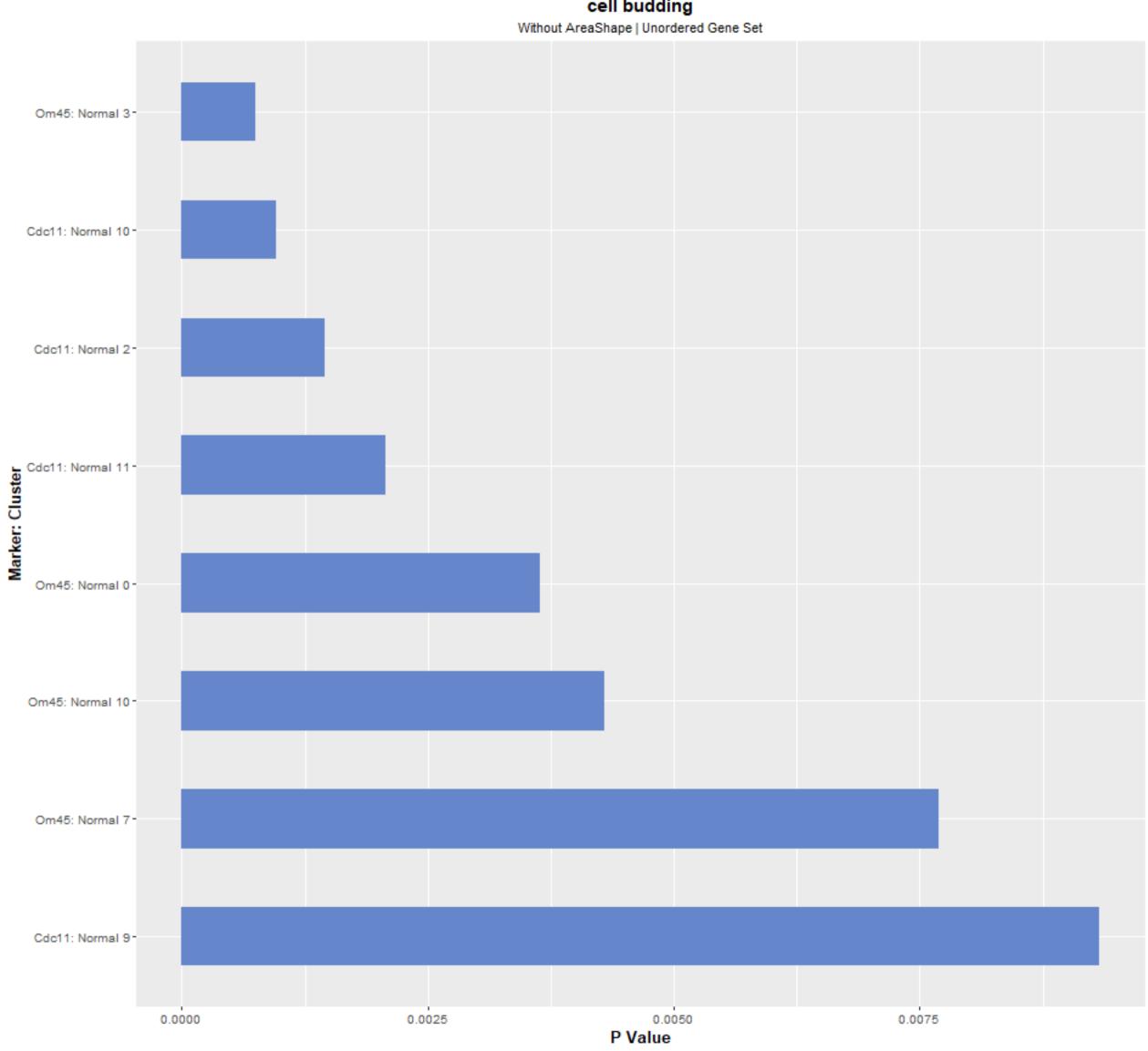
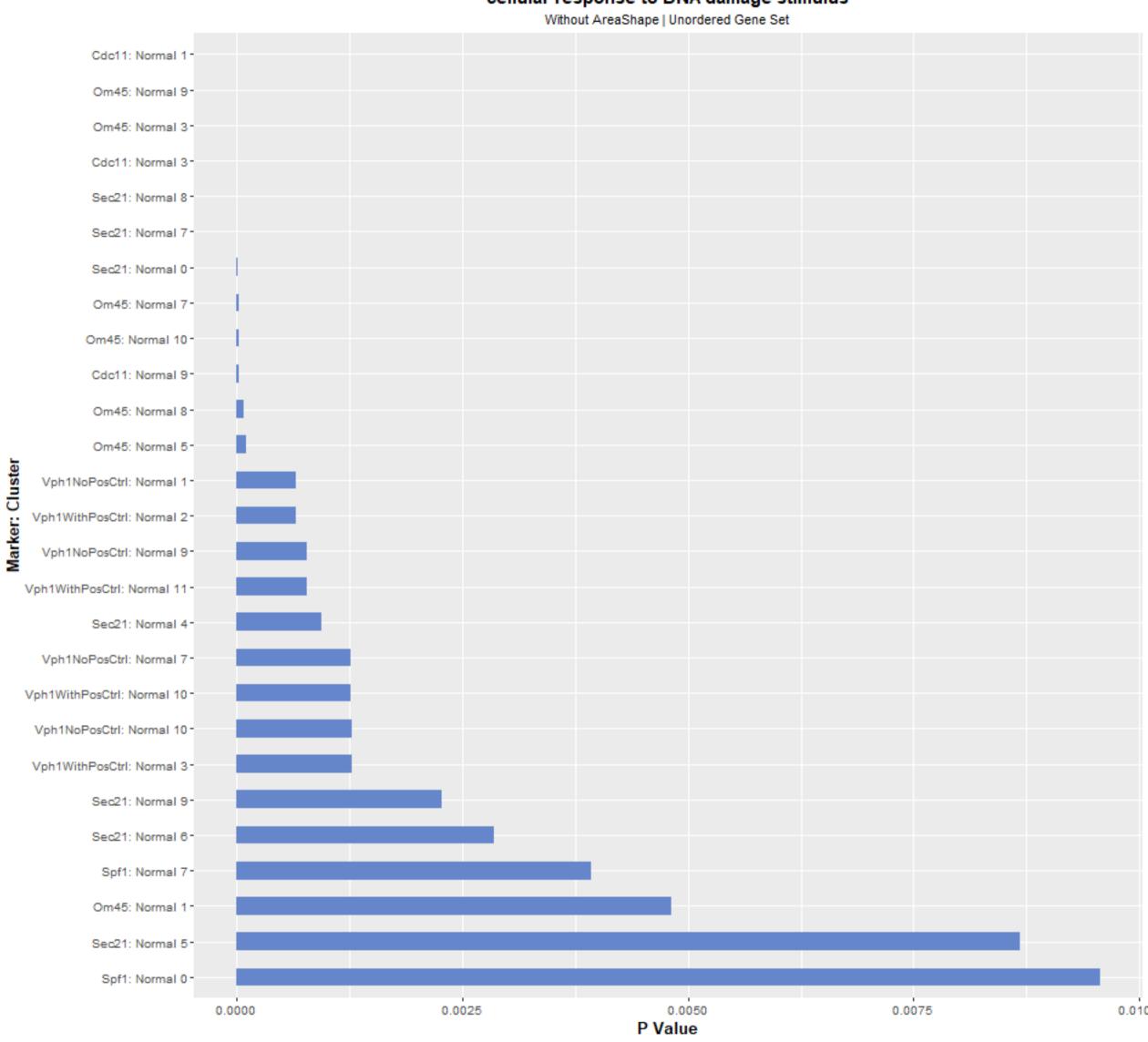
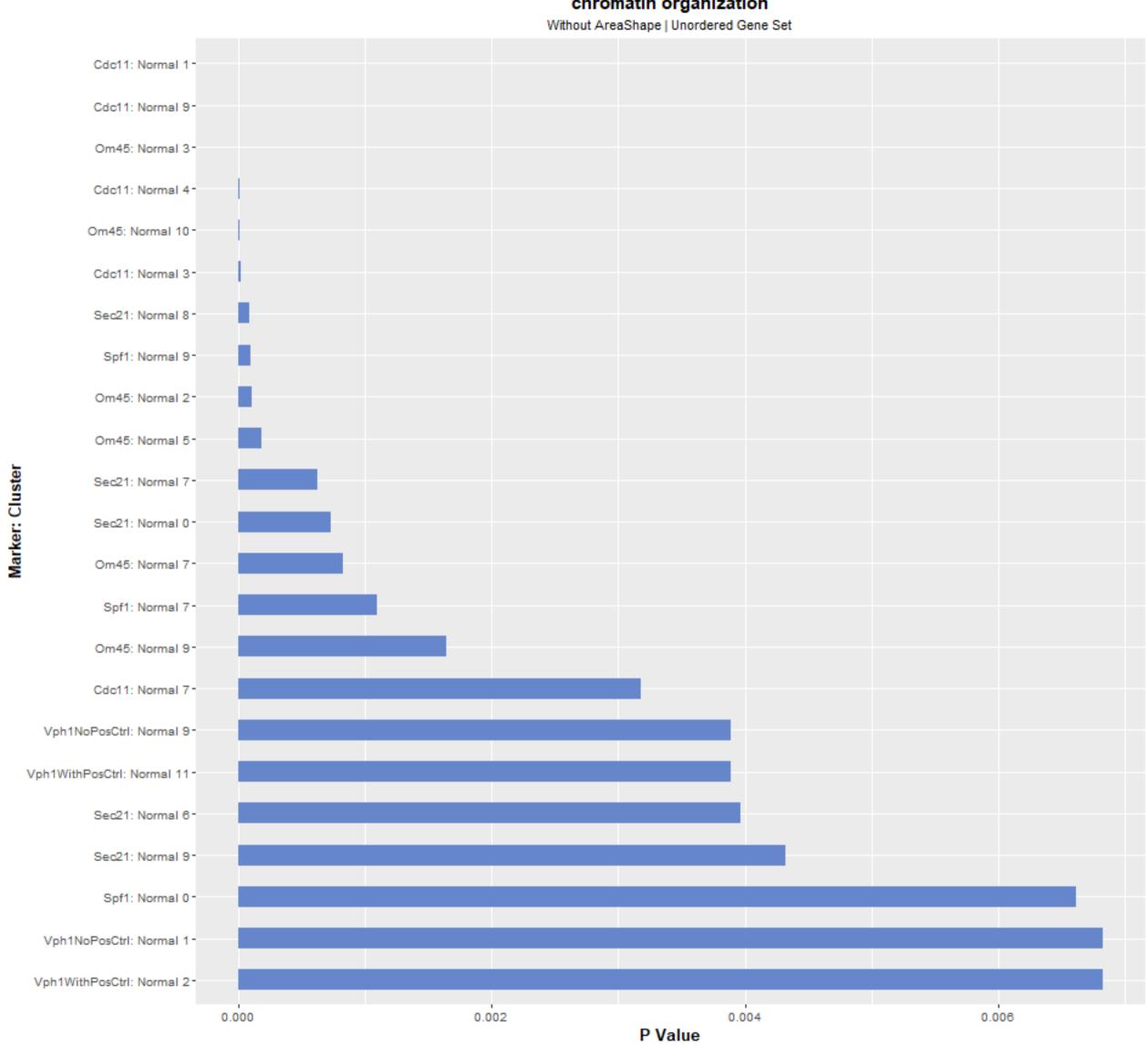
cell budding



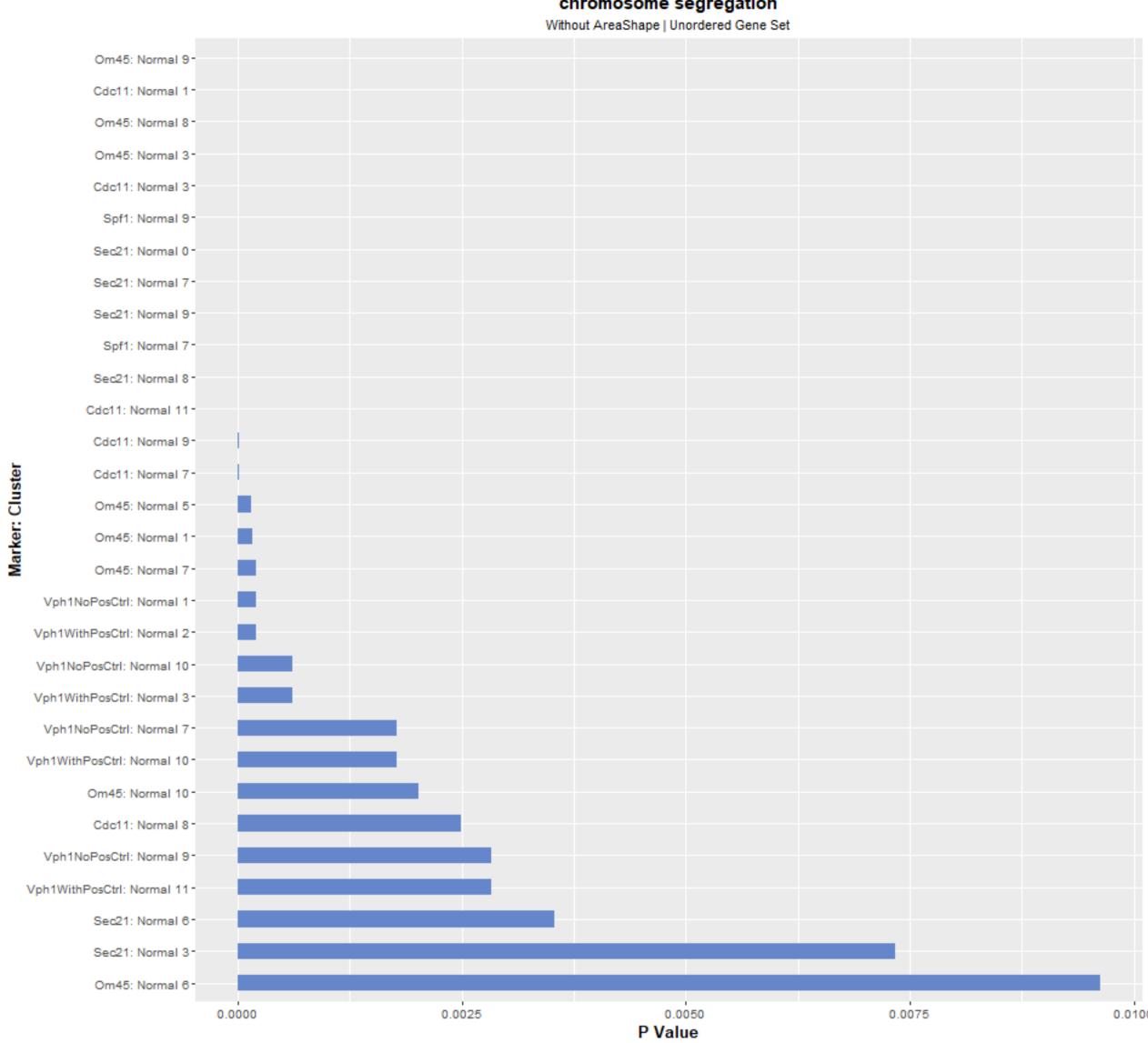
### cellular response to DNA damage stimulus

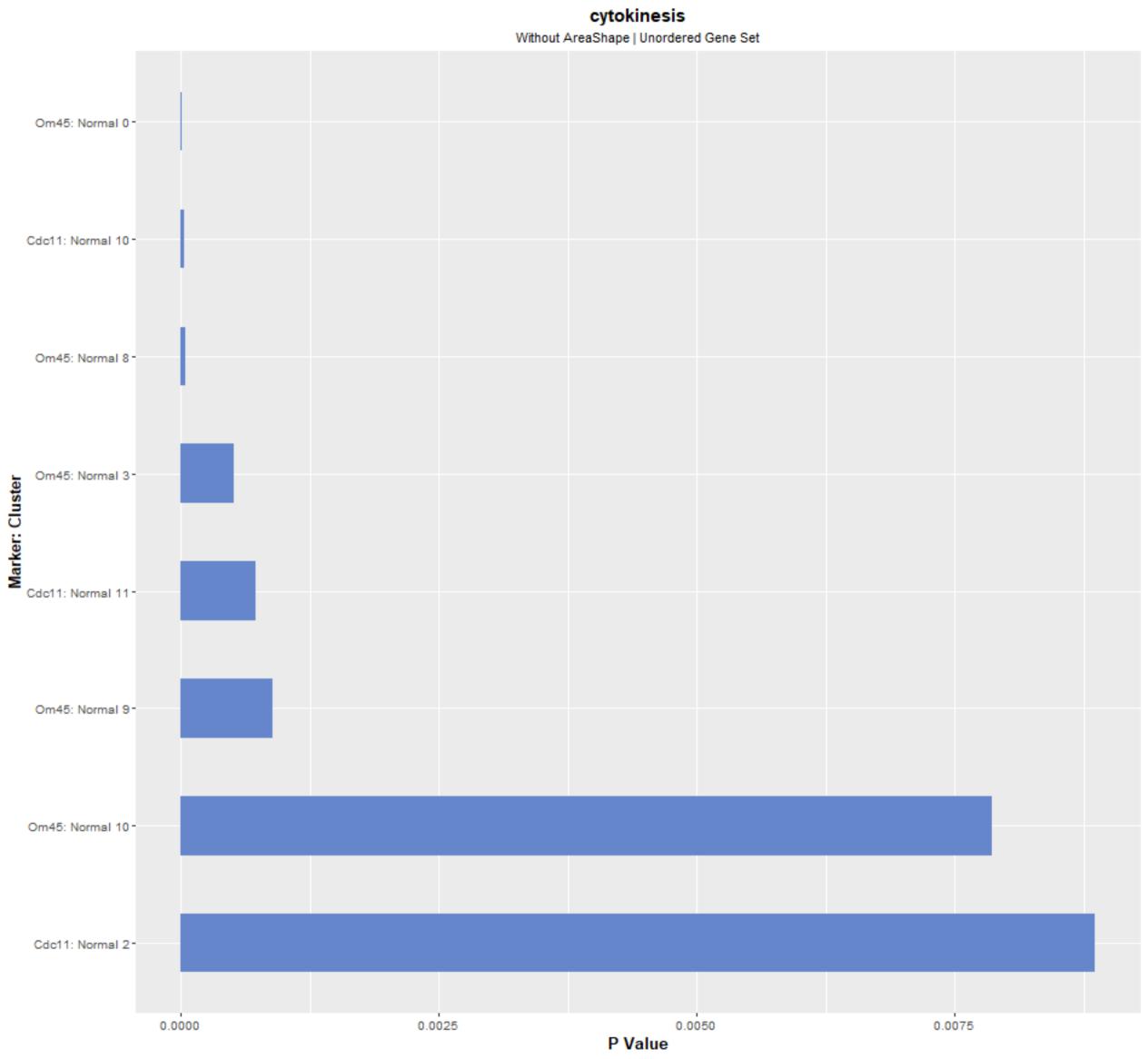


chromatin organization

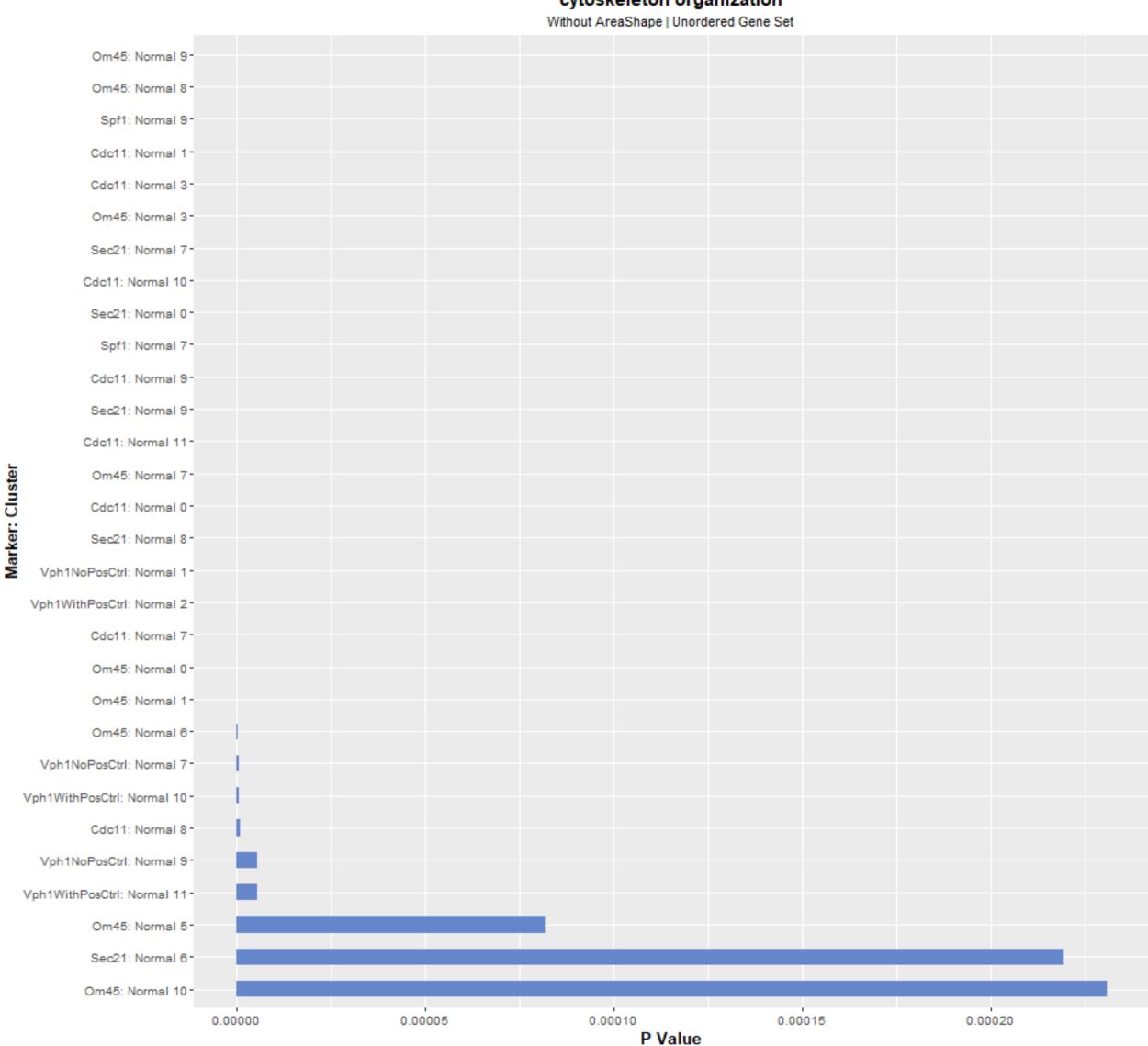


chromosome segregation

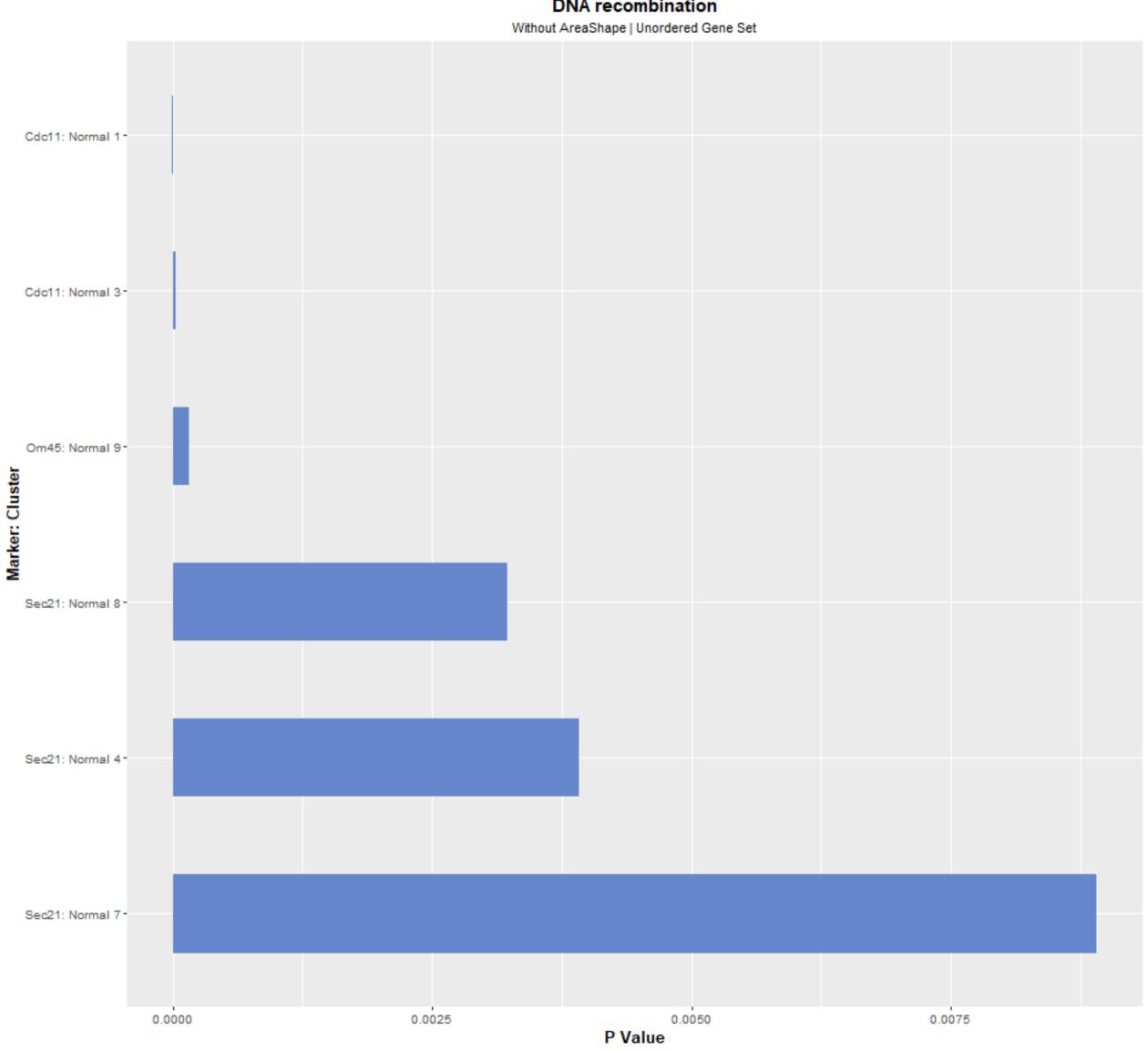




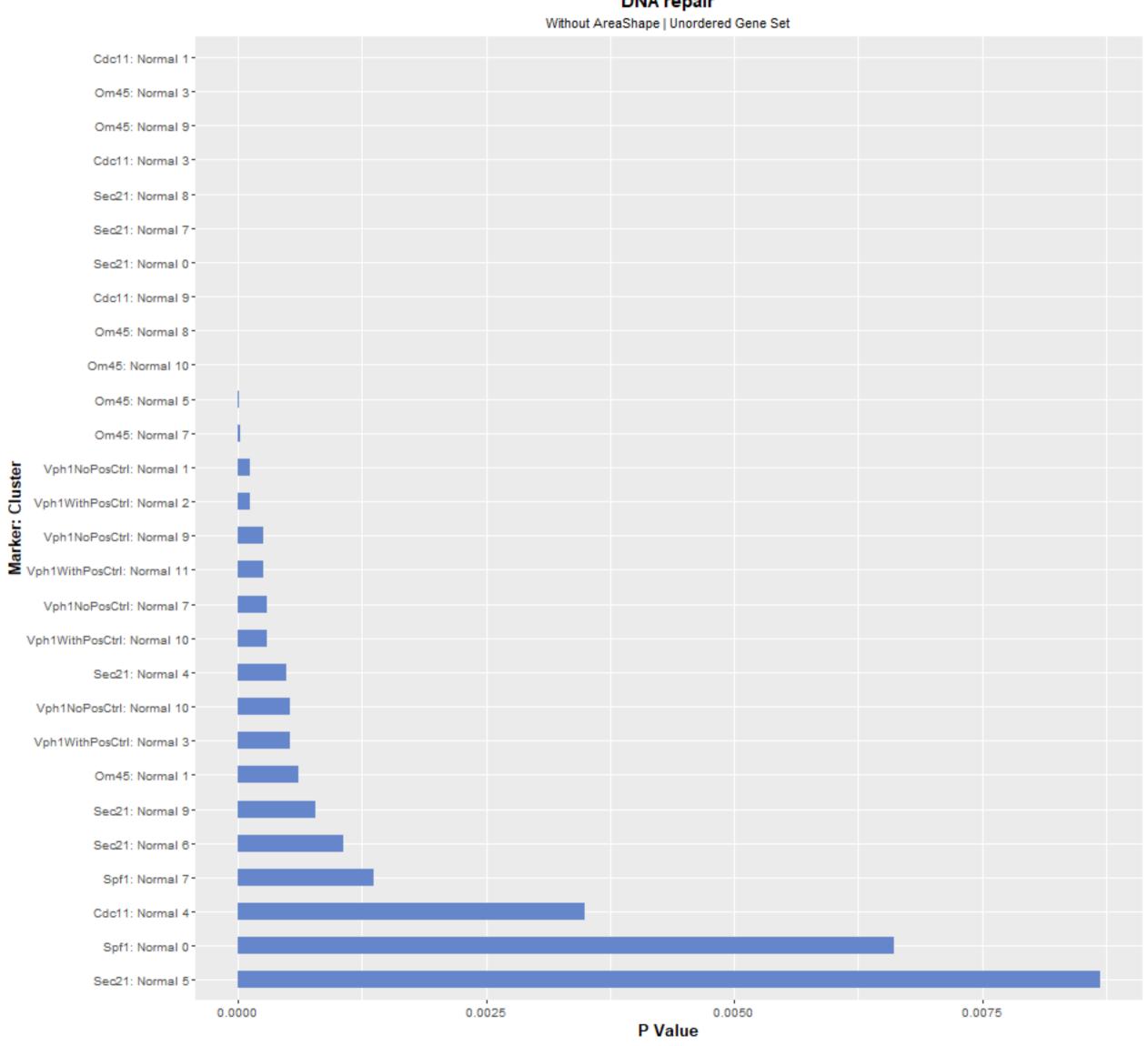
cytoskeleton organization



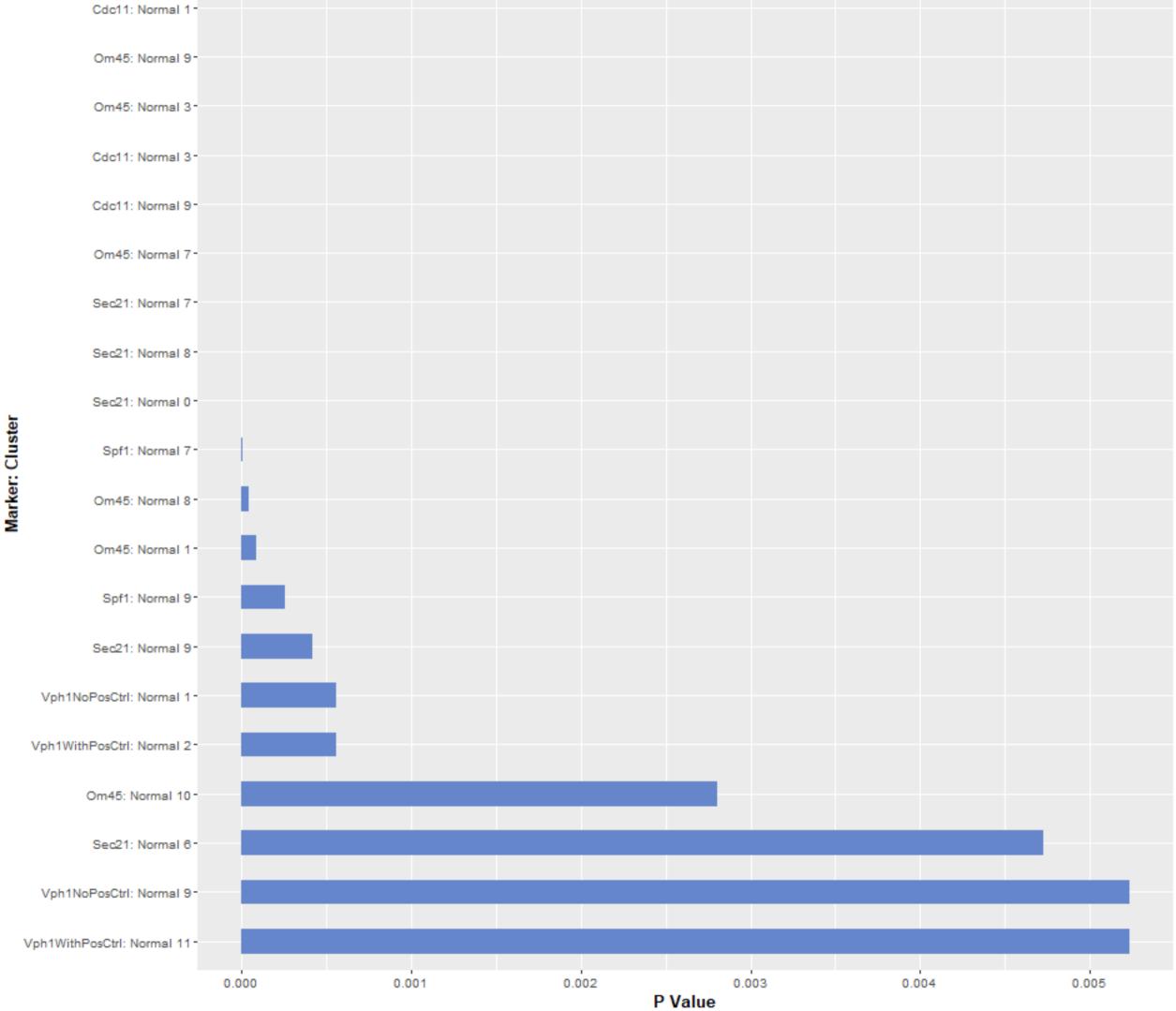
### **DNA** recombination



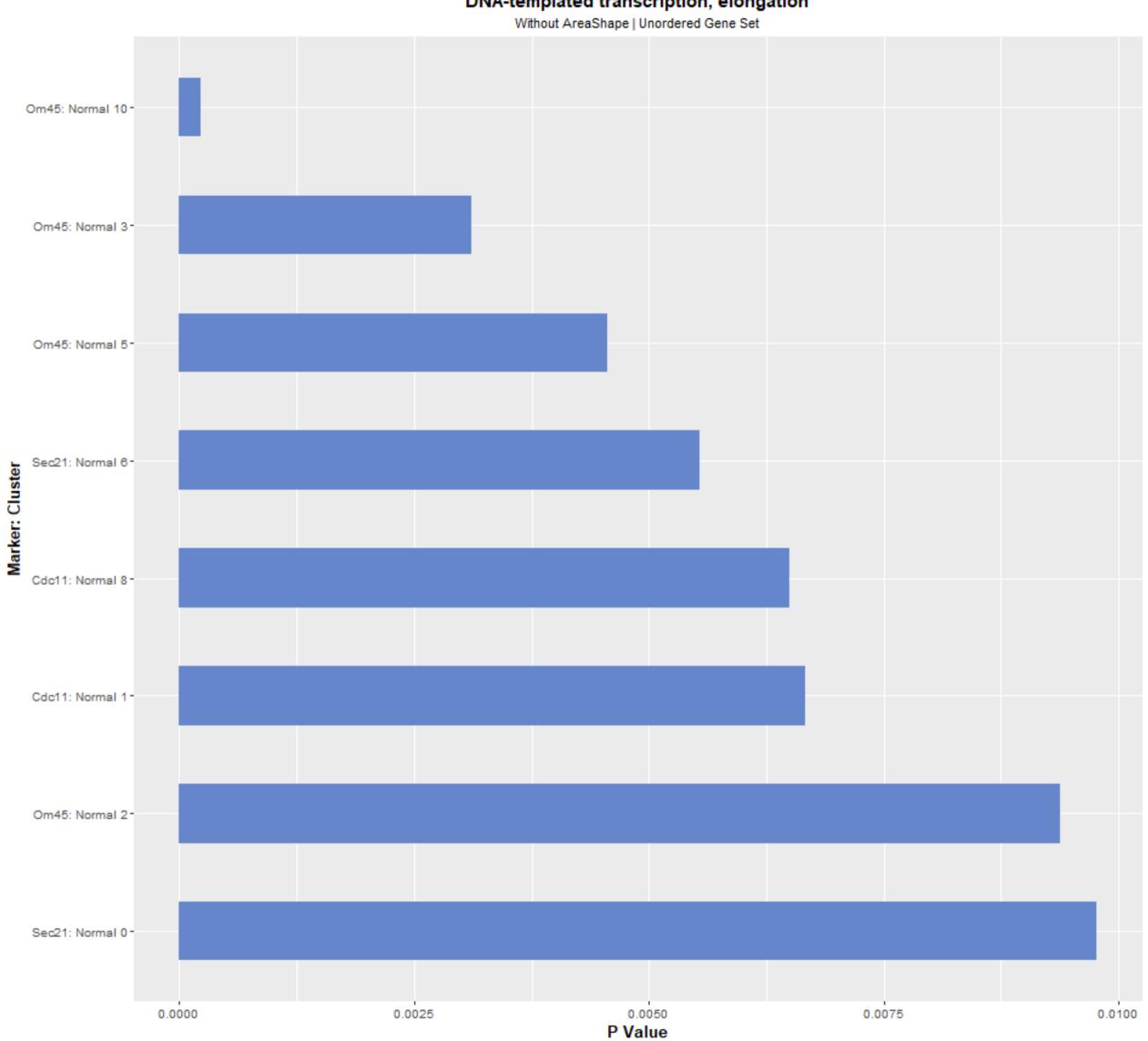
**DNA** repair



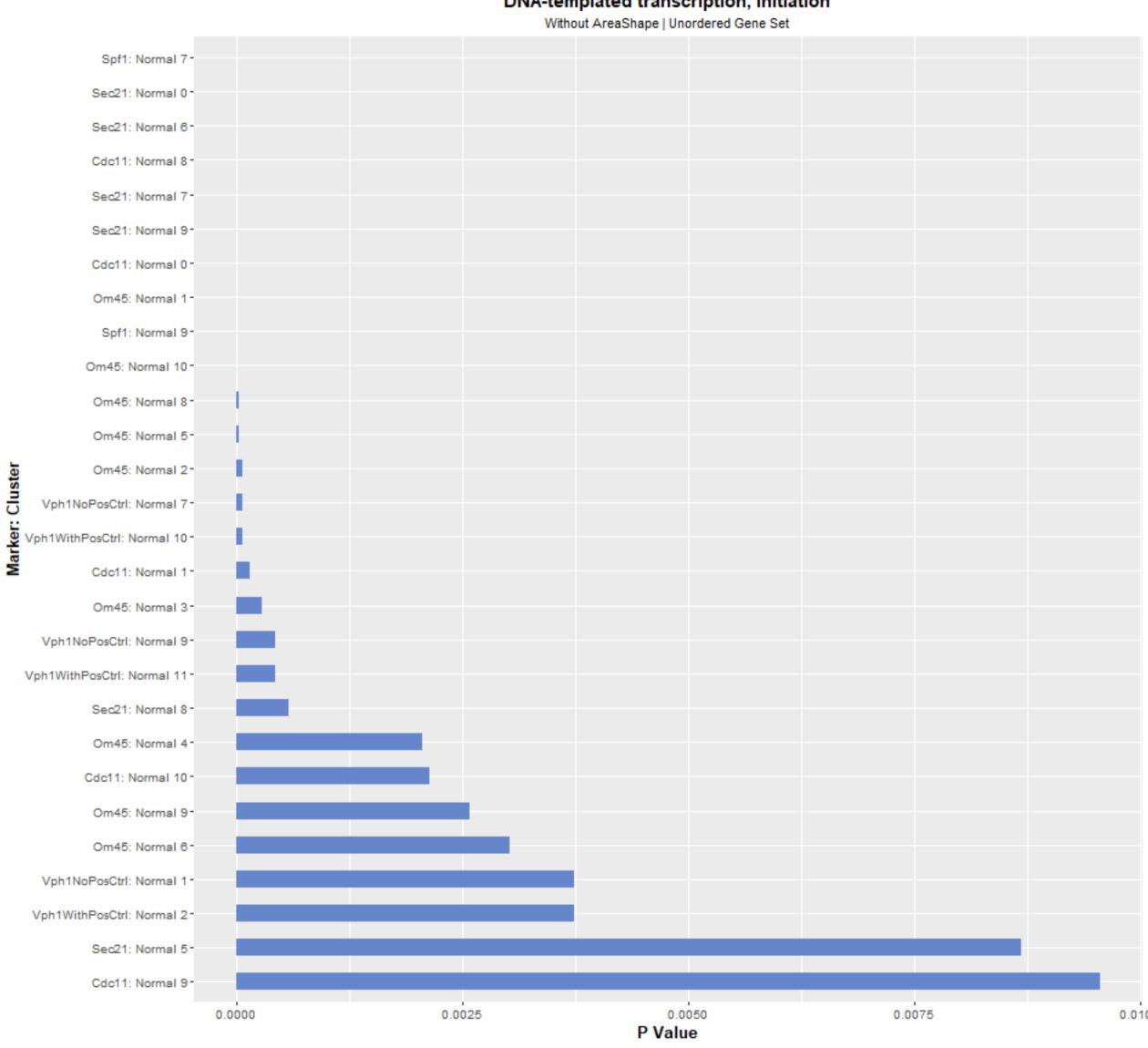
**DNA** replication Without AreaShape | Unordered Gene Set Cdc11: Normal 1-Om45: Normal 9 -Om45: Normal 3-Cdc11: Normal 31 Cdc11: Normal 91 Om45: Normal 7 -



### DNA-templated transcription, elongation



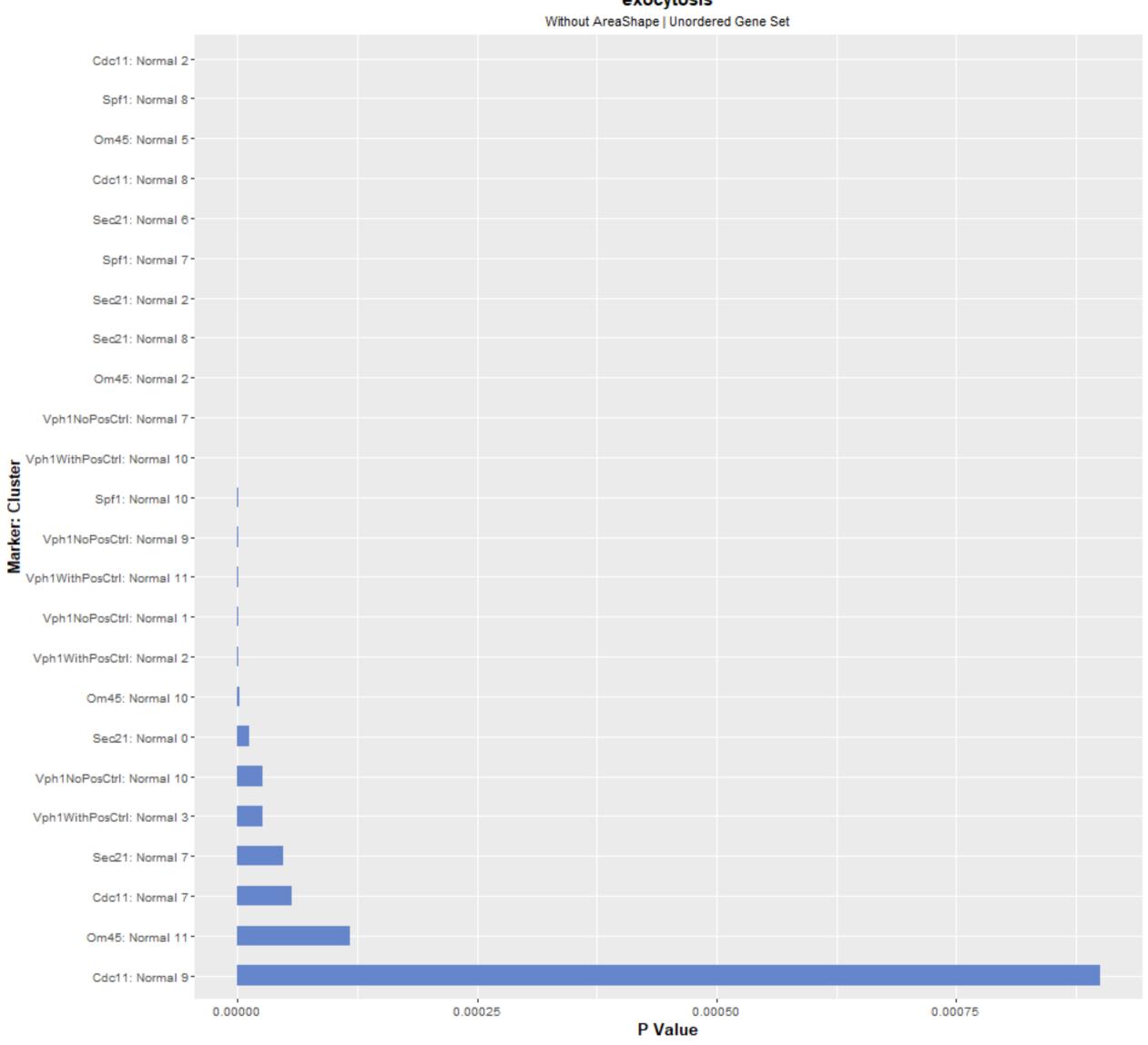
### DNA-templated transcription, initiation



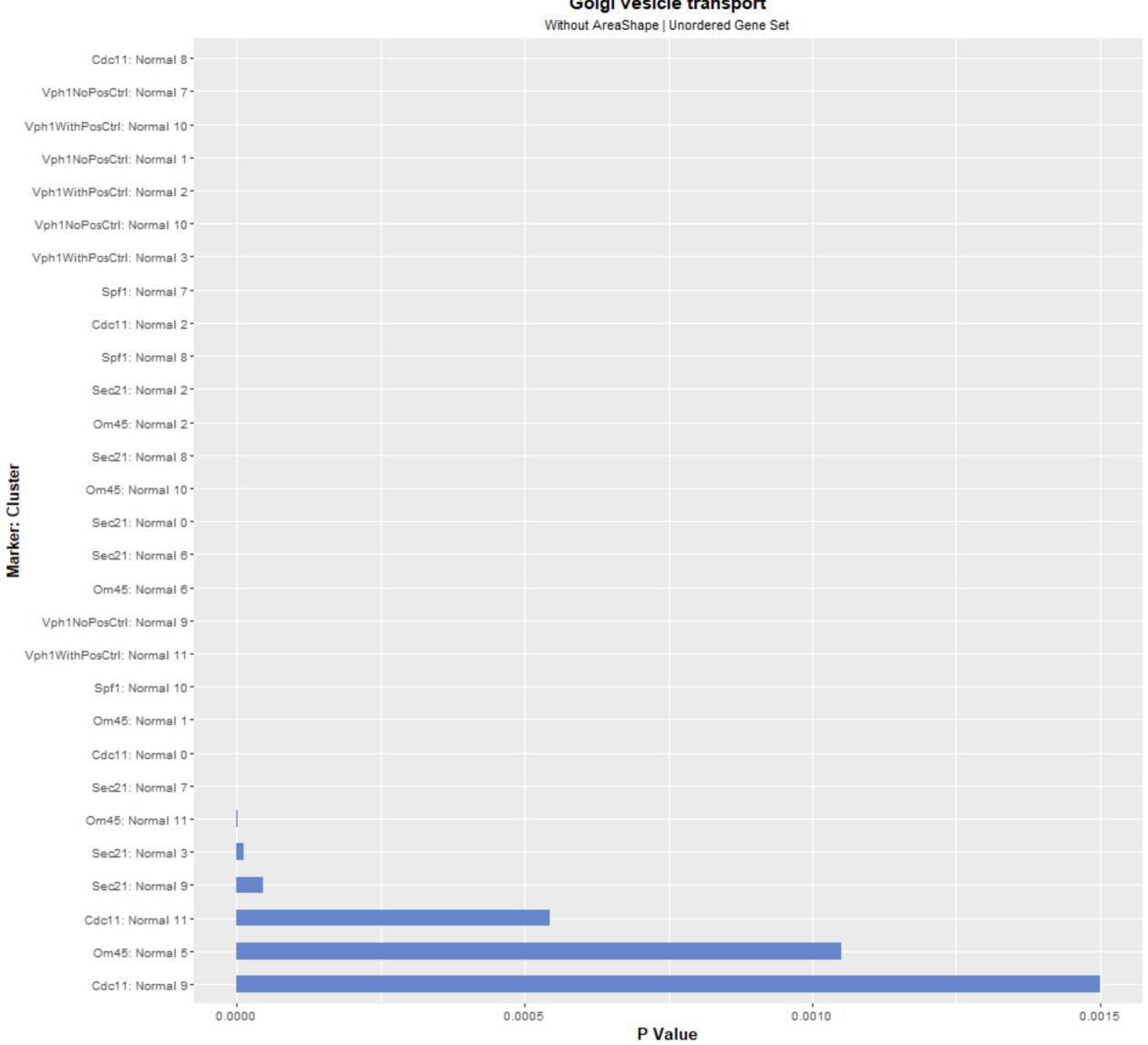
### DNA-templated transcription, termination Without AreaShape | Unordered Gene Set Vph1NoPosCtrl: Normal 7 Vph1WithPosCtrl: Normal 10 -Vph1NoPosCtrl: Normal 9 -Vph1WithPosCtrl: Normal 11 -Om45: Normal 10 -Marker: Cluster Om45: Normal 8 -Om45: Normal 31 Vph1NoPosCtrl: Normal 10 -Vph1WithPosCtrl: Normal 3 -Cdc11: Normal 8 -Vph1NoPosCtrl: Normal 1 -Vph1WithPosCtrl: Normal 2 -0.000 0.001 0.002 0.003 P Value

endocytosis Without AreaShape | Unordered Gene Set Cdc11: Normal 21 Marker: Cluster Cdc11: Normal 10 -0.004 0.000 0.002 0.006 0.008 P Value

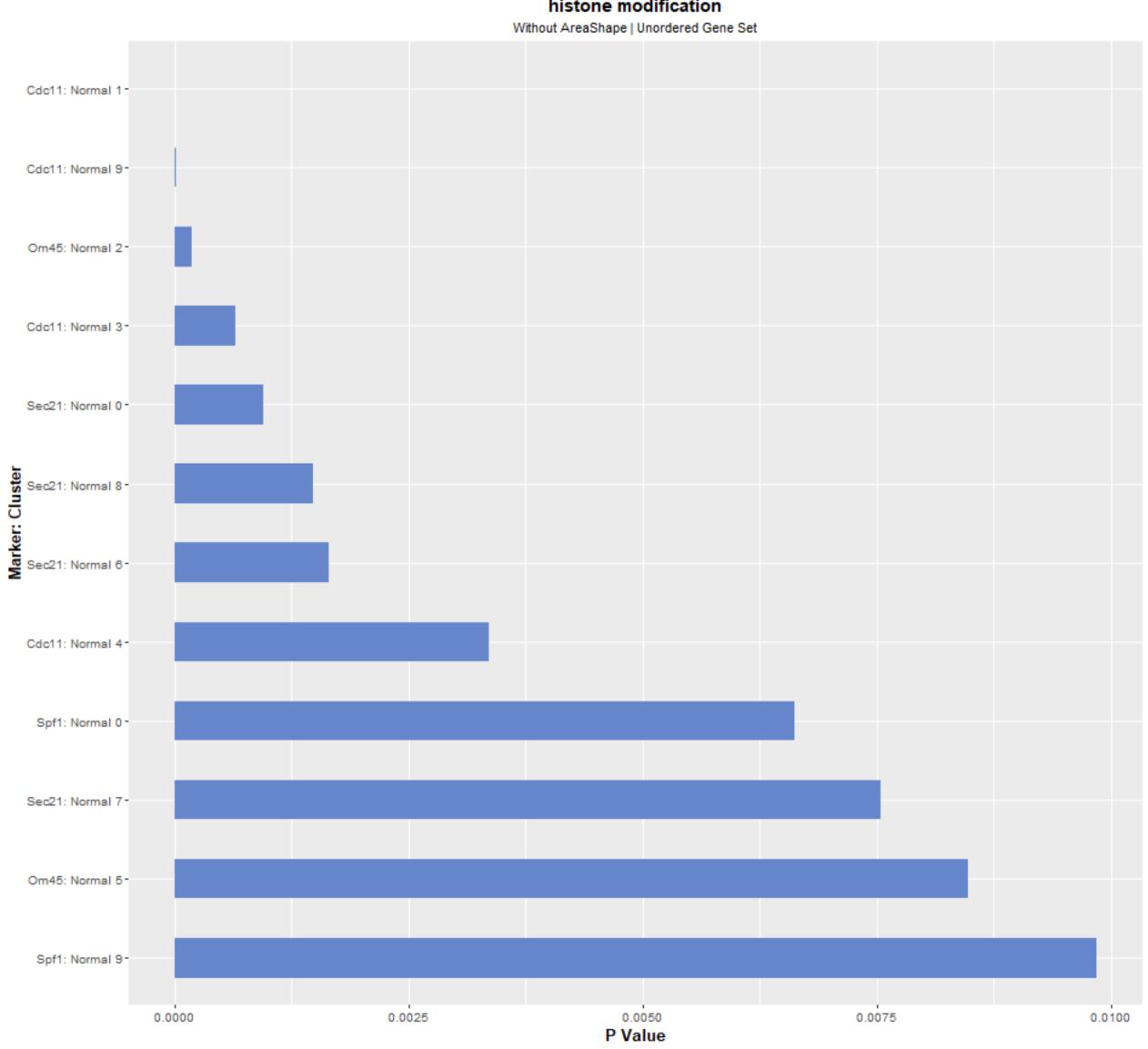
exocytosis



### Golgi vesicle transport

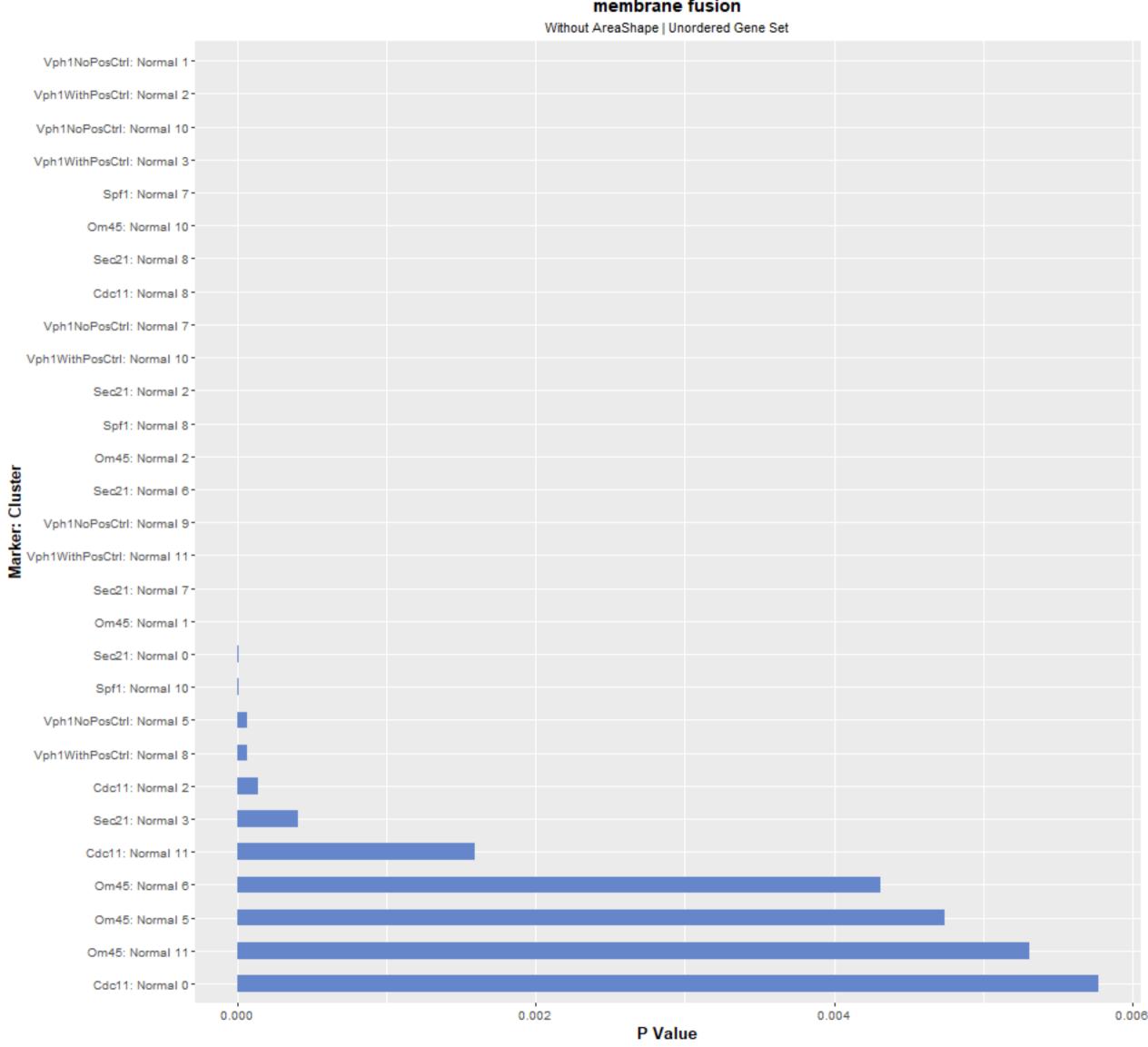


#### histone modification

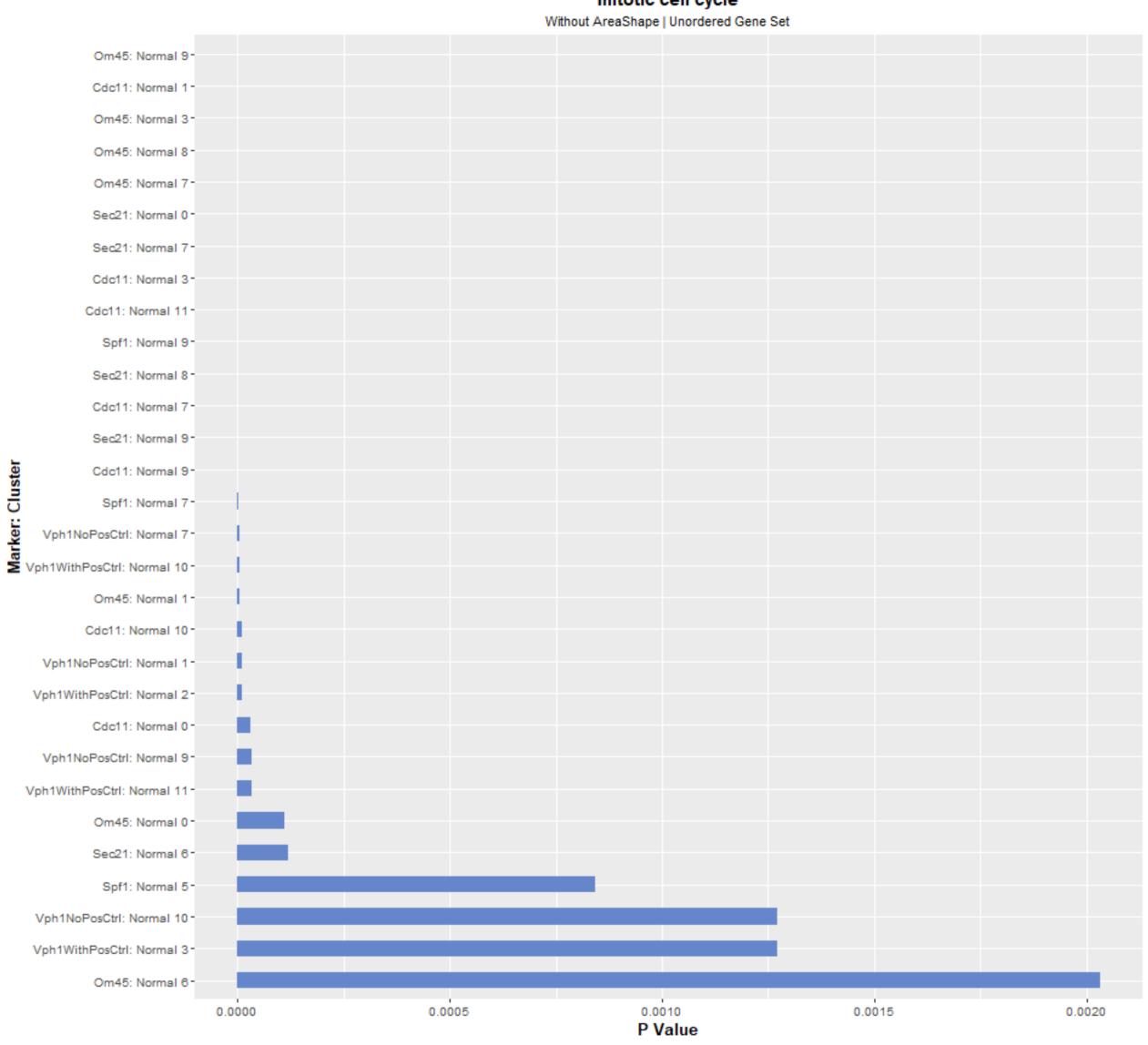


lipid metabolic process Without AreaShape | Unordered Gene Set Vph1NoPosCtrl: Normal 1 -Vph1WithPosCtrl: Normal 2-Vph1NoPosCtrl: Normal 9 -Vph1WithPosCtrl: Normal 11 -Cdc11: Normal 0 -Sec21: Normal 0 -Om45: Normal 31 Marker: Cluster Om45: Normal 1-Cdc11: Normal 8 -Om45: Normal 10 -Sec21: Normal 6-Om45: Normal 111 Sec21: Normal 8 -Om45: Normal 21 Om45: Normal 6-0.0050 0.0000 0.0025 0.0075 0.0100 P Value

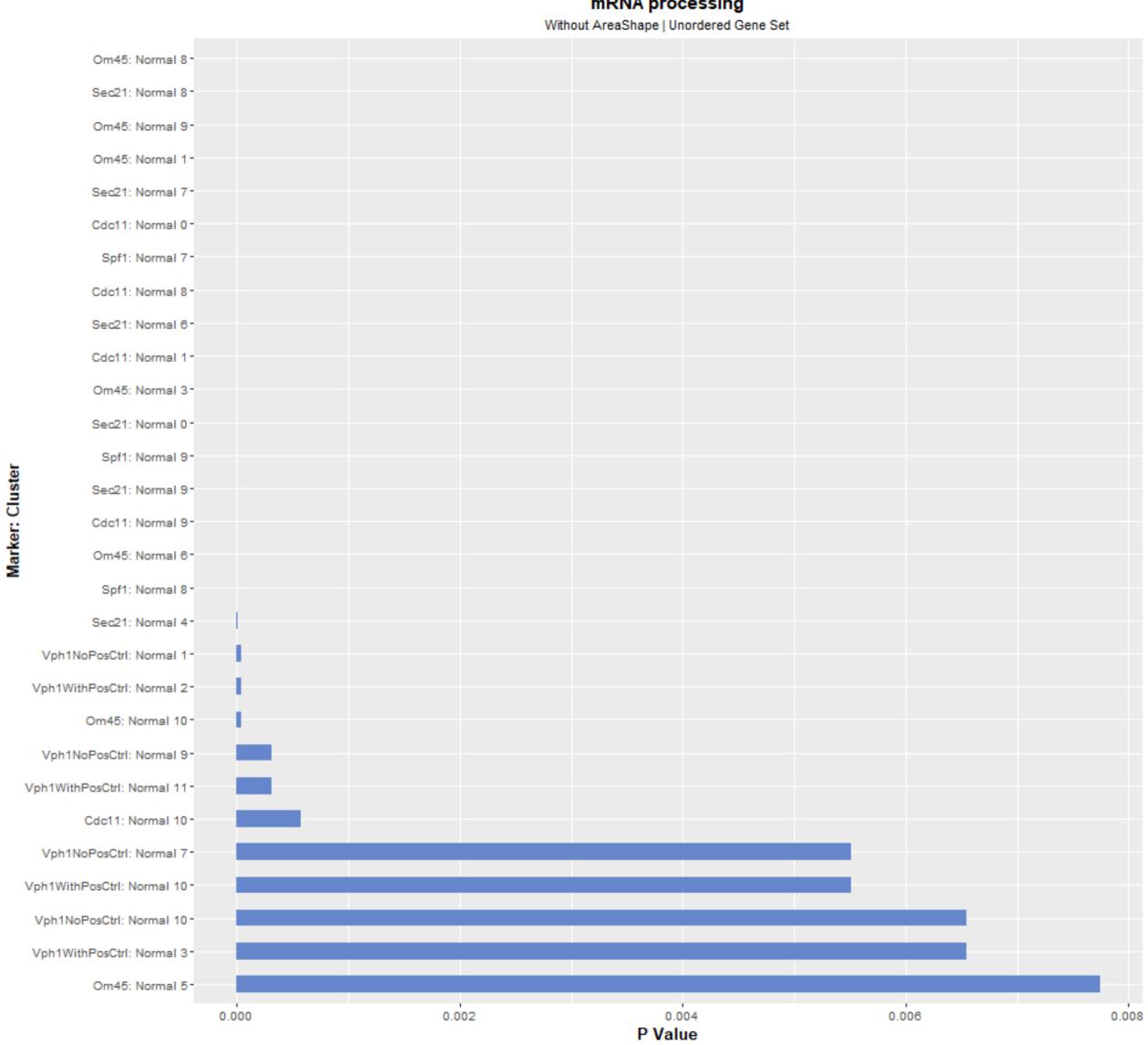
membrane fusion



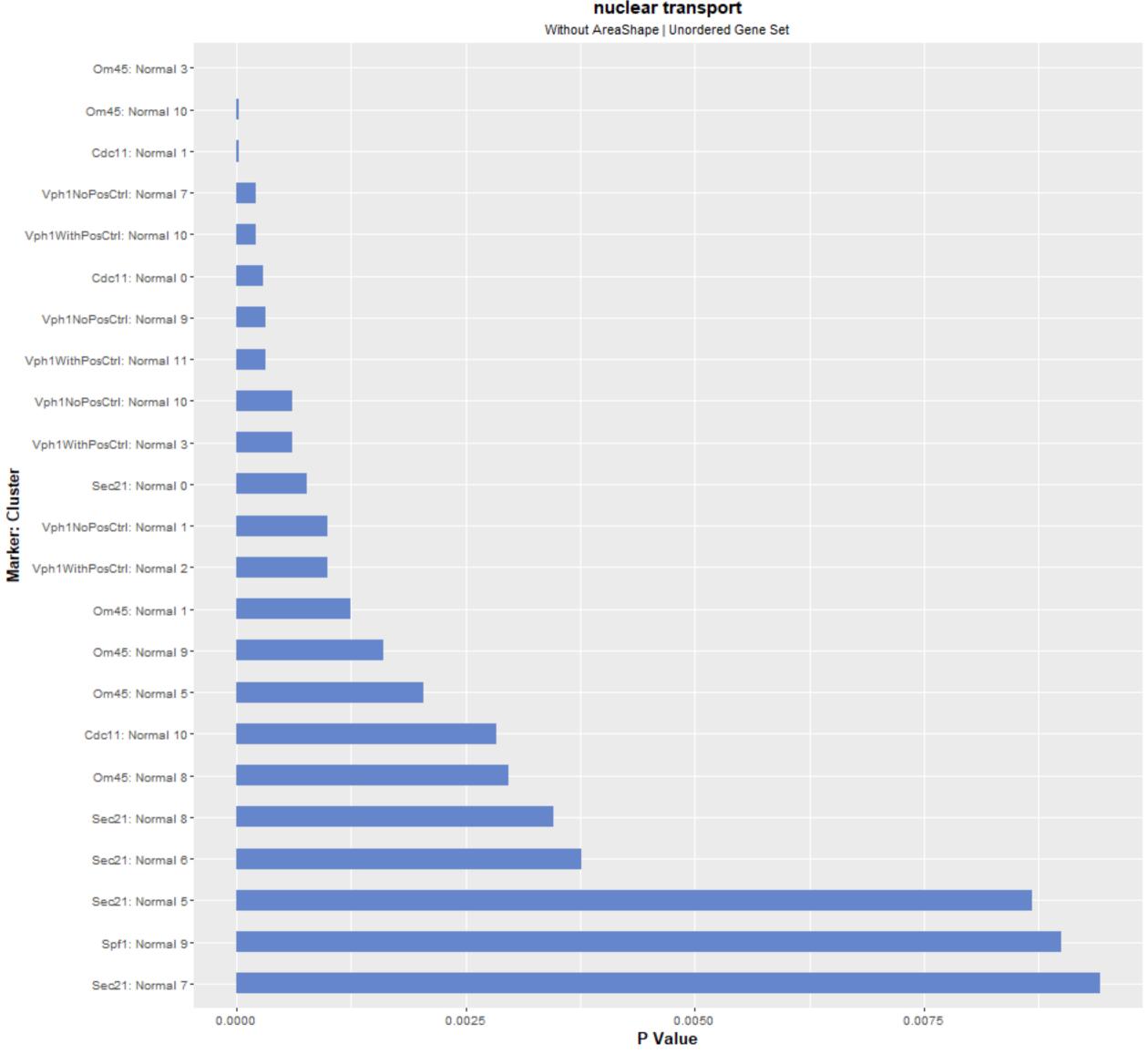
mitotic cell cycle



mRNA processing



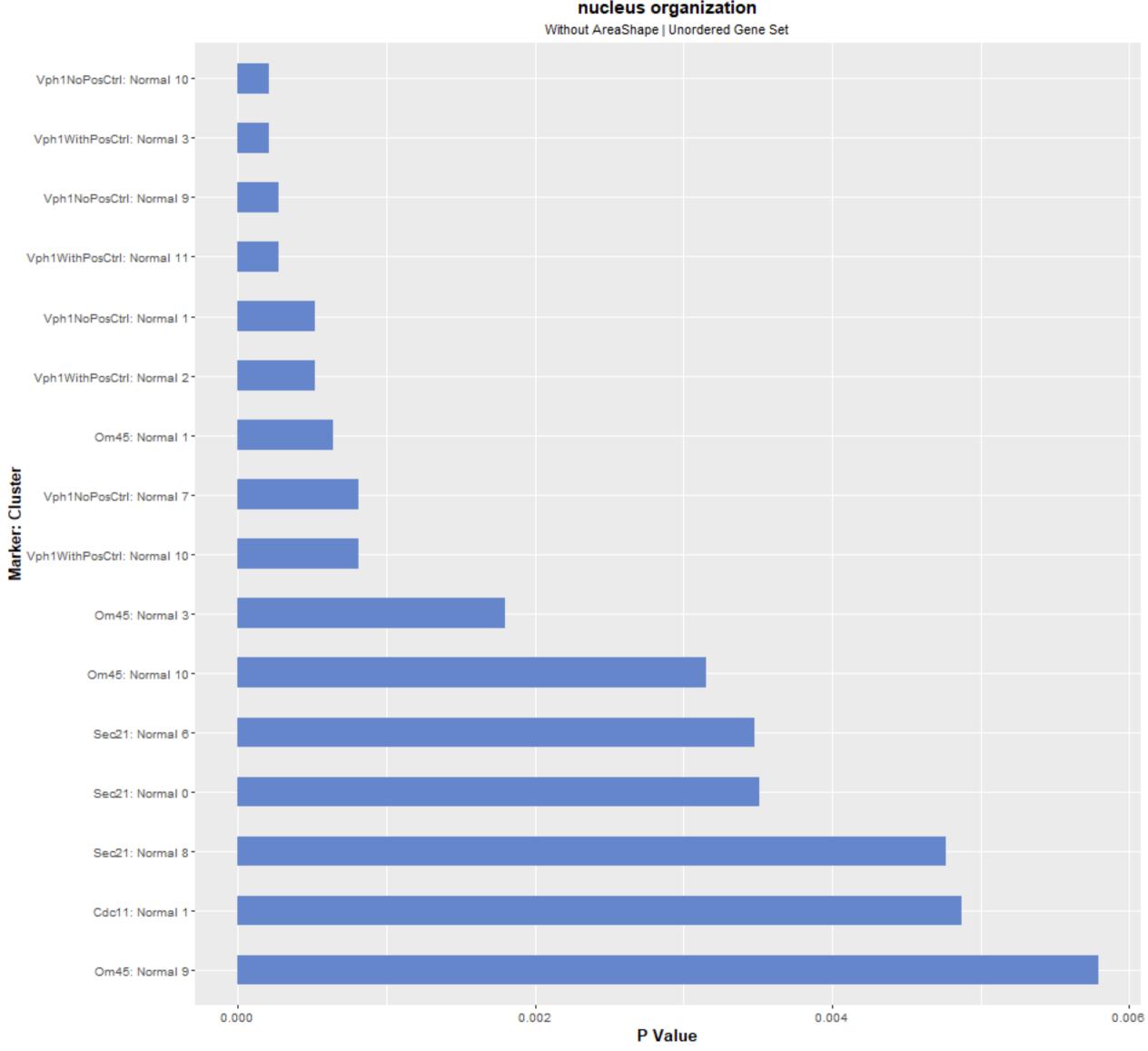
nuclear transport



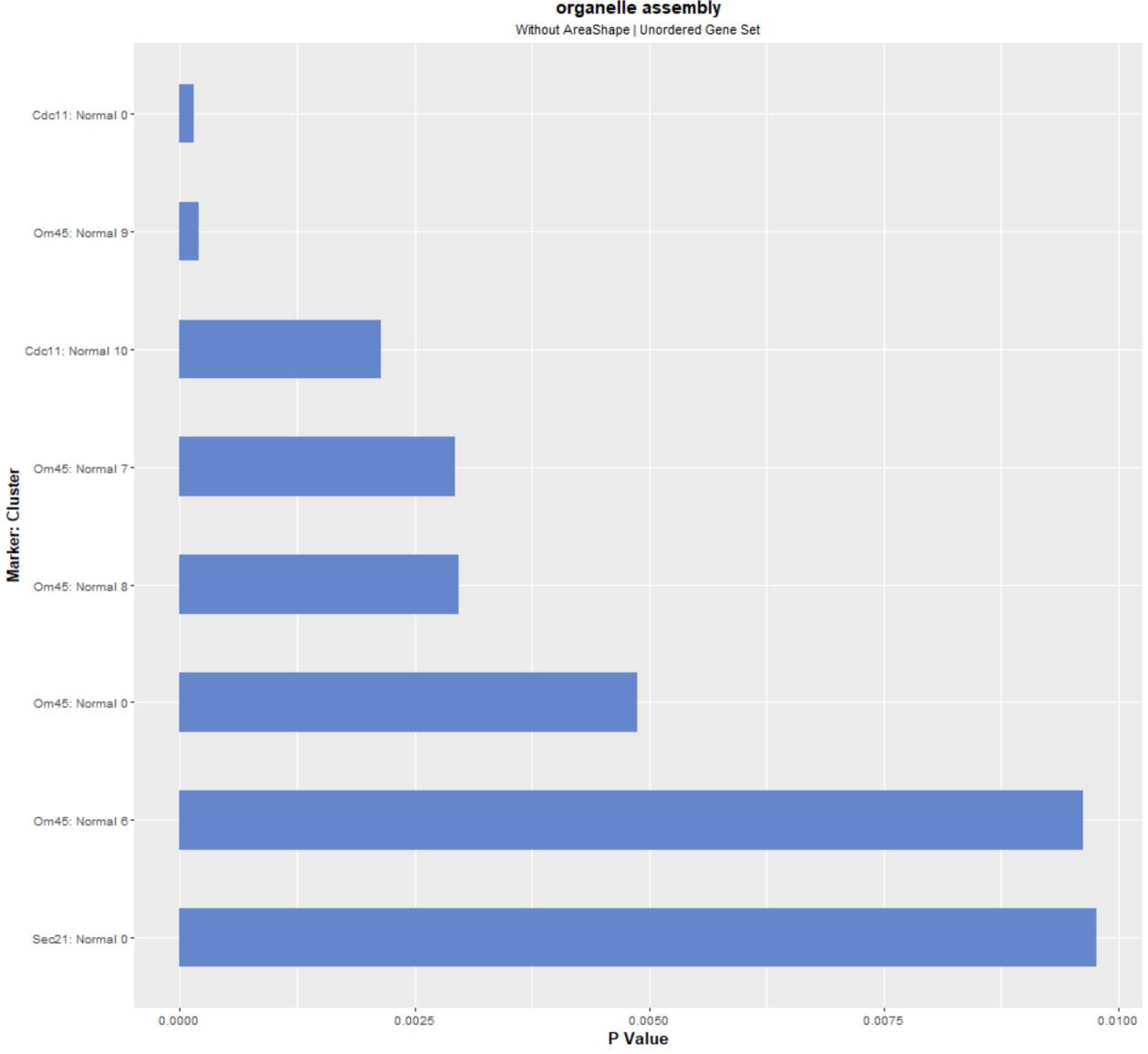
## nucleobase-containing compound transport Without AreaShape | Unordered Gene Set Cdc11: Normal 1-Cdc11: Normal 0 -Om45: Normal 31 Vph1NoPosCtrl: Normal 7 Vph1WithPosCtrl: Normal 10 -Marker: Cluster Sec21: Normal 61 Sec21: Normal 0 -Vph1NoPosCtrl: Normal 9 \* Vph1WithPosCtrl: Normal 11 -Sec21: Normal 8 -Sec21: Normal 51 0.0000 0.0025 0.0050 0.0075

P Value

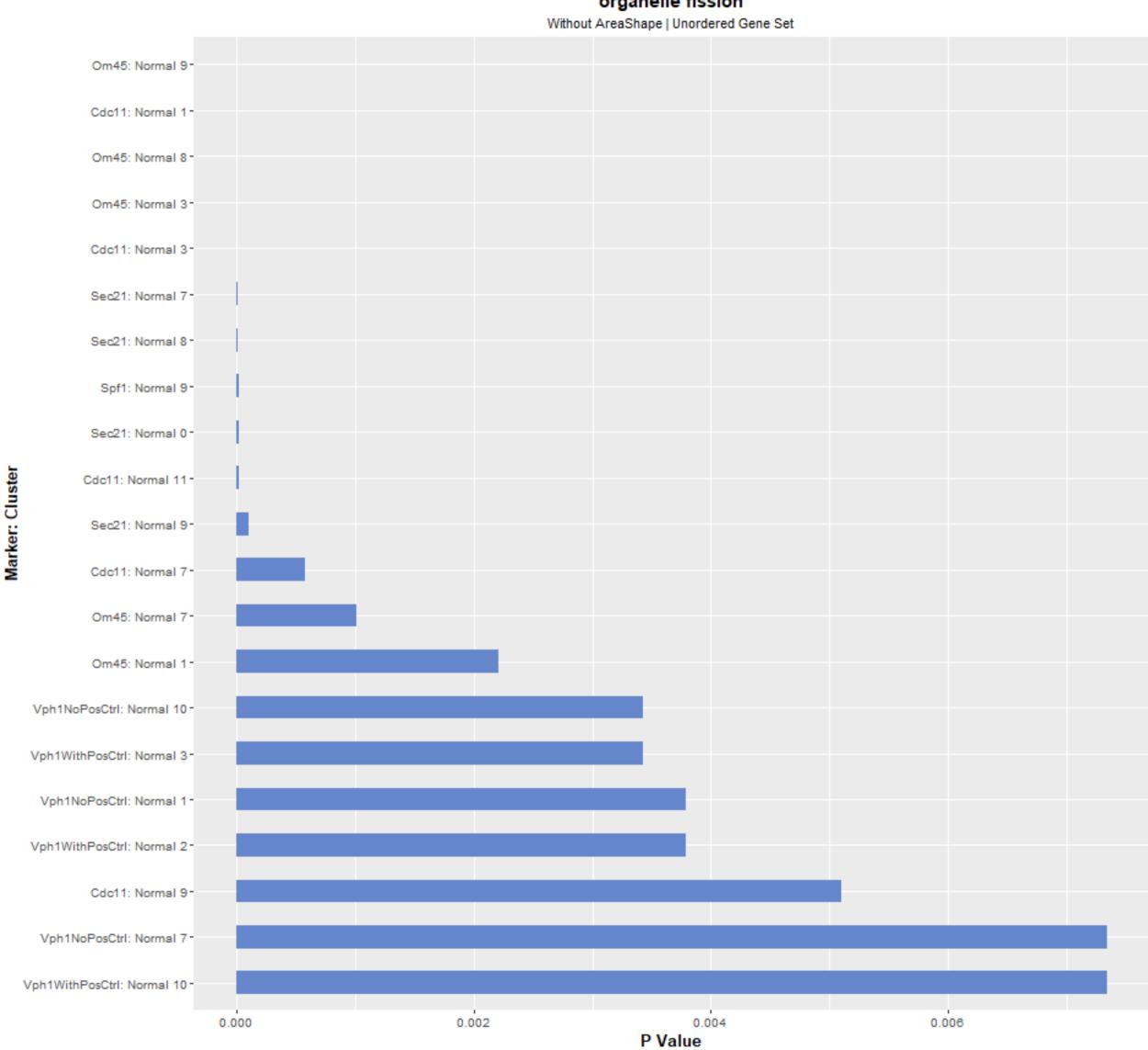
### nucleus organization



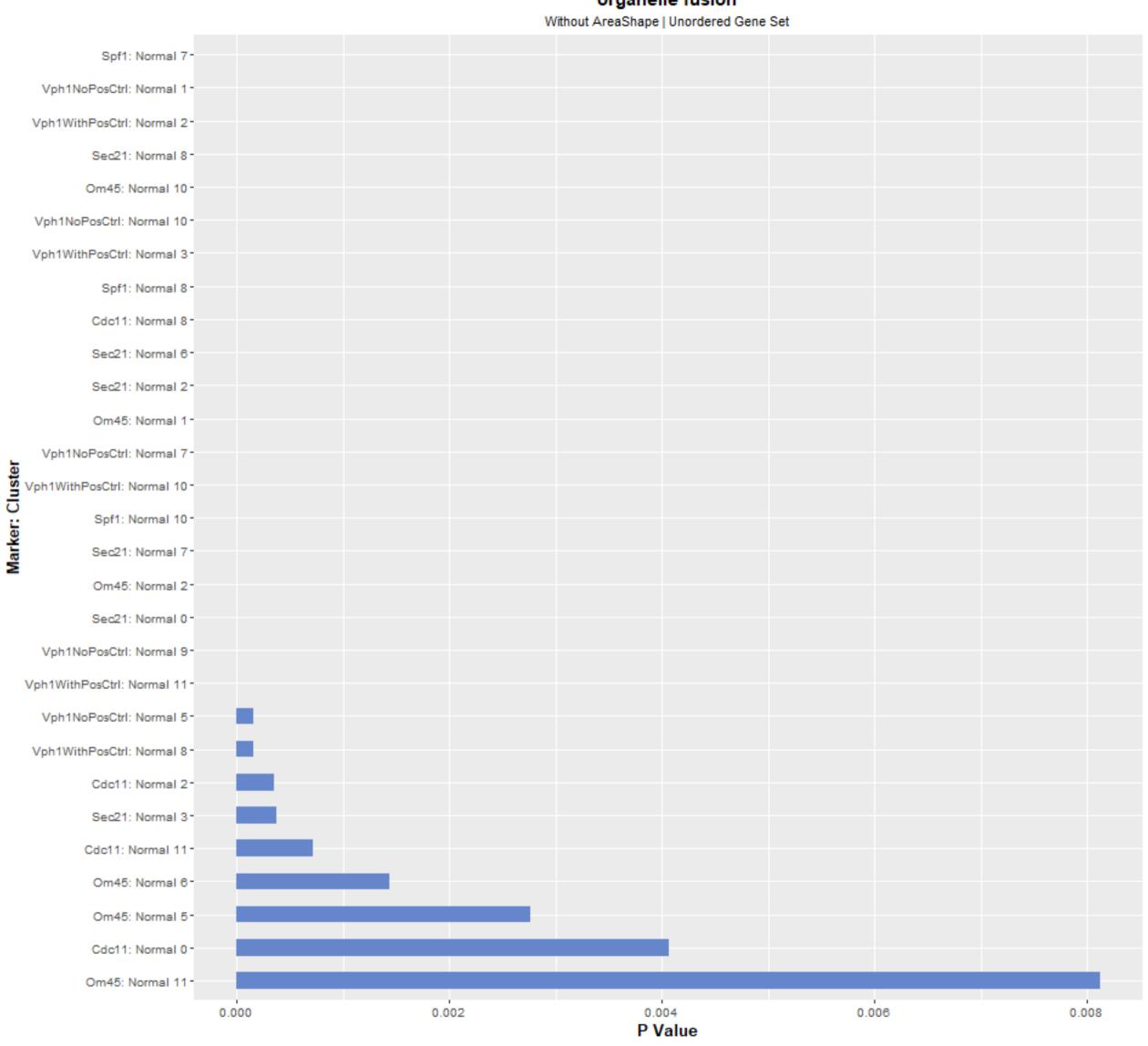
organelle assembly



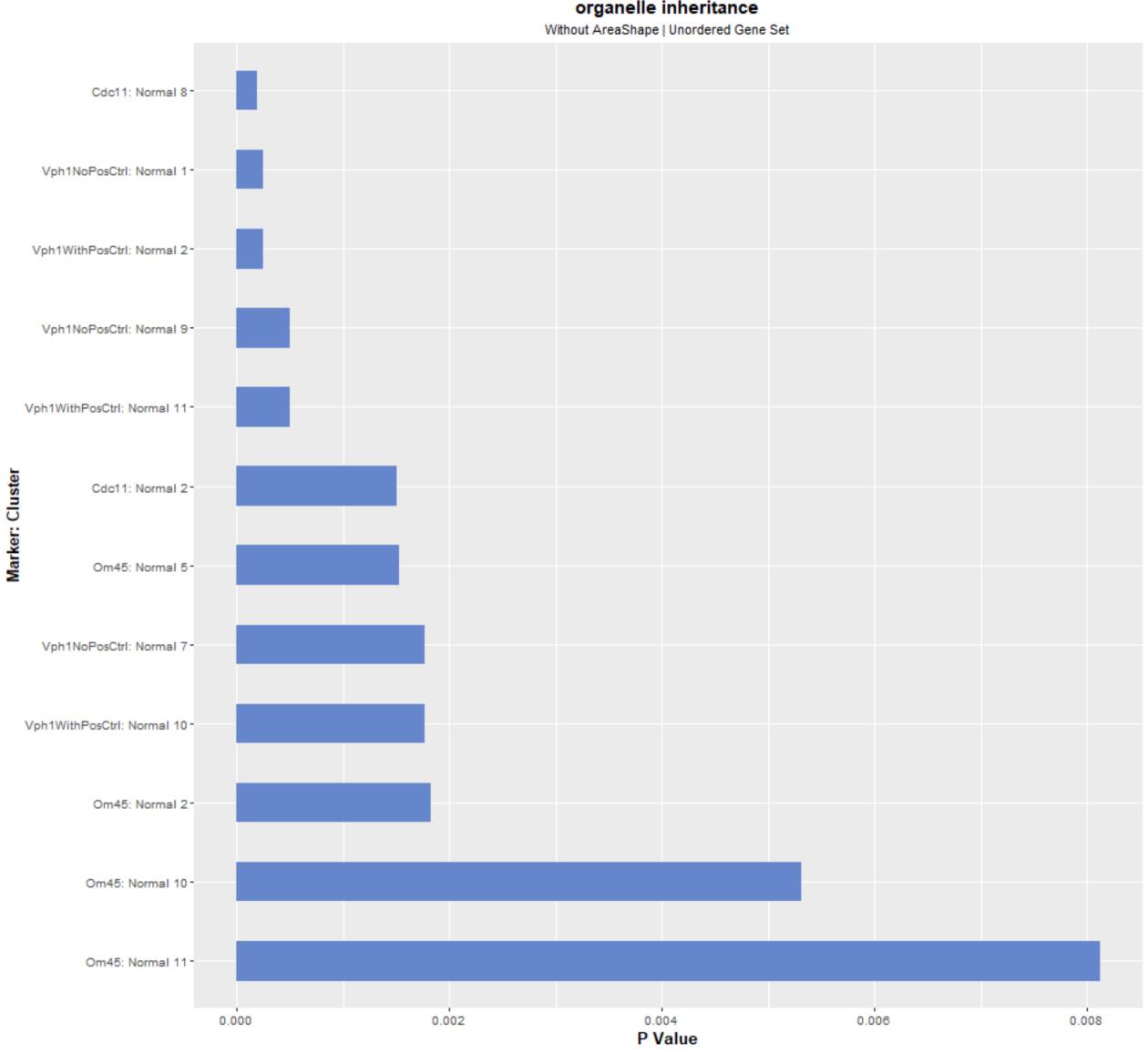
organelle fission



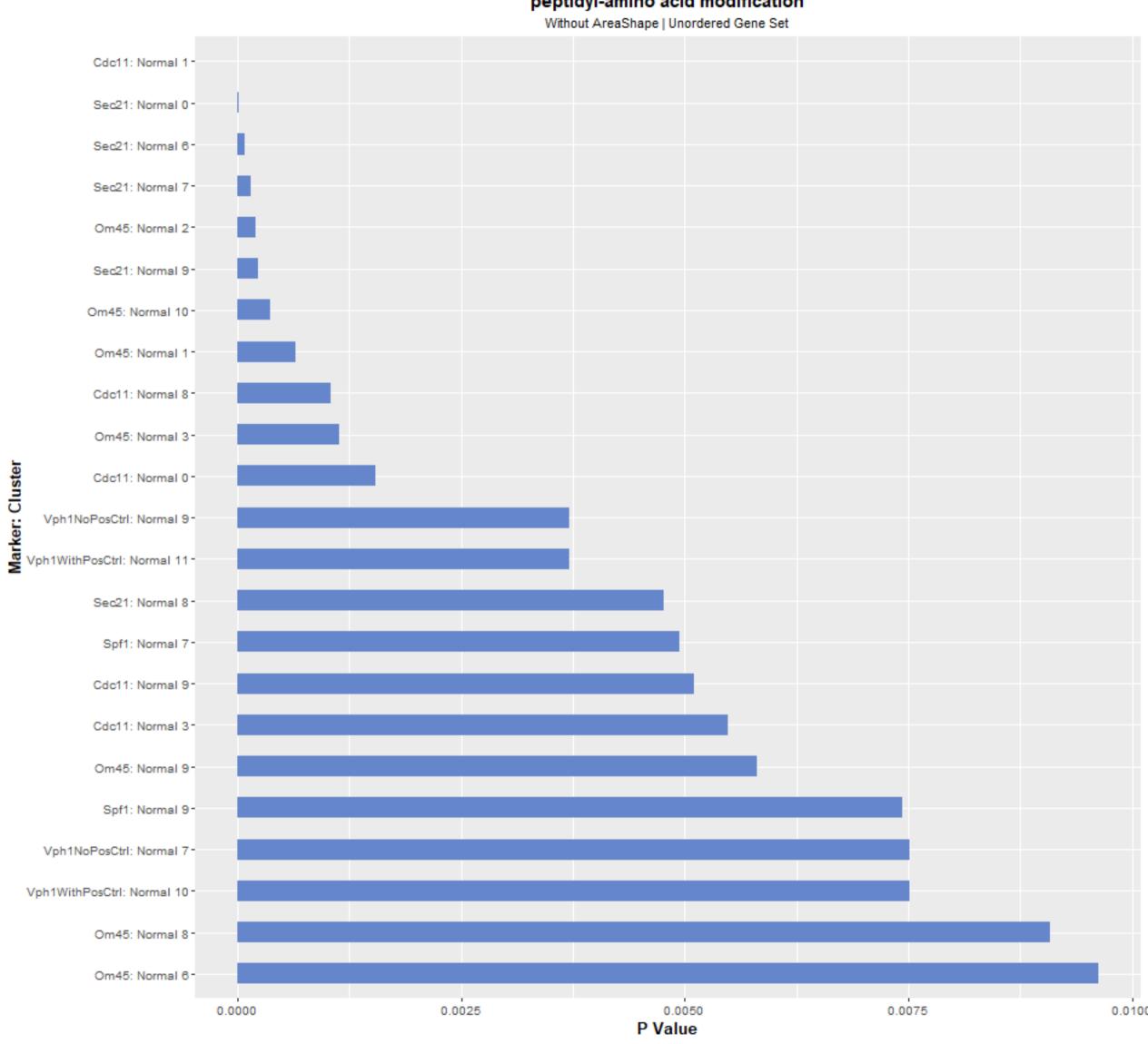
organelle fusion



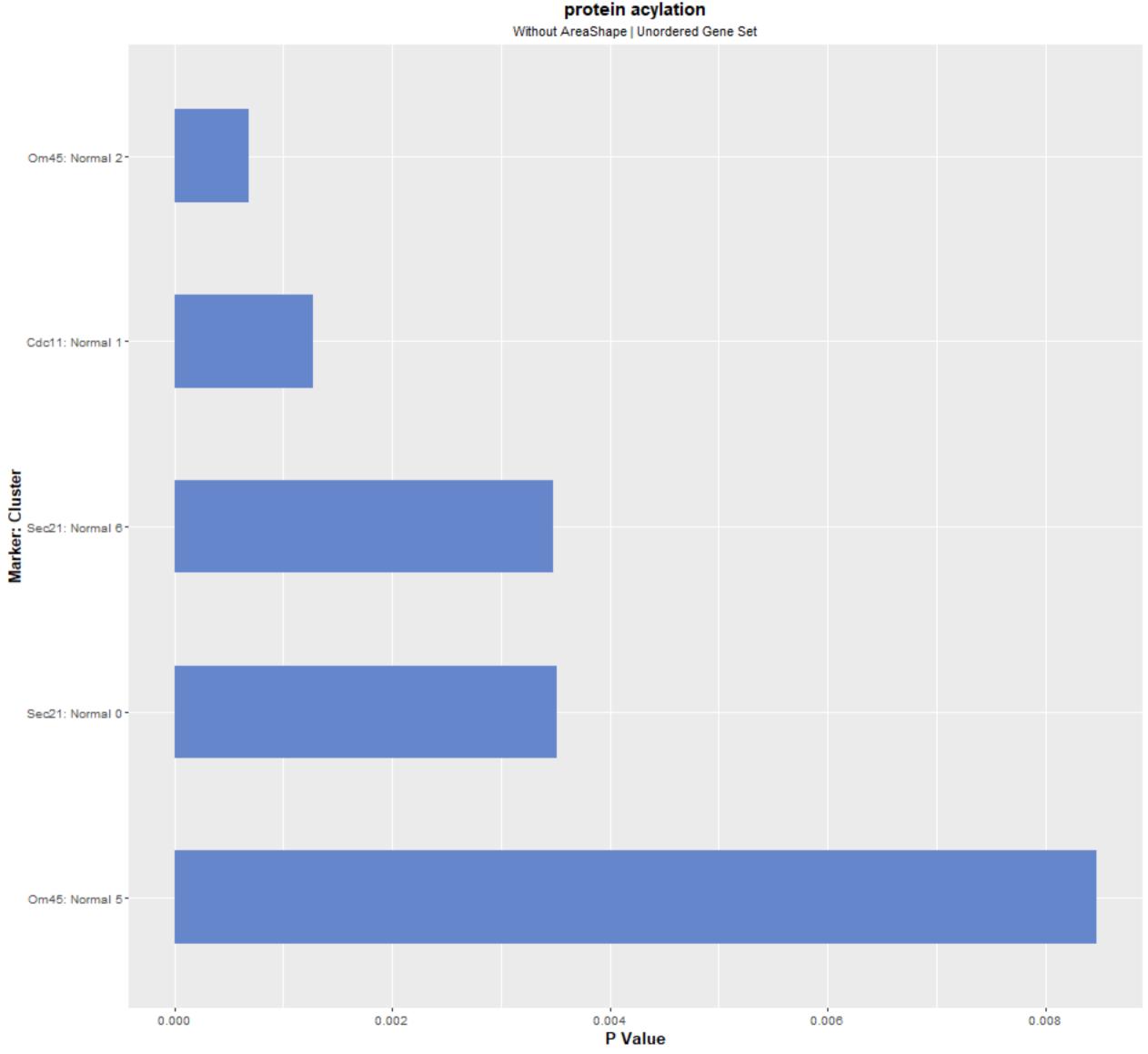
organelle inheritance



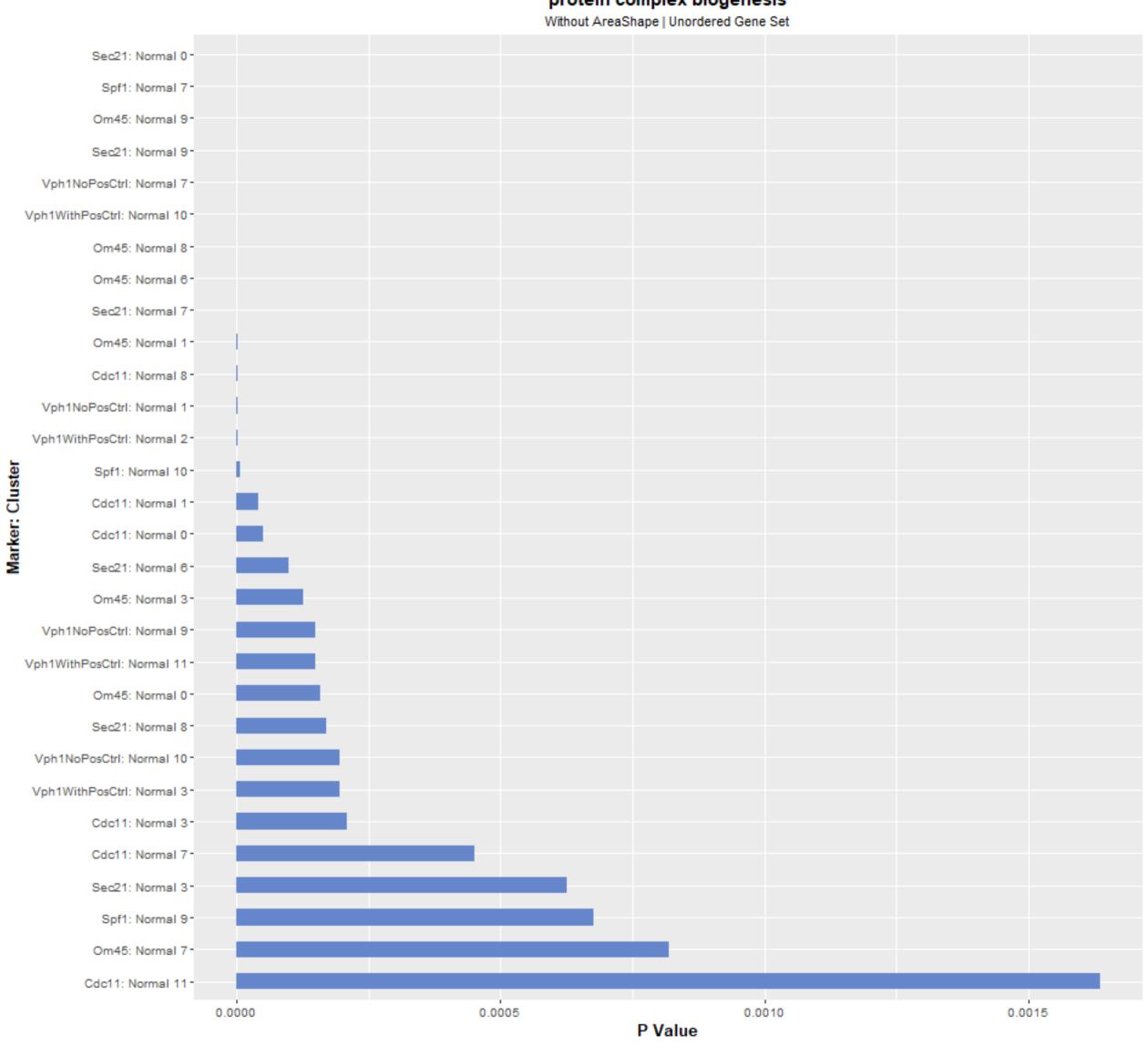
### peptidyl-amino acid modification



protein acylation



### protein complex biogenesis



protein glycosylation Without AreaShape | Unordered Gene Set Marker: Cluster: Code 11: Normal 2-0.0000 0.0005 0.0010 0.0015 P Value

protein lipidation Without AreaShape | Unordered Gene Set Cdc11: Normal 0 -Om45: Normal 6-Cdc11: Normal 8 -Om45: Normal 21 Om45: Normal 31 Spf1: Normal 7 -Marker: Cluster Om45: Normal 10 -Sec21: Normal 0 -Cdc11: Normal 10 -Vph1NoPosCtrl: Normal 1 -Vph1WithPosCtrl: Normal 2 Cdc11: Normal 4-Om45: Normal 1-0.000 0.002 0.004 0.006 P Value

# protein modification by small protein conjugation or removal Without AreaShape | Unordered Gene Set Om45: Normal 9 -Cdc11: Normal 1-Marker: Cluster Om45: Normal 8 -Om45: Normal 7 -0.0005 0.0010 0.0015 0.0000 0.0020 0.0025 P Value

protein phosphorylation Without AreaShape | Unordered Gene Set Om45: Normal 10 -Om45: Normal 8 -Om45: Normal 9 -Marker: Cluster Sec21: Normal 6-Vph1NoPosCtrl: Normal 7 -Vph1WithPosCtrl: Normal 10 -

0.0025

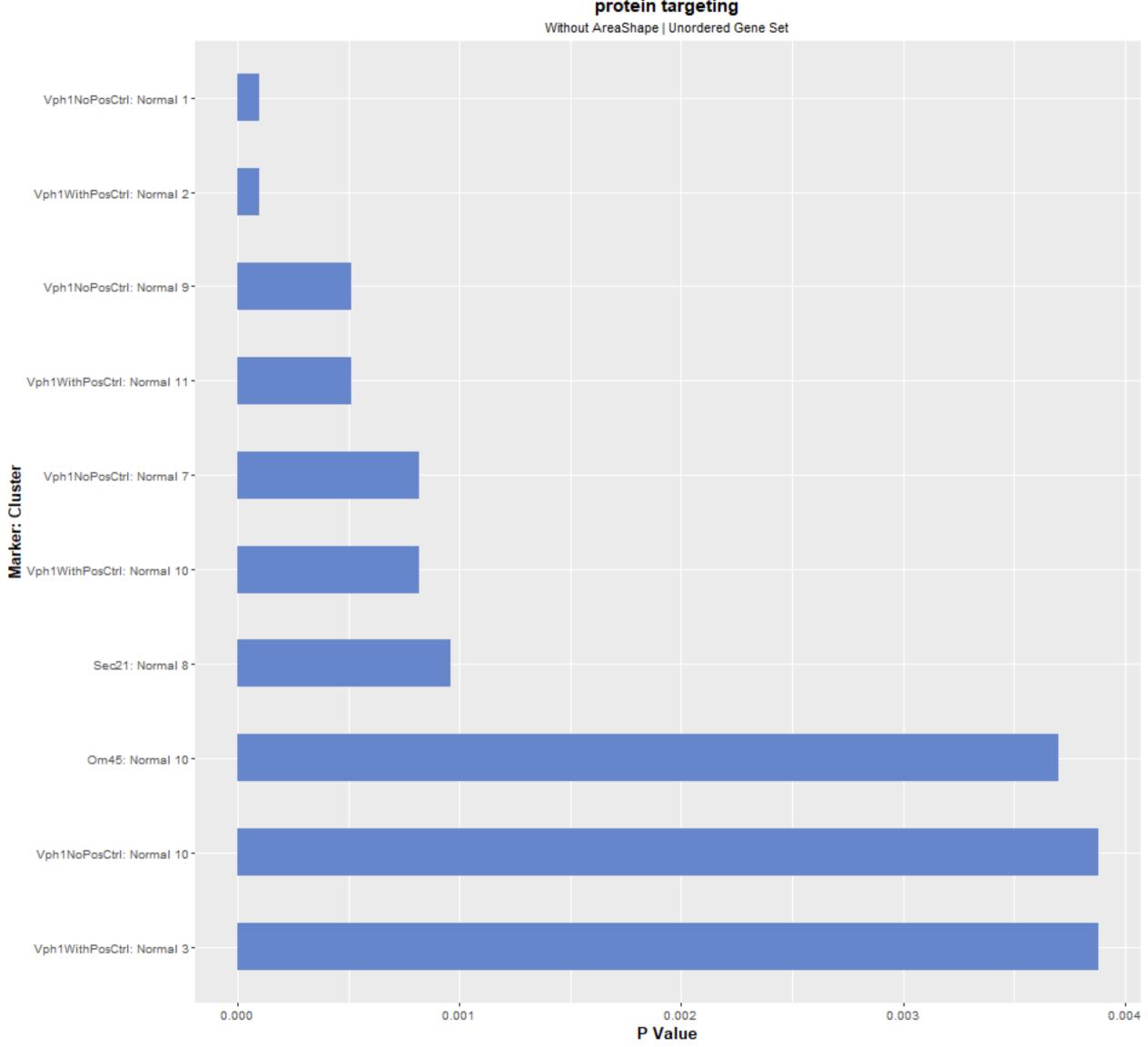
0.0000

0.0050

P Value

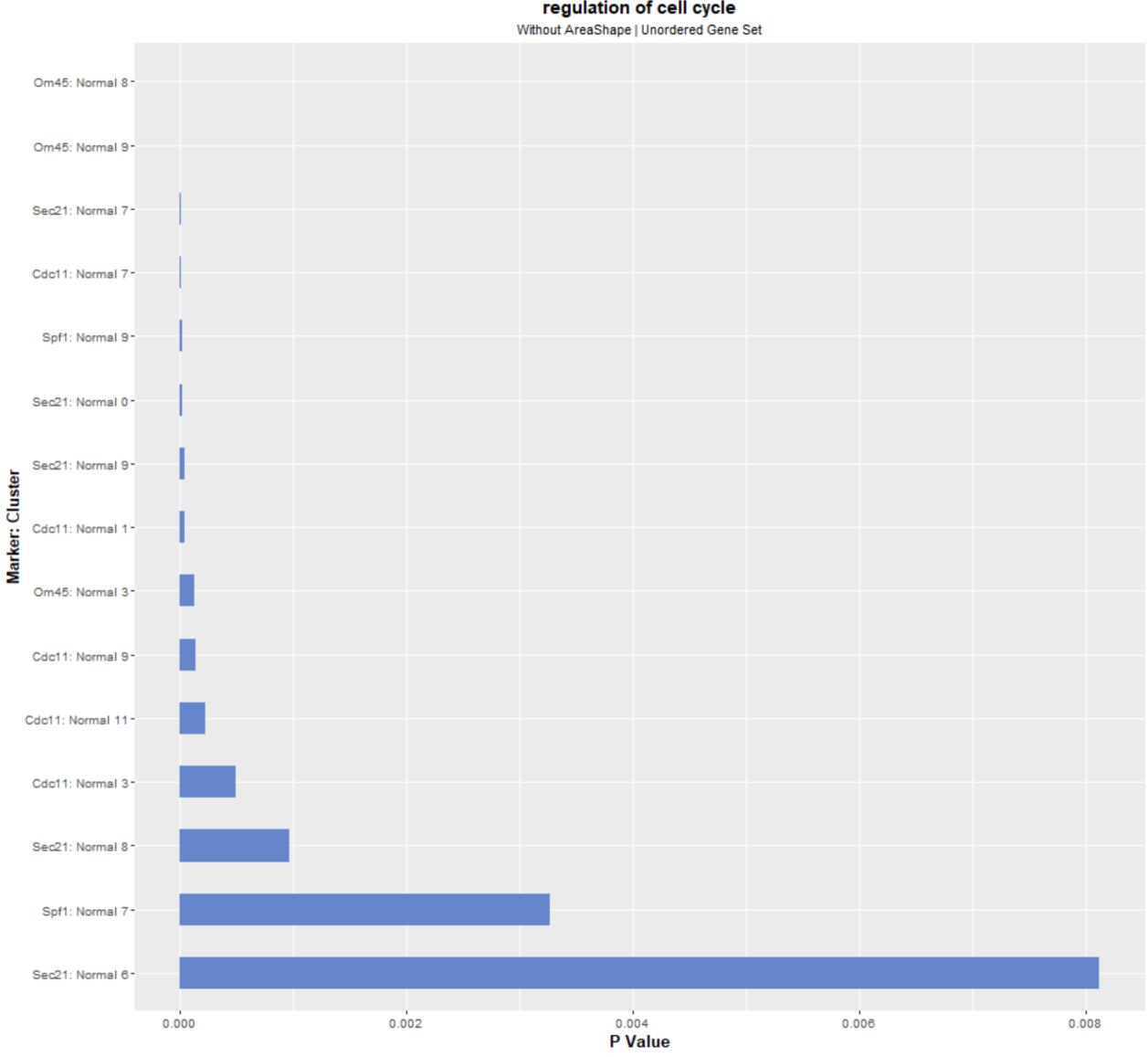
0.0075

protein targeting

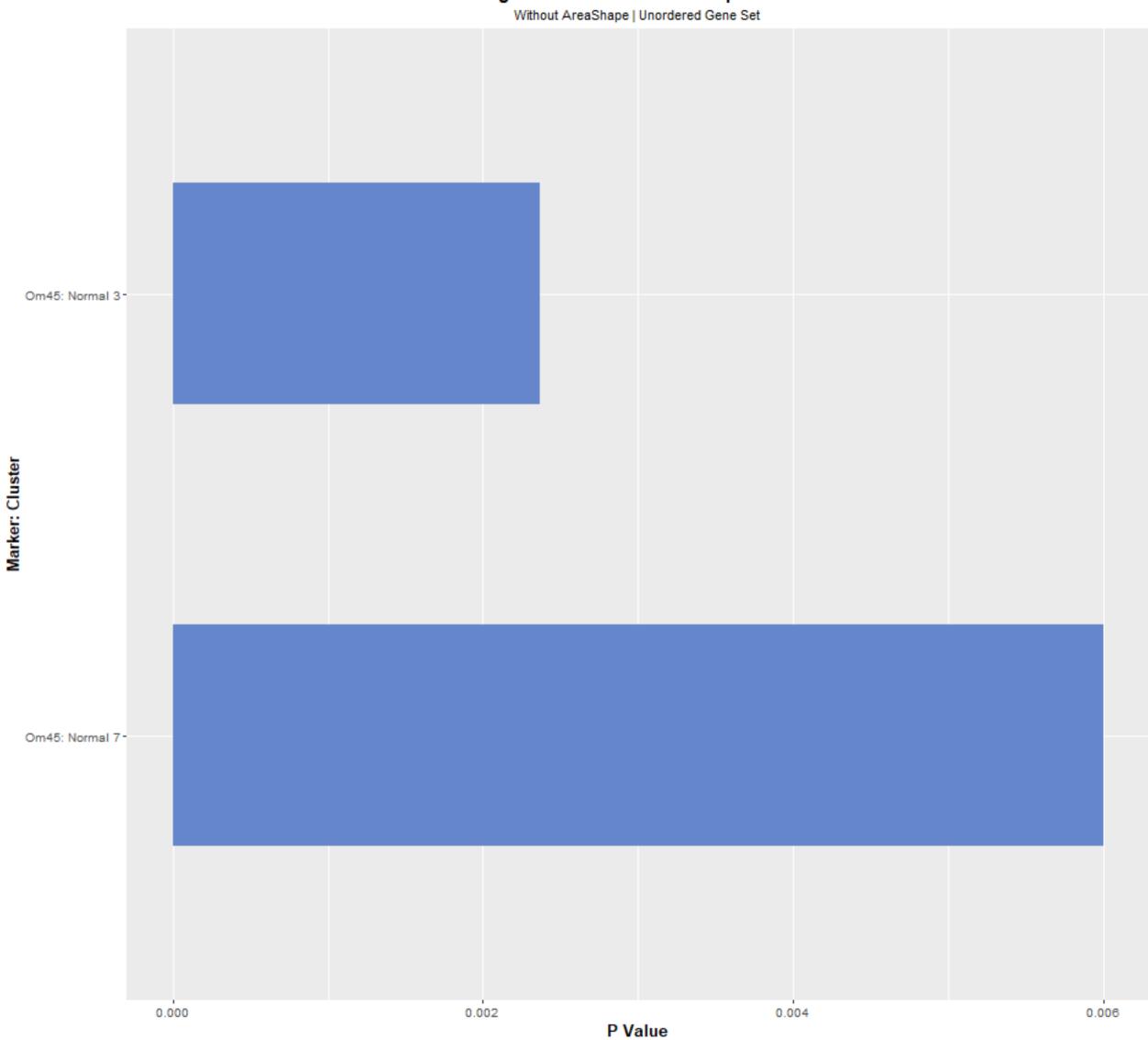


### proteolysis involved in cellular protein catabolic process Without AreaShape | Unordered Gene Set Om45: Normal 9 -Om45: Normal 8 -Spf1: Normal 10 -Om45: Normal 1-Om45: Normal 7 -Marker: Cluster Spf1: Normal 7 -Spf1: Normal 8 -Cdc11: Normal 31 Om45: Normal 3 -Om45: Normal 0 -Om45: Normal 61 0.0050 0.0100 0.0000 0.0025 0.0075 P Value

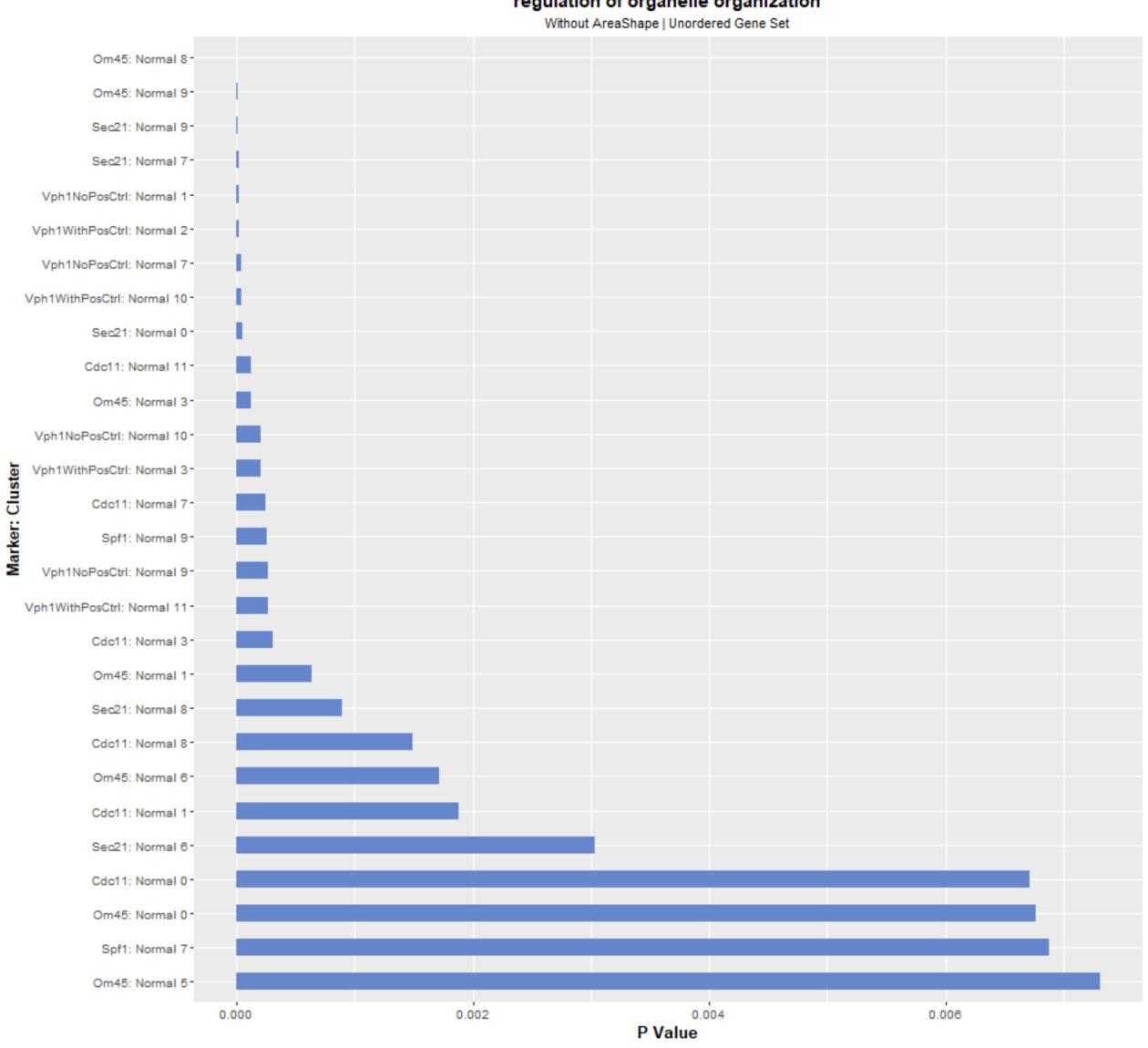
### regulation of cell cycle



# regulation of DNA metabolic process Without AreaShape | Unordered Gene Set



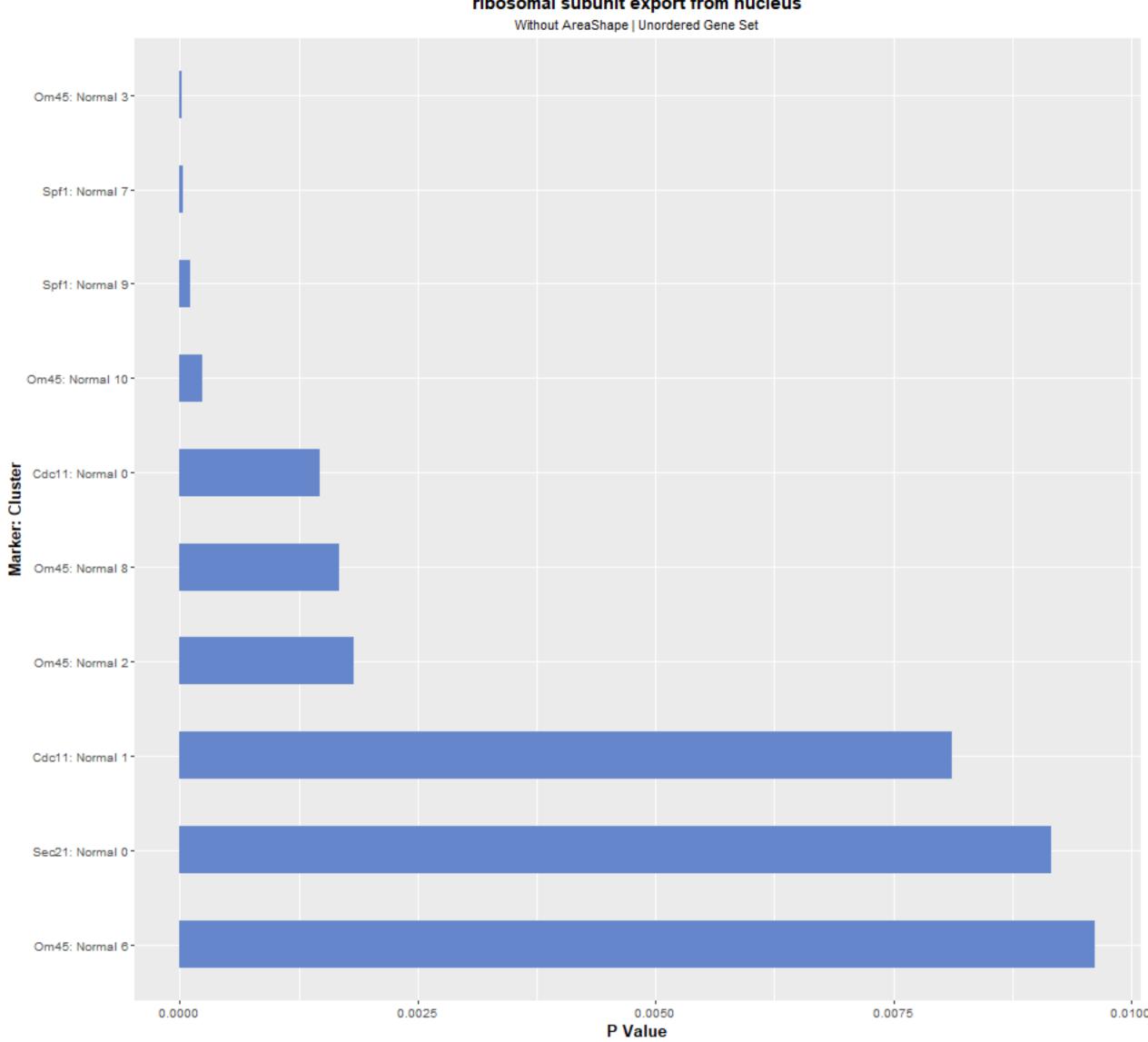
### regulation of organelle organization



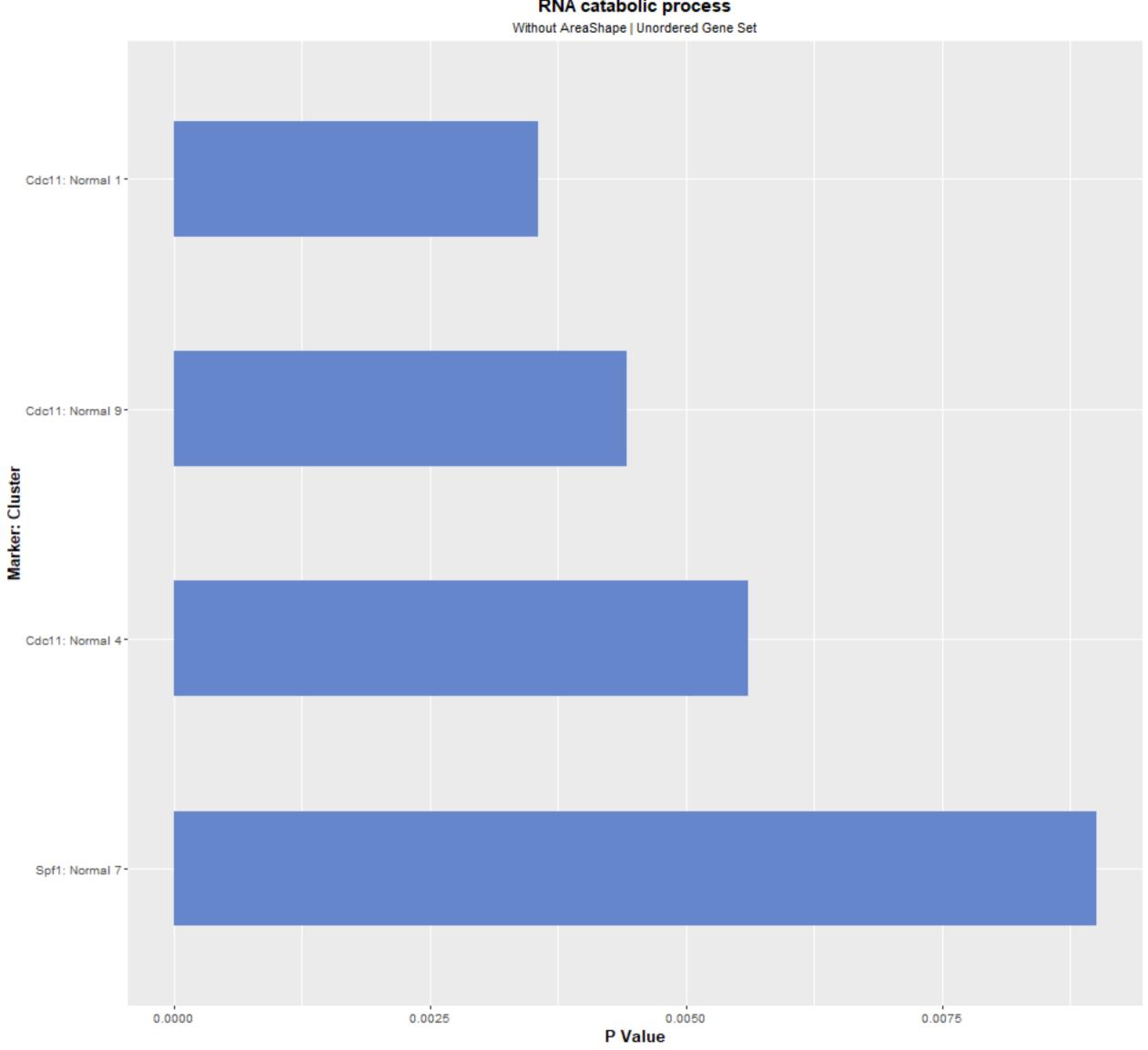
regulation of protein modification process Without AreaShape | Unordered Gene Set Cdc11: Normal 1-Sec21: Normal 8 -Om45: Normal 91 Marker: Cluster Sec21: Normal 0 -Vph1NoPosCtrl: Normal 9 -Vph1WithPosCtrl: Normal 11 -Spf1: Normal 9 -0.0050 0.0000 0.0025 0.0075 P Value

regulation of transport Without AreaShape | Unordered Gene Set Vph1NoPosCtrl: Normal 10 -Vph1WithPosCtrl: Normal 3 Marker: Cluster Om45: Normal 10 -Om45: Normal 51 0.004 0.006 0.000 0.002 P Value

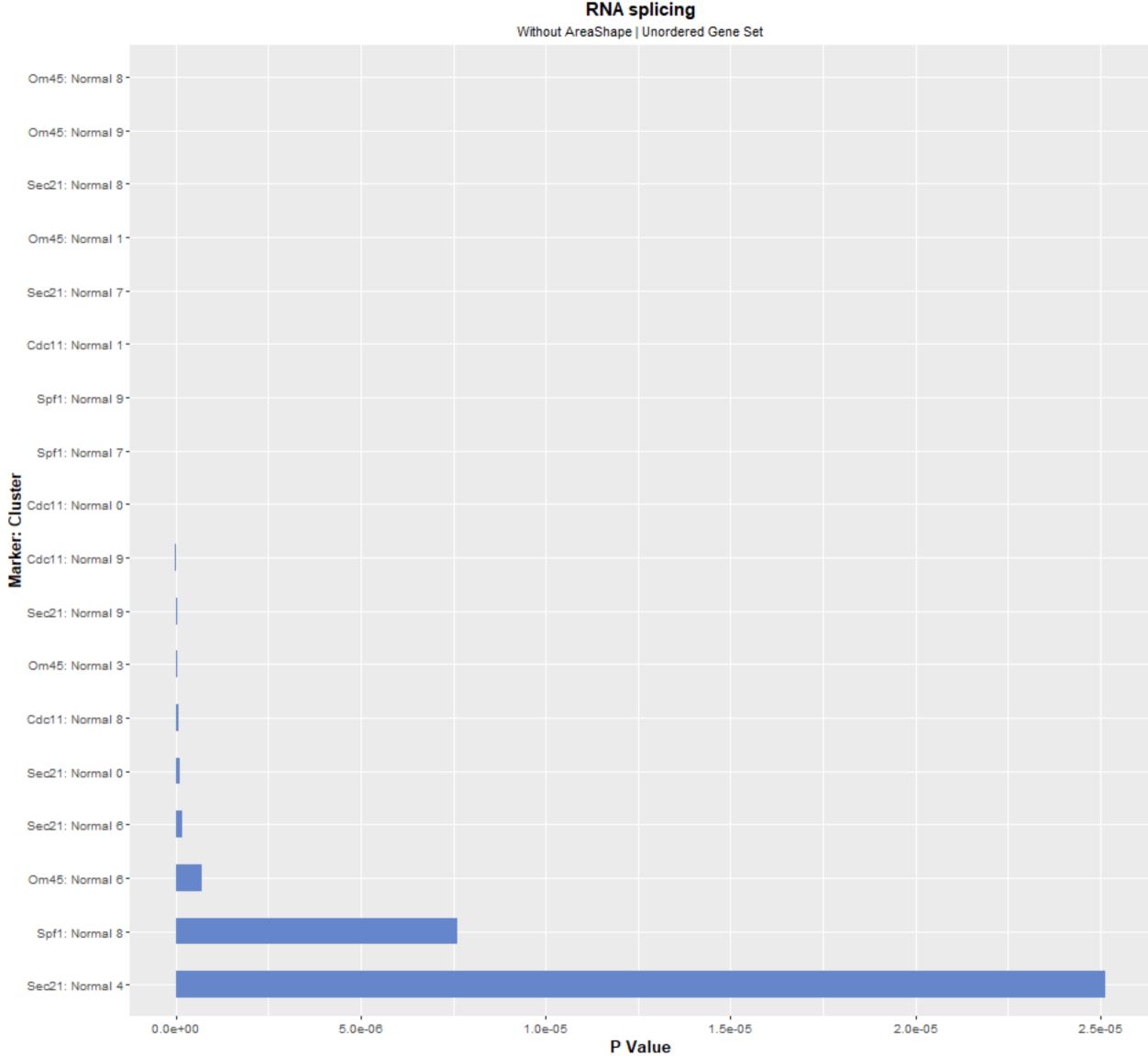
## ribosomal subunit export from nucleus



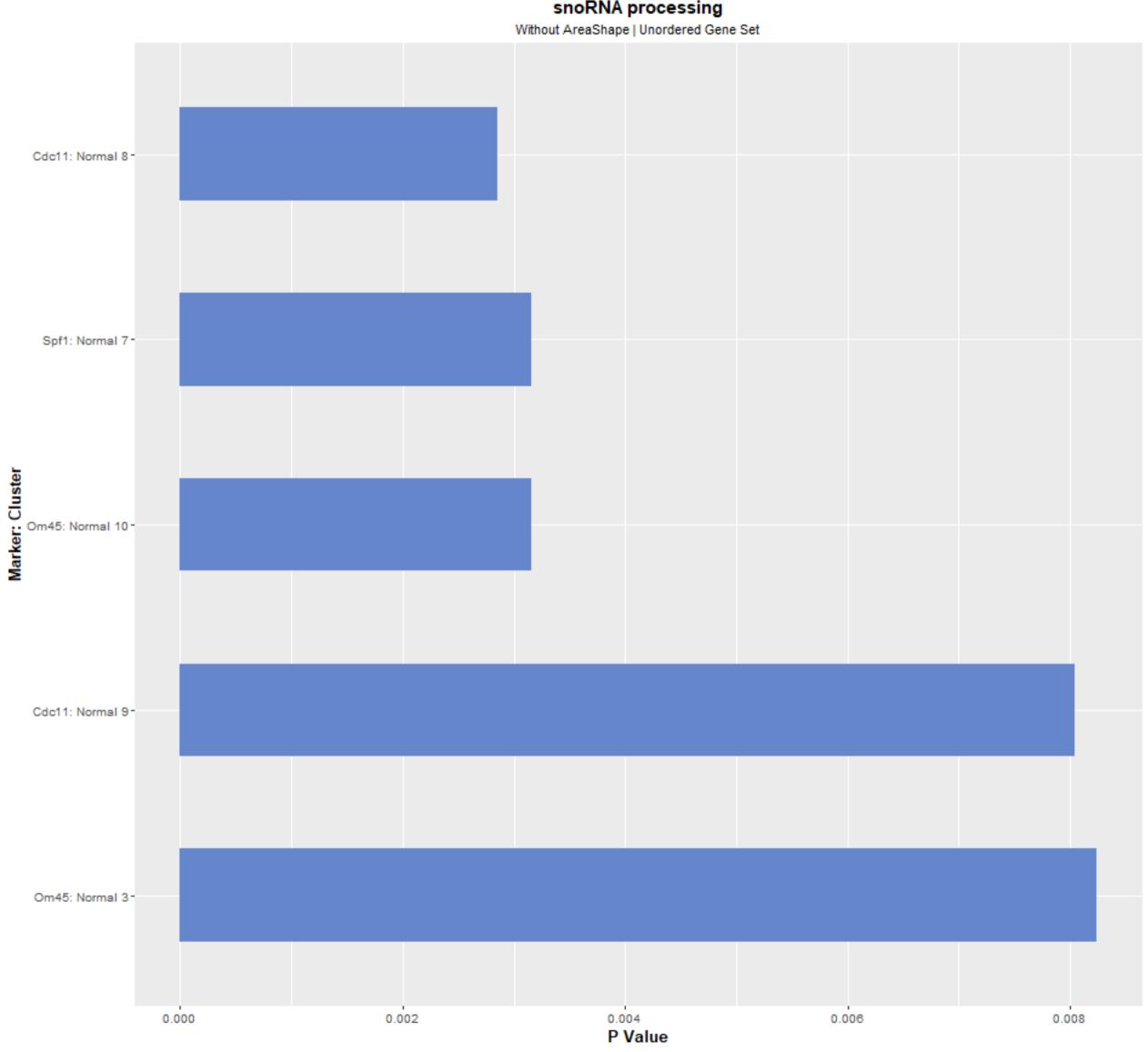
## **RNA** catabolic process



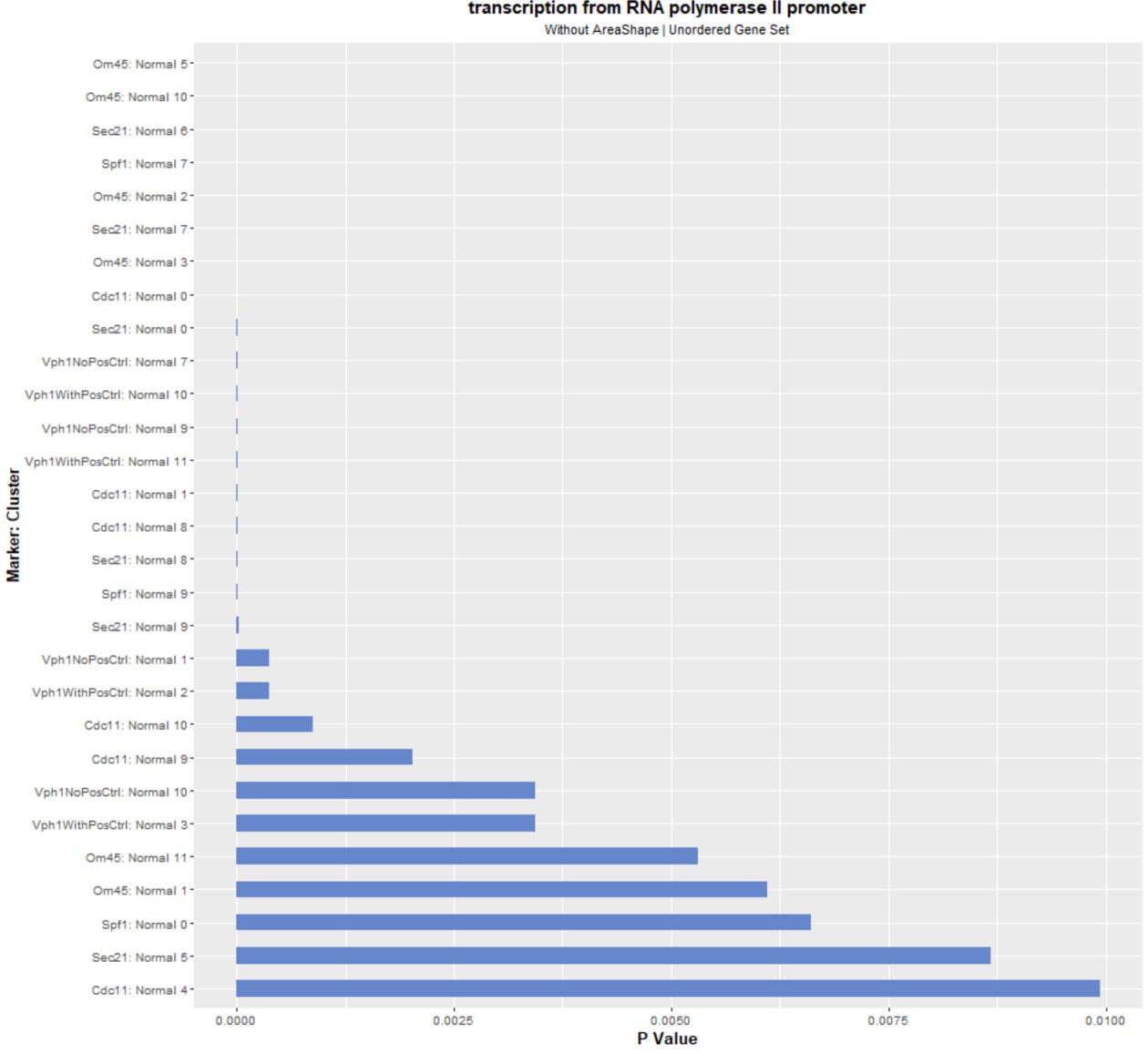
**RNA** splicing



# snoRNA processing



### transcription from RNA polymerase II promoter



translational initiation Without AreaShape | Unordered Gene Set Marker: Cluster: 0.0 Cluster 0 0.000 0.001 0.002 0.003 P Value

# tRNA aminoacylation for protein translation Without AreaShape | Unordered Gene Set Vph1NoPosCtrl: Normal 9 -Vph1WithPosCtrl: Normal 11 -Marker: Cluster Vph1NoPosCtrl: Normal 1 -Vph1WithPosCtrl: Normal 21 Om45: Normal 8 -0.0050 0.0100 0.0000 0.0025 0.0075 P Value

vacuole organization Without AreaShape | Unordered Gene Set Vph1NoPosCtrl: Normal 5 Vph1WithPosCtrl: Normal 8 -Marker: Cluster Sec21: Normal 6-Sec21: Normal 8 -0.004 0.002 0.006 0.000 P Value

vesicle organization

