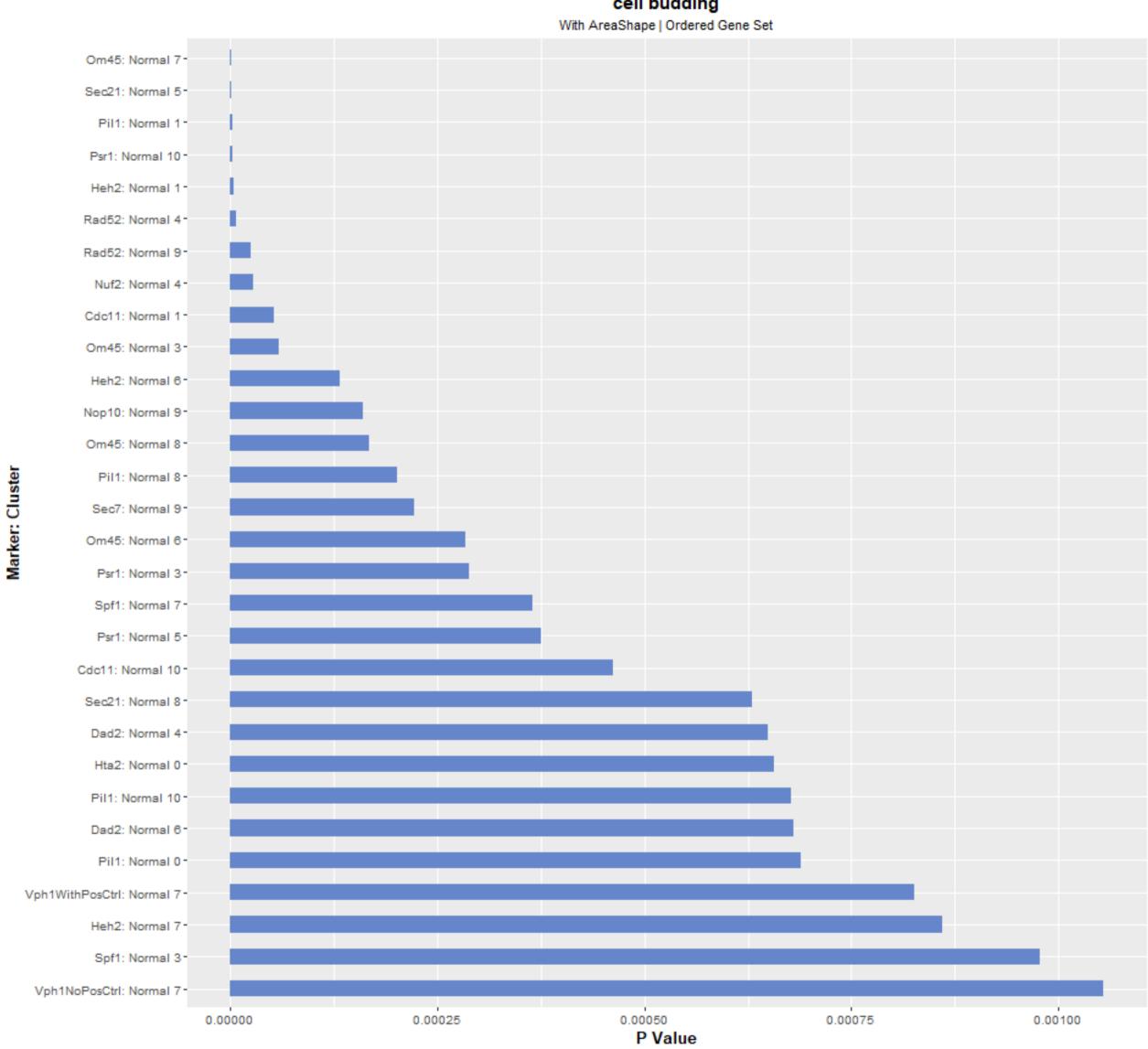
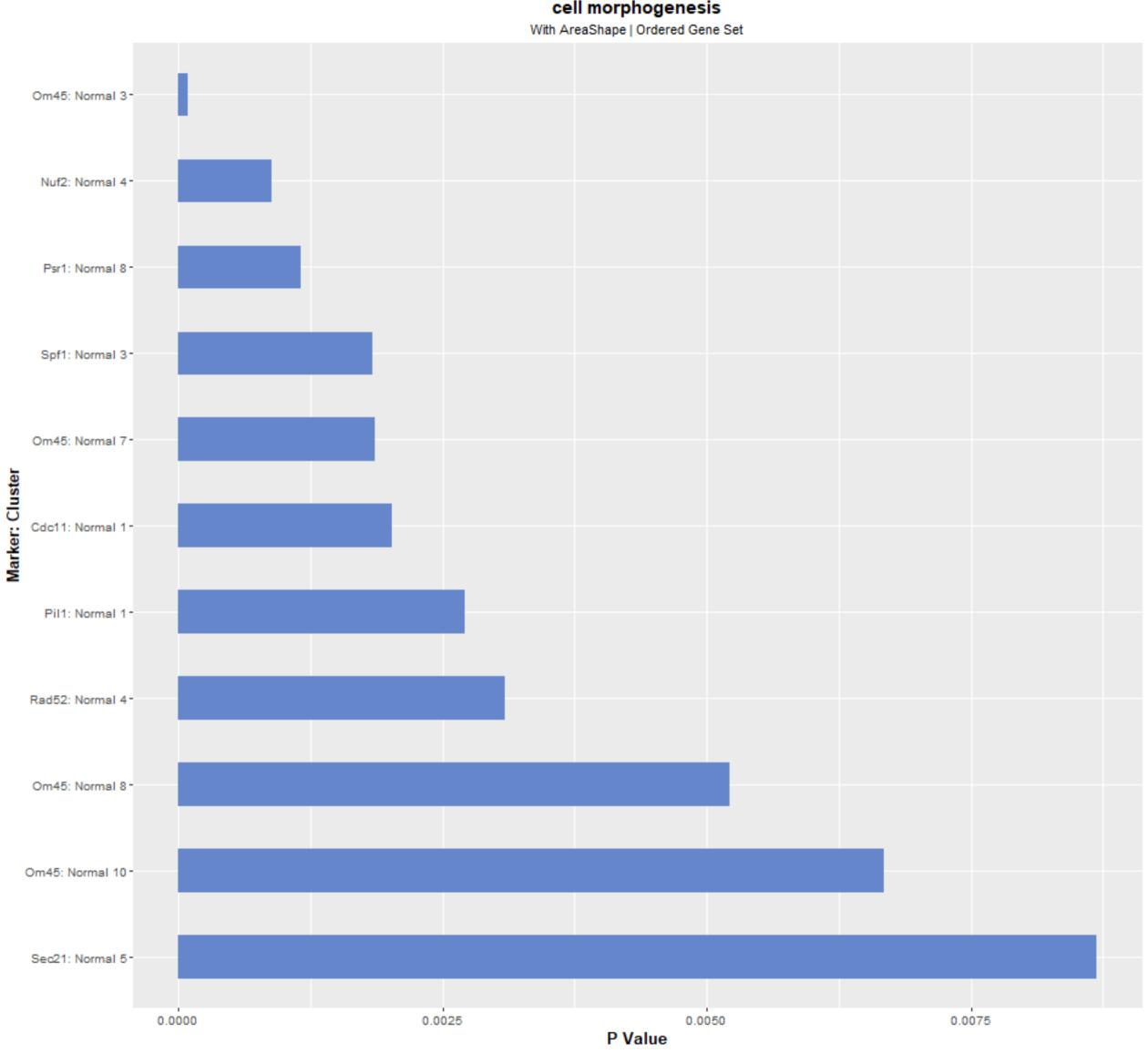
carbohydrate metabolic process With AreaShape | Ordered Gene Set 0.004 0.006 0.000 0.002 0.008 P Value

carbohydrate transport With AreaShape | Ordered Gene Set Marker: Cluster: Ser1: Normal 3-0.001 0.002 0.003 0.005 0.004 0.000 P Value

cell budding



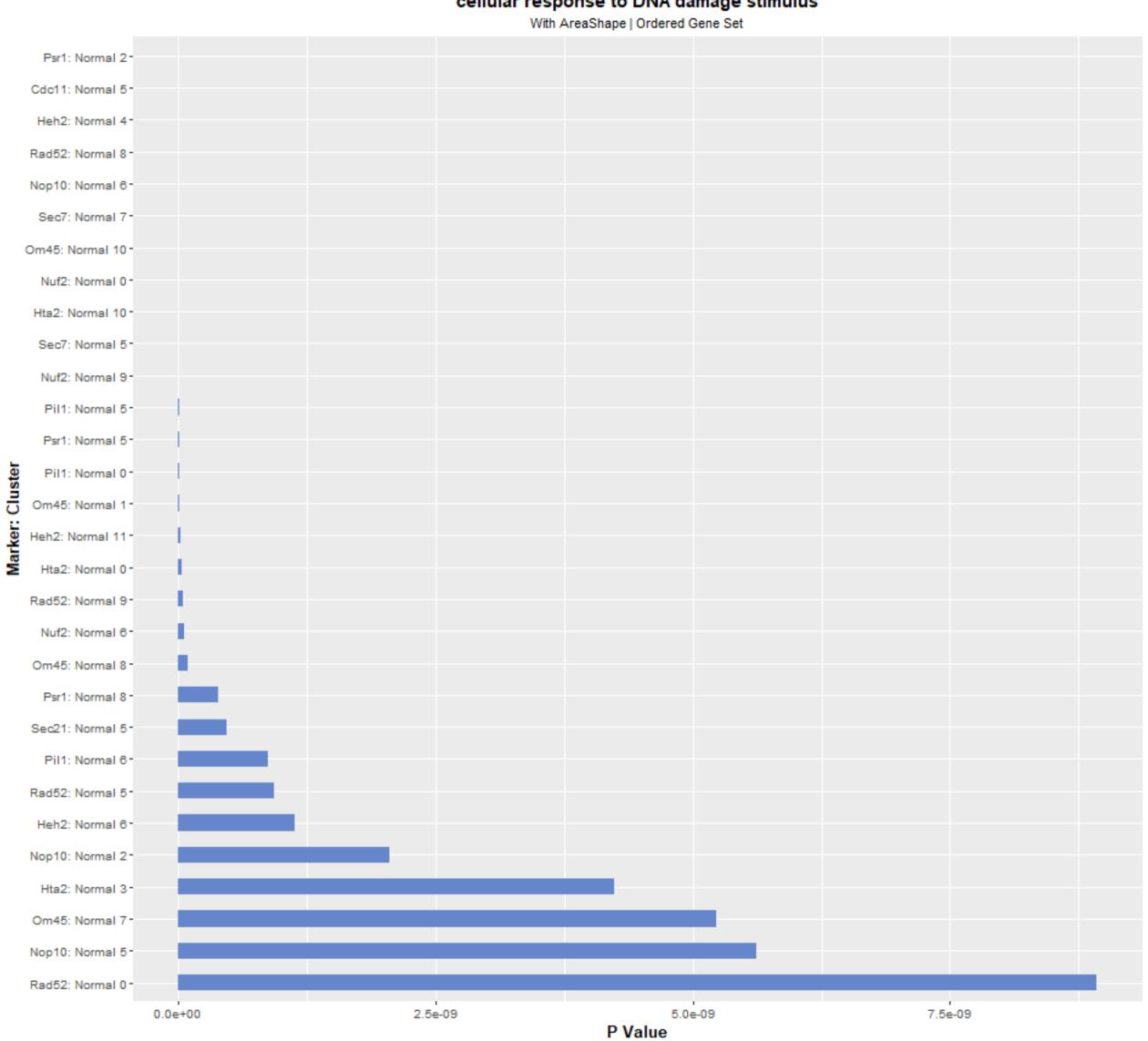
cell morphogenesis



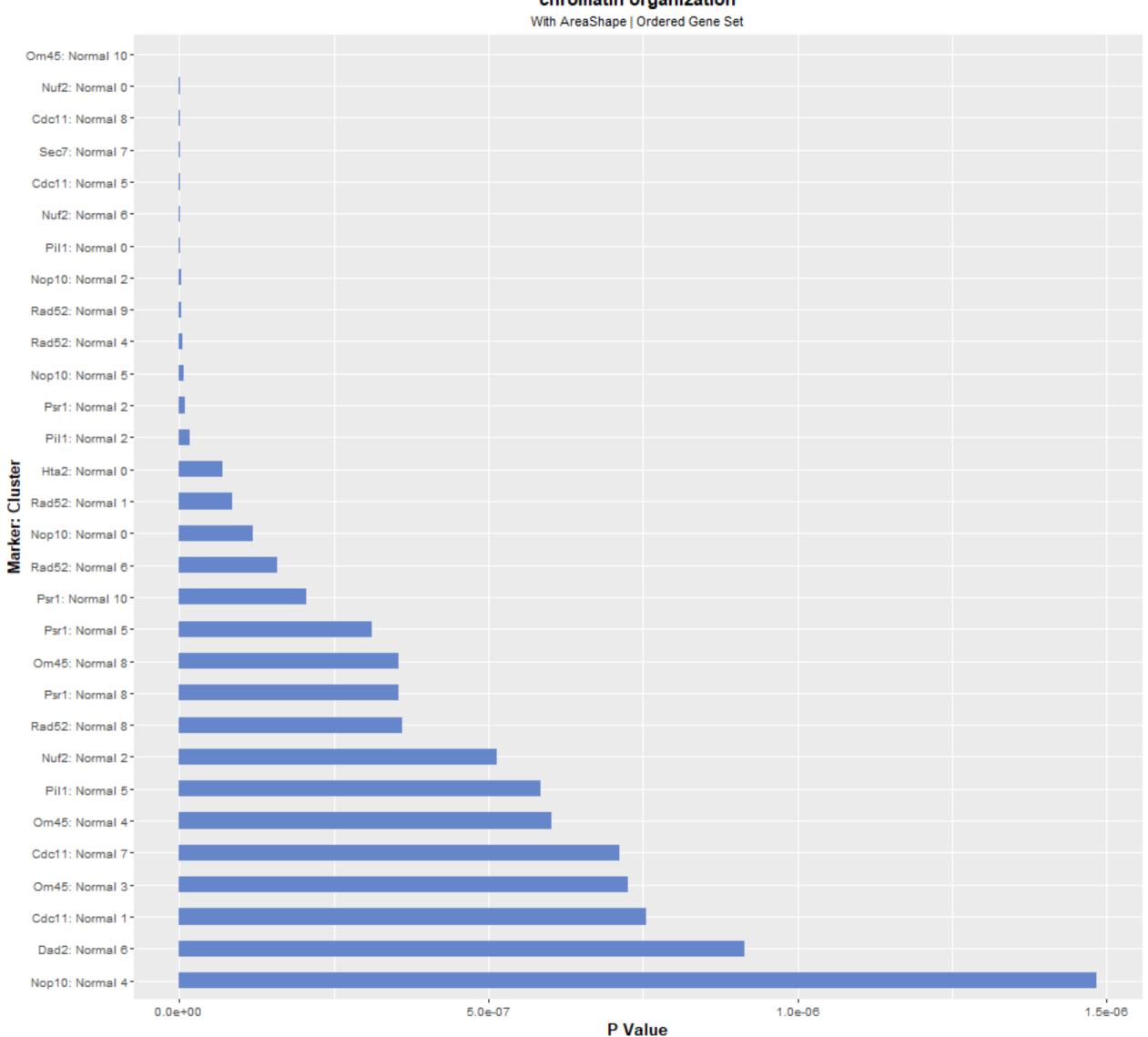
cell wall organization or biogenesis With AreaShape | Ordered Gene Set Cdc11: Normal 7 -Cdc11: Normal 6-Vph1WithPosCtrl: Normal 7 -Vph1NoPosCtrl: Normal 7 -Sec7: Normal 21 Marker: Cluster Psr1: Normal 31 Vph1NoPosCtrl: Normal 8 -Sec7: Normal 0 -Om45: Normal 8 -Nop10: Normal 10 -Vph1WithPosCtrl: Normal 2 Sec7: Normal 7 -0.0050 0.0100 0.0000 0.0025 0.0075 P Value

cellular amino acid metabolic process With AreaShape | Ordered Gene Set Cdc11: Normal 31 Marker: Cluster Sec7: Normal 10 -0.0010 0.0000 0.0005 0.0015 0.0020 P Value

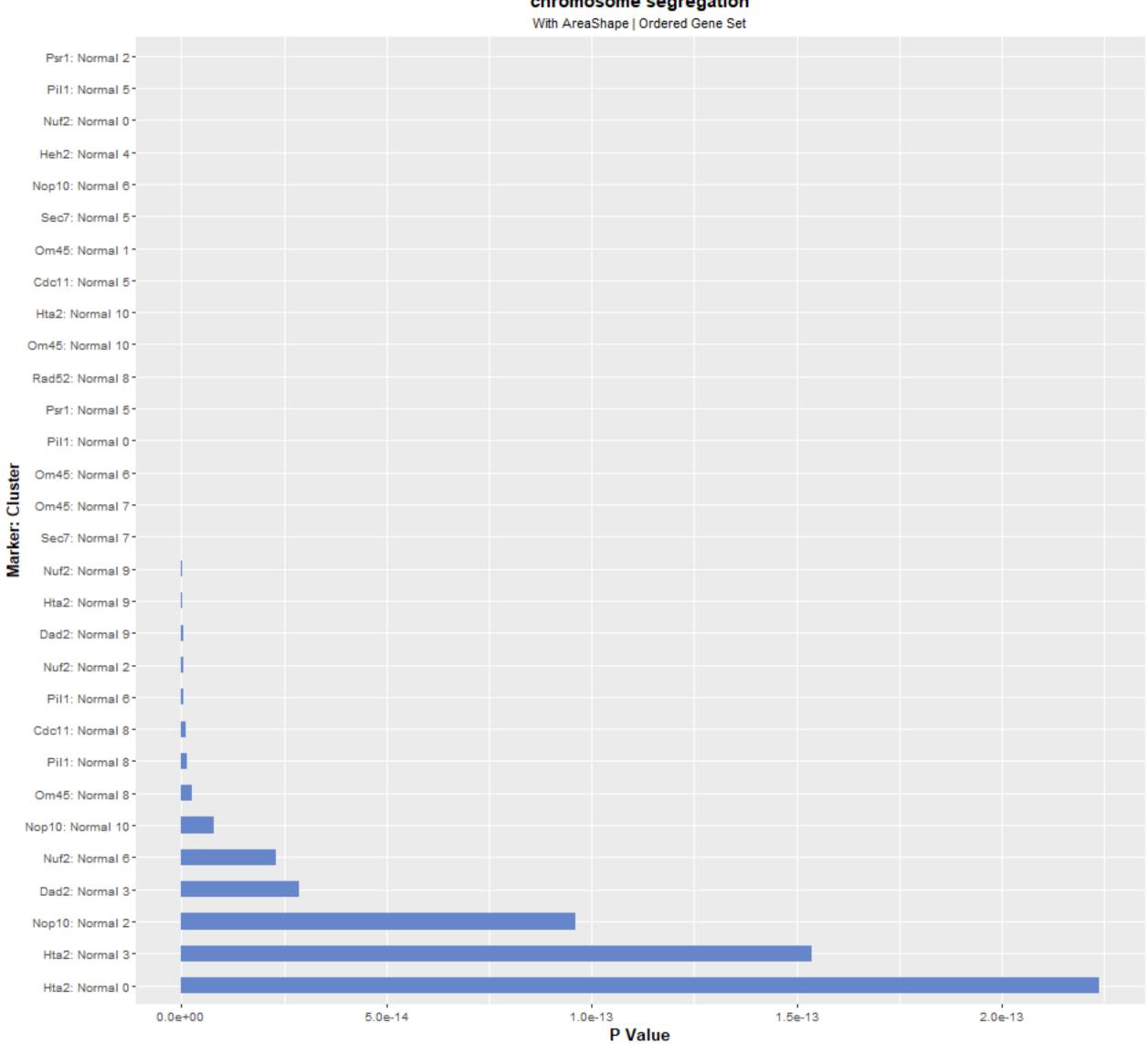
cellular response to DNA damage stimulus



chromatin organization

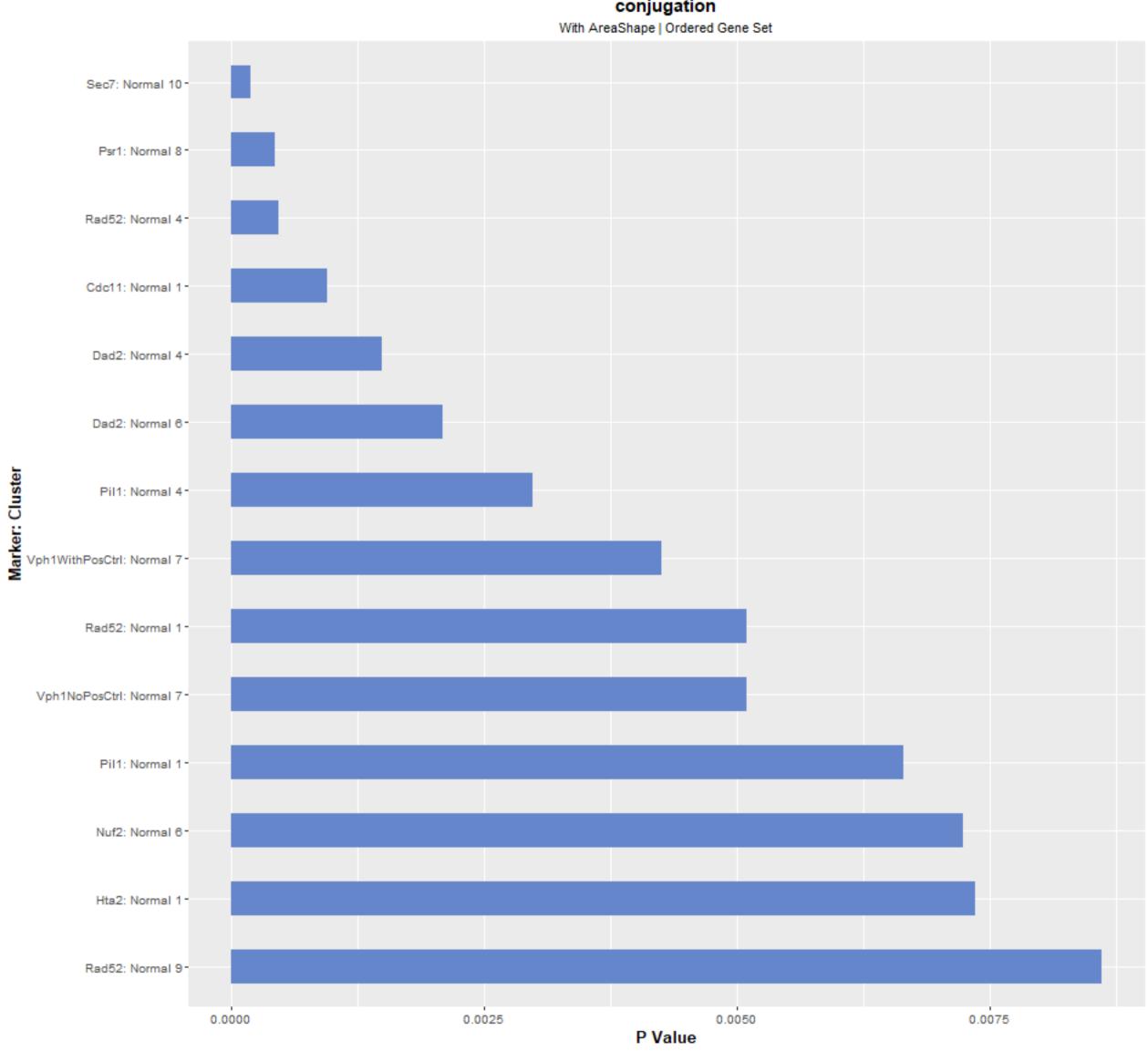


chromosome segregation

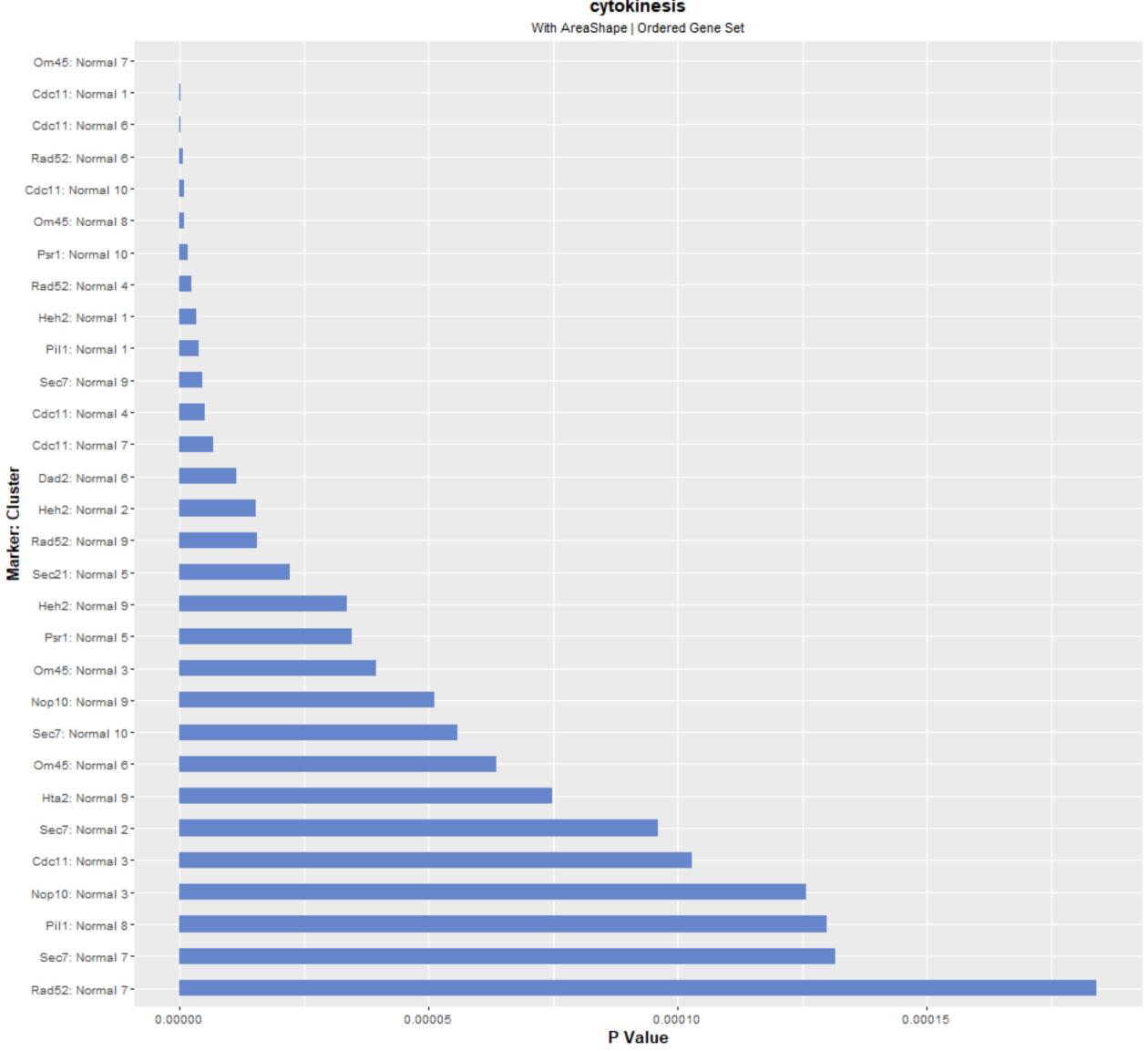


cofactor metabolic process With AreaShape | Ordered Gene Set Marker: Cluster: 0 c c la como de como 1e-04 0e+00 2e-04 P Value

conjugation

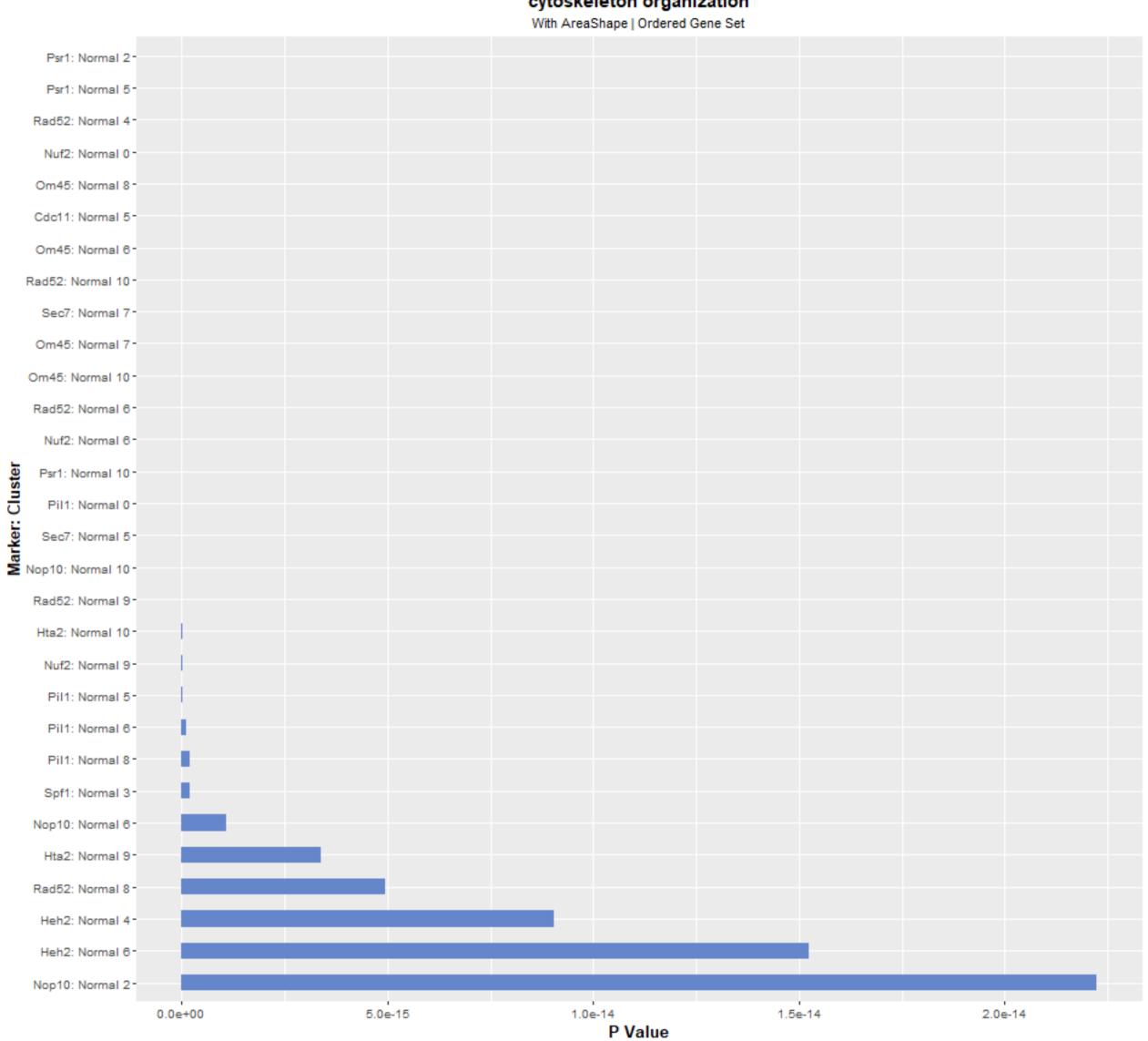


cytokinesis

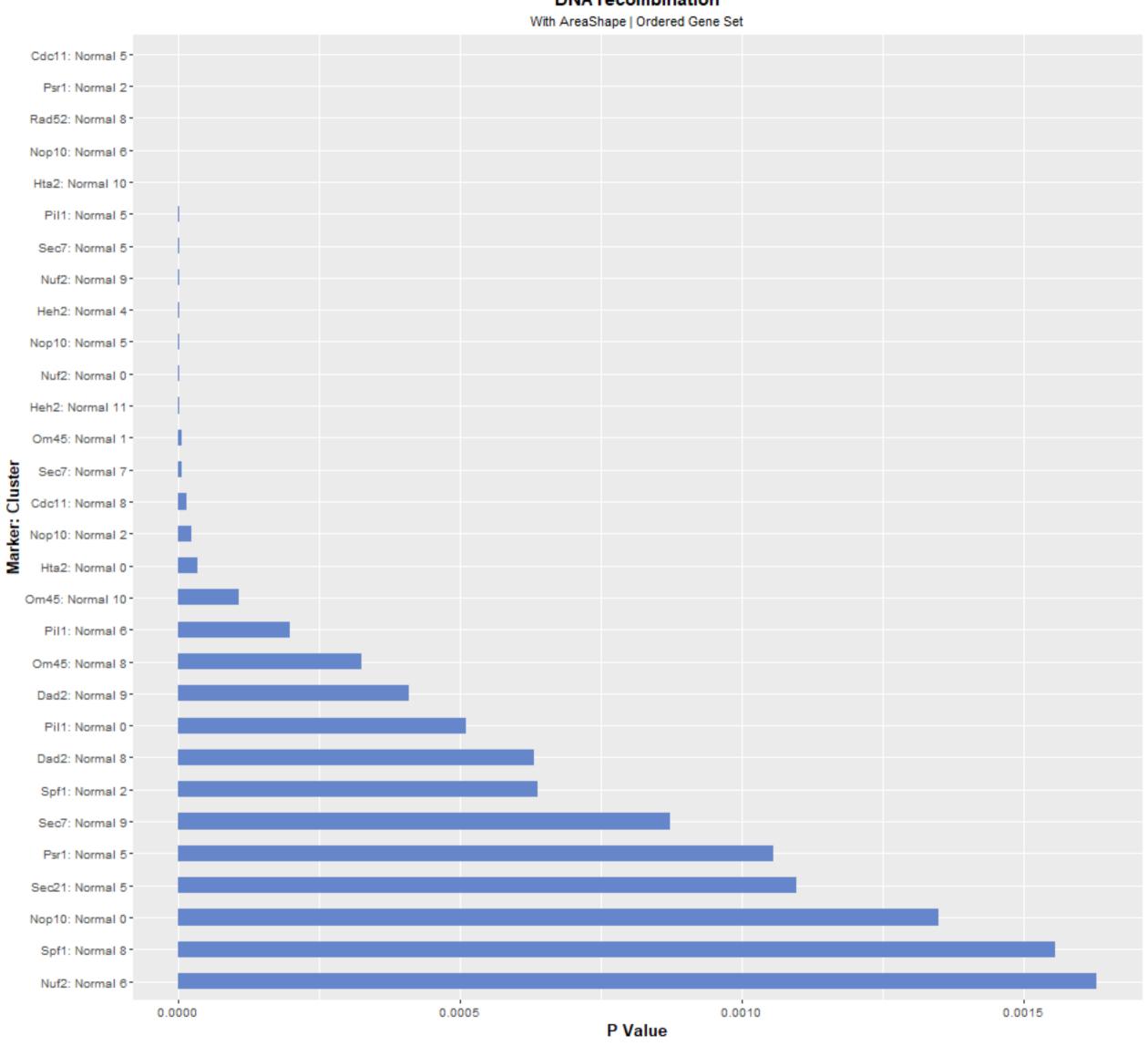


cytoplasmic translation With AreaShape | Ordered Gene Set Pil1: Normal 4-Marker: Cluster Rad52: Normal 1-2e-04 1e-04 3e-04 0e+00 4e-04 P Value

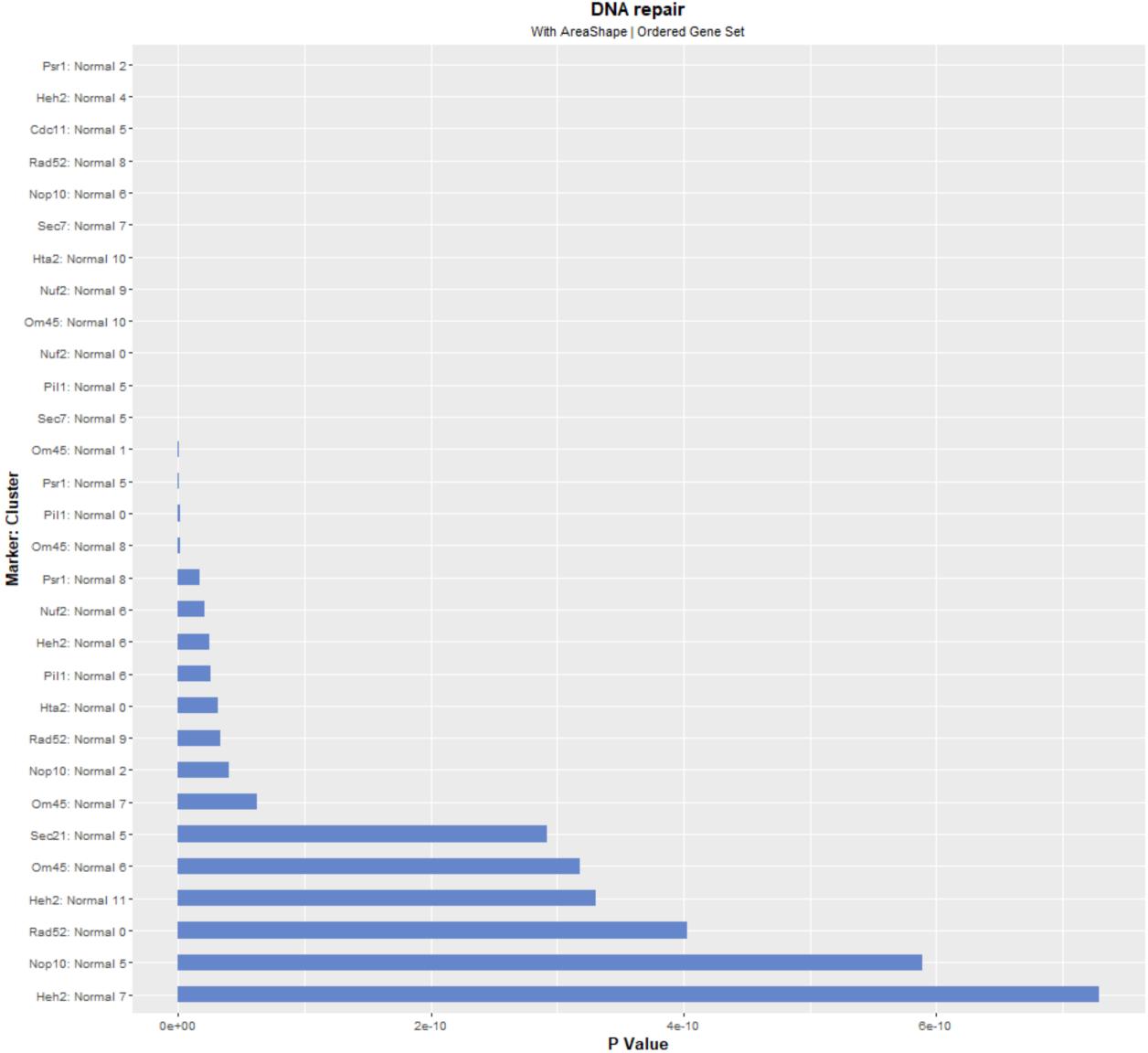
cytoskeleton organization



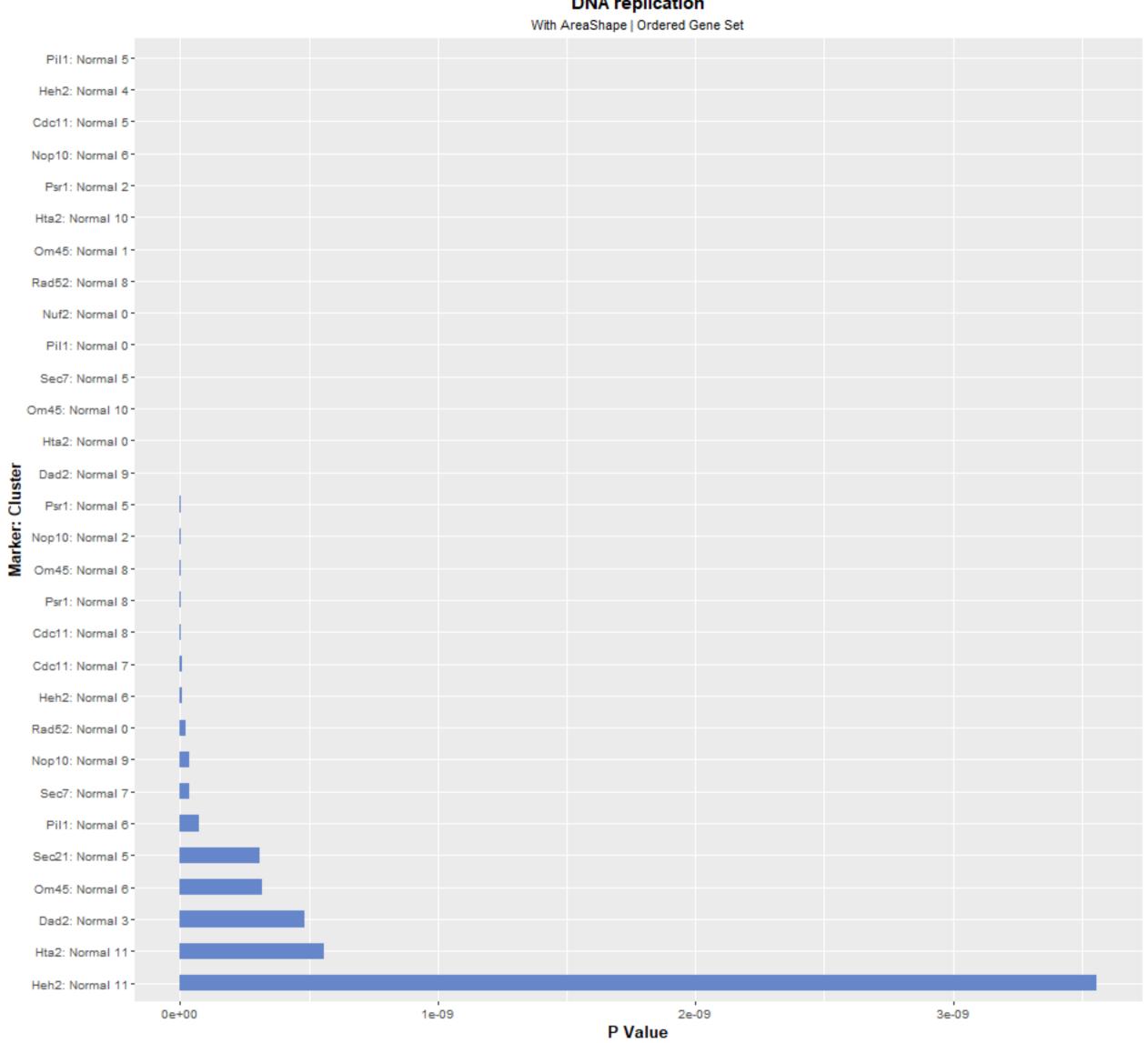
DNA recombination



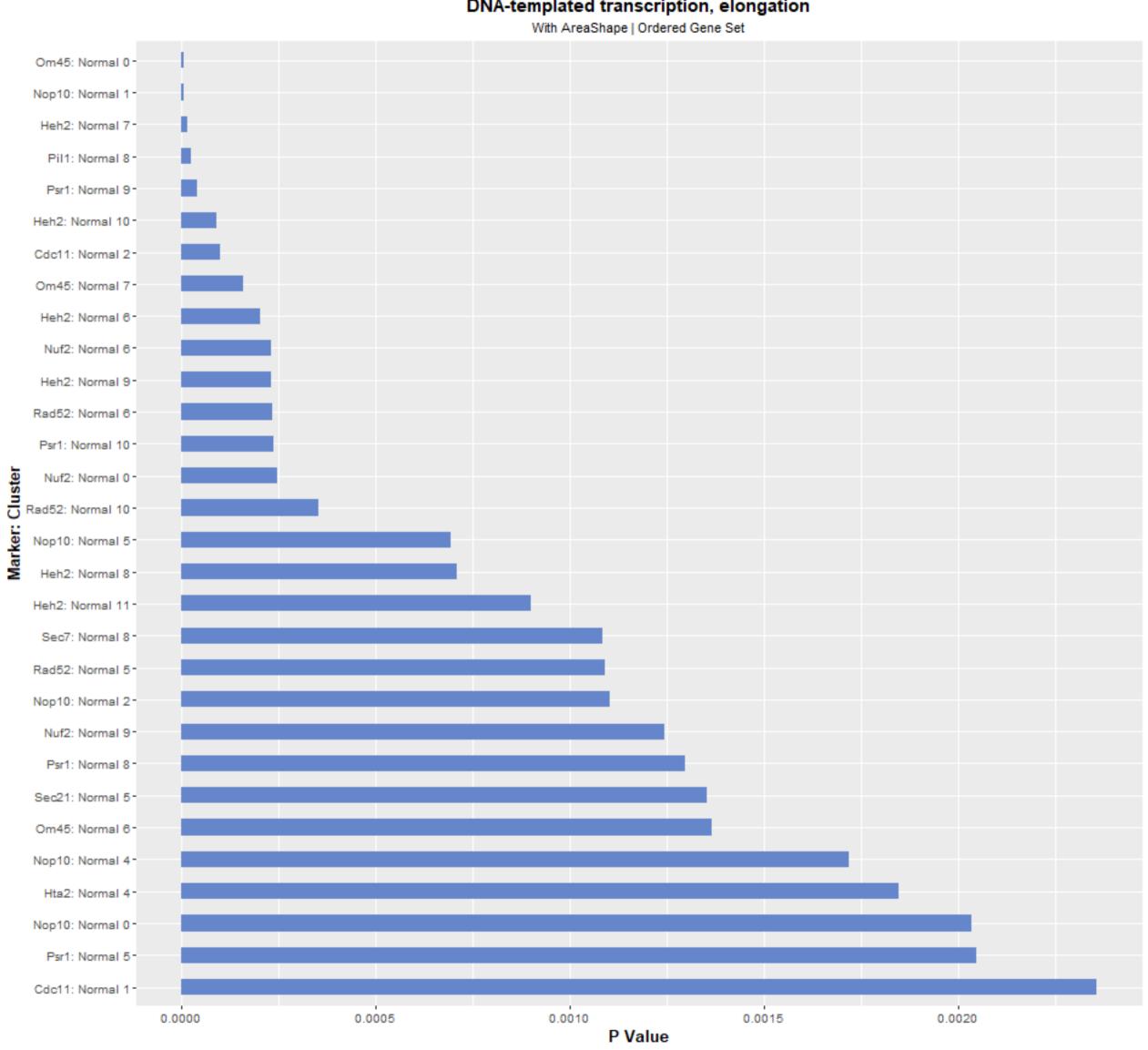
DNA repair



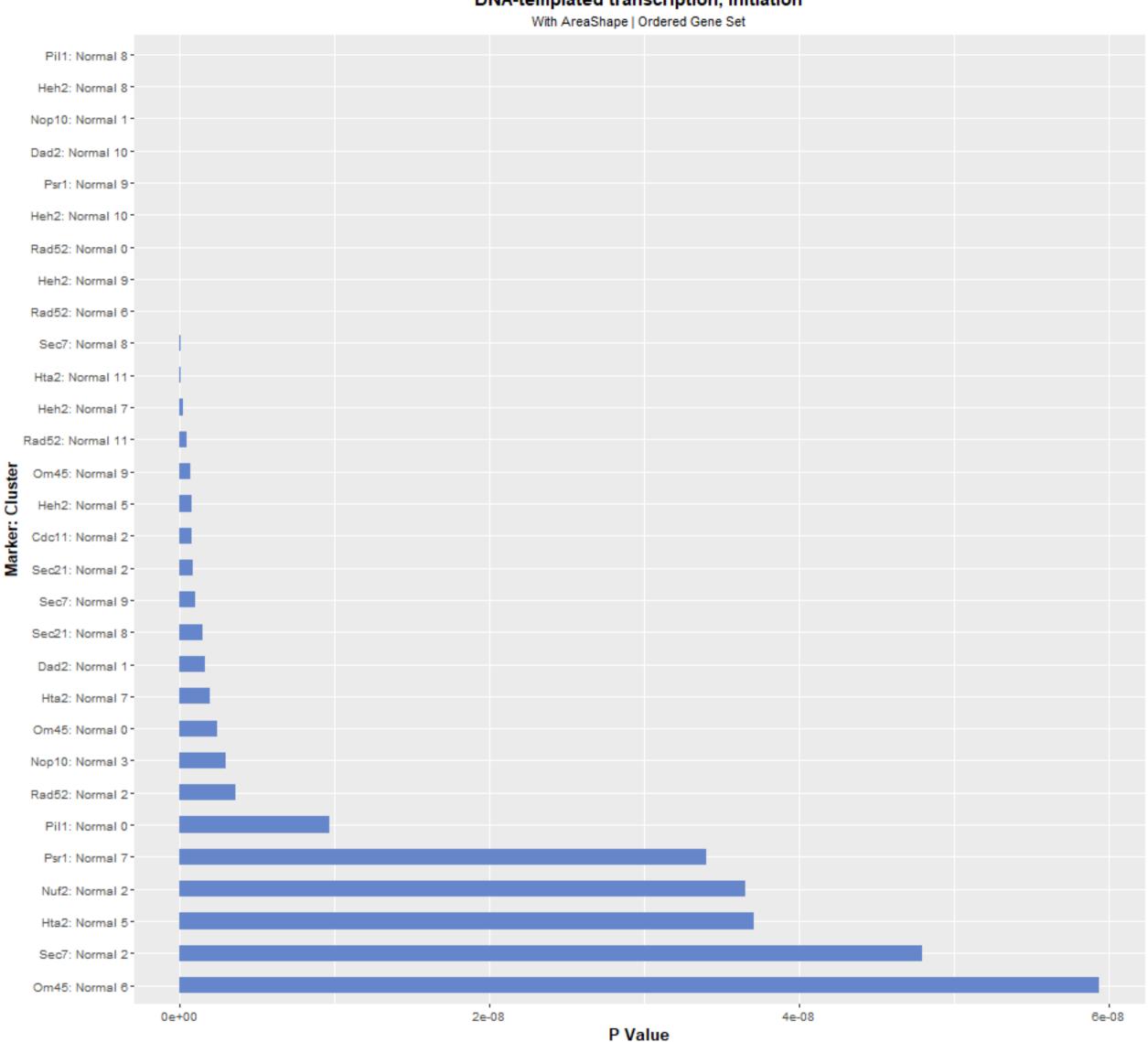
DNA replication



DNA-templated transcription, elongation



DNA-templated transcription, initiation



DNA-templated transcription, termination With AreaShape | Ordered Gene Set

0.002

P Value

0.003

Heh2: Normal 7

Heh2: Normal 9 -

Heh2: Normal 6-

Om45: Normal 7 -

Om45: Normal 3-

Om45: Normal 4-

Pil1: Normal 10 -

Nop10: Normal 1-

Om45: Normal 6-

Heh2: Normal 1-

Psr1: Normal 9 -

Heh2: Normal 8 -

Psr1: Normal 8 -

Om45: Normal 0 -

Sec7: Normal 21

Sec7: Normal 8 -

Psr1: Normal 10 -

Pil1: Normal 8 -

Pil1: Normal 6-

Nuf2: Normal 2 -

Nuf2: Normal 0 -

Psr1: Normal 21

Sec7: Normal 9 -

Sec7: Normal 41

0.000

0.001

Vph1NoPosCtrl: Normal 4-

Vph1WithPosCtrl: Normal 0 -

Vph1NoPosCtrl: Normal 3 -

Vph1WithPosCtrl: Normal 6 -

Vph1NoPosCtrl: Normal 5 -

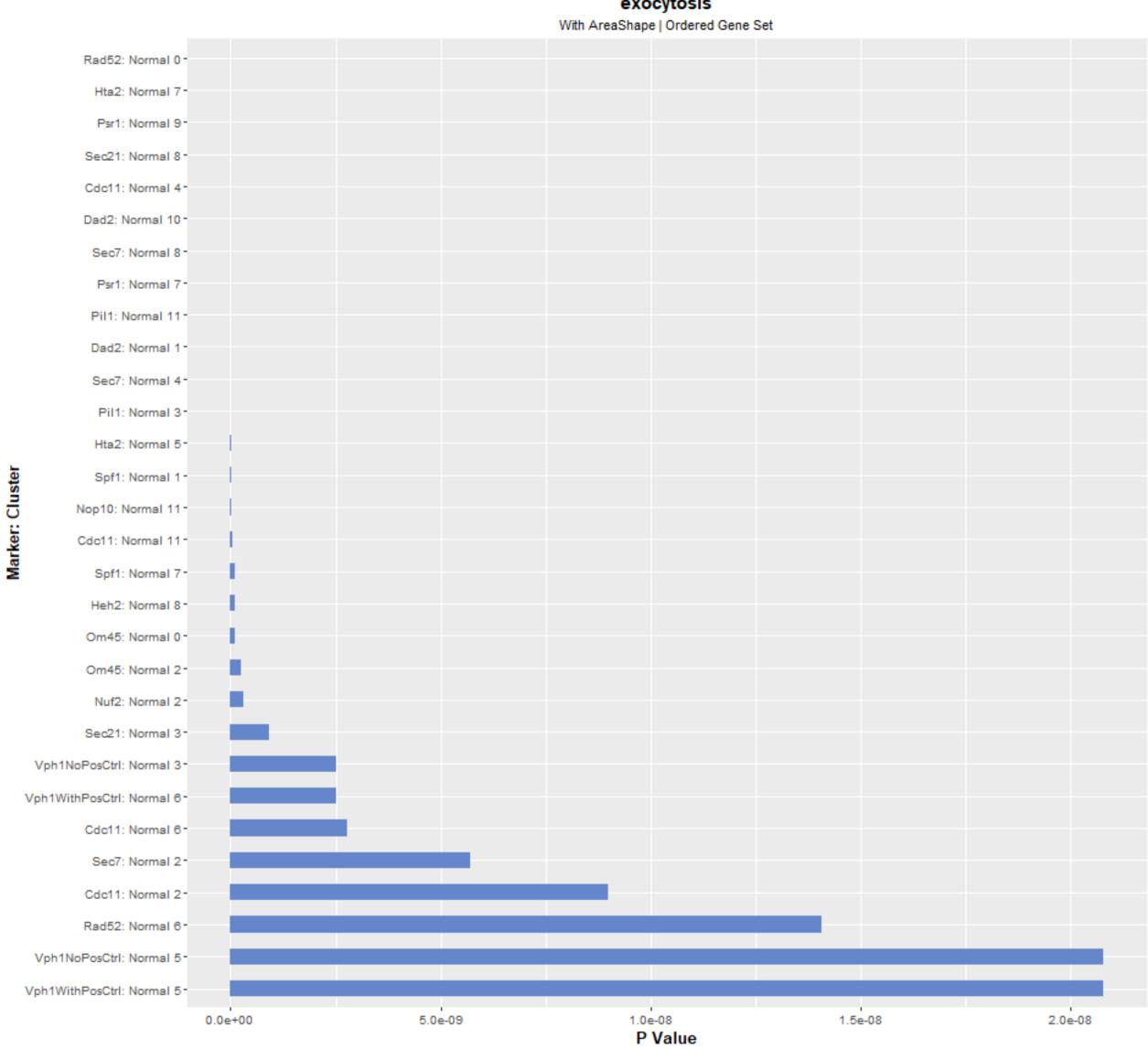
Vph1WithPosCtrl: Normal 5 -

Marker: Cluster

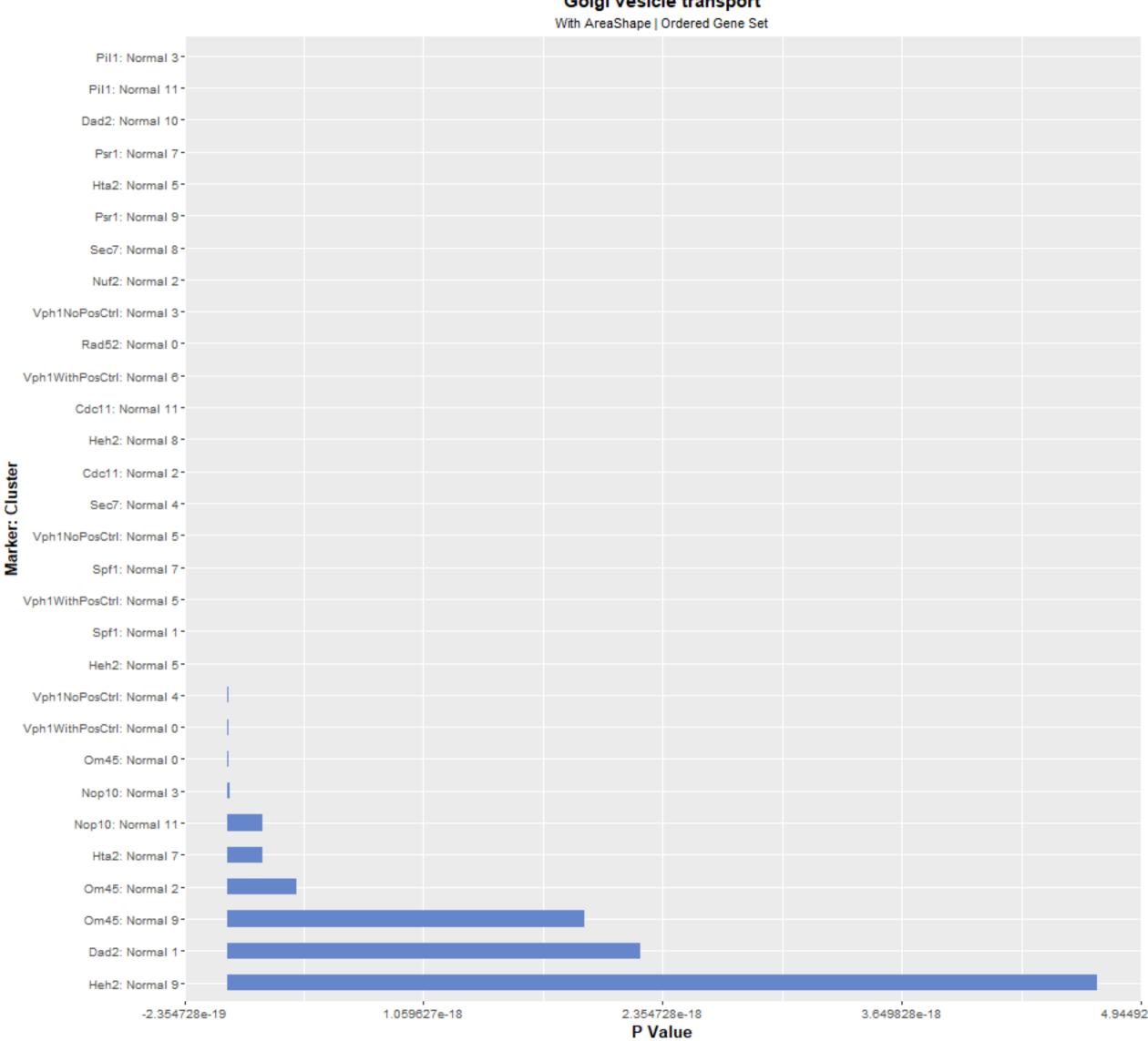
endocytosis With AreaShape | Ordered Gene Set Dad2: Normal 4-Spf1: Normal 7-Vph1WithPosCtrl: Normal 6 Vph1NoPosCtrl: Normal 3 Psr1: Normal 10 -Heh2: Normal 5 Om45: Normal 6-Dad2: Normal 7 -Marker: Cluster Heh2: Normal 7 -Rad52: Normal 10 -Om45: Normal 7 -Sec21: Normal 8 -Pil1: Normal 8 -Psr1: Normal 31 Pil1: Normal 4-Psr1: Normal 0 -Pil1: Normal 2-Pil1: Normal 1-0.0050 0.0100 0.0000 0.0025 0.0075 P Value

endosomal transport With AreaShape | Ordered Gene Set Psr1: Normal 0 -Pil1: Normal 1-Vph1WithPosCtrl: Normal 7 -Marker: Cluster Vph1NoPosCtrl: Normal 7 -Vph1NoPosCtrl: Normal 0 -Vph1WithPosCtrl: Normal 10 -0.0050 0.0000 0.0025 0.0075 P Value

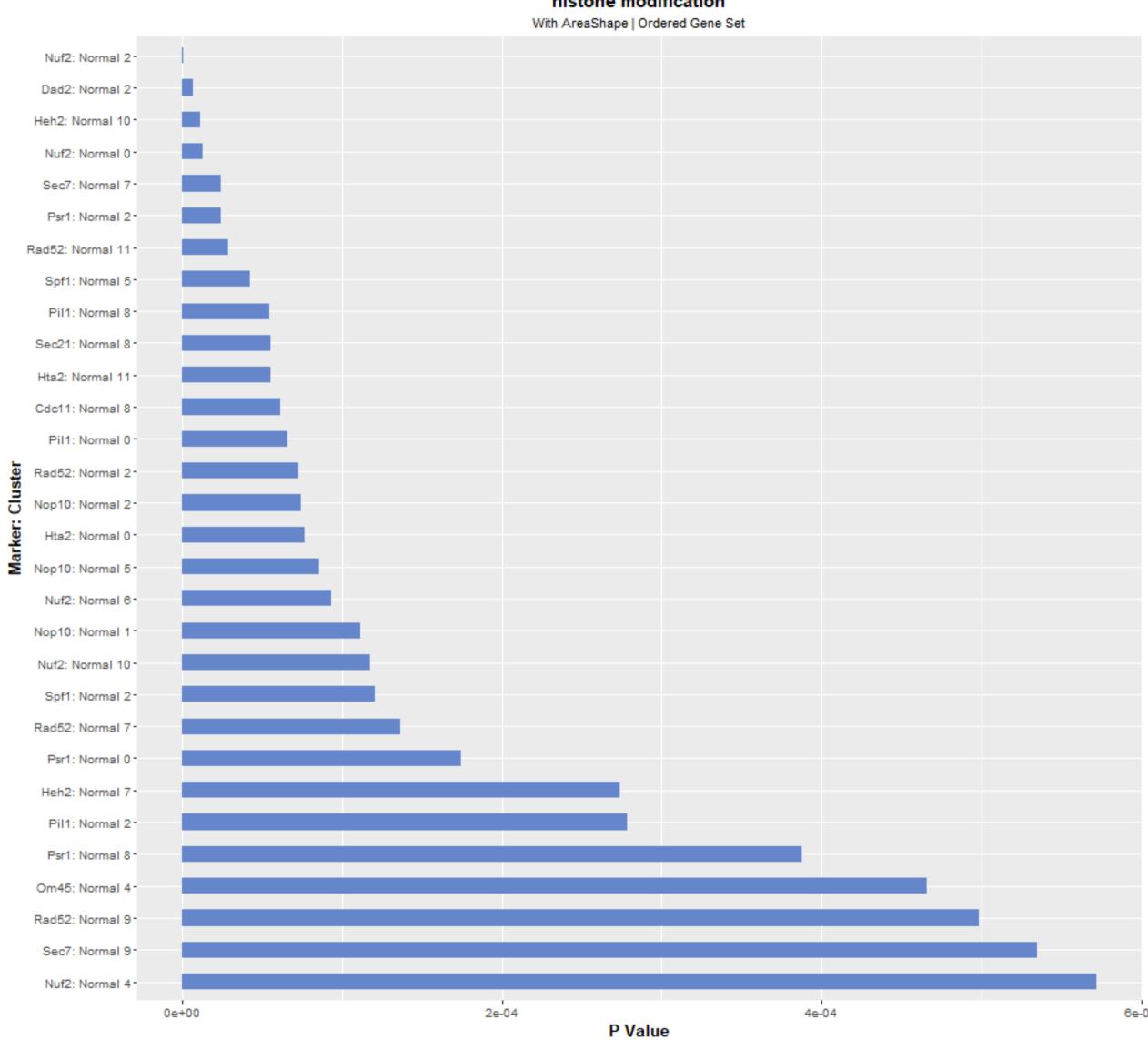
exocytosis



Golgi vesicle transport



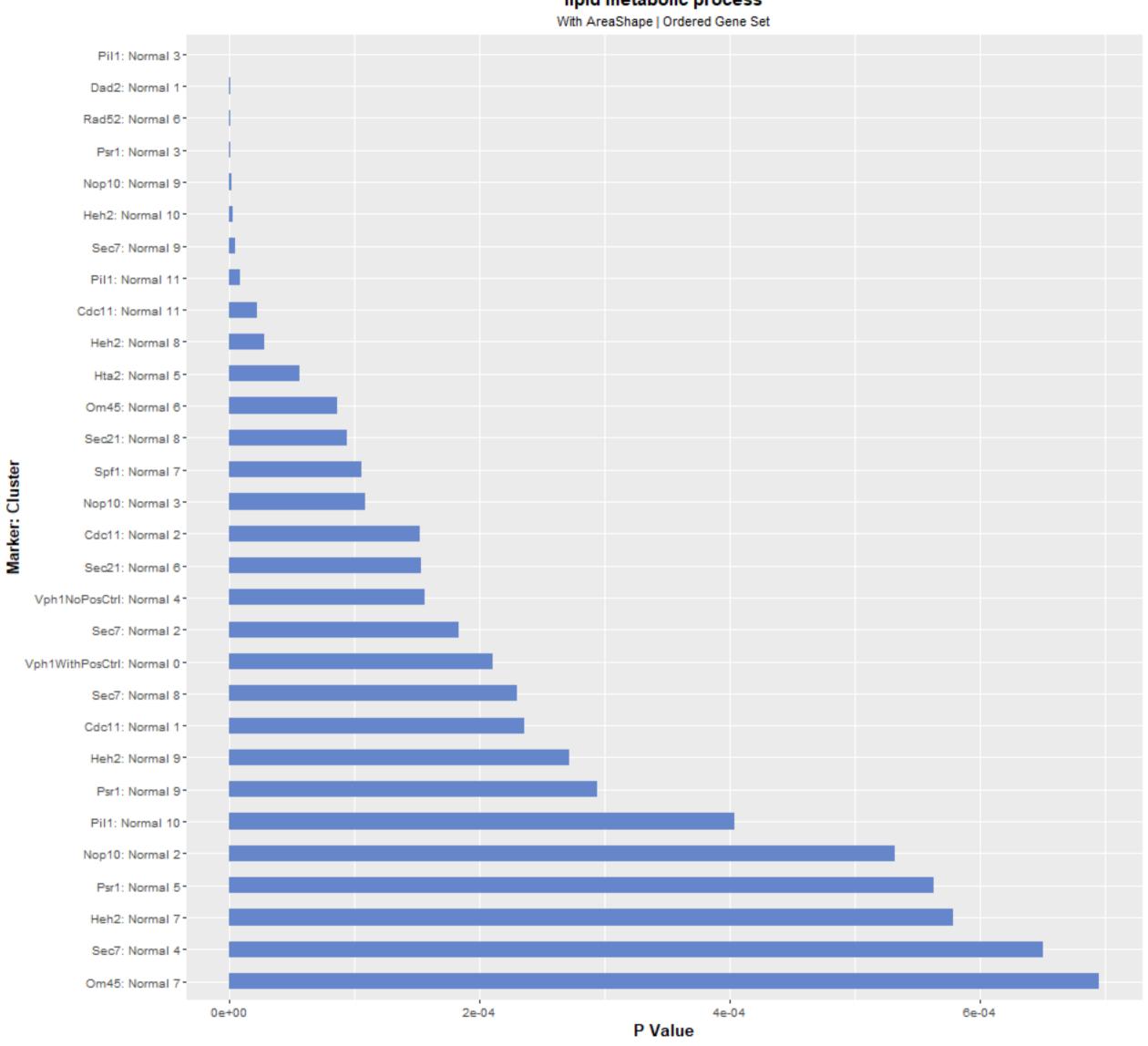
histone modification



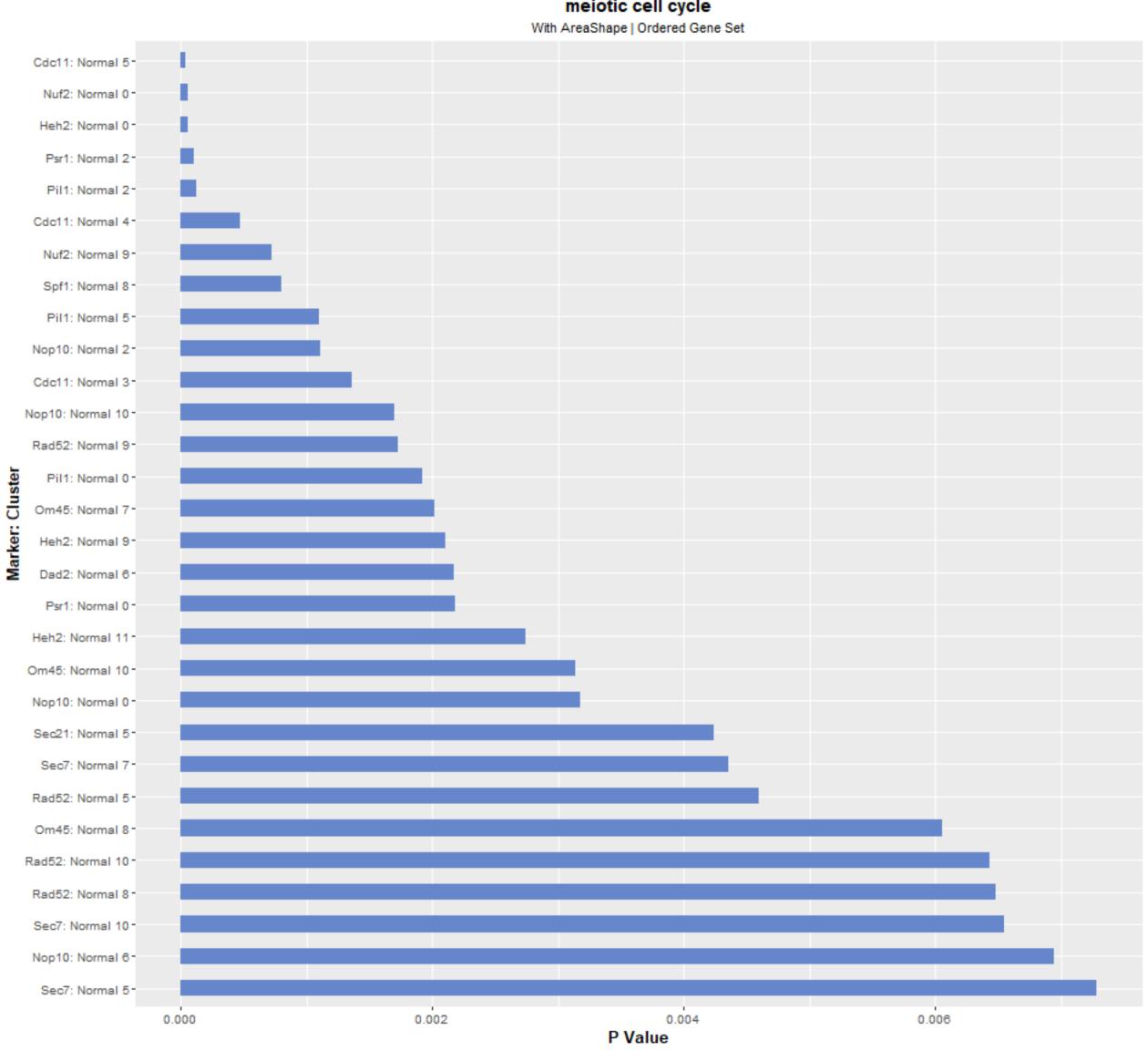
invasive growth in response to glucose limitation With AreaShape | Ordered Gene Set Om45: Normal 3-Psr1: Normal 0 -Rad52: Normal 1-Hta2: Normal 31 Spf1: Normal 21 Rad52: Normal 4-Rad52: Normal 91 Marker: Cluster Spf1: Normal 5-Vph1WithPosCtrl: Normal 7 -Vph1NoPosCtrl: Normal 7 Vph1NoPosCtrl: Normal 8 -Vph1WithPosCtrl: Normal 2 -Pil1: Normal 1-Pil1: Normal 21 Sec7: Normal 10 -0.0050 0.0000 0.0025 0.0075 P Value

ion transport With AreaShape | Ordered Gene Set Marker: Cluster: 0 c c la como de como 0.00050 0.00075 0.00000 0.00025 0.00100 P Value

lipid metabolic process



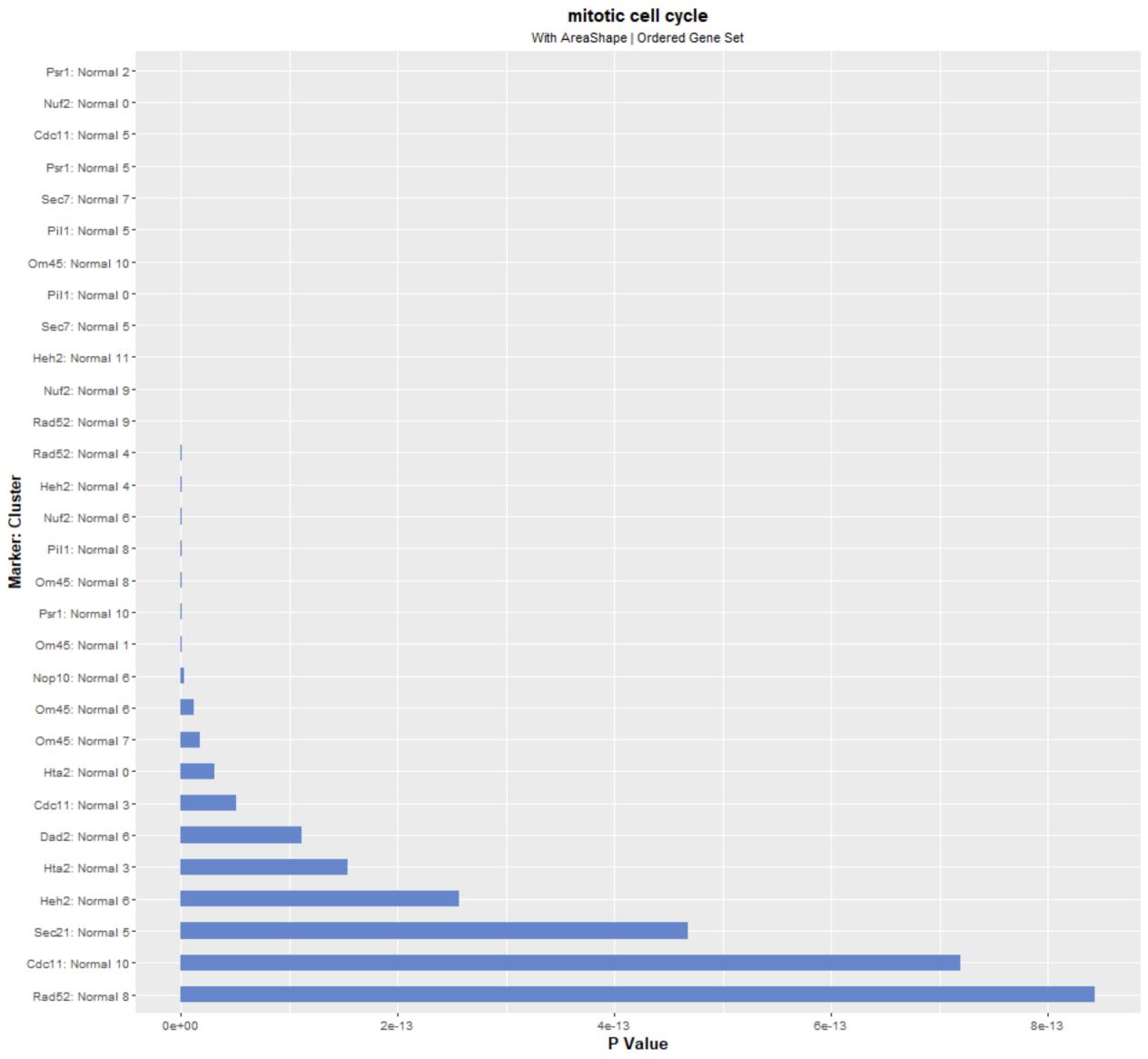
meiotic cell cycle



membrane fusion

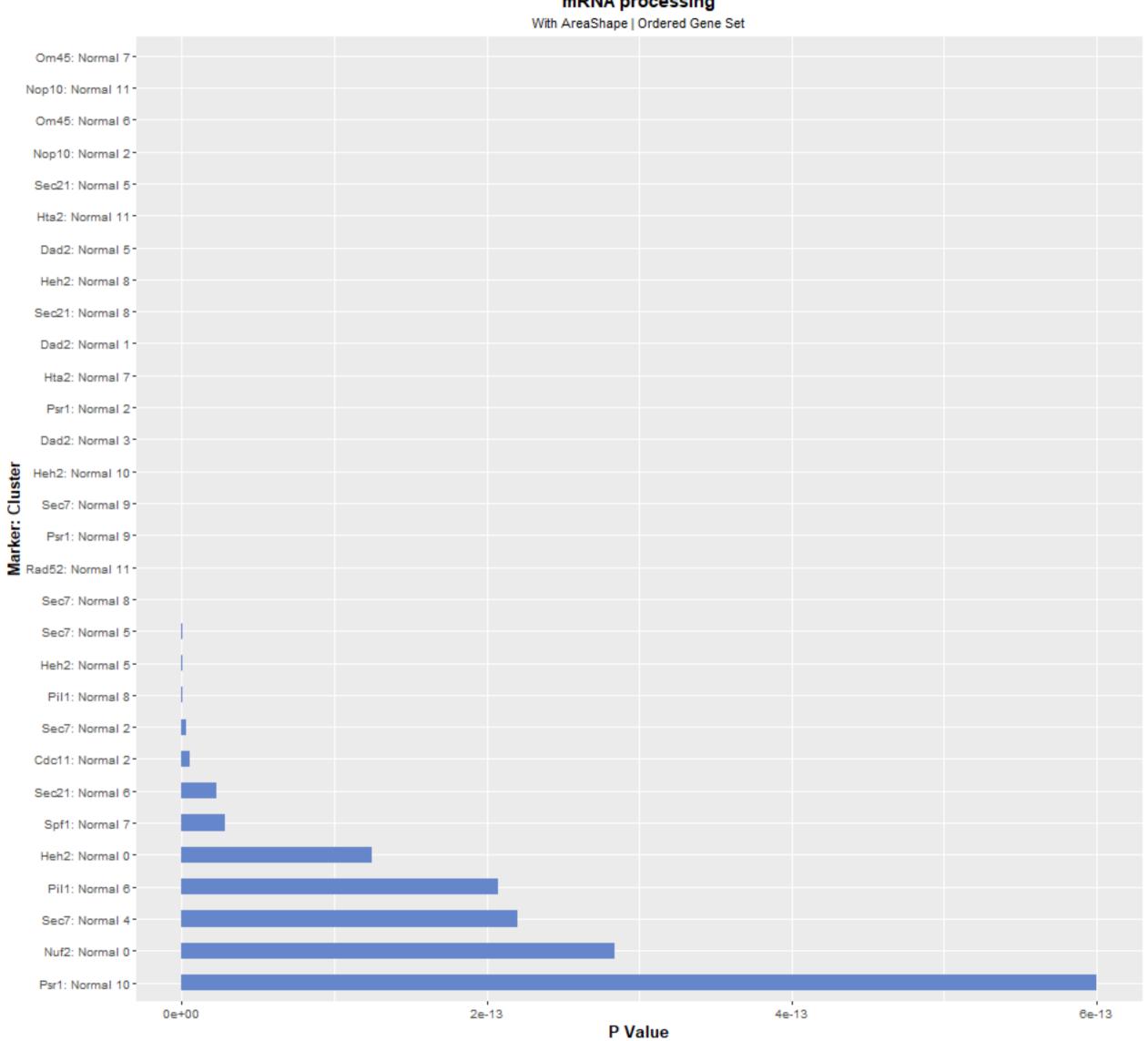
With AreaShape | Ordered Gene Set Pil1: Normal 11 Pil1: Normal 3-Dad2: Normal 10 -Cdc11: Normal 21 Psr1: Normal 9 -Spf1: Normal 7 -Om45: Normal 0 -Sec7: Normal 8 -Hta2: Normal 5-Vph1WithPosCtrl: Normal 5 -Rad52: Normal 0 -Psr1: Normal 7 -Vph1NoPosCtrl: Normal 5 -Marker: Cluster Sec7: Normal 21 Nuf2: Normal 2-Sec21: Normal 8 -Cdc11: Normal 11-Nop10: Normal 3-Vph1WithPosCtrl: Normal 6 -Vph1NoPosCtrl: Normal 3 -Sec21: Normal 31 Hta2: Normal 7 -Rad52: Normal 21 Spf1: Normal 1 -Heh2: Normal 8 -Heh2: Normal 9-Nop10: Normal 11-Om45: Normal 21 Sec7: Normal 41 Heh2: Normal 51 0e+00 4e-10 2e-10 6e-10 P Value

mitochondrion organization With AreaShape | Ordered Gene Set Om45: Normal 3 -Marker: Cluster Heh2: Normal 9 -0.003 0.000 0.001 0.002 P Value

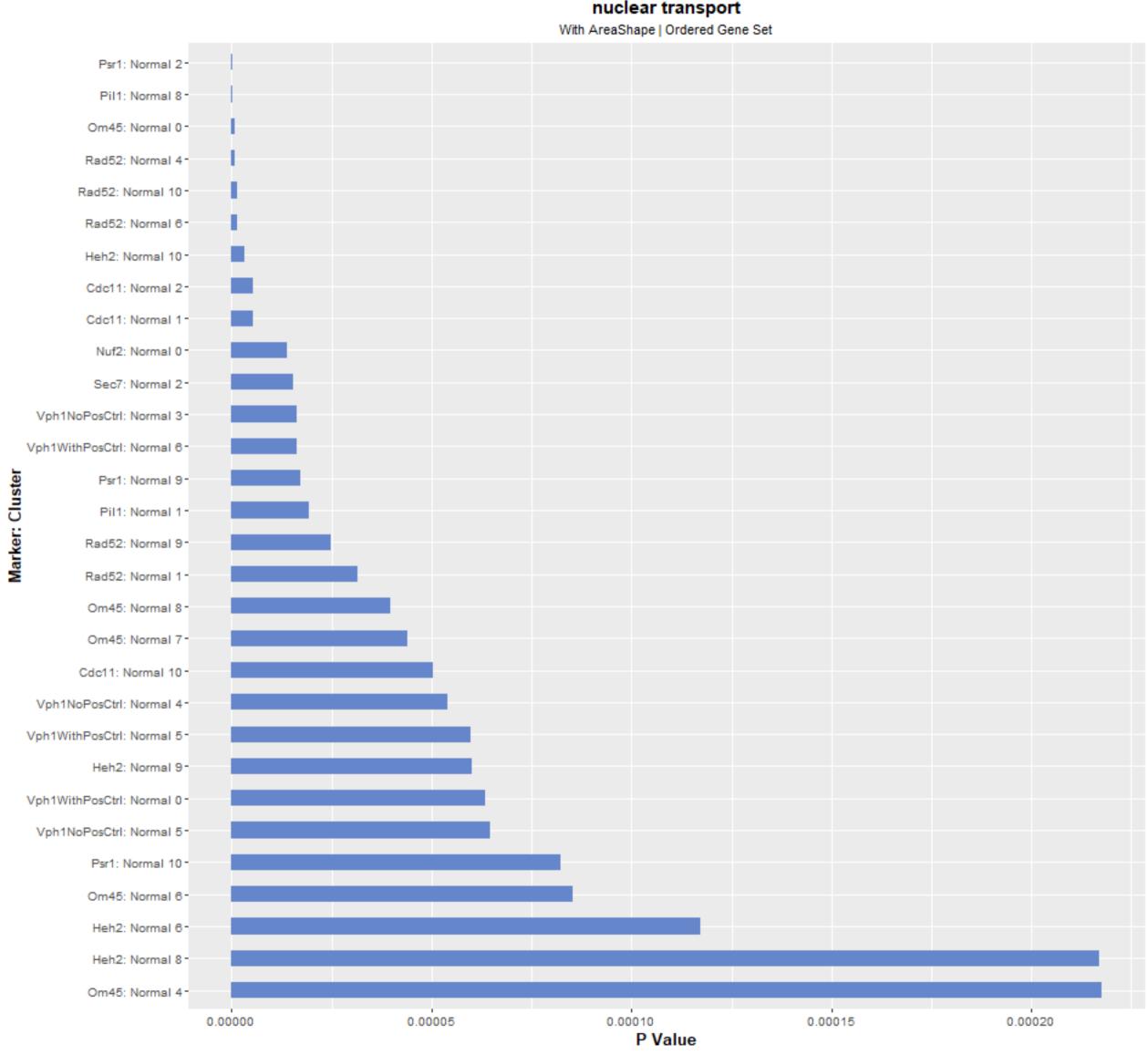


monocarboxylic acid metabolic process With AreaShape | Ordered Gene Set Marker: Cluster: Large Series 17-0.002 0.004 0.000 P Value

mRNA processing



nuclear transport

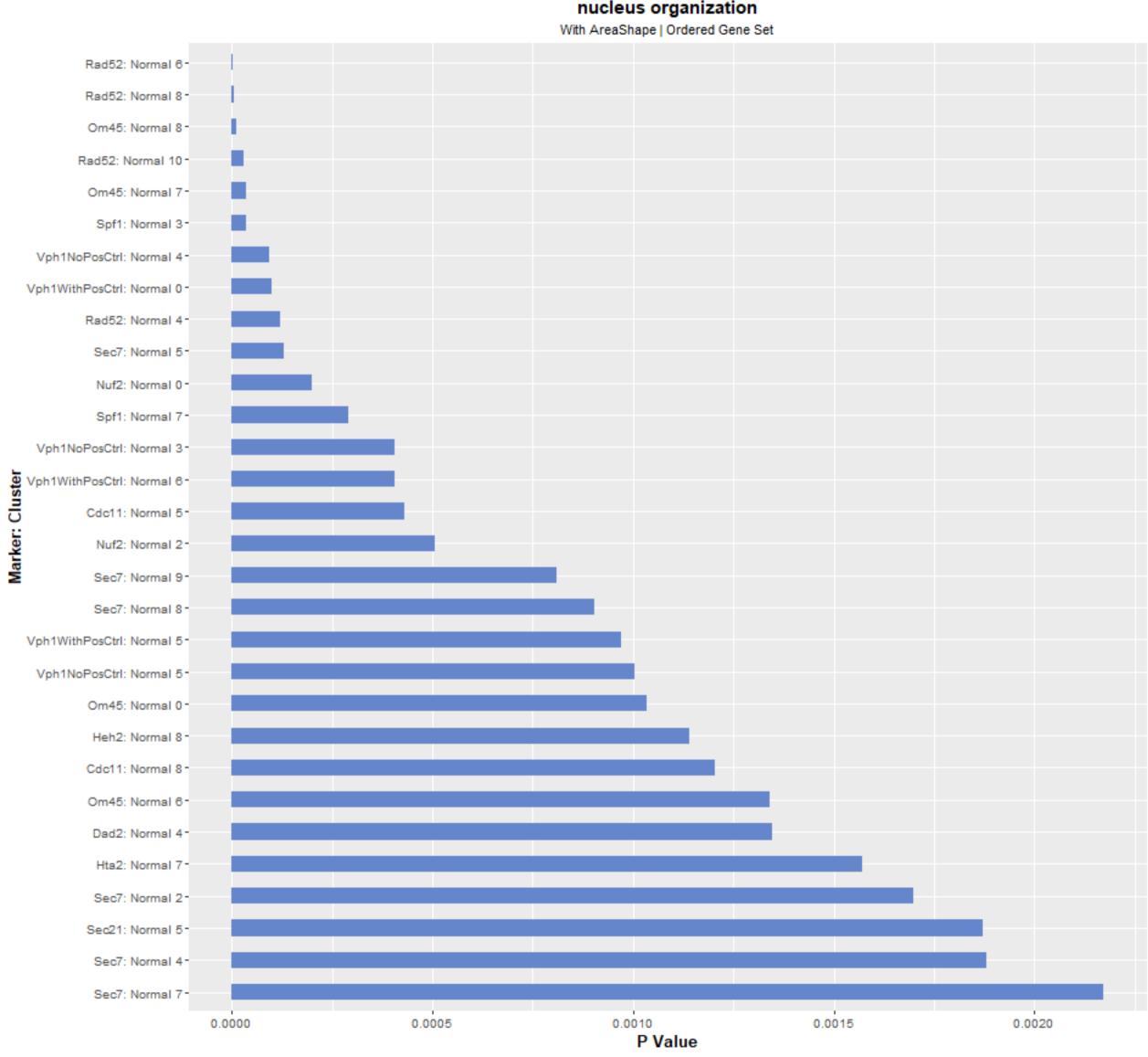


nucleobase-containing compound transport With AreaShape | Ordered Gene Set

Nuf2: Normal 0 -Om45: Normal 0 -Nuf2: Normal 6 -Nop10: Normal 0 -Vph1NoPosCtrl: Normal 3 -Vph1WithPosCtrl: Normal 6 -Vph1NoPosCtrl: Normal 5 -Vph1WithPosCtrl: Normal 5 -Nuf2: Normal 2 -Sec21: Normal 51 Sec21: Normal 8 -Psr1: Normal 2 -Om45: Normal 4-Marker: Cluster Heh2: Normal 10 -Sec21: Normal 1-Hta2: Normal 11 -Sec21: Normal 21 Heh2: Normal 9 -Rad52: Normal 10 -Pil1: Normal 8 -Psr1: Normal 0 -Vph1NoPosCtrl: Normal 4-Rad52: Normal 1 -Vph1WithPosCtrl: Normal 0 -Sec21: Normal 91 Cdc11: Normal 2-Rad52: Normal 9 -Rad52: Normal 11-Psr1: Normal 9 -Nuf2: Normal 9 -0.0000 0.0025 0.0050 0.0075 P Value

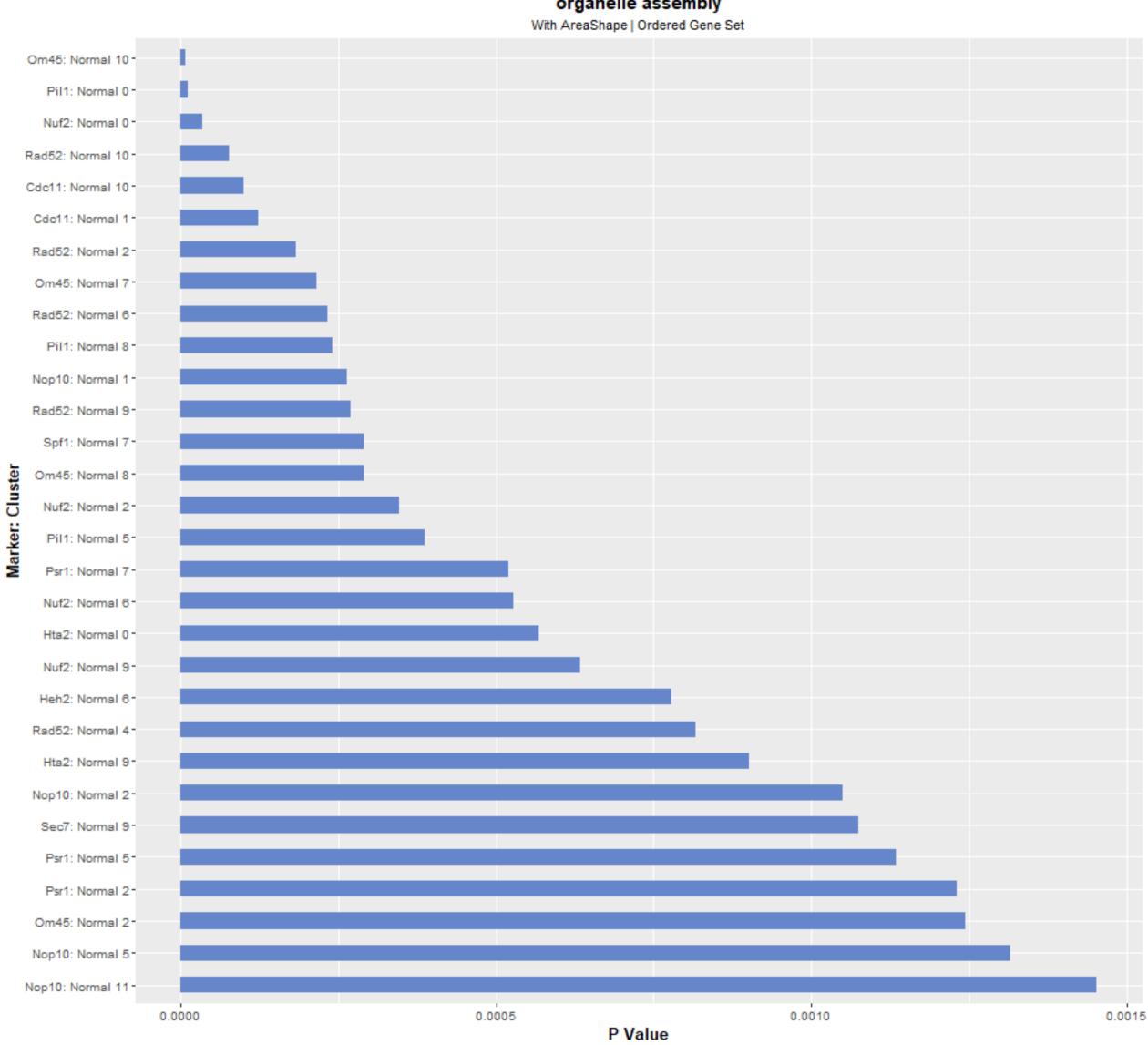
nucleobase-containing small molecule metabolic process With AreaShape | Ordered Gene Set Om45: Normal 31 Marker: Cluster Dad2: Normal 7 -0.001 0.002 0.003 0.004 0.000 P Value

nucleus organization

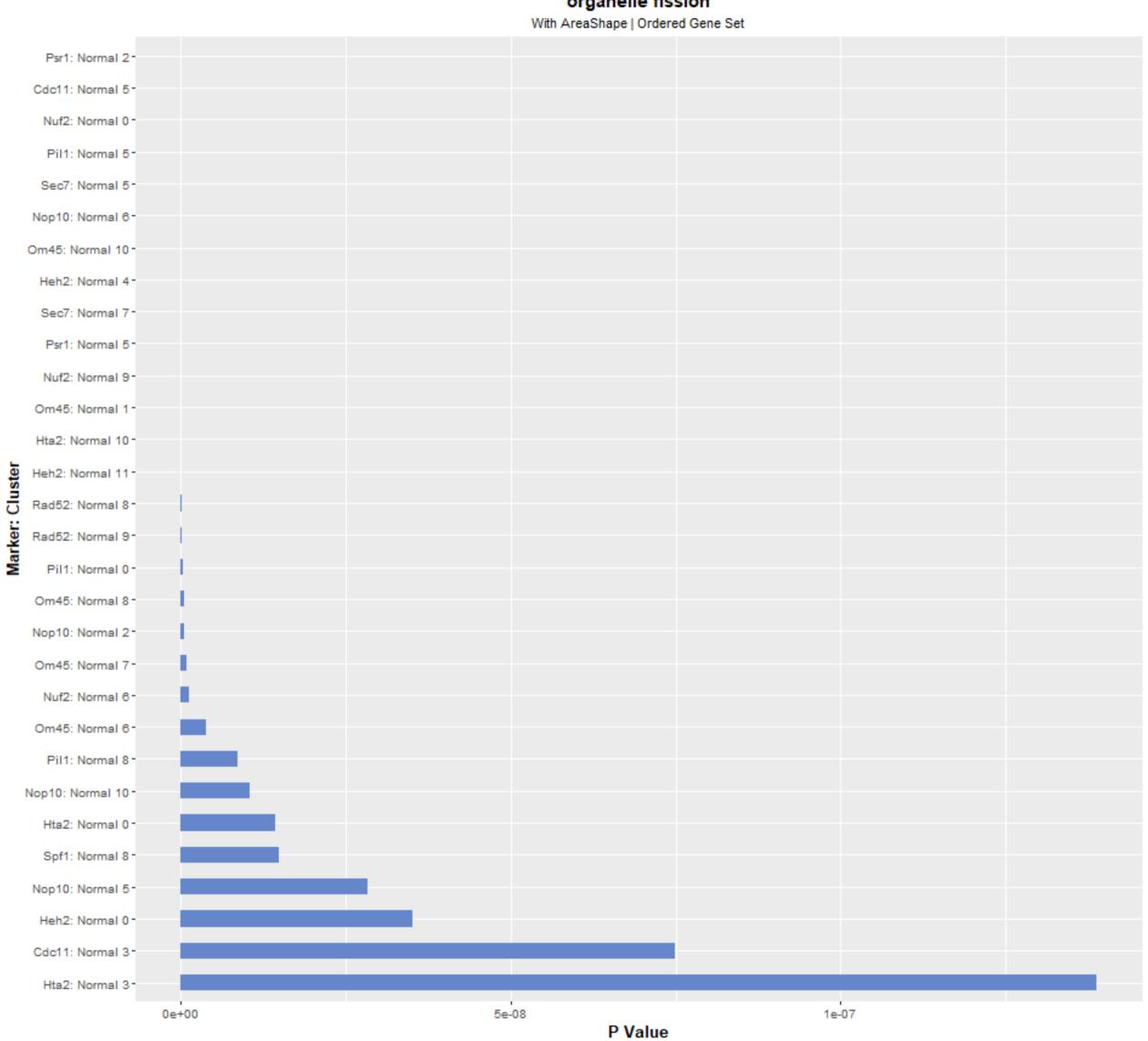


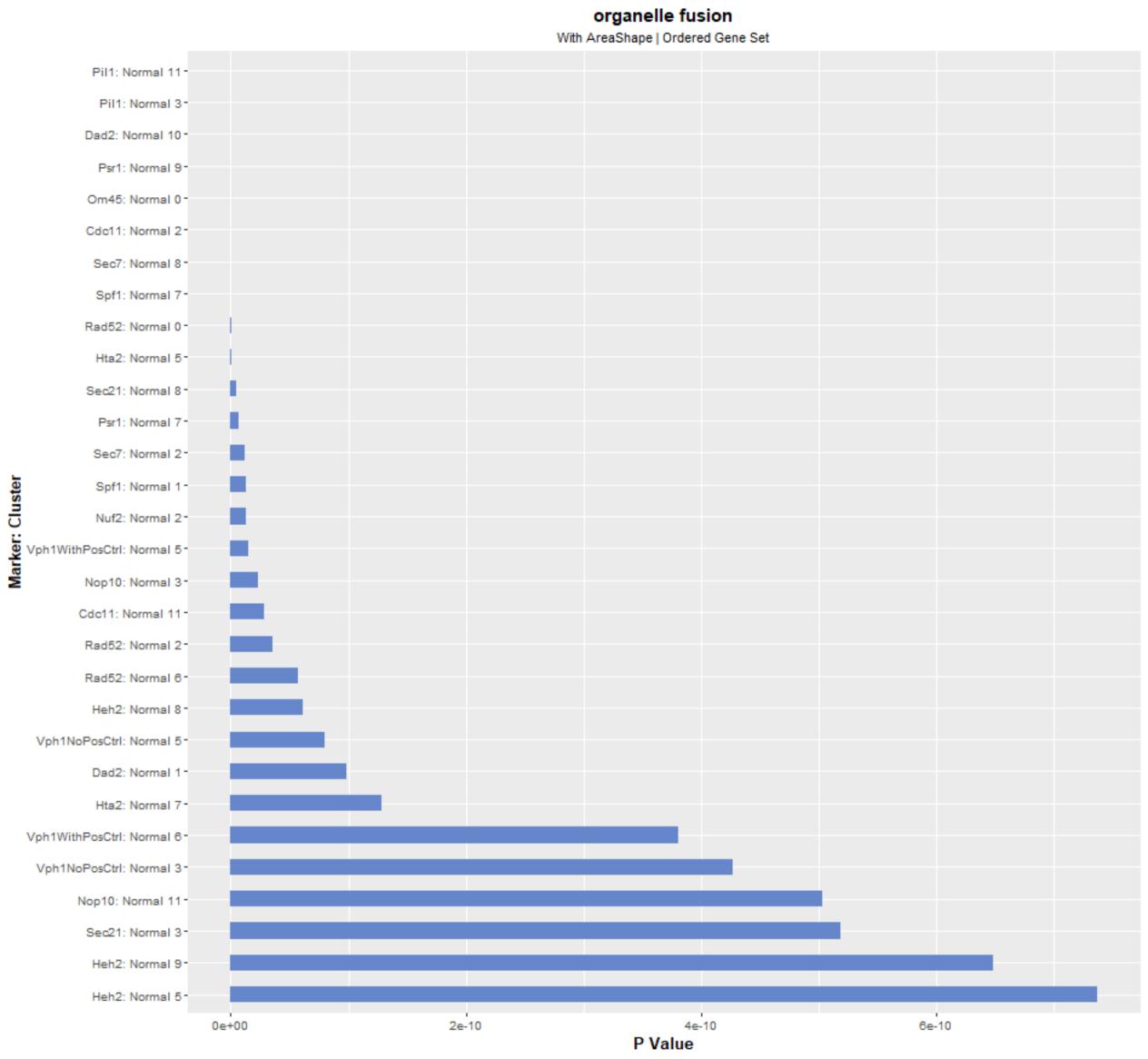
oligosaccharide metabolic process With AreaShape | Ordered Gene Set Pil1: Normal 6-Marker: Cluster Nuf2: Normal 6-0.008 0.004 0.000 0.002 0.006 P Value

organelle assembly

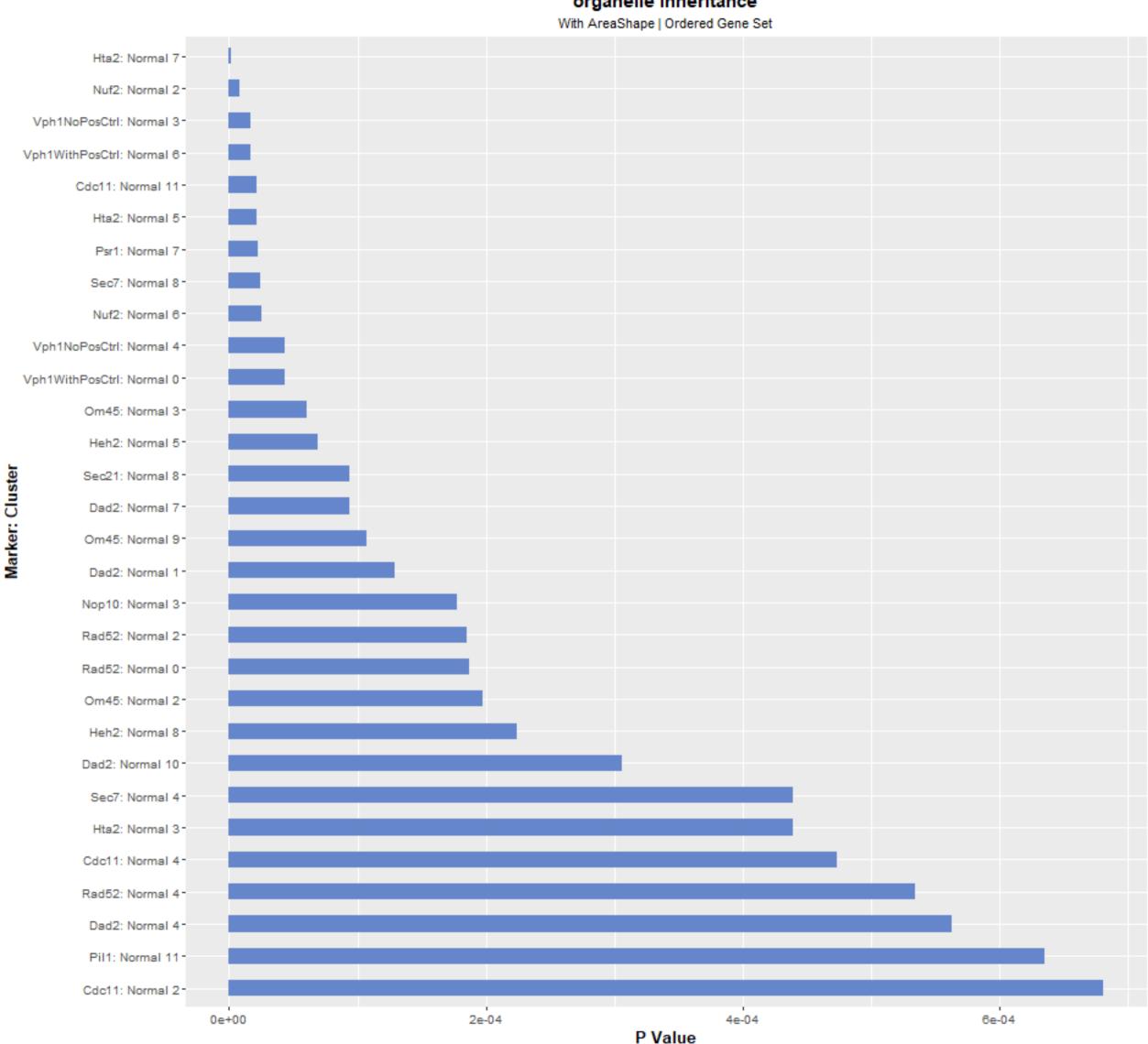


organelle fission





organelle inheritance



peptidyl-amino acid modification With AreaShape | Ordered Gene Set Nuf2: Normal 0 -Sec7: Normal 7 -Sec7: Normal 2-Pil1: Normal 0 -Psr1: Normal 2 -Sec7: Normal 5-Pil1: Normal 8 -Sec21: Normal 9 -Nuf2: Normal 6-Sec21: Normal 21 Heh2: Normal 10 -Sec21: Normal 6 -Heh2: Normal 7 Marker: Cluster Om45: Normal 6-Nop10: Normal 3-Dad2: Normal 1-Om45: Normal 8 -Sec21: Normal 8 -Heh2: Normal 6-Cdc11: Normal 51 Pil1: Normal 5-Rad52: Normal 4-Nuf2: Normal 2-Sec7: Normal 9 -Psr1: Normal 8 -Nuf2: Normal 9 -Om45: Normal 7 -Psr1: Normal 9 -Vph1NoPosCtrl: Normal 3 -Vph1WithPosCtrl: Normal 6

2e-04

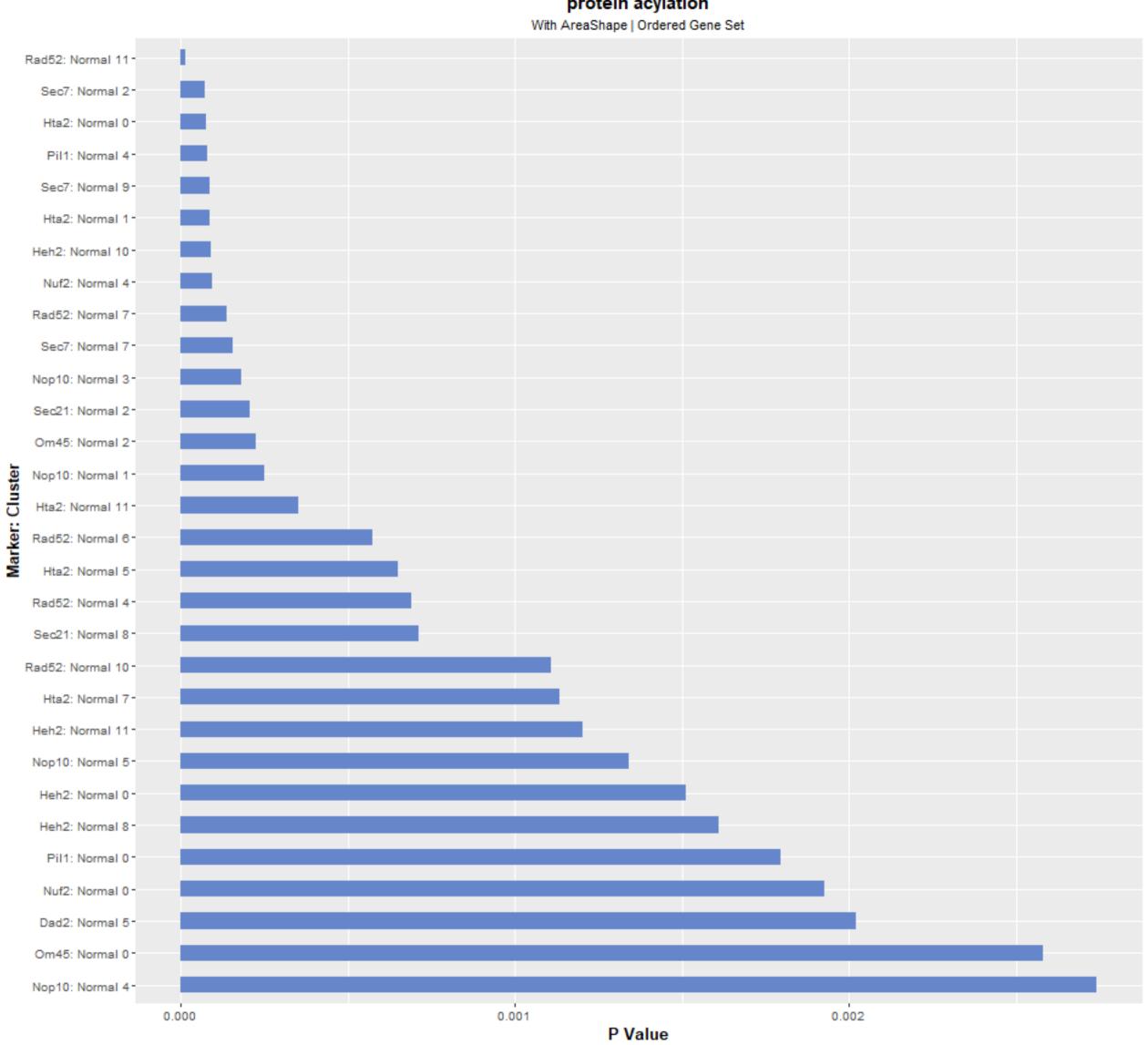
P Value

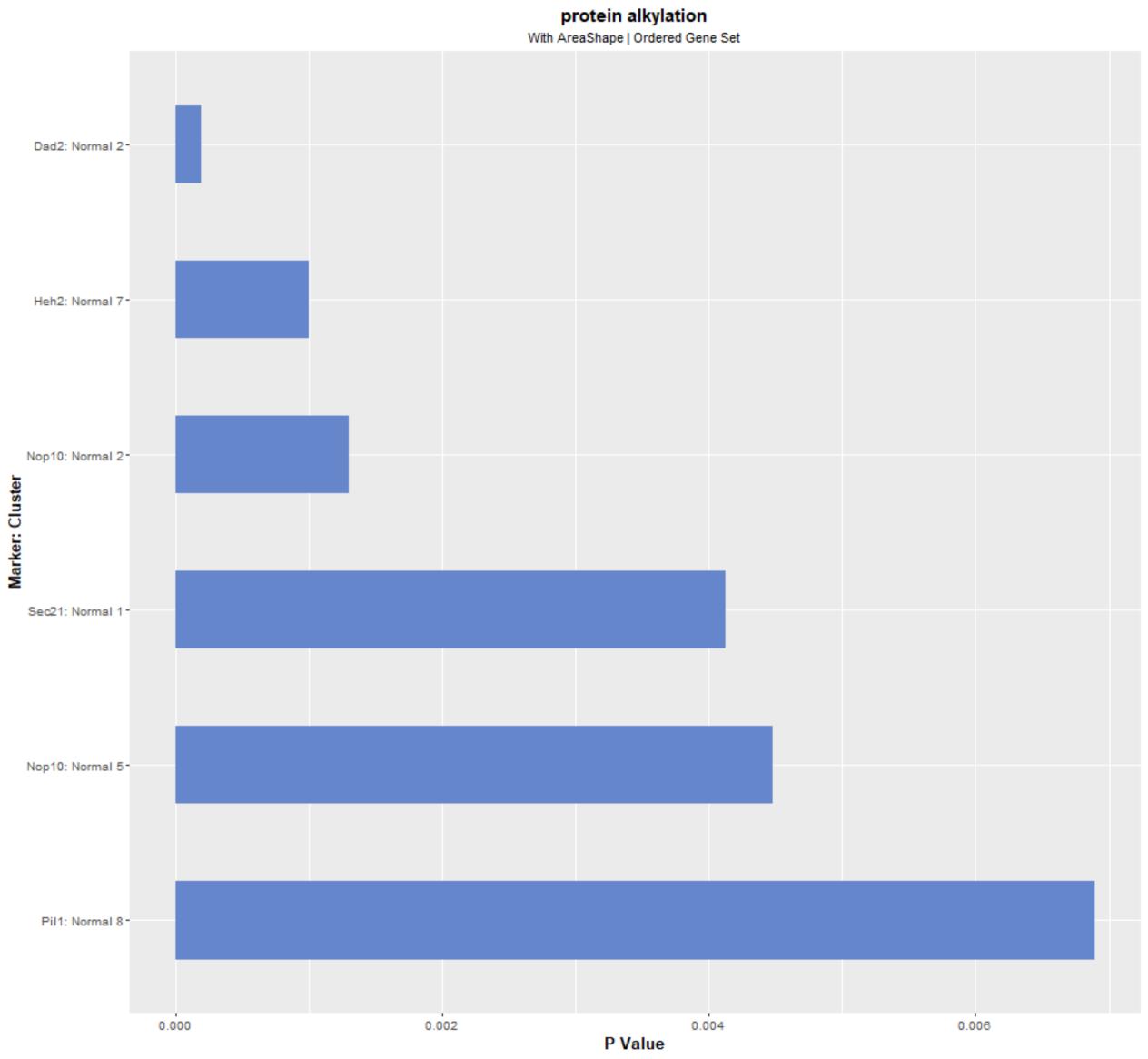
4e-04

6e-04

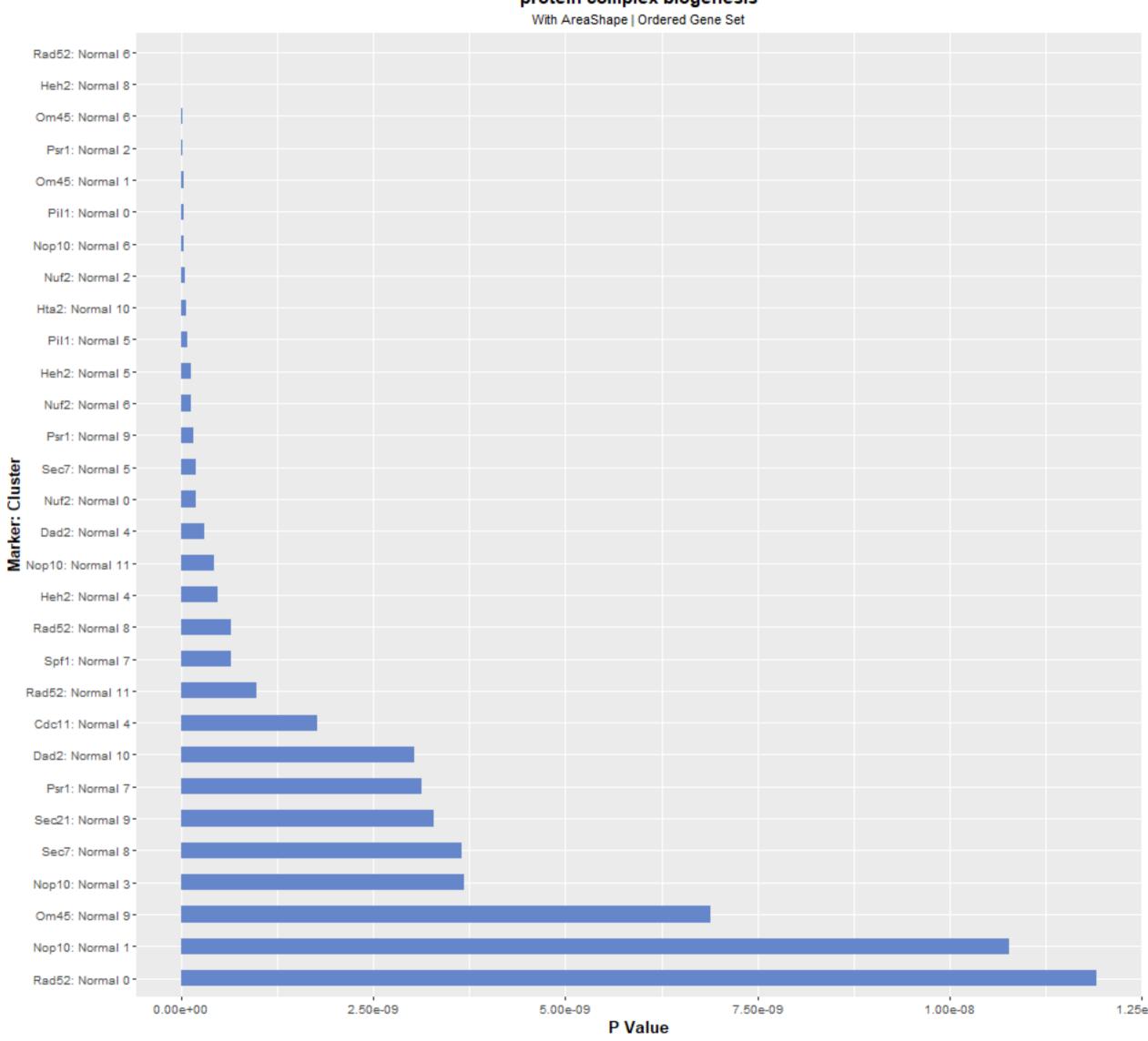
0e+00

protein acylation





protein complex biogenesis

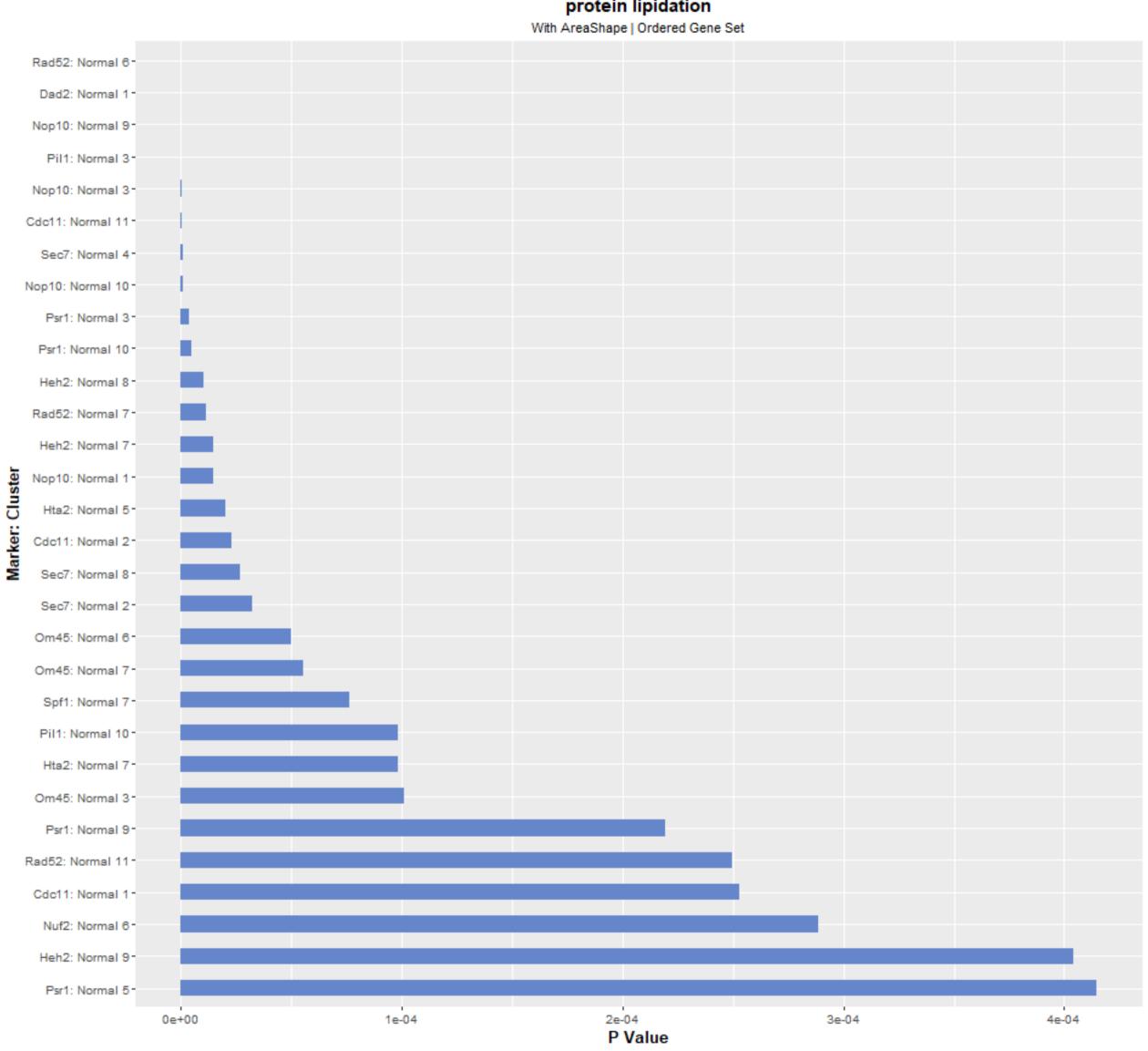


protein dephosphorylation With AreaShape | Ordered Gene Set Rad52: Normal 9 -Hta2: Normal 3-Marker: Cluster Pil1: Normal 4-Heh2: Normal 0 -Nop10: Normal 4-0.000 0.002 0.004 0.006 P Value

protein folding With AreaShape | Ordered Gene Set Marker: Cluster: Clus 0.002 0.000 0.004 0.006 P Value

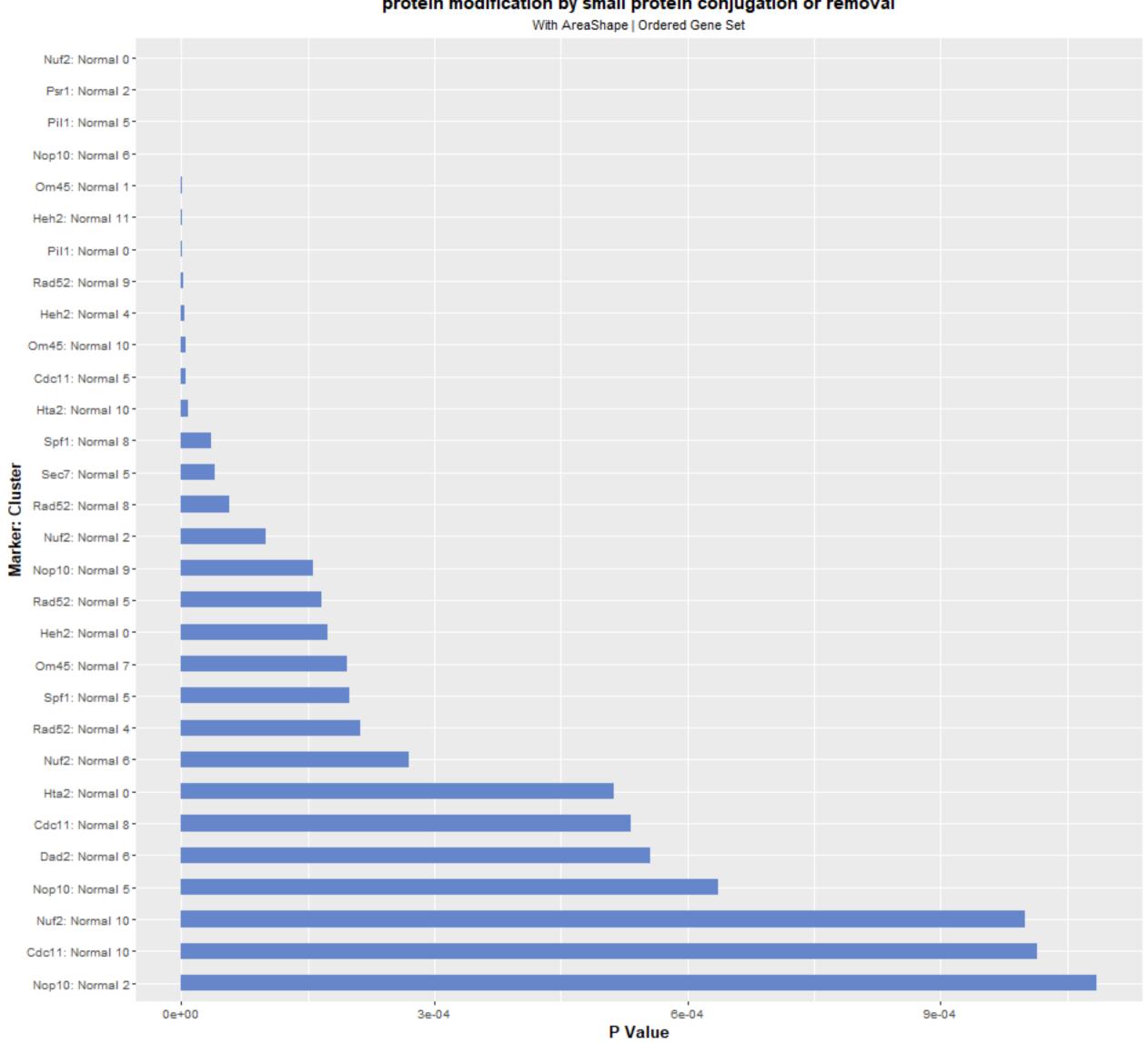
protein glycosylation With AreaShape | Ordered Gene Set Vph1WithPosCtrl: Normal 7 -Vph1NoPosCtrl: Normal 7 -Heh2: Normal 1-Dad2: Normal 8 -Sec7: Normal 9 -Marker: Cluster Nuf2: Normal 6-Heh2: Normal 7 -Vph1WithPosCtrl: Normal 2 Vph1NoPosCtrl: Normal 4-Vph1NoPosCtrl: Normal 8 -Vph1WithPosCtrl: Normal 0 -Dad2: Normal 1-0.0050 0.0000 0.0025 0.0075 P Value

protein lipidation

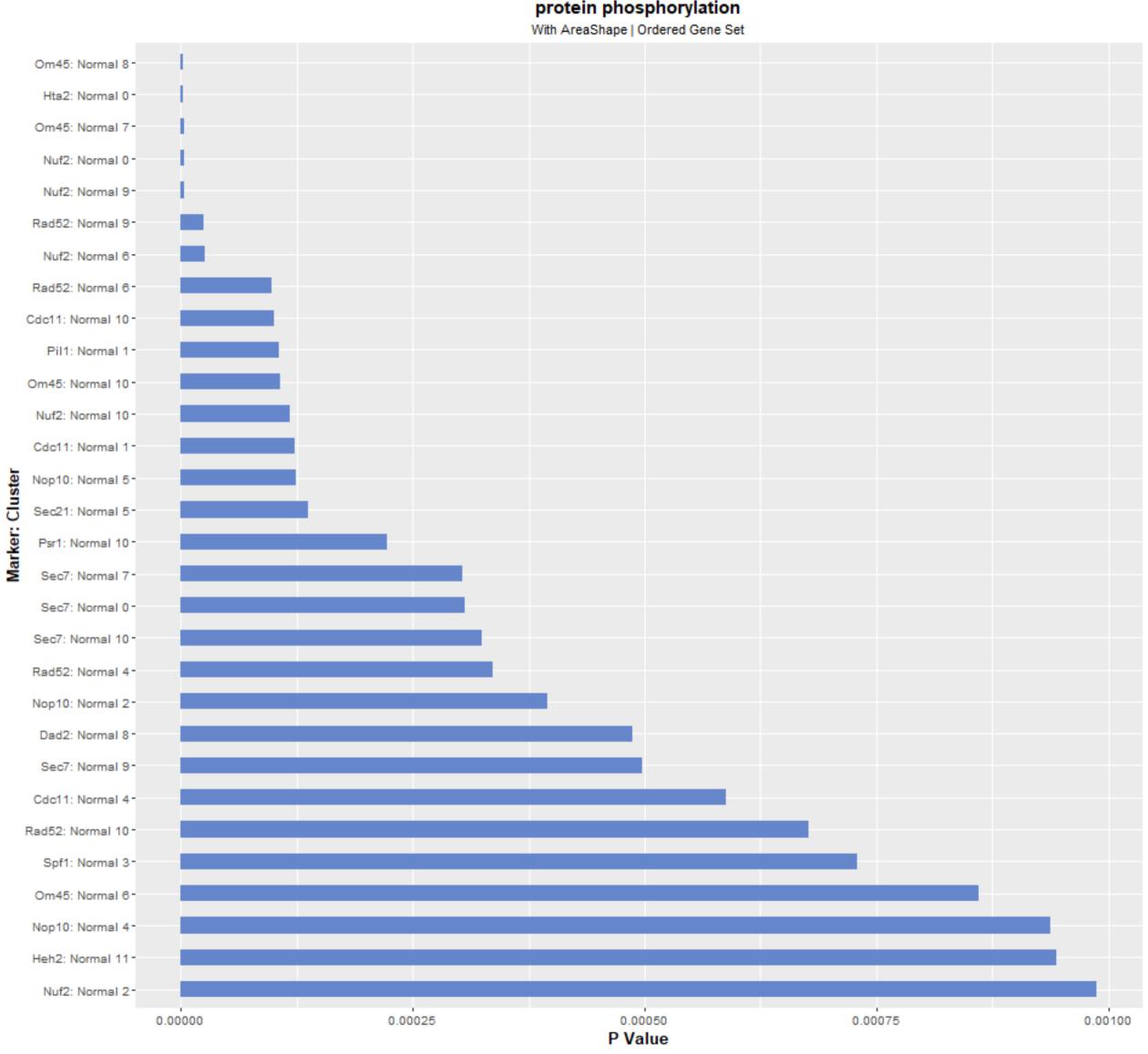


protein maturation With AreaShape | Ordered Gene Set Sec7: Normal 10 -Psr1: Normal 0 -Marker: Cluster Pil1: Normal 31 Nop10: Normal 3-0.004 0.000 0.002 0.006 0.008 P Value

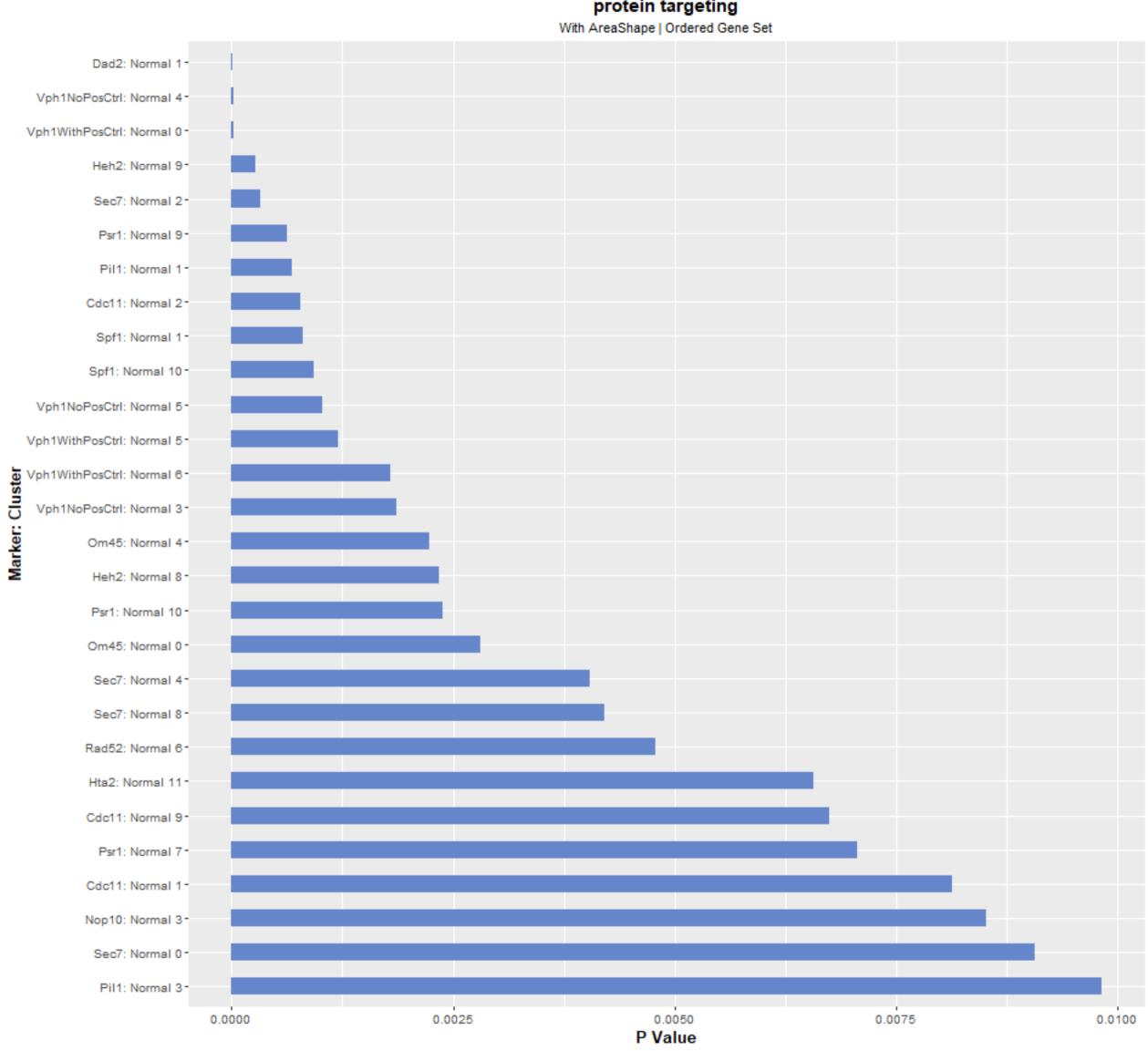
protein modification by small protein conjugation or removal



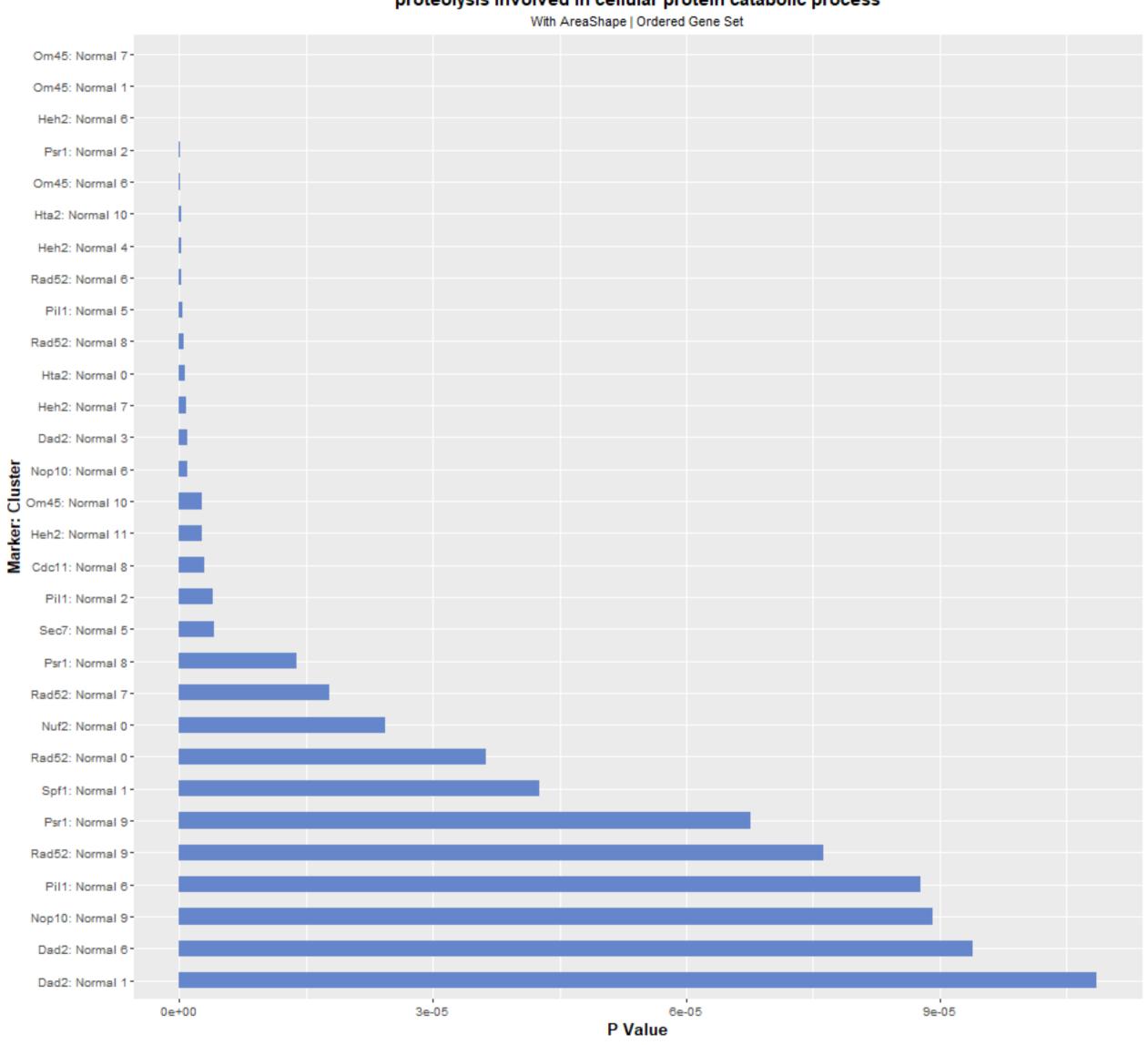
protein phosphorylation



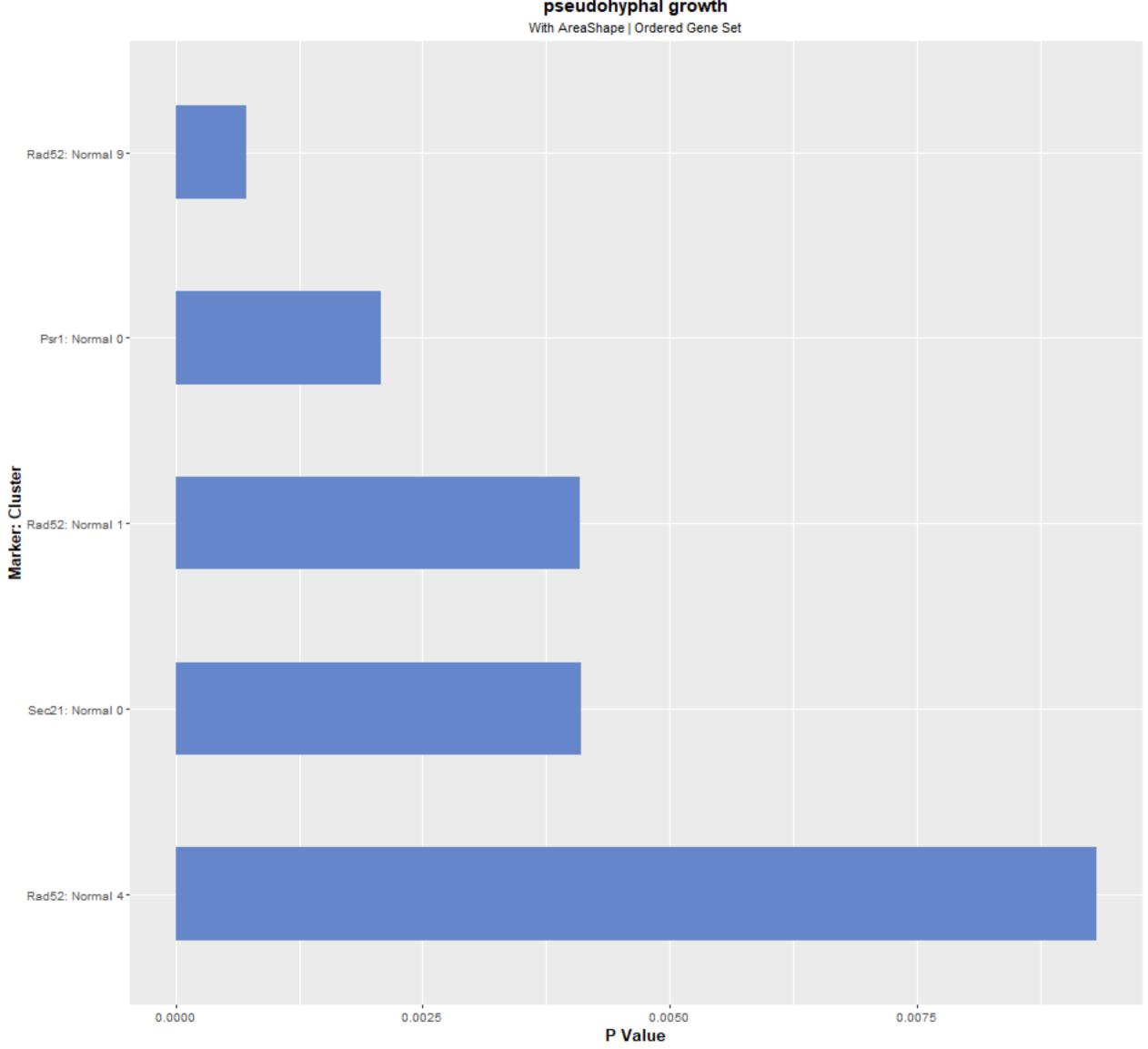
protein targeting



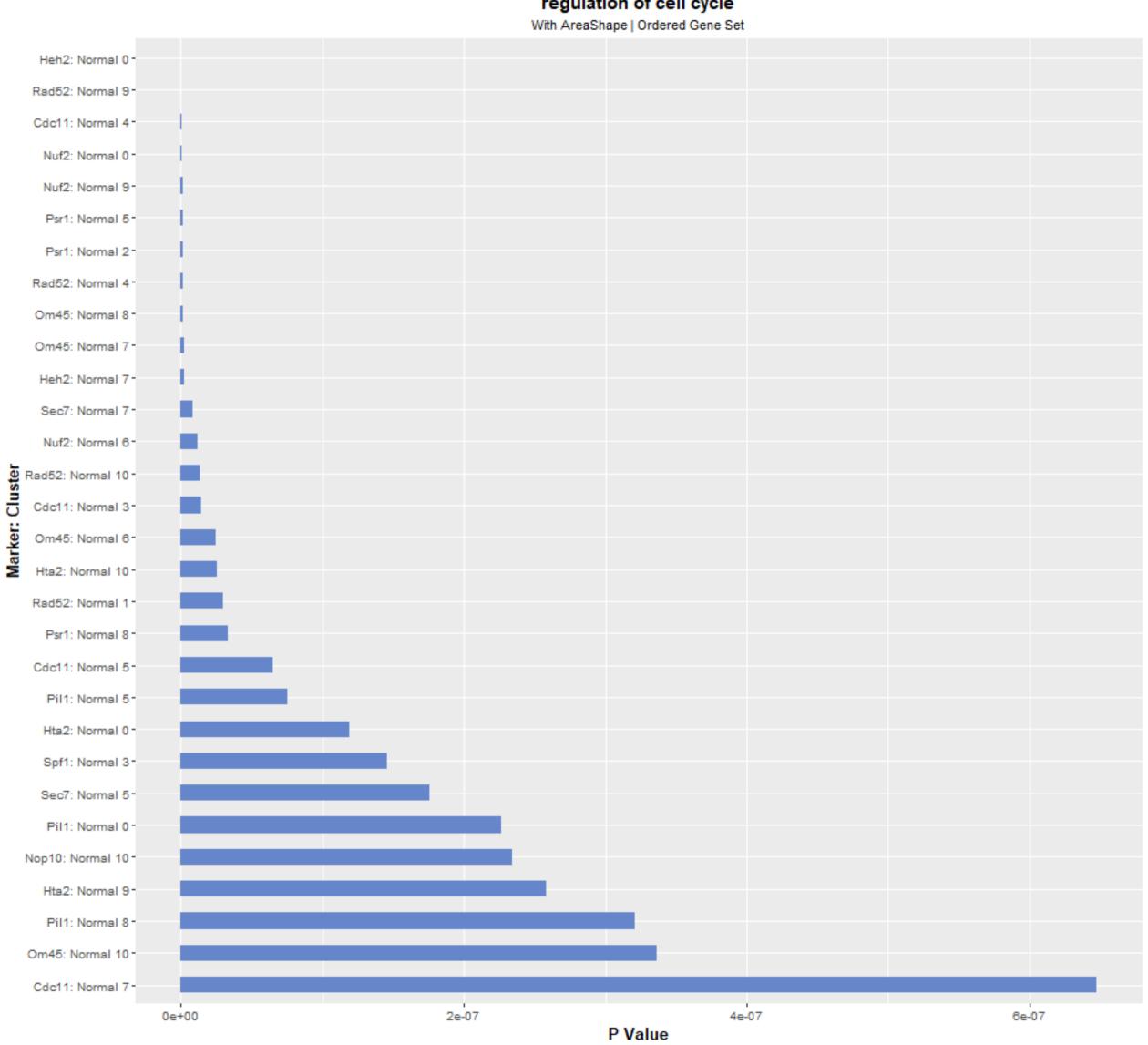
proteolysis involved in cellular protein catabolic process



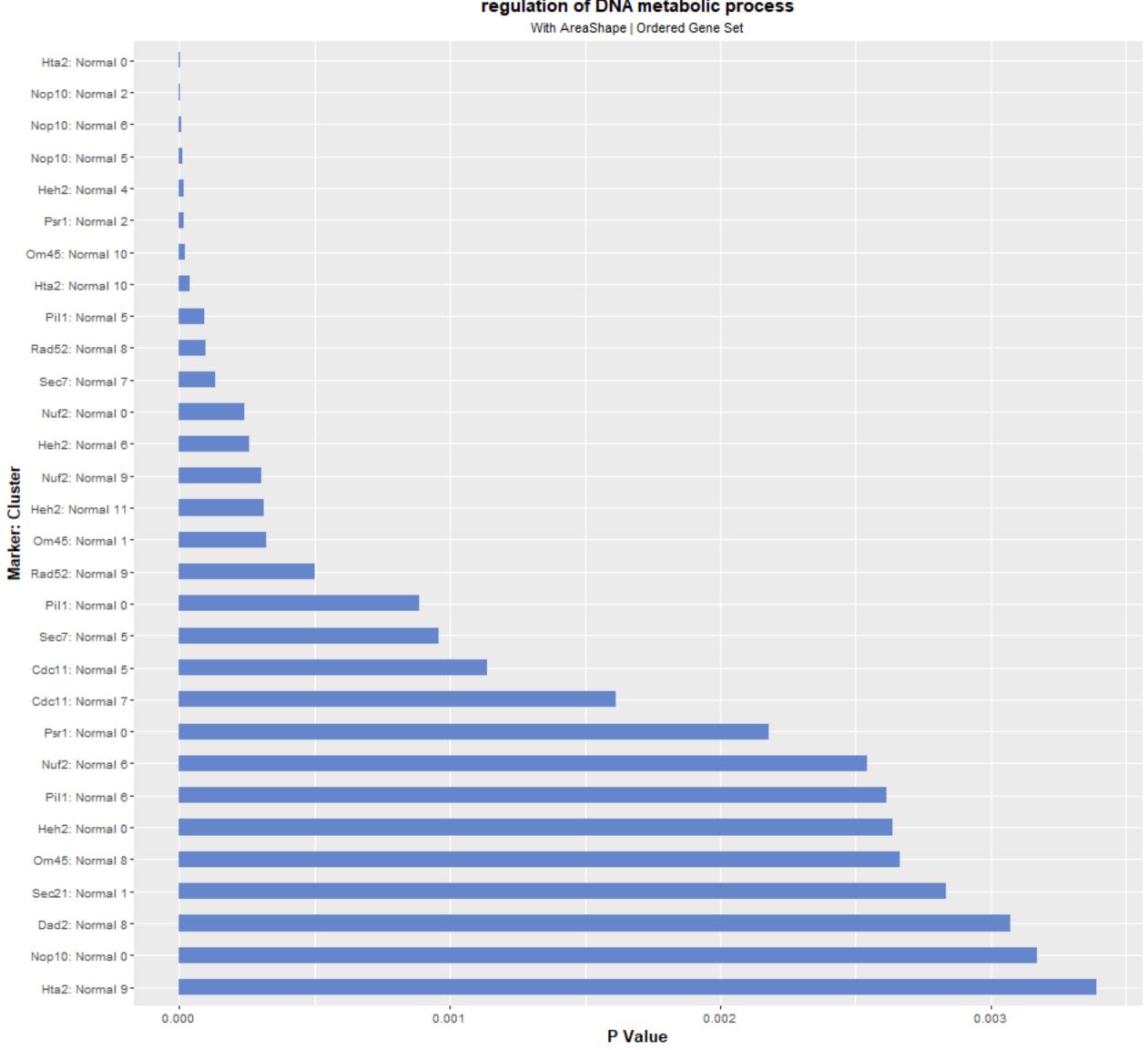
pseudohyphal growth



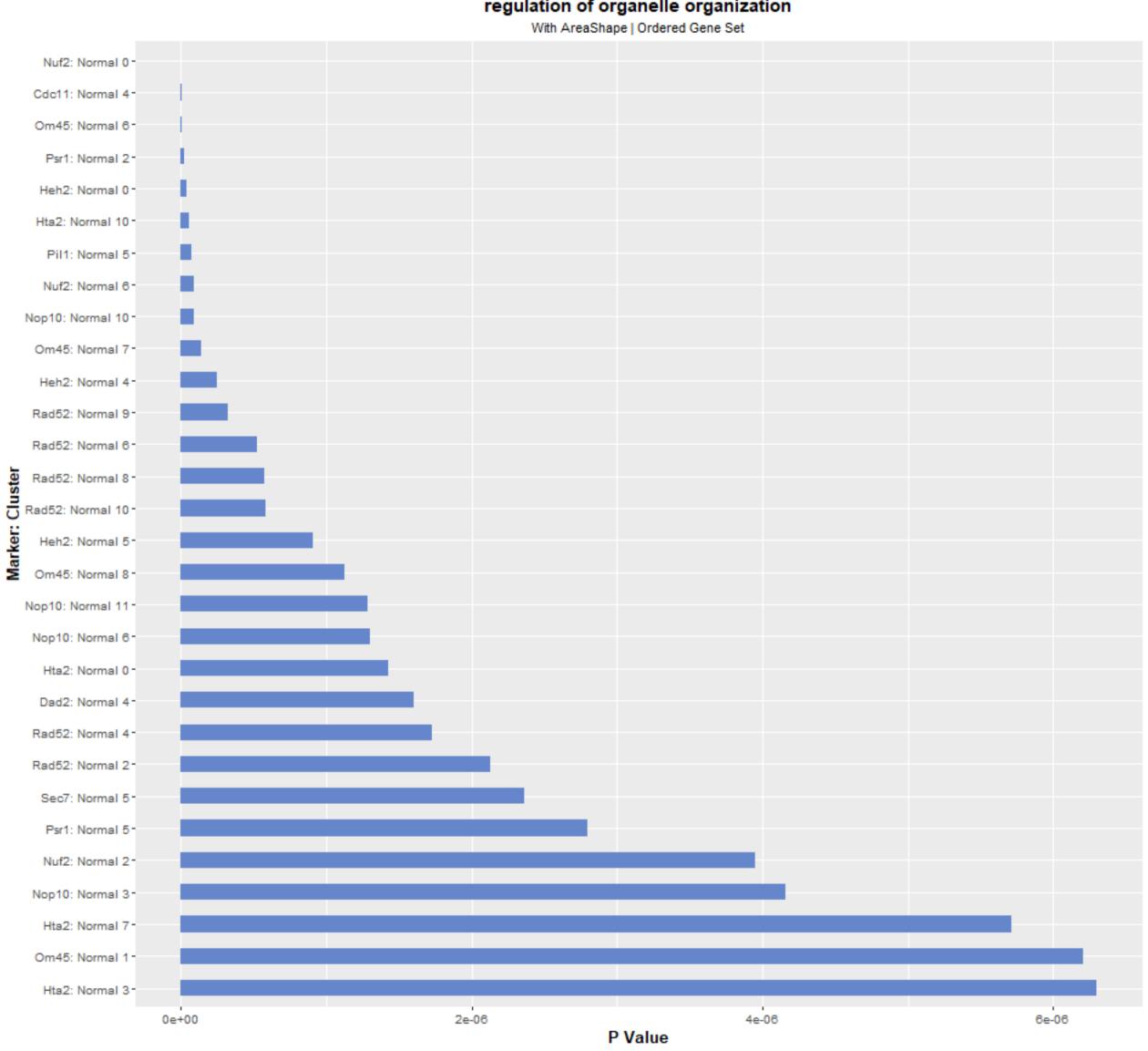
regulation of cell cycle



regulation of DNA metabolic process



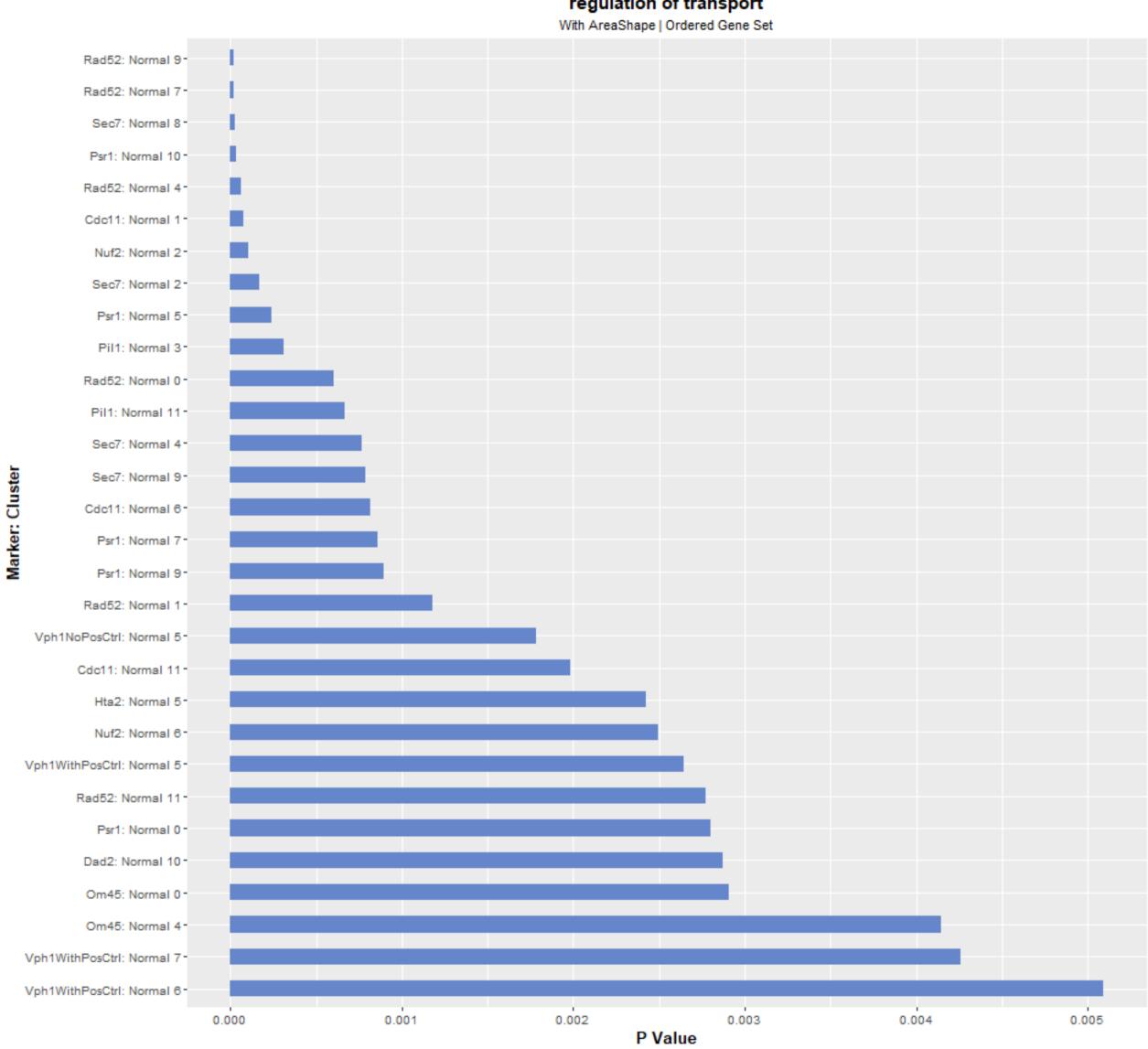
regulation of organelle organization



regulation of protein modification process With AreaShape | Ordered Gene Set Nuf2: Normal 0 -Rad52: Normal 9 -Rad52: Normal 4-Sec7: Normal 7 -Sec21: Normal 51 Pil1: Normal 0 -Nuf2: Normal 6 -Nop10: Normal 5-Psr1: Normal 2 -Nuf2: Normal 9 -Om45: Normal 10 -Cdc11: Normal 10 -Cdc11: Normal 5 Marker: Cluster Rad52: Normal 1 -Hta2: Normal 0 -Rad52: Normal 8 -Psr1: Normal 8 -Hta2: Normal 11 -Sec7: Normal 51 Pil1: Normal 8 -Nuf2: Normal 10 -Sec7: Normal 10 -Nop10: Normal 2-Sec7: Normal 9 -Pil1: Normal 21 Vph1NoPosCtrl: Normal 5 -Psr1: Normal 5 -Vph1WithPosCtrl: Normal 5 -Dad2: Normal 8 -Spf1: Normal 31 0.00050 0.00000 0.00025 0.00075 0.00100 P Value

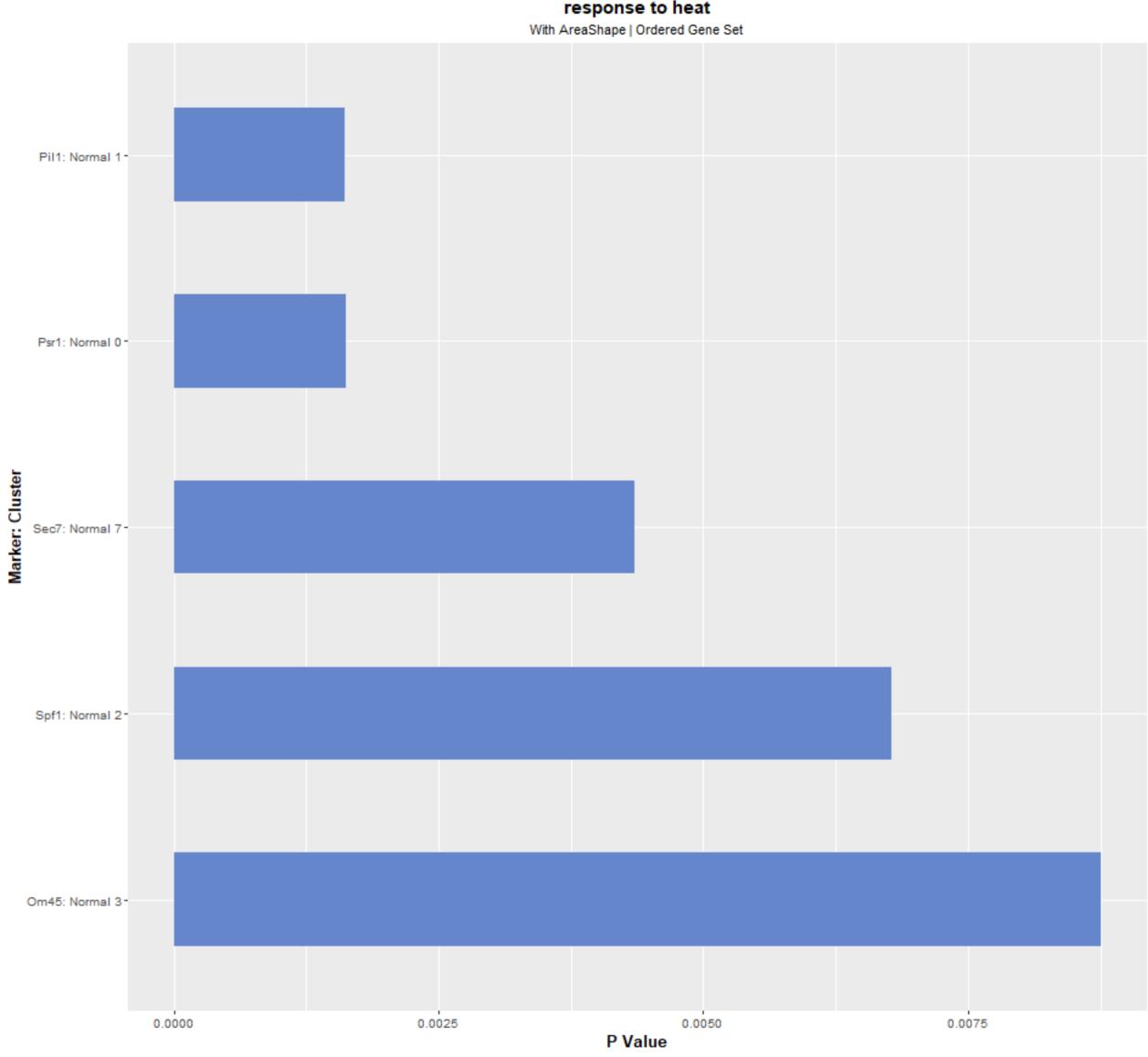
regulation of translation With AreaShape | Ordered Gene Set Heh2: Normal 7 Marker: Cluster Rad52: Normal 1-0.0050 0.0000 0.0025 0.0075 P Value

regulation of transport



response to chemical With AreaShape | Ordered Gene Set Marker: Cluster 0.002 0.004 0.001 0.000 0.003 P Value

response to heat

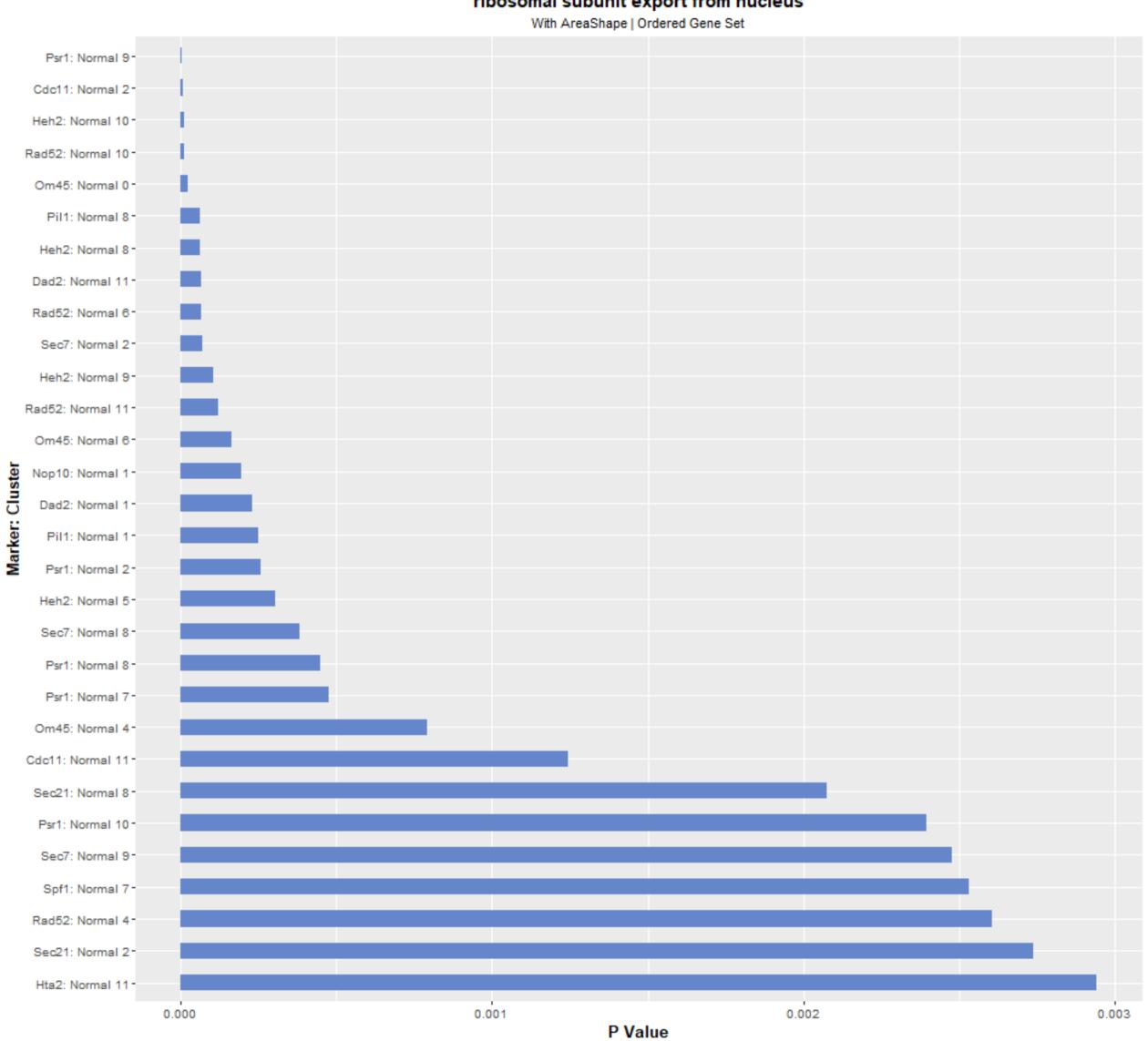


response to osmotic stress With AreaShape | Ordered Gene Set Heh2: Normal 0 -Marker: Cluster Nop10: Normal 0 -0.004 0.002 0.006 0.000 0.00 P Value

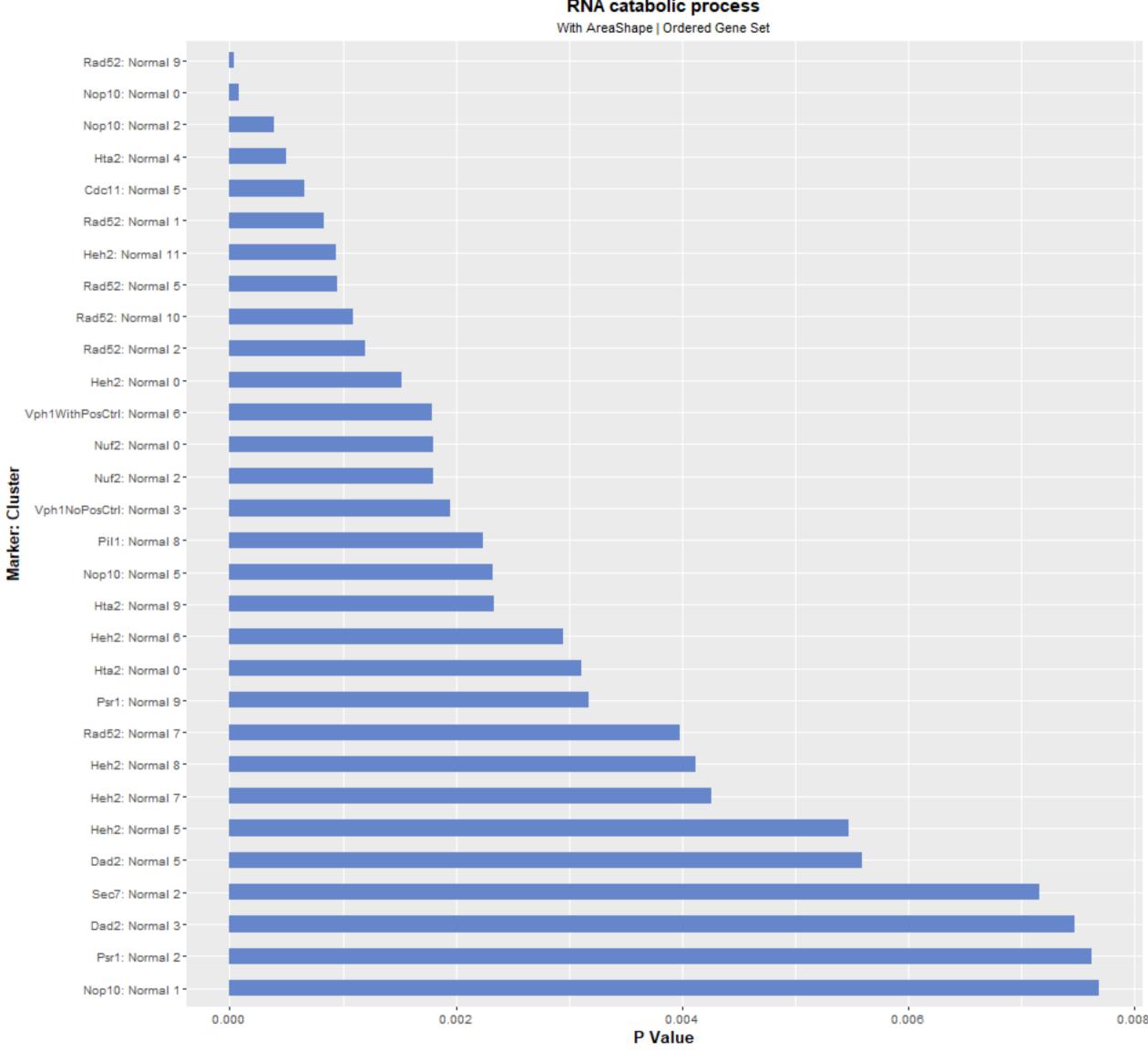
ribosomal large subunit biogenesis With AreaShape | Ordered Gene Set Sec7: Normal 21 Psr1: Normal 10 -Psr1: Normal 8 -Marker: Cluster Heh2: Normal 91 Psr1: Normal 9 -Pil1: Normal 10 -0.002 0.003 0.004 0.000 0.001 P Value

ribosomal small subunit biogenesis With AreaShape | Ordered Gene Set Marker: Cluster 0.002 0.000 0.001 0.003 0.004 P Value

ribosomal subunit export from nucleus



RNA catabolic process



RNA modification With AreaShape | Ordered Gene Set Sec21: Normal 6-Psr1: Normal 10 -Marker: Cluster Rad52: Normal 9 -Rad52: Normal 1-

0.004

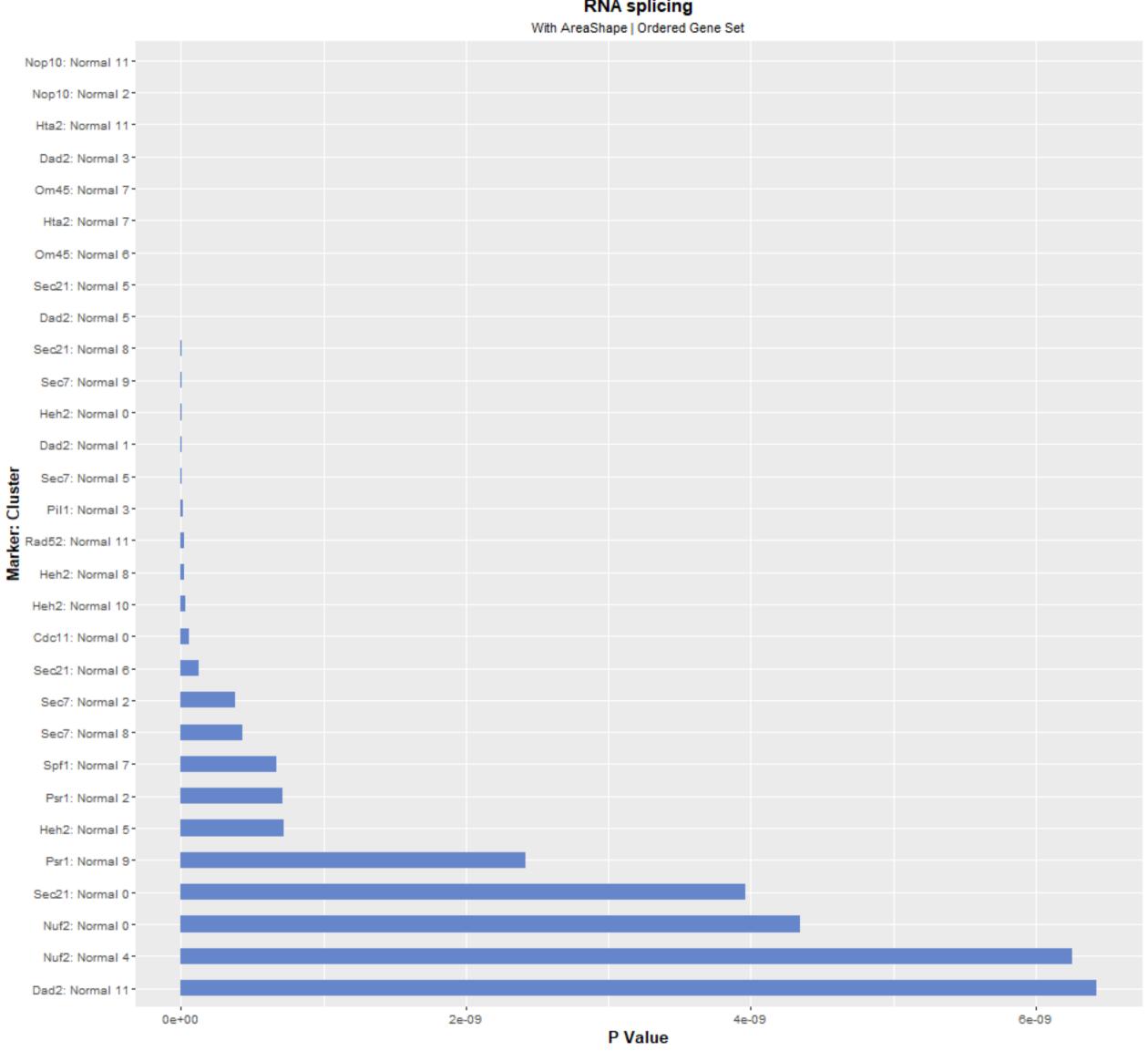
P Value

0.006

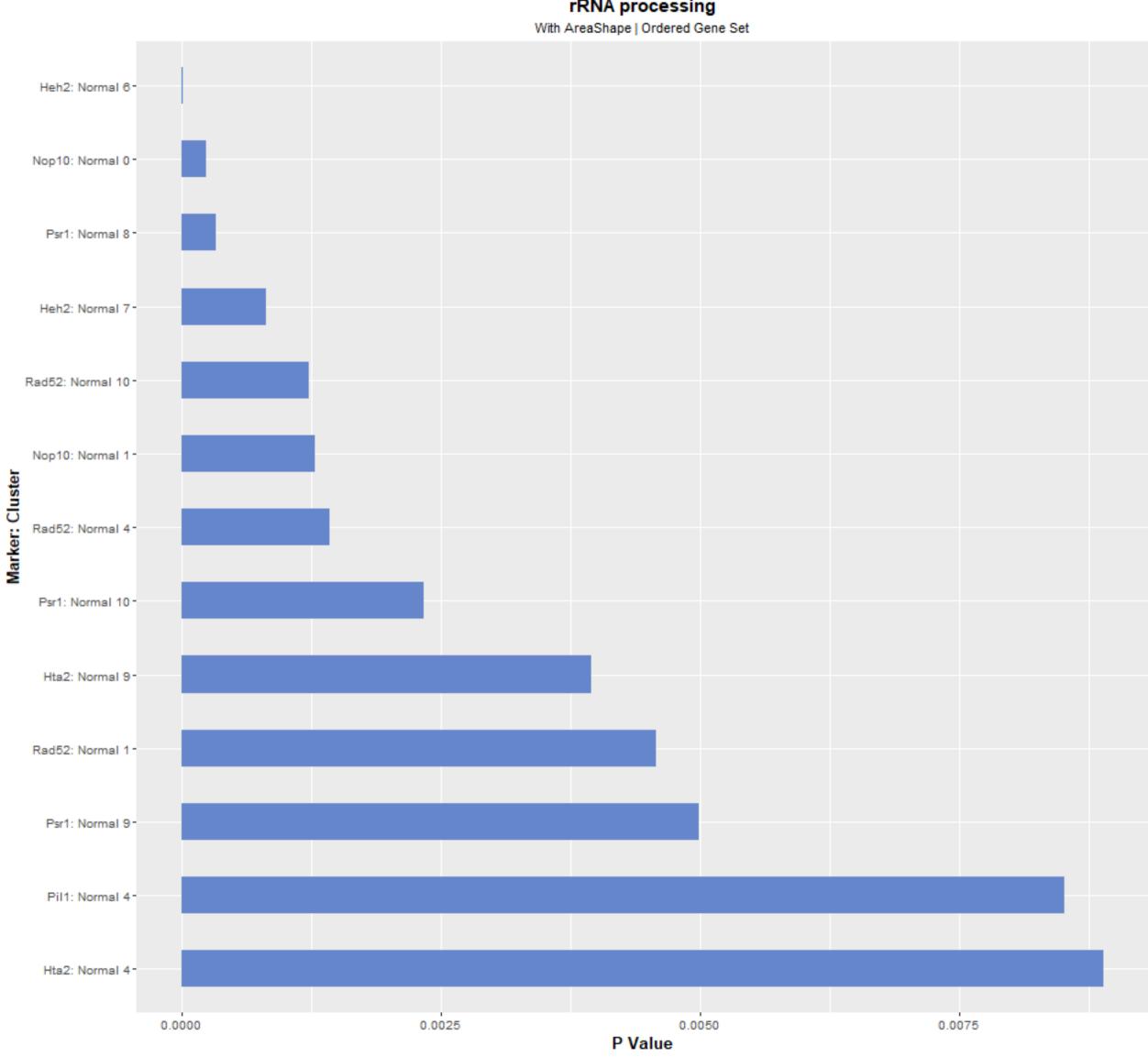
0.000

0.002

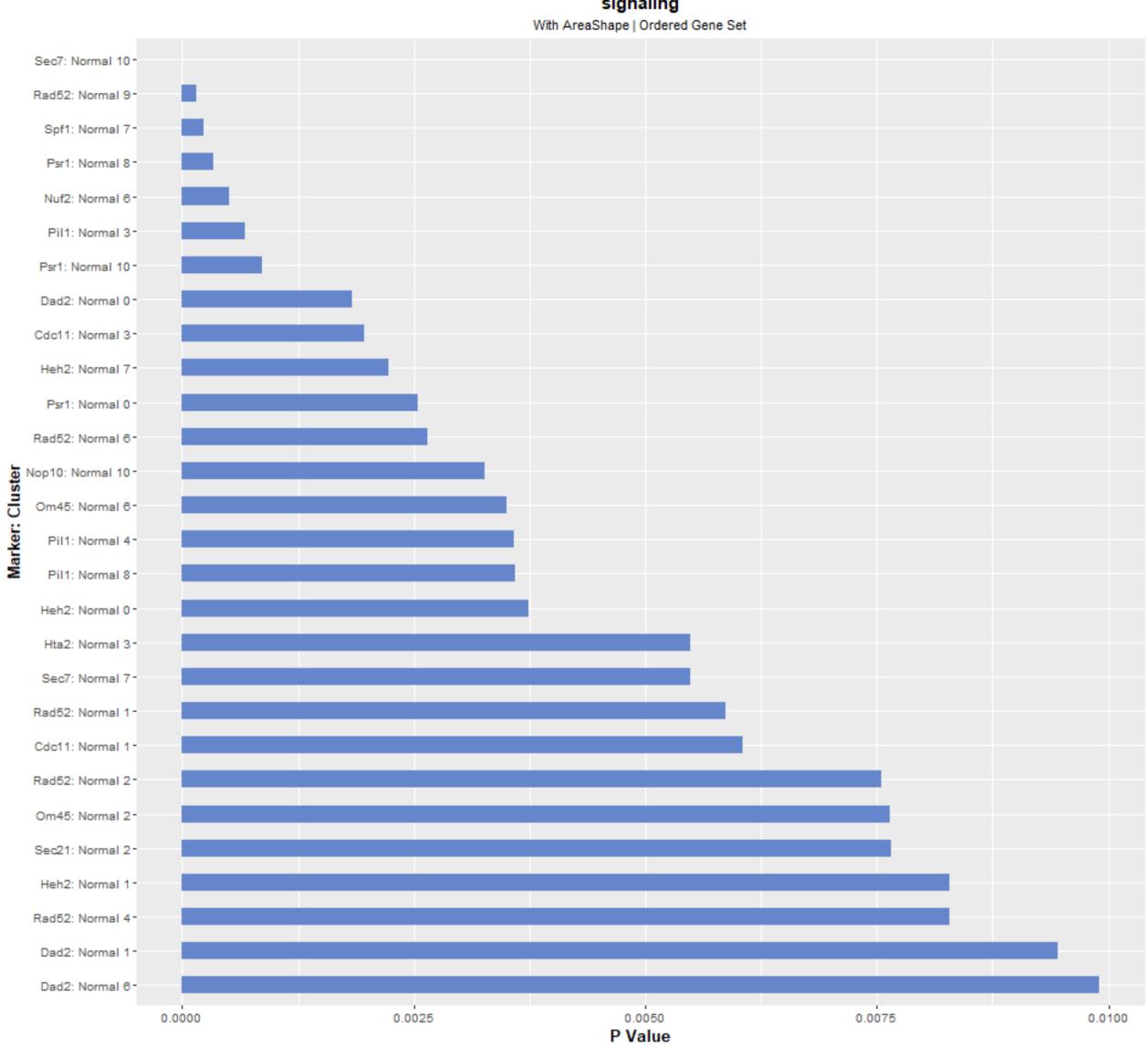
RNA splicing



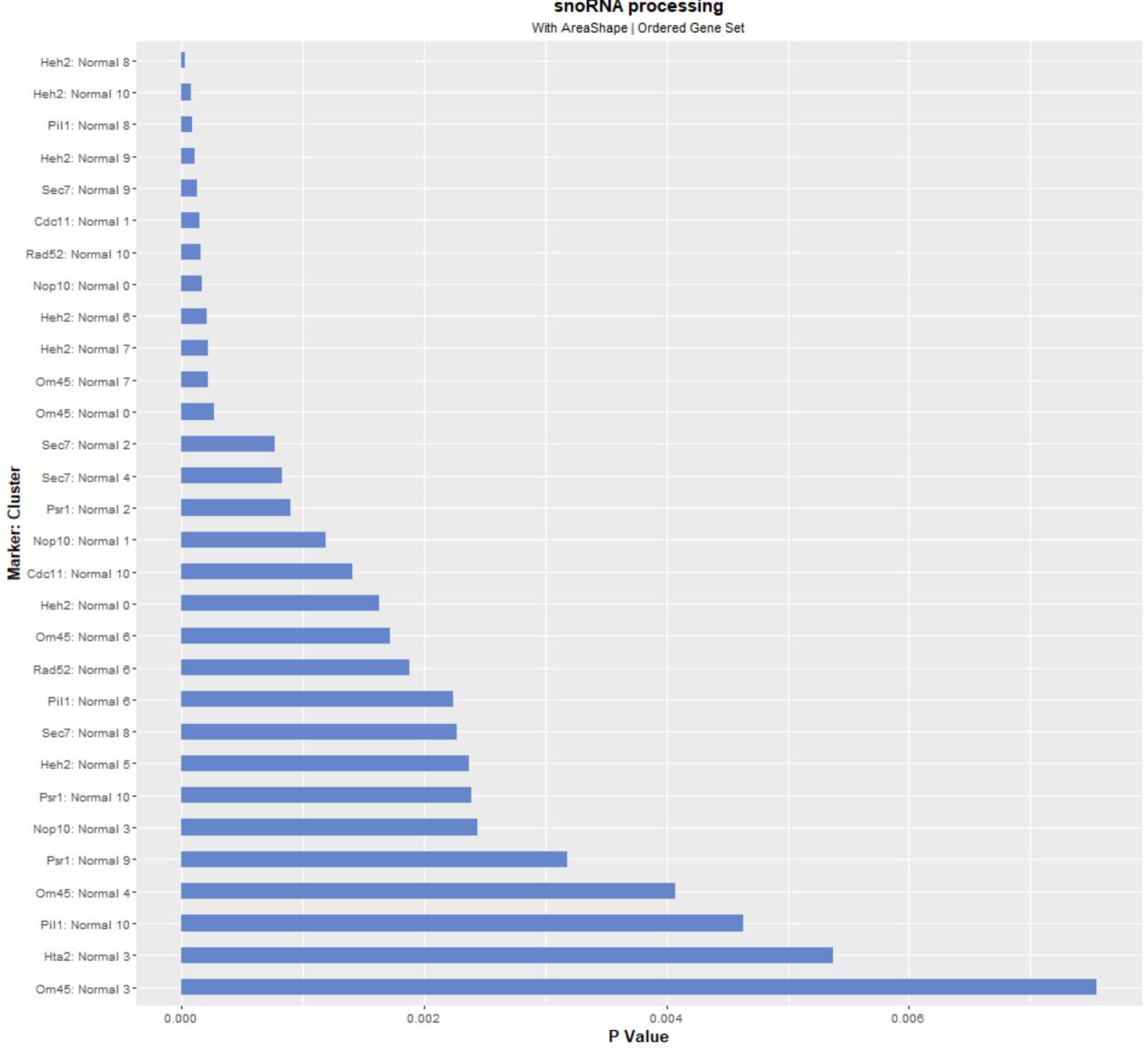
rRNA processing



signaling

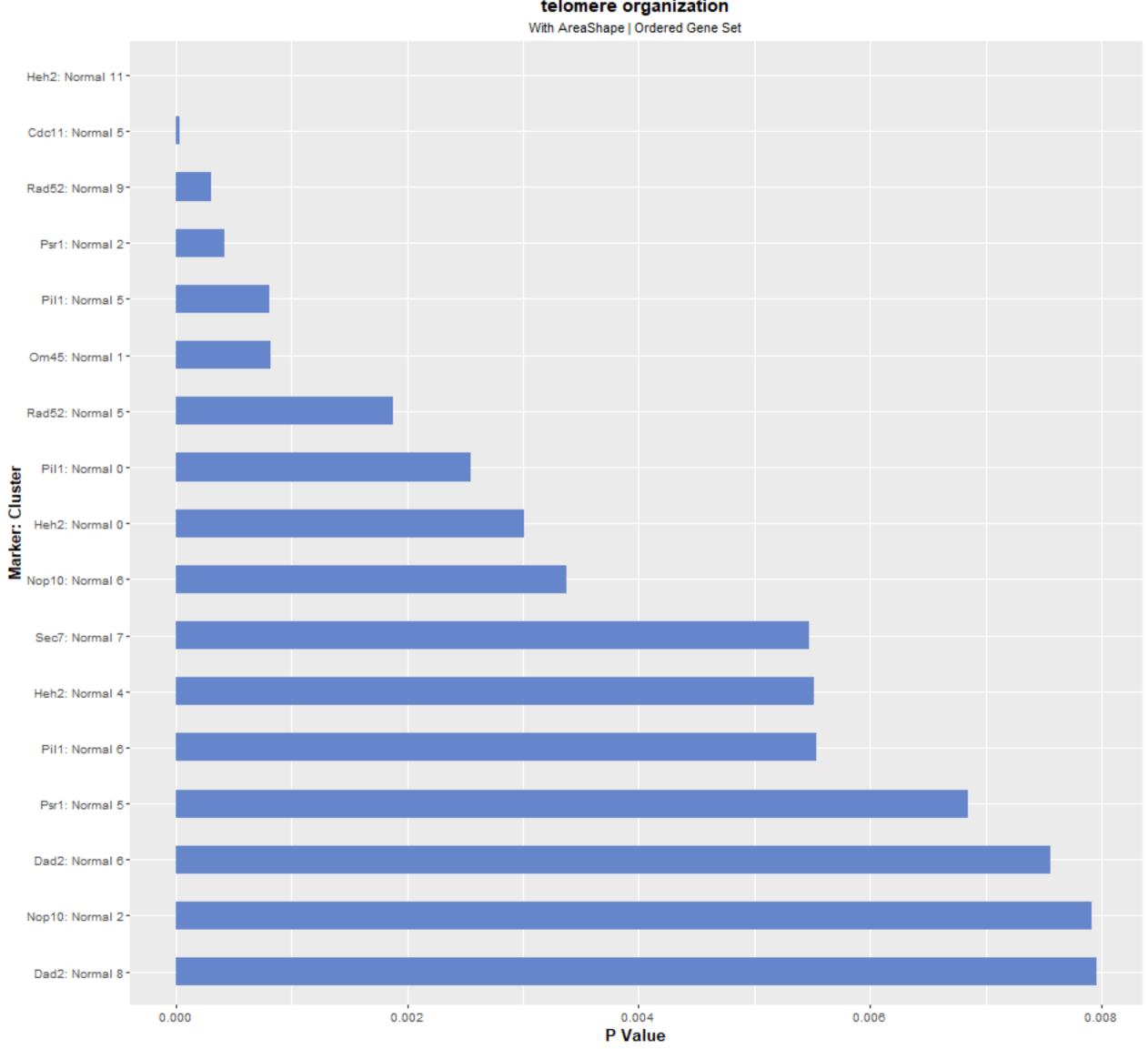


snoRNA processing



sporulation With AreaShape | Ordered Gene Set Rad52: Normal 5 Marker: Cluster Psr1: Normal 9 -Pil1: Normal 11-0.004 0.000 0.002 0.006 0.008 P Value

telomere organization



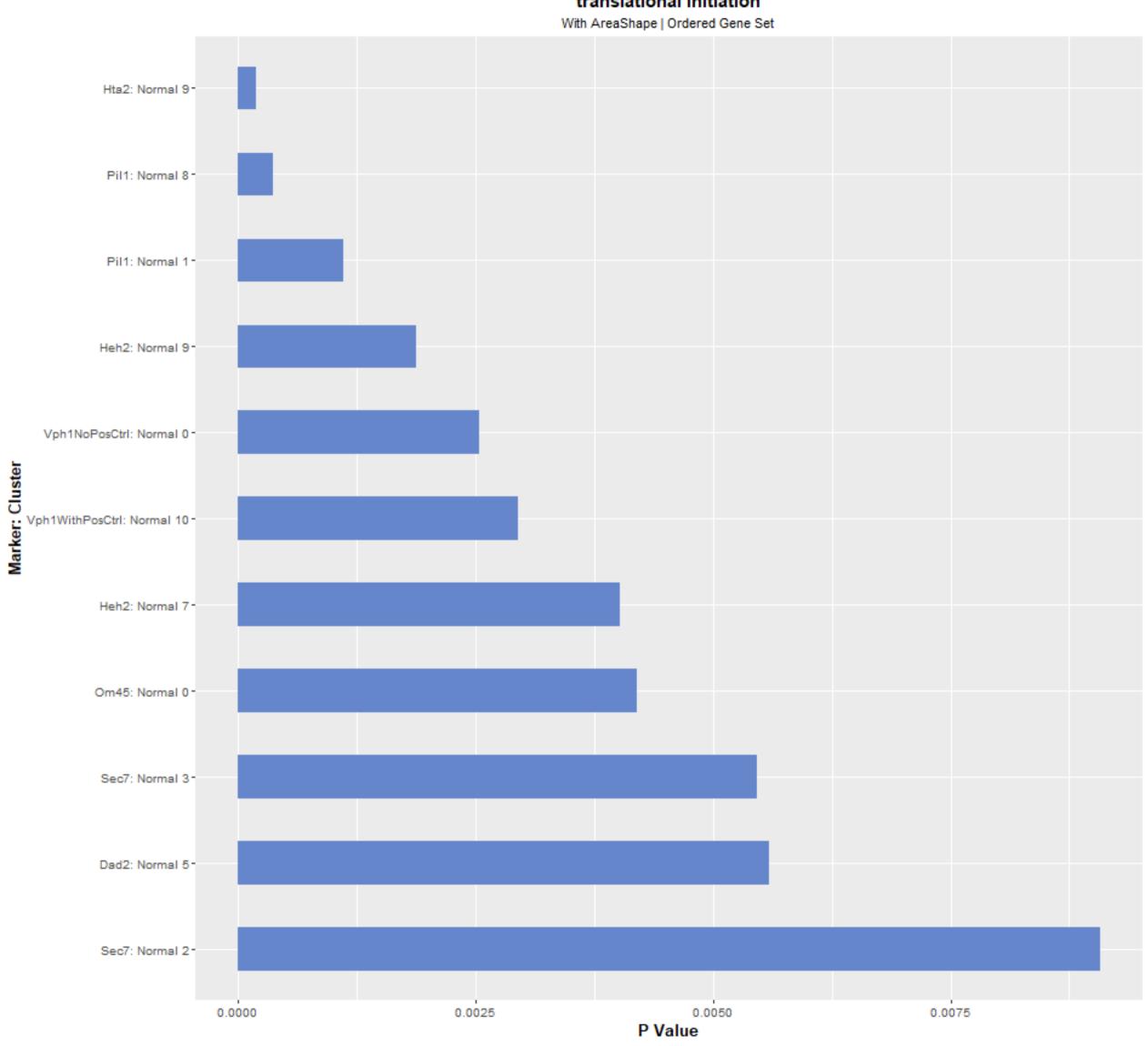
transcription from RNA polymerase I promoter With AreaShape | Ordered Gene Set Hta2: Normal 9 -Pil1: Normal 21 Pil1: Normal 1-Om45: Normal 3-Marker: Cluster Hta2: Normal 4-Nop10: Normal 1-Sec21: Normal 1-Dad2: Normal 1-Sec7: Normal 4-0.0050 0.0100 0.0000 0.0025 0.0075 P Value

transcription from RNA polymerase II promoter With AreaShape | Ordered Gene Set Om45: Normal 0 Sec21: Normal 8 -Rad52: Normal 6 -Nop10: Normal 1-Sec7: Normal 8 -Heh2: Normal 10 -Nuf2: Normal 2 -Psr1: Normal 9 Heh2: Normal 7 -Nop10: Normal 21 Sec7: Normal 91 Dad2: Normal 10 -Nuf2: Normal 6-Marker: Cluster Dad2: Normal 1 -Heh2: Normal 8 -Pil1: Normal 8 -Nuf2: Normal 0 -Rad52: Normal 10 -Psr1: Normal 10 -Rad52: Normal 0 -Sec7: Normal 21 Pil1: Normal 11 Psr1: Normal 8 -Sec21: Normal 21 Rad52: Normal 11 -Cdc11: Normal 21 Nuf2: Normal 4-Vph1NoPosCtrl: Normal 3 -Heh2: Normal 9 -Nop10: Normal 3-2e-07 6e-07 4e-07 0e+00 8e-07 P Value

transcription from RNA polymerase III promoter With AreaShape | Ordered Gene Set Hta2: Normal 4-Hta2: Normal 9 -Heh2: Normal 7 -Marker: Cluster Nop10: Normal 1-Heh2: Normal 6-Heh2: Normal 9 -0.002 0.004 0.000 P Value

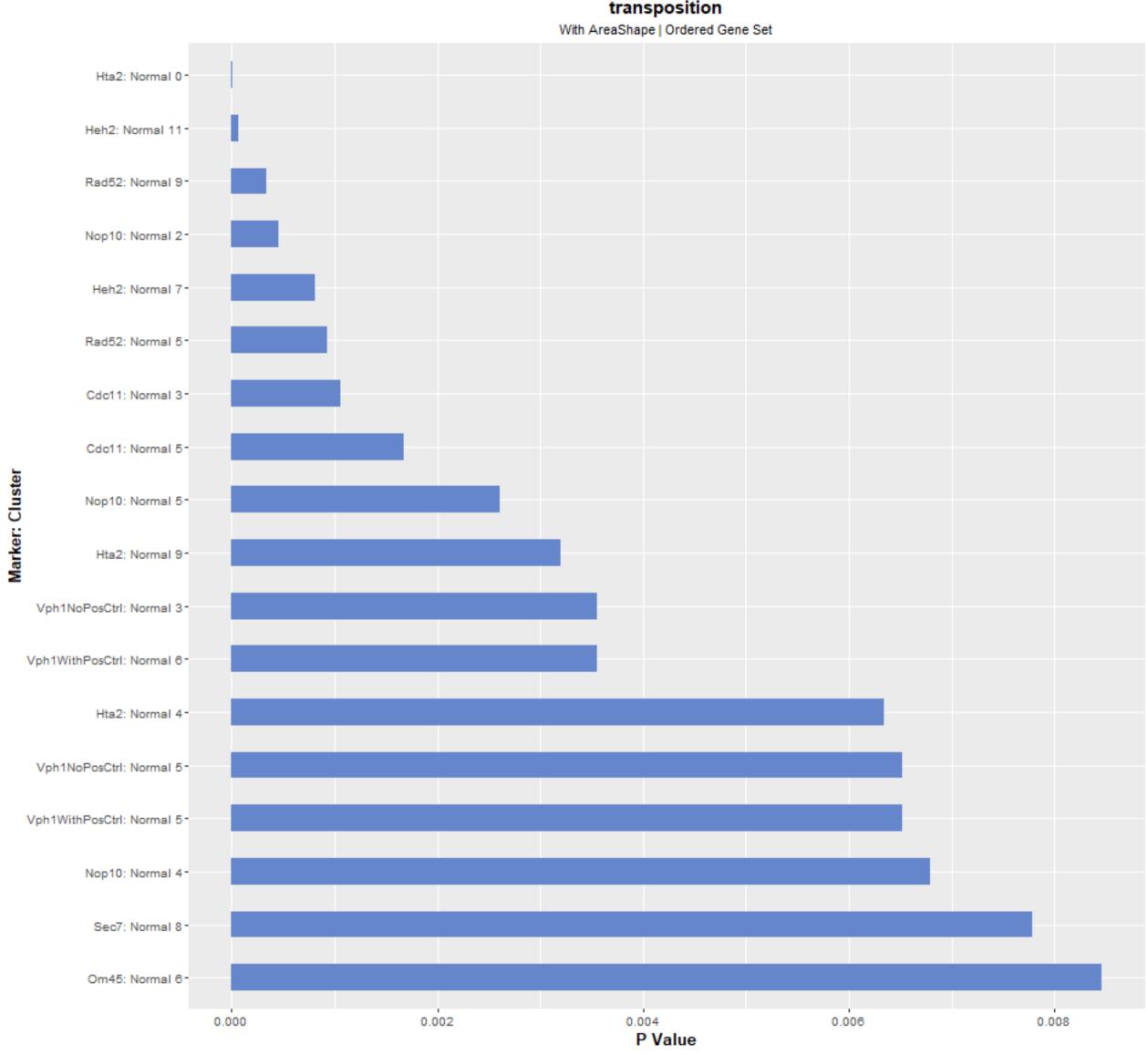
translational elongation With AreaShape | Ordered Gene Set Pil1: Normal 4-Dad2: Normal 6 -Marker: Cluster Pil1: Normal 1-Cdc11: Normal 1-0.0000 0.0025 0.0050 0.0075 P Value

translational initiation



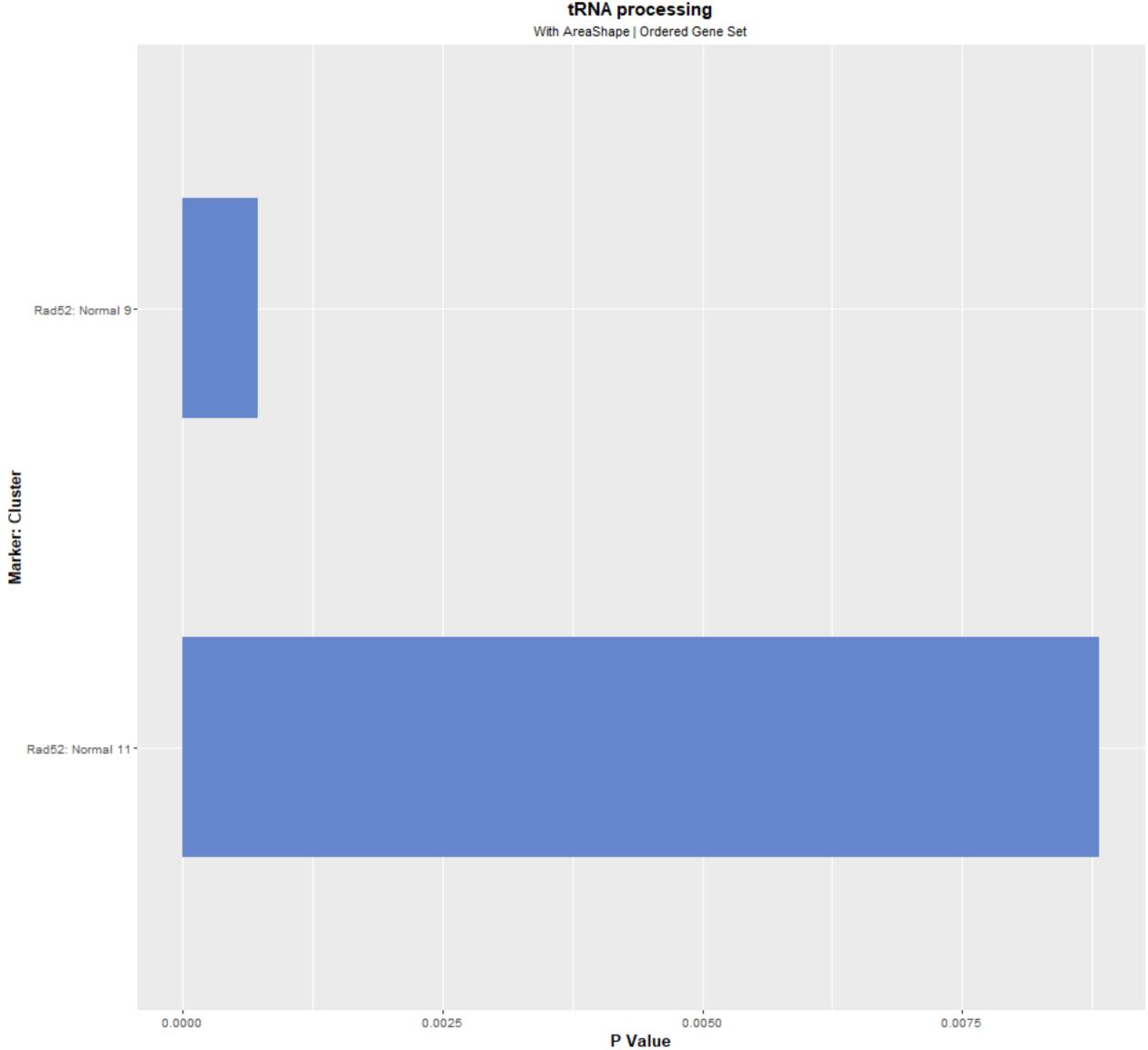
transmembrane transport With AreaShape | Ordered Gene Set Marker: Cluster: Heh2: Normal 9 -0.002 0.001 0.003 0.000 P Value

transposition



tRNA aminoacylation for protein translation With AreaShape | Ordered Gene Set Pil1: Normal 8 -Heh2: Normal 9 -Marker: Cluster: 0 Stemo (24 mol (24 m Heh2: Normal 8 -Om45: Normal 9 -0.002 0.001 0.003 0.000 P Value

tRNA processing



vacuole organization With AreaShape | Ordered Gene Set Psr1: Normal 9 -Sec21: Normal 8 -Nuf2: Normal 2 -Pil1: Normal 11 -Pil1: Normal 3-Cdc11: Normal 11-Rad52: Normal 2 -Sec7: Normal 8 -Dad2: Normal 10 -Psr1: Normal 7 -Vph1NoPosCtrl: Normal 3 -Heh2: Normal 5 Hta2: Normal 5 Marker: Cluster Spf1: Normal 7 -Nop10: Normal 0 -Vph1WithPosCtrl: Normal 6 -Heh2: Normal 8 -Psr1: Normal 0 -Cdc11: Normal 2-Om45: Normal 7 -Nop10: Normal 11 -Hta2: Normal 7 -Sec21: Normal 21 Vph1NoPosCtrl: Normal 4-Vph1WithPosCtrl: Normal 0 -Om45: Normal 0 -Om45: Normal 2-Sec7: Normal 4-Heh2: Normal 9-Vph1WithPosCtrl: Normal 7 0.000 0.001 0.002 0.003 0.004 0.005 P Value

vesicle organization

