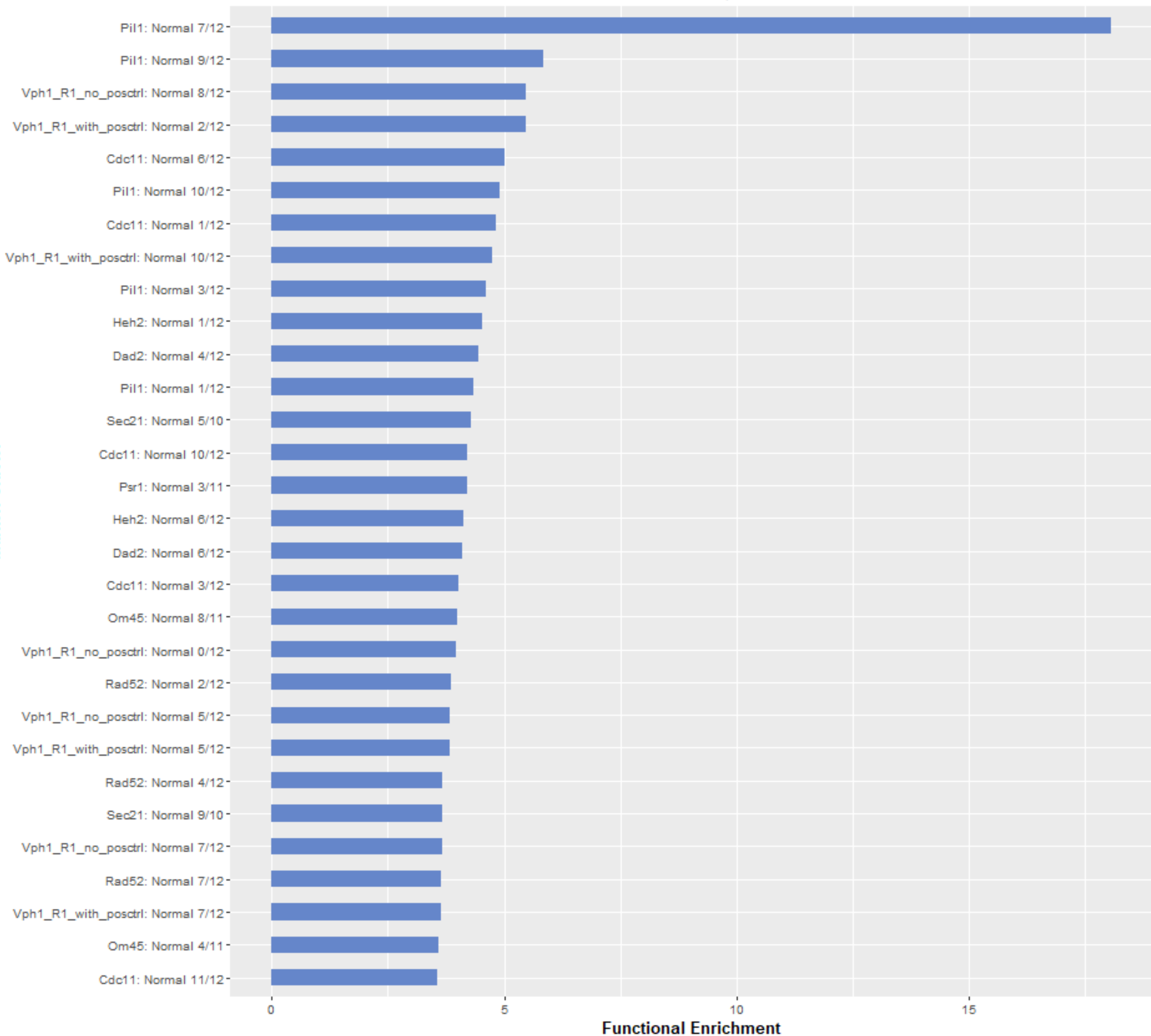


# cell budding

With AreaShape

Marker: Cluster



# cell morphogenesis

With AreaShape

Marker: Cluster

Om45: Normal 3/11

Om45: Normal 10/11

Pil1: Normal 1/12

0

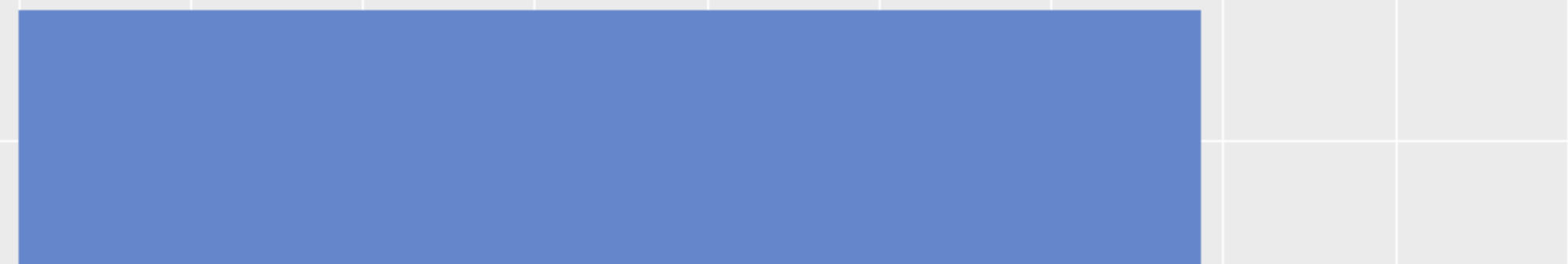
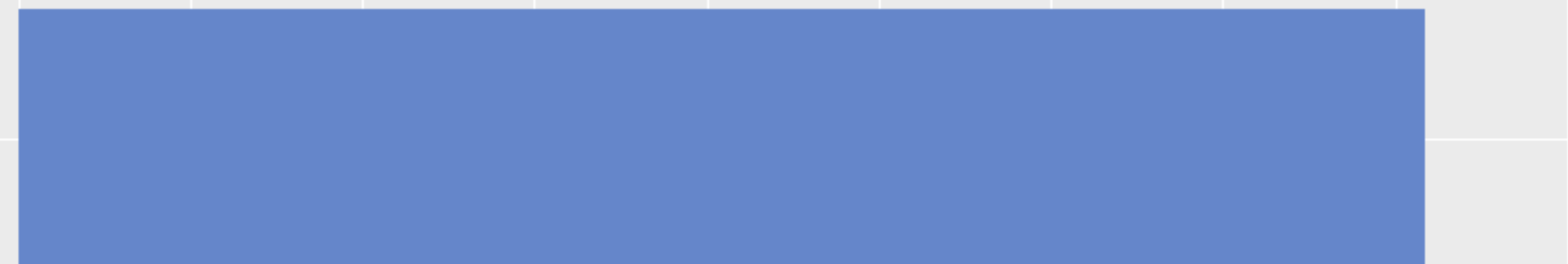
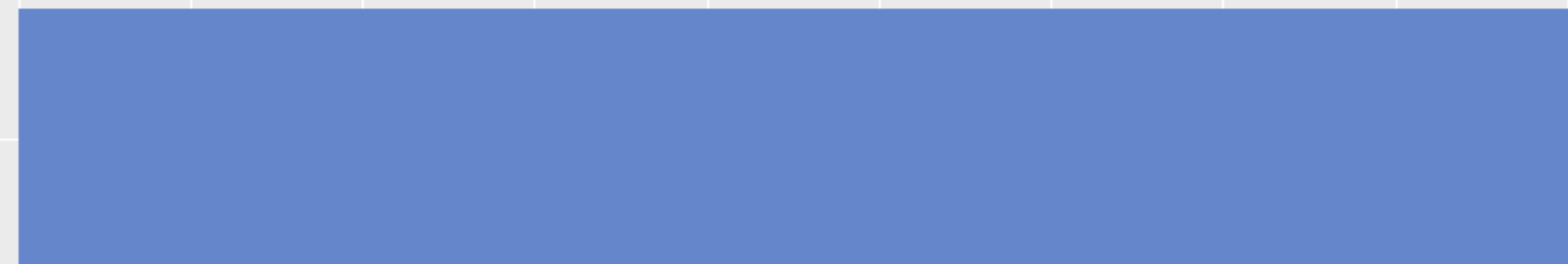
1

2

3

4

Functional Enrichment



# cell wall organization or biogenesis

With AreaShape

Marker: Cluster

Vph1\_R1\_no\_posctrl: Normal 8/12

Vph1\_R1\_with\_posctrl: Normal 2/12

Vph1\_R1\_no\_posctrl: Normal 7/12

Cdc11: Normal 6/12

Vph1\_R1\_with\_posctrl: Normal 7/12

Psr1: Normal 3/11

0.0

0.5

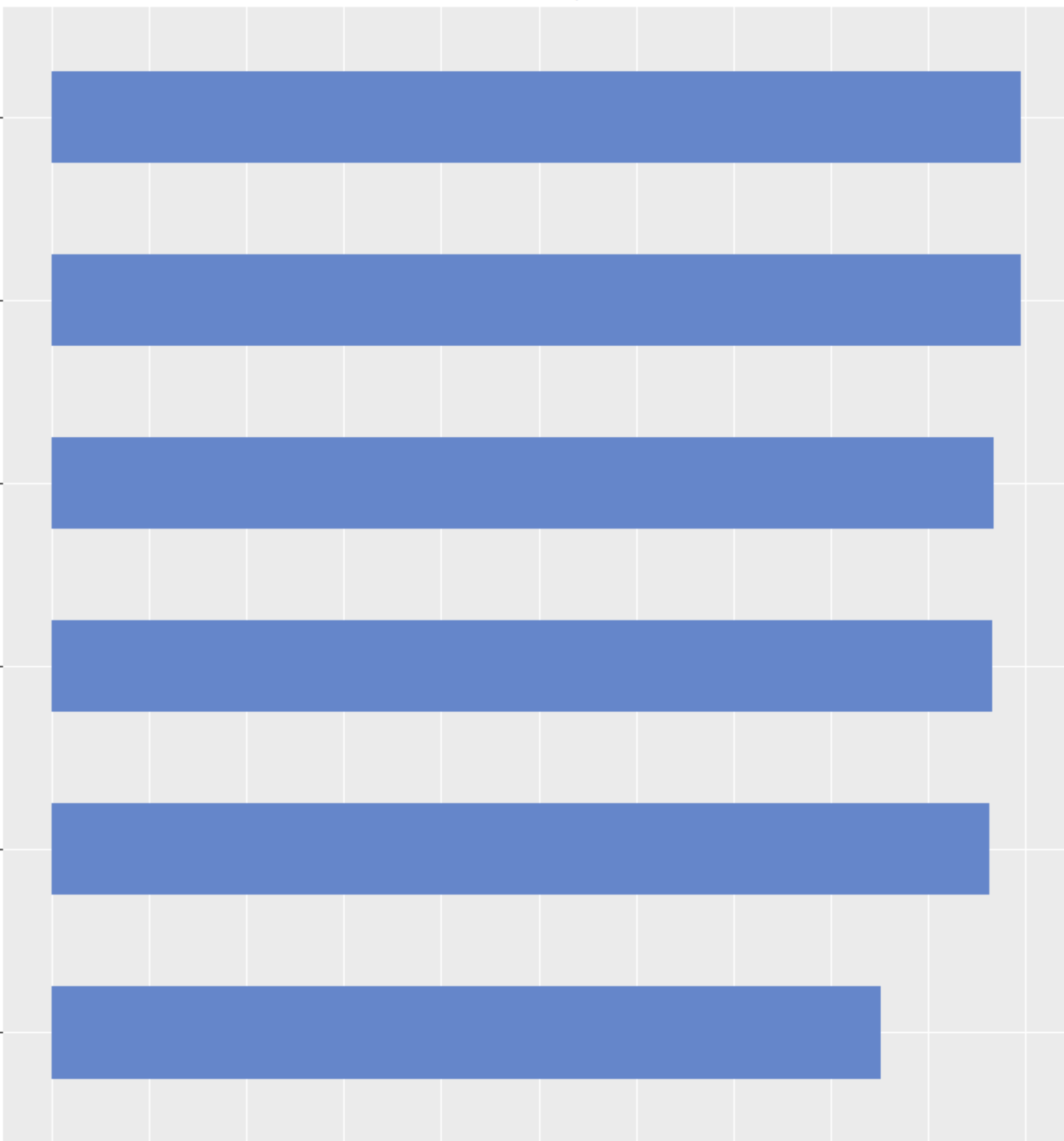
1.0

1.5

2.0

2.5

Functional Enrichment



# cellular amino acid metabolic process

With AreaShape

Marker: Cluster

Cdc11: Normal 3/12

0.0

0.5

1.0

1.5

2.0

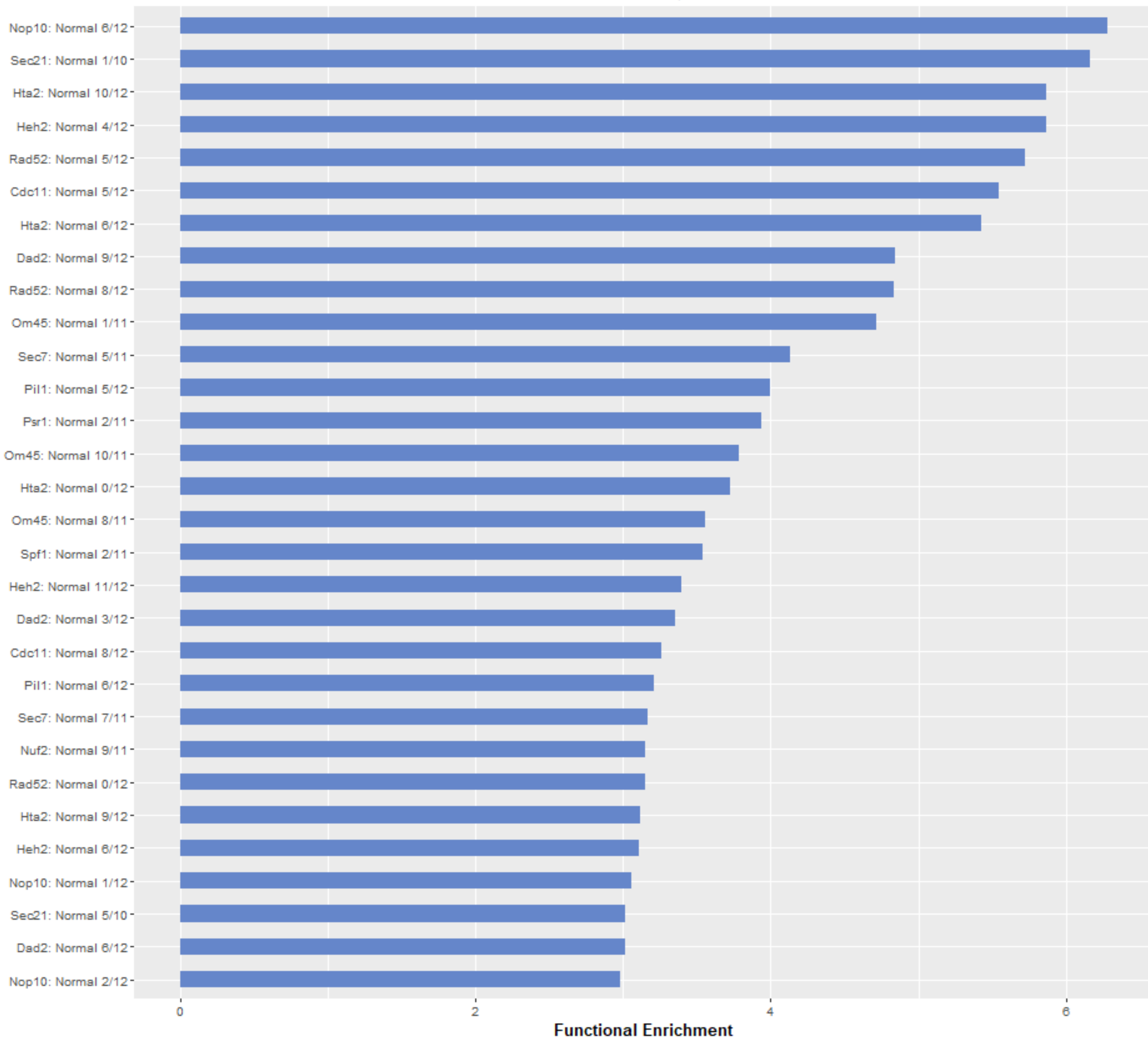
Functional Enrichment



# cellular response to DNA damage stimulus

With AreaShape

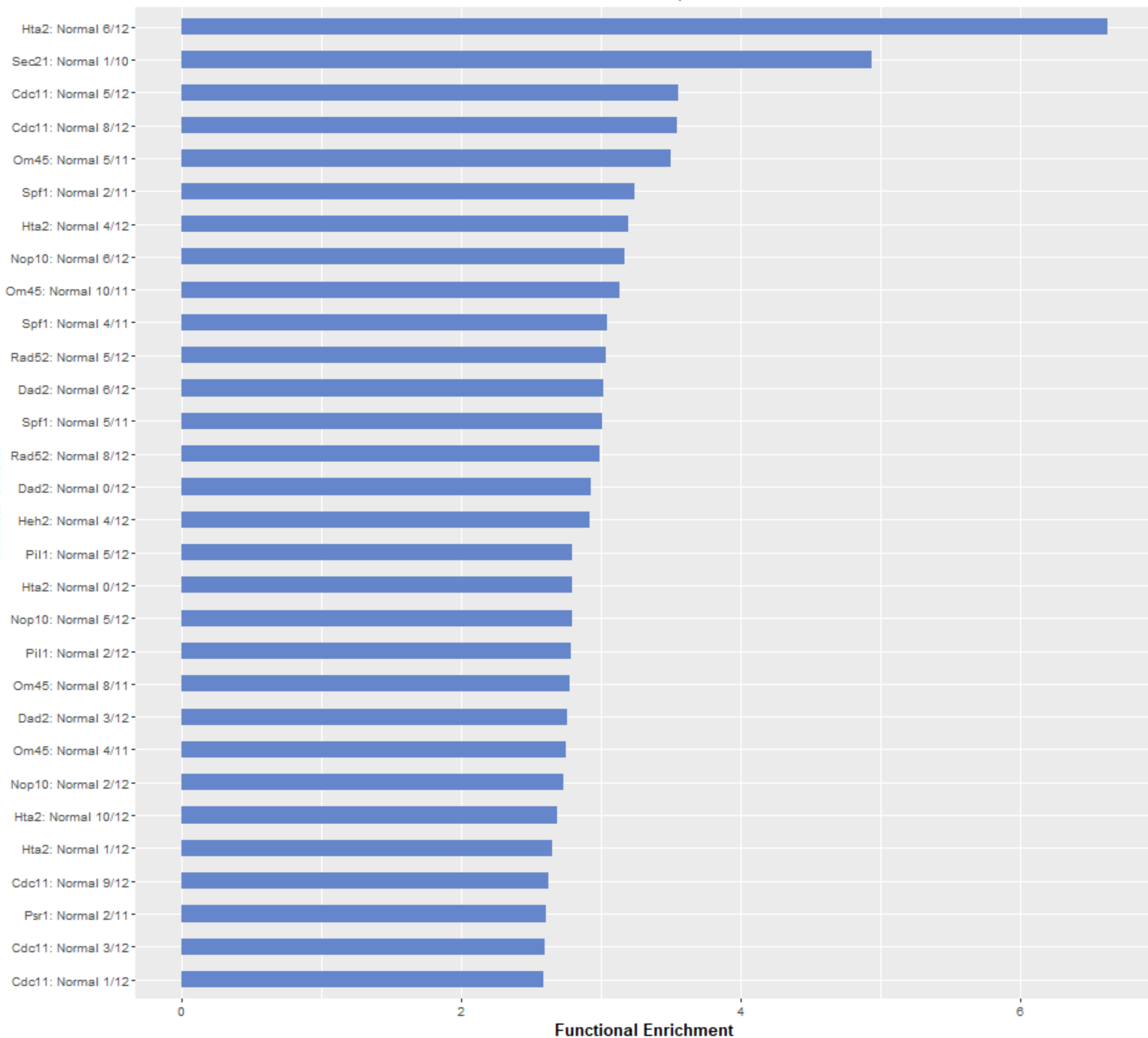
Marker: Cluster



# chromatin organization

With AreaShape

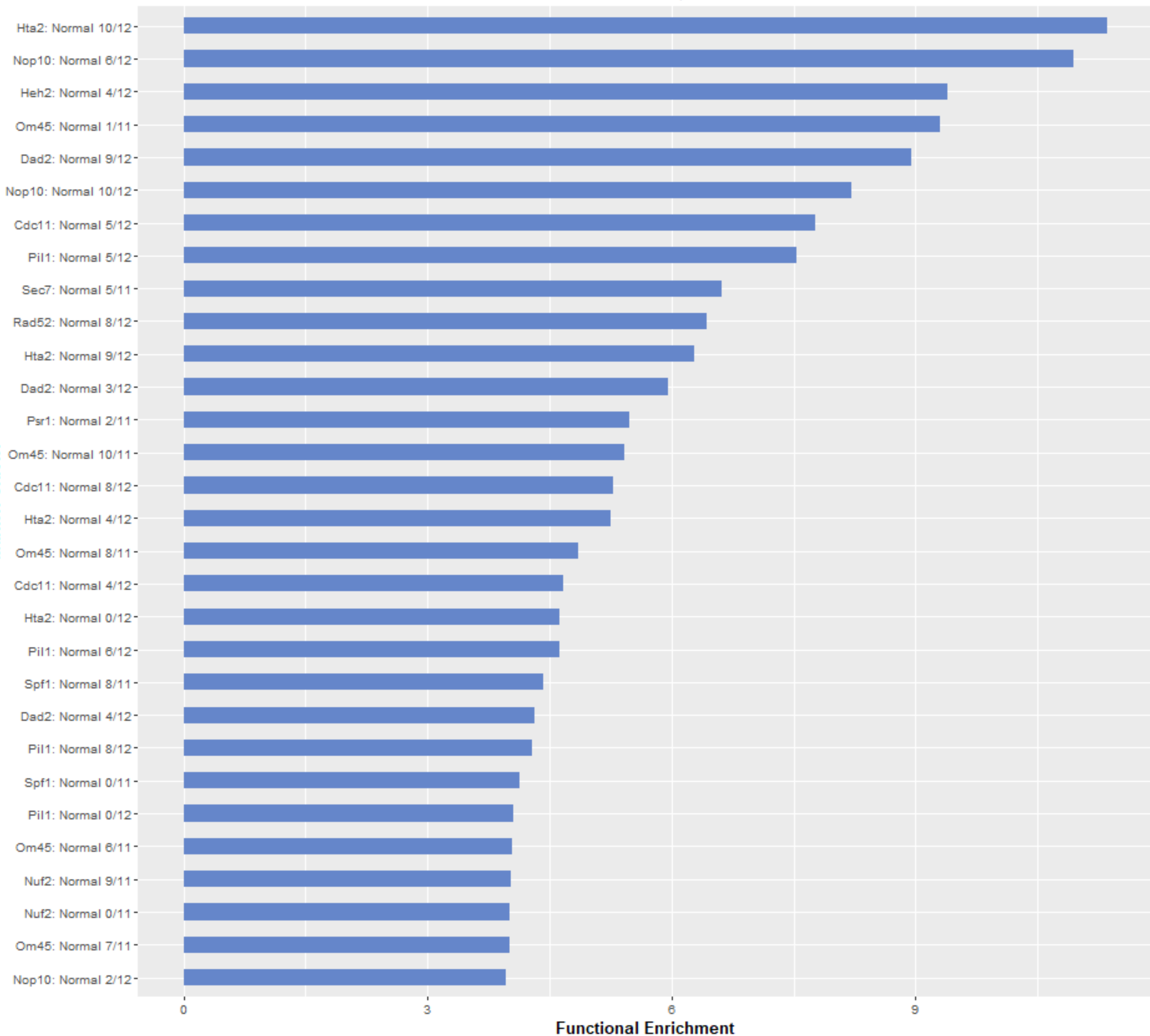
Marker: Cluster



# chromosome segregation

With AreaShape

Marker: Cluster



# cofactor metabolic process

With AreaShape

Marker: Cluster

Om45: Normal 3/11

0.0

0.5

1.0

1.5

2.0

Functional Enrichment





# conjugation

With AreaShape

Marker: Cluster

Dad2: Normal 0/12

Sec7: Normal 10/11

Pil1: Normal 4/12

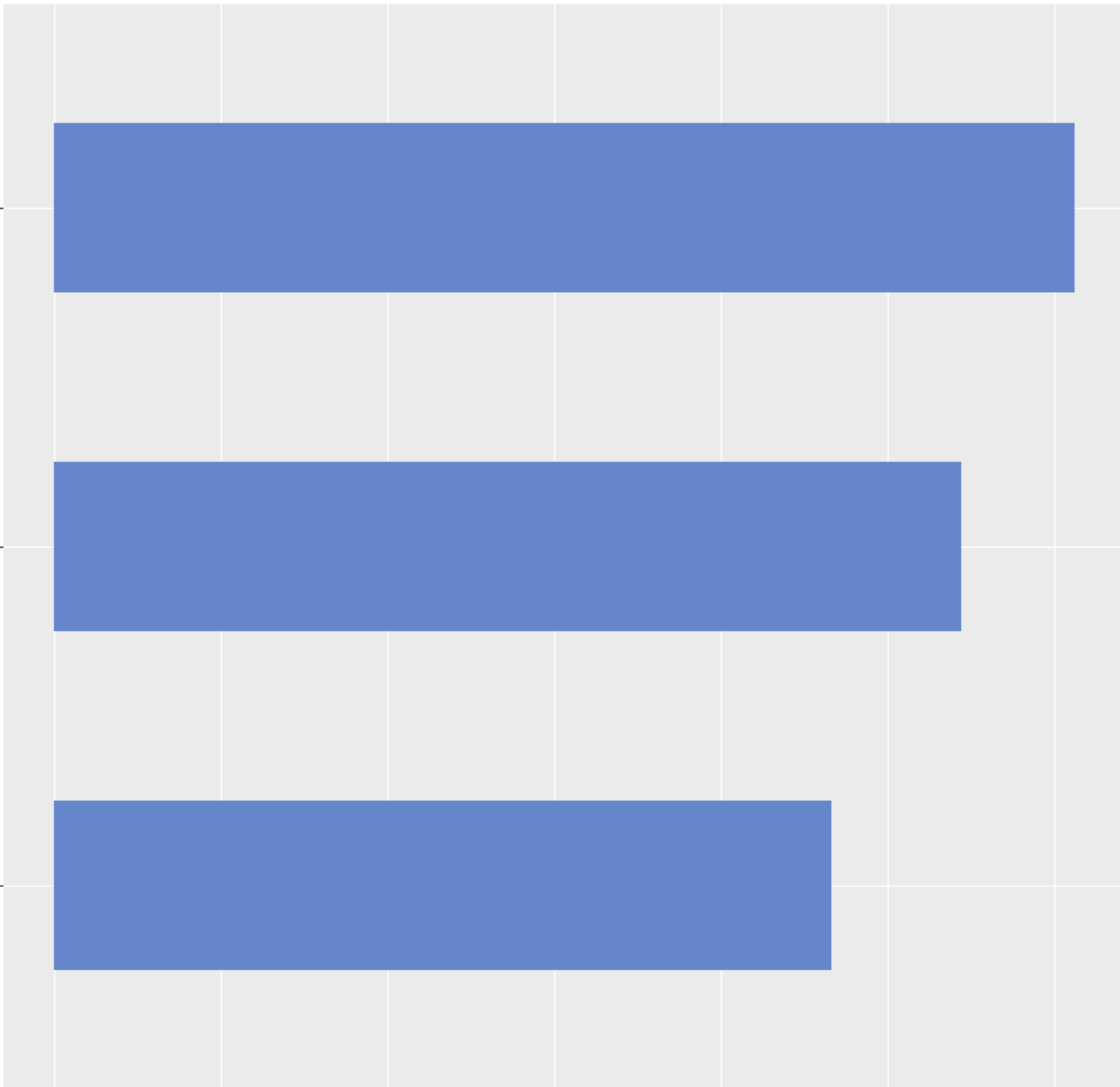
0

1

2

3

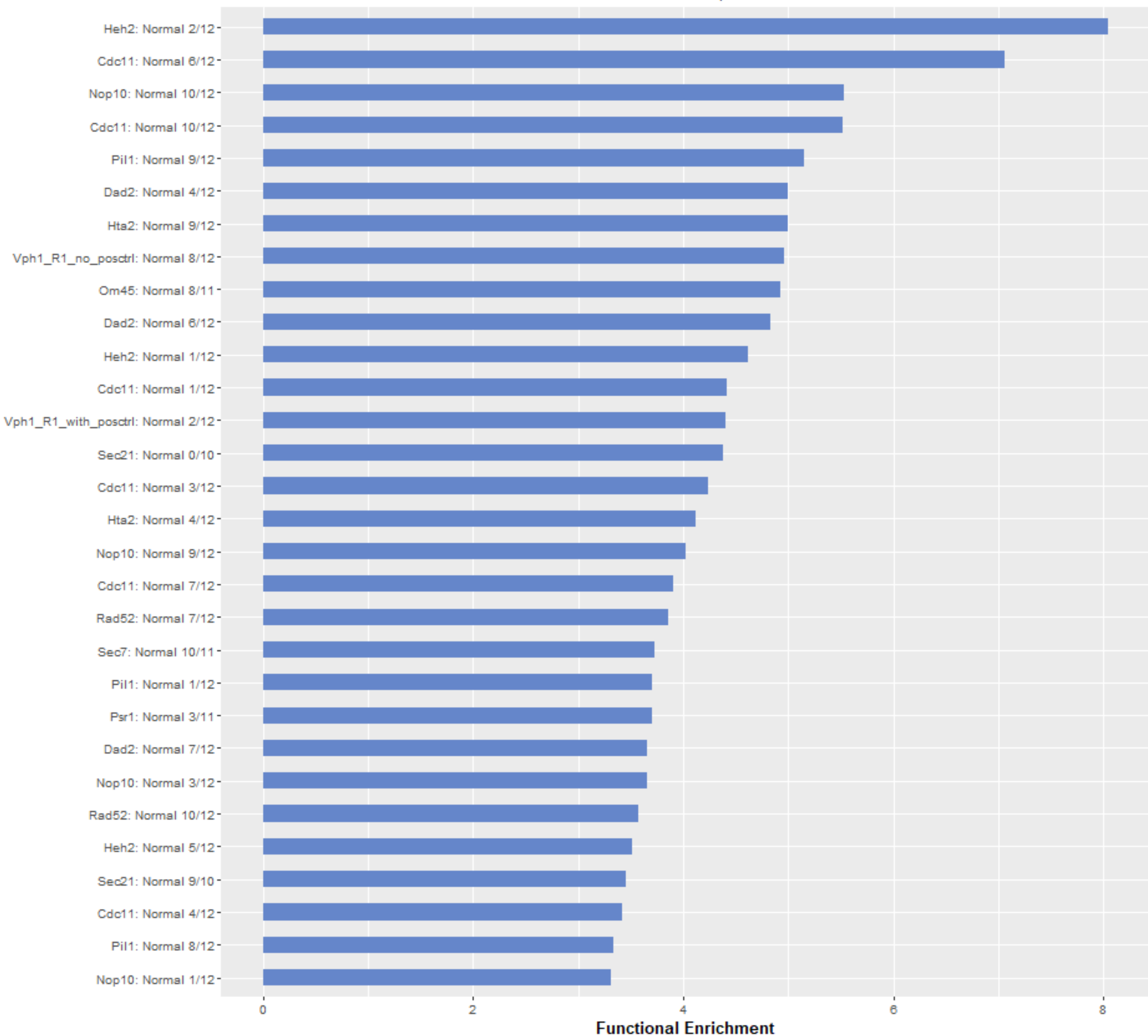
Functional Enrichment



# cytokinesis

With AreaShape

Marker: Cluster



# cytoplasmic translation

With AreaShape

Marker: Cluster

Pil1: Normal 4/12

Hta2: Normal 8/12

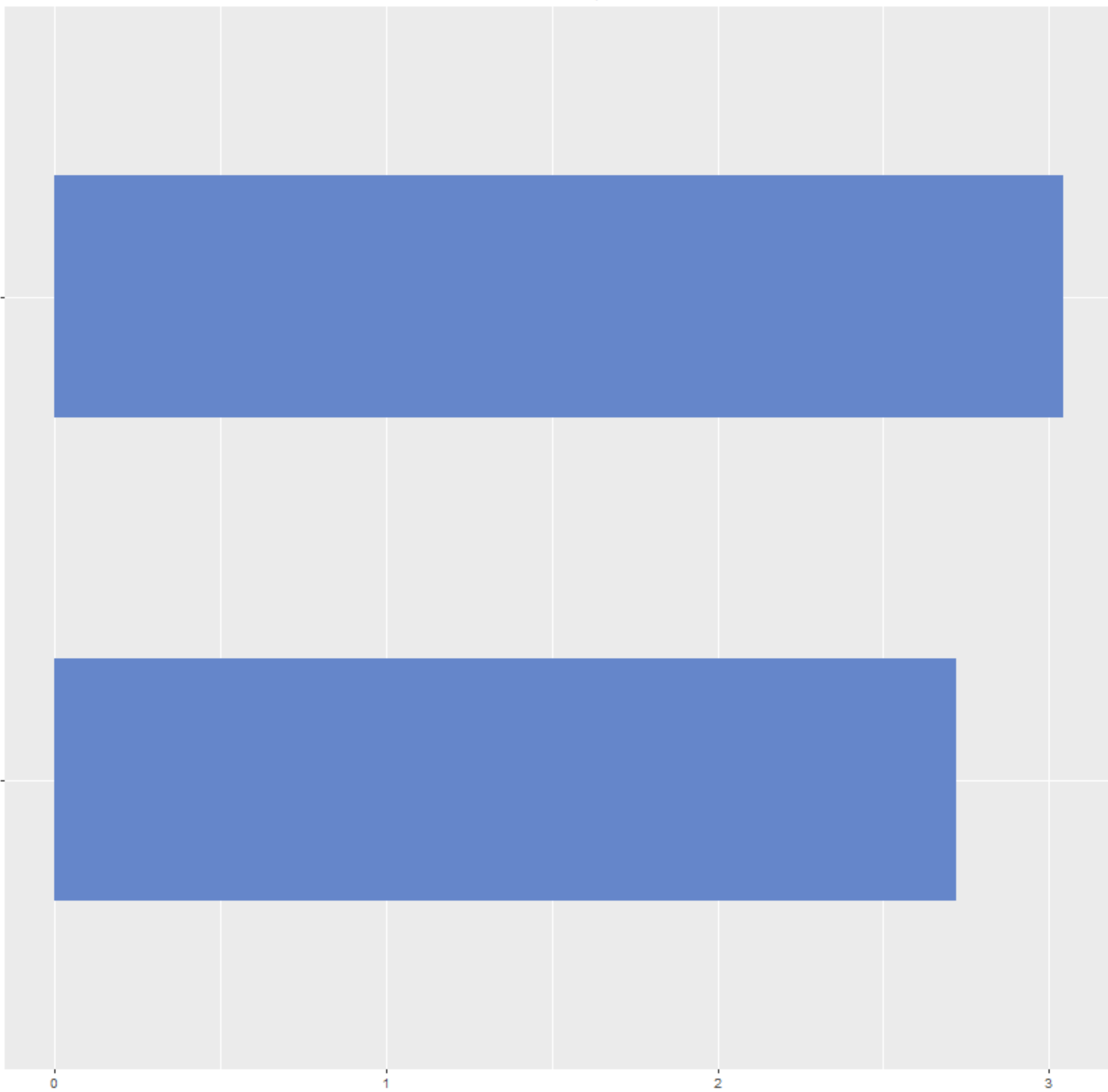
0

1

2

3

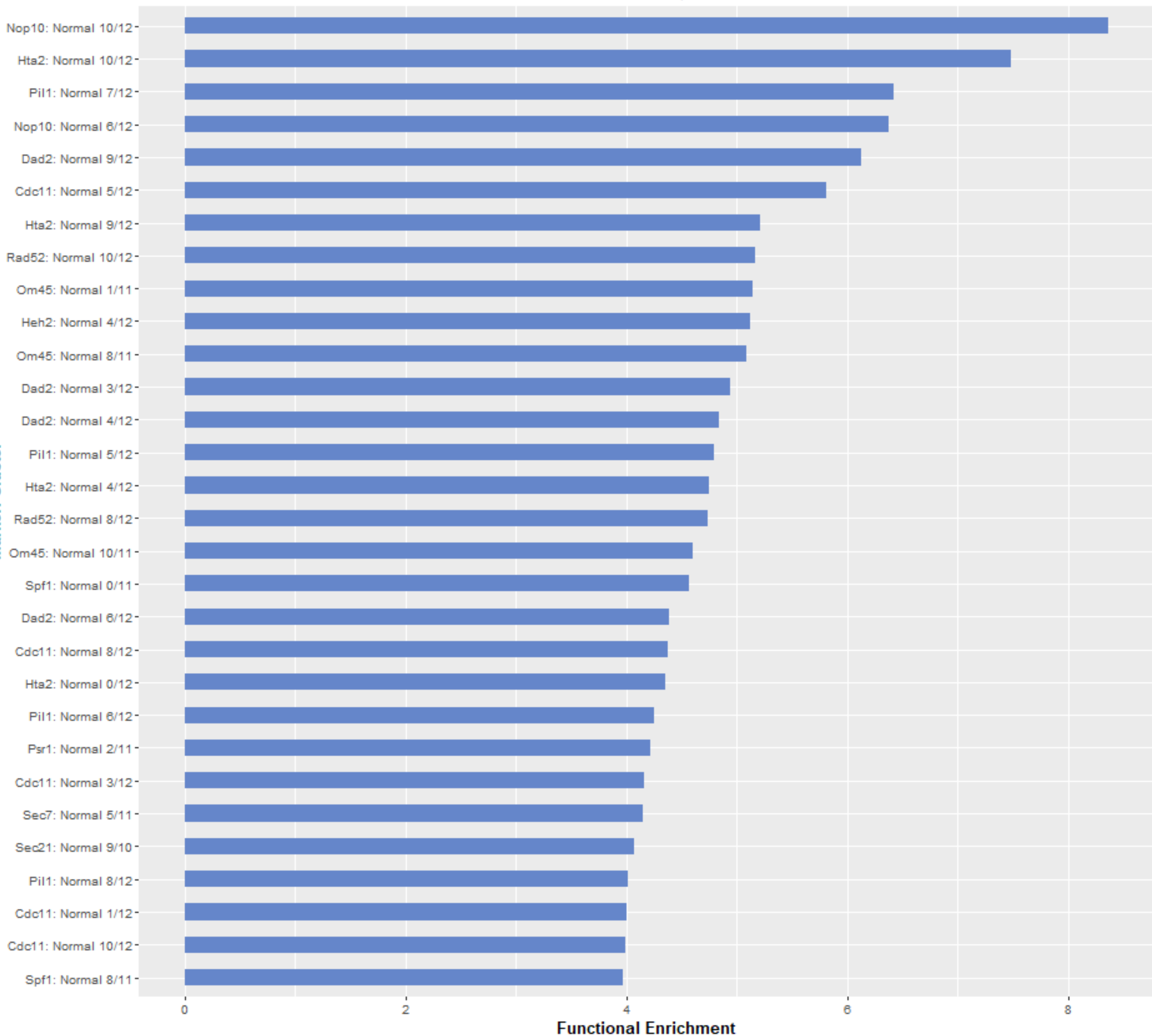
Functional Enrichment



# cytoskeleton organization

With AreaShape

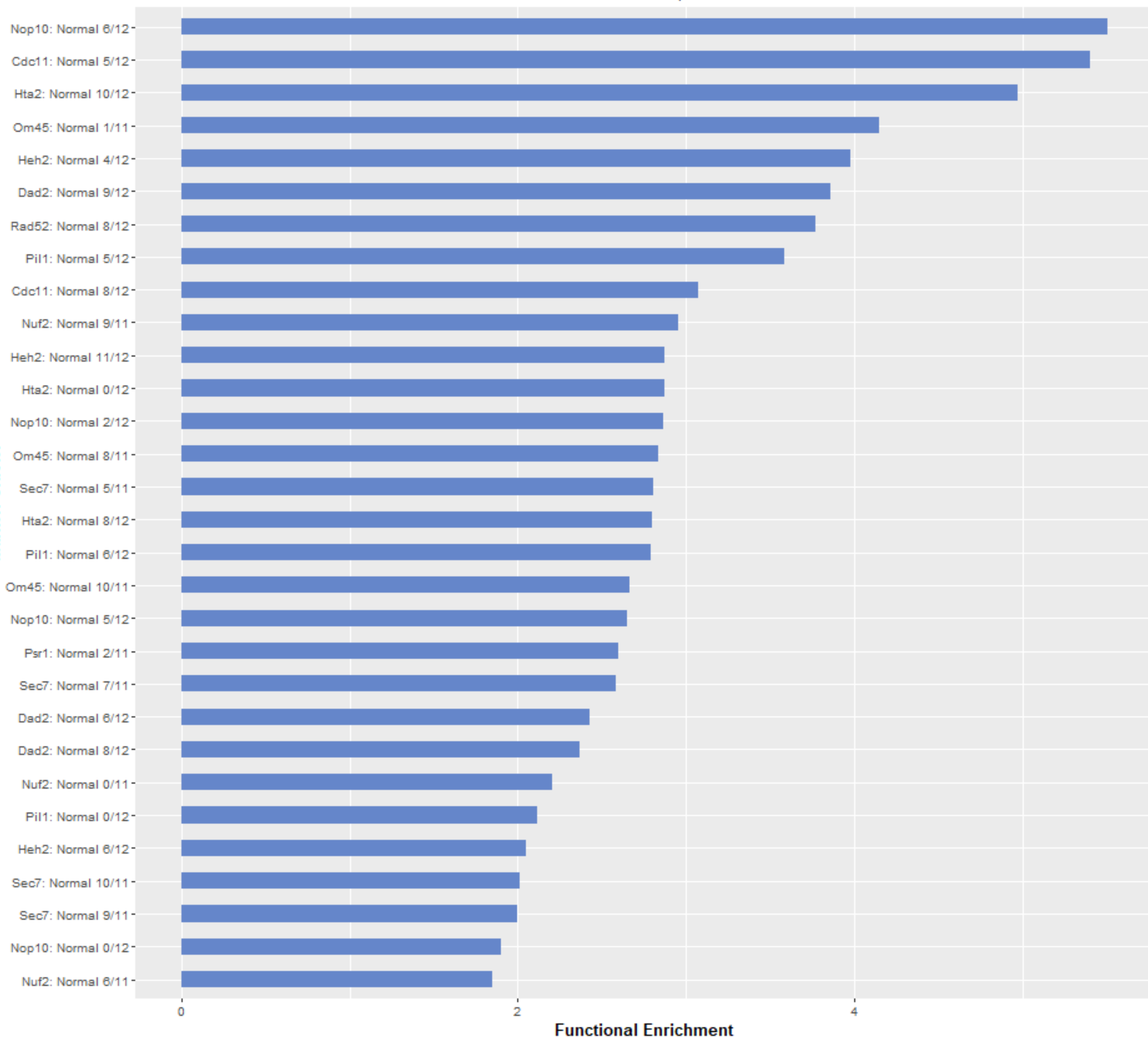
Marker: Cluster



# DNA recombination

With AreaShape

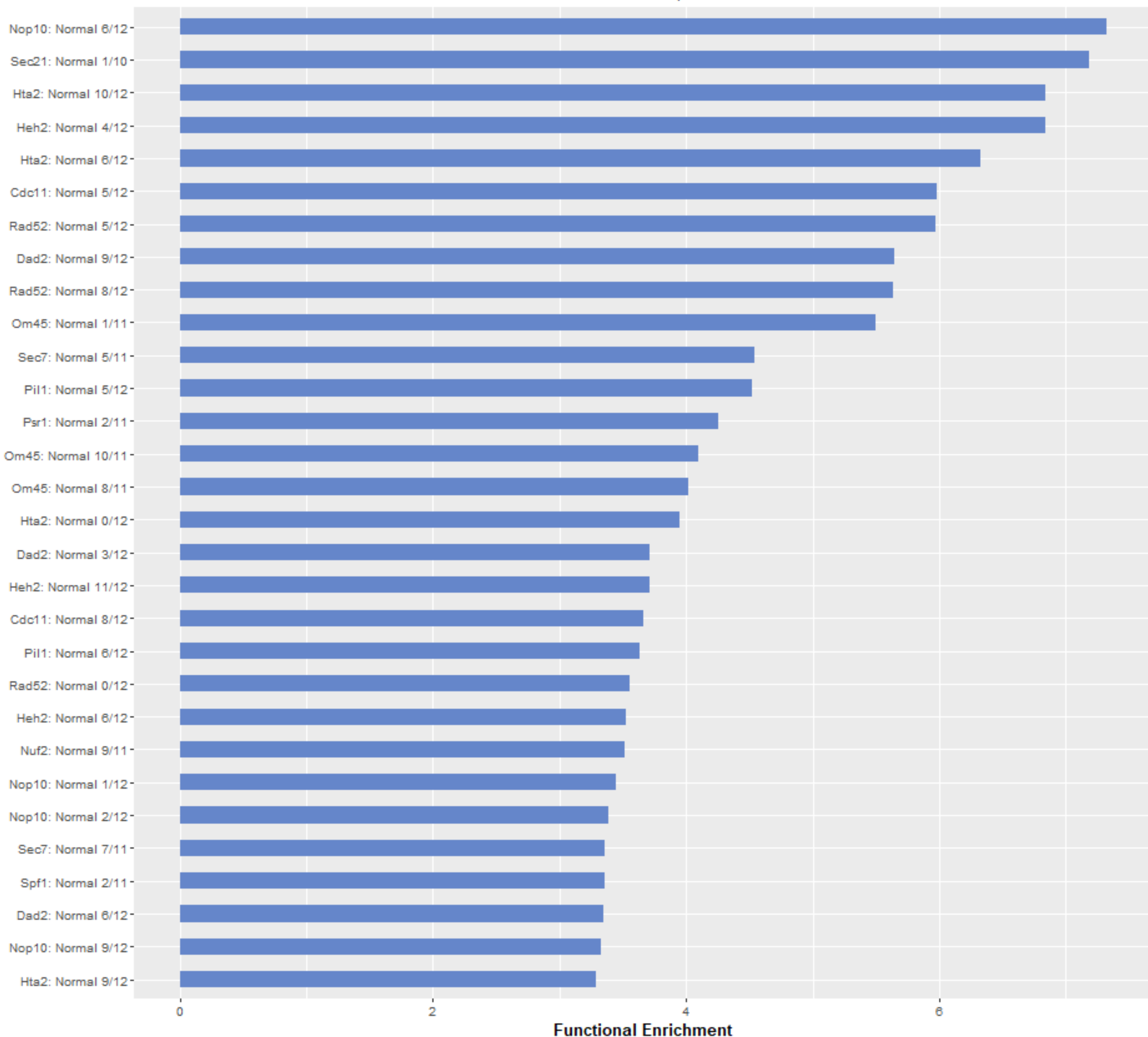
Marker: Cluster



# DNA repair

With AreaShape

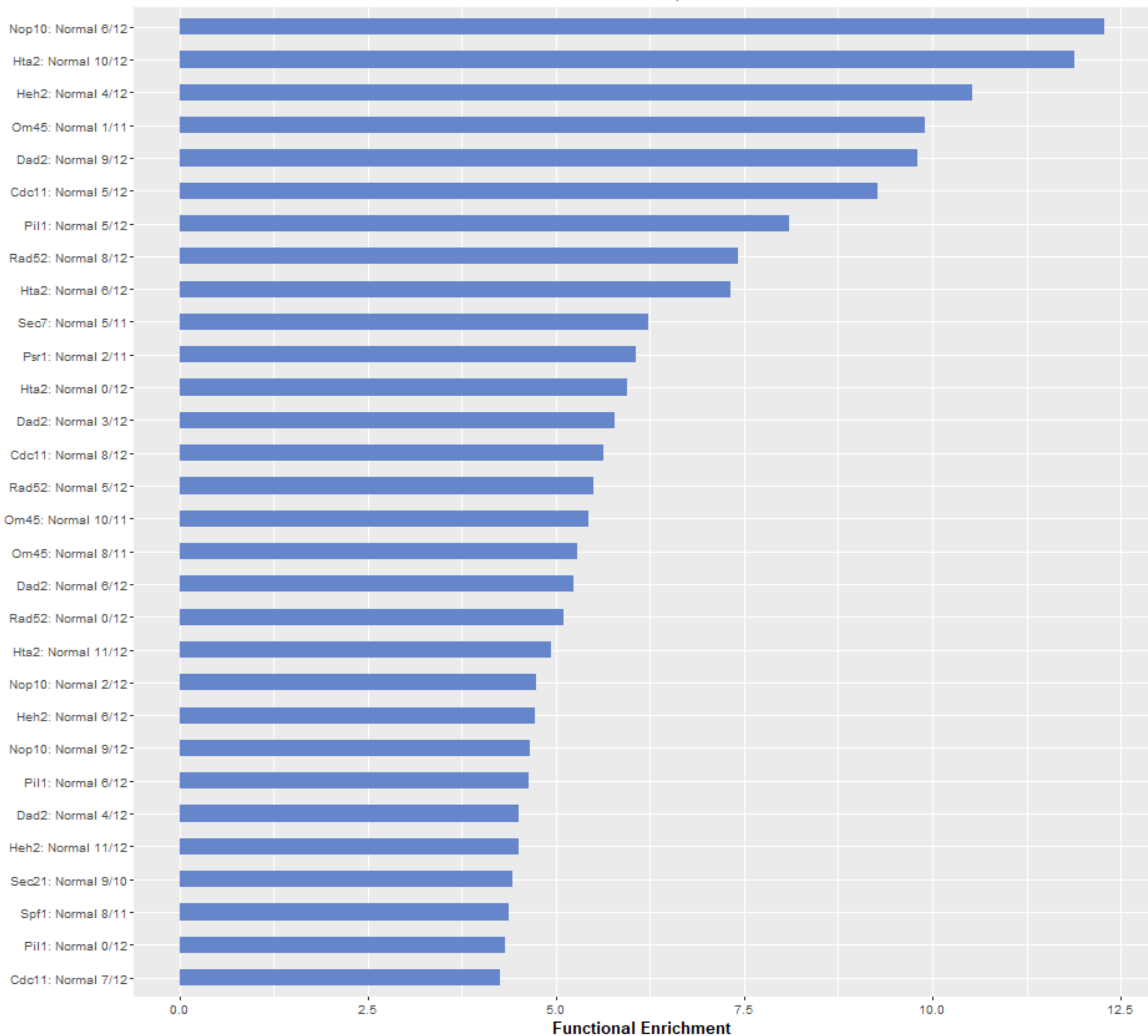
Marker: Cluster



# DNA replication

With AreaShape

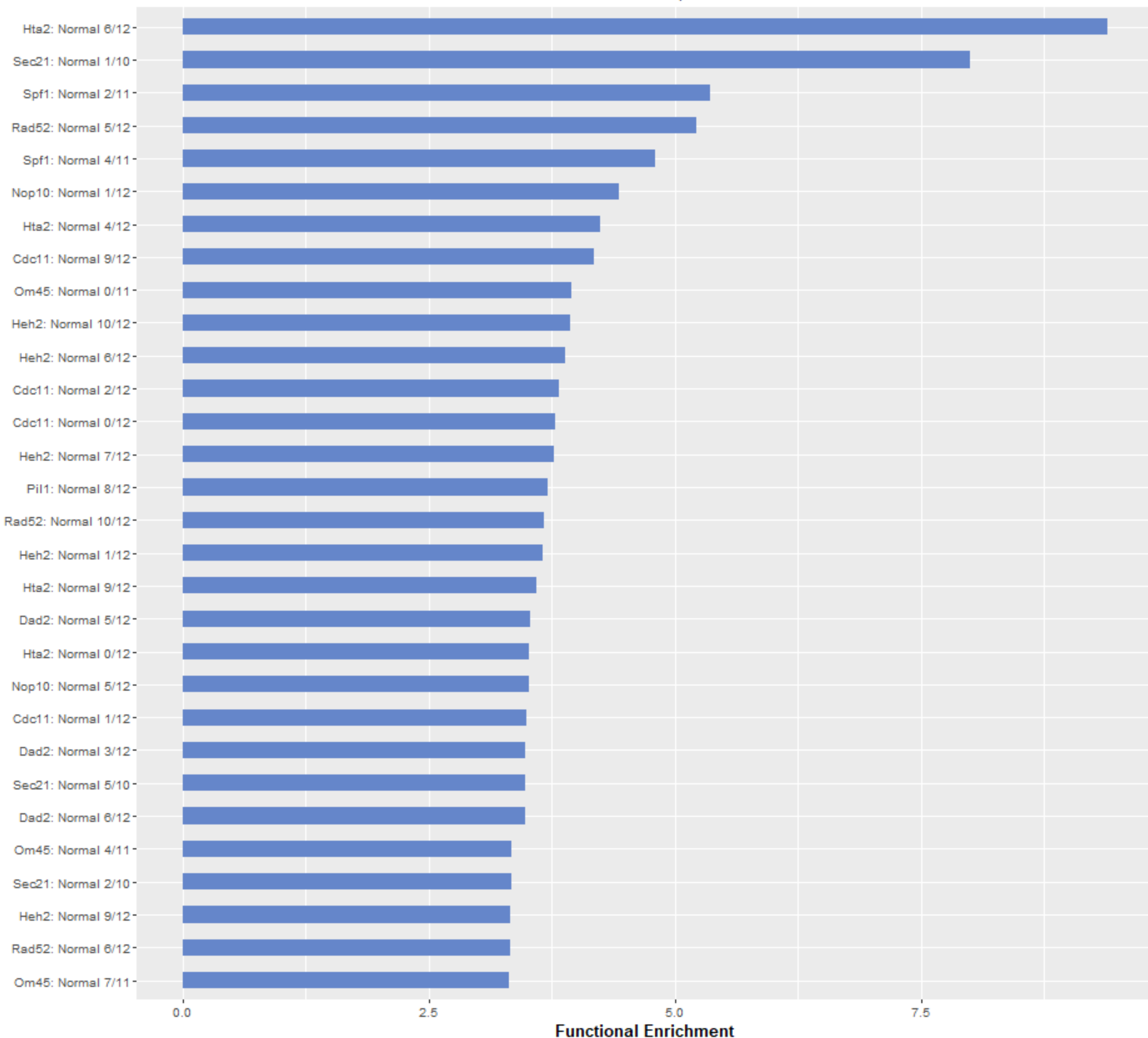
Marker: Cluster



# DNA-templated transcription, elongation

With AreaShape

Marker: Cluster

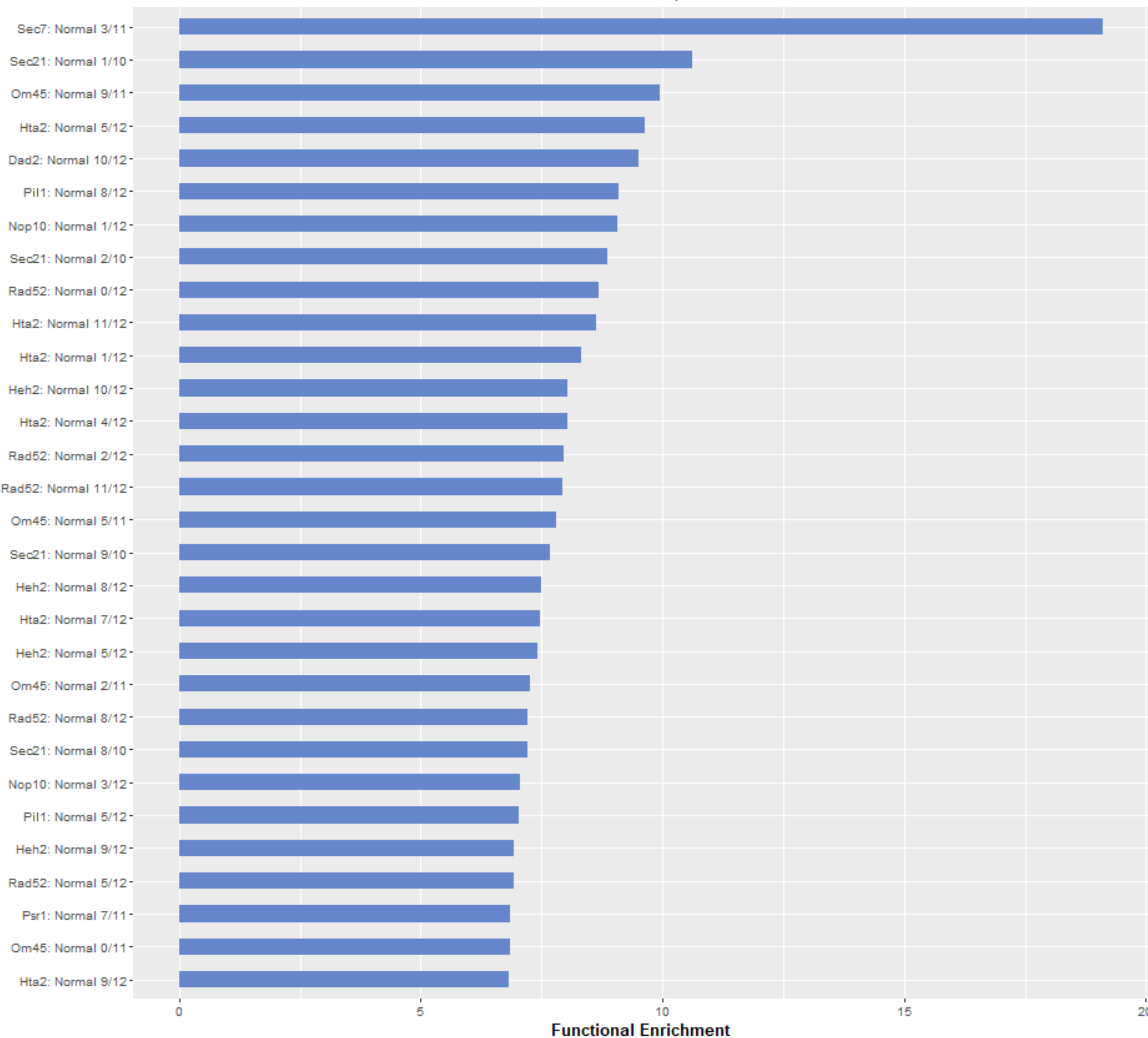




# DNA-templated transcription, initiation

With AreaShape

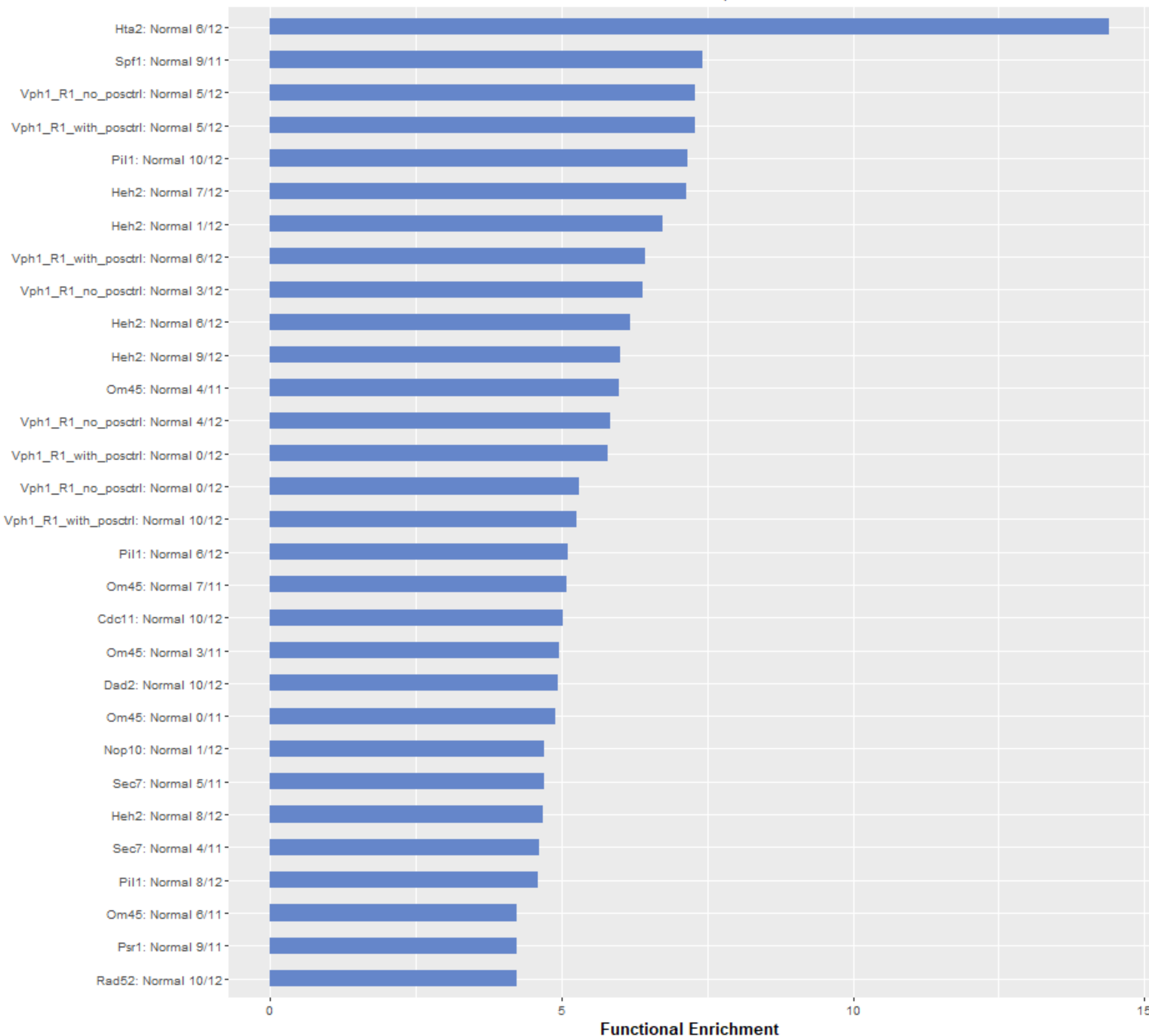
Marker: Cluster



# DNA-templated transcription, termination

With AreaShape

Marker: Cluster



# endocytosis

With AreaShape

Marker: Cluster

Pil1: Normal 7/12

Psr1: Normal 3/11

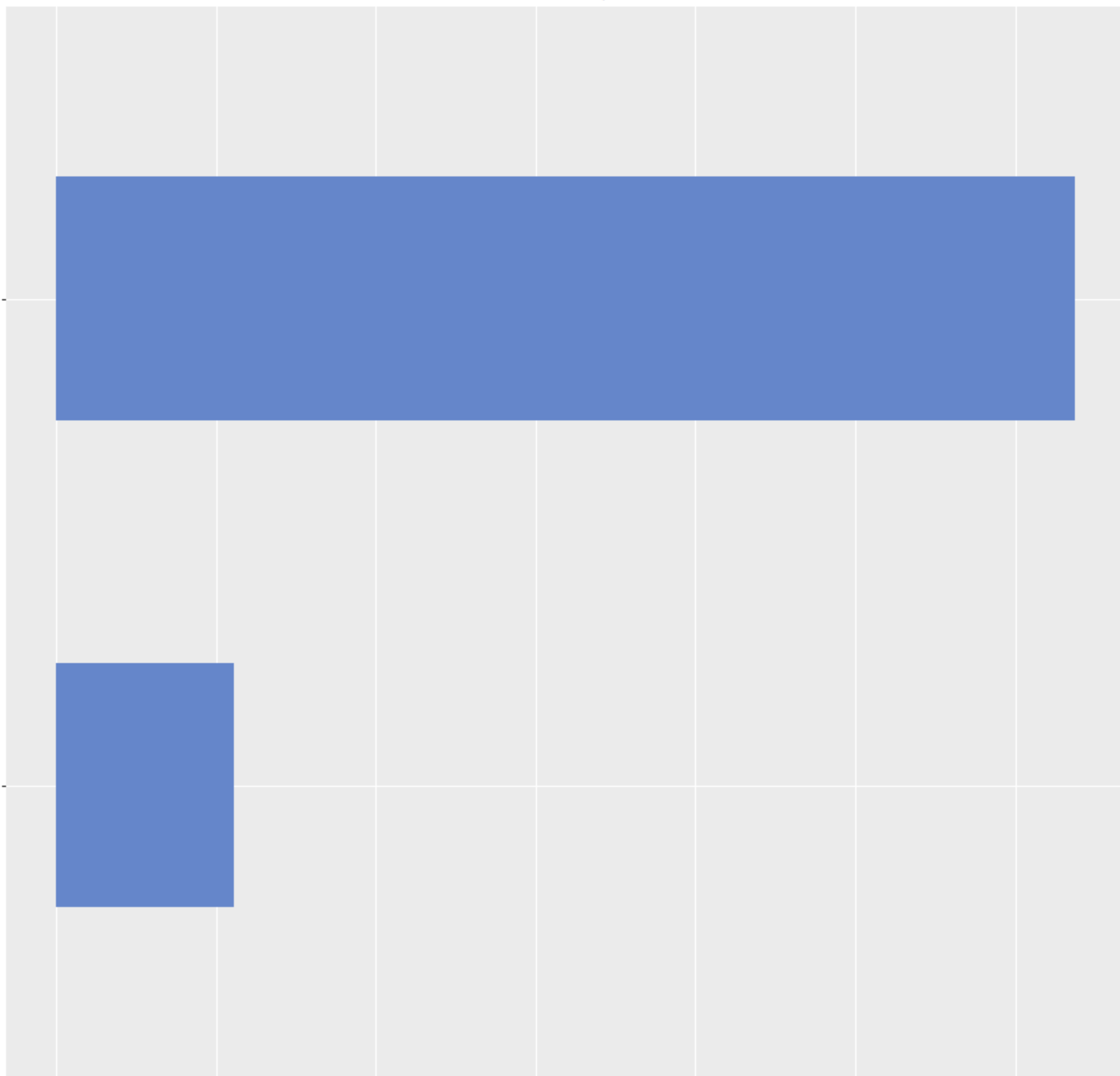
0

5

10

15

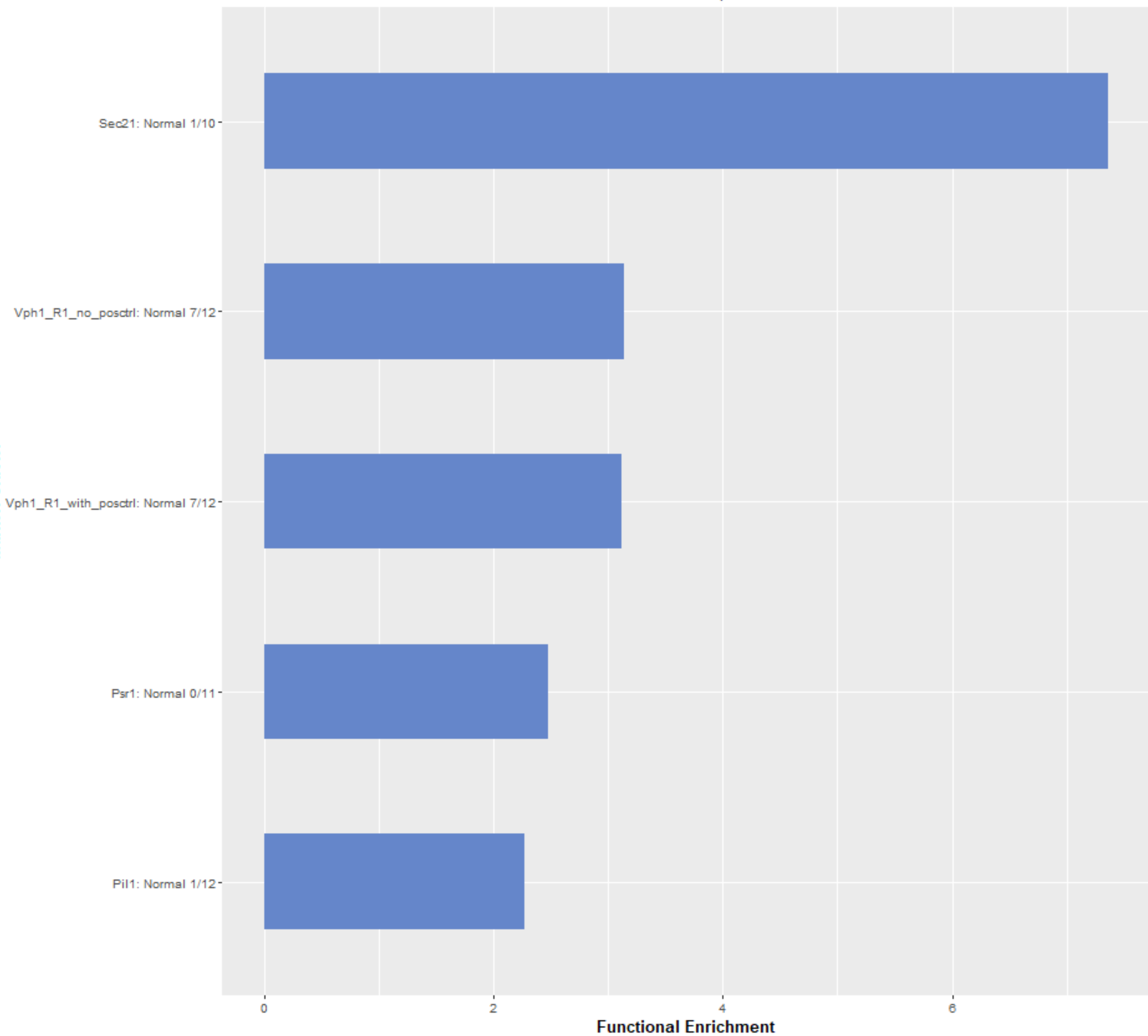
Functional Enrichment



# endosomal transport

With AreaShape

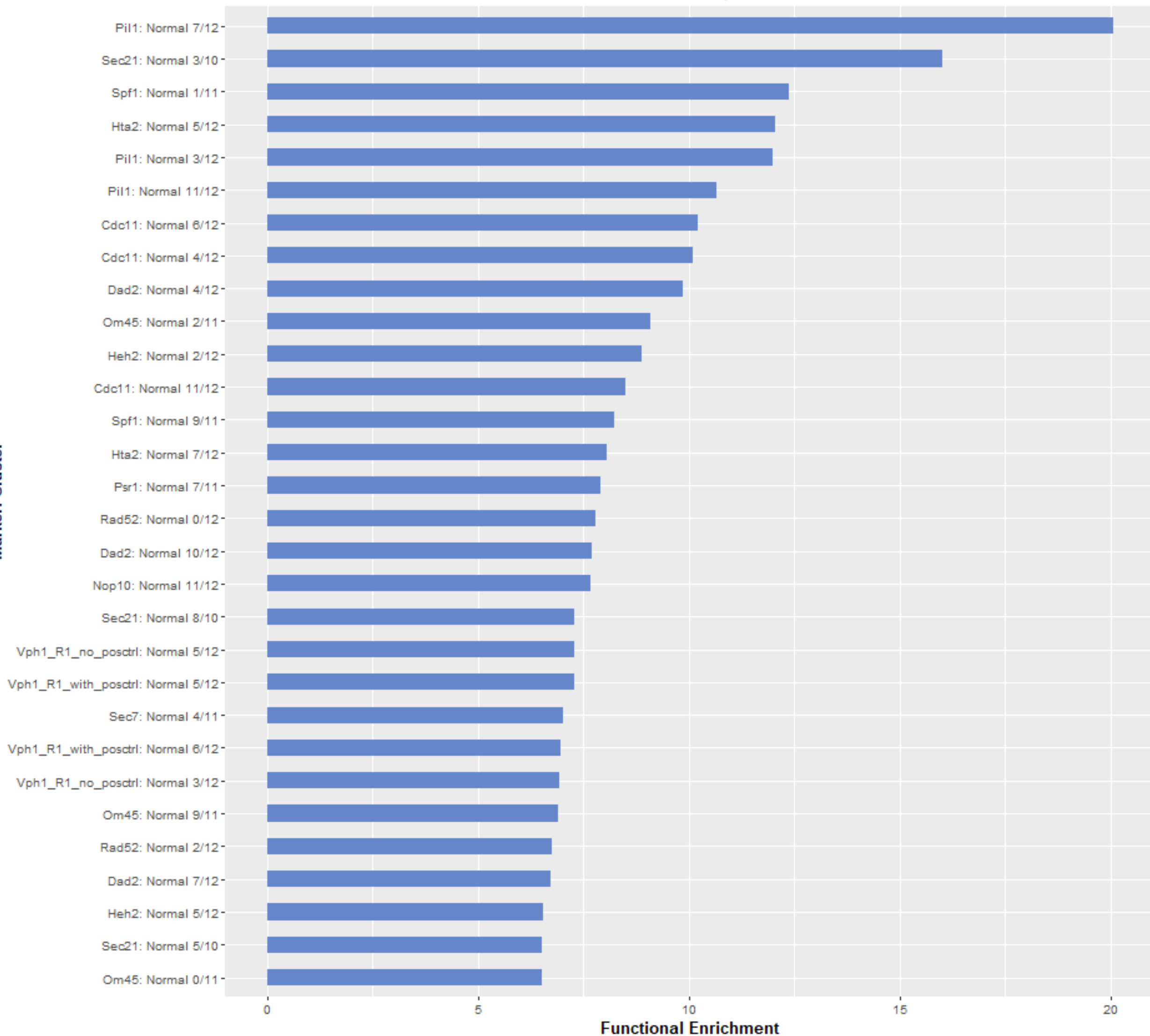
Marker: Cluster



# exocytosis

With AreaShape

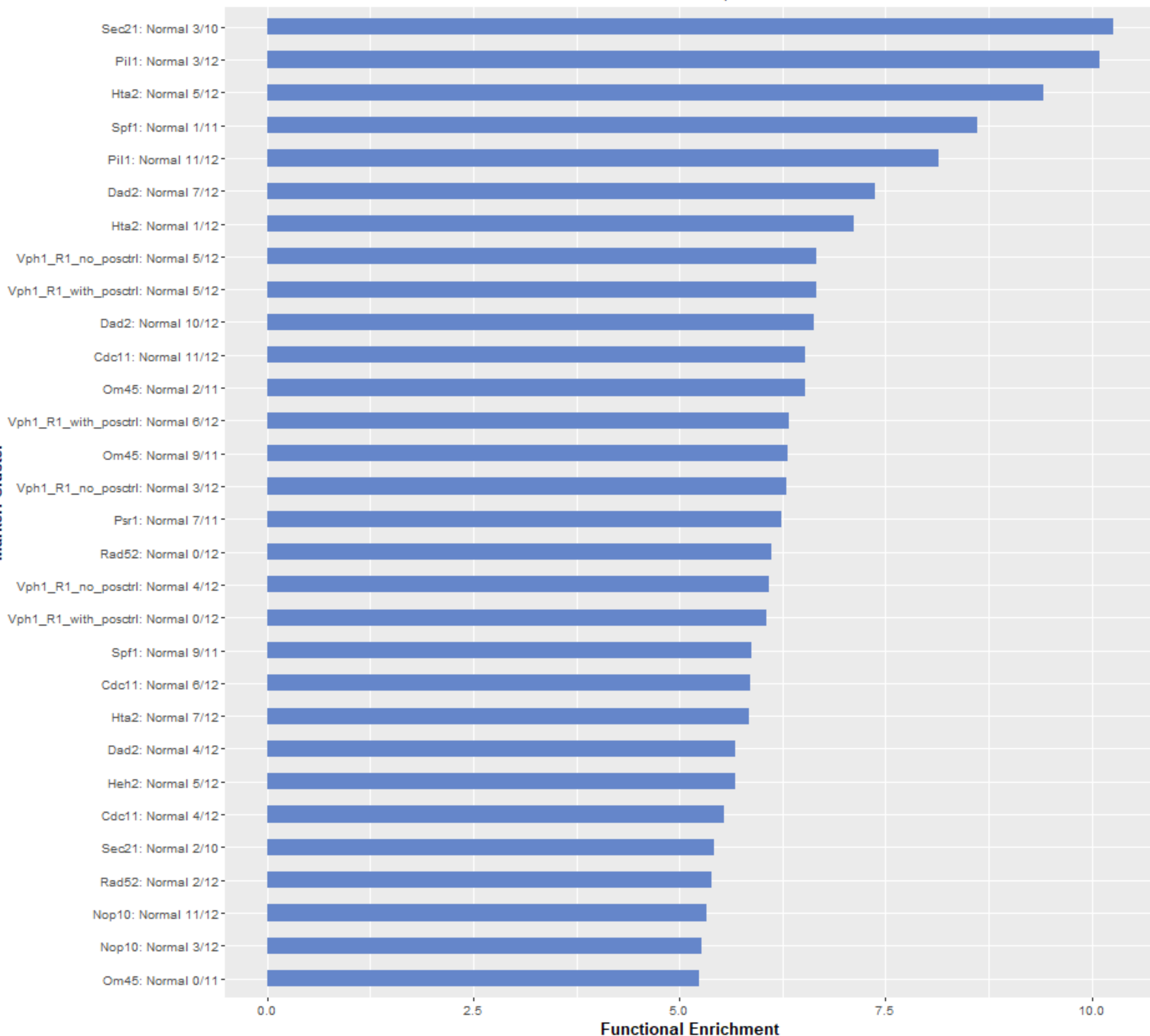
Marker: Cluster



# Golgi vesicle transport

With AreaShape

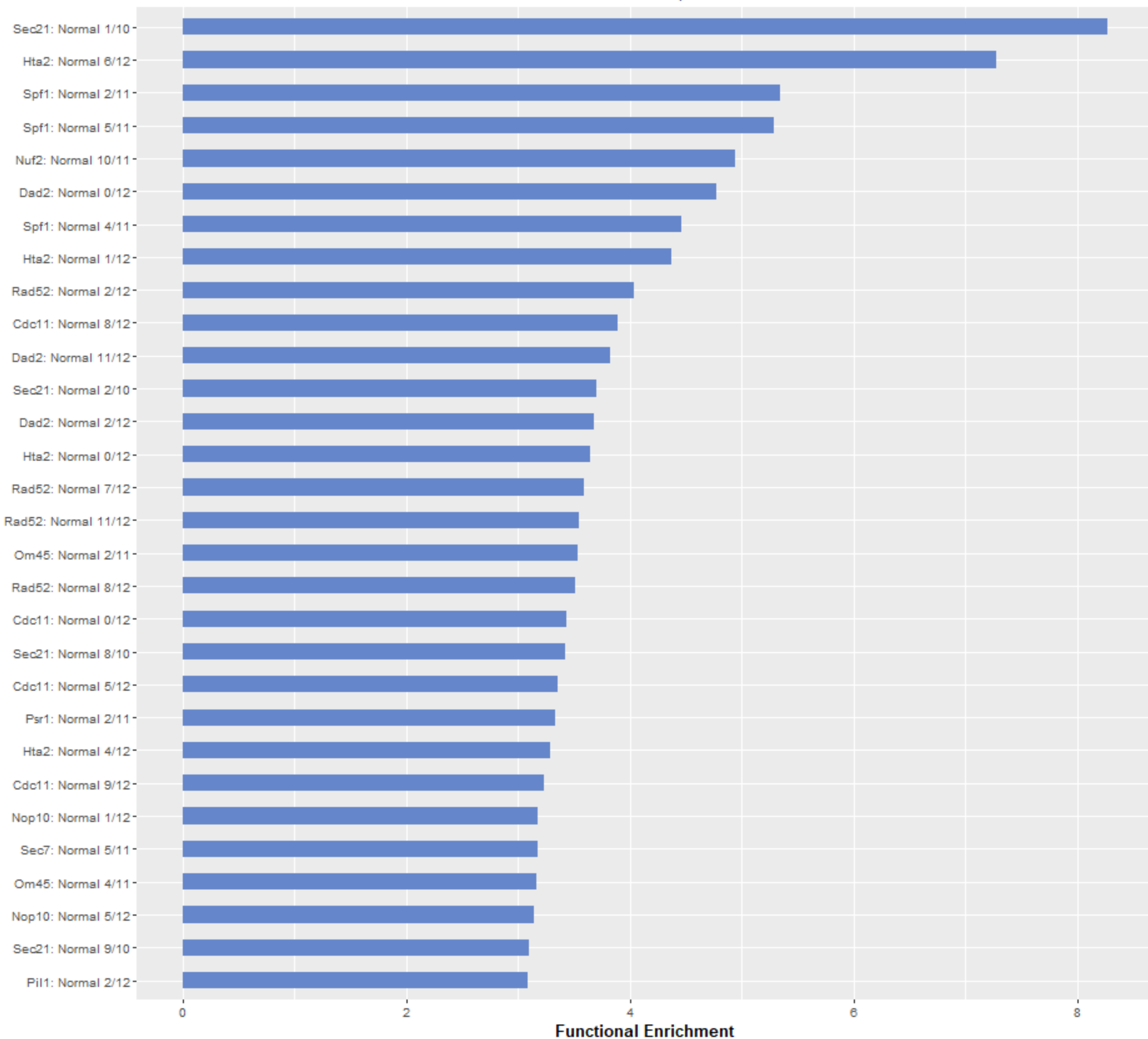
Marker: Cluster



# histone modification

With AreaShape

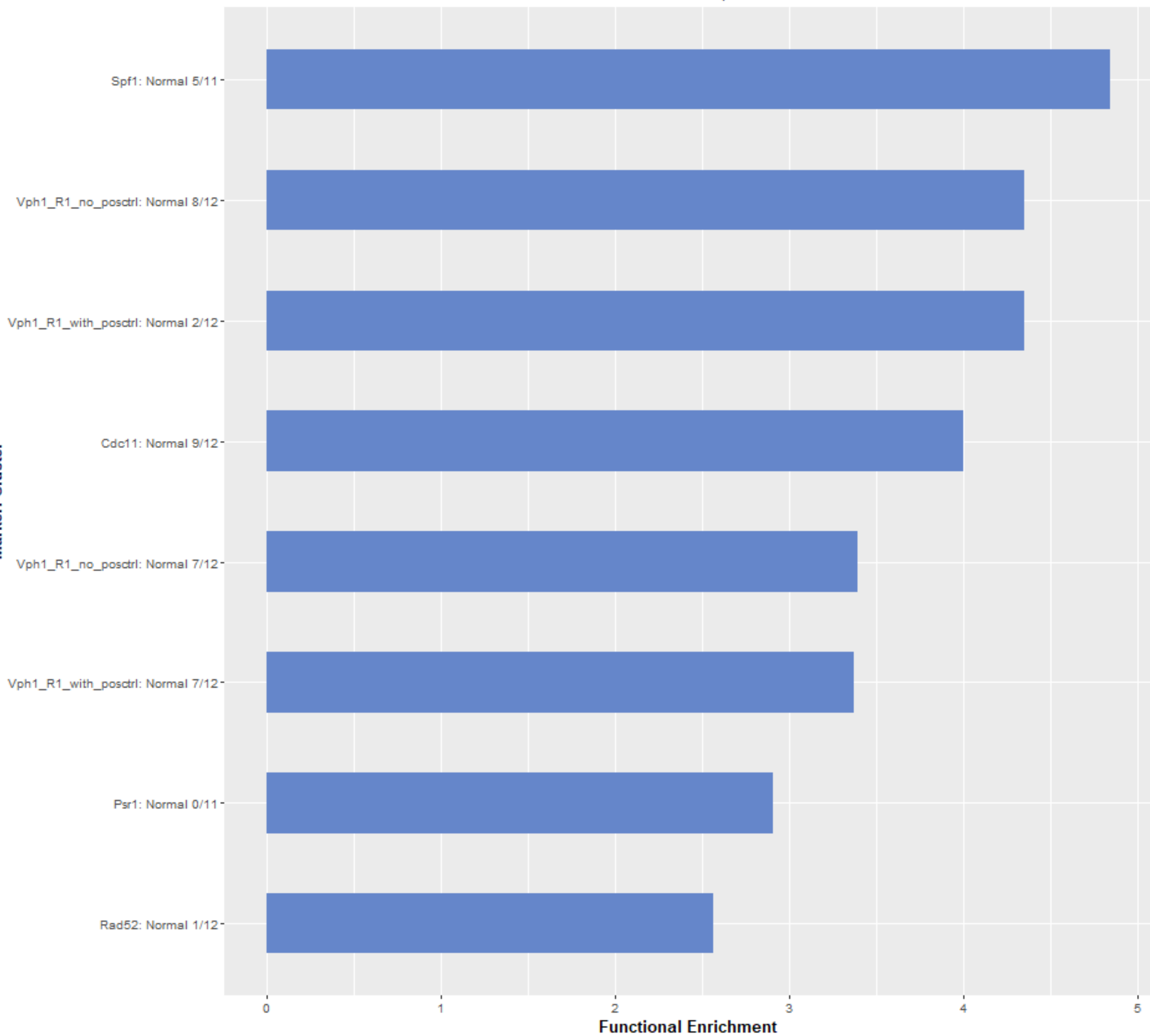
Marker: Cluster



# invasive growth in response to glucose limitation

With AreaShape

Marker: Cluster

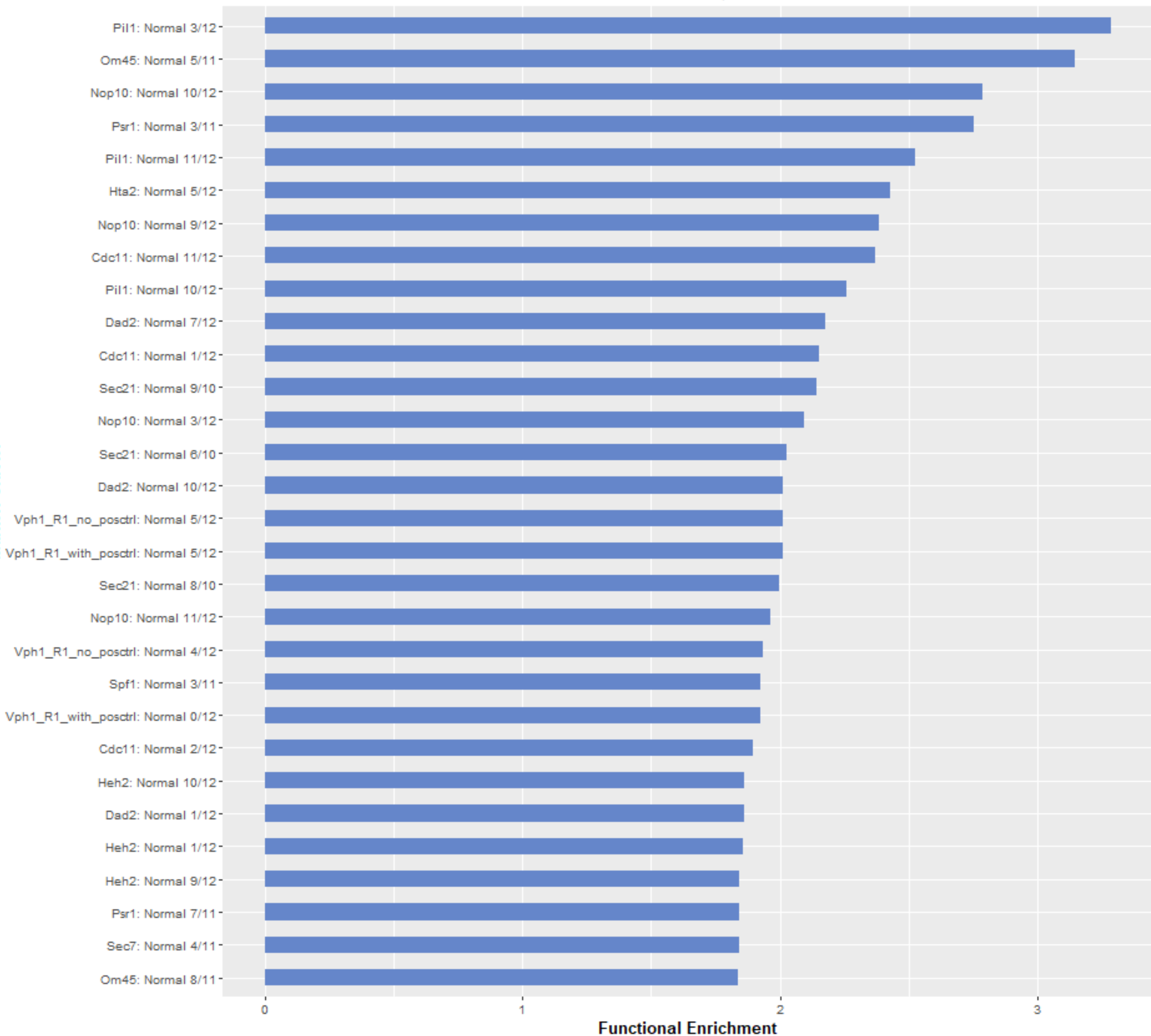




# lipid metabolic process

With AreaShape

Marker: Cluster



# meiotic cell cycle

With AreaShape

Marker: Cluster

Nop10: Normal 10/12

Cdc11: Normal 5/12

Heh2: Normal 0/12

Pil1: Normal 2/12

0.0

0.5

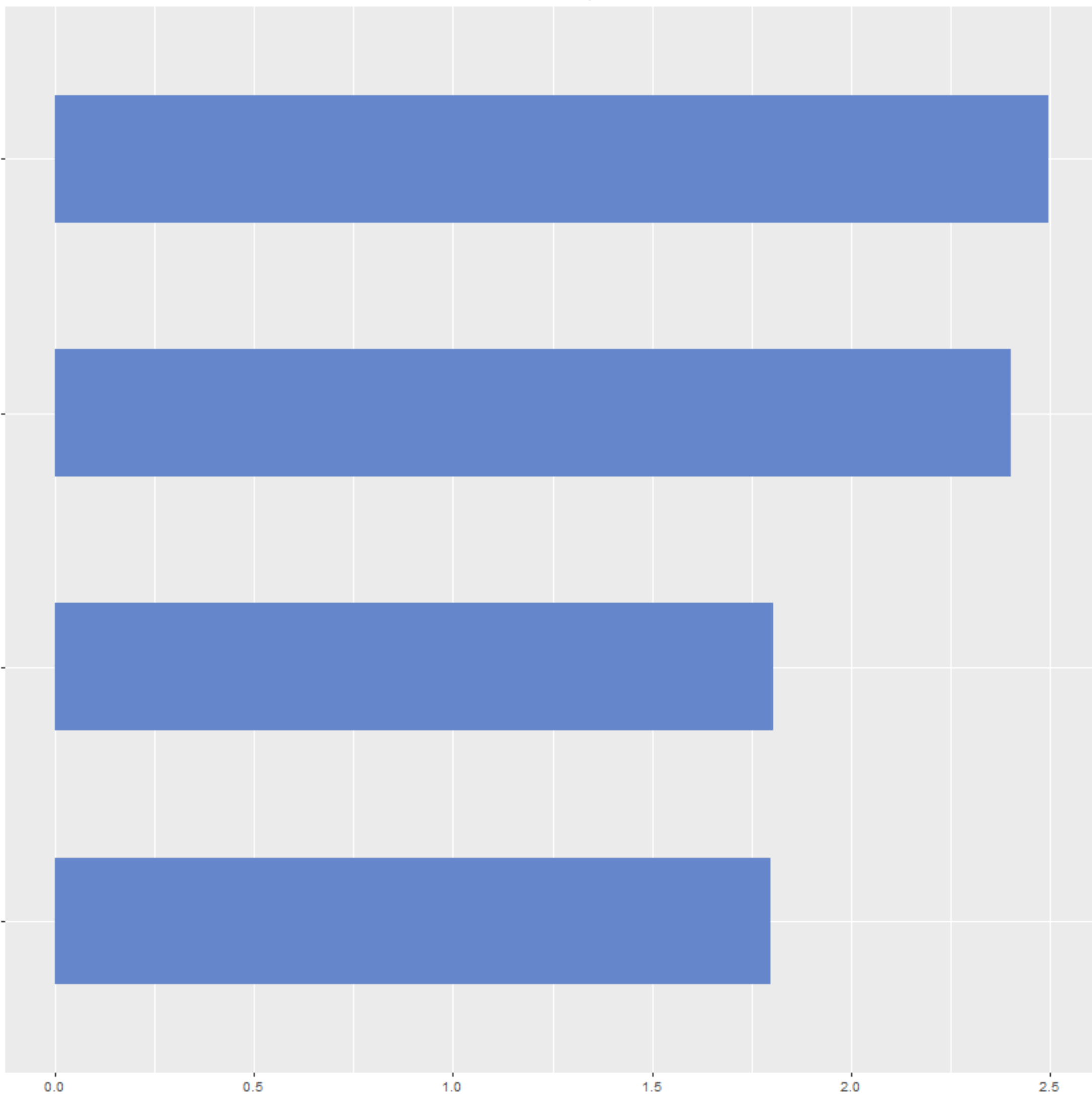
1.0

1.5

2.0

2.5

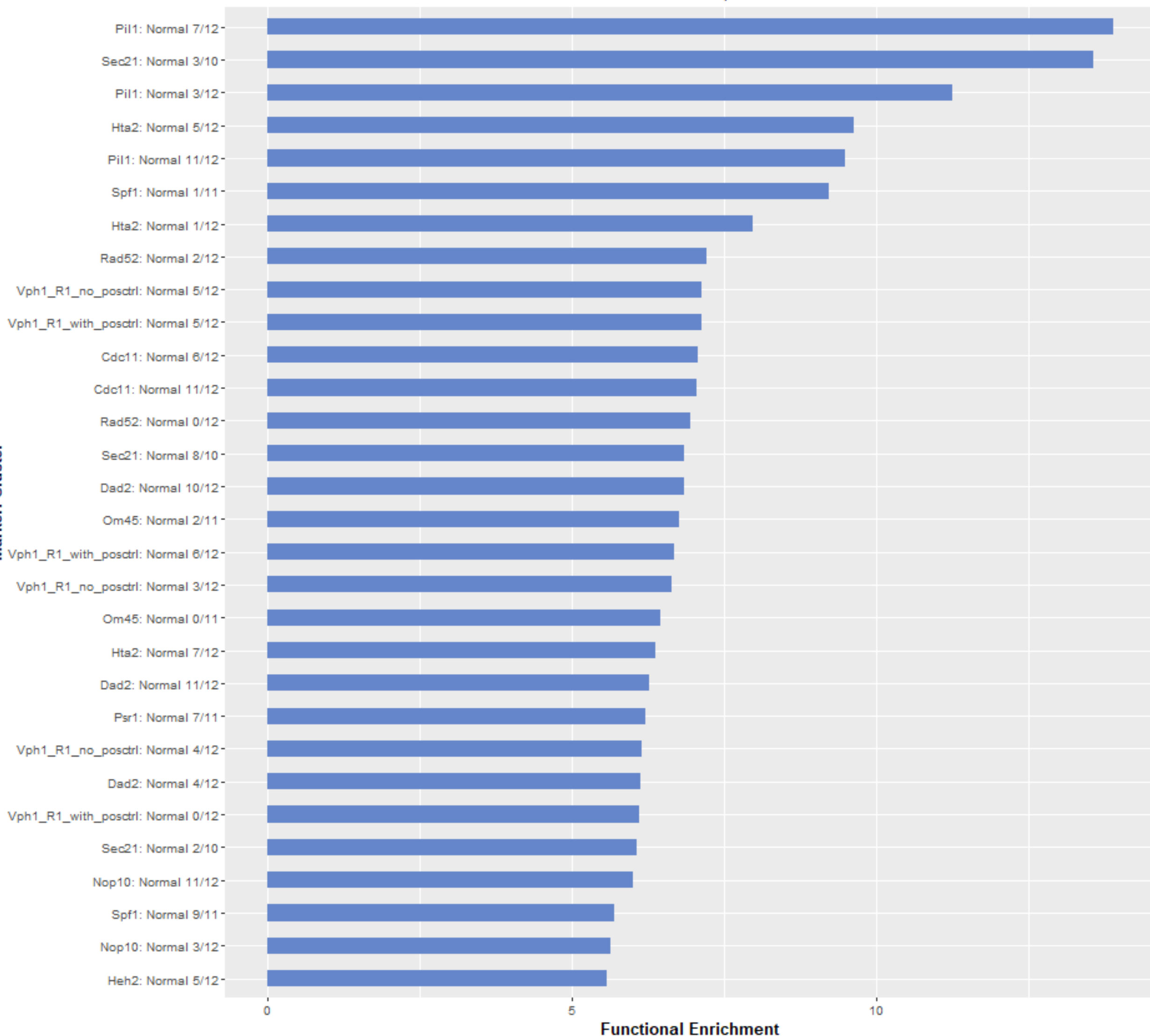
Functional Enrichment



# membrane fusion

With AreaShape

Marker: Cluster

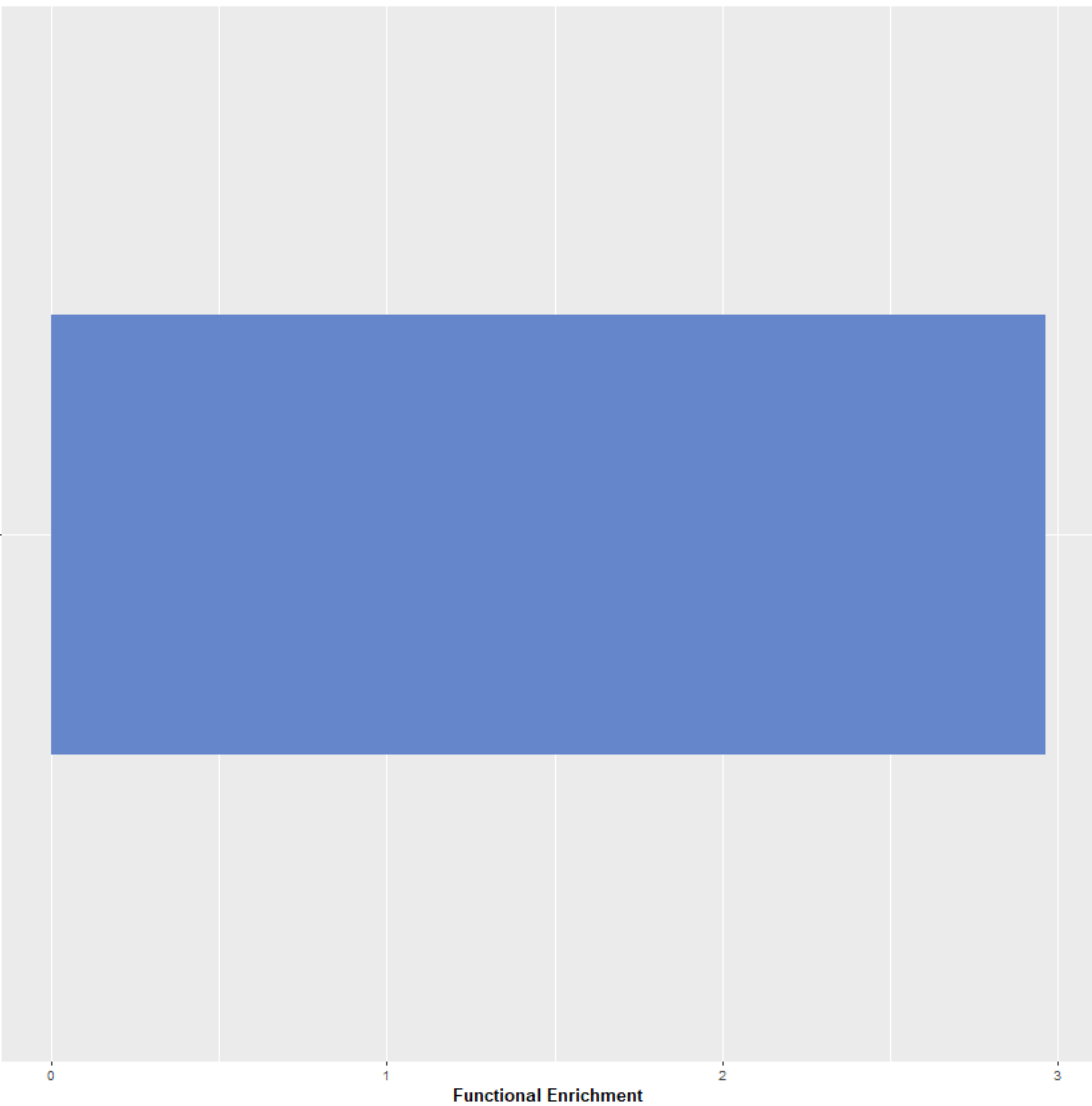


# mitochondrial translation

With AreaShape

Marker: Cluster

Om45: Normal 3/11



# mitochondrion organization

With AreaShape

Marker: Cluster

Om45: Normal 5/11

Om45: Normal 3/11

Om45: Normal 2/11

Om45: Normal 4/11

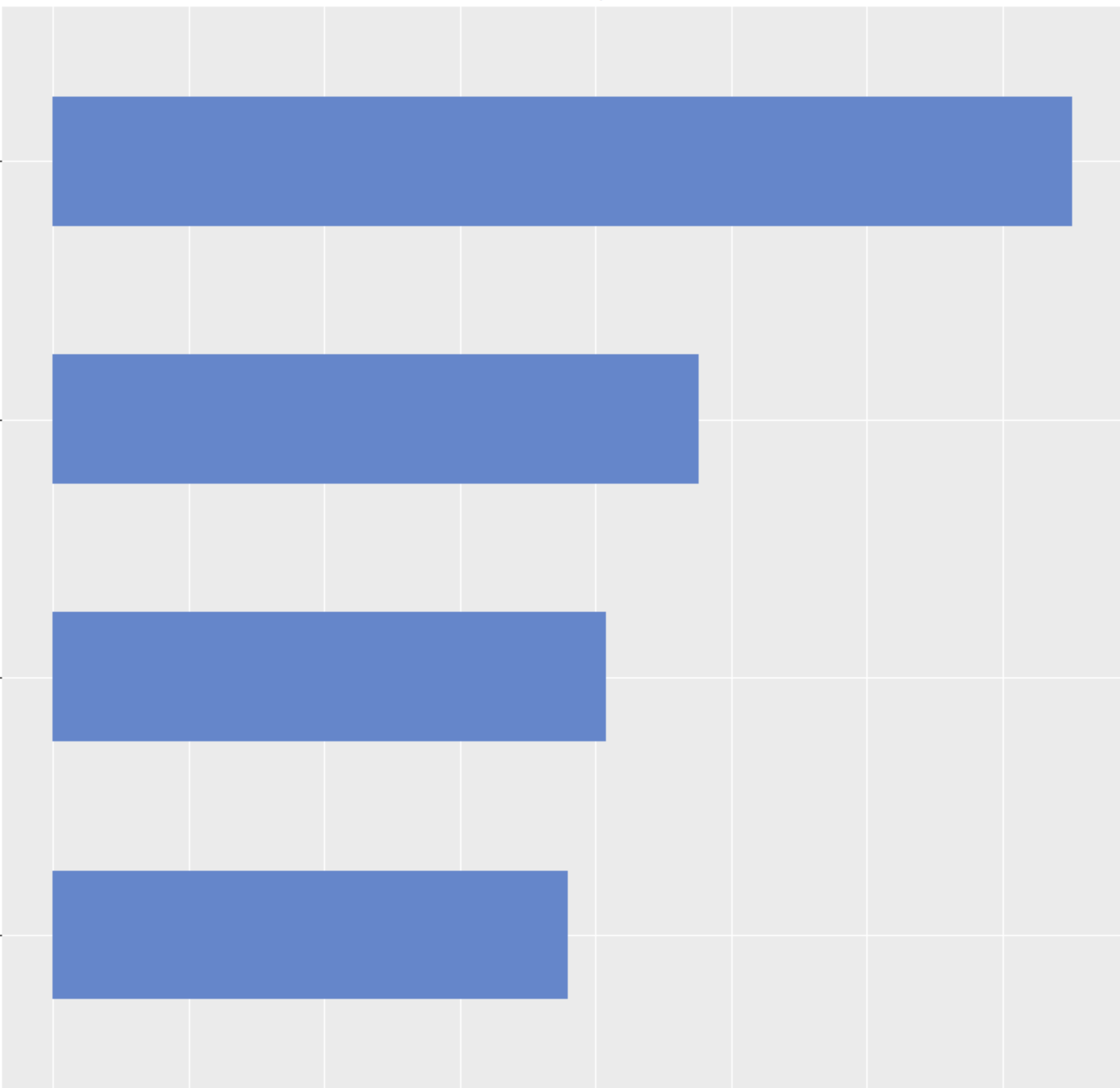
0

1

2

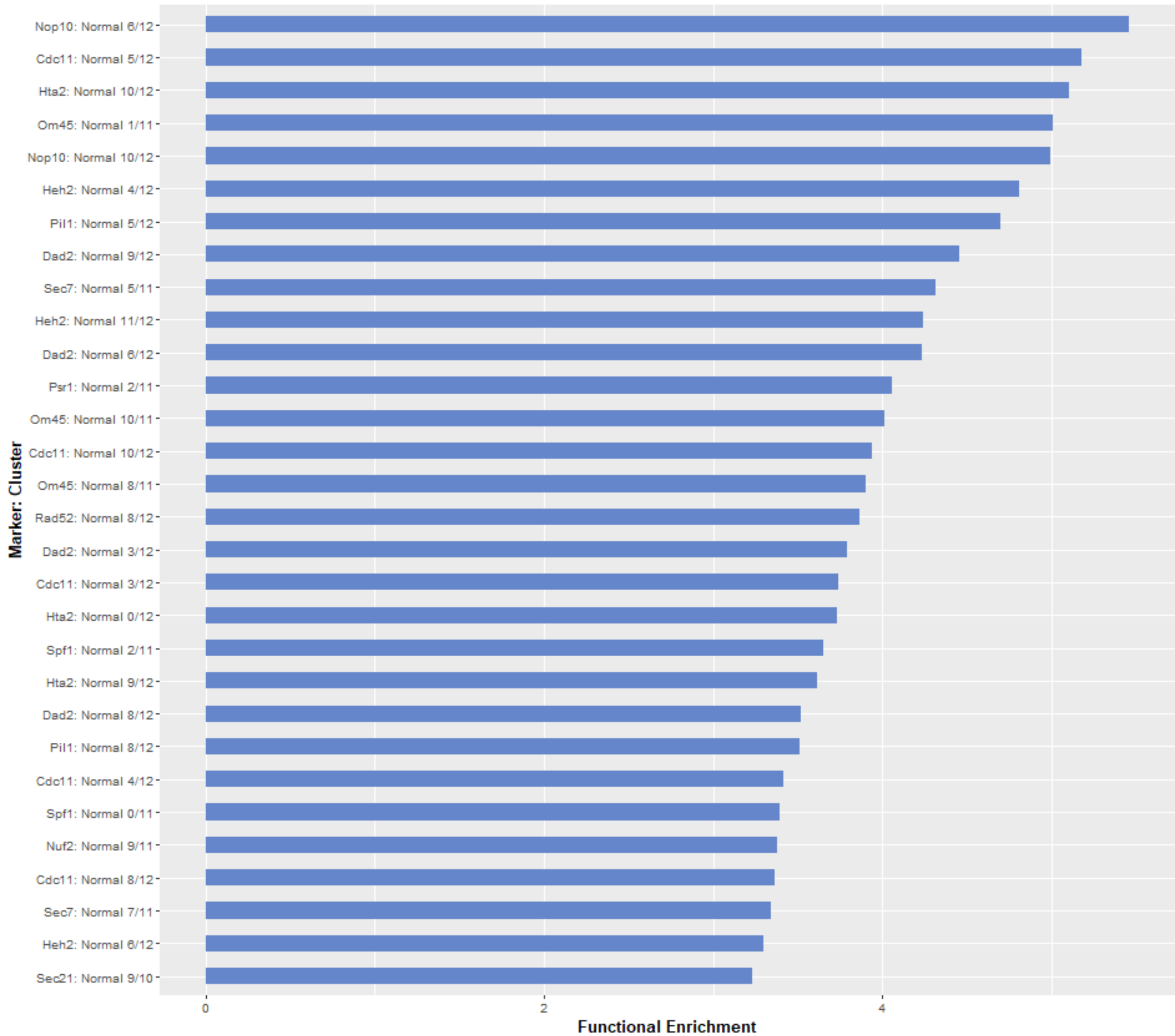
3

Functional Enrichment



mitotic cell cycle

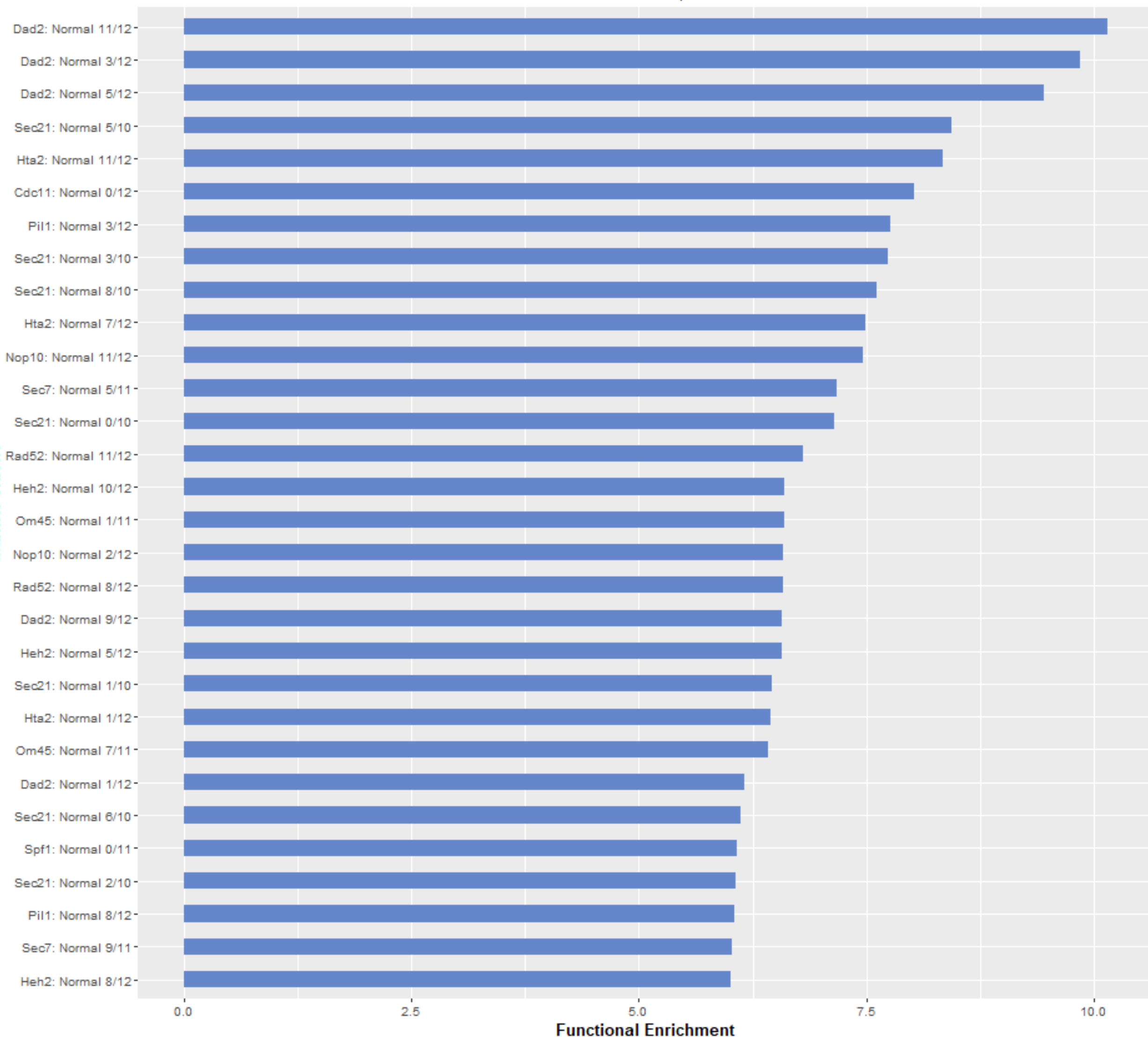
With AreaShape



# mRNA processing

With AreaShape

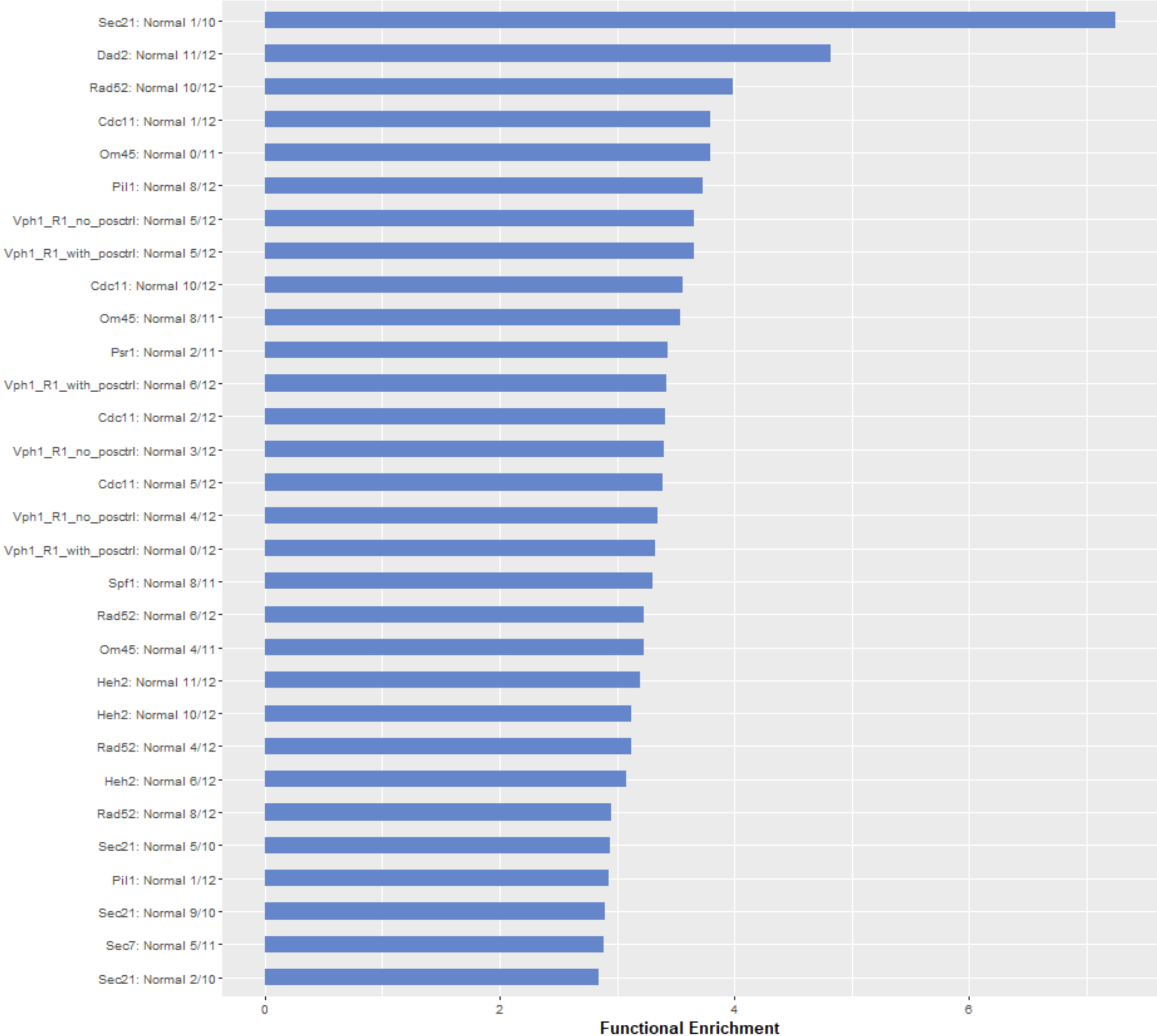
Marker: Cluster



nuclear transport

With AreaShape

Marker: Cluster

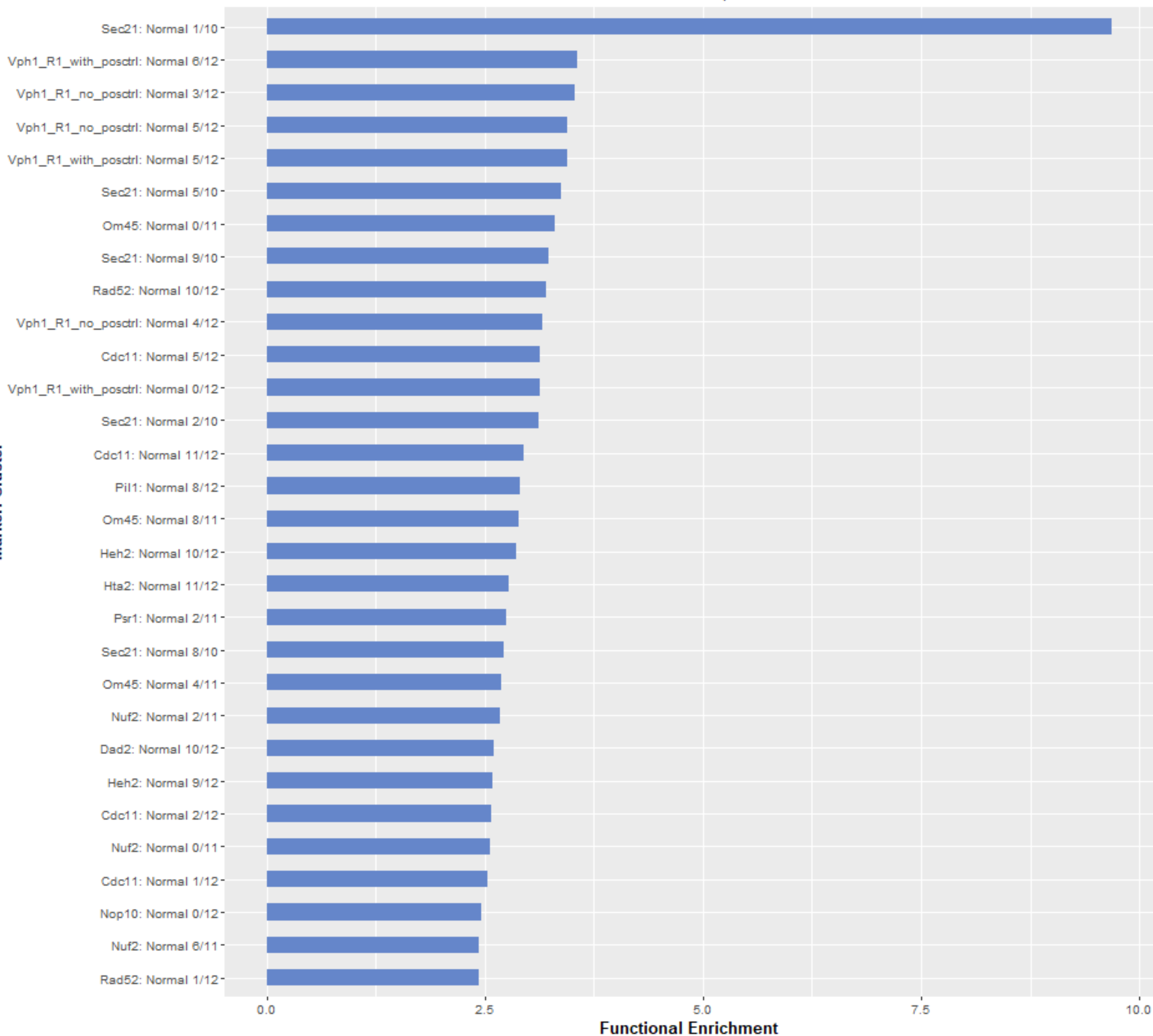




# nucleobase-containing compound transport

With AreaShape

Marker: Cluster



# nucleus organization

With AreaShape

Marker: Cluster

Rad52: Normal 8/12  
Om45: Normal 8/11  
Dad2: Normal 9/12  
Dad2: Normal 4/12  
Cdc11: Normal 5/12  
Sec7: Normal 5/11  
Rad52: Normal 10/12  
Dad2: Normal 3/12  
Spf1: Normal 3/11  
Cdc11: Normal 8/12  
Sec21: Normal 2/10  
Rad52: Normal 6/12  
Spf1: Normal 8/11  
Vph1\_R1\_no\_posctrl: Normal 4/12  
Vph1\_R1\_with\_posctrl: Normal 0/12  
Vph1\_R1\_no\_posctrl: Normal 5/12  
Vph1\_R1\_with\_posctrl: Normal 5/12  
Vph1\_R1\_with\_posctrl: Normal 6/12  
Vph1\_R1\_no\_posctrl: Normal 3/12  
Pil1: Normal 10/12  
Spf1: Normal 0/11  
Om45: Normal 1/11  
Hts2: Normal 7/12  
Spf1: Normal 7/11  
Om45: Normal 0/11  
Sec21: Normal 5/10  
Rad52: Normal 4/12  
Sec21: Normal 9/10  
Om45: Normal 7/11  
Cdc11: Normal 10/12

0

2

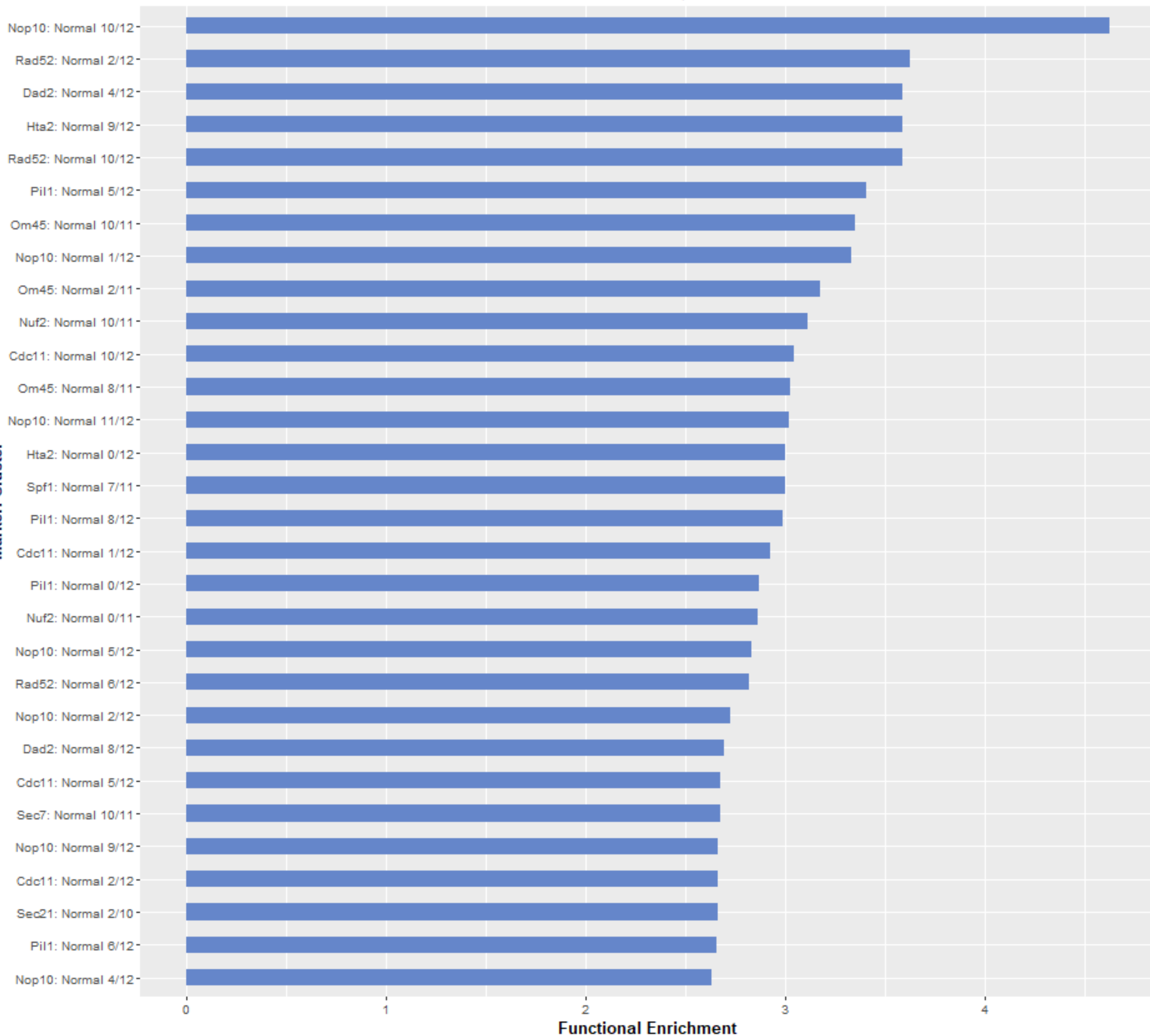
4

Functional Enrichment

# organelle assembly

With AreaShape

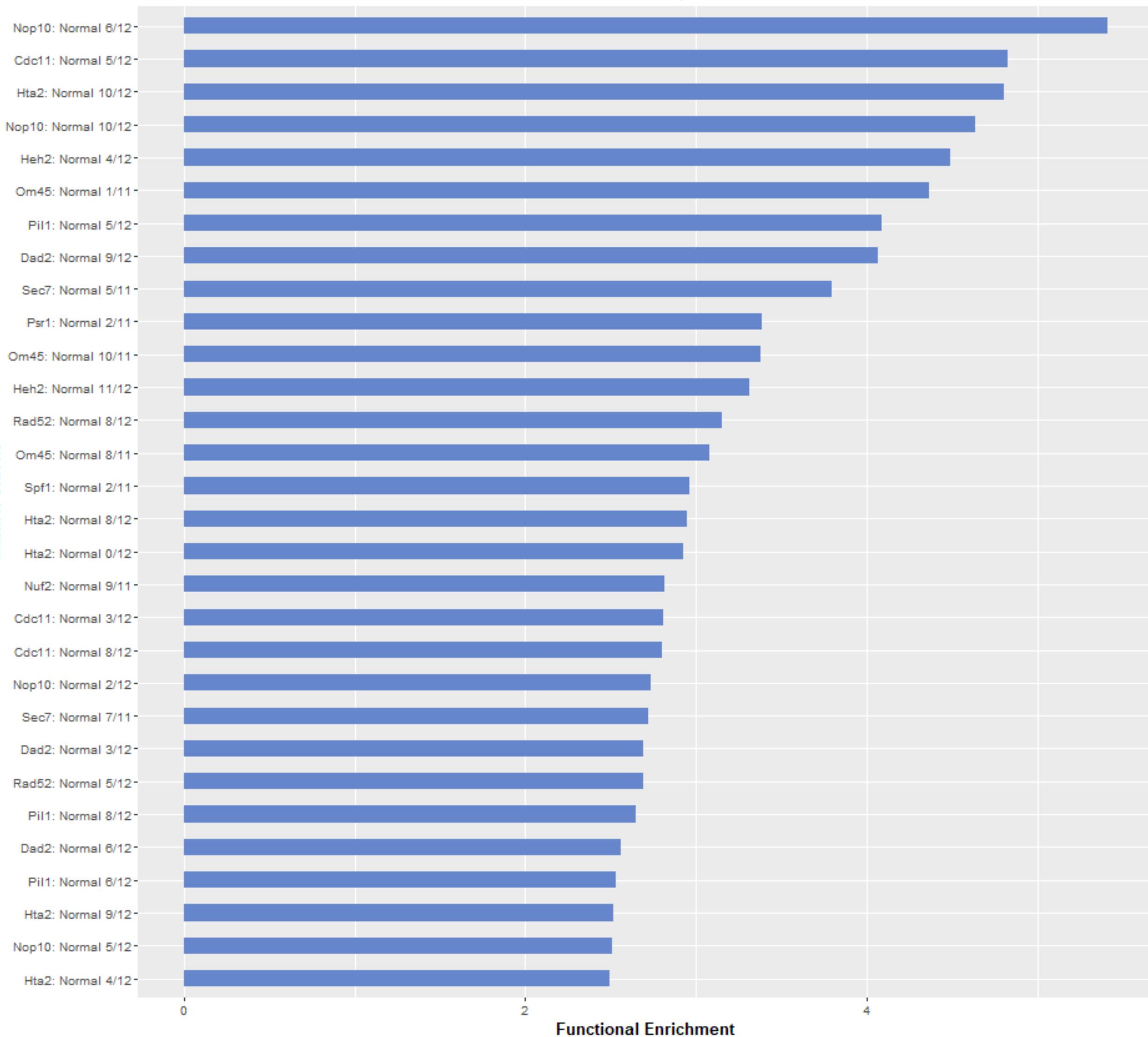
Marker: Cluster



# organelle fission

With AreaShape

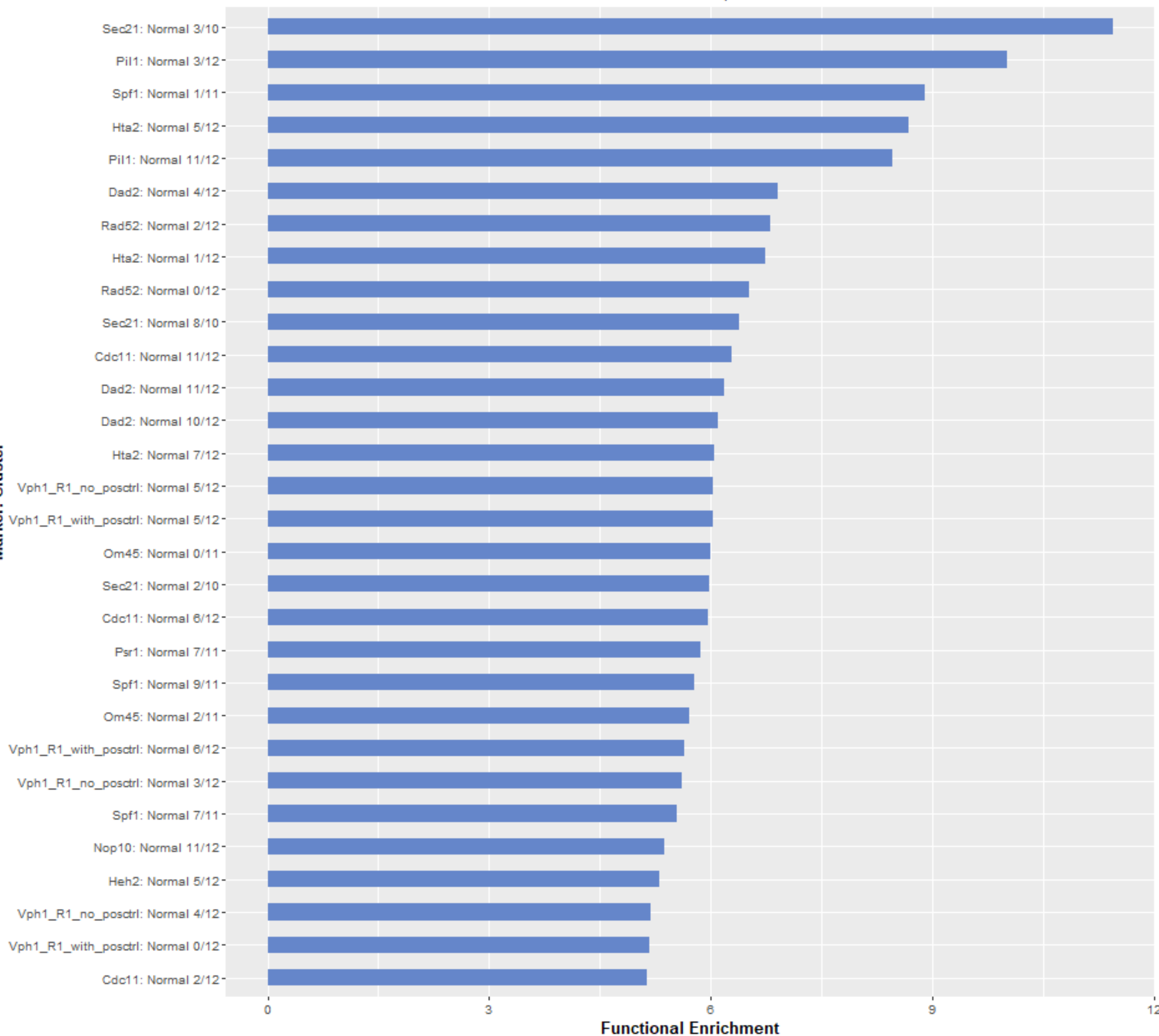
Marker: Cluster



# organelle fusion

With AreaShape

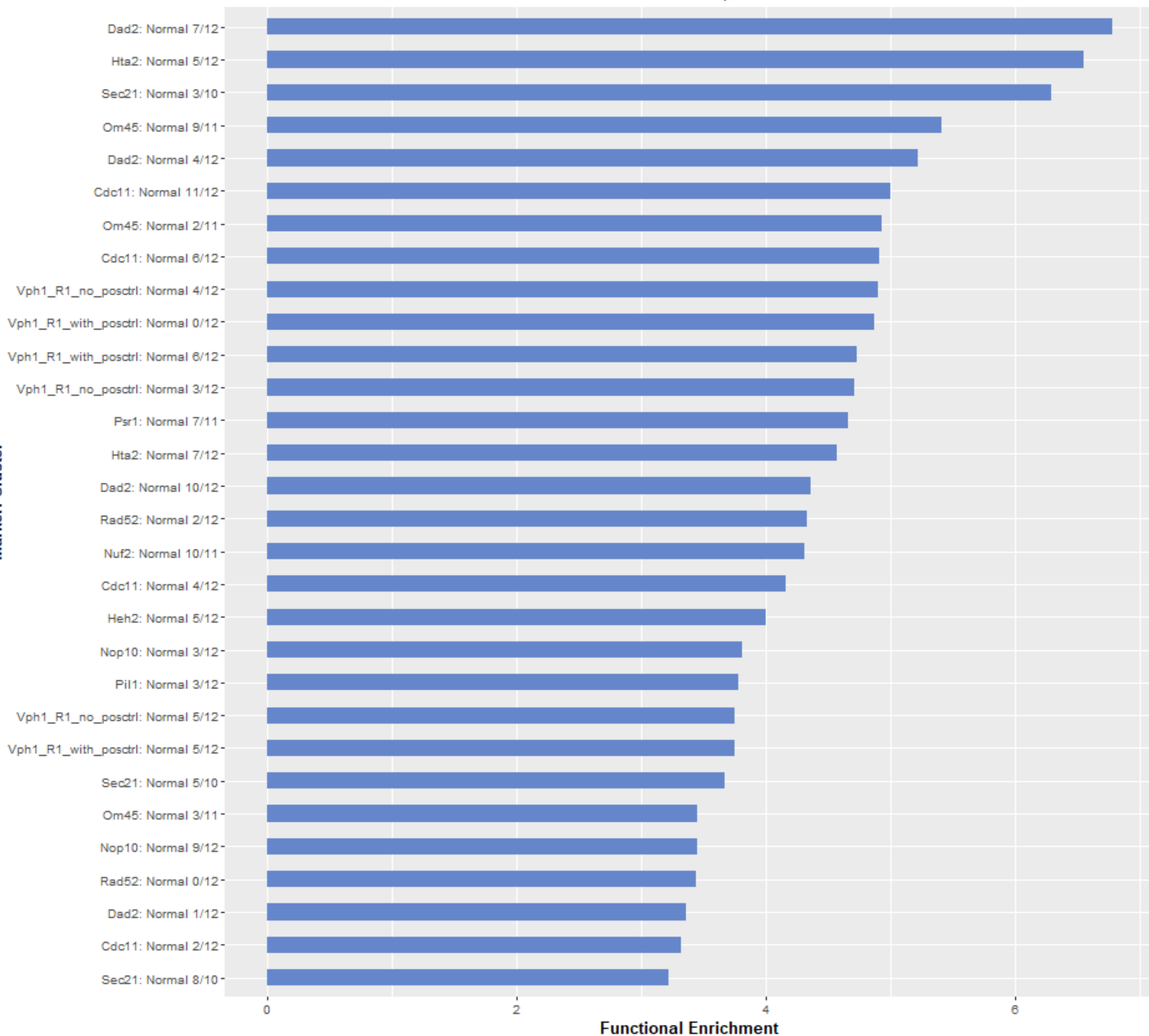
Marker: Cluster



# organelle inheritance

With AreaShape

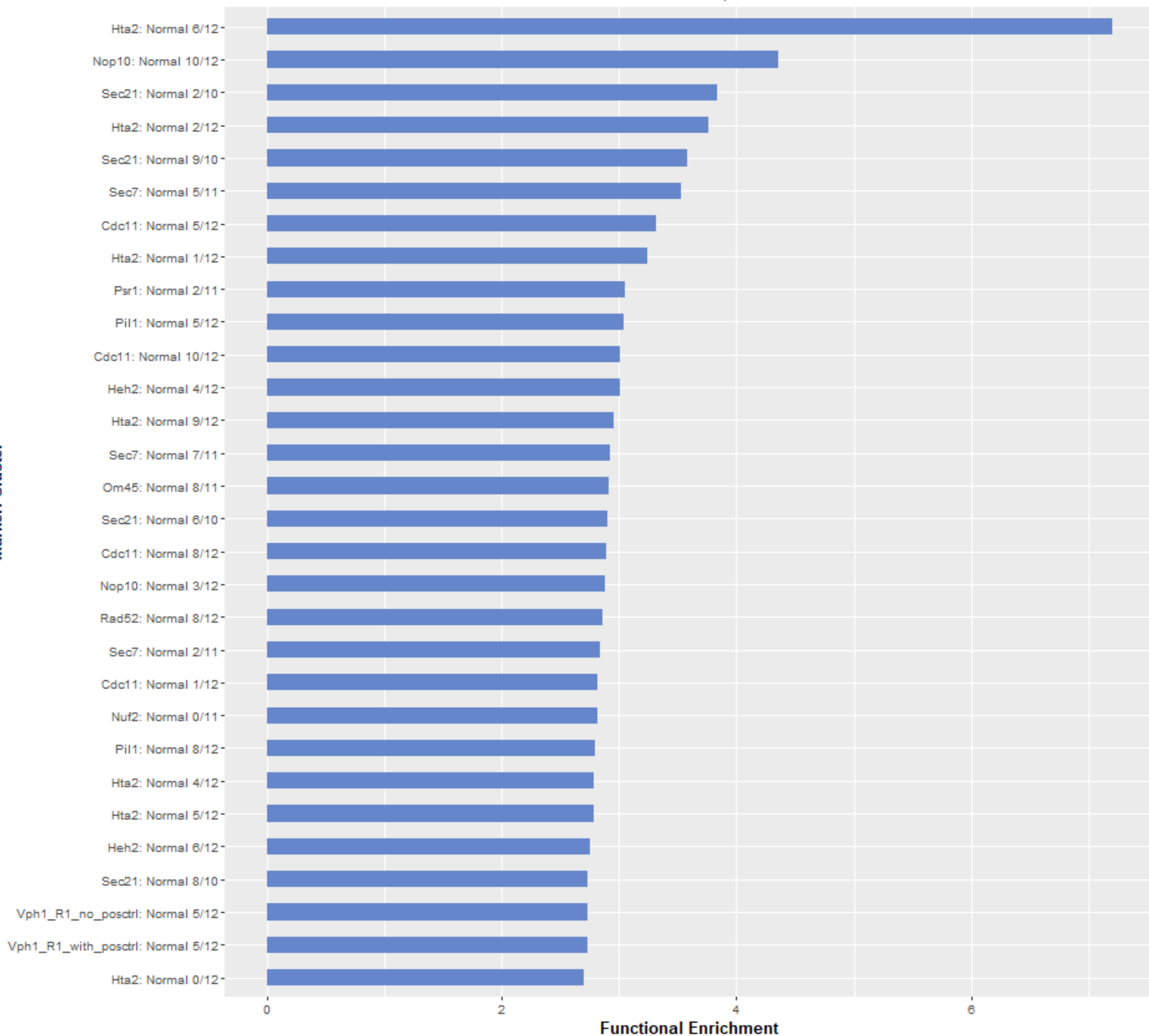
Marker: Cluster



# peptidyl-amino acid modification

With AreaShape

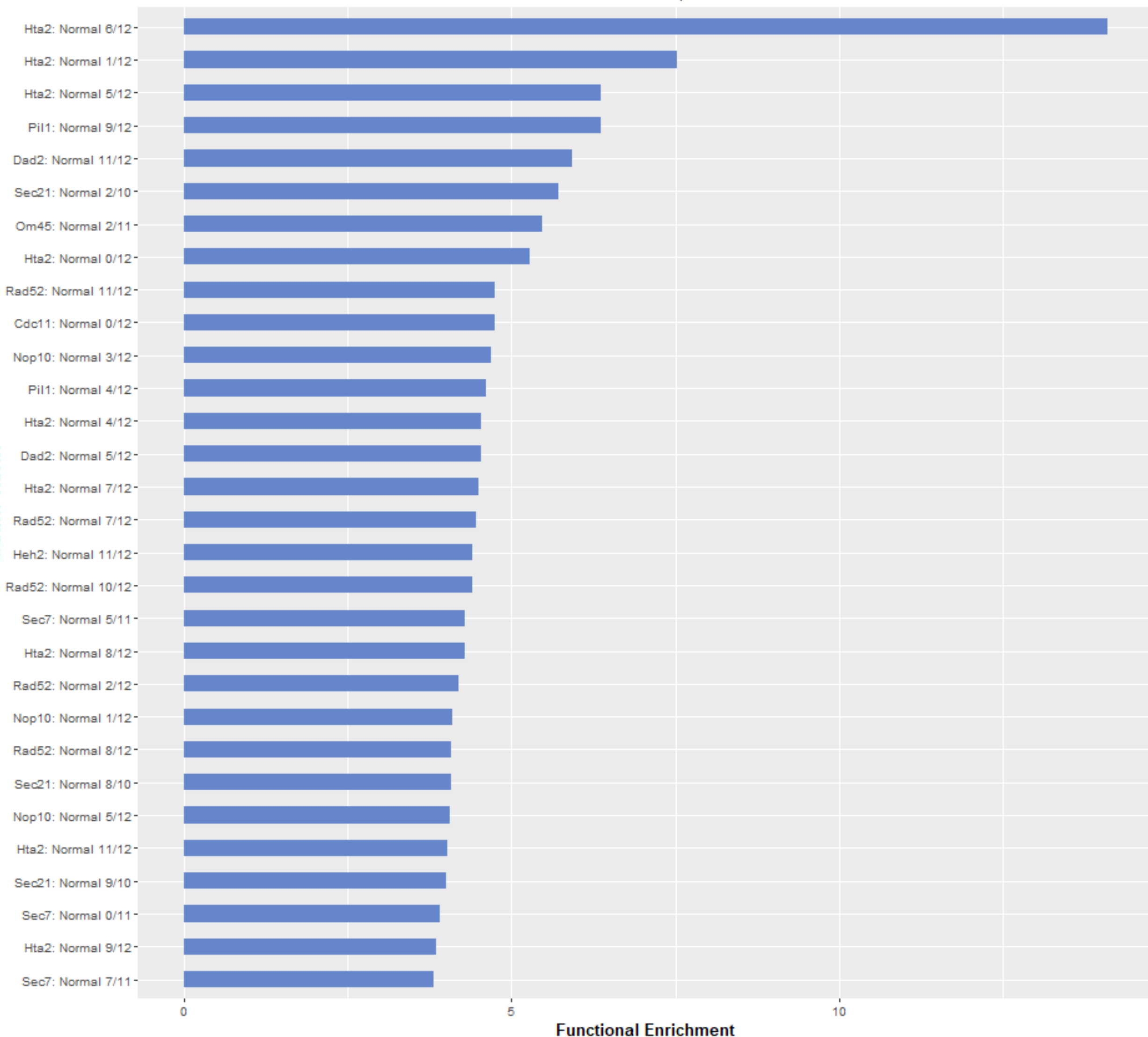
Marker: Cluster



# protein acylation

With AreaShape

Marker: Cluster





# protein alkylation

With AreaShape

Marker: Cluster

Sec21: Normal 1/10

Dad2: Normal 2/12

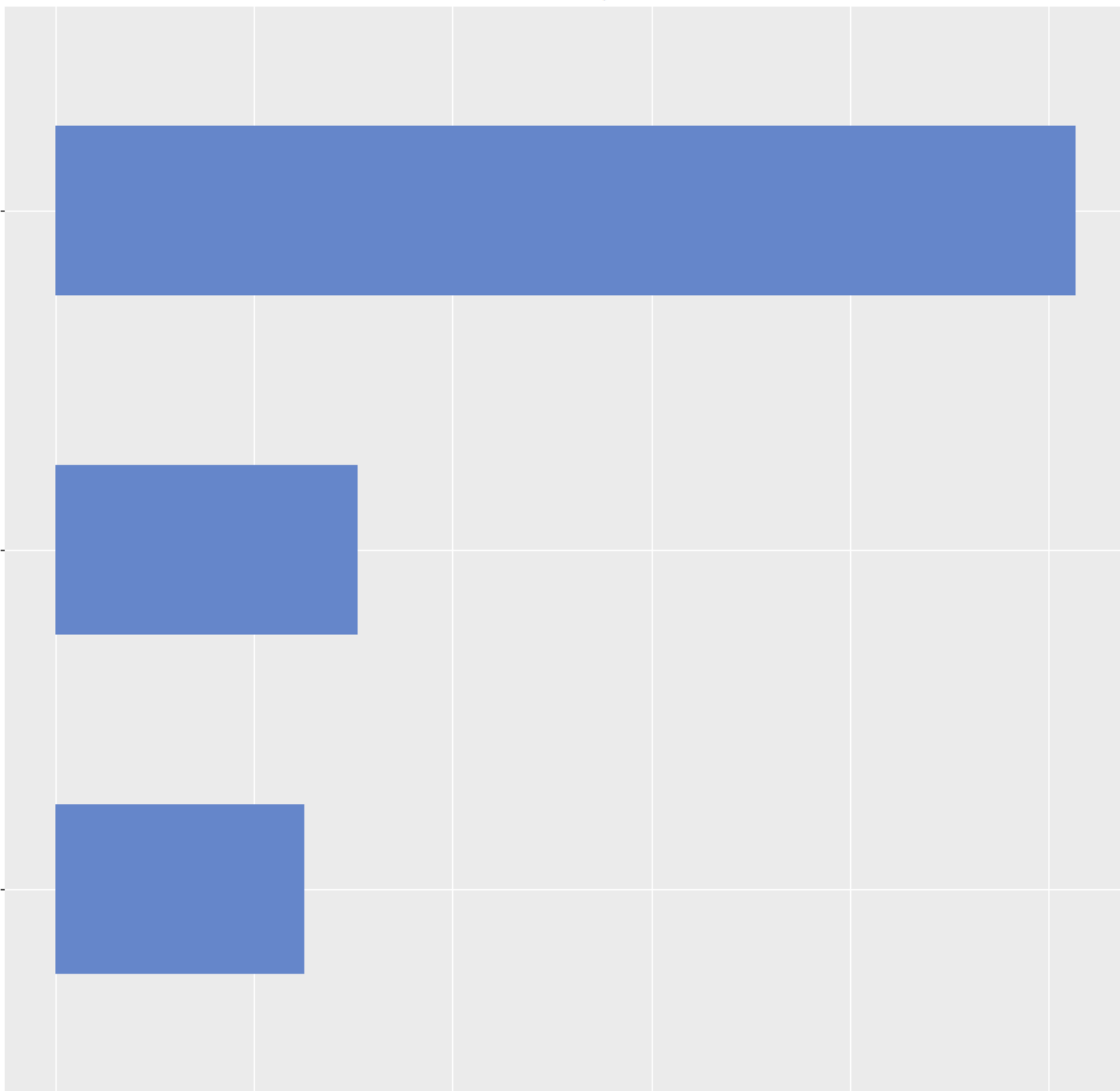
Nop10: Normal 2/12

0

5

10

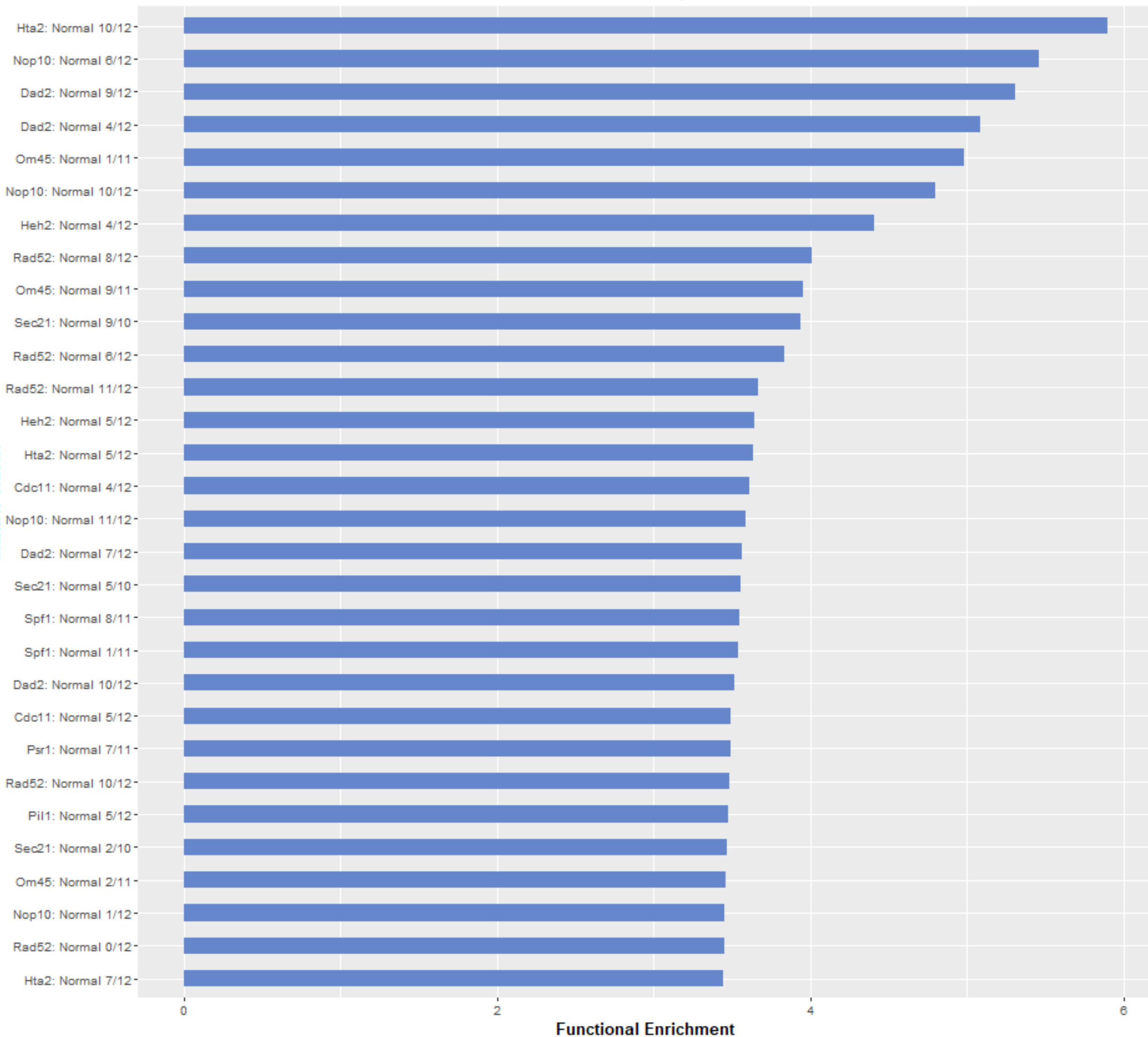
Functional Enrichment



# protein complex biogenesis

With AreaShape

Marker: Cluster



# protein dephosphorylation

With AreaShape

Marker: Cluster

Nop10: Normal 8/12

Heh2: Normal 0/12

Nop10: Normal 4/12

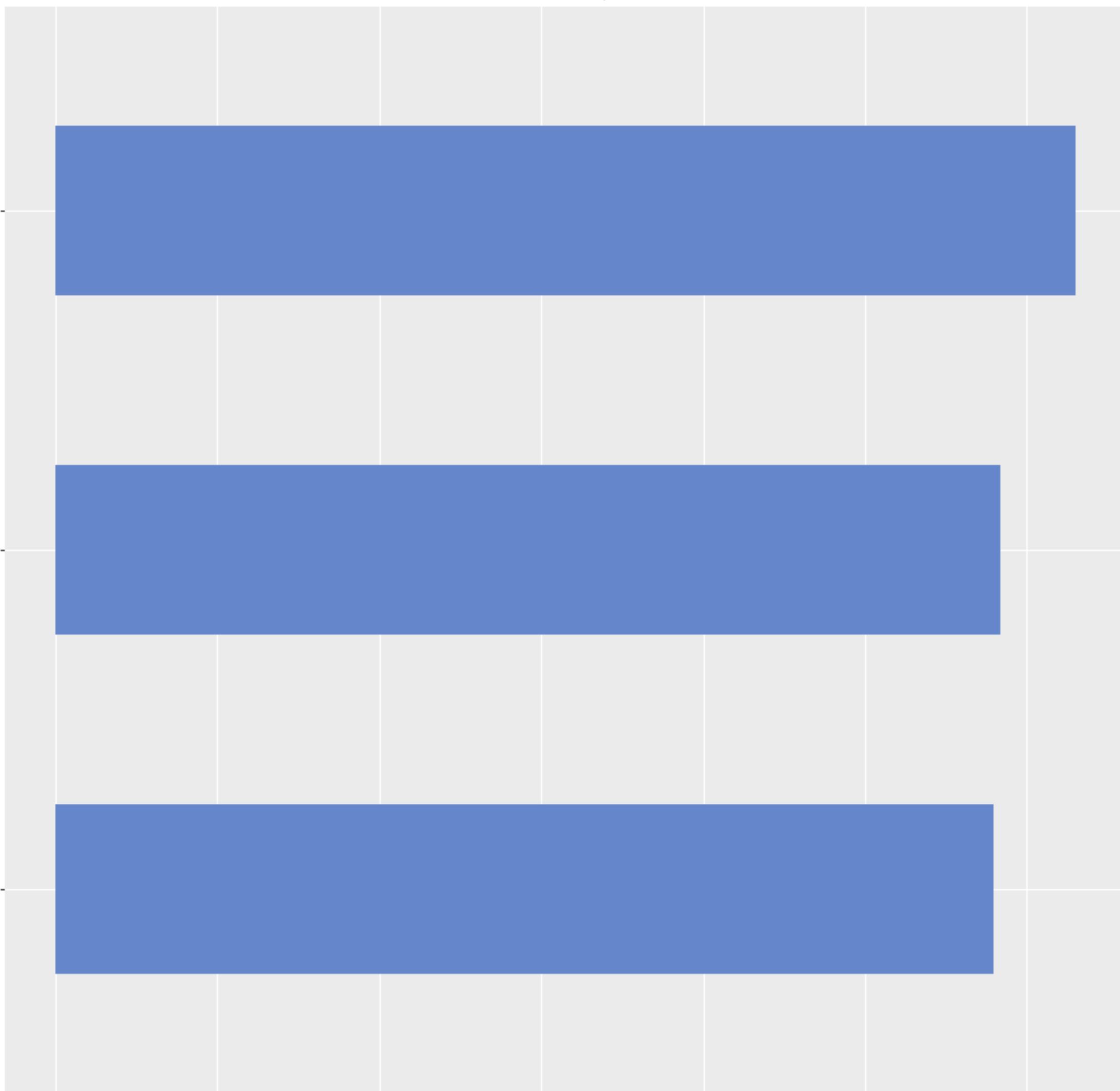
0

1

2

3

Functional Enrichment



# protein glycosylation

With AreaShape

Marker: Cluster

Vph1\_R1\_no\_posctrl: Normal 11/12

Vph1\_R1\_with\_posctrl: Normal 8/12

Vph1\_R1\_no\_posctrl: Normal 7/12

Vph1\_R1\_with\_posctrl: Normal 7/12

Vph1\_R1\_no\_posctrl: Normal 8/12

Vph1\_R1\_with\_posctrl: Normal 2/12

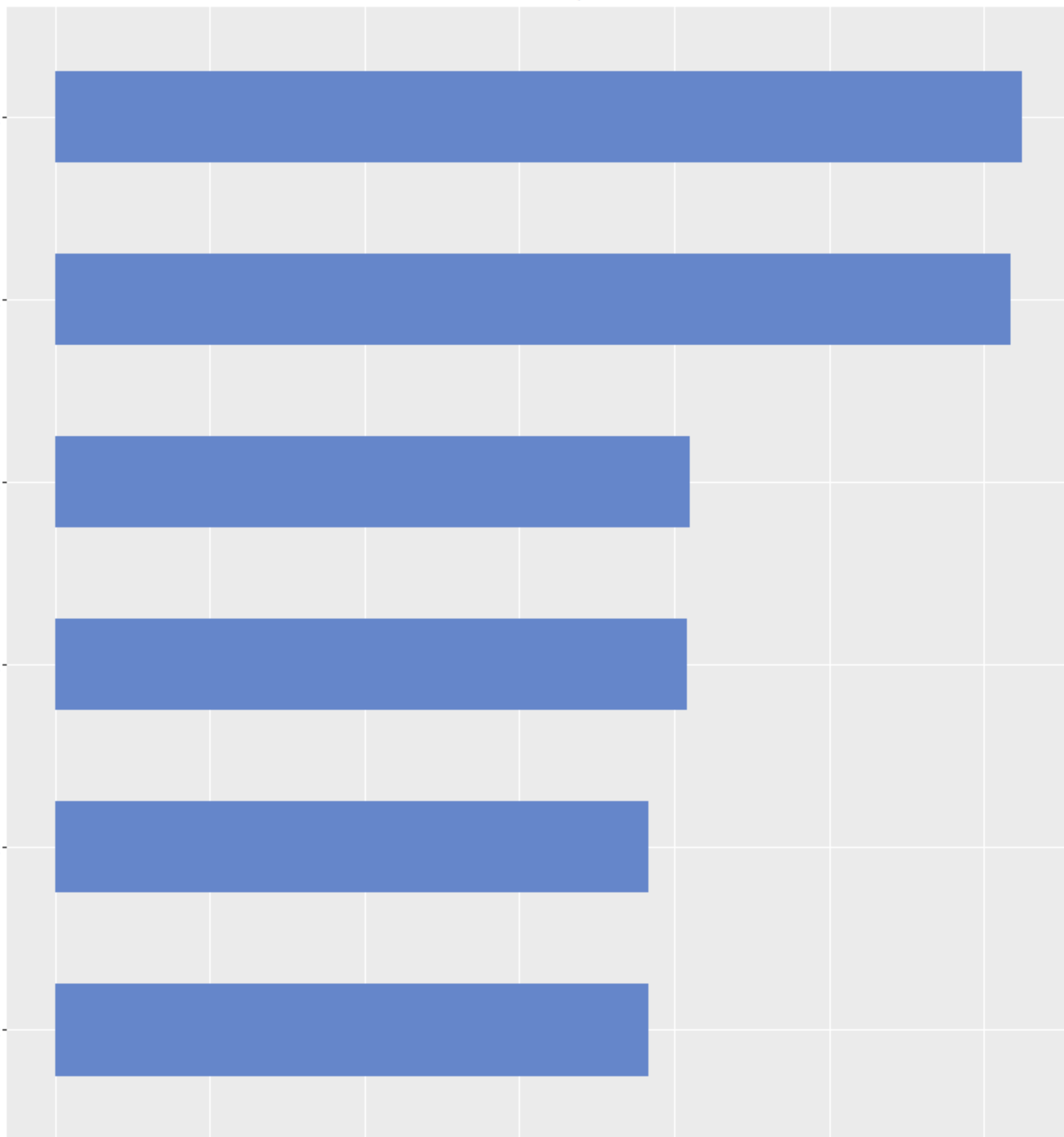
0

2

4

6

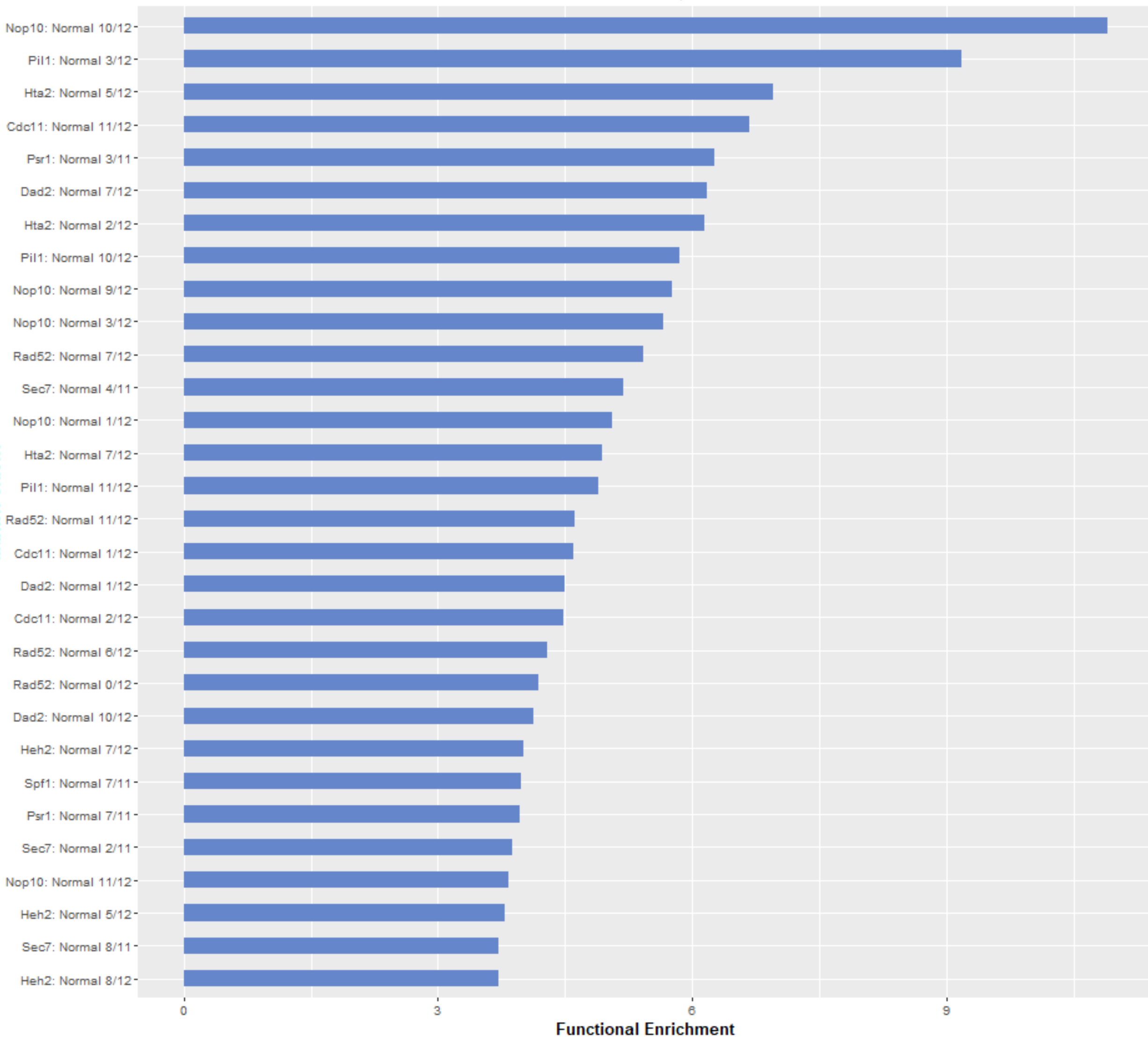
Functional Enrichment



# protein lipidation

With AreaShape

Marker: Cluster

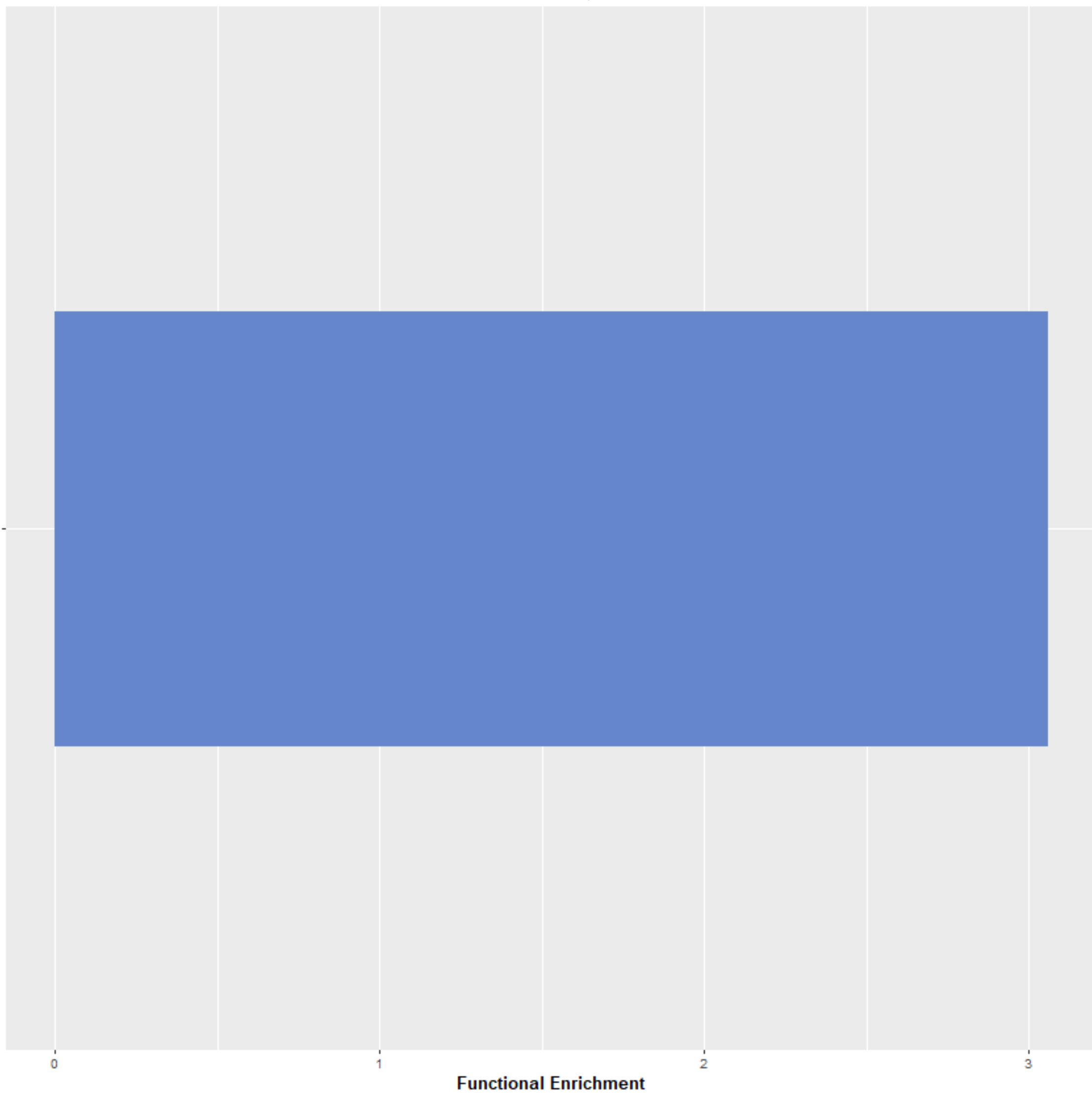


# protein maturation

With AreaShape

Marker: Cluster

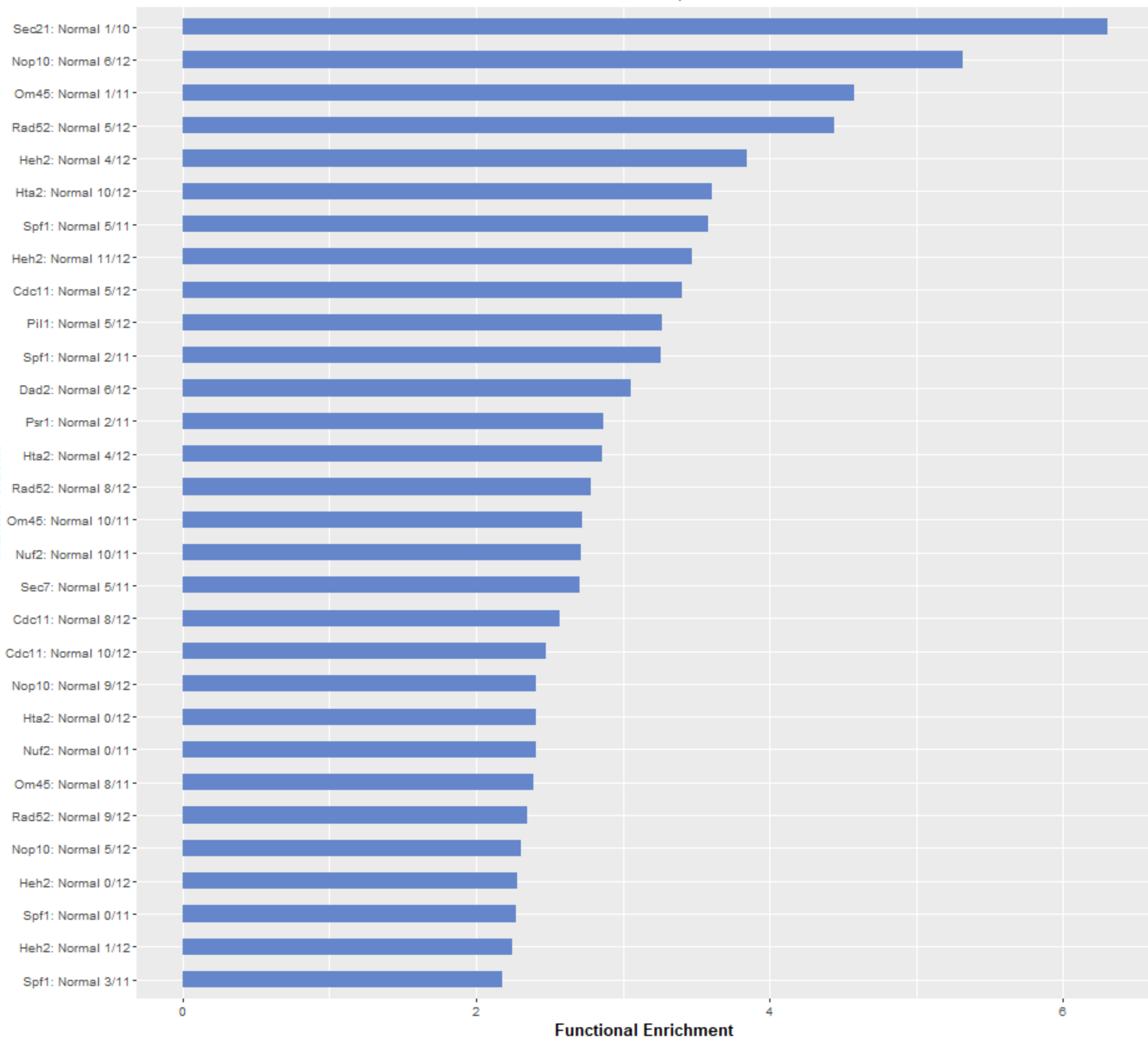
Psr1: Normal 0/11



# protein modification by small protein conjugation or removal

With AreaShape

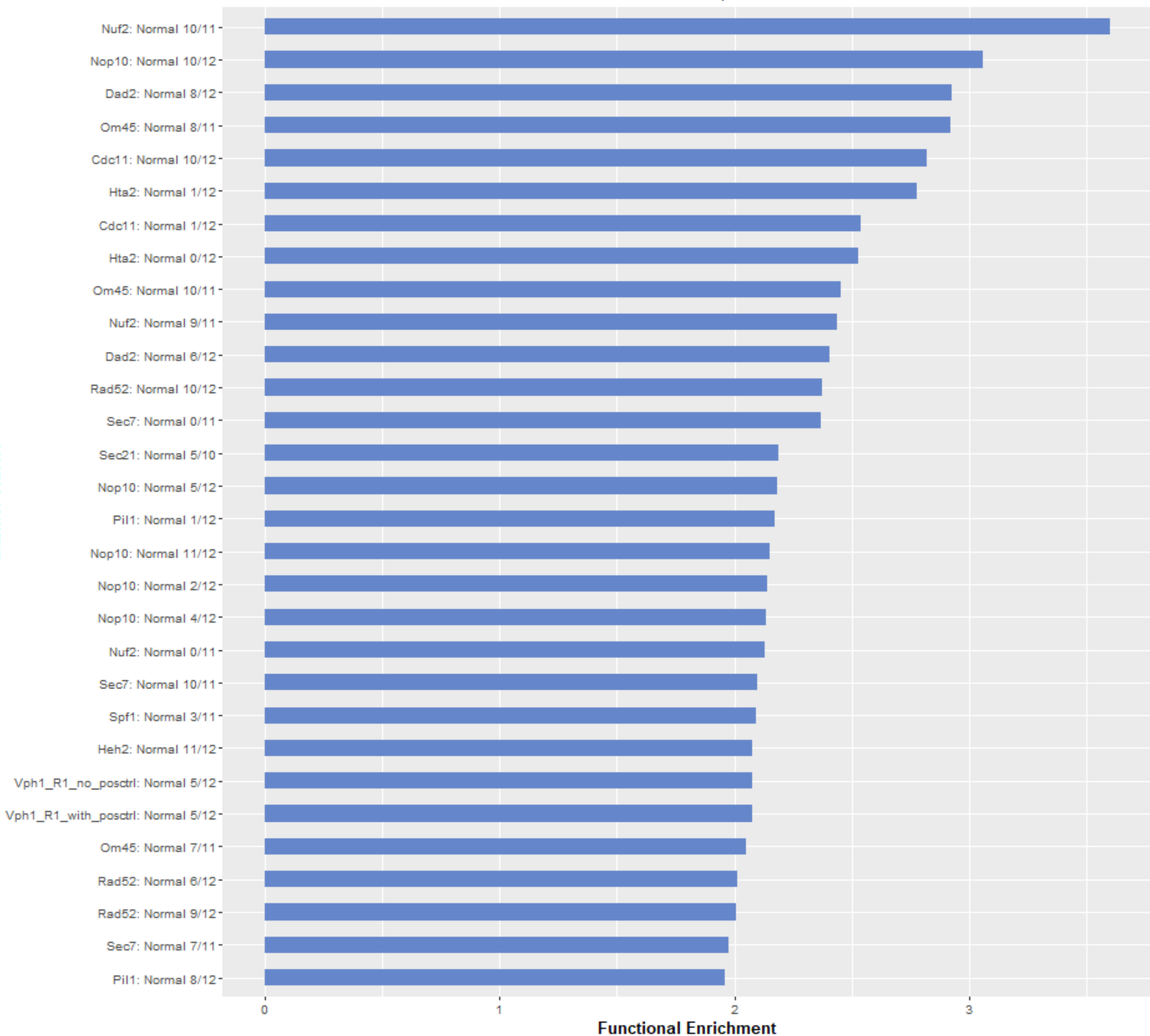
Marker: Cluster



# protein phosphorylation

With AreaShape

Marker: Cluster

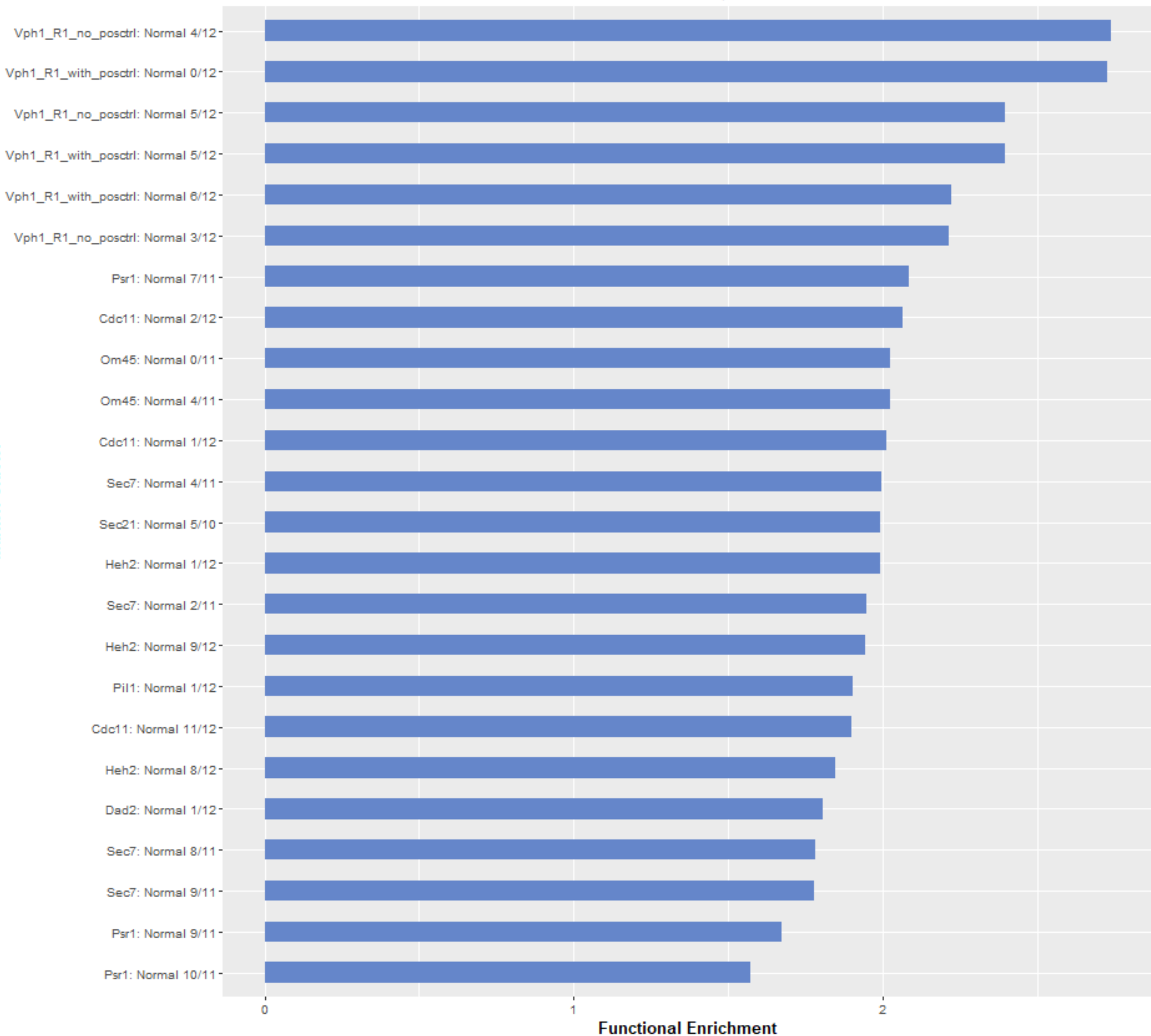




# protein targeting

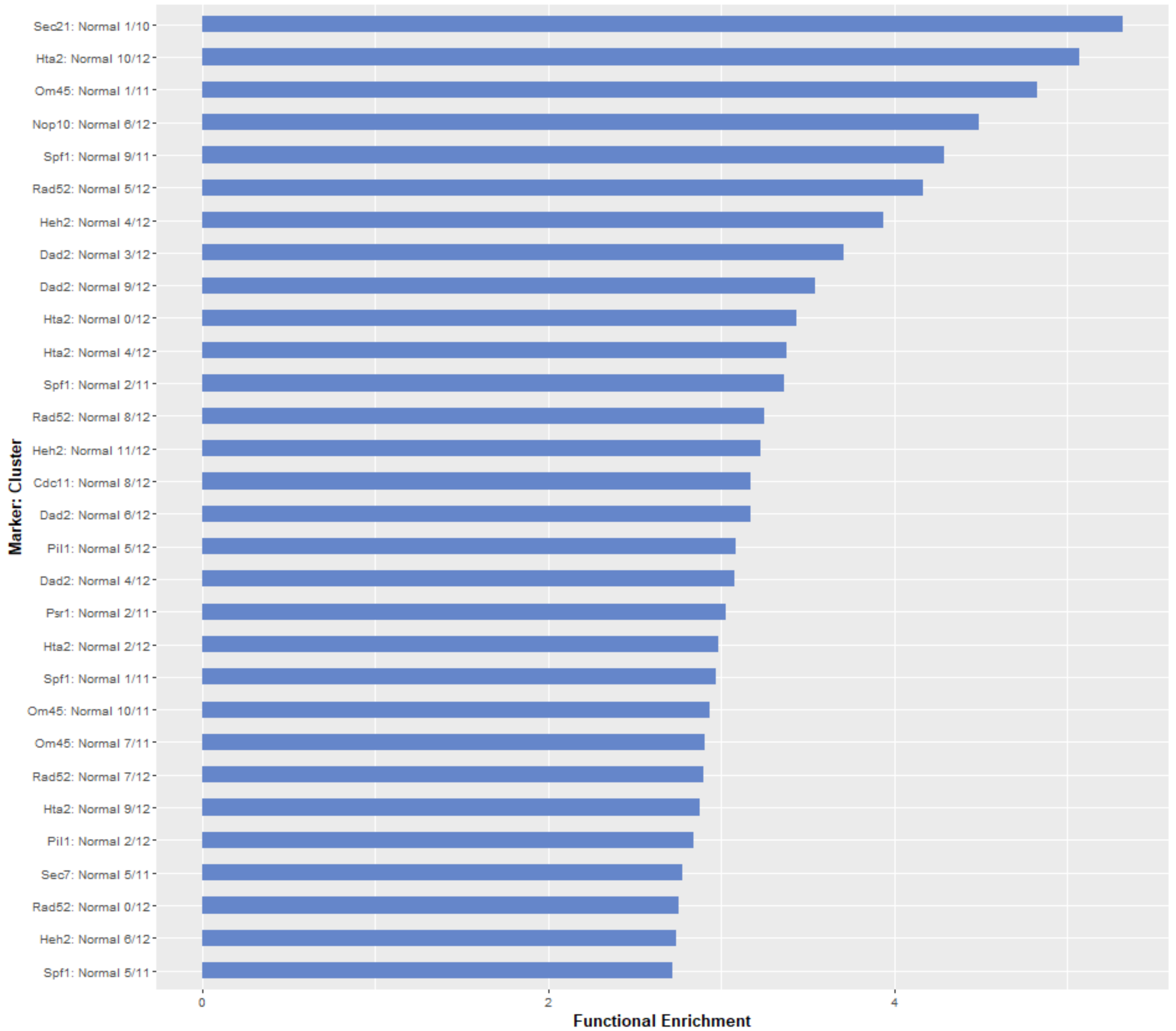
With AreaShape

Marker: Cluster



proteolysis involved in cellular protein catabolic process

With AreaShape



# pseudohyphal growth

With AreaShape

Marker: Cluster

Vph1\_R1\_no\_posctrl: Normal 8/12

Vph1\_R1\_with\_posctrl: Normal 2/12

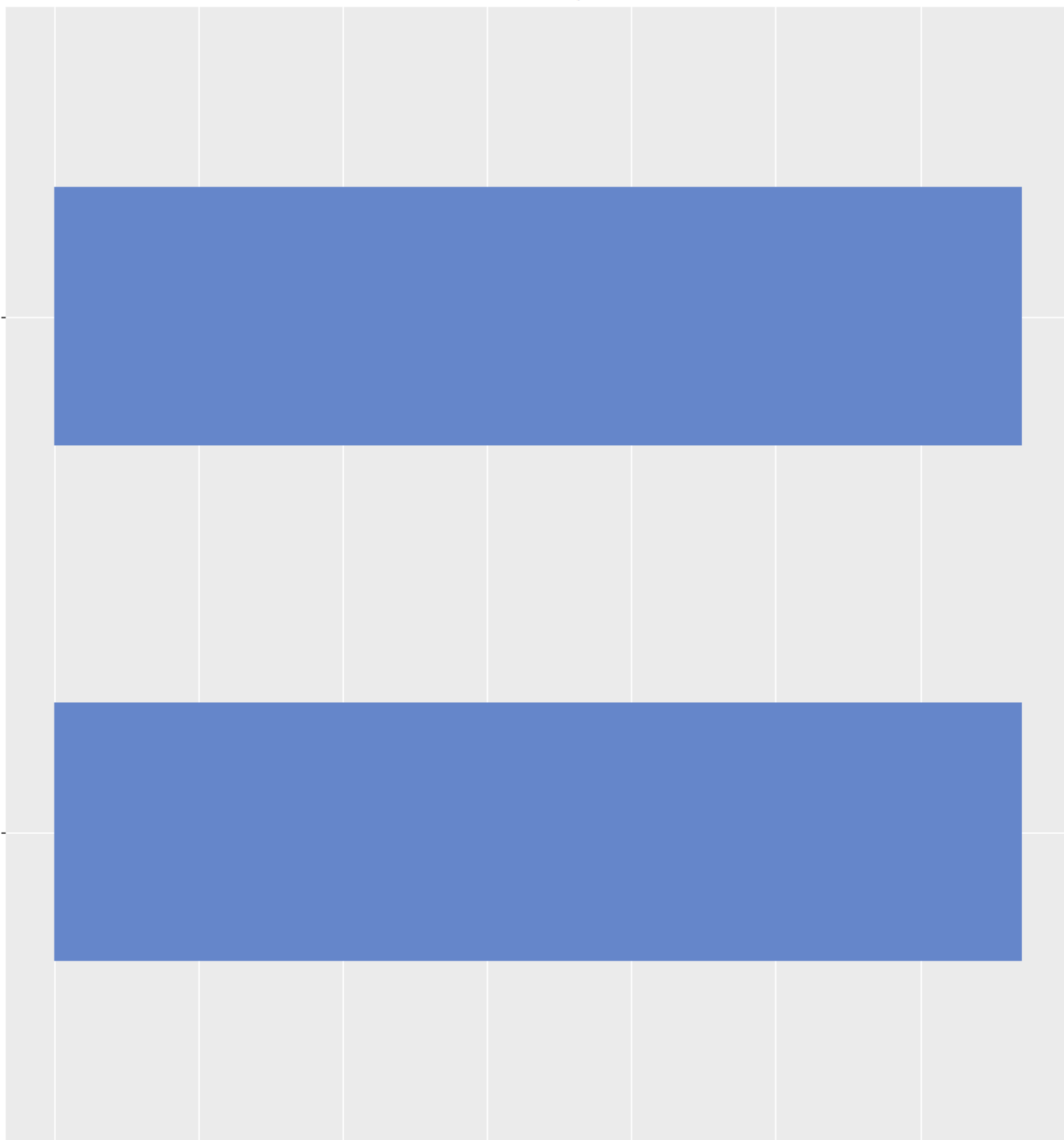
0

1

2

3

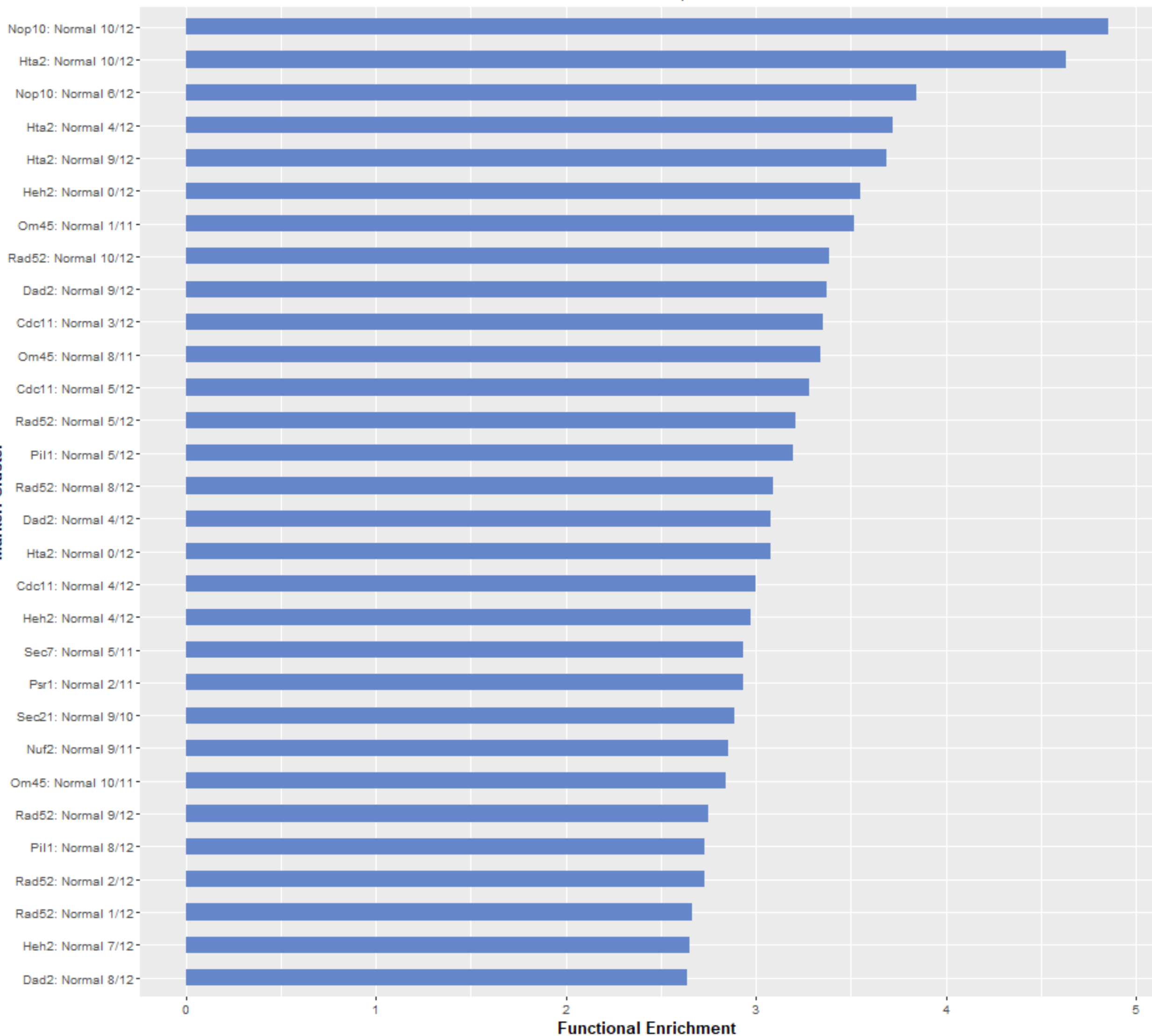
Functional Enrichment



# regulation of cell cycle

With AreaShape

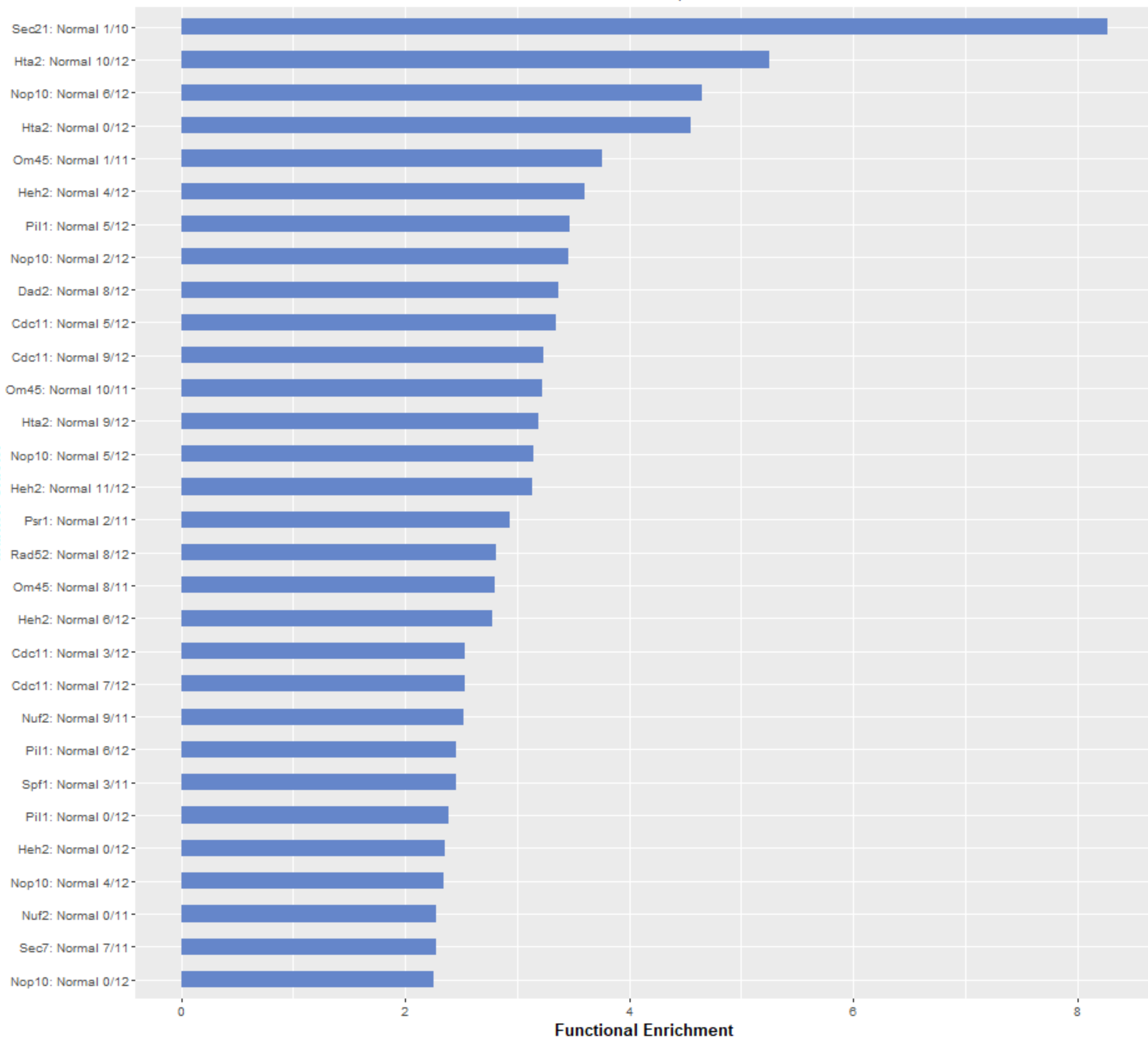
Marker: Cluster



# regulation of DNA metabolic process

With AreaShape

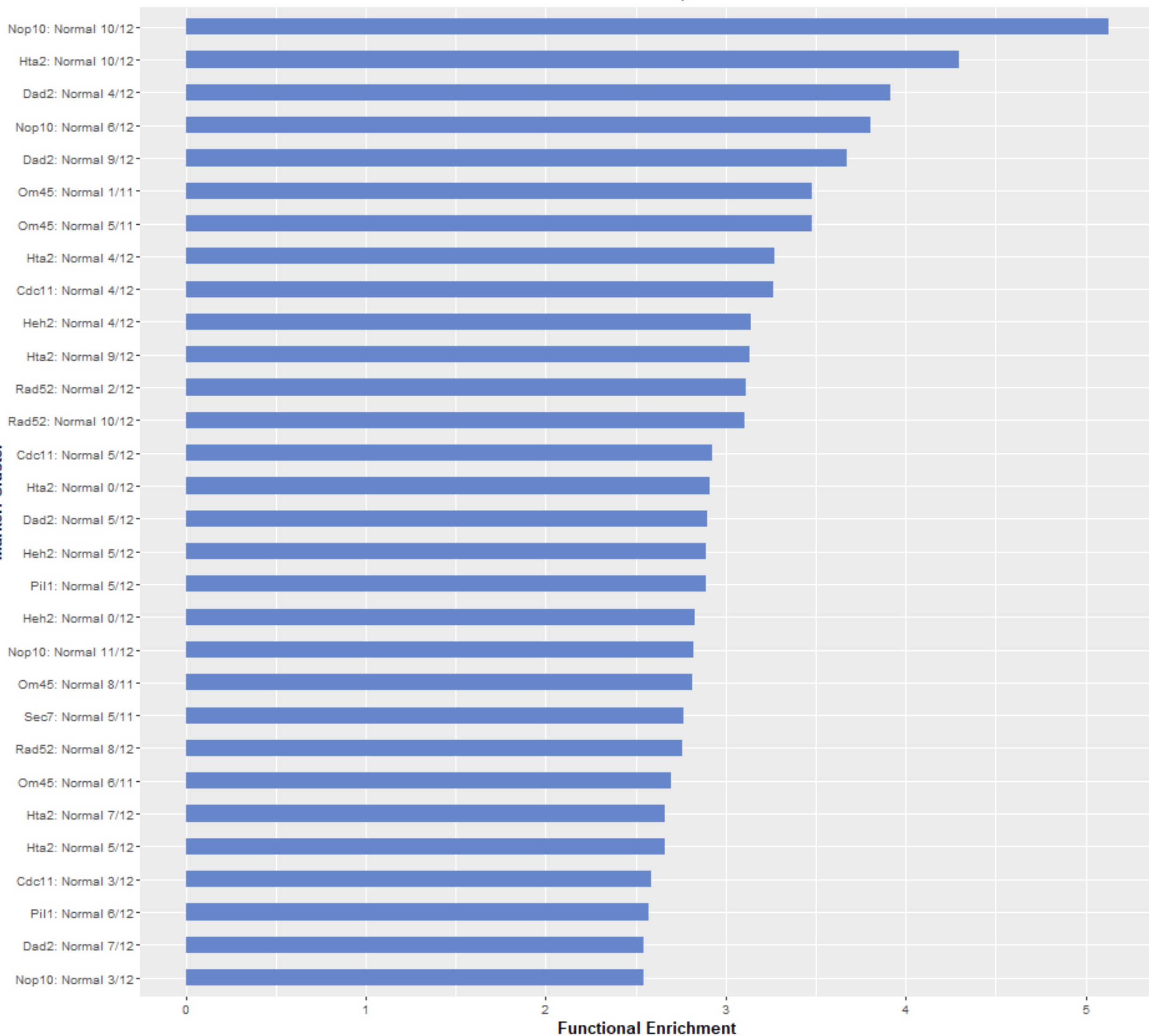
Marker: Cluster



# regulation of organelle organization

With AreaShape

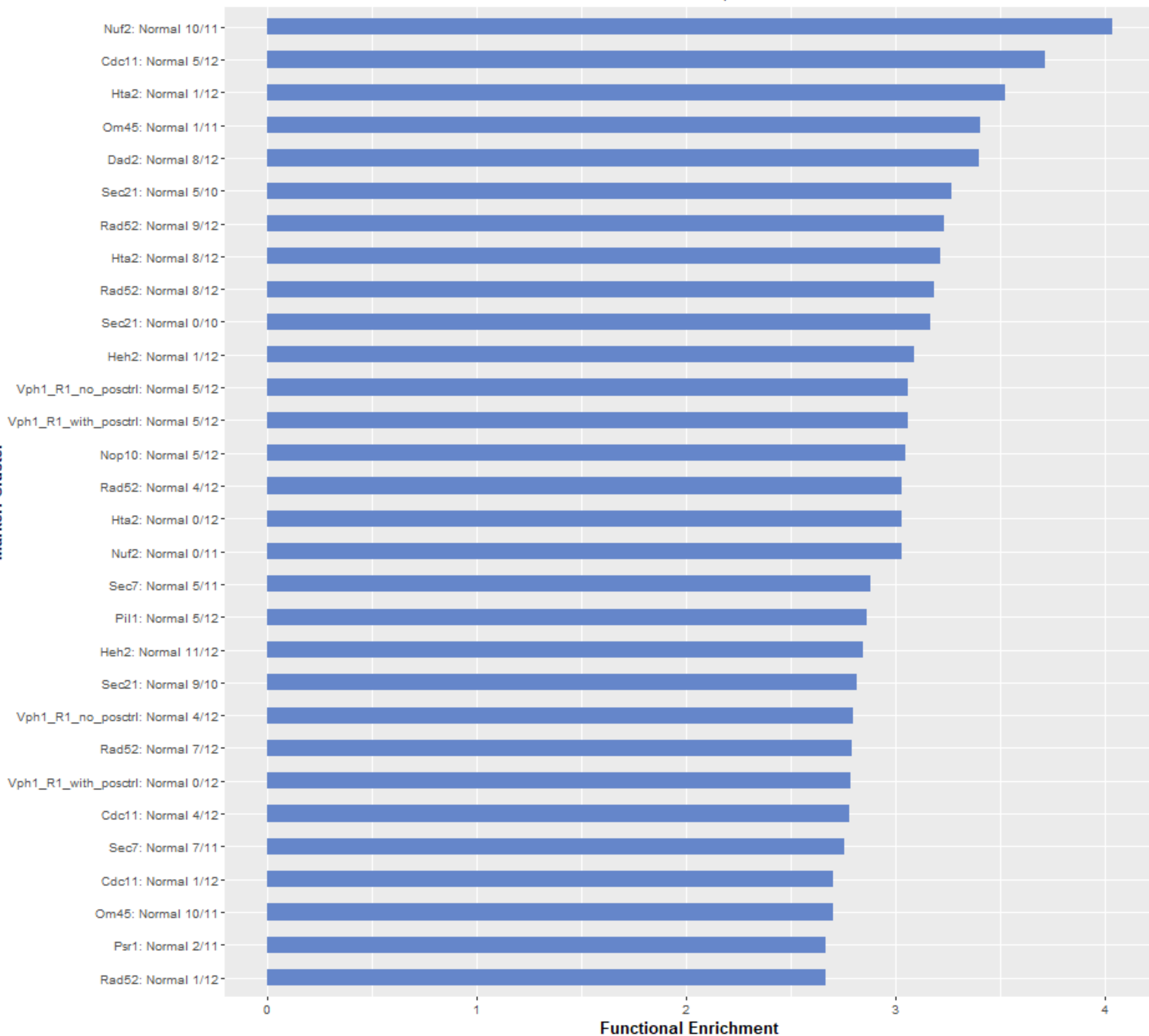
Marker: Cluster



# regulation of protein modification process

With AreaShape

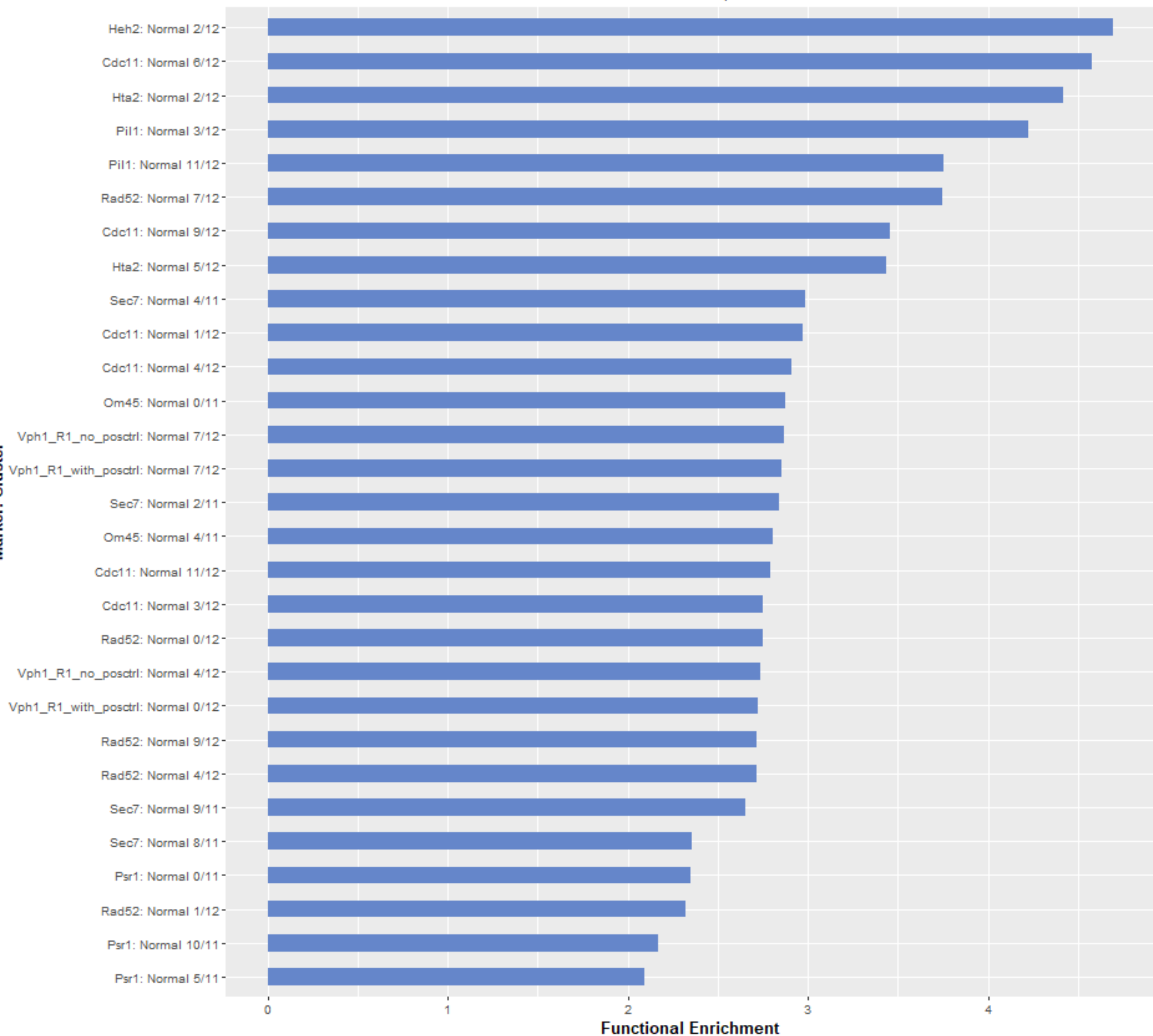
Marker: Cluster



# regulation of transport

With AreaShape

Marker: Cluster



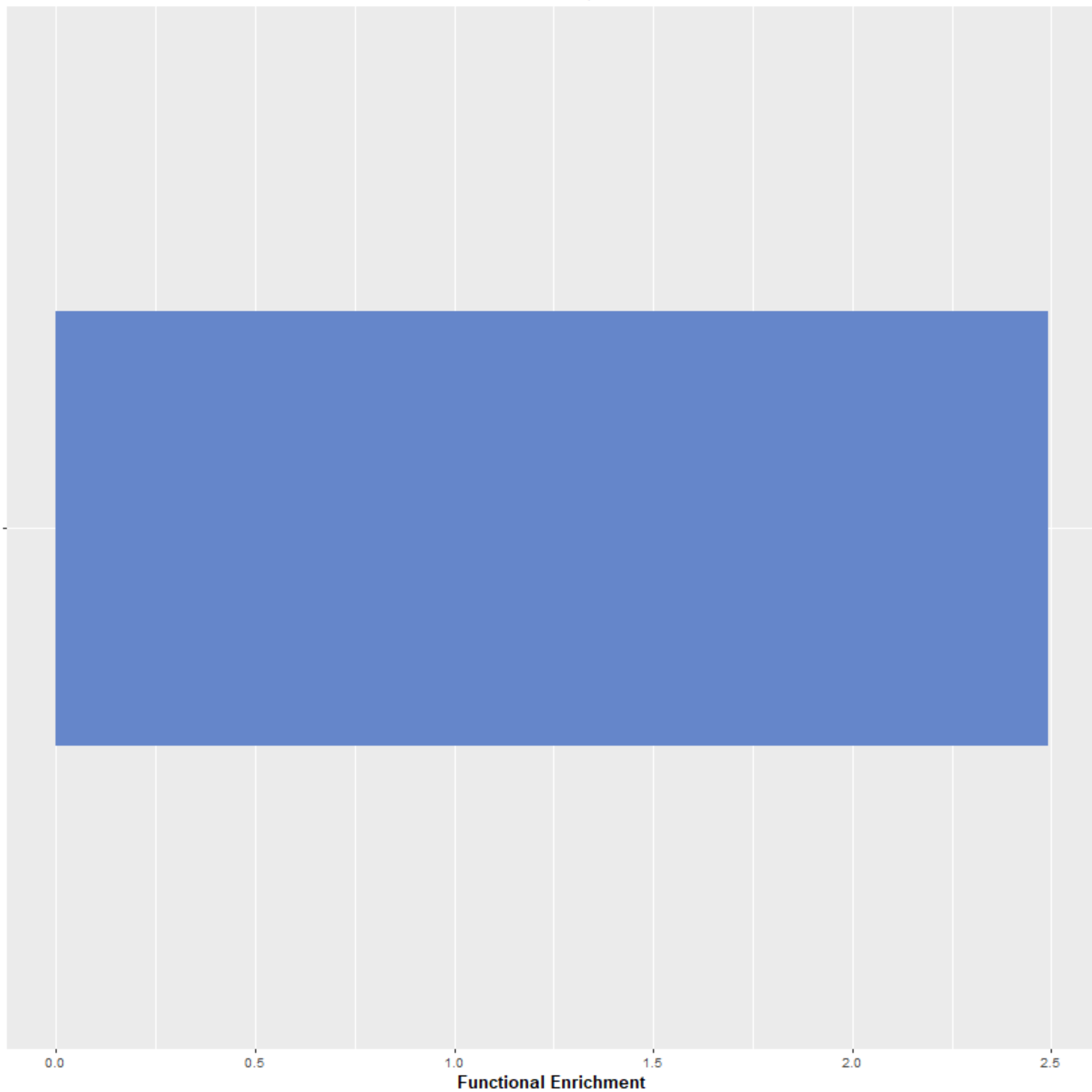


# response to heat

With AreaShape

Marker: Cluster

Psr1: Normal 0/11

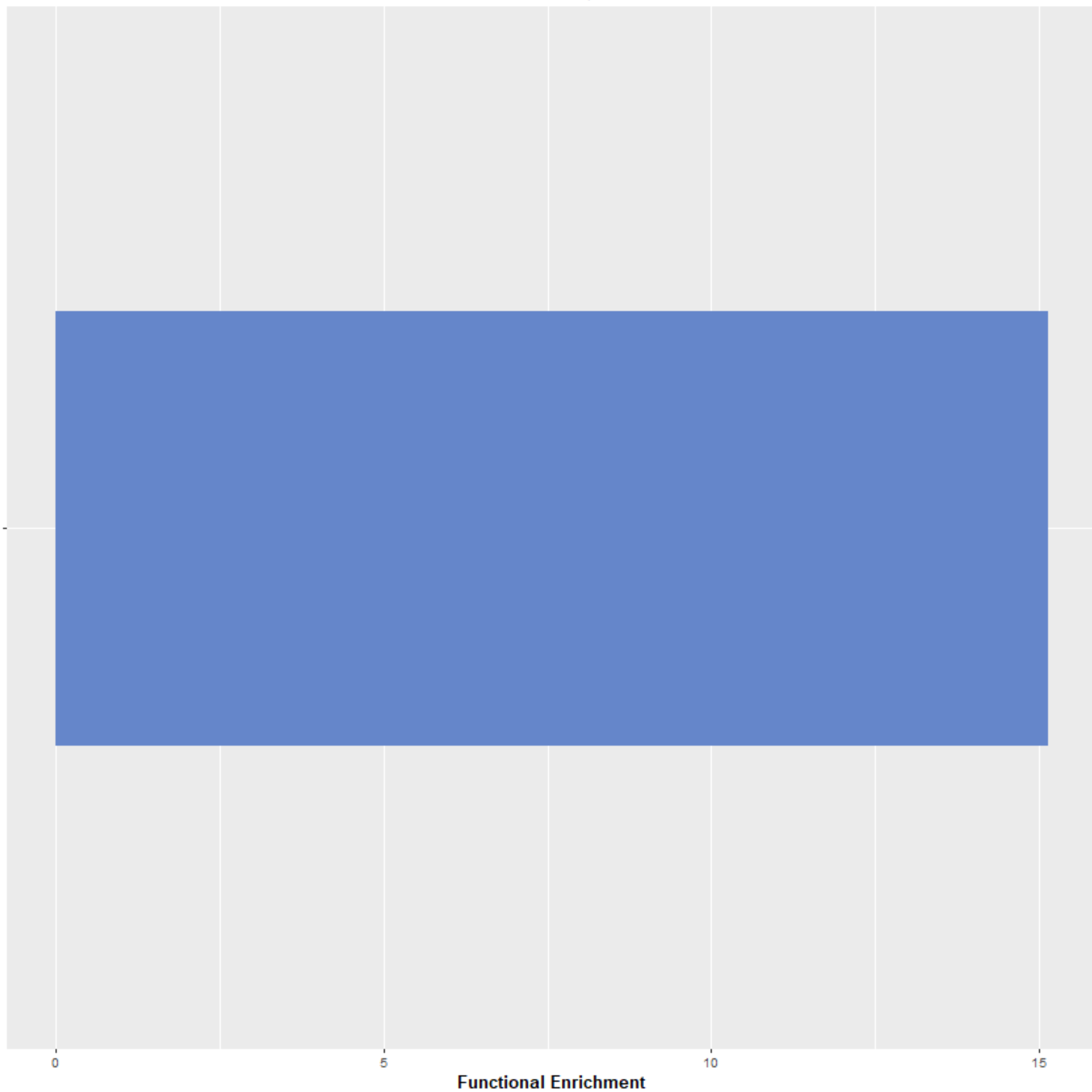


# response to starvation

With AreaShape

Marker: Cluster

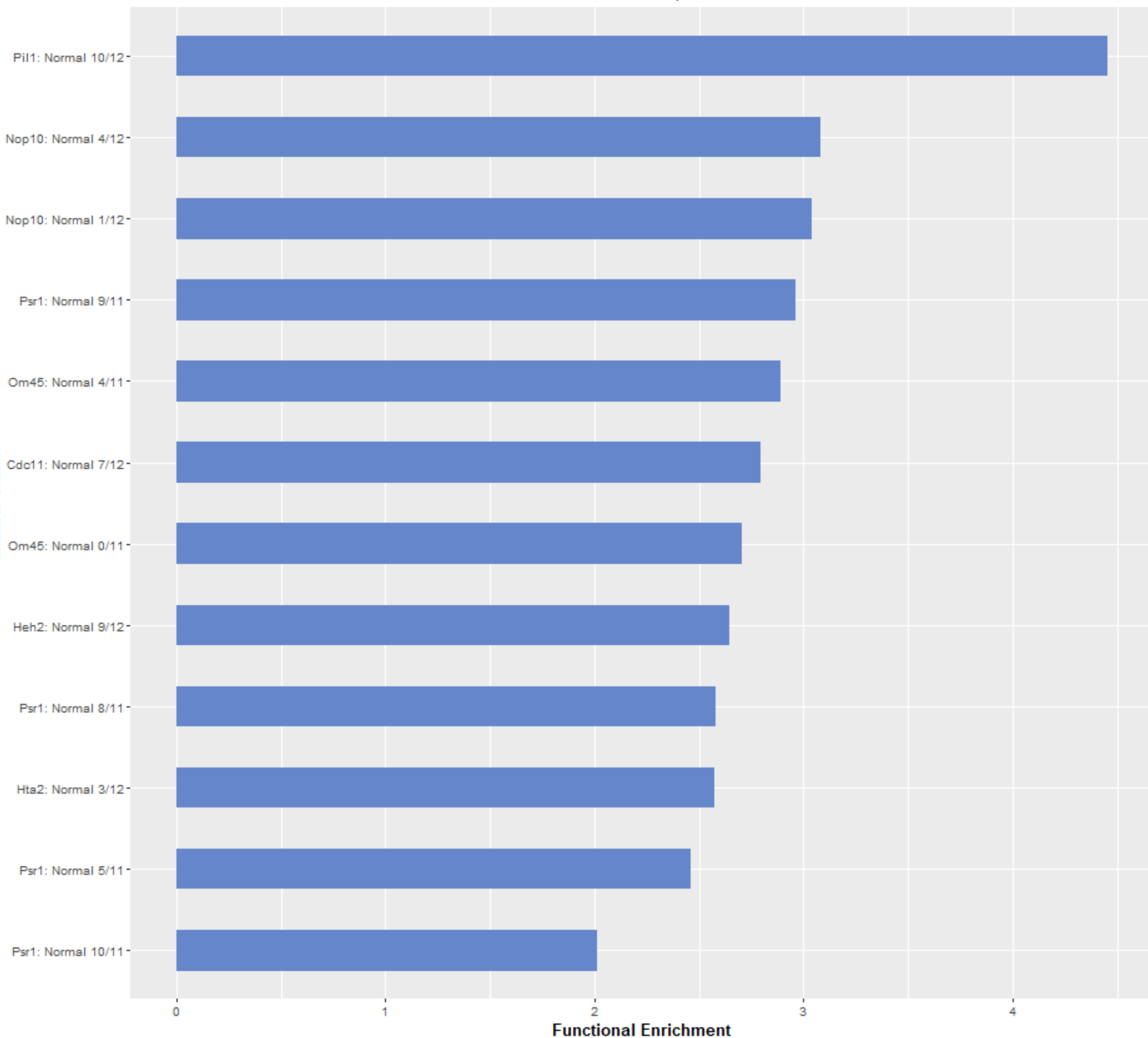
Psr1: Normal 6/11



# ribosomal large subunit biogenesis

With AreaShape

Marker: Cluster



# ribosomal small subunit biogenesis

With AreaShape

Marker: Cluster

Nop10: Normal 0/12

0.0

0.5

1.0

1.5

2.0

2.5

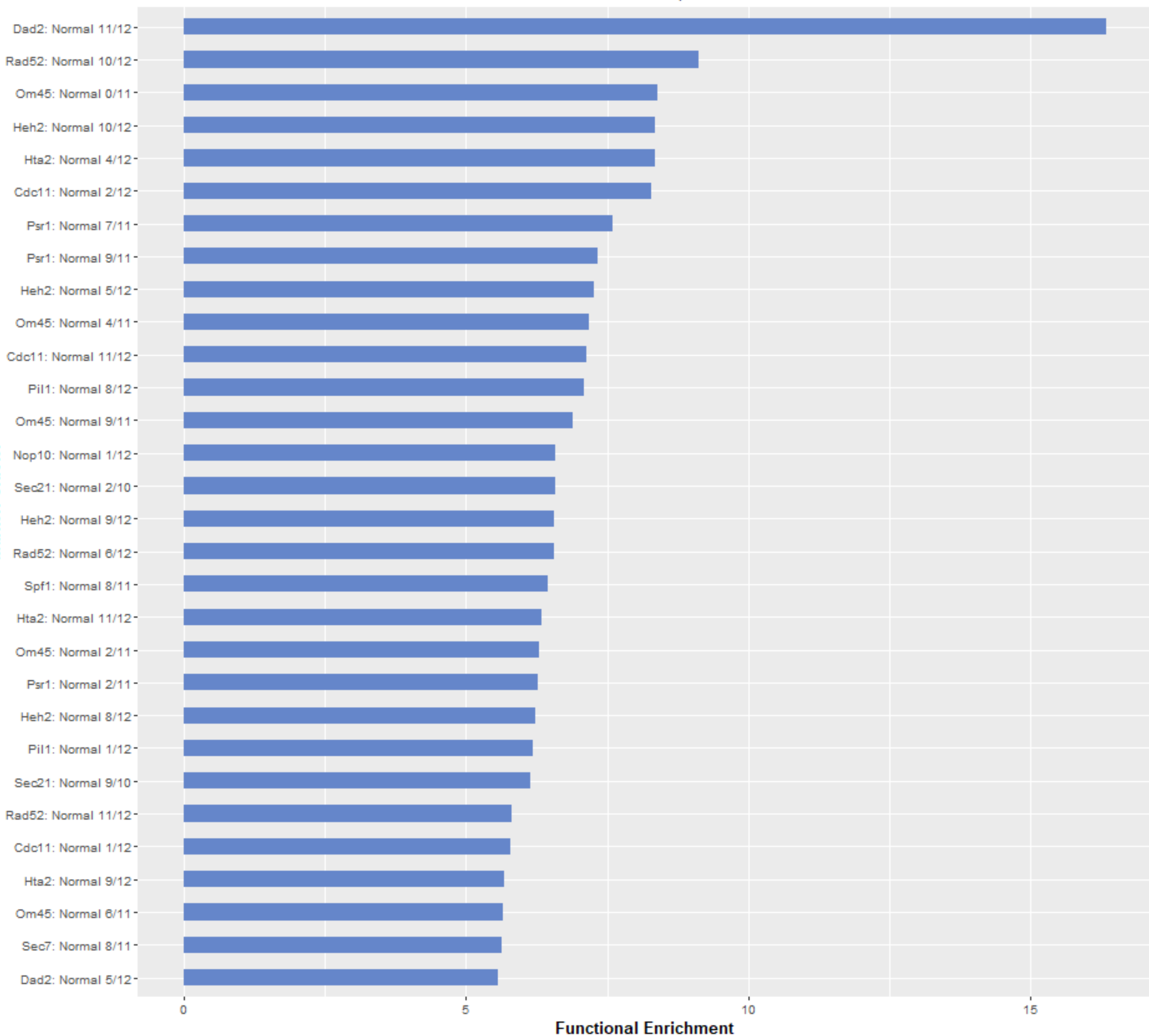
Functional Enrichment



# ribosomal subunit export from nucleus

With AreaShape

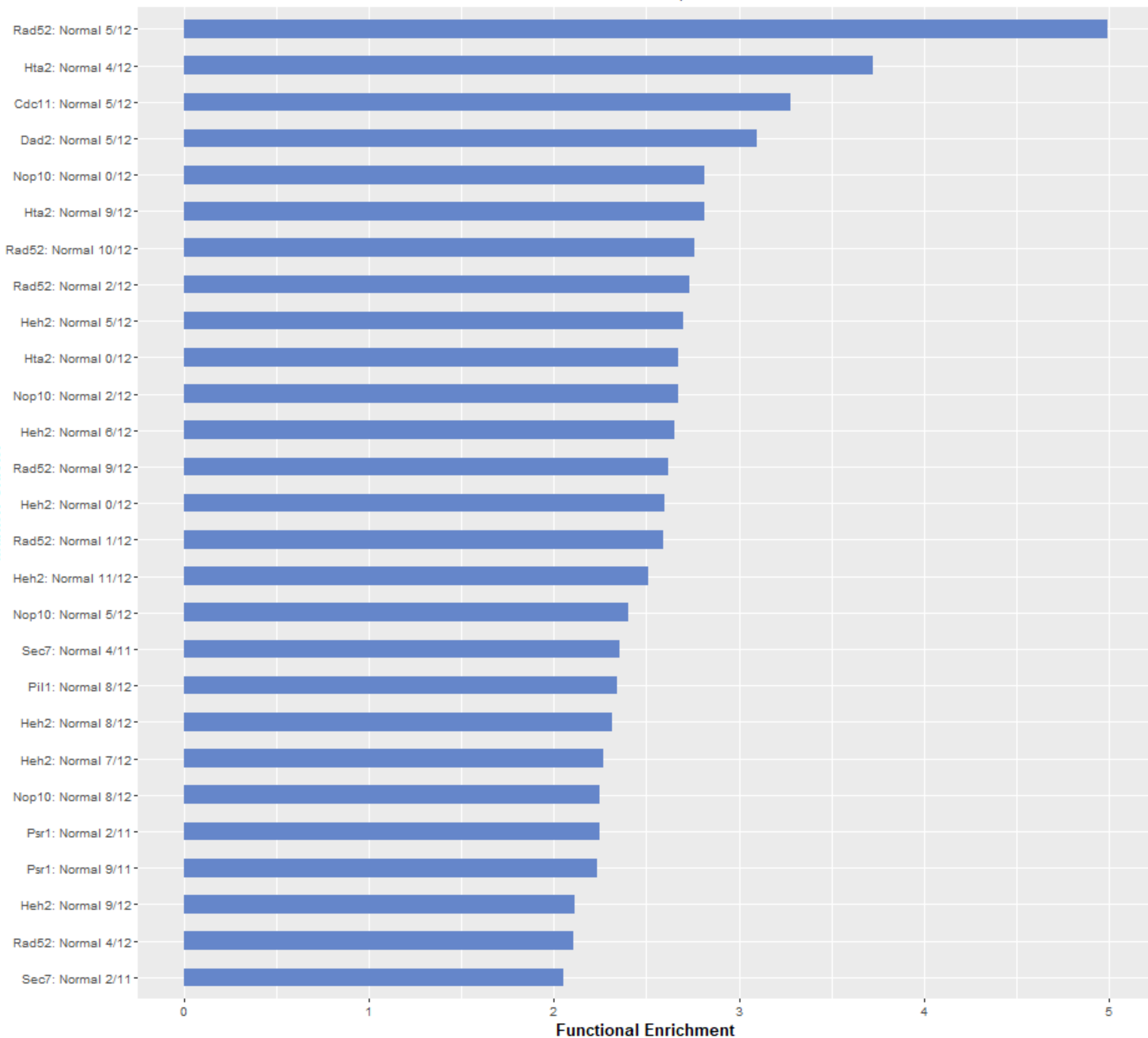
Marker: Cluster



# RNA catabolic process

With AreaShape

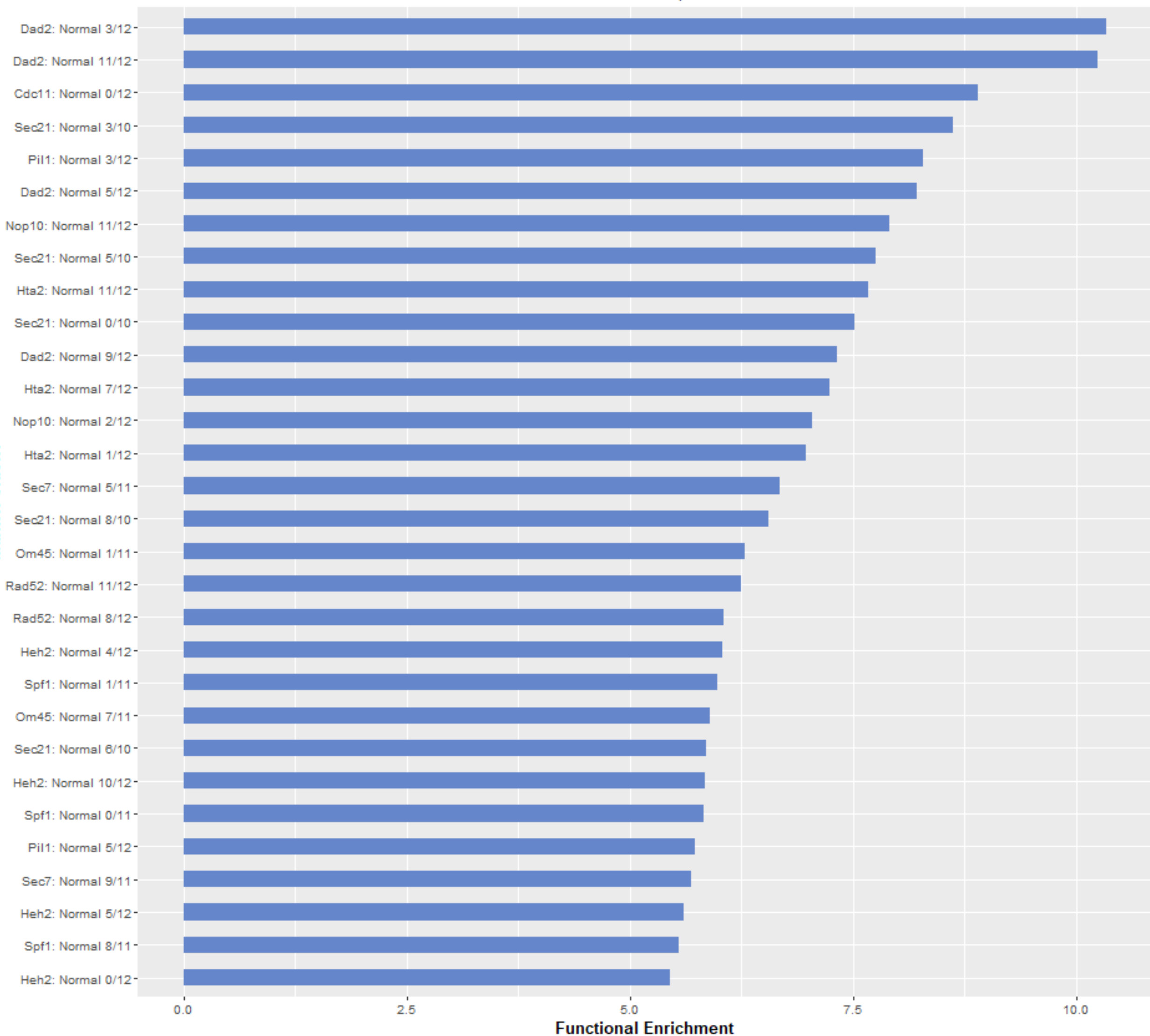
Marker: Cluster



# RNA splicing

With AreaShape

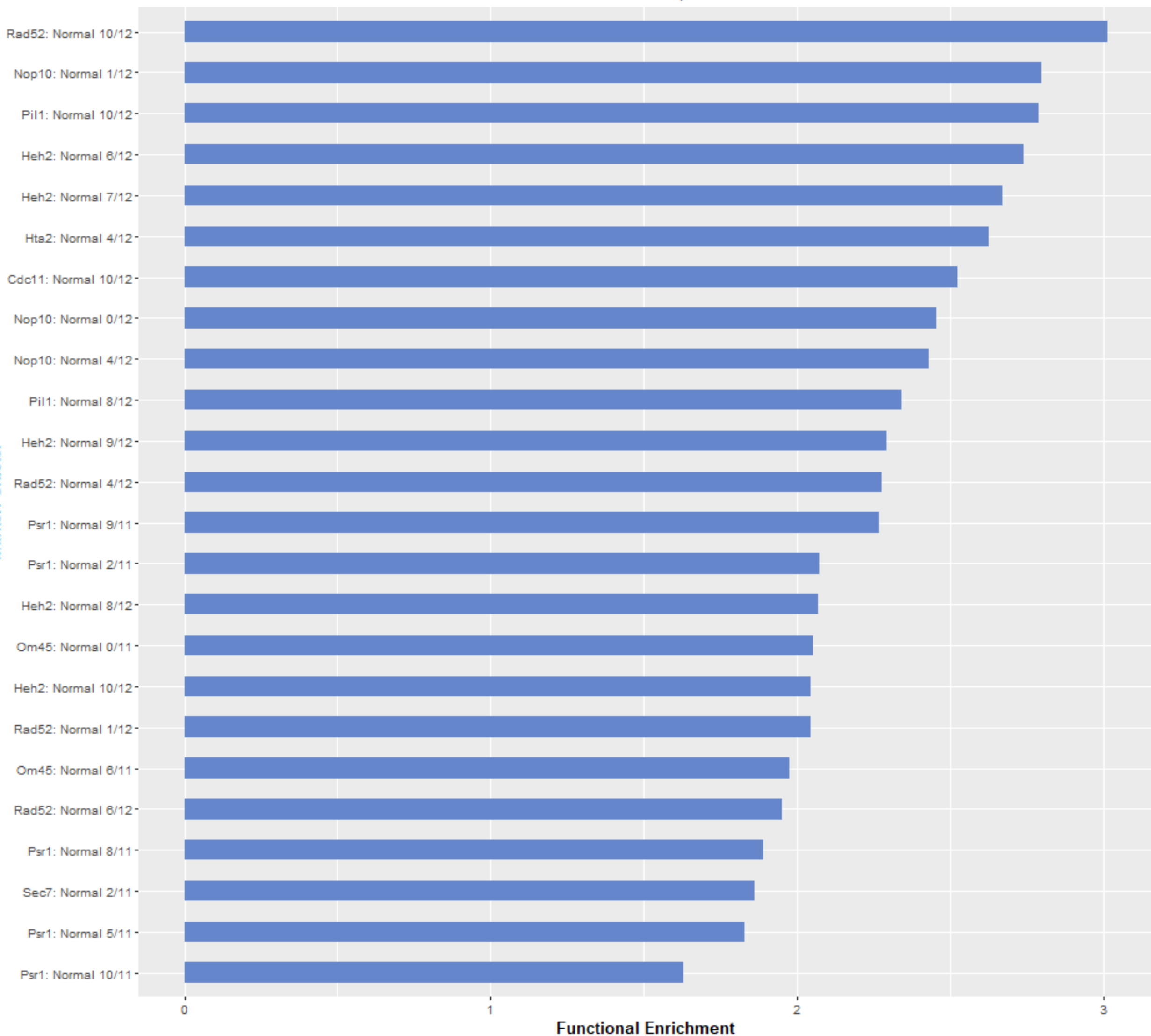
Marker: Cluster



# rRNA processing

With AreaShape

Marker: Cluster





**signaling**  
With AreaShape

**Marker: Cluster**

Dad2: Normal 0/12

Sec7: Normal 10/11

Cdc11: Normal 3/12

Rad52: Normal 9/12

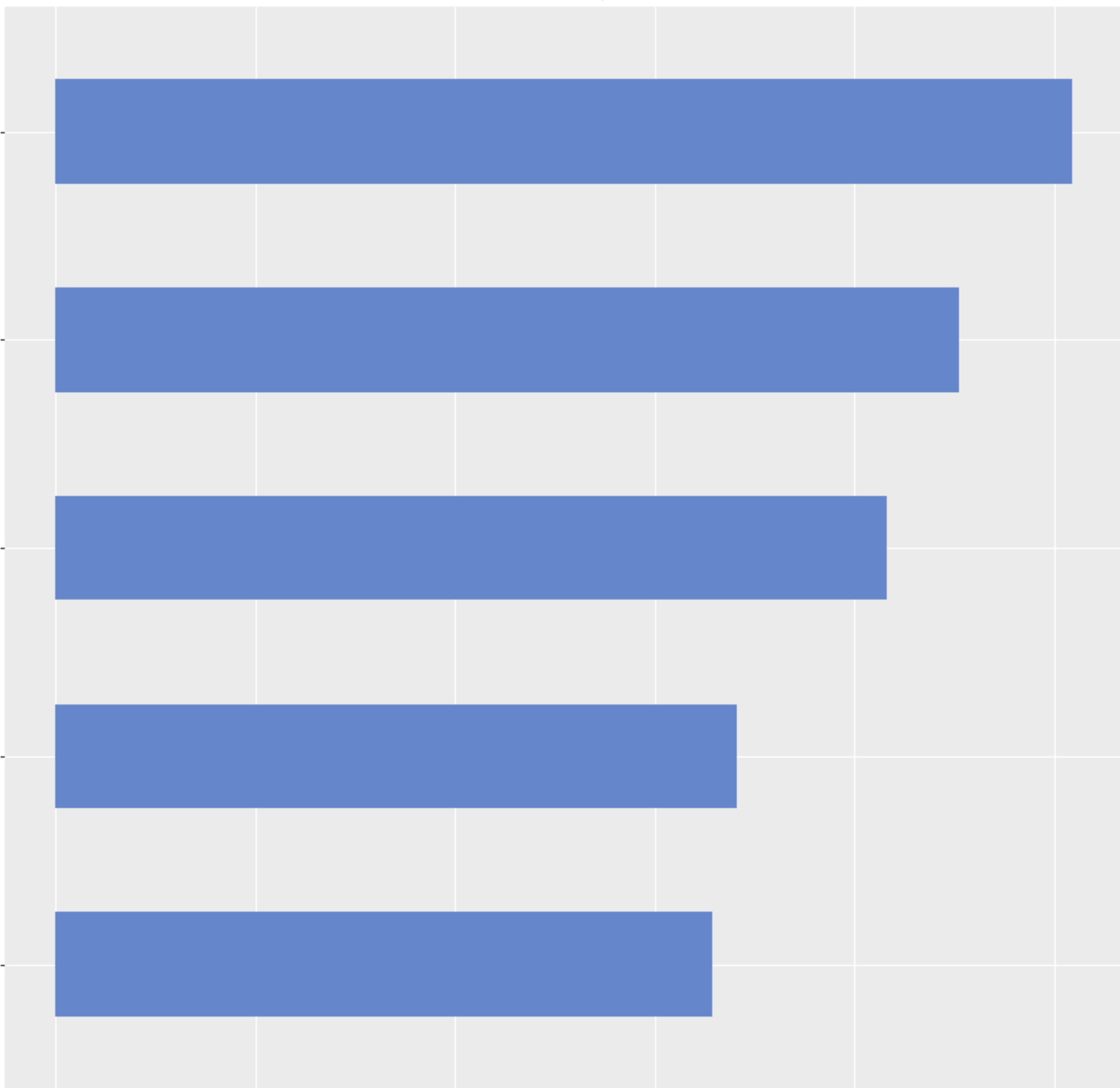
Psr1: Normal 0/11

0

1

2

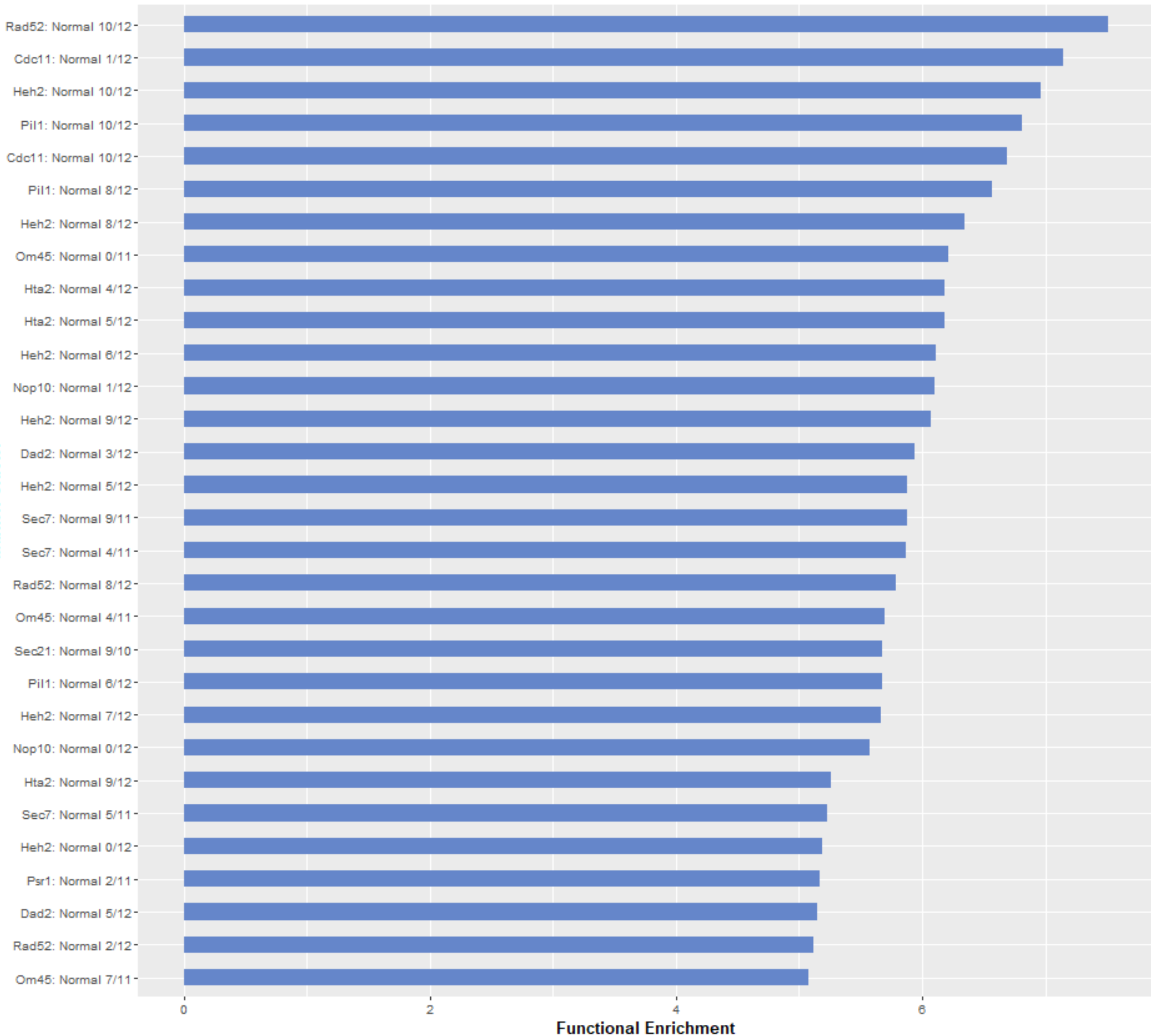
**Functional Enrichment**



# snoRNA processing

With AreaShape

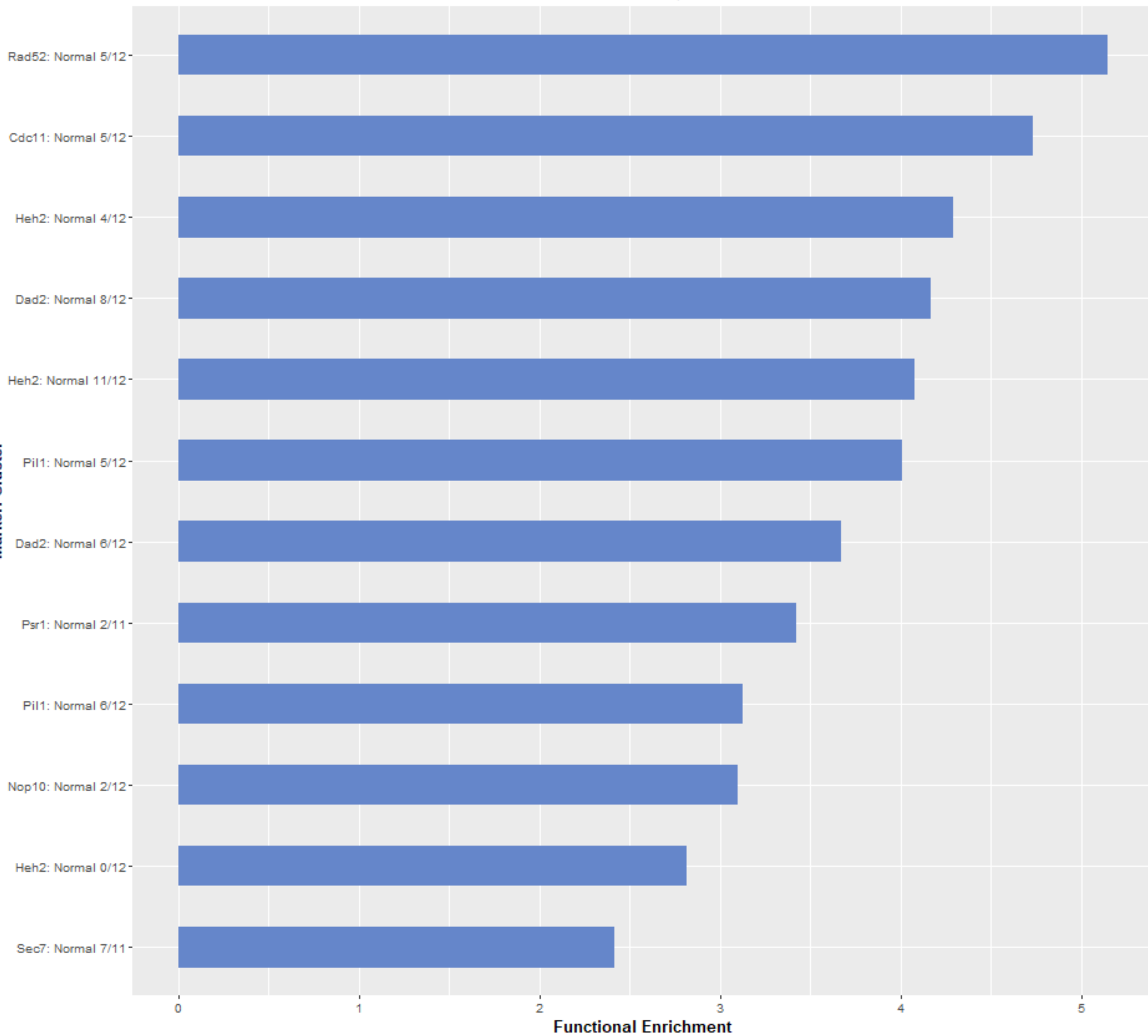
Marker: Cluster



# telomere organization

With AreaShape

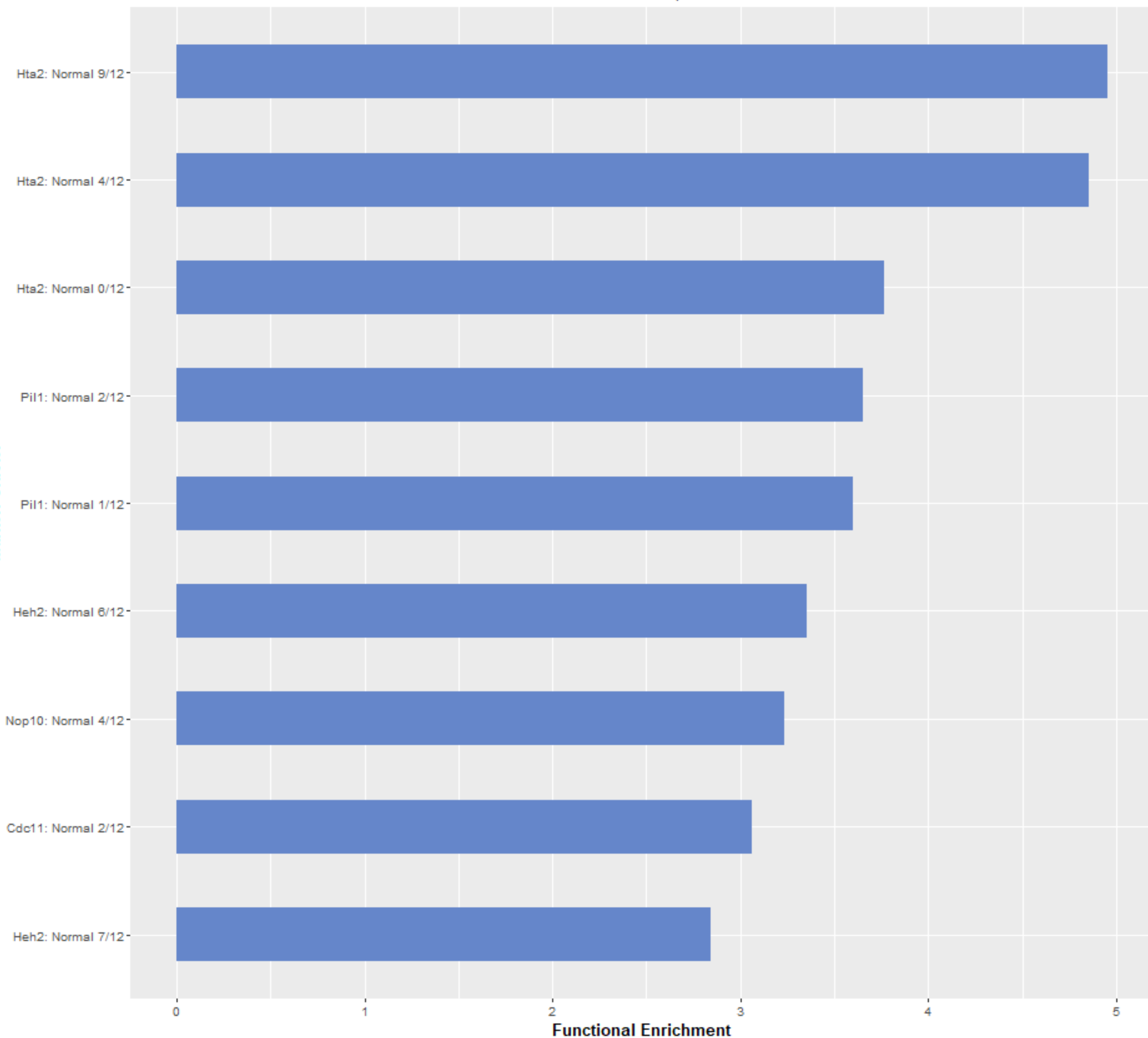
Marker: Cluster



# transcription from RNA polymerase I promoter

With AreaShape

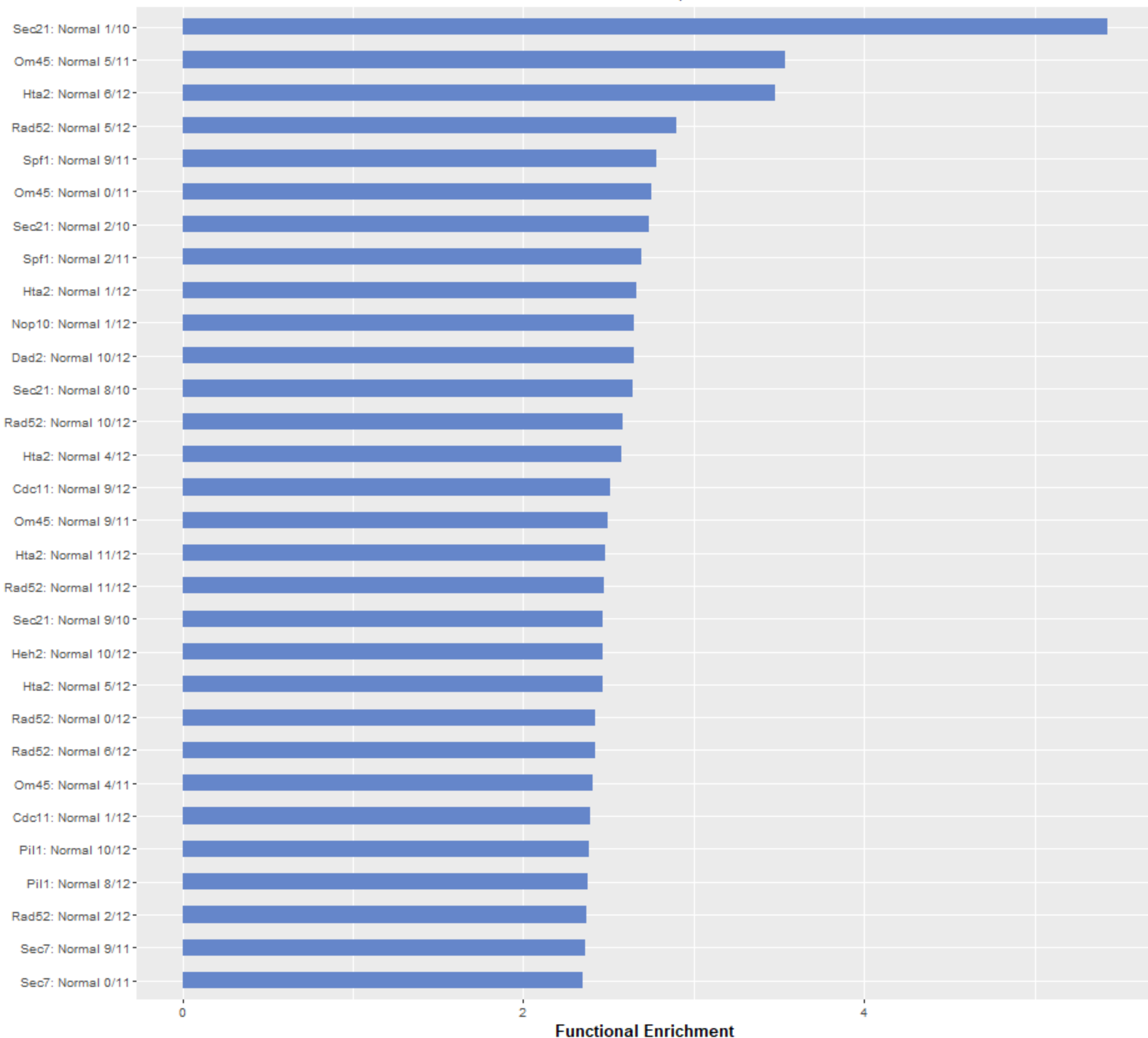
Marker: Cluster



# transcription from RNA polymerase II promoter

With AreaShape

Marker: Cluster



# transcription from RNA polymerase III promoter

With AreaShape

Marker: Cluster

Hta2: Normal 9/12

Hta2: Normal 4/12

Hta2: Normal 0/12

Heh2: Normal 6/12

Heh2: Normal 7/12

Nop10: Normal 1/12

Nop10: Normal 4/12

Heh2: Normal 9/12

0

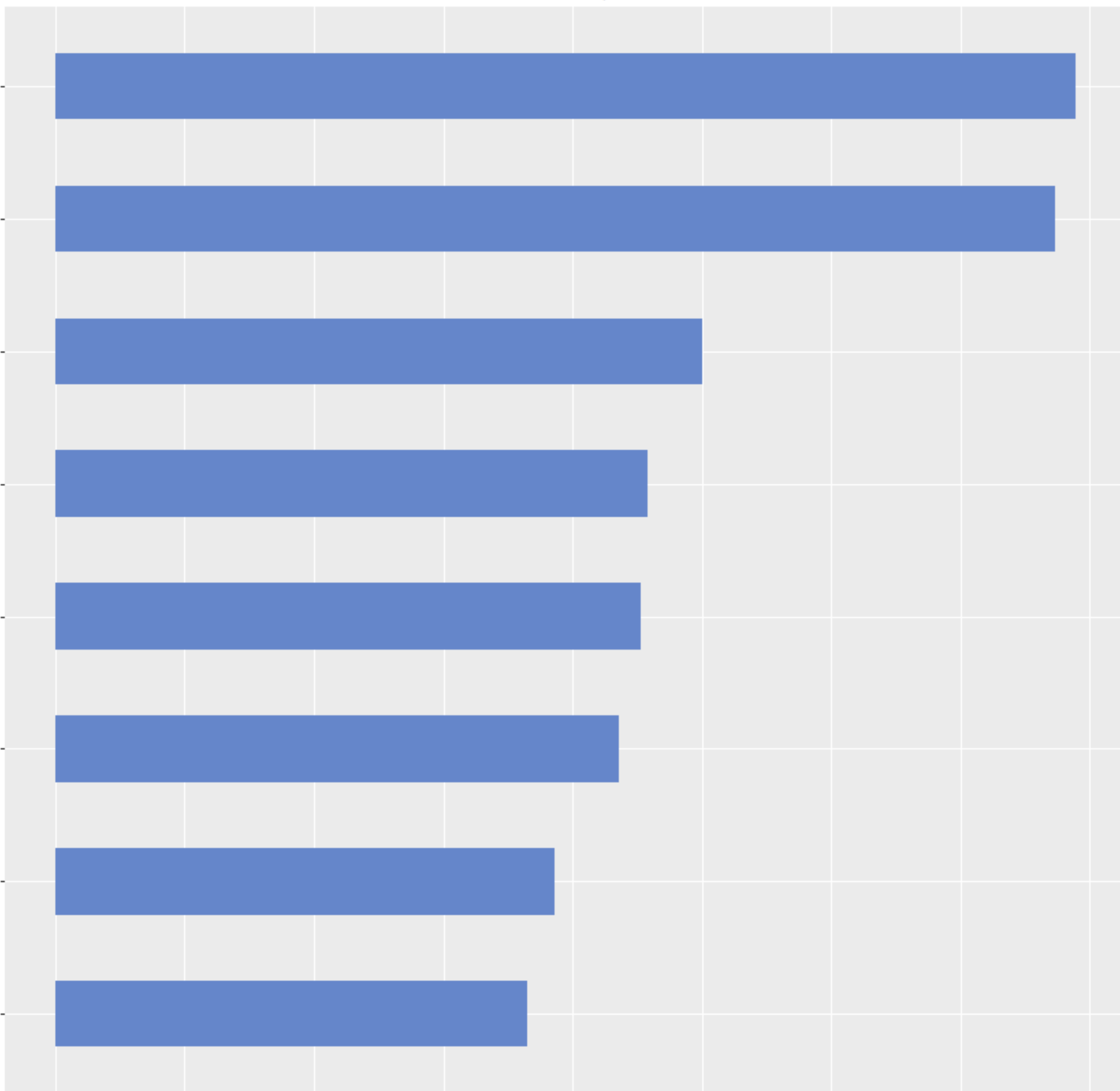
2

4

6

8

Functional Enrichment



# translational elongation

With AreaShape

Marker: Cluster

Spf1: Normal 4/11

Pil1: Normal 4/12

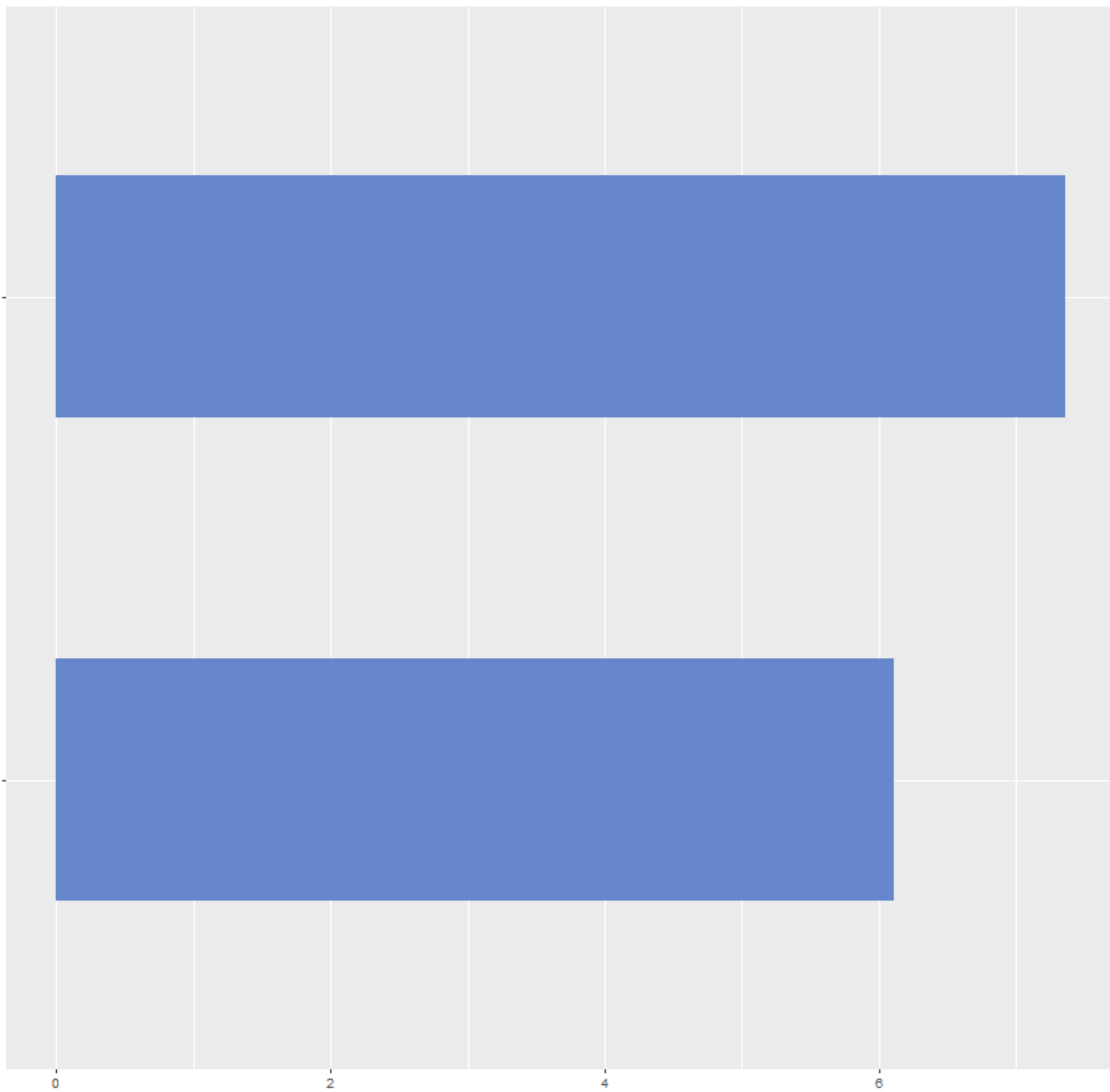
0

2

4

6

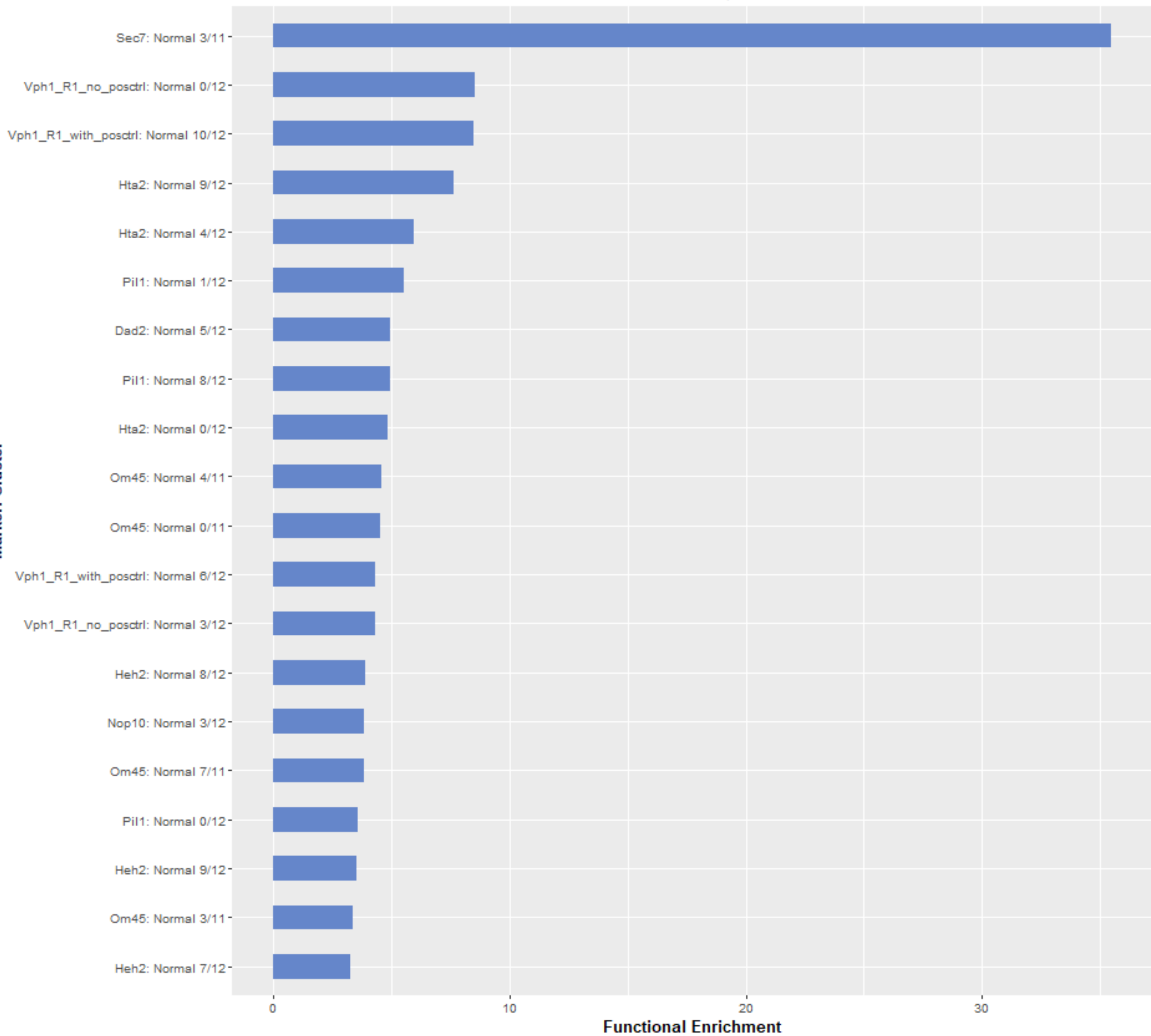
Functional Enrichment



# translational initiation

With AreaShape

Marker: Cluster





# transposition

With AreaShape

Marker: Cluster

Rad52: Normal 5/12  
Hta2: Normal 0/12  
Heh2: Normal 11/12  
Cdc11: Normal 5/12  
Dad2: Normal 0/12  
Cdc11: Normal 3/12  
Vph1\_R1\_no\_posctrl: Normal 5/12  
Vph1\_R1\_with\_posctrl: Normal 5/12  
Vph1\_R1\_with\_posctrl: Normal 6/12  
Vph1\_R1\_no\_posctrl: Normal 3/12  
Nop10: Normal 8/12  
Heh2: Normal 7/12  
Nop10: Normal 4/12  
Heh2: Normal 6/12  
Om45: Normal 6/11  
Rad52: Normal 9/12

0.0

2.5

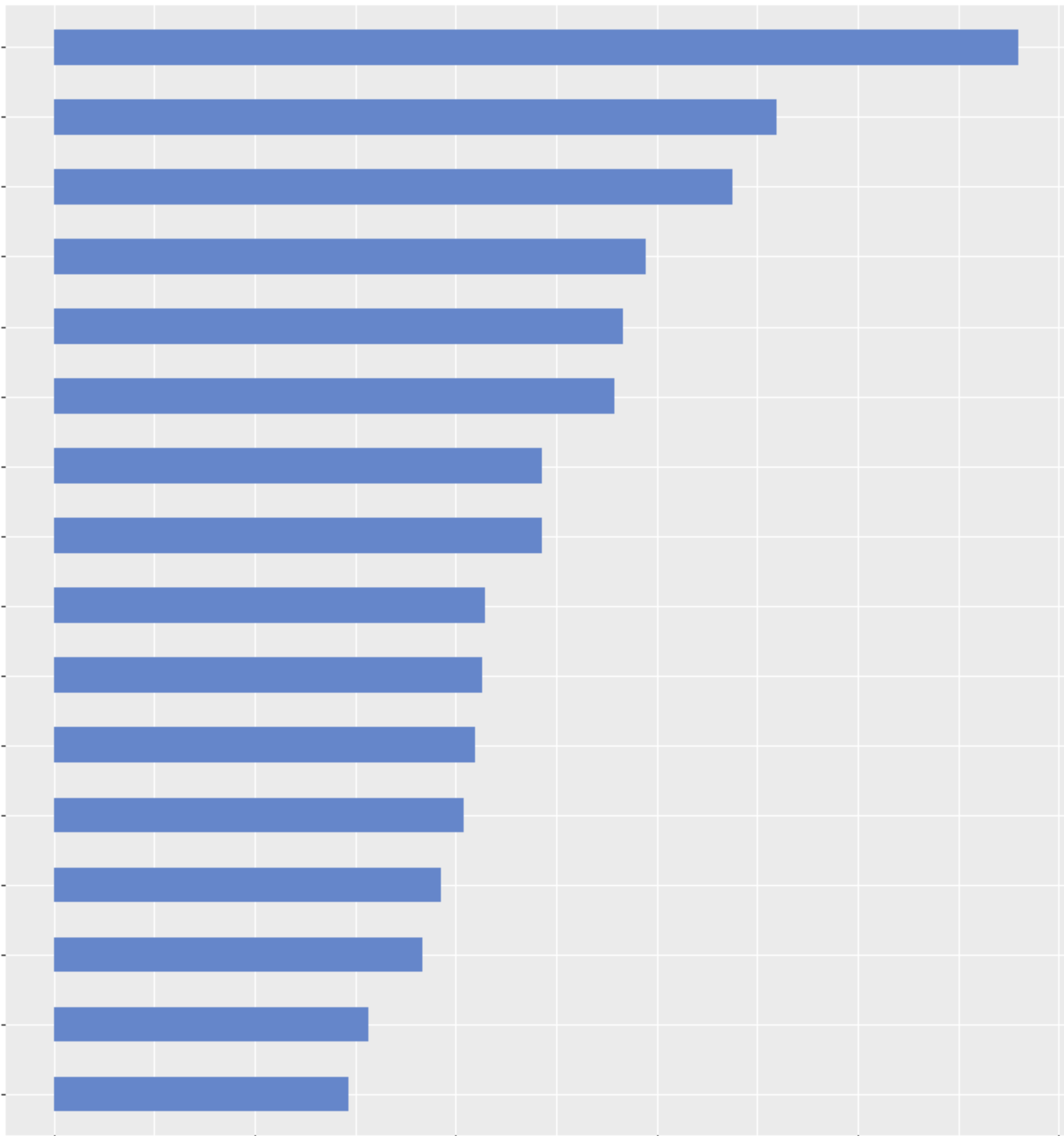
5.0

7.5

10.0

12.5

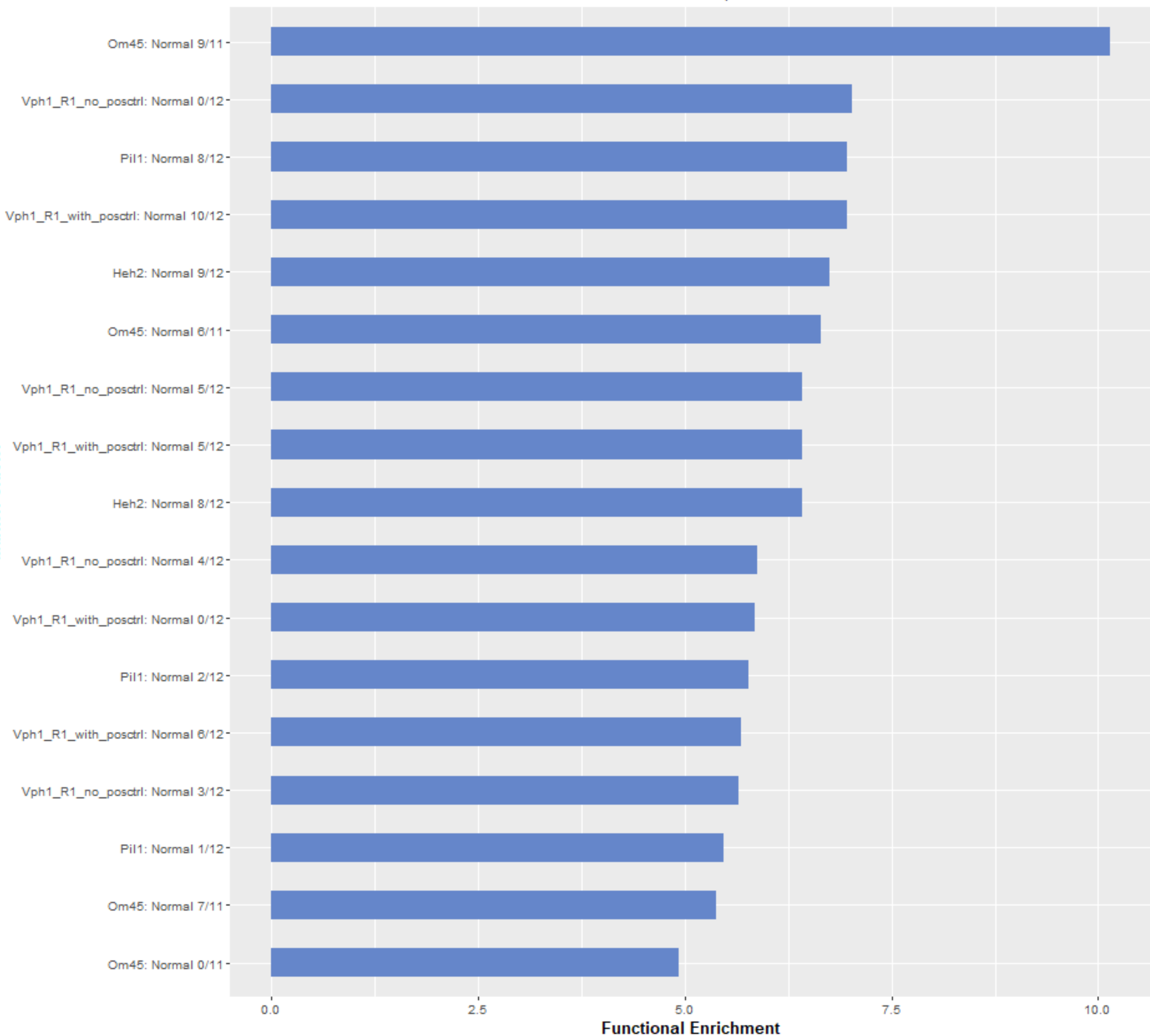
Functional Enrichment



# tRNA aminoacylation for protein translation

With AreaShape

Marker: Cluster



# tRNA processing

With AreaShape

Marker: Cluster

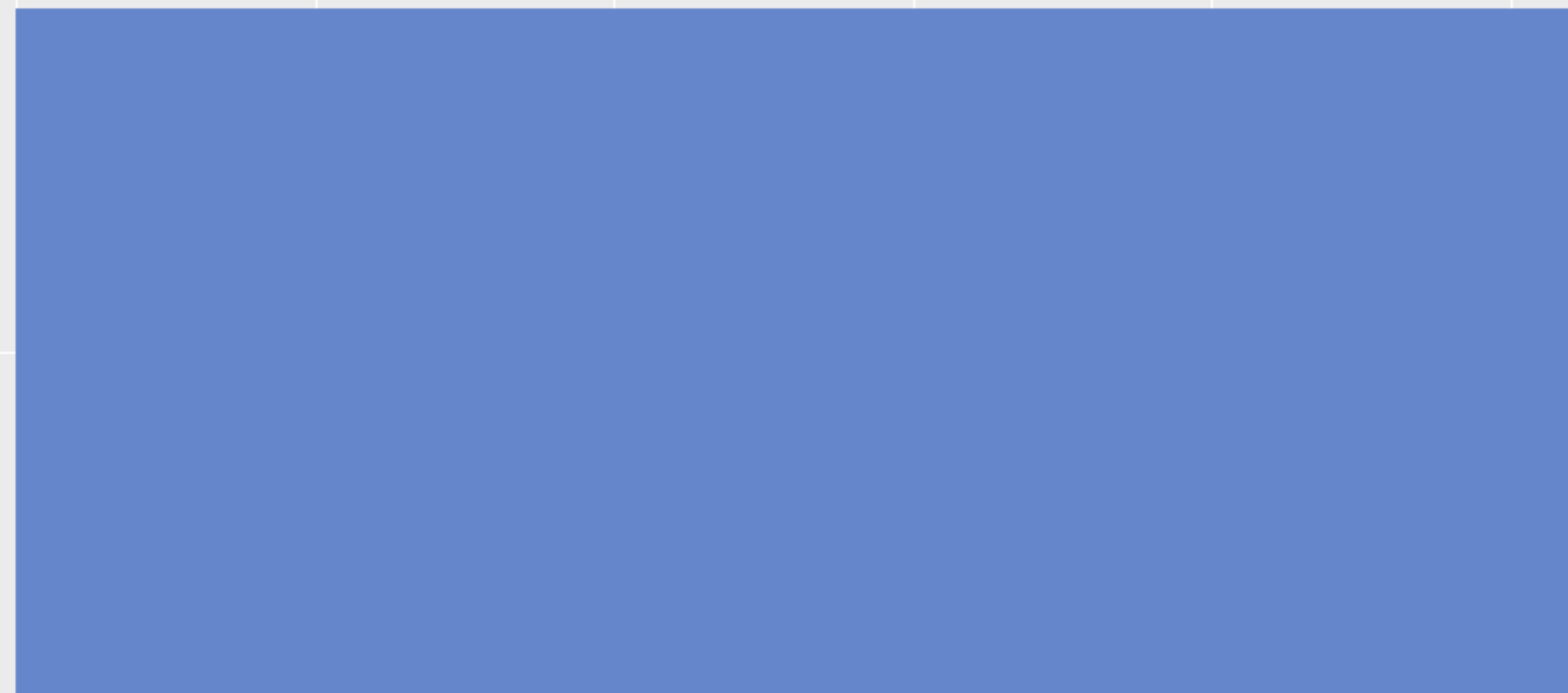
Rad52: Normal 7/12

0

1

2

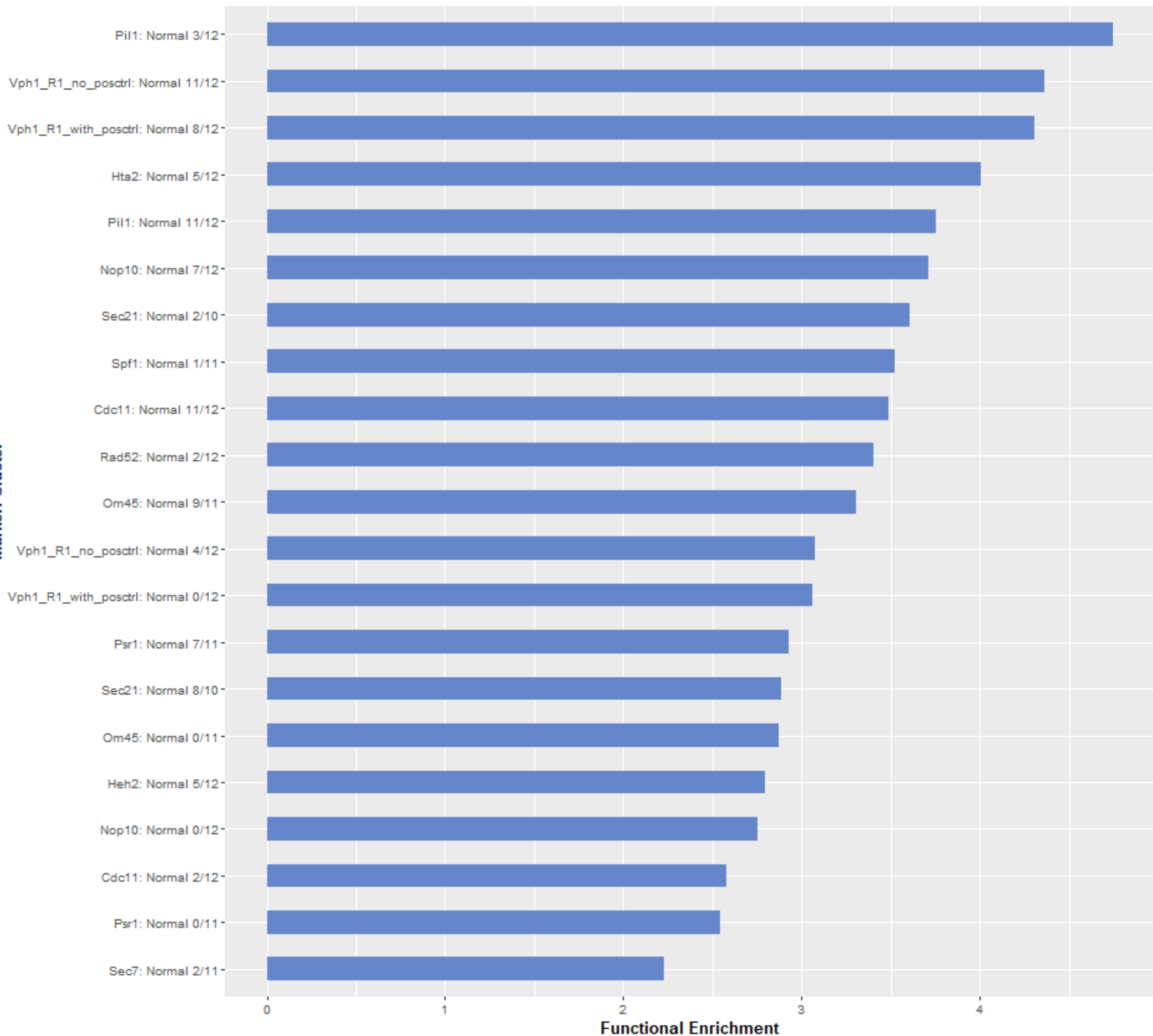
Functional Enrichment



# vacuole organization

With AreaShape

Marker: Cluster



# vesicle organization

With AreaShape

Marker: Cluster

