title: “Sunflower Rhythms 2020 Post-COSOPT Analysis” output: pdf_document: default html_notebook: default html_document: df_print: paged —

Setup the R environment

```
library(circular)
```

```
##
## Attaching package: 'circular'
```

```
## The following objects are masked from 'package:stats':
##
##     sd, var
```

```
library(clockplot)
library(ggplot2)
library(reshape2)
library(plyr)
library(stringr)
library(tools)
library(VennDiagram)
```

```
## Loading required package: grid
```

```
## Loading required package: futile.logger
```

```
knitr::opts_knit$set(root.dir='.')
```

Set thresholds and colors

```
min.p.mmc.beta <- 0.05
min.meanexplev <- 0.05
min.expressed.count <- 8
per.buffer <- 2
exp.min <- 10
amp.min <- 0.2
east.color <- 'orange'
west.color <- 'forestgreen'
```

Import and pre-process time course data

```
if (!file.exists('counts/east-counts.tsv')
    | !file.exists('counts/west-counts.tsv')
    | !file.exists('counts/merged-counts.tsv')
    | !file.exists('r-data/timecourse.rds')) {

  if (!dir.exists('r-data')) dir.create('r-data')

  counts <- read.table('counts/reanalysis_HA2015_HanXRQr1.0_mRNA_normalized_arranged.csv', sep=',', row
  # Remove bad replicates
  counts <- counts[, ! colnames(counts) %in% c('X4ea2', 'X10ea3', 'X16ea3', 'X10w3', 'X15w2')]

  # Output East and West counts files
  saveRDS(counts, 'r-data/counts.rds')
```

```r
# Extract Zeitgeber Time from column names
time.idx <- as.integer(sub("X([0-9]+)[ew][ae]?[1-3]{1}", "\\1", colnames(counts)))
times <- seq(0, 46, 2)
hour <- times[time.idx]
saveRDS(hour, 'r-data/hour.rds')


counts[] <- lapply(counts, as.numeric)
counts <- rbind(hour, counts)
rownames(counts)[1] <- 'Gene'


# Extract sample side from column names
west.samples <- grepl('w', colnames(counts))
east.samples <- grepl('e', colnames(counts))

side <- rep('', length(colnames(counts)))
side[west.samples] <- 'West'
side[east.samples] <- 'East'

saveRDS(side, 'r-data/side.rds')


west.counts <- counts[, west.samples]
east.counts <- counts[, east.samples]

write.table(east.counts, 'counts/east-counts.tsv', sep='\t', quote=F, col.names=F)
write.table(west.counts, 'counts/west-counts.tsv', sep='\t', quote=F, col.names=F)

saveRDS(east.counts[-1, ], 'r-data/east.counts.rds')
saveRDS(west.counts[-1, ], 'r-data/west.counts.rds')


# Get Merged Counts
west.counts.temp <- west.counts
east.counts.temp <- east.counts

colnames(west.counts.temp) <- sub('w', 'm', colnames(west.counts.temp))
colnames(east.counts.temp) <- sub('ea', 'm', colnames(east.counts.temp))

gene.ids <- rownames(counts)
merged.sample.ids <- intersect(colnames(west.counts.temp), colnames(east.counts.temp))
merged.counts = data.frame(matrix(vector(), length(gene.ids),
  length(merged.sample.ids), dimnames=list(gene.ids, merged.sample.ids)),
  stringsAsFactors=F)

for (sample.id in merged.sample.ids) {
  merged.counts[, colnames(merged.counts) == sample.id] <- rowMeans(cbind(
    west.counts.temp[, colnames(west.counts.temp) == sample.id],
    east.counts.temp[, colnames(east.counts.temp) == sample.id]
  ))
}
```

```
  write.table(merged.counts, 'counts/merged-counts.tsv', sep='\t', quote=F, col.names=F)
  saveRDS(merged.counts[-1, ], 'r-data/merged.counts.rds')


  # Prepare timecourse for plotting
  timecourse <- data.frame(hour, side, t(counts))
  timecourse.sides <- data.frame(hour, side, t(counts[rownames(counts) != "Gene", ]))
  hour.merged <- as.numeric(merged.counts[rownames(merged.counts) == "Gene", ])
  timecourse.merged <- data.frame(hour = hour.merged, side = "Merged", t(merged.counts[rownames(merged.
  timecourse.all <- rbind(timecourse.sides, timecourse.merged)
  timecourse.all <- melt(timecourse.all, id.vars=c('hour', 'side'), variable.name='gene', value.name='c
  timecourse <- ddply(timecourse.all, .(hour, side, gene), summarize, mean=mean(counts), stderr=sqrt(va
  saveRDS(timecourse, 'r-data/timecourse.rds')
}

if(!exists("timecourse")) timecourse <- readRDS('r-data/timecourse.rds')

timecourse.summary.mean <- dcast(timecourse, gene ~ side + hour, value.var = "mean")
timecourse.summary.stderr <- dcast(timecourse, gene ~ side + hour, value.var = "stderr")
timecourse.summary <- merge(timecourse.summary.mean, timecourse.summary.stderr, by = 'gene', all = TRUE
names(timecourse.summary)[names(timecourse.summary) == 'gene'] <- 'GeneID'
```

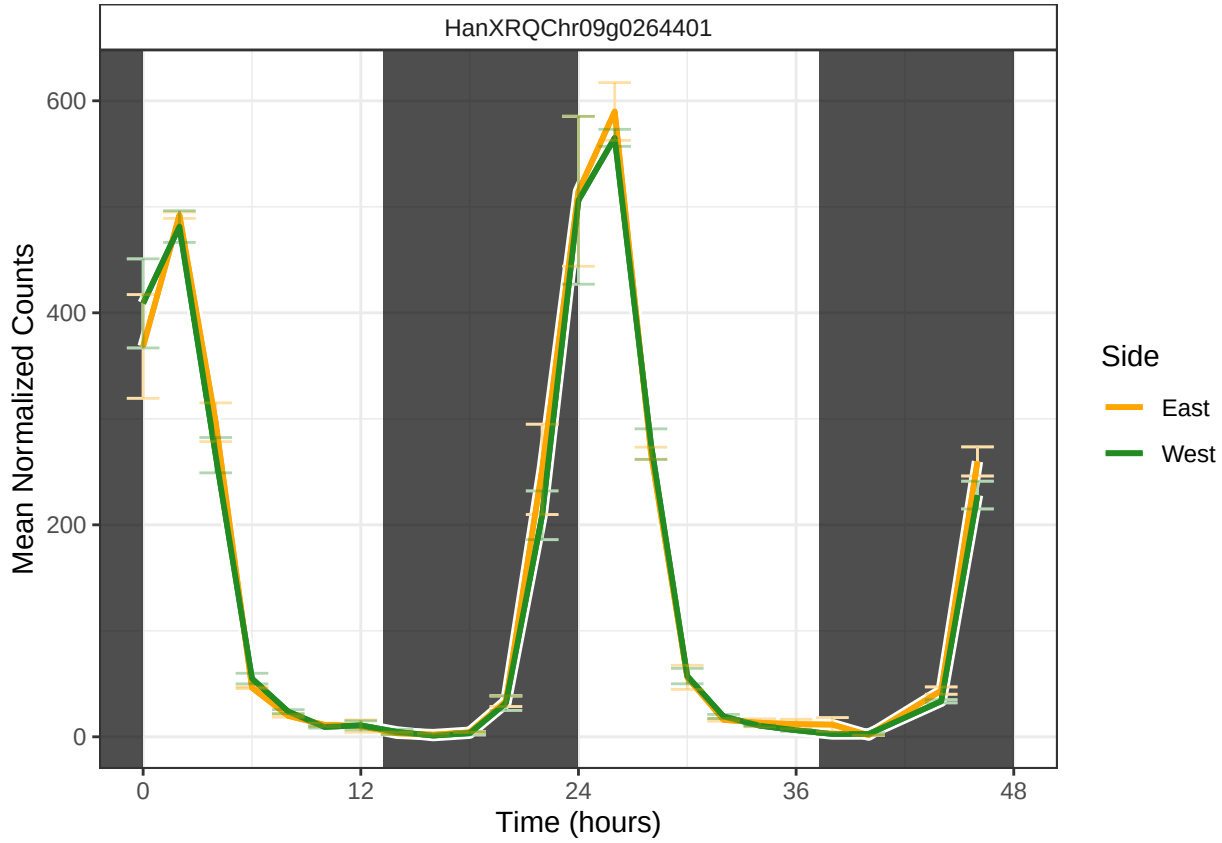
Function to plot timecourse data and demo

```
if (!dir.exists('plots')) dir.create('plots')

plot.timecourse <- function(gene.list, east.color='orange', west.color='forestgreen',
                            merged.color='black', plot.merged=FALSE,
                            double.plot=FALSE, side.by.side=FALSE, backlit=TRUE, theme.bw=TRUE,
                            lights.off=NULL, custom.daynight=NULL, night.alpha=0.7,
                            print.plot=TRUE, return.plot=FALSE, ncol=1, .timecourse=timecourse) {
  library(ggplot2)
  timecourse.subset <- .timecourse[.timecourse$gene %in% gene.list, ]
  if (plot.merged) {
    plot.colors <- c(east.color, west.color, merged.color)
  } else {
    plot.colors <- c(east.color, west.color)
    timecourse.subset <- subset(timecourse.subset, side != "Merged")
  }
  timecourse.subset$gene <- as.character(timecourse.subset$gene)

  if (double.plot) {
    timecourse.subset.copy <- timecourse.subset
    timecourse.subset.copy$hour <- timecourse.subset.copy$hour + 48
    timecourse.subset <- rbind(timecourse.subset, timecourse.subset.copy)
    x.breaks <- seq(0, 96, 12)
  } else {
    x.breaks <- seq(0, 48, 12)
  }

  p <- ggplot()

  daynight <- NULL
```

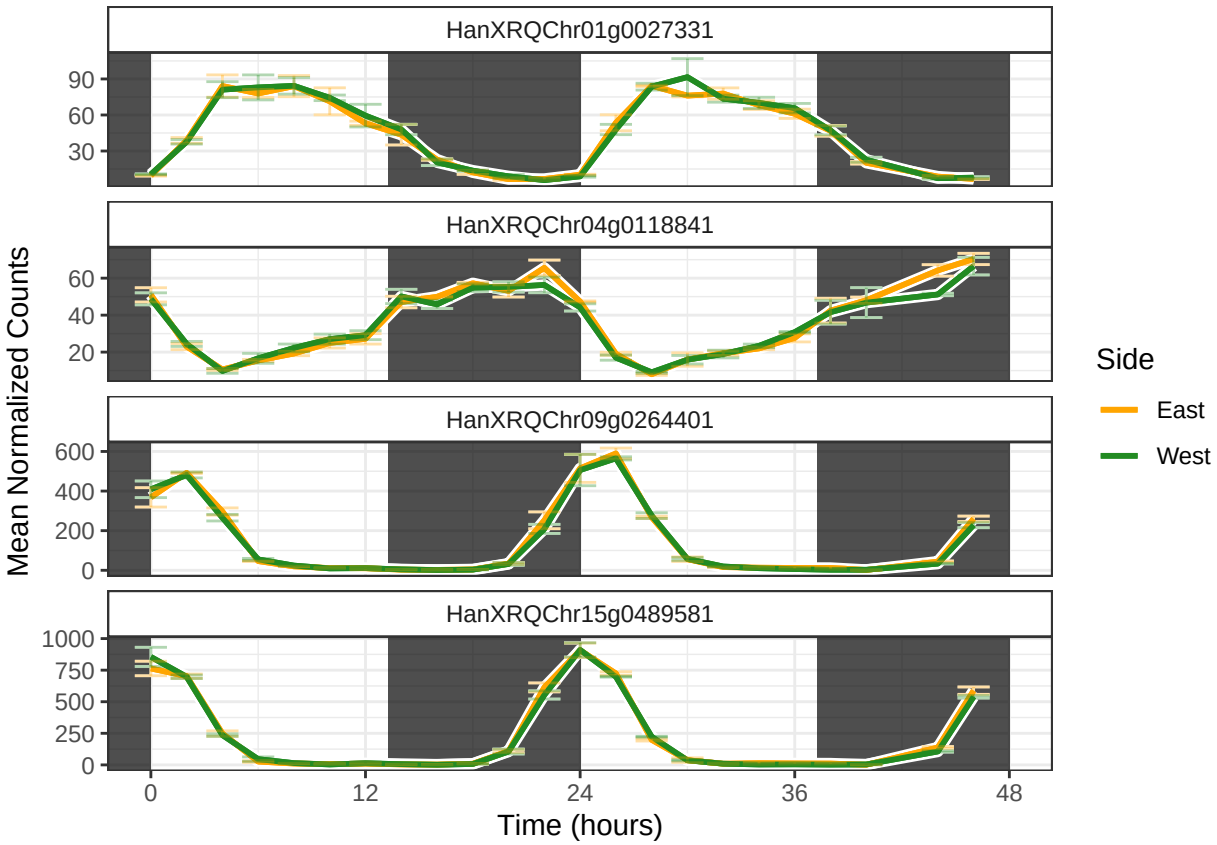
```
if(!is.null(custom.daynight)) {
  # Example of custom.daynight:
  # data.frame(daum=c(0, 24, 48, 72, 96), dusk=c(13.25 - 24, 13.25, 13.25 + 24, 13.25 + 48, 13.25 + 7
  daynight <- custom.daynight
} else if (!is.null(lights.off)) {
  lights.on <- seq(floor(min(timecourse.subset$hour) / 24), 24 * ceiling(max(timecourse.subset$hour) /
  daynight <- data.frame(dawn=lights.on, dusk=lights.on + lights.off %% 24 - 24)
}

if (!is.null(daynight)) {
  p <- p + geom_rect(data=daynight, aes(xmin=dawn, xmax=dusk), fill="black", ymin=-10000, ymax=10000,
}

if (backlit) {
   p <- p +
     geom_line(data=subset(timecourse.subset, side=='West'), aes(x=hour, y=mean), color='white', size=
     geom_line(data=subset(timecourse.subset, side=='East'), aes(x=hour, y=mean), color='white', size=

   if (plot.merged) {
     p <- p + geom_line(data=subset(timecourse.subset, side=='Merged'), aes(x=hour, y=mean), color='wh
   }

   p <- p +
     geom_errorbar(data=subset(timecourse.subset, side=='West'), aes(x=hour, ymin=mean-stderr, ymax=me
     geom_errorbar(data=subset(timecourse.subset, side=='East'), aes(x=hour, ymin=mean-stderr, ymax=me

   if (plot.merged) {
     p <- p + geom_errorbar(data=subset(timecourse.subset, side=='Merged'), aes(x=hour, ymin=mean-std
   }
}

p <- p +
     geom_line(data=timecourse.subset, aes(x=hour, y=mean, color=side), size=1) +
     geom_line(data=timecourse.subset, aes(x=hour, y=mean, color=side), size=1) +
     geom_errorbar(data=timecourse.subset, aes(x=hour, color=side, ymin=mean-stderr, ymax=mean+stderr)
     labs(x = 'Time (hours)', y = 'Mean Normalized Counts') +
     scale_x_continuous(breaks=x.breaks) +
     scale_color_manual(name='Side',values=plot.colors)

if (double.plot) {
  p <- p + coord_cartesian(xlim=c(0, 96), expand=T)
} else {
  p <- p + coord_cartesian(xlim=c(0, 48), expand=T)
}

if (side.by.side) {
  p <- p + facet_grid(gene ~ side, scales='free_y')
} else {
  p <- p + facet_wrap(~ gene, ncol=ncol, scales='free_y')
}

if (theme.bw) {
  p <- p + theme_bw() + theme(strip.background = element_rect(fill='white'))
```

```
  }

  if (print.plot) print(p)
  if (return.plot) p
}

demo.gene.list <- c('HanXRQChr09g0264401', 'HanXRQChr15g0489581', 'HanXRQChr04g0118841', 'HanXRQChr01g0
```

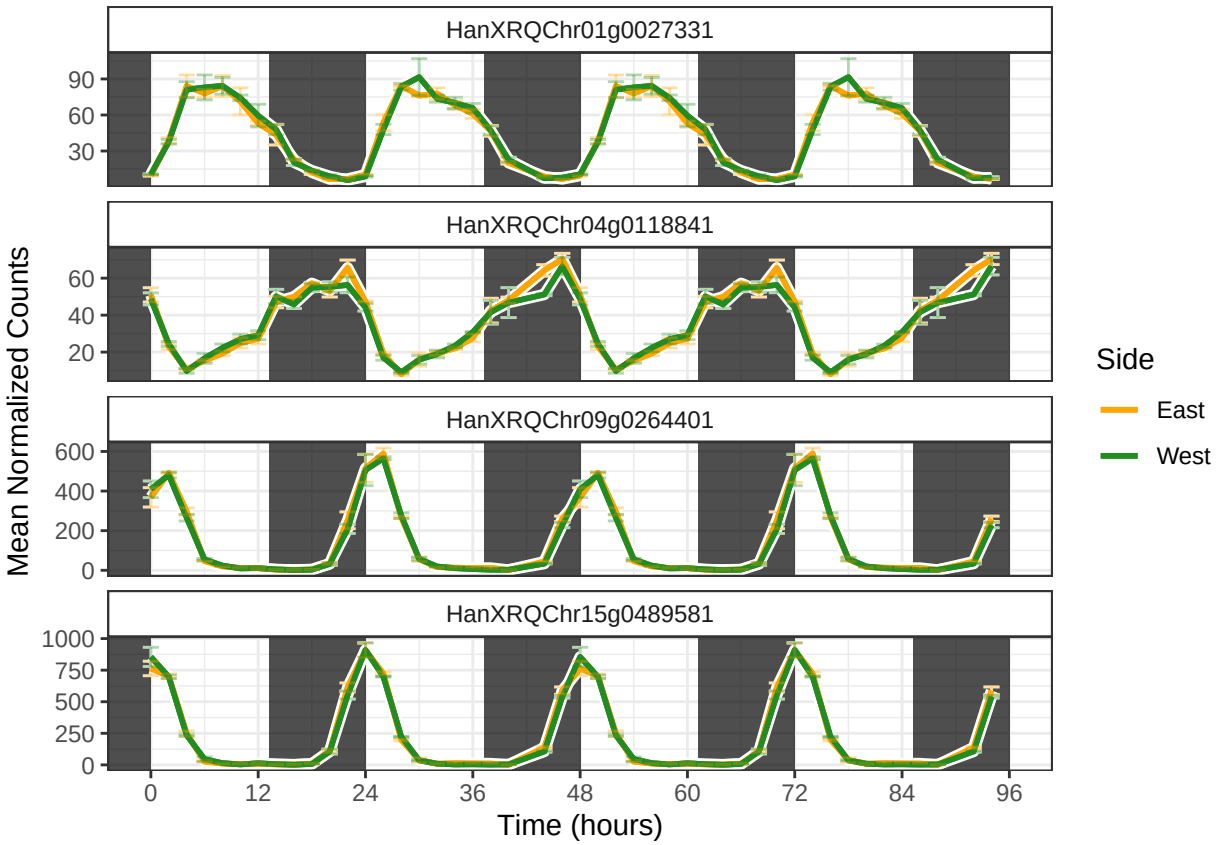
```
# Plot single gene
plot.timecourse(demo.gene.list[1], lights.off=13.25)
```



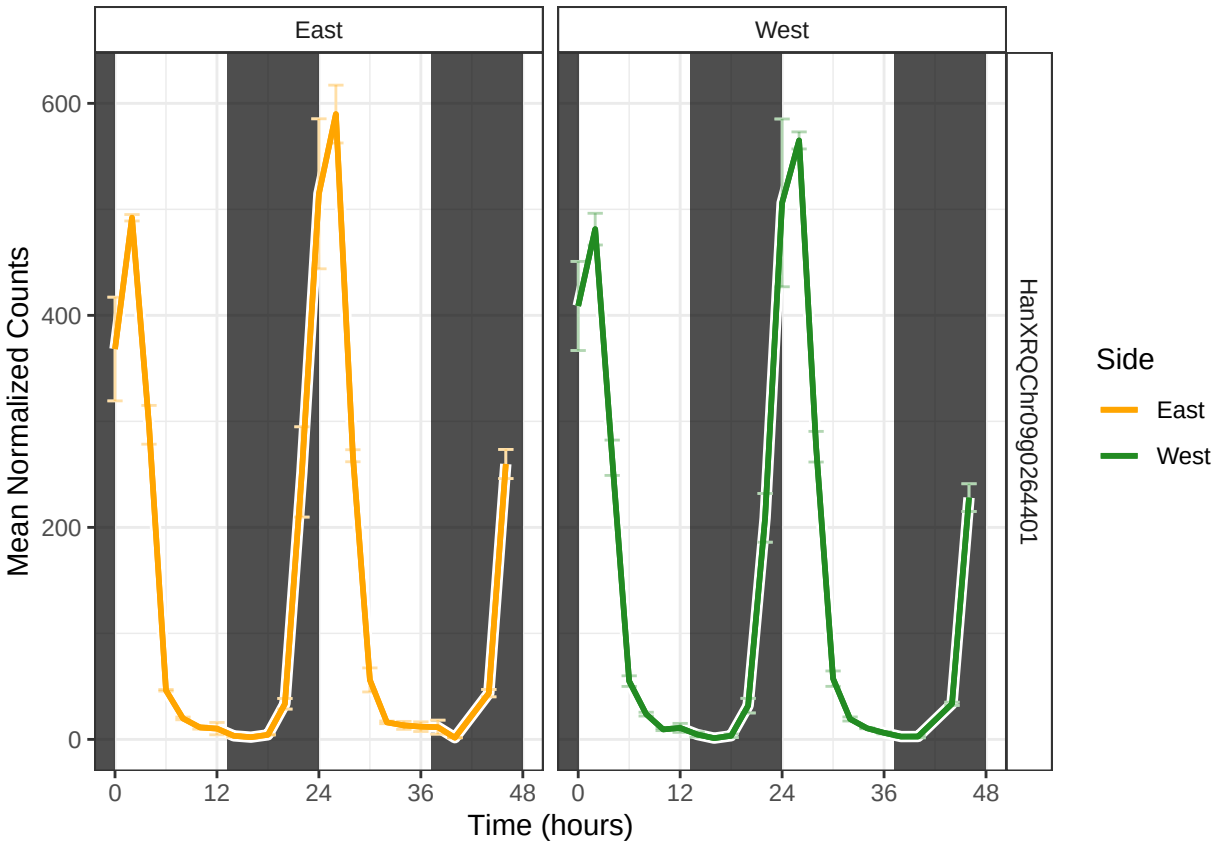

```
# Plot gene list
plot.timecourse(demo.gene.list, lights.off=13.25)
```



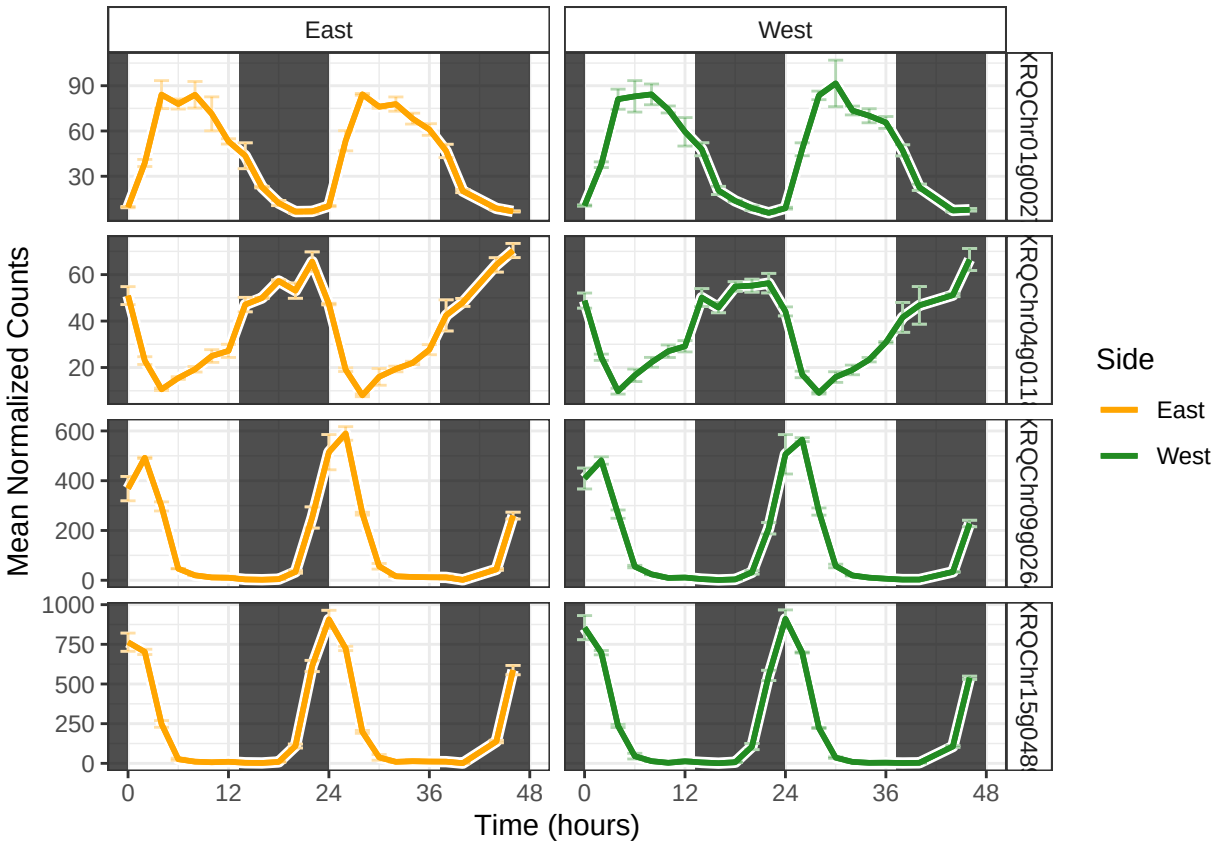

```
plot.timecourse(demo.gene.list, double.plot=TRUE, lights.off=13.25)
```



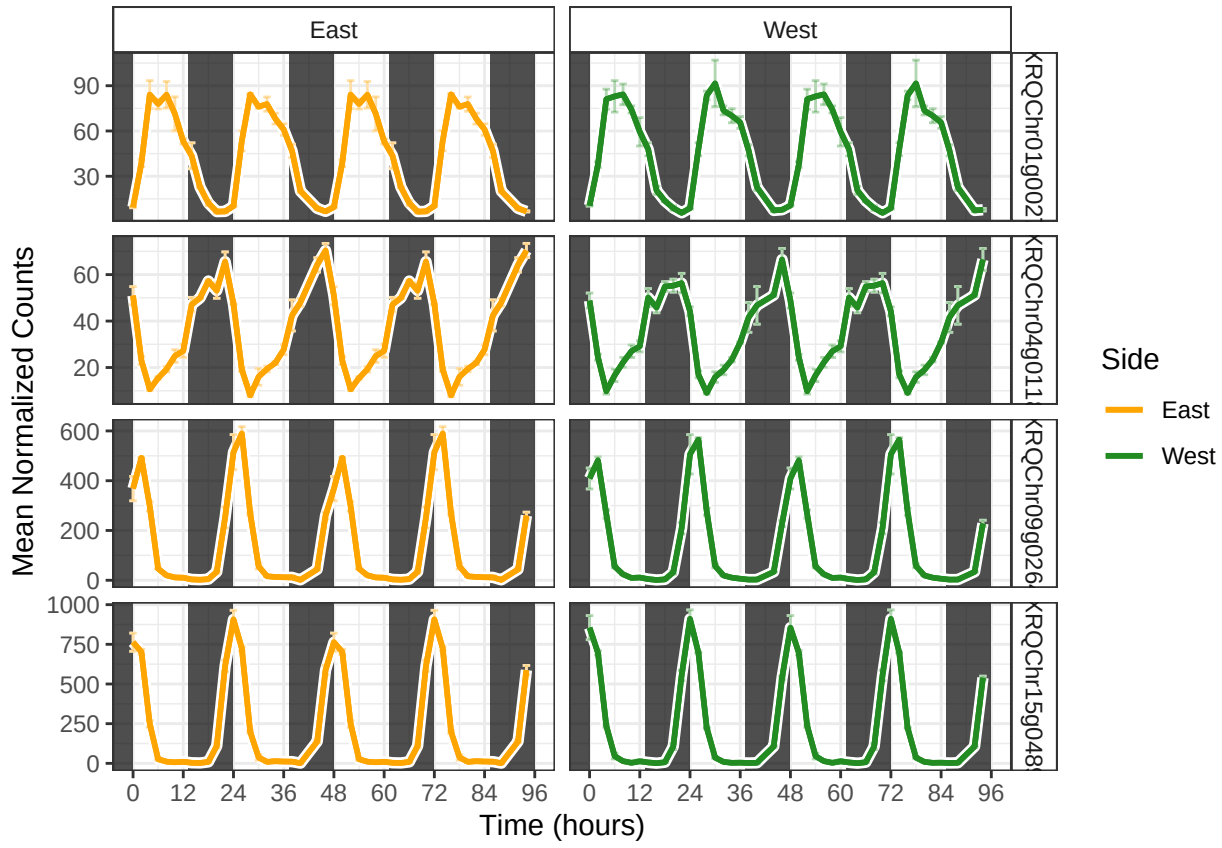

```
# Plot side-by-side
plot.timecourse(demo.gene.list[1], lights.off=13.25, side.by.side=TRUE)
```




```
plot.timecourse(demo.gene.list, lights.off=13.25, side.by.side=TRUE)
```




```
plot.timecourse(demo.gene.list, double.plot=TRUE, lights.off=13.25, side.by.side=TRUE)
```



Import COSOPT results and calculate additional metrics

We start with the COSOPT results files. They should have the folowing MD5 checksums:

```
4529c38ab3f52eb790416515f92774c3  cosopt/output-files/HA2015_HanXRQr1.0-East.cosopt-results.tsv
756c59834b09b678d05d4758bc995673  cosopt/output-files/HA2015_HanXRQr1.0-Merged.cosopt-results.tsv
f39d7991e9e917238172fd96d99bc38a  cosopt/output-files/HA2015_HanXRQr1.0-West.cosopt-results.tsv
```

```
md5sum(list.files('cosopt/output-files', pattern='.tsv', full.names=TRUE))
```

```
##   cosopt/output-files/HA2015_HanXRQr1.0-East.cosopt-results.tsv
##                               "4529c38ab3f52eb790416515f92774c3"
## cosopt/output-files/HA2015_HanXRQr1.0-Merged.cosopt-results.tsv
##                               "756c59834b09b678d05d4758bc995673"
##   cosopt/output-files/HA2015_HanXRQr1.0-West.cosopt-results.tsv
##                               "f39d7991e9e917238172fd96d99bc38a"
```

```
if (!dir.exists('cosopt-processed')) dir.create('cosopt-processed')

cosopt.east <- read.table('cosopt/output-files/HA2015_HanXRQr1.0-East.cosopt-results.tsv', h=T)
cosopt.merged <- read.table('cosopt/output-files/HA2015_HanXRQr1.0-Merged.cosopt-results.tsv', h=T)
cosopt.west <- read.table('cosopt/output-files/HA2015_HanXRQr1.0-West.cosopt-results.tsv', h=T)

cosopt.east$RelAmp <- cosopt.east$Beta / cosopt.east$MeanExpLev
cosopt.west$RelAmp <- cosopt.west$Beta / cosopt.west$MeanExpLev
cosopt.merged$RelAmp <- cosopt.merged$Beta / cosopt.merged$MeanExpLev
```

```r
cosopt.east$PeakPhase <- ifelse(cosopt.east$Phase <= 0, -cosopt.east$Phase, cosopt.east$Period - cosopt
cosopt.west$PeakPhase <- ifelse(cosopt.west$Phase <= 0, -cosopt.west$Phase, cosopt.west$Period - cosopt
cosopt.merged$PeakPhase <- ifelse(cosopt.merged$Phase <= 0, -cosopt.merged$Phase, cosopt.merged$Period

cosopt.east$PeakPhase[cosopt.east$PeakPhase >= 24] <- cosopt.east$PeakPhase[cosopt.east$PeakPhase >= 24
cosopt.west$PeakPhase[cosopt.west$PeakPhase >= 24] <- cosopt.west$PeakPhase[cosopt.west$PeakPhase >= 24
cosopt.merged$PeakPhase[cosopt.merged$PeakPhase >= 24] <- cosopt.merged$PeakPhase[cosopt.merged$PeakPhas


cosopt <- merge(cosopt.west, cosopt.east, by = 'GeneID', all = TRUE, suffixes = c('.W', '.E'))
cosopt <- merge(cosopt, cosopt.merged, by = 'GeneID', all = TRUE)


cosopt <- cosopt[, order(names(cosopt))]
rownames(cosopt) <- cosopt$GeneID

cosopt$phase.diff <- ifelse(
  abs(cosopt$PeakPhase.W - cosopt$PeakPhase.E) <= 12,
  cosopt$PeakPhase.W - cosopt$PeakPhase.E,
  ifelse(
    cosopt$PeakPhase.W - cosopt$PeakPhase.E < 0,
    cosopt$PeakPhase.W - cosopt$PeakPhase.E + 24,
    cosopt$PeakPhase.W - cosopt$PeakPhase.E - 24))

cosopt$amp.diff <- cosopt$RelAmp.W - cosopt$RelAmp.E

cosopt$exp.diff.log2 <- log(cosopt$MeanExpLev.W / cosopt$MeanExpLev.E, 2)

cosopt.processed.file <- 'cosopt-processed/cosopt-processed.txt'
write.table(cosopt, cosopt.processed.file, sep = "\t", quote = FALSE, col.names=NA)


# Expressed Genes

get.expressed.genes <- function(min.meanexplev = NULL, min.expressed.count = NULL) {
  if(is.null(min.meanexplev)) stop("No minimum expression level given.")

  mean.expression <- data.frame(
    east = rowMeans(timecourse.summary.mean[, grepl("East", names(timecourse.summary.mean))]),
    west = rowMeans(timecourse.summary.mean[, grepl("West", names(timecourse.summary.mean))]),
    merged = rowMeans(timecourse.summary.mean[, grepl("Merged", names(timecourse.summary.mean))])
  )
  rownames(mean.expression) <- timecourse.summary.mean$gene

  if(is.null(min.expressed.count)) {
    expressed.genes <- as.data.frame(mean.expression >= min.meanexplev)
    rownames(expressed.genes) <- rownames(mean.expression)
  } else {
    expressed.frequency <- data.frame(
      east = rowSums(timecourse.summary.mean[, grepl("East", names(timecourse.summary.mean))] > min.mean
      west = rowSums(timecourse.summary.mean[, grepl("West", names(timecourse.summary.mean))] > min.mean
      merged = rowSums(timecourse.summary.mean[, grepl("Merged", names(timecourse.summary.mean))] > min
    )
```

```
    rownames(expressed.frequency) <- timecourse.summary.mean$gene
    expressed.genes <- as.data.frame(expressed.frequency >= min.expressed.count)
    rownames(expressed.genes) <- rownames(expressed.frequency)
  }

  out <- list()
  out$mean.expression <- mean.expression
  out$expressed.genes <- expressed.genes
  return(out)
}

expressed.genes <- get.expressed.genes(
  min.meanexplev = min.meanexplev, min.expressed.count = min.expressed.count)
expressed <- expressed.genes$expressed
mean.expression <- expressed.genes$mean.expression

#Expressed in East: 40,291
sum(expressed$east)
```

```
## [1] 40291
```

```
#Expressed in West: 40,354
sum(expressed$west)
```

```
## [1] 40354
```

```
#Expressed in Merged: 40,228
sum(expressed$merged)
```

```
## [1] 40228
```

```
#Expressed in East or West: 40,739
sum(expressed$east | expressed$west)
```

```
## [1] 40739
```

```
#Expressed in East and West: 39,906
sum(expressed$east & expressed$west)
```

```
## [1] 39906
```

```
#Expressed in East, West, and Merged: 39,832
sum(expressed$east & expressed$west & expressed$merged)
```

```
## [1] 39832
```

```
#Expressed in East, West, or Merged: 40,781
sum(expressed$east | expressed$west | expressed$merged)
```

```
## [1] 40781
```

```
# Get rhythmic genes
rhythmic.east <- as.character(cosopt.east$GeneID[cosopt.east$pMMC.Beta < min.p.mmc.beta & cosopt.east$G
rhythmic.west <- as.character(cosopt.west$GeneID[cosopt.west$pMMC.Beta < min.p.mmc.beta & cosopt.west$G
rhythmic.both <- intersect(rhythmic.east, rhythmic.west)
rhythmic.merged <- as.character(cosopt.merged$GeneID[cosopt.merged$pMMC.Beta < min.p.mmc.beta & cosopt.m
rhythmic.all <- intersect(rhythmic.both, rhythmic.merged)
rhythmic.any <- union(rhythmic.merged, union(rhythmic.east, rhythmic.west))
```

```
length(intersect(rhythmic.merged, rhythmic.east))
```

```
## [1] 22005
```

```
# [1] 22005
length(intersect(rhythmic.merged, rhythmic.west))
```

```
## [1] 22014
```

```
# [1] 22014


rhythmic.east.only <- setdiff(rhythmic.east, rhythmic.both)
rhythmic.west.only <- setdiff(rhythmic.west, rhythmic.both)

length(rhythmic.east)
```

```
## [1] 23083
```

```
# [1] 23083
length(rhythmic.west)
```

```
## [1] 23172
```

```
# [1] 23172
length(rhythmic.merged)
```

```
## [1] 25778
```

```
# [1] 25778

length(rhythmic.both)
```

```
## [1] 19447
```

```
# [1] 19447
length(rhythmic.all)
```

```
## [1] 19409
```

```
# [1] 19409
length(rhythmic.any)
```

```
## [1] 27976
```

```
# [1] 27976

length(rhythmic.east.only)
```

```
## [1] 3636
```

```
# [1] 3636
length(rhythmic.west.only)
```

```
## [1] 3725
```

```
# [1] 3725


if (!dir.exists('rhythmic-genes')) dir.create('rhythmic-genes')
write.table(sort(rhythmic.east), "rhythmic-genes/rhythmic-east.txt", sep = "\t", quote = FALSE, col.nam
```

```
write.table(sort(rhythmic.west), "rhythmic-genes/rhythmic-west.txt", sep = "\t", quote = FALSE, col.name
write.table(sort(rhythmic.merged), "rhythmic-genes/rhythmic-merged.txt", sep = "\t", quote = FALSE, col
```

Rhythmic Counts Summary:

```
Total # of Genes: 49,262
Total # of Expressed Genes:

    East: 40,291
    West: 40,354
    East or West: 40,739
    East and West: 39,906
    Merged: 40,228
    East, West, or Merged: 39,832
    East, West, and Merged: 40,781


Rhythmic Genes in East or West time course: 26,808

    East only: 3,636 (13.6%)
    West only: 3,725 (13.9%)
    Both East and West: 19,447 (72.5%)

Rhythmic Genes in Merged time course: 25,778
Rhythmic Genes in any time course (East, West, and Merged): 27,976
Rhythmic Genes in all three time courses (East, West, and Merged): 19,409
```

	Rhythmic	Expressed	% Rhythmic
East	23,083	40,291	57.3%
West	23,172	40,354	57.4%
East or West	26,808	40,739	65.8%
East and West	19,447	39,906	48.7%
Merged	25,778	40,228	64.1%
East, West, or Merged	27,976	39,832	70.2%
East, West, and Merged	19,409	40,781	47.6%

Venn Diagram of Rhythmic Genes

```
threeway.Venn <- function(A, B, C, cat.names = c("A", "B", "C")){
  area1 <- length(A)
  area2 <- length(B)
  area3 <- length(C)
  n12 <- length(intersect(A,B))
  n23 <- length(intersect(B,C))
  n13 <- length(intersect(A,C))
  n123 <- length(intersect(intersect(A, B), intersect(B,C )))
  venn.plot <- draw.triple.venn(
    area1 = area1,
    area2 = area2,
    area3 = area3,
    n12 = n12,
    n23 = n23,
    n13 = n13,
    n123 = n123,
```

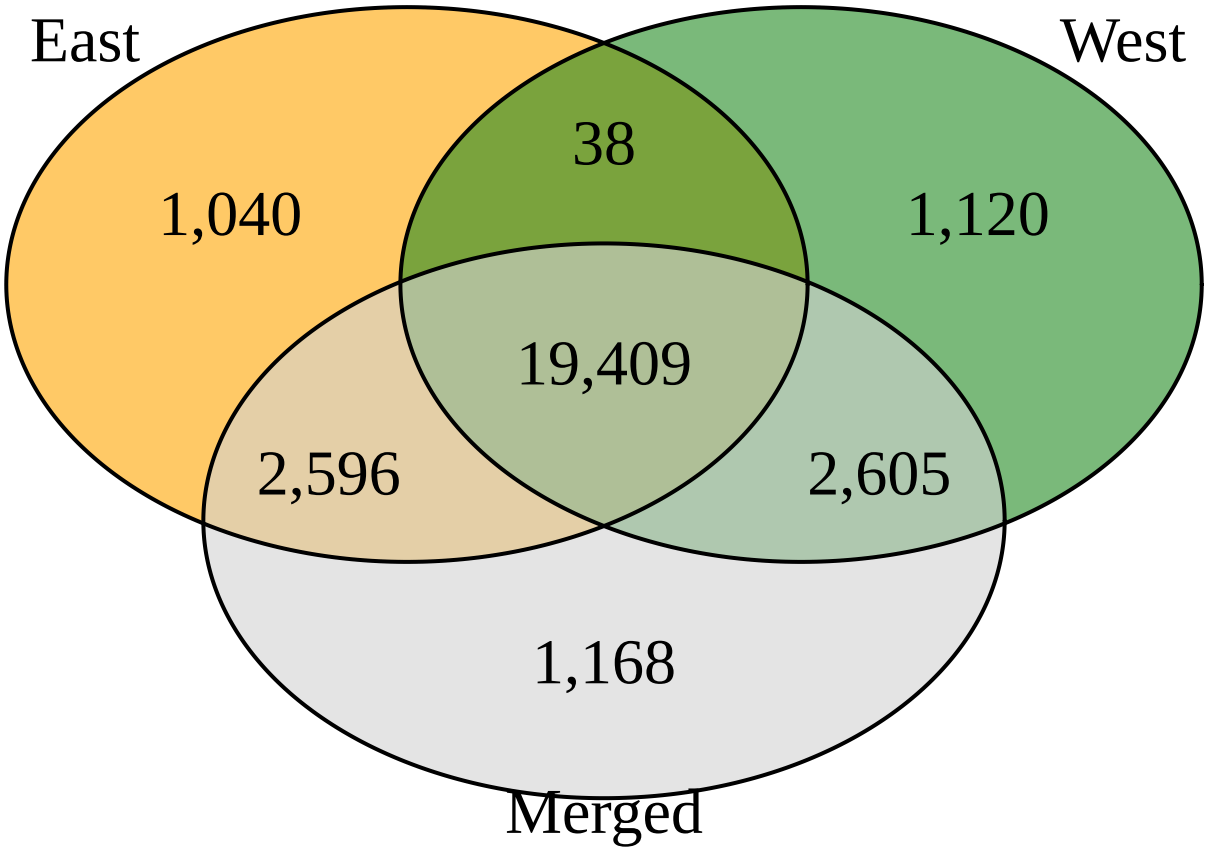
```
    category = cat.names,
    fill = c("orange", "forestgreen", "lightgray"),
    alpha = .6,
    cex = 2,
    cat.cex = 2,
  )

  # Add comma separators for larger numbers (https://stackoverflow.com/a/37240111/996114)
  idx <- sapply(venn.plot, function(i) grepl("text", i$name))
  for(i in 1:7){
    venn.plot[idx][[i]]$label <- format(as.numeric(venn.plot[idx][[i]]$label), big.mark=",", scientific=
  }
  venn.plot
}

png('plots/venn-rhythmic.png', w=7, h=7, u='in', res=150)
venn.rhythms <- threeway.Venn(rhythmic.east, rhythmic.west, rhythmic.merged, cat.names = c('East', 'West
grid.newpage()
grid.draw(venn.rhythms)
dev.off()
```

```
## pdf
##   2
```

```
pdf('plots/venn-rhythmic.pdf', w=7, h=7, useDingbats = FALSE)
grid.draw(venn.rhythms)
dev.off()
```

```
## pdf
##   2
```

```
grid.newpage()
grid.draw(venn.rhythms)
```

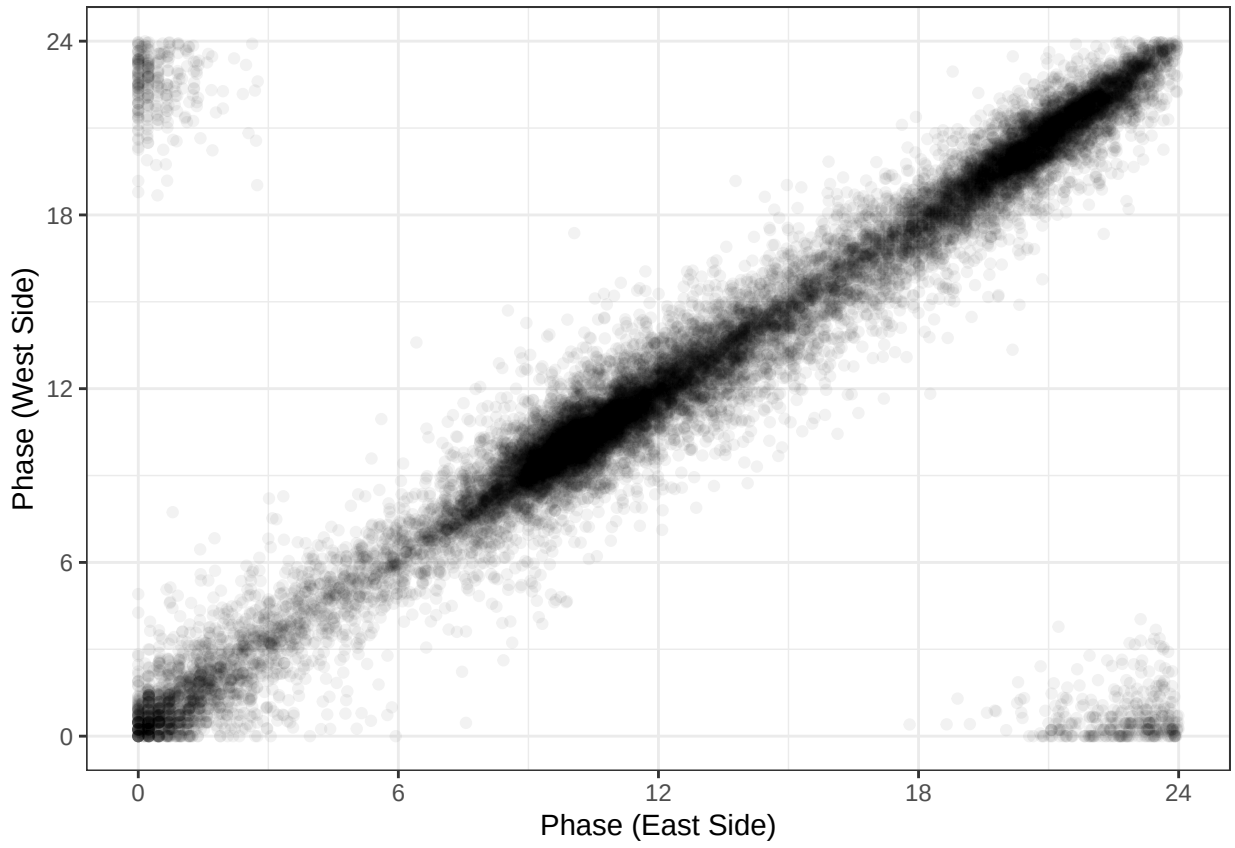


West vs East Phase

```
cor(subset(cosopt.east, GeneID %in% rhythmic.both)$PeakPhase, subset(cosopt.west, GeneID %in% rhythmic.b
```

```
## [1] -0.0003668416
```

```
cosopt.both <- subset(cosopt, GeneID %in% rhythmic.both)
ggplot(cosopt.both) +
  geom_point(aes(x = PeakPhase.E, y = PeakPhase.W), alpha=0.05) +
  scale_x_continuous(breaks=seq(0, 24, 6)) +
  scale_y_continuous(breaks=seq(0, 24, 6)) +
  xlab('Phase (East Side)') +
  ylab('Phase (West Side)') +
  theme_bw()
```




```
ggsave('plots/phases.west-vs-east.png', w=6, h=6)
ggsave('plots/phases.west-vs-east.pdf', w=6, h=6, useDingbats = FALSE)
```

Process Data for Phase Histograms

```
cosopt.east$side <- 'East'
cosopt.west$side <- 'West'
cosopt.east.west <- rbind(cosopt.east, cosopt.west)

histogram.data <- cosopt.east.west[cosopt.east.west$GeneID %in% rhythmic.both, c('GeneID', 'PeakPhase',
histogram.data <- subset(histogram.data, GeneID %in% rhythmic.both)
histogram.data$window <- 1
histogram.data.pre <- histogram.data
histogram.data.pre$PeakPhase <- histogram.data.pre$PeakPhase - 24
histogram.data.pre$window <- 0
histogram.data.post <- histogram.data
histogram.data.post$PeakPhase <- histogram.data.post$PeakPhase + 24
histogram.data.post$window <- 2

histogram.data.combined <- rbind(histogram.data.pre, histogram.data, histogram.data.post)

daynight <- data.frame(dawn=c(0, 24, 48, 72, 96), dusk=c(13.25 - 24, 13.25, 13.25 + 24, 13.25 + 48, 13.

temperatures <- read.table('environmental-data/temp-data-table.txt', sep="\t", header=TRUE)
temperatures$ScaledTempC <- ((temperatures$TempC - min(temperatures$TempC))* 1500) / (max(temperatures$

temperature.stats <- ddply(temperatures, .(Time), summarize, mean=mean(TempC), stderr=sqrt(var(TempC,na
```

```
##   |                                                                      |
```

```
temperature.stats.scaled <- ddply(temperatures, .(Time), summarize, mean=mean(ScaledTempC), stderr=sqrt
```

```
##   |                                                                      |
```

```
temperatures
```

```
##          Time TempC ScaledTempC
## 1  -0.6333333    17    157.8947
## 2  -0.6333333    17    157.8947
## 3   0.3666667    15      0.0000
## 4   0.3666667    17    157.8947
## 5   1.3666667    17    157.8947
## 6   1.3666667    18    236.8421
## 7   2.3666667    18    236.8421
## 8   2.3666667    19    315.7895
## 9   3.3666667    20    394.7368
## 10  3.3666667    22    552.6316
## 11  4.3666667    23    631.5789
## 12  4.3666667    24    710.5263
## 13  5.3666667    25    789.4737
## 14  5.3666667    26    868.4211
## 15  6.3666667    28   1026.3158
## 16  6.3666667    29   1105.2632
## 17  7.3666667    29   1105.2632
## 18  7.3666667    31   1263.1579
## 19  8.3666667    31   1263.1579
## 20  8.3666667    33   1421.0526
## 21  9.3666667    32   1342.1053
## 22  9.3666667    34   1500.0000
## 23 10.3666667    32   1342.1053
## 24 10.3666667    34   1500.0000
## 25 11.3666667    32   1342.1053
## 26 11.3666667    34   1500.0000
## 27 12.3666667    29   1105.2632
## 28 12.3666667    33   1421.0526
## 29 13.3666667    27    947.3684
## 30 13.3666667    30   1184.2105
## 31 14.3666667    24    710.5263
## 32 14.3666667    26    868.4211
## 33 15.3666667    22    552.6316
## 34 15.3666667    23    631.5789
## 35 16.3666667    21    473.6842
## 36 16.3666667    21    473.6842
## 37 17.3666667    20    394.7368
## 38 17.3666667    21    473.6842
## 39 18.3666667    20    394.7368
## 40 18.3666667    20    394.7368
## 41 19.3666667    19    315.7895
## 42 19.3666667    19    315.7895
## 43 20.3666667    19    315.7895
## 44 20.3666667    19    315.7895
## 45 21.3666667    19    315.7895
## 46 21.3666667    18    236.8421
```

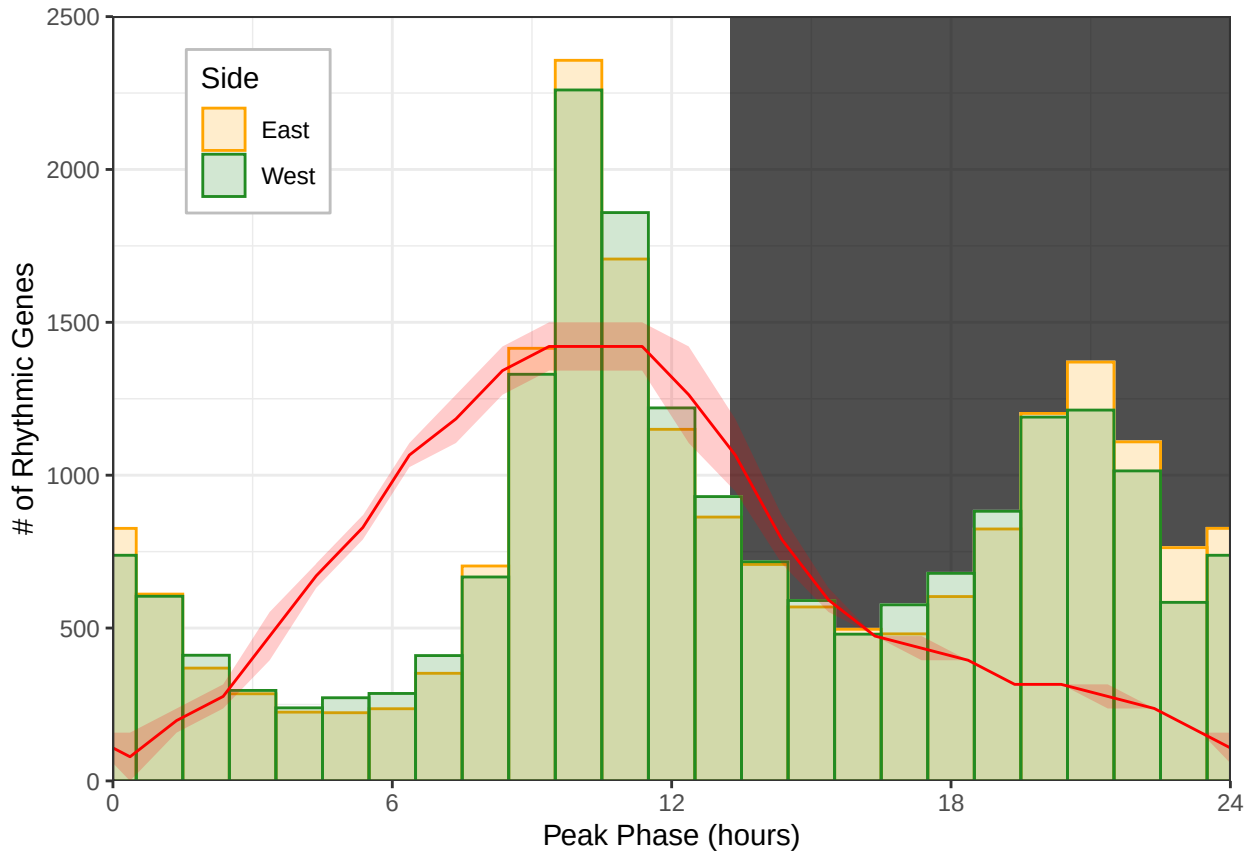
```
## 47 22.3666667    18    236.8421
## 48 22.3666667    18    236.8421
## 49 23.3666667    17    157.8947
## 50 23.3666667    17    157.8947
## 51 24.3666667    15      0.0000
## 52 24.3666667    17    157.8947
```

```
temperature.stats
```

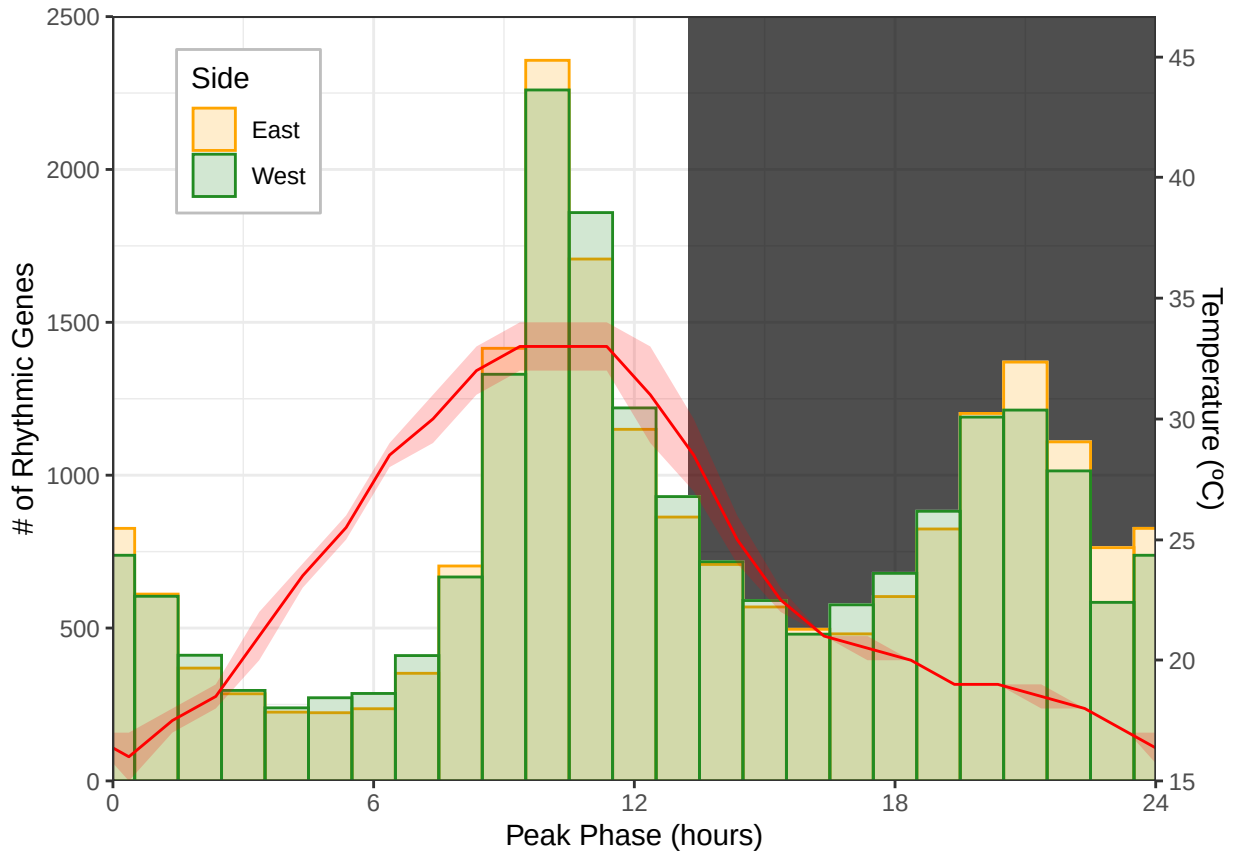
```
##          Time mean stderr
## 1  -0.6333333 17.0    0.0
## 2   0.3666667 16.0    1.0
## 3   1.3666667 17.5    0.5
## 4   2.3666667 18.5    0.5
## 5   3.3666667 21.0    1.0
## 6   4.3666667 23.5    0.5
## 7   5.3666667 25.5    0.5
## 8   6.3666667 28.5    0.5
## 9   7.3666667 30.0    1.0
## 10  8.3666667 32.0    1.0
## 11  9.3666667 33.0    1.0
## 12 10.3666667 33.0    1.0
## 13 11.3666667 33.0    1.0
## 14 12.3666667 31.0    2.0
## 15 13.3666667 28.5    1.5
## 16 14.3666667 25.0    1.0
## 17 15.3666667 22.5    0.5
## 18 16.3666667 21.0    0.0
## 19 17.3666667 20.5    0.5
## 20 18.3666667 20.0    0.0
## 21 19.3666667 19.0    0.0
## 22 20.3666667 19.0    0.0
## 23 21.3666667 18.5    0.5
## 24 22.3666667 18.0    0.0
## 25 23.3666667 17.0    0.0
## 26 24.3666667 16.0    1.0
```

Plot Phase Histograms

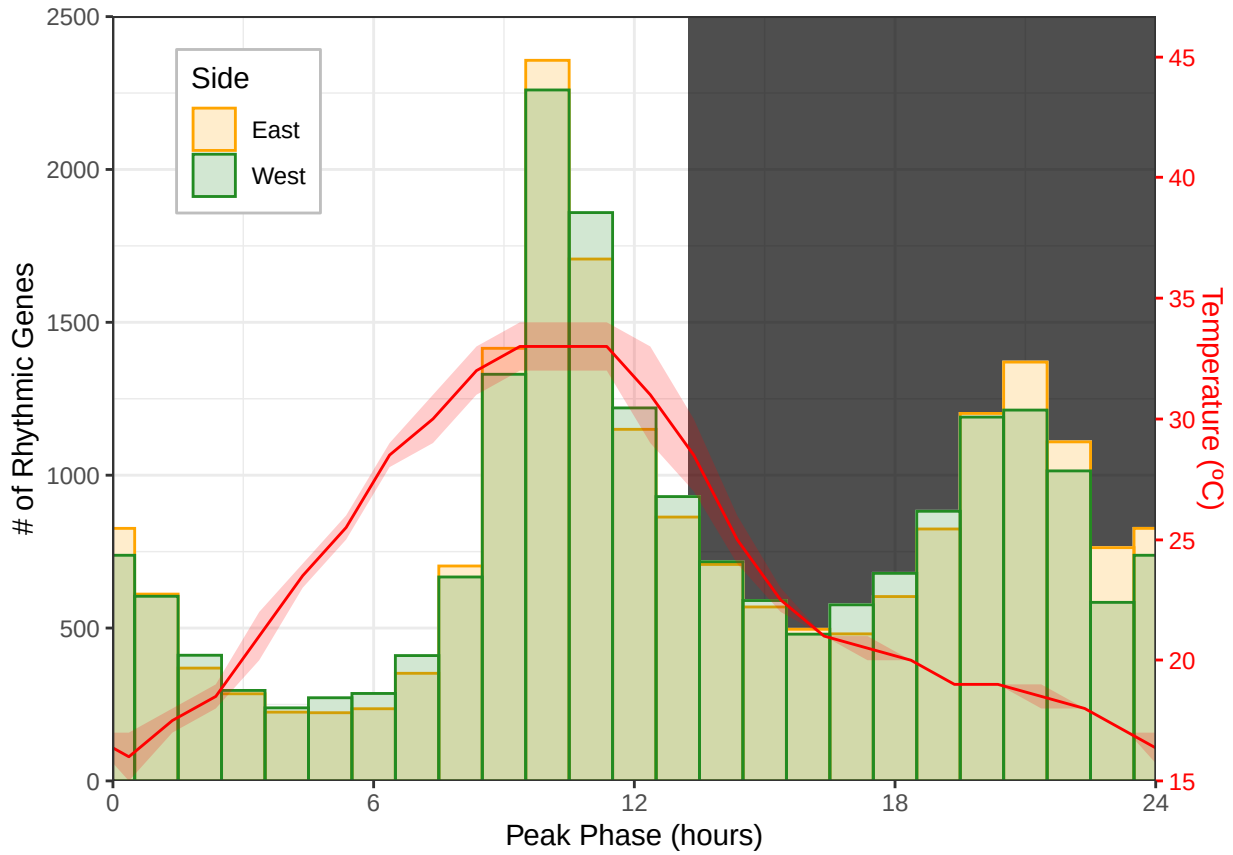
```
p <- ggplot() +
  geom_rect(data=daynight, aes(xmin=dawn, xmax=dusk), fill='black', ymin=-10000, ymax=10000, alpha=0.7) +
  geom_histogram(data=subset(histogram.data.combined, side=='West'), aes(x=PeakPhase, y=..count..), col
  geom_histogram(data=subset(histogram.data.combined, side=='East'), aes(x=PeakPhase, y=..count..), col
  geom_histogram(data=histogram.data.combined, aes(x=PeakPhase, color=side, fill=side, y=..count..), al
  geom_ribbon(data=temperature.stats.scaled, aes(x=Time, ymin=min, ymax=max), fill='red', alpha=0.2) +
  geom_line(data=temperature.stats.scaled, aes(x=Time, y=mean), color='red') +
  labs(x = 'Peak Phase (hours)', y = '# of Rhythmic Genes') +
  scale_color_manual(name = 'Side',values = c(east.color, west.color)) +
  scale_fill_manual(name = 'Side',values = c(east.color, west.color)) +
  scale_x_continuous(breaks=seq(0, 24, 6)) +
  coord_cartesian(xlim=c(0, 24), ylim=c(0, 2500), expand=F) +
  theme_bw() +
  theme(legend.position = c(.13, .85), legend.background = element_rect(linetype = 'solid',colour = 'gra
p
```



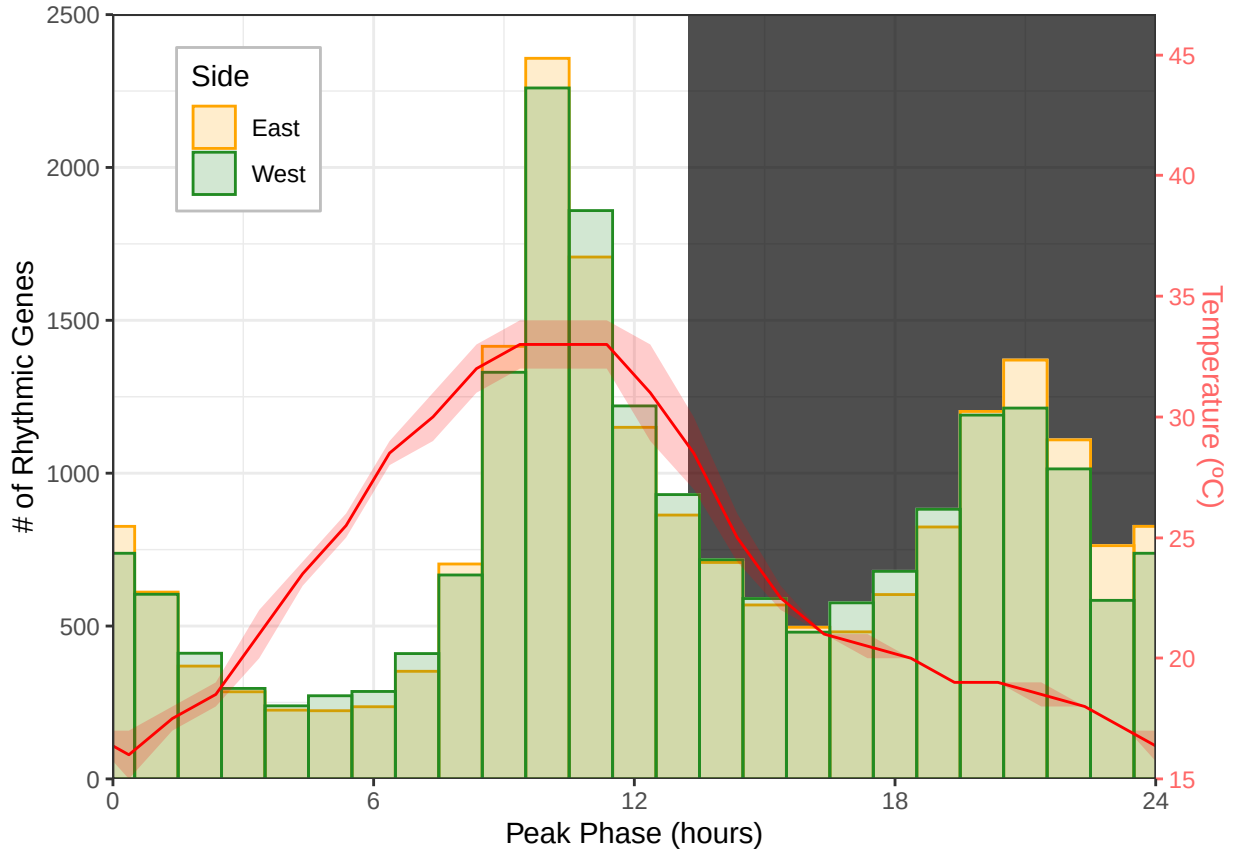

```
ggsave('plots/phase-histogram.temperature.png', w=6, h=5)
ggsave('plots/phase-histogram.temperature.pdf', w=6, h=5, useDingbats = FALSE)


scale_m <- (max(temperatures$TempC) - min(temperatures$TempC)) / (1500 - p$coordinates$limits$y[1])
scale_b <- min(temperatures$TempC)
scale_temp_max <- p$coordinates$limits$y[2] * scale_m + scale_b
scale_temp_min <- min(temperatures$TempC)
p + scale_y_continuous(sec.axis = sec_axis(~.*scale_m + scale_b, name = "Temperature (ºC)", breaks=seq(s
```




```
ggsave('plots/phase-histogram.temperature-axis.png', w=6, h=5)
ggsave('plots/phase-histogram.temperature-axis.pdf', w=6, h=5, useDingbats = FALSE)


p + scale_y_continuous(sec.axis = sec_axis(~.*scale_m + scale_b, name = "Temperature (ºC)", breaks=seq(
  theme(
    axis.title.y.right = element_text(color = "red"),
    axis.text.y.right = element_text(color = "red"),
    axis.ticks.y.right = element_line(color = "red"),
  )
```




```
ggsave('plots/phase-histogram.temperature-axis-red.png', w=6, h=5)
ggsave('plots/phase-histogram.temperature-axis-red.pdf', w=6, h=5, useDingbats = FALSE)


p + scale_y_continuous(sec.axis = sec_axis(~.*scale_m + scale_b, name = "Temperature (ºC)", breaks=seq(
  theme(
    axis.title.y.right = element_text(color = alpha("red", 0.6)),
    axis.text.y.right = element_text(color = alpha("red", 0.6)),
    axis.ticks.y.right = element_line(color = alpha("red", 0.6)),
  )
```




```
ggsave('plots/phase-histogram.temperature-axis-lightred.png', w=6, h=5)
ggsave('plots/phase-histogram.temperature-axis-lightred.pdf', w=6, h=5, useDingbats = FALSE)
```

The `cosopt-processed.txt` file that we just generated should have an MD5 checksum of `2fda73974466f805a22b1941b3f958f`

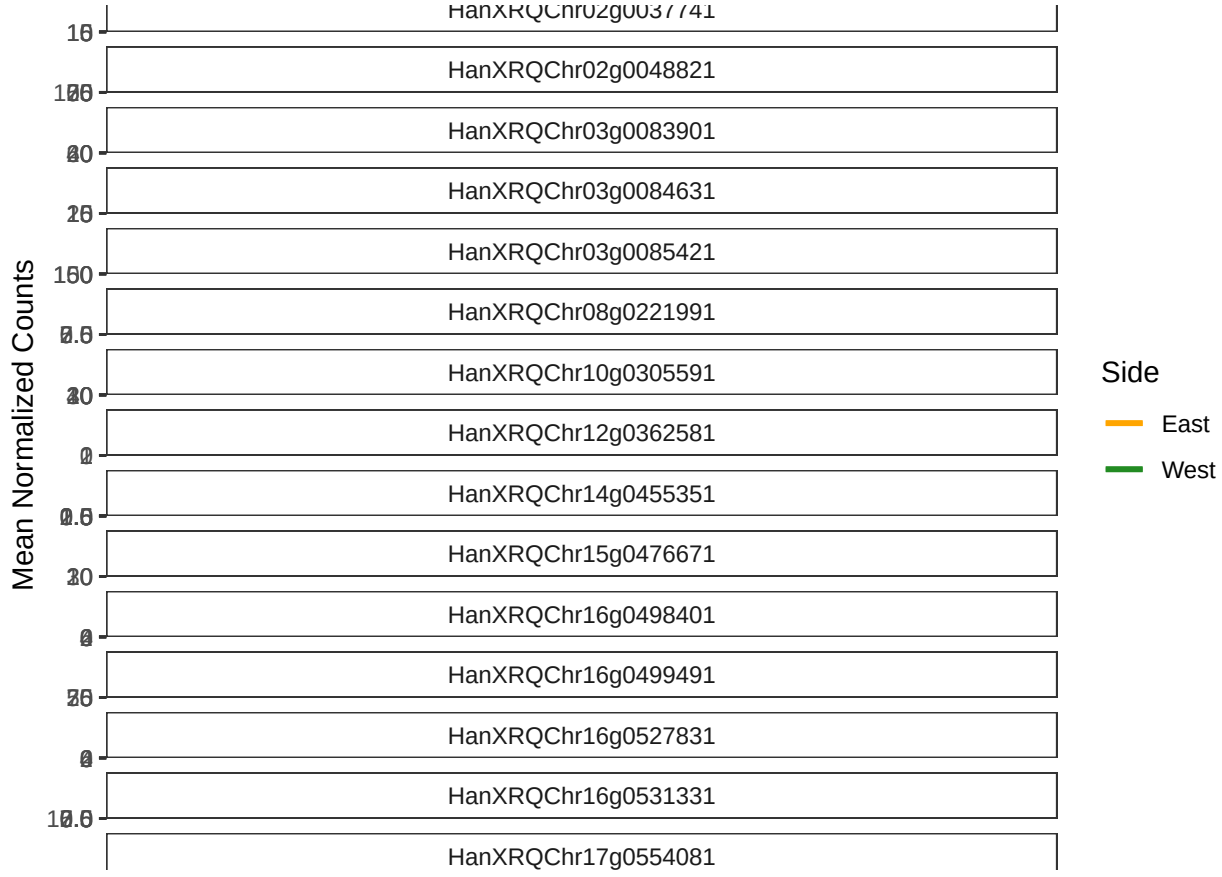
```
md5sum(cosopt.processed.file)
```

```
## cosopt-processed/cosopt-processed.txt
##    "713a7ed174948290a41708e29e9d65ab"
```

Plot Amplitude Differences Summary

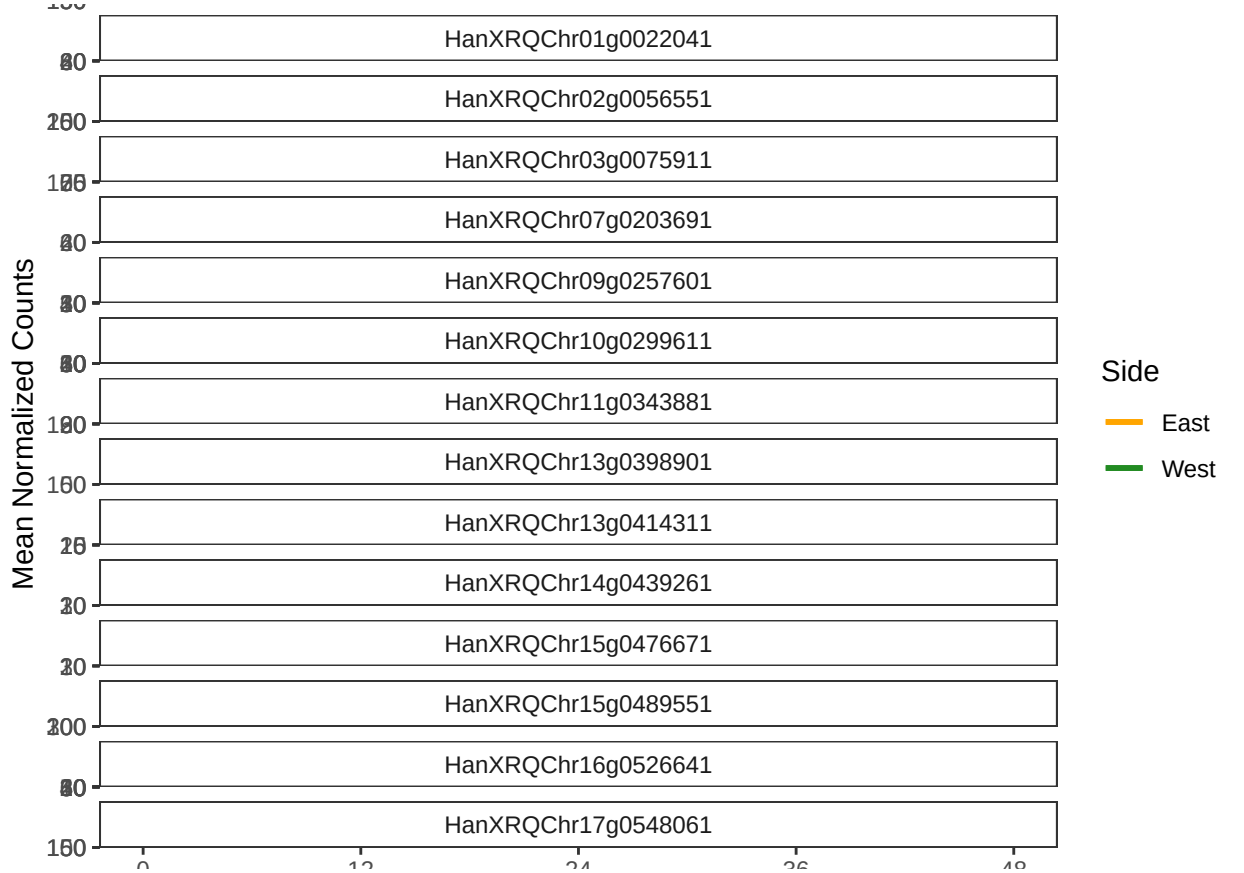
```
plot.ampdiff.summary <- function() {
  timecourse.subset <- subset(timecourse, side != "Merged")
  timecourse.w <- subset(timecourse.subset, gene %in% west.high)
  timecourse.e <- subset(timecourse.subset, gene %in% east.high)

  timecourse.w <- merge(timecourse.w, cosopt[, c('GeneID', 'MeanExpLev')], by.x='gene', by.y='GeneID')
  timecourse.e <- merge(timecourse.e, cosopt[, c('GeneID', 'MeanExpLev')], by.x='gene', by.y='GeneID')

  timecourse.w$mean.norm <- timecourse.w$mean / timecourse.w$MeanExpLev
  timecourse.e$mean.norm <- timecourse.e$mean / timecourse.e$MeanExpLev

  timecourse.w <- dcast(timecourse.w, hour ~ side, mean, value.var='mean.norm')
  timecourse.e <- dcast(timecourse.e, hour ~ side, mean, value.var='mean.norm')

  timecourse.w <- melt(timecourse.w, id.vars='hour', variable.name='side', value.name='mean.norm', na.r
```

```
  timecourse.e <- melt(timecourse.e, id.vars='hour', variable.name='side', value.name='mean.norm', na.rm
  timecourse.w$high.side <- paste0('West Higher (n=', length(west.high), ")")
  timecourse.e$high.side <- paste0('East Higher (n=', length(east.high), ")")
  timecourse.we <- rbind(timecourse.w, timecourse.e)

  p <- ggplot(timecourse.we, aes(x=hour, y=mean.norm, color=side)) +
         geom_line(size=1) +
         labs(x = 'Time (hours)', y = 'Mean of (Mean Normalized Counts / Mean Expression Level)') +
         scale_x_continuous(breaks=seq(0, 48, 12)) +
         scale_color_manual(name = 'Orientation',values = c(east.color, west.color)) +
         facet_wrap(~ high.side, ncol=1, scales='free_y')
  print(p)
  p
}

expdiff <- subset(cosopt, GeneID %in% rhythmic.both & abs(exp.diff.log2) > 0.6 & (MeanExpLev.W > 0.5 | M
plot.timecourse(expdiff$GeneID, lights.off = 13.25)
```

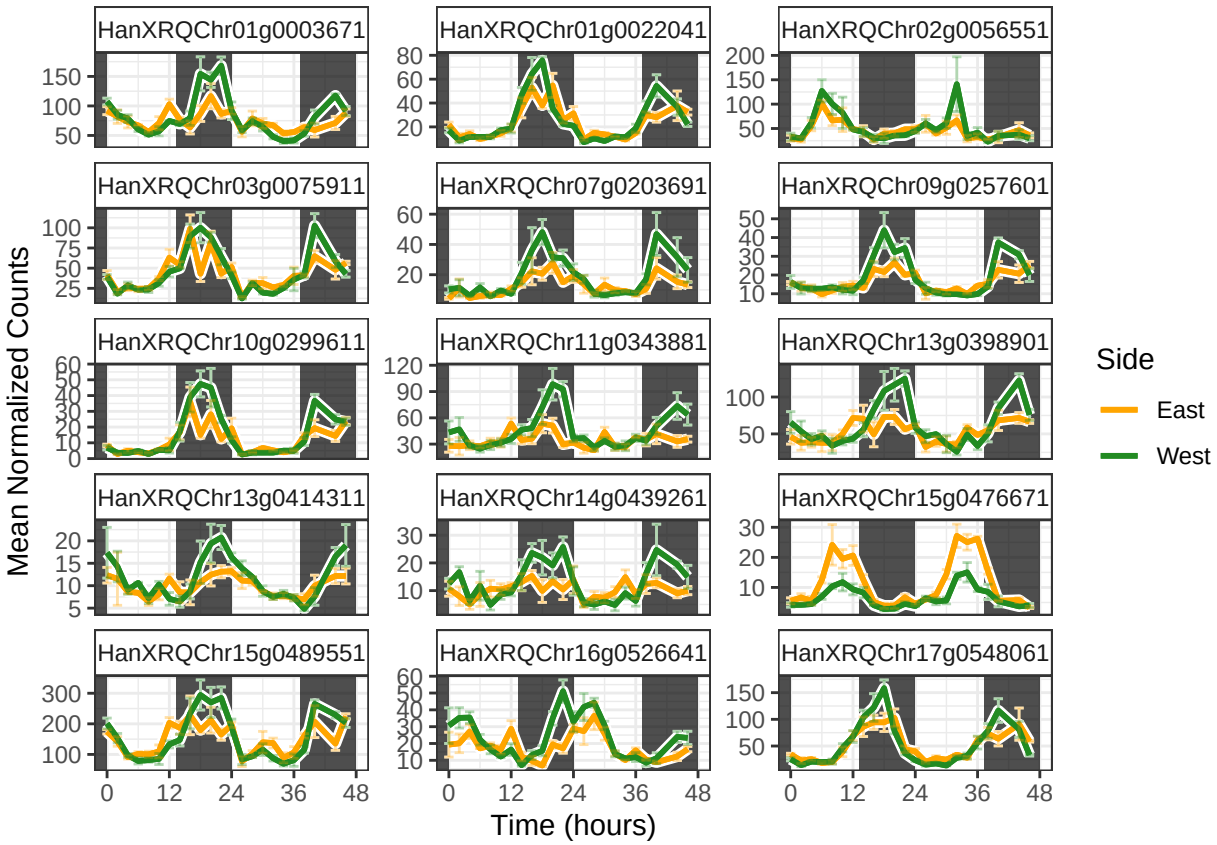



```
ggsave('plots/exp-diff.png', w=6, h=25)
ggsave('plots/exp-diff.pdf', w=6, h=25, useDingbats = FALSE)
write.table(expdiff, 'cosopt-processed/cosopt-processed.exp-diff.txt', sep = "\t", quote = FALSE, col.na

exp <- rownames(expdiff)
exp.e <- subset(cosopt, GeneID %in% exp & exp.diff.log2 < 0)$GeneID
exp.w <- subset(cosopt, GeneID %in% exp & exp.diff.log2 > 0)$GeneID
```

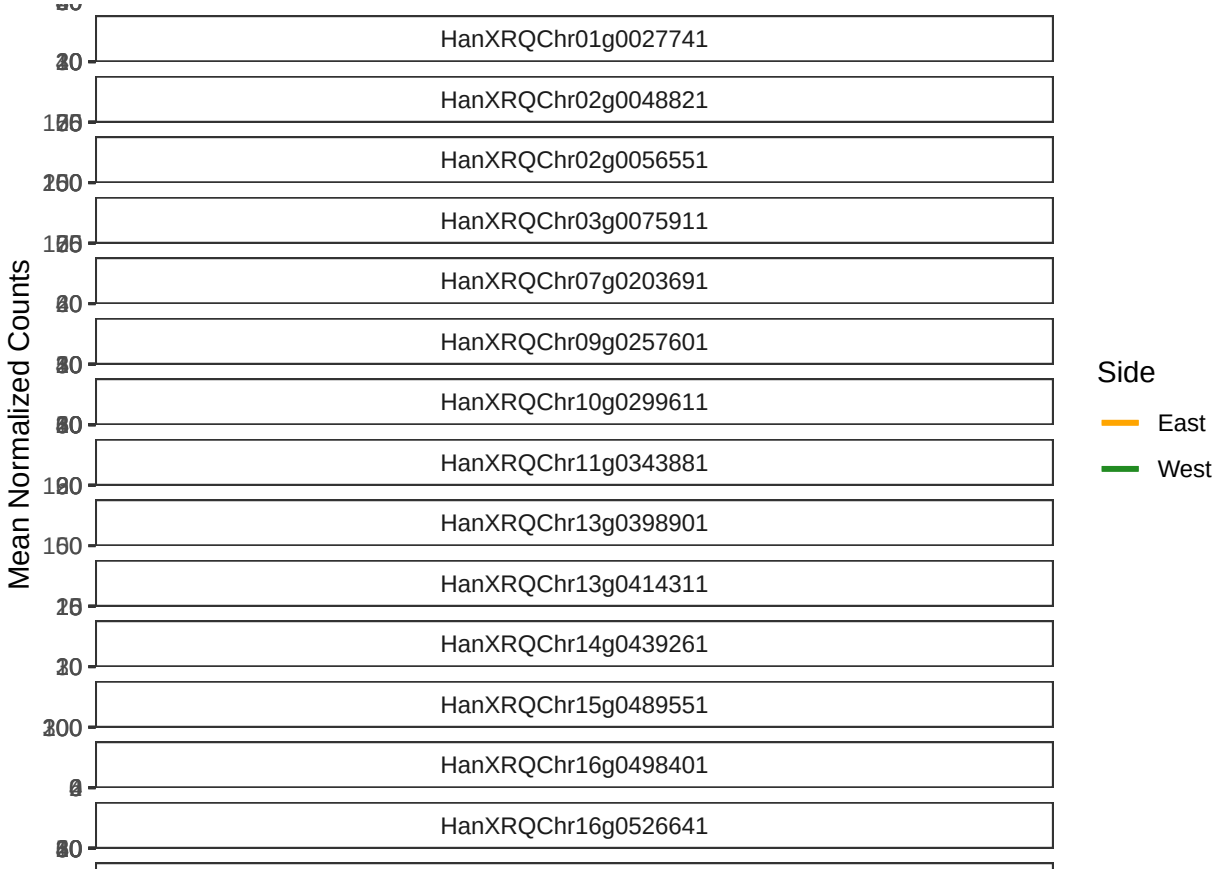
```
ampdiff <- subset(cosopt, GeneID %in% rhythmic.both & abs(amp.diff) > 0.25 & (MeanExpLev.E > 10 | MeanE
amp <- rownames(ampdiff)

amp.e <- subset(cosopt, GeneID %in% amp & amp.diff < 0)$GeneID
amp.w <- subset(cosopt, GeneID %in% amp & amp.diff > 0)$GeneID

plot.timecourse(amp, lights.off = 13.25)
```



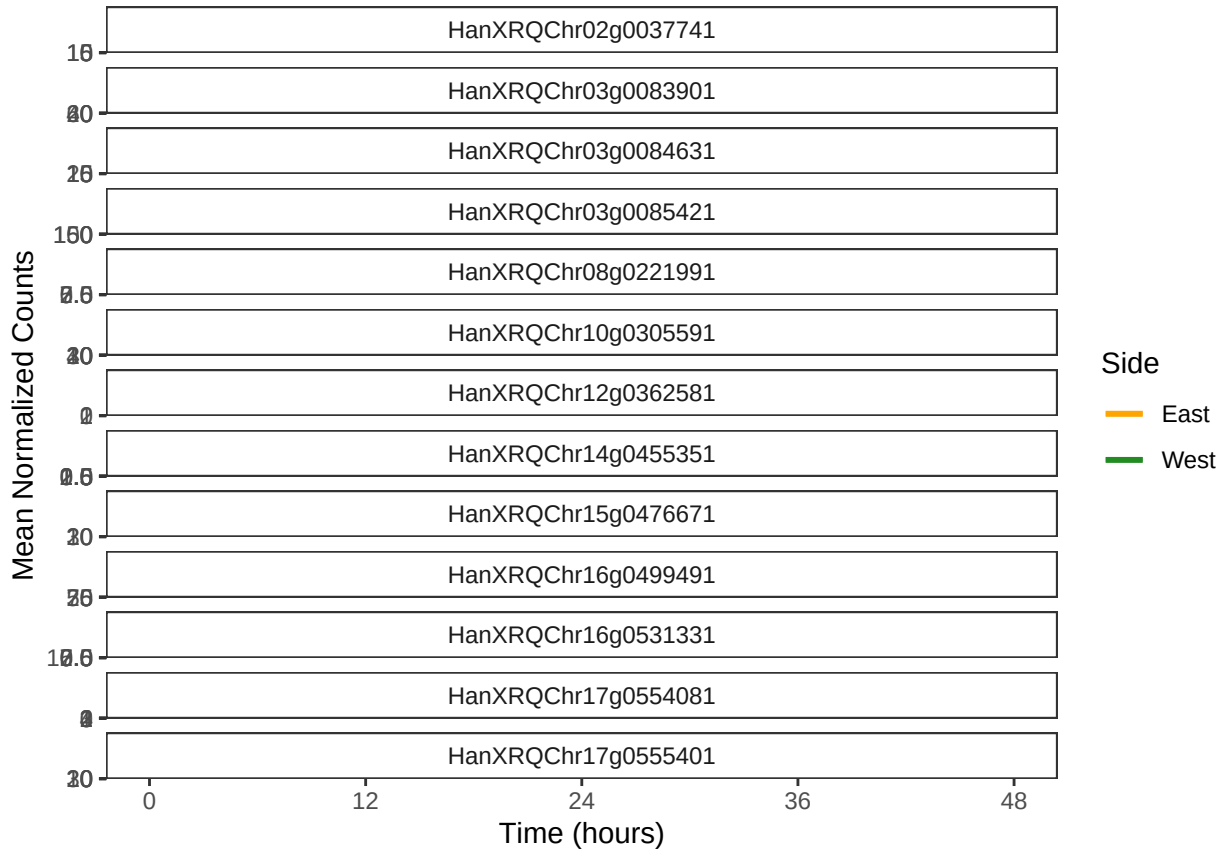

```
ggsave('plots/amp-diff.png', w=6, h=23)
ggsave('plots/amp-diff.pdf', w=6, h=23, useDingbats = FALSE)
plot.timecourse(amp, lights.off = 13.25, ncol = 3)
```



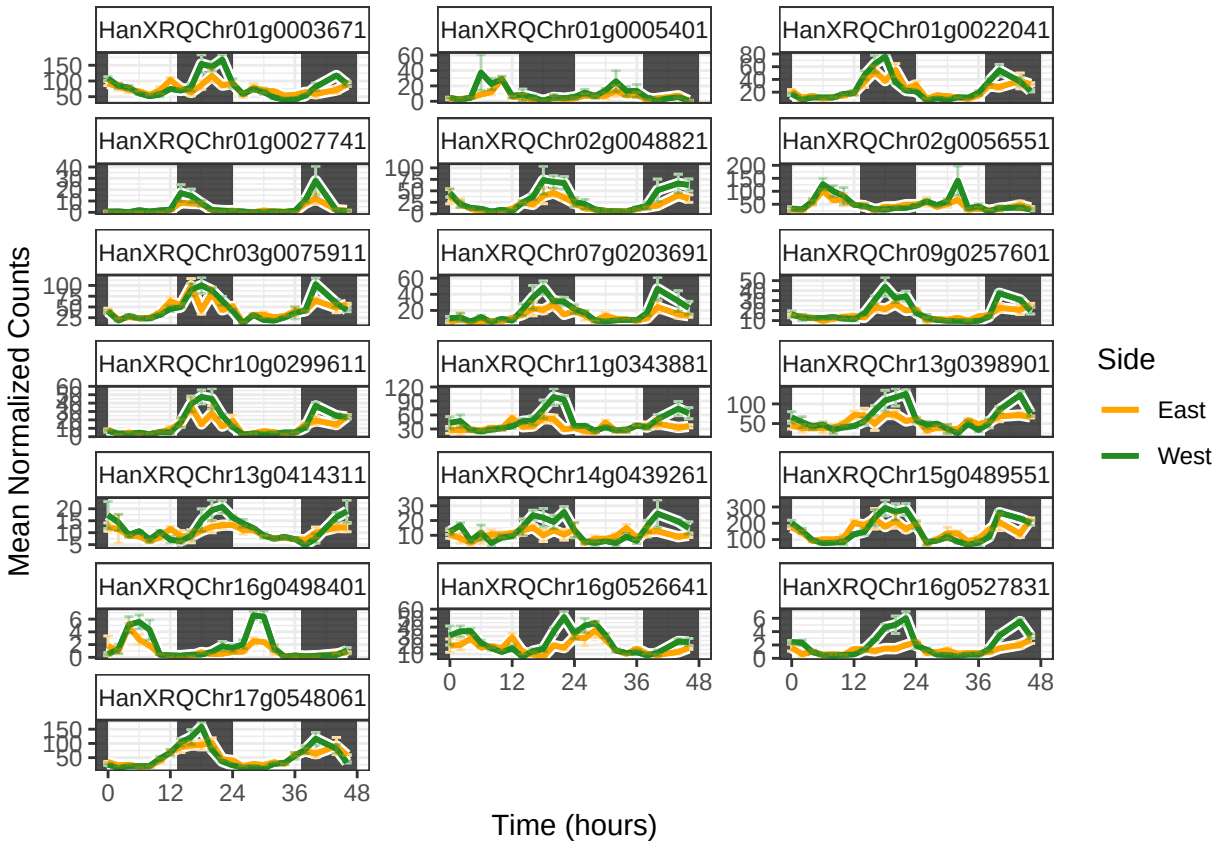

```
ggsave('plots/amp-diff.3col.standard-size.png', h=6.35, w=7.5)
ggsave('plots/amp-diff.3col.standard-size.pdf', h=6.35, w=7.5, useDingbats = FALSE)
write.table(ampdiff, 'cosopt-processed/cosopt-processed.amp-diff.txt', sep = "\t", quote = FALSE, col.na

west.high <- union(exp.w, amp.w)
east.high <- union(exp.e, amp.e)

plot.timecourse(west.high, lights.off = 13.25)
```



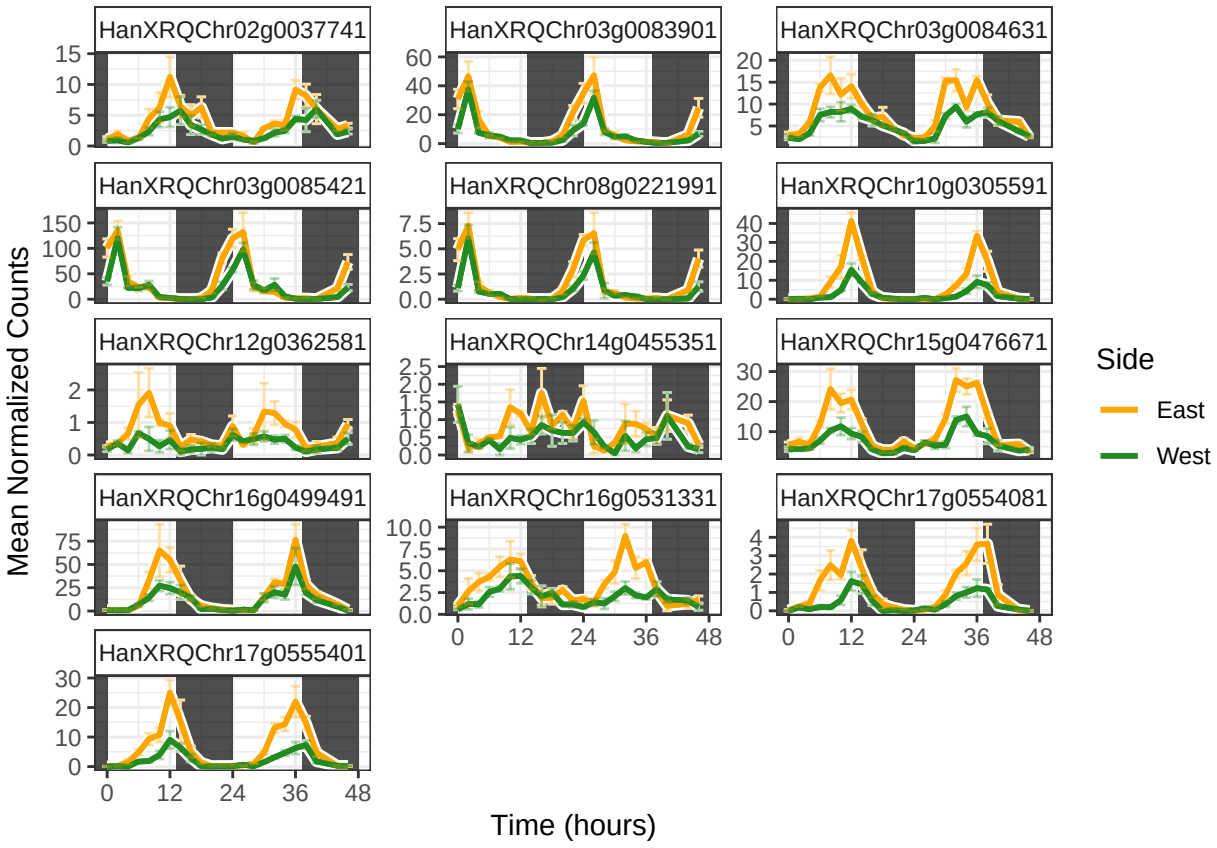

```
ggsave('plots/amp-exp-diff.west-high.png', w=6, h=30)
ggsave('plots/amp-exp-diff.west-high.pdf', w=6, h=30, useDingbats = FALSE)
plot.timecourse(east.high, lights.off = 13.25)
```



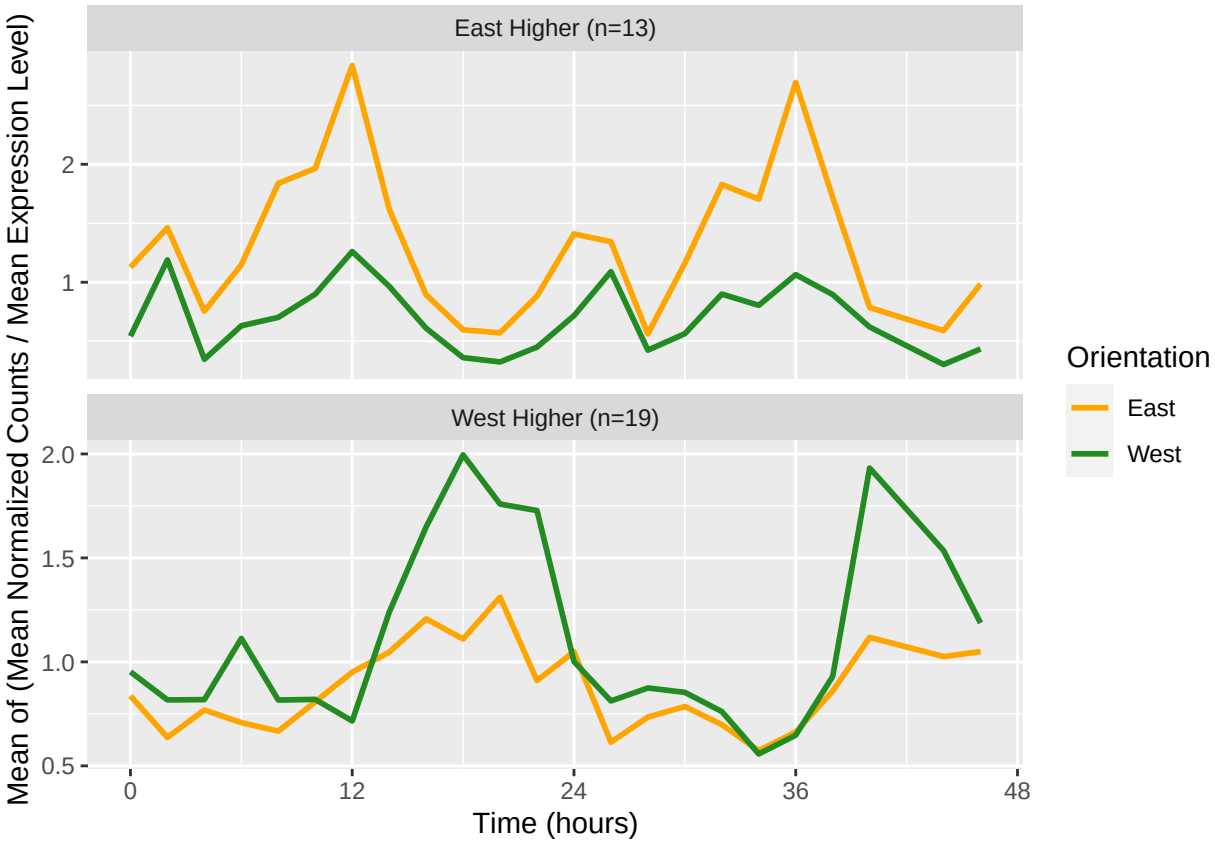

```
ggsave('plots/amp-exp-diff.east-high.png', w=6, h=21)
ggsave('plots/amp-exp-diff.east-high.pdf', w=6, h=21, useDingbats = FALSE)

plot.timecourse(west.high, lights.off = 13.25, ncol=3)
```

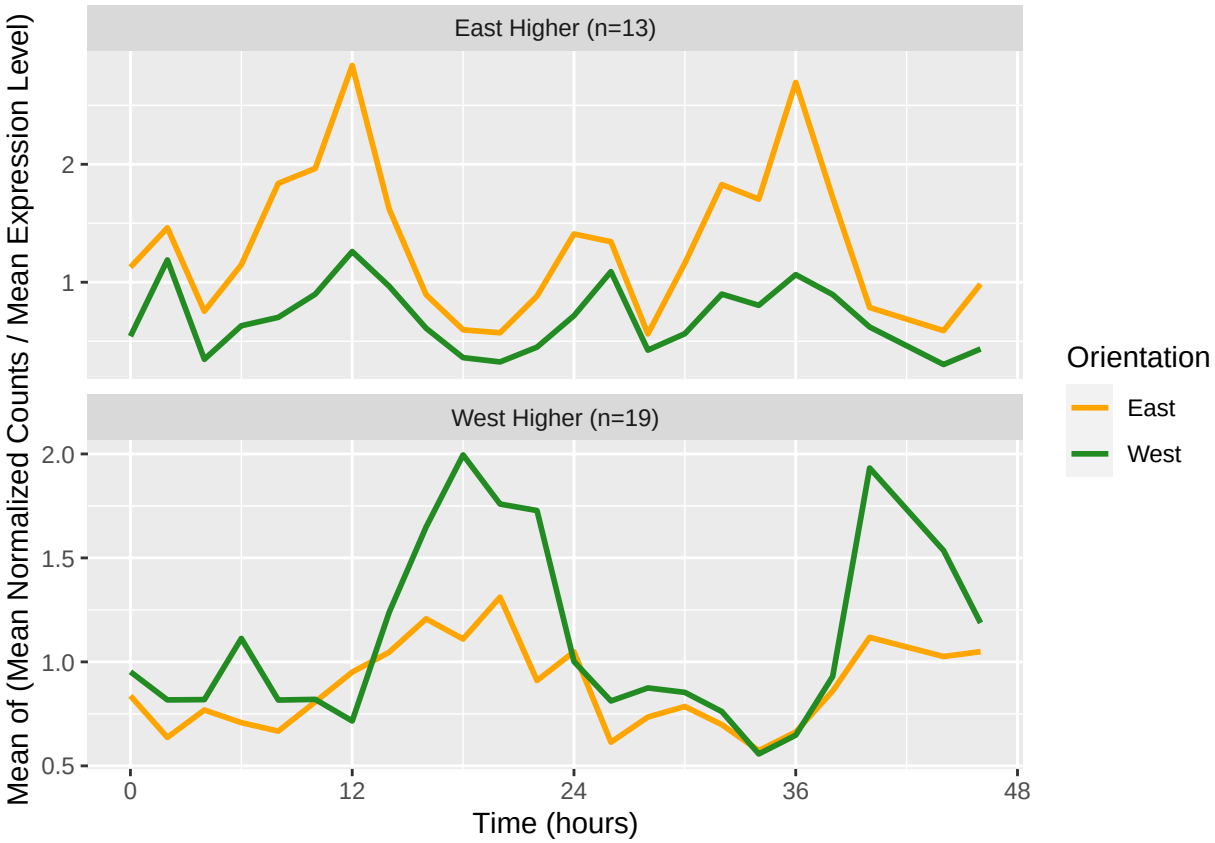



```
ggsave('plots/amp-exp-diff.west-high.3col.png', h=8.75, w=7.5)
ggsave('plots/amp-exp-diff.west-high.3col.pdf', h=8.75, w=7.5, useDingbats = FALSE)
plot.timecourse(east.high, lights.off = 13.25, ncol=3)
```

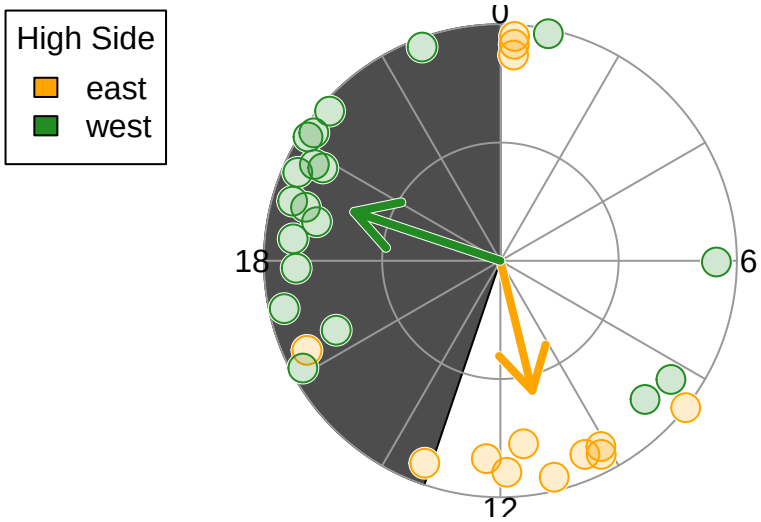



```
ggsave('plots/amp-exp-diff.east-high.3col.png', h=8.75, w=7.5)
ggsave('plots/amp-exp-diff.east-high.3col.pdf', h=8.75, w=7.5, useDingbats = FALSE)
ggsave('plots/amp-exp-diff.east-high.3col.standard-size.png', h=6.35, w=7.5)
ggsave('plots/amp-exp-diff.east-high.3col.standard-size.pdf', h=6.35, w=7.5, useDingbats = FALSE)

plot.ampdiff.summary()
```


East Higher (n=13)
West Higher (n=19)
Mean of (Mean Normalized Counts / Mean Expression Level)
2
1
2.0
1.5
1.0
0.5
0
12
24
36
48
Time (hours)
Orientation
East
West




```
# ggsave("plots/amp-exp-diff-summary.png", w=5, h=7)
write.table(subset(cosopt, GeneID %in% west.high), 'cosopt-processed/cosopt-processed.amp-exp-diff.west
write.table(subset(cosopt, GeneID %in% east.high), 'cosopt-processed/cosopt-processed.amp-exp-diff.east

# Polar
east.high.phase <- subset(cosopt, GeneID %in% east.high)$PeakPhase.E
west.high.phase <- subset(cosopt, GeneID %in% west.high)$PeakPhase.W

radius <- rep(1, length(east.high.phase) + length(west.high.phase))
phases <- c(east.high.phase, west.high.phase)
groups <- factor(c(rep('east', length(east.high.phase)), rep('west', length(west.high.phase))))
set.seed(1949); noise <- rnorm(length(radius), 0, 0.05)

polar.plot(radius + noise - max(noise), phases, pch=21, grp=groups, col=c(east.color, west.color), hours
```




```
png('plots/amp-exp-diff.png', w=7, h=7, u='in', res=150)
polar.plot(radius + noise - max(noise), phases, pch=21, grp=groups, col=c(east.color, west.color), hours
dev.off()
```

```
## pdf
##   2
```

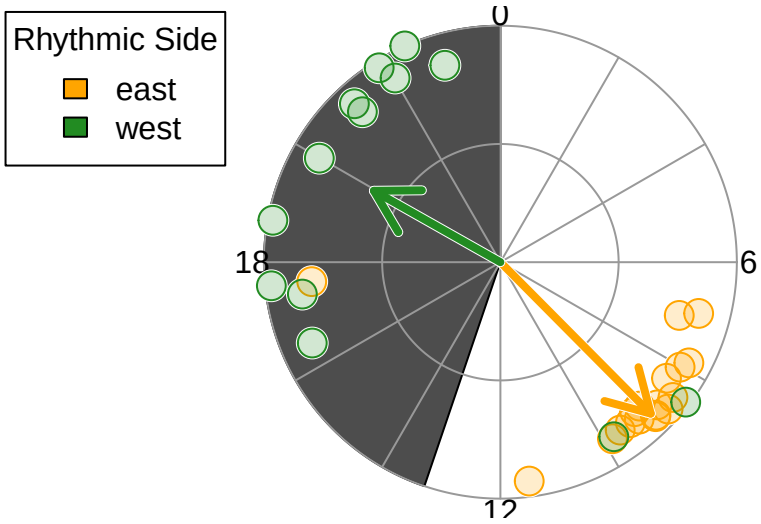
```
pdf('plots/amp-exp-diff.pdf', w=7, h=7, useDingbats = FALSE)
polar.plot(radius + noise - max(noise), phases, pch=21, grp=groups, col=c(east.color, west.color), hours
dev.off()
```

```
## pdf
##   2
```

Asymmetric Rhythm Polar Plot

```
asym.rhythm <- function(side, p1=0.01, p2=0.1, .cosopt=cosopt, amp.min=0, exp.min=0, per.buffer=0, per.
  if (side == 'east') {
    return(subset(.cosopt, pMMC.Beta.E < p1 & (is.na(pMMC.Beta.W) | pMMC.Beta.W >= p2) & RelAmp.E >= amp
  } else if (side == 'west') {
    return(subset(.cosopt, pMMC.Beta.W < p1 & (is.na(pMMC.Beta.E) | pMMC.Beta.E >= p2) & RelAmp.W >= amp
  } else {
    print("Need to provide a valid value for side: 'east' or 'west'.")
  }
}

east.rhythmic <- rownames(asym.rhythm(s='east', p1=0.001, p2=0.1, amp.min=amp.min, exp.min=exp.min, per
west.rhythmic <- rownames(asym.rhythm(s='west', p1=0.001, p2=0.1, amp.min=amp.min, exp.min=exp.min, per
```

```
east.phase <- subset(cosopt, GeneID %in% east.rhythmic)$PeakPhase.E
west.phase <- subset(cosopt, GeneID %in% west.rhythmic)$PeakPhase.W

write.table(subset(cosopt, GeneID %in% east.rhythmic), 'cosopt-processed/cosopt-processed.asymmetric-rhy
write.table(subset(cosopt, GeneID %in% west.rhythmic), 'cosopt-processed/cosopt-processed.asymmetric-rhy


radius <- rep(1, length(east.phase) + length(west.phase))
phases <- c(east.phase, west.phase)
groups <- factor(c(rep('east', length(east.phase)), rep('west', length(west.phase))))
set.seed(0709); noise <- rnorm(length(radius), 0, 0.05)

polar.plot(radius + noise - max(noise), phases, pch=21, grp=groups, col=c(east.color, west.color), hours
```




```
png('plots/asymmetric-rhythms.png', w=7, h=7, u='in', res=150)
polar.plot(radius + noise - max(noise), phases, pch=21, grp=groups, col=c(east.color, west.color), hours
dev.off()
```

```
## pdf
##   2
```

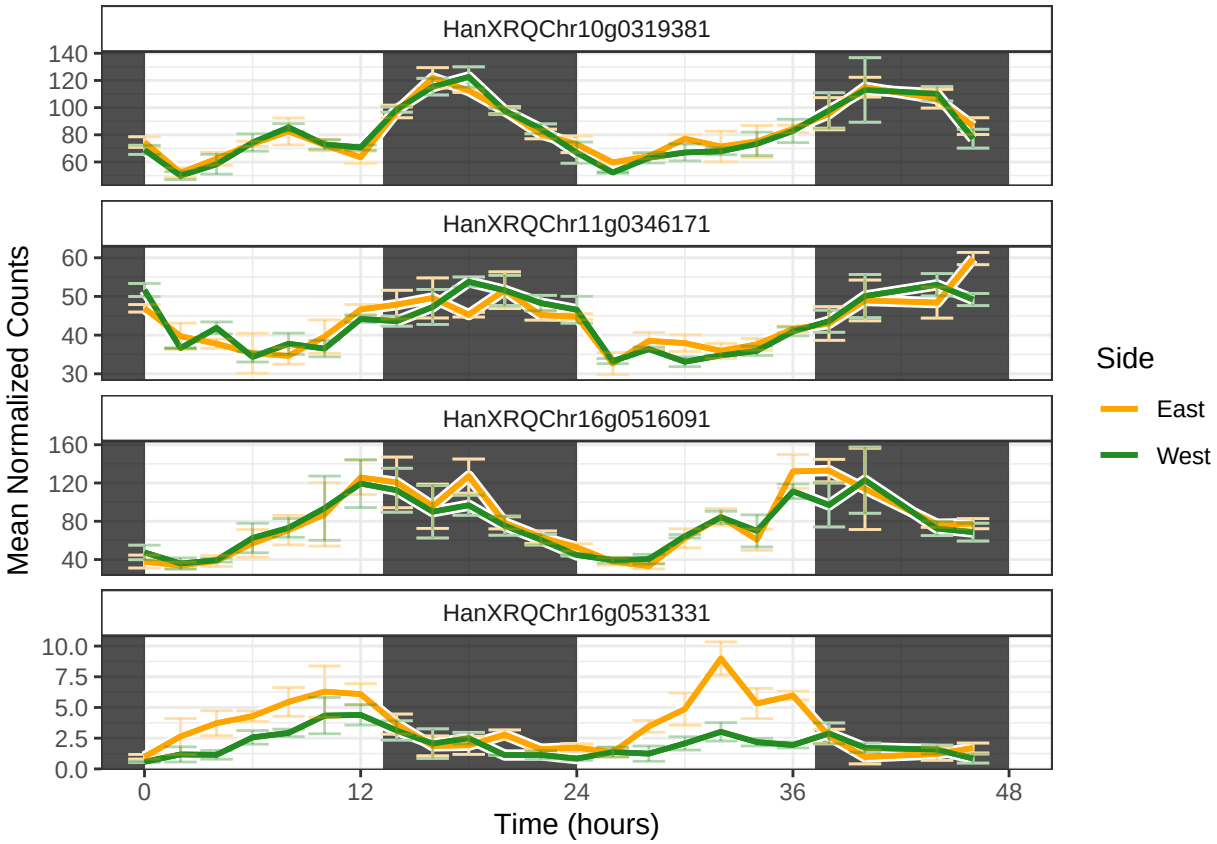
```
pdf('plots/asymmetric-rhythms.pdf', w=7, h=7, useDingbats = FALSE)
polar.plot(radius + noise - max(noise), phases, pch=21, grp=groups, col=c(east.color, west.color), hours
dev.off()
```

```
## pdf
```

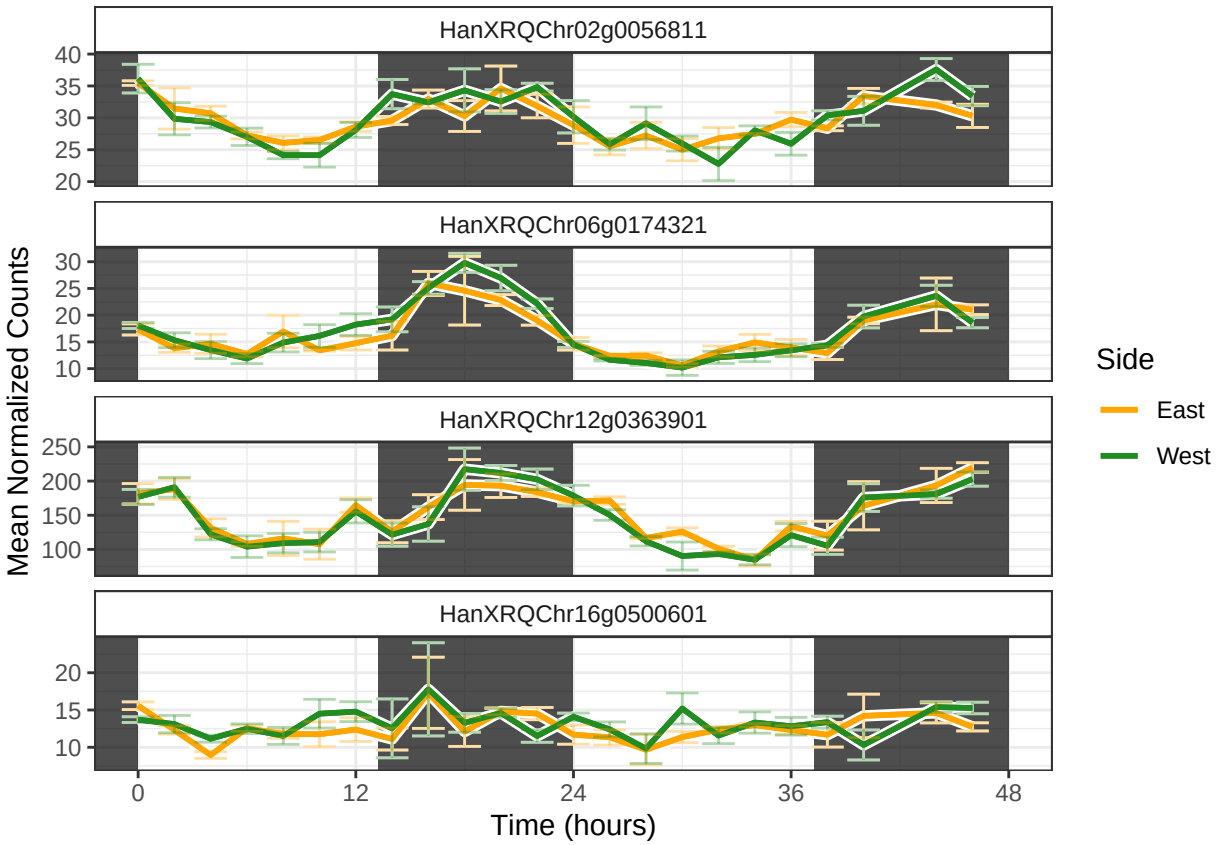
```
##    2
```

Plotting GWAS Candidates

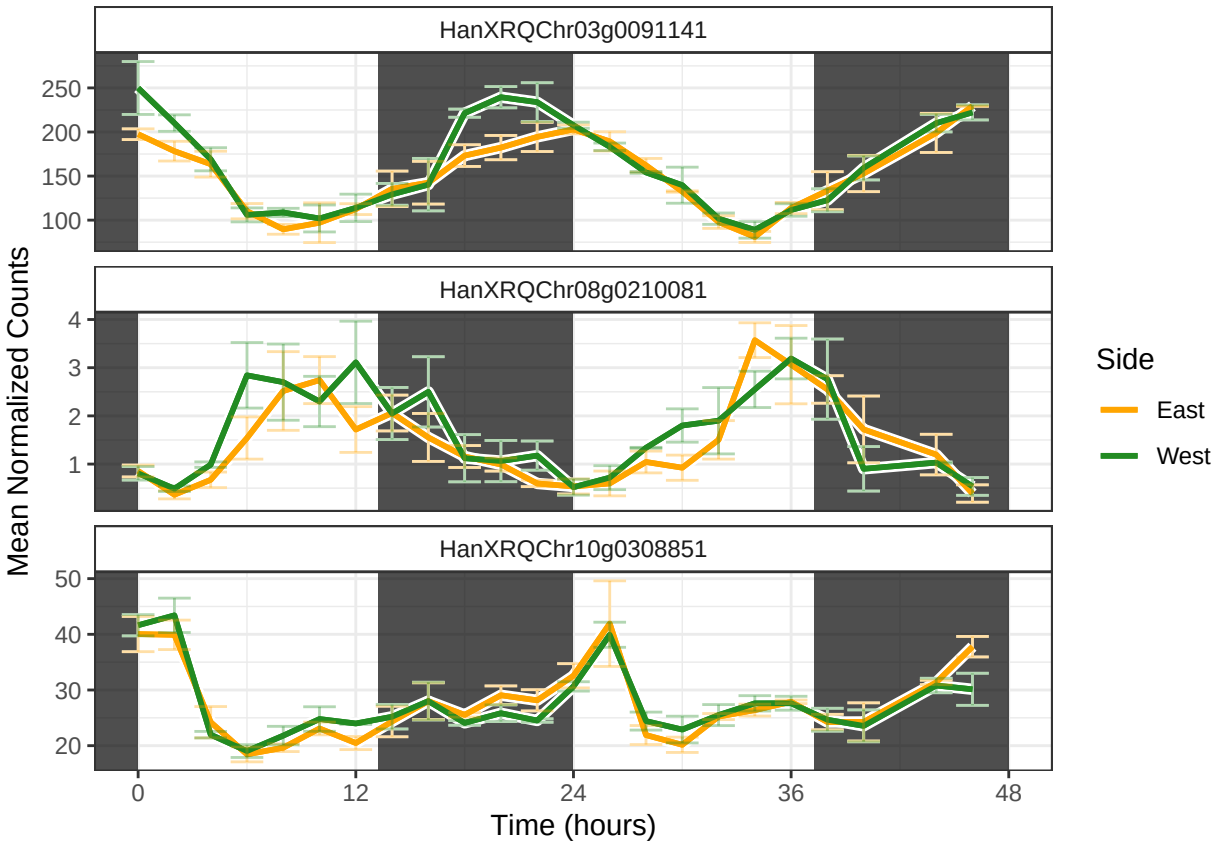
```
onset.time <- c('HanXRQChr10g0319381', 'HanXRQChr16g0516091', 'HanXRQChr16g0531331', 'HanXRQChr11g03461
nocturnal.reorientation <- c('HanXRQChr02g0056811', 'HanXRQChr16g0500601', 'HanXRQChr12g0363901', 'HanX
shoot.movement.pc1 <- c('HanXRQChr08g0210081', 'HanXRQChr03g0091141', 'HanXRQChr10g0308851')

plot.timecourse(onset.time, lights.off=13.25)
```




```
ggsave('plots/gwas.onset-time.png', w=4, h=6)
ggsave('plots/gwas.onset-time.pdf', w=4, h=6, useDingbats = FALSE)

plot.timecourse(nocturnal.reorientation, lights.off=13.25)
```

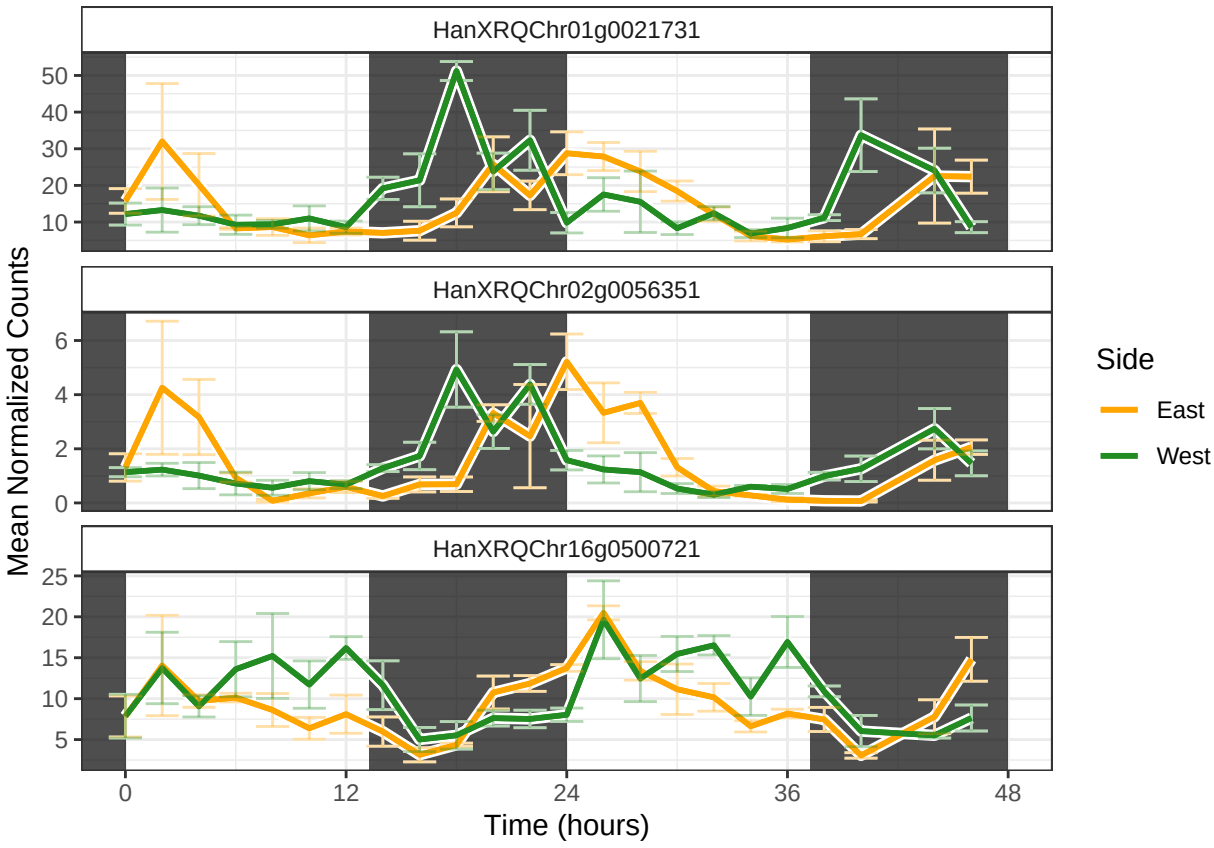



```
ggsave('plots/gwas.nocturnal-reorientation.png', w=4, h=6)
ggsave('plots/gwas.nocturnal-reorientation.pdf', w=4, h=6, useDingbats = FALSE)

plot.timecourse(shoot.movement.pc1, lights.off=13.25)
```

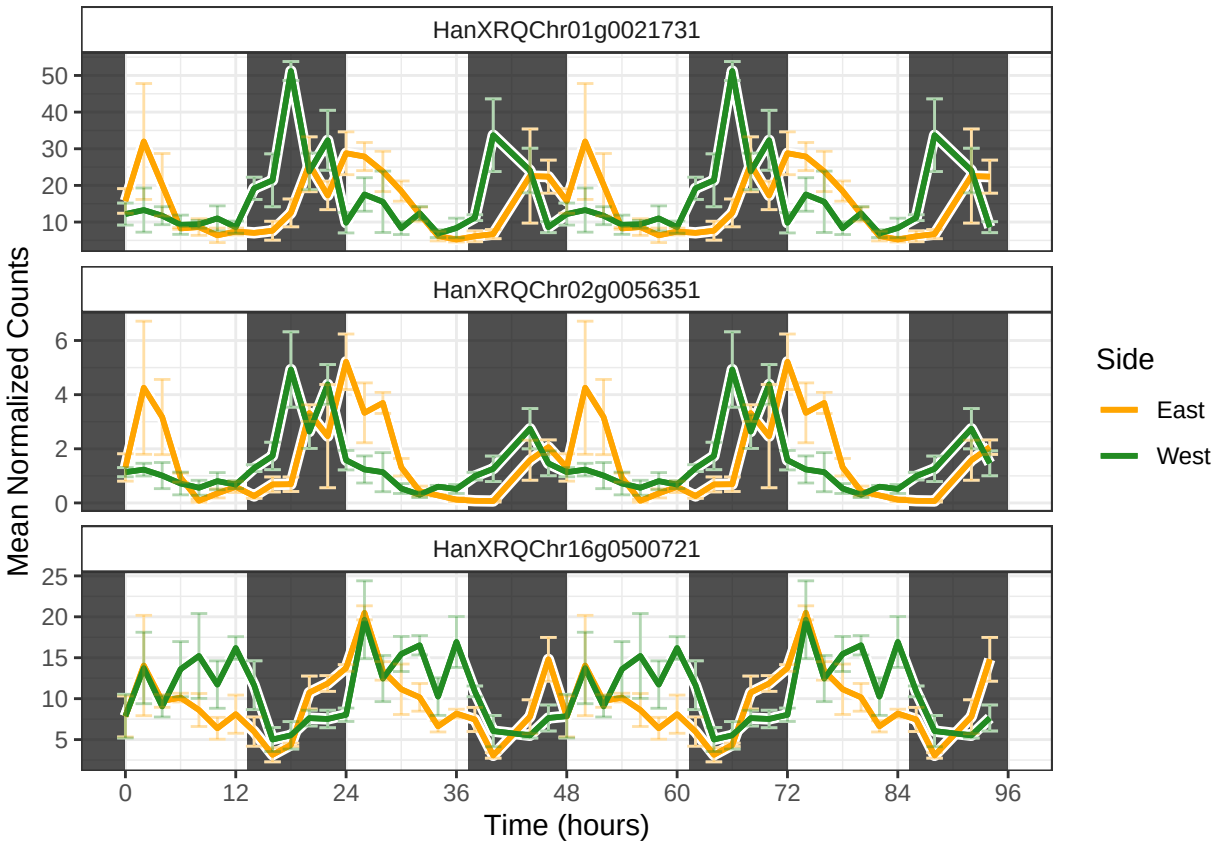



```
ggsave('plots/gwas.shoot-movement-pc1.png', w=4, h=4.7)
ggsave('plots/gwas.shoot-movement-pc1.pdf', w=4, h=4.7, useDingbats = FALSE)
```

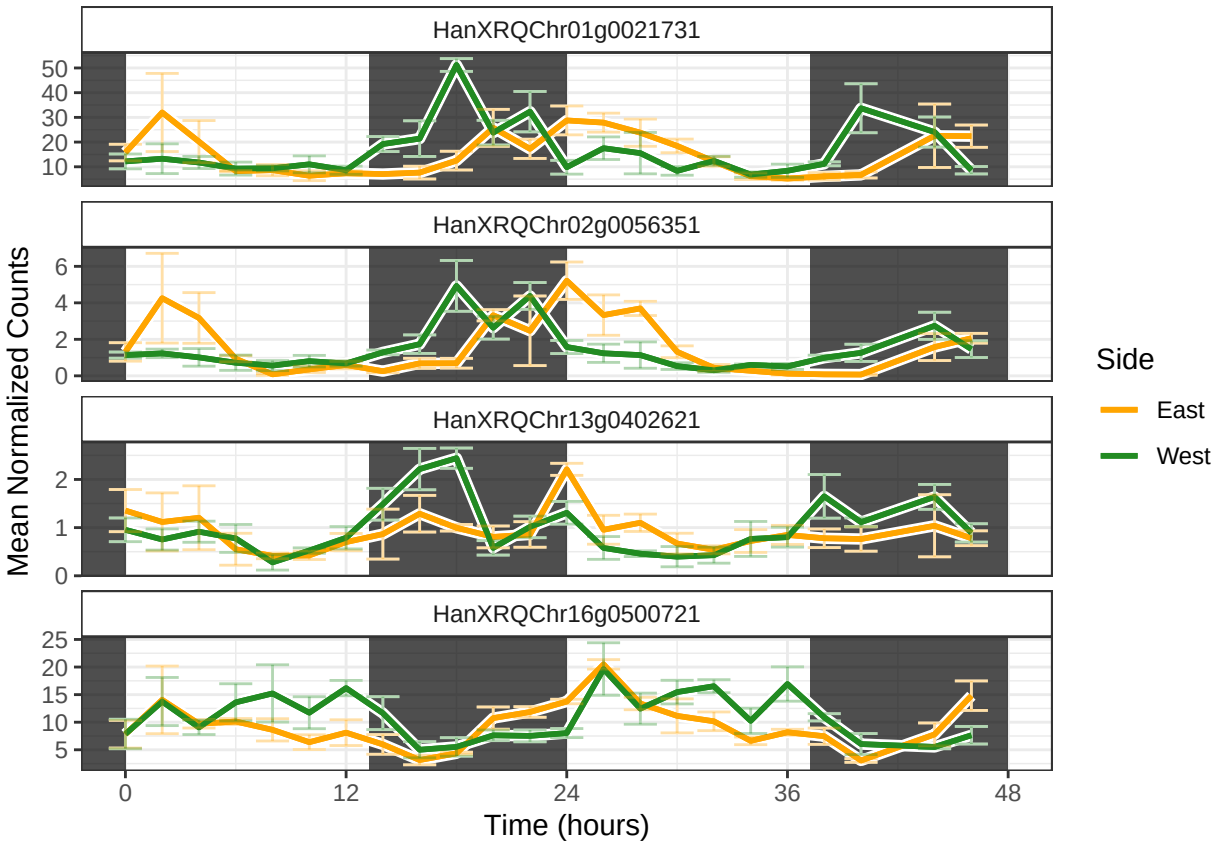
```
# Three genes implicated in Auxin- and Gibberillin-mediated growth are phase shifted between East and W
# HanXRQChr01g0021731 AT2G01420 PIN4 Auxin efflux carrier family protein
# HanXRQChr02g0056351 AT3G28857 PRE5: PACLOBUTRAZOL RESISTANCE 5 basic helix-loop-helix (bHLH) DNA-bind
# HanXRQChr16g0500721   AT3G04730   IAA16   indoleacetic acid-induced protein 16

# This one has a pMMC-Beta value of 0.05225100 for the East side and just misses the cutoff of 0.05.
# HanXRQChr13g0402621 AT4G38840 SAUR-like auxin-responsive protein family (According to https://academi

phase.shifted.genes <- c('HanXRQChr01g0021731', 'HanXRQChr02g0056351', 'HanXRQChr16g0500721')

plot.timecourse(phase.shifted.genes, lights.off = 13.25)
```



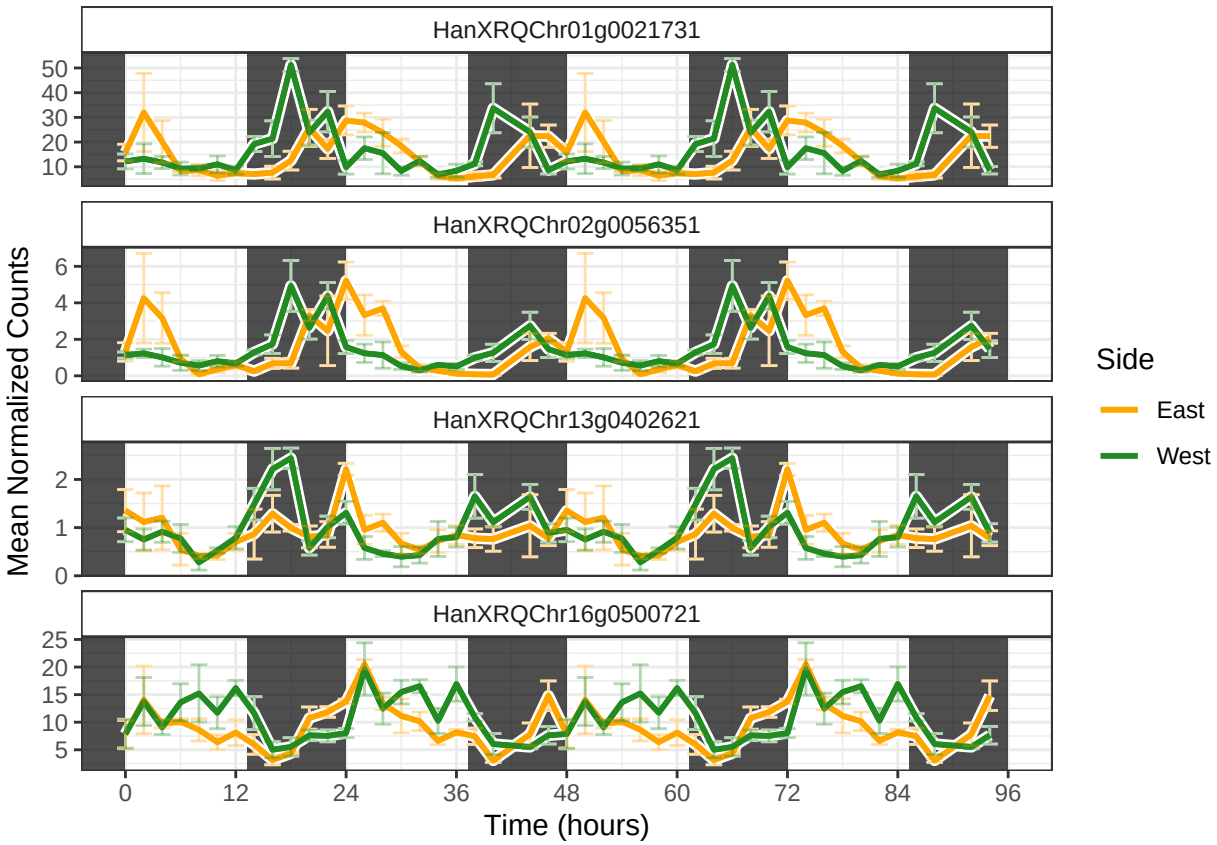

```
ggsave('plots/phase-shifted.png', w=4, h=4.7)
ggsave('plots/phase-shifted.pdf', w=4, h=4.7, useDingbats = FALSE)

plot.timecourse(phase.shifted.genes, lights.off = 13.25, double.plot = TRUE)
```




```
ggsave('plots/phase-shifted.double-plotted.png', w=6.5, h=4.7)
ggsave('plots/phase-shifted.double-plotted.pdf', w=6.5, h=4.7, useDingbats = FALSE)

plot.timecourse(c(phase.shifted.genes, 'HanXRQChr13g0402621'), lights.off = 13.25)
```

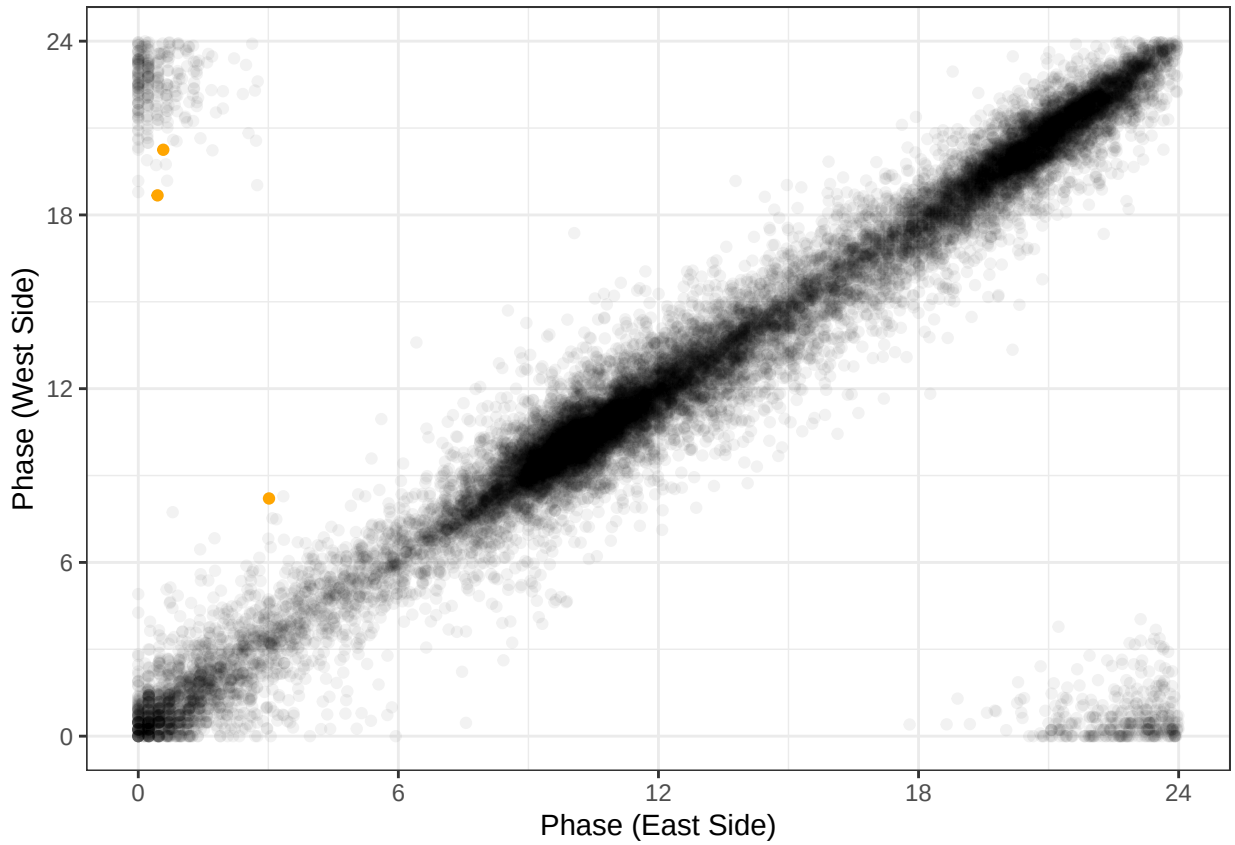



```
ggsave('plots/phase-shifted.with-SAUR14.png', w=4, h=6)
ggsave('plots/phase-shifted.with-SAUR14.pdf', w=4, h=6, useDingbats = FALSE)

plot.timecourse(c(phase.shifted.genes, 'HanXRQChr13g0402621'), lights.off = 13.25, double.plot = TRUE)
```

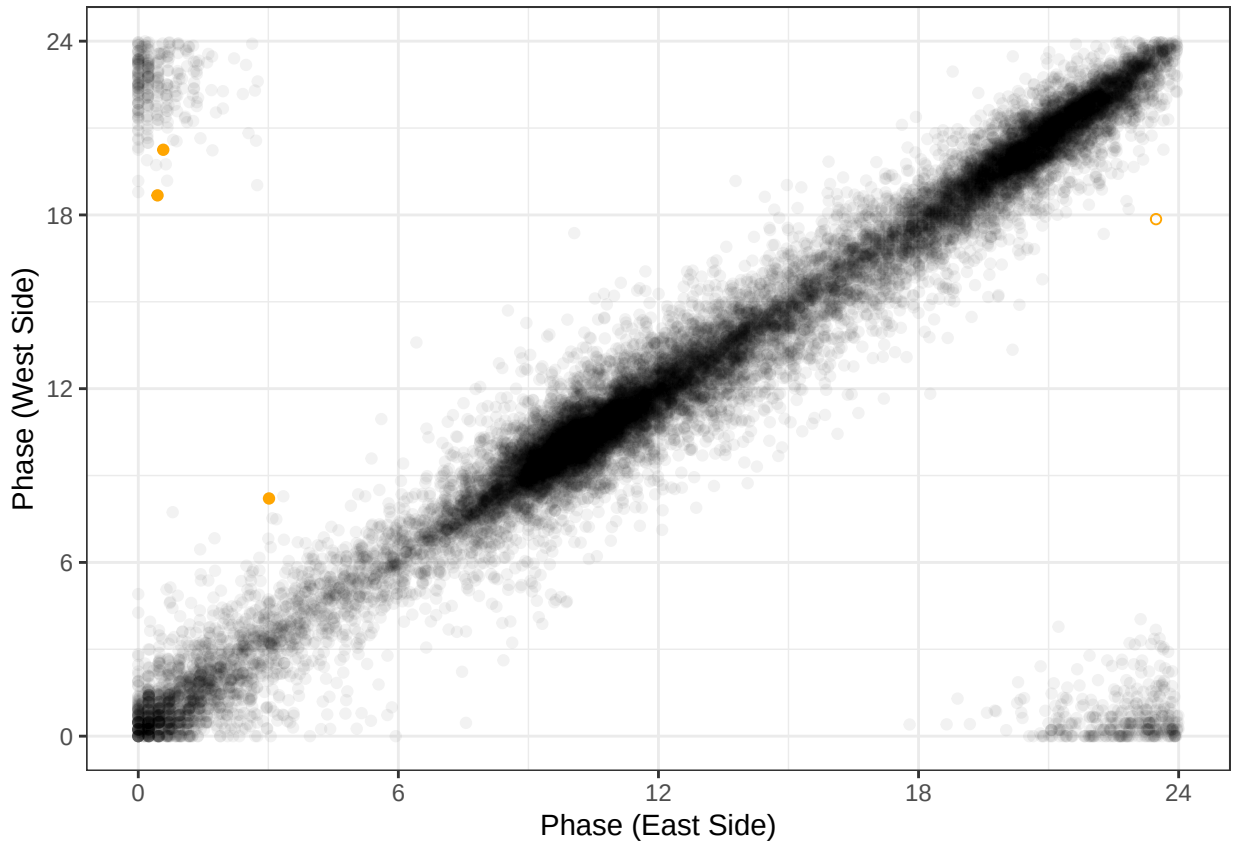



```
ggsave('plots/phase-shifted.double-plotted.with-SAUR14.png', w=6.5, h=6)
ggsave('plots/phase-shifted.double-plotted.with-SAUR14.pdf', w=6.5, h=6, useDingbats = FALSE)
```

```
phase.shifted.color <- 'orange'

cosopt.both.phaseshifted <- subset(cosopt.both, GeneID %in% phase.shifted.genes)
ggplot(cosopt.both) +
  geom_point(aes(x = PeakPhase.E, y = PeakPhase.W), alpha=0.05) +
  geom_point(data = subset(cosopt, GeneID %in% phase.shifted.genes), aes(x = PeakPhase.E, y = PeakPhase
  scale_x_continuous(breaks=seq(0, 24, 6)) +
  scale_y_continuous(breaks=seq(0, 24, 6)) +
  xlab('Phase (East Side)') +
  ylab('Phase (West Side)') +
  theme_bw()
```




```
ggsave('plots/phases.west-vs-east.highlight-shifted.png', w=6, h=6)
ggsave('plots/phases.west-vs-east.highlight-shifted.pdf', w=6, h=6, useDingbats = FALSE)

cosopt.both.phaseshifted <- subset(cosopt.both, GeneID %in% phase.shifted.genes)
ggplot(cosopt.both) +
  geom_point(aes(x = PeakPhase.E, y = PeakPhase.W), alpha=0.05) +
  geom_point(data = subset(cosopt, GeneID %in% phase.shifted.genes), aes(x = PeakPhase.E, y = PeakPhase
  geom_point(data = subset(cosopt, GeneID == 'HanXRQChr13g0402621'), aes(x = PeakPhase.E, y = PeakPhase
  scale_x_continuous(breaks=seq(0, 24, 6)) +
  scale_y_continuous(breaks=seq(0, 24, 6)) +
  xlab('Phase (East Side)') +
  ylab('Phase (West Side)') +
  theme_bw()
```




```
ggsave('plots/phases.west-vs-east.highlight-shifted.with-SAUR14.png', w=6, h=6)
ggsave('plots/phases.west-vs-east.highlight-shifted.with-SAUR14.pdf', w=6, h=6, useDingbats = FALSE)
```

Create Summary Table with Time Course Data, COSOPT results, etc.

```
# Merge time course data with COSOPT results
timecourse.cosopt.summary <- merge(timecourse.summary, cosopt, by = 'GeneID', all = TRUE)

# Record mean expression levels
timecourse.cosopt.summary$MeanExpressionEast <- mean.expression$east
timecourse.cosopt.summary$MeanExpressionWest <- mean.expression$west
timecourse.cosopt.summary$MeanExpressionMerged <- mean.expression$merged


# Mark rhythmic genes
timecourse.cosopt.summary$RhythmicEast[timecourse.cosopt.summary$GeneID %in% cosopt$GeneID] <- 0
timecourse.cosopt.summary$RhythmicWest[timecourse.cosopt.summary$GeneID %in% cosopt$GeneID] <- 0
timecourse.cosopt.summary$RhythmicBoth[timecourse.cosopt.summary$GeneID %in% cosopt$GeneID] <- 0
timecourse.cosopt.summary$RhythmicMerged[timecourse.cosopt.summary$GeneID %in% cosopt$GeneID] <- 0

timecourse.cosopt.summary$RhythmicEast[timecourse.cosopt.summary$GeneID %in% rhythmic.east] <- 1
timecourse.cosopt.summary$RhythmicWest[timecourse.cosopt.summary$GeneID %in% rhythmic.west] <- 1
timecourse.cosopt.summary$RhythmicBoth[timecourse.cosopt.summary$GeneID %in% rhythmic.both] <- 1
timecourse.cosopt.summary$RhythmicMerged[timecourse.cosopt.summary$GeneID %in% rhythmic.merged] <- 1


# Mark expressed genes
```

```
timecourse.cosopt.summary$ExpressedEast[timecourse.cosopt.summary$GeneID %in% cosopt$GeneID] <- 0
timecourse.cosopt.summary$ExpressedWest[timecourse.cosopt.summary$GeneID %in% cosopt$GeneID] <- 0
timecourse.cosopt.summary$ExpressedBoth[timecourse.cosopt.summary$GeneID %in% cosopt$GeneID] <- 0
timecourse.cosopt.summary$ExpressedMerged[timecourse.cosopt.summary$GeneID %in% cosopt$GeneID] <- 0

timecourse.cosopt.summary$ExpressedEast[timecourse.cosopt.summary$GeneID %in% rownames(expressed)[expres
timecourse.cosopt.summary$ExpressedWest[timecourse.cosopt.summary$GeneID %in% rownames(expressed)[expres
timecourse.cosopt.summary$ExpressedBoth[timecourse.cosopt.summary$GeneID %in% rownames(expressed)[expres
timecourse.cosopt.summary$ExpressedMerged[timecourse.cosopt.summary$GeneID %in% rownames(expressed)[expr


# Mark genes with higher amplitude or expression on one side
timecourse.cosopt.summary$AmpHigherEast[timecourse.cosopt.summary$GeneID %in% rhythmic.both] <- 0
timecourse.cosopt.summary$AmpHigherWest[timecourse.cosopt.summary$GeneID %in% rhythmic.both] <- 0
timecourse.cosopt.summary$AmpHigherEast[timecourse.cosopt.summary$GeneID %in% amp.e] <- 1
timecourse.cosopt.summary$AmpHigherWest[timecourse.cosopt.summary$GeneID %in% amp.w] <- 1

timecourse.cosopt.summary$ExpHigherEast[timecourse.cosopt.summary$GeneID %in% rhythmic.both] <- 0
timecourse.cosopt.summary$ExpHigherWest[timecourse.cosopt.summary$GeneID %in% rhythmic.both] <- 0
timecourse.cosopt.summary$ExpHigherEast[timecourse.cosopt.summary$GeneID %in% exp.e] <- 1
timecourse.cosopt.summary$ExpHigherWest[timecourse.cosopt.summary$GeneID %in% exp.w] <- 1

timecourse.cosopt.summary$AmpExpHigherEast[timecourse.cosopt.summary$GeneID %in% rhythmic.both] <- 0
timecourse.cosopt.summary$AmpExpHigherWest[timecourse.cosopt.summary$GeneID %in% rhythmic.both] <- 0
timecourse.cosopt.summary$AmpExpHigherEast[timecourse.cosopt.summary$GeneID %in% amp.e | timecourse.cos
timecourse.cosopt.summary$AmpExpHigherWest[timecourse.cosopt.summary$GeneID %in% amp.w | timecourse.cos


# Mark asymmetric cyclers (rhythmic on one side, but not the other)
timecourse.cosopt.summary$AsymmetricEast[timecourse.cosopt.summary$GeneID %in% union(rhythmic.east, rhy
timecourse.cosopt.summary$AsymmetricWest[timecourse.cosopt.summary$GeneID %in% union(rhythmic.east, rhy
timecourse.cosopt.summary$AsymmetricEast[timecourse.cosopt.summary$GeneID %in% east.rhythmic] <- 1
timecourse.cosopt.summary$AsymmetricWest[timecourse.cosopt.summary$GeneID %in% west.rhythmic] <- 1

head(timecourse.cosopt.summary, n=5)
```

```
##                     GeneID East_0h_mean East_2h_mean East_4h_mean East_6h_mean
## 1 HanXRQChr00c0001g0570931    0.9117024   0.45926241    0.4204598    0.2750039
## 2 HanXRQChr00c0003g0570971    0.1091173   0.07930041    0.3039131    0.2753755
## 3 HanXRQChr00c0003g0570981    0.4958849   0.40353149    0.5952826    0.4400805
## 4 HanXRQChr00c0004g0571001    5.6060333   4.89470893    5.5596748    5.6166944
## 5 HanXRQChr00c0004g0571011   11.1588551  15.52162866   22.0319606   21.7999671
##   East_8h_mean East_10h_mean East_12h_mean East_14h_mean East_16h_mean
## 1    0.4139209    0.50698195     0.4002296     0.2570277     0.7064449
## 2    0.2208127    0.06060066     0.2565281     0.1935906     0.2107729
## 3    0.6646679    0.49844351     0.5141270     0.6486378     0.7907490
## 4    6.2860724    6.26084198     6.9709343     8.8690336     9.9291800
## 5   25.3388315   24.38435423    19.6879723    14.2924269    15.3190341
##   East_18h_mean East_20h_mean East_22h_mean East_24h_mean East_26h_mean
## 1     0.3617501     0.7431298     0.1996955     0.2785472     0.5099242
## 2     0.2019911     0.1330436     0.2708863     0.1692589     0.1748185
## 3     0.6243119     0.7146057     0.5725981     0.8922424     0.9126925
## 4     9.0086614     9.7163352     6.6995663     5.6517962     6.6900929
## 5    16.0487244    13.5879497    17.5509128    15.1843145    20.3450989
```

```
##   East_28h_mean East_30h_mean East_32h_mean East_34h_mean East_36h_mean
## 1    0.48712893     0.9174001     0.2645752     0.8335053     0.9937369
## 2    0.09308733     0.0000000     0.2154461     0.2072242     0.1931378
## 3    0.86688849     0.4394522     0.6139451     0.4468905     0.5744472
## 4    5.69252070     5.4994014     4.5567243     6.7729709     6.2324946
## 5   20.83399118    21.1593221    22.4029475    23.3398537    25.2356634
##   East_38h_mean East_40h_mean East_44h_mean East_46h_mean West_0h_mean
## 1     0.8400430     0.5541328     0.7968898     0.2715544    0.3665759
## 2     0.2188712     0.3322028     0.2797127     0.2697980    0.1250066
## 3     0.8110953     0.8199693     1.1033019     0.7370958    0.8347580
## 4     9.4830179     8.6101784     9.9691223     7.5724658    6.2948094
## 5    19.2084475    13.3859965    18.6636127    18.1540090   13.2852110
##   West_2h_mean West_4h_mean West_6h_mean West_8h_mean West_10h_mean
## 1    0.6298716    0.8387638    0.4982465    0.2973809     0.8182397
## 2    0.2634719    0.1444436    0.1171651    0.2218034     0.1849692
## 3    0.4992268    0.6271347    0.2662168    0.8311336     0.7441114
## 4    4.3186672    6.6888407    6.0930987    7.6502346     7.2728022
## 5   16.6503097   20.2912081   21.7928923   25.9886879    26.6099122
##   West_12h_mean West_14h_mean West_16h_mean West_18h_mean West_20h_mean
## 1     0.4823134     0.2376923     0.6255419     0.3134011     0.3483086
## 2     0.1826446     0.2446365     0.3756466     0.1239564     0.1172849
## 3     0.7605737     0.5450553     0.7953738     1.3144125     0.3707426
## 4     7.0846240     9.6736792     7.2989631    10.1913688    10.5880762
## 5    22.0590107    17.2634986    14.8060528    17.9994852    15.9893356
##   West_22h_mean West_24h_mean West_26h_mean West_28h_mean West_30h_mean
## 1     0.2108630     0.3306077     0.4570837    0.42106947     1.0346923
## 2     0.3484867     0.3027098     0.2019638    0.06640825     0.1999967
## 3     0.7571385     0.7021352     0.7008402    0.69472634     0.9354931
## 4     6.7669680     5.7124289     5.7156136    6.09052839     7.3195046
## 5    18.3584199    13.6407907    18.3070608   16.35965598    25.2782878
##   West_32h_mean West_34h_mean West_36h_mean West_38h_mean West_40h_mean
## 1     0.3775487     0.3780953     1.0153553     0.8798077     0.4434399
## 2     0.2497154     0.4450860     0.4744737     0.2564431     0.2429383
## 3     0.6391529     0.5094483     1.0940143     0.9581114     0.8936439
## 4     5.8505074     6.6773925     7.7865504    10.0947371     8.6545831
## 5    23.1909166    24.4258443    23.4340058    17.5779978    12.8039267
##   West_44h_mean West_46h_mean Merged_0h_mean Merged_2h_mean Merged_4h_mean
## 1     0.6449330     0.6250404      0.6391391      0.5445670      0.6296118
## 2     0.2163135     0.3600761      0.1170620      0.1713862      0.2241784
## 3     0.9005424     0.9208543      0.6653214      0.4513792      0.6112087
## 4     7.7586798     7.0282456      5.9504214      4.6066881      6.1242577
## 5    18.0462215    17.5121522     12.2220331     16.0859692     21.1615843
##   Merged_6h_mean Merged_8h_mean Merged_10h_mean Merged_12h_mean Merged_14h_mean
## 1      0.3780742      0.3556509       0.6626108       0.4412715       0.2473600
## 2      0.2255616      0.2213080       0.1227849       0.2195863       0.2191135
## 3      0.3864247      0.7479007       0.6212775       0.6373503       0.5968465
## 4      4.9821429      6.9681535       6.7668221       7.0277791       9.2713564
## 5     21.8535890     25.6637597      25.4971332      20.8734915      15.7779628
##   Merged_16h_mean Merged_18h_mean Merged_20h_mean Merged_22h_mean
## 1       0.6659934       0.3375756       0.5457192       0.2052792
## 2       0.2932098       0.1629737       0.1251643       0.3096865
## 3       0.7930614       0.9693622       0.5426742       0.6648683
## 4       8.6140715       9.6000151      10.1522057       6.7332671
## 5      15.0625434      17.0241048      14.7886427      17.9546664
```

```
##   Merged_24h_mean Merged_26h_mean Merged_28h_mean Merged_30h_mean
## 1       0.3045775       0.4835040       0.4575030      0.63973595
## 2       0.2359843       0.1883911       0.1030196      0.07066642
## 3       0.7971888       0.8067663       0.8317997      0.60402152
## 4       5.6821125       6.2028532       5.6336810      5.46274041
## 5      14.4125526      19.3260799      18.2888865     20.97061753
##   Merged_32h_mean Merged_34h_mean Merged_36h_mean Merged_38h_mean
## 1       0.3210619       0.6058003       1.0045461       0.8599254
## 2       0.2325807       0.3261551       0.3338057       0.2376571
## 3       0.6265490       0.4781694       0.8342308       0.8846033
## 4       5.2036159       6.7251817       7.0095225       9.7888775
## 5      22.7969320      23.8828490      24.3348346      18.3932227
##   Merged_40h_mean Merged_44h_mean Merged_46h_mean East_0h_stderr East_2h_stderr
## 1       0.4987863       0.7209114       0.4482974     0.51888536     0.22023767
## 2       0.2875706       0.2480131       0.3149371     0.05774153     0.04006672
## 3       0.8568066       1.0019221       0.8289750     0.24316950     0.09346886
## 4       8.6323808       8.8639011       7.3003557     0.48788290     0.53699144
## 5      13.0949616      18.3549171      17.8330806     0.80726177     0.89031010
##   East_4h_stderr East_6h_stderr East_8h_stderr East_10h_stderr East_12h_stderr
## 1     0.21982503     0.16470500     0.12585793      0.15267188       0.2368528
## 2     0.05232181     0.05552109     0.01906768      0.03056394       0.1017951
## 3     0.10617768     0.21948279     0.22158508      0.20177774       0.2032670
## 4     0.85571722     0.56004232     0.69126780      0.61560685       0.3291396
## 5     4.51695765     1.39467615     2.51144988      5.71976722       1.4670510
##   East_14h_stderr East_16h_stderr East_18h_stderr East_20h_stderr
## 1      0.07466866       0.2883887       0.2772860      0.28226508
## 2      0.04669649       0.1064282       0.1175269      0.02559927
## 3      0.19091907       0.2982260       0.3047939      0.28249898
## 4      2.04777763       1.9125293       1.3224221      1.52700349
## 5      2.29847573       1.3051259       1.3508942      1.26038922
##   East_22h_stderr East_24h_stderr East_26h_stderr East_28h_stderr
## 1      0.04679541      0.03368115      0.07229755      0.07052773
## 2      0.15879990      0.06782794      0.12021884      0.09308733
## 3      0.15378347      0.10616874      0.20294814      0.13311444
## 4      1.63673522      1.14270815      0.66714847      0.80959695
## 5      2.30431472      1.96015747      1.63198142      0.74515121
##   East_30h_stderr East_32h_stderr East_34h_stderr East_36h_stderr
## 1      0.18747917      0.14128371      0.28242765     0.348733261
## 2      0.00000000      0.07403526      0.02366426     0.008979767
## 3      0.10798845      0.09532817      0.03075830     0.146235088
## 4      0.02499476      0.47049483      0.17526696     0.210853406
## 5      0.82954440      2.13929396      1.06118683     1.651712156
##   East_38h_stderr East_40h_stderr East_44h_stderr East_46h_stderr
## 1       0.2335623      0.16804911      0.14710853      0.13578561
## 2       0.1682888      0.05006363      0.07065581      0.01375465
## 3       0.3244117      0.12791362      0.16605026      0.07207517
## 4       1.9511321      0.66780981      0.90504328      0.79362952
## 5       1.2445824      0.52425397      1.03267652      0.61229346
##   West_0h_stderr West_2h_stderr West_4h_stderr West_6h_stderr West_8h_stderr
## 1     0.11027881     0.26599001     0.51539951     0.02756896      0.1062568
## 2     0.06446473     0.01948796     0.09509699     0.06434489      0.1689268
## 3     0.14939189     0.05378165     0.21479357     0.20332459      0.1362975
## 4     1.14111653     0.60346719     1.17659033     1.83433471      0.7469721
## 5     1.78600746     1.21480736     3.07656292     1.12658237      2.7555534
```

```
##   West_10h_stderr West_12h_stderr West_14h_stderr West_16h_stderr
## 1      0.16451441     0.089218243      0.04326365      0.24734057
## 2      0.05049299     0.007963469      0.13605317      0.06425125
## 3      0.24059398     0.152134104      0.29140678      0.10704522
## 4      0.53287244     0.457263046      0.93571941      1.91132827
## 5      3.40316164     2.746555302      1.36102900      0.89988803
##   West_18h_stderr West_20h_stderr West_22h_stderr West_24h_stderr
## 1      0.06548834      0.13310020      0.05254025       0.1837088
## 2      0.12395638      0.05925089      0.07142887       0.1305290
## 3      0.07484874      0.02234413      0.08988316       0.1371072
## 4      0.59283627      0.96947280      0.90857071       0.5796440
## 5      1.83353566      0.66165505      0.78459800       1.8709014
##   West_26h_stderr West_28h_stderr West_30h_stderr West_32h_stderr
## 1      0.07718986      0.11019653      0.67585358      0.11119440
## 2      0.12963690      0.06640825      0.05952557      0.02244022
## 3      0.16461992      0.03064384      0.16754889      0.05208067
## 4      0.87324153      0.64505189      2.00420819      0.53808176
## 5      1.70151966      1.43775503      4.62596875      0.92747972
##   West_34h_stderr West_36h_stderr West_38h_stderr West_40h_stderr
## 1      0.05840804       0.2947063       0.2493757       0.1668322
## 2      0.23083118       0.2877115       0.1057607       0.1458297
## 3      0.08103739       0.2479449       0.1087722       0.4669611
## 4      0.20871195       1.0072399       1.2132324       2.7557216
## 5      1.28114344       2.0530750       0.9943625       0.5712625
##   West_44h_stderr West_46h_stderr Merged_0h_stderr Merged_2h_stderr
## 1      0.43922303       0.1954358       0.27386622       0.17876656
## 2      0.07043235       0.1873304       0.05855184       0.02868705
## 3      0.09315458       0.2203679       0.16638355       0.04821517
## 4      0.79567345       1.0232390       0.33809296       0.18445752
## 5      0.80053181       1.1232488       1.28909205       0.17345952
##   Merged_4h_stderr Merged_6h_stderr Merged_8h_stderr Merged_10h_stderr
## 1       0.36147349      0.063626208       0.08599453        0.09386122
## 2       0.07304869      0.004711376       0.07536094        0.01898482
## 3       0.14141596      0.276125836       0.13684390        0.16047801
## 4       1.01615327      0.208334218       0.53032099        0.57082109
## 5       3.50050083      1.667950930       2.55311064        3.94170639
##   Merged_12h_stderr Merged_14h_stderr Merged_16h_stderr Merged_18h_stderr
## 1        0.09346653        0.02060531        0.25601364         0.1058988
## 2        0.04791591        0.08768712        0.02698078         0.1207417
## 3        0.17191487        0.19674193        0.16340663         0.1898213
## 4        0.38182002        1.48830424        1.63042502         0.9576292
## 5        1.85938847        1.76914034        1.08327013         0.2413207
##   Merged_20h_stderr Merged_22h_stderr Merged_24h_stderr Merged_26h_stderr
## 1        0.10916340       0.009620635        0.08592177       0.009295351
## 2        0.01699613       0.078827033        0.05621290       0.066803213
## 3        0.13095457       0.069302457        0.08688610       0.104402286
## 4        1.12969886       1.258834972        0.66361956       0.645854401
## 5        0.93940172       1.530651682        1.84648199       1.565232131
##   Merged_28h_stderr Merged_30h_stderr Merged_32h_stderr Merged_34h_stderr
## 1       0.005695347       0.150922206        0.11172473        0.13737028
## 2       0.103019620       0.008739765        0.03313899        0.12680534
## 3       0.058765471       0.041258726        0.06757415        0.02514776
## 4       0.863021574       0.556575451        0.48115114        0.18725476
## 5       1.082143198       1.356393067        1.26186672        1.12671118
```

```
##   Merged_36h_stderr Merged_38h_stderr Merged_40h_stderr Merged_44h_stderr
## 1         0.3020354        0.24055905        0.05189863        0.28880410
## 2         0.1441086        0.07133654        0.04816188        0.06215200
## 3         0.1953915        0.21629519        0.27694960        0.08517163
## 4         0.4248268        1.47253904        1.57933733        0.44364553
## 5         1.8194348        1.11854481        0.41624878        0.54279309
##   Merged_46h_stderr     Beta   Beta.E  Beta.W MeanExpLev MeanExpLev.E
## 1        0.03089423       NA       NA      NA         NA           NA
## 2        0.09199941 0.034317       NA      NA    0.21501           NA
## 3        0.14508214 0.088299 0.087048 0.09939    0.70022      0.66195
## 4        0.50231607 1.758000 1.816700 1.60300    7.14470      7.08820
## 5        0.73455879 4.366200 4.612000 4.64770   18.86900     18.85300
##   MeanExpLev.W PeakPhase PeakPhase.E PeakPhase.W Period Period.E Period.W
## 1           NA        NA          NA          NA     NA       NA       NA
## 2           NA    12.375          NA          NA   27.5       NA       NA
## 3       0.7528    18.486      20.436      16.872   23.7     26.2     22.2
## 4       7.2759    16.281      16.683      15.844   24.3     24.9     23.3
## 5      19.0860     9.000       8.550       9.503   22.5     22.5     22.1
##     Phase Phase.E Phase.W  pMMC.Beta pMMC.Beta.E pMMC.Beta.W    RelAmp
## 1      NA      NA      NA         NA          NA          NA        NA
## 2 -12.375      NA      NA 0.87212000          NA          NA 0.1596065
## 3   5.214   5.764   5.328 0.53278000  0.51955000   0.8765800 0.1261018
## 4   8.019   8.217   7.456 0.00080078  0.00083223   0.0066876 0.2460565
## 5  -9.000  -8.550  -9.503 0.00056347  0.00048054   0.0017195 0.2313954
##    RelAmp.E  RelAmp.W phase.diff      amp.diff exp.diff.log2 MeanExpressionEast
## 1        NA        NA         NA            NA            NA          0.5392629
## 2        NA        NA         NA            NA            NA          0.1943256
## 3 0.1315024 0.1320271     -3.564  0.0005247195    0.18554438          0.6600409
## 4 0.2562992 0.2203164     -0.839 -0.0359828145    0.03770640          7.0499357
## 5 0.2446295 0.2435136      0.953 -0.0011159318    0.01772067         18.8972119
##   MeanExpressionWest MeanExpressionMerged RhythmicEast RhythmicWest
## 1          0.5336901            0.5216305           NA           NA
## 2          0.2376365            0.2169911            0            0
## 3          0.7519496            0.7060308            0            0
## 4          7.3309088            7.1001045            1            1
## 5         19.2030819           18.9414963            1            1
##   RhythmicBoth RhythmicMerged ExpressedEast ExpressedWest ExpressedBoth
## 1           NA             NA            1             1            1
## 2            0              0            1             1            1
## 3            0              0            1             1            1
## 4            1              1            1             1            1
## 5            1              1            1             1            1
##   ExpressedMerged AmpHigherEast AmpHigherWest ExpHigherEast ExpHigherWest
## 1               1            NA            NA            NA            NA
## 2               1            NA            NA            NA            NA
## 3               1            NA            NA            NA            NA
## 4               1             0             0             0             0
## 5               1             0             0             0             0
##   AmpExpHigherEast AmpExpHigherWest AsymmetricEast AsymmetricWest
## 1               NA               NA             NA             NA
## 2               NA               NA             NA             NA
## 3               NA               NA             NA             NA
## 4                0                0              0              0
## 5                0                0              0              0
```

```
write.table(timecourse.cosopt.summary, "Expression-and-COSOPT-Summary.txt", sep = "\t", quote = FALSE, 
```