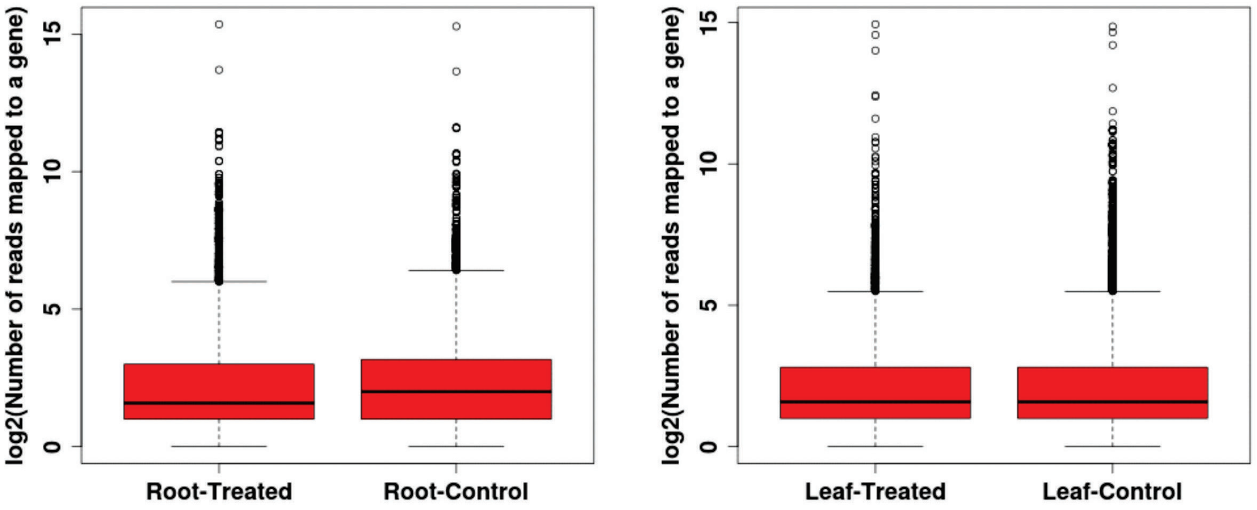

Figure S1 - Gene expression distribution between control and drought-stressed (treated) roots and leaves of the wheat cultivar MGS1 Aliança. Transcripts were obtained by 454 pyrosequencing of four libraries (control and treated roots, control and treated leaves) performed on a Genome Sequencer FLX Titanium instrument (Roche). Calculation was performed in DEGseq software for analysis of the statically differentially expressed transcripts in order to identify candidate genes associated to drought.