SUPPLEMENTARY MATERIAL

Fig. S1: see below
Table SI: *see below*
Table SII: see below

EXCEL file: 'supplement.XLS'
The file comprises 11 data sheets. Genes are listed according to the AGI codes.
Sheet 1 '301 genes': Statistical data for 301 genes showing transcript co-responses with the *BRI1* and *BAK1* genes. 44 genes subjected to RT-PCR analysis are highlighted.
Sheet 2 'Spearman rs', **sheet 3 'pvalue'**, and **sheet 4 'power'**: Bootstrap analysis results for 135 functionally classified genes. 44 genes subjected to RT-PCR analysis are highlighted.
Sheet 5 'complete Affx results': Expression analysis of 301 genes in expression profiles of BL-, EBL-, CS-, BRZ-, GA- and PAC-treated plants. Numbers give signal log ratios. Genes which were BR-induced / BR-repressed in at least two situations are highlighted in red / green. Genes subjected to RT-PCR analysis, and the *BRI1* and *BAK1* genes are in bold type. Detection p-values, signal log ratios, and change p-values were used to filter out significant changes in transcript levels (see text). Non-significant changes were left out in order to aid legibility.
Sheet 6 'Affx results BRs, BRZ': Expression analysis of 301 genes in expression profiles of BL- EBL-, CS-, and BRZ-treated.
Sheet 7 'Affx results GA3, PAC': Expression analysis of 301 genes in expression profiles of GA3- and PAC-treated plants.
Sheet 8 'nasc0271': Recovery of known BR-responsive genes in the nasc0271 database. BR-signalling genes, BR-biosynthesis genes, and known BR-responsive genes were used for transcript co-response analysis. Data were filtered for significant co-responses. Numbers give Spearman's correlation coefficients.
Sheet 9 'nasc0272': Recovery of known BR-responsive genes in the nasc0272 database.
Sheet 10 'nasc0273': Recovery of known BR-responsive genes in the nasc0273 database.
Sheet 11 'nasc profiles': Three data matrices were established using 123 expression profiles. The table specifies the experiments and profiles underlying the nasc0271, nasc0272, and nasc0273 matrices.
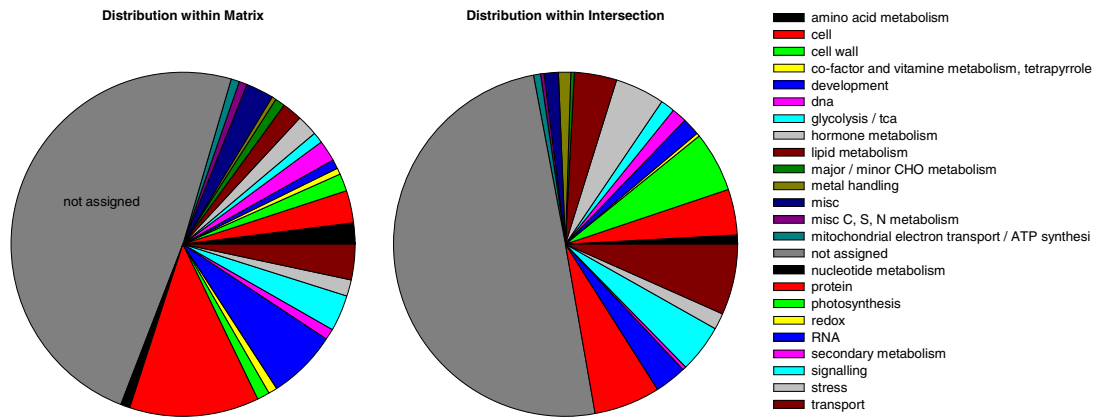
Distribution within Matrix

Distribution within Intersection

- ■ amino acid metabolism
- ■ cell
- ■ cell wall
- ■ co-factor and vitamine metabolism, tetrapyrrole
- ■ development
- ■ dna
- ■ glycolysis / tca
- ■ hormone metabolism
- ■ lipid metabolism
- ■ major / minor CHO metabolism
- ■ metal handling
- ■ misc
- ■ misc C, S, N metabolism
- ■ mitochondrial electron transport / ATP synthesi
- ■ not assigned
- ■ nucleotide metabolism
- ■ protein
- ■ photosynthesis
- ■ redox
- ■ RNA
- ■ secondary metabolism
- ■ signalling
- ■ stress
- ■ transport

Figure S1. Functional classification of 301 genes. Categories were deduced from the MapMan software (16) but slightly modified (Table SI).

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Table SI. Modified bins for functional classification of genes. Assignments into bins were taken from the MapMan software (16). Bins were merged as indicated within this table.

MapManBin	JointBin
fermentation	misc C, S, N metabolism
gluconeogenese/ glyoxylate cycle	misc C, S, N metabolism
biodegradation of xenobiotics	misc C, S, N metabolism
S-assimilation	misc C, S, N metabolism
polyamine metabolism	misc C, S, N metabolism
N-metabolism	misc C, S, N metabolism
C1-metabolism	misc C, S, N metabolism
OPP	misc C, S, N metabolism
control genes	control genes
tetrapyrrole synthesis	Co-factor and vitamine metabolism, tetrapyrrole synthesis
Co-factor and vitamine metabolism	Co-factor and vitamine metabolism, tetrapyrrole synthesis
glycolysis	glycolysis / TCA
TCA / org	glycolysis / TCA
minor CHO metabolism	major / minor CHO metabolism
major CHO metabolism	major / minor CHO metabolism
metal handling	metal handling
mitochondrial electron transport / ATP synthesis	mitochondrial electron transport / ATP synthesis
redox	redox
nucleotide metabolism	nucleotide metabolism
PS	PS
secondary metabolism	secondary metabolism
development	development
amino acid metabolism	amino acid metabolism
lipid metabolism	lipid metabolism
cell wall	cell wall
cell	cell
stress	stress
transport	transport
hormone metabolism	hormone metabolism
DNA	DNA
misc	misc
signalling	signalling
RNA	RNA
protein	protein
not assigned	not assigned

Table SII. RT-PCR analysis of 44 cell wall and growth-related genes in 12 situations used for the calculation of fold change values in Tables V and VI. C_T values were calculated from 3 technical replicates per experiment. C_T values of the *eIF1α* control gene were subtracted from C_T values of the genes of interest to account for different cDNA amounts. The resulting nC_T values were subtracted from an arbitrary value (i.e. 30). Numbers give the difference $(30 - nC_T)$ and the standard error (SE) of C_T values for each gene of interest. Higher numbers indicate stronger expression.

Gene		sterile culture			sterile culture			sterile culture			soil		
		WT	*cbb2*	*cbb3*	WT	WT control	WT BR	*dwf1-6*	*dwf1-6* control	*dwf1-6* BR	WT	*dwf1-6*	αCPD
		19d	19d	19d	14d	14d	14d	14d	14d	14d	28d	28d	28d
KCS1	At1g01120	8.8 ± 0.0	8.1 ± 0.0	7.5 ± 0.0	9.4 ± 0.0	9.0 ± 0.0	9.7 ± 0.0	8.5 ± 0.0	8.8 ± 0.0	9.4 ± 0.0	8.6 ± 0.0	6.7 ± 0.0	7.8 ± 0.0
PIP1.3	At1g01620	7.2 ± 0.0	6.6 ± 0.0	6.2 ± 0.0	8.3 ± 0.0	7.9 ± 0.0	7.8 ± 0.0	6.3 ± 0.1	6.5 ± 0.0	7.2 ± 0.0	7.3 ± 0.0	7.5 ± 0.0	7.8 ± 0.0
FLA9	At1g03870	6.1 ± 0.0	6.0 ± 0.0	6.5 ± 0.0	6.2 ± 0.0	5.9 ± 0.1	6.6 ± 0.1	5.5 ± 0.0	5.9 ± 0.0	6.5 ± 0.1	6.3 ± 0.0	6.1 ± 0.1	6.3 ± 0.0
	At1g27600	7.0 ± 0.0	7.2 ± 0.0	6.3 ± 0.0	6.3 ± 0.0	6.3 ± 0.0	7.6 ± 0.0	5.2 ± 0.0	5.4 ± 0.0	5.9 ± 0.0	6.2 ± 0.0	5.7 ± 0.0	5.1 ± 0.0
	At1g31310	3.2 ± 0.0	4.3 ± 0.0	4.0 ± 0.0	3.5 ± 0.0	3.7 ± 0.1	4.7 ± 0.0	3.7 ± 0.0	3.5 ± 0.1	3.7 ± 0.0	3.8 ± 0.1	4.7 ± 0.0	3.7 ± 0.0
AGP21	At1g55330	10.3 ± 0.0	8.3 ± 0.0	8.1 ± 0.0	11.0 ± 0.0	11.1 ± 0.0	11.2 ± 0.0	9.8 ± 0.0	10.2 ± 0.1	11.0 ± 0.0	10.5 ± 0.0	10.2 ± 0.0	9.2 ± 0.0
CYCD1.1	At1g70210	4.5 ± 0.1	4.9 ± 0.1	4.2 ± 0.0	4.8 ± 0.0	4.9 ± 0.0	3.5 ± 0.0	3.4 ± 0.0	3.2 ± 0.0	2.8 ± 0.0	4.4 ± 0.0	4.5 ± 0.0	4.4 ± 0.0
EXT	At2g06850	6.8 ± 0.0	6.4 ± 0.0	5.7 ± 0.0	8.4 ± 0.0	8.1 ± 0.0	8.3 ± 0.0	7.0 ± 0.0	7.4 ± 0.0	7.7 ± 0.0	7.6 ± 0.0	7.6 ± 0.0	8.0 ± 0.0
AGP9	At2g14890	10.2 ± 0.1	9.2 ± 0.0	9.4 ± 0.0	11.3 ± 0.4	10.8 ± 0.0	10.4 ± 0.0	10.4 ± 0.0	10.1 ± 0.0	10.1 ± 0.0	10.4 ± 0.0	10.2 ± 0.0	9.3 ± 0.0
PIP2.8	At2g16850	5.7 ± 0.0	4.3 ± 0.0	3.6 ± 0.0	5.6 ± 0.0	5.8 ± 0.1	5.4 ± 0.1	3.6 ± 0.2	4.3 ± 0.1	5.0 ± 0.0	5.4 ± 0.0	5.8 ± 0.0	5.1 ± 0.0
GRL1	At2g22840	5.9 ± 0.0	5.7 ± 0.2	5.1 ± 0.1	5.2 ± 0.0	5.3 ± 0.0	4.2 ± 0.0	4.9 ± 0.0	4.7 ± 0.0	4.0 ± 0.0	5.6 ± 0.1	6.5 ± 0.0	6.6 ± 0.1
GRL3	At2g36400	5.0 ± 0.0	5.0 ± 0.0	4.6 ± 0.0	5.9 ± 0.0	6.0 ± 0.1	5.1 ± 0.0	5.5 ± 0.0	5.7 ± 0.0	4.9 ± 0.0	5.0 ± 0.0	6.3 ± 0.1	6.2 ± 0.0
TIP1.1	At2g36830	7.5 ± 0.0	6.7 ± 0.0	7.2 ± 0.1	7.7 ± 0.0	7.9 ± 0.0	7.3 ± 0.0	7.2 ± 0.1	7.1 ± 0.0	7.5 ± 0.0	8.0 ± 0.0	8.5 ± 0.0	7.7 ± 0.0
PIP1.2	At2g45960	9.5 ± 0.0	8.6 ± 0.1	8.6 ± 0.0	9.2 ± 0.0	9.2 ± 0.1	8.6 ± 0.0	8.2 ± 0.1	8.3 ± 0.0	8.3 ± 0.0	9.7 ± 0.1	9.0 ± 0.0	9.6 ± 0.0
	At3g05910	8.4 ± 0.0	8.1 ± 0.0	7.7 ± 0.0	8.8 ± 0.0	8.9 ± 0.1	8.9 ± 0.0	8.5 ± 0.0	8.2 ± 0.1	8.9 ± 0.0	8.8 ± 0.0	7.9 ± 0.0	8.2 ± 0.1
TIP2.1	At3g16240	7.9 ± 0.0	7.2 ± 0.0	6.6 ± 0.0	9.5 ± 0.0	9.1 ± 0.1	8.9 ± 0.1	7.9 ± 0.1	8.1 ± 0.3	8.5 ± 0.0	9.4 ± 0.0	9.8 ± 0.0	9.4 ± 0.0
	At3g24480	9.8 ± 0.0	9.0 ± 0.1	9.0 ± 0.0	9.5 ± 0.0	9.5 ± 0.1	11.0 ± 0.0	9.0 ± 0.0	9.1 ± 0.0	10.0 ± 0.1	9.2 ± 0.0	8.4 ± 0.0	8.8 ± 0.4
TIP1.2	At3g26520	10.9 ± 0.0	9.8 ± 0.2	10.1 ± 0.1	11.9 ± 0.0	12.3 ± 0.0	11.7 ± 0.0	11.2 ± 0.0	11.5 ± 0.0	11.2 ± 0.0	11.5 ± 0.0	11.0 ± 0.0	10.7 ± 0.0

Gene	Locus												
CSLC4	At3g28180	3.5 ± 0.0	3.8 ± 0.1	2.5 ± 0.0	3.8 ± 0.1	4.4 ± 0.0	5.0 ± 0.0	3.3 ± 0.1	2.9 ± 0.0	4.6 ± 0.1	5.2 ± 0.0	5.5 ± 0.0	5.1 ± 0.0
PIP2.1	At3g53420	7.7 ± 0.0	7.1 ± 0.0	6.7 ± 0.0	8.6 ± 0.0	8.3 ± 0.0	7.7 ± 0.0	7.1 ± 0.0	7.7 ± 0.0	6.8 ± 0.0	8.9 ± 0.1	8.1 ± 0.0	8.9 ± 0.0
	At3g57790	7.3 ± 0.0	6.7 ± 0.0	6.6 ± 0.0	7.1 ± 0.2	7.5 ± 0.3	8.6 ± 0.0	6.7 ± 0.2	4.4 ± 0.0	6.5 ± 0.1	7.9 ± 0.0	6.4 ± 0.0	7.0 ± 0.0
PIP1.1	At3g61430	9.6 ± 0.0	9.0 ± 0.0	8.8 ± 0.0	9.6 ± 0.0	9.4 ± 0.0	9.2 ± 0.0	8.1 ± 0.0	8.4 ± 0.0	8.4 ± 0.1	9.7 ± 0.0	9.0 ± 0.1	9.5 ± 0.0
	At4g02500	7.9 ± 0.0	8.0 ± 0.0	7.7 ± 0.2	7.9 ± 0.0	8.0 ± 0.0	7.7 ± 0.0	7.8 ± 0.0	8.3 ± 0.0	8.4 ± 0.0	8.5 ± 0.0	8.2 ± 0.1	8.7 ± 0.0
SKU5	At4g12420	9.7 ± 0.0	9.2 ± 0.0	8.5 ± 0.0	10.4 ± 0.0	10.3 ± 0.0	10.5 ± 0.0	9.9 ± 0.0	10.3 ± 0.0	10.4 ± 0.0	9.3 ± 0.0	9.6 ± 0.1	9.4 ± 0.0
FLA2	At4g12730	10.2 ± 0.0	8.8 ± 0.0	8.7 ± 0.0	10.7 ± 0.0	10.2 ± 0.0	10.4 ± 0.0	10.1 ± 0.0	10.6 ± 0.0	10.6 ± 0.0	10.0 ± 0.0	9.6 ± 0.0	9.2 ± 0.1
	At4g13340	6.0 ± 0.1	5.8 ± 0.0	4.2 ± 0.2	7.0 ± 0.0	7.0 ± 0.0	7.9 ± 0.0	6.2 ± 0.1	6.6 ± 0.1	7.7 ± 0.0	7.0 ± 0.0	7.4 ± 0.0	6.1 ± 0.0
	At4g14130	6.0 ± 0.0	7.5 ± 0.0	5.9 ± 0.0	6.3 ± 0.1	5.9 ± 0.0	8.1 ± 0.0	7.9 ± 0.0	8.9 ± 0.0	6.9 ± 0.0	5.2 ± 0.0	9.0 ± 0.0	6.0 ± 0.0
	At4g18670	4.1 ± 0.0	3.4 ± 0.0	2.8 ± 0.2	3.2 ± 0.0	3.6 ± 0.0	3.2 ± 0.0	3.0 ± 0.1	3.0 ± 0.0	3.0 ± 0.0	3.4 ± 0.0	3.5 ± 0.0	3.2 ± 0.0
	At4g19410	8.5 ± 0.0	8.7 ± 0.3	8.3 ± 0.0	7.7 ± 0.1	7.9 ± 0.1	9.5 ± 0.0	7.4 ± 0.1	7.7 ± 0.0	7.8 ± 0.0	9.4 ± 0.0	9.3 ± 0.0	8.6 ± 0.0
PIP1.5	At4g23400	8.9 ± 0.0	8.1 ± 0.0	8.3 ± 0.0	9.8 ± 0.0	9.5 ± 0.1	8.9 ± 0.0	8.8 ± 0.0	9.1 ± 0.0	8.1 ± 0.0	9.1 ± 0.0	9.7 ± 0.0	9.5 ± 0.0
	At4g25260	7.1 ± 0.0	6.1 ± 0.0	5.9 ± 0.2	8.0 ± 0.0	7.6 ± 0.0	7.1 ± 0.1	7.6 ± 0.0	7.2 ± 0.4	7.0 ± 0.1	7.0 ± 0.0	6.1 ± 0.1	7.1 ± 0.0
	At4g25620	7.3 ± 0.0	7.8 ± 0.0	7.2 ± 0.0	7.8 ± 0.0	7.9 ± 0.0	8.1 ± 0.1	7.7 ± 0.0	7.9 ± 0.0	7.6 ± 0.0	7.3 ± 0.0	8.2 ± 0.1	8.1 ± 0.0
CSLC5	At4g31590	7.0 ± 0.0	7.0 ± 0.1	6.4 ± 0.0	5.8 ± 0.0	6.3 ± 0.0	5.2 ± 0.0	5.6 ± 0.0	5.4 ± 0.0	4.9 ± 0.4	6.1 ± 0.0	5.5 ± 0.0	6.1 ± 0.1
	At5g01210	6.7 ± 0.0	6.4 ± 0.1	6.7 ± 0.0	8.6 ± 0.0	7.9 ± 0.0	8.1 ± 0.0	8.6 ± 0.0	9.0 ± 0.0	8.4 ± 0.1	7.5 ± 0.0	7.4 ± 0.1	7.7 ± 0.0
CESA3	At5g05170	10.1 ± 0.2	10.1 ± 0.1	9.7 ± 0.1	10.3 ± 0.0	10.2 ± 0.0	10.2 ± 0.0	9.8 ± 0.0	10.1 ± 0.0	10.1 ± 0.0	9.4 ± 0.0	9.1 ± 0.0	9.2 ± 0.0
	At5g07830	6.6 ± 0.1	6.6 ± 0.0	6.3 ± 0.0	6.1 ± 0.1	6.1 ± 0.0	6.1 ± 0.0	6.4 ± 0.1	6.1 ± 0.0	6.7 ± 0.0	7.5 ± 0.0	6.5 ± 0.1	7.0 ± 0.1
TUB6	At5g12250	9.3 ± 0.0	8.9 ± 0.0	8.7 ± 0.0	9.1 ± 0.0	9.4 ± 0.0	9.1 ± 0.0	8.7 ± 0.1	8.8 ± 0.0	8.9 ± 0.0	9.5 ± 0.0	8.8 ± 0.0	8.5 ± 0.1
TUA3	At5g19770	7.3 ± 0.0	7.0 ± 0.0	7.1 ± 0.0	7.0 ± 0.1	7.6 ± 0.1	7.0 ± 0.0	6.8 ± 0.0	7.2 ± 0.0	7.3 ± 0.0	8.0 ± 0.0	7.3 ± 0.0	7.1 ± 0.0
DIN10	At5g20250	7.2 ± 0.1	6.7 ± 0.0	6.0 ± 0.0	9.2 ± 0.1	8.3 ± 0.0	9.5 ± 0.1	8.4 ± 0.0	9.3 ± 0.0	9.8 ± 0.0	7.6 ± 0.0	9.2 ± 0.0	7.1 ± 0.1
	At5g26665	5.8 ± 0.0	6.1 ± 0.0	5.4 ± 0.1	5.3 ± 0.0	5.3 ± 0.0	5.0 ± 0.0	5.4 ± 0.1	4.6 ± 0.0	4.3 ± 0.0	5.8 ± 0.0	5.5 ± 0.0	5.5 ± 0.1
	At5g43760	7.2 ± 0.0	6.4 ± 0.0	6.3 ± 0.0	7.4 ± 0.0	7.4 ± 0.1	7.3 ± 0.0	6.5 ± 0.0	7.0 ± 0.0	7.1 ± 0.0	6.7 ± 0.0	7.2 ± 0.0	7.3 ± 0.1
FLA1	At5g55730	7.2 ± 0.0	6.9 ± 0.0	7.2 ± 0.0	7.2 ± 0.0	6.8 ± 0.0	6.9 ± 0.0	7.2 ± 0.0	7.2 ± 0.0	6.5 ± 0.0	7.4 ± 0.0	7.0 ± 0.1	6.6 ± 0.0
CESA6	At5g64740	8.6 ± 0.0	8.5 ± 0.1	7.7 ± 0.0	8.1 ± 0.0	8.4 ± 0.0	8.4 ± 0.0	7.9 ± 0.1	7.8 ± 0.0	8.1 ± 0.0	8.8 ± 0.0	8.5 ± 0.0	9.3 ± 0.0
CYCD3.2	At5g67260	7.1 ± 0.0	7.0 ± 0.0	6.9 ± 0.1	6.8 ± 0.0	7.0 ± 0.0	5.7 ± 0.0	6.1 ± 0.0	6.1 ± 0.0	5.4 ± 0.0	6.5 ± 0.0	7.0 ± 0.0	6.6 ± 0.0