Supplementary Material

Figure.S1 Expression analysis of OsGSTU30 in transgenic line (A) SDS-PAGE gel demonstration of crude protein extracted from highest expressed L3 line and WT plant and, **(B)** Expression of OsGSTU30 (approx. 26 kDa) was detected with a monoclonal anti-GST antibody by Western blot. M: protein marker; WT: Wild type (col 0); L3: *OsGSTU30* expressing transgenic line.

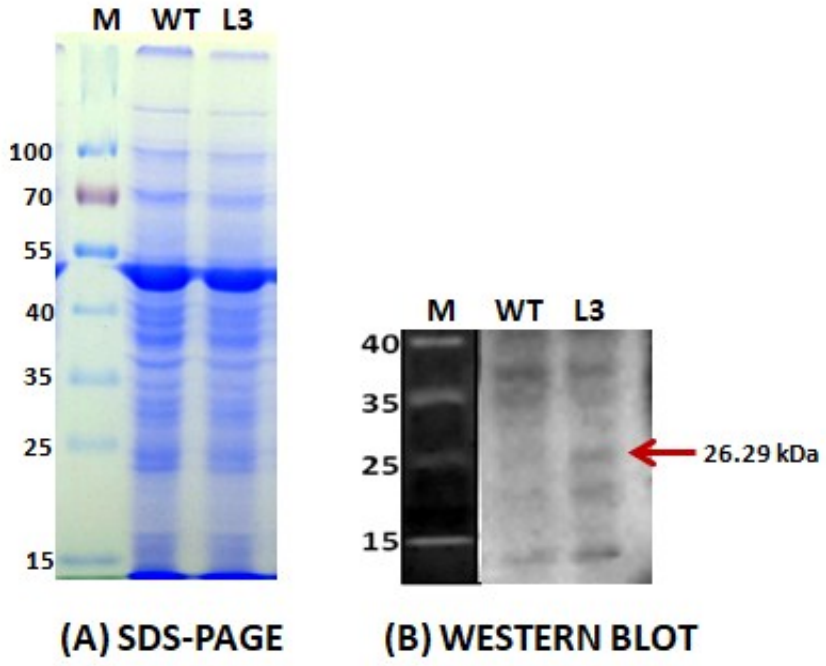

Figure S2. Response of WT and *OsGSTU30* expressing *Arabidopsis* transgenic lines to control and stress (Cr(VI) and drought) condition. **(A)** Sterilized seedlings were germinated on $^{1}/_{2}$ MS plate containing 15% PEG (for drought) and Cr(VI) (75 and 150µM). Tolerance of transgenic lines towards different concentrations of heavy metals was observed in comparison to the WT. Photographs were taken after 10 days of germination **(B)** Comparison of root length and, **(C)** Average fresh weight per seedling of transgenic lines and WT plants. Values are means ± SD from three independent experiments. Asterisks (student's t-test: *P<0.05; **P<0.01) indicate statistically significant difference between WT and transgenic lines.

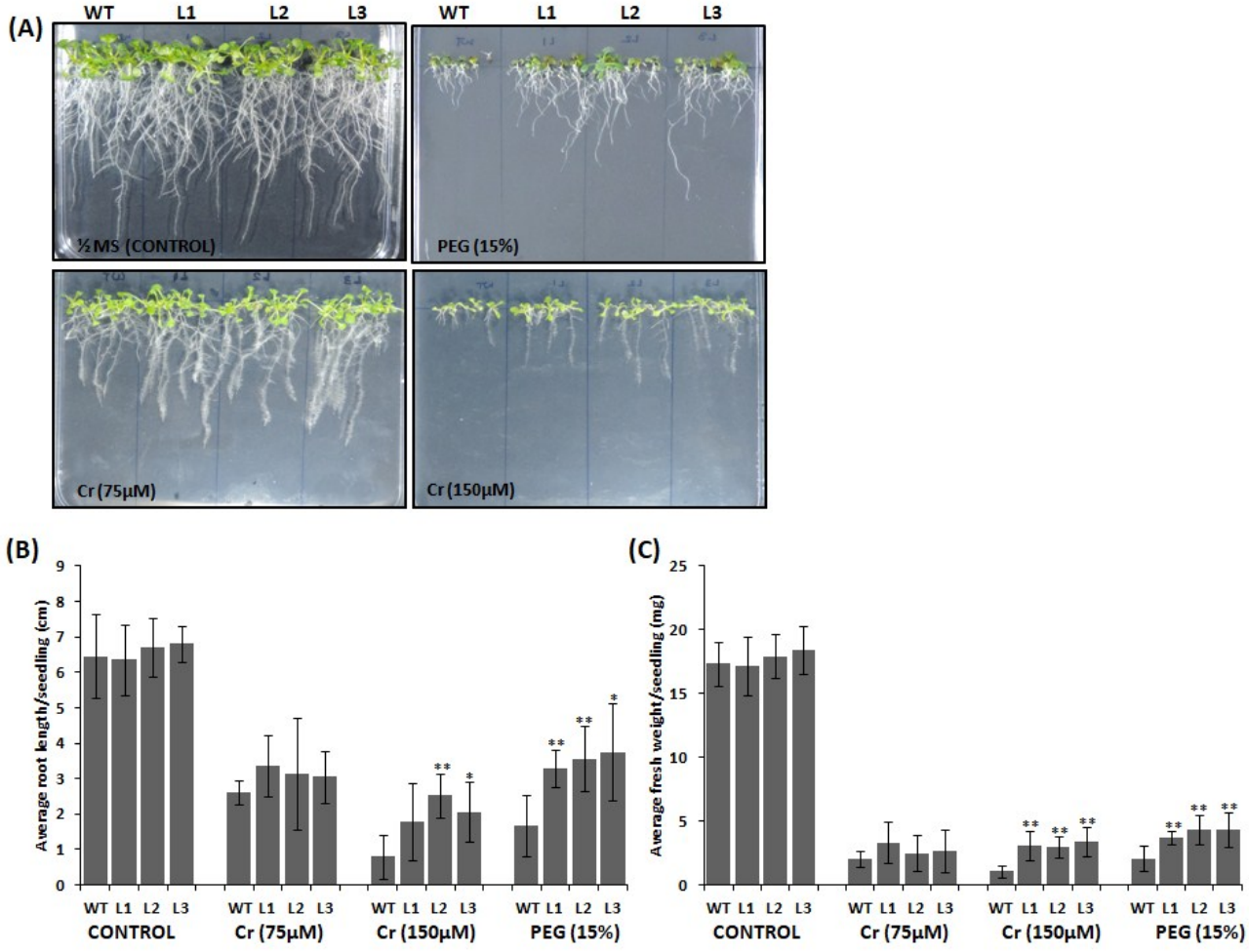

Figure S3. Response of WT and *OsGSTU30* expressing *Arabidopsis* transgenic lines to osmotic and salt stress. **(A)** For osmotic and salt stress, seeds were germinated on $^1/_2$ MS medium containing different concentrations of mannitol (150mM and 250mM) and NaCl (50mM and 100mM) respectively, Photograph was taken after 10 days of germination **(B)** Comparison of root length and, **(C)** Average fresh weight per seedling of transgenic lines and WT plants. Values are means ± SD from three independent experiments. Asterisks (student's t-test: *P<0.05; **P<0.01) indicate statistically significant difference between WT and transgenic lines.

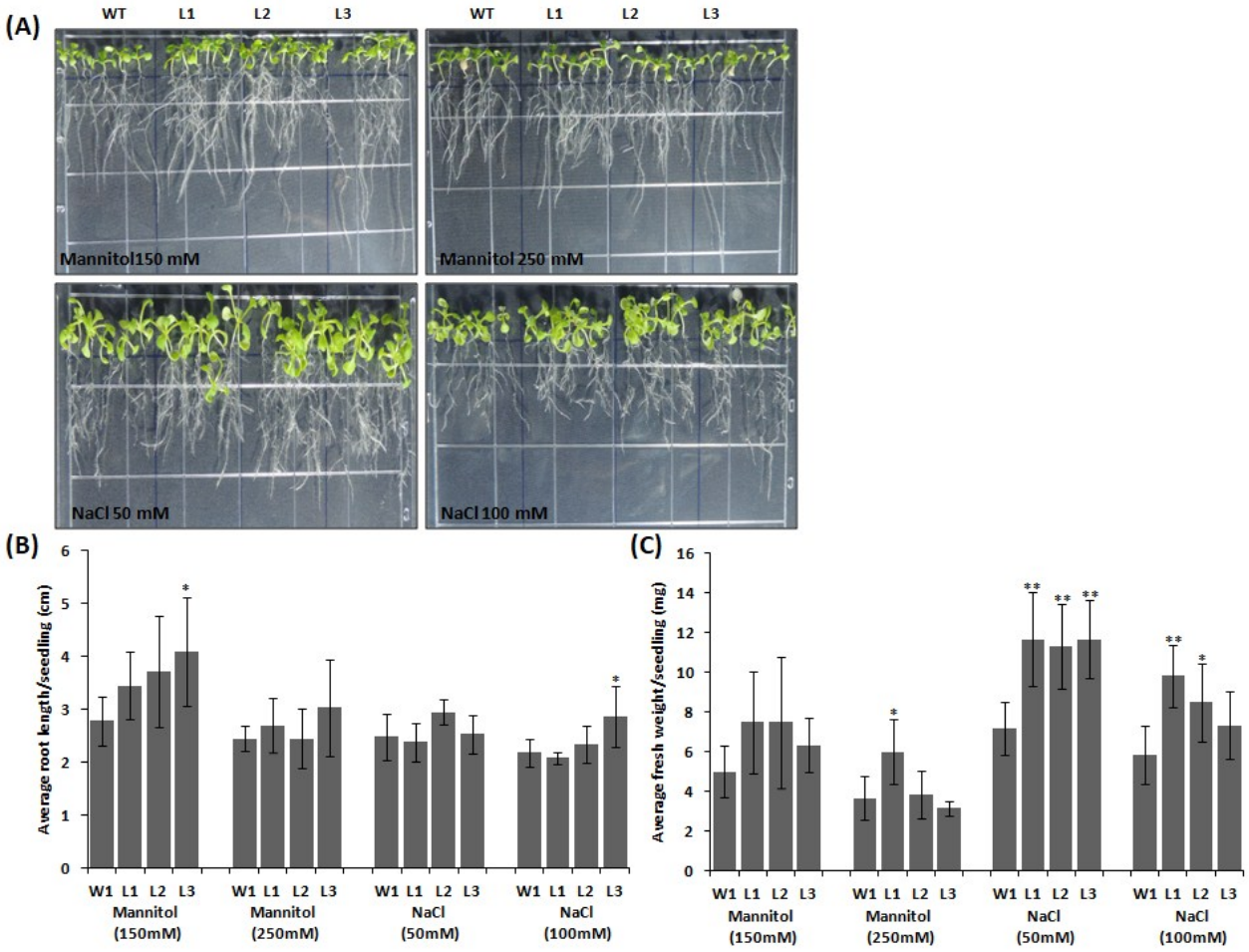

Figure S4. Phenotypic changes of WT and transgenic lines to heavy metal stress. (A) Sterilized seedlings were germinated on $^1/_2$ MS plate containing Cd (75µM), AsIII (10,25µM) and As(V)(100µM) for 10 days. Tolerance of transgenic lines towards different concentrations of heavy metals was observed in comparison to the WT **(B)** Comparison of root length and, **(C)** Average fresh weight per seedling of transgenic lines and WT plants. Values are means ± SD from three independent experiments. Asterisks (student's t-test: *P<0.05; **P<0.01; ***P<0.001) indicate statistically significant difference between WT and transgenic lines.

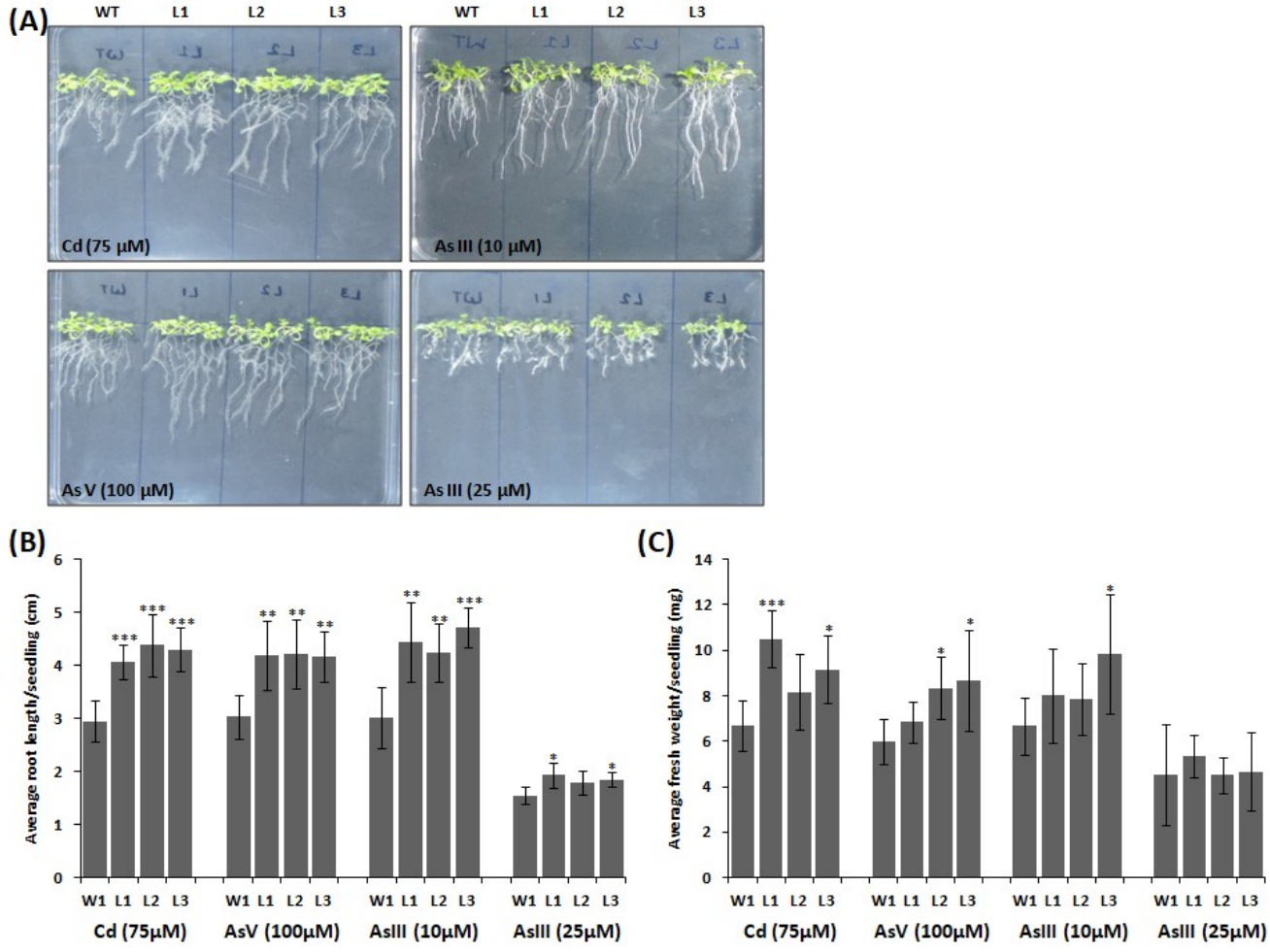

Figure S5. Docking of OsGSTU30-GSH complex models with 1-chloro-2,4-dinitrobenzene (CDNB), tert-Butyl hydroperoxide and Hydrogen peroxide substrates and the lowest energy configuration is shown in Ligplot (A,B,C) and UCSF Chimera (D,E,F) presentations respectively. Dashed lines in Ligplot indicate hydrogen bonds. Carbons are in black, nitrogens in blue, and oxygens in red. Figures were generated using UCSF Chimera and Ligplot+ softwares.

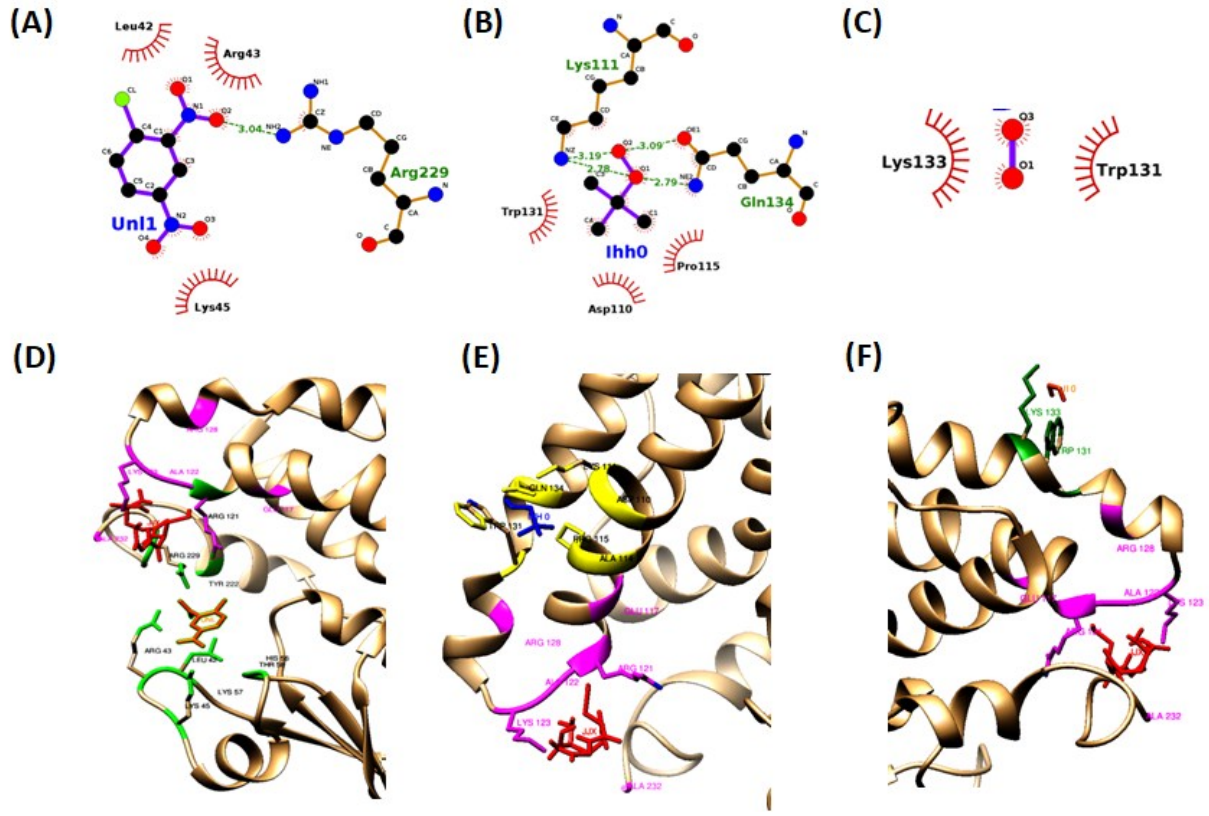

Figure S6. SDS-PAGE gel demonstration of OsGSTU30 protein expression and purification. Lane M indicates Protein marker (kDa), Lane UI : Cell lysate of un-induced BL21 *E. coli* cells containing the recombinant plasmid i.e. pETSUMO-OsGSTU30, Lane I : Cell lysate of induced BL21 *E. coli* cells containing the recombinant plasmid obtained at 12 h induction with 1 mM IPTG, and Lane P1 and P2 : Purified SUMO-tagged OsGSTU30 construct.

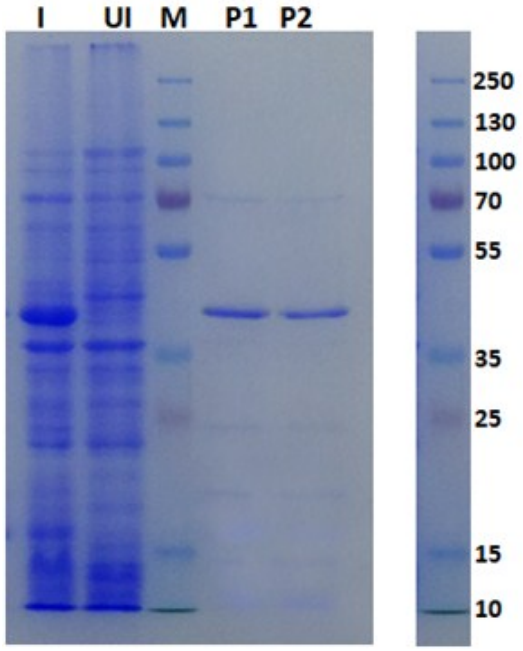

Figure S7. **Kinetic analysis of Purified OsGSTU30 protein**. **(A)** GST enzyme activity determination as a function of CDNB concentration in the presence of 2 mM GSH. **(B)** GPx like enzyme activity determination as a function of Cum-OOH concentration in the presence of 1 mM GSH. Data are represented as Linewaever–Burk representation. Apparent Km values were calculated from three separate experiments.

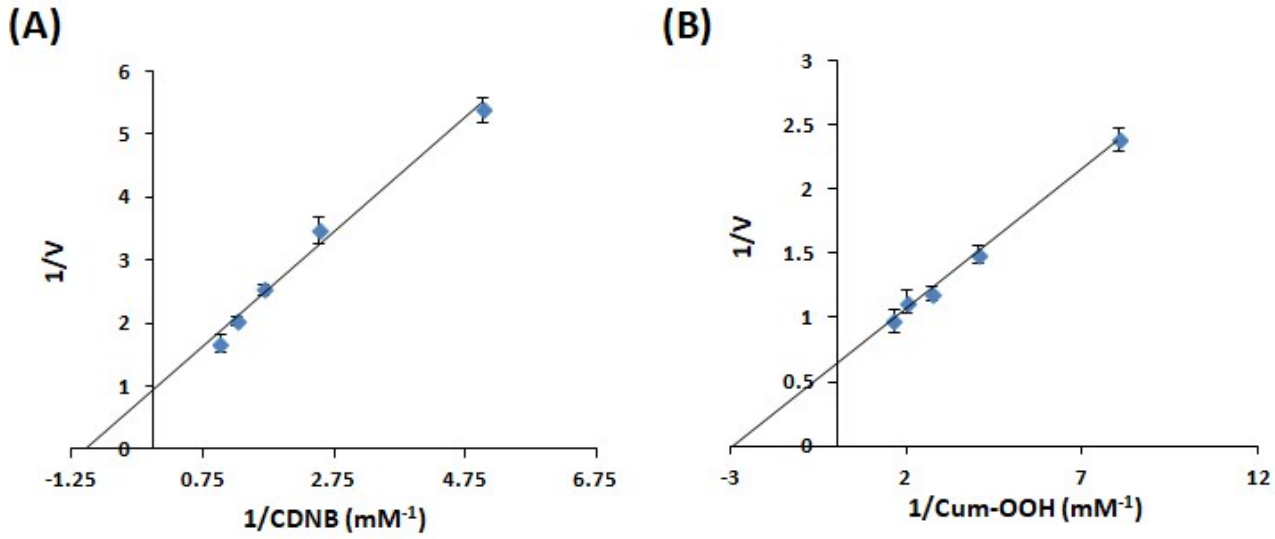

Figure. S8. Differential expression patterns of DEGs response to stress represented through Heat map according to FPKM values. Red and green color showed the relative expression of gene in *OsGST30* transgenic line (L3) and wild type plants (WT).

Figure. S9. Differential expression patterns of DEGs response to hormone stimulus represented through Heat map according to FPKM values. Red and green color showed the relative expression of gene in *OsGST30* transgenic line (L3) and wild type plants (WT).

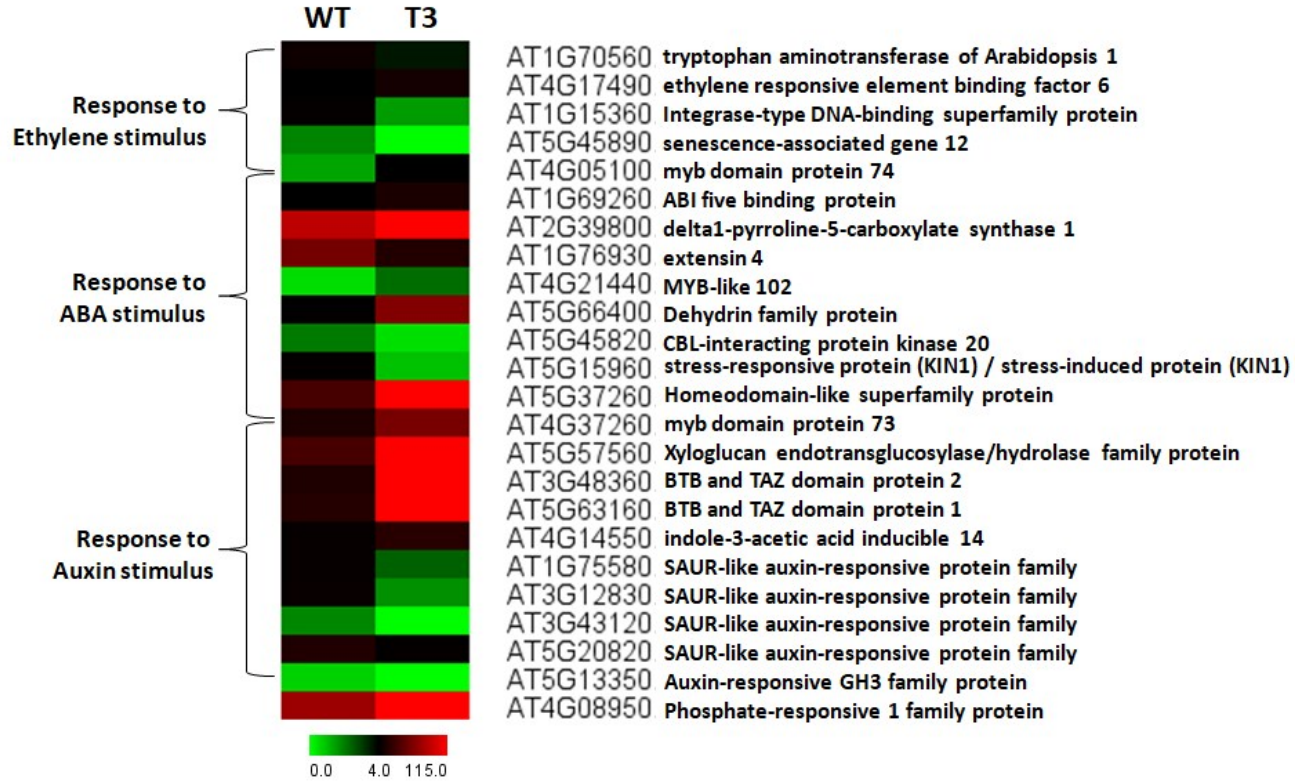

Figure. S10. Differential expression patterns of DEGs response to antioxidant activity represented through Heat map according to FPKM values. Red and green color showed the relative expression of gene in *OsGST30* transgenic line (L3) and wild type plants (WT).

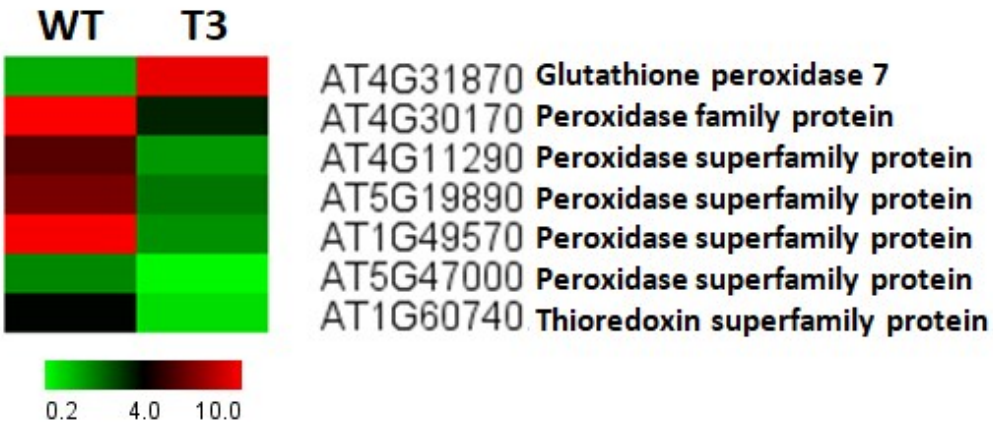

Figure. S11. Differential expression patterns of DEGs response to transcription factor activity represented through Heat map according to FPKM values. Red and green color showed the relative expression of gene in *OsGST30* transgenic line (L3) and wild type plants (WT).