

Table S2. Most abundant cis-regulatory elements present in the 1600 bp up-stream promoter regions of the *AhN4L-1* and *AhN4L-2* genes. Also shown are elements exclusively present in the promoter region of the *AhN4L-1* gene.

SHARED CIS-REGULATORY ELEMENTS	
Family	Function
AHBP (Recognized by homeobox proteins in Arabidopsis)	Regulation of genes involved in development processes (Trindade et al. 1999; Meng et al., 2020). Also present in nitric oxide-responsive genes that control growth, development, and responses to environmental stress conditions (Mukherjee et al., 2009; Shi et al., 2011).
GT-Box (Identified in light-regulated promoters)	Abundant in genes that control plant growth regulation and responses to numerous stress conditions. Found in the defense-related chalcone synthase gene in in soya and common bean plants (Lawton et al. 1991; Terzaghi and Cashmore 1995).
L1- Box (specific motifs for the expression of L1 proteins)	L1 proteins a known to control leaf and flower development. It is relevant in the proline-rich Proteoderma factor 1 protein, exclusive of the L1 layer of the apical meristem apical, the proteoderm and organ primordia (Abe et al. 2001; Lau et al. 2012).
MADS (Recognized by MADS-box TFs)	MADS-box transcription factors control diverse developmental processes in flowering plants including root, flower and fruit development. They are known to regulate the transition from vegetative to reproductive development. They are necessary for the development of flowering structures and floral meristems (e.g. via Sepallata 3 TF) (Becker and Theißen 2003; Angenent et al. 2009; Erdmann et al., 2010; Smaczniak et al. 2012).
DOF (DNA-binding One Zinc Finger)	The DOF family of TFs regulate plant responses to light and phytohormones. They also control seed maturation and germination. DOF TF genes are widely distributed, being found not only in gymnosperms and angiosperms but also in lower plants like mosses and algae (Noguero et al., 2013).
CIS-REGULATORY ELEMENTS PRESENT EXCLUSIVELY IN THE <i>AhN4L-1</i> GENE	
ABA-responsive and embryo-specification elements in the Dc3 promoter	Recognized by a class of sunflower bZIP transcription factors, <i>Dc3</i> promoter-binding factor-1 and 2 (DPBF-1 and 2) that are similar to the plant G-box binding factor GBF-4. Also found in the carrot (<i>Daucus carota</i>) <i>Dc3</i> gene promoter. <i>Dc3</i> expression is normally embryo-specific, and may be also induced by Arabidopsis abscisic acid (ABA). Also present in <i>ABI5</i> , an Arabidopsis ABA-responsive gene that encodes a bZIP transcription factor. <i>ABI5</i> regulates a subset of late embryogenesis-abundant (<i>LEA</i>) genes, whereas <i>abi5</i> mutants have pleiotropic defects in plant ABA responses; <i>GIA1</i> (growth-

	insensitivity to ABA) is identical to <i>ABI5</i> (Kim et al. 1997; Finkelstein and Lynch, 2000; Lopez-Molina and Chua, 2000).
Ethylene-responsive element (ERE)	Present in the E4 ethylene responsive element (ERE) of tomato (<i>Solanum lycopersicum</i>) and in the carnation <i>GST</i> genes; <i>GST1</i> is related to senescence. Also found in the 5'-LTR region of <i>TLC1.1</i> retrotransposon family in <i>Solanum chilense</i> . ERE motifs mediate ethylene-induced activation of the U3 promoter region (Montgomery et al., 1993; Itzhaki et al., 1994; Rawat et al., 2005; Tapia et al., 2005).
Recognized by meristematic WUSCHEL-type homeobox genes.	The Arabidopsis WUSCHEL (WUS) protein is involved in the specification of the stem cells in the shoot apical meristem (SAM) and in the specification and maintenance of the root apical meristem (RAM) stem cells of rice (Kamiya et al., 2003).
SP8a (ACTGTGTA) and SP8b (TACTATT) sequences present in genes coding for sporamin and beta-amylase of tuberous roots	Sporamin and beta-amylase are two prominent storage proteins that accumulate in tuberous roots of sweet potato. The expression of sporamin- and beta-amylase-coding genes is induced by the exogenous application of sucrose or polygalacturonic acid (Ishiguro and Nakamura, 1992, 1994).

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