

Supplementary Figures and Tables

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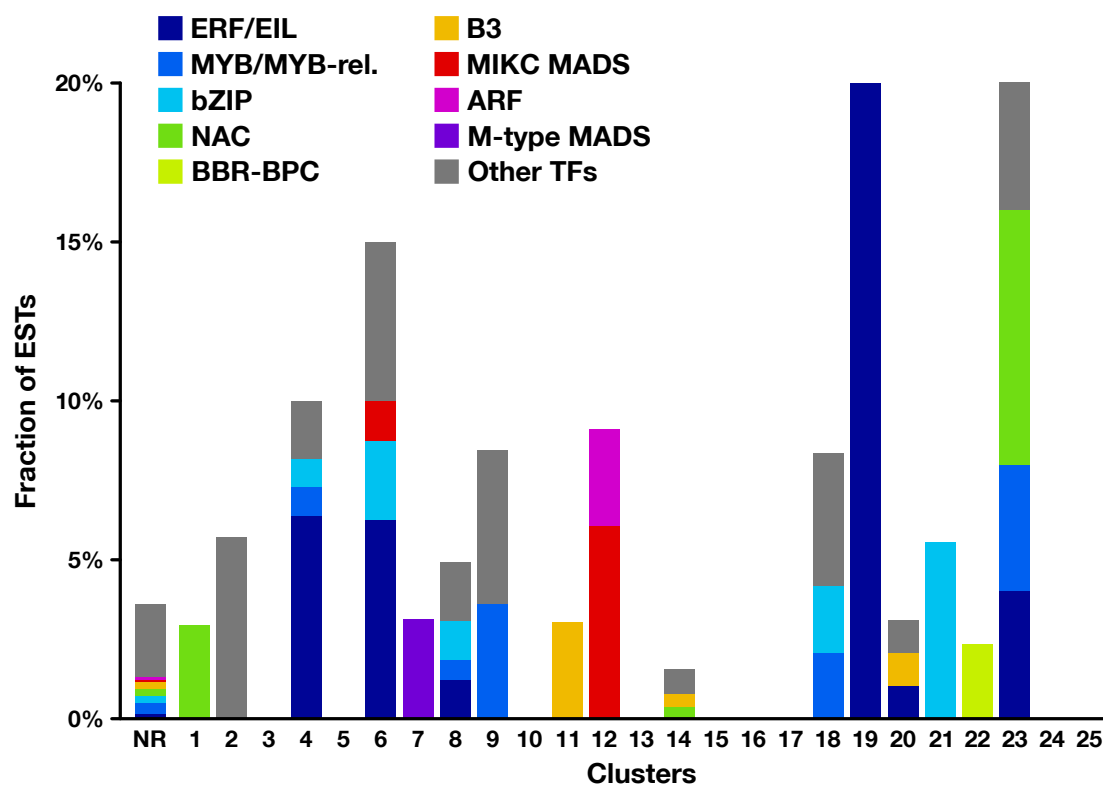


Figure S2. Graphical summary of *in silico* transcription factor predictions made in each cluster. The Plant-TFDB prediction tool was used on the best BLASTx hit for each EST to predict and classify sequences into transcription factor (TF) families.

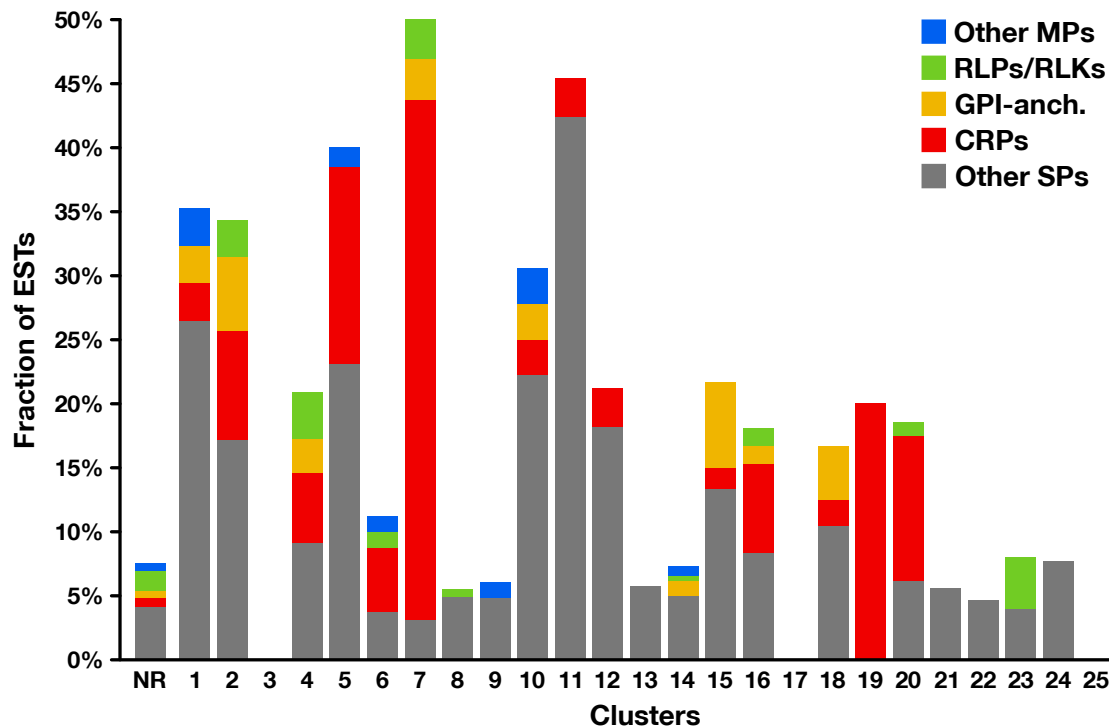


Figure S3. Graphical summary of *in silico* predictions made on secreted proteins in each cluster. SignalP was used on the best BLASTx hit for each EST to predict the presence of a signal peptide. GPI anchors were predicted using PredGPI. Remaining sequences were inspected for the presence of transmembrane helices with TMHMM. Sequences with one such helix were classified as potential receptor-like proteins or kinases (RLPs/RLKs); sequences with multiple transmembrane helices were classified as other membrane proteins. Sequences without a transmembrane helix nor a GPI anchor were split into cysteine-rich proteins (CRPs; mature peptide ≤ 150 aa, 6+ cysteines) and other non-membrane proteins.

Table S1. Number and proportion of genes regulated after each treatment, along with coregulation statistics across conditions and time points.. The number of up- and down-regulated genes in each category/overlap is given in columns “↑” and “↓”, respectively. The number of coregulated genes, i.e. having the same regulation in the two conditions compared, is given in columns “↑↑” (up/up) and “↓↓” (down/down). The number of genes in the overlap having opposite regulations are shown in column “Opp.”. Values given in column “*p*-values” express the significance of overlaps between gene sets; they were computed with a Fisher’s exact test. Local percentages (in black) were computed according to the total number of genes in each row. Global percentages (in gray) were computed according to the total number of genes regulated in the condition. In this table, “specific” refers to genes that are regulated in the considered condition but not in the other pollination conditions at the same time point.

(a) Genes regulated 6 h after conspecific compatible pollination (CCP)

Category	Regulated			Coregulated			Opp.	<i>p</i> -value
	all	↑	↓	↑↑	↓↓	total		
Total	125	68	57					
	100%	54.4%	45.6%					
	100%	54.4%	45.6%					
Specific	52	22	30					
	100%	42.3%	57.7%					
	41.6%	17.6%	24.0%					
Non specific	73	46	27					
	100%	63.0%	37.0%					
	58.4%	36.8%	21.6%					
Common to CIP 6 h	63	40	23	40	23	63	0	1.2×10^{-94}
	100%	63.5%	36.5%	63.5%	36.5%	100%	0.0%	
	50.4%	32.0%	18.4%	32.0%	18.4%	50.4%	0.0%	
Common to HCP 6 h	48	30	18	30	18	48	0	7.8×10^{-130}
	100%	62.5%	37.5%	62.5%	37.5%	100%	0.0%	
	38.4%	24.0%	14.4%	24.0%	14.4%	38.4%	0.0%	
Common to W 6 h	90	49	41	49	41	90	0	1.0×10^{-42}
	100%	54.4%	45.6%	54.4%	45.6%	100%	0.0%	
	72.0%	39.2%	32.8%	39.2%	32.8%	72.0%	0.0%	
Common to T 6 h	55	35	20	35	18	53	2	1.0×10^{-90}
	100%	63.6%	36.4%	63.6%	32.7%	96.4%	3.6%	
	44.0%	28.0%	16.0%	28.0%	14.4%	42.4%	1.6%	
Common to CCP 24 h	30	16	14	11	11	22	8	4.0×10^{-92}
	100%	53.3%	46.7%	36.7%	36.7%	73.3%	26.7%	
	24.0%	12.8%	11.2%	8.8%	8.8%	17.6%	6.4%	
Common to CCP 48 h	54	32	22	16	20	36	18	3.3×10^{-27}
	100%	59.3%	40.7%	29.6%	37.0%	66.7%	33.3%	
	43.2%	25.6%	17.6%	12.8%	16.0%	28.8%	14.4%	

Table S1. (continued)

(b) Genes regulated 6 h after conspecific incompatible pollination (CIP)

Category	Regulated			Coregulated			Opp.	<i>p</i> -value
	all	↑	↓	↑↑	↓↓	total		
Total	88	57	31					
	100%	64.8%	35.2%					
	100%	64.8%	35.2%					
Specific	22	15	7					
	100%	68.2%	31.8%					
	25.0%	17.0%	8.0%					
Non specific	66	42	24					
	100%	63.6%	36.4%					
	75.0%	47.7%	27.3%					
Common to CCP 6 h	63	40	23	40	23	63	0	4.0×10^{-28}
	100%	63.5%	36.5%	63.5%	36.5%	100%	0.0%	
	71.6%	45.5%	26.1%	45.5%	26.1%	71.6%	0.0%	
Common to HCP 6 h	41	26	15	26	15	41	0	8.6×10^{-78}
	100%	63.4%	36.6%	63.4%	36.6%	100%	0.0%	
	46.6%	29.5%	17.0%	29.5%	17.0%	46.6%	0.0%	
Common to W 6 h	63	39	24	39	24	63	0	1.4×10^{-27}
	100%	61.9%	38.1%	61.9%	38.1%	100%	0.0%	
	71.6%	44.3%	27.3%	44.3%	27.3%	71.6%	0.0%	
Common to T 6 h	46	31	15	31	14	45	1	9.1×10^{-52}
	100%	67.4%	32.6%	67.4%	30.4%	97.8%	2.2%	
	52.3%	35.2%	17.0%	35.2%	15.9%	51.1%	1.1%	
Common to CIP 24 h	16	10	6	9	6	15	1	4.5×10^{-113}
	100%	62.5%	37.5%	56.2%	37.5%	93.8%	6.2%	
	18.2%	11.4%	6.8%	10.2%	6.8%	17.0%	1.1%	
Common to CIP 48 h	17	14	3	13	2	15	2	1.5×10^{-97}
	100%	82.4%	17.6%	76.5%	11.8%	88.2%	11.8%	
	19.3%	15.9%	3.4%	14.8%	2.3%	17.0%	2.3%	

Table S1. (continued)

(c) Genes regulated 6 h after heterospecific compatible pollination (HCP)

Category	Regulated			Coregulated			Opp.	<i>p</i> -value
	all	↑	↓	↑↑	↓↓	total		
Total	64	43	21					
	100%	67.2%	32.8%					
	100%	67.2%	32.8%					
Specific	13	11	2					
	100%	84.6%	15.4%					
	20.3%	17.2%	3.1%					
Non specific	51	32	19					
	100%	62.7%	37.3%					
	79.7%	50.0%	29.7%					
Common to CCP 6 h	48	30	18	30	18	48	0	1.2×10^{-16}
	100%	62.5%	37.5%	62.5%	37.5%	100%	0.0%	
	75.0%	46.9%	28.1%	46.9%	28.1%	75.0%	0.0%	
Common to CIP 6 h	41	26	15	26	15	41	0	4.1×10^{-31}
	100%	63.4%	36.6%	63.4%	36.6%	100%	0.0%	
	64.1%	40.6%	23.4%	40.6%	23.4%	64.1%	0.0%	
Common to W 6 h	49	30	19	30	19	49	0	4.6×10^{-15}
	100%	61.2%	38.8%	61.2%	38.8%	100%	0.0%	
	76.6%	46.9%	29.7%	46.9%	29.7%	76.6%	0.0%	
Common to T 6 h	43	31	12	31	12	43	0	4.4×10^{-23}
	100%	72.1%	27.9%	72.1%	27.9%	100%	0.0%	
	67.2%	48.4%	18.8%	48.4%	18.8%	67.2%	0.0%	
Common to HCP 24 h	21	15	6	13	3	16	5	1.5×10^{-43}
	100%	71.4%	28.6%	61.9%	14.3%	76.2%	23.8%	
	32.8%	23.4%	9.4%	20.3%	4.7%	25.0%	7.8%	
Common to HCP 48 h	13	10	3	7	2	9	4	3.1×10^{-68}
	100%	76.9%	23.1%	53.8%	15.4%	69.2%	30.8%	
	20.3%	15.6%	4.7%	10.9%	3.1%	14.1%	6.2%	

Table S1. (continued)

(d) Genes regulated 24 h after conspecific compatible pollination (CCP)

Category	Regulated			Coregulated			Opp.	<i>p</i> -value
	all	↑	↓	↑↑	↓↓	total		
Total	354	151	203					
	100%	42.7%	57.3%					
	100%	42.7%	57.3%					
Specific	269	128	141					
	100%	47.6%	52.4%					
	76.0%	36.2%	39.8%					
Non specific	85	23	62					
	100%	27.1%	72.9%					
	24.0%	6.5%	17.5%					
Common to CIP 24 h	41	14	27	14	23	37	4	0
	100%	34.1%	65.9%	34.1%	56.1%	90.2%	9.8%	
	11.6%	4.0%	7.6%	4.0%	6.5%	10.5%	1.1%	
Common to HCP 24 h	58	14	44	8	17	25	33	6.1×10^{-307}
	100%	24.1%	75.9%	13.8%	29.3%	43.1%	56.9%	
	16.4%	4.0%	12.4%	2.3%	4.8%	7.1%	9.3%	
Common to W 24 h	61	24	37	24	37	61	0	0
	100%	39.3%	60.7%	39.3%	60.7%	100%	0.0%	
	17.2%	6.8%	10.5%	6.8%	10.5%	17.2%	0.0%	
Common to T 24 h	56	30	26	30	23	53	3	0
	100%	53.6%	46.4%	53.6%	41.1%	94.6%	5.4%	
	15.8%	8.5%	7.3%	8.5%	6.5%	15.0%	0.8%	
Common to CCP 6 h	30	14	16	11	11	22	8	0
	100%	46.7%	53.3%	36.7%	36.7%	73.3%	26.7%	
	8.5%	4.0%	4.5%	3.1%	3.1%	6.2%	2.3%	
Common to CCP 48 h	222	97	125	95	122	217	5	1.2×10^{-30}
	100%	43.7%	56.3%	42.8%	55.0%	97.7%	2.3%	
	62.7%	27.4%	35.3%	26.8%	34.5%	61.3%	1.4%	

Table S1. (continued)

(e) Genes regulated 24 h after conspecific incompatible pollination (CIP)

Category	Regulated			Coregulated			Opp.	<i>p</i> -value
	all	↑	↓	↑↑	↓↓	total		
Total	89	52	37					
	100%	58.4%	41.6%					
	100%	58.4%	41.6%					
Specific	17	9	8					
	100%	52.9%	47.1%					
	19.1%	10.1%	9.0%					
Non specific	72	43	29					
	100%	59.7%	40.3%					
	80.9%	48.3%	32.6%					
Common to CCP 24 h	41	18	23	14	23	37	4	1.9×10^{-38}
	100%	43.9%	56.1%	34.1%	56.1%	90.2%	9.8%	
	46.1%	20.2%	25.8%	15.7%	25.8%	41.6%	4.5%	
Common to HCP 24 h	45	34	11	15	6	21	24	8.4×10^{-38}
	100%	75.6%	24.4%	33.3%	13.3%	46.7%	53.3%	
	50.6%	38.2%	12.4%	16.9%	6.7%	23.6%	27.0%	
Common to W 24 h	33	24	9	23	9	32	1	6.6×10^{-78}
	100%	72.7%	27.3%	69.7%	27.3%	97.0%	3.0%	
	37.1%	27.0%	10.1%	25.8%	10.1%	36.0%	1.1%	
Common to T 24 h	30	24	6	24	5	29	1	2.4×10^{-70}
	100%	80.0%	20.0%	80.0%	16.7%	96.7%	3.3%	
	33.7%	27.0%	6.7%	27.0%	5.6%	32.6%	1.1%	
Common to CIP 6 h	16	9	7	9	6	15	1	6.0×10^{-115}
	100%	56.2%	43.8%	56.2%	37.5%	93.8%	6.2%	
	18.0%	10.1%	7.9%	10.1%	6.7%	16.9%	1.1%	
Common to CIP 48 h	28	10	18	9	18	27	1	6.0×10^{-79}
	100%	35.7%	64.3%	32.1%	64.3%	96.4%	3.6%	
	31.5%	11.2%	20.2%	10.1%	20.2%	30.3%	1.1%	

Table S1. (continued)

(f) Genes regulated 24 h after heterospecific compatible pollination (HCP)

Category	Regulated			Coregulated			Opp.	<i>p</i> -value
	all	↑	↓	↑↑	↓↓	total		
Total	285	140	145					
	100%	49.1%	50.9%					
	100%	49.1%	50.9%					
Specific	196	93	103					
	100%	47.4%	52.6%					
	68.8%	32.6%	36.1%					
Non specific	89	47	42					
	100%	52.8%	47.2%					
	31.2%	16.5%	14.7%					
Common to CCP 24 h	58	35	23	8	17	25	33	8.1×10^{-217}
	100%	60.3%	39.7%	13.8%	29.3%	43.1%	56.9%	
	20.4%	12.3%	8.1%	2.8%	6.0%	8.8%	11.6%	
Common to CIP 24 h	45	20	25	15	6	21	24	0
	100%	44.4%	55.6%	33.3%	13.3%	46.7%	53.3%	
	15.8%	7.0%	8.8%	5.3%	2.1%	7.4%	8.4%	
Common to W 24 h	37	10	27	5	5	10	27	0
	100%	27.0%	73.0%	13.5%	13.5%	27.0%	73.0%	
	13.0%	3.5%	9.5%	1.8%	1.8%	3.5%	9.5%	
Common to T 24 h	41	4	37	4	9	13	28	1.8×10^{-298}
	100%	9.8%	90.2%	9.8%	22.0%	31.7%	68.3%	
	14.4%	1.4%	13.0%	1.4%	3.2%	4.6%	9.8%	
Common to HCP 6 h	21	16	5	13	3	16	5	0
	100%	76.2%	23.8%	61.9%	14.3%	76.2%	23.8%	
	7.4%	5.6%	1.8%	4.6%	1.1%	5.6%	1.8%	
Common to HCP 48 h	128	70	58	70	58	128	0	3.0×10^{-199}
	100%	54.7%	45.3%	54.7%	45.3%	100%	0.0%	
	44.9%	24.6%	20.4%	24.6%	20.4%	44.9%	0.0%	

Table S1. (continued)

(g) Genes regulated 48 h after conspecific compatible pollination (CCP)

Category	Regulated			Coregulated			Opp.	<i>p</i> -value
	all	↑	↓	↑↑	↓↓	total		
Total	1018	515	503					
	100%	50.6%	49.4%					
	100%	50.6%	49.4%					
Specific	893	464	429					
	100%	52.0%	48.0%					
	87.7%	45.6%	42.1%					
Non specific	125	51	74					
	100%	40.8%	59.2%					
	12.3%	5.0%	7.3%					
Common to CIP 48 h	76	35	41	14	28	42	34	0
	100%	46.1%	53.9%	18.4%	36.8%	55.3%	44.7%	
	7.5%	3.4%	4.0%	1.4%	2.8%	4.1%	3.3%	
Common to HCP 48 h	60	24	36	13	11	24	36	0
	100%	40.0%	60.0%	21.7%	18.3%	40.0%	60.0%	
	5.9%	2.4%	3.5%	1.3%	1.1%	2.4%	3.5%	
Common to W 48 h	80	43	37	29	24	53	27	0
	100%	53.8%	46.2%	36.2%	30.0%	66.2%	33.8%	
	7.9%	4.2%	3.6%	2.8%	2.4%	5.2%	2.7%	
Common to T 48 h	43	16	27	16	21	37	6	0
	100%	37.2%	62.8%	37.2%	48.8%	86.0%	14.0%	
	4.2%	1.6%	2.7%	1.6%	2.1%	3.6%	0.6%	
Common to CCP 6 h	54	18	36	16	20	36	18	0
	100%	33.3%	66.7%	29.6%	37.0%	66.7%	33.3%	
	5.3%	1.8%	3.5%	1.6%	2.0%	3.5%	1.8%	
Common to CCP 24 h	222	98	124	95	122	217	5	0
	100%	44.1%	55.9%	42.8%	55.0%	97.7%	2.3%	
	21.8%	9.6%	12.2%	9.3%	12.0%	21.3%	0.5%	

Table S1. (continued)

(h) Genes regulated 48 h after conspecific incompatible pollination (CIP)

Category	Regulated			Coregulated			Opp.	<i>p</i> -value
	all	↑	↓	↑↑	↓↓	total		
Total	147	65	82					
	100%	44.2%	55.8%					
	100%	44.2%	55.8%					
Specific	60	33	27					
	100%	55.0%	45.0%					
	40.8%	22.4%	18.4%					
Non specific	87	32	55					
	100%	36.8%	63.2%					
	59.2%	21.8%	37.4%					
Common to CCP 48 h	76	27	49	14	28	42	34	3.4×10^{-22}
	100%	35.5%	64.5%	18.4%	36.8%	55.3%	44.7%	
	51.7%	18.4%	33.3%	9.5%	19.0%	28.6%	23.1%	
Common to HCP 48 h	22	14	8	8	0	8	14	8.7×10^{-165}
	100%	63.6%	36.4%	36.4%	0.0%	36.4%	63.6%	
	15.0%	9.5%	5.4%	5.4%	0.0%	5.4%	9.5%	
Common to W 48 h	77	40	37	40	36	76	1	2.0×10^{-75}
	100%	51.9%	48.1%	51.9%	46.8%	98.7%	1.3%	
	52.4%	27.2%	25.2%	27.2%	24.5%	51.7%	0.7%	
Common to T 48 h	19	12	7	12	6	18	1	2.3×10^{-197}
	100%	63.2%	36.8%	63.2%	31.6%	94.7%	5.3%	
	12.9%	8.2%	4.8%	8.2%	4.1%	12.2%	0.7%	
Common to CIP 6 h	17	14	3	13	2	15	2	3.5×10^{-201}
	100%	82.4%	17.6%	76.5%	11.8%	88.2%	11.8%	
	11.6%	9.5%	2.0%	8.8%	1.4%	10.2%	1.4%	
Common to CIP 24 h	28	9	19	9	18	27	1	1.1×10^{-180}
	100%	32.1%	67.9%	32.1%	64.3%	96.4%	3.6%	
	19.0%	6.1%	12.9%	6.1%	12.2%	18.4%	0.7%	

Table S1. (continued)

(i) Genes regulated 48 h after heterospecific compatible pollination (HCP)

Category	Regulated			Coregulated			Opp.	<i>p</i> -value
	all	↑	↓	↑↑	↓↓	total		
Total	166	97	69					
	100%	58.4%	41.6%					
	100%	58.4%	41.6%					
Specific	95	51	44					
	100%	53.7%	46.3%					
	57.2%	30.7%	26.5%					
Non specific	71	46	25					
	100%	64.8%	35.2%					
	42.8%	27.7%	15.1%					
Common to CCP 48 h	60	38	22	13	11	24	36	5.1×10^{-46}
	100%	63.3%	36.7%	21.7%	18.3%	40.0%	60.0%	
	36.1%	22.9%	13.3%	7.8%	6.6%	14.5%	21.7%	
Common to CIP 48 h	22	16	6	8	0	8	14	1.1×10^{-195}
	100%	72.7%	27.3%	36.4%	0.0%	36.4%	63.6%	
	13.3%	9.6%	3.6%	4.8%	0.0%	4.8%	8.4%	
Common to W 48 h	22	15	7	12	0	12	10	5.2×10^{-184}
	100%	68.2%	31.8%	54.5%	0.0%	54.5%	45.5%	
	13.3%	9.0%	4.2%	7.2%	0.0%	7.2%	6.0%	
Common to T 48 h	13	2	11	2	1	3	10	1.3×10^{-236}
	100%	15.4%	84.6%	15.4%	7.7%	23.1%	76.9%	
	7.8%	1.2%	6.6%	1.2%	0.6%	1.8%	6.0%	
Common to HCP 6 h	13	8	5	7	2	9	4	2.0×10^{-249}
	100%	61.5%	38.5%	53.8%	15.4%	69.2%	30.8%	
	7.8%	4.8%	3.0%	4.2%	1.2%	5.4%	2.4%	
Common to HCP 24 h	128	70	58	70	58	128	0	1.5×10^{-24}
	100%	54.7%	45.3%	54.7%	45.3%	100%	0.0%	
	77.1%	42.2%	34.9%	42.2%	34.9%	77.1%	0.0%	

Table S2. Summary of *in silico* transcription factor predictions made on genes modulated at a distance by pollination, with comparative enrichment analyses across conditions and clusters. The PlantTFDB prediction tool was used on the best BLASTx hit for each EST to predict and classify sequences into transcription factor (TF) families. Columns *Poll.* and *Rest* give the total number of genes regulated in at least one pollination condition, and the number of remaining genes, respectively. Asterisks (*) indicate a significant enrichment for a given prediction in a given sample (Fisher's exact test, $P < 0.05$).

(a) Genes regulated 6 h after pollination

Prediction	CCP 6 h		CIP 6 h		HCP 6 h		Poll.	Rest
	↑	↓	↑	↓	↑	↓		
ERF/EIL	1		*2	1	1		*17	8
MYB/MYB-rel.							7	18
bZIP							7	12
NAC							4	11
BBR-BPC							1	1
B3	1		1		1		3	12
MIKC MADS	1		*1				3	3
ARF	1		1				1	6
M-type MADS		*1					1	
Other TFs		1					21	121
Total TFs	4	2	5	1	2		65	192
Total	68	57	57	31	43	21	1441	5340

(b) Genes regulated 24 h after pollination

Prediction	CCP 24 h		CIP 24 h		HCP 24 h		Poll.	Rest
	↑	↓	↑	↓	↑	↓		
ERF/EIL	1	*10	*4	1	*9	2	*17	8
MYB/MYB-rel.	1	1			1	1	7	18
bZIP	1				*4	1	7	12
NAC	1	1			1		4	11
BBR-BPC				*1			1	1
B3							3	12
MIKC MADS		1				1	3	3
ARF							1	6
M-type MADS							1	
Other TFs	1	3			5	3	21	121
Total TFs	5	*16	4	2	*20	8	65	192
Total	151	203	52	37	140	145	1441	5340

Table S2. (continued)

(c) Genes regulated 48 h after pollination

Prediction	CCP 48 h		CIP 48 h		HCP 48 h		Poll.	Rest
	↑	↓	↑	↓	↑	↓		
ERF/EIL		*11	*3	1	*7	1	*17	8
MYB/MYB-rel.		3	*3		1	1	7	18
bZIP		*4			*3		7	12
NAC	2	1	*2			1	4	11
BBR-BPC							1	1
B3	2		1				3	12
MIKC MADS		1				1	3	3
ARF							1	6
M-type MADS		1					1	
Other TFs	2	12	1		1	3	21	121
Total TFs	6	*33	*10	1	*12	*7	65	192
Total	515	503	65	82	97	69	1441	5340

(d) Pollination-induced genes belonging to clusters 1–12

Prediction	Clusters												Poll.	Rest
	1	2	3	4	5	6	7	8	9	10	11	12		
ERF/EIL				*7		*5		2					*17	8
MYB/MYB-rel.				1				1	*3				7	18
bZIP				1		*2		2					7	12
NAC	1												4	11
BBR-BPC													1	1
B3											1		3	12
MIKC MADS						1						*2	3	3
ARF												*1	1	6
M-type MADS							*1						1	
Other TFs		2		2		4		3	4				21	121
Total TFs	1	2		*11		*12	1	8	*7		1	3	65	192
Total	34	35	15	110	65	80	32	163	83	36	33	33	1441	5340

Table S2. (continued)

(e) Pollination-induced genes belonging to clusters 13–25

Prediction	Clusters													Poll.	Rest
	13	14	15	16	17	18	19	20	21	22	23	24	25		
ERF/EIL							*1	1			1			*17	8
MYB/MYB-rel.						1					1			7	18
bZIP						1			*1					7	12
NAC		1									*2			4	11
BBR-BPC										*1				1	1
B3		1						1						3	12
MIKC MADS														3	3
ARF														1	6
M-type MADS														1	
Other TFs		2				2		1			1			21	121
Total TFs		4				4	1	3	1	1	*5			65	192
Total	52	260	60	72	10	48	5	97	18	43	25	13	19	1441	5340

Table S3. Summary of *in silico* signal peptide and subsequent predictions made on genes modulated at a distance by pollination, with comparative enrichment analyses across conditions and clusters. SignalP was used on the best BLASTx hit for each EST to predict the presence of a signal peptide. GPI anchors were predicted using PredGPI. Remaining sequences were inspected for the presence of transmembrane helices with TMHMM. Sequences with one such helix were classified as potential receptor-like proteins or kinases (RLPs/RLKs); sequences with multiple transmembrane helices were classified as other membrane proteins. Sequences without a transmembrane helix nor a GPI anchor were split into cysteine-rich proteins (CRPs; mature peptide ≤ 150 aa, 6+ cysteines) and other non-membrane proteins. Columns *Poll.* and *Rest* give the total number of genes regulated in at least one pollination condition, and the number of remaining genes, respectively. Asterisks (*) indicate a significant enrichment for a given prediction in a given sample (Fisher's exact test, $P < 0.05$).

(a) Genes regulated 6 h after pollination

Prediction	CCP 6 h		CIP 6 h		HCP 6 h		Poll.	Rest
	↑	↓	↑	↓	↑	↓		
CRPs	*9	*6	*6	*5	1	*2	*59	40
Other non-membrane	*18	1	*12		*14		*130	219
GPI-anchored		1		1			*18	28
RLPs/RLKs							12	*84
Other membrane					1		7	32
Total secreted	*27	8	*18	6	*16	2	*226	403
Total	68	57	57	31	43	21	1441	5340

(b) Genes regulated 24 h after pollination

Prediction	CCP 24 h		CIP 24 h		HCP 24 h		Poll.	Rest
	↑	↓	↑	↓	↑	↓		
CRPs	4	*14	*5	*6	4	*11	*59	40
Other non-membrane	12	*20	4	2	*20	13	*130	219
GPI-anchored		1			*5	3	*18	28
RLPs/RLKs		1			2		12	*84
Other membrane					1		7	32
Total secreted	16	*36	9	*8	*32	*27	*226	403
Total	151	203	52	37	140	145	1441	5340

Table S3. (continued)

(c) Genes regulated 48 h after pollination

Prediction	CCP 48 h		CIP 48 h		HCP 48 h		Poll.	Rest
	↑	↓	↑	↓	↑	↓		
CRPs	*14	*30		*7	3	*5	*59	40
Other non-membrane	*37	*52	6	*16	*12	*8	*130	219
GPI-anchored	*9	1		1	2	*3	*18	28
RLPs/RLKs	3	5	1	2	3		12	*84
Other membrane	2	4					7	32
Total secreted	*65	*92	7	*26	*20	*16	*226	403
Total	515	503	65	82	97	69	1441	5340

(d) Pollination-induced genes belonging to clusters 1–12

Prediction	Clusters												Poll.	Rest
	1	2	3	4	5	6	7	8	9	10	11	12		
CRPs	1	*3		*6	*10	*4	*13			1	1	1	*59	40
Other non-mb	*9	*6		10	*15	3	1	8	4	*8	*14	*6	*130	219
GPI-anchored	1	*2		*3			1			1			*18	28
RLPs/RLKs		1		4		1	1	1					12	*84
Other mb	1				1	1			1	1			7	32
Total secreted	*12	*12		*23	*26	9	*16	9	5	*11	*15	*7	*226	403
Total	34	35	15	110	65	80	32	163	83	36	33	33	1441	5340

(e) Pollination-induced genes belonging to clusters 13–25

Prediction	Clusters													Poll.	Rest
	13	14	15	16	17	18	19	20	21	22	23	24	25		
CRPs			1	*5		1	1	*11						*59	40
Other non-mb	3	13	*8	6		5		6	1	2	1	1		*130	219
GPI-anchored		3	*4	1		*2								*18	28
RLPs/RLKs		1		1				1			1			12	*84
Other mb		2												7	32
Total secreted	3	19	*13	*13		8	1	*18	1	2	2	1		*226	403
Total	52	260	60	72	10	48	5	97	18	43	25	13	19	1441	5340

Table S4. Summary of *in silico* metabolic pathway predictions made on genes modulated at a distance by pollination, with comparative enrichment analyses across conditions and clusters. The enzymes codes retrieved from BLAST and Blast2GO analyses were mapped to KEGG metabolic pathways. Columns *Poll.* and *Rest* give the total number of genes regulated in at least one pollination condition, and the number of remaining genes, respectively. Asterisks (*) indicate a significant enrichment for a given prediction in a given sample (Fisher's exact test, $P < 0.05$).

(a) Detailed view of metabolic pathway enrichment in each pollination condition

Metabolic pathway	6 HAP						24 HAP						48 HAP						Poll.	Rest
	CCP		CIP		HCP		CCP		CIP		HCP		CCP		CIP		HCP			
	↑	↓	↑	↓	↑	↓	↑	↓	↑	↓	↑	↓	↑	↓	↑	↓	↑	↓		
Total ESTs	68	57	57	31	43	21	151	203	52	37	140	145	515	503	65	82	97	69	1441	5340
ESTs involved in metabolic pathways	12	6	8	4	4	3	10	16	9	1	16	24	51	66	9	12	9	8	180	736
1. Carbohydrate metabolism																				
Amino sugar and nucleotide sugar metabolism [00520]	1	1	0	2	0	1	2	1	2	0	2	4	7	4	0	1	2	0	21	64
Ascorbate and aldarate metabolism [00053]	0	1	0	*2	0	1	1	1	0	0	0	0	1	1	0	0	1	0	6	28
Butanoate metabolism [00650]	0	0	0	0	0	0	0	0	0	0	0	2	0	3	0	0	0	1	5	15
C5-Branched dibasic acid metabolism [00660]	0	0	0	0	0	0	0	0	0	0	0	*2	2	0	0	0	0	0	4	8
Citrate cycle (TCA cycle) [00020]	0	0	0	0	0	0	0	0	0	0	0	*3	5	1	0	0	0	1	8	26
Fructose and mannose metabolism [00051]	0	0	0	0	0	0	1	0	0	0	0	0	1	3	0	1	0	0	5	29
Galactose metabolism [00052]	0	0	0	0	0	0	1	0	0	0	0	0	3	1	0	0	0	0	4	*53
Glycolysis / Gluconeogenesis [00010]	1	1	0	2	0	1	1	0	1	0	2	1	3	7	1	1	0	0	13	79
Glyoxylate and dicarboxylate metabolism [00630]	0	0	0	0	0	0	1	0	1	0	2	0	3	5	2	0	0	0	9	35
Inositol phosphate metabolism [00562]	0	0	0	1	0	0	0	0	0	0	0	2	1	1	0	0	0	0	4	24
Pentose and glucuronate interconversions [00040]	0	1	0	*2	0	1	0	1	0	0	1	0	2	2	0	0	1	0	7	32
Pentose phosphate pathway [00030]	1	0	0	0	0	0	0	0	0	0	0	0	2	2	0	1	0	0	4	34
Propanoate metabolism [00640]	0	0	0	0	0	0	0	0	1	0	2	2	2	*8	1	0	0	1	*12	18
Pyruvate metabolism [00620]	0	0	0	0	0	0	0	1	1	0	2	1	4	7	1	0	0	0	12	62
Starch and sucrose metabolism [00500]	1	0	0	0	0	1	0	3	1	0	1	1	2	3	0	1	1	0	10	58
2. Energy metabolism																				
Carbon fixation in photosynthetic organisms [00710]	1	0	0	0	0	0	0	0	0	0	0	0	2	4	0	1	0	0	6	33
Carbon fixation pathways in prokaryotes [00720]	0	0	0	0	0	0	0	0	1	0	2	2	5	*7	1	0	0	1	13	27
Methane metabolism [00680]	0	1	0	*2	0	1	1	0	1	0	2	0	3	5	1	1	0	0	10	34
Nitrogen metabolism [00910]	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	3	13
Oxidative phosphorylation [00190]	0	0	0	1	0	1	1	1	0	1	0	0	0	2	0	0	0	0	4	35
Photosynthesis [00195]	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	*1	0	0	2	1
Sulfur metabolism [00920]	0	0	1	0	1	0	0	0	0	0	1	0	0	3	0	0	0	0	3	17
3. Lipid metabolism																				
alpha-Linolenic acid metabolism [00592]	0	*2	0	*2	0	1	1	2	0	0	0	1	4	4	1	2	0	1	*13	22
Arachidonic acid metabolism [00590]	0	0	0	0	0	0	0	2	0	0	0	2	0	3	0	1	0	0	6	14
Ether lipid metabolism [00565]	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	1	4
Fatty acid biosynthesis [00061]	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	3	18
Fatty acid degradation [00071]	0	*2	0	*2	0	1	0	0	0	0	0	0	0	*7	0	0	0	0	10	30
Fatty acid elongation [00062]	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	2	19
Glycerolipid metabolism [00561]	0	0	0	0	0	0	0	0	0	0	1	2	0	1	0	0	1	0	4	28
Glycerophospholipid metabolism [00564]	0	*2	0	1	0	1	0	2	0	1	2	2	0	2	1	1	2	1	9	30
Linoleic acid metabolism [00591]	0	0	0	0	0	0	0	1	0	0	0	1	0	2	0	*2	0	0	4	9
Sphingolipid metabolism [00600]	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	2	*47
Steroid biosynthesis [00100]	0	0	0	0	0	0	0	*2	1	0	0	*3	*6	0	0	0	0	0	*8	4
Steroid hormone biosynthesis [00140]	1	0	1	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	2	17
4. Nucleotide metabolism																				
Purine metabolism [00230]	0	0	1	0	1	0	2	2	0	0	3	1	9	7	1	*5	1	1	21	69
Pyrimidine metabolism [00240]	0	0	0	0	0	0	1	0	0	0	0	0	4	1	*2	1	0	0	6	24
5. Amino acid metabolism																				
Alanine, aspartate and glutamate metabolism [00250]	0	0	0	0	0	0	0	2	0	0	0	1	0	4	0	0	0	1	6	21
Arginine and proline metabolism [00330]	0	0	0	0	0	0	0	0	1	0	3	0	1	5	0	0	*3	0	9	41
Arginine biosynthesis [00220]	0	0	0	0	0	0	0	0	0	0	0	1	1	2	0	0	0	1	4	16
Cysteine and methionine metabolism [00270]	1	0	1	0	0	0	0	1	0	0	1	1	3	8	0	1	0	0	12	48
Glycine, serine and threonine metabolism [00260]	0	1	0	*2	0	1	1	1	0	0	0	0	3	1	0	0	0	1	7	44
Histidine metabolism [00340]	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	4	17
Lysine biosynthesis [00300]	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	2	10
Lysine degradation [00310]	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	3	32
Phenylalanine metabolism [00360]	0	0	0	0	0	0	0	0	1	0	2	2	2	*11	1	0	0	2	15	38
Phenylalanine, tyrosine and tryptophan biosynthesis [00400]	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	1	0	5	19
Tryptophan metabolism [00380]	0	0	0	0	0	0	0	0	0	0	0	0	1	6	1	0	0	0	8	34
Tyrosine metabolism [00350]	2	1	*2	*2	0	1	0	0	0	0	0	0	1	2	1	0	0	1	8	31
Valine, leucine and isoleucine biosynthesis [00290]	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	15
Valine, leucine and isoleucine degradation [00280]	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	4	25
6. Metabolism of other amino acids																				
beta-Alanine metabolism [00410]	0	0	0	0	0	0	0	0	0	0	0	1	1	3	0	0	0	*2	6	20
Cyanoamino acid metabolism [00460]	0	0	0	0	0	0	1	1	0	0	2	0	3	0	0	1	1	0	6	16
Glutathione metabolism [00480]	0	0	0	0	0	0	2	1	1	0	2	*4	3	8	0	1	1	2	17	43
Selenocompound metabolism [00450]	0	0	1	0	1	0	0	0	0	0	1	0	2	3	0	0	0	0	5	9
Taurine and hypotaurine metabolism [00430]	0	0	0	0	0	0	0	0	0	0	*2	0	1	0	0	0	1	0	2	7
→ cf. page suivante																				

→ cf. page suivante

Table S4. (continued)

Metabolic pathway	6 HAP			24 HAP			48 HAP			Poll.	Rest
	CCP	CIP	HCP	CCP	CIP	HCP	CCP	CIP	HCP		
	↑ ↓	↑ ↓	↑ ↓	↑ ↓	↑ ↓	↑ ↓	↑ ↓	↑ ↓	↑ ↓		
7. Glycan biosynthesis and metabolism											
Glycosaminoglycan degradation [00531]	0	0	0	0	0	0	0	0	0	2	27
Glycosphingolipid biosynthesis - ganglio series [00604]	0	0	0	0	0	0	0	0	0	2	26
N-Glycan biosynthesis [00510]	0	0	0	0	0	0	0	1	0	1	9
Other glycan degradation [00511]	0	0	0	1	0	0	3	0	1	1	38
8. Metabolism of cofactors and vitamins											
Folate biosynthesis [00790]	0	0	0	0	0	0	0	2	0	0	15
Nicotinate and nicotinamide metabolism [00760]	0	0	0	1	0	0	2	0	0	0	12
One carbon pool by folate [00670]	0	0	0	1	0	0	3	2	0	0	14
Pantothenate and CoA biosynthesis [00770]	0	0	0	0	0	0	1	0	0	0	19
Porphyrin and chlorophyll metabolism [00860]	0	*2	0	0	2	1	0	2	0	1	21
Retinol metabolism [00830]	0	1	0	*2	0	0	0	1	0	0	17
Riboflavin metabolism [00740]	0	0	0	0	0	0	0	1	0	0	13
Thiamine metabolism [00730]	0	0	0	0	0	0	3	1	0	*2	18
Ubiquinone and other terpenoid-quinone biosynthesis [00130]	*5	0	*4	0	*3	0	1	0	0	*6	22
9. Metabolism of terpenoids and polyketides											
Biosynthesis of vancomycin group antibiotics [01055]	0	0	0	0	*2	0	*1	0	0	0	0
Carotenoid biosynthesis [00906]	0	0	0	0	0	0	*2	0	0	0	11
Diterpenoid biosynthesis [00904]	0	0	0	0	*3	0	0	0	*4	0	1
Geraniol degradation [00281]	0	0	0	0	0	0	0	0	3	0	12
Insect hormone biosynthesis [00981]	0	0	0	0	0	0	0	0	1	0	7
Limonene and pinene degradation [00903]	0	0	0	0	0	0	0	3	0	0	10
Polyketide sugar unit biosynthesis [00523]	0	0	0	0	*2	0	*1	0	0	0	0
Terpenoid backbone biosynthesis [00900]	0	0	0	0	0	1	1	0	2	3	9
10. Biosynthesis of other secondary metabolites											
Acarbose and validamycin biosynthesis [00525]	0	0	0	0	*2	0	*1	0	0	0	0
Anthocyanin biosynthesis [00942]	0	0	0	0	0	0	*2	0	0	0	2
Betalain biosynthesis [00965]	*2	0	*2	0	0	0	0	0	*1	0	1
Caffeine metabolism [00232]	0	0	0	0	0	0	0	0	1	0	10
Flavone and flavonol biosynthesis [00944]	1	0	1	0	0	0	0	*2	0	0	3
Indole alkaloid biosynthesis [00901]	0	0	0	0	0	0	0	1	0	0	6
Isoquinoline alkaloid biosynthesis [00950]	1	0	1	0	0	0	0	1	2	1	11
Monobactam biosynthesis [00261]	0	0	*1	0	*1	0	0	0	*2	0	2
Novobiocin biosynthesis [00401]	0	0	0	0	0	0	0	0	2	0	5
Penicillin and cephalosporin biosynthesis [00311]	0	0	0	0	0	0	0	1	0	0	14
Phenylpropanoid biosynthesis [00940]	1	1	0	0	0	1	2	2	4	8	46
Streptomycin biosynthesis [00521]	0	0	0	0	*2	0	1	0	0	0	9
Tropane, piperidine and pyridine alkaloid biosynthesis [00960]	0	0	0	0	0	0	1	2	0	1	13
11. Xenobiotics biodegradation and metabolism											
Aminobenzoate degradation [00627]	*5	0	*4	0	*3	0	0	0	2	4	21
Benzoate degradation [00362]	1	0	0	0	0	0	0	0	2	0	12
Caprolactam degradation [00930]	0	0	0	0	0	0	0	0	2	0	10
Chloroalkane and chloroalkene degradation [00625]	0	1	0	*2	0	1	0	1	0	1	13
Chlorocyclohexane and chlorobenzene degradation [00361]	*6	0	*4	0	*3	0	0	0	0	0	5
Drug metabolism - cytochrome P450 [00982]	0	1	0	*2	0	1	1	1	0	0	32
Drug metabolism - other enzymes [00983]	0	0	0	0	0	2	1	3	6	4	41
Fluorobenzoate degradation [00364]	*1	0	0	0	0	0	0	0	0	0	2
Metabolism of xenobiotics by cytochrome P450 [00980]	0	1	0	*2	0	1	1	1	0	0	34
Naphthalene degradation [00626]	0	1	0	*2	0	*1	0	0	0	0	5
Styrene degradation [00643]	0	0	0	0	0	0	0	0	1	1	9
Toluene degradation [00623]	1	0	0	0	0	0	0	0	0	0	7

(b) Detailed view of metabolic pathway enrichment in each cluster

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Table S4. (continued)

Prediction	Clusters																									Poll.	Rest
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25		
7. Glycan biosynthesis and metabolism																											
Glycosaminoglycan degradation [00531]	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	2	27
Glycosphingolipid biosynthesis - ganglio series [00604]	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	2	26
N-Glycan biosynthesis [00510]	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	9
Other glycan degradation [00511]	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	4	38
8. Metabolism of cofactors and vitamins																											
Folate biosynthesis [00790]	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	15
Nicotinate and nicotinamide metabolism [00760]	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	2	12
One carbon pool by folate [00670]	0	0	0	0	0	0	2	0	0	0	0	0	0	*3	0	0	0	0	0	0	0	0	0	0	0	5	14
Pantothenate and CoA biosynthesis [00770]	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2	19
Porphyrin and chlorophyll metabolism [00860]	1	0	0	1	1	0	1	0	0	0	0	0	1	0	0	0	0	0	0	2	0	0	0	0	*2	9	21
Retinol metabolism [00830]	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	*2	0	3	17
Riboflavin metabolism [00740]	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	13
Thiamine metabolism [00730]	0	0	0	0	0	0	1	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	4	18
Ubiquinone and other terpenoid-quinone biosynth. [00130]	0	0	0	0	0	0	*5	1	0	0	*4	0	0	0	0	0	0	0	0	1	0	0	0	0	0	11	22
9. Metabolism of terpenoids and polyketides																											
Biosynthesis of vancomycin group antibiotics [01055]	0	0	0	0	0	0	0	0	0	0	0	0	0	1	*1	0	0	0	0	*1	0	0	0	0	0	*3	0
Carotenoid biosynthesis [00906]	0	*2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	11
Diterpenoid biosynthesis [00904]	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	*4	0	0	*4	1
Geraniol degradation [00281]	0	0	0	0	1	0	*2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	12
Insect hormone biosynthesis [00981]	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	7
Limonene and pinene degradation [00903]	0	0	0	0	0	0	*3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	10
Polyketide sugar unit biosynthesis [00523]	0	0	0	0	0	0	0	0	0	0	0	0	0	1	*1	0	0	0	0	*1	0	0	0	0	0	*3	0
Terpenoid backbone biosynthesis [00900]	0	0	0	0	0	0	0	*3	0	0	0	0	0	0	0	0	0	0	0	*2	0	0	0	0	0	5	9
10. Biosynthesis of other secondary metabolites																											
Acarbose and validamycin biosynthesis [00525]	0	0	0	0	0	0	0	0	0	0	0	0	0	1	*1	0	0	0	0	*1	0	0	0	0	0	*3	0
Anthocyanin biosynthesis [00942]	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	*2	0	0	0	0	0	2	2
Betalain biosynthesis [00965]	0	0	0	0	0	0	0	0	0	0	*2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1
Caffeine metabolism [00232]	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	10
Flavone and flavonol biosynthesis [00944]	0	0	0	0	0	0	0	0	0	0	*1	0	0	0	0	0	0	0	*2	0	0	0	0	0	0	3	4
Indole alkaloid biosynthesis [00901]	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	6
Isoquinoline alkaloid biosynthesis [00950]	0	0	0	0	0	0	1	1	0	0	1	0	0	0	0	0	0	0	0	*3	0	0	1	0	0	7	11
Monobactam biosynthesis [00261]	0	0	0	0	0	0	*2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2
Novobiocin biosynthesis [00401]	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	5
Penicillin and cephalosporin biosynthesis [00311]	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2	14
Phenylpropanoid biosynthesis [00940]	1	0	0	0	2	0	*6	0	1	0	0	0	3	1	0	0	0	0	1	0	0	0	1	0	0	16	46
Streptomycin biosynthesis [00521]	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0	0	0	3	9
Tropane, piperidine and pyridine alkaloid biosynth. [00960]	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	*1	0	0	*2	0	0	0	0	0	5	13
11. Xenobiotics biodegradation and metabolism																											
Aminobenzoate degradation [00627]	1	0	0	0	1	0	0	2	0	1	0	*4	0	1	1	0	0	0	0	0	1	0	0	0	0	12	21
Benzoate degradation [00362]	0	0	0	0	0	0	*2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	3	12
Caprolactam degradation [00930]	0	0	0	0	0	0	*2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	10
Chloroalkane and chloroalkene degradation [00625]	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	*1	0	0	0	0	0	0	*2	0	4	13
Chlorocyclohexane and chlorobenzene degradation [00361]	0	0	0	0	0	0	0	0	0	0	*5	0	0	0	0	0	0	0	0	1	0	0	0	0	0	*6	5
Drug metabolism - cytochrome P450 [00982]	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0	1	0	*2	0	8	32
Drug metabolism - other enzymes [00983]	0	1	0	0	1	0	1	1	0	0	0	0	3	0	0	0	0	0	*4	0	1	*2	0	0	0	14	41
Fluorobenzoate degradation [00364]	0	0	0	0	0	0	0	0	0	0	*1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2
Metabolism of xenobiotics by cytochrome P450 [00980]	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	2	0	1	0	*2	0	0	8	34
Naphthalene degradation [00626]	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	*2	0	2	5
Styrene degradation [00643]	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2	9
Toluene degradation [00623]	0	0	0	0	0	0	0	0	0	0	*1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	7