or more nucleic acids comprising, consisting essentially of or consisting of the nucleotide sequence set forth in any one of SEQ ID NOs: 1–27, a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 28–44, a nucleotide sequence that is at least 95% identical to the nucleotide sequence set forth in any one of SEQ ID NOs: 1–  
10 27, a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence that is at least 95% identical to the amino acid sequence of any one of SEQ ID NOs: 28–44, a nucleotide sequence that is complementary to any one of the aforementioned nucleotide sequences and/or a nucleotide sequence that specifically hybridizes to any one of the aforementioned nucleotide sequences under stringent hybridization conditions; and producing a  
15 plant from the plant part.

In some embodiments, the present invention provides a method of producing a plant having enhanced abiotic stress tolerance, the method comprising introducing, into a plant part, one or more nucleic acids comprising, consisting essentially of or consisting of the nucleotide sequence set forth in any one of SEQ ID NOs: 1–27, a nucleotide sequence that encodes a polypeptide  
20 comprising the amino acid sequence of any one of SEQ ID NOs: 28–44, a nucleotide sequence that is at least 95% identical to the nucleotide sequence set forth in any one of SEQ ID NOs: 1–27, a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence that is at least 95% identical to the amino acid sequence of any one of SEQ ID NOs: 28–44, a nucleotide sequence that is complementary to any one of the aforementioned nucleotide  
25 sequences and/or a nucleotide sequence that specifically hybridizes to any one of the aforementioned nucleotide sequences under stringent hybridization conditions; and producing a plant from the plant part.

In some embodiments, the present invention provides a method of producing a plant enhanced abiotic stress tolerance, the method comprising crossing a first parent plant or plant  
30 part with a second parent plant or plant part, wherein the first parent plant or plant part comprises within its genome one or more exogenous nucleic acids comprising, consisting essentially of or consisting of the nucleotide sequence set forth in any one of SEQ ID NOs: 1–27, a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence of any one of SEQ ID  
NOs: 28–44, a nucleotide sequence that is at least 95% identical to the nucleotide sequence set  
35 forth in any one of SEQ ID NOs: 1–27, a nucleotide sequence that encodes a polypeptide

comprising an amino acid sequence that is at least 95% identical to the amino acid sequence of any one of SEQ ID NOs: 28–44, a nucleotide sequence that is complementary to any one of the aforementioned nucleotide sequences and/or a nucleotide sequence that specifically hybridizes to any one of the aforementioned nucleotide sequences under stringent hybridization conditions.

5 The foregoing and other objects and aspects of the present invention are explained in detail in the drawings and specification set forth below.

### BRIEF DESCRIPTION OF THE DRAWINGS

10 Figs. 1A–1H are graphs showing the relative expression levels of endogenous *Oryza sativa ssp japonica COBRA-like protein 4 (OsCOBL4)* (1A–1D) and endogenous *Oryza sativa ssp japonica ERF62 (OsERF62)* (1E–1H) in upland rice variety *Oryza sativa ssp japonica cv. IRAT109* (IRAT109; Zhihong, *High quality Japonica upland rice variety IRAT109 and its cultivation techniques*. ANHUI AGR. No. 06 (1994); publically available from China Agricultural University) and lowland rice variety *Oryza sativa ssp japonica cv. Nipponbare* (Nipponbare; 15 *Lowland rice variety "Nipponbare"*. BULL. AGR. SCI. TECH. No. 02 (1973); publicly available from China Agricultural University) under various growth conditions: 1A,1E = abscisic acid (ABA) treatment; 1B,1F = dehydration treatment; 1C,1G = H<sub>2</sub>O<sub>2</sub> treatment; 1D,1H = PEG treatment.

Fig. 2A shows an agarose gel containing DNA fragments from Nipponbare rice plants, 20 wherein lane M is a molecular weight standard with fragments 2000, 1000, 750, 500, or 250 base pairs in size (from top to bottom), lane P is a positive control, plasmid pMDC32, lane W is a wild-type Nipponbare rice plant. Lanes 1-10 are T<sub>0</sub>-generation *OsCOBL4<sub>IRAT109</sub>* transgenic Nipponbare rice plants.

Fig. 2B shows an agarose gel containing DNA fragments from Nipponbare rice plants, 25 wherein lane M is a molecular weight standard with fragments 2000, 1000, 750, 500, or 250 base pairs in size (from top to bottom), lane P is a positive control, plasmid pMDC32, lane W is a wild-type Nipponbare rice plant, and lanes 1-8 are T<sub>0</sub>-generation *OsERF62<sub>IRAT109</sub>* transgenic Nipponbare rice plants.

Fig. 3A is a graph showing the relative expression levels of *OsCOBL4* in wild-type 30 Nipponbare rice plants (WT) and T<sub>2</sub>-generation *OsCOBL4<sub>IRAT109</sub>* transgenic Nipponbare rice plants (T6, T8, T9).

Fig. 3B is a graph showing the relative expression levels of *OsERF62* in wild-type Nipponbare rice plants (WT) and T<sub>2</sub>-generation *OsERF62<sub>IRAT109</sub>* transgenic Nipponbare rice plants (OE4, OE5).

Figs. 4A–4B shows wild-type Nipponbare rice plants (WT), T<sub>2</sub>-generation *OsCOBL4*<sub>IRAT109</sub> transgenic Nipponbare rice plants (T6, T8) and T<sub>2</sub>-generation *OsERF62*<sub>IRAT109</sub> transgenic Nipponbare rice plants (OE4, OE5) before and after PEG-simulated drought stress treatment.

Fig. 5A–5B shows wild-type Nipponbare rice plants (WT), T<sub>2</sub>-generation *OsCOBL4*<sub>IRAT109</sub> transgenic Nipponbare rice plants (T6, T8, T9) and T<sub>2</sub>-generation *OsERF62*<sub>IRAT109</sub> transgenic Nipponbare rice plants (OE4, OE5) before and after mannitol-induced osmotic stress treatment.

Fig. 6A–6B show wild-type Nipponbare rice plants (WT), T<sub>2</sub>-generation *OsCOBL4*<sub>IRAT109</sub> transgenic Nipponbare rice plants (T6, T8, T9) and T<sub>2</sub>-generation *OsERF62*<sub>IRAT109</sub> transgenic Nipponbare rice plants (OE4, OE5) before and after drought stress treatment.

Fig. 7 is a multiple sequence alignment showing the amino acid sequences of *OsCOBL4*<sub>IRAT109</sub> and several of its homologues. The underlined section of sequences represents an N-terminal signal peptide. The section of sequences encompassed by the box represents a conserved CCVS domain. Point mutations between *OsCOBL4*<sub>IRAT109</sub> and *OsCOBL4*<sub>Nipponbare</sub> are circled.

Fig. 8 shows the variation between *OsCOBL4*<sub>IRAT109</sub> and *OsCOBL4*<sub>Nipponbare</sub>.

Fig. 9A shows tissues from *ProCOBL4-IRAT109::GUS* transgenic IRAT109 rice plants and *ProCOBL4-IRAT109::GUS* transgenic Nipponbare rice plants following GUS staining.

Fig. 9B is a graph showing the results of real-time fluorescence quantitative PCR analyses of the relative expression levels of *OsCOBL4* in *ProCOBL4-IRAT109::GUS* transgenic IRAT109 rice plants and *ProCOBL4-IRAT109::GUS* transgenic Nipponbare rice plants. The standard error bars shown therein are based on three replicates.

Fig. 10 is a graph showing the results of real-time fluorescence quantitative PCR analyses of the relative expression levels of GUS in *ProNipponbare::GUS* transgenic Nipponbare rice plants (BPN), *ProIRAT109e::GUS* transgenic Nipponbare rice plants (BPI), *ProNipponbare (-600C>T)::GUS* transgenic Nipponbare rice plants (BPMA), *ProNipponbare (-369G>T)::GUS* transgenic Nipponbare rice plants (BPMB), and *ProNipponbare (-169C>T)::GUS* transgenic Nipponbare rice plants (BPMC).

Fig. 11 shows the subcellular localization of GFP-fused IRAT109 *OsCOBL4*<sub>IRAT109</sub> in *N. benthamiana* leaves following Agrobacterium-mediated transformation. Leaves were treated with 10% NaCl to separate cell walls and protoplasts.

Fig. 12 is a graph showing the relative expression levels of *OsCOBL4* (referred to as DBL9 in the figure legend) in wild-type Nipponbare rice plants (WT), *IRAT109* *OsCOBL4*<sub>IRAT109</sub> transgenic Nipponbare rice plants (OEI-6, OEI-8, OEI-9) and *OsCOBL4*<sub>Nipponbare</sub> transgenic Nipponbare rice plants (OEN-2, OEN-6, OEN-8).

Fig. 13A shows wild-type Nipponbare rice plants (WT), *IRAT109* *OsCOBL4*<sub>IRAT109</sub> transgenic Nipponbare rice plants (OEI-6, OEI-9) and *OsCOBL4*<sub>Nipponbare</sub> transgenic Nipponbare

rice plants (OEN-2, OEN-8) before (upper panels) and after (lower panels) drought stress treatment.

Fig. 13B is a graph showing the survival rates of wild-type Nipponbare rice plants (WT), *IRAT109* OsCOBL4<sub>*IRAT109*</sub> transgenic Nipponbare rice plants (OEI-6, OEI-8) and  
5 OsCOBL4<sub>*Nipponbare*</sub> transgenic Nipponbare rice plants (OEN-2, OEN-6) following drought stress treatment. The standard error bars shown therein are based on three replicates. \* = significance at  $p < 0.05$ . \*\* = significance at  $p < 0.01$ .

Fig. 14A shows wild-type Nipponbare rice plants (WT), OsCOBL4<sub>*IRAT109*</sub> transgenic Nipponbare rice plants (OEI-6, OEI-8) and OsCOBL4<sub>*Nipponbare*</sub> transgenic Nipponbare rice plants  
10 (OEN-2, OEN-6) before and after physiological dehydration stress treatment.

Fig. 14B is a graph showing the survival rates of wild-type Nipponbare rice plants (WT), OsCOBL4<sub>*IRAT109*</sub> transgenic Nipponbare rice plants (OEI-6, OEI-8) and OsCOBL4<sub>*Nipponbare*</sub> transgenic Nipponbare rice plants (OEN-2, OEN-6) following physiological dehydration drought stress treatment. The standard error bars shown therein are based on three replicates. \* =  
15 significance at  $p < 0.05$ . \*\* = significance at  $p < 0.01$ .

Fig. 15A shows wild-type Nipponbare rice plants (WT), OsCOBL4<sub>*IRAT109*</sub> transgenic Nipponbare rice plants (OEI-6, OEI-9) and OsCOBL4<sub>*Nipponbare*</sub> transgenic Nipponbare rice plants (OEN-2, OEN-8) following a control treatment (Normal) or an osmotic stress treatment (Mannitol).

Fig. 15B is a graph showing the relative heights of wild-type Nipponbare rice plants (WT), OsCOBL4<sub>*IRAT109*</sub> transgenic Nipponbare rice plants (OEI-6, OEI-8) and OsCOBL4<sub>*Nipponbare*</sub> transgenic Nipponbare rice plants (OEN-2, OEN-8) following an osmotic stress treatment. The standard error bars shown therein are based on three replicates. \* = significance at  $p < 0.05$ . \*\* = significance at  $p < 0.01$ .  
20

Fig. 15C is a graph showing the relative weights of wild-type Nipponbare rice plants (WT), OsCOBL4<sub>*IRAT109*</sub> transgenic Nipponbare rice plants (OEI-6, OEI-8) and OsCOBL4<sub>*Nipponbare*</sub> transgenic Nipponbare rice plants (OEN-2, OEN-8) following an osmotic stress treatment. The standard error bars shown therein are based on three replicates. \* = significance at  $p < 0.05$ . \*\* = significance at  $p < 0.01$ .  
25

Fig. 16A shows wild-type Nipponbare rice plants (WT), OsCOBL4<sub>*IRAT109*</sub> transgenic Nipponbare rice plants (OEI-6, OEI-9) and OsCOBL4<sub>*Nipponbare*</sub> transgenic Nipponbare rice plants (OEN-2, OEN-8) following a control treatment (Normal) or a salt stress treatment (NaCl).  
30

Fig. 16B is a graph showing the relative heights of wild-type Nipponbare rice plants (WT), OsCOBL4<sub>*IRAT109*</sub> transgenic Nipponbare rice plants (OEI-6, OEI-8) and OsCOBL4<sub>*Nipponbare*</sub> transgenic Nipponbare rice plants (OEN-2, OEN-8) following salt stress treatment. The standard  
35

error bars shown therein are based on three replicates. \* = significance at  $p < 0.05$ . \*\* = significance at  $p < 0.01$ .

Fig. 16C is a graph showing the relative weights of wild-type Nipponbare rice plants (WT), OsCOBL4<sub>IRAT109</sub> transgenic Nipponbare rice plants (OEI-6, OEI-8) and OsCOBL4<sub>Nipponbare</sub> transgenic Nipponbare rice plants (OEN-2, OEN-8) following salt stress treatment. The standard error bars shown therein are based on three replicates. \* = significance at  $p < 0.05$ . \*\* = significance at  $p < 0.01$ .

Fig. 17A shows wild-type Nipponbare rice plants (WT), OsCOBL4<sub>IRAT109</sub> transgenic Nipponbare rice plants (OEI-6, OEI-8) and OsCOBL4<sub>Nipponbare</sub> transgenic Nipponbare rice plants (OEN-2, OEN-6) before and after low-temperature stress treatment.

Fig. 17B is a graph showing the relative membrane permeativities of wild-type Nipponbare rice plants (WT), OsCOBL4<sub>IRAT109</sub> transgenic Nipponbare rice plants (OEI-6, OEI-8) and OsCOBL4<sub>Nipponbare</sub> transgenic Nipponbare rice plants (OEN-2, OEN-6) following low-temperature stress treatment. The standard error bars shown therein are based on three replicates. \* = significance at  $p < 0.05$ . \*\* = significance at  $p < 0.01$ .

Fig. 17C is a graph showing the survival rates of wild-type Nipponbare rice plants (WT), OsCOBL4<sub>IRAT109</sub> transgenic Nipponbare rice plants (OEI-6, OEI-8) and OsCOBL4<sub>Nipponbare</sub> transgenic Nipponbare rice plants (OEN-2, OEN-6) following a low-temperature stress treatment. The standard error bars shown therein are based on three replicates. \* = significance at  $p < 0.05$ . \*\* = significance at  $p < 0.01$ .

Fig. 18 shows the accumulation of reactive oxygen species in leaves taken from wild-type Nipponbare rice plants (WT) and OsCOBL4<sub>IRAT109</sub> transgenic Nipponbare rice plants (OEI) following control treatment (Mock), dehydration stress treatment (Dehydration), low-temperature stress treatment (Cold) or salt stress treatment (NaCl). Reactive oxygen species were detected using DAB staining.

Fig. 19 is a graph showing the sugar composition of cell walls taken from wild-type Nipponbare rice plants (WT), OsCOBL4<sub>IRAT109</sub> transgenic Nipponbare rice plants (OEI) and OsCOBL4<sub>Nipponbare</sub> transgenic Nipponbare rice plants (OEN). The values shown therein are means  $\pm$  standard error. \* = significance at  $p < 0.05$ . \*\* = significance at  $p < 0.01$ .

Fig. 20 is a multiple sequence alignment showing the amino acid sequences of OsERF62<sub>IRAT109</sub> and several of its homologues. The underlined sections of sequences represent an N-terminal MCGGAI(L/I) motif and a nuclear localization signal (NIL), respectively. The section of sequences encompassed by the box represents a conserved AP2 domain.

Fig. 21 shows the results of real-time fluorescence quantitative PCR analyses of the relative expression levels of native *OsERF62* in IRAT109 rice plants and Nipponbare rice plants at

various time points during PEG-simulated drought stress treatment, physiological dehydration drought stress treatment, low-temperature stress treatment, H<sub>2</sub>O<sub>2</sub> treatment, ethylene treatment, ABA treatment, or GA treatment. The standard error bars shown therein are based on three replicates.

5 Fig. 22 is a graph showing the results of real-time fluorescence quantitative PCR analyses of the relative expression levels of native *OsERF62* in tissues from IRAT109 rice plants and Nipponbare rice plants.

Fig. 23 shows the subcellular localization of GFP-fused ERF62 in onion epithelium following particle bombardment-mediated transformation. Leaves were treated with 10% NaCl  
10 to separate cell walls and protoplasts.

Fig. 24A shows maps of various GAL4BD yeast expression vectors used to test the transaction activity of *OsERF62*: A1 = full-length *OsERF62* fused to GAL4BD; A2 = amino acids 1-167 of *OsERF62* fused to GAL4BD; A3 = amino acids 1-106 of *OsERF62* fused to GAL4BD; A4 = amino acids 162-335 of *OsERF62* fused to GAL4BD; A5 = amino acids 230-  
15 335 of GAL4BD fused to GAL4BD.

Fig. 24B-D show the results of an *in vivo* yeast assay using the GAL4BD yeast expression vectors depicted in Fig. 24A. + = positive control. - = negative control.

Fig. 25A is a graph showing the relative expression levels of *OsERF62* in wild-type Nipponbare rice plants (WT) and *OsERF62* transgenic Nipponbare rice plants (OE1, OE2, OE3, OE4, OE5, OE7, OE9). The standard error bars shown therein are based on three replicates.  
20 Triangle = line used for further analysis.

Fig. 25B is a graph showing the relative expression levels of *OsERF62* in wild-type Nipponbare rice plants (WT) and transgenic Nipponbare rice plants expressing an RNA interference molecule directed at *OsERF62* (RI1, RI4, RI6, RI9, RI10, RI12, RI14). The standard error bars shown therein are based on three replicates. Triangle = line used for further analysis.  
25

Fig. 26A shows wild-type Nipponbare rice plants (WT) and *OsERF62* transgenic Nipponbare rice plants (OE4, OE7) before and after physiological dehydration stress treatment.

Fig. 26B is a graph showing the survival rates of wild-type Nipponbare rice plants (WT) and *OsERF62* transgenic Nipponbare rice plants (OE4, OE7) following physiological dehydration drought stress treatment. The standard error bars shown therein are based on three replicates. \*\* = significance at p<0.01.  
30

Fig. 27A shows wild-type Nipponbare rice plants (WT) and *OsERF62* transgenic Nipponbare rice plants (OE4, OE7) before and after drought stress treatment.

Fig. 27B is a graph showing the survival rates of wild-type Nipponbare rice plants (WT) and *OsERF62* transgenic Nipponbare rice plants (OE4, OE7) following drought stress treatment.  
35

The standard error bars shown therein are based on three replicates. \* = significance at  $p < 0.05$ . \*\* = significance at  $p < 0.01$ .

Fig. 27C shows wild-type Nipponbare rice plants (WT) and transgenic Nipponbare rice plants expressing an RNA interference molecule directed at *OsERF62* (RI4, RI10) before and after drought stress treatment.

Fig. 27D is a graph showing the survival rates of wild-type Nipponbare rice plants (WT) and transgenic Nipponbare rice plants expressing an RNA interference molecule directed at *OsERF62* (RI4, RI10) following drought stress treatment. The standard error bars shown therein are based on three replicates. \* = significance at  $p < 0.05$ . \*\* = significance at  $p < 0.01$ .

Fig. 28A shows wild-type Nipponbare rice plants (WT), *OsERF62* transgenic Nipponbare rice plants (OE4, OE7), and transgenic Nipponbare rice plants expressing an RNA interference molecule directed at *OsERF62* (RI6, RI10) following control treatment (Normal) or salt stress treatment (NaCl).

Fig. 28B is a graph showing the relative shoot lengths of wild-type Nipponbare rice plants (WT), *OsERF62* transgenic Nipponbare rice plants (OE4, OE7), and transgenic Nipponbare rice plants expressing an RNA interference molecule directed at *OsERF62* (RI6, RI10) following salt stress treatment. The standard error bars shown therein are based on three replicates. \* = significance at  $p < 0.05$ . \*\* = significance at  $p < 0.01$ .

Fig. 28C is a graph showing the relative weights of wild-type Nipponbare rice plants (WT), *OsERF62* transgenic Nipponbare rice plants (OE4, OE7), and transgenic Nipponbare rice plants expressing an RNA interference molecule directed at *OsERF62* (RI6, RI10) following salt stress treatment. The standard error bars shown therein are based on three replicates. \* = significance at  $p < 0.05$ . \*\* = significance at  $p < 0.01$ .

Fig. 29A shows wild-type Nipponbare rice plants (WT), *OsERF62* transgenic Nipponbare rice plants (OE4, OE7), and transgenic Nipponbare rice plants expressing an RNA interference molecule directed at *OsERF62* (RI6, RI10) following control treatment (Normal) or osmotic stress treatment (Mannitol).

Fig. 29B is a graph showing the relative shoot lengths of wild-type Nipponbare rice plants (WT), *OsERF62* transgenic Nipponbare rice plants (OE4, OE7), and transgenic Nipponbare rice plants expressing an RNA interference molecule directed at *OsERF62* (RI6, RI10) following osmotic stress treatment. The standard error bars shown therein are based on three replicates. \* = significance at  $p < 0.05$ . \*\* = significance at  $p < 0.01$ .

Fig. 29C is a graph showing the relative weights of wild-type Nipponbare rice plants (WT), *OsERF62* transgenic Nipponbare rice plants (OE4, OE7), and transgenic Nipponbare rice plants expressing an RNA interference molecule directed at *OsERF62* (RI6, RI10) following osmotic

stress treatment. The standard error bars shown therein are based on three replicates. \* = significance at  $p < 0.05$ . \*\* = significance at  $p < 0.01$ .

Fig. 30A shows the germination performance of wild-type Nipponbare rice plants (WT) and *OsERF62* transgenic Nipponbare rice plants (OE4, OE7) grown on medium comprising 0, 2, 3, or 5  $\mu$ M ABA.

Fig. 30B is a graph showing the germination rates of wild-type Nipponbare rice plants (WT) and *OsERF62* transgenic Nipponbare rice plants (OE4, OE7) grown on medium comprising 0, 2, 3, or 5  $\mu$ M ABA. The standard error bars shown therein are based on three replicates.

Fig. 30C shows wild-type Nipponbare rice plants (WT), *OsERF62* transgenic Nipponbare rice plants (OE4, OE7), and transgenic Nipponbare rice plants expressing an RNA interference molecule directed at *OsERF62* (RI6, RI10) grown on medium comprising 0  $\mu$ M ABA (Normal) or 3  $\mu$ M ABA (ABA).

Fig. 30D is a graph showing the relative shoot lengths of wild-type Nipponbare rice plants (WT), *OsERF62* transgenic Nipponbare rice plants (OE4, OE7), and transgenic Nipponbare rice plants expressing an RNA interference molecule directed at *OsERF62* (RI6, RI10) grown on medium comprising 3  $\mu$ M ABA. The standard error bars shown therein are based on three replicates. \* = significance at  $p < 0.05$ . \*\* = significance at  $p < 0.01$ .

Fig. 30E is a graph showing the relative weights of wild-type Nipponbare rice plants (WT), *OsERF62* transgenic Nipponbare rice plants (OE4, OE7), and transgenic Nipponbare rice plants expressing an RNA interference molecule directed at *OsERF62* (RI6, RI10) grown on medium comprising 3  $\mu$ M ABA. The standard error bars shown therein are based on three replicates. \* = significance at  $p < 0.05$ . \*\* = significance at  $p < 0.01$ .

Fig. 31 is a graph showing water loss of leaves taken from wild-type Nipponbare rice plants (WT), *OsERF62* transgenic Nipponbare rice plants (OE7), and transgenic Nipponbare rice plants expressing an RNA interference molecule directed at *OsERF62* (RI10). The standard error bars shown therein are based on three replicates.

Fig. 32 shows the accumulation of reactive oxygen species in leaves taken from wild-type Nipponbare rice plants (WT), *OsERF62* transgenic Nipponbare rice plants (OE7), and transgenic Nipponbare rice plants expressing an RNA interference molecule directed at *OsERF62* (RI10) following control treatment (No Stress), dehydration stress treatment (Dehydration stress), or simulated drought stress treatment (20% PEG stress). Reactive oxygen species were detected using DAB staining.

Fig. 33A shows wild-type Nipponbare rice plants (WT), *OsERF62* transgenic Nipponbare rice plants (OE4, OE7), and transgenic Nipponbare rice plants expressing an RNA interference

molecule directed at *OsERF62* (RI6, RI10) following control treatment (Normal) or oxidative stress treatment (MV).

Fig. 33B is a graph showing the relative shoot lengths of wild-type Nipponbare rice plants (WT), *OsERF62* transgenic Nipponbare rice plants (OE4, OE7), and transgenic Nipponbare rice plants expressing an RNA interference molecule directed at *OsERF62* (RI6, RI10) following oxidative stress treatment (MV). The standard error bars shown therein are based on three replicates. \*\* = significance at  $p < 0.01$ .

Fig. 33C is a graph showing the relative weights of wild-type Nipponbare rice plants (WT), *OsERF62* transgenic Nipponbare rice plants (OE4, OE7), and transgenic Nipponbare rice plants expressing an RNA interference molecule directed at *OsERF62* (RI6, RI10) following oxidative stress treatment (MV). The standard error bars shown therein are based on three replicates. \* = significance at  $p < 0.05$ . \*\* = significance at  $p < 0.01$ .

Fig. 34 shows the relative mRNA levels of genes associated with reactive oxygen species scavenging (*APX1*, *APX2*, *catB*, *POD1*, *POD2*, and *DSMI*) in wild-type Nipponbare rice plants (WT), *OsERF62* transgenic Nipponbare rice plants (OE4, OE7), and transgenic Nipponbare rice plants expressing an RNA interference molecule directed at *OsERF62* (RI6, RI10). The standard error bars shown therein are based on three replicates.

Fig. 35 is a graphing showing the relative ethylene emissions of wild-type Nipponbare rice plants (WT), *OsERF62* transgenic Nipponbare rice plants (OE4, OE7), and transgenic Nipponbare rice plants expressing an RNA interference molecule directed at *OsERF62* (RI6, RI10). The standard error bars shown therein are based on three replicates.

Fig. 36 shows the relative mRNA levels of genes associated with ethylene biosynthesis (*ACO3*, *ASC6*, *ASC2*, *ACO2*) in wild-type Nipponbare rice plants (WT), *OsERF62* transgenic Nipponbare rice plants (OE4, OE7), and transgenic Nipponbare rice plants expressing an RNA interference molecule directed at *OsERF62* (RI6, RI10). The standard error bars shown therein are based on three replicates.

#### DETAILED DESCRIPTION

The present invention provides compositions and methods for identifying, selecting and/or producing plants and plant parts having enhanced abiotic stress tolerances (e.g., enhanced drought tolerances, enhanced osmotic stress tolerances, enhanced salt stress tolerances and/or enhanced temperature stress tolerances), as well as plants and plant parts identified, selected and/or produced using compositions and methods of the present invention.

Although the following terms are believed to be well understood by one of ordinary skill in the art, the following definitions are set forth to facilitate understanding of the presently disclosed subject matter.

5 All technical and scientific terms used herein, unless otherwise defined below, are intended to have the same meaning as commonly understood by one of ordinary skill in the art. References to techniques employed herein are intended to refer to the techniques as commonly understood in the art, including variations on those techniques or substitutions of equivalent techniques that would be apparent to one of skill in the art.

10 All patents, patent publications, non-patent publications referenced herein are incorporated by reference in their entireties for all purposes and to the same extent as if each was specifically and individually indicated to be incorporated by reference.

As used herein, the terms "a" or "an" or "the" may refer to one or more than one, unless the context clearly and unequivocally indicates otherwise. For example, "an" endogenous nucleic acid can mean one endogenous nucleic acid or a plurality of endogenous nucleic acids.

15 As used herein, the term "and/or" refers to and encompasses any and all possible combinations of one or more of the associated listed items, as well as the lack of combinations when interpreted in the alternative ("or").

As used herein, the term "about," when used in reference to a measurable value such as an amount of mass, dose, time, temperature, and the like, refers to a variation of 0.1%, 0.25%, 0.5%,  
20 0.75%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15% or even 20% of the specified amount. Thus, if a given composition is described as comprising "about 50% X," it is to be understood that, in some embodiments, the composition comprises 50% X whilst in other embodiments it may comprise anywhere from 40 to 60% X (*i.e.*,  $50 \pm 10\%$ ).

As used herein, the terms "abiotic stress" and "abiotic stress conditions" refer to non-living  
25 factors that negatively affect a plant's ability to grow, reproduce and/or survive (*e.g.*, drought, flooding, extreme temperatures, extreme light conditions, extreme osmotic pressures, extreme salt concentrations, high winds, natural disasters and poor edaphic conditions (*e.g.*, extreme soil pH, nutrient-deficient soil, compacted soil, etc.)).

As used herein, the terms "abiotic stress tolerance" and "abiotic stress tolerant" refer to a  
30 plant's ability to endure and/or thrive under abiotic stress conditions. When used in reference to a plant part, the terms refer to the ability of a plant that arises from that plant part to endure and/or thrive under abiotic stress conditions.

A characteristic is "associated with" a trait when it is linked to it and when the presence of the characteristic is an indicator of whether and/or to what extent the desired trait or trait form  
35 will occur in a plant/plant part comprising the characteristic. Similarly, a characteristic is

"associated with" an allele when it is linked to it and when the presence of the characteristic is an indicator of whether the allele is present in a plant/plant part comprising the characteristic. For example, "a characteristic associated with enhanced drought tolerance" refers to a characteristic whose presence or absence can be used to predict whether and/or to what extent a plant will display a drought tolerant phenotype.

As used herein, the terms "backcross" and "backcrossing" refer to the process whereby a progeny plant is repeatedly crossed back to one of its parents. In a backcrossing scheme, the "donor" parent refers to the parental plant with the desired allele or locus to be introgressed. The "recipient" parent (used one or more times) or "recurrent" parent (used two or more times) refers to the parental plant into which the gene or locus is being introgressed. The initial cross gives rise to the F1 generation. The term "BC1" refers to the second use of the recurrent parent, "BC2" refers to the third use of the recurrent parent, and so on.

As used herein, the transitional phrase "consisting essentially of" is to be interpreted as encompassing the recited materials or steps and those that do not materially affect the basic and novel characteristic(s) of the claimed invention.

As used herein, the terms "cross" or "crossed" refer to the fusion of gametes via pollination to produce progeny (e.g., cells, seeds or plants). The term encompasses both sexual crosses (the pollination of one plant by another) and selfing (self-pollination, e.g., when the pollen and ovule are from the same plant). The term "crossing" refers to the act of fusing gametes via pollination to produce progeny.

As used herein, the terms "cultivar" and "variety" refer to a group of similar plants that by structural or genetic features and/or performance can be distinguished from other cultivars/varieties within the same species.

As used herein, the terms "decrease," "decreases," "decreasing" and similar terms refer to a reduction of at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more. In some embodiments, the reduction results in no or essentially no activity (*i.e.*, an insignificant or undetectable amount of activity).

As used herein, the terms "drought tolerance" and "drought tolerant" refer to a plant's ability to endure and/or thrive under drought stress conditions. When used in reference to a plant part, the terms refer to the ability of a plant that arises from that plant part to endure and/or thrive under drought conditions. In general, a plant or plant part is designated as "drought tolerant" if it displays "enhanced drought tolerance."

As used herein, the term "COBL4 protein" refers to a protein belonging to the COBRA family, such as *Oryza sativa ssp japonica* cv. *IRAT109* COBRA-like 4 protein (OsCOBL4<sub>IRAT109</sub>),

*Oryza sativa ssp japonica cv. Nipponbare* COBRA-like 4 protein (OsCOBL4<sub>Nipponbare</sub>) and homologues thereof. Examples of COBL4 proteins include, but are not limited to, proteins having the amino acid sequence of any one of SEQ ID NOs: 28–35 and proteins having an amino acid sequence that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the amino acid sequence of any one of SEQ ID NOs: 28–35. In some embodiments, the COBL4 protein comprises an N-terminal signal peptide that is at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 1 to 27 of SEQ ID NO: 28–35 and/or a CVS domain that is at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 226 to 229 of SEQ ID NO: 28–35. In some embodiments, the COBL4 protein is encoded by a nucleic acid comprising a nucleotide sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to any one of SEQ ID NOs: 1–13.

As used herein, the term "ERF62 protein" refers to an AP2 domain-containing protein, such as *Oryza sativa ssp japonica cv. IRAT109* ERF62 (OsERF62-IRAT109), *Oryza sativa ssp japonica cv. IRAT109* Japonica Group ERF71 (OsERF71-IRAT109; Rice Genome Annotation Project Accession No. LOC\_Os06g09390.1) and homologues thereof. Examples of ERF62 proteins include, but are not limited to, proteins having the amino acid sequence of any one of SEQ ID NOs: 36–44 and proteins having an amino acid sequence that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the amino acid sequence of any one of SEQ ID NOs: 36–44. In some embodiments, the ERF62 protein comprises an AP2 domain that is at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 95 to 167 of SEQ ID NO: 36–44 and/or an N-terminal MCGGAI(L/I) motif that is at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 1 to 7 of SEQ ID NO: 36–44. In some embodiments, the ERF62 protein is encoded by a nucleic acid comprising a nucleotide sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to any one of SEQ ID NOs: 14–27.

As used herein, the term "enhanced abiotic stress tolerance" refers to an improvement in the ability of a plant or plant part to grow, reproduce and/or survive under abiotic stress conditions, as compared to one or more controls (*e.g.*, a native plant/plant part of the same species). "Enhanced abiotic stress tolerance" may refer to any improvement in a plant's or plant part's ability to thrive and/or endure when grown under abiotic stress conditions, including, but not limited to, decreased water loss, decreased accumulation of one or more reactive oxygen species, decreased accumulation of one or more salts, increased salt excretion, increased accumulation of one or more dehydrins, improved root architecture, improved osmotic pressure regulation,

increased accumulation of one or more late embryogenesis abundant proteins, increased survival rate, increased growth rate, increased height, increased chlorophyll content and/or increased yield (*e.g.*, increased biomass, increased seed yield, increased grain yield at standard moisture percentage (YGSMN), increased grain moisture at harvest (GMSTP), increased grain weight per plot (GWTPN), increased percent yield recovery (PYREC), decreased yield reduction (YRED), and/or decreased percent barren (PB)) when grown under abiotic stress conditions. A plant or plant part that exhibits enhanced abiotic stress tolerance may be designated as "abiotic stress tolerant."

As used herein, the term "enhanced drought tolerance" refers to an improvement in one or more water optimization traits as compared to one or more controls (*e.g.*, a native plant/plant part of the same species). A plant or plant part that exhibits decreased water loss, decreased accumulation of one or more reactive oxygen species, decreased accumulation of one or more salts, increased salt excretion, increased accumulation of one or more dehydrins, improved root architecture, improved osmotic pressure regulation, increased accumulation of one or more late embryogenesis abundant proteins, increased survival rate, increased growth rate, increased height, increased chlorophyll content and/or increased yield (*e.g.*, increased biomass, increased seed yield, increased YGSMN, increased GMSTP, increased GWTPN, increased PYREC, decreased YRED, and/or decreased PB) as compared to a control plant (*e.g.*, one or both of its parents) when each is grown under the same drought stress conditions displays enhanced drought tolerance and may be designated as "drought tolerant." In some embodiments, the plant or plant part exhibits an increased survival rate after being subjected to PED-simulated drought stress conditions (*e.g.*, incubation in a 200g/L PEG6000 solution).

As used herein, the term "enhanced osmotic stress tolerance" refers to an improvement in one or more osmotic pressure optimization traits as compared to one or more controls (*e.g.*, a native plant/plant part of the same species). A plant or plant part that exhibits decreased water loss, decreased accumulation of one or more reactive oxygen species, decreased accumulation of one or more salts, increased salt excretion, increased accumulation of one or more dehydrins, improved root architecture, improved osmotic pressure regulation, increased accumulation of one or more late embryogenesis abundant proteins, increased survival rate, increased growth rate, increased height, increased chlorophyll content and/or increased yield (*e.g.*, increased biomass, increased seed yield, increased YGSMN, increased GMSTP, increased GWTPN, increased PYREC, decreased YRED, and/or decreased PB) as compared to a control plant (*e.g.*, one or both of its parents) when each is grown under the same osmotic stress conditions displays enhanced osmotic stress tolerance and may be designated as "osmotic stress tolerant." In some

embodiments, the plant or plant part exhibits an increased survival rate after being subjected to mannitol-induced osmotic stress conditions. (*e.g.*, incubation in a 200 mM mannitol solution).

As used herein, the term "enhanced salt stress tolerance" refers to an improvement in one or more salt optimization traits as compared to one or more controls (*e.g.*, a native plant/plant part of the same species). A plant or plant part that exhibits decreased water loss, decreased accumulation of one or more reactive oxygen species, decreased accumulation of one or more salts, increased salt excretion, increased accumulation of one or more dehydrins, improved root architecture, improved osmotic pressure regulation, increased accumulation of one or more late embryogenesis abundant proteins, increased survival rate, increased growth rate, increased height, increased chlorophyll content and/or increased yield (*e.g.*, increased biomass, increased seed yield, increased YGSMN, increased GMSTP, increased GWTPN, increased PYREC, decreased YRED, and/or decreased PB) as compared to a control plant (*e.g.*, one or both of its parents) when each is grown under the same salt stress conditions displays enhanced salt stress tolerance and may be designated as "salt stress tolerant."

As used herein, the term "enhanced temperature stress tolerance" refers to an improvement in one or more temperature tolerance traits as compared to one or more controls (*e.g.*, a native plant/plant part of the same species). A plant or plant part that exhibits decreased water loss, decreased accumulation of one or more reactive oxygen species, decreased accumulation of one or more salts, increased salt excretion, increased accumulation of one or more dehydrins, improved root architecture, improved osmotic pressure regulation, increased accumulation of one or more late embryogenesis abundant proteins, increased survival rate, increased growth rate, increased height, increased biomass, increased chlorophyll content, increased grain yield at standard moisture percentage (YGSMN), increased GMSTP, increased GWTPN, increased PYREC, decreased YRED, and/or decreased PB as compared to a control plant (*e.g.*, one or both of its parents) when each is grown under the same temperature stress conditions displays enhanced temperature stress tolerance and may be designated as "temperature stress tolerant."

It is to be understood that "drought tolerant," "osmotic stress tolerant," "salt stress tolerant," and "temperature stress tolerant" plants and plant parts may also be referred to as a "abiotic stress tolerant" because drought stress, osmotic stress, salt stress and temperature stress are all abiotic stresses.

As used herein, with respect to nucleic acids, the term "exogenous" refers to a nucleic acid that is not in the natural genetic background of the cell/organism in which it resides. In some embodiments, the exogenous nucleic acid comprises one or more nucleic acid sequences that are not found in the natural genetic background of the cell/organism. In some embodiments, the

exogenous nucleic acid comprises one or more additional copies of a nucleic acid that is endogenous to the cell/organism.

As used herein with respect to nucleotide sequences, the terms "express" and "expression" refer to transcription and/or translation of the sequences.

5 As used herein with respect to nucleic acids, the term "fragment" refers to a nucleic acid that is reduced in length relative to a reference nucleic acid and that comprises, consists essentially of and/or consists of a nucleotide sequence of contiguous nucleotides identical or almost identical (*e.g.*, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical) to a corresponding portion of the reference nucleic acid. Such a nucleic acid fragment may be, where  
10 appropriate, included in a larger polynucleotide of which it is a constituent. In some embodiments, the nucleic acid fragment comprises, consists essentially of or consists of at least about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 300, 350, 400, 450, 500, or more consecutive nucleotides. In some embodiments, the nucleic acid fragment comprises, consists essentially of or consists of  
15 less than about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 300, 350, 400, 450 or 500 consecutive nucleotides.

As used herein with respect to polypeptides, the term "fragment" refers to a polypeptide that is reduced in length relative to a reference polypeptide and that comprises, consists essentially of  
20 and/or consists of an amino acid sequence of contiguous amino acids identical or almost identical (*e.g.*, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical) to a corresponding portion of the reference polypeptide. Such a polypeptide fragment may be, where appropriate, included in a larger polypeptide of which it is a constituent. In some embodiments, the polypeptide fragment comprises, consists essentially of or consists of at least about 2, 3, 4, 5,  
25 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 300, 350, 400, 450, 500, or more consecutive amino acids. In some embodiments, the polypeptide fragment comprises, consists essentially of or consists of less than about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 300, 350, 400, 450 or 500 consecutive amino acids.

30 As used herein with respect to nucleic acids, the term "functional fragment" refers to nucleic acid that encodes a functional fragment of a polypeptide.

As used herein with respect to polypeptides, the term "functional fragment" refers to polypeptide fragment that retains at least about 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more of at least  
35 one biological activity of the full-length polypeptide (*e.g.*, the ability to up- or down-regulate

gene expression). In some embodiments, the functional fragment actually has a higher level of at least one biological activity of the full-length polypeptide.

As used herein, the term "germplasm" refers to genetic material of or from an individual plant, a group of plants (e.g., a plant line, variety or family), or a clone derived from a plant line, variety, species, or culture. The genetic material can be part of a cell, tissue or organism, or can be isolated from a cell, tissue or organism.

As used herein, the term "heterologous" refers to a nucleotide/polypeptide that originates from a foreign species, or, if from the same species, is substantially modified from its native form in composition and/or genomic locus by deliberate human intervention.

As used herein, the terms "increase," "increases," "increasing" and similar terms refer to an elevation of at least about 20%, 25%, 30%, 35%, 40%, 45%, 50%, 75%, 100%, 125%, 150%, 175%, 200%, 350%, 300%, 350%, 400%, 450%, 500% or more.

As used herein, the term "informative fragment" refers to a nucleotide sequence comprising a fragment of a larger nucleotide sequence, wherein the fragment allows for the identification of one or more alleles within the larger nucleotide sequence. For example, an informative fragment of the nucleotide sequence of SEQ ID NO: 1 comprises a fragment of the nucleotide sequence of SEQ ID NO: 1 and allows for the identification of one or more alleles located within the portion of the nucleotide sequence corresponding to that fragment of SEQ ID NO: 1.

As used herein with respect to nucleotides and polypeptides, the term "isolated" refers to a nucleotide or polypeptide that is substantially free of cellular material, viral material, culture medium (when produced by recombinant DNA techniques), or chemical precursors or other chemicals (when chemically synthesized). An "isolated fragment" is a fragment of a nucleotide or polypeptide that is not naturally occurring as a fragment and would not be found in the natural state. "Isolated" does not mean that the preparation is technically pure (homogeneous), but rather that it is sufficiently pure to provide the nucleotide or polypeptide in a form in which it can be used for the intended purpose. In certain embodiments, the composition comprising the nucleotide or polypeptide is at least about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% or more pure.

As used herein with respect to cells, the term "isolated" refers to a cell that is separated from other components with which it is normally associated in its natural state. For example, an isolated plant cell may be a plant cell in culture medium and/or a plant cell in a suitable carrier. "Isolated" does not mean that the preparation is technically pure (homogeneous), but rather that it is sufficiently pure to provide the cell in a form in which it can be used for the intended purpose. In certain embodiments, the composition comprising the cell is at least about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% or more pure.

As used herein with respect to nucleic acids, the term "nonfunctional fragment" refers to nucleic acid that encodes a nonfunctional fragment of a polypeptide.

As used herein with respect to polypeptides, the term "nonfunctional fragment" refers to polypeptide fragment that exhibits none or essentially none (*i.e.*, less than about 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1% or less) of the biological activities of the full-length polypeptide.

As used herein with respect to nucleic acids, proteins, plant cells, plant parts, plants, viruses and bacteria, the term "nonnaturally occurring" refers to a nucleic acids, proteins, plant parts, plants, viruses or bacteria that does not naturally exist in nature. In some embodiments, the nonnaturally occurring plant part, plant, virus or bacteria comprises one of more exogenous nucleotide sequences. For example, in some embodiments, the nonnaturally occurring plant part, plant, virus or bacteria comprises one or more nonnaturally occurring copies of a naturally occurring nucleotide sequence (*i.e.*, extraneous copies of a gene that naturally occurs in that species). Nonnaturally occurring plants and plant parts may be produced by any suitable method, including, but not limited to, transforming a plant or plant part with an exogenous nucleic acid, transfecting a plant or plant part with an exogenous nucleic acid, and crossing a naturally occurring plant or plant part with a nonnaturally occurring plant or plant part. It is to be understood that all nucleic acids, proteins, plant parts, plants, viruses and bacteria provided by the present invention are nonnaturally occurring.

As used herein, the term "nucleic acid" refers to deoxyribonucleotide, ribonucleotide and deoxyribonucleotide-ribonucleotide polymers in either single- or double-stranded form and, unless otherwise limited, encompasses analogues having the essential nature of natural nucleotides in that they hybridize to single-stranded nucleic acids in a manner similar to naturally occurring nucleotides (*e.g.*, peptide nucleic acids).

As used herein, the term "nucleotide" refers to a monomeric unit from which DNA or RNA polymers are constructed and which consists of a purine or pyrimidine base, a pentose, and a phosphoric acid group. Nucleotides (usually found in their 5'-monophosphate form) are referred to by their single letter designation as follows: "A" for adenylate or deoxyadenylate (for RNA or DNA, respectively), "C" for cytidylate or deoxycytidylate, "G" for guanylate or deoxyguanylate, "U" for uridylate, "T" for deoxythymidylate, "R" for purines (A or G), "Y" for pyrimidines (C or T), "K" for G or T, "H" for A or C or T, "I" for inosine, and "N" for any nucleotide.

As used herein, the terms "nucleotide sequence," "polynucleotide," "nucleic acid sequence," "nucleic acid molecule" and "nucleic acid fragment" refer to a polymer of RNA, DNA, or RNA and DNA that is single- or double-stranded, optionally containing synthetic, non-natural and/or altered nucleotide bases.

As used herein, the term "nucleotide sequence identity" refers to the presence of identical nucleotides at corresponding positions of two polynucleotides. Polynucleotides have "identical" sequences if the sequence of nucleotides in the two polynucleotides is the same when aligned for maximum correspondence (e.g., in a comparison window). Sequence comparison between two or more polynucleotides is generally performed by comparing portions of the two sequences over a comparison window to identify and compare local regions of sequence similarity. The comparison window is generally from about 20 to 200 contiguous nucleotides. The "percentage of sequence identity" for polynucleotides, such as about 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 98, 99 or 100 percent sequence identity, can be determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window can include additions or deletions (i.e., gaps) as compared to the reference sequence for optimal alignment of the two sequences. The percentage is calculated by: (a) determining the number of positions at which the identical nucleic acid base occurs in both sequences; (b) dividing the number of matched positions by the total number of positions in the window of comparison; and (c) multiplying the result by 100. Optimal alignment of sequences for comparison can also be conducted by computerized implementations of known algorithms, or by visual inspection. Readily available sequence comparison and multiple sequence alignment algorithms are, respectively, the Basic Local Alignment Search Tool (BLAST) and ClustalW programs, both available on the internet. Other suitable programs include, but are not limited to, GAP, BestFit, Plot Similarity, and FASTA, which are part of the Accelrys GCG Package available from Accelrys, Inc. of San Diego, California, United States of America. In some embodiments, a percentage of sequence identity refers to sequence identity over the full length of one of the sequences being compared. In some embodiments, a calculation to determine a percentage of sequence identity does not include in the calculation any nucleotide positions in which either of the compared nucleic acids includes an "N" (i.e., where any nucleotide could be present at that position).

As used herein with respect to nucleic acids, the term "operably linked" refers to a functional linkage between two or more nucleic acids. For example, a promoter sequence may be described as being "operably linked" to a heterologous nucleic acid sequence because the promoter sequences initiates and/or mediates transcription of the heterologous nucleic acid sequence. In some embodiments, the operably linked nucleic acid sequences are contiguous and/or are in the same reading frame.

As used herein, the term "osmotic pressure optimization trait" refers to any trait that can be shown to influence the growth, yield and/or survival of a plant under different sets of growth conditions related to osmotic pressure.

As used herein, the terms "osmotic stress tolerance" and "osmotic stress tolerant" refer to a plant's ability to endure and/or thrive under osmotic stress conditions. When used in reference to a plant part, the terms refer to the ability of a plant that arises from that plant part to endure and/or thrive under osmotic stress conditions. In general, a plant or plant part is designated as

5 "osmotic stress tolerant" if it displays "enhanced osmotic stress tolerance."

As used herein, the term "percent barren" (PB) refers to the percentage of plants in a given area (e.g., plot) with no grain. It is typically expressed in terms of the percentage of plants per plot and can be calculated as:

$$10 \quad \frac{\text{number of plants in the plot with no grain}}{\text{total number of plants in the plot}} \times 100$$

As used herein, the term "percent yield recovery" (PYREC) refers to the effect an allele and/or combination of alleles has on the yield of a plant grown under stress conditions (e.g., drought stress conditions) as compared to that of a plant that is genetically identical except

15 insofar as it lacks the allele and/or combination of alleles. PYREC is calculated as:

$$20 \quad 1 - \frac{\text{yield under non-stress (w/ allele(s) of interest)} - \text{yield under stress conditions (w/ allele(s) of interest)}}{\text{yield under non-stress (w/out allele(s) of interest)} - \text{yield under stress conditions (w/out allele(s) of interest)}} \times 100$$

By way of example and not limitation, if a control plant yields 200 bushels under full irrigation conditions, but yields only 100 bushels under drought stress conditions, then its percentage yield loss would be calculated at 50%. If an otherwise genetically identical hybrid that contains the allele(s) of interest yields 125 bushels under drought stress conditions and 200 bushels under full irrigation conditions, then the percentage yield loss would be calculated as 37.5% and the PYREC would be calculated as 25% [1.00-(200-125)/(200-100)x100)].

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As used herein, the terms "phenotype," "phenotypic trait" or "trait" refer to one or more traits of an organism. The phenotype can be observable to the naked eye, or by any other means of evaluation known in the art, e.g., microscopy, biochemical analysis, or an electromechanical assay. In some cases, a phenotype is directly controlled by a single gene or genetic locus, i.e., a "single gene trait." In other cases, a phenotype is the result of several genes. It is noted that, as used herein, the term "water optimization phenotype" takes into account environmental

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conditions that might affect water optimization such that the water optimization effect is real and reproducible.

As used herein, the term "plant" may refer to any suitable plant, including, but not limited to, spermatophytes (*e.g.*, angiosperms and gymnosperms) and embryophytes (*e.g.*, bryophytes, ferns and fern allies). In some embodiments, the plant is a monocotyledonous (monocot) plant such as a rice, maize, wheat, barley, sorghum, millet, oat, triticale, rye, buckwheat, fonio, quinoa, sugar cane, bamboo, banana, ginger, onion, lily, daffodil, iris, amaryllis, orchid, canna, bluebell, tulip, garlic, secale, einkorn, spelt, emmer, durum, kamut, grass (*e.g.*, gramma grass), teff, milo, flax, *Tripsacum sp.*, or teosinte plant. In some embodiments, the plant is a dicotyledonous (dicot) plant such as a blackberry, raspberry, strawberry, barberry, bearberry, blueberry, coffee berry, cranberry, crowberry, currant, elderberry, gooseberry, goji berry, honeyberry, lemon, lime, lingonberry, mangosteen, orange, pepper, persimmon, pomegranate, prune, cotton, clover, acai, plum, peach, nectarin, cherry, guava, almond, pecan, walnut, amaranth, apple, sweet pea, pear, potato, soybean, sugar beet, sunflower, sweet potato, tamarind, tea, tobacco or tomato plant.

As used herein, the term "plant cell" refers to a cell existing in, taken from and/or derived from a plant (*e.g.*, a cell derived from a plant cell/tissue culture). Thus, the term "plant cell" may refer to an isolated plant cell, a plant cell in a culture, a plant cell in an isolated tissue/organ and/or a plant cell in a whole plant.

As used herein, the term "plant part" refers to at least a fragment of a whole plant or to a cell culture or tissue culture derived from a plant. Thus, the term "plant part" may refer to plant cells, plant tissues and plant organs, as well as cell/tissue cultures derived from plant cells, plant tissues and plant cultures. Embodiments of the present invention may comprise and/or make use of any suitable plant part, including, but not limited to, anthers, branches, buds, calli, clumps, cobs, cotyledons, ears, embryos, filaments, flowers, fruits, husks, kernels, leaves, lodicules, ovaries, palea, panicles, pedicels, pods, pollen, protoplasts, roots, root tips, seeds, silks, stalks, stems, stigma, styles, and tassels. In some embodiments, the plant part is a plant germplasm.

As used herein, the term "polynucleotide" refers to a deoxyribopolynucleotide, ribopolynucleotide or analogs thereof that have the essential nature of a natural deoxyribopolynucleotide/ribonucleotide in that they hybridize, under stringent hybridization conditions, to substantially the same nucleotide sequence as naturally occurring nucleotides and/or allow translation into the same amino acid(s) as the naturally occurring nucleotide(s). A polynucleotide can be full-length or a subsequence of a native or heterologous structural or regulatory gene. Unless otherwise indicated, the term includes reference to the specified sequence as well as the complementary sequence thereof. Thus, DNAs or RNAs with backbones modified for stability or for other reasons are "polynucleotides" as that term is intended herein.

Moreover, DNAs or RNAs comprising unusual bases, such as inosine or modified bases, such as tritylated bases, to name just two examples, are polynucleotides as the term is used herein. It will be appreciated that a great variety of modifications have been made to DNA and RNA that serve many useful purposes known to those of skill in the art. The term polynucleotide as it is employed herein embraces such chemically, enzymatically or metabolically modified forms of polynucleotides, as well as the chemical forms of DNA and RNA characteristic of viruses and cells, including inter alia, simple and complex cells.

As used herein, the terms "polypeptide," "peptide" and "protein" refer to a polymer of amino acid residues. The terms encompass amino acid polymers in which one or more amino acid residue is an artificial chemical analogue of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers.

As used herein, the terms "progeny" and "progeny plant" refer to a plant generated from a vegetative or sexual reproduction from one or more parent plants. A progeny plant may be obtained by cloning or selfing a single parent plant, or by crossing two parental plants.

As used herein, the terms "promoter" and "promoter sequence" refer to nucleic acid sequences involved in the regulation of transcription initiation. A "plant promoter" is a promoter capable of initiating transcription in plant cells. Exemplary plant promoters include, but are not limited to, those that are obtained from plants, plant viruses and bacteria that comprise genes expressed in plant cells such *Agrobacterium* or *Rhizobium*. A "tissue-specific promoter" is a promoter that preferentially initiates transcription in a certain tissues. A "stress-inducible promoter" is a promoter that preferentially initiates transcription under certain environmental conditions. A "developmental stage-specific promoter" is a promoter that preferentially initiates transcription during certain developmental stages.

As used herein, the term "salt optimization trait" refers to any trait that can be shown to influence the growth, yield and/or survival of a plant under different sets of growth conditions related to salt availability.

As used herein, the terms "salt stress tolerance" and "salt stress tolerant" refer to a plant's ability to endure and/or thrive under salt stress conditions (*i.e.*, low salt concentrations and/or high salt concentrations). When used in reference to a plant part, the terms refer to the ability of a plant that arises from that plant part to endure and/or thrive under salt stress conditions. In general, a plant or plant part is designated as "salt stress tolerant" if it displays "enhanced salt stress tolerance."

As used herein, the terms "selectively hybridize" and "specifically hybridize" refer to the hybridization of a nucleic acid sequence to a specified nucleic acid target sequence, wherein the nucleic acid sequence preferentially hybridizes to the specified nucleic acid target sequence (*e.g.*,

at least about a two-fold difference as compared to its hybridization with non-target nucleic acid sequences) to the substantial exclusion of non-target nucleic acids.

As used herein, the term "stringent hybridization conditions" refers to conditions under which a nucleic acid will selectively hybridize to a target nucleic acid sequence. In some  
5 embodiments, stringent hybridization conditions comprise 7% sodium dodecyl sulfate (SDS), 0.5 M Na<sub>3</sub>PO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 2x SSC, 0.1% SDS at 50°C. In some embodiments, stringent hybridization conditions comprise 7% SDS, 0.5 M Na<sub>3</sub>PO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 1x SSC, 0.1% SDS at 50°C. In some embodiments, stringent hybridization conditions comprise 7% SDS, 0.5 M Na<sub>3</sub>PO<sub>4</sub>, 1 mM EDTA at 50°C with washing  
10 in 0.5x SSC, 0.1% SDS at 50°C. In some embodiments, stringent hybridization conditions comprise 7% SDS, 0.5 M Na<sub>3</sub>PO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 0.1x SSC, 0.1% SDS at 50°C. In some embodiments, stringent hybridization conditions comprise 7% SDS, 0.5 M Na<sub>3</sub>PO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 0.1x SSC, 0.1% SDS at 65°C. In some embodiments, stringent hybridization conditions comprise 6x SSC, 0.5% SDS at 65°C with  
15 washing in 2x SSC, 0.1% SDS and 1x SSC, 0.1% SDS at 65°C. In some embodiments, stringent hybridization conditions comprise a wash stringency of 50% formamide with 5x Denhardt's solution, 0.5% SDS and 1x SSPE at 42°C.

As used herein, the terms "temperature stress tolerance" and "temperature stress tolerant" refer to a plant's ability to endure and/or thrive under temperature stress conditions (*i.e.*, low  
20 temperature conditions and/or high temperature conditions). When used in reference to a plant part, the terms refer to the ability of a plant that arises from that plant part to endure and/or thrive under temperature stress conditions. In general, a plant or plant part is designated as "temperature stress tolerant" if it displays "enhanced temperature stress tolerance."

As used herein, the term "temperature tolerance trait" refers to any trait that can be shown to  
25 influence the growth, yield and/or survival of a plant under different sets of growth conditions related to temperature.

As used herein, the terms "transfection" and "transduction" refer to the uptake of an exogenous nucleic acid (RNA and/or DNA) by a plant cell. A cell has been "transfected" or "transduced" with an exogenous nucleic acid when such nucleic acid has been introduced or  
30 delivered into the cell. A cell has been "transformed" by an exogenous nucleic acid when the transfected or transduced nucleic acid imparts a phenotypic change to the cell and/or a change in an activity or function of the cell. The transforming nucleic acid can be integrated (covalently linked) into chromosomal DNA making up the genome of the cell or it can be present as a stable plasmid.

As used herein with respect to plants and plant parts, the term "transgenic" refers to a plant or plant part that comprises one or more exogenous nucleic acids. Generally, the exogenous nucleic acid is stably integrated within the genome such that the polynucleotide is passed on to successive generations. The exogenous nucleic acid may be integrated into the genome alone or as part of a recombinant expression cassette. "Transgenic" may be used to designate any plant or plant part the genotype of which has been altered by the presence of an exogenous nucleic acid, including those transgenics initially so altered and those created by sexual crosses or asexual propagation from the initial transgenic. As used herein, the term "transgenic" does not encompass the alteration of the genome (chromosomal or extra-chromosomal) by conventional plant breeding methods or by naturally occurring events such as random cross-fertilization, non-recombinant viral infection, non-recombinant bacterial transformation, non-recombinant transposition or spontaneous mutation.

As used herein, the term "vector" refers to a nucleic acid molecule for the cloning of and/or transfer of a nucleic acid into a cell. A vector may be a replicon to which another nucleotide sequence may be attached to allow for replication of the attached nucleotide sequence. A "replicon" can be any genetic element (*e.g.*, plasmid, phage, cosmid, chromosome, viral genome) that functions as an autonomous unit of nucleic acid replication *in vivo* (*i.e.*, is capable of replication under its own control). The term "vector" includes both viral and nonviral (*e.g.*, plasmid) nucleic acid molecules for introducing a nucleic acid into a cell *in vitro*, *ex vivo*, and/or *in vivo*. A large number of vectors known in the art may be used to manipulate nucleic acids, incorporate response elements and promoters into genes, etc. For example, the insertion of nucleic acid fragments corresponding to response elements and promoters into a suitable vector can be accomplished by ligating the appropriate nucleic acid fragments into a chosen vector that has complementary cohesive termini. Alternatively, the ends of the nucleic acid molecules may be enzymatically modified or any site may be produced by ligating nucleotide sequences (linkers) to the nucleic acid termini. Such vectors may be engineered to contain sequences encoding selectable markers that provide for the selection of cells that contain the vector and/or have incorporated the nucleic acid of the vector into the cellular genome. Such markers allow identification and/or selection of host cells that incorporate and express the proteins encoded by the marker. A "recombinant" vector refers to a viral or non-viral vector that comprises one or more heterologous nucleotide sequences (*i.e.*, transgenes). Vectors may be introduced into cells by any suitable method known in the art, including, but not limited to, transfection, electroporation, microinjection, transduction, cell fusion, DEAE dextran, calcium phosphate precipitation, lipofection (lysosome fusion), and use of a gene gun or nucleic acid vector transporter.

As used herein, the term "water optimization trait" refers to any trait that can be shown to influence the yield of a plant under different sets of growth conditions related to water availability.

As used herein, the term "yield reduction" (YD) refers to the degree to which yield is reduced in plants grown under stress conditions. YD is calculated as:

$$\frac{\text{yield under non-stress conditions} - \text{yield under stress conditions}}{\text{yield under non-stress conditions}} \times 100$$

The present invention provides nonnaturally occurring nucleic acids useful for enhancing abiotic stress tolerance (*e.g.*, drought stress tolerance, osmotic stress tolerance, salt stress tolerance and/or temperature stress tolerance) in a plant or plant part.

Nucleic acids of the present invention may comprise any nucleotide sequence(s) the expression of which increases the expression and/or activity of one or more COBL4 proteins and/or ERF62 proteins in a plant or plant part, thereby enhancing the abiotic stress tolerance of the plant or plant part.

Nucleic acids of the present invention may comprise, consist essentially of or consist of a nucleotide sequence that encodes one or more COBL4 proteins and/or one or more ERF62 proteins. For example, in some embodiments, the nucleic acid comprises, consists essentially of or consists of a nucleotide sequence that encodes one or more of SEQ ID NOs: 28–44 (*e.g.*, the nucleotide sequence of any one of SEQ ID NOs: 1–27. In some embodiments, each COBL4 protein encoded by the nucleotide sequence has an amino acid sequence that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 99.5% or more identical to the amino acid sequence of one or more of SEQ ID NOs: 1–13. In some embodiments, each ERF62 protein encoded by the nucleotide sequence has an amino acid sequence that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 99.5% or more identical to the amino acid sequence of one or more of SEQ ID NOs: 14–27.

Nucleic acids of the present invention may comprise, consist essentially of or consist of:

- (a) one or more of the nucleotide sequences set forth in SEQ ID NOs: 1–27;
- (b) one or more nucleotide sequences that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of the nucleotide sequences set forth in SEQ ID NOs: 1–27;

- (c) one or more nucleotide sequences that encodes a polypeptide comprising, consisting essentially of or consisting of the amino acid sequence set forth in any one of SEQ ID NOs: 28–44;
- (d) one or more nucleotide sequences that encodes a polypeptide comprising, consisting essentially of or consisting of an amino acid sequence that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of the amino acid sequences set forth in SEQ ID NOs: 28–44;
- (e) a nucleotide sequence that is complementary to any one of the nucleotide sequences described in (a) to (d) above;
- (f) a nucleotide sequence that hybridizes to any one of the nucleotide sequences described in (a) to (e) above under stringent hybridization conditions;
- (g) a functional fragment of any one of the nucleotide sequences described in (a) to (f) above, wherein the functional fragment encodes a polypeptide that comprises an N-terminal signal peptide sequence that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 1 to 27 of SEQ ID NO: 28 and a CCVS domain that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 226 to 229 of SEQ ID NO: 28; and/or
- (h) a functional fragment of any one of the nucleotide sequences described in (a) to (f) above, wherein the functional fragment encodes a polypeptide that comprises an AP2 domain that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 110 to 167 of SEQ ID NO: 36.

Nucleic acids of the present invention may comprise any suitable promoter sequence(s), including, but not limited to, constitutive promoters, tissue-specific promoters, stress-inducible promoters and developmental stage-specific promoters.

In some embodiments, the nucleic acid comprises one or more constitutive promoter sequences. For example, the nucleic acid may comprise one or more CaMV 19S, CaMV 35S, *Arabidopsis* At6669, maize H3 histone, rice actin, actin 2, rice cyclophilin, pEMU, GOS2, constitutive root tip CT2, and/or ubiquitin (e.g., maize *Ubi*) promoter sequences. Thus, in some embodiments, the nucleic acid comprises a nucleotide sequence encoding one or more COBL4

proteins and/or one or more ERF62 proteins operably linked to one or more constitutive promoter sequences.

In some embodiments, the nucleic acid comprises one or more tissue-specific promoter sequences. For example, the nucleic acid may comprise one or more leaf-, ligule-, node-,  
5 panicle-, root-, sheath-, stem-, and/or vascular bundle-specific promoter sequences. Thus, in some embodiments, the nucleic acid comprises a nucleotide sequence encoding one or more COBL4 proteins and/or one or more ERF62 proteins operably linked to one or more tissue-specific promoter sequences.

In some embodiments, the nucleic acid comprises one or more stress-inducible promoter  
10 sequences. For example, the nucleic acid may comprise one or more drought stress-inducible, salt stress-inducible, heat stress-inducible, light stress-inducible and/or osmotic stress-inducible promoter sequences. Thus, in some embodiments, the nucleic acid comprises a nucleotide sequence encoding one or more COBL4 proteins and/or one or more ERF62 proteins operably linked to one or more stress-inducible promoter sequences.

15 In some embodiments, the nucleic acid comprises one or more developmental stage-specific promoter sequences. For example, the nucleic acid may comprise a promoter sequence that drives expression prior to and/or during the seedling and/or reproductive stage(s) of development. Thus, in some embodiments, the nucleic acid comprises a nucleotide sequence encoding one or more COBL4 proteins and/or one or more ERF62 proteins operably linked to one or more  
20 developmental stage-specific promoter sequences.

In some embodiments, the nucleic acid comprises one or more termination sequences. For example, the nucleic acid may comprise a termination sequence comprising a stop signal for RNA polymerase and a polyadenylation signal for polyadenylase. Thus, in some embodiments, the nucleic acid comprises a nucleotide sequence encoding one or more COBL4 proteins and/or  
25 one or more ERF62 proteins operably linked to one or more termination sequences.

In some embodiments, the nucleic acid comprises codons specific for expression in plants.

In some embodiments, the nucleic acid is an isolated nucleotide.

Nucleic acids of the present invention may comprise any suitable transgene(s), including, but not limited to, transgenes that encode gene products that provide herbicide-resistance, pest-  
30 resistance and/or disease-resistance.

In some embodiments, the nucleic acid comprises one or more transgenes encoding a gene product that provides resistance to one or more herbicides. For example, the nucleic acid may comprise a transgene that encodes a gene product that provides glyphosate-, Sulfonylurea-, imidazolinione-, dicamba-, glufisinate-, phenoxy propionic acid-, cyclohexime-, triazine-,  
35 benzonitrile-, and/or broxynil-resistance.

In some embodiments, the nucleic acid comprises one or more transgenes encoding a gene product that provides resistance to one or more pests. For example, the nucleic acid may comprise a transgene that encodes a gene product that provides bacterial-, fungal, gastropod-, insect-, nematode-, oomycete-, phytoplasma-, protozoa-, and/or viral-resistance.

5 In some embodiments, the nucleic acid comprises one or more transgenes encoding a gene product that provides resistance to one or more diseases.

Nucleic acids of the present invention may encode any suitable epitope tag, including, but not limited to, poly-Arg tags (*e.g.*, RRRRR and RRRRRR) and poly-His tags (*e.g.*, HHHHHH). In some embodiments, the nucleic acid comprises a nucleotide sequence encoding a poly-Arg tag, a poly-His tag, a FLAG tag (*i.e.*, DYKDDDDK), a Strep-tag II™ (GE Healthcare, Pittsburgh, PA, USA) (*i.e.*, WSH PQFEK), and/or a c-myc tag (*i.e.*, EQKLISEEDL).

Nucleic acids of the present invention may comprise any suitable number of nucleotides. In some embodiments, the nucleic acid is 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400, 1450, 1500, 1550, 1600, 1650, 1700, 1750, 1800, 1850, 1900, 1950, 2000 or more nucleotides in length. In some embodiments, the nucleic acid is less than about 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400, 1450, 1500, 1550, 1600, 1650, 1700, 1750, 1800, 1850, 1900, 1950 or 2000 nucleotides in length. In some embodiments, the nucleic acid is about 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400, 1450, 1500, 1550, 1600, 1650, 1700, 1750, 1800, 1850, 1900, 1950 or 2000 nucleotides in length.

In some embodiments, the expression and/or activity of one or more COBL4 proteins and/or one or more ERF62 proteins in a plant or plant part expressing a nucleic acid of the present invention is increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300% or more as compared to a control plant (*e.g.*, a native plant of the same species) grown under the same (or substantially the same) environmental conditions. For example, the expression and/or activity of OsCOBL4 may be increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300% or more in a rice plant expressing a nucleic acid comprising any one of SEQ ID NOs: 1–13. Similarly, the expression and/or activity of OsERF62 may be

increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300% or more in a rice plant expressing a nucleic acid comprising any one of SEQ ID NOs: 14–27.

In some embodiments, the abiotic stress tolerance (*e.g.*, drought stress tolerance, osmotic stress tolerance, salt stress tolerance and/or temperature stress tolerance) of a plant or plant part expressing a nucleic acid of the present invention is increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300% or more as compared to a control plant or plant part (*e.g.*, a native plant of the same species) grown under the same (or substantially the same) environmental conditions. For example, the drought stress tolerance of a plant or plant part expressing any one of SEQ ID NOs: 1–27 may be increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300% or more as compared to a control plant or plant part grown under the same (or substantially the same) drought stress conditions.

Plants and plant parts expressing nucleic acids of the present invention may exhibit a variety of abiotic stress tolerant phenotypes, including, but not limited to, decreased water loss, decreased accumulation of one or more reactive oxygen species, decreased accumulation of one or more salts, increased salt excretion, increased accumulation of one or more dehydrins, improved root architecture, improved osmotic pressure regulation, increased accumulation of one or more late embryogenesis abundant proteins, increased survival rate, increased growth rate, increased height, increased chlorophyll content and/or increased yield (*e.g.*, increased biomass, increased seed yield, increased grain yield at standard moisture percentage (YGSMN), increased grain moisture at harvest (GMSTP), increased grain weight per plot (GWTPN), increased percent yield recovery (PYREC), decreased yield reduction (YRED), and/or decreased percent barren (PB)) when grown under abiotic stress conditions (*e.g.*, drought stress conditions, osmotic stress conditions, salt stress conditions and/or temperature stress conditions). In some embodiments, one or more abiotic stress tolerant phenotypes is increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300%, or more as compared to a control plant or plant part (*e.g.*, a native plant of the same species) when each is grown under the same (or substantially the same) environmental conditions.

In some embodiments, the yield (*e.g.*, seed yield, biomass, GWTPN, PYREC and/or YGSMN) of a plant or plant part expressing a nucleic acid of the present invention is increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300% or more as compared to

a control plant or plant part (*e.g.*, a native plant of the same species) grown under the same (or substantially the same) environmental conditions. For example, the seed yield and/or biomass of a plant or plant part expressing any one of SEQ ID NOs: 1–27 may be increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300% or more as compared to a control plant or plant part grown under the same (or substantially the same) drought stress conditions.

In some embodiments, the accumulation of dehydrins and/or late embryogenesis abundant proteins, survival rate, growth potential, height, chlorophyll content and/or GMSTP of a plant or plant part expressing a nucleic acid of the present invention is increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300% or more as compared to a control plant or plant part (*e.g.*, a native plant of the same species) grown under the same (or substantially the same) environmental conditions. For example, the survival rate and/or chlorophyll content of a plant or plant part expressing any one of SEQ ID NOs: 1–27 may be increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300% or more as compared to a control plant or plant part grown under the same (or substantially the same) drought stress conditions.

In some embodiments, the water loss, accumulation of reactive oxygen species, accumulation of salts, YRED, and/or PB of a plant or plant part expressing a nucleic acid of the present invention is decreased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more as compared to a control plant or plant part (*e.g.*, a native plant of the same species) grown under the same (or substantially the same) environmental conditions. For example, the YRED and/or PB of a plant expressing any one of SEQ ID NOs: 1–27 may be decreased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more as compared to a control plant grown under the same (or substantially the same) drought stress conditions.

In some embodiments, the root architecture and/or osmotic pressure regulation of a plant or plant part expressing a nucleic acid of the present invention is improved as compared to a control plant or plant part (*e.g.*, a native plant of the same species) grown under the same (or substantially the same) environmental conditions. For example, the root architecture and/or osmotic pressure regulation of a plant or plant part expressing any one of SEQ ID NOs: 1–27 may be improved as compared to a control plant or plant part grown under the same (or substantially the same) drought stress conditions.

The present invention also provides expression cassettes comprising one or more nucleic acids of the present invention. In some embodiments, the expression cassette comprises a nucleic acid encoding a nucleic acid that confers at least one property (*e.g.*, resistance to a selection agent) that can be used to detect, identify or select transformed plant cells and tissues.

5 The present invention also provides vectors comprising one or more nucleic acids and/or expression cassettes of the present invention. In some embodiments, the vector is a pROKI, pBin438, pCAMBIA (*e.g.*, pCAMBIA1302, pCAMBIA2301, pCAMBIA1301, pCAMBIA1391-Xa, pCAMBIA1391-Xb) (CAMBIA Co., Brisbane, Australia) or pBI121 vector.

10 The present invention also provides recombinant viruses and recombinant bacteria comprising one or more nucleic acids, expression cassettes and/or vectors of the present invention.

The present invention also provides nonnaturally occurring proteins useful for enhancing abiotic stress tolerance (*e.g.*, drought stress tolerance, osmotic stress tolerance, salt stress tolerance and/or temperature stress tolerance) in a plant or plant part.

15 Proteins of the present invention may comprise any amino acid sequence the expression of which enhances the abiotic stress tolerance of a plant or plant part. In some embodiments, the protein comprises, consists essentially of or consists of an amino acid sequence that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% 99.5% or more identical to the amino acid sequence of one or more of SEQ ID NOs: 28–44. In some  
20 embodiments, the protein comprises a functional fragment of a COBL4 protein (*e.g.*, a functional fragment of any one of SEQ ID NOs: 28–35) and, optionally, comprises an N-terminal signal peptide sequence that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids XXX to YYY of SEQ ID NO: 28–35 and/or a C CVS domain that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%,  
25 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids XXX to YYY of SEQ ID NO: 28–35. In some embodiments, the protein comprises a functional fragment of a ERF62 protein (*e.g.*, a functional fragment of any one of SEQ ID NOs: 36–44) and, optionally, comprises an AP2 domain that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 110 to 167 of SEQ ID  
30 NO: 36–44

In some embodiments, the protein is an isolated protein.

Proteins of the present invention may comprise any suitable epitope tag, including, but not limited to, poly-Arg tags (*e.g.*, RRRRR and RRRRRR) and poly-His tags (*e.g.*, HHHHHH). In some embodiments, the nucleic acid comprises a nucleotide sequence encoding a poly-Arg tag, a

poly-His tag, a FLAG tag (*i.e.*, DYKDDDDK), a Strep-tag II™ (GE Healthcare, Pittsburgh, PA, USA) (*i.e.*, WSHPOFEK), and/or a c-myc tag (*i.e.*, EQKLISEEDL).

Proteins of the present invention may comprise any suitable number of amino acids. In some embodiments, the proteins is 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 450, 500 or more amino acids in length. In some embodiments, the protein is less than about 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 450 or 500 amino acids in length. In some embodiments, the protein is about 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 450 or 500 amino acids in length.

In some embodiments, the expression and/or activity of one or more COBL4 proteins and/or one or more ERF62 proteins in a plant or plant part expressing a protein of the present invention is increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300% or more as compared to a control plant (*e.g.*, a native plant of the same species) grown under the same (or substantially the same) environmental conditions. For example, the expression and/or activity of OsCOBL4 may be increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300% or more in a rice plant expressing a nucleic acid encoding any one of SEQ ID NOs: 28–35. Similarly, the expression and/or activity of OsEF62 may be increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300% or more in a rice plant expressing a nucleic acid encoding any one of SEQ ID NOs: 36–44.

In some embodiments, the abiotic stress tolerance (*e.g.*, drought stress tolerance, osmotic stress tolerance, salt stress tolerance and/or temperature stress tolerance) of a plant expressing a protein of the present invention is increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300% or more as compared to a control plant (*e.g.*, a native plant of the same species) grown under the same (or substantially the same) environmental conditions. For example, the drought stress tolerance of a plant or plant part expressing any one of SEQ ID NOs: 28–44 may be increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300% or more as compared to a control plant grown under the same (or substantially the same) drought stress conditions.

Plants and plant parts expressing proteins of the present invention may exhibit a variety of abiotic stress tolerant phenotypes, including, but not limited to, decreased water loss, decreased accumulation of one or more reactive oxygen species, decreased accumulation of one or more salts, increased salt excretion, increased accumulation of one or more dehydrins, improved root architecture, improved osmotic pressure regulation, increased accumulation of one or more late embryogenesis abundant proteins, increased survival rate, increased growth rate, increased height, increased chlorophyll content and/or increased yield (*e.g.*, increased biomass, increased seed yield, increased grain yield at standard moisture percentage (YGSMN), increased grain moisture at harvest (GMSTP), increased grain weight per plot (GWTPN), increased percent yield recovery (PYREC), decreased yield reduction (YRED), and/or decreased percent barren (PB)) when grown under abiotic stress conditions (*e.g.*, drought stress conditions, osmotic stress conditions, salt stress conditions and/or temperature stress conditions). In some embodiments, one or more abiotic stress tolerant phenotypes is increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300%, or more as compared to a control plant or plant part (*e.g.*, a native plant of the same species) when each is grown under the same (or substantially the same) environmental conditions.

In some embodiments, the yield (*e.g.*, seed yield, biomass, GWTPN, PYREC and/or YGSMN) of a plant or plant part expressing a protein of the present invention is increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300% or more as compared to a control plant or plant part (*e.g.*, a native plant of the same species) grown under the same (or substantially the same) environmental conditions. For example, the seed yield and/or biomass of a plant or plant part expressing any one of SEQ ID NOs: 28–44 may be increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300% or more as compared to a control plant or plant part grown under the same (or substantially the same) drought stress conditions.

In some embodiments, the accumulation of dehydrins and/or late embryogenesis abundant proteins, survival rate, growth potential, height, chlorophyll content and/or GMSTP of a plant or plant part expressing a protein of the present invention is increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300% or more as compared to a control plant or plant part (*e.g.*, a native plant of the same species) grown under the same (or substantially the same) environmental conditions. For example, the survival rate and/or chlorophyll content of a plant or plant part expressing any one of SEQ ID NOs: 28–44 may be increased by at least about 5%,

10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300% or more as compared to a control plant or plant part grown under the same (or substantially the same) drought stress conditions.

In some embodiments, the water loss, accumulation of reactive oxygen species, YRED,  
5 and/or PB of a plant or plant part expressing a protein of the present invention is decreased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more as compared to a control plant or plant part (*e.g.*, a native plant of the same species) grown under the same (or substantially the same) environmental conditions. For example, the YRED and/or PB of a plant expressing any one of  
10 SEQ ID NOs: 28-44 may be decreased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more as compared to a control plant grown under the same (or substantially the same) drought stress conditions.

In some embodiments, the root architecture and/or osmotic pressure regulation of a plant or  
15 plant part expressing a protein of the present invention is improved as compared to a control plant (*e.g.*, a native plant of the same species) grown under the same (or substantially the same) environmental conditions. For example, the root architecture and/or osmotic pressure regulation of a plant or plant part expressing any one of SEQ ID NOs: 28-44 may be improved as compared to a control plant or plant part grown under the same (or substantially the same)  
20 drought stress conditions.

The present invention extends to uses of nucleic acids, expression cassettes, vectors, recombinant viruses, recombinant bacteria and proteins of the present invention, including, but not limited to, uses for enhancing abiotic stress tolerance (*e.g.*, drought stress tolerance, osmotic stress tolerance, salt stress tolerance and/or temperature stress tolerance) in a plant or plant part  
25 and uses for identifying, selecting and/or producing abiotic stress tolerant plants (*e.g.*, drought stress tolerant, osmotic stress tolerant, salt stress tolerant and/or temperature stress tolerant plants and plant parts).

The present invention also provides nonnaturally occurring plants and plant parts having enhanced abiotic stress tolerance.

30 Plants and plant parts of the present invention may comprise any suitable exogenous nucleic acid(s). In some embodiments, the plant or plant part comprises at least one exogenous nucleic acid that encodes one or more proteins of the present invention and/or comprises, consists essentially of or consists of one or more nucleic acids of the present invention.

In some embodiments, the plant or plant part comprises within its genome an exogenous  
35 nucleic acid that comprises, consists essentially of or consists of:

- (a) one or more of the nucleotide sequences set forth in SEQ ID NOs: 1–27;
- (b) one or more nucleotide sequences that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of the nucleotide sequences set forth in SEQ ID NOs: 1–27;
- (c) one or more nucleotide sequences that encodes a polypeptide comprising, consisting essentially of or consisting of the amino acid sequence set forth in any one of SEQ ID NOs: 28–44;
- (d) one or more nucleotide sequences that encodes a polypeptide comprising, consisting essentially of or consisting of an amino acid sequence that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of the amino acid sequences set forth in SEQ ID NOs: 28–44;
- (e) a nucleotide sequence that is complementary to any one of the nucleotide sequences described in (a) to (d) above;
- (f) a nucleotide sequence that hybridizes to any one of the nucleotide sequences described in (a) to (e) above under stringent hybridization conditions;
- (g) a functional fragment of any one of the nucleotide sequences described in (a) to (f) above, wherein the functional fragment encodes a polypeptide that comprises an N-terminal signal peptide sequence that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 1 to 27 of SEQ ID NO: 28 and a CCVS domain that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 226 to 229 of SEQ ID NO: 28; and/or
- (h) a functional fragment of any one of the nucleotide sequences described in (a) to (f) above, wherein the functional fragment encodes a polypeptide that comprises an AP2 domain that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 110 to 167 of SEQ ID NO: 36.

In some embodiments, the plant or plant part comprises an exogenous nucleic acid comprising one or more constitutive promoter sequences. For example, the plant or plant part may comprise an exogenous nucleic acid that comprises one or more CaMV 19S, CaMV 35S, *Arabidopsis* At6669, maize H3 histone, rice actin, actin 2, rice cyclophilin, pEMU, GOS2,

constitutive root tip CT2, and/or ubiquitin (*e.g.*, maize *Ubi*) promoter sequences. Thus, in some embodiments, the plant or plant part comprises an exogenous nucleic acid that comprises one or more of the nucleotide sequences described in (a) to (tt) above operably linked to one or more constitutive promoter sequences.

5 In some embodiments, the plant or plant part comprises an exogenous nucleic acid comprising one or more tissue-specific promoter sequences. For example, the plant or plant part may comprise an exogenous nucleic acid that comprises one or more leaf-, ligule-, node-, panicle-, root-, sheath-, stem-, and/or vascular bundle-specific promoter sequences. Thus, in some embodiments, the plant or plant part comprises an exogenous nucleic acid that comprises  
10 one or more of the nucleotide sequences described in (a) to (tt) above operably linked to one or more tissue-specific promoter sequences.

In some embodiments, the plant or plant part comprises an exogenous nucleic acid comprising one or more stress-inducible promoter sequences. For example, the plant or plant part may comprise an exogenous nucleic acid that comprises one or more drought stress-inducible,  
15 osmotic stress-inducible, salt-inducible, temperature stress-inducible, and/or light stress-inducible promoter sequences. Thus, in some embodiments, the plant or plant part comprises an exogenous nucleic acid that comprises one or more of the nucleotide sequences described in (a) to (tt) above operably linked to one or more stress-inducible promoter sequences.

In some embodiments, the plant or plant part comprises an exogenous nucleic acid  
20 comprising one or more developmental stage-specific promoter sequences. For example, the plant or plant part may comprise an exogenous nucleic acid that comprises a promoter sequence that drives expression prior to and/or during the seedling and/or reproductive stage(s) of development. Thus, in some embodiments, the nucleic acid comprises one or more of the nucleotide sequences described in (a) to (tt) above operably linked to one or more developmental  
25 stage-specific promoter sequences. In some embodiments, the plant or plant part comprises an exogenous nucleic acid comprising one or more termination sequences. For example, the plant or plant part may comprise an exogenous nucleic acid that comprises a termination sequence comprising a stop signal for RNA polymerase and a polyadenylation signal for polyadenylase. Thus, in some embodiments, the plant or plant part comprises an exogenous nucleic acid that  
30 comprises one or more of the nucleotide sequences describes in (a) to (tt) above operably linked to one or more termination sequences.

In some embodiments, plants and plant parts of the present invention exhibit increased expression and/or activity of one or more COBL4 proteins (*e.g.*, increased microfibril orientating activity), increased expression and/or activity of one or more ERF62 proteins (*e.g.*, increased  
35 DNA binding activity).

In some embodiments, the plant or plant part expresses one or more COBL4 proteins (*e.g.*, a COBL4 protein having an amino acid sequence that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the amino acid sequence of one or more of SEQ ID NOs: 1–13) at an increased level as compared to a control plant or plant part (*e.g.*, a native plant of the same species) when each is grown under the same (or substantially the same) environmental conditions. In some such embodiments, expression of the COBL4 protein(s) is increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300%, or more as compared to the control plant.

In some embodiments, the plant or plant part expresses one or more ERF62 proteins (*e.g.*, an ERF62 protein having an amino acid sequence that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the amino acid sequence of one or more of SEQ ID NOs: 14–27) at an increased level as compared to a control plant or plant part (*e.g.*, a native plant of the same species) when each is grown under the same (or substantially the same) environmental conditions. In some such embodiments, expression of the ERF62 protein(s) is increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300%, or more as compared to the control plant.

Plants and plant parts of the present invention may exhibit a variety of abiotic stress tolerant phenotypes, including, but not limited to, decreased water loss, decreased accumulation of one or more reactive oxygen species, decreased accumulation of one or more salts, increased salt excretion, increased accumulation of one or more dehydrins, improved root architecture, improved osmotic pressure regulation, increased accumulation of one or more late embryogenesis abundant proteins, increased survival rate, increased growth rate, increased height, increased chlorophyll content and/or increased yield (*e.g.*, increased biomass, increased seed yield, increased grain yield at standard moisture percentage (YGSMN), increased grain moisture at harvest (GMSTP), increased grain weight per plot (GWTPN), increased percent yield recovery (PYREC), decreased yield reduction (YRED), and/or decreased percent barren (PB)) when grown under abiotic stress conditions (*e.g.*, drought stress conditions, osmotic stress conditions, salt stress conditions and/or temperature stress conditions). In some embodiments, one or more abiotic stress tolerant phenotypes is increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300%, or more as compared to a control plant or plant part (*e.g.*, a native plant of the same species) when each is grown under the same (or substantially the same) environmental conditions.

In some embodiments, the yield (*e.g.*, seed yield, biomass, GWTPN, PYREC and/or YGSMN) of the plant or plant part is increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300% or more as compared to a control plant or plant part (*e.g.*, a native plant of the same species) grown under the same (or substantially the same) environmental conditions. For example, the seed yield and/or biomass of the plant or plant part may be increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300% or more as compared to a control plant or plant part grown under the same (or substantially the same) drought stress conditions.

In some embodiments, the accumulation of dehydrins and/or late embryogenesis abundant proteins, survival rate, growth potential, height, chlorophyll content and/or GMSTP of the plant or plant part is increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300% or more as compared to a control plant or plant part (*e.g.*, a native plant of the same species) grown under the same (or substantially the same) environmental conditions. For example, the survival rate and/or chlorophyll content of the plant or plant part may be increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300% or more as compared to a control plant or plant part grown under the same (or substantially the same) drought stress conditions.

In some embodiments, the water loss, accumulation of reactive oxygen species, YRED, and/or PB of the plant or plant part is decreased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more as compared to a control plant or plant part (*e.g.*, a native plant of the same species) grown under the same (or substantially the same) environmental conditions. For example, the YRED and/or PB of the plant may be decreased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more as compared to a control plant grown under the same (or substantially the same) drought stress conditions.

In some embodiments, the root architecture and/or osmotic pressure regulation of the plant or plant part is improved as compared to a control plant (*e.g.*, a native plant of the same species) grown under the same (or substantially the same) environmental conditions. For example, the root architecture and/or osmotic pressure regulation of the plant or plant part may be improved as compared to a control plant or plant part grown under the same (or substantially the same) drought stress conditions.

Plants and plant parts of the present invention may be of any suitable plant type, including, but not limited to, plants belonging to the superfamily Viridiplantae. In some embodiments the plant or plant part is a fodder crop, a food crop, an ornamental plant, a tree or a shrub. For example, in some embodiments, the plant or plant part is a variety of *Acer* spp., *Actinidia* spp.,

5 *Abelmoschus* spp., *Agropyron* spp., *Allium* spp., *Amaranthus* spp., *Ananas comosus*, *Annona* spp., *Apium graveolens*, *Arachis* spp., *Artocarpus* spp., *Asparagus officinalis*, *Avena* spp. (e.g. *Avena sativa*, *Avena fatua*, *Avena byzantina*, *Avena fatua* var. *sativa*, *Avena hybrida* ), *Averrhoa carambola*, *Benincasa hispida*, *Bertholletia excelsea*, *Beta vulgaris*, *Brassica* spp. (e.g. *Brassica napus*, *Brassica rapa* ssp. [canola, oilseed rape, turnip rape]), *Cadaba farinosa*, *Camellia*

10 *sinensis*, *Canna indica*, *Capsicum* spp., *Carex elata*, *Carica papaya*, *Carissa macrocarpa*, *Carya* spp., *Carthamus tinctorius*, *Castanea* spp., *Cichorium endivia*, *Cinnamomum* spp., *Citrullus lanatus*, *Citrus* spp., *Cocos* spp., *Coffea* spp., *Colocasia esculenta*, *Cola* spp., *Coriandrum sativum*, *Corylus* spp., *Crataegus* spp., *Crocus sativus*, *Cucurbita* spp., *Cucumis* spp., *Cynara* spp., *Daucus carota*, *Desmodium* spp., *Dimocarpus longan*, *Dioscorea* spp., *Diospyros* spp.,

15 *Echinochloa* spp., *Elaeis* (e.g. *Elaeis guineensis*, *Elaeis oleifera* ), *Eleusine coracana*, *Eriobotrya japonica*, *Eugenia uniflora*, *Fagopyrum* spp., *Fagus* spp., *Ficus carica*, *Fortunella* spp., *Fragaria* spp., *Ginkgo biloba*, *Glycine* spp. (e.g. *Glycine max*, *Soja hispida* or *Soja max* ), *Gossypium hirsutum*, *Helianthus* spp. (e.g. *Helianthus annuus* ), *Hemerocallis fulva*, *Hibiscus* spp., *Hordeum* spp. (e.g. *Hordeum vulgare* ), *Ipomoea batatas*, *Juglans* spp., *Lactuca sativa*,

20 *Lathyrus* spp., *Lens culinaris*, *Linum usitatissimum*, *Litchi chinensis*, *Lotus* spp., *Luffa acutangula*, *Lupinus* spp., *Luzula sylvatica*, *Lycopersicon* spp. (e.g. *Lycopersicon esculentum*, *Lycopersicon lycopersicum*, *Lycopersicon pyriforme* ), *Macrotyloma* spp., *Malus* spp., *Malpighia emarginata*, *Mammea americana*, *Mangifera indica*, *Manihot* spp., *Manilkara zapota*, *Medicago sativa*, *Melilotus* spp., *Mentha* spp., *Miscanthus* spp., *Momordica* spp., *Morus nigra*, *Musa* spp.,

25 *Nicotiana* spp., *Olea* spp., *Opuntia* spp., *Ornithopus* spp., *Oryza* spp. (e.g. *Oryza sativa*, *Oryza latifolia*), *Panicum miliaceum*, *Passiflora edulis*, *Pastinaca sativa*, *Persea* spp., *Petroselinum crispum*, *Phaseolus* spp., *Phoenix* spp., *Physalis* spp., *Pinus* spp., *Pistacia vera*, *Pisum* spp., *Poa* spp., *Populus* spp., *Prosopis* spp., *Prunus* spp., *Psidium* spp., *Punica granatum*, *Pyrus communis*, *Quercus* spp., *Raphanus sativus*, *Rheum rhabarbarum*, *Ribes* spp., *Ricinus communis*, *Rubus*

30 spp., *Saccharum* spp., *Sambucus* spp., *Secale cereale*, *Sesamum* spp., *Sinapis* sp., *Solanum* spp. (e.g. *Solanum tuberosum*, *Solanum integrifolium* or *Solanum lycopersicum* ), *Sorghum bicolor*, *Spinacia* spp., *Syzygium* spp., *Tagetes* spp., *Tamarindus indica*, *Theobroma cacao*, *Trifolium* spp., *Triticosecale rimpaui*, *Triticum* spp. (e.g. *Triticum aestivum*, *Triticum durum*, *Triticum turgidum*, *Triticum hybernum*, *Triticum macha*, *Triticum sativum* or *Triticum vulgare* ),

35 *Tropaeolum minus*, *Tropaeolum majus*, *Vaccinium* spp., *Vicia* spp., *Vigna* spp., *Viola odorata*,

*Vitis* spp., *Zea mays*, *Zizania palustris* or *Ziziphus* spp., amongst others. In some embodiments, the plant or plant part is a rice, maize, wheat, barley, sorghum, millet, oat, triticale, rye, buckwheat, fonio, quinoa, sugar cane, bamboo, banana, ginger, onion, lily, daffodil, iris, amaryllis, orchid, canna, bluebell, tulip, garlic, secale, einkorn, spelt, emmer, durum, kamut, grass (*e.g.*, gramma grass), teff, milo, flax, *Tripsacum* sp., or teosinte plant or plant part. In some  
 5 embodiments, the plant or plant part is a blackberry, raspberry, strawberry, barberry, bearberry, blueberry, coffee berry, cranberry, crowberry, currant, elderberry, gooseberry, goji berry, honeyberry, lemon, lime, lingonberry, mangosteen, orange, pepper, persimmon, pomegranate, prune, cotton, clover, acai, plum, peach, nectarin, cherry, guava, almond, pecan, walnut, apple,  
 10 amaranth, sweet pea, pear, potato, soybean, sugar beet, sunflower, sweet potato, tamarind, tea, tobacco or tomato plant or plant part.

Plants and plant parts of the present invention may be produced using any suitable method, including, but not limited to, methods of the present invention.

The present invention extends to products harvested from plants and plant parts of the  
 15 present invention, including, but not limited to, plant cells and harvestable plant parts such as seeds, leaves, fruits, flowers, stems, rhizomes, tubers and bulbs. In some embodiments, the harvested product is a plant cell (*e.g.*, a embryo or ovule) or plant part capable of producing a plant or plant part having increased expression and/or activity of one or more COBL4 proteins, increased expression and/or activity of one or more ERF62 proteins, and/or enhanced abiotic  
 20 stress tolerance (*e.g.*, enhanced drought tolerance, enhanced osmotic stress tolerance, enhanced salt stress tolerance and/or enhanced temperature stress tolerance). In some embodiments, the harvested product is a plant cell (*e.g.*, a embryo or ovule) or plant part capable of producing a plant or plant that exhibits decreased water loss, decreased accumulation of one or more reactive oxygen species, decreased accumulation of one or more salts, increased salt excretion, increased  
 25 accumulation of one or more dehydrins, improved root architecture, improved osmotic pressure regulation, increased accumulation of one or more late embryogenesis abundant proteins, increased survival rate, increased growth rate, increased height, increased chlorophyll content and/or increased yield (*e.g.*, increased biomass, increased seed yield, increased grain yield at standard moisture percentage (YGSMN), increased grain moisture at harvest (GMSTP),  
 30 increased grain weight per plot (GWTPN), increased percent yield recovery (PYREC), decreased yield reduction (YRED), and/or decreased percent barren (PB)) when grown under abiotic stress conditions (*e.g.*, drought stress conditions, osmotic stress conditions, salt stress conditions and/or temperature stress conditions).

The present invention also extends to products derived from harvestable plant parts,  
 35 including, but not limited to, dry pellets and powders, oils, fats, fatty acids, starches and proteins.

The present invention also provides methods of enhancing abiotic stress tolerance (*e.g.*, drought stress tolerance, osmotic stress tolerance, salt stress tolerance and/or temperature stress tolerance) in a plant or plant part.

Abiotic stress tolerance (*e.g.*, drought stress tolerance, osmotic stress tolerance, salt stress tolerance and/or temperature stress tolerance) may be enhanced by increasing the expression and/or activity of one or more COBL4 proteins and/or by increasing the expression and/or activity of one or more ERF62 proteins. Thus, methods of enhancing abiotic stress tolerance in a plant or plant part may comprise, consist essentially of or consist of increasing the expression and/or activity of one or more COBL4 proteins and/or one or more ERF62 proteins in the plant or plant part.

The expression and/or activity of COBL4 proteins may be increased via any suitable method, including, but not limited to, overexpression of native COBL4 proteins, expression of exogenous COBL4 proteins, overexpression of one or more COBL4 precursors, down-regulation and/or inhibition of one or more COBL4 inhibitors, overexpression of one or more native enzymes involved in COBL4 synthesis and expression of one or more exogenous enzymes involved in COBL4 synthesis. In some embodiments, the expression and/or activity of one or more COBL4 proteins is increased by:

- (a) increasing the expression and/or activity of one or more native COBL4 proteins in the plant or plant part; and/or
- (b) increasing the expression and/or activity of one or more exogenous COBL4 proteins in the plant or plant part;
- (c) increasing the expression and/or activity of one or more COBL4 protein precursors in the plant or plant part;
- (d) decreasing the expression and/or activity of one or more COBL4 protein inhibitors in the plant or plant part;
- (e) increasing the expression and/or activity of one or more native enzymes involved in COBL4 protein synthesis in the plant or plant part; and/or
- (f) increasing the expression and/or activity of one or more exogenous enzymes involved in COBL4 protein synthesis in the plant or plant part.

In some embodiments of the present invention, the expression of one or more COBL4 proteins is increased by introducing an exogenous nucleic acid encoding the COBL4 protein(s) into the plant or plant part. For example, in some embodiments, an exogenous nucleic acid encoding one or more of SEQ ID NOs: 27–35 (*e.g.*, an exogenous nucleic acid comprising one or

more of SEQ ID NOs: 1–13) is introduced into the plant or plant part, thereby increasing expression of the COBL4 protein(s).

The expression and/or activity of ERF62 proteins may be increased via any suitable method, including, but not limited to, overexpression of native ERF62 proteins, expression of exogenous  
5 ERF62 proteins, overexpression of one or more ERF62 precursors, down-regulation and/or inhibition of one or more ERF62 inhibitors, overexpression of one or more native enzymes involved in ERF62 synthesis and expression of one or more exogenous enzymes involved in ERF62 synthesis. In some embodiments, the expression and/or activity of one or more ERF62 proteins is/are increased by:

- 10 (a) increasing the expression and/or activity of one or more native ERF62 proteins in the plant or plant part; and/or
- (b) increasing the expression and/or activity of one or more exogenous ERF62 proteins in the plant or plant part;
- (c) increasing the expression and/or activity of one or more ERF62 protein precursors  
15 in the plant or plant part;
- (d) decreasing the expression and/or activity of one or more ERF62 protein inhibitors in the plant or plant part;
- (e) increasing the expression and/or activity of one or more native enzymes involved in ERF62 protein synthesis in the plant or plant part; and/or
- 20 (f) increasing the expression and/or activity of one or more exogenous enzymes involved in ERF62 protein synthesis in the plant or plant part.

In some embodiments of the present invention, the expression of one or more ERF62 proteins is increased by introducing an exogenous nucleic acid encoding the ERF62 protein(s)  
25 into the plant or plant part. For example, in some embodiments, an exogenous nucleic acid encoding one or more of SEQ ID NOs: 36–44 (e.g., an exogenous nucleic acid comprising one or more of SEQ ID NOs: 14–27) is introduced into the plant or plant part, thereby increasing expression of the ERF62 protein(s).

Thus, in some embodiments, abiotic stress tolerance (e.g., drought stress tolerance, osmotic  
30 stress tolerance, salt stress tolerance and/or temperature stress tolerance) may be enhanced by introducing/expressing an exogenous nucleic acid comprising:

- (a) one or more of the nucleotide sequences set forth in SEQ ID NOs: 1–27;
- (b) one or more nucleotide sequences that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more

identical to one or more of the nucleotide sequences set forth in SEQ ID NOs: 1–27;

(c) one or more nucleotide sequences that encodes a polypeptide comprising, consisting essentially of or consisting of the amino acid sequence set forth in any one of SEQ ID NOs: 28–44;

(d) one or more nucleotide sequences that encodes a polypeptide comprising, consisting essentially of or consisting of an amino acid sequence that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of the amino acid sequences set forth in SEQ ID NOs: 28–44;

(e) a nucleotide sequence that is complementary to any one of the nucleotide sequences described in (a) to (d) above;

(f) a nucleotide sequence that hybridizes to any one of the nucleotide sequences described in (a) to (e) above under stringent hybridization conditions;

(g) a functional fragment of any one of the nucleotide sequences described in (a) to (f) above, wherein the functional fragment encodes a polypeptide that comprises an N-terminal signal peptide sequence that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 1 to 27 of SEQ ID NO: 28 and a CCVS domain that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 226 to 229 of SEQ ID NO: 28; and/or

(h) a functional fragment of any one of the nucleotide sequences described in (a) to (f) above, wherein the functional fragment encodes a polypeptide that comprises an AP2 domain that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 110 to 167 of SEQ ID NO: 36.

The present invention also provides methods of identifying, selecting and/or producing a plant or plant part having enhanced abiotic stress tolerance (*e.g.*, enhanced drought tolerance, enhanced osmotic stress tolerance, enhanced salt stress tolerance and/or enhanced temperature stress tolerance).

Methods of identifying plants and plant parts having enhanced abiotic stress tolerance may comprise, consist essentially of or consist of detecting, in the plant or plant part, a nucleic acid (*e.g.*, an exogenous nucleic acid) comprising:

- (a) one or more of the nucleotide sequences set forth in SEQ ID NOs: 1–27;
- (b) one or more nucleotide sequences that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of the nucleotide sequences set forth in SEQ ID NOs: 1–27;
- (c) one or more nucleotide sequences that encodes a polypeptide comprising, consisting essentially of or consisting of the amino acid sequence set forth in any one of SEQ ID NOs: 28–44;
- (d) one or more nucleotide sequences that encodes a polypeptide comprising, consisting essentially of or consisting of an amino acid sequence that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of the amino acid sequences set forth in SEQ ID NOs: 28–44;
- (e) a nucleotide sequence that is complementary to any one of the nucleotide sequences described in (a) to (d) above;
- (f) a nucleotide sequence that hybridizes to any one of the nucleotide sequences described in (a) to (e) above under stringent hybridization conditions;
- (g) a functional fragment of any one of the nucleotide sequences described in (a) to (f) above, wherein the functional fragment encodes a polypeptide that comprises an N-terminal signal peptide sequence that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 1 to 27 of SEQ ID NO: 28 and a CCVS domain that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 226 to 229 of SEQ ID NO: 28; and/or
- (h) a functional fragment of any one of the nucleotide sequences described in (a) to (f) above, wherein the functional fragment encodes a polypeptide that comprises an AP2 domain that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 110 to 167 of SEQ ID NO: 36.

Methods of producing plants and plant parts having enhanced abiotic stress tolerance may comprise, consist essentially of or consist of:

- (a) detecting, in a plant part, the presence of a nucleic acid (*e.g.*, an exogenous nucleic acid) encoding one or more COBL4 proteins and/or one or more ERF62

proteins (*e.g.*, a nucleic acid comprising a nucleotide sequence that is at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the nucleotide sequence set forth in any one of SEQ ID NOs: 1–27), and producing a plant from the plant part;

- 5 (b) introducing, into a plant part, an exogenous nucleic acid encoding one or more COBL4 proteins and/or one or more ERF62 proteins (*e.g.*, an exogenous nucleic acid comprising a nucleotide sequence that is at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the nucleotide sequence set forth in any one of SEQ ID NOs: 1–27), and growing  
10 the plant part into a plant; such methods may further comprise detecting the exogenous nucleic acid in the plant part and/or in the plant produced from the plant part;
- (c) introducing, into a plant part, an exogenous nucleic acid encoding one or more COBL4 proteins and/or one or more ERF62 proteins (*e.g.*, an exogenous nucleic  
15 acid comprising a nucleotide sequence that is at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the nucleotide sequence set forth in any one of SEQ ID NOs: 1–27), detecting the presence of the exogenous nucleic acid in the plant part, and growing the plant part into a plant;
- 20 (d) crossing a first parent plant or plant part with a second parent plant or plant part, wherein the first parent plant or plant part comprises within its genome a nucleic acid (*e.g.*, an exogenous nucleic acid) encoding one or more COBL4 proteins and/or one or more ERF62 proteins (*e.g.*, an exogenous nucleic acid comprising a  
25 nucleotide sequence that is at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the nucleotide sequence set forth in any one of SEQ ID NOs: 1–27); and/or
- (e) introgressing an exogenous nucleic acid encoding one or more COBL4 proteins and/or one or more ERF62 proteins (*e.g.*, an exogenous nucleic acid comprising a  
30 nucleotide sequence that is at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the nucleotide sequence set forth in any one of SEQ ID NOs: 1–27) into a plant or plant part lacking the exogenous nucleic acid.

In some embodiments, methods of producing plants having enhanced abiotic stress  
35 tolerance comprise, consist essentially of or consist of detecting, in a plant part, the presence of

a nucleic acid (*e.g.*, an exogenous nucleic acid) comprising, consisting essentially of or consisting of:

- (a) one or more of the nucleotide sequences set forth in SEQ ID NOs: 1–27;
- (b) one or more nucleotide sequences that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of the nucleotide sequences set forth in SEQ ID NOs: 1–27;
- (c) one or more nucleotide sequences that encodes a polypeptide comprising, consisting essentially of or consisting of the amino acid sequence set forth in any one of SEQ ID NOs: 28–44;
- (d) one or more nucleotide sequences that encodes a polypeptide comprising, consisting essentially of or consisting of an amino acid sequence that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of the amino acid sequences set forth in SEQ ID NOs: 28–44;
- (e) a nucleotide sequence that is complementary to any one of the nucleotide sequences described in (a) to (d) above;
- (f) a nucleotide sequence that hybridizes to any one of the nucleotide sequences described in (a) to (e) above under stringent hybridization conditions;
- (g) a functional fragment of any one of the nucleotide sequences described in (a) to (f) above, wherein the functional fragment encodes a polypeptide that comprises an N-terminal signal peptide sequence that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 1 to 27 of SEQ ID NO: 28 and a CCVS domain that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 226 to 229 of SEQ ID NO: 28; and/or
- (h) a functional fragment of any one of the nucleotide sequences described in (a) to (f) above, wherein the functional fragment encodes a polypeptide that comprises an AP2 domain that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 110 to 167 of SEQ ID NO: 36; and

producing a plant from the plant part.

In some embodiments, methods of producing plants having enhanced abiotic stress tolerance comprise, consist essentially of or consist of introducing, into a plant part, an exogenous nucleic acid comprising, consisting essentially of or consisting of:

- (a) one or more of the nucleotide sequences set forth in SEQ ID NOs: 1–27;
- 5 (b) one or more nucleotide sequences that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of the nucleotide sequences set forth in SEQ ID NOs: 1–27;
- (c) one or more nucleotide sequences that encodes a polypeptide comprising, consisting essentially of or consisting of the amino acid sequence set forth in any one of SEQ ID NOs: 28–44;
- 10 (d) one or more nucleotide sequences that encodes a polypeptide comprising, consisting essentially of or consisting of an amino acid sequence that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of the amino acid sequences set forth in SEQ ID NOs: 28–44;
- 15 (e) a nucleotide sequence that is complementary to any one of the nucleotide sequences described in (a) to (d) above;
- (f) a nucleotide sequence that hybridizes to any one of the nucleotide sequences described in (a) to (e) above under stringent hybridization conditions;
- 20 (g) a functional fragment of any one of the nucleotide sequences described in (a) to (f) above, wherein the functional fragment encodes a polypeptide that comprises an N-terminal signal peptide sequence that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 1 to 27 of SEQ ID NO: 28 and a CCVS domain that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 226 to 229 of SEQ ID NO: 28; and/or
- 25 (h) a functional fragment of any one of the nucleotide sequences described in (a) to (f) above, wherein the functional fragment encodes a polypeptide that comprises an AP2 domain that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 110 to 167 of SEQ ID NO: 36; and
- 30

growing the plant part into a plant.

In some embodiments, methods of producing plants having enhanced abiotic stress tolerance comprise, consist essentially of or consist of crossing a first parent plant or plant part with a second parent plant or plant part, wherein the first parent plant or plant part comprises within its genome a nucleic acid (*e.g.*, an exogenous nucleic acid) comprising, consisting essentially of or consisting of:

- (a) one or more of the nucleotide sequences set forth in SEQ ID NOs: 1–27;
- (b) one or more nucleotide sequences that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of the nucleotide sequences set forth in SEQ ID NOs: 1–27;
- (c) one or more nucleotide sequences that encodes a polypeptide comprising, consisting essentially of or consisting of the amino acid sequence set forth in any one of SEQ ID NOs: 28–44;
- (d) one or more nucleotide sequences that encodes a polypeptide comprising, consisting essentially of or consisting of an amino acid sequence that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of the amino acid sequences set forth in SEQ ID NOs: 28–44;
- (e) a nucleotide sequence that is complementary to any one of the nucleotide sequences described in (a) to (d) above;
- (f) a nucleotide sequence that hybridizes to any one of the nucleotide sequences described in (a) to (e) above under stringent hybridization conditions;
- (g) a functional fragment of any one of the nucleotide sequences described in (a) to (f) above, wherein the functional fragment encodes a polypeptide that comprises an N-terminal signal peptide sequence that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 1 to 27 of SEQ ID NO: 28 and a CCVS domain that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 226 to 229 of SEQ ID NO: 28; and/or
- (h) a functional fragment of any one of the nucleotide sequences described in (a) to (f) above, wherein the functional fragment encodes a polypeptide that comprises an AP2 domain that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 110 to 167 of SEQ ID NO: 36.

In some embodiments, methods of producing plants having enhanced abiotic stress tolerance comprise, consist essentially of or consist of crossing a first plant or plant part that comprises an exogenous nucleic acid encoding one or more COBL4 proteins and/or one or more ERF62 proteins with a second plant or plant part that lacks the exogenous nucleic acid and repeatedly backcrossing progeny plants comprising the exogenous nucleic acid (or a functional fragment thereof) with the second plant or plant part to produce an introgressed plant or plant part comprising the exogenous nucleic acid (or a functional fragment thereof). Such methods may further comprise selecting the introgressed plant or plant part (for inclusion in a breeding program, for example).

In some embodiments, methods of producing plants and plant parts having enhanced abiotic stress tolerance comprise, consist essentially of or consist of crossing a first plant or plant part that comprises an exogenous nucleic acid with a second plant or plant part that lacks the exogenous nucleic acid and repeatedly backcrossing progeny plants comprising the exogenous nucleic acid (or a functional fragment thereof) with the second plant or plant part to produce an introgressed plant or plant part comprising the exogenous nucleic acid (or a functional fragment thereof), wherein the exogenous nucleic acid comprises, consists essentially of or consists of:

- (a) one or more of the nucleotide sequences set forth in SEQ ID NOs: 1–27;
- (b) one or more nucleotide sequences that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of the nucleotide sequences set forth in SEQ ID NOs: 1–27;
- (c) one or more nucleotide sequences that encodes a polypeptide comprising, consisting essentially of or consisting of the amino acid sequence set forth in any one of SEQ ID NOs: 28–44;
- (d) one or more nucleotide sequences that encodes a polypeptide comprising, consisting essentially of or consisting of an amino acid sequence that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of the amino acid sequences set forth in SEQ ID NOs: 28–44;
- (e) a nucleotide sequence that is complementary to any one of the nucleotide sequences described in (a) to (d) above;
- (f) a nucleotide sequence that hybridizes to any one of the nucleotide sequences described in (a) to (e) above under stringent hybridization conditions;

(g) a functional fragment of any one of the nucleotide sequences described in (a) to (f) above, wherein the functional fragment encodes a polypeptide that comprises an N-terminal signal peptide sequence that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 1 to 27 of SEQ ID NO: 28 and a CCVS domain that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 226 to 229 of SEQ ID NO: 28; and/or

(h) a functional fragment of any one of the nucleotide sequences described in (a) to (f) above, wherein the functional fragment encodes a polypeptide that comprises an AP2 domain that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to amino acids 110 to 167 of SEQ ID NO: 36.

Such methods may further comprise selecting the introgressed plant or plant part (for inclusion in a breeding program, for example).

Any suitable nucleic acid may be detected in/introduced into the plant or plant part, including, but not limited to, nucleic acids of the present invention. In some embodiments, the nucleic acid detected in/introduced into the plant or plant part is a nucleic acid encoding one or more of SEQ ID NOs: 28–44 (*e.g.*, an exogenous nucleic acid comprising one or more of SEQ ID NOs: 1–27).

Exogenous nucleic acids may be introduced into the plant or plant part via any suitable method, including, but not limited to, microparticle bombardment, liposome-mediated transfection, receptor-mediated delivery, *Agrobacterium*-mediated transformation and/or whiskers-mediated transformation. In some embodiments, the exogenous nucleic acid is introduced into a plant part by crossing a first plant or plant part comprising the exogenous nucleic acid with a second plant or plant part that lacks the exogenous nucleic acid.

Nucleic acids encoding COBL4 proteins and/or ERF62 proteins may be detected using any suitable method, including, but not limited to, DNA sequencing, mass spectrometry and capillary electrophoresis. In some embodiments, the nucleic acid (or an informative fragment thereof) is detected in one or more amplification products from a nucleic acid sample from the plant or plant part. In some such embodiments, the amplification product(s) comprise(s) the nucleotide sequence of any one of SEQ ID NOs: 1–27, the reverse complement thereof, an informative fragment thereof, or an informative fragment of the reverse complement thereof.

Nucleic acids encoding COBL4 proteins and/or ERF62 proteins may be detected using any suitable probe. In some embodiments, the nucleic acid (or an informative fragment thereof) is detected using a probe comprising the nucleotide sequence of any one of SEQ ID NOs: 1–27, the reverse complement thereof, an informative fragment thereof, or an informative fragment of the reverse complement thereof. In some embodiments, the probe comprises one or more detectable moieties, such as digoxigenin, fluorescein, acridine-ester, biotin, alkaline phosphatase, horseradish peroxidase,  $\beta$ -glucuronidase,  $\beta$ -galactosidase, luciferase, ferritin or a radioactive isotope.

Methods of the present invention may be used to identify, select and/or produce plants and plant parts that exhibit a variety of abiotic stress tolerant phenotypes, including, but not limited to, decreased water loss, decreased accumulation of one or more reactive oxygen species, decreased accumulation of one or more salts, increased salt excretion, increased accumulation of one or more dehydrins, improved root architecture, improved osmotic pressure regulation, increased accumulation of one or more late embryogenesis abundant proteins, increased survival rate, increased growth rate, increased height, increased chlorophyll content and/or increased yield (*e.g.*, increased biomass, increased seed yield, increased grain yield at standard moisture percentage (YGSMN), increased grain moisture at harvest (GMSTP), increased grain weight per plot (GWTPN), increased percent yield recovery (PYREC), decreased yield reduction (YRED), and/or decreased percent barren (PB)) when grown under abiotic stress conditions (*e.g.*, drought stress conditions, osmotic stress conditions, salt stress conditions and/or temperature stress conditions). In some embodiments, one or more abiotic stress tolerant phenotypes is increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300%, or more as compared to a control plant or plant part (*e.g.*, a native plant of the same species) when each is grown under the same (or substantially the same) environmental conditions.

In some embodiments, the plant or plant part expresses one or more COBL4 proteins (*e.g.*, one or more proteins having the amino sequence that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the amino sequence one or more of SEQ ID NOs: 28–35) at an increased level as compared to a control plant or plant part (*e.g.*, a native plant of the same species) when each is grown under the same (or substantially the same) environmental conditions. In some such embodiments, expression of the COBL4 protein(s) is increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300%, or more as compared to the control plant or plant part.

In some embodiments, the plant or plant part expresses one or more ERF62 proteins (*e.g.*, one or more proteins having the amino sequence that is at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the amino sequence one or more of SEQ ID NOs: 36–44) at an increased level as compared to a control plant or plant part (*e.g.*, a native plant of the same species) when each is grown under the same (or substantially the same) environmental conditions. In some such embodiments, expression of the ERF62 protein(s) is increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300%, or more as compared to the control plant or plant part.

In some embodiments, the yield (*e.g.*, seed yield, biomass, GWTPN, PYREC and/or YGSMN) of the plant or plant part is increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300% or more as compared to a control plant or plant part (*e.g.*, a native plant of the same species) grown under the same (or substantially the same) environmental conditions. For example, the seed yield and/or biomass of the plant or plant part may be increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300% or more as compared to a control plant or plant part grown under the same (or substantially the same) drought stress conditions.

In some embodiments, the accumulation of dehydrins and/or late embryogenesis abundant proteins, survival rate, growth potential, height, chlorophyll content and/or GMSTP of the plant or plant part is increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300% or more as compared to a control plant or plant part (*e.g.*, a native plant of the same species) grown under the same (or substantially the same) environmental conditions. For example, the survival rate and/or chlorophyll content of the plant or plant part may be increased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 250%, 300% or more as compared to a control plant or plant part grown under the same (or substantially the same) drought stress conditions.

In some embodiments, the water loss, accumulation of reactive oxygen species, YRED, and/or PB of the plant or plant part is decreased by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more as compared to a control plant or plant part (*e.g.*, a native plant of the same species) grown under the same (or substantially the same) environmental conditions. For example, the YRED and/or PB of the plant may be decreased by at least about 5%, 10%, 15%,

20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more as compared to a control plant grown under the same (or substantially the same) drought stress conditions.

In some embodiments, the root architecture and/or osmotic pressure regulation of the plant or plant part is improved as compared to a control plant (e.g., a native plant of the same species) grown under the same (or substantially the same) environmental conditions. For example, the root architecture and/or osmotic pressure regulation of the plant or plant part may be improved as compared to a control plant or plant part grown under the same (or substantially the same) drought stress conditions.

Methods of the present invention may be used to identify, select and/or produce plants and plant parts of any suitable plant type, including, but not limited to, plants belonging to the superfamily Viridiplantae. In some embodiments the plant or plant part is a fodder crop, a food crop, an ornamental plant, a tree or a shrub. For example, in some embodiments, the plant or plant part is a variety of *Acer* spp., *Actinidia* spp., *Abelmoschus* spp., *Agropyron* spp., *Allium* spp., *Amaranthus* spp., *Ananas comosus*, *Annona* spp., *Apium graveolens*, *Arachis* spp., *Artocarpus* spp., *Asparagus officinalis*, *Avena* spp. (e.g. *Avena sativa*, *Avena fatua*, *Avena byzantina*, *Avena fatua* var. *sativa*, *Avena hybrida* ), *Averrhoa carambola*, *Benincasa hispida*, *Bertholletia excelsea*, *Beta vulgaris*, *Brassica* spp. (e.g. *Brassica napus*, *Brassica rapa* ssp. [canola, oilseed rape, turnip rape]), *Cadaba farinosa*, *Camellia sinensis*, *Canna indica*, *Capsicum* spp., *Carex elata*, *Carica papaya*, *Carissa macrocarpa*, *Carya* spp., *Carthamus tinctorius*, *Castanea* spp., *Cichorium endivia*, *Cinnamomum* spp., *Citrullus lanatus*, *Citrus* spp., *Cocos* spp., *Coffea* spp., *Colocasia esculenta*, *Cola* spp., *Coriandrum sativum*, *Corylus* spp., *Crataegus* spp., *Crocus sativus*, *Cucurbita* spp., *Cucumis* spp., *Cynara* spp., *Daucus carota*, *Desmodium* spp., *Dimocarpus longan*, *Dioscorea* spp., *Diospyros* spp., *Echinochloa* spp., *Elaeis* (e.g. *Elaeis guineensis*, *Elaeis oleifera* ), *Eleusine coracana*, *Eriobotrya japonica*, *Eugenia uniflora*, *Fagopyrum* spp., *Fagus* spp., *Ficus carica*, *Fortunella* spp., *Fragaria* spp., *Ginkgo biloba*, *Glycine* spp. (e.g. *Glycine max*, *Soja hispida* or *Soja max* ), *Gossypium hirsutum*, *Helianthus* spp. (e.g. *Helianthus annuus* ), *Hemerocallis fulva*, *Hibiscus* spp., *Hordeum* spp. (e.g. *Hordeum vulgare* ), *Ipomoea batatas*, *Juglans* spp., *Lactuca sativa*, *Lathyrus* spp., *Lens culinaris*, *Linum usitatissimum*, *Litchi chinensis*, *Lotus* spp., *Luffa acutangula*, *Lupinus* spp., *Luzula sylvatica*, *Lycopersicon* spp. (e.g. *Lycopersicon esculentum*, *Lycopersicon lycopersicum*, *Lycopersicon pyriforme* ), *Macrotyloma* spp., *Malus* spp., *Malpighia emarginata*, *Mammea americana*, *Mangifera indica*, *Manihot* spp., *Manilkara zapota*, *Medicago sativa*, *Melilotus* spp., *Mentha* spp., *Miscanthus* spp., *Momordica* spp., *Morus nigra*, *Musa* spp., *Nicotiana* spp., *Olea* spp., *Opuntia* spp., *Ornithopus* spp., *Oryza* spp. (e.g. *Oryza sativa*, *Oryza latifolia*), *Panicum*

*miliaceum*, *Passiflora edulis*, *Pastinaca sativa*, *Persea* spp., *Petroselinum crispum*, *Phaseolus* spp., *Phoenix* spp., *Physalis* spp., *Pinus* spp., *Pistacia vera*, *Pisum* spp., *Poa* spp., *Populus* spp., *Prosopis* spp., *Prunus* spp., *Psidium* spp., *Punica granatum*, *Pyrus communis*, *Quercus* spp., *Raphanus sativus*, *Rheum rhabarbarum*, *Ribes* spp., *Ricinus communis*, *Rubus* spp., *Saccharum* spp., *Sambucus* spp., *Secale cereale*, *Sesamum* spp., *Sinapis* sp., *Solanum* spp. (e.g. *Solanum tuberosum*, *Solanum integrifolium* or *Solanum lycopersicum*), *Sorghum bicolor*, *Spinacia* spp., *Syzygium* spp., *Tagetes* spp., *Tamarindus indica*, *Theobroma cacao*, *Trifolium* spp., *Triticosecale rimpaii*, *Triticum* spp. (e.g. *Triticum aestivum*, *Triticum durum*, *Triticum turgidum*, *Triticum hybernum*, *Triticum macha*, *Triticum sativum* or *Triticum vulgare*), *Tropaeolum minus*, *Tropaeolum majus*, *Vaccinium* spp., *Vicia* spp., *Vigna* spp., *Viola odorata*, *Vitis* spp., *Zea mays*, *Zizania palustris* or *Ziziphus* spp., amongst others.

In some embodiments, the plant or plant part is a rice, maize, wheat, barley, sorghum, millet, oat, triticale, rye, buckwheat, fonio, quinoa, sugar cane, bamboo, banana, ginger, onion, lily, daffodil, iris, amaryllis, orchid, canna, bluebell, tulip, garlic, secale, einkorn, spelt, emmer, durum, kamut, grass (e.g., gramma grass), teff, milo, flax, *Tripsacum* sp., or teosinte plant or plant part. In some embodiments, the plant or plant part is a blackberry, raspberry, strawberry, barberry, bearberry, blueberry, coffee berry, cranberry, crowberry, currant, elderberry, gooseberry, goji berry, honeyberry, lemon, lime, lingonberry, mangosteen, orange, pepper, persimmon, pomegranate, prune, cotton, clover, acai, plum, peach, nectarin, cherry, guava, almond, pecan, walnut, apple, amaranth, sweet pea, pear, potato, soybean, sugar beet, sunflower, sweet potato, tamarind, tea, tobacco or tomato plant or plant part.

The present invention extends to products harvested from plants and plant parts produced according to methods of the present invention, including, but not limited to, plant cells and harvestable plant parts such as seeds, leaves, fruits, flowers, stems, rhizomes, tubers and bulbs. In some embodiments, the harvested product is a plant cell (e.g., a embryo or ovule) or plant part capable of producing a plant or plant part having increased expression and/or activity of one or more COBL4 proteins, increased expression and/or activity of one or more ERF62 proteins, and/or enhanced abiotic stress tolerance (e.g., enhanced drought tolerance, enhanced osmotic stress tolerance, enhanced salt stress tolerance and/or enhanced temperature stress tolerance). In some embodiments, the harvested product is a plant cell (e.g., a embryo or ovule) or plant part capable of producing a plant or plant that exhibits decreased water loss, decreased accumulation of one or more reactive oxygen species, decreased accumulation of one or more salts, increased salt excretion, increased accumulation of one or more dehydrins, improved root architecture, improved osmotic pressure regulation, increased accumulation of one or more late embryogenesis abundant proteins, increased survival rate, increased growth rate, increased

height, increased chlorophyll content and/or increased yield (e.g., increased biomass, increased seed yield, increased grain yield at standard moisture percentage (YGSMN), increased grain moisture at harvest (GMSTP), increased grain weight per plot (GWTPN), increased percent yield recovery (PYREC), decreased yield reduction (YRED), and/or decreased percent barren (PB))  
5 when grown under abiotic stress conditions (e.g., drought stress conditions, osmotic stress conditions, salt stress conditions and/or temperature stress conditions).

The present invention also extends to products derived from plants produced according to methods of the present invention, including, but not limited to, dry pellets and powders, oils, fats, fatty acids, starches and proteins.

#### EXAMPLES

The following examples are not intended to be a detailed catalog of all the different ways in which the present invention may be implemented or of all the features that may be added to the present invention. Persons skilled in the art will appreciate that numerous variations and  
15 additions to the various embodiments may be made without departing from the present invention. Hence, the following descriptions are intended to illustrate some particular embodiments of the invention, and not to exhaustively specify all permutations, combinations and variations thereof.

#### Example 1

##### Over-expression of *OsCOBL4* or *OsERF62* enhances abiotic stress tolerance

Exposure to abiotic stress conditions resulted in the upregulation of both *OsCOBL4* expression and *OsERF62* expression (Figs. 1A–1H), indicating that *OsCOBL4* and *OsERF62* are associated with one or more abiotic stress responses. As shown in Figs. 4A–6B, overexpression  
25 of *OsCOBL4* and *OsERF62* gave rise to enhanced abiotic stress tolerance in transgenic rice plants.

##### Part I. *OsCOBL4* and *OsERF62* expression were upregulated in rice exposed to abiotic stress conditions

Water-cultured four-week-old seedlings of upland rice variety IRAT109 and lowland rice variety Nipponbare were subjected to the following abiotic stress treatments: ABA treatment (roots were soaked in 100  $\mu$ M ABA solution and cultured under illumination for 1, 2, 4, 6, 9, 12, 24 or 36 hours); dehydration treatment (roots were left in the air for 1, 2, 3, 4, 5, 6 or 8 hours);  
35  $H_2O_2$  treatment (roots were soaked in 1 mM  $H_2O_2$  solution and left in the air 1, 2, 4, 6, 9, 12 or

24 hours); PEG treatment (roots were soaked in 200 g/L polyethylene glycol (PEG6000) aqueous solution for 1, 2, 4, 6, 9, 12 or 24 hours); or control treatment (roots remained in water culture). Following treatment, leaves were collected and quickly frozen using liquid nitrogen and stored at -80°C for further use.

5 Total RNA was extracted from the harvested leaves and purified. Reverse transcription was performed using M-MLV reverse transcriptase to synthesize cDNA, then the cDNA was used as a template to amplify 244 bp fragments of *OsCOBL4* (forward primer: 5'-TGTGTTTCTCTCTCGTCGTTTCG-3' (corresponding to nucleotides 756 to 777 of SEQ ID NO 3); reverse primer: 5'-TCTTTGAGCATCAAGTGCCAGT-3' (corresponding to nucleotides 958 to 979 of SEQ ID NO: 3)); a 142 bp fragment of *OsERF62* gene (forward primer: 5'-ATGGCTTGCTTGATTACCGAA-3' (corresponding to nucleotides 1203 to 1223 of SEQ ID NO 16); reverse primer: 5'-AGACCCCGTAAAAGTAGCCCA-3' (corresponding to nucleotides 1324 to 1344 of SEQ ID NO: 16)); and a 255bp fragment (255bp) of the Nipponbare Actin gene (forward primer: 5'-ATTGGCACCACACATTCTAC-3'; reverse primer: 5'-ATAACCTTCGTAGATTGGGACT-3'), which was used as an internal reference for real-time quantitative analysis.

Real-time fluorescence quantitative PCR was carried out on a real-time fluorescence quantitative PCR apparatus (Applied Biosystems® 7500 Real Time PCR system, Life Technologies, Grand Island, NY, USA); one parallel experiment was performed with three repetitions. The relative expression levels of *OsCOBL4*, *OsERF62*, and *Actin* were calculated by the method reported by Livak KJ and Schmittgen TD (*Analysis of relative gene expression data using real-time quantitative PCR and the 2(-Delta Delta C(T)) Method*, METHODS 25(4):402 (2001).

As shown in Figs. 1A–1H, the expressions of *OsCOBL4* and *OsERF62* were upregulated in response to each of the abiotic stress treatments, indicating that *OsCOBL4* and *OsERF62* are associated with one or more abiotic stress responses (more particularly, to one or more drought stress responses). The expression of *OsCOBL4* was greater in upland rice variety IRAT109 than in lowland rice variety Nipponbare.

## 30 Part II. Isolation of genes associated with enhanced abiotic stress tolerance

Seedlings of upland rice variety IRAT109 were cultivated under normal conditions. Total RNA was extracted using the Trizol method and purified. Reverse transcription was performed using M-MLV reverse transcriptase to obtain cDNA. Using the cDNA as a template, two genes were amplified: *OsCOBL4*<sub>IRAT109</sub> (forward primer: 5'-

TTGGCGCGCCACACACCGAGTCATCGCTCG-3' (the underlined nucleotides are the digestion recognition sequence of restriction endonuclease *AscI*); reverse primer: 5'-CCTTAATTAACCCCTGCCACGAATCTGCTAT-3' (the underlined bases are the digestion recognition sequence of restriction endonuclease *PacI*)) and *OsERF62<sub>IRAT109</sub>* (forward primer: 5'-CGGGGTACCAAAGGCATTTCGCAACACACA-3' (the underlined base pairs are the digestion recognition sequence of restriction endonuclease *KpnI*); reverse primer: 5'-CCTTAATTAACCAAAAATACATTACGACTGGAC-3' (the underlined nucleotides are the digestion recognition sequence of restriction endonuclease *PacI*)). The amplification products were subjected to agarose gel electrophoresis, and amplification products corresponding to *OsCOBL4<sub>IRAT109</sub>* and *OsERF62<sub>IRAT109</sub>* were recovered and purified for sequencing.

The sequence of the 1589 bp fragment corresponding to *OsCOBL4<sub>IRAT109</sub>* is shown herein as SEQ ID NO: 3. *OsCOBL4<sub>IRAT109</sub>* (SEQ ID NO: 28) is encoded by nucleotides 78 to 1355 of SEQ ID NO: 3 (shown herein as SEQ ID NO: 1). Nucleotides 11 to 1579 of SEQ ID NO: 3 (shown herein as SEQ ID NO: 2) represent the full-length cDNA sequence encoding *OsCOBL4<sub>IRAT109</sub>*.

The sequence of the 1580 bp fragment corresponding to *OsERF62<sub>IRAT109</sub>* is shown as SEQ ID NO: 16. *OsERF62<sub>IRAT109</sub>* (SEQ ID NO: 36) is encoded by nucleotides 102 to 1106 of SEQ ID NO: 16 (shown herein as SEQ ID NO: 14). Nucleotides 10 to 1570 of SEQ ID NO: 16 (shown herein as SEQ ID NO: 15) represent the full-length cDNA sequence encoding *OsERF62<sub>IRAT109</sub>*.

### Part III. Construction of recombinant expression vectors comprising *OsCOBL4* or *OsERF62*

The 1589 bp DNA fragment corresponding to *OsCOBL4<sub>IRAT109</sub>* was cleaved by double digestion with *AscI* and *PacI*, and the digestion product was ligated into a pMDC32 vector (Farre and Kay, *PRR7 protein levels are regulated by light and the circadian clock in Arabidopsis*, PLANT J. 52:548 (2007); publicly available from China Agricultural University) between the *AscI* and *PacI* digestion sites (*i.e.*, downstream of the dual tobacco mosaic virus 35S promoter) to produce a recombinant 35S::*OsCOBL4<sub>IRAT109</sub>* vector.

The 1580 bp DNA fragment corresponding to *OsERF62<sub>IRAT109</sub>* was cleaved by double digestion with *KpnI* and *PacI*, and the digestion product was ligated into a pMDC32 vector between the *KpnI* and *PacI* digestion sites (*i.e.*, downstream of the dual tobacco mosaic virus 35S promoter) to produce a recombinant 35S::*OsEF62<sub>IRAT109</sub>* vector.

Proper insertion of the *OsCOBL4<sub>IRAT109</sub>* and *OsERF62<sub>IRAT109</sub>* digestion products was verified by sequencing and enzyme digestion.

Part IV. Production of recombinant *Agrobacterium tumefaciens* comprising 35S::OsCOBL4<sub>IRAT109</sub> or 35S::OsERF62<sub>IRAT109</sub>

*Agrobacterium tumefaciens* EHA105 (Shiwu et al., *Study on factors affecting conversion efficiency of Agrobacterium tumefaciens EHA105 competent cells*, J. TROPICAL BIOL. 3(1) (March 2012); publicly available from China Agricultural University) was transformed with recombinant 35S::OsCOBL4<sub>IRAT109</sub> vector or recombinant 35S::OsERF62<sub>IRAT109</sub> vector using the freeze-thaw method to produce recombinant *Agrobacterium* EHA105/35S::OsCOBL4<sub>IRAT109</sub> and recombinant *Agrobacterium* EHA105/35S::OsERF62<sub>IRAT109</sub>.

Part V. Production of transgenic Nipponbare rice plants expressing OsCOBL4<sub>IRAT109</sub> or OsERF62<sub>IRAT109</sub>

Embryogenic calli of lowland rice variety Nipponbare were infected with recombinant *Agrobacterium* EHA105/35S::OsCOBL4<sub>IRAT109</sub> or recombinant *Agrobacterium* EHA105/35S::OsERF62<sub>IRAT109</sub> to produce T<sub>0</sub>-generation OsCOBL4<sub>IRAT109</sub> transgenic Nipponbare rice lines and T<sub>0</sub>-generation OsERF62<sub>IRAT109</sub> transgenic Nipponbare rice lines:

(Step 1) Recombinant *Agrobacterium* EHA105/35S::OsCOBL4 and recombinant *Agrobacterium* EHA105/35S::OsERF62 were separately spread YEP culture media (10 g/L peptone + 10 g/L yeast extract + 5 g/L NaCl + 15 g/L agar powder, 50 mg/L kanamycin, 20 mg/L rifampin, pH 7.0) and cultured at 28°C for 2-3 days. A single bacterial plaque from each culture was picked and inoculated into separate YEP liquid media (10 g/L peptone + 10 g/L yeast extract + 5 g/L NaCl + 15 g/L agar powder, 50 mg/L kanamycin, 20 mg/L rifampin, pH 7.0), cultured at 28°C at 240 rpm until OD<sub>600</sub> reached 0.8-1.0, then inoculated in an inoculation amount of 1% into fresh YEP liquid medium and cultured at 28°C at 240 rpm until OD<sub>600</sub> reached 0.5-0.6. Cells were collected by centrifugation, resuspended in AAM culture media (AA salts (AA large amount, AA microamount, iron salts) + MS vitamins + AA amino acids + 500 mg/L casein hydrolysate + 68.5 g/L sucrose + 36 g/L glucose + 20 mg/L acetosyringone, pH 5.2) and cultured at 28°C at 240 rpm until OD<sub>600</sub> reached 0.3-0.4. The resulting cultures were used as infection solutions in Step 2.

(Step 2) Embryogenic calli of lowland rice variety Nipponbare were soaked in one of the infection solutions for 30 min and then removed. After removing excess infection solution with sterile filter paper, the calli were cultured in separate co-culture media (NB medium basic components (N6 macroelements, B5 microelements, B5 organic components, 150 mg/L inositol, 300 mg/L casein hydrolysate, 500 mg/L glutamine, 600 mg/L proline, 30 g/L sucrose, and 3 g/L

plant gels) + 2 mg/L 2,4-D + 10 g/L glucose + 20 mg/L acetosyringone, pH 5.4) for 2-3 days.

(Step 3) Calli co-cultured in Step 2 were rinsed 3-4 times with sterile water under oscillation, and then washed with 500 mg/L cephalosporin aqueous solution under oscillation for 40 min until the supernatant was completely clear. Washed calli were taken out and put into sterile culture dishes containing filter paper and air-dried at 0.4 m/s for 4 hours. Dried calli were transferred to delay-screening culture media (NB medium basic components + 2 mg/L 2,4-D+ 500 mg/L cephalosporin, pH 5.8) and cultured in the dark for 3-7 days, then transferred to consecutive screening culture media (3-4 weeks for each screening medium; first screening medium: NB medium basic components + 2 mg/L 2,4-D+ 500 mg/L cephalosporin + 50 mg/L hygromycin, pH 5.8; second screening medium: NB medium basic components + 2 mg/L 2,4-D + 50 mg/L hygromycin, pH 5.8).

(Step 4) Calli screened in Step 3 were cultured in pre-differentiation culture media (NB medium basic components + 1 mg/L 6-BA + 2 mg/L NAA + 5 mg/L ABA + 50 mg/L hygromycin, pH 5.8) in the dark for 2-3 weeks and then transferred to differentiation culture media (NB medium basic components + 2 mg/L 6-BA+ 1 mg/L NAA + 1 mg/L KT + 50 mg/L hygromycin, pH 5.8) where they were cultured under illumination for 2-3 weeks; when buds grew to a length of about 1 cm, the cultures were transferred to sound seedling culture media (1/2 MS medium basic components + 0.5 mg/L NAA + 0.25 mg/L paclobutrazol, pH 5.8) and cultured for 30 days. The sealing films were removed, and the hardening-seedling cultures were performed for one week, then the seedlings were transplanted into soil.

(Step 5) T<sub>0</sub>-generation *OsCOBL4*<sub>IRAT109</sub> transgenic Nipponbare rice plants and T<sub>0</sub>-generation *OsERF62*<sub>IRAT109</sub> transgenic Nipponbare rice plants were identified by PCR at the DNA level using hygromycin phosphotransferase (*HPT*) as the target gene (forward primer: 5'-AAAAGTTCGACAGCGTCTCCGACC-3'; reverse primer: 5'-TCTACACAGCCATCGGTCCAGACG-3'). The target fragment was 919 nucleotides in length. Plants containing the target fragment were deemed positive and plants lacking the target fragment were deemed negative. Figs. 2A-2B.

The transgenic plants produced in Step 4 and deemed positive in Step 5 are referred to as T<sub>0</sub>-generation transgenic Nipponbare rice plants. The T<sub>1</sub> generation comprises seeds produced by selfing T<sub>0</sub> generation plants and plants growing therefrom. The T<sub>2</sub> generation comprises seeds produced by selfing the T<sub>1</sub> generation and plants growing therefrom. T<sub>3</sub> generation comprises seeds produced by selfing T<sub>2</sub> generation plants and plants growing therefrom.

## Part VI. Overexpression of *OsCOBL4* and *OsERF62* in transgenic Nipponbare rice

Leaves were collected from wild-type Nipponbare rice lines, T<sub>2</sub>-generation *OsCOBL4*<sub>IRAT109</sub> transgenic Nipponbare rice lines and T<sub>2</sub>-generation *OsERF62*<sub>IRAT109</sub> transgenic Nipponbare rice lines, all of which were planted in an open field. Total RNA was extracted from the leaves using the TRIZOL method and purified. Reverse transcription was performed using M-MLV reverse transcriptase to synthesize cDNA, then the cDNA was used as a template to amplify 244 bp fragments of *OsCOBL4* (forward primer: 5'-TGTGTTTCTCTCTCGTCGTTTCG-3' (corresponding to nucleotides 756 to 777 of SEQ ID NO 3); reverse primer: 5'-TCTTTGAGCATCAAGTGCCAGT-3' (corresponding to nucleotides 958 to 979 of SEQ ID NO: 3)); a 142 bp fragment of *OsERF62* gene (forward primer: 5'-ATGGCTTGCTTGATTACCGAA-3' (corresponding to nucleotides 1203 to 1223 of SEQ ID NO 16); reverse primer: 5'-AGACCCCGTAAAAGTAGCCCA-3' (corresponding to nucleotides 1324 to 1344 of SEQ ID NO: 16)); and a 255bp fragment (255bp) of the Nipponbare Actin gene (forward primer: 5'-ATTTGGCACCACACATTCTAC-3'; reverse primer: 5'-ATAACCTTCGTAGATTGGGACT-3'), which was used as an internal reference for real-time quantitative analysis.

Real-time fluorescence quantitative PCR was carried out on a real-time fluorescence quantitative PCR apparatus (Applied Biosystems® 7500 Real Time PCR system, Life Technologies, Grand Island, NY, USA); one parallel experiment was performed with three repetitions. The relative expression levels of *OsCOBL4*, *OsERF62*, and *Actin* were calculated by the method reported by Livak KJ and Schmittgen TD (*Analysis of relative gene expression data using real-time quantitative PCR and the 2(-Delta Delta C(T)) Method*, METHODS 25(4):402 (2001).

As shown in Figs. 3A–3B, respectively, the expression of *OsCOBL4* and *OsERF62* in the T<sub>2</sub>-generation *OsCOBL4*<sub>IRAT109</sub> transgenic Nipponbare rice lines (T6, T8, T9) and T<sub>2</sub>-generation *OsERF62*<sub>IRAT109</sub> transgenic Nipponbare rice lines (T6, T8, T9) were significantly higher than in the WT lines.

#### Part VII. Overexpression of *OsCOBL4* and *OsERF62* gave rise to enhanced abiotic stress tolerance in rice plants grown under simulated drought stress conditions

Wild-type lowland rice variety Nipponbare lines (WT) were subjected to PEG-simulated drought stress conditions, along with two T<sub>2</sub>-generation *OsCOBL4*<sub>IRAT109</sub> transgenic Nipponbare rice lines (T6 and T8) and two T<sub>2</sub>-generation *OsERF62*<sub>IRAT109</sub> transgenic Nipponbare rice lines (OE4 and OE5), each of which were positively identified by PCR in Step 5 of Part V.

Seeds of individual plant lines were sterilized with 20% NaClO. Seeds of the T<sub>2</sub>-generation

*OsCOBL4<sub>IRAT109</sub>* transgenic Nipponbare rice lines (T6 and T8) and the T<sub>2</sub>-generation *OsERF62<sub>IRAT109</sub>* transgenic Nipponbare rice lines (OE4 and OE5) were soaked in sterile water containing 50 mg/L hygromycin for 2 days. WT seeds were soaked in sterile water free of hygromycin for 2 days. The soaked seeds were washed with sterile water containing 50 mg/L

5 hygromycin, and forced to germinate for 2-3 days after excess water was removed.

Seeds having the same (or substantially the same) growth potential under normal growth conditions were selected and transferred to PCR plates, the bottom of which were hollowed out. Thirty T6, T8, OE4 or OE5 plants were planted on each PCR plate, using WT plants as controls, and cultured with a Hoagland nutrient fluid (1.43 mM NH<sub>4</sub>NO<sub>3</sub>, 0.27 mM NaH<sub>2</sub>PO<sub>4</sub>·2H<sub>2</sub>O, 0.51

10 mM K<sub>2</sub>SO<sub>4</sub>, 1.0 mM CaCl<sub>2</sub>, 1.46 mM MnSO<sub>4</sub>·7H<sub>2</sub>O, 0.19 mM Na<sub>2</sub>SiO<sub>3</sub>, 9.5 μM MnCl<sub>2</sub>·4H<sub>2</sub>O,  $7.5 \times 10^{-2}$  μM (NH<sub>4</sub>)<sub>6</sub>Mo<sub>7</sub>O<sub>24</sub>·4H<sub>2</sub>O, 18.8 μM H<sub>3</sub>BO<sub>3</sub>, 0.15 μM ZnSO<sub>4</sub>·7H<sub>2</sub>O, 0.16 μM CuSO<sub>4</sub>·5H<sub>2</sub>O, 35.6 μM FeCl<sub>3</sub>·6H<sub>2</sub>O, pH 5.5-6.0) in an illuminated culture room until they grew to the two-leaf one-apical bud stage, at which point the PCR plates were transferred into an aqueous solution containing 200 g/L PEG6000 for 3 days and then transferred to sterile water for

15 7 days. The number of surviving plants was counted, and the survival rates (*i.e.*, the percentage of the number of surviving plants to the total number of plants subjected to the stress treatment) were calculated.

As shown in Figs. 4A–4B and Table 1, the survival rates of *OsCOBL4<sub>IRAT109</sub>* transgenic Nipponbare rice lines and *OsERF62<sub>IRAT109</sub>* transgenic Nipponbare rice lines were significantly

20 higher than that of WT Nipponbare rice lines, indicating that overexpression of *OsCOBL4* and/or *OsERF62* gave rise to enhanced abiotic stress tolerance (more particularly, enhanced drought stress tolerance).

|         | Plant Line | Survival Rate  |
|---------|------------|----------------|
| Group 1 | T6         | 92.96±3.53**   |
|         | WT         | 46.67±3.33     |
| Group 2 | T8         | 66.69±2.17**   |
|         | WT         | 35.56±2.22     |
| Group 3 | OE4        | 100 ± 0**      |
|         | WT         | 33.33 ± 6.67   |
| Group 4 | OE5        | 62.22 ± 6.19** |
|         | WT         | 10 ± 5.57      |

25 Table 1. Survival rates of seedlings grown under PEG-simulated drought stress conditions.

\*\* = significance at p<0.01 as compared with WT.

Part VIII. Overexpression of *OsCOBL4* and *OsERF62* gave rise to enhanced abiotic stress tolerance in rice plants grown under osmotic stress conditions

5 Wild-type lowland rice variety Nipponbare lines (WT) were subjected to osmotic stress conditions, along with three T<sub>2</sub>-generation *OsCOBL4*<sub>IRAT109</sub> transgenic Nipponbare rice lines (T6, T8, T9) and two T<sub>2</sub>-generation *OsERF62*<sub>IRAT109</sub> transgenic Nipponbare rice lines (OE4 and OE5), each of which were positively identified by PCR in Step 5 of Part V.

10 Seeds of individual plant lines were dehulled and sterilized with 20% NaClO. Seeds of the T<sub>2</sub>-generation *OsCOBL4*<sub>IRAT109</sub> transgenic Nipponbare rice lines (T6, T8, T9) and the T<sub>2</sub>-generation *OsERF62*<sub>IRAT109</sub> transgenic Nipponbare rice lines (OE4 and OE5) were allowed to germinate on 1/2 MS media containing 50 mg/L hygromycin at 28°C with a light rhythm of 12-hour illumination and 12-hour darkness every day. WT seeds were allowed to germinate on a 1/2 MS medium free of hygromycin at 28°C with a light rhythm of 12-hour illumination and 12-hour  
15 darkness every day.

Germinated seeds having the same or substantially the same growth potential under normal conditions were selected and transferred to 1/2 MS media containing 0 mmol/L or 200 mmol/L mannitol and cultured at 28°C for 7-10 days with a light rhythm of 12-hour illumination and 12-hour darkness every day. The heights and fresh weights of the plants were measured, the  
20 percentage of the heights of the plants treated with 200 mmol/L mannitol to the heights of the plants treated with 0 mmol/L mannitol were calculated and recorded as relative plant heights (%), and the percentages of the fresh weights of the plants treated with 200 mmol/L mannitol to the fresh weights of the plants treated with 0 mmol/L mannitol were calculated and recorded as relative fresh weights (%).

25 As shown in Figs. 5A–5B and Table 2 below, the plant heights and fresh weights of the *OsCOBL4*<sub>IRAT109</sub> transgenic Nipponbare rice lines and the *OsERF62*<sub>IRAT109</sub> transgenic Nipponbare rice lines exposed to 200 mmol/L mannitol were significantly higher than that of WT Nipponbare rice lines, indicating that overexpression of *OsCOBL4* and/or *OsERF62* gave rise to enhanced abiotic stress tolerance (more particularly, enhanced osmotic stress tolerance).

30

|         | Plant Line | Relative Height | Relative Weight |
|---------|------------|-----------------|-----------------|
| Group 1 | WT         | 68.03±1.15      | 72.79±2.85      |
|         | T6         | 81.90±1.86**    | 91.93±4.10**    |
|         | T8         | 76.95±1.93**    | 94.78±3.61**    |
|         | T9         | 75.18±1.41**    | 97.73±2.72**    |

|         |     |                       |                       |
|---------|-----|-----------------------|-----------------------|
| Group 2 | WT  | $58.72 \pm 1.19$      | $76.93 \pm 3.74$      |
|         | OE4 | $63.22 \pm 1.78^{**}$ | $88.15 \pm 3.67^{**}$ |
|         | OE5 | $75.90 \pm 3.07^{**}$ | $97.96 \pm 5.17^{**}$ |

Table 2. Growth of seedlings grown under mannitol-induced osmotic stress conditions.

\*\* = significance at  $p < 0.01$  as compared with WT.

5      Part IX. Overexpression of *OsCOBL4* and *OsERF62* gave rise to enhanced abiotic stress tolerance in rice plants grown under drought stress conditions

Wild-type lowland rice variety Nipponbare lines (WT) were subjected to drought stress conditions, along with three T<sub>2</sub>-generation *OsCOBL4*<sub>IRAT109</sub> transgenic Nipponbare rice lines (T6, T8, T9) and two T<sub>2</sub>-generation *OsERF62*<sub>IRAT109</sub> transgenic Nipponbare rice lines (OE4 and OE5),  
10 each of which were positively identified by PCR in Step 5 of Part V.

Seeds of individual plant lines were sterilized with 20% NaClO. Seeds of the T<sub>2</sub>-generation *OsCOBL4*<sub>IRAT109</sub> transgenic Nipponbare rice lines (T6, T8, T9) and the T<sub>2</sub>-generation *OsERF62*<sub>IRAT109</sub> transgenic Nipponbare rice lines (OE4 and OE5) were soaked in sterile water  
15 containing 50 mg/L hygromycin for 2 days. WT seeds were soaked in sterile water free of hygromycin for 2 days. The soaked seeds were washed with sterile water containing 50 mg/L hygromycin, and forced to germinate for 2-3 days after excess water was removed. The soaked seeds were washed with sterile water containing 50 mg/L hygromycin, and forced to germinate for 3–4 days after excess water was removed.

20      Seeds having the same or substantially the same growth potential under normal conditions were selected and transplanted into flower pots. Fifteen WT, T6, T8, T9, OE4 or OE5 plants were planted in each pot and grown under normal conditions unto they grew to the four-leaf stage, at which point the plants were subjected to a water shortage (*i.e.*, were not watered) for one week and then rehydration for 10 days. The number of surviving plants was counted, and  
25 the survival rates (*i.e.*, the percentage of the number of surviving plants to the total number of plants subjected to the stress treatment) were calculated.

As shown in Figs. 6A–6B and Table 3 below, the survival rates of *OsCOBL4*<sub>IRAT109</sub> transgenic Nipponbare rice lines and *OsERF62*<sub>IRAT109</sub> transgenic Nipponbare rice lines were significantly higher than that of WT Nipponbare rice lines, indicating that overexpression of  
30 *OsCOBL4* and/or *OsERF62* gave rise to enhanced abiotic stress tolerance (more particularly, enhanced drought stress tolerance).

|         | Plant Line | Survival Rate  |
|---------|------------|----------------|
| Group 1 | T6         | 41.67±10.14*   |
|         | WT         | 6.67±6.67      |
| Group 2 | T8         | 43.33±3.33**   |
|         | WT         | 13.33±6.67     |
| Group 3 | T9         | 56.67±3.33**   |
|         | WT         | 21.67±1.67     |
| Group 4 | OE4        | 93.33 ± 6.67** |
|         | WT         | 28.33 ± 6.01   |
| Group 5 | OE5        | 46.67 ± 21.67* |
|         | WT         | 21.67 ± 1.67   |

Table 3. Survival rates of seedlings grown under drought stress conditions.

\* = significance at p<0.05 as compared with WT. \*\* = significance at p<0.01 as compared with WT.

5 Thus, it was shown that both *OsCOBL4* and *OsERF62* give rise to enhanced abiotic stress tolerance (more particularly, enhanced drought tolerance and enhanced osmotic stress tolerance).

Example 2

10 Over-expression of *OsCOBL4* enhances abiotic stress tolerance

As shown in Figs. 13A–17C, overexpression of *OsCOBL4*<sub>IRAT109</sub> or *OsCOBL4*<sub>Nipponbare</sub> gave rise to enhanced abiotic stress tolerance in transgenic rice plants.

15 Part I. Bioinformatic analysis of *OsCOBL4*

*OsCOBL4* encodes a protein that comprises 425 amino acids and that has an N-terminal signal peptide sequence and a CCVS domain, which are both typical of proteins belonging to the COBRA family. Fig. 7. Both the nucleotide and amino acid sequences of *OsCOBL4* vary  
20 between typical upland rice varieties (e.g., IRAT109 and Haogelao) and lowland rice varieties (e.g., Nipponbare and Yuefu): three SNPs in the promoter region; four SNPs in the exon region, which lead to the variation of four amino acids; seven SNPs and 1 Indel in the introns; and four SNPs in the 3'UTR. Fig. 8.

Part II. Expression pattern of *OsCOBL4<sub>IRAT109</sub>* in various tissues and organs of plants

GUS staining was performed on various tissues and organs of *Pro<sub>COBL4IRAT109</sub>::GUS* transgenic IRAT rice plants and *Pro<sub>COBL4IRAT109</sub>::GUS* transgenic Nipponbare rice plants. As shown in Fig. 9A, *OsCOBL4<sub>IRAT109</sub>* was expressed at the seedling stage in the root, sheath, and leaf, and at the reproductive stage in the root, sheath, vascular bundle, stem, node, ligule, leaf and panicle. As shown in Fig. 9B, the expression of *OsCOBL4<sub>IRAT109</sub>* in IRAT109 was relatively low in the stem at the productive stage, was more highly expressed in the root, sheath, and leaf at the seedling stage, and in the root, leaf, sheath, and panicle at the productive stage. Also as shown in Fig. 9B, the expression of *OsCOBL4<sub>IRAT109</sub>* in Nipponbare was generally lower than in IRAT109, with higher expression in the root and leaf at the seedling stage and in the root at the productive stage, with low expression in the stem at the productive stage. Thus, it was observed that *OsCOBL4* was constitutively expressed in various tissues and organs of IRAT109 and Nipponbare, that expression levels differed with respect to both tissue and reproductive stage, and that expression was generally higher in IRAT109 than in Nipponbare.

Part III. Differences in the expression patterns of *OsCOBL4<sub>IRAT109</sub>* and *OsCOBL4<sub>Nipponbare</sub>* may be explained by differences in their respective promoter regions

As noted in Part I above, the promoter region of *OsCOBL4* varies contains three SNPs with respect to upland rice variety IRAT109 and lowland rice variety Nipponbare. In order to determine whether those three SNPs were responsible for the differences in expression levels seen in Part III, five *Pro::GUS* vectors were constructed: BPN (*Pro<sub>Nipponbare</sub>::GUS*), BPI (*Pro<sub>IRAT109</sub>::GUS*), BPMA (*Pro<sub>Nipponbare</sub> (-600C>T)::GUS*), BPMB (*Pro<sub>Nipponbare</sub> (-369G>T)::GUS*), and BPMB (*Pro<sub>Nipponbare</sub> (-169C>T)::GUS*). The five vectors were transferred into Nipponbare through Agrobacterium-mediated transformation, and single copies of homozygous T<sub>2</sub> generation line were obtained. Quantitative PCR analysis of the expression level of the GUS gene was performed to reflect the initiation capabilities of the five promoters by the magnitude of the expression of the GUS gene. The results showed that the expression level of GUS in the BPI transgenic plants was the highest, followed by that of BPMB, BPMA, and BPMB, and GUS is lowest expressed in BPN. Fig. 9. It was postulated that the three SNP variations in the promoter region led to the different expression level of the *OsCOBL4* between the upland rice variety IRAT109 and lowland rice variety Nipponbare and that each contributed to the increase of the expression to some degree.

Part IV. Subcellular localization of *OsCOBL4<sub>IRAT109</sub>*

For determining the subcellular localization of *COBL4*, *OsCOBL4<sub>IRAT109</sub>* was ligated into a pMDC83 vector to produce a *GFP-OsCOBL4<sub>IRAT109</sub>* expression vector. The *GFP-OsCOBL4<sub>IRAT109</sub>* expression vector transferred into tobacco plants through Agrobacterium-mediated transformation. As shown in Fig. 11, GFP-*OsCOBL4<sub>IRAT109</sub>* was expressed in the cell membranes and cell walls of the tobacco plants.

Part V. Overexpression of *OsCOBL4<sub>IRAT109</sub>* and *OsCOBL4<sub>Nipponbare</sub>* gave rise to enhanced abiotic stress tolerance in rice plants grown under abiotic stress conditions

*OsCOBL4<sub>IRAT109</sub>* and *OsCOBL4<sub>Nipponbare</sub>* were isolated and amplified as described in Example 1, Part II, ligated into a pMDC32 vector as described in Example 1, Part III, transformed into *Agrobacterium tumefaciens EHA105* as described in Example I, Part IV, and introduced into Nipponbare rice plants as described in Example I, Part V. Fig. 12 shows the relative *OsCOBL4* expression levels in wild-type Nipponbare rice plants (WT), *OsCOBL4<sub>IRAT109</sub>* transgenic Nipponbare rice plants (OEI-6, OEI-8, OEI-9) and *OsCOBL4<sub>Nipponbare</sub>* transgenic Nipponbare rice plants (OEN-2, OEN-6, OEN-8).

Overexpression of *OsCOBL4<sub>IRAT109</sub>* and *OsCOBL4<sub>Nipponbare</sub>* gave rise to enhanced abiotic stress tolerance in rice plants grown under drought stress conditions

Wild-type Nipponbare lines (WT), T<sub>2</sub>-generation *OsCOBL4<sub>IRAT109</sub>* transgenic Nipponbare rice lines (OEI) and T<sub>2</sub>-generation *OsCOBL4<sub>Nipponbare</sub>* transgenic Nipponbare rice lines (OEN) were subjected to drought stress conditions as described in Example 1, Part IX. As shown in Fig. 13 and Table 4 below, the survival rates of the OEI and OEN lines were significantly higher than that of WT lines, indicating that overexpression of both *OsCOBL4<sub>IRAT109</sub>* and *OsCOBL4<sub>Nipponbare</sub>* gives rise to enhanced abiotic stress tolerance (more particularly, enhanced drought stress tolerance).

|         | Plant Line | Survival Rate |
|---------|------------|---------------|
| Group 1 | OEI        | 56.67%–68%**  |
|         | WT         | 6.67%–15%     |
| Group 2 | OEN        | 43.33%–80%**  |
|         | WT         | 6.67%–28.33%  |

Table 4. Survival rates of seedlings grown under drought stress conditions.

\* = significance at  $p<0.05$  as compared with WT. \*\* = significance at  $p<0.01$  as compared with WT.

Overexpression of  $OsCOBL4_{IRAT109}$  and  $OsCOBL4_{Nipponbare}$  gave rise to enhanced abiotic stress tolerance in rice plants grown under simulated drought stress conditions

Wild-type Nipponbare lines (WT), T<sub>2</sub>-generation  $OsCOBL4_{IRAT109}$  transgenic Nipponbare rice lines (OEI) and T<sub>2</sub>-generation  $OsCOBL4_{Nipponbare}$  transgenic Nipponbare rice lines (OEN) were subjected to PEG-simulated drought stress conditions as described in Example 1, Part VII. As shown in Fig. 14 and Table 5 below, the survival rates of the OEI and OEN lines were significantly higher than that of WT lines, indicating that overexpression of both  $OsCOBL4_{IRAT109}$  and  $OsCOBL4_{Nipponbare}$  gave rise to enhanced abiotic stress tolerance (more particularly, enhanced drought stress tolerance).

|         | Plant Line | Survival Rate   |
|---------|------------|-----------------|
| Group 1 | OEI        | 66.39%–92.96%** |
|         | WT         | 35.55%–46.67%   |
| Group 2 | OEN        | 93.33%–100%**   |
|         | WT         | 23.77%–46.67%   |

Table 5. Survival rates of seedlings grown under PEG-simulated drought stress conditions.

\*\* = significance at  $p<0.01$  as compared with WT.

Overexpression of  $OsCOBL4_{IRAT109}$  and  $OsCOBL4_{Nipponbare}$  gave rise to enhanced abiotic stress tolerance in rice plants grown under osmotic stress conditions

Wild-type Nipponbare lines (WT), T<sub>2</sub>-generation  $OsCOBL4_{IRAT109}$  transgenic Nipponbare rice lines (OEI) and T<sub>2</sub>-generation  $OsCOBL4_{Nipponbare}$  transgenic Nipponbare rice lines (OEN) were subjected to drought stress conditions as described in Example 1, Part VIII. As shown in Fig. 15 and Table 6 below, the plant heights and fresh weights of the OEI and OEN lines were significantly higher than that of WT lines, indicating that overexpression of both  $OsCOBL4_{IRAT109}$  and  $OsCOBL4_{Nipponbare}$  gave rise to enhanced abiotic stress tolerance (more particularly, enhanced osmotic stress tolerance).

| Plant Line | Relative Height | Relative Weight |
|------------|-----------------|-----------------|
| WT         | 68.03%          | 72.8%           |

|      |           |          |
|------|-----------|----------|
| OEI6 | 81.91% ** | 91.93%** |
| OEI8 | 76.95%**  | 94.78%** |
| OEN2 | 81.03%**  | 98.03%** |
| OEN8 | 76.39% ** | 95.34%** |

Table 6. Growth of seedlings grown under mannitol-induced osmotic stress conditions.

\*\* = significance at p<0.01 as compared with WT.

5        Overexpression of *OsCOBL4*<sub>IRAT109</sub> and *OsCOBL4*<sub>Nipponbare</sub> gave rise to enhanced abiotic stress tolerance in rice plants grown under salt stress conditions

Wild-type Nipponbare lines (WT), T<sub>2</sub>-generation *OsCOBL4*<sub>IRAT109</sub> transgenic Nipponbare rice lines (OEI) and T<sub>2</sub>-generation *OsCOBL4*<sub>Nipponbare</sub> transgenic Nipponbare rice lines (OEN) were subjected to salt stress conditions as follows: Seedlings that normally germinated for 2 - 3  
10 days and had uniform growth were transferred to a 1/2 MS medium containing 0 and 150 mmol/L NaCl, respectively. The plants were grown for 7 d in a light incubator, and then measured for the shoot length and fresh weight. The relative shoot length and fresh weight prior and post stress treatment were used as evaluation criteria. As shown in Fig. 16 and Table 7 below, the plant heights and fresh weights of the OEI and OEN lines were significantly higher than that  
15 of WT lines, indicating that overexpression of both *OsCOBL4*<sub>IRAT109</sub> and *OsCOBL4*<sub>Nipponbare</sub> gave rise to enhanced abiotic stress tolerance (more particularly, enhanced salt stress tolerance).

| Plant Line | Relative Height | Relative Weight |
|------------|-----------------|-----------------|
| WT         | 36.93%          | 47.32%          |
| OEI6       | 43.3% **        | 64.08% **       |
| OEI8       | 45.48%**        | 67.88%**        |
| OEN2       | 44.68%**        | 58.43%**        |
| OEN8       | 43.05% **       | 54.3%**         |

Table 7. Growth of seedlings grown under salt stress conditions. \* = significance at p<0.05 as  
20 compared with WT. \*\* = significance at p<0.01 as compared with WT.

Overexpression of *OsCOBL4*<sub>IRAT109</sub> and *OsCOBL4*<sub>Nipponbare</sub> gave rise to enhanced abiotic stress tolerance in rice plants grown under low-temperature stress conditions

Wild-type Nipponbare lines (WT), T<sub>2</sub>-generation *OsCOBL4*<sub>IRAT109</sub> transgenic Nipponbare  
25 rice lines (OEI) and T<sub>2</sub>-generation *OsCOBL4*<sub>Nipponbare</sub> transgenic Nipponbare rice lines (OEN)

were subjected to drought stress conditions. WT, OEI and OEN seeds were sterilized, germination promoted, and then cultivated in pots, each pot having 15 transgenic plants and 15 WT controls. After growing to 4-leaf stage in a light incubator under normal conditions, the pot was transferred to an artificial climate chamber of 4°C for low-temperature stress treatment, during which the performance was observed, and the change in the membrane permeability was detected. After 3 days of stressing, the normal growth conditions were recovered, and the survival rate was calculated after 7 days. As shown in Figure 17, during the low temperature treatment, the membrane permeability of the WT lines rose more quickly than that of the OEI and OEN lines. Survival rate analysis showed that the survival rate of the OEI6 plants was 56.67%, compared to 15% of that of the WT plants; the survival rate of the OEI8 plants was 65%, compared to 6.67% of that of the WT plants; the survival rate of the OEN2 plants was 43.33%, compared to 6.67% of that of the WT plants; and the survival of the OEN6 plants was 80%, compared to 28.33% of that of the WT plants, indicating that overexpression of both *OsCOBL4<sub>IRAT109</sub>* and *OsCOBL4<sub>Nipponbare</sub>* gave rise to enhanced abiotic stress tolerance (more particularly, enhanced low-temperature stress tolerance).

Thus, it was shown that both *OsCOBL4<sub>IRAT109</sub>* and *OsCOBL4<sub>Nipponbare</sub>* give rise to enhanced abiotic stress tolerance (more particularly, enhanced drought tolerance, enhanced osmotic stress tolerance, enhanced salt stress tolerance and enhanced low-temperature stress tolerance). It was therefore postulated that the genetic differences between *OsCOBL4<sub>IRAT109</sub>* and *OsCOBL4<sub>Nipponbare</sub>* do not significantly influence the anti-abiotic stress properties/performance of the resultant proteins.

#### Part VI. Analysis of reactive oxygen species (ROS) accumulation in *OsCOBL4* transgenic plants

Wild-type Nipponbare lines (WT) and *OsCOBL4<sub>IRAT109</sub>* transgenic Nipponbare rice lines (OEI) were grown in a nutrient solution for 3 weeks were treated with dehydration for 8 h, with 4°C cold for 24 h, or with 150 mmol/L NaCl for 24h , and then analyzed for ROS accumulation by DAB staining. As shown in Fig. 18, after dehydration, low temperature and high salt stress treatments, ROS accumulation in the OEI lines was lower than in the WT lines, indicating that overexpression of *OsCOBL4<sub>IRAT109</sub>* gave rise to a more potent ROS scavenger system, as compared to WT plants.

#### Part VII. Ingredient analysis of cell wall of *COBL4* transgenic plants

It was previously reported that the members of the COBRA gene family are involved in the formation of plant cell walls and the synthesis of cellulose. In order to ascertain whether *OsCOBL4* is involved in the synthesis of plant cell walls, cell walls in the roots of seedlings of wild-type Nipponbare lines (WT) were analyzed, along with cell walls in the roots of seedlings of two T<sub>2</sub>-generation *OsCOBL4*<sub>IRAT109</sub> transgenic Nipponbare rice lines (OEI6, OEI8) and two T<sub>2</sub>-generation *OsCOBL4*<sub>Nipponbare</sub> transgenic Nipponbare rice lines (OEN6, OEN8) at seedling stage were analyzed. As shown in Fig. 19, glucose (Glc), Xylose (Xyl), and cellulose levels were decreased in both OEI plants and OEN plants, whereas the levels of rhamnose (Rha), fucose (Fuc), mannose (Man), galactose (Gal), and arabinose (Ara) were increased, indicating that *OsCOBL4* overexpression may enhance abiotic stress tolerance by effecting the monosaccharide content of plant cell walls.

### Example 3

#### Over-expression of *OsERF62* enhances abiotic stress tolerance

As shown in Figs. 26A–36, overexpression of *OsERF62* gave rise to enhanced abiotic stress tolerance in transgenic rice plants.

#### Part I. Bioinformatic analysis of *OsERF62*

*OsERF62* encodes a protein that comprises 335 amino acids and that has a molecular weight of 35760.44 Da and an isoelectric point of 6.0764. Comparison and analysis of protein homology showed that *OsERF62* has a conservative AP2 domain in the region from positions 110 to 167, which is quite highly homologous to previously reported ERF transcription factors. Fig. 20. The amino acids at positions 14 and 19 in the conservative domain are alanine (A) and aspartic acid (D), respectively, which is a feature typical of ERF transcription factors.

#### Part II. *OsERF62* expression was upregulated in rice exposed to abiotic stress conditions

Water-cultured three-week-old seedlings of upland rice variety IRAT109 and lowland rice variety Nipponbare were subjected to the following abiotic stress treatments: PEG treatment (roots were soaked in 200 g/L polyethylene glycol (PEG6000) aqueous solution for 1, 2, 4, 6, 9, 12 or 24 hours); dehydration treatment (roots were left in the air for 1, 2, 4, 6, 9, 12 or 24 hours); salt treatment (roots were soaked in 200 mM NaCl for 1, 2, 4, 6, 9, 12 or 24 hours); cold treatment (seedlings were transferred to an artificial climate chamber of 4°C for 1, 2, 4, 6, 9, 12

or 24 hours); H<sub>2</sub>O<sub>2</sub> treatment (roots were soaked in 1 mM H<sub>2</sub>O<sub>2</sub> solution and left in the air 1, 2, 4, 6, 9, 12 or 24 hours); ABA treatment (roots were soaked in 100 μM ABA solution and cultured under illumination for 1, 2, 4, 6, 9, 12 or 24 hours); ethylene treatment (roots were soaked in 1mM ethylene for 1, 2, 4, 6, 9, 12 or 24 hours); GA treatment (roots were soaked in 100 μM GA for 1, 2, 4, 6, 9, 12 or 24 hours); or control treatment (roots remained in water culture). Following treatment, leaves were collected and quickly frozen using liquid nitrogen and stored at -80°C for further use.

Total RNA was extracted from the harvested leaves and the relative expression levels of *OsERF62* and *Actin* were calculated as described above in Example 1, Part I.

As shown in Fig. 21, the expression of *OsERF62* in both IRAT109 and Nipponbare rice plants was upregulated in response to each of the abiotic stress treatments, indicating that *OsERF62* is associated with one or more abiotic stress responses. *OsERF62* expression gradually increased in both Nipponbare and IRAT109 4 h after stress treatment with 20% PEG, and reached the highest respectively at 6 h in Nipponbare (24.86 times) and at 9 h in IRAT109 (12.72 times). *OsERF62* expression gradually increased in both Nipponbare and IRAT109 4 h after dehydration stress treatment, and reached the highest at 8 h (8.69 times in Nipponbare and 12.71 times in IRAT109). *OsERF62* expression gradually increased in both Nipponbare and IRAT109 2 h after stress treatment with NaCl, and reached the highest at 6 h (22.29 times in Nipponbare and 16.74 times in IRAT109). *OsERF62* expression increased in both Nipponbare and IRAT109 2 h after stress treatment with H<sub>2</sub>O<sub>2</sub>, reached a peak at 9 h in Nipponbare (8.89 times) followed by a gradual decrease, and reached a peak at 6 h in IRAT109 followed by a gradual decrease (6.12 times). *OsERF62* expression gradually increased in both Nipponbare and IRAT109 2 h after treatment with ABA, and reached the highest at 6 h (3.35 times in Nipponbare and 3.02 times in IRAT109). *OsERF62* expression in Nipponbare was up-regulated 1 h after treatment with ethylene, and reached the highest at 9 h (209.54 times), and increased at 2 h in IRAT109 and reached the highest at 9 h (202.19 times). Under treatment with GA, the expression was remarkably up-regulated at 9 h in Nipponbare (209.95 times), and was started to inductively express at 4 h, and reached the highest at 9 h (225.41 times) in IRAT109. These results suggest that *OsERF62* is strongly inductively expressed in both Nipponbare and IRAT109 in response to abiotic stress conditions, particularly drought stress conditions, osmotic stress conditions and salt stress conditions.

### Part III. Expression analysis of *OsERF62* in various tissues of plants

Reverse transcription of RNA extracted from the roots, stems, sheaths, leaves and panicles

of upland rice variety IRAT109 and lowland rice variety Nipponbare showed that *OsERF62* was maximally expressed in the root at both the seedling and reproductive stages, and was minimally expressed in the sheath and leaf at the seedling stage. Fig. 22.

#### 5 Part IV. Subcellular localization analysis of *OsERF62*

*OsERF62* was ligated into a pMDC83 vector to produce an *OsERF62*-GFP expression vector. GFP was located at C-terminus of the *OsERF62* protein. The vector was transformed into onion epithelial cells through particle bombardment. A relatively strong fluorescence signal was  
10 observed in the nuclei under confocal laser scanning microscope (Fig. 23), indicating that *OsERF62* is a nuclei protein, which is consistent with its proposed role as a transcription factor.

#### Part V. Analysis of transactivation activity and domain of *OsERF62* protein

15 For analyzing the transactivation activity and domain of *OsERF62* protein, full-length and deletion ORF fragments of *OsERF62* were constructed into a yeast expression vector pGBKT7, and for determining the activation domain of *OsERF62* protein, the AP2 domain of *OsERF62* was divided into five regions based on the positions thereof—A1: full-length, 335 aa; A2: 1-106 aa; A3: 1-167 aa; A4: 162-335 aa; A5: 230-335aa—which were fused to the yeast GAL4BD  
20 fusion expression vector pGBKT7, and then used to transform the yeast strain AH109. Fig. 24A. As shown in Figs. 24B–24D, yeasts transformed with A1, A4, A5 and positive vectors grew normally on SD/-Trp-His-Ade/X-á-gal plate and developed a blue appearance, while the yeasts transformed with A2, A3, and negative control failed to grow normally. These results suggest that *OsERF62* had transactivation activity and that the transactivation domain of *OsERF62* is  
25 located in a region from positions 230 to 335 at C-terminus of the protein sequence.

#### Part VI. Response of *OsERF62* OE and suppression expression transgenic plants to abiotic stress

30 For further determining the role and functions of *OsERF62* under abiotic stress conditions, *OsERF62* overexpression and *OsERF62* RNAi vectors were constructed and transformed into the lowland rice variety Nipponbare through *Agrobacterium*-mediated transformation to produce *OsERF62* transgenic Nipponbare rice lines (OE) and *OsERF62*-RNAi transgenic Nipponbare rice lines (RI). Quantitative PCR analysis showed that five transformation events of significantly  
35 increased expression occurred in ten individual OE transgenic plants (Fig. 25A), and that seven

transformation events of significantly decreased expression occurred in 14 individual RNA-interference plants (Fig. 25B). The OE plants having the highest expression (OE4, OE7) and the RNA-interference plants having the lowest expression (RI6, RI10) were selected for subsequent experimental analysis.

5

Overexpression of *OsERF62* gave rise to enhanced abiotic stress tolerance in rice plants grown under simulated drought stress conditions

Wild-type Nipponbare lines (WT) and T<sub>2</sub>-generation *OsERF62* transgenic Nipponbare rice lines (OE) were subjected to PEG-simulated drought stress conditions as described in Example 1, Part VII. As shown in Figs. 26A–26B and Table 8 below, the survival rates of the OE lines were significantly higher than that of WT lines, indicating that overexpression of *OsERF62* gave rise to enhanced abiotic stress tolerance (more particularly, enhanced drought stress tolerance).

10

| Plant Line | Survival Rate |
|------------|---------------|
| OE4        | 90%**         |
| WT         | 33.33%%       |
| OE7        | 62.22%**      |
| WT         | 10%           |

Table 8. Survival rates of seedlings grown under PEG-simulated drought stress conditions.

15

\*\* = significance at  $p < 0.01$  as compared with WT.

Drought stress tolerance of *OsERF62* OE and RNAi transgenic plants at seedling stage

Wild-type Nipponbare lines (WT), T<sub>2</sub>-generation *OsERF62* transgenic Nipponbare rice lines (OE) and T<sub>2</sub>-generation *OsERF62-RNAi* transgenic Nipponbare rice lines (RI) were subjected to drought stress conditions as described in Example 1, Part IX. As shown in Figs. 27A–27D and Table 9 below, the survival rates of the OE lines were significantly higher than that of WT lines, while the survival rates of the RI lines were significantly lower than that of the WT lines, indicating that overexpression of *OsERF62* gave rise to enhanced abiotic stress tolerance (more particularly, enhanced drought stress tolerance). These results suggest that suppression of *OsERF62* expression may attenuate a plant's drought stress response(s).

20

25

|         | Plant Line | Survival Rate |
|---------|------------|---------------|
| Group 1 | OE4        | 73.33%**      |
|         | WT         | 28.33%        |

|         |      |          |
|---------|------|----------|
| Group 2 | OE7  | 46.637%* |
|         | WT   | 21.67%   |
| Group 3 | RI4  | 20%**    |
|         | WT   | 80%      |
| Group 4 | RI10 | 12.22%*  |
|         | WT   | 58.33%   |

Table 9. Survival rates of seedlings grown under drought stress conditions. \* = significance at p<0.05 as compared with WT. \*\* = significance at p<0.01 as compared with WT.

5        Salt stress tolerance assay of OsERF62 OE and RNAi transgenic plants

Wild-type Nipponbare lines (WT), T<sub>2</sub>-generation *OsERF62* transgenic Nipponbare rice lines (OE) and T<sub>2</sub>-generation *OsERF62-RNAi* transgenic Nipponbare rice lines (RI) were subjected to salt stress conditions as described in Example 2, Part V. As shown in Figs. 28A–28C and Table 10 below, both the plant heights and fresh weights of the OE lines were significantly higher than that of WT lines and RI lines, indicating that overexpression of *OsERF62* gave rise to enhanced abiotic stress tolerance (more particularly, enhanced drought stress tolerance). These results suggest that suppression of *OsERF62* expression may attenuate a plant's salt stress response(s).

|            |                 |                 |
|------------|-----------------|-----------------|
| Plant Line | Relative Height | Relative Weight |
| WT         | 32.38%          | 53.53%          |
| OE4        | 36.01%*         | 63.29%**        |
| OE7        | 38.86%**        | 58.77%*         |
| RI6        | 30.84%          | 46.63%**        |
| RI10       | 29.18%*         | 35.2%**         |

Table 10. Growth of seedlings grown under salt stress conditions. \* = significance at p<0.05 as compared with WT. \*\* = significance at p<0.01 as compared with WT.

20        High osmotic stress tolerance assay of OsERF62 OE, and RNAi transgenic plants

Wild-type Nipponbare lines (WT), T<sub>2</sub>-generation *OsERF62* transgenic Nipponbare rice lines (OE) and T<sub>2</sub>-generation *OsERF62-RNAi* transgenic Nipponbare rice lines (RI) were subjected to osmotic stress conditions as described in Example 1, Part VIII. As shown in Figs. 29A–29C and Table 11 below, both the plant heights and fresh weights of the OE lines were

significantly higher than that of WT lines and RI lines, indicating that overexpression of *OsERF62* gave rise to enhanced abiotic stress tolerance (more particularly, enhanced osmotic stress tolerance). These results suggest that suppression of *OsERF62* expression may attenuate a plant's osmotic stress response(s).

5

| Plant Line | Relative Height | Relative Weight |
|------------|-----------------|-----------------|
| WT         | 61.35%          | 83.04%          |
| OE4        | 63.97%          | 88.24%          |
| OE7        | 70.03%**        | 99.15%**        |
| RI6        | 58.51%*         | 71.11%**        |
| RI10       | 55.54%*         | 57.22%**        |

Table 11. Growth of seedlings grown under mannitol-induced osmotic stress conditions.

\*\* = significance at  $p < 0.01$  as compared with WT.

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*ABA sensitivity assay of OsERF62 OE and RNAi transgenic plants at seedling stage*

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It was observed that the expression of *OsERF62* was induced by ABA. Therefore, for analyzing the function of *OsERF62* in ABA signaling pathway, ABA sensitivity tests of wild-type Nipponbare lines (WT),  $T_2$ -generation *OsCOBL4<sub>IRAT109</sub>* transgenic Nipponbare rice lines (OE) and were conducted at seedling stage. The seeds of WT plants and homozygous OE plants were unshelled and sterilized, then cultivated in 1/2 MS medium containing 0, 2, 3, and 5  $\mu$ M ABA for 7 d. The germination rates were calculated. In the presence of ABA, the germination rate of the *OsERF62*-OE plants was higher than that of the control. Fig. 30A–30C. The seedlings of WT plants, OE plants and RI plants that were normally germinated in 1/2MS medium for 2-3 d and had the uniform growth status were transferred to 1/2 MS medium containing 0 and 3  $\mu$ M ABA, grown in a light incubator for 7 d, and then measured for the shoot length and fresh weight. As shown in Fig. 30B, at 0  $\mu$ M ABA, there was no obvious difference in growing performances between the WT plants and the OE plants. However, in the medium containing 3  $\mu$ M ABA, the relative shoot length of the *OsERF62*-OE plants was 20.78%-25.87%, and the relative fresh weight was 33.75%-42.21%; while the relative shoot length of the WT was 29.78%, and the relative fresh weight was 44.84%; and the relative shoot length of the *OsERF62*-RI plants was 20.78%-25.87%, and the relative fresh weight was 33.75%-42.21%. These results suggest that overexpression of *OsERF62* may reduce the sensitivity of plants to ABA at germination stage, and that suppression of *OsERF62* expression may increase the sensitivity of transgenic plants to ABA.

Water loss assay of *OsERF62* OE, and *RNAi* transgenic plants

A direct behavior in response of the plants to drought stress is to effectively reduce the water loss in plants under drought conditions. For further analyzing the contribution of *OsERF62* to abiotic stress tolerance (particularly drought stress tolerance), water loss was analyzed in detached leaves of wild-type Nipponbare lines (WT), T<sub>2</sub>-generation *OsERF62* transgenic Nipponbare rice lines (OE) and T<sub>2</sub>-generation *OsERF62-RNAi* transgenic Nipponbare rice lines (RI). As shown in Fig. 31, water loss was lowest in the leaves of OE plants and highest in the leaves of RI plants. The ability to reduce water loss might partly account for the contribution of *OsERF62* to enhanced abiotic stress tolerance (particularly, enhanced drought stress tolerance) in plants.

Part VII. Oxidative stress tolerance assay of *OsERF62* OE and suppression expression transgenic plants

Under drought stress, reactive oxygen species (ROS) such as O<sup>•</sup> and H<sub>2</sub>O<sub>2</sub> were accumulated in plants, and excessive accumulation of ROS could lead to oxidative stress (Miller *et al.*, 2010; Zhu, 2001). *OsERF62* was strongly induced to express by H<sub>2</sub>O<sub>2</sub>, and the tolerance to drought stress of transgenic plants over-expressing *OsERF62* was improved. In order to analyze the effect of *OsERF62* on ROS accumulation, ROS accumulations in wild-type Nipponbare lines (WT), T<sub>2</sub>-generation *OsERF62* transgenic Nipponbare rice plants (OE) and T<sub>2</sub>-generation *OsERF62-RNAi* transgenic Nipponbare rice plants (RI) were detected under dehydration and simulated stress with 20% PEG treatment. Plants normally grown for 3 weeks were dehydrated for 6 h, and then treated in a nutrient solution containing 20% PEG for 24 h. After treatment, the leaves were subjected to DAB staining, then decolorized, and observed. Untreated plants were used as a control. As shown in Fig. 32, in the absence of stress, all the background levels of H<sub>2</sub>O<sub>2</sub> in the WT, OE and RI plants were quite low, and after dehydration and stress treatment with 20% PEG, the leaves of the RI plants were deepest colored and the leaves of OE plants were least colored. These results suggest that that overexpression of *OsERF62* may reduce the accumulation of ROS under abiotic stress conditions (particularly drought stress conditions), thereby reducing harm to the plant.

Excessive accumulation of H<sub>2</sub>O<sub>2</sub> could lead to oxidative stress, thereby destroying the life cycle of the cells. The results above showed that overexpression of *OsERF62* may reduce the accumulation of H<sub>2</sub>O<sub>2</sub> in plants under abiotic stress conditions (particularly drought stress conditions), thereby avoiding serious damage caused by ROS.

To find out what role *OsERF62* plays in oxidative stress, the performance of OE plants and RI plants under oxidative stress was also investigated. Seedlings of WT plants, OE plants, and RI plants that were normally germinated in 1/2MS MS medium for 2-3 d and had uniform growth status were transferred to 1/2MS medium containing 0 or 2 mM MV and grown for 7 d. Then the shoot length and fresh weight were measured. As shown in Fig. 33, under treatment with MV, the relative shoot length of OE plants was higher than that of WT and RI plants; likewise, the relative fresh weight of OE plants was also significantly higher than that of WT and RI plants, indicating that overexpression of *OsERF62* gave rise to enhanced abiotic stress tolerance (more particularly, enhanced oxidative stress tolerance).

Under drought stress, the ROS content accumulated in OE transgenic plants is lower than that in WT plants, and is higher in RI plants than that in WT plants. Therefore, it was postulated that *OsERF62* reduced the ROS accumulated in the plants by regulating the expression of one or more ROS scavenge-related genes. To verify the postulation, ROS scavenge related genes were analyzed, including *APX1*, *APX2*, *catB*, *DSM*, *POD1* and *POD2*. As shown in Fig. 34, although there was no significant change in *DSM* 1 expression, the expression levels of *APX1*, *APX2*, *catB*, *POD1*, and *POD2* in OE plants were significantly higher than in WT plants, and were slightly lower in RI plants than that in WT plants. These results suggest that overexpression of *OsERF62* may reduce the accumulation of ROS in plants by regulating the expression of ROS scavenge related gene, thereby alleviating the damage of drought stress to plants.

#### Part VIII. *OsERF62* affected emission of ethylene from rice

Ethylene plays an important role in regulating the drought tolerance of plants. *OsERF62* expression was strongly induced by ethylene (Example 3, Part II), and previously reported ERF genes, such as *OsERF3*, *DERF1*, and *SERF1*, respond to ethylene. To determine whether the improvements in abiotic stress tolerance caused by *OsERF62* overexpression are correlated with the anti-drought pathway regulated by ethylene, the ethylene emissions from wild-type Nipponbare lines (WT), T<sub>2</sub>-generation *OsERF62* transgenic Nipponbare rice plants (OE) and T<sub>2</sub>-generation *OsERF62-RNAi* transgenic Nipponbare rice plants (RI) were analyzed.

Seedlings germinated for 3 d in a normal medium were transferred to a glass tube (diameter: 4.8 cm; height: 14.8 cm) containing 50 ml 1/2 MS medium (10 plants each), grown for 7 d, and then sealed for 24 h. The emission of ethylene from the plants was determined by high resolution gas chromatography. An empty tube without rice was used as a control. For more intuitively expressing the difference in the biosynthesis of ethylene between WT and the transgenic plants, the biosynthesis of ethylene in WT was designated as a reference value of 100, with which the

biosynthesis of ethylene from the transgenic plants was compared, the production of ethylene from the plants being represented by relative ethylene biosynthesis. As shown in Fig. 35, the emission of ethylene from OE plants was higher than that of WT plants, and the emission of ethylene from RI plants was lower than that of WT plants. The relative emissions of ethylene from OE4 and OE7 transgenic plants were 139.22 and 174.6, and were 73.9 and 89.66 from RI6 and RI10 suppression expression plants, indicating that *OsERF62* is involved in the regulation of the biosynthesis of ethylene in rice.

Because *OsERF62* was strongly induced to express in both Nipponbare and IRAT109 by ethylene, and because over expression of *OsERF62* could improve the emission of ethylene from the transgenic plants, the expression of ethylene biosynthesis related genes *ACO2*, *ACO3*, *ASC2*, and *ASC6* were analyzed. As shown in Fig. 36, the expressions of *ACO3* and *ASC6* in OE plants were improved, and were decreased in RI. These results suggest that *OsERF62* might affect the biosynthesis of ethylene by regulating the expressions of ethylene biosynthesis related genes *ACO3* and *ASC6*, thereby regulating the drought tolerance of the plant.

The foregoing is illustrative of the present invention and is not to be construed as limiting thereof. Although a few exemplary embodiments of this invention have been described, those skilled in the art will readily appreciate that many modifications are possible in the exemplary embodiments without materially departing from the novel teachings and advantages of this invention. Accordingly, all such modifications are intended to be included within the scope of the present invention.

## CLAIMS

1. A plant or plant part having within its genome an exogenous nucleic acid that  
5 comprises:
- (a) the nucleotide sequence set forth in SEQ ID NO: IRAT1091;
  - (b) the nucleotide sequence set forth in SEQ ID NO: IRAT1092;
  - (c) the nucleotide sequence set forth in SEQ ID NO: IRAT1093;
  - (d) the nucleotide sequence set forth in SEQ ID NO: 4;
  - 10 (e) the nucleotide sequence set forth in SEQ ID NO: 5;
  - (f) the nucleotide sequence set forth in SEQ ID NO: 6;
  - (g) the nucleotide sequence set forth in SEQ ID NO: 7;
  - (h) the nucleotide sequence set forth in SEQ ID NO: 8;
  - (i) the nucleotide sequence set forth in SEQ ID NO: 9;
  - 15 (j) the nucleotide sequence set forth in SEQ ID NO: 10;
  - (k) the nucleotide sequence set forth in SEQ ID NO: 11;
  - (l) the nucleotide sequence set forth in SEQ ID NO: 12;
  - (m) the nucleotide sequence set forth in SEQ ID NO: 13;
  - (n) the nucleotide sequence set forth in SEQ ID NO: 14;
  - 20 (o) the nucleotide sequence set forth in SEQ ID NO: 15;
  - (p) the nucleotide sequence set forth in SEQ ID NO: 16;
  - (q) the nucleotide sequence set forth in SEQ ID NO: 17;
  - (r) the nucleotide sequence set forth in SEQ ID NO: 18;
  - (s) the nucleotide sequence set forth in SEQ ID NO: 19;
  - 25 (t) the nucleotide sequence set forth in SEQ ID NO: 20;
  - (u) the nucleotide sequence set forth in SEQ ID NO: 21;
  - (v) the nucleotide sequence set forth in SEQ ID NO: 22;
  - (w) the nucleotide sequence set forth in SEQ ID NO: 23;
  - (x) the nucleotide sequence set forth in SEQ ID NO: 24;
  - 30 (y) the nucleotide sequence set forth in SEQ ID NO: 25;
  - (z) the nucleotide sequence set forth in SEQ ID NO: 26;
  - (aa) the nucleotide sequence set forth in SEQ ID NO: 27;
  - (bb) a nucleotide sequence that is at least 95% identical to the nucleotide sequence of  
any one of (a) to (aa) above;

(cc) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 28–3528;

(dd) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 29;

5 (ee) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 30;

(ff) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 31;

10 (gg) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 32;

(hh) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 33;

(ii) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 34;

15 (jj) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 35;

(kk) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 36;

20 (ll) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 37;

(mm) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 38;

(nn) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 39;

25 (oo) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 40;

(pp) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 41;

30 (qq) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 42;

(rr) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 43;

(ss) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 44;

(tt) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: IRAT10928–44;

(uu) a nucleotide sequence that is complementary to the nucleotide sequence of any one of (a) to (tt) above;

(vv) a nucleotide sequence that hybridizes to the nucleotide sequence of any one of (a) to (uu) above under stringent hybridization conditions;

(ww) a functional fragment of any one of (a) to (vv) above, wherein the functional fragment encodes a polypeptide that comprises an N-terminal signal peptide sequence that is at least 95% identical to amino acids 1 to 27 of SEQ ID NO: 28–3528 and a CCVS domain that is at least 95% identical to amino acids 226 to 229 of SEQ ID NO: 28–3528; and/or

(xx) a functional fragment of any one of (a) to (vv) above, wherein the functional fragment encodes a polypeptide that comprises an AP2 domain that is at least 95% identical to amino acids 110 to 167 of SEQ ID NO: 36.

15

2. The plant or plant part of claim 1, wherein the exogenous nucleic acid further comprises a tissue-specific promoter sequence, optionally a leaf-, ligule-, node-, panicle-, root-, sheath-, stem-, and/or vascular bundle-specific promoter sequence.

20

3. The plant or plant part of any one of claims 1 to 2, wherein the exogenous nucleic acid is expressed in a leaf, ligule, node, panicle, root, sheath, stem, and/or vascular bundle of the plant or plant part.

25

4. The plant or plant part of any one of claims 1 to 3, wherein the exogenous nucleic acid further comprises a stress-inducible promoter sequence, optionally a drought stress-, osmotic stress-, salt stress- and/or temperature stress-inducible promoter sequence.

30

5. The plant or plant part of any one of claims 1 to 4, wherein the exogenous nucleic acid further comprises a developmental stage-specific promoter sequence, optionally a promoter sequence that drives expression prior to and/or during the seedling and/or reproductive stage(s) of development.

6. The plant or plant part of any one of claims 1 to 5, wherein the exogenous nucleic acid comprises codons specific for expression in plants.

35

7. The plant or plant part of any one of claims 1 to 6, wherein the plant or plant part further comprises a transgene that encodes a gene product that provides resistance to one or more herbicides, optionally glyphosate-, sulfonylurea-, imidazolinone-, dicamba-, glufisinate-, phenoxy proprionic acid-, cyclohexime-, triazine-, benzonitrile-, and/or broxynil-resistance.

8. The plant or plant part of any one of claims 1 to 7, wherein the plant or plant part further comprises a transgene that encodes a gene product that provides resistance to one or more pests, optionally bacterial-, fungal, gastropod-, insect-, nematode-, oomycete-, phytoplasma-, protozoa-, and/or viral-resistance.

9. The plant or plant part of any one of claims 1 to 8, wherein the plant or plant part further comprises a transgene that encodes a gene product that provides resistance to one or more diseases.

10. The plant or plant part of any one of claims 1 to 9, wherein the plant or plant part expresses a protein encoded by the exogenous nucleic acid at an elevated level as compared to a control plant or plant part of the same species grown under the same environmental conditions.

11. The plant or plant part of any one of claims 1 to 10, wherein the plant or plant part exhibits enhanced abiotic stress tolerance relative to a control plant or plant part of the same species grown under the same environmental conditions, optionally enhanced drought stress tolerance, enhanced osmotic stress tolerance, enhanced salt stress tolerance and/or enhanced temperature stress tolerance.

12. The plant or plant part of claim 11, wherein enhanced abiotic stress tolerance comprises decreased water loss, decreased accumulation of one or more reactive oxygen species, decreased accumulation of one or more salts, increased salt excretion, increased accumulation of one or more dehydrins, improved root architecture, improved osmotic pressure regulation, increased accumulation of one or more late embryogenesis abundant proteins, increased survival rate, increased growth rate, increased height, increased chlorophyll content and/or increased yield (e.g., increased biomass, increased seed yield, increased grain yield at standard moisture percentage (YGSMN), increased grain moisture at harvest (GMSTP), increased grain weight per plot (GWTPN), increased percent yield recovery (PYREC), decreased yield reduction (YRED), and/or decreased percent barren (PB)) relative to the control plant or plant part.

13. The plant or plant part of any one of claims 1 to 12, wherein the plant or plant part exhibits increased yield relative to a control plant or plant part of the same species grown under the same environmental conditions, optionally increased seed yield and/or increased biomass.

5 14. The plant or plant part of claim 13, wherein the seed yield and/or biomass of the plant or plant part is increased by at least about 20% relative to the control plant or plant part.

10 15. The plant or plant part of any one of claims 1 to 14, wherein the plant or plant part exhibits increased grain yield at standard moisture percentage (YGSMN), increased grain weight per plot (GWTPN), increased percent yield recovery (PYREC), decreased yield reduction (YRED), and/or decreased percent barren (PB) relative to a control plant or plant part of the same species grown under the same environmental conditions.

15 16. The plant or plant part of claim 15, wherein the YGSMN, GWTPN and/or PYREC of the plant or plant part is increased by at least about 20% relative to the control plant or plant part.

20 17. The plant or plant part of any one of claims 15 to 16, wherein the YRED and/or PB of the plant or plant part is decreased by at least about 20% relative to the control plant or plant part.

18. The plant or plant part of any one of claims 1 to 17, wherein the plant or plant part is a monocot.

25 19. The plant or plant part of claim 18, wherein the monocot is rice, maize, wheat, barley, oats, rye, millet, sorghum, triticale, secale, einkorn, spelt, emmer, teff, milo, flax, gramma grass, *Tripsacum sp.*, or teosinte.

30 20. The plant or plant part of any one of claims 1 to 19, wherein the plant or plant part is a dicot.

21. The plant or plant part of claim 20, wherein the dicot is cotton, potato, soybean, sugar beet, sunflower, tobacco or tomato.

35 22. A nonnaturally occurring nucleic acid, comprising:

- (a) the nucleotide sequence set forth in SEQ ID NO: 1;
- (b) the nucleotide sequence set forth in SEQ ID NO: 2;
- (c) the nucleotide sequence set forth in SEQ ID NO: 3;
- (d) the nucleotide sequence set forth in SEQ ID NO: 4;
- 5 (e) the nucleotide sequence set forth in SEQ ID NO: 5;
- (f) the nucleotide sequence set forth in SEQ ID NO: 6;
- (g) the nucleotide sequence set forth in SEQ ID NO: 7;
- (h) the nucleotide sequence set forth in SEQ ID NO: 8;
- (i) the nucleotide sequence set forth in SEQ ID NO: 9;
- 10 (j) the nucleotide sequence set forth in SEQ ID NO: 10;
- (k) the nucleotide sequence set forth in SEQ ID NO: 11;
- (l) the nucleotide sequence set forth in SEQ ID NO: 12;
- (m) the nucleotide sequence set forth in SEQ ID NO: 13;
- (n) the nucleotide sequence set forth in SEQ ID NO: 14;
- 15 (o) the nucleotide sequence set forth in SEQ ID NO: 15;
- (p) the nucleotide sequence set forth in SEQ ID NO: 16;
- (q) the nucleotide sequence set forth in SEQ ID NO: 17;
- (r) the nucleotide sequence set forth in SEQ ID NO: 18;
- (s) the nucleotide sequence set forth in SEQ ID NO: 19;
- 20 (t) the nucleotide sequence set forth in SEQ ID NO: 20;
- (u) the nucleotide sequence set forth in SEQ ID NO: 21;
- (v) the nucleotide sequence set forth in SEQ ID NO: 22;
- (w) the nucleotide sequence set forth in SEQ ID NO: 23;
- (x) the nucleotide sequence set forth in SEQ ID NO: 24;
- 25 (y) the nucleotide sequence set forth in SEQ ID NO: 25;
- (z) the nucleotide sequence set forth in SEQ ID NO: 26;
- (aa) the nucleotide sequence set forth in SEQ ID NO: 27;
- (bb) a nucleotide sequence that is at least 95% identical to the nucleotide sequence of  
any one of (a) to (aa) above;
- 30 (cc) a nucleotide sequence that encodes a polypeptide comprising the amino acid  
sequence set forth in SEQ ID NO: 28;
- (dd) a nucleotide sequence that encodes a polypeptide comprising the amino acid  
sequence set forth in SEQ ID NO: 29;
- (ee) a nucleotide sequence that encodes a polypeptide comprising the amino acid  
35 sequence set forth in SEQ ID NO: 30;

- (ff) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 31;
- (gg) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 32;
- 5 (hh) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 33;
- (ii) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 34;
- (jj) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 35;
- 10 (kk) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 36;
- (ll) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 37;
- 15 (mm) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 38;
- (nn) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 39;
- (oo) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 40;
- 20 (pp) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 41;
- (qq) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 42;
- 25 (rr) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 43;
- (ss) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 44;
- (tt) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 28–44;
- 30 (uu) a nucleotide sequence that is complementary to the nucleotide sequence of any one of (a) to (tt) above;
- (vv) a nucleotide sequence that hybridizes to the nucleotide sequence of any one of (a) to (uu) above under stringent hybridization conditions;
- 35

- (ww) a functional fragment of any one of (a) to (vv) above, wherein the functional fragment encodes a polypeptide that comprises an N-terminal signal peptide sequence that is at least 95% identical to amino acids 1 to 27 of SEQ ID NO: 28 and a CCVS domain that is at least 95% identical to amino acids 226 to 229 of SEQ ID NO: 28; and/or
- (xx) a functional fragment of any one of (a) to (vv) above, wherein the functional fragment encodes a polypeptide that comprises an AP2 domain that is at least 95% identical to amino acids 110 to 167 of SEQ ID NO: 36.

23. The nonnaturally occurring nucleic acid of claim 22, further comprising a tissue-specific promoter sequence, optionally a leaf-, ligule-, node-, panicle-, root-, sheath-, stem-, and/or vascular bundle-specific promoter sequence.

24. The nonnaturally occurring nucleic acid of any one of claims 22 to 23, further comprising a stress-inducible promoter sequence, optionally a drought stress-, osmotic stress-, salt stress- and/or temperature stress-inducible promoter sequence.

25. The nonnaturally occurring nucleic acid of any one of claims 22 to 24, further comprising a developmental stage-specific promoter sequence, optionally a promoter sequence that drives expression prior to and/or during the seedling and/or reproductive stage(s) of development.

26. The nonnaturally occurring nucleic acid of any one of claims 22 to 25, further comprising a transgene that encodes a gene product that provides resistance to one or more herbicides, optionally glyphosate-, sulfonylurea-, imidazolinione-, dicamba-, glufisinate-, phenoxy proprionic acid-, cyclohexime-, triazine-, benzonitrile-, and/or broxynil-resistance.

27. The nonnaturally occurring nucleic acid of any one of claims 22 to 26, further comprising a transgene that encodes a gene product that provides resistance to one or more pests, optionally bacterial-, fungal, gastropod-, insect-, nematode-, oomycete-, phytoplasma-, protozoa- and/or viral-resistance.

28. The nonnaturally occurring nucleic acid of any one of claims 22 to 27, further comprising a transgene that encodes a gene product that provides resistance to one or more diseases.

29. The nonnaturally occurring nucleic acid of any one of claims 22 to 28, wherein the nonnaturally occurring nucleic acid comprises codons specific for expression in plants.

5 30. The nonnaturally occurring nucleic acid of any one of claims 22 to 29, wherein the nonnaturally occurring nucleic acid is expressed in a leaf, ligule, node, panicle, root, sheath, stem, and/or vascular bundle of a plant.

10 31. An expression cassette comprising the nonnaturally occurring nucleic acid of any one of claims 22 to 30.

32. A vector comprising the nonnaturally occurring nucleic acid of any one of claims 22 to 30.

15 33. A vector comprising the expression cassette of claim 31.

34. A use of the nonnaturally occurring nucleic acid of any one of claims 22 to 30 for enhancing abiotic stress tolerance in a plant or plant part, optionally drought stress tolerance, osmotic stress tolerance, salt stress tolerance and/or temperature stress tolerance.

20 35. A use of the expression cassette of claim 31 for enhancing abiotic stress tolerance in a plant or plant part, optionally drought stress tolerance, osmotic stress tolerance, salt stress tolerance and/or temperature stress tolerance.

25 36. A use of the vector of any one of claims 32 to 33 for enhancing abiotic stress tolerance in a plant or plant part, optionally drought stress tolerance, osmotic stress tolerance, salt stress tolerance and/or temperature stress tolerance.

30 37. The use of any one of claims 34 to 36, wherein enhancing abiotic stress tolerance comprises decreasing water loss, decreasing accumulation of one or more reactive oxygen species, decreasing accumulation of one or more salts, increased salt excretion, increased accumulation of one or more dehydrins, improving root architecture, improving osmotic pressure regulation, increasing accumulation of one or more late embryogenesis abundant proteins, increasing survival rate, increasing growth rate, increasing height, increasing chlorophyll content  
35 and/or increasing yield (e.g., increasing biomass, increasing seed yield, increasing grain yield at

standard moisture percentage (YGSMN), increasing grain moisture at harvest (GMSTP), increasing grain weight per plot (GWTPN), increasing percent yield recovery (PYREC), decreasing yield reduction (YRED), and/or decreasing percent barren (PB)) relative to the control plant or plant part.

5

38. The use of claim 37, wherein the drought stress tolerance, osmotic stress tolerance, salt stress tolerance and/or temperature stress tolerance of the plant or plant part is increased by at least about 20% relative to the control plant or plant part.

10

39. The use of any one of claims 34 to 38, wherein the yield of the plant or plant part is increased as compared to a control plant or plant part of the same species grown under the same environmental conditions.

15

40. The use of claim 39, wherein the seed yield and/or biomass of the plant or plant part is increased by at least about 20% relative to the control plant or plant part.

20

41. The use of any one of claims 34 to 40, wherein the plant or plant part exhibits increased grain yield at standard moisture percentage (YGSMN), increased grain weight per plot (GWTPN), increased percent yield recovery (PYREC), decreased yield reduction (YRED), and/or decreased percent barren (PB) as compared to a control plant or plant part of the same species grown under the same environmental conditions.

25

42. The use of claim 41, wherein the YGSMN, GWTPN and/or PYREC of the plant or plant part is increased by at least about 20% relative to the control plant or plant part.

43. The use of any one of claims 41 to 42, wherein the YRED and/or PB of the plant or plant part is decreased by at least about 20% relative to the control plant or plant part.

30

44. The use of any one of claims 34 to 43, wherein the use comprises:  
transforming a plant cell with the nonnaturally occurring nucleic acid of any one of claims 22 to 30; and  
growing the transformed plant cell into the plant or plant part.

35

45. The use of any one of claims 34 to 43, wherein the use comprises:  
transforming a plant cell with the expression cassette of claim 31; and

growing the transformed plant cell into the plant or plant part.

46. The use of any one of claims 34 to 43, wherein the use comprises:  
transforming a plant cell with the vector of any one of claims 32 to 34; and  
growing the transformed plant cell into the plant or plant part.

47. The use of any one of claims 44 to 46 as it depends from any one of claims 37 to 43, further comprising selecting the plant or plant part based upon the increased yield of the plant or plant part.

48. The use of any one of claims 44 to 46 as it depends from any one of claims 41 to 43, further comprising selecting the plant or plant part based upon the increased YGSMN, increased GWTPN, increased PYREC, decreased YRED and/or decreased PB of the plant or plant part.

49. The use of any one of claims 34 to 48, wherein the plant is a monocot.

50. The use of any one of claims 34 to 48, wherein the plant is rice, maize, wheat, barley, oats, rye, millet, sorghum, buckwheat, fonio, quinoa, sugar cane, bamboo, durum, kamut, triticale, secale, einkorn, spelt, emmer, teff, milo, flax, banana, ginger, onion, lily, daffodil, iris, amaryllis, orchid, canna, bluebell, tulip, garlic, gramma grass, *Tripsacum sp.*, or teosinte.

51. The use of any one of claims 34 to 48, wherein the plant is a dicot.

52. The use of any one of claims 34 to 48, wherein the plant is soybean, tobacco, sunflower or cotton.

53. A method of identifying a plant or plant part having enhanced abiotic stress tolerance as compared to a control plant or plant part, comprising:

detecting, in the plant or plant part, a nucleic acid comprising:

- (a) the nucleotide sequence set forth in SEQ ID NO: 1;
- (b) the nucleotide sequence set forth in SEQ ID NO: 2;
- (c) the nucleotide sequence set forth in SEQ ID NO: 3;
- (d) the nucleotide sequence set forth in SEQ ID NO: 4;
- (e) the nucleotide sequence set forth in SEQ ID NO: 5;

- 5 (f) the nucleotide sequence set forth in SEQ ID NO: 6;
- (g) the nucleotide sequence set forth in SEQ ID NO: 7;
- (h) the nucleotide sequence set forth in SEQ ID NO: 8;
- (i) the nucleotide sequence set forth in SEQ ID NO: 9;
- (j) the nucleotide sequence set forth in SEQ ID NO: 10;
- (k) the nucleotide sequence set forth in SEQ ID NO: 11;
- (l) the nucleotide sequence set forth in SEQ ID NO: 12;
- (m) the nucleotide sequence set forth in SEQ ID NO: 13;
- (n) the nucleotide sequence set forth in SEQ ID NO: 14;
- 10 (o) the nucleotide sequence set forth in SEQ ID NO: 15;
- (p) the nucleotide sequence set forth in SEQ ID NO: 16;
- (q) the nucleotide sequence set forth in SEQ ID NO: 17;
- (r) the nucleotide sequence set forth in SEQ ID NO: 18;
- (s) the nucleotide sequence set forth in SEQ ID NO: 19;
- 15 (t) the nucleotide sequence set forth in SEQ ID NO: 20;
- (u) the nucleotide sequence set forth in SEQ ID NO: 21;
- (v) the nucleotide sequence set forth in SEQ ID NO: 22;
- (w) the nucleotide sequence set forth in SEQ ID NO: 23;
- (x) the nucleotide sequence set forth in SEQ ID NO: 24;
- 20 (y) the nucleotide sequence set forth in SEQ ID NO: 25;
- (z) the nucleotide sequence set forth in SEQ ID NO: 26;
- (aa) the nucleotide sequence set forth in SEQ ID NO: 27;
- (bb) a nucleotide sequence that is at least 95% identical to the nucleotide sequence of any one of (a) to (aa) above;
- 25 (cc) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 28;
- (dd) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 29;
- (ee) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 30;
- 30 (ff) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 31;
- (gg) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 32;

- (hh) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 33;
- (ii) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 34;
- 5 (jj) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 35;
- (kk) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 36;
- 10 (ll) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 37;
- (mm) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 38;
- (nn) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 39;
- 15 (oo) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 40;
- (pp) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 41;
- 20 (qq) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 42;
- (rr) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 43;
- (ss) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 44;
- 25 (tt) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 28–44;
- (uu) a nucleotide sequence that is complementary to the nucleotide sequence of any one of (a) to (tt) above;
- 30 (vv) a nucleotide sequence that hybridizes to the nucleotide sequence of any one of (a) to (uu) above under stringent hybridization conditions;
- (ww) a functional fragment of any one of (a) to (vv) above, wherein the functional fragment encodes a polypeptide that comprises an N-terminal signal peptide sequence that is at least 95% identical to amino acids 1 to

27 of SEQ ID NO: 28 and a CCVS domain that is at least 95% identical to amino acids 226 to 229 of SEQ ID NO: 28; and/or

(xx) a functional fragment of any one of (a) to (vv) above, wherein the functional fragment encodes a polypeptide that comprises an AP2 domain

5 that is at least 95% identical to amino acids 110 to 167 of SEQ ID NO: 36; thereby identifying a plant or plant part having enhanced abiotic stress tolerance.

54. The method of claim 53, wherein the exogenous nucleic acid or an informative fragment thereof is detected in an amplification product from a nucleic acid sample from the  
10 plant or plant part.

55. The method of any one of claims 53 to 54, wherein the exogenous nucleic acid is detected using a probe comprising the nucleotide sequence of any one of SEQ ID NOs: 1–27, the reverse complement thereof, an informative fragment thereof, or an informative fragment of the  
15 reverse complement thereof.

56. The method of claim 55, wherein the probe comprises a detectable moiety.

57. A method of enhancing abiotic stress tolerance in a plant, comprising:  
20 expressing in the plant an exogenous nucleic acid comprising:

- (a) the nucleotide sequence set forth in SEQ ID NO: 1;
- (b) the nucleotide sequence set forth in SEQ ID NO: 2;
- (c) the nucleotide sequence set forth in SEQ ID NO: 3;
- (d) the nucleotide sequence set forth in SEQ ID NO: 4;
- 25 (e) the nucleotide sequence set forth in SEQ ID NO: 5;
- (f) the nucleotide sequence set forth in SEQ ID NO: 6;
- (g) the nucleotide sequence set forth in SEQ ID NO: 7;
- (h) the nucleotide sequence set forth in SEQ ID NO: 8;
- (i) the nucleotide sequence set forth in SEQ ID NO: 9;
- 30 (j) the nucleotide sequence set forth in SEQ ID NO: 10;
- (k) the nucleotide sequence set forth in SEQ ID NO: 11;
- (l) the nucleotide sequence set forth in SEQ ID NO: 12;
- (m) the nucleotide sequence set forth in SEQ ID NO: 13;
- (n) the nucleotide sequence set forth in SEQ ID NO: 14;
- 35 (o) the nucleotide sequence set forth in SEQ ID NO: 15;

- (p) the nucleotide sequence set forth in SEQ ID NO: 16;
- (q) the nucleotide sequence set forth in SEQ ID NO: 17;
- (r) the nucleotide sequence set forth in SEQ ID NO: 18;
- (s) the nucleotide sequence set forth in SEQ ID NO: 19;
- 5 (t) the nucleotide sequence set forth in SEQ ID NO: 20;
- (u) the nucleotide sequence set forth in SEQ ID NO: 21;
- (v) the nucleotide sequence set forth in SEQ ID NO: 22;
- (w) the nucleotide sequence set forth in SEQ ID NO: 23;
- (x) the nucleotide sequence set forth in SEQ ID NO: 24;
- 10 (y) the nucleotide sequence set forth in SEQ ID NO: 25;
- (z) the nucleotide sequence set forth in SEQ ID NO: 26;
- (aa) the nucleotide sequence set forth in SEQ ID NO: 27;
- (bb) a nucleotide sequence that is at least 95% identical to the nucleotide sequence of any one of (a) to (aa) above;
- 15 (cc) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 28;
- (dd) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 29;
- (ee) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 30;
- 20 (ff) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 31;
- (gg) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 32;
- 25 (hh) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 33;
- (ii) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 34;
- (jj) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 35;
- 30 (kk) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 36;
- (ll) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 37;

- (mm) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 38;
- (nn) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 39;
- 5 (oo) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 40;
- (pp) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 41;
- 10 (qq) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 42;
- (rr) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 43;
- (ss) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 44;
- 15 (tt) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 28–44;
- (uu) a nucleotide sequence that is complementary to the nucleotide sequence of any one of (a) to (tt) above;
- 20 (vv) a nucleotide sequence that hybridizes to the nucleotide sequence of any one of (a) to (uu) above under stringent hybridization conditions;
- (ww) a functional fragment of any one of (a) to (vv) above, wherein the functional fragment encodes a polypeptide that comprises an N-terminal signal peptide sequence that is at least 95% identical to amino acids 1 to 27 of SEQ ID NO: 28 and a CCVS domain that is at least 95% identical to amino acids 226 to 229 of SEQ ID NO: 28; and/or
- 25 (xx) a functional fragment of any one of (a) to (vv) above, wherein the functional fragment encodes a polypeptide that comprises an AP2 domain that is at least 95% identical to amino acids 110 to 167 of SEQ ID NO: 36;
- 30 wherein expression of the exogenous nucleic acid results in enhanced abiotic stress tolerance in the plant as compared to a control plant of the same species grown under the same environmental conditions.

58. The method of claim 57, further comprising introducing the exogenous nucleic acid into the plant.

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59. The method of claim 57, further comprising introducing the exogenous nucleic acid into a plant part and producing the plant from the plant part.

5 60. A method of producing a plant having enhanced abiotic stress tolerance, comprising:

detecting, in a plant part, an exogenous nucleic acid comprising:

- (a) the nucleotide sequence set forth in SEQ ID NO: 1;
- (b) the nucleotide sequence set forth in SEQ ID NO: 2;
- 10 (c) the nucleotide sequence set forth in SEQ ID NO: 3;
- (d) the nucleotide sequence set forth in SEQ ID NO: 4;
- (e) the nucleotide sequence set forth in SEQ ID NO: 5;
- (f) the nucleotide sequence set forth in SEQ ID NO: 6;
- (g) the nucleotide sequence set forth in SEQ ID NO: 7;
- 15 (h) the nucleotide sequence set forth in SEQ ID NO: 8;
- (i) the nucleotide sequence set forth in SEQ ID NO: 9;
- (j) the nucleotide sequence set forth in SEQ ID NO: 10;
- (k) the nucleotide sequence set forth in SEQ ID NO: 11;
- (l) the nucleotide sequence set forth in SEQ ID NO: 12;
- 20 (m) the nucleotide sequence set forth in SEQ ID NO: 13;
- (n) the nucleotide sequence set forth in SEQ ID NO: 14;
- (o) the nucleotide sequence set forth in SEQ ID NO: 15;
- (p) the nucleotide sequence set forth in SEQ ID NO: 16;
- (q) the nucleotide sequence set forth in SEQ ID NO: 17;
- 25 (r) the nucleotide sequence set forth in SEQ ID NO: 18;
- (s) the nucleotide sequence set forth in SEQ ID NO: 19;
- (t) the nucleotide sequence set forth in SEQ ID NO: 20;
- (u) the nucleotide sequence set forth in SEQ ID NO: 21;
- (v) the nucleotide sequence set forth in SEQ ID NO: 22;
- 30 (w) the nucleotide sequence set forth in SEQ ID NO: 23;
- (x) the nucleotide sequence set forth in SEQ ID NO: 24;
- (y) the nucleotide sequence set forth in SEQ ID NO: 25;
- (z) the nucleotide sequence set forth in SEQ ID NO: 26;
- (aa) the nucleotide sequence set forth in SEQ ID NO: 27;

- (bb) a nucleotide sequence that is at least 95% identical to the nucleotide sequence of any one of (a) to (aa) above;
- (cc) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 28;
- 5 (dd) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 29;
- (ee) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 30;
- 10 (ff) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 31;
- (gg) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 32;
- (hh) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 33;
- 15 (ii) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 34;
- (jj) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 35;
- (kk) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 36;
- 20 (ll) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 37;
- (mm) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 38;
- 25 (nn) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 39;
- (oo) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 40;
- (pp) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 41;
- 30 (qq) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 42;
- (rr) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 43;

- (ss) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 44;
- (tt) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 28–44;
- (uu) a nucleotide sequence that is complementary to the nucleotide sequence of any one of (a) to (tt) above;
- (vv) a nucleotide sequence that hybridizes to the nucleotide sequence of any one of (a) to (uu) above under stringent hybridization conditions;
- (ww) a functional fragment of any one of (a) to (vv) above, wherein the functional fragment encodes a polypeptide that comprises an N-terminal signal peptide sequence that is at least 95% identical to amino acids 1 to 27 of SEQ ID NO: 28 and a CCVS domain that is at least 95% identical to amino acids 226 to 229 of SEQ ID NO: 28; and/or
- (xx) a functional fragment of any one of (a) to (vv) above, wherein the functional fragment encodes a polypeptide that comprises an AP2 domain that is at least 95% identical to amino acids 110 to 167 of SEQ ID NO: 36; and

producing a plant from the plant part,

- thereby producing a plant having enhanced abiotic stress tolerance as compared to a control plant of the same species grown under the same environmental conditions.

61. A method of producing a plant having enhanced abiotic stress tolerance, comprising:

- introducing an exogenous nucleic acid into a plant part, wherein the exogenous nucleic acid comprises:

- (a) the nucleotide sequence set forth in SEQ ID NO: 1;
- (b) the nucleotide sequence set forth in SEQ ID NO: 2;
- (c) the nucleotide sequence set forth in SEQ ID NO: 3;
- (d) the nucleotide sequence set forth in SEQ ID NO: 4;
- (e) the nucleotide sequence set forth in SEQ ID NO: 5;
- (f) the nucleotide sequence set forth in SEQ ID NO: 6;
- (g) the nucleotide sequence set forth in SEQ ID NO: 7;
- (h) the nucleotide sequence set forth in SEQ ID NO: 8;
- (i) the nucleotide sequence set forth in SEQ ID NO: 9;

- 5 (j) the nucleotide sequence set forth in SEQ ID NO: 10;  
(k) the nucleotide sequence set forth in SEQ ID NO: 11;  
(l) the nucleotide sequence set forth in SEQ ID NO: 12;  
(m) the nucleotide sequence set forth in SEQ ID NO: 13;  
(n) the nucleotide sequence set forth in SEQ ID NO: 14;  
(o) the nucleotide sequence set forth in SEQ ID NO: 15;  
(p) the nucleotide sequence set forth in SEQ ID NO: 16;  
(q) the nucleotide sequence set forth in SEQ ID NO: 17;  
(r) the nucleotide sequence set forth in SEQ ID NO: 18;  
10 (s) the nucleotide sequence set forth in SEQ ID NO: 19;  
(t) the nucleotide sequence set forth in SEQ ID NO: 20;  
(u) the nucleotide sequence set forth in SEQ ID NO: 21;  
(v) the nucleotide sequence set forth in SEQ ID NO: 22;  
(w) the nucleotide sequence set forth in SEQ ID NO: 23;  
15 (x) the nucleotide sequence set forth in SEQ ID NO: 24;  
(y) the nucleotide sequence set forth in SEQ ID NO: 25;  
(z) the nucleotide sequence set forth in SEQ ID NO: 26;  
(aa) the nucleotide sequence set forth in SEQ ID NO: 27;  
(bb) a nucleotide sequence that is at least 95% identical to the nucleotide  
20 sequence of any one of (a) to (aa) above;  
(cc) a nucleotide sequence that encodes a polypeptide comprising the amino  
acid sequence set forth in SEQ ID NO: 28;  
(dd) a nucleotide sequence that encodes a polypeptide comprising the amino  
acid sequence set forth in SEQ ID NO: 29;  
25 (ee) a nucleotide sequence that encodes a polypeptide comprising the amino  
acid sequence set forth in SEQ ID NO: 30;  
(ff) a nucleotide sequence that encodes a polypeptide comprising the amino  
acid sequence set forth in SEQ ID NO: 31;  
(gg) a nucleotide sequence that encodes a polypeptide comprising the amino  
30 acid sequence set forth in SEQ ID NO: 32;  
(hh) a nucleotide sequence that encodes a polypeptide comprising the amino  
acid sequence set forth in SEQ ID NO: 33;  
(ii) a nucleotide sequence that encodes a polypeptide comprising the amino  
acid sequence set forth in SEQ ID NO: 34;

- (jj) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 35;
- (kk) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 36;
- 5 (ll) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 37;
- (mm) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 38;
- 10 (nn) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 39;
- (oo) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 40;
- (pp) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 41;
- 15 (qq) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 42;
- (rr) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 43;
- 20 (ss) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 44;
- (tt) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 28–44;
- 25 (uu) a nucleotide sequence that is complementary to the nucleotide sequence of any one of (a) to (tt) above;
- (vv) a nucleotide sequence that hybridizes to the nucleotide sequence of any one of (a) to (uu) above under stringent hybridization conditions;
- 30 (ww) a functional fragment of any one of (a) to (vv) above, wherein the functional fragment encodes a polypeptide that comprises an N-terminal signal peptide sequence that is at least 95% identical to amino acids 1 to 27 of SEQ ID NO: 28 and a CCVS domain that is at least 95% identical to amino acids 226 to 229 of SEQ ID NO: 28; and/or
- (xx) a functional fragment of any one of (a) to (vv) above, wherein the functional fragment encodes a polypeptide that comprises an AP2 domain

that is at least 95% identical to amino acids 110 to 167 of SEQ ID NO: 36;  
and

growing the plant part into a plant that expresses the exogenous nucleic acid and that has enhanced abiotic stress tolerance as compared to a control plant of the same species that has not  
5 been transformed with the exogenous nucleic acid grown under the same environmental conditions.

62. The method of claim 61, wherein the exogenous nucleic acid is introduced into the plant part by microparticle bombardment, Agrobacterium-mediated transformation and/or  
10 whiskers-mediated transformation.

63. A method of producing a plant having enhanced abiotic stress tolerance, comprising:

crossing a first parent plant or plant part with a second parent plant or plant part, wherein  
15 the first parent plant or plant part comprises within its genome an exogenous nucleic acid that comprises:

- (a) the nucleotide sequence set forth in SEQ ID NO: 1;
- (b) the nucleotide sequence set forth in SEQ ID NO: 2;
- (c) the nucleotide sequence set forth in SEQ ID NO: 3;
- 20 (d) the nucleotide sequence set forth in SEQ ID NO: 4;
- (e) the nucleotide sequence set forth in SEQ ID NO: 5;
- (f) the nucleotide sequence set forth in SEQ ID NO: 6;
- (g) the nucleotide sequence set forth in SEQ ID NO: 7;
- (h) the nucleotide sequence set forth in SEQ ID NO: 8;
- 25 (i) the nucleotide sequence set forth in SEQ ID NO: 9;
- (j) the nucleotide sequence set forth in SEQ ID NO: 10;
- (k) the nucleotide sequence set forth in SEQ ID NO: 11;
- (l) the nucleotide sequence set forth in SEQ ID NO: 12;
- (m) the nucleotide sequence set forth in SEQ ID NO: 13;
- 30 (n) the nucleotide sequence set forth in SEQ ID NO: 14;
- (o) the nucleotide sequence set forth in SEQ ID NO: 15;
- (p) the nucleotide sequence set forth in SEQ ID NO: 16;
- (q) the nucleotide sequence set forth in SEQ ID NO: 17;
- (r) the nucleotide sequence set forth in SEQ ID NO: 18;
- 35 (s) the nucleotide sequence set forth in SEQ ID NO: 19;

- 5 (t) the nucleotide sequence set forth in SEQ ID NO: 20;
- (u) the nucleotide sequence set forth in SEQ ID NO: 21;
- (v) the nucleotide sequence set forth in SEQ ID NO: 22;
- (w) the nucleotide sequence set forth in SEQ ID NO: 23;
- 5 (x) the nucleotide sequence set forth in SEQ ID NO: 24;
- (y) the nucleotide sequence set forth in SEQ ID NO: 25;
- (z) the nucleotide sequence set forth in SEQ ID NO: 26;
- (aa) the nucleotide sequence set forth in SEQ ID NO: 27;
- 10 (bb) a nucleotide sequence that is at least 95% identical to the nucleotide sequence of any one of (a) to (aa) above;
- (cc) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 28;
- (dd) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 29;
- 15 (ee) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 30;
- (ff) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 31;
- (gg) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 32;
- 20 (hh) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 33;
- (ii) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 34;
- 25 (jj) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 35;
- (kk) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 36;
- (ll) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 37;
- 30 (mm) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 38;
- (nn) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 39;

- (oo) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 40;
- (pp) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 41;
- 5 (qq) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 42;
- (rr) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 43;
- 10 (ss) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 44;
- (tt) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 28–44;
- 15 (uu) a nucleotide sequence that is complementary to the nucleotide sequence of any one of (a) to (tt) above;
- (vv) a nucleotide sequence that hybridizes to the nucleotide sequence of any one of (a) to (uu) above under stringent hybridization conditions;
- 20 (ww) a functional fragment of any one of (a) to (vv) above, wherein the functional fragment encodes a polypeptide that comprises an N-terminal signal peptide sequence that is at least 95% identical to amino acids 1 to 27 of SEQ ID NO: 28 and a CCVS domain that is at least 95% identical to amino acids 226 to 229 of SEQ ID NO: 28; and/or
- 25 (xx) a functional fragment of any one of (a) to (vv) above, wherein the functional fragment encodes a polypeptide that comprises an AP2 domain that is at least 95% identical to amino acids 110 to 167 of SEQ ID NO: 36;

thereby producing a progeny generation,

wherein the progeny generation comprises at least one plant that possesses the exogenous nucleic acid within its genome and that exhibits abiotic enhanced stress tolerance as compared to a control plant of the same species grown under the same environmental conditions.

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64. The method of any one of claims 60 to 63, further comprising:

selecting for a plant having elevated expression of a protein encoded by the exogenous nucleic acid relative to the control plant.

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65. The method of any one of claims 60 to 64, further comprising:

selecting for a plant having increased seed yield and/or increased biomass, relative to the control plant.

66. The method of any one of claims 60 to 65, further comprising:

5 selecting for a plant having increased YGSMN, increased GWTPN, increased PYREC, decreased YRED, and/or decreased PB relative to the control plant.

67. The method of any one of claims 57 to 66, wherein expression of a protein encoded by the exogenous nucleic acid is increased in the plant relative to the control plant.

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68. The method of claim 67, wherein the expression of the protein in the plant is increased by at least about 20% relative to the control plant.

69. The method of any one of claims 57 to 68, wherein the drought stress tolerance, osmotic stress tolerance, salt stress tolerance and/or temperature stress tolerance of the plant is increased relative to the control plant.

15

70. The method of claim 69, wherein the drought stress tolerance, osmotic stress tolerance, salt stress tolerance and/or temperature stress tolerance of the plant is increased by at least about 20% relative to the control plant.

20

71. The method of any one of claims 57 to 70, wherein the yield, optionally the seed yield and/or biomass, of the plant is increased relative to the control plant.

72. The method of claim 71, wherein the seed yield and/or biomass of the plant is increased by at least about 20% relative to the control plant.

25

73. The method of any one of claims 57 to 72, wherein the plant exhibits increased YGSMN, increased GWTPN, increased PYREC, decreased YRED, and/or decreased PB relative to the control plant.

30

74. The method of claim 73, wherein the YGSMN, GWTPN and/or PYREC of the plant is increased by at least about 20% relative to the control plant.

75. The method of any one of claims 73 to 74, wherein the YRED and/or PB of the plant is decreased by at least about 20% relative to the control plant.

76. The method of any one of claims 57 to 75, wherein the exogenous nucleic acid comprises a tissue-specific promoter sequence, optionally a leaf-, ligule-, node-, panicle-, root-, sheath-, stem-, and/or vascular bundle-specific promoter sequence.

77. The method of any one of claims 57 to 76, wherein the exogenous nucleic acid comprises a stress-inducible promoter sequence, optionally a drought stress-, osmotic stress-, salt stress- and/or temperature stress-inducible promoter sequence.

78. The method of any one of claims 57 to 77, wherein the exogenous nucleic acid comprises a developmental stage-specific promoter sequence, optionally a promoter sequence that drives expression prior to and/or during the seedling and/or reproductive stage(s) of development.

79. The method of any one of claims 57 to 78, wherein the exogenous nucleic acid is expressed in a leaf, ligule, node, panicle, root, sheath, stem, and/or vascular bundle of the plant.

80. The method of any one of claims 57 to 79, wherein the plant is a monocot.

81. The method of any one of claims 57 to 79, wherein the plant is a rice, maize, wheat, barley, oats, rye, millet, sorghum, triticale, secale, einkorn, spelt, emmer, teff, milo, flax gramma grass, *Tripsacum sp.* or teosinte plant.

82. The method of any one of claims 57 to 79, wherein the plant is a dicot.

83. The method of any one of claims 57 to 79, wherein the plant is a cotton, potato, soybean, sugar beet, sunflower, tobacco or tomato plant.

84. The method of any one of claims 57 to 83, wherein the exogenous nucleic acid comprises codons specific for expression in plants.

85. A plant cell from the plant or plant part of any one of claims 1 to 21.

86. A plant cell comprising the nonnaturally occurring nucleic acid of any one of claims 22 to 30.

87. A plant cell comprising the expression cassette of claim 31.

88. A plant cell comprising the vector of any one of claims 32 to 33.

89. The plant cell of any one of claims 85 to 88, wherein the plant cell is an egg cell.

90. The plant cell of any one of claims 85 to 88, wherein the plant cell is a sperm cell.

91. The plant cell of any one of claims 85 to 90, wherein the plant cell is capable of producing a plant having enhanced abiotic stress tolerance as compared to a control plant of the same species grown under the same environmental conditions, optionally enhanced drought stress tolerance, enhanced osmotic stress tolerance, enhanced salt stress tolerance and/or enhanced temperature stress tolerance.

92. The plant cell of claim 91, wherein the drought stress tolerance, osmotic stress tolerance, salt stress tolerance and/or temperature stress tolerance of the plant produced from the plant cell is increased by at least about 20% relative to the control plant.

93. The plant cell of any one of claims 85 to 92, wherein the plant cell is capable of producing a plant having increased yield, optionally increased seed yield and/or biomass, as compared to a control plant of the same species grown under the same environmental conditions.

94. The plant cell of claim 93, wherein the seed yield and/or biomass of the plant produced from the plant cell is increased by at least about 20% relative to the control plant.

95. The plant cell of any one of claims 85 to 94, wherein the plant cell is capable of producing a plant having increased YGSMN, increased GWTPN, increased PYREC, decreased YRED, and/or decreased PB relative to a control plant of the same species grown under the same environmental conditions.

96. The plant cell of claim 95, wherein the YGSMN, GWTPN and/or PYREC of the plant produced from the plant cell is increased by at least about 20% relative to the control plant.

97. The plant cell of any one of claims 95 to 96, wherein the YRED and/or PB of the plant produced from the plant cell is decreased by at least about 20% relative to the control plant.

5 98. A plant comprising the nonnaturally occurring nucleic acid of any one of claims 22 to 30.

99. A plant comprising the expression cassette of claim 31.

10 100. A plant comprising the vector of any one of claims 32 to 33.

101. A plant comprising the plant cell of any one of claims 85 to 97.

102. A plant produced according to the method of any one of claims 60 to 84.

15 103. A plant produced from the plant cell of any one of claims 85 to 97.

104. The plant of any one of claims 98 to 103, wherein the plant expresses a protein encoded by the nonnaturally occurring nucleic acid at an elevated level as compared to a control  
20 plant of the same species grown under the same environmental conditions.

105. The plant of any one of claims 98 to 104, wherein the plant exhibits enhanced abiotic stress tolerance relative to a control plant of the same species grown under the same environmental conditions, optionally enhanced drought stress tolerance, enhanced osmotic stress  
25 tolerance, enhanced salt stress tolerance and/or enhanced temperature stress tolerance.

106. The plant of claim 105, wherein the drought stress tolerance, osmotic stress tolerance, salt stress tolerance and/or temperature stress tolerance of the plant is increased by at least about 20% relative to the control plant.

30 107. The plant of any one of claims 98 to 106, wherein the plant exhibits increased yield, optionally increased seed yield and/or biomass, relative to a control plant of the same species grown under the same environmental conditions.

108. The plant of claim 107, wherein the seed yield and/or biomass of the plant is increased by at least about 20% relative to the control plant.

109. The plant of any one of claims 98 to 108, wherein the plant exhibits increased YGSMN, increased GWTPN, increased PYREC, decreased YRED, and/or decreased PB relative to a control plant of the same species grown under the same environmental conditions.

110. The plant of claim 109, wherein the YGSMN, GWTPN and/or PYREC of the plant is increased by at least about 20% relative to the control plant.

111. The plant of any one of claims 109 to 110, wherein the YRED and/or PB of the plant is decreased by at least about 20% relative to the control plant.

112. A seed from the plant of any one of claims 1 to 21 and 98 to 111.

113. The seed of claim 112, wherein the seed comprises:

- (a) the nucleotide sequence set forth in SEQ ID NO: 1;
- (b) the nucleotide sequence set forth in SEQ ID NO: 2;
- (c) the nucleotide sequence set forth in SEQ ID NO: 3;
- (d) the nucleotide sequence set forth in SEQ ID NO: 4;
- (e) the nucleotide sequence set forth in SEQ ID NO: 5;
- (f) the nucleotide sequence set forth in SEQ ID NO: 6;
- (g) the nucleotide sequence set forth in SEQ ID NO: 7;
- (h) the nucleotide sequence set forth in SEQ ID NO: 8;
- (i) the nucleotide sequence set forth in SEQ ID NO: 9;
- (j) the nucleotide sequence set forth in SEQ ID NO: 10;
- (k) the nucleotide sequence set forth in SEQ ID NO: 11;
- (l) the nucleotide sequence set forth in SEQ ID NO: 12;
- (m) the nucleotide sequence set forth in SEQ ID NO: 13;
- (n) the nucleotide sequence set forth in SEQ ID NO: 14;
- (o) the nucleotide sequence set forth in SEQ ID NO: 15;
- (p) the nucleotide sequence set forth in SEQ ID NO: 16;
- (q) the nucleotide sequence set forth in SEQ ID NO: 17;
- (r) the nucleotide sequence set forth in SEQ ID NO: 18;
- (s) the nucleotide sequence set forth in SEQ ID NO: 19;

- (t) the nucleotide sequence set forth in SEQ ID NO: 20;
- (u) the nucleotide sequence set forth in SEQ ID NO: 21;
- (v) the nucleotide sequence set forth in SEQ ID NO: 22;
- (w) the nucleotide sequence set forth in SEQ ID NO: 23;
- 5 (x) the nucleotide sequence set forth in SEQ ID NO: 24;
- (y) the nucleotide sequence set forth in SEQ ID NO: 25;
- (z) the nucleotide sequence set forth in SEQ ID NO: 26;
- (aa) the nucleotide sequence set forth in SEQ ID NO: 27;
- (bb) a nucleotide sequence that is at least 95% identical to the nucleotide sequence of  
10 any one of (a) to (aa) above;
- (cc) a nucleotide sequence that encodes a polypeptide comprising the amino acid  
sequence set forth in SEQ ID NO: 28;
- (dd) a nucleotide sequence that encodes a polypeptide comprising the amino acid  
sequence set forth in SEQ ID NO: 29;
- 15 (ee) a nucleotide sequence that encodes a polypeptide comprising the amino acid  
sequence set forth in SEQ ID NO: 30;
- (ff) a nucleotide sequence that encodes a polypeptide comprising the amino acid  
sequence set forth in SEQ ID NO: 31;
- (gg) a nucleotide sequence that encodes a polypeptide comprising the amino acid  
20 sequence set forth in SEQ ID NO: 32;
- (hh) a nucleotide sequence that encodes a polypeptide comprising the amino acid  
sequence set forth in SEQ ID NO: 33;
- (ii) a nucleotide sequence that encodes a polypeptide comprising the amino acid  
sequence set forth in SEQ ID NO: 34;
- 25 (jj) a nucleotide sequence that encodes a polypeptide comprising the amino acid  
sequence set forth in SEQ ID NO: 35;
- (kk) a nucleotide sequence that encodes a polypeptide comprising the amino acid  
sequence set forth in SEQ ID NO: 36;
- (ll) a nucleotide sequence that encodes a polypeptide comprising the amino acid  
30 sequence set forth in SEQ ID NO: 37;
- (mm) a nucleotide sequence that encodes a polypeptide comprising the amino acid  
sequence set forth in SEQ ID NO: 38;
- (nn) a nucleotide sequence that encodes a polypeptide comprising the amino acid  
sequence set forth in SEQ ID NO: 39;

- (oo) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 40;
- (pp) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 41;
- 5 (qq) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 42;
- (rr) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 43;
- 10 (ss) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 44;
- (tt) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 28–44;
- 15 (uu) a nucleotide sequence that is complementary to the nucleotide sequence of any one of (a) to (tt) above;
- (vv) a nucleotide sequence that hybridizes to the nucleotide sequence of any one of (a) to (uu) above under stringent hybridization conditions;
- 20 (ww) a functional fragment of any one of (a) to (vv) above, wherein the functional fragment encodes a polypeptide that comprises an N-terminal signal peptide sequence that is at least 95% identical to amino acids 1 to 27 of SEQ ID NO: 28 and a CCVS domain that is at least 95% identical to amino acids 226 to 229 of SEQ ID NO: 28; and/or
- 25 (xx) a functional fragment of any one of (a) to (vv) above, wherein the functional fragment encodes a polypeptide that comprises an AP2 domain that is at least 95% identical to amino acids 110 to 167 of SEQ ID NO: 36.
114. A plant grown from the seed of any one of claims 112 to 113.
115. A product harvested from the plant of any one of claims 1 to 21, 98 to 111 and  
30 114.
116. A processed product produced from the harvested product of claim 115.
117. A crop comprising a plurality of the plant of any one of claims 1 to 21, 98 to 111  
35 and 114.

118. A nonnaturally occurring protein comprising:

- (a) the amino acid sequence set forth in SEQ ID NO: 28;
- (b) the amino acid sequence set forth in SEQ ID NO: 29;
- (c) the amino acid sequence set forth in SEQ ID NO: 30;
- (d) the amino acid sequence set forth in SEQ ID NO: 31;
- (e) the amino acid sequence set forth in SEQ ID NO: 32;
- (f) the amino acid sequence set forth in SEQ ID NO: 33;
- (g) the amino acid sequence set forth in SEQ ID NO: 34;
- (h) the amino acid sequence set forth in SEQ ID NO: 35;
- (i) the amino acid sequence set forth in SEQ ID NO: 36;
- (j) the amino acid sequence set forth in SEQ ID NO: 37;
- (k) the amino acid sequence set forth in SEQ ID NO: 38;
- (l) the amino acid sequence set forth in SEQ ID NO: 39;
- (m) the amino acid sequence set forth in SEQ ID NO: 40;
- (n) the amino acid sequence set forth in SEQ ID NO: 41;
- (o) the amino acid sequence set forth in SEQ ID NO: 42;
- (p) the amino acid sequence set forth in SEQ ID NO: 43;
- (q) the amino acid sequence set forth in SEQ ID NO: 44;
- (r) an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 28–44;
- (s) a functional fragment of any one of (a) to (r) above, wherein the functional fragment comprises an N-terminal signal peptide sequence that is at least 95% identical to amino acids 1 to 27 of SEQ ID NO: 28 and a CCVS domain that is at least 95% identical to amino acids 226 to 229 of SEQ ID NO: 28; and/or
- (t) a functional fragment of any one of (a) to (q) above, wherein the functional fragment comprises an AP2 domain that is at least 95% identical to amino acids 110 to 167 of SEQ ID NO: 36.

119. The nonnaturally occurring protein of claim 118, further comprising a poly-Arg tag, a poly-His tag, a FLAG tag, a strep-tag II, and/or a c-myc tag.

120. A recombinant bacteria comprising:

- (a) the nucleotide sequence set forth in SEQ ID NO: 1;
- (b) the nucleotide sequence set forth in SEQ ID NO: 2;

- (c) the nucleotide sequence set forth in SEQ ID NO: 3;
- (d) the nucleotide sequence set forth in SEQ ID NO: 4;
- (e) the nucleotide sequence set forth in SEQ ID NO: 5;
- (f) the nucleotide sequence set forth in SEQ ID NO: 6;
- 5 (g) the nucleotide sequence set forth in SEQ ID NO: 7;
- (h) the nucleotide sequence set forth in SEQ ID NO: 8;
- (i) the nucleotide sequence set forth in SEQ ID NO: 9;
- (j) the nucleotide sequence set forth in SEQ ID NO: 10;
- (k) the nucleotide sequence set forth in SEQ ID NO: 11;
- 10 (l) the nucleotide sequence set forth in SEQ ID NO: 12;
- (m) the nucleotide sequence set forth in SEQ ID NO: 13;
- (n) the nucleotide sequence set forth in SEQ ID NO: 14;
- (o) the nucleotide sequence set forth in SEQ ID NO: 15;
- (p) the nucleotide sequence set forth in SEQ ID NO: 16;
- 15 (q) the nucleotide sequence set forth in SEQ ID NO: 17;
- (r) the nucleotide sequence set forth in SEQ ID NO: 18;
- (s) the nucleotide sequence set forth in SEQ ID NO: 19;
- (t) the nucleotide sequence set forth in SEQ ID NO: 20;
- (u) the nucleotide sequence set forth in SEQ ID NO: 21;
- 20 (v) the nucleotide sequence set forth in SEQ ID NO: 22;
- (w) the nucleotide sequence set forth in SEQ ID NO: 23;
- (x) the nucleotide sequence set forth in SEQ ID NO: 24;
- (y) the nucleotide sequence set forth in SEQ ID NO: 25;
- (z) the nucleotide sequence set forth in SEQ ID NO: 26;
- 25 (aa) the nucleotide sequence set forth in SEQ ID NO: 27;
- (bb) a nucleotide sequence that is at least 95% identical to the nucleotide sequence of any one of (a) to (aa) above;
- (cc) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 28;
- 30 (dd) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 29;
- (ee) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 30;
- (ff) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 31;
- 35

- (gg) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 32;
- (hh) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 33;
- 5 (ii) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 34;
- (jj) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 35;
- (kk) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 36;
- 10 (ll) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 37;
- (mm) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 38;
- 15 (nn) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 39;
- (oo) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 40;
- (pp) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 41;
- 20 (qq) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 42;
- (rr) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 43;
- 25 (ss) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 44;
- (tt) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 28–44;
- 30 (uu) a nucleotide sequence that is complementary to the nucleotide sequence of any one of (a) to (tt) above;
- (vv) a nucleotide sequence that hybridizes to the nucleotide sequence of any one of (a) to (uu) above under stringent hybridization conditions;
- (ww) a functional fragment of any one of (a) to (vv) above, wherein the functional fragment encodes a polypeptide that comprises an N-terminal signal peptide
- 35

sequence that is at least 95% identical to amino acids 1 to 27 of SEQ ID NO: 28 and a CCVS domain that is at least 95% identical to amino acids 226 to 229 of SEQ ID NO: 28; and/or

- (xx) a functional fragment of any one of (a) to (vv) above, wherein the functional fragment encodes a polypeptide that comprises an AP2 domain that is at least 95% identical to amino acids 110 to 167 of SEQ ID NO: 36.

121. A recombinant virus comprising:

- (a) the nucleotide sequence set forth in SEQ ID NO: 1;
- (b) the nucleotide sequence set forth in SEQ ID NO: 2;
- (c) the nucleotide sequence set forth in SEQ ID NO: 3;
- (d) the nucleotide sequence set forth in SEQ ID NO: 4;
- (e) the nucleotide sequence set forth in SEQ ID NO: 5;
- (f) the nucleotide sequence set forth in SEQ ID NO: 6;
- (g) the nucleotide sequence set forth in SEQ ID NO: 7;
- (h) the nucleotide sequence set forth in SEQ ID NO: 8;
- (i) the nucleotide sequence set forth in SEQ ID NO: 9;
- (j) the nucleotide sequence set forth in SEQ ID NO: 10;
- (k) the nucleotide sequence set forth in SEQ ID NO: 11;
- (l) the nucleotide sequence set forth in SEQ ID NO: 12;
- (m) the nucleotide sequence set forth in SEQ ID NO: 13;
- (n) the nucleotide sequence set forth in SEQ ID NO: 14;
- (o) the nucleotide sequence set forth in SEQ ID NO: 15;
- (p) the nucleotide sequence set forth in SEQ ID NO: 16;
- (q) the nucleotide sequence set forth in SEQ ID NO: 17;
- (r) the nucleotide sequence set forth in SEQ ID NO: 18;
- (s) the nucleotide sequence set forth in SEQ ID NO: 19;
- (t) the nucleotide sequence set forth in SEQ ID NO: 20;
- (u) the nucleotide sequence set forth in SEQ ID NO: 21;
- (v) the nucleotide sequence set forth in SEQ ID NO: 22;
- (w) the nucleotide sequence set forth in SEQ ID NO: 23;
- (x) the nucleotide sequence set forth in SEQ ID NO: 24;
- (y) the nucleotide sequence set forth in SEQ ID NO: 25;
- (z) the nucleotide sequence set forth in SEQ ID NO: 26;
- (aa) the nucleotide sequence set forth in SEQ ID NO: 27;

- (bb) a nucleotide sequence that is at least 95% identical to the nucleotide sequence of any one of (a) to (aa) above;
- (cc) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 28;
- 5 (dd) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 29;
- (ee) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 30;
- 10 (ff) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 31;
- (gg) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 32;
- (hh) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 33;
- 15 (ii) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 34;
- (jj) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 35;
- 20 (kk) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 36;
- (ll) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 37;
- (mm) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 38;
- 25 (nn) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 39;
- (oo) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 40;
- 30 (pp) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 41;
- (qq) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 42;
- (rr) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 43;

- (ss) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 44;
- (tt) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 28–44;
- (uu) a nucleotide sequence that is complementary to the nucleotide sequence of any one of (a) to (tt) above;
- (vv) a nucleotide sequence that hybridizes to the nucleotide sequence of any one of (a) to (uu) above under stringent hybridization conditions;
- (ww) a functional fragment of any one of (a) to (vv) above, wherein the functional fragment encodes a polypeptide that comprises an N-terminal signal peptide sequence that is at least 95% identical to amino acids 1 to 27 of SEQ ID NO: 28 and a CCVS domain that is at least 95% identical to amino acids 226 to 229 of SEQ ID NO: 28; and/or
- (xx) a functional fragment of any one of (a) to (vv) above, wherein the functional fragment encodes a polypeptide that comprises an AP2 domain that is at least 95% identical to amino acids 110 to 167 of SEQ ID NO: 36.

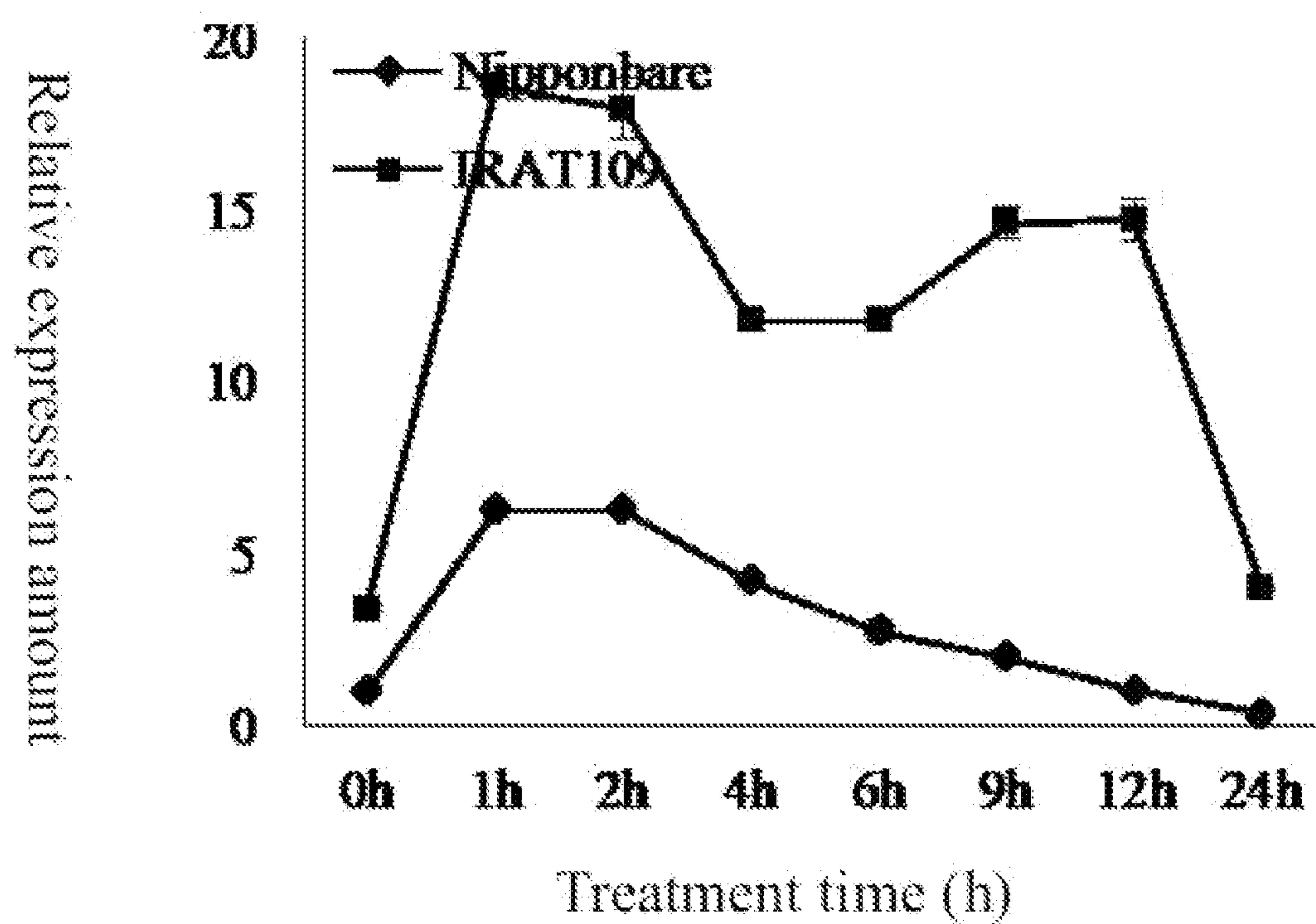


Fig. 1A

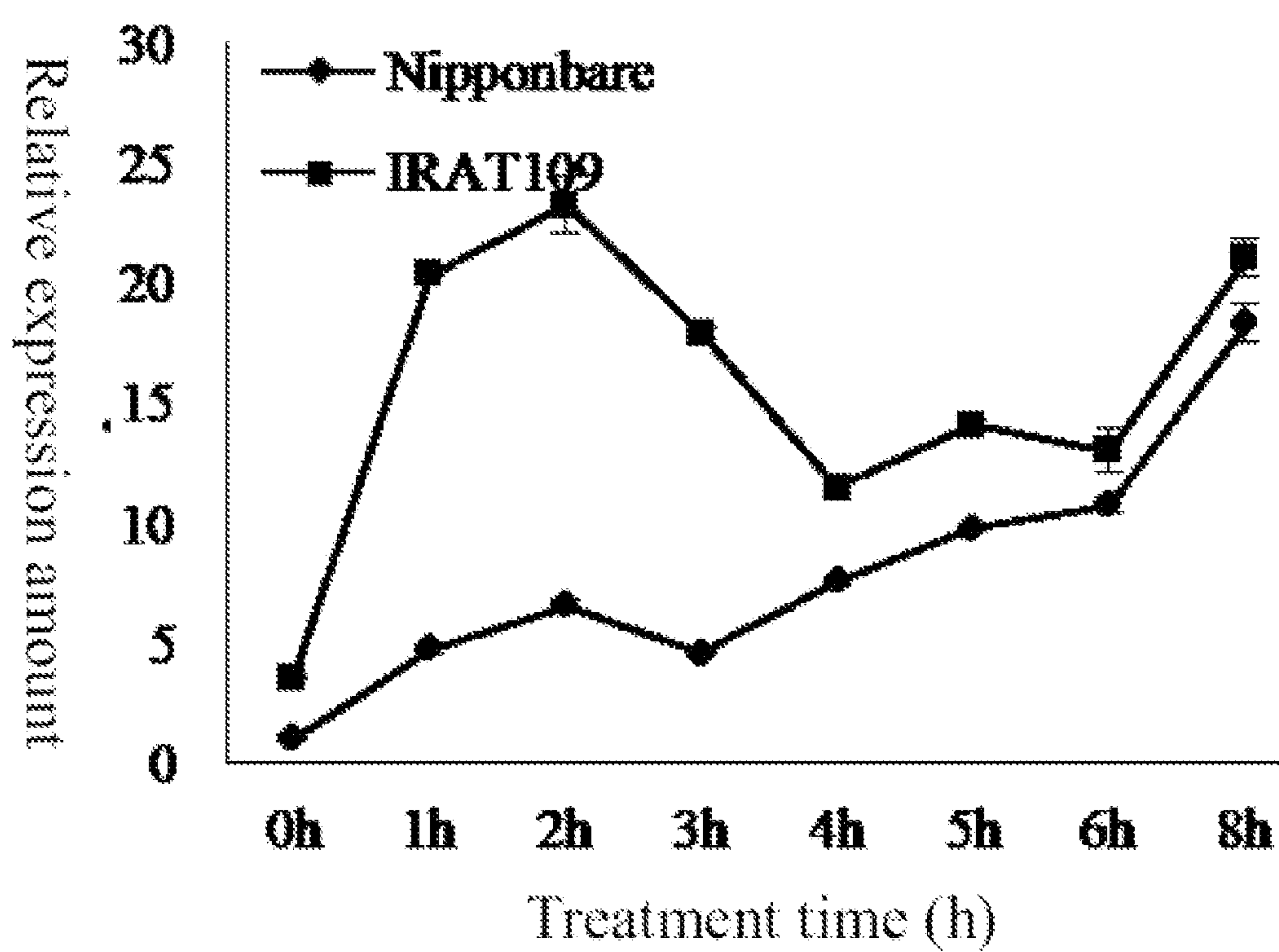


Fig. 1B

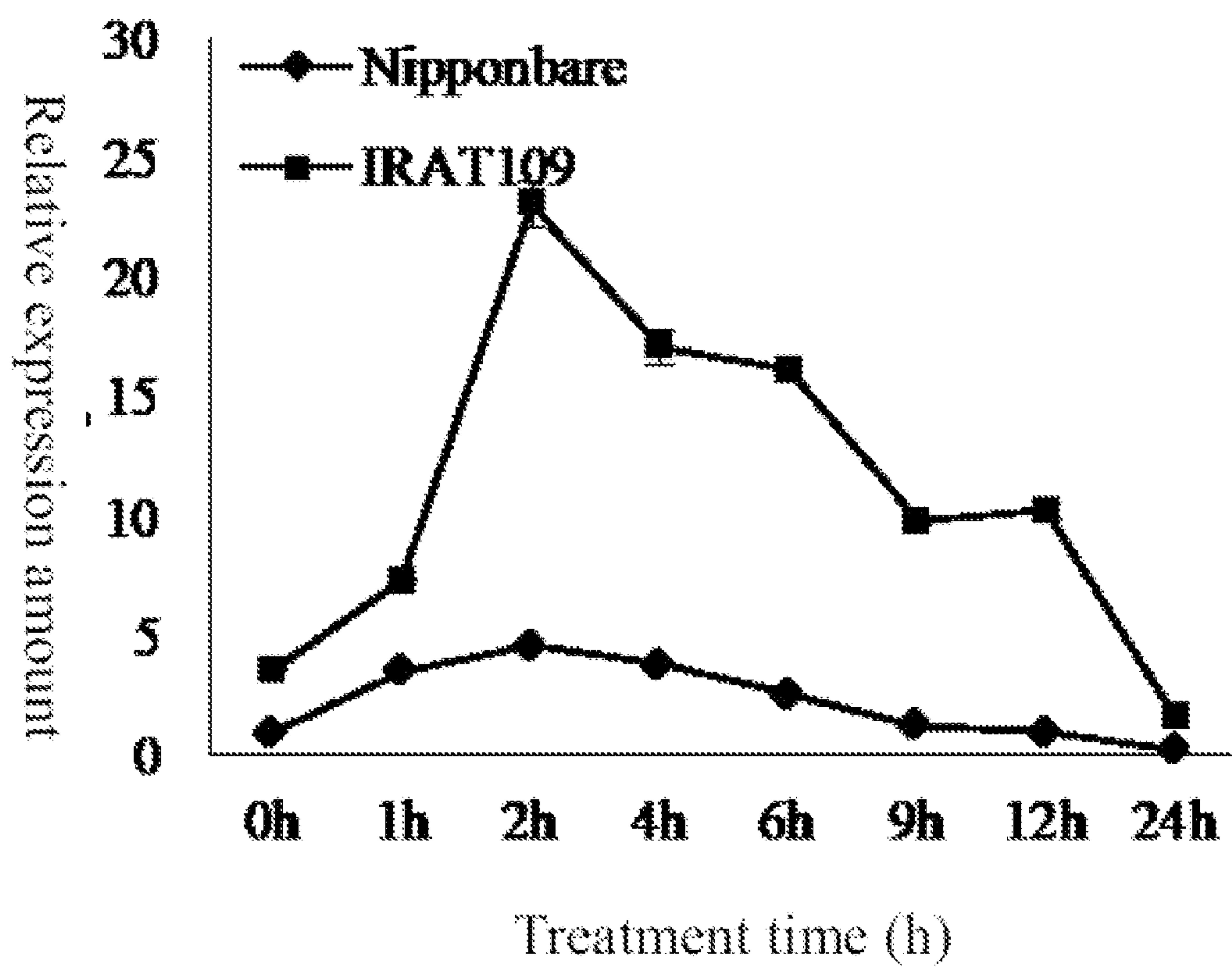


Fig. 1C

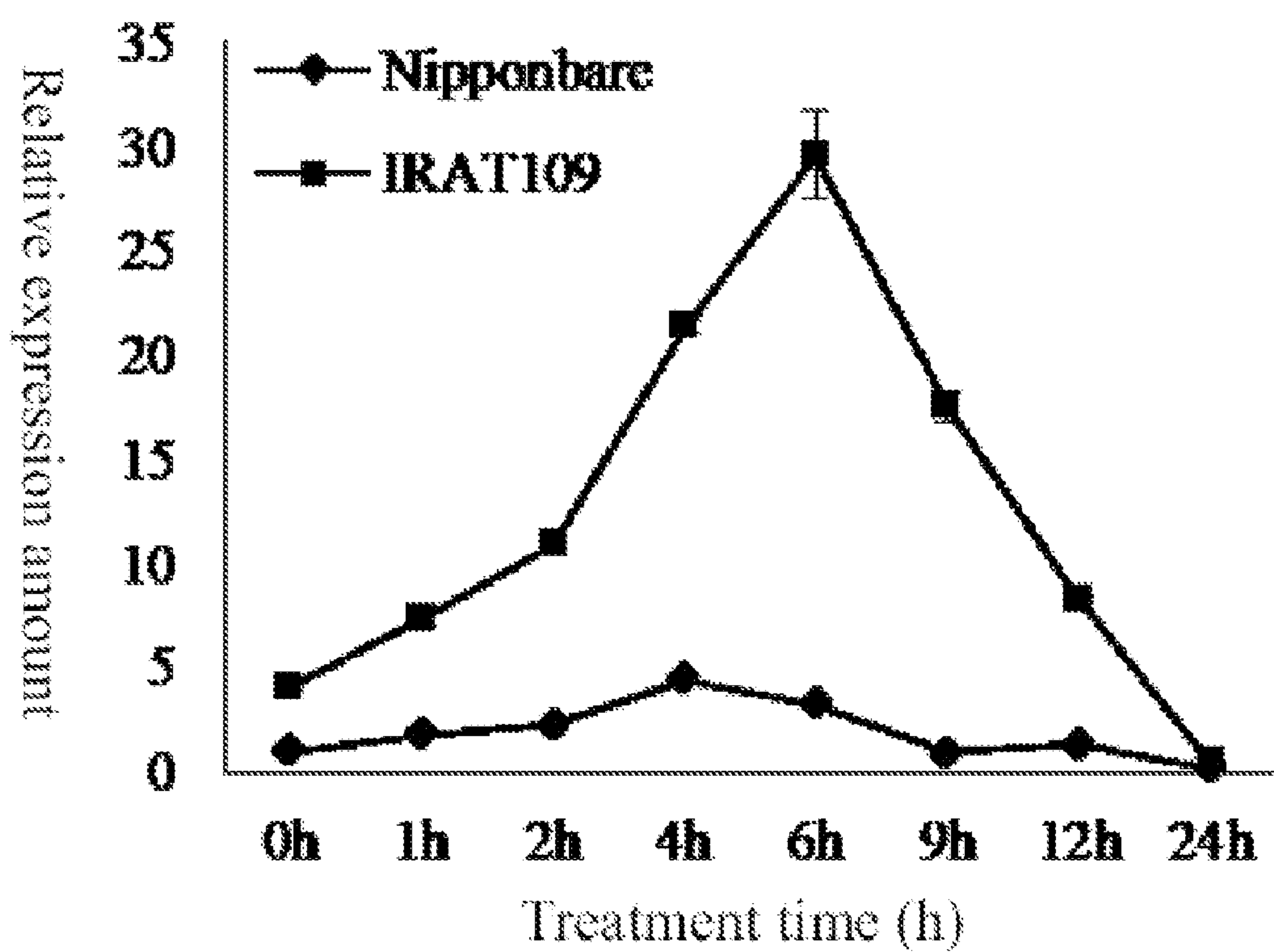
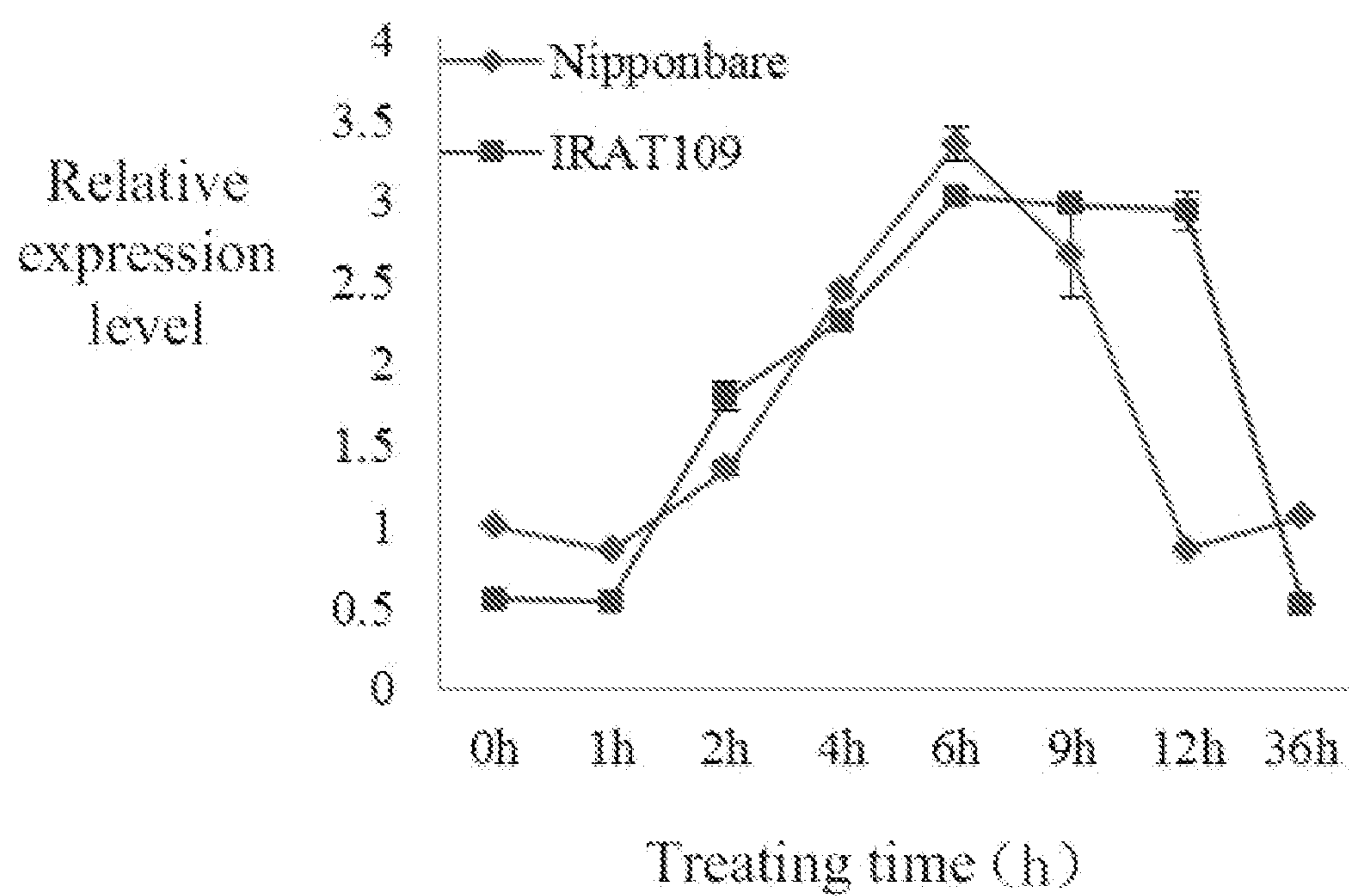
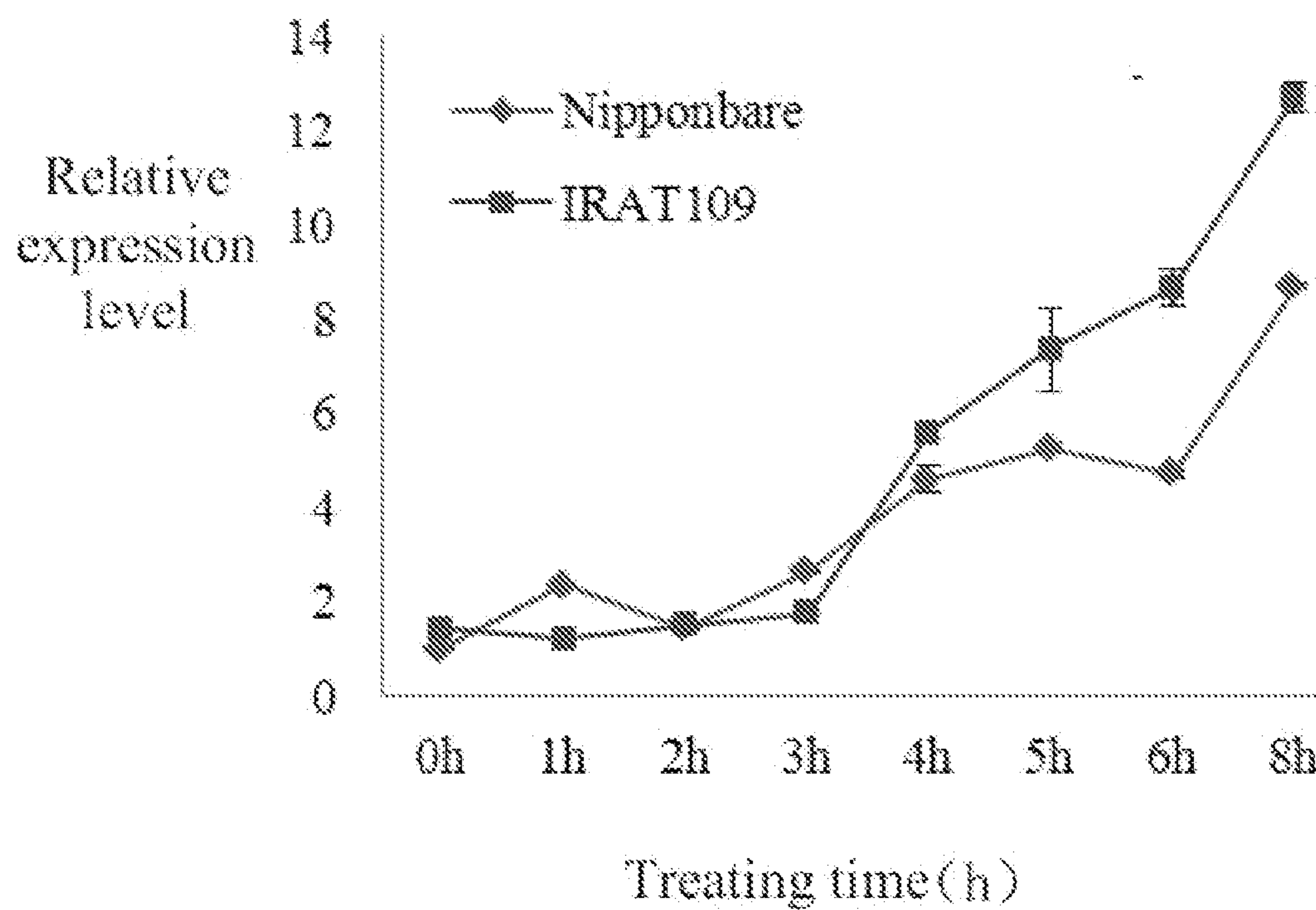
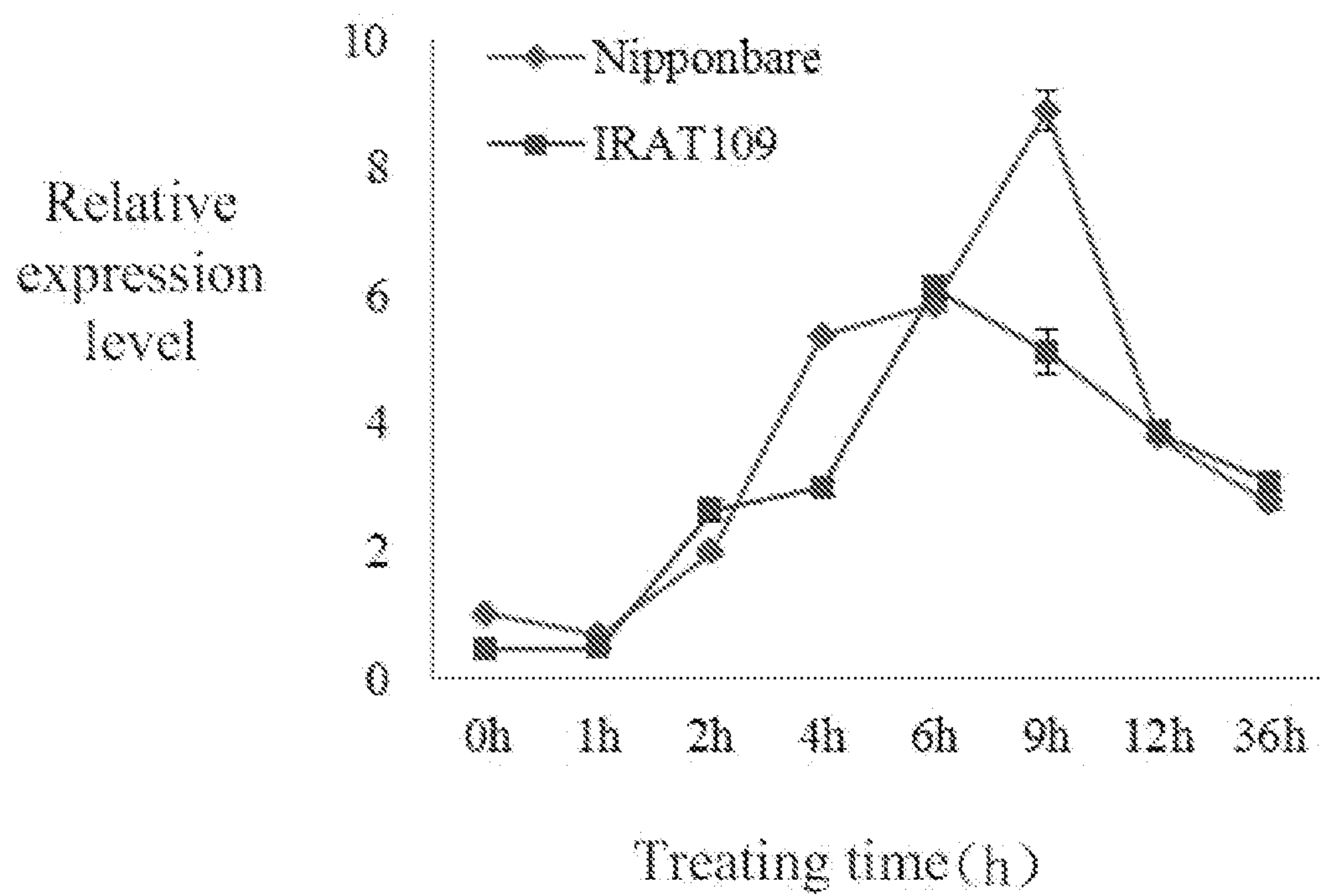
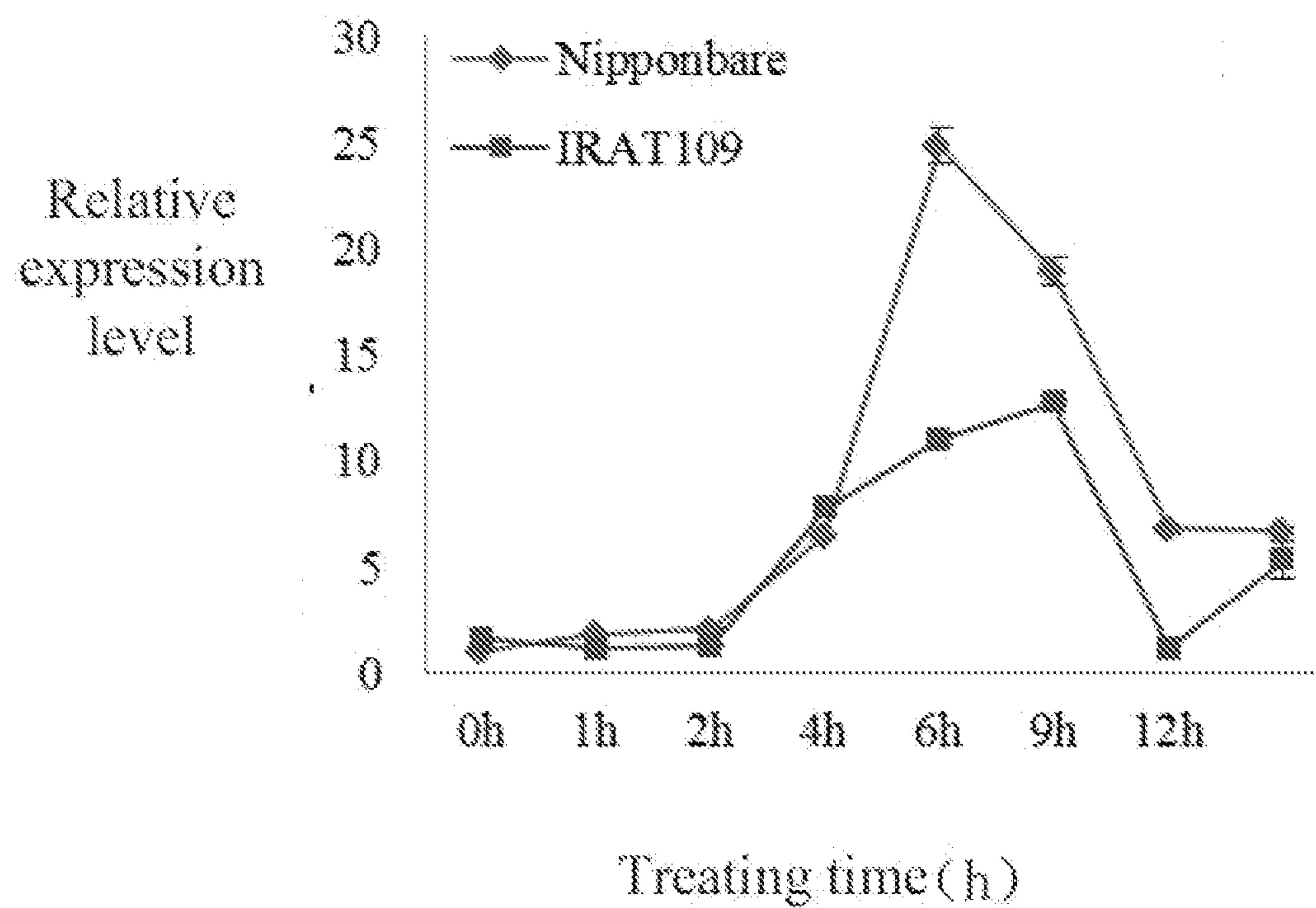


Fig. 1D

**Fig. 1E****Fig. 1F**

**Fig. 1G****Fig. 1H**

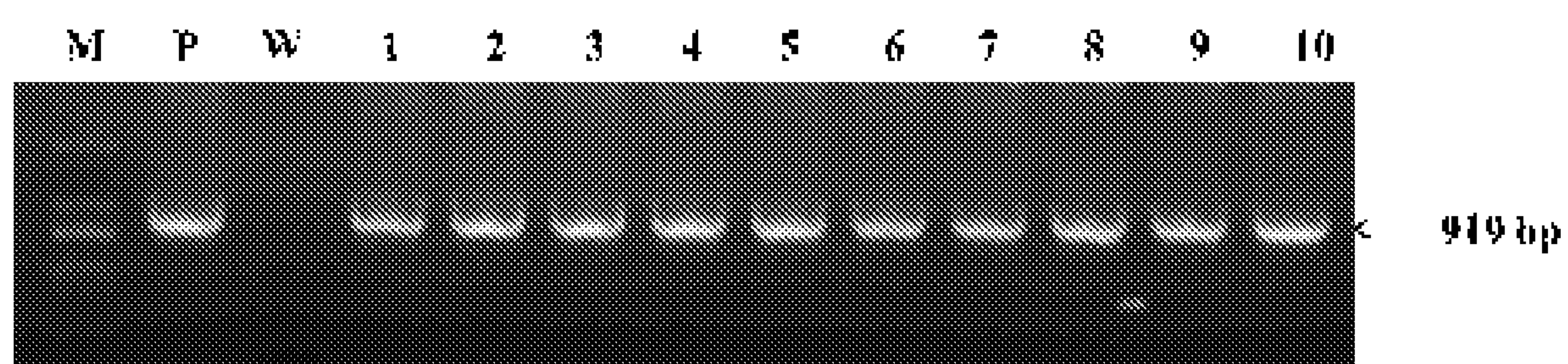


Fig. 2A

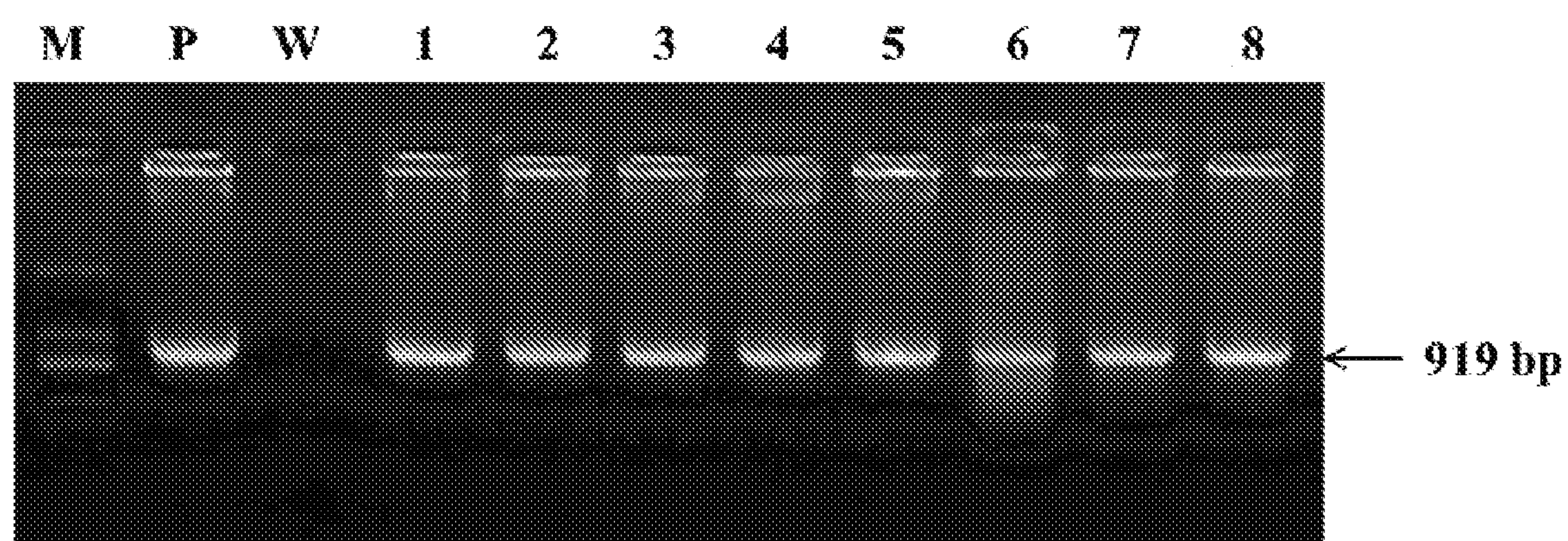


Fig. 2B

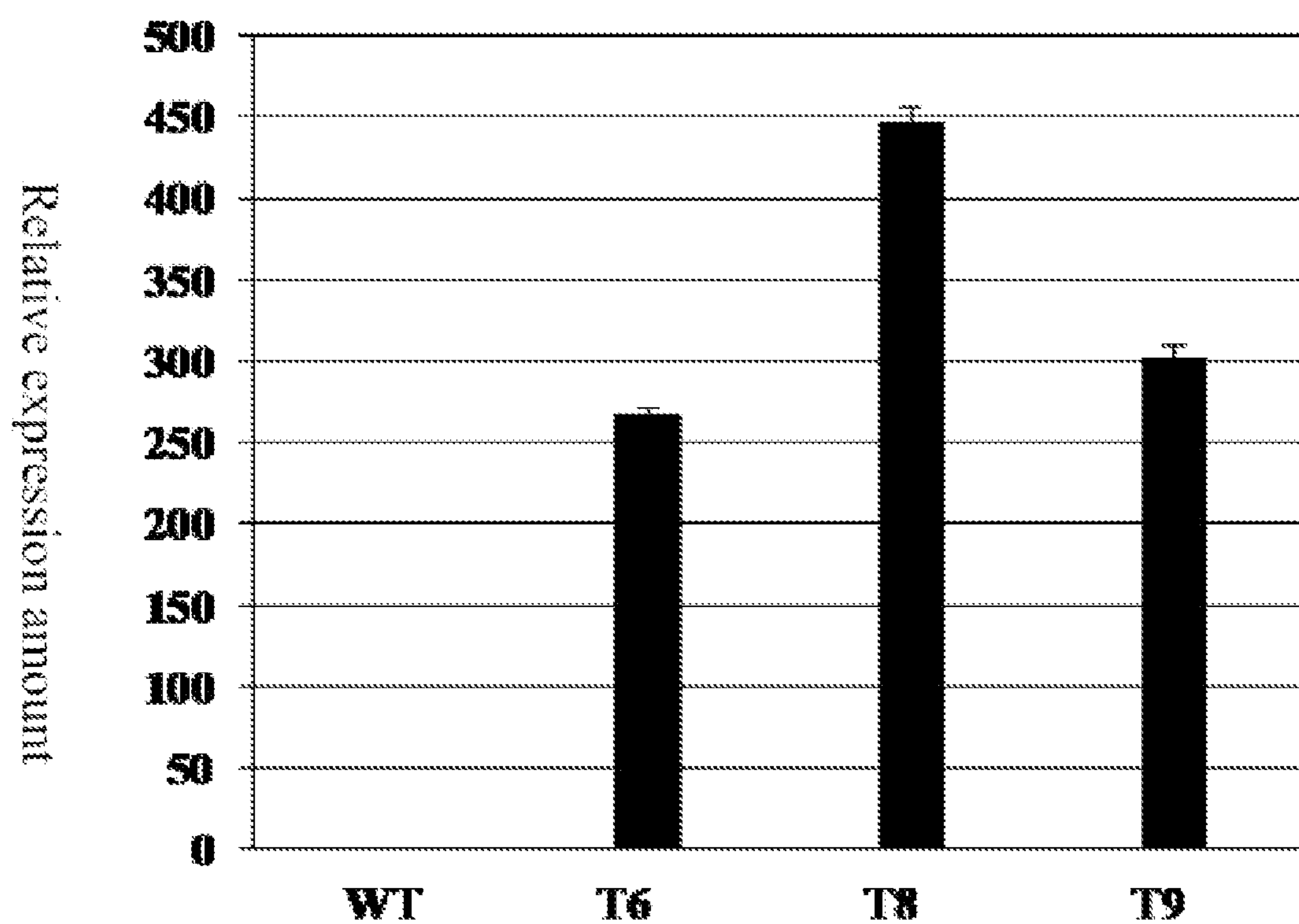


Fig. 3A

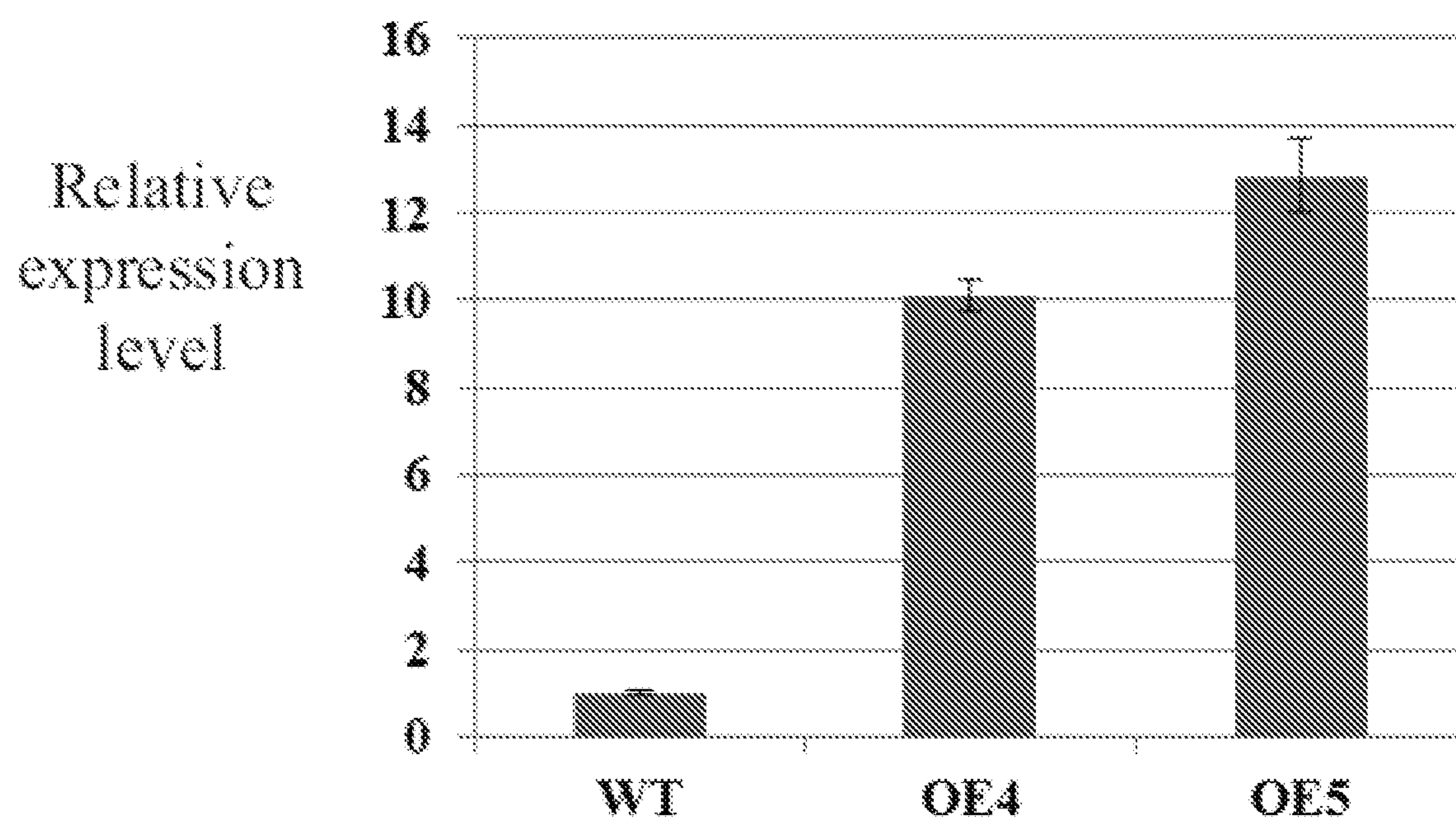


Fig. 3B

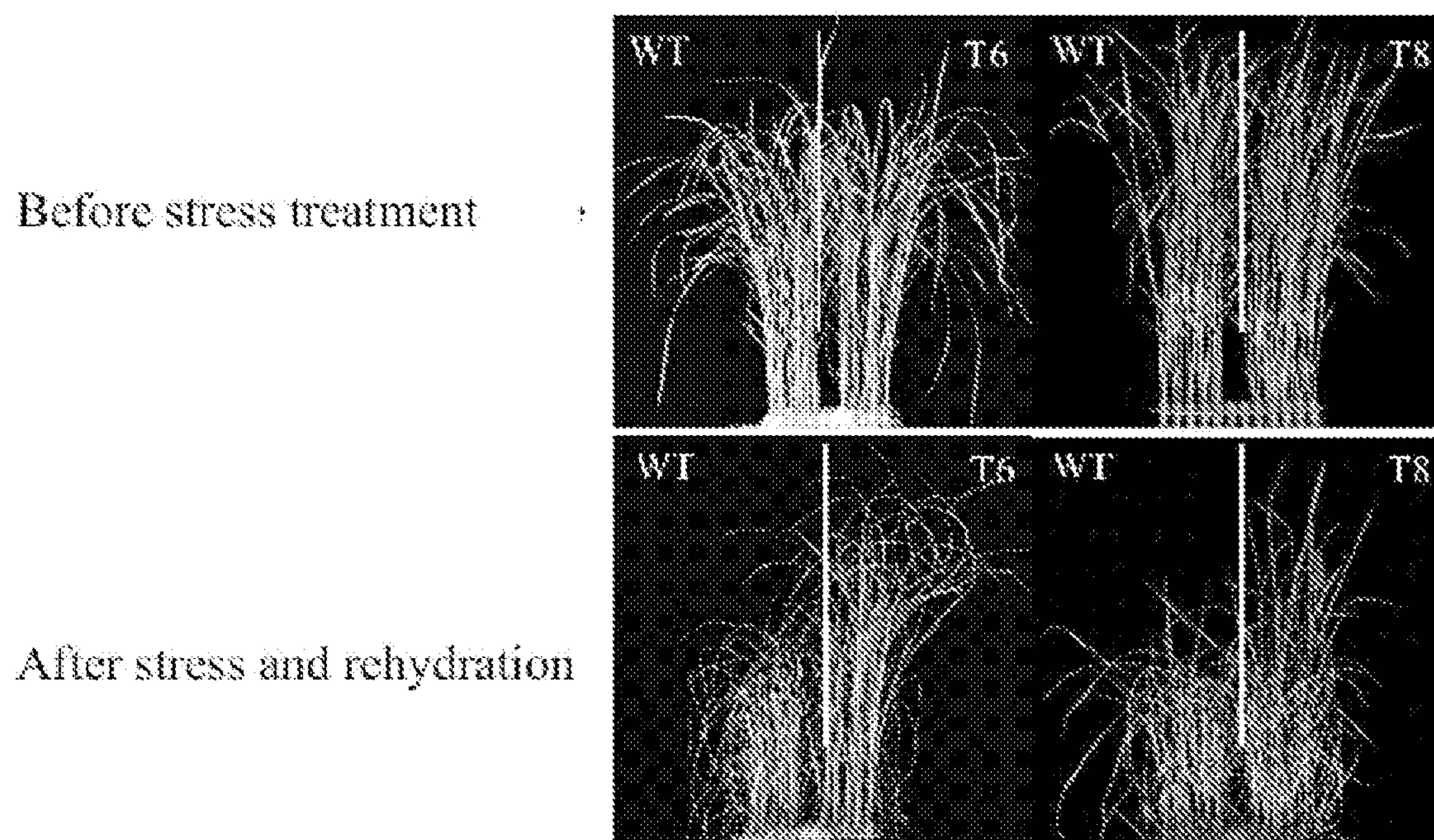


Fig. 4A

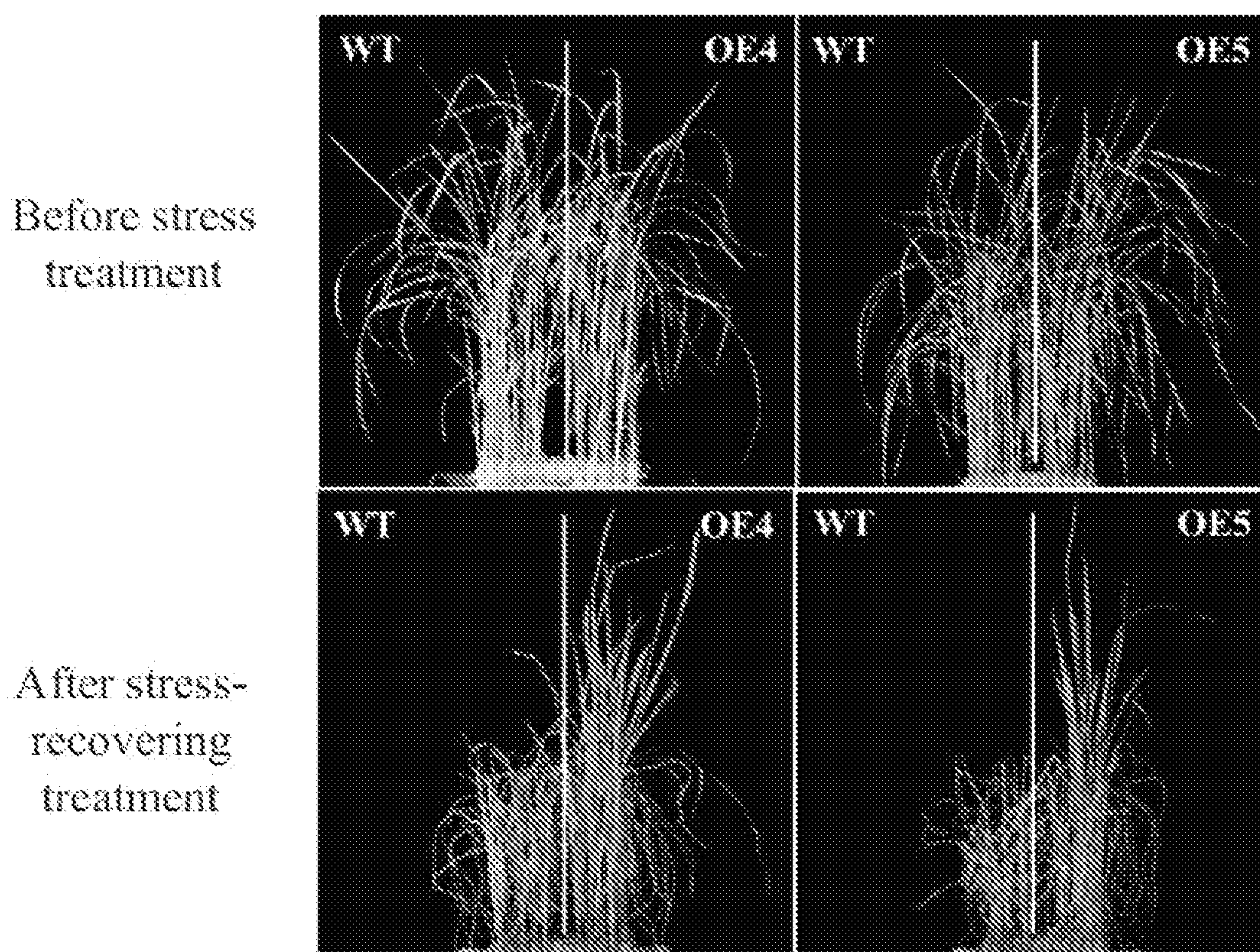


Fig. 4B

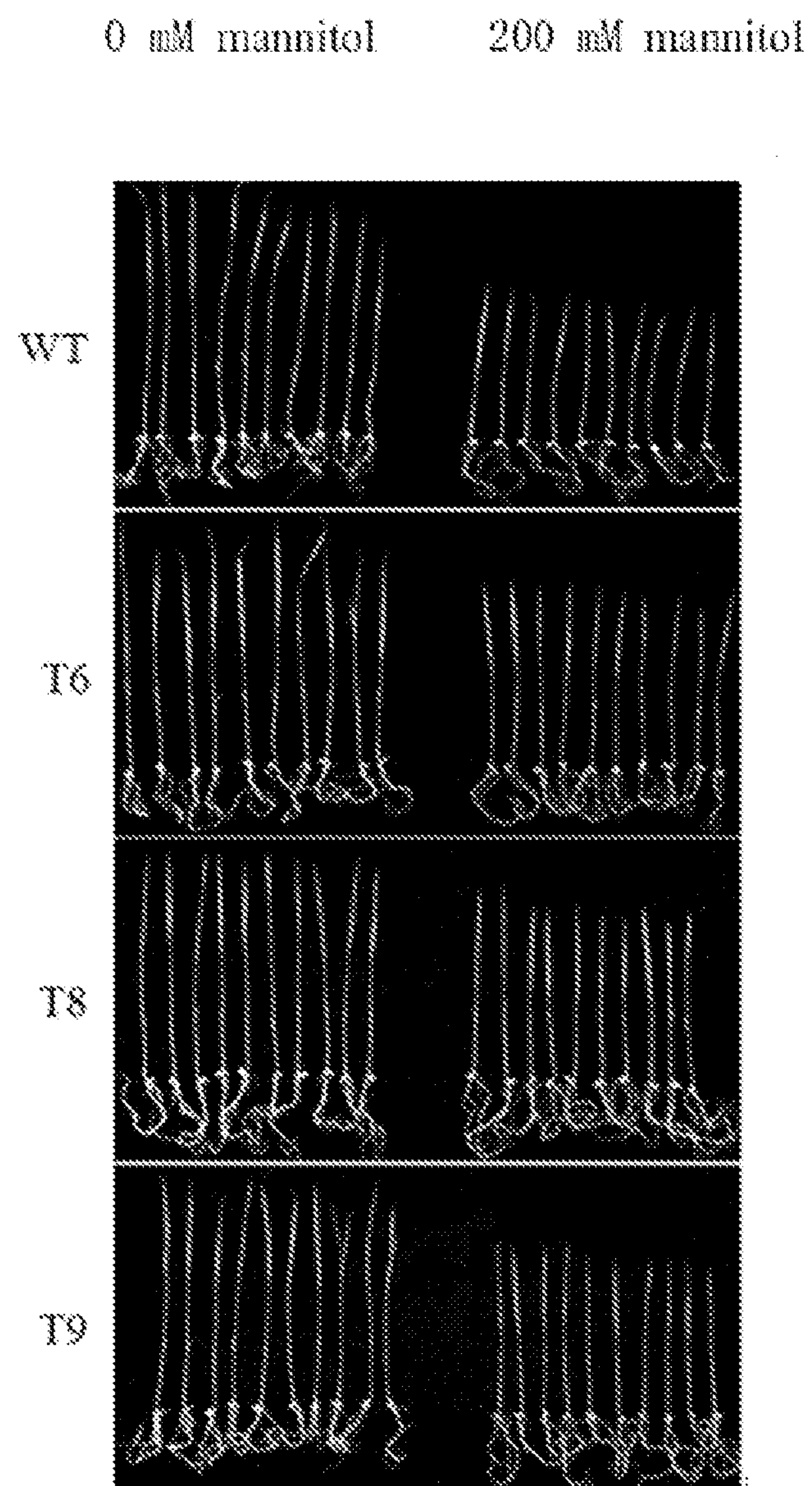


Fig. 5A

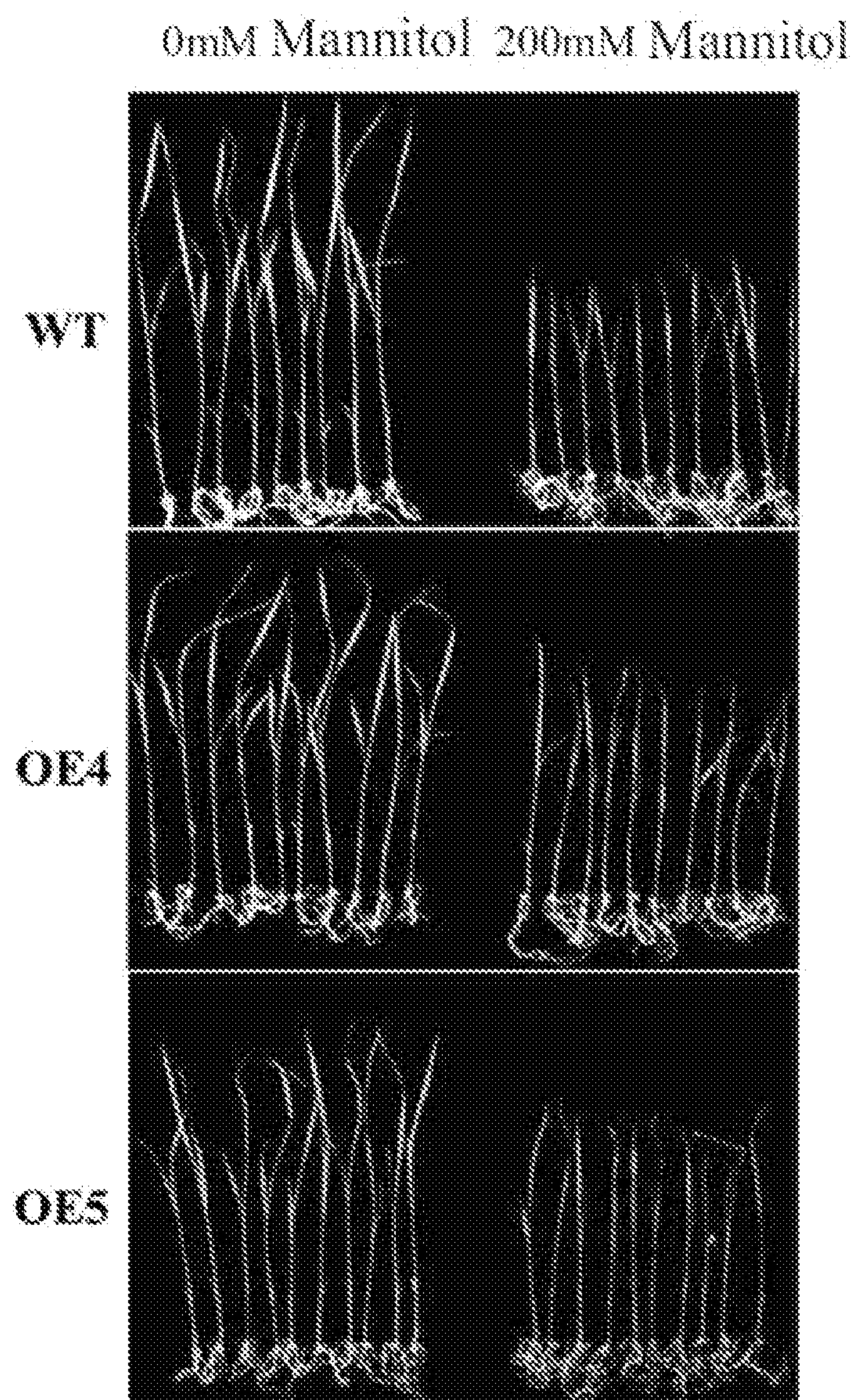


Fig. 5B

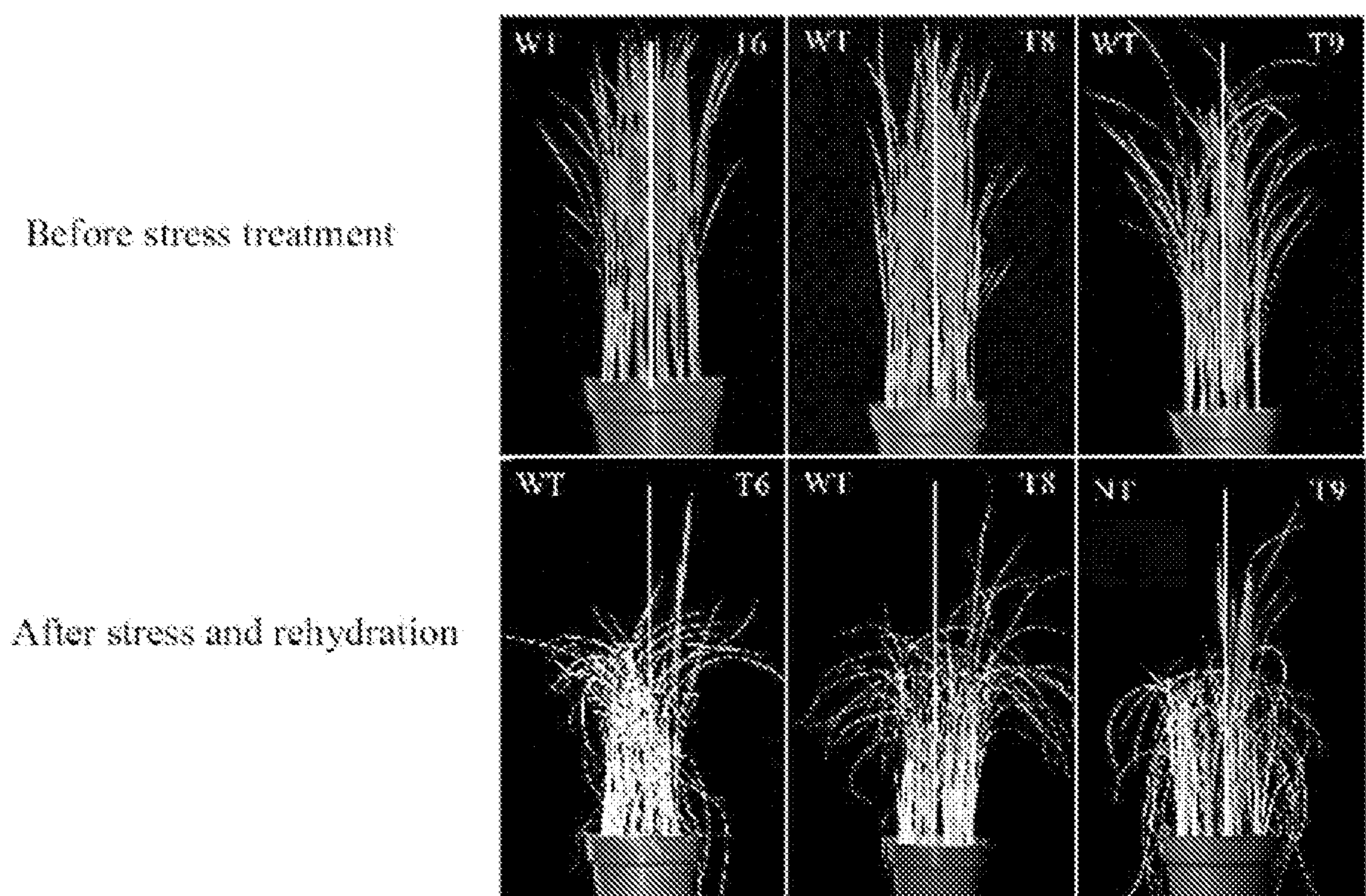


Fig. 6A

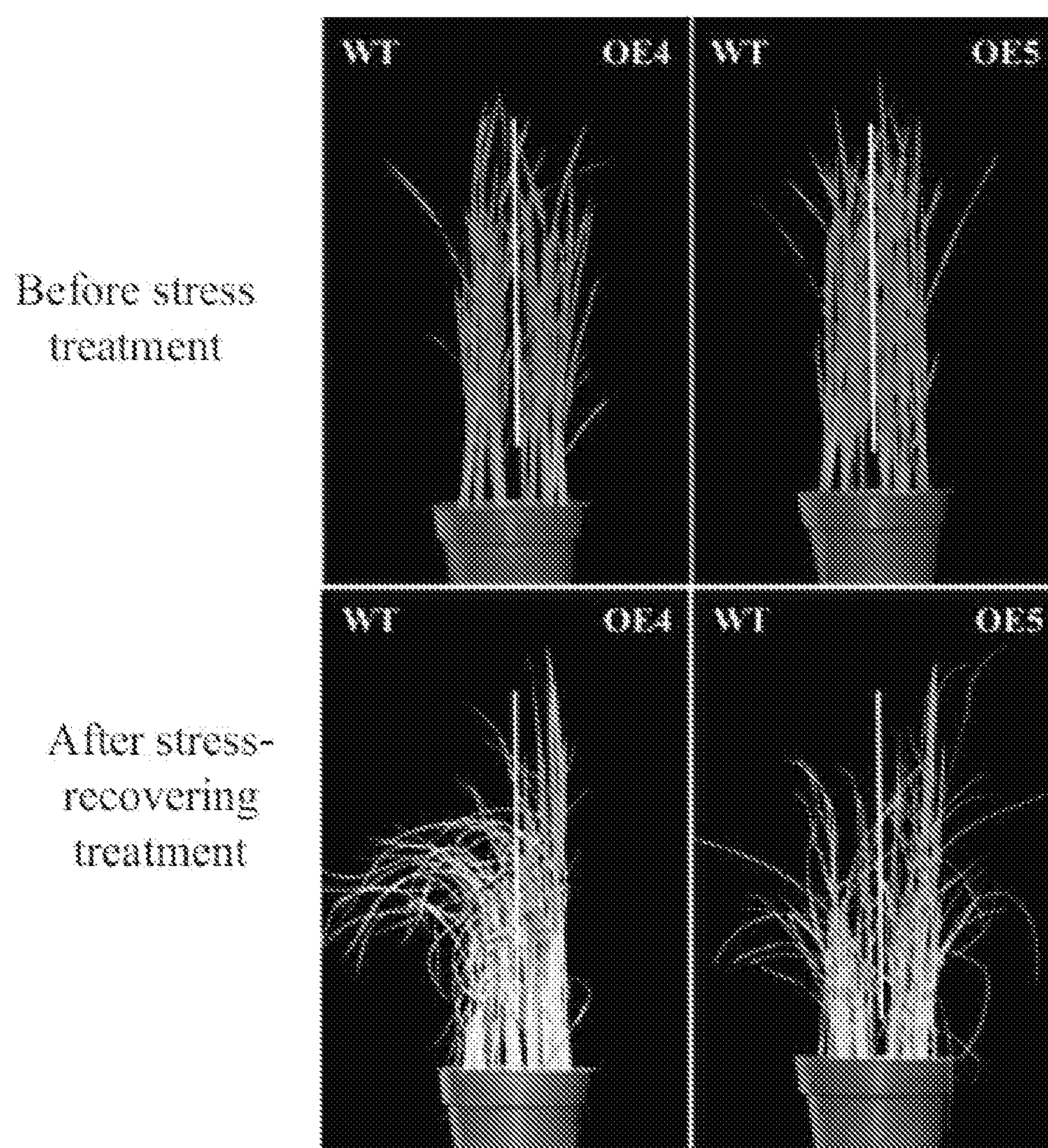
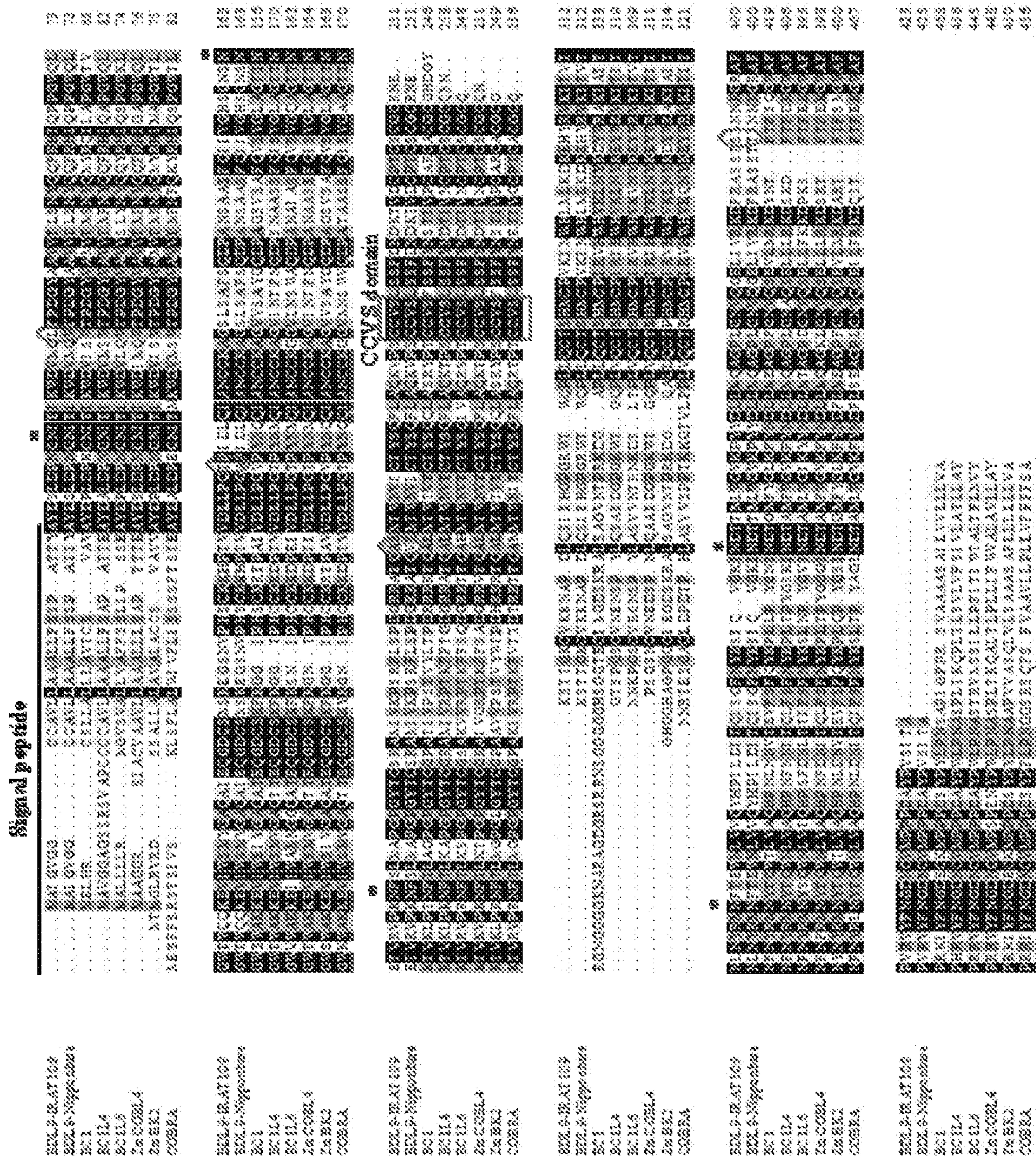


Fig. 6B



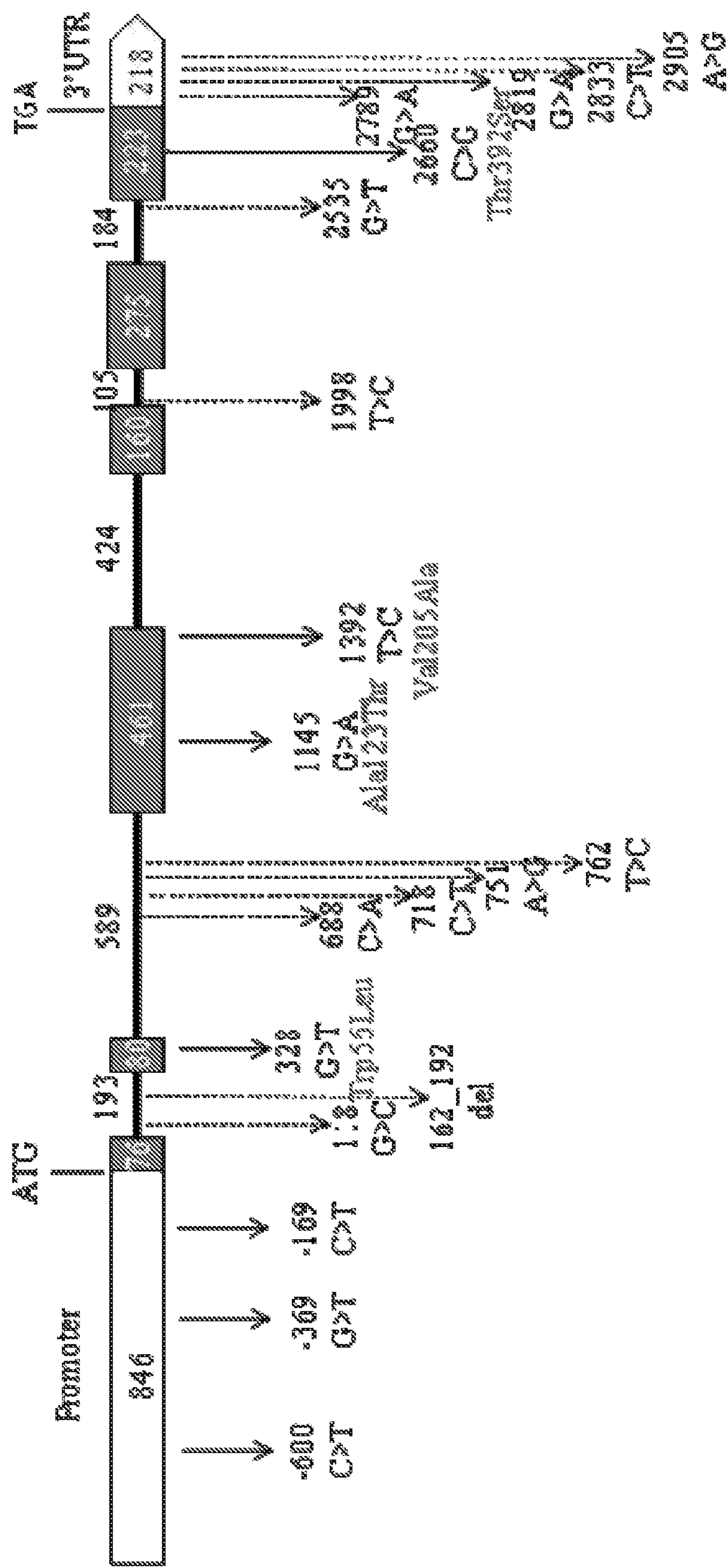


Fig. 8

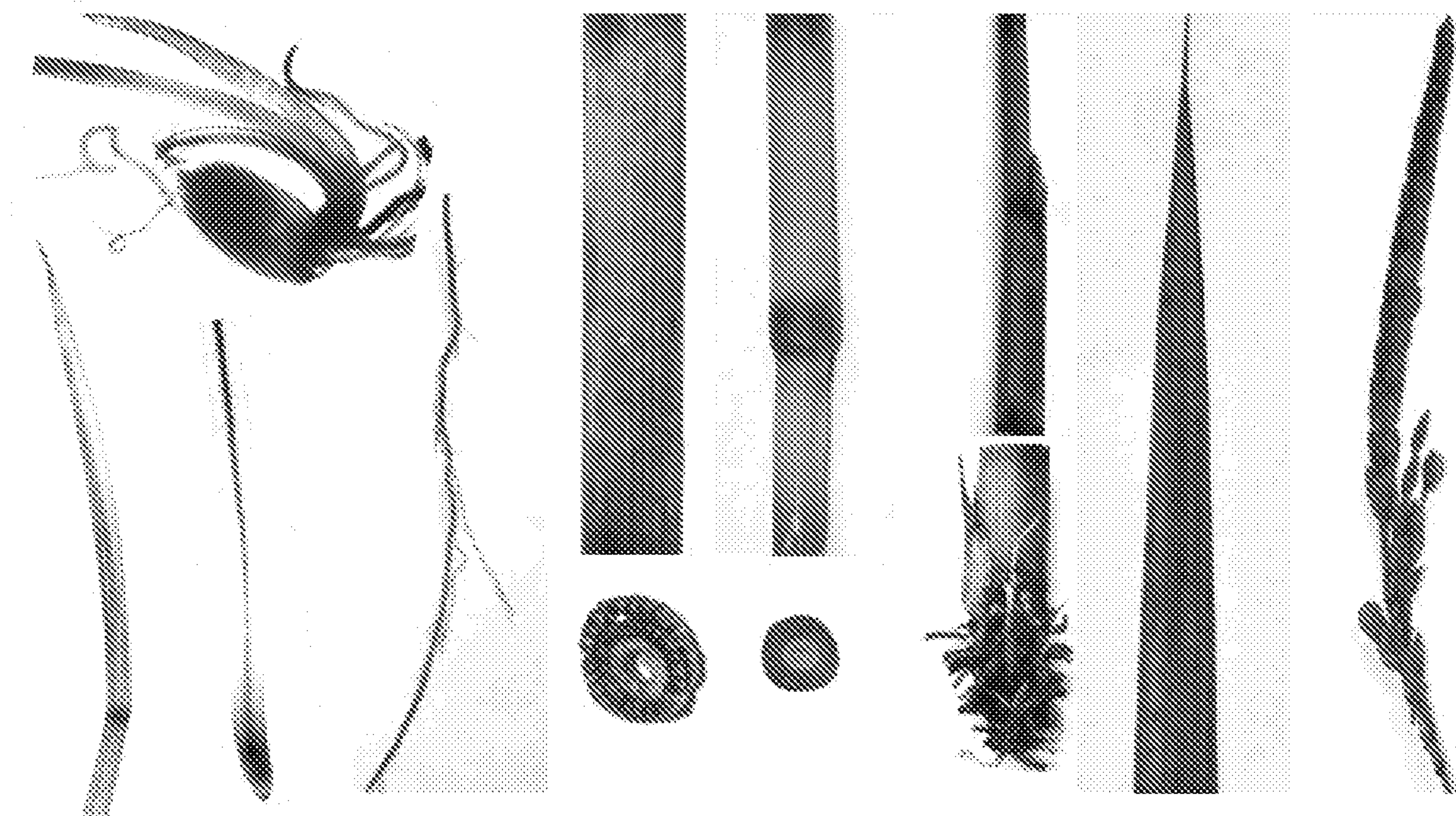


Fig. 9A

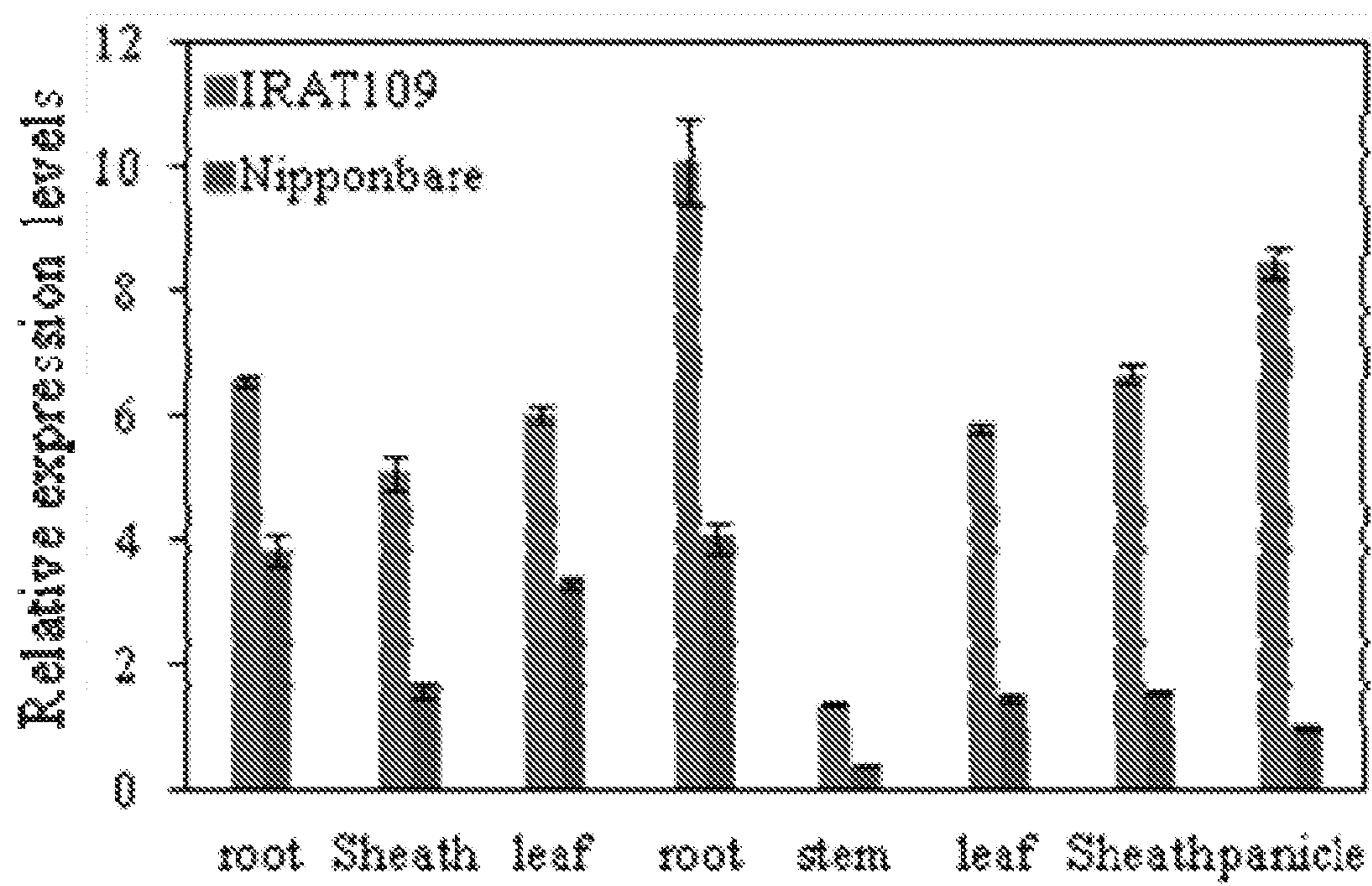


Fig. 9B

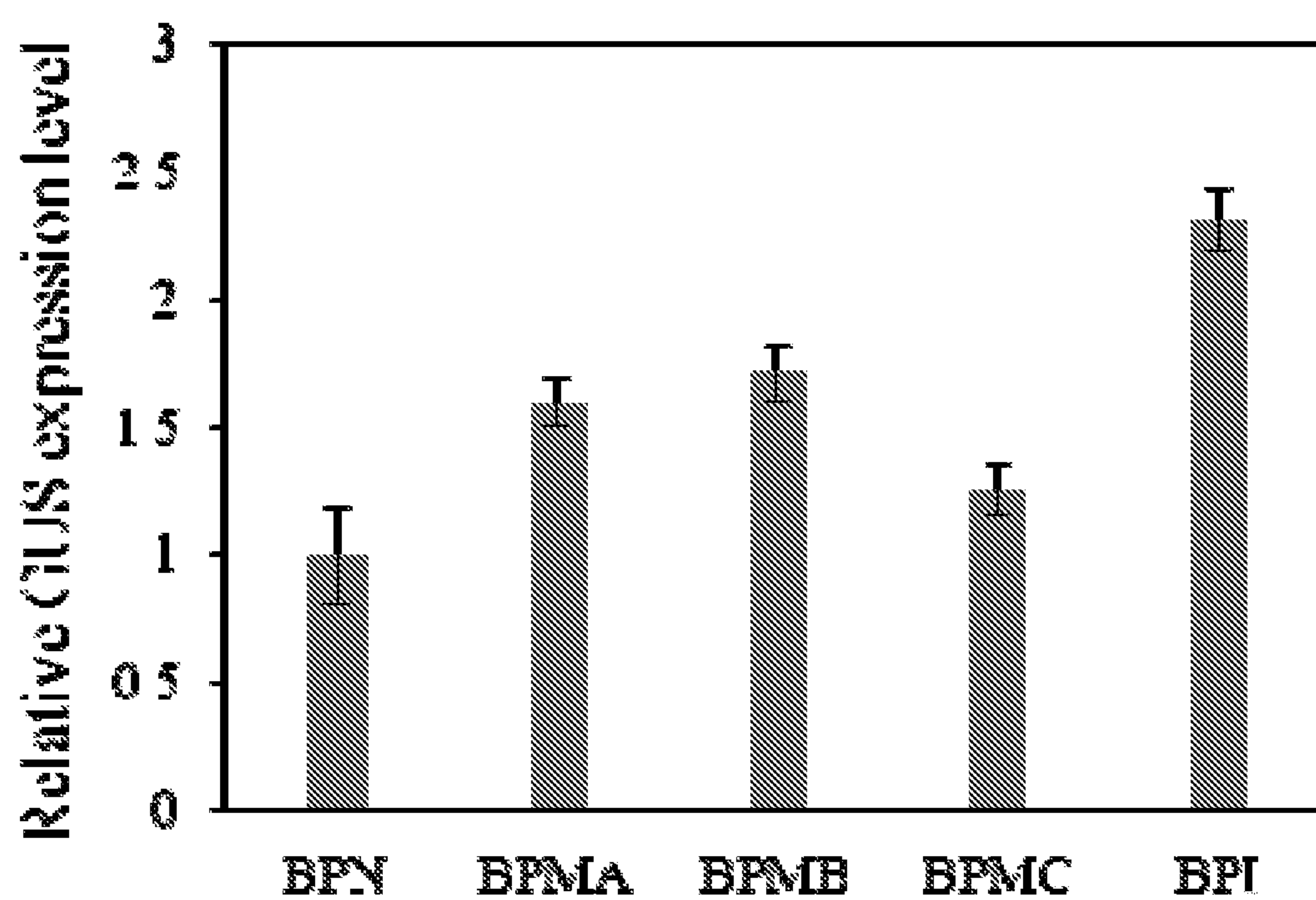


Fig. 10

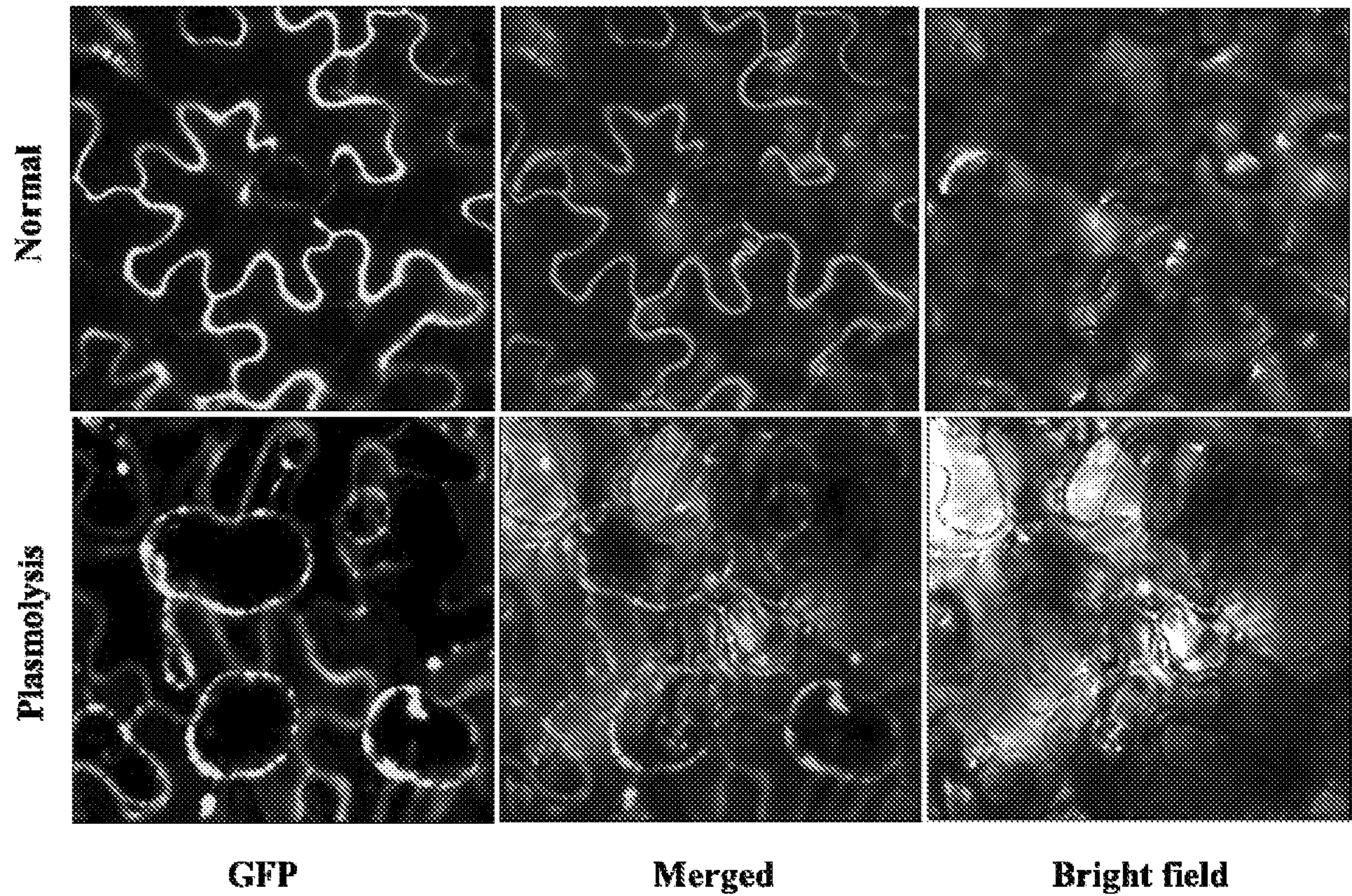


Fig. 11

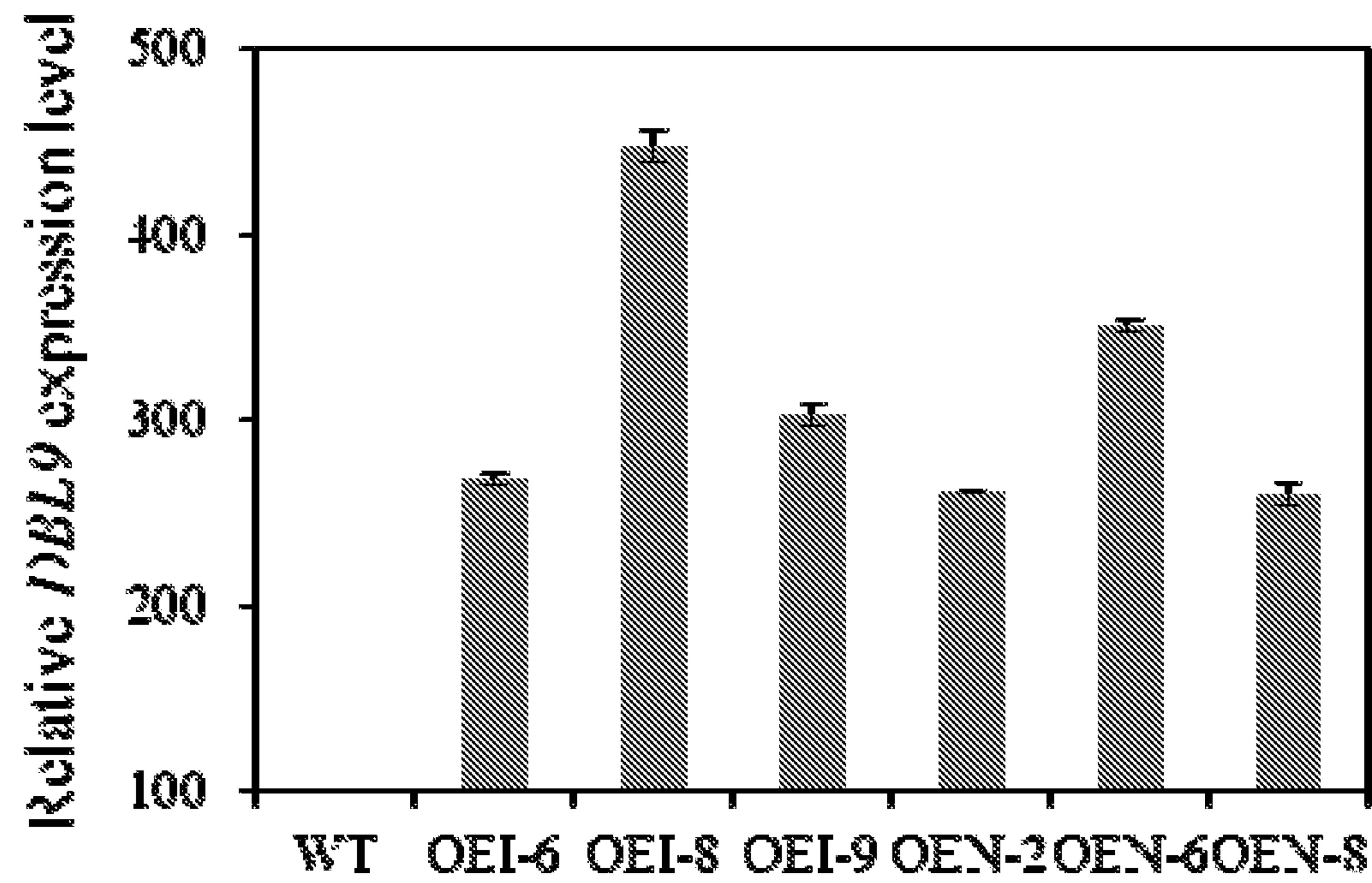


Fig. 12

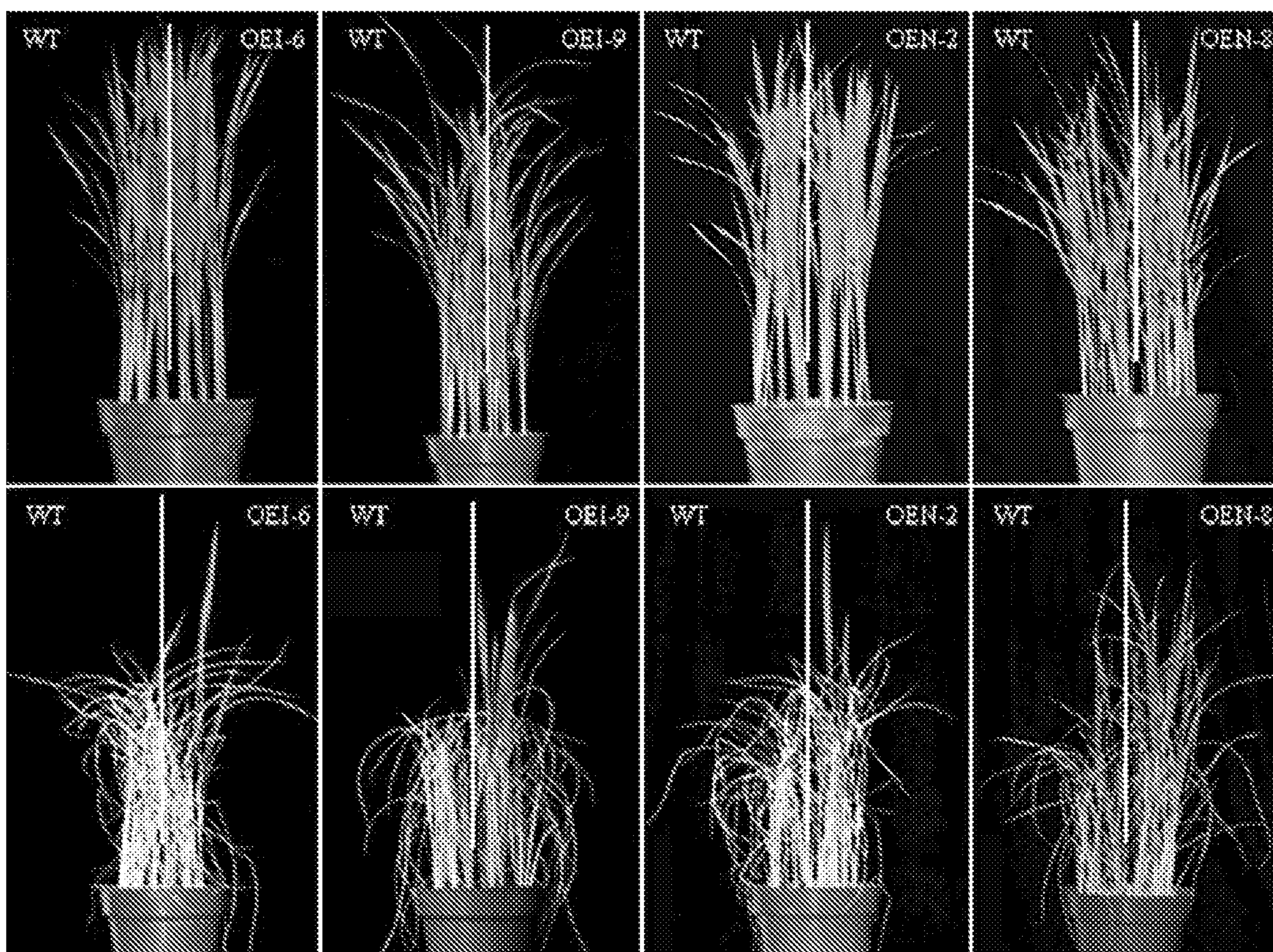


Fig. 13A

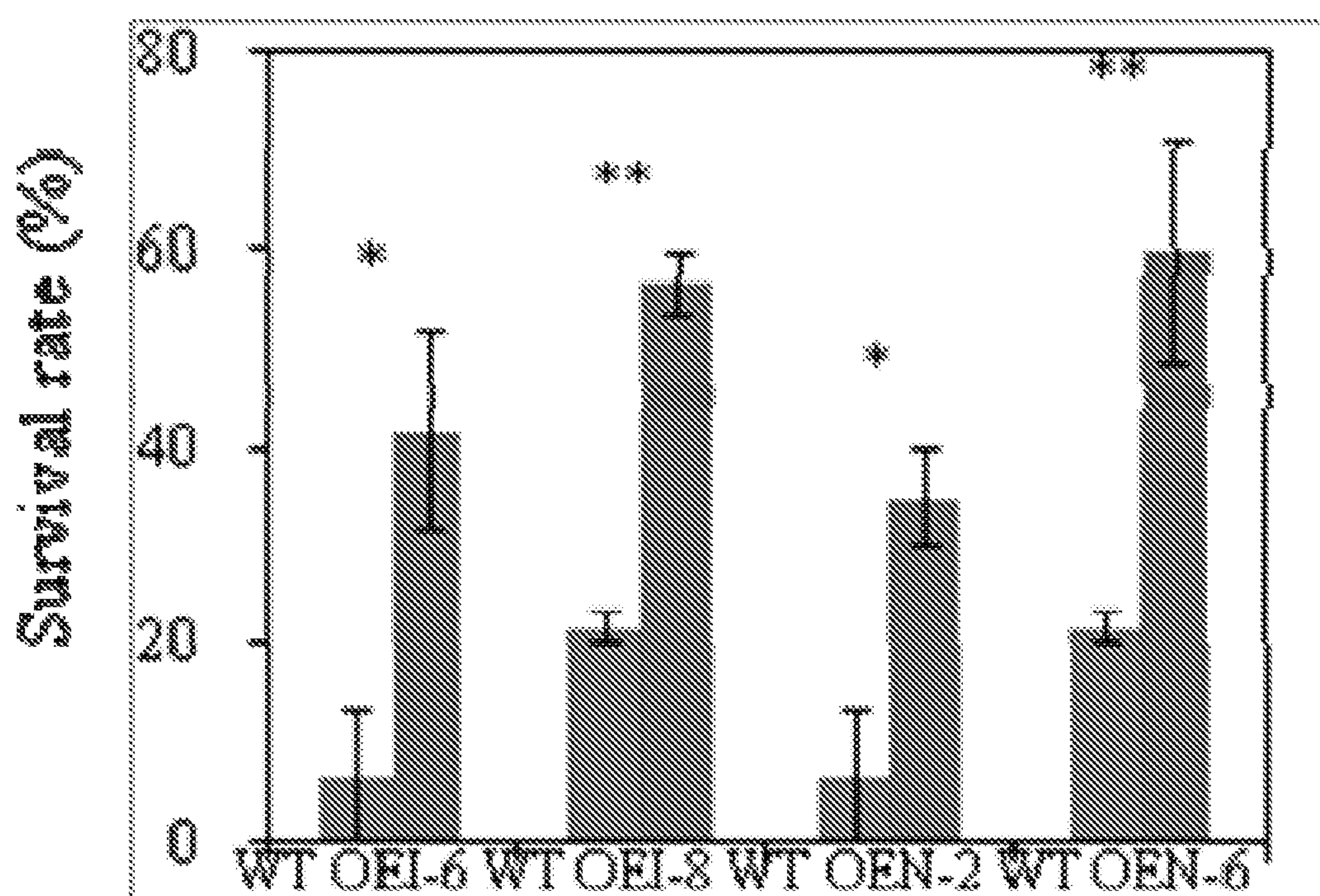


Fig. 13B

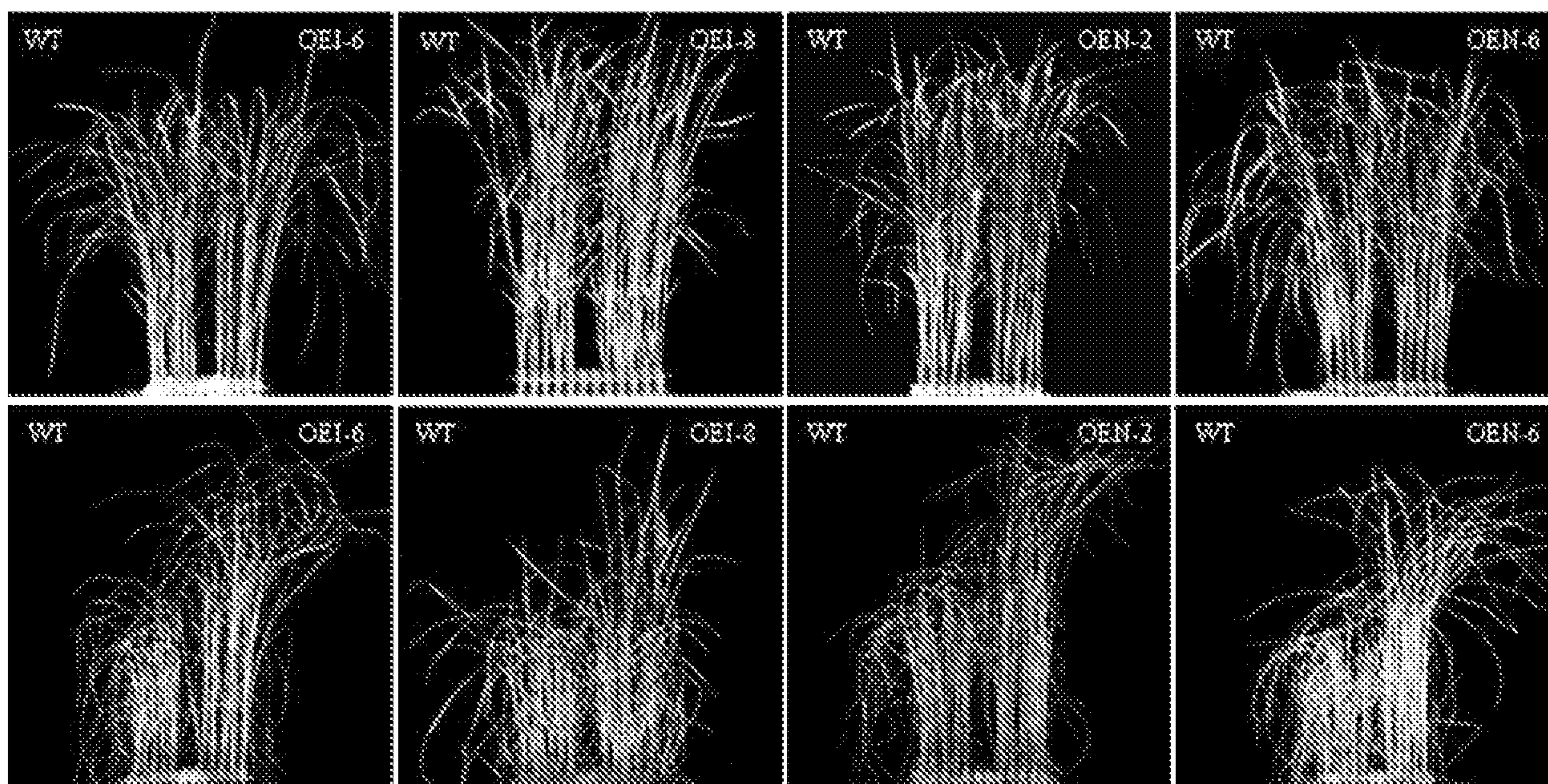


Fig. 14A

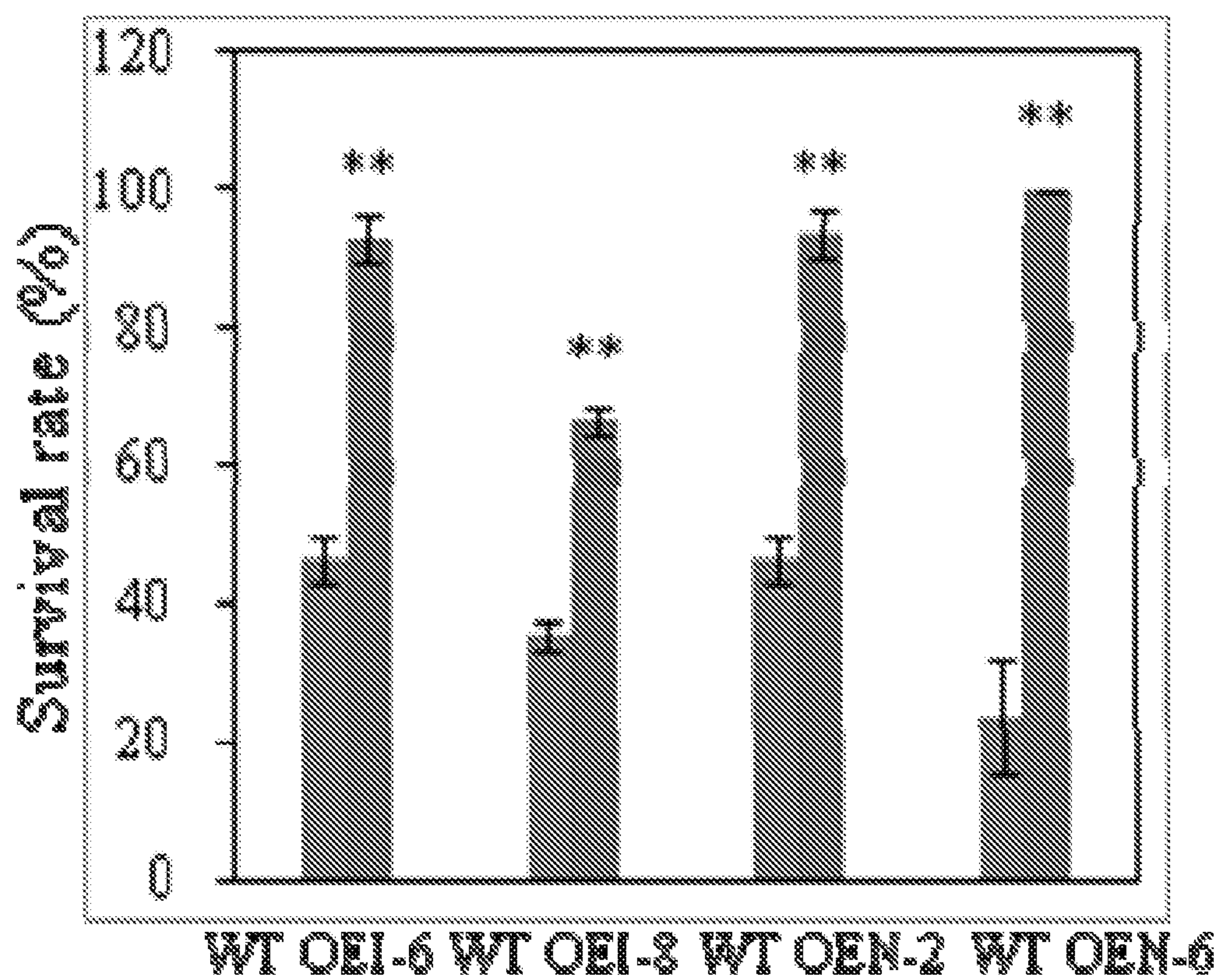


Fig. 14B

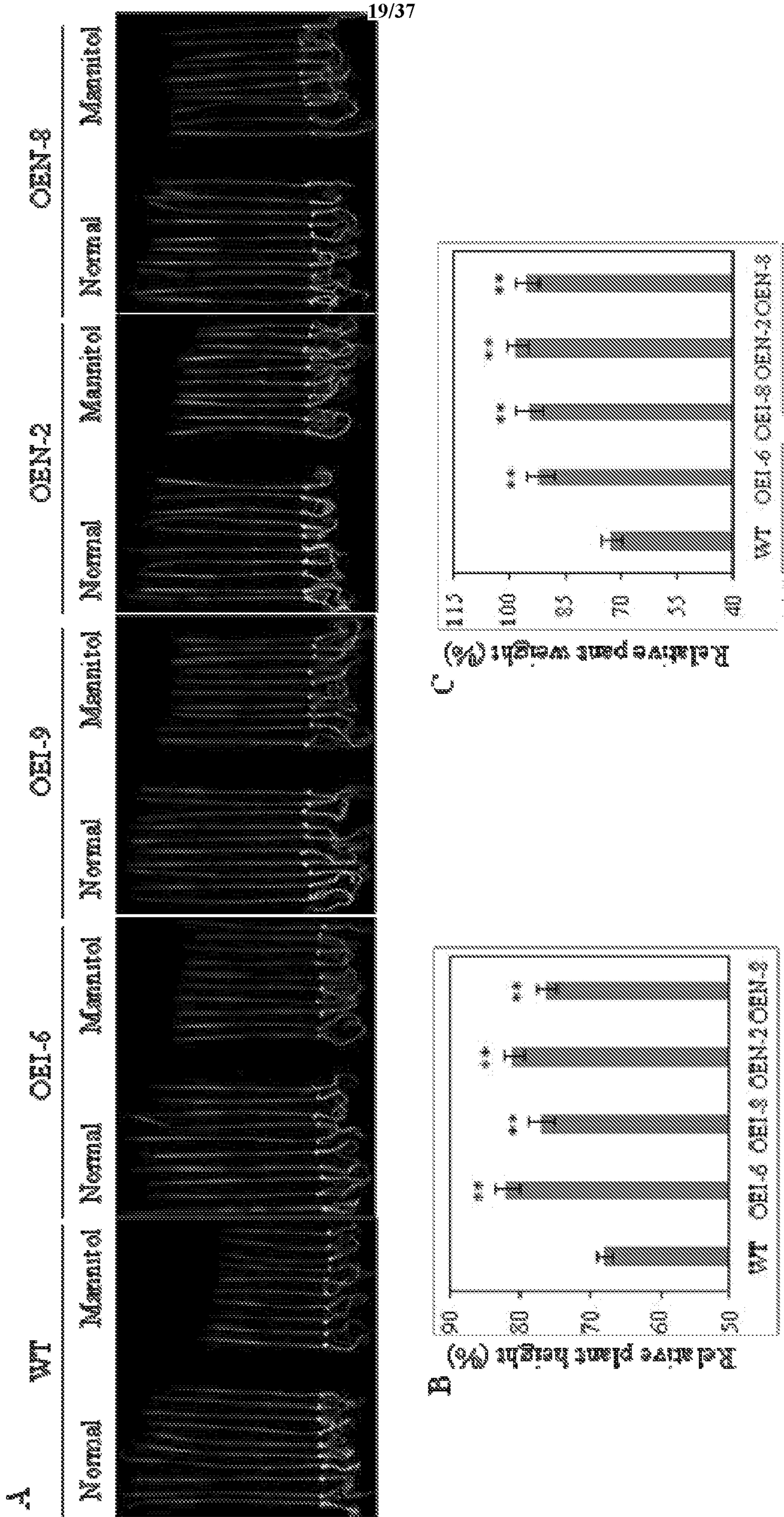


Fig. 15

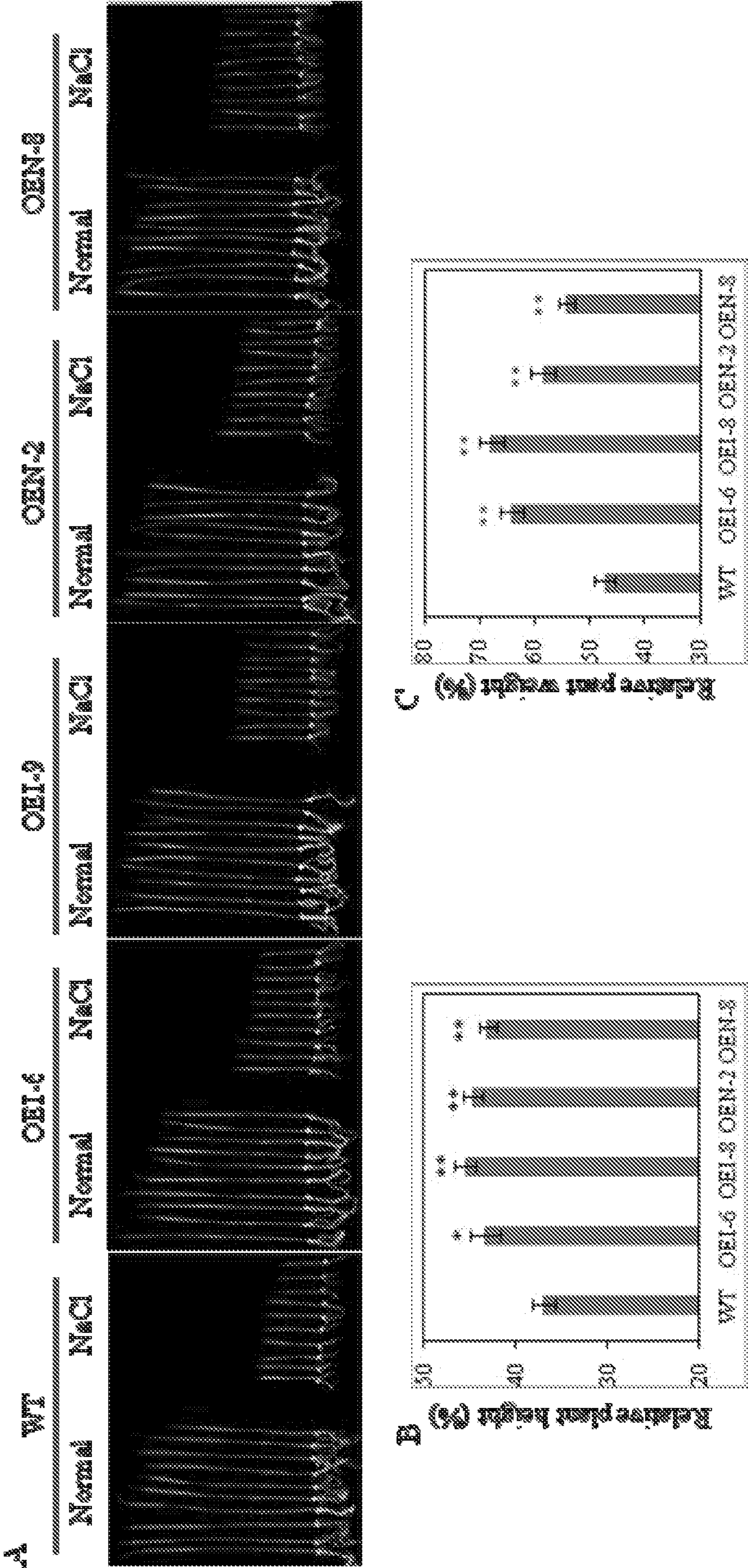


Fig. 16

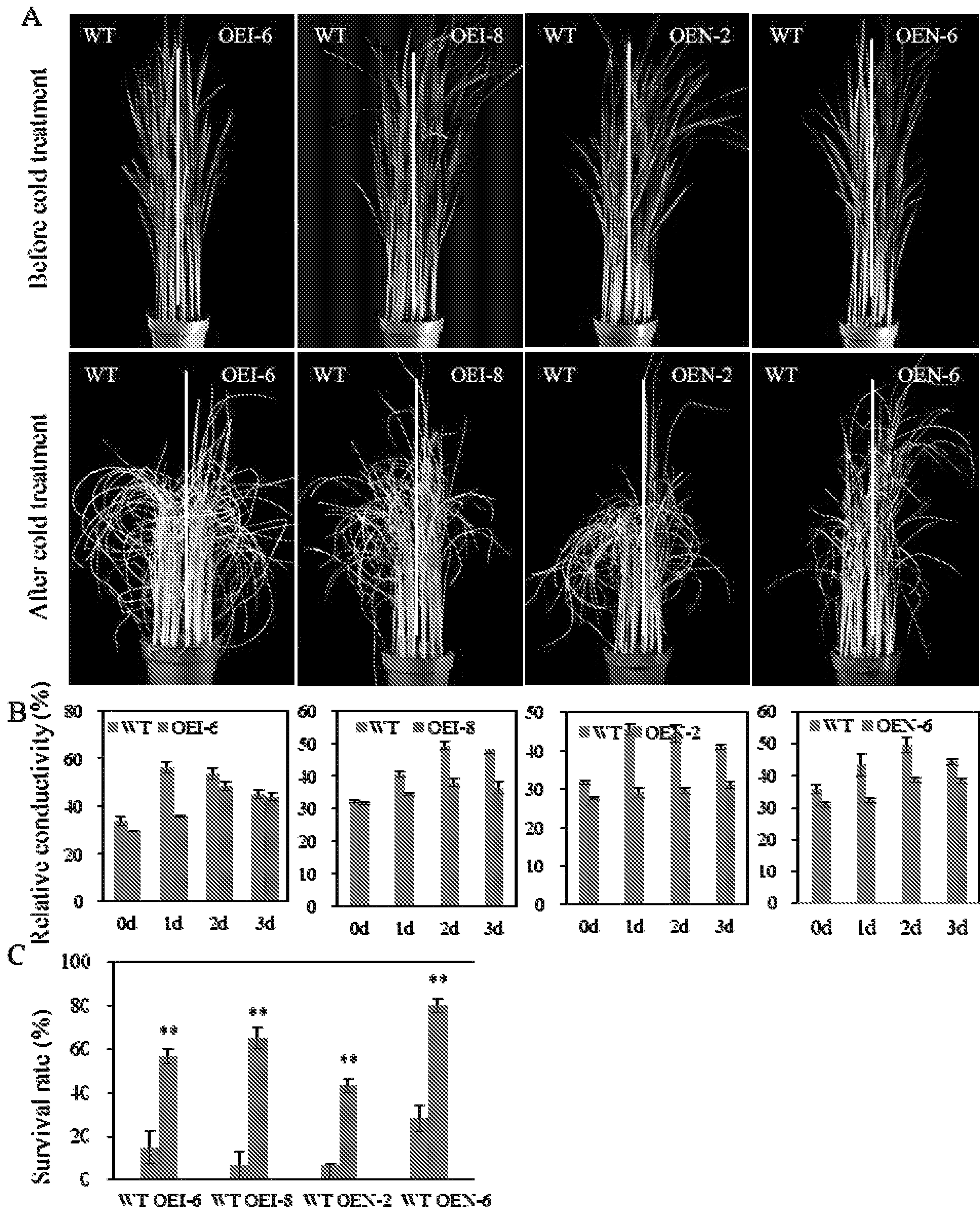


Fig. 17

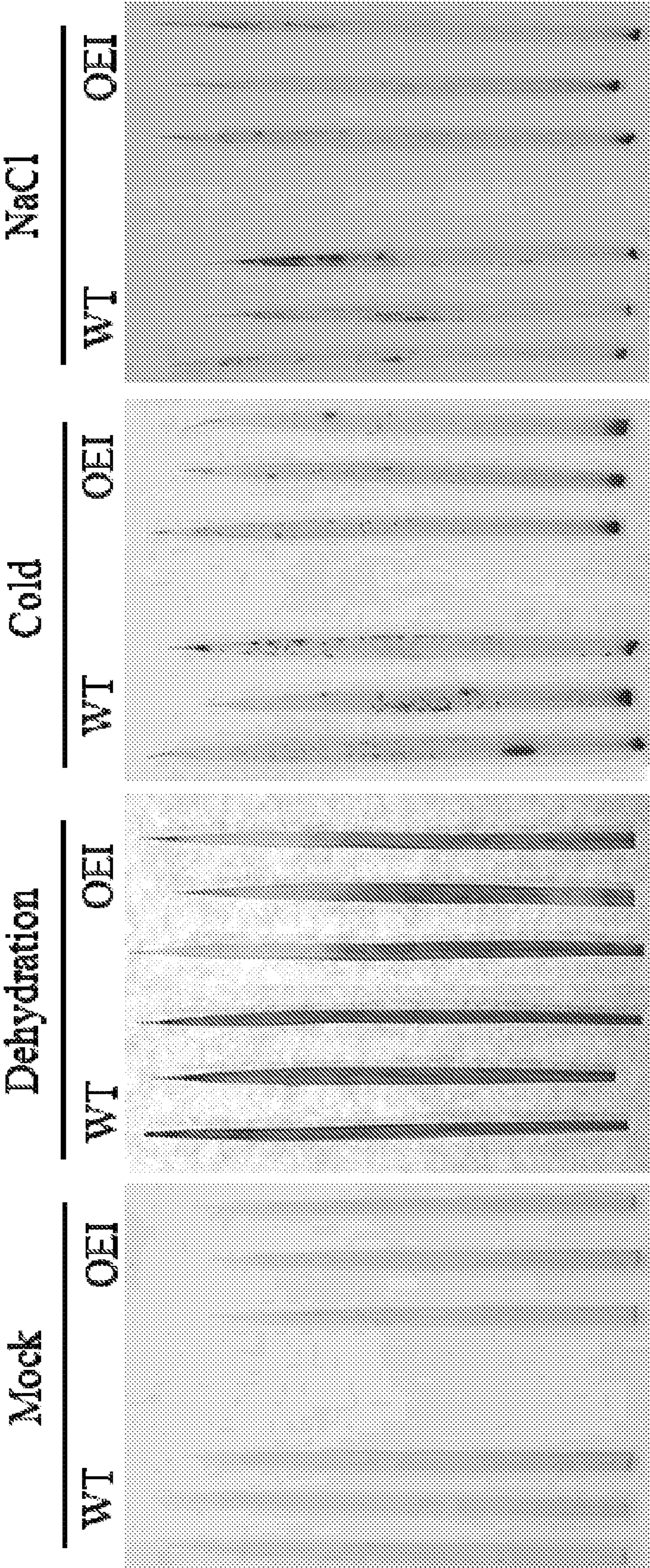


Fig. 18

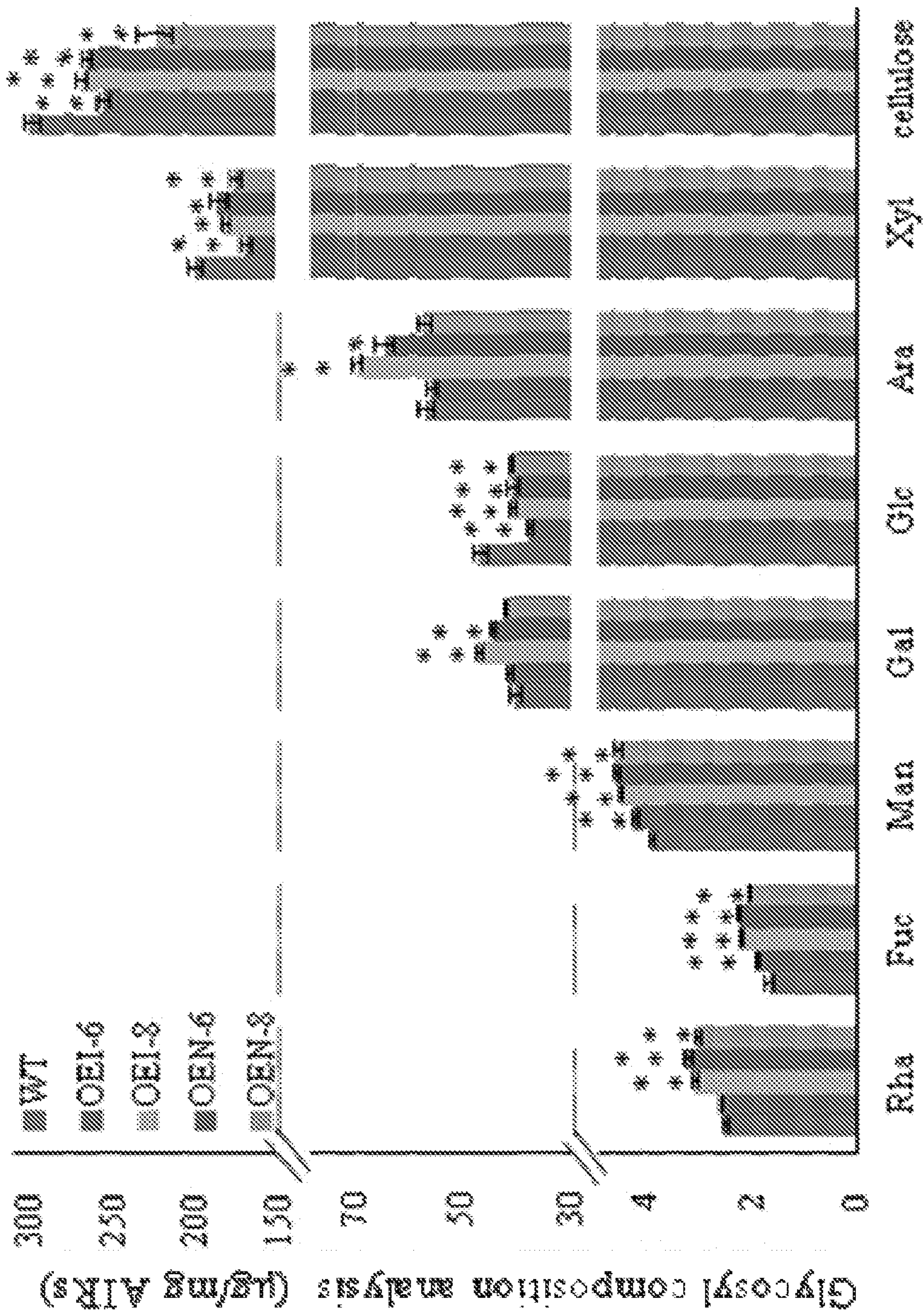


Fig. 19

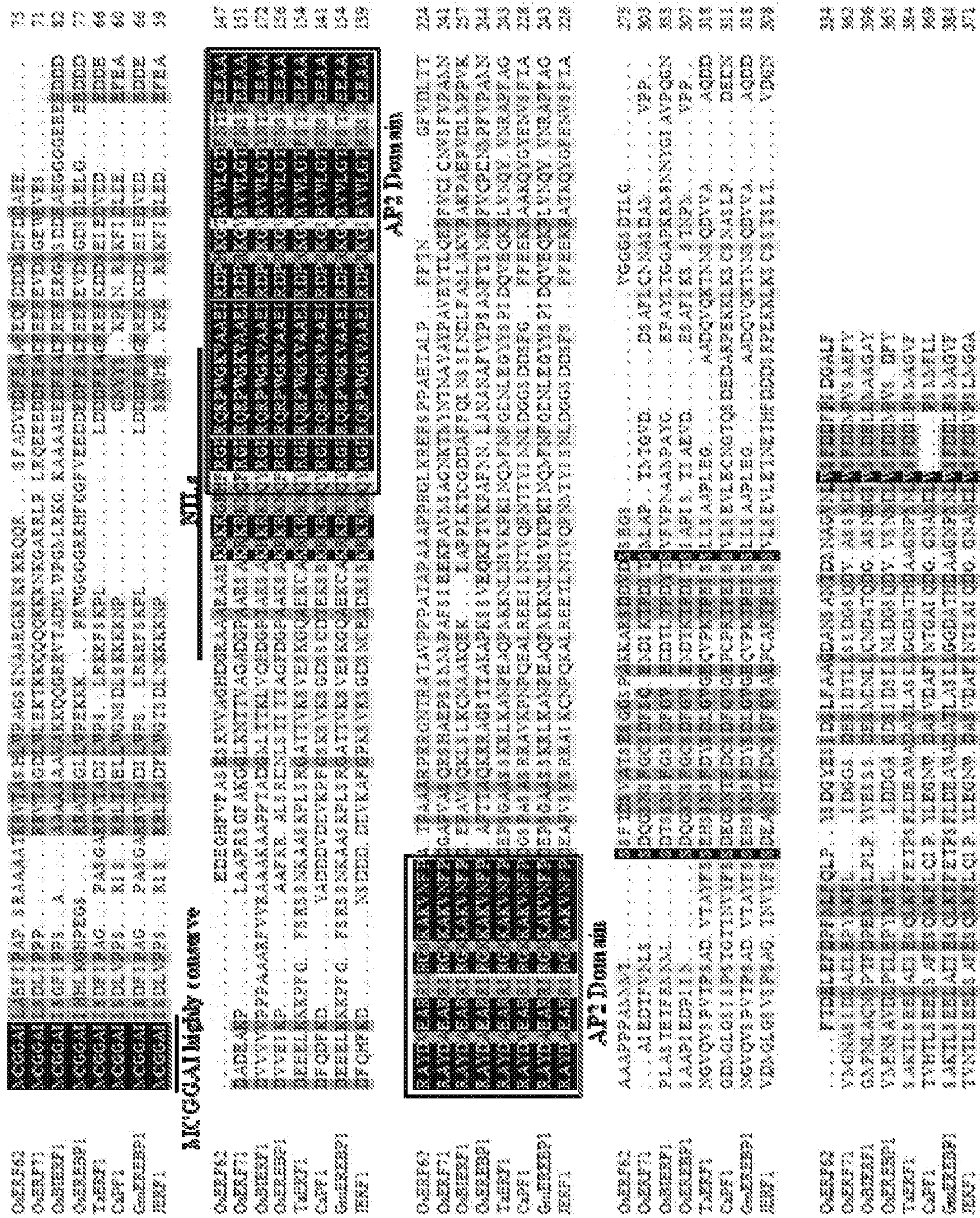


**Fig. 20**

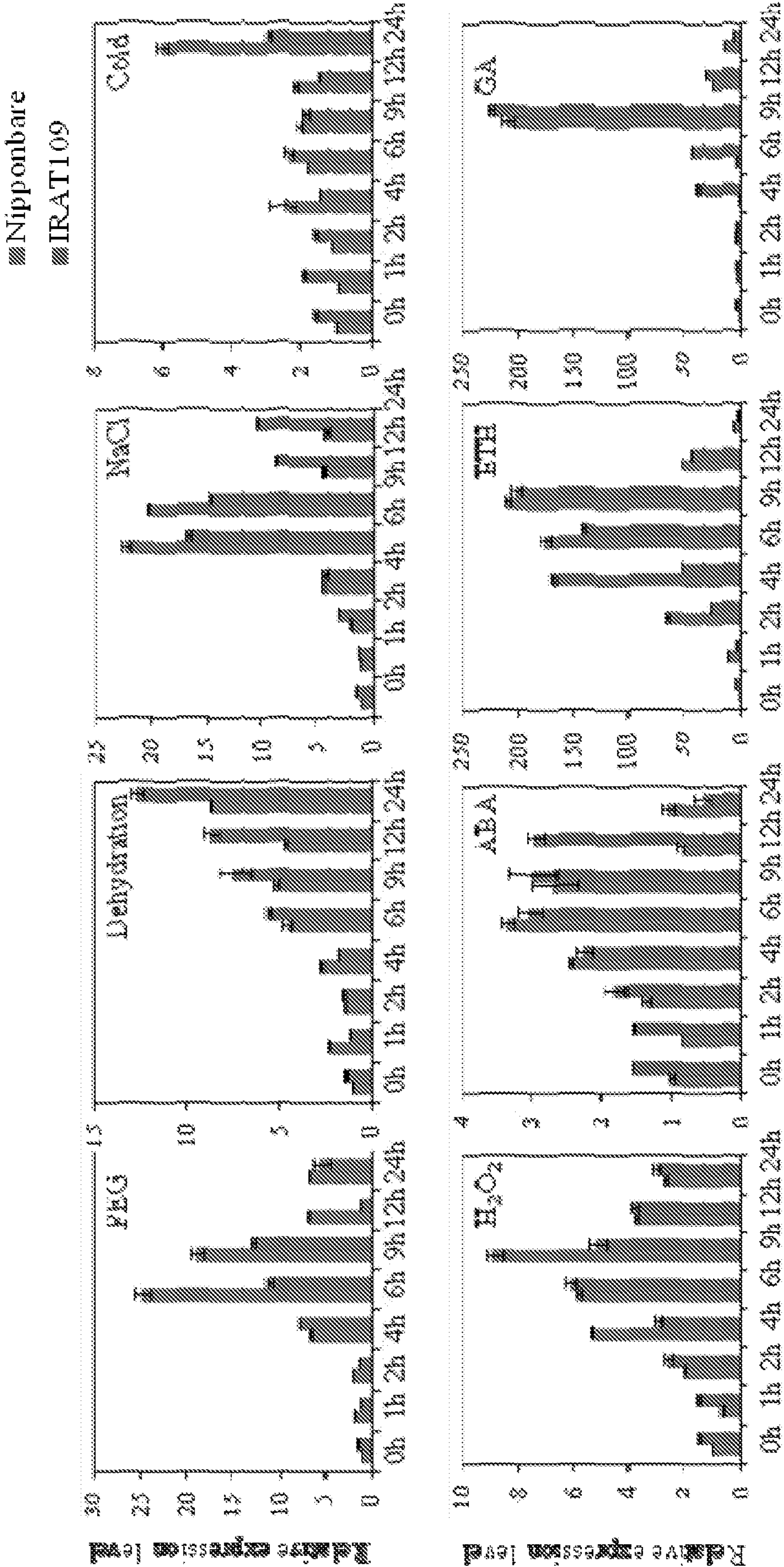


Fig. 21

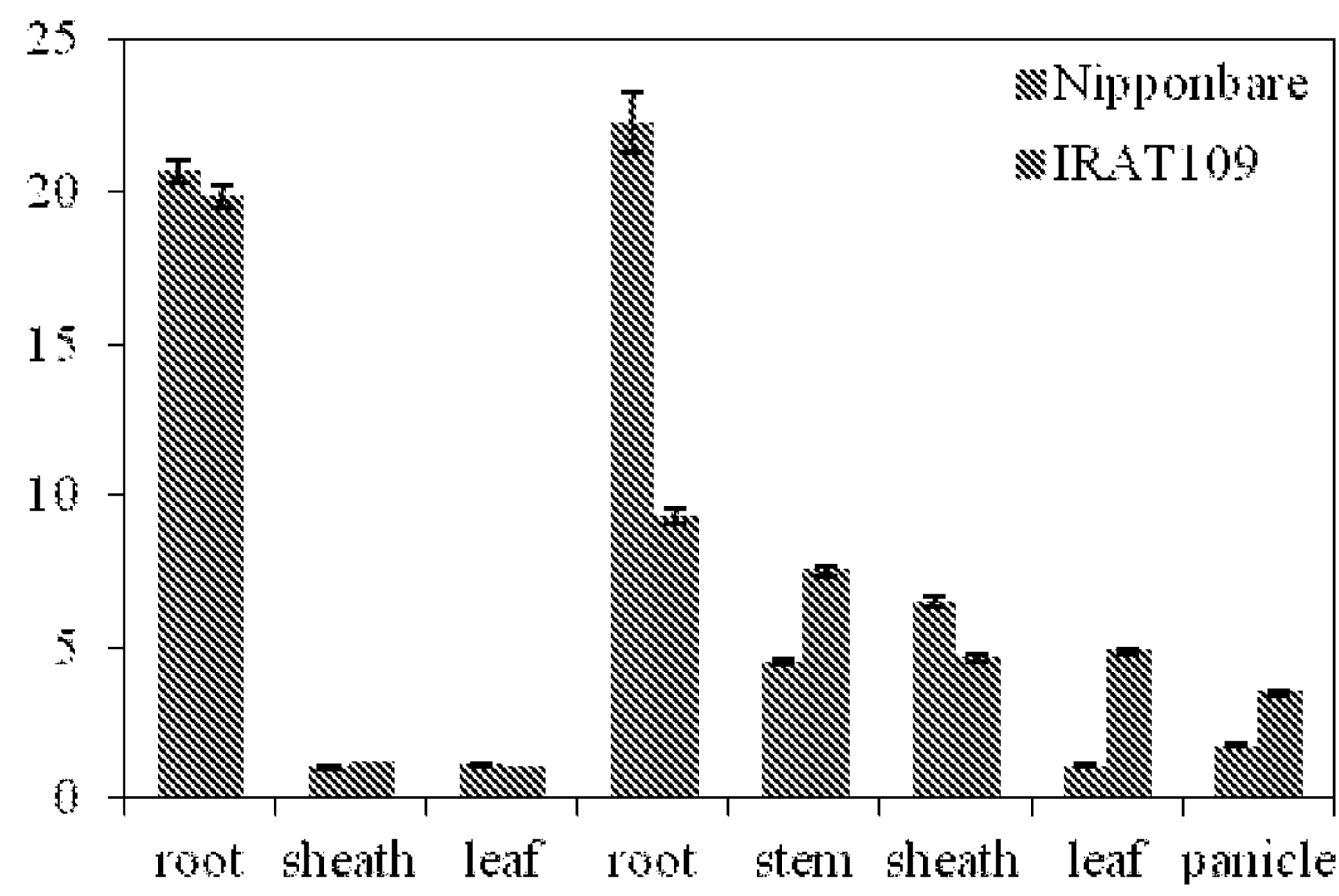


Fig. 22

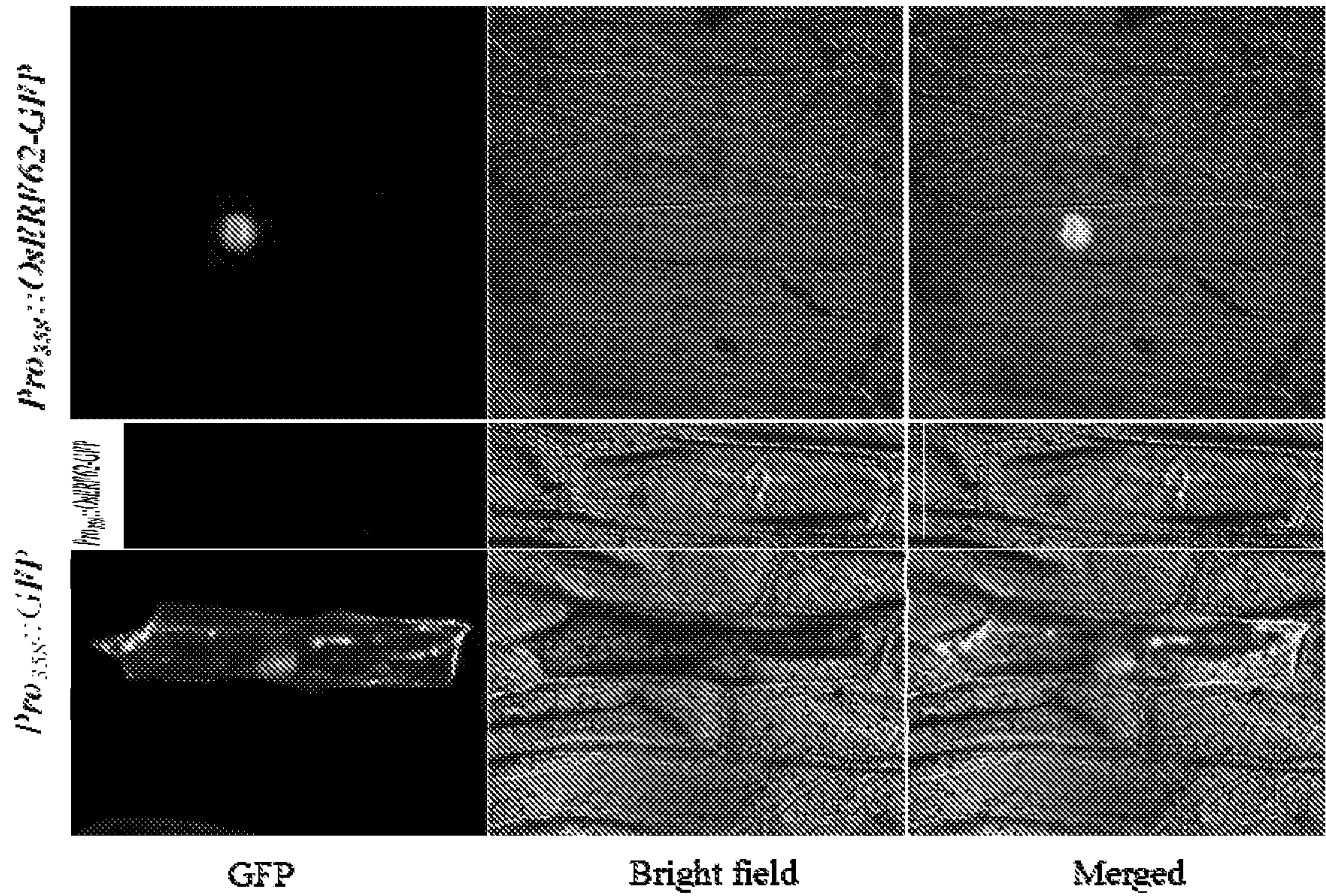


Fig. 23

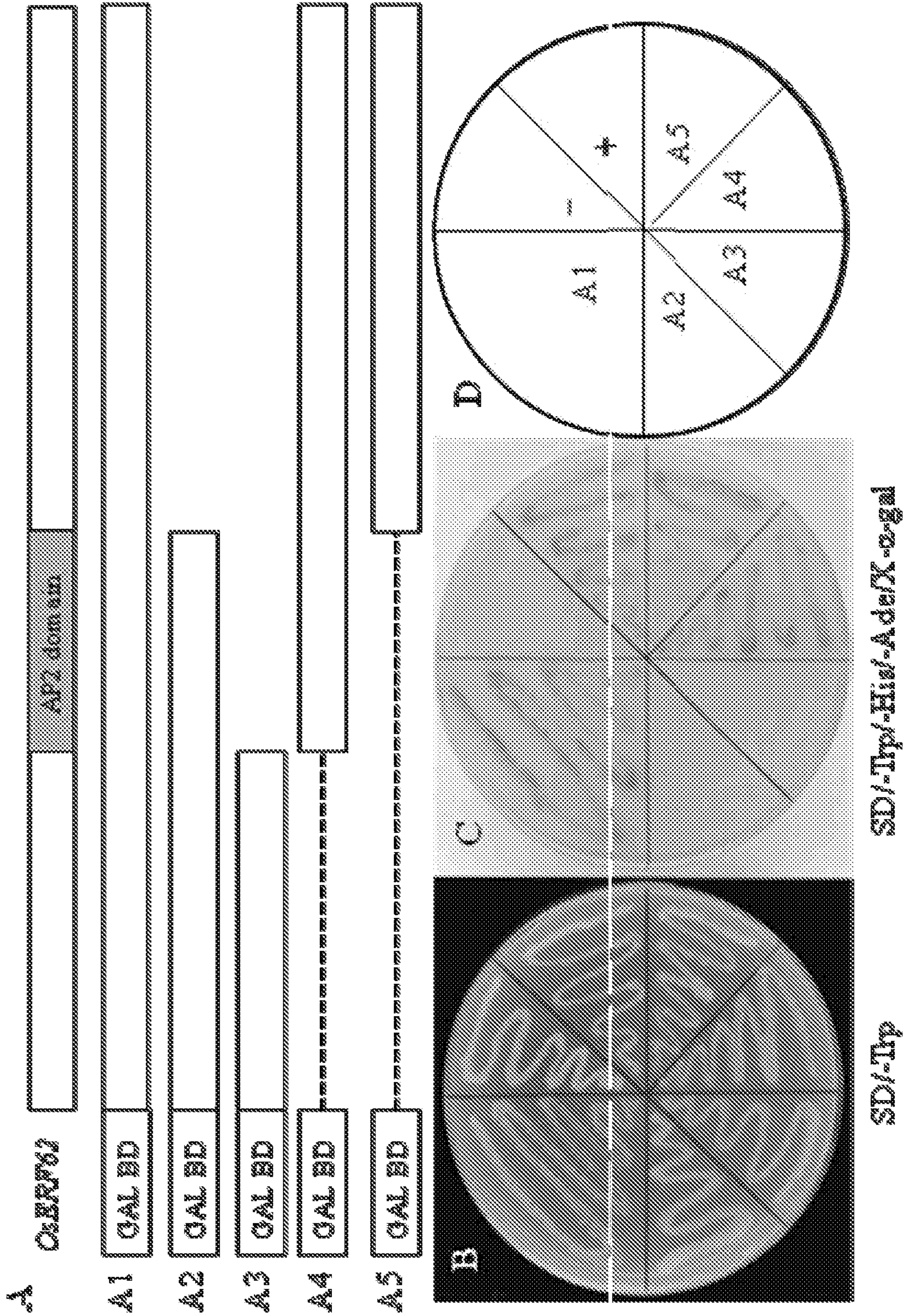


Fig. 24

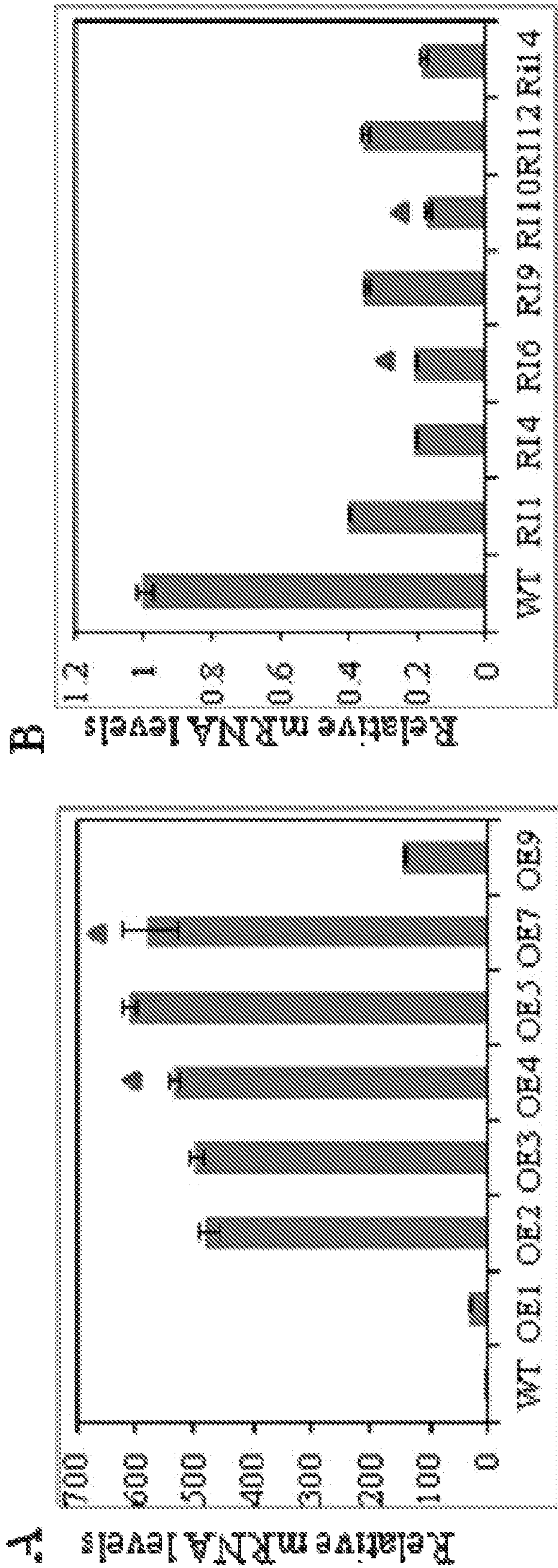


Fig. 25

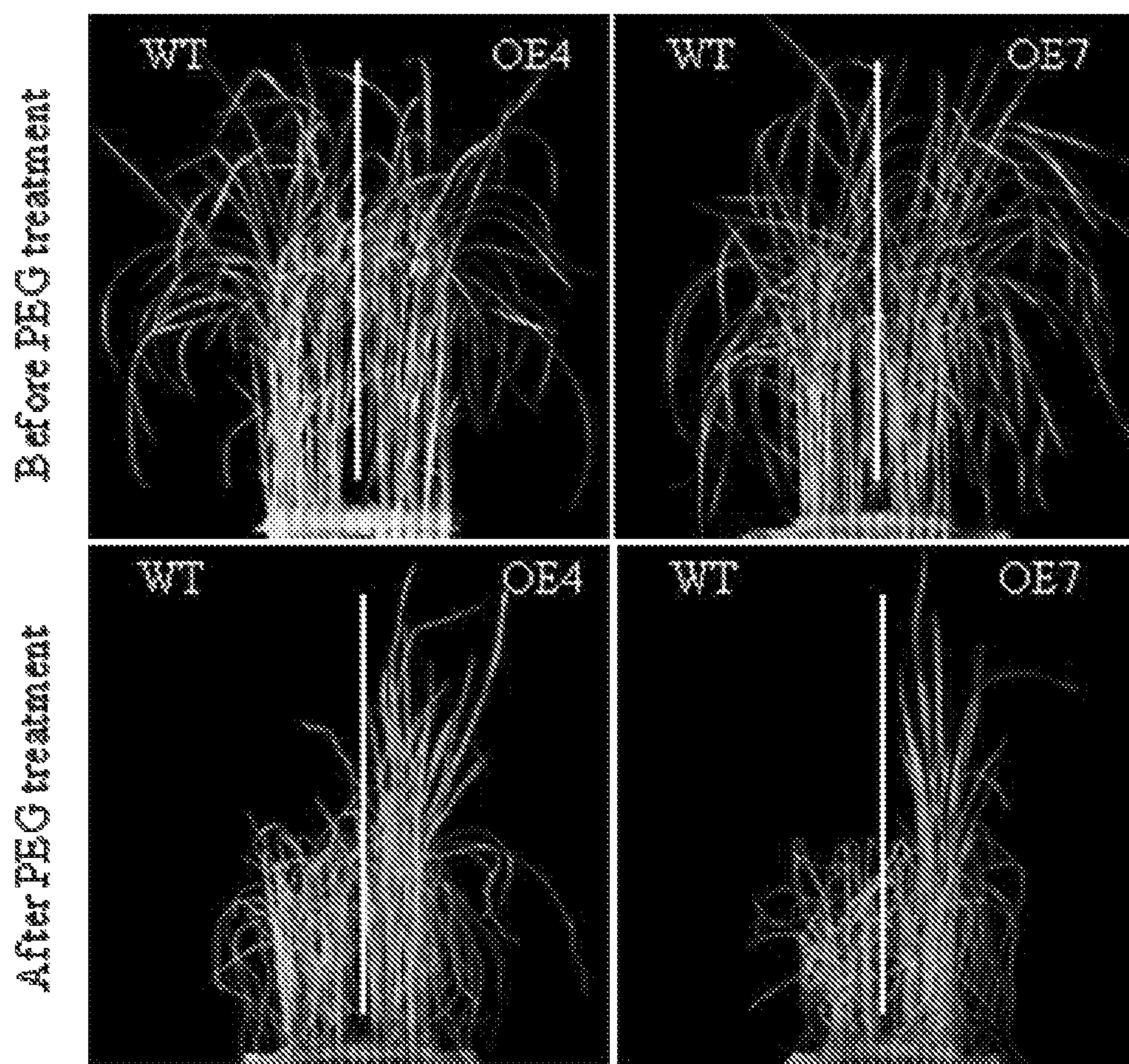


Fig. 26A

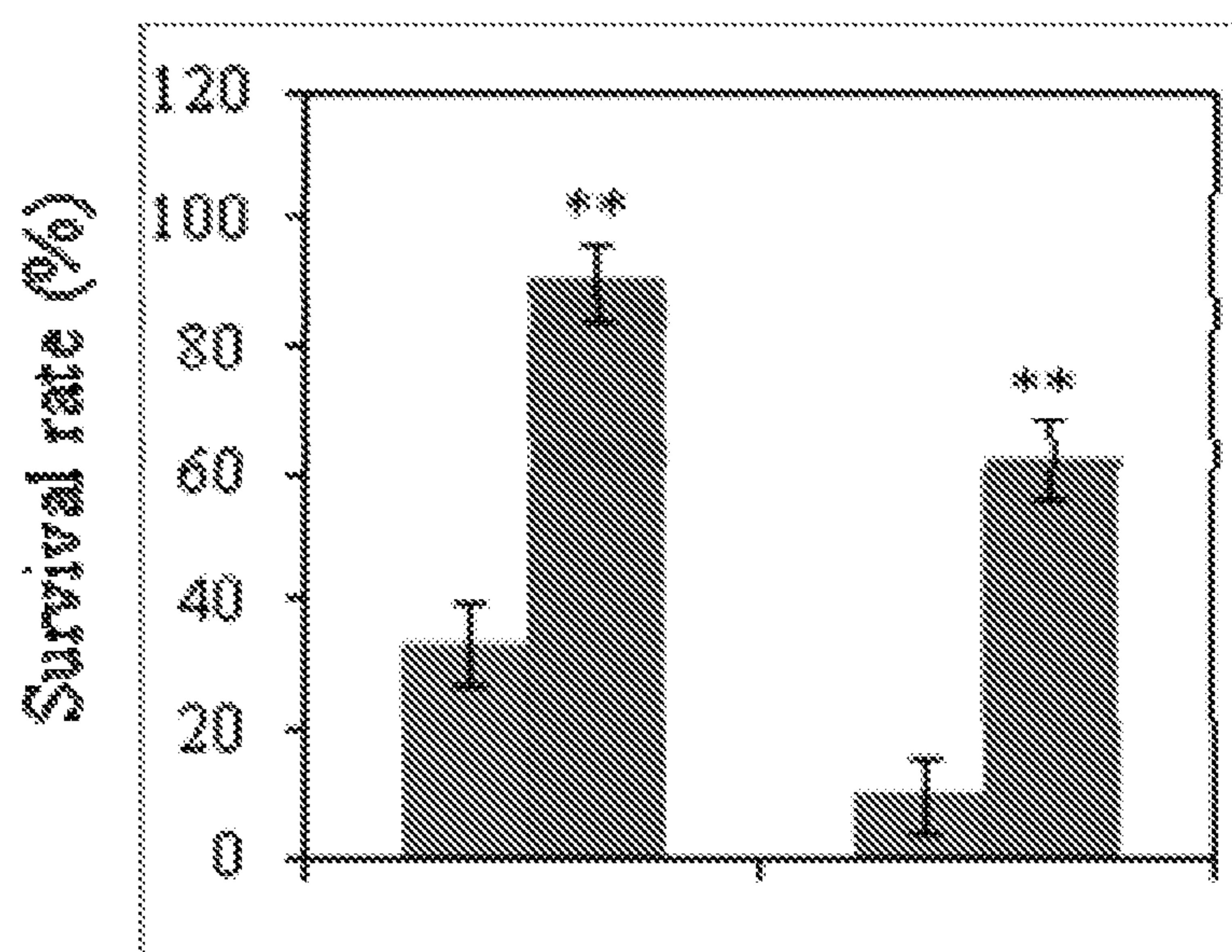


Fig. 26B

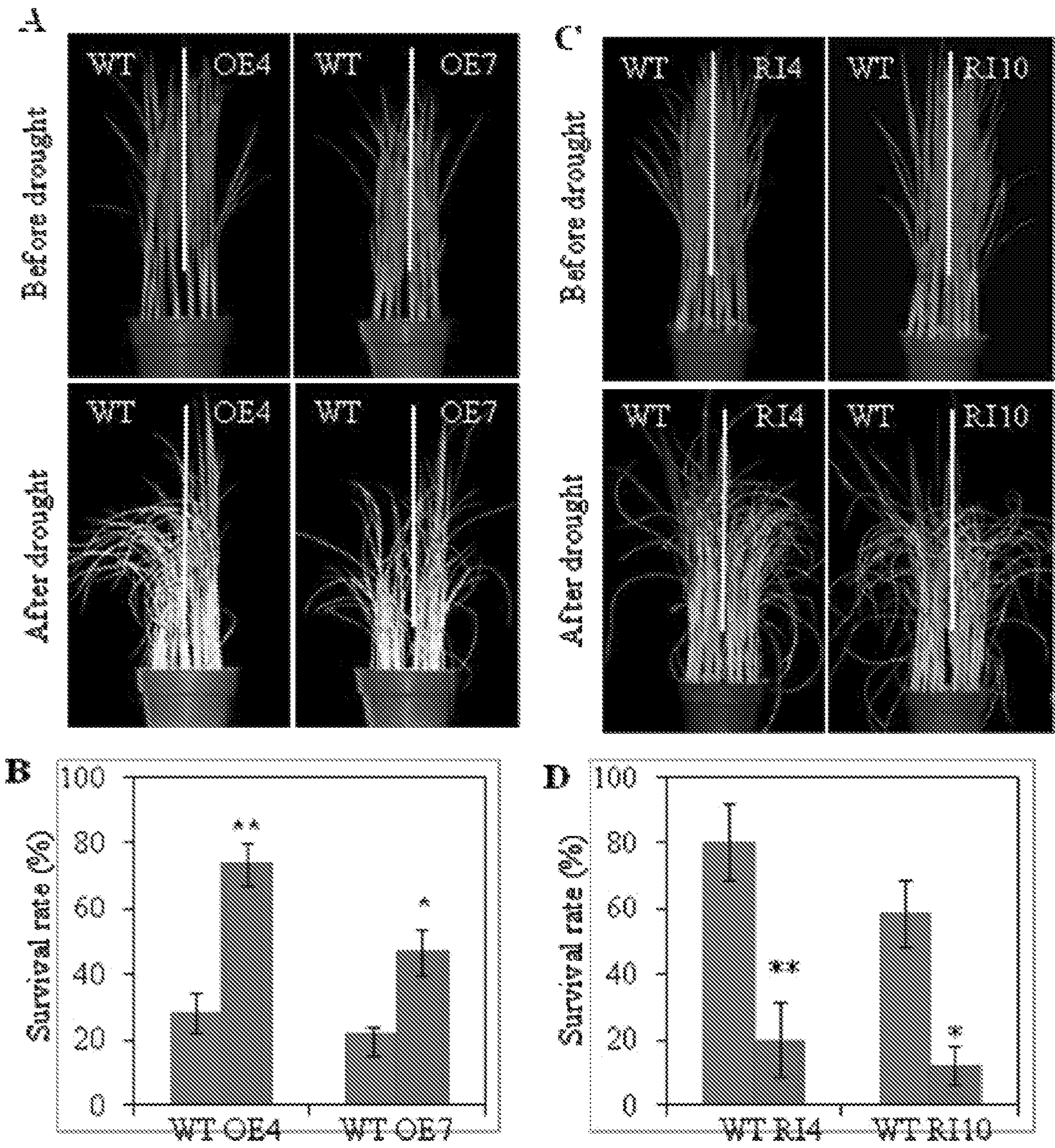


Fig. 27

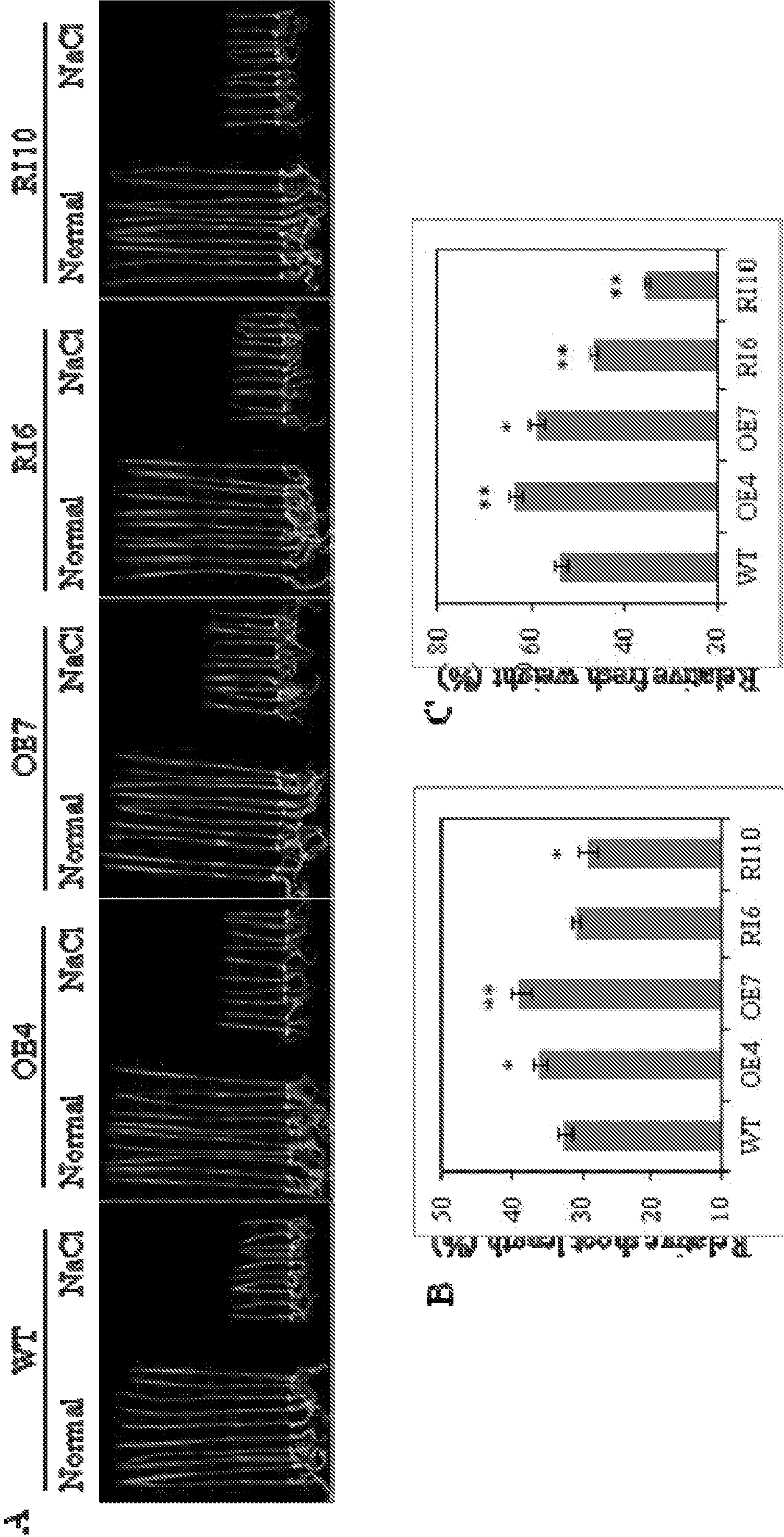


Fig. 28

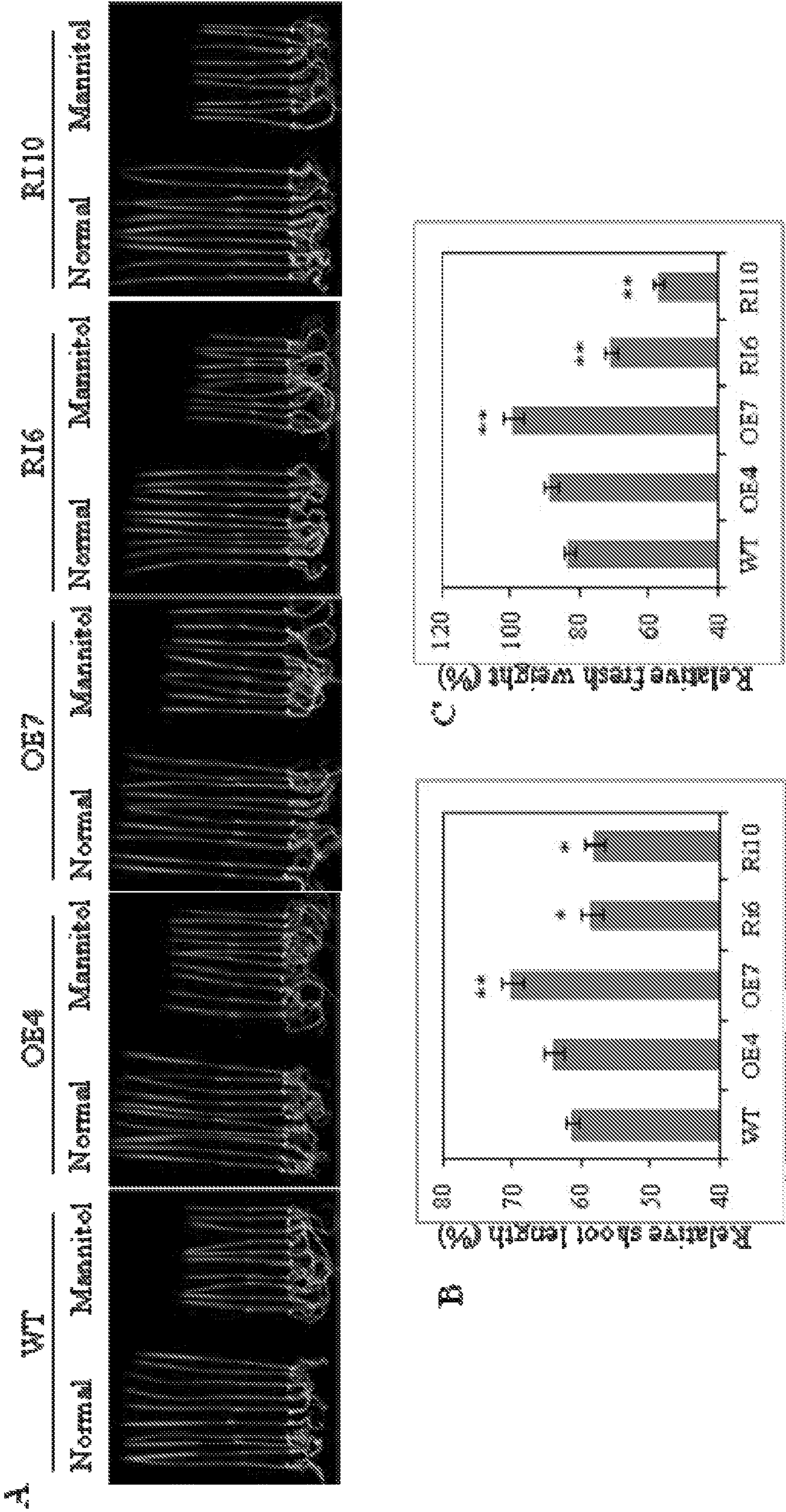
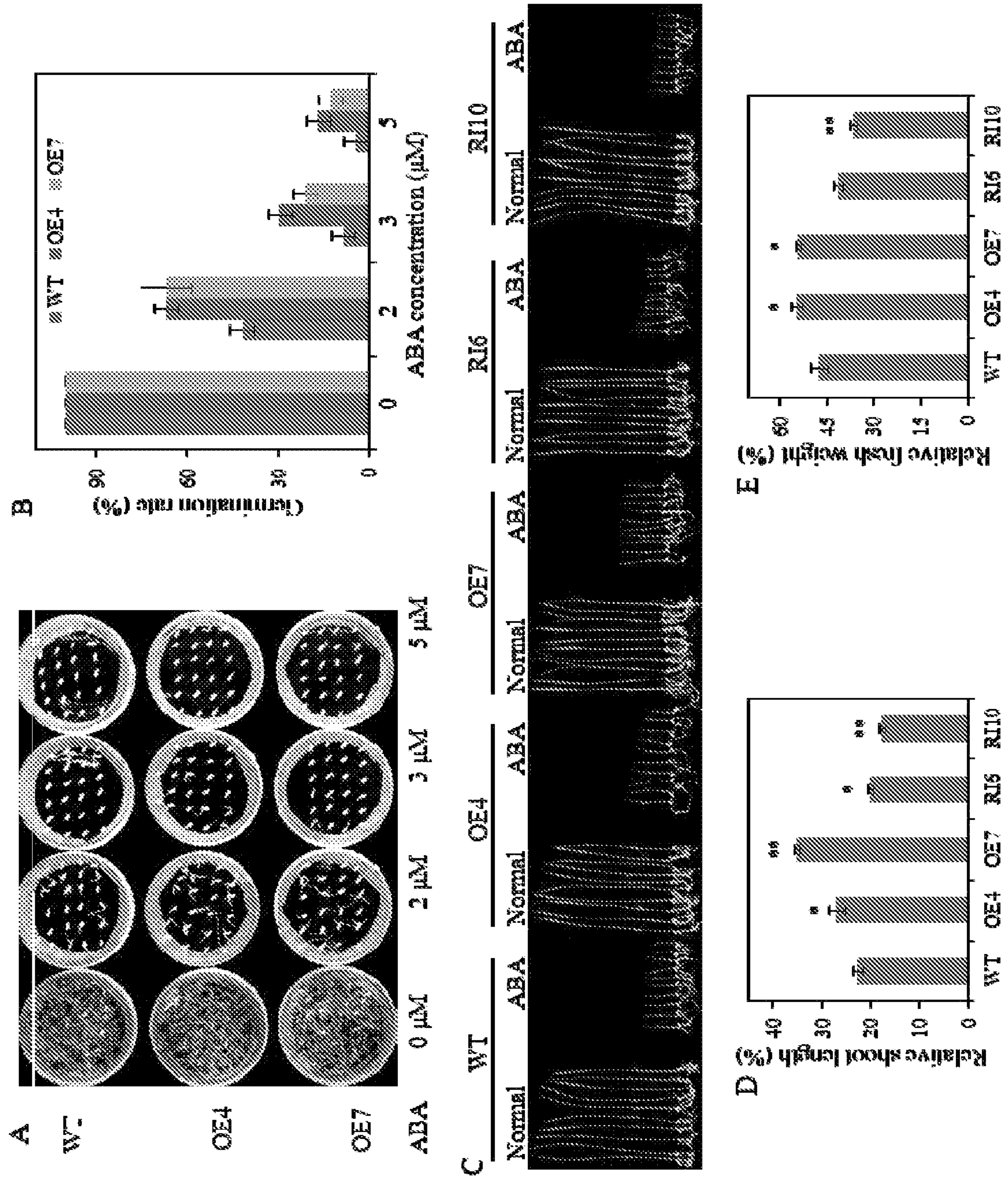


Fig. 29



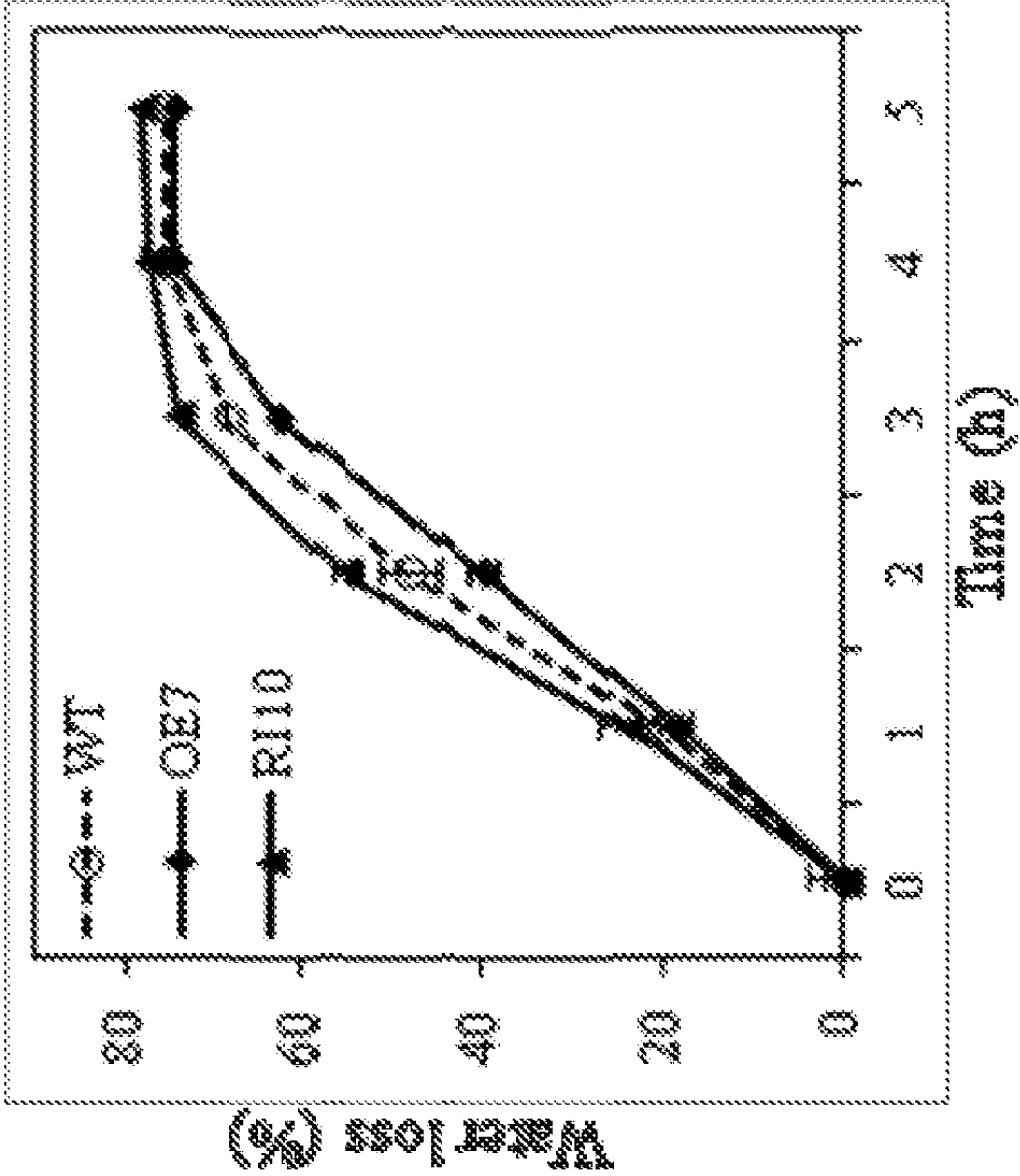


Fig. 31

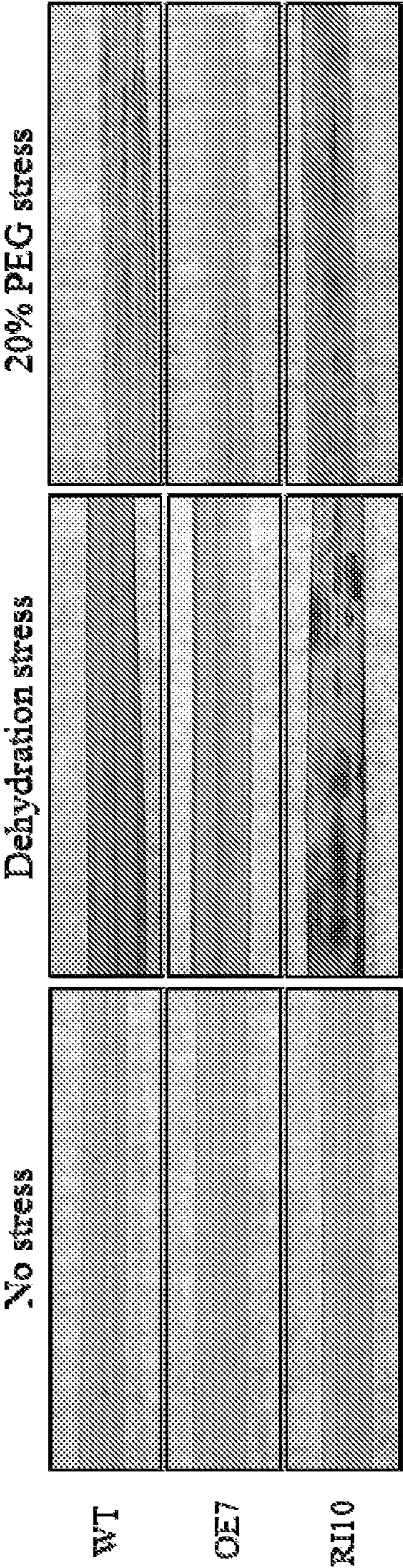


Fig. 32

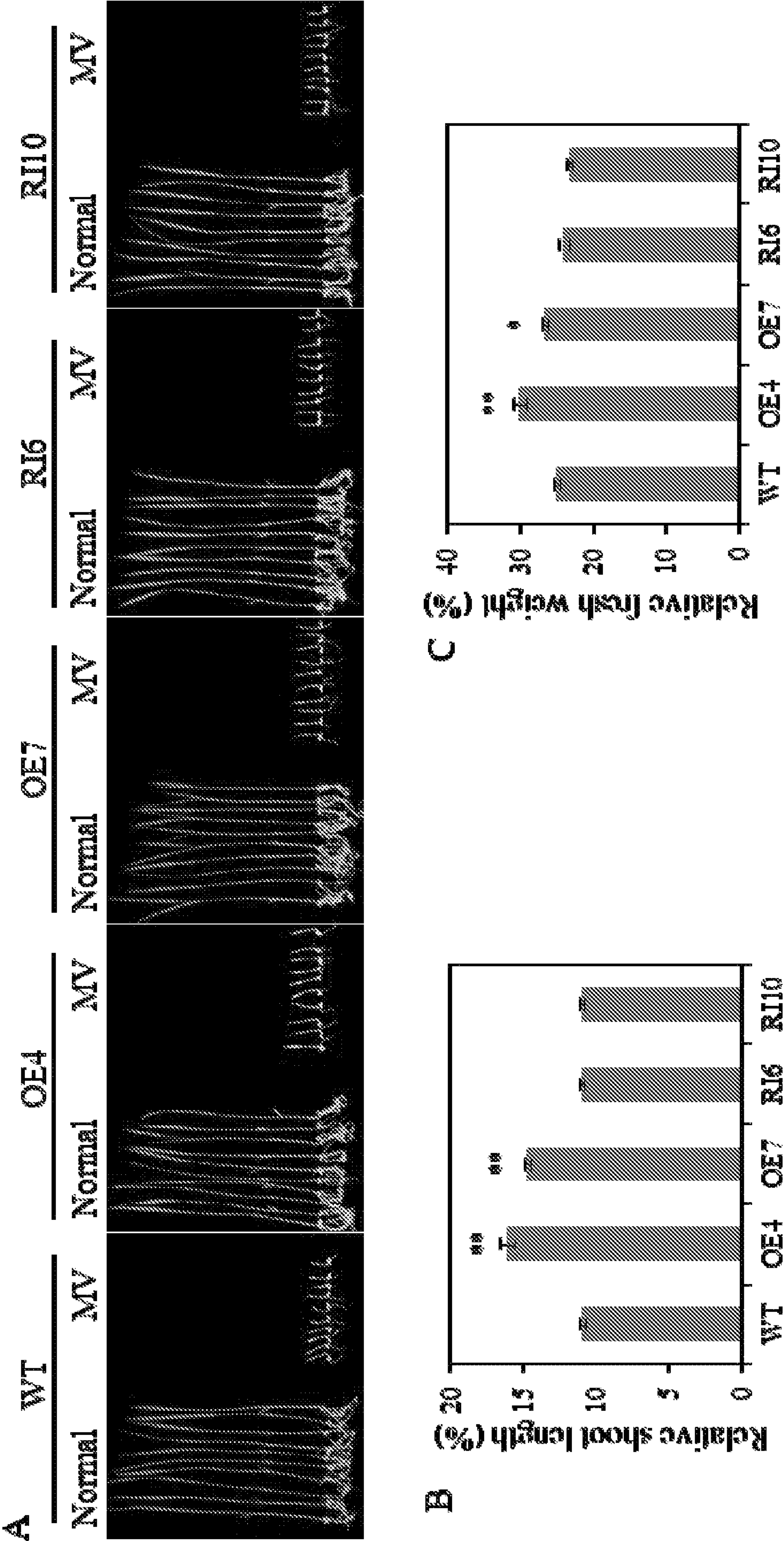


Fig. 33

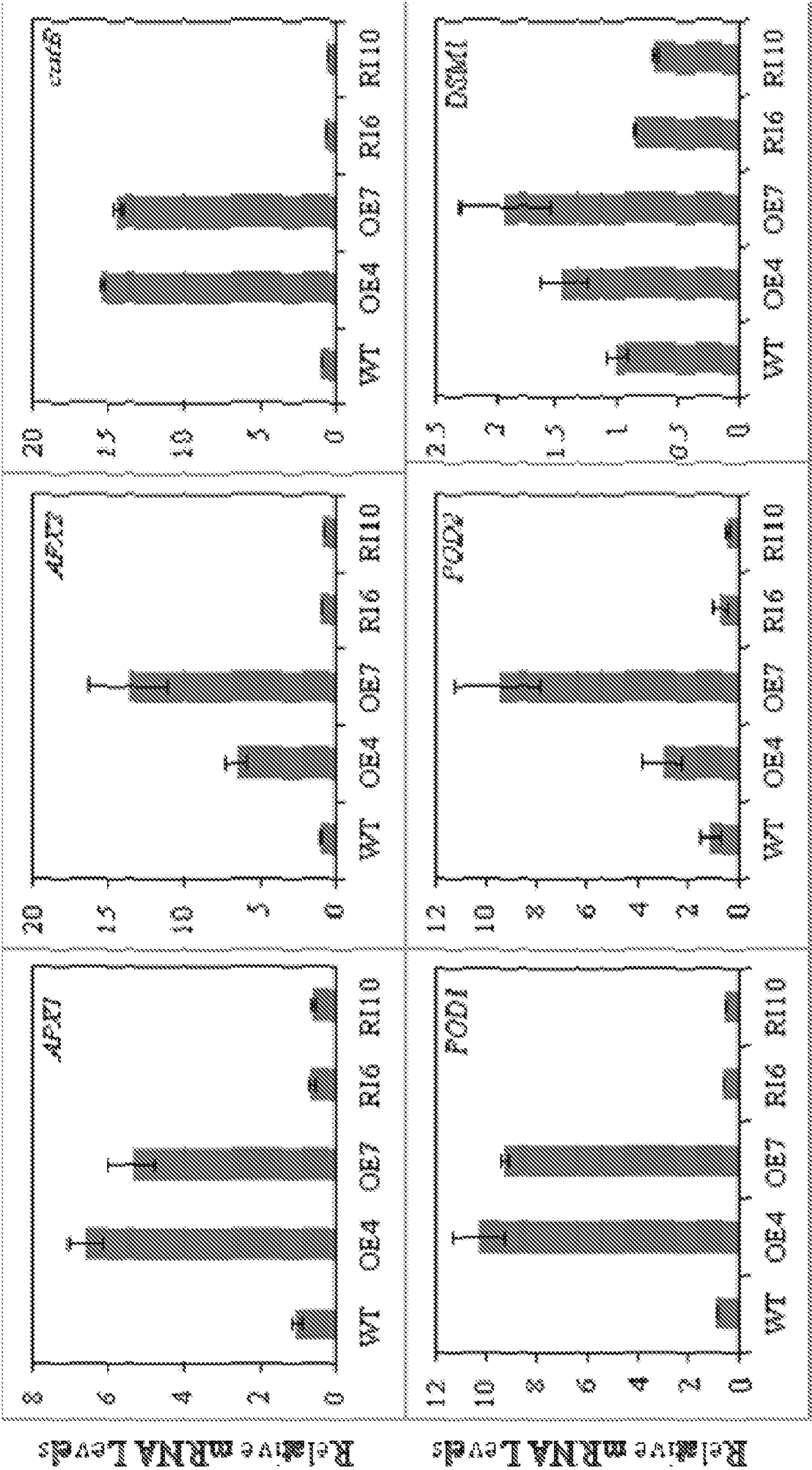


Fig. 34

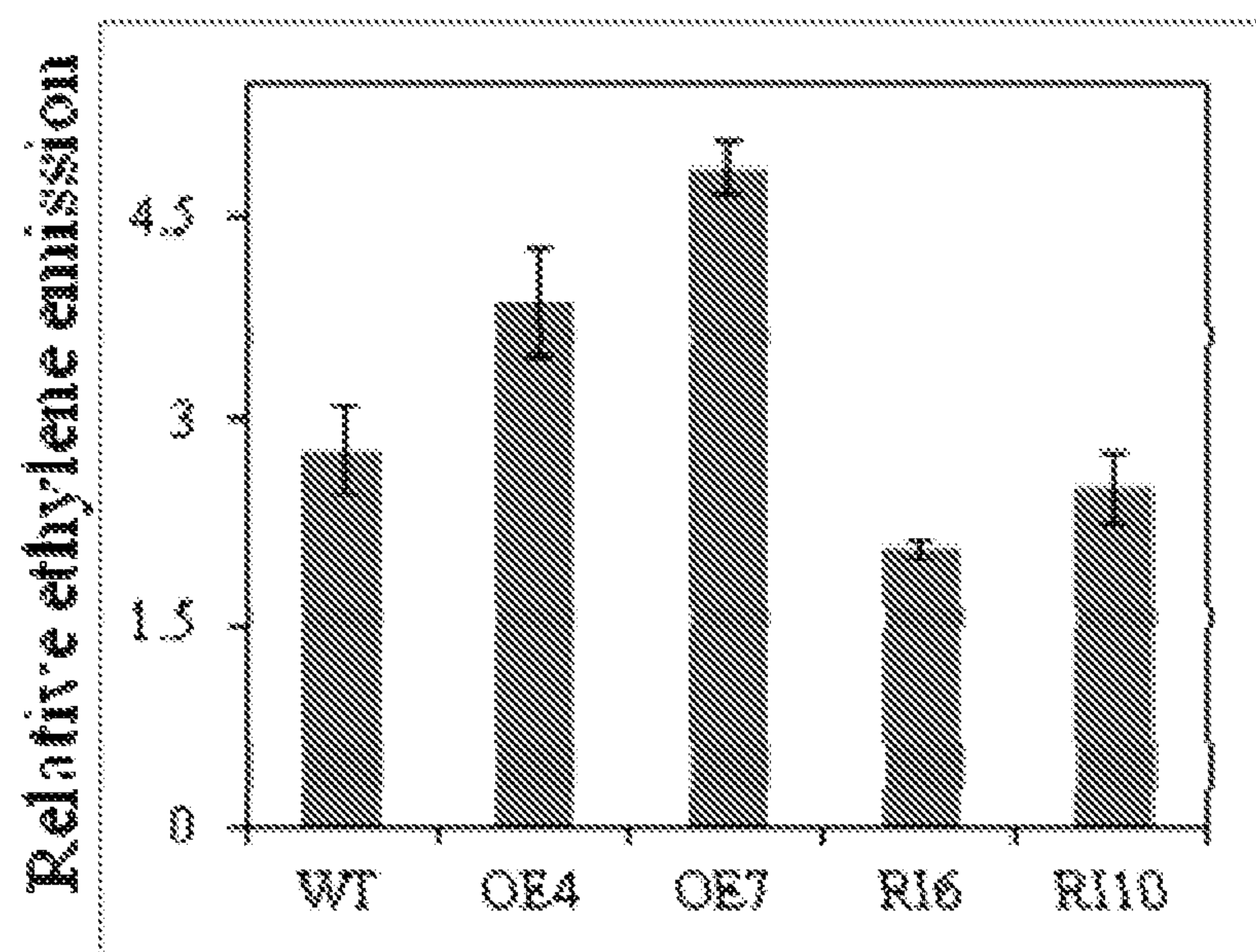


Fig. 35

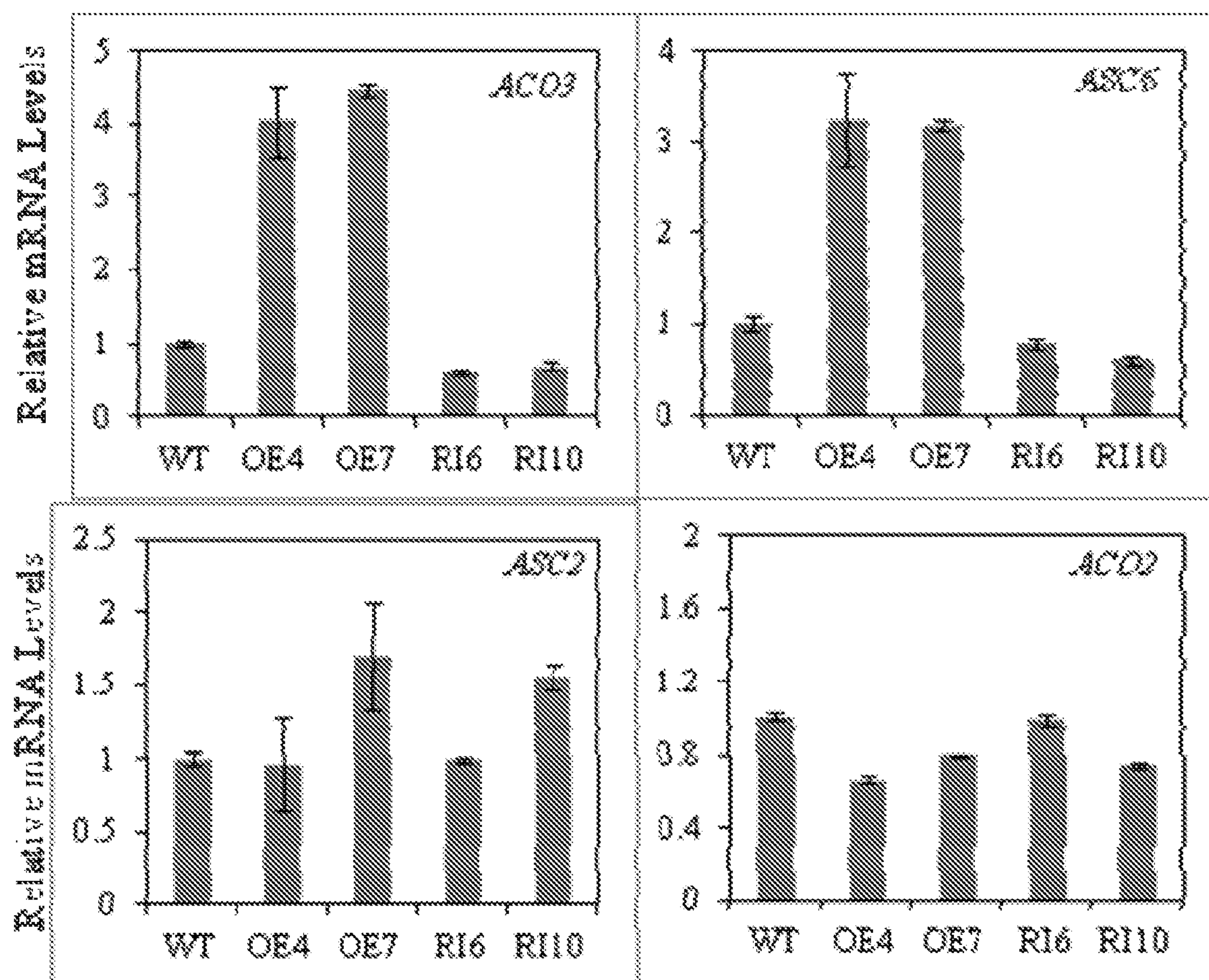


Fig. 36