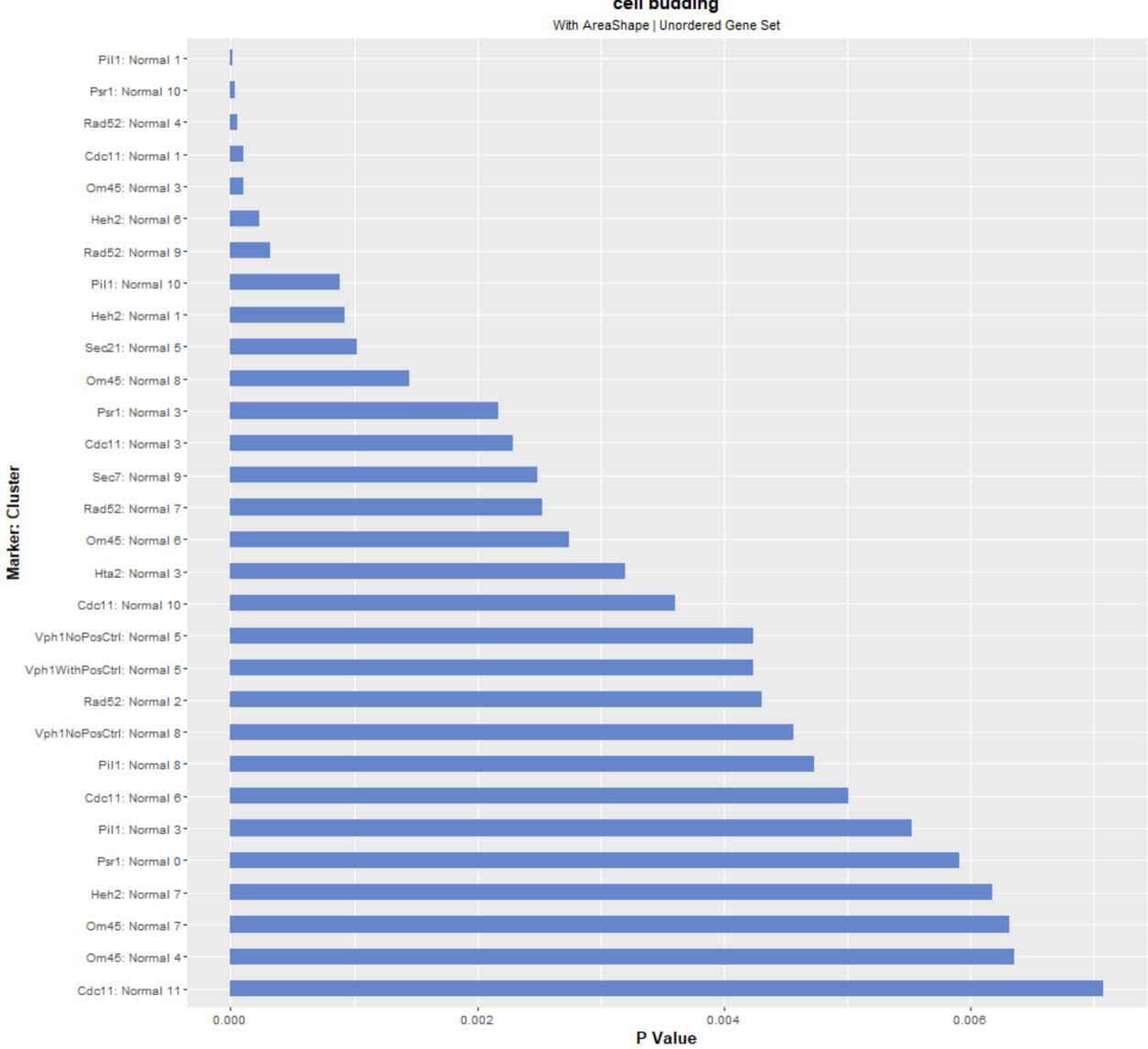
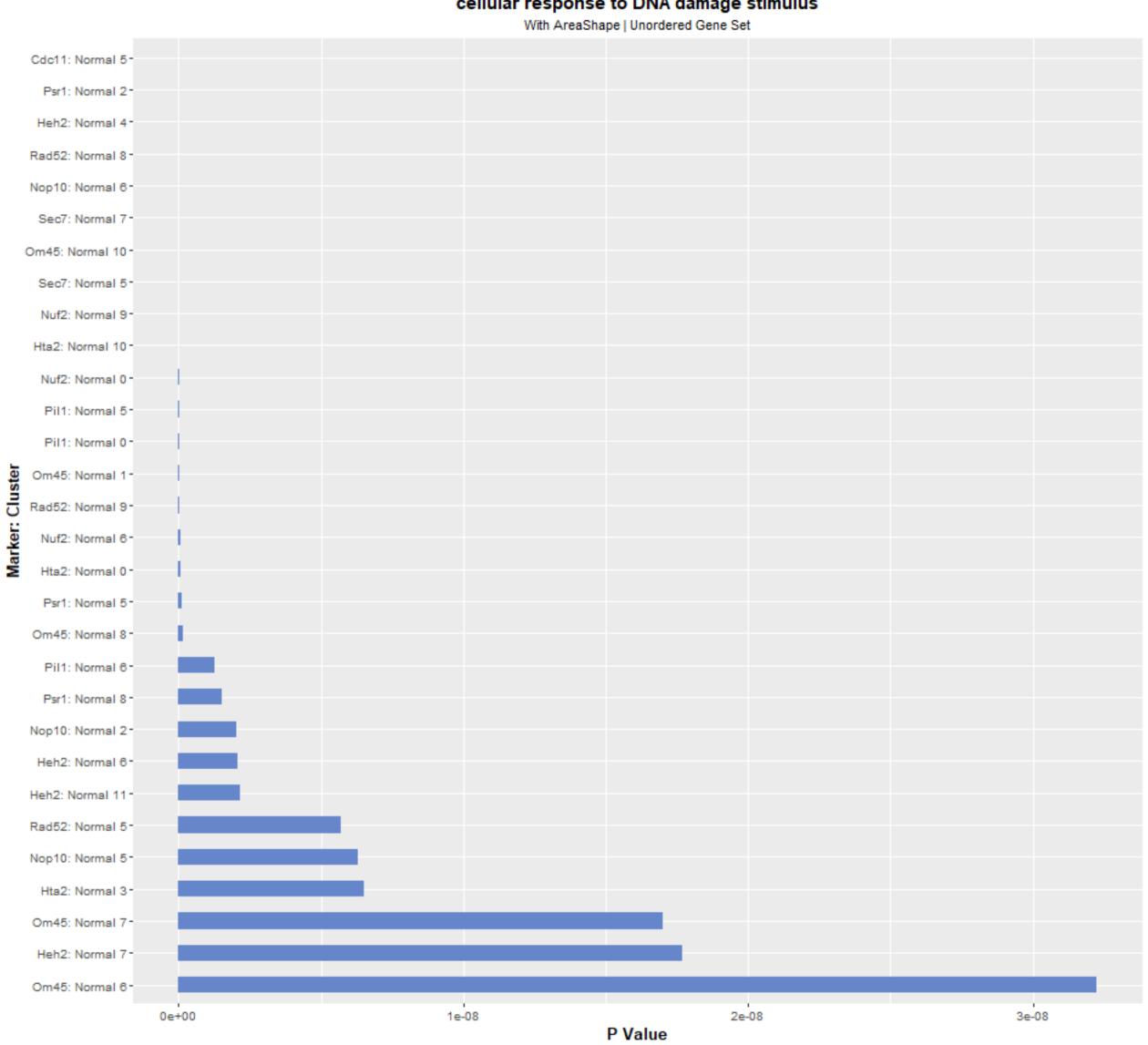
cell budding

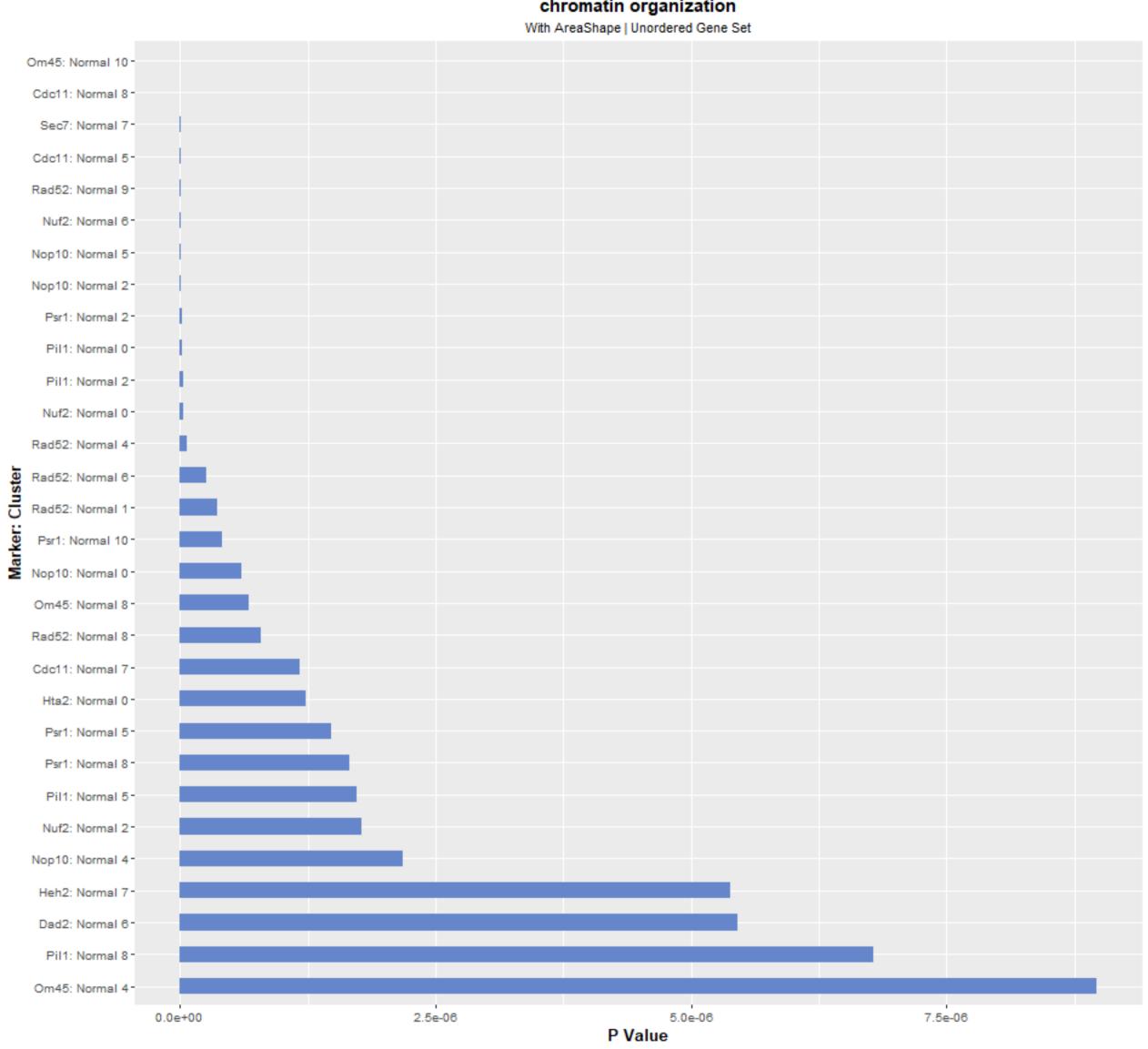


cell morphogenesis With AreaShape | Unordered Gene Set Marker: Cluster: 0 c c la como de como 0.000050 0.000 0.000000 0.000025 0.000075 0.000100 P Value

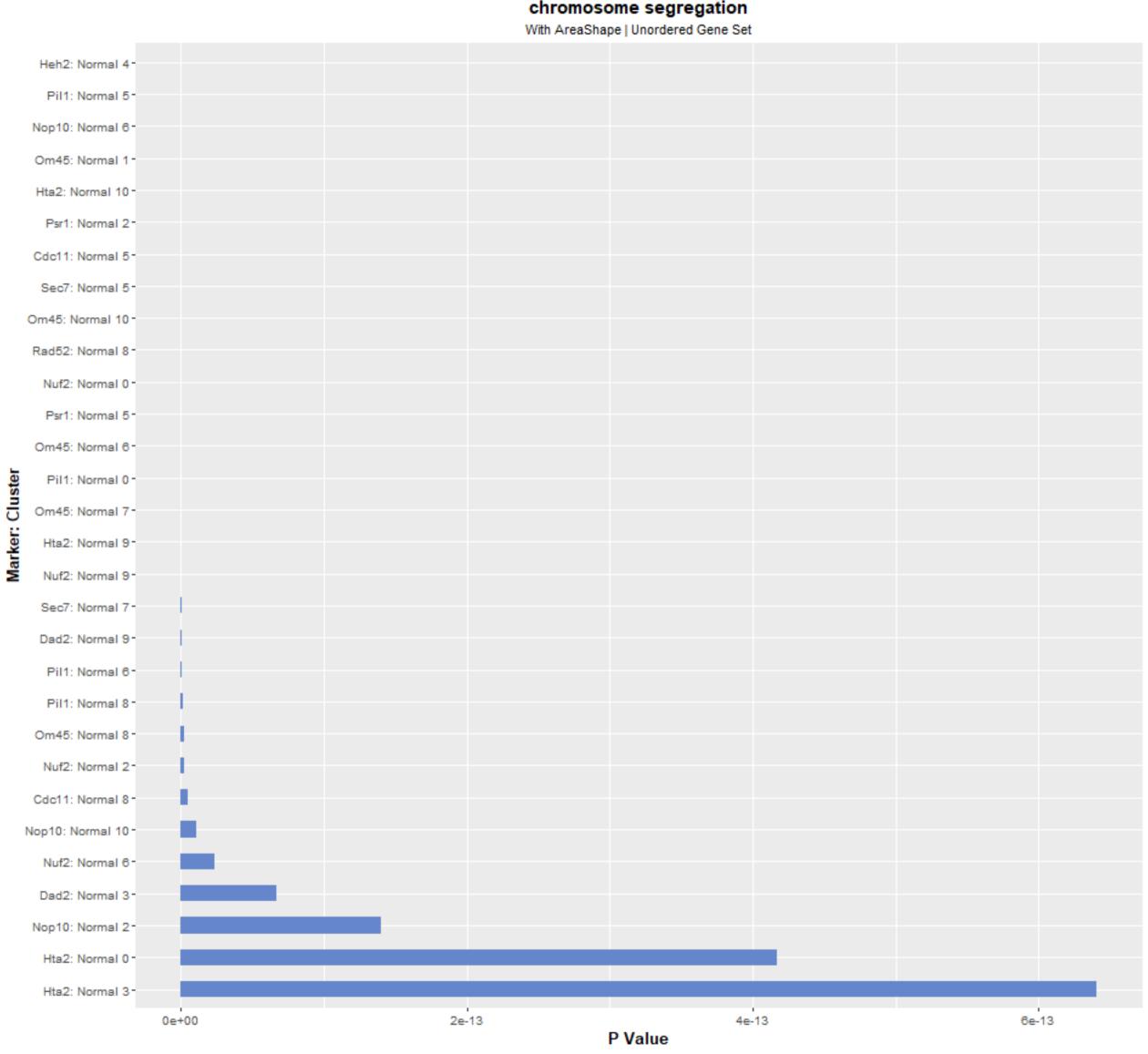
cellular response to DNA damage stimulus



chromatin organization



chromosome segregation

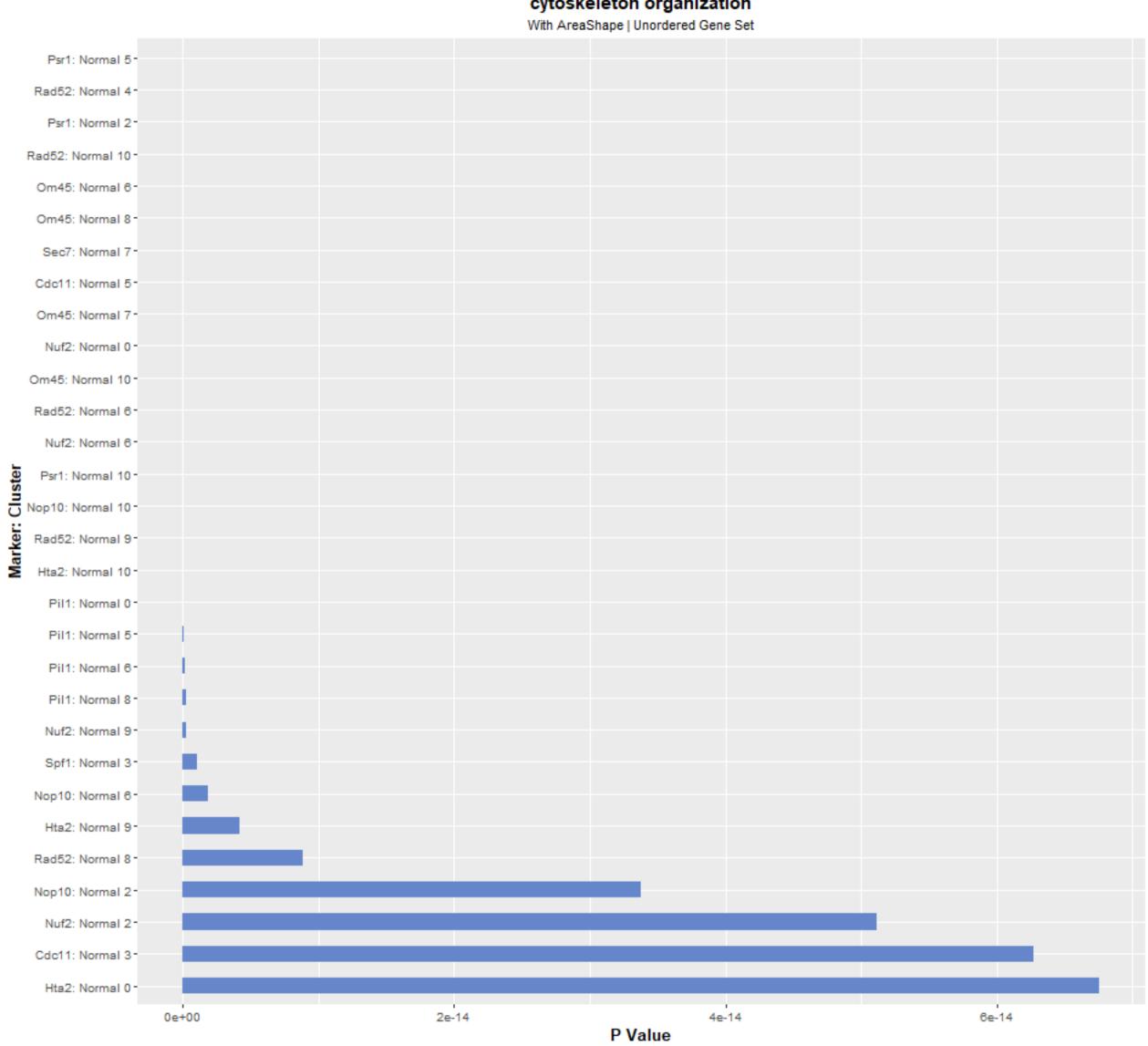


conjugation With AreaShape | Unordered Gene Set Marker: Cluster: Sec7: Normal 10 -0.00000 0.00005 0.00010 0.00015 0.00020 P Value

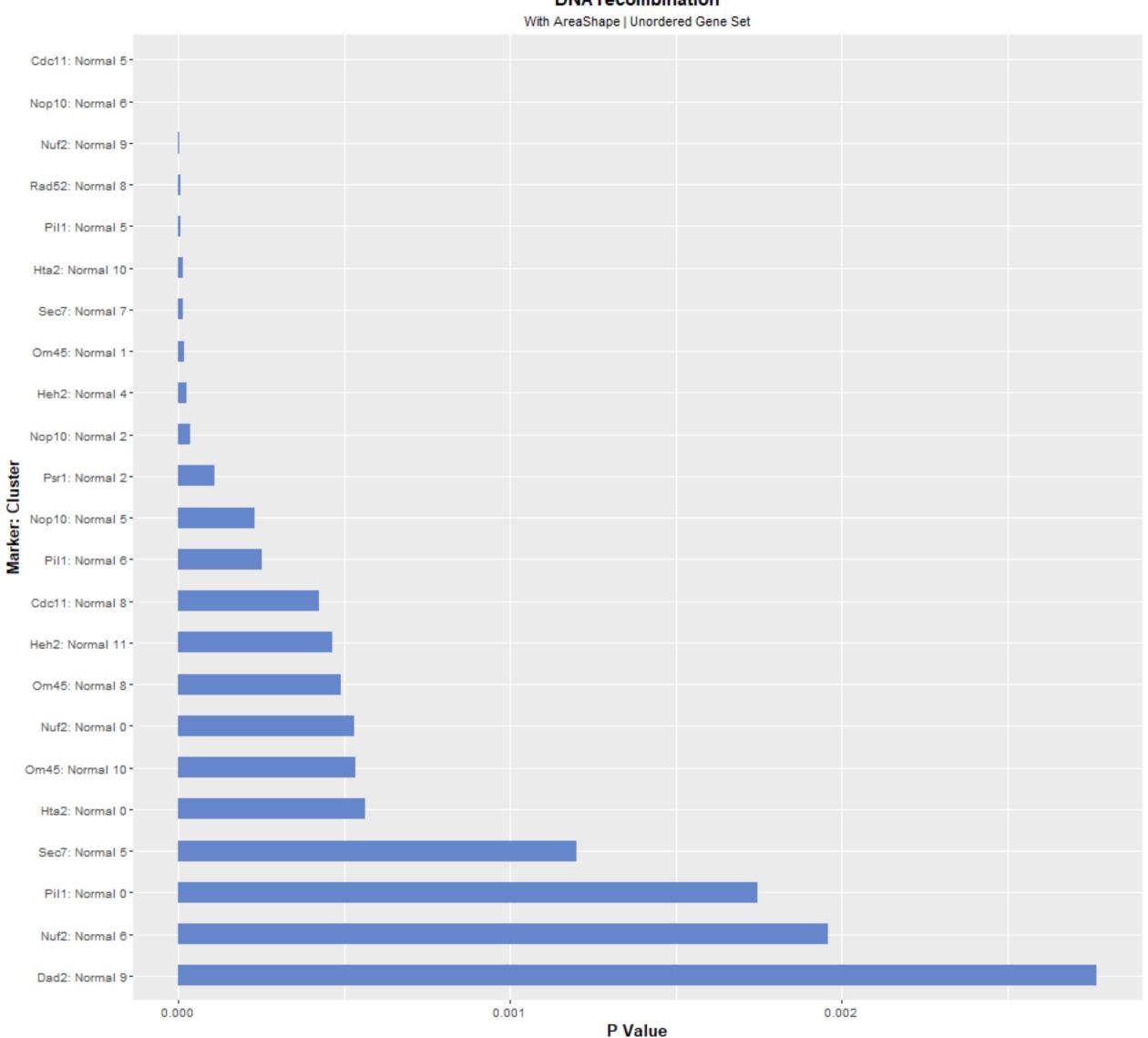
cytokinesis With AreaShape | Unordered Gene Set Cdc11: Normal 6 Om45: Normal 8 -Psr1: Normal 10 -Cdc11: Normal 10 -Cdc11: Normal 7 -Heh2: Normal 2 -Pil1: Normal 1-Cdc11: Normal 1-Om45: Normal 3-Nop10: Normal 9-Heh2: Normal 1-Sec7: Normal 10 -Om45: Normal 6-Marker: Cluster Rad52: Normal 4-Hta2: Normal 9 -Cdc11: Normal 31 Sec7: Normal 21 Rad52: Normal 6-Rad52: Normal 9 -Dad2: Normal 6-Rad52: Normal 7 -Nop10: Normal 3-Om45: Normal 7 -Sec7: Normal 7 -Pil1: Normal 8 -Psr1: Normal 5 -Dad2: Normal 4-Heh2: Normal 51 Nop10: Normal 0 -Psr1: Normal 0 -0.00000 0.00025 0.00050 0.00075 P Value

cytoplasmic translation With AreaShape | Unordered Gene Set Marker: Cluster 0.002 P Value 0.004 0.001 0.003 0.000

cytoskeleton organization

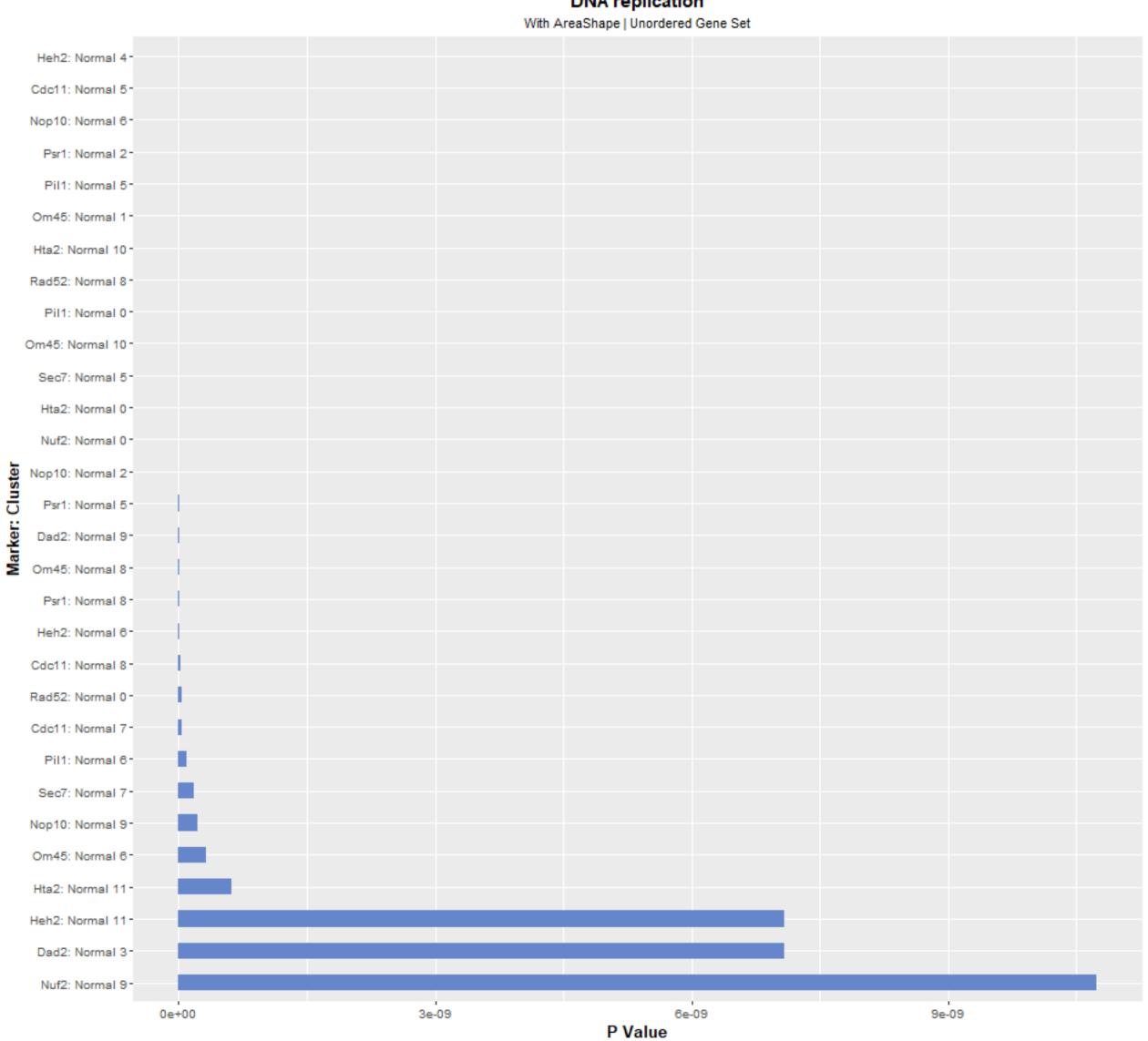


DNA recombination

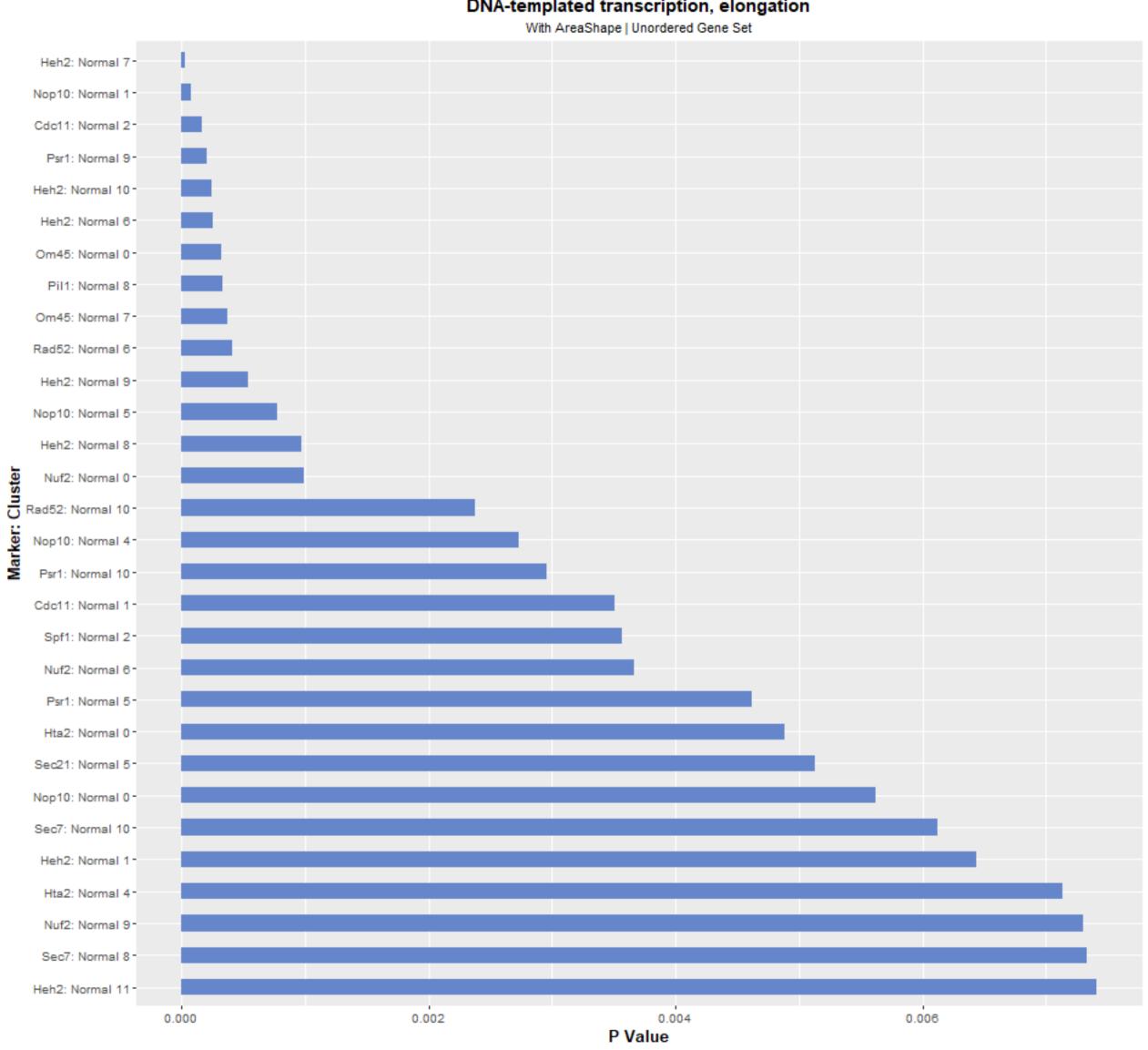


DNA repair With AreaShape | Unordered Gene Set Heh2: Normal 4 Psr1: Normal 2 -Cdc11: Normal 5 Rad52: Normal 8 -Nop10: Normal 6-Sec7: Normal 7 -Nuf2: Normal 9 -Om45: Normal 10 -Hta2: Normal 10 -Pil1: Normal 5-Sec7: Normal 5-Om45: Normal 1-Pil1: Normal 0 -Marker: Cluster Nuf2: Normal 0 -Om45: Normal 8 -Psr1: Normal 5 -Nuf2: Normal 6-Rad52: Normal 9 -Pil1: Normal 6-Nop10: Normal 2-Heh2: Normal 6-Hta2: Normal 0 -Psr1: Normal 8 -Om45: Normal 7 -Om45: Normal 6-Heh2: Normal 11-Nop10: Normal 5-Heh2: Normal 7 -Rad52: Normal 0 -Nop10: Normal 1-0e+00 2e-09 3e-09 4e-09 1e-09 P Value

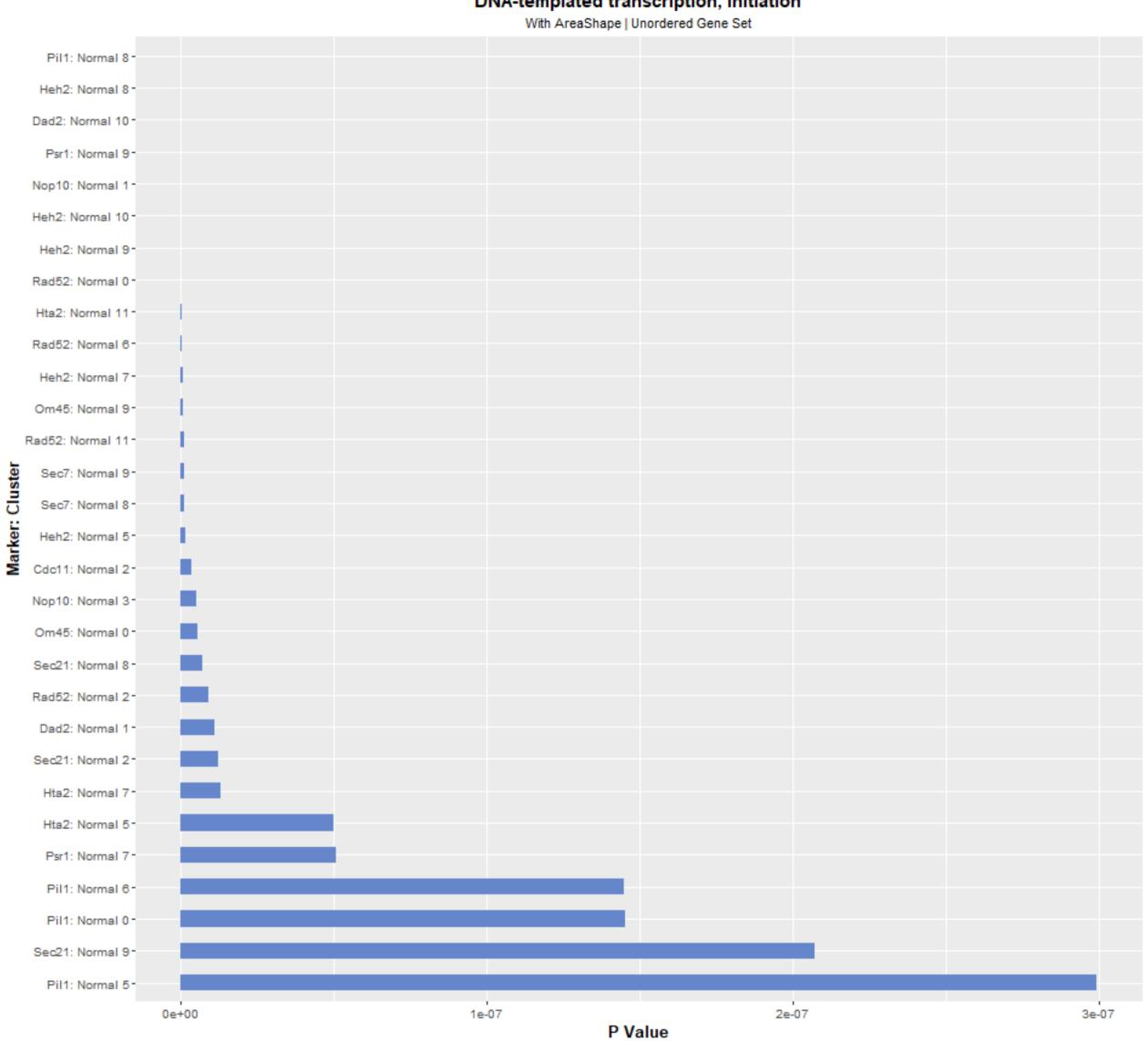
DNA replication



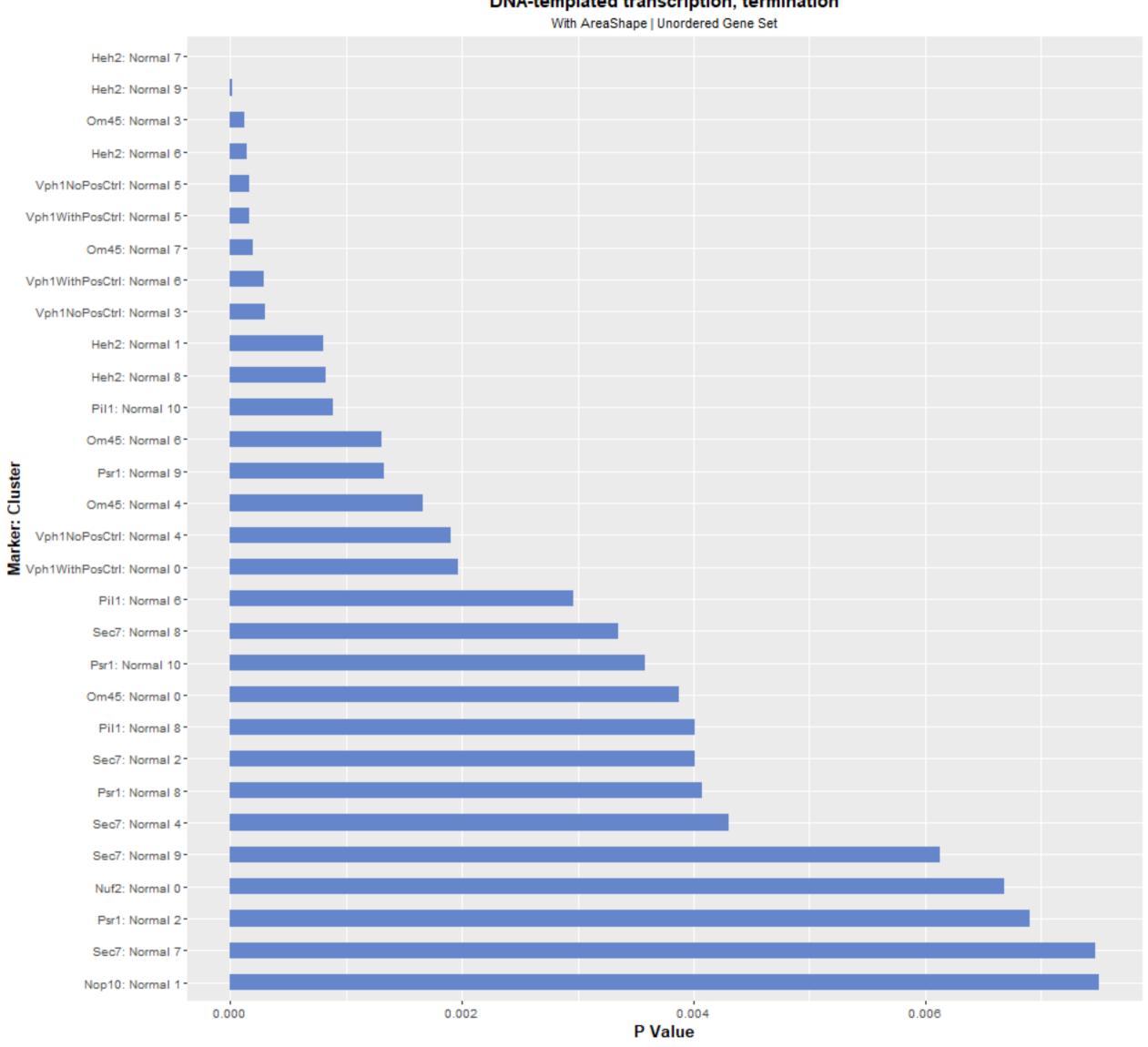
DNA-templated transcription, elongation



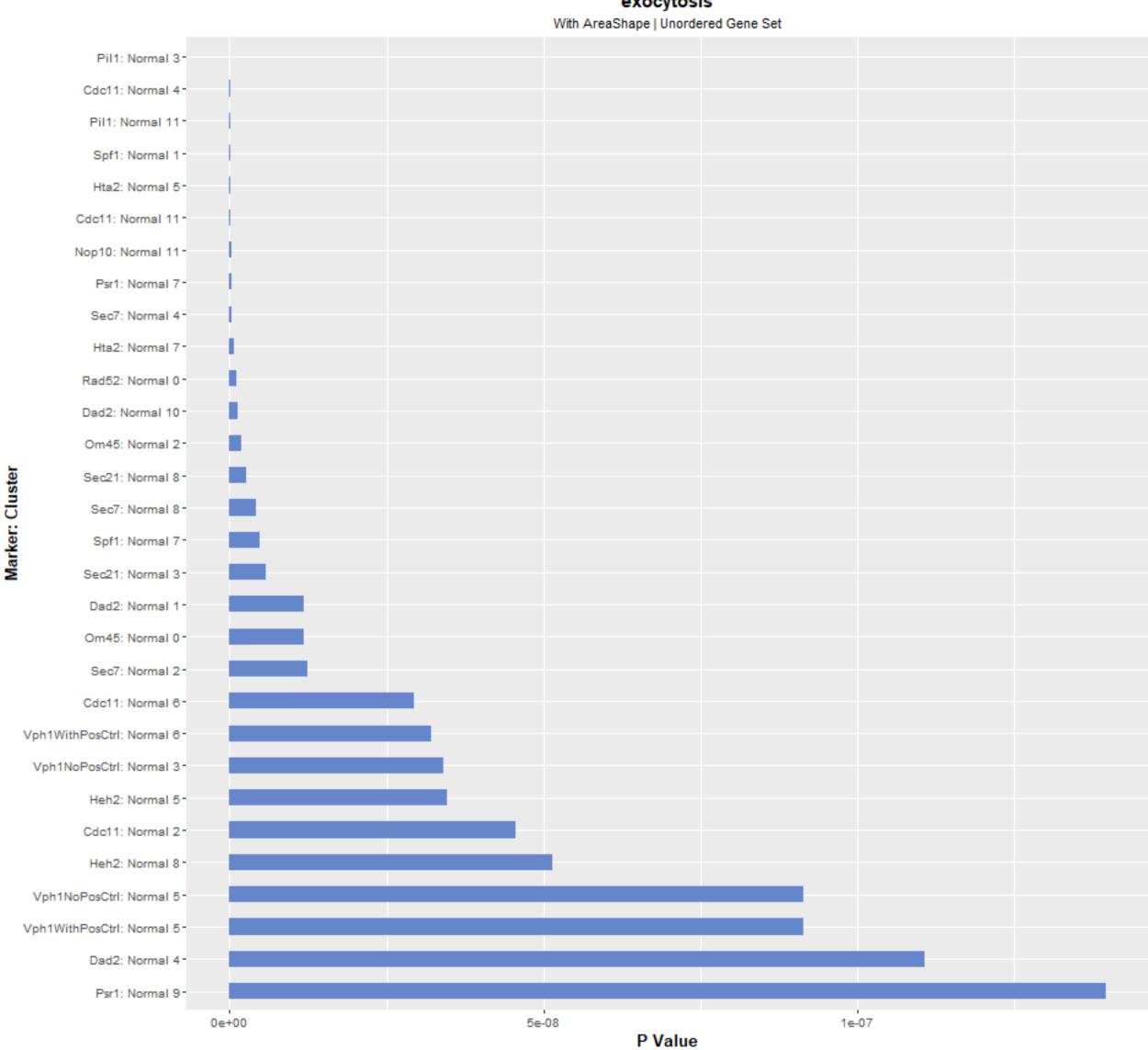
DNA-templated transcription, initiation



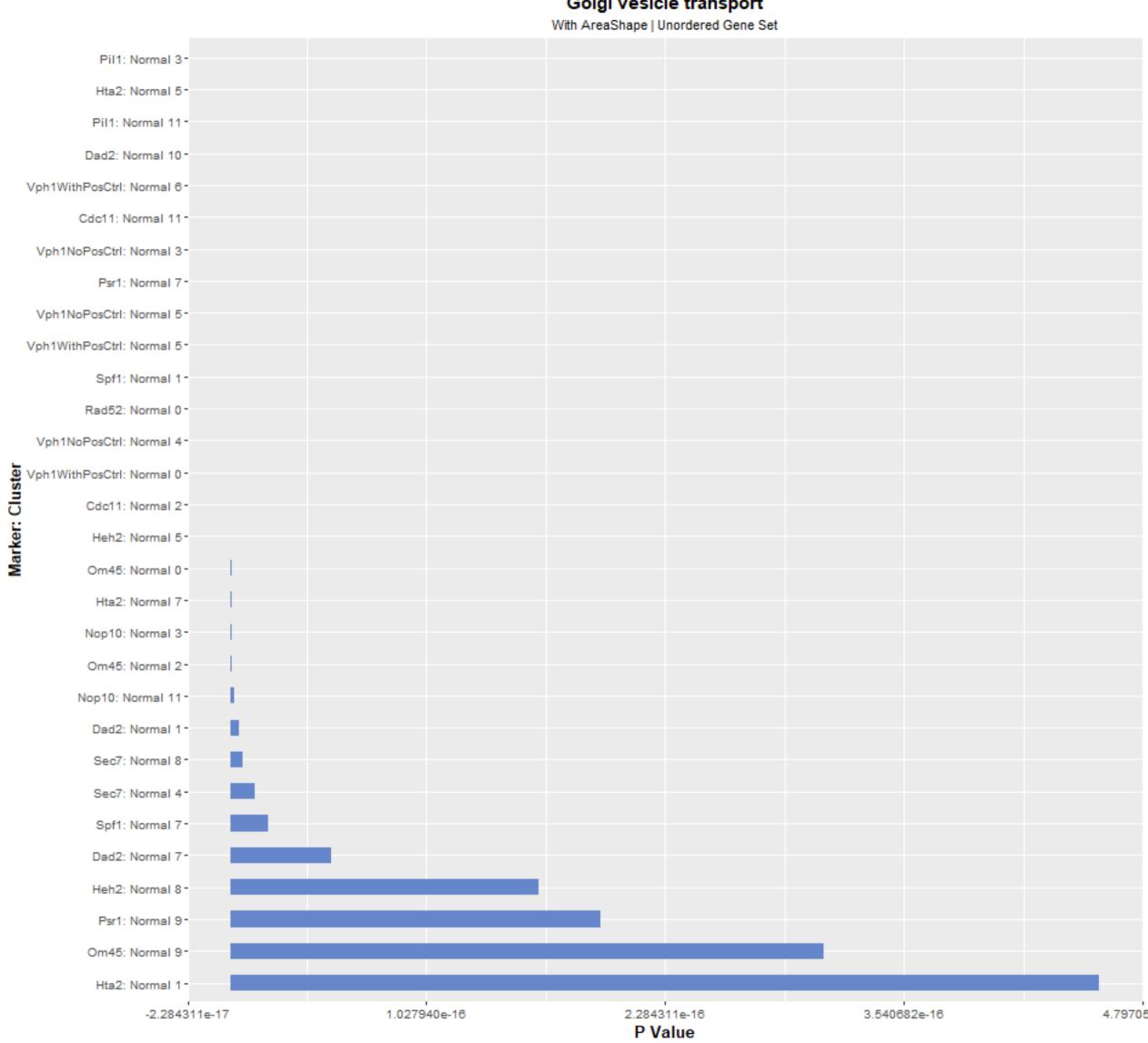
DNA-templated transcription, termination



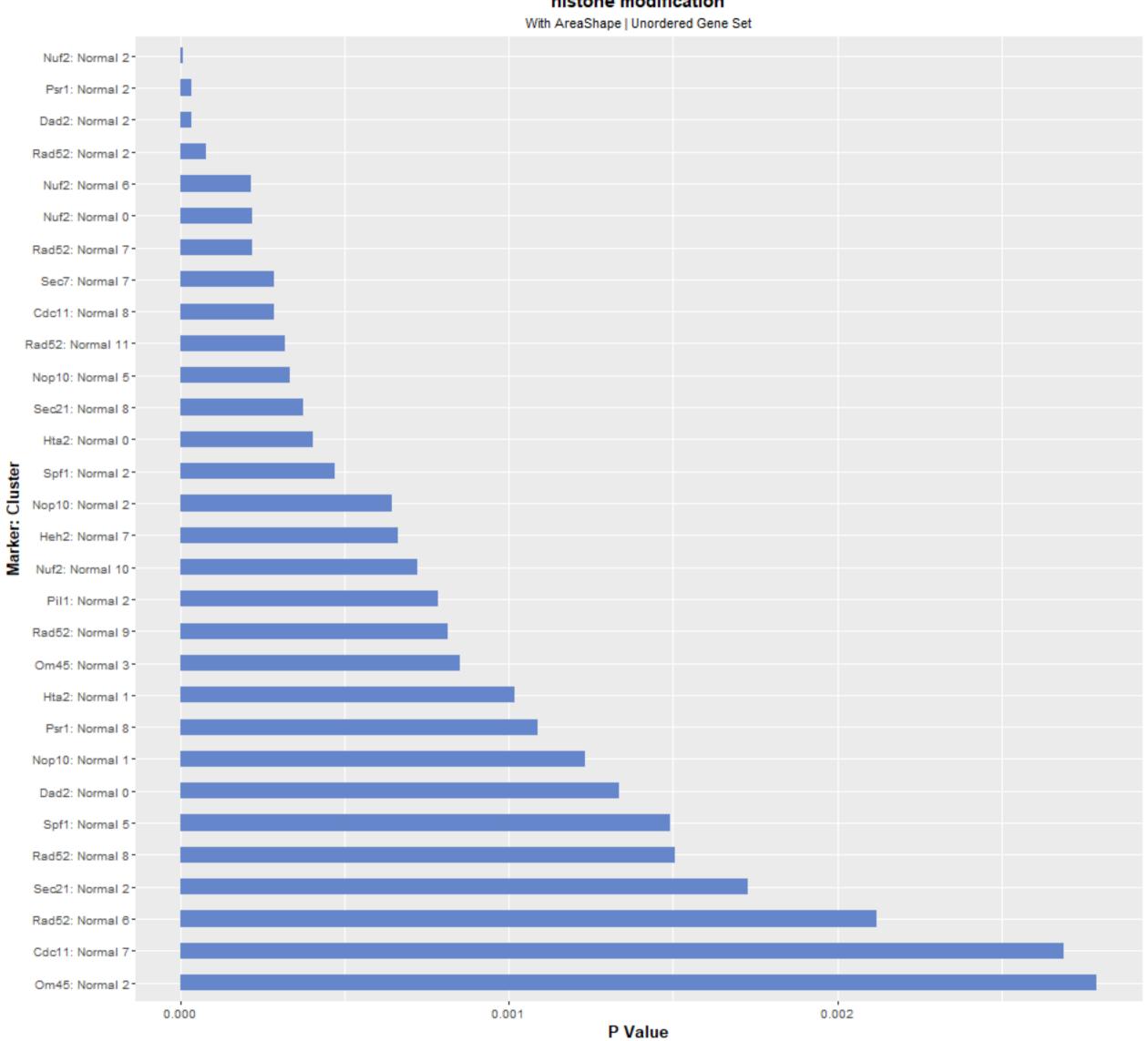
exocytosis



Golgi vesicle transport

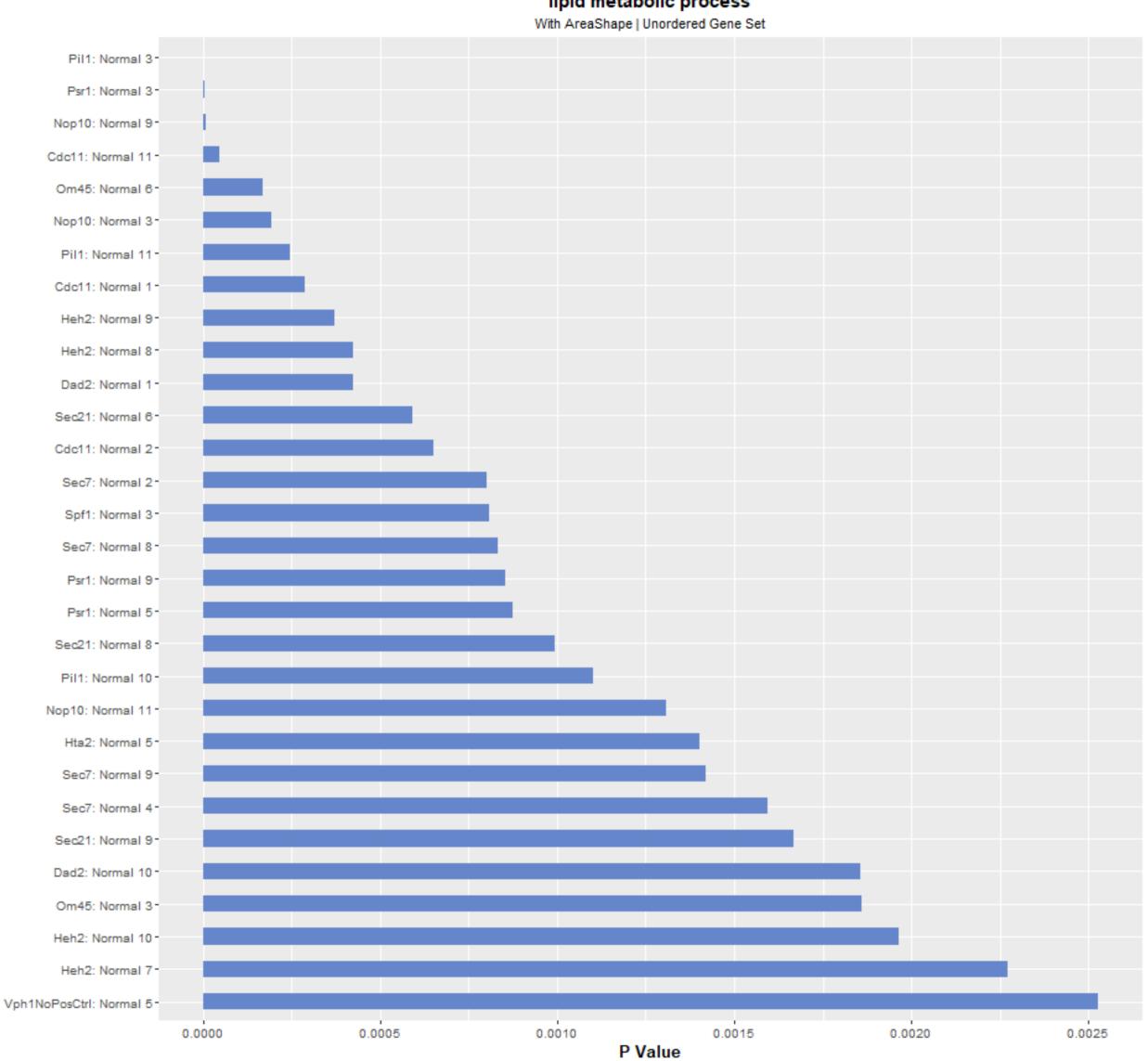


histone modification



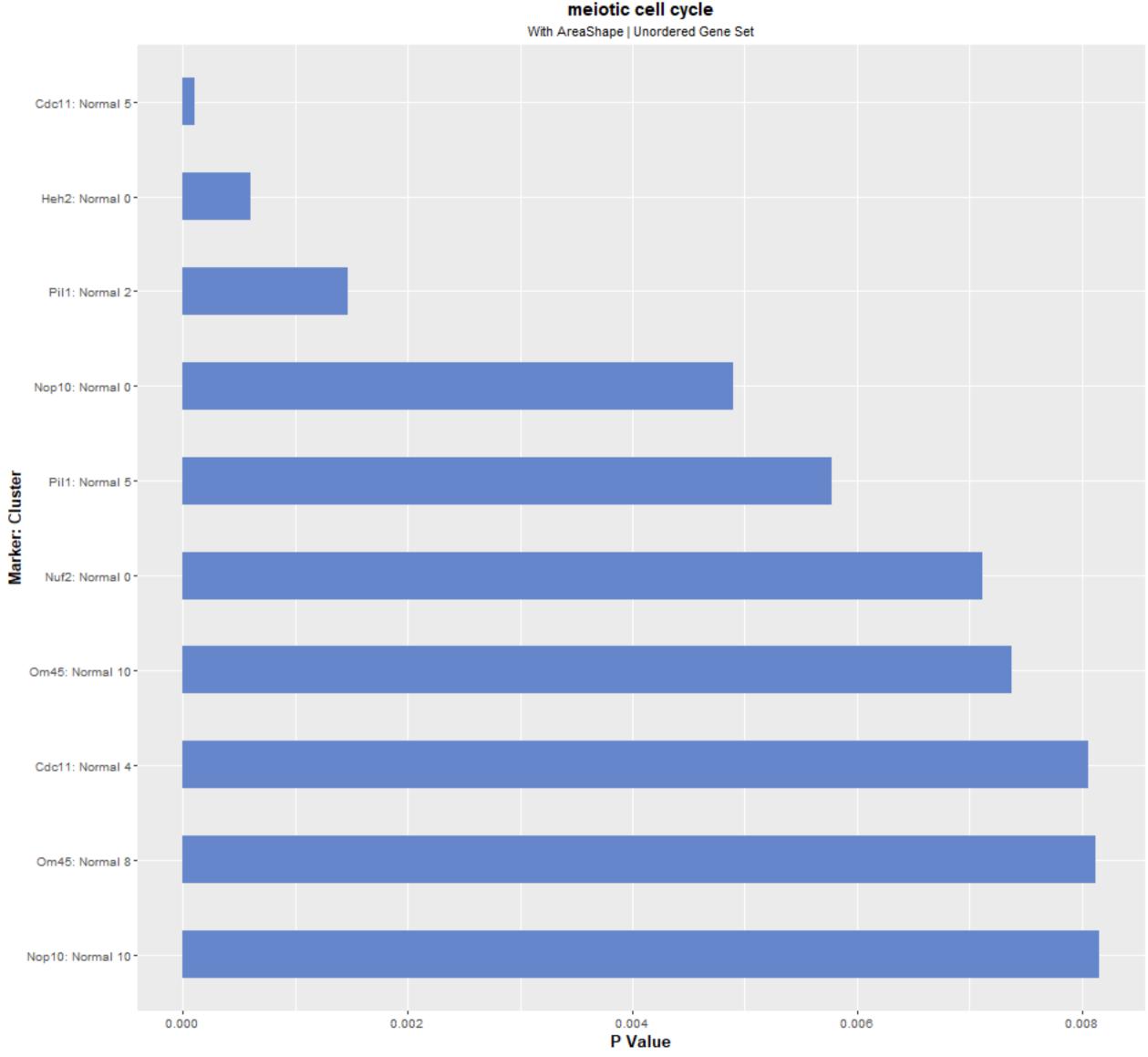
invasive growth in response to glucose limitation With AreaShape | Unordered Gene Set Psr1: Normal 0 -Marker: Cluster Rad52: Normal 1-0.0000 0.0025 0.0050 0.0075 P Value

lipid metabolic process



Marker: Cluster

meiotic cell cycle

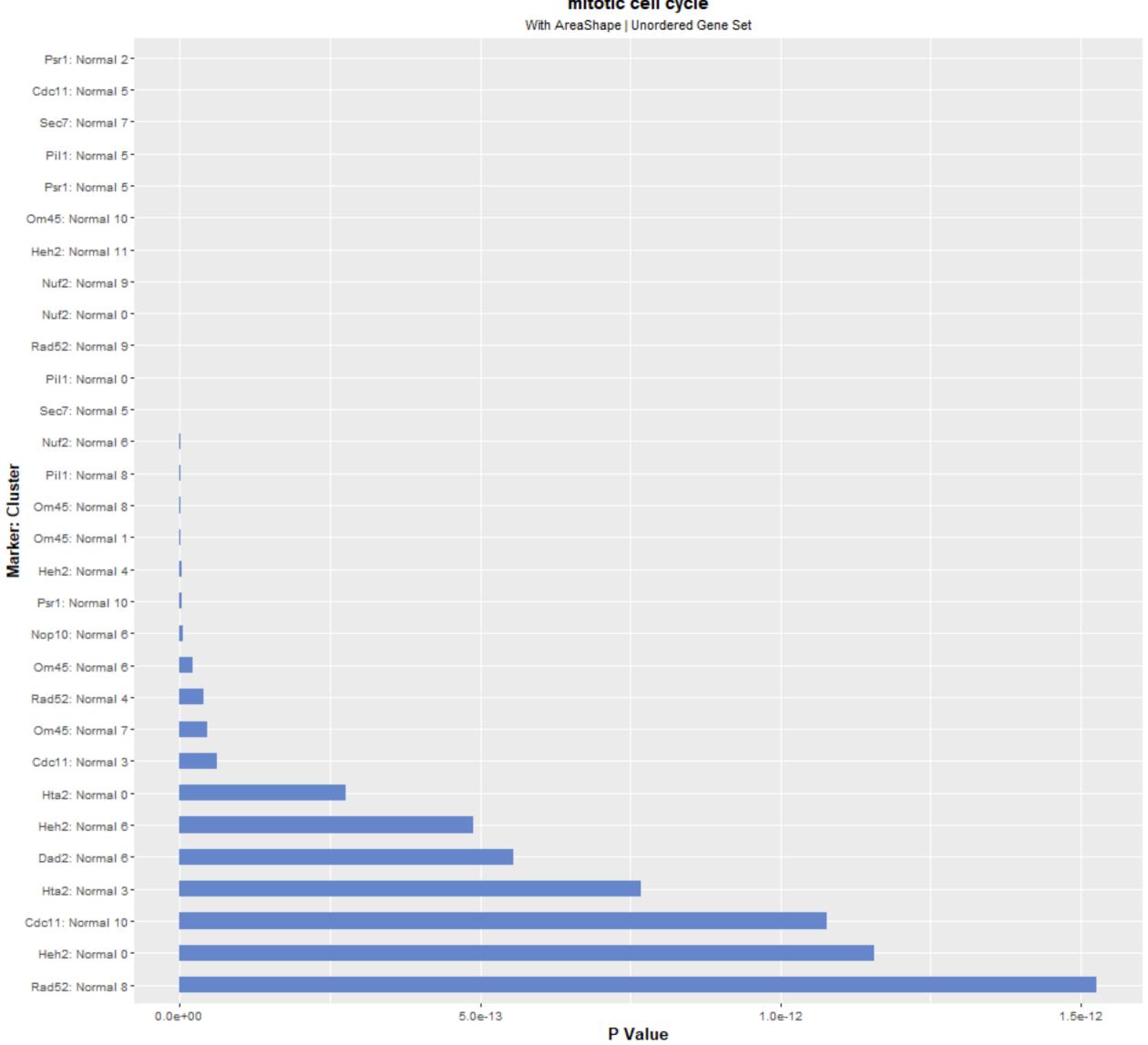


membrane fusion

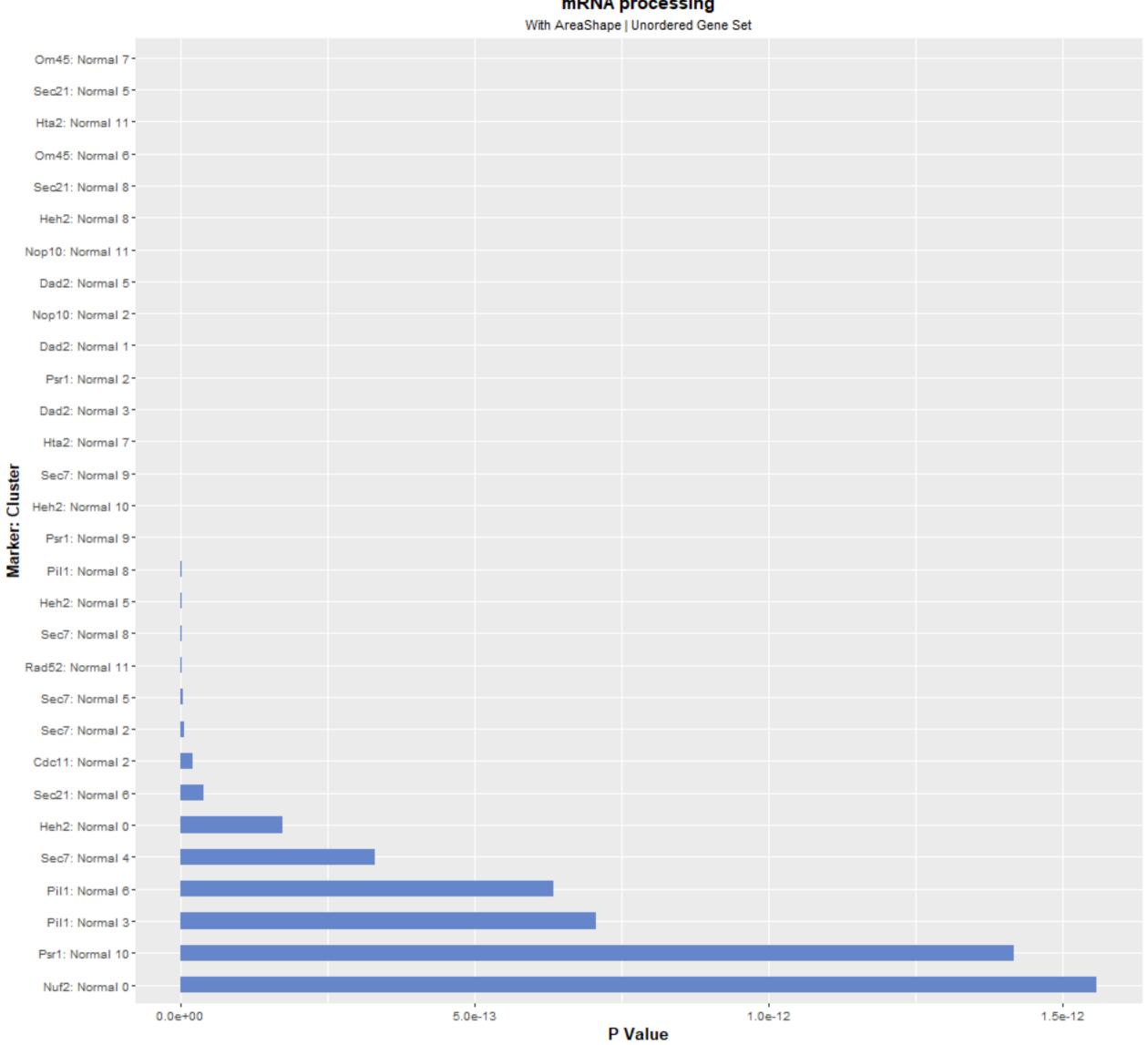
With AreaShape | Unordered Gene Set Pil1: Normal 3 Pil1: Normal 11-Sec21: Normal 8 -Sec7: Normal 2-Om45: Normal 0 -Hta2: Normal 5 -Rad52: Normal 0 -Cdc11: Normal 11 -Dad2: Normal 10 -Rad52: Normal 2-Vph1WithPosCtrl: Normal 6 -Vph1NoPosCtrl: Normal 3 -Vph1NoPosCtrl: Normal 5 -Vph1WithPosCtrl: Normal 5 Spf1: Normal 1 Spf1: Normal 7 Cdc11: Normal 2 -Sec21: Normal 3-Psr1: Normal 7 -Nop10: Normal 11-Sec7: Normal 8 -Hta2: Normal 7 -Dad2: Normal 1-Sec7: Normal 41 Nop10: Normal 3-Vph1NoPosCtrl: Normal 4-Vph1WithPosCtrl: Normal 0 -Heh2: Normal 51 Rad52: Normal 6 -Om45: Normal 21 1e-08 2e-08 4e-08 5e-08 0e+00 3e-08 P Value

mitochondrion organization With AreaShape | Unordered Gene Set Marker: Cluster: 0 c c la como de como 1e-03 0e+00 5e-04 P Value

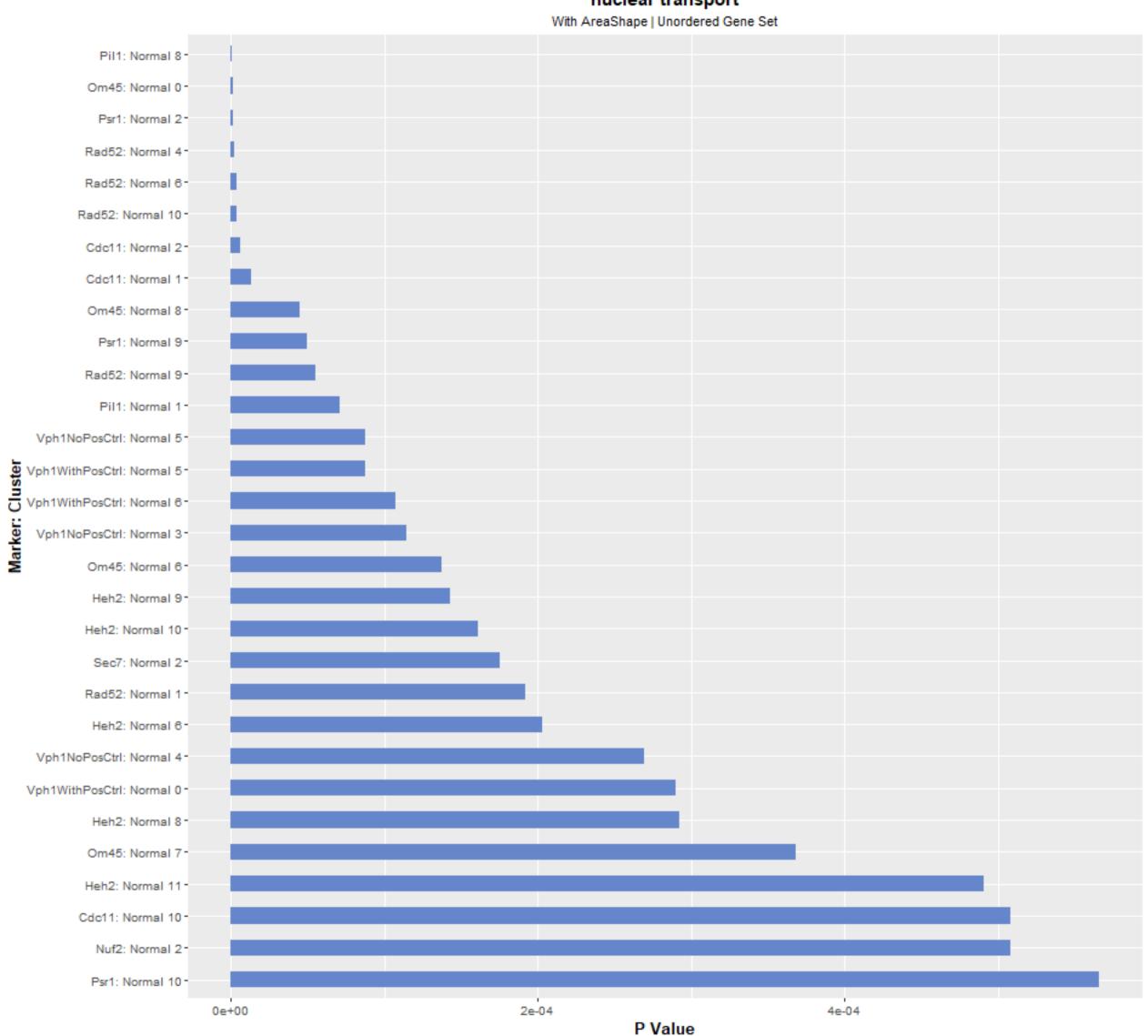
mitotic cell cycle



mRNA processing

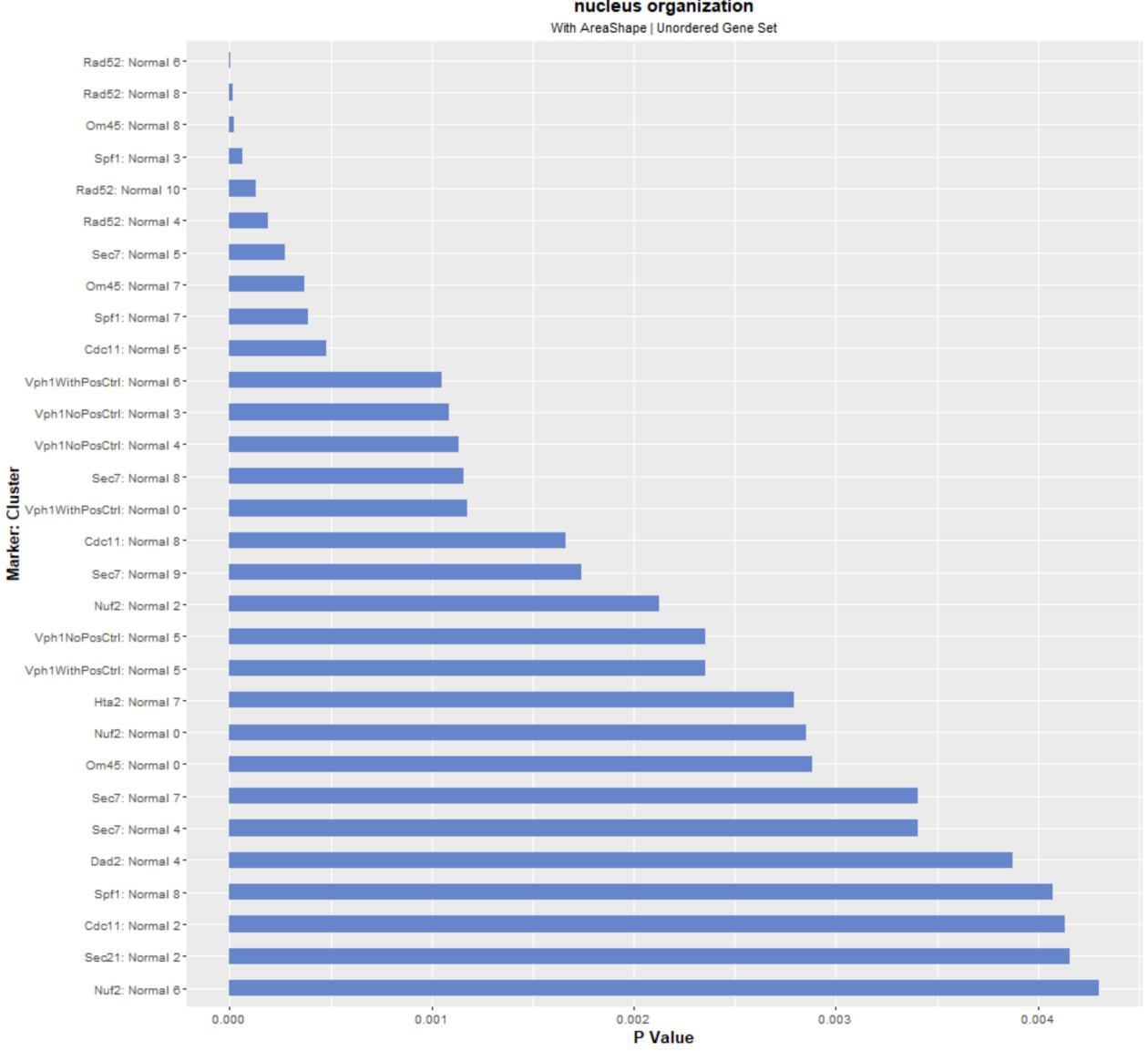


nuclear transport

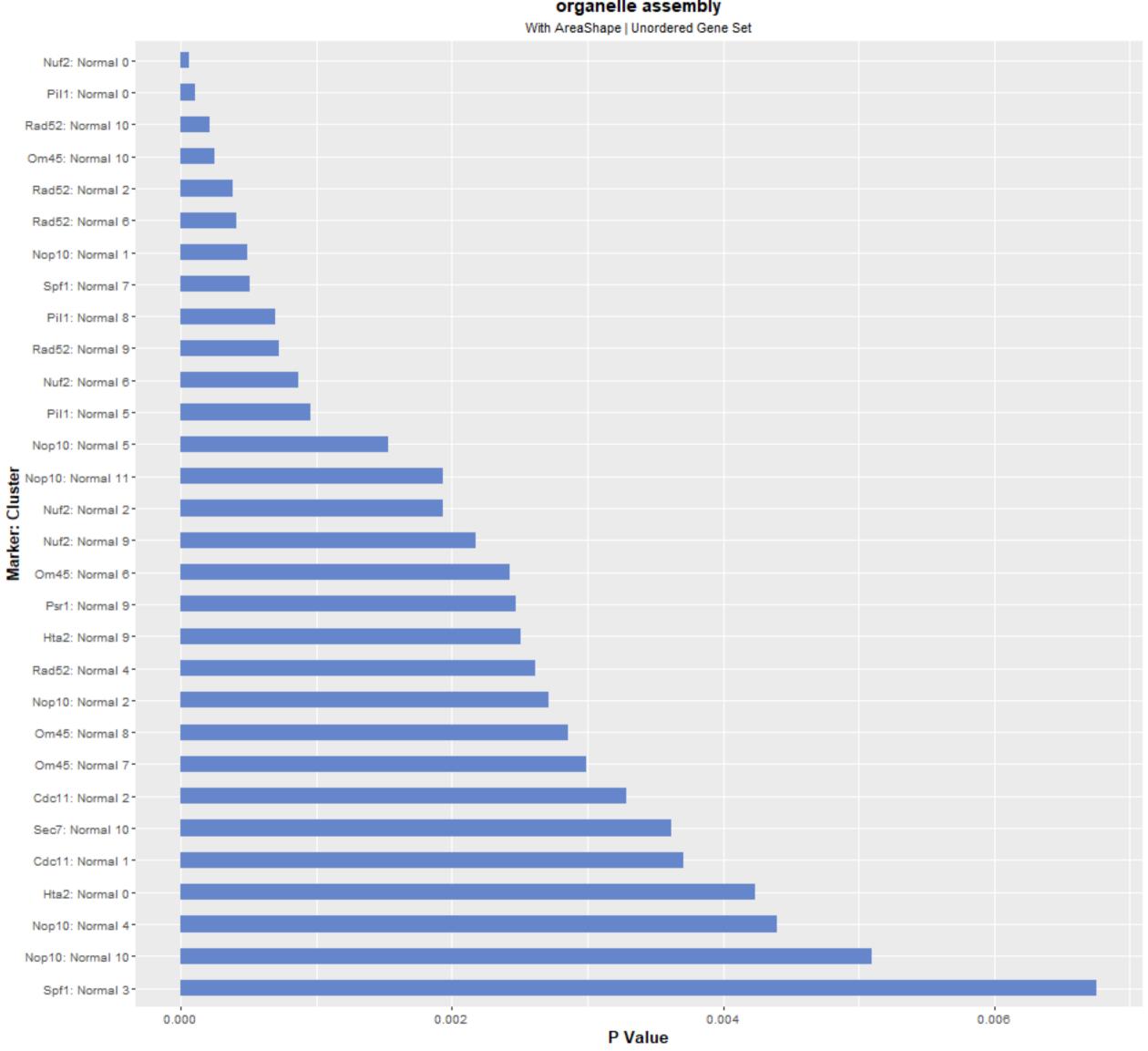


nucleobase-containing compound transport With AreaShape | Unordered Gene Set Nuf2: Normal 21 Vph1WithPosCtrl: Normal 6 -Vph1NoPosCtrl: Normal 3 Nuf2: Normal 6-Om45: Normal 0 -Vph1NoPosCtrl: Normal 5 -Vph1WithPosCtrl: Normal 5 -Sec21: Normal 51 Marker: Cluster Nuf2: Normal 0 -Sec21: Normal 1-Rad52: Normal 10 -Pil1: Normal 8 -Psr1: Normal 21 Vph1NoPosCtrl: Normal 4-Vph1WithPosCtrl: Normal 0 -Heh2: Normal 91 Heh2: Normal 10 -Sec21: Normal 9 -0.0050 0.0000 0.0025 0.0075 0.010 P Value

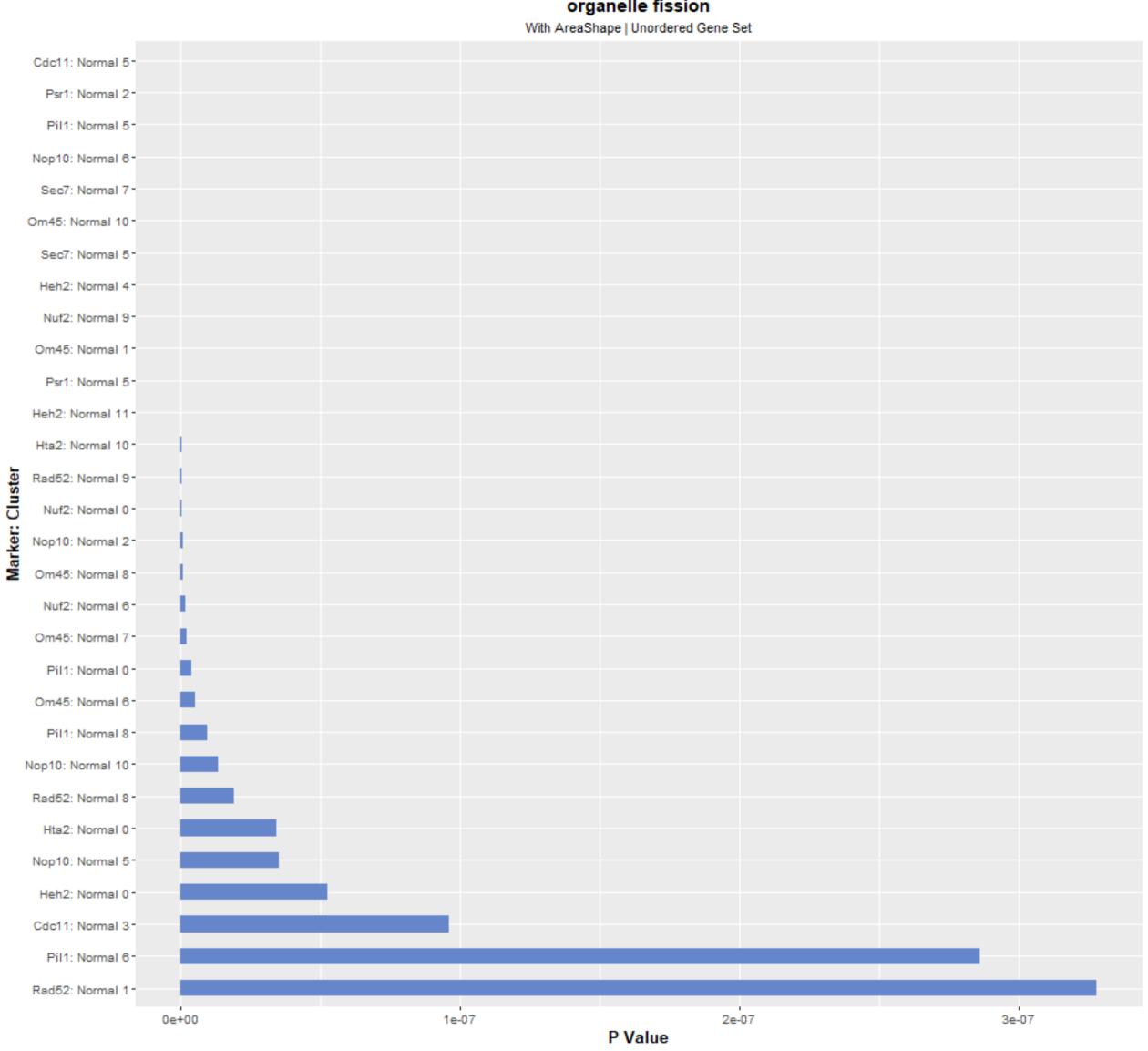
nucleus organization



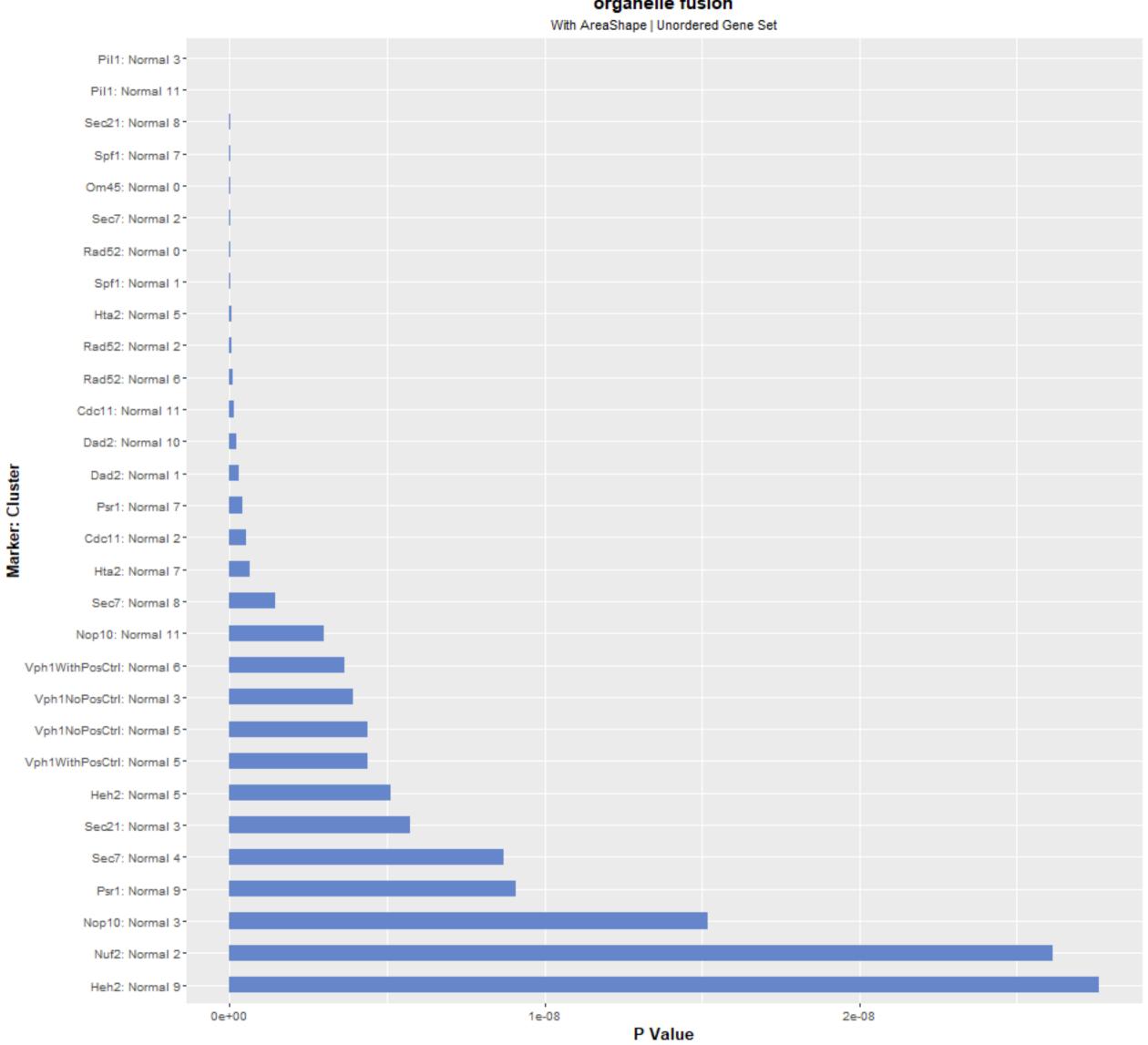
organelle assembly



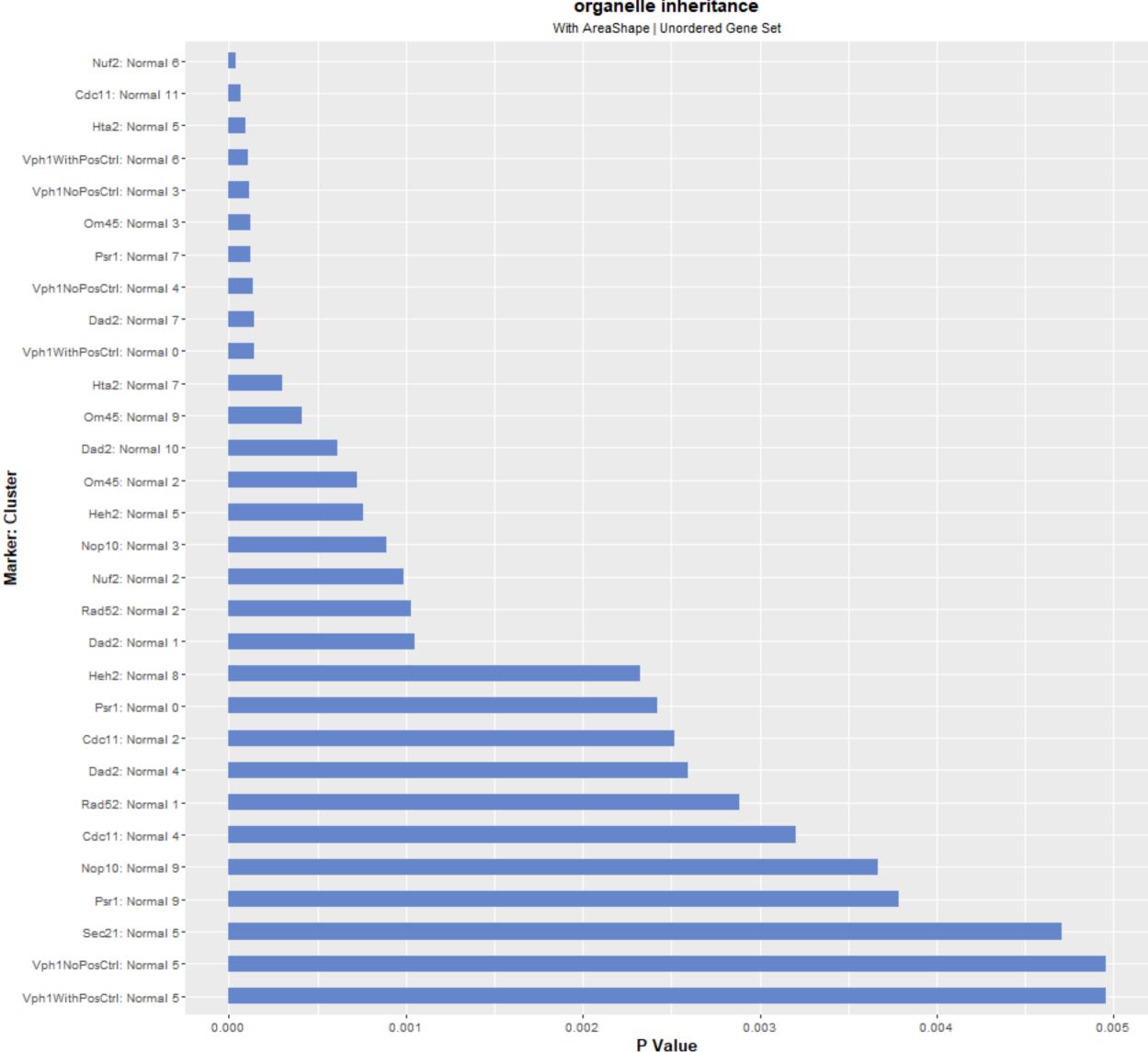
organelle fission



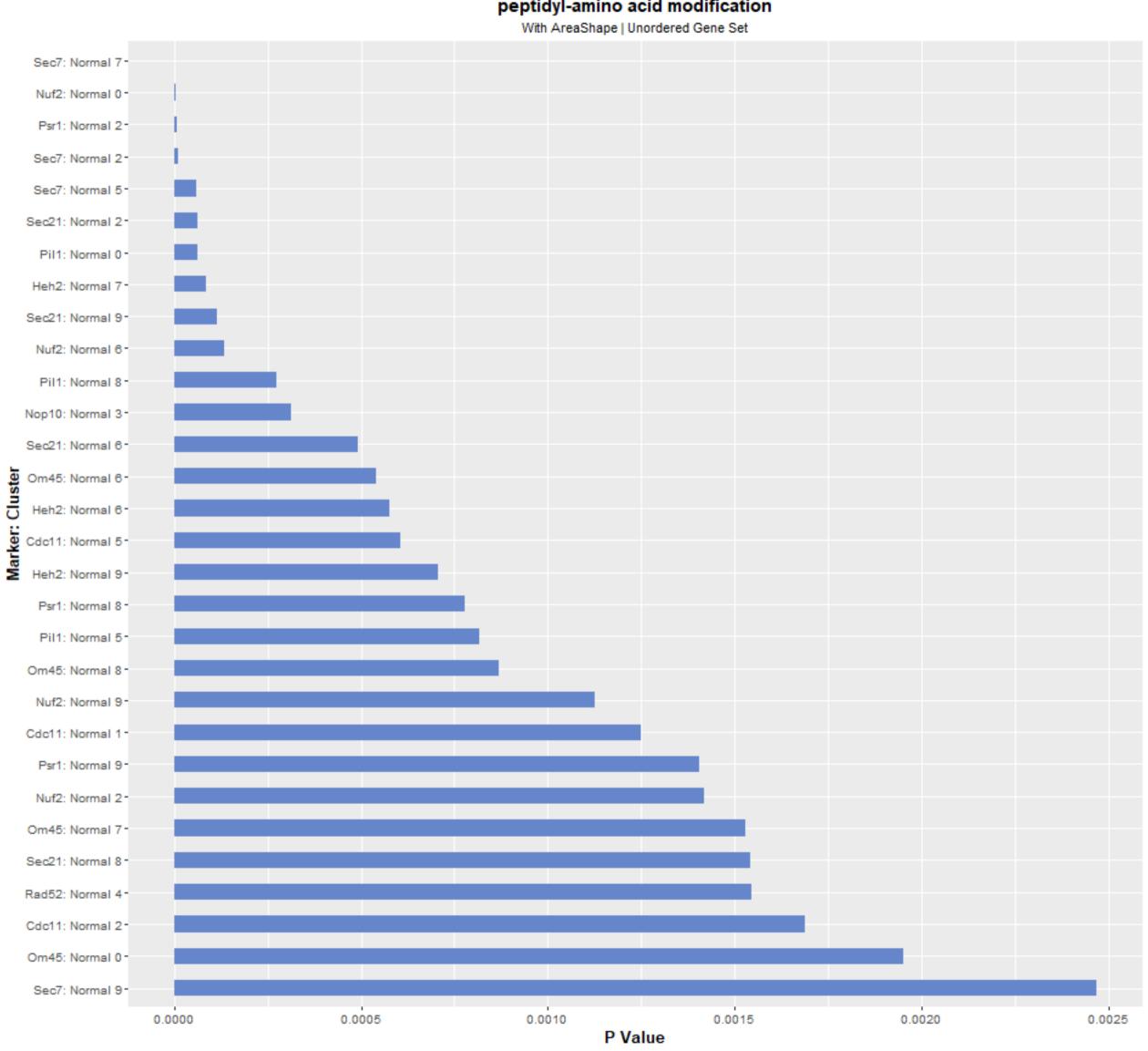
organelle fusion



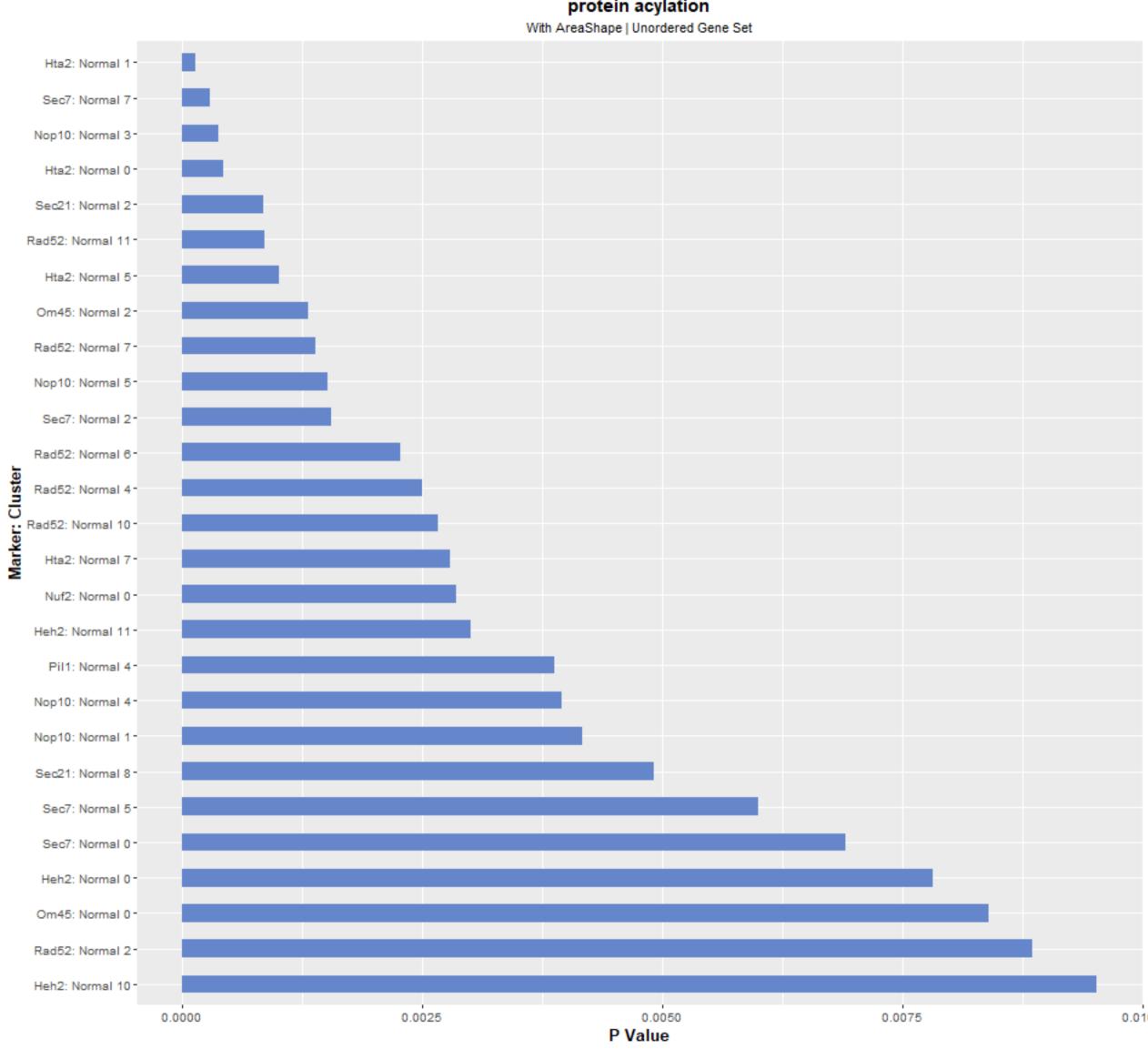
organelle inheritance



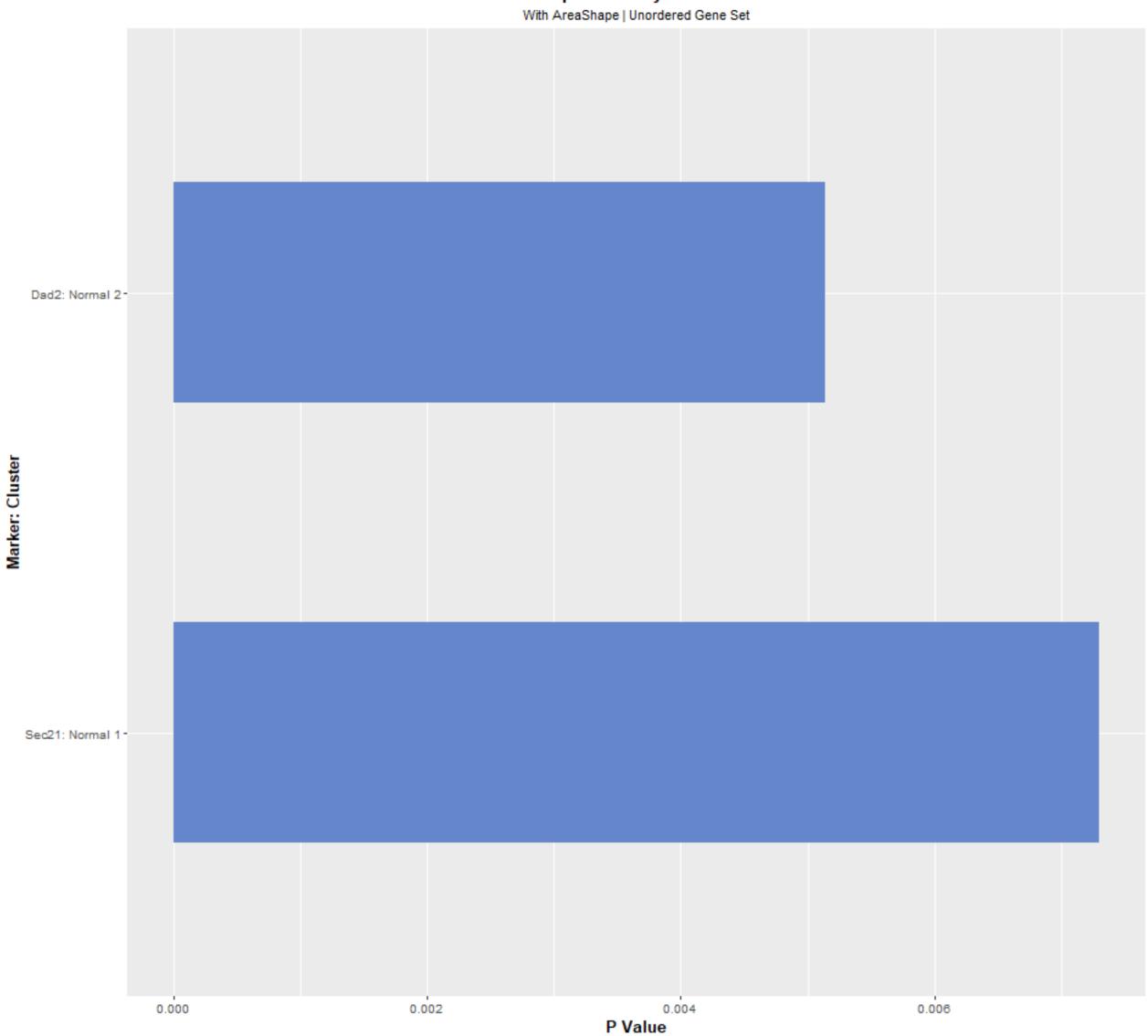
peptidyl-amino acid modification



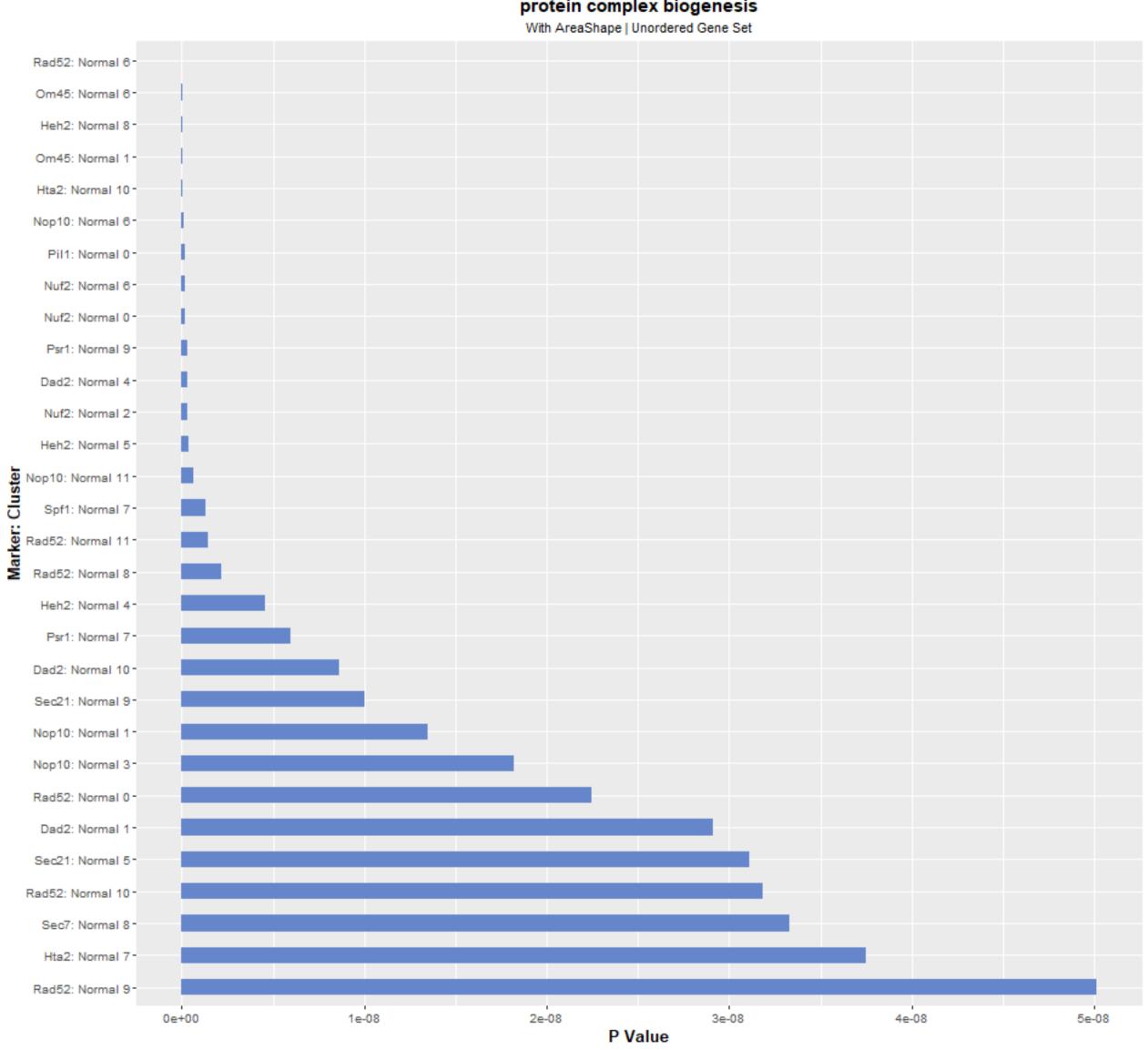
protein acylation



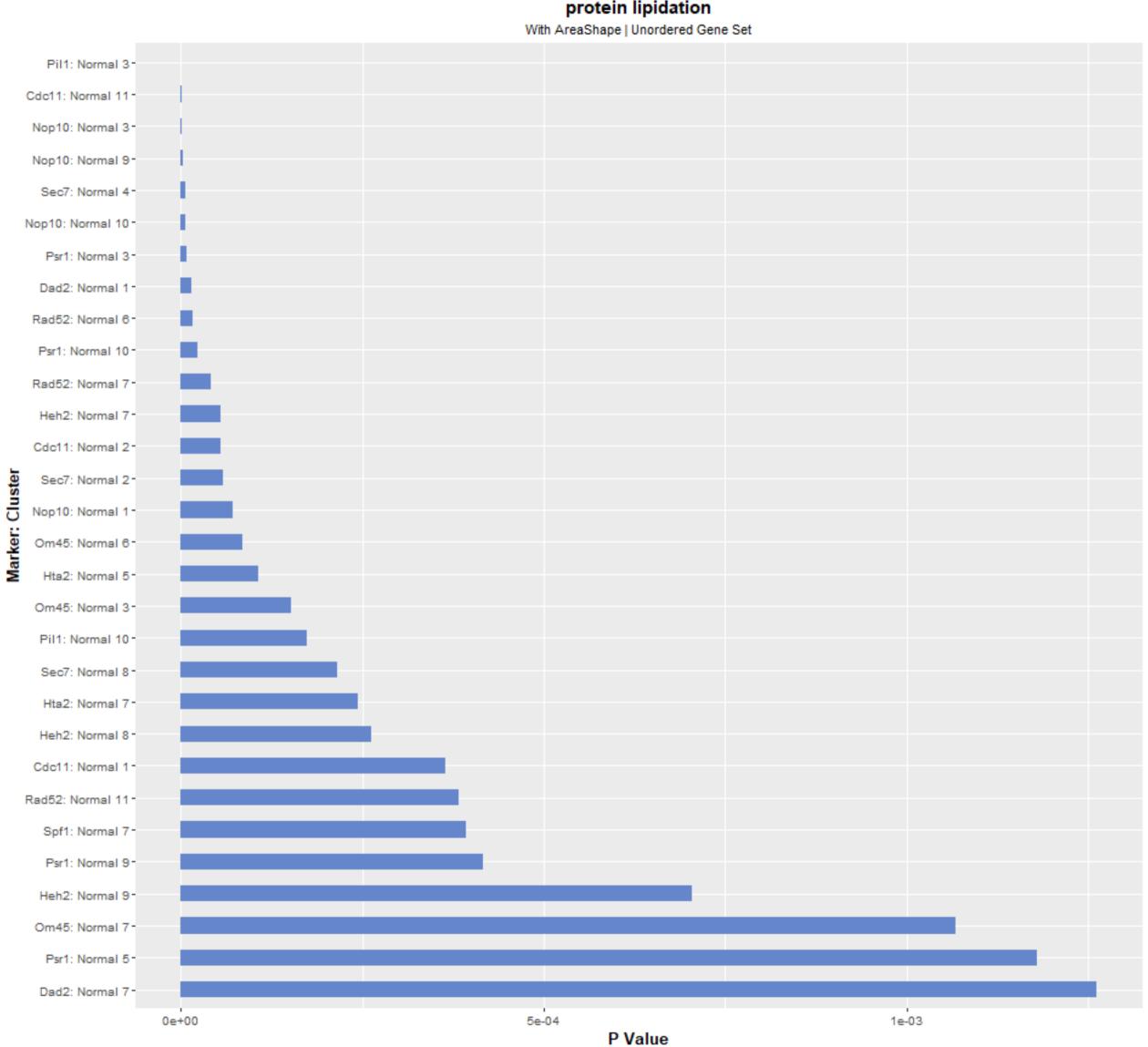
protein alkylation



protein complex biogenesis

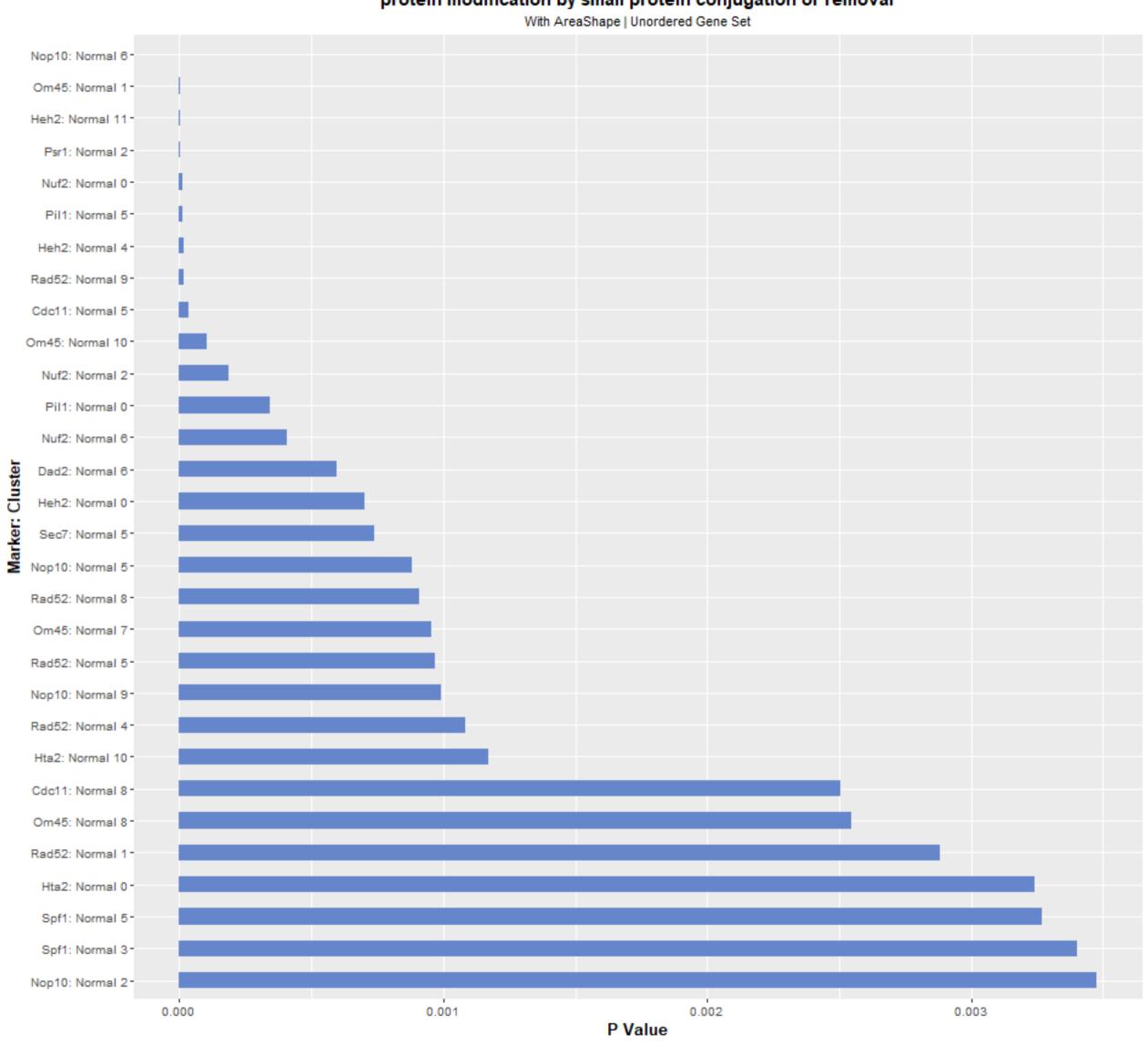


protein lipidation

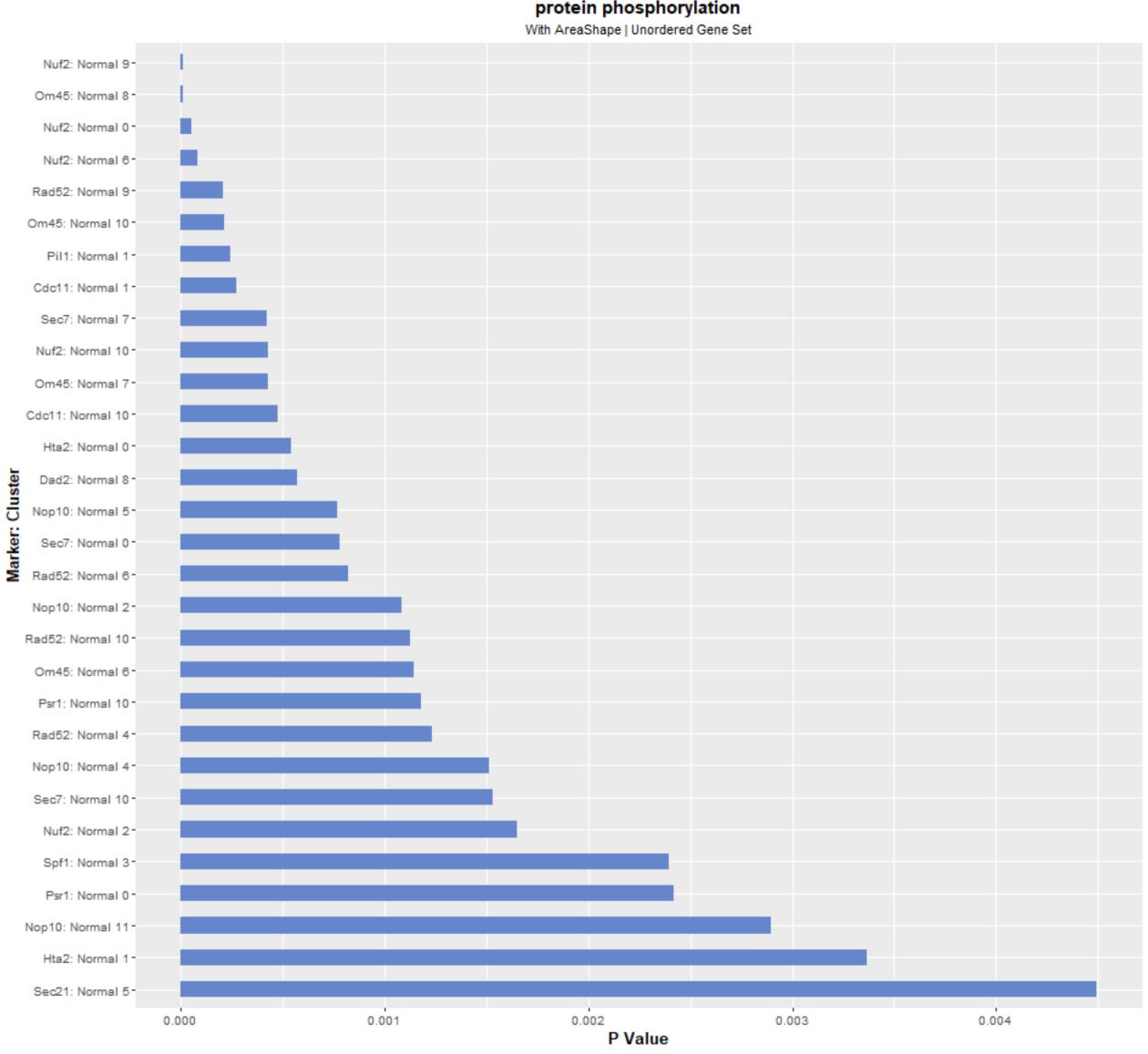


protein maturation With AreaShape | Unordered Gene Set Marker: Cluster ... Ser ... Cluster ... Cl 0.004 0.000 0.002 0.006 0.008 P Value

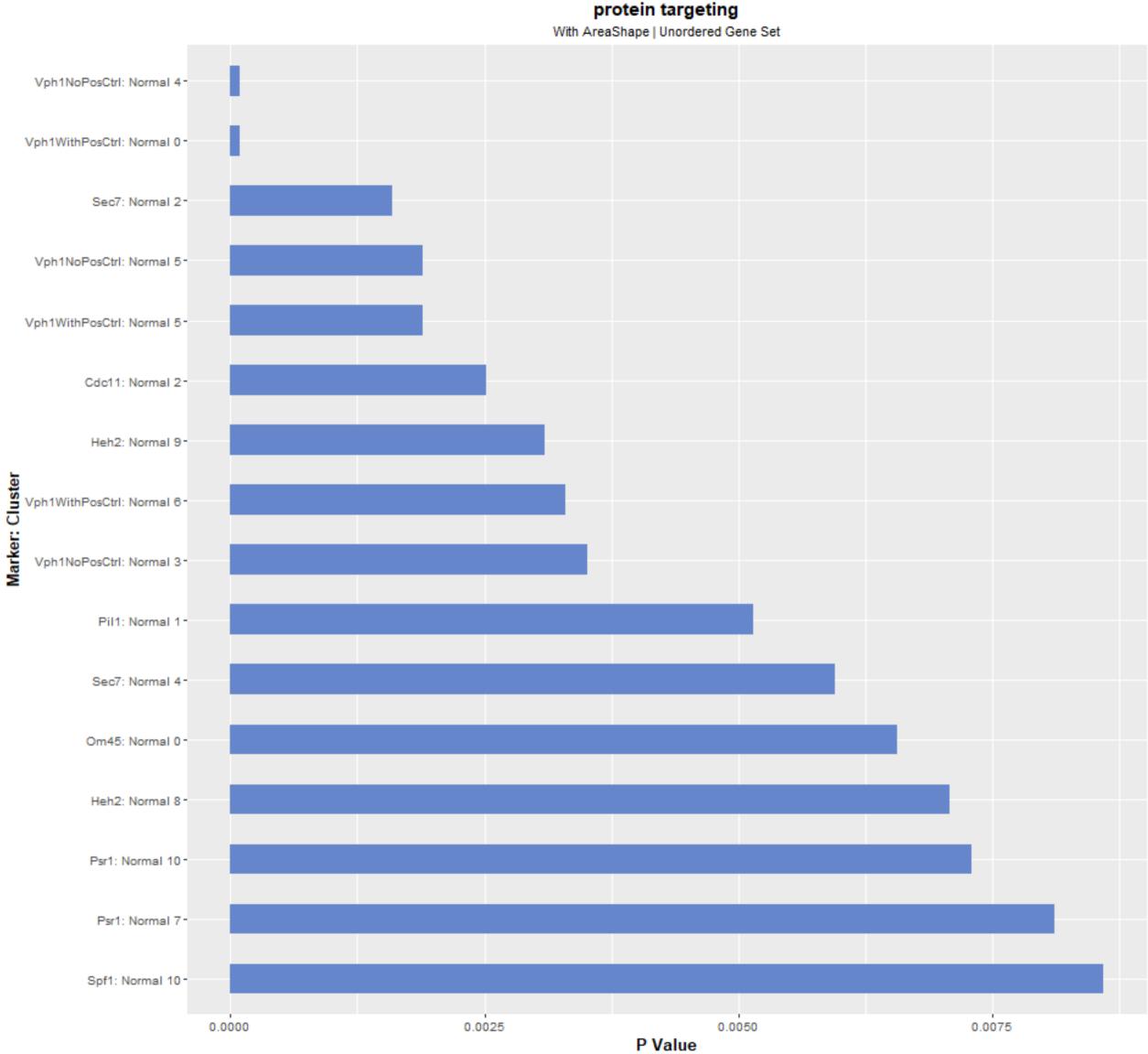
protein modification by small protein conjugation or removal



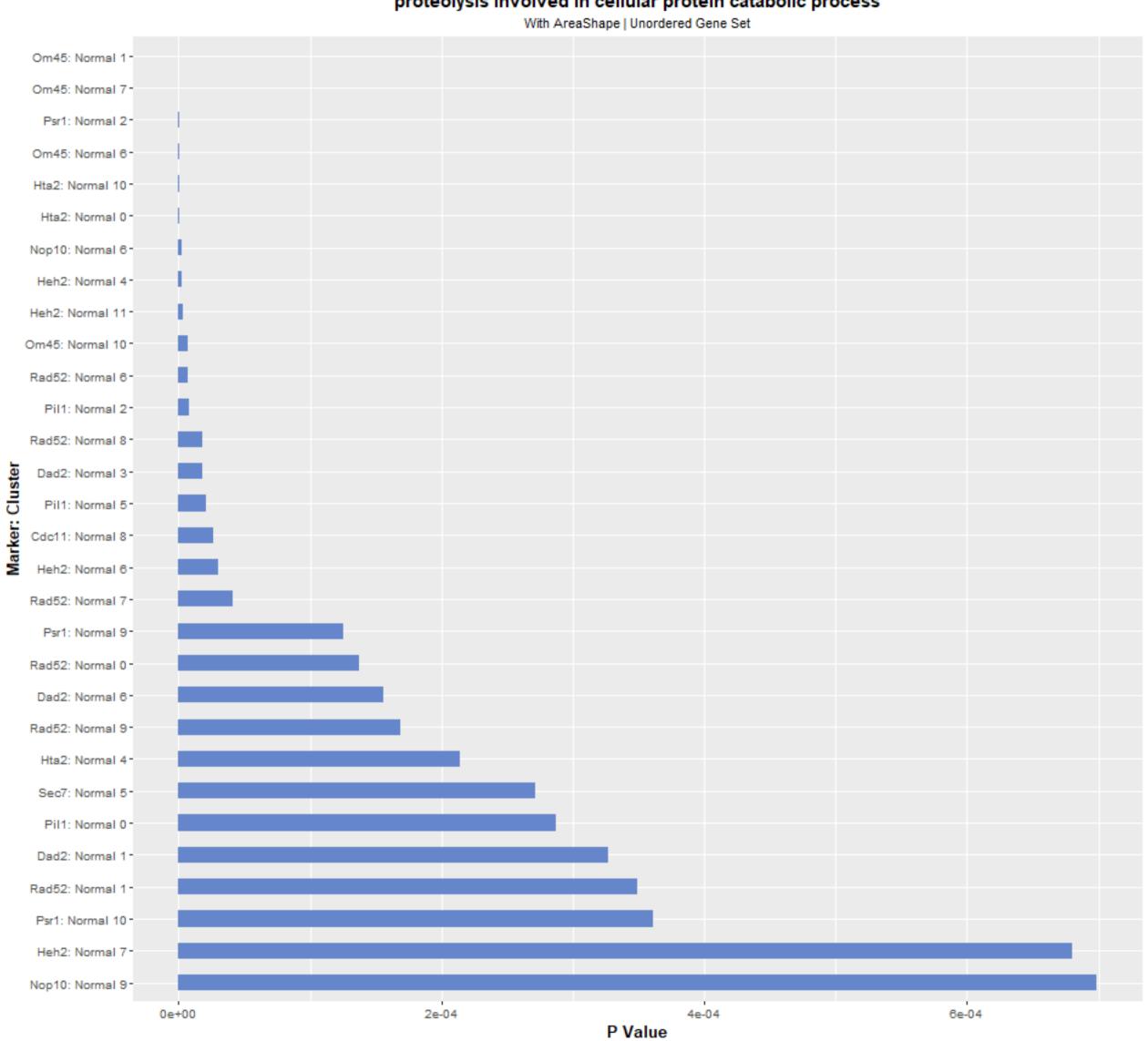
protein phosphorylation



protein targeting

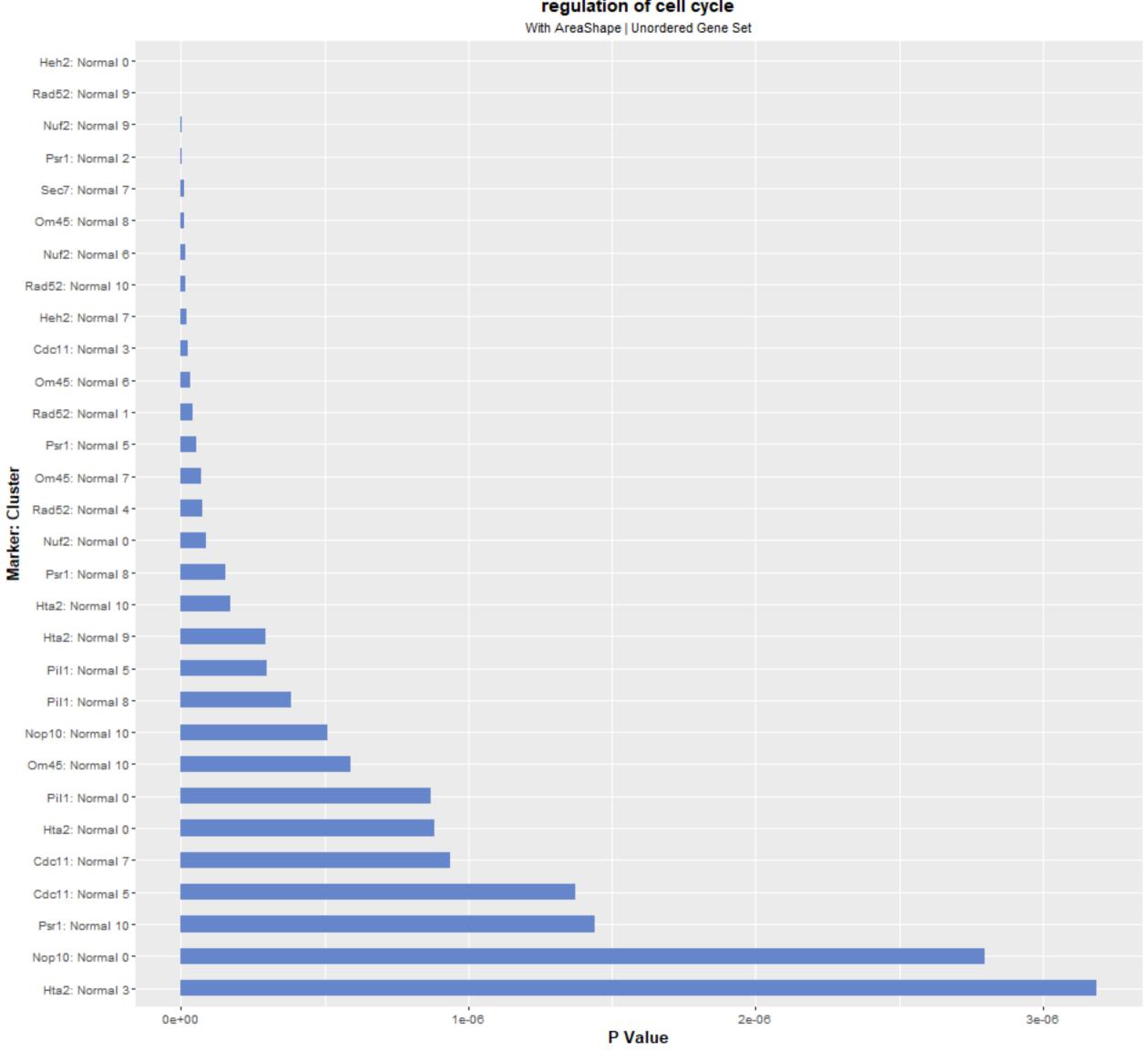


proteolysis involved in cellular protein catabolic process

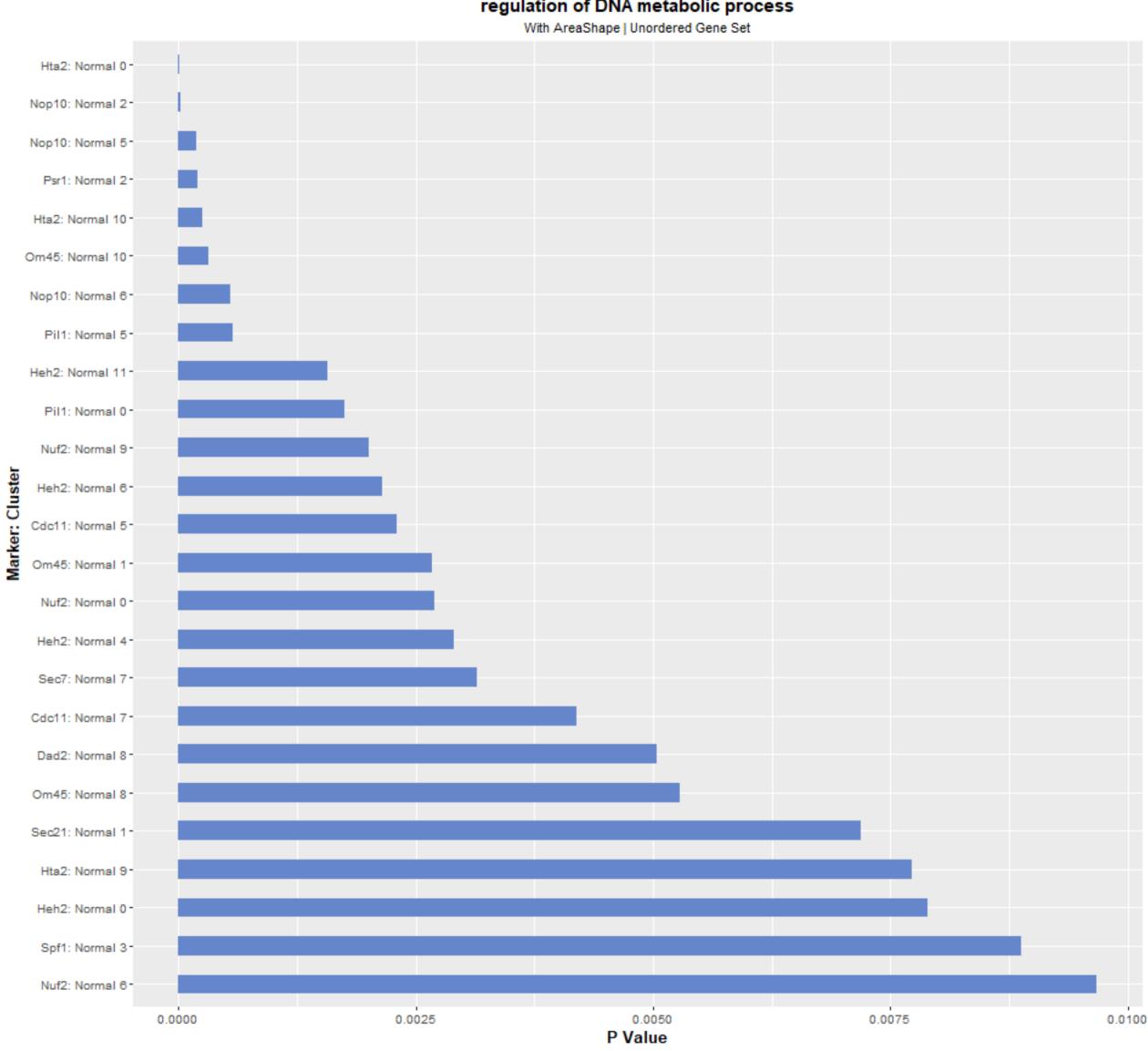


pseudohyphal growth With AreaShape | Unordered Gene Set Marker: Cluster: 6 Land 22: Normal 9-0.0050 0.0025 0.0075 0.0000 P Value

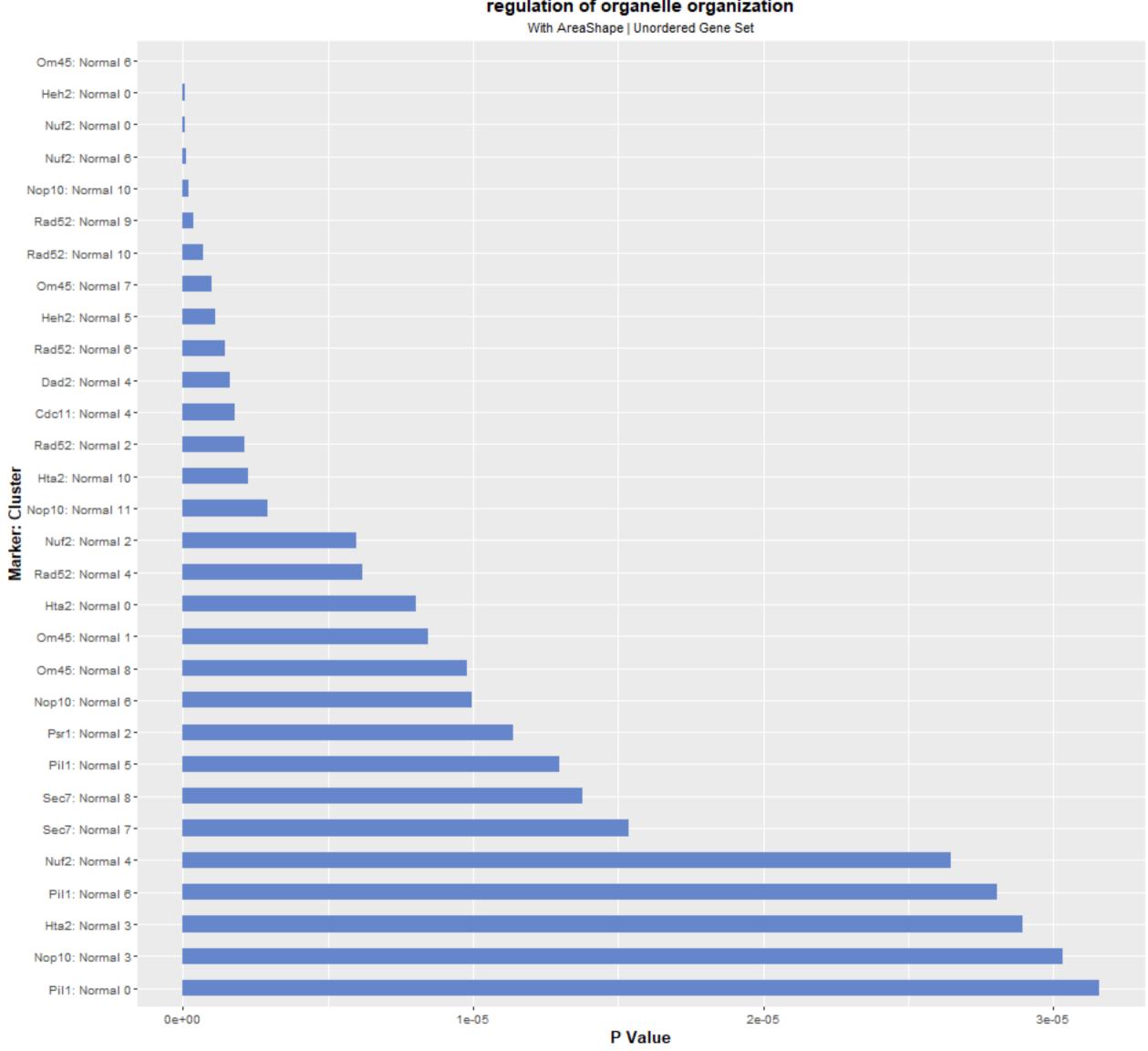
regulation of cell cycle



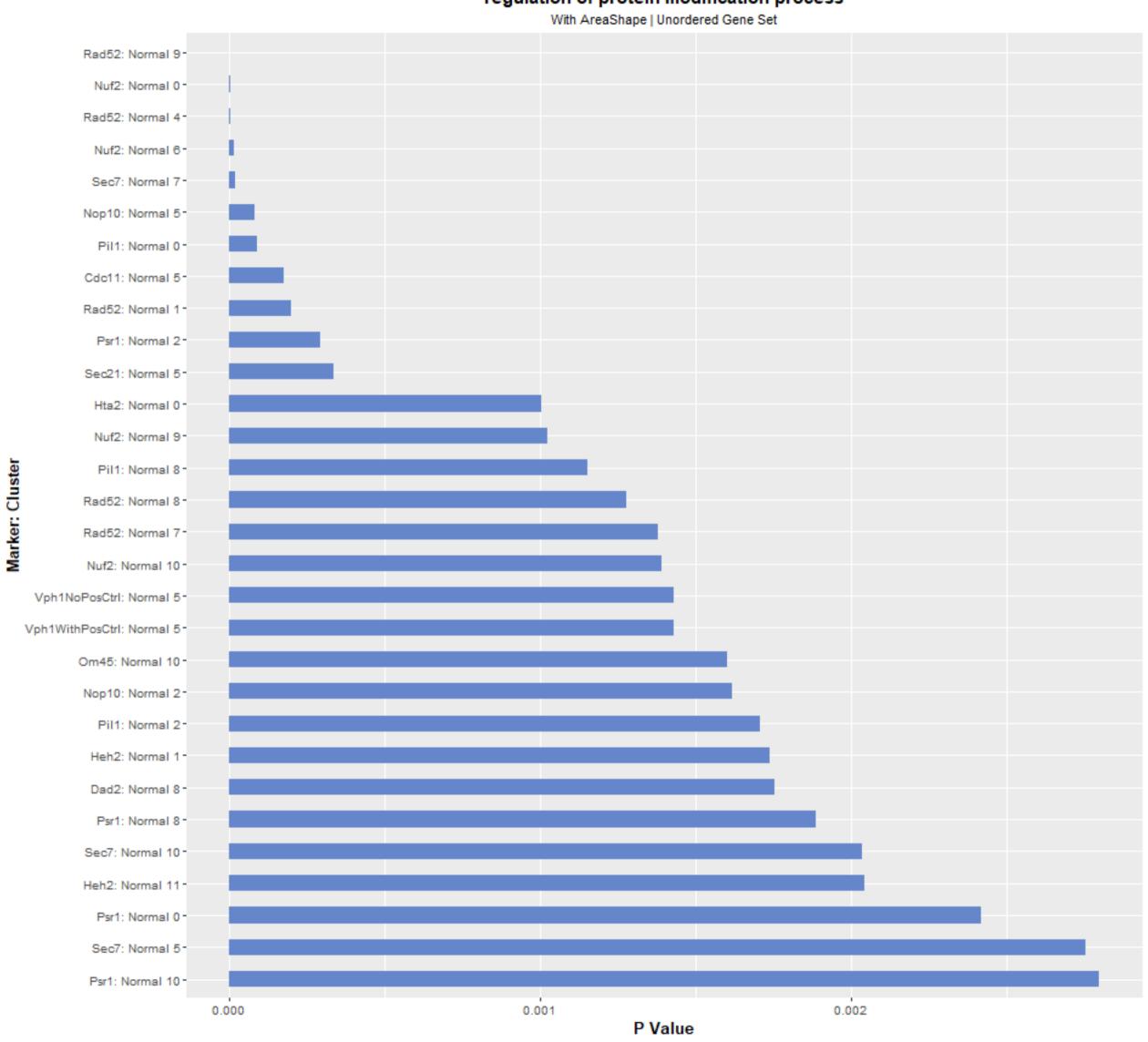
regulation of DNA metabolic process



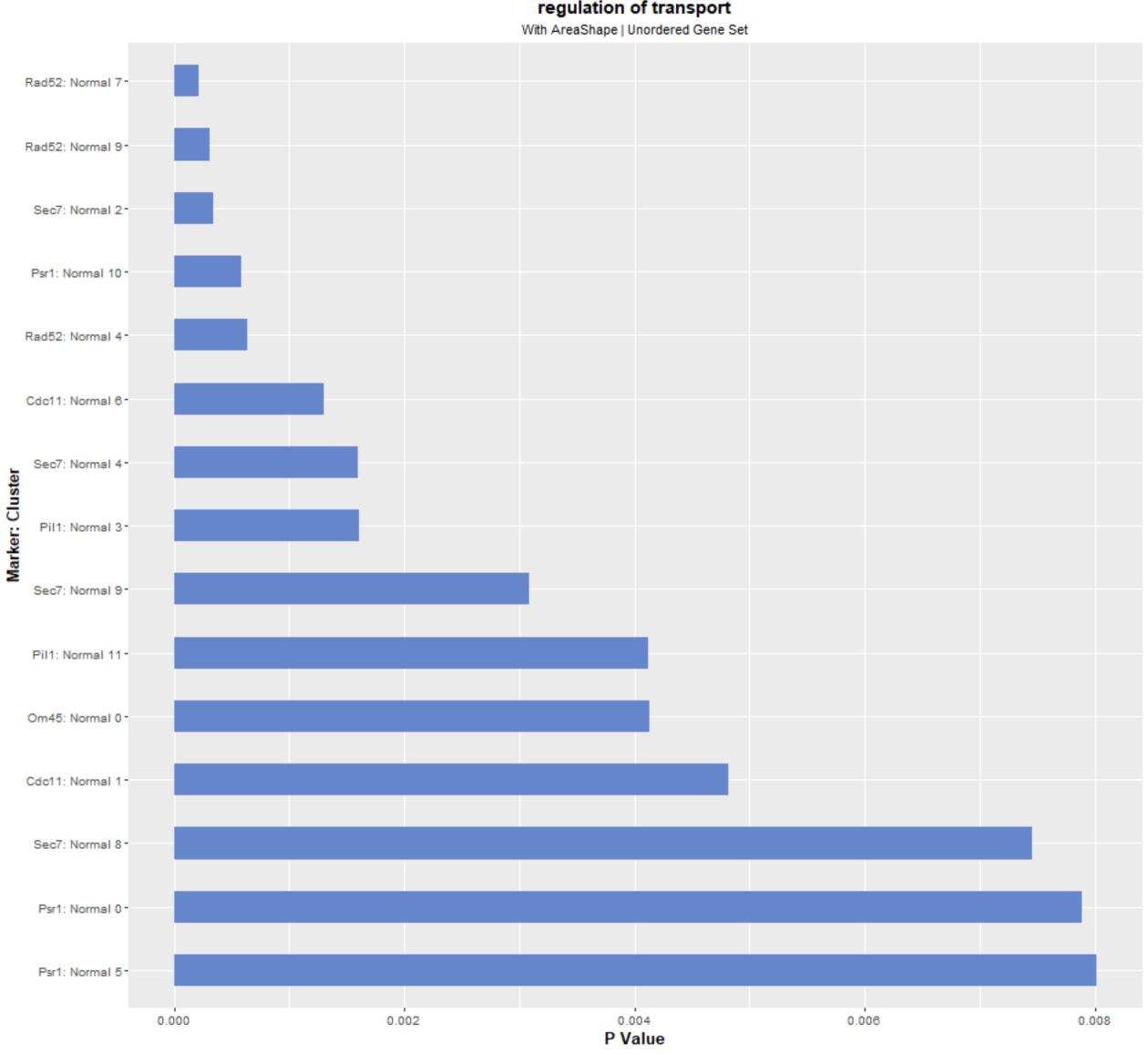
regulation of organelle organization



regulation of protein modification process



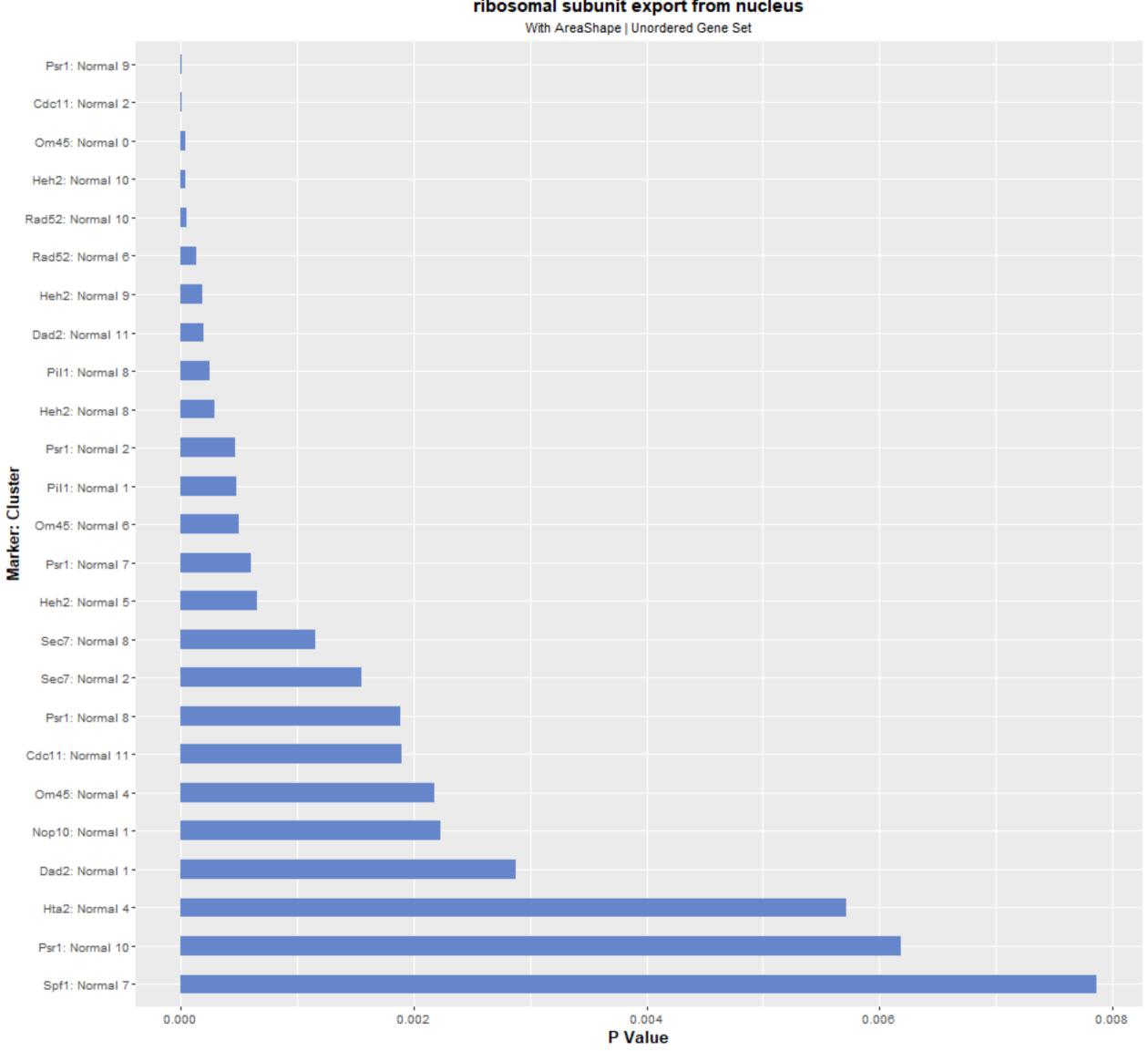
regulation of transport



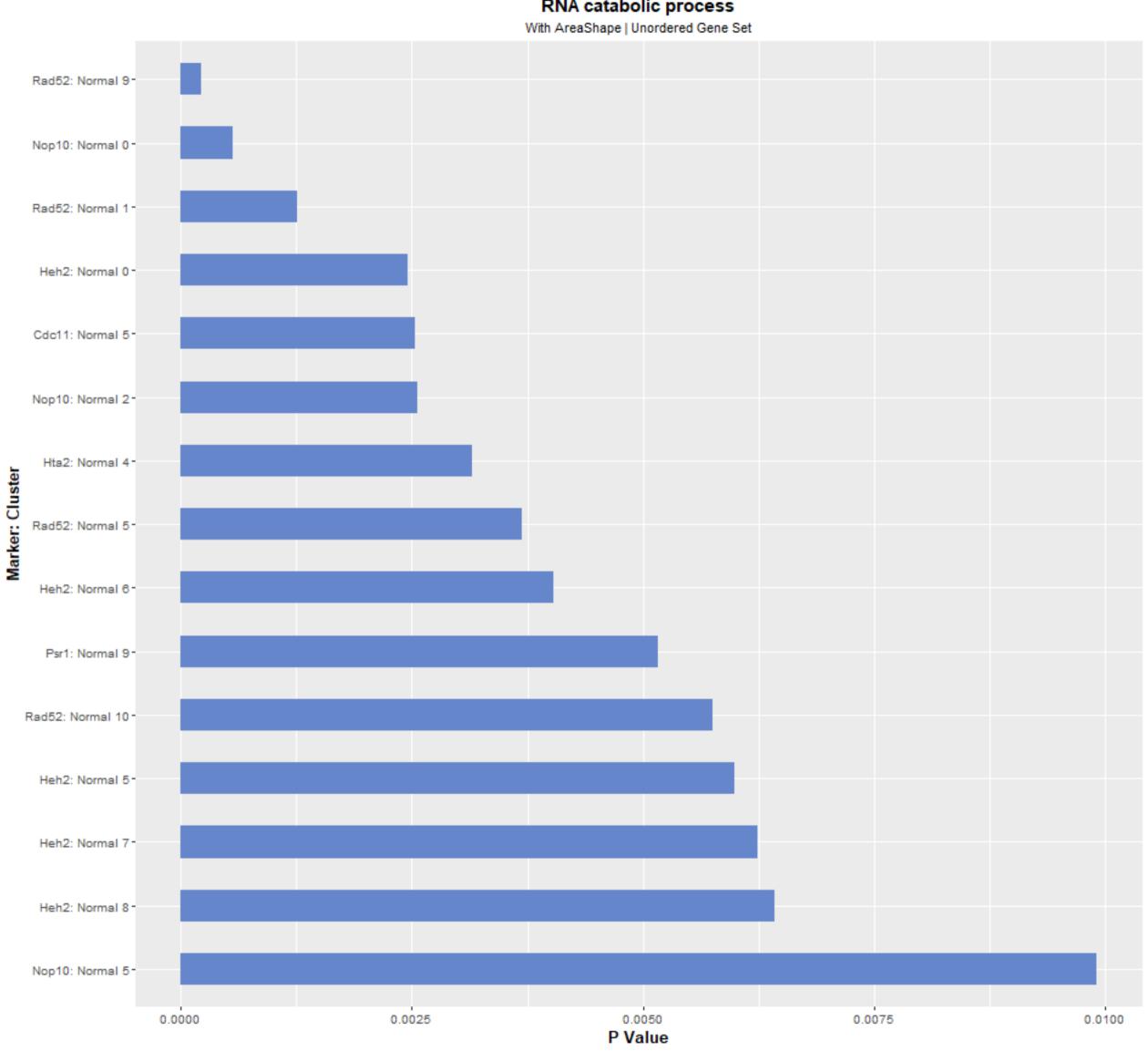
response to heat With AreaShape | Unordered Gene Set Marker: Cluster ... Ser ... Cluster ... Cl 0.004 0.000 0.002 0.006 0.008 P Value

ribosomal large subunit biogenesis With AreaShape | Unordered Gene Set Pil1: Normal 10 -Marker: Cluster Psr1: Normal 9 -0.0050 0.0000 0.0025 0.0075 P Value

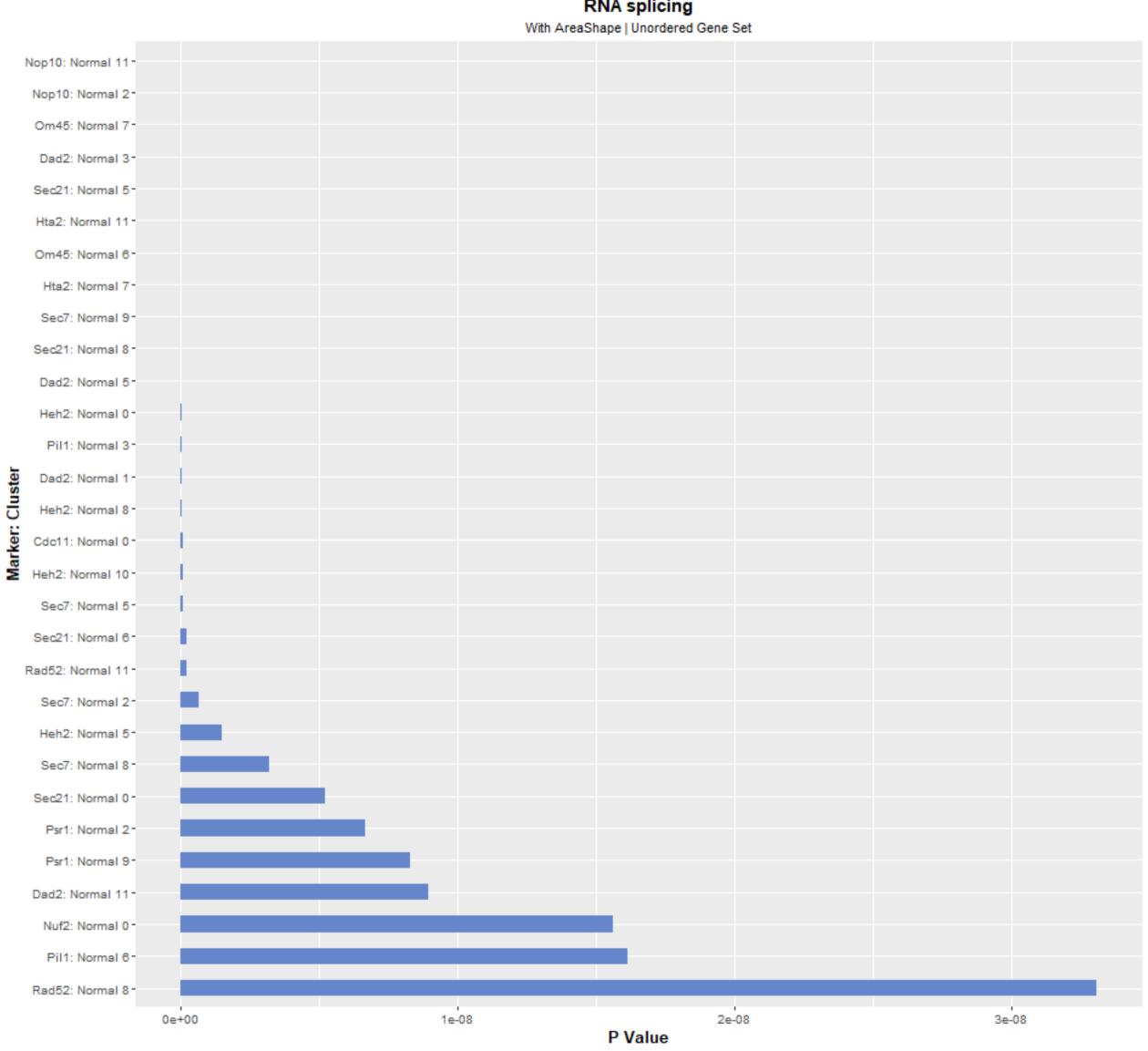
ribosomal subunit export from nucleus



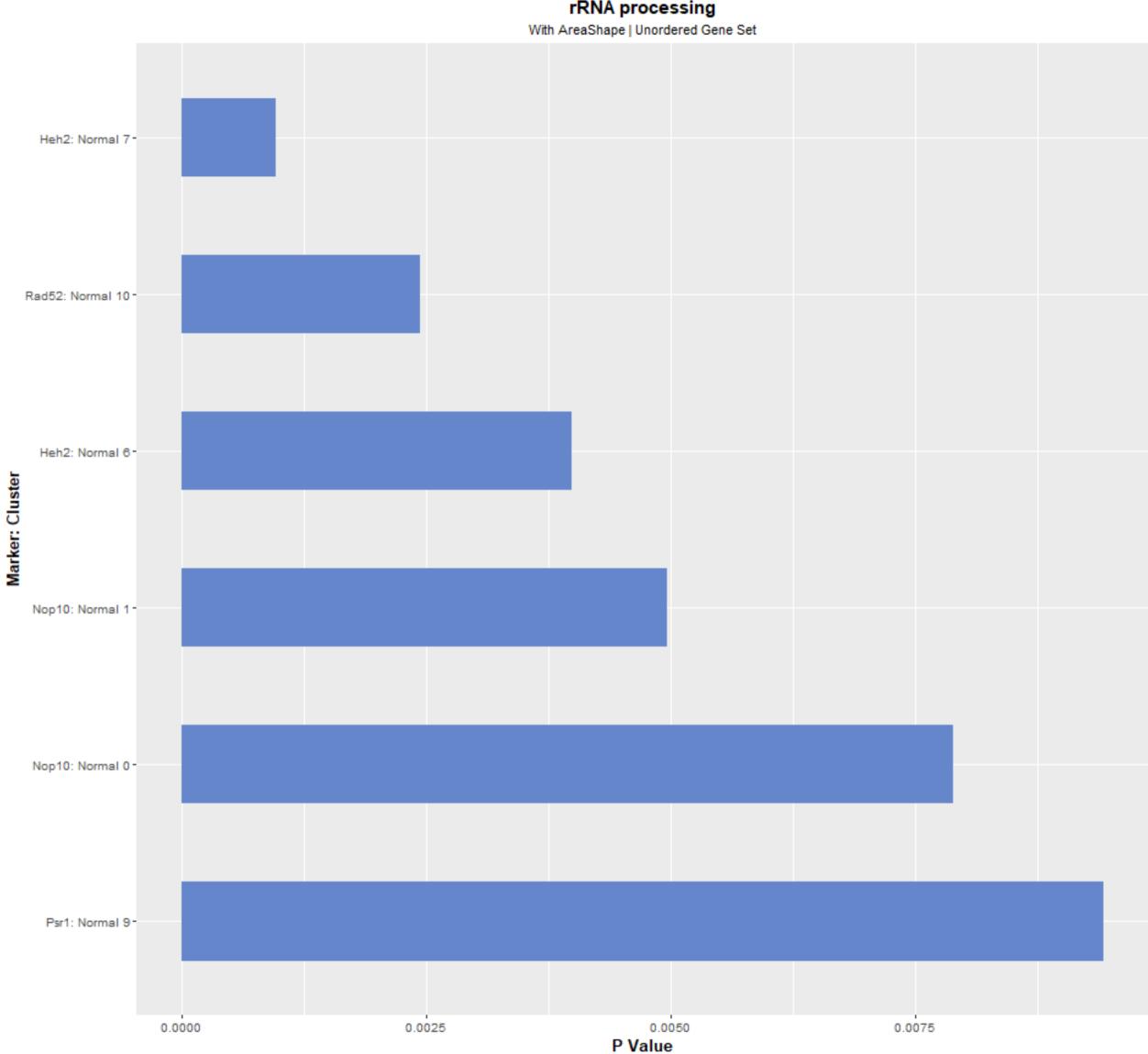
RNA catabolic process



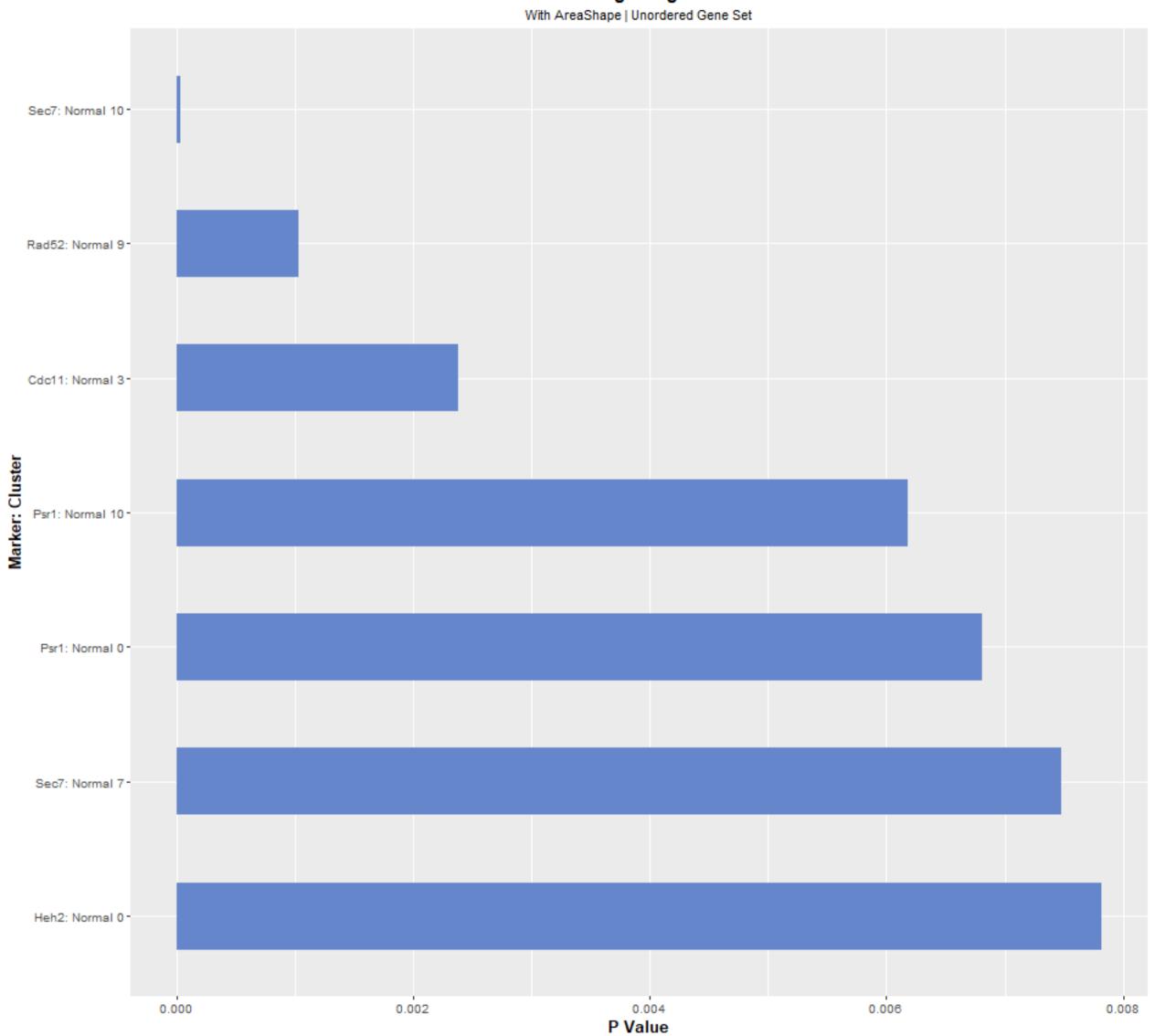
RNA splicing



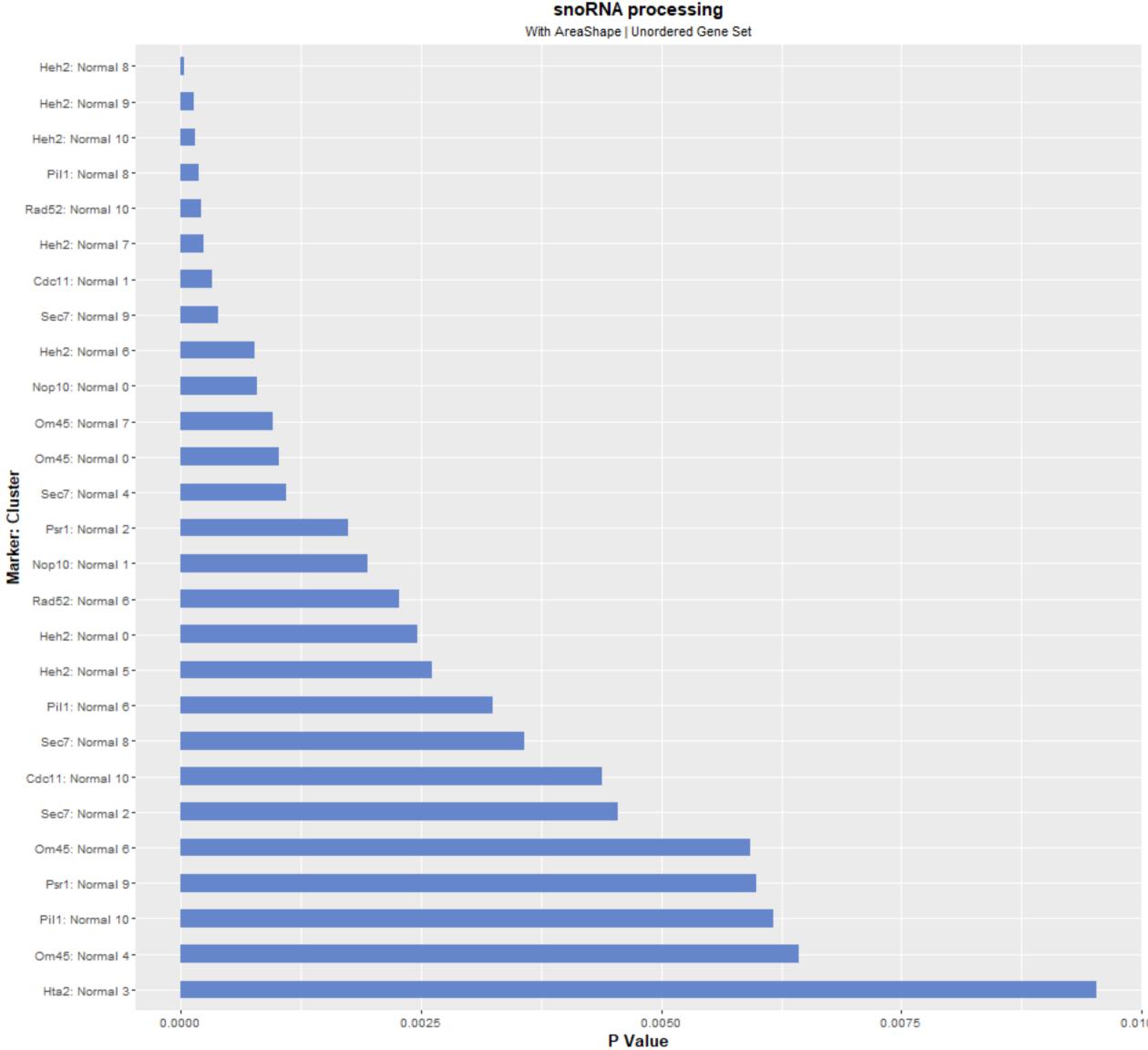
rRNA processing



signaling



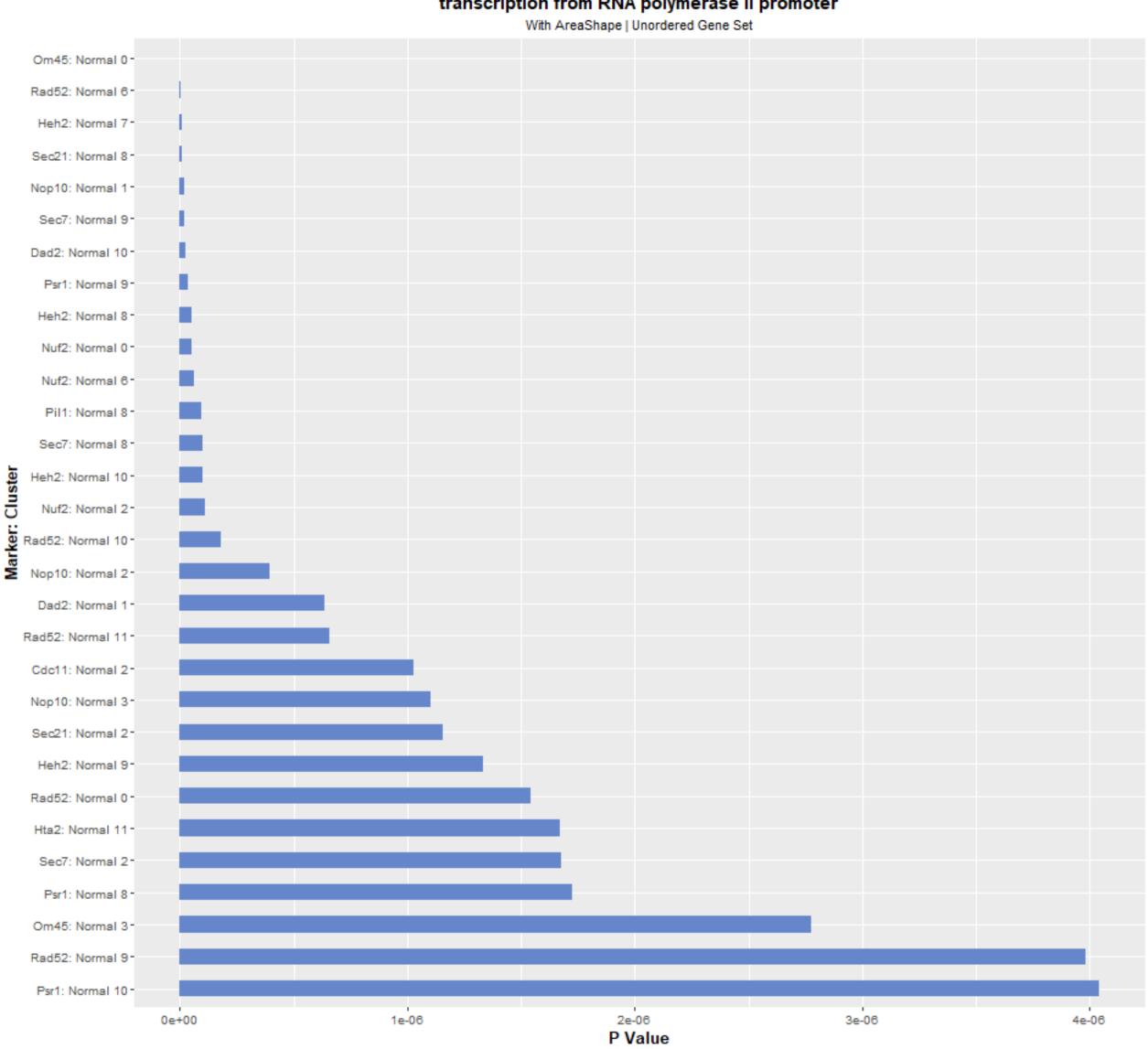
snoRNA processing



telomere organization With AreaShape | Unordered Gene Set Cdc11: Normal 5-Psr1: Normal 2 -Marker: Cluster: Heh2: Normal 11-Pil1: Normal 5-Heh2: Normal 41 0.010 0.0050 0.0000 0.0025 0.0075 P Value

transcription from RNA polymerase I promoter With AreaShape | Unordered Gene Set 0.002 0.004 0.006 0.000 P Value

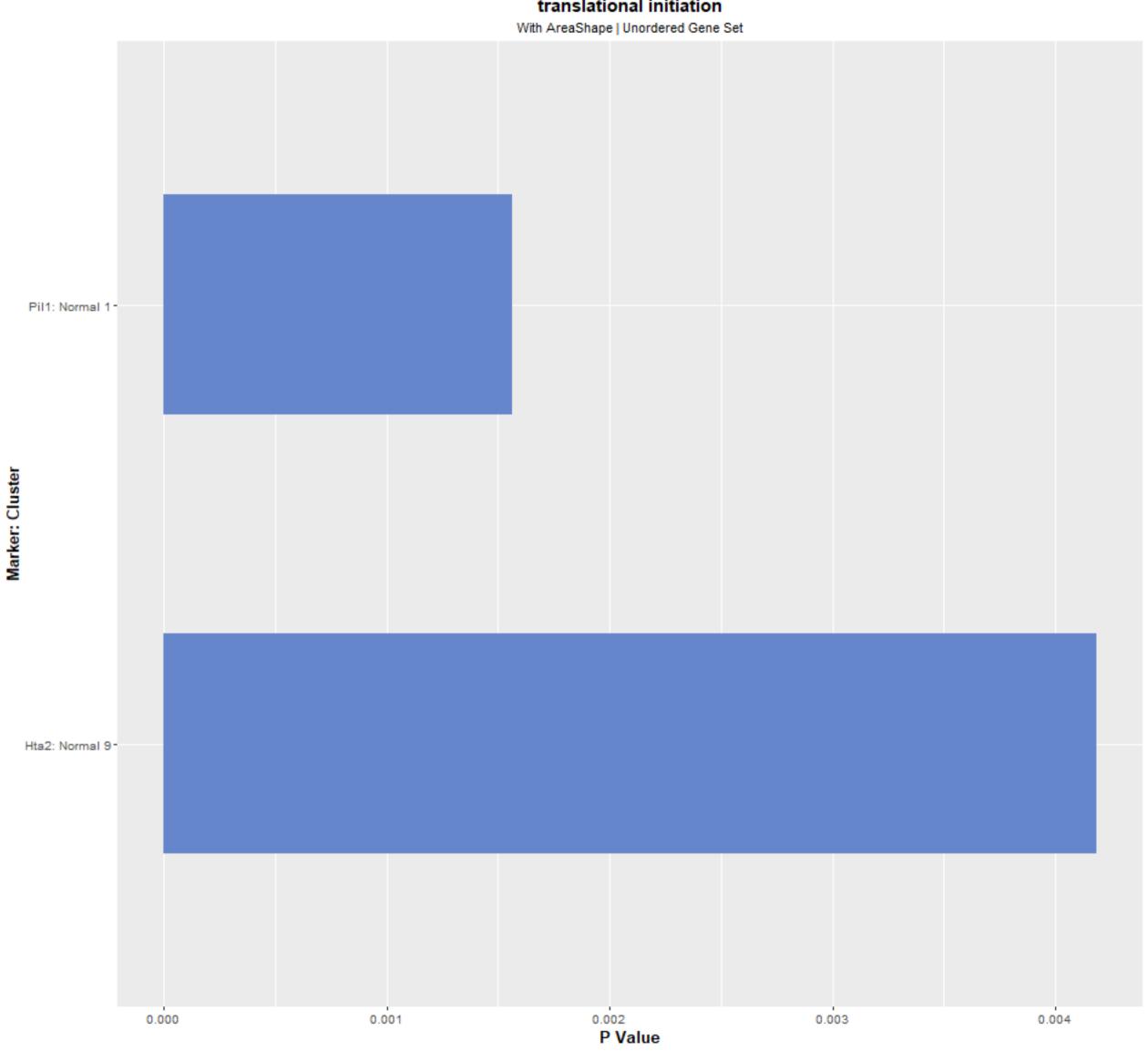
transcription from RNA polymerase II promoter



transcription from RNA polymerase III promoter With AreaShape | Unordered Gene Set Hta2: Normal 9 -Marker: Cluster: Heh2: Normal 7 -Hta2: Normal 4-0.002 0.000 0.001 0.003 0.004 P Value

translational elongation With AreaShape | Unordered Gene Set Marker: Cluster 0.002 0.004 0.001 0.003 0.000 P Value

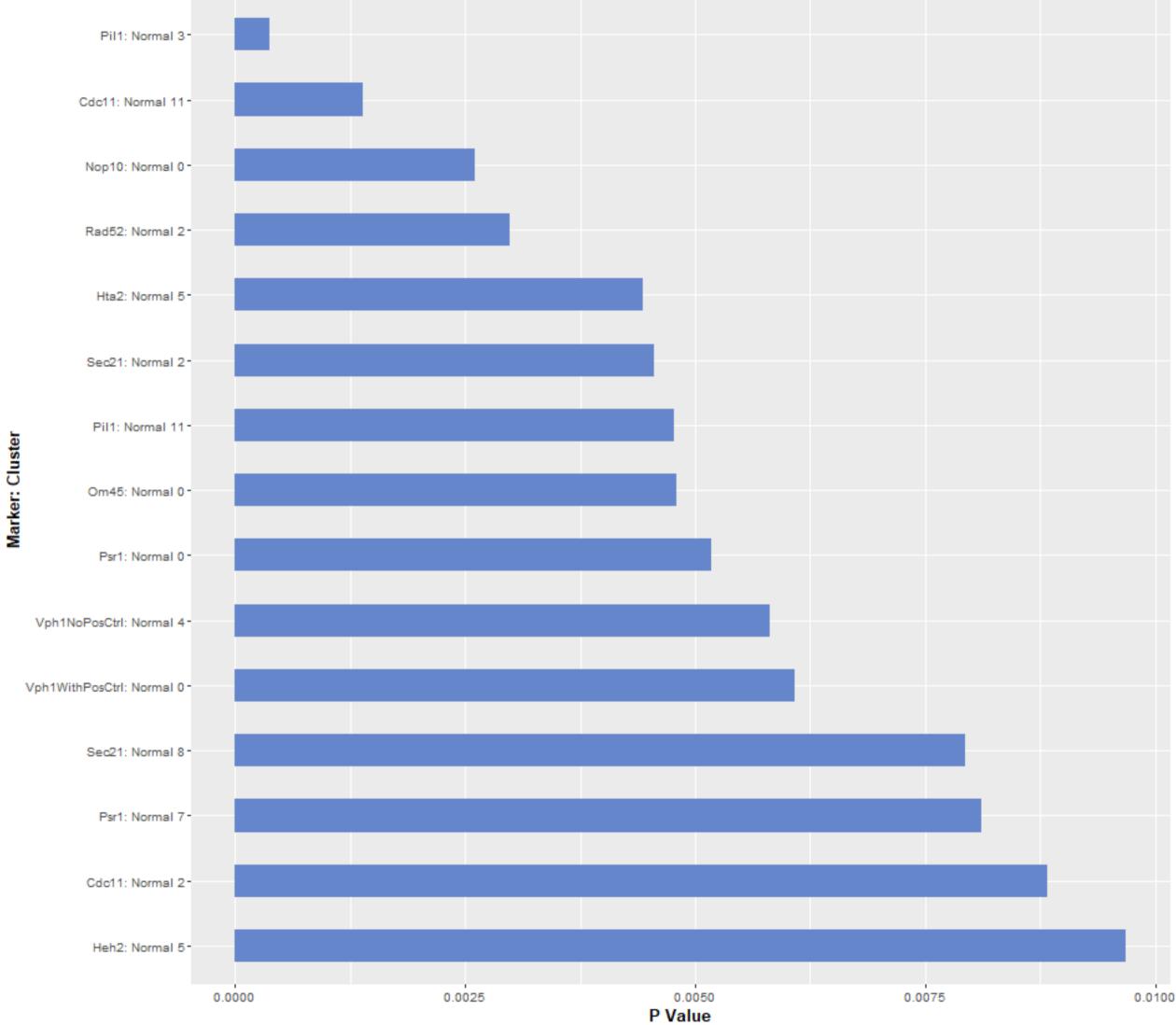
translational initiation



transposition With AreaShape | Unordered Gene Set Hta2: Normal 0 -Heh2: Normal 11 -Heh2: Normal 7 -Cdc11: Normal 3-Marker: Cluster Cdc11: Normal 5-Rad52: Normal 5 -Vph1NoPosCtrl: Normal 5 Vph1WithPosCtrl: Normal 5 0.0025 0.0050 0.0000 0.0075 P Value

tRNA aminoacylation for protein translation With AreaShape | Unordered Gene Set Om45: Normal 6 -Heh2: Normal 9 -Marker: Cluster: Heh2: Normal 8 -Pil1: Normal 8 -Om45: Normal 9 -0.002 0.004 0.006 0.000 P Value

vacuole organization With AreaShape | Unordered Gene Set Pil1: Normal 3-Cdc11: Normal 111



vesicle organization

