CannabinoidAccumLineGraphs

```
library(readxl)
setwd("~/2019 Hemp Field Trials/2019 CBD TRIALS/Data Analysis/Cannabinoid Data")
Cannabinoids2019 <- read_excel("CBDTrial2019.xlsx")
```

```
## New names:
## * `` -> ...18
## * `` -> ...26
## * `` -> ...33
## * `` -> ...36
```

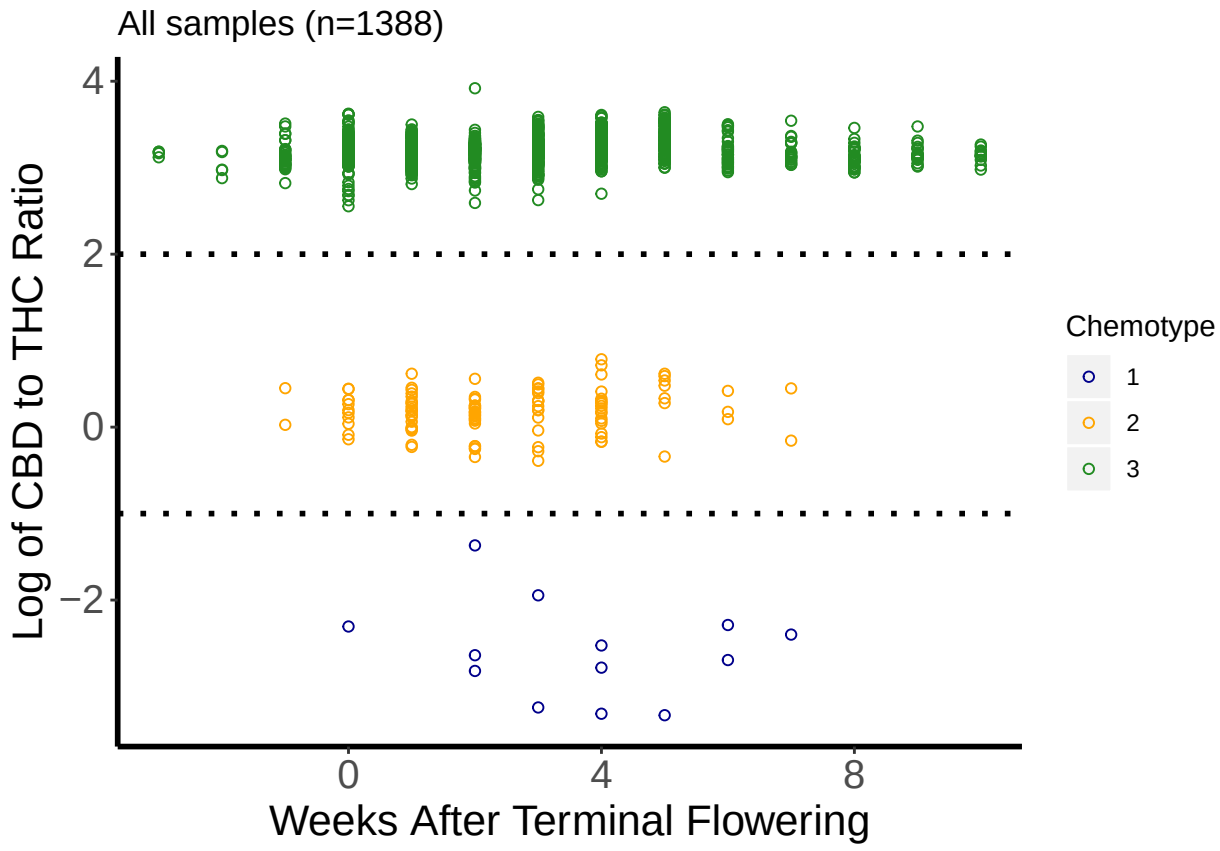
```
Cannabinoids2019$Chemotype = as.factor(Cannabinoids2019$Chemotype)
library(ggplot2)

ChemotypeIII = subset(Cannabinoids2019, Chemotype=="3")
ChemotypeII = subset(Cannabinoids2019, Chemotype=="2")
ChemotypeI = subset(Cannabinoids2019, Chemotype=="1")
```

```
#Make list of cultivars
cultivars = vector()
for(i in Cannabinoids2019$Cultivar) {
  if(i %in% cultivars) {}
  else{cultivars = append(cultivars, i)}
}
cultivars
```

```
##  [1] "A2R4"              "A2R4 (E)"          "AC/DC"
##  [4] "Brilliance"        "Cherry 307"        "Cherry 308"
##  [7] "Cherry 5"          "Deschutes"         "Deschutes (E)"
## [10] "FL 49"             "FL 58"             "FL 70"
## [13] "FL 70x70"          "FL 71"             "FL 71x71"
## [16] "FL 80"             "KG9201"            "KG9202"
## [19] "Late Sue"          "GVA.H.19.1097"     "GVA.H.19.1097 (E)"
## [22] "NY Cherry"         "Otto II"           "RN 13a"
## [25] "RN 16"             "RN 17"             "RN 19"
## [28] "GVA.H.19.1039"     "Rogue"             "Rogue (E)"
## [31] "T2"                "Tangerine"         "TJs CBD"
## [34] "Umpqua"            "Umpqua (E)"
```

```
ggplot(data = Cannabinoids2019, aes(y=log(CBDtoTHC), x=WeeksPostFlower, color=Chemotype,na.rm=TRUE))+
  #geom_line(stat="summary", size=1,aes(color=Chemotype))+
  geom_point(shape=1, aes(color=Chemotype))+
  scale_color_manual(values=c("blue4","Orange", "forestgreen"))+
  labs(title=paste("All samples (n=", nrow(Cannabinoids2019),")", sep=""), y="Log of CBD to THC Ratio",
  geom_abline(intercept=2,slope=0, color="Black", size=1,linetype=3)+
```

```
  geom_abline(intercept=-1,slope=0, color="Black", size=1,linetype=3)+
  theme(axis.text = element_text(angle = 0, hjust = , vjust=.45, size=15),
        axis.title = element_text(size=16),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        panel.background = element_blank(),
        axis.line = element_line(color="black", size = 1))
```




```
linegraphTHC = function(cultivar){

  subs = subset(Cannabinoids2019, Cultivar == cultivar)

  if(min(as.numeric(subs$Chemotype))==3){
  ggplot(data = subs, aes(y=THCtot, x=WeeksPostFlower, fill=Chemotype,na.rm=TRUE))+
  geom_line(stat="summary", size=1,aes(color=Chemotype))+
  geom_point(shape=4, aes(color=Chemotype))+
  geom_abline(intercept=.3,slope=0, color="Black", size=1,linetype=3)+
  scale_color_manual(values=c("forestgreen"))+
  labs(title=paste(cultivar, " (n=", nrow(subs),")", sep=""), y="Total Potential THC", x="Weeks After T
  geom_errorbar(stat="summary", size=1,width=.1,na.rm=T)+
  theme(axis.text = element_text(angle = 0, hjust = , vjust=.45, size=15),
        axis.title = element_text(size=16),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        panel.background = element_blank(),
```

```
        axis.line = element_line(color="black", size = 1))
  }

  else if(min(as.numeric(subs$Chemotype))==2){
  ggplot(data = subs, aes(y=THCtot, x=WeeksPostFlower, fill=Chemotype,na.rm=TRUE))+
  geom_line(stat="summary", size=1,aes(color=Chemotype))+
  geom_point(shape=4, aes(color=Chemotype))+
  geom_abline(intercept=.3,slope=0, color="Black", size=1,linetype=3)+
  scale_color_manual(values=c("orange","forestgreen"))+
  labs(title=paste(cultivar, " (n=", nrow(subs),")", sep=""), y="Total Potential THC", x="Weeks After To
  geom_errorbar(stat="summary", size=1,width=.1,na.rm=T)+
  theme(axis.text = element_text(angle = 0, hjust = , vjust=.45, size=15),
        axis.title = element_text(size=16),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        panel.background = element_blank(),
        axis.line = element_line(color="black", size = 1))
  }

  else{
  ggplot(data = subs, aes(y=THCtot, x=WeeksPostFlower, fill=Chemotype,na.rm=TRUE))+
  geom_line(stat="summary", size=1,aes(color=Chemotype))+
  geom_point(shape=4, aes(color=Chemotype))+
  geom_abline(intercept=.3,slope=0, color="Black", size=1,linetype=3)+
  scale_color_manual(values=c("blue4","Orange","forestgreen"))+
  labs(title=paste(cultivar, " (n=", nrow(subs),")", sep=""), y="Total Potential THC", x="Weeks After To
  geom_errorbar(stat="summary", size=1,width=.1,na.rm=T)+
  theme(axis.text = element_text(angle = 0, hjust = , vjust=.45, size=15),
        axis.title = element_text(size=16),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        panel.background = element_blank(),
        axis.line = element_line(color="black", size = 1))
  }
}
```

```
linegraphCBD = function(cultivar){

  subs = subset(Cannabinoids2019, Cultivar == cultivar)

  if(min(as.numeric(subs$Chemotype))==3){
  ggplot(data = subs, aes(y=CBDtot, x=WeeksPostFlower, fill=Chemotype,na.rm=TRUE))+
  geom_line(stat="summary", size=1,aes(color=Chemotype))+
  geom_point(shape=4, aes(color=Chemotype))+
  scale_color_manual(values=c("forestgreen"))+
  labs(title=paste(cultivar, " (n=", nrow(subs),")", sep=""), y="Total Potential CBD", x="Weeks After To
  geom_errorbar(stat="summary", size=1,width=.1,na.rm=T)+
  theme(axis.text = element_text(angle = 0, hjust = , vjust=.45, size=15),
        axis.title = element_text(size=16),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        panel.background = element_blank(),
        axis.line = element_line(color="black", size = 1))
```

```
  }

  else if(min(as.numeric(subs$Chemotype))==2){
  ggplot(data = subs, aes(y=CBDtot, x=WeeksPostFlower, fill=Chemotype,na.rm=TRUE))+
  geom_line(stat="summary", size=1,aes(color=Chemotype))+
  geom_point(shape=4, aes(color=Chemotype))+
  scale_color_manual(values=c("orange","forestgreen"))+
  labs(title=paste(cultivar, " (n=", nrow(subs),")", sep=""), y="Total Potential CBD", x="Weeks After To
  geom_errorbar(stat="summary", size=1,width=.1,na.rm=T)+
  theme(axis.text = element_text(angle = 0, hjust = , vjust=.45, size=15),
        axis.title = element_text(size=16),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        panel.background = element_blank(),
        axis.line = element_line(color="black", size = 1))
  }

  else{
  ggplot(data = subs, aes(y=CBDtot, x=WeeksPostFlower, fill=Chemotype,na.rm=TRUE))+
  geom_line(stat="summary", size=1,aes(color=Chemotype))+
  geom_point(shape=4, aes(color=Chemotype))+
  scale_color_manual(values=c("blue4","Orange","forestgreen"))+
  labs(title=paste(cultivar, " (n=", nrow(subs),")", sep=""), y="Total Potential CBD", x="Weeks After To
  geom_errorbar(stat="summary", size=1,width=.1,na.rm=T)+
  theme(axis.text = element_text(angle = 0, hjust = , vjust=.45, size=15),
        axis.title = element_text(size=16),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        panel.background = element_blank(),
        axis.line = element_line(color="black", size = 1))
  }
}
```

```
linegraphTOTAL = function(cultivar){

  subs = subset(Cannabinoids2019, Cultivar == cultivar)

  if(min(as.numeric(subs$Chemotype))==3){
  ggplot(data = subs, aes(y=TotalCannabinoids, x=WeeksPostFlower, fill=Chemotype,na.rm=TRUE))+
  geom_line(stat="summary", size=1,aes(color=Chemotype))+
  geom_point(shape=4, aes(color=Chemotype))+
  scale_color_manual(values=c("forestgreen"))+
  labs(title=paste(cultivar, " (n=", nrow(subs),")", sep=""), y="Total Cannabinoids", x="Weeks After Tes
  geom_errorbar(stat="summary", size=1,width=.1,na.rm=T)+
  theme(axis.text = element_text(angle = 0, hjust = , vjust=.45, size=15),
        axis.title = element_text(size=16),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        panel.background = element_blank(),
        axis.line = element_line(color="black", size = 1))
  }

  else if(min(as.numeric(subs$Chemotype))==2){
```

```
  ggplot(data = subs, aes(y=TotalCannabinoids, x=WeeksPostFlower, fill=Chemotype,na.rm=TRUE))+
  geom_line(stat="summary", size=1,aes(color=Chemotype))+
  geom_point(shape=4, aes(color=Chemotype))+
  scale_color_manual(values=c("orange","forestgreen"))+
  labs(title=paste(cultivar, " (n=", nrow(subs),")", sep=""), y="Total Cannabinoids", x="Weeks After Tr
  geom_errorbar(stat="summary", size=1,width=.1,na.rm=T)+
  theme(axis.text = element_text(angle = 0, hjust = , vjust=.45, size=15),
        axis.title = element_text(size=16),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        panel.background = element_blank(),
        axis.line = element_line(color="black", size = 1))
  }

  else{
  ggplot(data = subs, aes(y=TotalCannabinoids, x=WeeksPostFlower, fill=Chemotype,na.rm=TRUE))+
  geom_line(stat="summary", size=1,aes(color=Chemotype))+
  geom_point(shape=4, aes(color=Chemotype))+
  scale_color_manual(values=c("blue4","Orange","forestgreen"))+
  labs(title=paste(cultivar, " (n=", nrow(subs),")", sep=""), y="Total Cannabinoids", x="Weeks After Tr
  geom_errorbar(stat="summary", size=1,width=.1,na.rm=T)+
  theme(axis.text = element_text(angle = 0, hjust = , vjust=.45, size=15),
        axis.title = element_text(size=16),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        panel.background = element_blank(),
        axis.line = element_line(color="black", size = 1))
  }
}
```

```
for(cv in cultivars){
  print(linegraphCBD(cv))
  print(linegraphTHC(cv))
  print(linegraphTOTAL(cv))
}
```

```
## No summary function supplied, defaulting to `mean_se()
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```

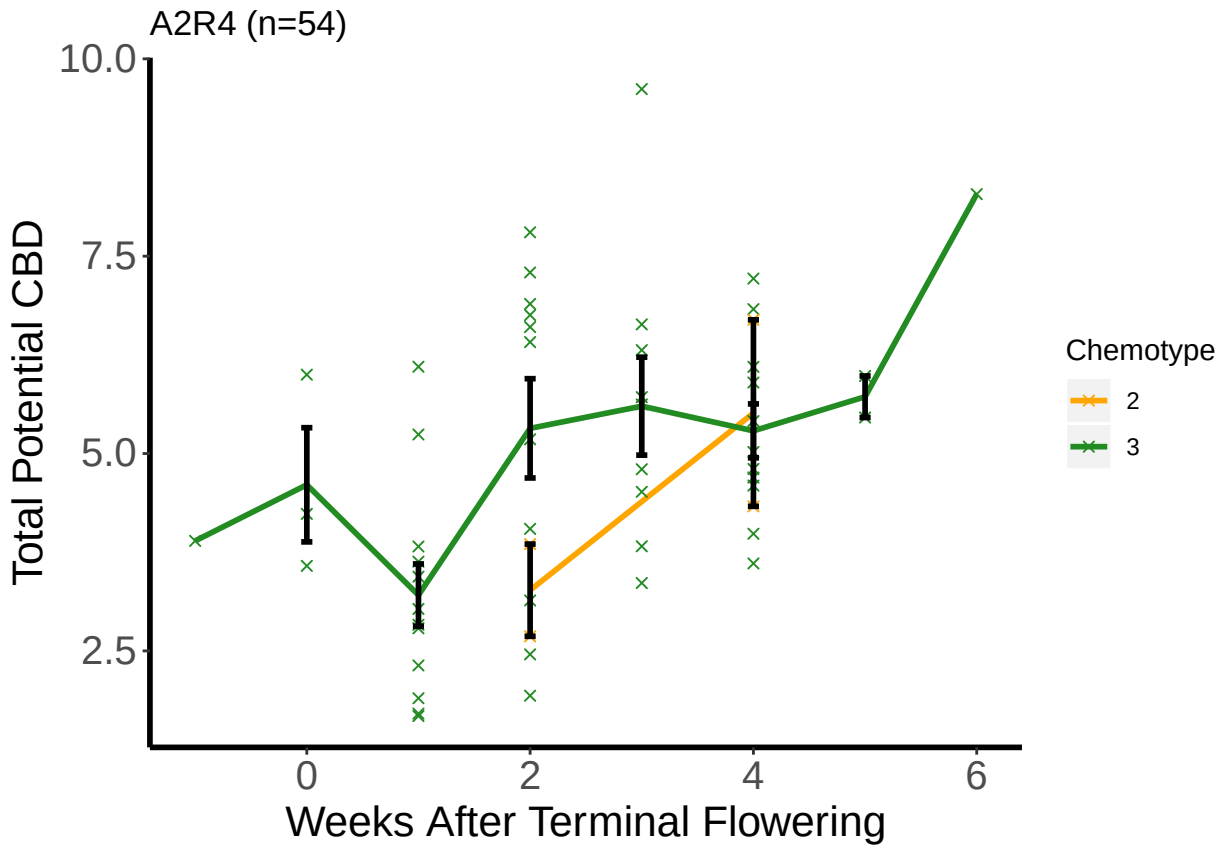


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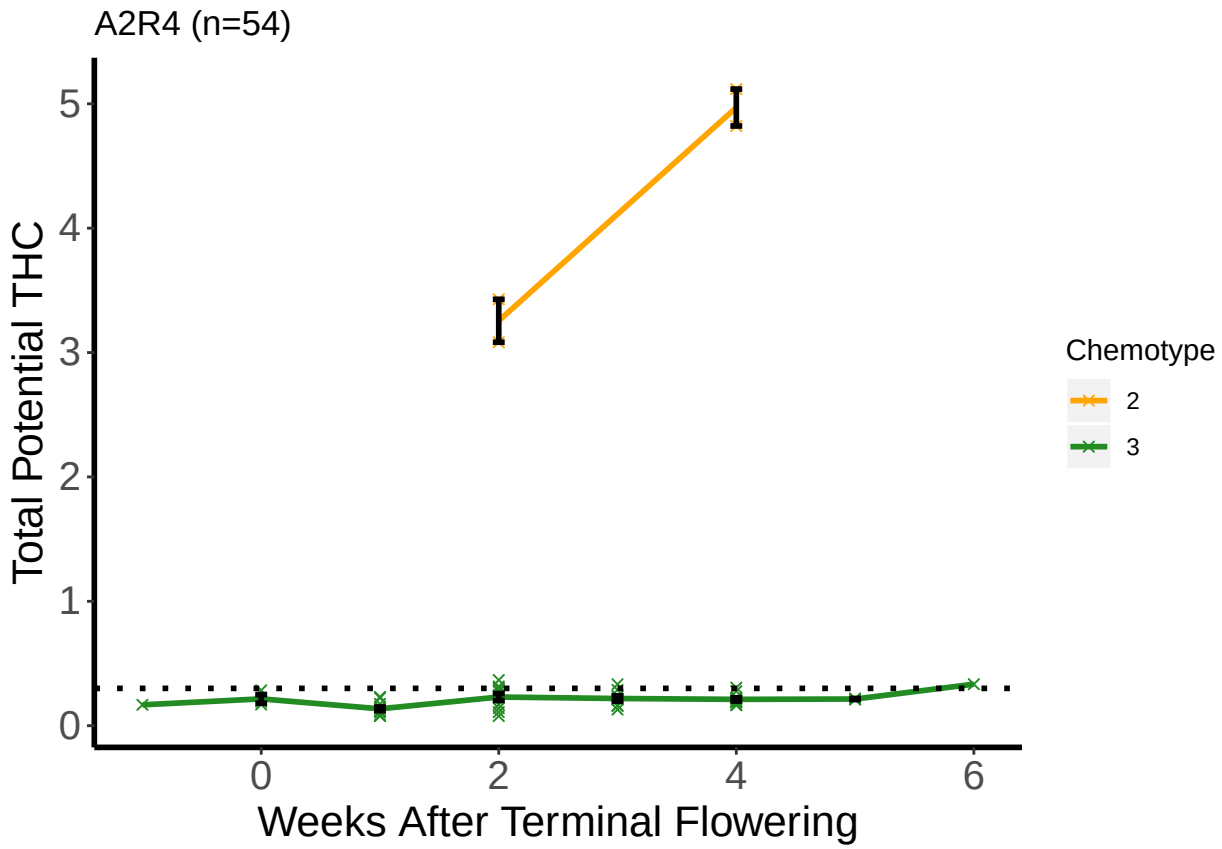


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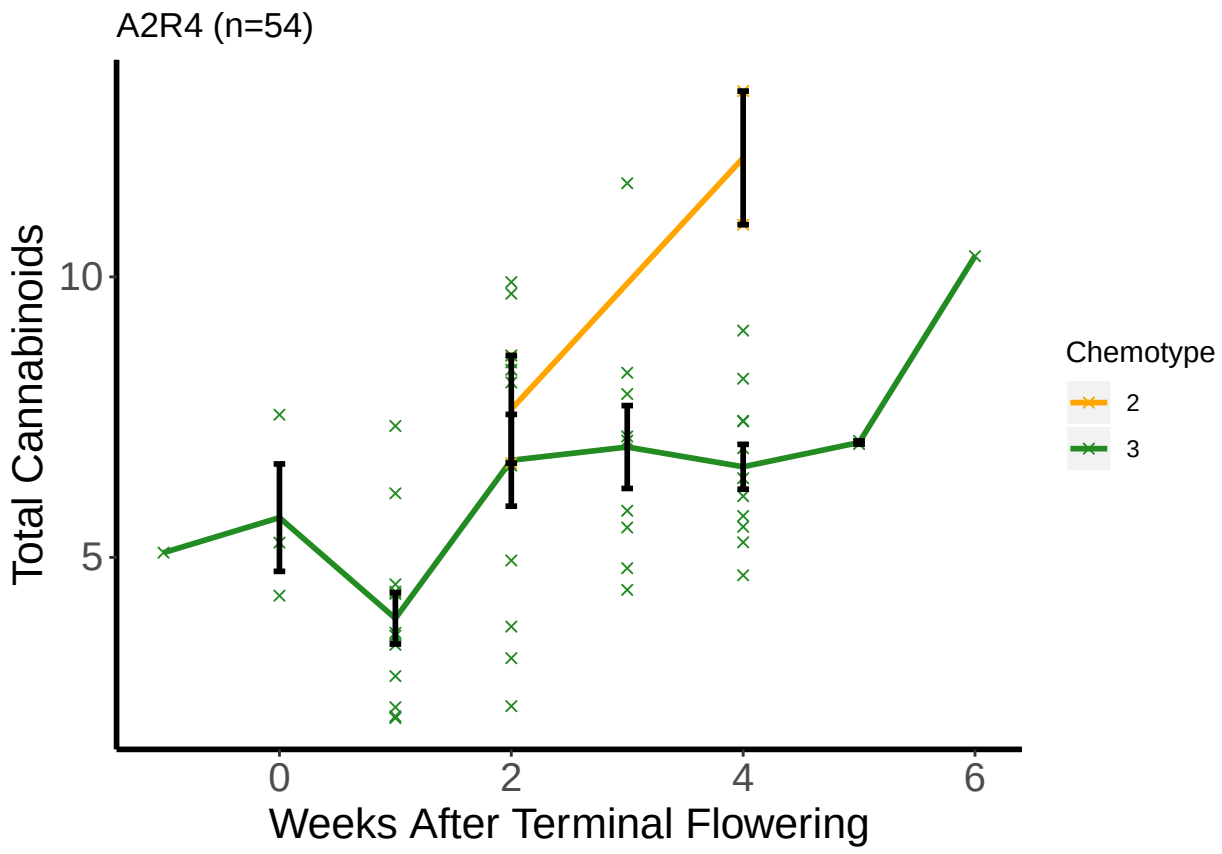


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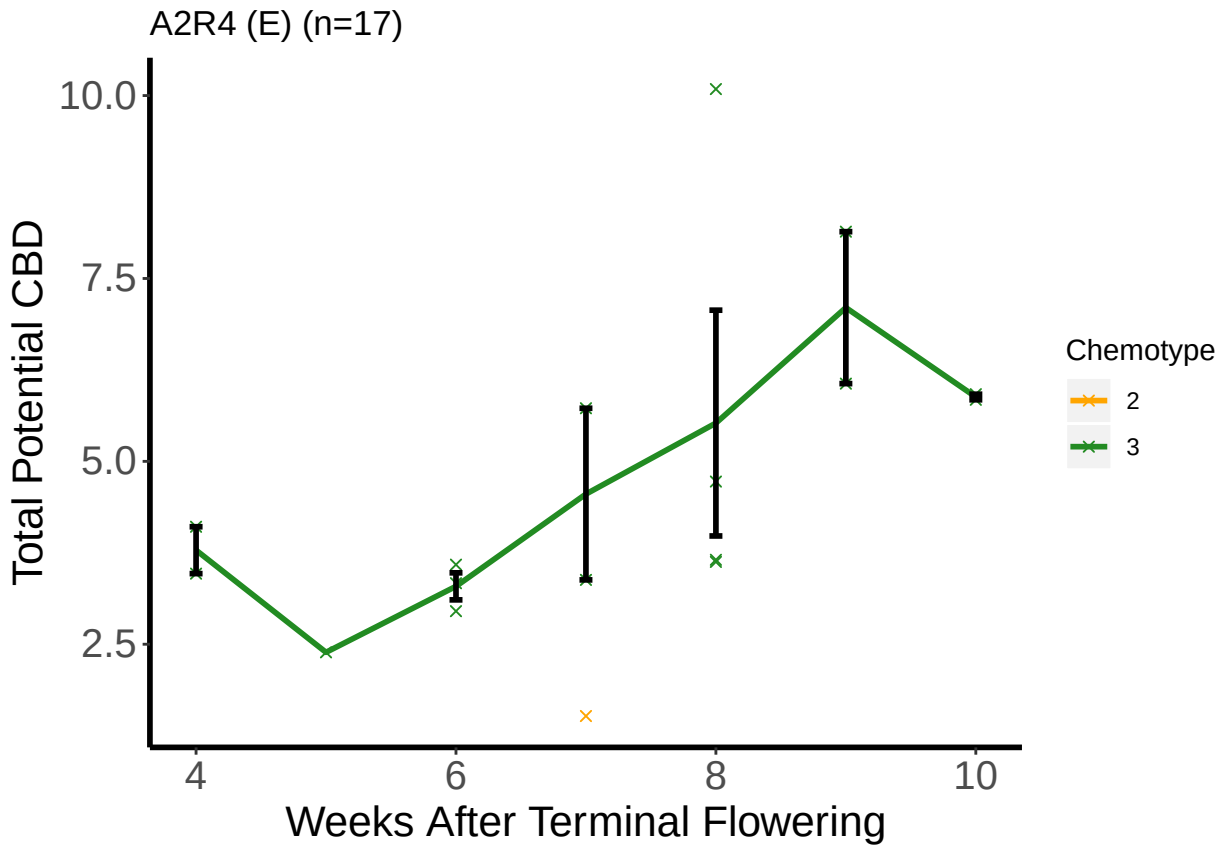


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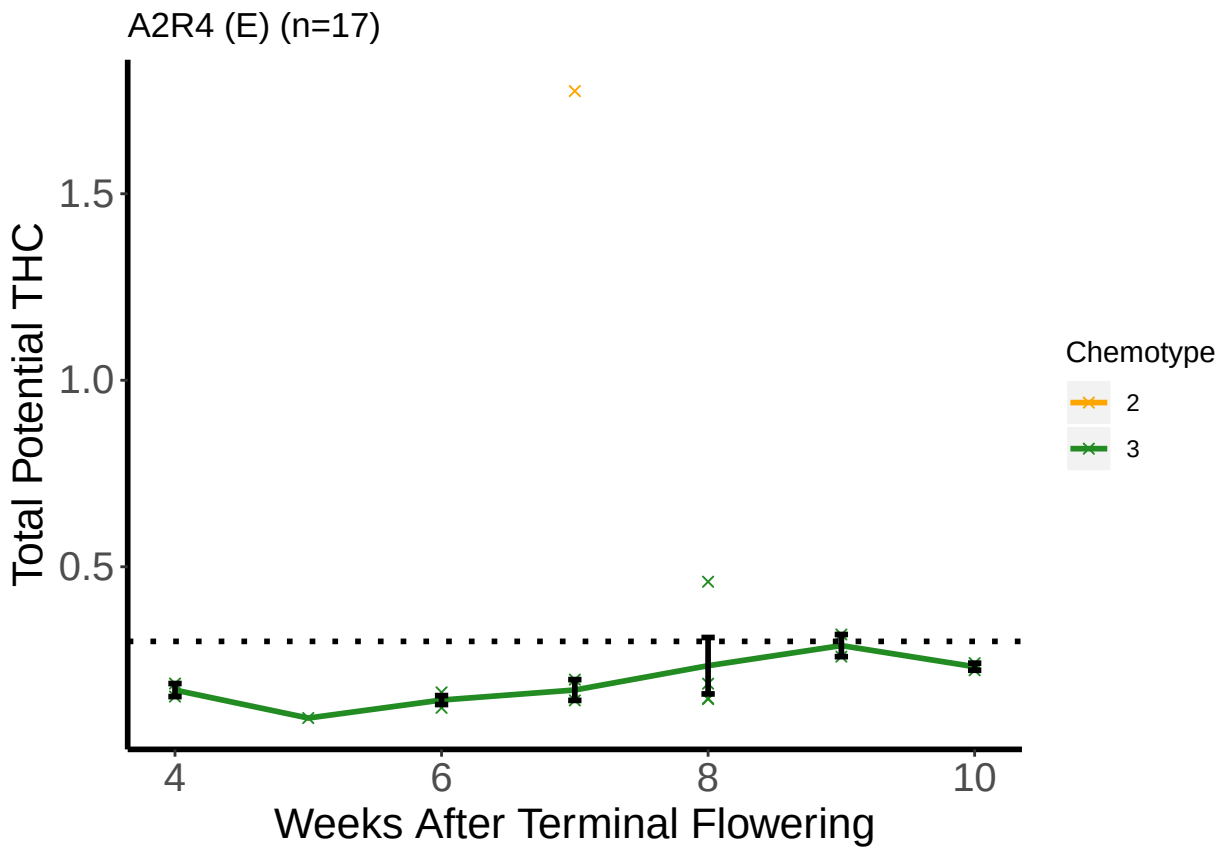


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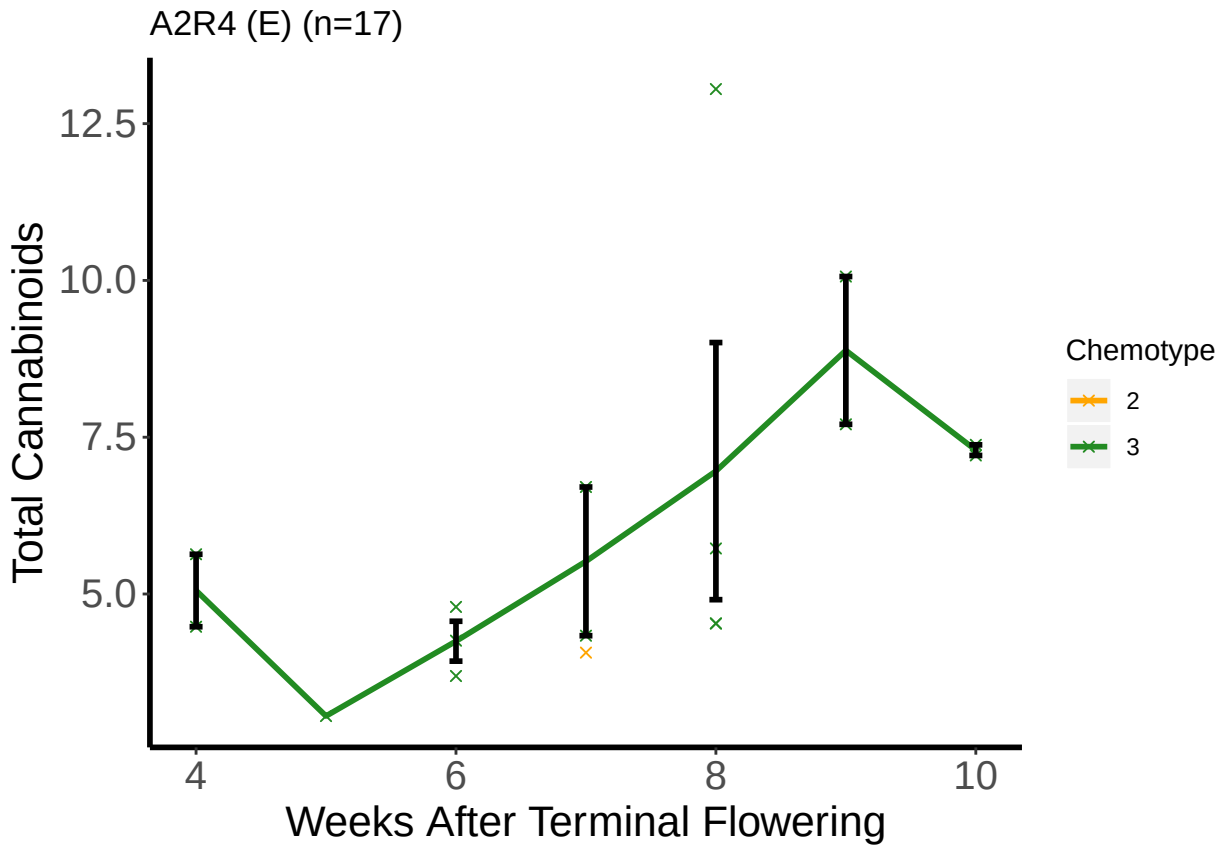


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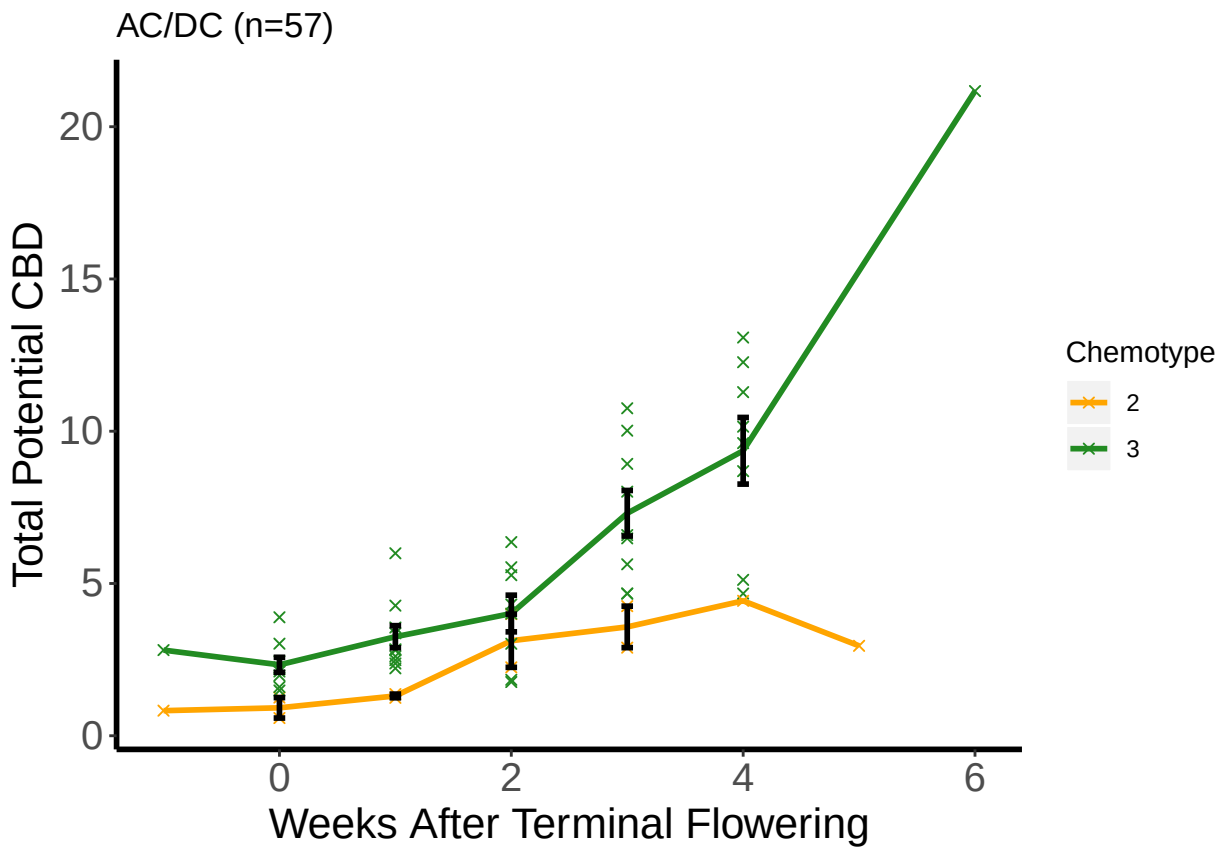


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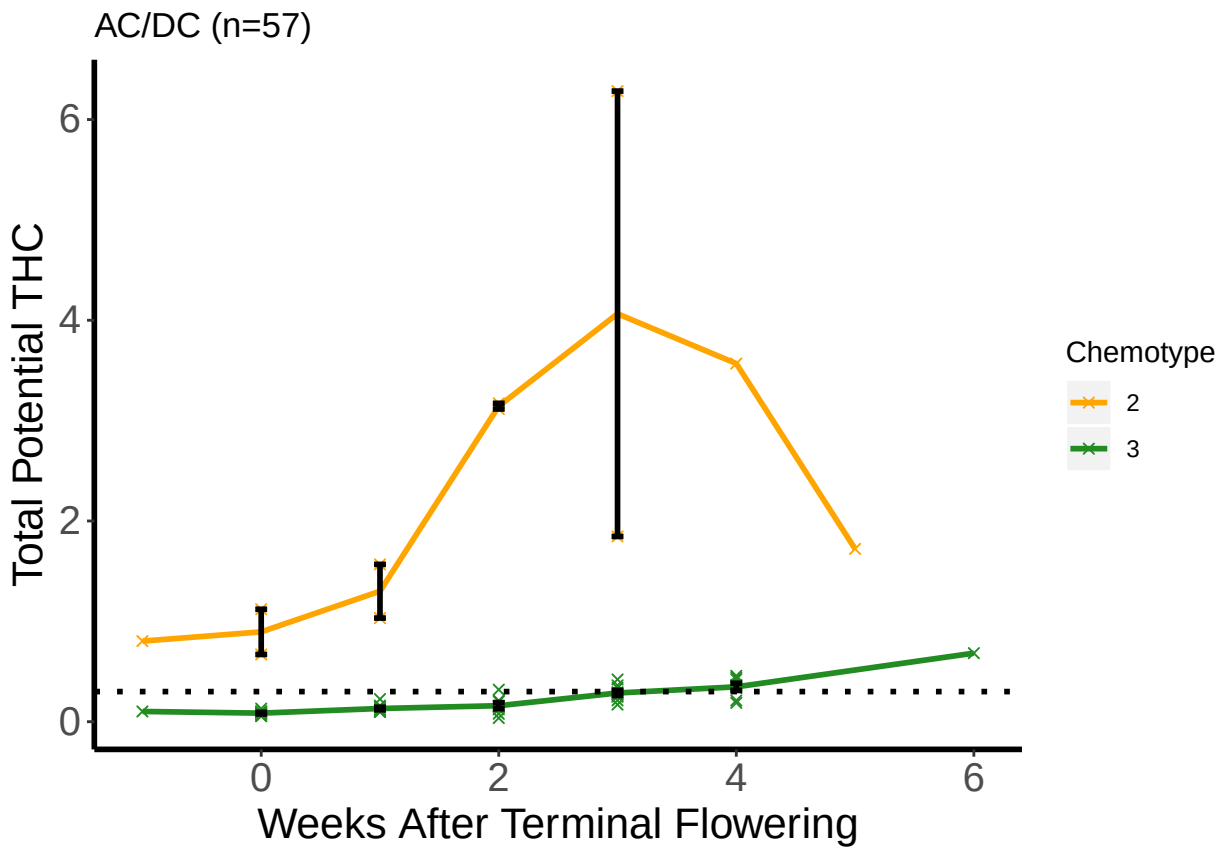


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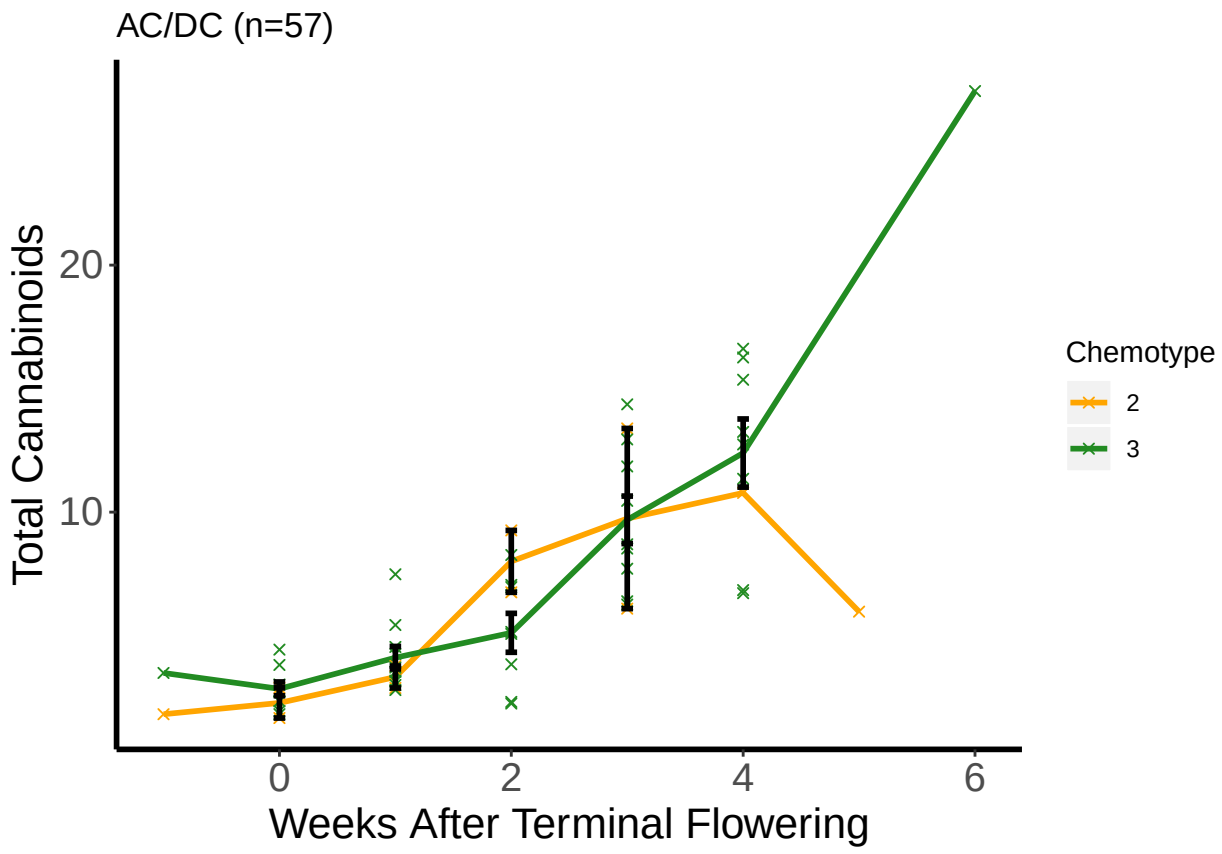


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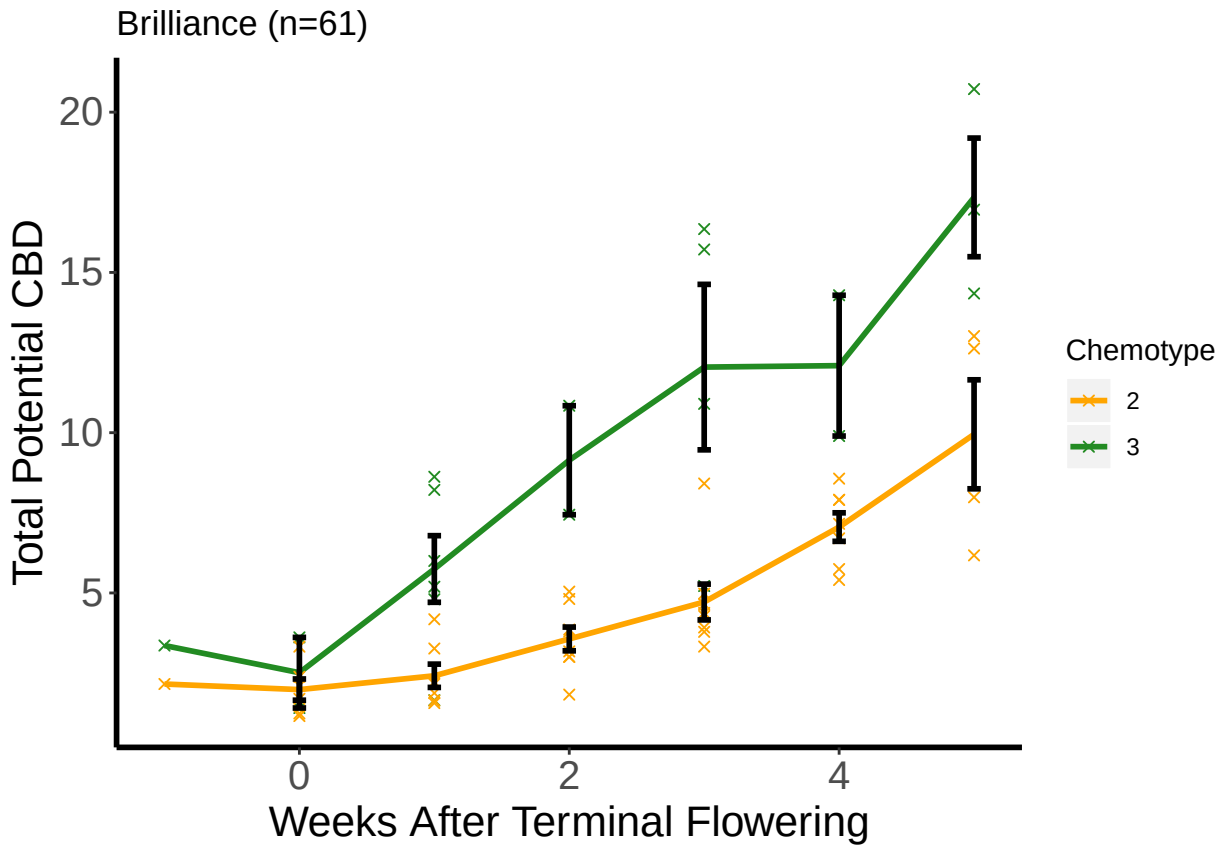


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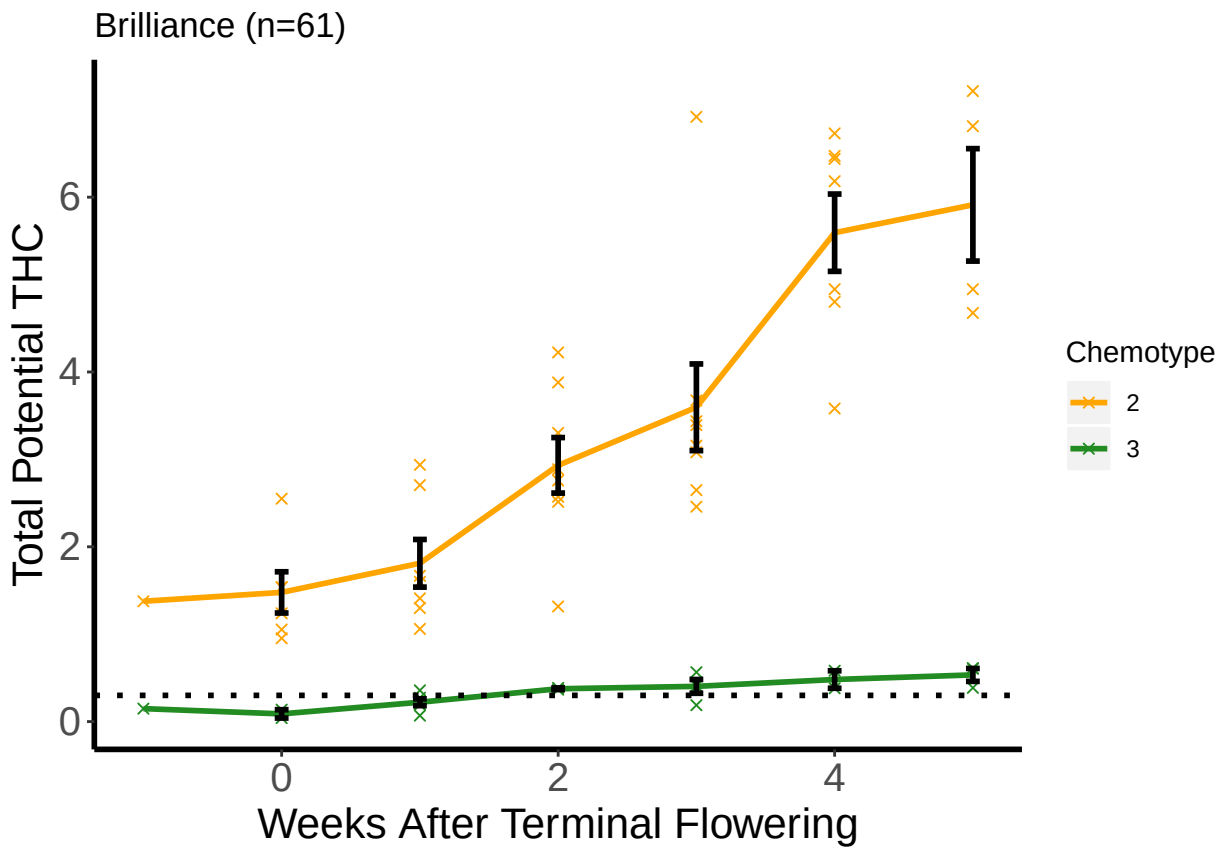


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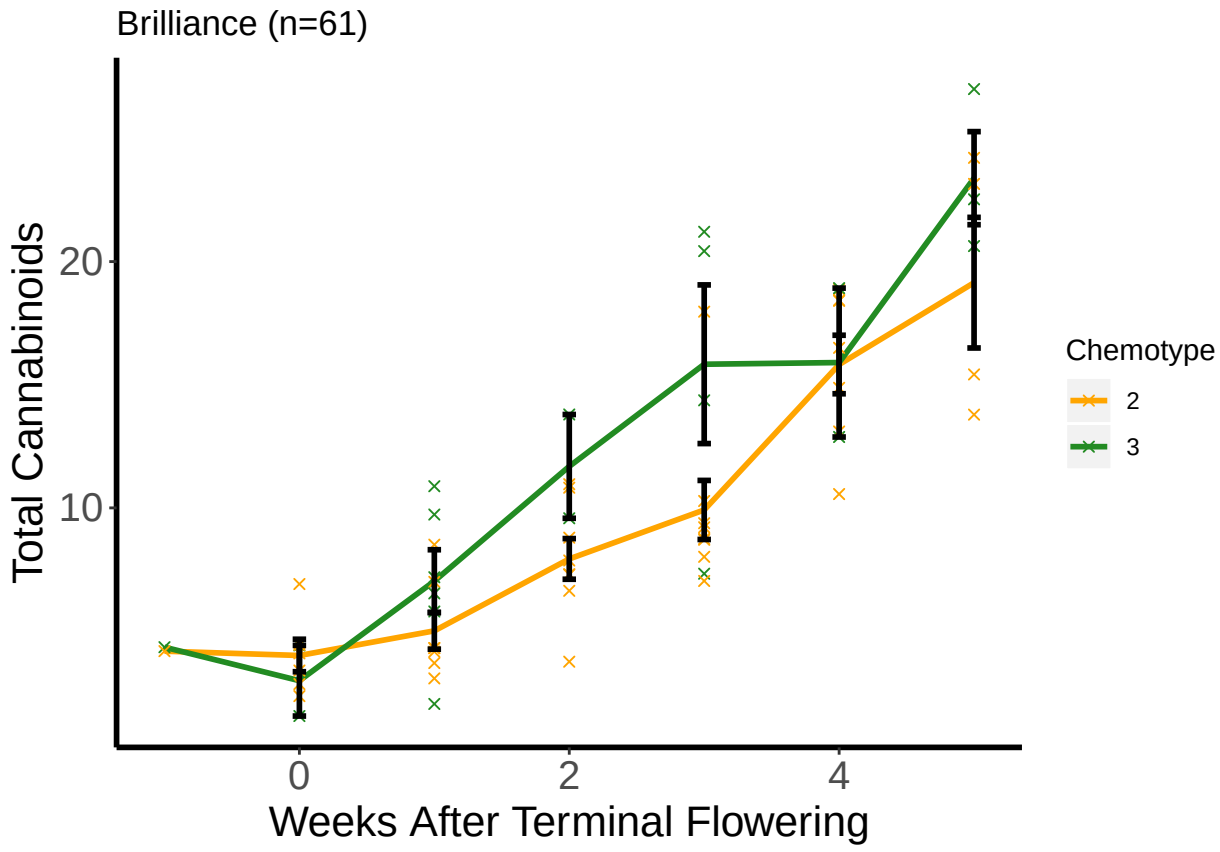


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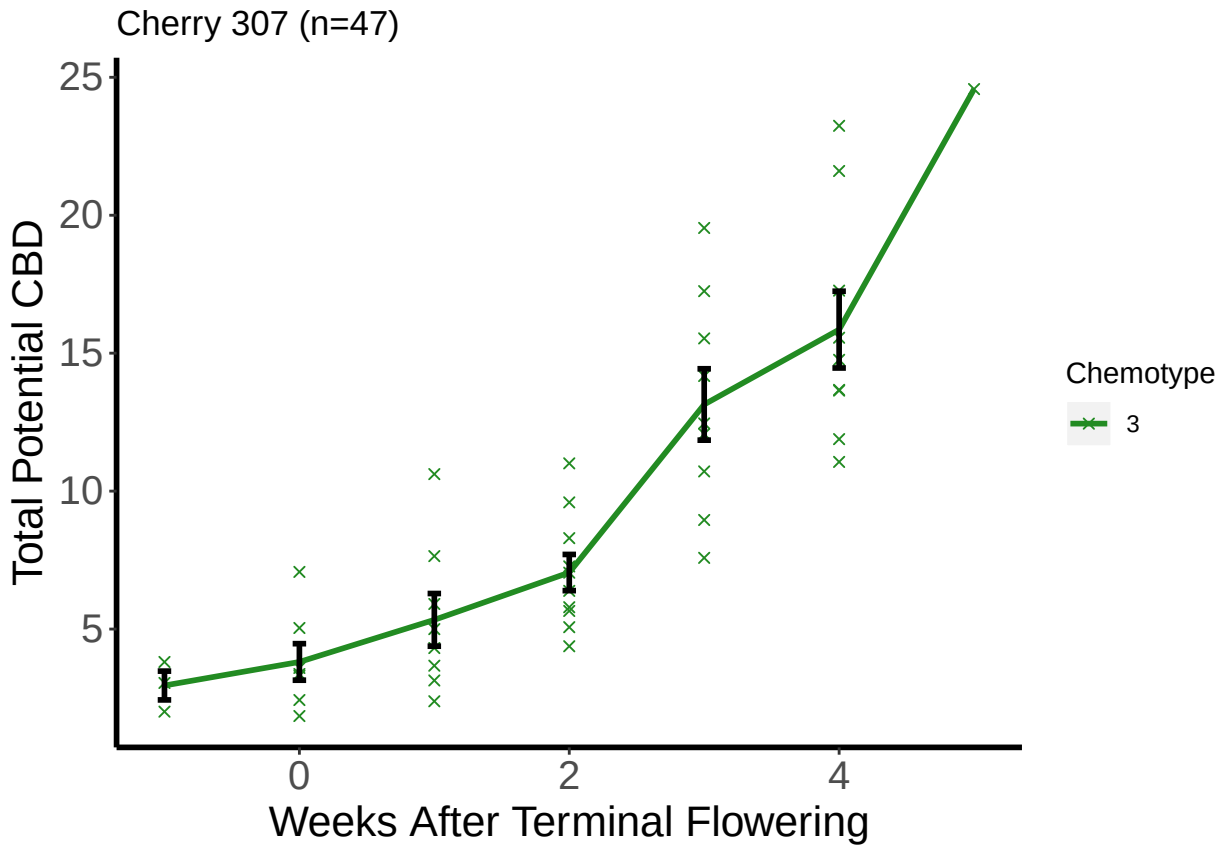


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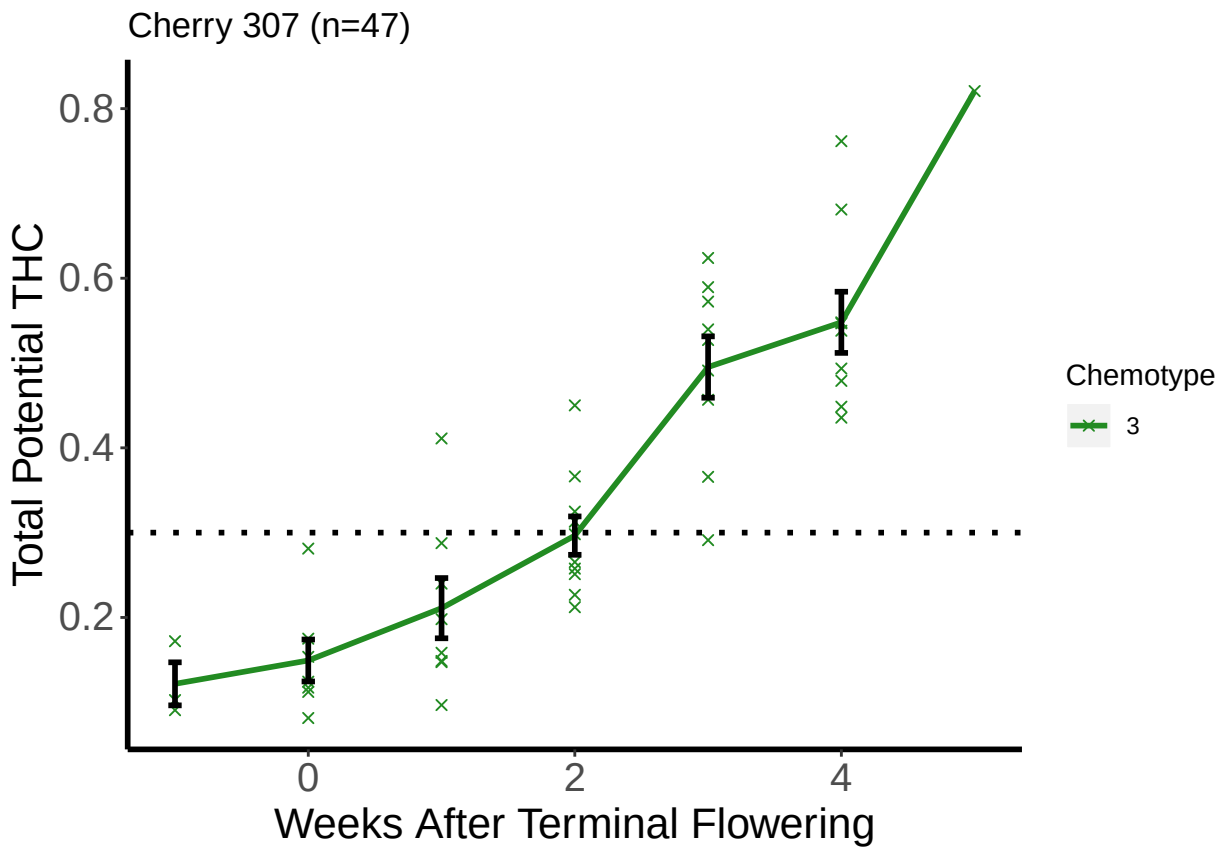


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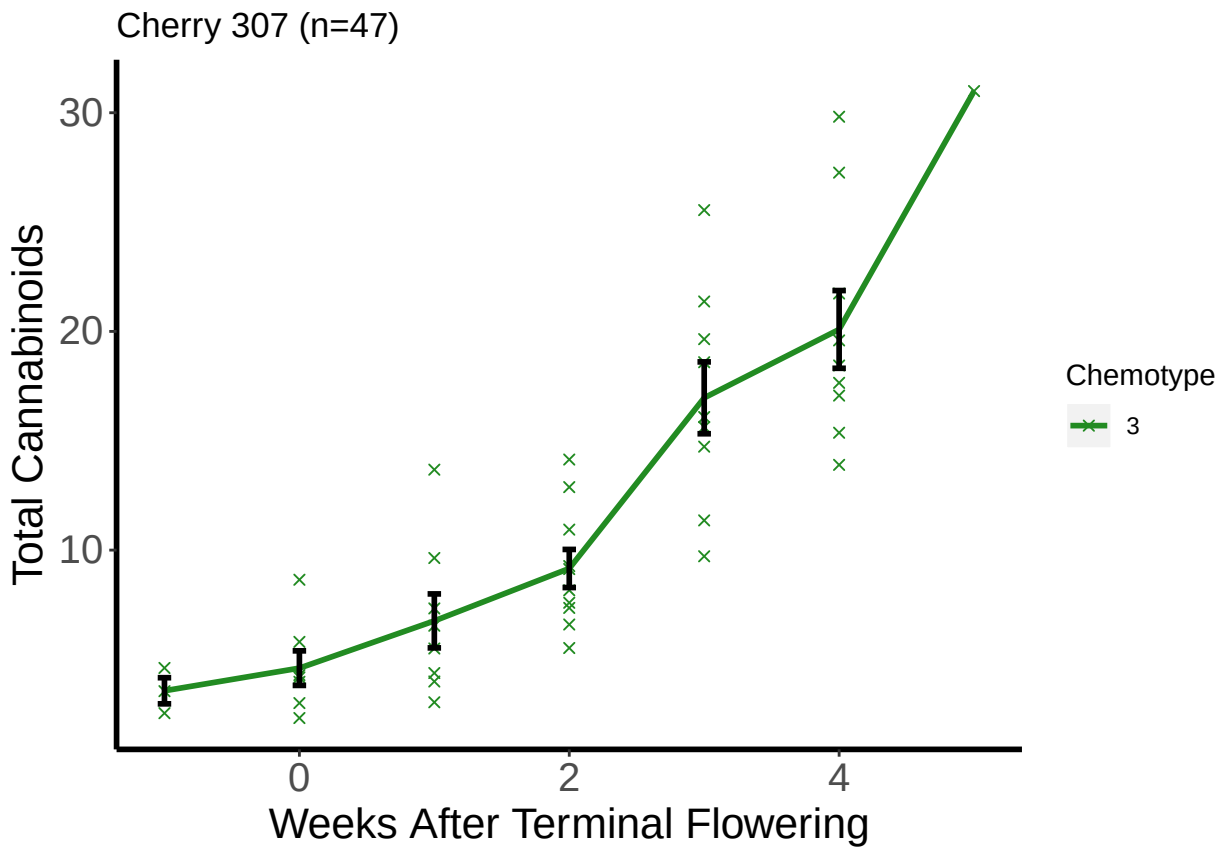


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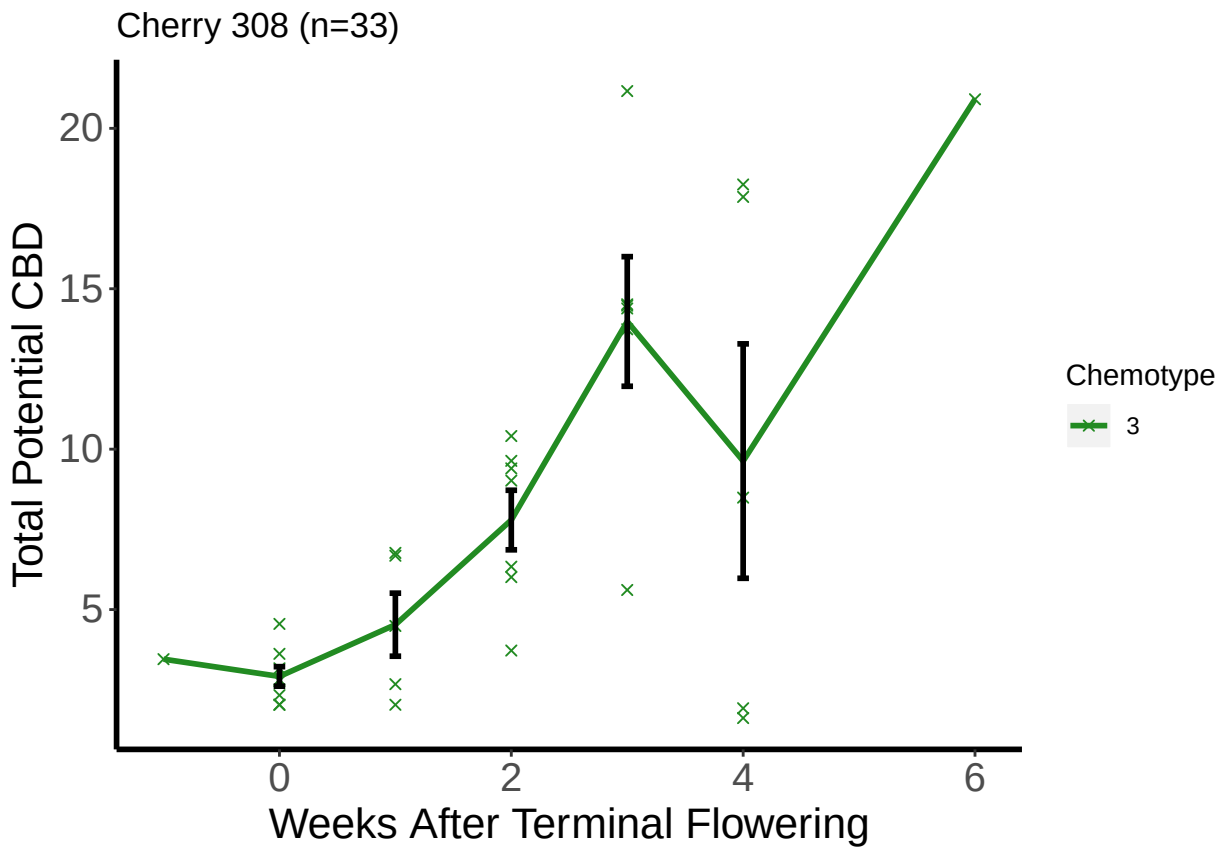


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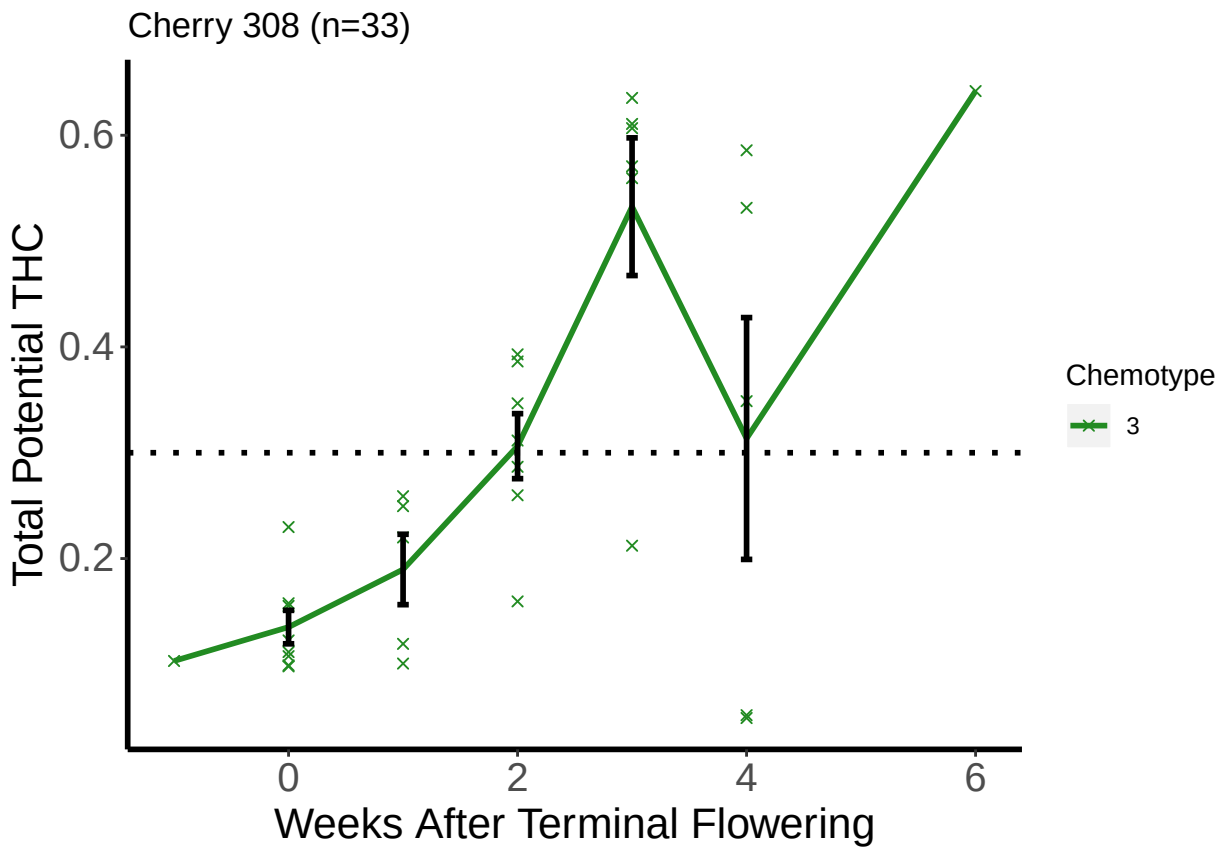


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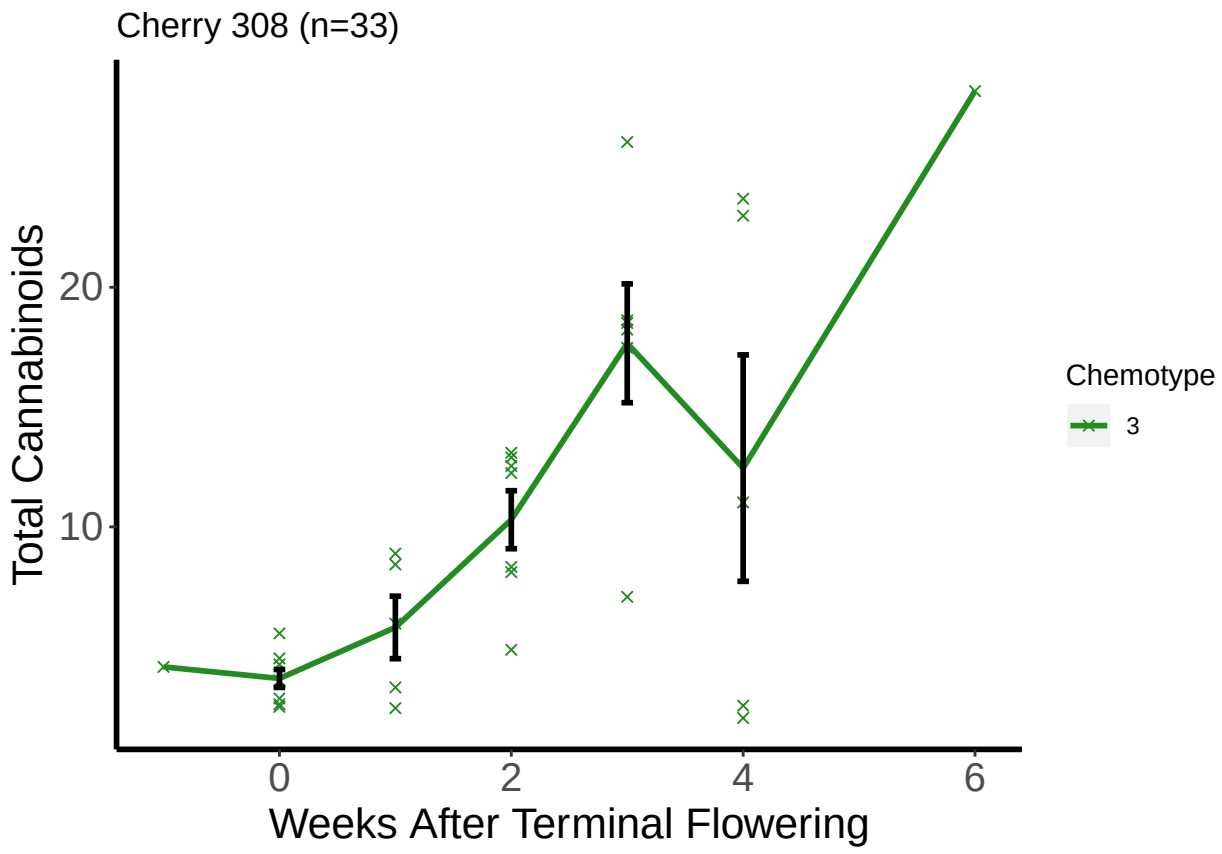


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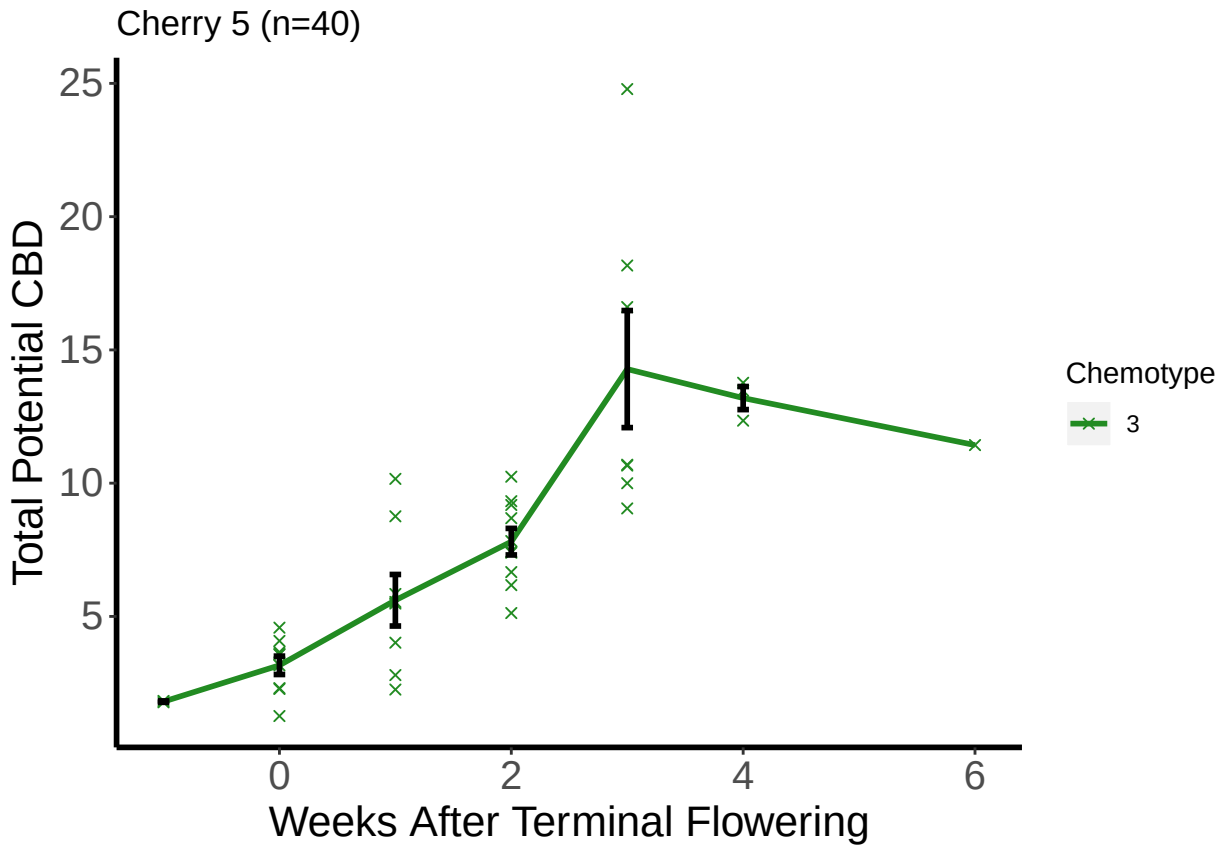


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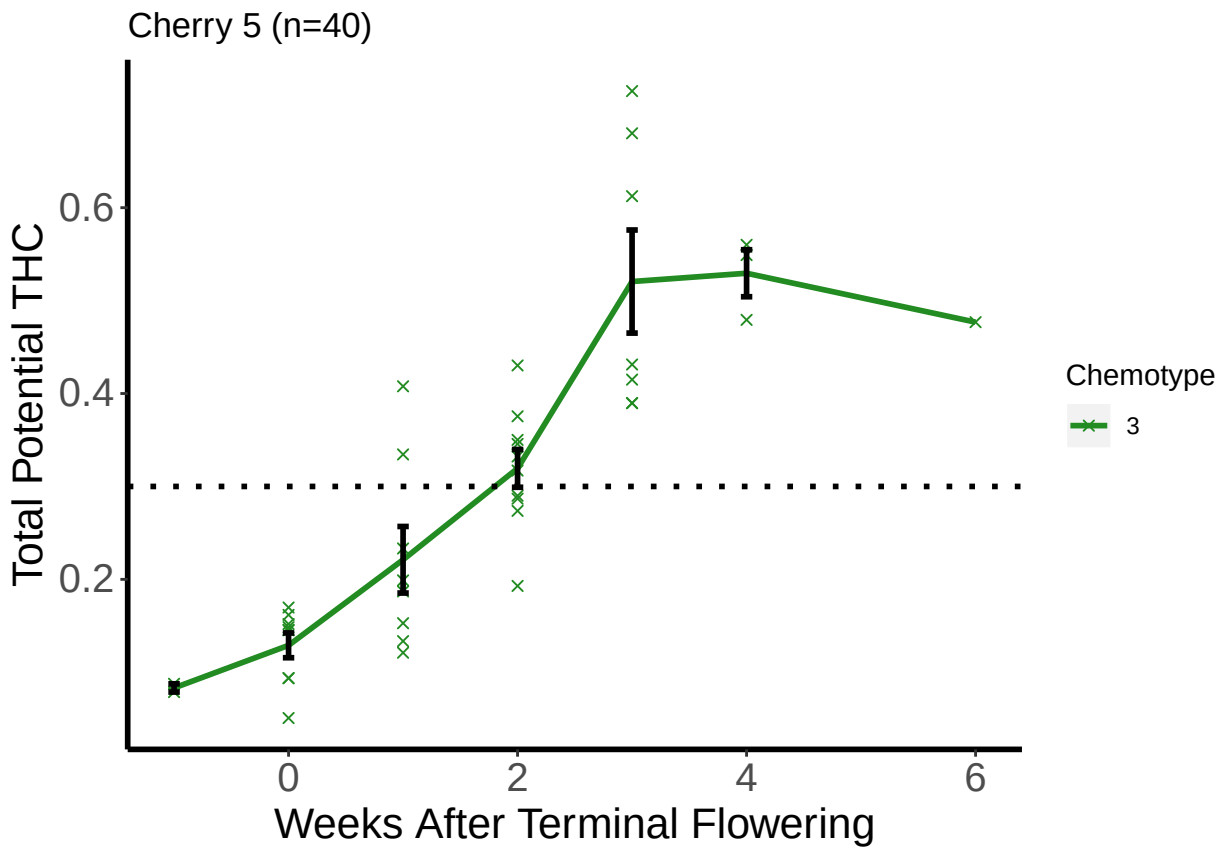


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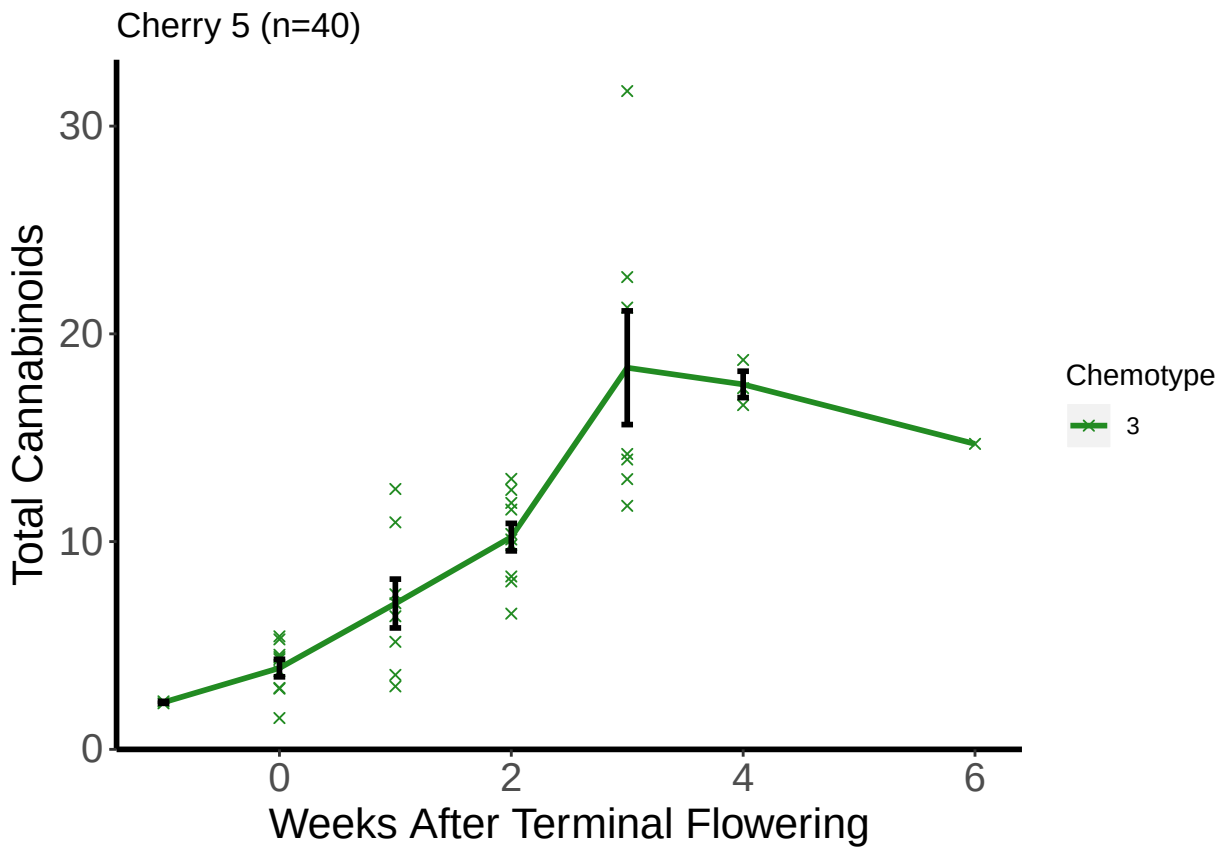


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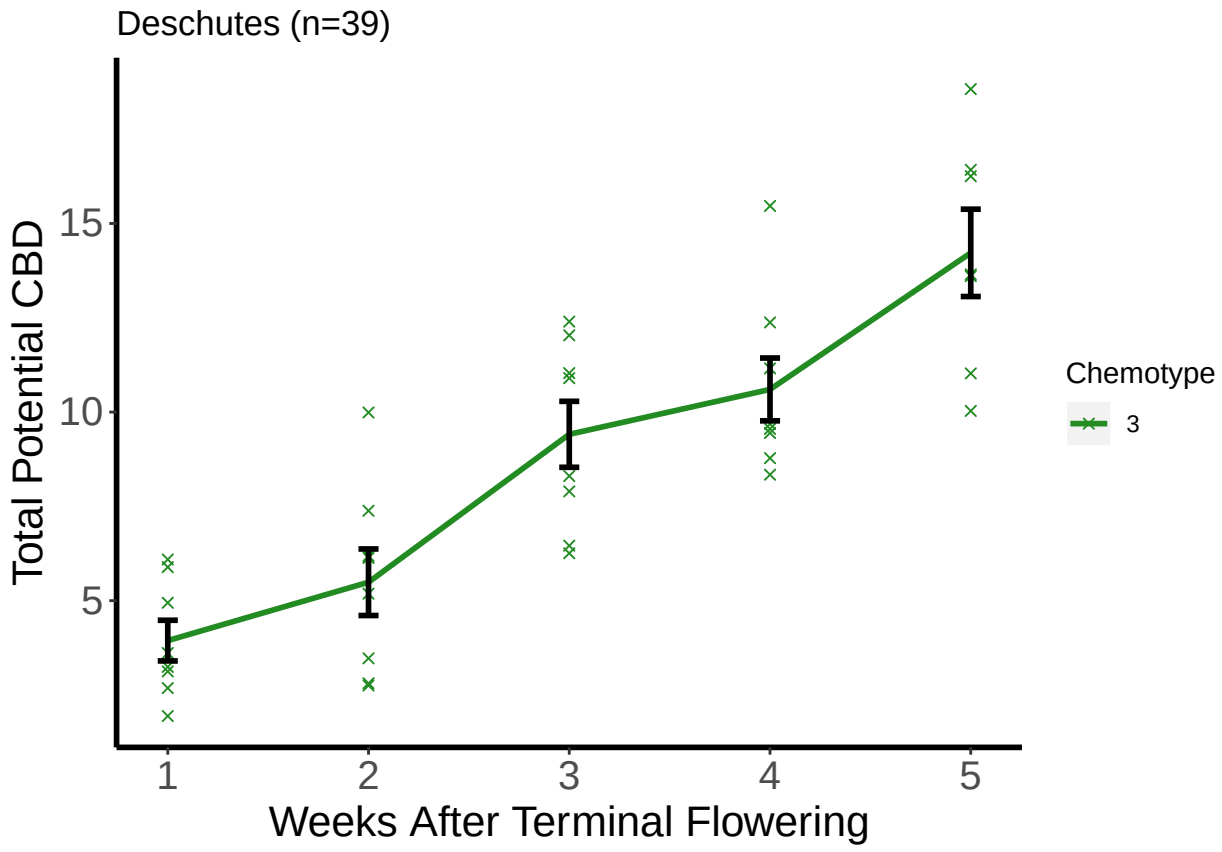


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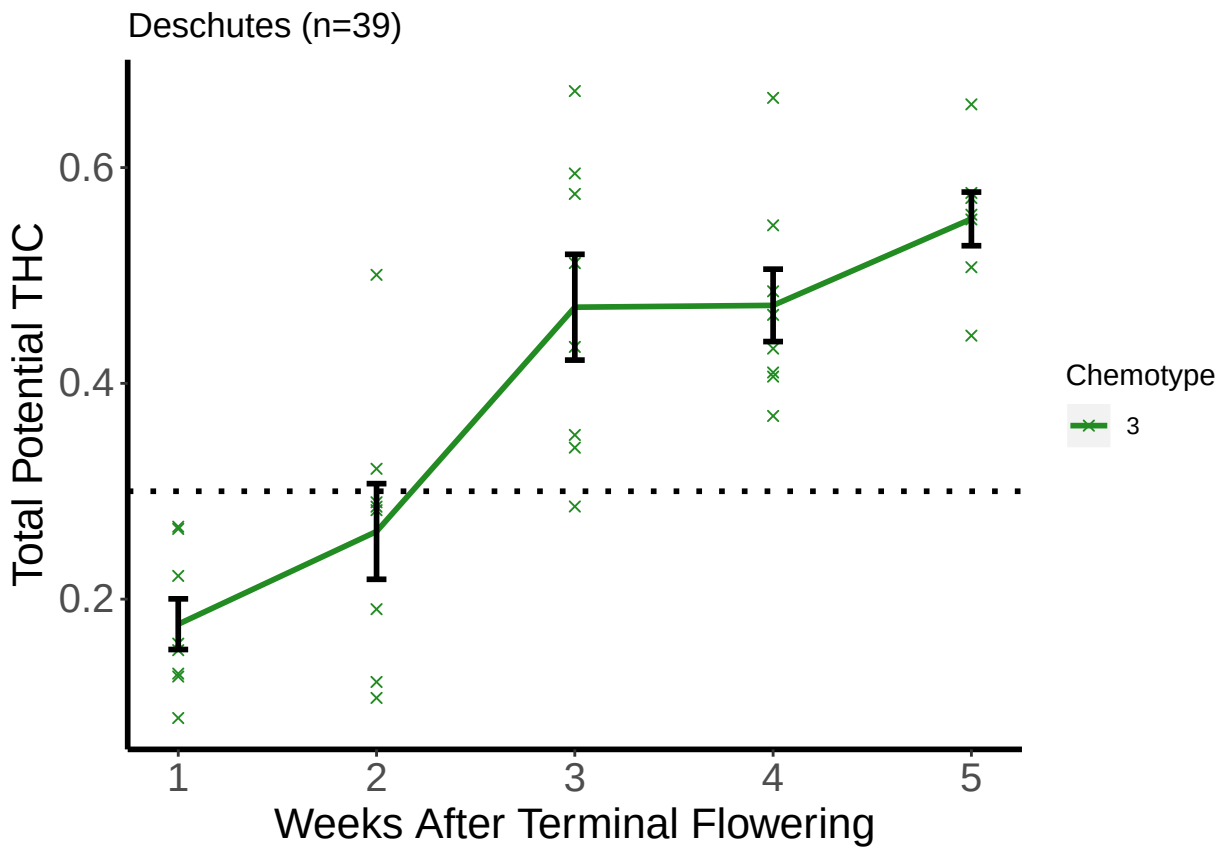


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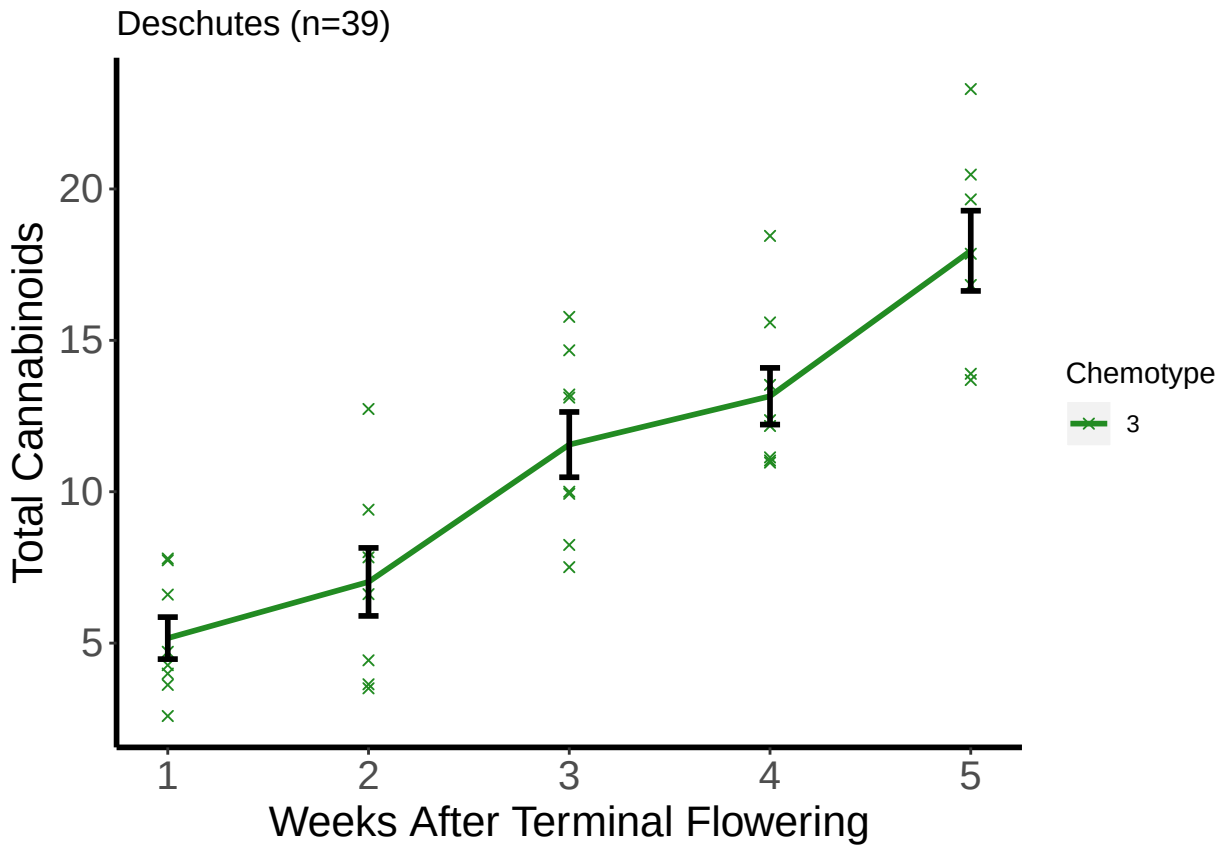


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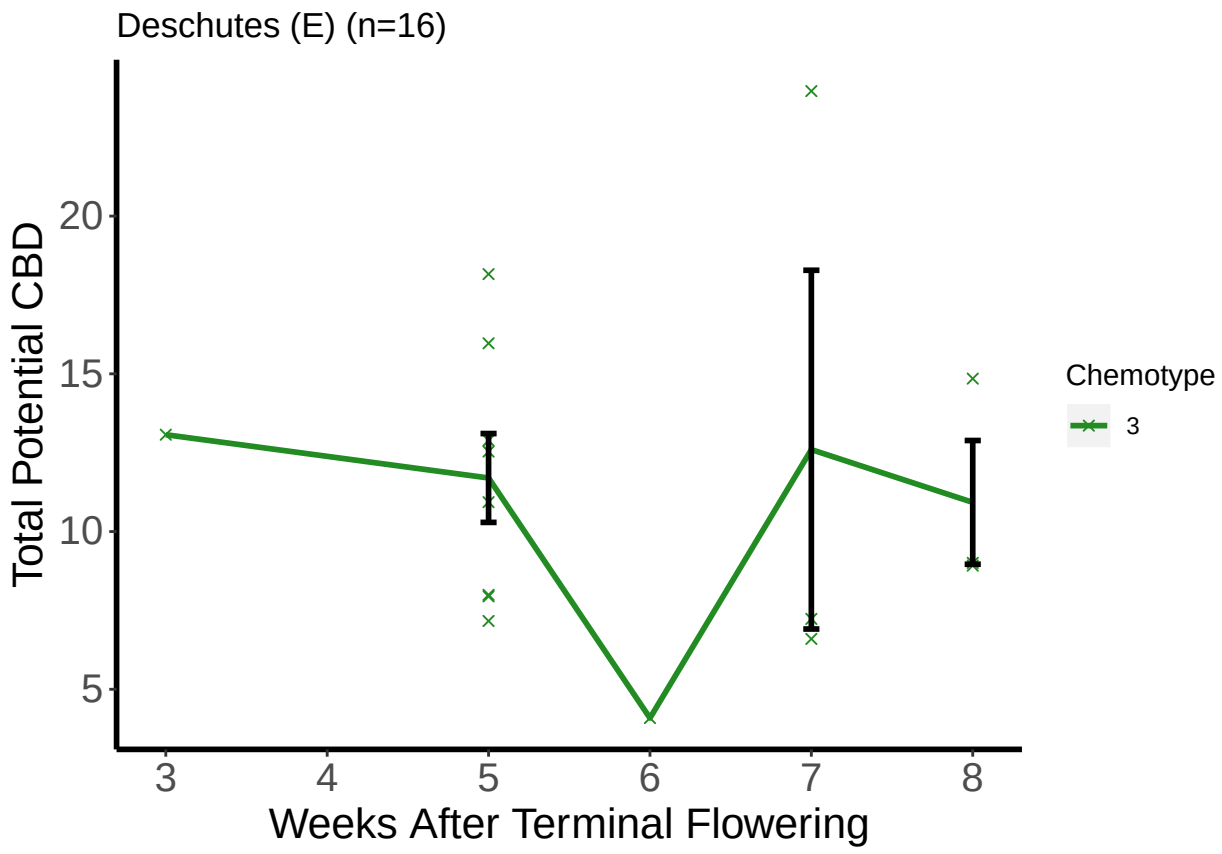


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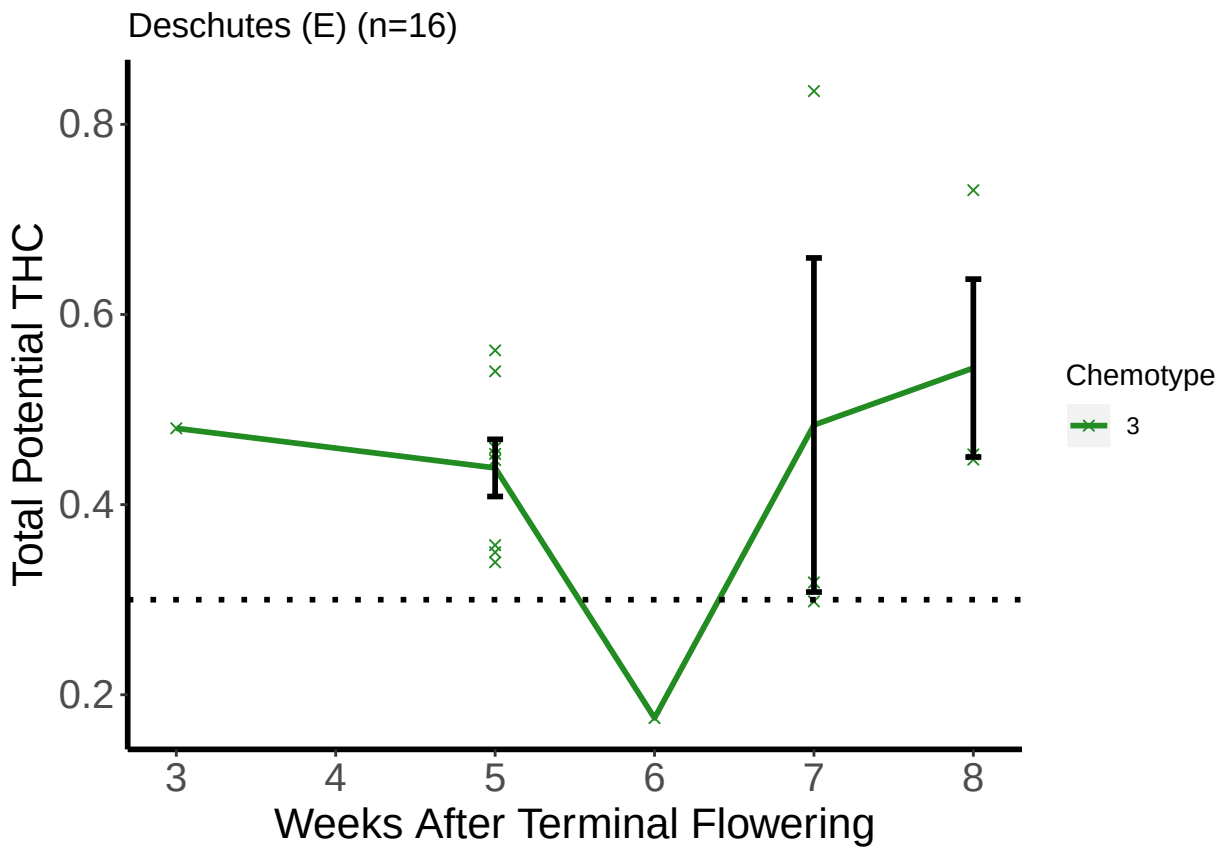


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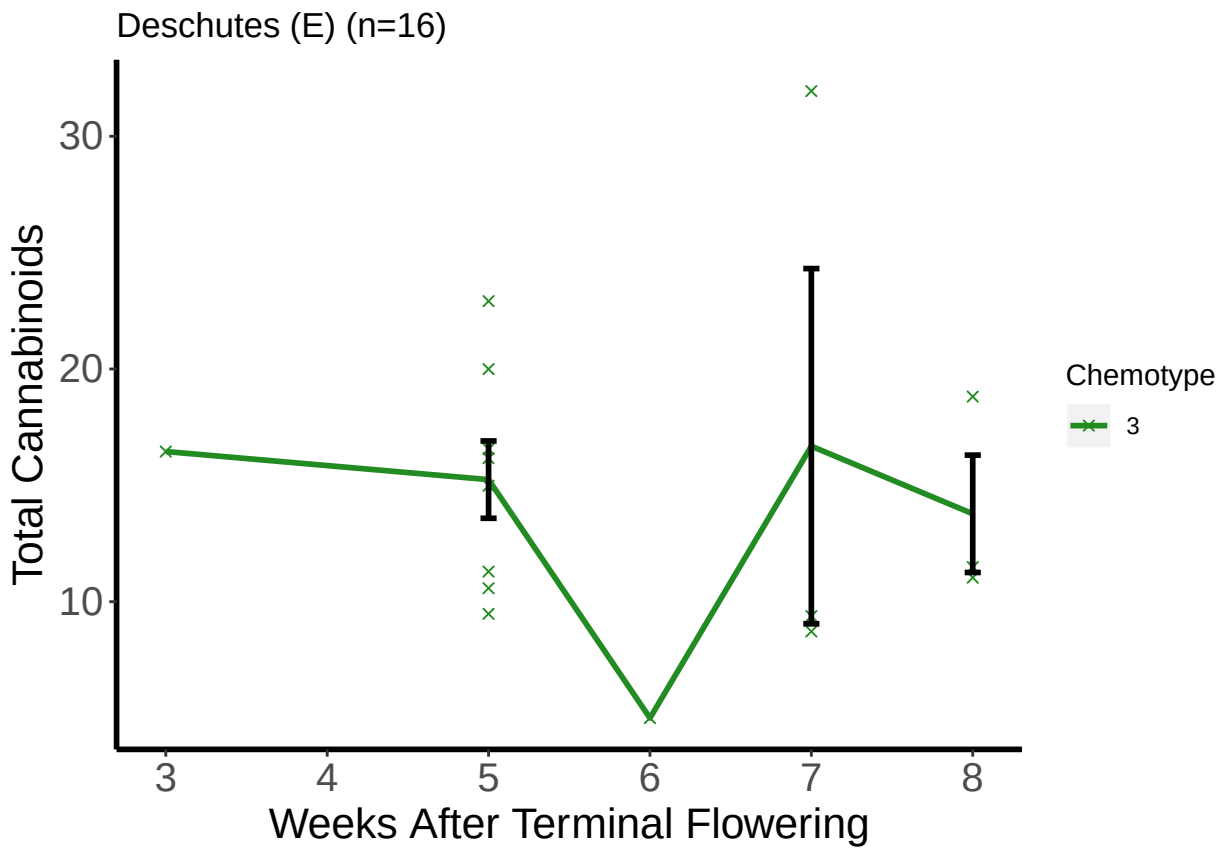


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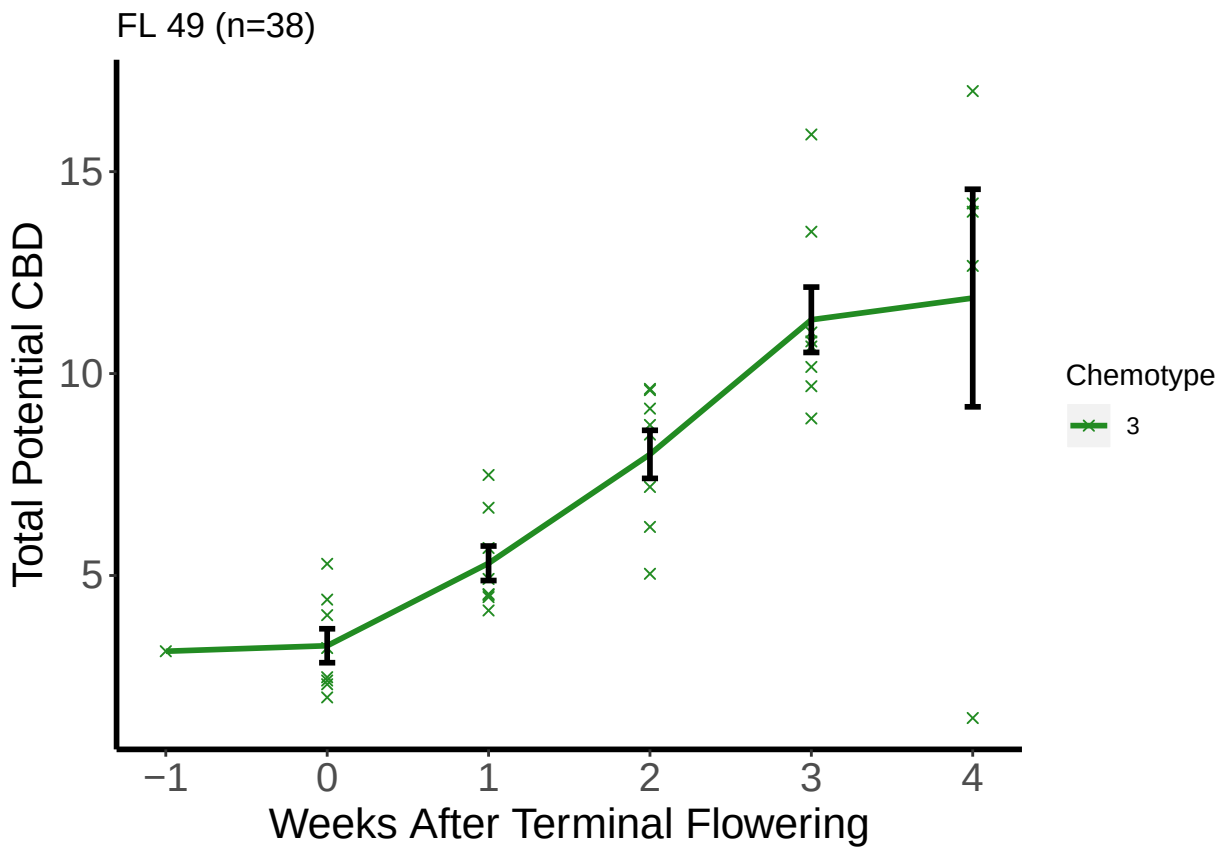


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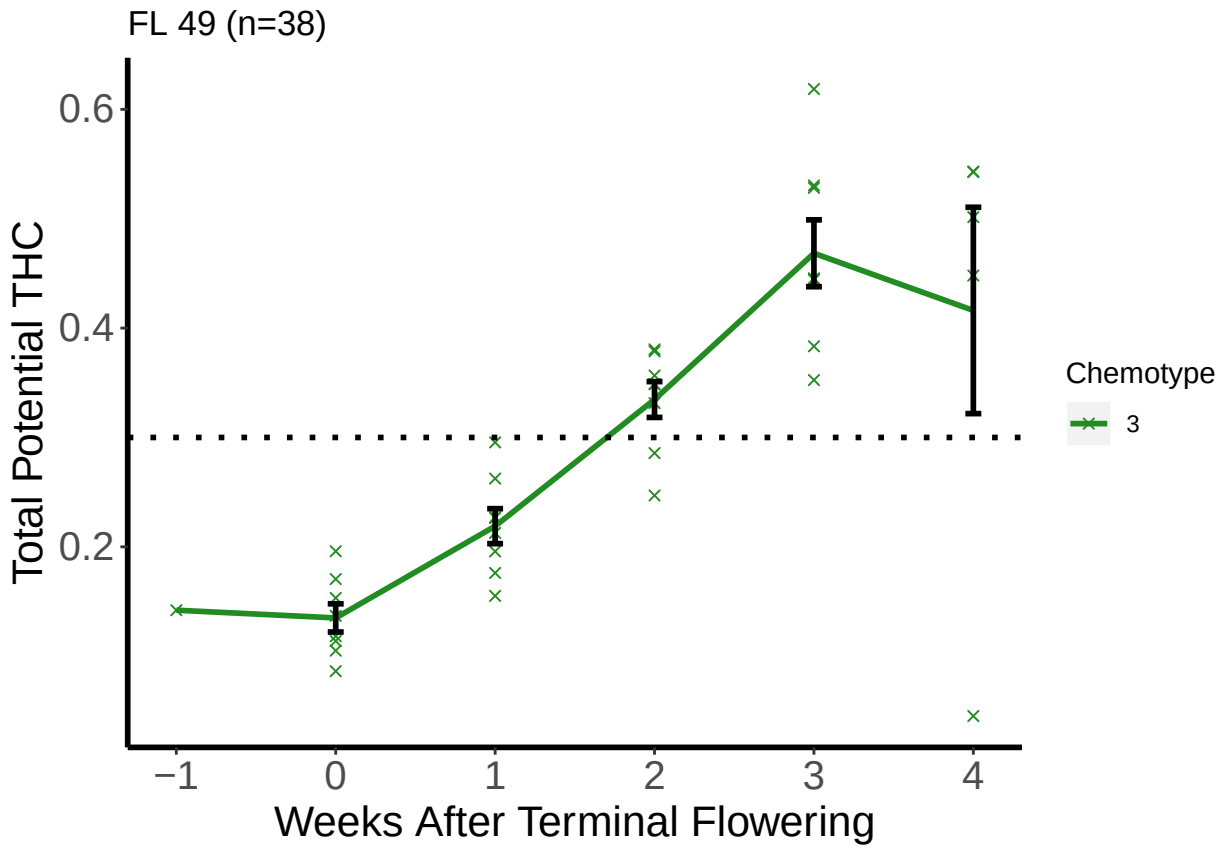


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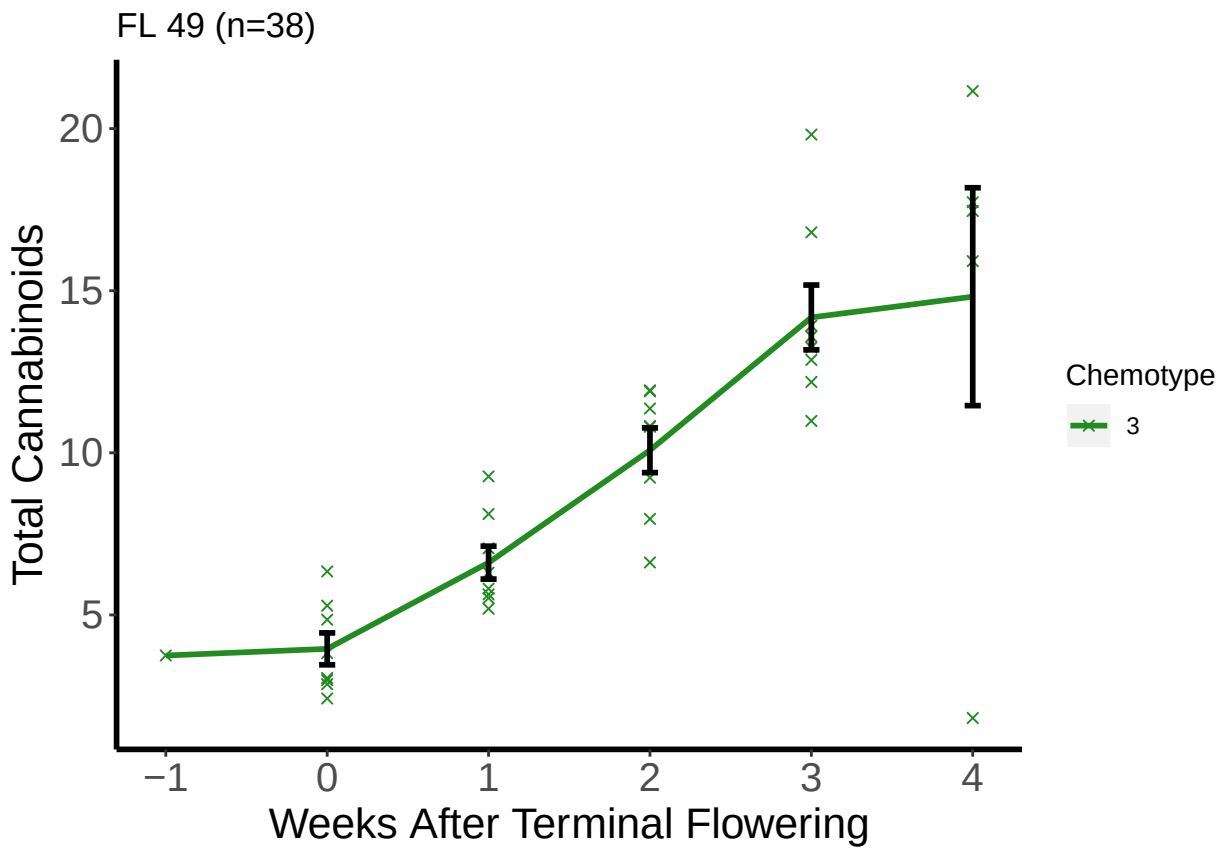


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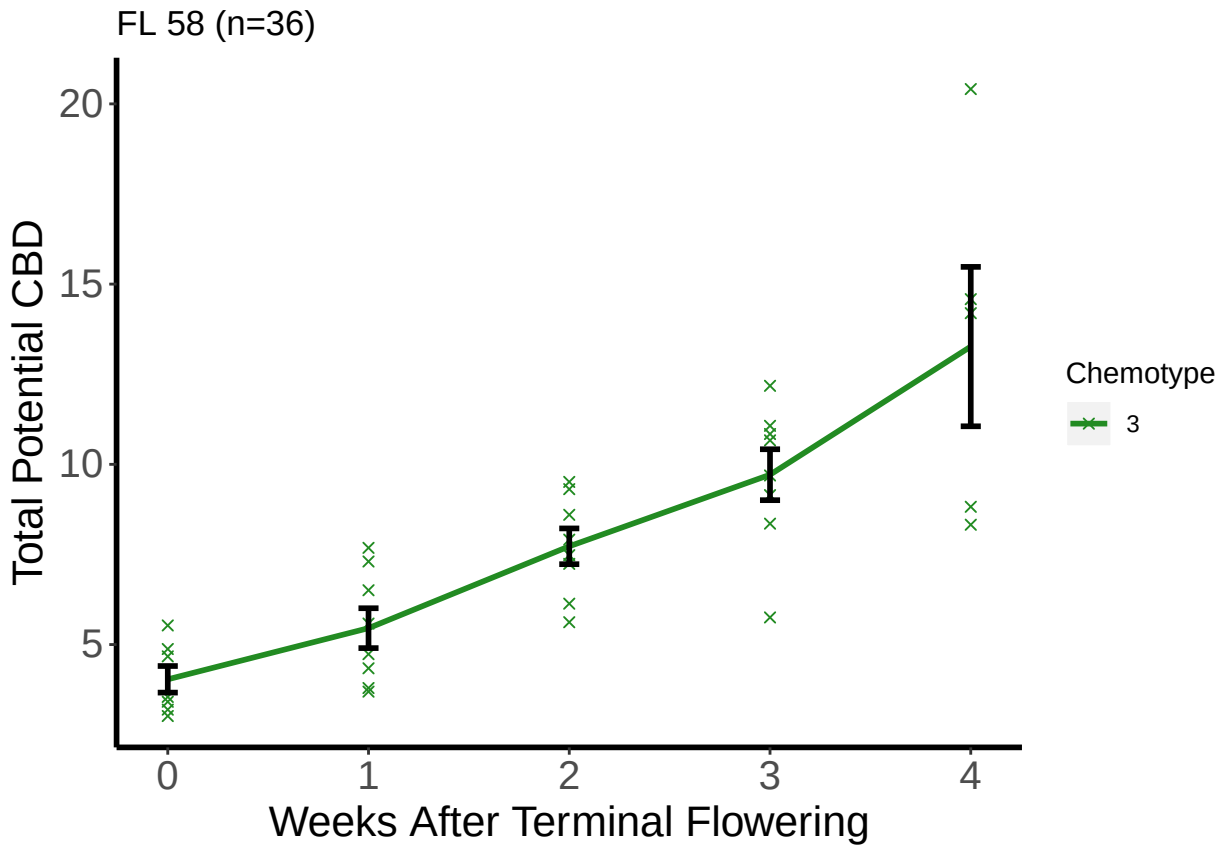


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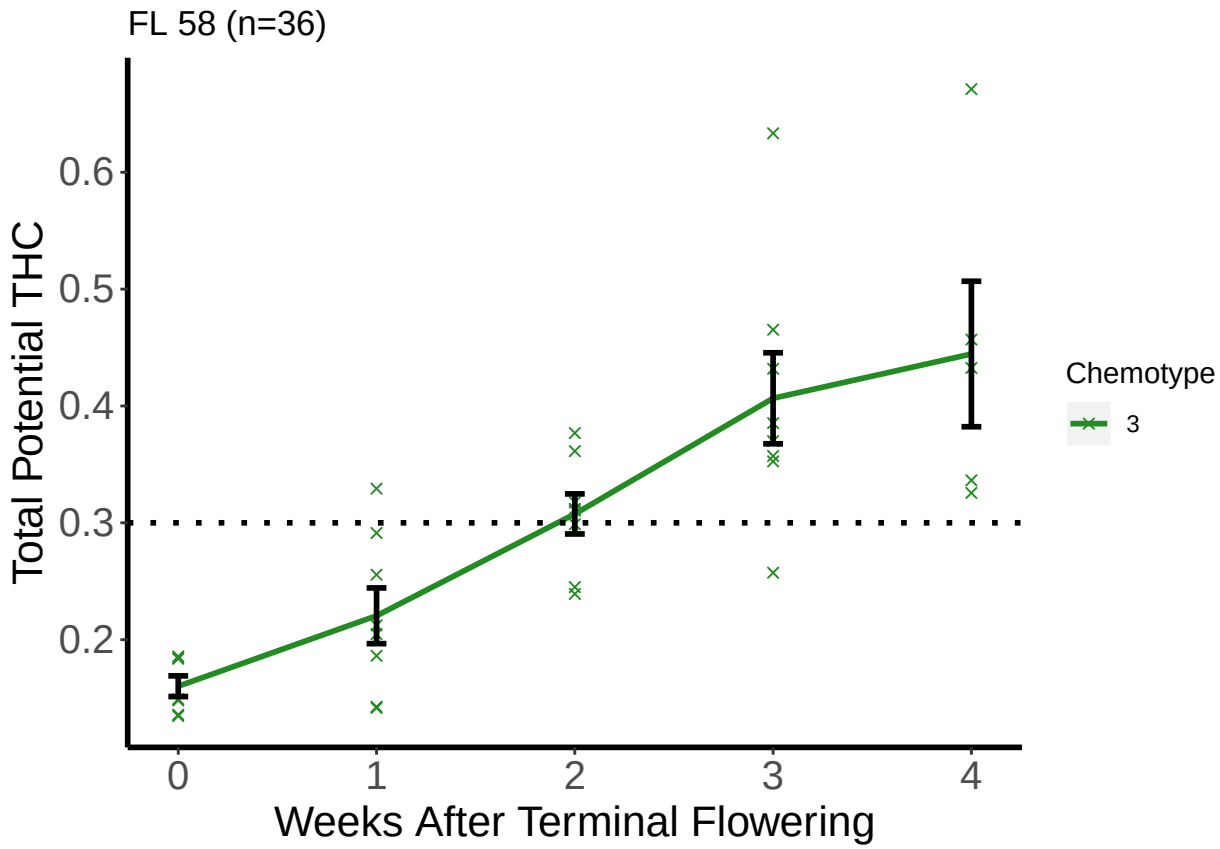


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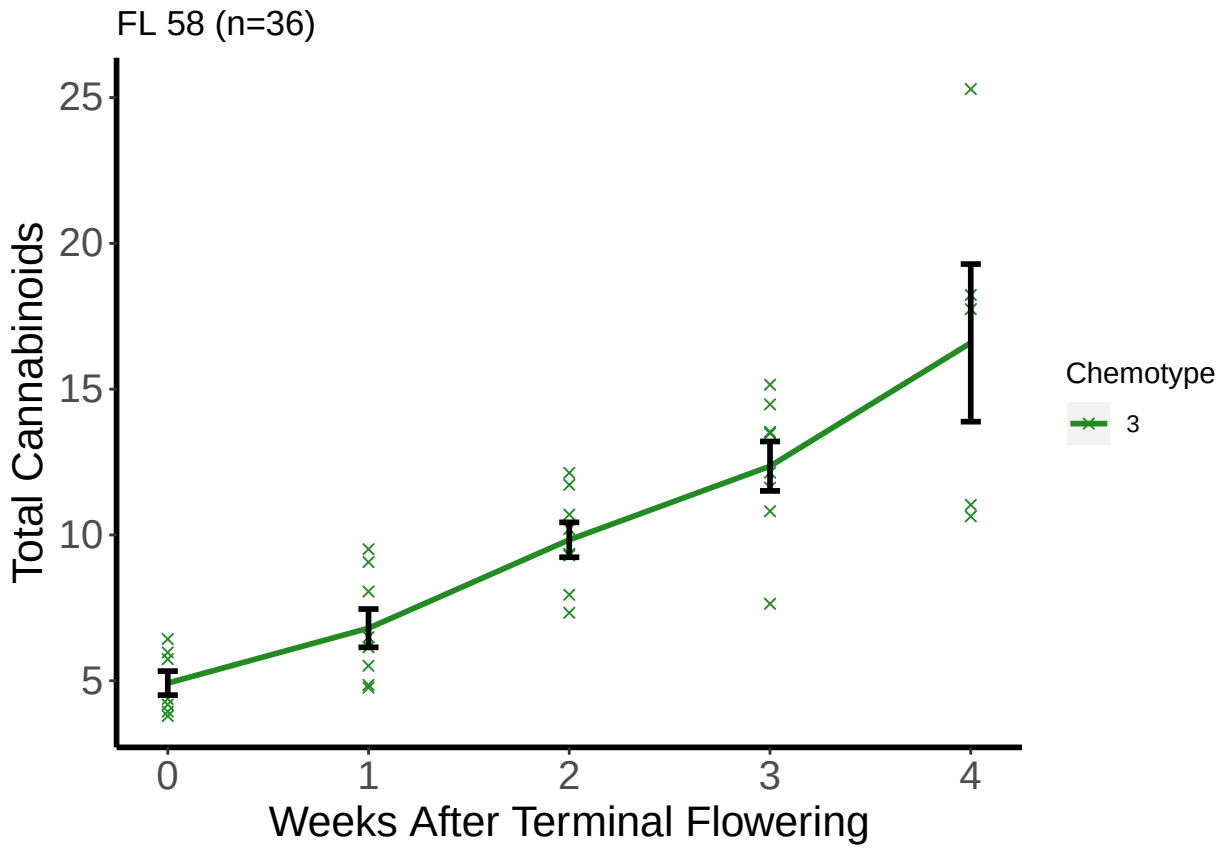


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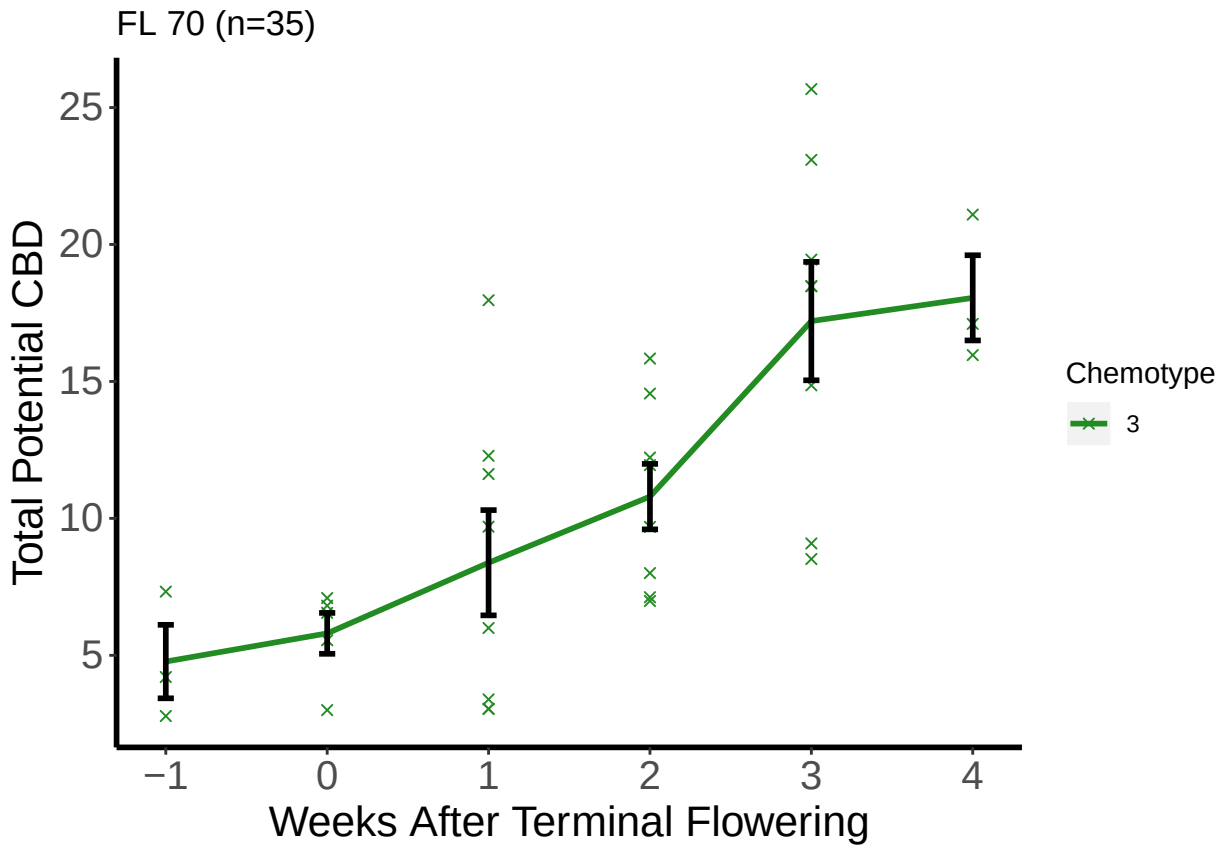


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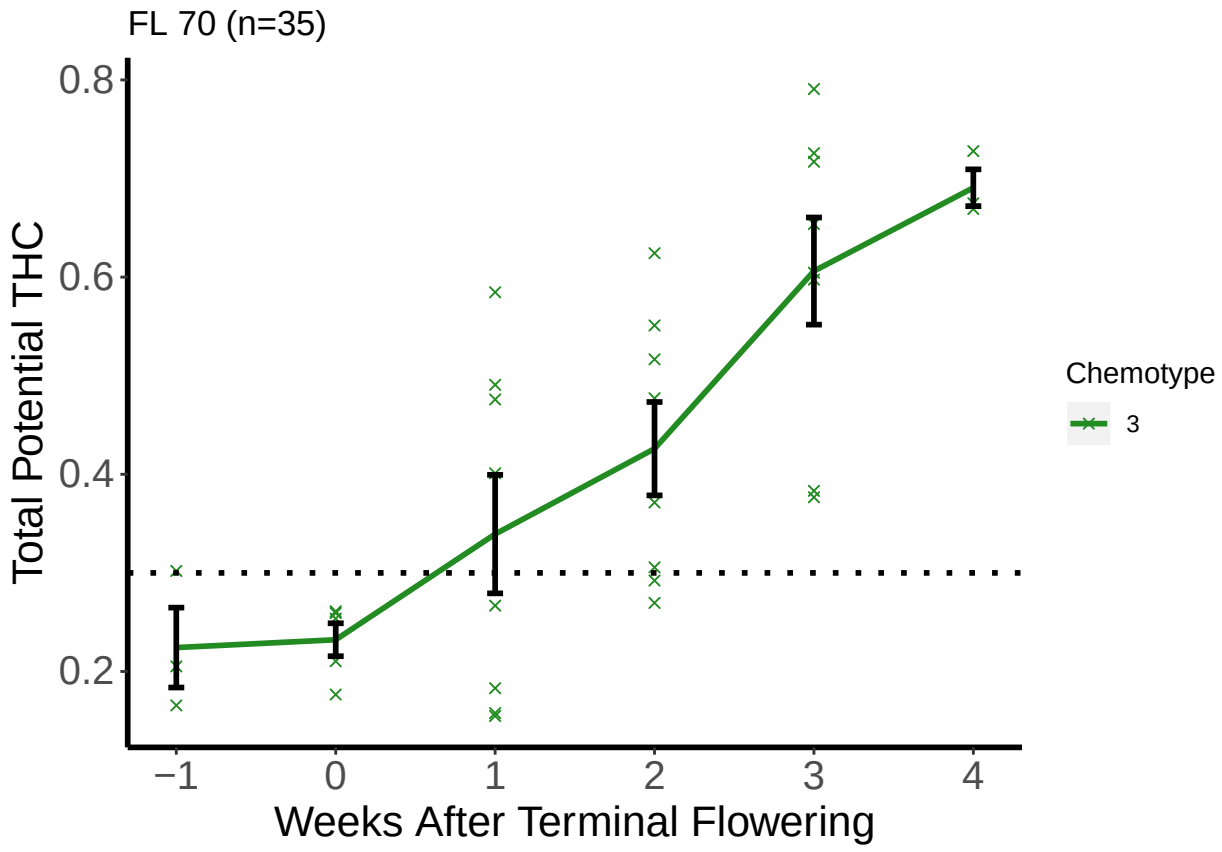


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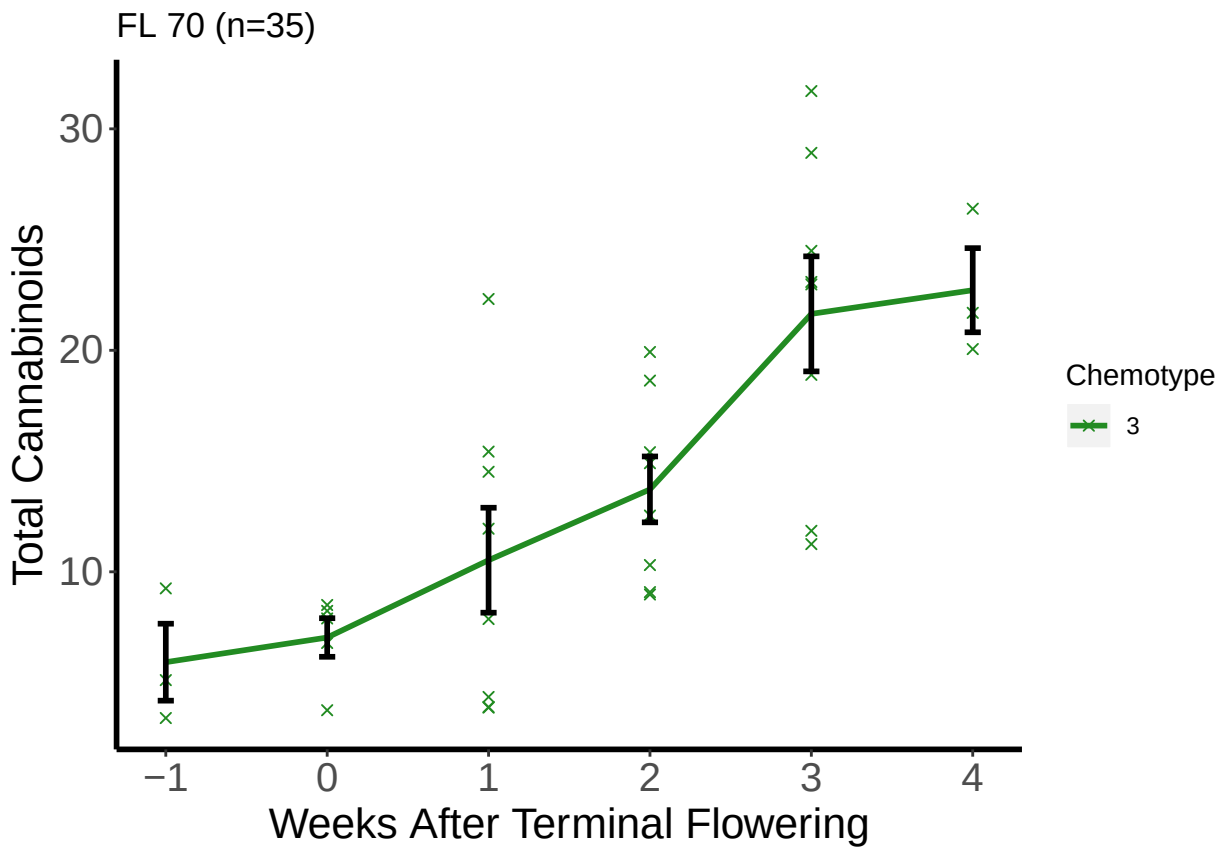


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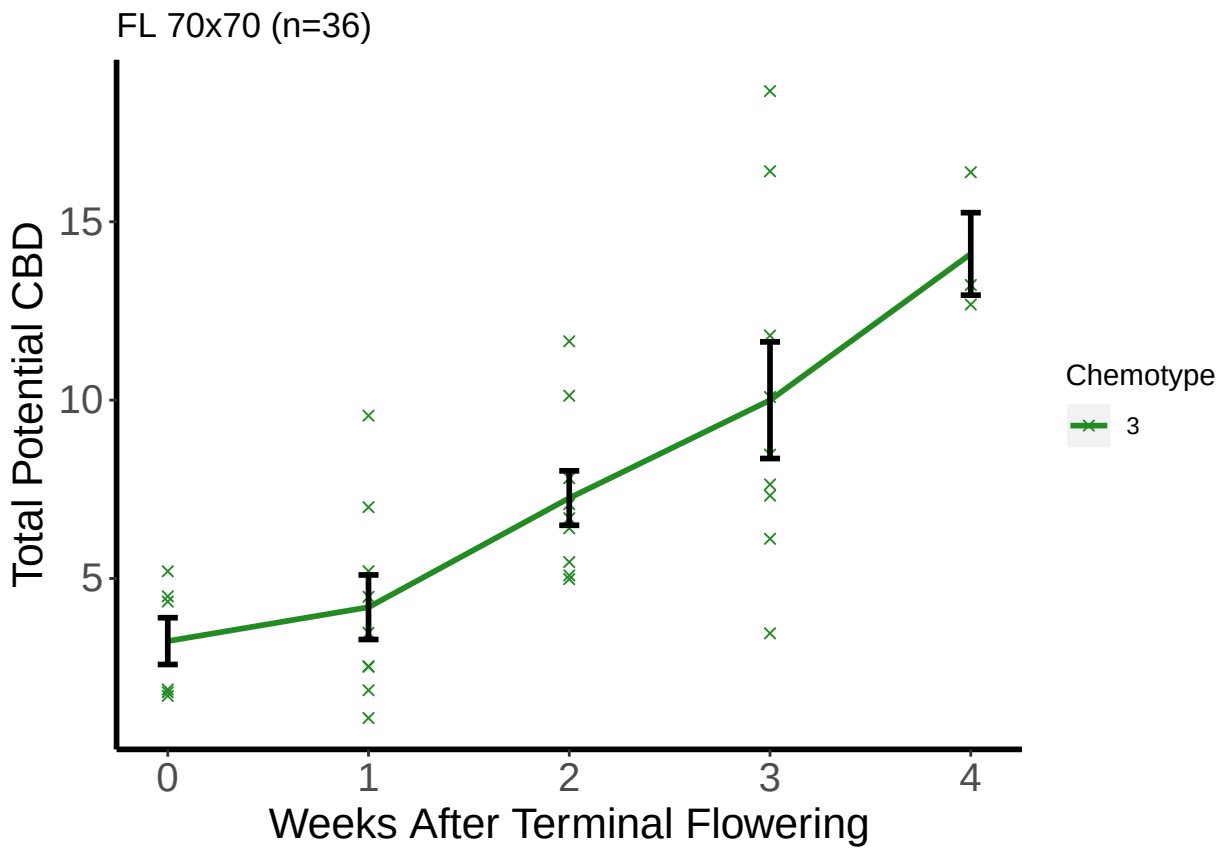


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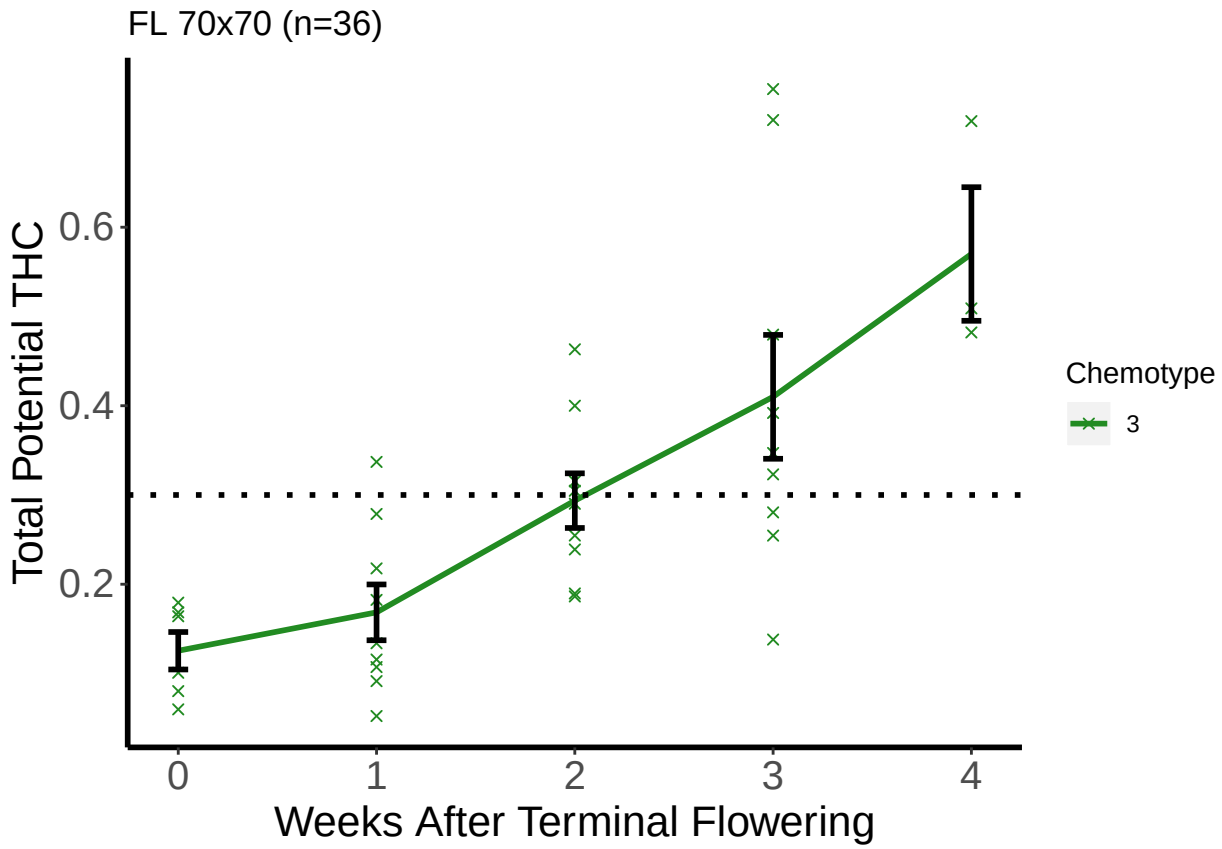


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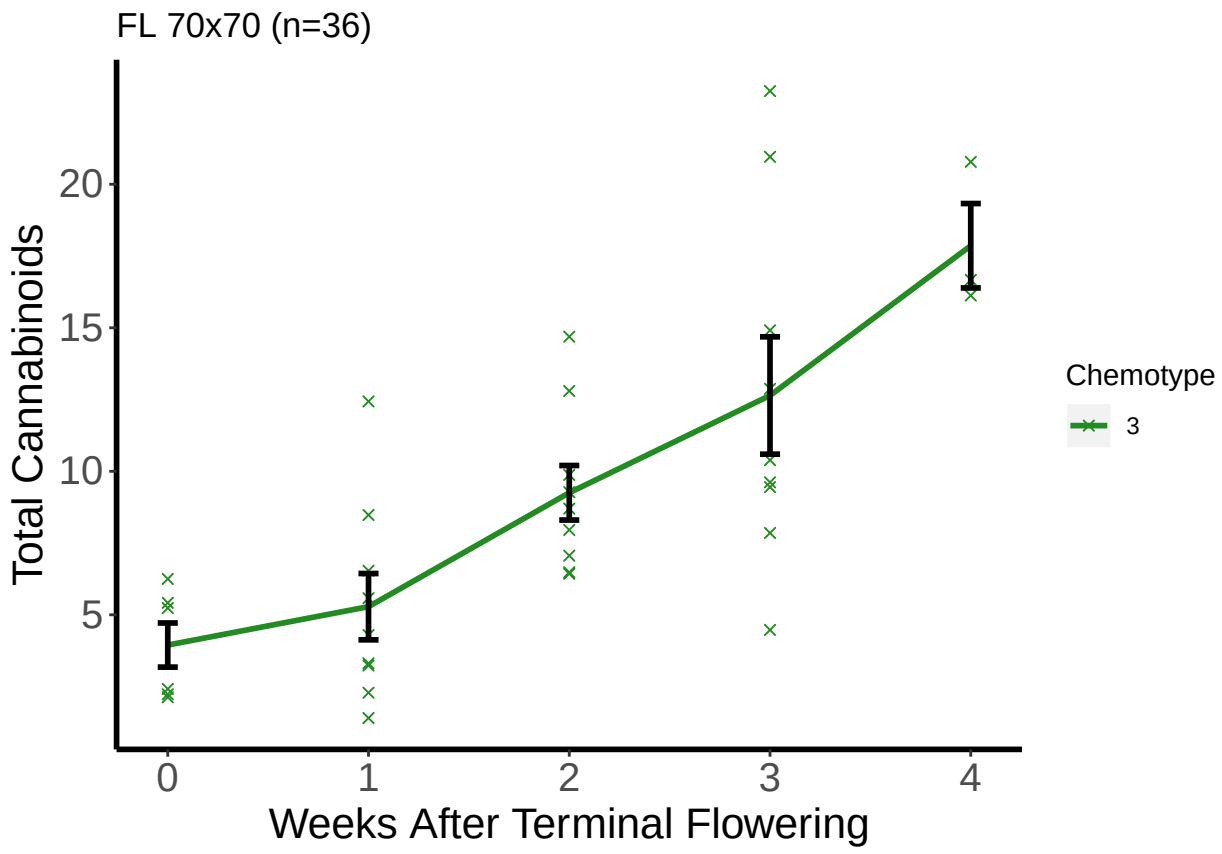


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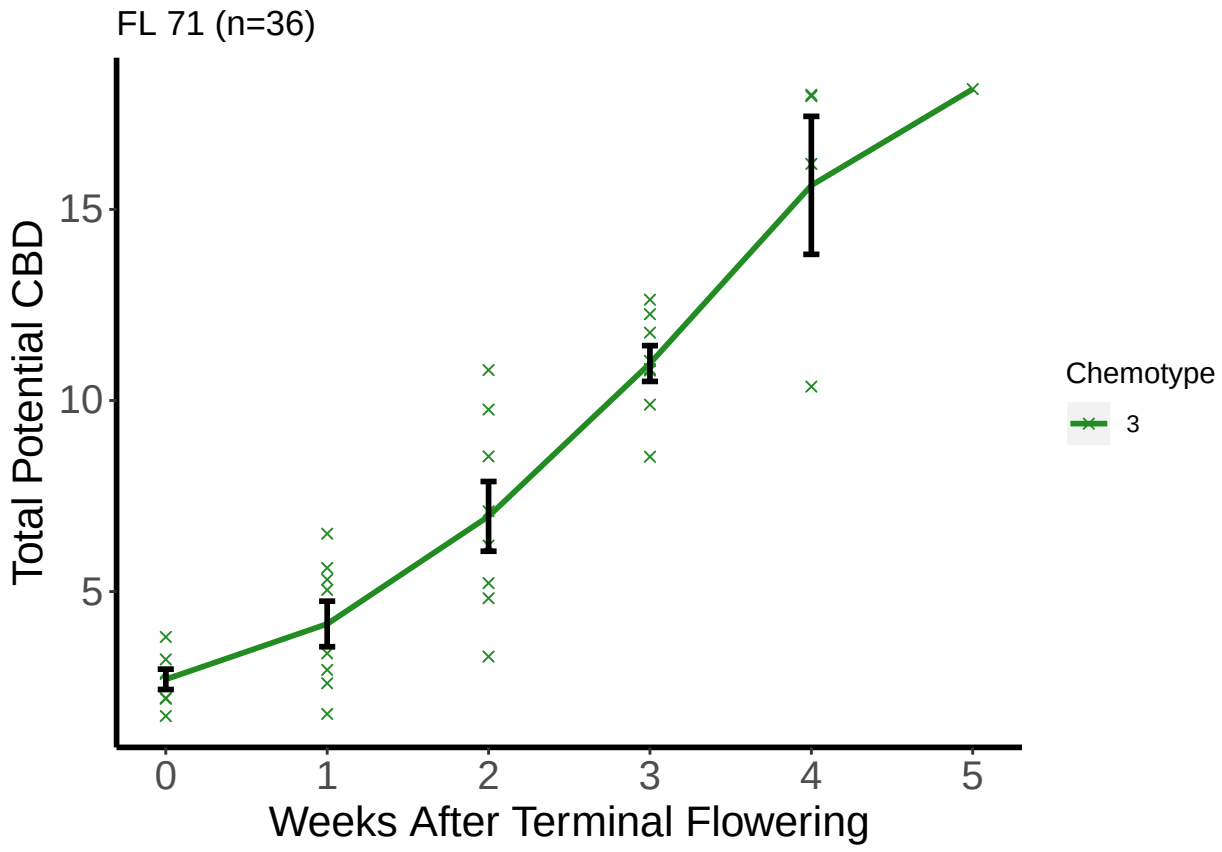


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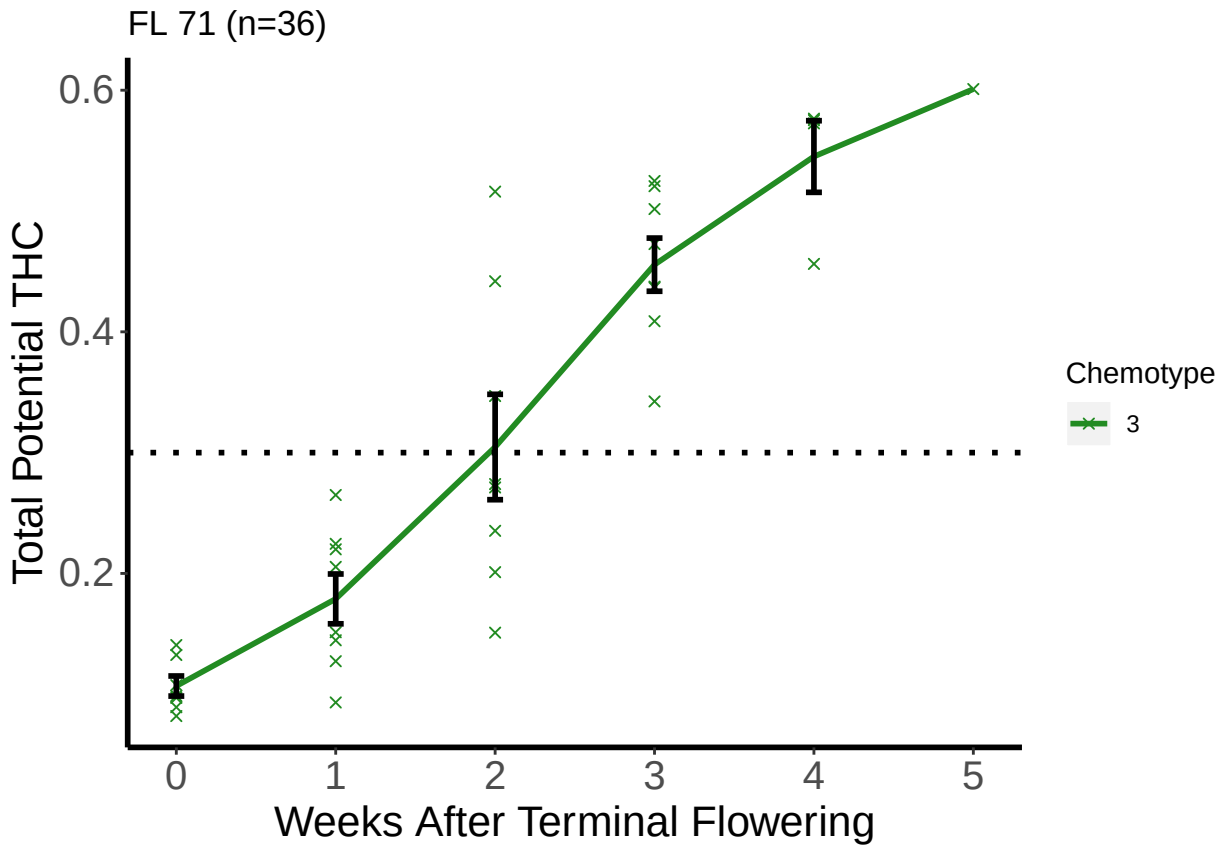


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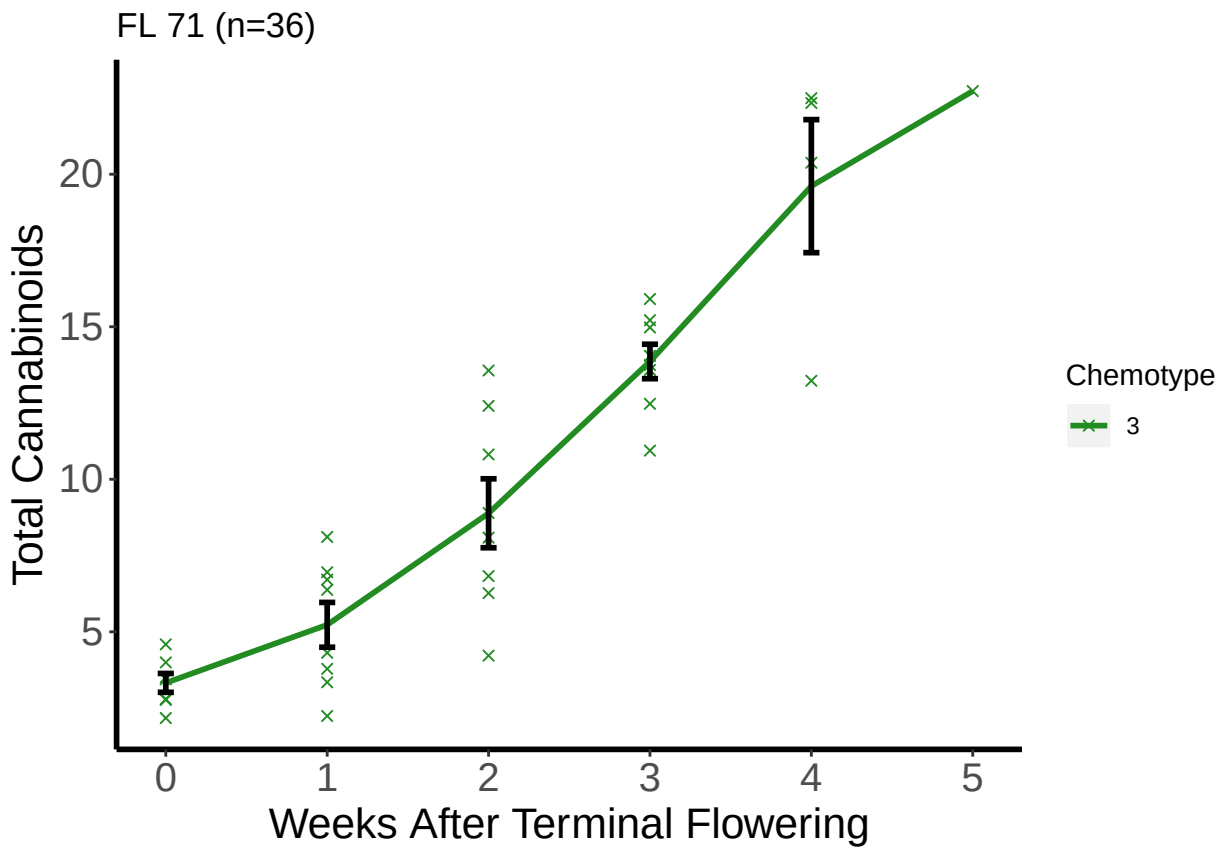


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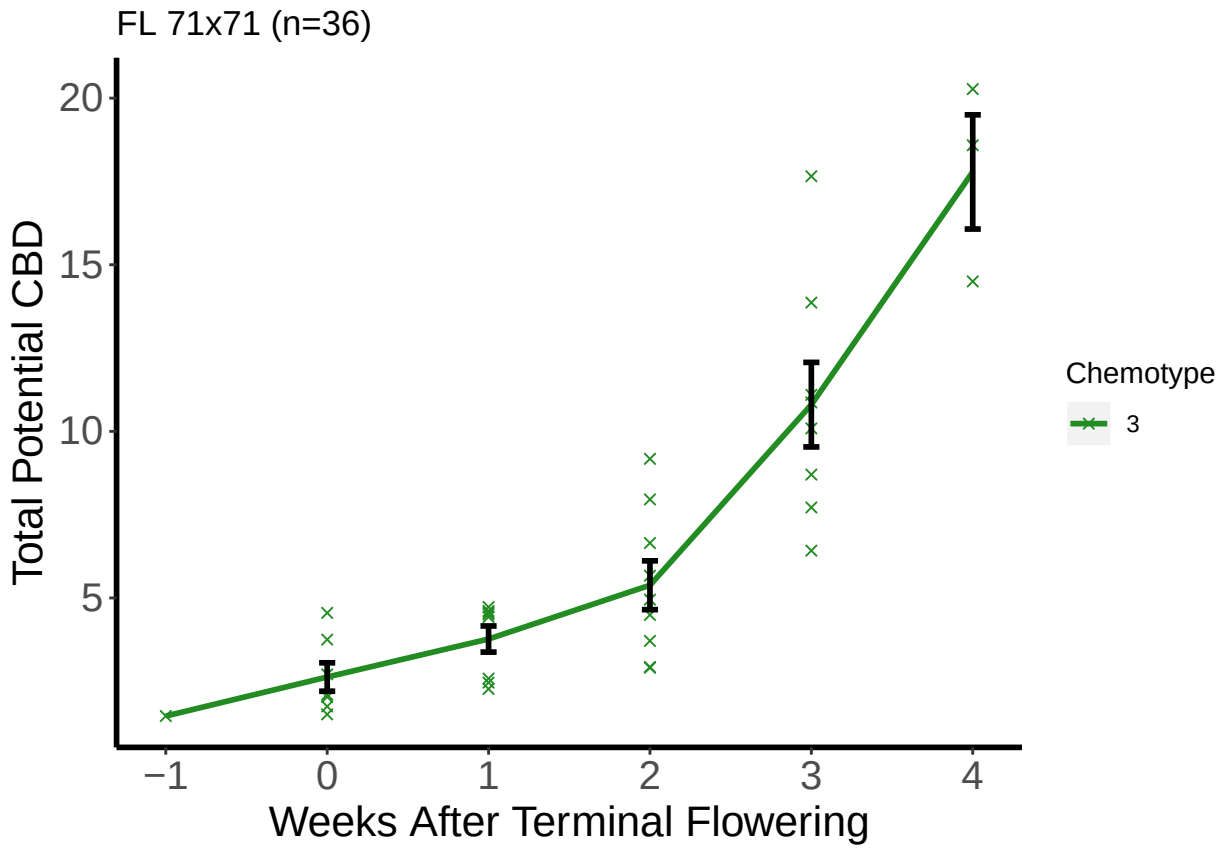


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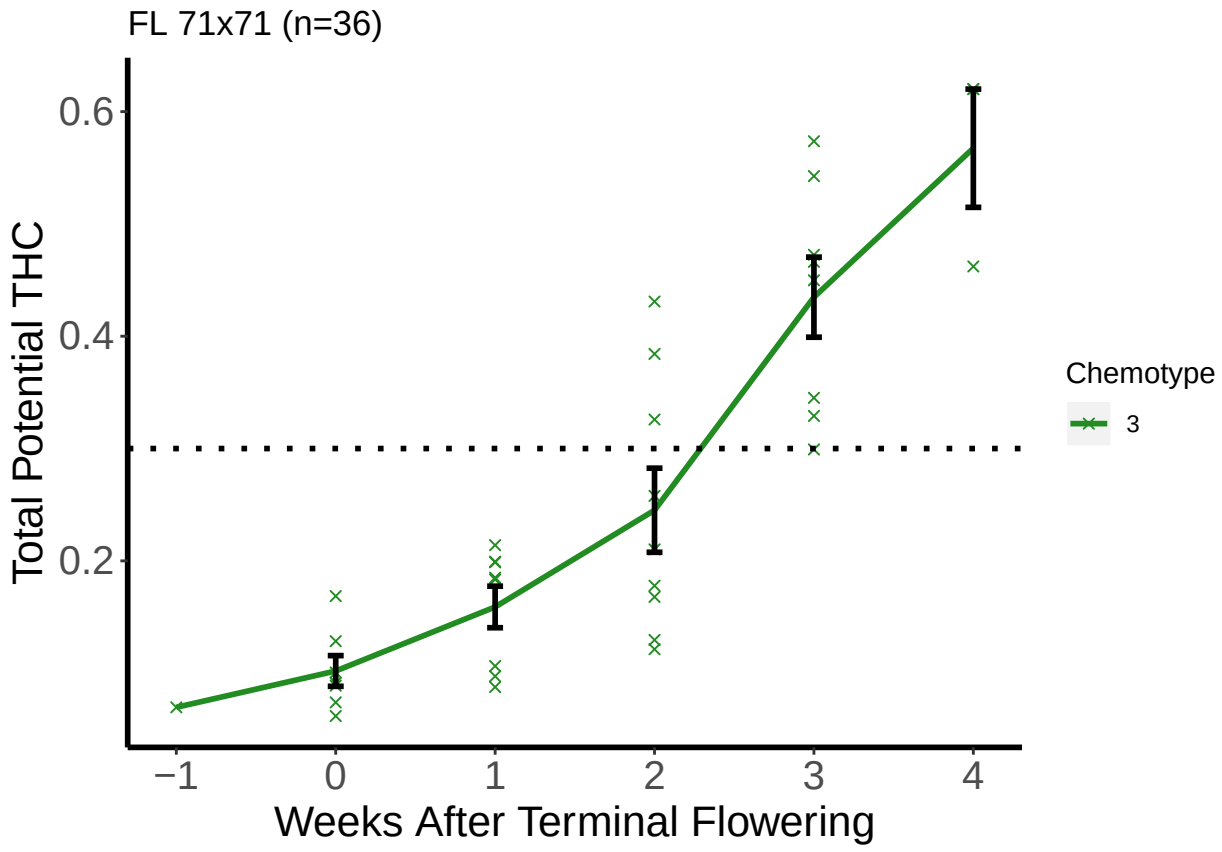


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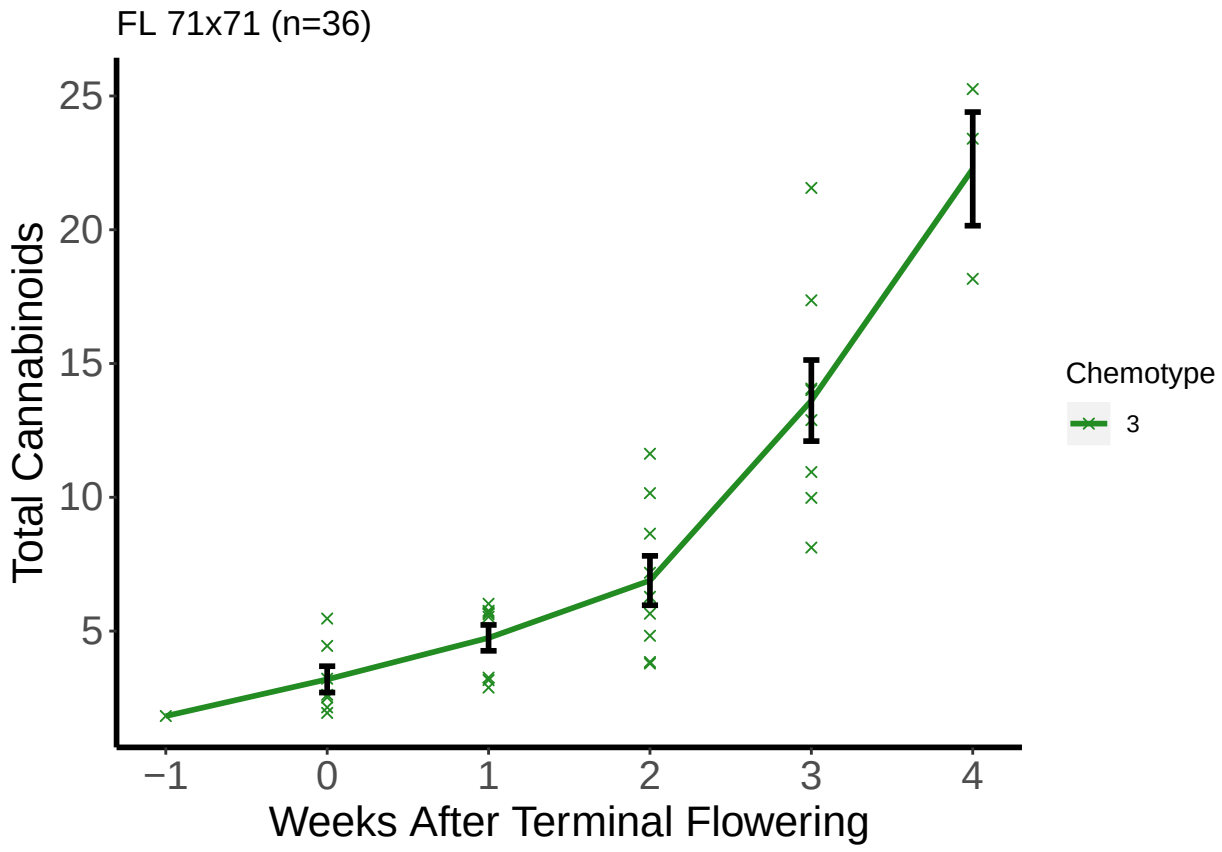


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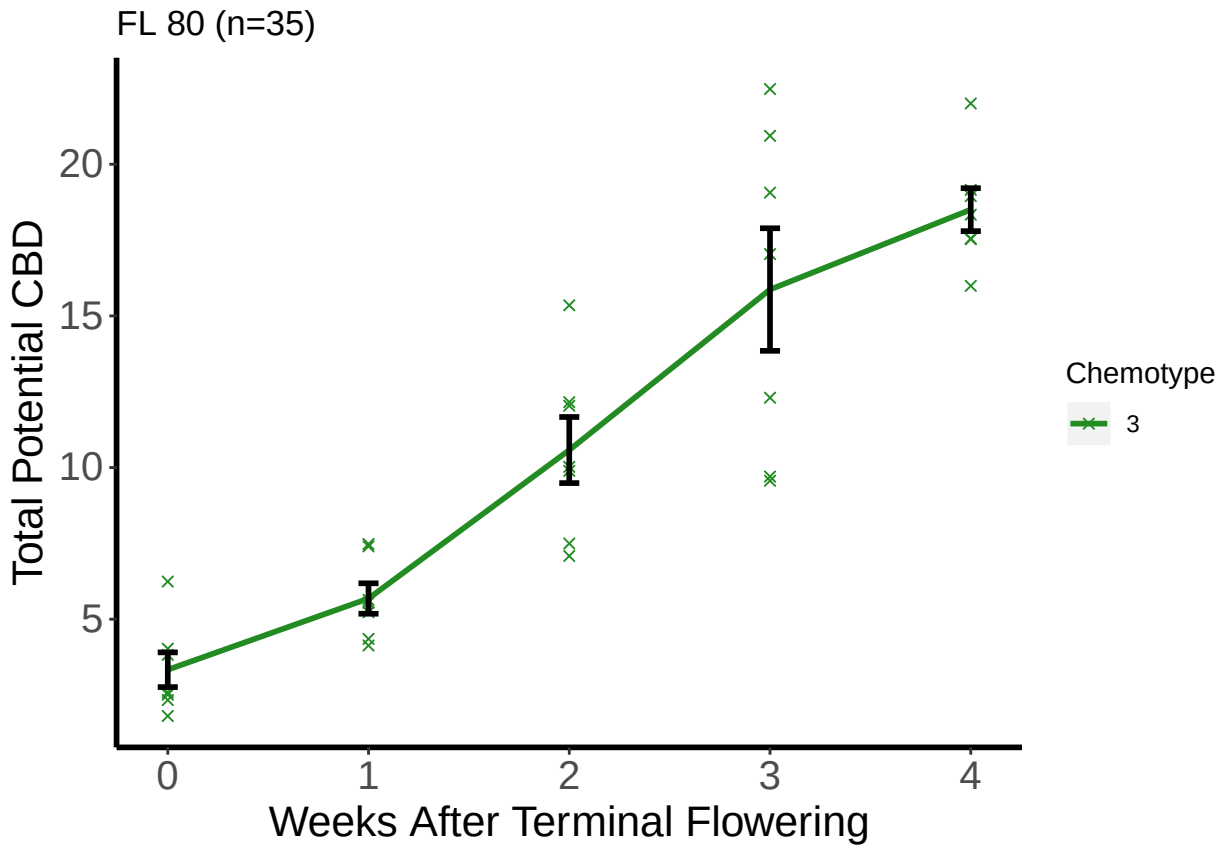


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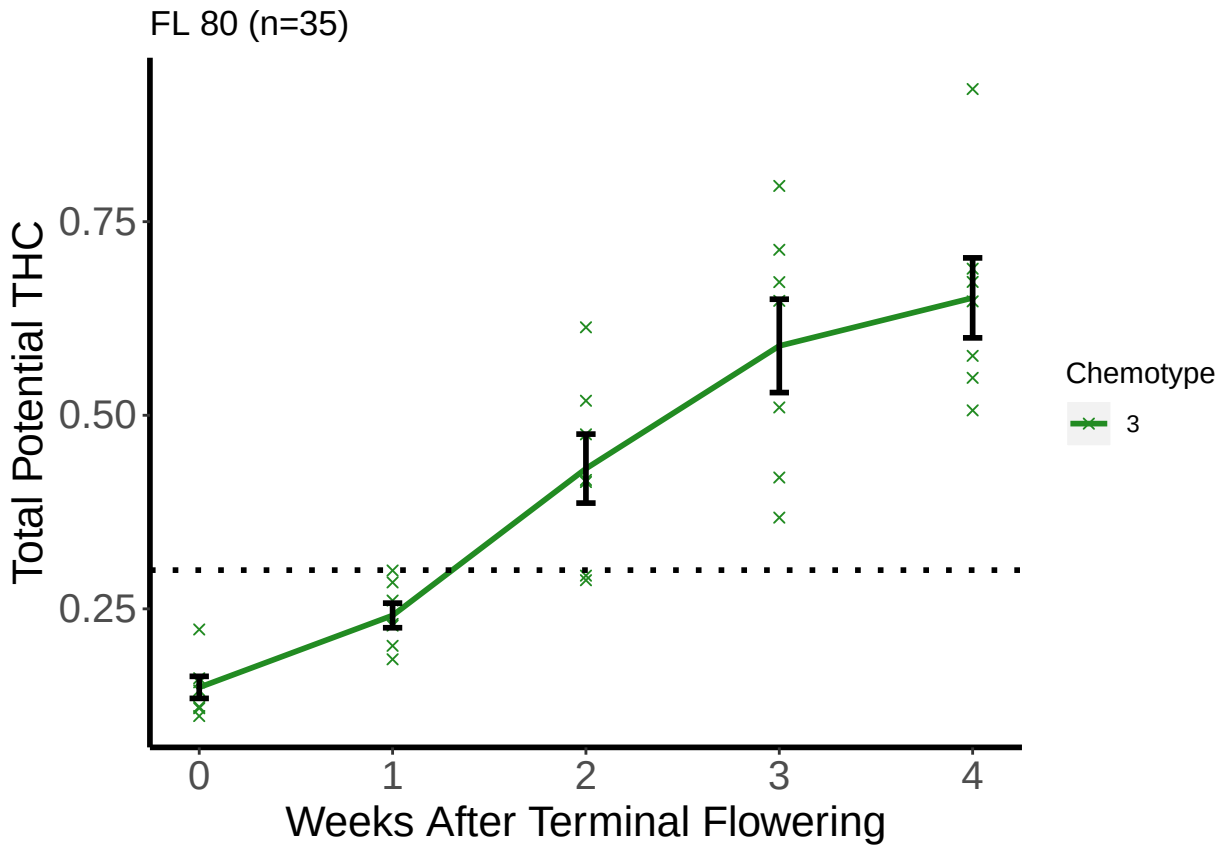


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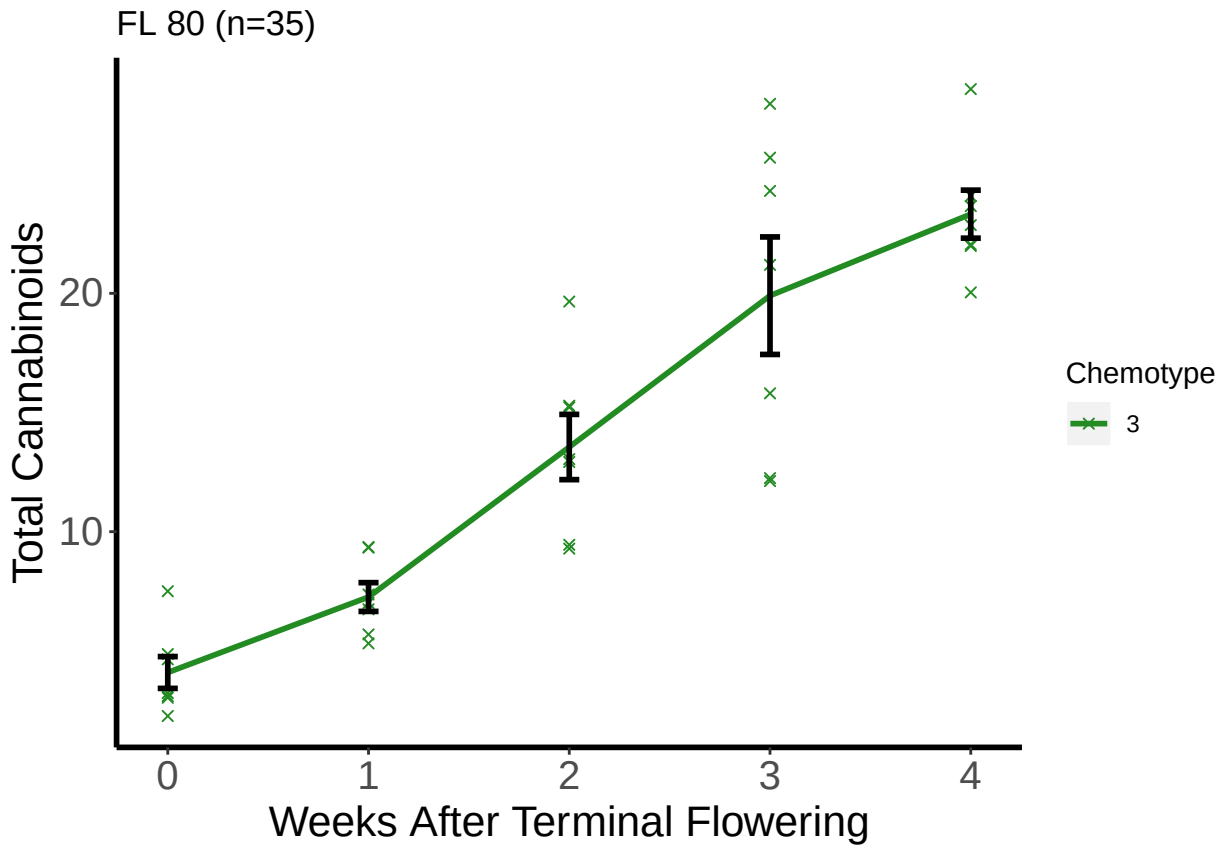


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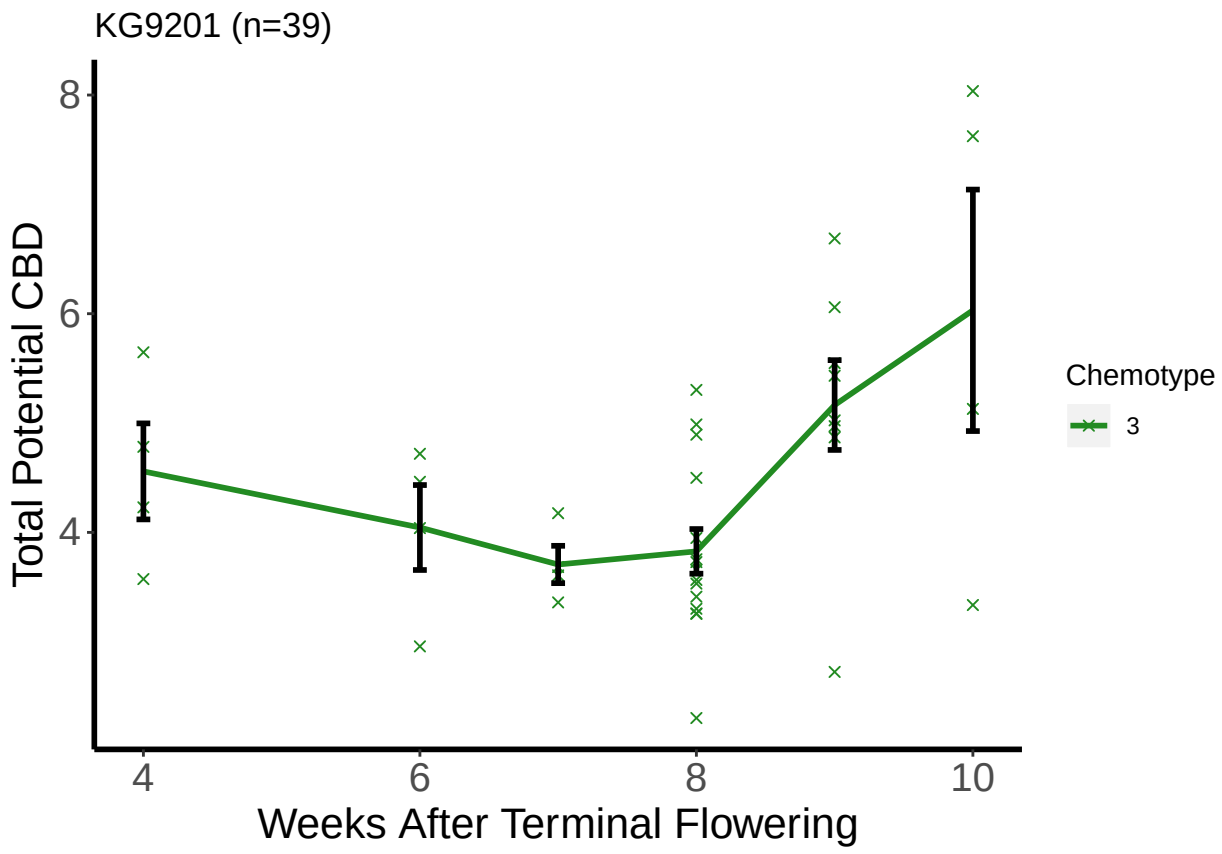


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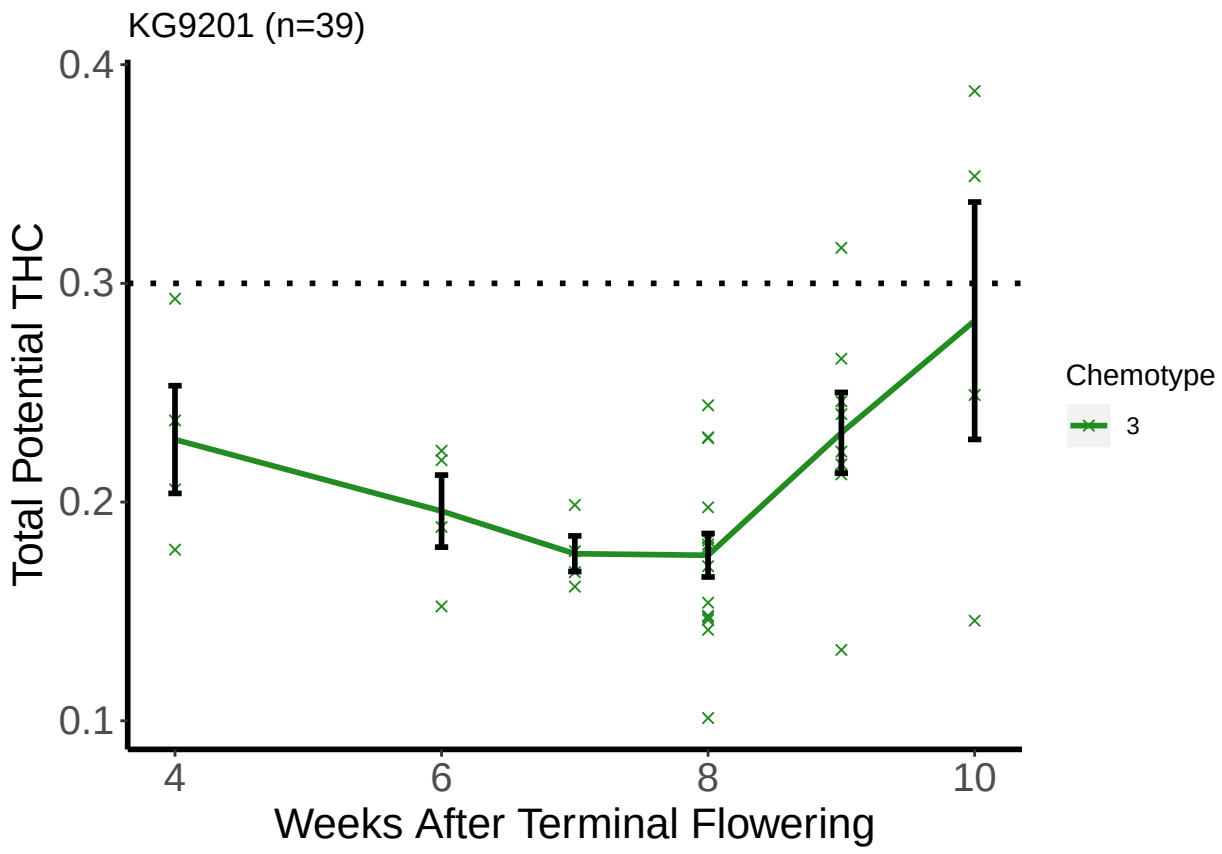


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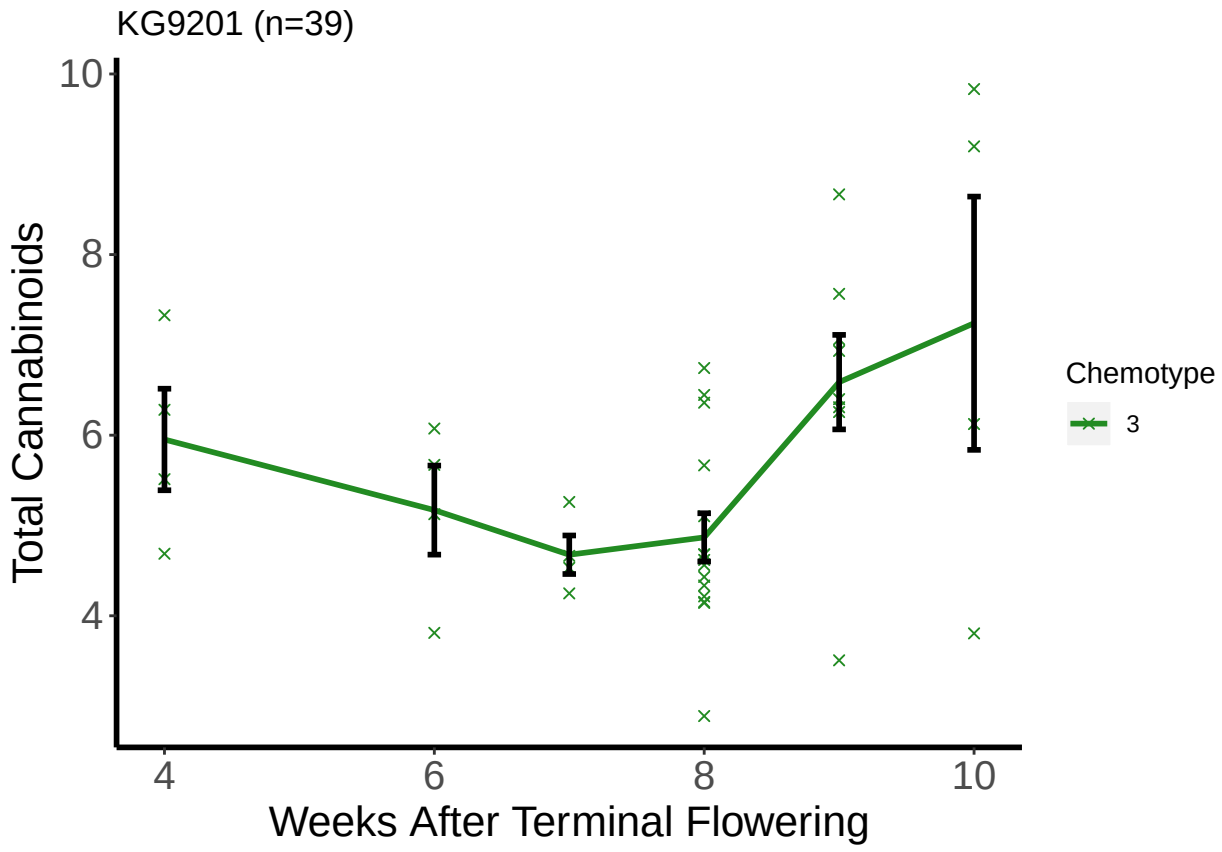


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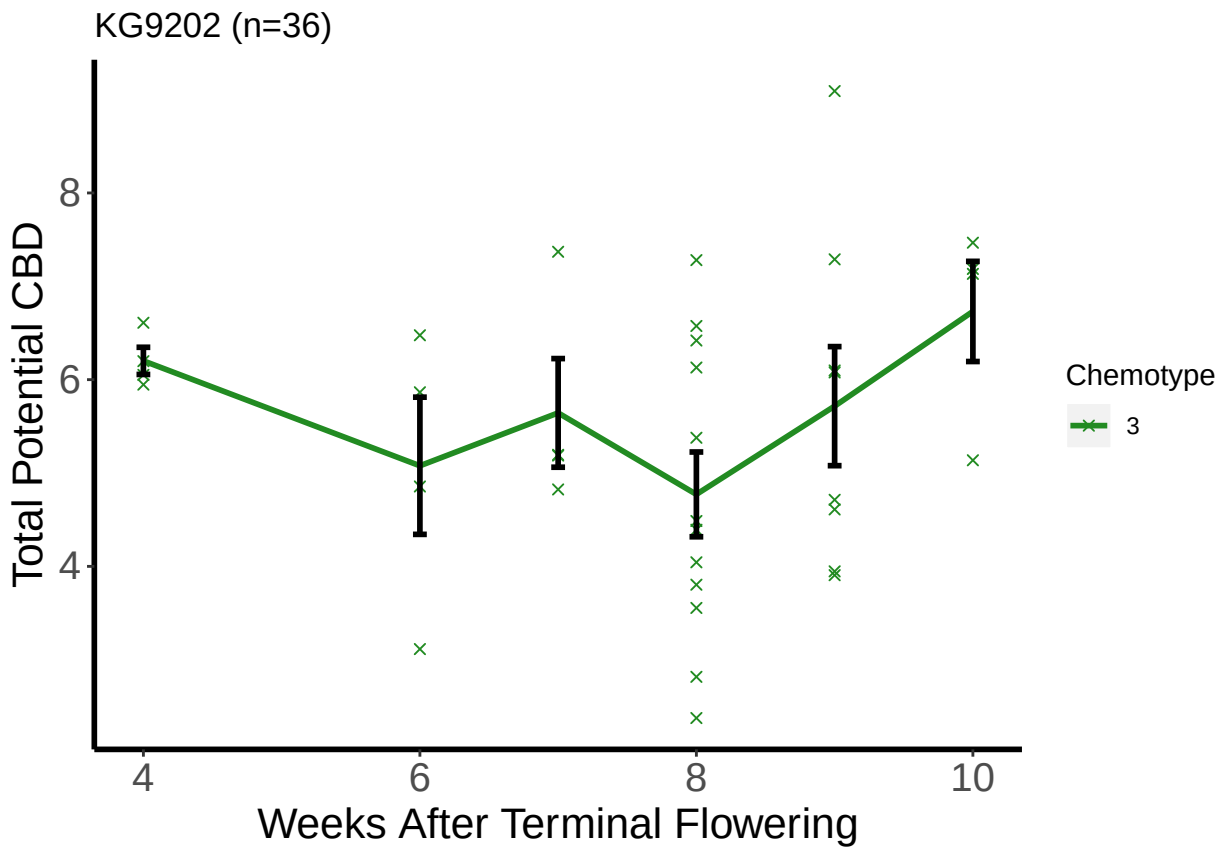


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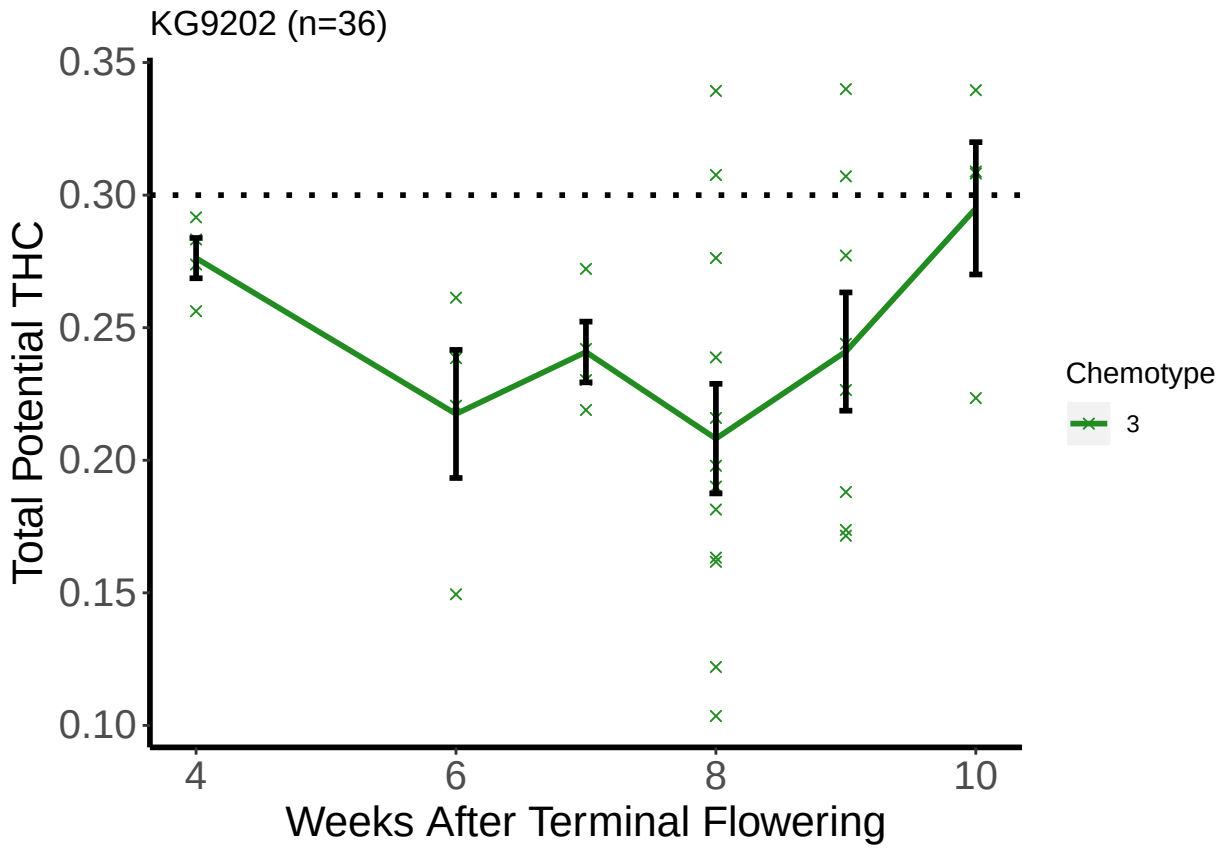


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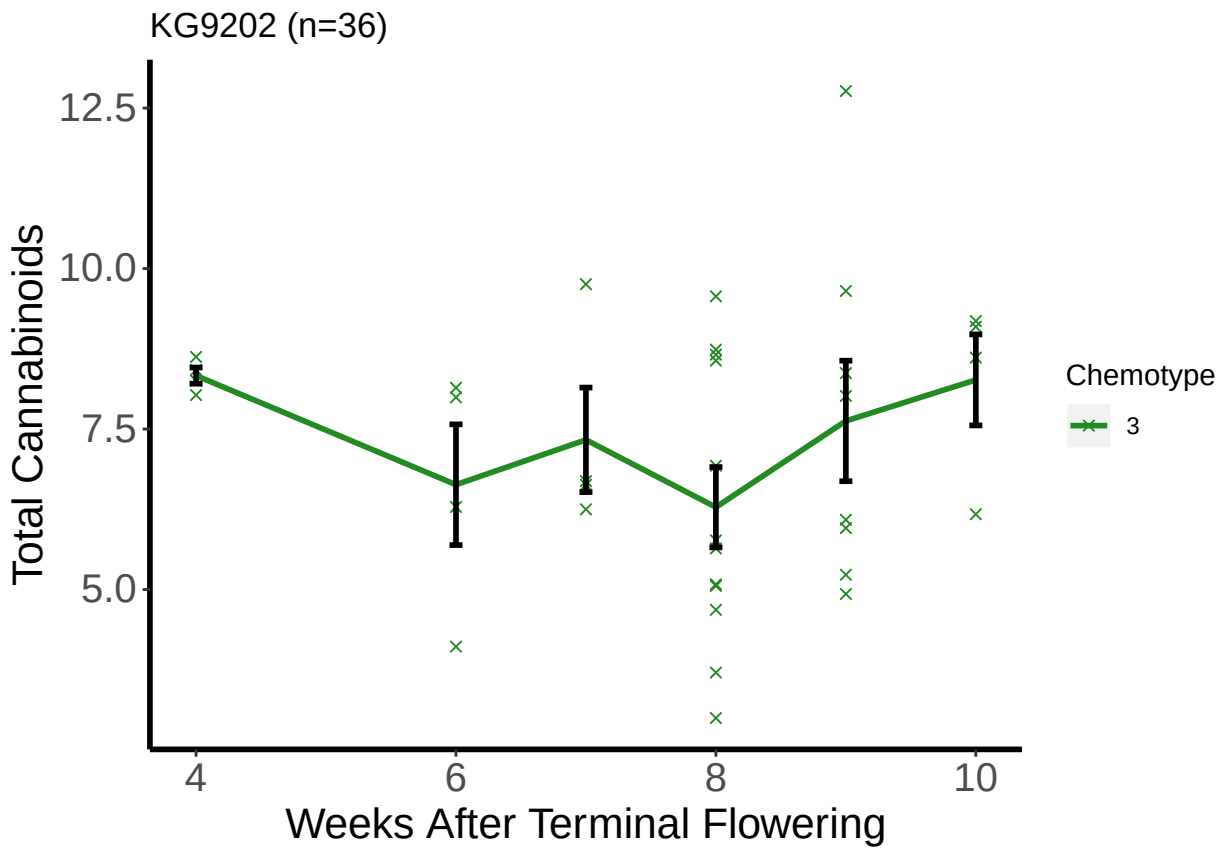


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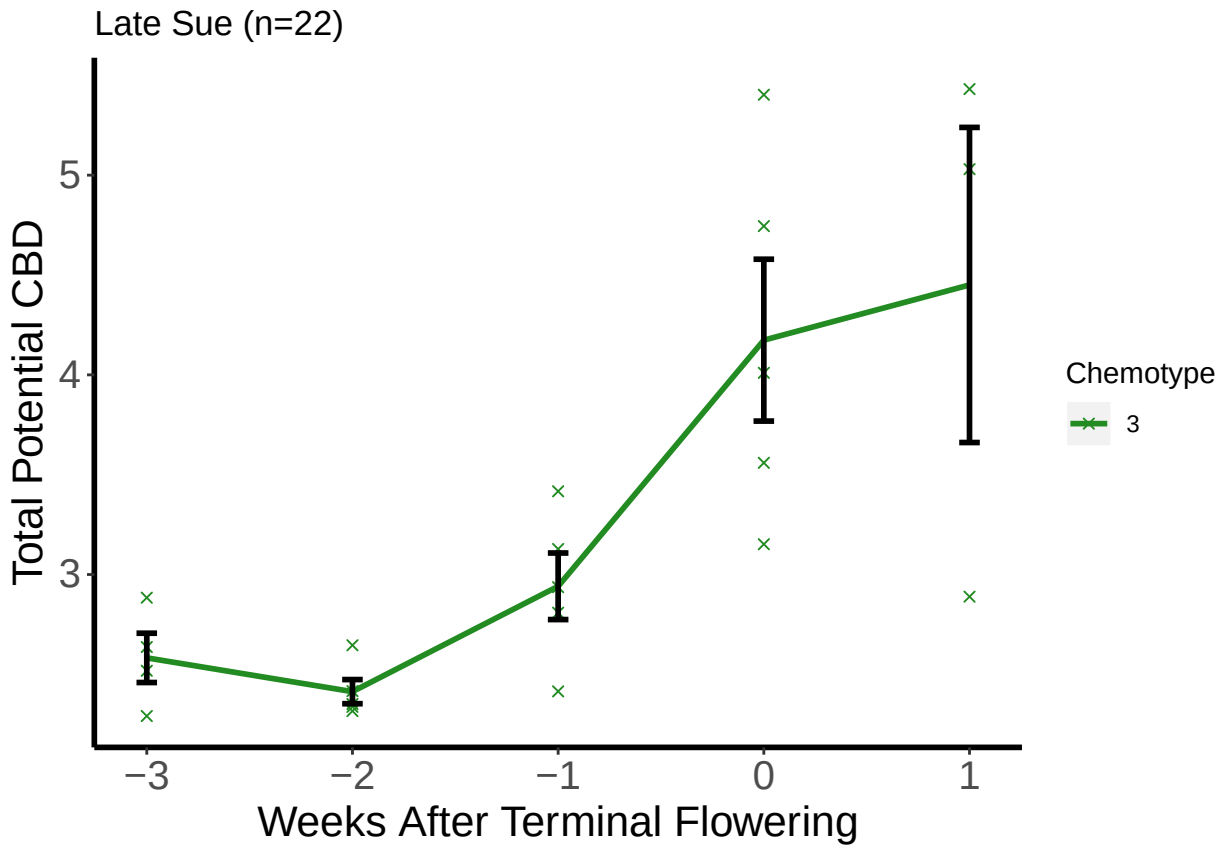


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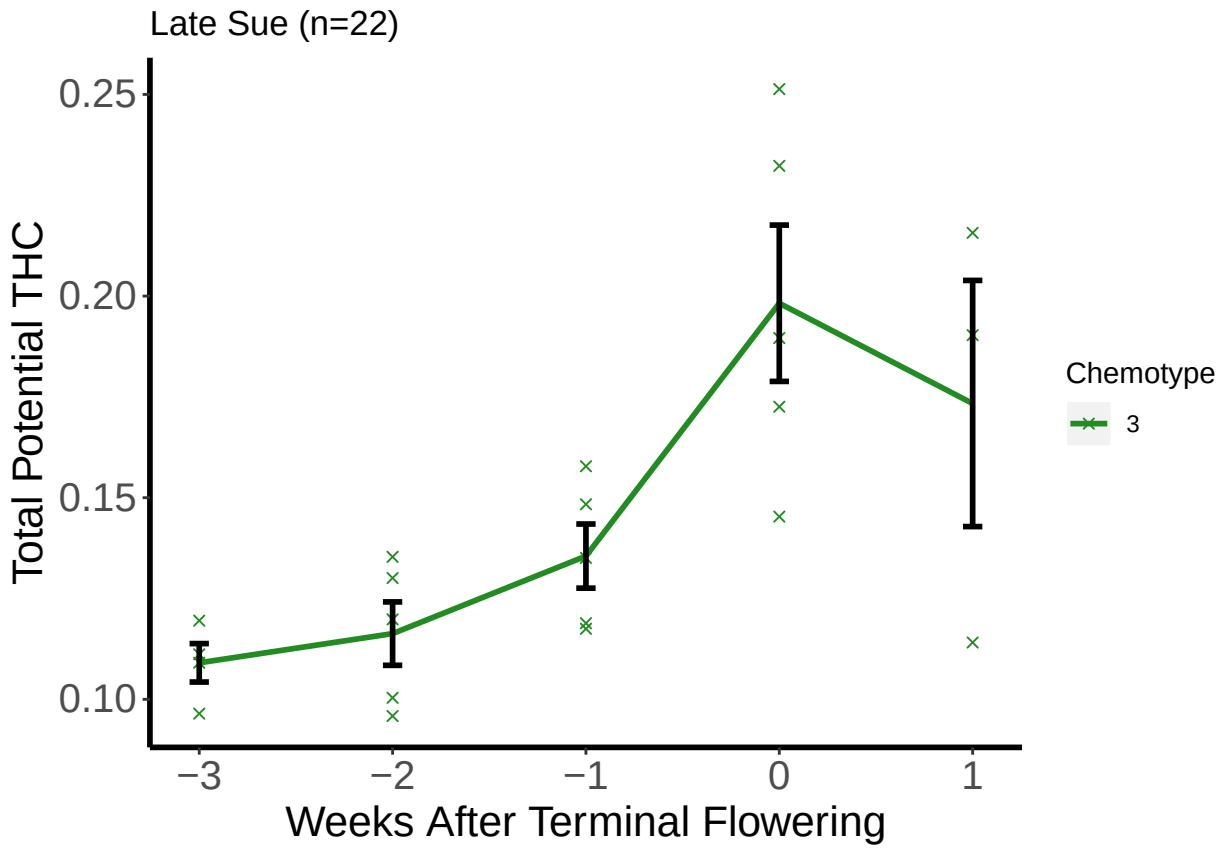


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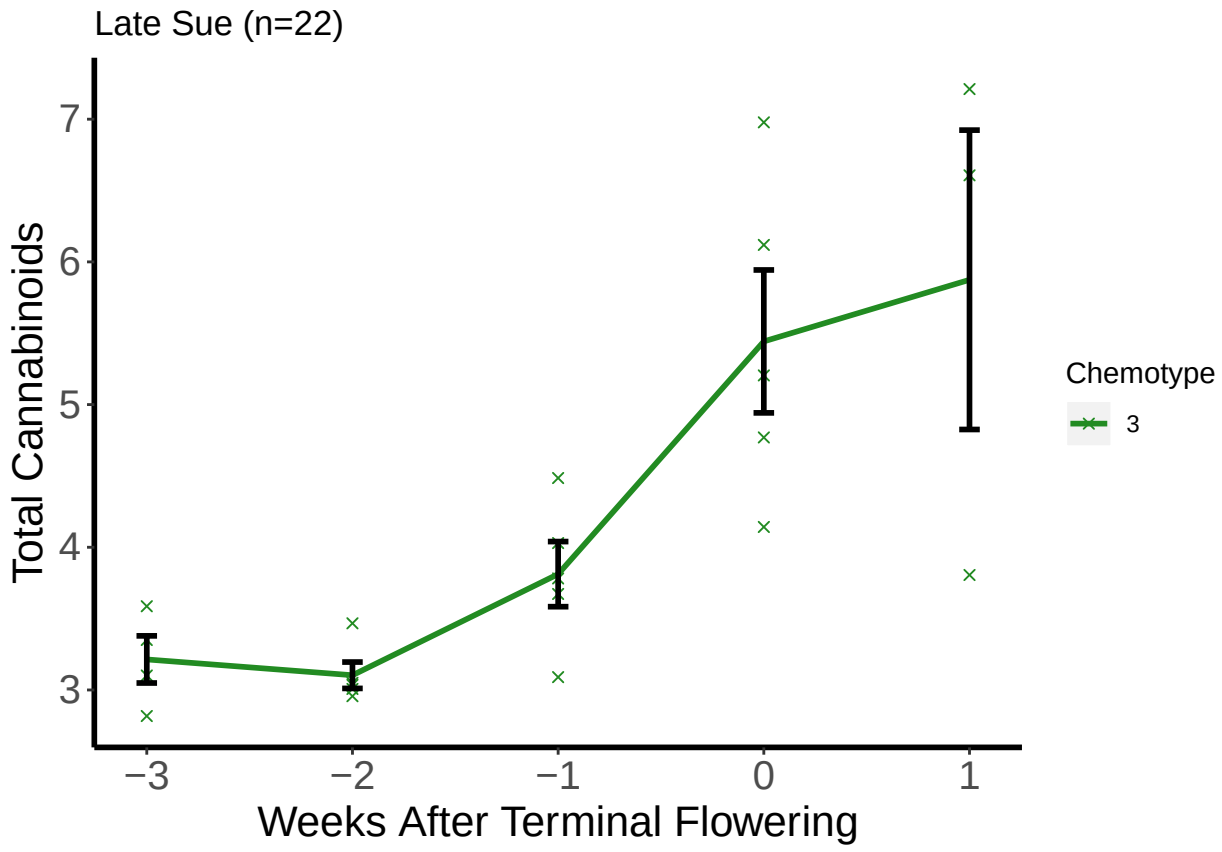


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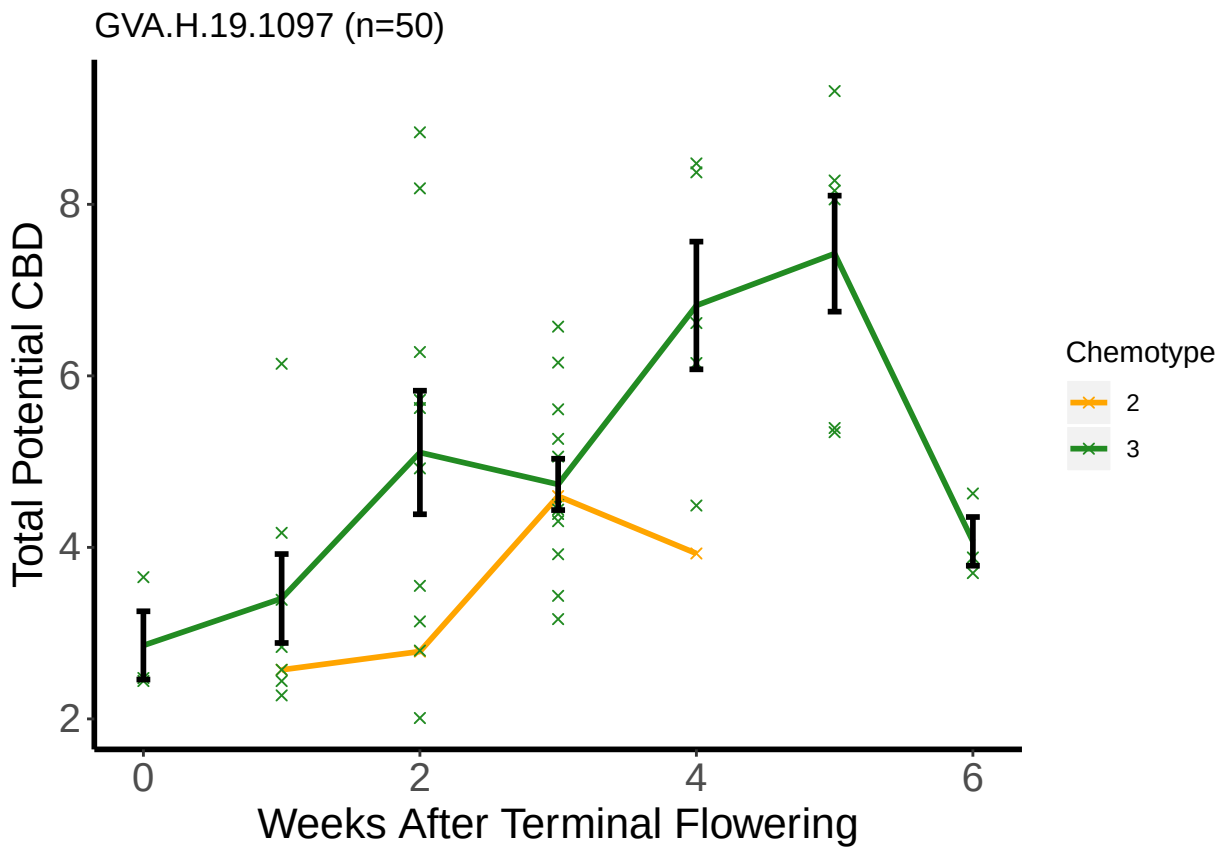


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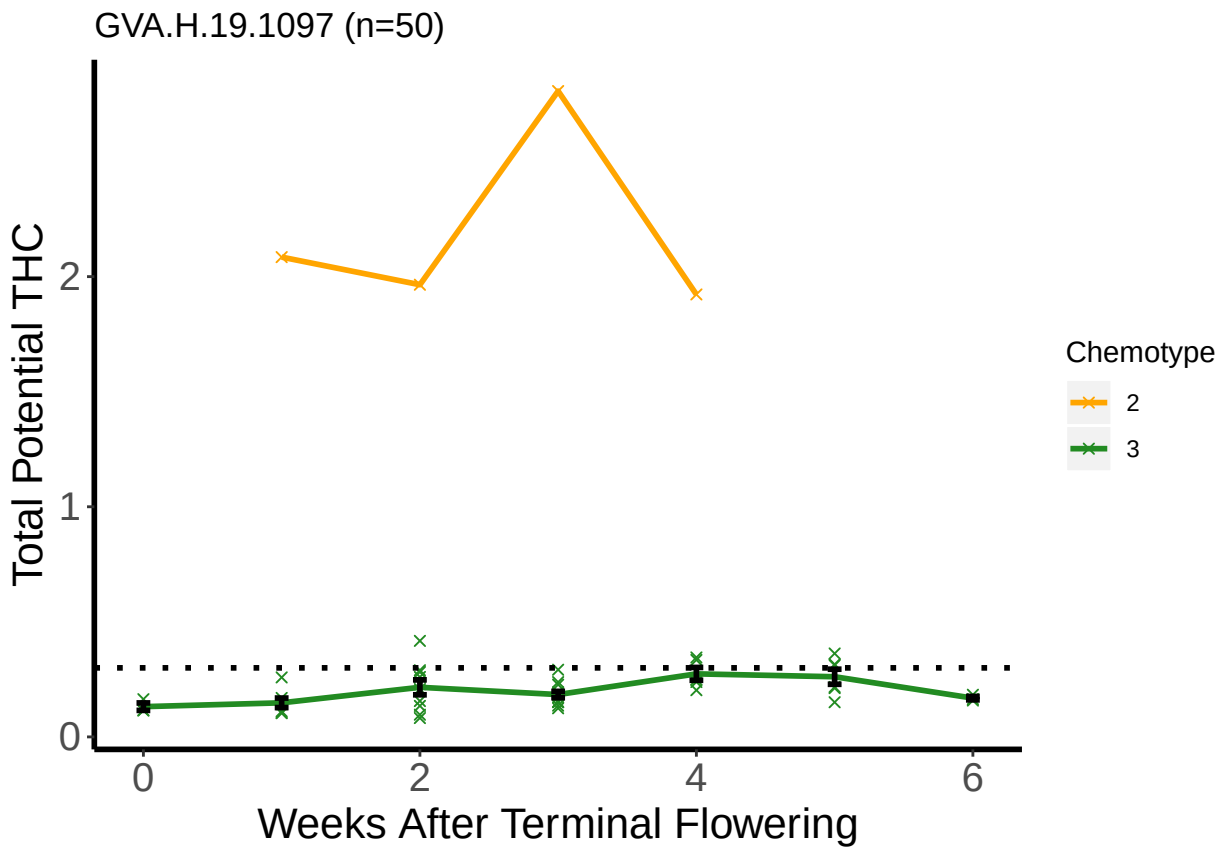


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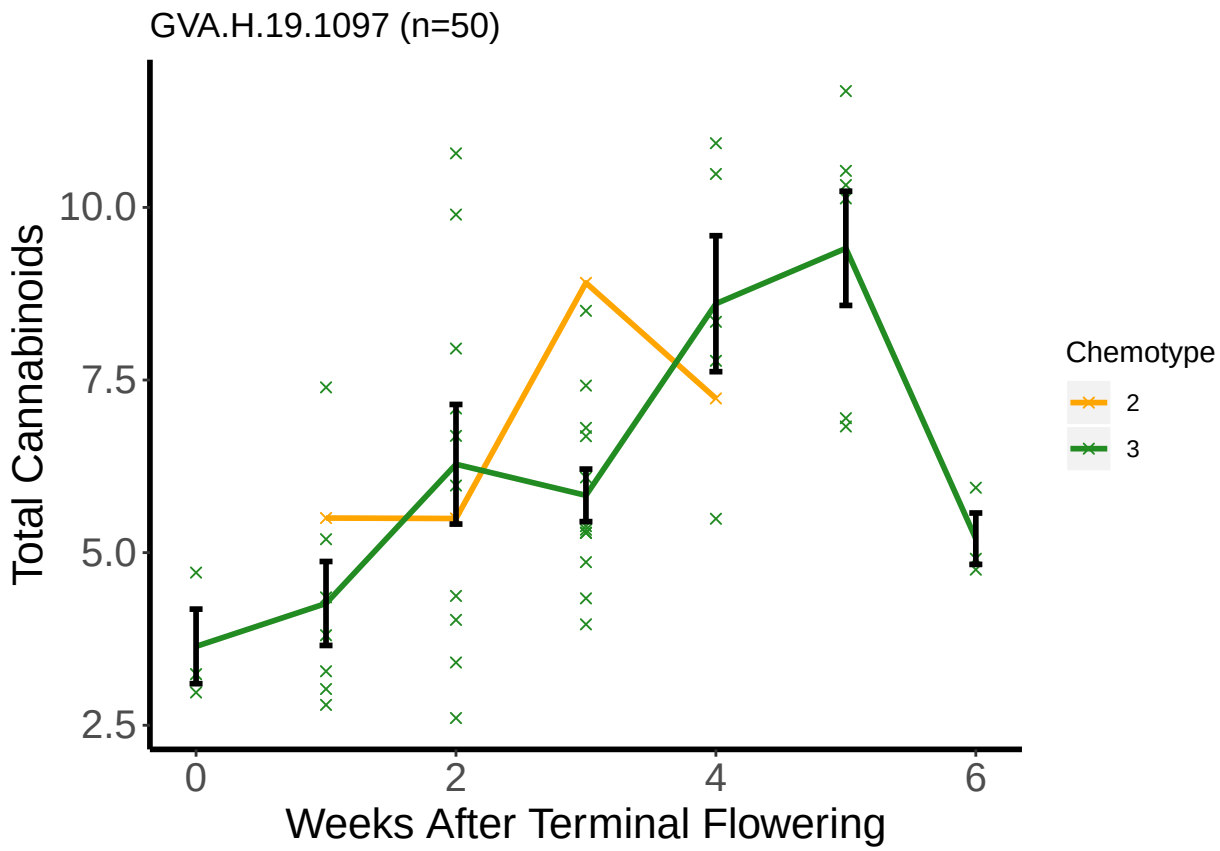


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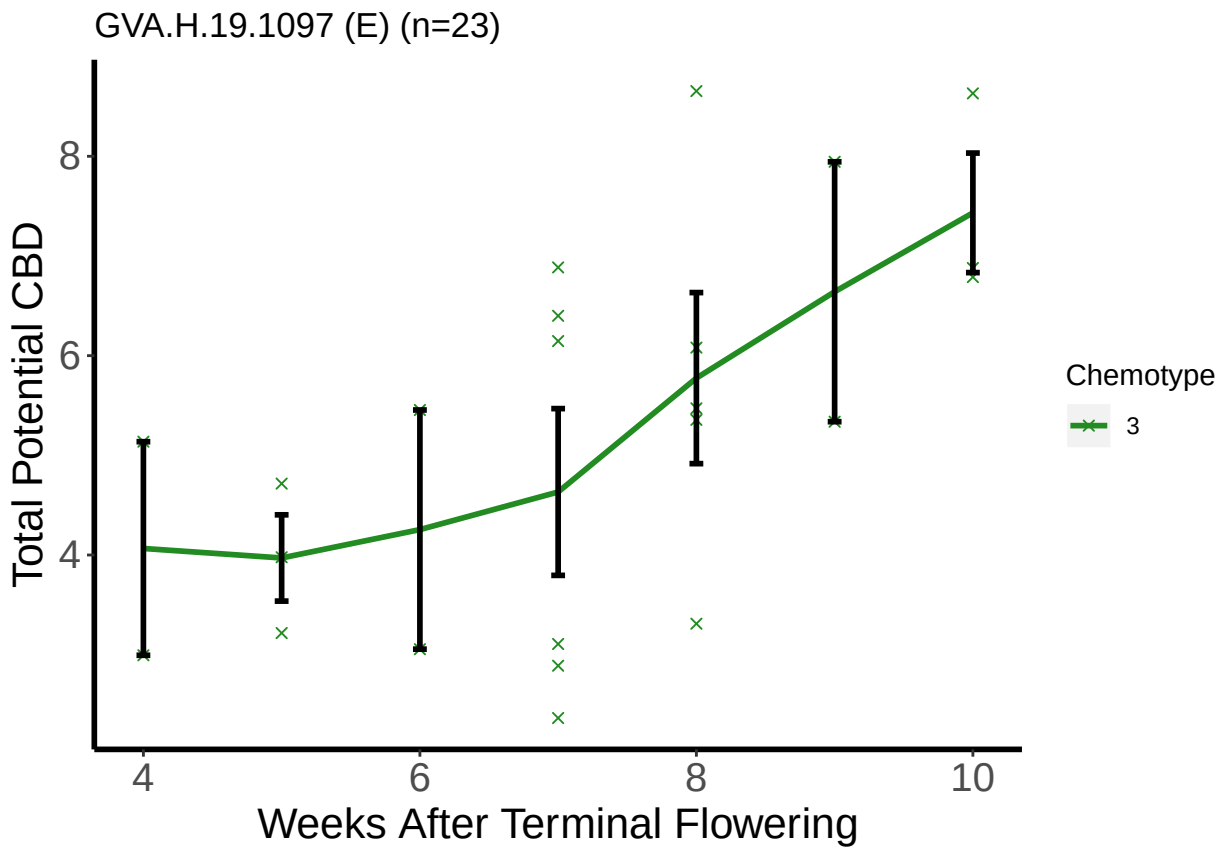


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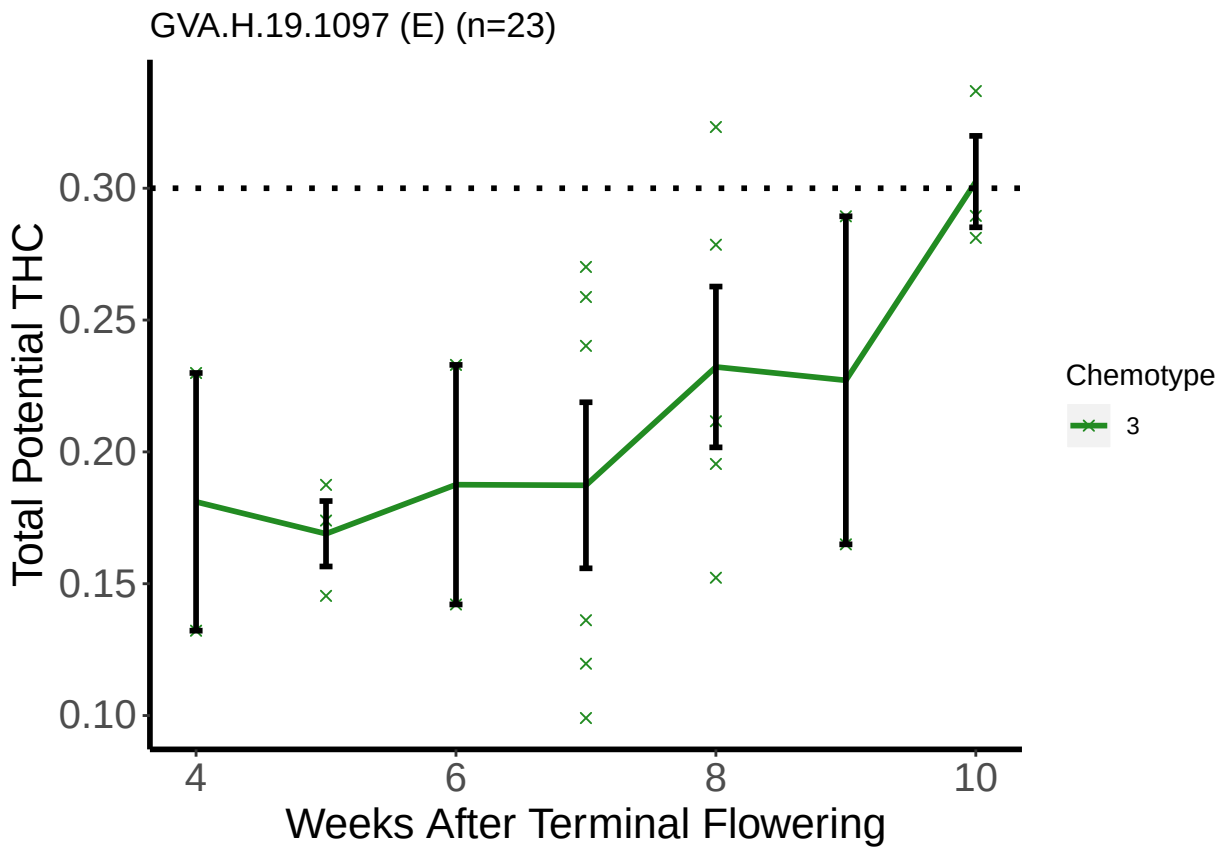


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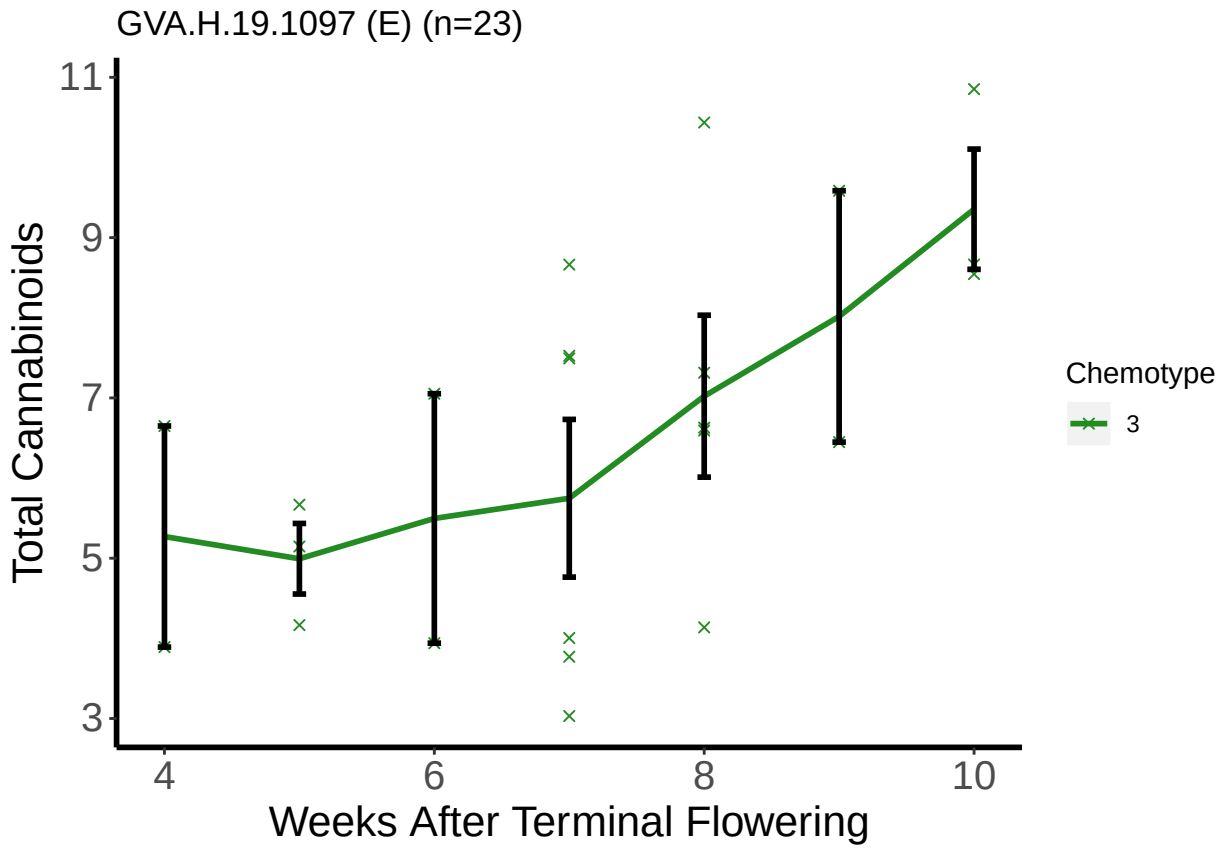


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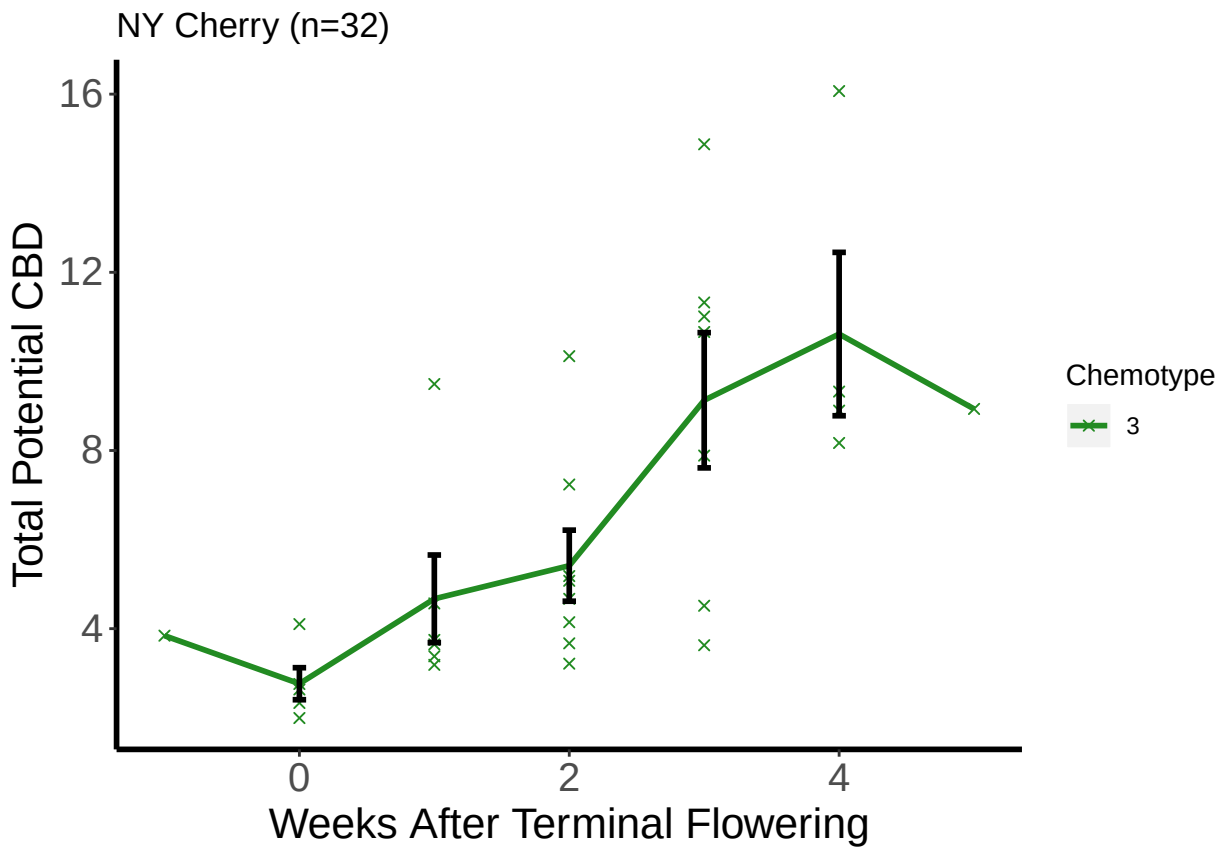


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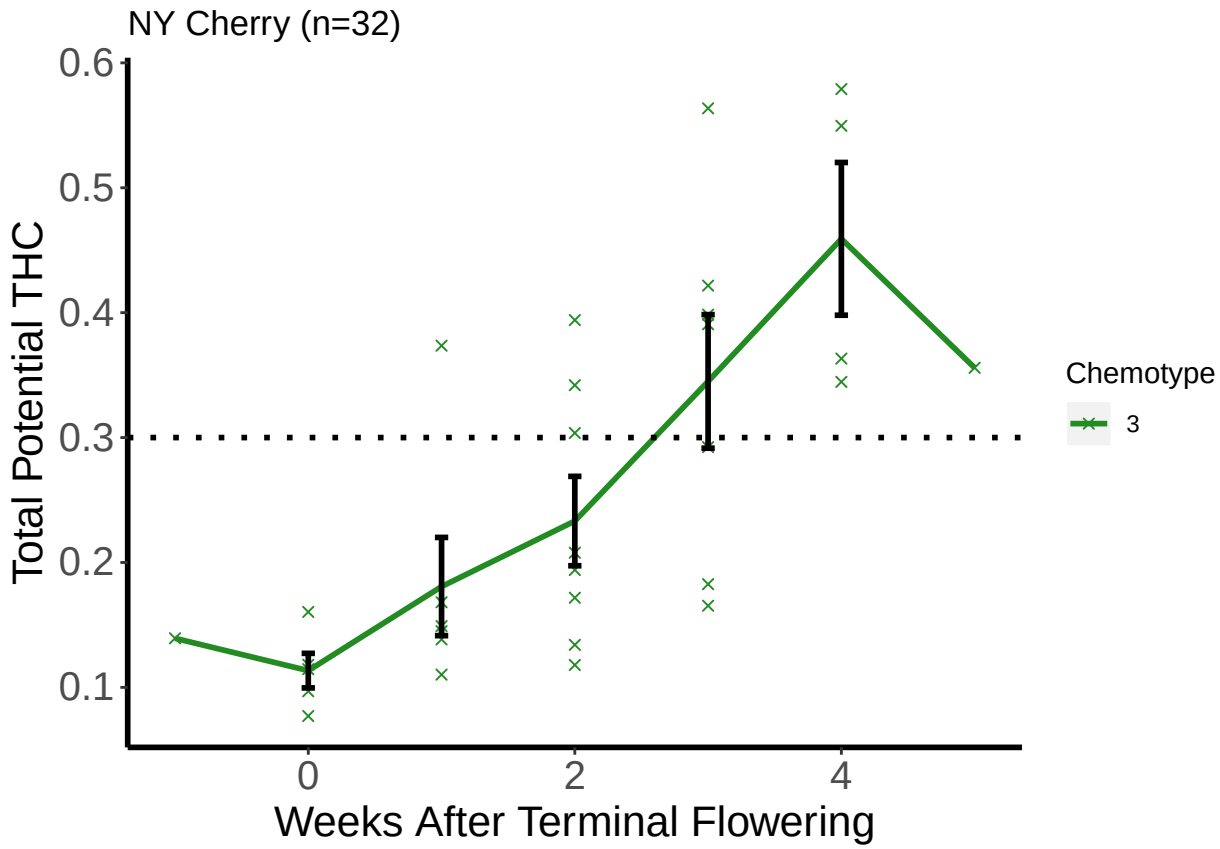


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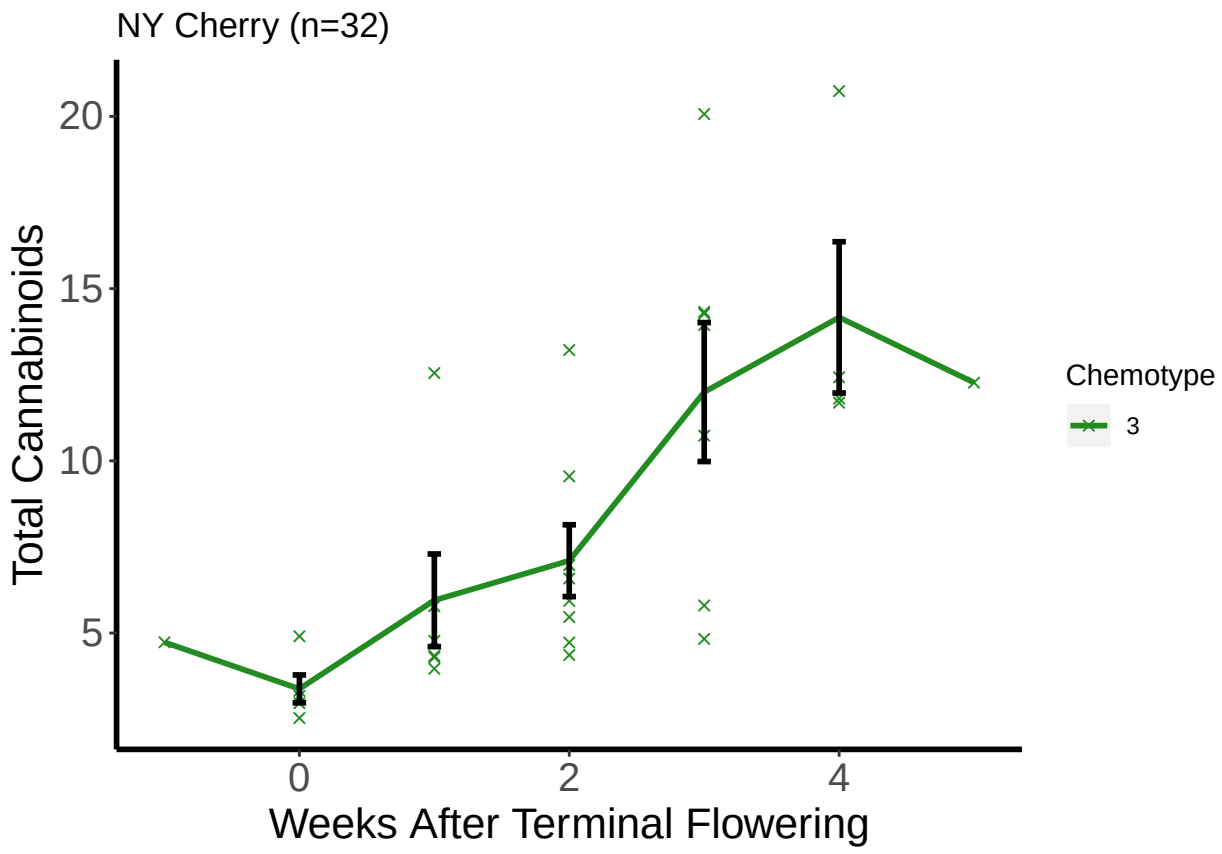


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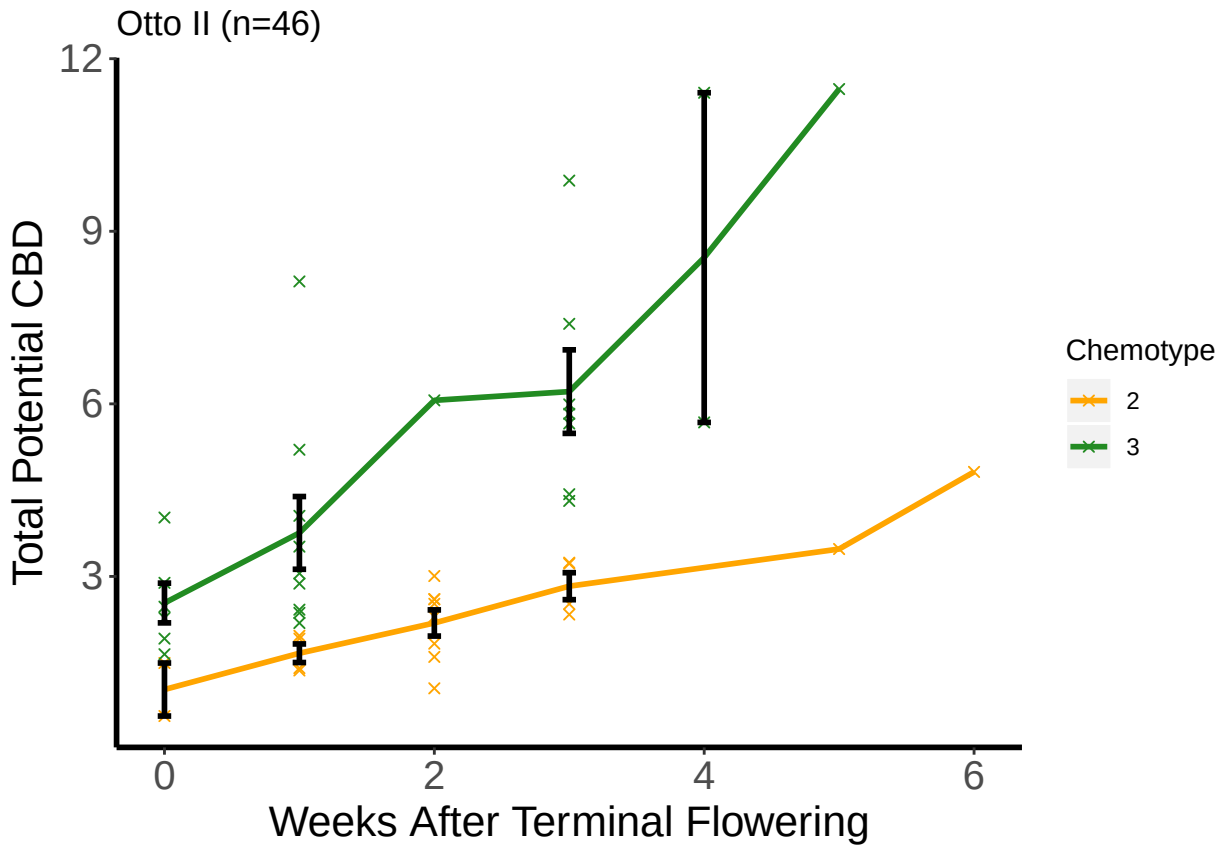


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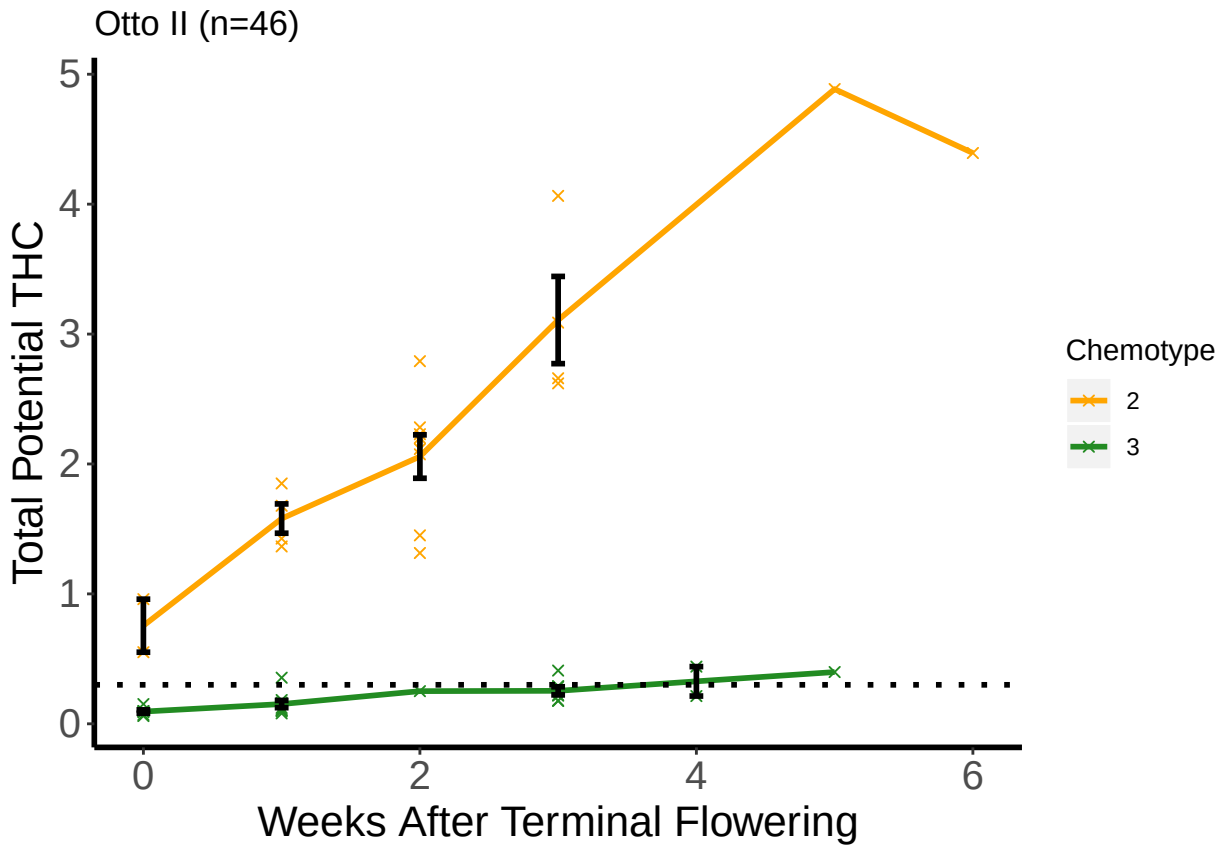


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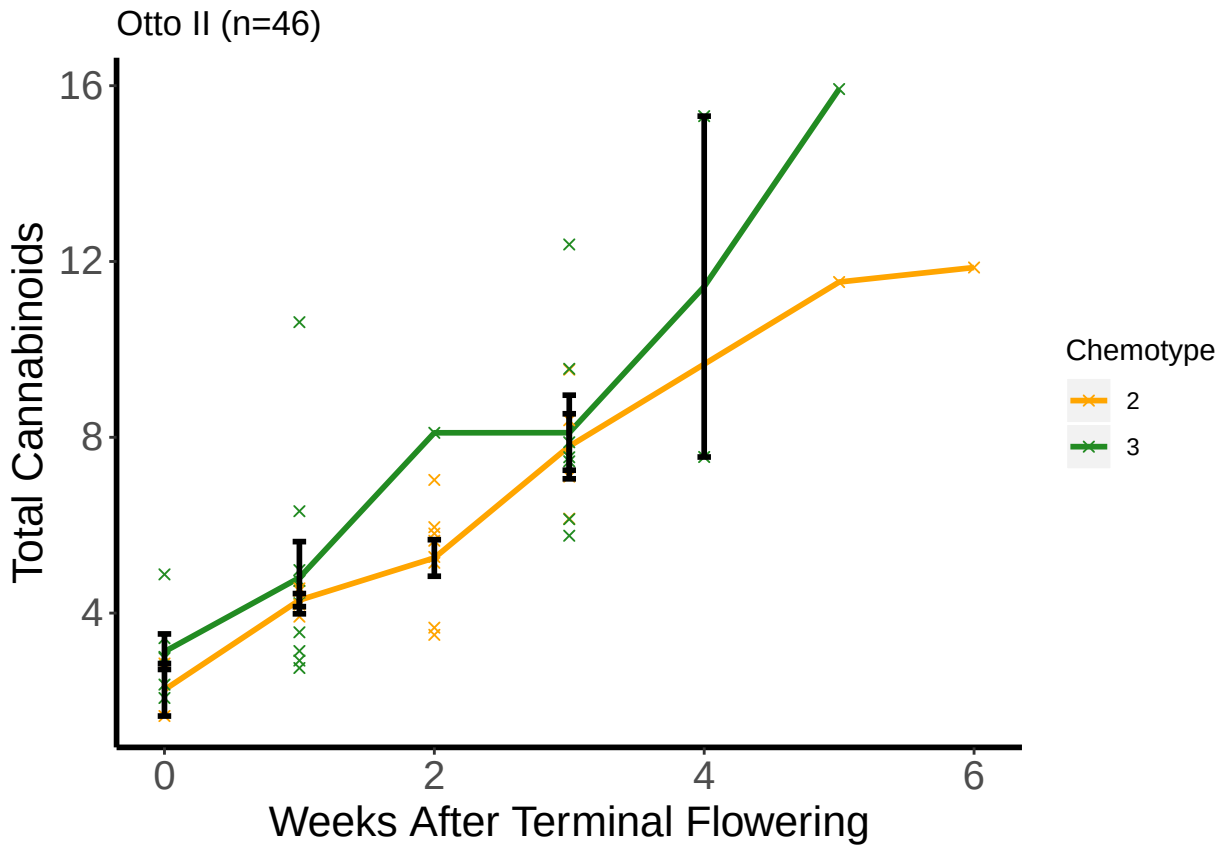


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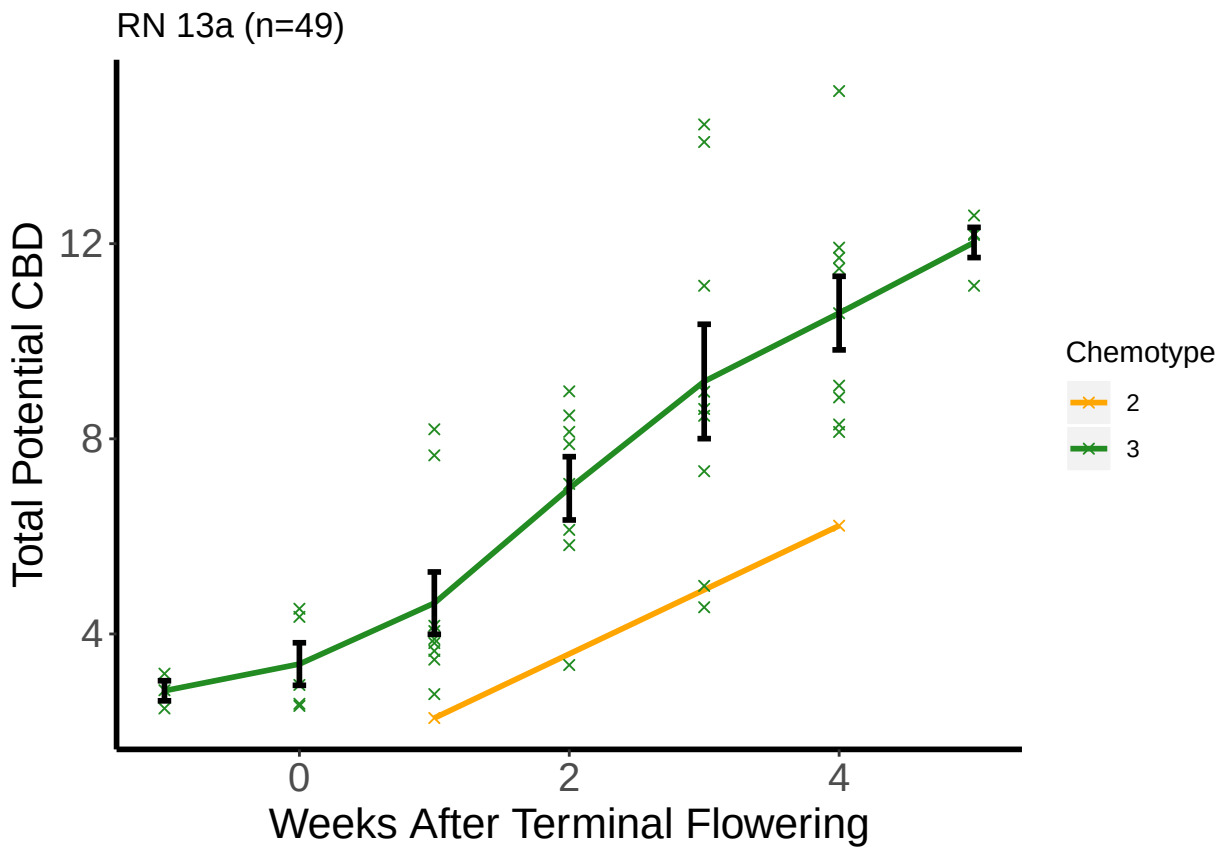


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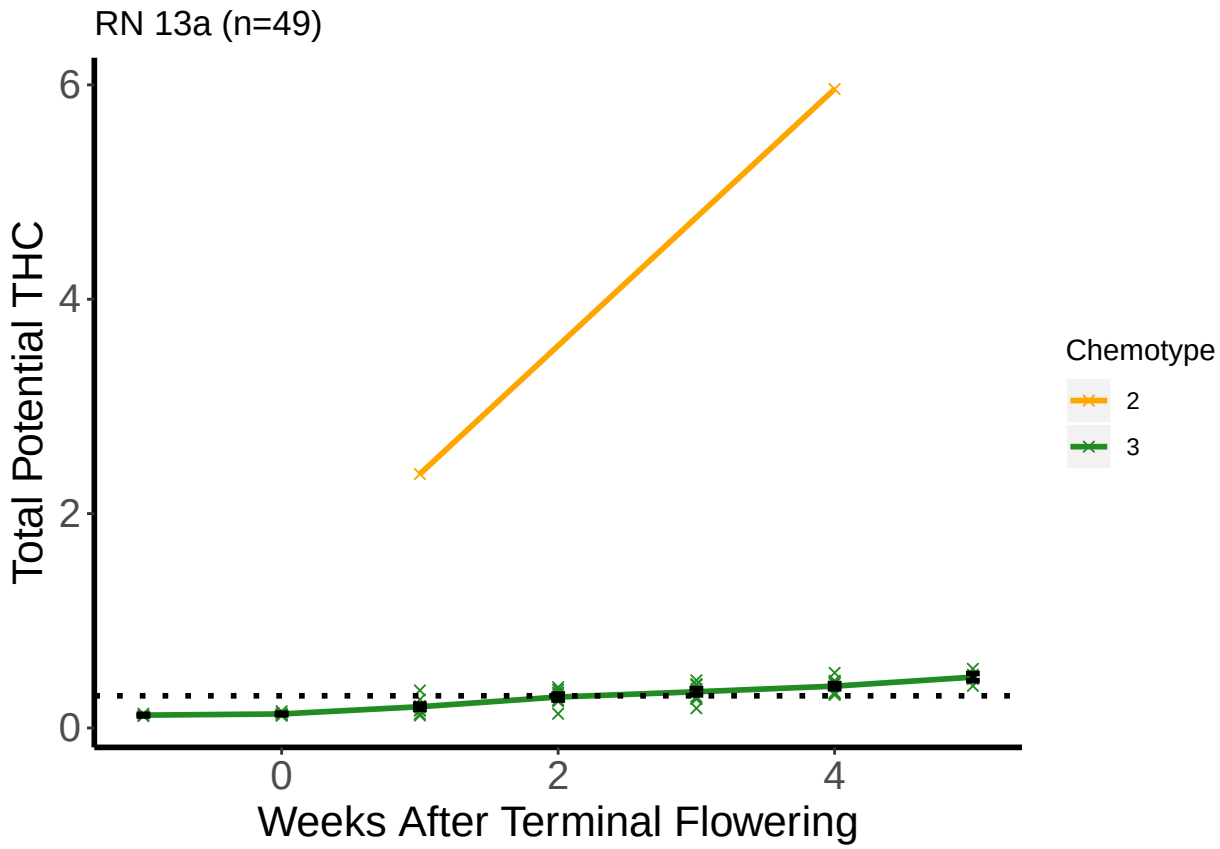


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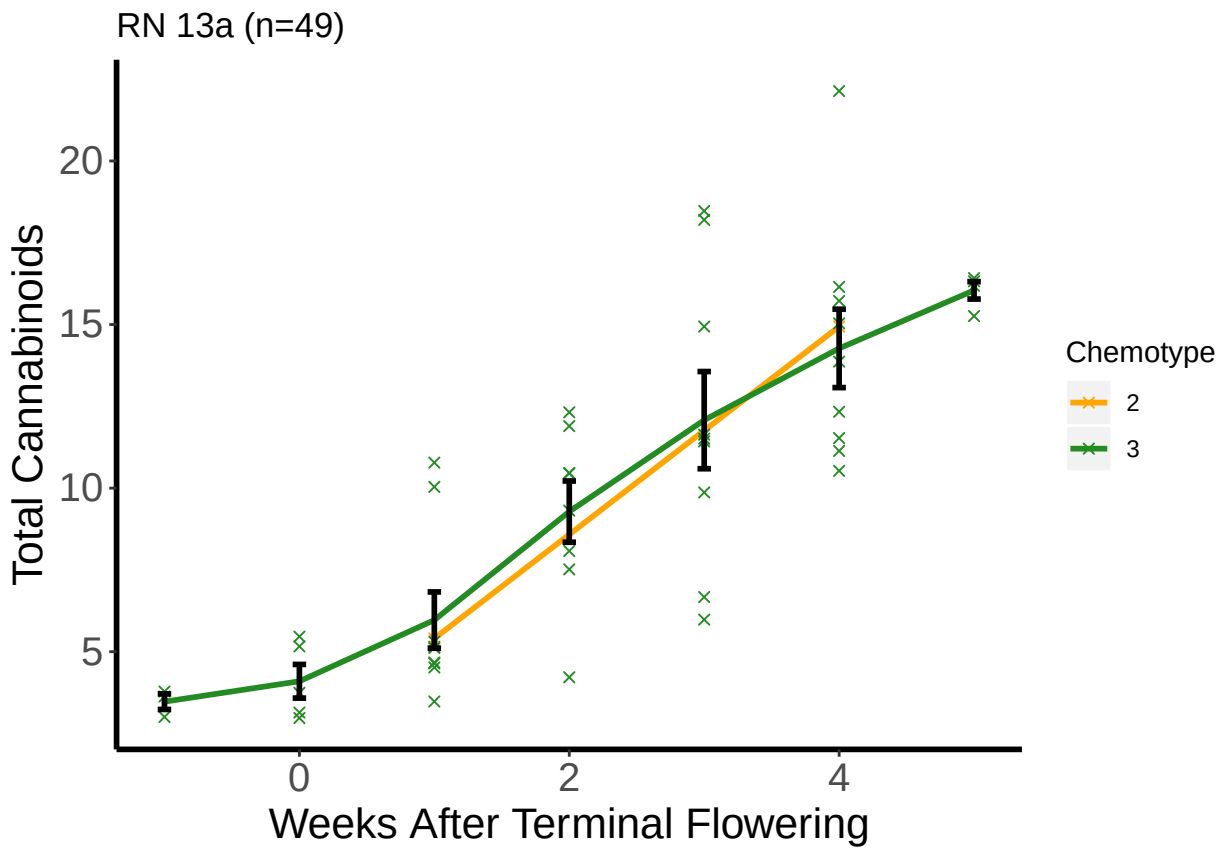


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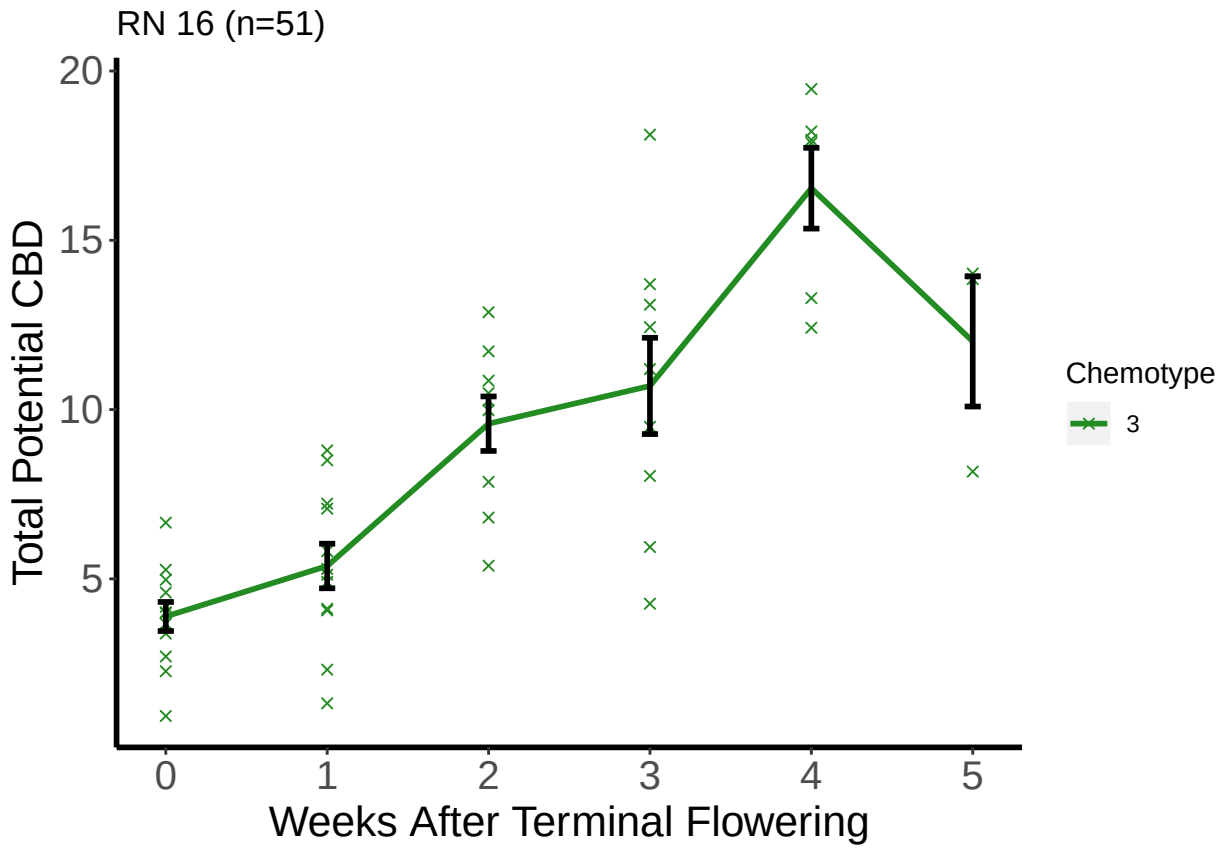


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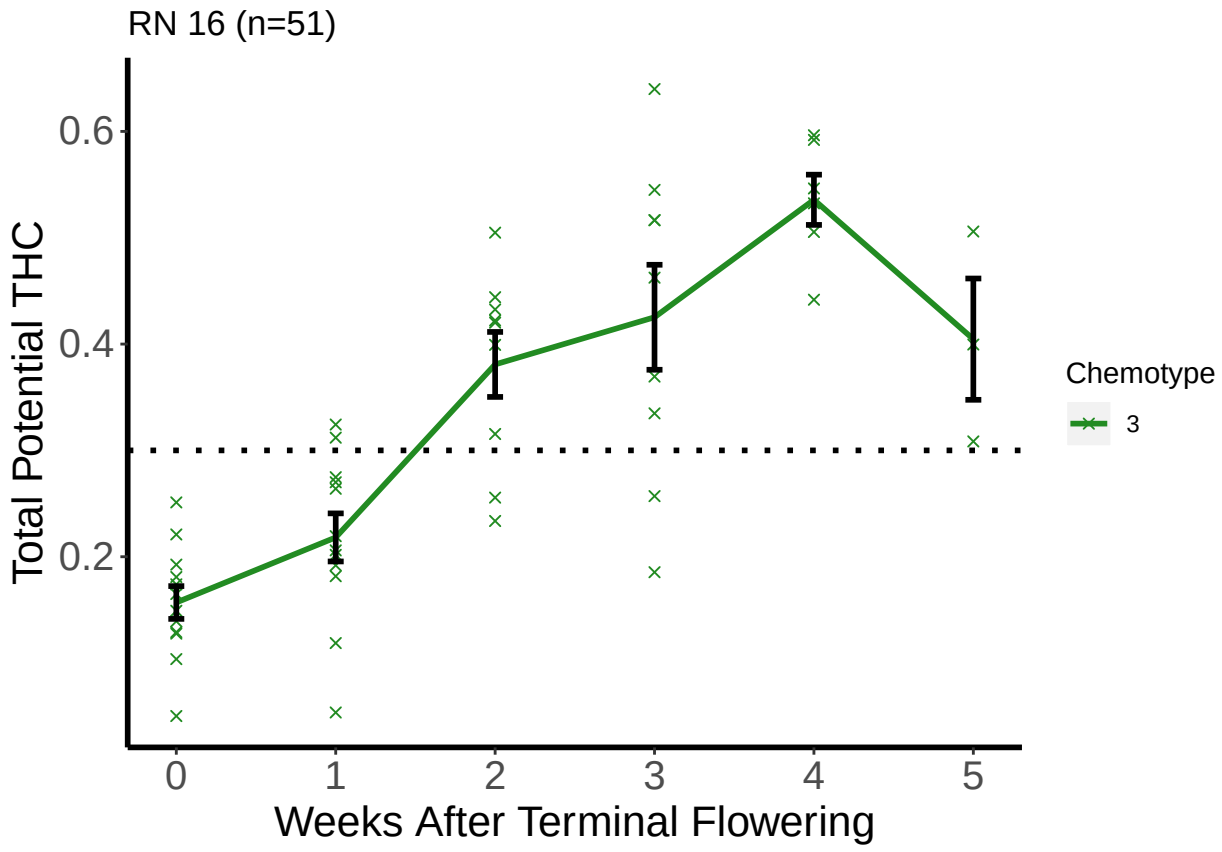


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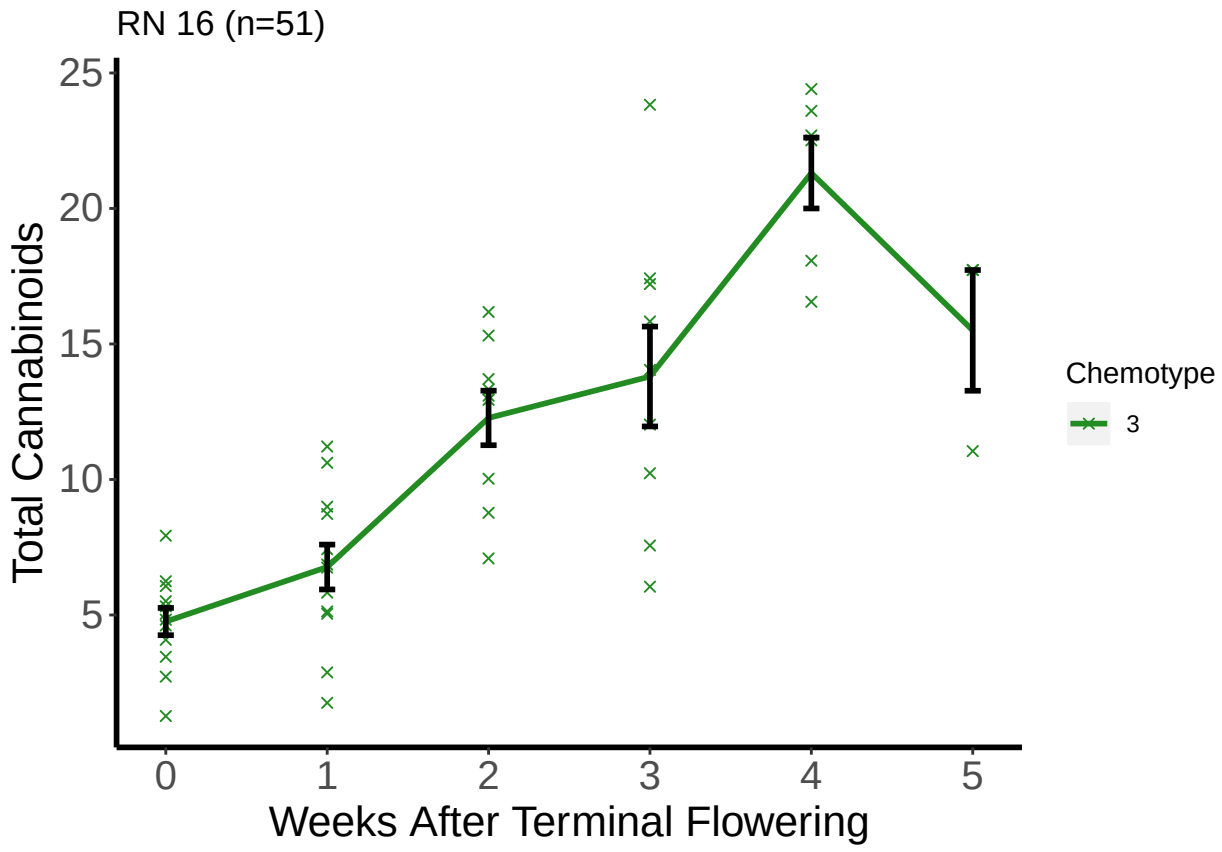


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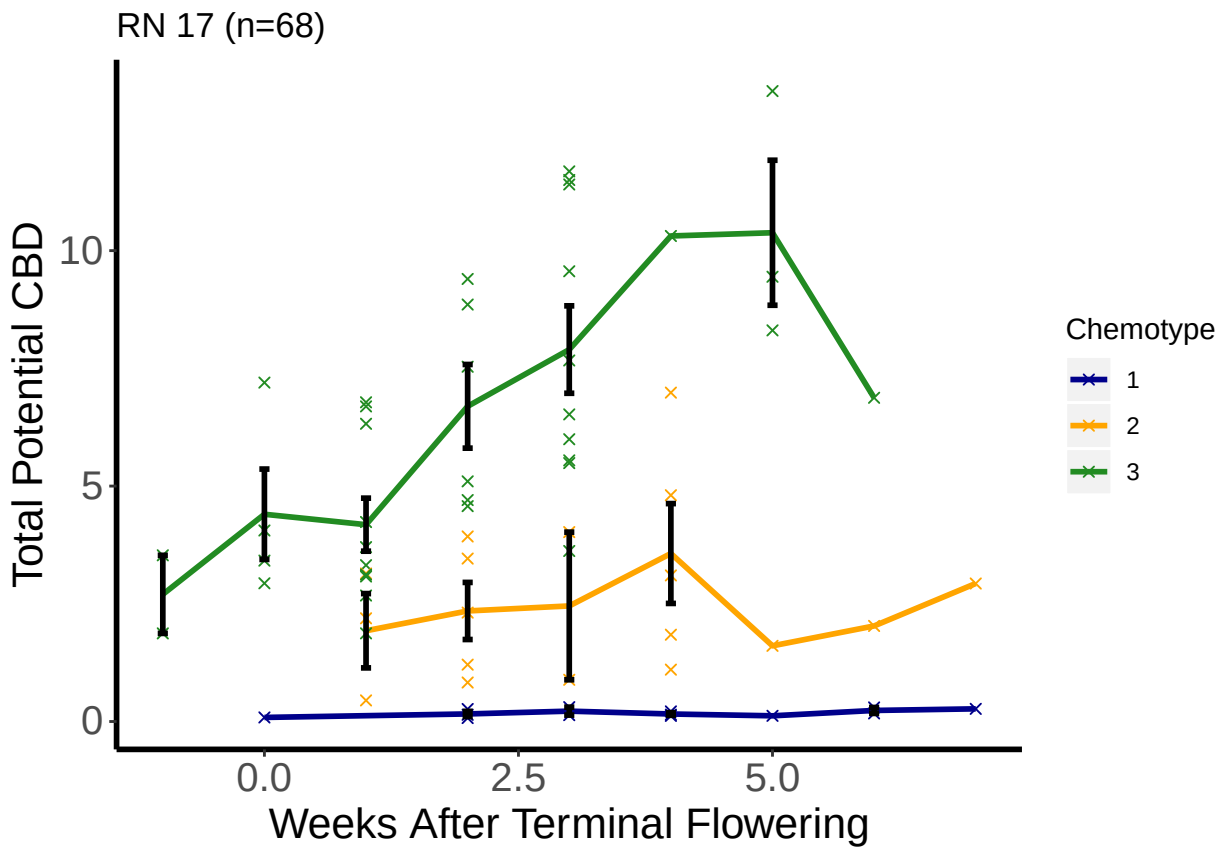


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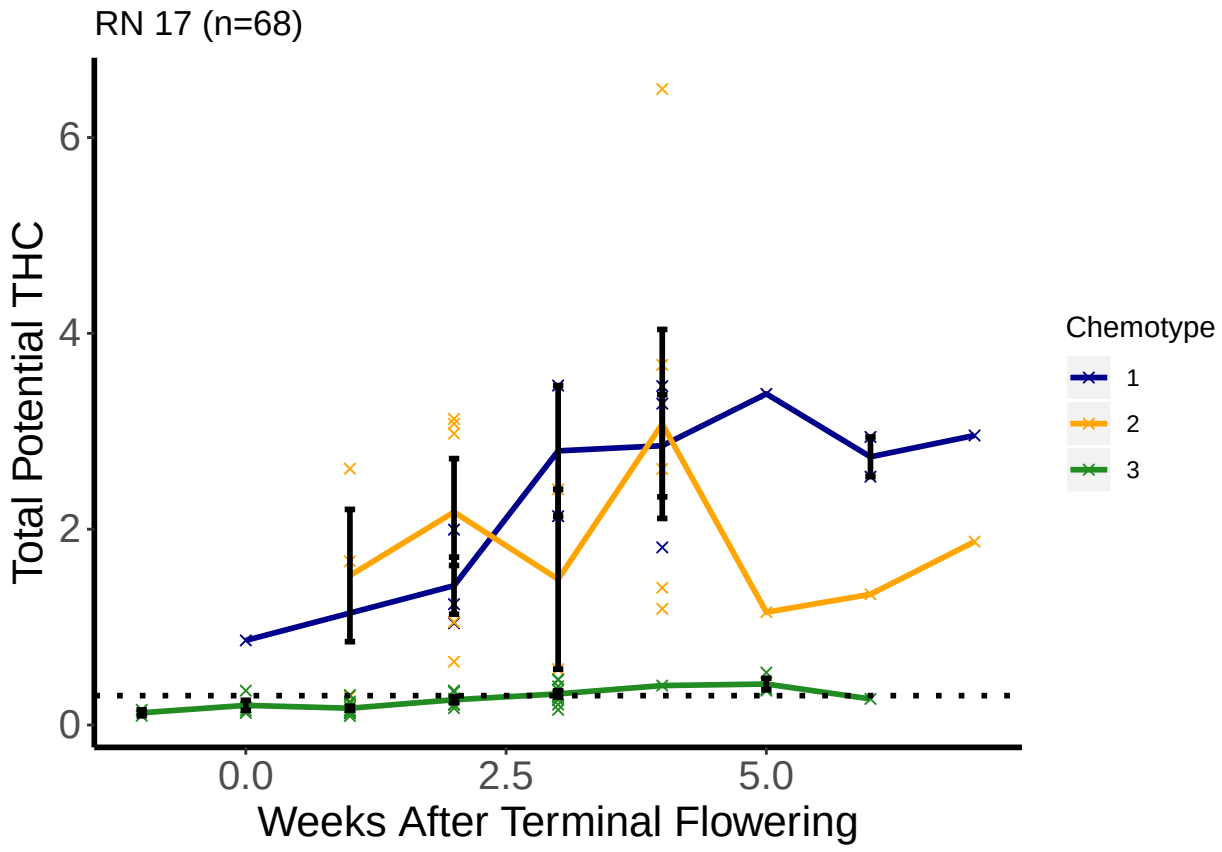


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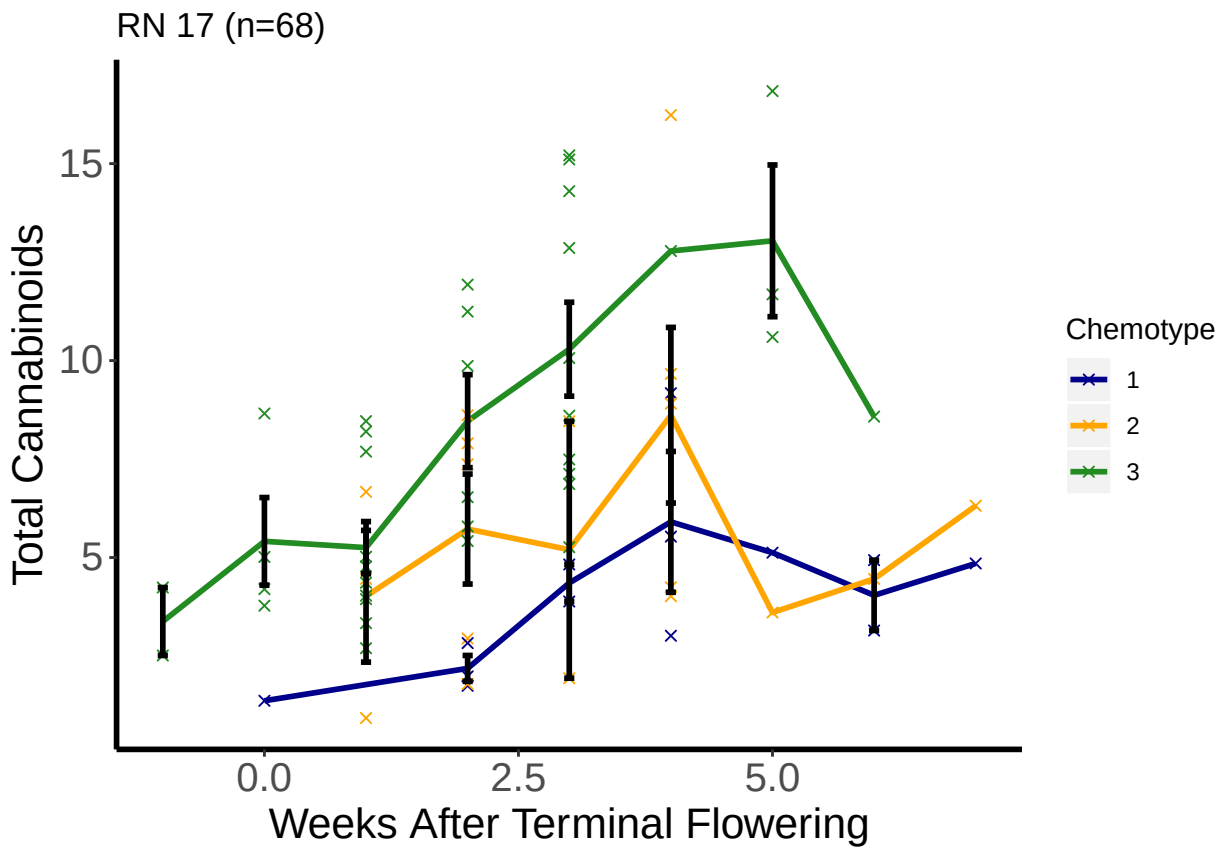


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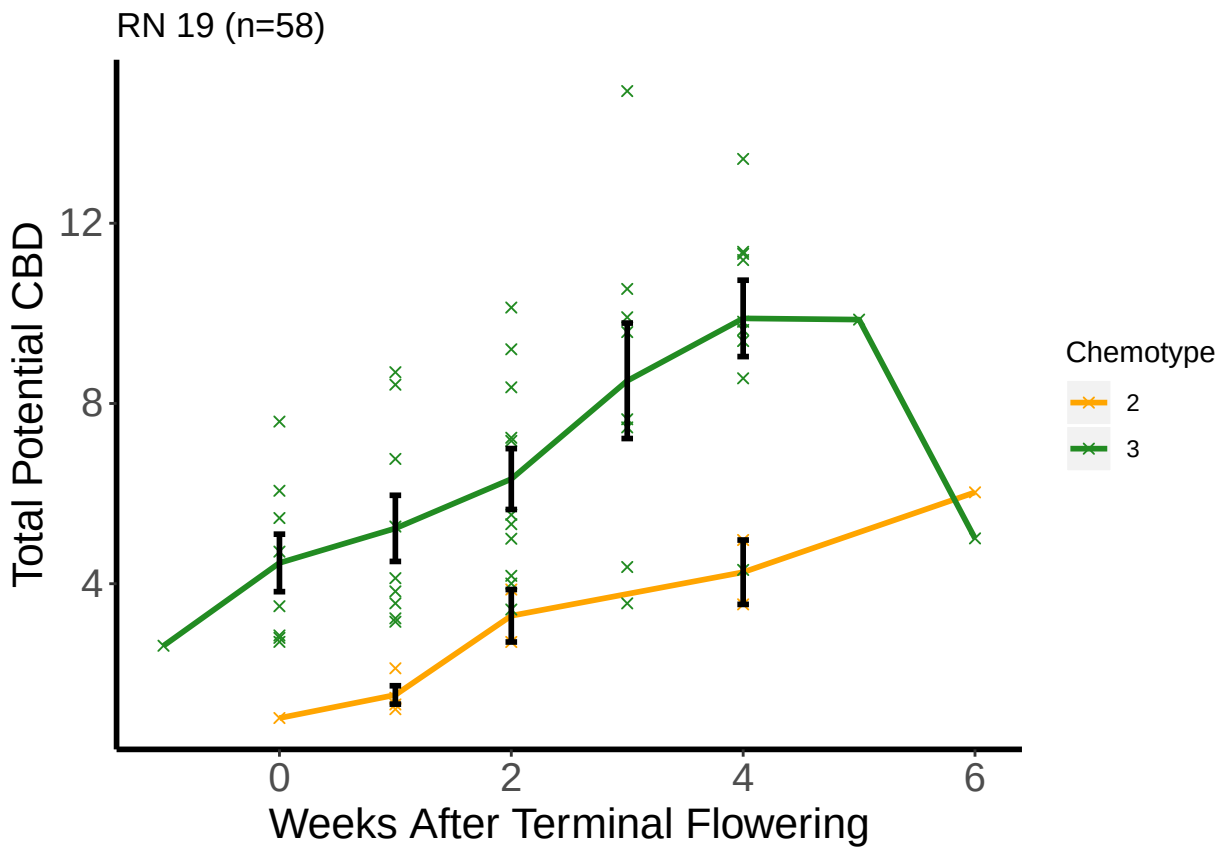


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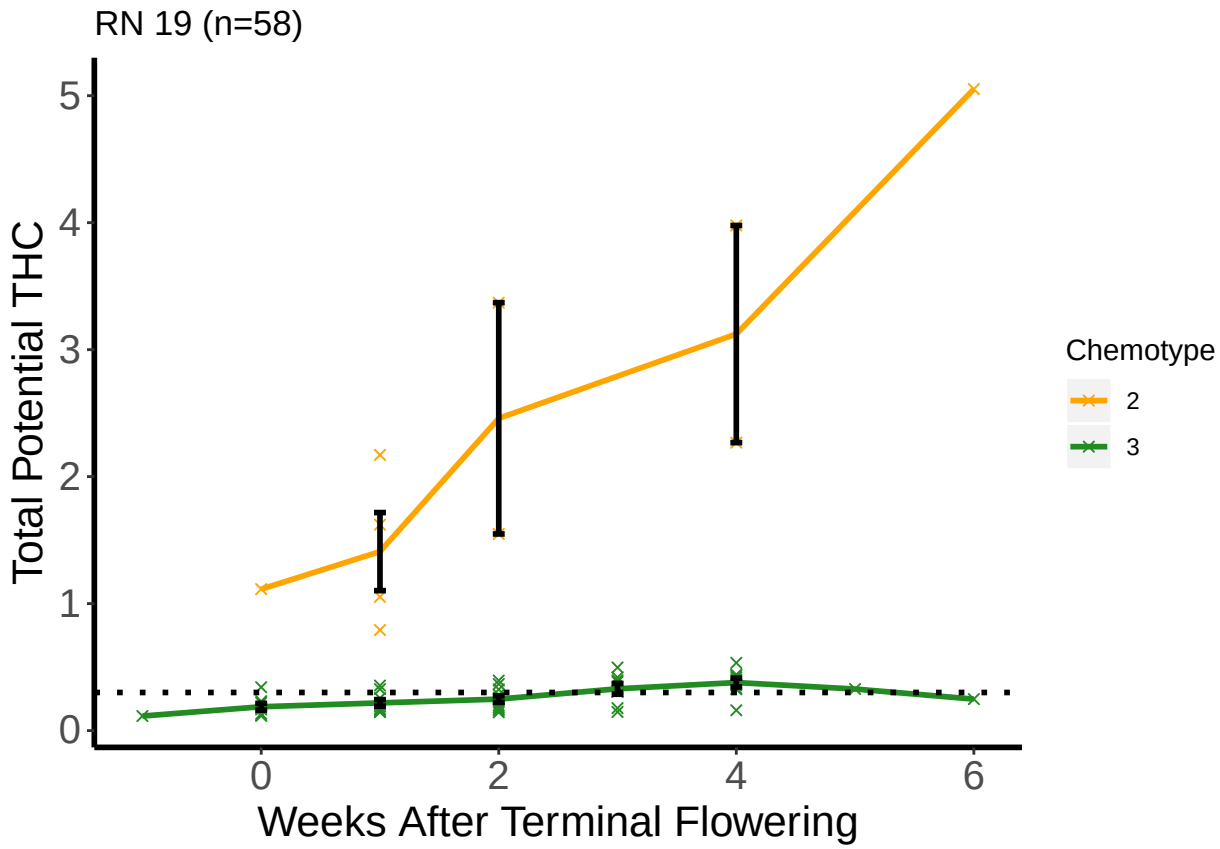


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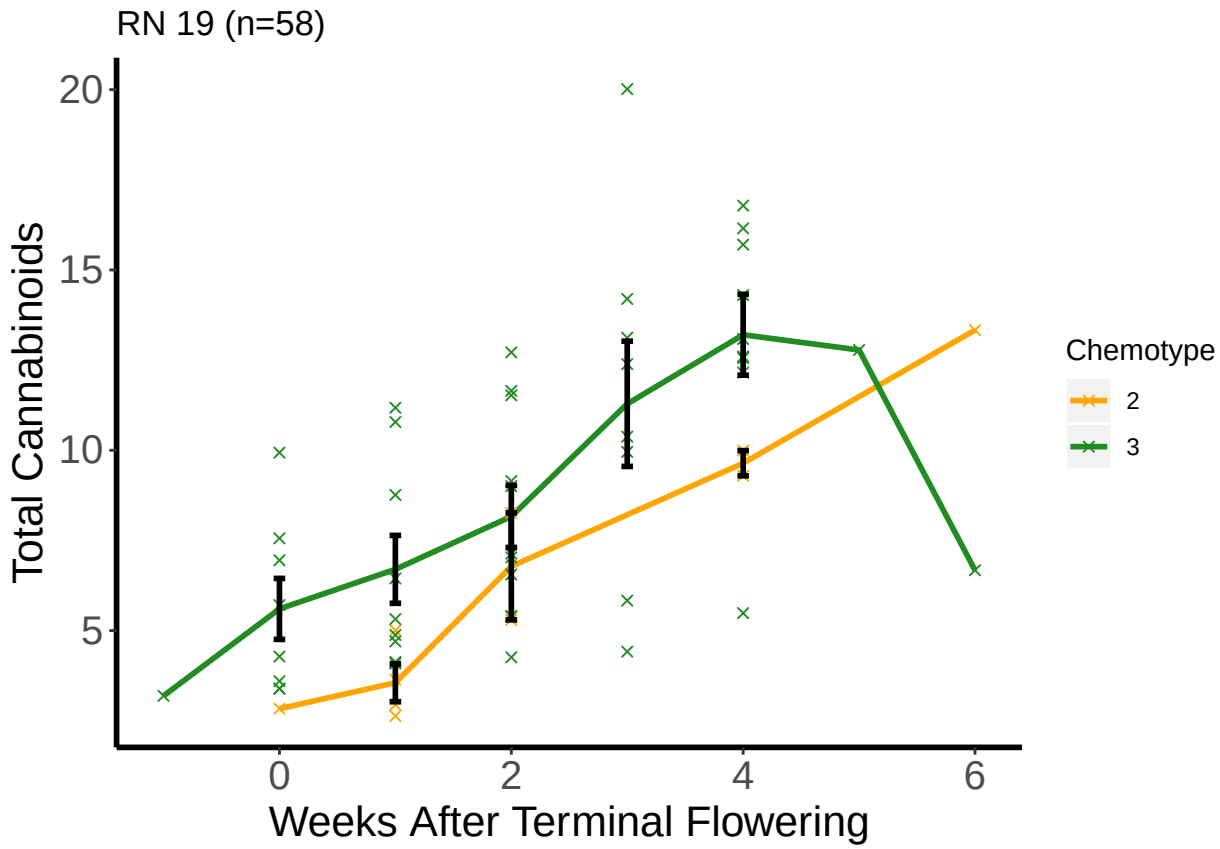


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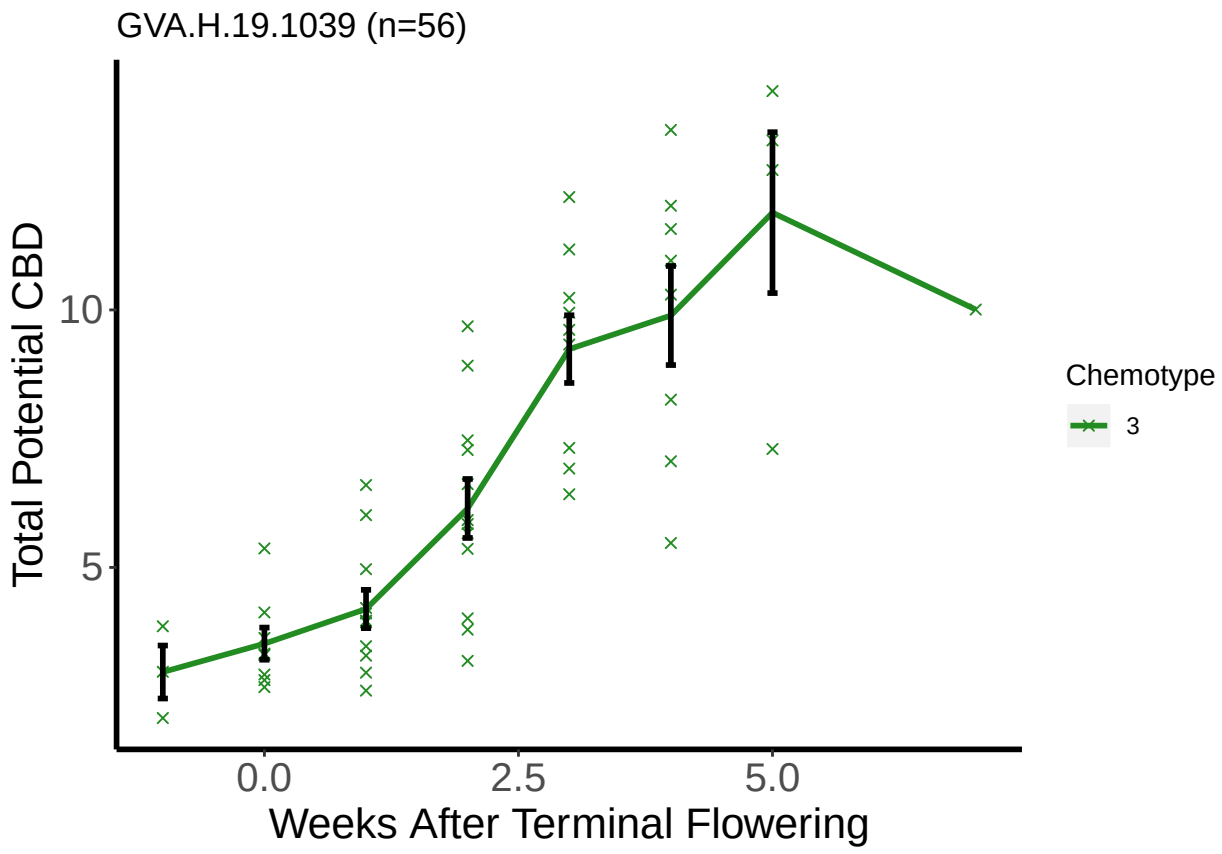


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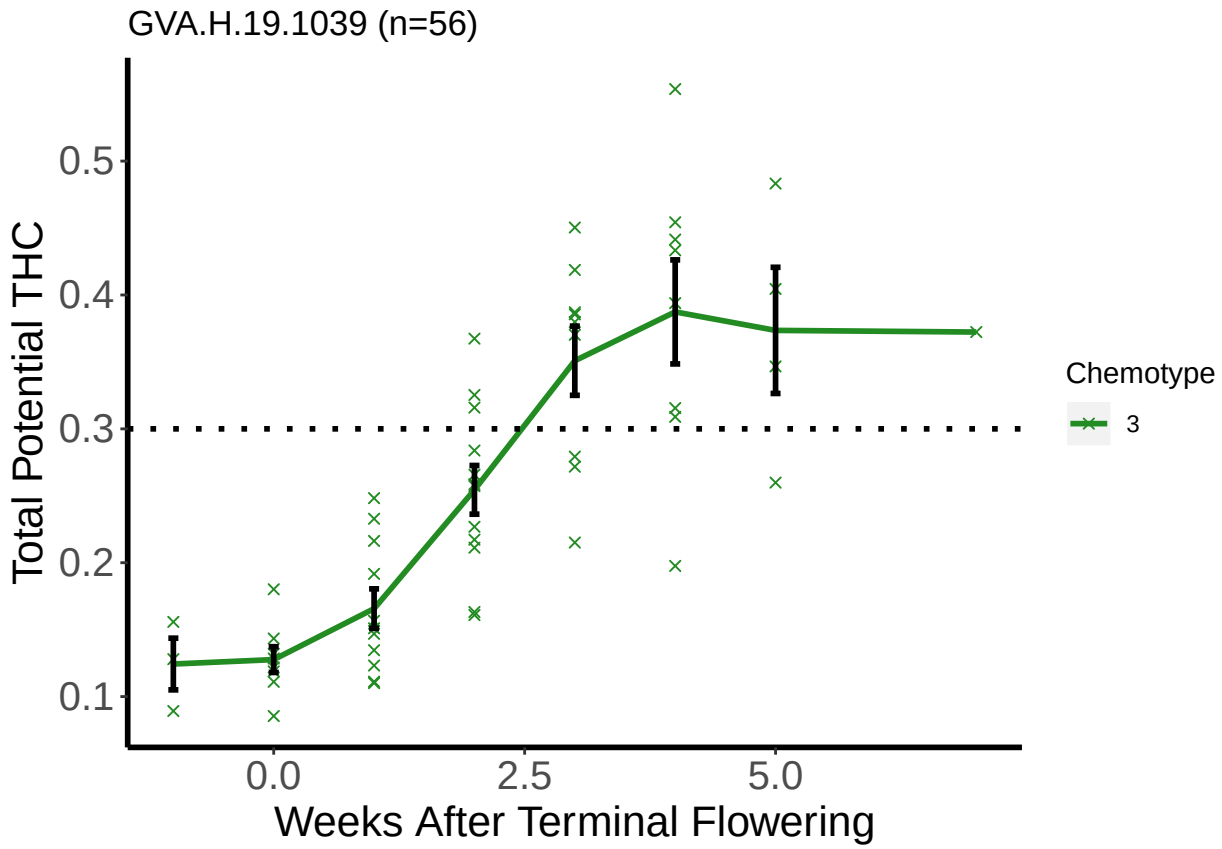


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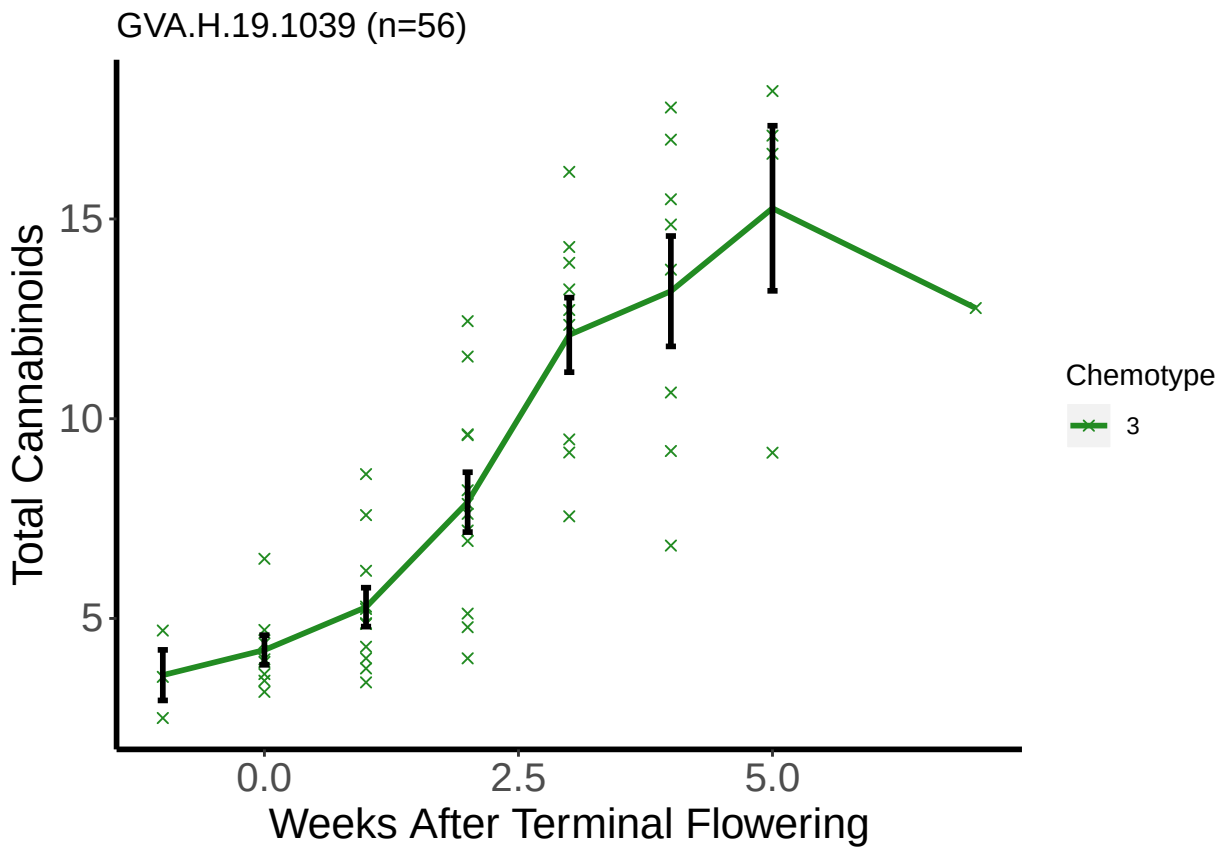


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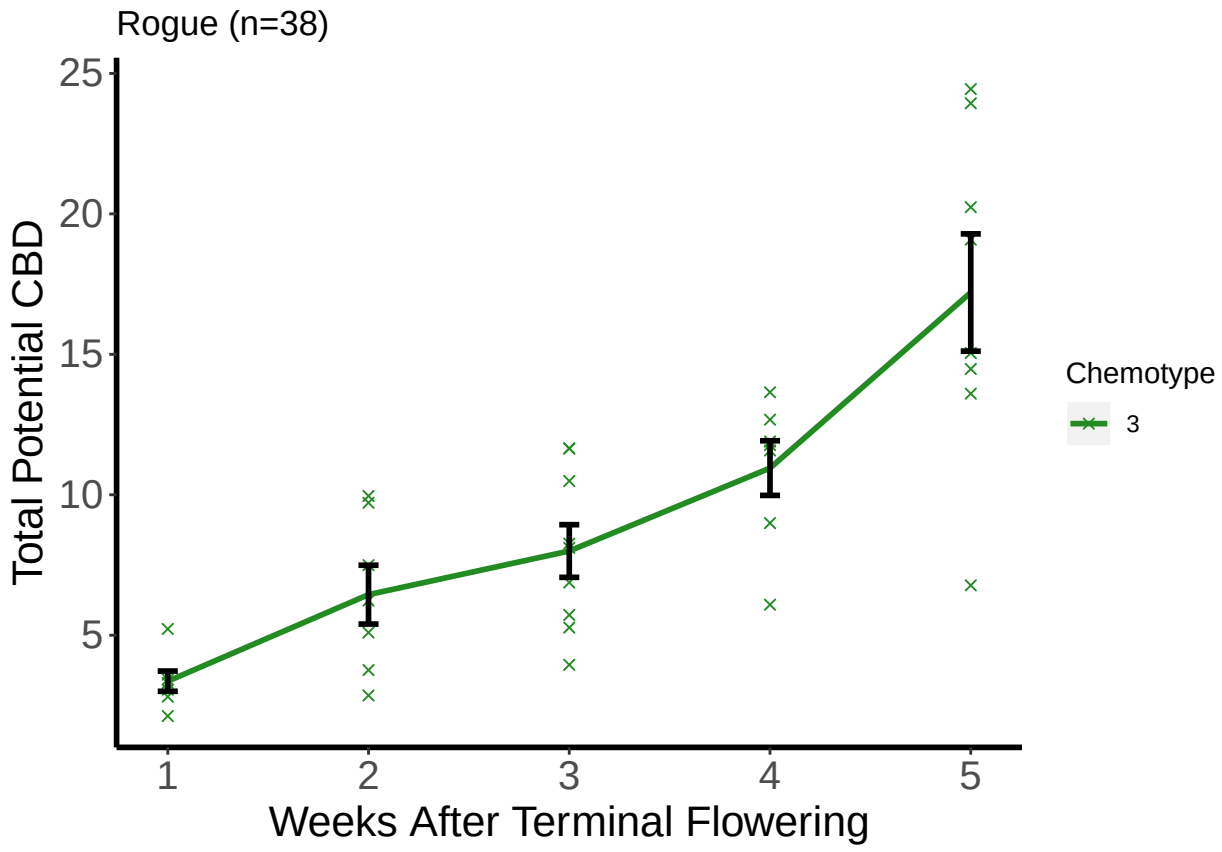


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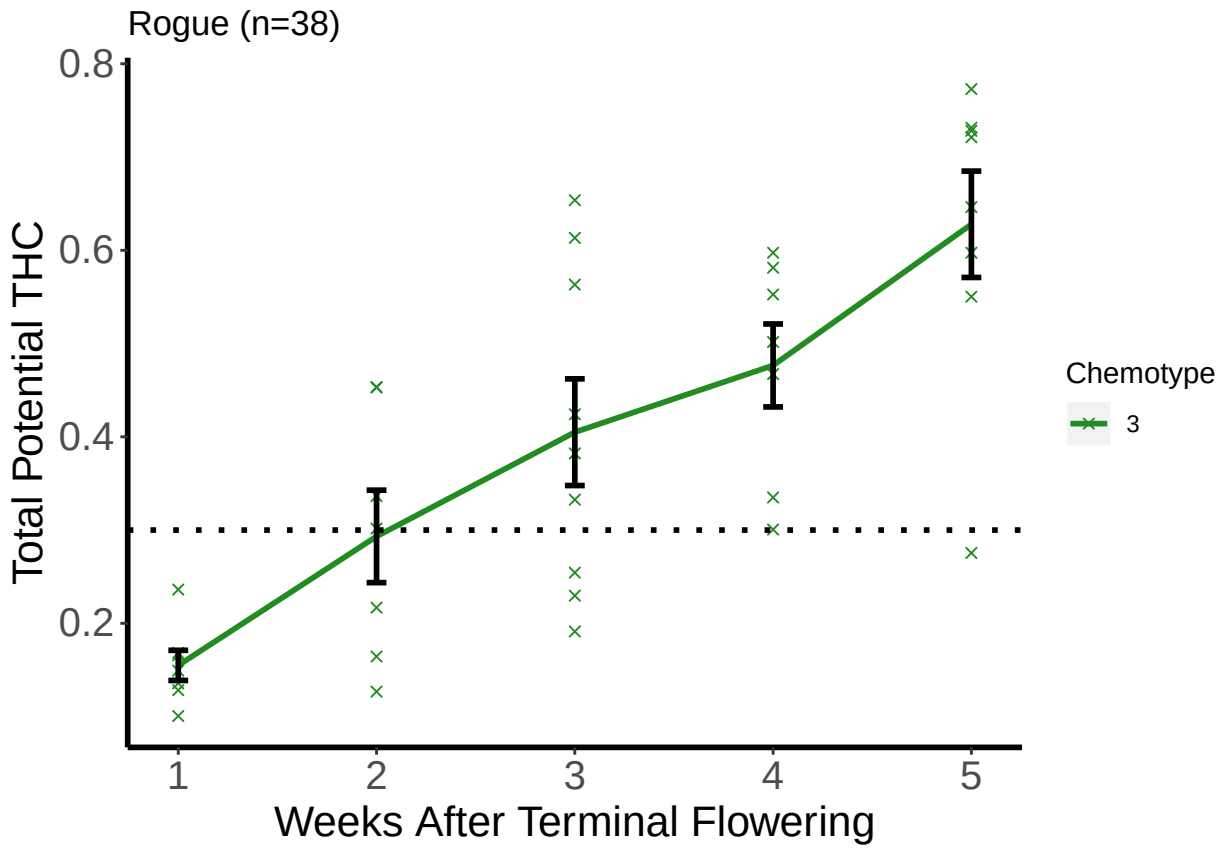


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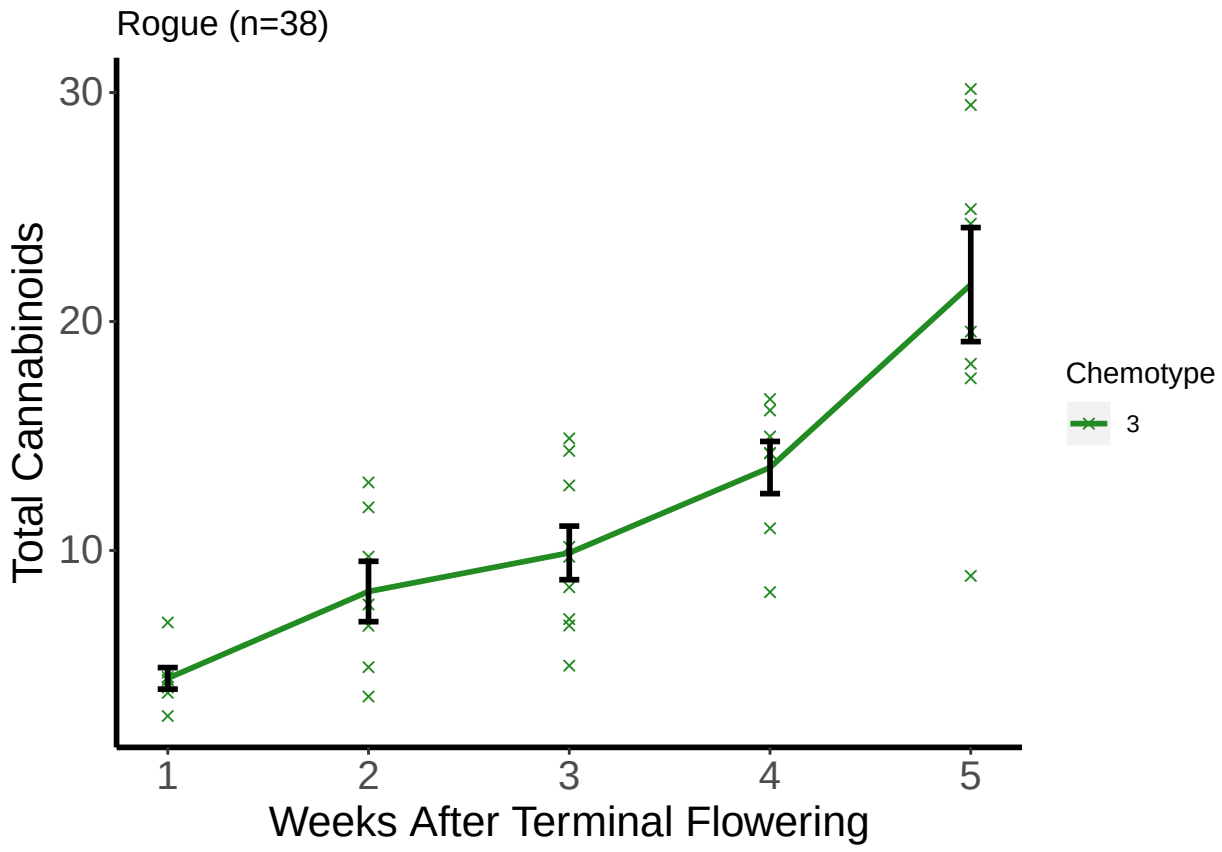


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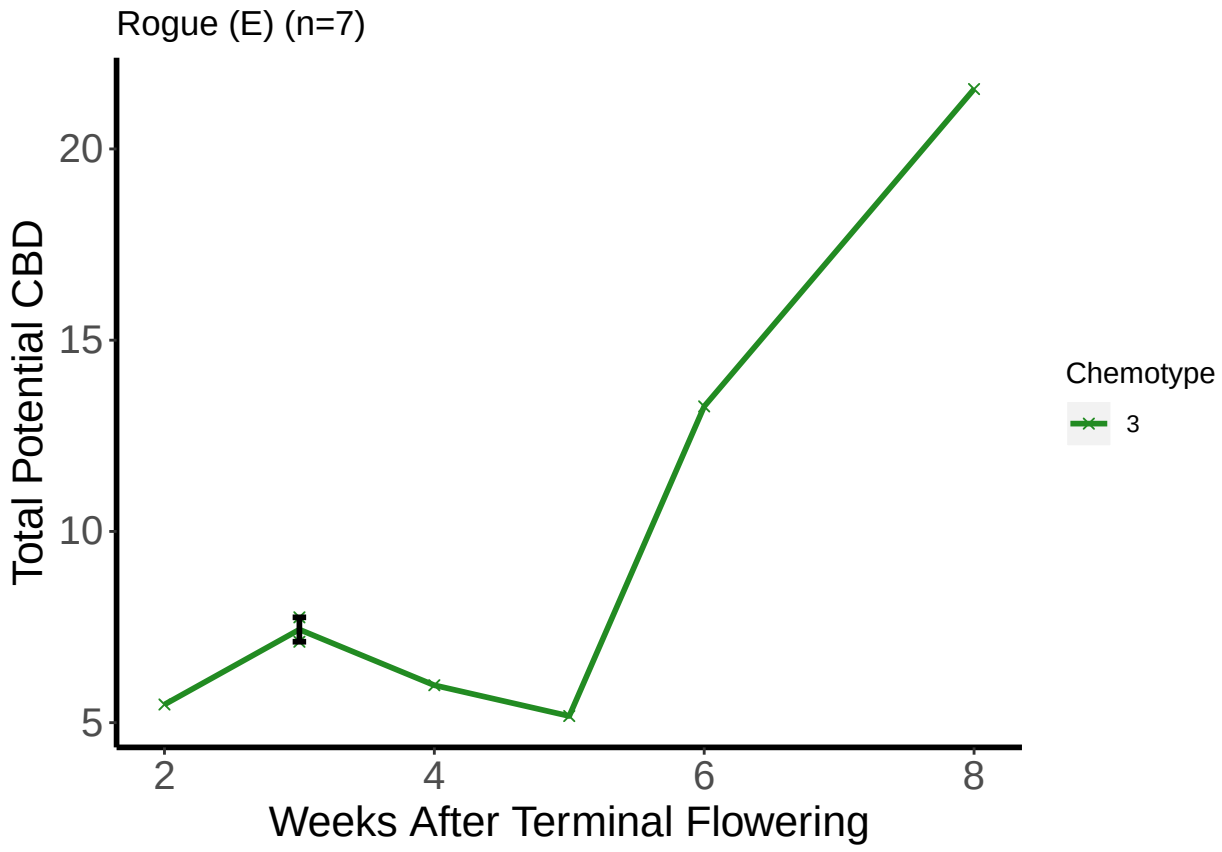


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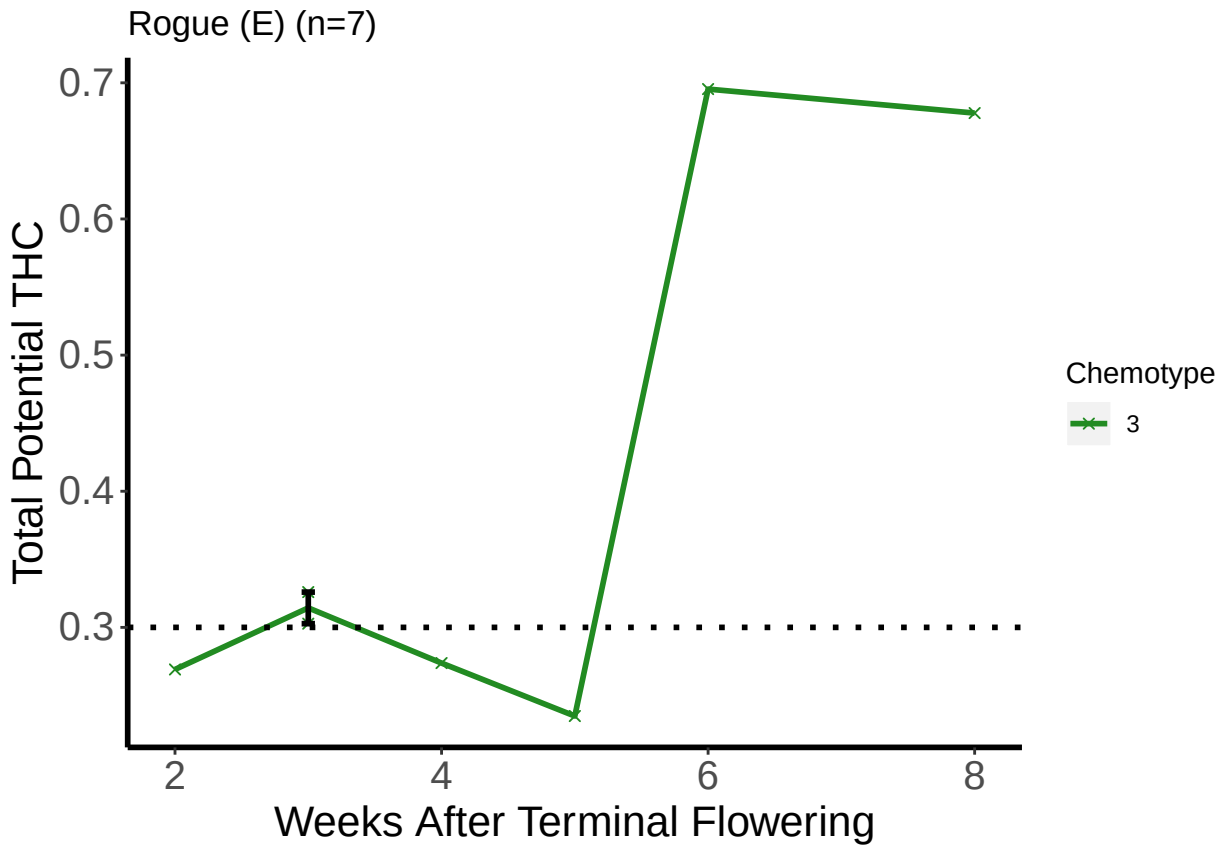


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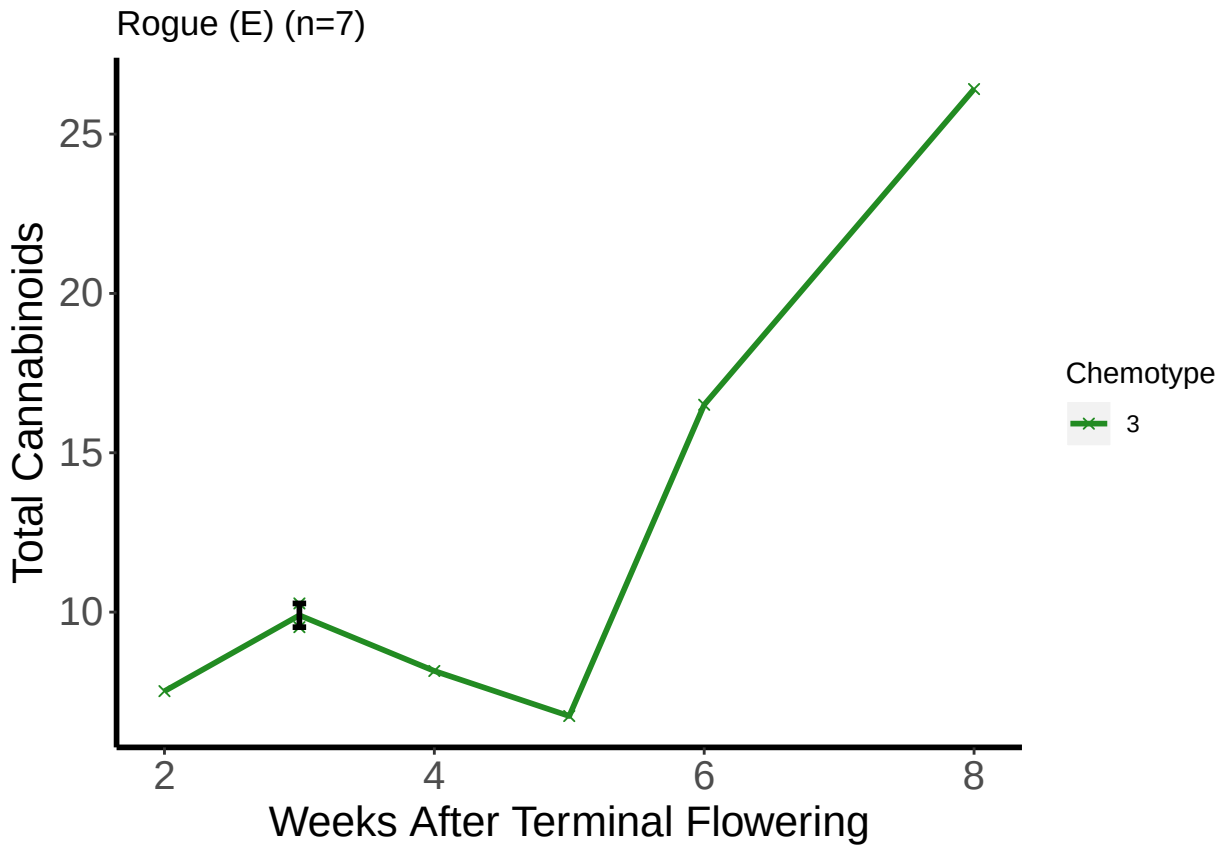


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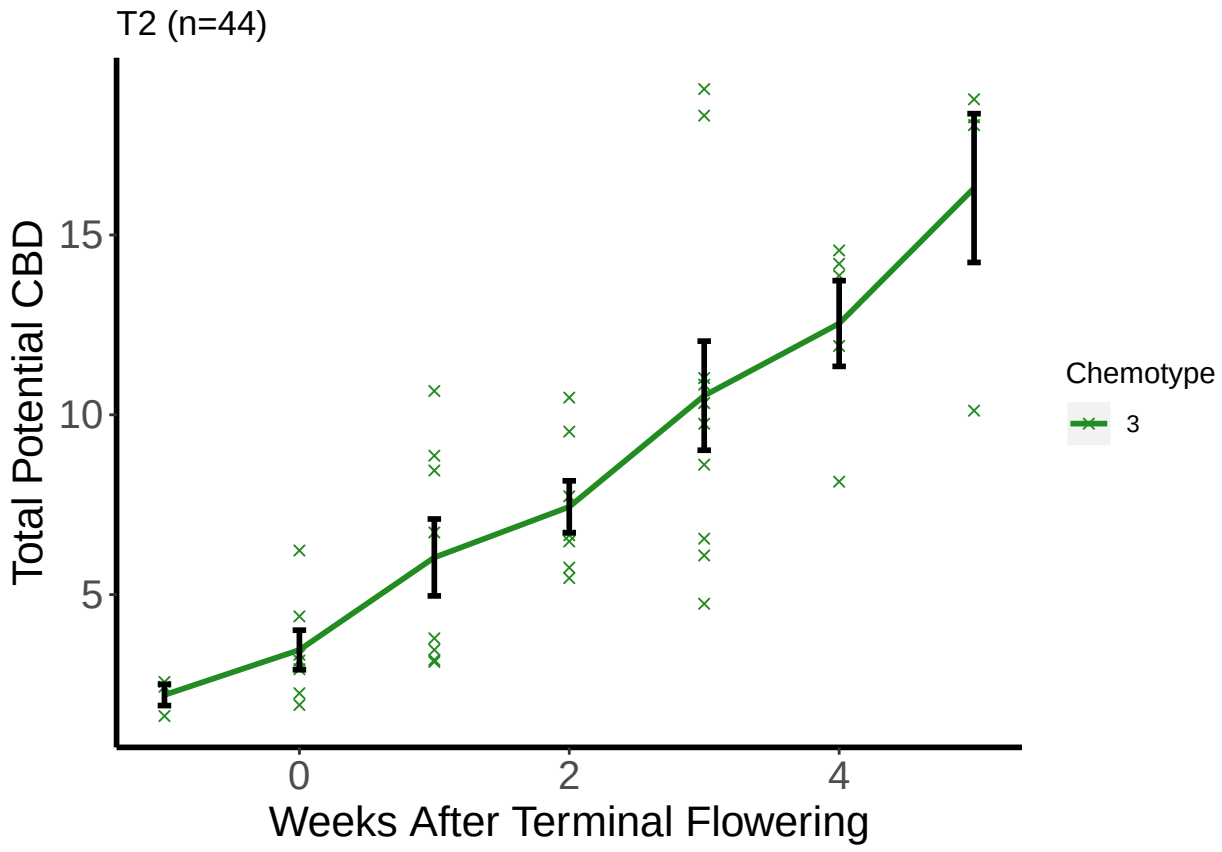


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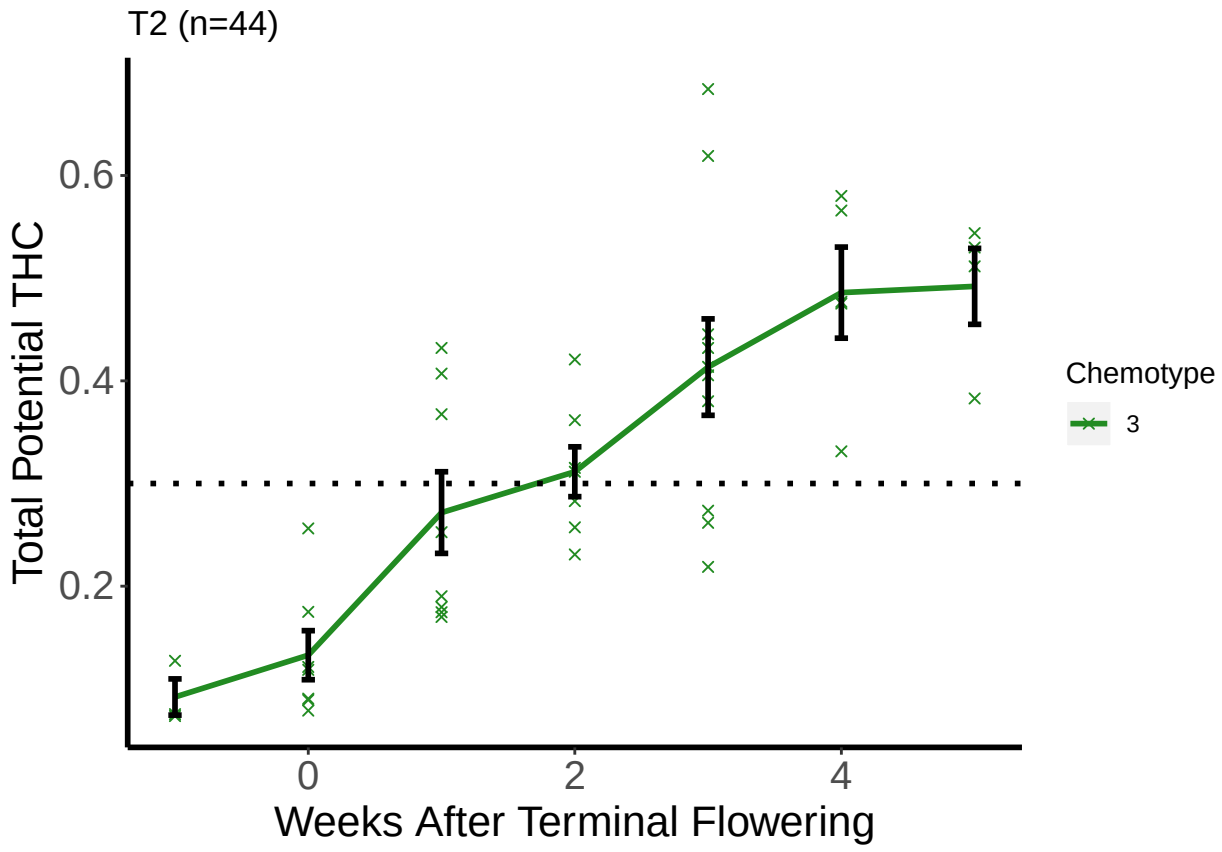


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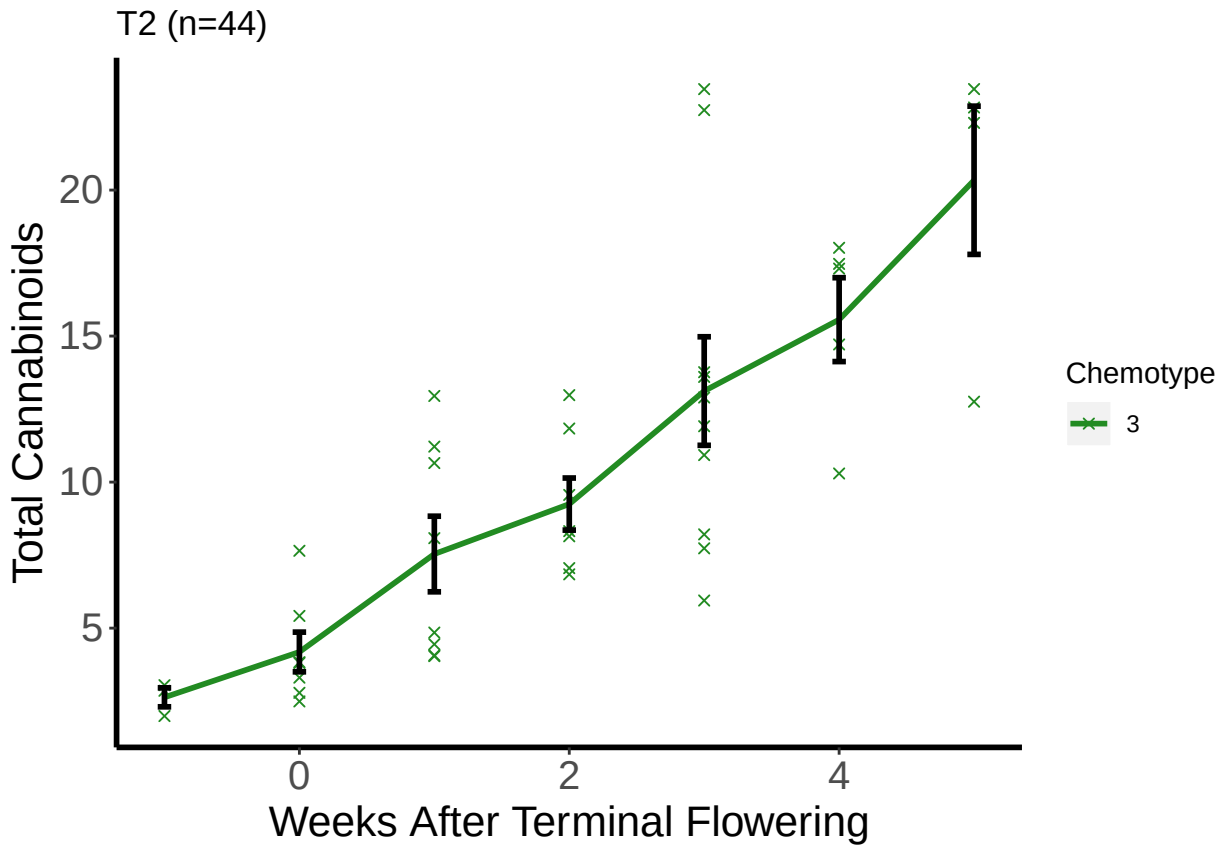


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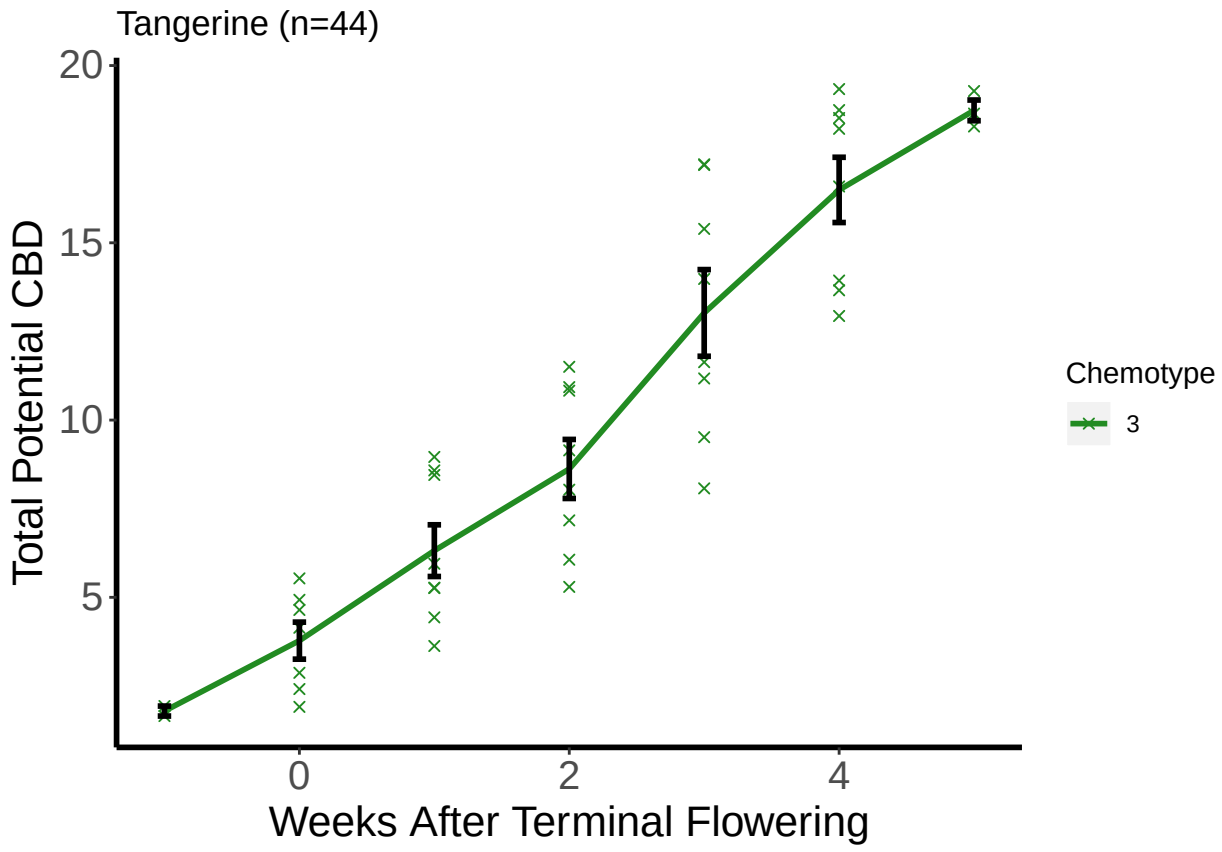


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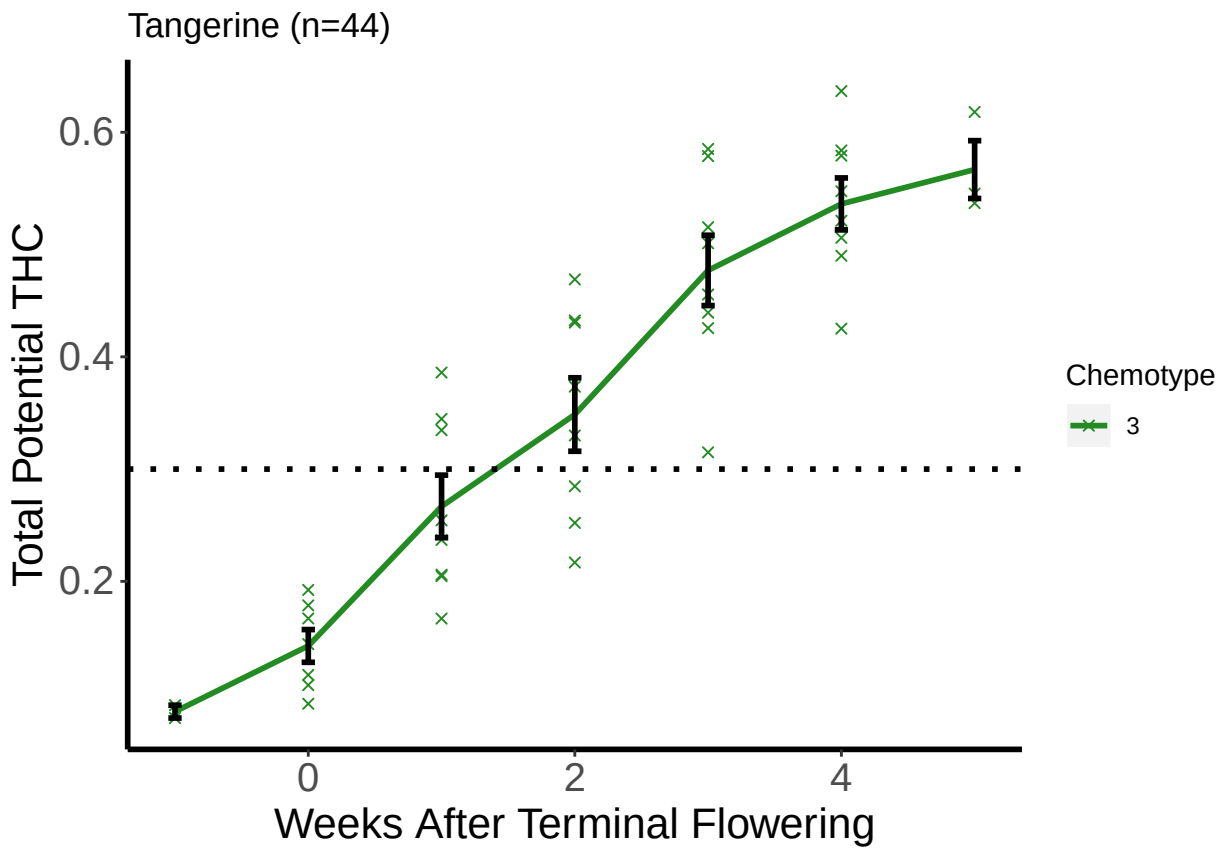


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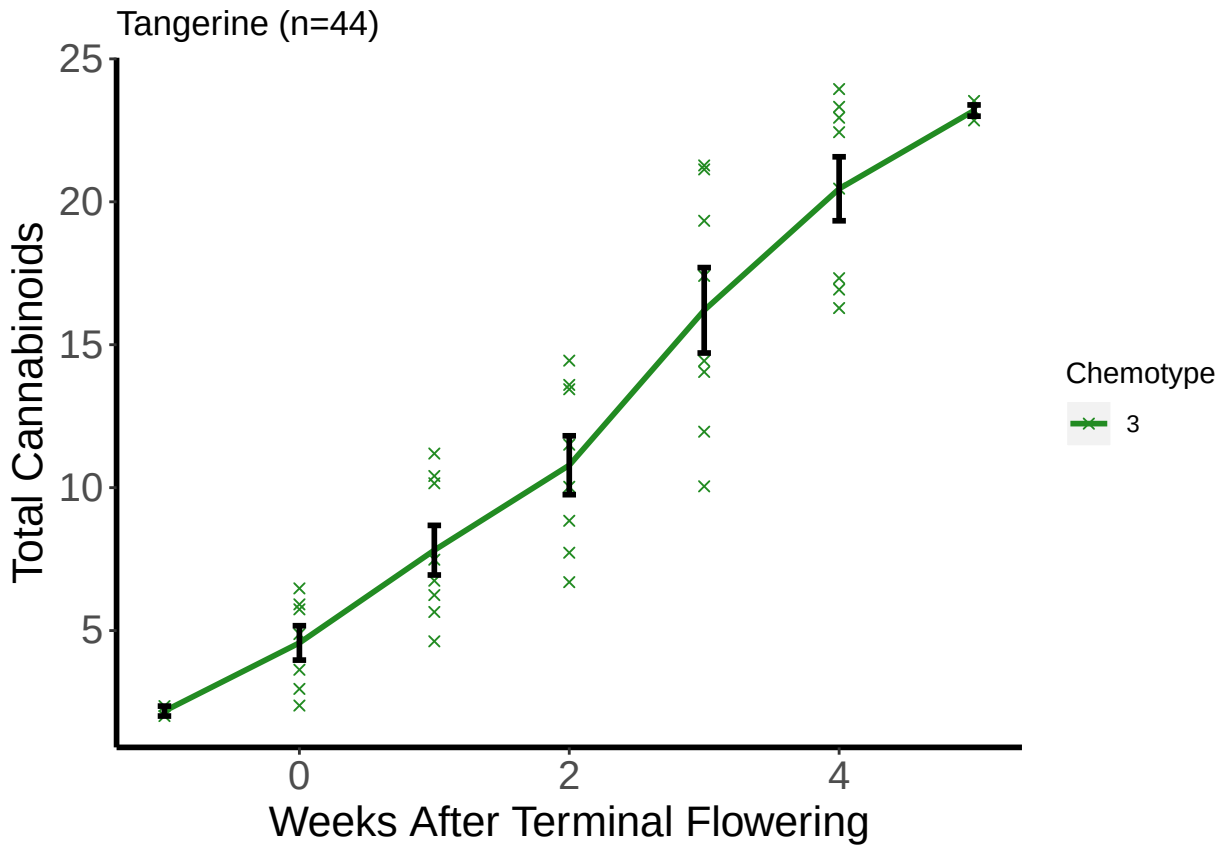


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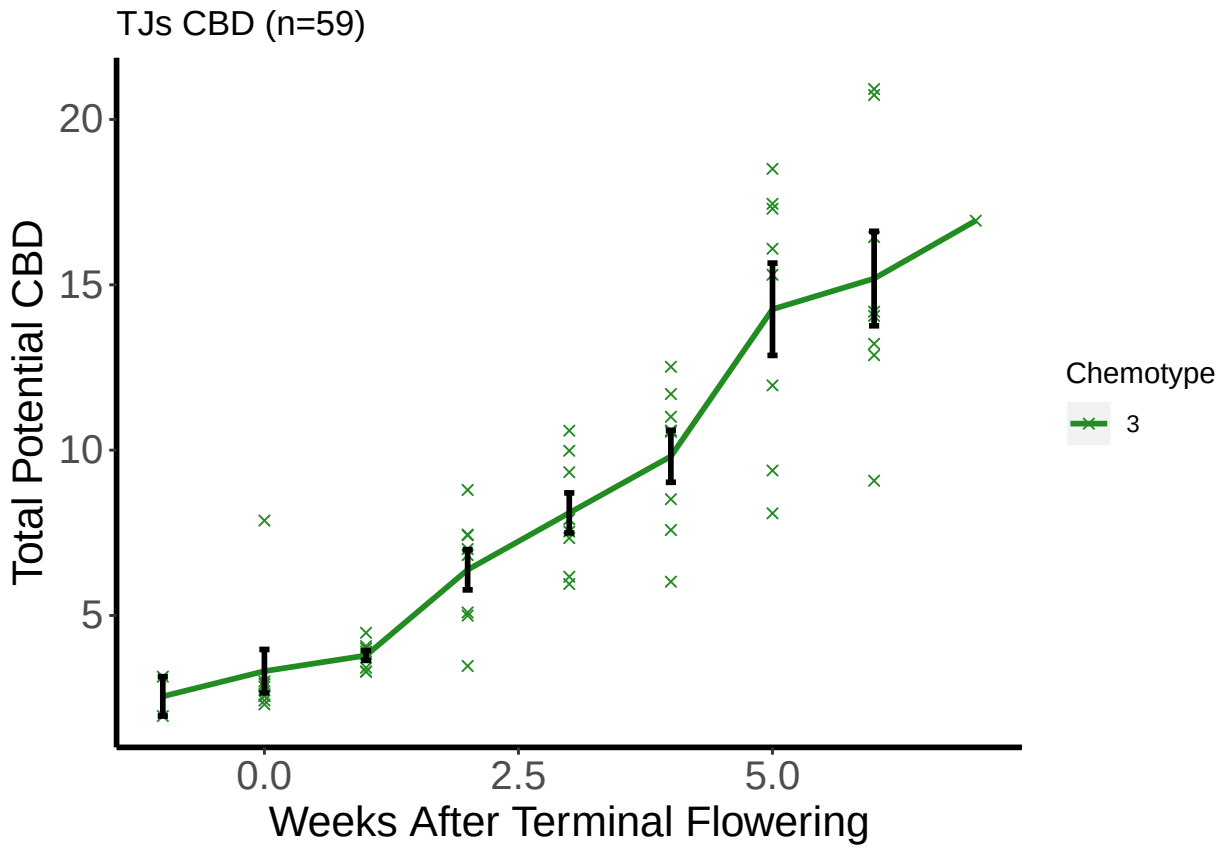


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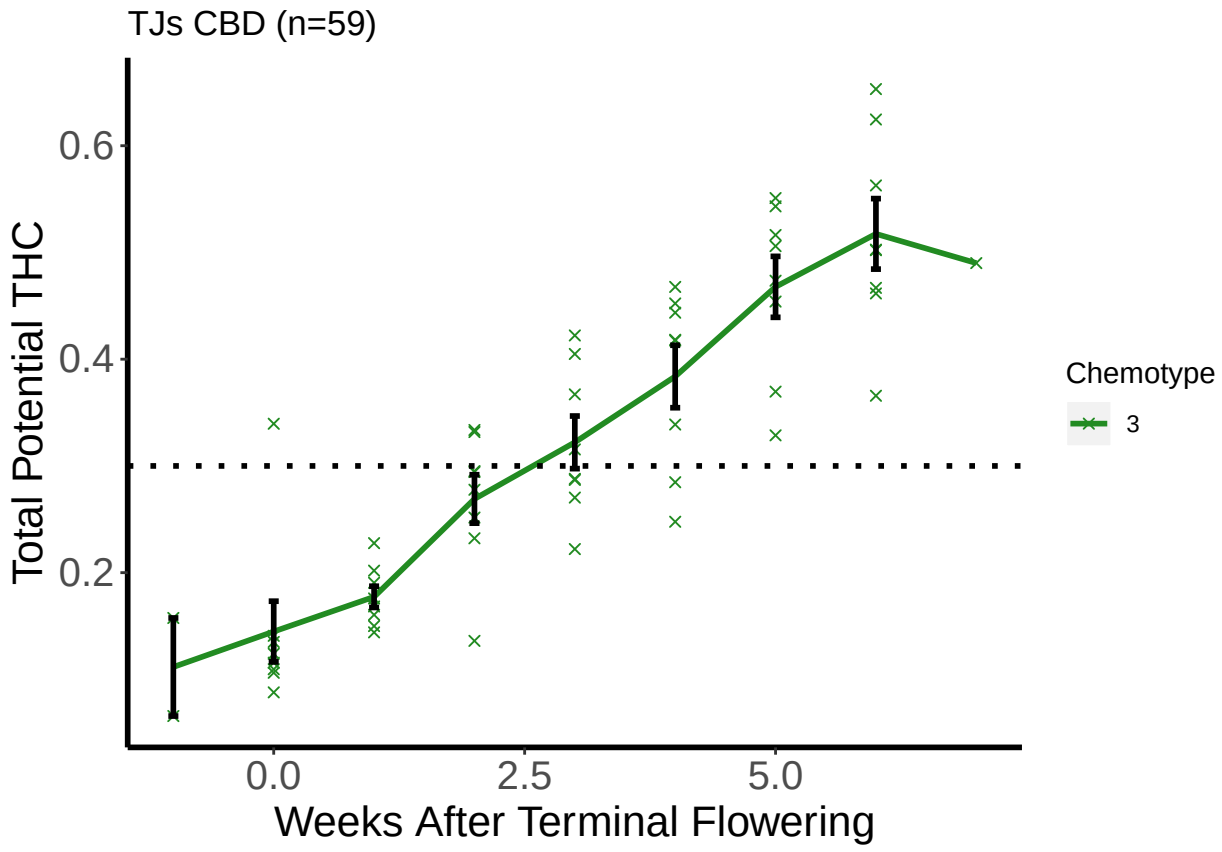


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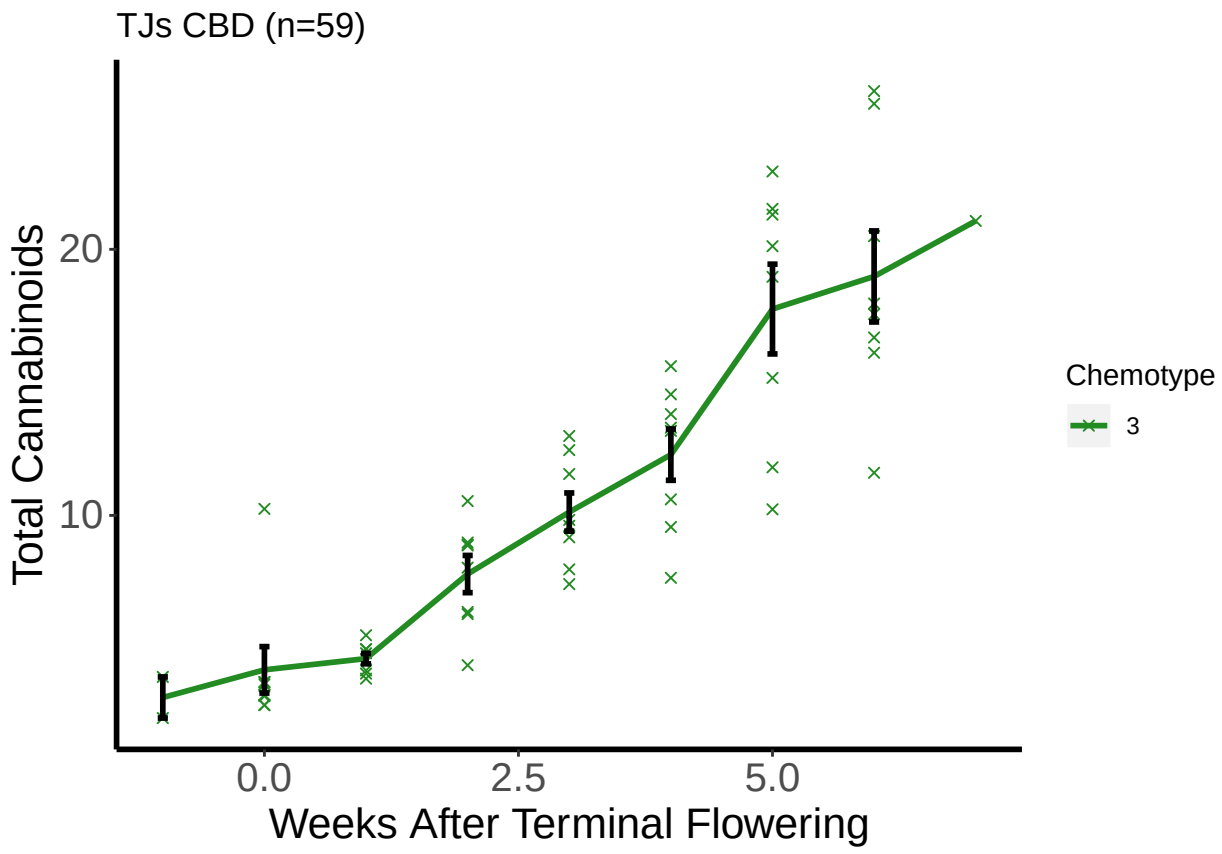


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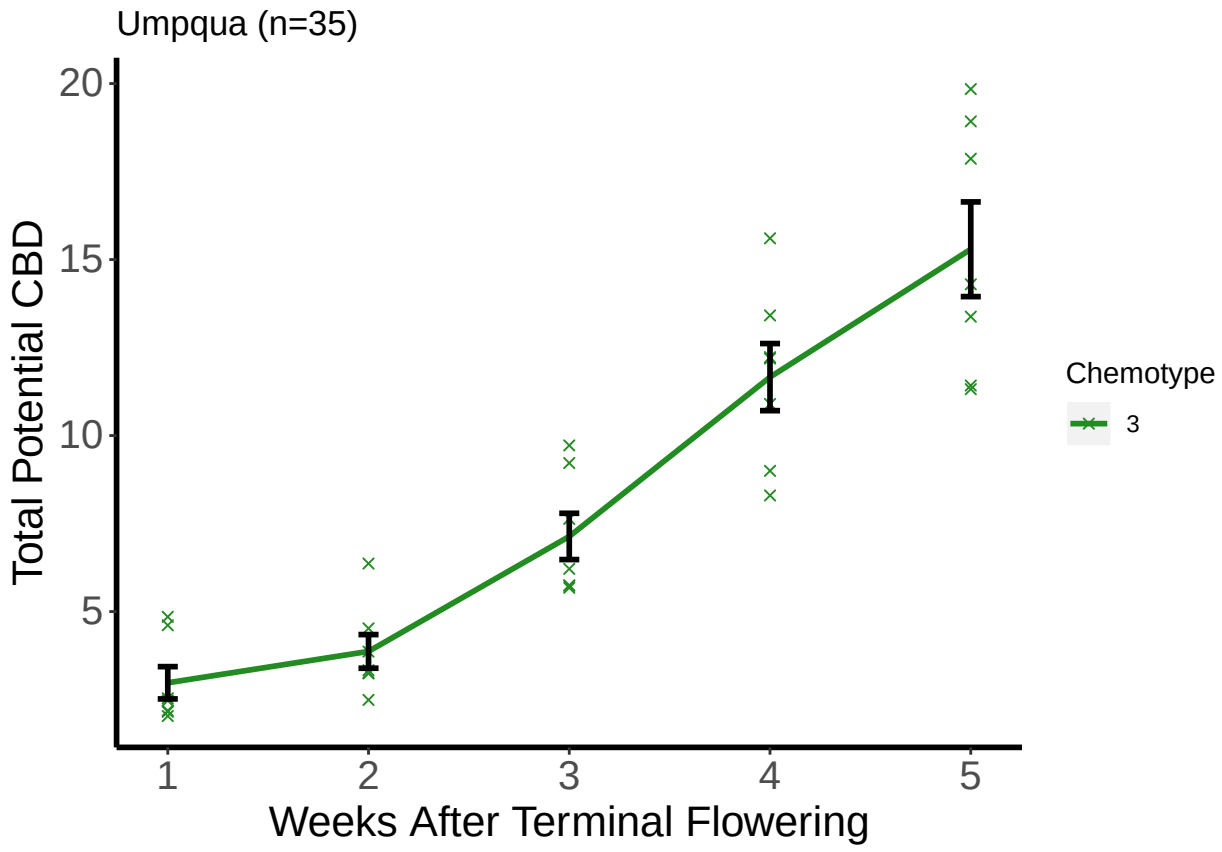


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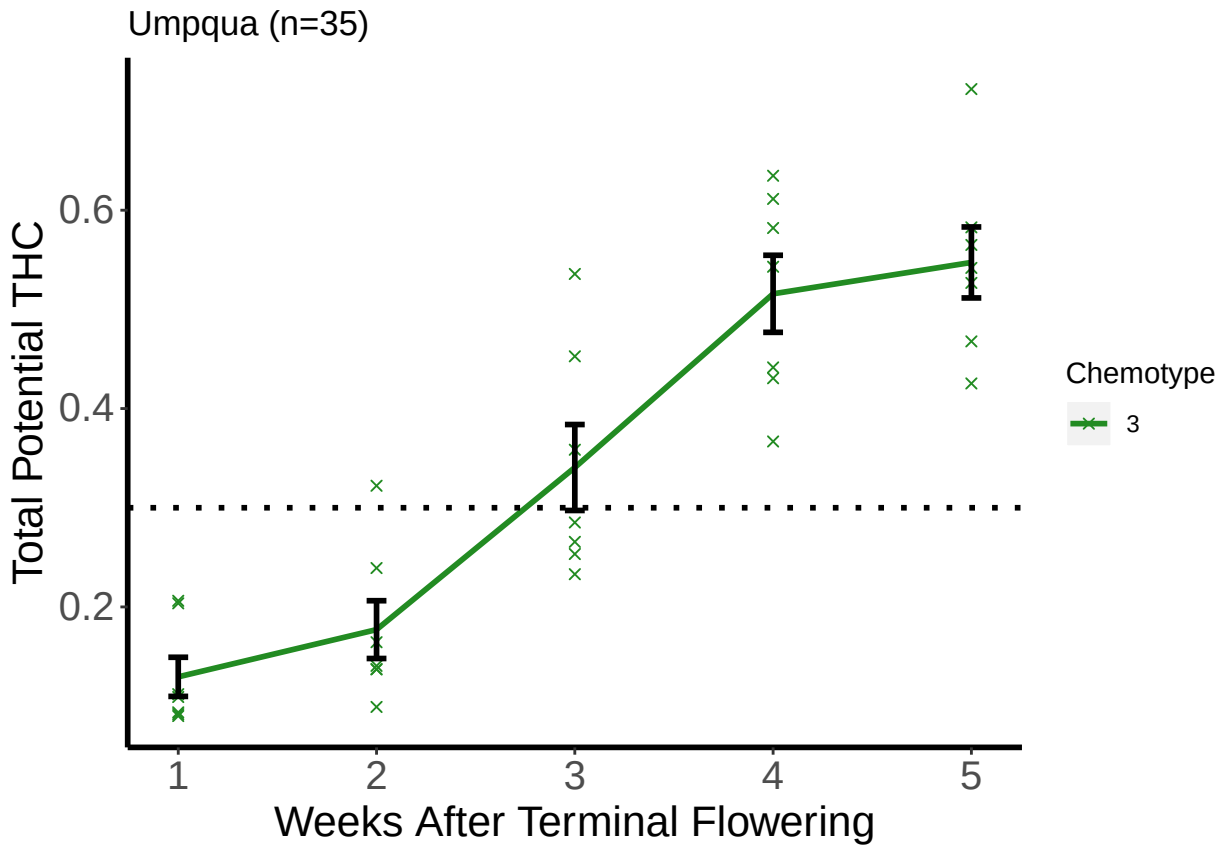


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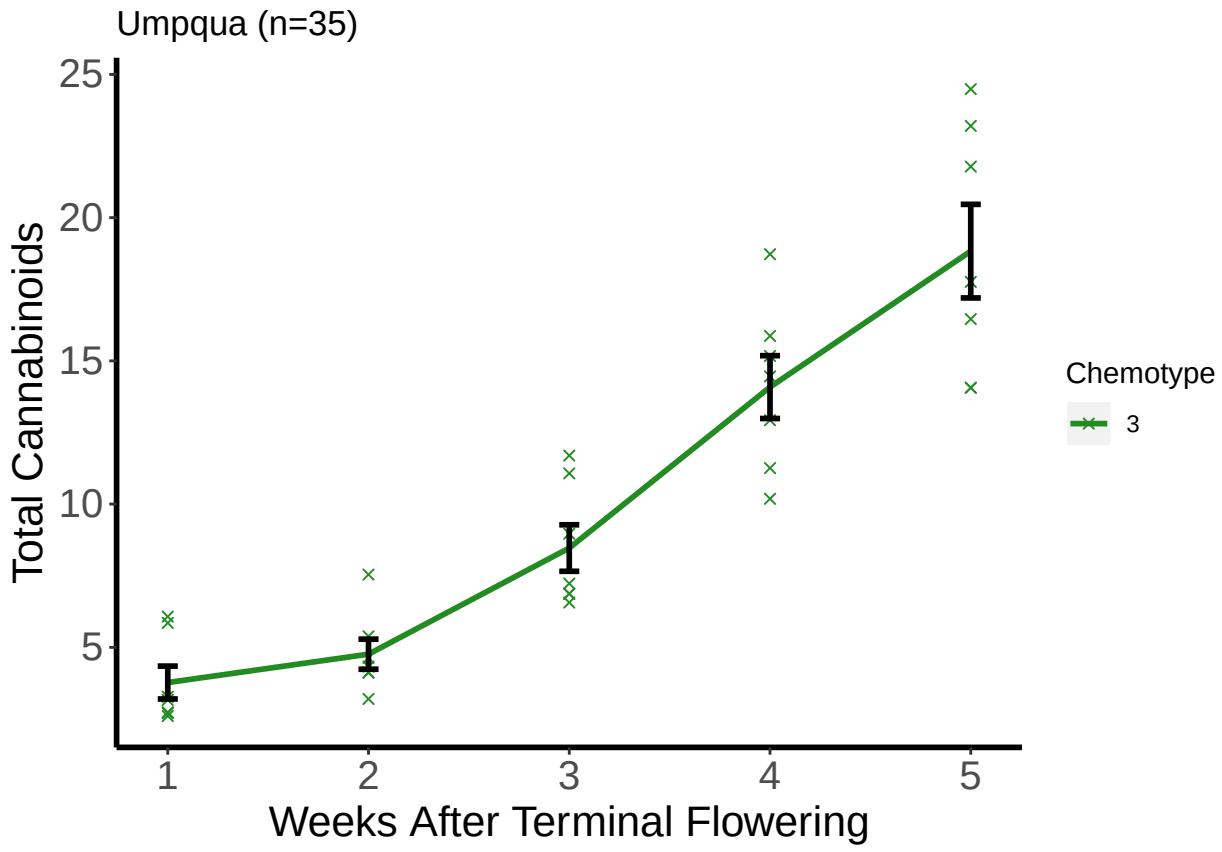


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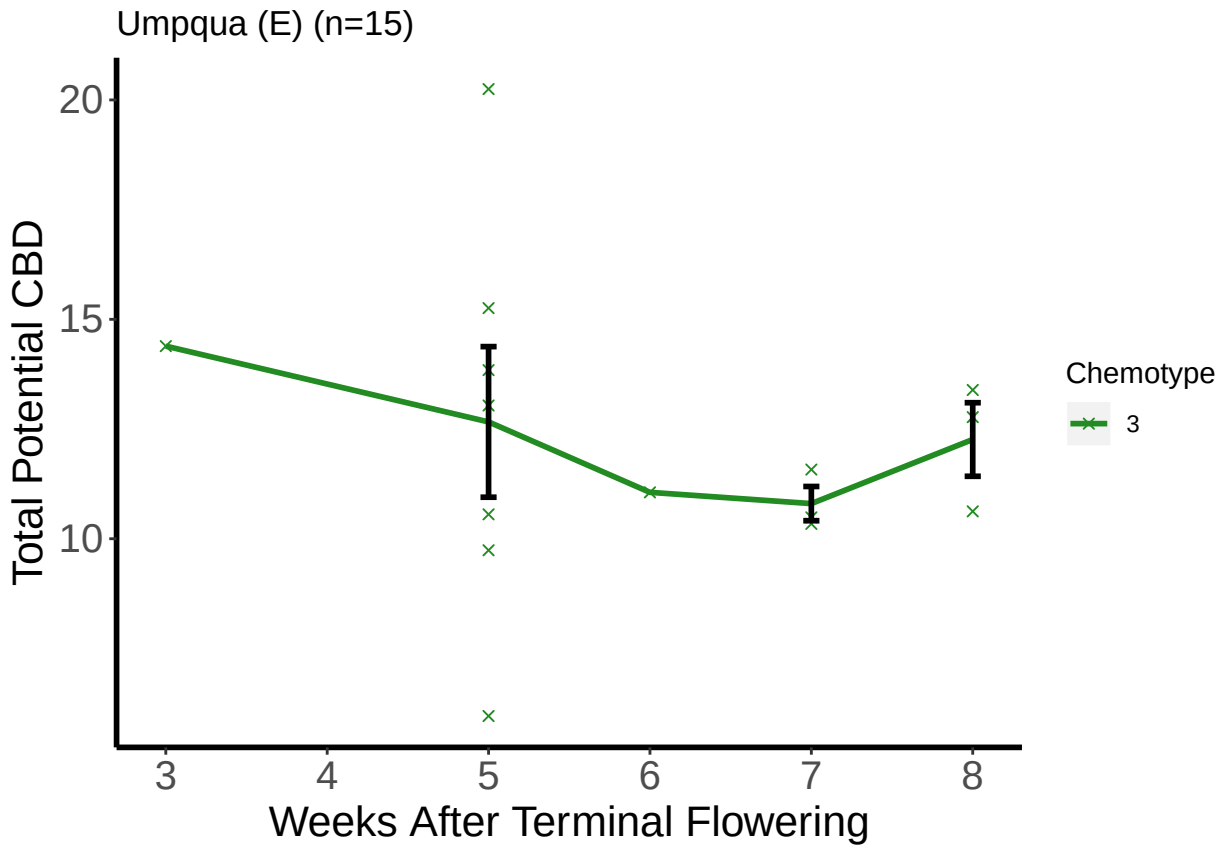


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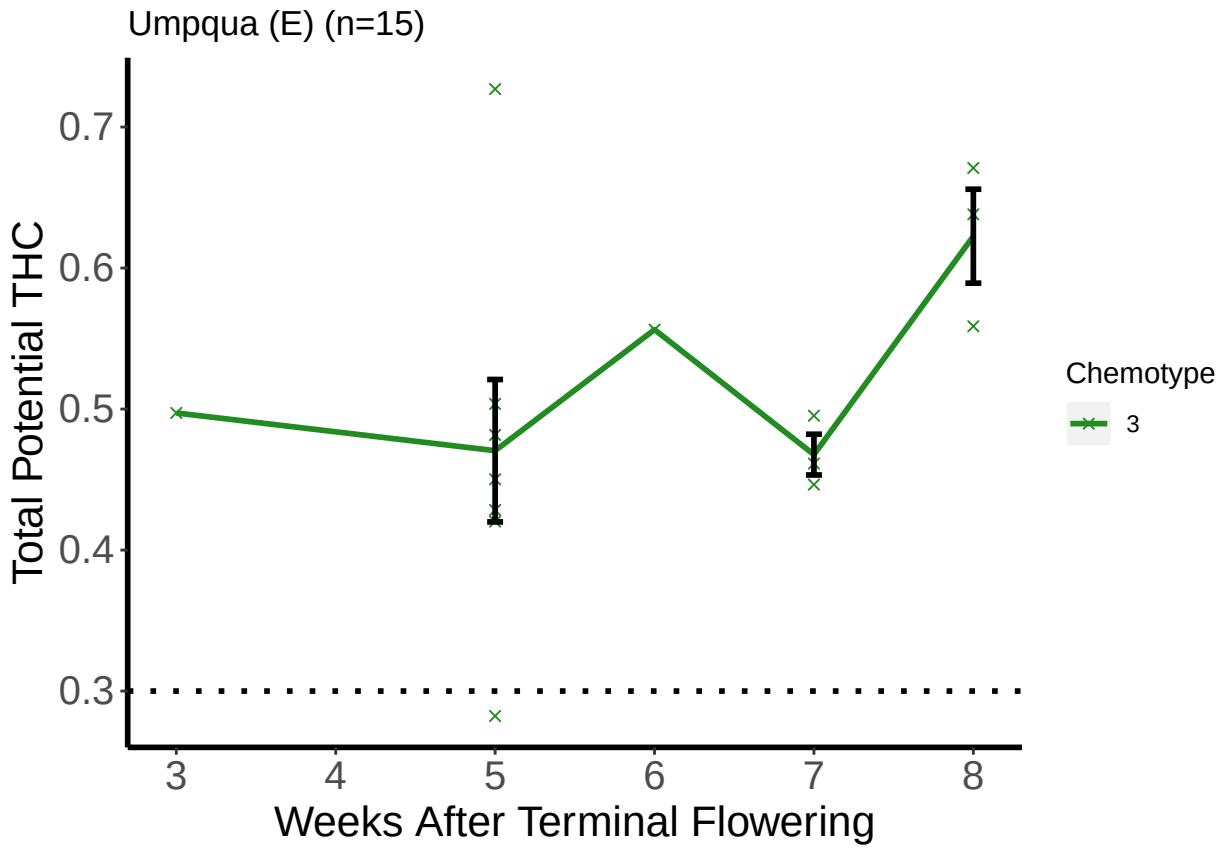


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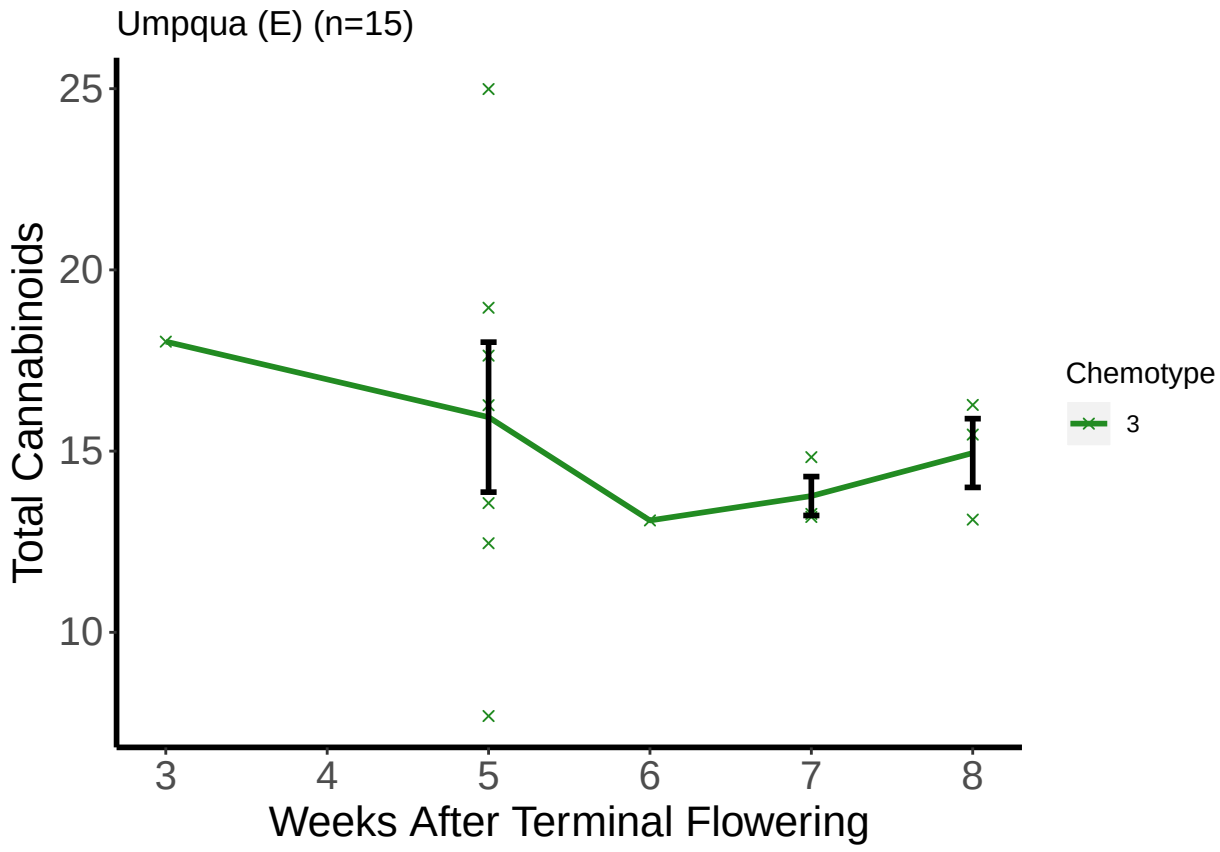
Umpqua (E) (n=15)
Total Cannabinoids
25
20
15
10
3
4
5
6
7
8
Weeks After Terminal Flowering
Chemotype
3