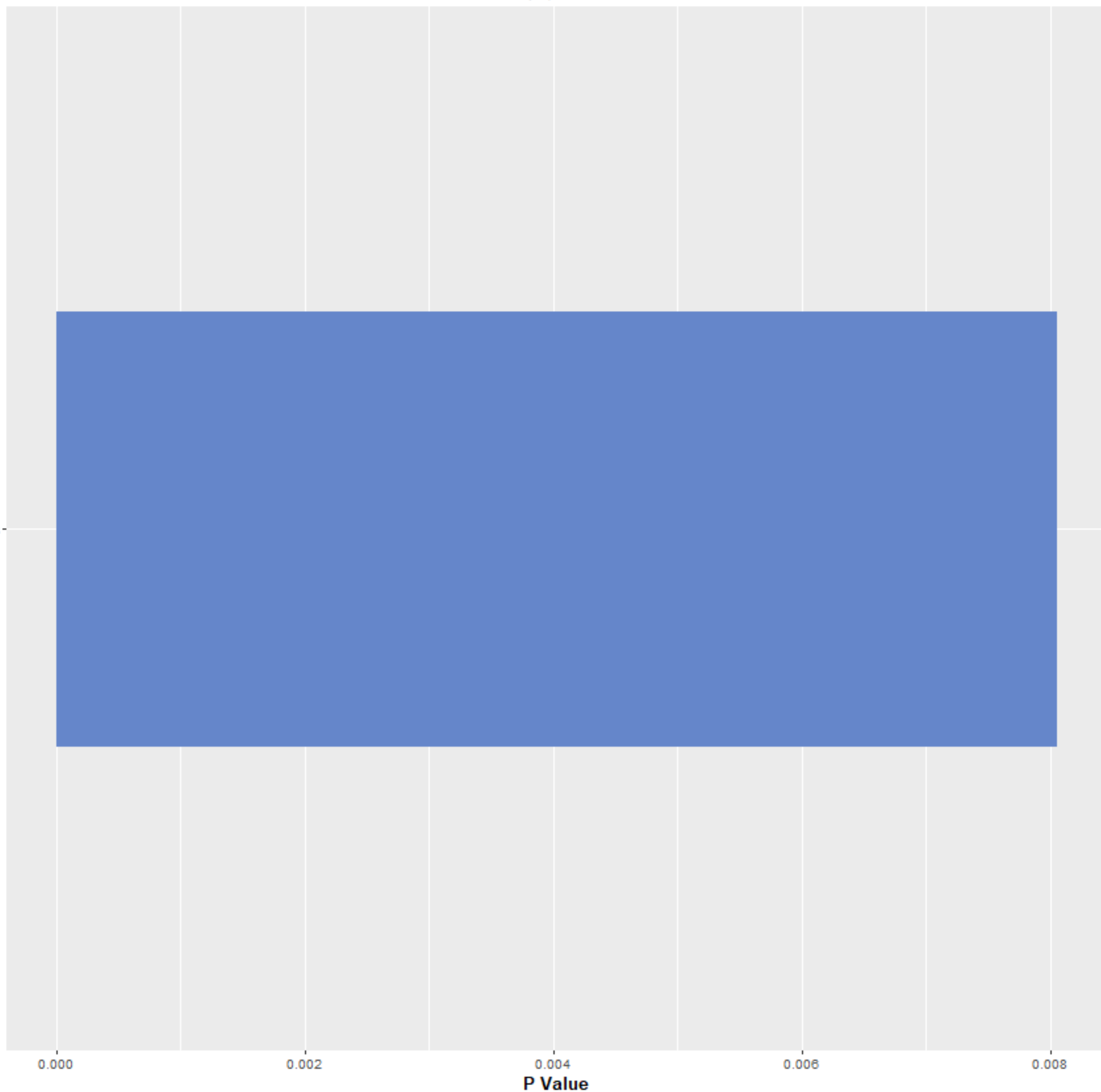


# carbohydrate metabolic process

With AreaShape | Ordered Gene Set

Marker: Cluster

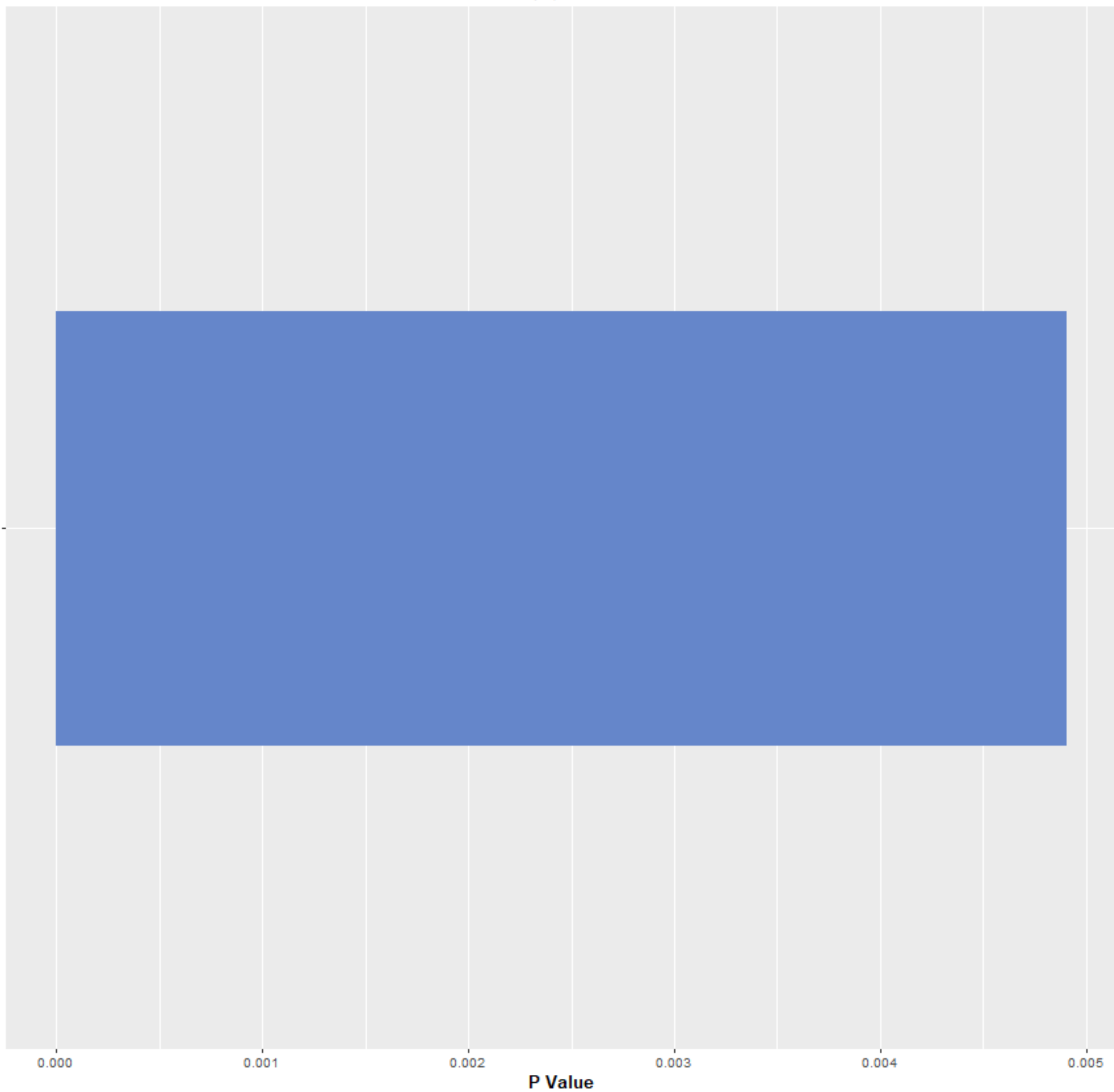
Om45: Normal 3



**carbohydrate transport**  
With AreaShape | Ordered Gene Set

**Marker: Cluster**

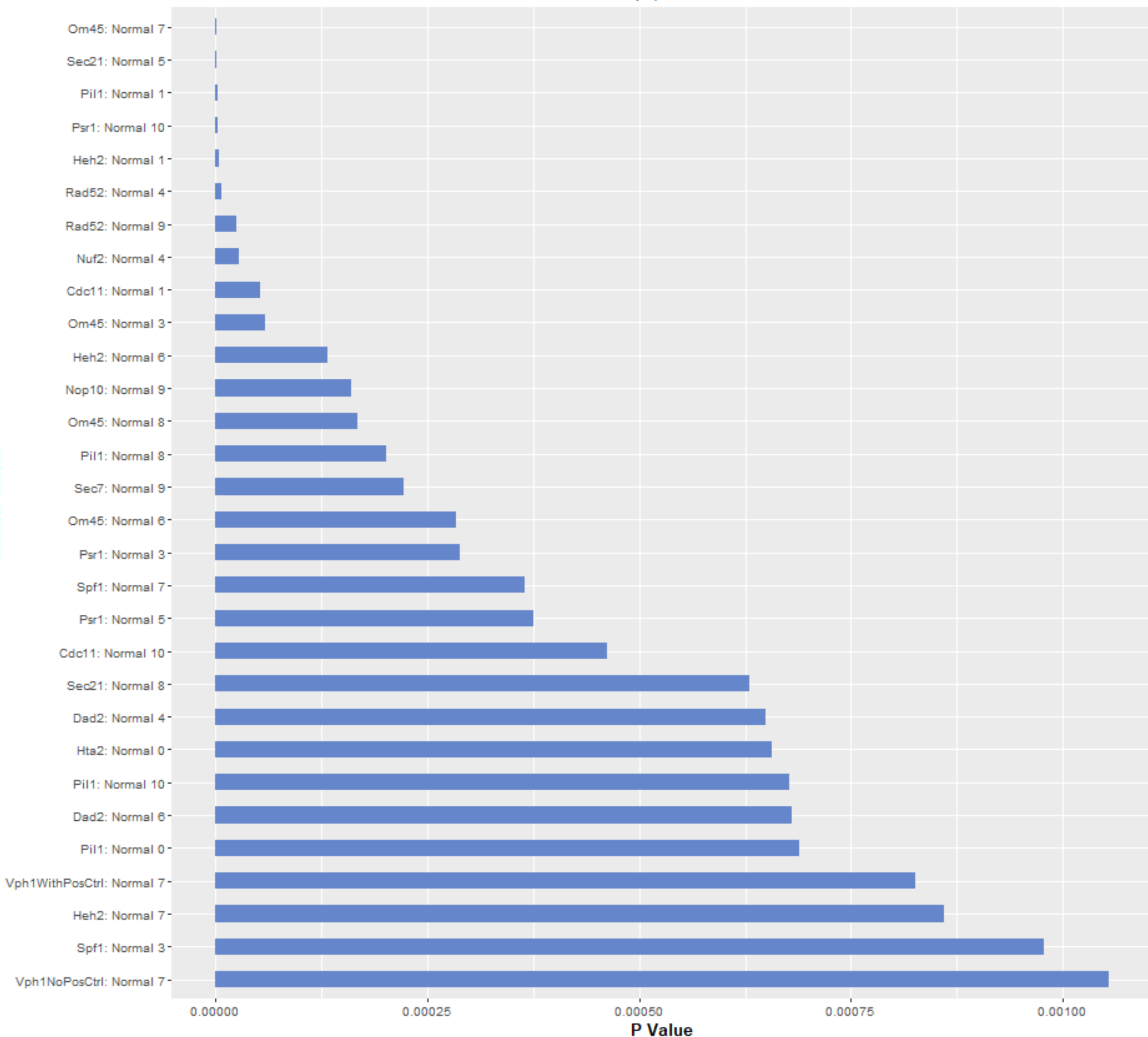
Psr1: Normal 3



# cell budding

With AreaShape | Ordered Gene Set

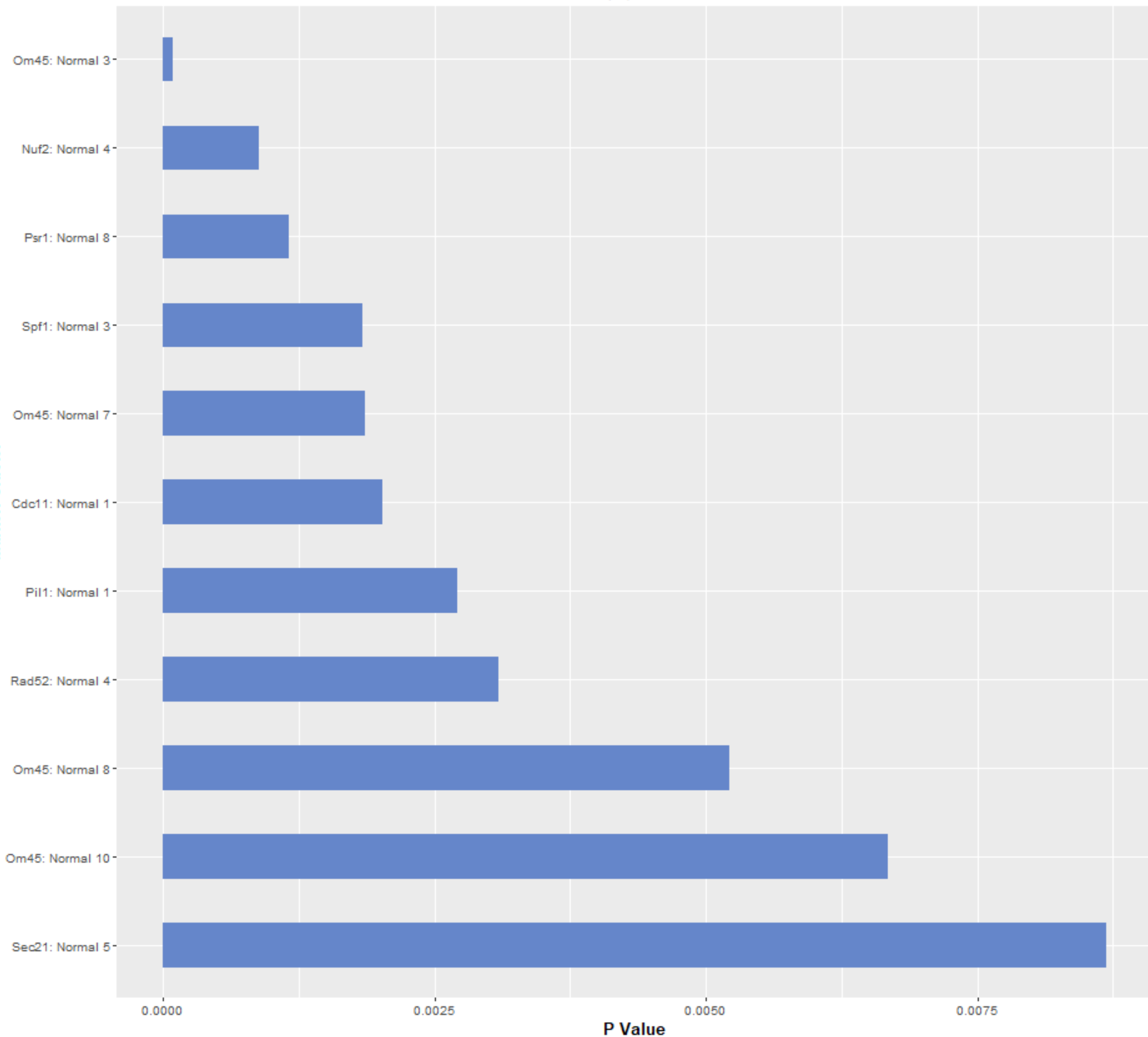
Marker: Cluster



# cell morphogenesis

With AreaShape | Ordered Gene Set

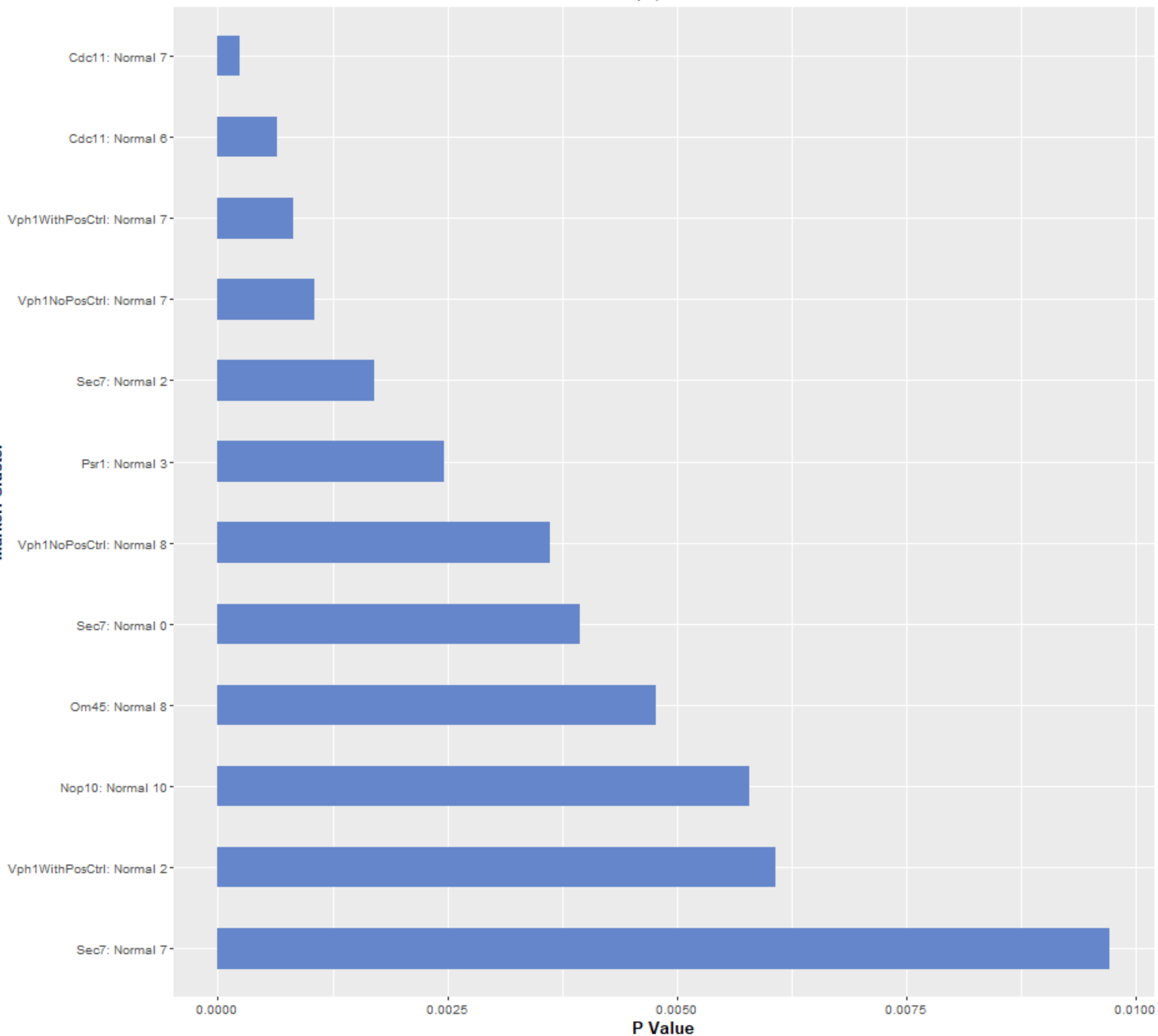
Marker: Cluster



# cell wall organization or biogenesis

With AreaShape | Ordered Gene Set

Marker: Cluster



# cellular amino acid metabolic process

With AreaShape | Ordered Gene Set

Marker: Cluster

Cdc11: Normal 3

Sec7: Normal 10

0.0000

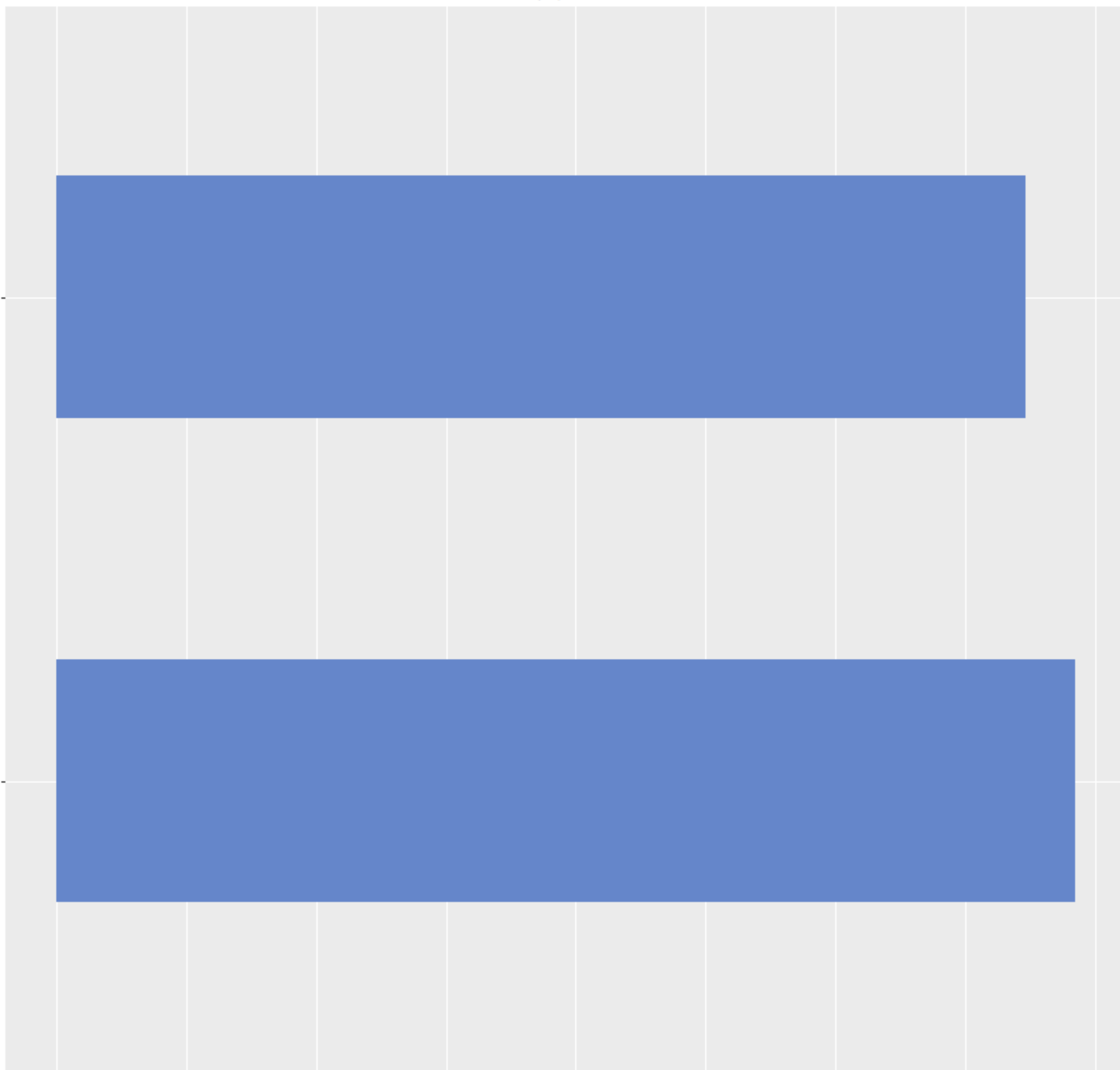
0.0005

0.0010

0.0015

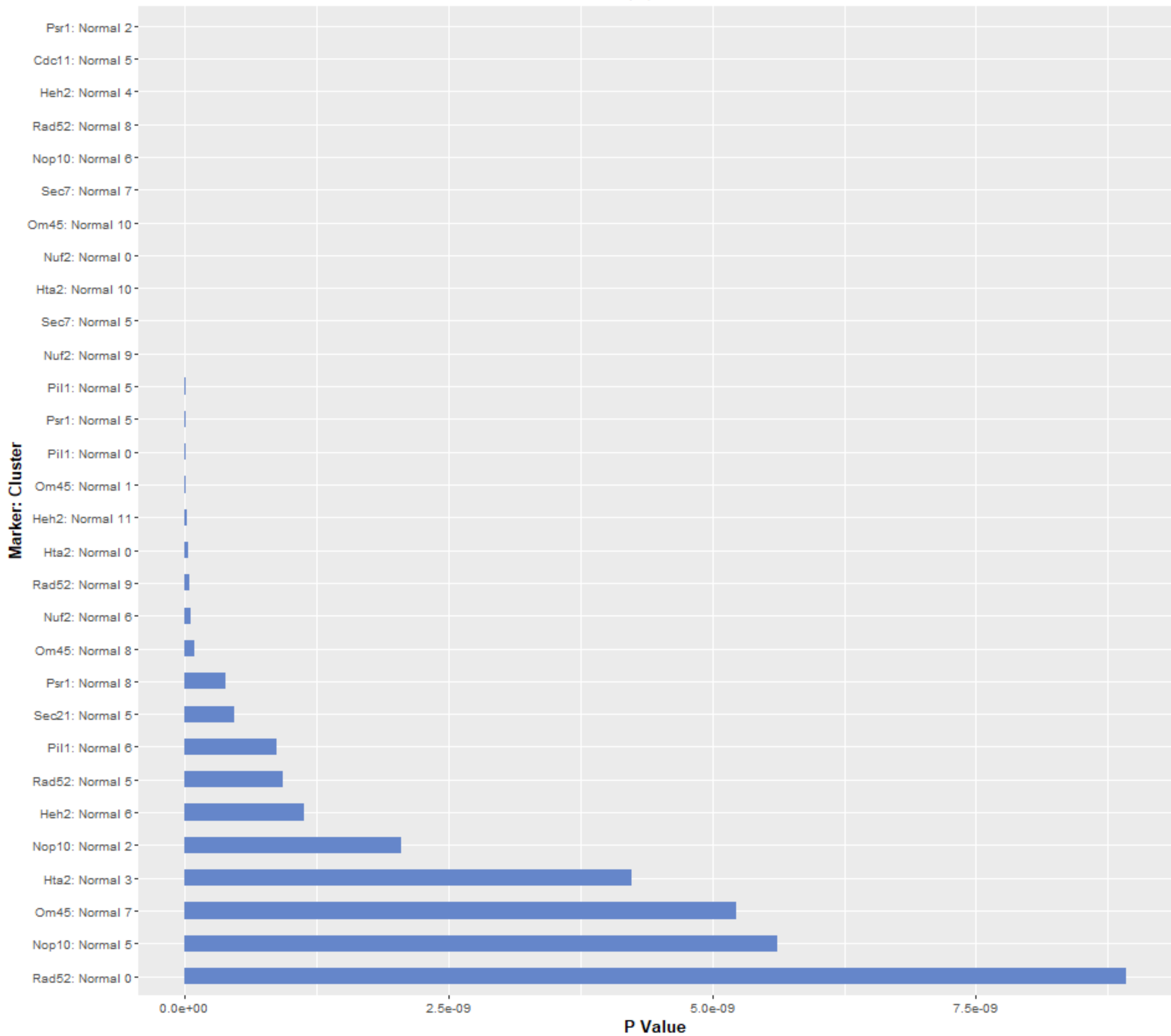
0.0020

P Value

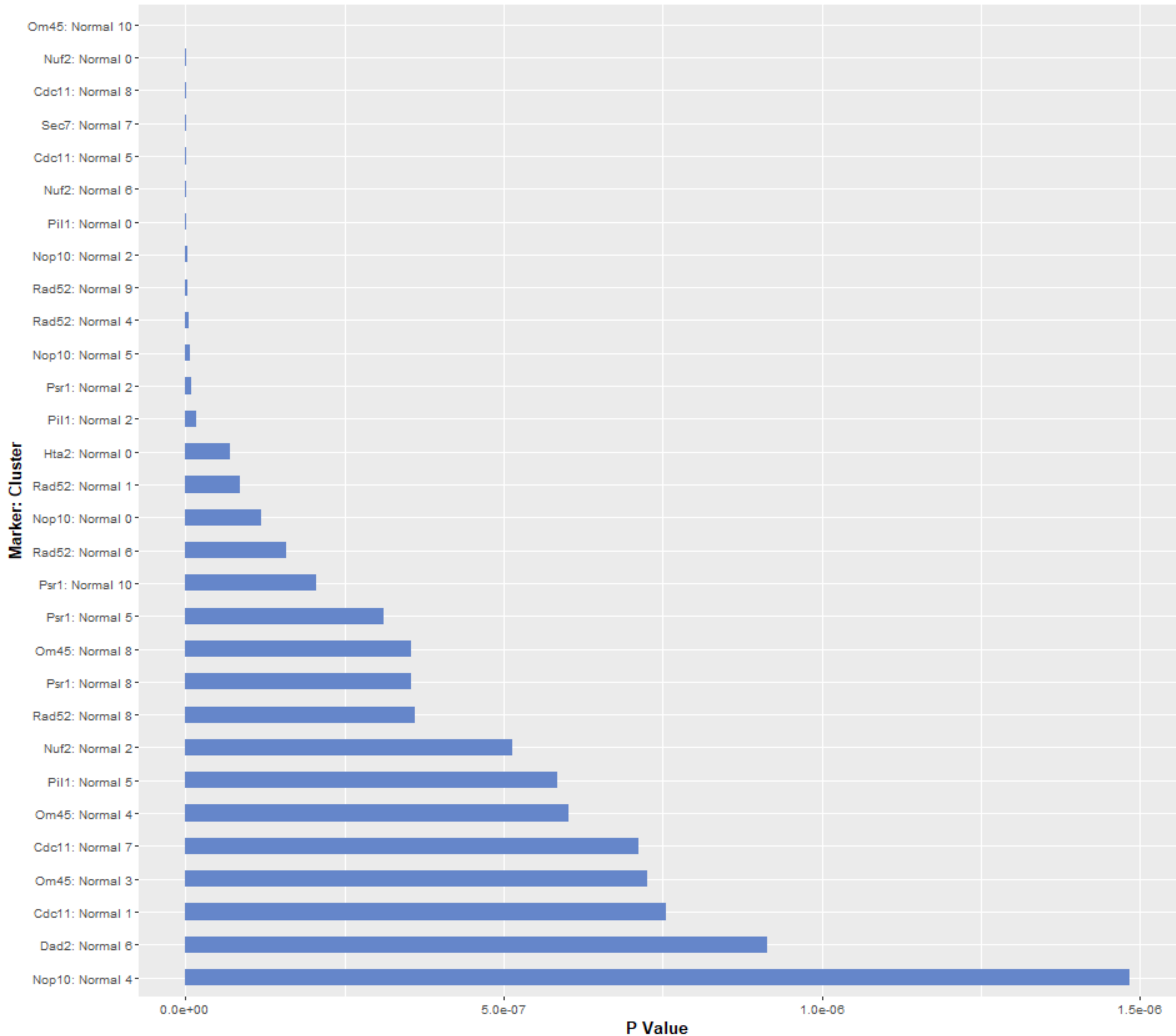


# cellular response to DNA damage stimulus

With AreaShape | Ordered Gene Set



chromatin organization  
With AreaShape | Ordered Gene Set

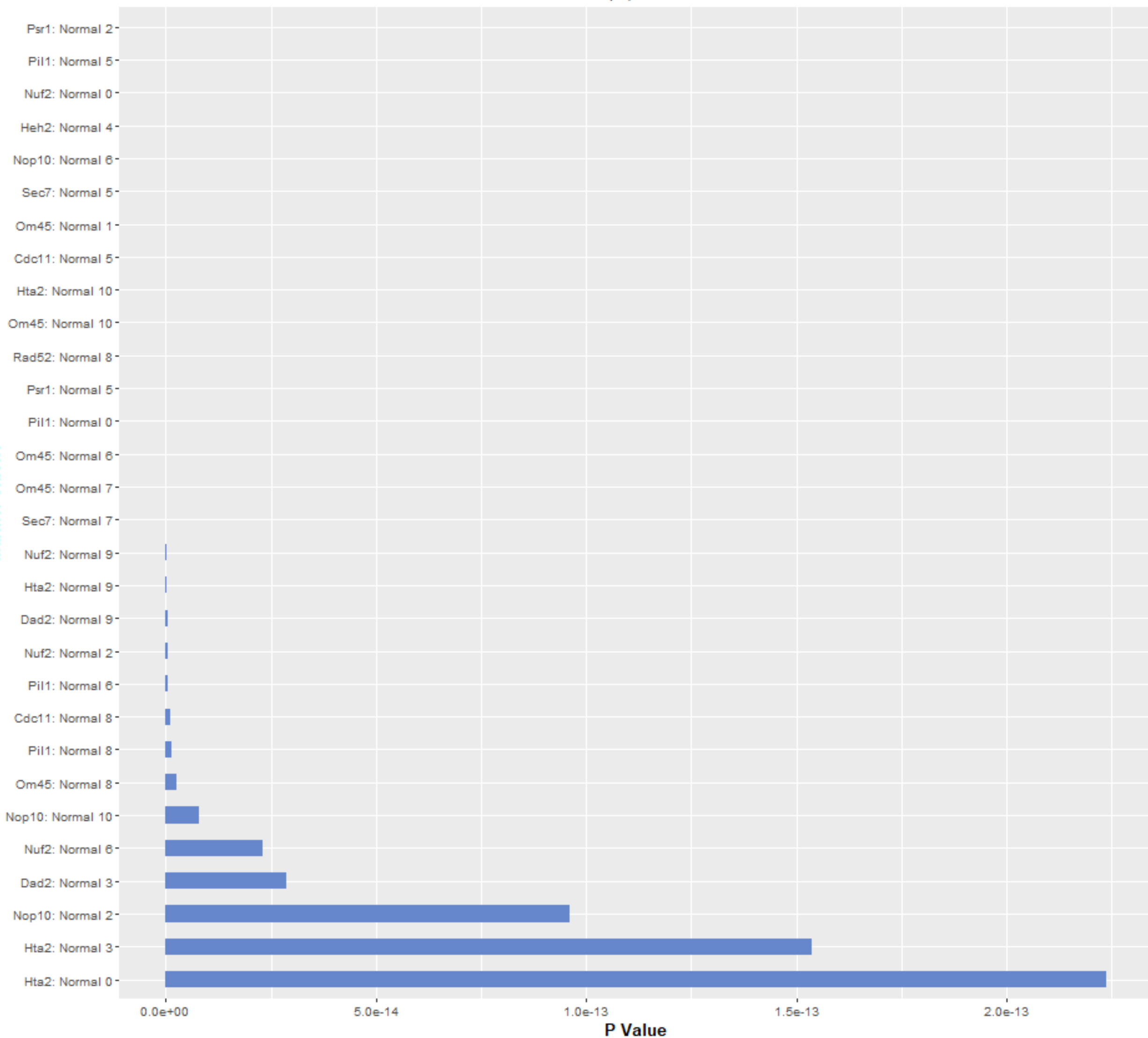




# chromosome segregation

With AreaShape | Ordered Gene Set

Marker: Cluster



# cofactor metabolic process

With AreaShape | Ordered Gene Set

Marker: Cluster

Om45: Normal 3

0e+00

1e-04

2e-04

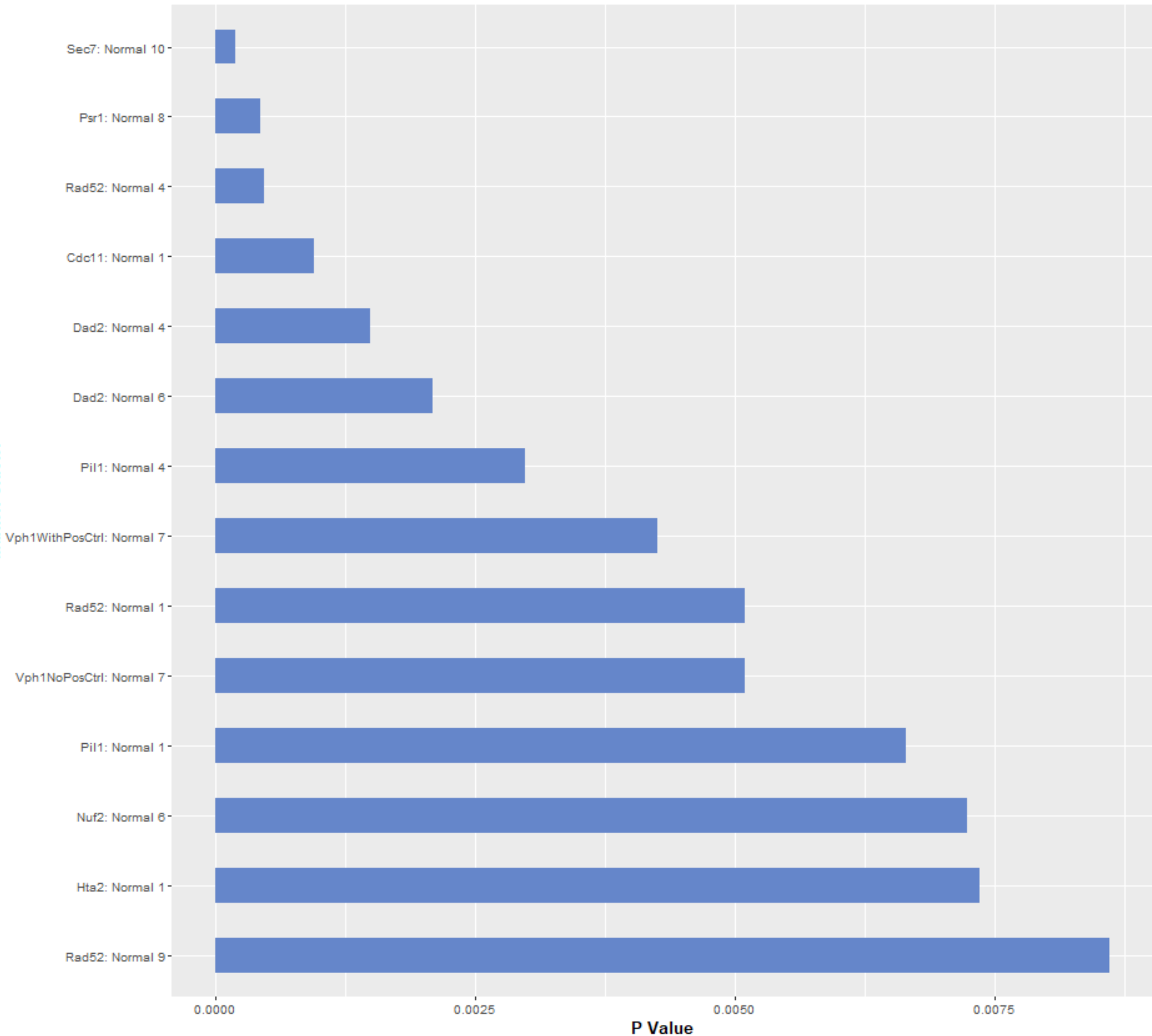
P Value



# conjugation

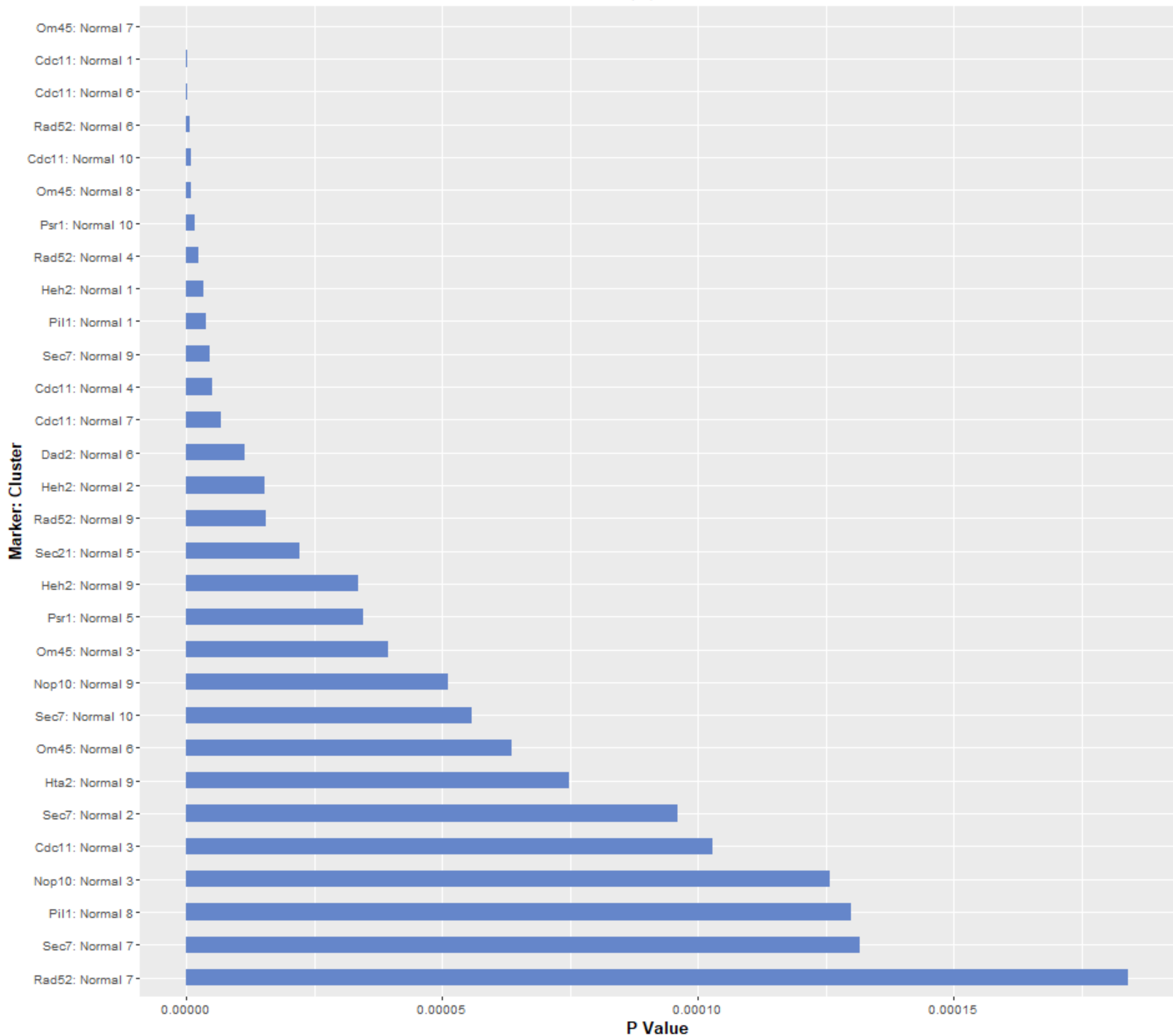
With AreaShape | Ordered Gene Set

Marker: Cluster

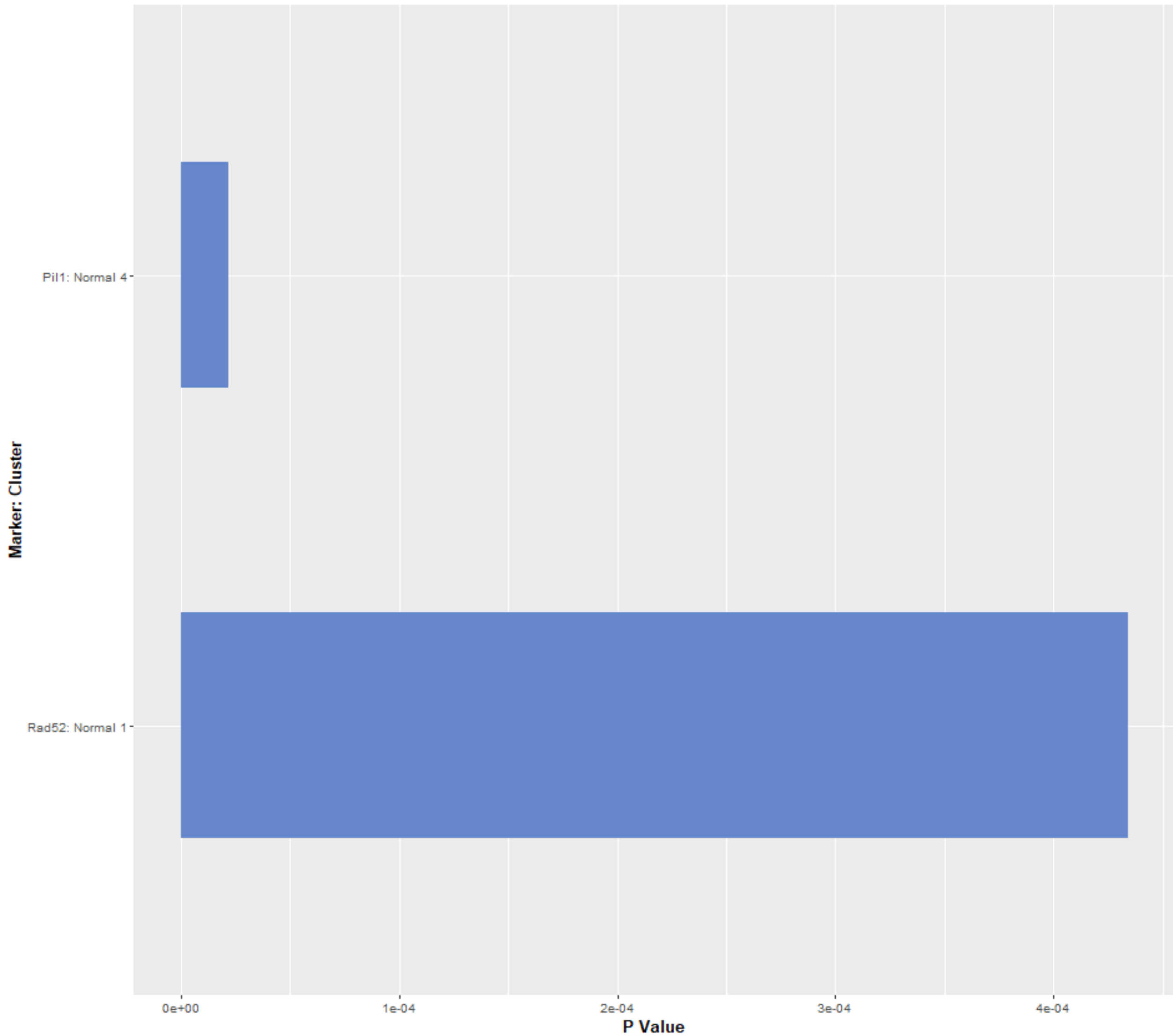


# cytokinesis

With AreaShape | Ordered Gene Set



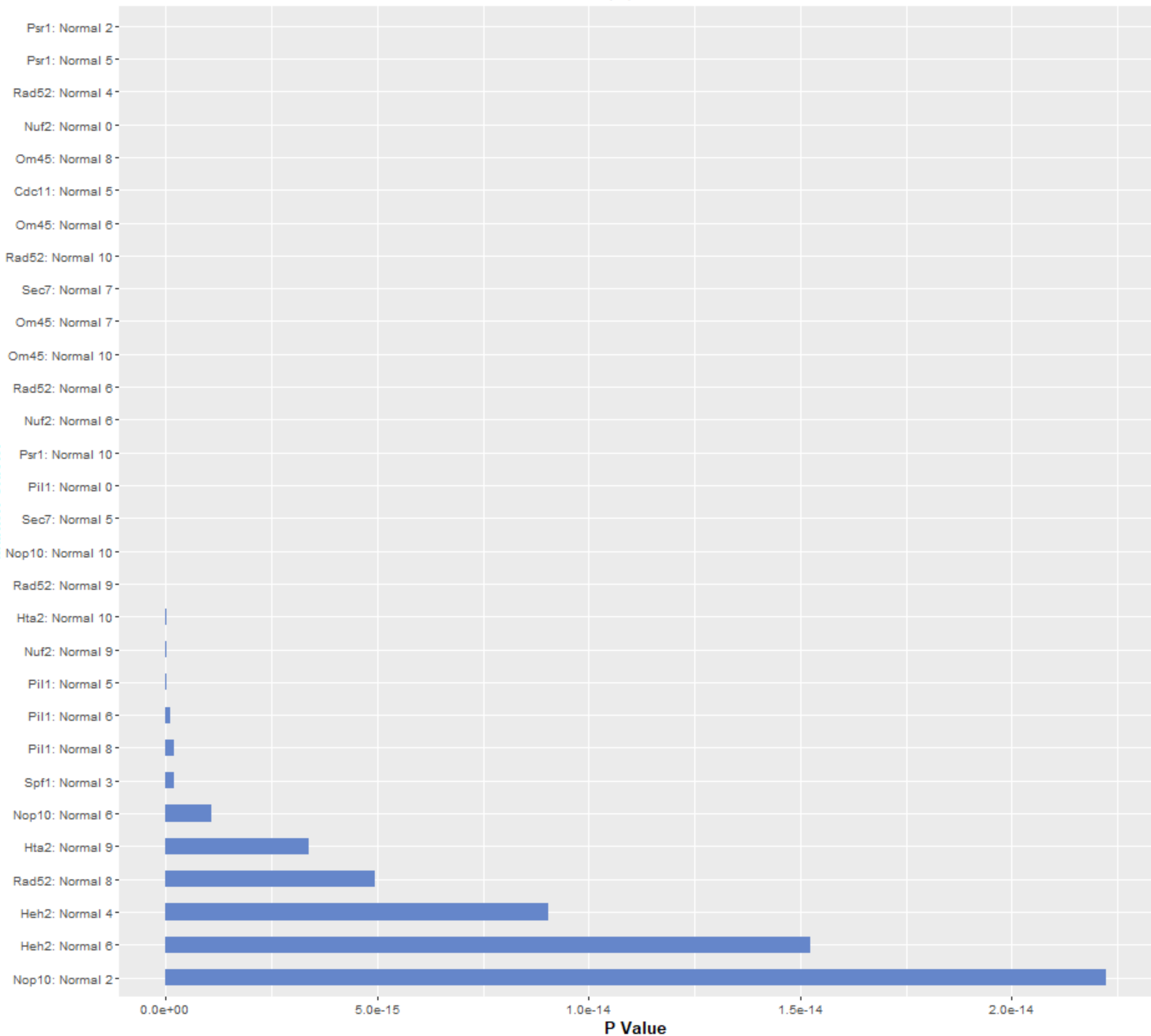
**cytoplasmic translation**  
With AreaShape | Ordered Gene Set



# cytoskeleton organization

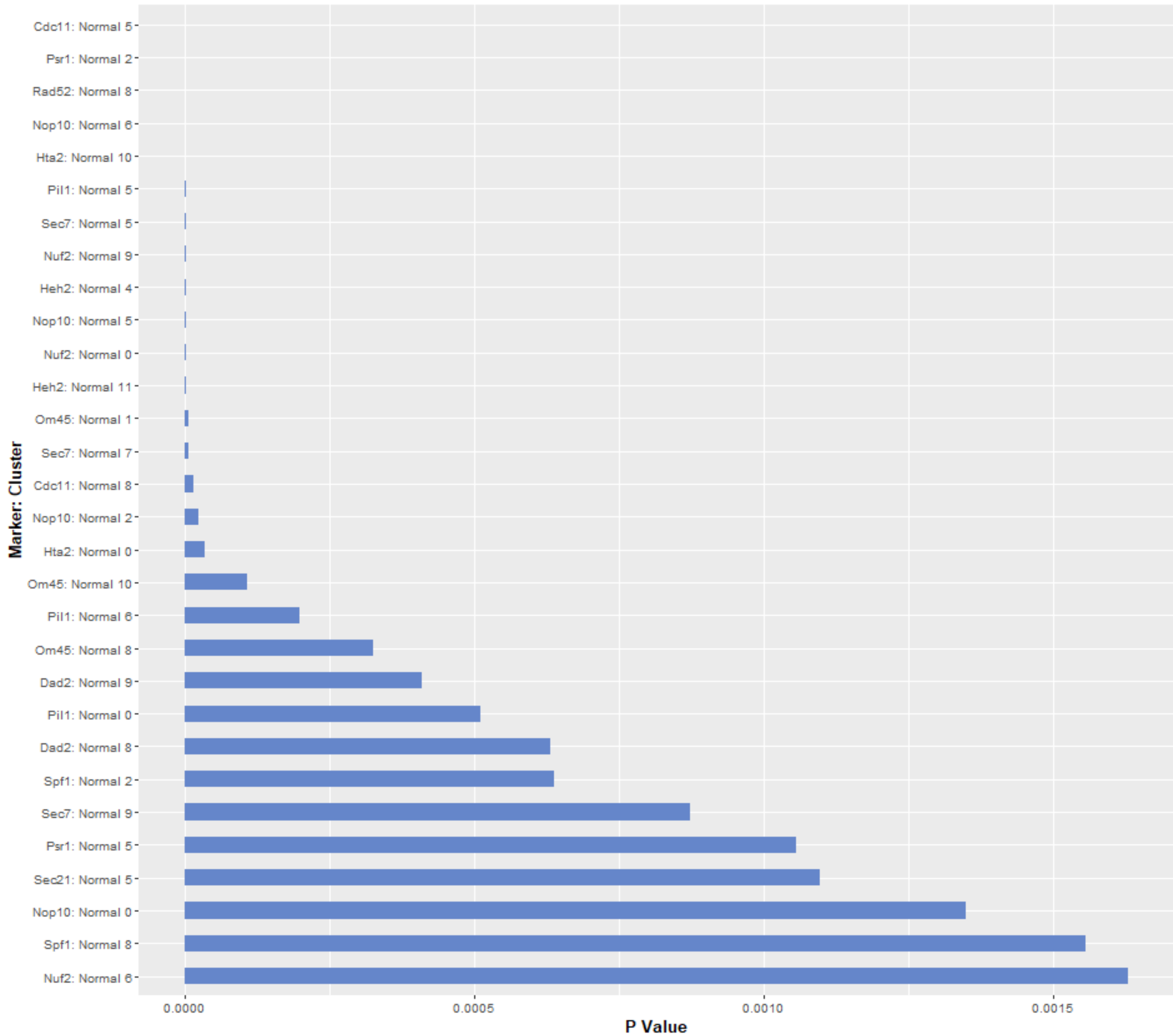
With AreaShape | Ordered Gene Set

Marker: Cluster



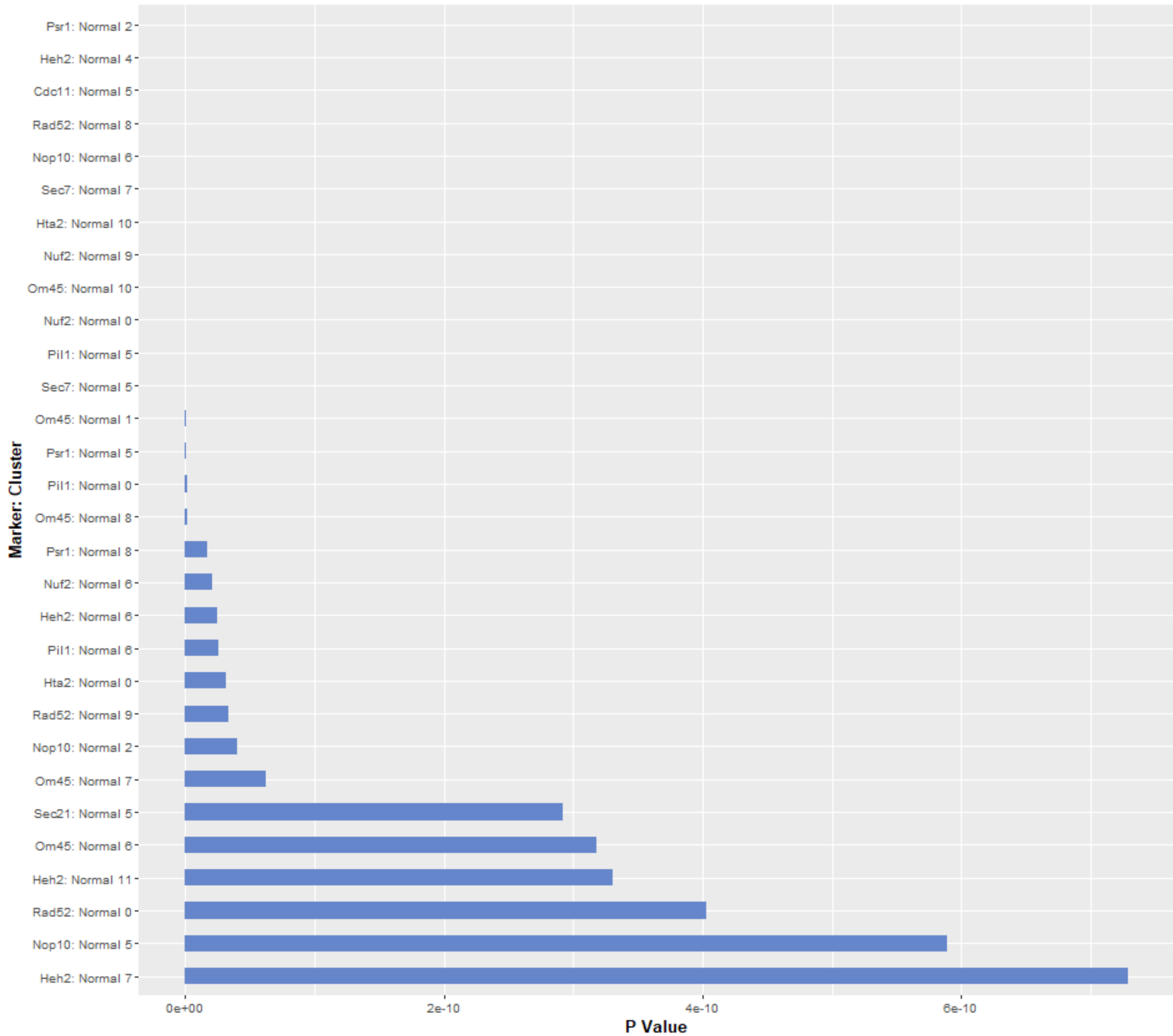
# DNA recombination

With AreaShape | Ordered Gene Set



# DNA repair

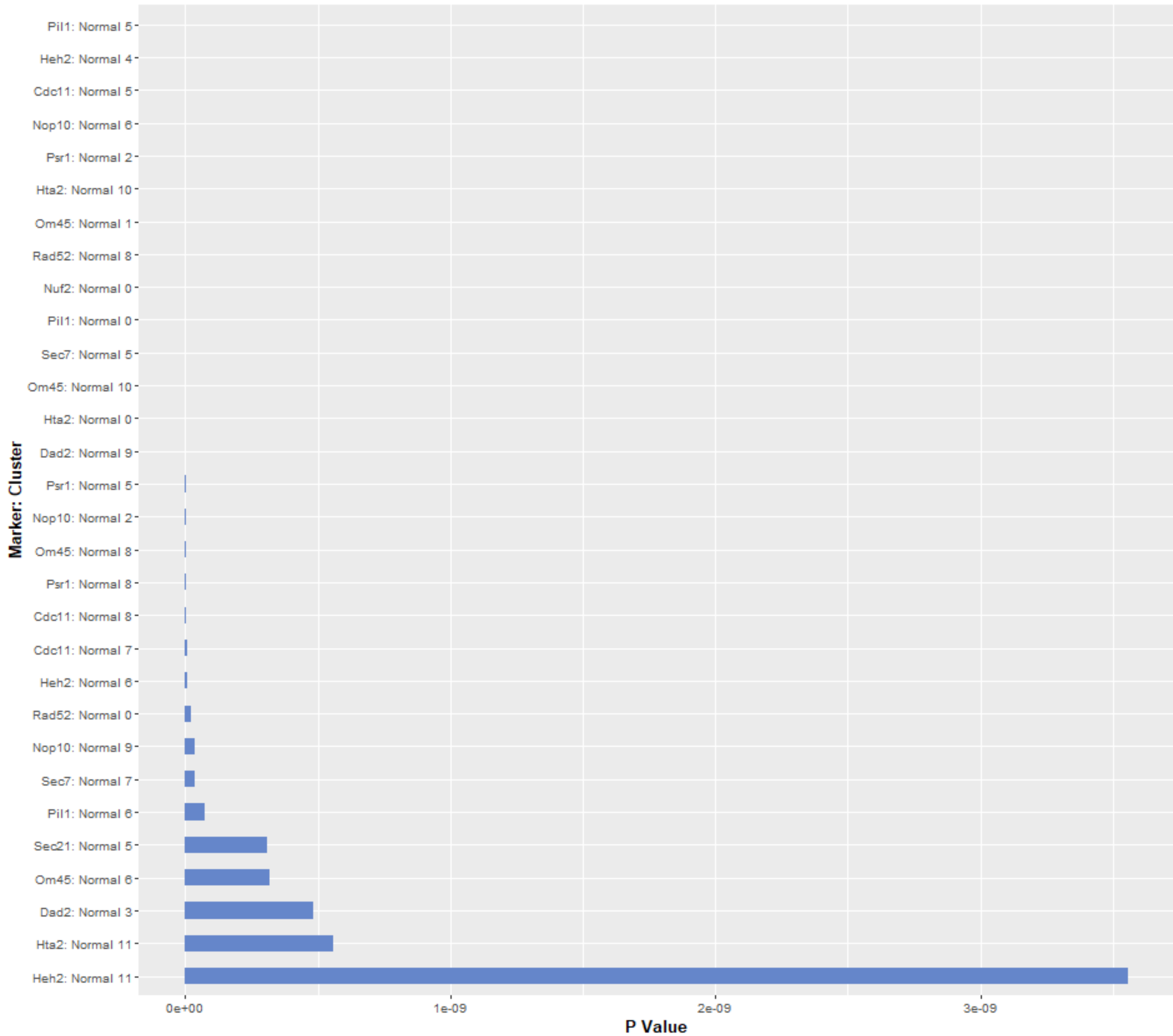
With AreaShape | Ordered Gene Set





# DNA replication

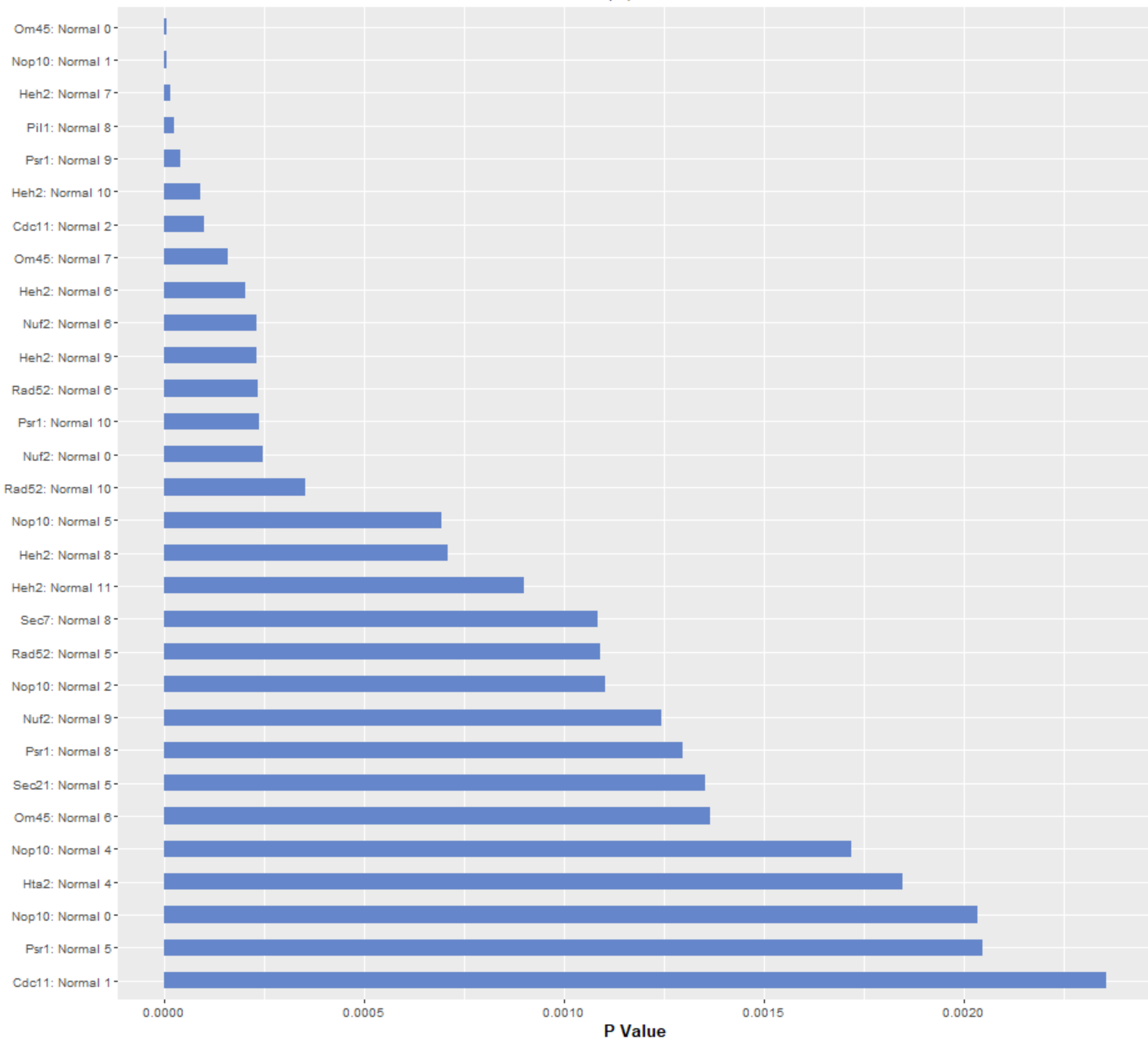
With AreaShape | Ordered Gene Set



# DNA-templated transcription, elongation

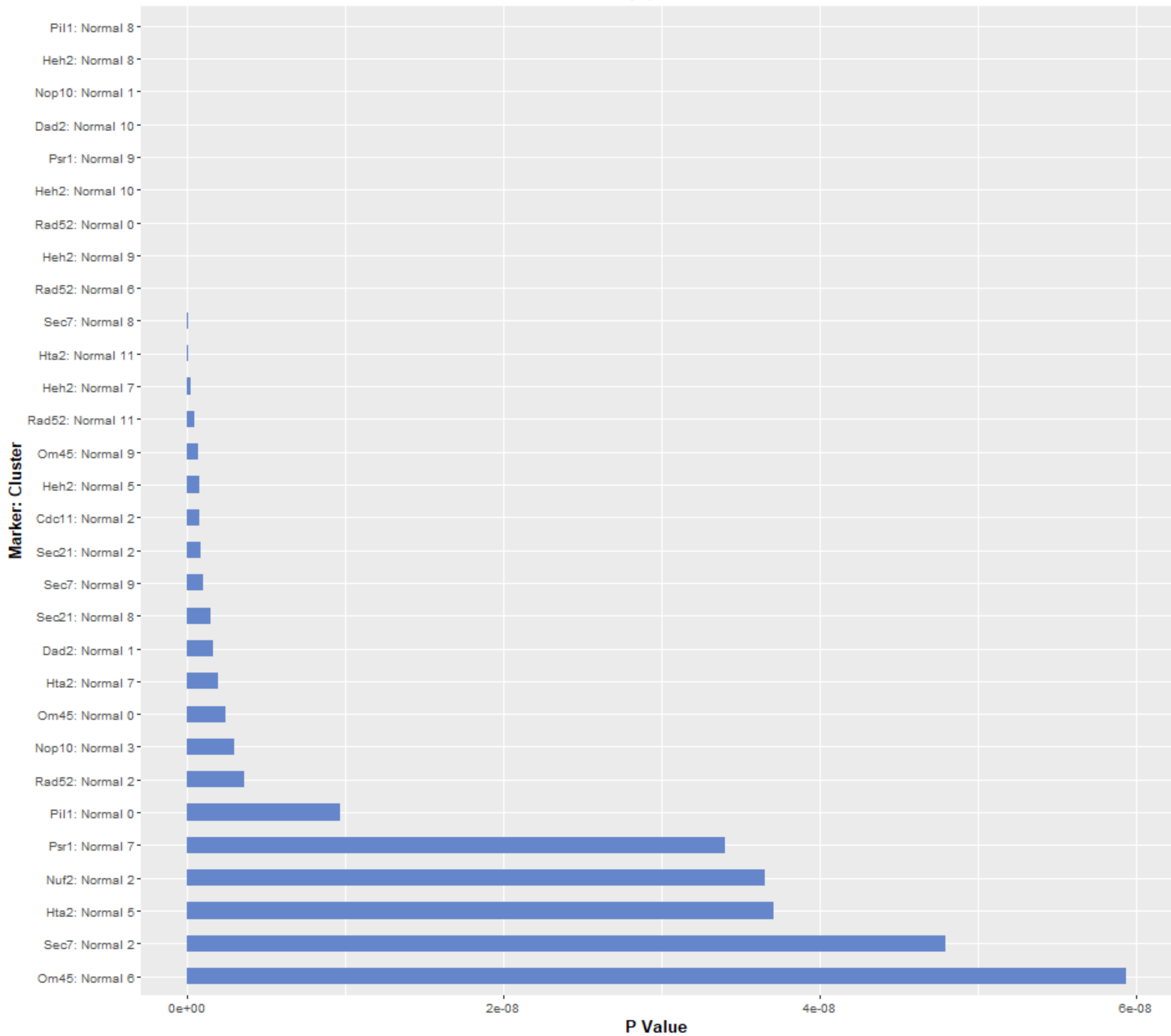
With AreaShape | Ordered Gene Set

Marker: Cluster



# DNA-templated transcription, initiation

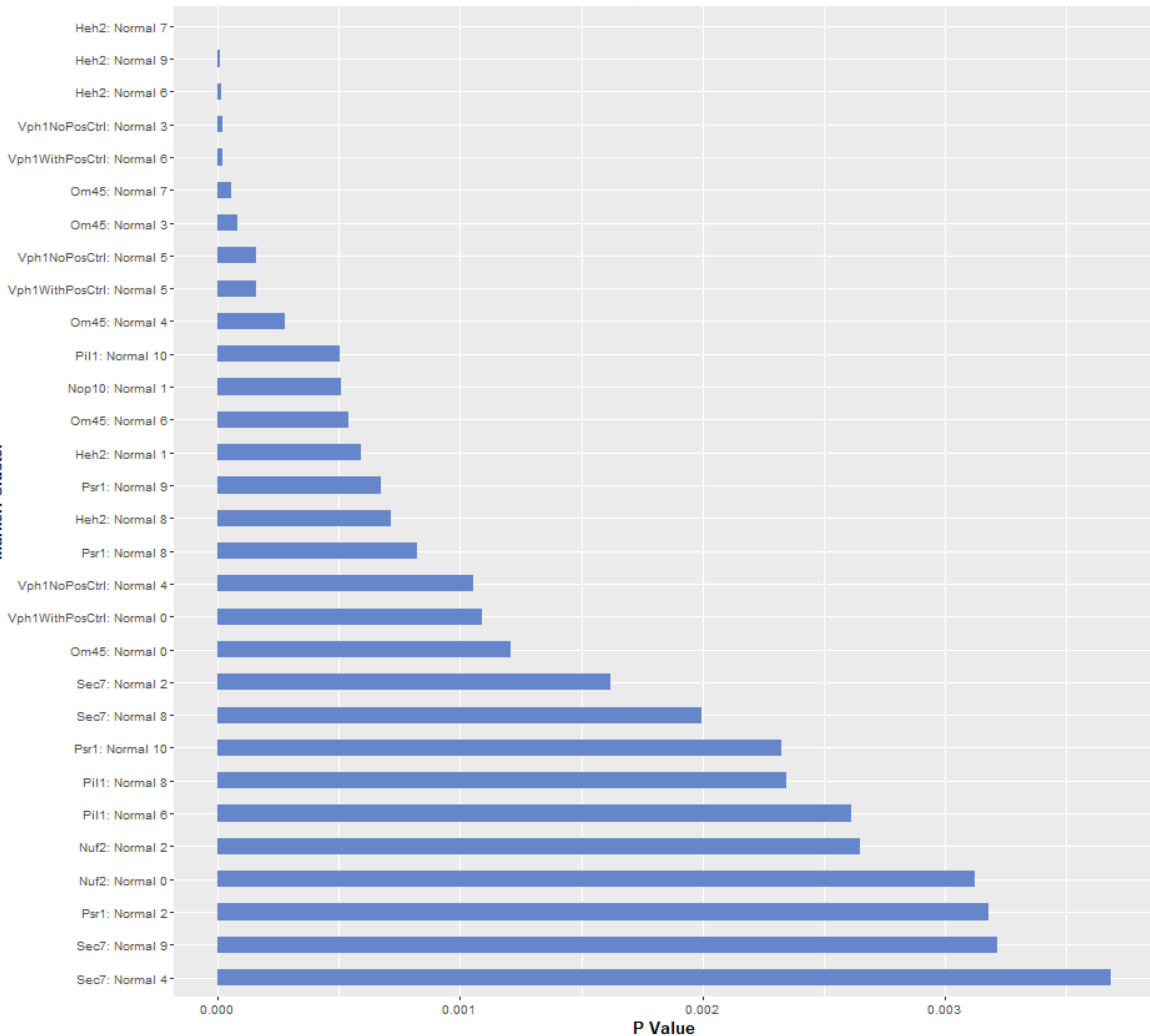
With AreaShape | Ordered Gene Set



# DNA-templated transcription, termination

With AreaShape | Ordered Gene Set

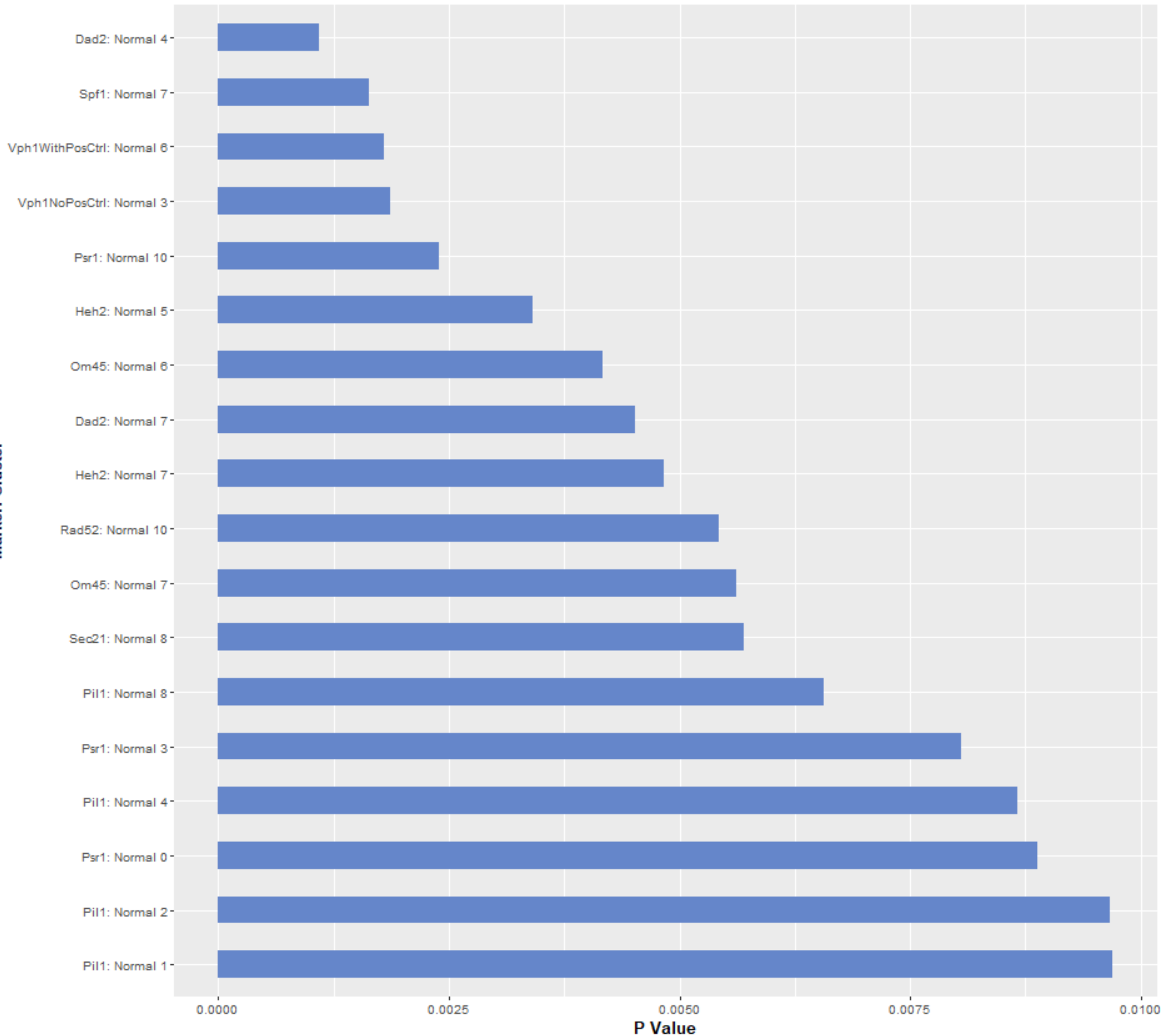
Marker: Cluster



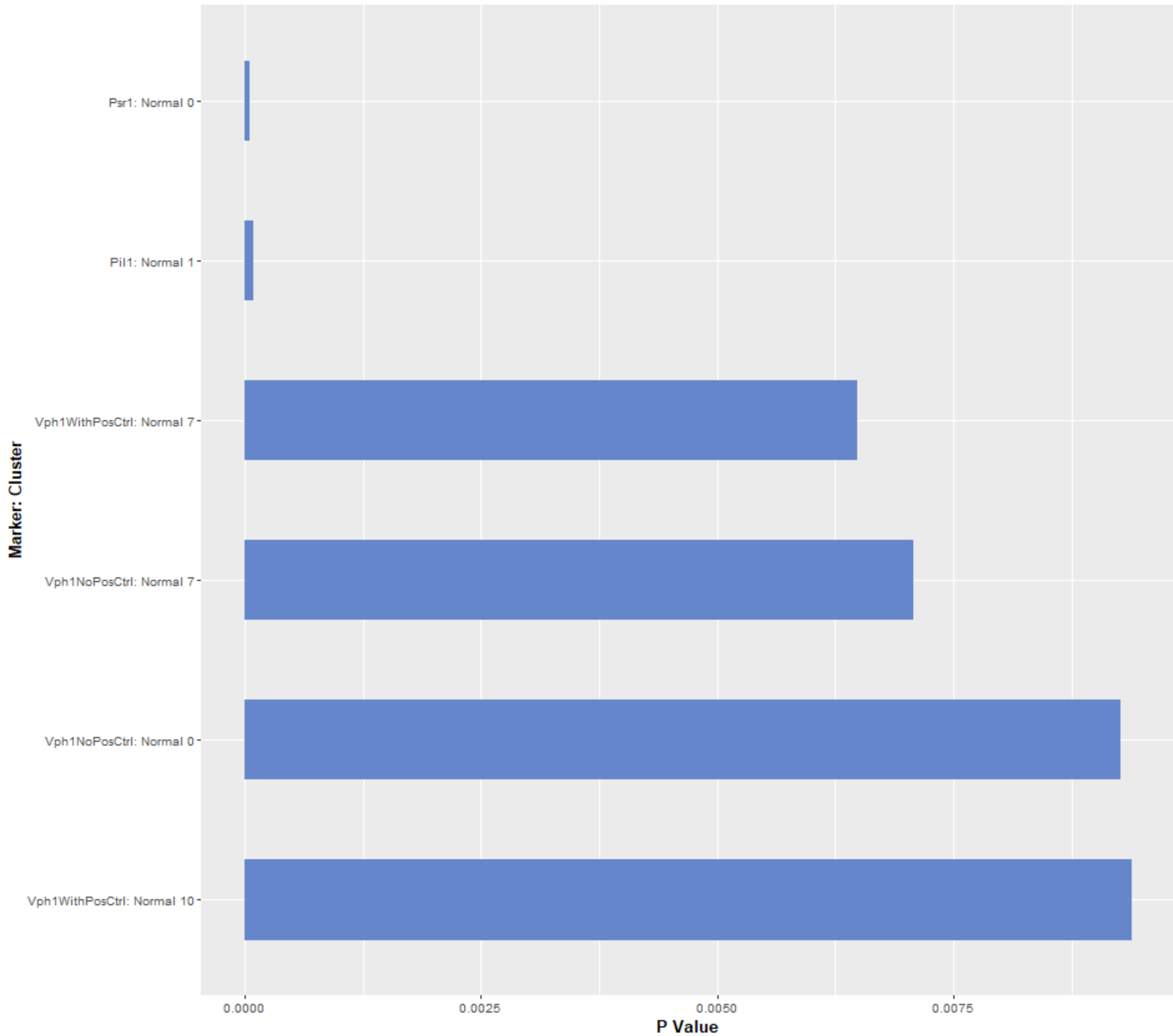
# endocytosis

With AreaShape | Ordered Gene Set

Marker: Cluster



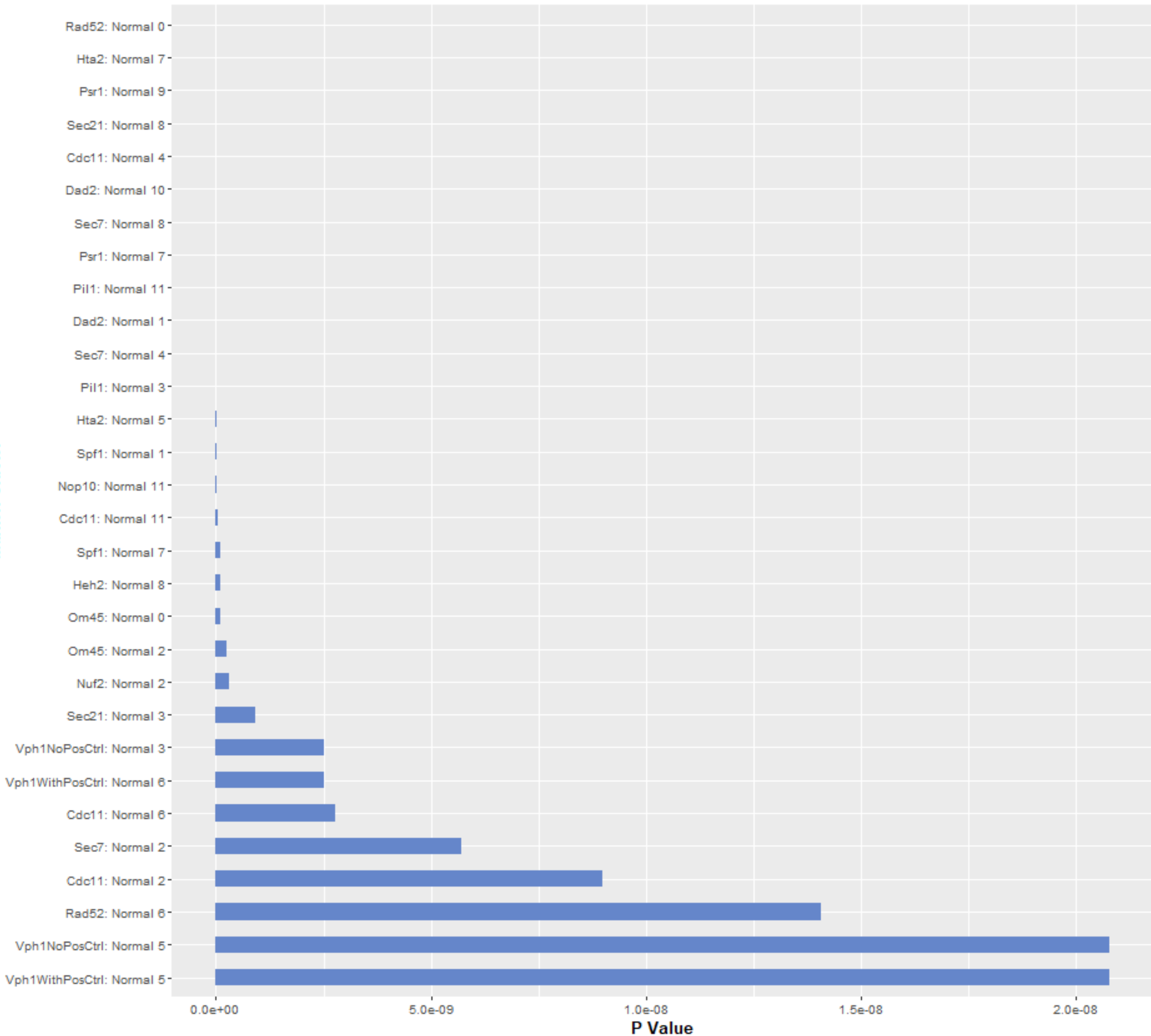
**endosomal transport**  
With AreaShape | Ordered Gene Set



# exocytosis

With AreaShape | Ordered Gene Set

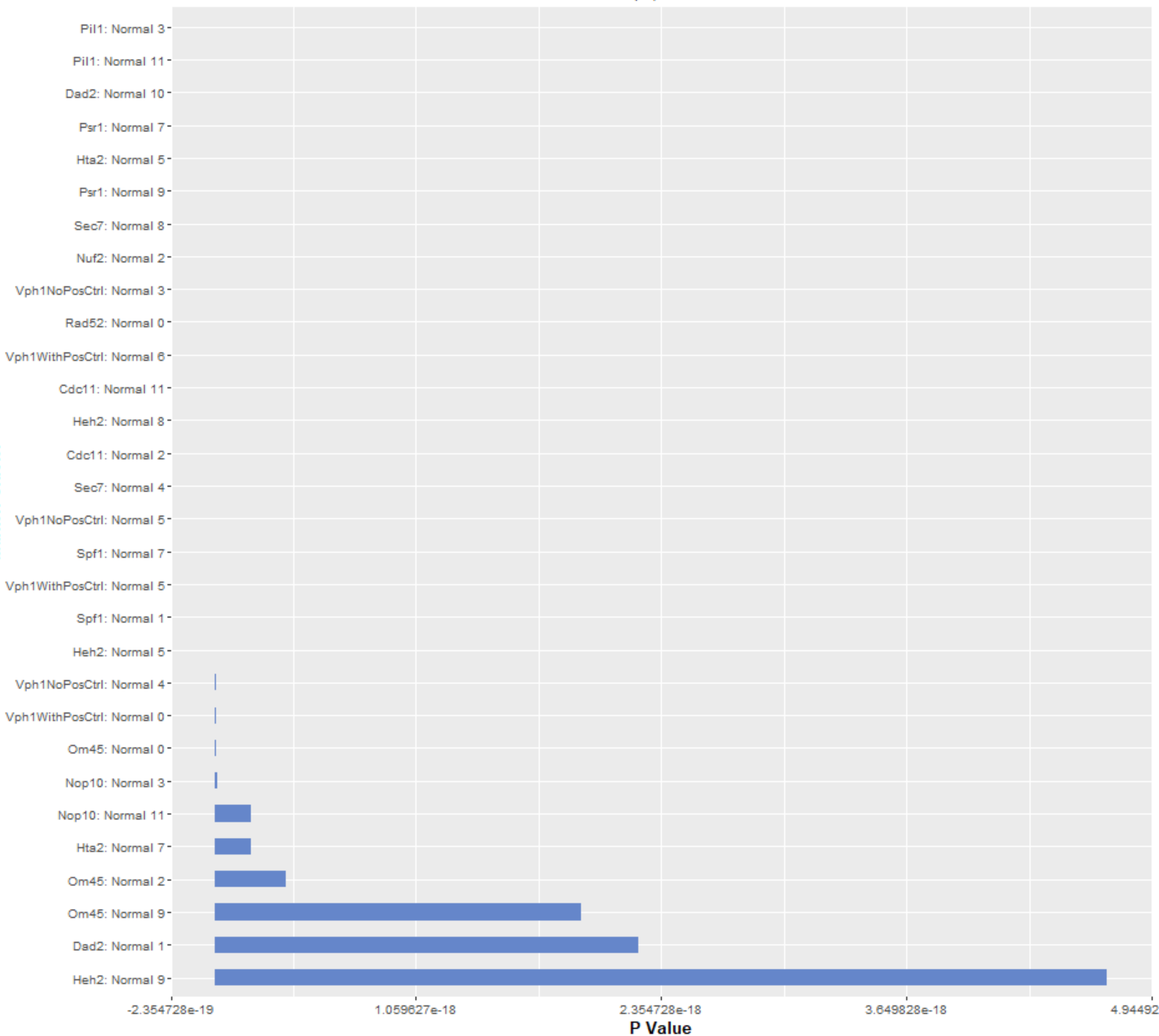
Marker: Cluster



# Golgi vesicle transport

With AreaShape | Ordered Gene Set

Marker: Cluster

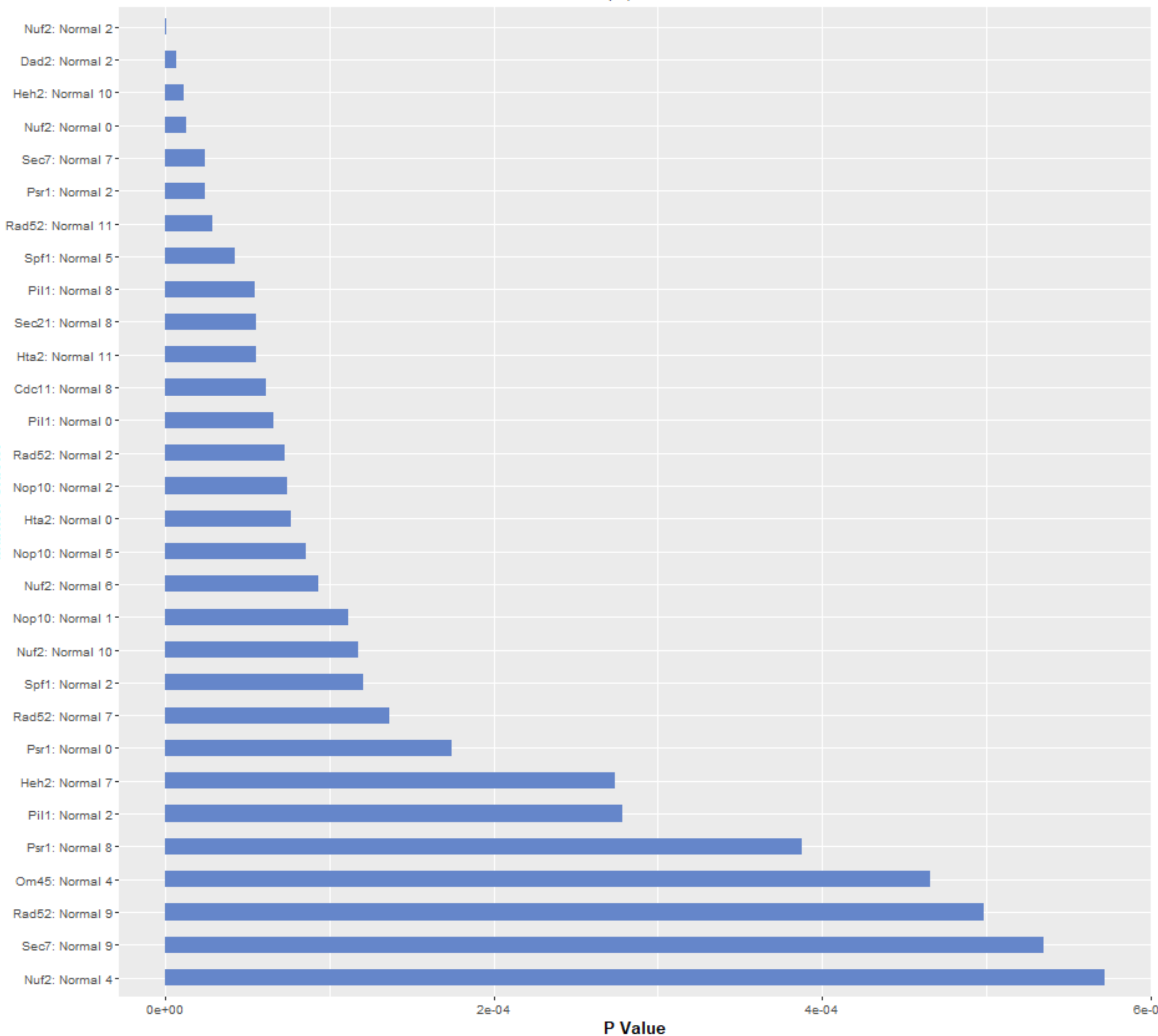




# histone modification

With AreaShape | Ordered Gene Set

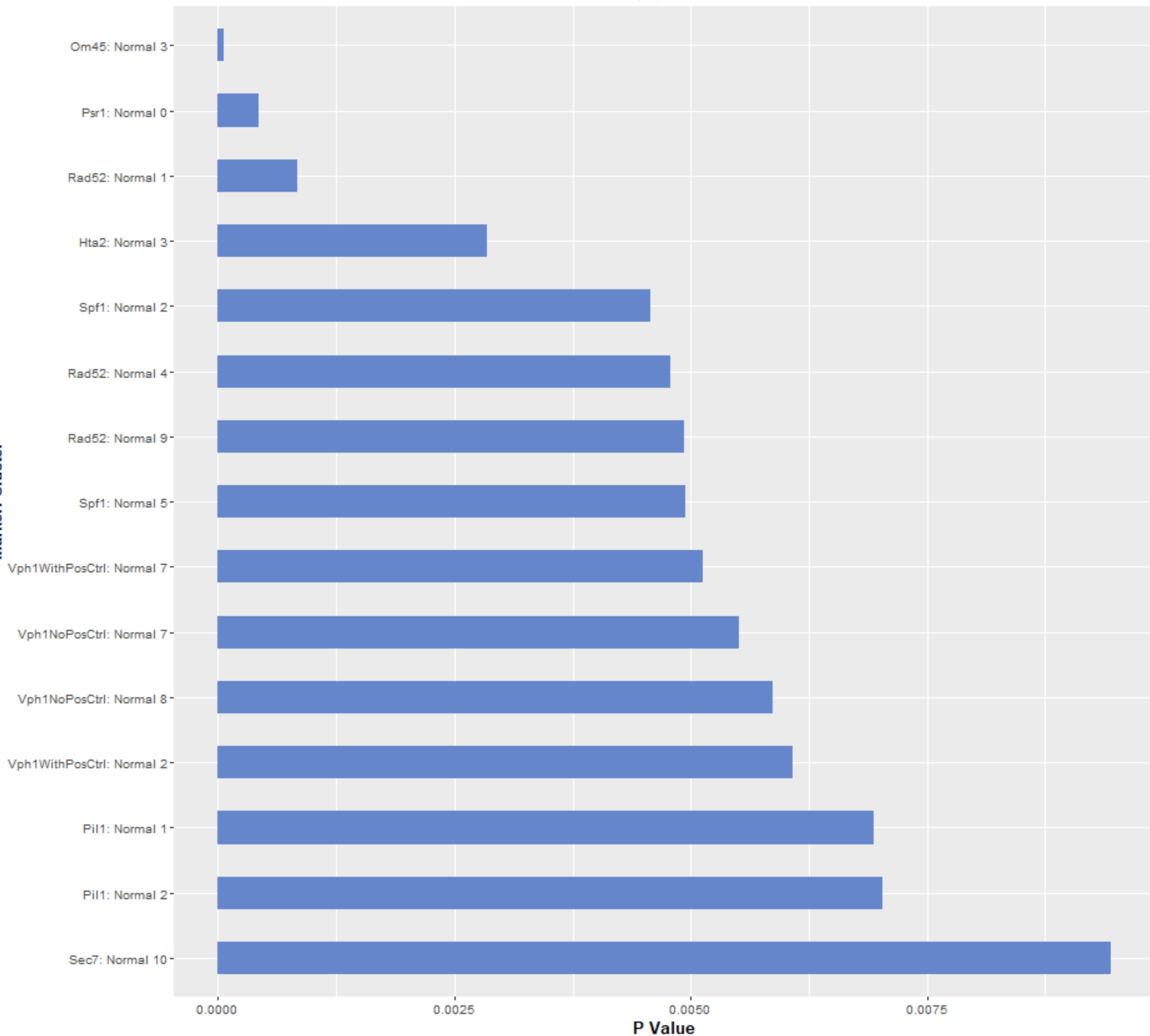
Marker: Cluster



# invasive growth in response to glucose limitation

With AreaShape | Ordered Gene Set

Marker: Cluster



# ion transport

With AreaShape | Ordered Gene Set

Marker: Cluster

Om45: Normal 3

0.00000

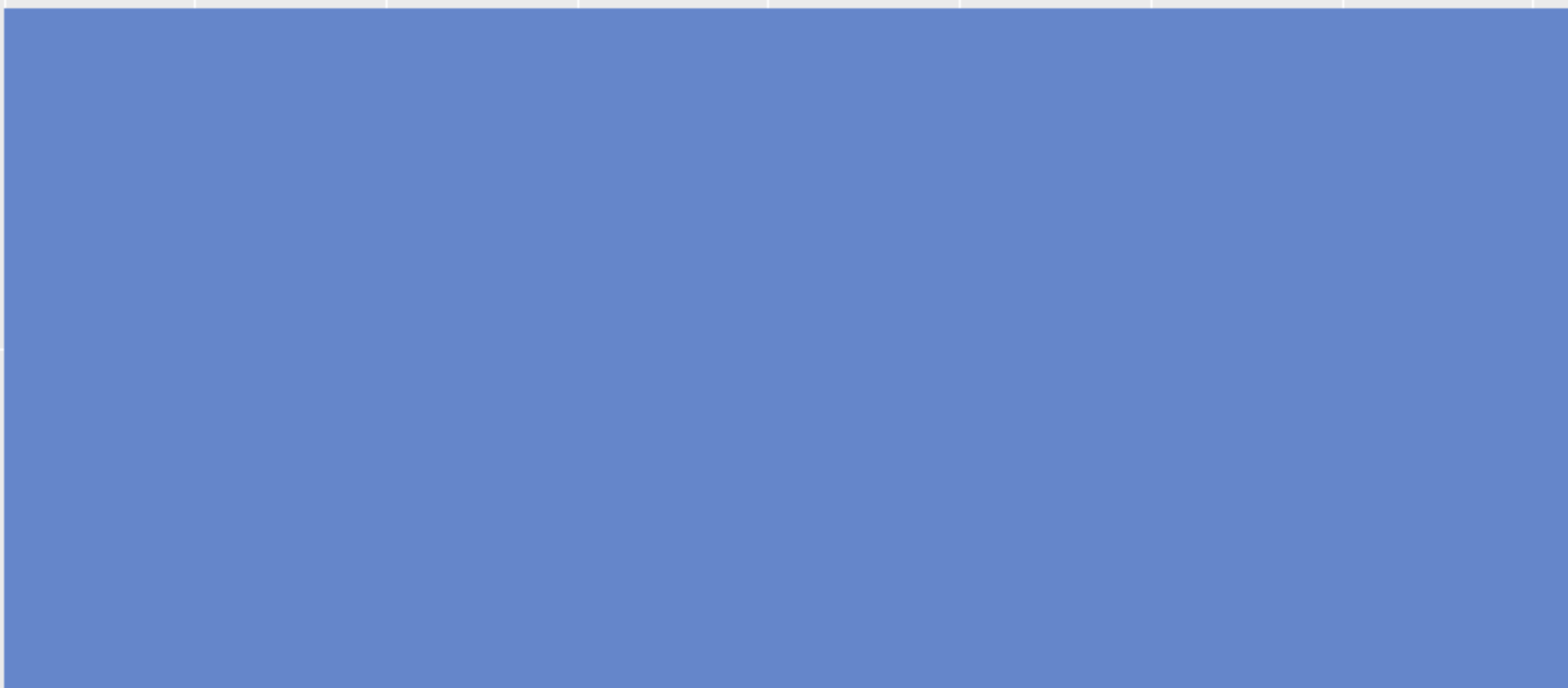
0.00025

0.00050

0.00075

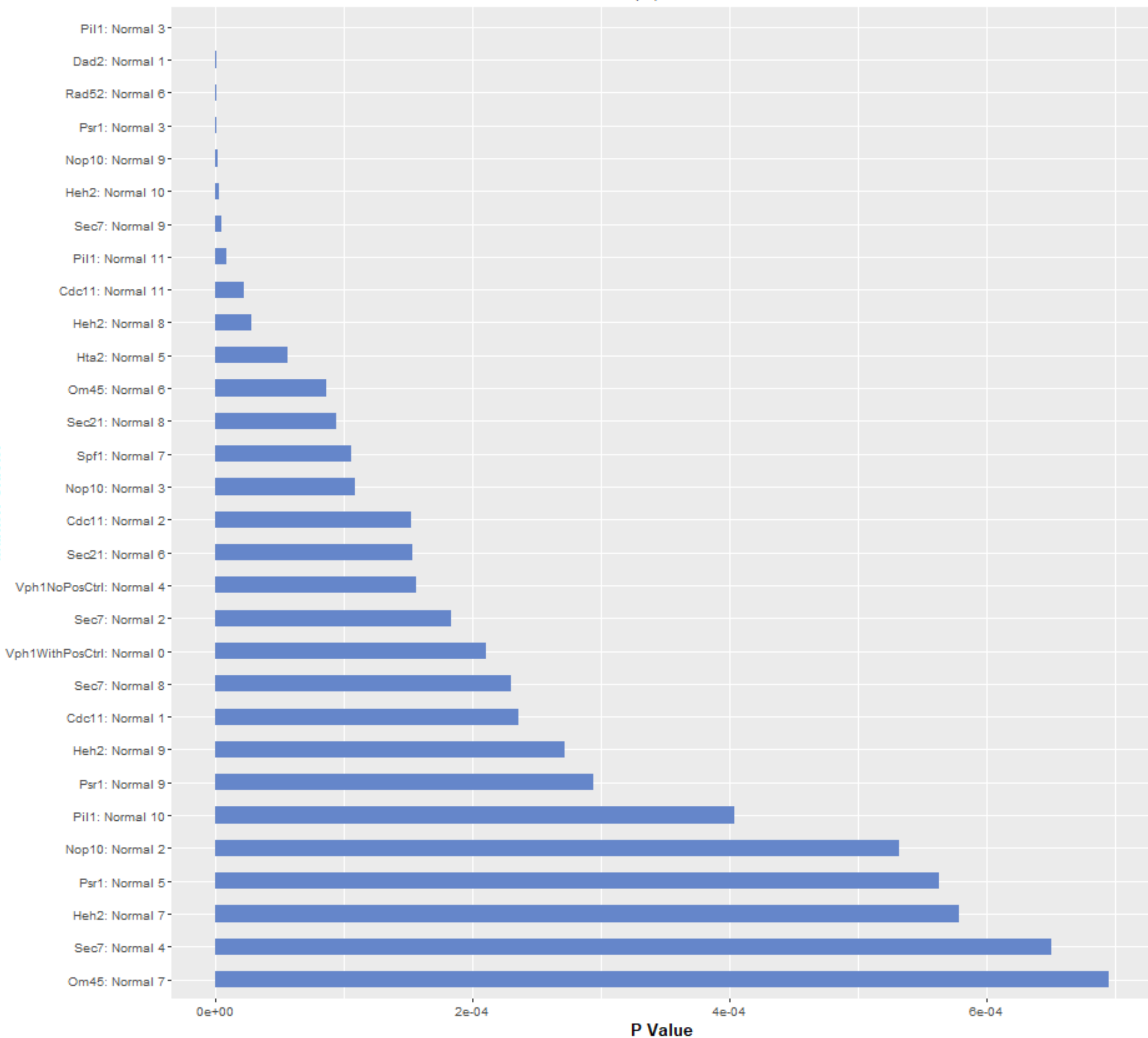
0.00100

P Value

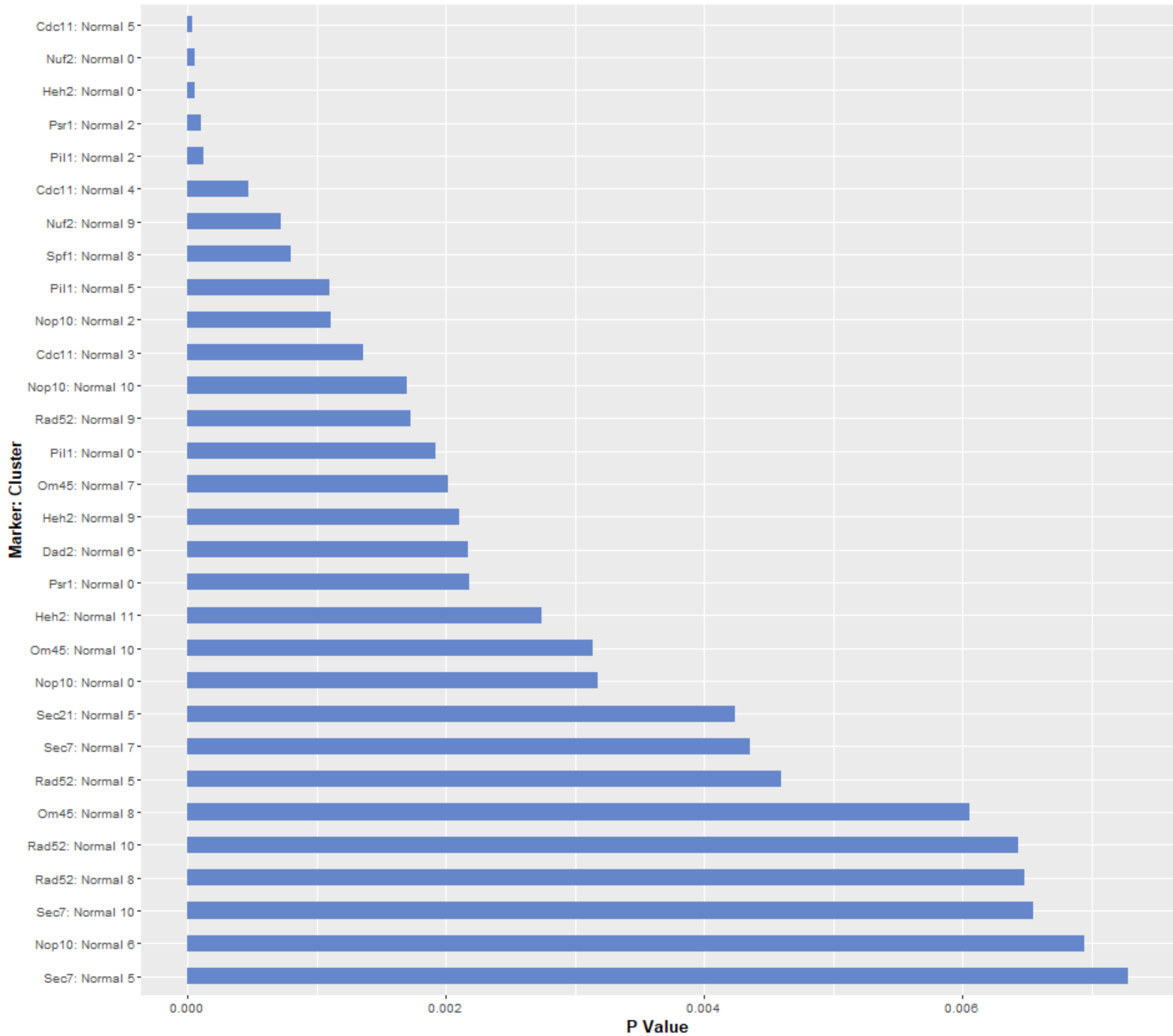


**lipid metabolic process**  
With AreaShape | Ordered Gene Set

Marker: Cluster



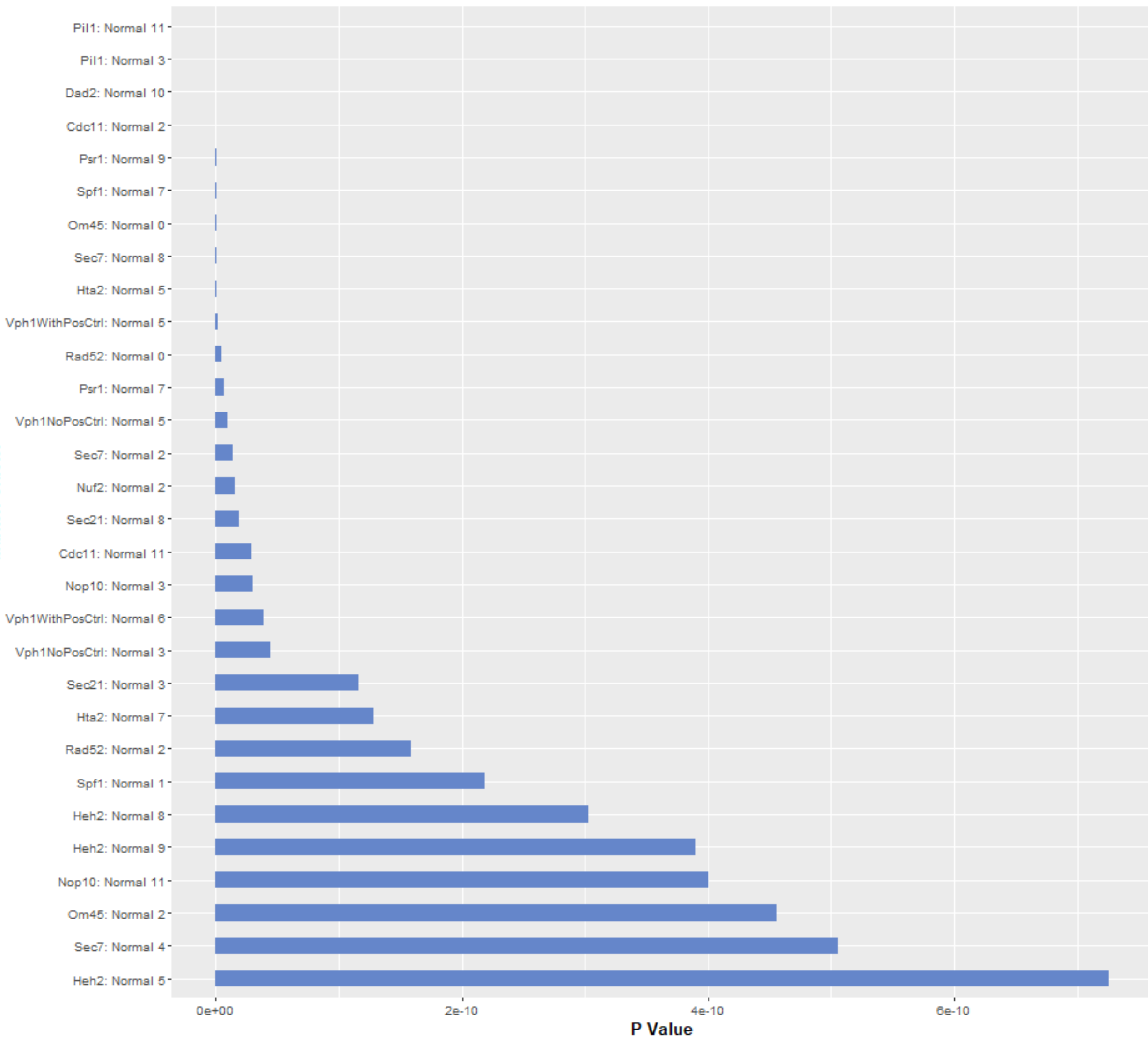
**meiotic cell cycle**  
With AreaShape | Ordered Gene Set



# membrane fusion

With AreaShape | Ordered Gene Set

Marker: Cluster



# mitochondrion organization

With AreaShape | Ordered Gene Set

Marker: Cluster

Om45: Normal 3

Heh2: Normal 9

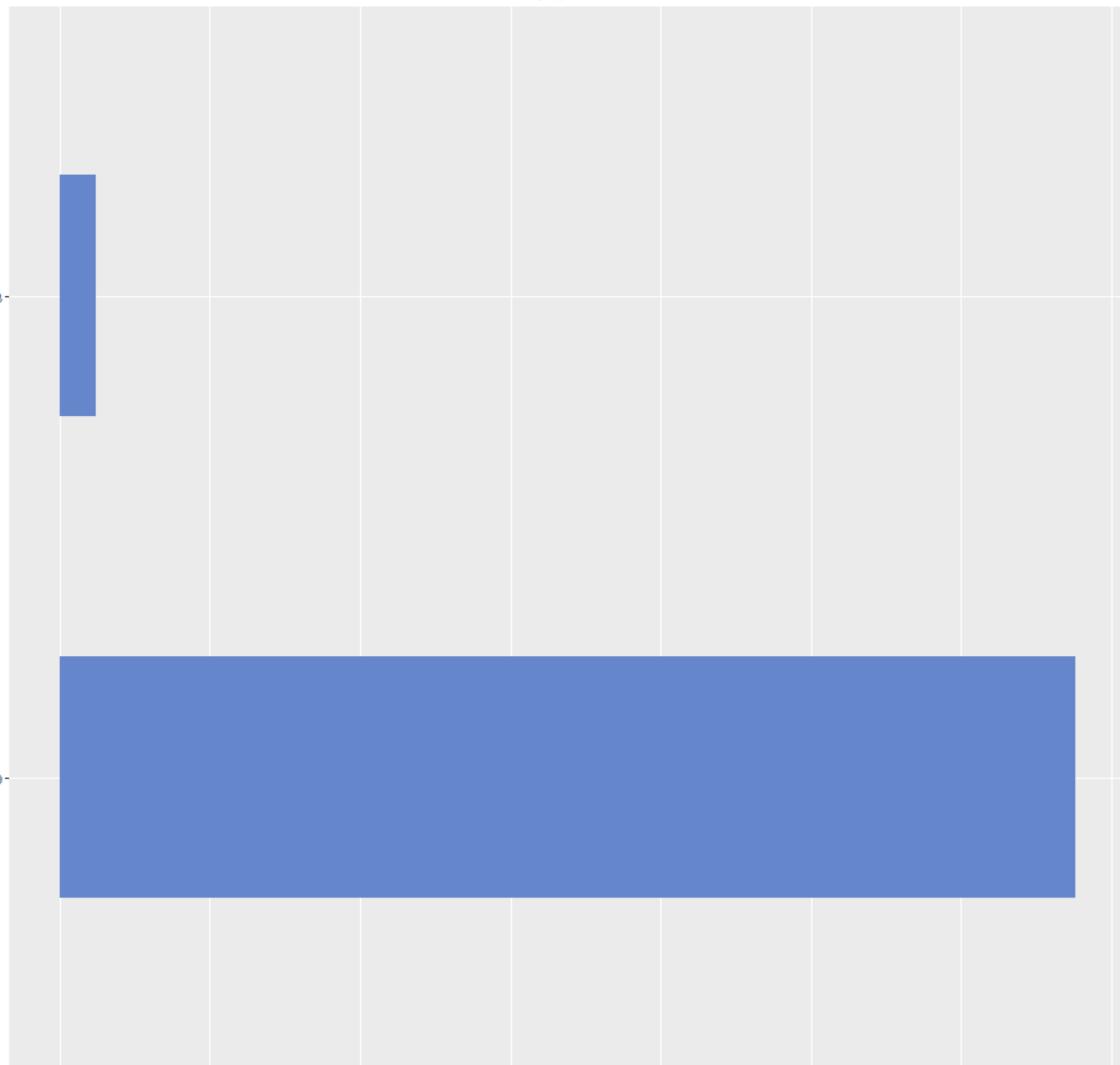
0.000

0.001

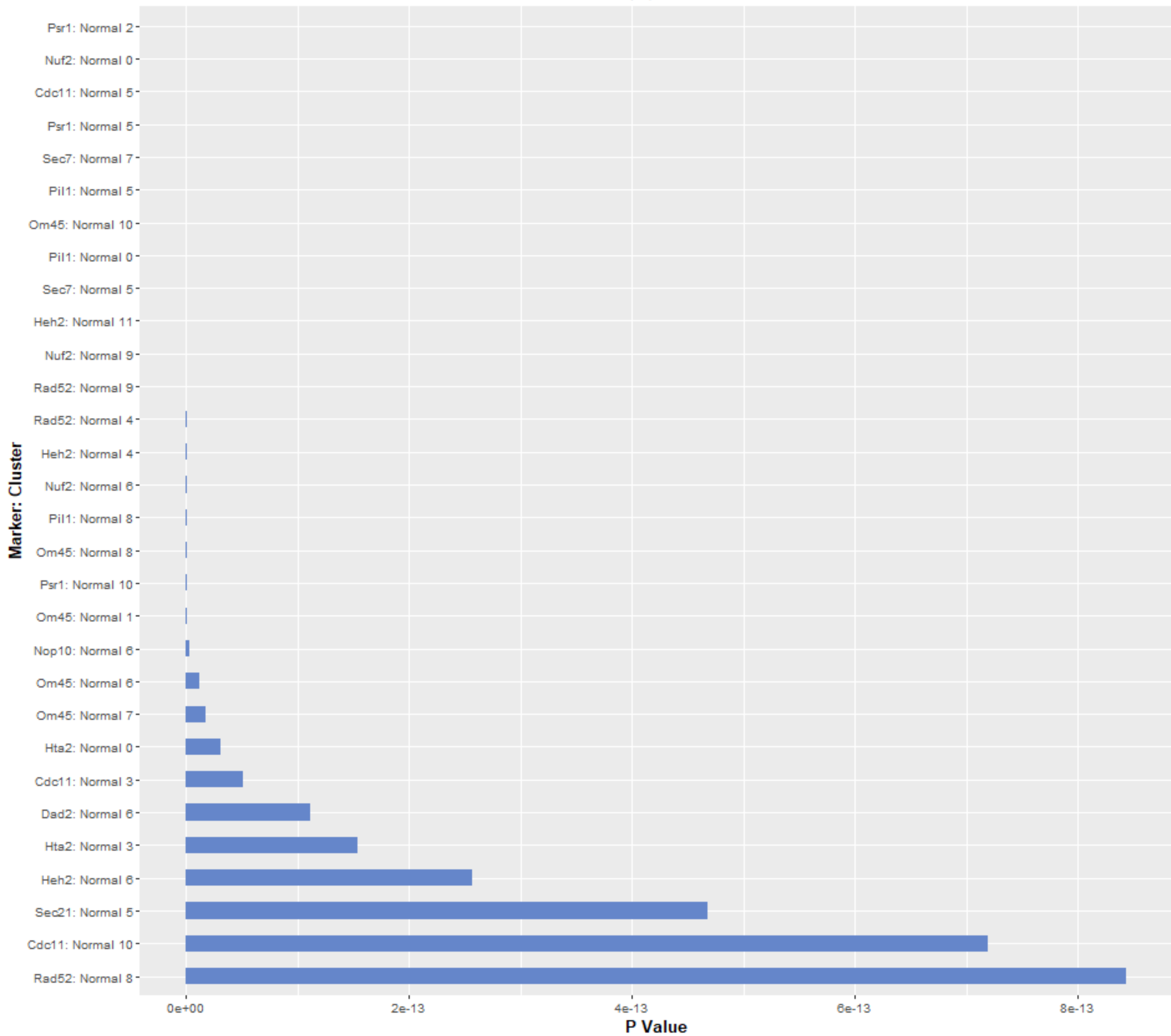
0.002

0.003

P Value



**mitotic cell cycle**  
With AreaShape | Ordered Gene Set





# monocarboxylic acid metabolic process

With AreaShape | Ordered Gene Set

Marker: Cluster

Psr1: Normal 7

0.000

0.002

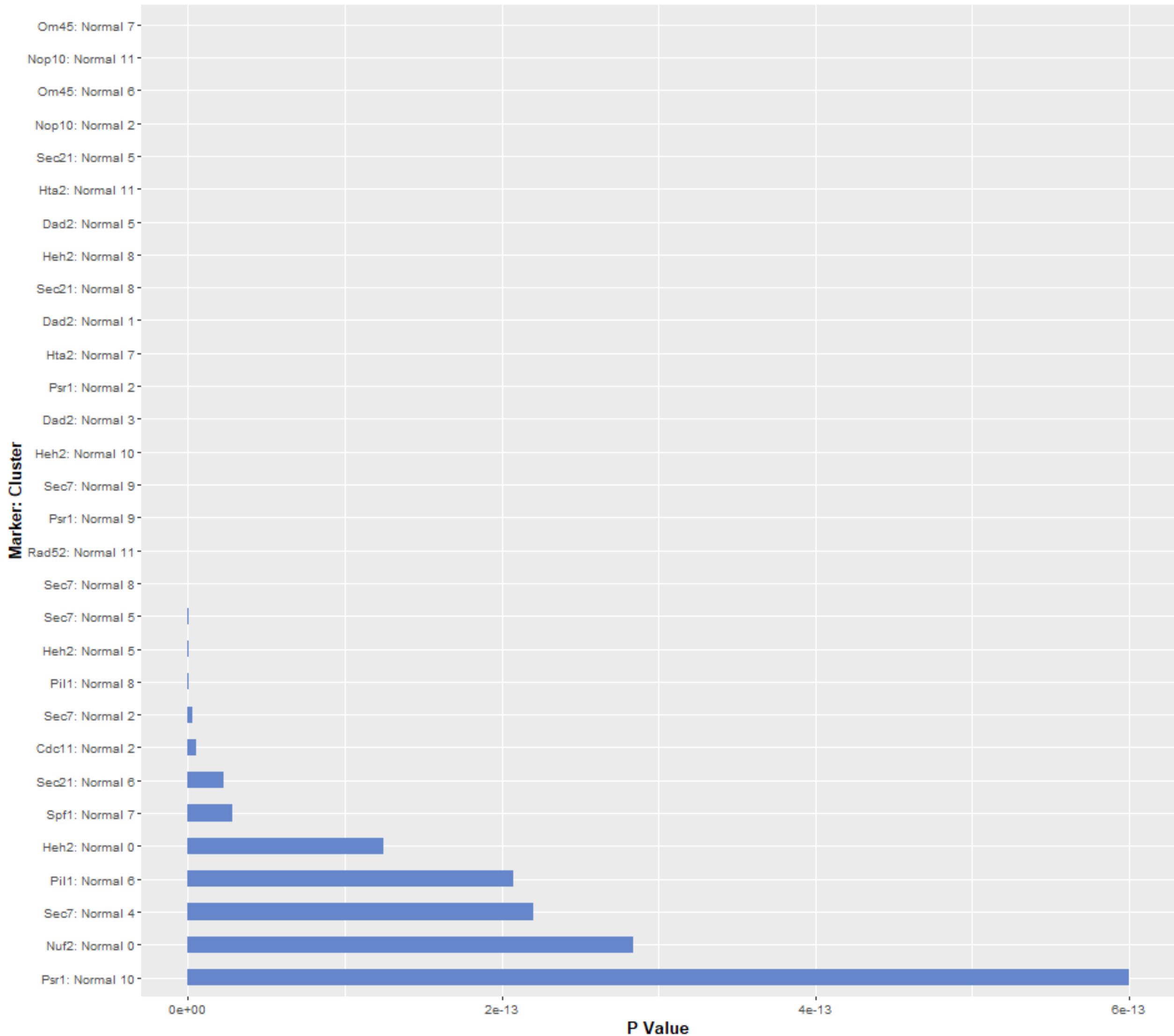
P Value

0.004



# mRNA processing

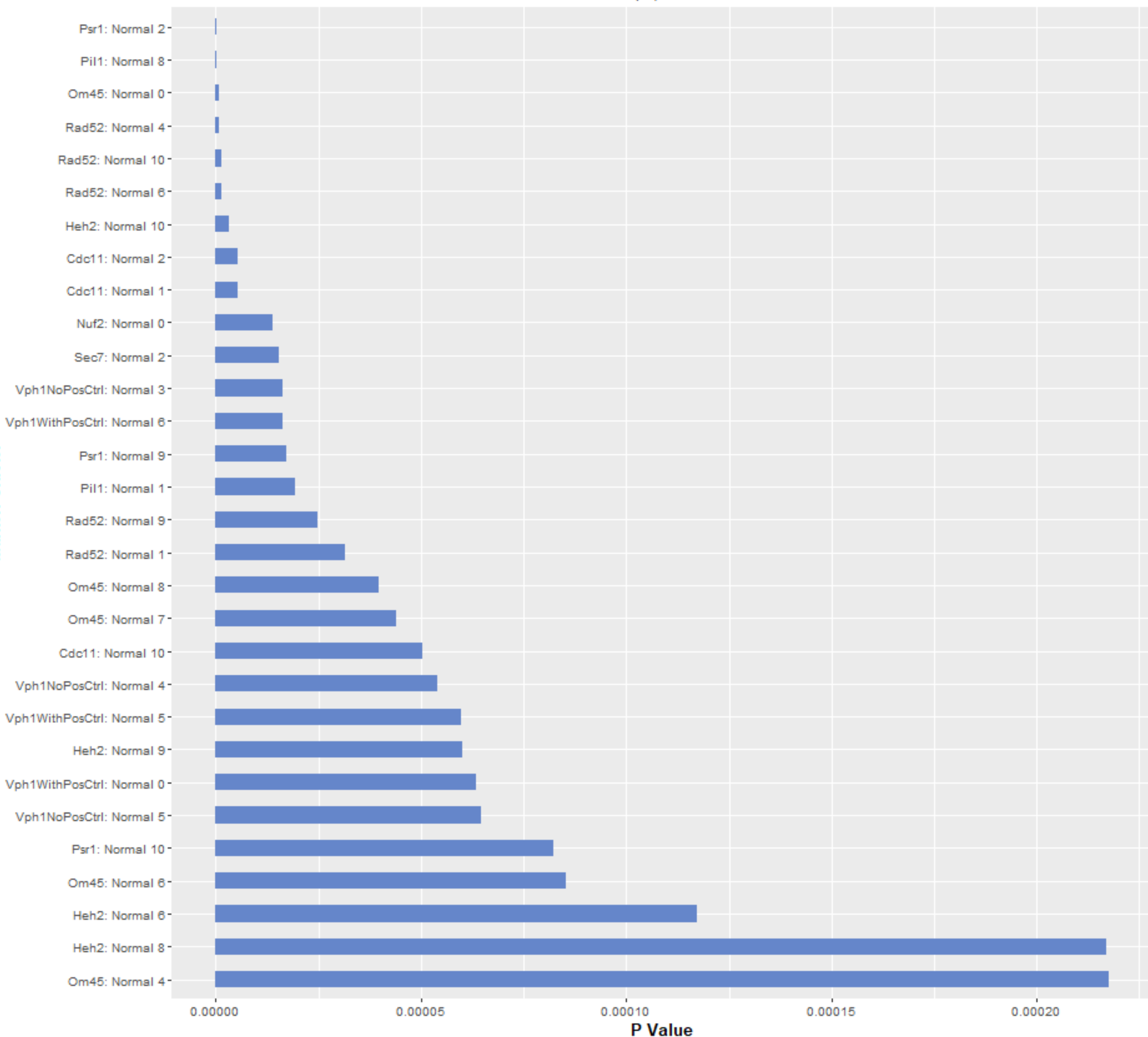
With AreaShape | Ordered Gene Set



# nuclear transport

With AreaShape | Ordered Gene Set

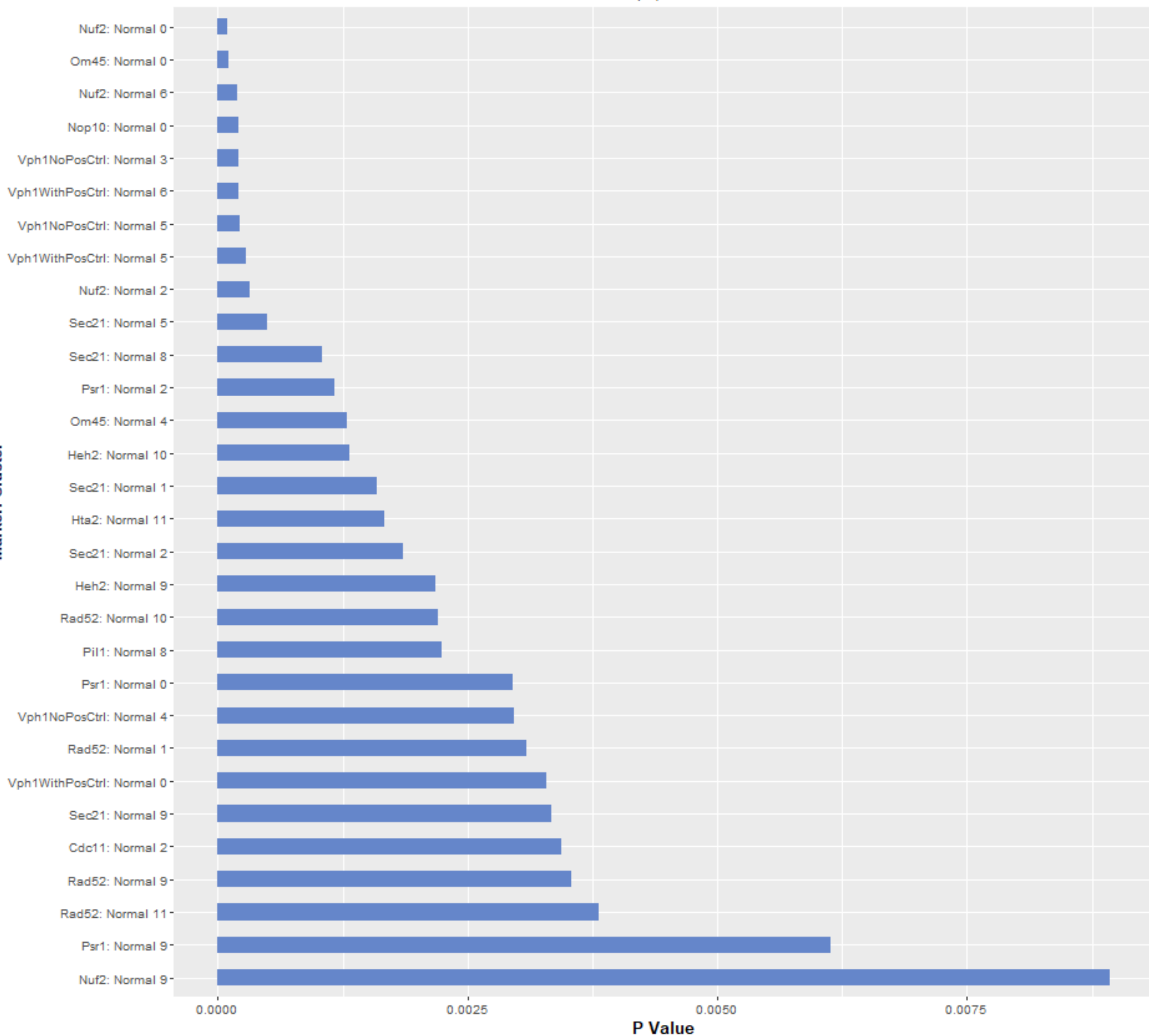
Marker: Cluster



# nucleobase-containing compound transport

With AreaShape | Ordered Gene Set

Marker: Cluster



# nucleobase-containing small molecule metabolic process

With AreaShape | Ordered Gene Set

Marker: Cluster

Om45: Normal 3

Dad2: Normal 7

0.000

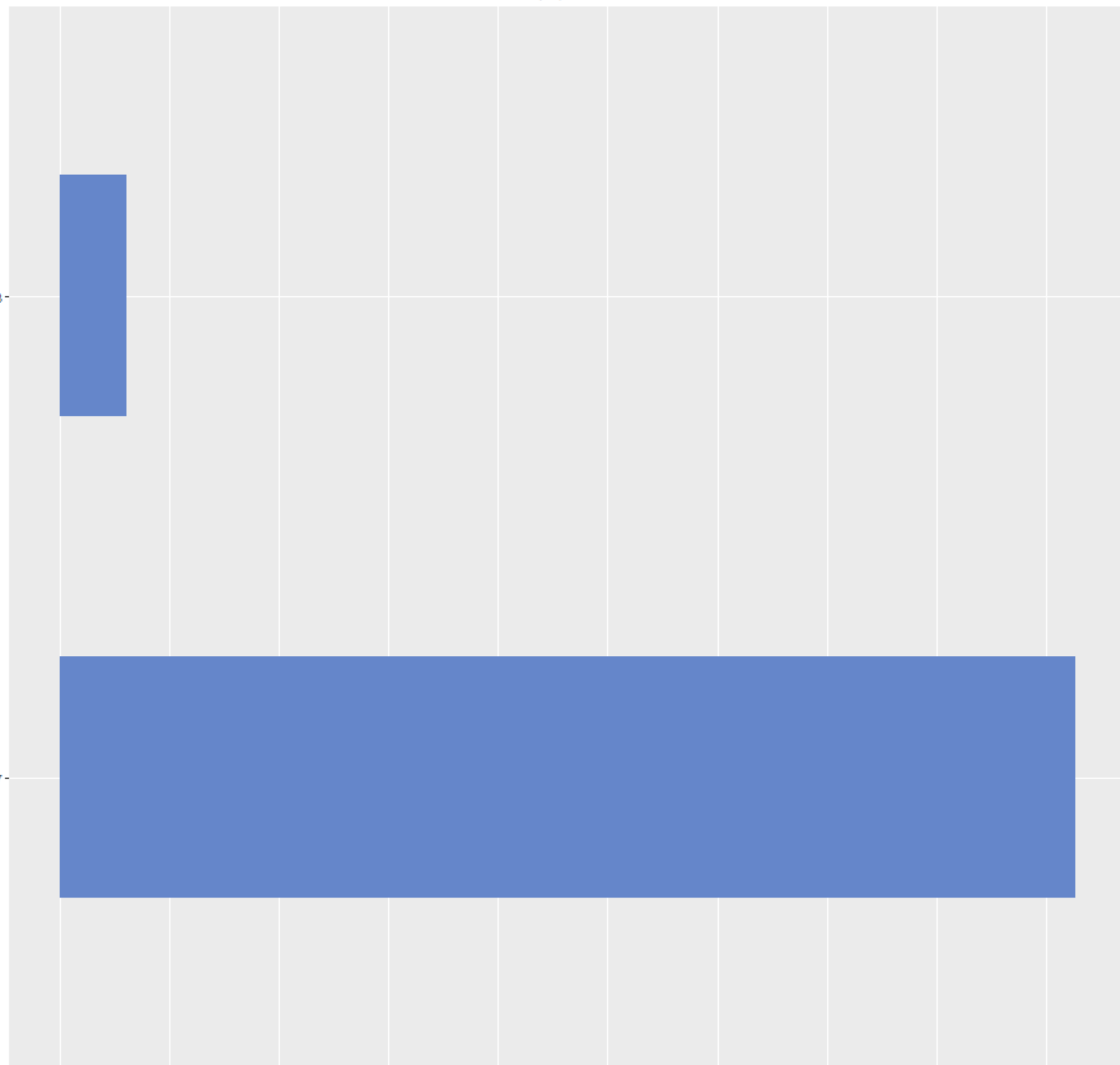
0.001

0.002

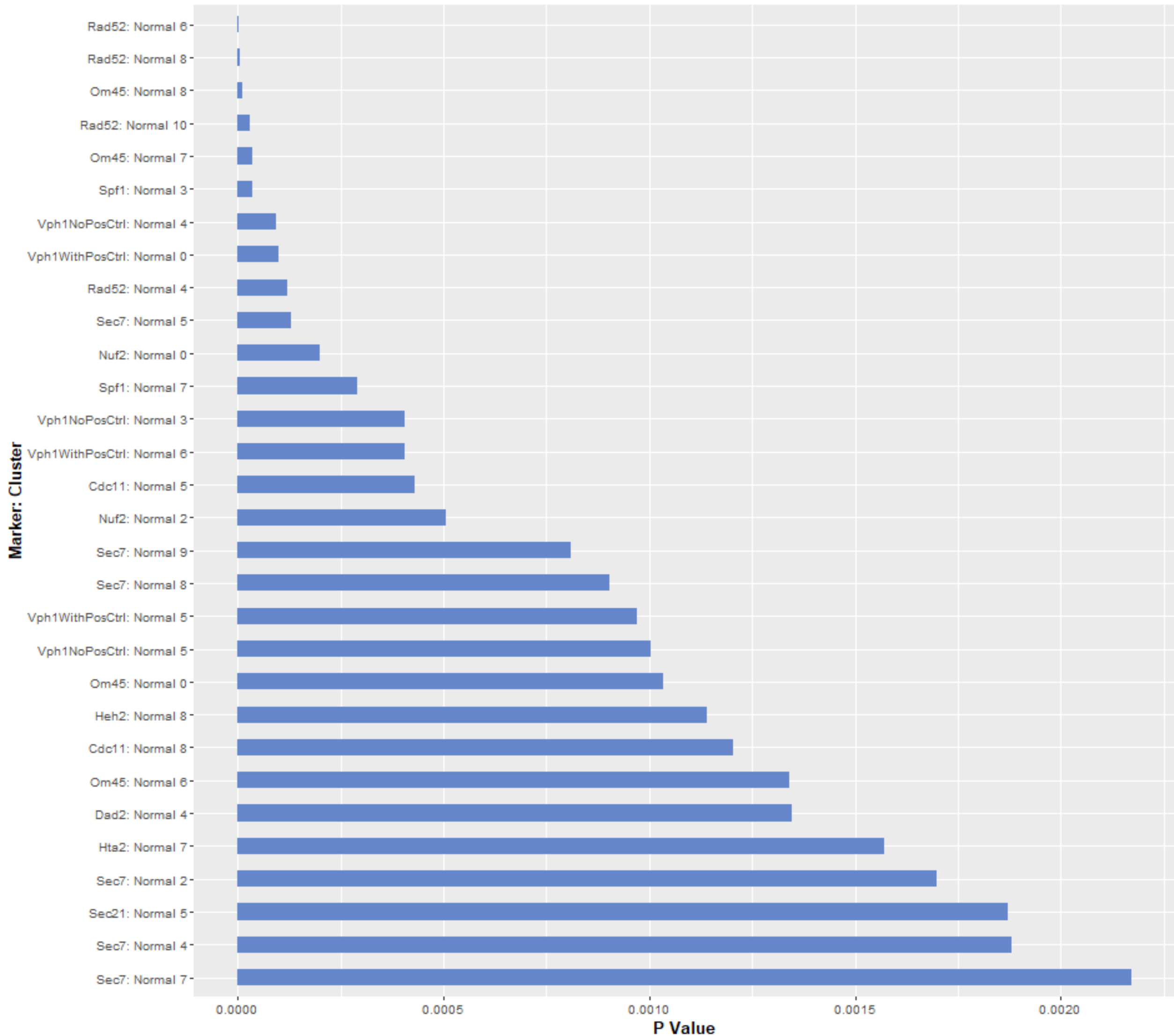
0.003

0.004

P Value



nucleus organization  
With AreaShape | Ordered Gene Set



# oligosaccharide metabolic process

With AreaShape | Ordered Gene Set

Marker: Cluster

Pil1: Normal 6

Nuf2: Normal 6

0.000

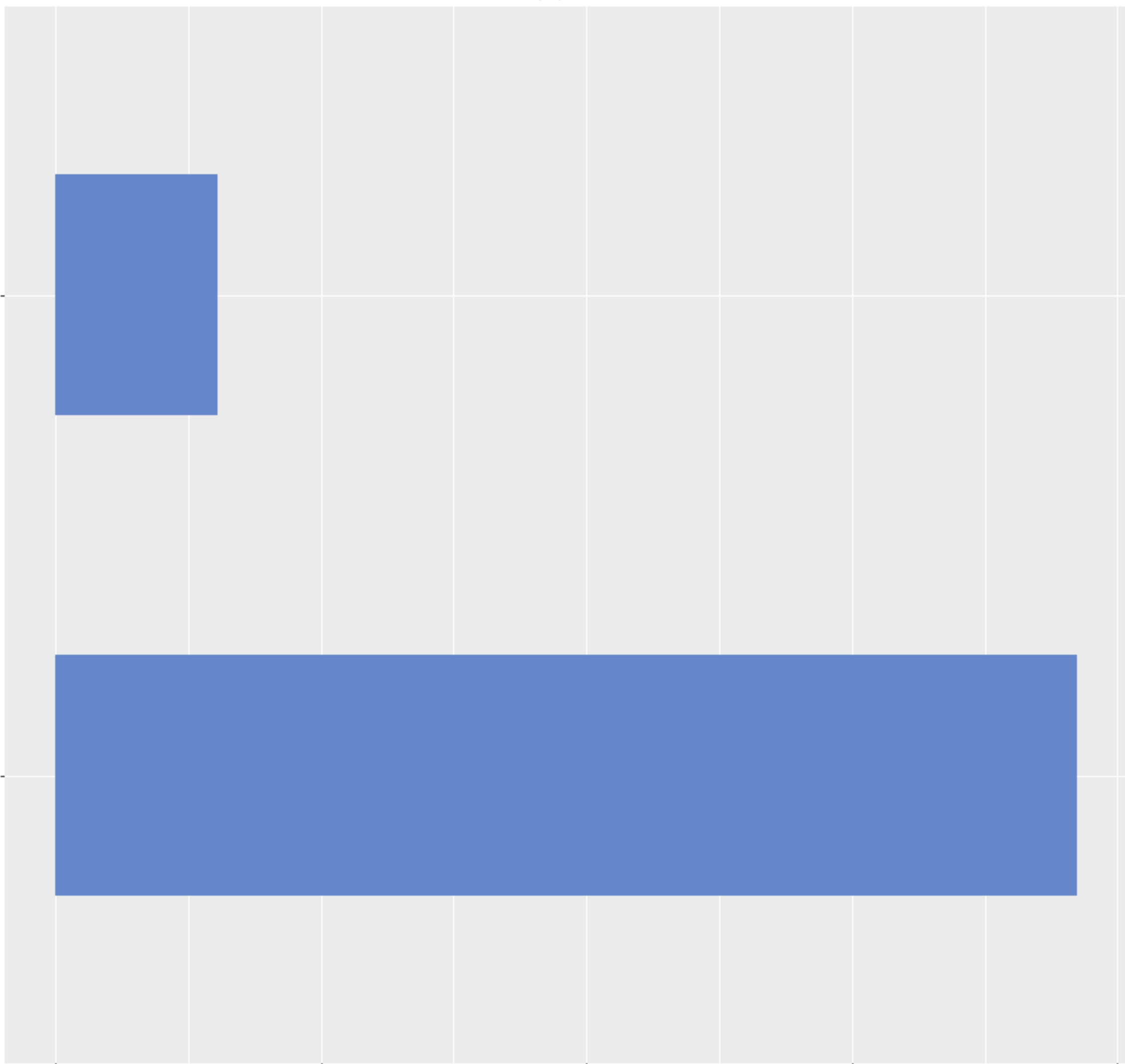
0.002

0.004

0.006

0.008

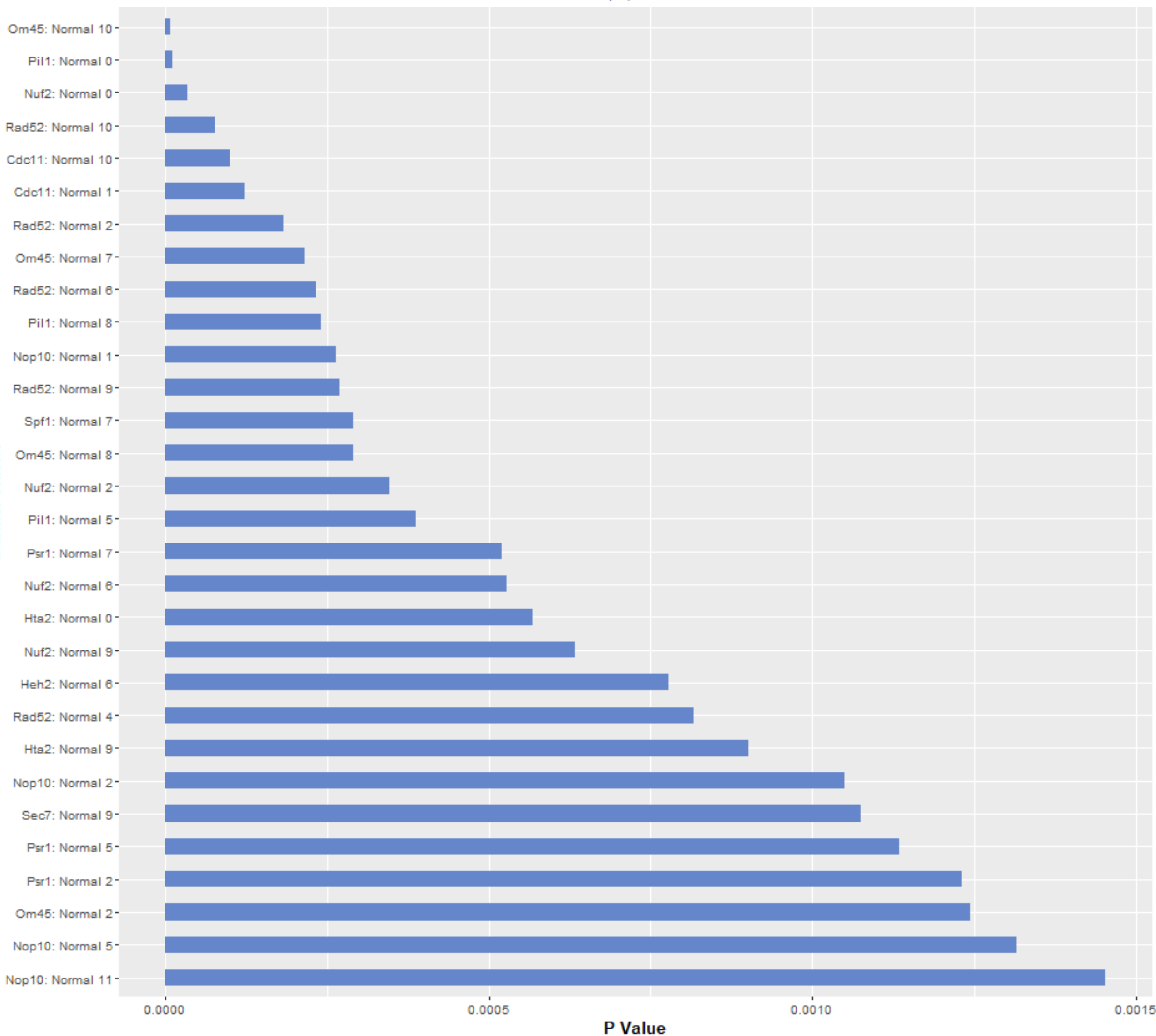
P Value



# organelle assembly

With AreaShape | Ordered Gene Set

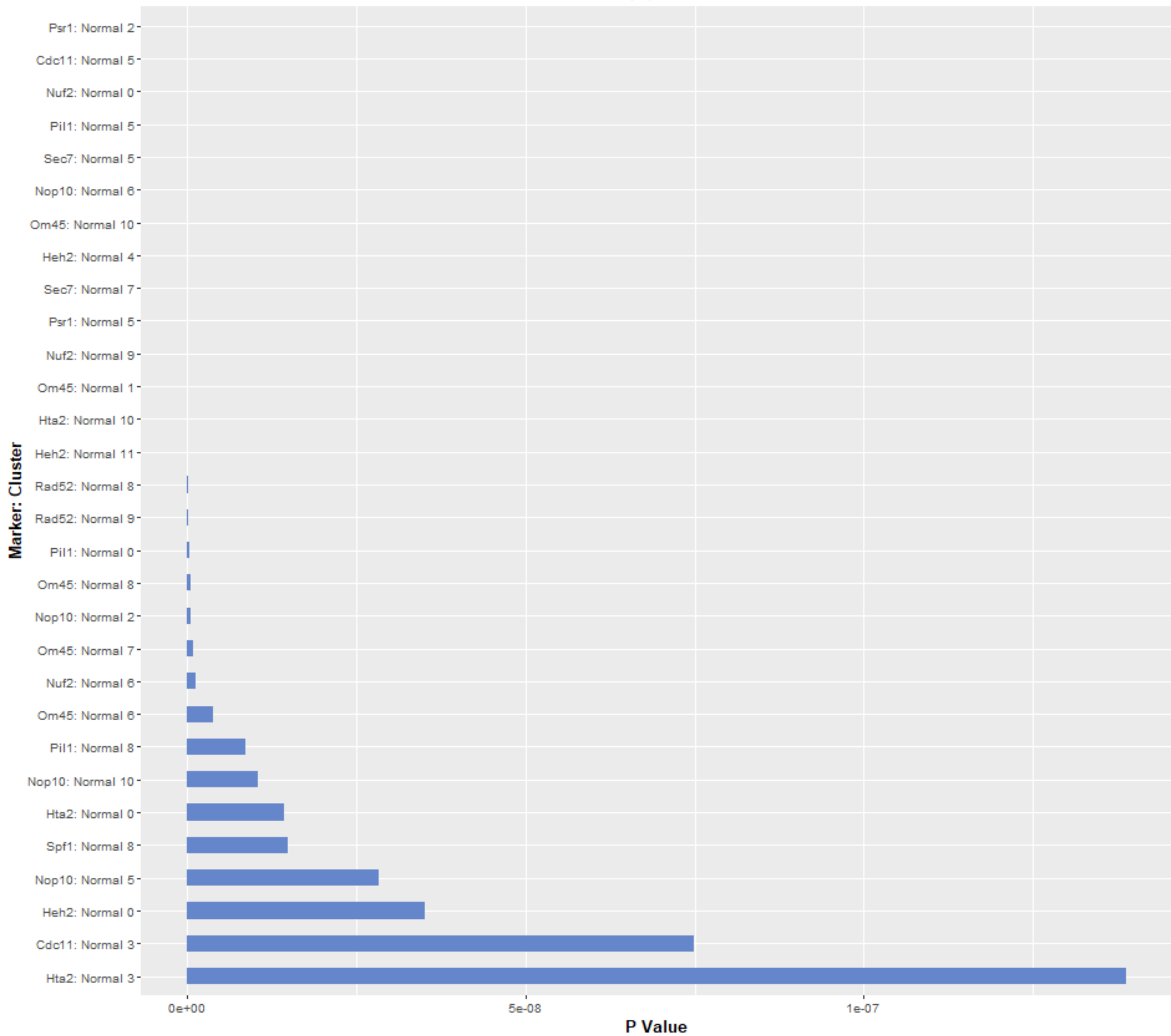
Marker: Cluster





# organelle fission

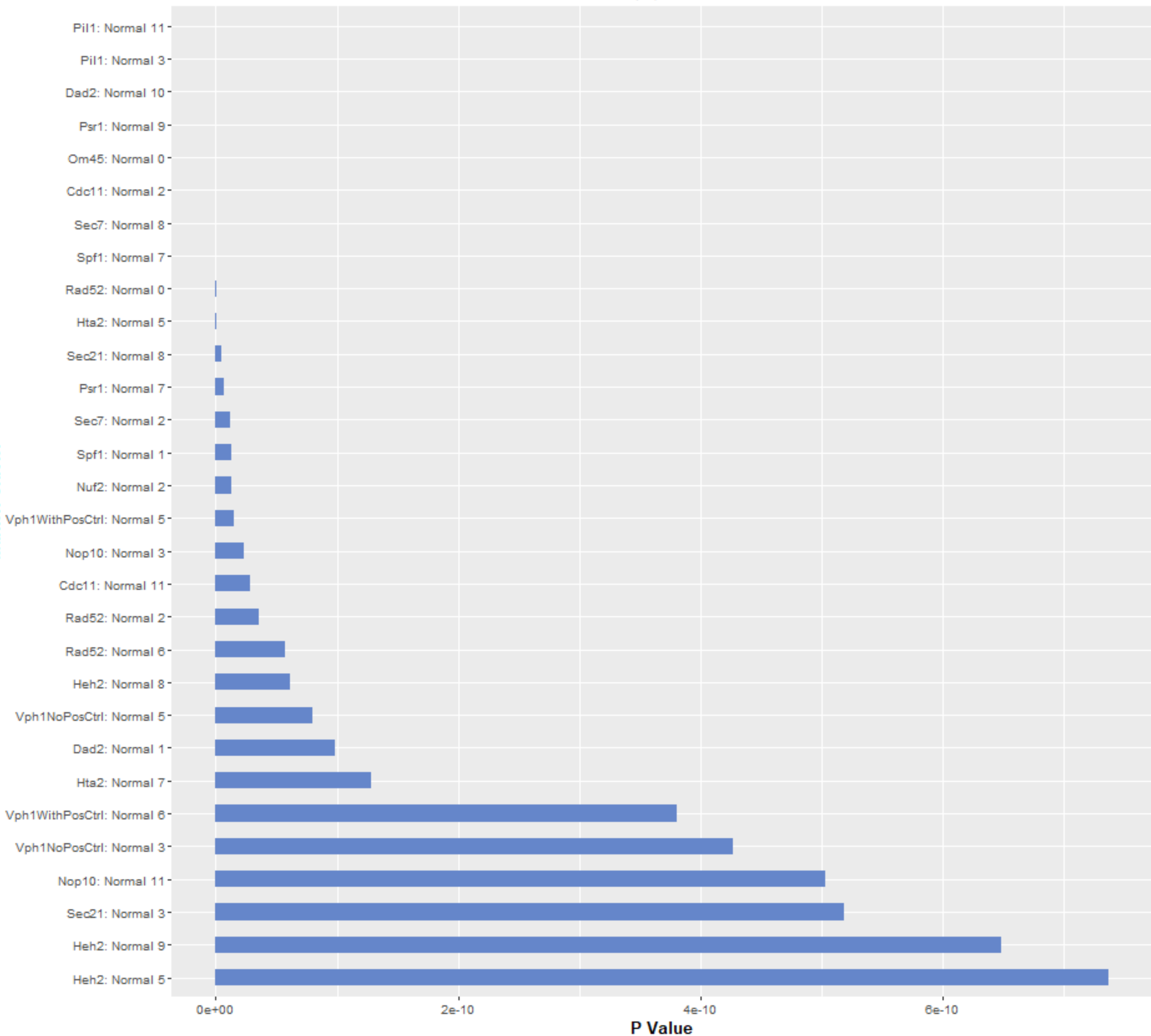
With AreaShape | Ordered Gene Set



# organelle fusion

With AreaShape | Ordered Gene Set

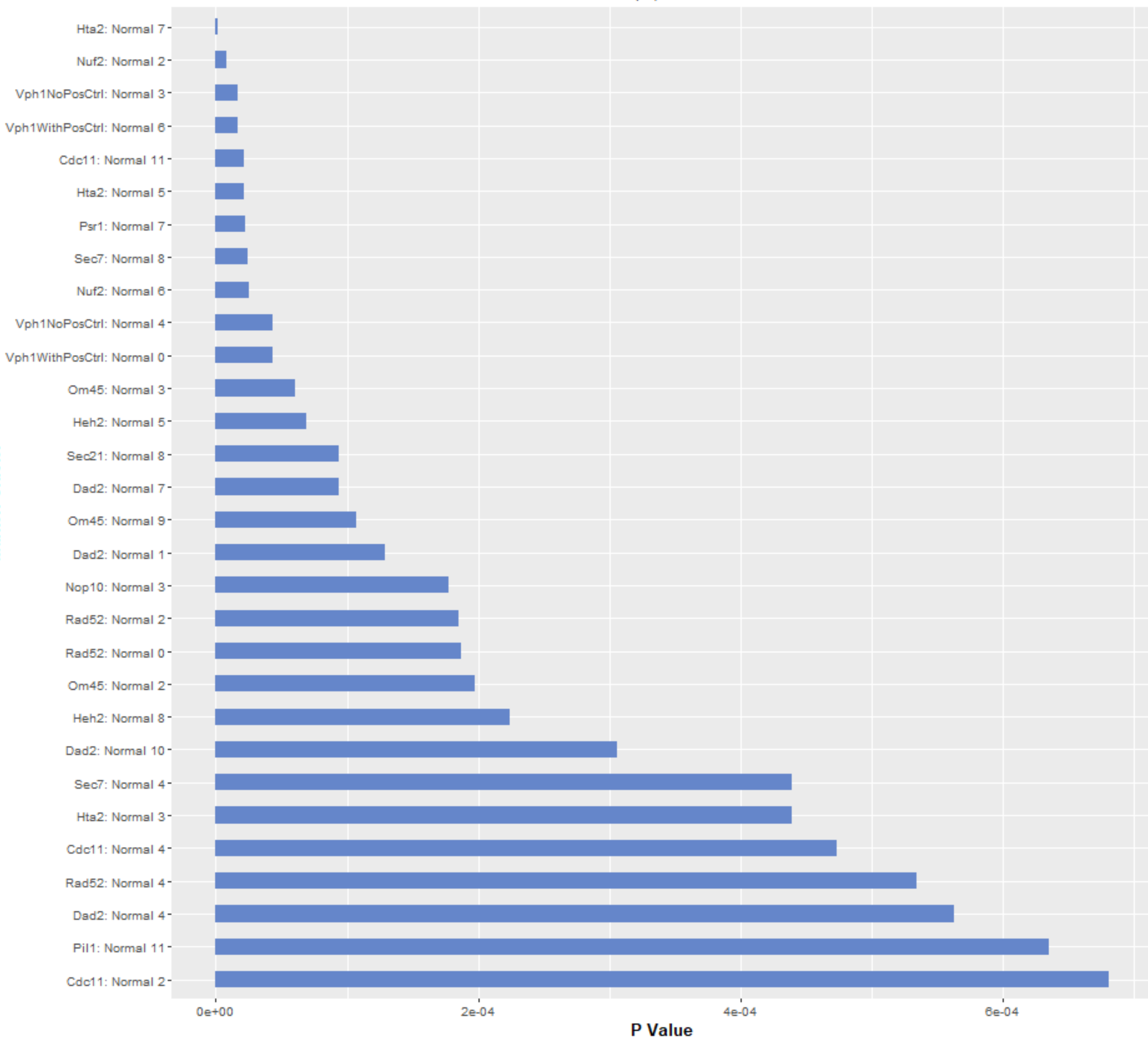
Marker: Cluster



# organelle inheritance

With AreaShape | Ordered Gene Set

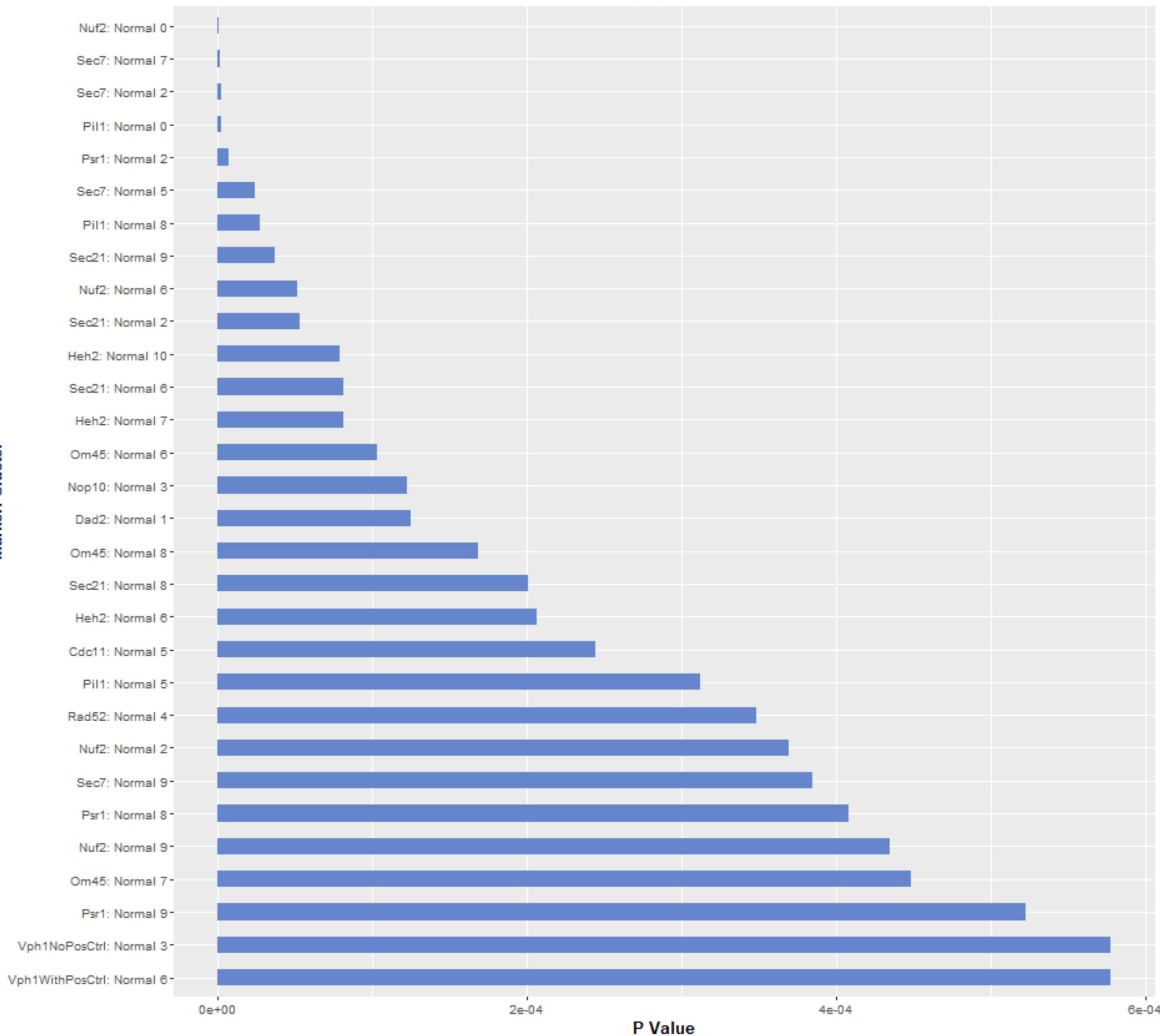
Marker: Cluster



# peptidyl-amino acid modification

With AreaShape | Ordered Gene Set

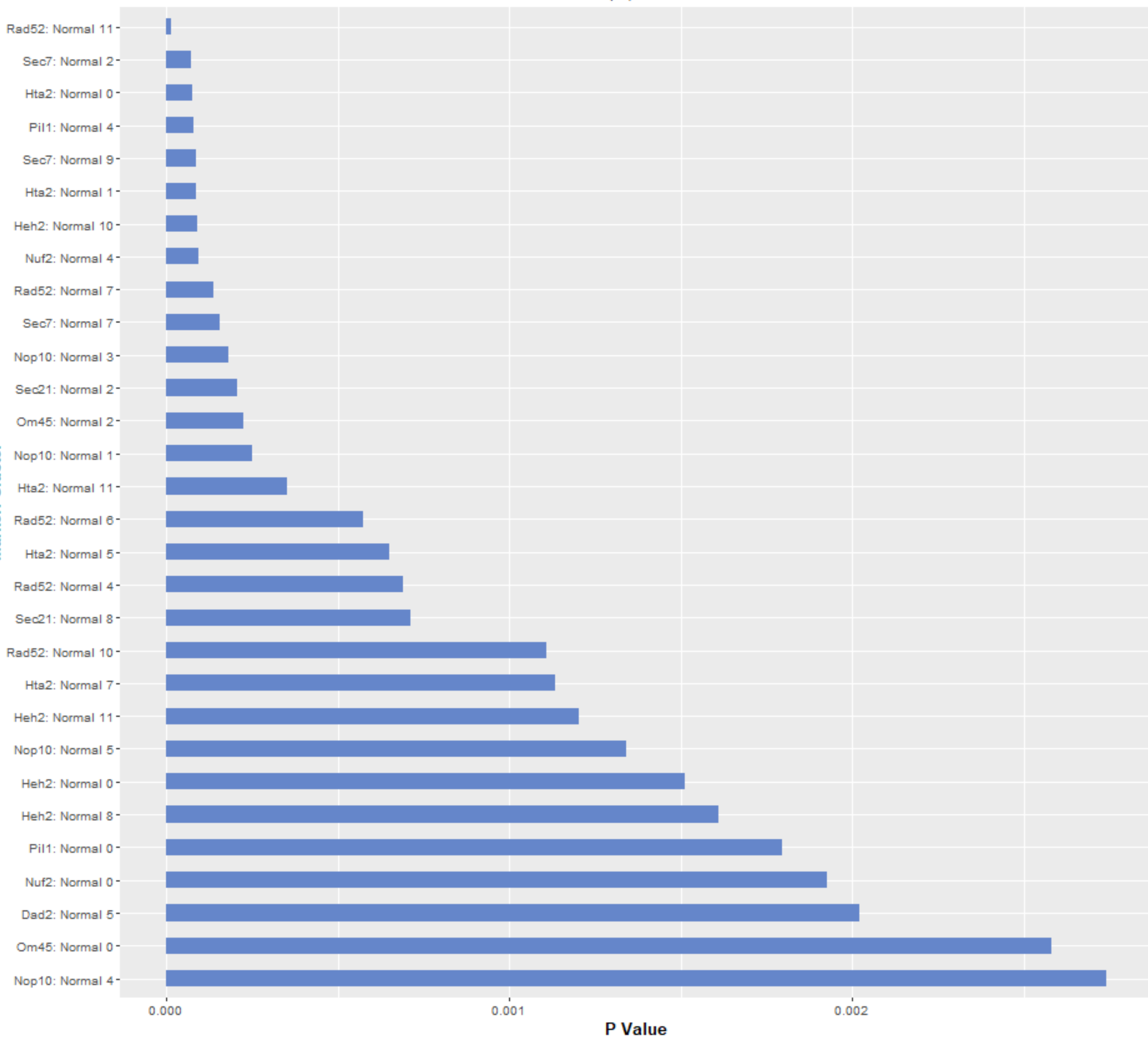
Marker: Cluster



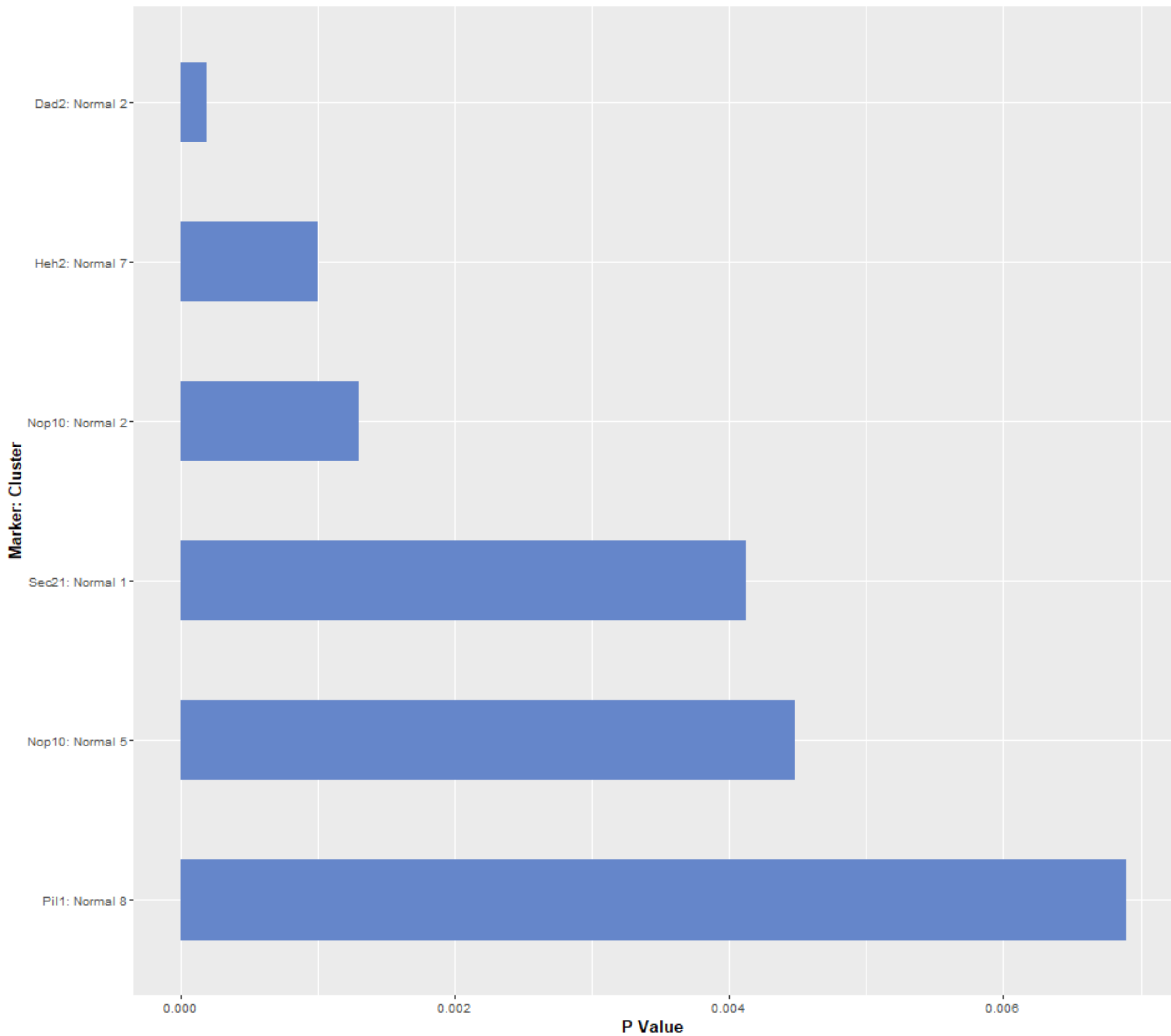
# protein acylation

With AreaShape | Ordered Gene Set

Marker: Cluster

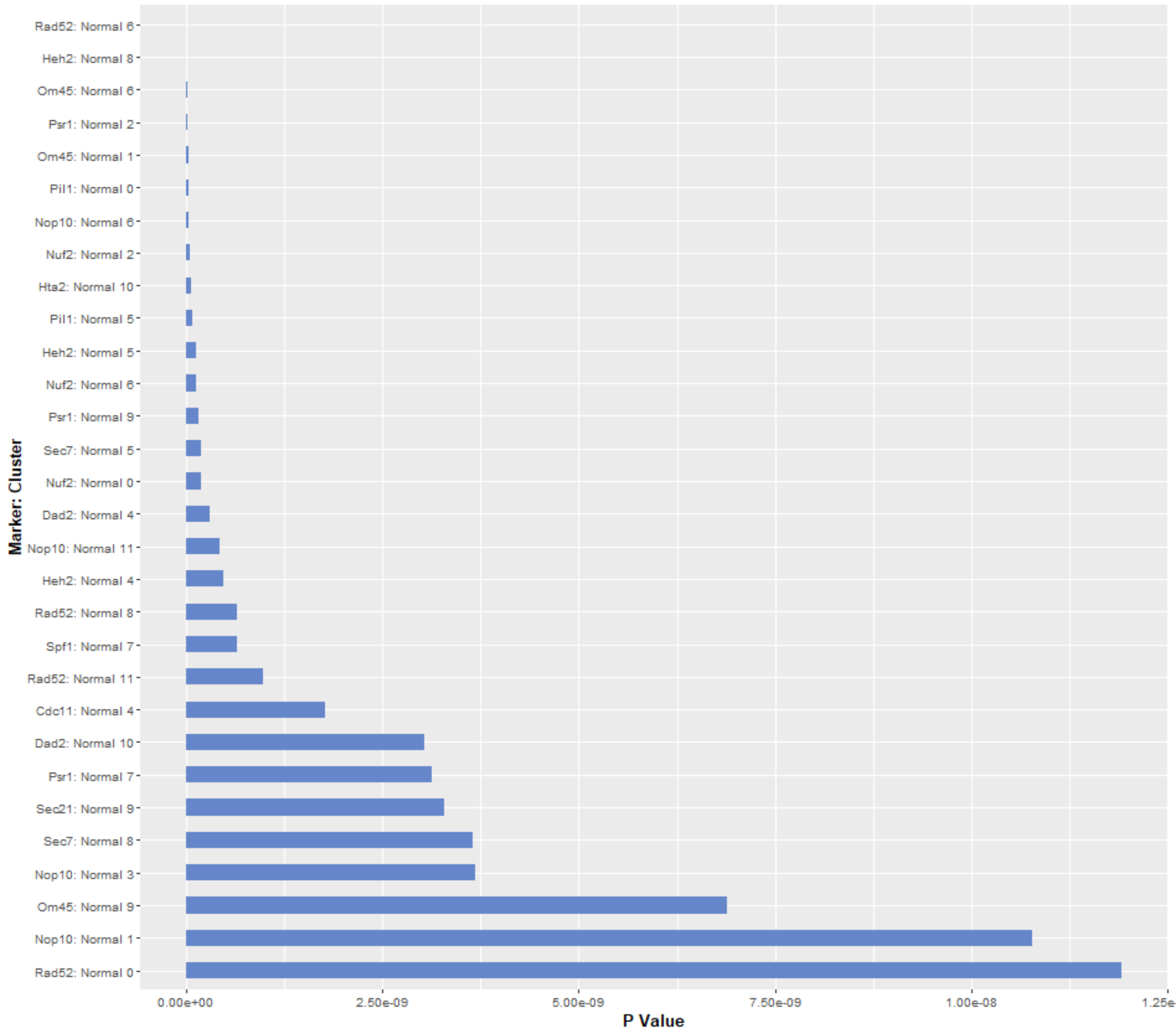


**protein alkylation**  
With AreaShape | Ordered Gene Set



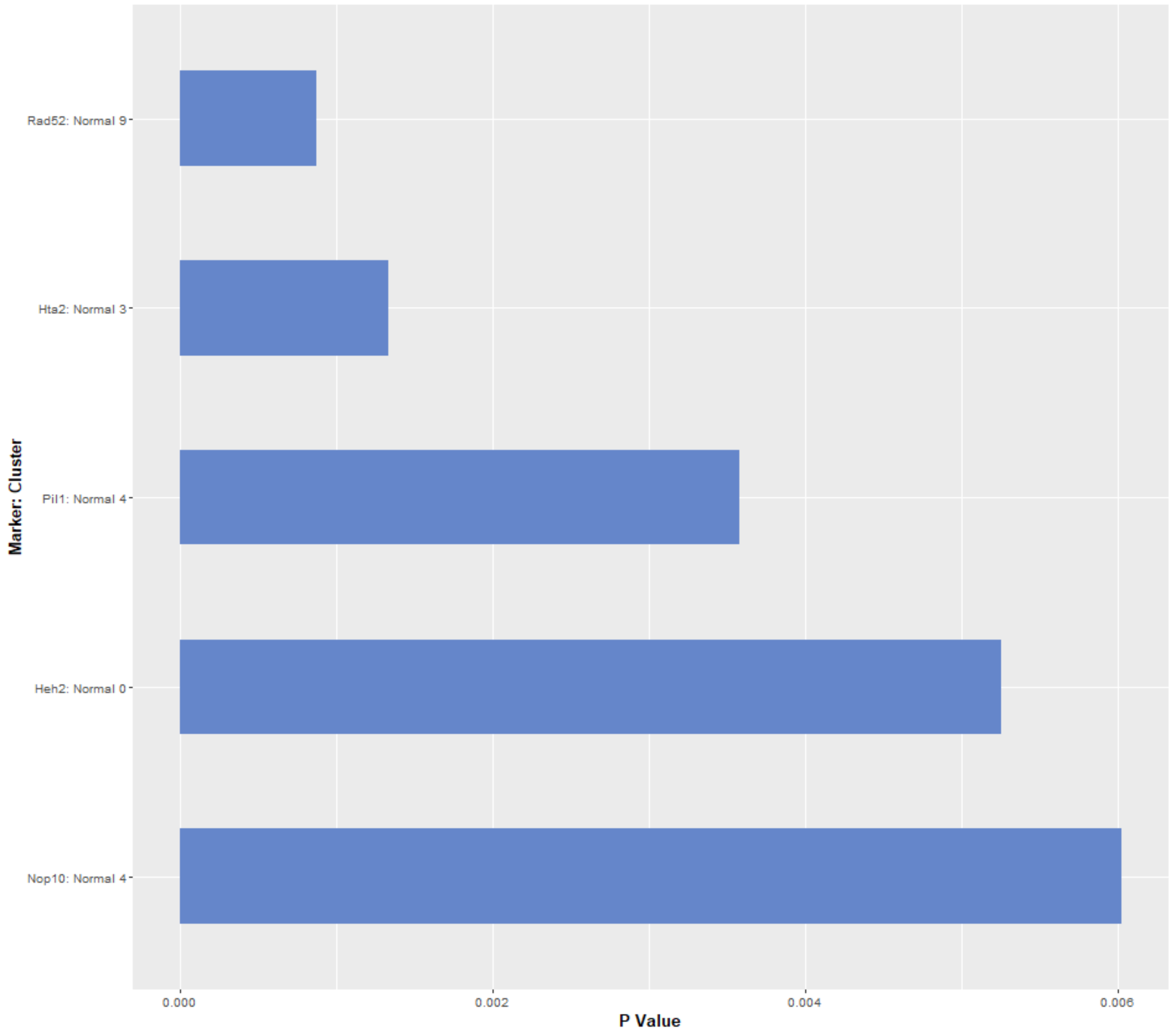
protein complex biogenesis

With AreaShape | Ordered Gene Set



protein dephosphorylation

With AreaShape | Ordered Gene Set





# protein folding

With AreaShape | Ordered Gene Set

Marker: Cluster

Rad52: Normal 1

0.000

0.002

0.004

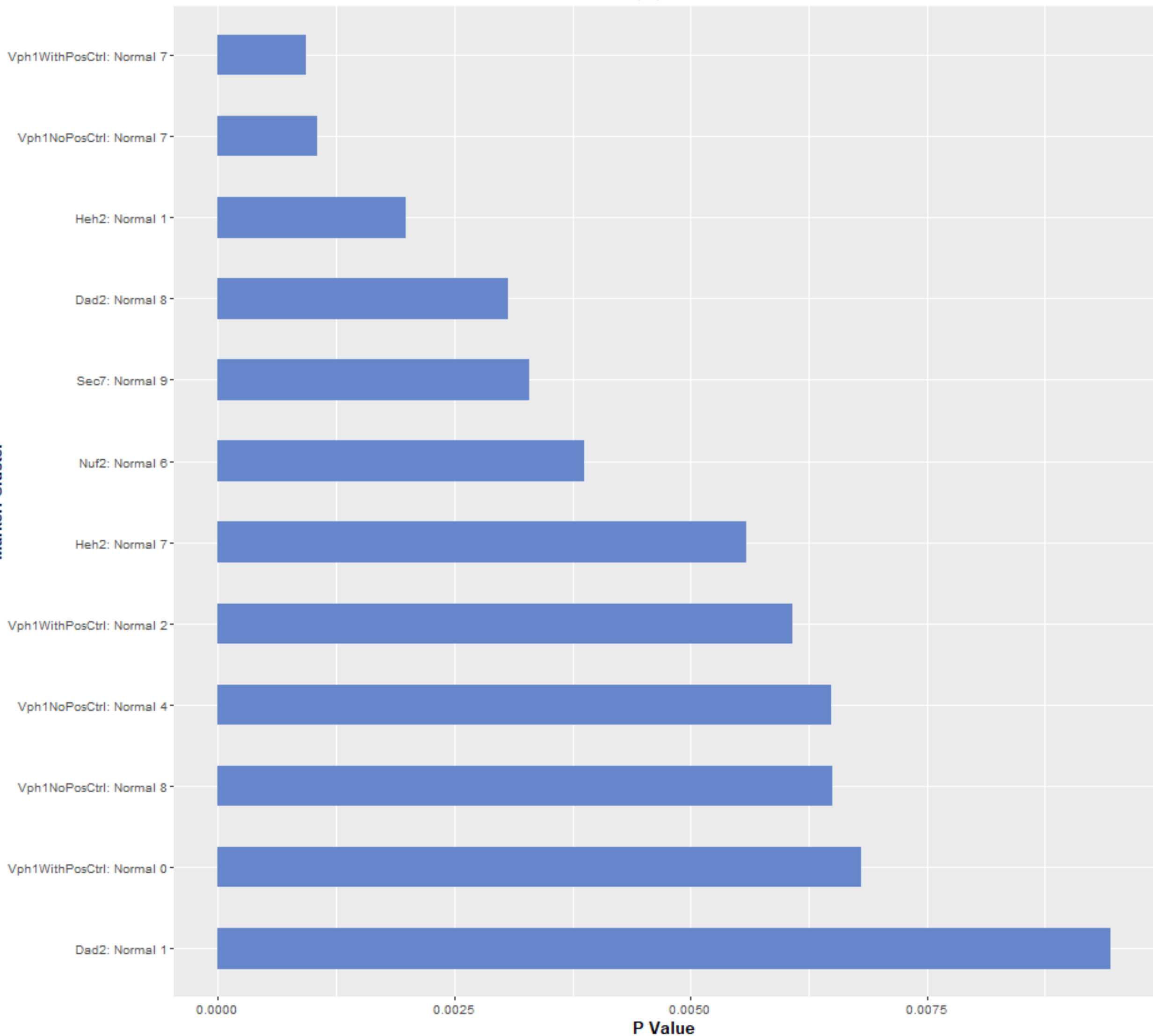
0.006

P Value



**protein glycosylation**  
With AreaShape | Ordered Gene Set

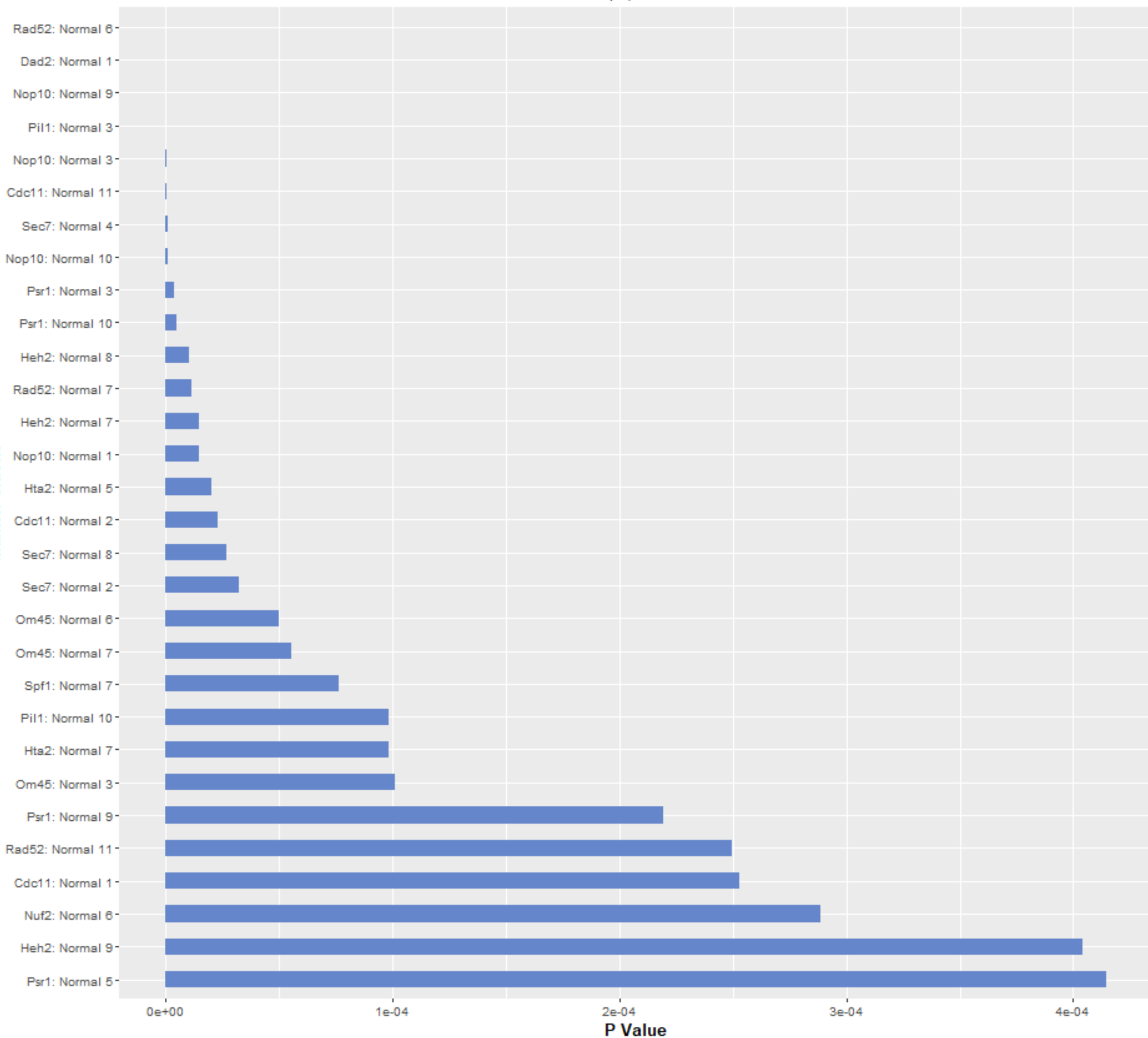
**Marker: Cluster**



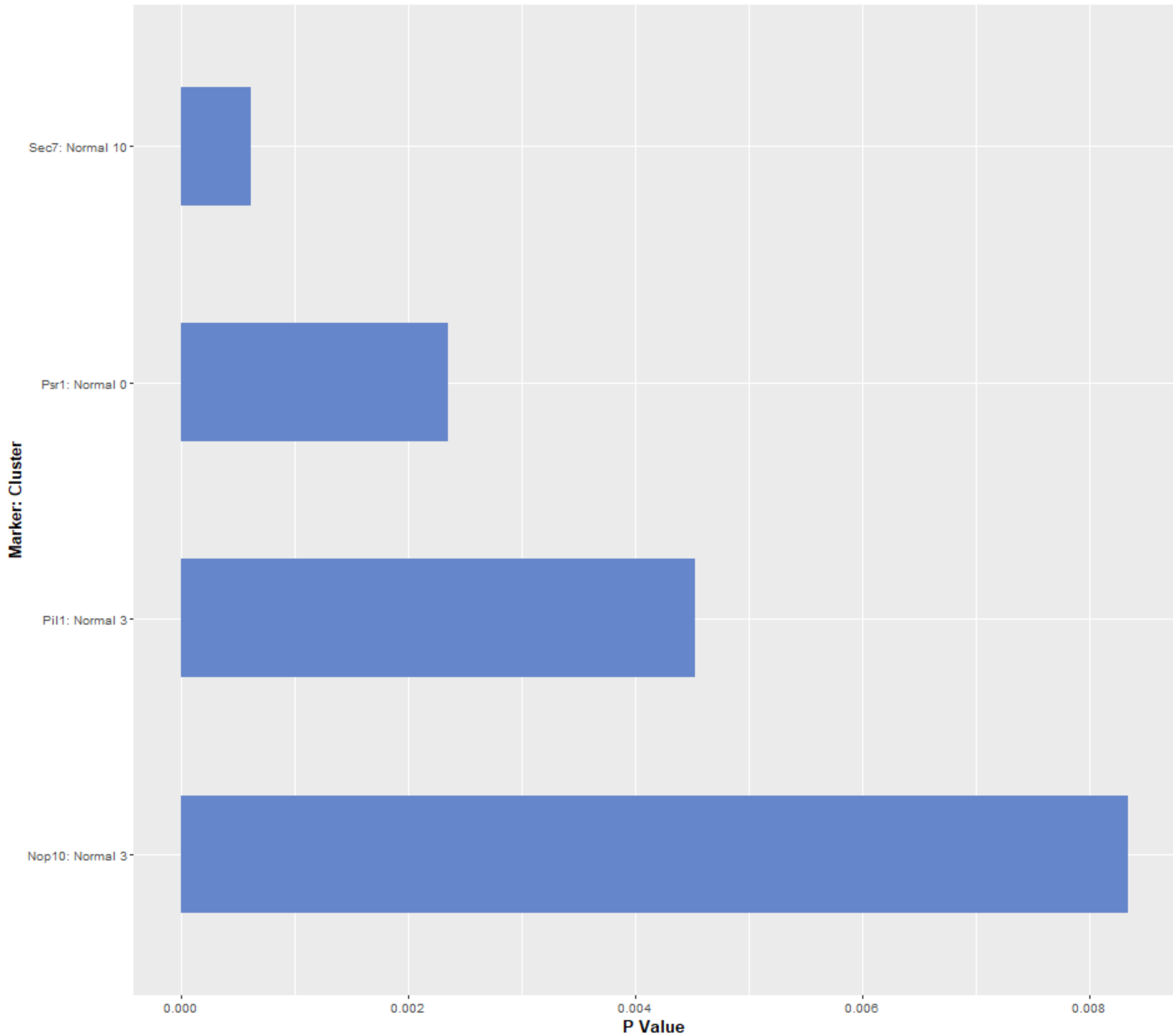
# protein lipidation

With AreaShape | Ordered Gene Set

Marker: Cluster

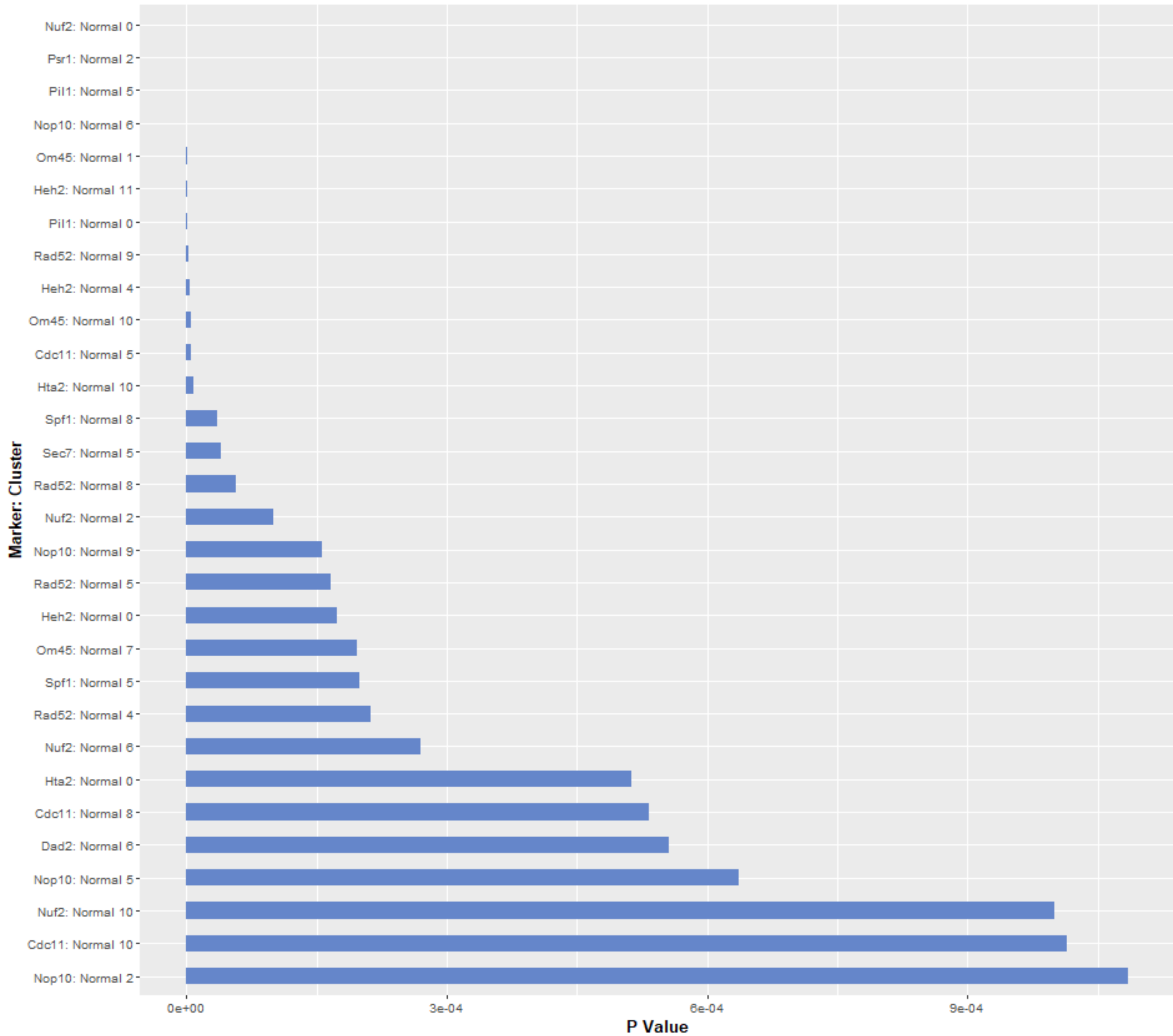


**protein maturation**  
With AreaShape | Ordered Gene Set



# protein modification by small protein conjugation or removal

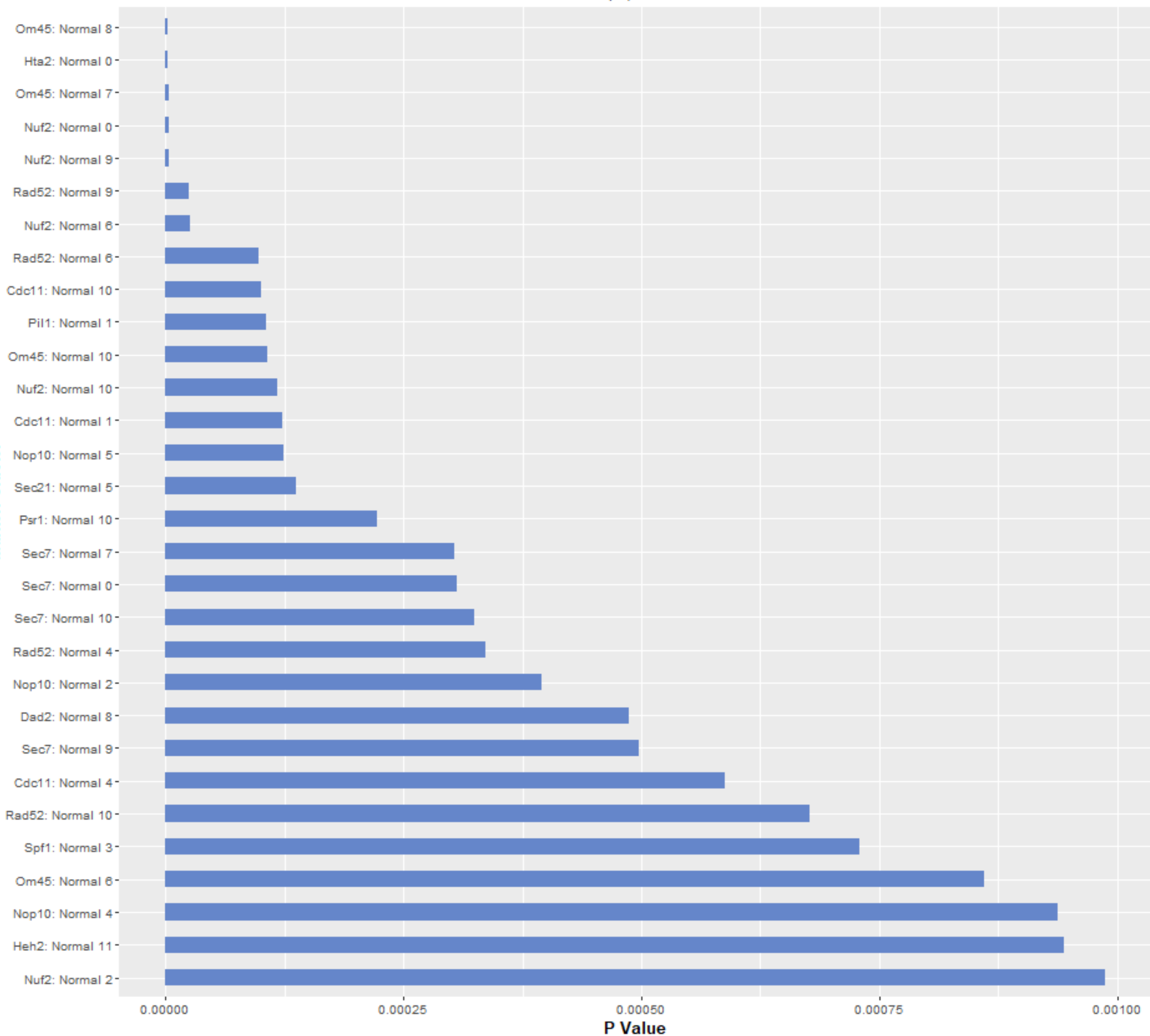
With AreaShape | Ordered Gene Set



# protein phosphorylation

With AreaShape | Ordered Gene Set

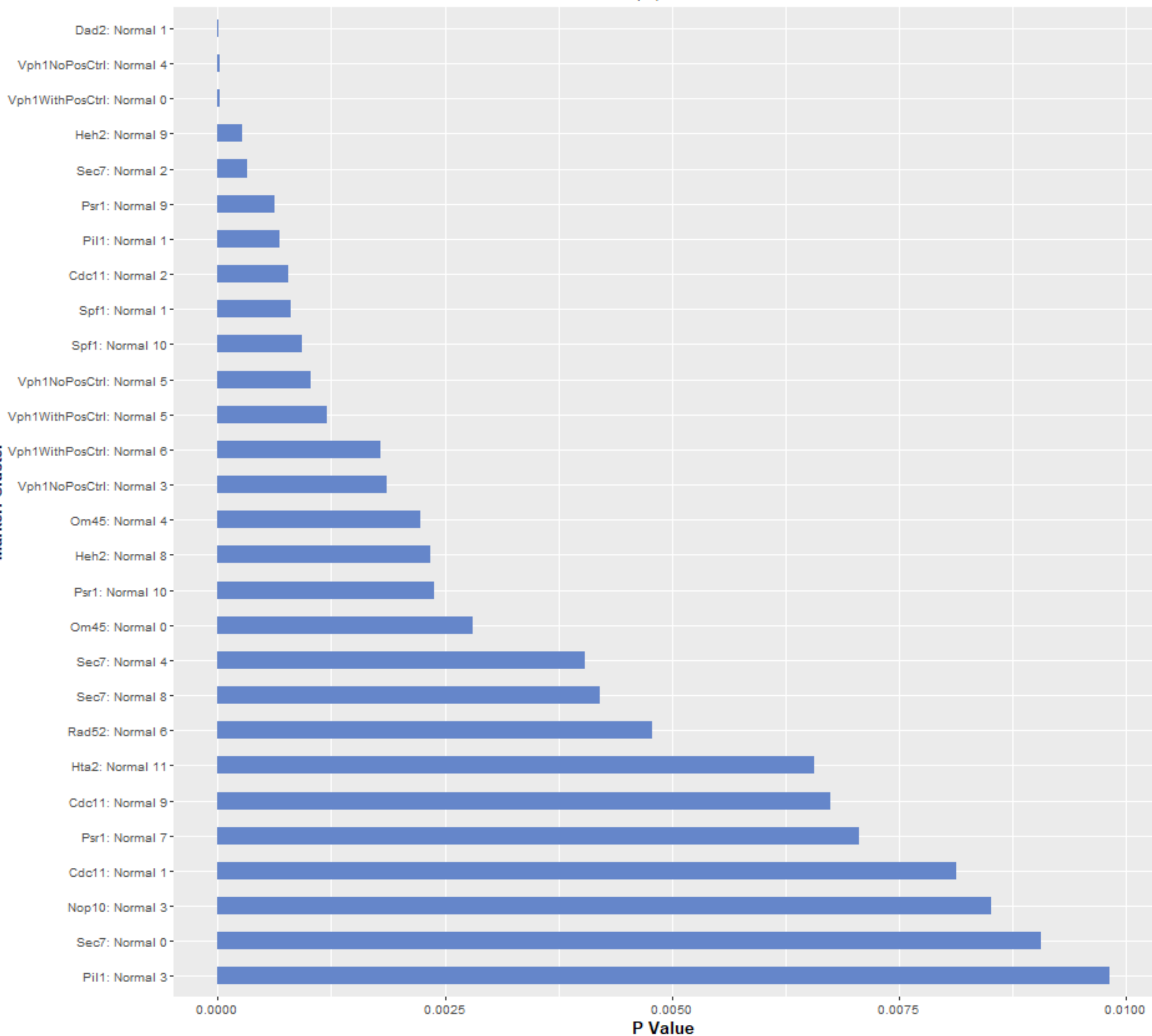
Marker: Cluster



# protein targeting

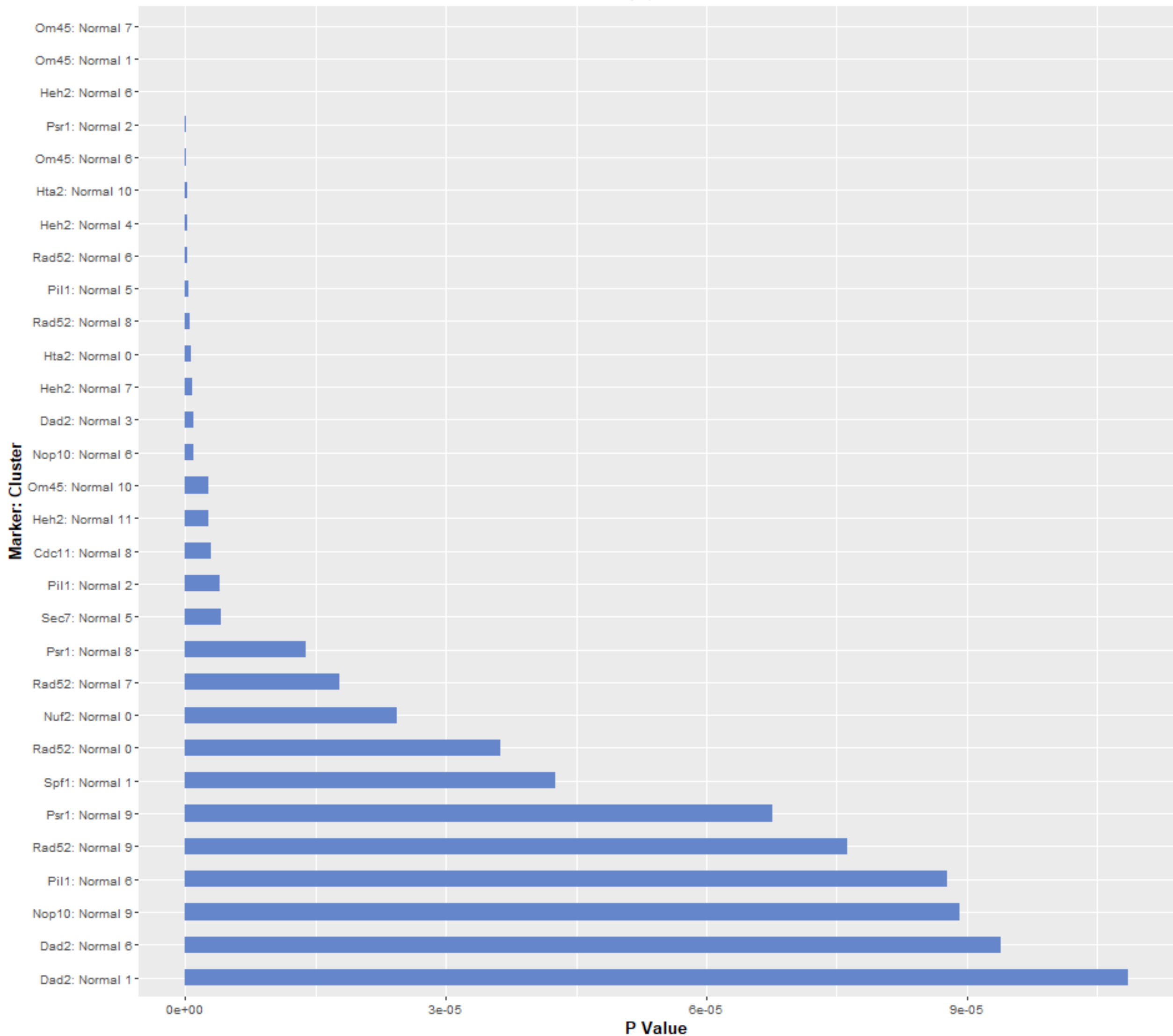
With AreaShape | Ordered Gene Set

Marker: Cluster



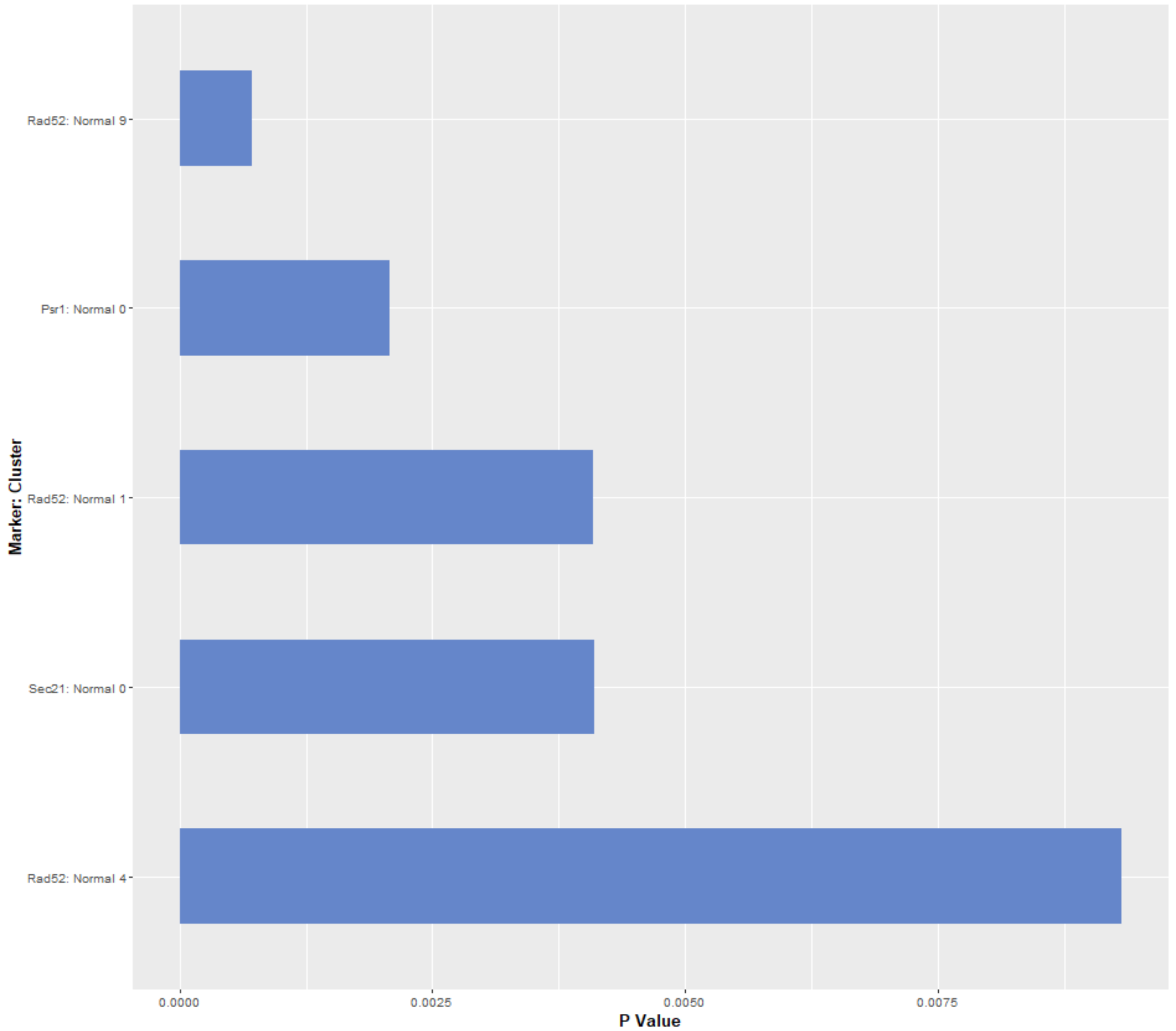
# proteolysis involved in cellular protein catabolic process

With AreaShape | Ordered Gene Set

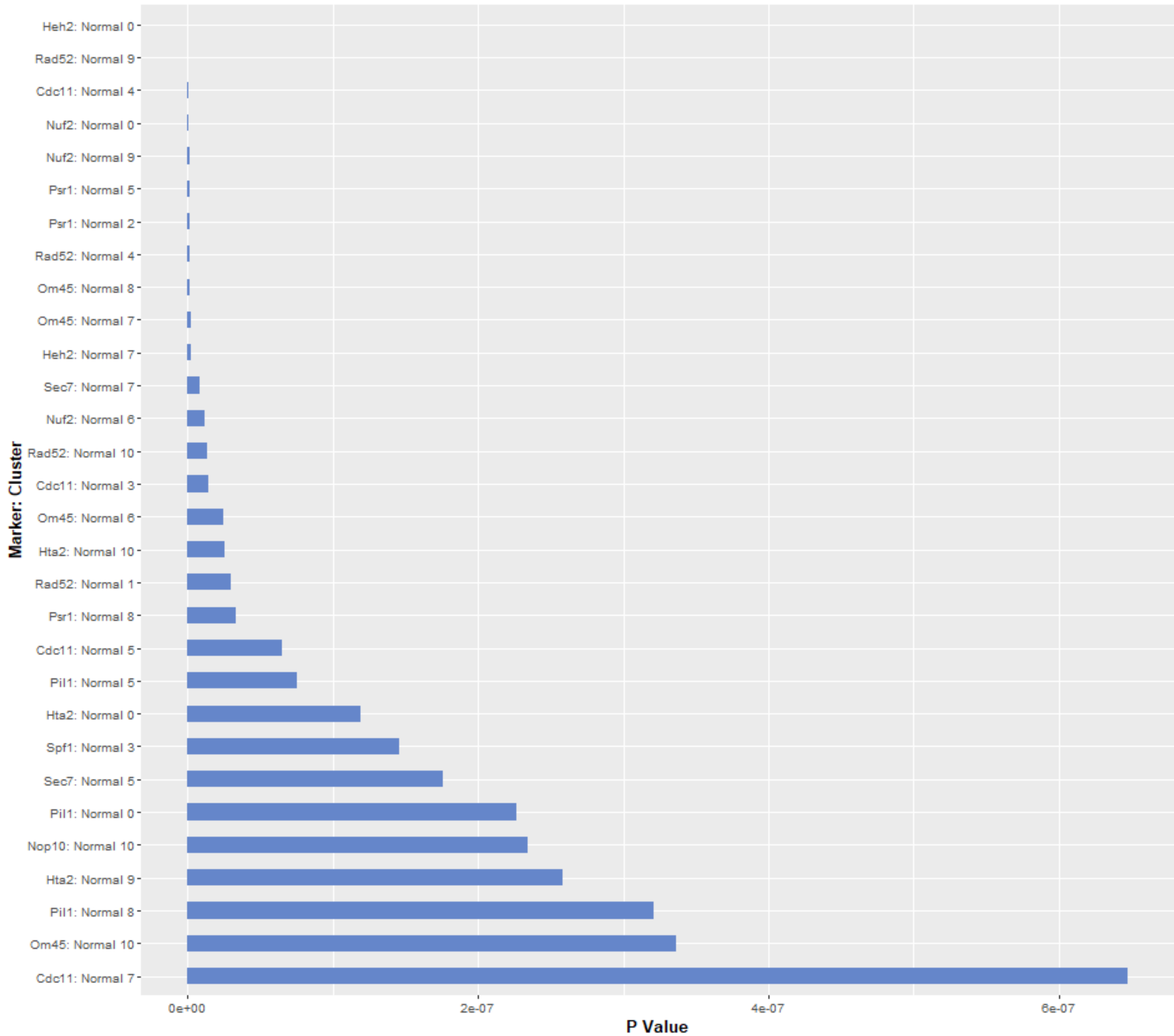




pseudohyphal growth  
With AreaShape | Ordered Gene Set

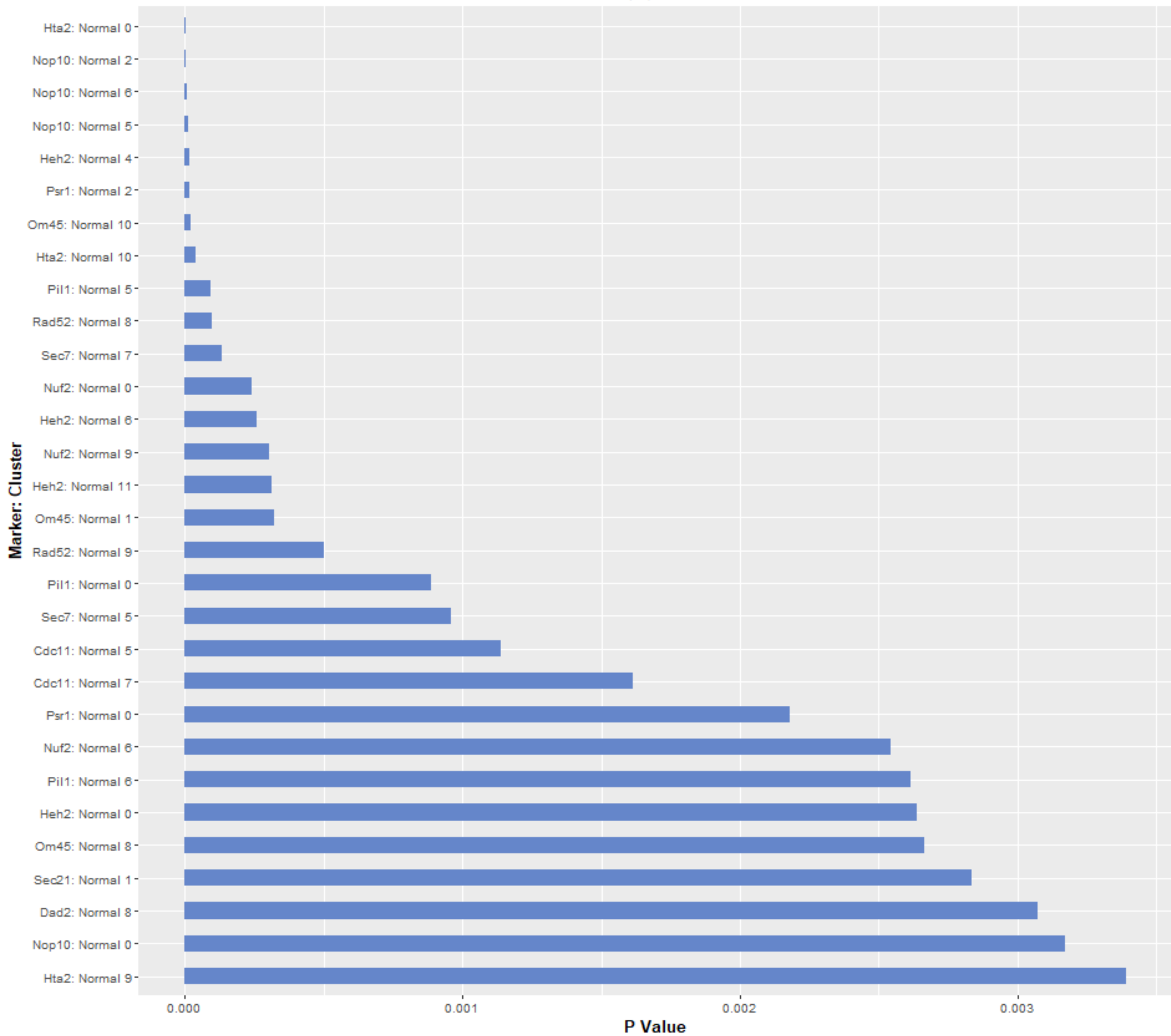


regulation of cell cycle  
With AreaShape | Ordered Gene Set



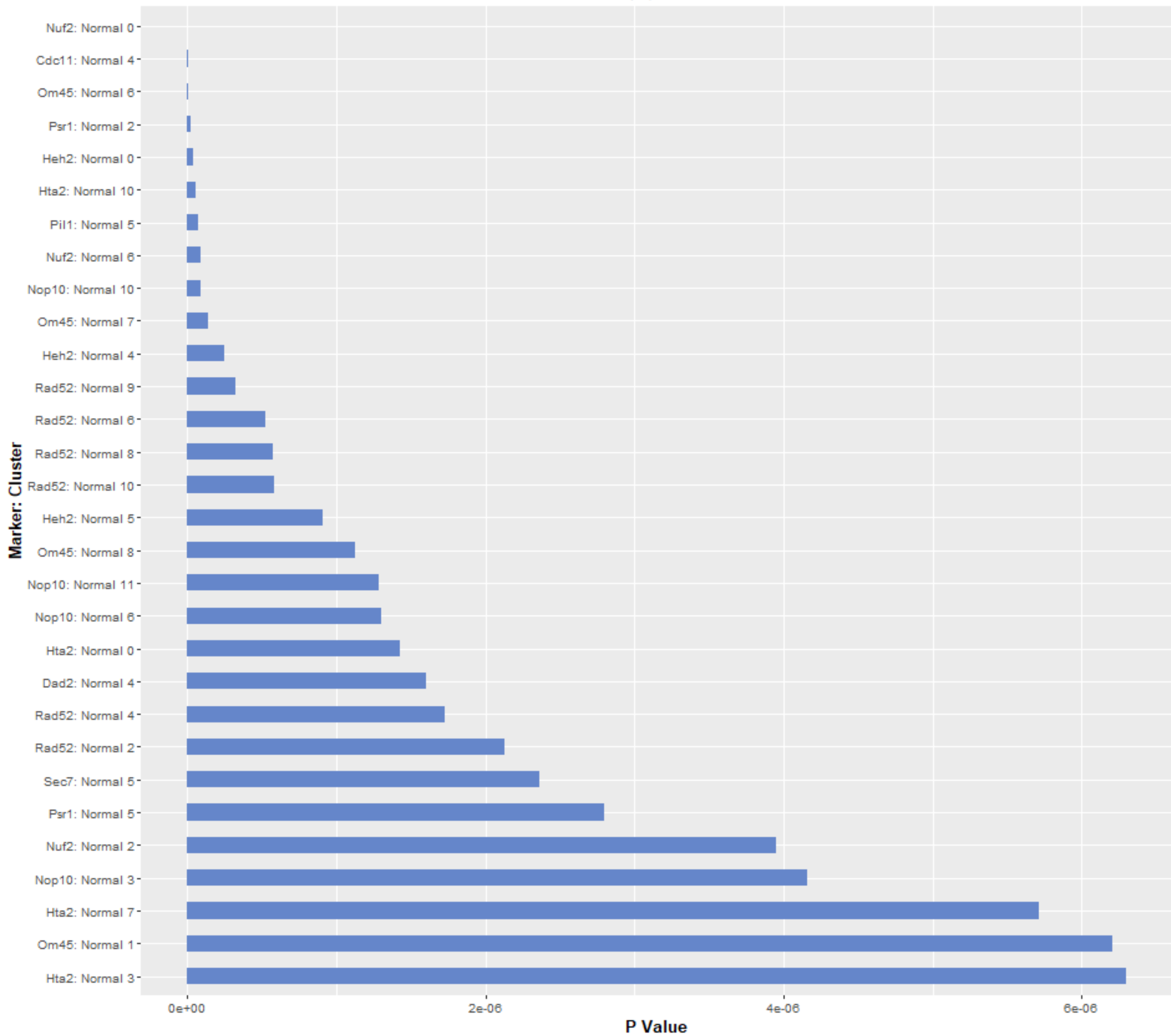
# regulation of DNA metabolic process

With AreaShape | Ordered Gene Set



# regulation of organelle organization

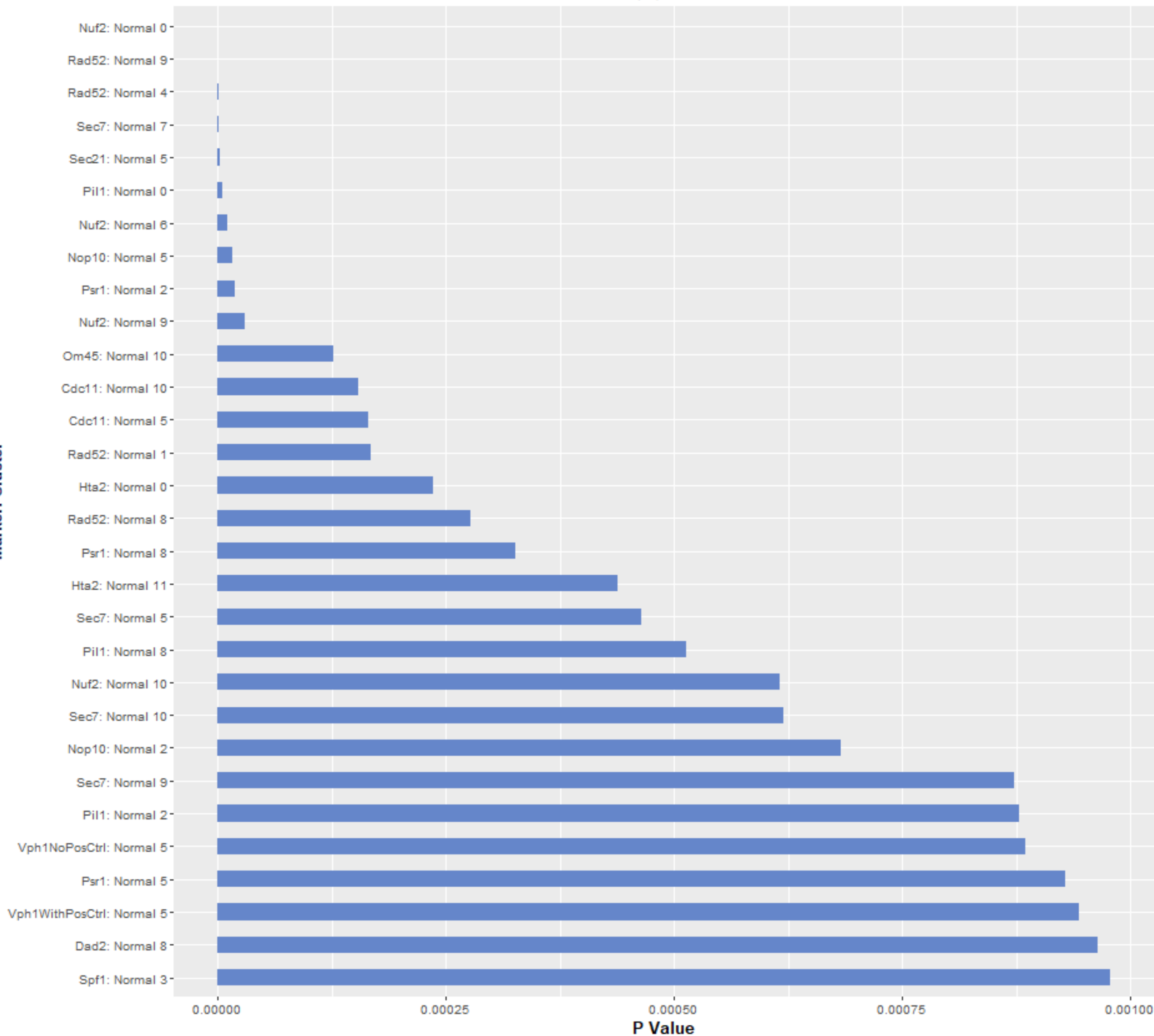
With AreaShape | Ordered Gene Set



# regulation of protein modification process

With AreaShape | Ordered Gene Set

Marker: Cluster



# regulation of translation

With AreaShape | Ordered Gene Set

Marker: Cluster

Heh2: Normal 7

Rad52: Normal 1

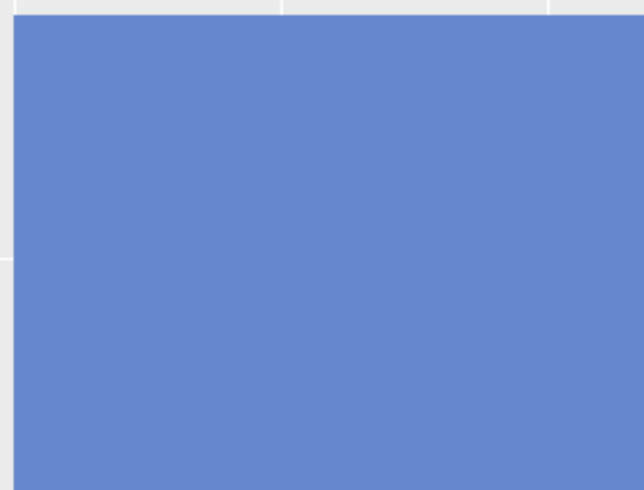
0.0000

0.0025

0.0050

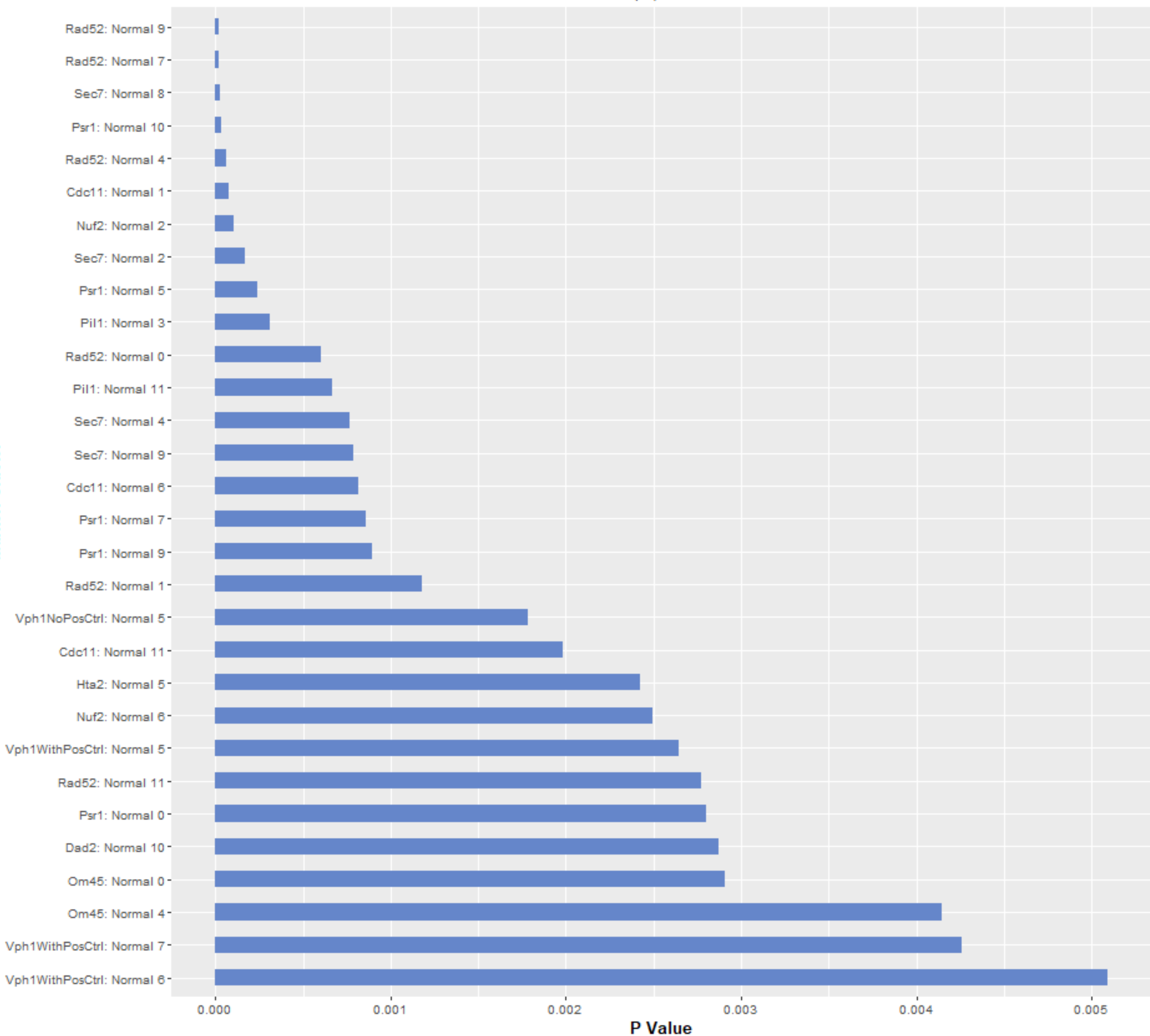
0.0075

P Value



**regulation of transport**  
With AreaShape | Ordered Gene Set

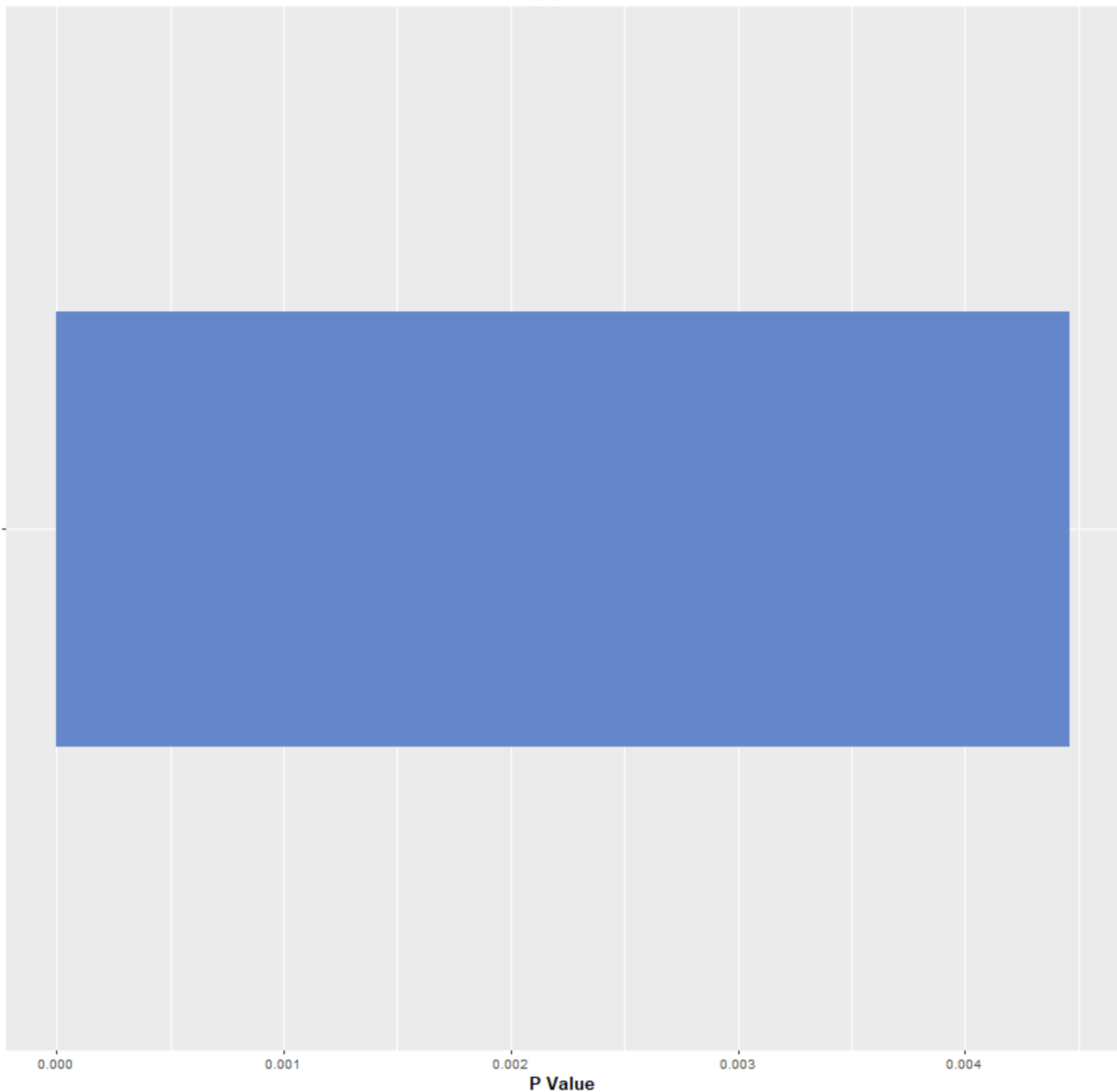
**Marker: Cluster**



**response to chemical**  
With AreaShape | Ordered Gene Set

**Marker: Cluster**

Pil1: Normal 4





**response to heat**  
With AreaShape | Ordered Gene Set

**Marker: Cluster**

Pil1: Normal 1

Psr1: Normal 0

Sec7: Normal 7

Spf1: Normal 2

Om45: Normal 3

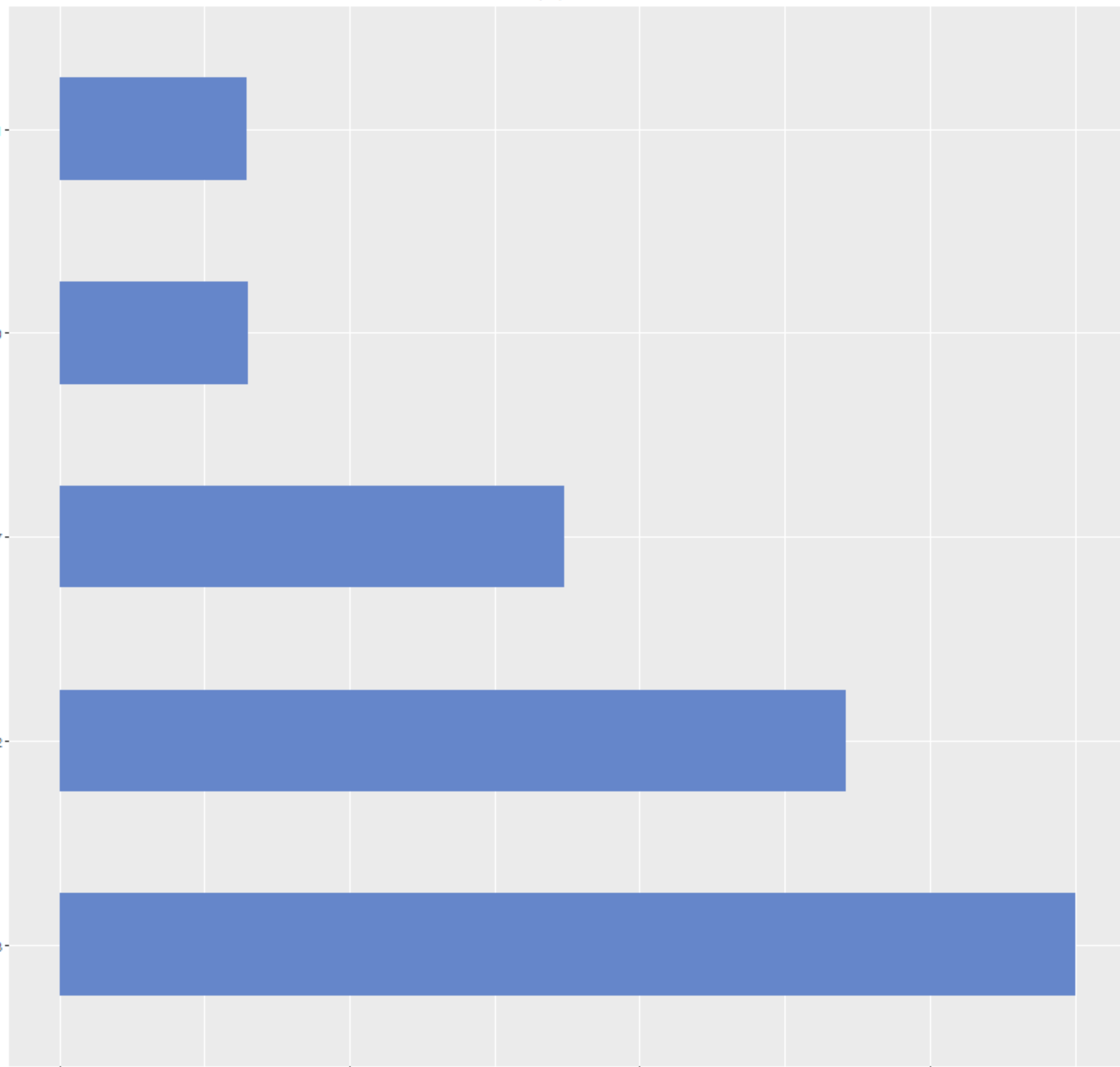
0.0000

0.0025

0.0050

0.0075

**P Value**



# response to osmotic stress

With AreaShape | Ordered Gene Set

Marker: Cluster

Heh2: Normal 0

Nop10: Normal 0

0.000

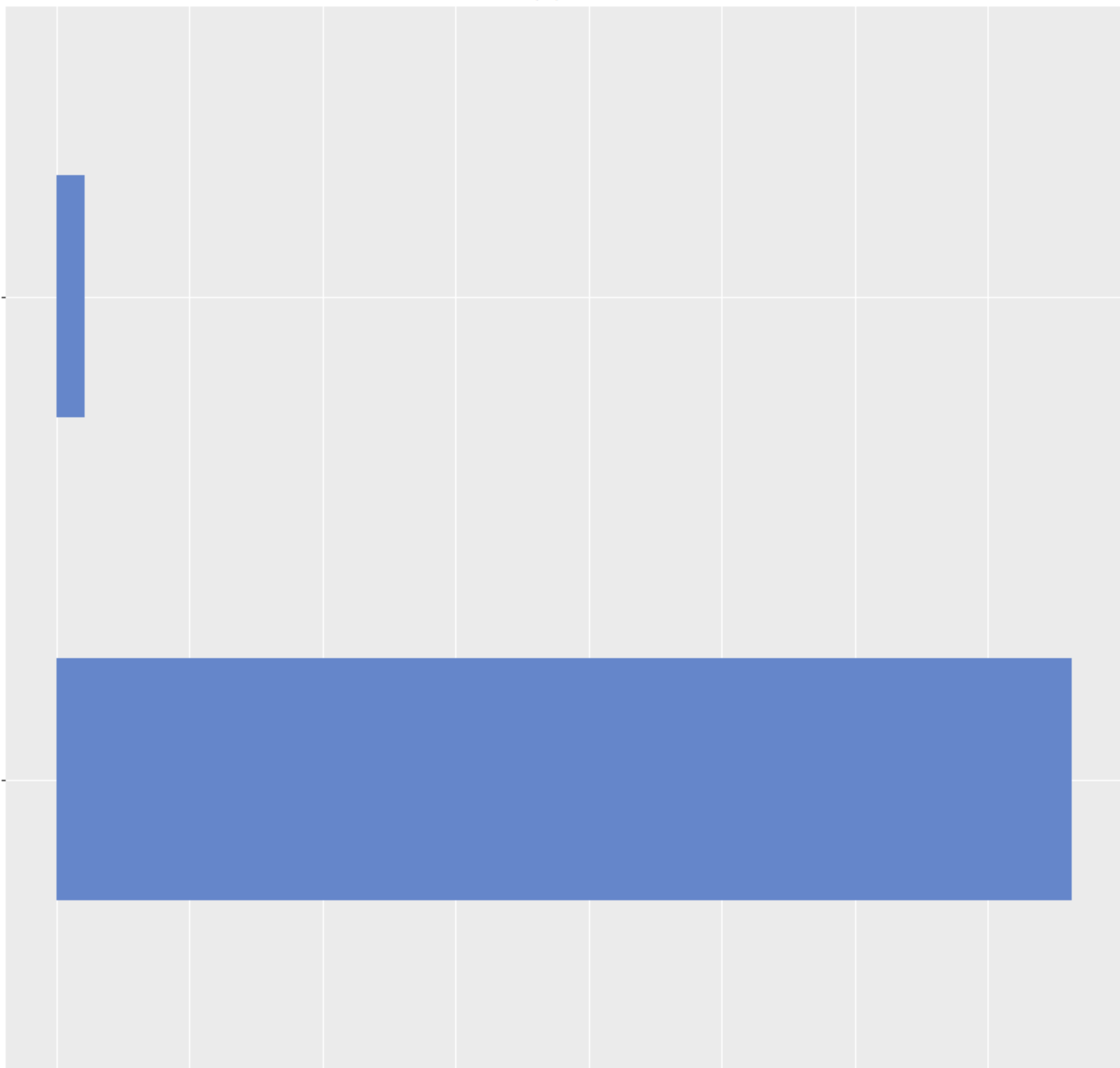
0.002

0.004

0.006

0.008

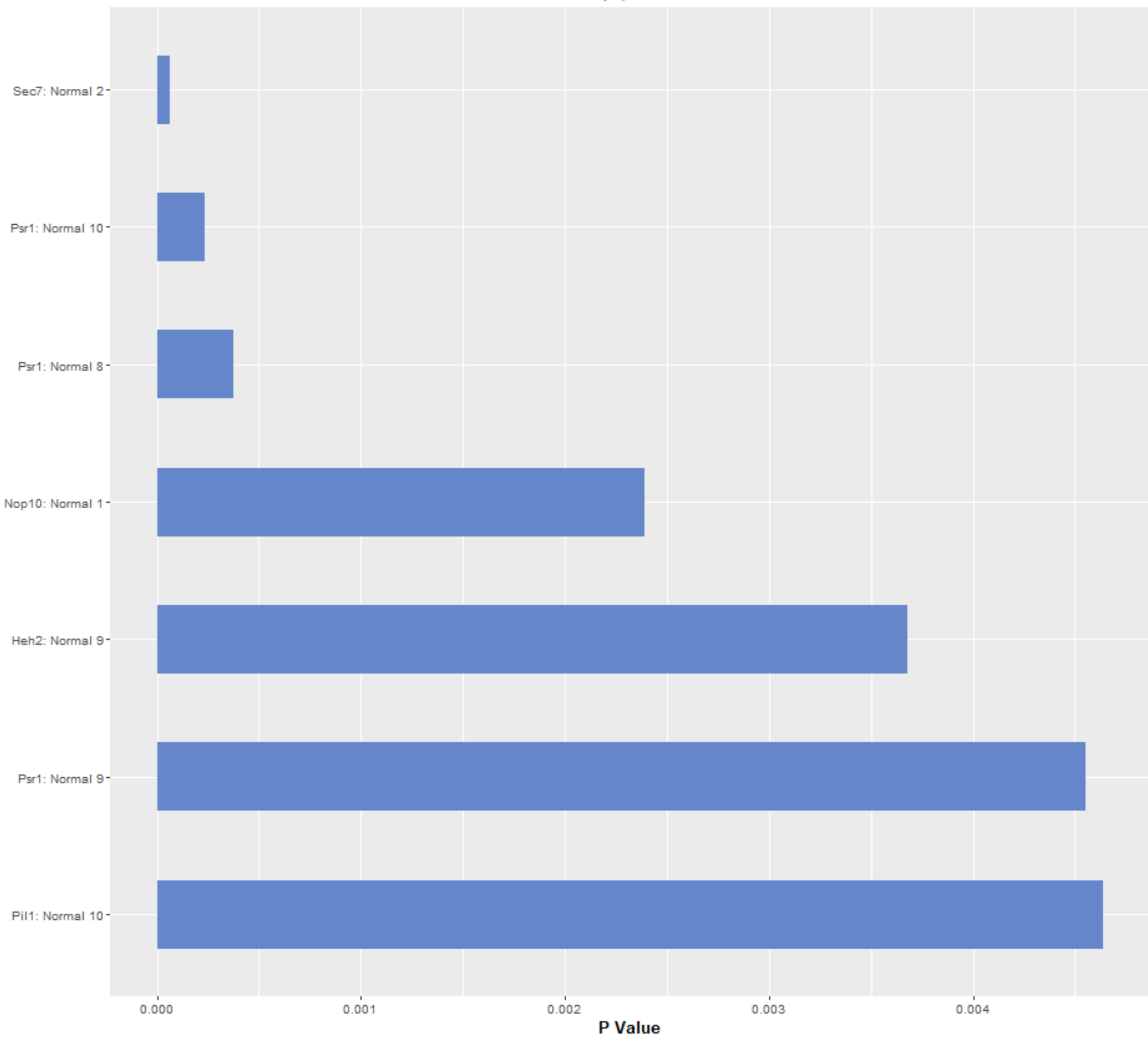
P Value



# ribosomal large subunit biogenesis

With AreaShape | Ordered Gene Set

Marker: Cluster



# ribosomal small subunit biogenesis

With AreaShape | Ordered Gene Set

Marker: Cluster

Pil1: Normal 4

0.000

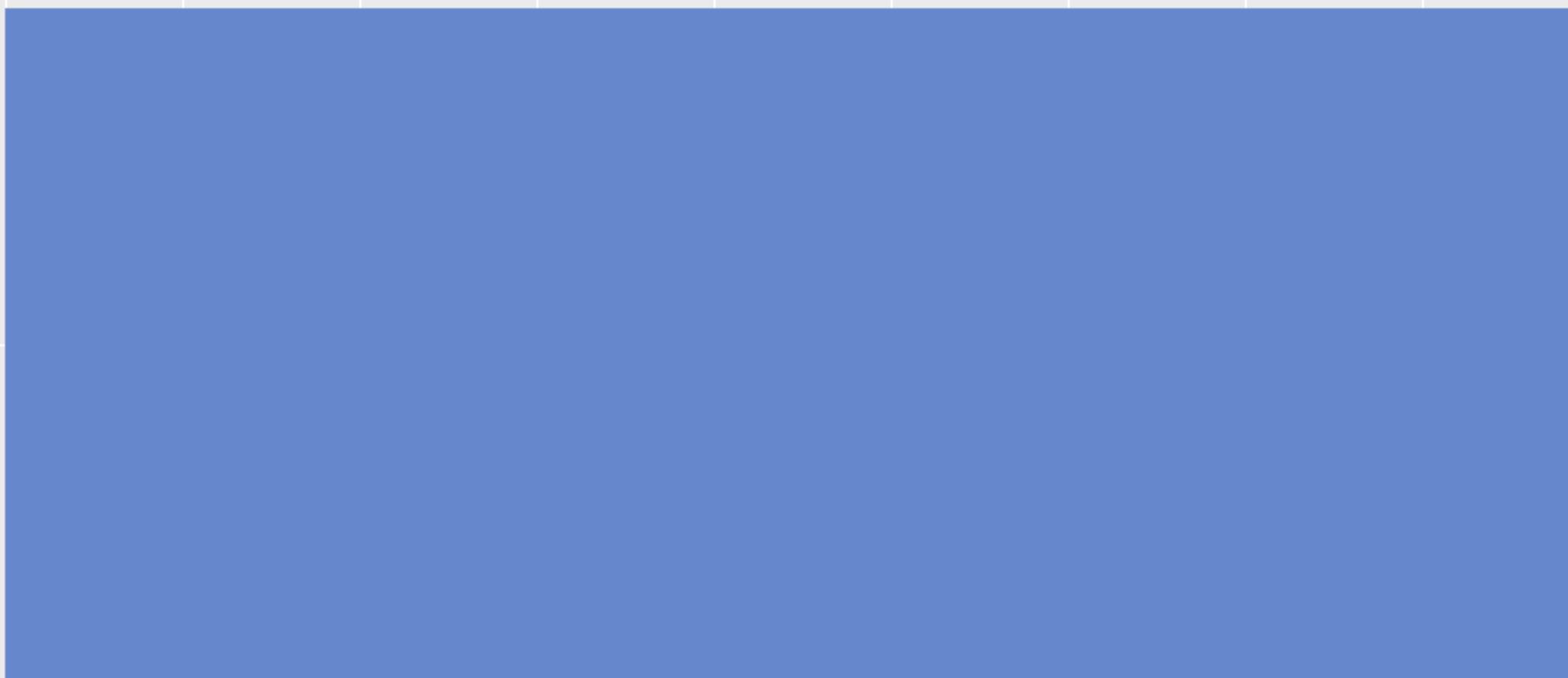
0.001

0.002

0.003

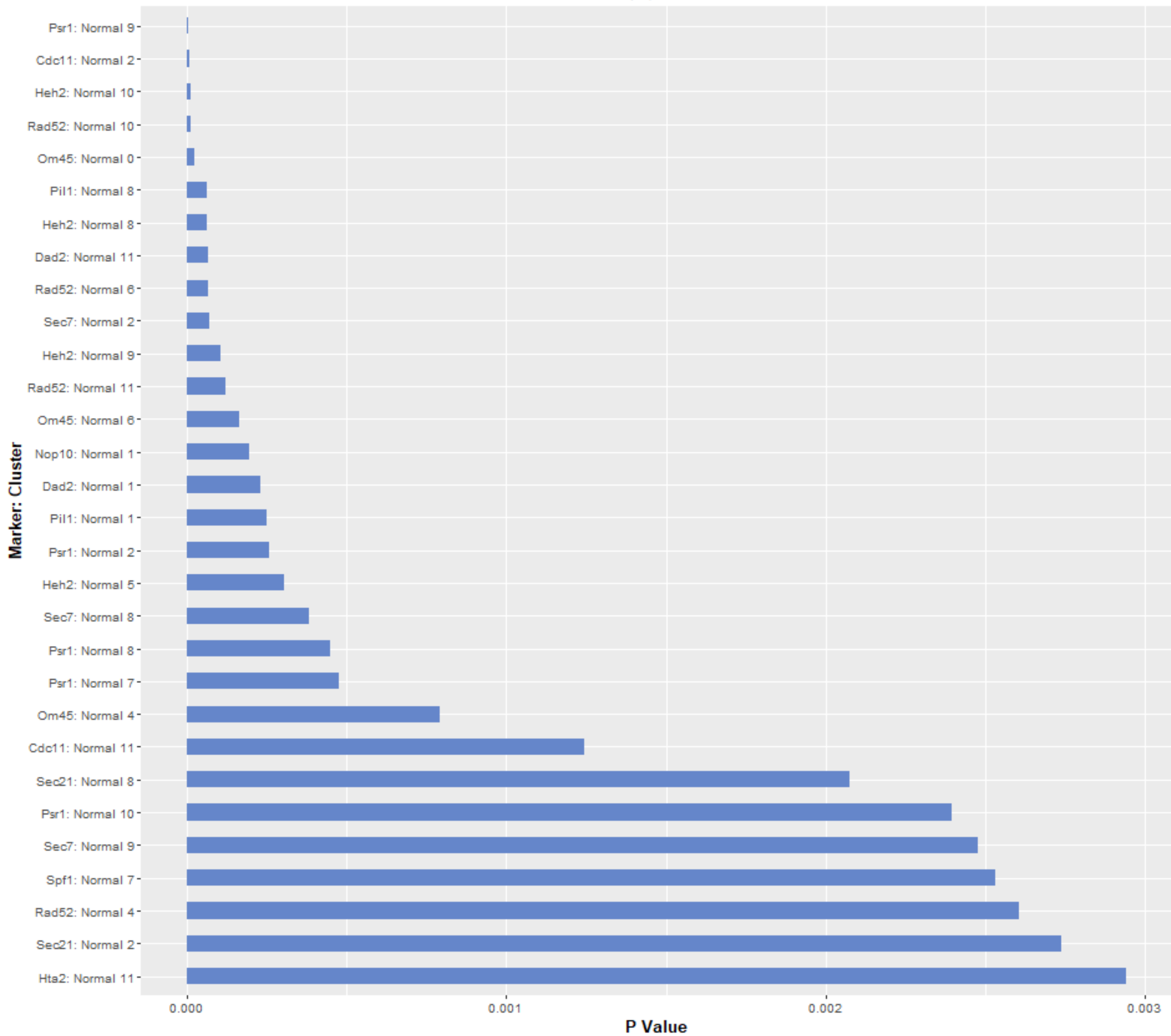
0.004

P Value



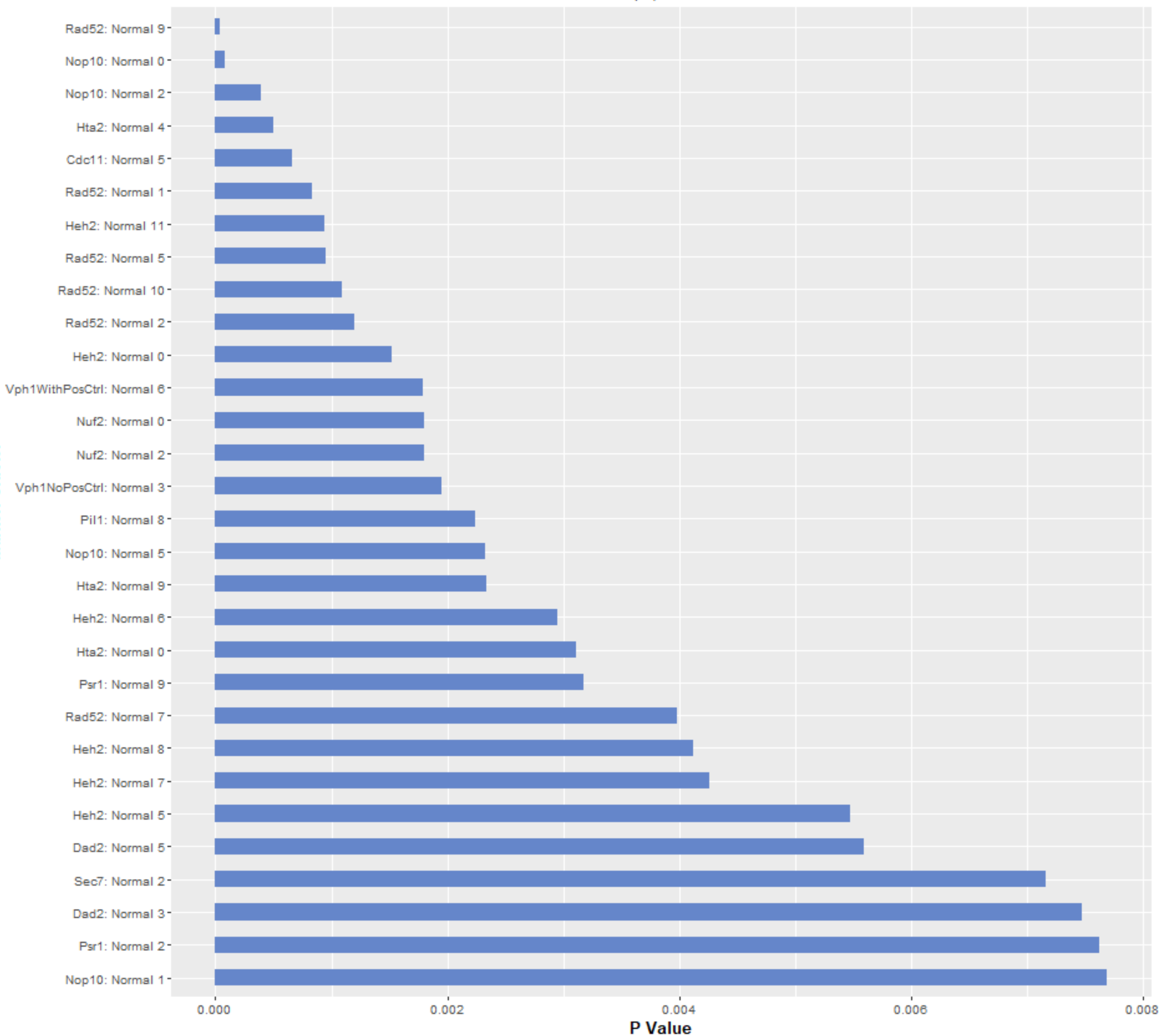
# ribosomal subunit export from nucleus

With AreaShape | Ordered Gene Set

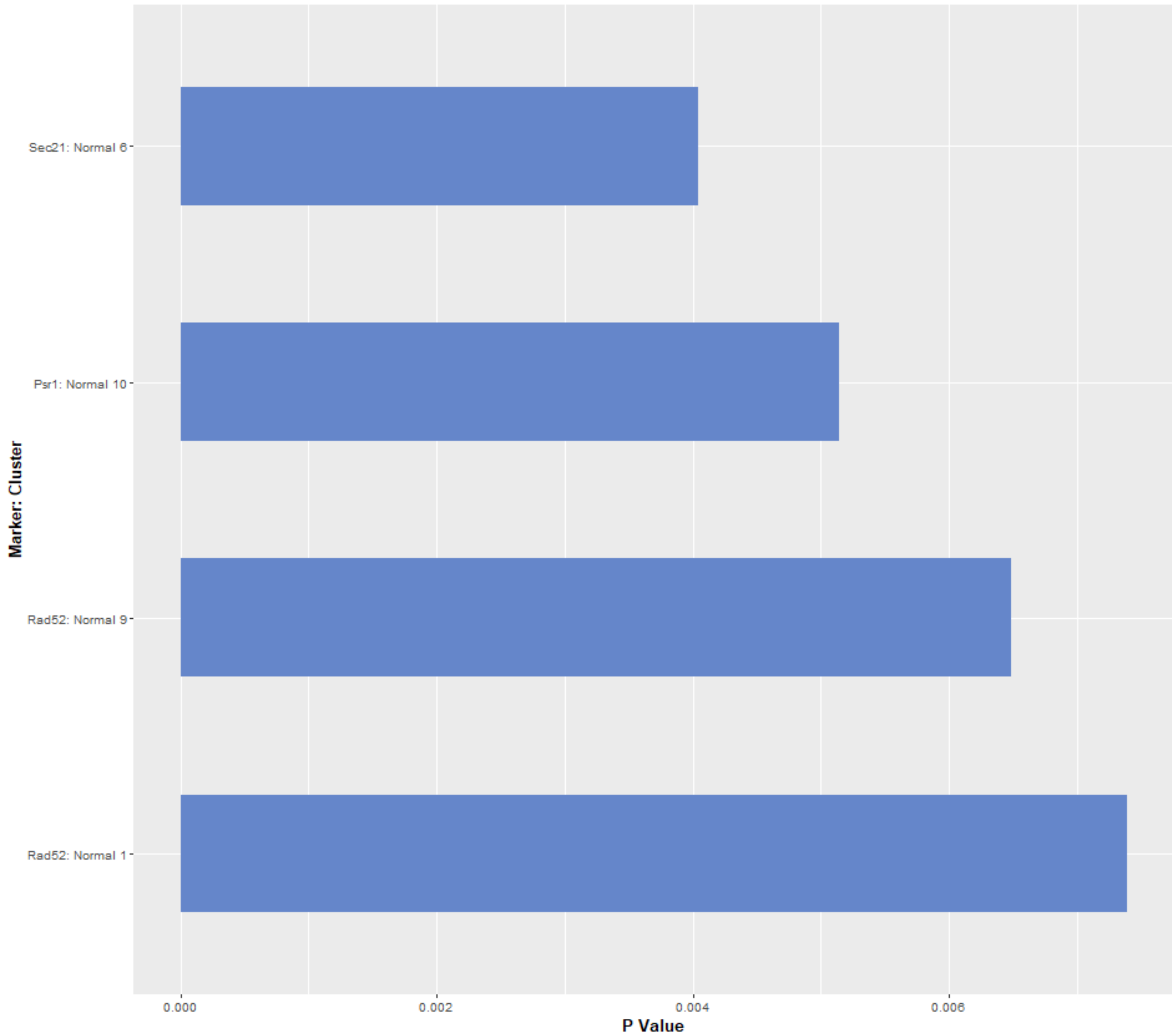


RNA catabolic process  
With AreaShape | Ordered Gene Set

Marker: Cluster

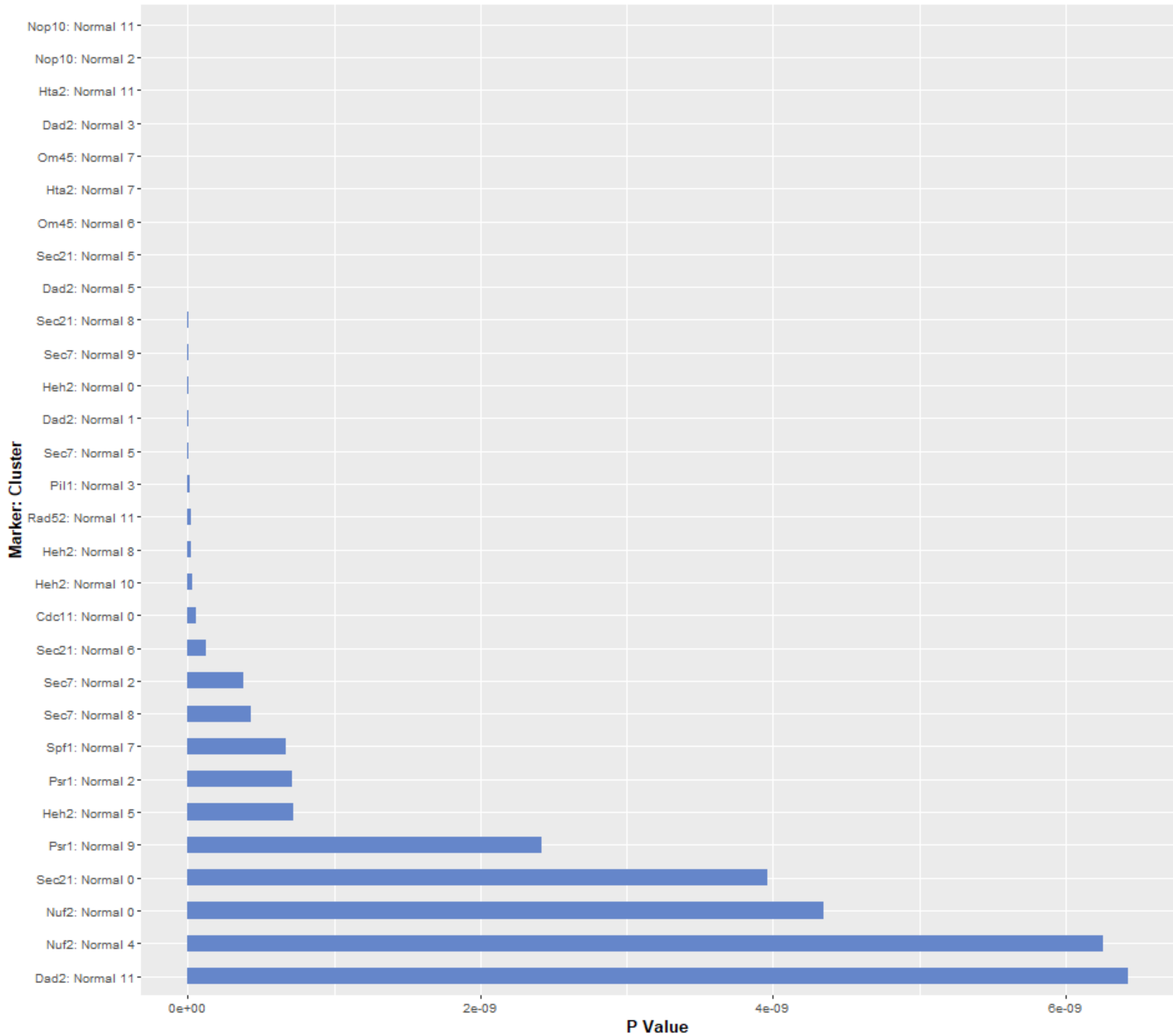


**RNA modification**  
With AreaShape | Ordered Gene Set



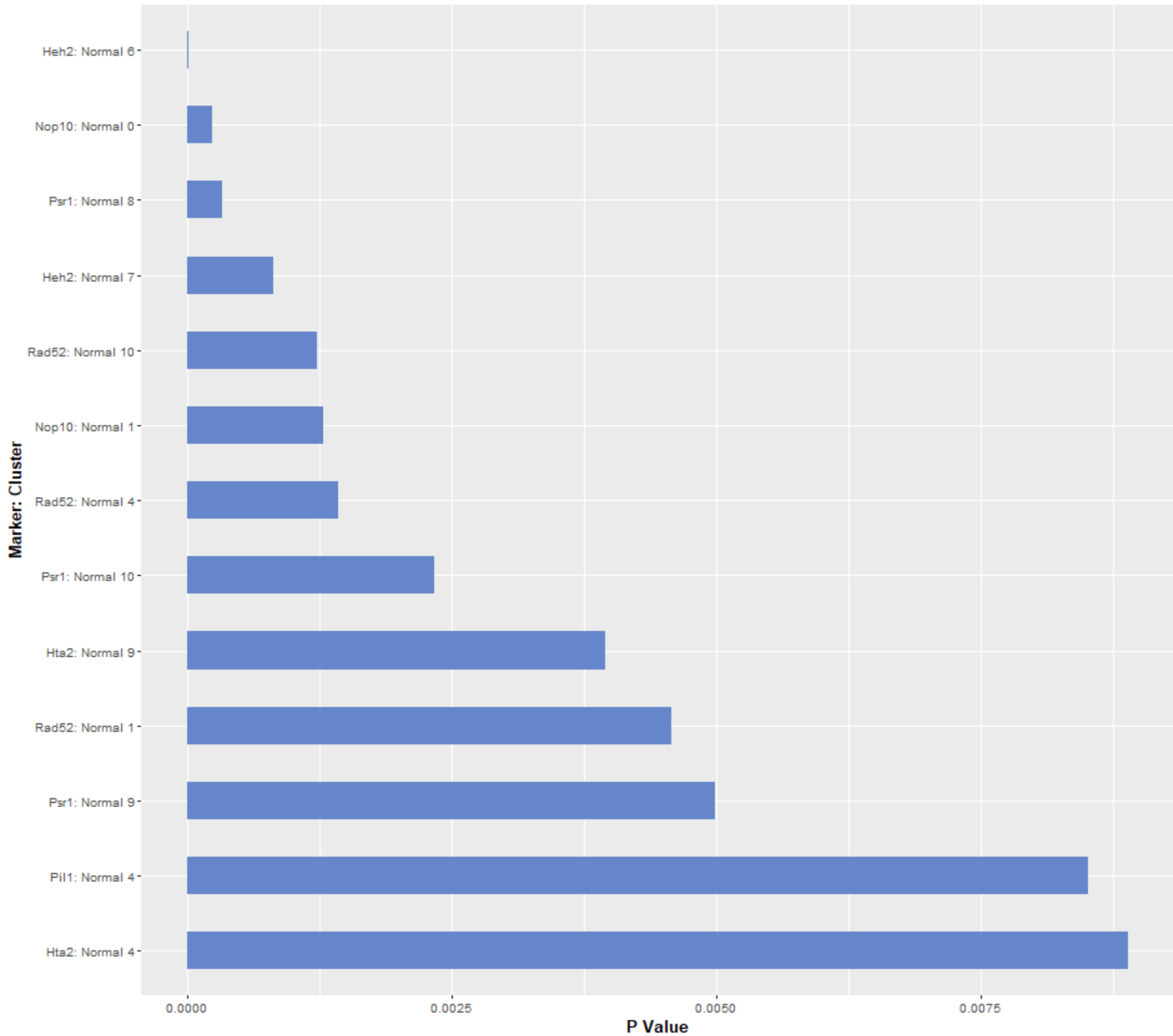
# RNA splicing

With AreaShape | Ordered Gene Set





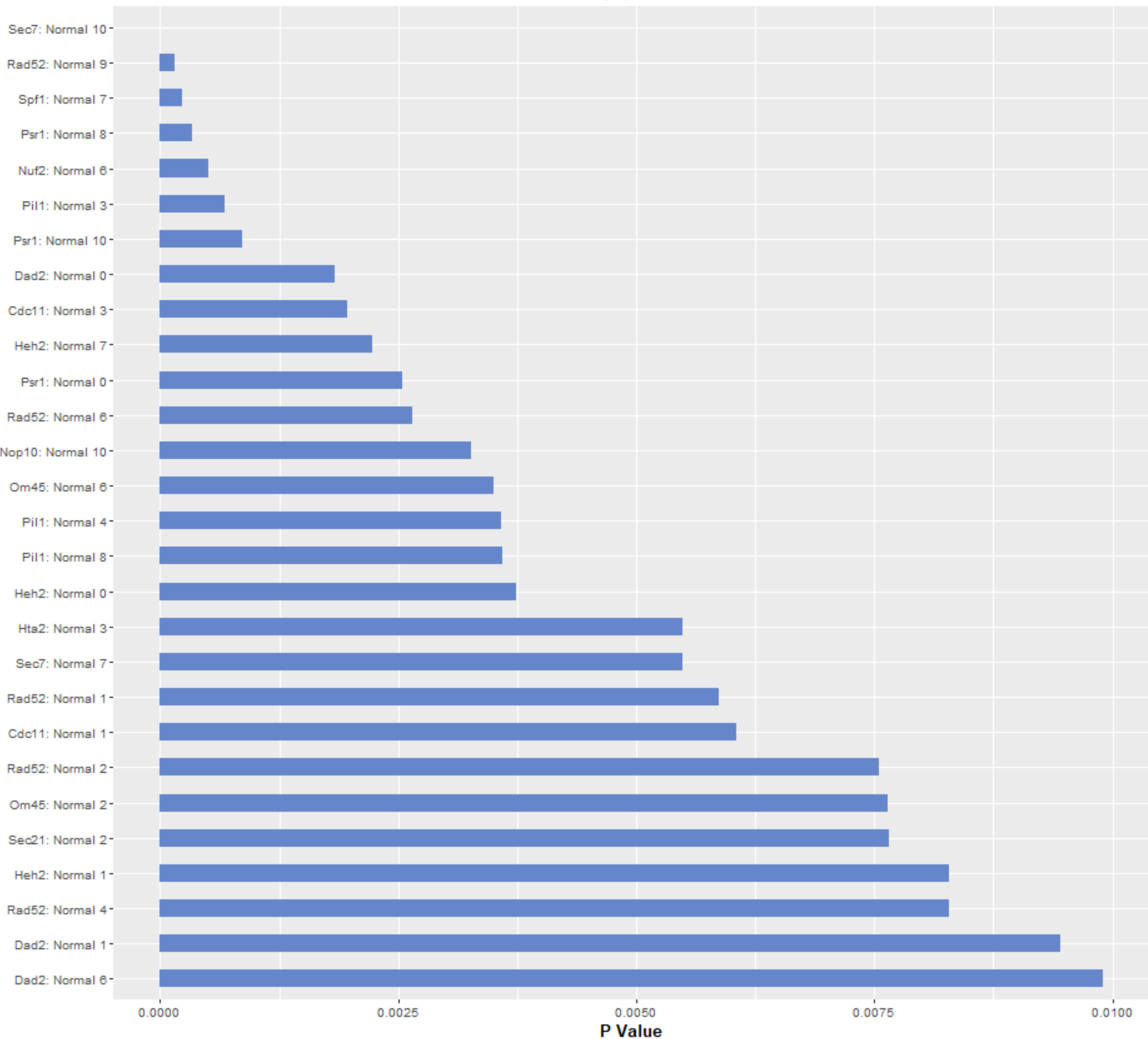
**rRNA processing**  
With AreaShape | Ordered Gene Set



# signaling

With AreaShape | Ordered Gene Set

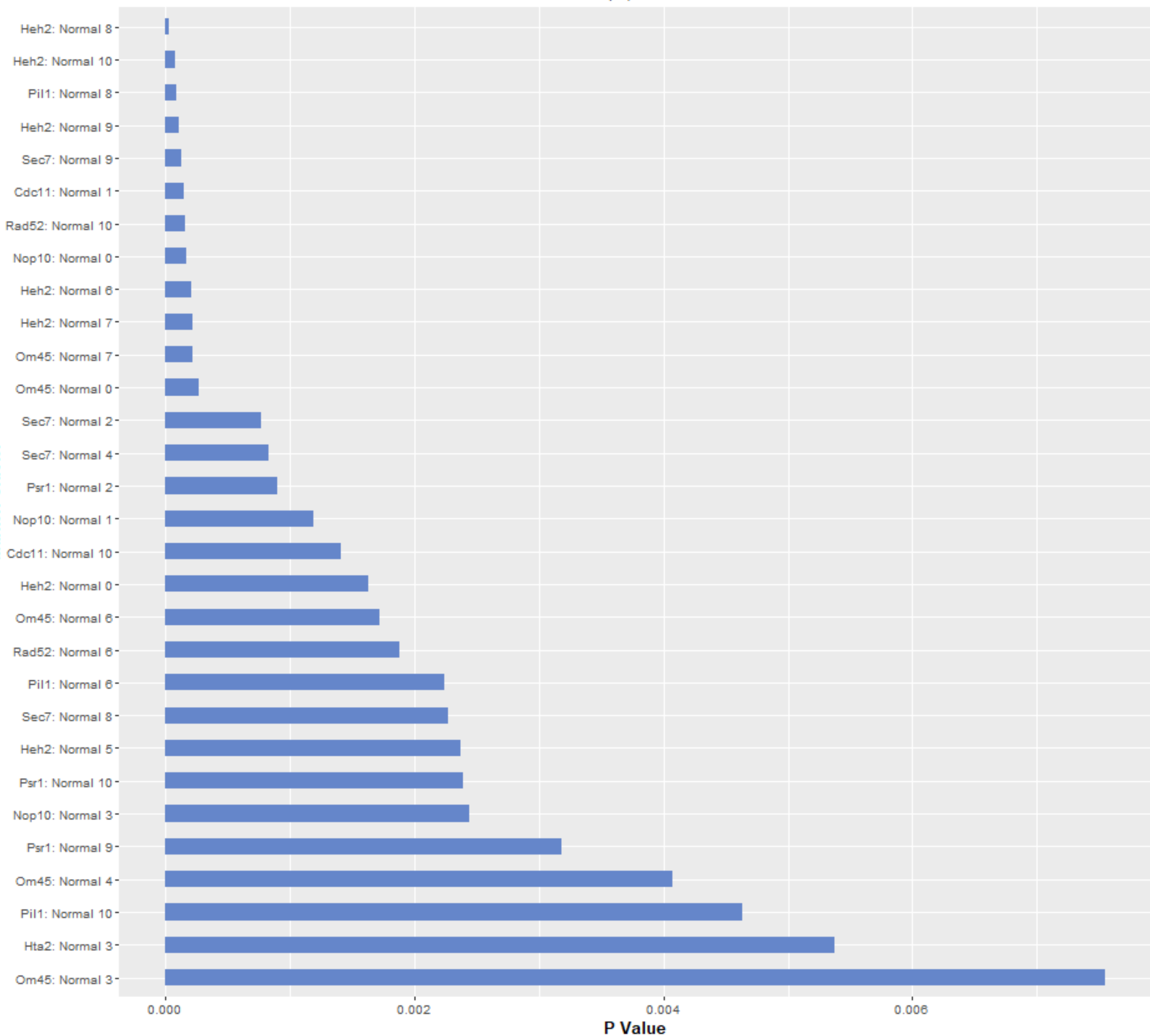
Marker: Cluster



# snoRNA processing

With AreaShape | Ordered Gene Set

Marker: Cluster



# sporulation

With AreaShape | Ordered Gene Set

Marker: Cluster

Rad52: Normal 5

Psr1: Normal 9

Pil1: Normal 11

0.000

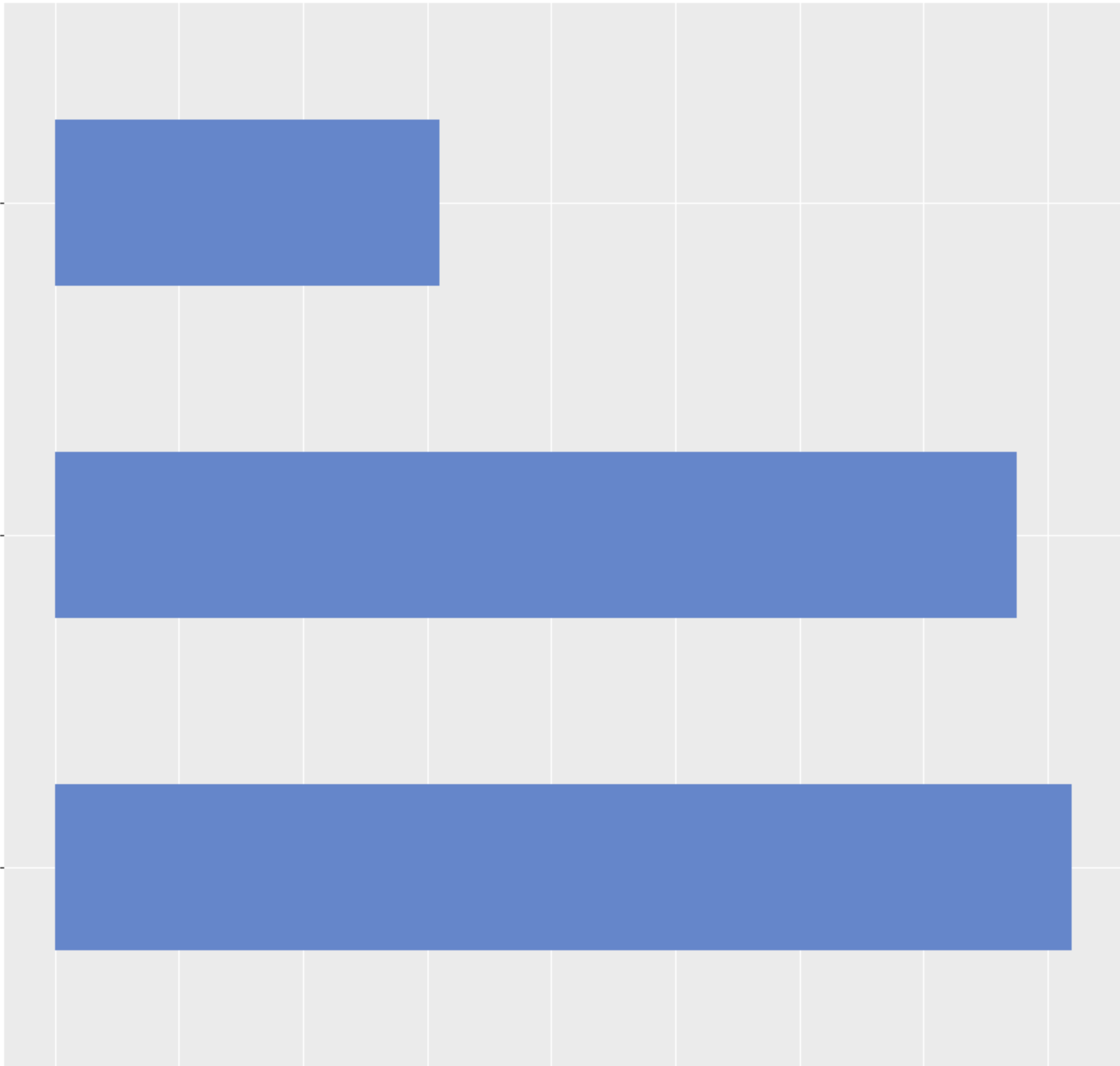
0.002

0.004

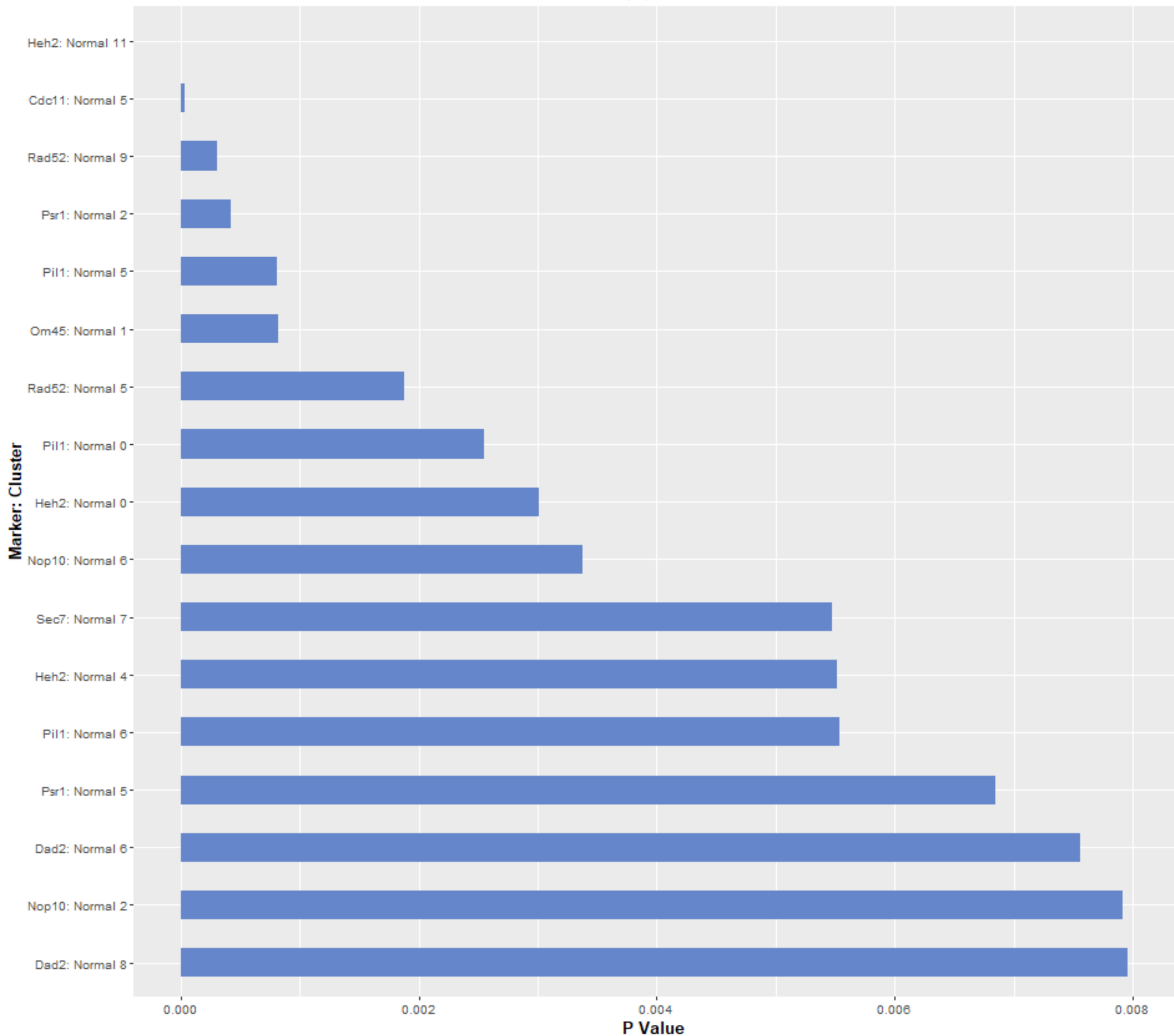
0.006

0.008

P Value



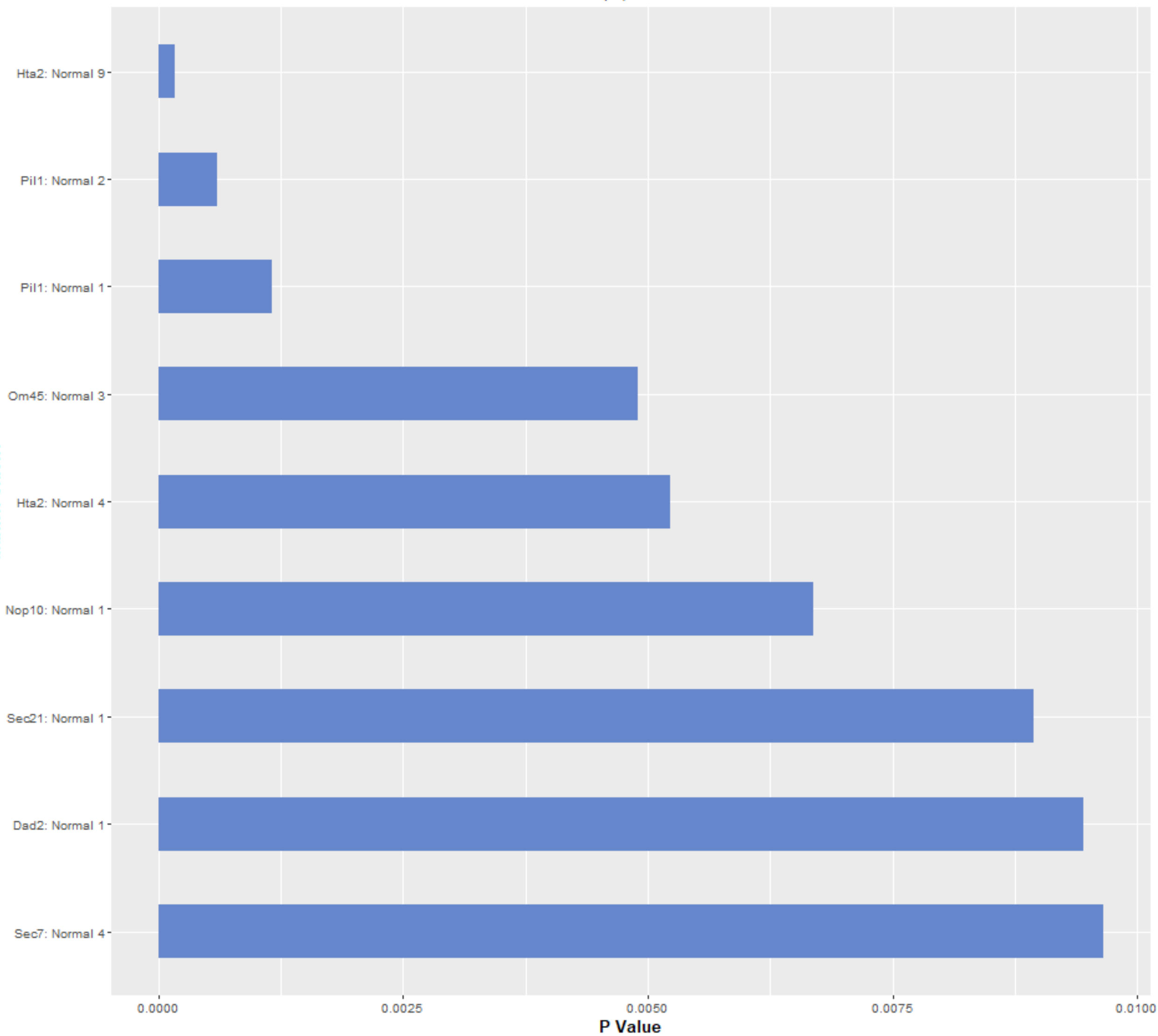
telomere organization  
With AreaShape | Ordered Gene Set



# transcription from RNA polymerase I promoter

With AreaShape | Ordered Gene Set

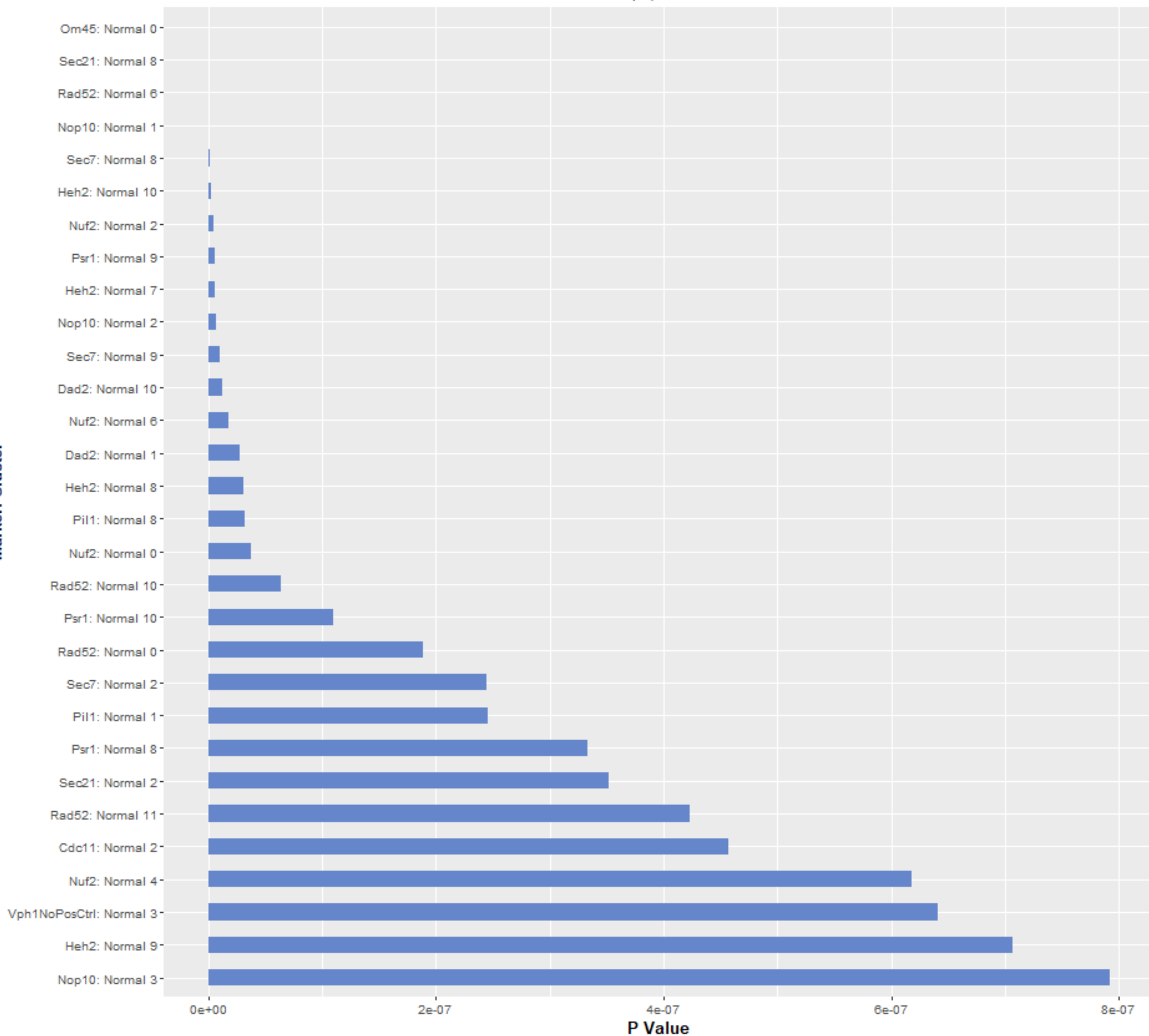
Marker: Cluster



# transcription from RNA polymerase II promoter

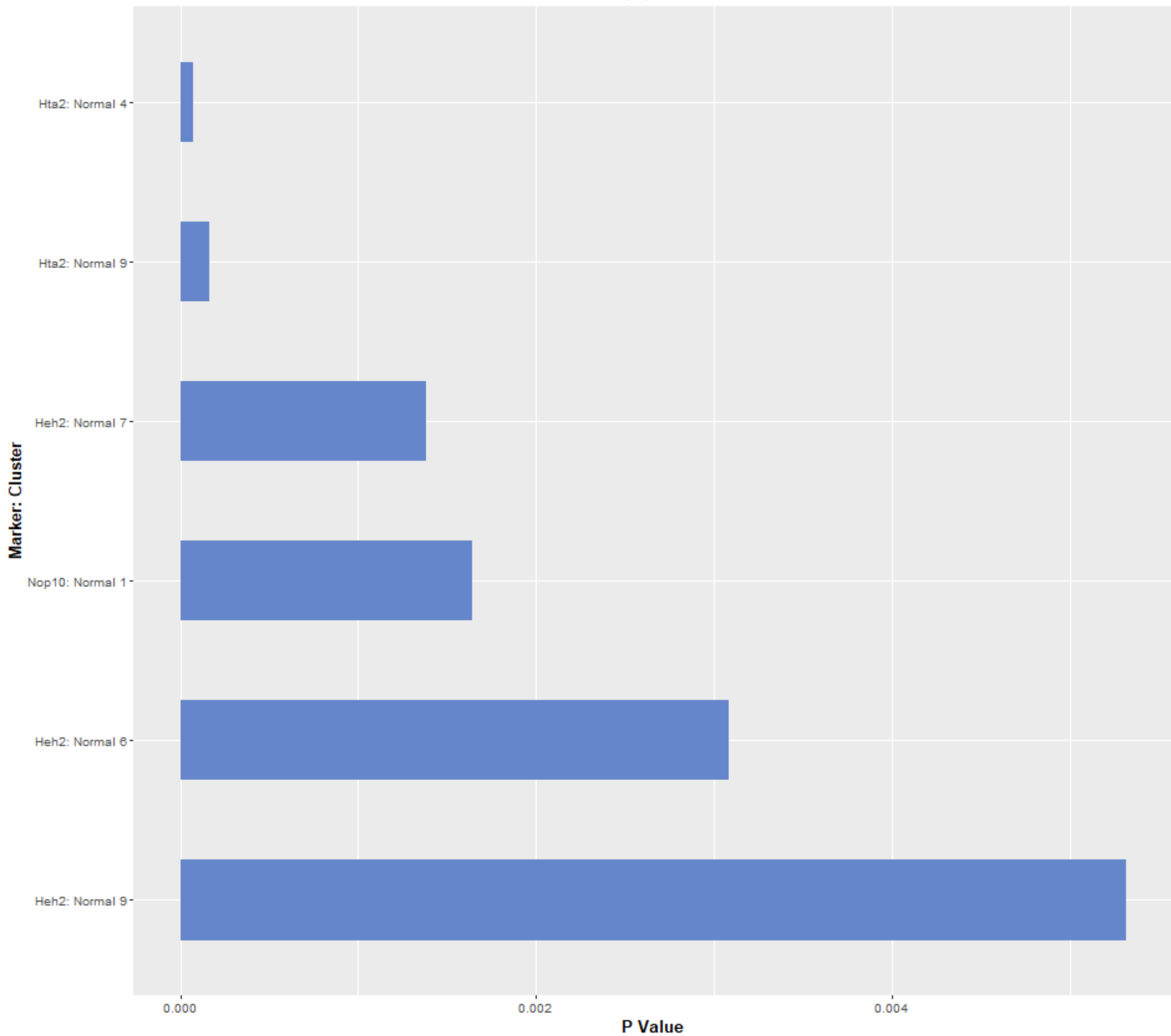
With AreaShape | Ordered Gene Set

Marker: Cluster



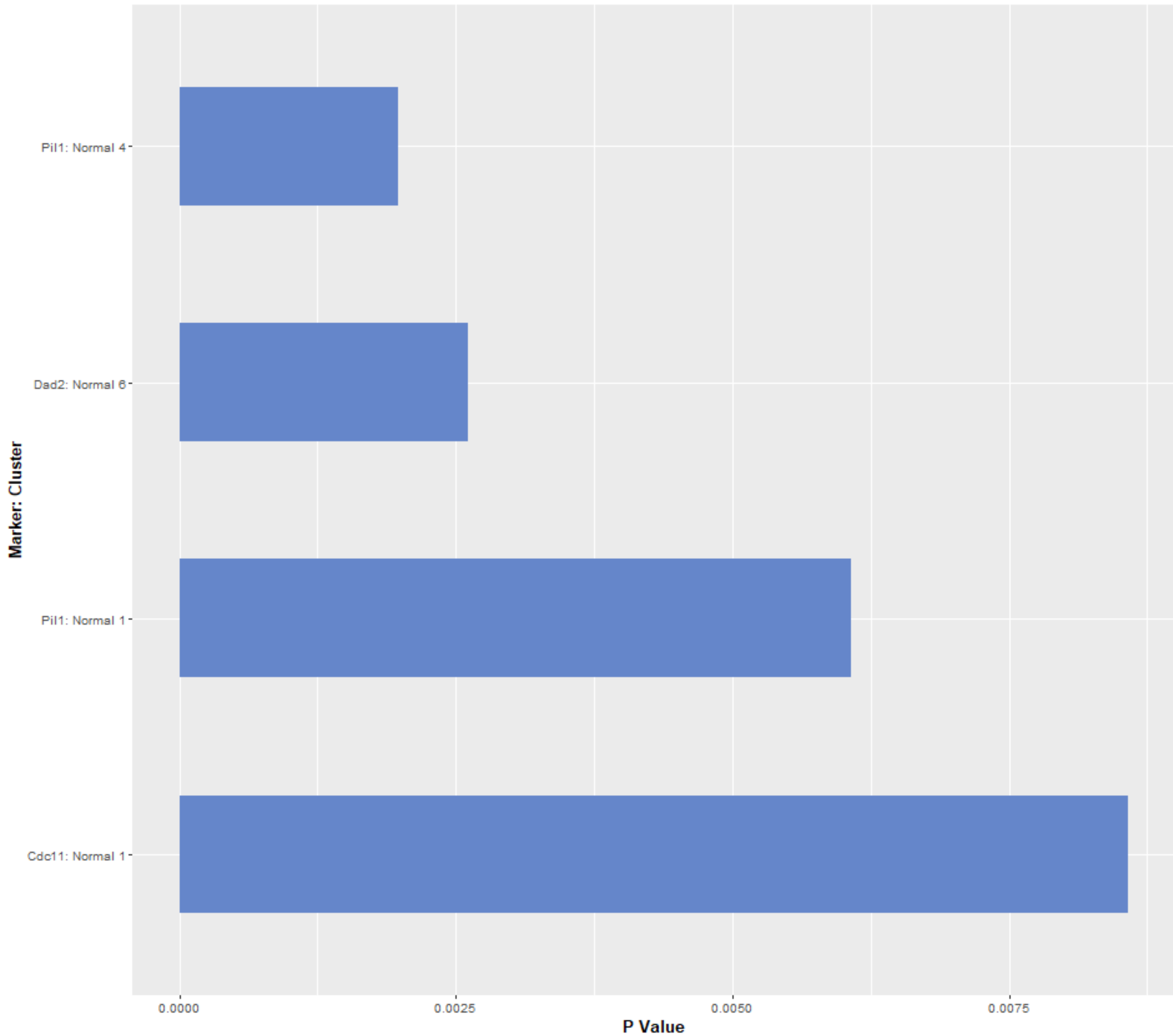
# transcription from RNA polymerase III promoter

With AreaShape | Ordered Gene Set





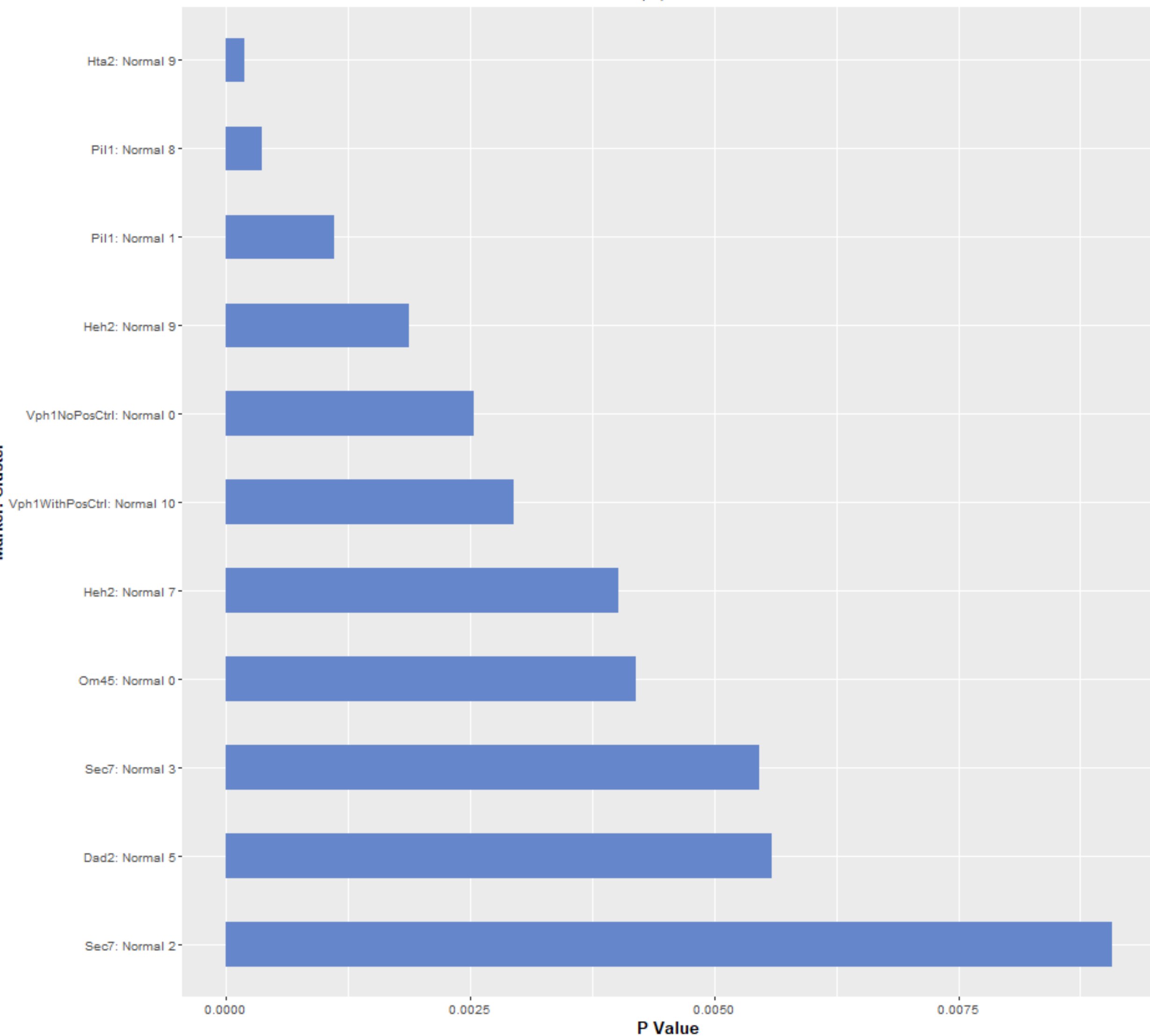
**translational elongation**  
With AreaShape | Ordered Gene Set



# translational initiation

With AreaShape | Ordered Gene Set

Marker: Cluster



# transmembrane transport

With AreaShape | Ordered Gene Set

Marker: Cluster

Heh2: Normal 9

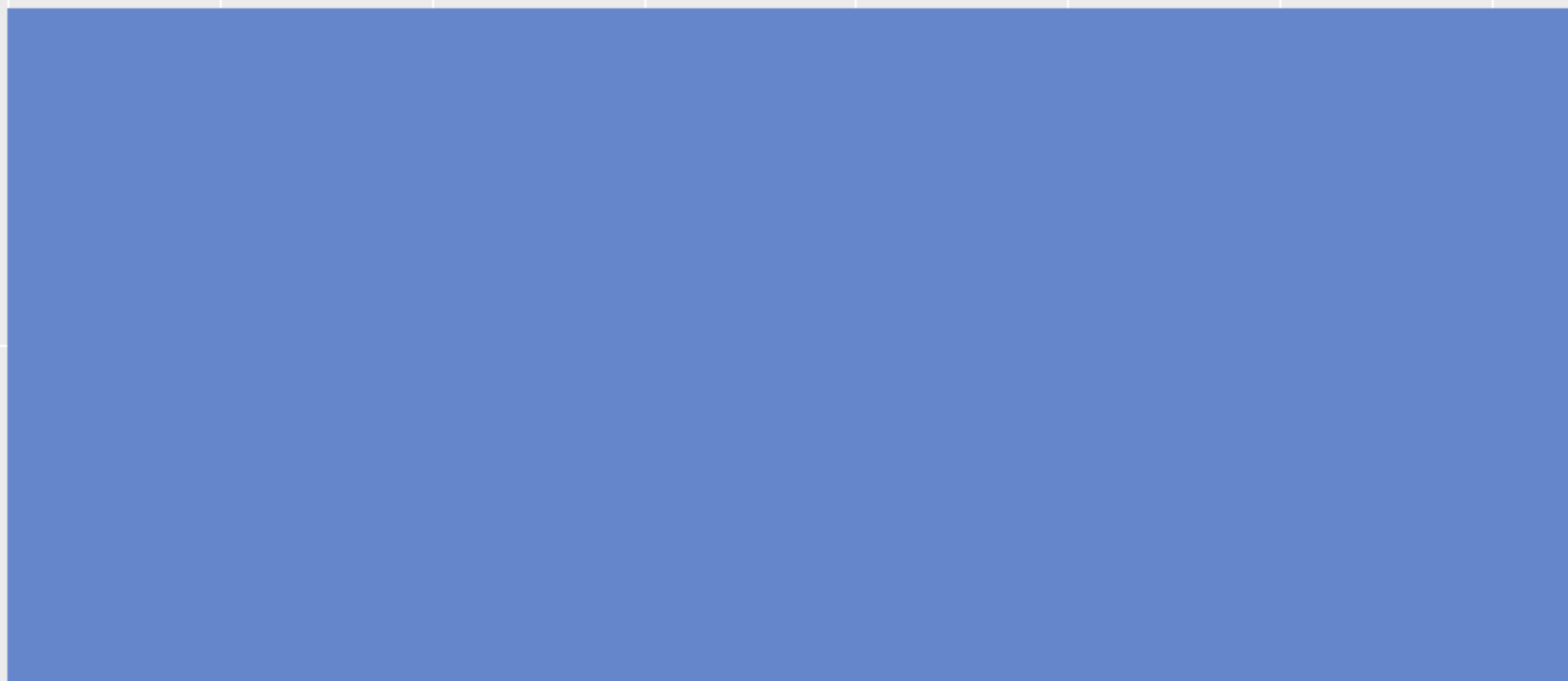
0.000

0.001

0.002

0.003

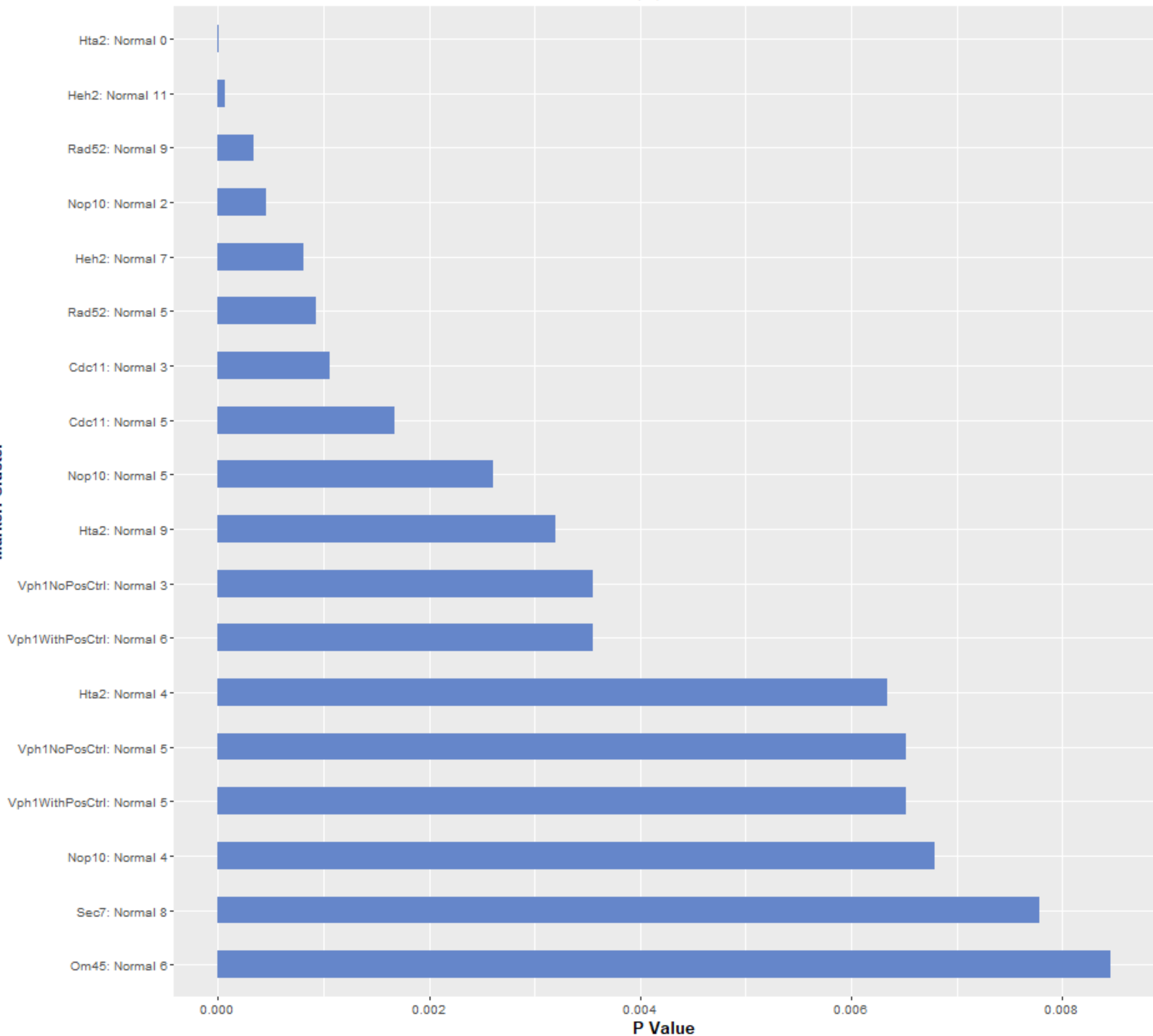
P Value



# transposition

With AreaShape | Ordered Gene Set

Marker: Cluster



# tRNA aminoacylation for protein translation

With AreaShape | Ordered Gene Set

Marker: Cluster

Pil1: Normal 8

Heh2: Normal 9

Om45: Normal 8

Heh2: Normal 8

Om45: Normal 9

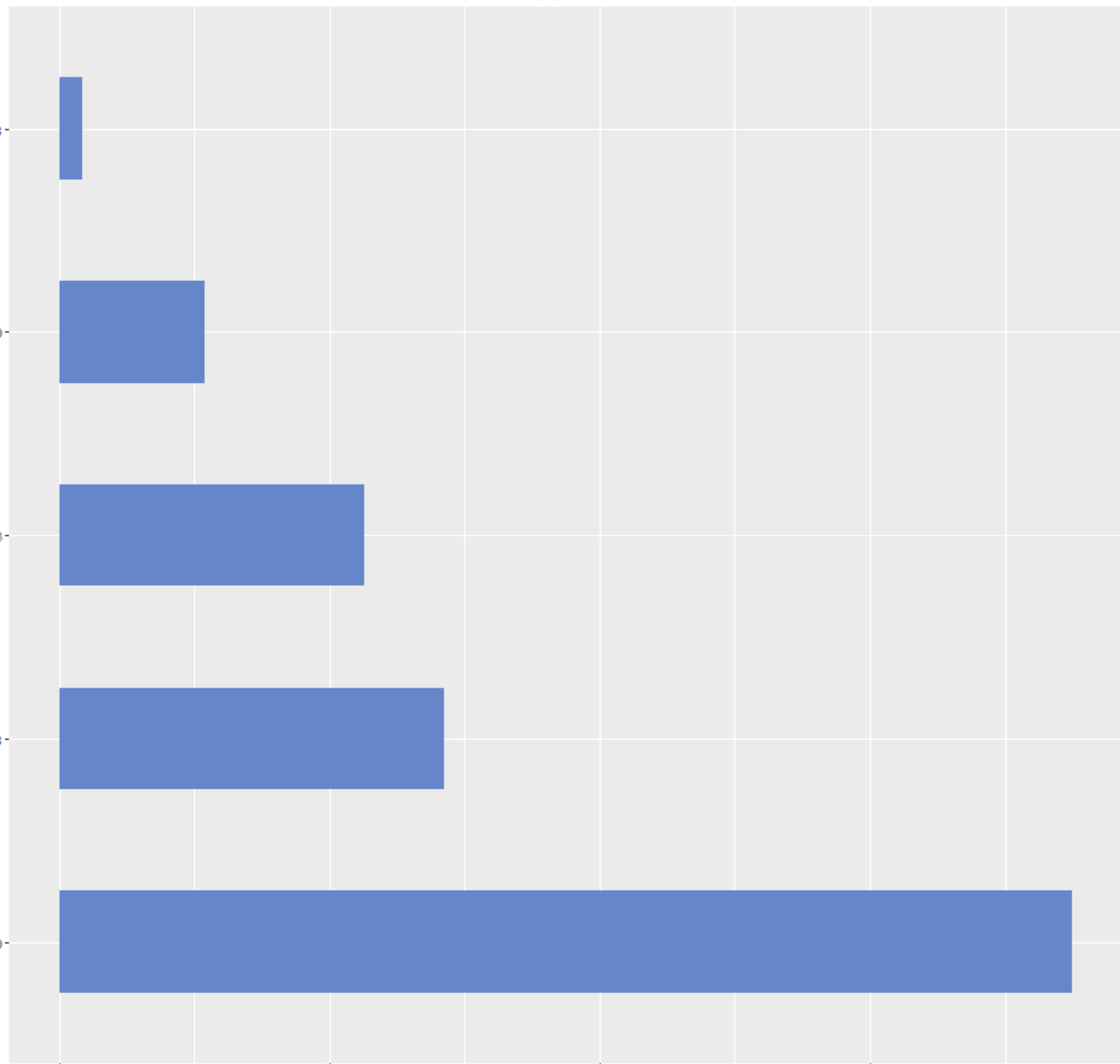
0.000

0.001

0.002

0.003

P Value



# tRNA processing

With AreaShape | Ordered Gene Set

Marker: Cluster

Rad52: Normal 9

Rad52: Normal 11

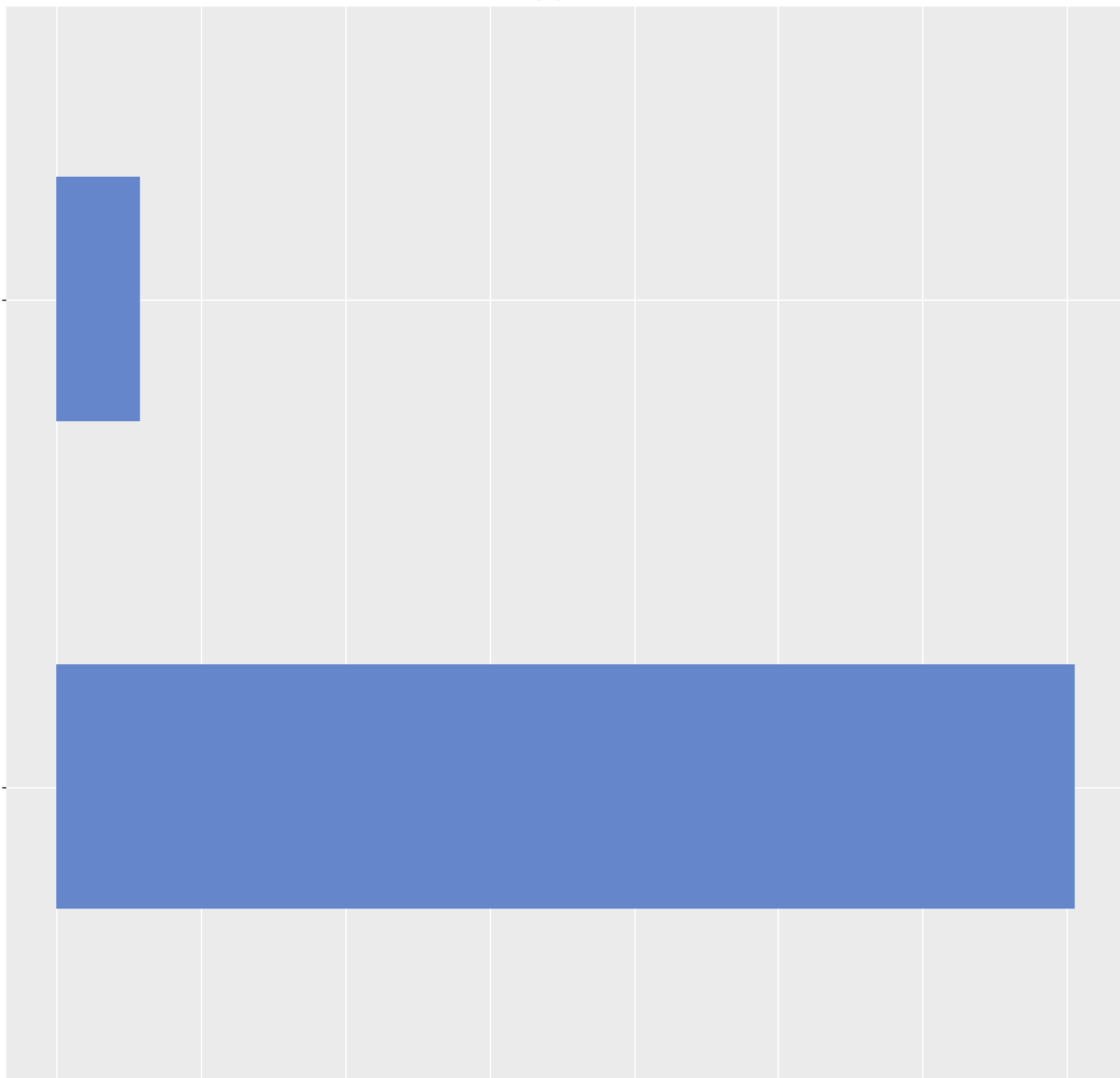
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0.0025

0.0050

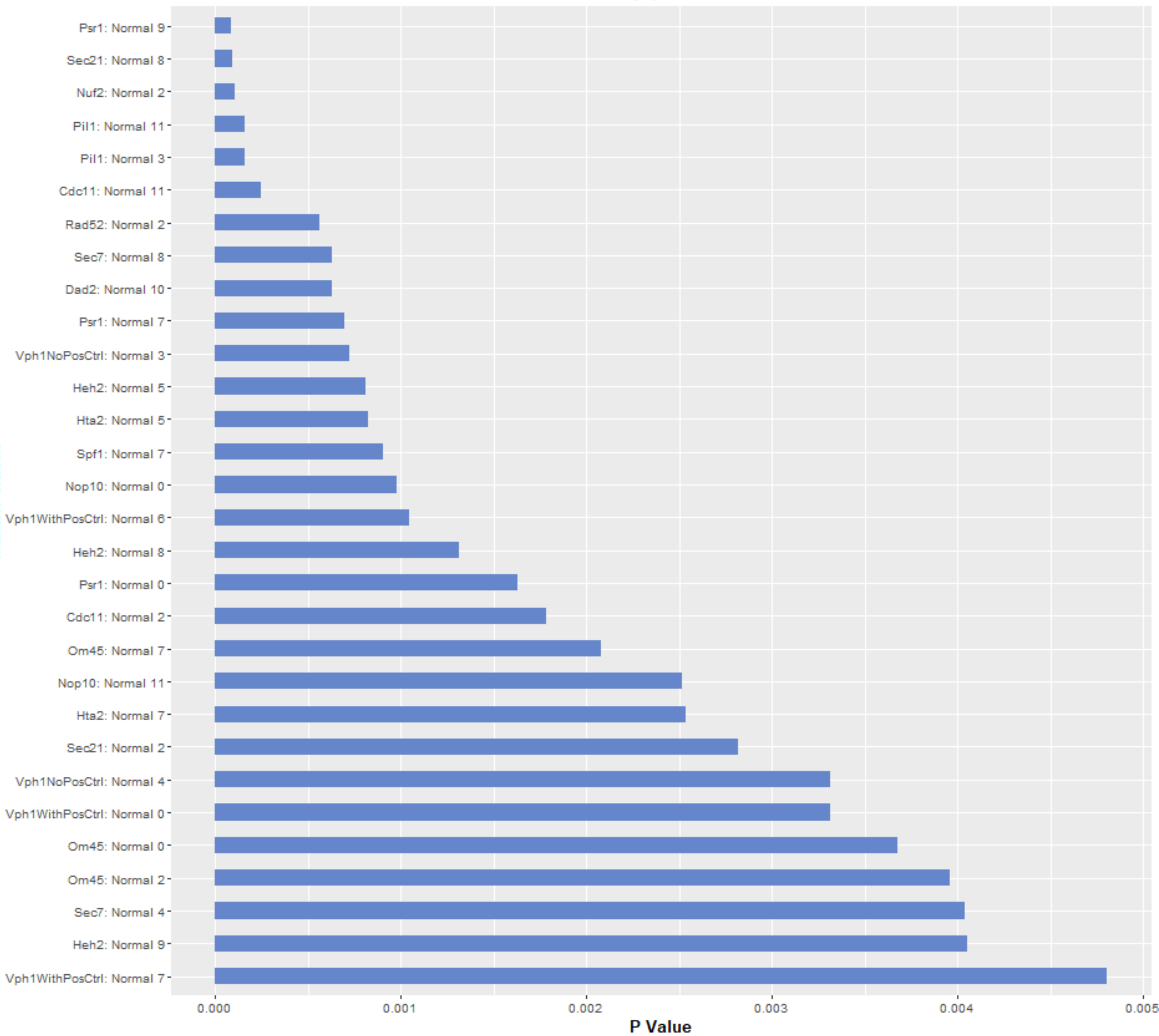
0.0075

P Value



**vacuole organization**  
With AreaShape | Ordered Gene Set

**Marker: Cluster**



vesicle organization  
With AreaShape | Ordered Gene Set

