

Description of Additional Supplementary Files

File name: Supplementary Data 1

Description: Differentially expressed receiver plant genes (DEGs) in response to sender stimulation by wounding and flg22 in cut and connected CMN treatments.

File name: Supplementary Data 2

Description: GO-term enrichment for the 1880 upregulated and 3005 downregulated receiver plant DEGs in the connected CMN treatment. Functional enrichment is based on Fisher exact test with Hochberg (FDR) correction using agriGO v2.0. Significantly enriched functions ($p < 0.05$; $FDR < 0.05$) for each ontology category - biological process, molecular function and cell compartment – are highlighted in bold and coloured.

File name: Supplementary Data 3

Description: Assignment of plant stress and defence bin for functional enrichment analysis of CMN-mediated receiver plant DEGs.

File name: Supplementary Data 4

Description: Source data for compound identification using LC-HRMS and HS-GC- Page 8 of 21 MS as well as rCCA and correlation network between transcriptome and metabolome datasets.

File name: Supplementary Data 5

Description: Measured necrotic area (cm²) on *Medicago truncatula* leaves. Raw data values for Figure 4 and Supplemental Figure 8.

File name: Supplementary Data 6

Description: Comparison of transcription factors, auxin transporters, P45 and UGT enzyme fold change in receiver from "connected" and "cut" treatments.

File name: Supplementary Data 7

Description: Correspondence of gene expression data from RNA-seq experiment and rt-qPCR analysis with an independent sample set.