Minmum module size & cut height

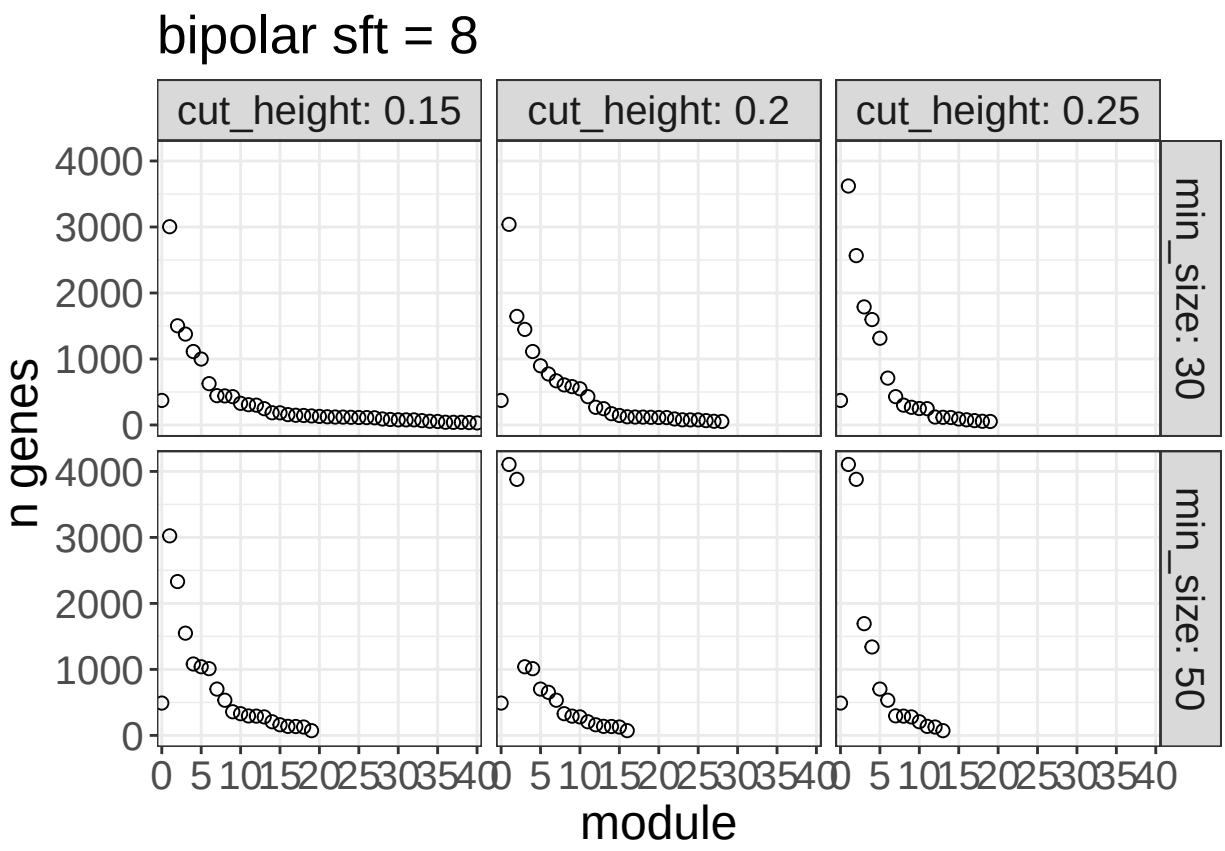
Rachel Smith

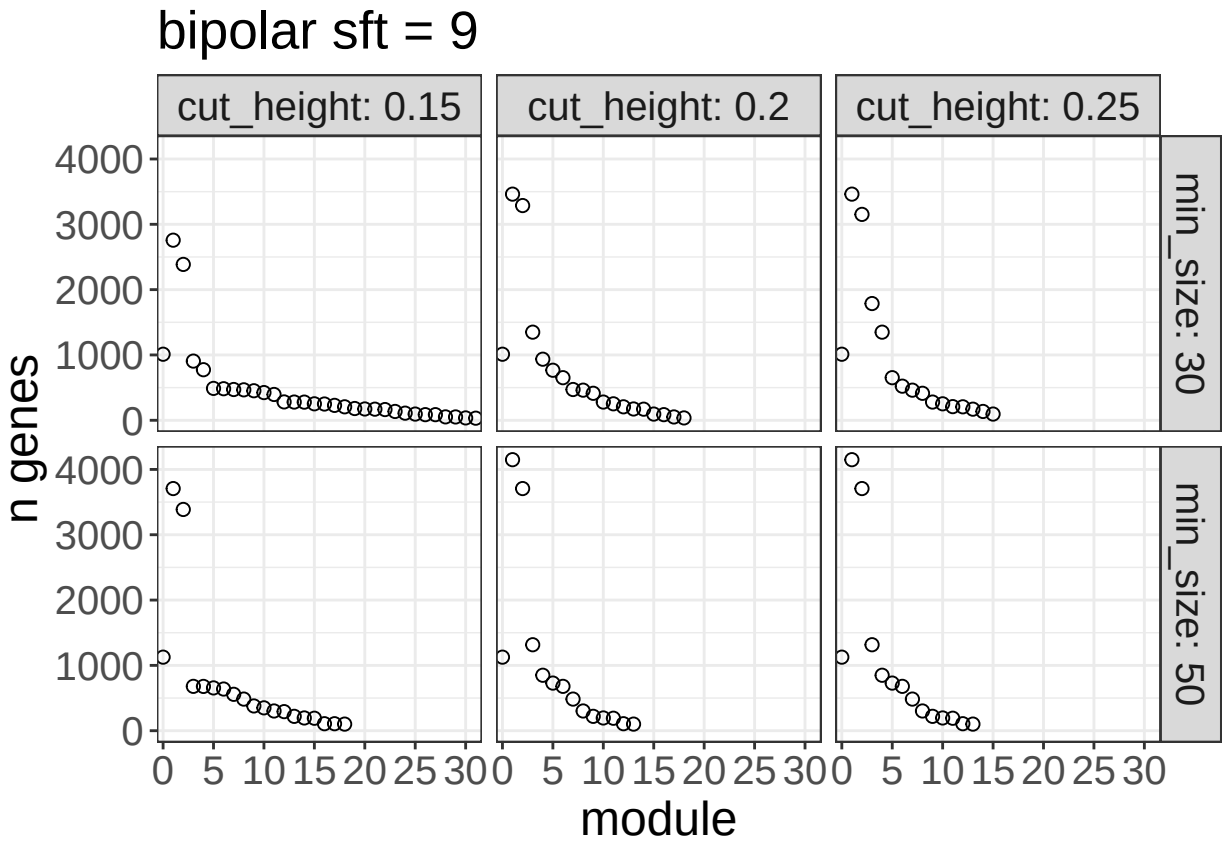
2022-07-01

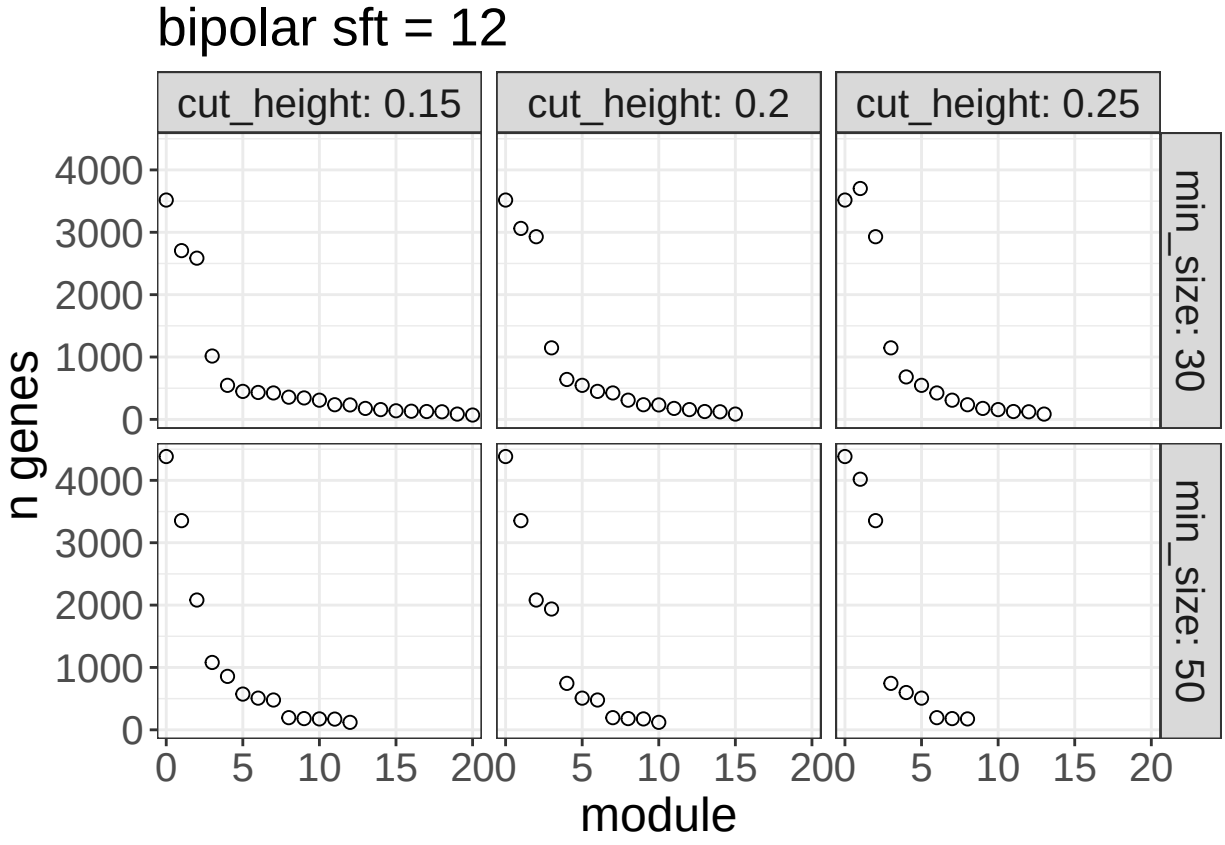
SELECT SFT POWERS HERE

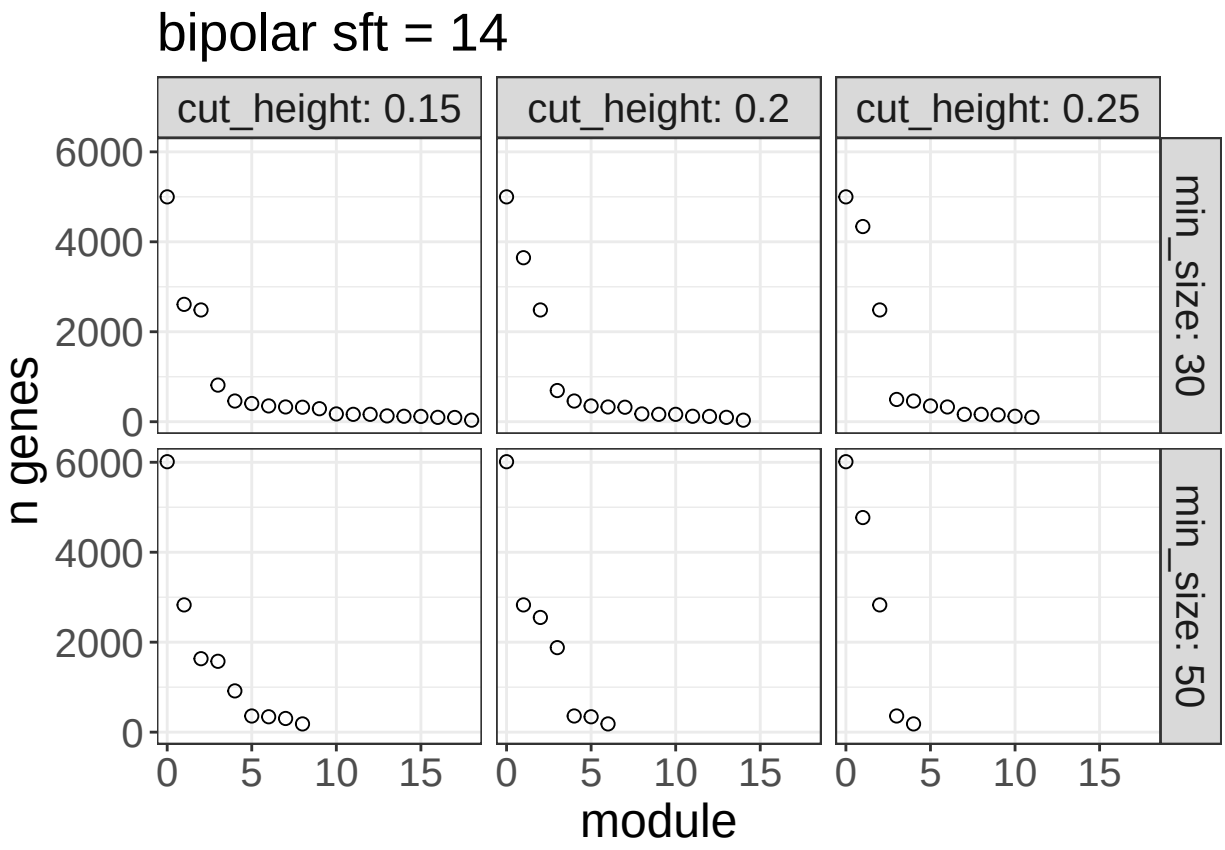
```
dx <- "bipolar"

powers <- c(8, 9, 12, 14)
```




bipolar sft = 9
cut_height: 0.15
cut_height: 0.2
cut_height: 0.25
min_size: 30
min_size: 50
n genes
module


bipolar sft = 12
cut_height: 0.15
cut_height: 0.2
cut_height: 0.25
min_size: 30
min_size: 50
n genes
module


bipolar sft = 14
cut_height: 0.15
cut_height: 0.2
cut_height: 0.25
min_size: 30
min_size: 50
n genes
module
0
2000
4000
6000
0
5
10
15