Frontloading_RMD

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Call modules representing higher expression by naive clams throughout the subseqent exposures

- 'Naive_modules' == all mods of interest

```
day7.brown     <- day7.ModMem %>% dplyr::filter(moduleColor %in% 'brown')     %>% dplyr::mutate(day ='Day
day14.brown    <- day14.ModMem %>% dplyr::filter(moduleColor %in% 'brown')    %>% dplyr::mutate(day ='Day
day21.blue     <- day21.ModMem %>% dplyr::filter(moduleColor %in% 'blue')     %>% dplyr::mutate(day ='Day
day21.magenta  <- day21.ModMem %>% dplyr::filter(moduleColor %in% 'magenta')  %>% dplyr::mutate(day ='Day

Naive_modules <- rbind(day7.brown, day14.brown, day21.blue, day21.magenta)
```

- 'NaiveResponse_genes_data' call all genes that occured THREE times in 'Naive_modules'
- Why? These genes are represent those with persistant high expression relative to the pre-exposed (primed) clams!
- there are 315 total genes in this category

```
NaiveResponse_genes <- Naive_modules %>%
                       dplyr::group_by(Pgen_ID) %>%
                       dplyr::summarise(count = n()) %>%
                       dplyr::filter(count == 3)
# View(NaiveResponse_genes)
NaiveResponse_genes         = NaiveResponse_genes$Pgen_ID
NaiveResponse_genes_ANNOT   = match(NaiveResponse_genes, annot$V1)
NaiveResponse_genes_data    <- data.frame(geneSymbol = annot$V1[NaiveResponse_genes_ANNOT],
                                          Annotation = annot$V7[NaiveResponse_genes_ANNOT])
# nrow(NaiveResponse_genes_data) # 315 genes present on all sampling days
```

Calculate the contorl ratio (Y axis) and the foldchangie ratio (x axis)

```
# Day 7 gene expression
Day_WGCNA_genes <- Day7_exp_data %>%
  dplyr::filter(Gene %in% NaiveResponse_genes)
Day7_WGCNA_genes_melted    <- Day_WGCNA_genes %>%
  reshape2::melt(id.var = 'Gene') %>%
  dplyr::rename(Sample.Name = variable)
```

```r
Day7_WGCNA_genes_Merge <- merge(Day7_WGCNA_genes_melted, Day7_Master.Exp.Metadata, by = 'Sample.Name')
  dplyr::group_by(Gene, All_Treatment) %>%
  dplyr::select(!'Sample.Name') %>%
  dplyr::summarise(meanExp = mean(value))
```

`summarise()` has grouped output by 'Gene'. You can override using the `.groups` argument.

```r
Day7_READY <- dcast(Day7_WGCNA_genes_Merge, Gene ~ All_Treatment)
```

Using meanExp as value column: use value.var to override.

```r
for (i in 1:nrow(Day7_READY)) {
          # Moderate - higher expression AM > AA
        if (Day7_READY$AM[i] > Day7_READY$AA[i]) {
          Day7_READY$wgcna.xall_mod[i] <- ( (Day7_READY$MM[i] / Day7_READY$MA[i]) / (Day7_READY$AM[i] /
          Day7_READY$wgcna.yall_mod[i] <- (Day7_READY$MA[i] / Day7_READY$AA[i]) # Y Axis - this is simp
            } else {
               Day7_READY$wgcna.xall_mod[i] <- NA  # X axis  - call NA
               Day7_READY$wgcna.yall_mod[i] <- NA # Y Axis  - call NA
            }
          # Severe - higher expression AS > AA
        if (Day7_READY$AS[i] > Day7_READY$AA[i]) {
          Day7_READY$wgcna.xall_sev[i] <- ( (Day7_READY$MS[i] / Day7_READY$MA[i]) / (Day7_READY$AS[i]
          Day7_READY$wgcna.yall_sev[i] <- (Day7_READY$MA[i] / Day7_READY$AA[i])                # Y Axis -
            } else {
               Day7_READY$wgcna.xall_sev[i] <- NA  # X axis  - call NA
               Day7_READY$wgcna.yall_sev[i] <- NA # Y Axis  - call NA
            }
}
# Day7_READY

# Day 14 gene expression
Day_WGCNA_genes <- Day14_exp_data %>%
  dplyr::filter(Gene %in% NaiveResponse_genes)
Day14_WGCNA_genes_melted      <- Day_WGCNA_genes %>%
  reshape2::melt(id.var = 'Gene') %>%
  dplyr::rename(Sample.Name = variable)
Day14_WGCNA_genes_Merge <- merge(Day14_WGCNA_genes_melted, Day14_Master.Exp.Metadata, by = 'Sample.Name
  dplyr::group_by(Gene, All_Treatment) %>%
  dplyr::select(!'Sample.Name') %>%
  dplyr::summarise(meanExp = mean(value))
```

`summarise()` has grouped output by 'Gene'. You can override using the `.groups` argument.

```r
Day14_READY <- dcast(Day14_WGCNA_genes_Merge, Gene ~ All_Treatment)
```

Using meanExp as value column: use value.var to override.

```r
for (i in 1:nrow(Day14_READY)) {
        # Moderate - higher expression AM > AA
      if (Day14_READY$AM[i] > Day14_READY$AA[i]) {
        Day14_READY$wgcna.xall_mod[i] <- ( (Day14_READY$MM[i] / Day14_READY$MA[i]) / (Day14_READY$AM[
        Day14_READY$wgcna.yall_mod[i] <- (Day14_READY$MA[i] / Day14_READY$AA[i]) # Y Axis - this is s
          } else {
            Day14_READY$wgcna.xall_mod[i] <- NA  # X axis  - call NA
            Day14_READY$wgcna.yall_mod[i] <- NA # Y Axis  - call NA
          }
        # Severe - higher expression AS > AA
      if (Day14_READY$AS[i] > Day14_READY$AA[i]) {
        Day14_READY$wgcna.xall_sev[i] <- ( (Day14_READY$MS[i] / Day14_READY$MA[i]) / (Day14_READY$AS
        Day14_READY$wgcna.yall_sev[i] <- (Day14_READY$MA[i] / Day14_READY$AA[i])             # Y Axi
          } else {
            Day14_READY$wgcna.xall_sev[i] <- NA  # X axis  - call NA
            Day14_READY$wgcna.yall_sev[i] <- NA # Y Axis  - call NA
          }
}
# Day14_READY


# Day 21 gene expression
Day_WGCNA_genes <- Day21_exp_data %>%
  dplyr::filter(Gene %in% NaiveResponse_genes)
Day21_WGCNA_genes_melted    <- Day_WGCNA_genes %>%
  reshape2::melt(id.var = 'Gene') %>%
  dplyr::rename(Sample.Name = variable)
Day21_WGCNA_genes_Merge <- merge(Day21_WGCNA_genes_melted, Day21_Master.Exp.Metadata, by = 'Sample.Name
  dplyr::group_by(Gene, All_Treatment) %>%
  dplyr::select(!'Sample.Name') %>%
  dplyr::summarise(meanExp = mean(value))
```

`summarise()` has grouped output by 'Gene'. You can override using the `.groups` argument.

```r
Day21_READY <- dcast(Day21_WGCNA_genes_Merge, Gene ~ All_Treatment)
```

Using meanExp as value column: use value.var to override.

```r
for (i in 1:nrow(Day21_READY)) {
        # Moderate - higher expression AM > AA
      if (Day21_READY$AAM[i] > Day21_READY$AAA[i]) {
        Day21_READY$wgcna.xall_mod[i] <- ( (Day21_READY$MAM[i] / Day21_READY$MAA[i]) / (Day21_READY$A
        Day21_READY$wgcna.yall_mod[i] <- (Day21_READY$MAA[i] / Day21_READY$AAA[i]) # Y Axis - this is
          } else {
            Day21_READY$wgcna.xall_mod[i] <- NA  # X axis  - call NA
            Day21_READY$wgcna.yall_mod[i] <- NA # Y Axis  - call NA
          }
}
# Day21_READY
```

Day 7
Frontloaded genes; response to moderate pCO2
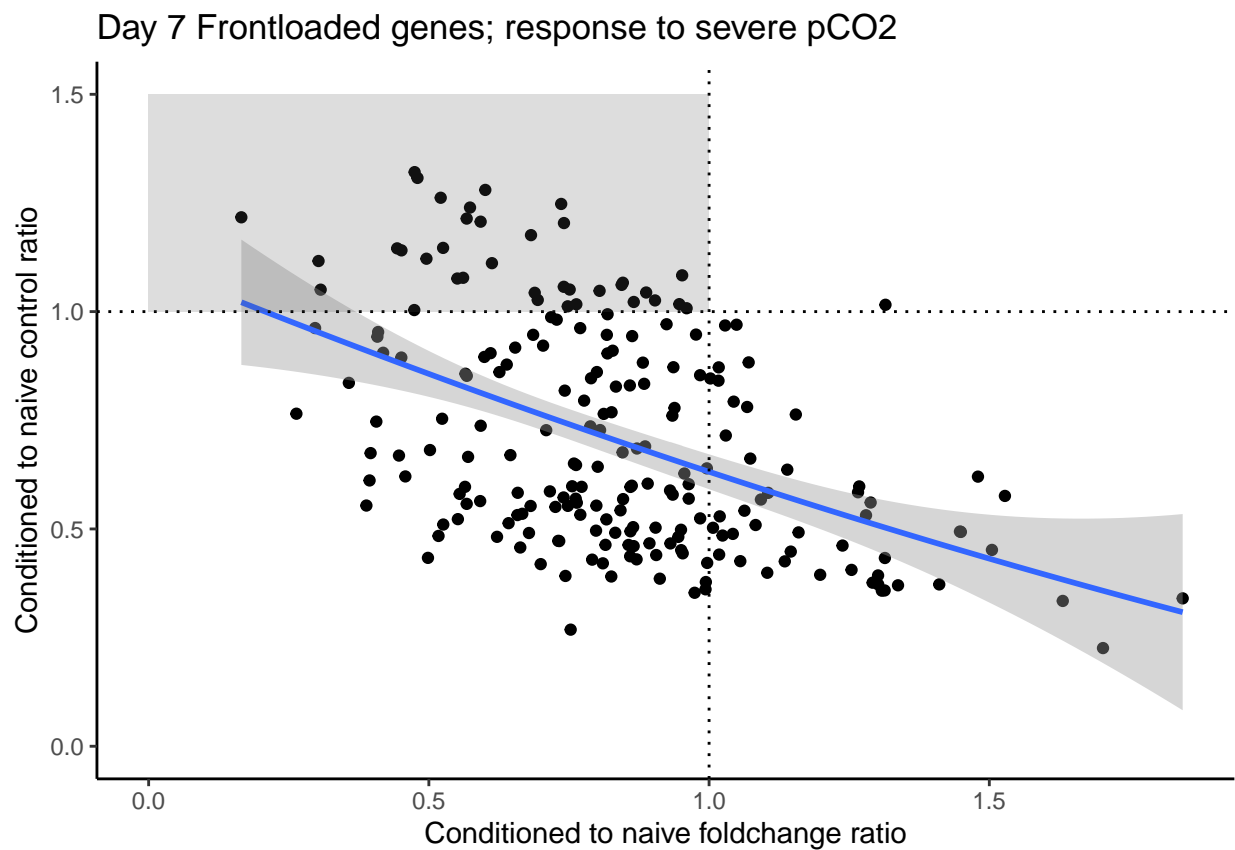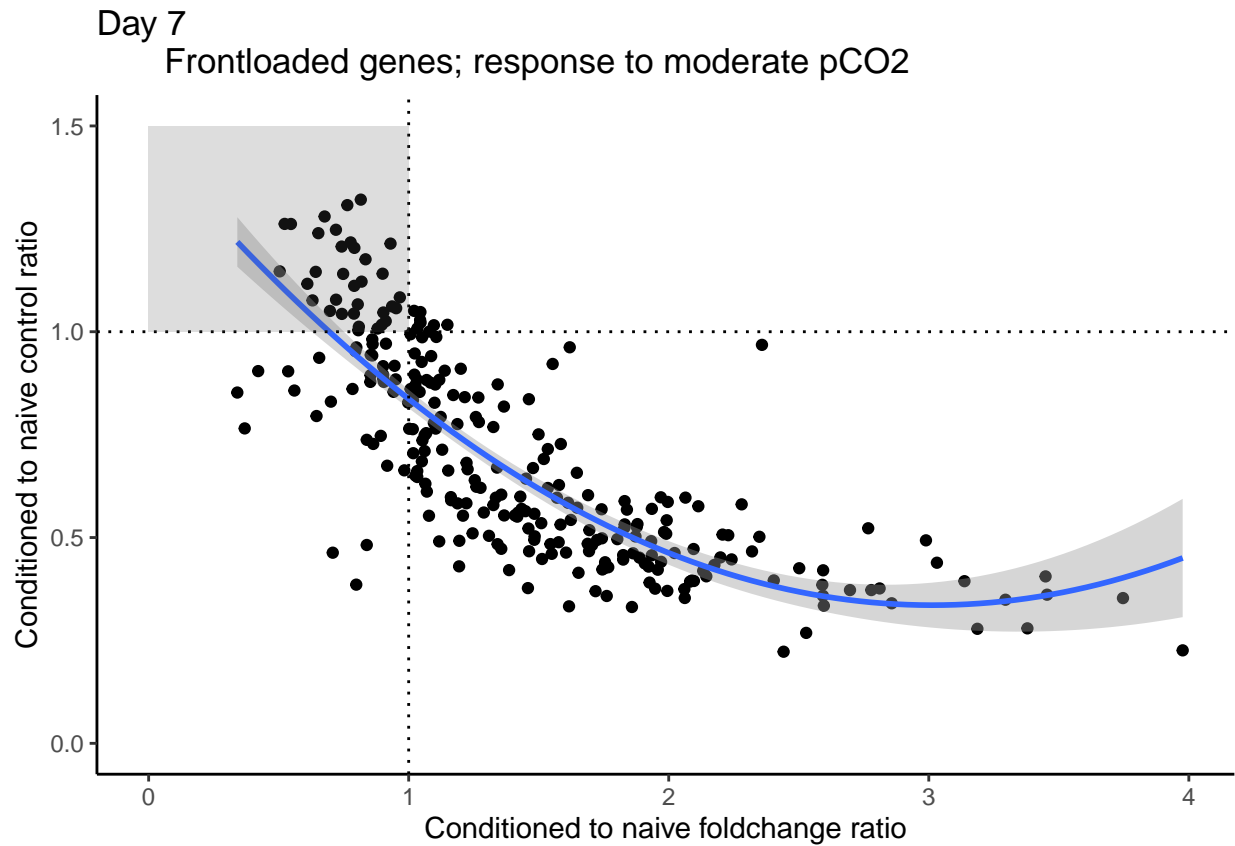
Day 7 Frontloaded genes; response to severe pCO2

Day 7 - Frontloaded genes (Table)

```
# MODERATE second treatment
Day7.wgcna.frontloaded_genes_mod <- Day7_READY %>%
                            dplyr::filter(wgcna.xall_mod < 1) %>%
                            dplyr::filter(wgcna.yall_mod > 1) %>%
                            dplyr::select('Gene')


Day7.wgcna.frontloadprobes_mod          = Day7.wgcna.frontloaded_genes_mod$Gene
probes2annot_mod                        = match(Day7.wgcna.frontloadprobes_mod, annot$V1)
Day7.wgcna.frontloaded_mod_ANNOT        = data.frame(geneSymbol = annot$V1[probes2annot_mod],
                                                Genes = annot$V7[probes2annot_mod])

kable(Day7.wgcna.frontloaded_mod_ANNOT)
```

geneSymbol	Genes
PGEN_.00g026480	Ras-related protein Rab-32B
PGEN_.00g027620	V-type proton ATPase subunit D (V-ATPase subunit D) (Vacuolar proton pump subunit D)
PGEN_.00g048930	Alcohol dehydrogenase class-3 (EC 1.1.1.1) (Alcohol dehydrogenase class-III) (Glutathione-dependen
PGEN_.00g073190	Apolipophorins [Cleaved into: Apolipophorin-2 (Apolipophorin II) (apoLp-2); Apolipophorin-1 (Apo
PGEN_.00g082240	Alpha-galactosidase A (EC 3.2.1.22) (Alpha-D-galactosidase A) (Alpha-D-galactoside galactohydrola
PGEN_.00g093570	NA
PGEN_.00g111730	V-type proton ATPase catalytic subunit A (V-ATPase subunit A) (EC 7.1.2.2) (V-ATPase 69 kDa s
PGEN_.00g116940	Glutathione peroxidase (PcGPx) (Se-PcGPx) (EC 1.11.1.9)
PGEN_.00g127120	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial (EC 3.1.2.4) (3-hydroxyisobutyryl-coenzyme A hy
PGEN_.00g127760	Long-chain specific acyl-CoA dehydrogenase, mitochondrial (LCAD) (EC 1.3.8.8)
PGEN_.00g130790	All-trans-retinol 13,14-reductase (EC 1.3.99.23) (All-trans-13,14-dihydroretinol saturase A) (RetSat
PGEN_.00g153080	Hermansky-Pudlak syndrome 5 protein (Alpha-integrin-binding protein 63) (Ruby-eye protein 2 hom
PGEN_.00g186500	D-aspartate oxidase (DASOX) (DDO) (EC 1.4.3.1)
PGEN_.00g199980	NA
PGEN_.00g201290	Putative D-cysteine desulfhydrase 1, mitochondrial (EC 4.4.1.15) (OsD-CDes1) (D-CDes1)
PGEN_.00g203570	15-hydroxyprostaglandin dehydrogenase [NAD(+)] (15-PGDH) (EC 1.1.1.141) (Prostaglandin dehyd
PGEN_.00g204750	TBC1 domain family member 22A
PGEN_.00g213350	Carnitine O-palmitoyltransferase 2, mitochondrial (EC 2.3.1.21) (Carnitine palmitoyltransferase II) (
PGEN_.00g213740	Soma ferritin (EC 1.16.3.1)
PGEN_.00g236660	NA
PGEN_.00g245510	NA
PGEN_.00g261210	Cytochrome P450 4Z1 (EC 1.14.14.1) (CYPIVZ1)
PGEN_.00g273190	Putative phosphoenolpyruvate synthase (Putative PEP synthase) (Pyruvate, water dikinase)
PGEN_.00g285980	Dimethylaniline monooxygenase [N-oxide-forming] 5 (EC 1.14.13.8) (Dimethylaniline oxidase 5) (Hep
PGEN_.00g298200	Cathepsin B (EC 3.4.22.1) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heav
PGEN_.00g298410	Cathepsin B (EC 3.4.22.1) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heav
PGEN_.00g300030	Peroxisomal acyl-coenzyme A oxidase 1 (AOX) (EC 1.3.3.6) (Palmitoyl-CoA oxidase) [Cleaved into:
PGEN_.00g305330	Poly(U)-specific endoribonuclease (EC 3.1.-.-) (Placental protein 11-related protein) (PP11-related p
PGEN_.00g306890	Adenylyl cyclase-associated protein 1 (CAP 1)
PGEN_.00g308530	Protein hunchback (Fragment)
PGEN_.00g312490	Tetratricopeptide repeat protein 39C (TPR repeat protein 39C)
PGEN_.00g313730	WASH complex subunit 2A
PGEN_.00g317830	Solute carrier family 12 member 9
PGEN_.00g334080	NA
PGEN_.00g345680	Cathepsin L1 (EC 3.4.22.15) (Cathepsin L) [Cleaved into: Cathepsin L1 heavy chain; Cathepsin L1

```r
# SEVERE second treatment
Day7.wgcna.frontloaded_genes_sev <- Day7_READY %>%
                            dplyr::filter(wgcna.xall_sev < 1) %>%
                            dplyr::filter(wgcna.yall_sev > 1) %>%
                            dplyr::select('Gene')

Day7.wgcna.frontloadprobes_sev        = Day7.wgcna.frontloaded_genes_sev$Gene
probes2annot_sev                      = match(Day7.wgcna.frontloadprobes_sev, annot$V1)
Day7.wgcna.frontloaded_sev_ANNOT      = data.frame(geneSymbol = annot$V1[probes2annot_sev],
                                          Genes = annot$V7[probes2annot_sev])

kable(Day7.wgcna.frontloaded_sev_ANNOT)
```

geneSymbol	Genes
PGEN_.00g026480	Ras-related protein Rab-32B
PGEN_.00g027620	V-type proton ATPase subunit D (V-ATPase subunit D) (Vacuolar proton pump subunit D)
PGEN_.00g032500	NA
PGEN_.00g036250	Ethanolamine-phosphate cytidylyltransferase (EC 2.7.7.14) (CTP:phosphoethanolamine cytidylyltra
PGEN_.00g048930	Alcohol dehydrogenase class-3 (EC 1.1.1.1) (Alcohol dehydrogenase class-III) (Glutathione-dependen
PGEN_.00g064470	Catalase (EC 1.11.1.6)
PGEN_.00g073190	Apolipophorins [Cleaved into: Apolipophorin-2 (Apolipophorin II) (apoLp-2); Apolipophorin-1 (Apo
PGEN_.00g082240	Alpha-galactosidase A (EC 3.2.1.22) (Alpha-D-galactosidase A) (Alpha-D-galactoside galactohydrola
PGEN_.00g093570	NA
PGEN_.00g111730	V-type proton ATPase catalytic subunit A (V-ATPase subunit A) (EC 7.1.2.2) (V-ATPase 69 kDa s
PGEN_.00g116940	Glutathione peroxidase (PcGPx) (Se-PcGPx) (EC 1.11.1.9)
PGEN_.00g127120	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial (EC 3.1.2.4) (3-hydroxyisobutyryl-coenzyme A hy
PGEN_.00g130790	All-trans-retinol 13,14-reductase (EC 1.3.99.23) (All-trans-13,14-dihydroretinol saturase A) (RetSat
PGEN_.00g132070	Vacuolar protein sorting-associated protein 29 (Vesicle protein sorting 29)
PGEN_.00g153080	Hermansky-Pudlak syndrome 5 protein (Alpha-integrin-binding protein 63) (Ruby-eye protein 2 hom
PGEN_.00g199980	NA
PGEN_.00g201290	Putative D-cysteine desulfhydrase 1, mitochondrial (EC 4.4.1.15) (OsD-CDes1) (D-CDes1)
PGEN_.00g203570	15-hydroxyprostaglandin dehydrogenase [NAD(+)] (15-PGDH) (EC 1.1.1.141) (Prostaglandin dehyd
PGEN_.00g204750	TBC1 domain family member 22A
PGEN_.00g213350	Carnitine O-palmitoyltransferase 2, mitochondrial (EC 2.3.1.21) (Carnitine palmitoyltransferase II)
PGEN_.00g213740	Soma ferritin (EC 1.16.3.1)
PGEN_.00g236660	NA
PGEN_.00g245510	NA
PGEN_.00g261210	Cytochrome P450 4Z1 (EC 1.14.14.1) (CYPIVZ1)
PGEN_.00g273190	Putative phosphoenolpyruvate synthase (Putative PEP synthase) (Pyruvate, water dikinase)
PGEN_.00g282910	FK506-binding protein 15 (FKBP-15) (133 kDa FK506-binding protein) (133 kDa FKBP) (FKBP-1
PGEN_.00g285980	Dimethylaniline monooxygenase [N-oxide-forming] 5 (EC 1.14.13.8) (Dimethylaniline oxidase 5) (Hep
PGEN_.00g298200	Cathepsin B (EC 3.4.22.1) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heav
PGEN_.00g298410	Cathepsin B (EC 3.4.22.1) (Cathepsin B1) [Cleaved into: Cathepsin B light chain; Cathepsin B heav
PGEN_.00g300030	Peroxisomal acyl-coenzyme A oxidase 1 (AOX) (EC 1.3.3.6) (Palmitoyl-CoA oxidase) [Cleaved into:
PGEN_.00g305330	Poly(U)-specific endoribonuclease (EC 3.1.-.-) (Placental protein 11-related protein) (PP11-related p
PGEN_.00g308530	Protein hunchback (Fragment)
PGEN_.00g312490	Tetratricopeptide repeat protein 39C (TPR repeat protein 39C)
PGEN_.00g313730	WASH complex subunit 2A
PGEN_.00g317830	Solute carrier family 12 member 9
PGEN_.00g334080	NA
PGEN_.00g345680	Cathepsin L1 (EC 3.4.22.15) (Cathepsin L) [Cleaved into: Cathepsin L1 heavy chain; Cathepsin L1

Day 14
Frontloaded genes; response to moderate pCO2
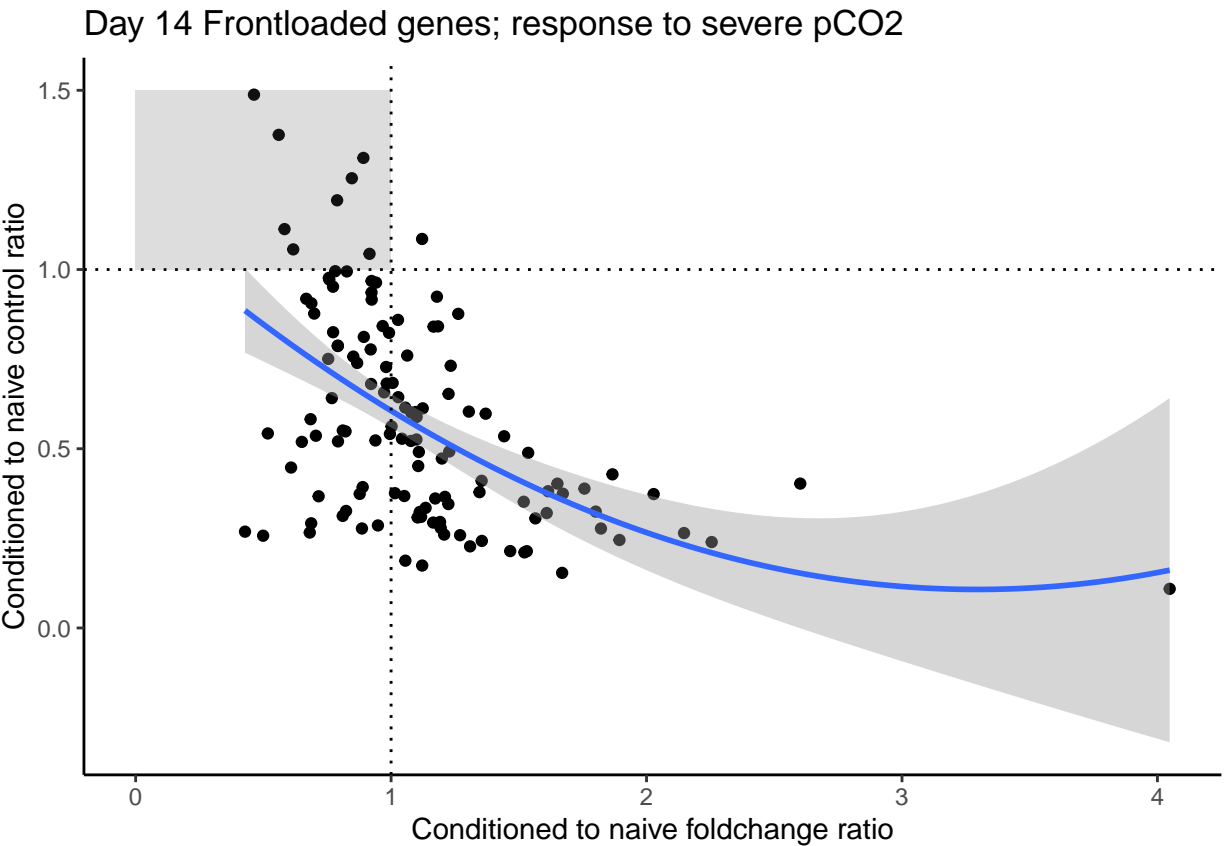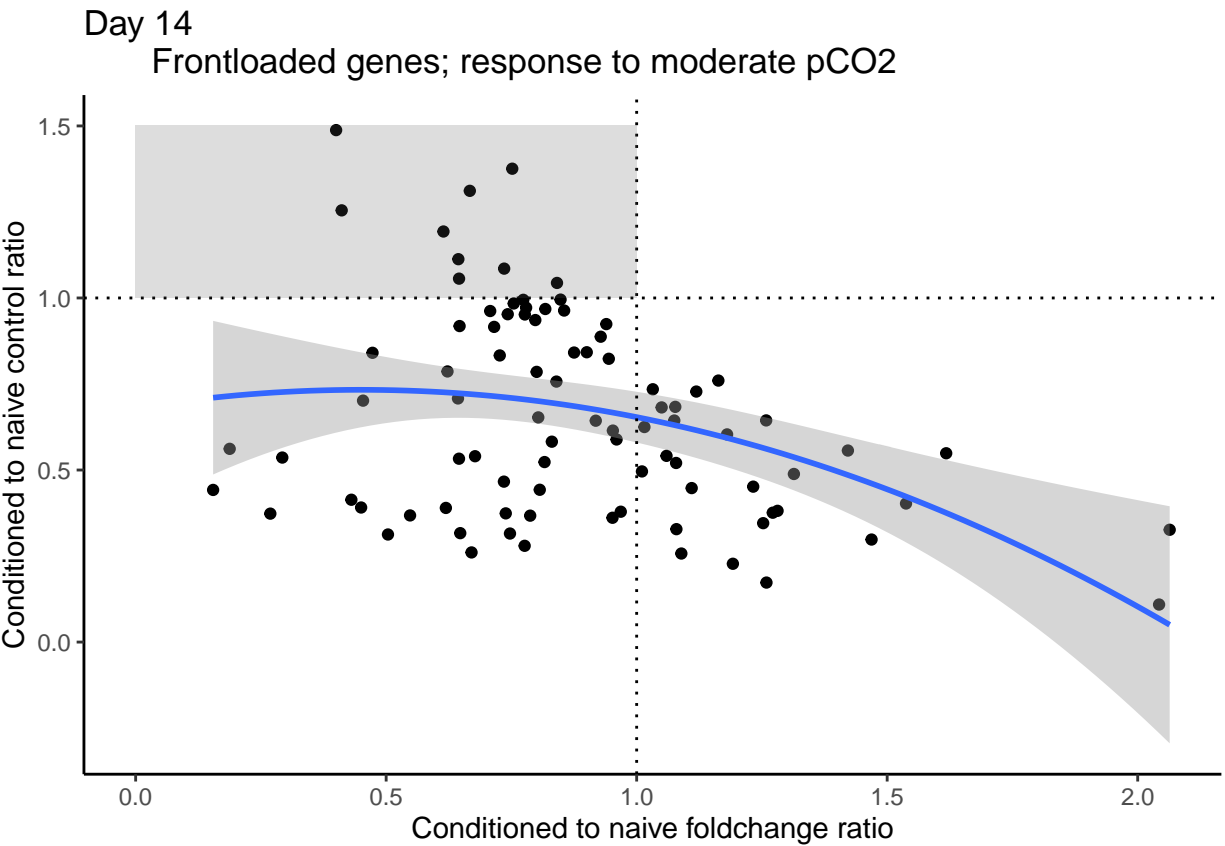
Day 14 Frontloaded genes; response to severe pCO2

Day 14 - Frontloaded genes (Table)

```
# MODERATE second treatment
Day14.wgcna.frontloaded_genes_mod <- Day14_READY %>%
                        dplyr::filter(wgcna.xall_mod < 1) %>%
                        dplyr::filter(wgcna.yall_mod > 1) %>%
                        dplyr::select('Gene') # %>%

Day14.wgcna.frontloadprobes_mod         = Day14.wgcna.frontloaded_genes_mod$Gene
probes2annot_mod                        = match(Day14.wgcna.frontloadprobes_mod, annot$V1)
Day14.wgcna.frontloaded_mod_ANNOT       = data.frame(geneSymbol = annot$V1[probes2annot_mod],
                                            Genes = annot$V7[probes2annot_mod])
kable(Day14.wgcna.frontloaded_mod_ANNOT)
```

geneSymbol	Genes
PGEN_.00g034480	ATP-binding cassette sub-family A member 5
PGEN_.00g047170	RUN and FYVE domain-containing protein 2
PGEN_.00g113630	Calponin-3 (Calponin, acidic isoform) (Calponin, non-muscle isoform)
PGEN_.00g228160	Collagen alpha-2(IV) chain
PGEN_.00g241240	NA
PGEN_.00g247890	NA
PGEN_.00g252190	Myosin regulatory light chain, smooth muscle
PGEN_.00g279950	Ribosome-recycling factor, mitochondrial (RRF) (Ribosome-releasing factor, mitochondrial)
PGEN_.00g334420	NA

```
# SEVERE second treatment
Day14.wgcna.frontloaded_genes_sev <- Day14_READY %>%
                        dplyr::filter(wgcna.xall_sev < 1) %>%
                        dplyr::filter(wgcna.yall_sev > 1) %>%
                        dplyr::select('Gene') # %>%

Day14.wgcna.frontloadprobes_sev         = Day14.wgcna.frontloaded_genes_sev$Gene
probes2annot_sev                        = match(Day14.wgcna.frontloadprobes_sev, annot$V1)
Day14.wgcna.frontloaded_sev_ANNOT       = data.frame(geneSymbol = annot$V1[probes2annot_sev],
                                            Genes = annot$V7[probes2annot_sev])
kable(Day14.wgcna.frontloaded_sev_ANNOT)
```

geneSymbol	Genes
PGEN_.00g034480	ATP-binding cassette sub-family A member 5
PGEN_.00g047170	RUN and FYVE domain-containing protein 2
PGEN_.00g113630	Calponin-3 (Calponin, acidic isoform) (Calponin, non-muscle isoform)
PGEN_.00g228160	Collagen alpha-2(IV) chain
PGEN_.00g247890	NA
PGEN_.00g252190	Myosin regulatory light chain, smooth muscle
PGEN_.00g279950	Ribosome-recycling factor, mitochondrial (RRF) (Ribosome-releasing factor, mitochondrial)
PGEN_.00g334420	NA

Day 21 - Frontloaded genes (Plot)

Day 21
Frontloaded genes; response to moderate pCO2
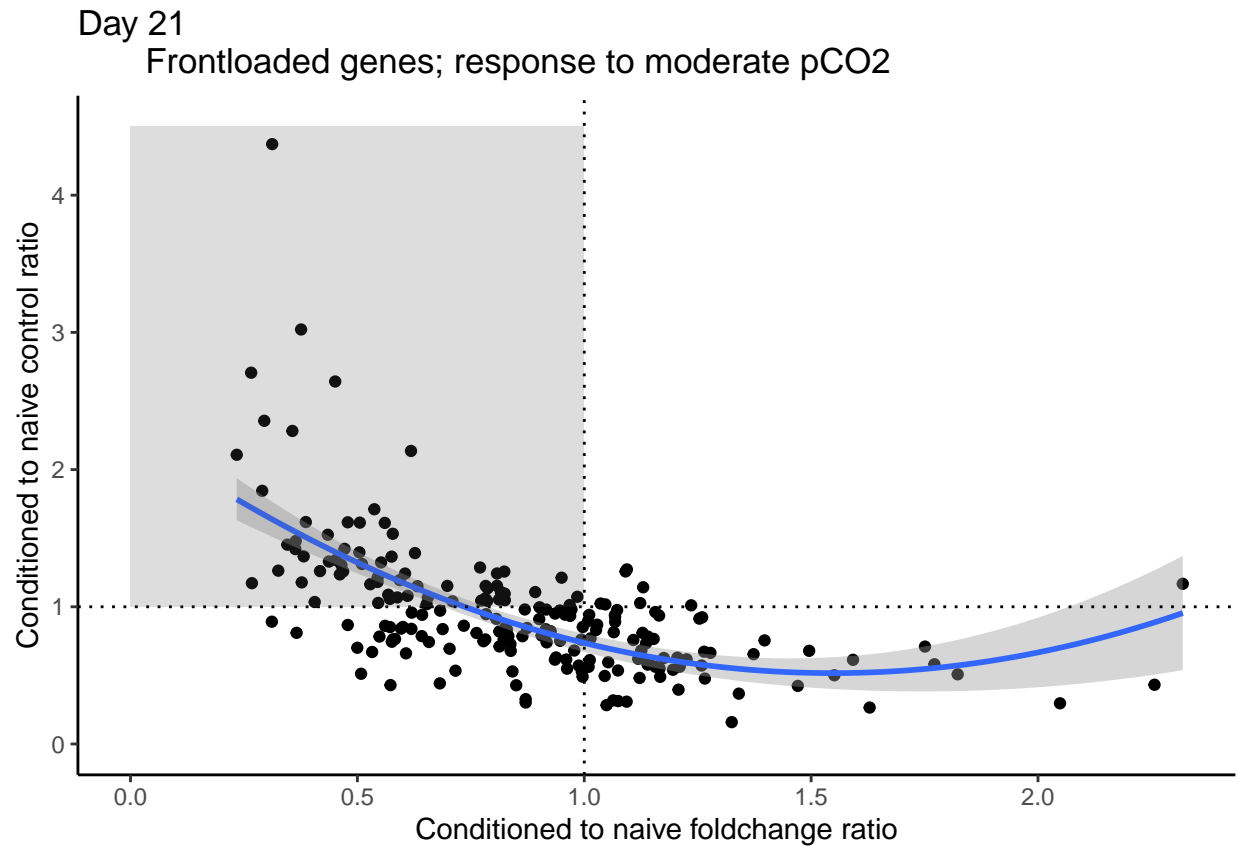
Day 21 - Frontloaded genes (Table)

```
# MODERATE second treatment
Day21.wgcna.frontloaded_genes_mod <- Day21_READY %>%
                          dplyr::filter(wgcna.xall_mod < 1) %>%
                          dplyr::filter(wgcna.yall_mod > 1) %>%
                          dplyr::select('Gene') # %>%

Day21.wgcna.frontloadprobes_mod        = Day21.wgcna.frontloaded_genes_mod$Gene
probes2annot_mod                       = match(Day21.wgcna.frontloadprobes_mod, annot$V1)
Day21.wgcna.frontloaded_mod_ANNOT      = data.frame(geneSymbol = annot$V1[probes2annot_mod],
                                          Genes = annot$V7[probes2annot_mod])
kable(Day21.wgcna.frontloaded_mod_ANNOT)
```

geneSymbol	Genes
PGEN_.00g003940	Regucalcin (RC) (Gluconolactonase) (GNL) (EC 3.1.1.17) (Senescence marker protein 30) (SMP-30)
PGEN_.00g006490	Beta,beta-carotene 15,15'-dioxygenase (EC 1.13.11.63) (Beta-carotene dioxygenase 1) (Beta-carotene
PGEN_.00g008880	Hydroxysteroid dehydrogenase-like protein 2 (EC 1.-.-.-)
PGEN_.00g014860	Molybdenum cofactor biosynthesis protein 1 [Includes: GTP 3',8-cyclase (EC 4.1.99.22) (Molybdenu
PGEN_.00g018570	Mammalian ependymin-related protein 1 (MERP-1)
PGEN_.00g024970	NA
PGEN_.00g027970	NA
PGEN_.00g030010	Homeobox protein prospero
PGEN_.00g031490	NA
PGEN_.00g035820	Prosaposin (Proactivator polypeptide) [Cleaved into: Saposin-A (Protein A); Saposin-B (Cerebroside
PGEN_.00g039520	NA
PGEN_.00g042910	Sulfotransferase 1C4 (ST1C4) (EC 2.8.2.-) (Sulfotransferase 1C2) (SULT1C#2)
PGEN_.00g046630	L-rhamnonate dehydratase (RhamD) (EC 4.2.1.90)
PGEN_.00g047200	Trypsin beta (EC 3.4.21.4)
PGEN_.00g048930	Alcohol dehydrogenase class-3 (EC 1.1.1.1) (Alcohol dehydrogenase class-III) (Glutathione-depender
PGEN_.00g049840	Meprin A subunit alpha (EC 3.4.24.18) (Endopeptidase-2) (Endopeptidase-24.18 subunit alpha) (E-2
PGEN_.00g064390	Putative defense protein 1 (DFP-1)
PGEN_.00g070040	Apolipophorins [Cleaved into: Apolipophorin-2 (Apolipophorin II) (apoLp-2); Apolipophorin-1 (Apo
PGEN_.00g077860	Sorting nexin-12
PGEN_.00g084890	Protocadherin-11 X-linked (Protocadherin-11) (Protocadherin on the X chromosome)
PGEN_.00g085780	Transforming growth factor-beta-induced protein ig-h3 (Beta ig-h3) (Kerato-epithelin) (RGD-contain
PGEN_.00g095390	Transforming growth factor-beta-induced protein ig-h3 (Beta ig-h3)
PGEN_.00g106710	NA
PGEN_.00g114200	Caprin-2 (C1q domain-containing protein 1) (Cytoplasmic activation/proliferation-associated protein
PGEN_.00g114370	NA
PGEN_.00g119160	Perlucin
PGEN_.00g121940	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic (GPD-C) (GPDH-C) (EC 1.1.1.8)
PGEN_.00g122110	Poly(rC)-binding protein 3 (Alpha-CP3) (PCBP3-overlapping transcript) (PCBP3-overlapping trans
PGEN_.00g122510	NA
PGEN_.00g123000	NA
PGEN_.00g130020	Fatty acid-binding protein 1
PGEN_.00g130760	NA
PGEN_.00g133710	NA
PGEN_.00g135600	Peroxisomal acyl-coenzyme A oxidase 3 (EC 1.3.3.6) (Branched-chain acyl-CoA oxidase) (BRCACox
PGEN_.00g150640	Oxysterol-binding protein 2 (Oxysterol-binding protein-related protein 4) (ORP-4) (OSBP-related p
PGEN_.00g155300	NA
PGEN_.00g155710	RUN domain-containing protein 1
PGEN_.00g156260	Prostaglandin reductase-3 (PTGR-3) (EC 1.3.1.48) (15-oxoprostaglandin 13-reductase) (Zinc-binding
PGEN_.00g169020	NA
PGEN_.00g187320	Interferon-induced very large GTPase 1 (Very large-inducible GTPase-1) (VLIG-1)
PGEN_.00g199190	NA
PGEN_.00g204750	TBC1 domain family member 22A
PGEN_.00g214740	Adiponectin receptor protein
PGEN_.00g228160	Collagen alpha-2(IV) chain
PGEN_.00g237580	Pancreatic triacylglycerol lipase (PL) (PTL) (Pancreatic lipase) (EC 3.1.1.3) (Fragment)
PGEN_.00g240360	NA
PGEN_.00g248130	NA
PGEN_.00g251840	Copper homeostasis protein cutC homolog
PGEN_.00g258220	NA
PGEN_.00g265000	NA
PGEN_.00g273190	Putative phosphoenolpyruvate synthase (Putative PEP synthase) (Pyruvate, water dikinase)
PGEN_.00g281080	NA
PGEN_.00g281550	DBH-like monooxygenase protein 1 (EC 1.14.17.-) (DBH-related protein) (Monooxygenase X)
PGEN_.00g285980	Dimethylaniline monooxygenase [N-oxide-forming] 5 (EC 1.14.13.8) (Dimethylaniline oxidase 5) (Hep
PGEN_.00g286040	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial (MCAD) (EC 1.3.8.7)
PGEN_.00g293270	Perlucin-like protein
PGEN_.00g306160	NA