**Supplementary materials and methods**

**Plant material, growth conditions and histological analyses**

*Arabidopsis thaliana* ecotype Columbia-0 (Col-0) was the wild-type for the generation of all plant material described in this study. General plant handling and transformation protocols as well as β-glucuronidase (GUS) staining followed standard procedures (Weigel and Glazebrook, 2001). The *ces-1* line was identified in the SIGnAL database (SALK Institute) and corresponds to line SALK_082100. This line segregated kanamycin resistance 3:1 and was defined by the absence of CES transcript.

For hypocotyl elongation assays mother plants were cultivated in a controlled environment of 16 hr/8 hr light/dark cycle (100 μmol m⁻² s⁻¹ white light) at a temperature of 21°C/17°C (±1). Seeds of all lines used in one experiment were harvested at the same time and plated on ATS medium (Lincoln et al., 1990). Hypocotyl elongation assays were performed as described previously (Poppenberger et al., 2005). For hypocotyl growth response assays 24-epiBL (OlChemIm Ltd, Olomouc, Czech Republic) and Brz2001 (Sekimata et al., 2001) were dissolved in DMSO and added to ATS medium in the required concentrations. Seeds were incubated on vertical plates either in the dark (following a 4 hr light impulse) or in the light and hypocotyl elongation was measured at different time-points. For each experiment the 20 tallest seedlings originating from 40 seeds (to correct for late germination) were analyzed in 3 replicates and the standard error (SE) was calculated.

For quantitative PCR analysis 10-day-old seedlings were grown vertically on ATS plates and transferred to flasks containing liquid ATS medium and incubated for 48 hr on an orbital shaker at 20 rpm. 24-epiBL and Brz2001 were then added to the flasks in the indicated concentrations and after incubation seedlings were ground in liquid nitrogen.
**Western blotting**

For Western blot analysis 100 mg of plant material was ground to a fine powder and extracted with 300 μl loading buffer (66 mM TRIS/HCl pH=6.8, 133 mM DTT, 2.7% SDS, 13% glycerol and 0.01% bromophenol blue). 20 μl of this extract were separated by SDS-PAGE (10% gel) and blotted onto Immobilon P (Millipore Cooperation, Bedford, MA, USA). Membranes were probed with a rabbit anti-c-Myc antibody. Alkaline phosphatase-conjugated goat anti-rabbit IgG (Santa Cruz Biotechnology, CA) was used as secondary antibody and detected by enhanced chemiluminescence using CDP-Star reagent (Amersham Biosciences).

**Protein interaction assays and kinase assays**

For yeast two-hybrid assays, CES, BEE1 and BEE3 were PCR amplified from Col-0 cDNA using specific primers and cloned into GAL4 bait (pGADT7) and prey (pGBK7) vectors, respectively (Clontech). The sequenced constructs were introduced into the yeast two-hybrid strain PJ69-4A (James *et al.*, 1996) and β-galactosidase activity was assayed.

Kinase assays were performed as described previously (Rozhon *et al.*, 2010).

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Supplementary figure legends

Figure S1 Analysis of CES-YFP subcellular localization in *Arabidopsis* plants stably transformed with 35Spro:CES-YFP. CES-YFP localizes diffusely to the nucleus in 14-day-old seedlings of 35Spro:CES-YFP. Nuclear compartmentalization was induced by application of 1 μM 24-epiBL for 2 h to plants pre-treated with 2.5 μM Brz2001 for 24 h. Application of Brz2001 on its own did not induce nuclear body formation.

Figure S2 Analysis of BEE1-YFP and BEE3-YFP subcellular localization and interactions of CES with BEE1 and BEE3 in yeast two-hybrid assays. (A) 35Spro:BEE1-YFP reporter expression in *Arabidopsis* protoplasts treated with 24-epiBL (1 μM) 2 hr as compared to untreated controls. (B) 35Spro:BEE3-YFP reporter expression in *Arabidopsis* protoplasts treated with 24-epiBL (1 μM) for 2 hr as compared to untreated controls. (C) Images of a representative 35Spro:CES-CFP and 35Spro:BEE3-YFP co-expressing protoplast after 2 hr of 24-epiBL treatment. (D) Quantitative yeast two-hybrid analysis of ß-galactosidase activity in cells transformed with combinations of CES and BEE1, BEE3 resp. as compared to control strains. Data points represent the average of three replicates. The standard deviation is shown.
BR-induced genes significantly up-regulated in ces-D and their expression in 35Sp:cMyc-CES-SRDX plants.

| Public ID | ces-D/Col-0 | SRDX/Col-0 | Gene symbol | Description |
|-----------|-------------|-------------|-------------|-------------|
| At4g25810 | 1.3         | 2.42        | XTR6       | Xyloglucan-xyloglucosyl transferase |
| At4g16563 | 3.8         | 2.34        | PH1        | Phosphate-induced 1 |
| At1g35140 | 3           | 1.84        | LRX2       | Extensin; structural constituent of cell wall |
| At3g45970 | 3           | 1.16        | D2N2       | Dark-induced 2 |
| At1g62440 | 1.1         | 1.13        | SLAH3      | SLAC1 homologue 3 |
| At3g60140 | 2.3         | 0.22        | AIEXLA1    | Expansin-like |
| At5g24030 | 3           | 1.55        | SLAH3      | SLAC1 homologue 3 |
| At1g10550 | 1.3         | 1.82        | XTH33      | Xyloglucan-xyloglucosyl transferase |
| At3g35290 | 3           | 0.94        | --         | -- |
| At2g19800 | 1.2         | 3.30        | MIOX2      | Myo-inositol oxygenase 2 |
| At4g38400 | 1.2         | 1.17        | AIEXLA2    | Expansin-like |
| At5g57550 | 2           | 2.84        | XTR3       | Xyloglucan-xyloglucosyl transferase |
| At3g93530 | 3           | 1.39        | --         | -- |
| At1g77640 | 3           | 0.86        | --         | -- |
| At2g27920 | 2.3         | 0.73        | SCPL51     | Serine carboxypeptidase |
| At3g46480 | 3           | 0.80        | --         | -- |
| At2g34510 | 2.9         | 1.46        | --         | Anchored to membrane |
| At5g08950 | 1.2         | 2.54        | --         | -- |
| At2g47440 | 1.2         | 0.89        | --         | Heat shock protein folding |
| At2g42580 | 3           | 1.41        | TTL3       | Leaf vascular tissue pattern formation |
| At5g43800 | 3           | 1.18        | THE1       | Regulation of cell growth |
| At3g06070 | 3           | 0.46        | --         | -- |
| At3g41080 | 3           | 1.66        | --         | -- |
| At5g13220 | 3           | 1.83        | AHS1       | Jasmonate-associated 1 |
| At1g23030 | 1.3         | 1.04        | Ubiquitin-protein ligase activity |
| At5g57650 | 1.3         | 0.71        | TCH4       | Xyloglucan-xyloglucosyl transferase |
| At5g06720 | 1.2         | 1.59        | --         | Hydrogen peroxide catalytic process |
| At2g16060 | 4           | 1.64        | AHB1       | Oxygen transporter activity |
| At3g47340 | 4           | 1.68        | ASN1       | Dark-induced; amino acid biosynthesis |
| At2g33570 | 3           | 1.11        | --         | -- |
| At3g62720 | 3           | 1.28        | ATXT1      | Xylosyltransferase 1 |
| At1g11260 | 2.3         | 1.32        | --         | -- |
| At4g35320 | 2.3         | 0.75        | --         | -- |
| At2g14900 | 2.3         | 1.09        | Endomembrane system |
| At3g54030 | 3           | 3.15        | --         | -- |
| At1g66160 | 3           | 1.20        | --         | -- |
| At4g39830 | 2.3         | 0.88        | --         | -- |
| At2g32150 | 2.3         | 0.88        | Hydrolyase activity |
| At3g05060 | 2.3         | 0.88        | --         | -- |
| At1g44350 | 3           | 1.44        | IIA-Leucine resistant (IRL)-like gene 6 |
| At5g39580 | 3           | 2.66        | Hydrogen peroxide catalytic process |
| At5g06870 | 3           | 1.01        | PGIP2      | Polygalacturonase inhibiting protein 2 |
| At3g05900 | 3           | 1.26        | TTL4       | Tetratricopeptide-repeat thioredoxin-like 4 |
| At2g28400 | 2.3         | 0.94        | --         | -- |
| At4g31800 | 3           | 3.63        | --         | -- |
| At4g22560 | 2.3         | 1.02        | --         | -- |
| At3g06770 | 3           | 0.79        | --         | -- |
| At3g30775 | 4           | 2.70        | ERD5       | Early responsive to dehydration 5 |
| At2g34300 | 2.9         | 1.25        | --         | -- |
| At5g58670 | 2.3         | 0.74        | ATPLC1     | Phospholipase C, lipid metabolic process |
| At4g31000 | 3           | 1.94        | --         | -- |
| At5g03120 | 2.3         | 1.00        | --         | -- |
| At2g34930 | 1.2         | 3.63        | --         | -- |
| At5g01040 | 2.0         | 1.26        | LAC8       | Laccase 8 |
| At1g76900 | 2.0         | 1.16        | --         | -- |
| At1g08370 | 2.0         | 1.34        | FLA9       | Fasciclin-like arabinogalactan-protein 9 |

*a* Ratio of the microarray intensity of the ces-D mutant and Col-0 controls.

*b* Student's t-Test p-value.

*c* FDR q-value.

A ratio of the microarray intensity of the dominant-negative over-expressor line CES-SRDX #203 and Col-0 controls.

References: 1, Goda et al. 2002; 2, Goda et al. 2004; 3, He et al., 2005; 4, Müssig et al., 2002
**Supplementary Table 4**

Genes involved in the regulation of transcription (GO 0006355) significantly up-regulated in cesD.

| Public ID | cesD/Col-0 Ratio<sup>a</sup> | p-value<sup>b</sup> | q-value<sup>c</sup> | CES-SRDX/Col-0 Ratio<sup>a</sup> | p-value<sup>b</sup> | q-value<sup>c</sup> | Gene symbol | Description |
|-----------|-------------------------------|---------------------|---------------------|-------------------------------|---------------------|---------------------|-------------|-------------|
| At1g65330 | 26.51                         | 0.0000              | 0.0028              | 0.91                          | 0.9087              | 0.5854              | PHE2        | Agamous-like transcription factor |
| At1g18710 | 18.91                         | 0.0087              | 0.0390              | 1.15                          | 0.8588              | 0.5721              | AtMYB47     | Myb-type transcription factor, responsive to IAA |
| At2g44010 | 14.61                         | 0.0091              | 0.0400              | 1.67                          | 0.2417              | 0.3046              | ---         | Transcription factor activity, shade avoidance |
| At3g15170 | 13.57                         | 0.0198              | 0.0603              | 0.69                          | 0.6267              | 0.4925              | CUC1        | Shoot apical meristem formation |
| At2g28700 | 9.95                          | 0.0157              | 0.0529              | 2.15                          | 0.4733              | 0.4284              | AGL46       | Agamous-like, transcription factor activity |
| At5g53980 | 6.85                          | 0.0028              | 0.0223              | 0.69                          | 0.4032              | 0.3963              | ATHB52      | Homeodomain leucine zipper class I |
| At2g34600 | 5.58                          | 0.0031              | 0.0236              | 2.43                          | 0.0458              | 0.1294              | JAZ7        | Response to JA and chitin |
| At3g54340 | 5.00                          | 0.0144              | 0.0504              | 9.35                          | 0.0015              | 0.0261              | AP3         | Floral homoeotic gene |
| At1g22130 | 3.28                          | 0.0345              | 0.0835              | 1.09                          | 0.9219              | 0.5891              | AGL104      | Agamous-like; pollen development, tube growth |
| At1g77640 | 3.12                          | 0.0008              | 0.0126              | 0.86                          | 0.3818              | 0.3859              | ---         | Contains a AP2 domain |
| At1g01250 | 2.77                          | 0.0265              | 0.0719              | 3.90                          | 0.0008              | 0.0209              | ---         | Putative transcription factor of unknown function |
| At4g28190 | 2.75                          | 0.0009              | 0.0129              | 1.11                          | 0.3676              | 0.3784              | ULT1        | Regulation of inflorescence meristem growth |
| At5g50570 | 2.75                          | 0.0000              | 0.0040              | 0.91                          | 0.3766              | 0.3832              | ---         | Putative SBP-box binding transcription factor |
| At1g44830 | 2.70                          | 0.0001              | 0.0061              | 1.74                          | 0.0671              | 0.1564              | ---         | ERF/AP2 transcription factor family |
| At3g58120 | 2.62                          | 0.0004              | 0.0088              | 0.91                          | 0.3981              | 0.3939              | ---         | BZIP family transcription factors |
| At5g13220 | 2.50                          | 0.0017              | 0.0179              | 1.83                          | 0.0169              | 0.0786              | JAS1        | Overexpression enhances insensitivity to MeJA |
| At4g37850 | 2.50                          | 0.0039              | 0.0265              | 1.54                          | 0.3549              | 0.3718              | ---         | Basic helix-loop-helix (bHLH) family protein |
| At1g21910 | 2.45                          | 0.0016              | 0.0173              | 1.25                          | 0.0819              | 0.1733              | ---         | ERF/AP2 transcription factor |
| At3g16770 | 2.34                          | 0.0001              | 0.0059              | 1.04                          | 0.5265              | 0.4523              | ATEBP       | Suppressor of Bax-induced cell death |
| At4g36730 | 2.28                          | 0.0004              | 0.0091              | 1.29                          | 0.0670              | 0.1563              | GFB1        | bZIP transcription factor, G-box binding |
| At2g30590 | 2.25                          | 0.0004              | 0.0088              | 1.48                          | 0.0131              | 0.0702              | WRKY21      | WRKY DNA-binding protein, unknown function |
| At2g14210 | 2.20                          | 0.0042              | 0.0272              | 0.90                          | 0.8068              | 0.5726              | ANR1        | Agamous-like, response to nutrient |
| At2g42380 | 2.15                          | 0.0255              | 0.0702              | 0.13                          | 0.0090              | 0.0072              | ---         | Heterodimerizes with AtZIP61, binds G-boxes |
| At5g60850 | 2.14                          | 0.0028              | 0.0225              | 0.52                          | 0.0001              | 0.0116              | OBP4        | Zinc finger protein |
| At4g31800 | 2.13                          | 0.0006              | 0.0107              | 3.63                          | 0.0001              | 0.0101              | WRKY18      | Pathogen-induced transcription factor |
| At5g10140 | 2.08                          | 0.0006              | 0.0107              | 2.25                          | 0.0000              | 0.0082              | FLC         | Agamous-like; negative regulation of flower development |

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<sup>a</sup> Ratio of the microarray intensity of the cesD mutant and Col-0 controls.

<sup>b</sup> t-Test p-value.

<sup>c</sup> FDR q-value.

<sup>d</sup> Ratio of the microarray intensity of the dominat-negative over-expressor line CES-SRDX #203 and Col-0 controls.
**Supplementary Table 5**

Sequences of primers used in this study.

| Name                      | Sequence                                           |
|---------------------------|----------------------------------------------------|
| Primers used for cloning and sequencing |                                                    |
| CEspGBK7-T-fw             | 5' AAGCATATGATGGACGGGTGGACGACGTCATTGAAATGCATCCATAG 3' |
| CEspGBK7-rv               | 5' TGGCGAATCCTCAGAAGGAGTGAAGGTGAATGAGTGAAGATGAACTG 3' |
| CEspGBK7-T-rw             | 5' GTACCTGGAAGGATGGACGTAATGAGTGAAGGTGAATGAGTGAAGATGAACTG 3' |
| CEspGBK7-fw               | 5' TGCGAATCCTCAGAAGGAGTGAAGGTGAATGAGTGAAGATGAACTG 3' |
| BEE1pGBK7-T-fw            | 5' TCTGAATGCATTCATATGCAATGTCATGCAGGAGGAATTGAGTGAAGATGAACTG 3' |
| BEE1pGBK7-rv              | 5' GAGGACCGAAGGAGTGAAGGTGAATGAGTGAAGATGAACTG 3' |
| BEE1pGBK7-T-rw            | 5' TCTGAATGCATTCATATGCAATGTCATGCAGGAGGAATTGAGTGAAGATGAACTG 3' |
| BEE3pGBK7-fw              | 5' CACATGCGGAGATCTCTCTCTCGA 3' |
| BEE3pGBK7-rv              | 5' CAAGAATCGAAGGAGTGAAGGTGAATGAGTGAAGATGAACTG 3' |
| CESSfusions-fw-c          | 5' CTACGAAATCGGCAAGGATGTGAATGAGTGAAGATGAACTG 3' |
| CEStranscGUS-rv-a         | 5' CTGCGAATCCTCAGAAGGAGTGAAGGTGAATGAGTGAAGATGAACTG 3' |
| pGWR8-8-BEE1-1            | 5' GATACCGAAGGAGTGAAGGTGAATGAGTGAAGATGAACTG 3' |
| pGWR8-8-SEE1-2            | 5' GCCCGCCCTAAGGAGGATGTGAATGAGTGAAGATGAACTG 3' |
| pGWR8-8-SEE1-3            | 5' ACCATGCGAAGGAGTGAATGAGTGAAGATGAACTG 3' |
| pGWR8-8-SEE1-2            | 5' GCCCGCCCTAAGGAGGATGTGAATGAGTGAAGATGAACTG 3' |
| pGWR8-8-SES-1             | 5' ACCATGCGAAGGAGTGAATGAGTGAAGATGAACTG 3' |
| PGWKR-8-SES-2             | 5' GAGGAGGAGGAGTGAAGGTGAATGAGTGAAGATGAACTG 3' |
| SOER2                     | 5' GCGGATGCAGACGTTACATGCCAGATGATATGAGATGAACTG 3' |
| SOEL2                     | 5' TGATGCGATATCAGCTGCAGGCAACACTTATAC 3' |

| Primers used for RT-semi quantitative PCR |                                                    |
| Atlg25320RT-fw            | 5' GTATACCGCCTTCCGAGGATGTGAATGAGTGAAGATGAACTG 3' |
| Atlg25320RT-rv            | 5' GATATGCGATTCCGAGGATGTGAATGAGTGAAGATGAACTG 3' |
| Atlg25340RT-T-fw          | 5' GATATGCGATTCCGAGGATGTGAATGAGTGAAGATGAACTG 3' |
| Atlg25340RT-rv            | 5' GATATGCGATTCCGAGGATGTGAATGAGTGAAGATGAACTG 3' |
| CERSRT-fw                 | 5' CTGCGAATCCTCAGGCAAGGATGTGAATGAGTGAAGATGAACTG 3' |
| CERSRT-rv                 | 5' CTGCGAATCCTCAGGCAAGGATGTGAATGAGTGAAGATGAACTG 3' |
| CPDRT-fw                  | 5' TCGTGAATCCTCAGGCAAGGATGTGAATGAGTGAAGATGAACTG 3' |
| CPDRT-rv                  | 5' TCGTGAATCCTCAGGCAAGGATGTGAATGAGTGAAGATGAACTG 3' |
| DWF4RT-fw                 | 5' TCGTGAATCCTCAGGCAAGGATGTGAATGAGTGAAGATGAACTG 3' |
| DWF4RT-rv                 | 5' TCGTGAATCCTCAGGCAAGGATGTGAATGAGTGAAGATGAACTG 3' |
| ROT3-fw                   | 5' TCGTGAATCCTCAGGCAAGGATGTGAATGAGTGAAGATGAACTG 3' |
| ROT3-rv                   | 5' TCGTGAATCCTCAGGCAAGGATGTGAATGAGTGAAGATGAACTG 3' |
| UBQ5-fw                   | 5' TCGTGAATCCTCAGGCAAGGATGTGAATGAGTGAAGATGAACTG 3' |
| UBQ5-rv                   | 5' TCGTGAATCCTCAGGCAAGGATGTGAATGAGTGAAGATGAACTG 3' |

| Primers used for RT-qPCR |                                                    |
|--------------------------|---------------------------------------------------|
| CPD-1                     | 5' CTTACGCGGAGGATGTGAATGAGTGAAGATGAACTG 3' |
| CPD-2                     | 5' TCGTGAATCCTCAGGCAAGGATGTGAATGAGTGAAGATGAACTG 3' |
| DWF4RT-3                  | 5' TCGTGAATCCTCAGGCAAGGATGTGAATGAGTGAAGATGAACTG 3' |
| DWF4RT-4                  | 5' TCGTGAATCCTCAGGCAAGGATGTGAATGAGTGAAGATGAACTG 3' |
| ROT3-3                    | 5' TCGTGAATCCTCAGGCAAGGATGTGAATGAGTGAAGATGAACTG 3' |
| ROT3-4                    | 5' TCGTGAATCCTCAGGCAAGGATGTGAATGAGTGAAGATGAACTG 3' |
| UBQ5-1                    | 5' TCGTGAATCCTCAGGCAAGGATGTGAATGAGTGAAGATGAACTG 3' |
| UBQ5-2                    | 5' TCGTGAATCCTCAGGCAAGGATGTGAATGAGTGAAGATGAACTG 3' |

| Primers used for ChIP-semi quantitative PCR |                                                    |
|-----------------------------|---------------------------------------------------|
| CPD-ChIP-1                   | 5' TTATCGCGGAGCAGGTAATGCGGATGGTGAATGAGTGAAGATGAACTG 3' |
| CPD-ChIP-2                   | 5' TTATCGCGGAGCAGGTAATGCGGATGGTGAATGAGTGAAGATGAACTG 3' |
| CPD-ChIP-3                   | 5' TTATCGCGGAGCAGGTAATGCGGATGGTGAATGAGTGAAGATGAACTG 3' |
| CPD-ChIP-4                   | 5' TTATCGCGGAGCAGGTAATGCGGATGGTGAATGAGTGAAGATGAACTG 3' |
| CPD-ChIP-5                   | 5' TTATCGCGGAGCAGGTAATGCGGATGGTGAATGAGTGAAGATGAACTG 3' |
| CPD-ChIP-6                   | 5' TTATCGCGGAGCAGGTAATGCGGATGGTGAATGAGTGAAGATGAACTG 3' |
| CPD-ChIP-7                   | 5' TTATCGCGGAGCAGGTAATGCGGATGGTGAATGAGTGAAGATGAACTG 3' |
| CPD-ChIP-8                   | 5' TTATCGCGGAGCAGGTAATGCGGATGGTGAATGAGTGAAGATGAACTG 3' |
| CPD-ChIP-9                   | 5' TTATCGCGGAGCAGGTAATGCGGATGGTGAATGAGTGAAGATGAACTG 3' |
| CPD-ChIP-10                  | 5' TTATCGCGGAGCAGGTAATGCGGATGGTGAATGAGTGAAGATGAACTG 3' |
| CPD-ChIP-13                  | 5' TTATCGCGGAGCAGGTAATGCGGATGGTGAATGAGTGAAGATGAACTG 3' |
| CPD-ChIP-14                  | 5' TTATCGCGGAGCAGGTAATGCGGATGGTGAATGAGTGAAGATGAACTG 3' |
| CPD-ChIP-15                  | 5' TTATCGCGGAGCAGGTAATGCGGATGGTGAATGAGTGAAGATGAACTG 3' |
| CPD-ChIP-16                  | 5' TTATCGCGGAGCAGGTAATGCGGATGGTGAATGAGTGAAGATGAACTG 3' |

| Primers used for ChIP-qPCR |                                                    |
|-----------------------------|---------------------------------------------------|
| SS-F''                     | 5' GAGGATGCGGAGCAGGTAATGCGGATGGTGAATGAGTGAAGATGAACTG 3' |
| SS-R''                     | 5' GAGGATGCGGAGCAGGTAATGCGGATGGTGAATGAGTGAAGATGAACTG 3' |
| CPD-qPCR-9                  | 5' GAGGATGCGGAGCAGGTAATGCGGATGGTGAATGAGTGAAGATGAACTG 3' |
| CPD-qPCR-10                 | 5' GAGGATGCGGAGCAGGTAATGCGGATGGTGAATGAGTGAAGATGAACTG 3' |
| COR15a-ChIP-1              | 5' GAGGATGCGGAGCAGGTAATGCGGATGGTGAATGAGTGAAGATGAACTG 3' |
| COR15a-ChIP-2              | 5' GAGGATGCGGAGCAGGTAATGCGGATGGTGAATGAGTGAAGATGAACTG 3' |
**Supplementary Table 5**
(continued)

| Name                      | Sequence                      | 3'               |
|---------------------------|-------------------------------|------------------|
| COR15a-ChIP-3             | 5' TGTTGGCGGACATACATTG        |                  |
| COR15a-ChIP-4             | 5' TCGTCTCATTTCTCCAG          |                  |
| COR15b-ChIP-1             | 5' GATAATGCAATGCCAAAAA        |                  |
| COR15b-ChIP-2             | 5' TCTCGACCAATGAGAATCCA       |                  |
| CYP718-ChIP-3             | 5' ACATACAGCCGAGCCACCTG       |                  |
| CYP718-ChIP-4             | 5' TGGATGGGTCTCTTCTACCTC      |                  |
| CYP724a1-ChIP-1           | 5' CATGAGGTTCCCCAAATTACG      |                  |
| CYP724a1-ChIP-2           | 5' TTCTCTAAAAAGAGGAATGAAAGAA |                  |
| DIN11-ChIP-1              | 5' TCAAAGGATTGGATCTACCTC      |                  |
| DIN11-ChIP-2              | 5' TCAAGCGTGAAGTAGTTTGGAG     |                  |
| DWF4-ChIP-1               | 5' CTCTGTCGTCATGCCTTC         |                  |
| DWF4-ChIP-2               | 5' CAATGATTCCGGAATGG          |                  |
| JR2-ChIP-1                | 5' ACACAGTTTTAGATCAGGAAGG     |                  |
| JR2-ChIP-2                | 5' GCCAATGGTTTTCACATTGTC      |                  |
| KIN1-ChIP-1               | 5' CCGACATAAGGCAAAACTCGA      |                  |
| KIN1-ChIP-2               | 5' GATGTGGTGGCAGGATAGA        |                  |
| PHE2-ChIP-1               | 5' GAATTTGCGGATGAGTT          |                  |
| PHE2-ChIP-2               | 5' TTTGGAAACATTTCAAGTTT       |                  |

| Name                      | Sequence                      | 3'               |
|---------------------------|-------------------------------|------------------|
| Reference: Le et al. (2010) |                               |                  |