

Supporting Information

Luxurious nitrogen fertilization of two sugarcane genotypes contrasting for lignin causes changes in the stem proteome related to carbon, nitrogen and oxidant metabolism but does not alter lignin content

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Table S1: Protein identification in sugarcane stems of IACSP04-627 and IACSP04-065 genotypes using Proteome Discoverer and MaxQuant platforms.

Table S2: Proteins exclusively detected in cultivar IACSP04-065 in control or fertilized treatment.

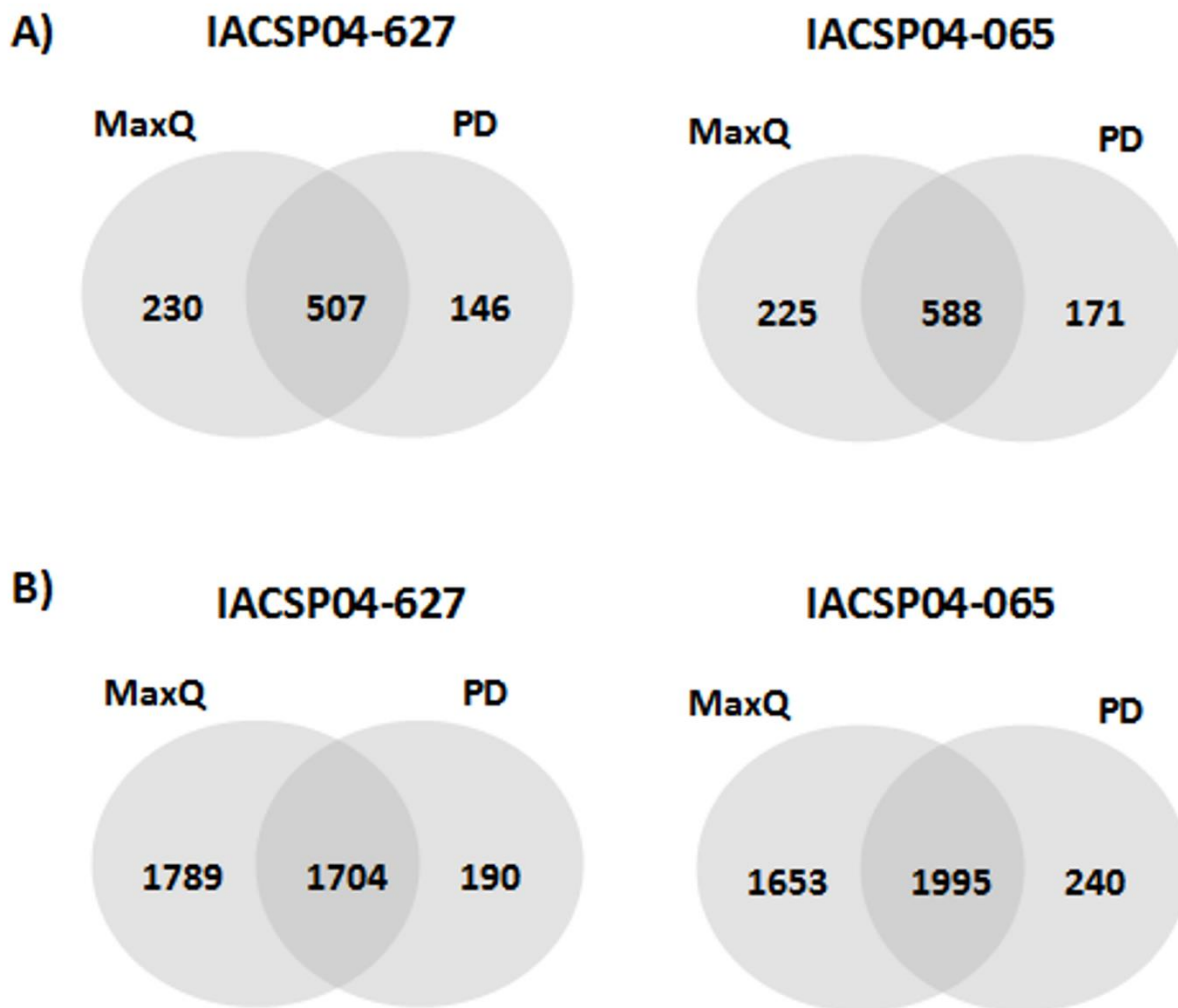
Table S3: Proteins exclusively detected in cultivar IACSP04-627 in control or fertilized treatment.

Table S4: Differentiating proteins identified in cultivar IACSP04-627 under nitrogen fertilization treatment.

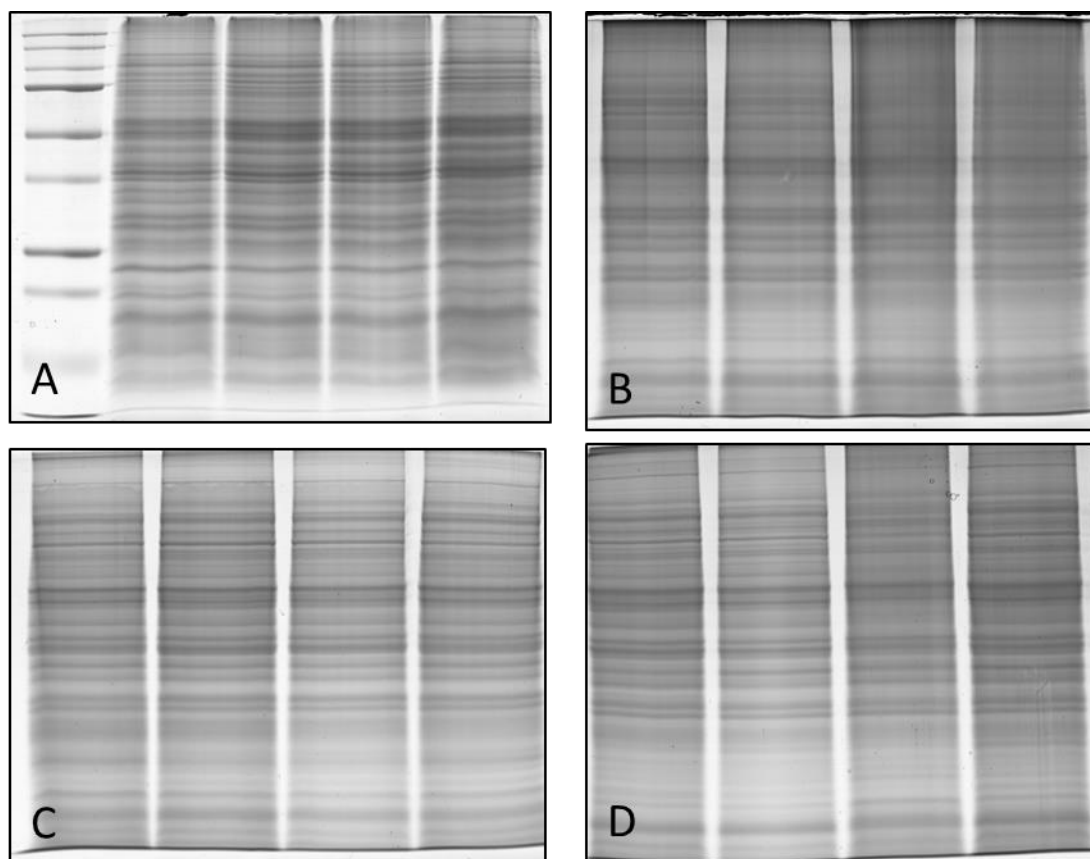
Table S5: Differentiating proteins identified in cultivar IACSP04-065 under nitrogen fertilization treatment.

Table S6: Functional categorization and relative abundance of proteins differently accumulated and exclusively found in IACSP04-065 after N fertilization.

Table S7: Functional categorization and relative abundance of proteins differently accumulated and exclusively found in IACSP04-627 after N fertilization.



Supplementary Figure S1: Proteome-wide identification in sugarcane stems of contrasting genotypes for lignin content using MaxQuant (MaxQ) and Proteome Discoverer (PD) platforms. A) Venn diagrams of protein groups identified. B) Venn diagrams of peptides identified.



Supplementary Figure S2: SDS-PAGE of proteins samples extracted from sugarcane stems. Each lane represents one biological replicate. A) control samples of IACSP04-065; B) nitrogen treated samples of IACSP04-065; C) control samples of IACSP04-627; D) nitrogen treated samples of IACSP04-627. First left lane on A represents the molecular weight distribution.