Supplementary Note: Circadian and light signaling evolutionary linkage

Core circadian clock and light signaling genes brought into genetic linkage across the green lineage

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Phenotypes of core circadian clock genes in \textit{Arabidopsis}

The first plant circadian clock mutant described in \textit{Arabidopsis} was timing of cab expression 1 (\textit{toc}1) that has short free-running period (FRP) under continuous conditions and early flowering phenotypes (Millar et al., 1995; Somers et al., 1998). It was later cloned and shown to encode \textit{PSEUDO-RESPONSE REGULATOR (PRR1)} with conserved CCT (CONSTANS, CO-like, and TOC1) and REC (receiver) domains (Strayer et al., 2000). \textit{TOC1/PRR1} is part of a five gene family including \textit{PRR3}, \textit{PRR5}, \textit{PRR7}, and \textit{PRR9} that is regulated in “circadian waves of expression” with peak gene expression at Zeitgeber (ZT, German for “time giver”) 13, 11, 8, 7 and 4 hours (hrs) after lights on (dawn) respectively in long day conditions (16 hrs light/8 hrs dark) (Matsushika et al., 2000; Michael et al., 2008). The loss of evening expressed \textit{PRRs} (\textit{PRR1/3/5}) result in short FRP, while the morning expressed \textit{PRRs} (\textit{PRR7/9}) result in a long FRP (Michael et al., 2003; Salomé and McClung, 2005). Loss of \textit{PRR9} results in differential impact depending on the output rhythm assayed; there is a change in the phase of circadian regulated leaf movement, and core clock gene expression displayed a long FRP (Michael et al., 2003; Salomé and McClung, 2005). Similarly, \textit{PRR7} is essential for the cycling of \textit{CCA1} in the shoots but not in the roots, suggesting that it has tissue specific roles in circadian clock regulation (Nimmo and Laird, 2021). The double mutant combination of \textit{PRR7} and \textit{PRR9} (\textit{prr7/9}) results in loss of temperature compensation and very long FRP, suggesting that they have independent functions in the circadian clock consistent with not being direct paralogs of one another or having similar expression (Figure 1; Supplemental Table S4) (Farré et al., 2005; Salomé and McClung, 2005).

The second family of core circadian clock genes identified were \textit{LATE ELONGATED HYPOCOTYL (LHY)} and \textit{CIRCADIAN CLOCK ASSOCIATED 1 (CCA1)}, which are part of a sub-family of the large myeloblastosis (MYB) transcription factors (TF) family defined by the “SHAQKYF” protein motif (\textit{sMYB}) (Schaffer et al., 1998; Wang and Tobin, 1998). Both \textit{LHY} and \textit{CCA1} have peak expression at dawn regardless of entraining conditions (different photocycles and thermocycles) or under driven (diurnal) or free-run (circadian) conditions (Michael et al., 2008). Gain of function (overexpression) of either \textit{LHY} or \textit{CCA1} results in arrhythmic leaf movement, hypocotyl elongation, and gene expression of clock-controlled genes (Schaffer et al., 1998; Wang and Tobin, 1998). In contrast, loss of function of either result in a short FRP (3 hrs) and early flowering under short days (SD), although hypocotyl length and flowering time are wild type under long days (LD) (Green and Tobin, 1999; Alabadi et al., 2002; Mizoguchi et al., 2005).
2002; Oda et al., 2007). The double mutant (cca1/lhy) results in an even shorter FRP (6 hrs) than the single mutant, early flowering and plants with very small stature, suggesting that these orthologs are partly redundant in the core clock (Mizoguchi et al., 2002; Lu et al., 2009; Salomé et al., 2010).

In addition to CCA1 and LHY, the sMYB sub-family consists of eight other genes that share both the “SHAQKYF” motif as well as dawn-specific expression and thus were named REVEILLE (RVE) (Chaudhury et al., 1999). RVE3, RVE4, RVE5, RVE6, and RVE8 form a sub-clade of the RVEs since they also share the LHY-CCA1-like (LCL) domain and hence have also been referred to as LCL3, LCL1, LCL4, LCL2, and LCL5 respectively (Farinas and Mas, 2011). The LCL sub-clade are generally expressed at dawn like the other RVEs except RVE6/LCL2 only cycles under LD and SD conditions (not under circadian free-run conditions), and RVE4 peaks in the afternoon under thermocycles (Michael et al., 2008). In contrast, RVE1, RVE2 and RVE7 peak at ZT0 (dawn), ZT18 (midnight) and ZT07 (afternoon) respectively (Supplemental Figure S1) (Michael et al., 2008).

The first RVE gene described was an gain of function (overexpression) line of RVE7/EARLY-PHYTOCHROME-RESPONSIVE 1 (EPR1) that didn’t result in circadian period defects but did cause late flowering under LD and repressed its own expression consistent with it forming a slave oscillator (Kuno et al., 2003). Next, an overexpressing line of RVE2/CIRCADIAN 1 (CIR1) was described that resulted in short FRP, delayed flowering, longer hypocotyls and reduced seed germination in the dark (Zhang et al., 2007). Similar to RVE7, loss of RVE1 did not result in a defect in FRP, but it does result in changes in growth due to alterations in the auxin pathway (Rawat et al., 2009). The LCL sub-clade was the last to be described beginning with RVE8/LCL5; overexpression results in a shorter FRP and late flowering under both LD and SD, while loss of function causes a long FRP and early flowering (Farinas and Mas, 2011; Rawat et al., 2011). Loss of function of either of the closely related RVE4/LCL1 or RVE6/LCL2 does not result in a FRP change, but the double (rve4/8, 27 hrs; rve6/8, 26 hrs) or triple (rve4/6/8, 28 hrs) with RVE8/LCL5 results in a progressively longer FRP (Figure 1) (Hsu et al., 2013). Loss of function of either RVE3/LCL3 or RVE5/LCL4 also do not result in FRP changes, while the double mutant (rve3/5) has a slightly shorter FRP and the quintuple mutant (rve3/4/5/6/8) has a a even longer FRP (28 hrs) (Gray et al., 2017).

Since both the sMYB and PRR gene families are redundant, combinatorial mutation analysis provides clues as to significance of the CCA1-PRR9 and RVE4-PRR7 genetic linkages. One study has looked at the loss of the CCA1-PRR9 linkage but in the context of other redundant genes LHY and PRR7 (Salomé et al., 2010). The double mutant prr7/9 results in a very long FRP, yet when CCA1 or LHY are reduced using artificial microRNAs (amiR) silencing technology, the period is shortened almost to wild type FRP, while loss of both CCA1 and LHY has a similar short FRP as the lhy/cca1 (Salomé et al., 2010). These results suggest that the CCA1-PRR9 linkage results in reciprocal impacts on FRP, but that CCA1 and LHY are epistatic to PRR7 and PRR9 impacts on FRP.

In contrast to the lhy/cca1 double mutant that results in plants with a smaller stature, the rve4/6/8 triple mutant results in larger plants and the increased growth that is dependent on PIF4 and PIF5 (Gray et al., 2017). However, loss of both lhy/cca1 and rve4/6/8 (lhy/cca1/rve4/6/8 quintuple) restores the growth defect and FRP, suggesting that the the two clades of sMYB have reciprocal and dispensable roles in maintaining timing information and
growth (Shalit-Kaneh et al., 2018). So what are these specific feedback loops used for? While the *lhy/cca1/rve4/6/8* quintuple has restored growth and FRP, the circadian clock is less robust with decreased amplitude and suboptimal response to adverse environmental conditions (Shalit-Kaneh et al., 2018). Since *CCA1-LHY*-mediated temperature compensation requires both *PRR7* and *PRR9* (Salomé et al., 2010), it is possible that the *CCA1-PRR9* and *RVE4-PRR7* linkages represented inherited positive and negative respectively regulators of growth through the *PIFs* in a thermo and photo-sensitive way. To this end, the *PRR9* and *RVE4* phase of expression is shifted by 4 hours under thermocycles (while *CCA1* and *PRR7* are not), suggesting differential integration of thermocycle information (Michael et al., 2008).

**Gene neighborhoods in plant genomes**

Gene order in eukaryotes is generally poorly conserved resulting in seemingly random organization across chromosomes in contrast to prokaryotes where genes are often organized in functional arrays, or operons (Rocha, 2008). However, with more high-quality genomes and analytical tools it has become clear that there is in fact some level of gene clustering in eukaryotes and that some gene order is conserved evolutionarily (Hurst et al., 2004; Michalak, 2008). Two different studies across a collection of eukaryotic genomes spanning from plants to humans revealed that functionally and transcriptionally related genes are found in non-random clusters in the genome (Lee and Sonnhammer, 2003; Dávila López et al., 2010). In humans, bidirectional promoters play a role in proximally co-expressed genes (Adachi and Lieber, 2002; Trinklein et al., 2004). In yeast, essential genes are more likely to be found in clusters where the recombination rate is lower and this is independent of co-expression, suggesting that at some level genetics plays a role at preserving gene order (Pál and Hurst, 2003).

While many studies focus on identifying clusters based on functional or co-expression information, several tools have been developed to take an unbiased approach to find “gene neighborhoods,” or Proximal Ortholog Gene (POG) pairs of non-homologous genes (Winter et al., 2016; Marcat-Houben and Gabaldón, 2020; Foflonker and Blaby-Haas, 2021). Leveraging an evolutionary approach, up to 32% of the gene space across 341 fungal genomes are found in gene neighborhoods with many representing metabolic clusters (Marcat-Houben and Gabaldón, 2019). In algal genomes far fewer gene neighborhoods were identified, but they revealed several non-metabolic novel pathways (Foflonker and Blaby-Haas, 2021).

In plants a systematic look for gene neighbors has primarily been restricted to metabolic pathways (Osborn, 2010; Kautsar et al., 2017; Nützmann et al., 2018; Nützmann et al., 2020; Bharadwaj et al., 2021), or co-expressed genes (Williams and Bowles, 2004; Zhan et al., 2006; Chen et al., 2010). Plants are special amongst the eukaryotes since they undergo extensive whole genome duplication (WGD) and polyploidy events followed by rounds of fractionation that greatly increases the random order of genes and decreases gene synteny across lineages (Vision, 2005; Cheng et al., 2018). For instance, it has been shown across an array of high-quality genomes of mammals and plants that only closely related plants retain a similar level of synteny that is found across all mammals (Zhao and Schranz, 2019). Therefore, the *sMYB-PRR* and *PIF3-PHYA* evolutionarily conserved non-homologous gene clusters involved in a genetic network (as opposed to a metabolic pathway) are the first to be described across plant genomes.
The evolutionary significance of the environmental robustness model

The increasing closeness of the gene linkages appears around the same time as the rise to dominance of angiosperms over gymnosperms and ferns during the Cretaceous (Condamine et al., 2020). The phenotypic and species diversity of the angiosperm has been attributed to the multiple rounds of whole genome duplication (polyploidy) and fractionation (Soltis et al., 2009), which is the process by which the gene linkages are moving closer together over evolutionary time. There are two forces at work here: first, polyploidy often brings together distant genomes (allopolyploidy), which is thought to be maintained due to hybrid vigor enabling the ability to thrive in harsh/disparate environments or an asexual lifestyle (Fawcett et al., 2009; Cheng et al., 2018). Second, polyploids are ultimately reduced back to diploids (Zhao et al., 2017), which must thrive in their specific environment, yet sex is risky because it would be easy to make an unwanted genetic combination for a local environment (Freeling, 2017).

It is thought that the major innovation that led to the dominance of angiosperm was the flower and the specific relationship that it fostered with pollinators (Supplementary Figure S10) (Regal, 1977). Therefore, the linkage of light and circadian genes ensures that plants are tuned to exploit their specific environments, inheriting the correct combination for their local conditions so they will grow optimally under different seasons (Michael et al., 2003; Dodd et al., 2005). Another burst of polyploidy occurred at the Cretaceous/Tertiary (K/Pg) boundary that coincided with several natural disasters (Fawcett et al., 2009), and at this time the light and circadian gene linkages moved closer together in almost all species tested, except the grasses. This suggests that most plants “doubled down” on ensuring that the circadian system was inherited for a specific location; maybe the global decreasing temperature and carbon dioxide made it more likely that plants specially tuned for their environment would thrive and reproduce (Condamine et al., 2020).

At the same time, grasses became the most successful angiosperms and started to fill new ecological niches such as shaded forests and later open plains (Linder et al., 2018). Grasses are completely wind pollinated and flower at specific times of day (TOD) (Friedman and Barrett, 2009), suggesting they have taken the exact opposite route from other angiosperms and aggressively ensure every progeny has a new combination of circadian and light alleles. In essence, every pollination event represents a wide-hybrid that experiences heterosis or hybrid vigor, which enables it to outcompete populations in its new location. This strategy has been termed the “Viking syndrome” describing the ability of the grasses to colonize, persist and transform their environments (Linder et al., 2018). Taken together, the close genetic linkage favors animal pollination where specific circadian timing states are maintained; whereas the broken linkages favors wind pollination where diverse circadian states enable possible colonization of new environments.
Supplemental Figure S1. Expression of core circadian clock genes in *Arabidopsis*. Core circadian clock genes grouped by gene family or function. A) RVE1 (blue), RVE2 (orange) and RVE7 (grey). B) RVE3 (blue), RVE5 (orange), and RVE7 (grey). C) RVE4 (blue) and RVE8 (orange). D) PRR1 (blue), PRR3 (orange), PRR5 (grey), PRR7 (yellow) and PRR9 (aqua); E) GI (blue), ELF3 (orange), ELF4 (grey), and LUX (yellow). F) ZTL (blue), LKP2 (orange) and FKF1 (grey). Normalized RNA-seq expression was plotted over the day with grey boxes representing the dark period.
Supplemental Figure S2. Syntenic orthologs and expression of core circadian clock genes. A) The syntenic block for LUX (top) and BOA (bottom). B) The expression for LUX (blue) and BOA (orange). C) The syntenic block for RVE3 (top) and RVE5 (bottom). D) The expression RVE3 (blue), RVE5 (orange) and RVE6 (grey). E) The syntenic block for LKP2 (top) and ZTL (bottom). F) The expression of ZTL (grey), LKP2 (orange) and FKF1 (blue). Key syntenic relationships (red) and other syntenic genes (grey) for the entire syntenic block. In the syntenic plots the genes on the positive strand (blue) and negative strand (green).
Supplemental Figure S3. **PIF3** and **PHYA** linkage conserved back to *Amborella*. **PIF3** syntenic relationships (red), **PHYA** syntenic relationships (blue) and other syntenic genes (grey) for the entire syntenic block. Genes on the positive strand (blue) and negative strand (green). A) Syntenic blocks between *Amborella* (*Amborella trichopoda*), grape (*Vitis vinifera*) and *Arabidopsis* (*Arabidopsis thaliana*). B) Syntenic blocks between grape (*Vitis vinifera*) and soy (*Glycine max*).
Supplemental Figure S4. Syntenic sMYB-PRR pairs between Amborella and grape. LHY/CCA1 syntenic relationships (red), PRR3/5/7/9 syntenic relationships (blue) and other syntenic genes (grey) for the entire syntenic block. Genes on the positive strand (blue) and negative strand (green). A) Syntenic blocks between Amborella (Amborella trichopoda) and grape (Vitis vinifera) for the RVE4/8-PRR3/7. B) A) Syntenic blocks between Amborella (Amborella trichopoda) and grape (Vitis vinifera) for the LHY/CCA1-PRR5/9.
Supplemental Figure S5. CCA1/LHY lineage across monocots and eudicots. Both trees are pre-generated from the PLAZA dicot and monocot web pages. Gene names are on the tips of the tree and domain structure is depicted to the left. A) Monocot LHY/CCA1 tree; and B) Eudicot LHY/CCA1 tree. CCA1 genes boxed.
Supplemental Figure S6. The sMYB-PRR syntenic block in pineapple reveals relationships across monocots. LHY/CCA1/RVE syntenic relationships (red), PRR3/5/7/9 syntenic relationships (blue) and other syntenic genes (grey) for the entire syntenic block. Genes on the positive strand (blue) and negative strand (green). A) Pineapple (Ananas comosus) versus oro (Oropetium thomaeum); B) pineapple versus orchid (Apostasia shenzhenica); C) pineapple versus coconut (Cocos nucifera); D) pineapple versus palm (Elaeis guineensis).
Supplemental Figure S7. Different sMYB-PRR combinations are found across plant genomes with distinct whole genome duplication (WGD) events. LHY/CCA1/RVE syntenic relationships (red), PRR3/5/7/9 syntenic relationships (blue) and other syntenic genes (grey) for the entire syntenic block. Genes on the positive strand (blue) and negative strand (green). A) Amborella versus cassava (Manihot esculenta); B) Sequoia (Sequoiadendron giganteum) versus Amborella; C) Cuscuta (Caustralis; Cuscuta australis) versus Inil (Ipomoea nil) D) Eight different sMYB-PRR combinations and genome examples for each; this is not meant to be an exhaustive list.
Supplemental Figure S8. *PIF3-PHYA* are expressed at distinct times of day in *Arabidopsis* and soybean. A) *Arabidopsis* *PHYA* (blue) shows peak expression at ZT11, while *PIF3* (orange) has peak expression ZT16. B) One syntenic pair of the four *PIF3-PHYA* linkages in soybean robustly cycles under circadian conditions with *PHYA* (blue) peaking at CT8 and *PIF3* (orange) peaking at CT17. ZT; Zeitgeber Time. CT; Circadian Time.
Supplemental Figure S9. Circadian clock and light signaling genes are duplicated in Ostreococcus. A) CRYPTOCHROME (CRY/UVR) family in Ostreococcus; all CRY2 genes (blue box) and duplicated CRY2 genes in O. lucimarinus (brown box). B) Dotplot of O. lucimarinus (Ol) showing both the CRY2 and PRR5 duplications. C) PRR genes across Arabidopsis, Chlamydomonas (red box) and Ostreococcus (blue box). All of the PRR from Ostreococcus (Ol, O. lucimarinus; Or, O. tauri; and Or) and the duplicated PRR5 in Ol (luci).
Supplemental Tables

Supplemental Table S1. *Arabidopsis* circadian clock, light signaling and flowering time genes.

| Gene name       | Gene ID     | Gene name       | Gene ID     |
|-----------------|-------------|-----------------|-------------|
| sMYB family     | light/flowering |                |             |
| CCA1            | AT2G46830   | ARR3            | At1g59940   |
| LHY             | AT1G01060   | ARR4            | At1g10470   |
| RVE1            | AT5G17300   | bHLH69          | At4g30980   |
| RVE2            | AT5G37260   | bHLH92          | At5g43650   |
| RVE3            | AT1G01520   | CCR1            | At4g39260   |
| RVE4            | AT5G02840   | CCR2            | At2g21660   |
| RVE5            | AT4G01280   | COL2            | At3g02380   |
| RVE6            | AT5G52660   | COL9            | At3g07650   |
| RVE7            | AT1G18330   | COP1            | At2g32950   |
| RVE8            | AT3G09600   | CRB             | At1g09340   |
| PRR family      |             | CRY1            | At4g08920   |
| PRR1            | AT5G61380   | DET1            | At4g10180   |
| PRR3            | AT5G60100   | EID1            | At4g02440   |
| PRR5            | AT5G24470   | FHY3            | At3g22170   |
| PRR7            | AT5G02810   | FIO1            | At2g21070   |
| PRR9            | AT2G46790   | FLC             | At5g10140   |
| ZTL             | HYH         | FT              | At1g65480   |
| ZTL             | AT5G57360   | LIP1            | At2g20860   |
| LKP2            | AT2G18915   | LNK1            | AT5G64170   |
| FKF1            | AT1G68050   | LNK2            | AT3G54500   |
| GI              | AT1G22770   | PHYA            | At1g09570   |
| ELF3            | AT2G25930   | PIF3            | At1g09530   |
|     |        |        |        |
|-----|--------|--------|--------|
| ELF4 | AT2G40080 | PRMT5 | At4g31120 |
| PCL1/LUX | AT3G46640 | SEC   | At3g04240 |
| LUX-like | AT5G59570 | SFR6  | At4g04920 |
| SPA1 |        |        | At2g46340 |
| TEJ  | AT2G31870 | SPY   | At3g11540 |
| TIC  | AT3G22380 | SRR1  | At5g59560 |
| CDF3 | AT3G47500 | STN7  | At1g68830 |
| CHE  | AT5G08330 |        |        |
| CKB3 | AT3G60250 |        |        |
| CKB4 | AT2G44680 |        |        |
Supplemental Table S2. Syntenic regions for core circadian clock genes in *Arabidopsis*.

| Gene | Gene ID 1 | Gene ID 2 | Gene ID 1 | Gene ID 2 | Gene ID 1 | Gene ID 2 | Gene ID 1 | Gene ID 2 | Gene ID 1 | Gene ID 2 |
|------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| LHY  | AT1G01060.1 | AT2G46830.1 | CCA1      | AT1G01160.1 | AT4G00850.1 |
|      | AT1G01120.1 | AT2G46720.1 |           | AT1G01170.1 | AT4G00860.1 |
|      | AT1G01190.1 | AT2G46660.1 |           | AT1G01225.1 | AT4G00905.1 |
|      | AT1G01240.1 | AT2G46550.1 |           | AT1G01340.2 | AT4G01010.1 |
|      | AT1G01260.1 | AT2G46510.1 |           | AT1G01350.1 | AT4G01023.1 |
|      | AT1G01340.2 | AT2G46430.1 |           | AT1G01360.1 | AT4G01026.1 |
|      | AT1G01380.1 | AT2G46410.1 |           | AT1G01380.1 | AT4G01060.1 |
|      | AT1G01440.1 | AT2G46380.1 |           | AT1G01420.1 | AT4G01070.2 |
|      | AT1G01453.1 | AT2G46300.1 |           | AT1G01430.1 | AT4G01080.1 |
|      | AT1G01440.1 | AT4G01090.1 |           | AT1G01440.1 | AT4G01090.1 |
|      | AT2G18650.1 | AT5G57750.1 |           | AT1G01453.1 | AT4G01110.1 |
|      | AT2G18730.1 | AT5G57690.1 |           | AT1G01460.1 | AT4G01190.1 |
|      | AT2G18750.1 | AT5G57580.1 | RVE3      | AT1G01520.1 | AT4G01280.1 | RVE5 |
|      | AT2G18800.1 | AT5G57550.1 |           | AT1G01540.2 | AT4G01330.1 |
|      | AT2G18876.1 | AT5G57410.3 |           | AT1G01550.1 | AT4G01360.1 |
|      | AT2G18880.1 | AT5G57380.1 |           | AT1G01560.2 | AT4G01370.1 |
|      | AT2G18915.1 | AT5G57360.2 | ZTL       | AT3G46350.1 | AT5G59270.1 |
|      | AT2G18960.1 | AT5G57350.1 |           | AT3G46440.1 | AT5G59290.2 |
|      | AT2G19160.1 | AT5G57270.1 |           | AT3G46590.1 | AT5G59300.1 |
|      | AT2G19230.1 | AT5G57210.1 |           | AT3G46520.1 | AT5G59370.1 |
|      | AT5G64960.1 | AT5G10270.1 |           | AT3G46580.1 | AT5G59380.1 |
|      | AT5G64990.1 | AT5G10260.1 |           | AT3G46590.1 | AT5G59430.3 |
|      | AT5G65010.1 | AT5G10240.1 |           | AT3G46600.1 | AT5G59450.1 |
|      | AT5G65020.1 | AT5G10220.1 |           | AT3G46613.1 | AT5G59510.1 |
|      | AT5G65030.1 | AT5G10210.1 |           | AT3G46620.1 | AT5G59550.1 |
| MAF5 | AT5G65080.1 | AT5G10140.1 | FLC | LUX | AT3G46640.3 | AT5G59570.1 | BOA |
|------|-------------|-------------|-----|-----|-------------|-------------|-----|
| AT5G65100.1 | AT5G10120.1 |             |     |     | AT3G46650.1 | AT5G59580.1 |     |
| AT5G65120.1 | AT5G10110.1 |             |     |     |             |             |     |
| AT5G65140.1 | AT5G10100.1 |             |     | AT3G09300.1 | AT5G02100.1 |     |
| AT5G65160.1 | AT5G10090.1 | AT3G09340.1 | AT5G02170.2 |     |
| AT5G65180.1 | AT5G10060.1 | AT3G09370.1 | AT5G02320.1 |     |
| AT5G65205.1 | AT5G10050.1 | AT3G09390.1 | AT5G02380.1 |     |
| AT5G65207.1 | AT5G10040.1 | AT3G09400.1 | AT5G02400.1 |     |
| AT5G65210.1 | AT5G10030.1 | AT3G09440.1 | AT5G02500.1 |     |
|             |             | AT3G09470.1 | AT5G02502.1 |     |
| AT5G08190.1 | AT5G23090.1 |             |     | AT3G09480.1 | AT5G02570.1 |     |
| AT5G08200.1 | AT5G23130.1 |             |     | AT3G09490.1 | AT5G02590.1 |     |
| AT5G08230.1 | AT5G23150.1 | AT3G09500.1 | AT5G02610.1 |     |
| AT5G08240.1 | AT5G23160.1 | AT3G09550.1 | AT5G02620.1 |     |
| AT5G08250.1 | AT5G23190.1 | AT3G09570.1 | AT5G02630.1 |     |
| AT5G08270.1 | AT5G23200.1 | AT3G09590.1 | AT5G02730.1 |     |
| AT5G08300.1 | AT5G23250.1 | RVE8 | AT3G09600.1 | AT5G02840.1 | RVE4       |     |
| AT5G08330.1 | AT5G23280.1 | TCP7 | AT3G09630.1 | AT5G02870.1 |     |
| AT5G08335.1 | AT5G23320.1 |             | AT3G09670.1 | AT5G02950.1 |     |
| AT5G08340.2 | AT5G23330.1 |             | AT3G09680.1 | AT5G02960.1 |     |
| AT5G08350.1 | AT5G23350.1 |             | AT3G09690.1 | AT5G02970.1 |     |
| AT5G08360.1 | AT5G23380.1 |             | AT3G09700.1 | AT5G03030.1 |     |
| AT5G08390.1 | AT5G23430.1 |             | AT3G09710.1 | AT5G03040.1 |     |
| AT5G08410.1 | AT5G23440.1 |             | AT3G09760.1 | AT5G03180.1 |     |
| AT5G08430.1 | AT5G23480.1 |             | AT3G09770.1 | AT5G03200.1 |     |
| AT5G08440.1 | AT5G23490.1 |             | AT3G09790.1 | AT5G03240.1 |     |
| AT5G08500.1 | AT5G23575.1 |             | AT3G09810.1 | AT5G03290.1 |     |
| AT5G08520.1 | AT5G23650.1 |             | AT3G09820.1 | AT5G03300.1 |     |
|             |             |             | AT3G09840.1 | AT5G03340.1 |     |
Supplemental Table S3. Synonymous substitution (Ks) across *Arabidopsis* sMYB proteins. Coloring (from green to red) indicates the magnitude of the Ks value where green is a high number representing genes that are evolutionarily distant, and red indicates a low Ks value representing genes that are evolutionarily close.

| Gene name | Gene ID | CCA1 | LHY | RVE1 | RVE2 | RVE3 | RVE4 | RVE5 | RVE6 | RVE7 | RVE8 |
|-----------|---------|------|-----|------|------|------|------|------|------|------|------|
| CCA1      | AT2G46830 | 2.8531 | 3.2959 | 3.8734 | 3.8241 | 3.8795 | 3.8421 | 3.6285 | 3.9743 | 2.1194 |
| LHY       | AT1G01060 | 2.8531 | 3.9771 | 3.8654 | 3.8257 | 4.2384 | 3.9251 | 3.9332 | 3.9372 | 3.8884 |
| RVE1      | AT5G17300 | 3.2959 | 3.9771 | 3.9174 | 1.8631 | 5.648  | 2.3697 | 2.3213 | 4.0707 | 4.3232 |
| RVE2      | AT5G37260 | 3.8734 | 3.8654 | 3.9174 | 3.8757 | 2.2745 | 3.495  | 3.8795 | 3.742  | 2.4353 |
| RVE3      | AT1G01520 | 3.8241 | 3.8257 | 1.8631 | 3.8757 | 3.8886 | 1.2433 | 3.9338 | 3.8388 | 3.8348 |
| RVE4      | AT5G02840 | 3.8795 | 4.2384 | 5.648  | 2.2745 | 3.8886 | 2.1927 | 3.9253 | 3.92   | 0.8413 |
| RVE5      | AT4G01280 | 3.8421 | 3.9251 | 2.3697 | 3.495  | 1.2433 | 2.1927 | 3.9399 | 2.0931 | 1.9066 |
| RVE6      | AT5G52860 | 3.6285 | 3.9332 | 2.3213 | 3.8795 | 3.9338 | 3.9253 | 3.9399 | 3.9268 | 4.6156 |
| RVE7      | AT1G18330 | 3.9743 | 3.9372 | 4.0707 | 3.742  | 3.8388 | 3.92   | 2.0931 | 3.9268 | 3.9438 |
| RVE8      | AT3G09600 | 2.1194 | 3.8884 | 4.3232 | 2.4353 | 3.8348 | 0.8413 | 1.9066 | 4.6156 | 3.9438 |
Supplemental Table S4. Synonymous substitution (Ks) across *Arabidopsis* PRR proteins. Coloring (from green to red) indicates the magnitude of the Ks value where green is a high number representing genes that are evolutionarily distant, and red indicates a low Ks value representing genes that are evolutionarily close.

| Gene name | Gene ID       | PRR1  | PRR3  | PRR5  | PRR7  | PRR9  |
|-----------|---------------|-------|-------|-------|-------|-------|
| PRR1      | AT5G61380     | 4.1647|       | 4.3028| 4.2329|       |
| PRR3      | AT5G60100     | 4.1647| 4.2775|       | 4.2402| 2.641 |
| PRR5      | AT5G24470     | 4.2759| 4.2775| 4.381 |       | 2.328 |
| PRR7      | AT5G02810     | 4.3028| 4.2402| 4.381 |       | 2.5112|
| PRR9      | AT2G46790     | 4.2329| 2.641 | 2.328 | 2.5112|       |
Supplemental Table S5. Genetic linkages between *CCA1/LHY*-PRR5/9 and *RVE4/8-PRR3/7* from PLAZA dicot 4.5. For each species the number of genetic linkages is presented.

| Abbreviation | Common Name                  | TaxID  | PubMedID   | LHY/CCA1-PRR5/9 | RVE4/8-PRR3/7 | Total linkages |
|--------------|-------------------------------|--------|------------|-----------------|---------------|----------------|
| ach          | *Actinidia chinensis*         | 3625   | 24136039   | 0               | 0             | 0              |
| Ahy          | *Amaranthus hypochondriacus*  | NA     | NA         | 1               | 2             | 3              |
| aip          | *Arachis ipaensis*            | 130453 | 26901068   | 0               | 1             | 1              |
| aly          | *Arabidopsis lyrata*          | 59689  | 26382944   | 1               | 1             | 2              |
| ath          | *Arabidopsis thaliana*        | 3702   | 27862469   | 1               | 1             | 2              |
| atr          | *Amborella trichopoda*        | 13333  | 24357323   | 1               | 1             | 2              |
| bol          | *Brassica oleracea*           | 109376 | 24852848   | 1               | 0             | 1              |
| bra          | *Brassica rapa*               | 3711   | 21873998   | 0               | 1             | 1              |
| bvu          | *Beta vulgaris*               | 161934 | 24352233   | 1               | 0             | 1              |
| can          | *Capsicum annuum*             | 4072   | 24441736   | 0               | 0             | 0              |
| car          | *Cicer arietinum*             | 3827   | 23354103   | 1               | 1             | 2              |
| ccaj         | *Cajanus cajan*               | 3821   | 22057054   | 0               | 0             | 0              |
| ccan         | *Coffea canephora*            | 49390  | 25190796   | 1               | 1             | 2              |
| ccl          | *Citrus clementina*           | 85681  | 24908277   | 1               | 1             | 2              |
| cla          | *Citrus lanatus*              | 3654   | 23179023   | 0               | 0             | 0              |
| cme          | *Cucumis melo*                | 3656   | 22753475   | 0               | 0             | 0              |
| col          | *Corchorus olitorius*         | 93759  | 28134914   | 1               | 0             | 1              |
| CPA          | *Carica papaya*               | 3649   | 18432245   | 0               | 0             | 0              |
| cqu          | *Chenopodium quinoa*          | 63459  | 28178233   | 2               | 0             | 2              |
| cre          | *Chlamydomonas reinhardtii*   | 3055   | 17932292   | 0               | 0             | 0              |
| cru          | *Capsella rubella*            | 81985  | 23749190   | 1               | 1             | 2              |
| csa          | *Cucumis sativus L.*          | 3659   | NA         | 0               | 0             | 0              |
| dca          | *Daucus carota*               | 4039   | 27158781   | 0               | 0             | 0              |
| egr          | *Eucalyptus grandis*          | 71139  | 24919147   | 0               | 0             | 0              |
| egut         | *Erythranthe guttata*         | 4155   | 24225854   | 0               | 1             | 1              |
| Code | Species Name                      | Accession | GenBank ID  | SRA | NCBI | JGI |
|------|----------------------------------|-----------|-------------|-----|------|-----|
| fve  | Fragaria vesca                  | 57918     | 21186353    | 0   | 1    | 1   |
| gma  | Glycine max                     | 3847      | 20075913    | 4   | 2    | 6   |
| gra  | Gossypium raimondii             | 29730     | 22922876    | 1   | 1    | 2   |
| hbr  | Hevea brasiliensis              | 3981      | 27255837    | 1   | 2    | 3   |
| mco  | Micromonas commoda              | 296587    | 19359590    | 0   | 0    | 0   |
| mdo  | Malus domestica                 | 3750      | 20802477    | 0   | 0    | 0   |
| mes  | Manihot esculenta               | 3983      | 22523606    | 0   | 0    | 0   |
| mpo  | Marchantia polymorpha           | 3197      | 28985561    | 0   | 0    | 0   |
| mtr  | Medicago truncatula             | 3880      | 22089132    | 1   | 1    | 2   |
| nnu  | Nelumbo nucifera                | 4432      | 23663246    | 0   | 1    | 1   |
| osa  | Oryza sativa ssp. japonica      | 39947     | 16100779    | 0   | 0    | 0   |
| pab  | Picea abies                     | 3329      | 23698360    | 0   | 0    | 0   |
| pax  | Petunia axillaris               | 33119     | 27255838    | 0   | 0    | 0   |
| pbr  | Pyrus bretschneideri             | 225117    | 23149293    | 0   | 1    | 1   |
| ppa  | Physcomitrella patens           | 3218      | 18079367    | 0   | 0    | 0   |
| ppe  | Prunus persica                  | 3760      | 23525075    | 0   | 1    | 1   |
| ptr  | Populus trichocarpa             | 3694      | 16973872    | 2   | 0    | 2   |
| rco  | Ricinus communis                | 3988      | 20729833    | 0   | 1    | 1   |
| sly  | Solanum lycopersicum            | 4081      | 22660326    | 1   | 0    | 1   |
| smo  | Selaginella moellendorffii      | 88036     | 21551031    | 0   | 0    | 0   |
| spa  | Schrenkiella parvula            | 98039     | 21822265    | 1   | 1    | 2   |
| stu  | Solanum tuberosum               | 4113      | 21743474    | 0   | 1    | 1   |
| tca  | Theobroma cacao                 | 3641      | 21186351    | 1   | 1    | 2   |
| tha  | Tarenaya hassleriana            | 28532     | 23983221    | 1   | 2    | 3   |
| tpr  | Trifolium pratense              | 57577     | 26617401    | 1   | 0    | 1   |
| ugi  | Utricularia gibba               | 13748     | 23665961    | 0   | 0    | 0   |
| vra  | Vigna radiata var. radiata      | 157791    | 25384727    | 1   | 1    | 2   |
| vvi  | Vitis vinifera                  | 29760     | 17721507    | 1   | 1    | 2   |
| zju  | Ziziphus jujuba                 | 326968    | 25350882    | 0   | 0    | 0   |
| zma | Zea mays | 4577 | 19965430 | 0 | 0 | 0 |
Supplemental Table S6. Number of syntenic blocks and genetic linkages between CCA1/LHY-PRR5/9, RVE4/8-PRR3/7 and PIF3-PHYA. The number under each individual gene pair is the number of syntenic blocks found per species. The number under the genetic linkages represents the number of species sharing genetic linkages with that species.

| species             | Clade            | Order       | CCA1/LHY | RVE4/8 | PRR3/7 | PRR5/9 | PHYA | PIF3 | RVE4/8-PRR3/7 | LHY/CCA1-PRR5/9 | PIF3-PHYA |
|---------------------|------------------|-------------|----------|--------|--------|--------|------|------|---------------|-----------------|-----------|
| Amborella trichopoda| Basal-Angiosperm | Amborellales| 1 1 1 2 1 1 | 23     | 29     | 42     |
| Nymphaea tetragona  | Basal-Angiosperm | Nymphaeales | 1 0 2 2 1 1 | 0 2    | 41     |
| Nelumbo nucifera    | Basal-Eudicots   | Proteales   | 1 1 2 2 0 2 | 46     | 50     | 0      |
| Macleaya cordata    | Basal-Eudicots   | Ranunculales| 2 1 1 1 1 1 | 44     | 6      | 72     |
| Papaver somniferum  | Basal-Eudicots   | Ranunculales| 2 2 1 2 2 2 | 11     | 50     | 108    |
| Aquilegia coerulea  | Basal-Eudicots   | Ranunculales| 1 1 2 0 1 1 | 24     | 0      | 1      |
| Vitis vinifera      | Basal-Eudicots   | Vitales     | 1 1 4 2 1 2 | 22     | 56     | 72     |
| Cinnamomum micranthum | Magnoliids      | Magnoliales | 2 0 2 3 1 2 | 0      | 59     | 64     |
| Persea americana    | Magnoliids       | Magnoliales | 2 0 2 3 1 2 | 0      | 40     | 0      |
| Liriodendron chinense | Magnoliids      | Magnoliales | 3 0 4 2 1 2 | 1      | 35     | 55     |
| Spirodela polyrhiza | Monocots         | Alismatales | 2 1 1 1 2 2 | 0      | 2      | 0      |
| Zostera marina      | Monocots         | Alismatales | 0 0 0 0 0 2 | 0      | 0      | 0      |
| Elaeis guineensis   | Monocots         | Arecales    | 1 1 3 0 1 4 | 50     | 1      | 41     |
| Phoenix dactylifera | Monocots         | Arecales    | 1 1 2 0 1 2 | 39     | 0      | 0      |
| Asparagus officinalis | Monocots         | Asparagales | 1 1 1 0 1 5 | 17     | 0      | 31     |
| Apostasia shenzhenica | Monocots        | Asparagales | 1 1 2 0 1 1 | 6      | 0      | 0      |
| Phalaeopsis equestris | Monocots         | Asparagales | 1 0 1 0 1 0 | 0      | 0      | 0      |
| Xerophyta viscosa   | Monocots         | Pandanales  | 0 1 3 1 1 3 | 0      | 0      | 2      |
| Ananas comosus      | Monocots         | Poales      | 1 1 2 0 1 2 | 47     | 0      | 59     |
| Brachypodium distachyon | Monocots        | Poales      | 0 0 2 0 0 2 | 0      | 0      | 0      |
| Echinochloa crus-galli | Monocots        | Poales      | 0 0 4 0 0 6 | 0      | 0      | 0      |
| Hordeum vulgare     | Monocots         | Poales      | 0 0 2 0 0 1 | 0      | 0      | 0      |
| leersia perrieri    | Monocots         | Poales      | 0 0 3 0 0 2 | 0      | 0      | 0      |
| Species                        | Order      | Family     | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 |
|-------------------------------|------------|------------|---|---|---|---|---|---|---|---|---|
| *Capsicum chinense*           | Monocots   | Poales     | 0 | 0 | 2 | 0 | 0 | 1 | 0 | 0 | 0 |
| *Cuscuta campestris*          | Monocots   | Poales     | 0 | 0 | 3 | 0 | 0 | 2 | 0 | 0 | 0 |
| *Kalanchoe*                   | Monocots   | Poales     | 0 | 0 | 3 | 0 | 0 | 2 | 0 | 0 | 0 |
| *Malania oleifera*            | Monocots   | Poales     | 0 | 0 | 2 | 0 | 0 | 1 | 0 | 0 | 0 |
| *Olea europaea*               | Monocots   | Poales     | 0 | 0 | 3 | 0 | 0 | 2 | 0 | 0 | 0 |
| *Chenopodium quinoa hypochondriacus* | Super-Asterids | Caryophyllales | 2 | 1 | 2 | 2 | 2 | 2 | 46 | 58 | 0 |
| *Beta vulgaris*               | Super-Asterids | Caryophyllales | 1 | 1 | 2 | 1 | 1 | 0 | 0 | 0 | 0 |
| *Beta vulgaris*               | Super-Asterids | Caryophyllales | 1 | 1 | 1 | 2 | 1 | 1 | 0 | 0 | 0 |
| *Beta vulgaris*               | Super-Asterids | Caryophyllales | 1 | 1 | 2 | 1 | 1 | 0 | 0 | 0 | 0 |
| *Beta vulgaris*               | Super-Asterids | Caryophyllales | 1 | 1 | 3 | 4 | 2 | 2 | 7 | 59 | 0 |
| *Actinidia chinensis*         | Super-Asterids | Ericales | 1 | 2 | 5 | 3 | 3 | 3 | 0 | 0 | 131 |
| *Actinidia eriantha*          | Super-Asterids | Ericales | 2 | 3 | 6 | 3 | 3 | 4 | 1 | 1 | 85 |
| *Coffea canephora*            | Super-Asterids | Gentianales | 1 | 1 | 2 | 1 | 1 | 1 | 27 | 0 | 0 |
| *Olea europaea*               | Super-Asterids | Lamiales | 1 | 2 | 4 | 3 | 1 | 3 | 0 | 0 | 0 |
| *Sesamum indicum*             | Super-Asterids | Lamiales | 1 | 1 | 1 | 2 | 2 | 1 | 55 | 0 | 76 |
| *Olecrania guttata*           | Super-Asterids | Lamiales | 1 | 1 | 2 | 2 | 2 | 1 | 53 | 0 | 74 |
| *Malania oleifera*            | Super-Asterids | Santalales | 1 | 0 | 1 | 1 | 1 | 1 | 0 | 0 | 70 |
| *Kalanchoe fedtschenkoi*      | Super-Asterids | Saxifragales | 2 | 1 | 5 | 2 | 2 | 2 | 0 | 17 | 71 |
| *Cuscuta campestris*          | Super-Asterids | Solanales | 1 | 2 | 8 | 2 | 2 | 0 | 52 | 0 | 0 |
| *Ipomoea nil*                 | Super-Asterids | Solanales | 0 | 1 | 3 | 3 | 1 | 2 | 41 | 0 | 0 |
| *Capsicum annuum*             | Super-Asterids | Solanales | 1 | 1 | 4 | 2 | 0 | 1 | 1 | 33 | 0 |
| *Capsicum baccatum*           | Super-Asterids | Solanales | 2 | 1 | 2 | 2 | 0 | 1 | 0 | 32 | 0 |
| *Capsicum chinense*           | Super-Asterids | Solanales | 1 | 1 | 2 | 2 | 0 | 1 | 0 | 0 | 0 |
| Species                        | Class         | Order       | Value 1 | Value 2 | Value 3 | Value 4 | Value 5 | Value 6 |
|-------------------------------|---------------|-------------|---------|---------|---------|---------|---------|---------|
| Petunia axillaris             | Super-Asterids| Solanales   | 0       | 1       | 3       | 3       | 0       | 2       |
| Solanum lycopersicum          | Super-Asterids| Solanales   | 1       | 1       | 3       | 2       | 0       | 1       |
| Solanum pennellii             | Super-Asterids| Solanales   | 1       | 1       | 2       | 2       | 0       | 1       |
| Solanum tuberosum             | Super-Asterids| Solanales   | 1       | 1       | 0       | 2       | 0       | 1       |
| Aethionema arabicum           | Super-Rosids  | Brassicales | 2       | 2       | 2       | 2       | 1       | 3       |
| Arabidopsis lyrata            | Super-Rosids  | Brassicales | 2       | 2       | 4       | 2       | 1       | 6       |
| Arabidopsis thaliana          | Super-Rosids  | Brassicales | 2       | 2       | 2       | 3       | 1       | 4       |
| Arabis alpina                 | Super-Rosids  | Brassicales | 0       | 2       | 1       | 0       | 0       | 5       |
| Boechera stricta              | Super-Rosids  | Brassicales | 2       | 2       | 2       | 2       | 1       | 4       |
| Brassica napus                | Super-Rosids  | Brassicales | 3       | 10      | 7       | 9       | 4       | 15      |
| Brassica oleracea             | Super-Rosids  | Brassicales | 4       | 5       | 3       | 4       | 2       | 8       |
| Brassica rapa                 | Super-Rosids  | Brassicales | 4       | 4       | 3       | 3       | 2       | 8       |
| Camelina sativa               | Super-Rosids  | Brassicales | 5       | 8       | 6       | 6       | 3       | 10      |
| Capsella rubella              | Super-Rosids  | Brassicales | 2       | 2       | 3       | 2       | 1       | 4       |
| Lepidium meyenii              | Super-Rosids  | Brassicales | 6       | 8       | 9       | 8       | 4       | 12      |
| Schrenkiella parvula           | Super-Rosids  | Brassicales | 1       | 1       | 2       | 2       | 1       | 5       |
| Thellungiella halophila        | Super-Rosids  | Brassicales | 1       | 2       | 5       | 2       | 1       | 3       |
| Thellungiella salsuginea      | Super-Rosids  | Brassicales | 1       | 2       | 2       | 2       | 1       | 3       |
| Carica papaya                 | Super-Rosids  | Brassicales | 1       | 1       | 2       | 2       | 1       | 1       |
| Cleome gynandra               | Super-Rosids  | Brassicales | 3       | 1       | 1       | 4       | 0       | 3       |
| Tarenaya hasseriana           | Super-Rosids  | Brassicales | 5       | 2       | 6       | 4       | 2       | 6       |
| Begonia fuchsiioides           | Super-Rosids  | Cucurbitales| 7       | 1       | 2       | 7       | 2       | 2       |
| Citrullus lanatus             | Super-Rosids  | Cucurbitales| 1       | 1       | 1       | 1       | 0       | 1       |
| Cucumis melo                  | Super-Rosids  | Cucurbitales| 1       | 1       | 1       | 1       | 0       | 1       |
| Cucumis sativus               | Super-Rosids  | Cucurbitales| 1       | 1       | 1       | 1       | 0       | 1       |
| Cucurbita maxima              | Super-Rosids  | Cucurbitales| 2       | 0       | 2       | 3       | 0       | 2       |
| Datisca glomerata             | Super-Rosids  | Cucurbitales| 1       | 1       | 2       | 1       | 0       | 1       |
| Ammopiptanthus nanus          | Super-Rosids  | Fabales     | 0       | 1       | 2       | 3       | 1       | 2       |
| Arachis duranensis            | Super-Rosids  | Fabales     | 2       | 2       | 2       | 2       | 3       | 4       |
| Cajanus cajan                 | Super-Rosids  | Fabales     | 1       | 1       | 1       | 2       | 2       | 4       |
| Cicer arietinum               | Super-Rosids  | Fabales     | 1       | 0       | 2       | 2       | 2       | 2       |
| Species                | Super-Order   | Super-Families | Family | 1  | 2  | 3  | 4  | 5  | 6  | 7  | 8  | 9  | 10 |
|------------------------|---------------|----------------|--------|----|----|----|----|----|----|----|----|----|----|
| Glycine max            | Super-Rosids  | Fabales        |        | 4  | 4  | 4  | 6  | 4  | 8  | 53 | 61 | 337 |
| Lotus japonicus        | Super-Rosids  | Fabales        |        | 1  | 1  | 1  | 8  | 1  | 3  | 51 | 52 | 75  |
| Lupinus angustifolius  | Super-Rosids  | Fabales        |        | 3  | 1  | 2  | 3  | 3  | 7  | 0  | 55 | 181 |
| Medicago truncatula    | Super-Rosids  | Fabales        |        | 1  | 1  | 2  | 3  | 1  | 3  | 55 | 51 | 92  |
| Phaseolus vulgaris     | Super-Rosids  | Fabales        |        | 3  | 2  | 3  | 3  | 2  | 3  | 53 | 62 | 117 |
| Trifolium pratense     | Super-Rosids  | Fabales        |        | 1  | 1  | 1  | 2  | 1  | 3  | 0  | 54 | 53  |
| Vigna angularis        | Super-Rosids  | Fabales        |        | 2  | 2  | 3  | 3  | 2  | 4  | 31 | 51 | 180 |
| Vigna radiata          | Super-Rosids  | Fabales        |        | 2  | 2  | 4  | 2  | 2  | 3  | 40 | 47 | 165 |
| Betula pendula         | Super-Rosids  | Fagales        |        | 1  | 1  | 2  | 3  | 1  | 2  | 0  | 56 | 22  |
| Casuarina glauca       | Super-Rosids  | Fagales        |        | 1  | 1  | 2  | 2  | 1  | 2  | 48 | 57 | 57  |
| Quercus robur          | Super-Rosids  | Fagales        |        | 2  | 1  | 3  | 1  | 1  | 3  | 52 | 5  | 7   |
| Carya illinoiensis     | Super-Rosids  | Fagales        |        | 1  | 0  | 3  | 2  | 0  | 3  | 0  | 0  | 0   |
| Manihot esculenta      | Super-Rosids  | Malpighiales   |        | 2  | 1  | 5  | 3  | 1  | 3  | 16 | 58 | 78  |
| Ricinus communis       | Super-Rosids  | Malpighiales   |        | 1  | 1  | 4  | 2  | 1  | 2  | 54 | 53 | 76  |
| Linum usitatissimum    | Super-Rosids  | Malpighiales   |        | 5  | 2  | 2  | 6  | 0  | 2  | 50 | 7  | 0   |
| Populus trichocarpa    | Super-Rosids  | Malpighiales   |        | 4  | 2  | 2  | 4  | 1  | 3  | 0  | 60 | 77  |
| Durio zibethinus       | Super-Rosids  | Malvales       |        | 2  | 2  | 5  | 4  | 0  | 4  | 57 | 0  | 0   |
| Gossypium barbadense   | Super-Rosids  | Malvales       |        | 5  | 2  | 8  | 9  | 0  | 6  | 47 | 58 | 2   |
| Gossypium hirsutum     | Super-Rosids  | Malvales       |        | 6  | 2  | 8  | 8  | 0  | 6  | 47 | 58 | 2   |
| Gossypium raimondii    | Super-Rosids  | Malvales       |        | 3  | 1  | 5  | 4  | 0  | 3  | 46 | 59 | 0   |
| Theobroma cacao        | Super-Rosids  | Malvales       |        | 1  | 1  | 3  | 2  | 1  | 2  | 52 | 58 | 78  |
| Punica granatum        | Super-Rosids  | Myrtales       |        | 1  | 1  | 2  | 2  | 2  | 3  | 49 | 0  | 74  |
| Eucalyptus grandis     | Super-Rosids  | Myrtales       |        | 1  | 1  | 2  | 1  | 1  | 3  | 0  | 0  | 3   |
| Trema orientale        | Super-Rosids  | Rosales        |        | 1  | 1  | 3  | 2  | 1  | 2  | 51 | 54 | 71  |
| Morus notabilis        | Super-Rosids  | Rosales        |        | 1  | 1  | 5  | 2  | 1  | 2  | 50 | 55 | 75  |
| Ziziphus jujuba        | Super-Rosids  | Rosales        |        | 1  | 0  | 3  | 2  | 3  | 2  | 0  | 2  | 79  |
| Dryas drummondii       | Super-Rosids  | Rosales        |        | 1  | 1  | 2  | 2  | 1  | 1  | 53 | 51 | 75  |
| Fragaria vesca         | Super-Rosids  | Rosales        |        | 2  | 1  | 1  | 2  | 1  | 1  | 51 | 60 | 61  |
| Malus domestica        | Super-Rosids  | Rosales        |        | 2  | 1  | 5  | 3  | 2  | 3  | 57 | 54 | 149 |
| Prunus mume            | Super-Rosids  | Rosales        |        | 1  | 1  | 1  | 1  | 1  | 1  | 53 | 0  | 74  |
| Prunus persica         | Super-Rosids  | Rosales        |        | 2  | 1  | 1  | 2  | 1  | 1  | 52 | 55 | 76  |
| Species                     | Super-Order | Order   | 2  | 1  | 4  | 2  | 2  | 3  | 54 | 1  | 74 |
|-----------------------------|-------------|---------|----|----|----|----|----|----|----|----|----|
| Pyrus x bretschneideri      | Super-Rosids| Rosales | 2  | 1  | 4  | 2  | 2  | 3  | 54 | 1  | 74 |
| Rosa chinensis              | Super-Rosids| Rosales | 1  | 1  | 2  | 2  | 1  | 2  | 50 | 58 | 73 |
| Rubus occidentalis          | Super-Rosids| Rosales | 1  | 1  | 2  | 2  | 1  | 1  | 53 | 1  | 76 |
| Parasponia andersonii       | Super-Rosids| Rosales | 1  | 1  | 3  | 2  | 1  | 2  | 0  | 32 | 75 |
| Citrus maxima               | Super-Rosids| Sapindales| 1  | 0  | 3  | 2  | 1  | 2  | 0  | 58 | 58 |
| Citrus sinensis             | Super-Rosids| Sapindales| 1  | 1  | 5  | 1  | 1  | 2  | 43 | 59 | 52 |
| Xanthoceras sorbifolium     | Super-Rosids| Sapindales| 1  | 0  | 2  | 2  | 1  | 2  | 0  | 58 | 75 |
**Supplemental Table S7. Summary of syntenic blocks across 123 plant genome assemblies for circadian genes.**

| Family name | CCA1/LHY | RVE4/8 | PRR3/7 | PRR5/9 | PHYA | PIF3 |
|-------------|----------|--------|--------|--------|------|------|
| Syntenic blocks (#) | 182 | 152 | 345 | 264 | 129 | 330 |
| Most syntenic blocks (#) | 7 | 10 | 9 | 9 | 4 | 15 |
| Fewest syntenic blocks (#) | 0 | 0 | 0 | 0 | 0 | 0 |
| Median syntenic blocks (#) | 1 | 1 | 2 | 2 | 1 | 2 |
| Average syntenic blocks (#) | 1.5 | 1.2 | 2.8 | 2.1 | 1 | 2.7 |
| Zero syntenic blocks | 23 | 28 | 2 | 24 | 37 | 4 |
| Total genomes tested (#) | 123 | 123 | 123 | 123 | 123 | 123 |
| missing (%) | 18.70% | 22.80% | 1.60% | 19.50% | 30.10% | 3.30% |
| present (%) | 81.30% | 77.20% | 98.40% | 80.50% | 69.90% | 96.70% |
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