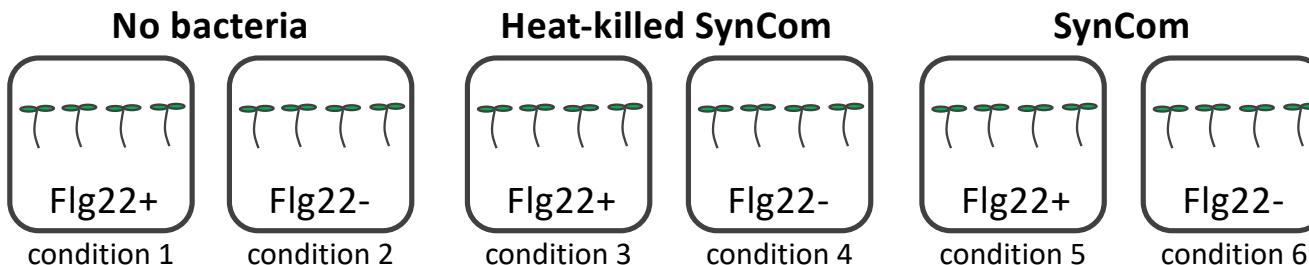


Experimental design

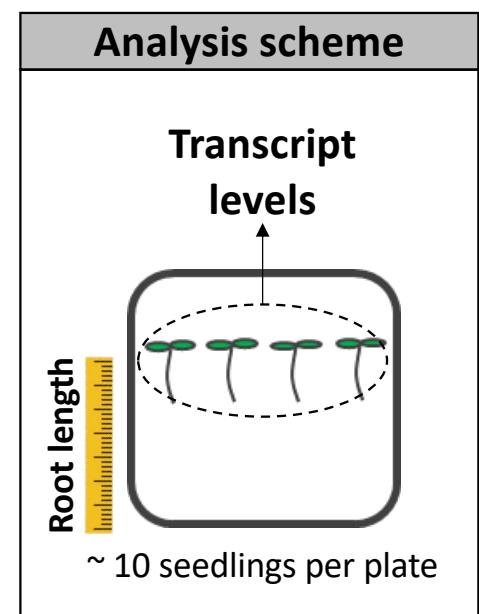
A

Variables				
Bacteria	flg22	Time	Tissue	Experiment
No bacteria	flg22 ⁻ (0 µM)	1 day	Roots	e1 (3 replicates)
Heat-killed SynCom	flg22 ⁺ (1 µM)	12 days		e2 (3 replicates)
SynCom				e3 (3 replicates)

B

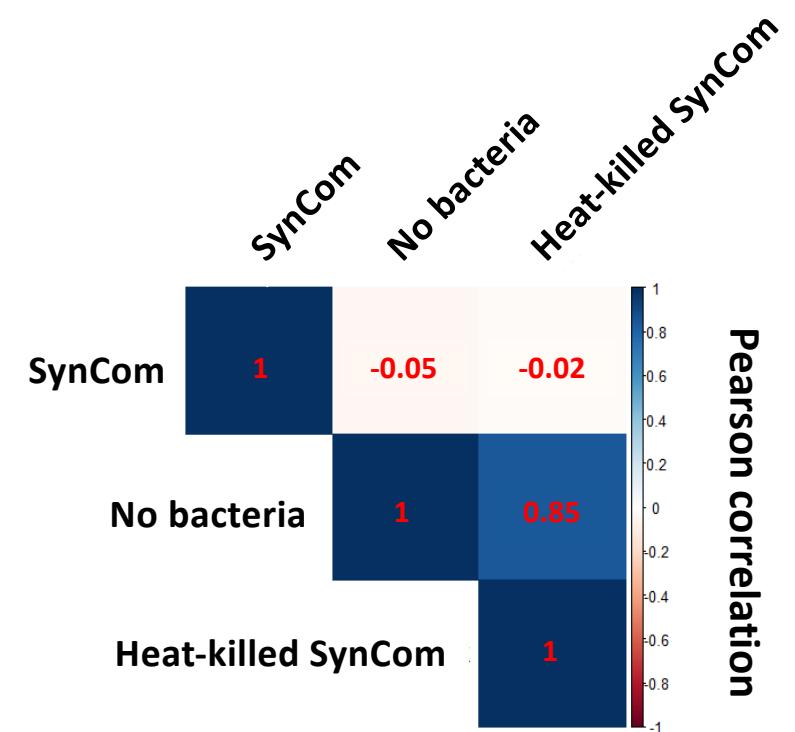
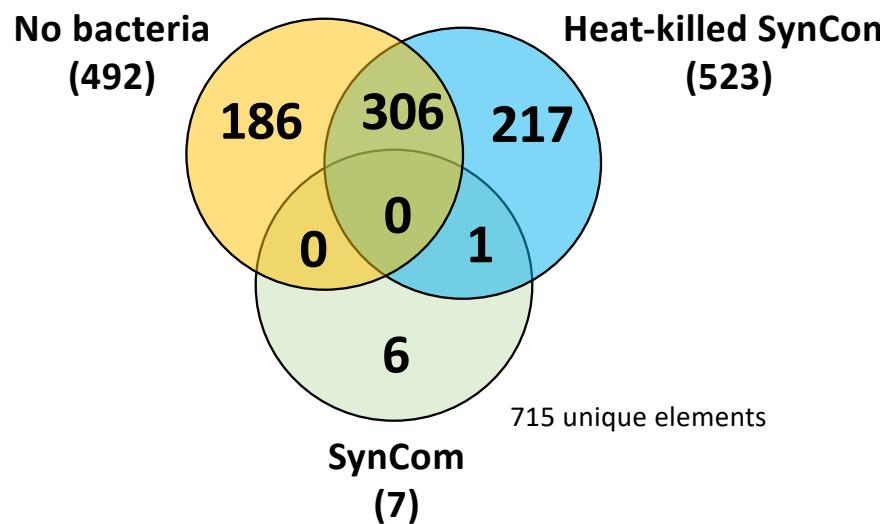
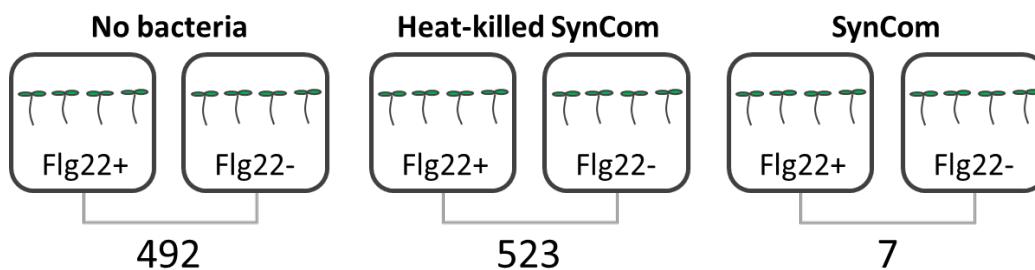


C



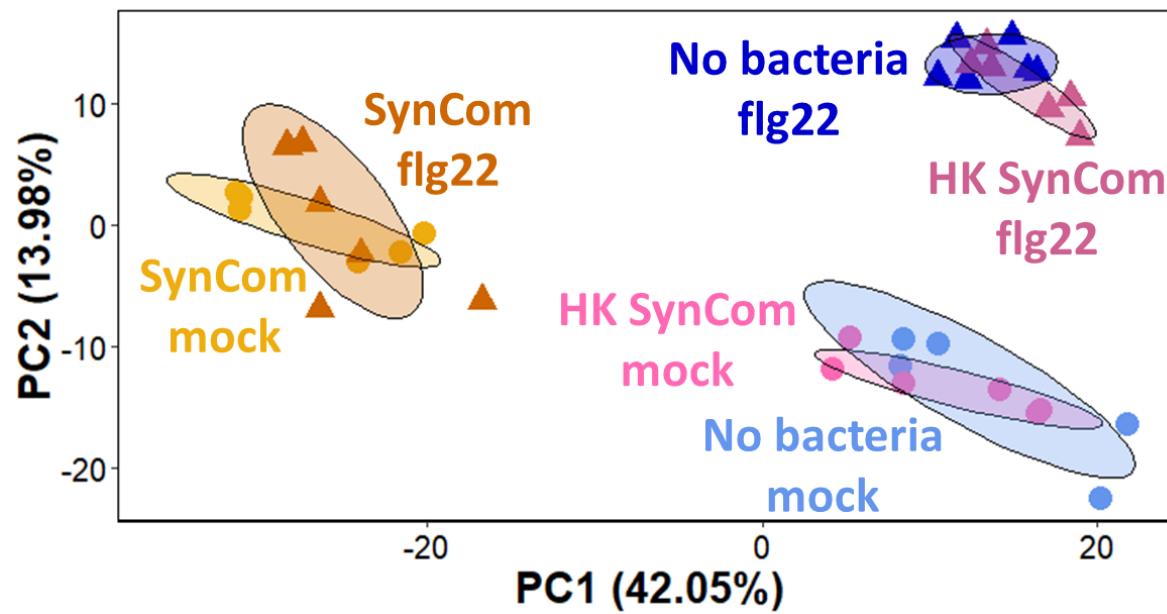
The root response to flg22 is altered in the presence of the SynCom

Number of genes responsive to flg22

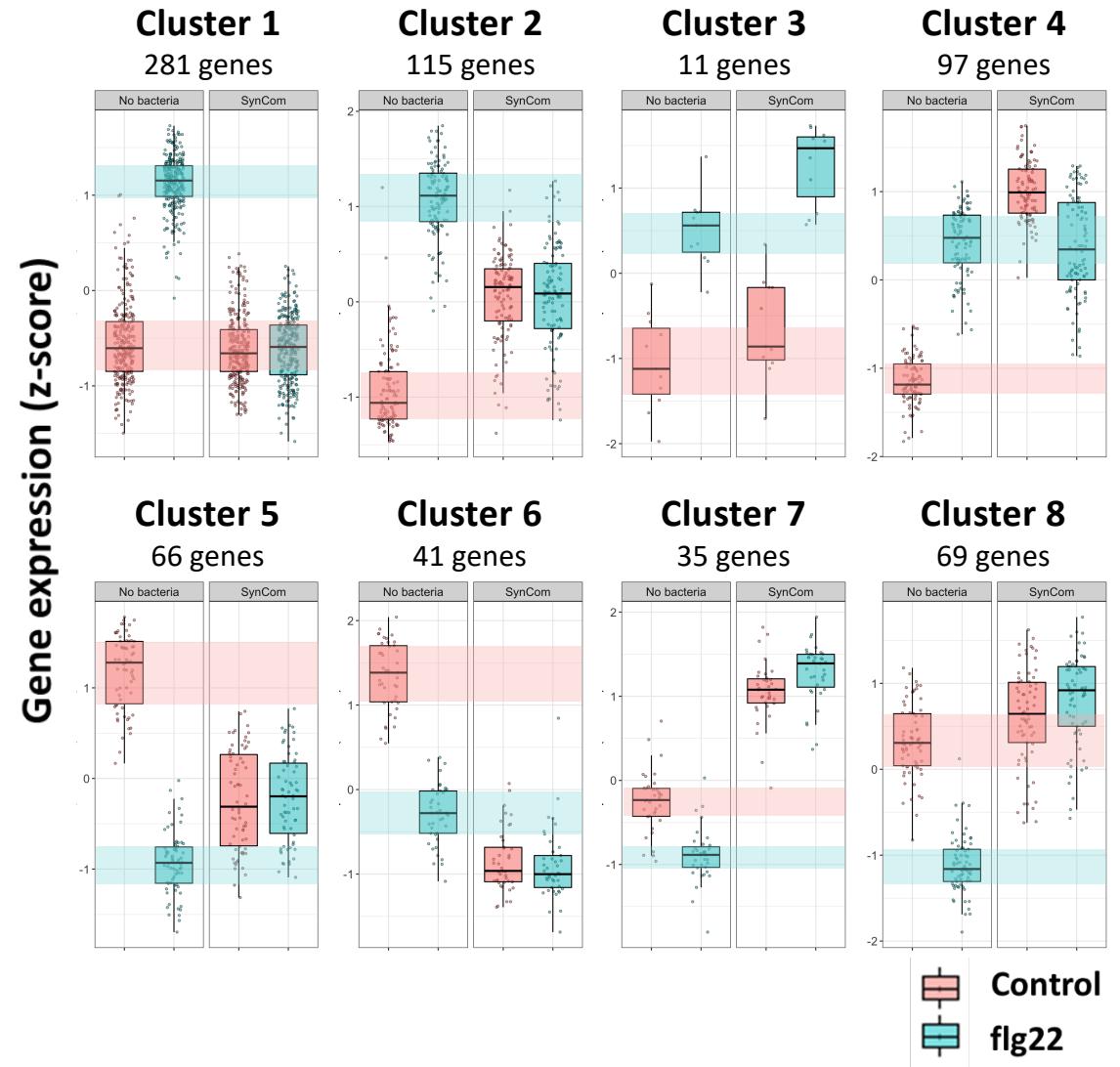
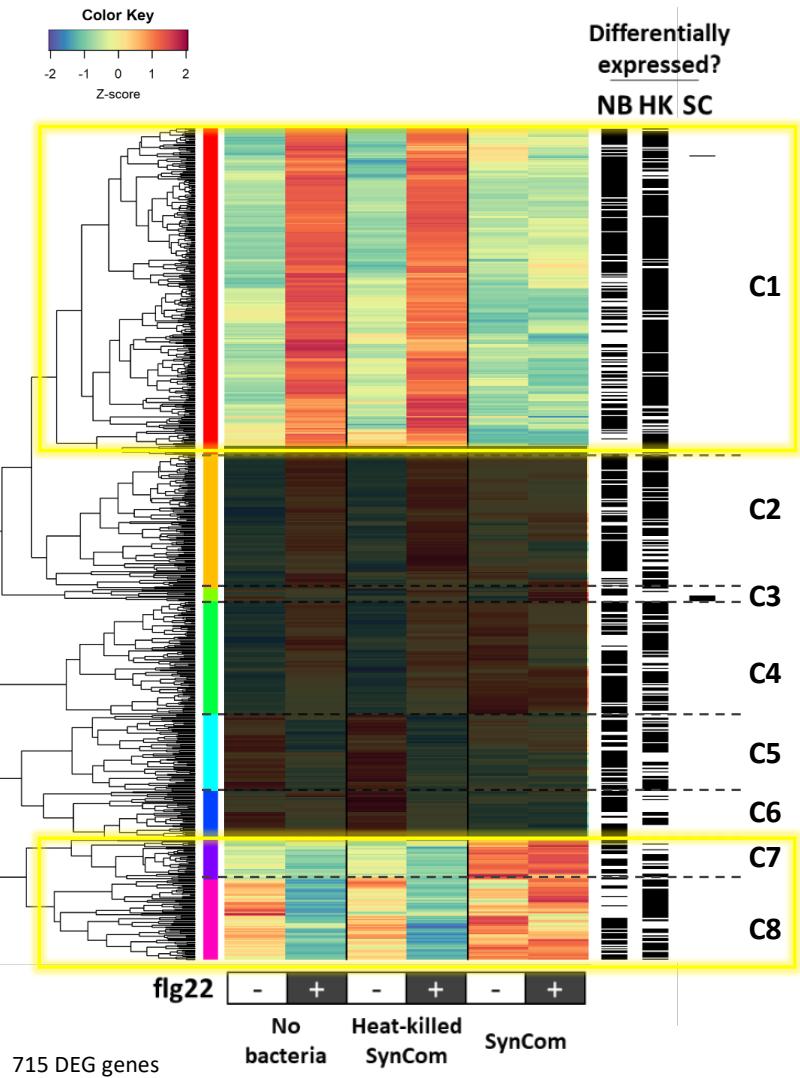


Correlation among flg22 responses

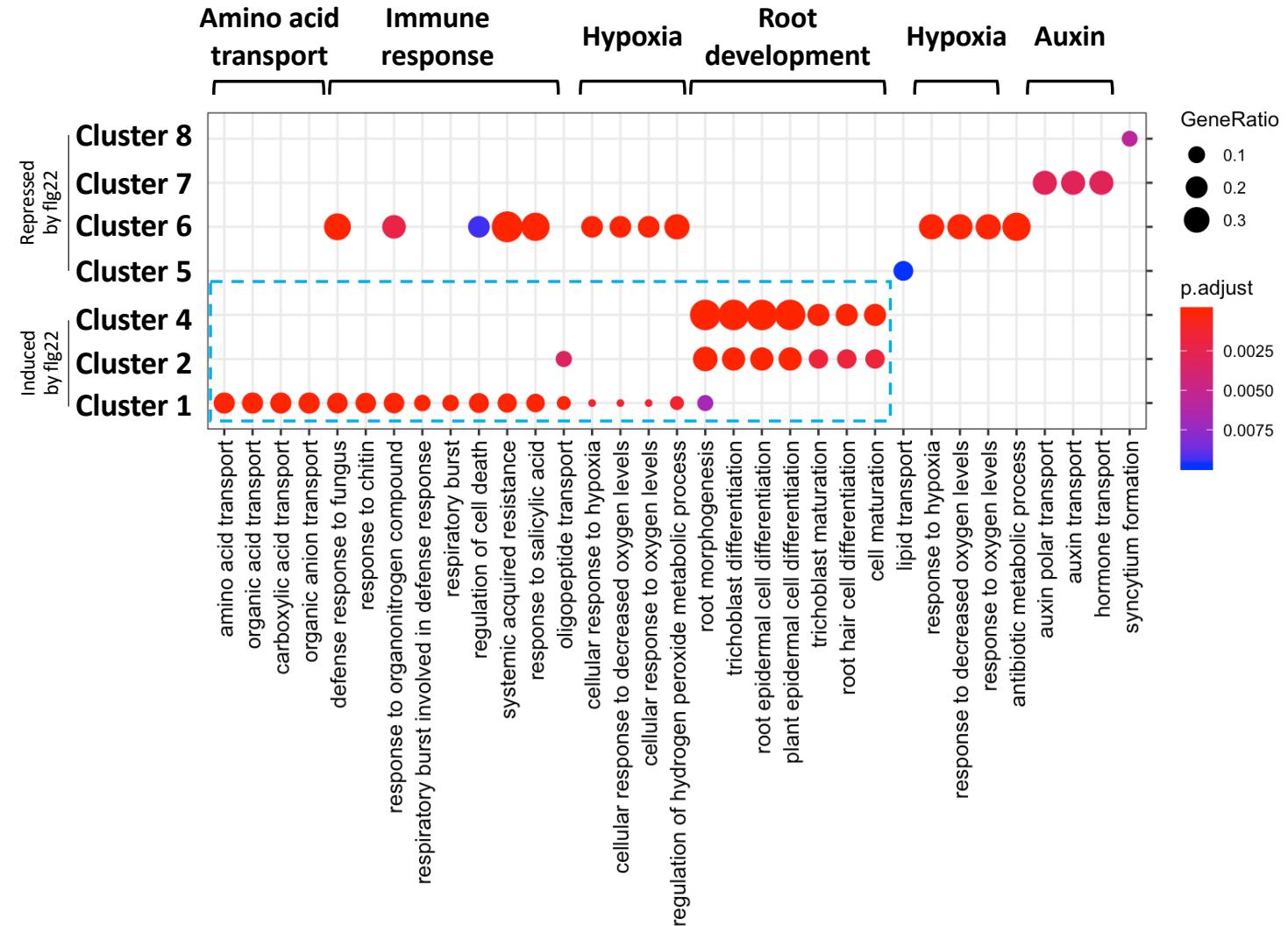
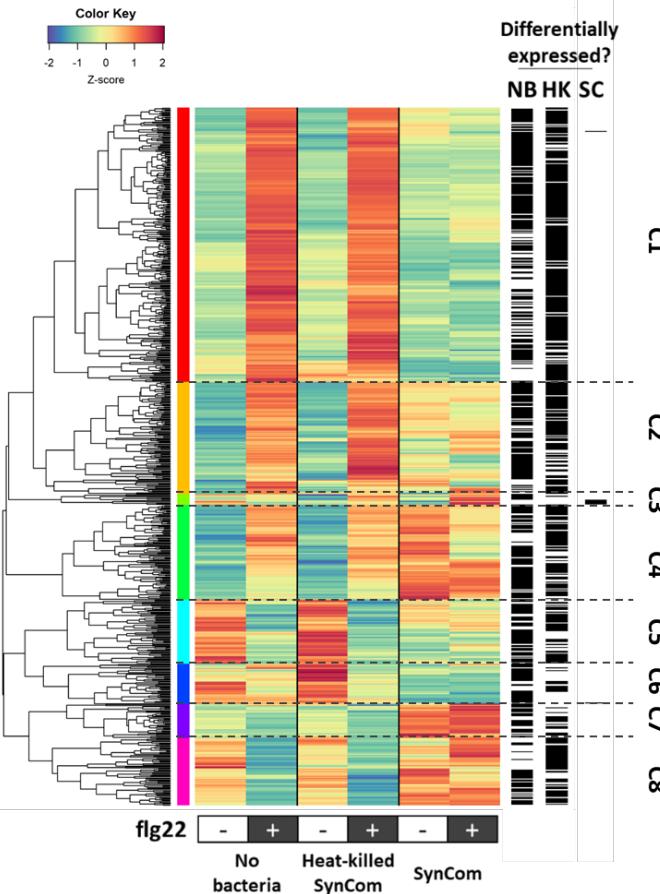
The response to flg22 is altered in the presence of the SynCom



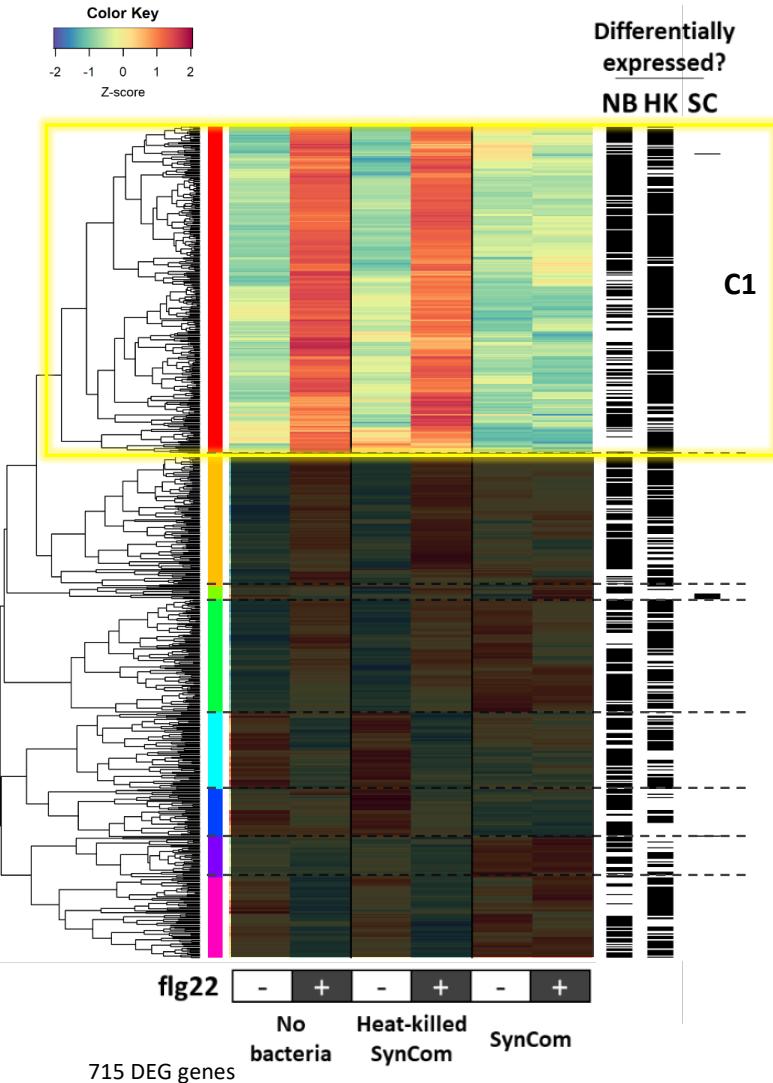
The root response to flg22 is altered in the presence of the SynCom



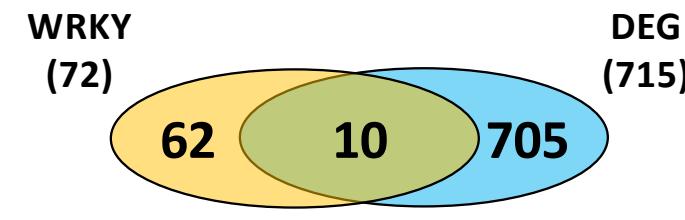
Gene Ontology (GO) enrichment analyses



Enriched gene families in cluster 1



Enriched gene families		FDR
Gene Set Name(No. Genes)		
CLASS_III_PEROXIDASE(73)		3.40E-06
RECEPTOR_KINASE-LIKE_PROTEIN_FAMILY(307)		1.97E-03
MONOLIGNOL BIOSYNTHESIS_COMT-LIKE(13)		1.97E-03
WRKY_TRANSCRIPTION_FACTOR_FAMILY(72)		1.97E-03
WRKY_TRANSCRIPTION_FACTOR_SUPERFAMILY_GROUP_II-B(8)		0.0119
CARBOHYDRATE ESTERASE_GENE_FAMILIES_CARBOHYDRATE ESTERASE_FAMILY_8(56)		0.0222
GLYCOSIDE_HYDROLASE_GENE_FAMILIES_GLYCOSIDE_HYDROLASE_FAMILY_19(15)		0.04



10/72 WRKYS are DE
7 are in cluster 1

WRKY8 WRKY33
WRKY28 WRKY42
WRKY30 WRKY61
WRKY31

WRKYS per cluster

- C1 – 7
- C2 – 0
- C3 – 0
- C4 – 1
- C5 – 2
- C6 – 0
- C7 – 0
- C8 – 0

70% of the WRKYS that are up-regulated by flg22 in roots have the activation prevented by the SynCom (cluster1)

The activation of WRKYs is suppressed by the SynCom

