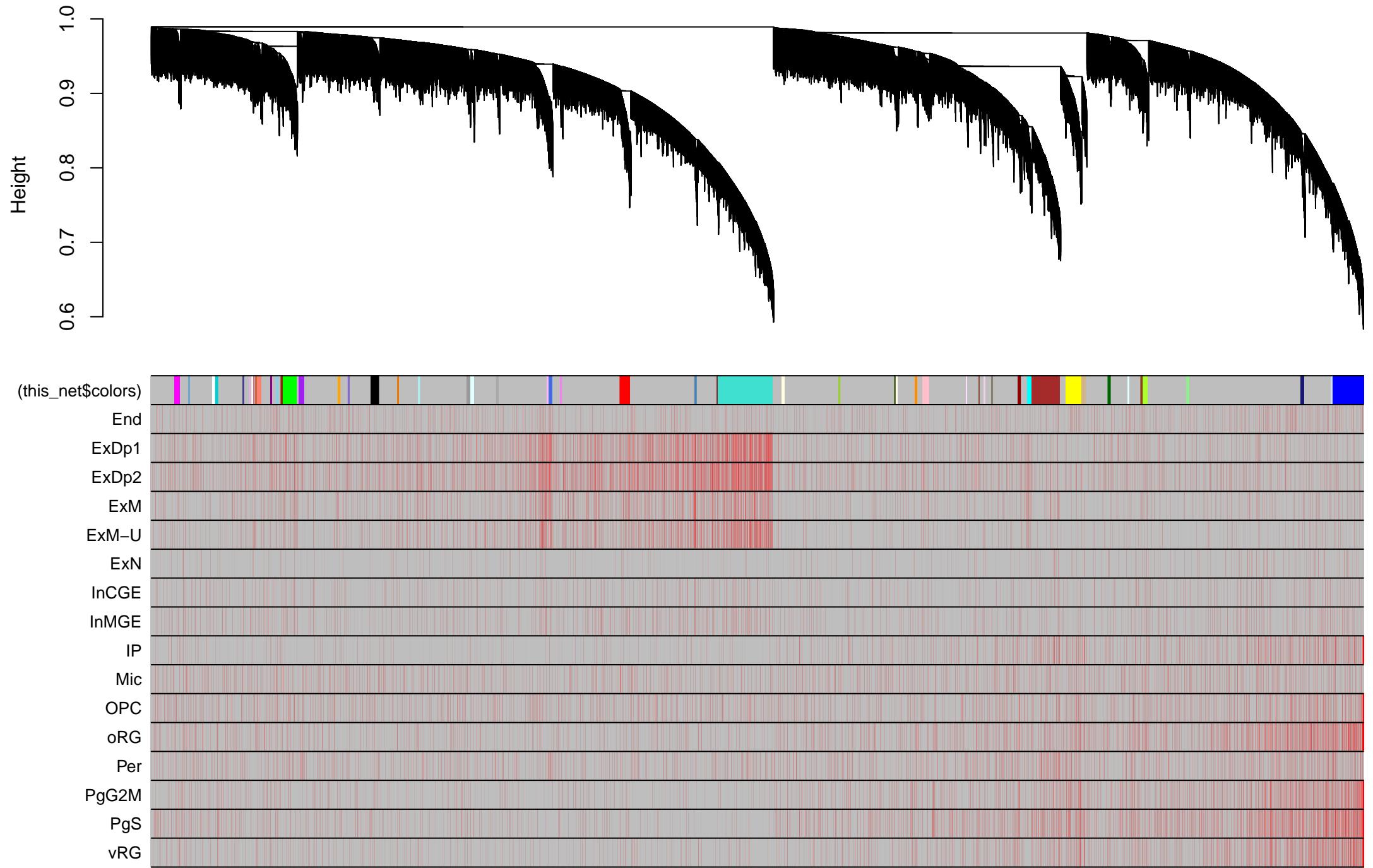
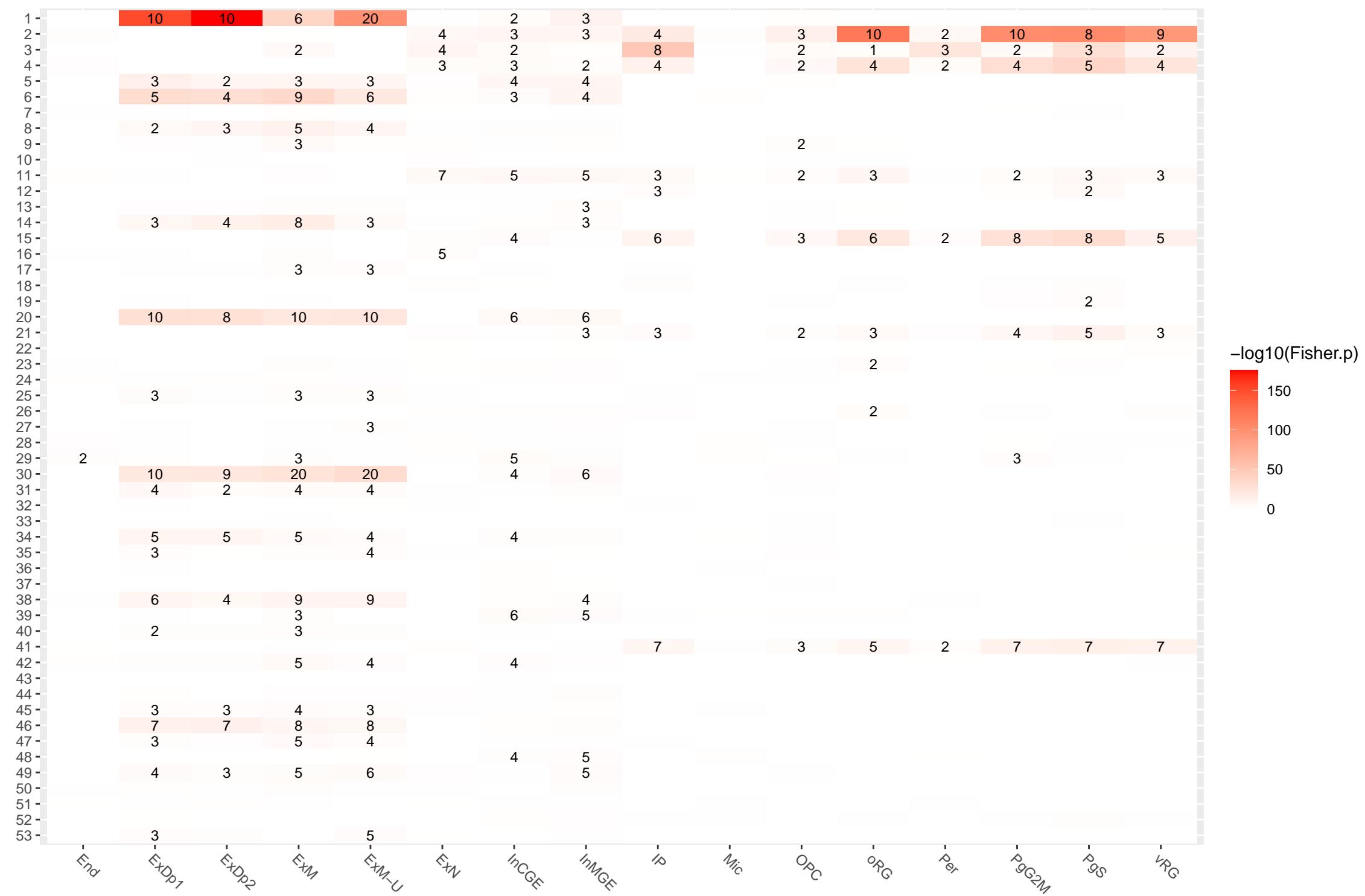
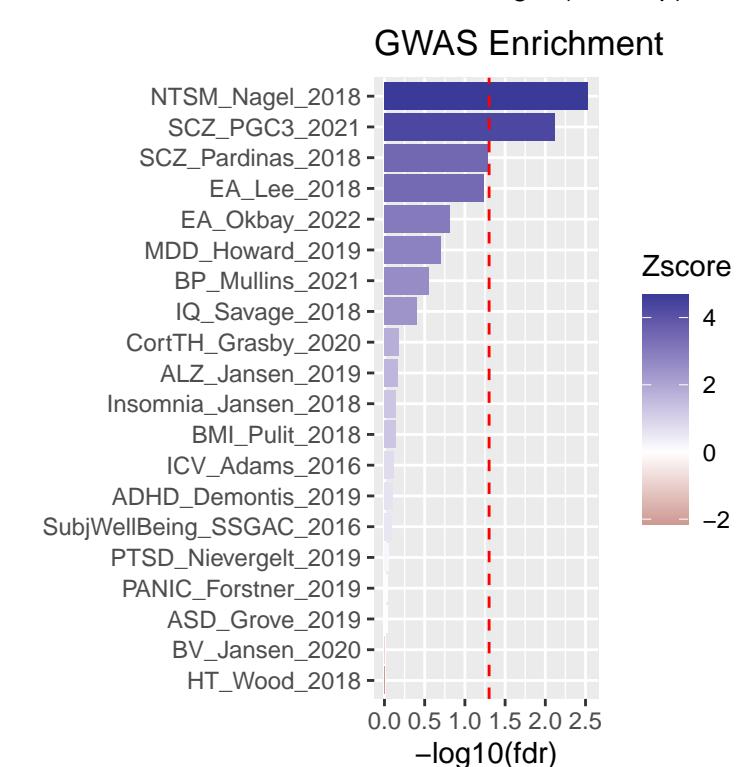
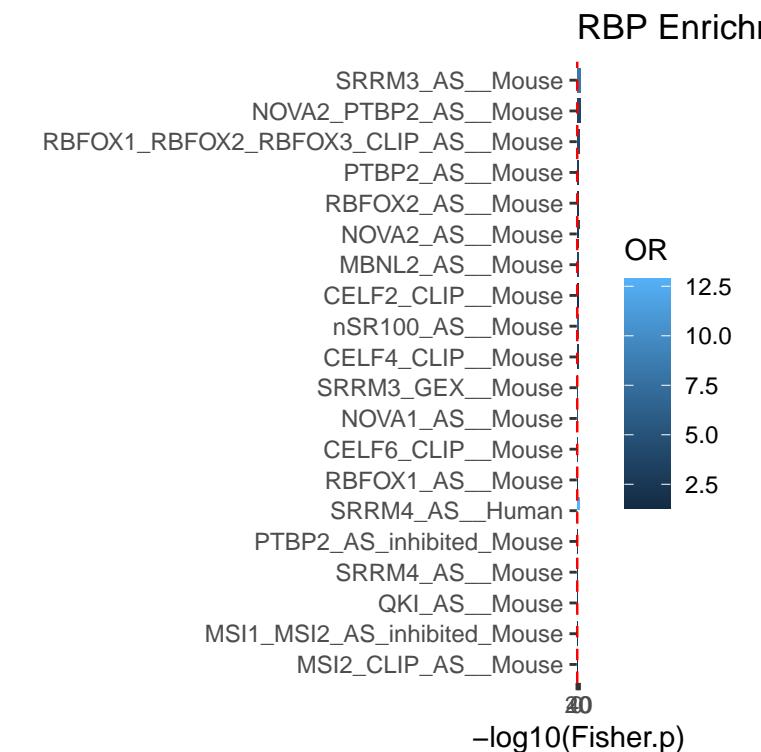
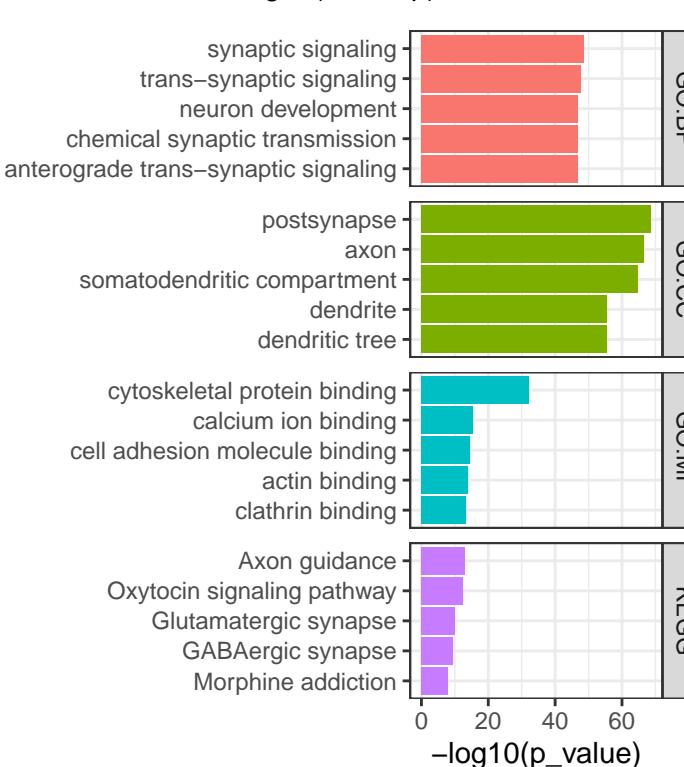
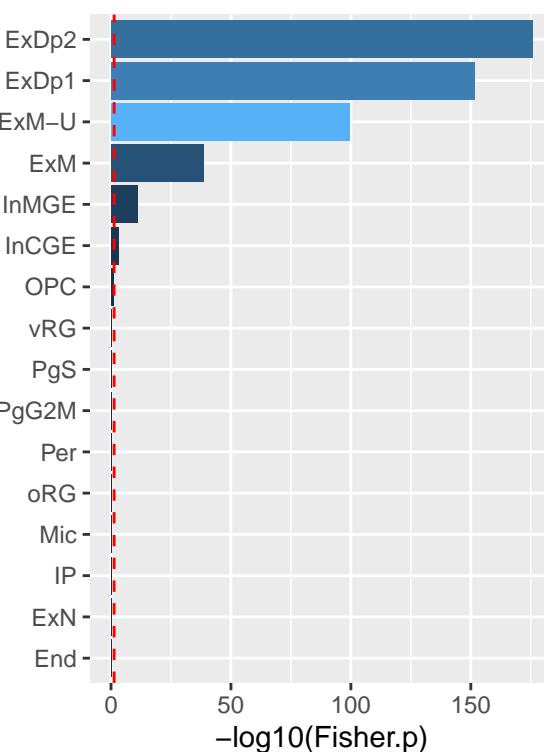
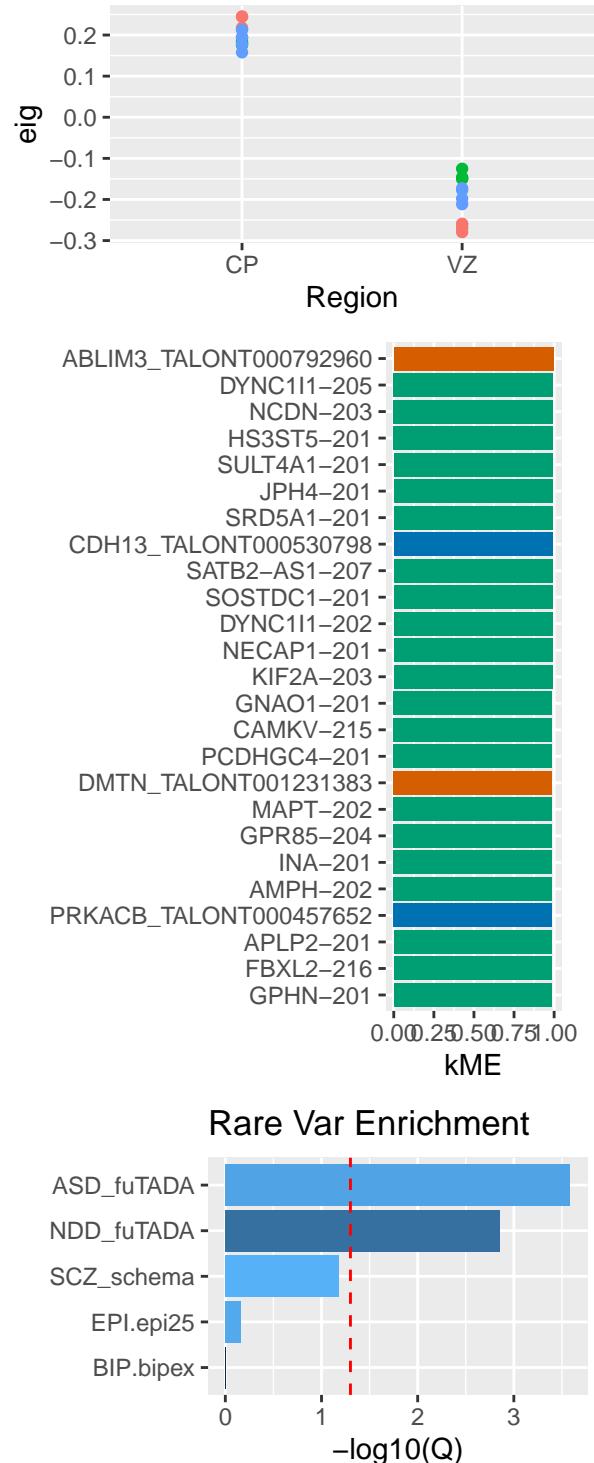


## Cluster Dendrogram

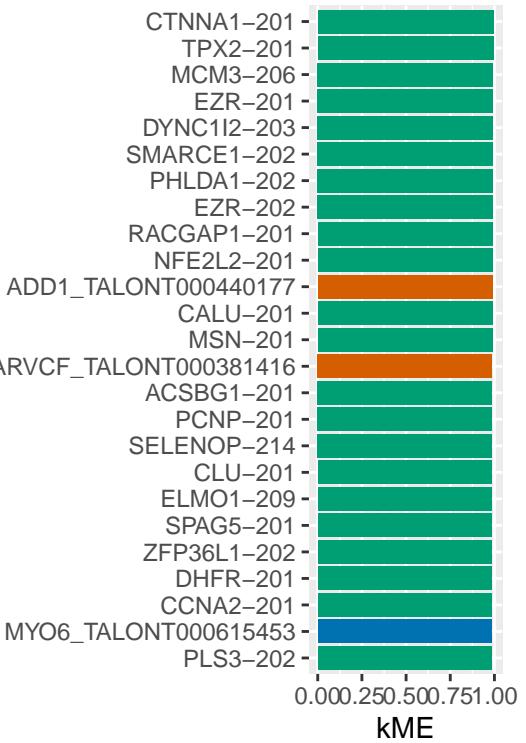
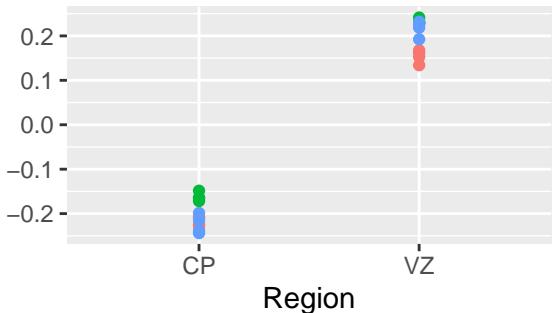




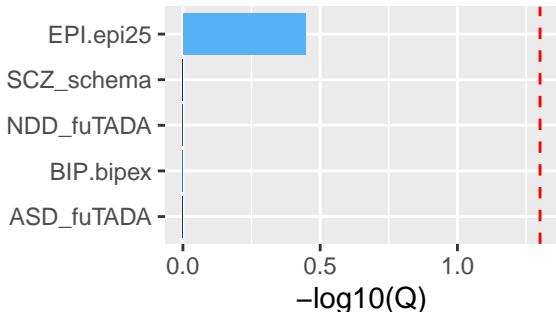
# Module 1: turquoise n=4153



## Module 2: blue n=2274

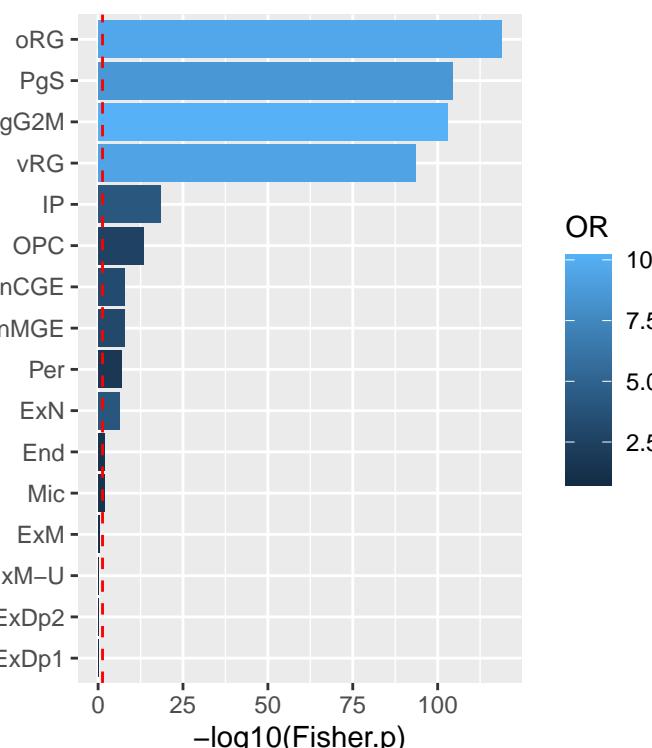


### Rare Var Enrichment



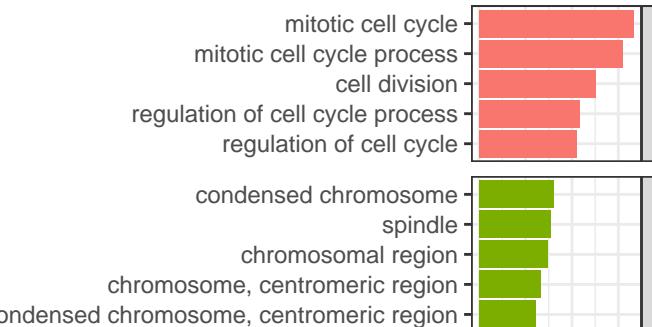
### Subject

- 209 (red)
- 334 (green)
- 336 (blue)

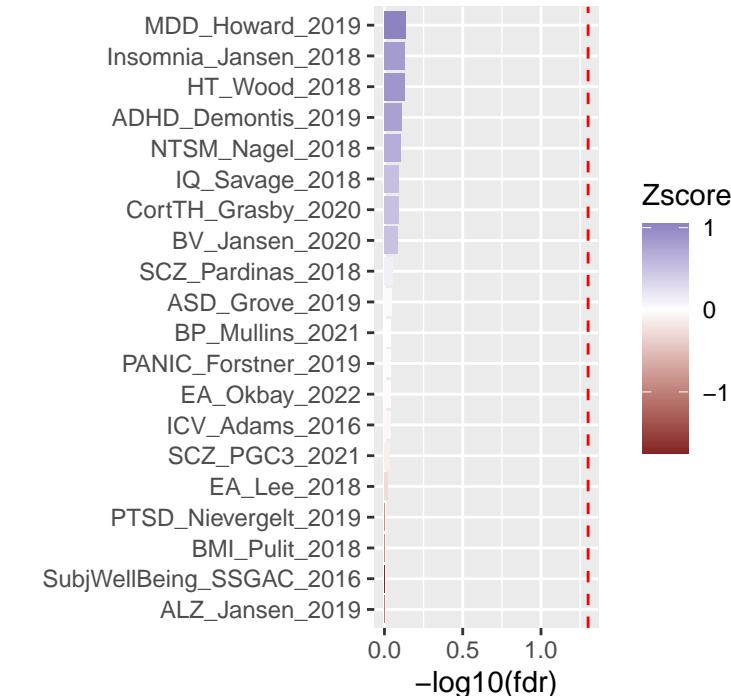


### OR

10.0  
7.5  
5.0  
2.5



### GWAS Enrichment



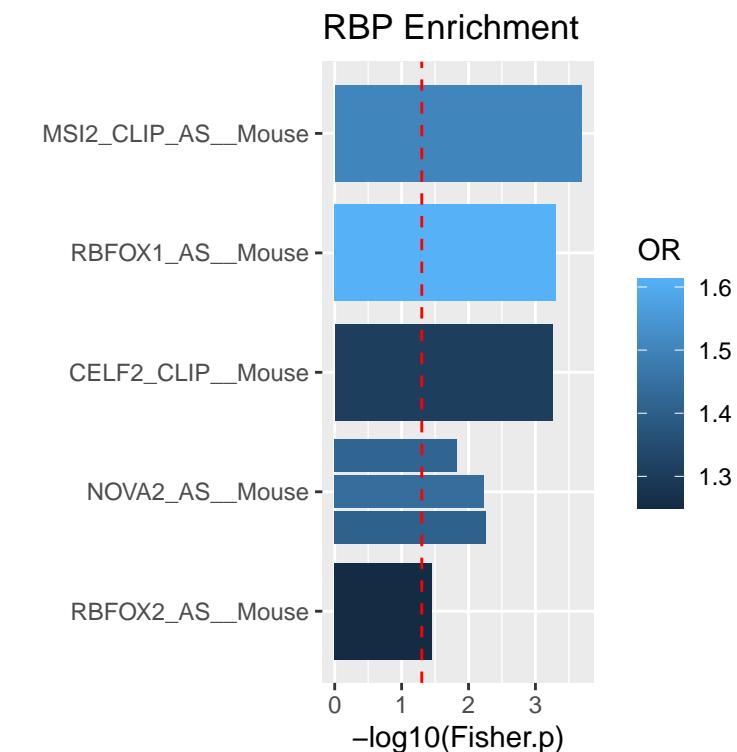
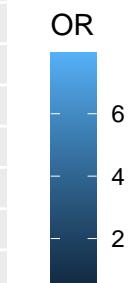
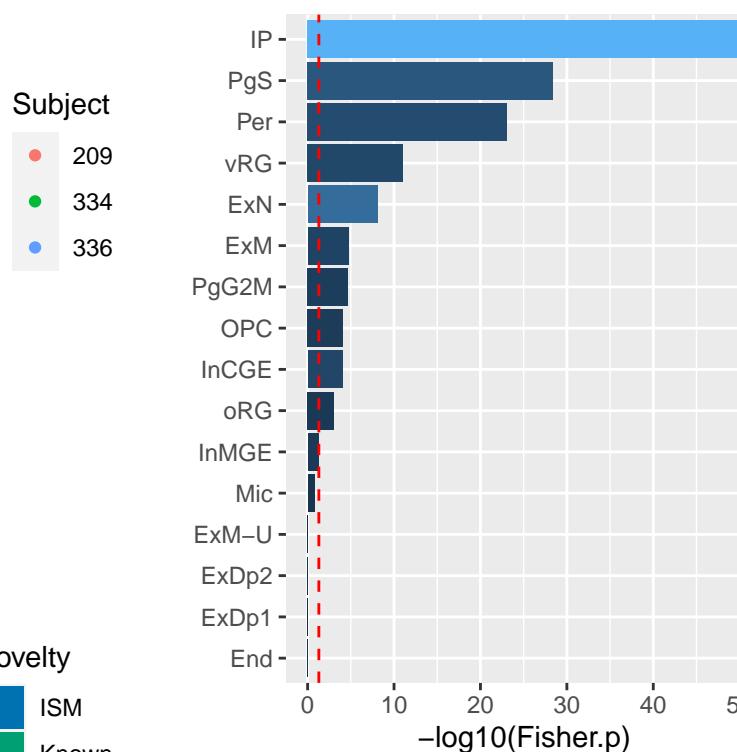
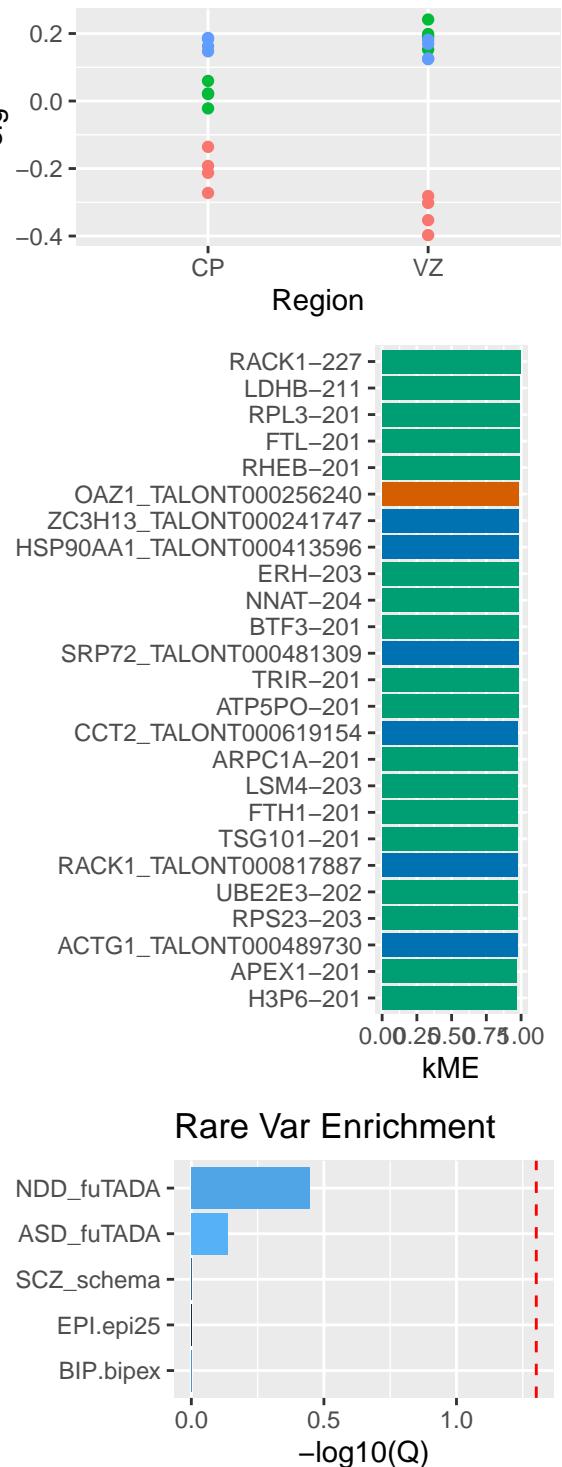
### OR

12  
9  
6  
3

### Zscore

1  
0  
-1

### Module 3: brown n=2161



translation  
peptide biosynthetic process  
peptide metabolic process  
cytoplasmic translation  
amide biosynthetic process

ribosomal subunit  
mitochondrial protein-containing complex  
mitochondrial inner membrane  
organelle inner membrane  
cytosolic ribosome

structural constituent of ribosome  
mRNA binding  
oxidoreduction-driven active transmembrane transporter activity  
ribonucleoprotein complex binding  
electron transfer activity

Ribosome  
Parkinson disease  
Huntington disease  
Amyotrophic lateral sclerosis  
Prion disease

GO:BP

GO:CC

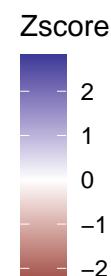
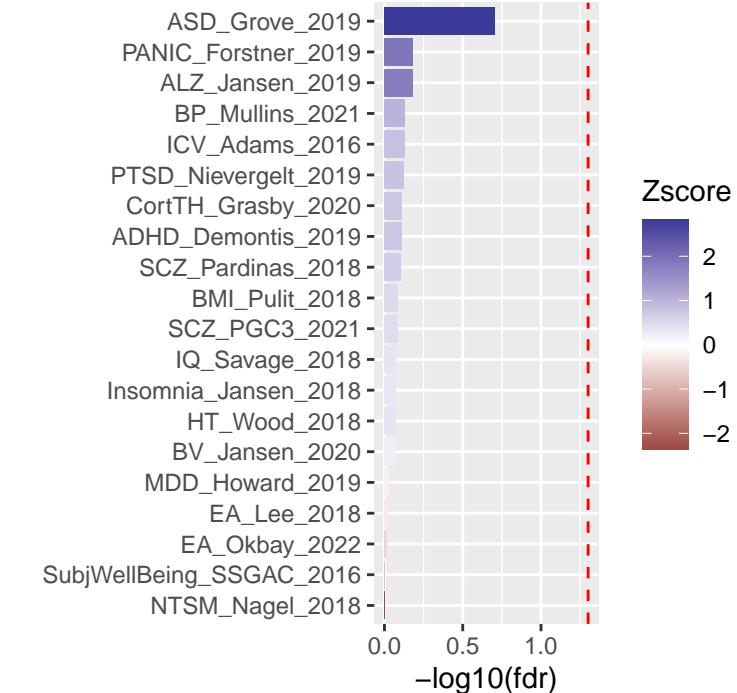
GO:MF

KEGG

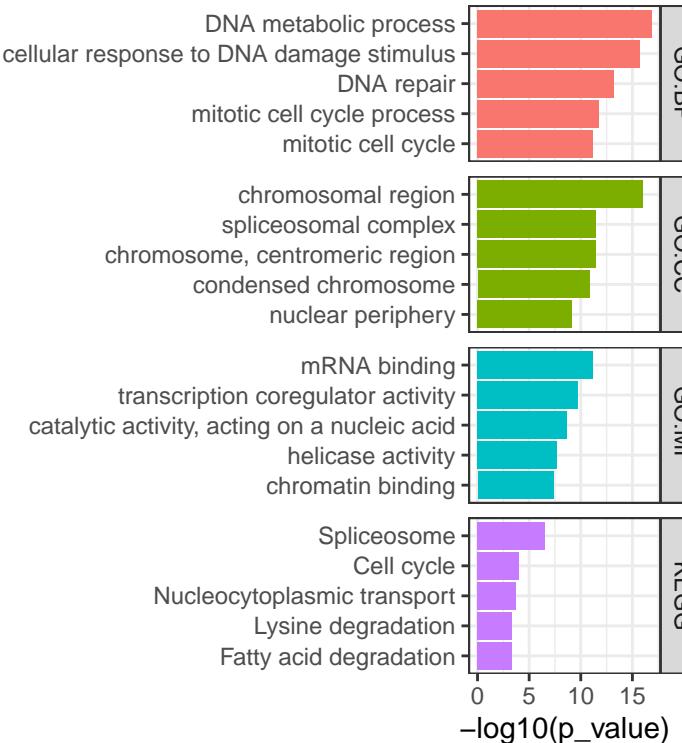
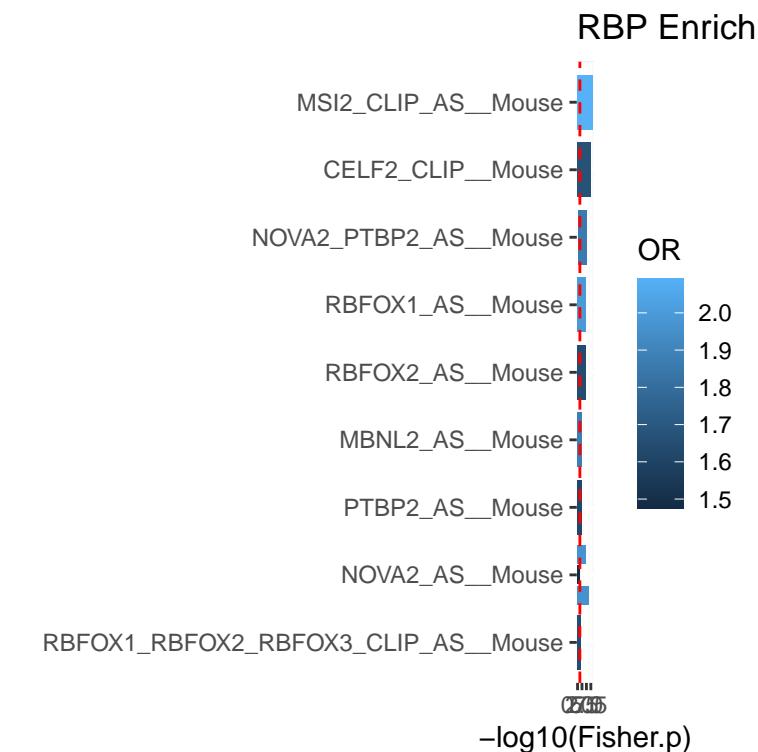
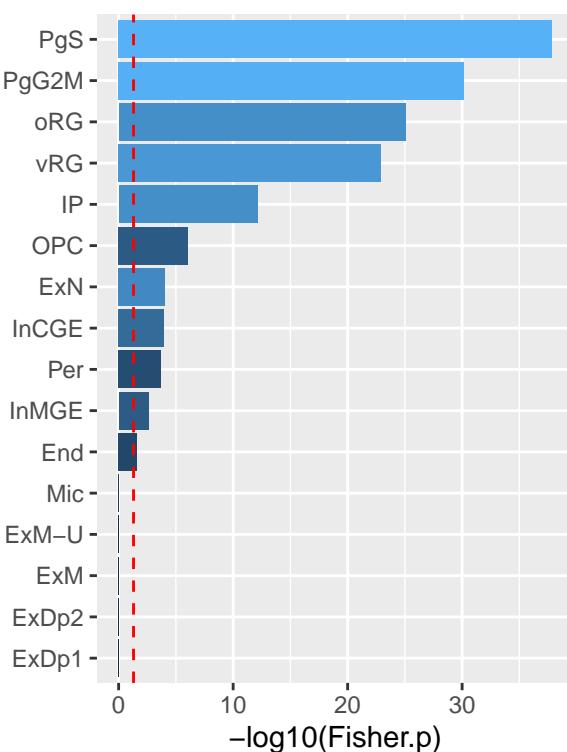
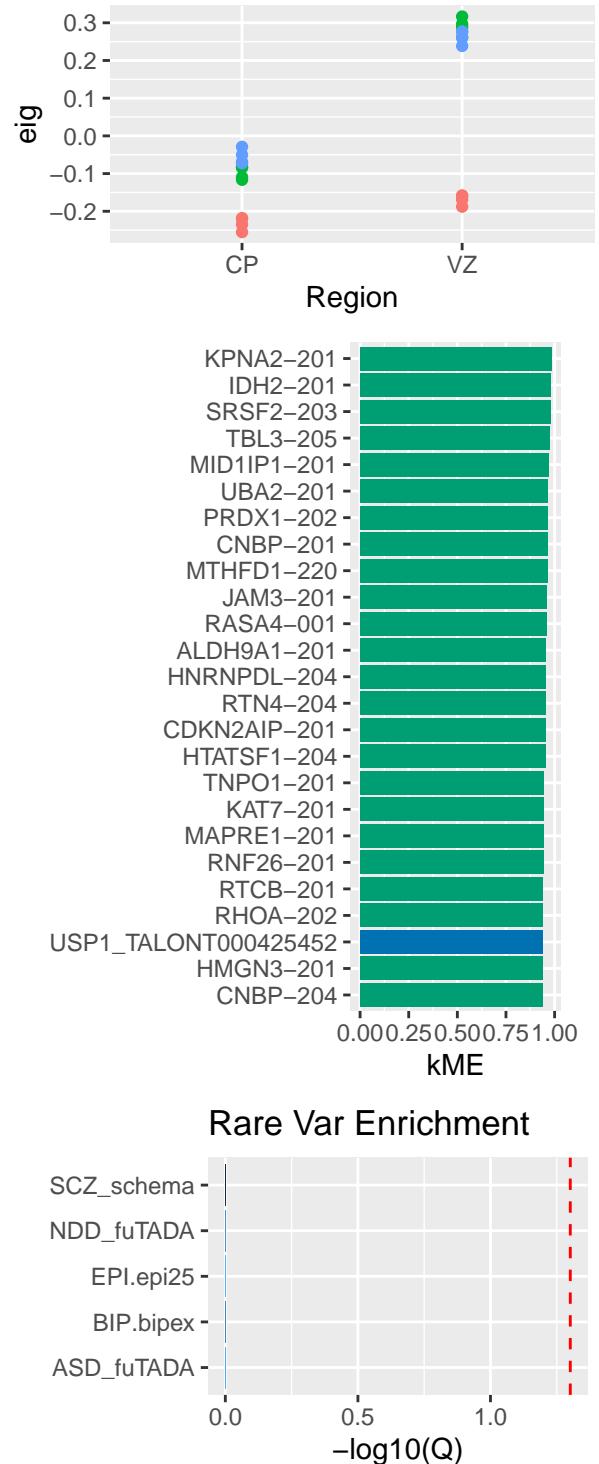
$-\log_{10}(p_{\text{v}})$

$-\log_{10}(\text{fdr})$

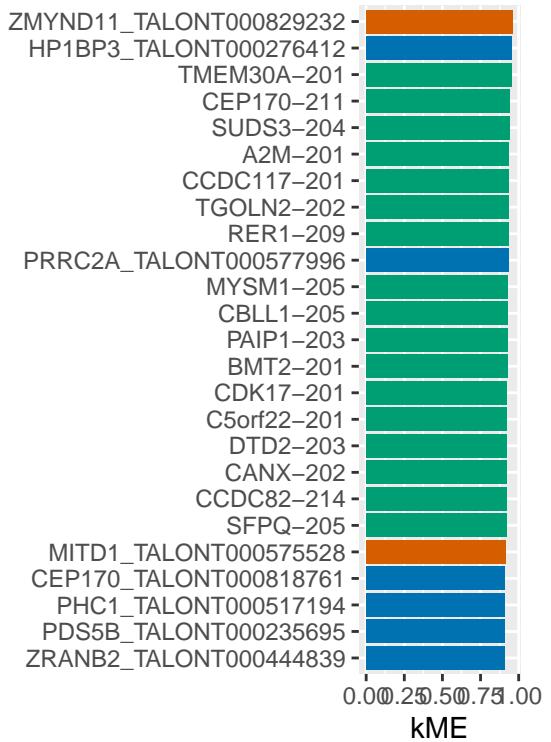
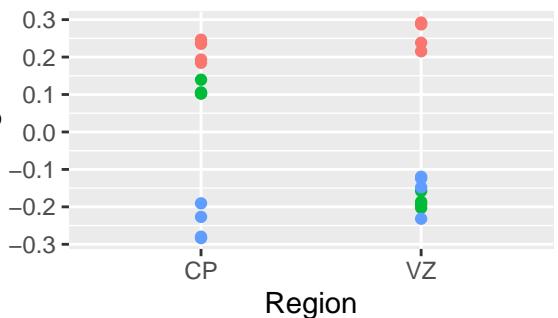
### GWAS Enrichment



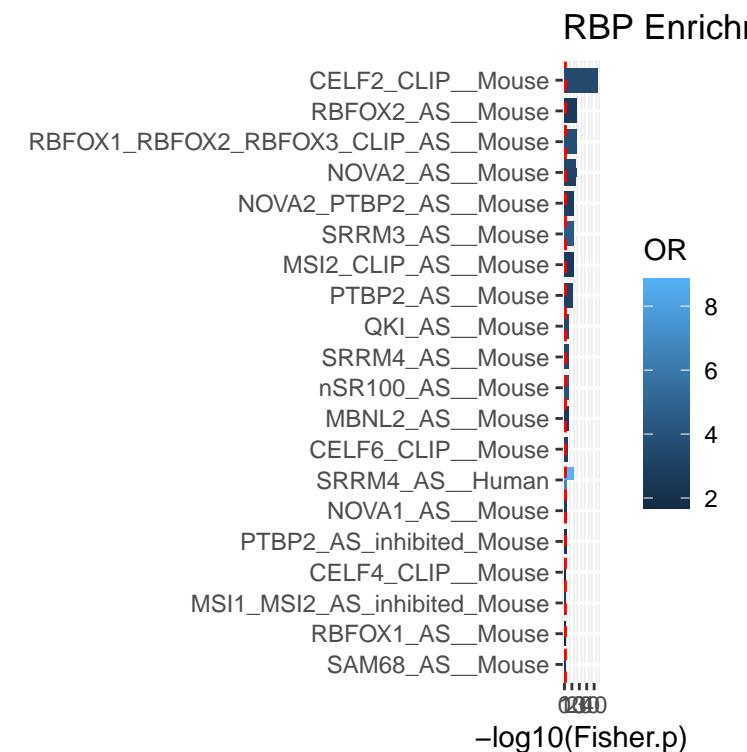
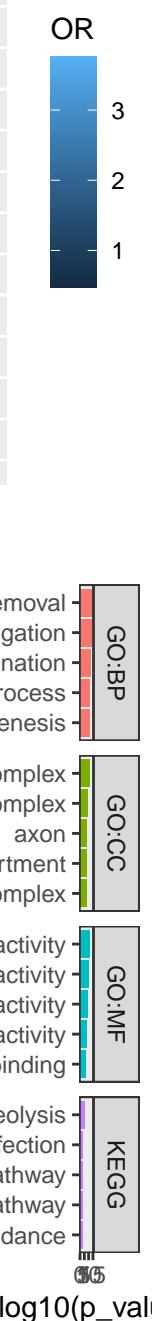
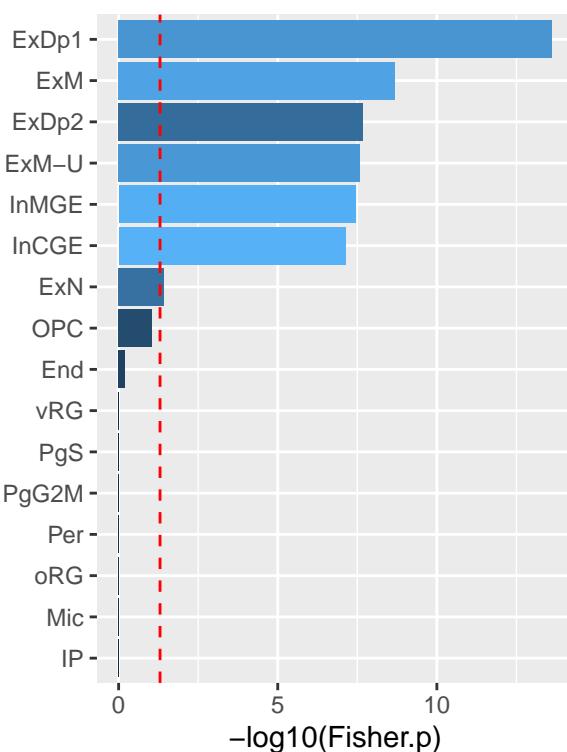
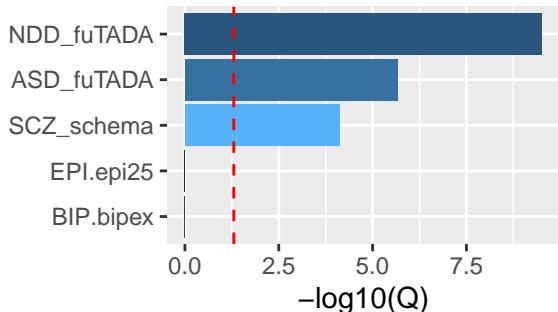
## Module 4: yellow n=1196



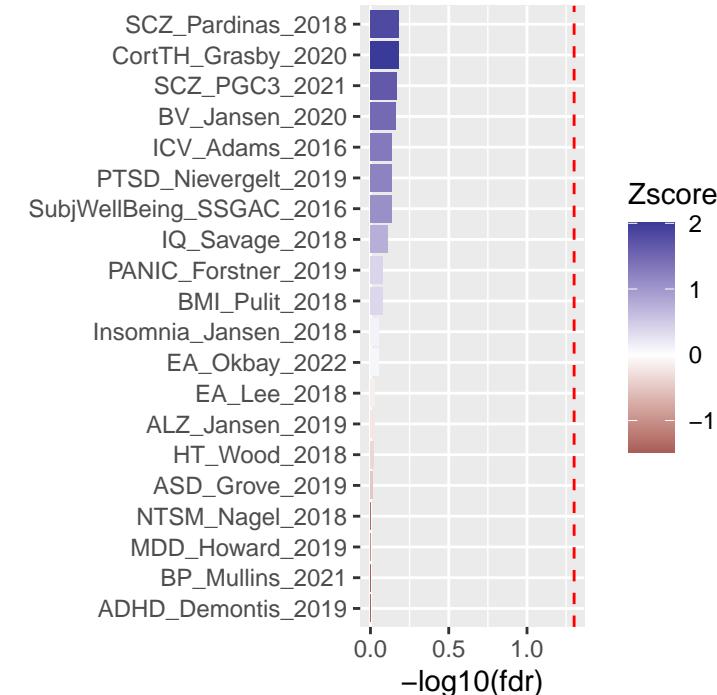
## Module 5: green n=1065



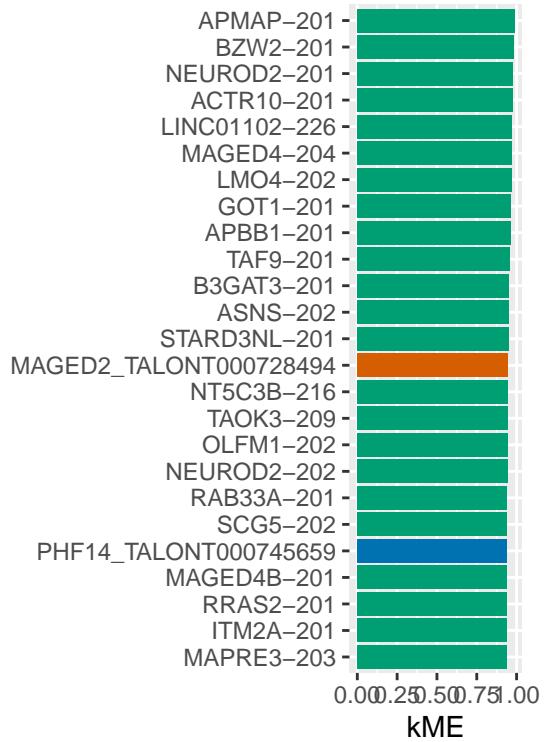
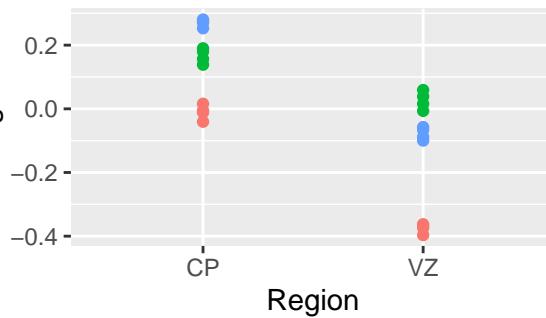
## Rare Var Enrichment



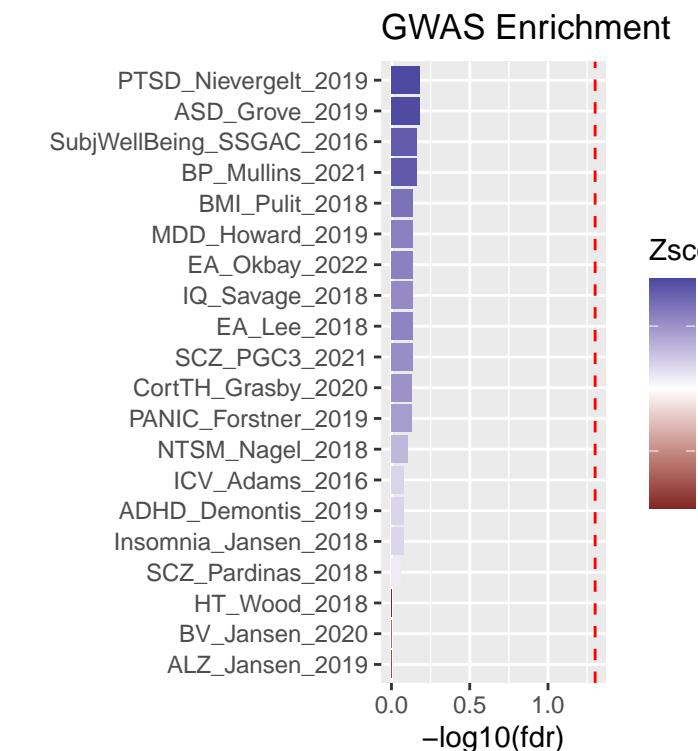
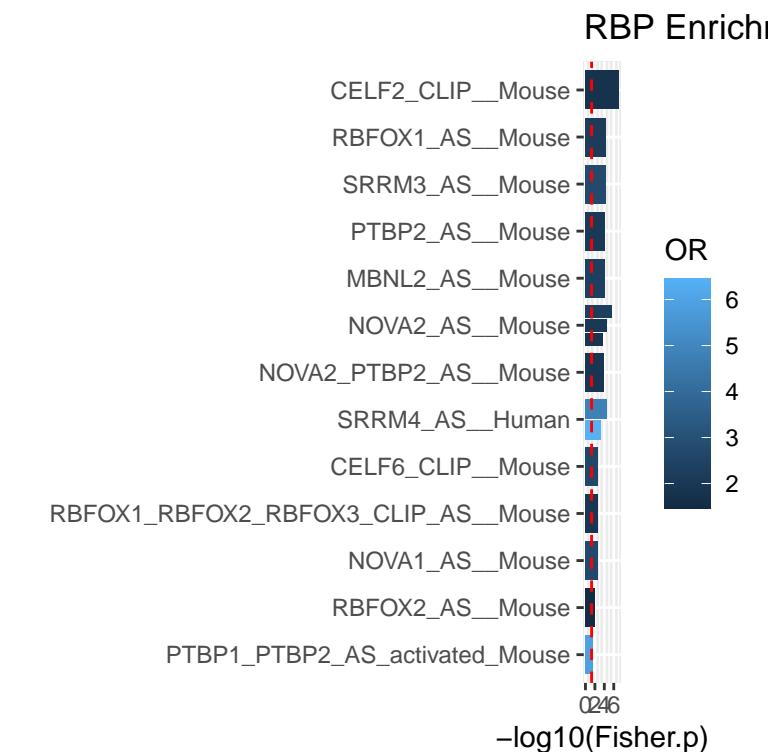
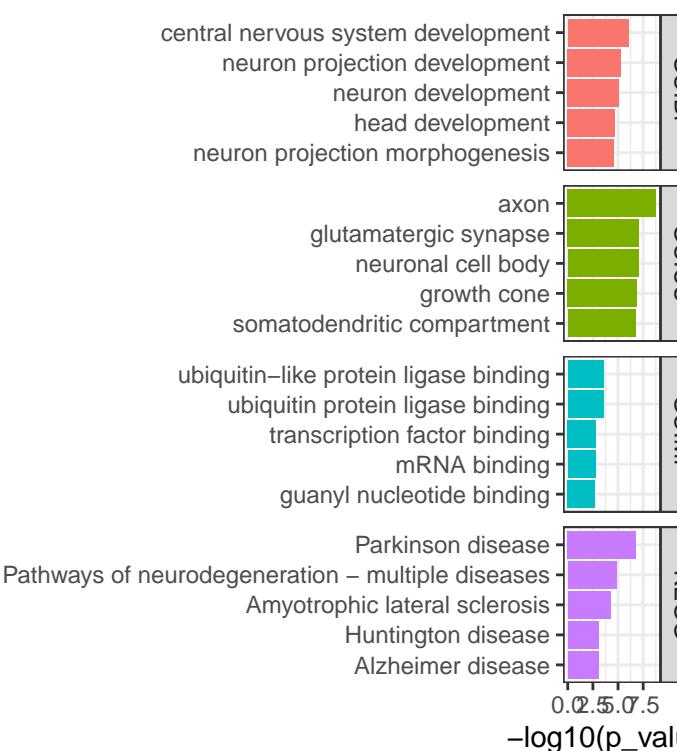
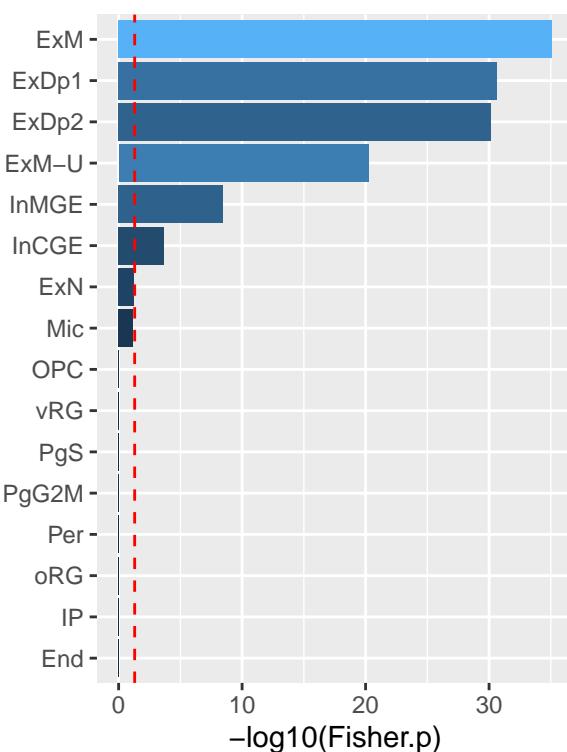
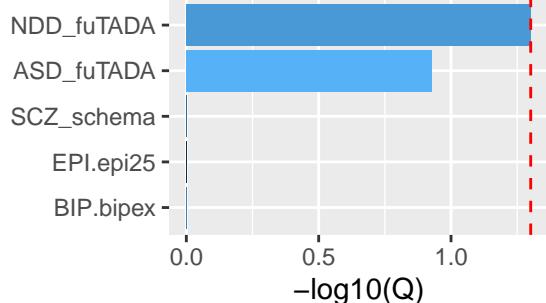
## GWAS Enrichment



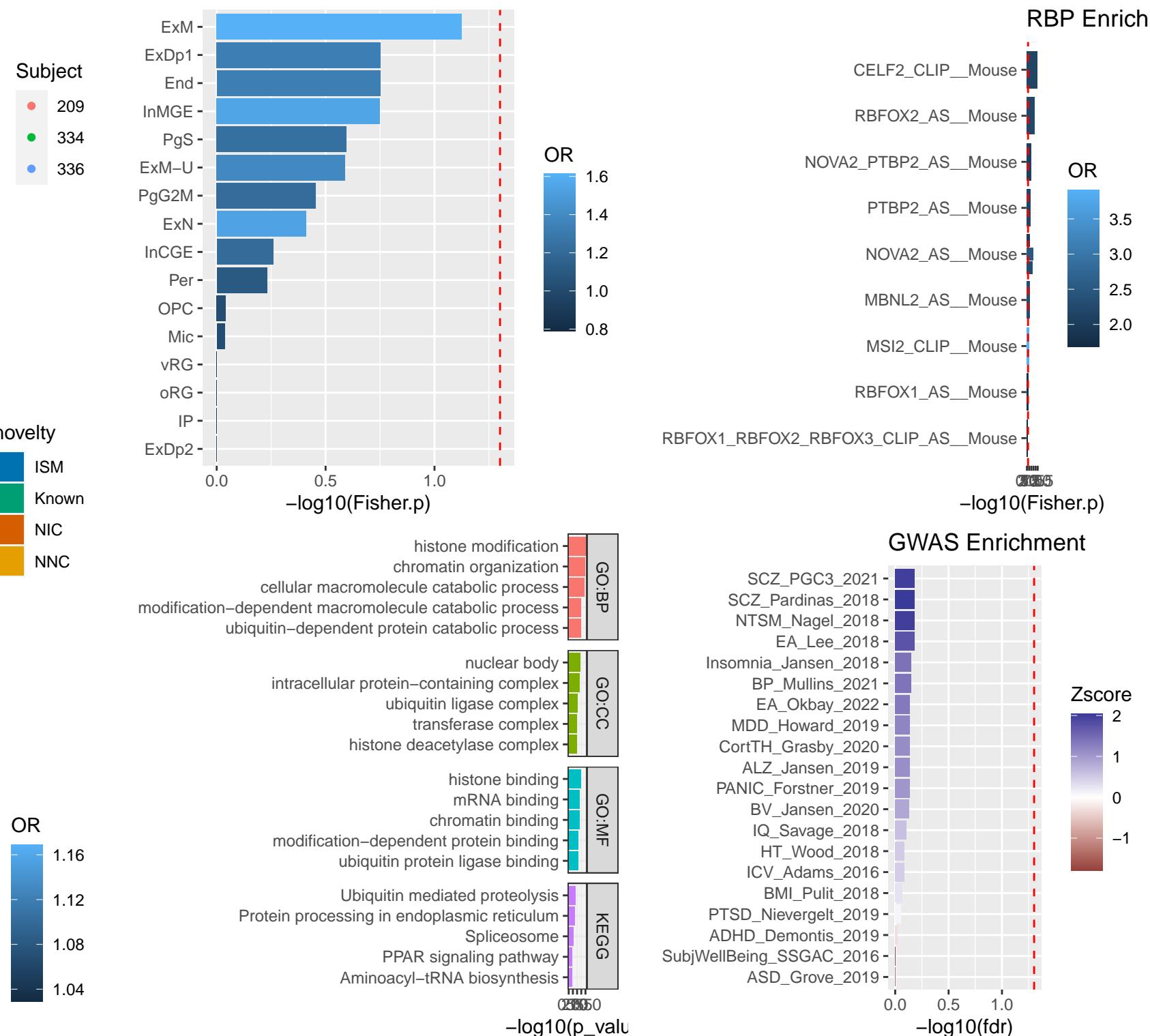
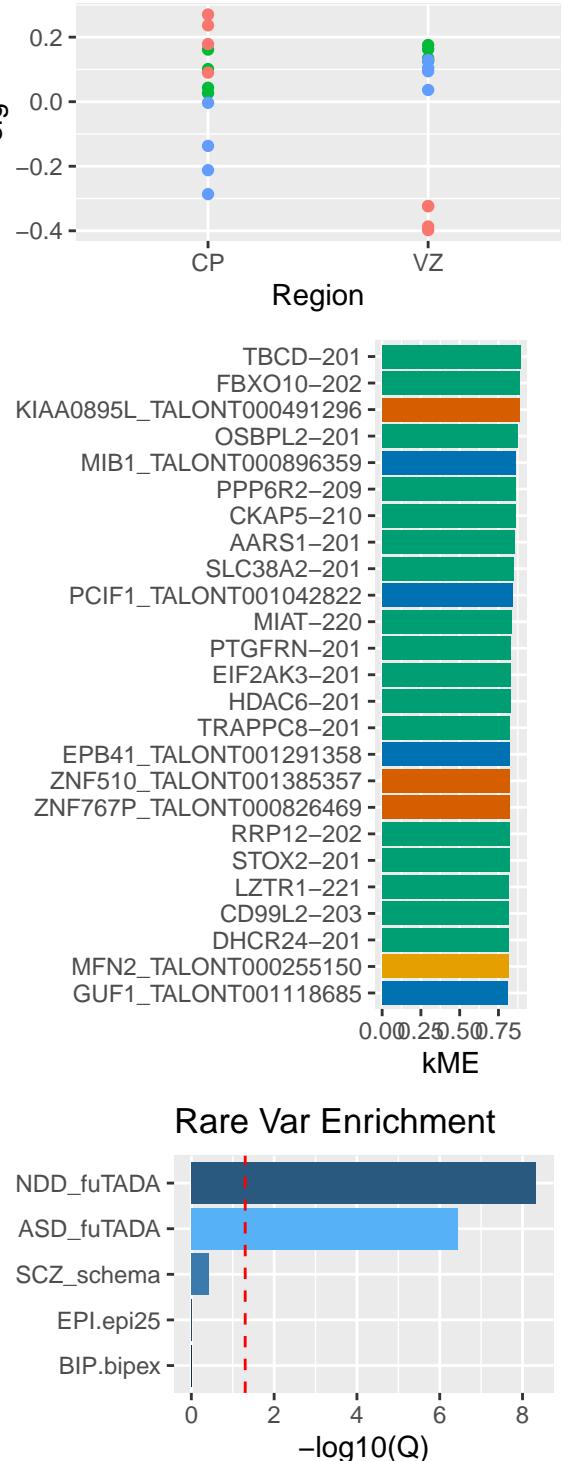
## Module 6: red n=805



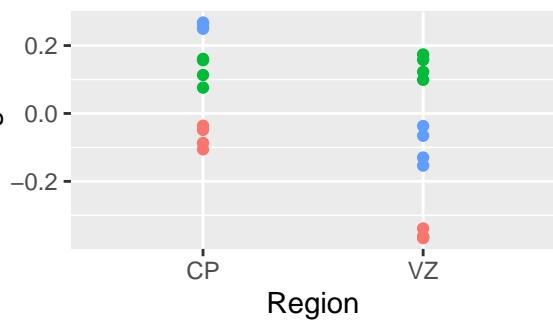
### Rare Var Enrichment



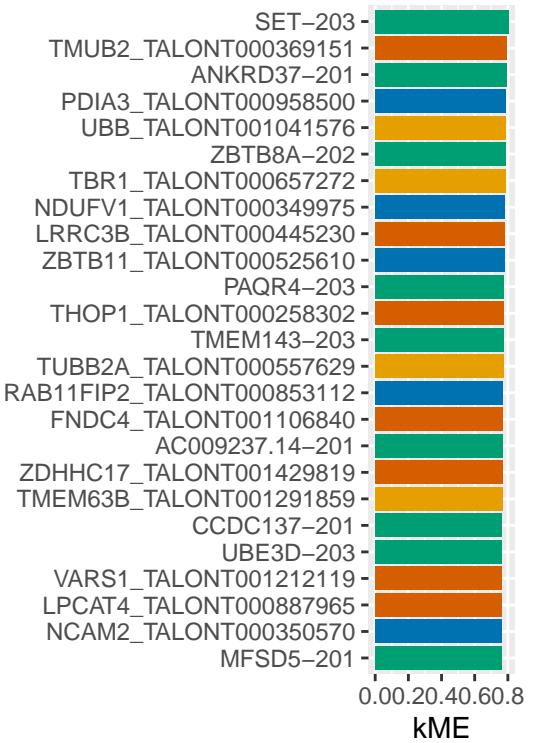
## Module 7: black n=662



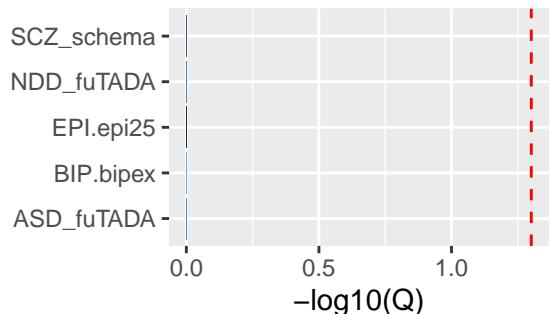
## Module 8: pink n=525



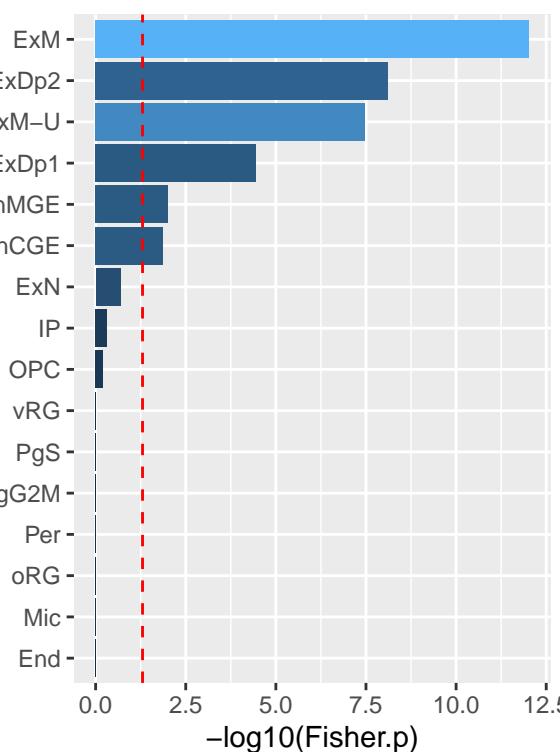
Subject  
209  
334  
336



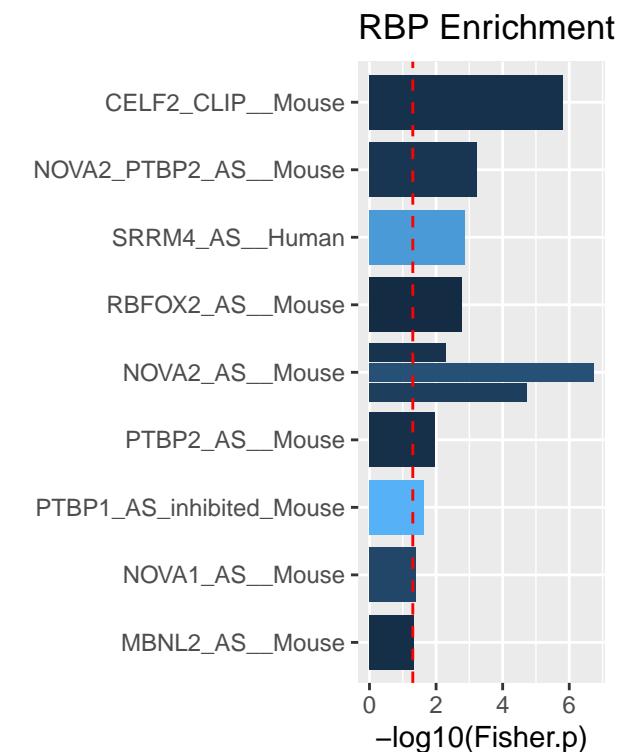
### Rare Var Enrichment



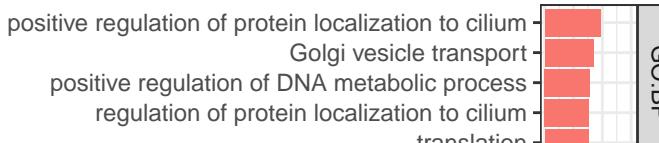
OR  
1.05  
1.00  
0.95  
0.90



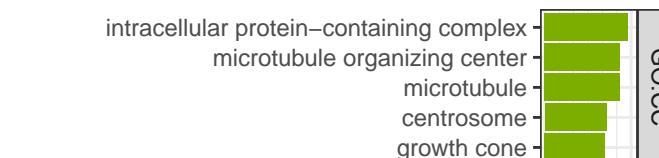
OR  
4  
3  
2  
1



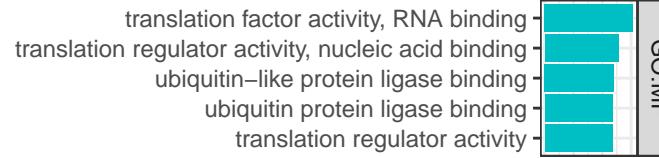
OR  
4  
3  
2



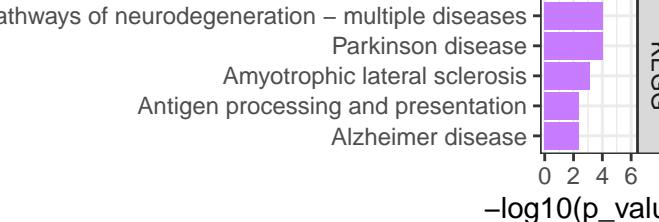
GO:BP



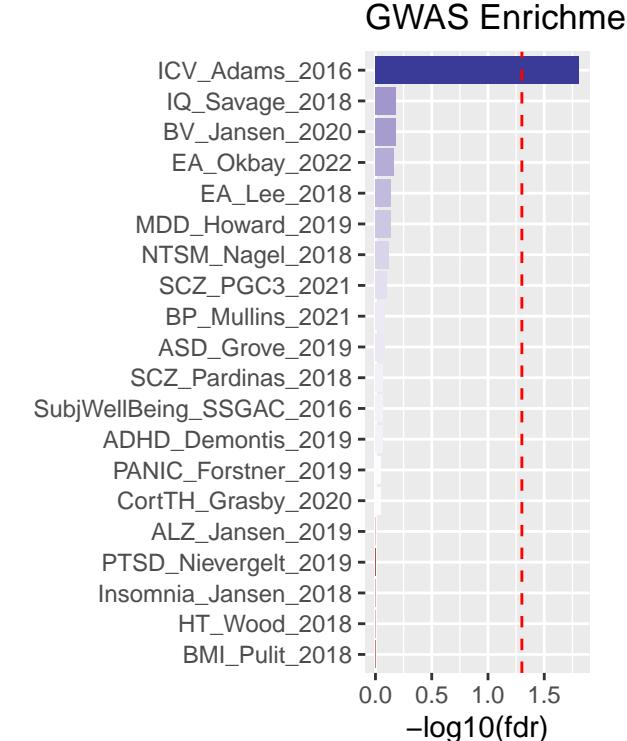
GO:CC



GO:MF

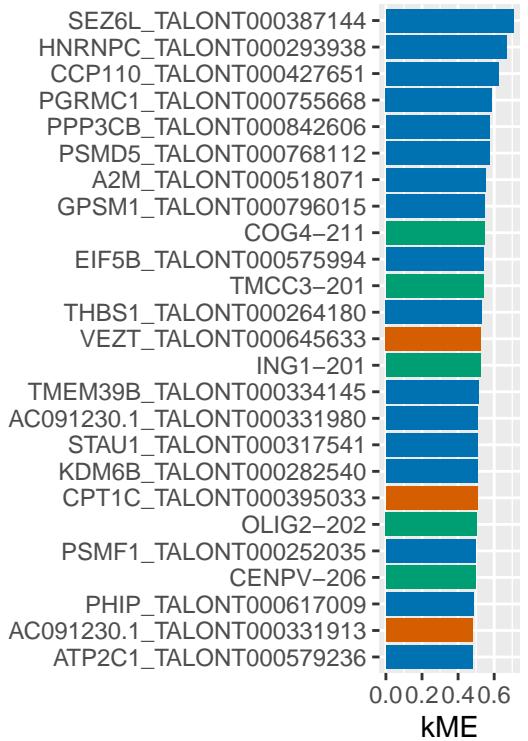
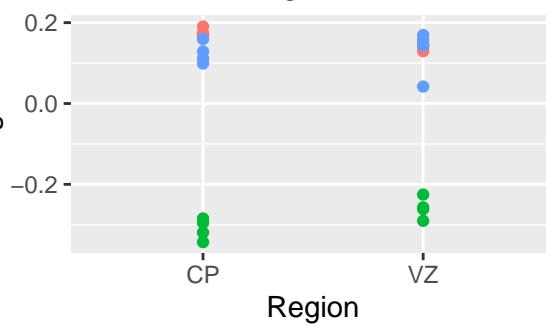


KEGG

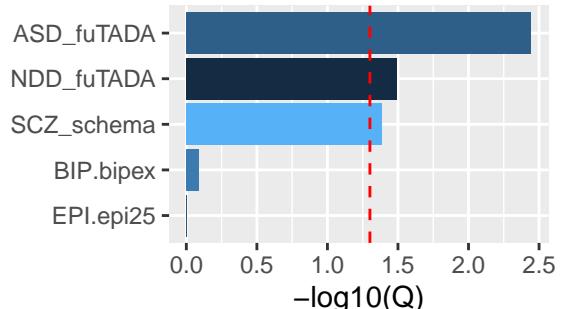


Zscore  
2  
0  
-2

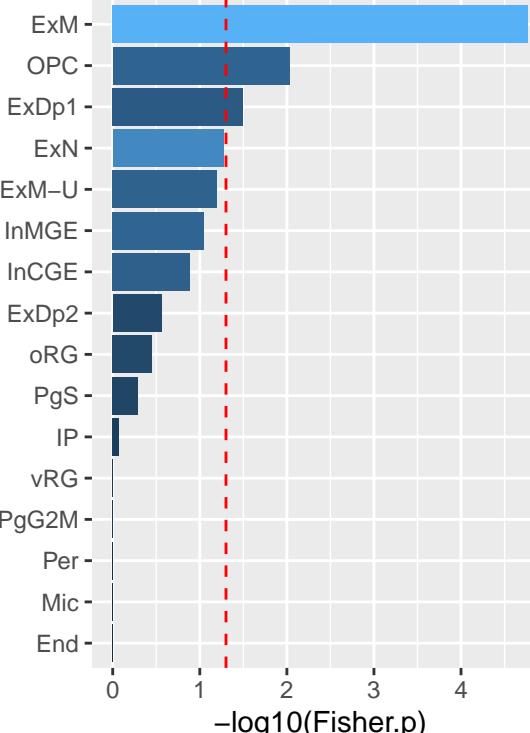
## Module 9: magenta n=420



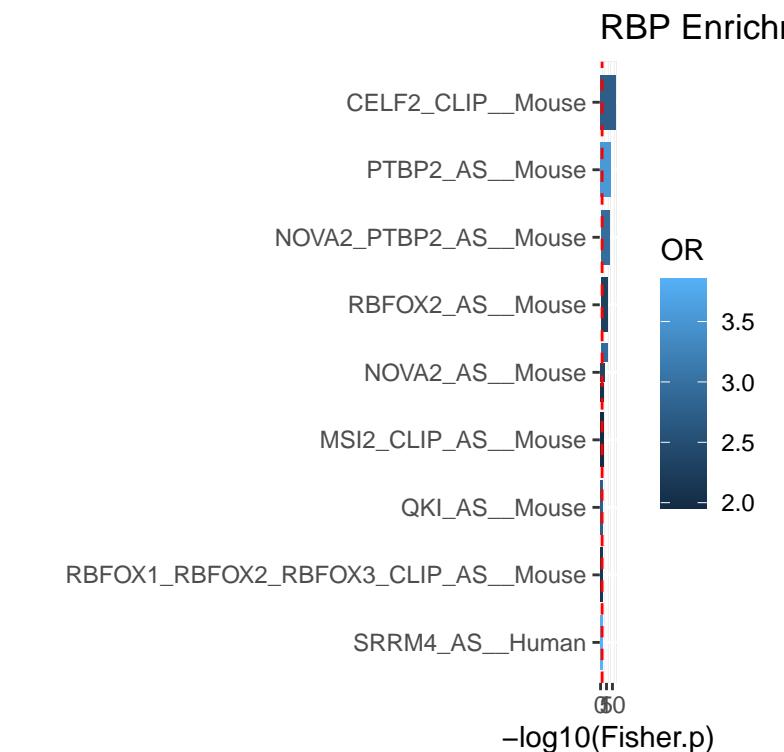
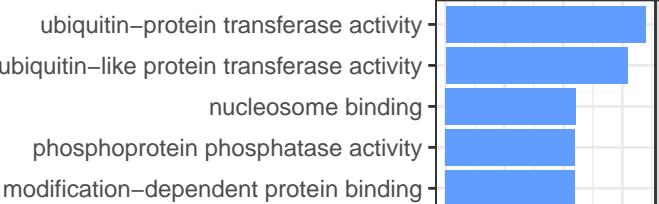
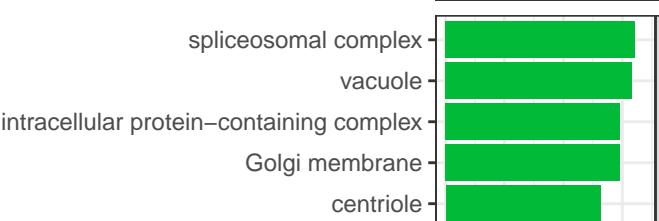
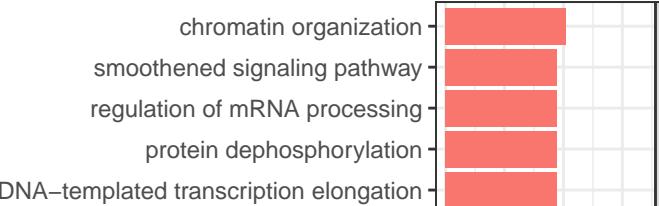
## Rare Var Enrichment



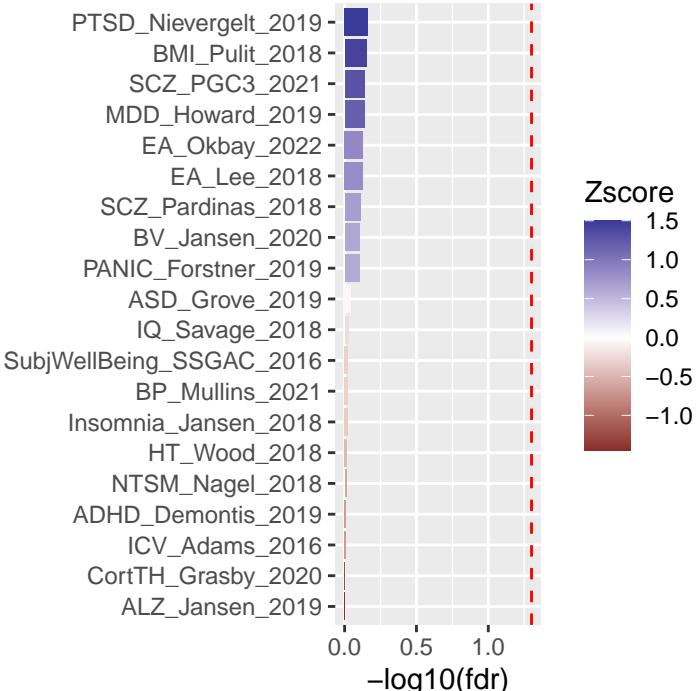
Subject  
209  
334  
336



OR

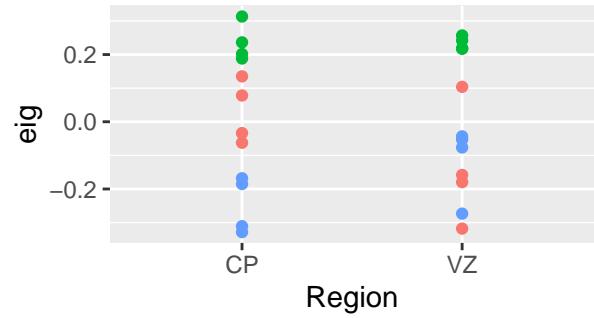


## GWAS Enrichment



Zscore  
1.5  
1.0  
0.5  
0.0  
-0.5  
-1.0

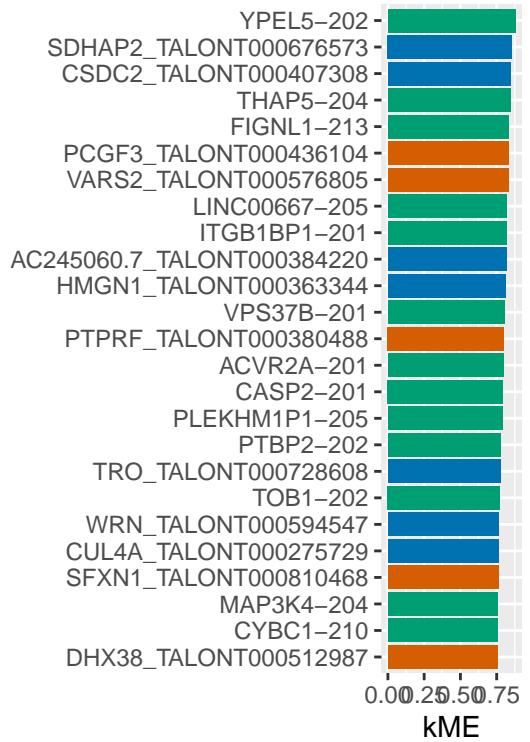
## Module 10: purple n=419



Subject

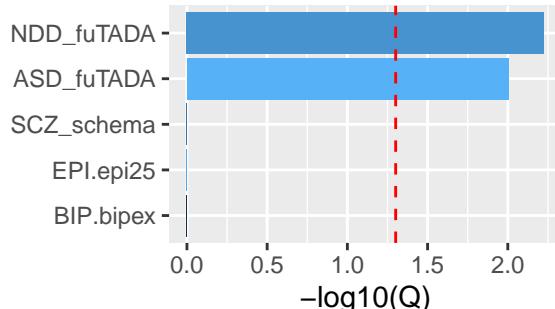
- 209
- 334
- 336

Region

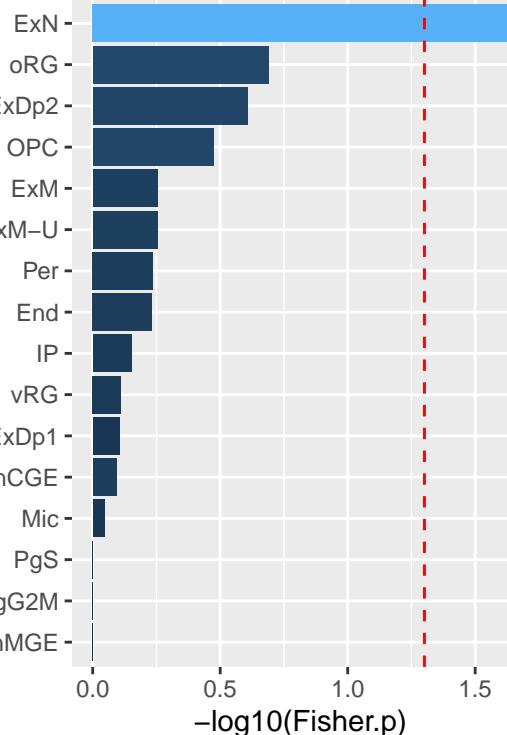


kME

### Rare Var Enrichment

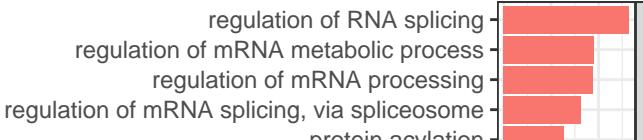


-log10(Q)

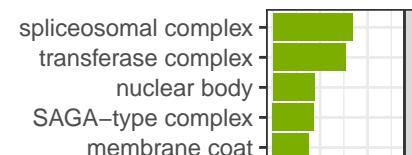


OR

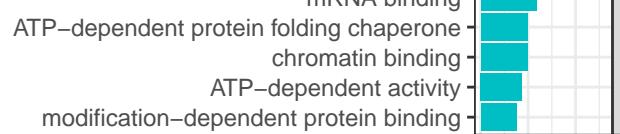
-log10(Fisher.p)



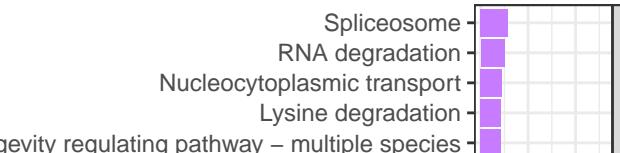
GO:BP



GO:CC



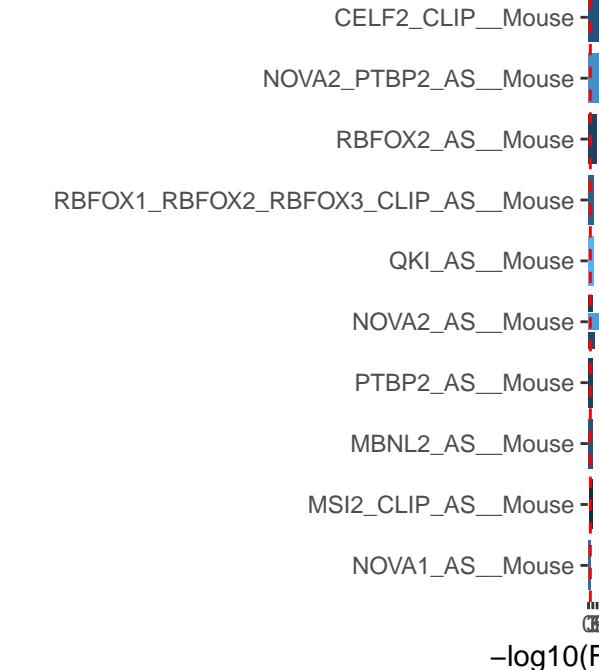
GO:MF



KEGG

-log10(p\_value)

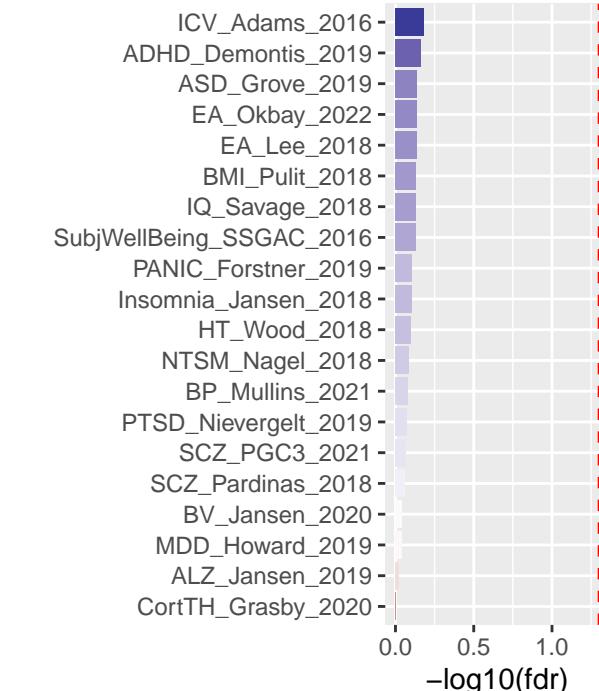
RBP Enrich



OR

-log10(Fisher.p)

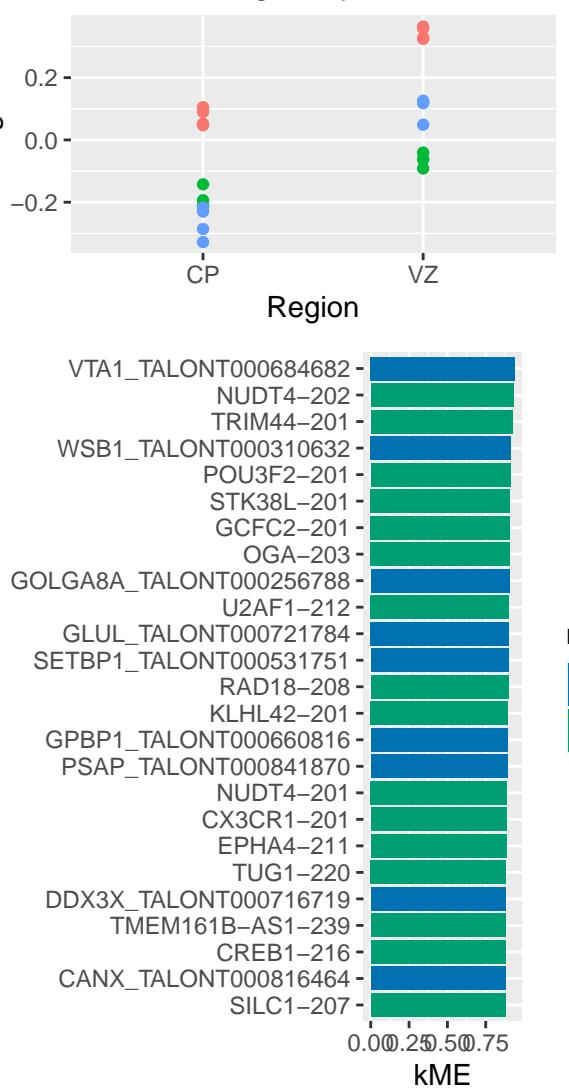
### GWAS Enrichment



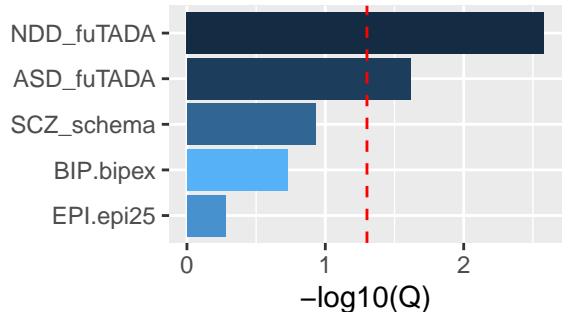
Zscore

-log10(fdr)

## Module 11: greenyellow n=383



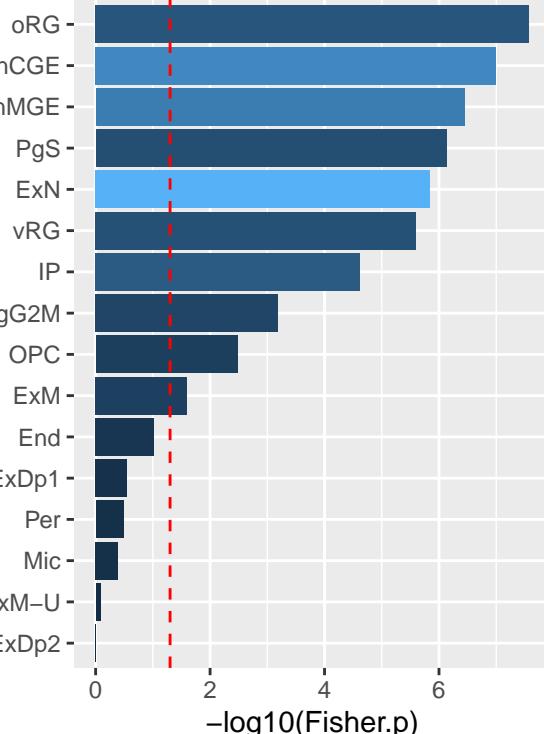
### Rare Var Enrichment



### Subject

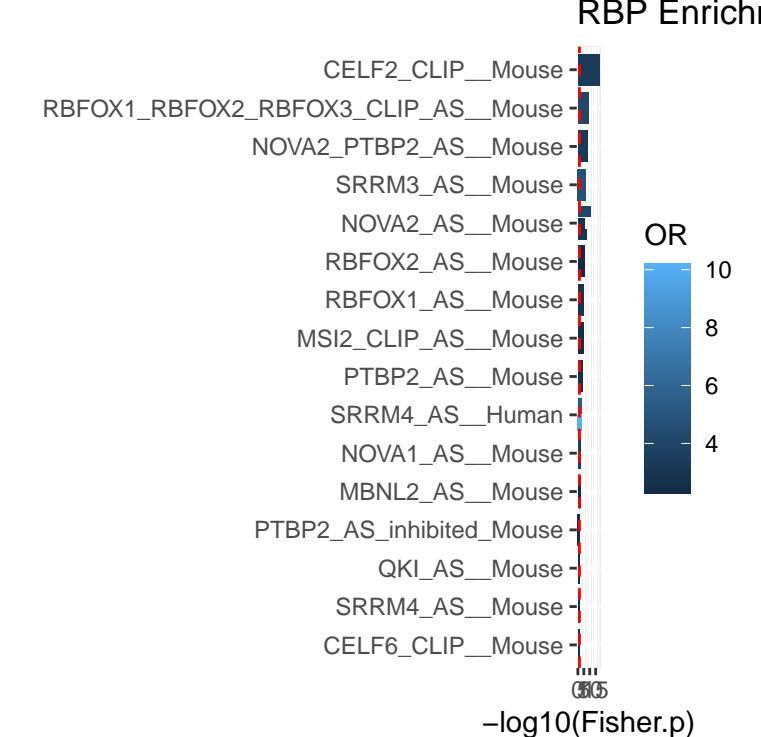
209  
334  
336

Region



OR

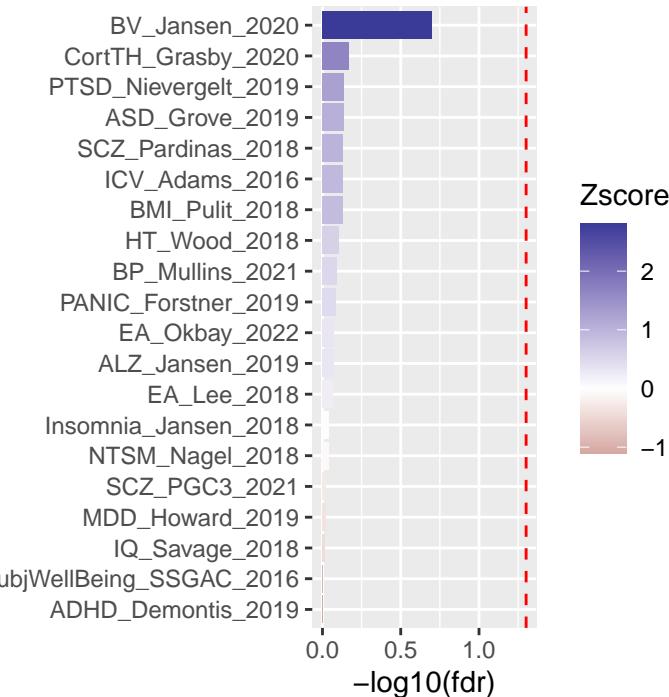
6  
4  
2



OR

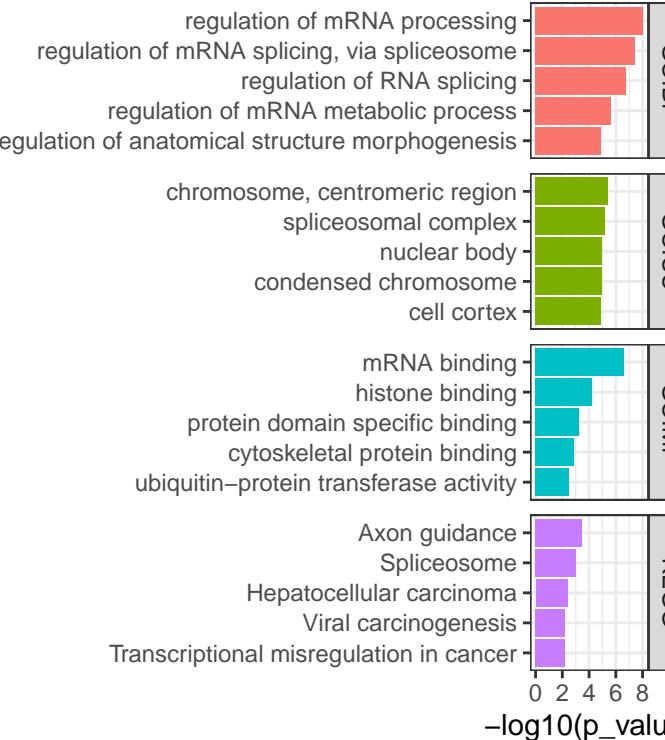
10  
8  
6  
4

### GWAS Enrichment

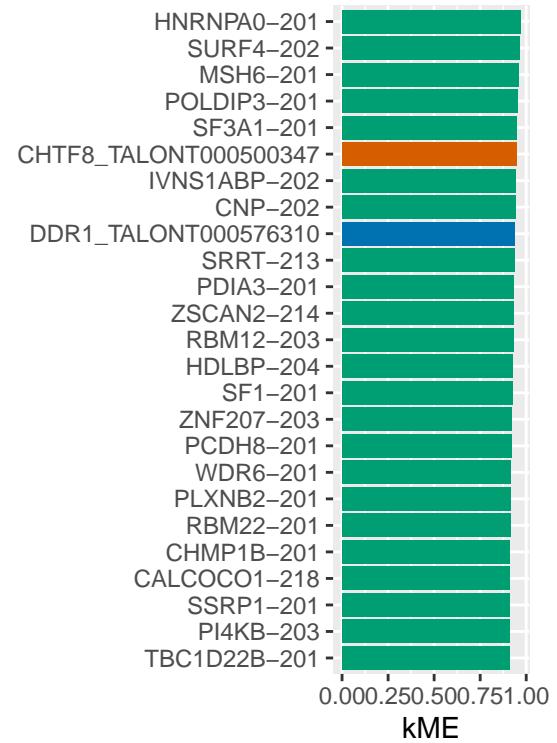
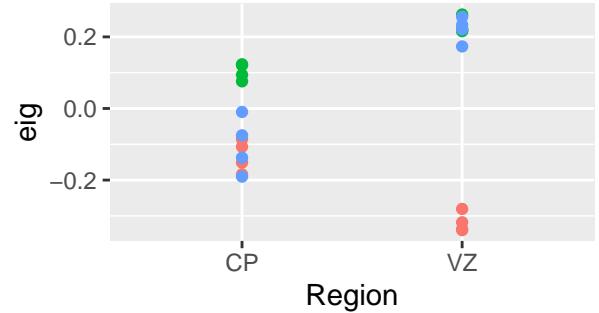


Zscore

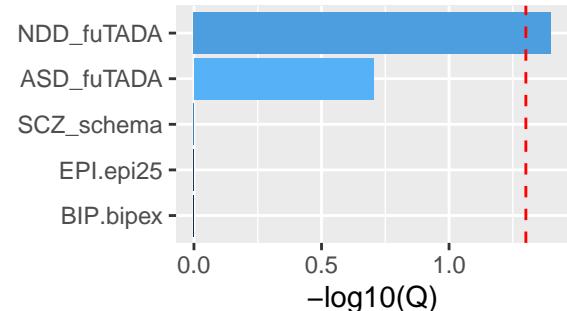
2  
1  
0  
-1



## Module 12: tan n=379

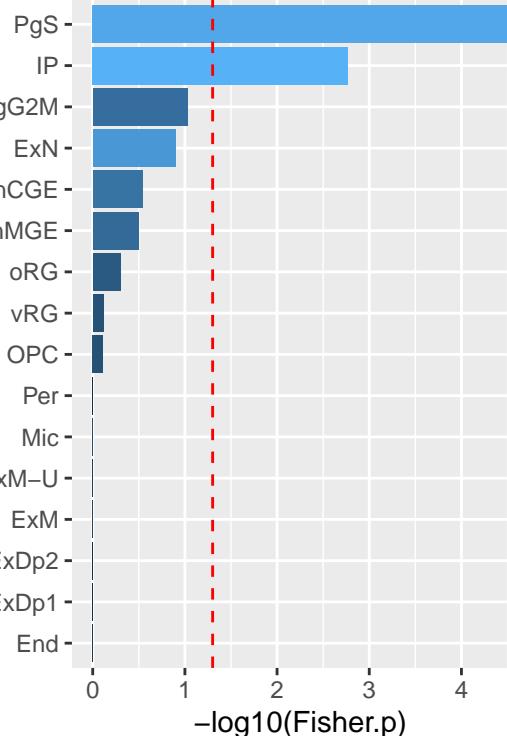


### Rare Var Enrichment

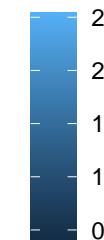


### Subject

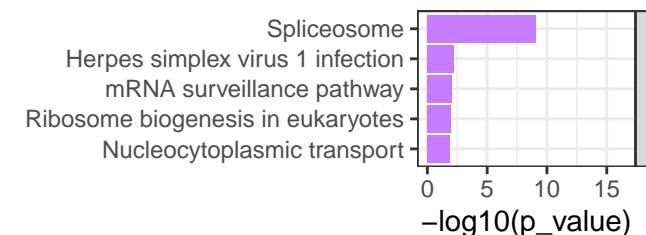
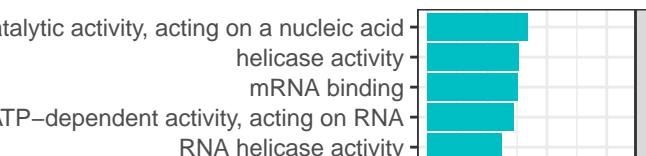
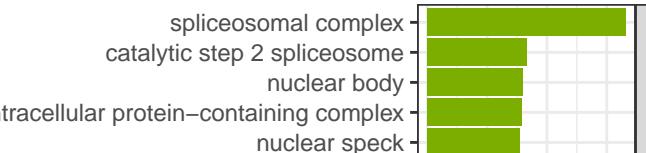
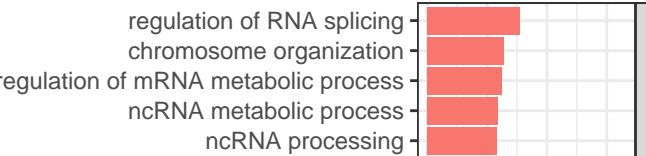
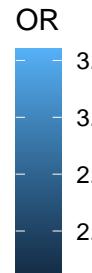
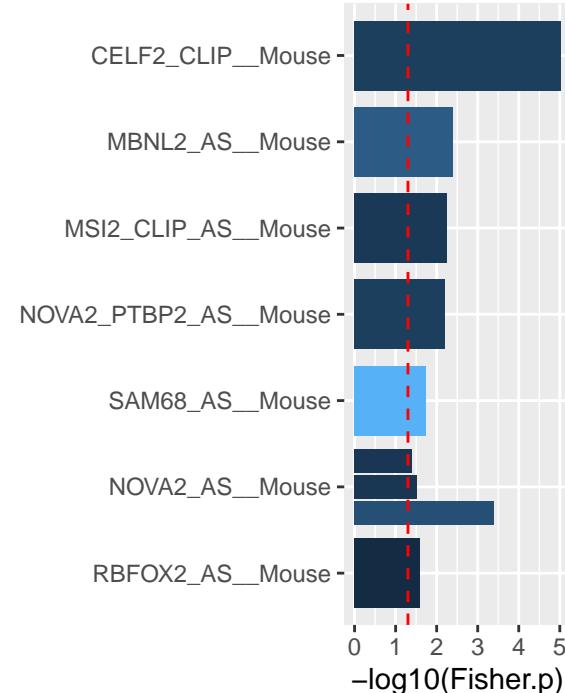
- 209 (red)
- 334 (green)
- 336 (blue)



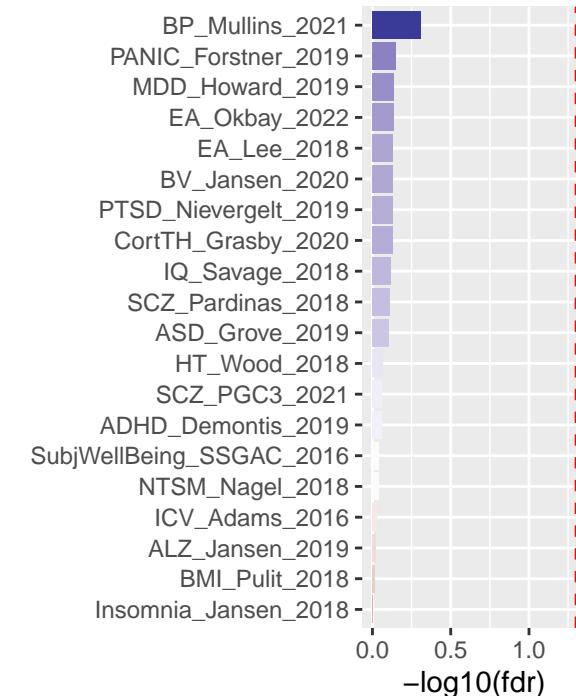
### OR



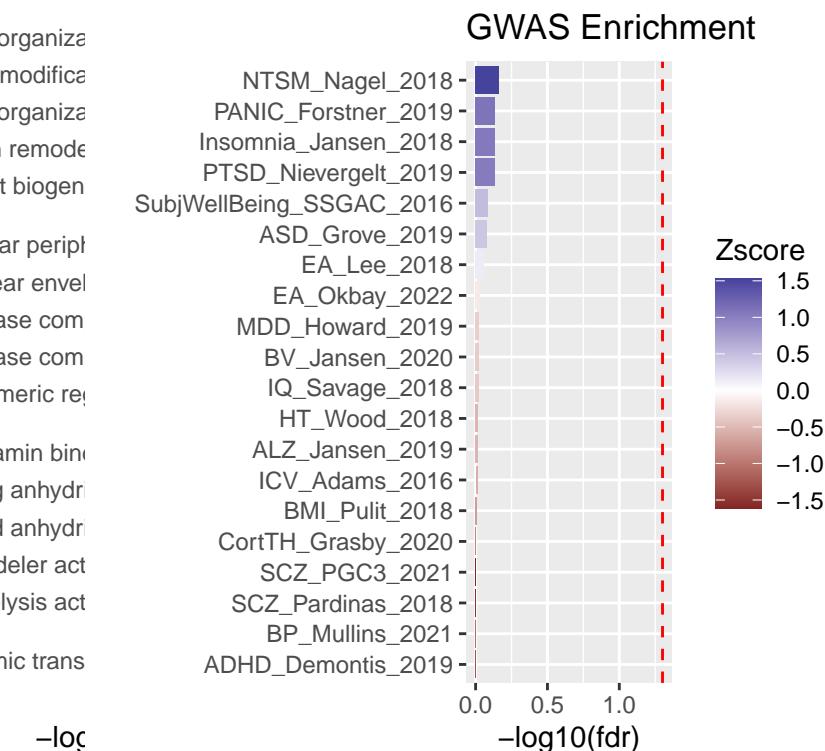
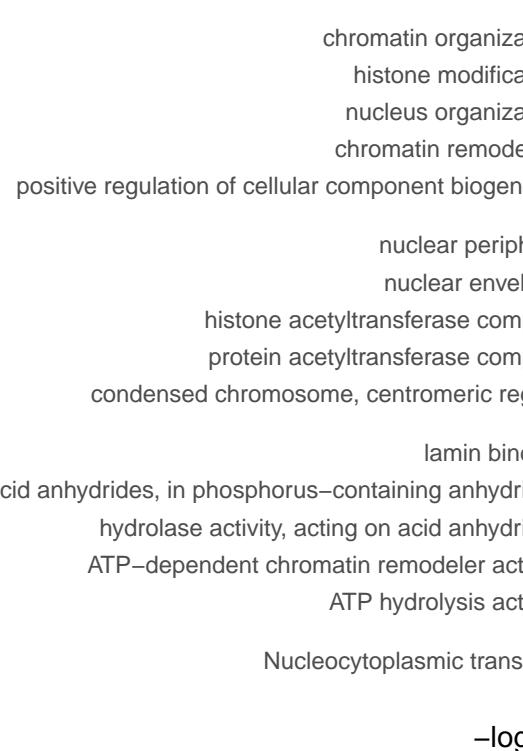
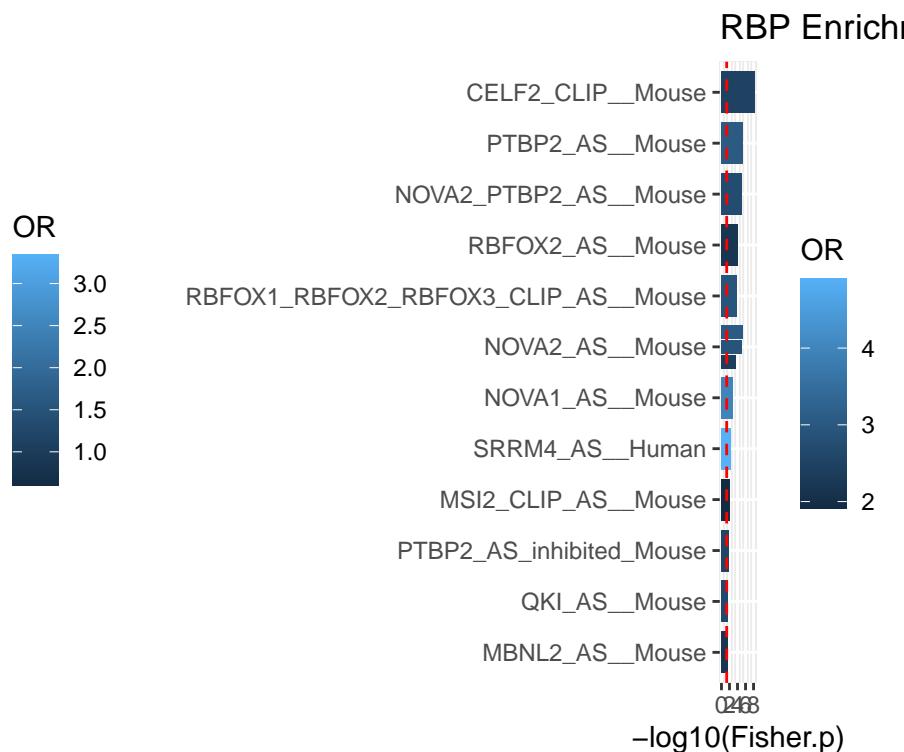
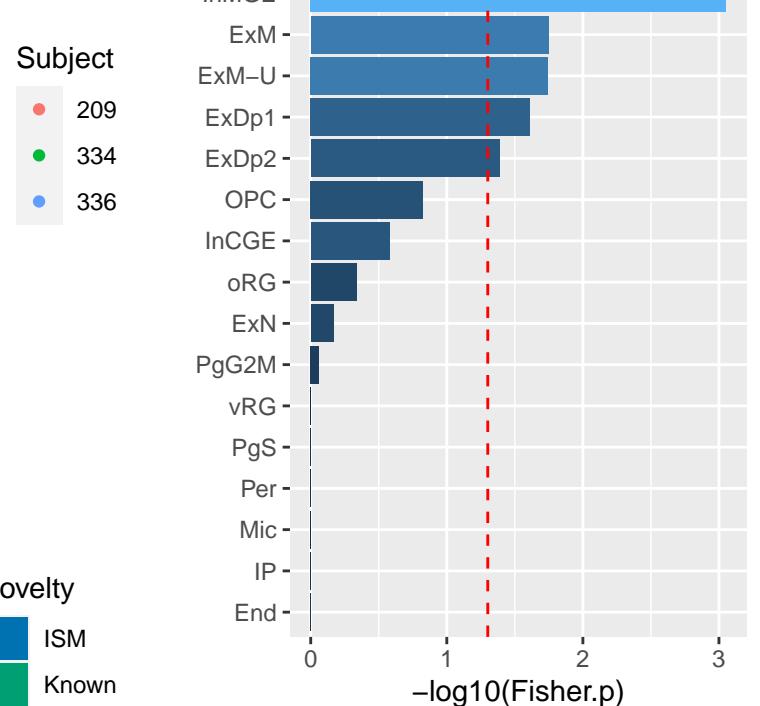
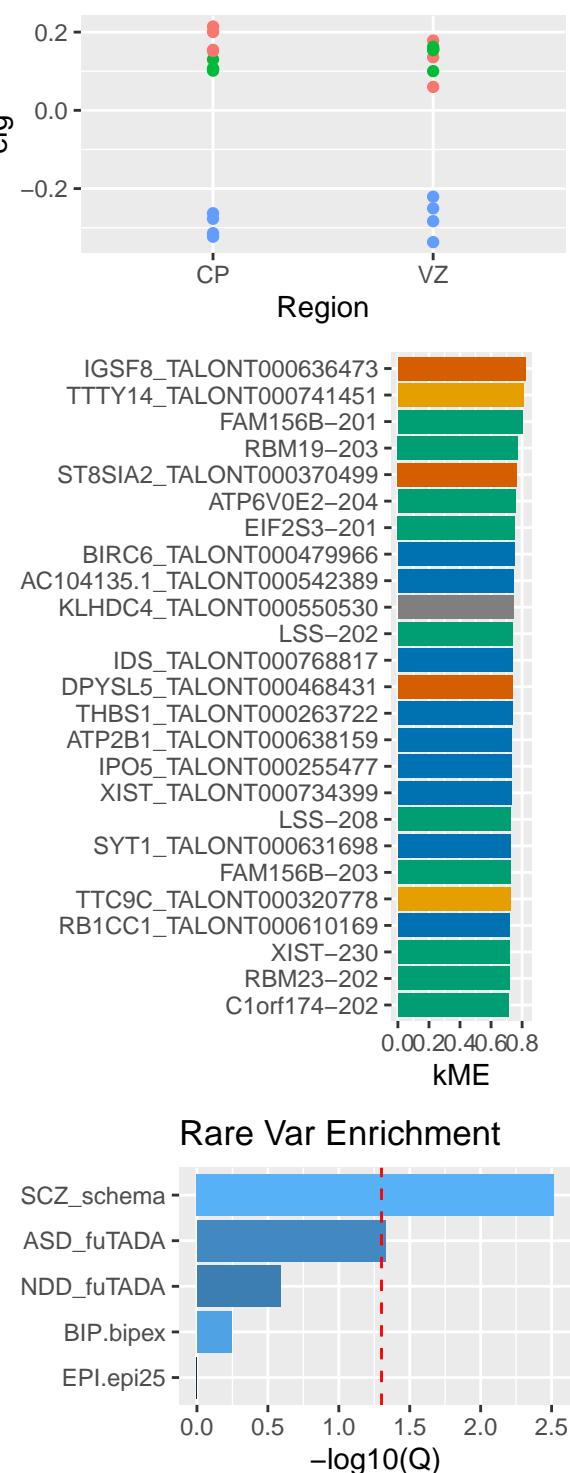
### RBP Enrichment



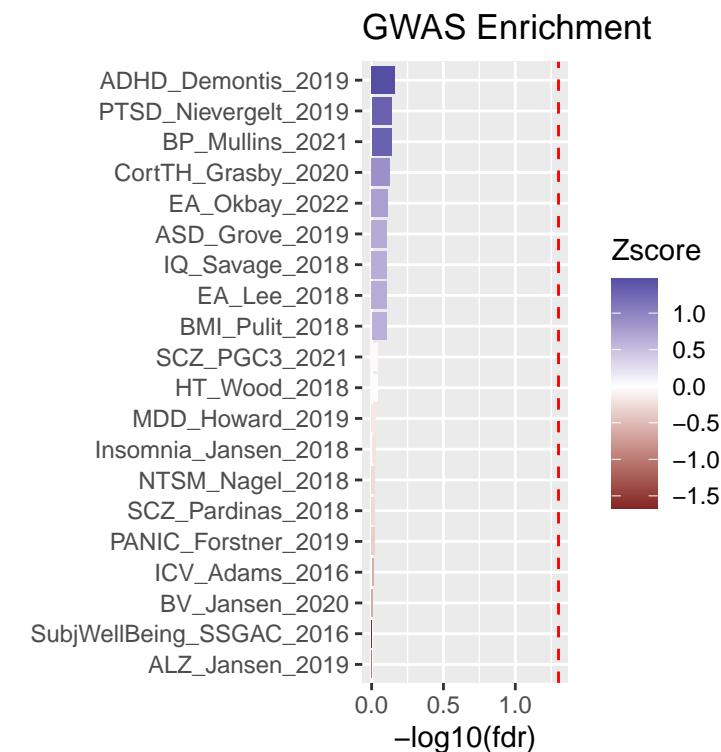
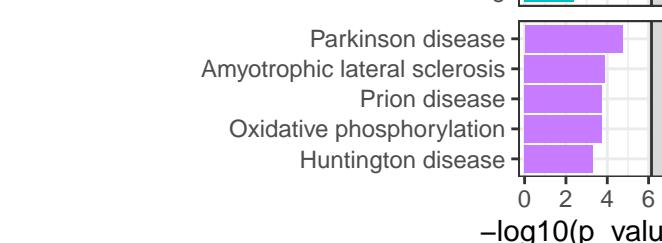
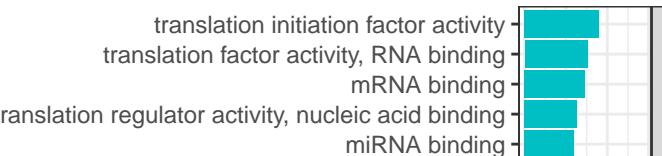
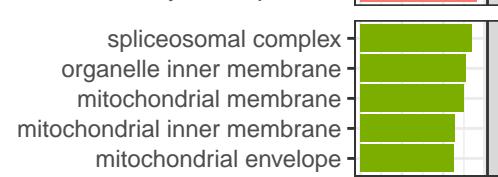
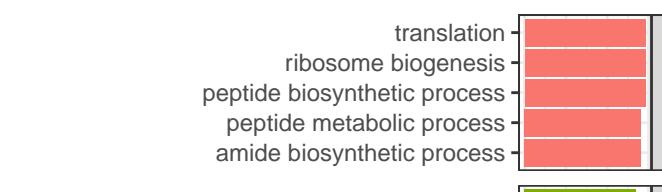
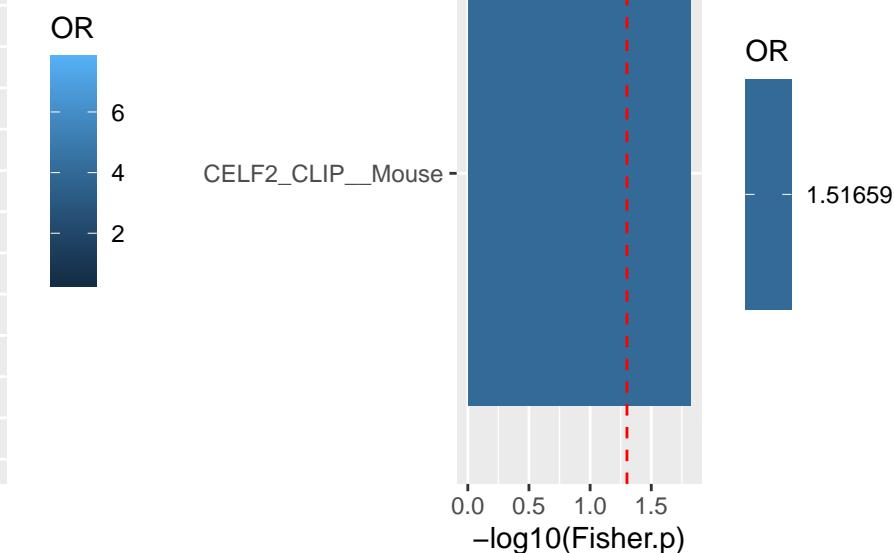
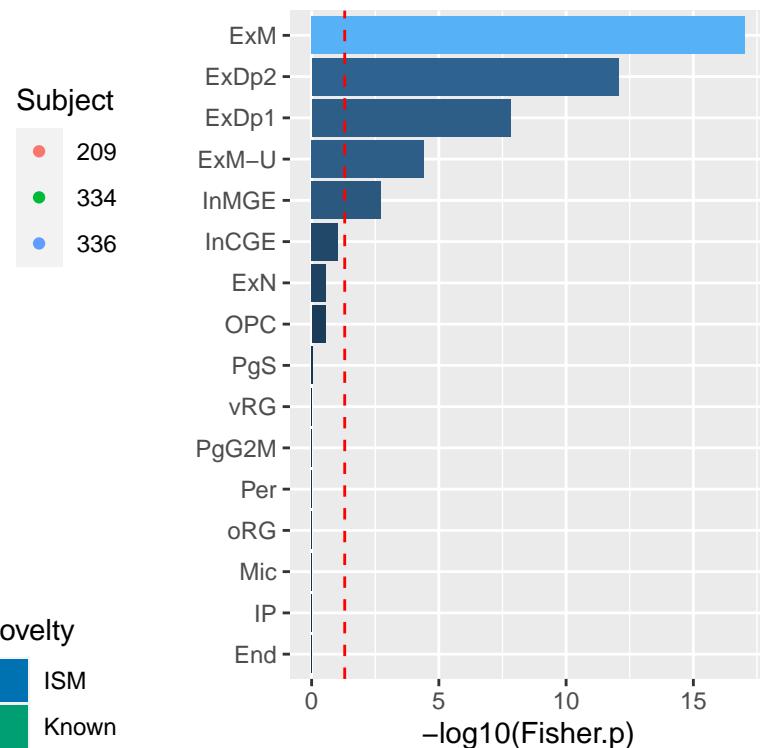
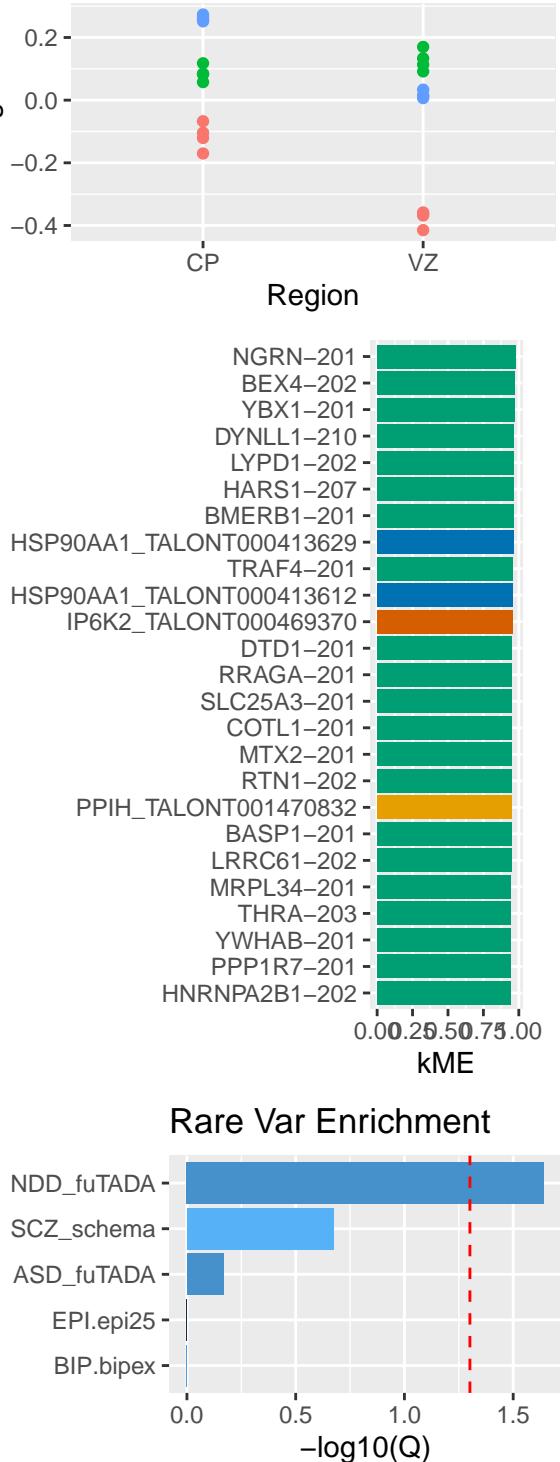
### GWAS Enrichment



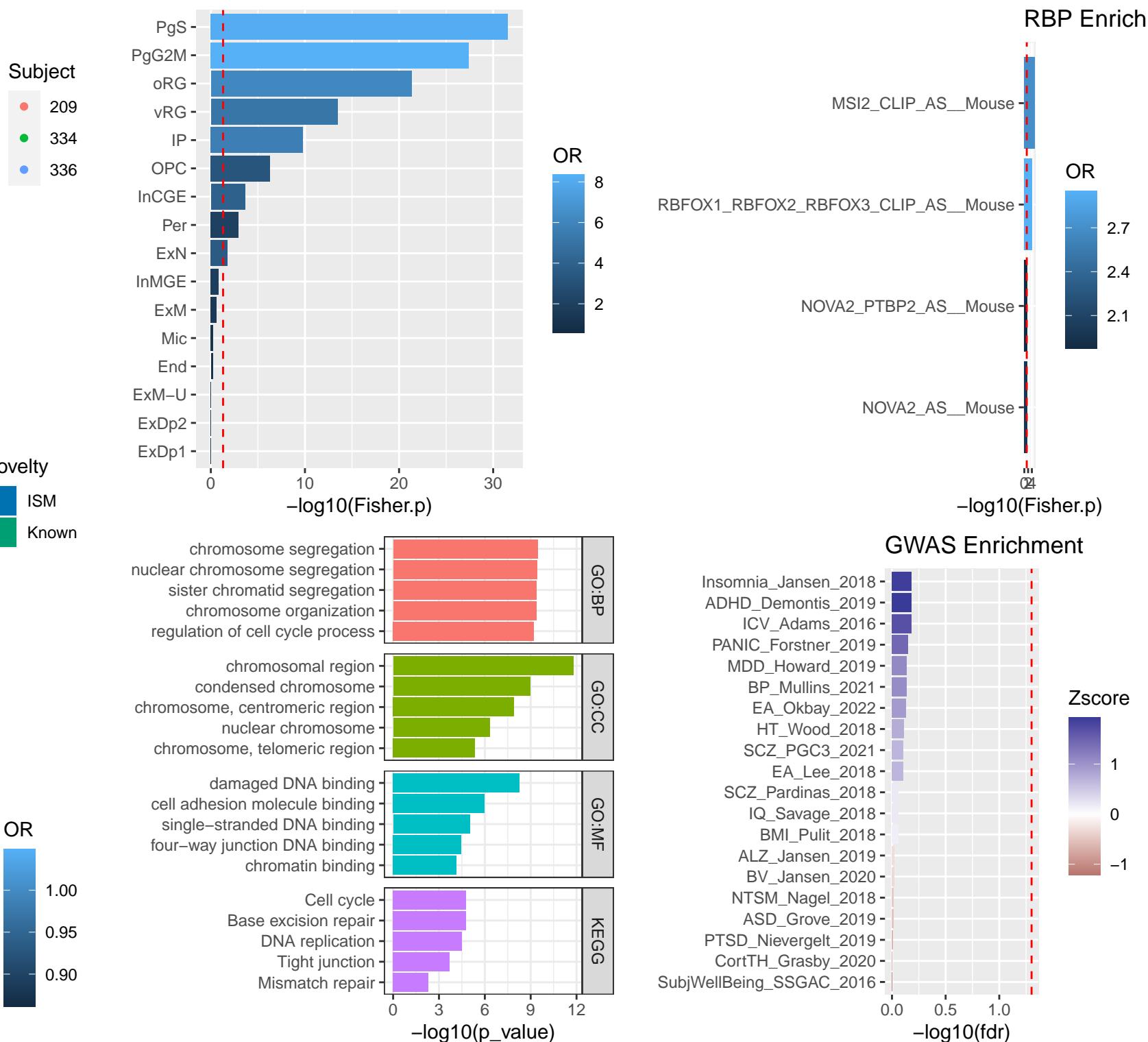
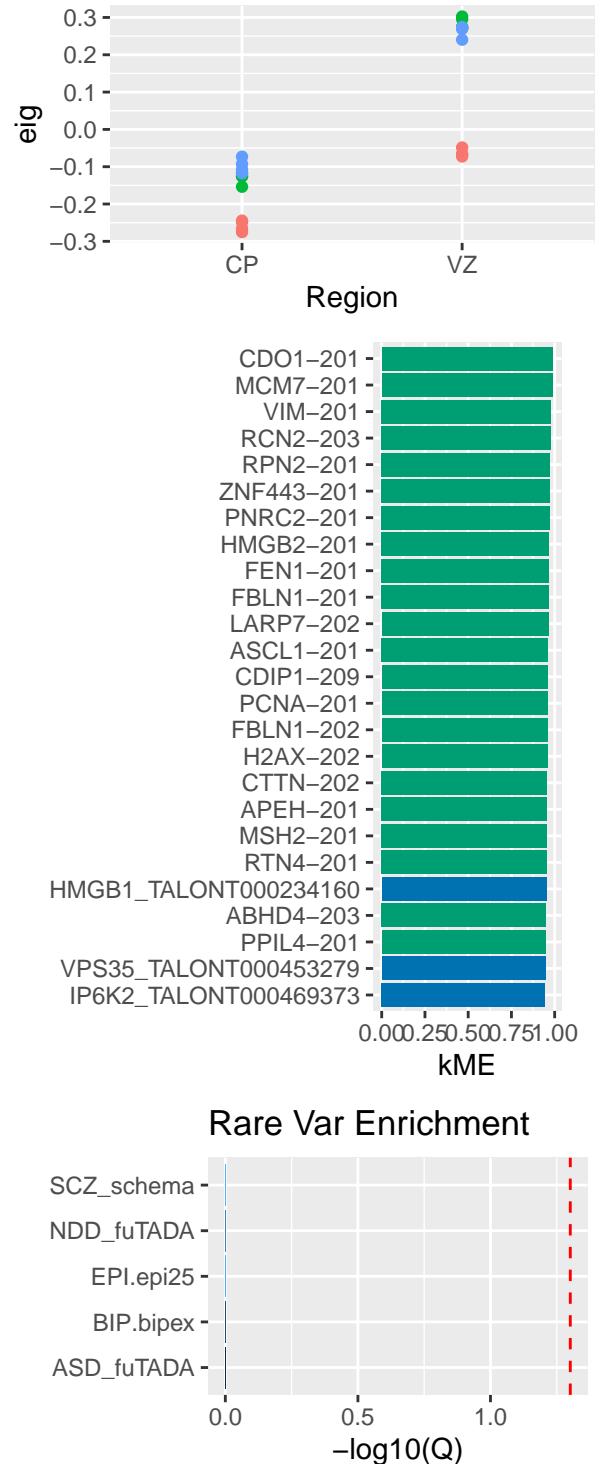
# Module 13: salmon n=346



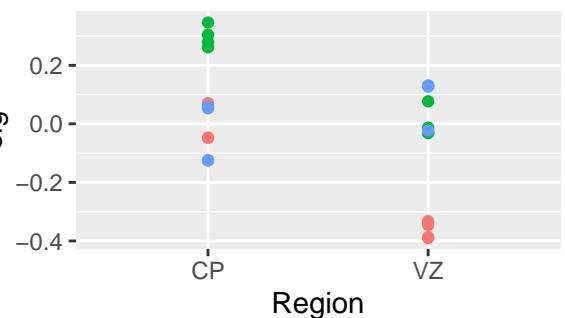
## Module 14: cyan n=340



# Module 15: midnightblue n=286



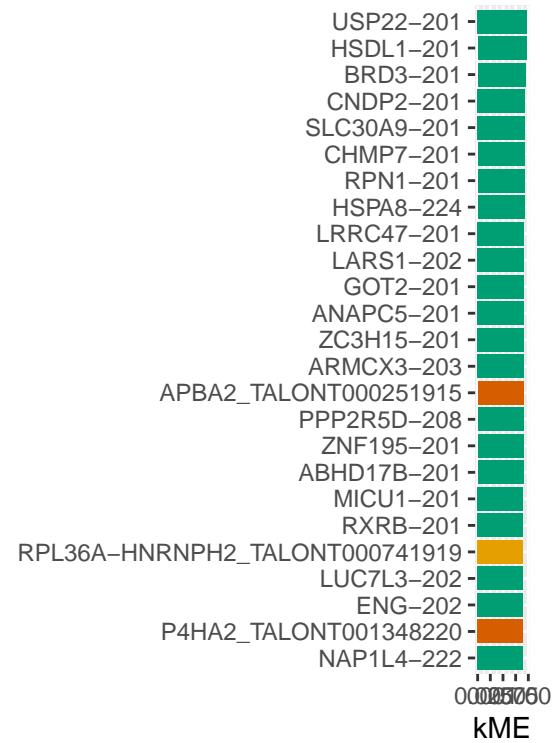
## Module 16: lightcyan n=274



Subject

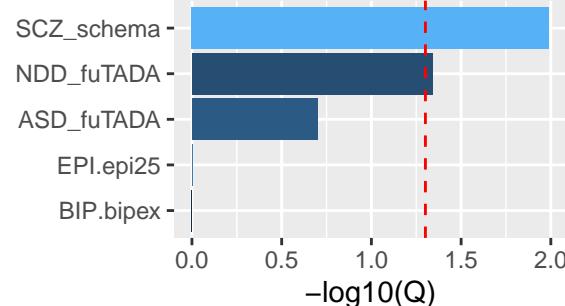
- 209
- 334
- 336

Region



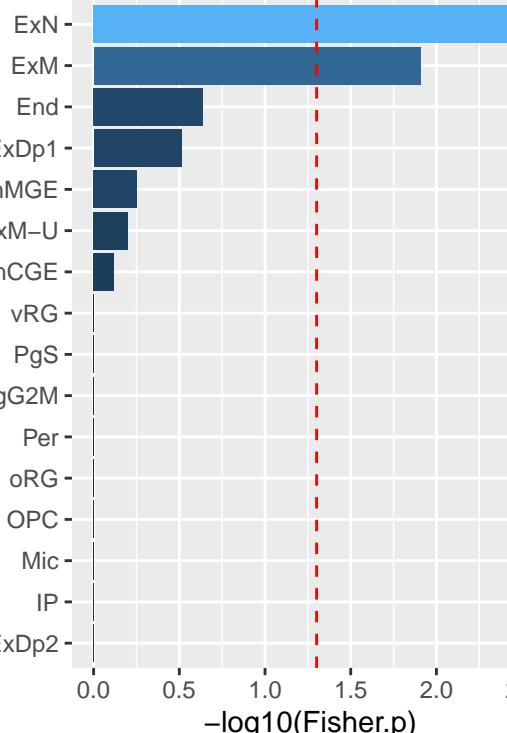
kME

Rare Var Enrichment



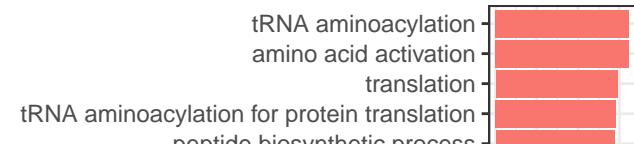
OR

- 1.0
- 1.1
- 1.2
- 1.3

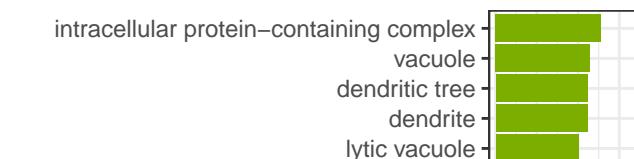


OR

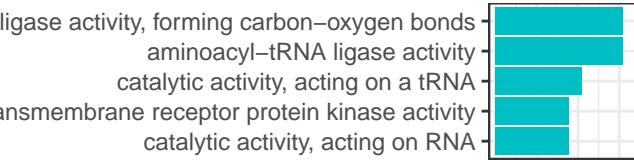
- 1
- 2
- 3
- 4



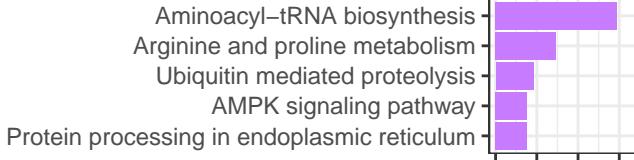
GO:BP



GO:CC

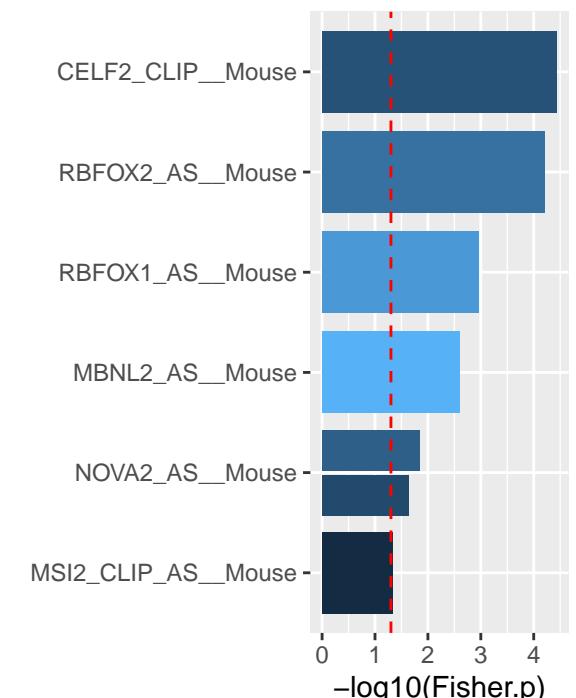


GO:MF



KEGG

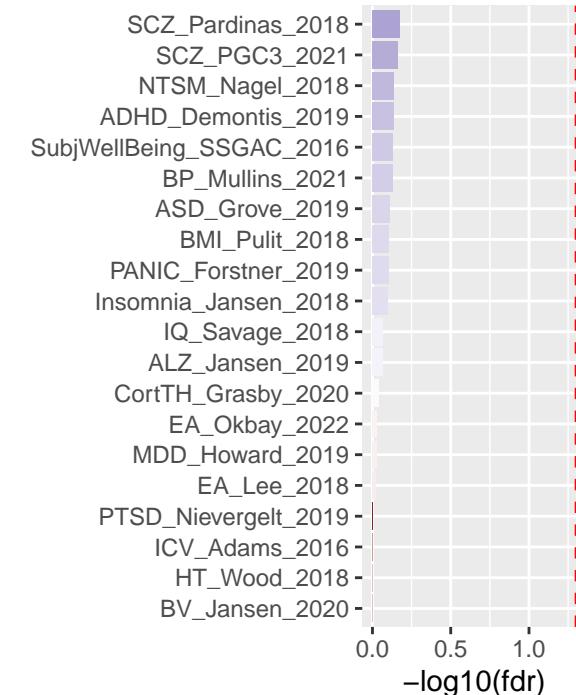
## RBP Enrichment



OR

- 1.75
- 2.00
- 2.25
- 2.50

## GWAS Enrichment

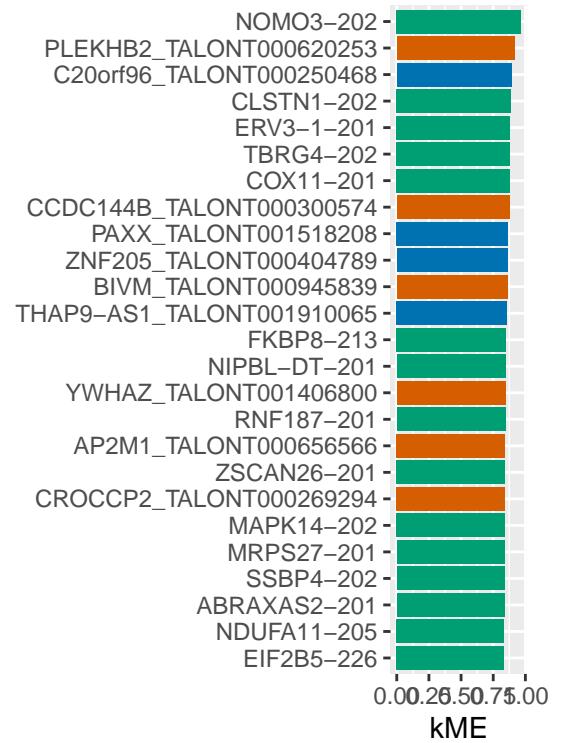
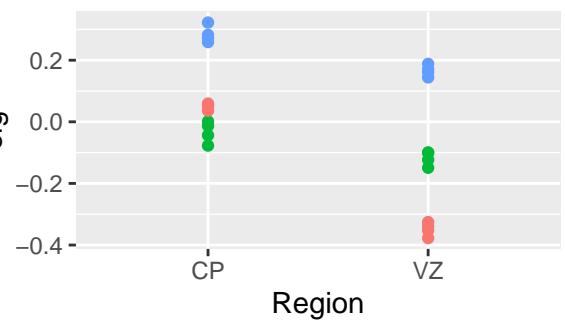


Zscore

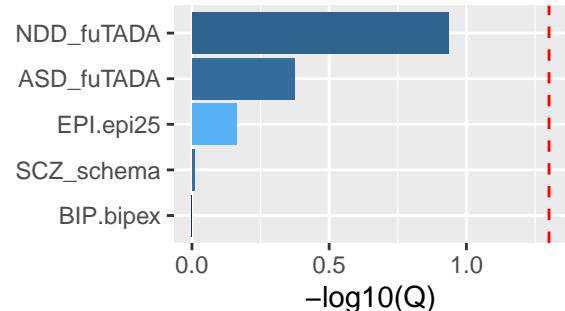
- 3
- 2
- 1
- 0
- 1

-log10(fdr)

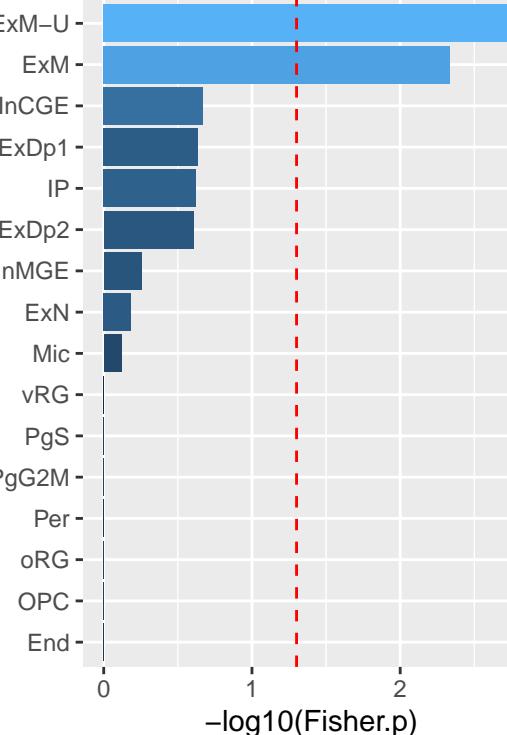
## Module 17: grey60 n=274



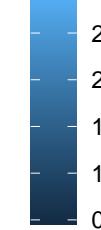
### Rare Var Enrichment



### Subject



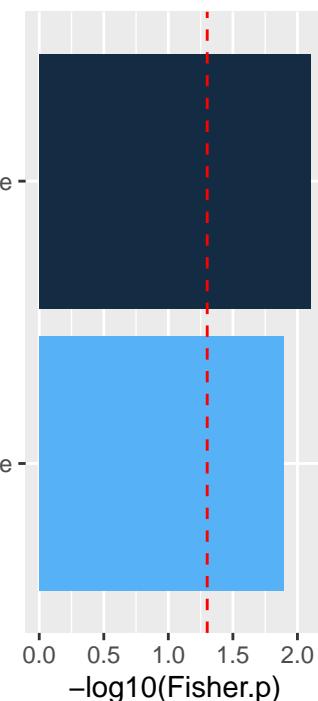
### OR



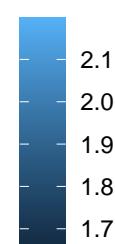
CELF2\_CLIP\_\_Mouse

RBFOX1\_AS\_\_Mouse

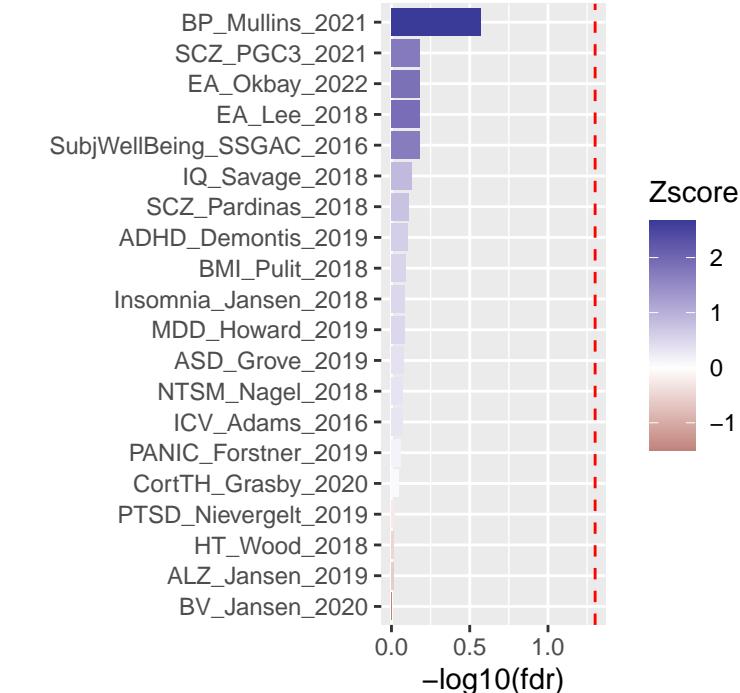
## RBP Enrichment



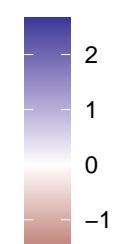
### OR



## GWAS Enrichment



### Zscore

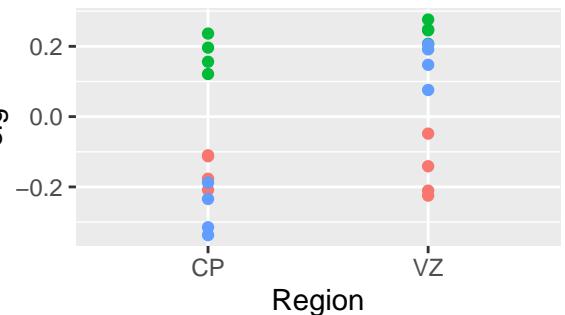


regulation of postsynaptic membrane neurotransmitter receptor activity, negative regulation of nuclear-transcribed mRNA catabolic process, nonsense-mediated mRNA decay, negative regulation of mRNA metabolism process, negative regulation of mRNA catabolic process, establishment of protein localization to postsynaptic membrane, synaptic transmission, mitochondrial ribosome, mitochondrial electron transport chain, glutamatergic synapse, disordered domain specific protein binding, cytoskeletal protein binding, tubulin binding, transferase activity, transferring phosphorus-containing groups, kinase activity, Fatty acid metabolic process, Oocyte development, Huntington's disease

transferase activity, transferring phosphorus-containing groups, kinase activity

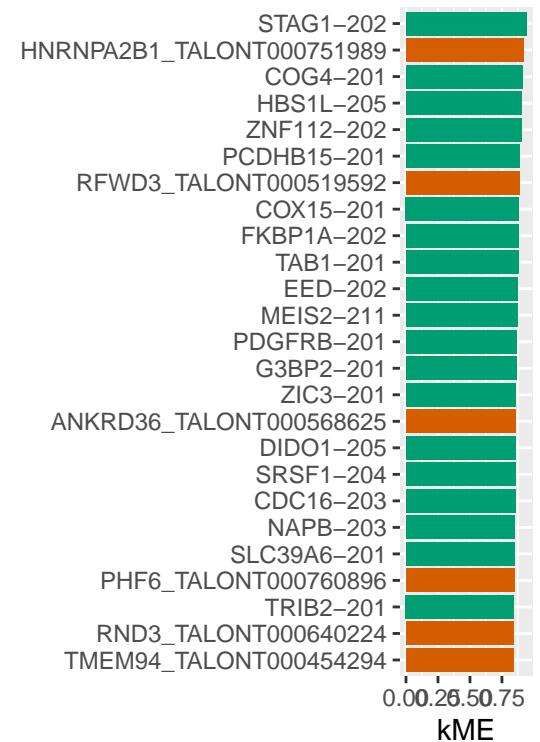
Fatty acid metabolic process, Oocyte development, Huntington's disease

## Module 18: lightgreen n=266



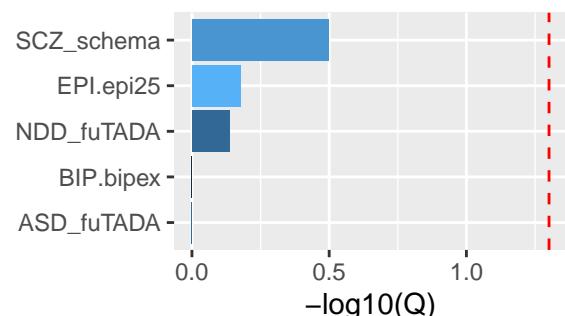
Subject

- 209
- 334
- 336



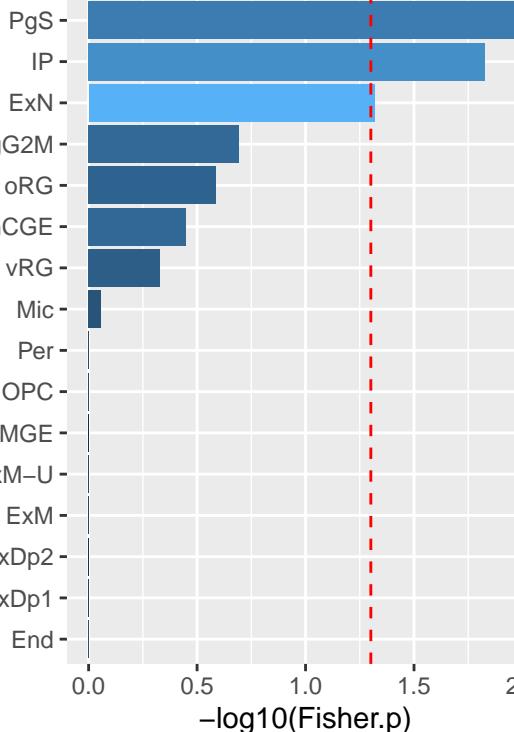
KME

### Rare Var Enrichment



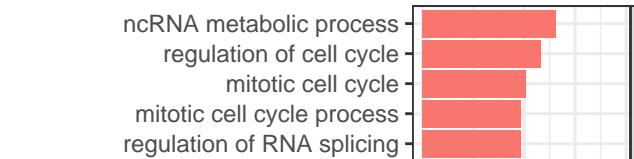
OR

- 0.8
- 0.9
- 1.0
- 1.1
- 1.2

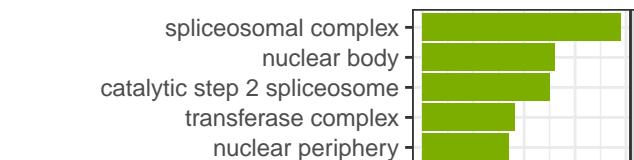


OR

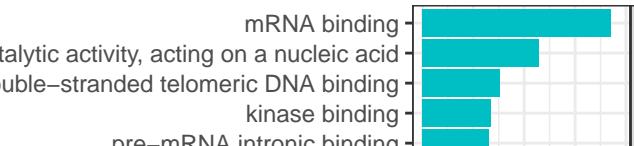
- 0
- 1
- 2
- 3
- 4



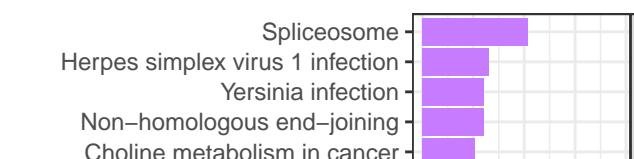
GO:BP



GO:CC

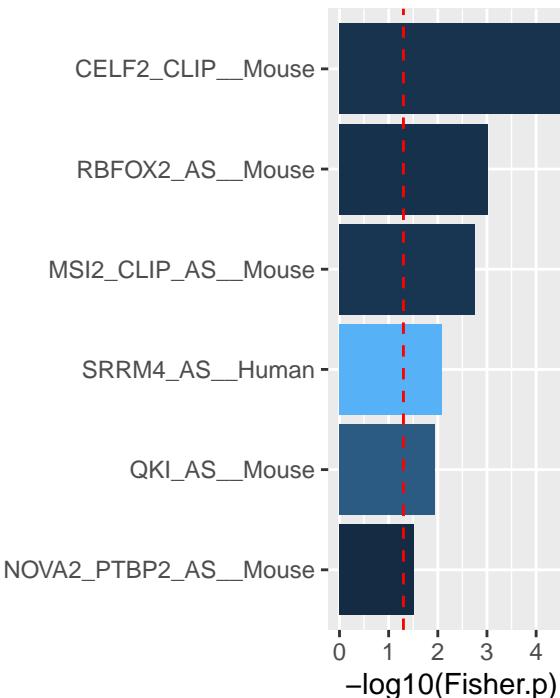


GO:MF



KEGG

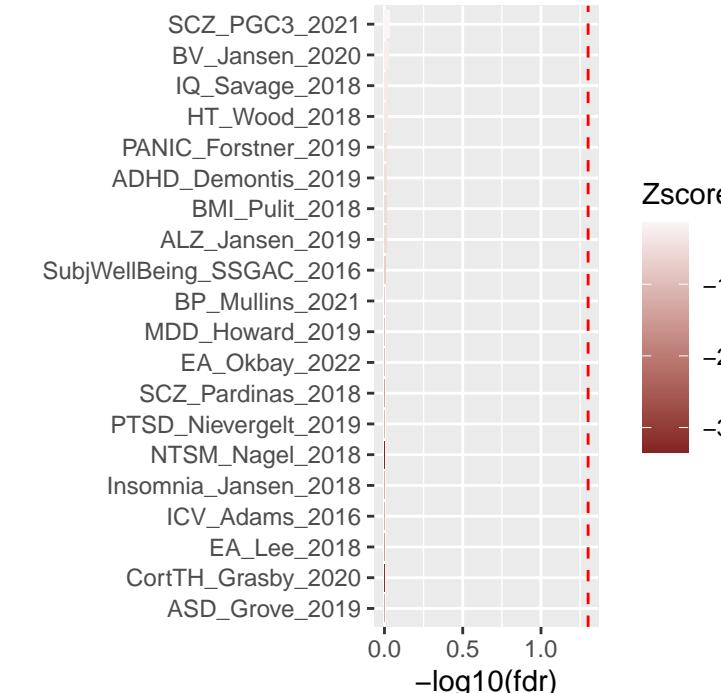
## RBP Enrichment



OR

- 2
- 3
- 4

## GWAS Enrichment

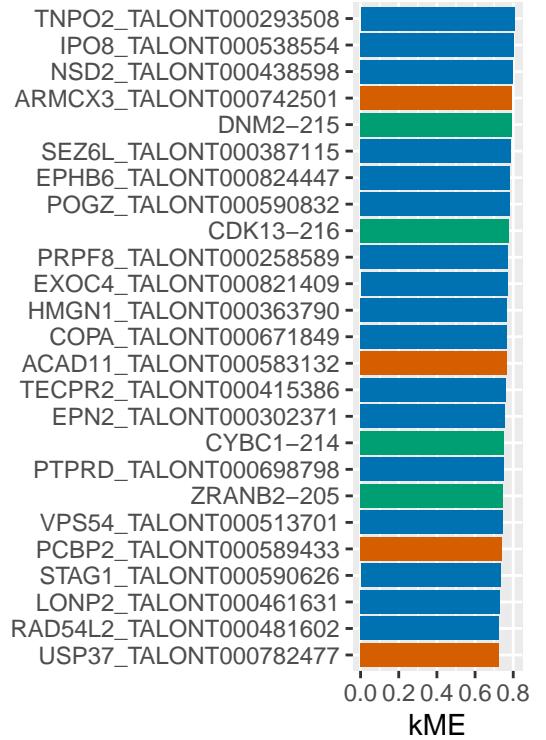
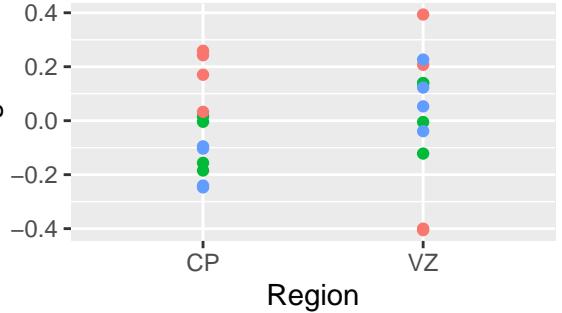


Zscore

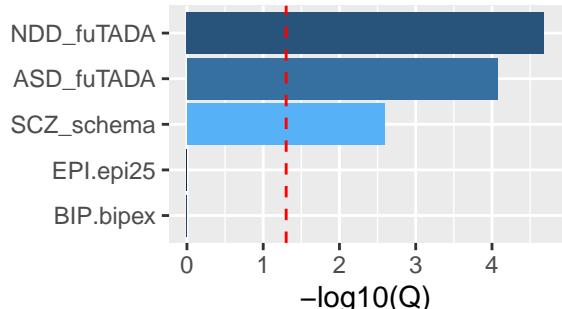
- -1
- -2
- -3

-log10(fdr)

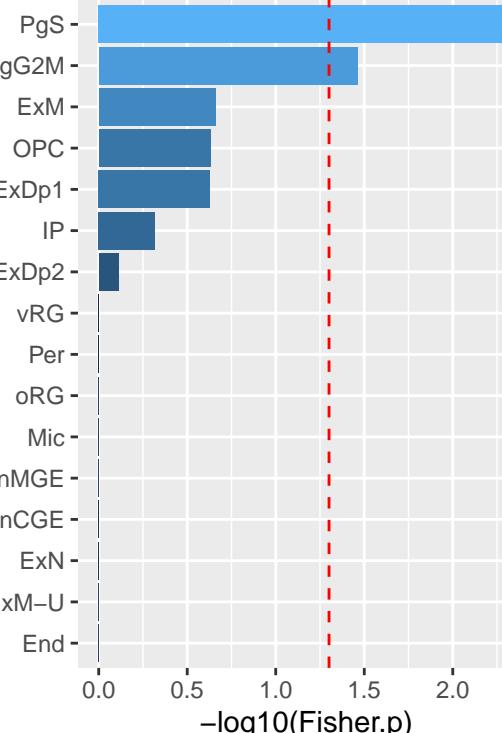
# Module 19: lightyellow n=264



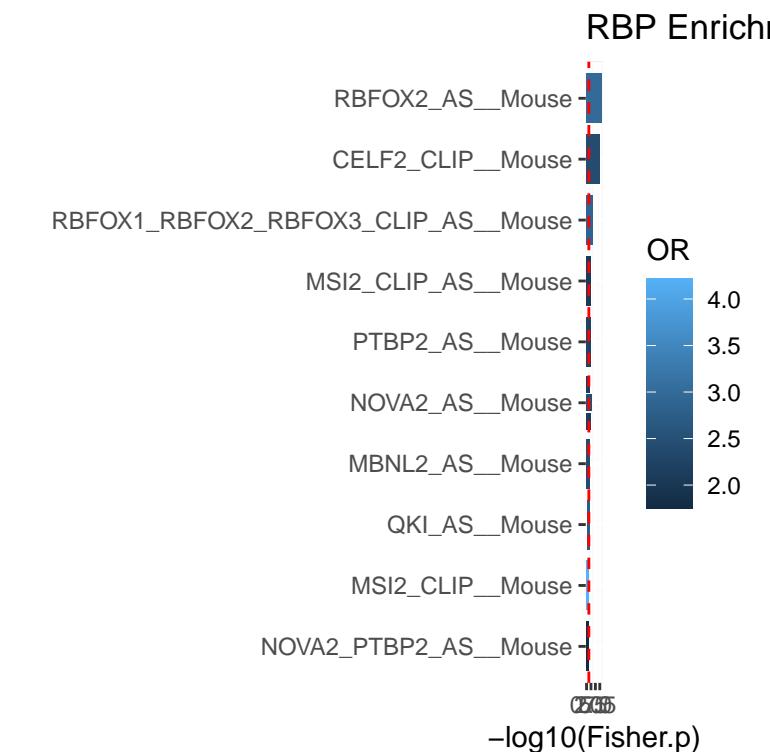
## Rare Var Enrichment



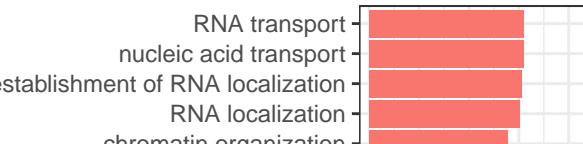
Subject  
209  
334  
336



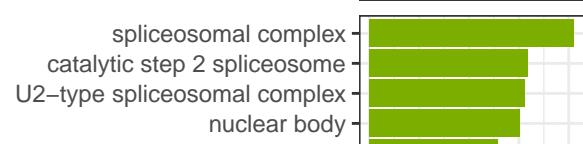
OR



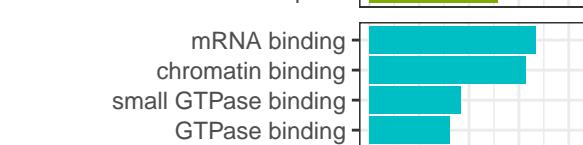
OR



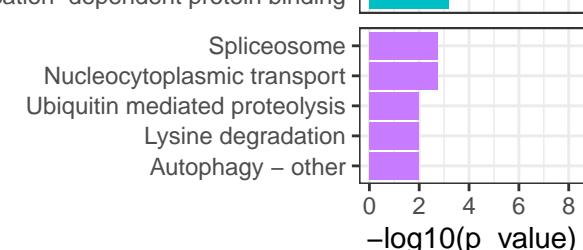
GO:BP



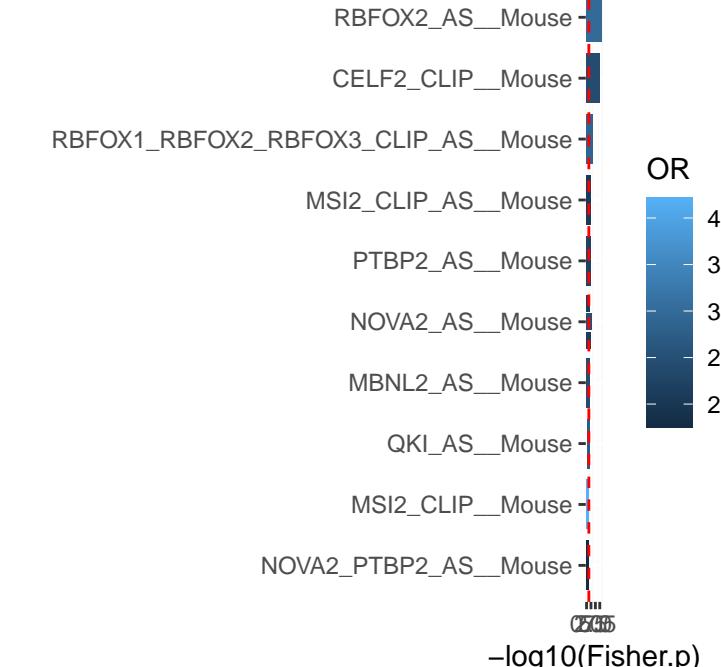
GO:CC



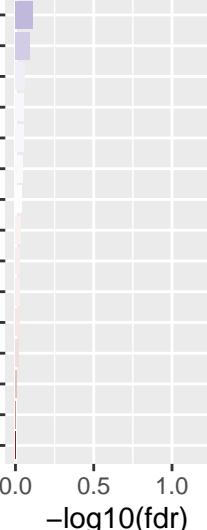
GO:MF



KEGG

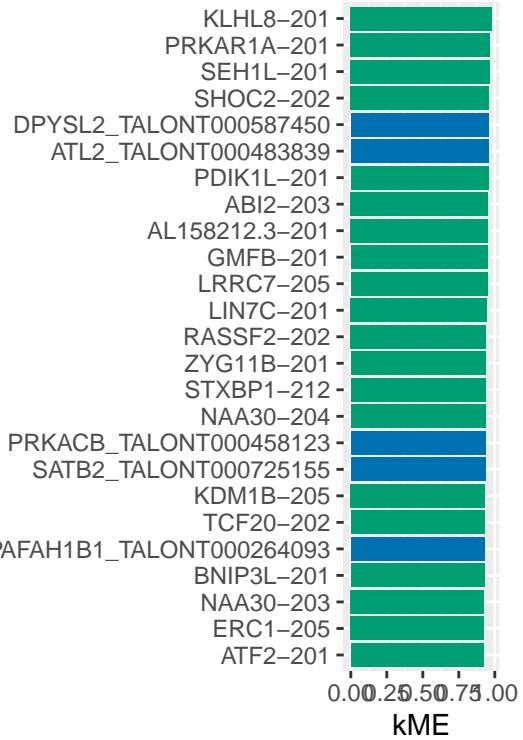
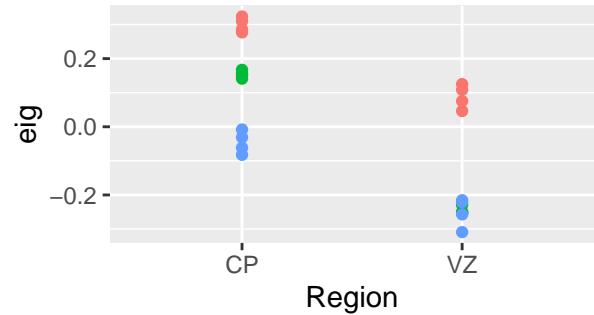


Zscore

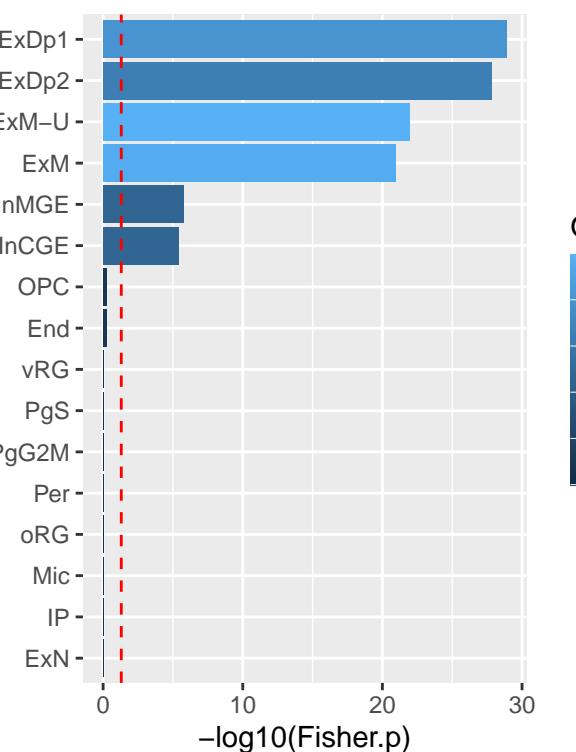
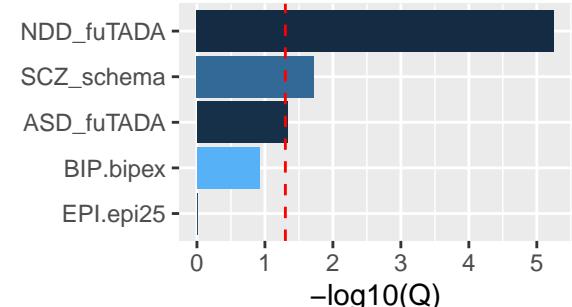


-log10(fdr)

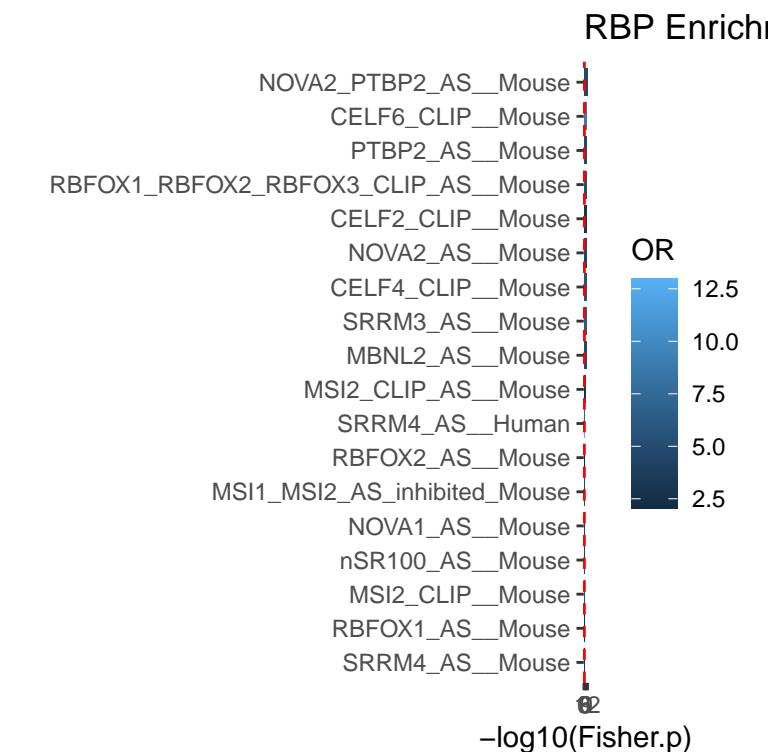
# Module 20: royalblue n=256



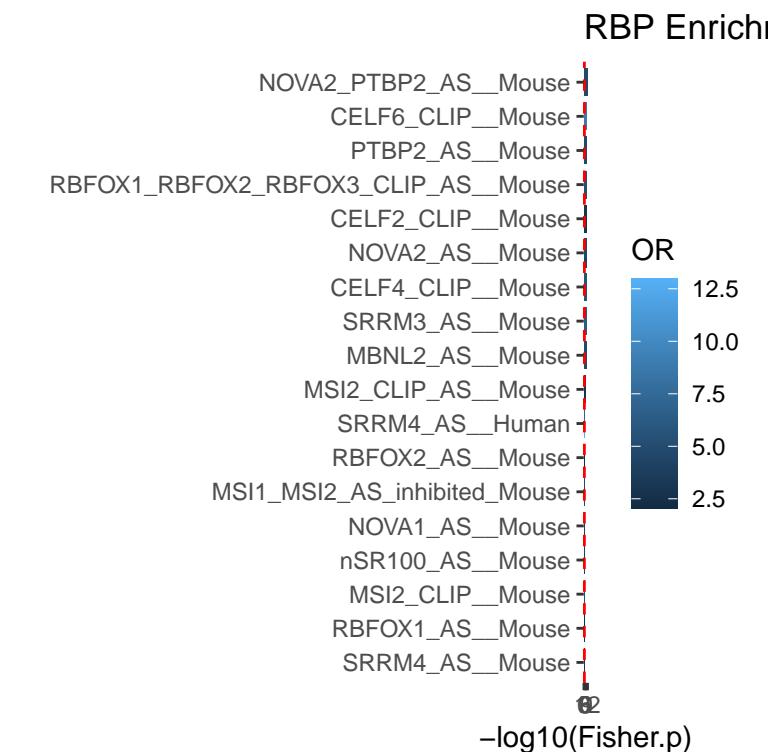
## Rare Var Enrichment



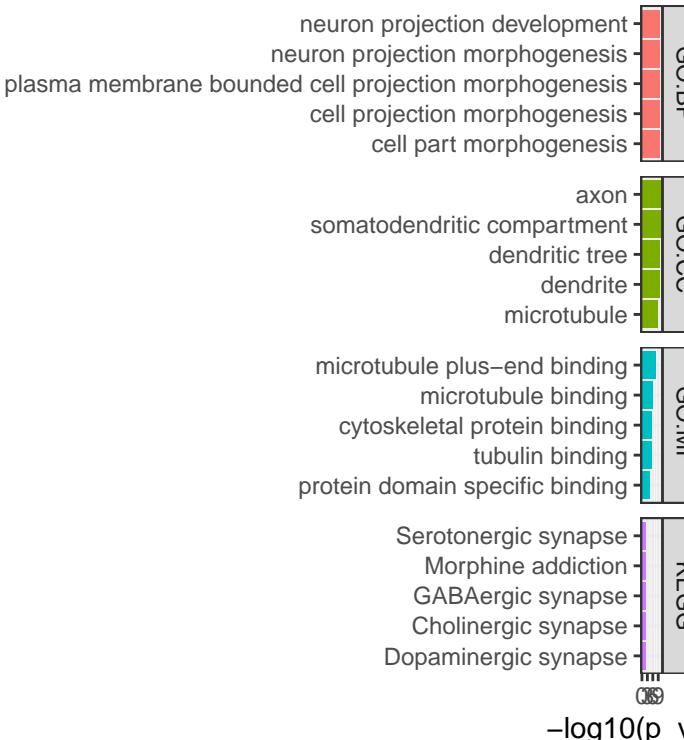
OR



OR



OR

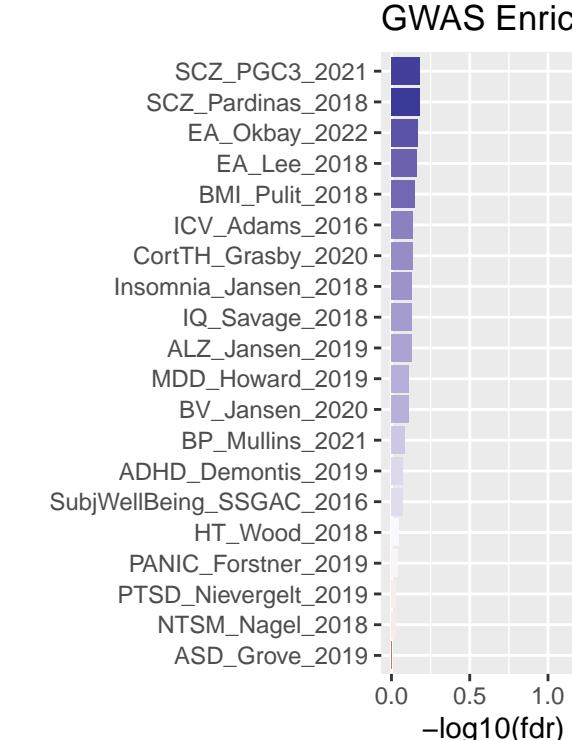


GO:BP

GO:CC

GO:MF

KEGG



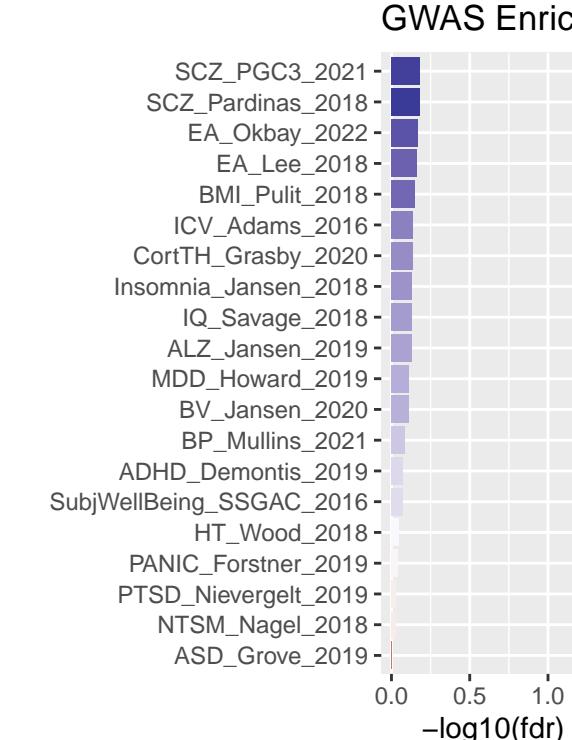
GO:BP

GO:CC

GO:MF

KEGG

Zscore



GO:BP

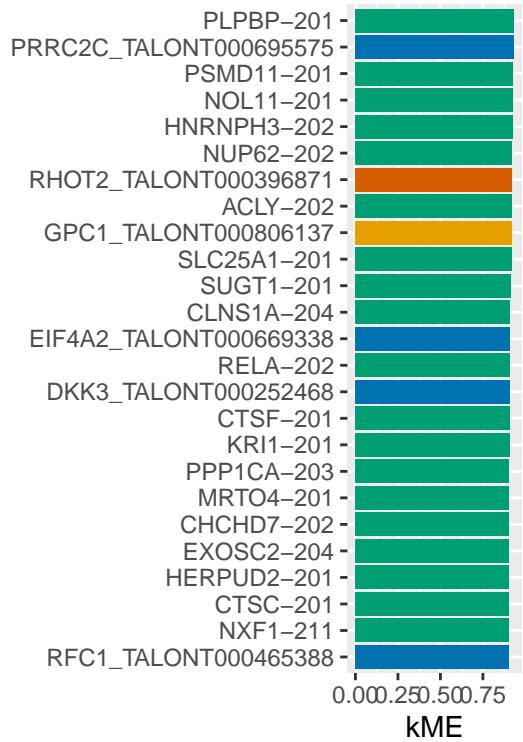
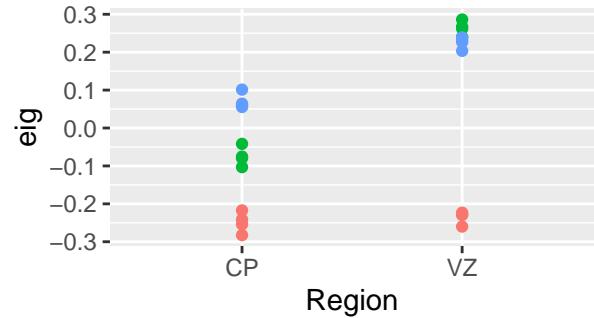
GO:CC

GO:MF

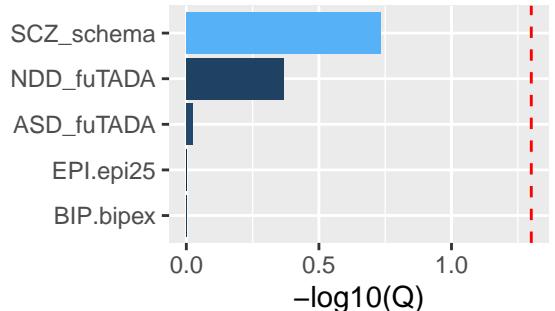
KEGG

-log10(fdr)

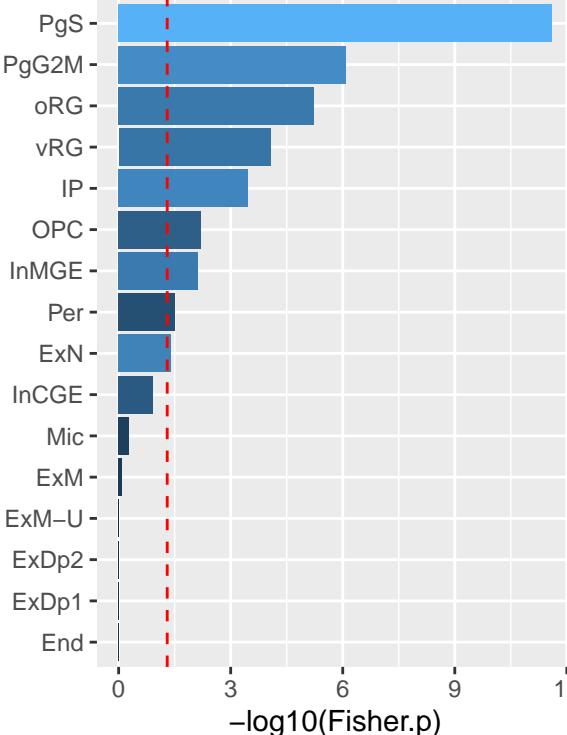
# Module 21: darkred n=247



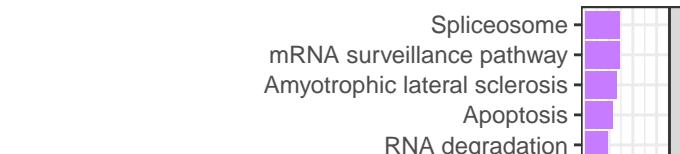
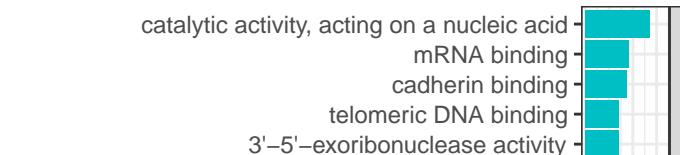
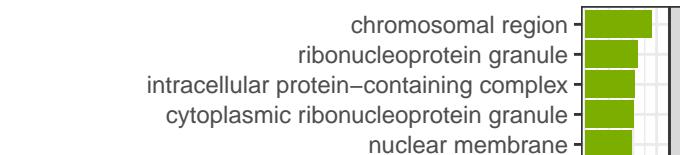
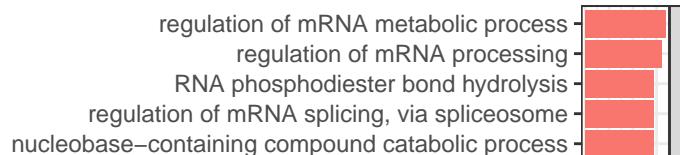
## Rare Var Enrichment



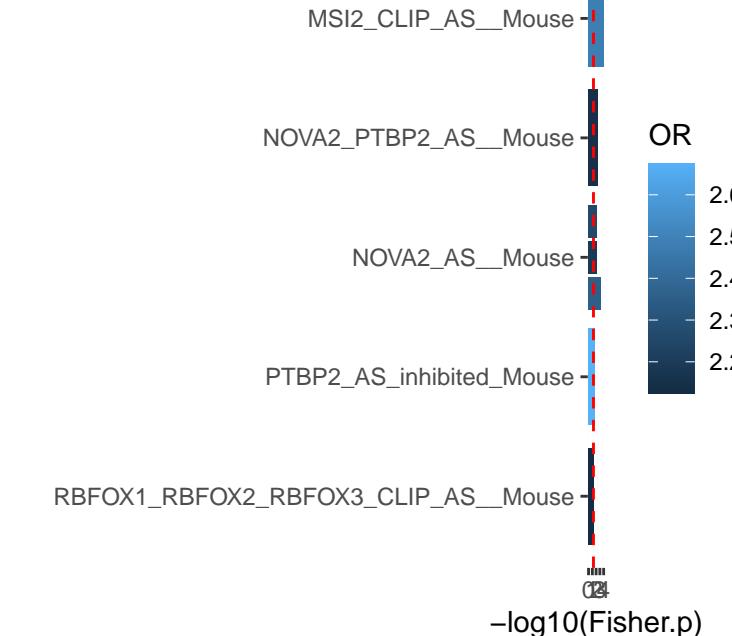
Subject  
209  
334  
336



OR  
4  
3  
2  
1

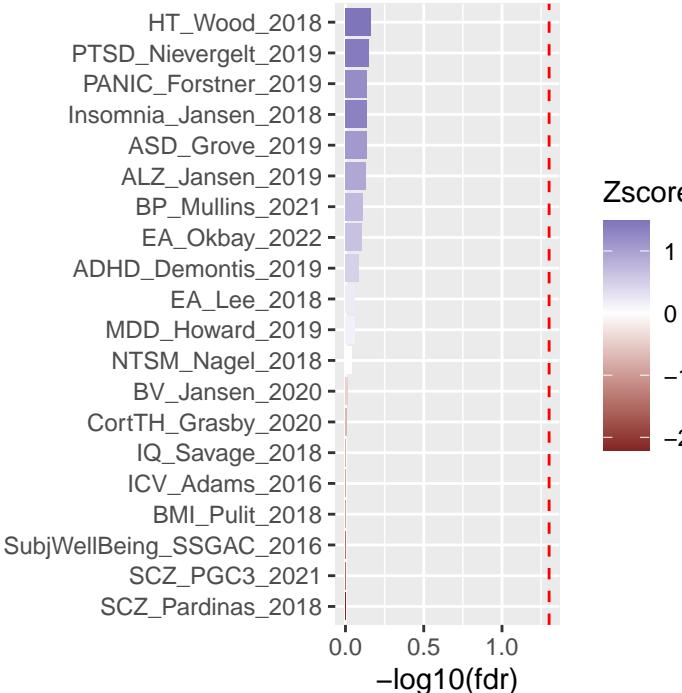


RBP Enrich



OR  
2.6  
2.5  
2.4  
2.3  
2.2

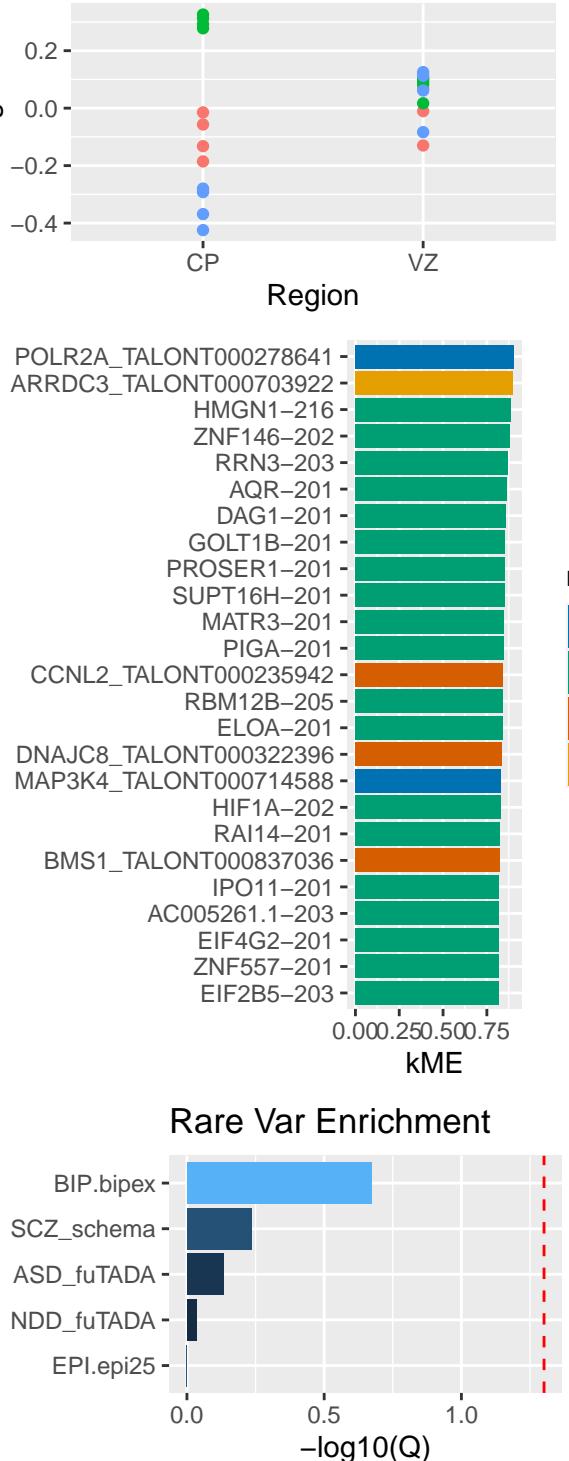
## GWAS Enrichment



Zscore  
1  
0  
-1  
-2

-log10(fdr)

## Module 22: darkgreen n=240

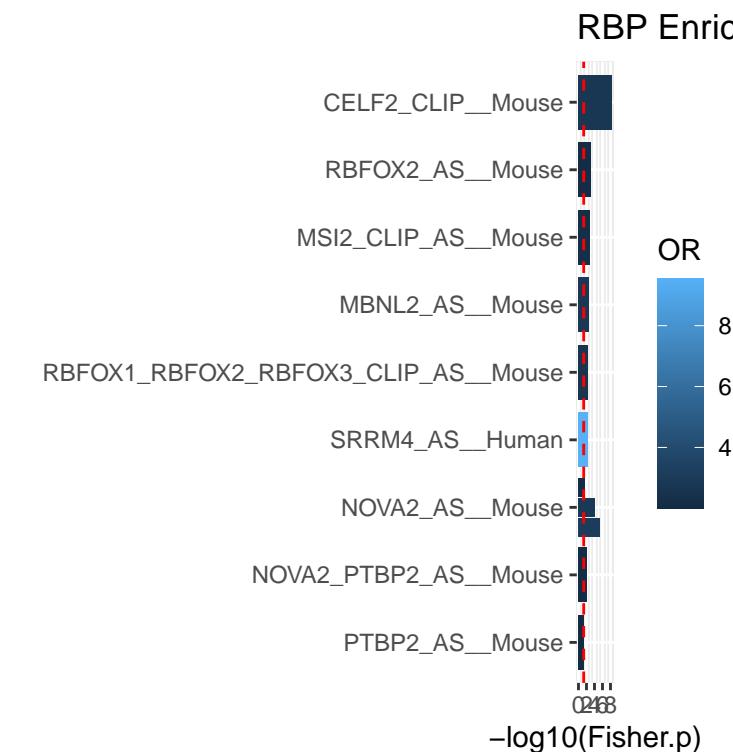
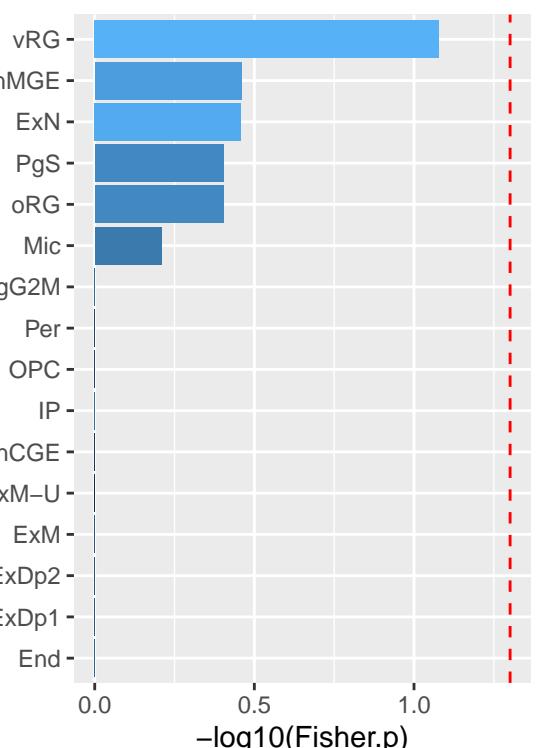


Subject

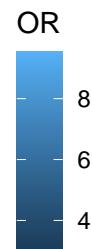
- 209
- 334
- 336

novelty

- ISM
- Known
- NIC
- NNC



RBP Enrich



regulation of RNA splicing  
protein modification by small protein conjugation or removal  
RNA transport  
nucleic acid transport  
establishment of RNA localization

nuclear body  
nuclear speck  
spliceosomal complex  
intracellular protein-containing complex  
nuclear periphery

poly-purine tract binding  
single-stranded RNA binding  
mRNA binding  
poly(A) binding  
poly(G) binding

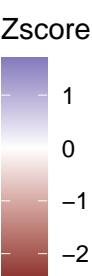
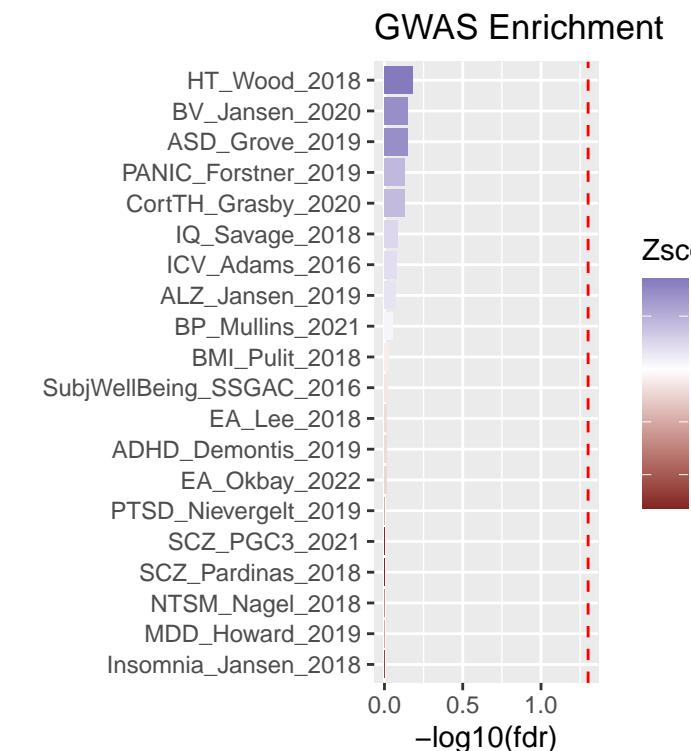
Herpes simplex virus 1 infection  
Nucleocytoplasmic transport  
Spliceosome  
Viral myocarditis  
Autophagy – animal

GO:BP

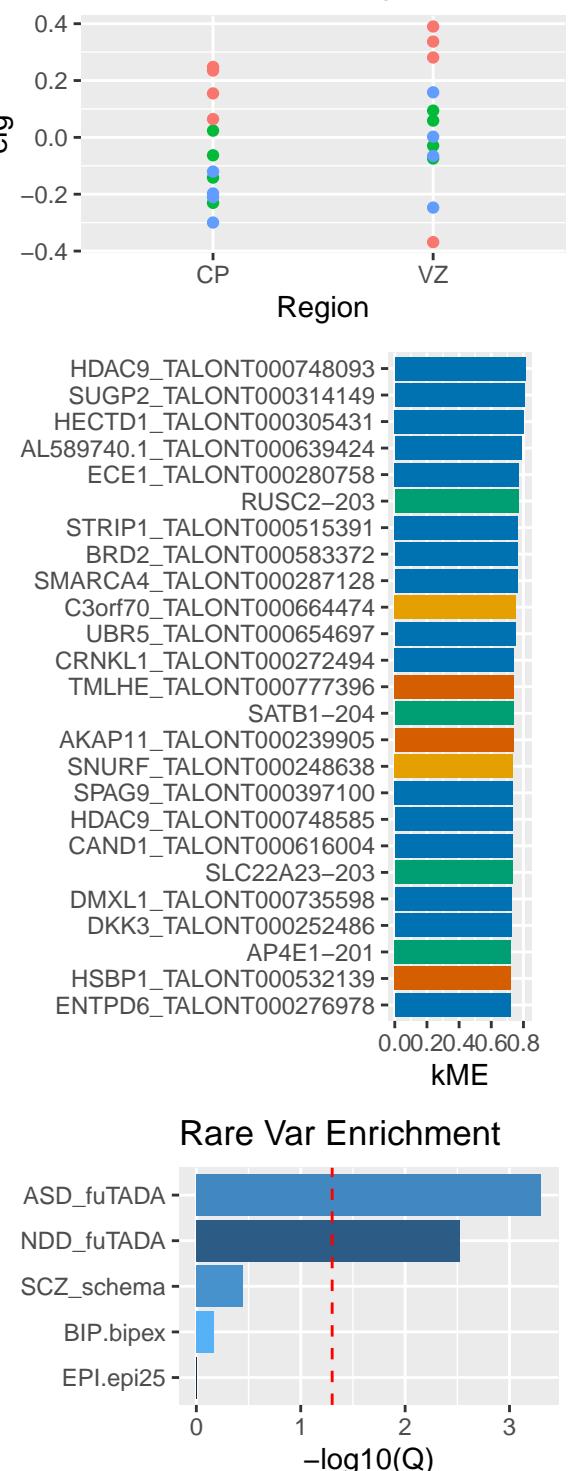
GO:CC

GO:MF

KEGG



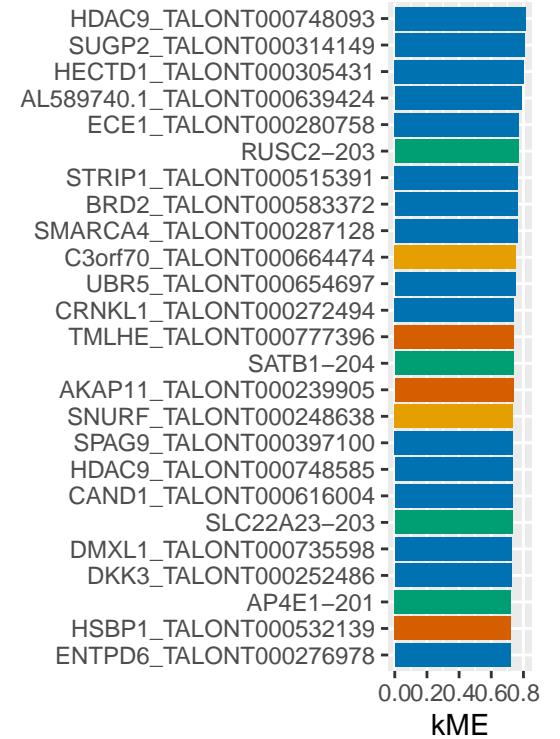
# Module 23: darkturquoise n=238



**Subject**

- 209 (red dots)
- 334 (green dots)
- 336 (blue dots)

**Region**



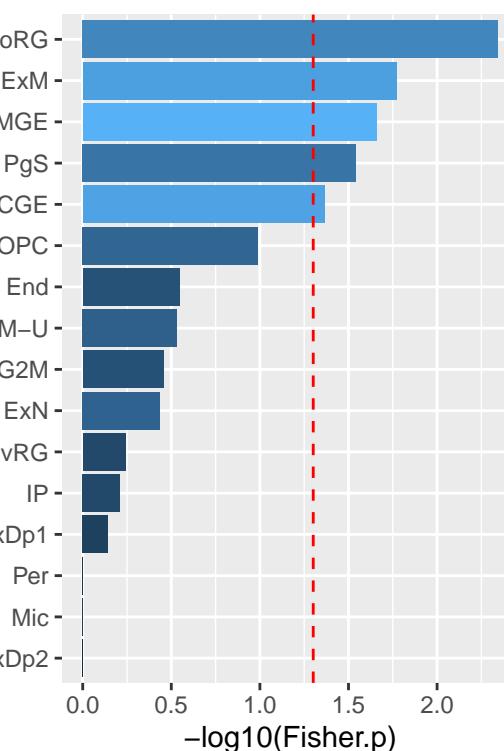
**novelty**

- ISM
- Known
- NIC
- NNC

**OR**

- 1.00
- 1.05
- 1.10
- 1.15
- 1.20

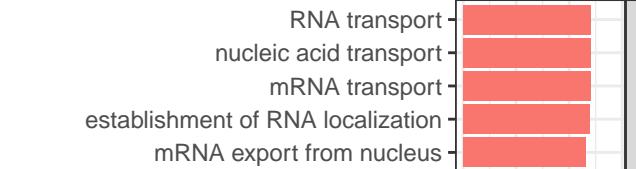
$-\log_{10}(Q)$



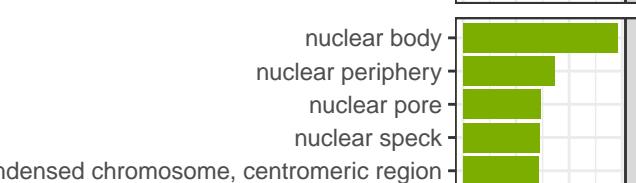
**OR**

2.5  
2.0  
1.5  
1.0

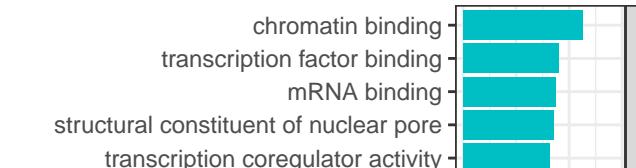
$-\log_{10}(\text{Fisher.p})$



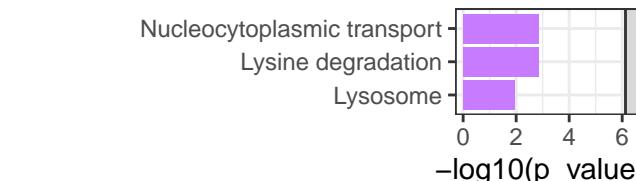
**GO:BP**



**GO:CC**

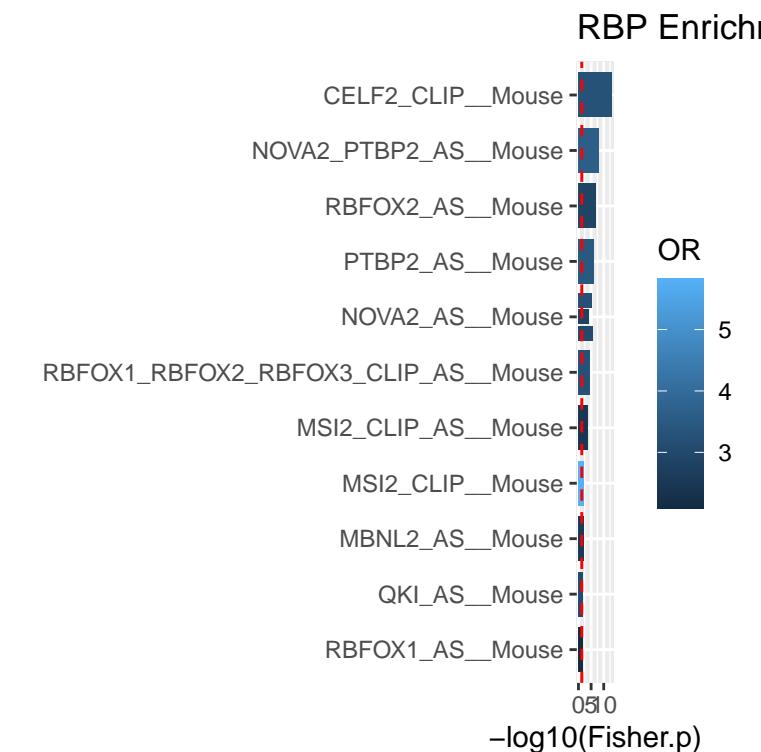


**GO:MF**



**KEGG**

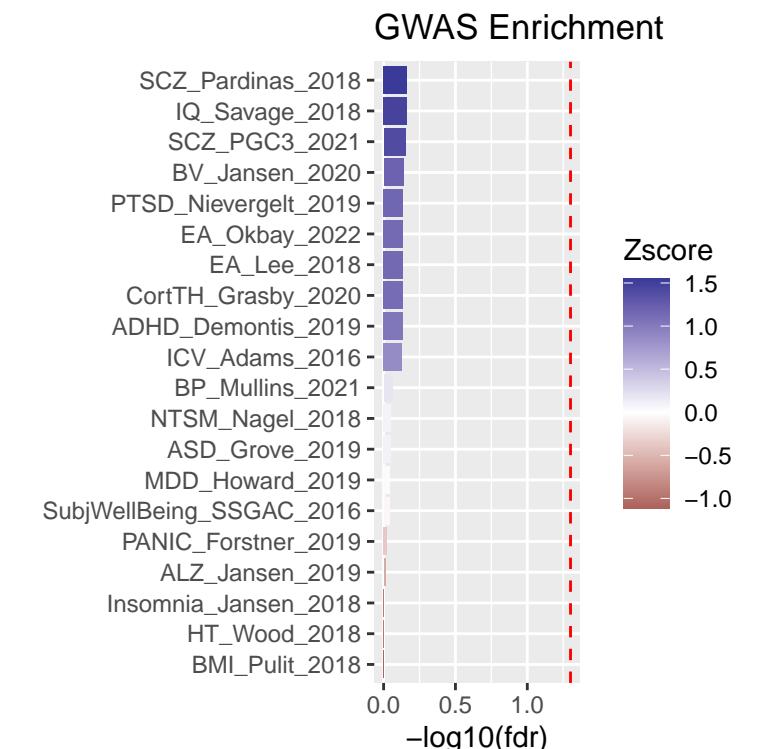
$-\log_{10}(p_{\text{value}})$



**OR**

5  
4  
3

$-\log_{10}(\text{Fisher.p})$

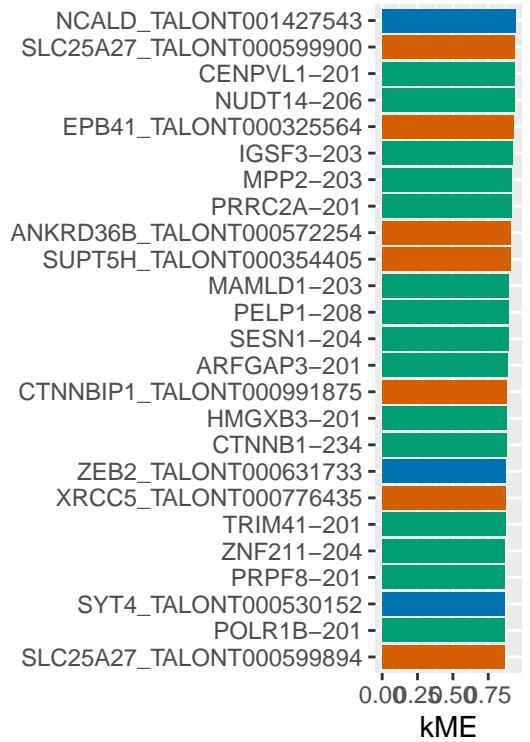
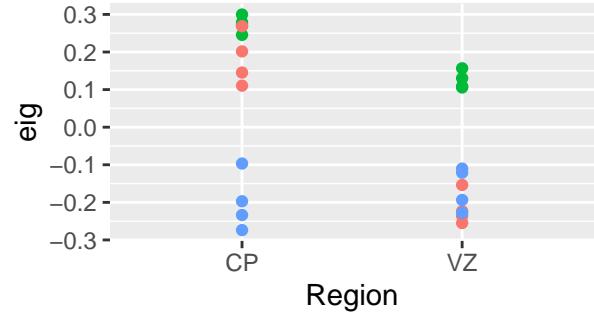


**Zscore**

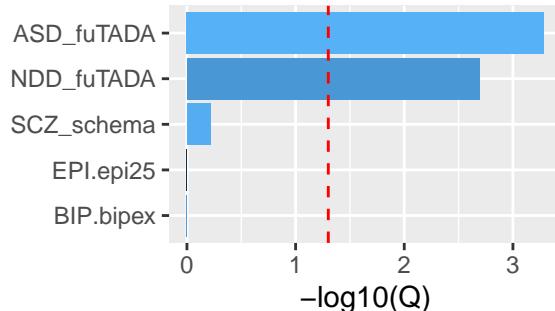
1.5  
1.0  
0.5  
0.0  
-0.5  
-1.0

$-\log_{10}(\text{fdr})$

# Module 24: darkgrey n=221

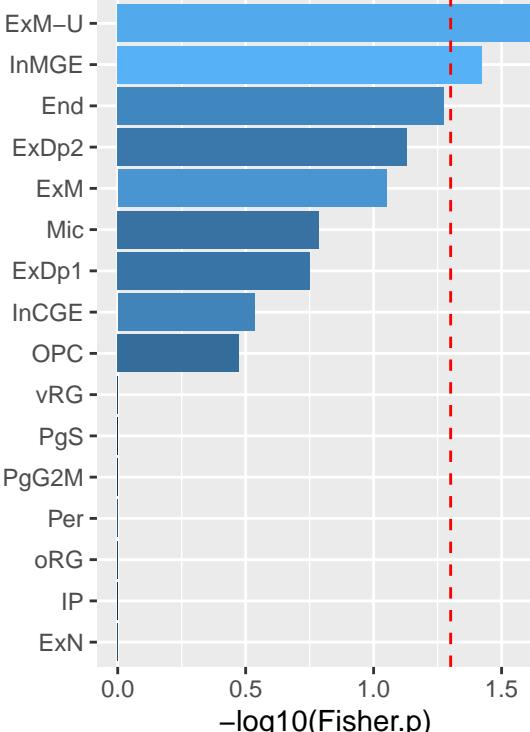


## Rare Var Enrichment

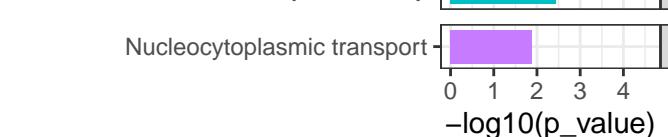
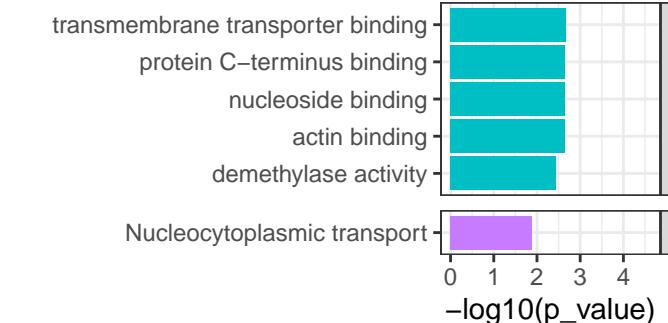
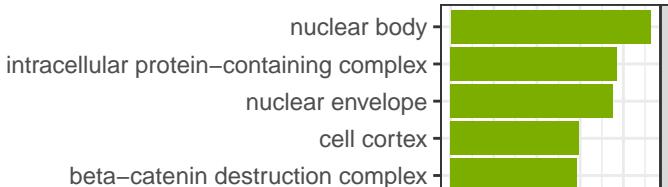


## Subject

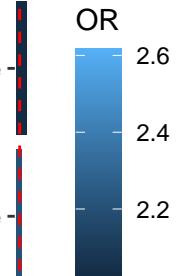
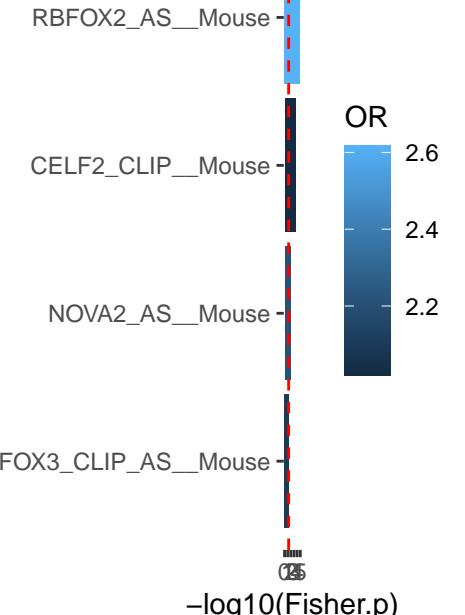
- 209
- 334
- 336



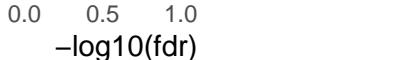
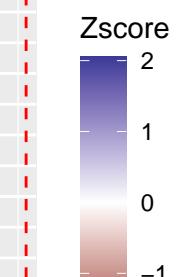
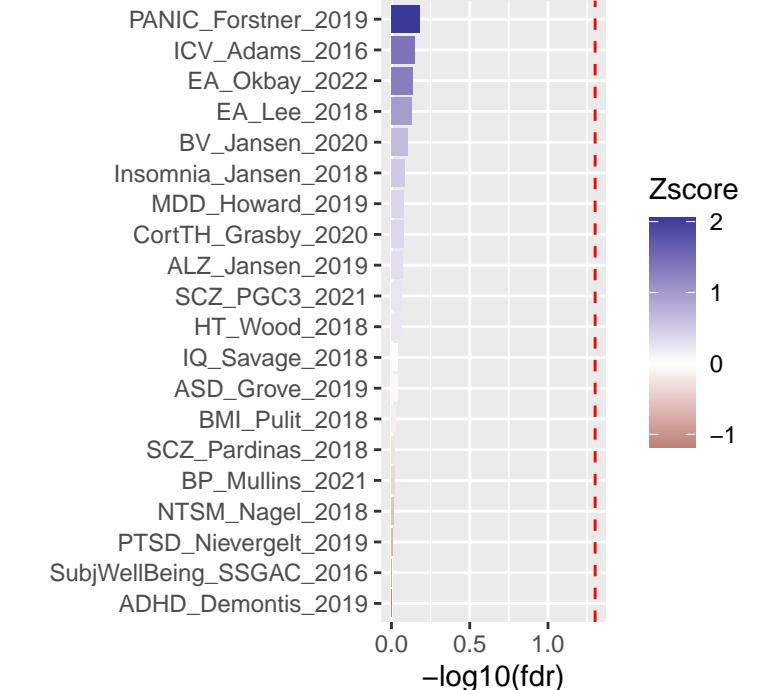
## OR



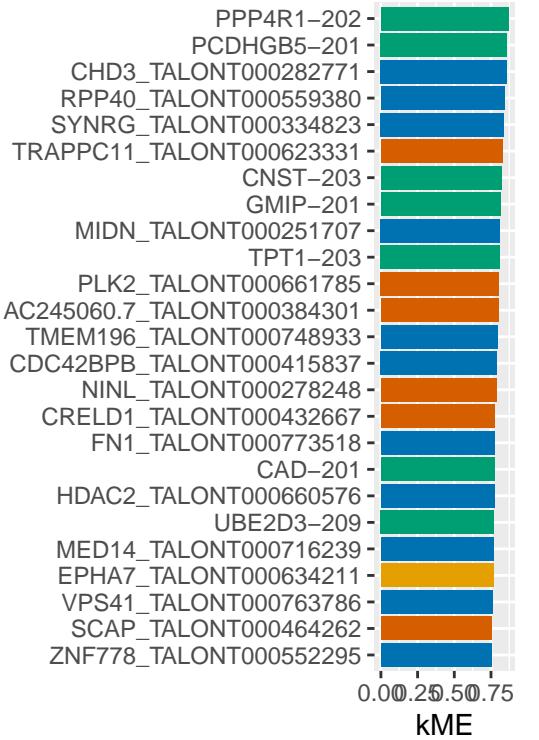
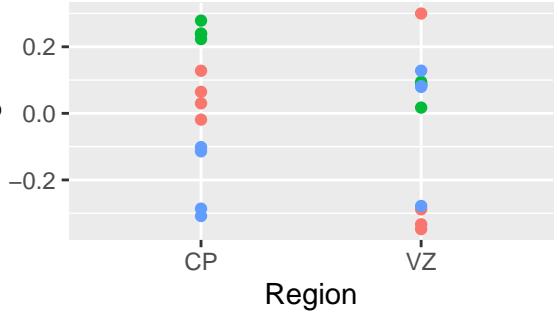
## RBP Enrichment



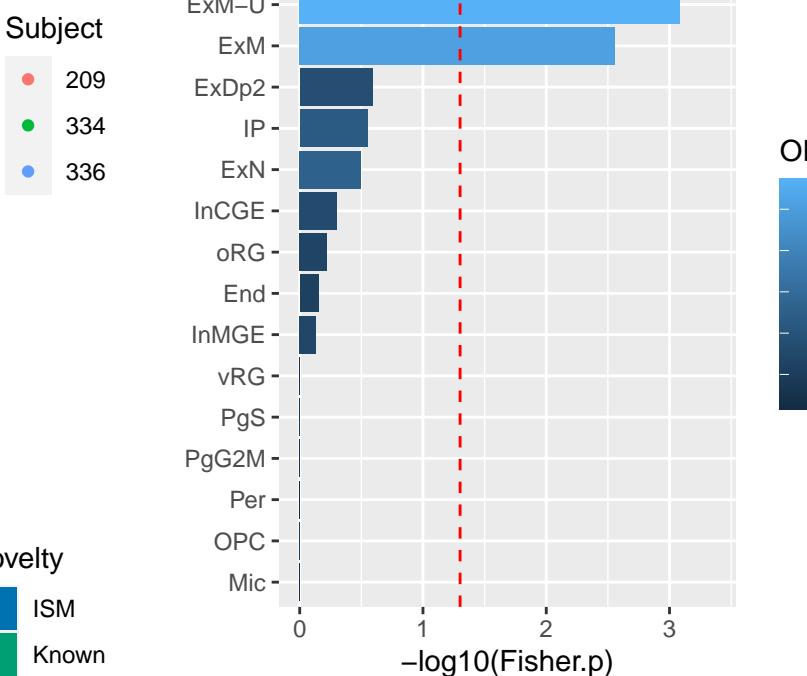
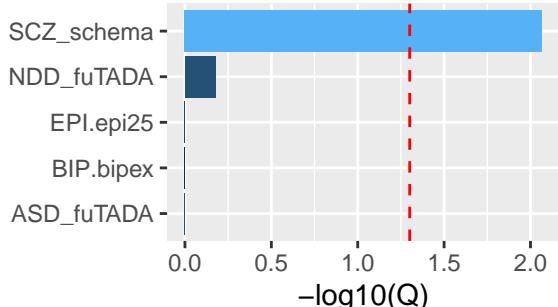
## GWAS Enrichment



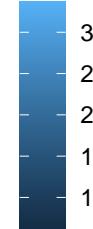
## Module 25: orange n=217



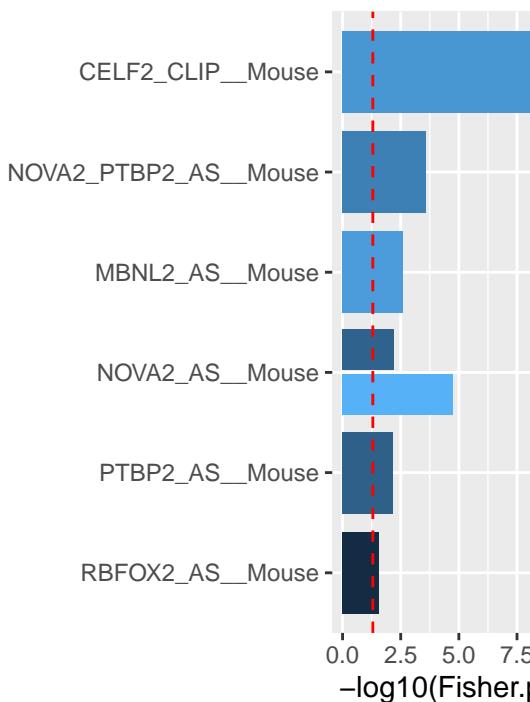
### Rare Var Enrichment



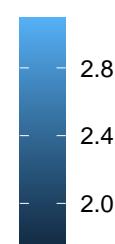
OR



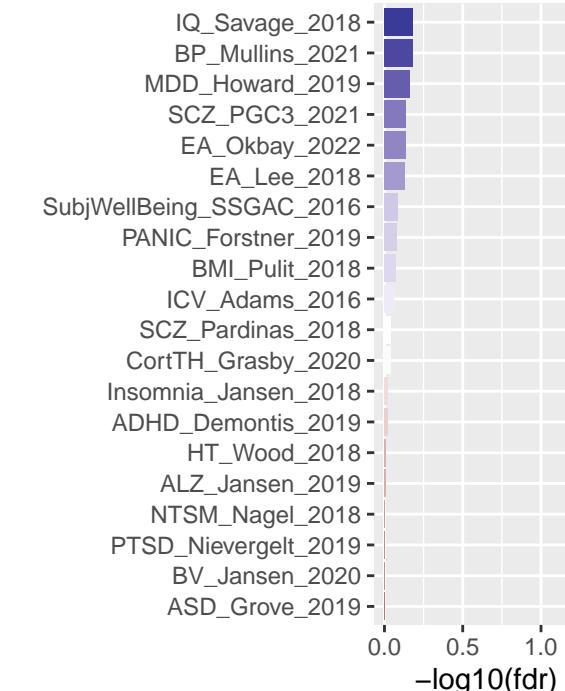
### RBP Enrichment



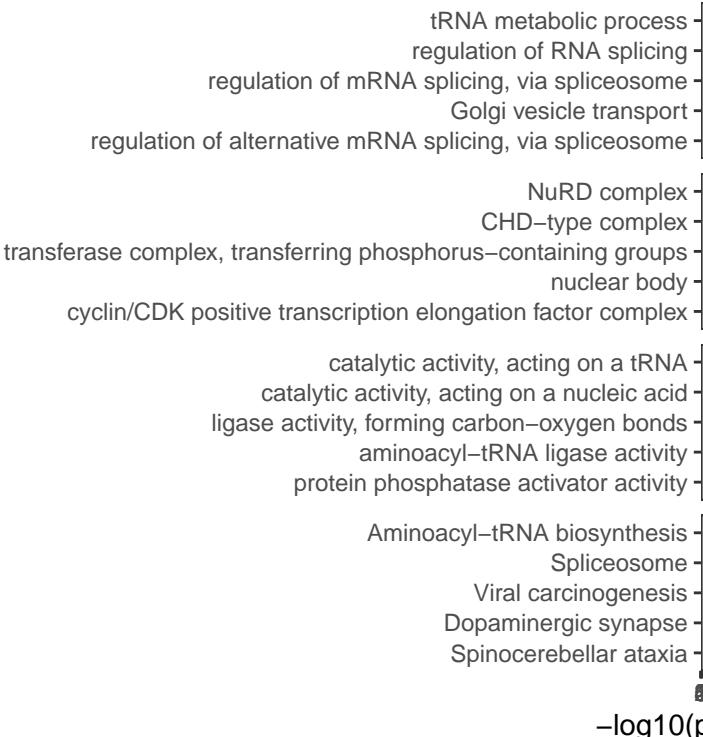
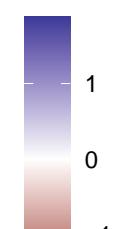
OR



### GWAS Enrichment



Zscore



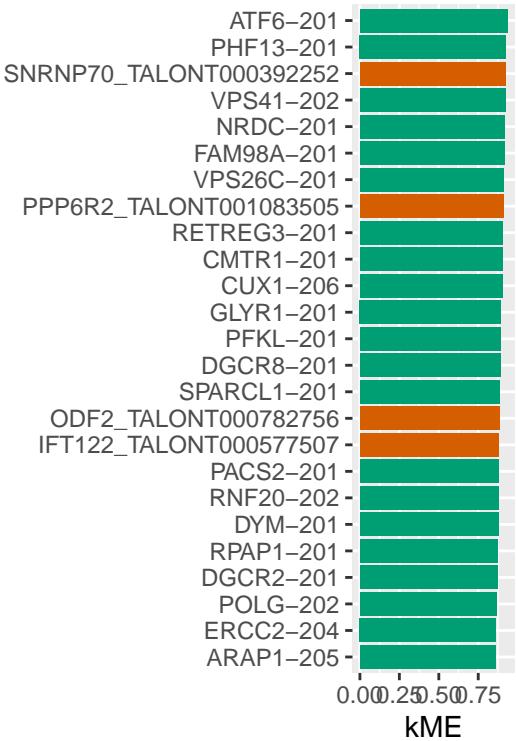
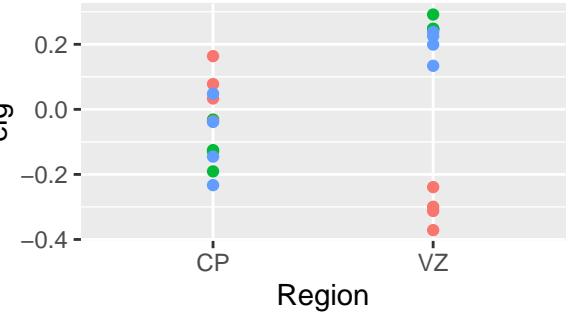
OR



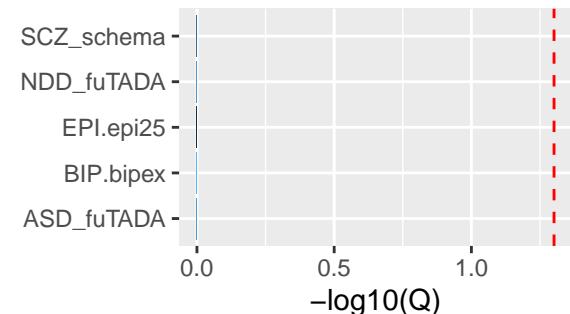
-log10(p\_v)

-log10(fdr)

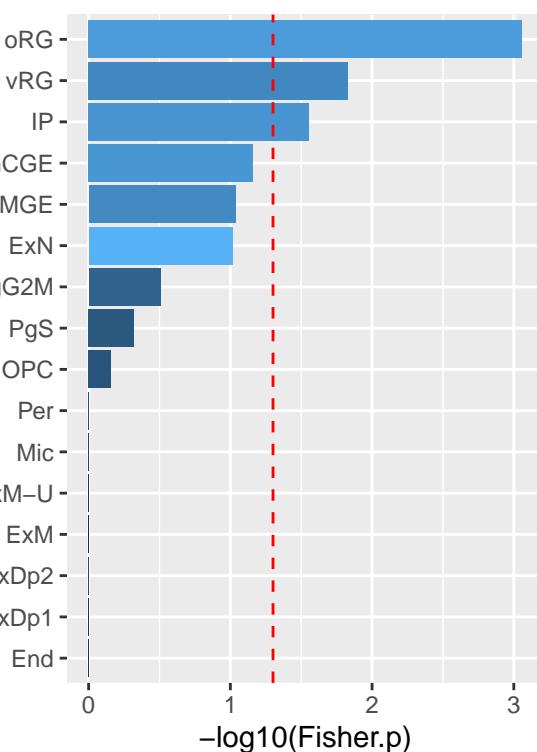
## Module 26: darkorange n=210



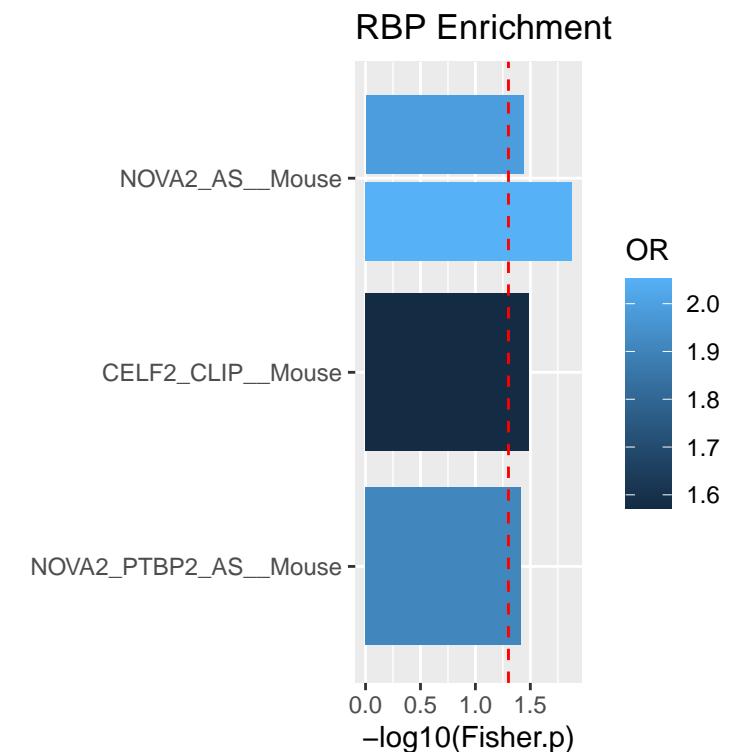
### Rare Var Enrichment



Subject  
209  
334  
336



OR  
2  
1



OR  
2.0  
1.9  
1.8  
1.7  
1.6

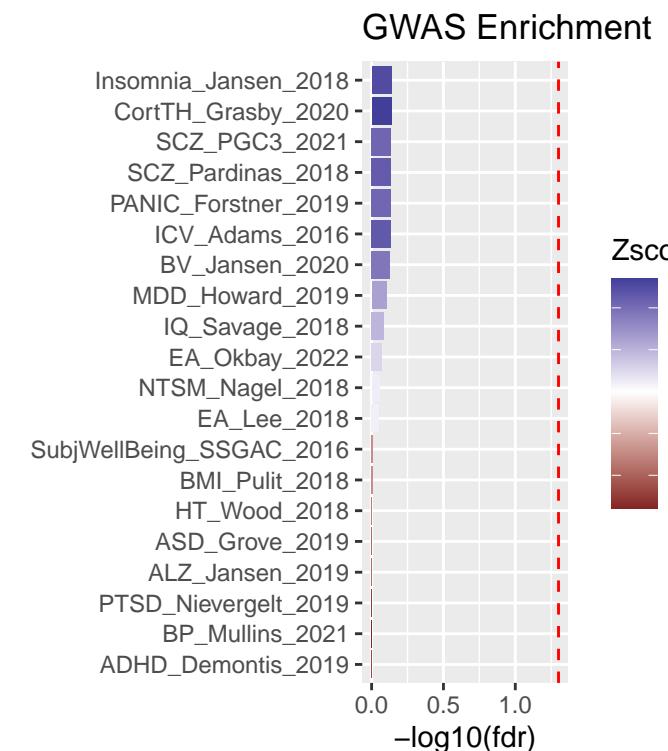
ncRNA processing  
ncRNA metabolic process  
macromolecule methylation  
methylation  
positive regulation of histone modification  
  
intracellular protein-containing complex  
transferase complex  
chromatin silencing complex  
pigment granule  
  
histone binding  
ubiquitin protein ligase binding  
ribonucleoprotein complex binding  
ubiquitin-like protein ligase binding  
catalytic activity, acting on a nucleic acid  
  
Spliceosome  
Nucleotide excision repair  
mRNA surveillance pathway  
Citrate cycle (TCA cycle)  
Basal transcription factors

GO:BP

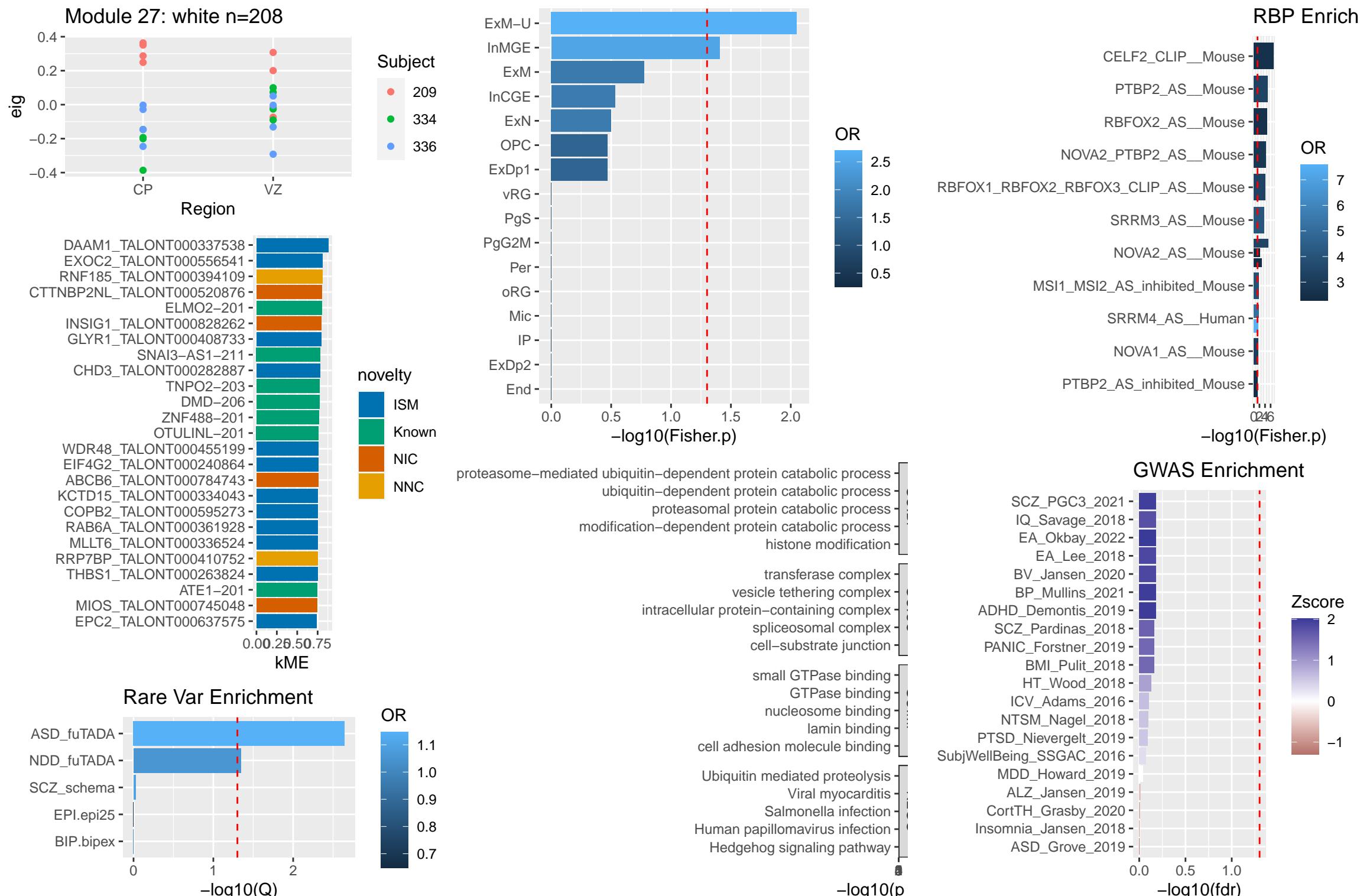
GO:CC

GO:MF

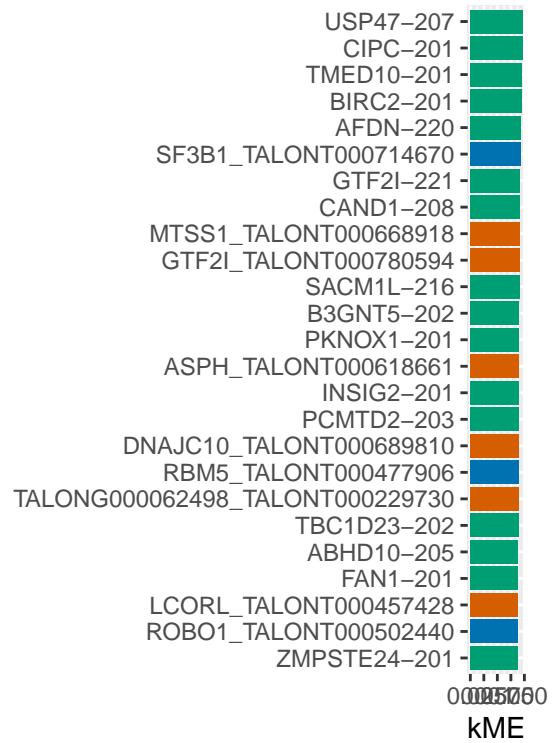
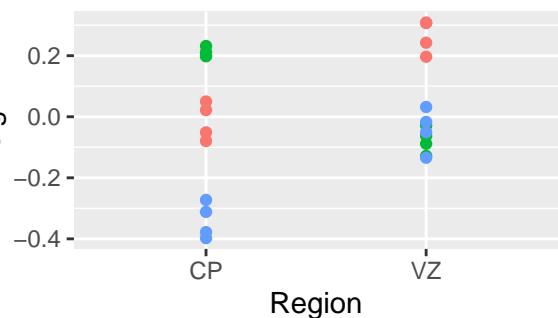
KEGG



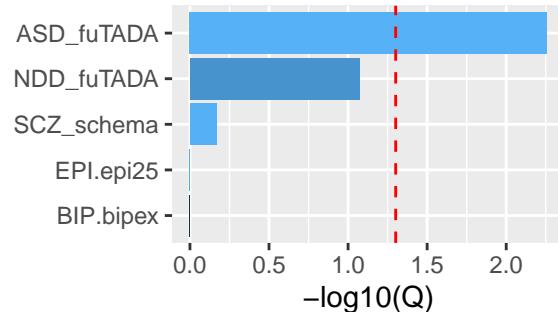
Zscore  
1.0  
0.5  
0.0  
-0.5  
-1.0



# Module 28: skyblue n=202

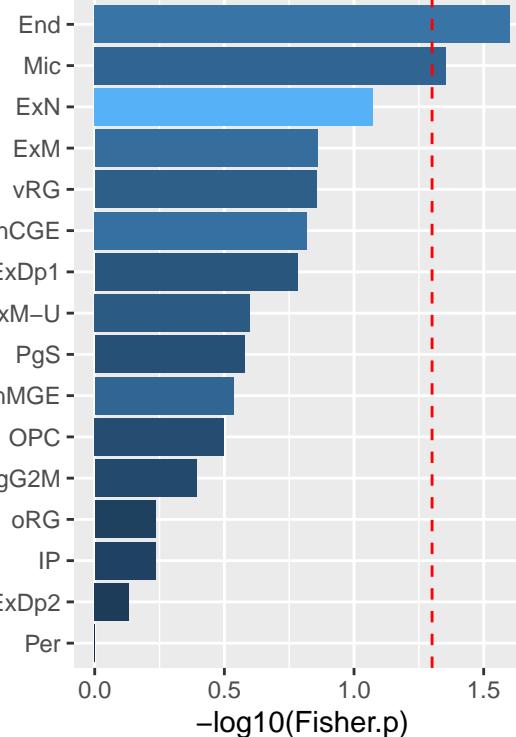


## Rare Var Enrichment

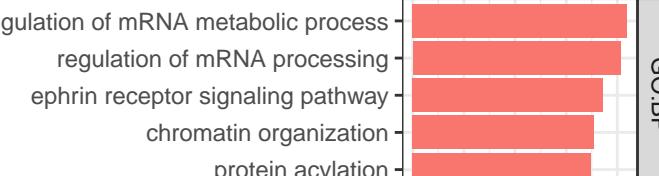


Subject  
209  
334  
336

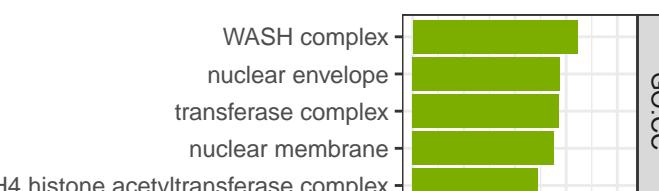
novelty  
ISM  
Known  
NIC



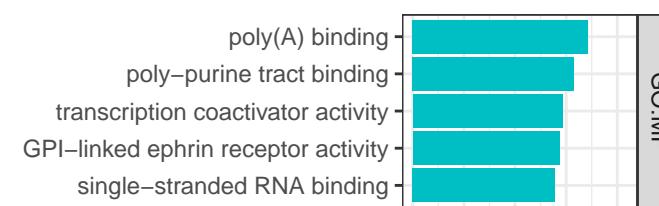
OR  
3.0  
2.5  
2.0  
1.5  
1.0



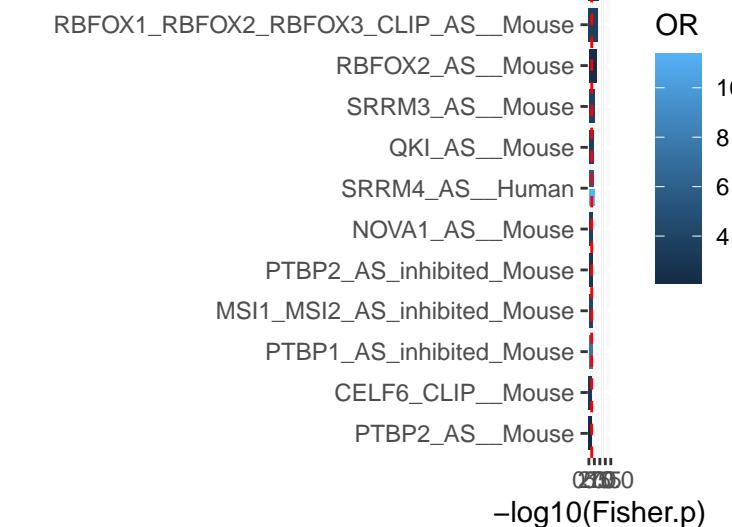
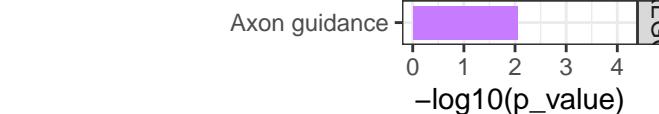
GO:BP



GO:CC

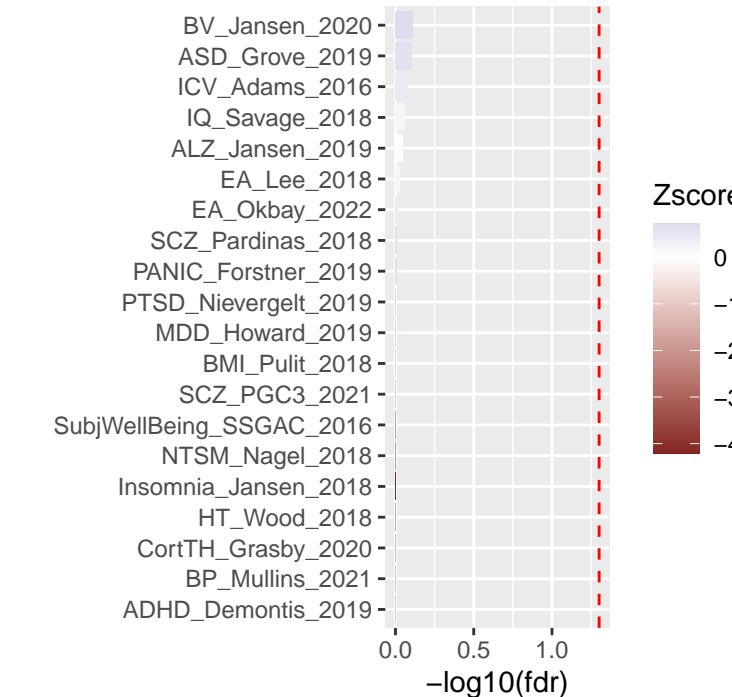


GO:MF



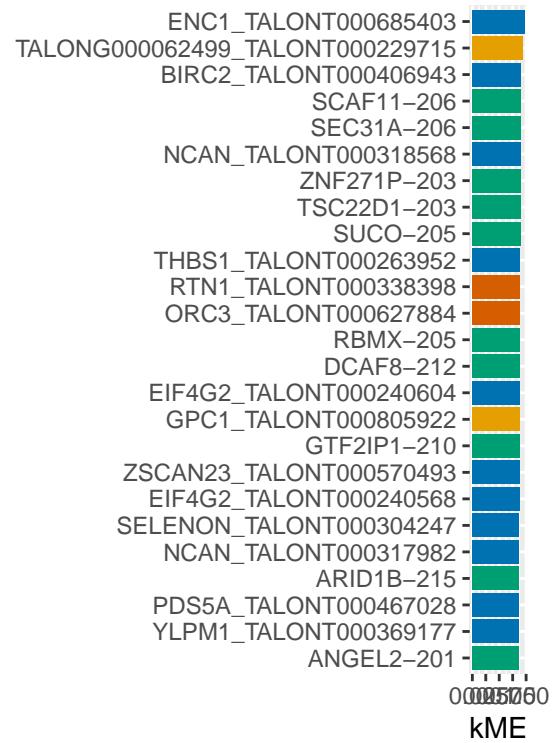
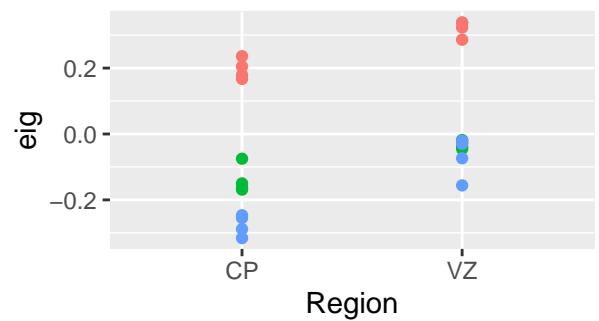
OR  
10  
8  
6  
4

## GWAS Enrichment

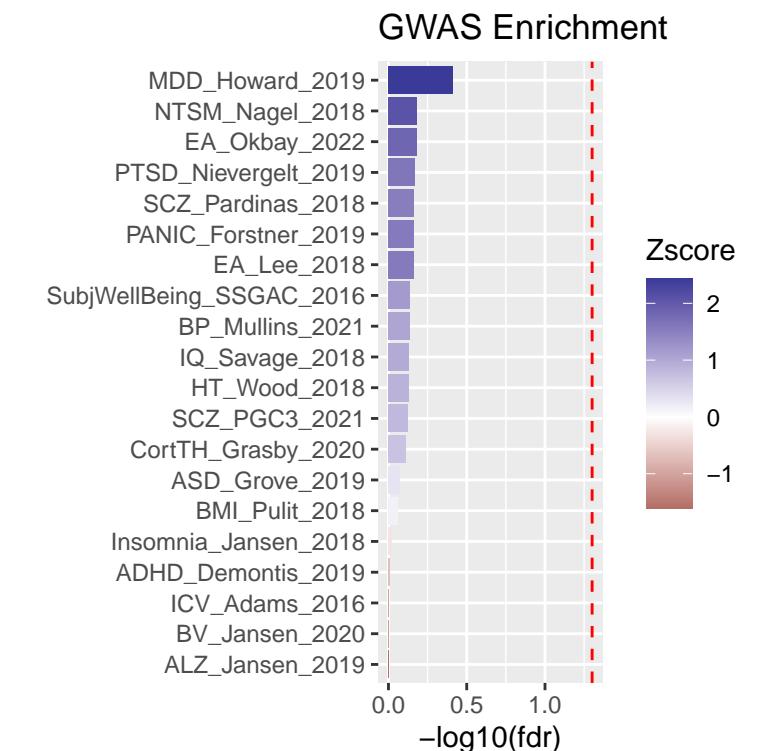
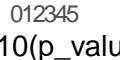
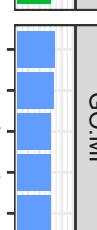
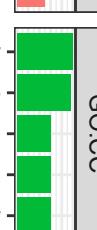
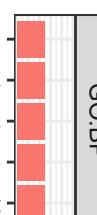
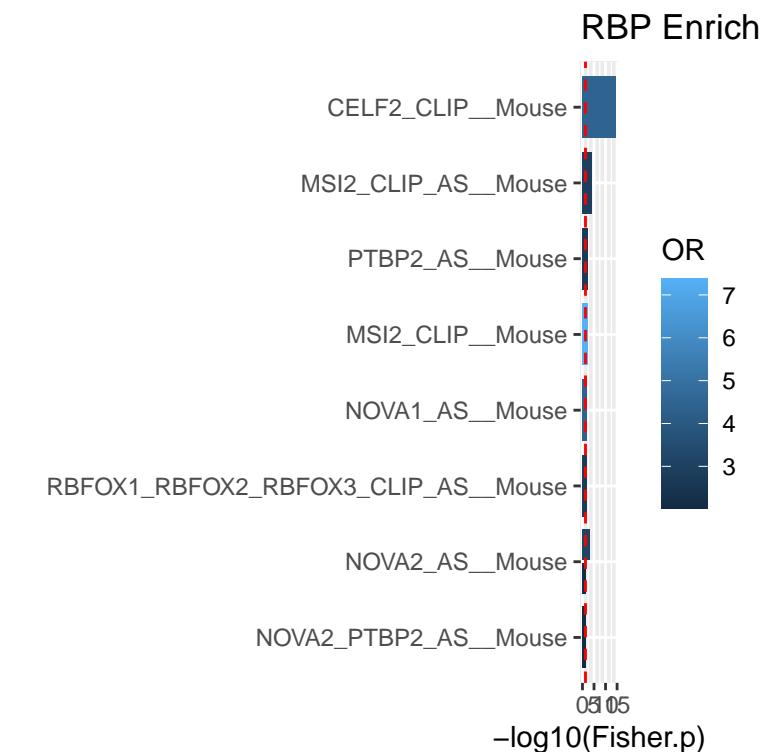
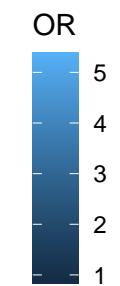
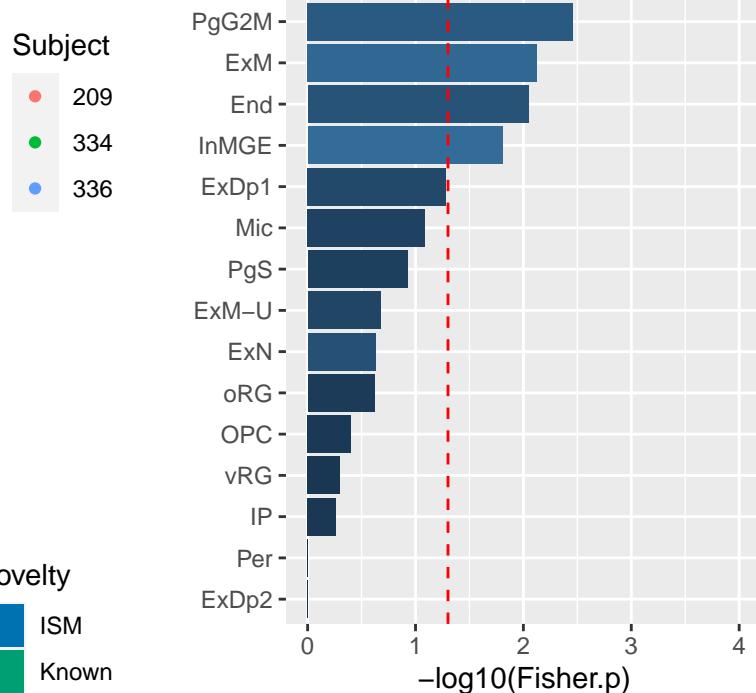
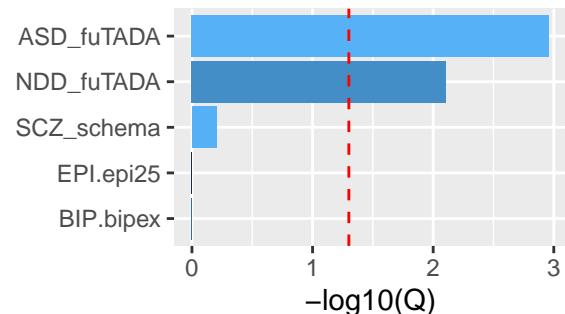


Zscore  
0  
-1  
-2  
-3  
-4

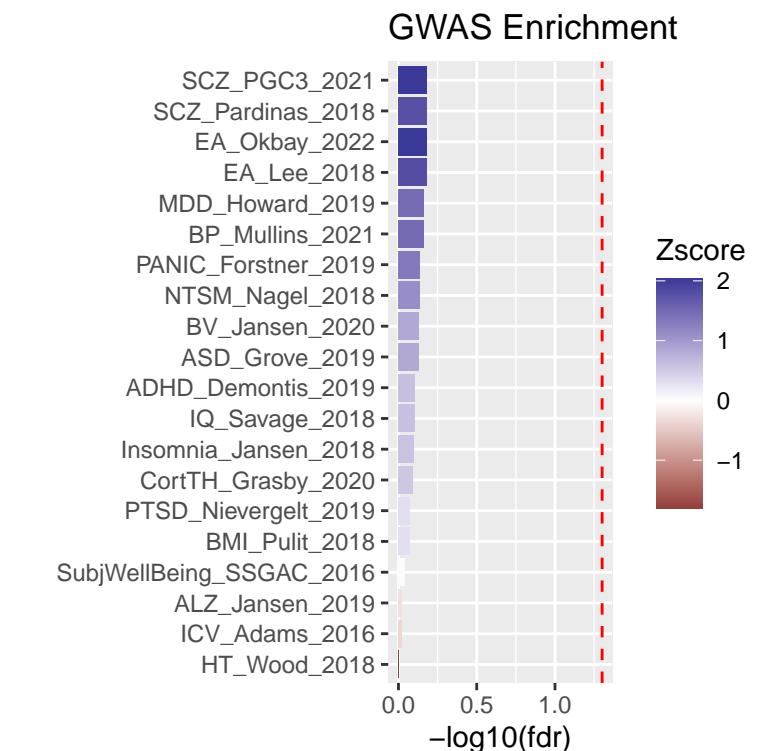
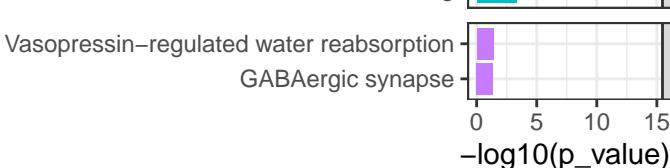
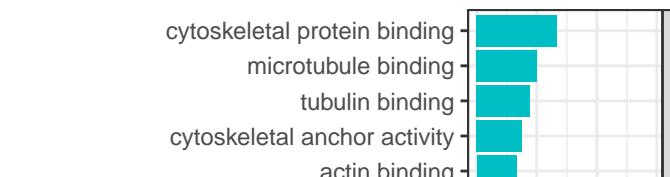
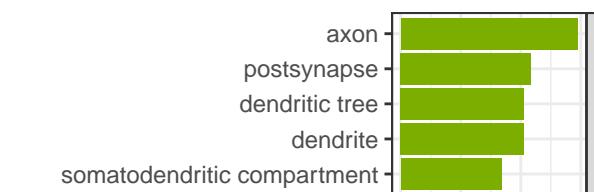
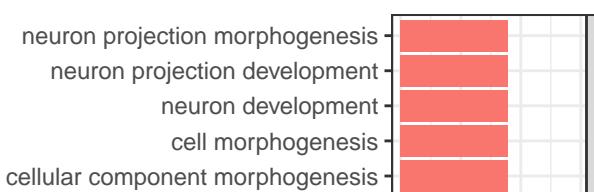
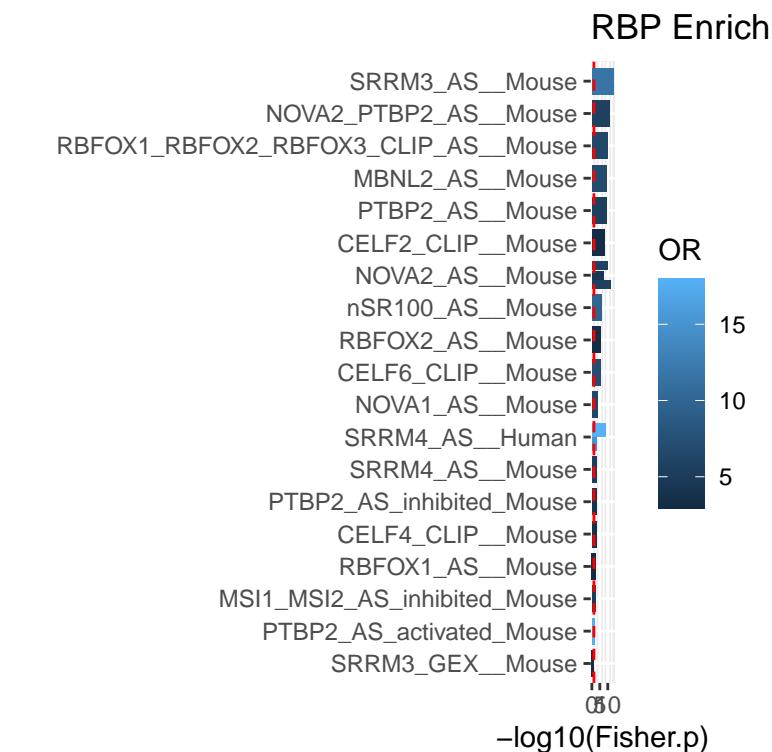
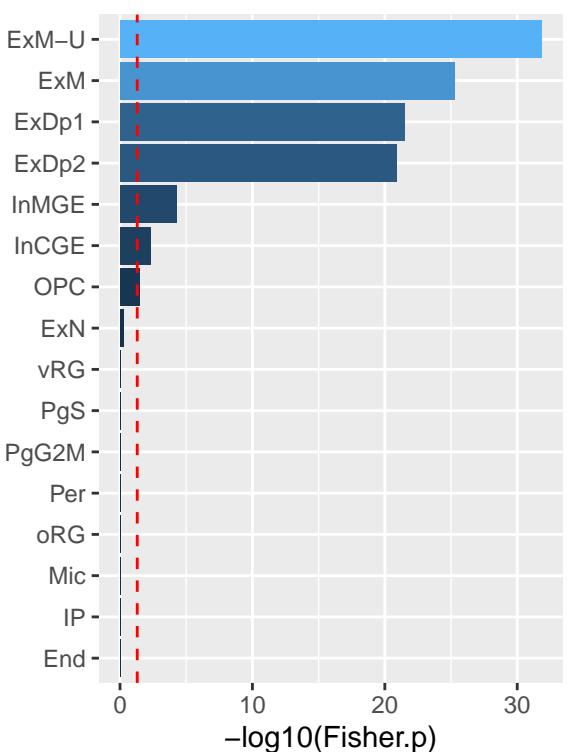
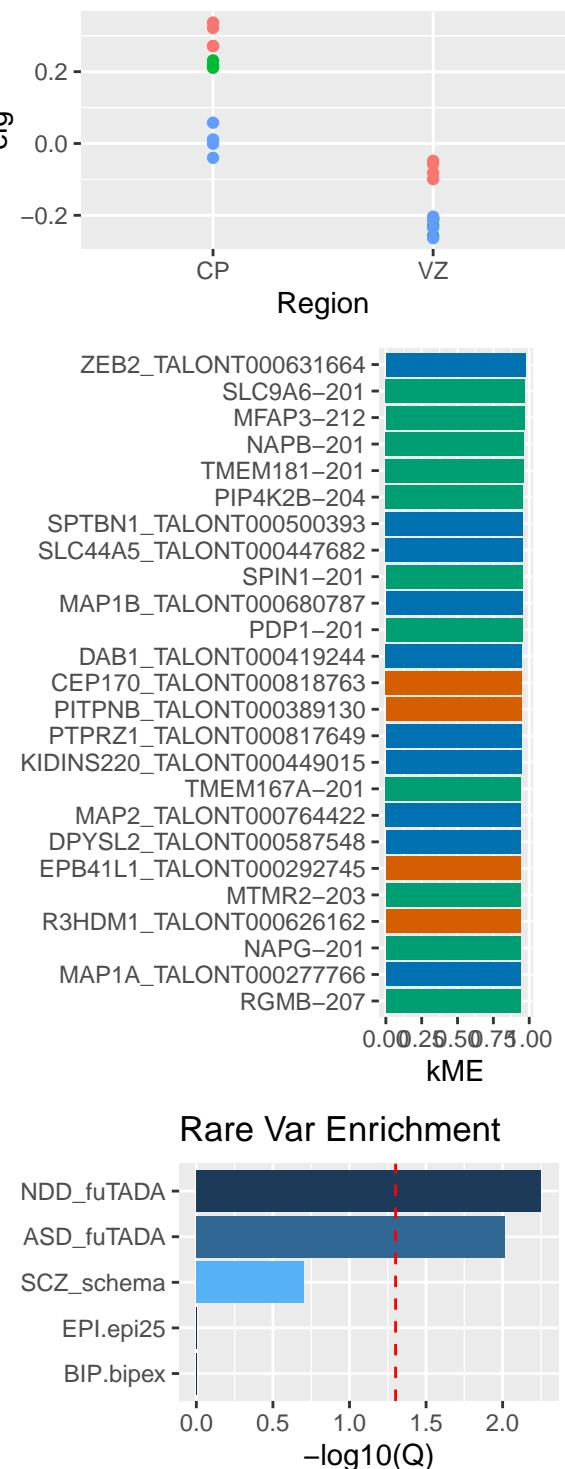
# Module 29: saddlebrown n=189



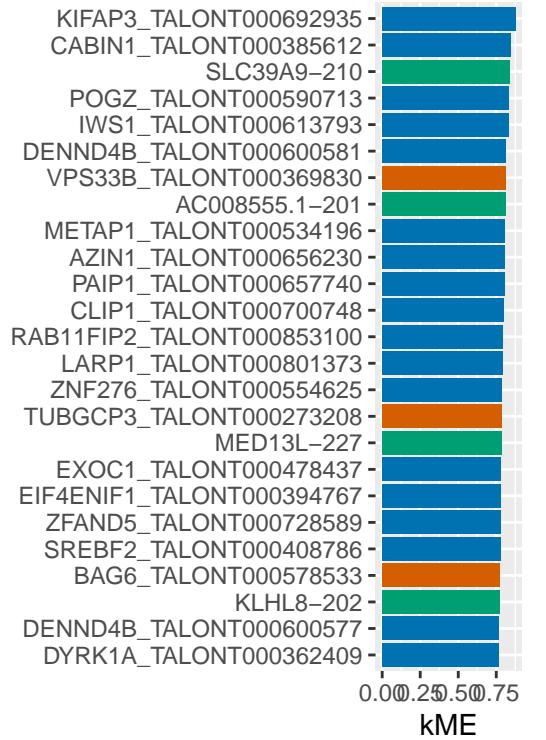
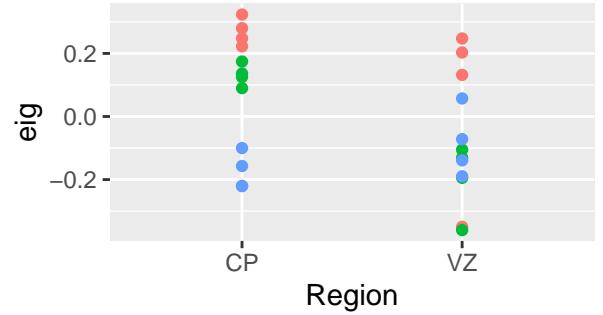
## Rare Var Enrichment



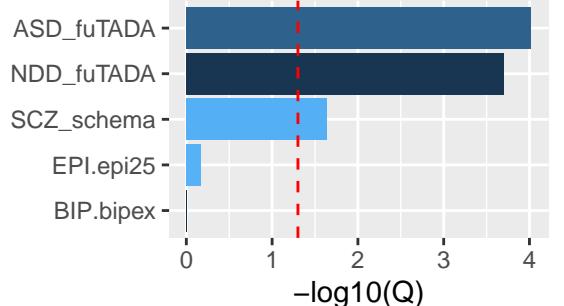
# Module 30: steelblue n=172



# Module 31: paleturquoise n=169

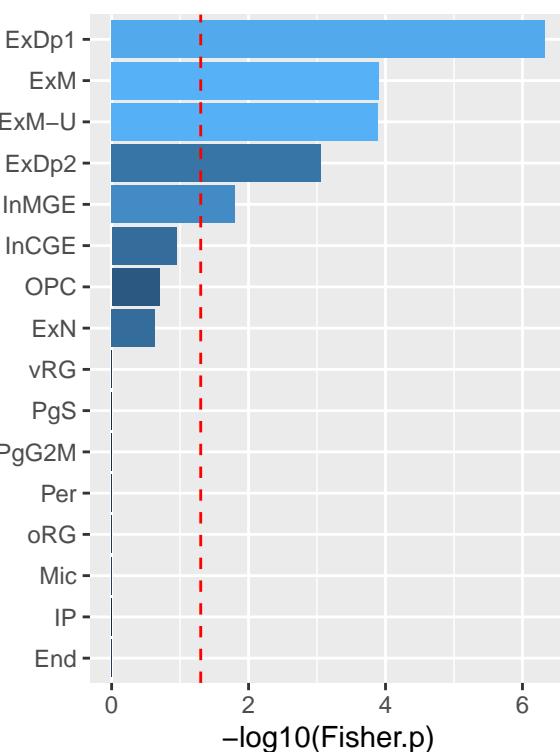


## Rare Var Enrichment

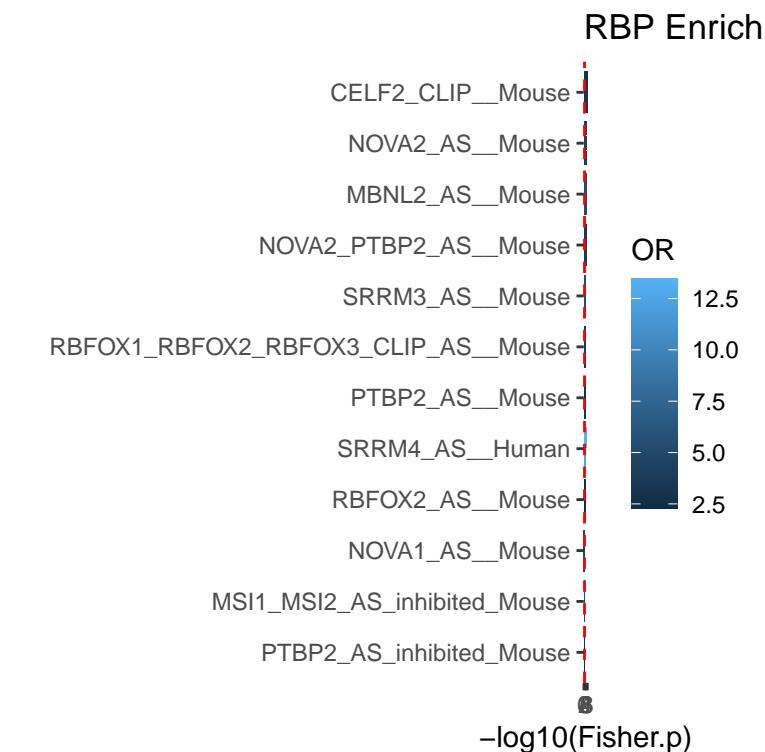


Subject  
209  
334  
336

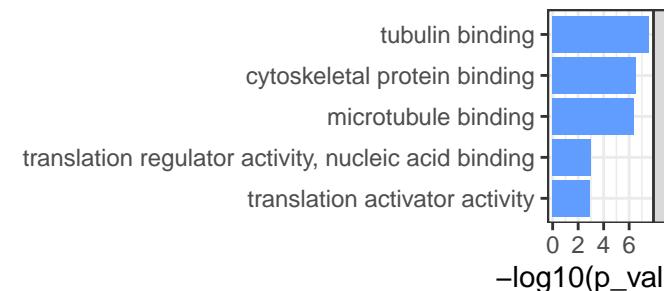
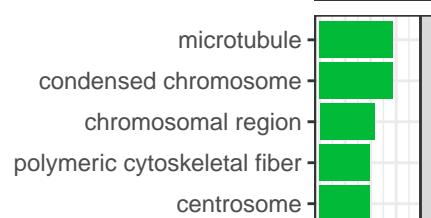
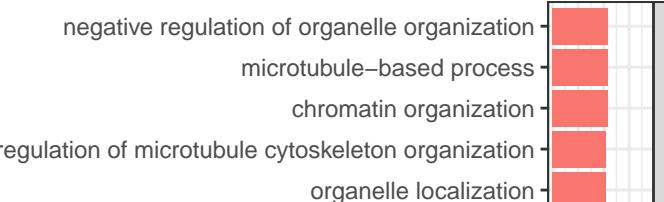
novelty  
ISM  
Known  
NIC



OR  
0 1 2 3 4



OR  
0 2.5 5.0 7.5 10.0 12.5

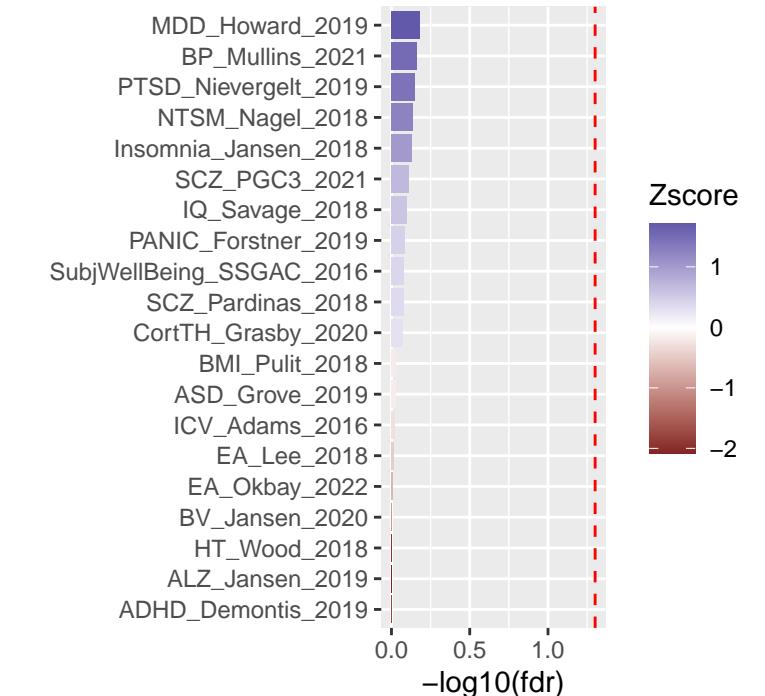


-log10(p\_value)

CELF2\_CLIP\_Mouse  
NOVA2\_AS\_Mouse  
MBNL2\_AS\_Mouse  
NOVA2\_PTBP2\_AS\_Mouse  
SRRM3\_AS\_Mouse

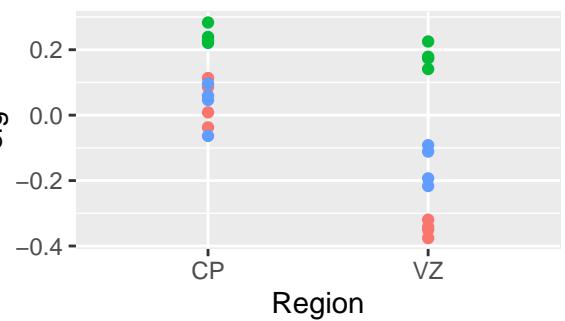
RBFOX1\_RBFOX2\_RBFOX3\_CLIP\_AS\_Mouse  
PTBP2\_AS\_Mouse  
SRRM4\_AS\_Human  
RBFOX2\_AS\_Mouse  
NOVA1\_AS\_Mouse  
MSI1\_MSII\_AS\_inhibited\_Mouse  
PTBP2\_AS\_inhibited\_Mouse

## GWAS Enrichment



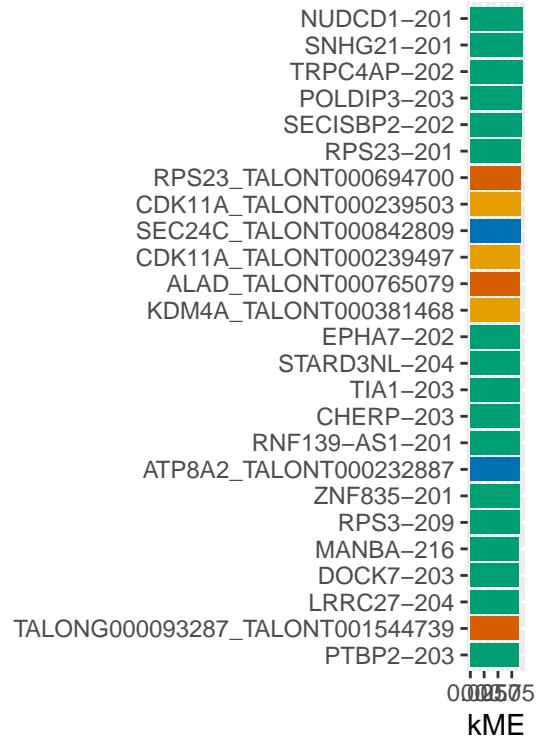
Zscore  
-2 -1 0 1

### Module 32: violet n=168

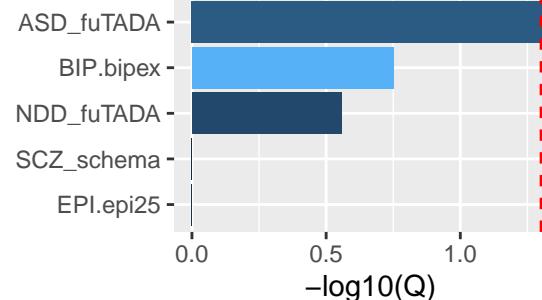


Subject  
209  
334  
336

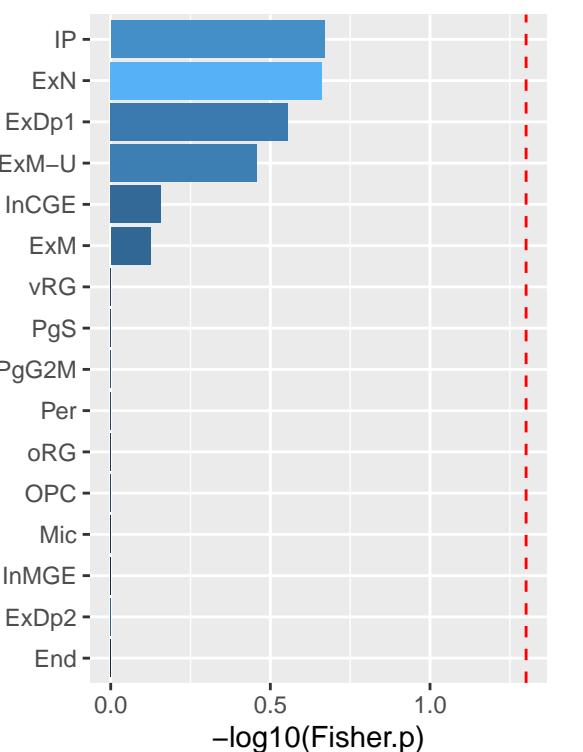
Region



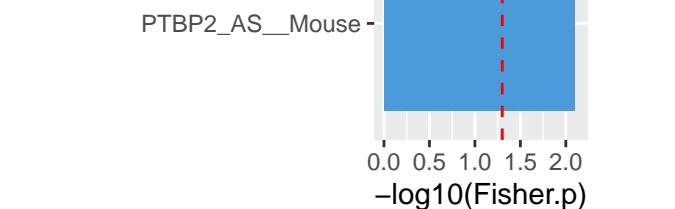
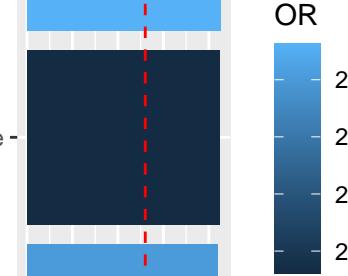
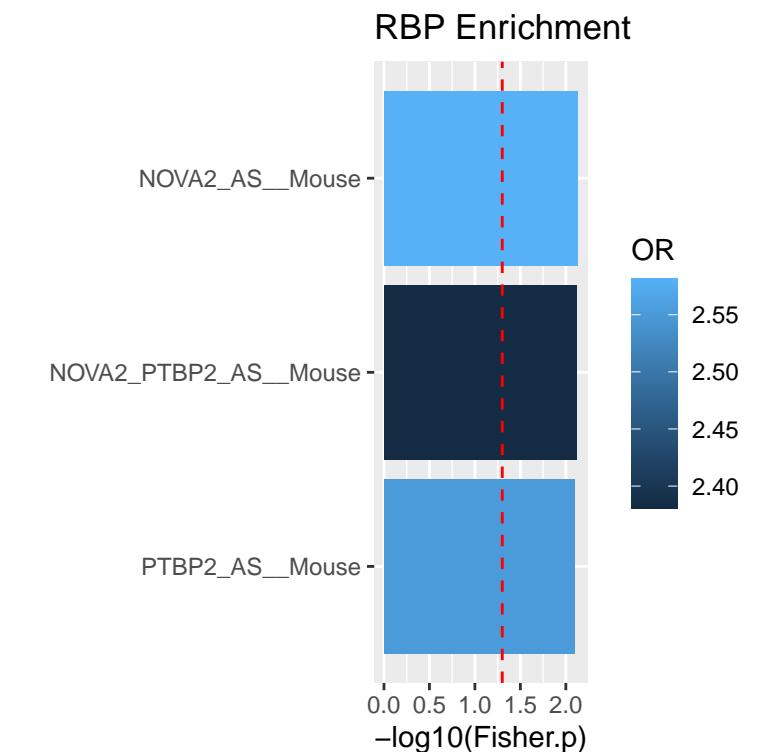
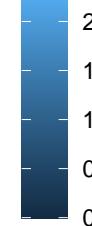
Rare Var Enrichment



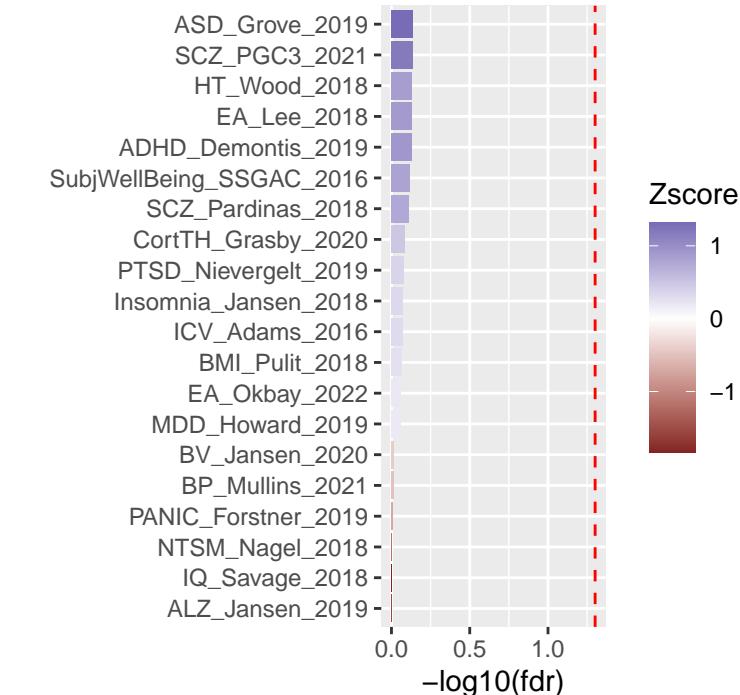
OR  
1.4  
1.2  
1.0



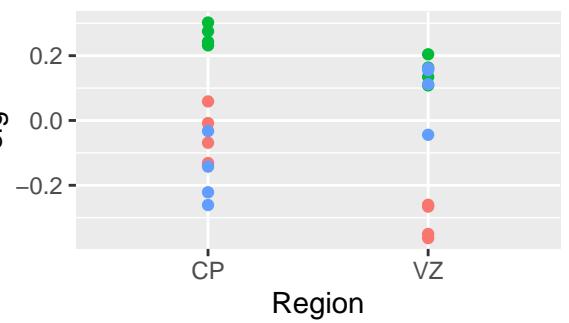
OR



GWAS Enrichment



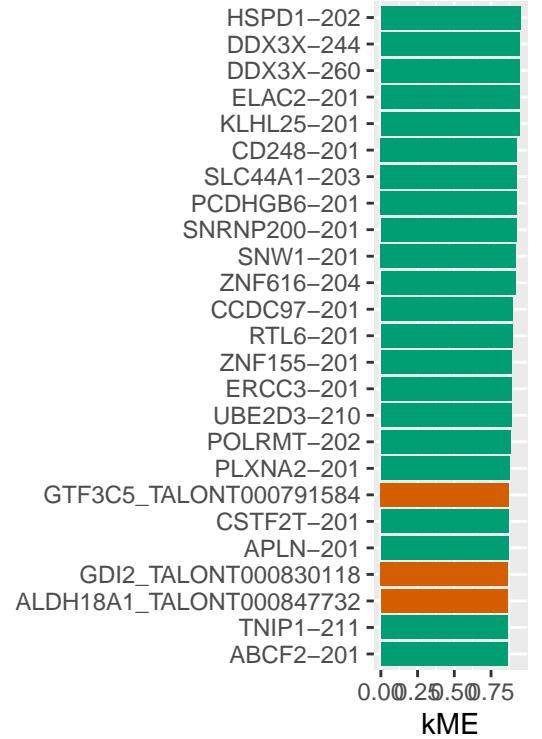
### Module 33: darkolivegreen n=163



Subject

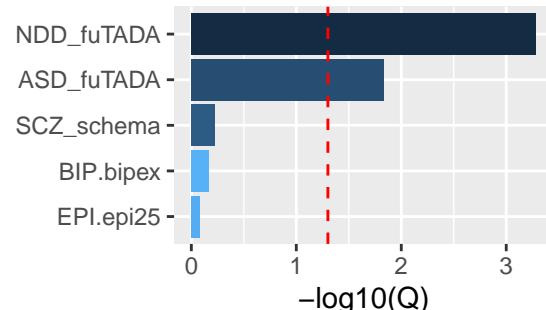
- 209
- 334
- 336

Region



kME

### Rare Var Enrichment

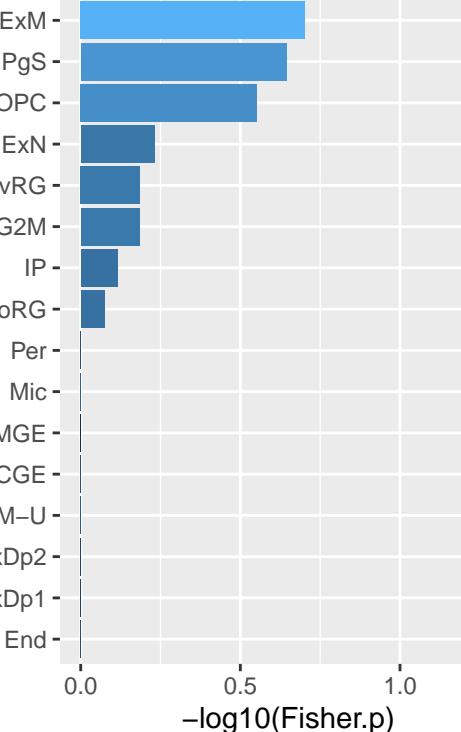


OR

- 1.10
- 1.15
- 1.20
- 1.25

OR

- 0.00
- 0.50
- 1.00
- 1.50

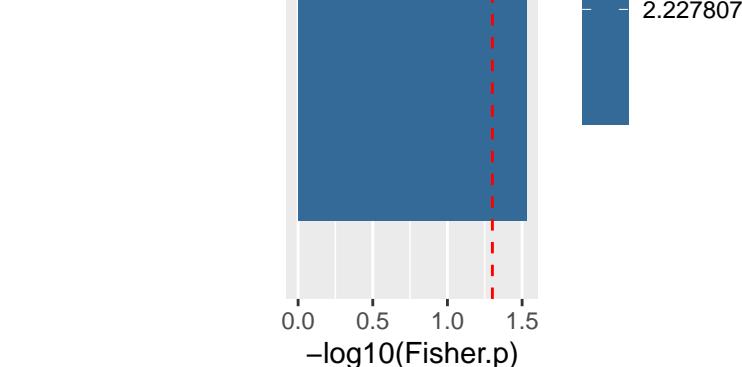


-log10(Fisher.p)

OR

- 0.0
- 0.5
- 1.0
- 1.5

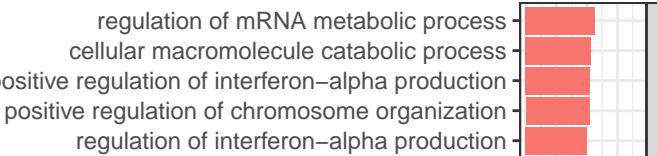
PTBP2\_AS\_Mouse



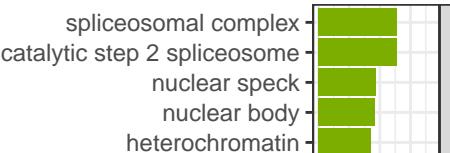
OR

- 2.227807

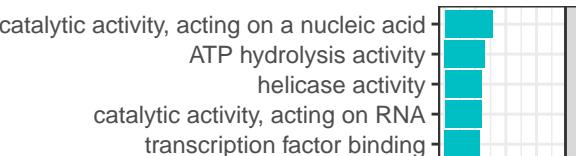
-log10(Fisher.p)



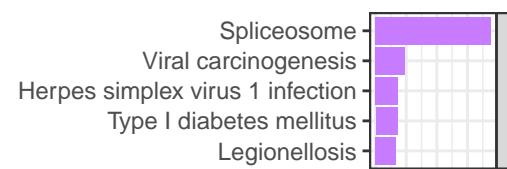
GO:BP



GO:CC



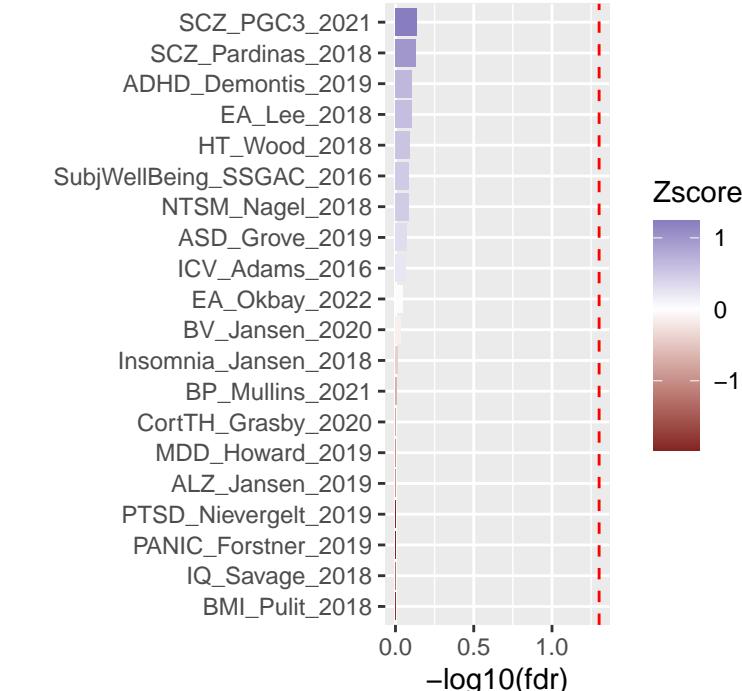
GO:MF



KEGG

-log10(p\_value)

### GWAS Enrichment

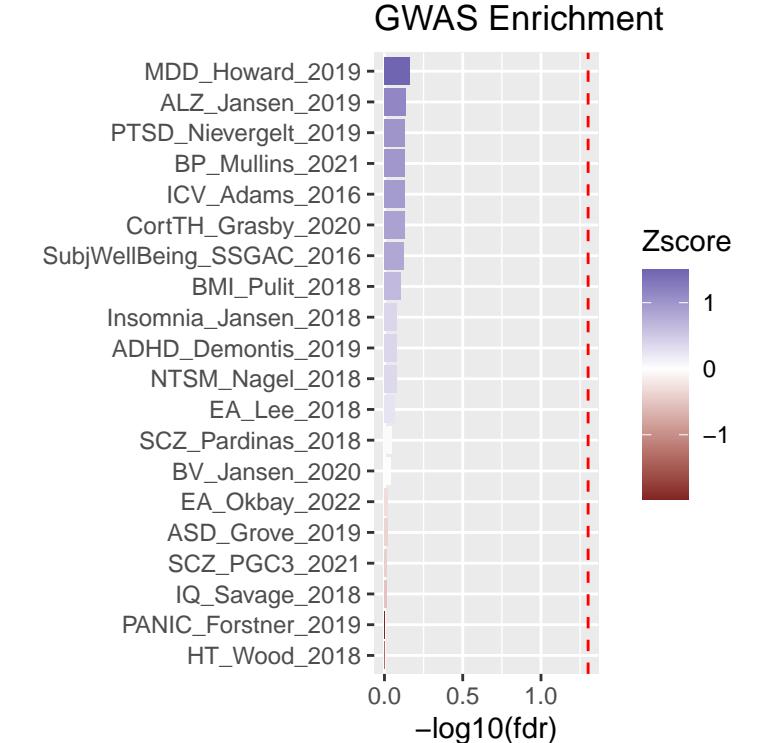
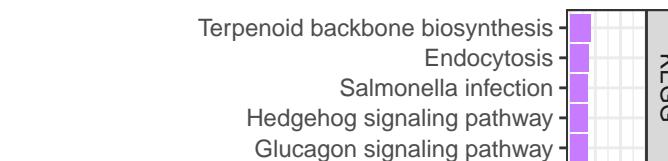
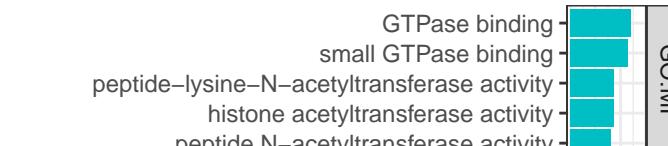
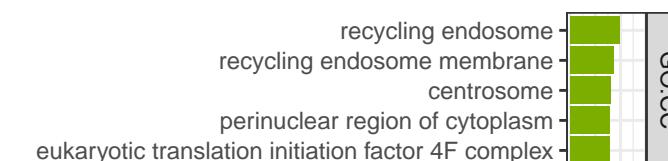
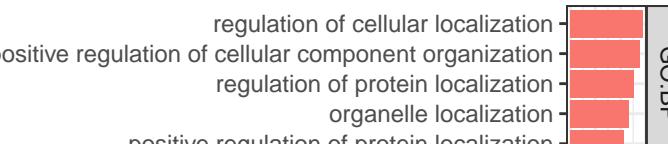
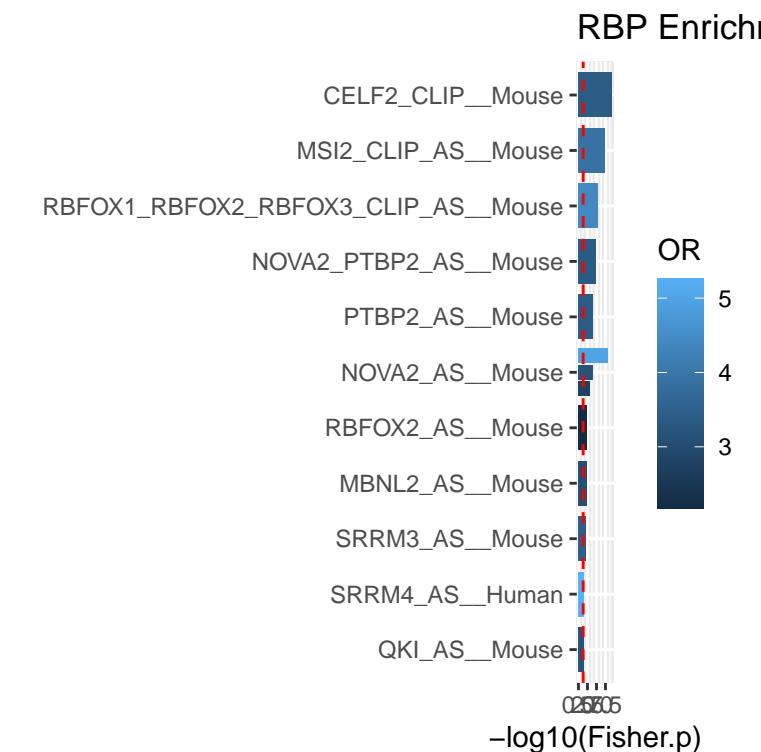
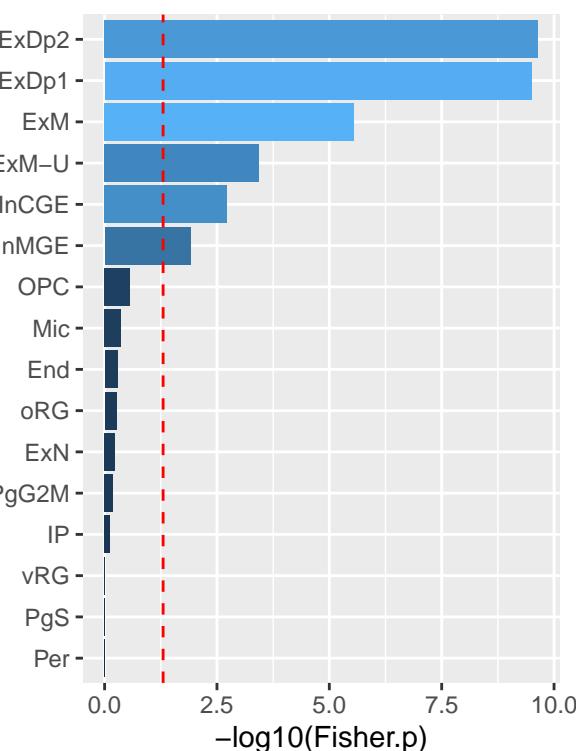
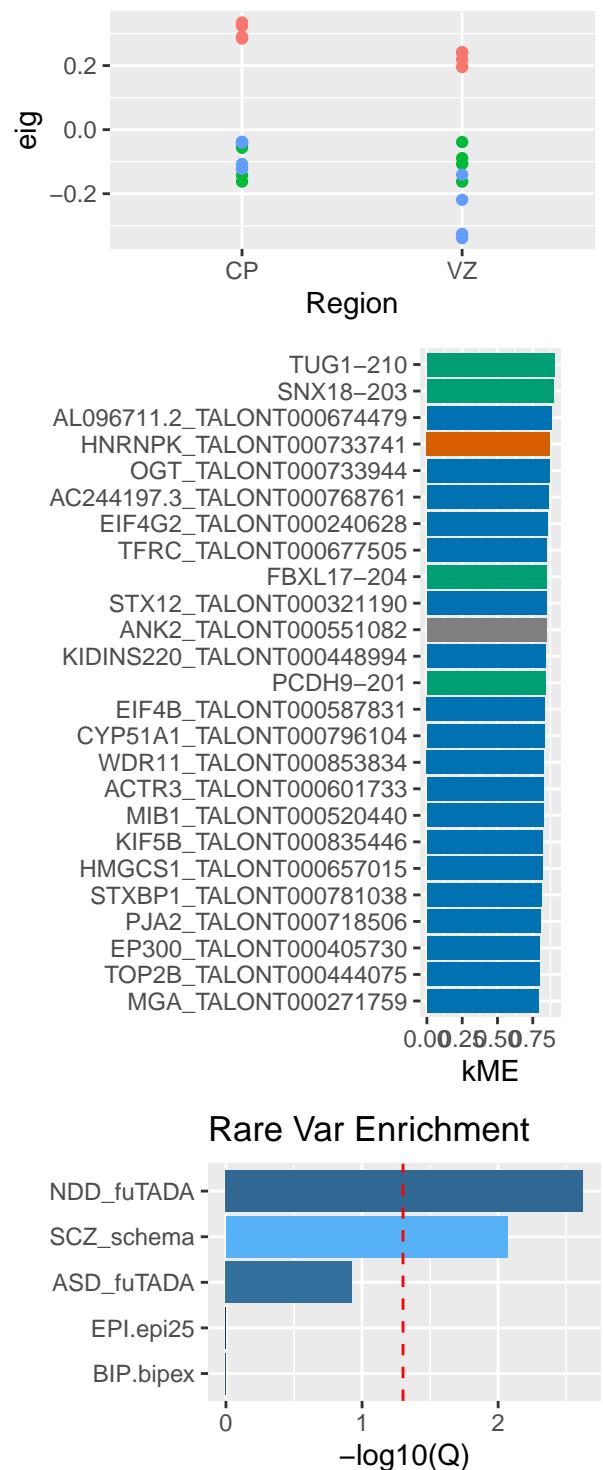


Zscore

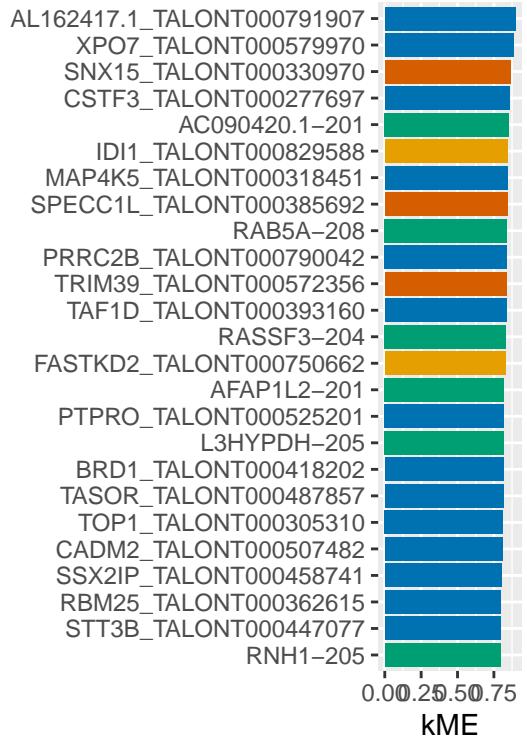
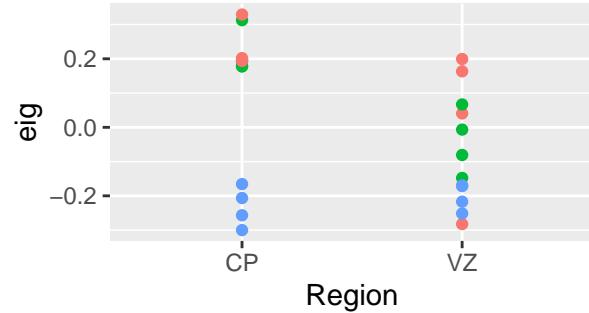
- 1
- 0
- 1

-log10(fdr)

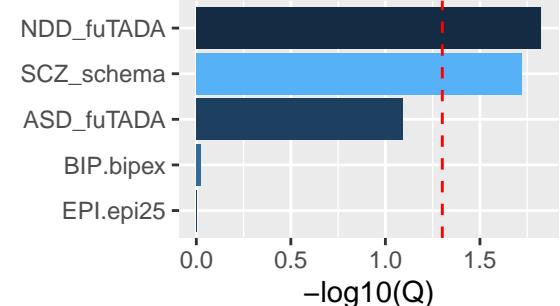
# Module 34: darkmagenta n=161



# Module 35: sienna3 n=160



## Rare Var Enrichment

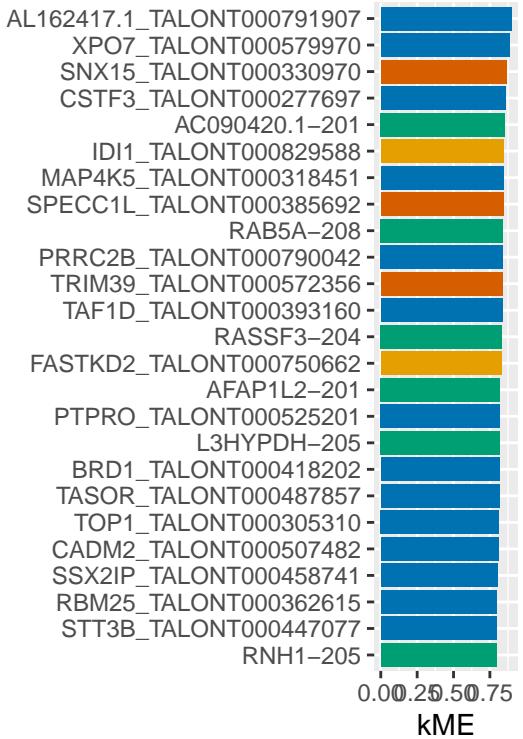


## Subject

209  
334  
336

## novelty

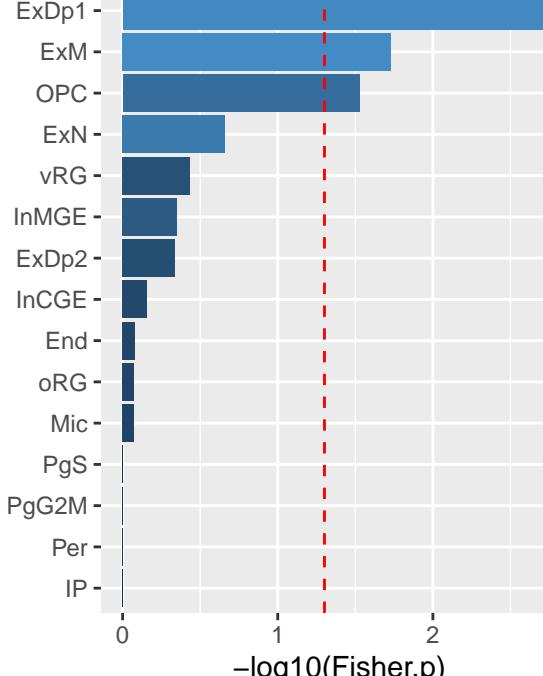
ISM  
Known  
NIC  
NNC



## OR

1.30  
1.25  
1.20  
1.15  
1.10

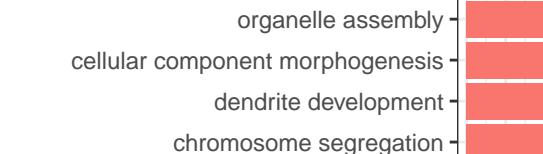
## ExM-U



## OR

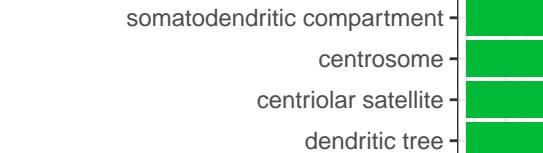
3  
2  
1

## cellular macromolecule catabolic process



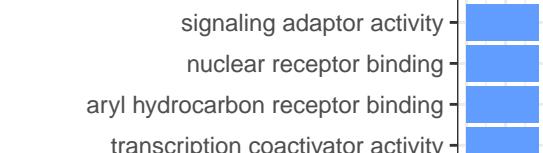
GO:BP

## microtubule organizing center



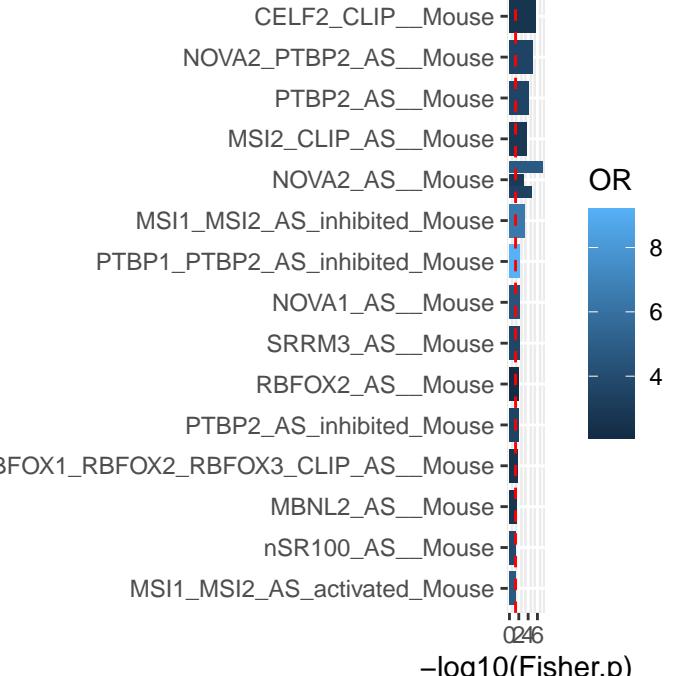
GO:CC

## protein-macromolecule adaptor activity



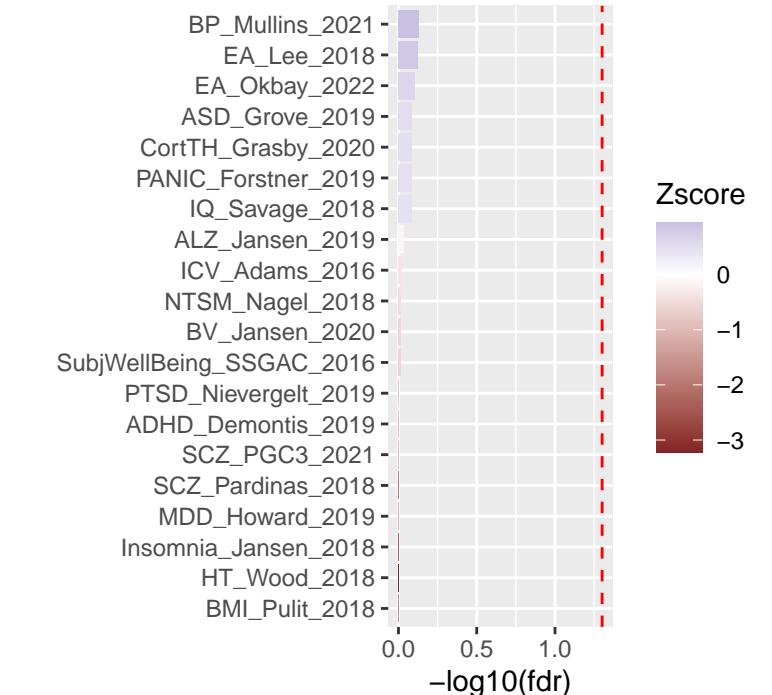
GO:MF

## RBP Enrichment

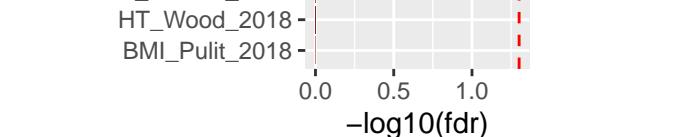


OR  
8  
6  
4

## GWAS Enrichment

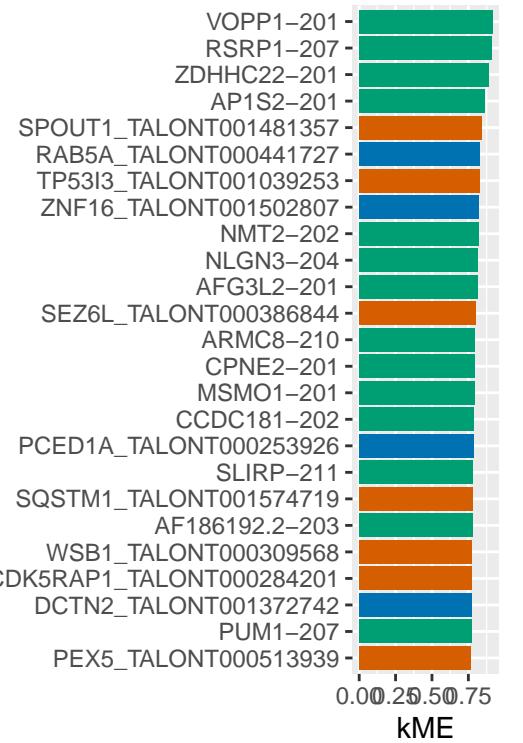
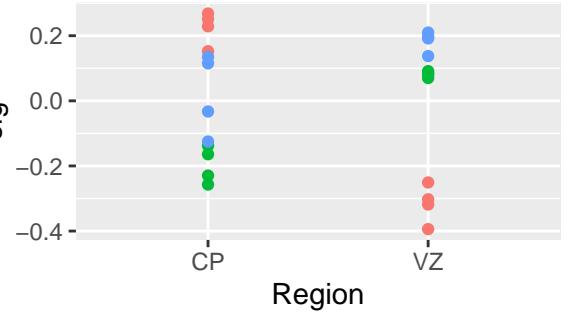


Zscore  
0  
-1  
-2  
-3

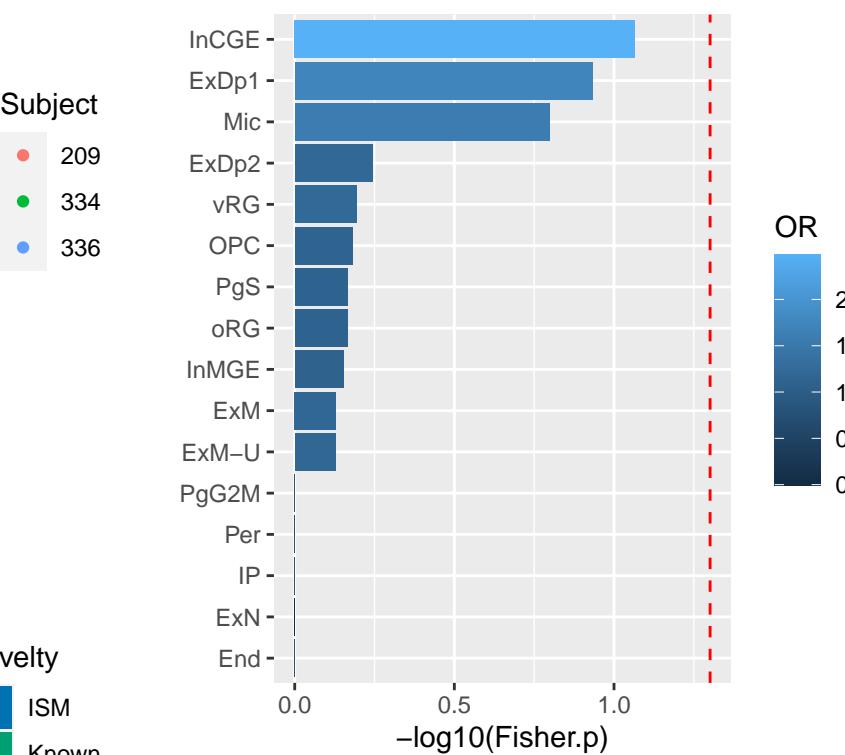
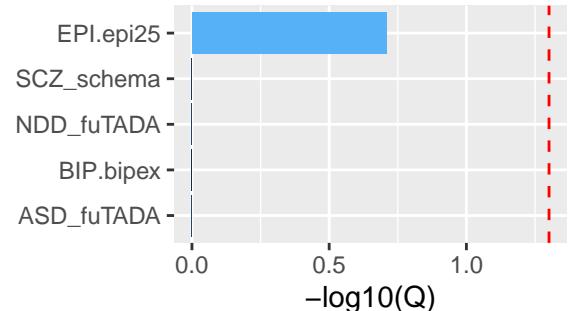


-log10(fdr)

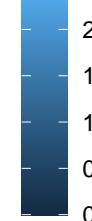
### Module 36: yellowgreen n=156



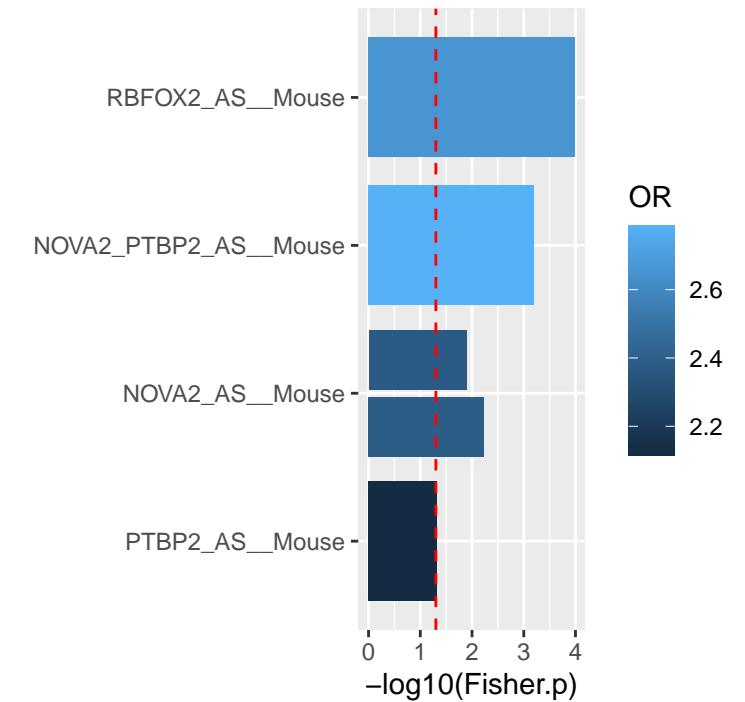
### Rare Var Enrichment



OR



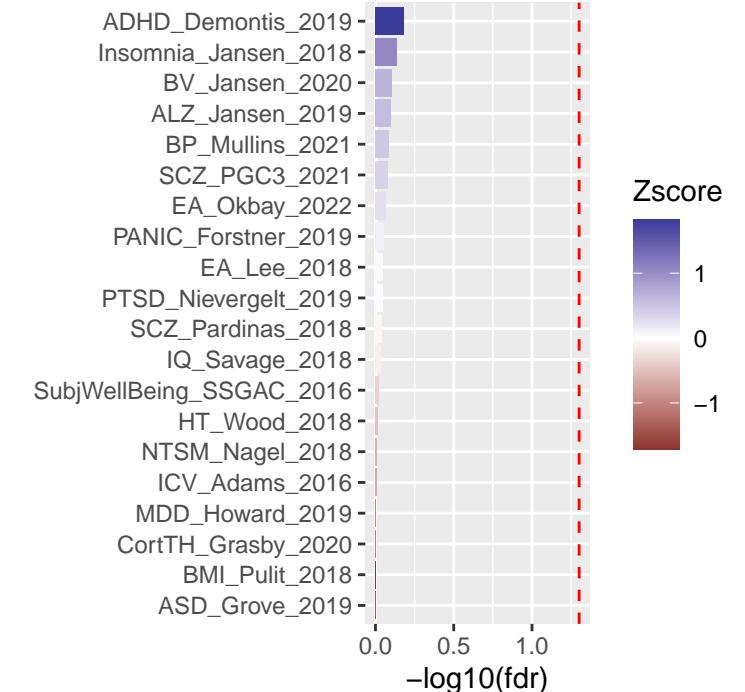
### RBP Enrichment



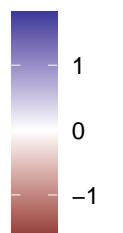
OR



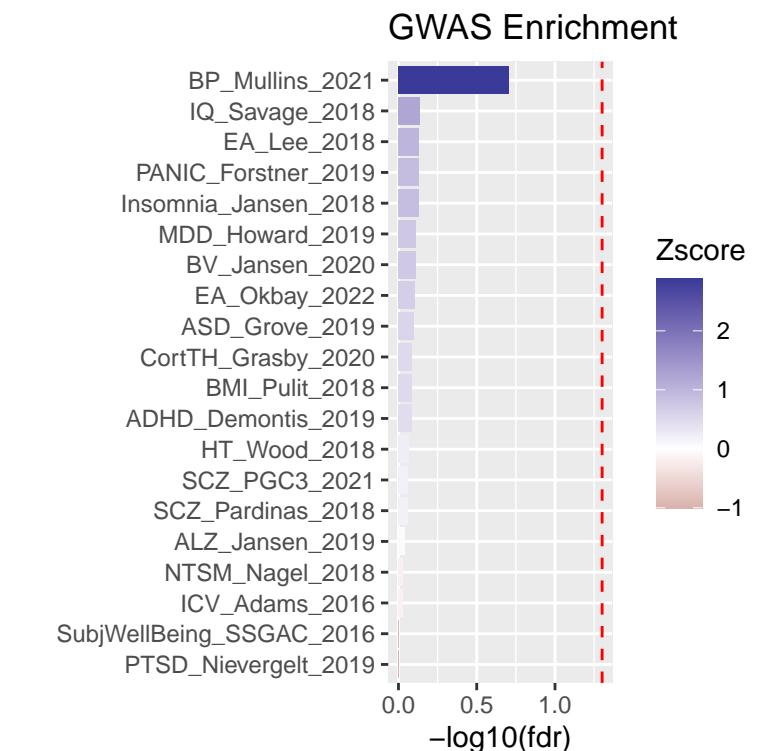
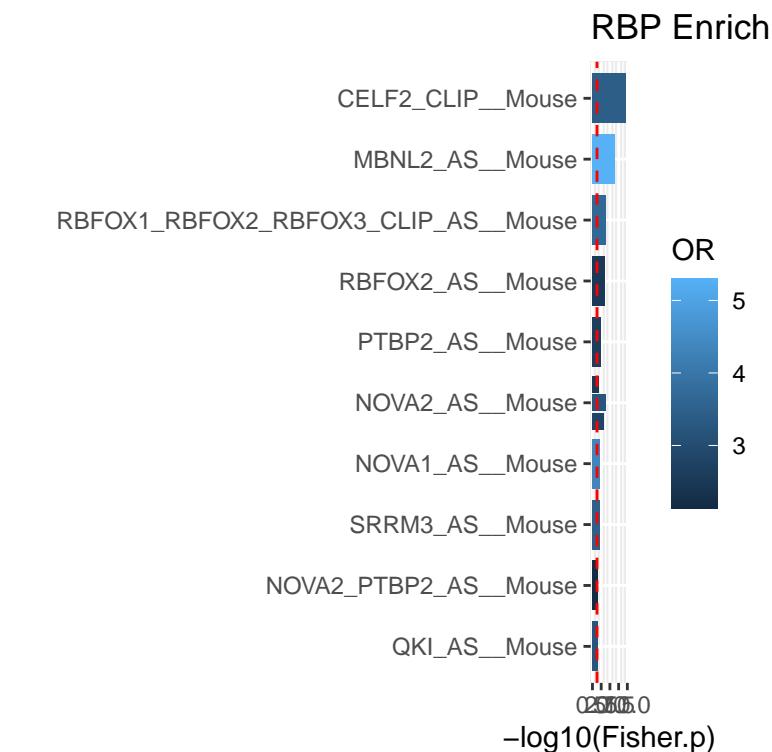
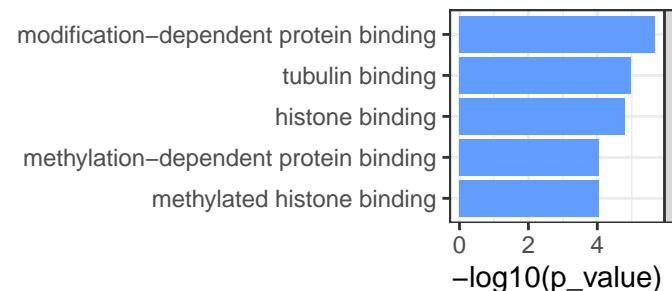
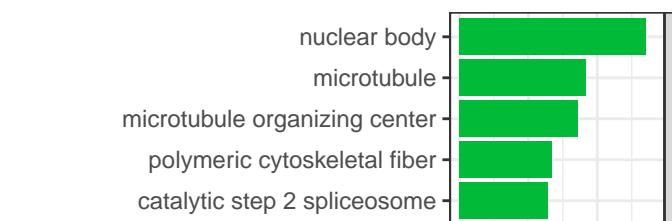
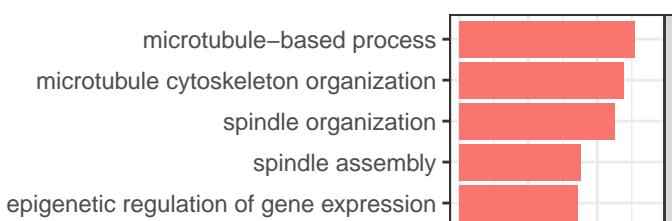
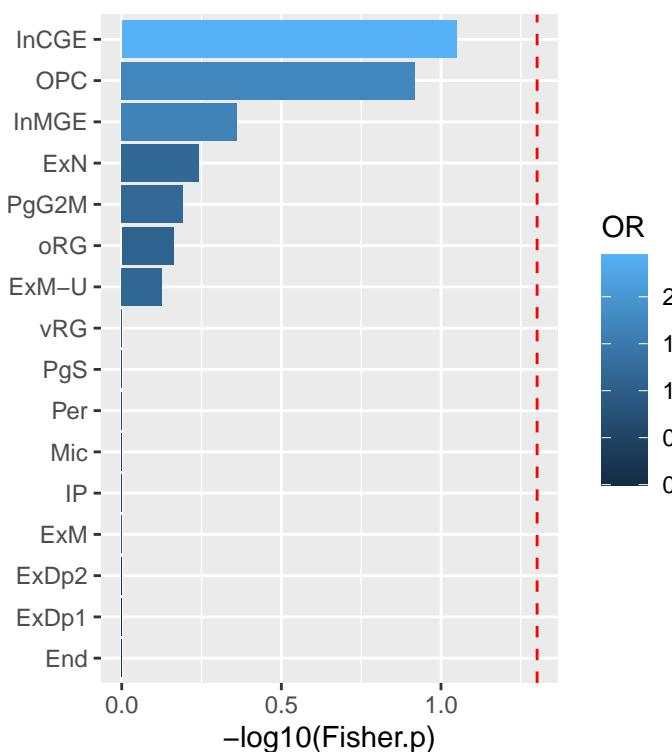
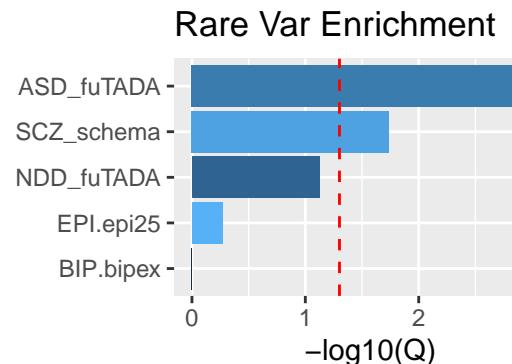
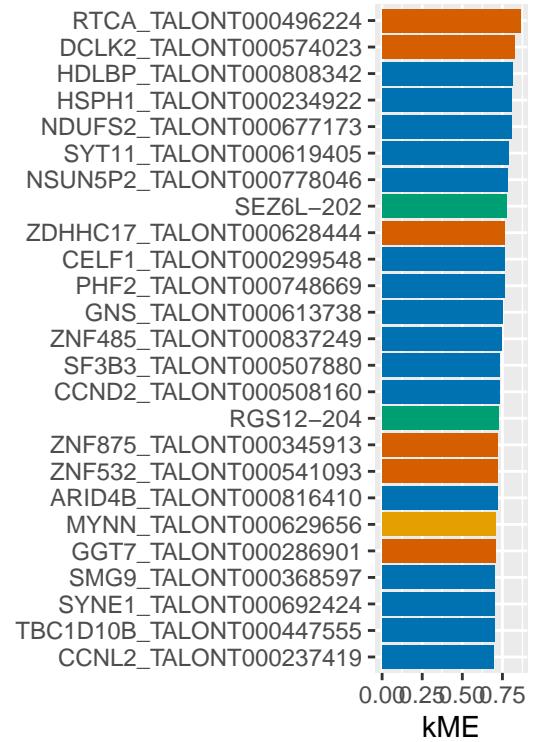
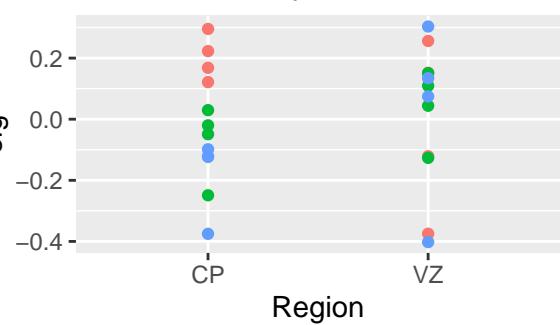
### GWAS Enrichment



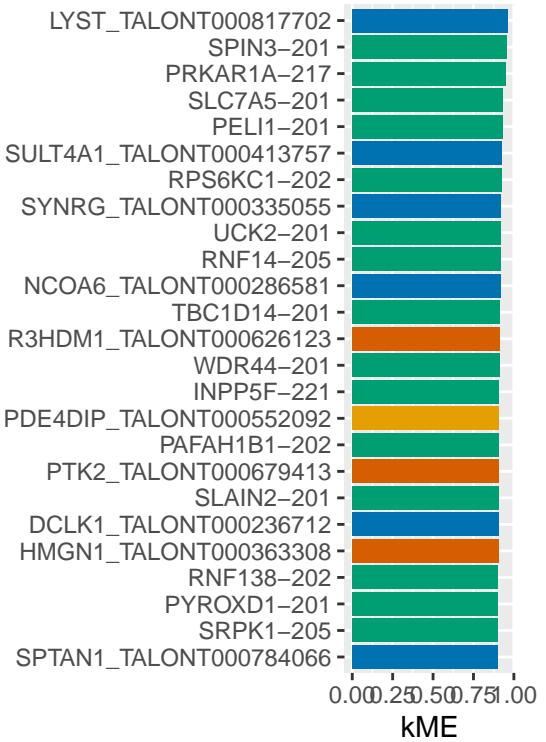
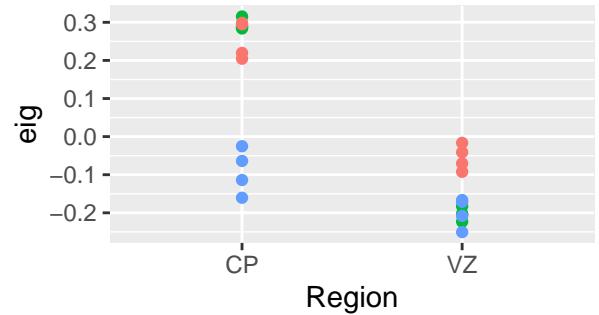
Zscore



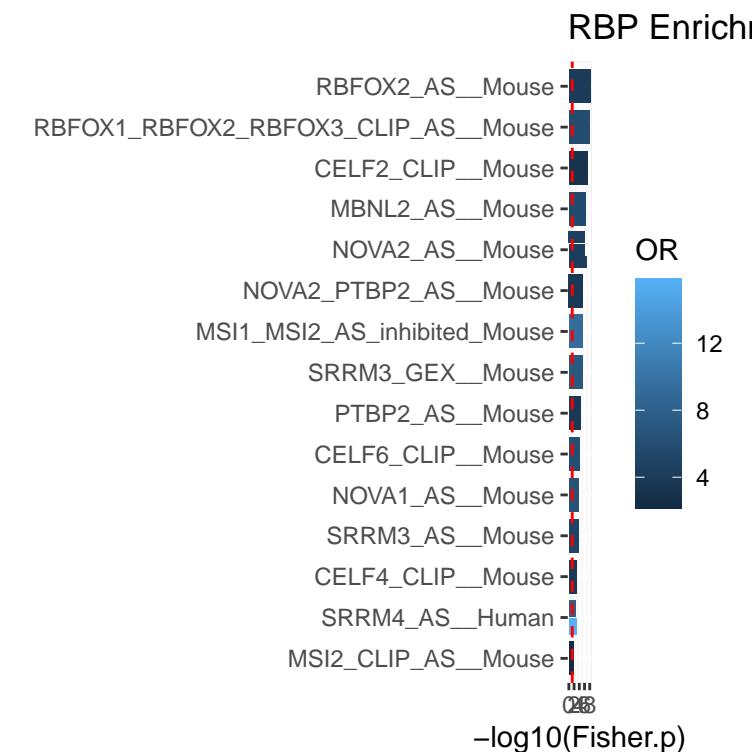
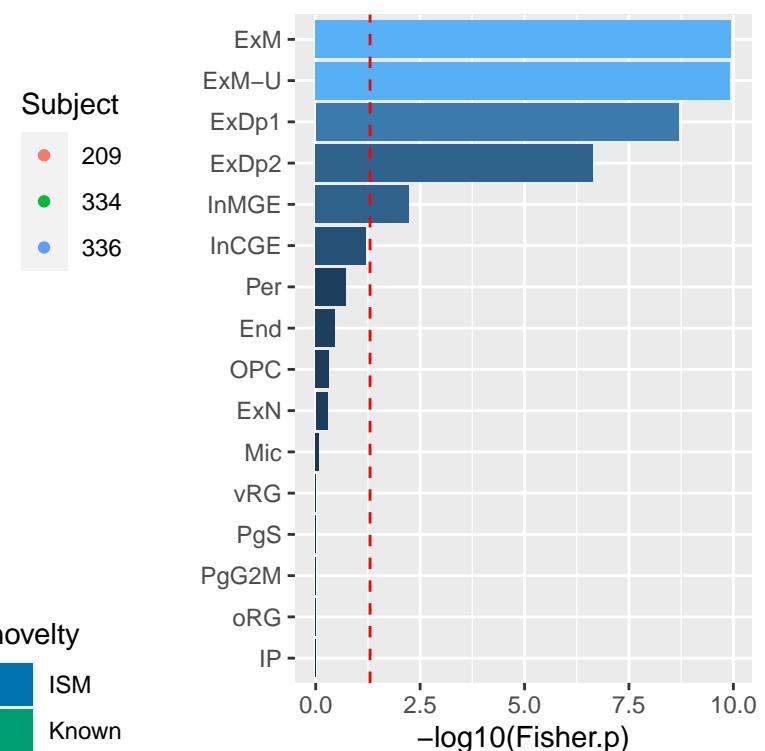
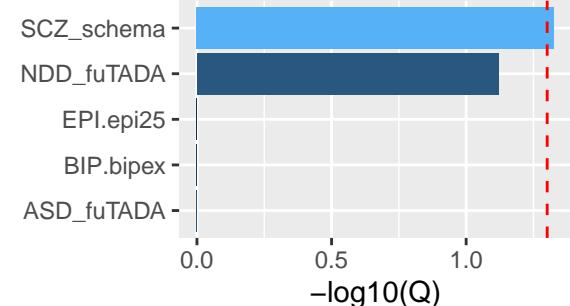
# Module 37: skyblue3 n=150



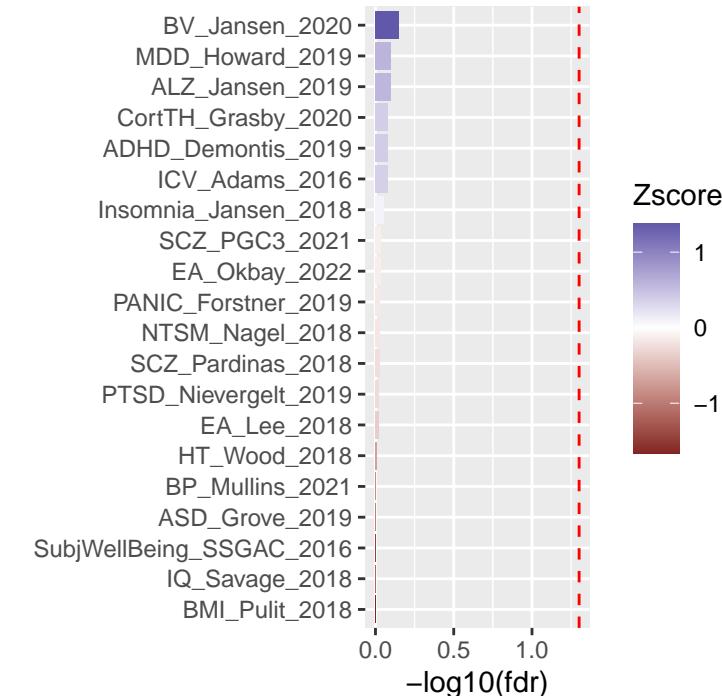
# Module 38: plum1 n=148



## Rare Var Enrichment



## GWAS Enrichment



cell morphogenesis  
cell part morphogenesis  
cellular component morphogenesis  
neuron development  
adult locomotory behavior

postsynapse  
clathrin-coated vesicle  
axon  
somatodendritic compartment  
dendritic tree

cytoskeletal protein binding  
tubulin binding  
microtubule binding  
GTPase binding

Phosphatidylinositol signaling system  
Bacterial invasion of epithelial cells

GO:BP

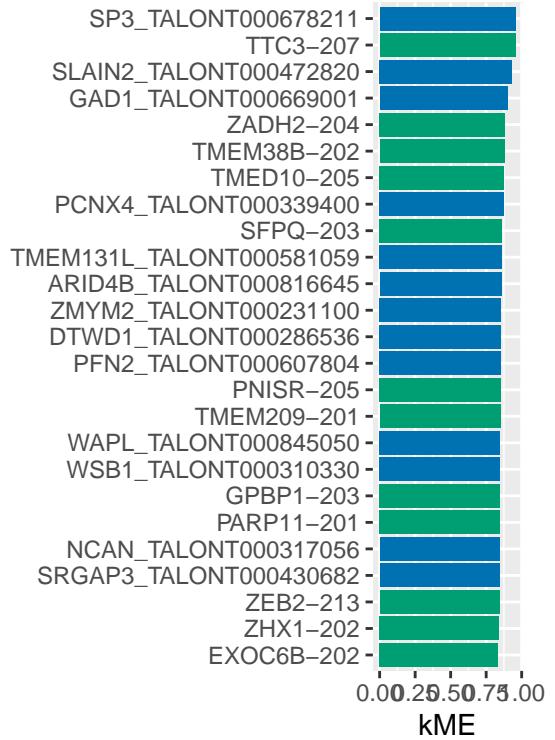
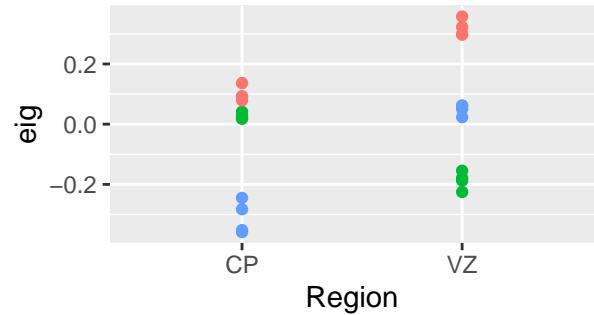
GO:CC

GO:MF

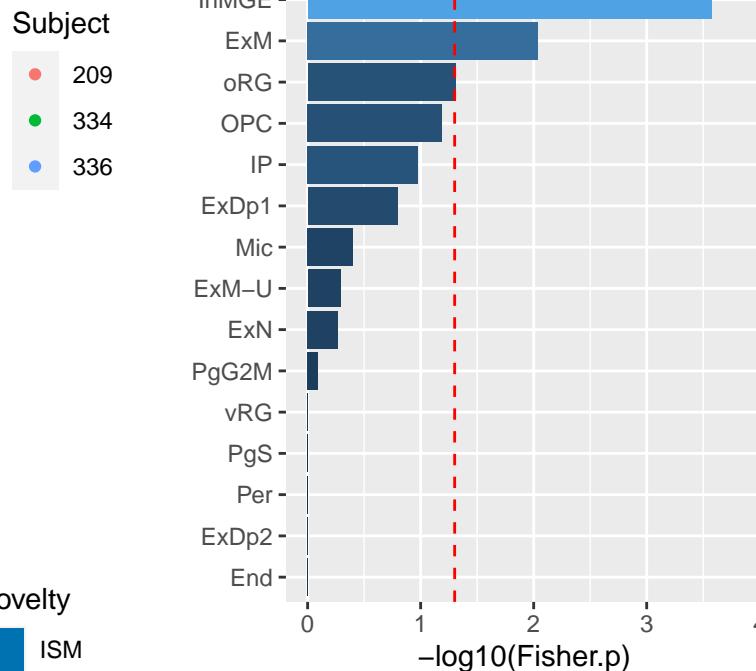
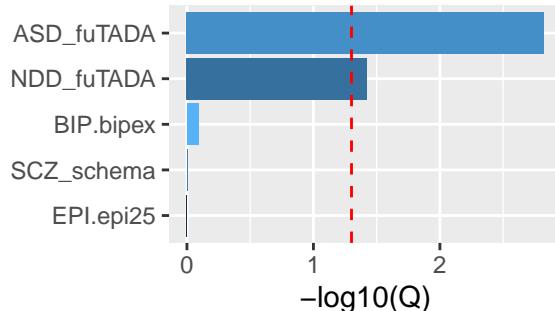
KEGG

-log10(p\_val)

# Module 39: orangered4 n=148



## Rare Var Enrichment



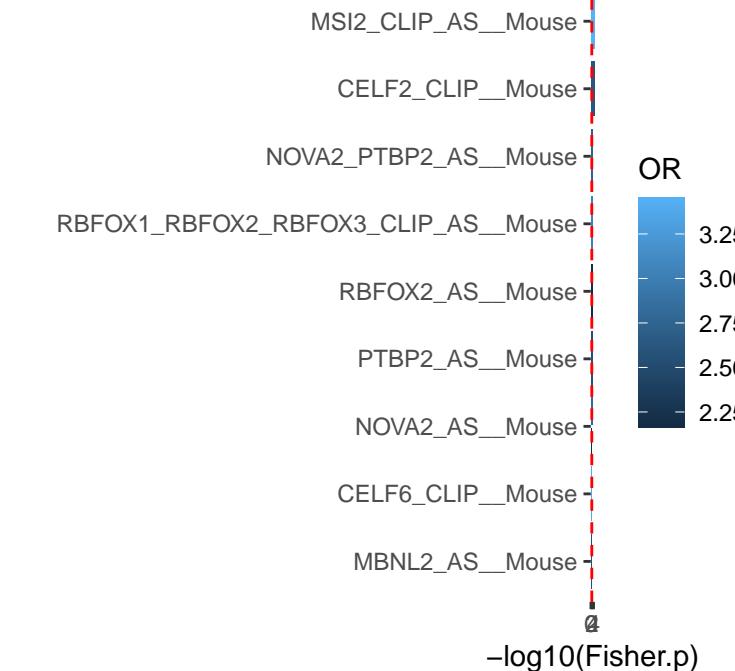
OR

5  
4  
3  
2  
1

-log10(Fisher.p)

positive regulation of cellular component organization  
epigenetic regulation of gene expression  
regulation of plasma membrane bounded cell projection organization  
regulation of cell projection organization  
positive regulation of cellular component biogenesis  
nuclear body  
chromatin silencing complex  
nuclear speck  
chromatin  
microtubule plus-end  
chromatin binding  
DNA topoisomerase activity  
transcription coregulator activity  
protein kinase regulator activity  
protein domain specific binding

RBP Enrich

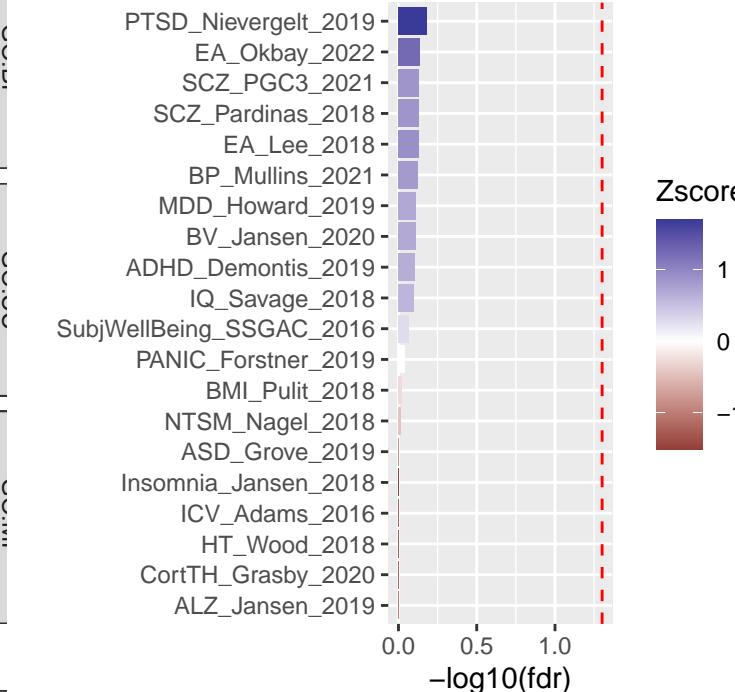


OR

3.25  
3.00  
2.75  
2.50  
2.25

-log10(Fisher.p)

## GWAS Enrichment

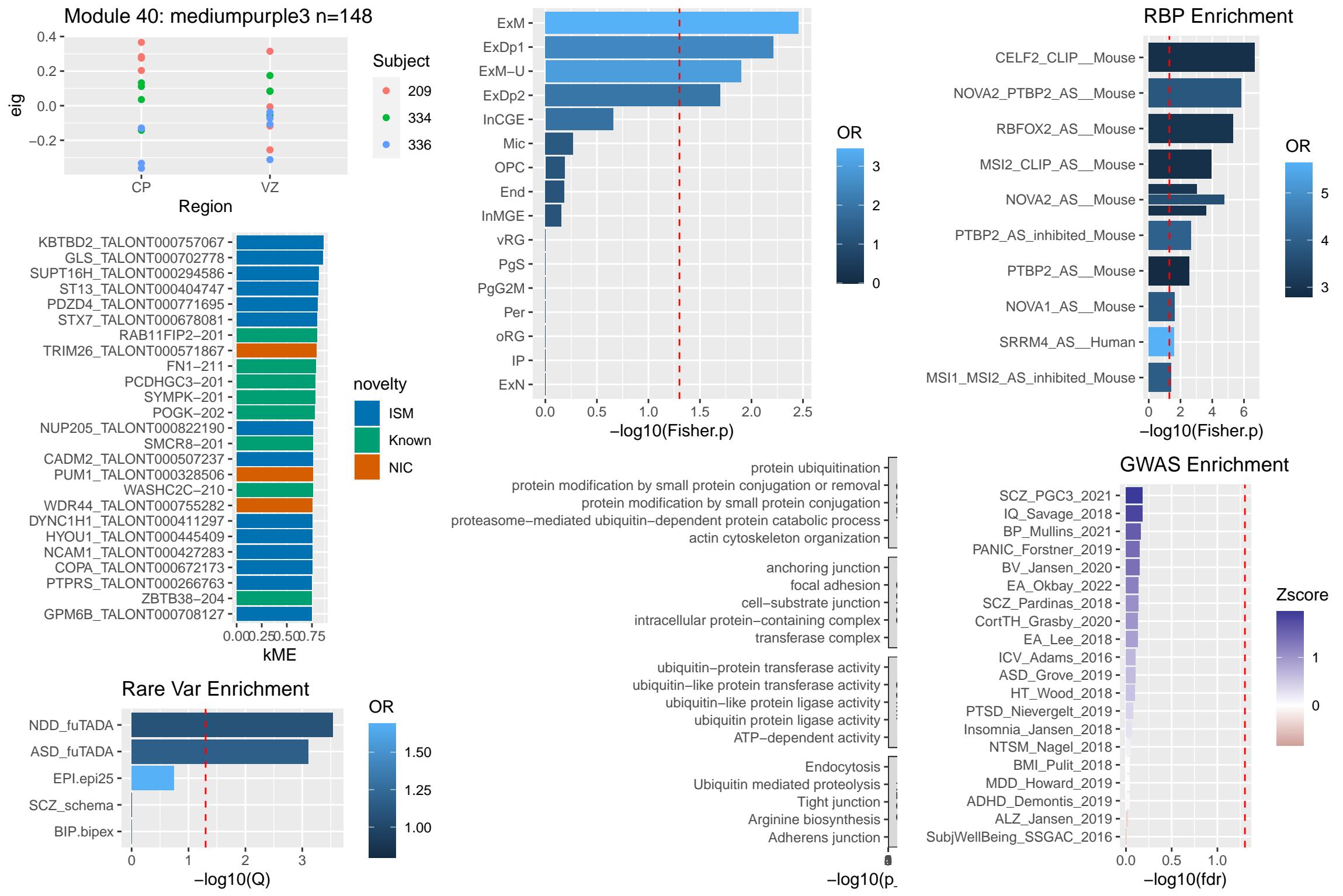


Zscore

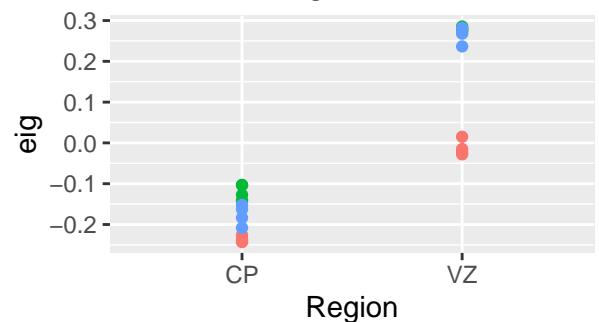
1  
0  
-1

-log10(p\_

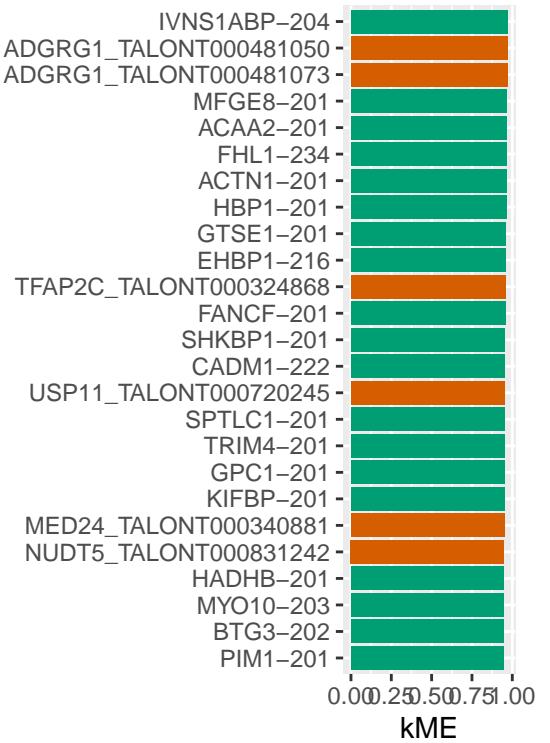
-log10(fdr)



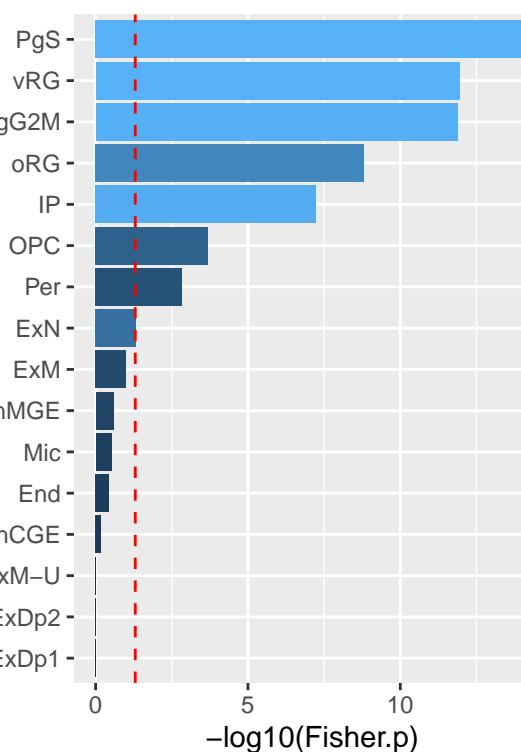
# Module 41: lightsteelblue1 n=145



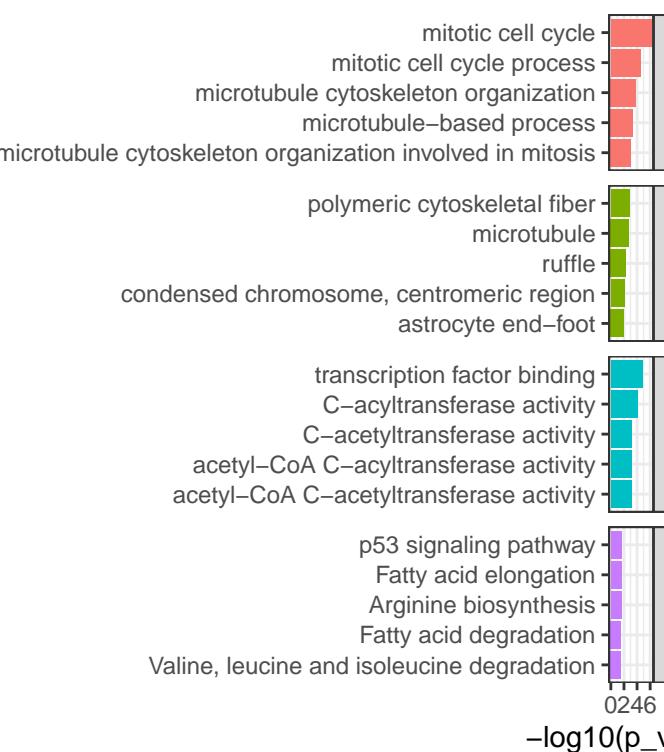
Subject  
209  
334  
336



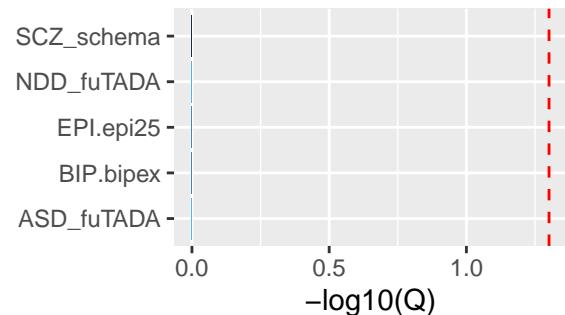
novelty  
Known  
NIC



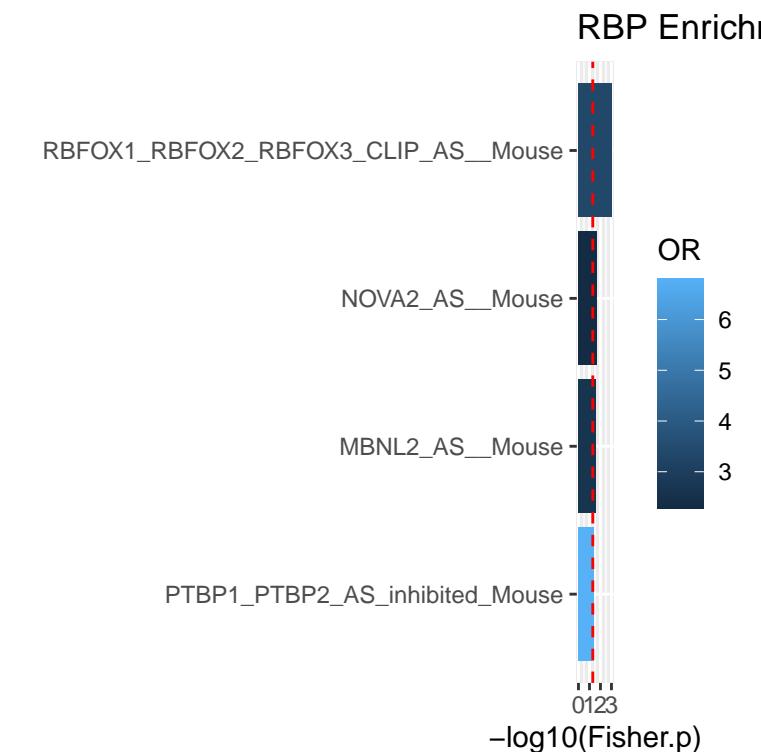
OR  
6  
4  
2



## Rare Var Enrichment

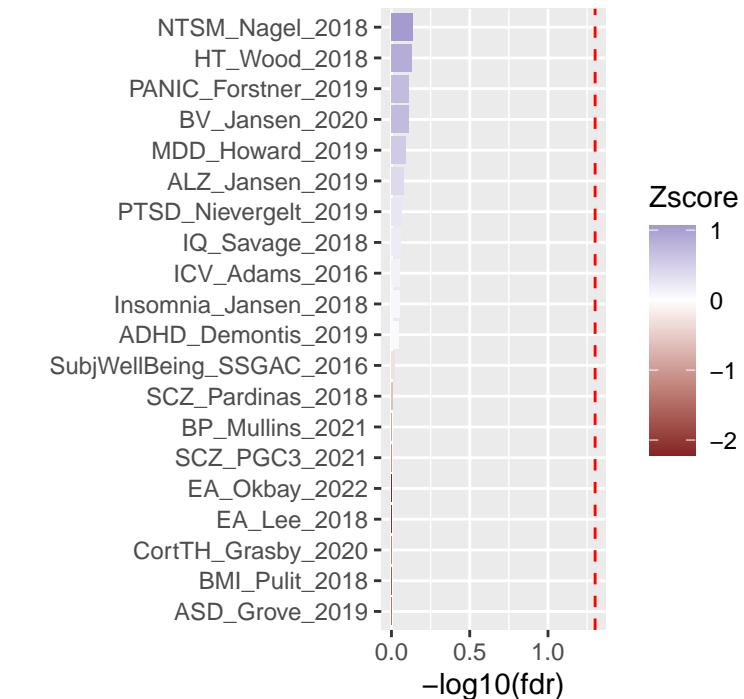


OR  
1.0  
0.9  
0.8



OR  
6  
5  
4  
3

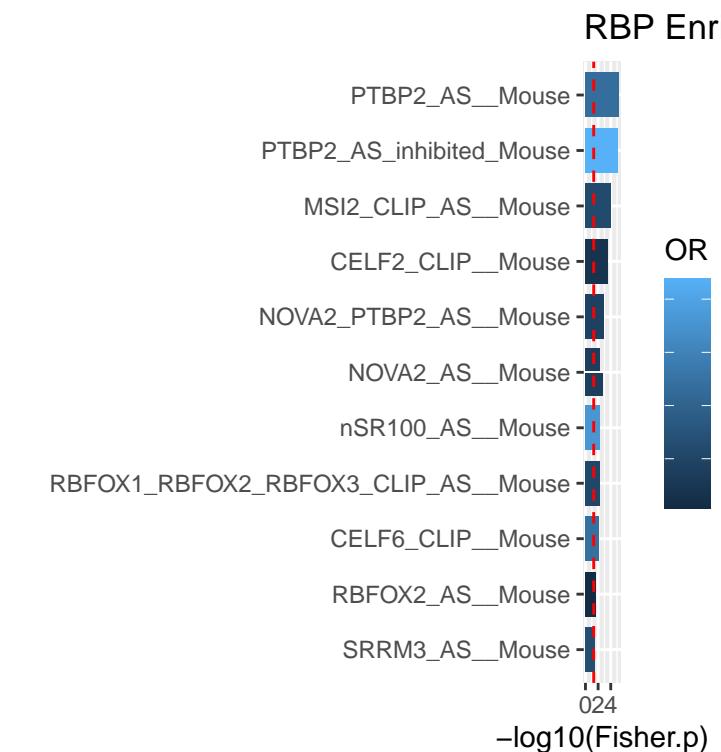
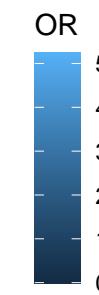
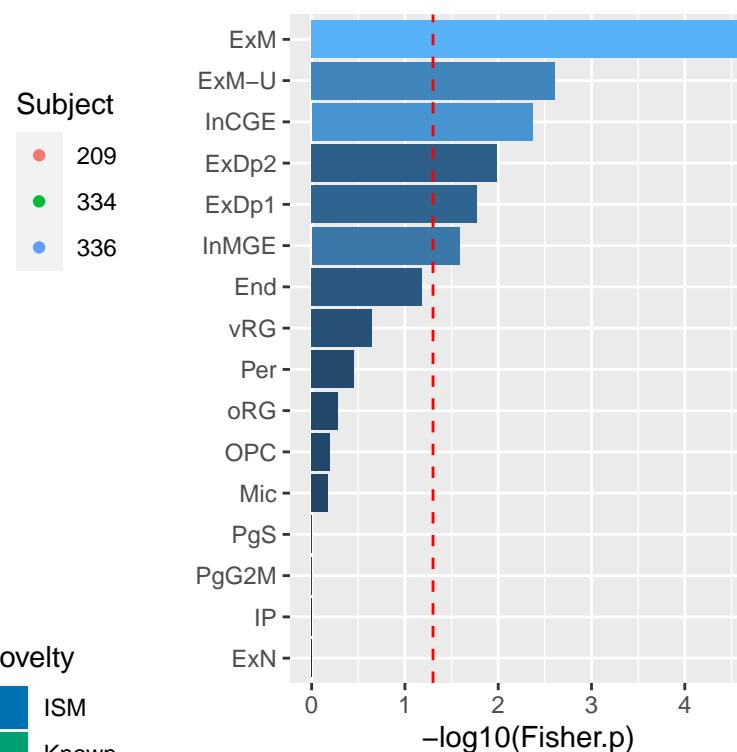
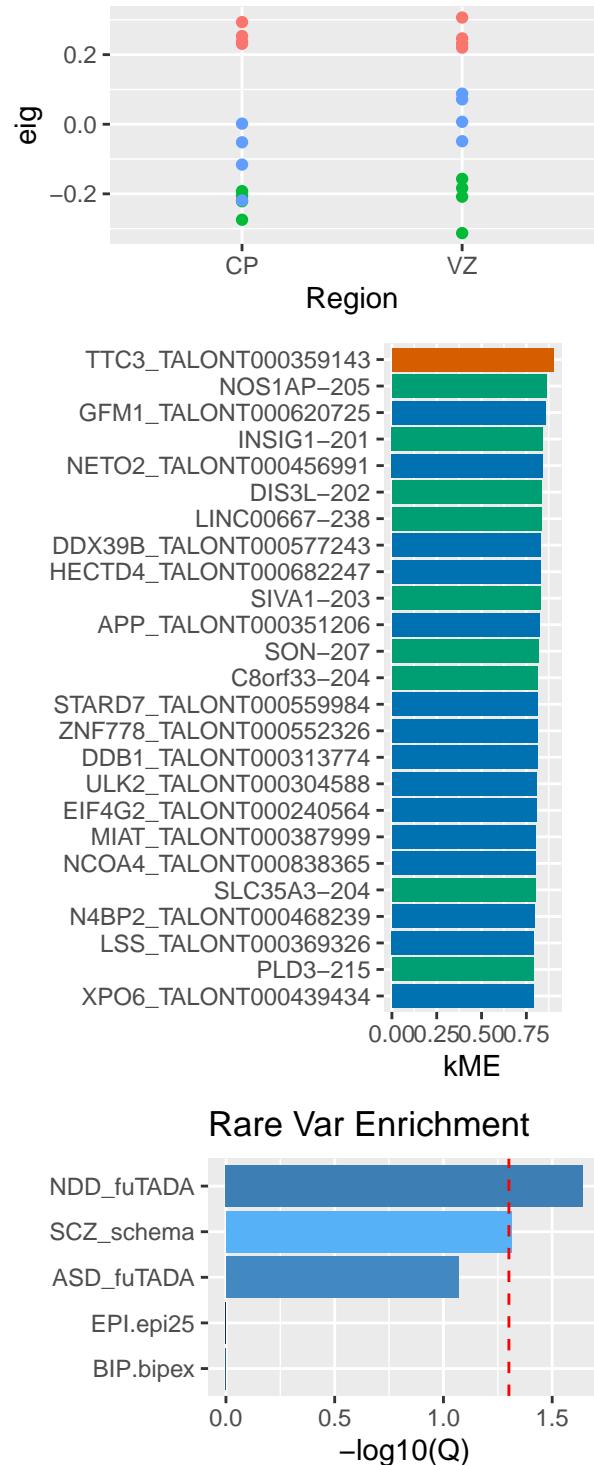
## GWAS Enrichment



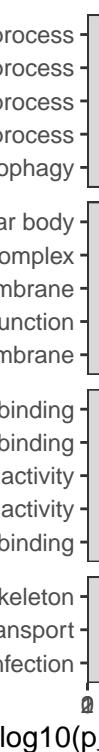
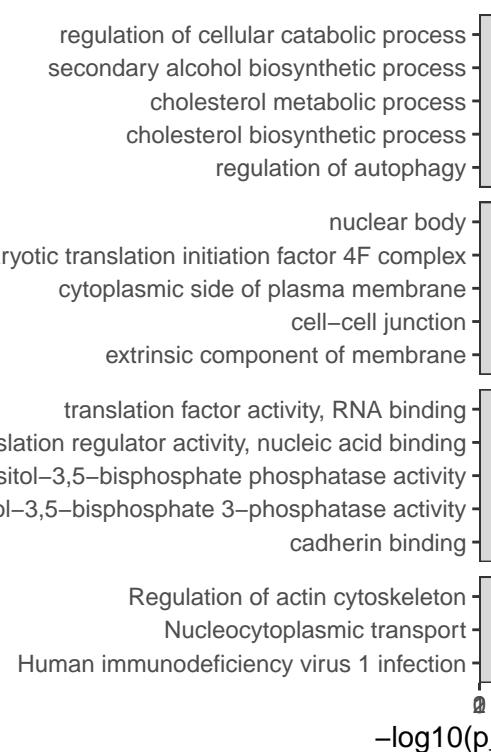
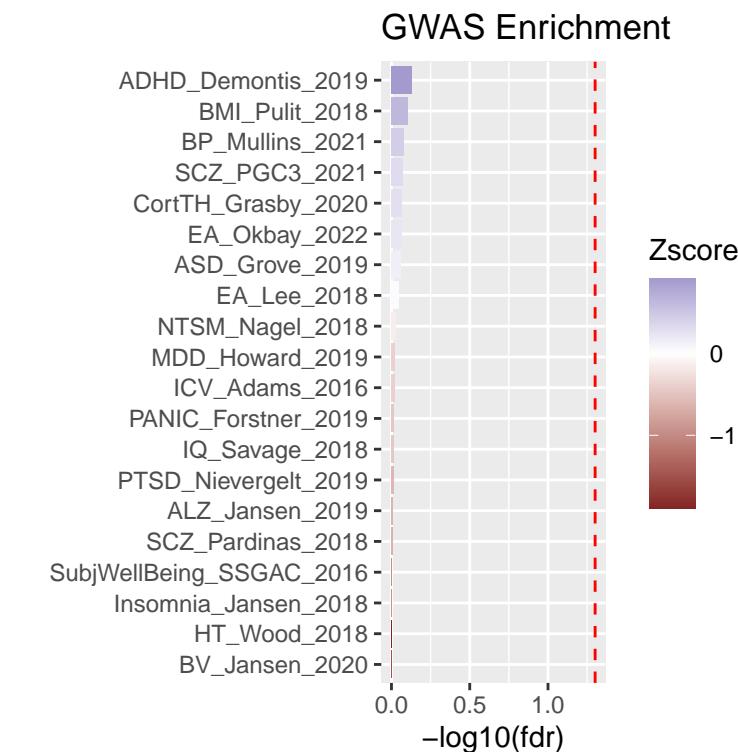
Zscore  
1  
0  
-1  
-2

-log10(fdr)

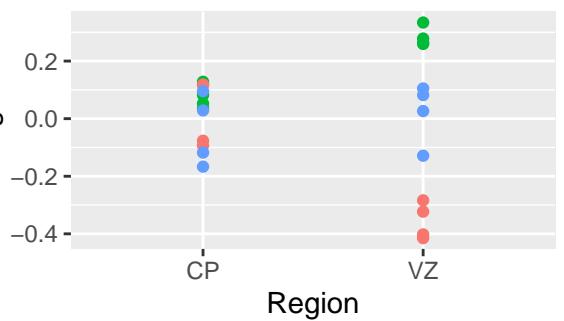
## Module 42: lightcyan1 n=140



## GWAS Enrichment

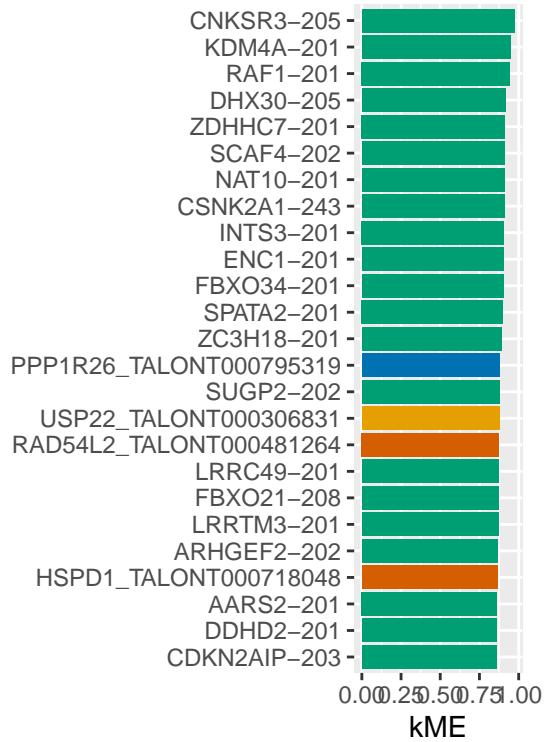


## Module 43: ivory n=135



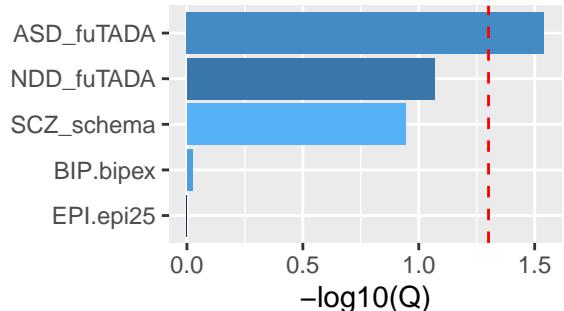
Subject  
209  
334  
336

Region



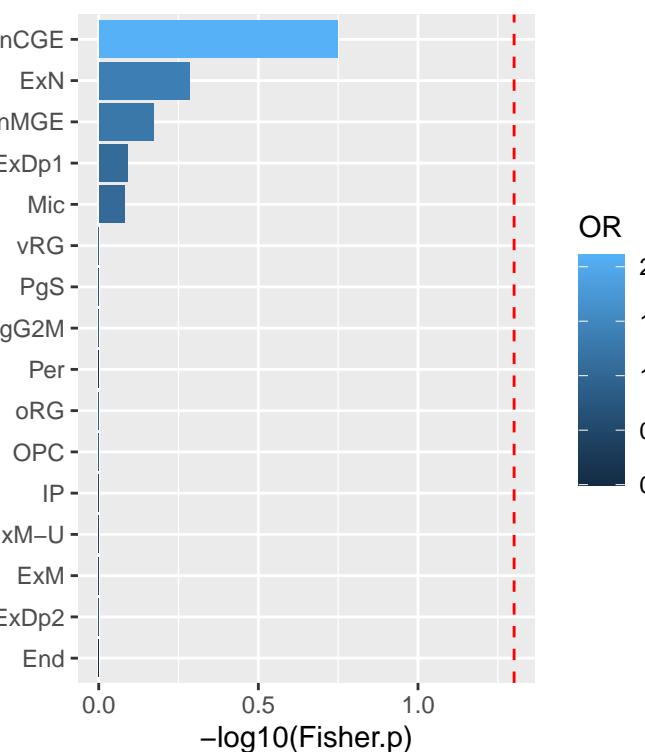
kME

### Rare Var Enrichment



OR  
1.2  
1.1  
1.0  
0.9  
0.8

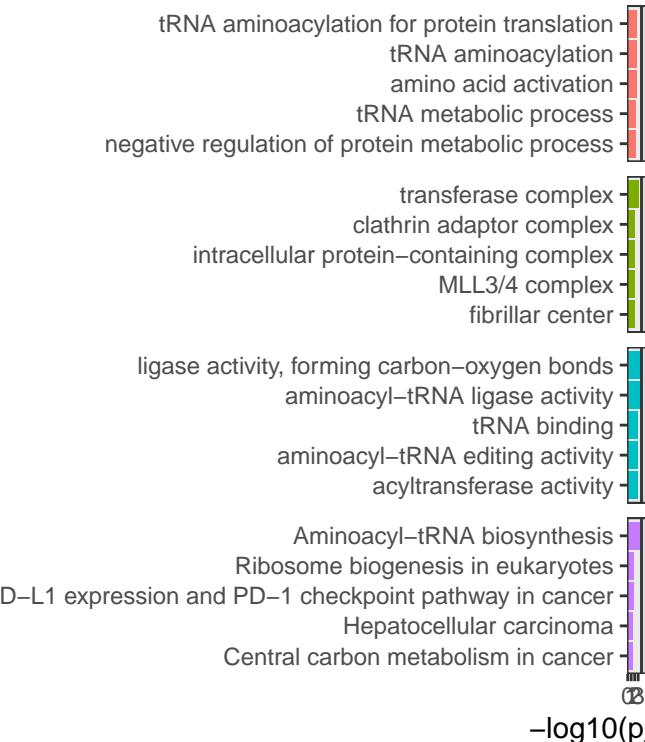
-log10(Q)



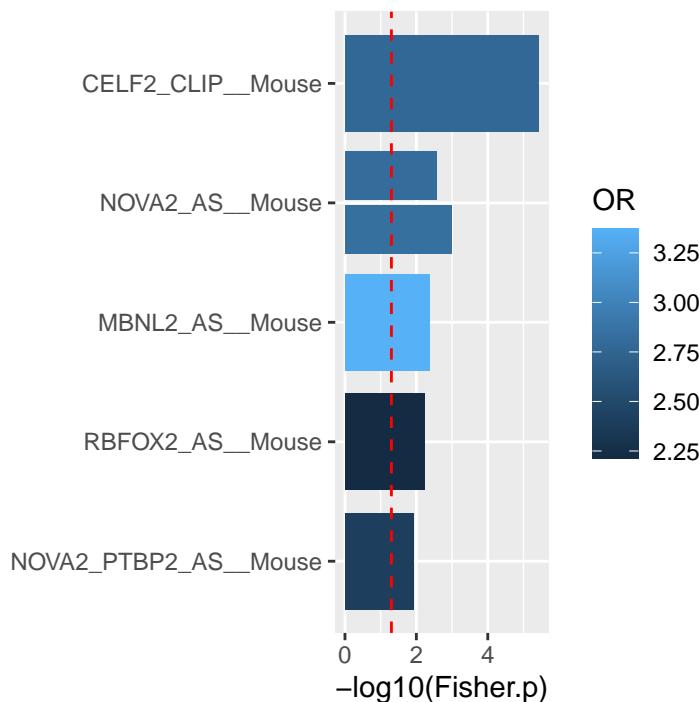
OR

2.0  
1.5  
1.0  
0.5  
0.0

-log10(Fisher.p)



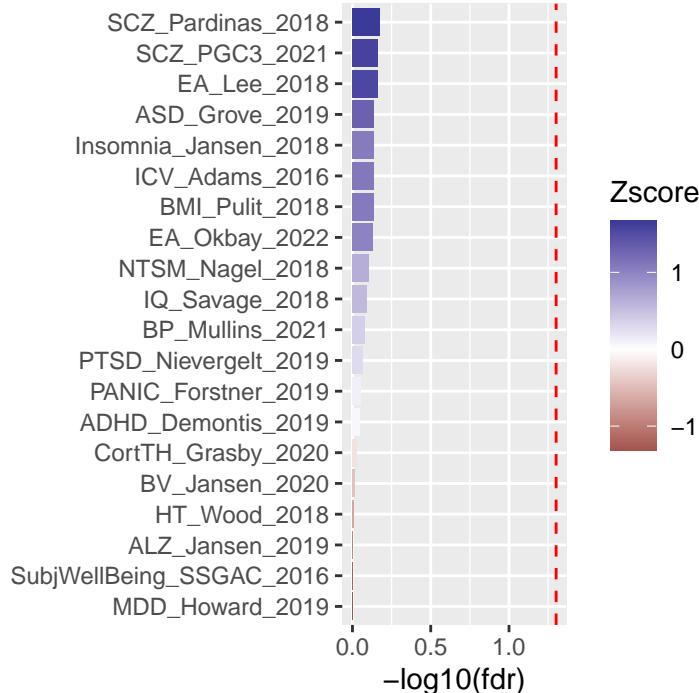
## RBP Enrichment



OR  
3.25  
3.00  
2.75  
2.50  
2.25

-log10(Fisher.p)

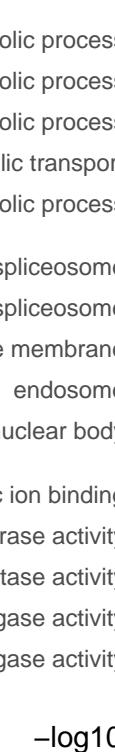
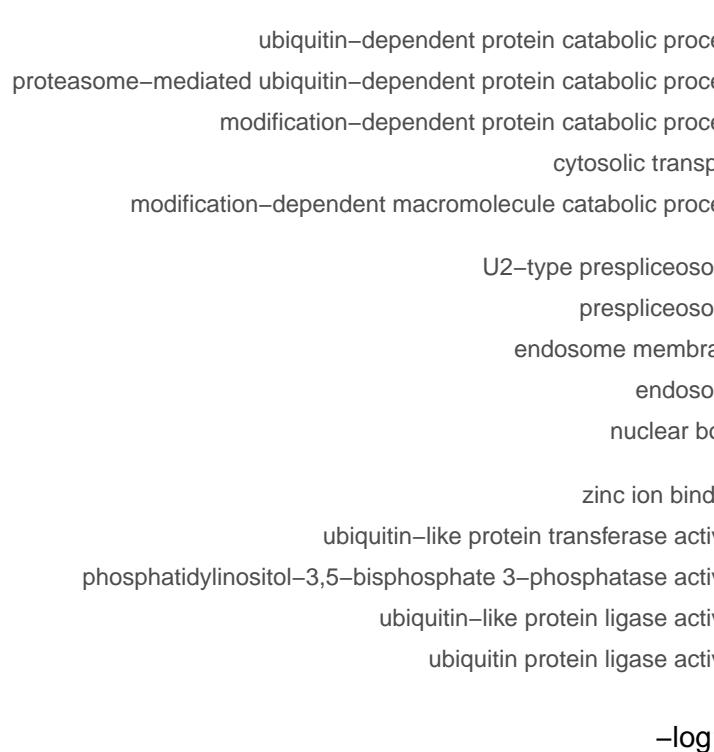
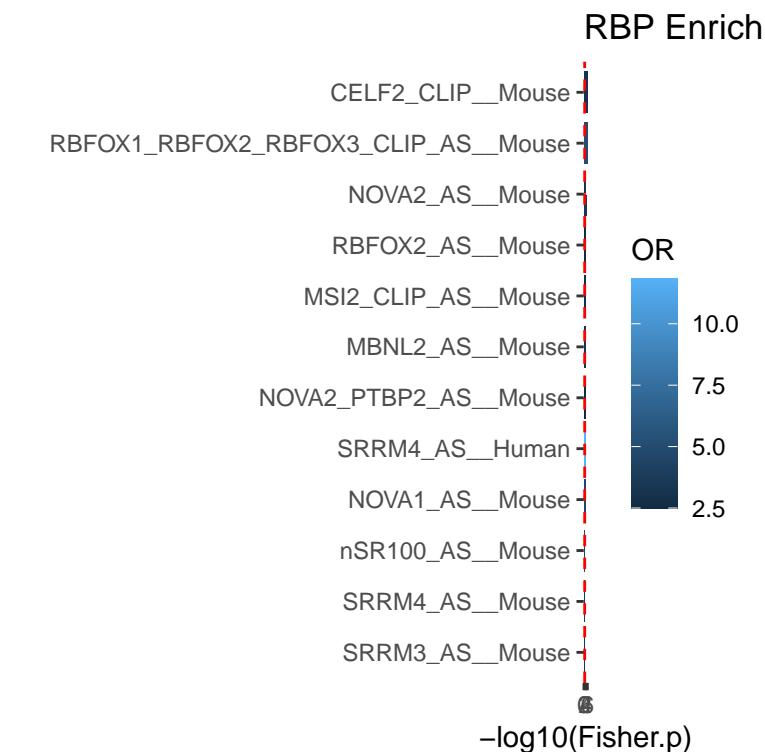
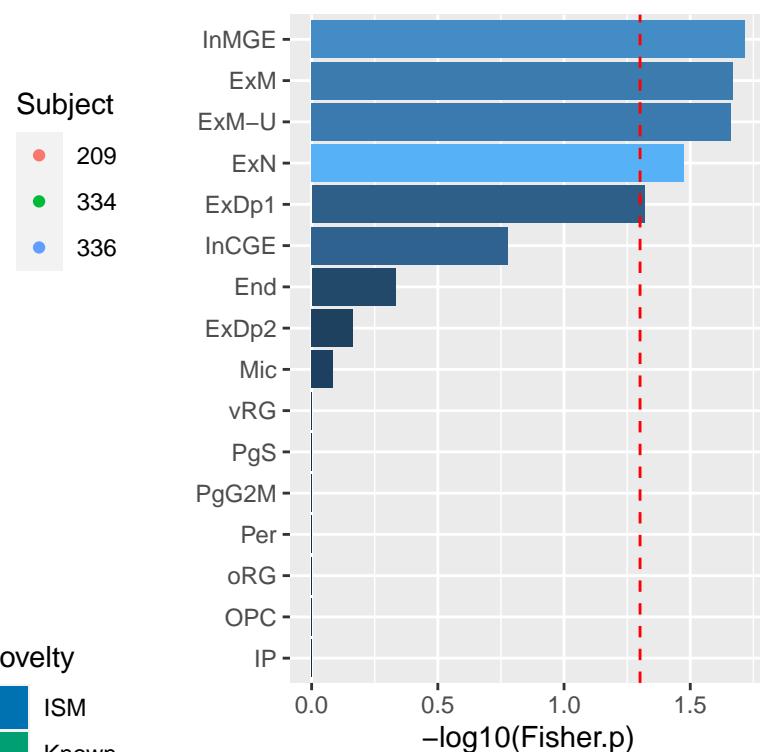
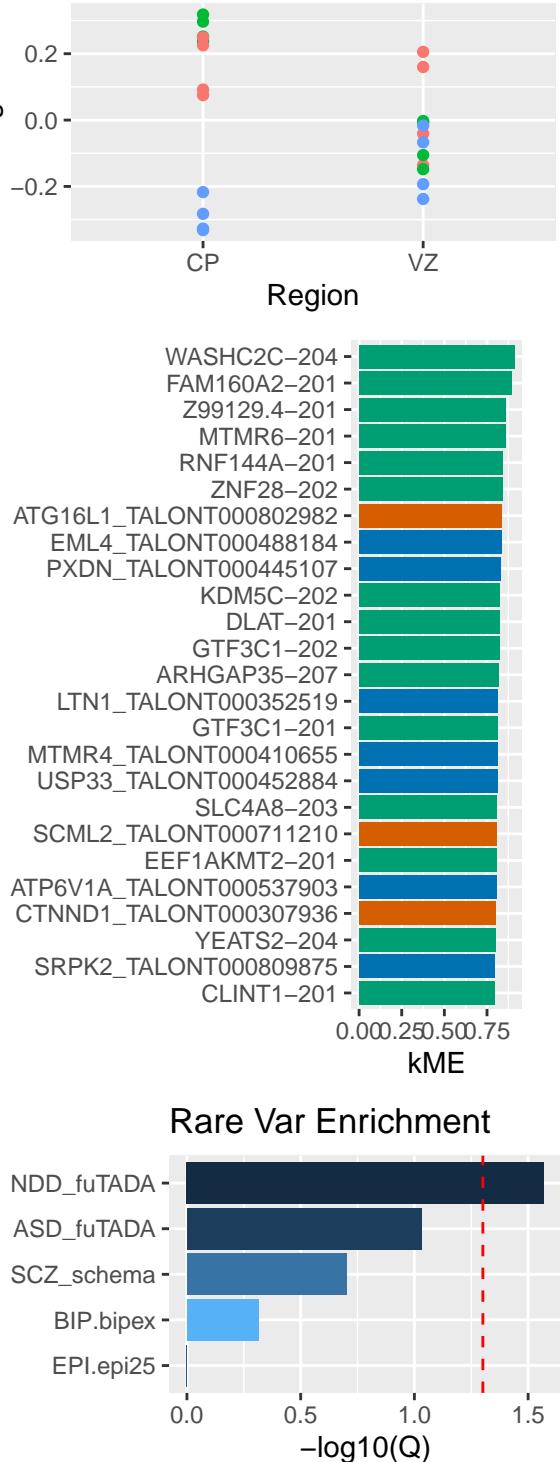
## GWAS Enrichment



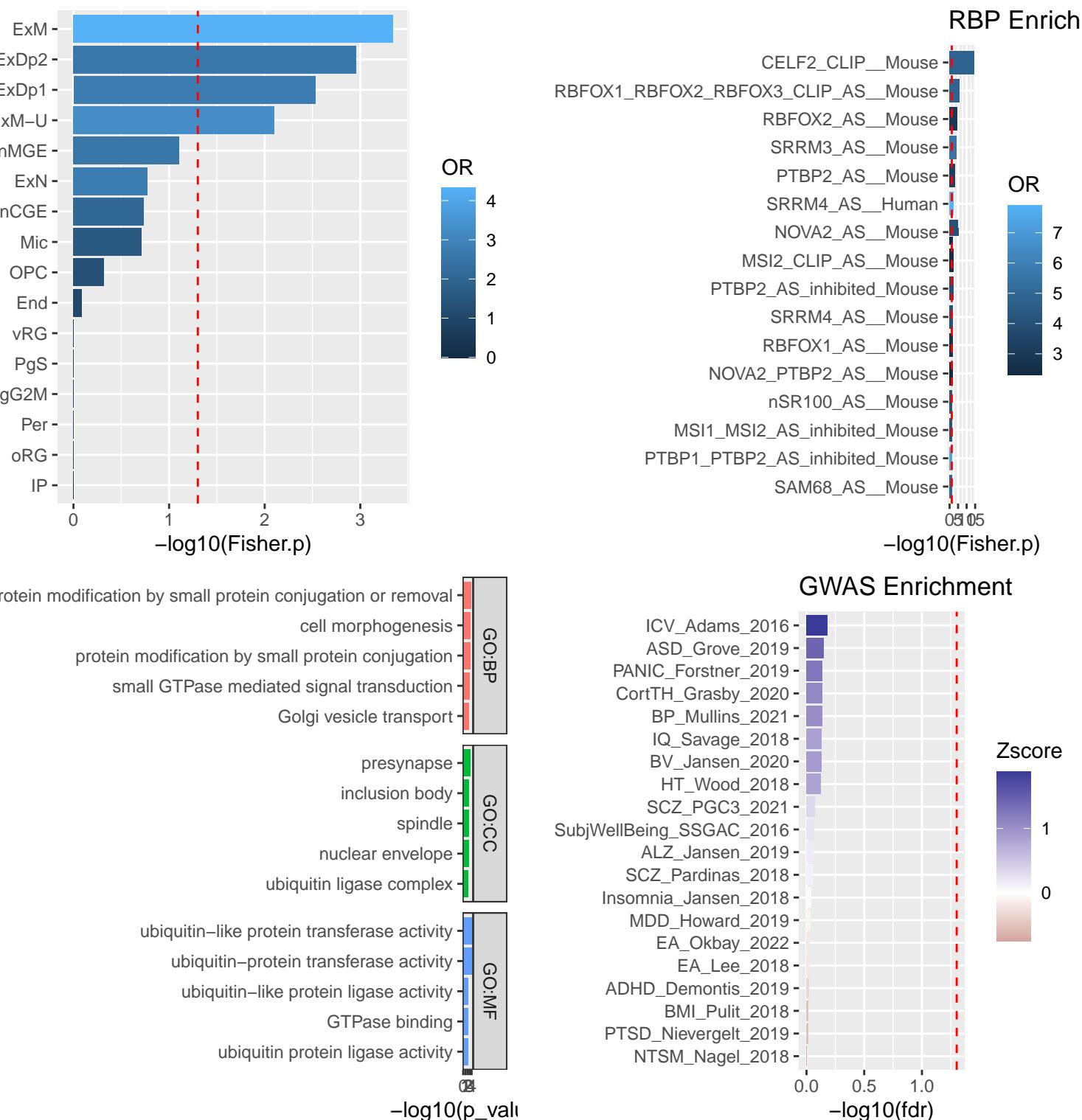
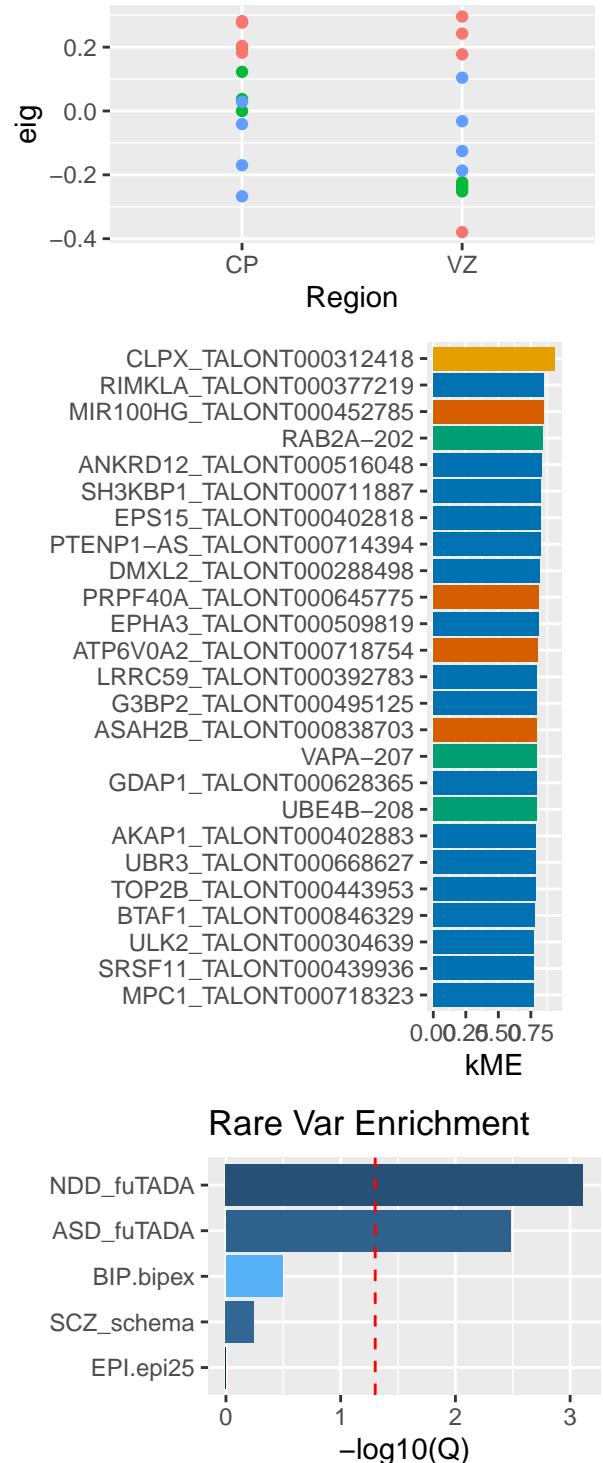
Zscore  
1  
0  
-1

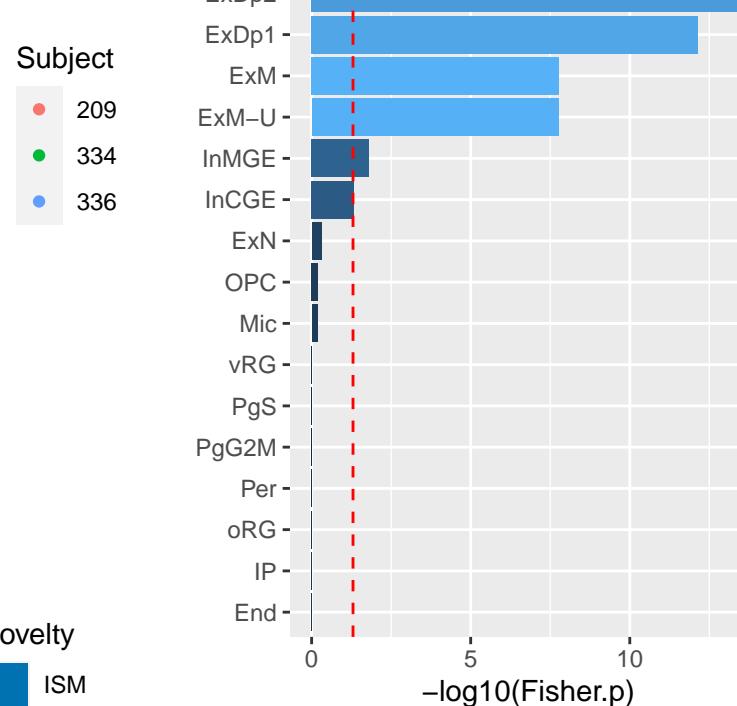
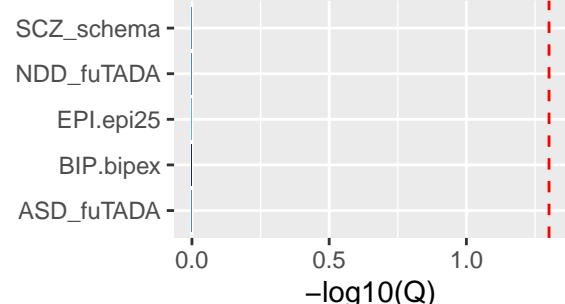
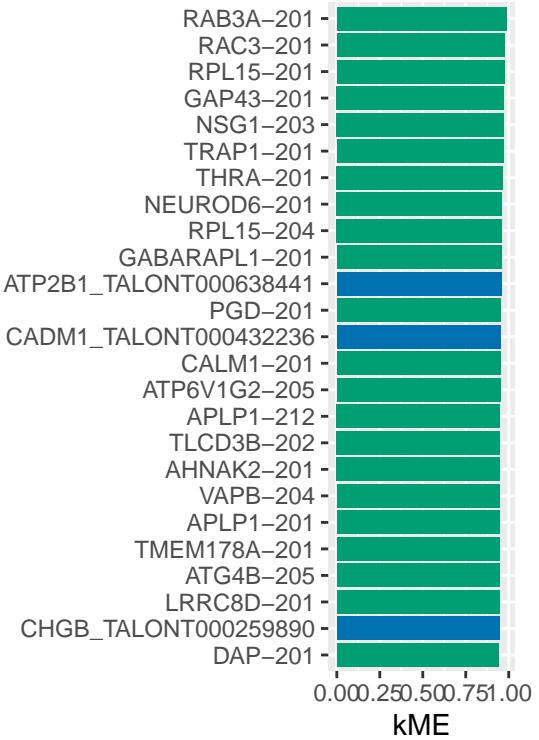
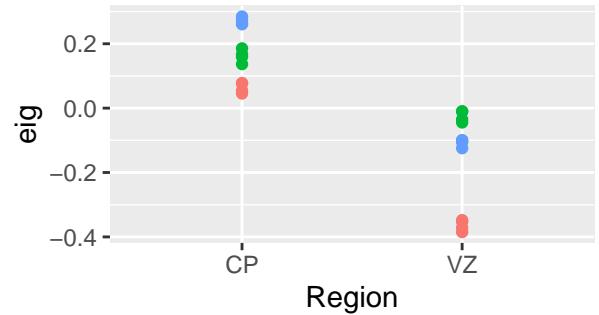
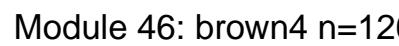
-log10(fdr)

# Module 44: floralwhite n=135



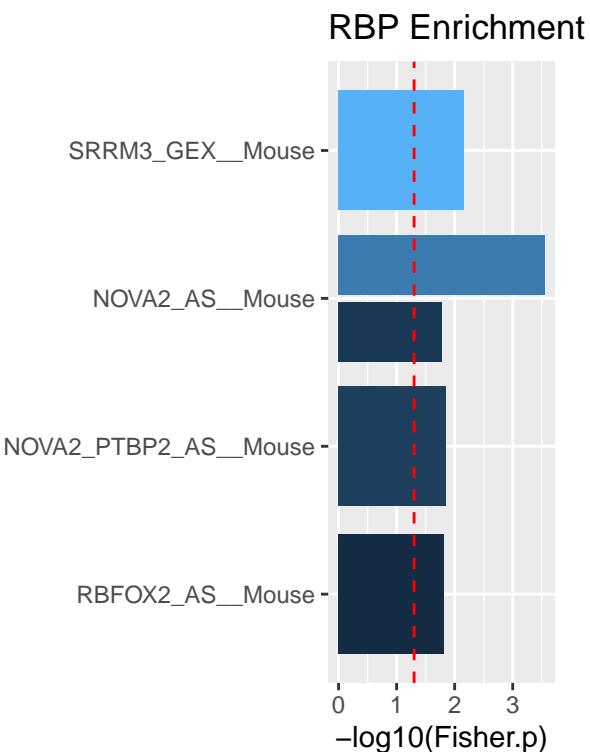
# Module 45: darkorange2 n=134



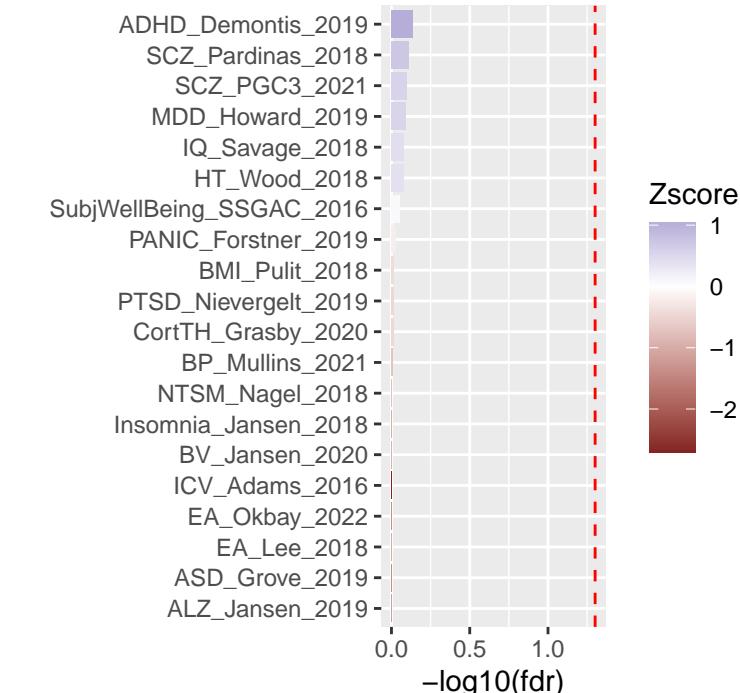


central nervous system development  
cell morphogenesis involved in neuron differentiation  
axonogenesis  
axon development  
central nervous system neuron development  
  
site of polarized growth  
growth cones  
distal axon  
intrinsic component of synaptic vesicle membrane  
synaptic vesicle membrane  
ribonucleoside triphosphate phosphatase activity  
pyrophosphatase activity  
protein domain specific binding  
acid anhydrides, in phosphorus-containing anhydrides  
hydrolase activity, acting on acid anhydrides

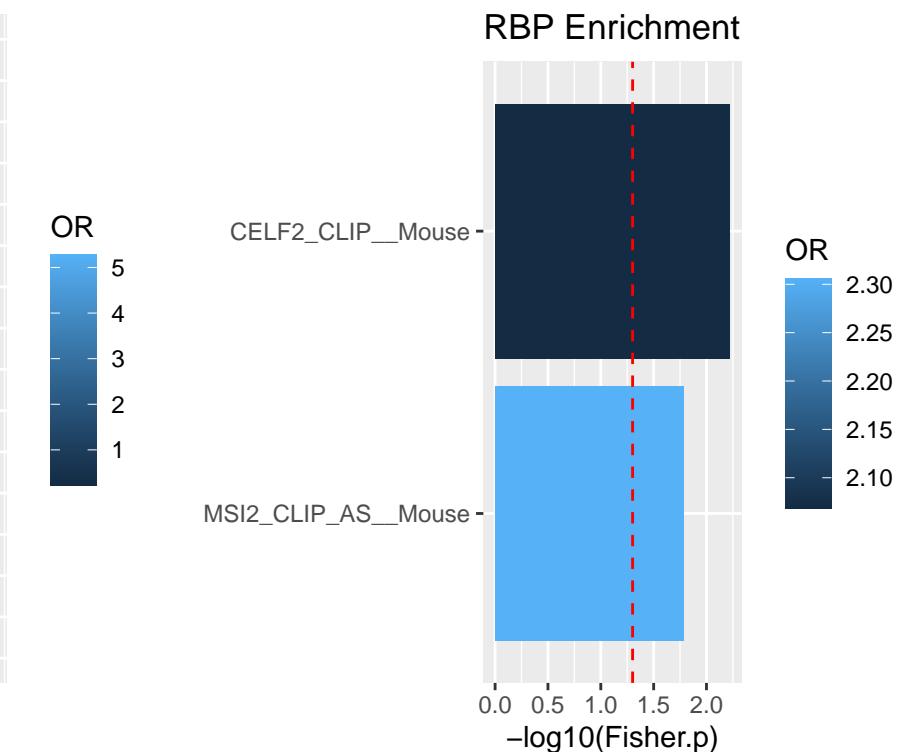
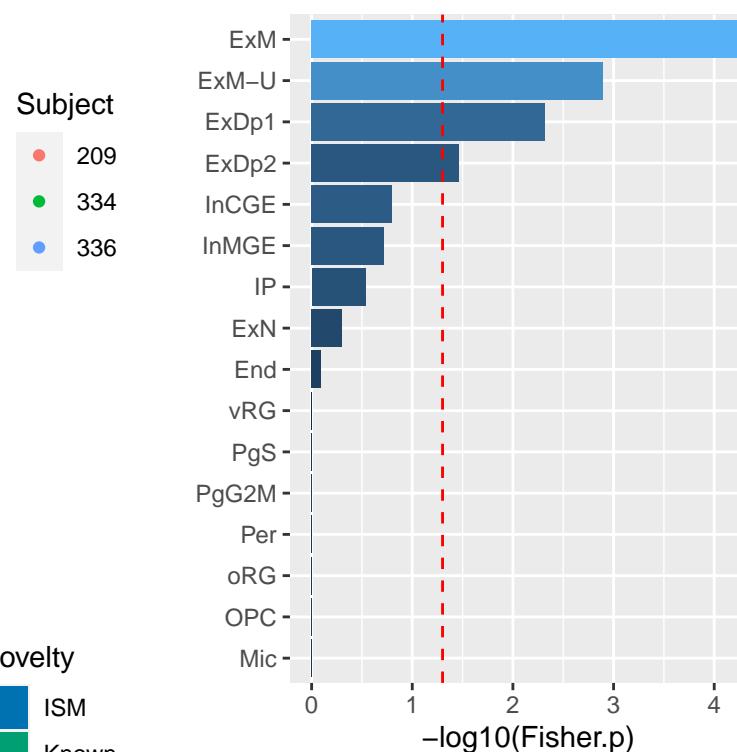
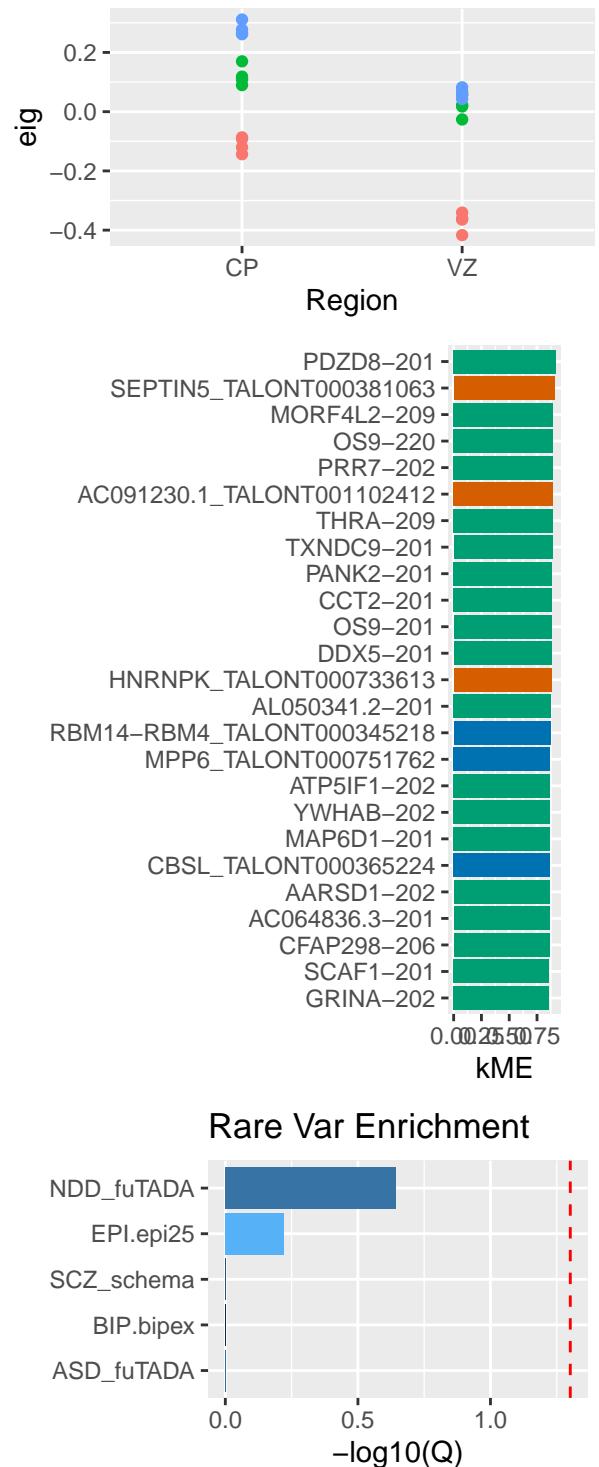
Endocrine and other factor-regulated calcium reabsorption  
cAMP signaling pathway  
Autophagy – Cytosolic calcium  
Salivary secretion



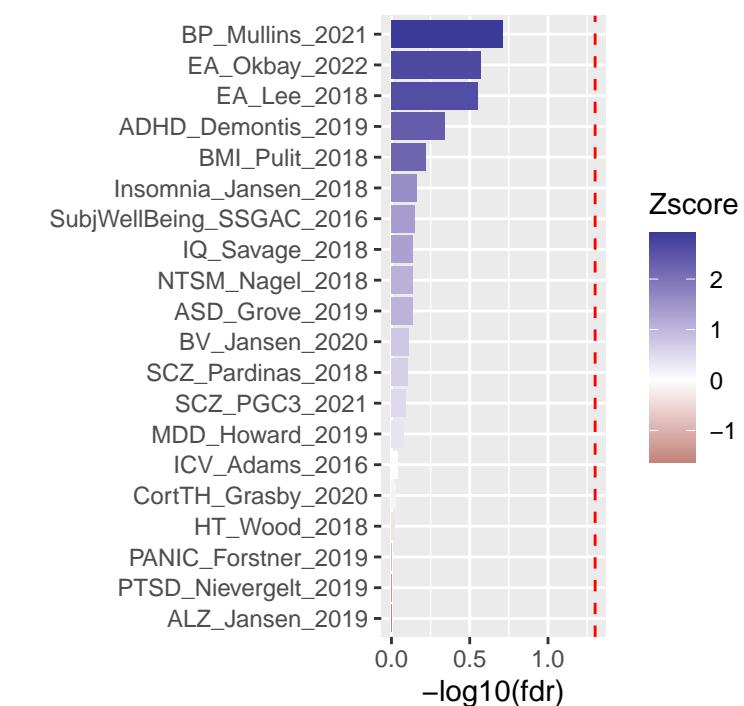
## RBP Enrichment



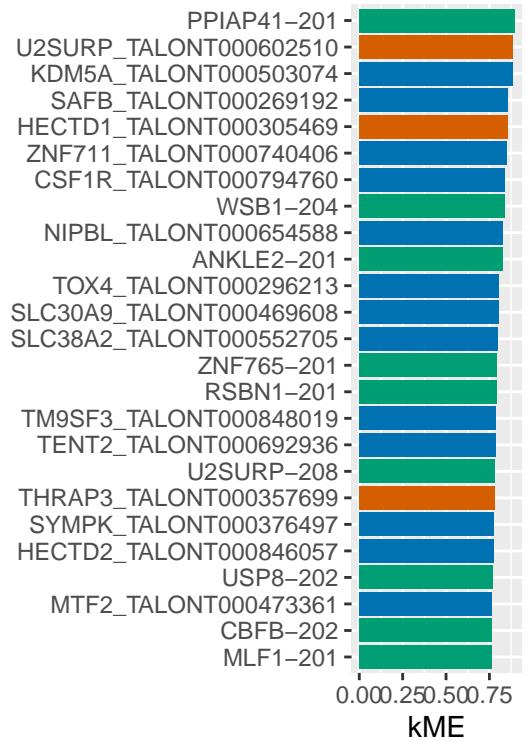
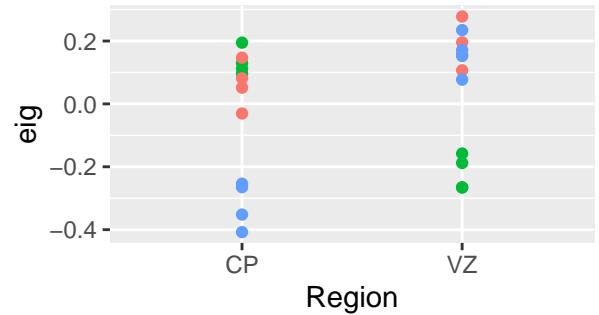
## Module 47: bisque4 n=126



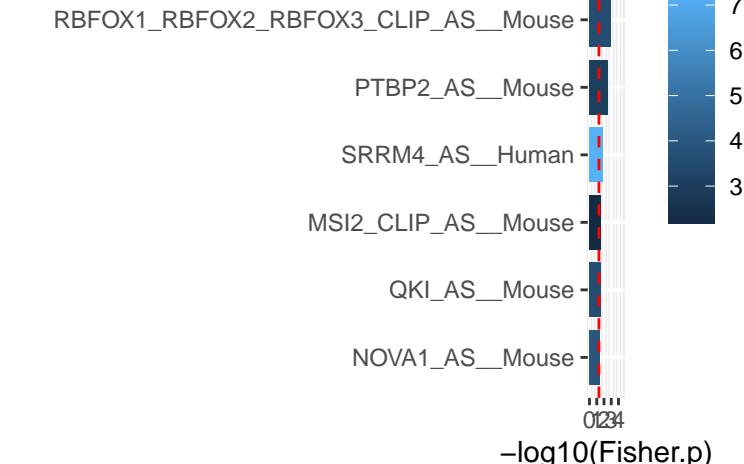
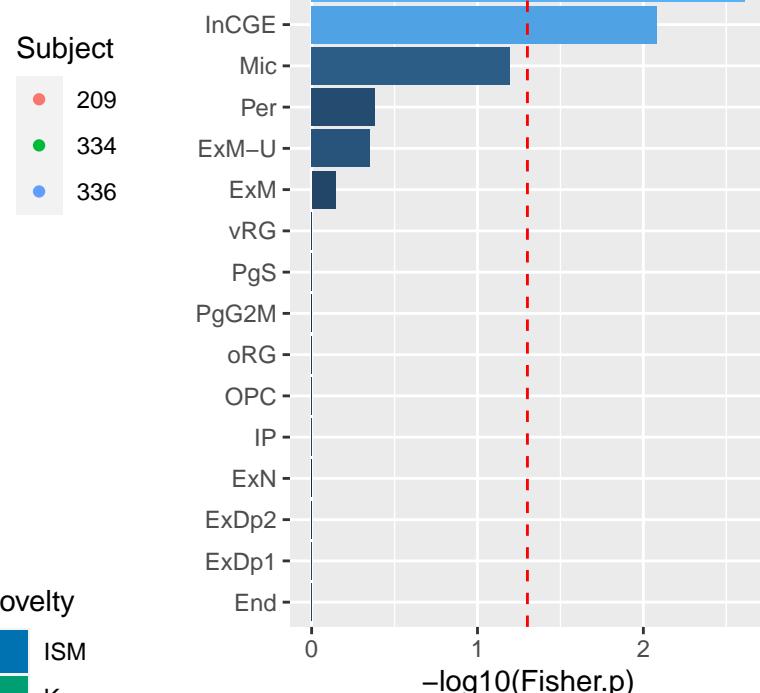
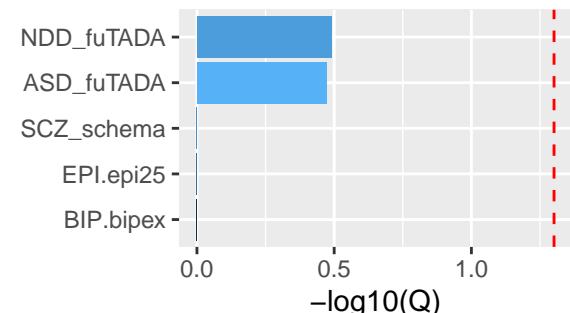
## GWAS Enrichment



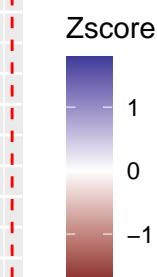
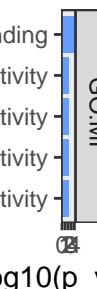
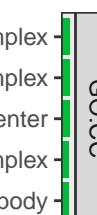
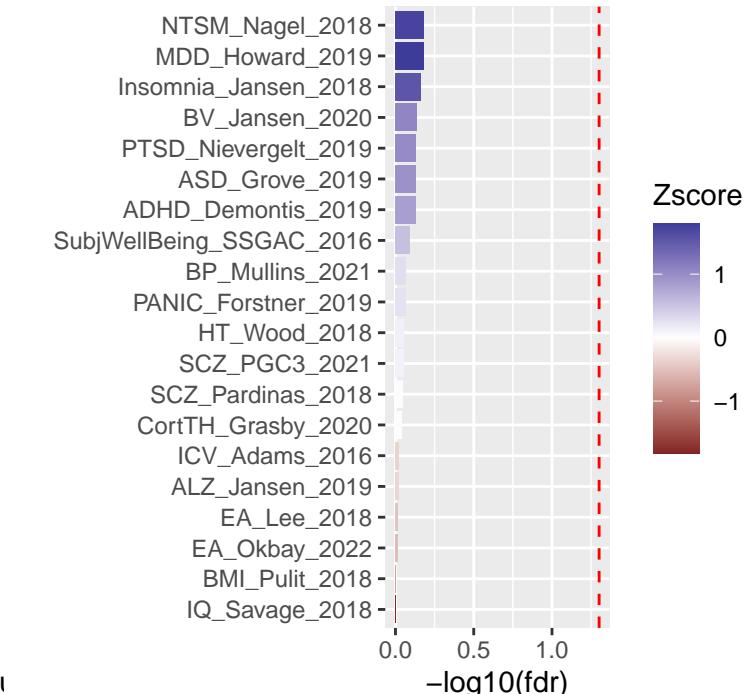
# Module 48: darkslateblue n=119



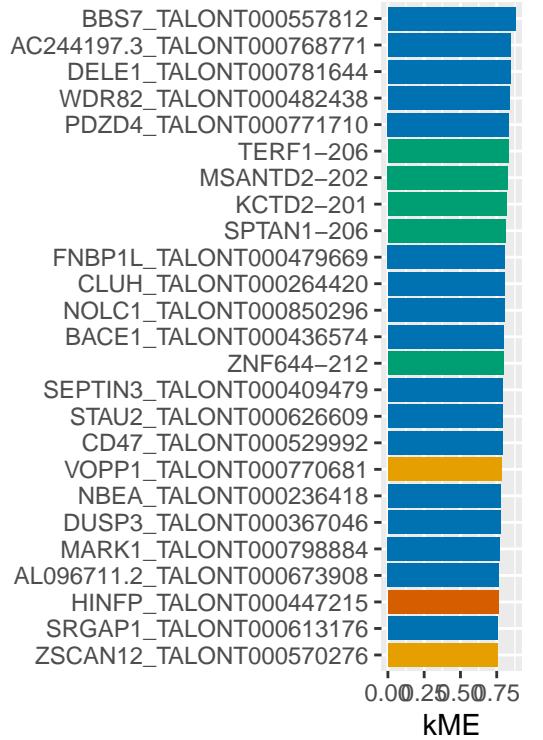
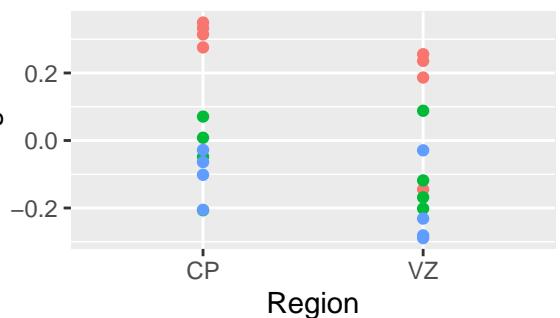
## Rare Var Enrichment



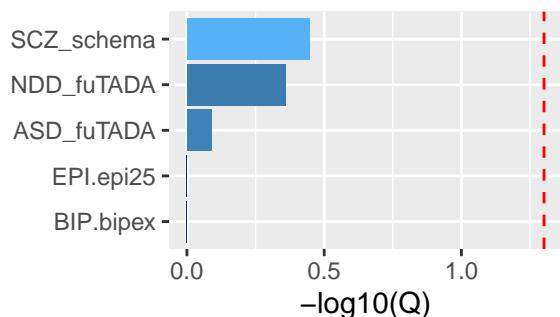
## GWAS Enrichment



# Module 49: plum2 n=116



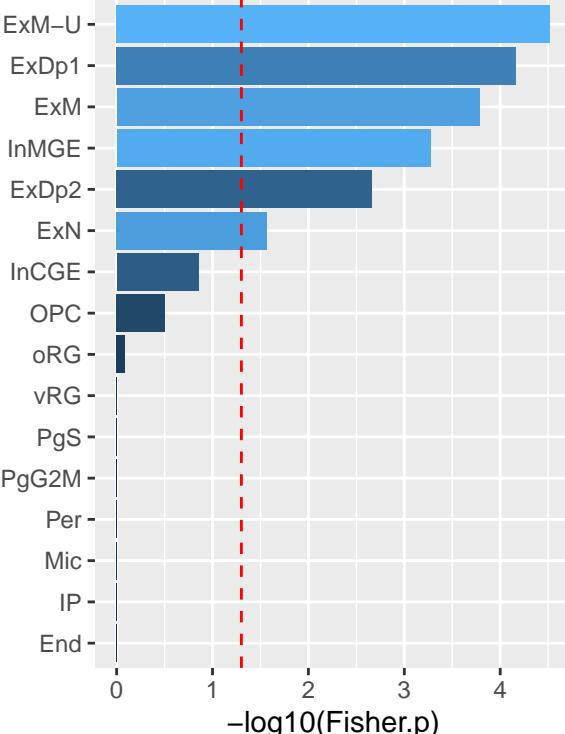
## Rare Var Enrichment



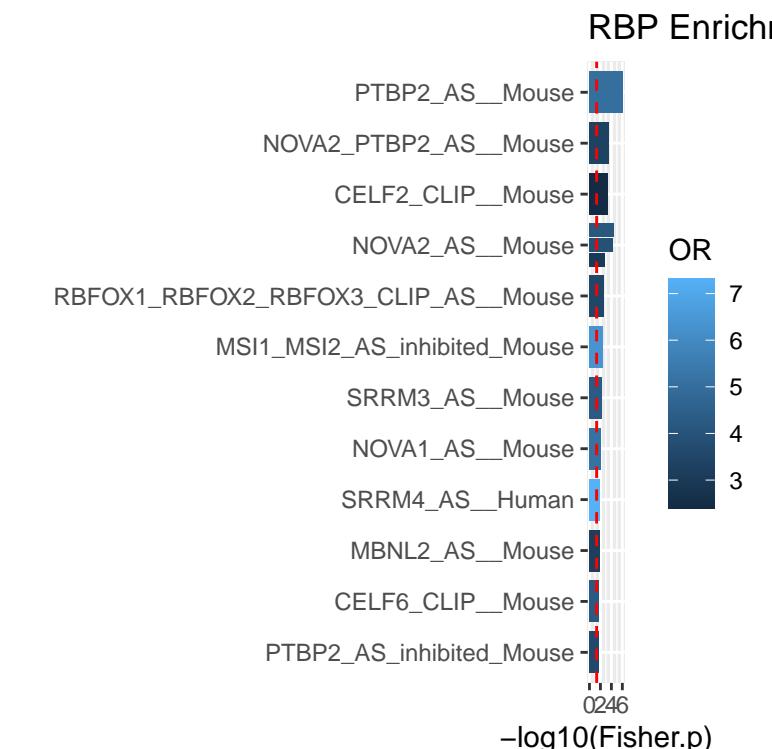
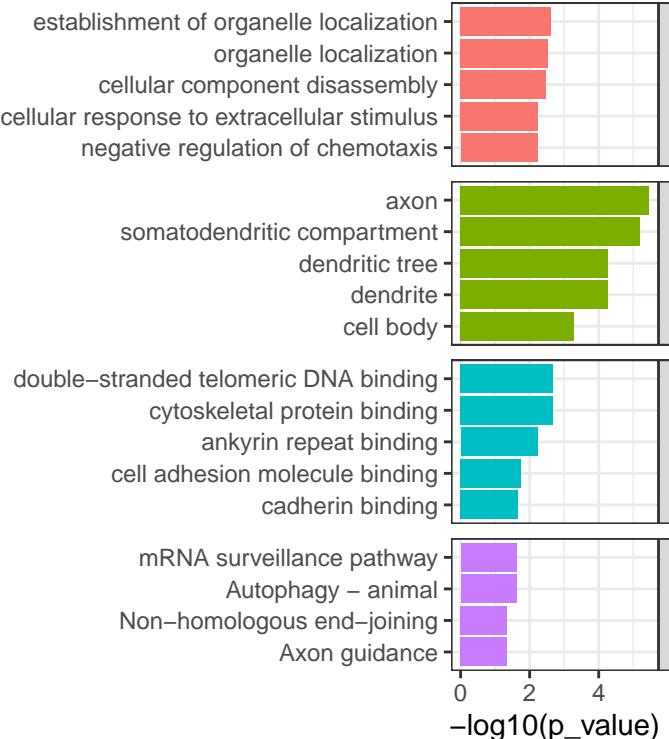
Subject  
209  
334  
336

novelty  
ISM  
Known  
NIC  
NNC

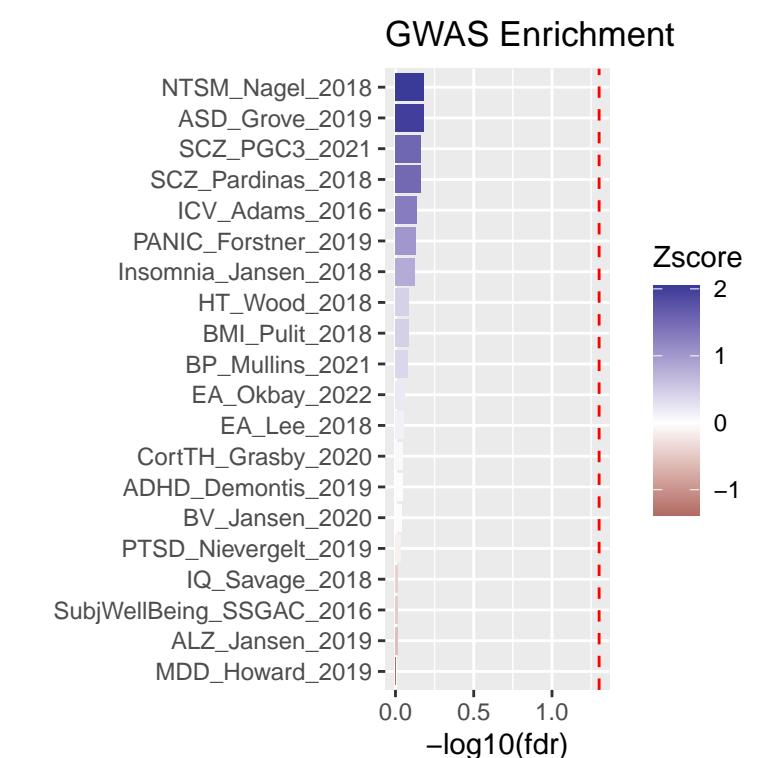
OR  
1.2  
1.1  
1.0  
0.9  
0.8



OR  
5  
4  
3  
2  
1

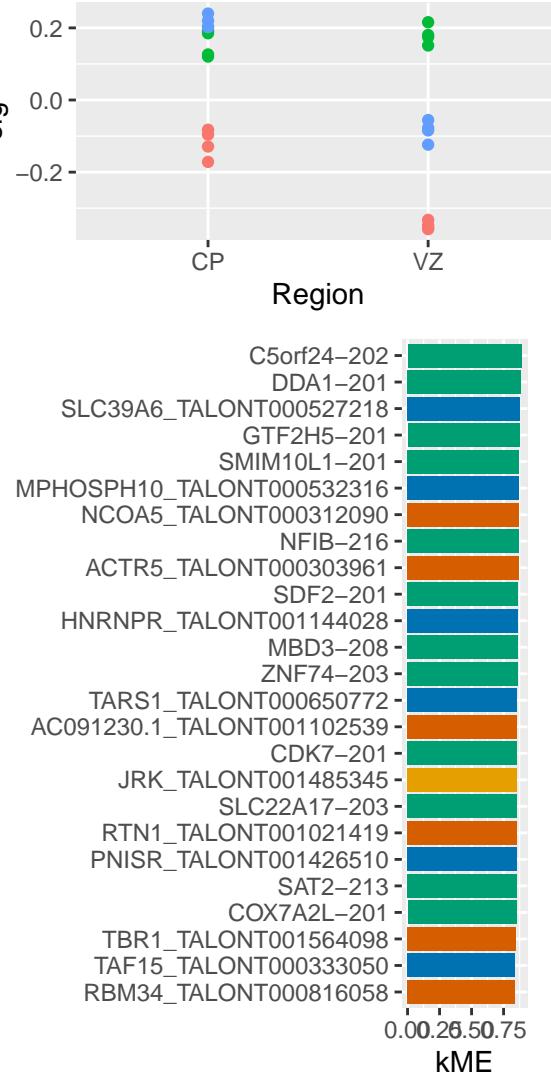


OR  
7  
6  
5  
4  
3

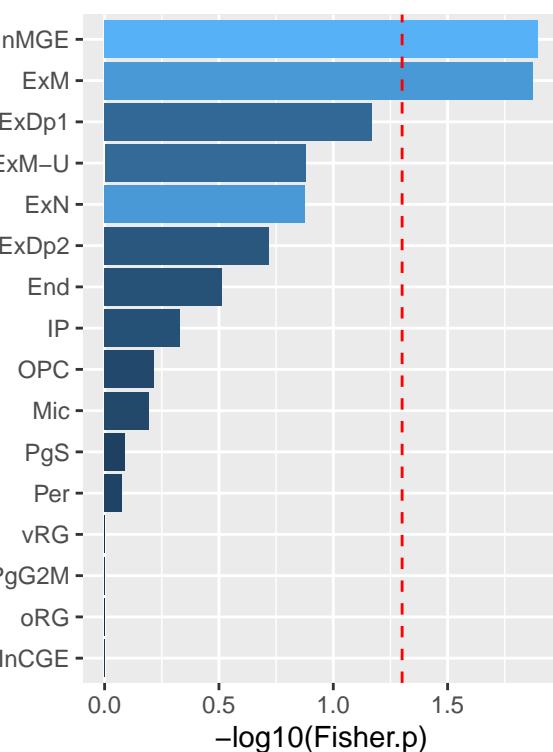
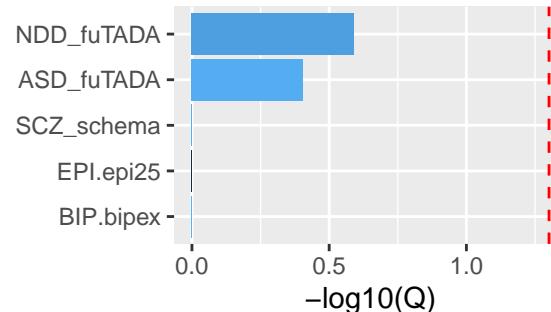


Zscore  
2  
1  
0  
-1

## Module 50: thistle2 n=115

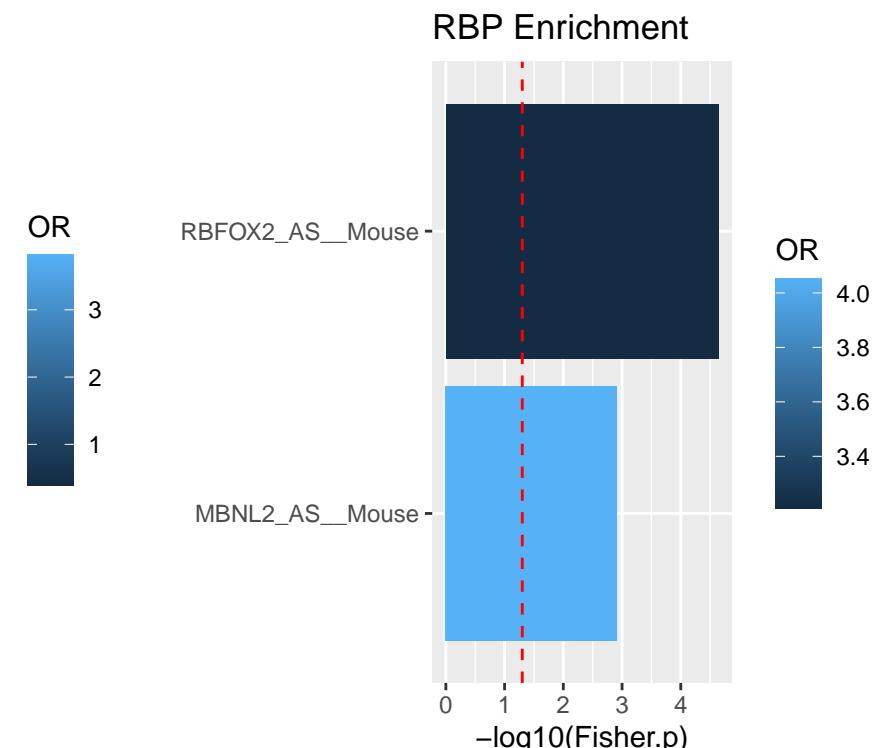


## Rare Var Enrichment



ncRNA metabolic proc  
positive regulation of protein localization to chromosome, telomeric reg  
regulation of protein localization to chromosome, telomeric reg  
telomerase RNA localiza  
RNA localization to nuc  
transcription factor TFIIH holo com  
transcription factor TFIIH core com  
chaperone com  
intracellular protein-containing com  
carboxy-terminal domain protein kinase com  
mRNA bind

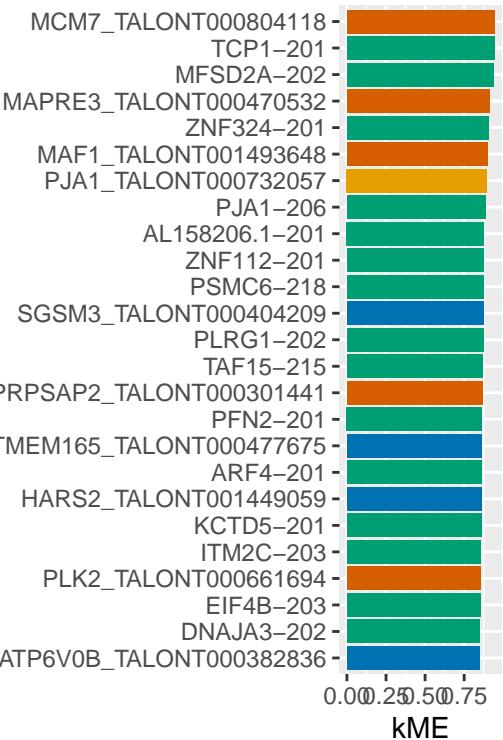
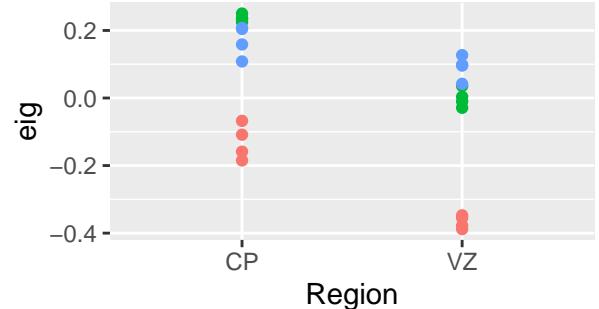
ase activity, acting on acid anhydrides, in phosphorus-containing anhydri  
hydrolase activity, acting on acid anhydri  
low-density lipoprotein particle receptor bind  
ATP-dependent protein folding chaper  
Basal transcription fac  
Synaptic vesicle c  
Nucleotide excision re



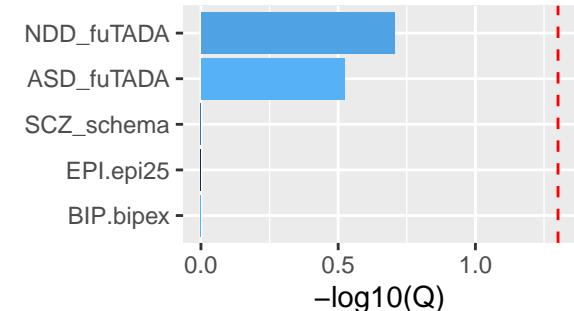
## GWAS Enrichment



# Module 51: thistle1 n=112

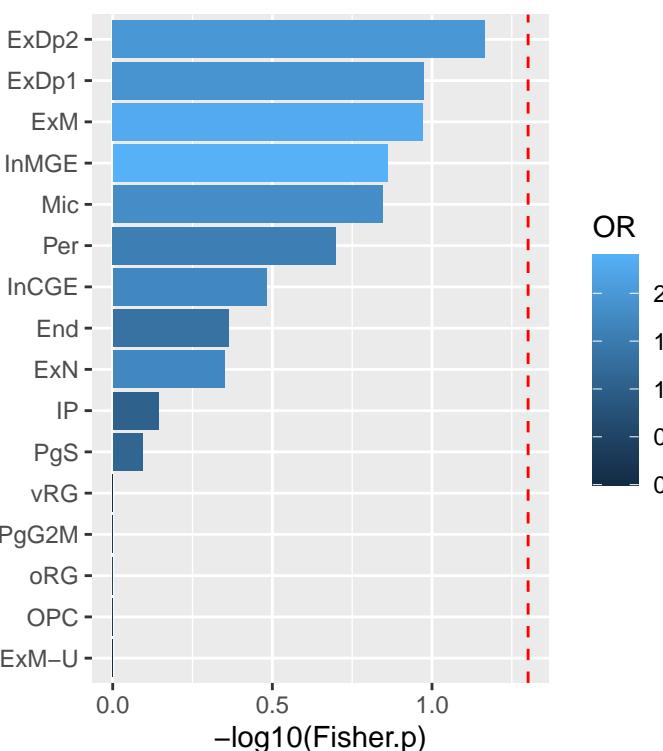


## Rare Var Enrichment

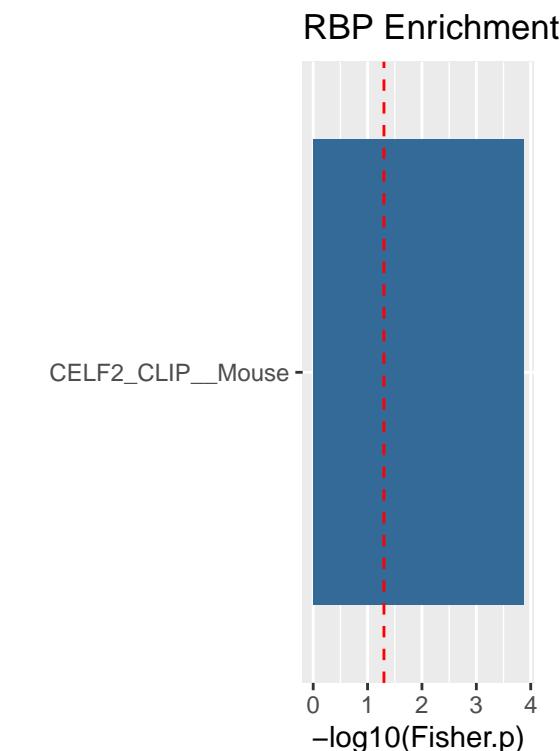
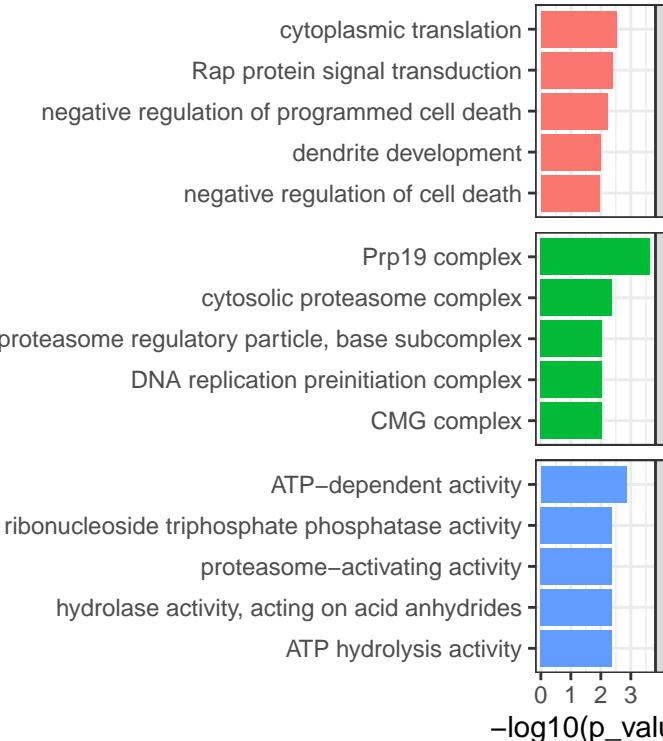


Subject  
209  
334  
336

novelty  
ISM  
Known  
NIC  
NNC



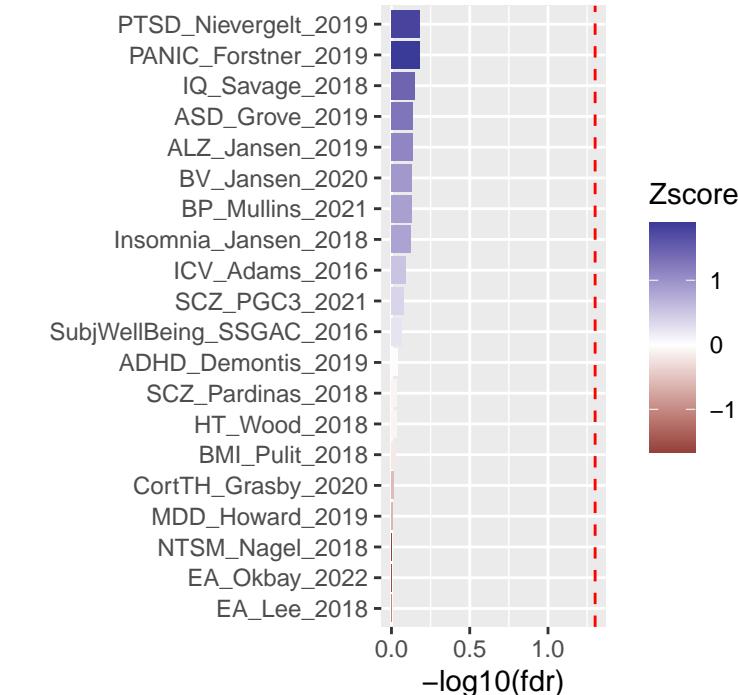
OR  
2.0  
1.5  
1.0  
0.5  
0.0



CELF2\_CLIP\_\_Mouse

OR  
2.668463

## GWAS Enrichment



Zscore  
1  
0  
-1

## RBP Enrichment

## Module 52: salmon4 n=103

