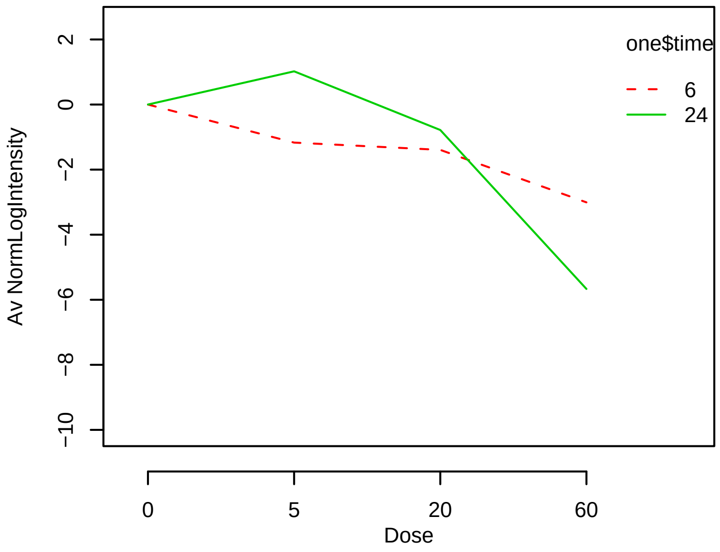
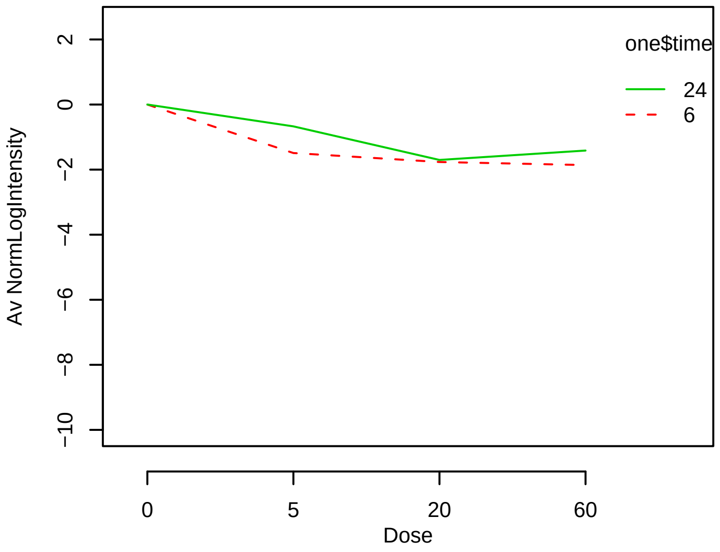
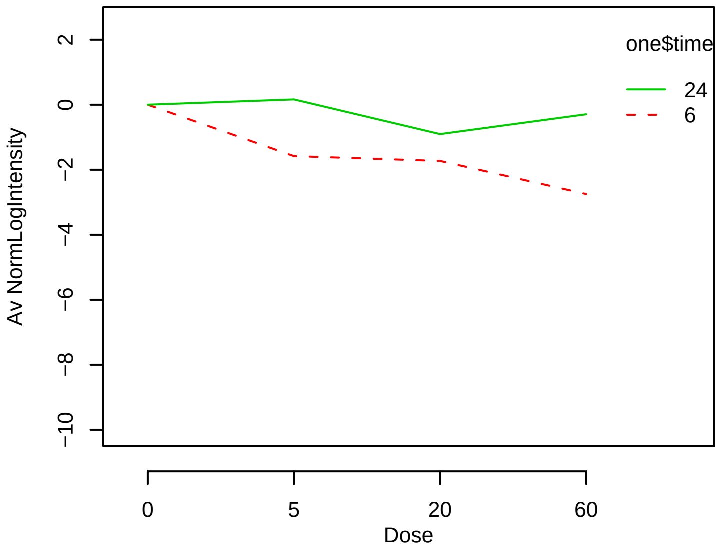
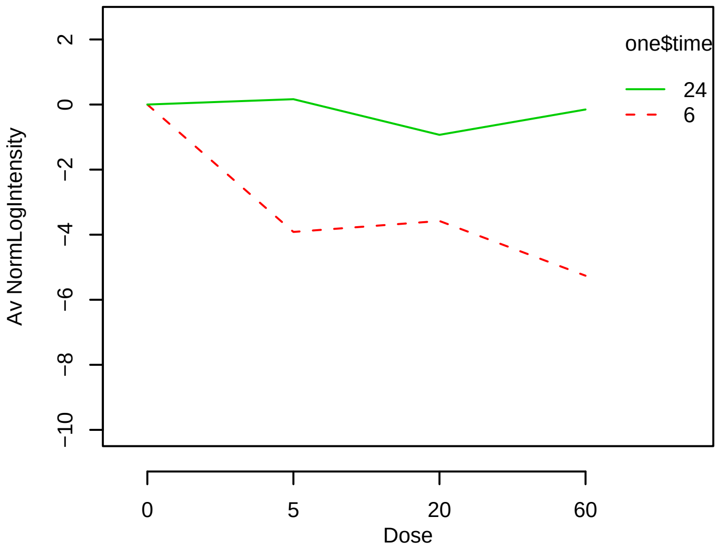
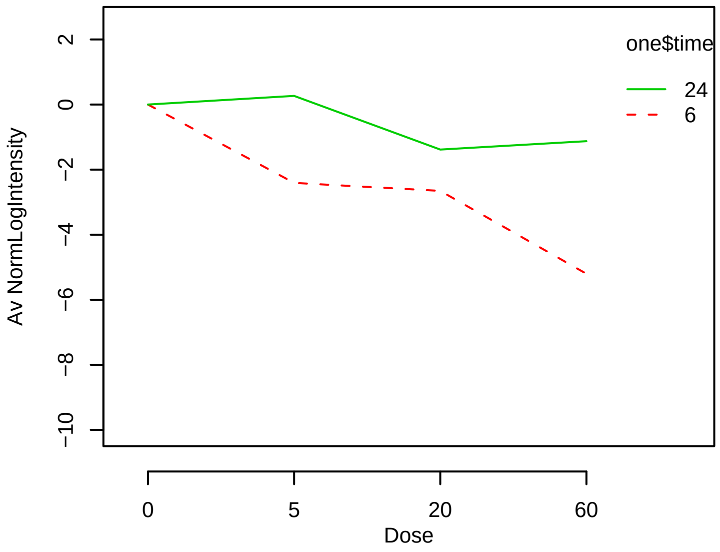
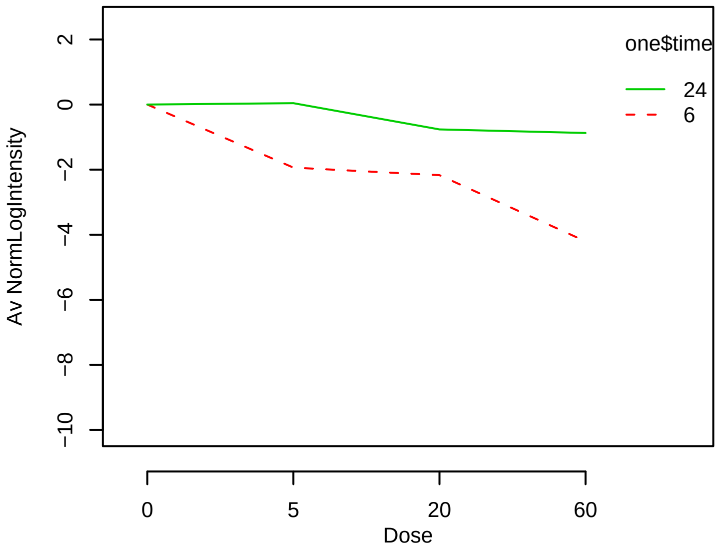

GO_0000018 : regulation of DNA recombination


GO_0000038 : very−long−chain fatty acid metabolism

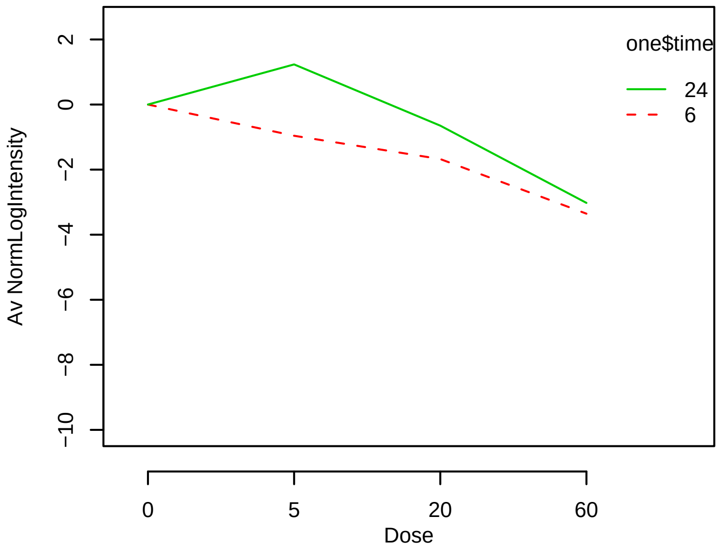

GO_0000041 : transition metal ion transport


GO_0000045 : autophagic vacuole formation

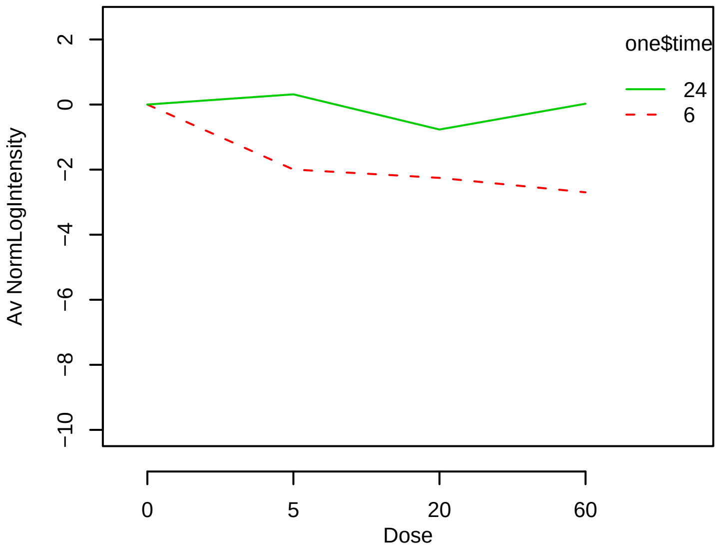

GO_0000050 : urea cycle


GO_0000051 : urea cycle intermediate metabolism

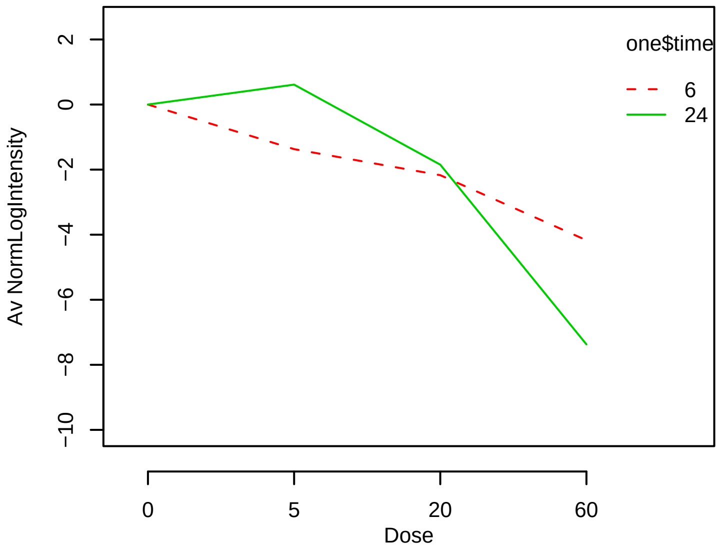
GO_0000059 : protein import into nucleus\, docking



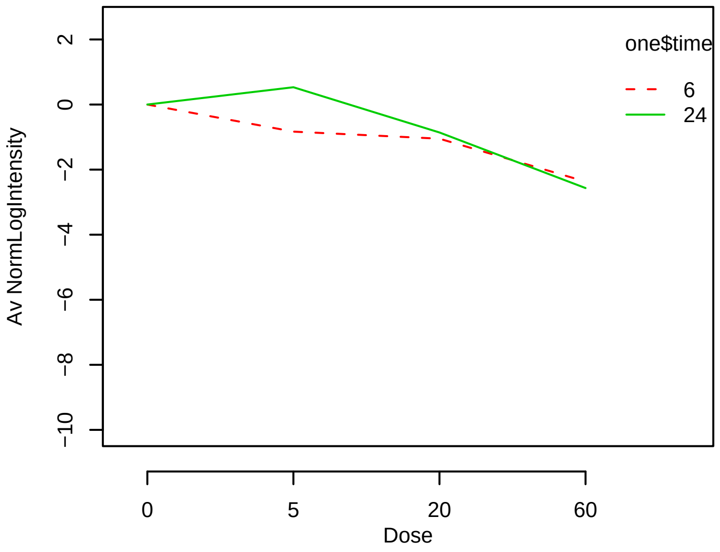
GO_0000060 : protein import into nucleus\, translocation



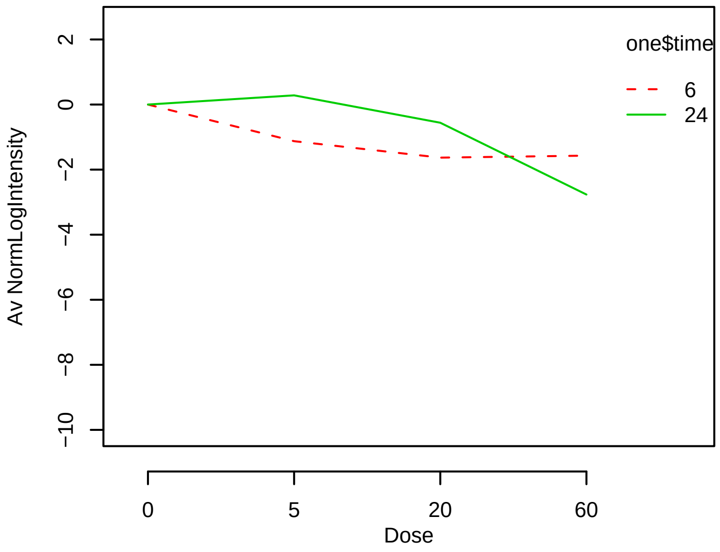
GO_0000070 : mitotic sister chromatid segregation



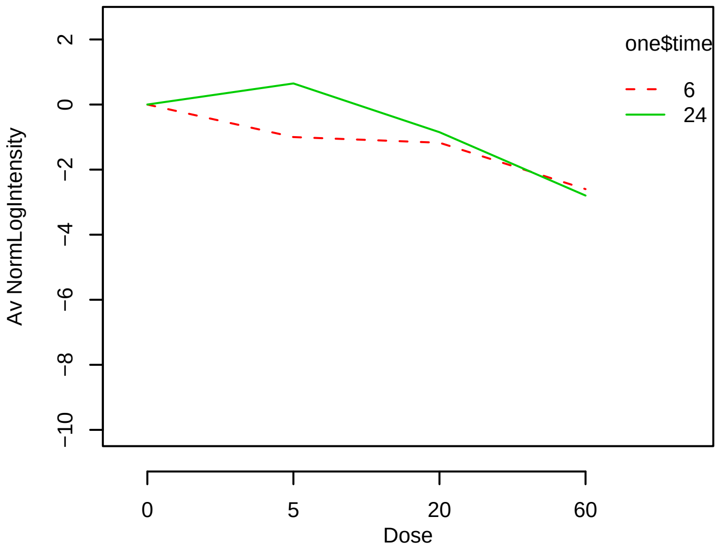
GO_0000075 : cell cycle checkpoint

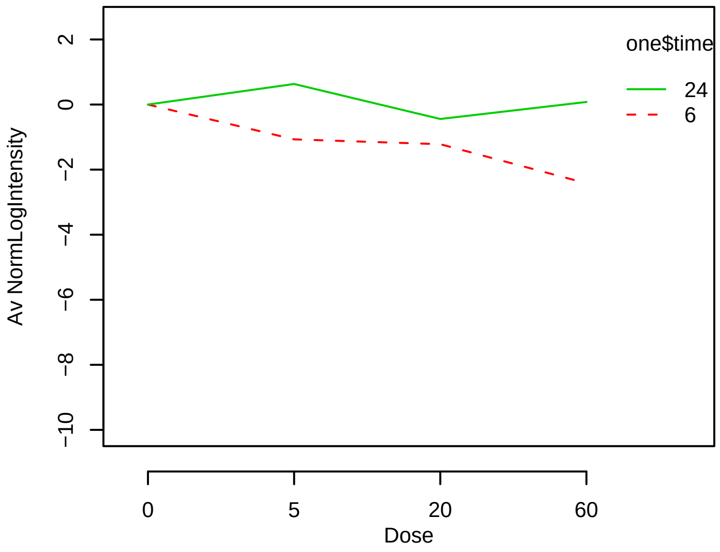


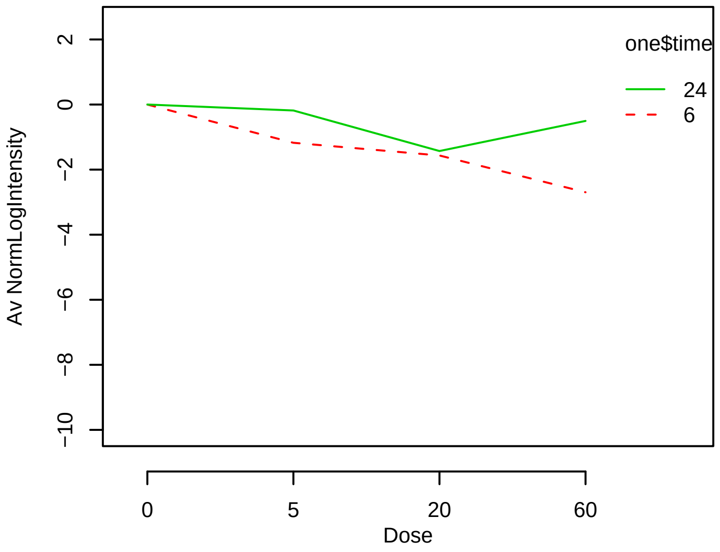
GO_0000076 : DNA replication checkpoint

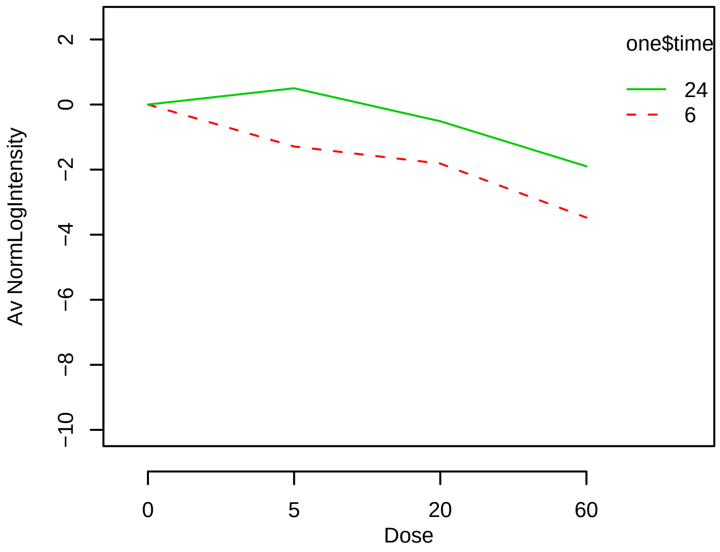


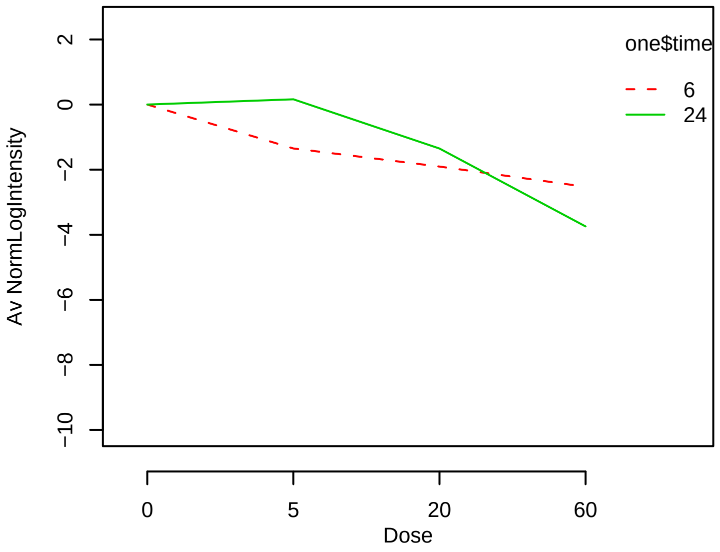
GO_0000077 : DNA damage checkpoint

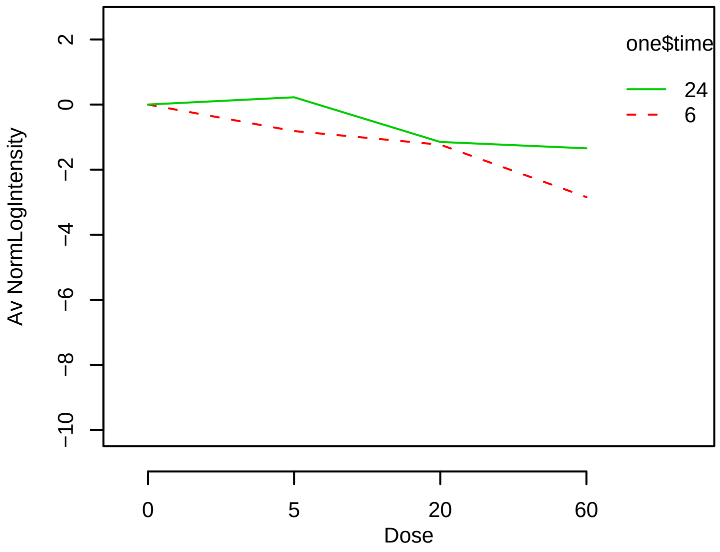


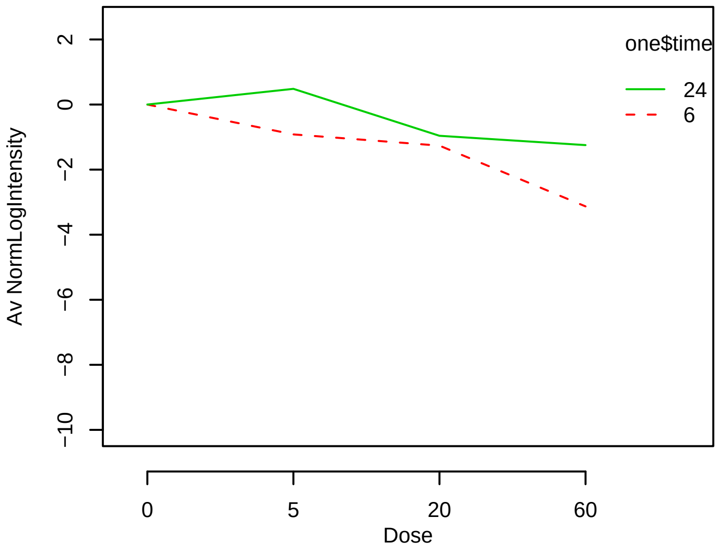

GO_0000079 : regulation of cyclin−dependent protein kinase

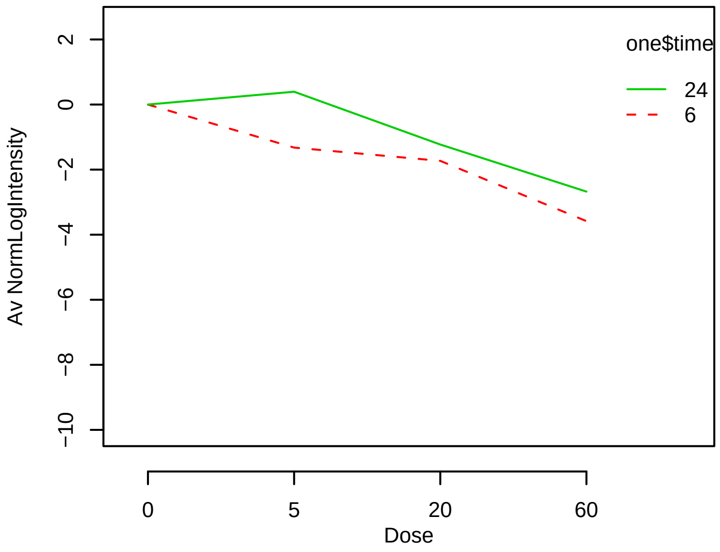

GO_0000080 : G1 phase of mitotic cell cycle

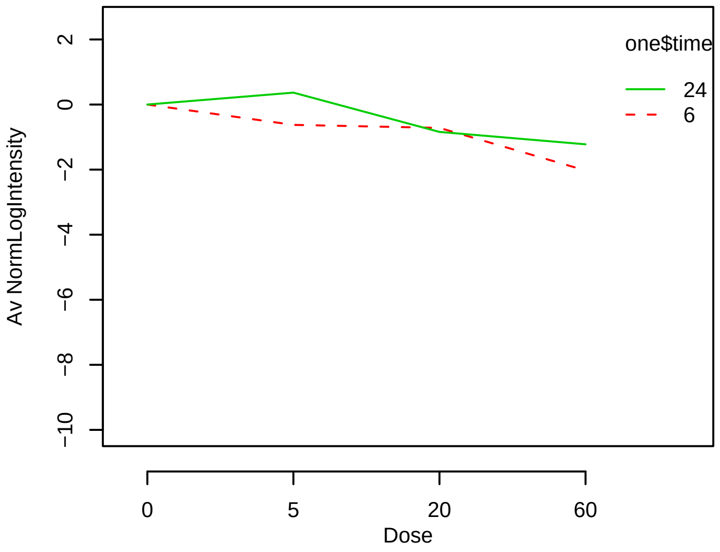

GO_0000082 : G1/S transition of mitotic cell cycle

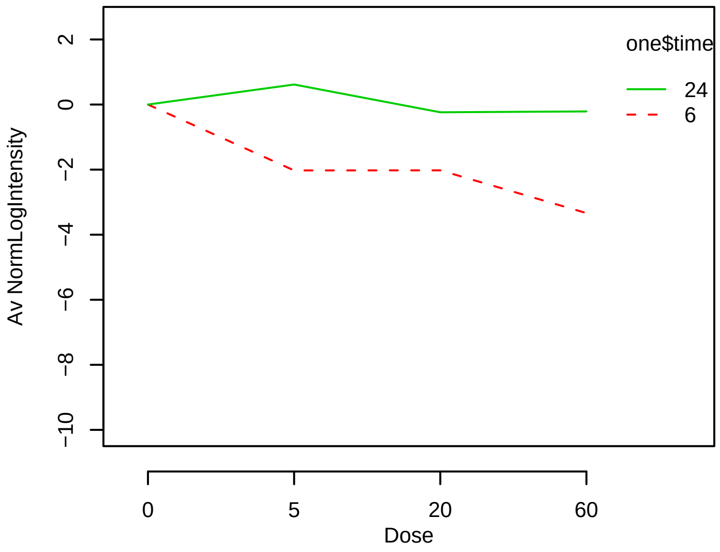

GO_0000084 : S phase of mitotic cell cycle

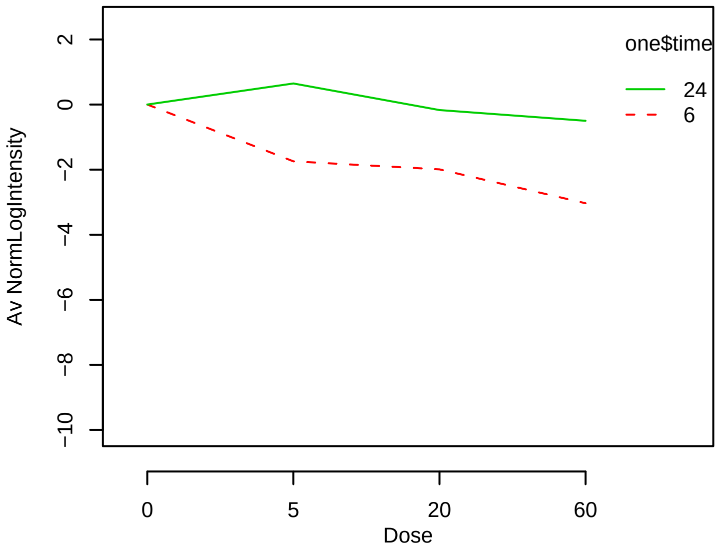

GO_0000085 : G2 phase of mitotic cell cycle

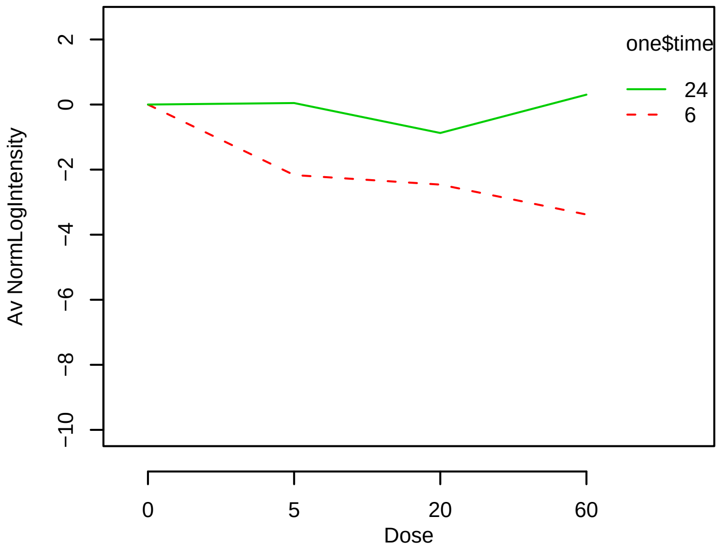

GO_0000086 : G2/M transition of mitotic cell cycle

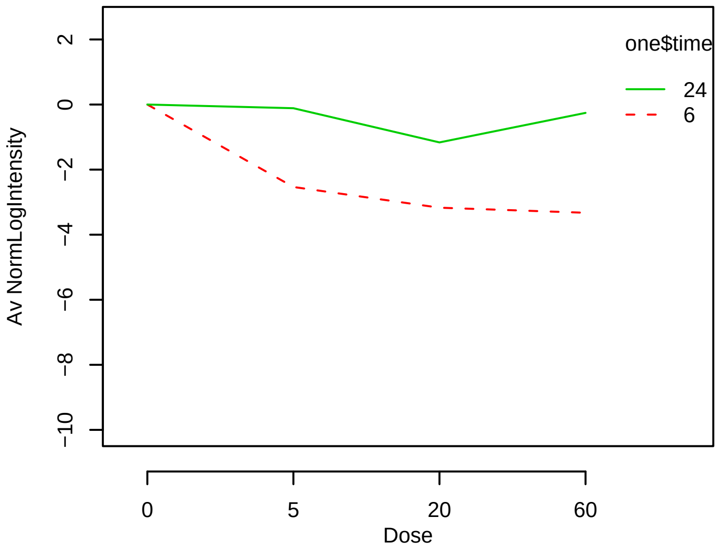

GO_0000087 : M phase of mitotic cell cycle


GO_0000090 : mitotic anaphase

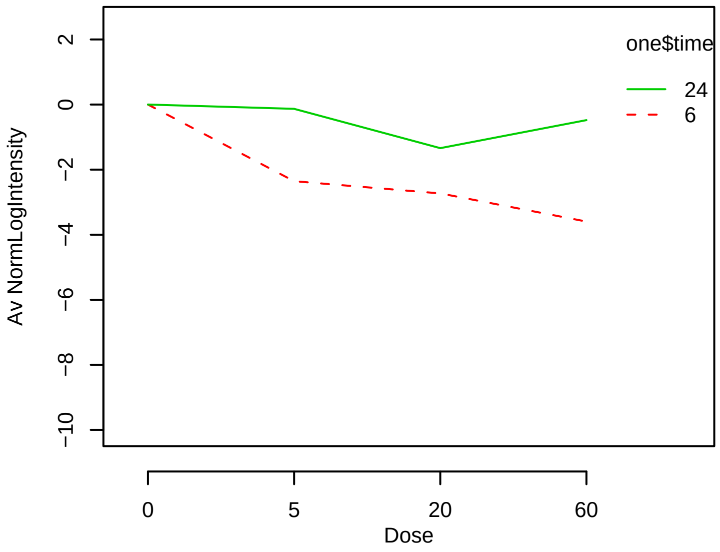

GO_0000096 : sulfur amino acid metabolism


GO_0000097 : sulfur amino acid biosynthesis

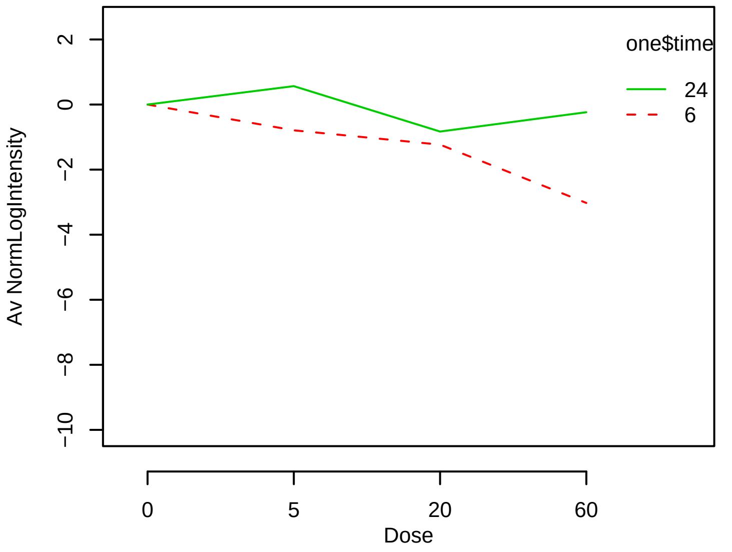

GO_0000122 : negative regulation of transcription from RNA


_0000160 : two−component signal transduction system (pho

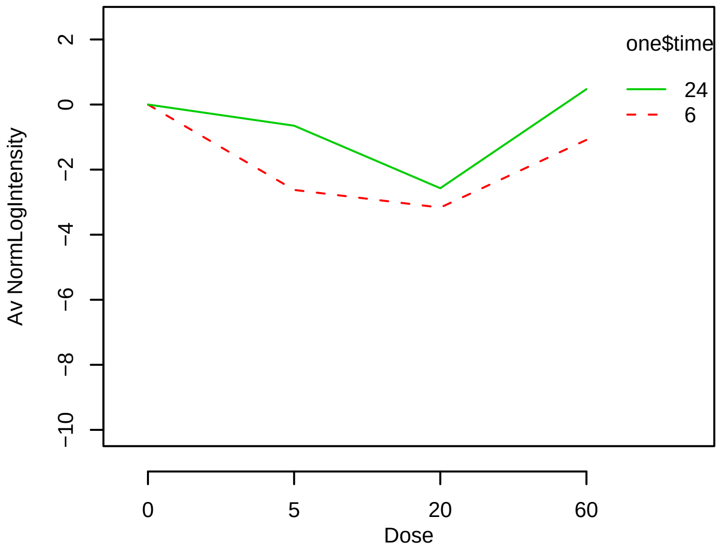
GO_0000165 : MAPKKK cascade



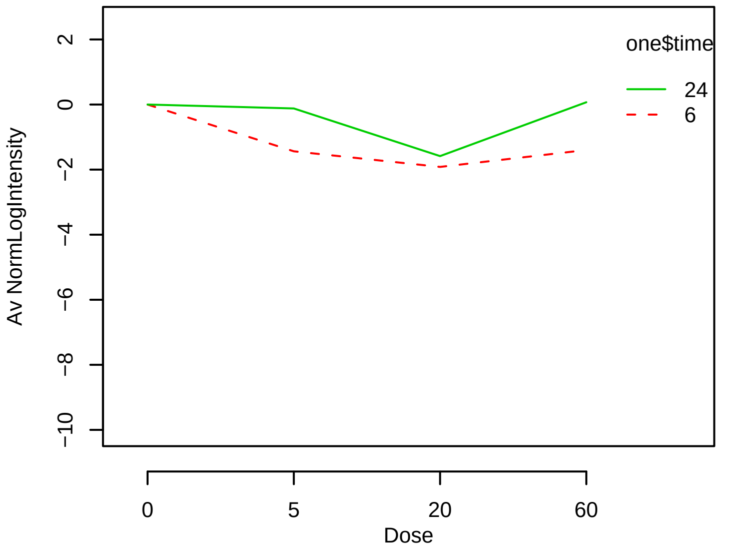
GO_0000184 : mRNA catabolism\, nonsense−mediated dec



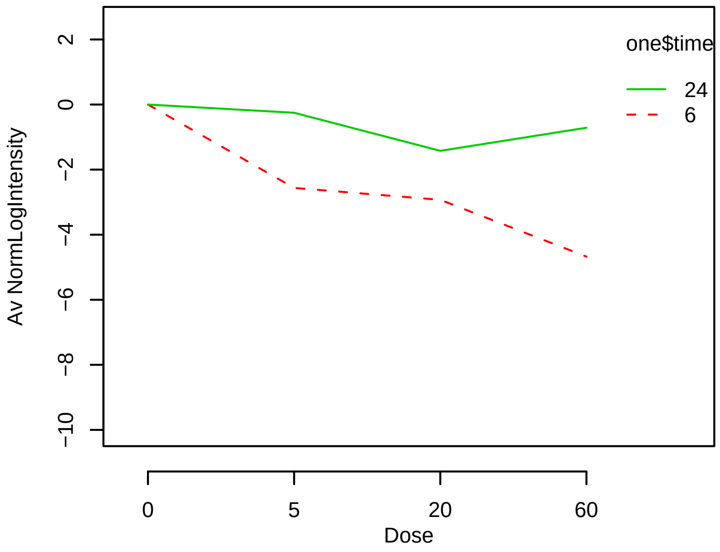
GO_0000185 : activation of MAPKKK activity



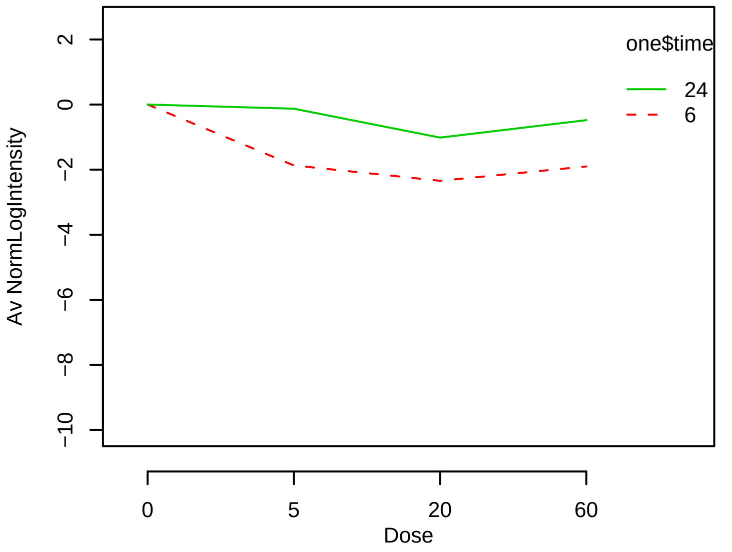
GO_0000186 : activation of MAPKK activity



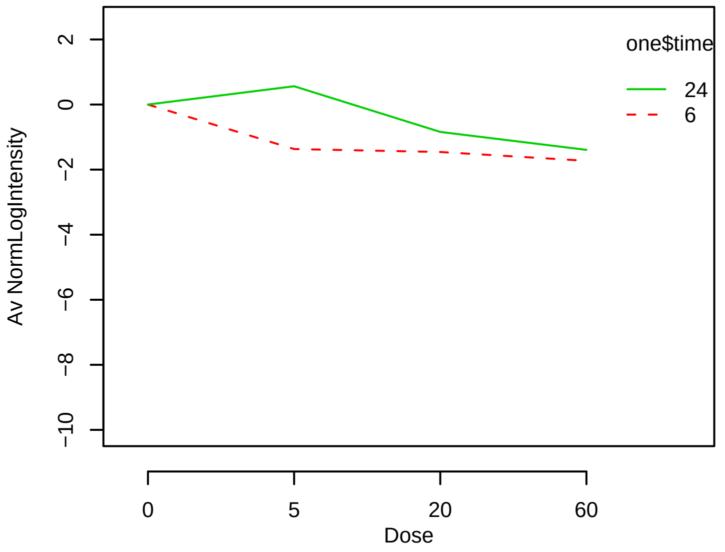
GO_0000187 : activation of MAPK activity



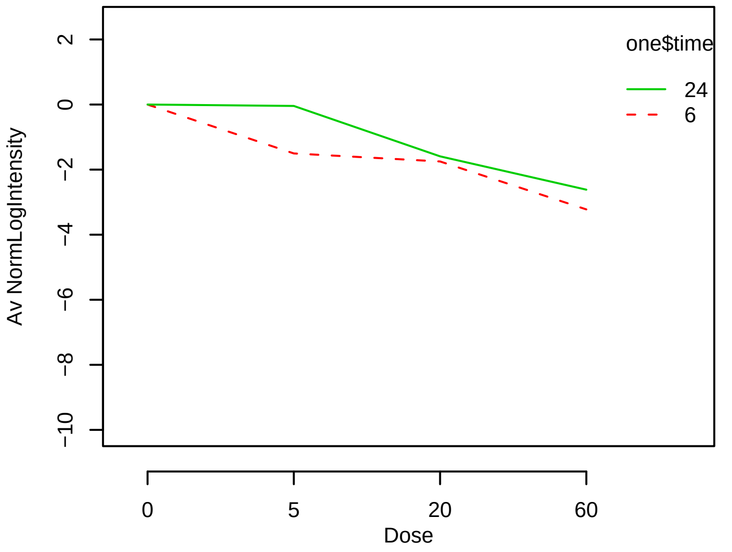
GO_0000188 : inactivation of MAPK activity



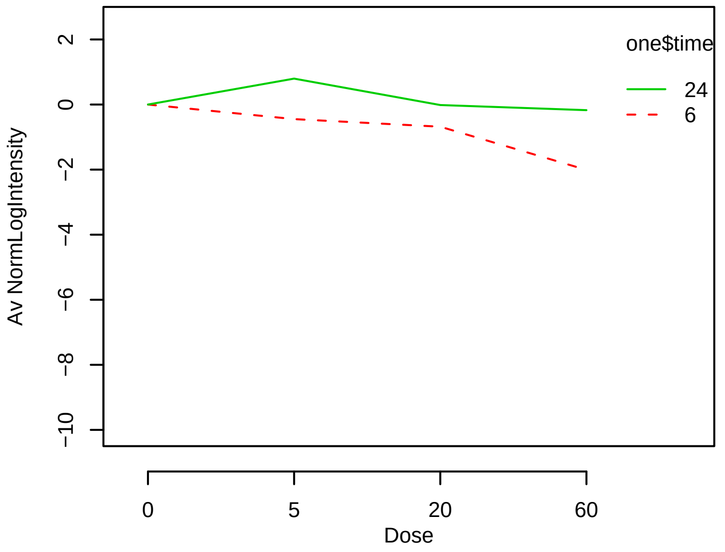
GO_0000209 : protein polyubiquitination



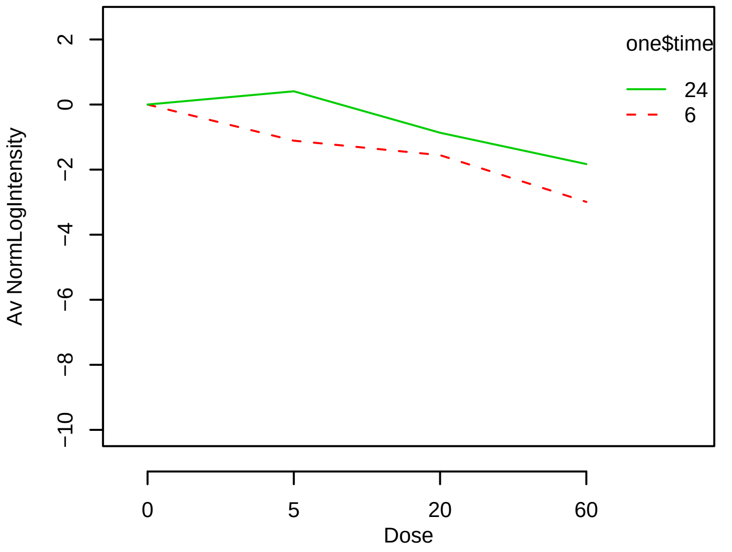
O_0000226 : microtubule cytoskeleton organization and biog



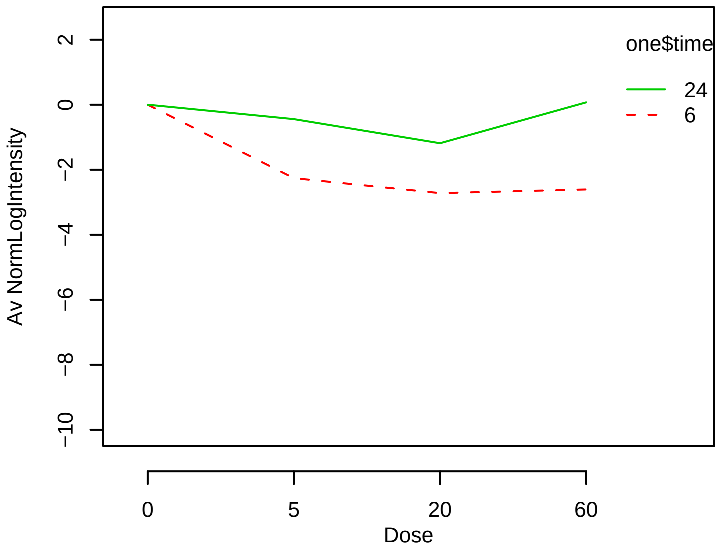
GO_0000244 : assembly of spliceosomal tri−snRNP



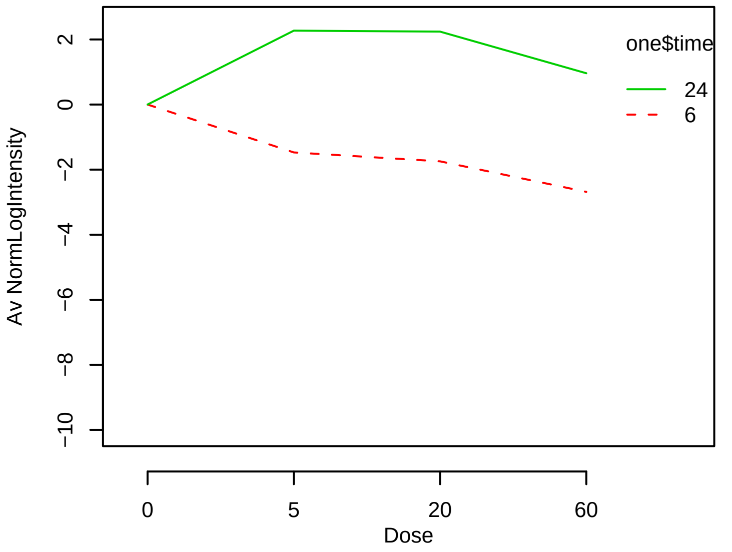
GO_0000245 : spliceosome assembly



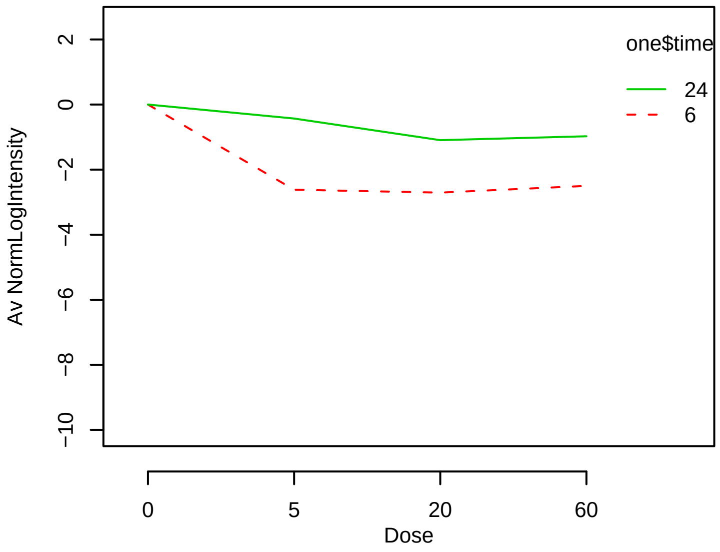
GO_0000270 : peptidoglycan metabolism



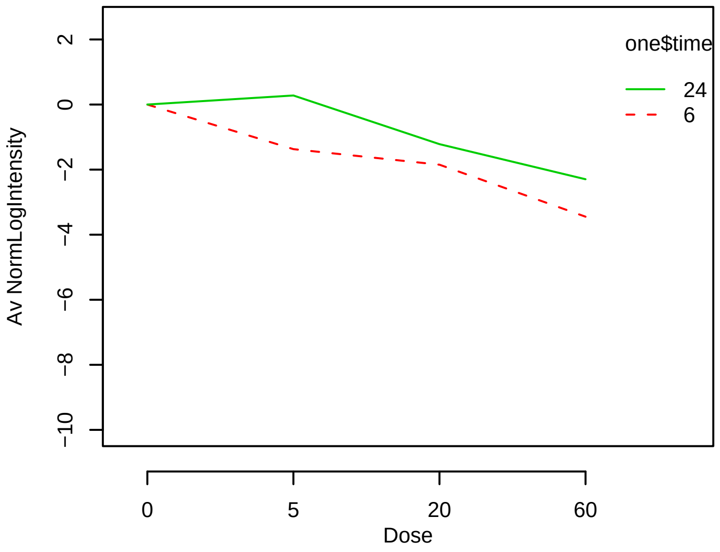
GO_0000271 : polysaccharide biosynthesis



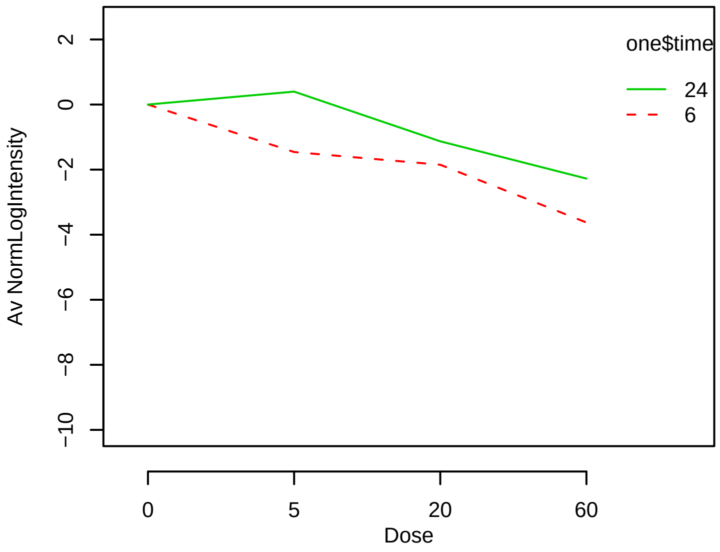
GO_0000272 : polysaccharide catabolism



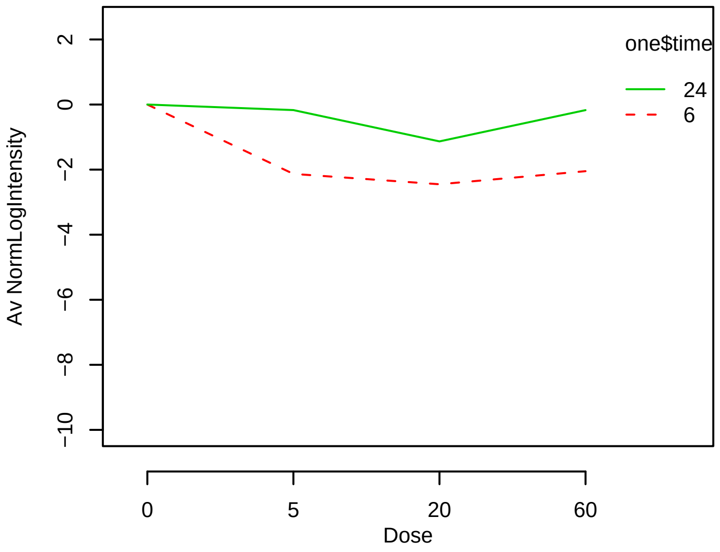
GO_0000278 : mitotic cell cycle



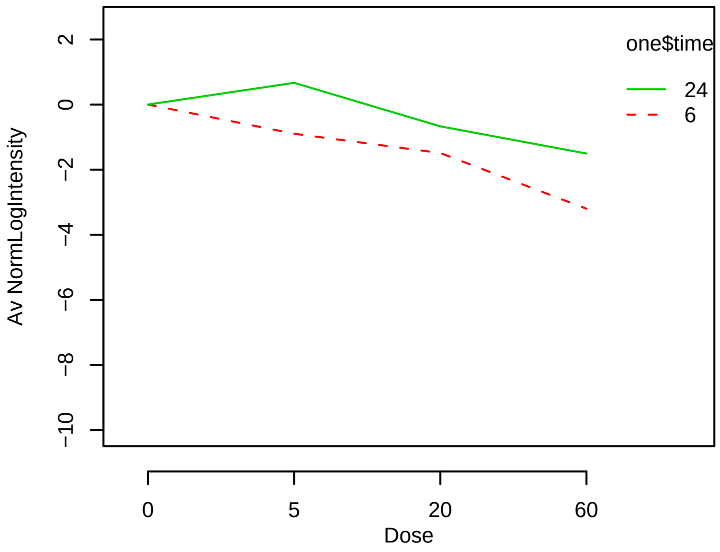
GO_0000279 : M phase



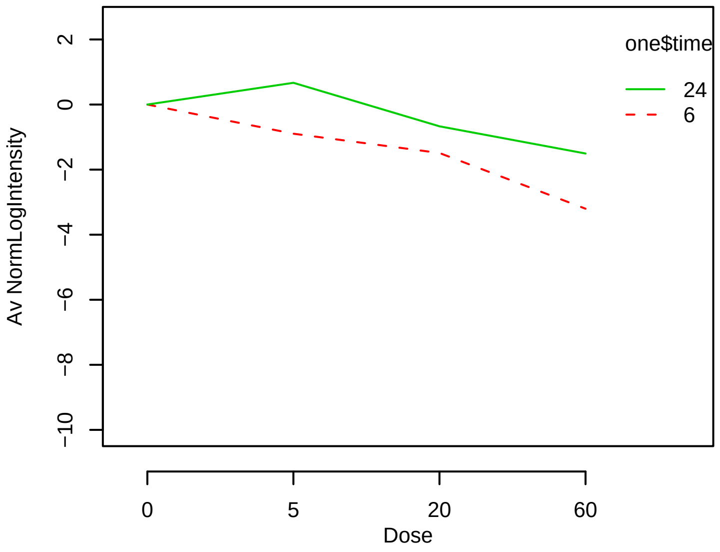
GO_0000302 : response to reactive oxygen species

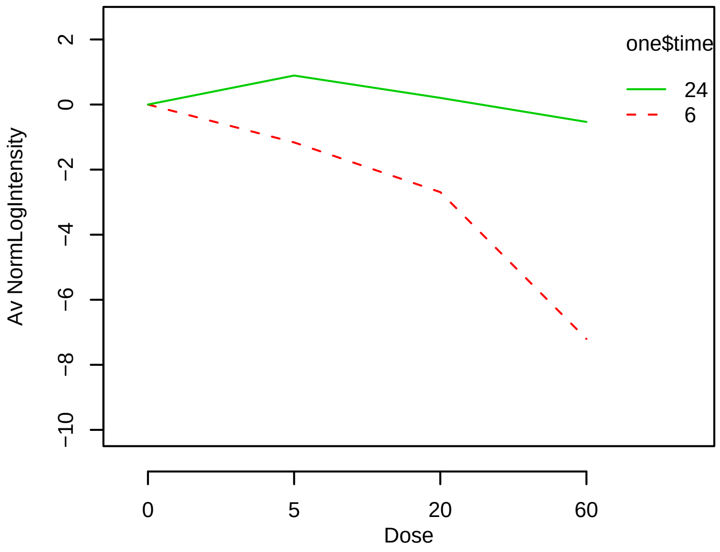


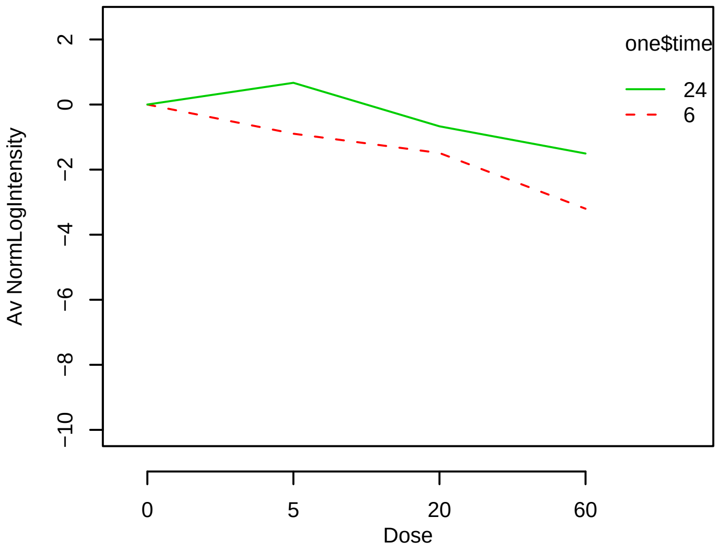
GO_0000375 : RNA splicing\, via transesterification reactio

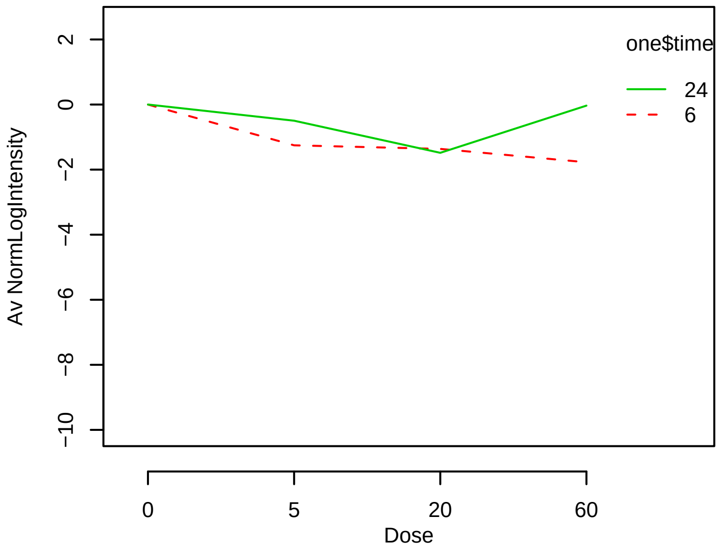


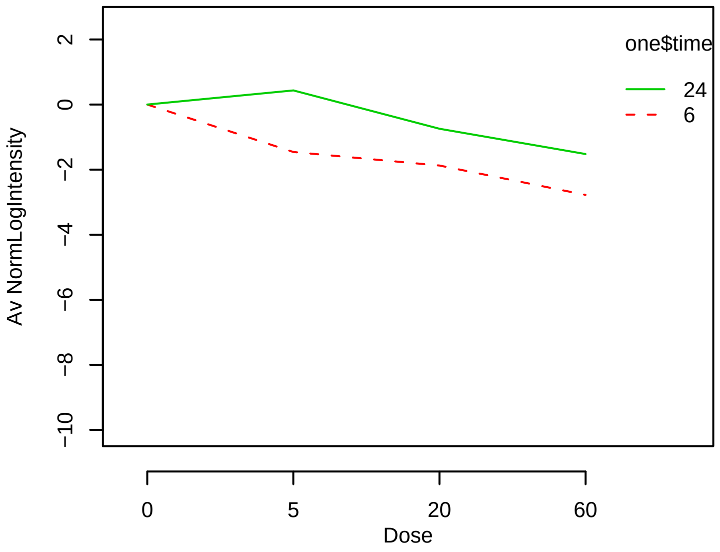
GO_0000377 : RNA splicing\, via transesterification reaction

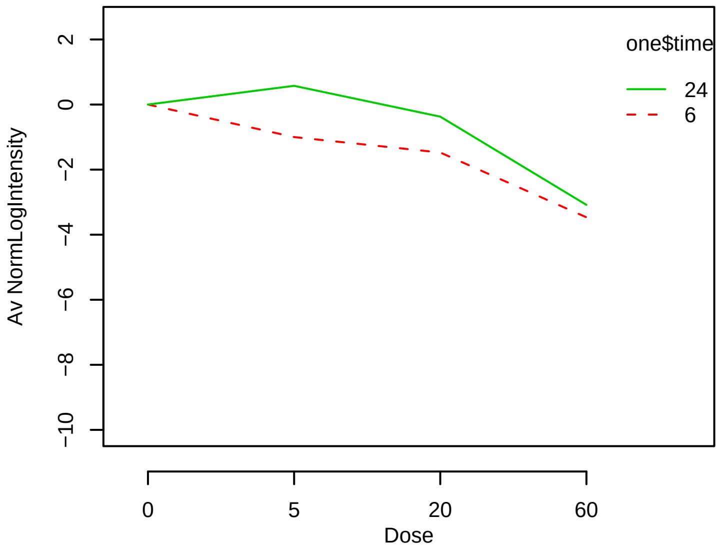


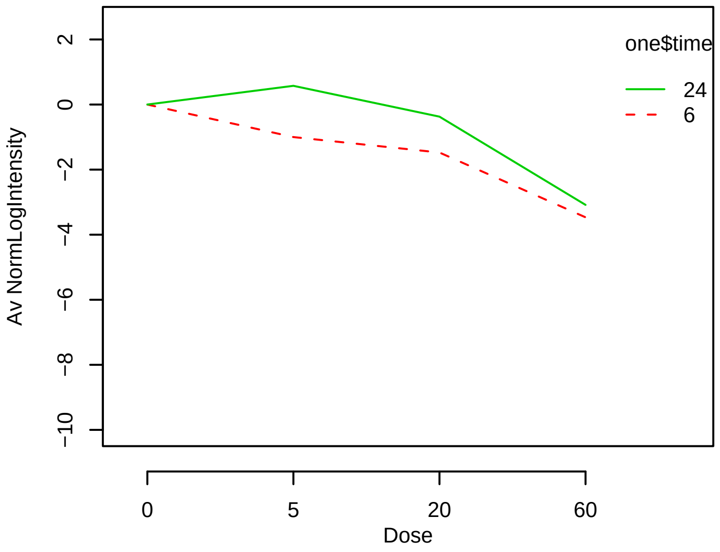

GO_0000387 : spliceosomal snRNP biogenesis

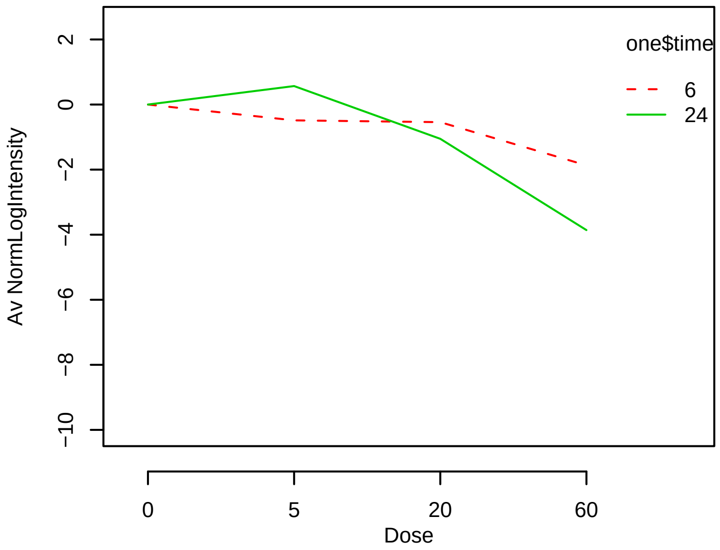

GO_0000398 : nuclear mRNA splicing\, via spliceosome

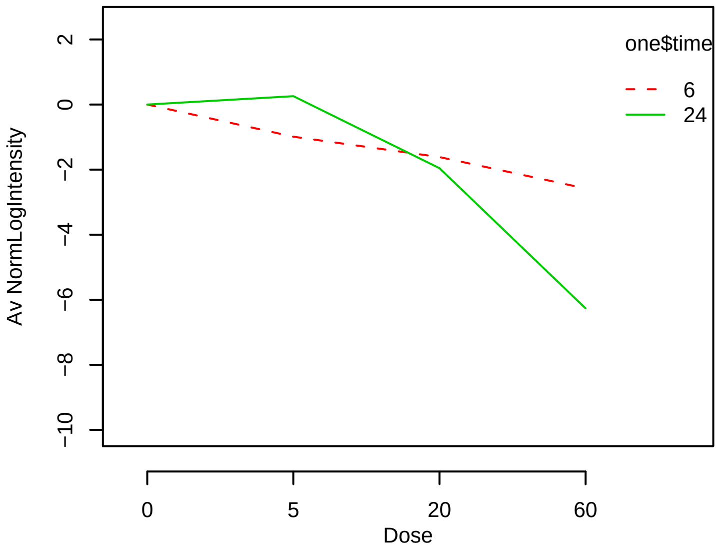

GO_0000578 : embryonic axis specification

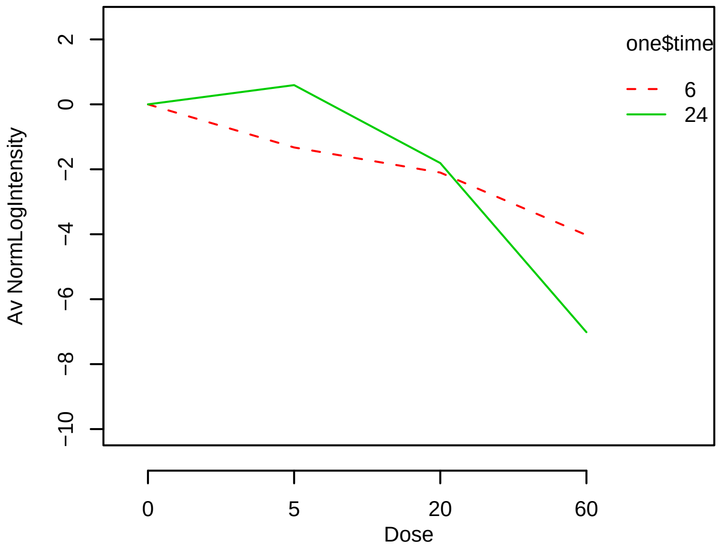

GO_0000723 : telomere maintenance

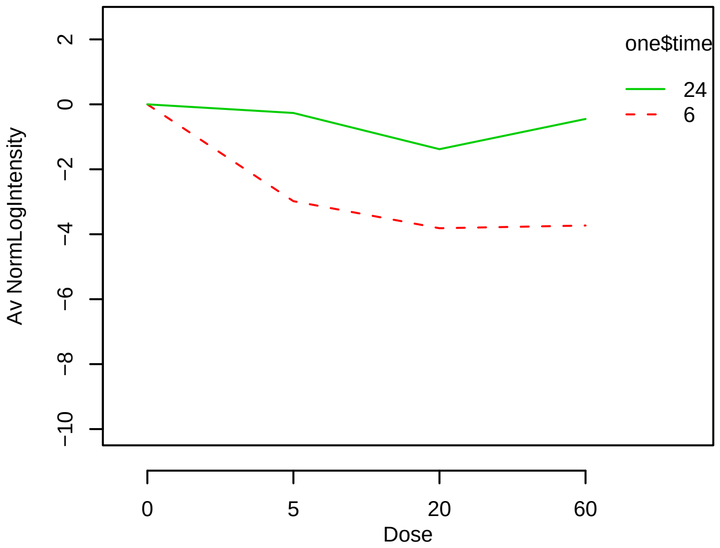

O_0000724 : double−strand break repair via homologous rec

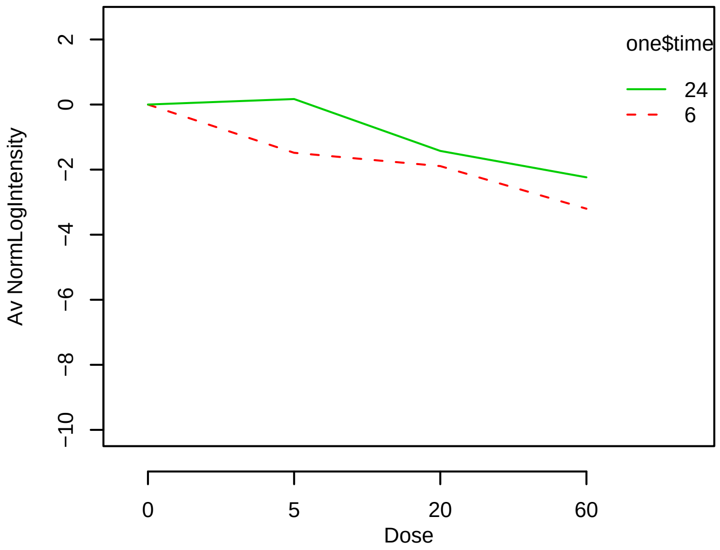

GO_0000725 : recombinational repair

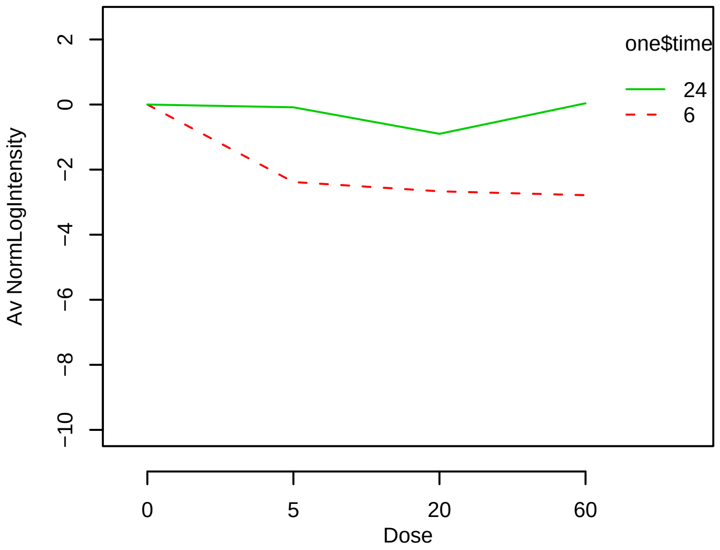

GO_0000726 : non−recombinational repair


GO_0000731 : DNA synthesis during DNA repair

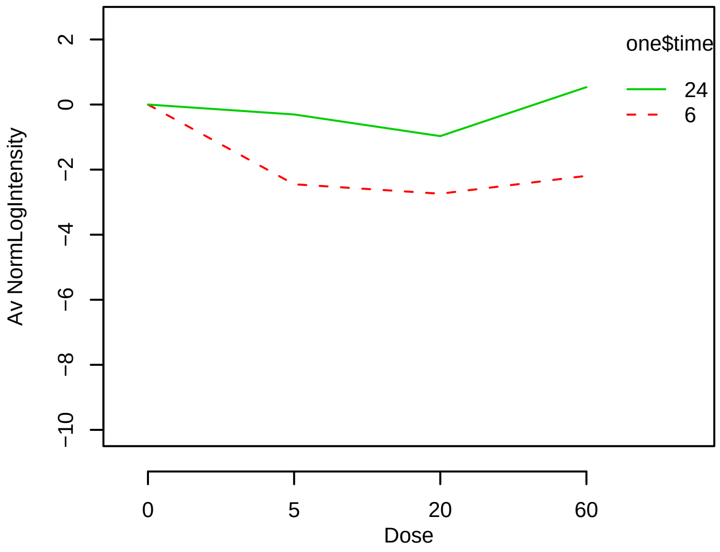

GO_0000819 : sister chromatid segregation


GO_0000904 : cellular morphogenesis during differentiatio

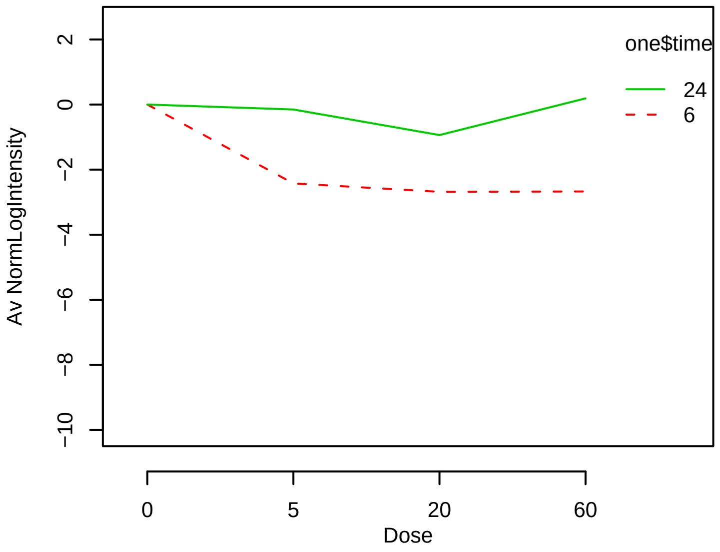

GO_0000910 : cytokinesis


GO_0001501 : skeletal development

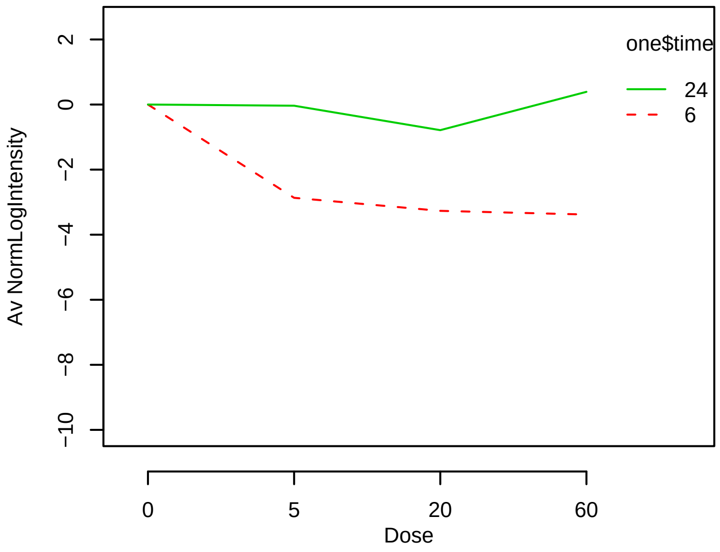
GO_0001502 : cartilage condensation



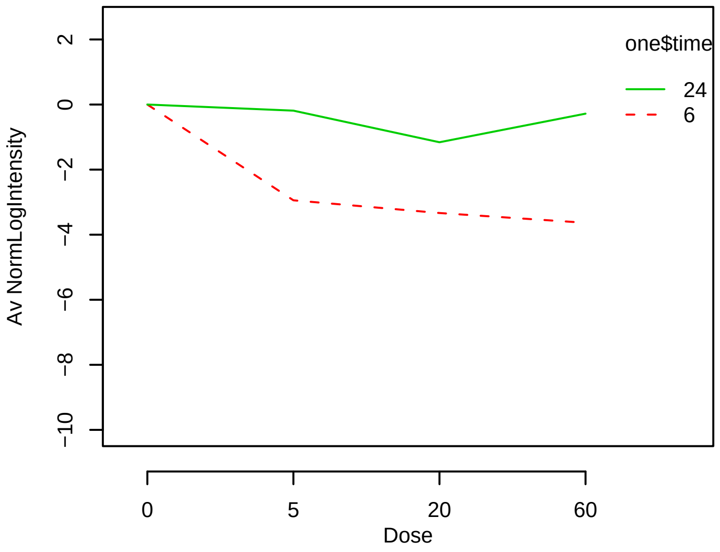
GO_0001503 : ossification



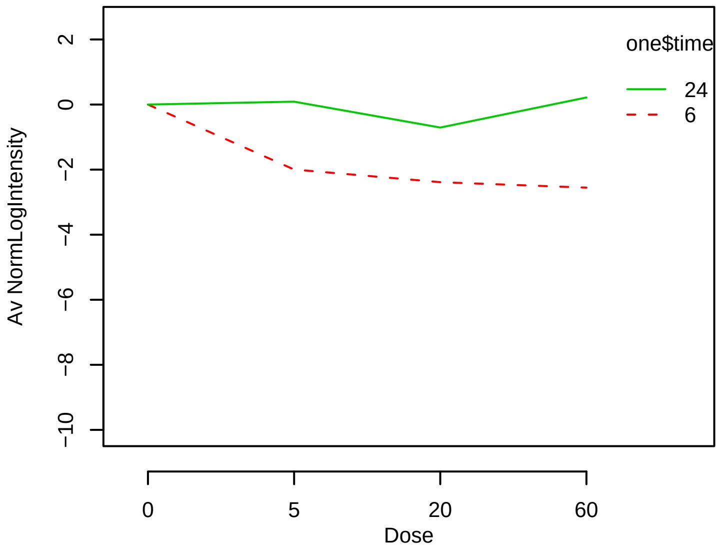
GO_0001504 : neurotransmitter uptake



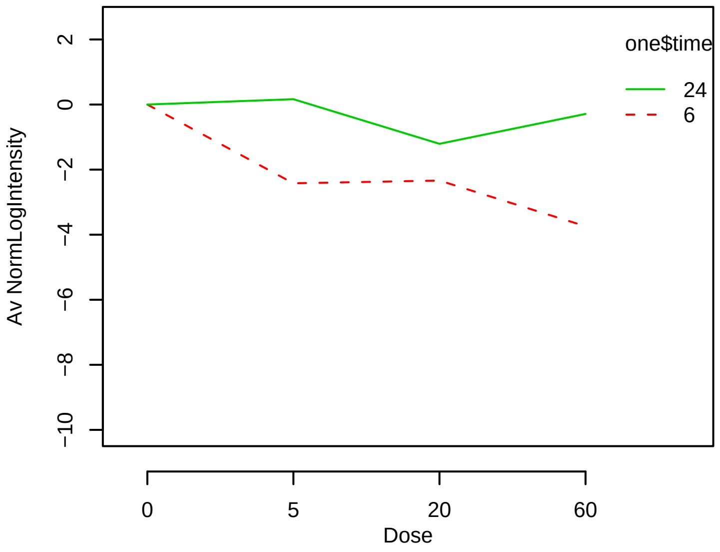
GO_0001505 : regulation of neurotransmitter levels



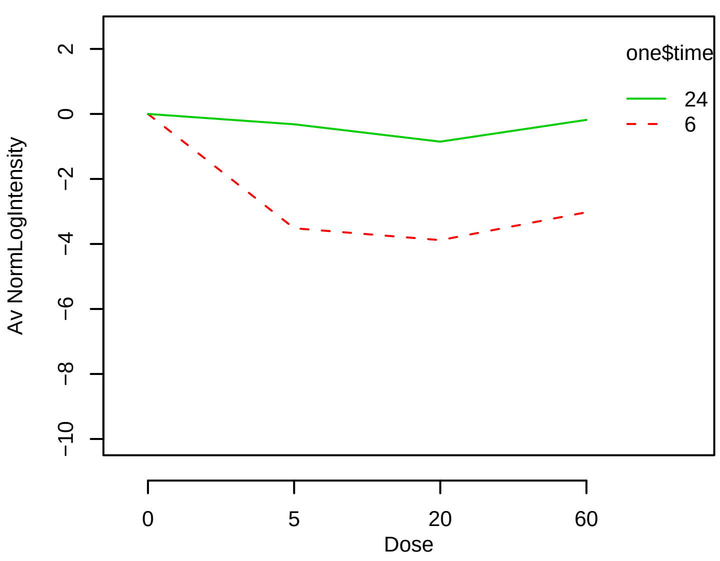
GO_0001508 : regulation of action potential



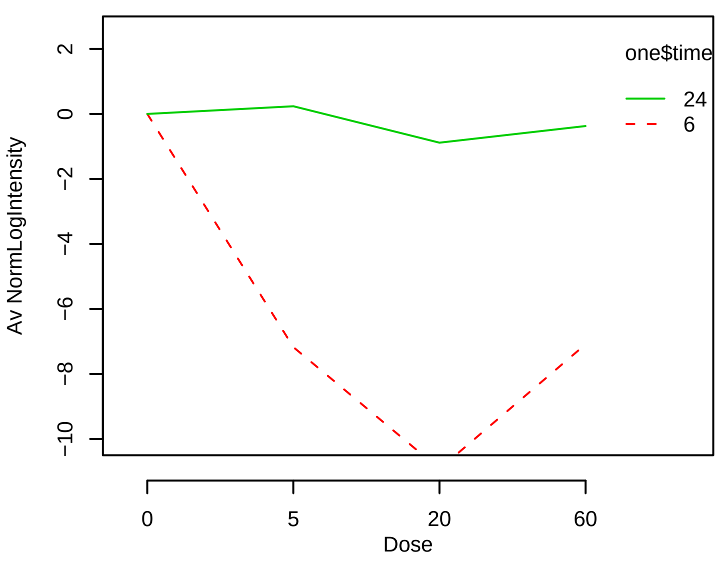
GO_0001514 : selenocysteine incorporation



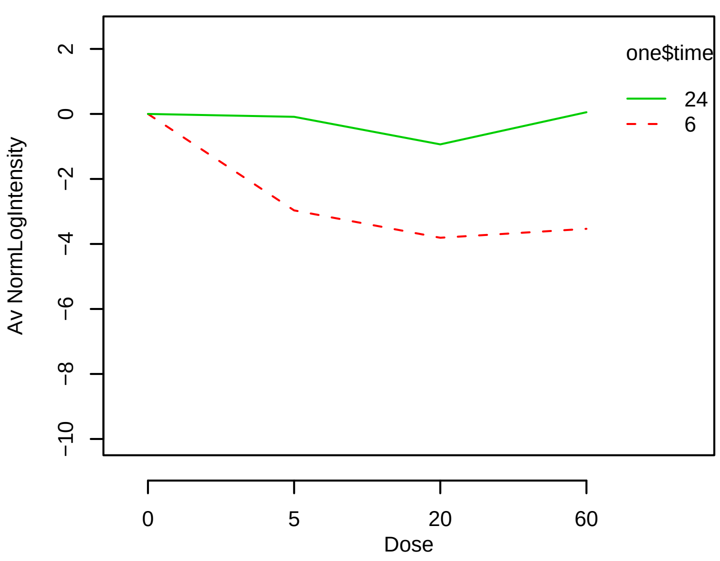
GO_0001516 : prostaglandin biosynthesis



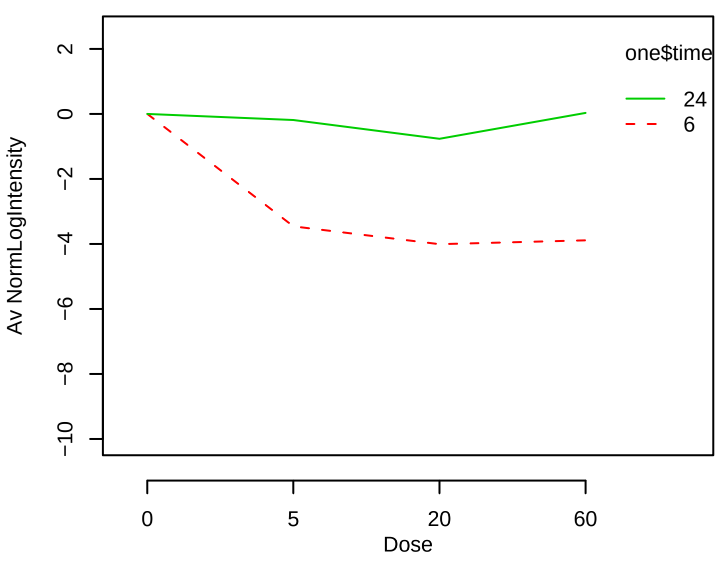
GO_0001523 : retinoid metabolism



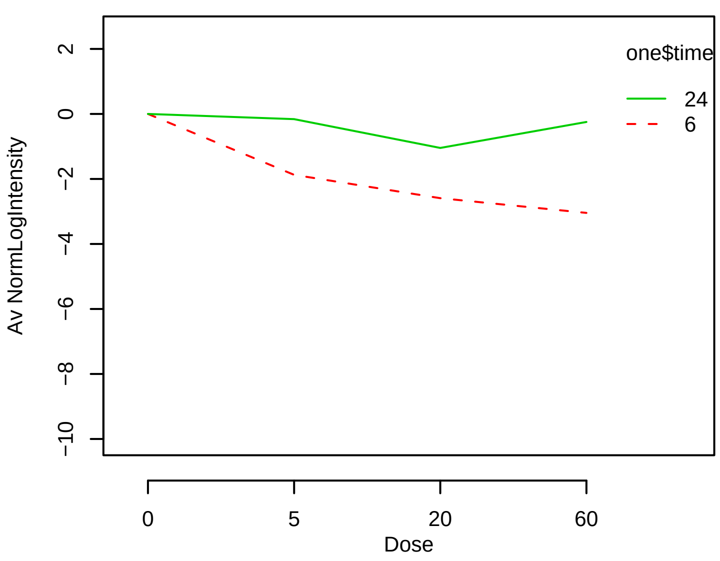
GO_0001525 : angiogenesis



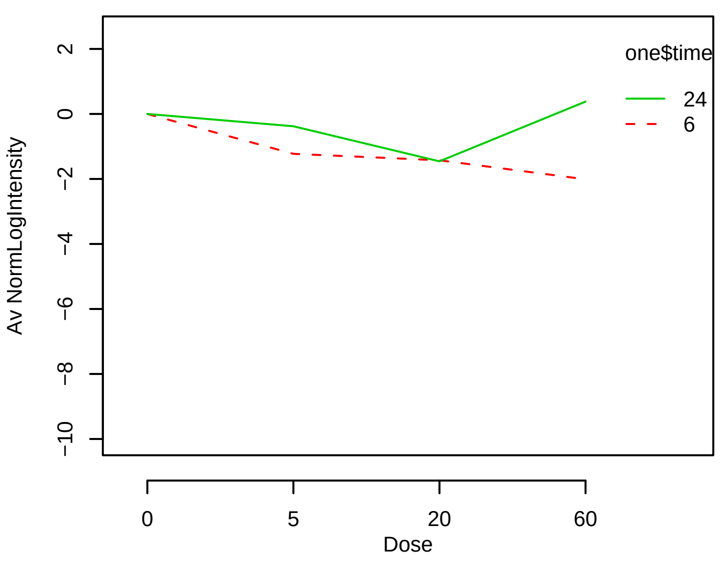
GO_0001539 : ciliary or flagellar motility

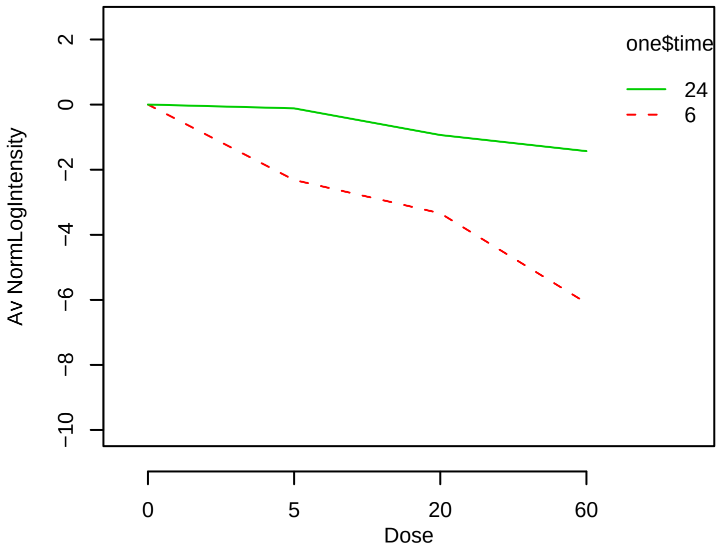


GO_0001541 : ovarian follicle development

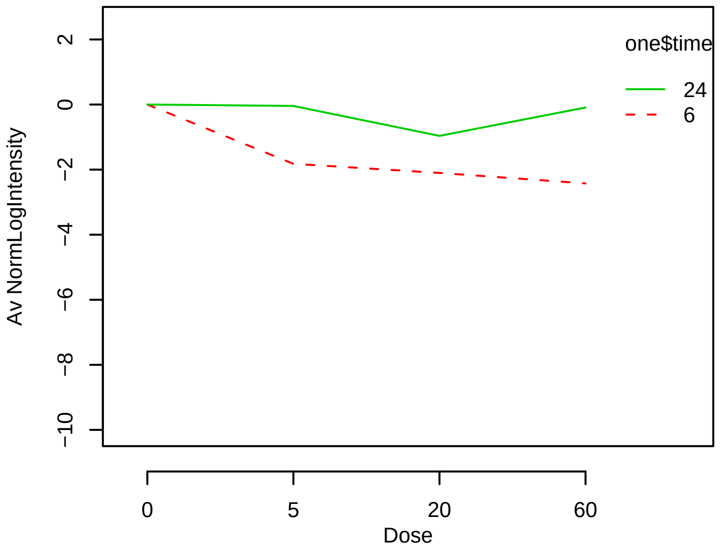


GO_0001542 : ovulation (sensu Mammalia)

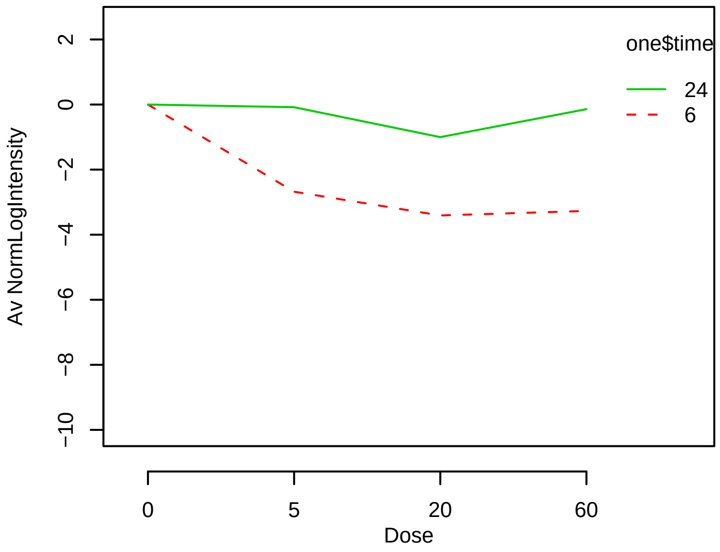




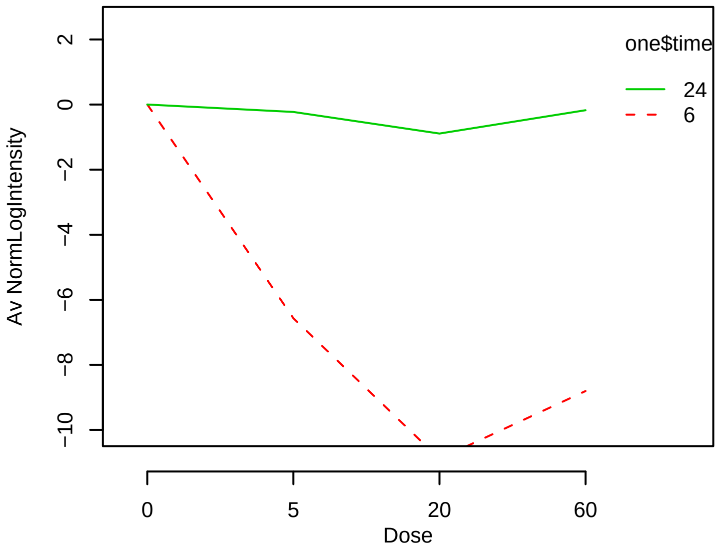
GO_0001556 : oocyte maturation



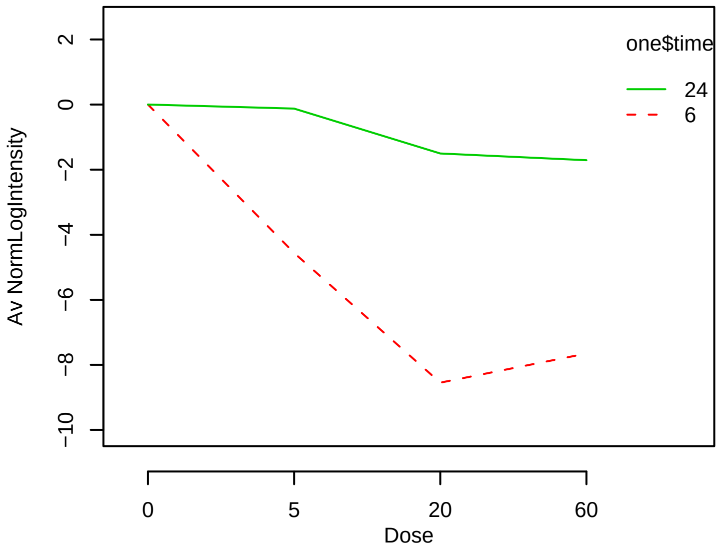
GO_0001558 : regulation of cell growth



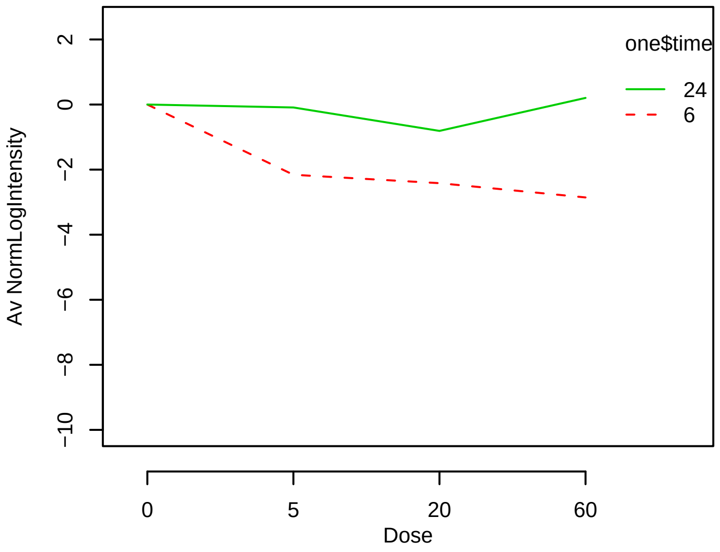
GO_0001568 : blood vessel development



GO_0001569 : patterning of blood vessels

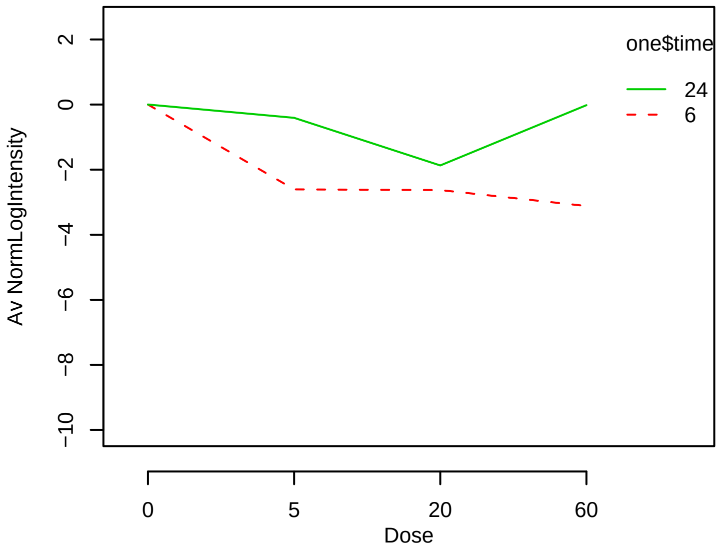


GO_0001570 : vasculogenesis

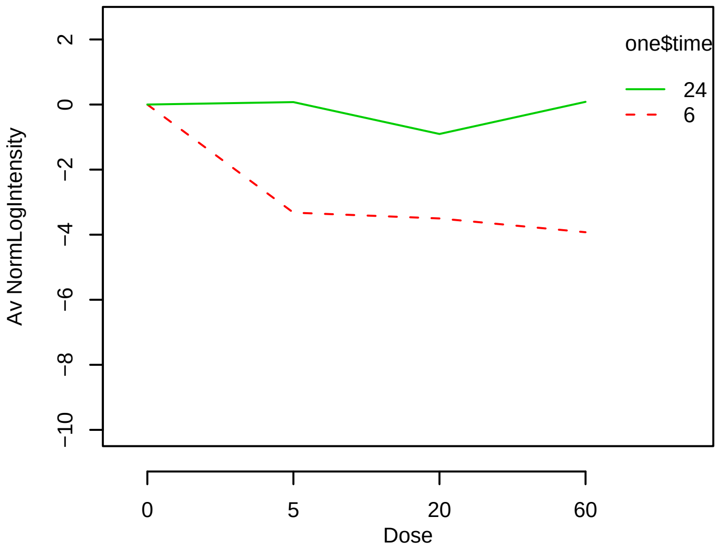


GO_0001573 : ganglioside metabolism

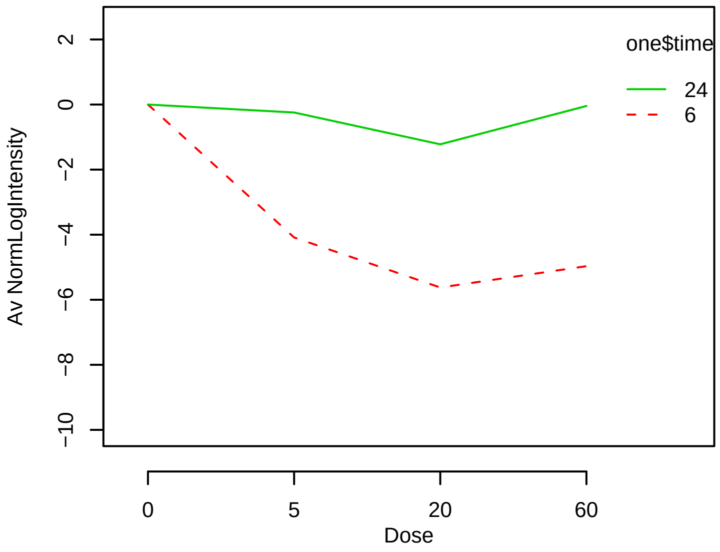
GO_0001578 : microtubule bundle formation



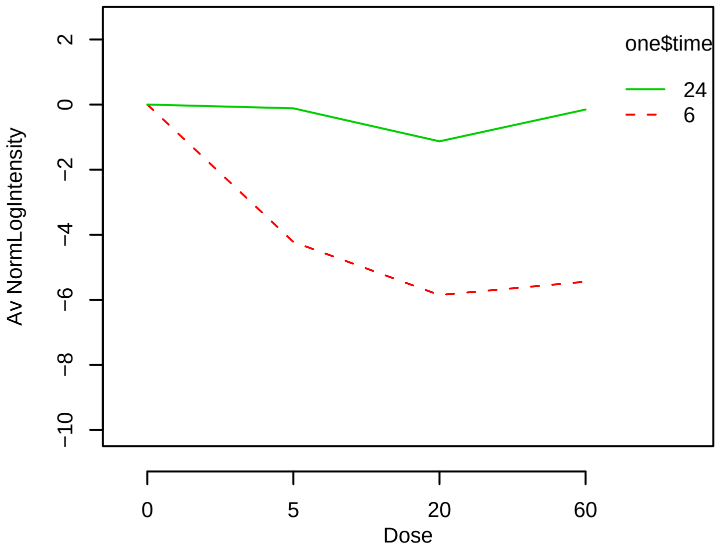
GO_0001649 : osteoblast differentiation



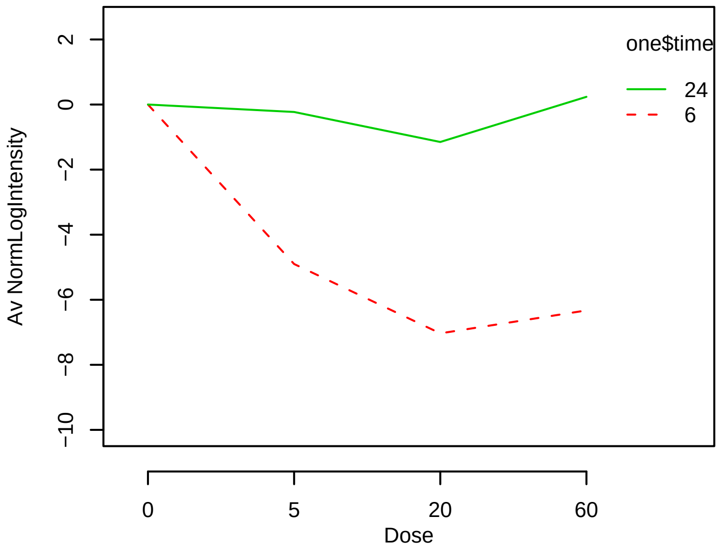
GO_0001654 : eye development



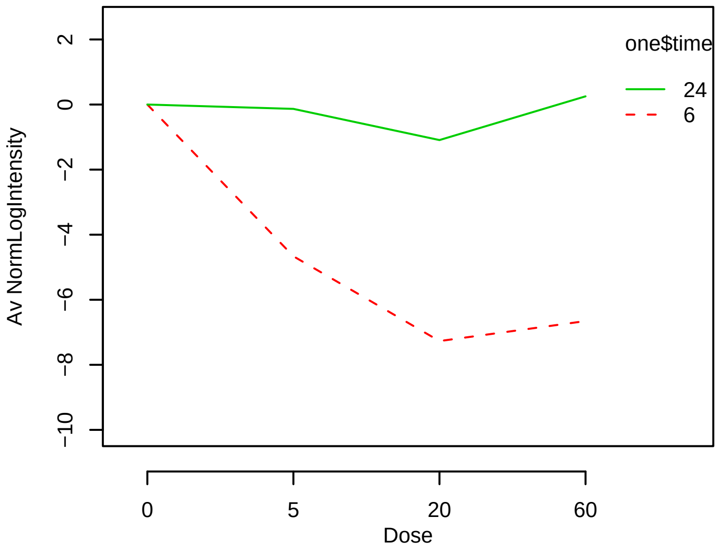
GO_0001655 : urogenital system development

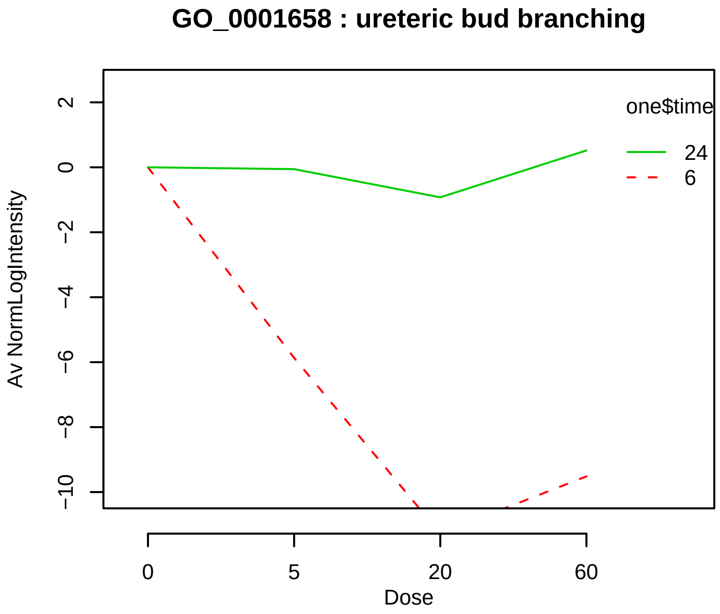


GO_0001656 : metanephros development

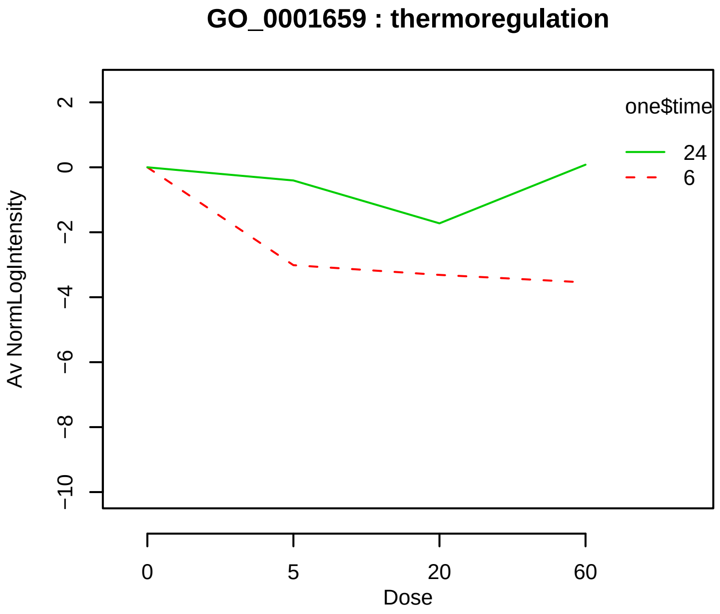


GO_0001657 : ureteric bud development

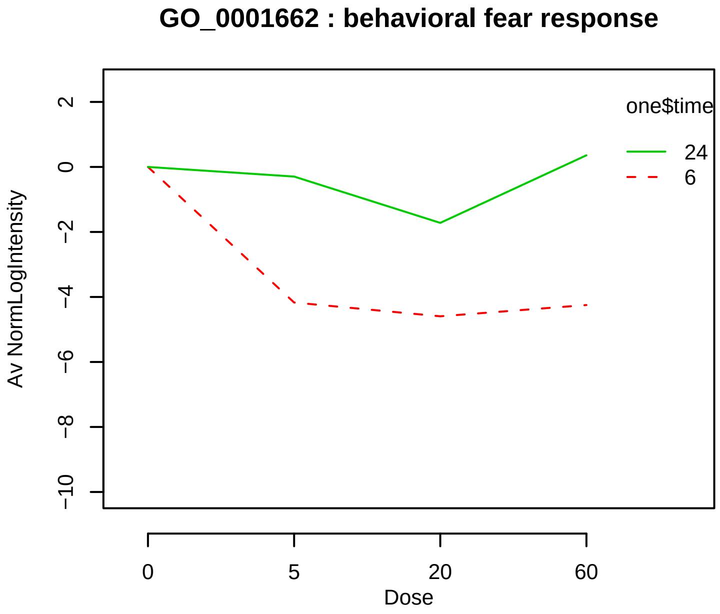




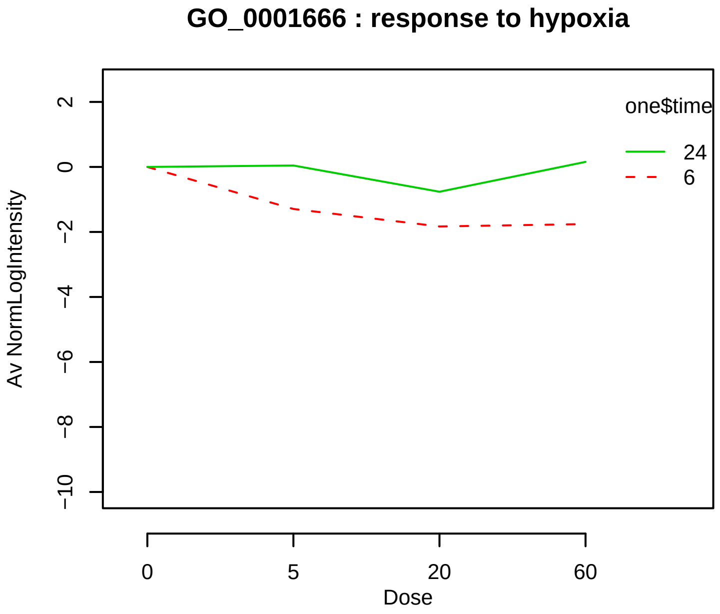
GO_0001658 : ureteric bud branching



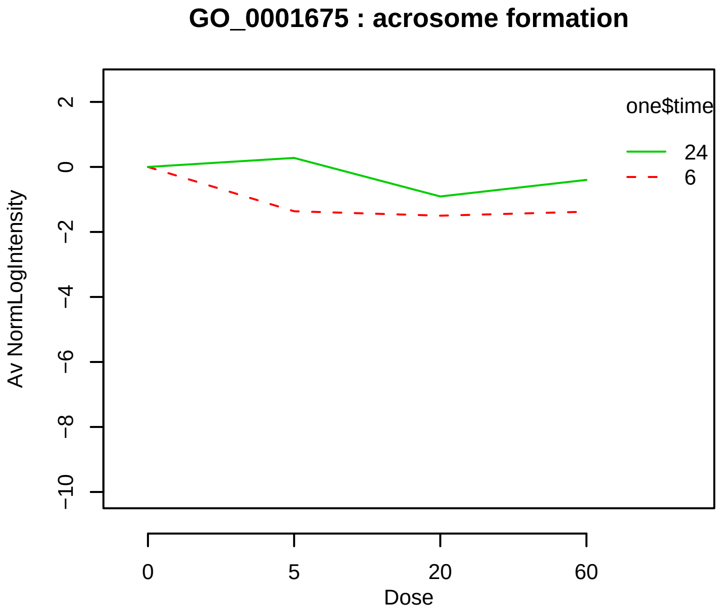
GO_0001659 : thermoregulation



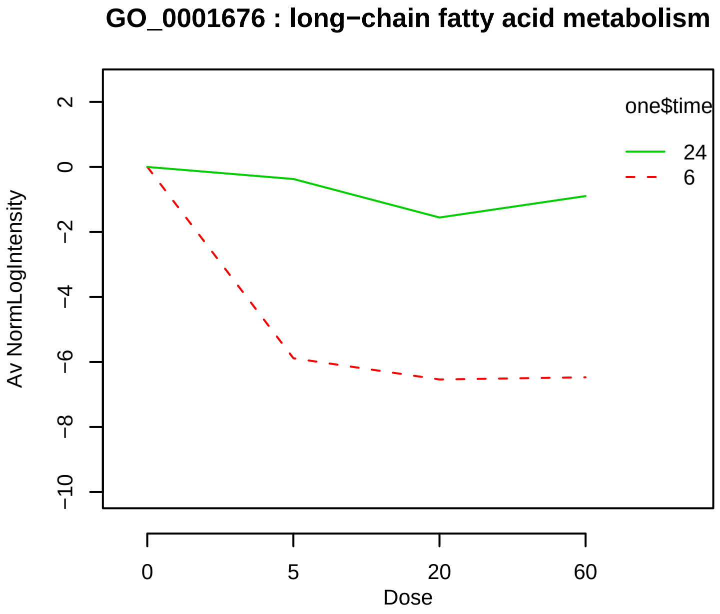
GO_0001662 : behavioral fear response



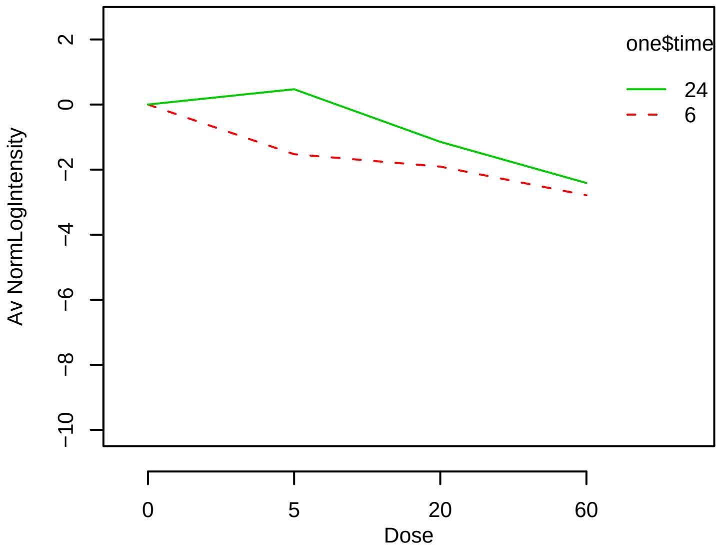
GO_0001666 : response to hypoxia

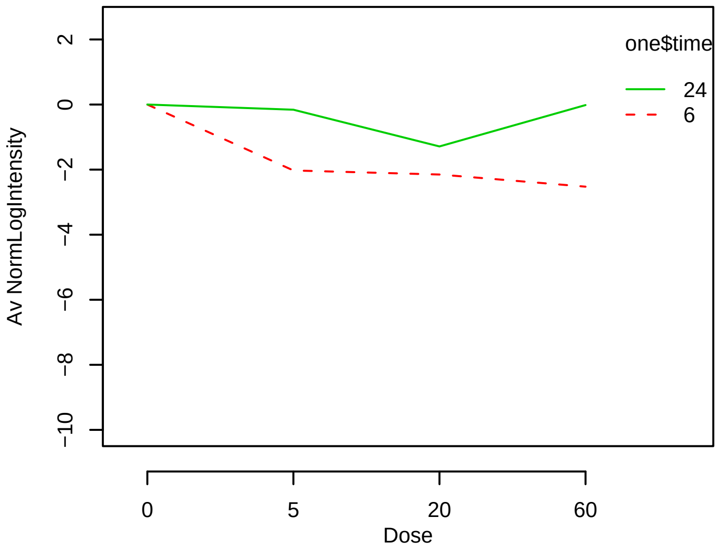


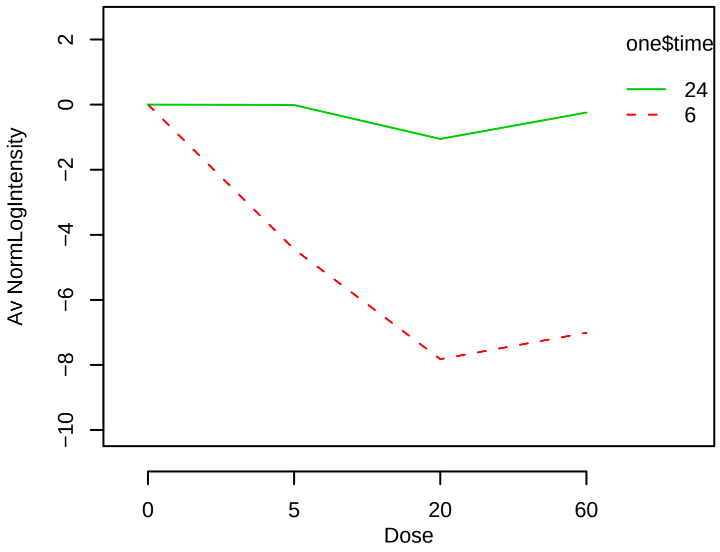
GO_0001675 : acrosome formation

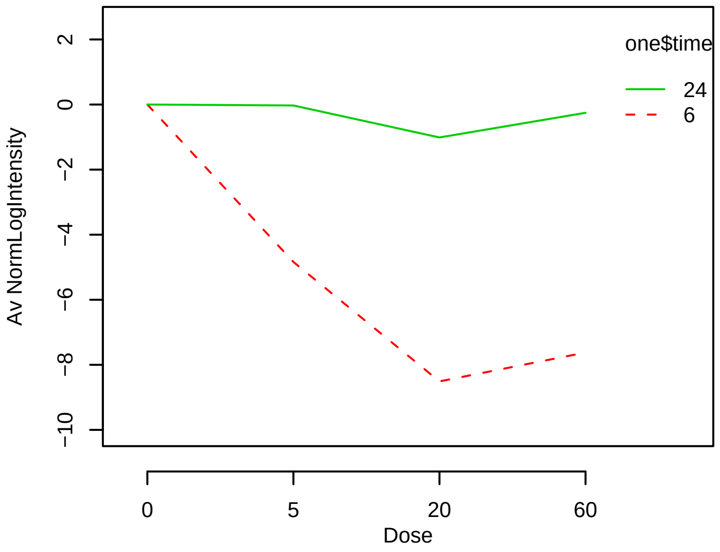


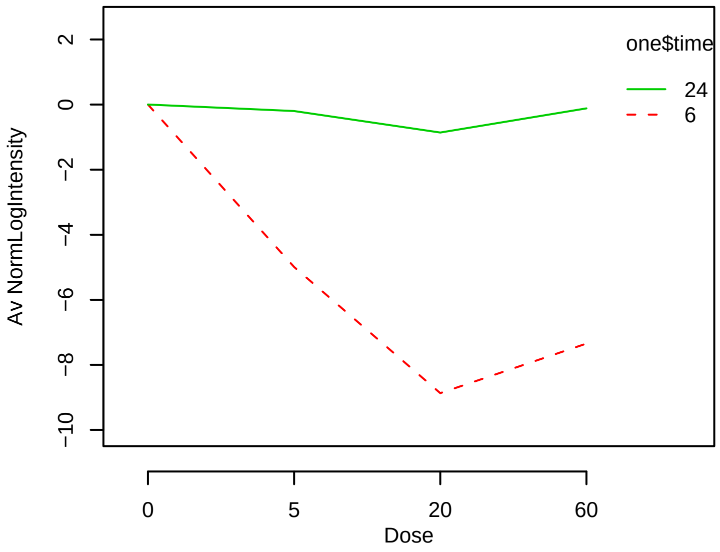
GO_0001676 : long−chain fatty acid metabolism

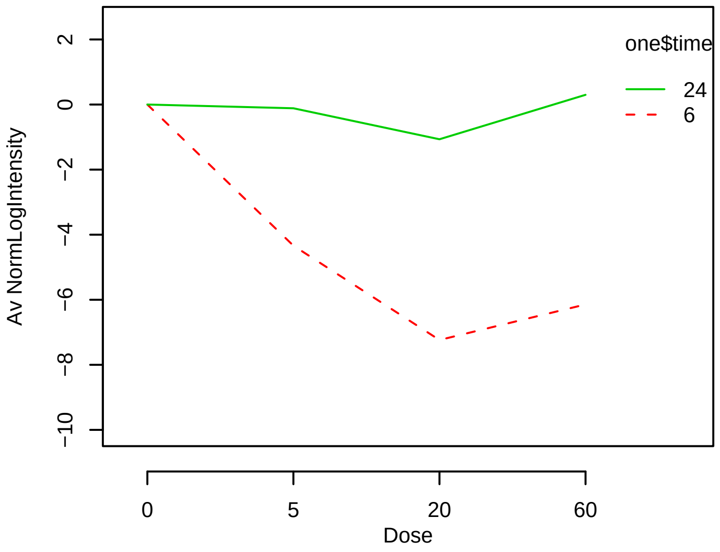

GO_0001701 : embryonic development (sensu Mammalia)


GO_0001702 : gastrulation (sensu Deuterostomia)

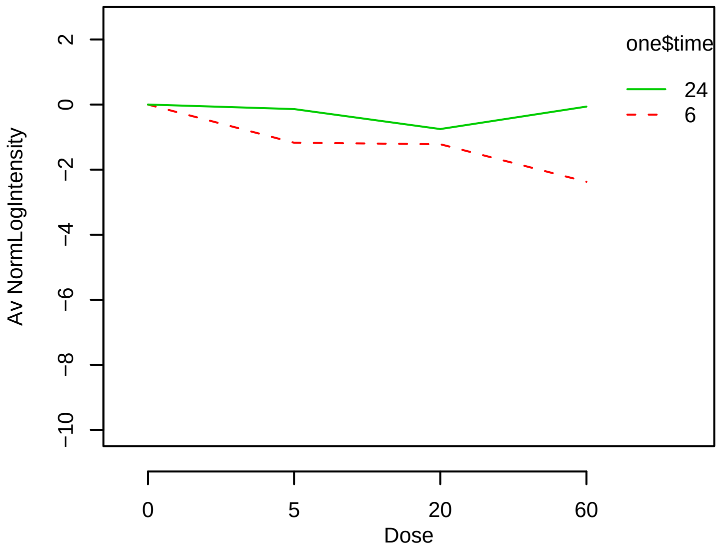

GO_0001704 : formation of primary germ layer


GO_0001707 : mesoderm formation

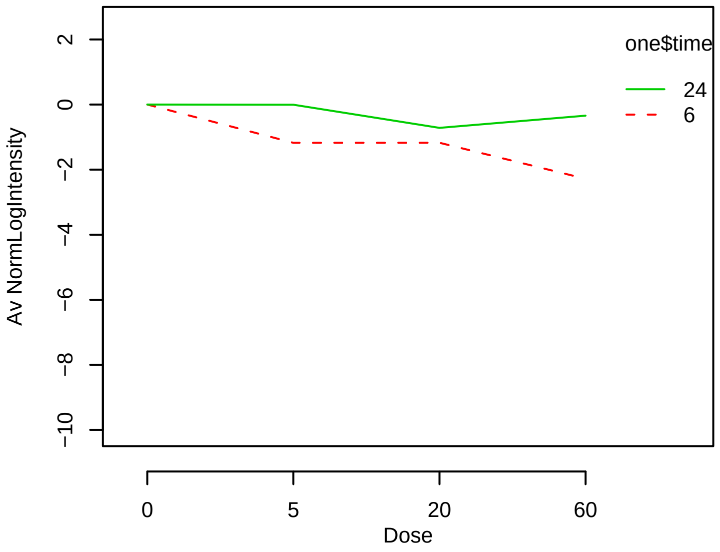

GO_0001708 : cell fate specification


GO_0001709 : cell fate determination

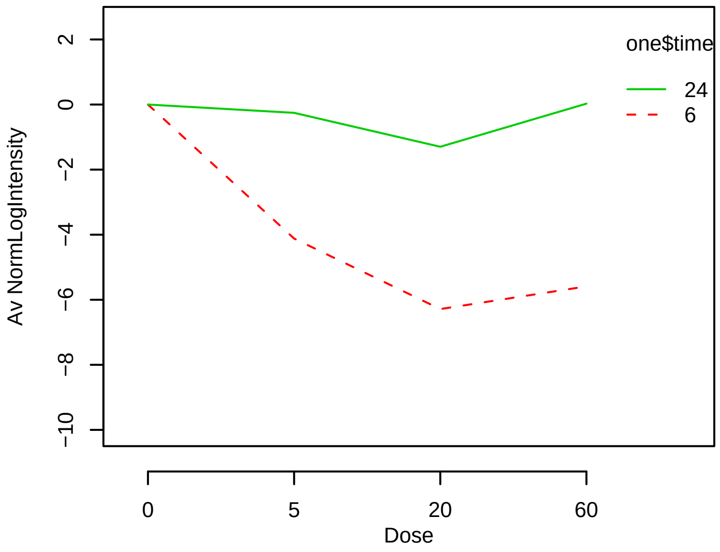
GO_0001736 : establishment of planar polarity



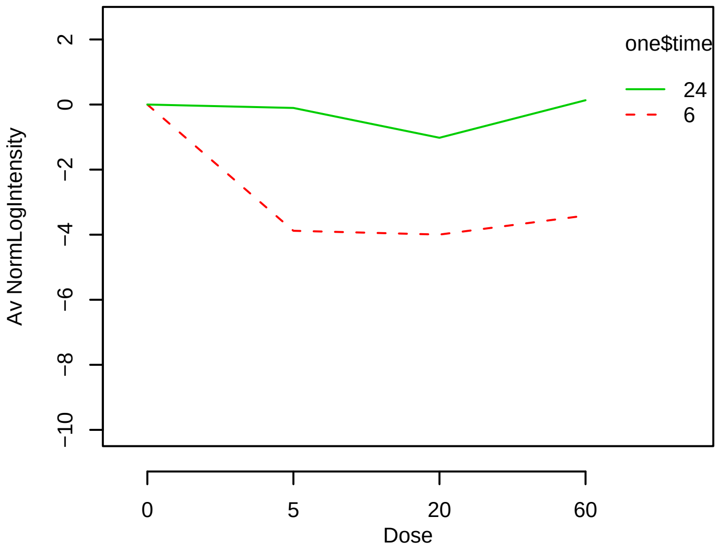
GO_0001738 : morphogenesis of a polarized epithelium



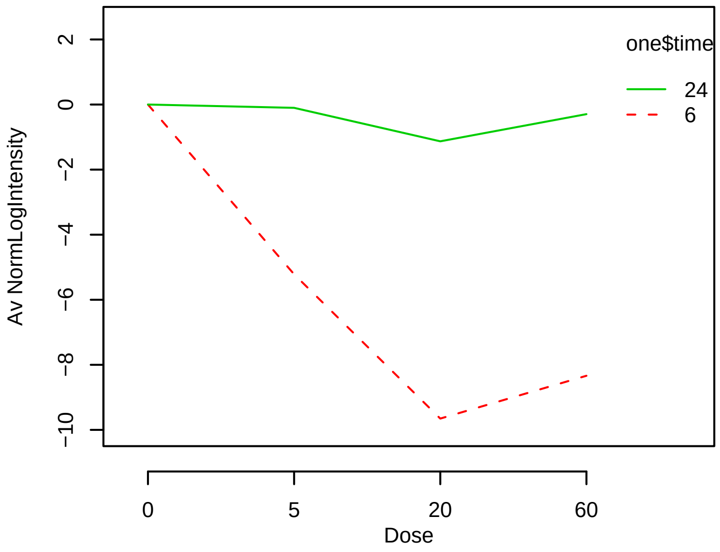
GO_0001747 : eye development (sensu Mammalia)



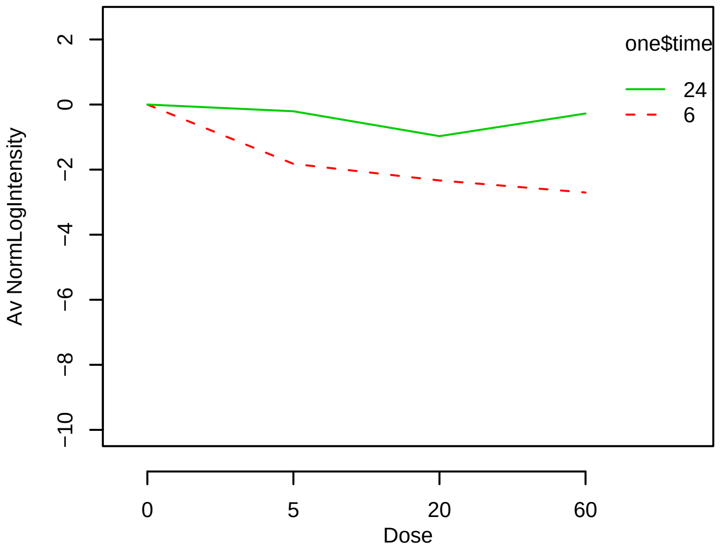
GO_0001754 : eye photoreceptor cell differentiation

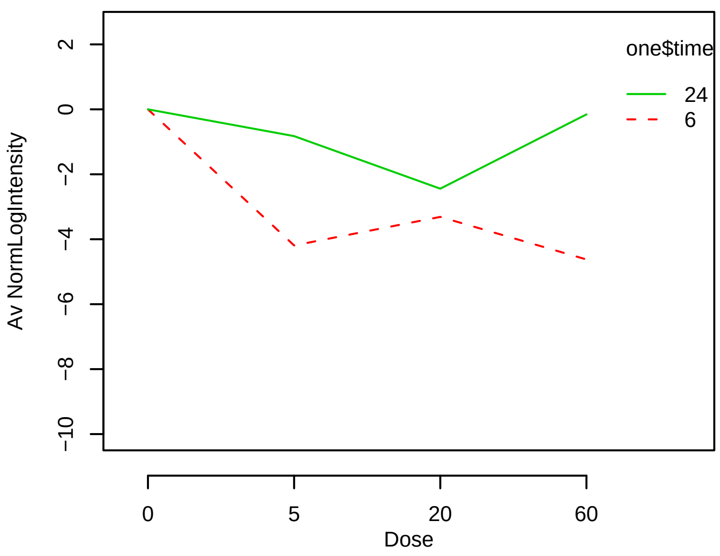


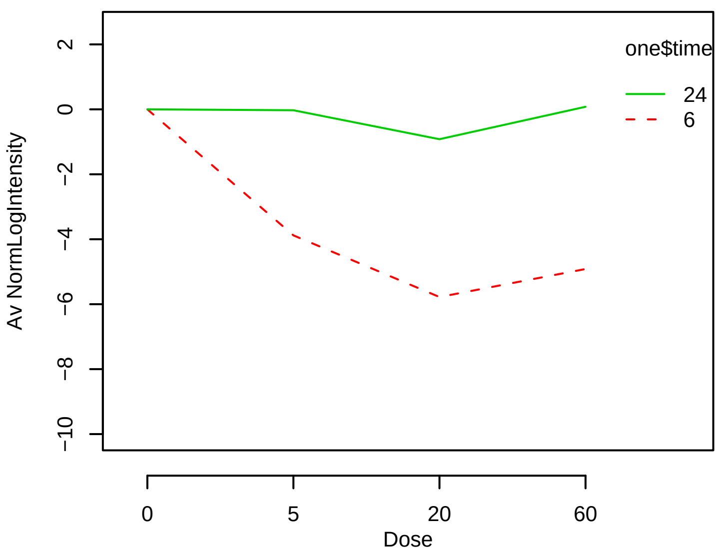
GO_0001755 : neural crest cell migration

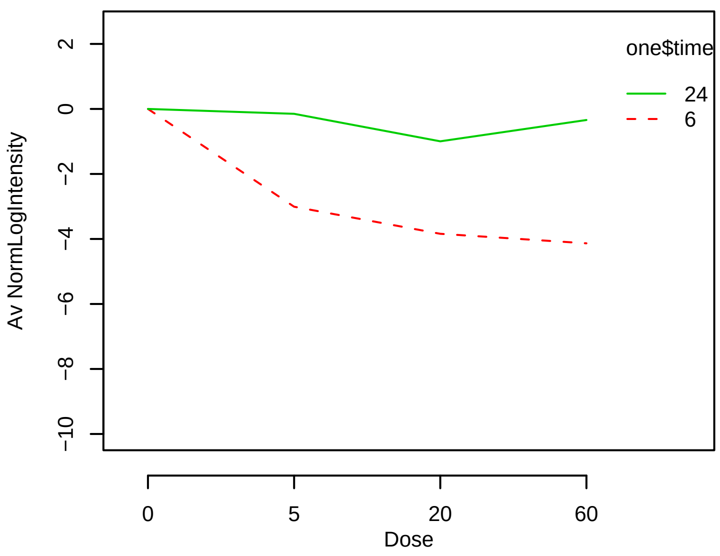


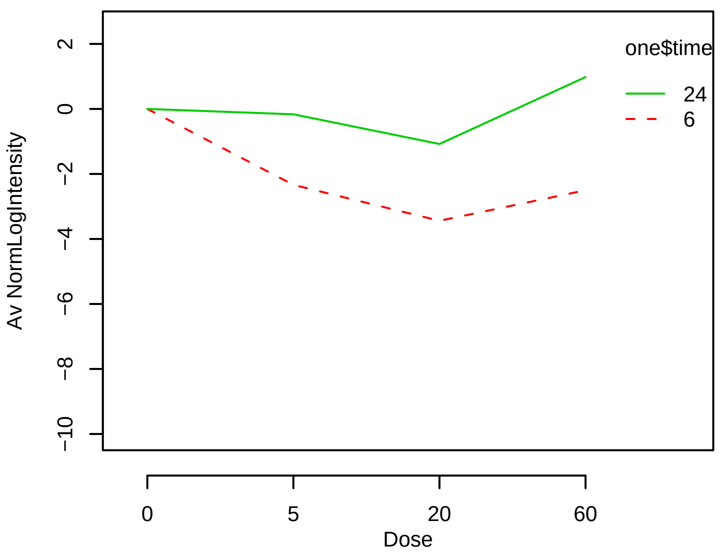
GO_0001756 : somitogenesis

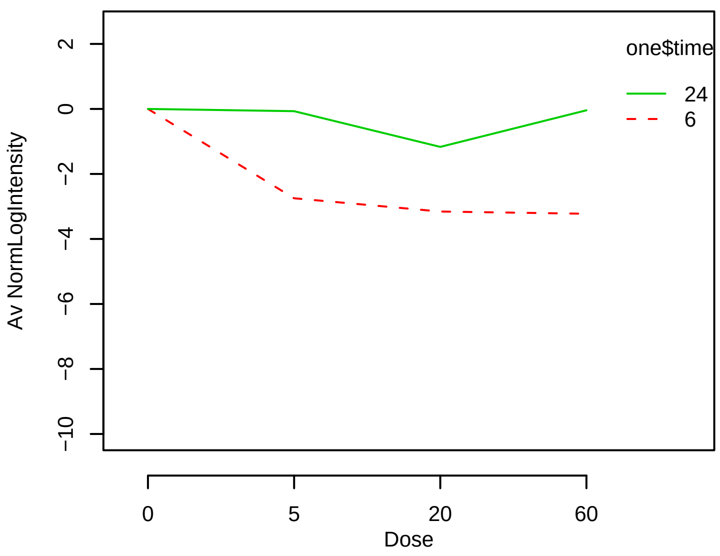


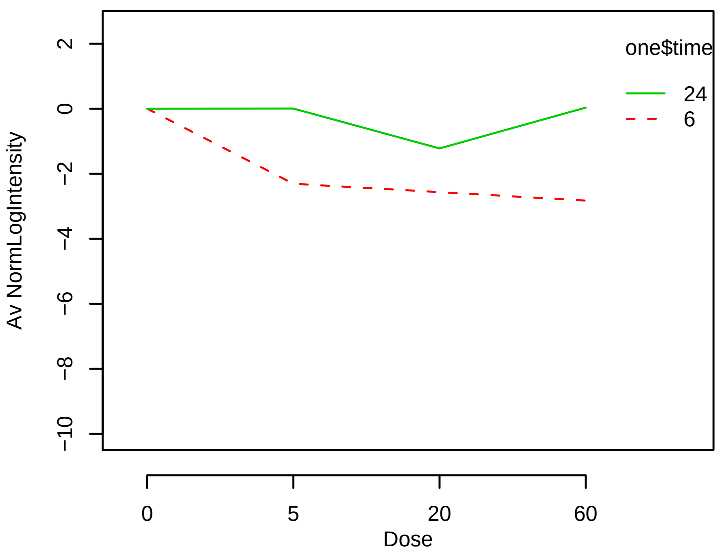

GO_0001759 : induction of an organ

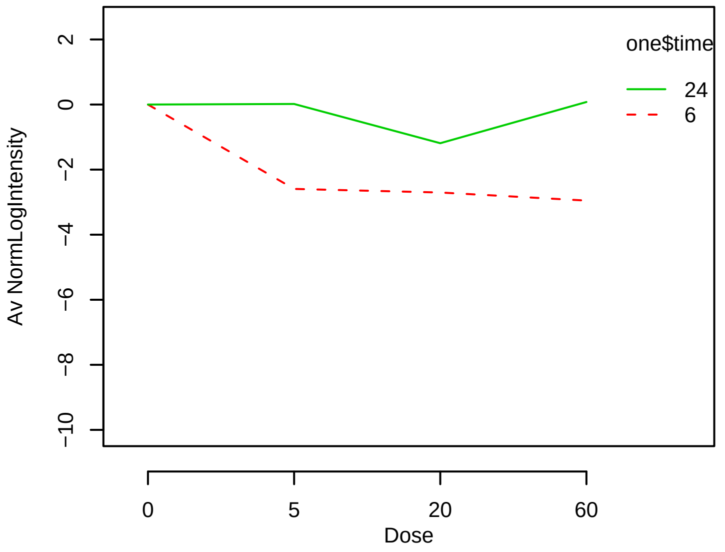

GO_0001763 : morphogenesis of a branching structure

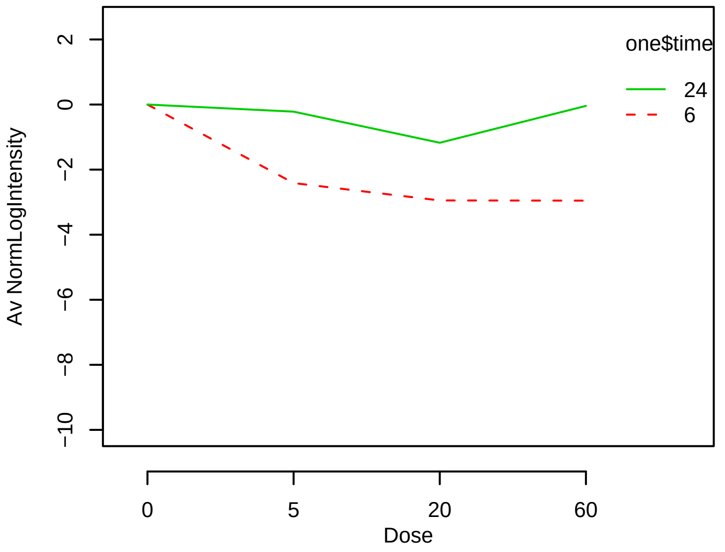

GO_0001764 : neuron migration

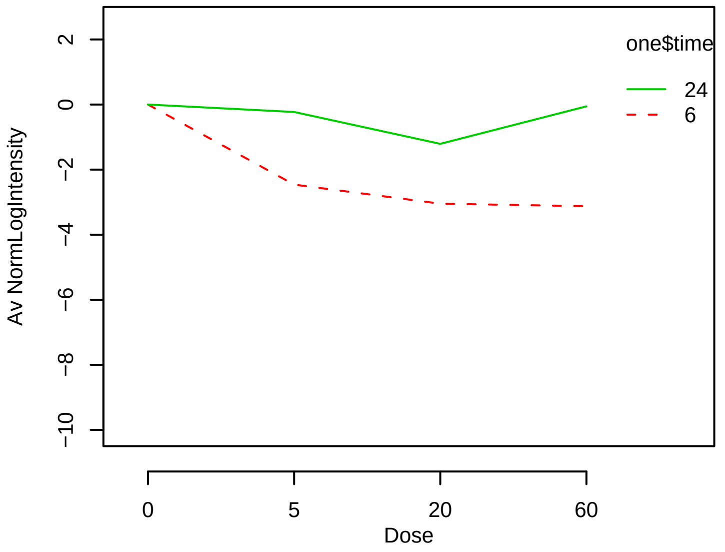

GO_0001773 : myeloid dendritic cell activation

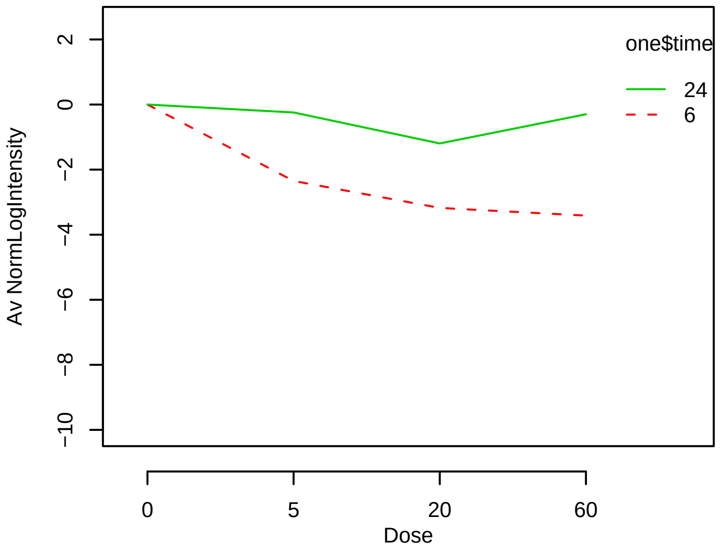

GO_0001775 : cell activation

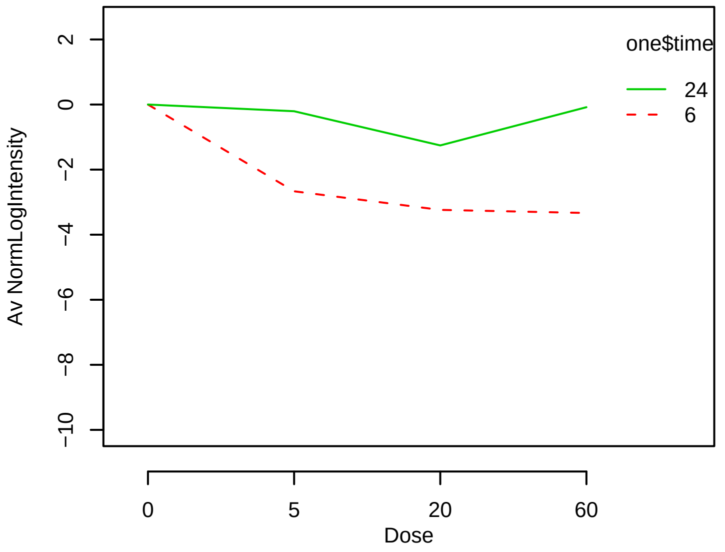

GO_0001776 : leukocyte homeostasis

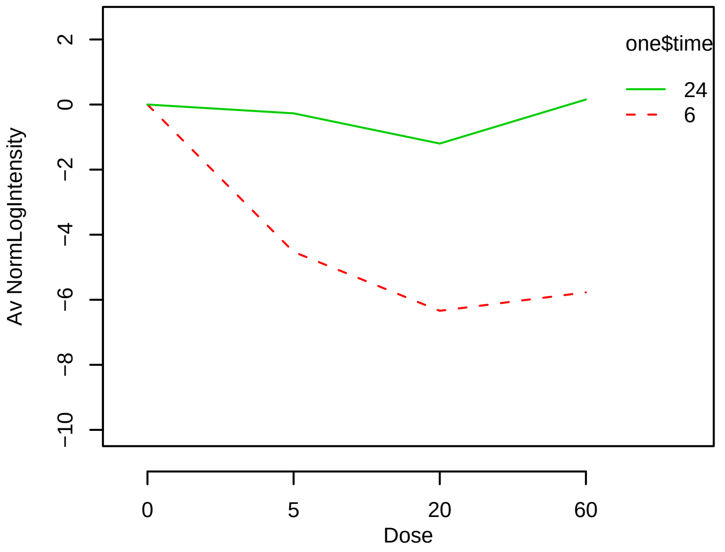

GO_0001782 : B cell homeostasis

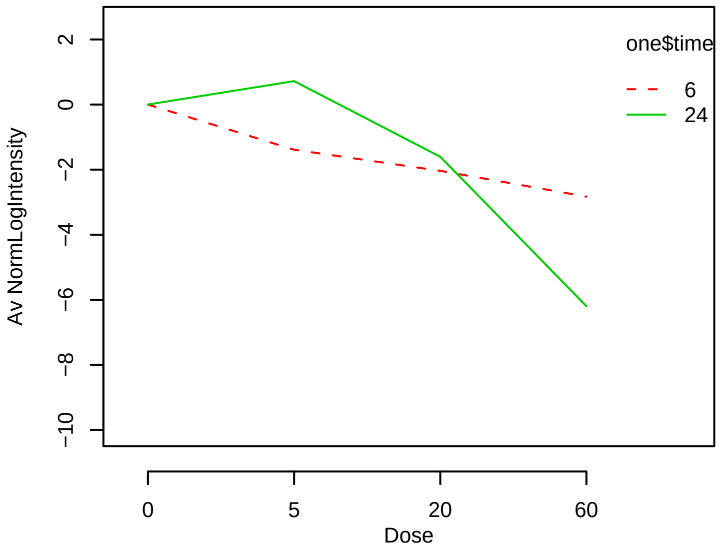

GO_0001816 : cytokine production

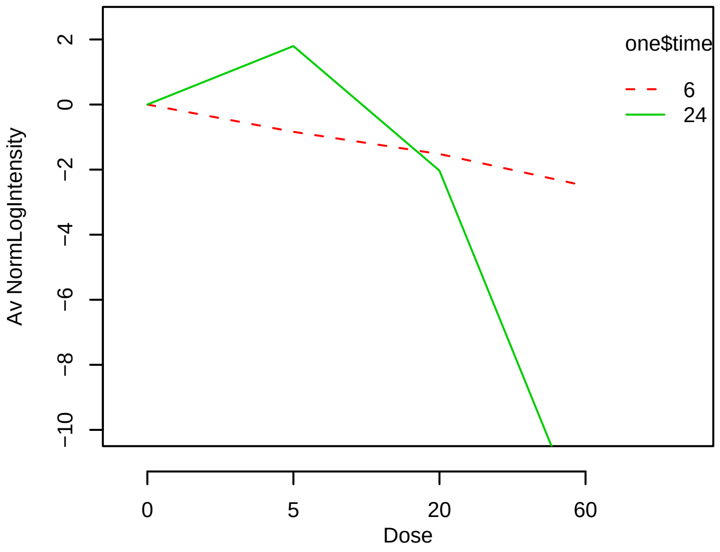

GO_0001817 : regulation of cytokine production

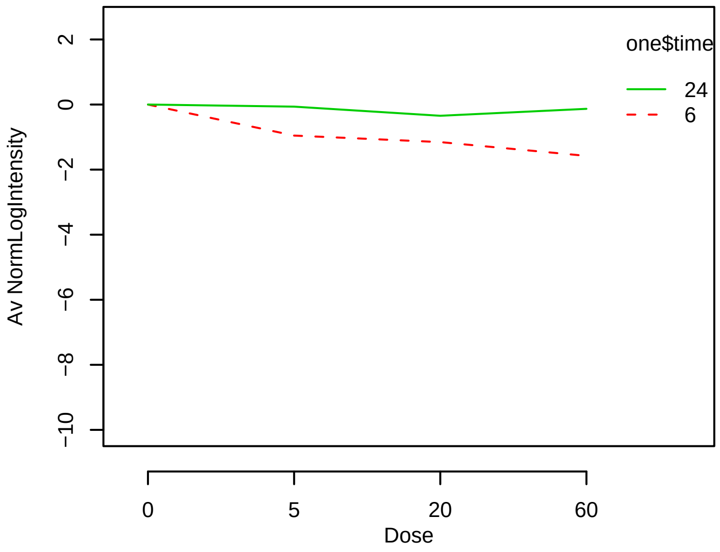

GO_0001818 : negative regulation of cytokine production

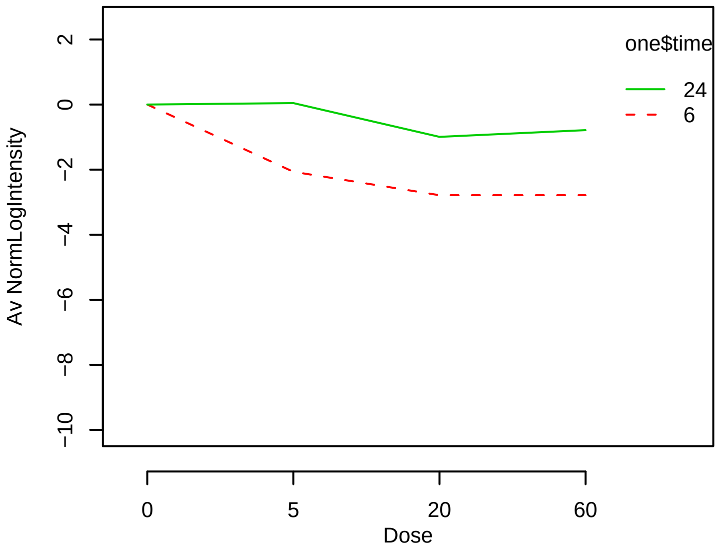

GO_0001819 : positive regulation of cytokine production

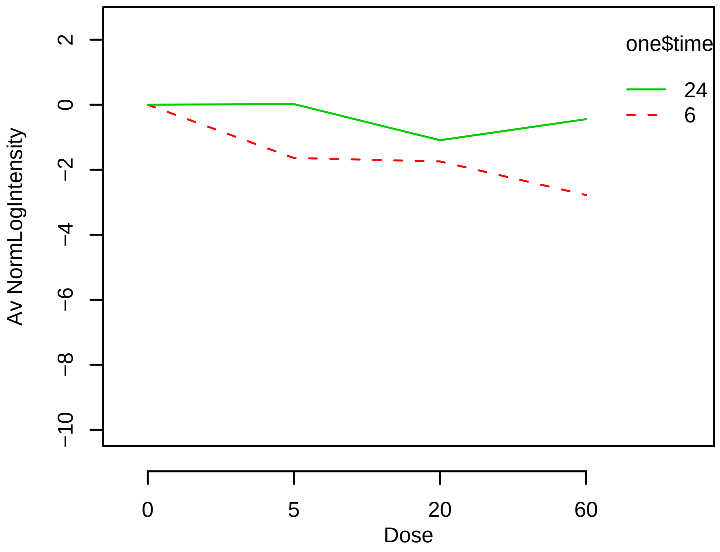

GO_0001822 : kidney development

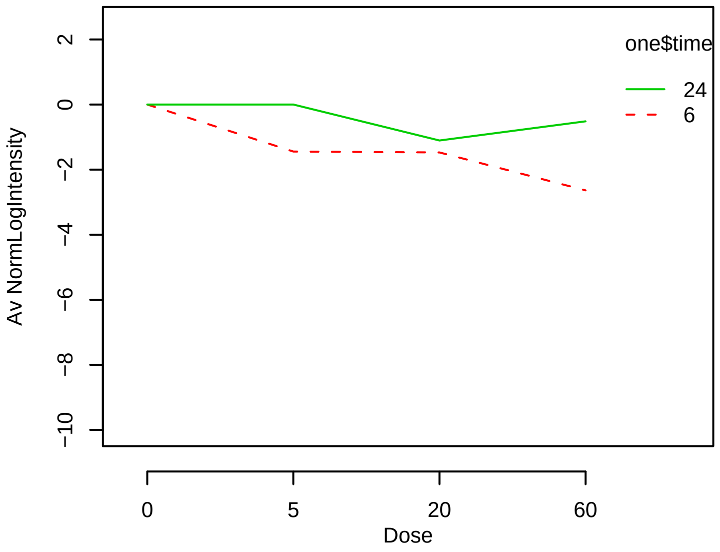

GO_0001824 : blastocyst development


GO_0001832 : blastocyst growth

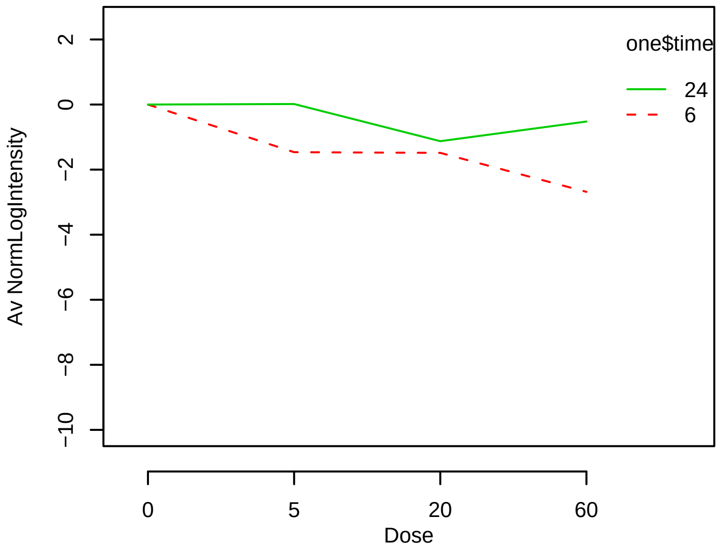

GO_0001836 : release of cytochrome c from mitochondri


GO_0001837 : epithelial to mesenchymal transition

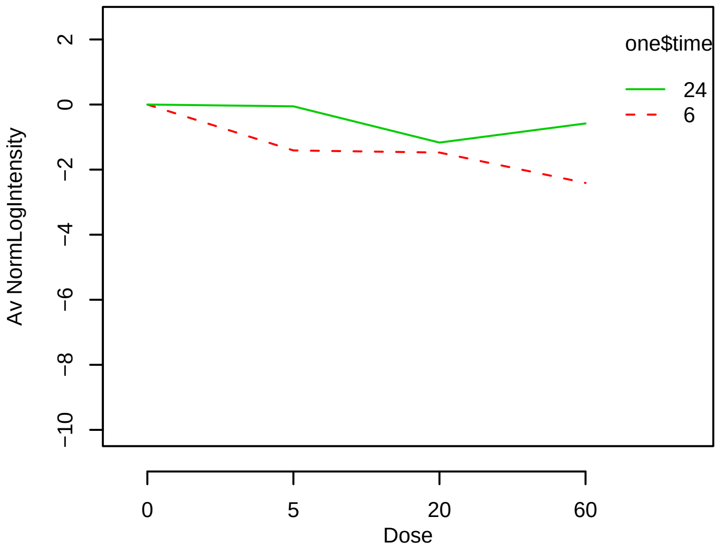

GO_0001838 : embryonic epithelial tube formation


GO_0001839 : neural plate morphogenesis

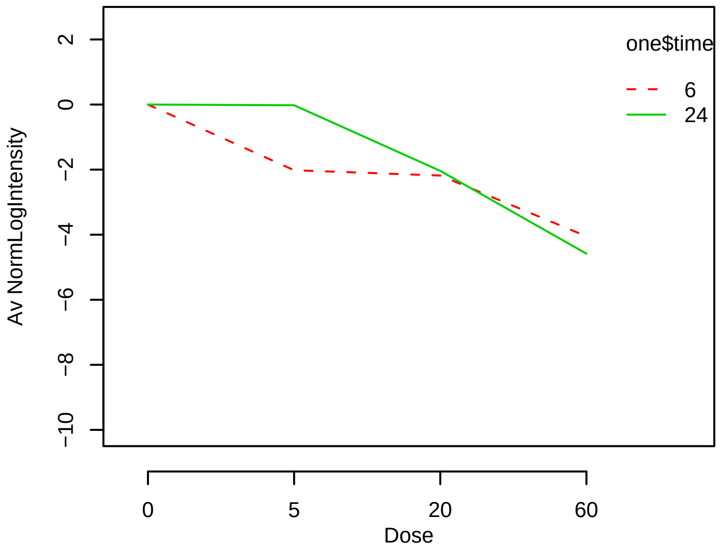
GO_0001841 : neural tube formation



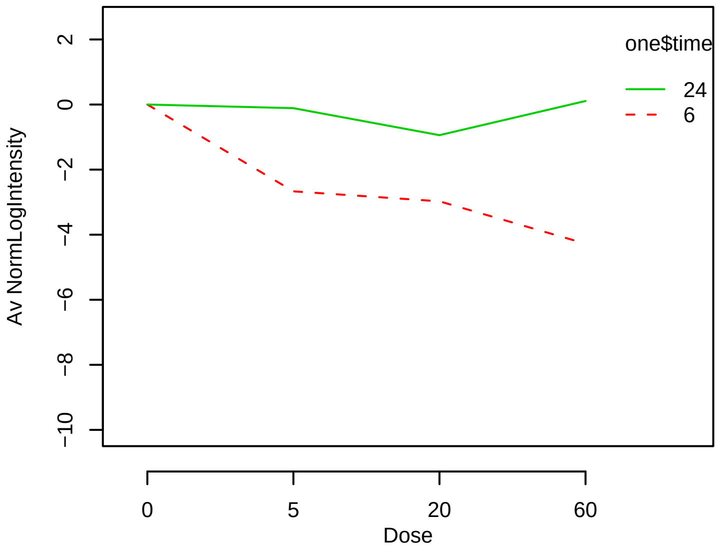
GO_0001843 : neural tube closure



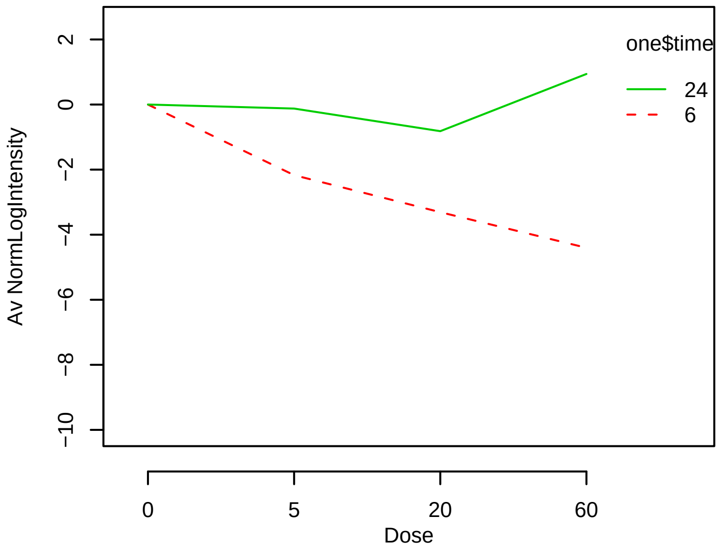
GO_0001889 : liver development



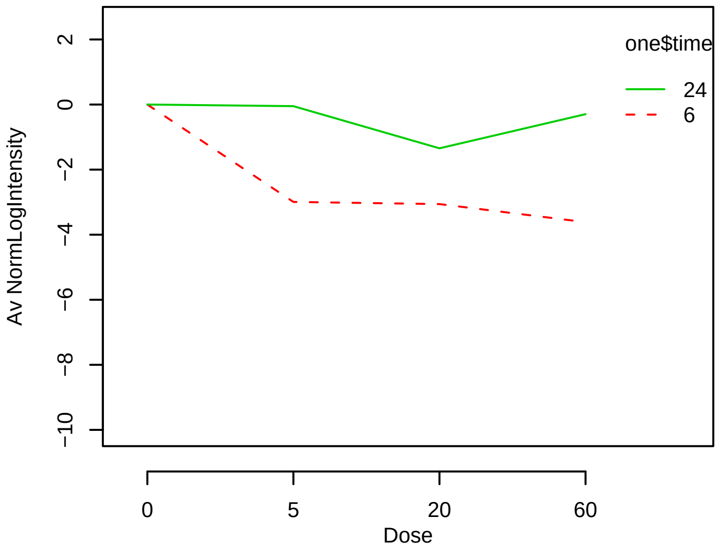
GO_0001890 : placenta development

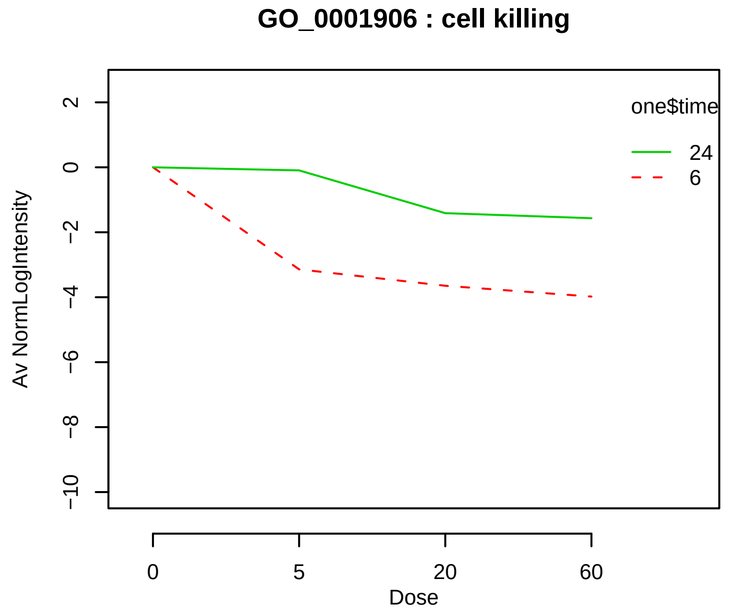


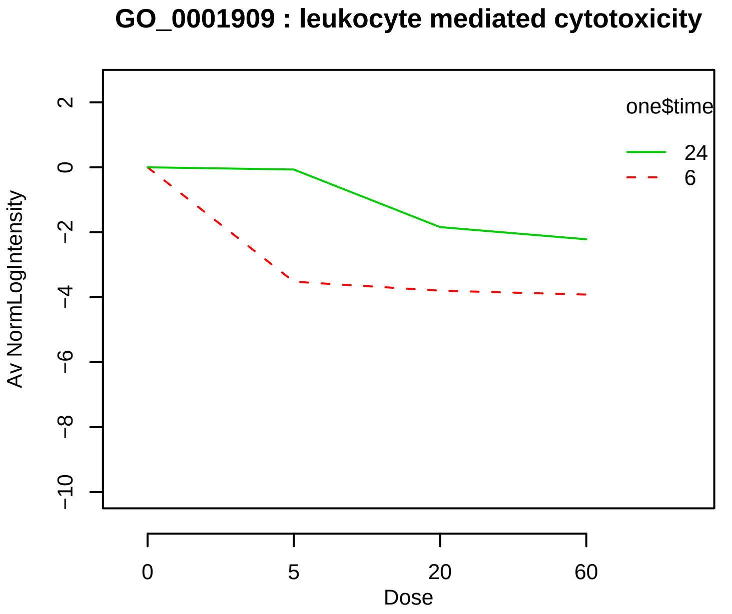
GO_0001892 : embryonic placenta development

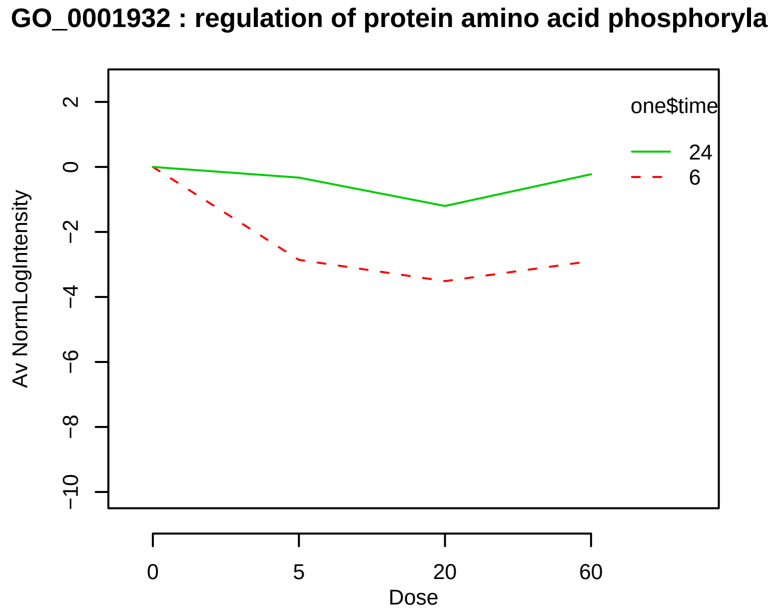


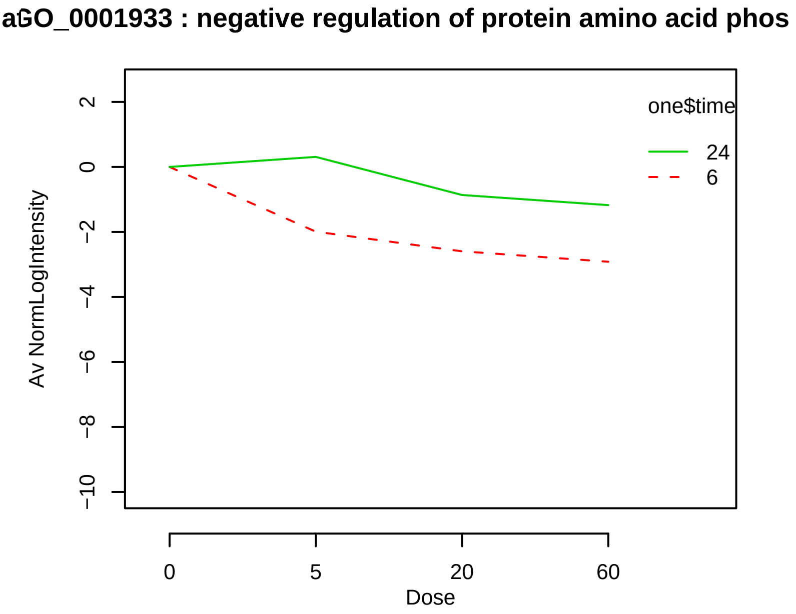
GO_0001894 : tissue homeostasis

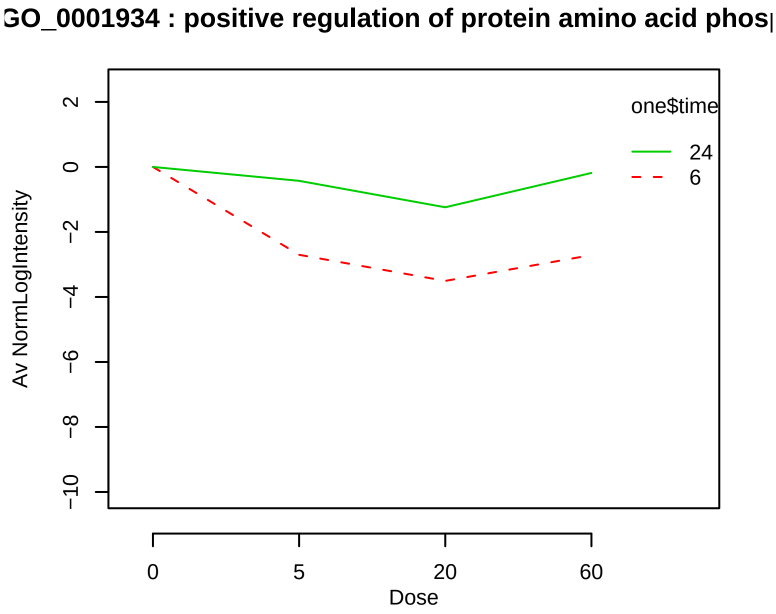


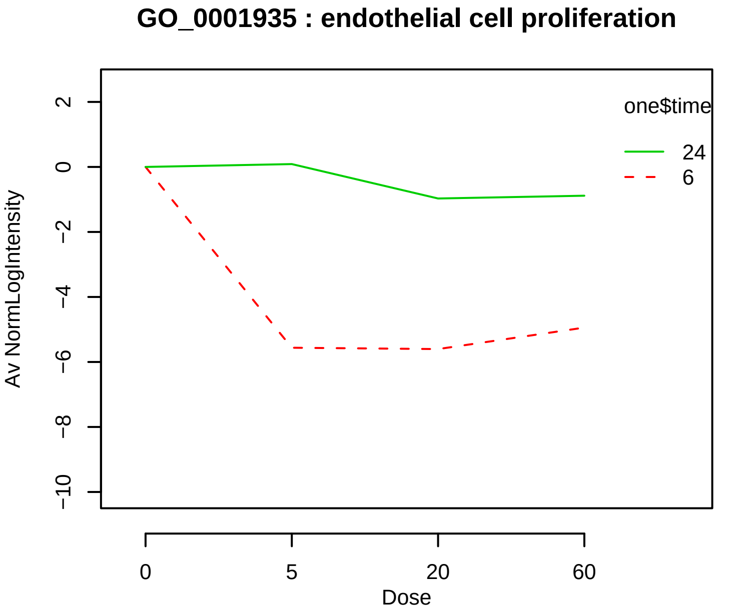

GO_0001906 : cell killing


GO_0001909 : leukocyte mediated cytotoxicity

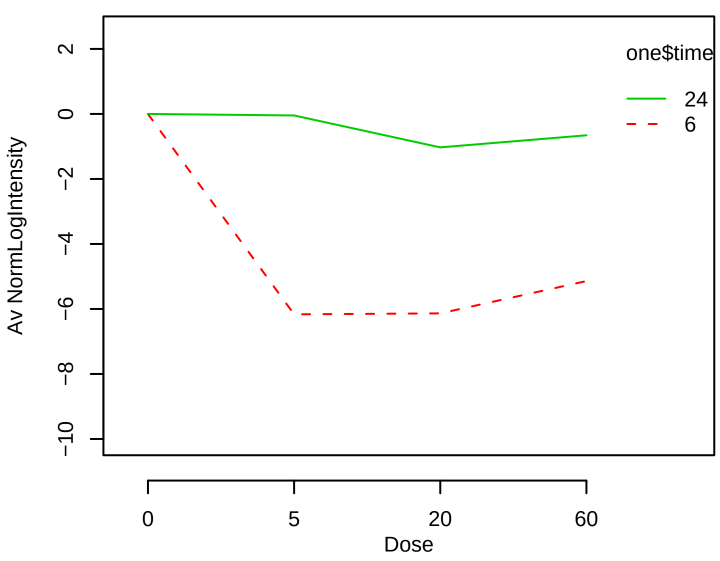

GO_0001932 : regulation of protein amino acid phosphoryla


GO_0001933 : negative regulation of protein amino acid phos

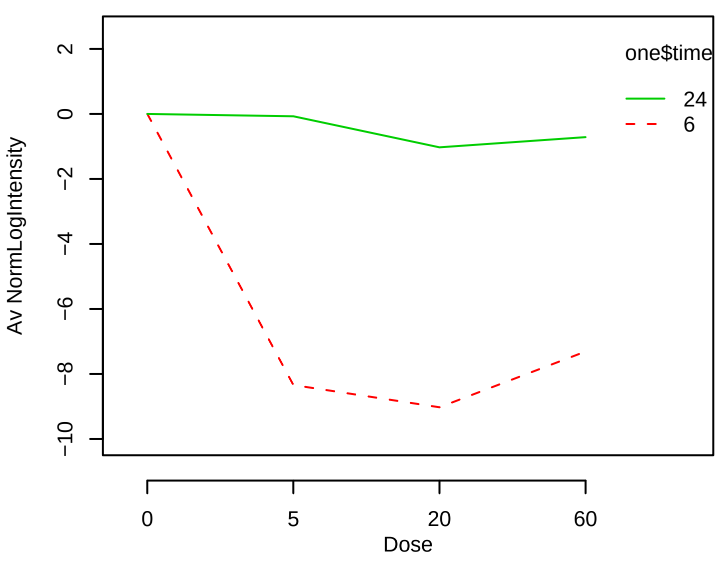

GO_0001934 : positive regulation of protein amino acid phos


GO_0001935 : endothelial cell proliferation

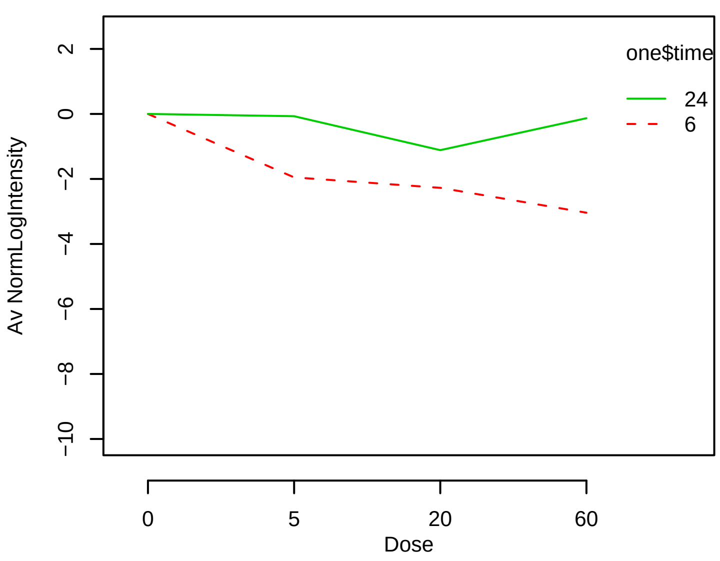
GO_0001936 : regulation of endothelial cell proliferation



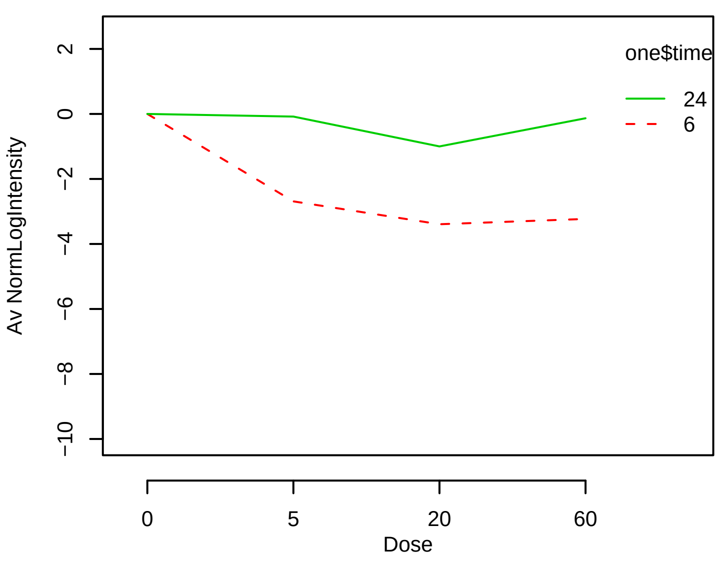
GO_0001937 : negative regulation of endothelial cell prolife



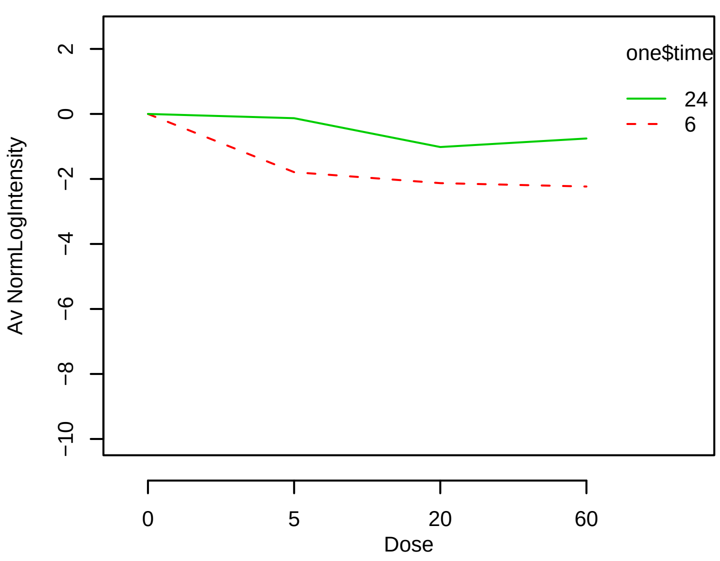
GO_0001942 : hair follicle development



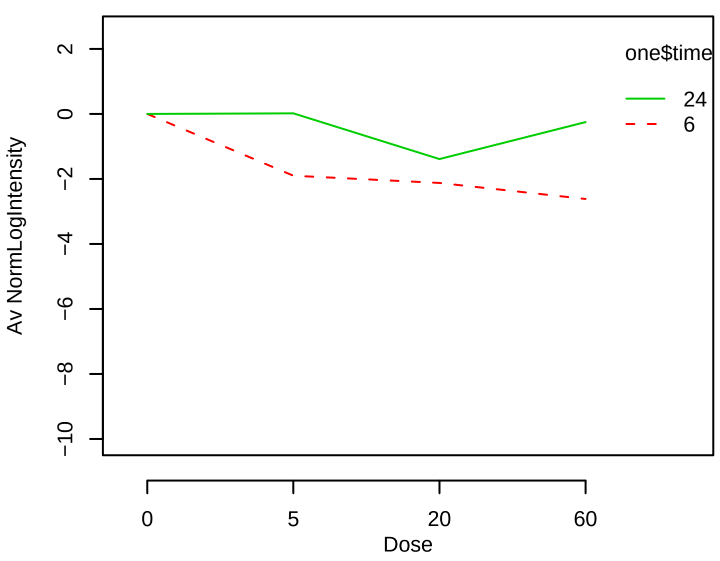
GO_0001944 : vasculature development

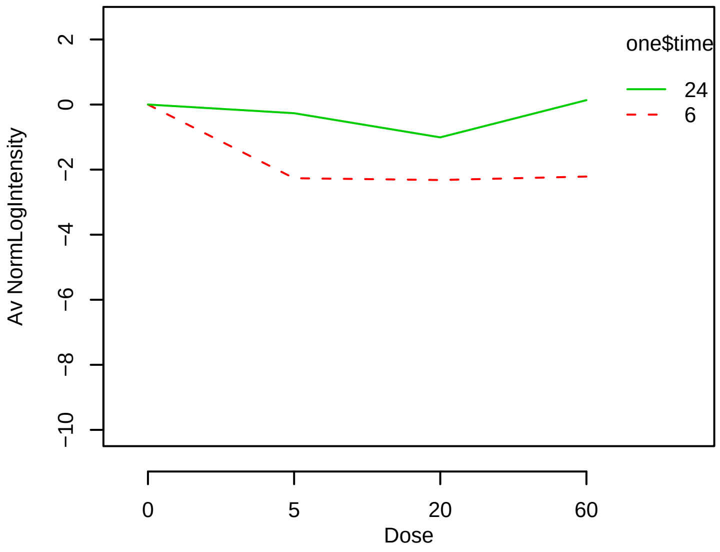


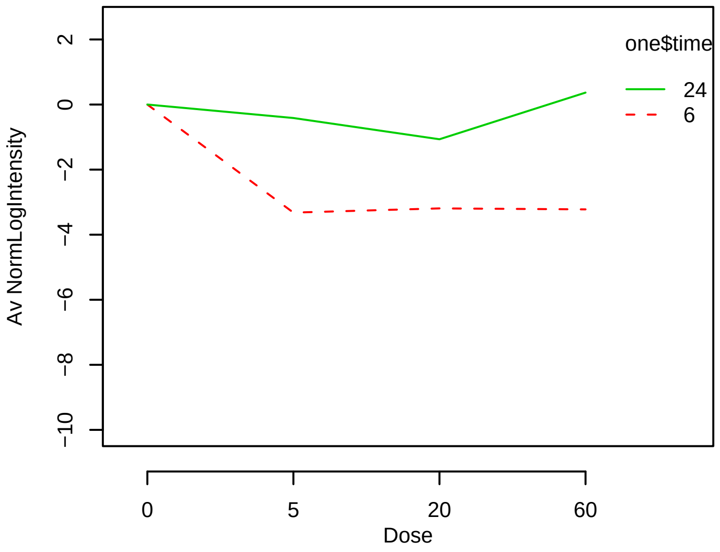
GO_0001947 : heart looping

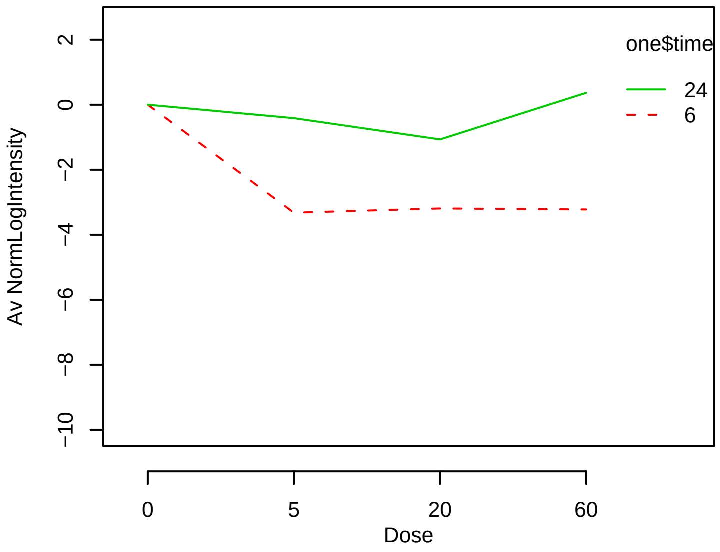


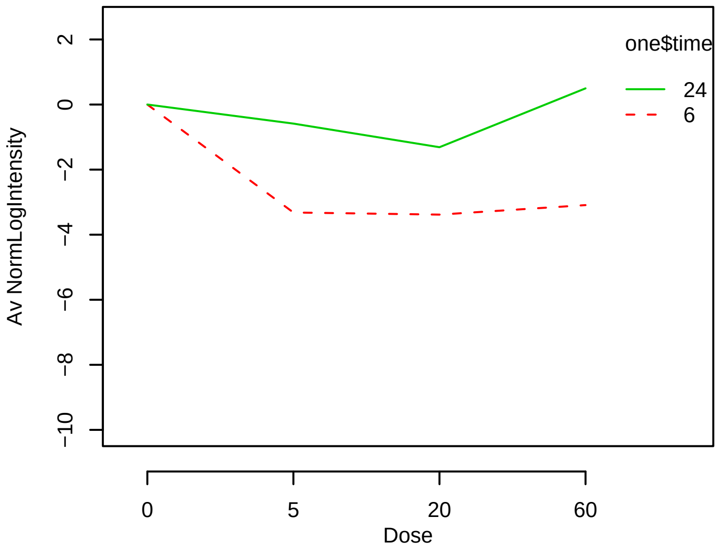
GO_0001952 : regulation of cell−matrix adhesion

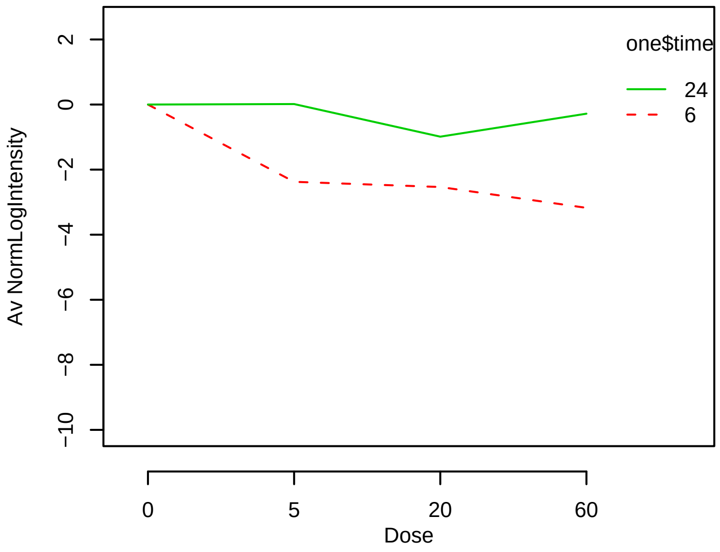


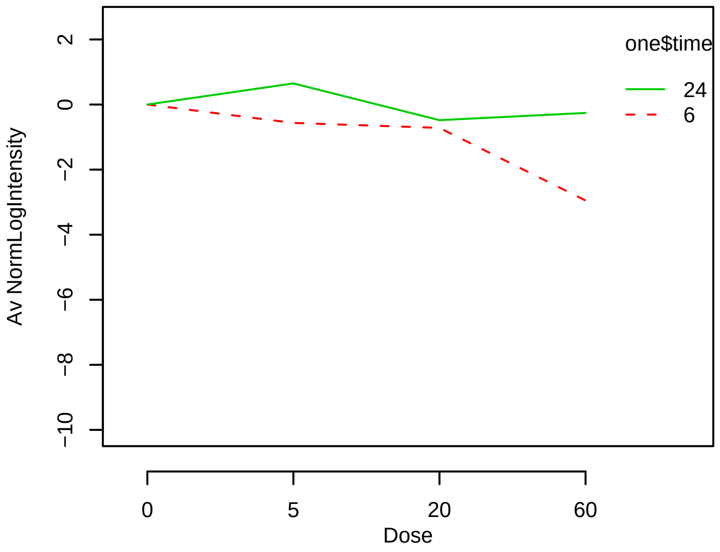

GO_0001974 : blood vessel remodeling

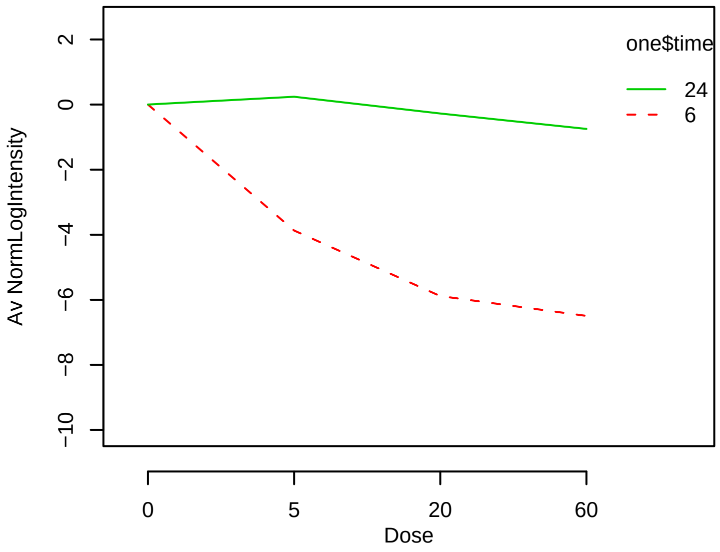

GO_0001976 : fast regulation of arterial pressure


GO_0001990 : regulation of blood pressure by hormones

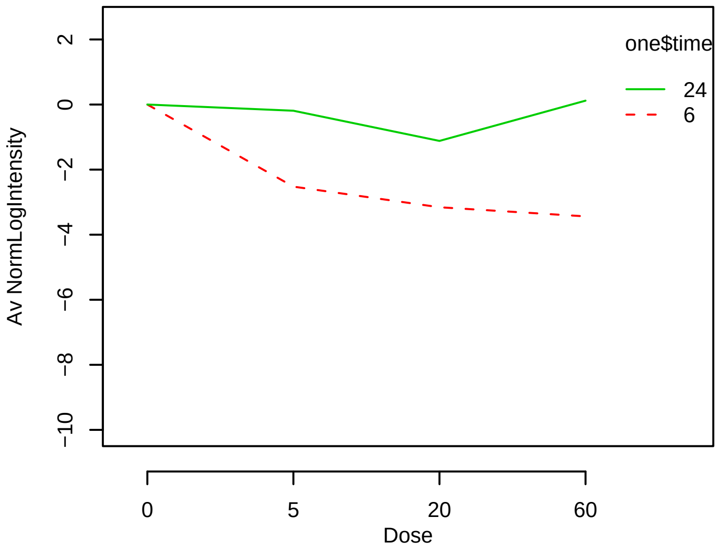

GO_0001993 : norepinephrine−epinephrine regulation of bloo


GO_0002009 : morphogenesis of an epithelium

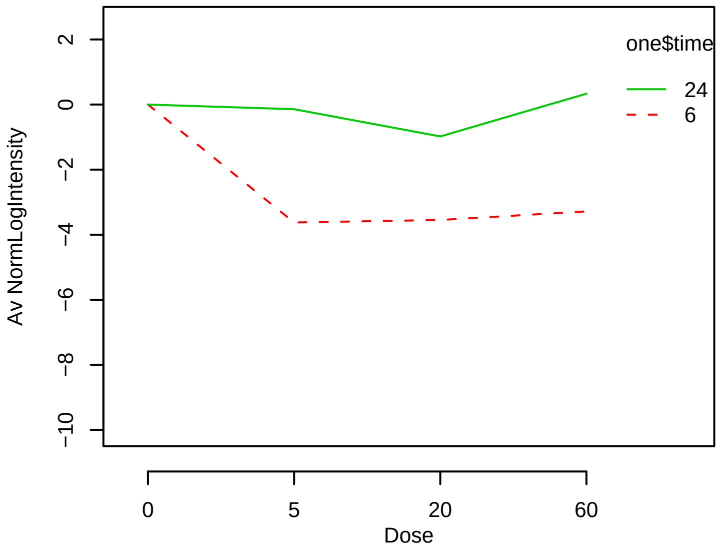

GO_0002011 : morphogenesis of an epithelial sheet



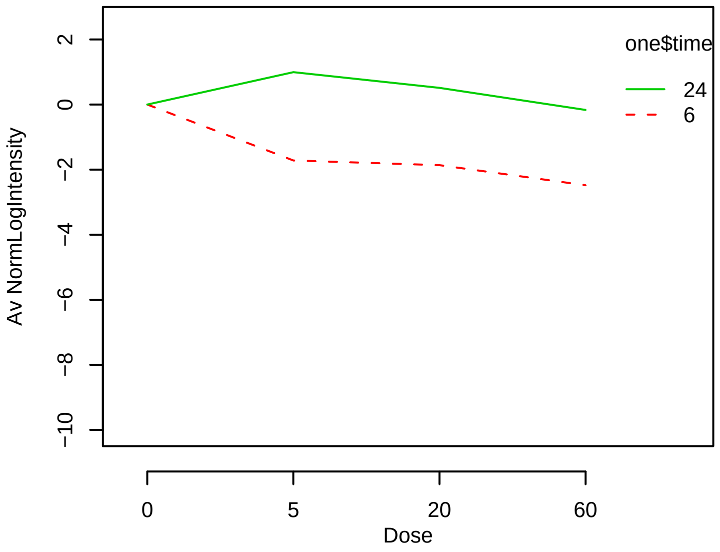
GO_0002026 : cardiac inotropy



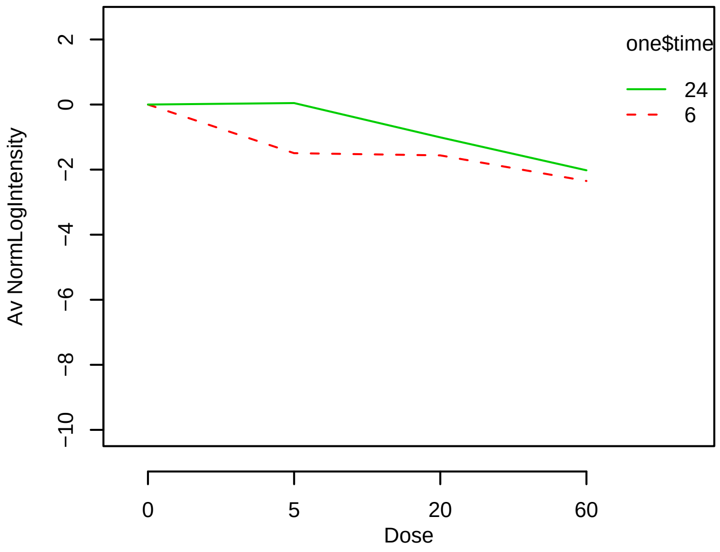
GO_0002443 : leukocyte mediated immunity



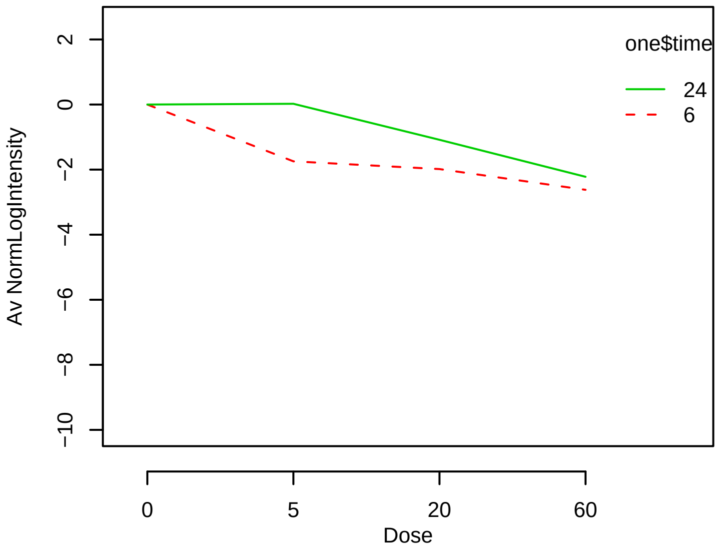
GO_0005513 : detection of calcium ion



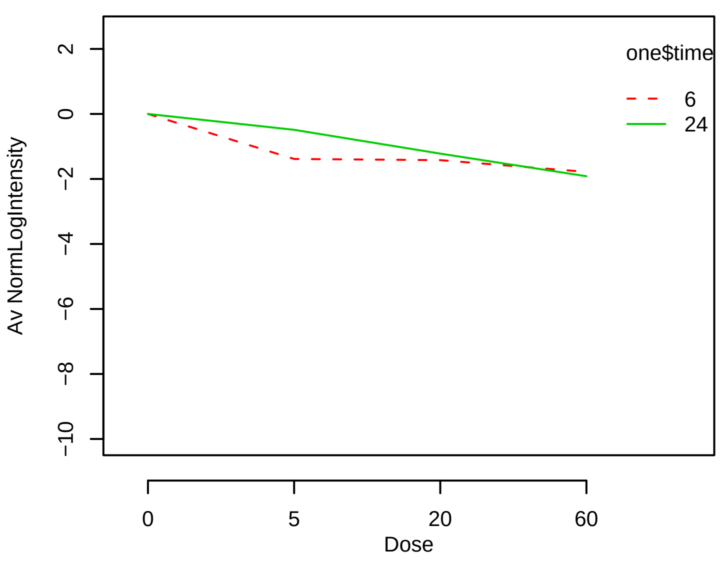
GO_0005976 : polysaccharide metabolism



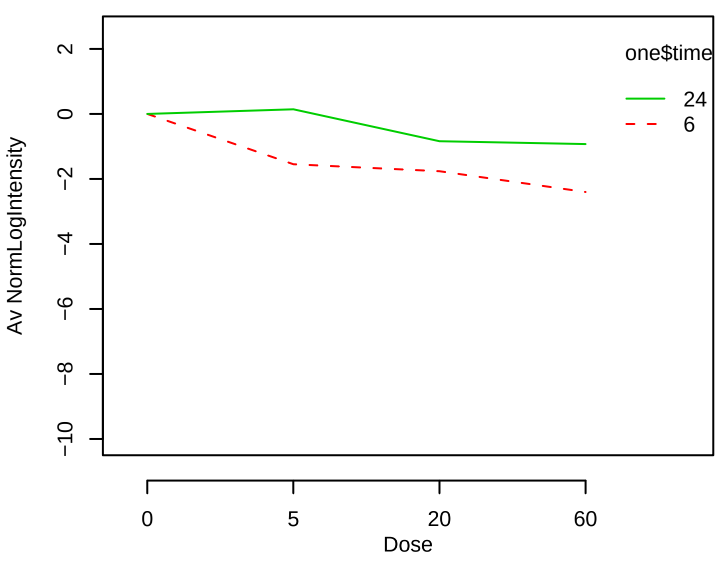
GO_0005977 : glycogen metabolism



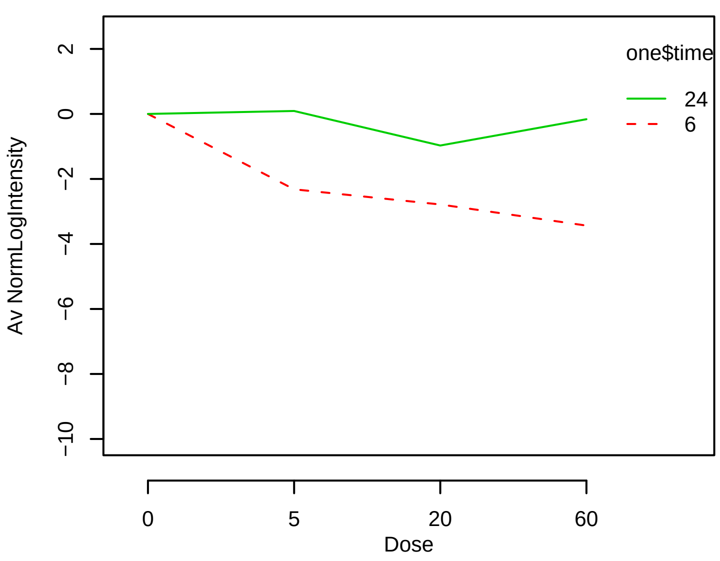
GO_0005978 : glycogen biosynthesis



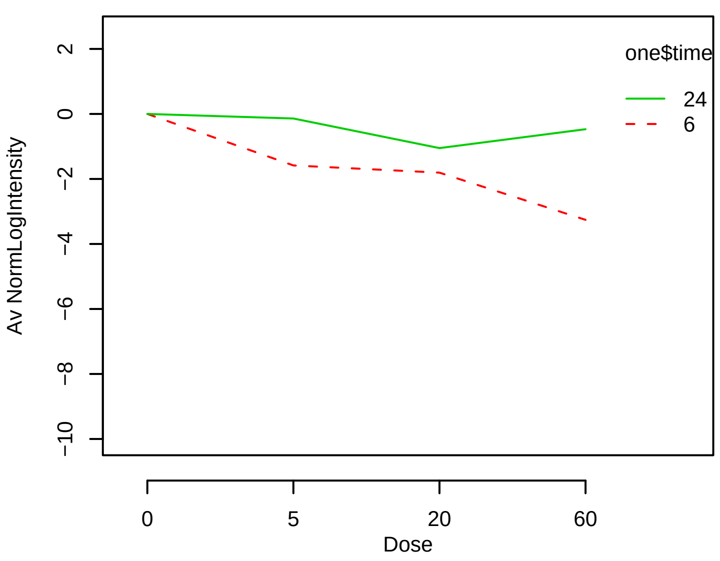
GO_0005980 : glycogen catabolism



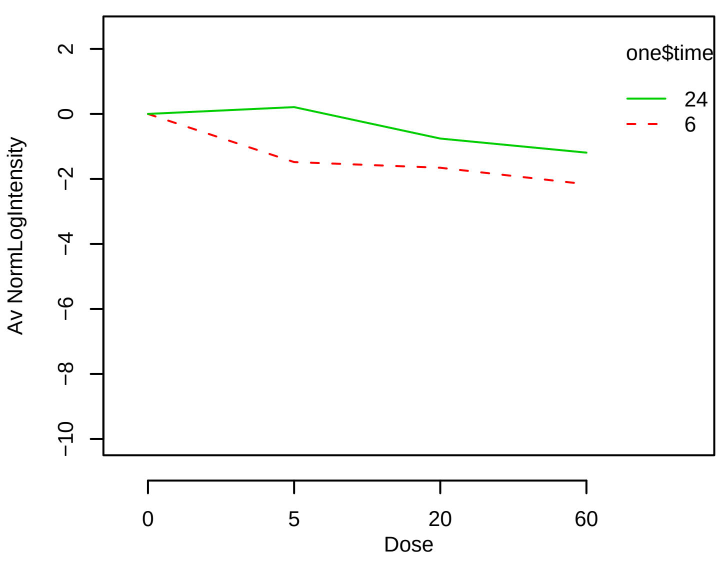
GO_0005996 : monosaccharide metabolism



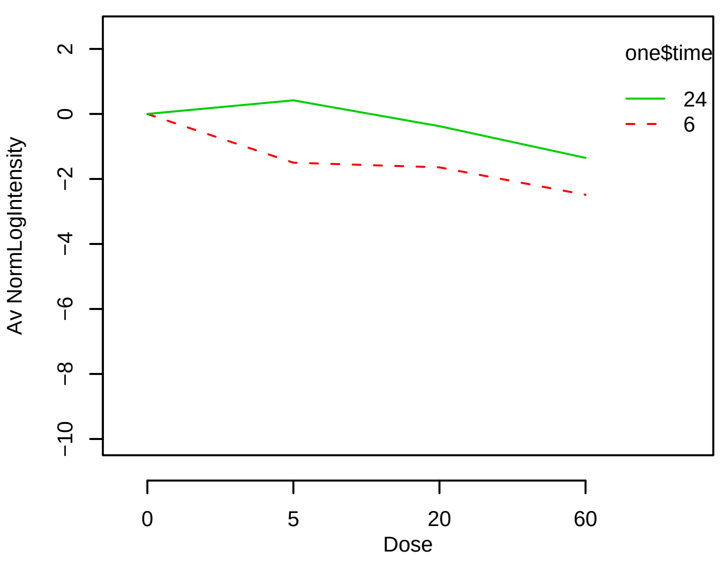
GO_0006000 : fructose metabolism



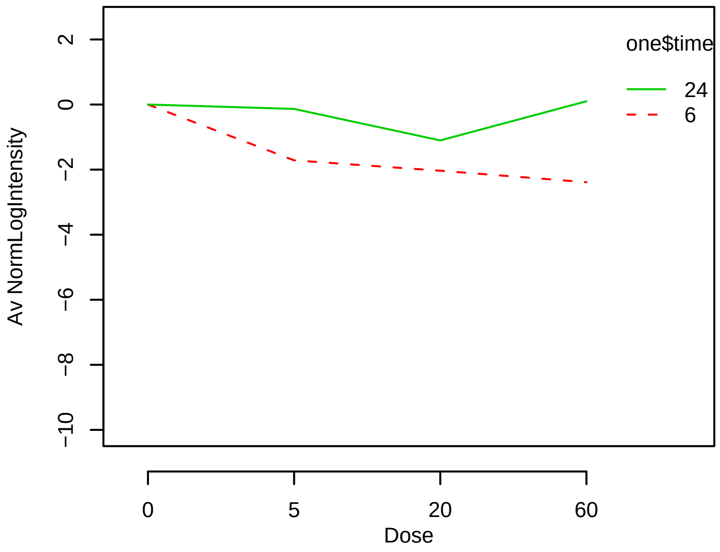
GO_0006004 : fucose metabolism

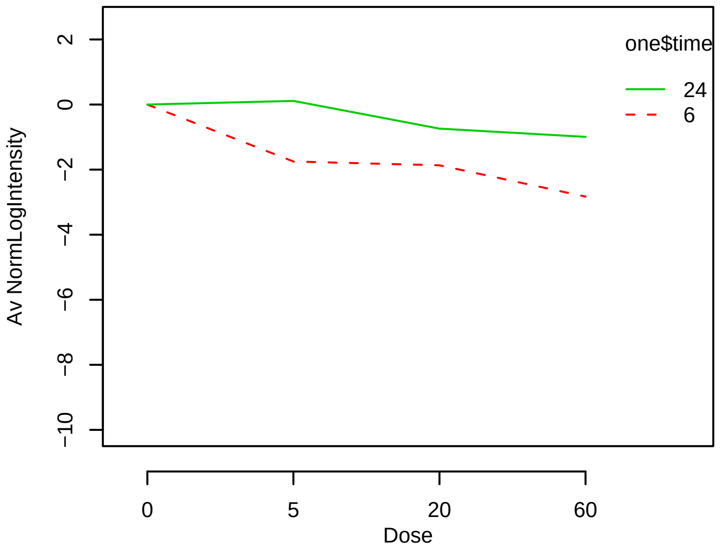


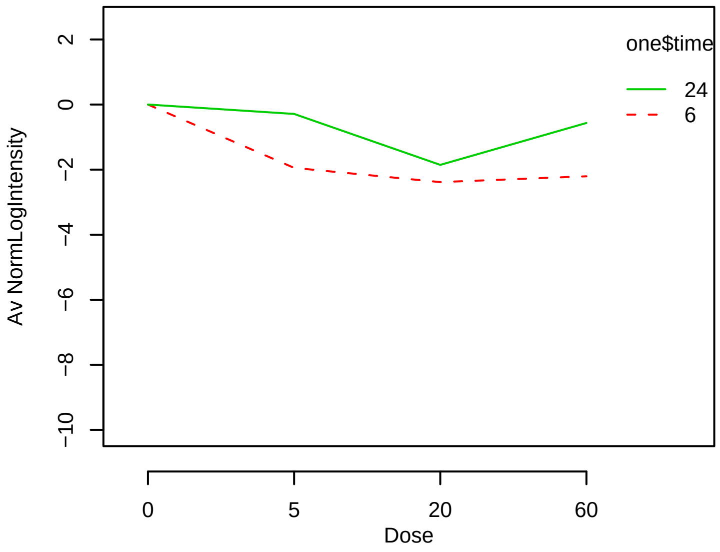
GO_0006006 : glucose metabolism

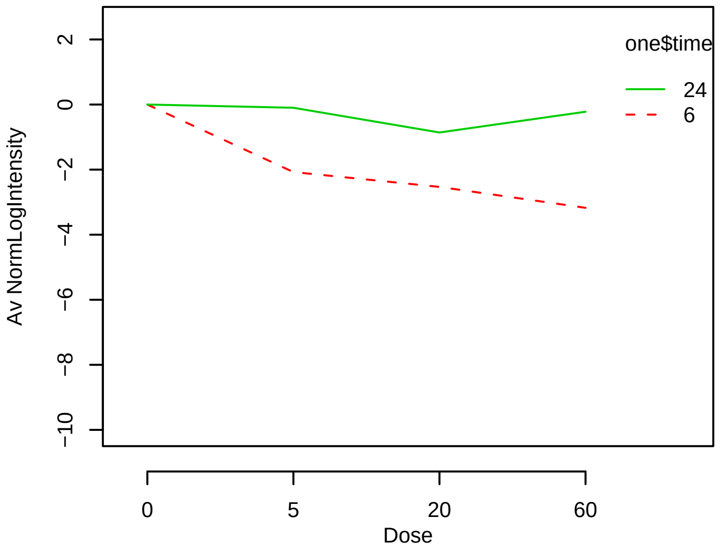


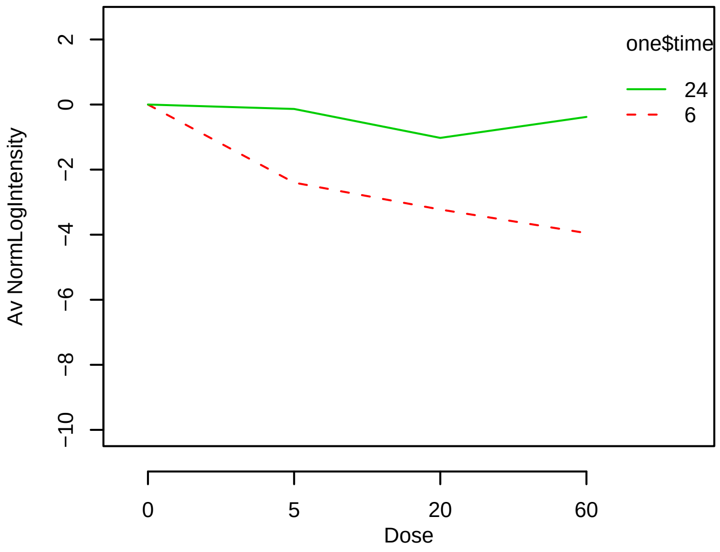
GO_0006007 : glucose catabolism

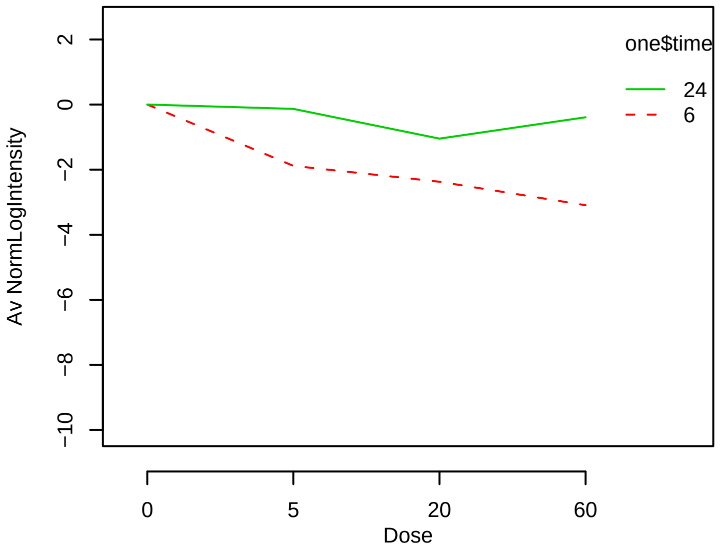

GO_0006012 : galactose metabolism

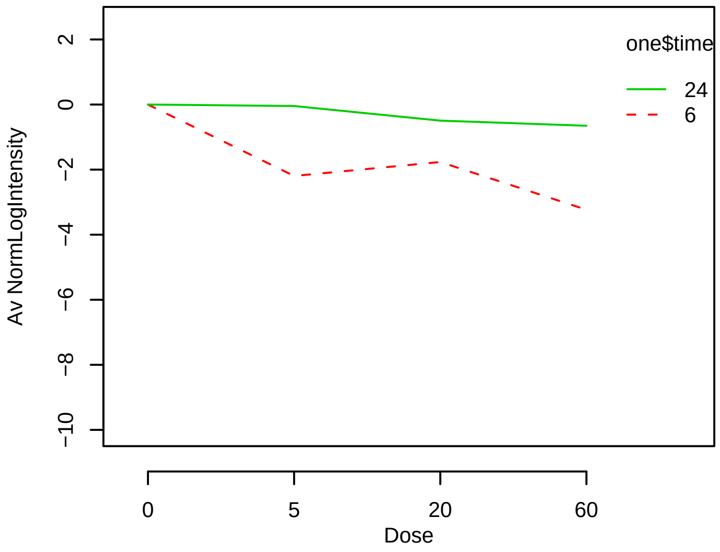

GO_0006013 : mannose metabolism


GO_0006020 : myo−inositol metabolism

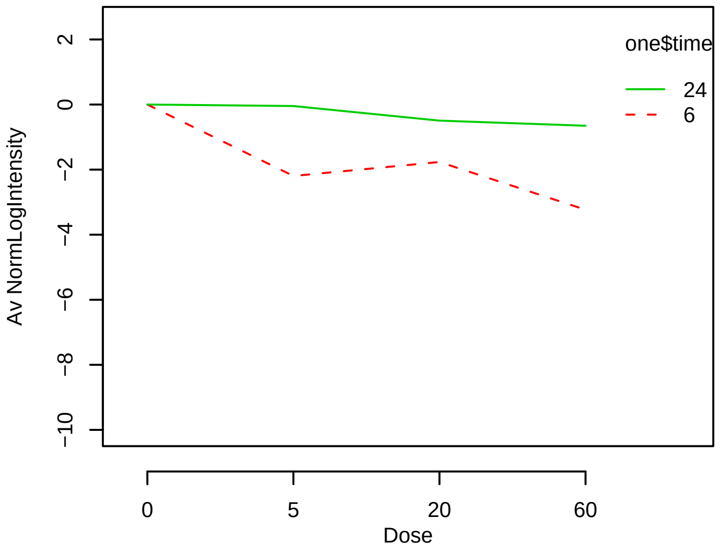

GO_0006022 : aminoglycan metabolism


GO_0006023 : aminoglycan biosynthesis

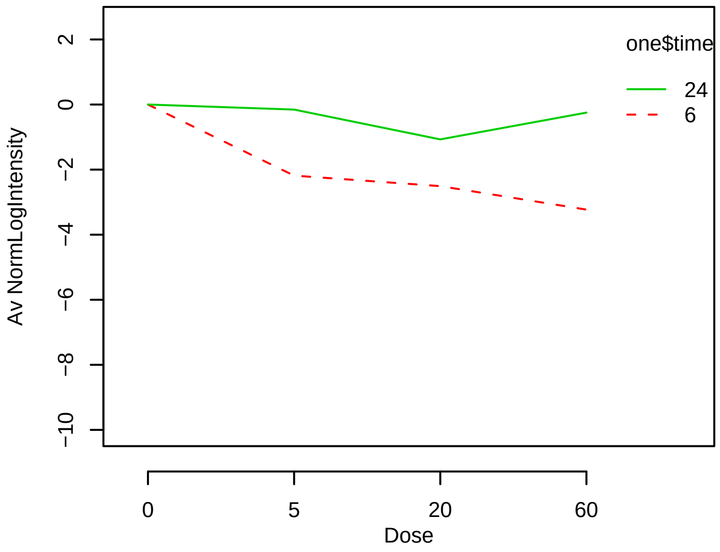

GO_0006024 : glycosaminoglycan biosynthesis



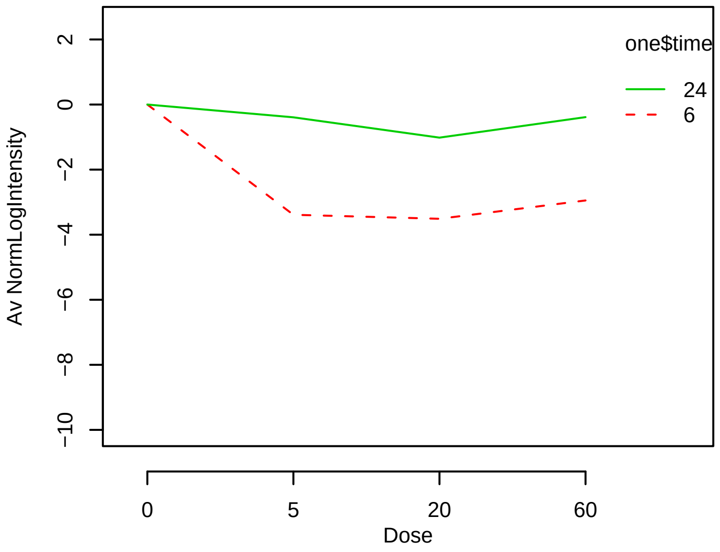
GO_0006026 : aminoglycan catabolism



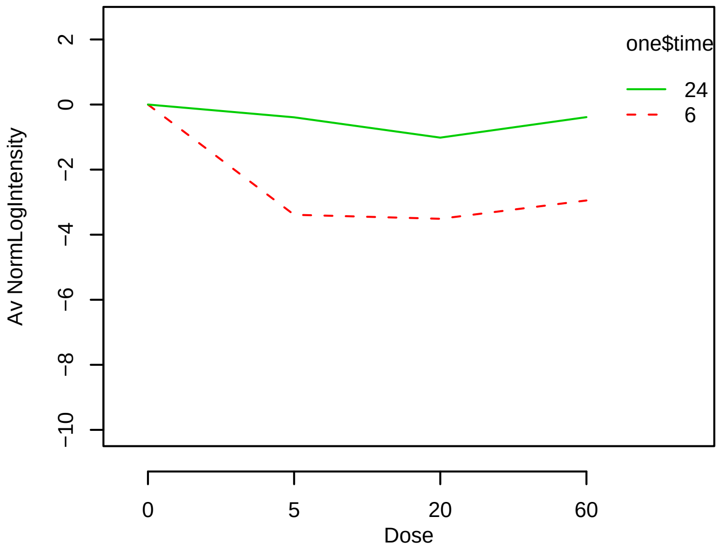
GO_0006027 : glycosaminoglycan catabolism



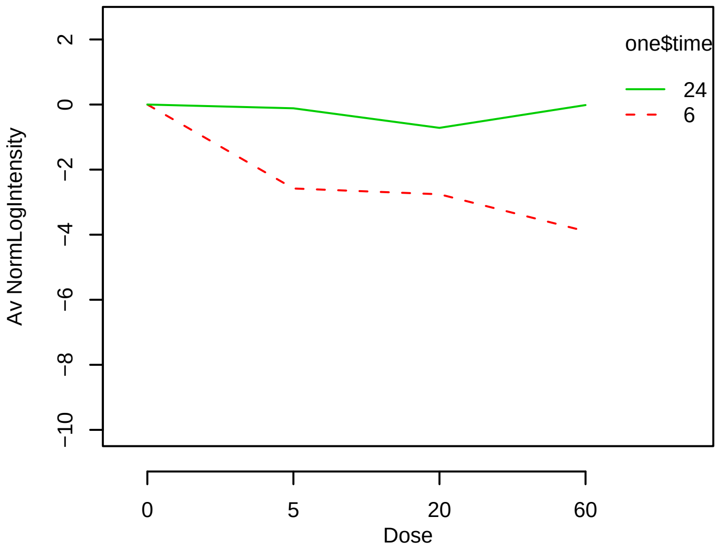
GO_0006029 : proteoglycan metabolism



GO_0006030 : chitin metabolism

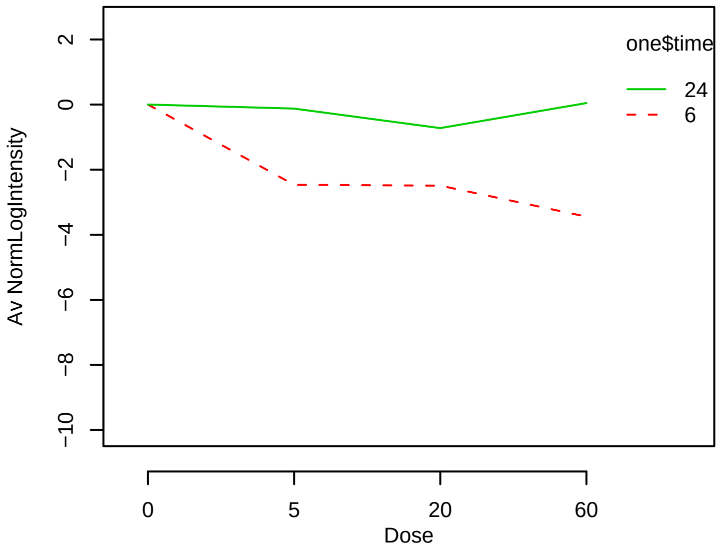


GO_0006032 : chitin catabolism

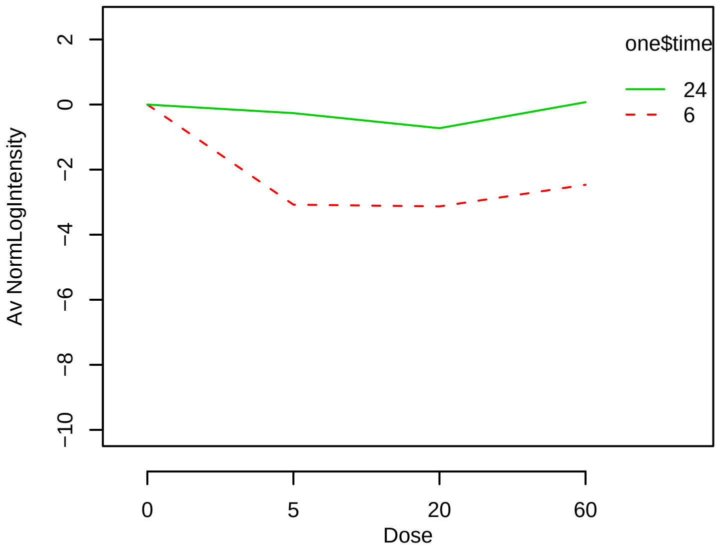


GO_0006040 : amino sugar metabolism

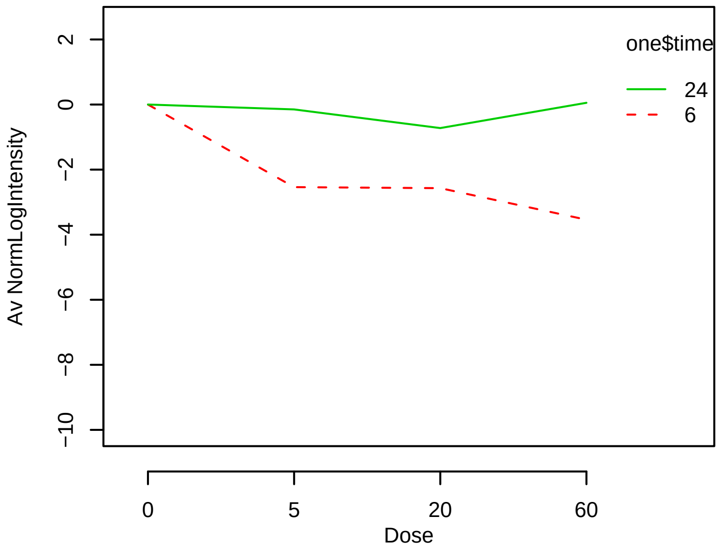
GO_0006041 : glucosamine metabolism



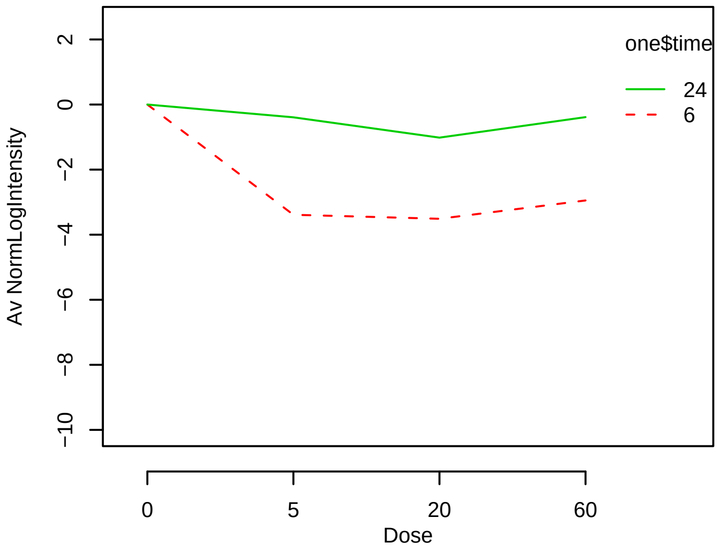
GO_0006043 : glucosamine catabolism



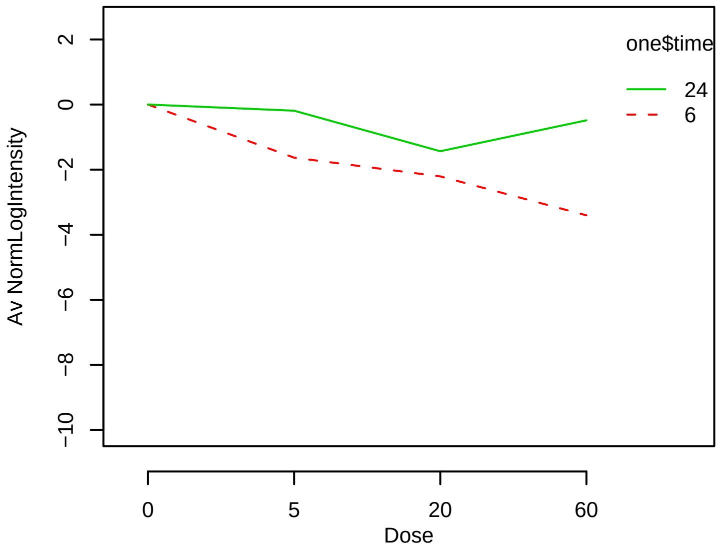
GO_0006044 : N−acetylglucosamine metabolism



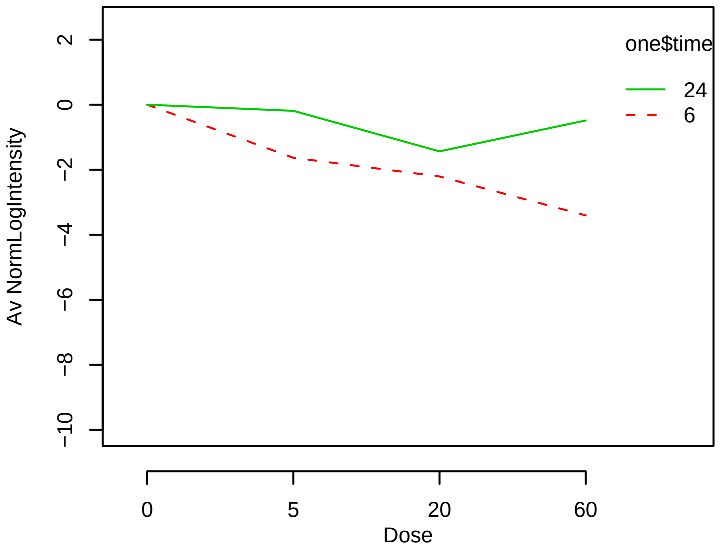
GO_0006046 : N−acetylglucosamine catabolism

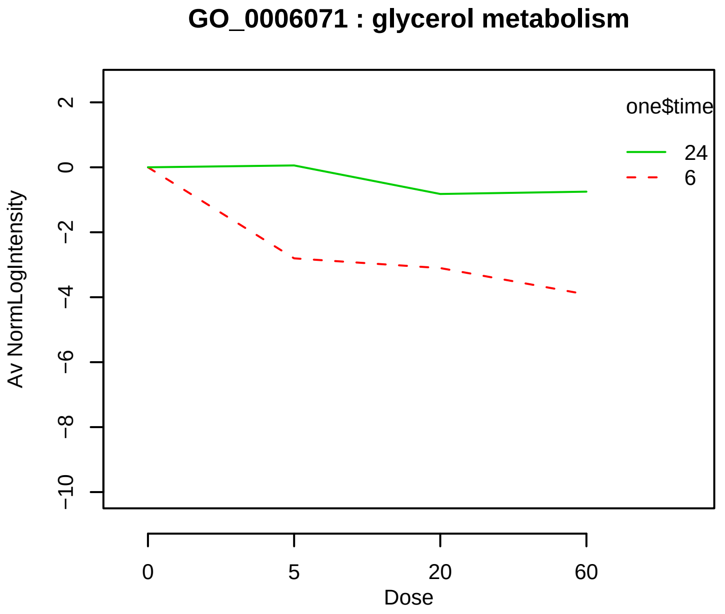


GO_0006067 : ethanol metabolism

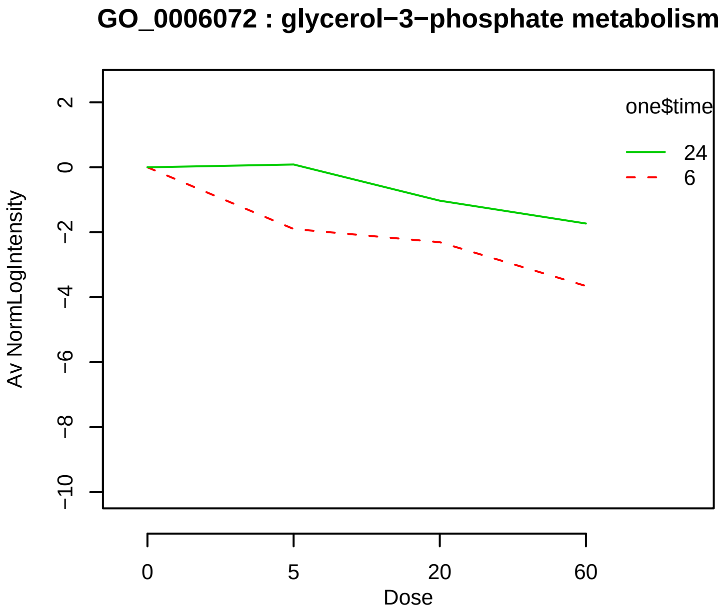


GO_0006069 : ethanol oxidation

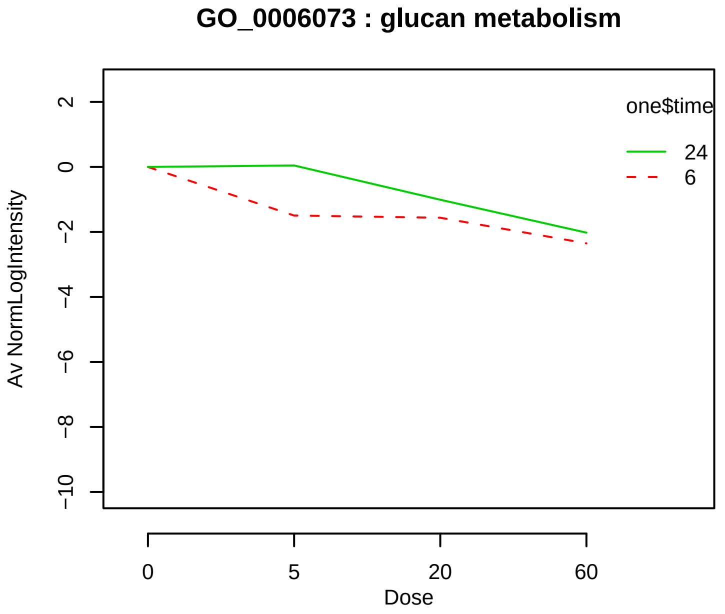




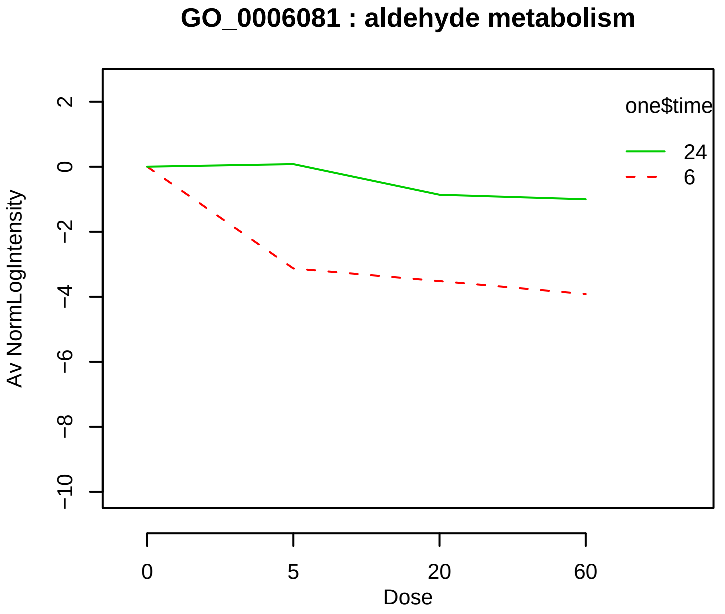
GO_0006071 : glycerol metabolism



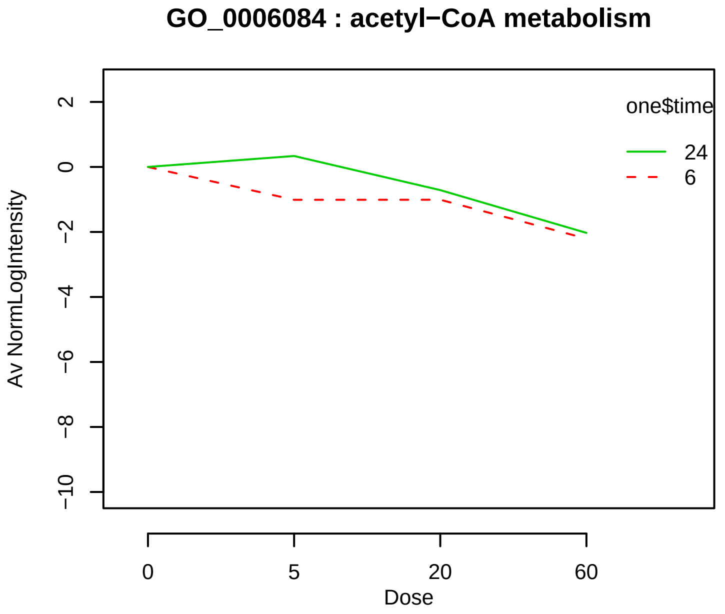
GO_0006072 : glycerol−3−phosphate metabolism



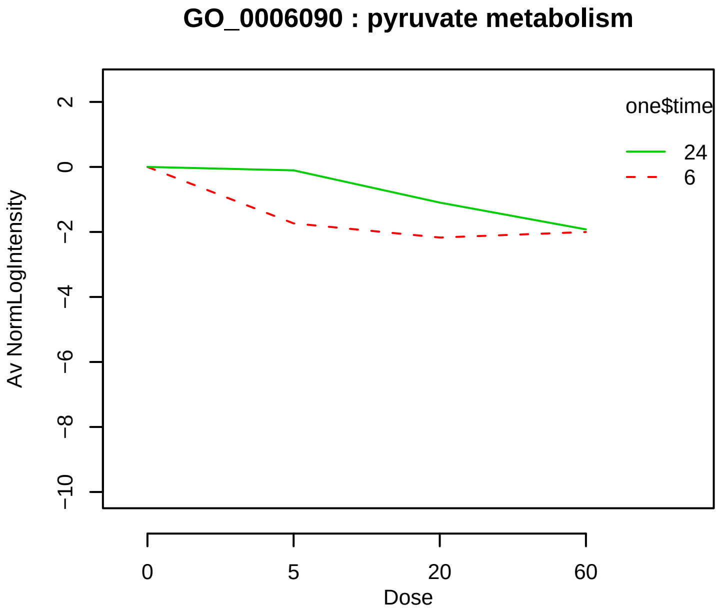
GO_0006073 : glucan metabolism



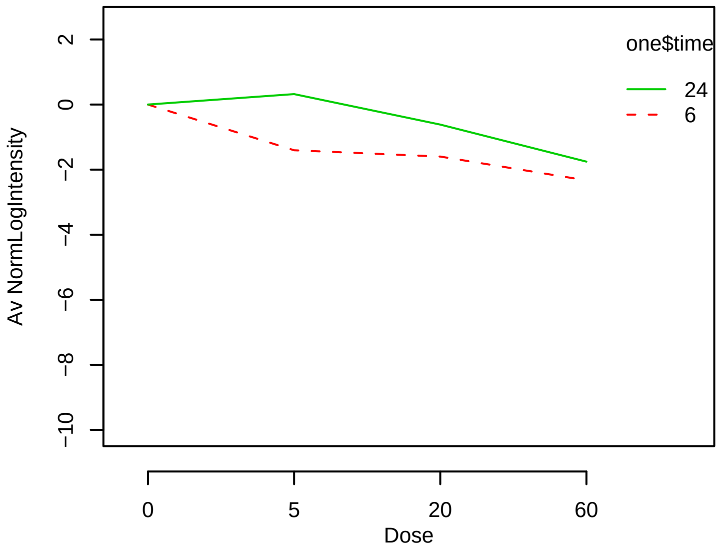
GO_0006081 : aldehyde metabolism

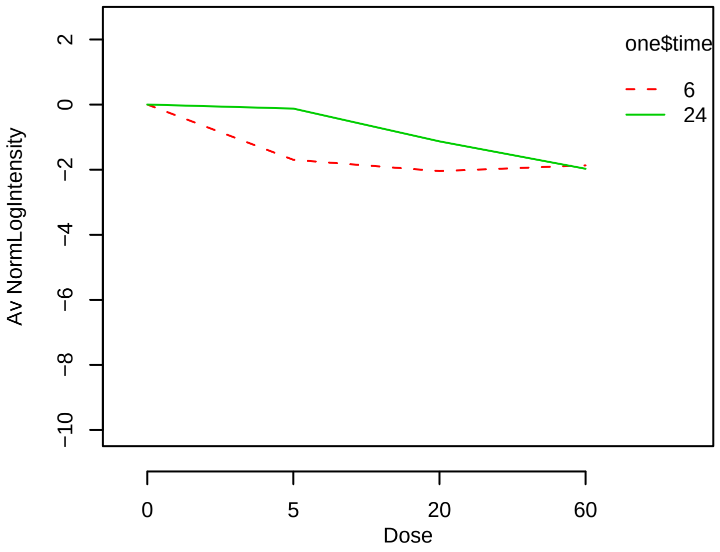


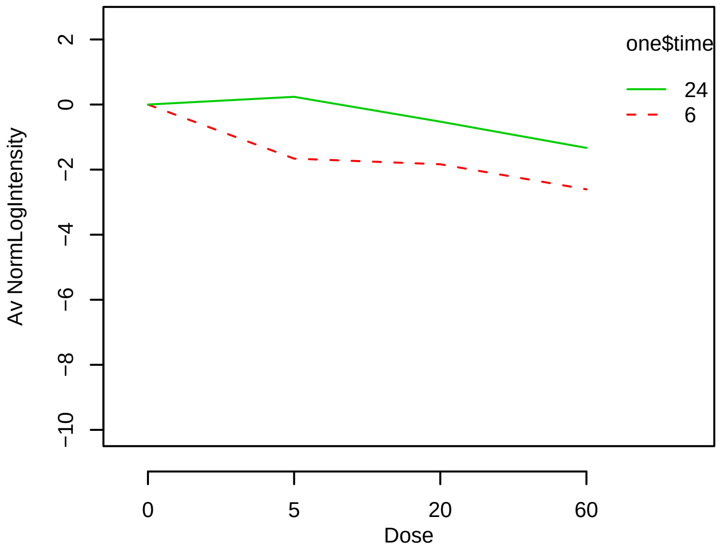
GO_0006084 : acetyl−CoA metabolism

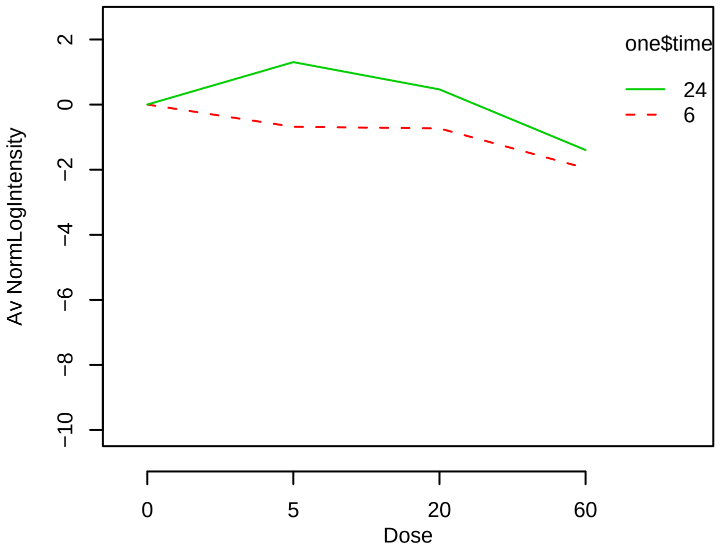


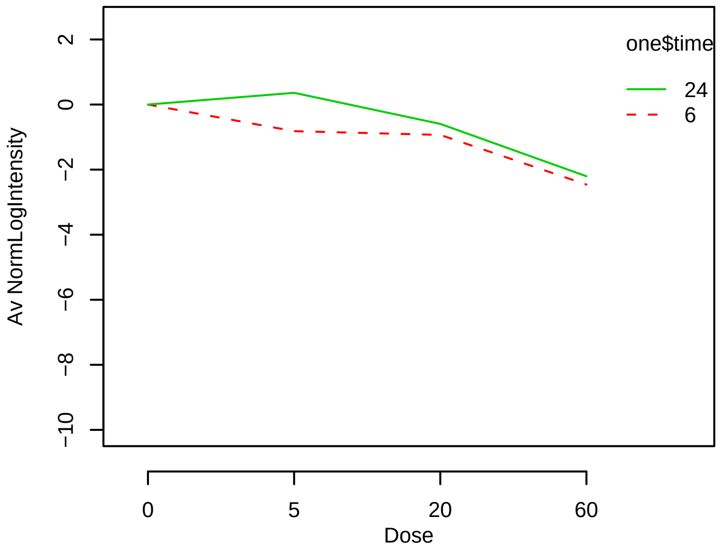
GO_0006090 : pyruvate metabolism

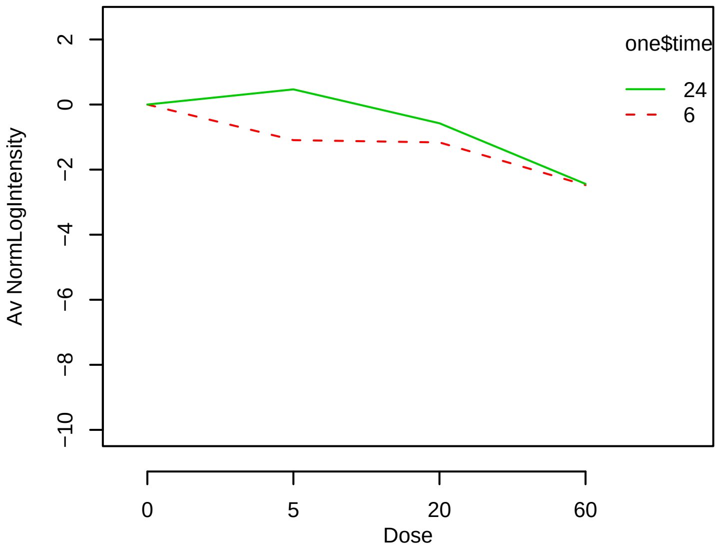

GO_0006092 : main pathways of carbohydrate metabolism


GO_0006094 : gluconeogenesis

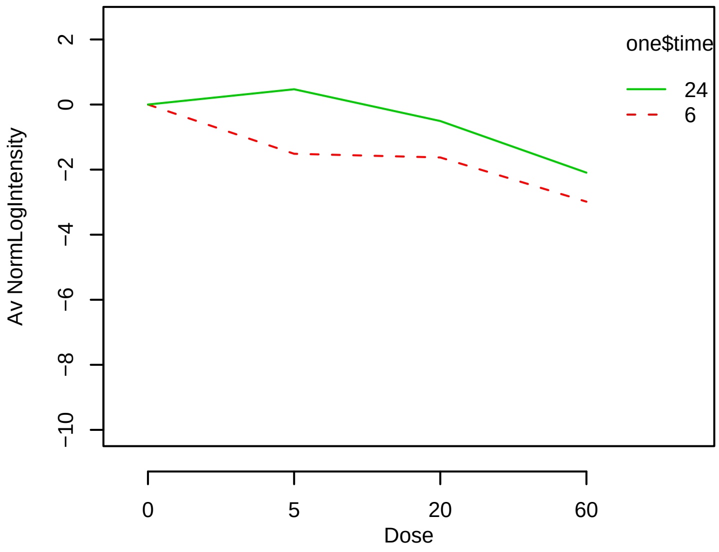

GO_0006096 : glycolysis


GO_0006098 : pentose−phosphate shunt

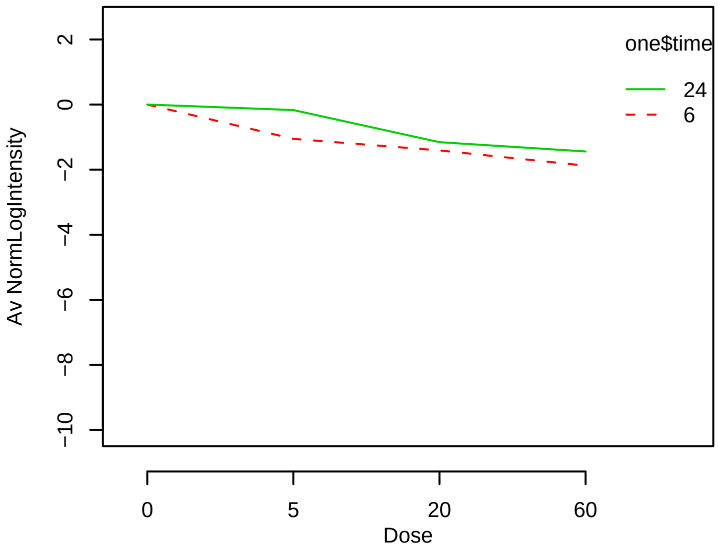

GO_0006099 : tricarboxylic acid cycle


GO_0006100 : tricarboxylic acid cycle intermediate metaboli

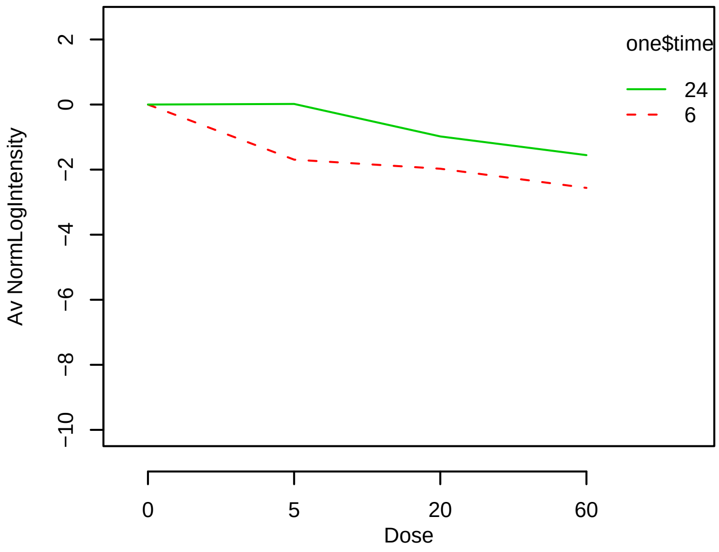
GO_0006108 : malate metabolism



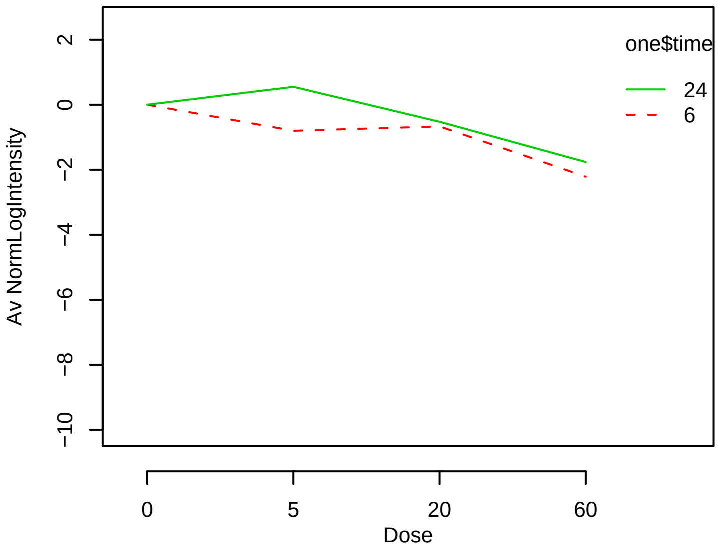
GO_0006109 : regulation of carbohydrate metabolism



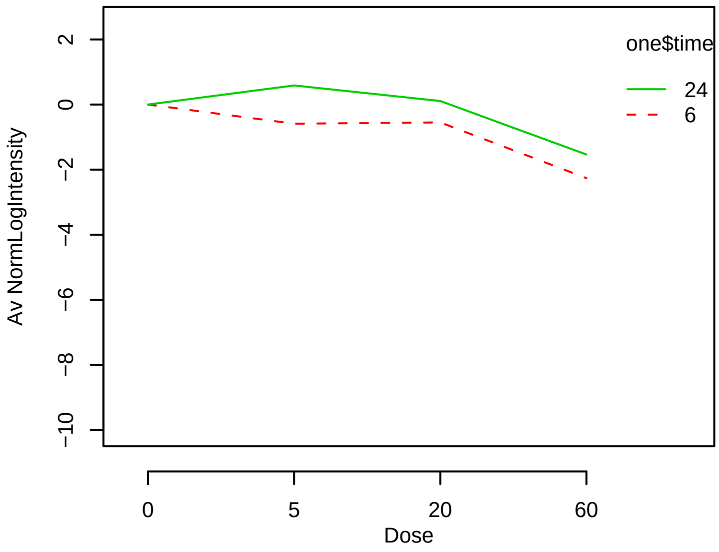
GO_0006112 : energy reserve metabolism



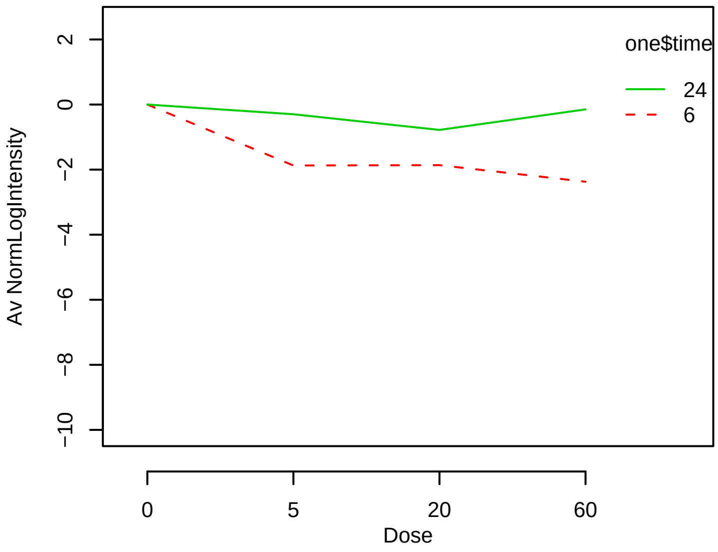
GO_0006119 : oxidative phosphorylation

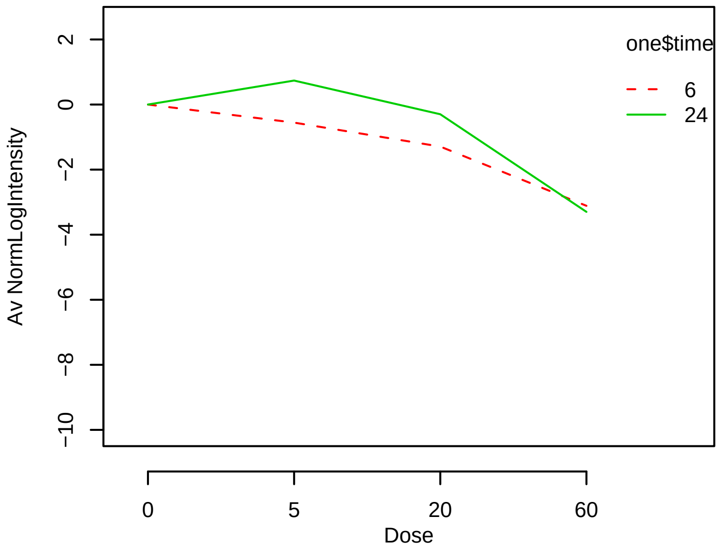


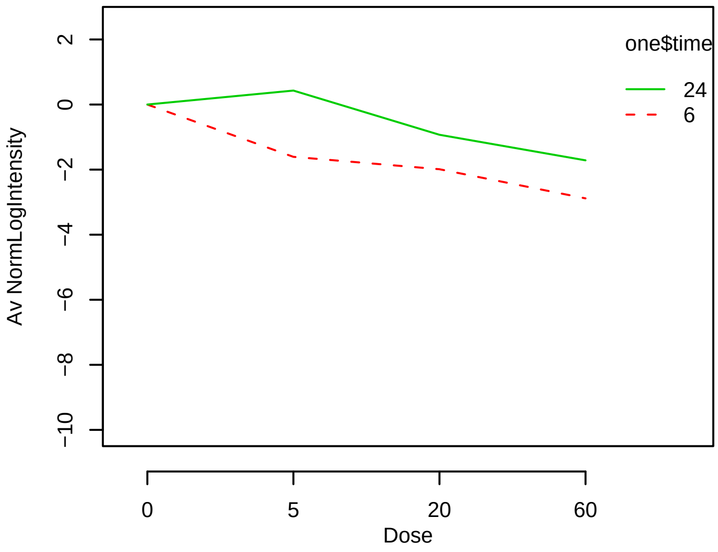
O_0006120 : mitochondrial electron transport\, NADH to ubi

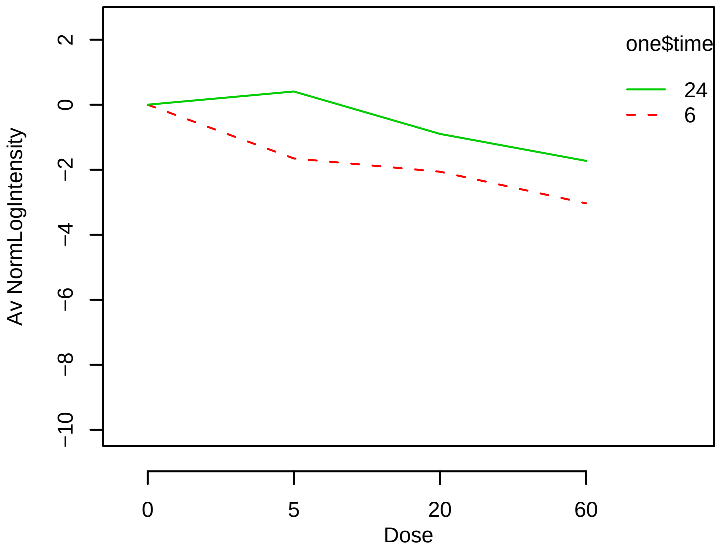


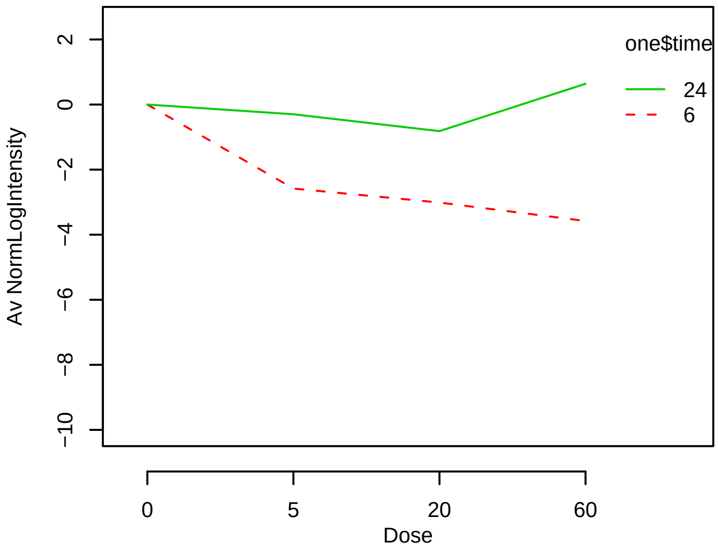
GO_0006140 : regulation of nucleotide metabolism

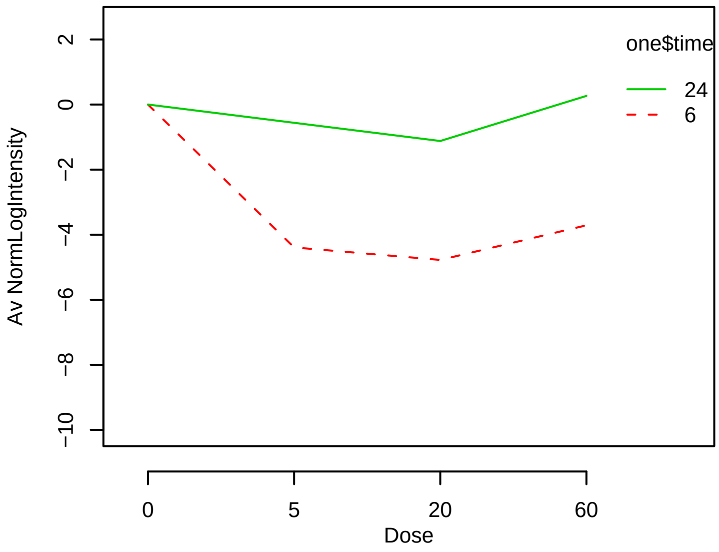


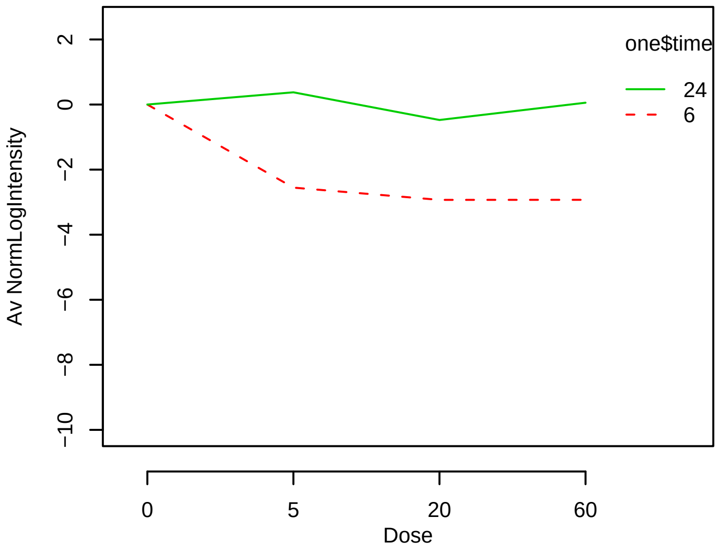

GO_0006144 : purine base metabolism


GO_0006163 : purine nucleotide metabolism

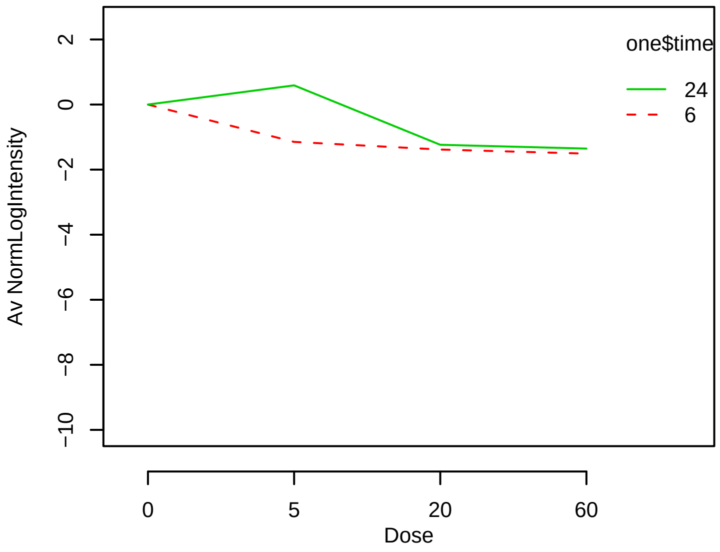

GO_0006164 : purine nucleotide biosynthesis


GO_0006171 : cAMP biosynthesis

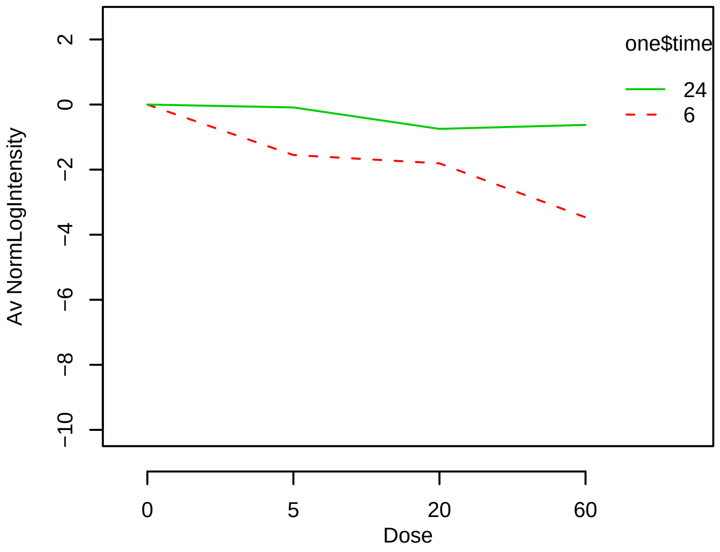

GO_0006182 : cGMP biosynthesis


GO_0006183 : GTP biosynthesis

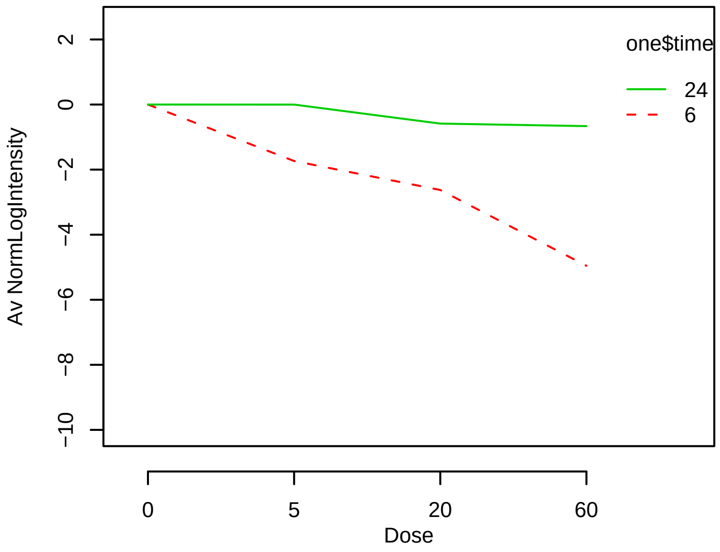
GO_0006195 : purine nucleotide catabolism



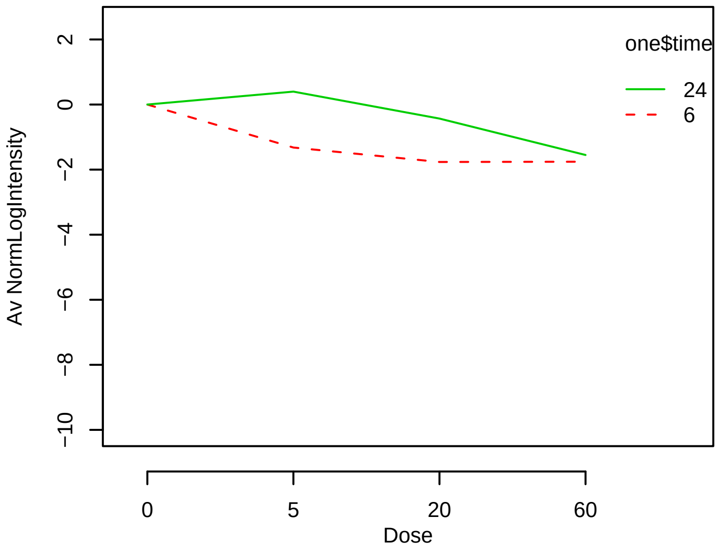
GO_0006206 : pyrimidine base metabolism



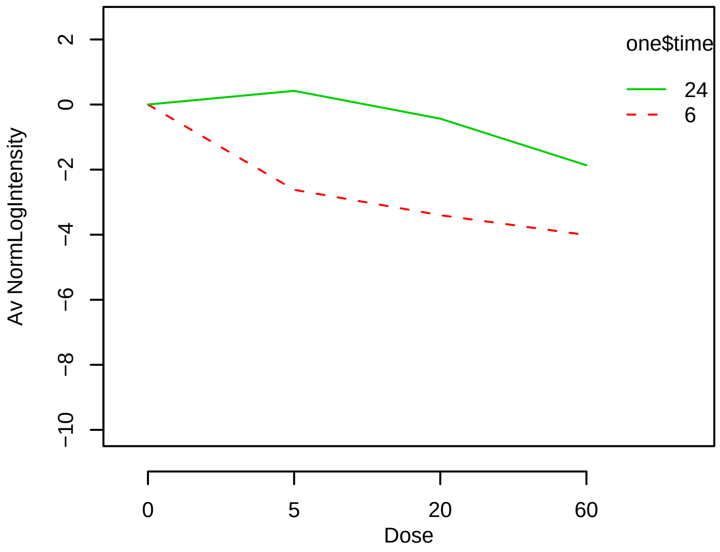
GO_0006207 : ’de novo’ pyrimidine base biosynthesis



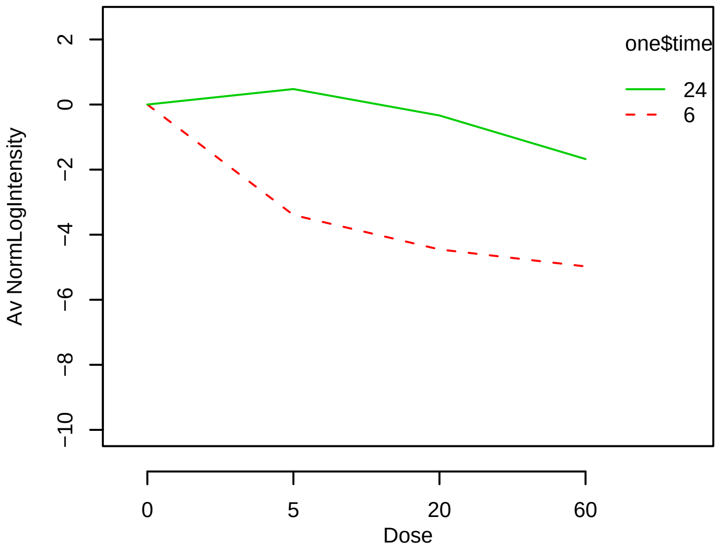
GO_0006213 : pyrimidine nucleoside metabolism

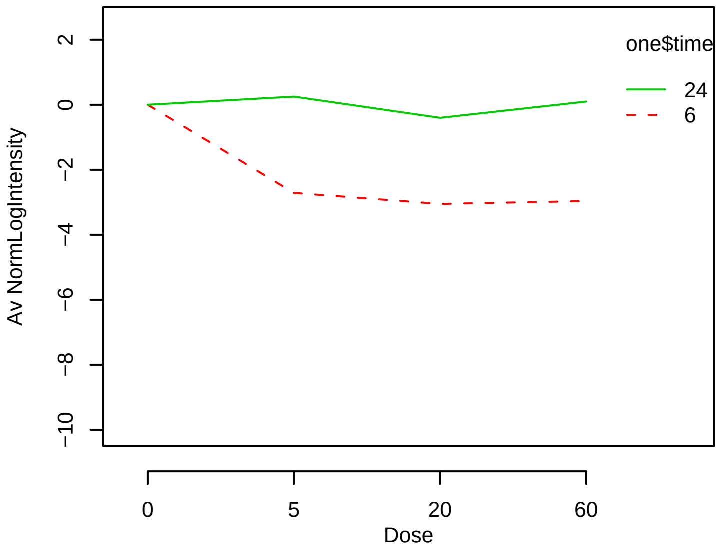


GO_0006220 : pyrimidine nucleotide metabolism

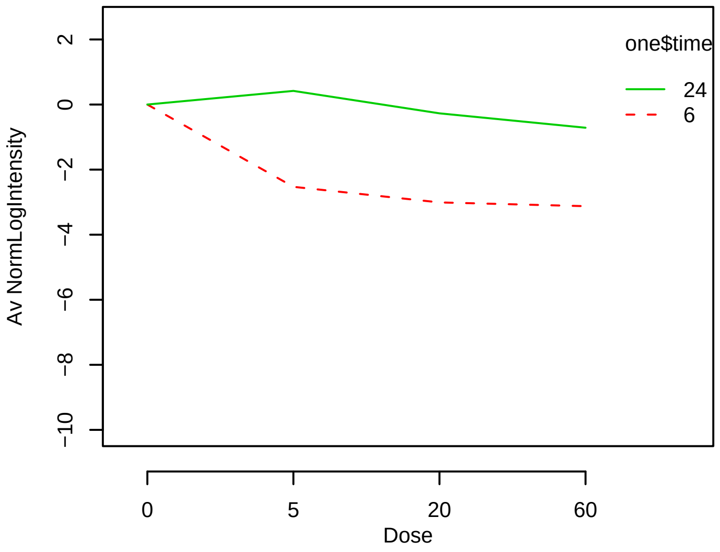


GO_0006221 : pyrimidine nucleotide biosynthesis

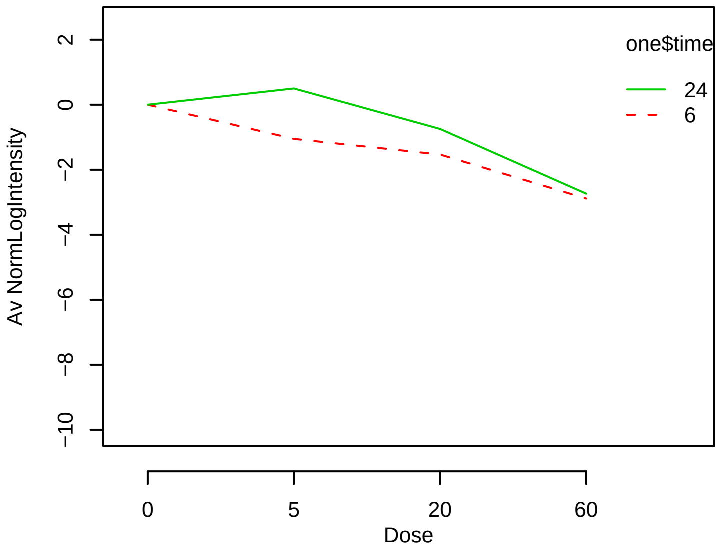




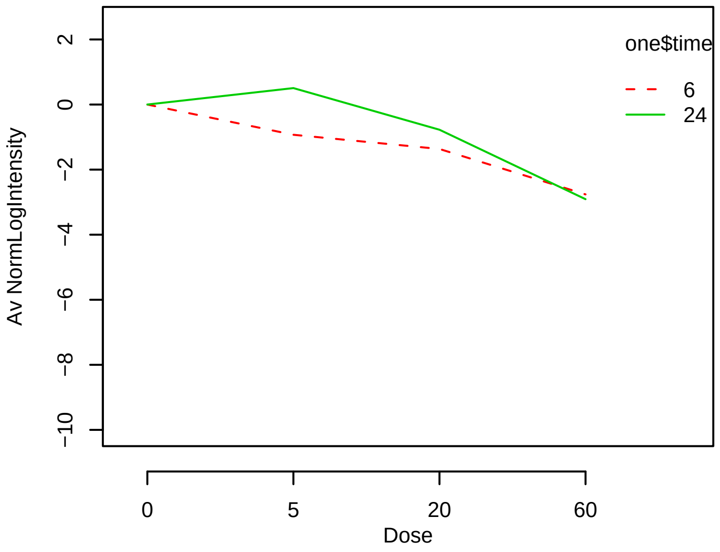
GO_0006228 : UTP biosynthesis



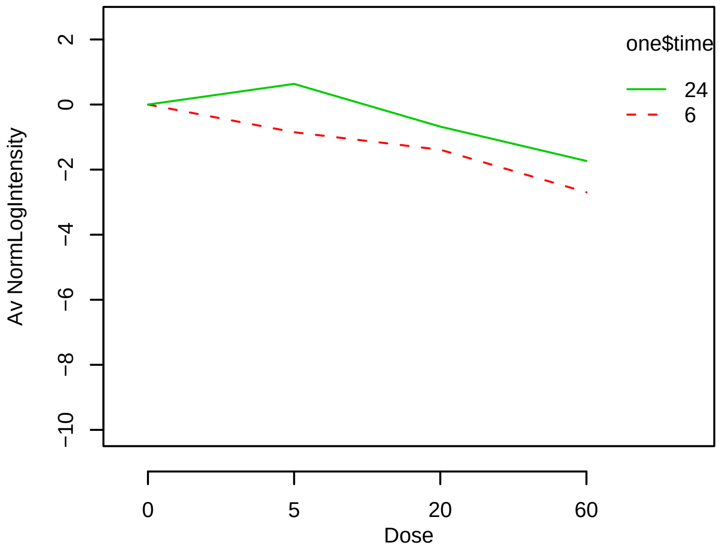
GO_0006241 : CTP biosynthesis



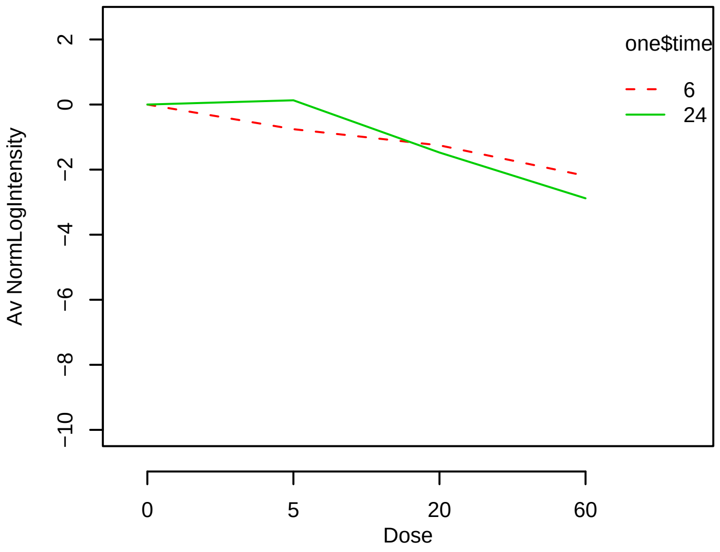
GO_0006260 : DNA replication



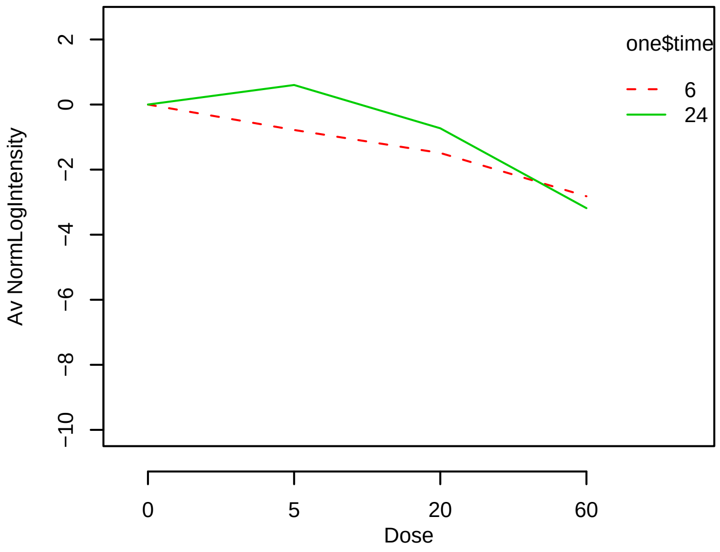
GO_0006261 : DNA−dependent DNA replication

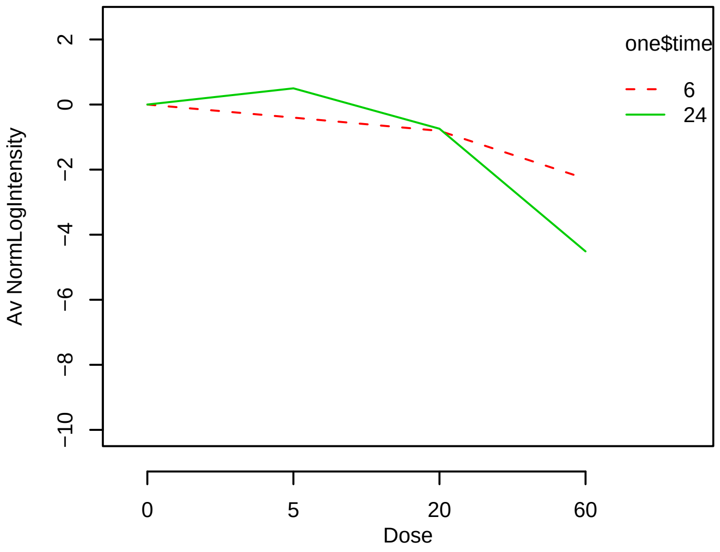


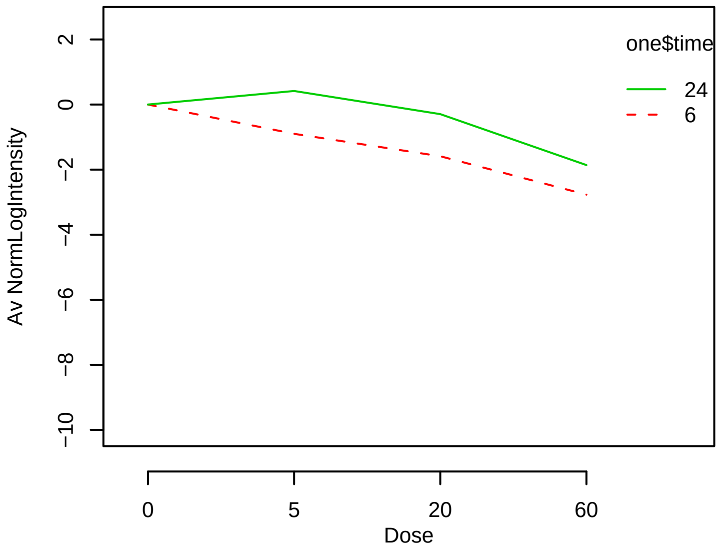
GO_0006265 : DNA topological change

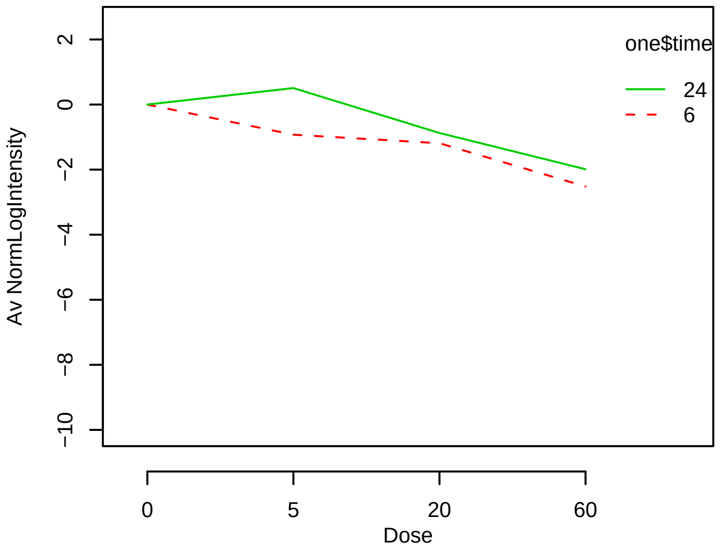


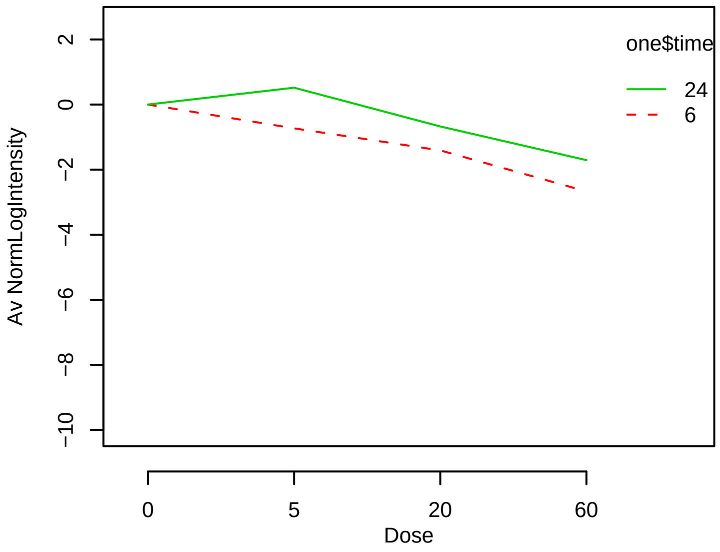
GO_0006268 : DNA unwinding during replication

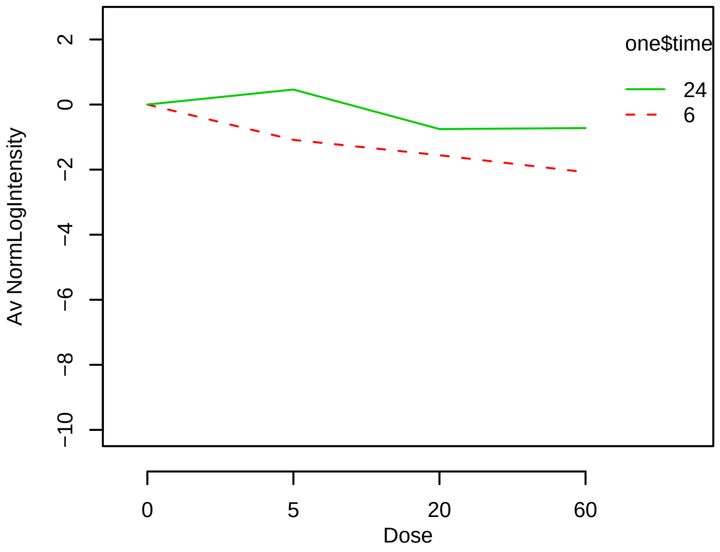

GO_0006270 : DNA replication initiation

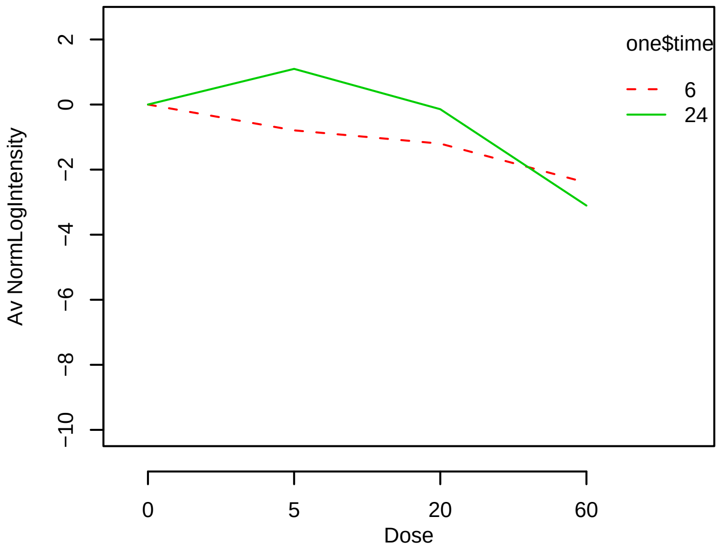

GO_0006271 : DNA strand elongation


GO_0006275 : regulation of DNA replication

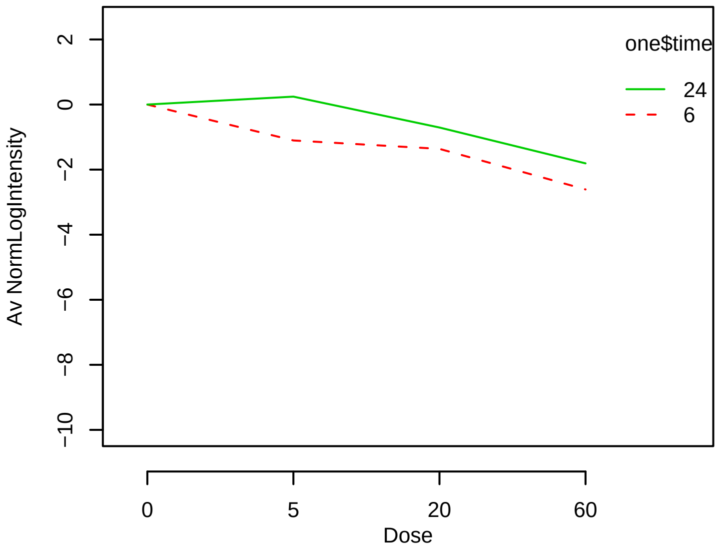

GO_0006281 : DNA repair


GO_0006282 : regulation of DNA repair

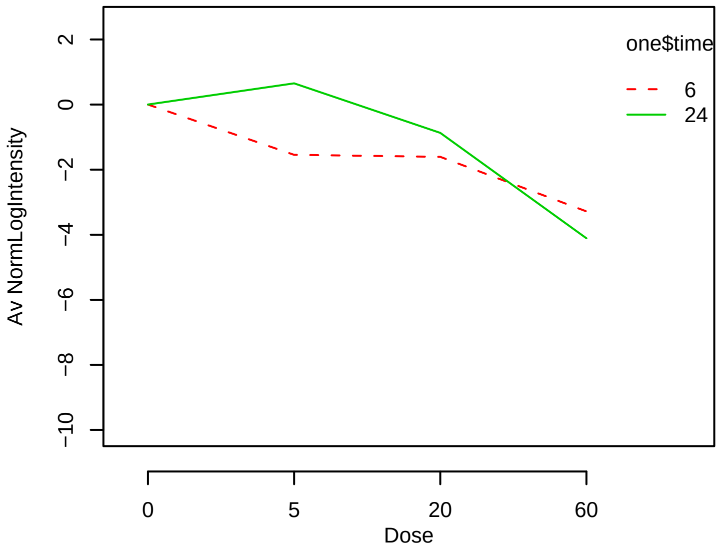

GO_0006283 : transcription−coupled nucleotide−excision re



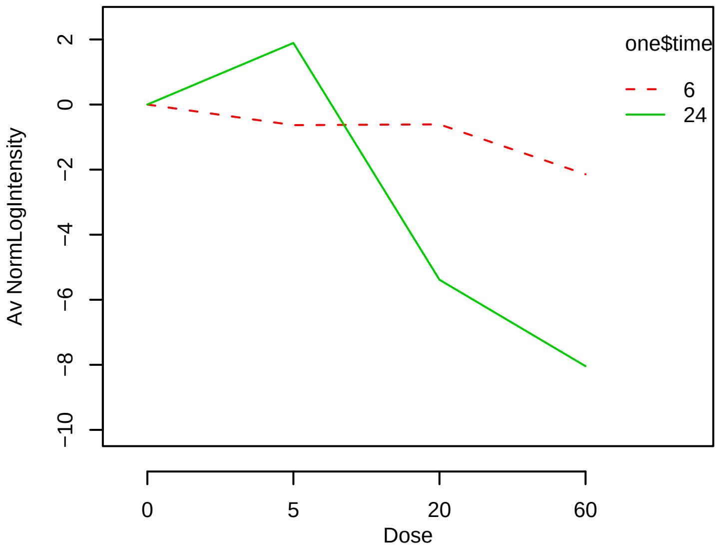
GO_0006284 : base−excision repair



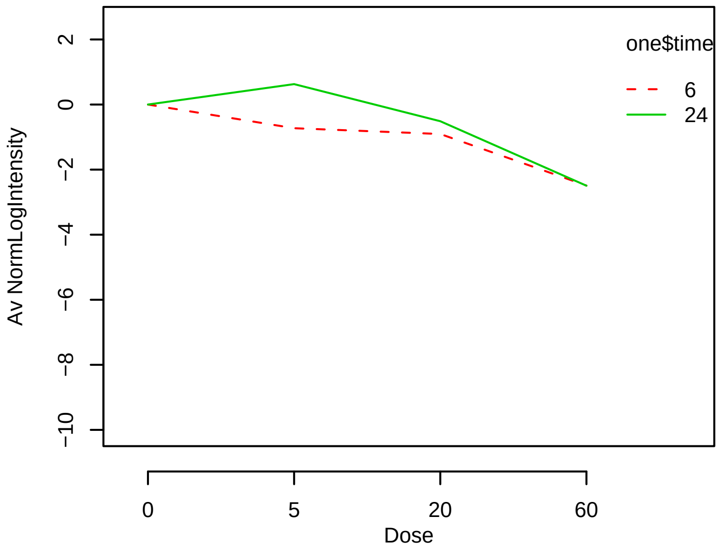
GO_0006289 : nucleotide−excision repair



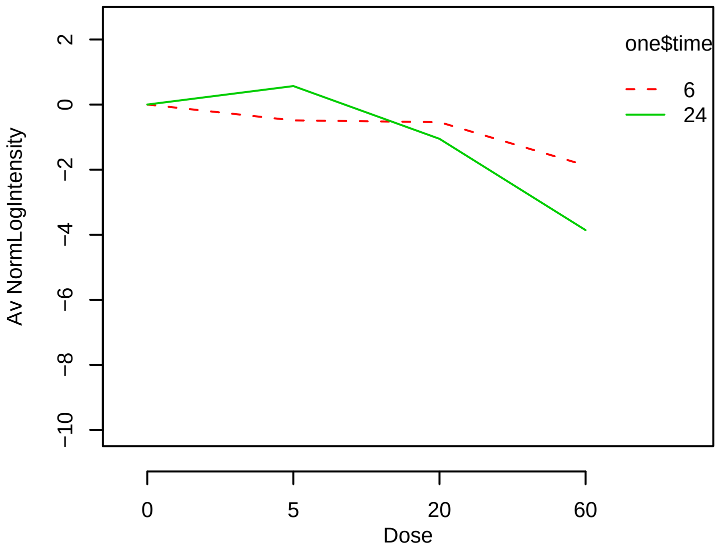
GO_0006298 : mismatch repair



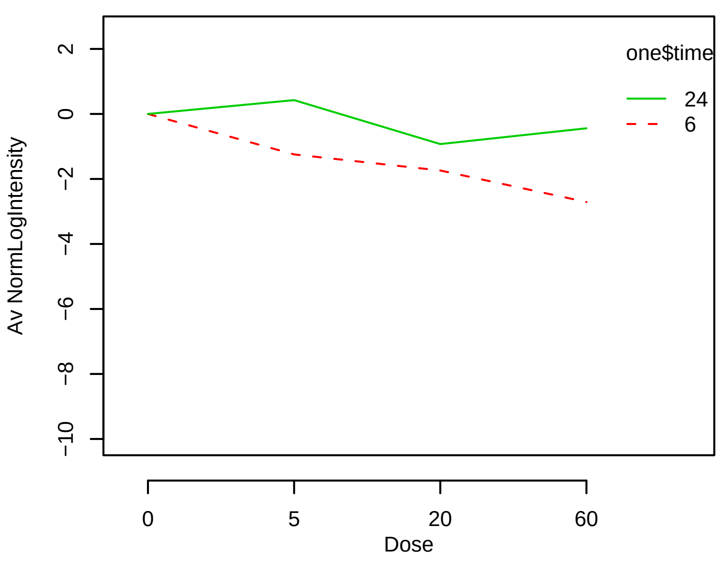
GO_0006301 : postreplication repair



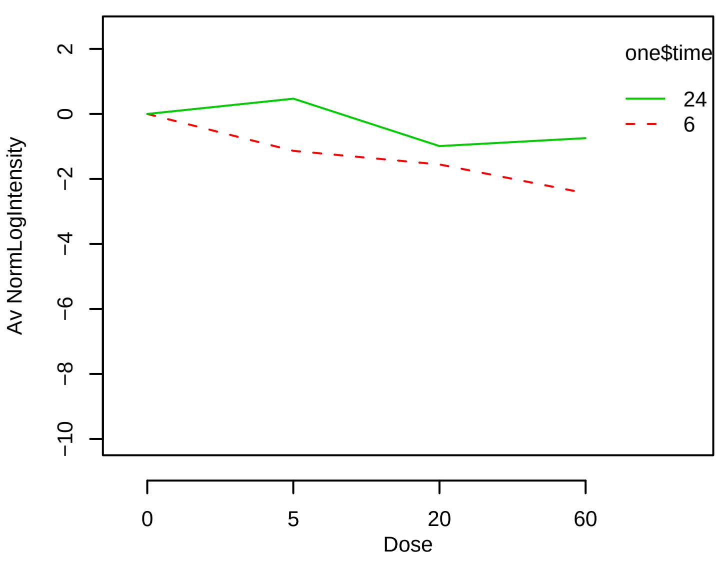
GO_0006302 : double−strand break repair



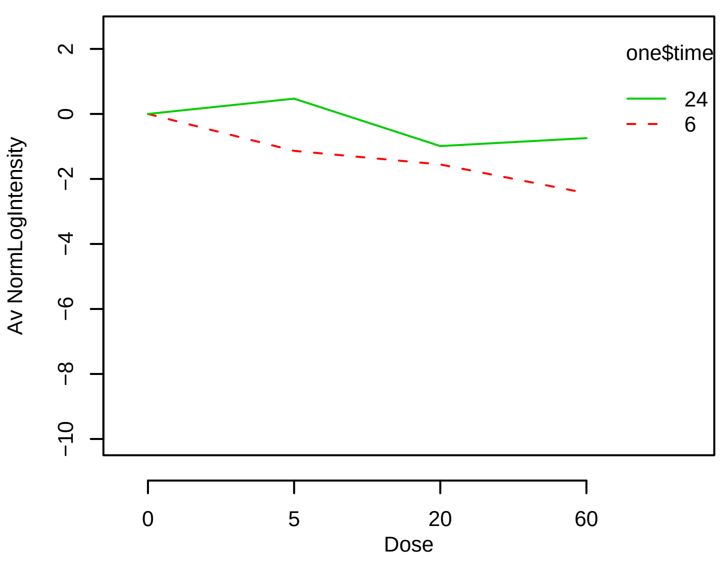
O_0006303 : double−strand break repair via nonhomologous



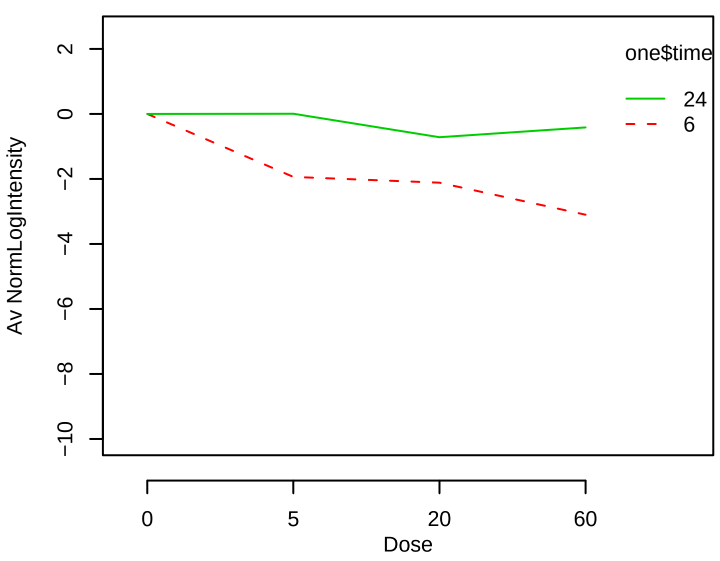
GO_0006304 : DNA modification



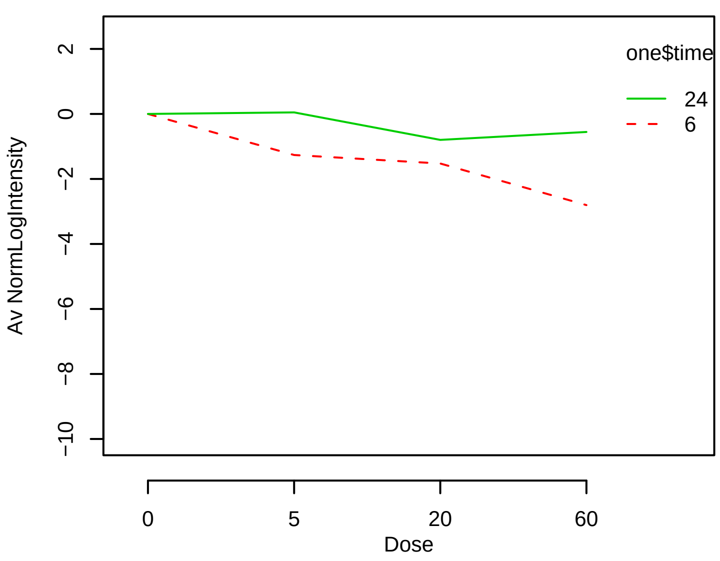
GO_0006305 : DNA alkylation



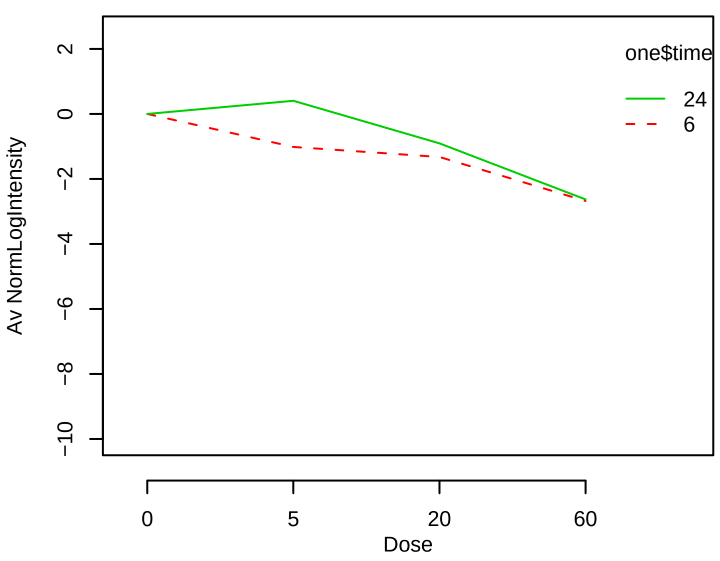
GO_0006306 : DNA methylation



GO_0006308 : DNA catabolism

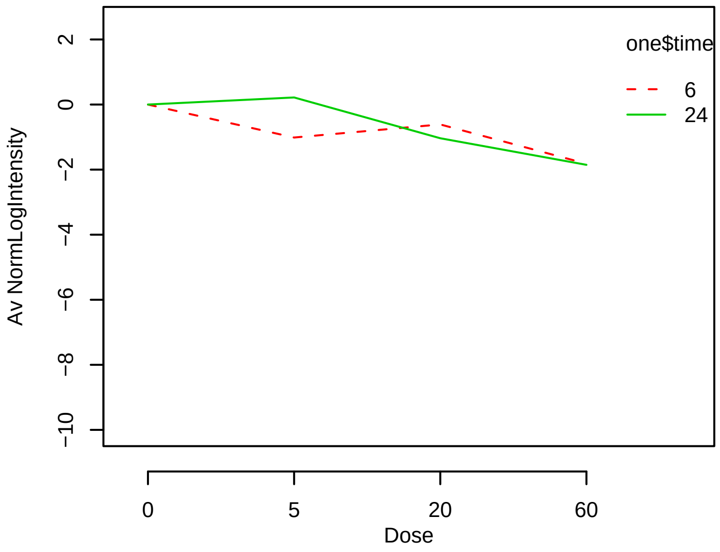


GO_0006309 : DNA fragmentation during apoptosis

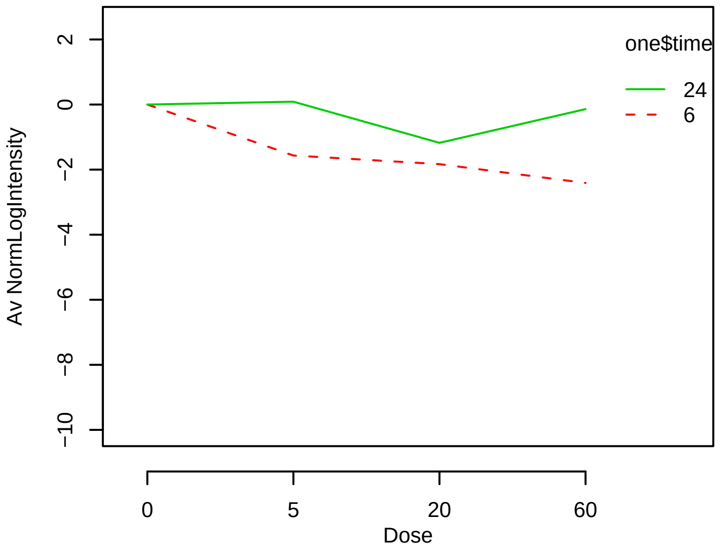


GO_0006310 : DNA recombination

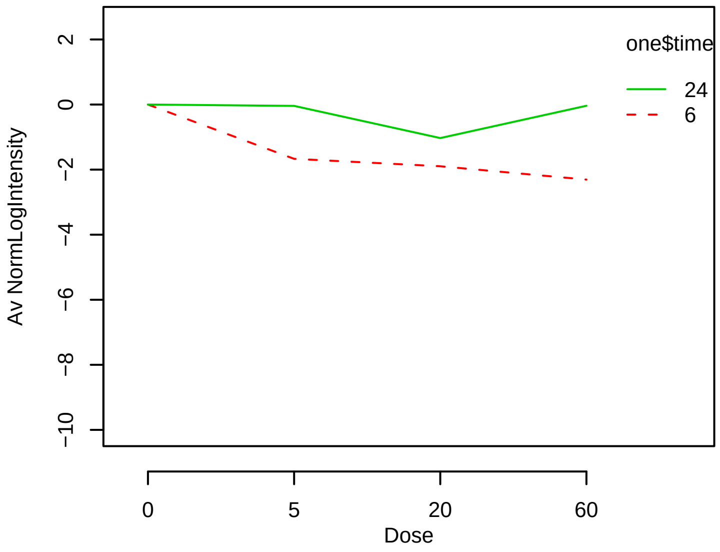
GO_0006312 : mitotic recombination



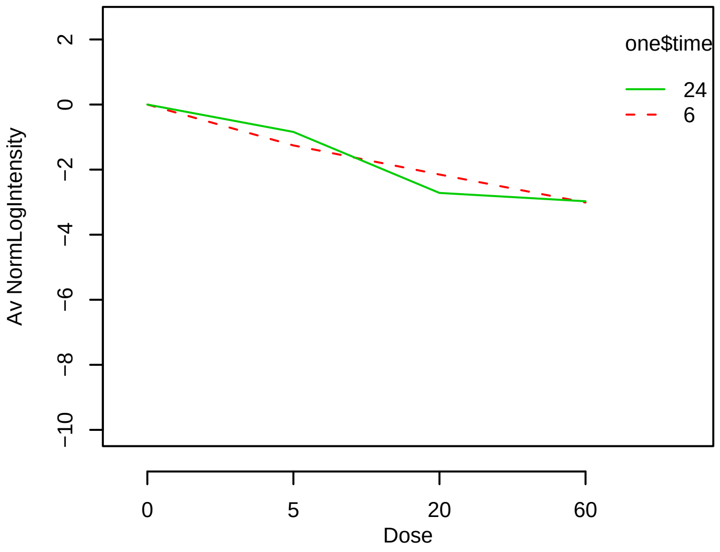
GO_0006333 : chromatin assembly or disassembly



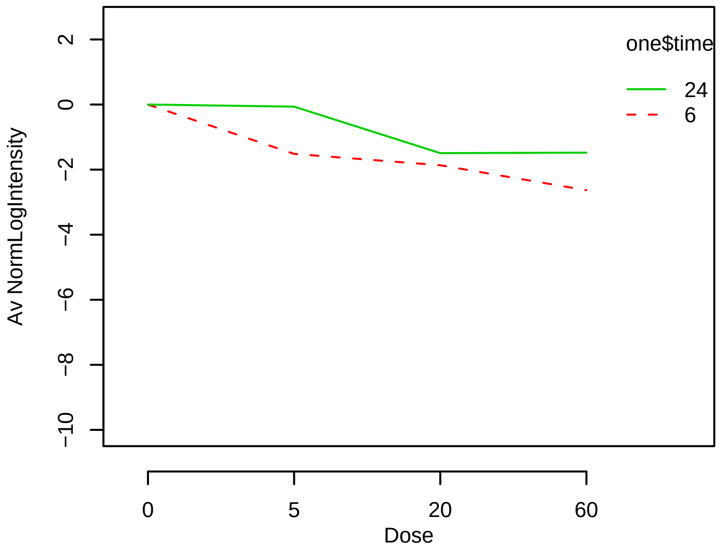
GO_0006334 : nucleosome assembly



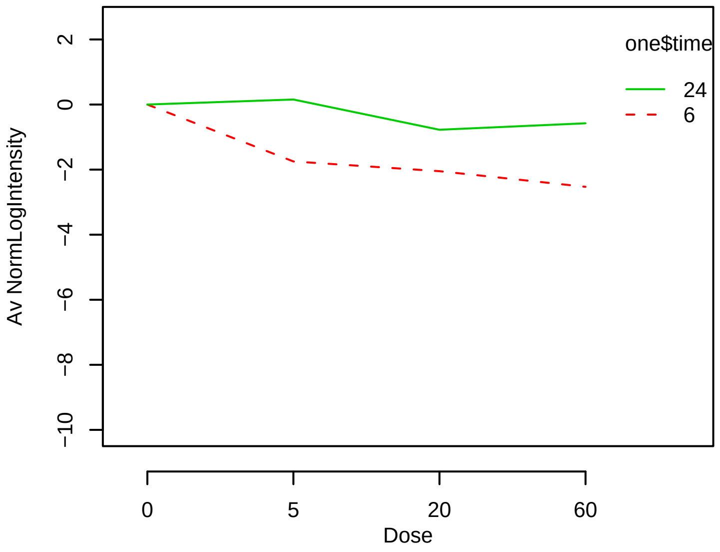
GO_0006337 : nucleosome disassembly



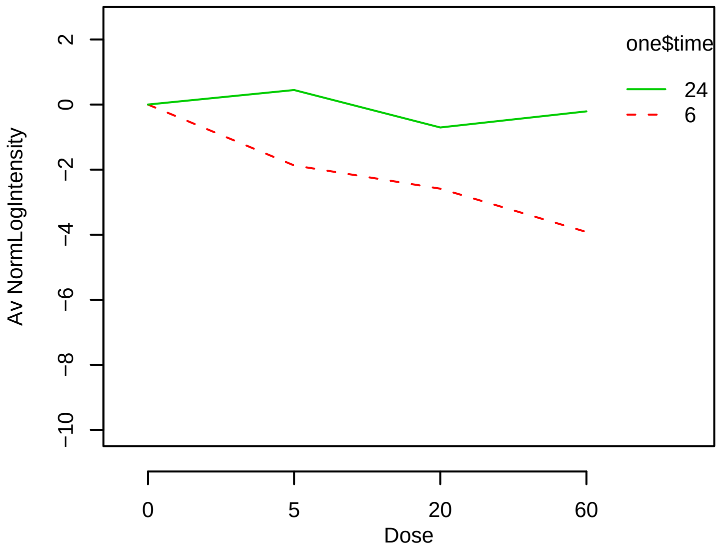
GO_0006338 : chromatin remodeling



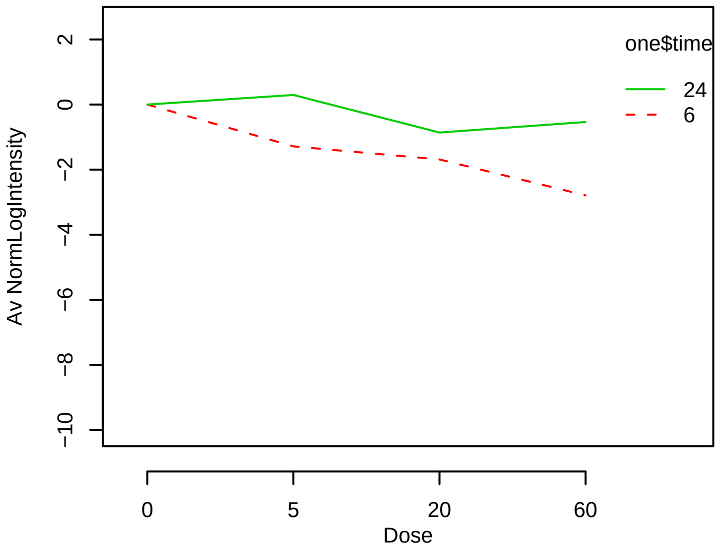
GO_0006342 : chromatin silencing



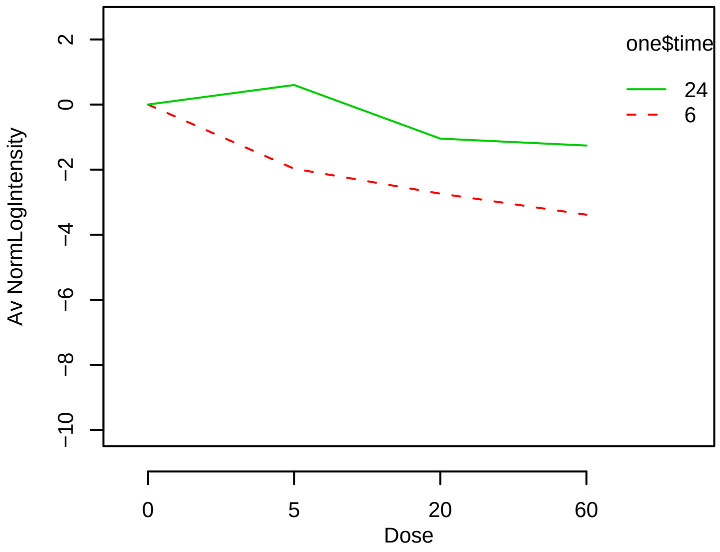
GO_0006349 : imprinting



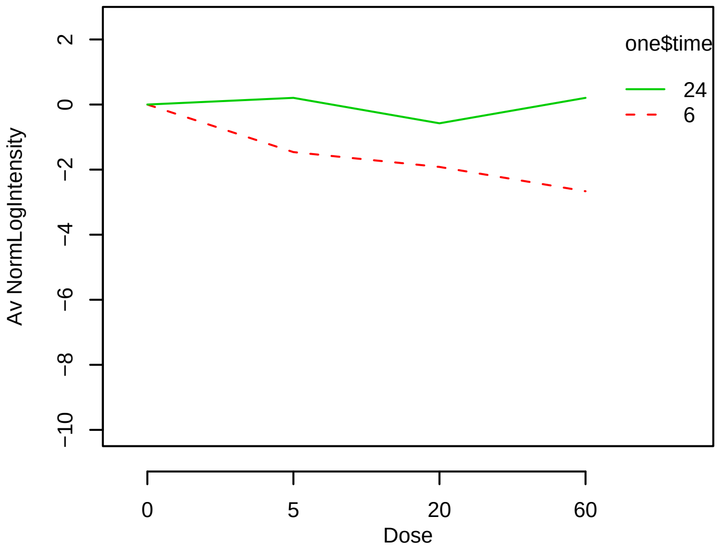
GO_0006352 : transcription initiation



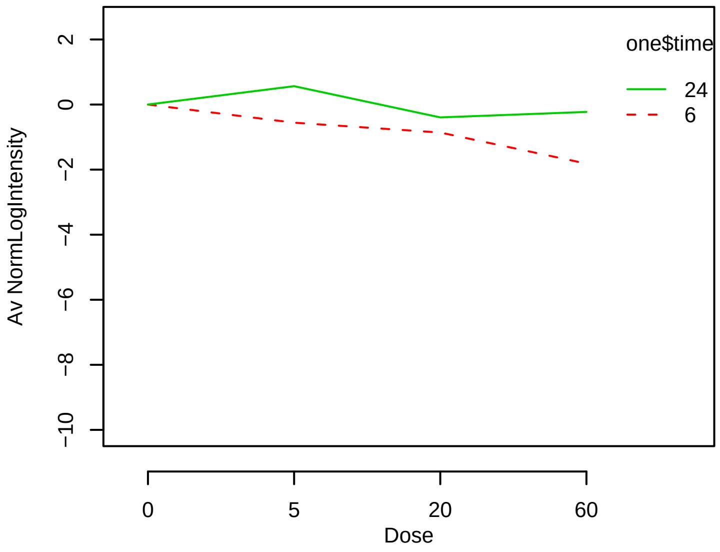
GO_0006353 : transcription termination



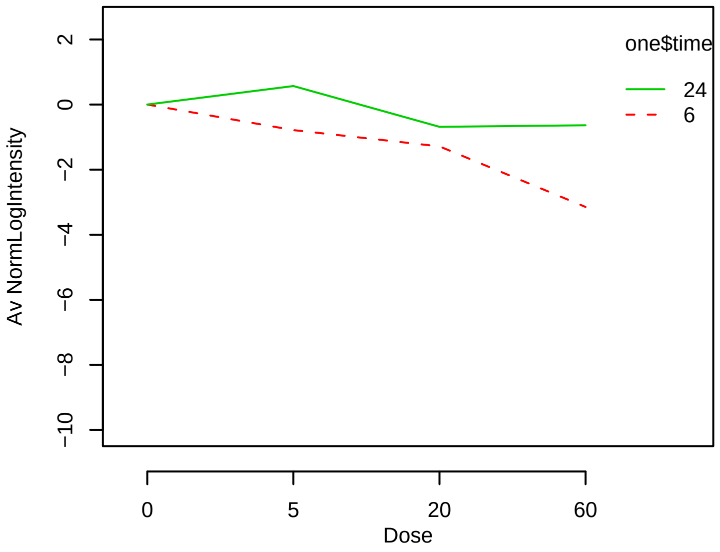
GO_0006354 : RNA elongation

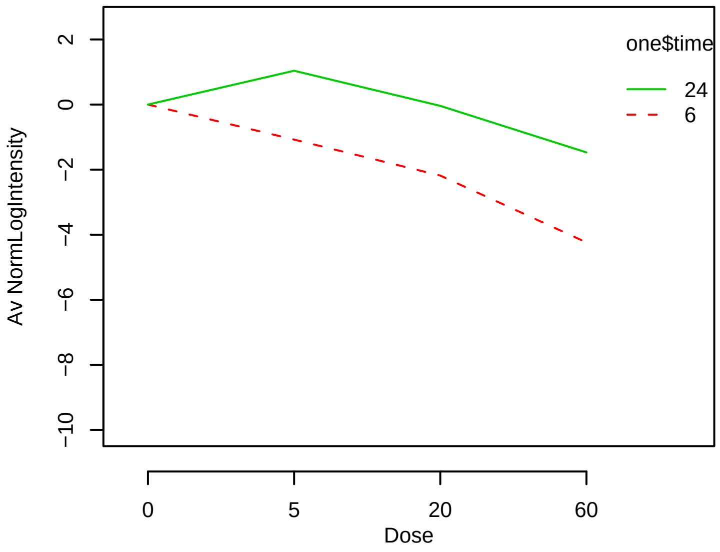


GO_0006359 : regulation of transcription from RNA polymera

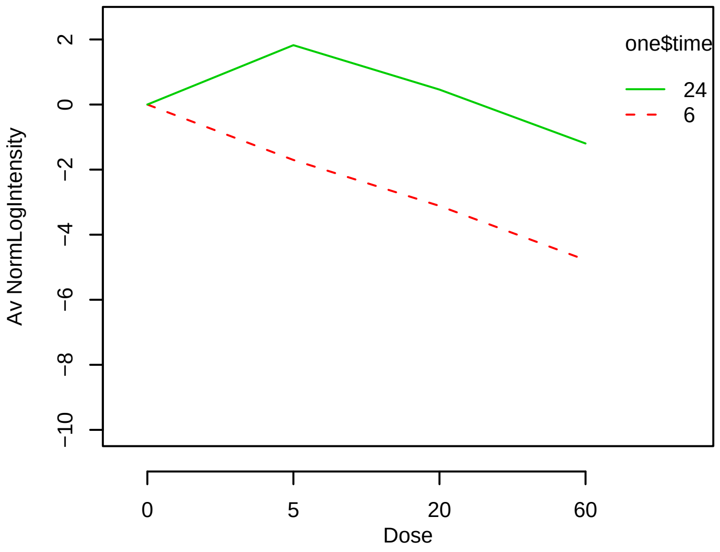


GO_0006360 : transcription from RNA polymerase I promot

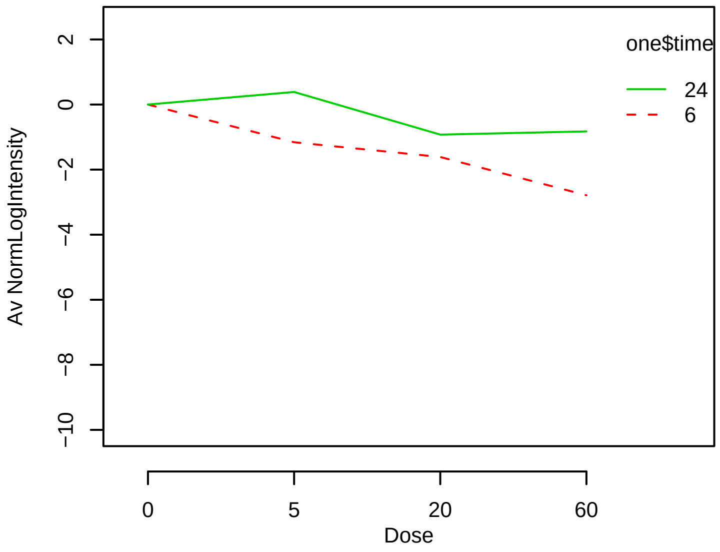




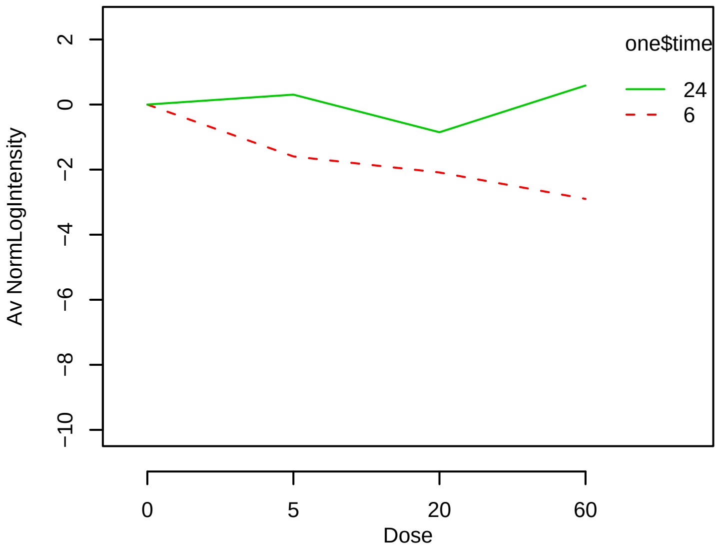
GO_0006364 : rRNA processing



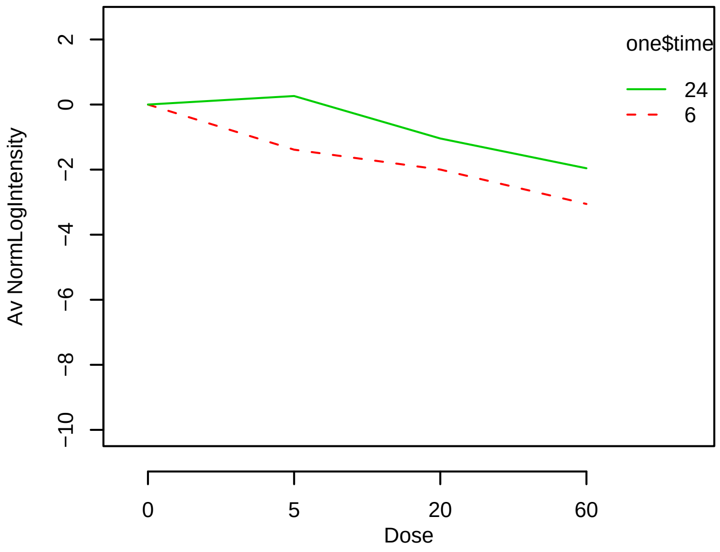
GO_0006365 : 35S primary transcript processing



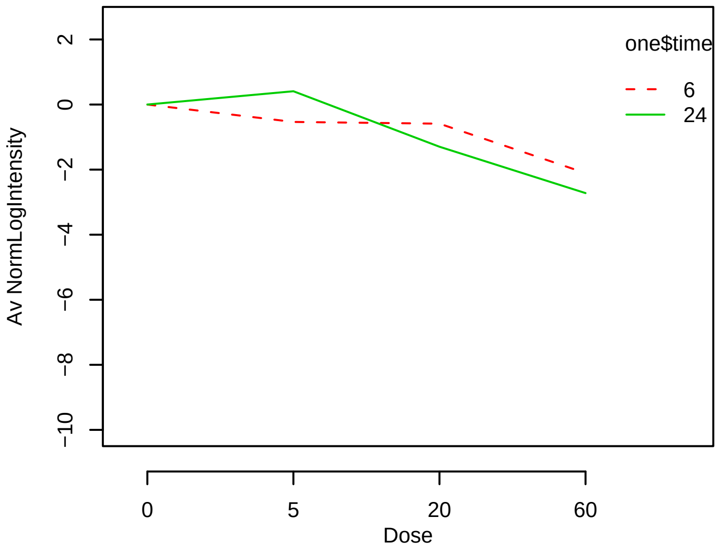
GO_0006367 : transcription initiation from RNA polymerase I



GO_0006368 : RNA elongation from RNA polymerase II prom

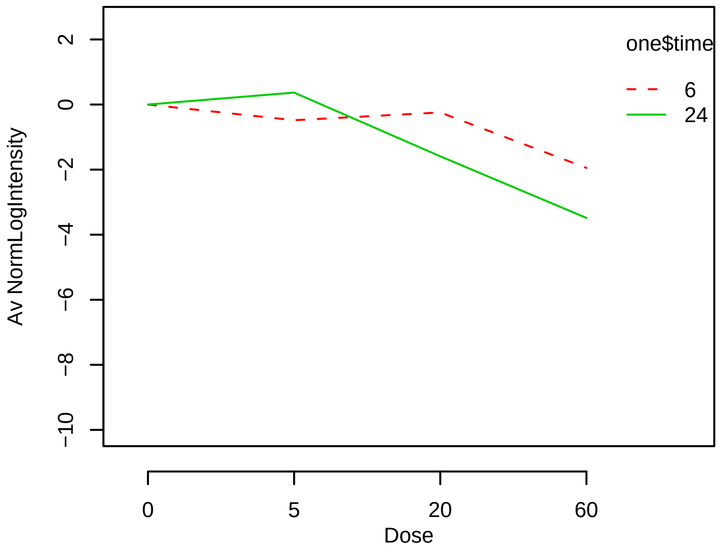


GO_0006376 : mRNA splice site selection

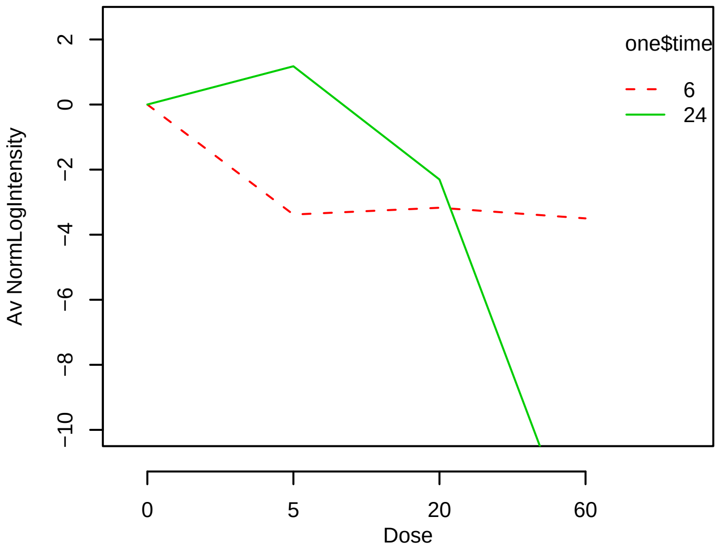


GO_0006378 : mRNA polyadenylation

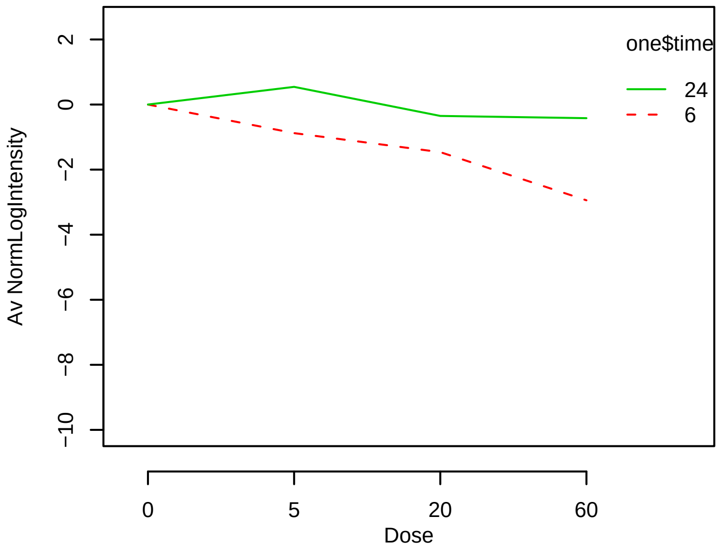
GO_0006379 : mRNA cleavage



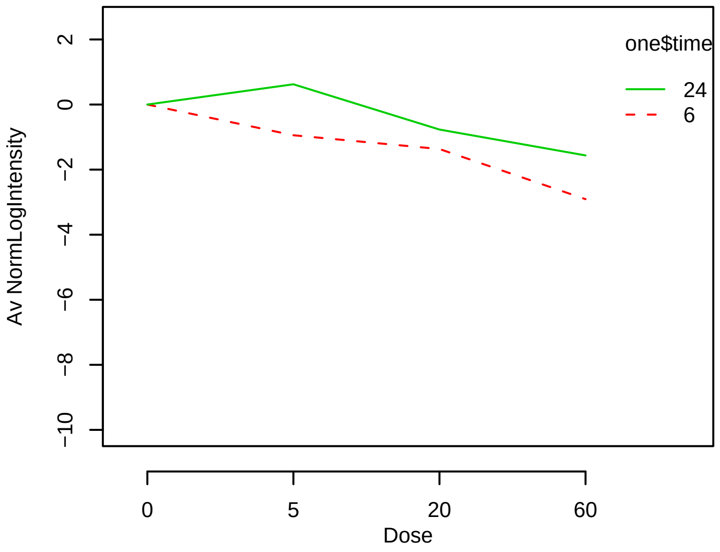
GO_0006381 : mRNA editing



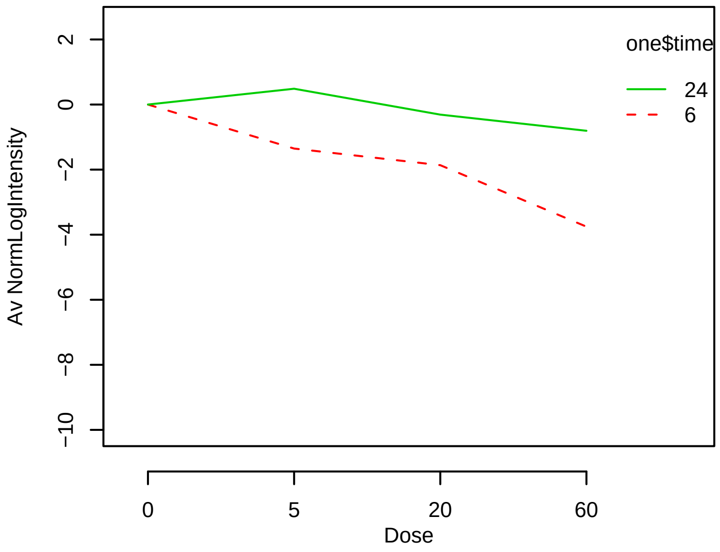
GO_0006383 : transcription from RNA polymerase III promo



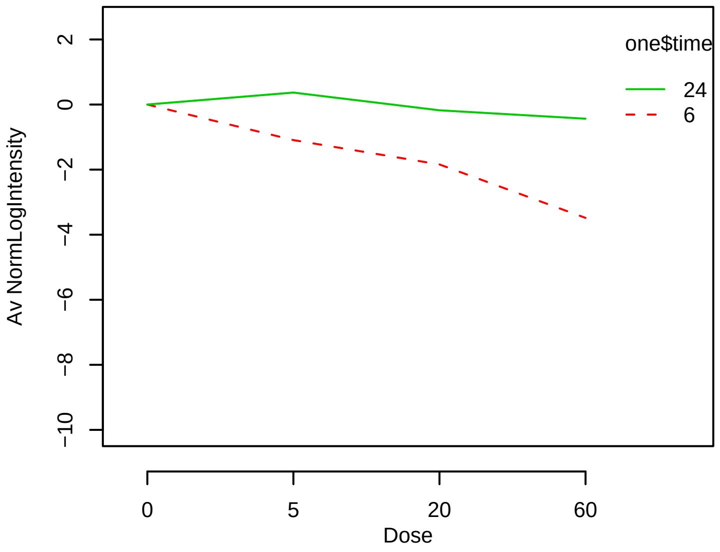
GO_0006397 : mRNA processing



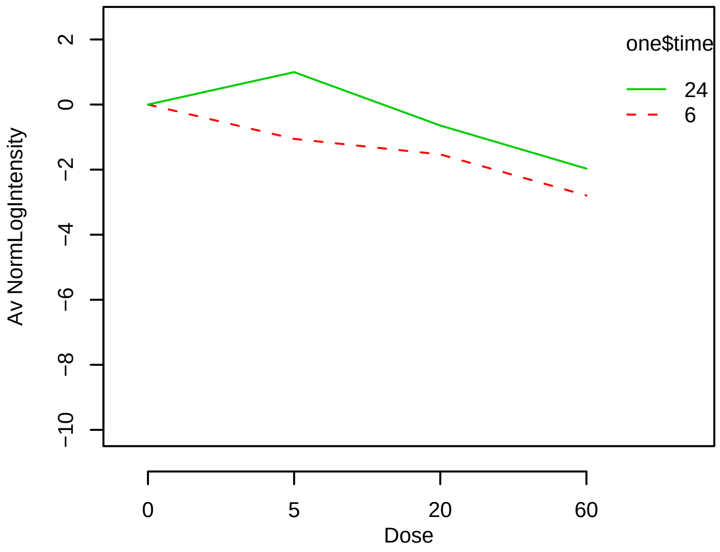
GO_0006399 : tRNA metabolism



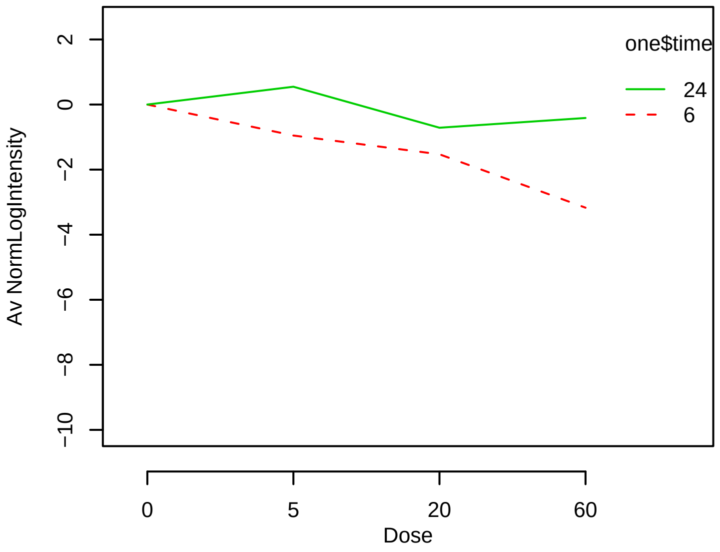
GO_0006400 : tRNA modification



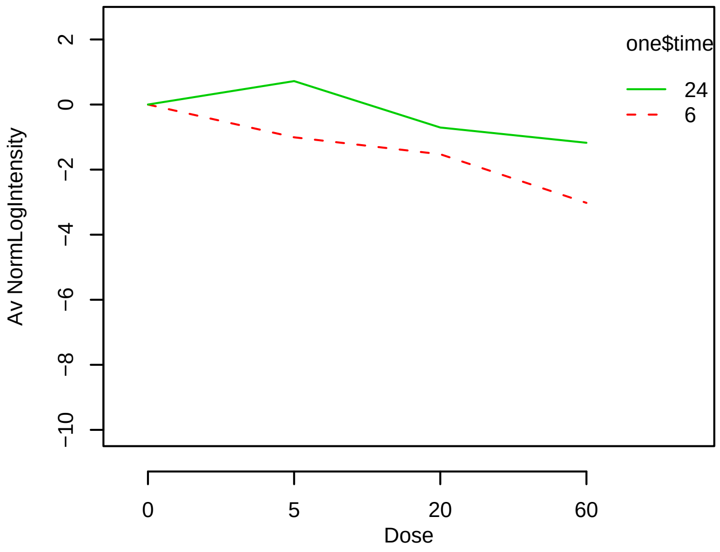
GO_0006401 : RNA catabolism



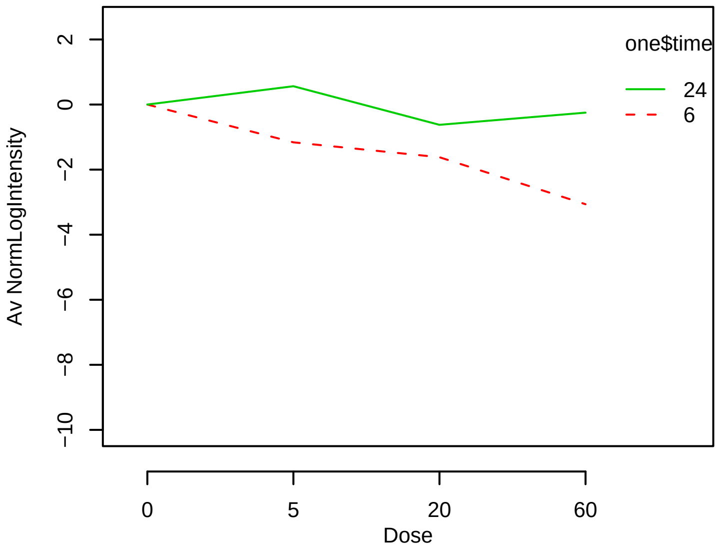
GO_0006402 : mRNA catabolism



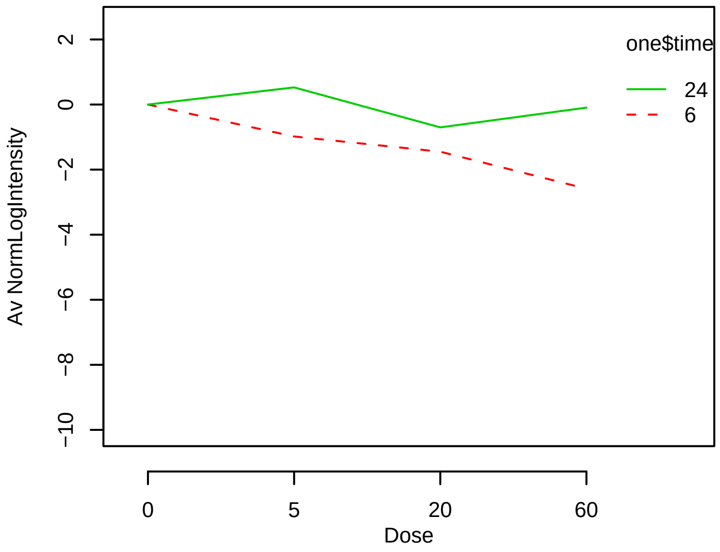
GO_0006403 : RNA localization



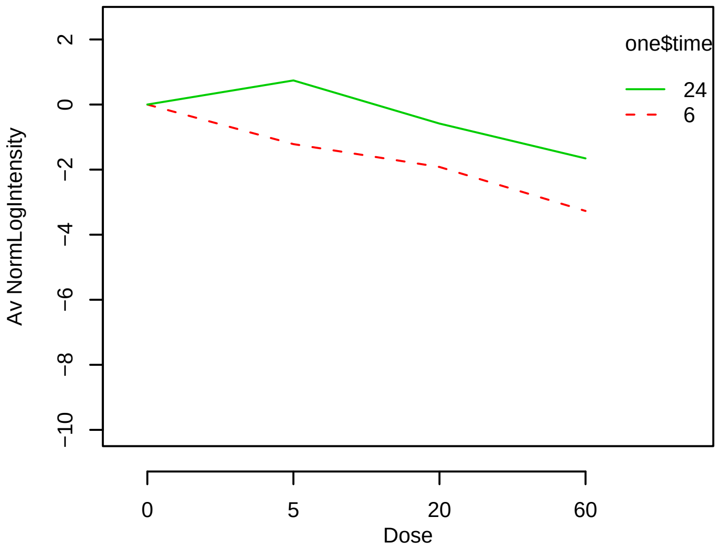
GO_0006405 : RNA export from nucleus



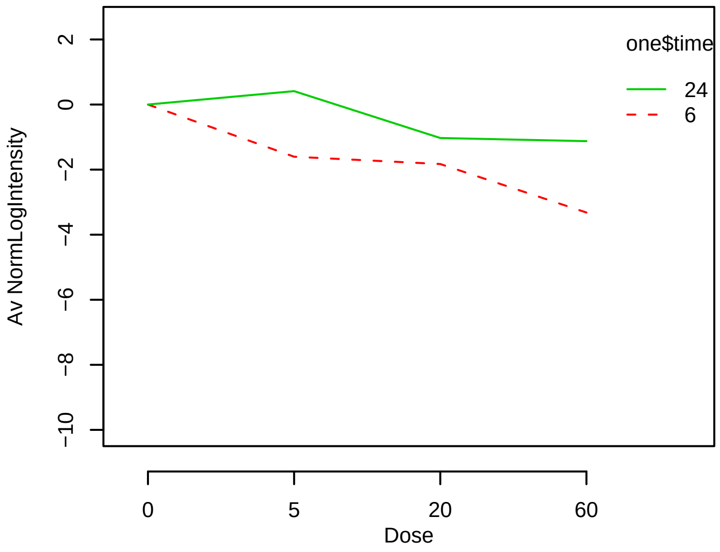
GO_0006406 : mRNA export from nucleus



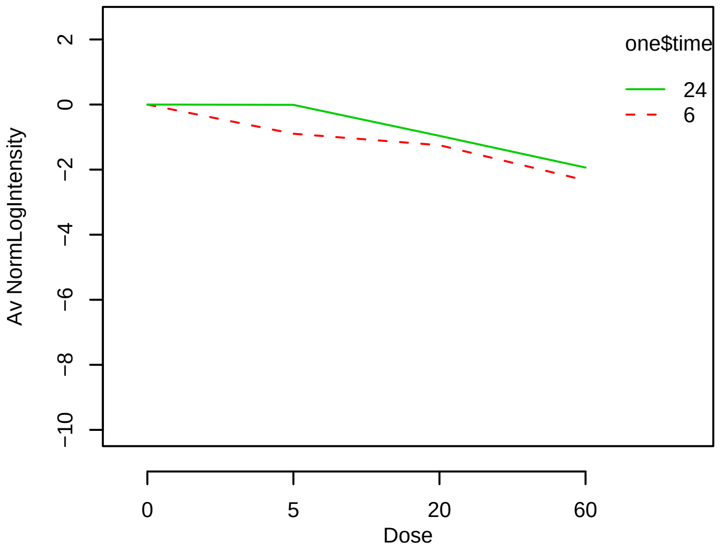
GO_0006413 : translational initiation



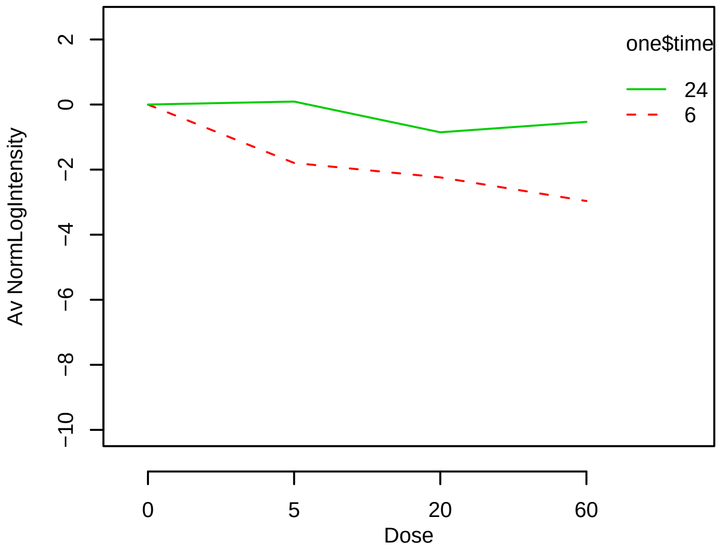
GO_0006414 : translational elongation



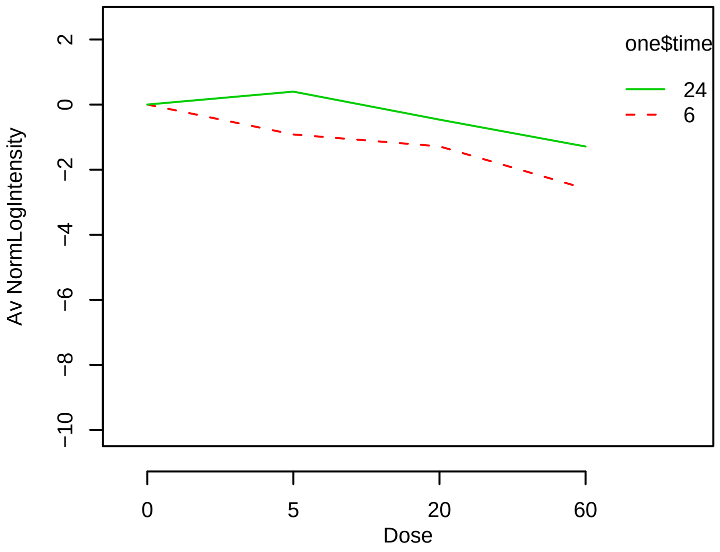
GO_0006415 : translational termination



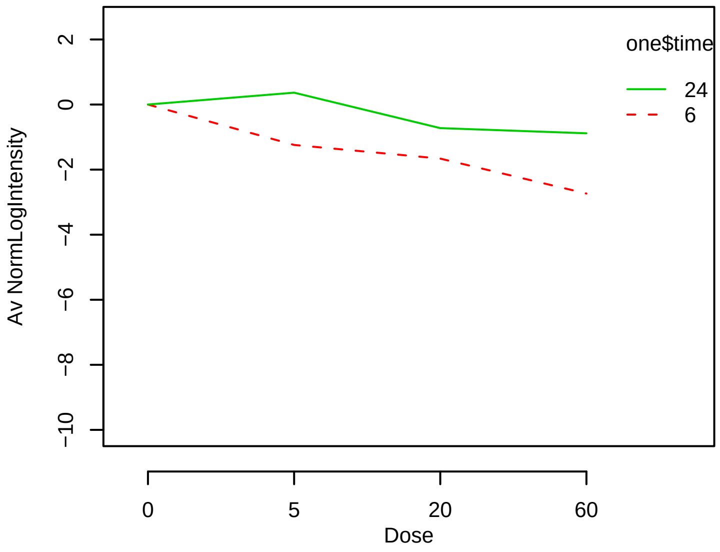
GO_0006417 : regulation of protein biosynthesis



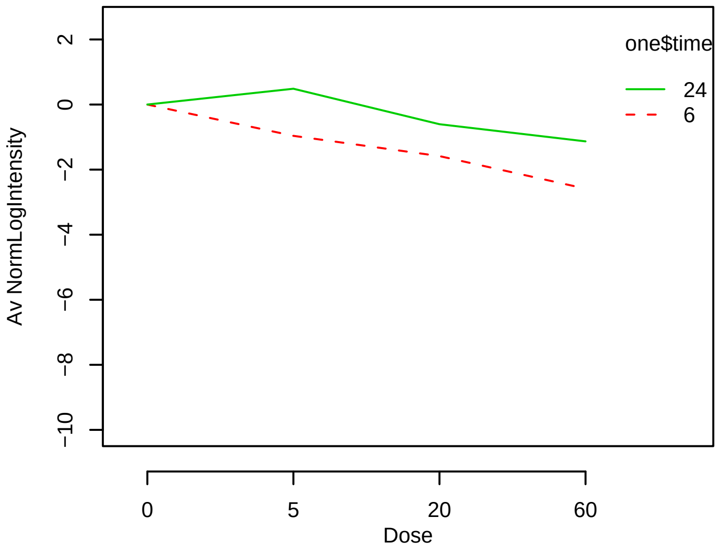
GO_0006418 : tRNA aminoacylation for protein translatio

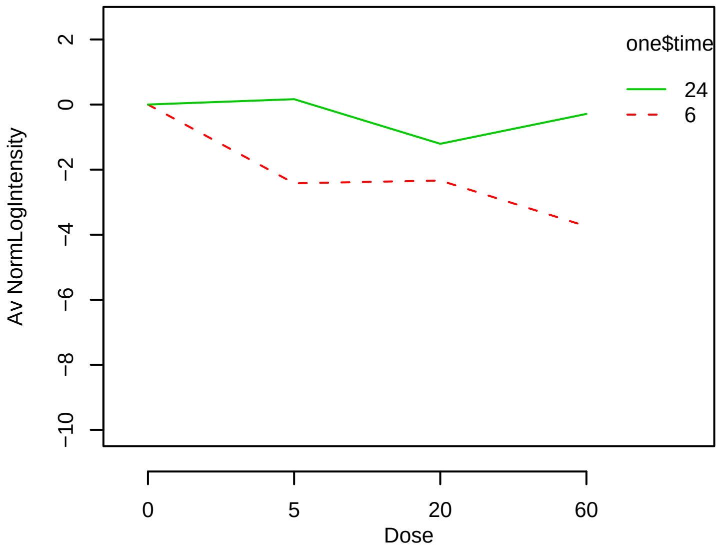


GO_0006445 : regulation of translation

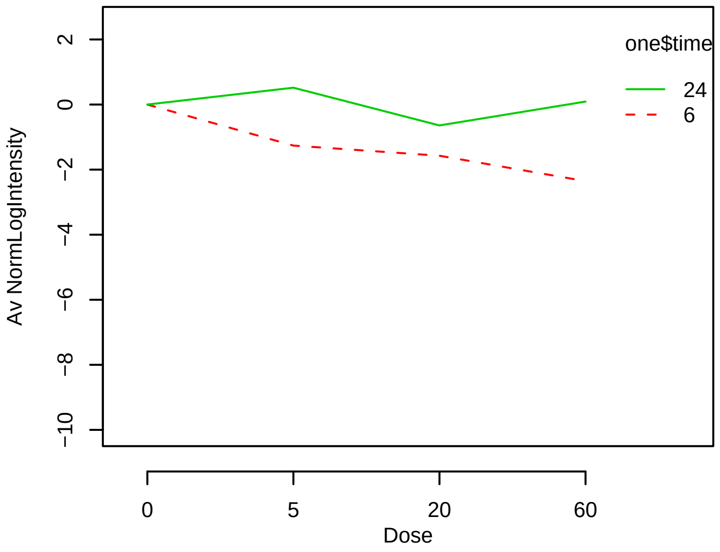


GO_0006446 : regulation of translational initiation

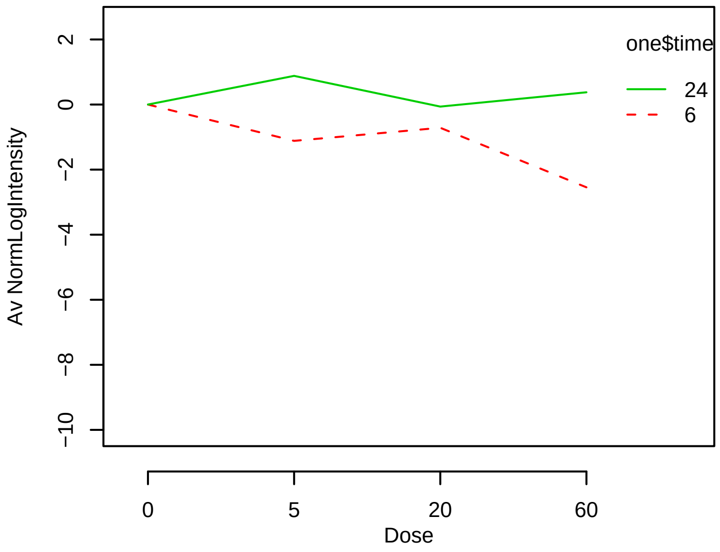




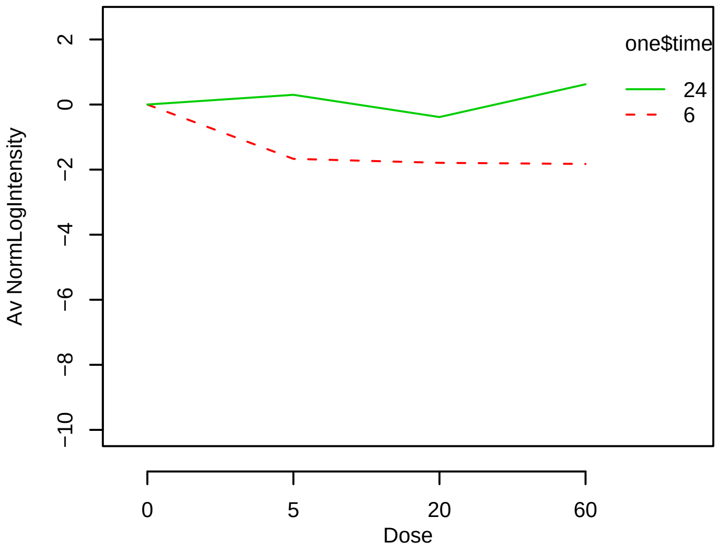
GO_0006451 : translational readthrough



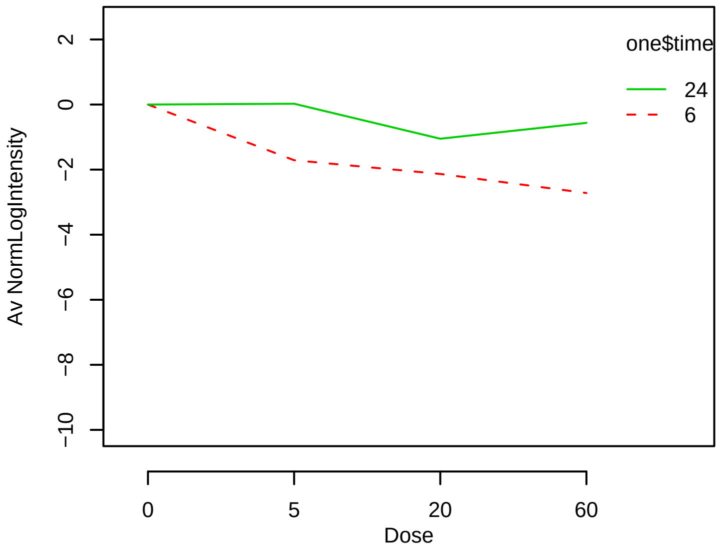
GO_0006457 : protein folding



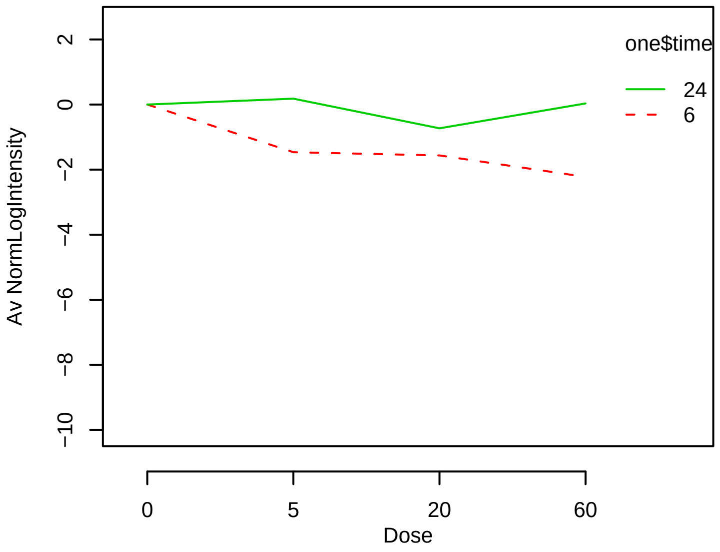
GO_0006465 : signal peptide processing



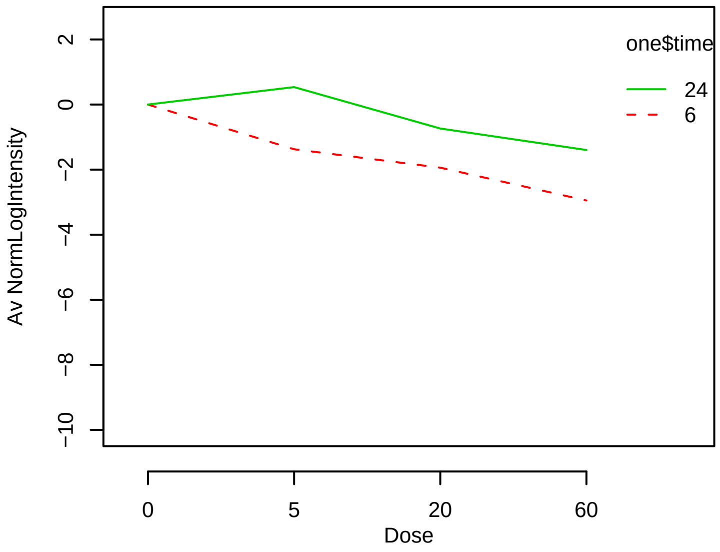
GO_0006469 : negative regulation of protein kinase activit

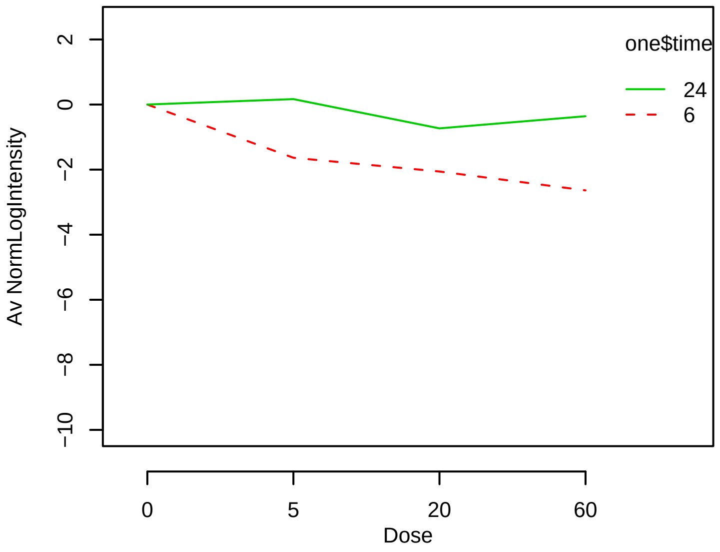


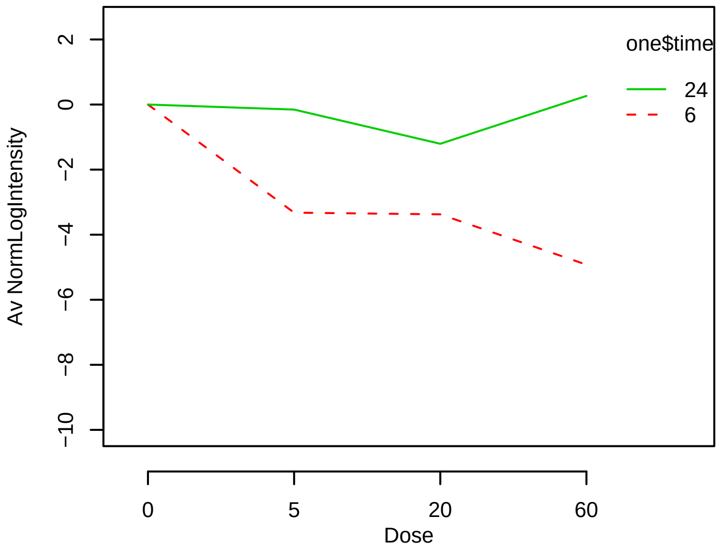
GO_0006470 : protein amino acid dephosphorylation

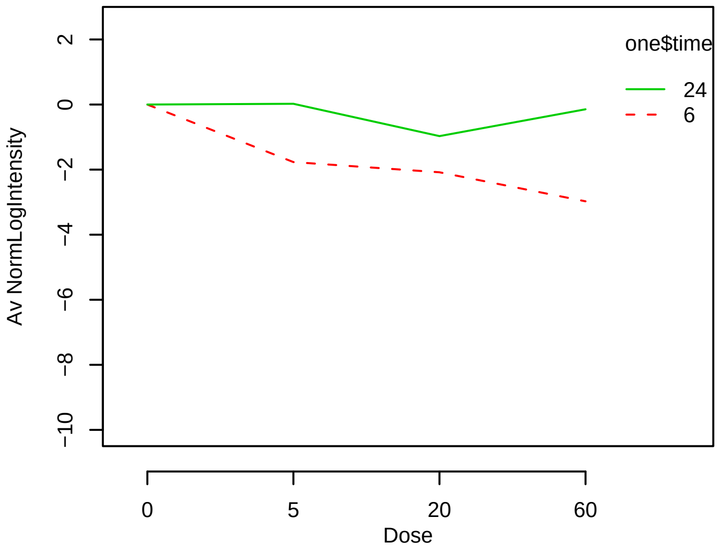


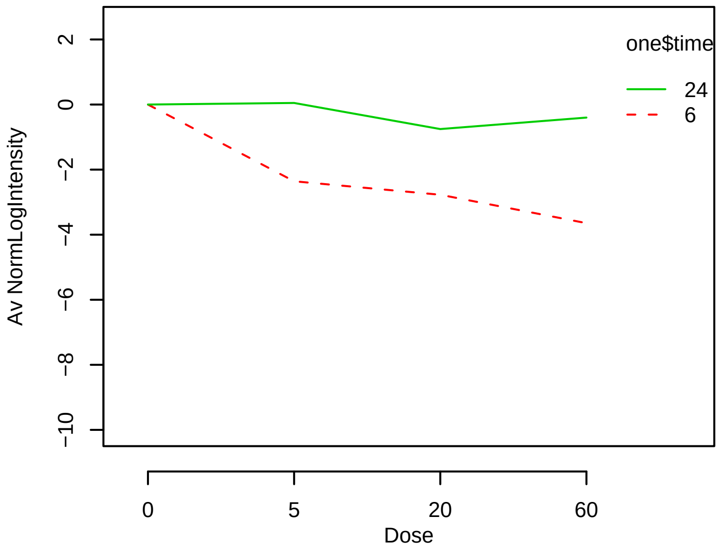
GO_0006471 : protein amino acid ADP−ribosylation

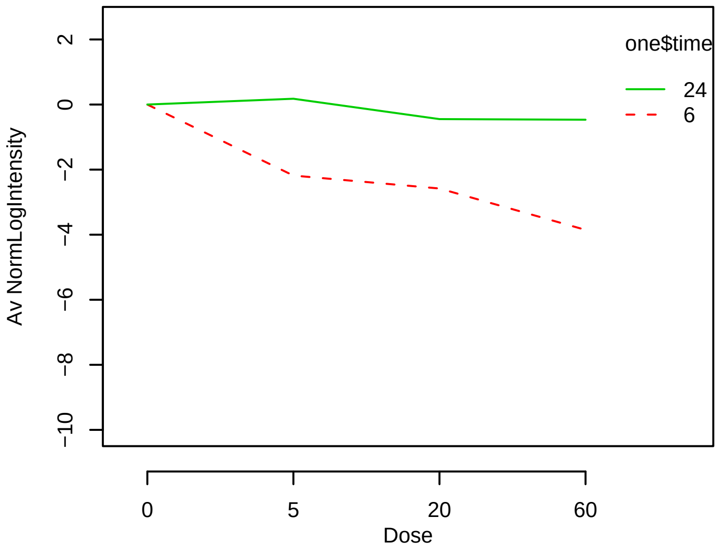

GO_0006473 : protein amino acid acetylation

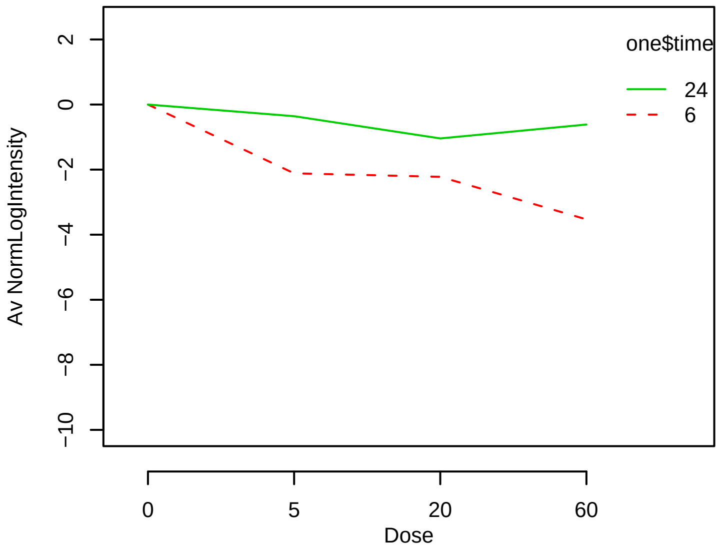

GO_0006476 : protein amino acid deacetylation


GO_0006477 : protein amino acid sulfation

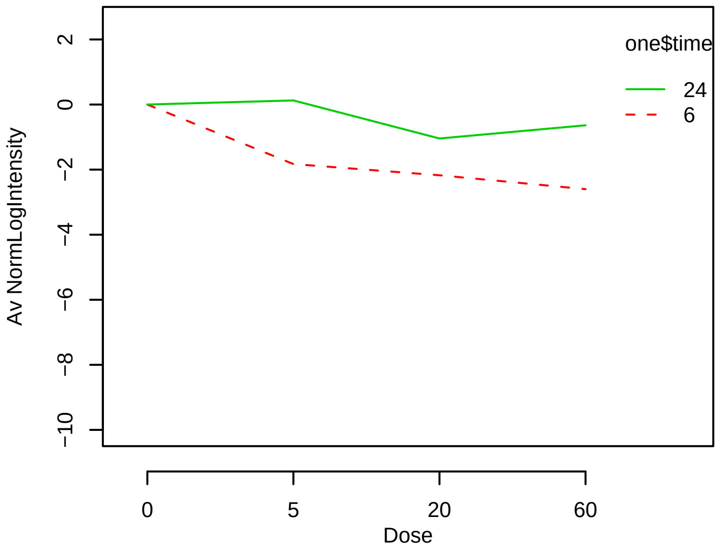

GO_0006479 : protein amino acid methylation


GO_0006486 : protein amino acid glycosylation

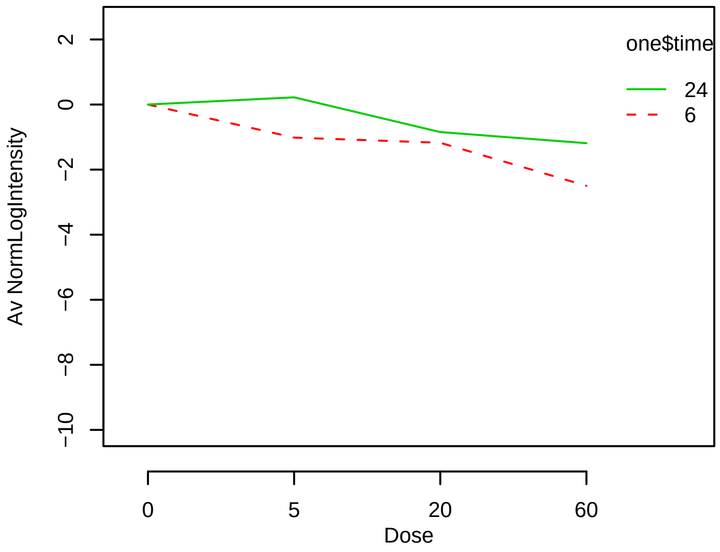

GO_0006487 : protein amino acid N−linked glycosylation



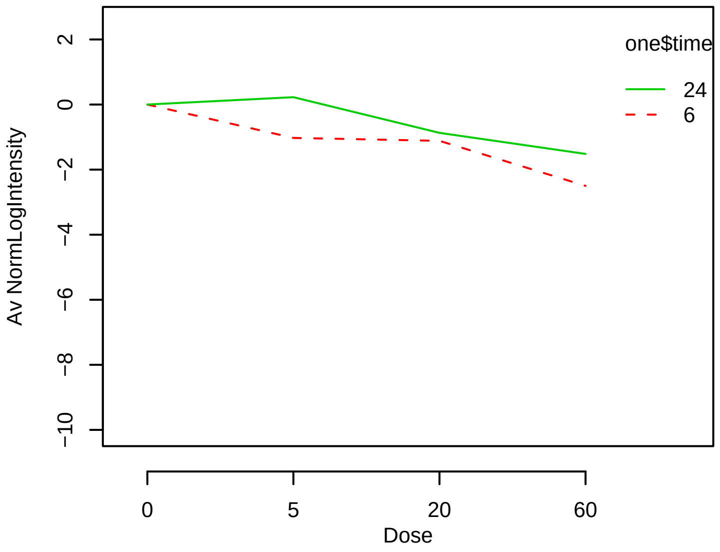
GO_0006491 : N−glycan processing



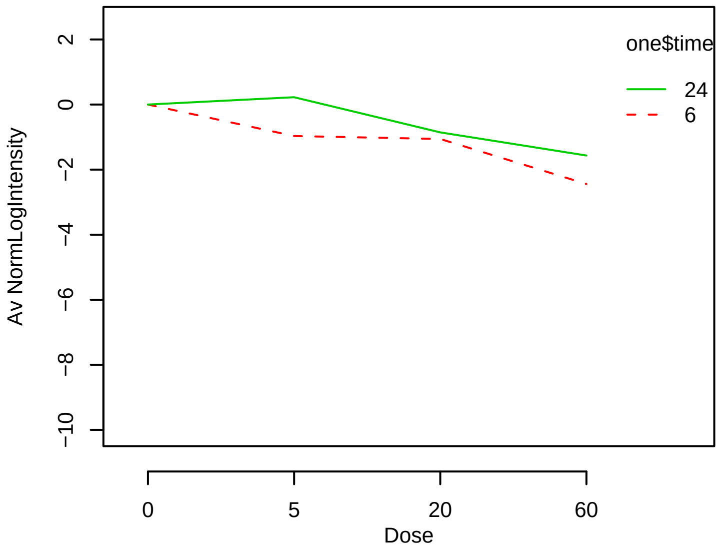
GO_0006493 : protein amino acid O−linked glycosylation



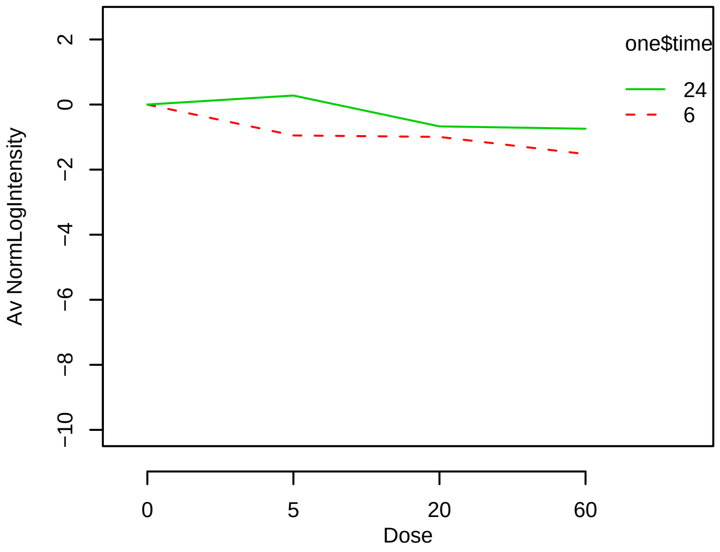
GO_0006497 : protein amino acid lipidation



GO_0006505 : GPI anchor metabolism

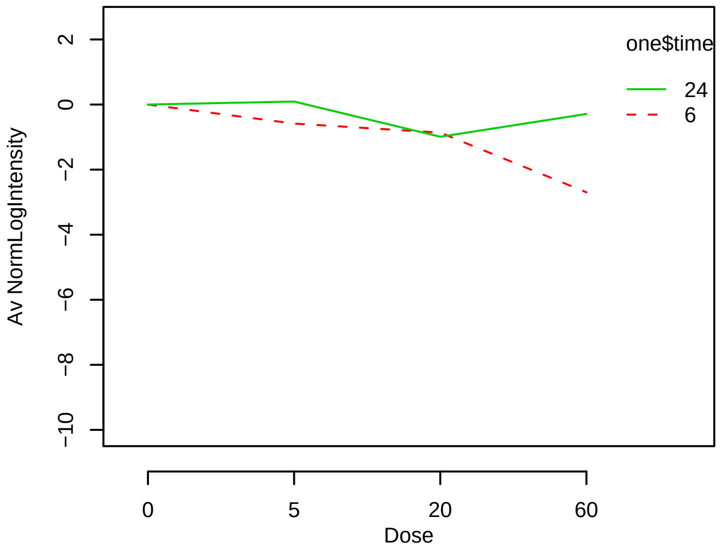


GO_0006506 : GPI anchor biosynthesis

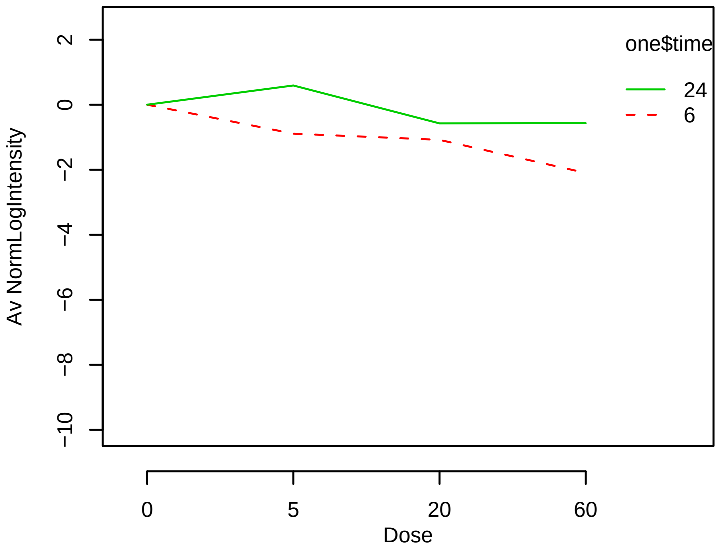


GO_0006509 : membrane protein ectodomain proteolysis

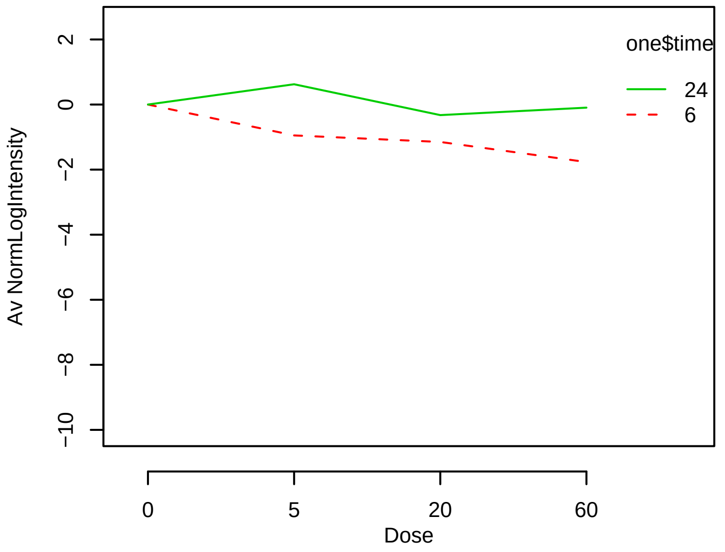
GO_0006510 : ATP−dependent proteolysis



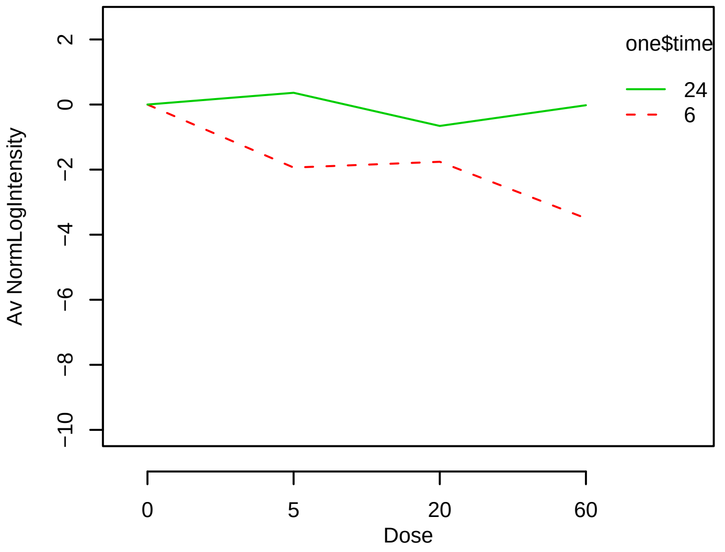
GO_0006511 : ubiquitin−dependent protein catabolism



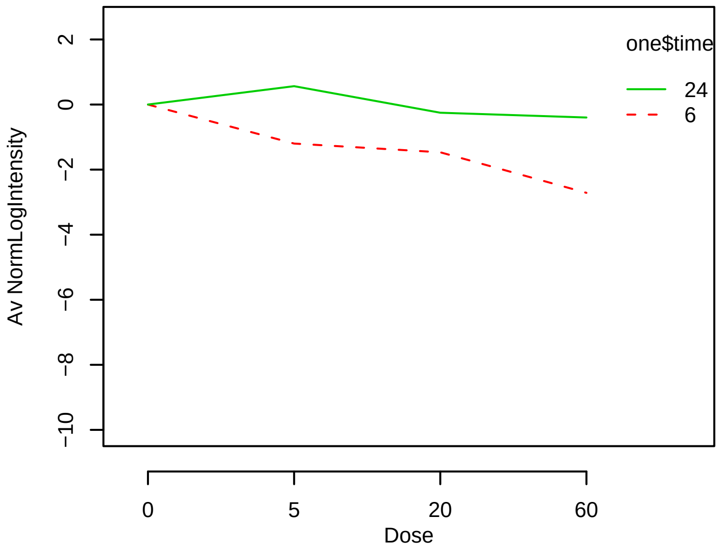
GO_0006515 : misfolded or incompletely synthesized protein



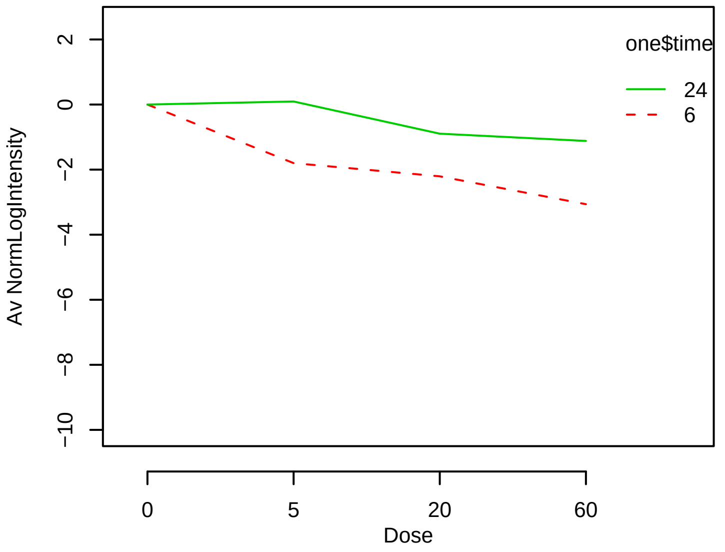
GO_0006516 : glycoprotein catabolism



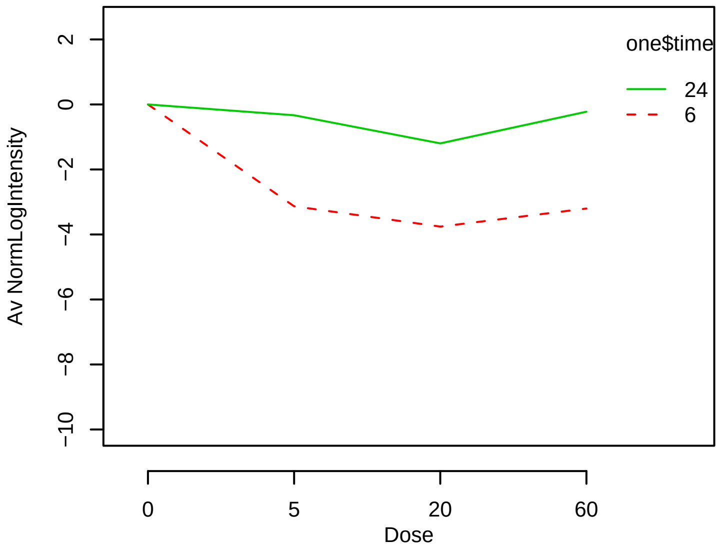
GO_0006518 : peptide metabolism



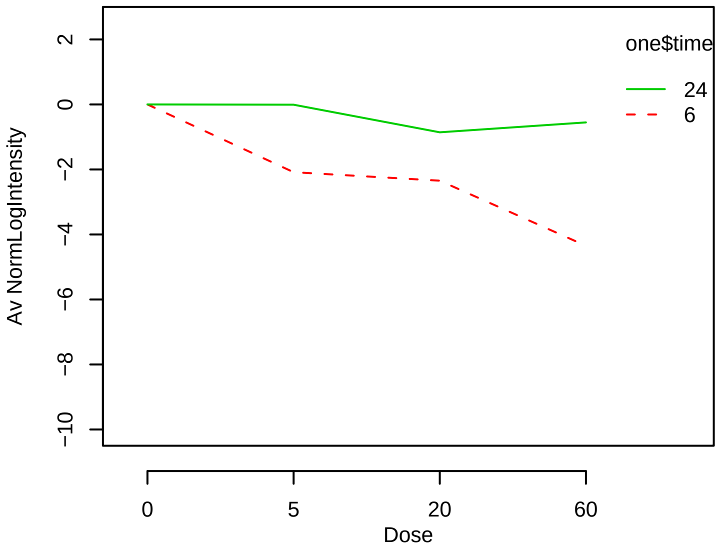
GO_0006520 : amino acid metabolism



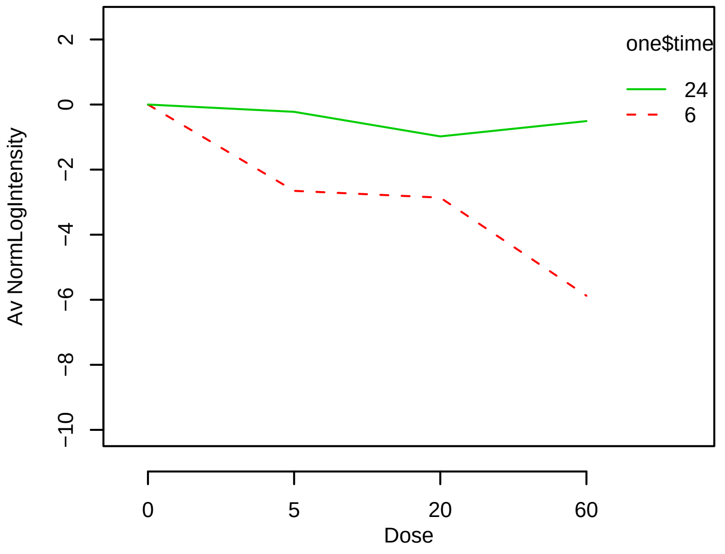
GO_0006521 : regulation of amino acid metabolism



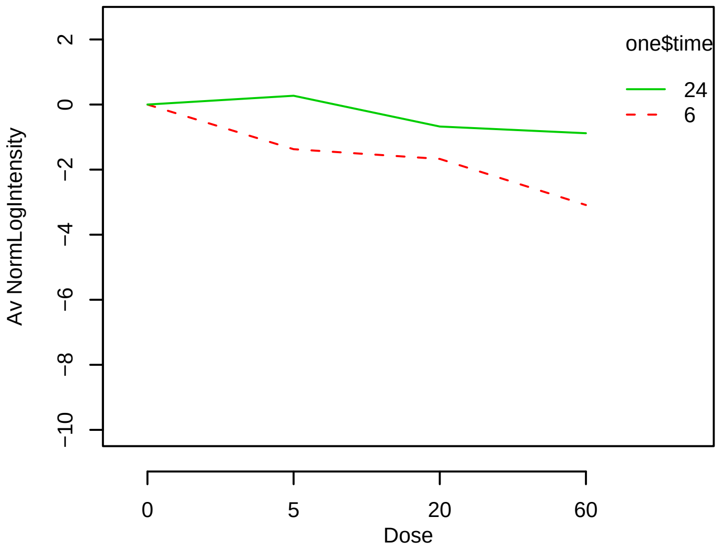
GO_0006525 : arginine metabolism



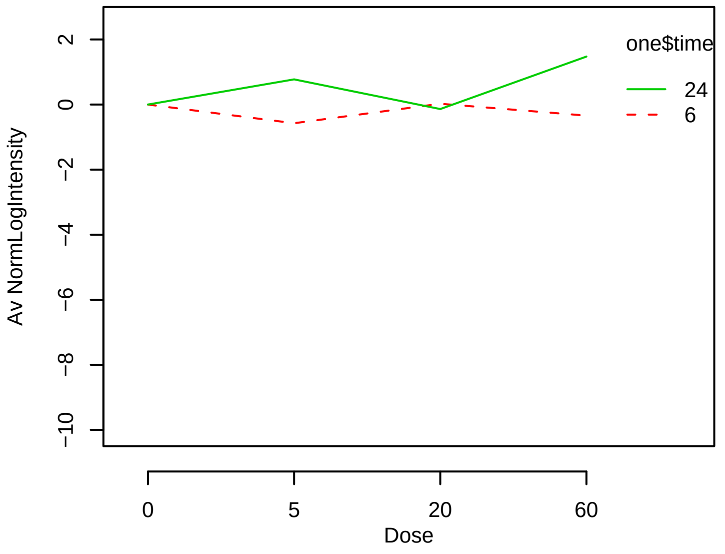
GO_0006526 : arginine biosynthesis



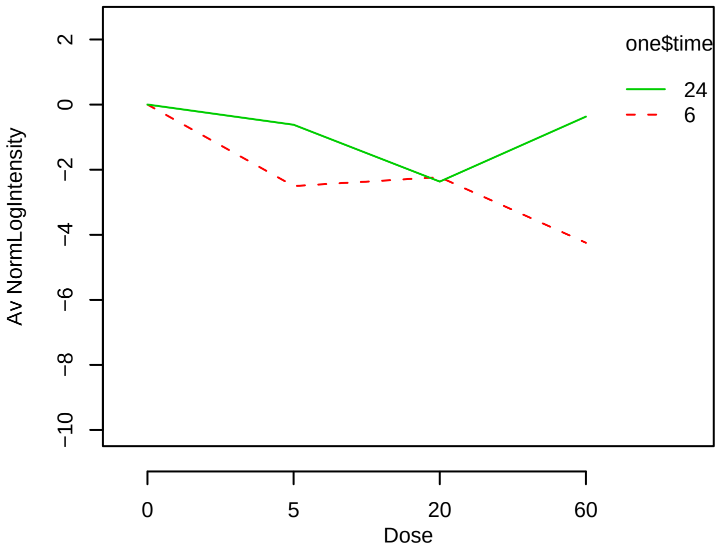
GO_0006527 : arginine catabolism



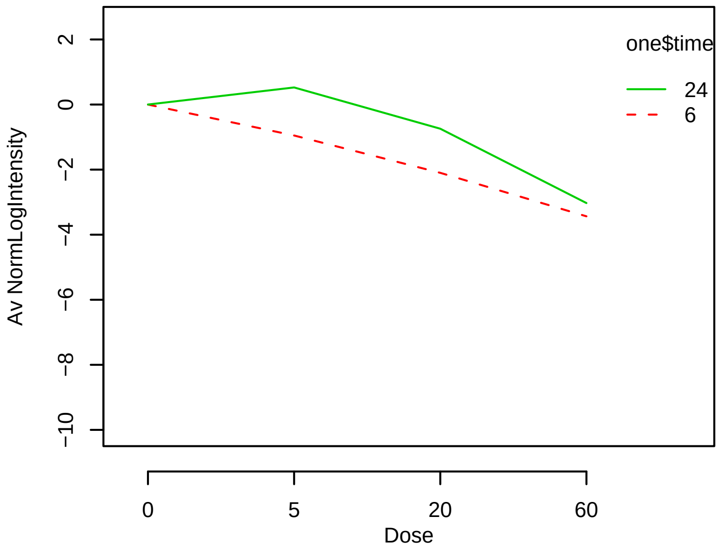
GO_0006534 : cysteine metabolism



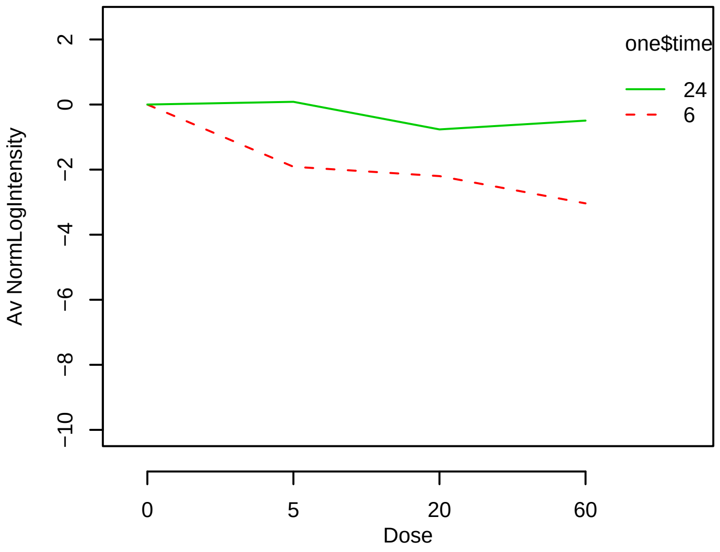
GO_0006536 : glutamate metabolism



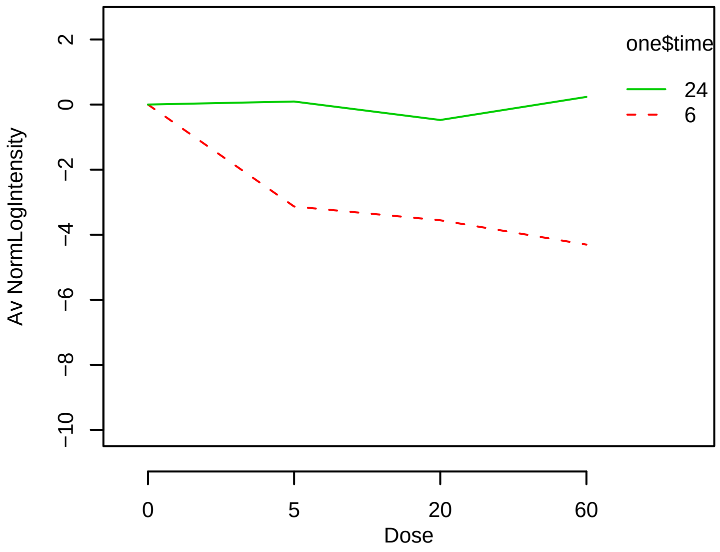
GO_0006541 : glutamine metabolism



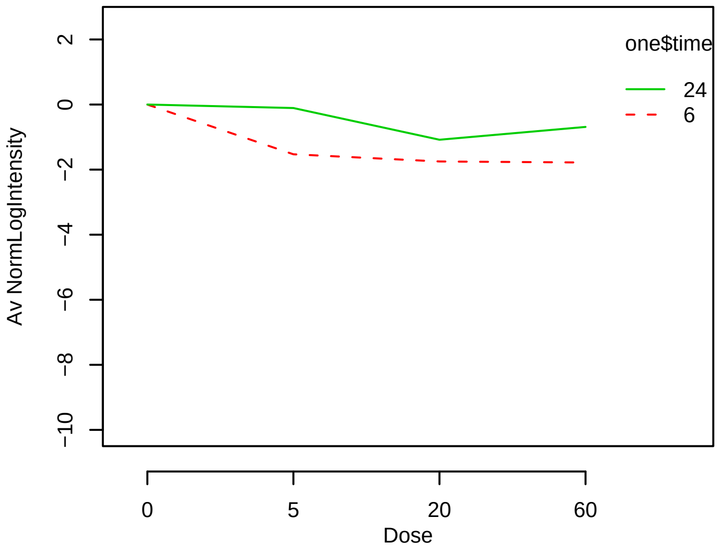
GO_0006544 : glycine metabolism



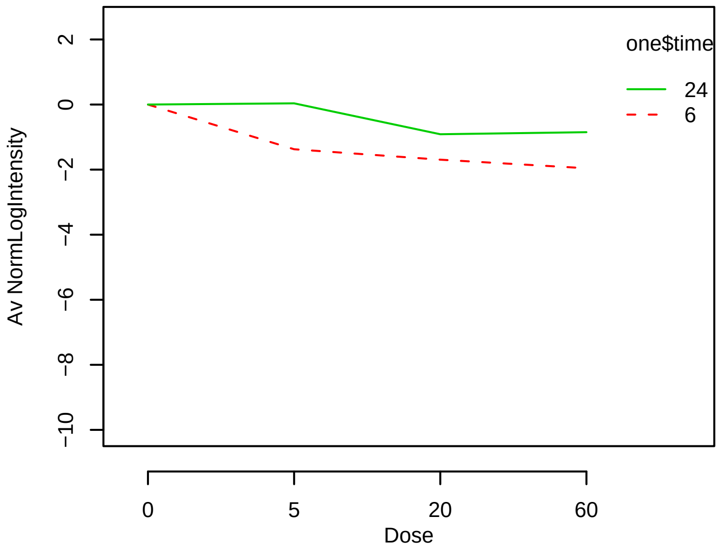
GO_0006546 : glycine catabolism



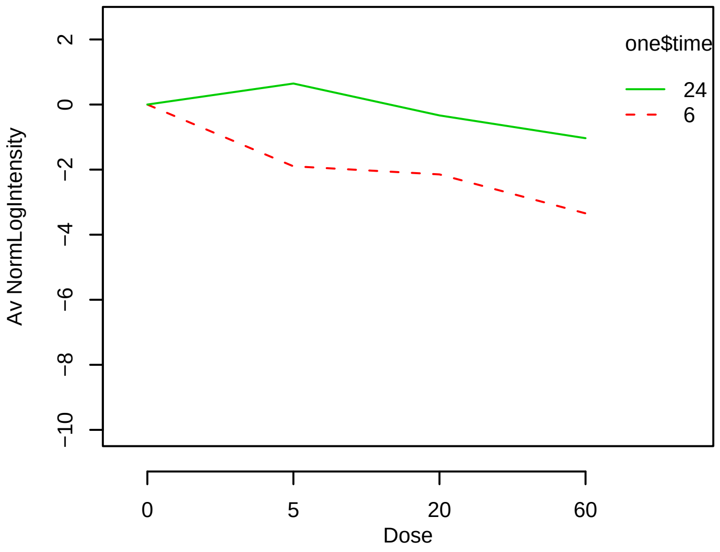
GO_0006547 : histidine metabolism

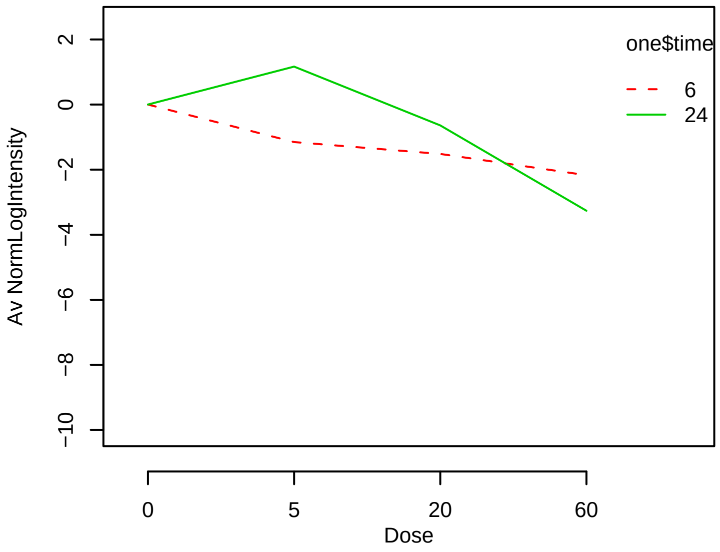


GO_0006548 : histidine catabolism

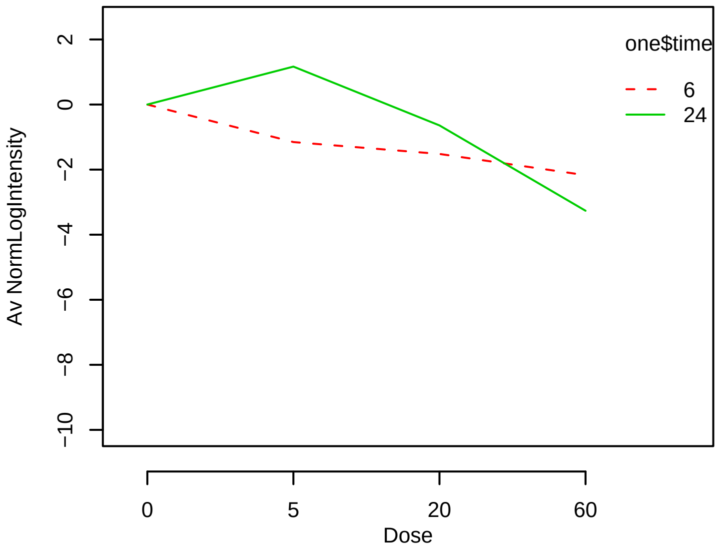


GO_0006555 : methionine metabolism

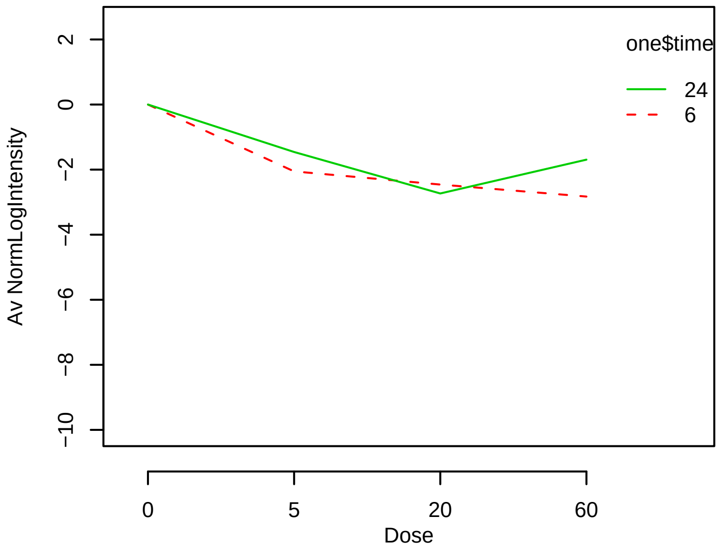




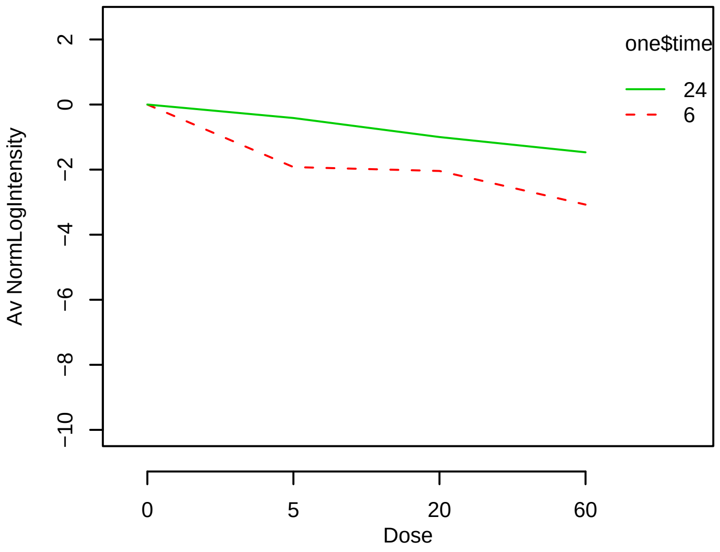
GO_0006558 : L−phenylalanine metabolism



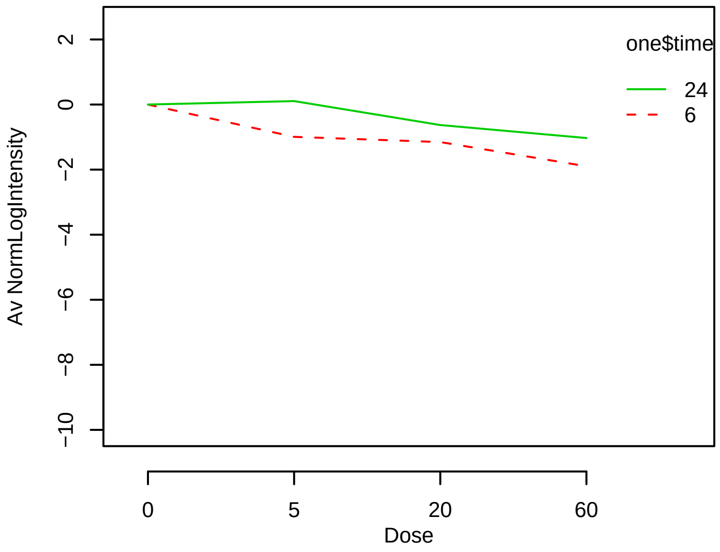
GO_0006559 : L−phenylalanine catabolism



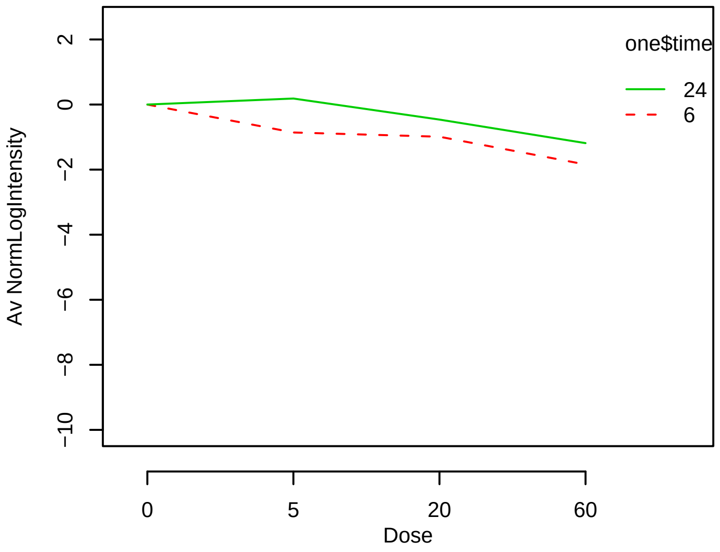
GO_0006560 : proline metabolism



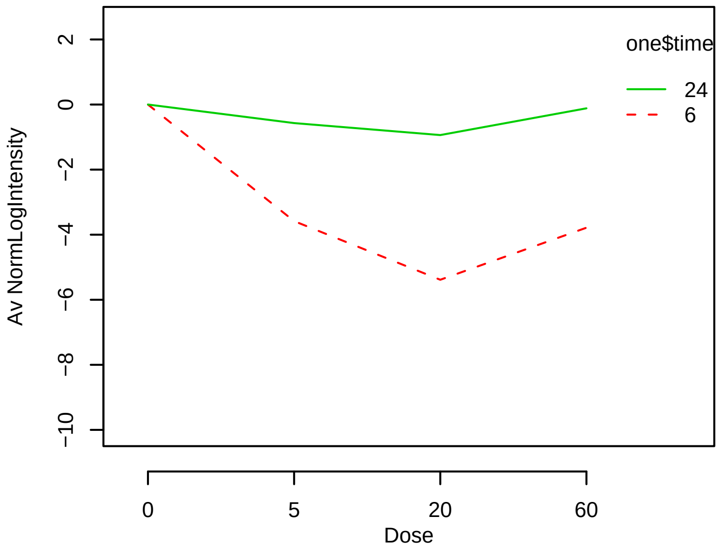
GO_0006561 : proline biosynthesis

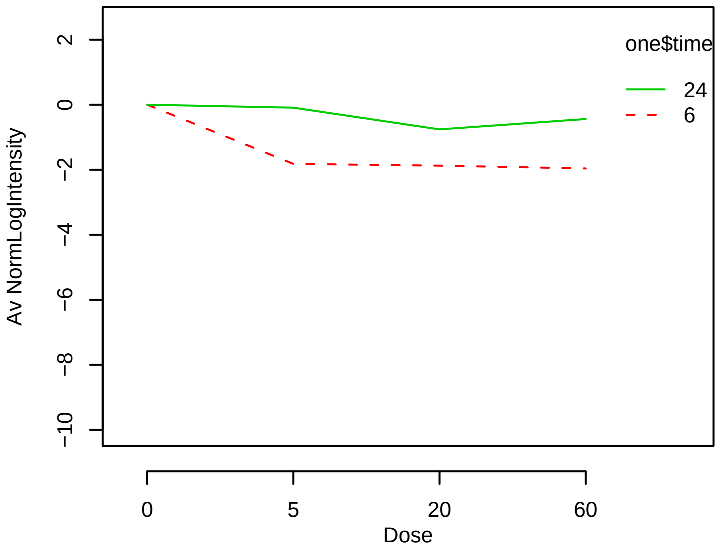


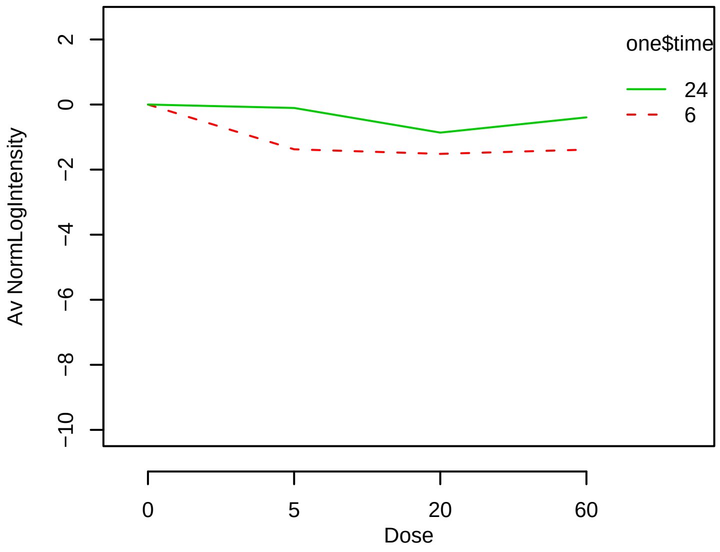
GO_0006563 : L−serine metabolism

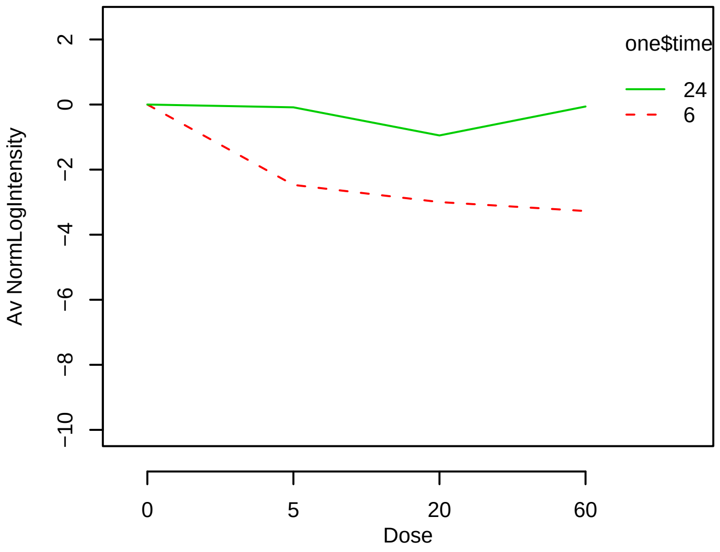


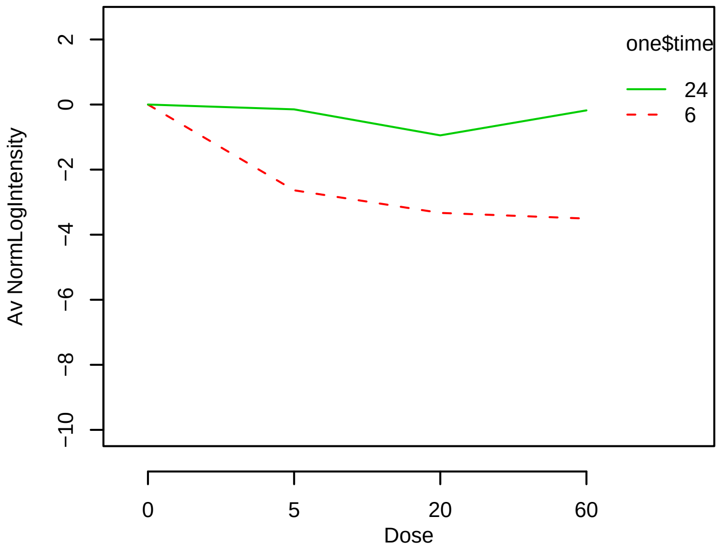
GO_0006564 : L−serine biosynthesis

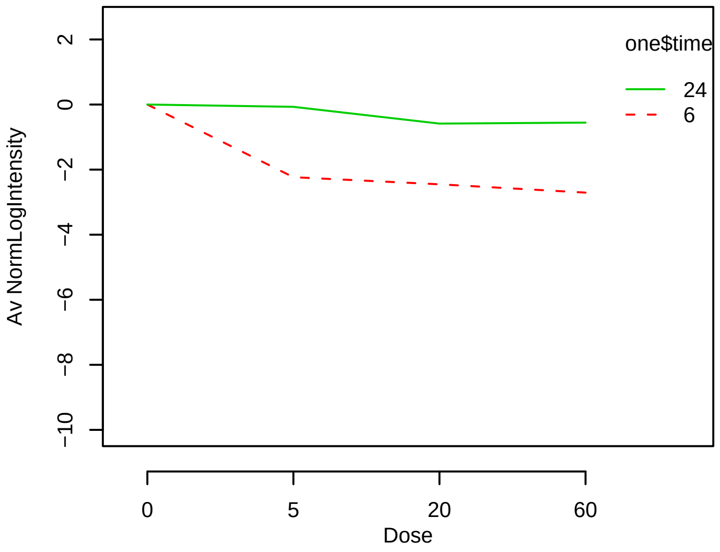

GO_0006568 : tryptophan metabolism

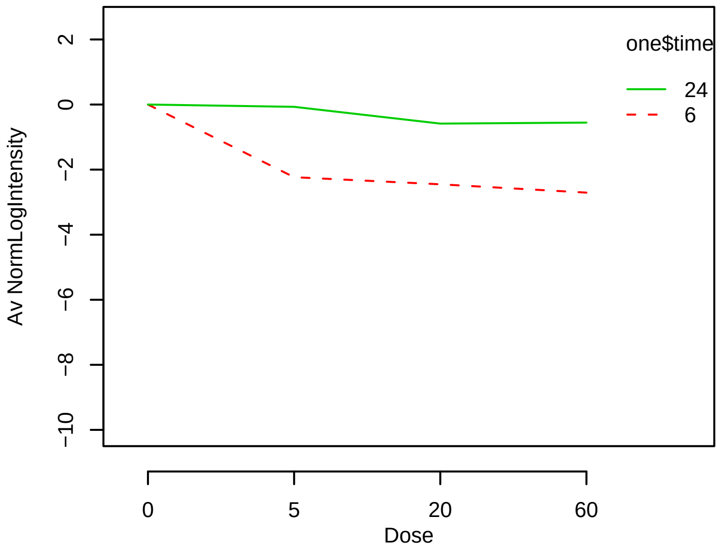

GO_0006570 : tyrosine metabolism

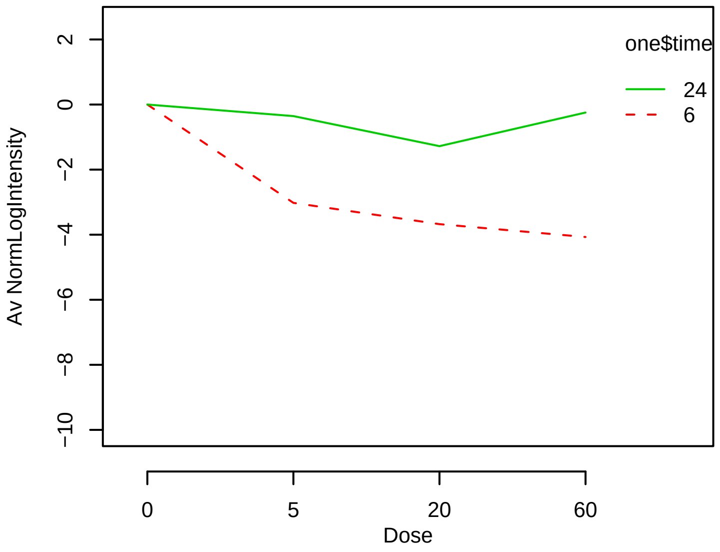

GO_0006572 : tyrosine catabolism

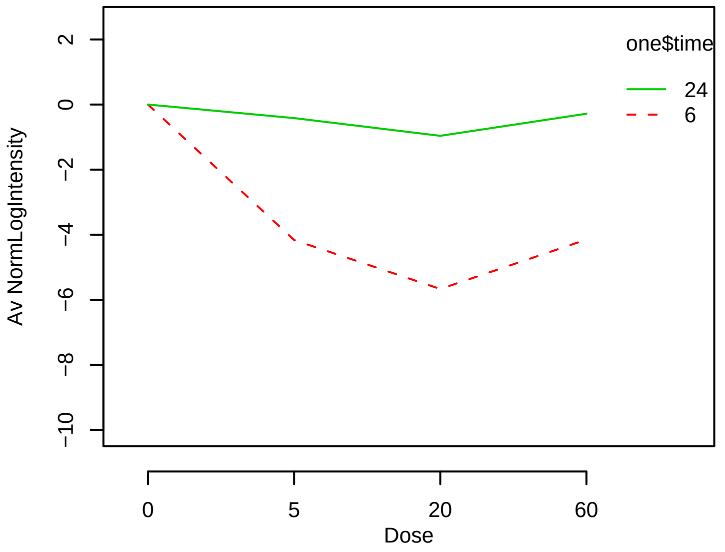

GO_0006575 : amino acid derivative metabolism

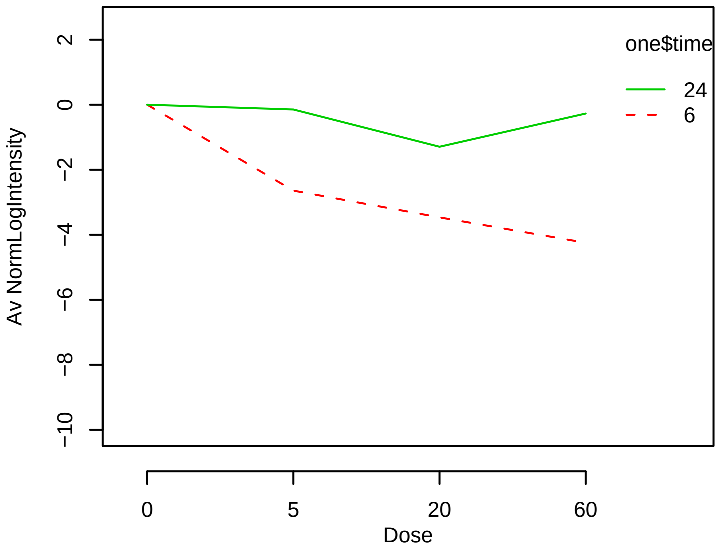

GO_0006576 : biogenic amine metabolism

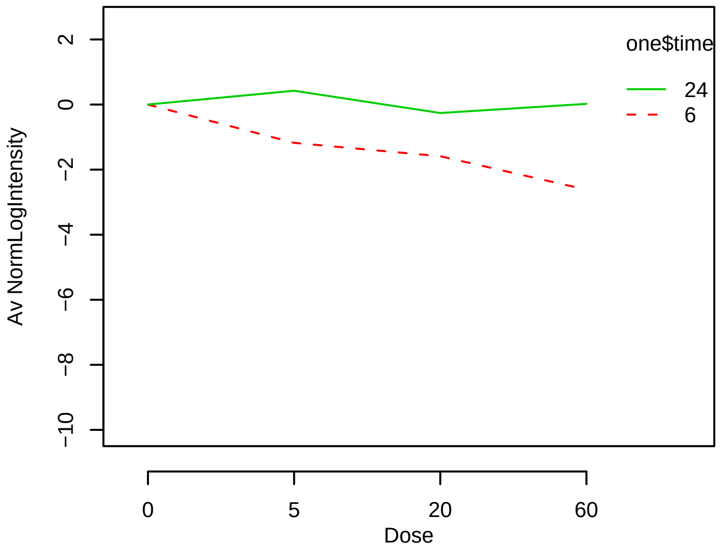

GO_0006582 : melanin metabolism

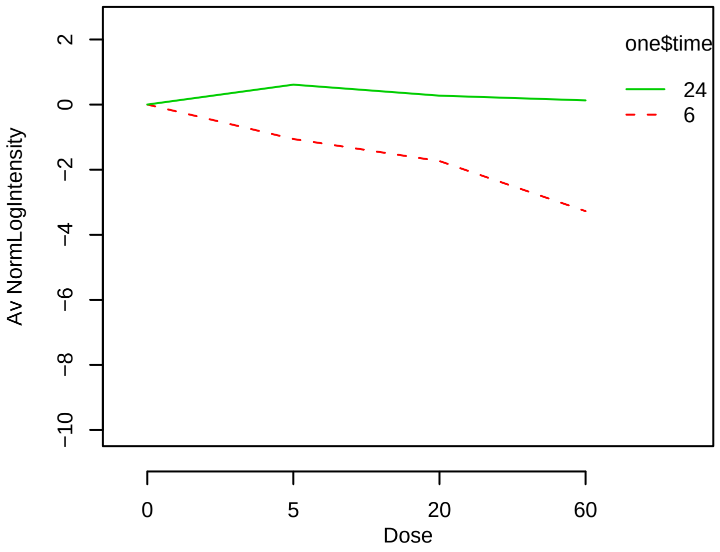

GO_0006583 : melanin biosynthesis from tyrosine


GO_0006584 : catecholamine metabolism

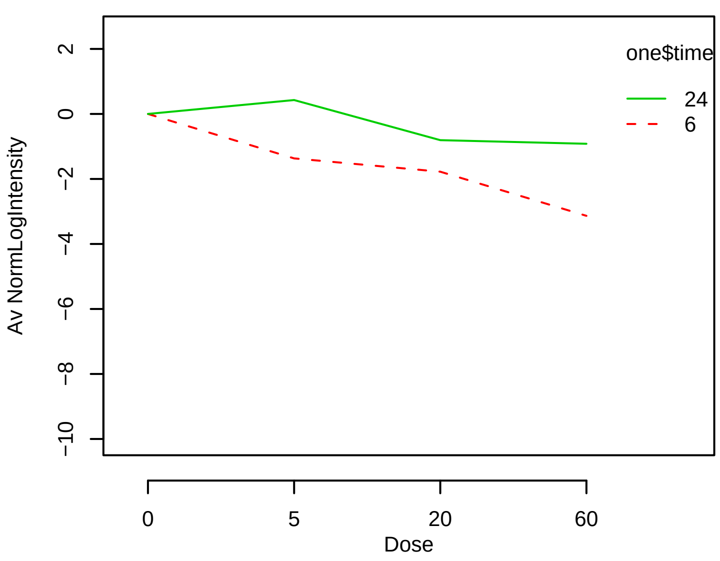

GO_0006586 : indolalkylamine metabolism


GO_0006590 : thyroid hormone generation

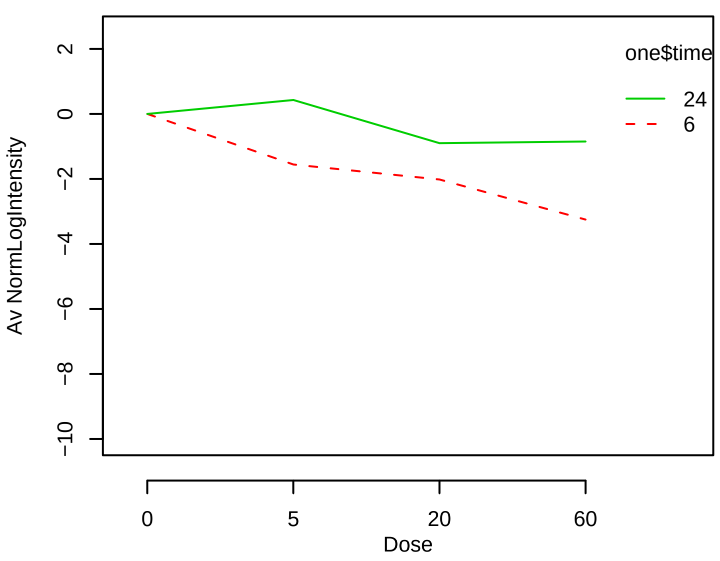

GO_0006595 : polyamine metabolism


GO_0006596 : polyamine biosynthesis

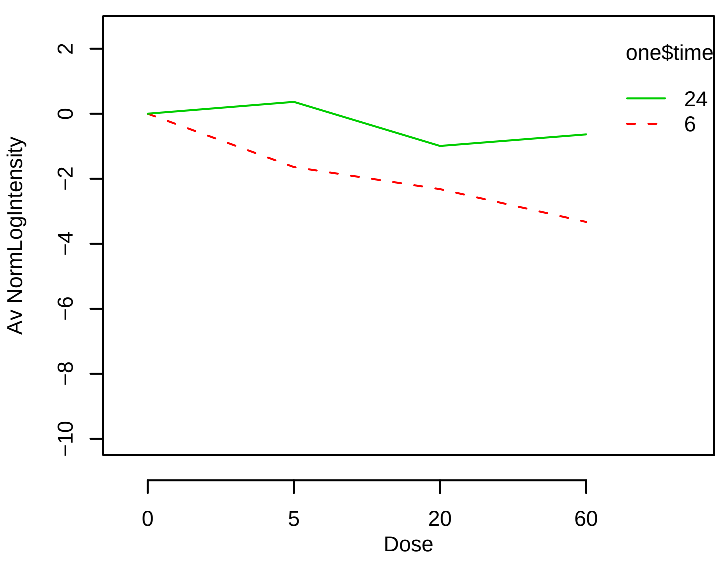
GO_0006605 : protein targeting



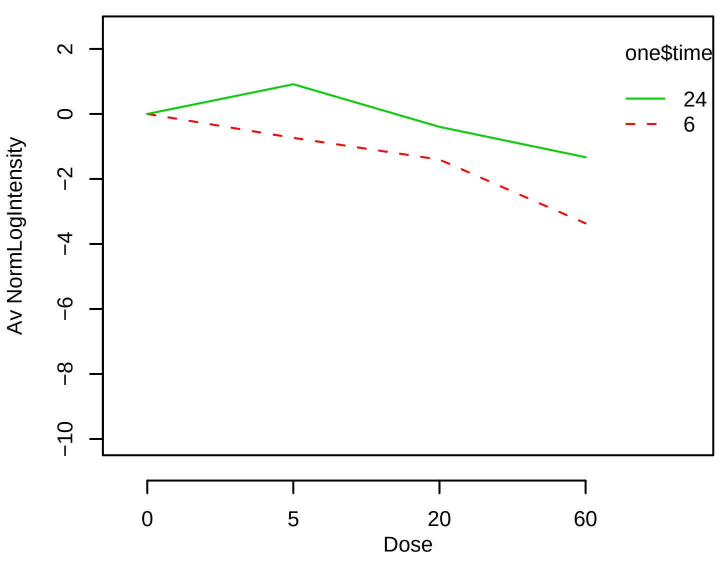
GO_0006606 : protein import into nucleus



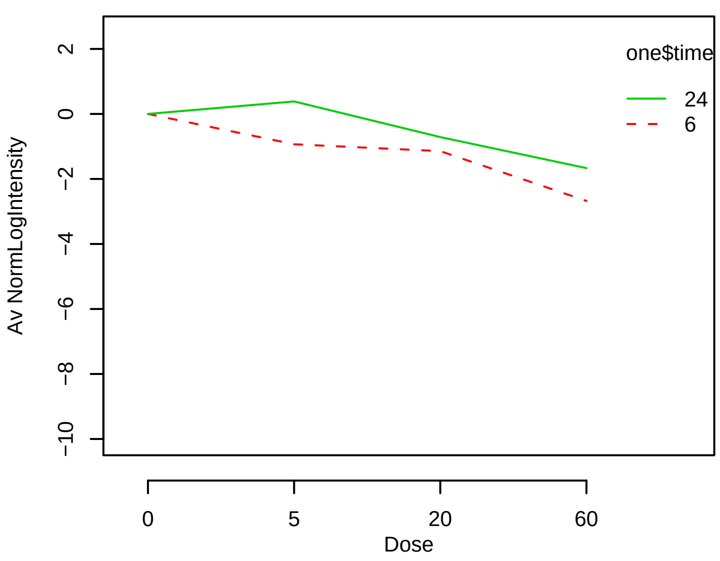
GO_0006607 : NLS−bearing substrate import into nucleus



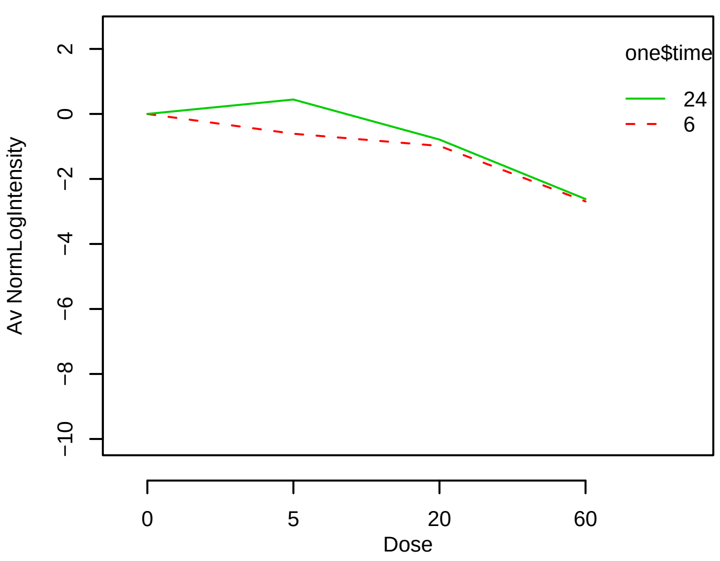
GO_0006611 : protein export from nucleus

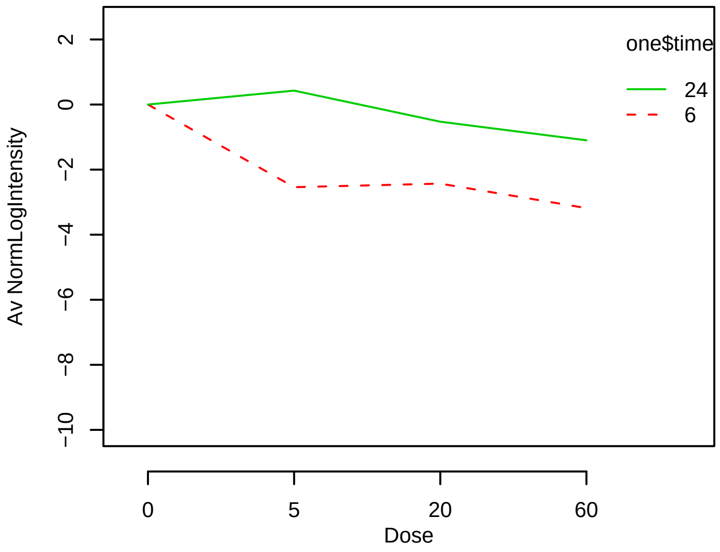


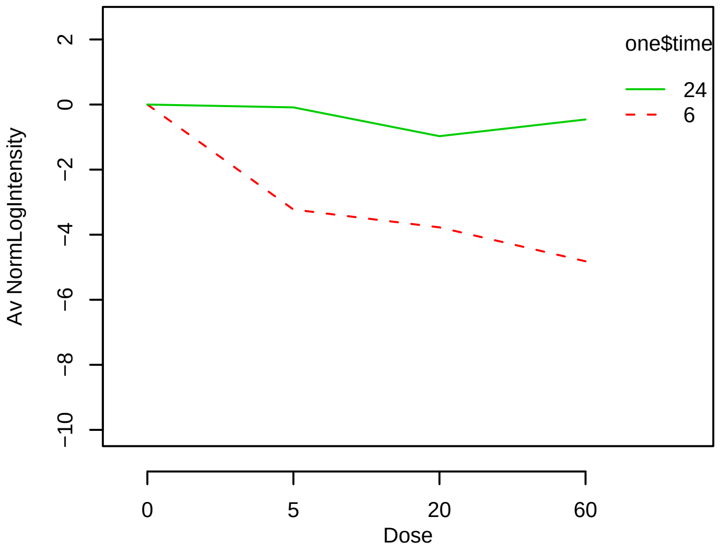
GO_0006612 : protein targeting to membrane

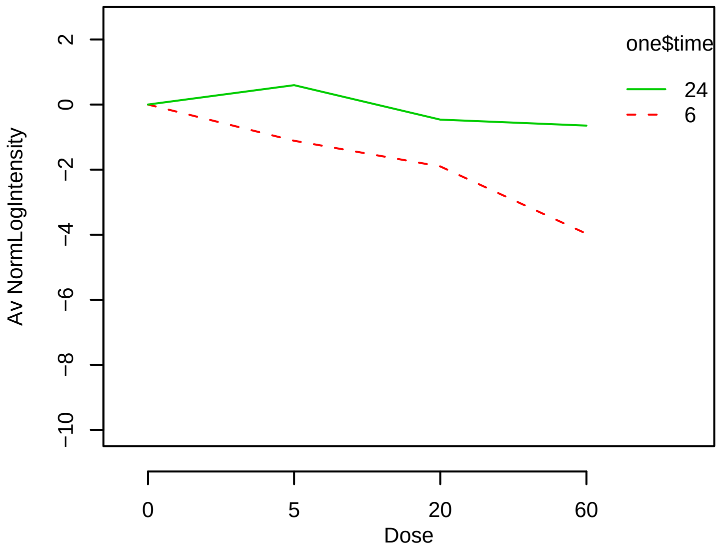


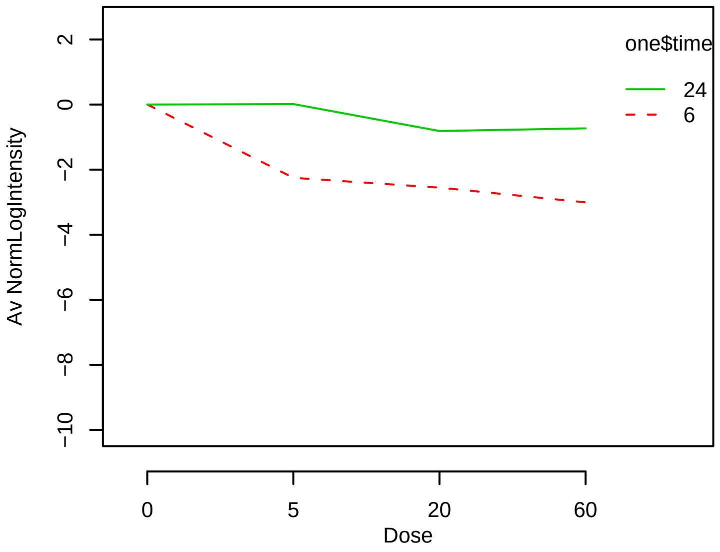
GO_0006613 : cotranslational protein targeting to membra

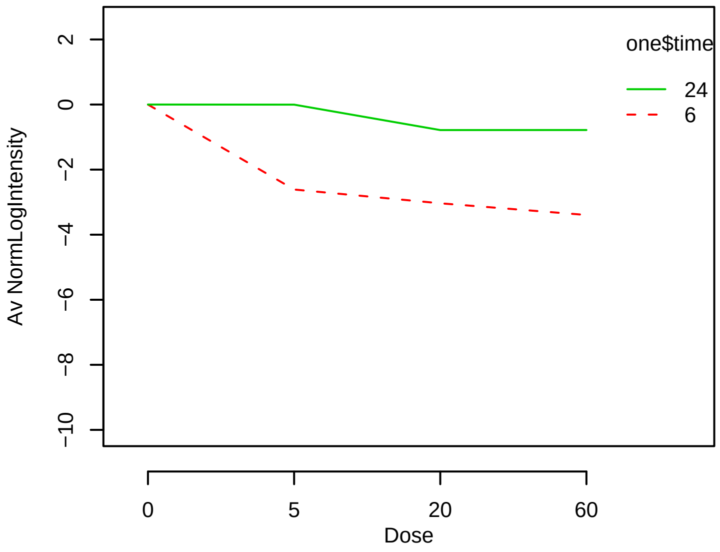


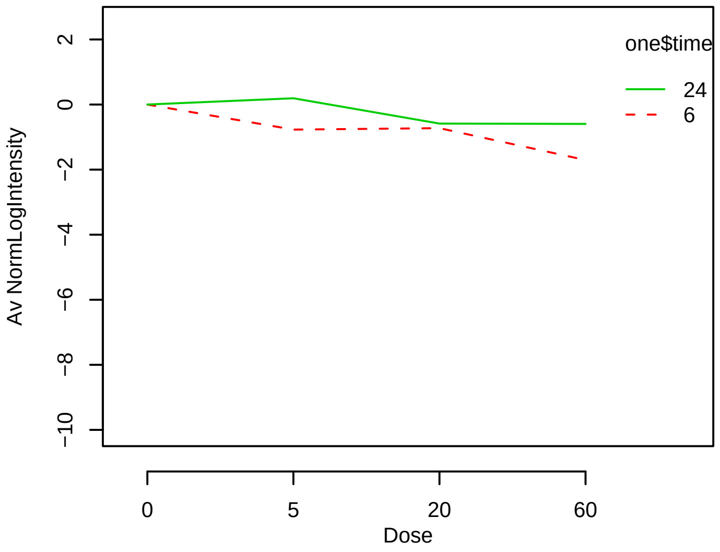

GO_0006621 : protein retention in ER


GO_0006625 : protein targeting to peroxisome

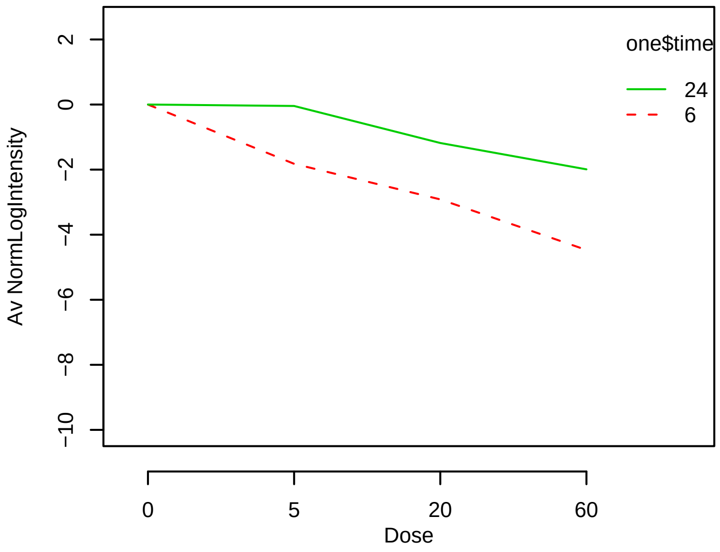

GO_0006626 : protein targeting to mitochondrion


GO_0006631 : fatty acid metabolism

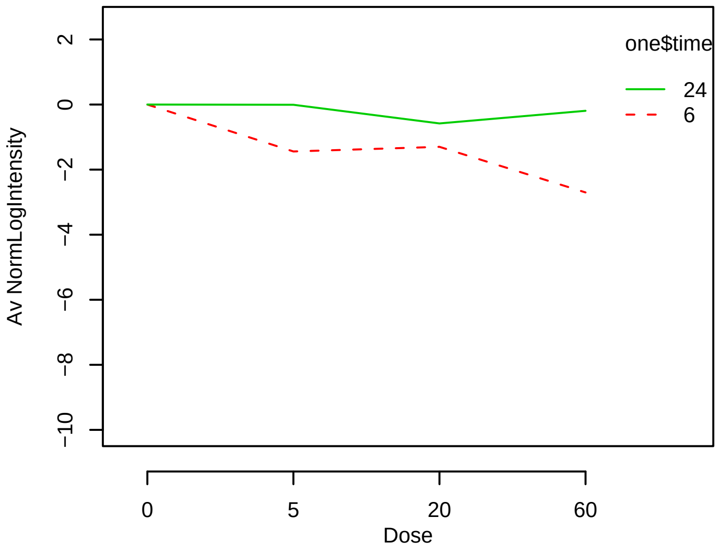

GO_0006633 : fatty acid biosynthesis


GO_0006635 : fatty acid beta−oxidation

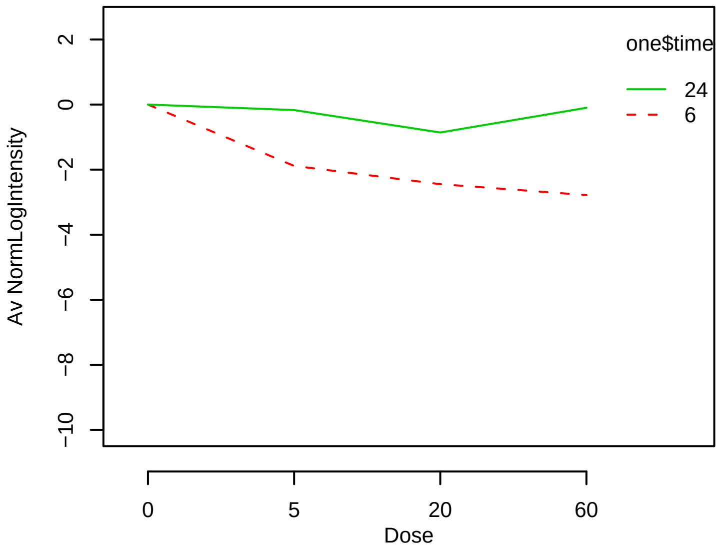
GO_0006636 : fatty acid desaturation



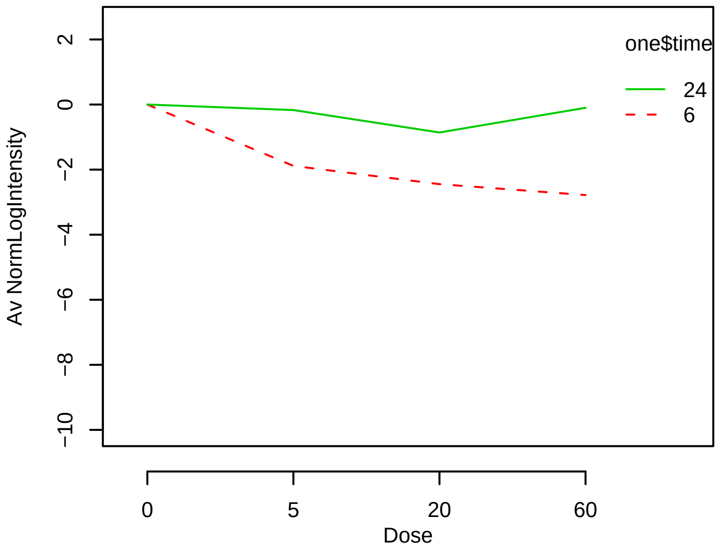
GO_0006637 : acyl−CoA metabolism



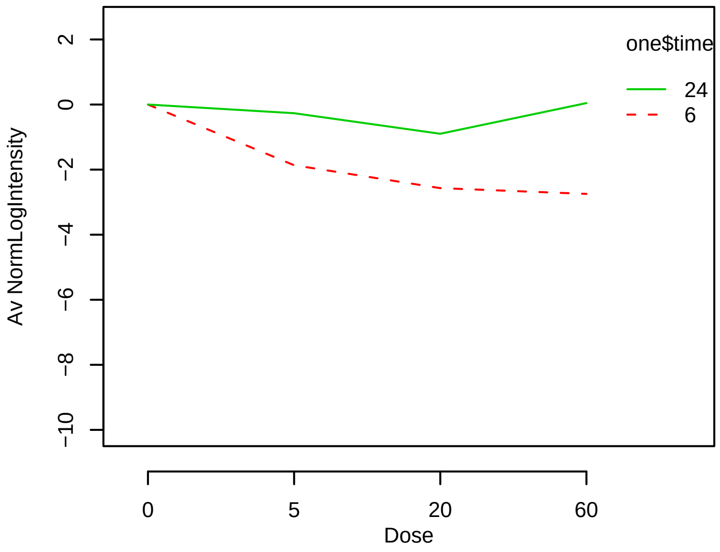
GO_0006638 : neutral lipid metabolism



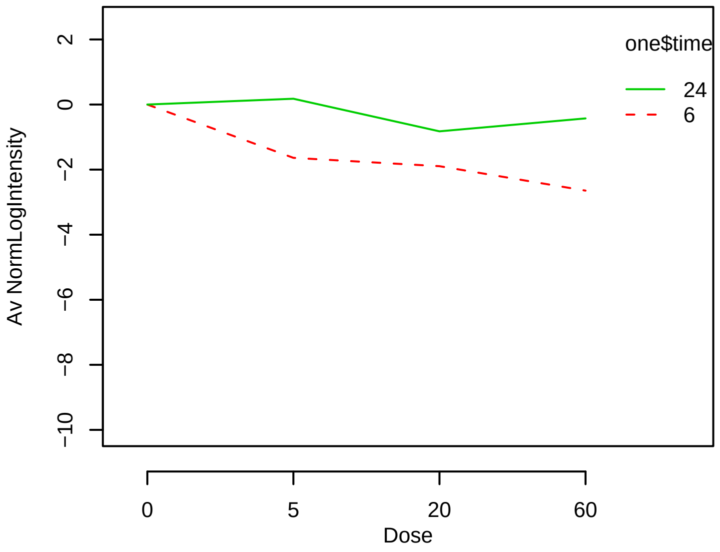
GO_0006639 : acylglycerol metabolism



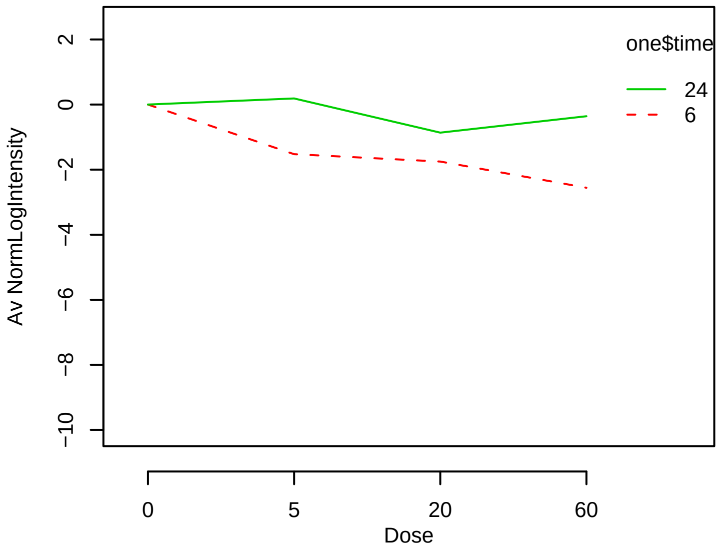
GO_0006641 : triacylglycerol metabolism



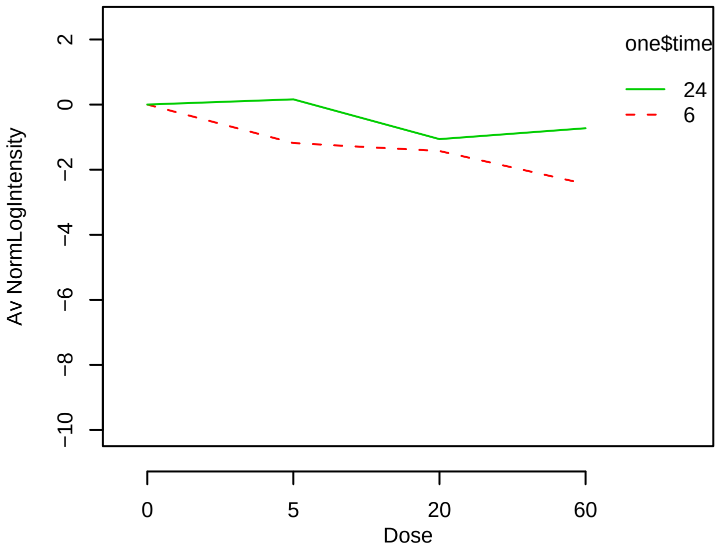
GO_0006643 : membrane lipid metabolism



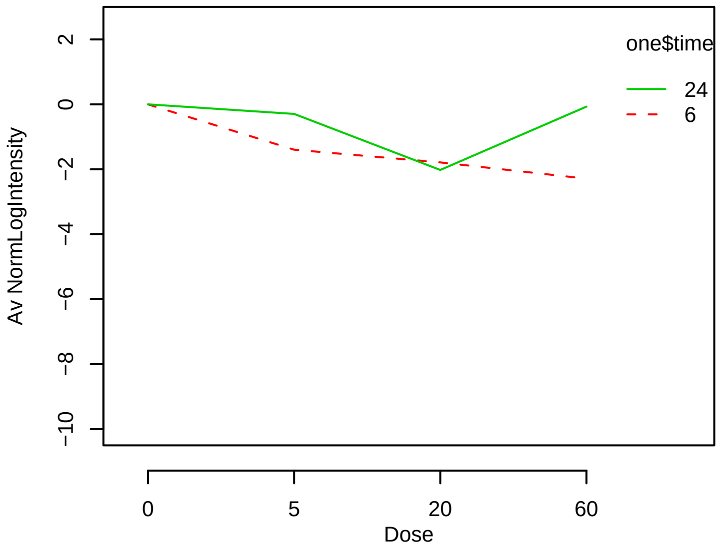
GO_0006644 : phospholipid metabolism



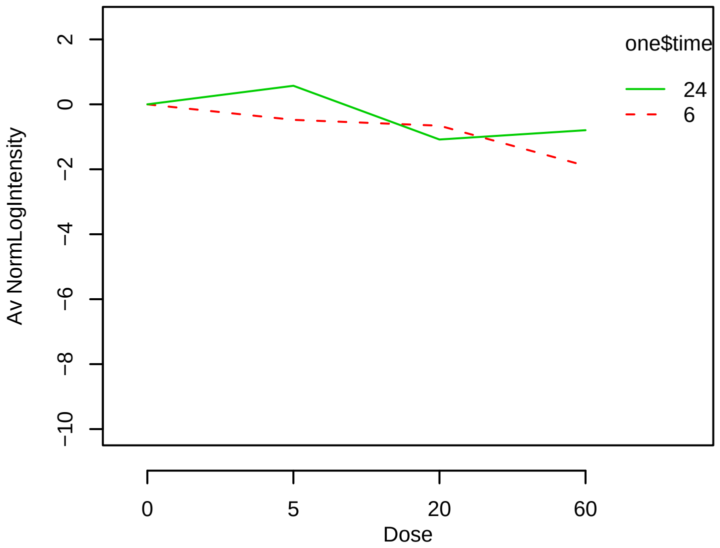
GO_0006650 : glycerophospholipid metabolism



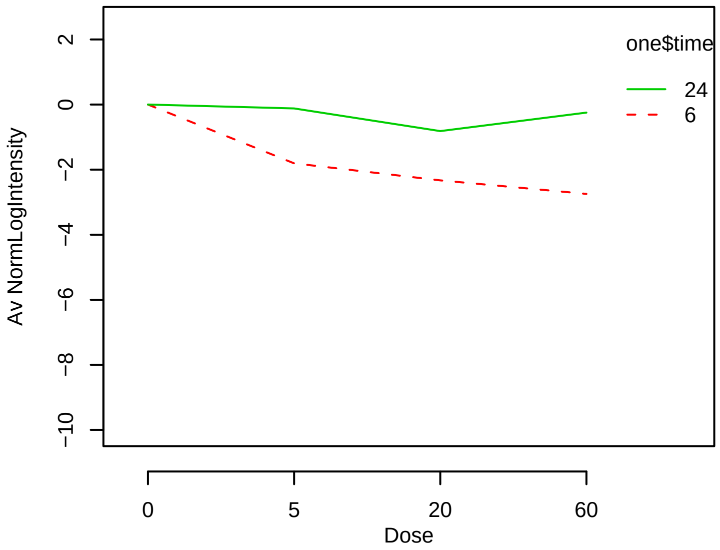
GO_0006656 : phosphatidylcholine biosynthesis



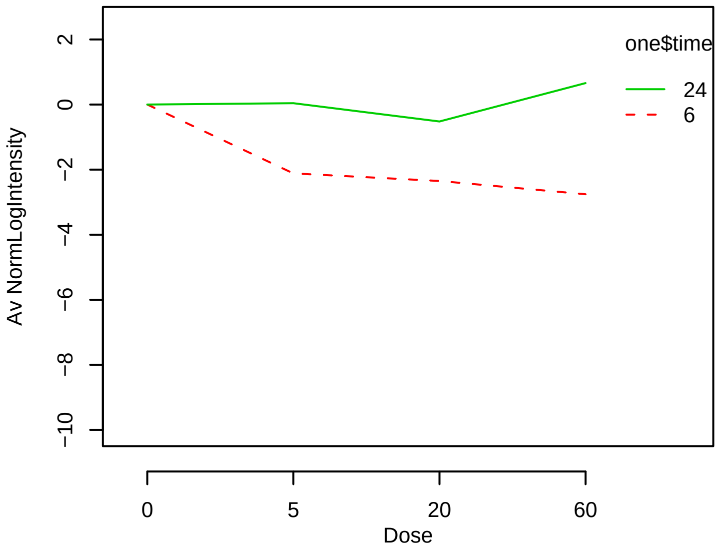
GO_0006661 : phosphatidylinositol biosynthesis

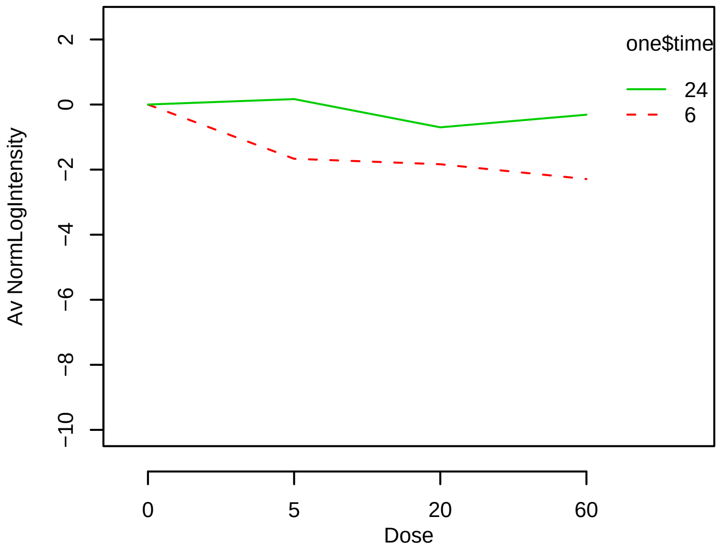


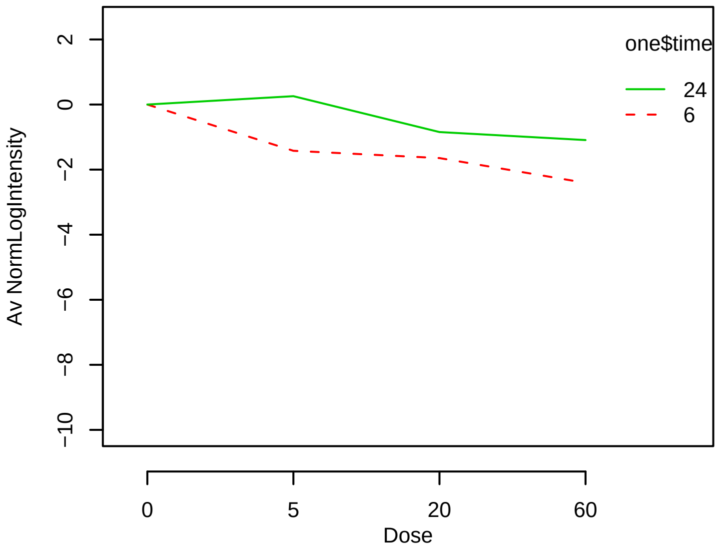
GO_0006662 : glycerol ether metabolism

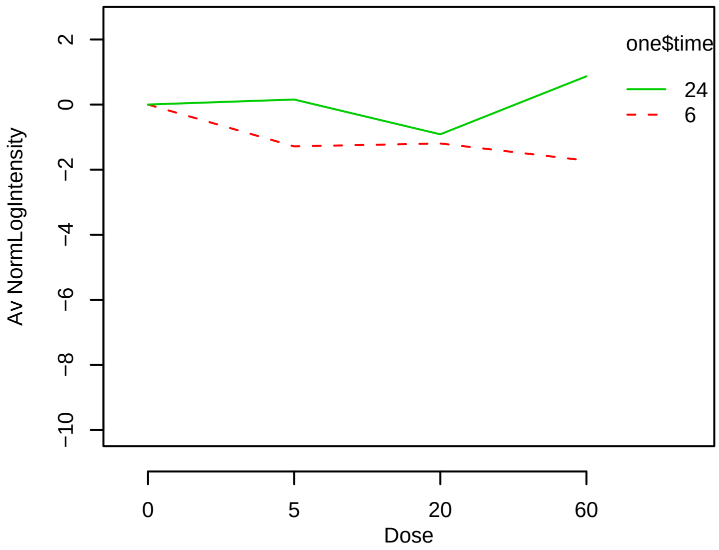


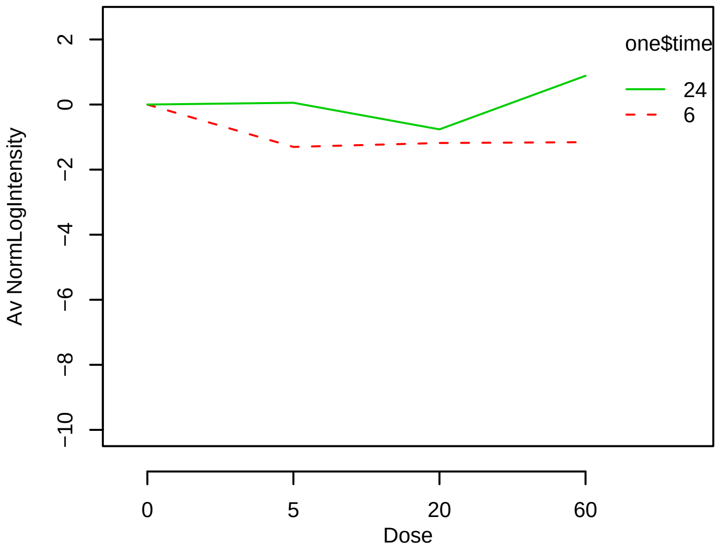
GO_0006664 : glycolipid metabolism

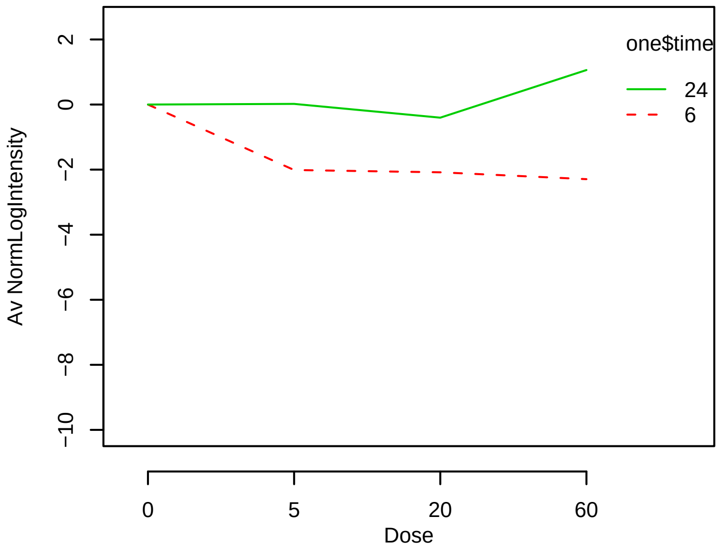


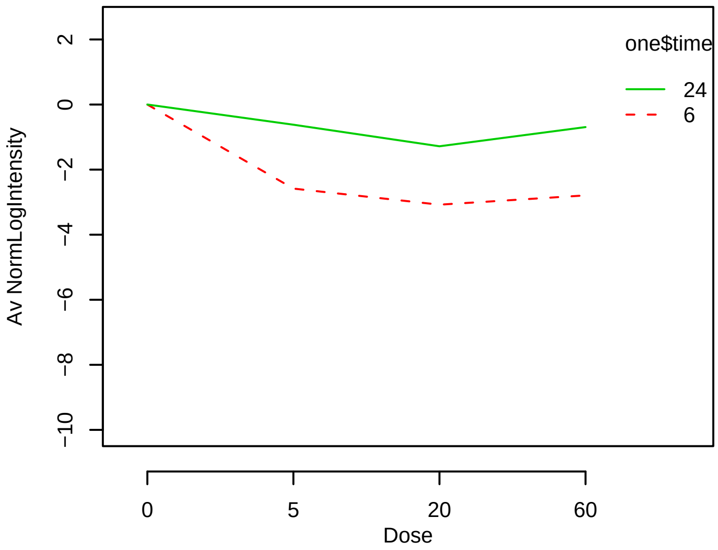

GO_0006665 : sphingolipid metabolism

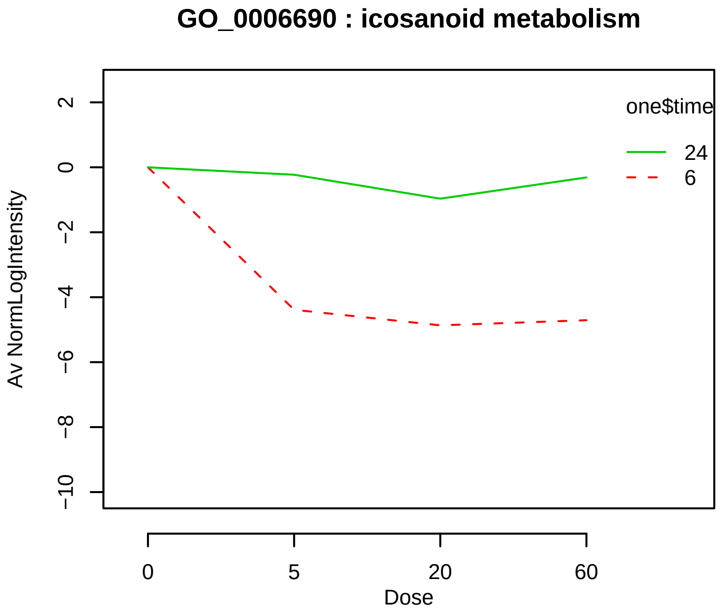

GO_0006672 : ceramide metabolism

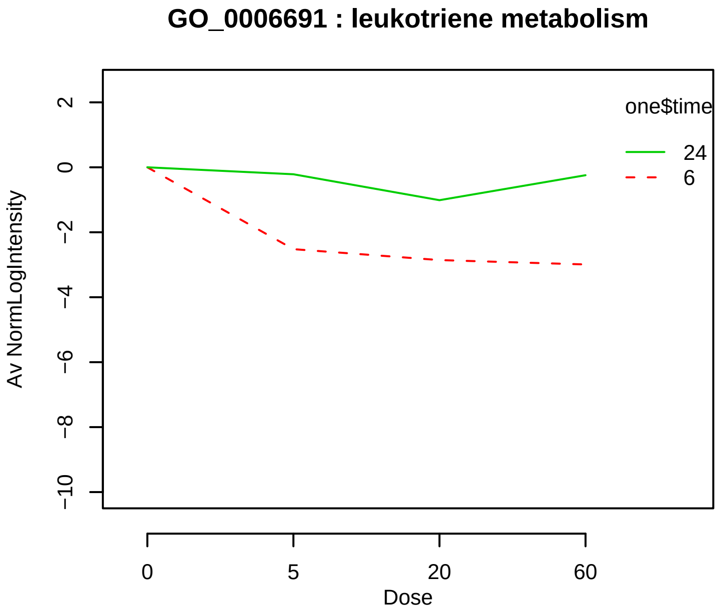

GO_0006677 : glycosylceramide metabolism

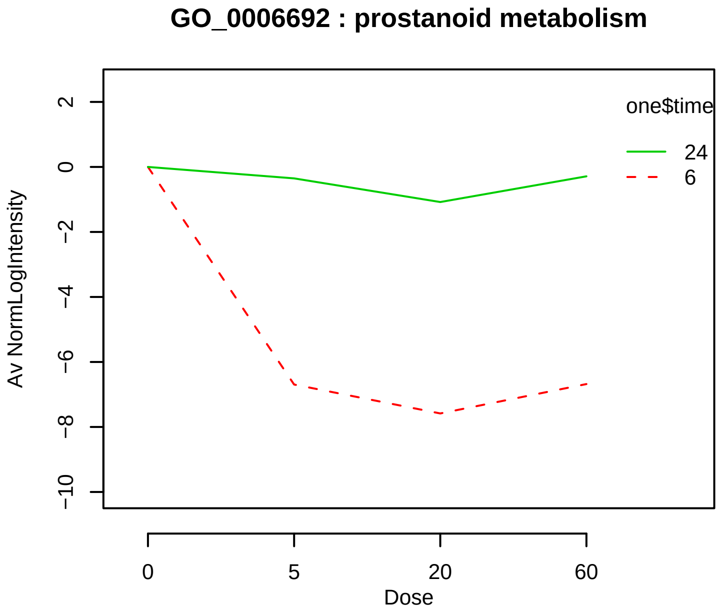

GO_0006684 : sphingomyelin metabolism

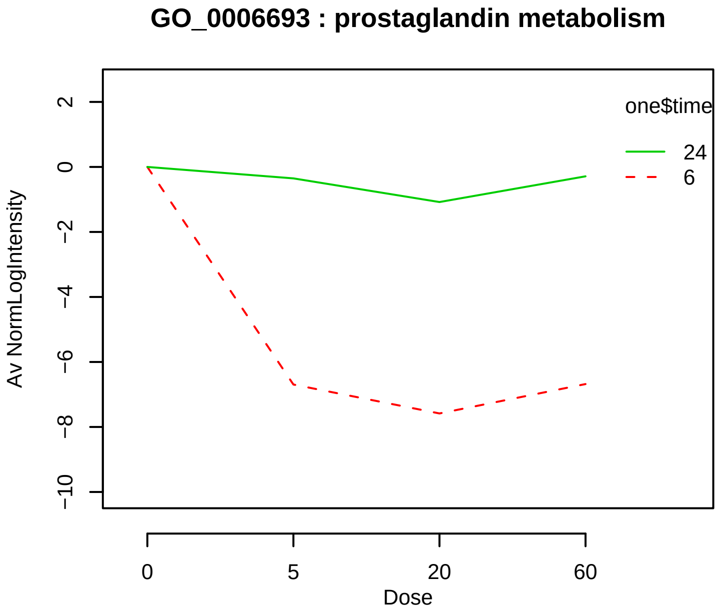

GO_0006687 : glycosphingolipid metabolism

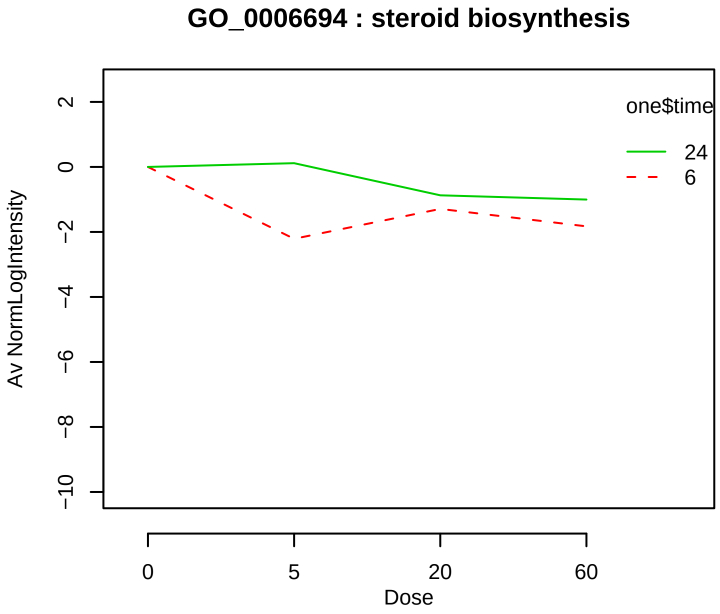

GO_0006688 : glycosphingolipid biosynthesis

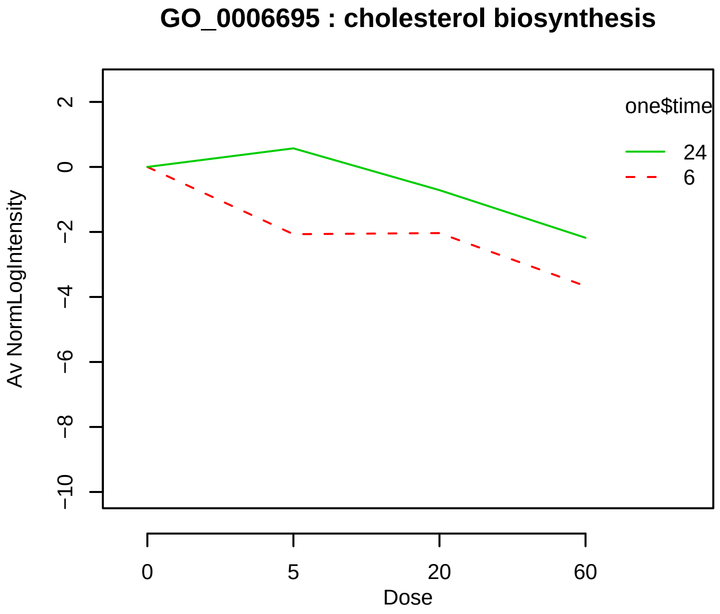

GO_0006690 : icosanoid metabolism

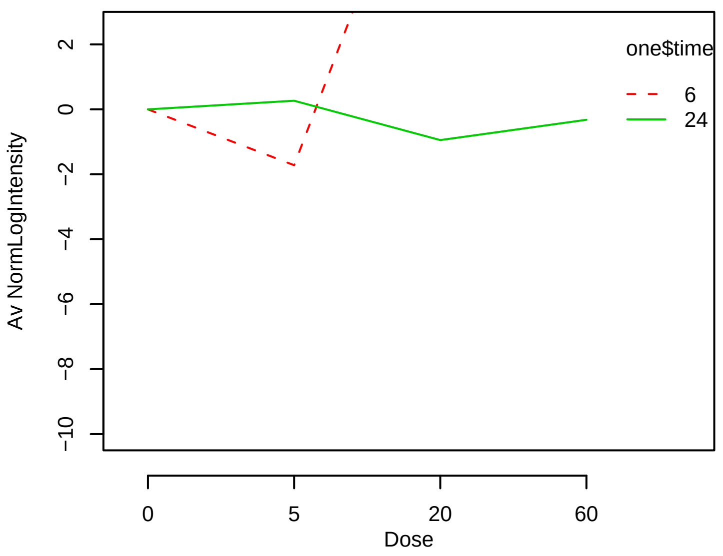

GO_0006691 : leukotriene metabolism


GO_0006692 : prostanoid metabolism

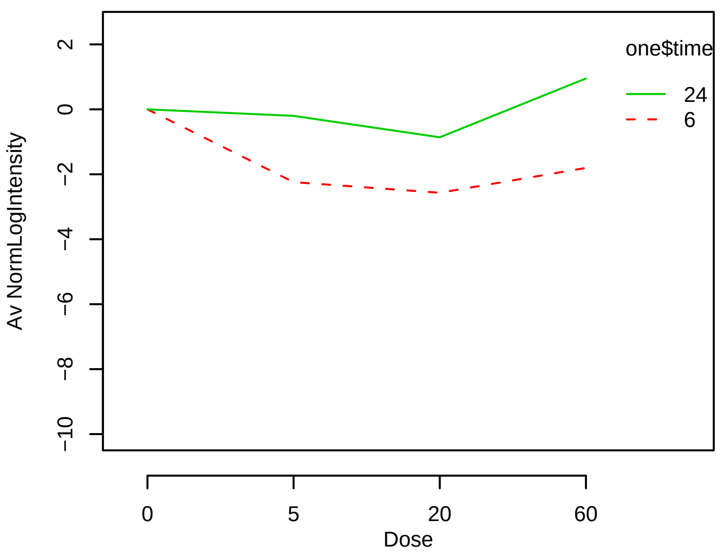

GO_0006693 : prostaglandin metabolism


GO_0006694 : steroid biosynthesis

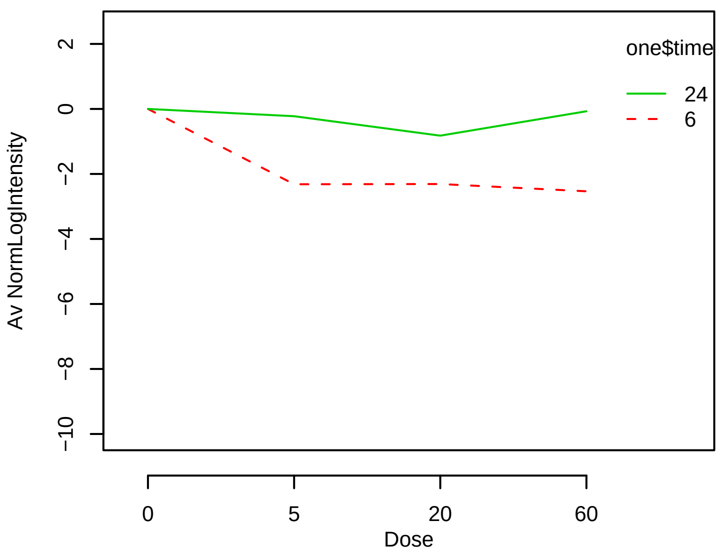

GO_0006695 : cholesterol biosynthesis



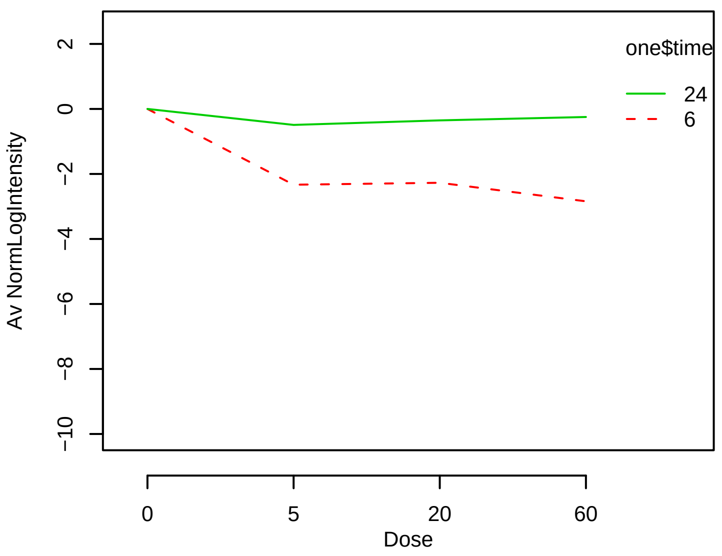
GO_0006699 : bile acid biosynthesis



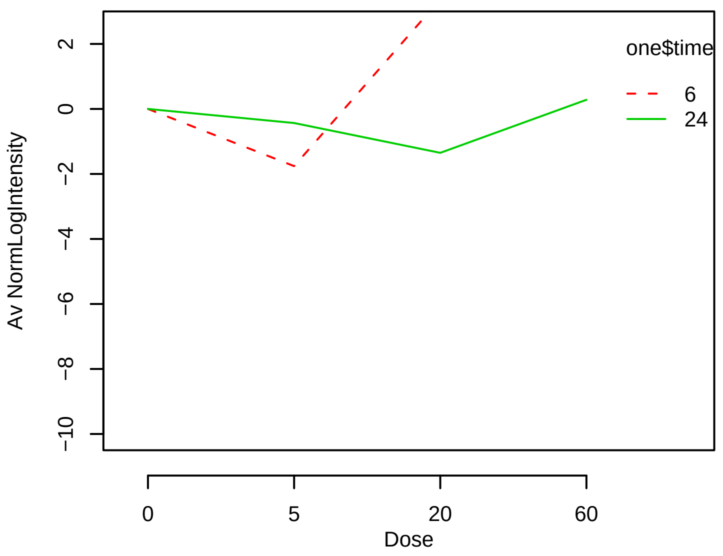
GO_0006700 : C21−steroid hormone biosynthesis



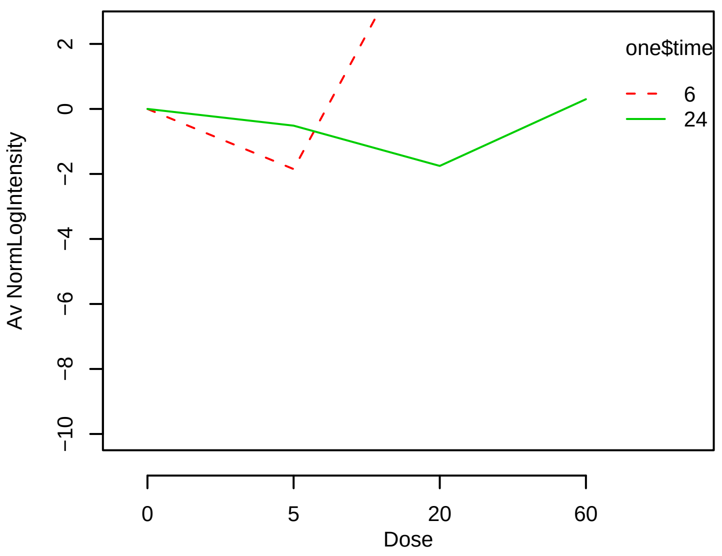
GO_0006702 : androgen biosynthesis



GO_0006703 : estrogen biosynthesis

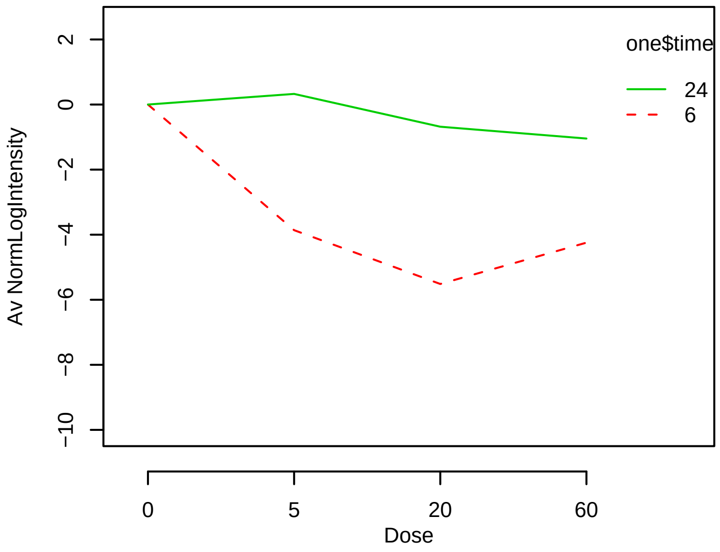


GO_0006706 : steroid catabolism

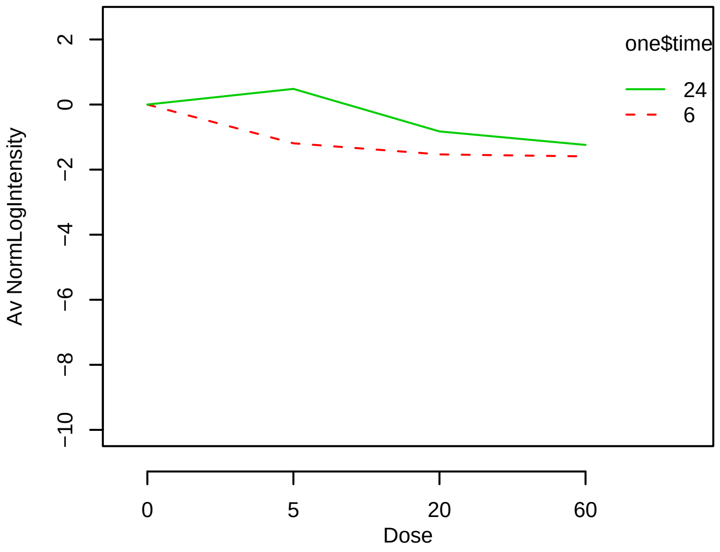


GO_0006707 : cholesterol catabolism

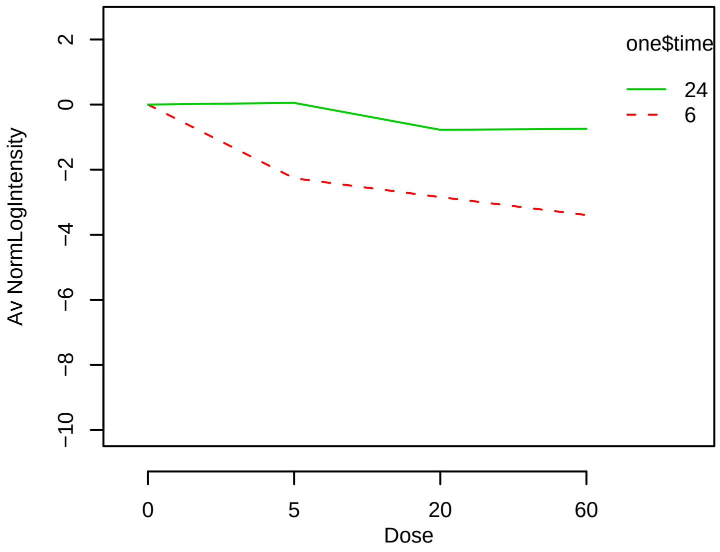
GO_0006720 : isoprenoid metabolism



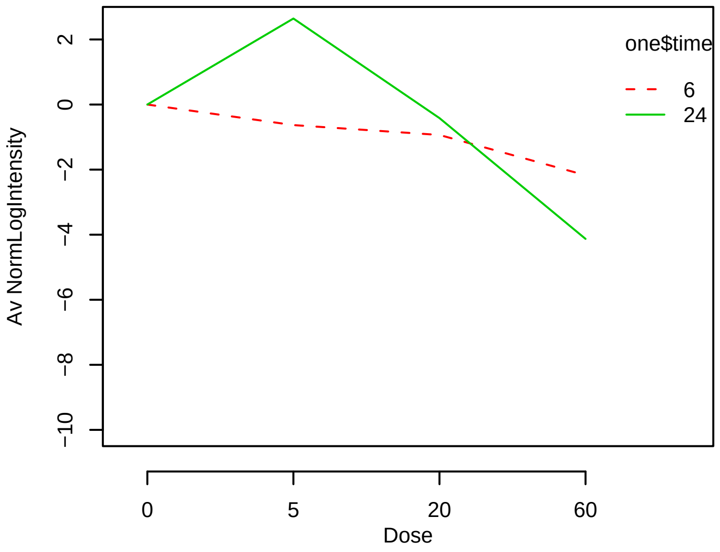
GO_0006721 : terpenoid metabolism



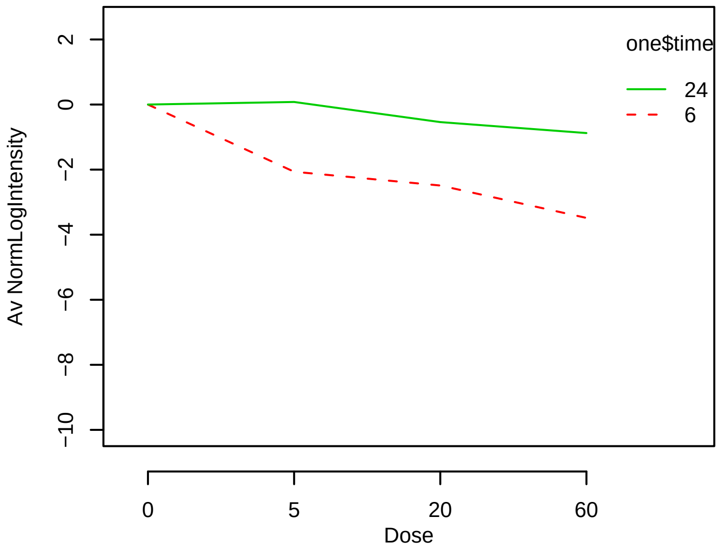
GO_0006725 : aromatic compound metabolism



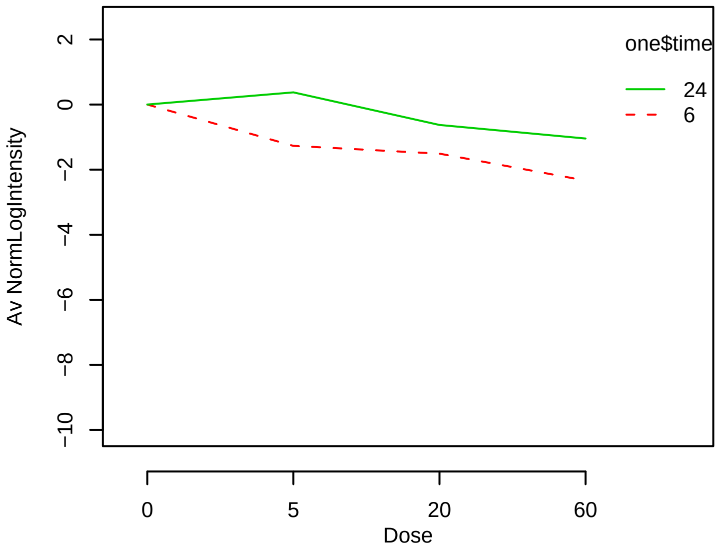
GO_0006729 : tetrahydrobiopterin biosynthesis

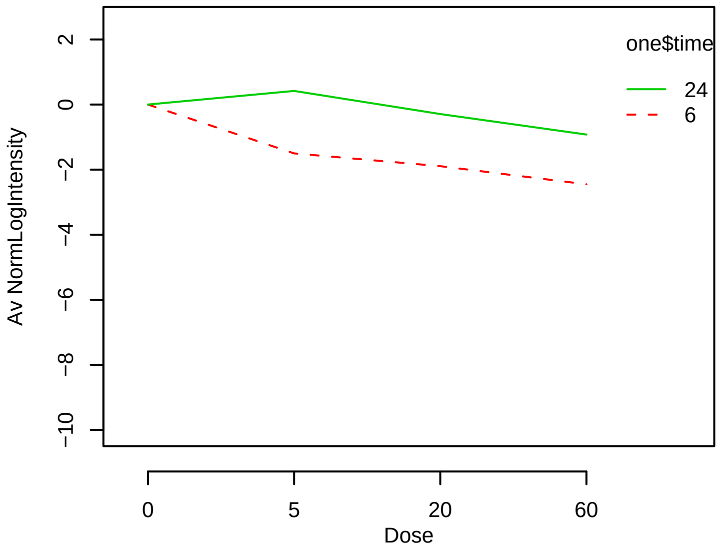


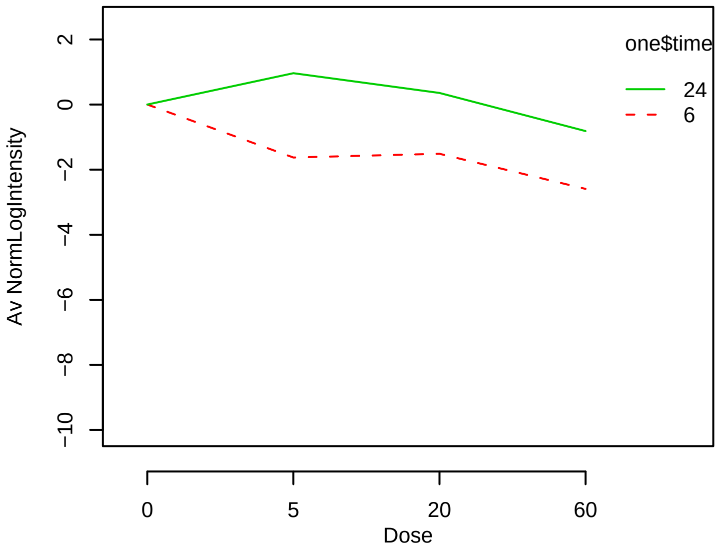
GO_0006730 : one−carbon compound metabolism

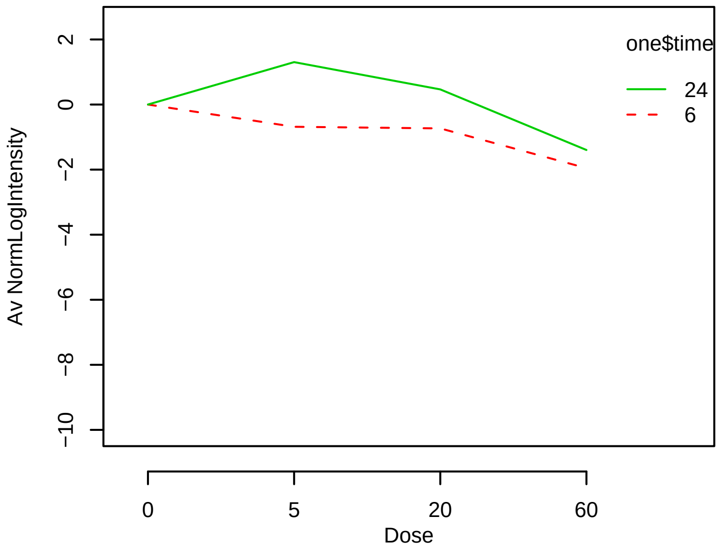


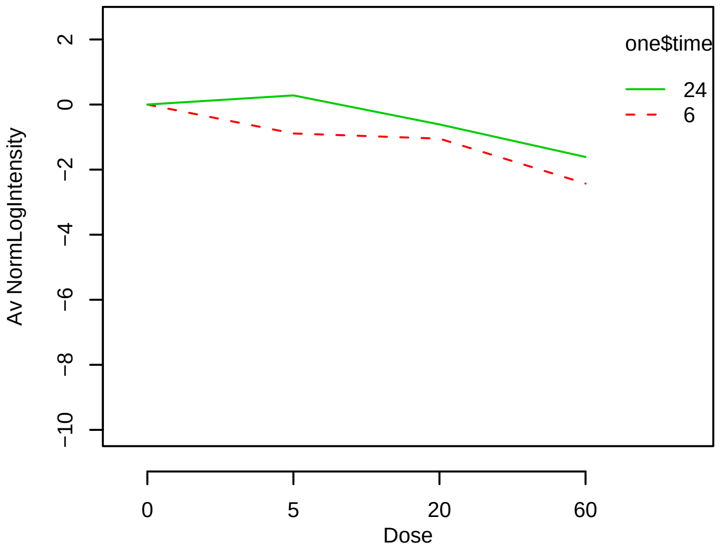
GO_0006732 : coenzyme metabolism

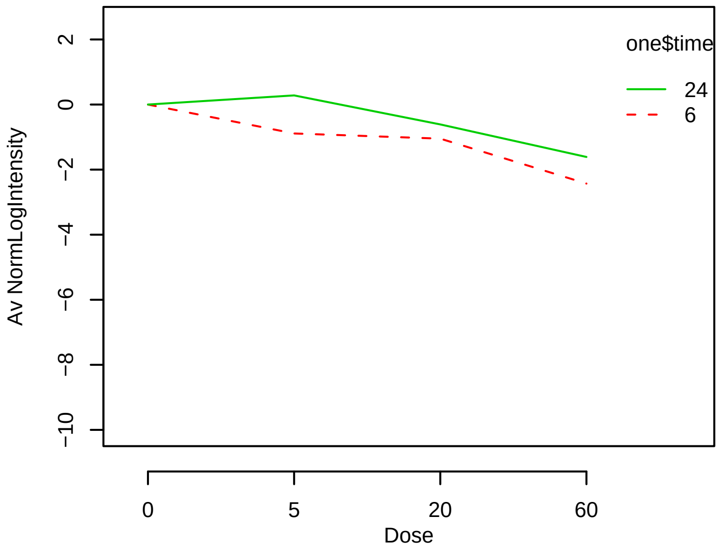


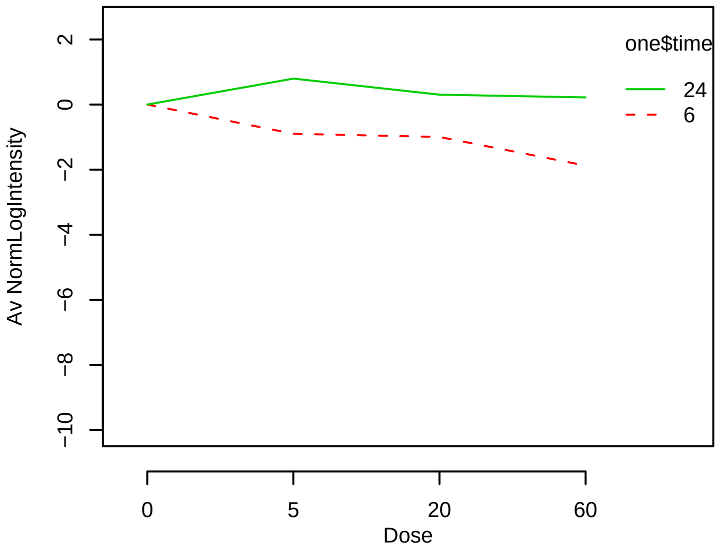

GO_0006733 : oxidoreduction coenzyme metabolism

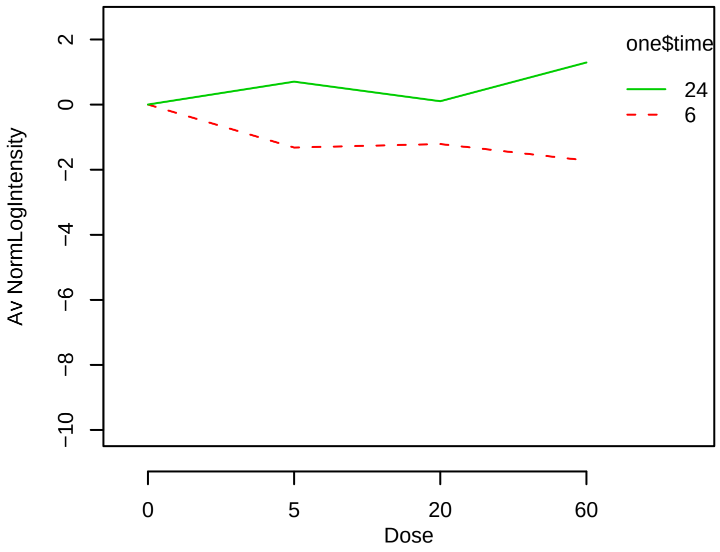

GO_0006739 : NADP metabolism

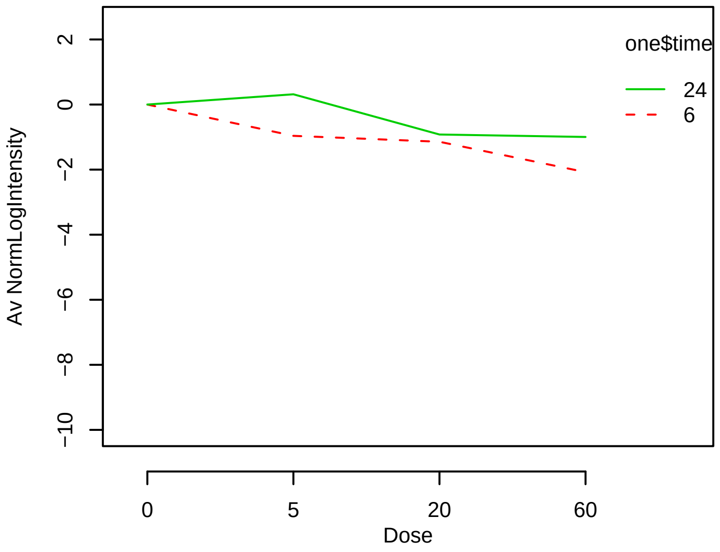

GO_0006740 : NADPH regeneration

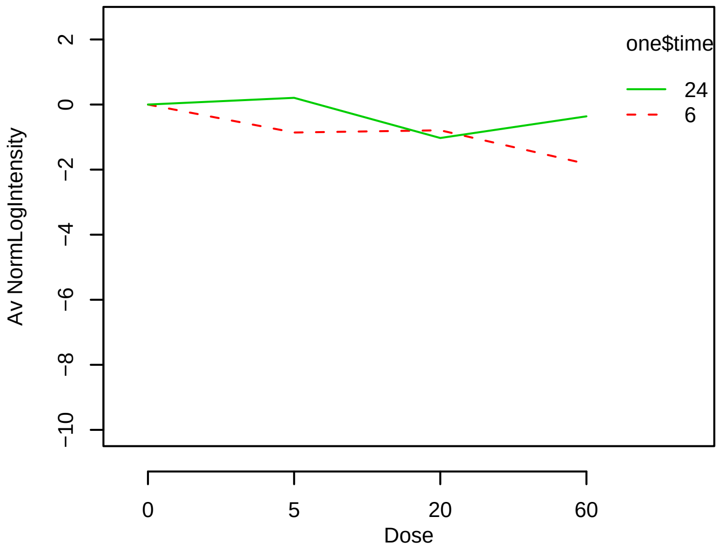

GO_0006743 : ubiquinone metabolism

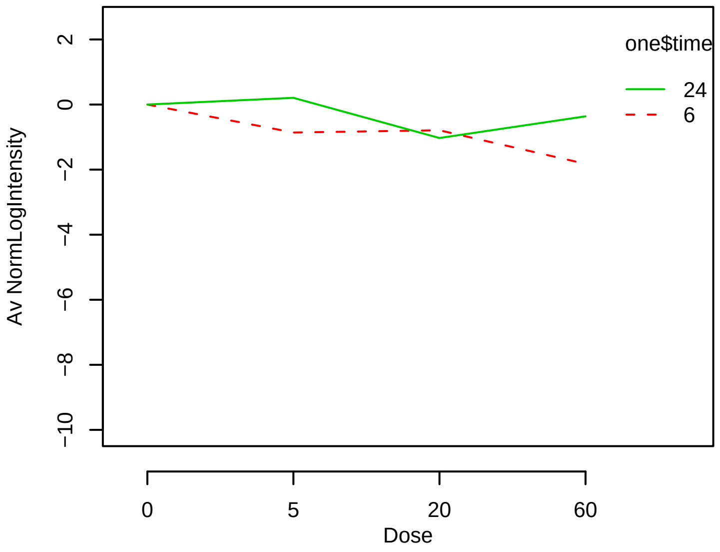

GO_0006744 : ubiquinone biosynthesis

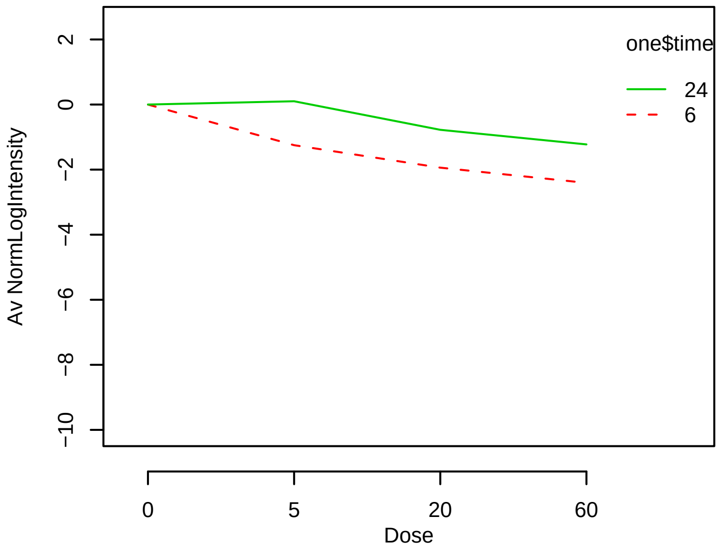

GO_0006749 : glutathione metabolism

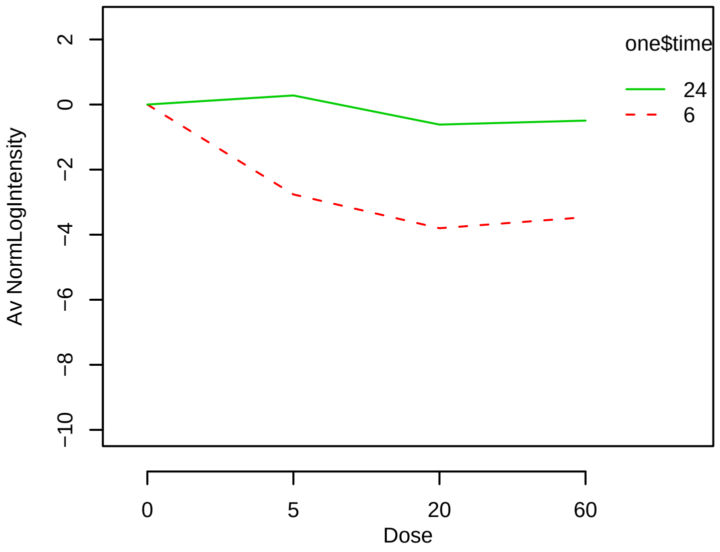

GO_0006750 : glutathione biosynthesis


GO_0006752 : group transfer coenzyme metabolism

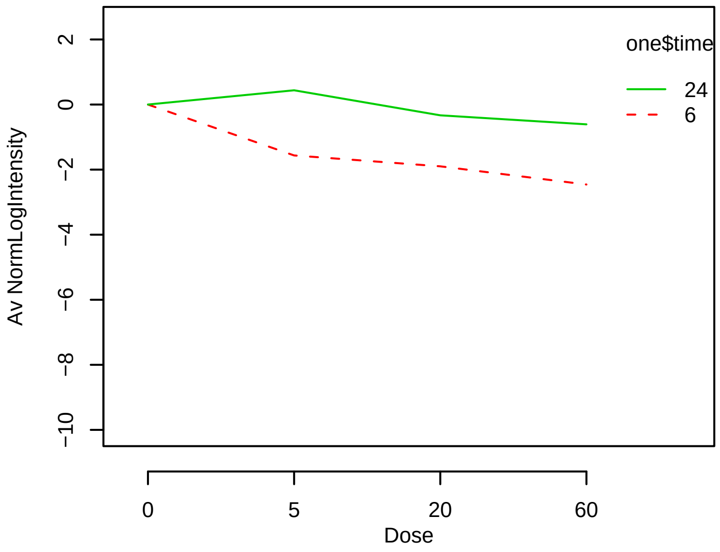

GO_0006753 : nucleoside phosphate metabolism


GO_0006754 : ATP biosynthesis

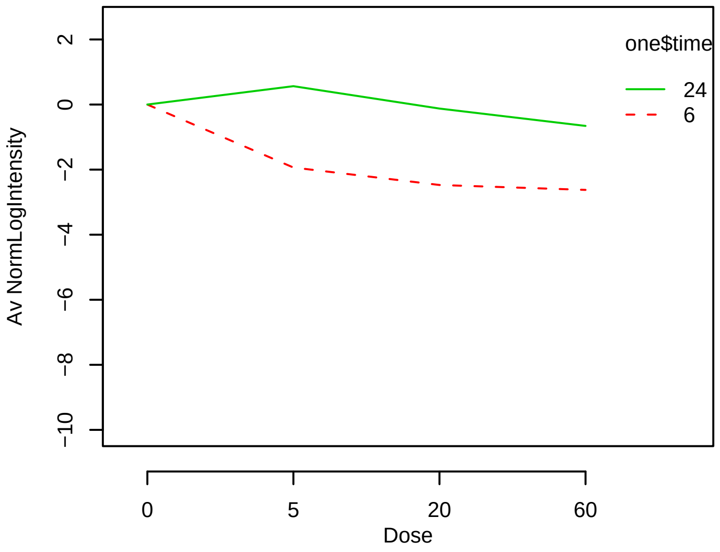

GO_0006760 : folic acid and derivative metabolism


GO_0006766 : vitamin metabolism

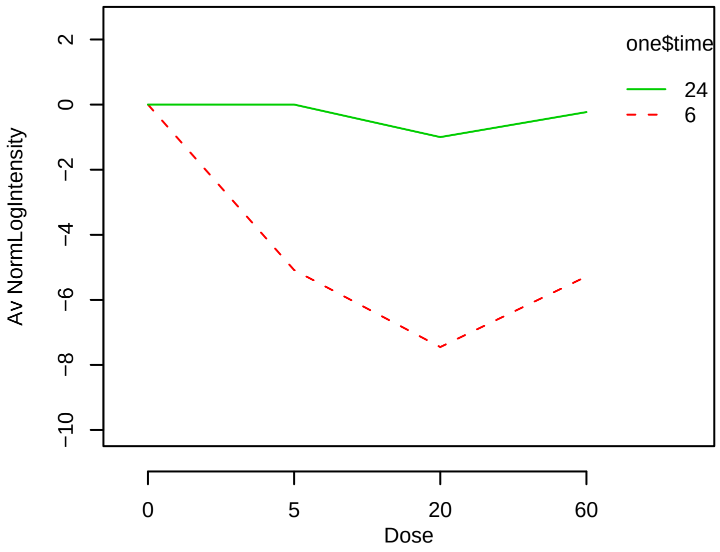
GO_0006767 : water−soluble vitamin metabolism



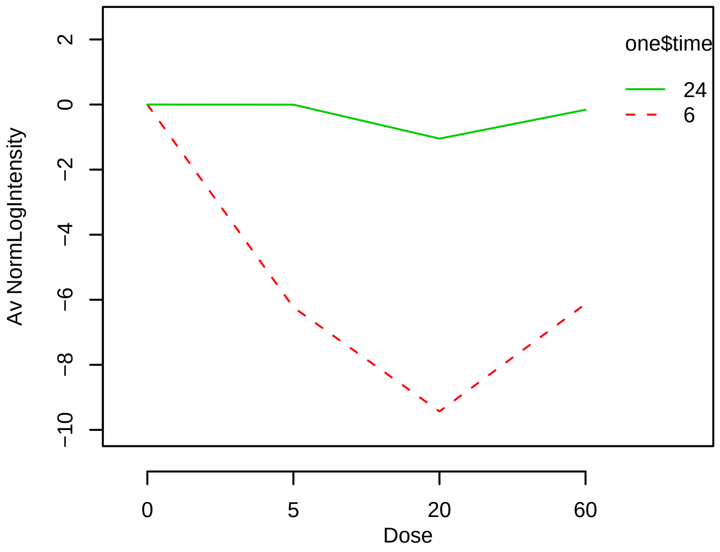
GO_0006769 : nicotinamide metabolism



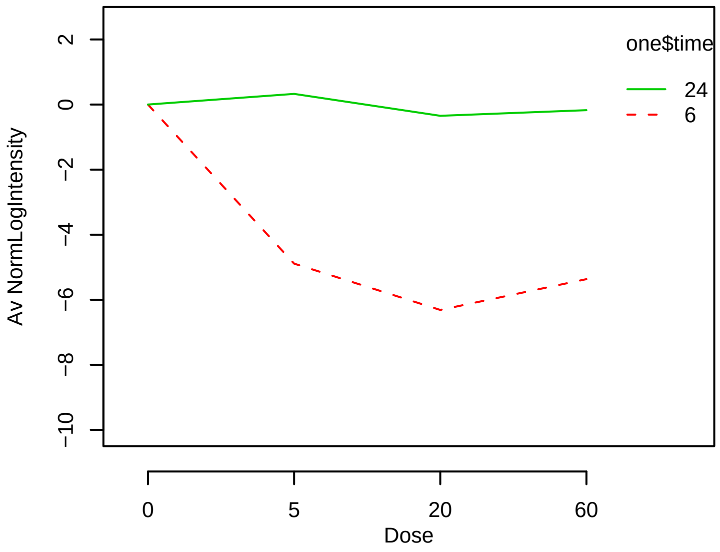
GO_0006775 : fat−soluble vitamin metabolism



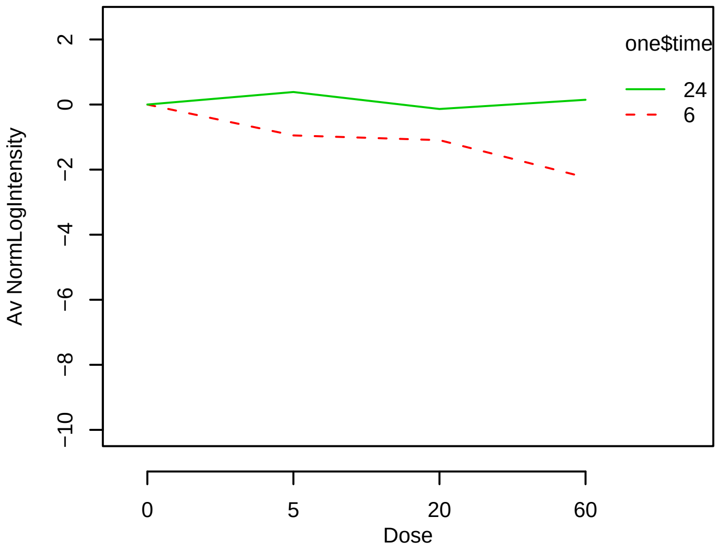
GO_0006776 : vitamin A metabolism



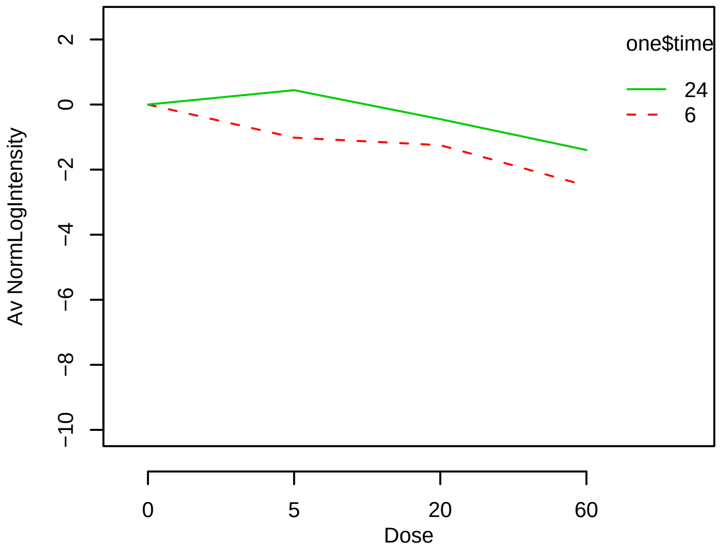
GO_0006777 : Mo−molybdopterin cofactor biosynthesis



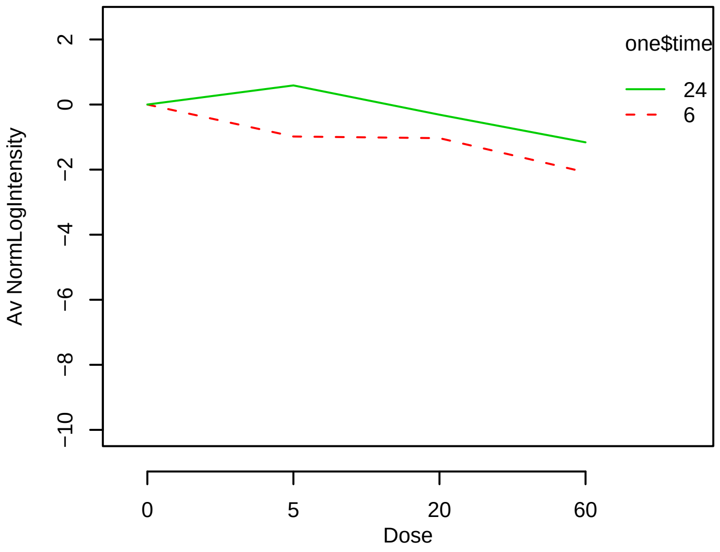
GO_0006778 : porphyrin metabolism



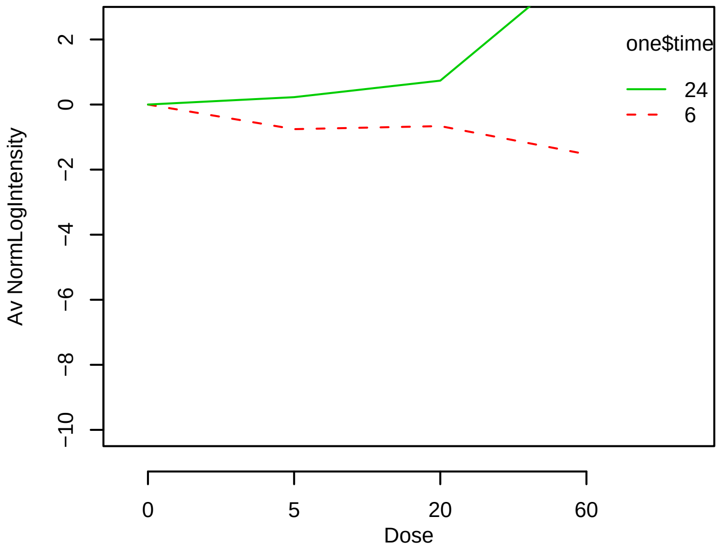
GO_0006779 : porphyrin biosynthesis



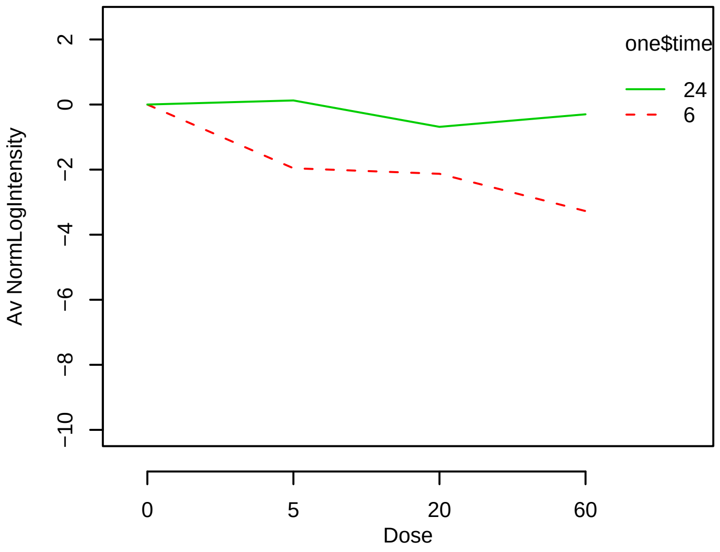
GO_0006783 : heme biosynthesis



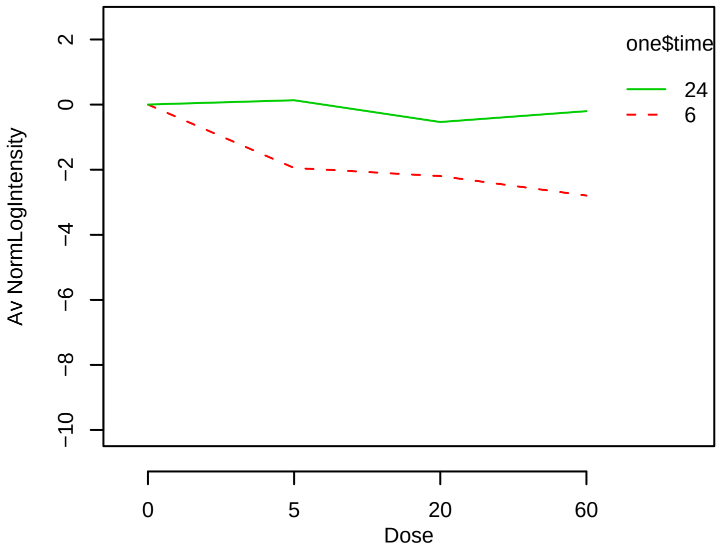
GO_0006787 : porphyrin catabolism



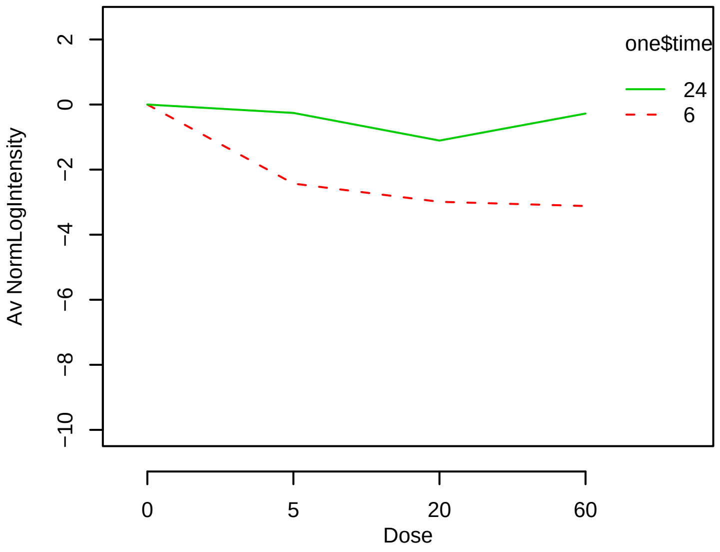
GO_0006790 : sulfur metabolism

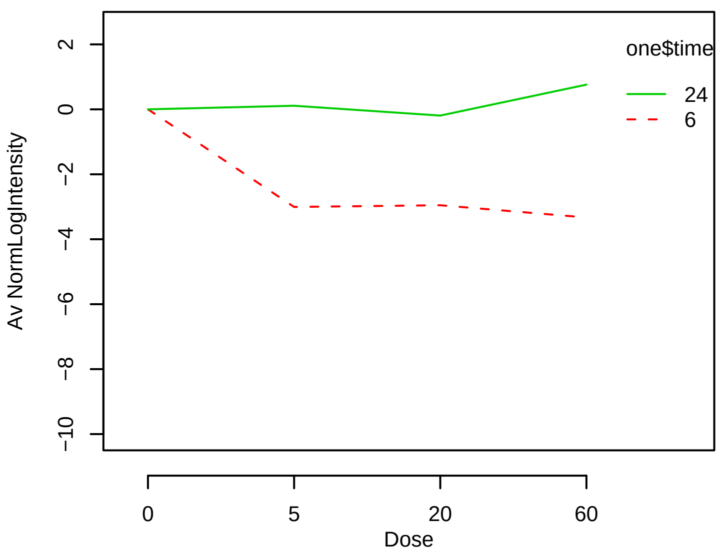


GO_0006800 : oxygen and reactive oxygen species metaboli

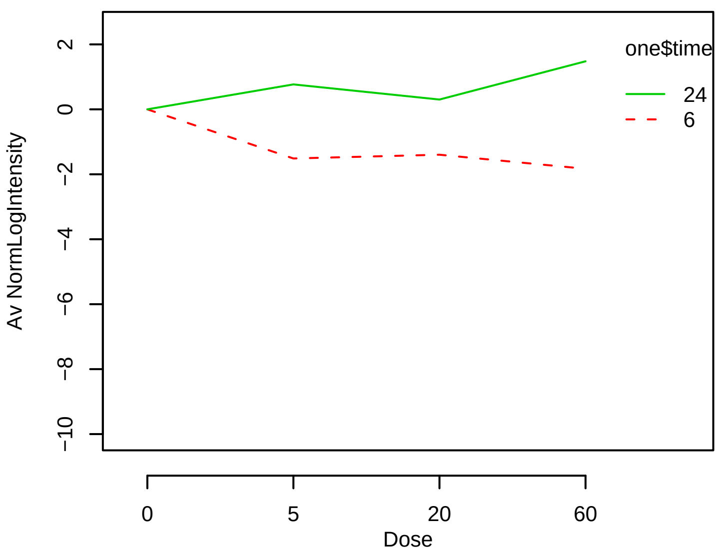


GO_0006801 : superoxide metabolism

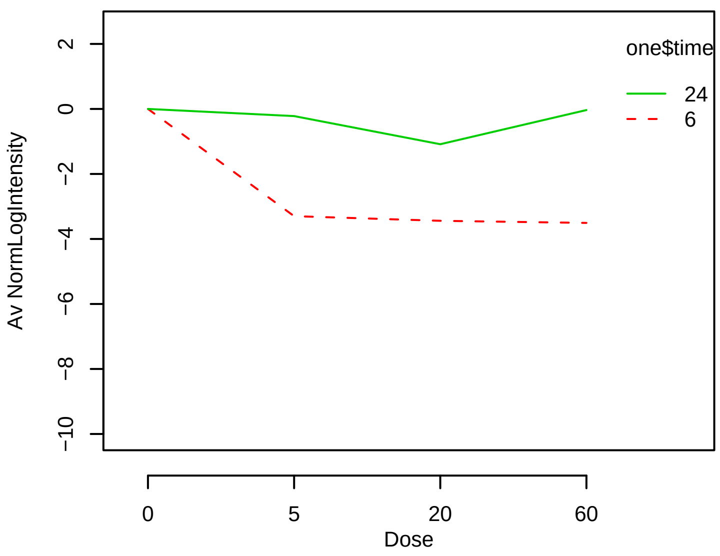




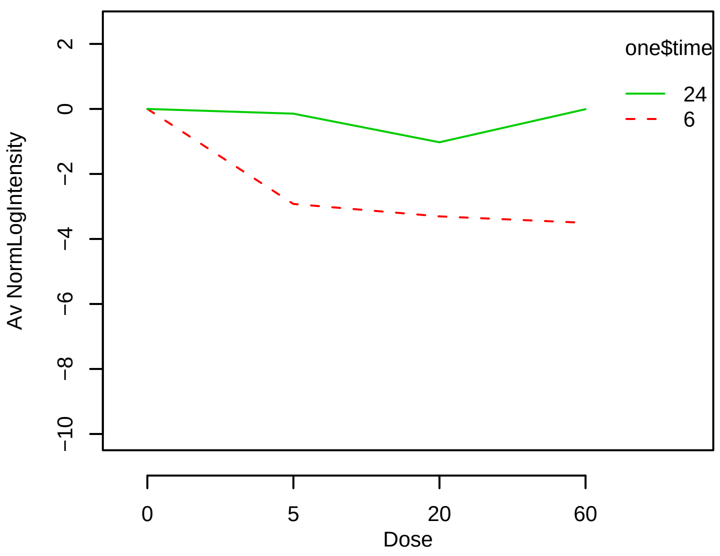
GO_0006805 : xenobiotic metabolism



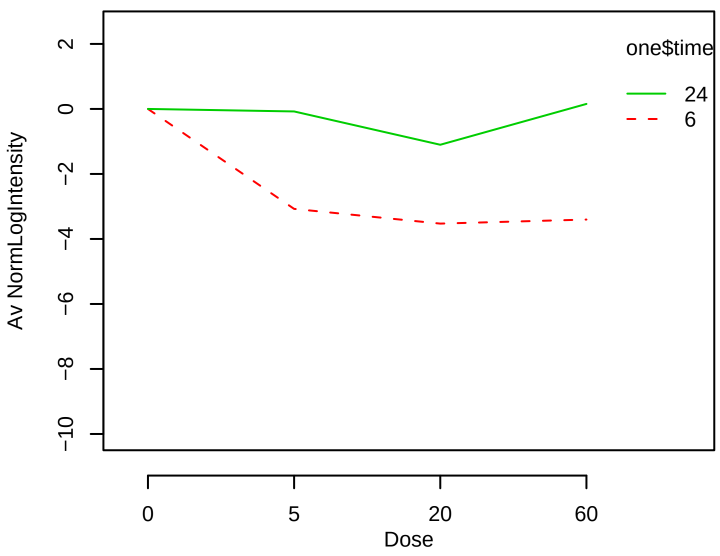
GO_0006809 : nitric oxide biosynthesis



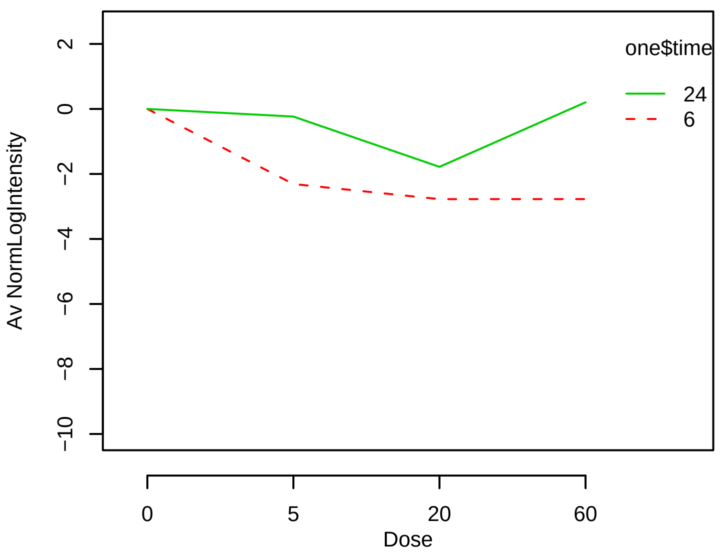
GO_0006813 : potassium ion transport



GO_0006814 : sodium ion transport

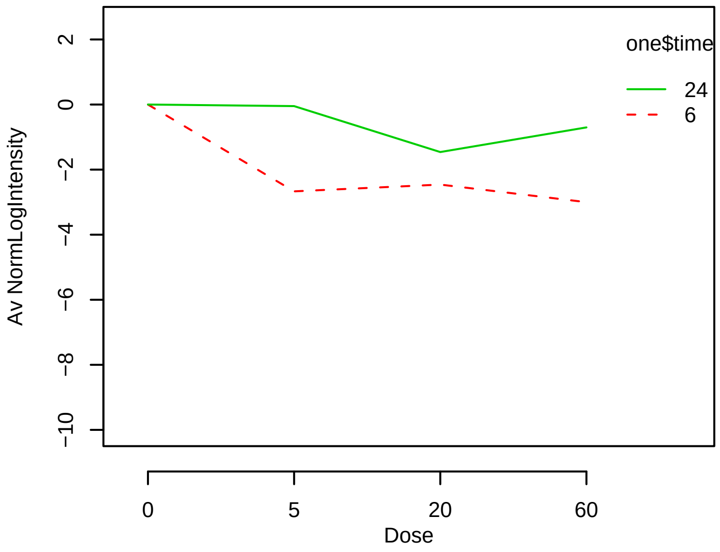


GO_0006816 : calcium ion transport

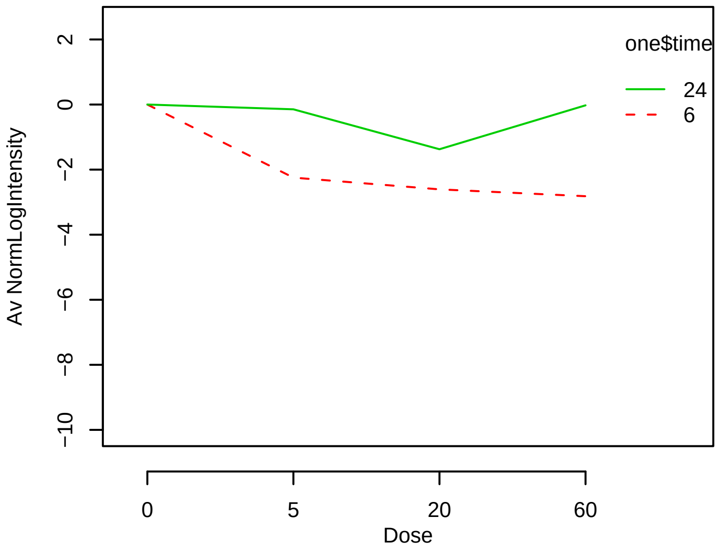


GO_0006817 : phosphate transport

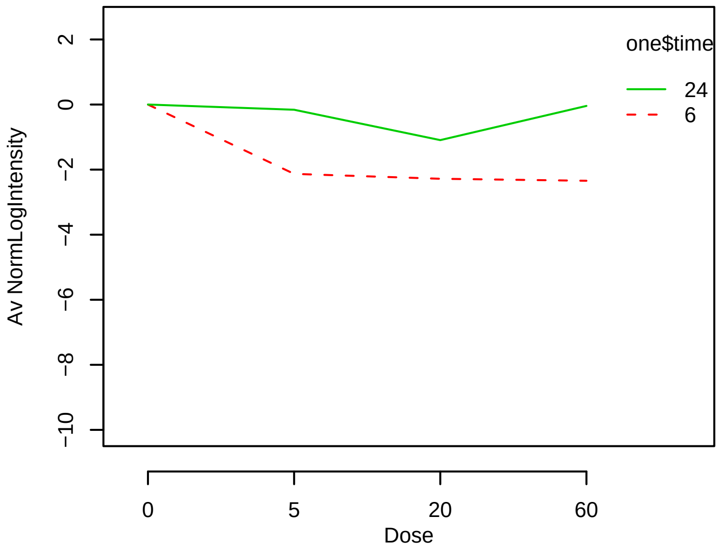
GO_0006818 : hydrogen transport



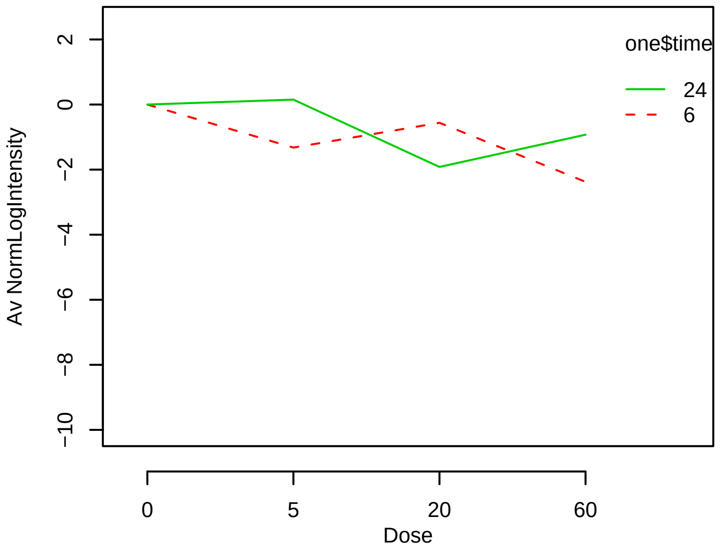
GO_0006820 : anion transport



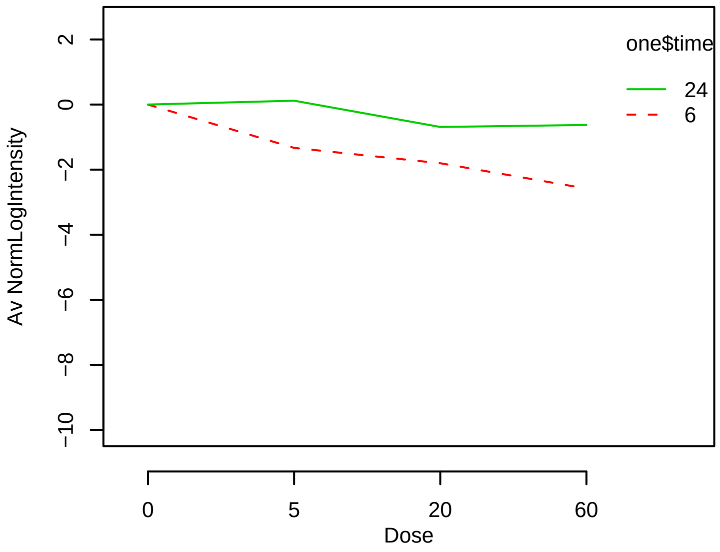
GO_0006821 : chloride transport



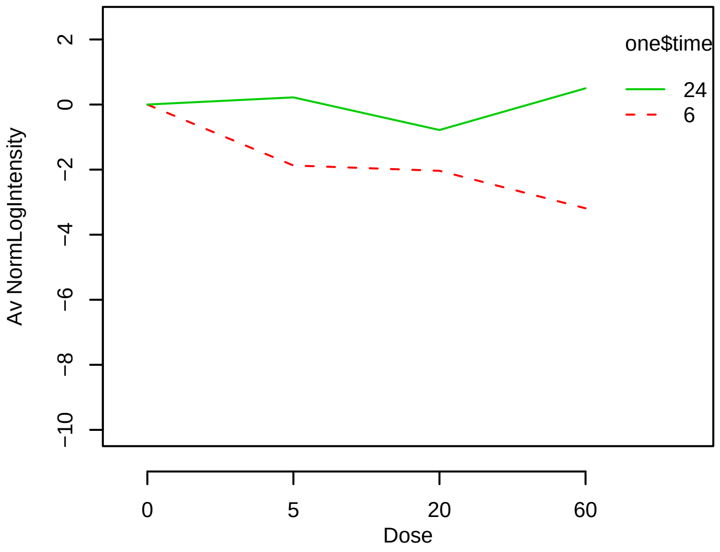
GO_0006825 : copper ion transport



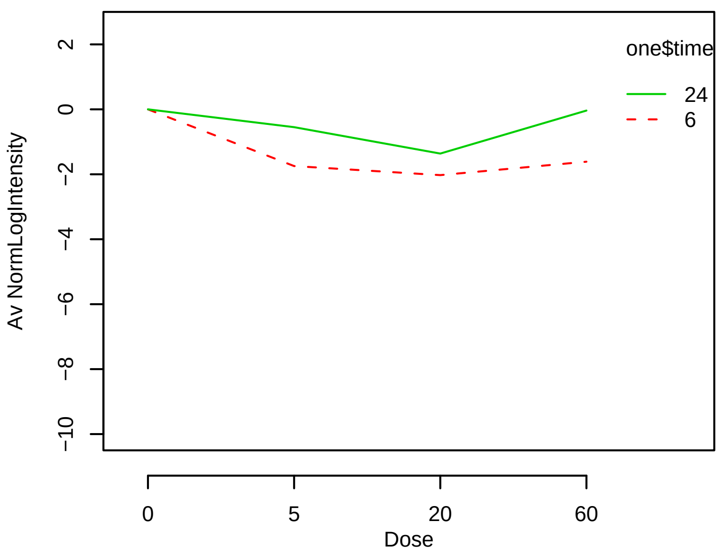
GO_0006826 : iron ion transport



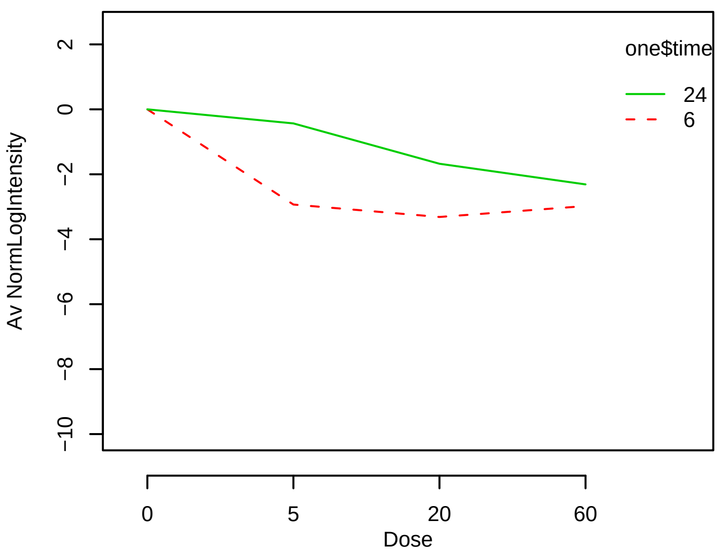
GO_0006829 : zinc ion transport



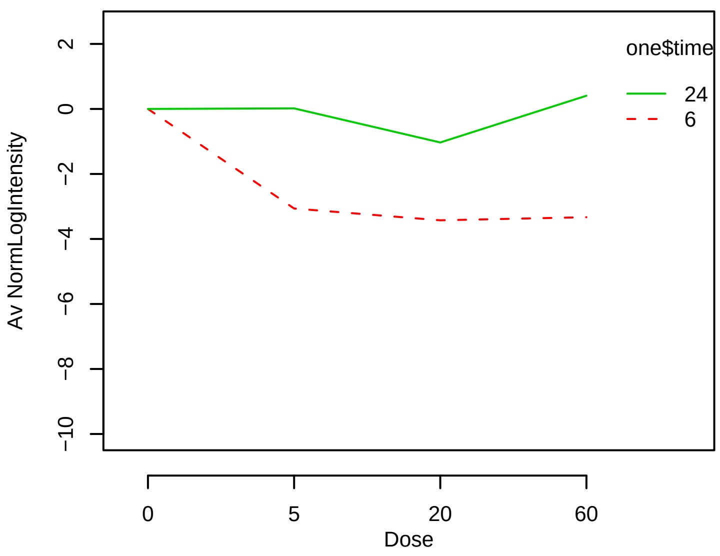
GO_0006833 : water transport



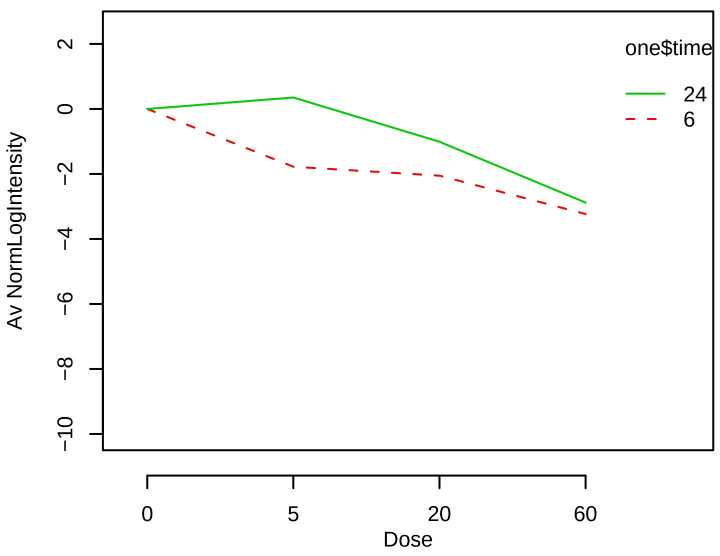
GO_0006835 : dicarboxylic acid transport



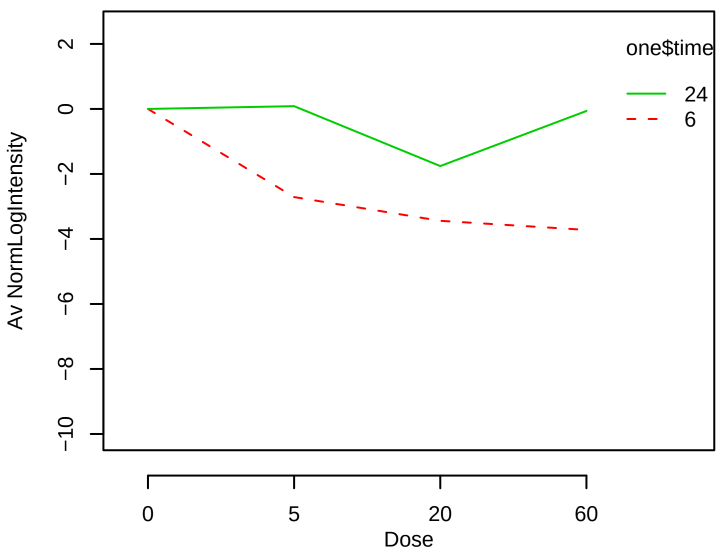
GO_0006836 : neurotransmitter transport



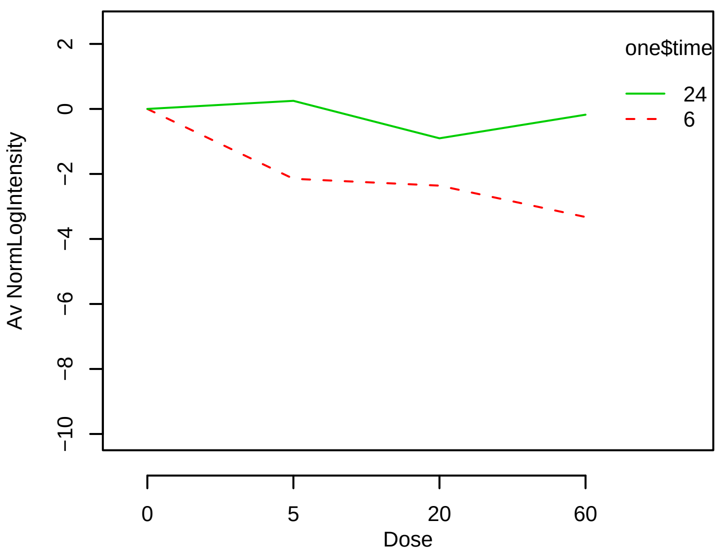
GO_0006839 : mitochondrial transport

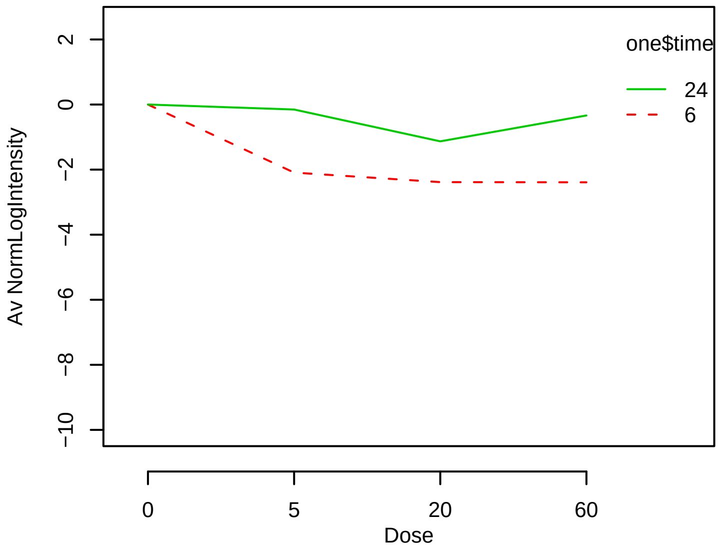


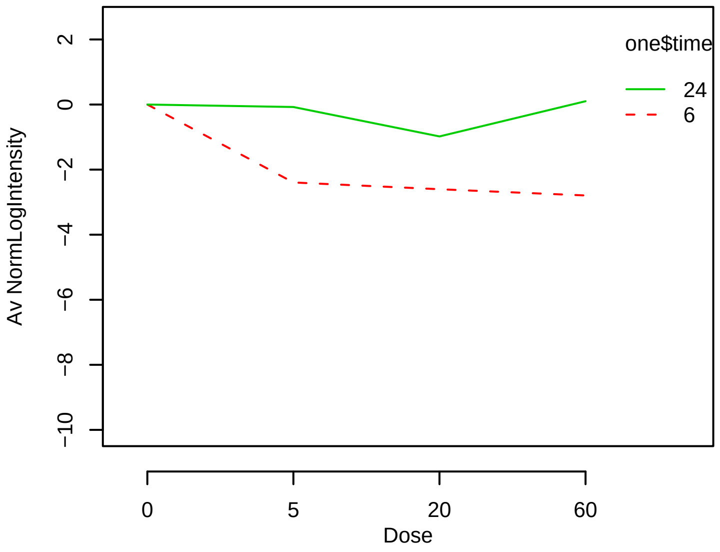
GO_0006857 : oligopeptide transport

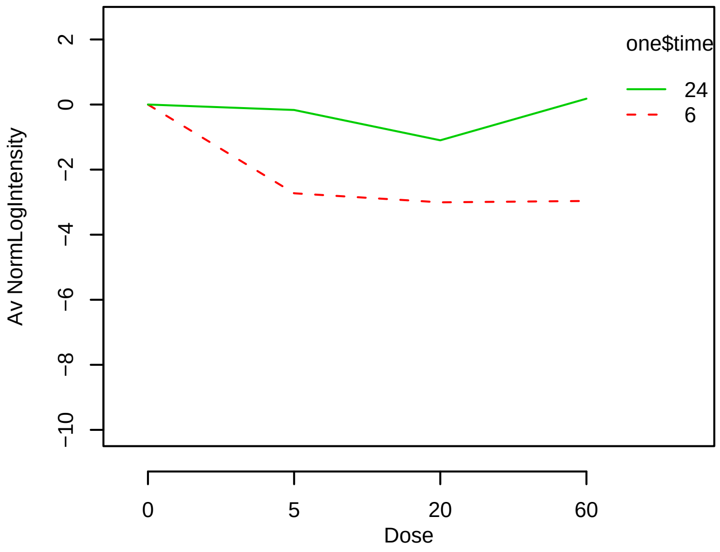


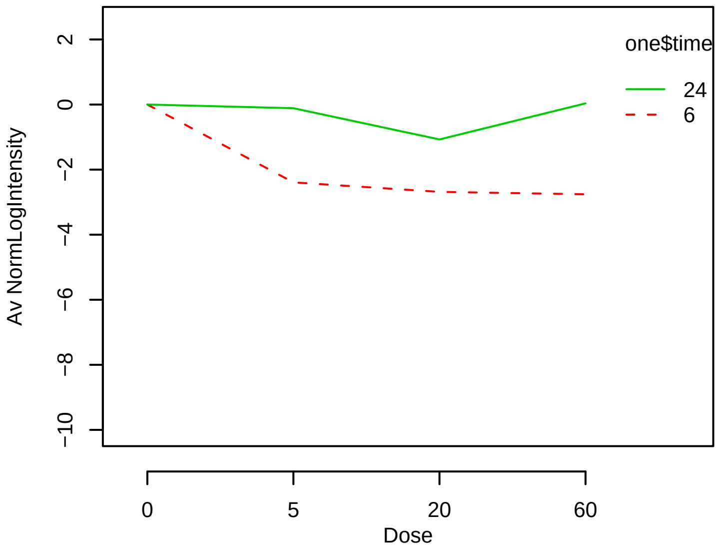
GO_0006865 : amino acid transport

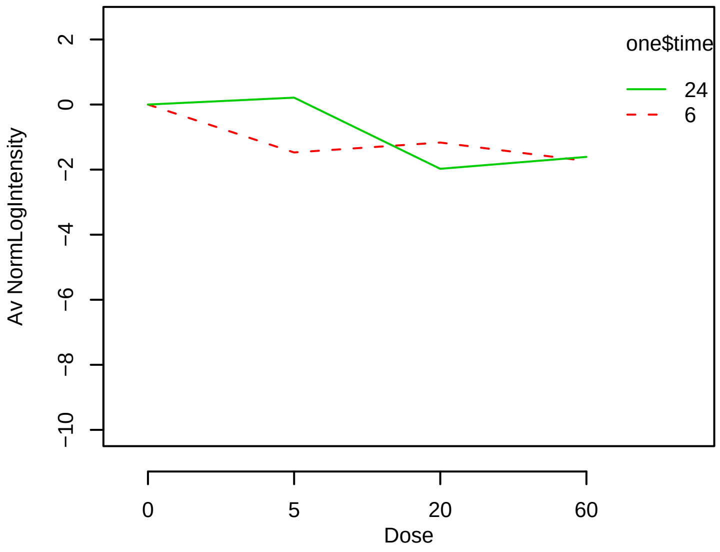


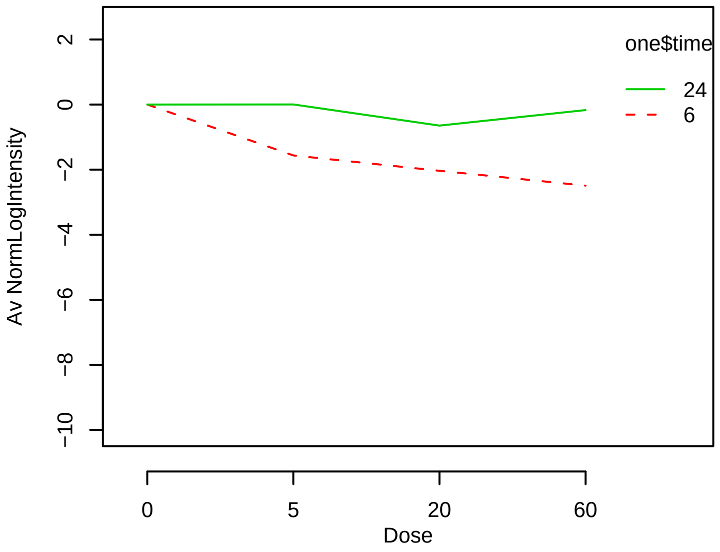

GO_0006869 : lipid transport

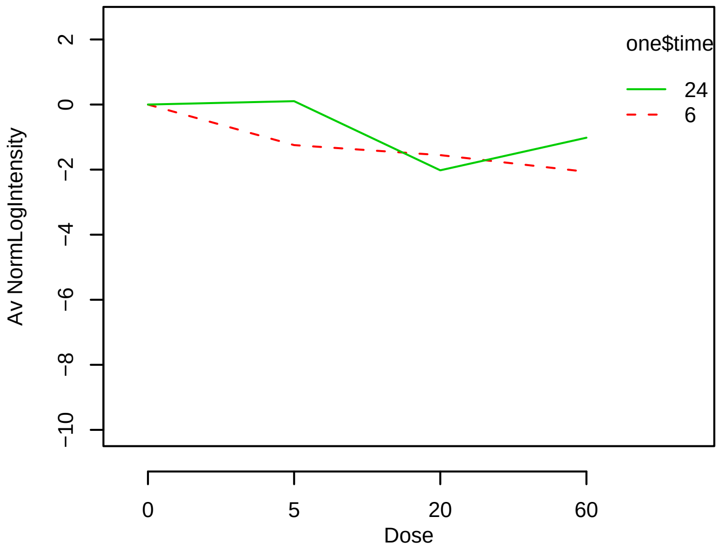

GO_0006873 : cell ion homeostasis

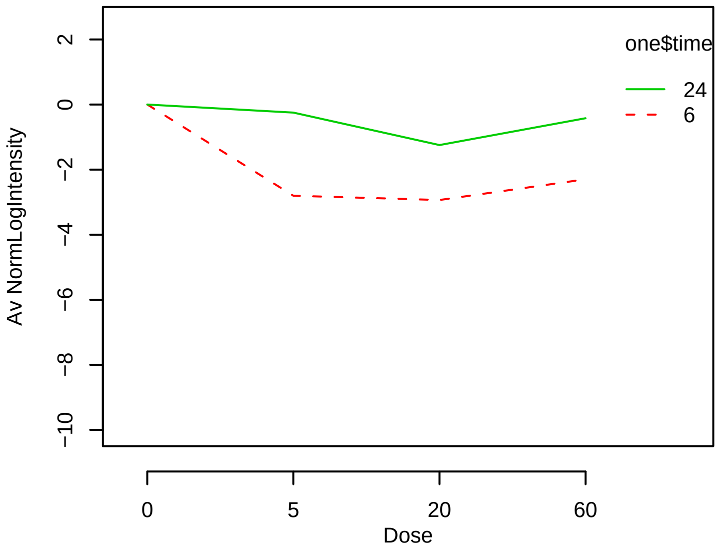

GO_0006874 : calcium ion homeostasis

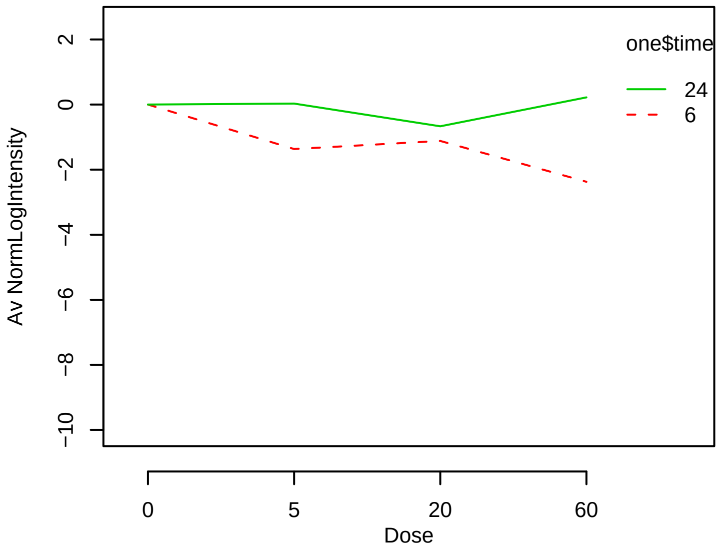

GO_0006875 : metal ion homeostasis

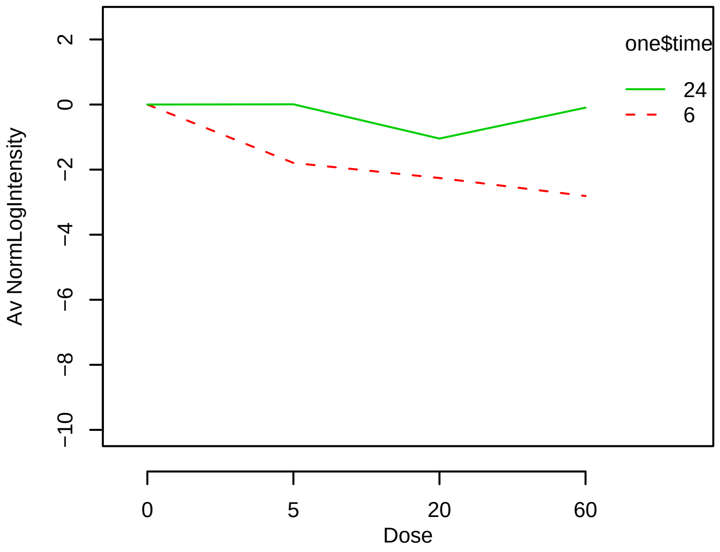

GO_0006878 : copper ion homeostasis

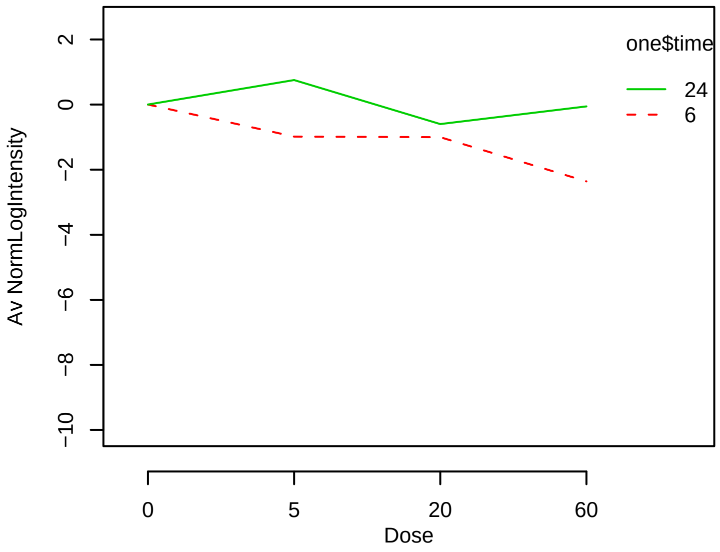

GO_0006879 : iron ion homeostasis

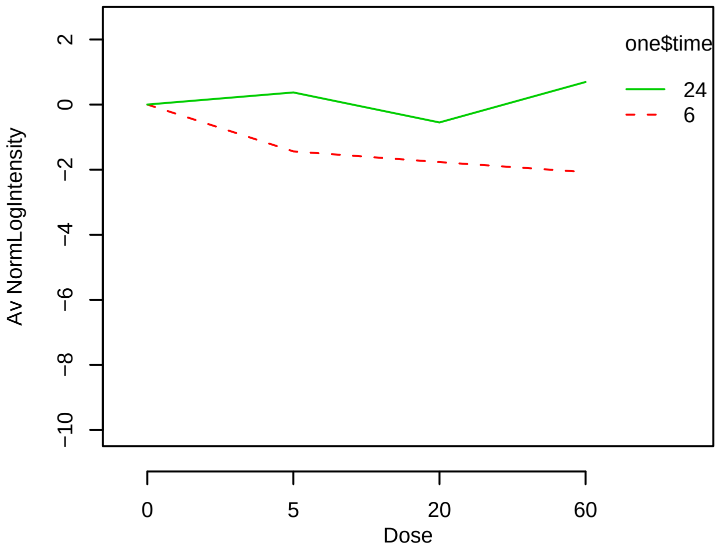

GO_0006882 : zinc ion homeostasis


GO_0006884 : regulation of cell volume

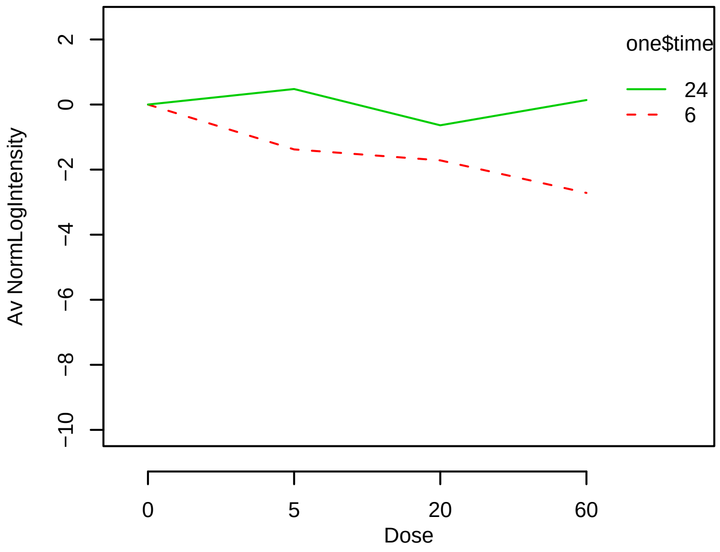

GO_0006885 : regulation of pH


GO_0006887 : exocytosis

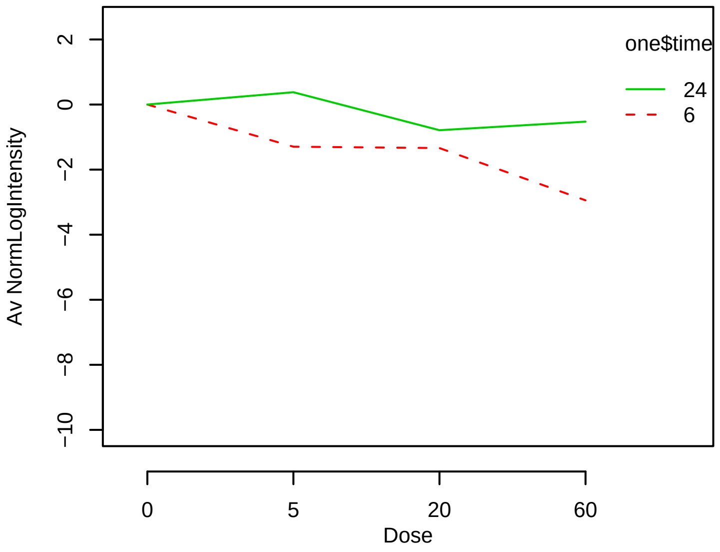

GO_0006888 : ER to Golgi vesicle−mediated transport


GO_0006890 : retrograde vesicle−mediated transport\, Golgi

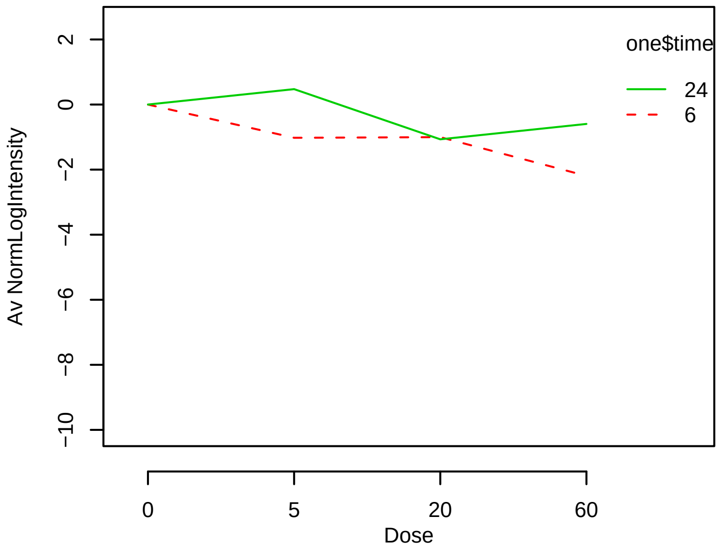
GO_0006891 : intra−Golgi vesicle−mediated transport



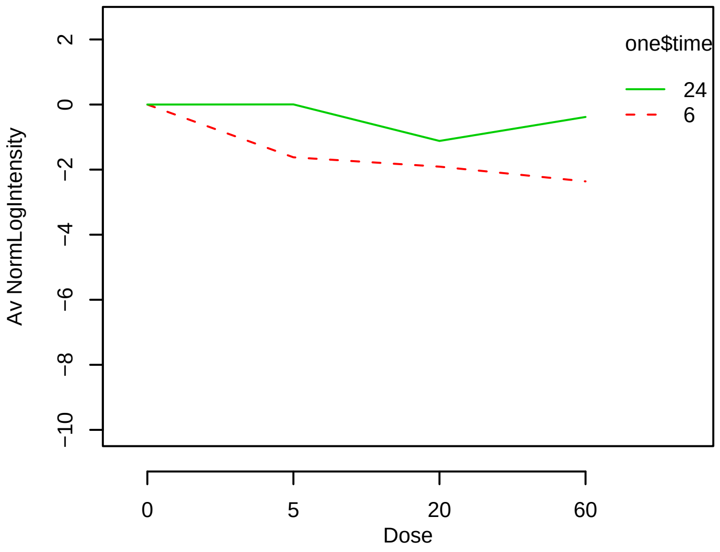
GO_0006892 : post−Golgi vesicle−mediated transport



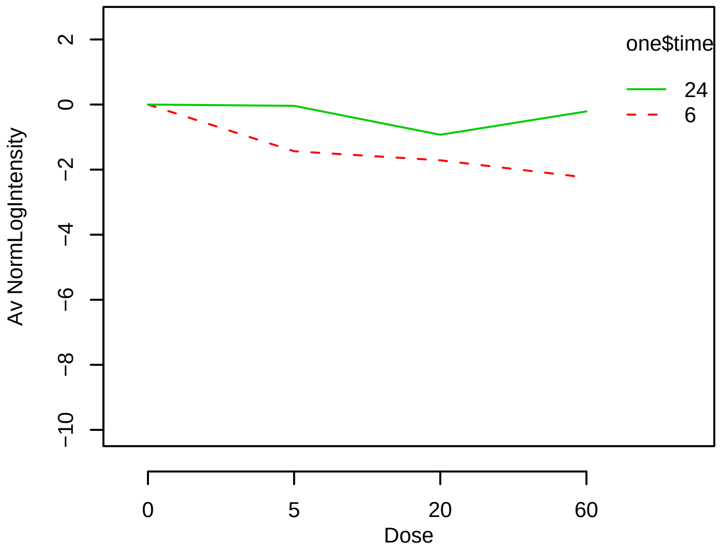
GO_0006895 : Golgi to endosome transport



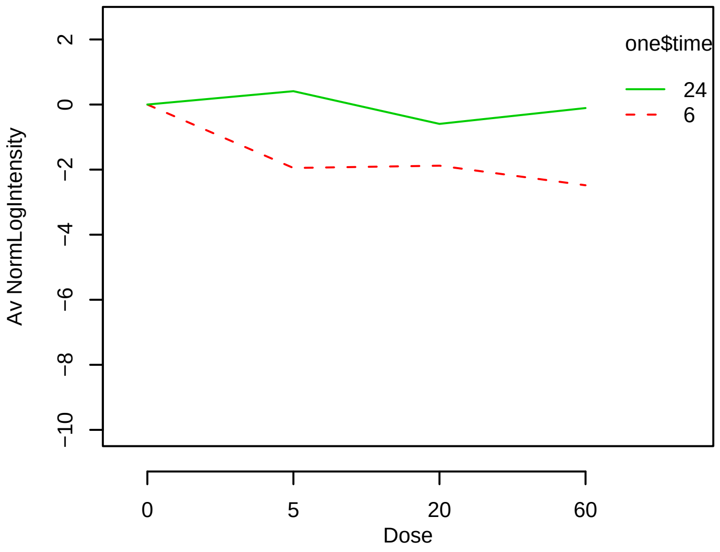
GO_0006897 : endocytosis

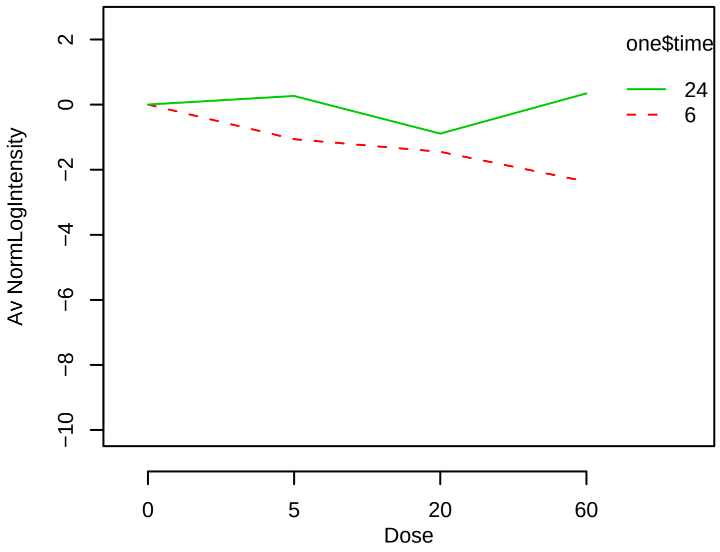


GO_0006898 : receptor−mediated endocytosis

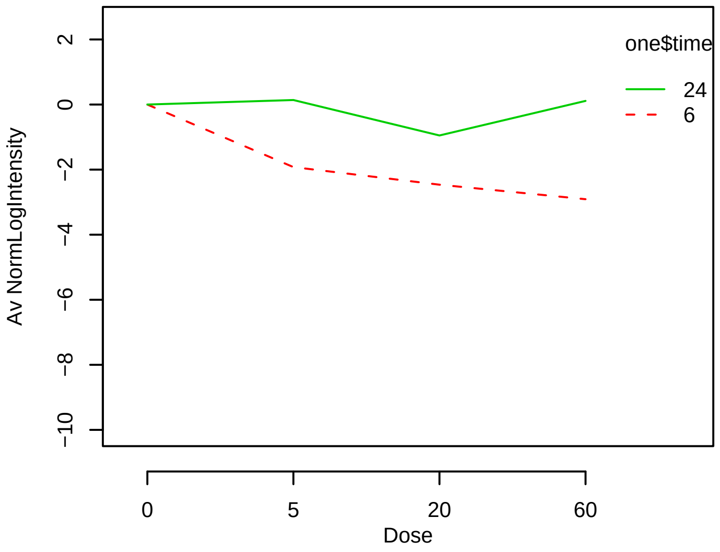


GO_0006903 : vesicle targeting

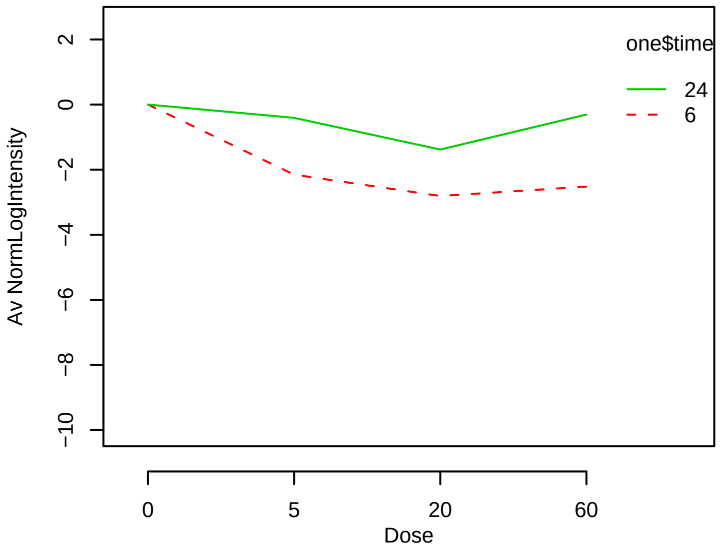




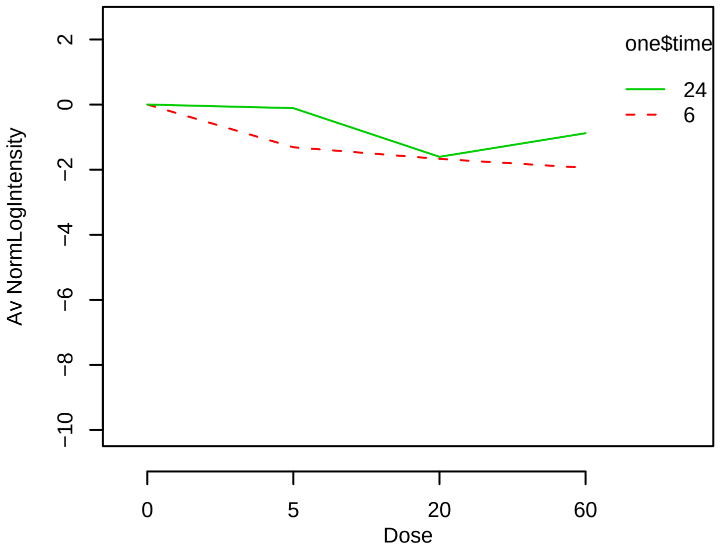
GO_0006904 : vesicle docking during exocytosis



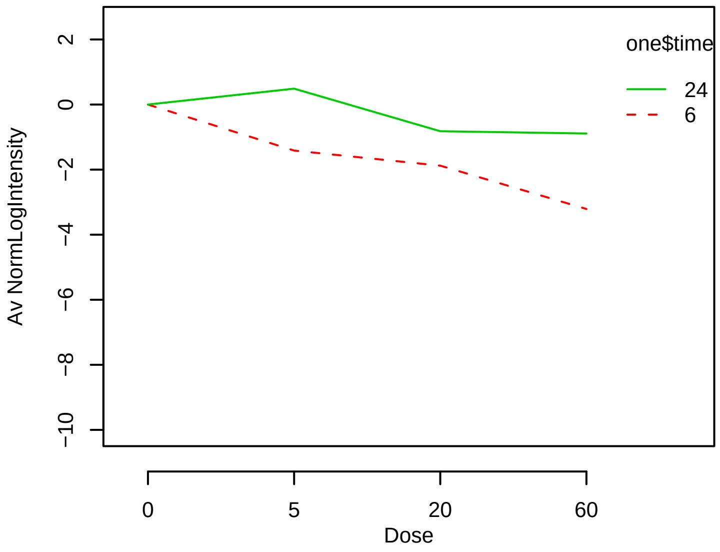
GO_0006906 : vesicle fusion



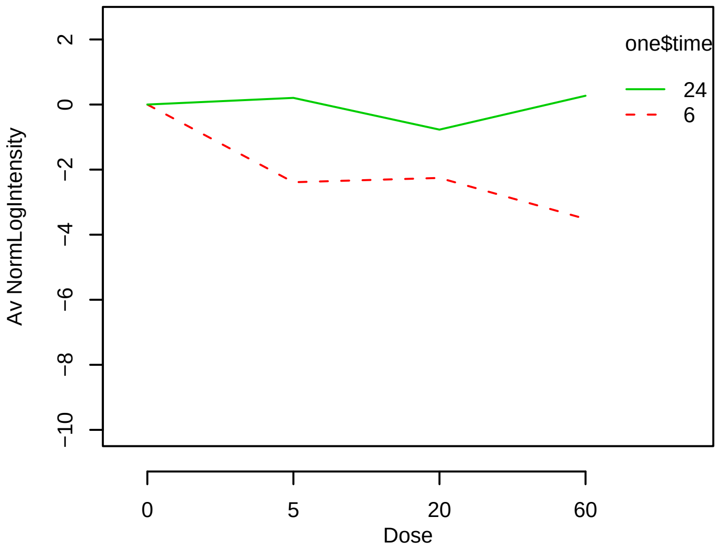
GO_0006909 : phagocytosis



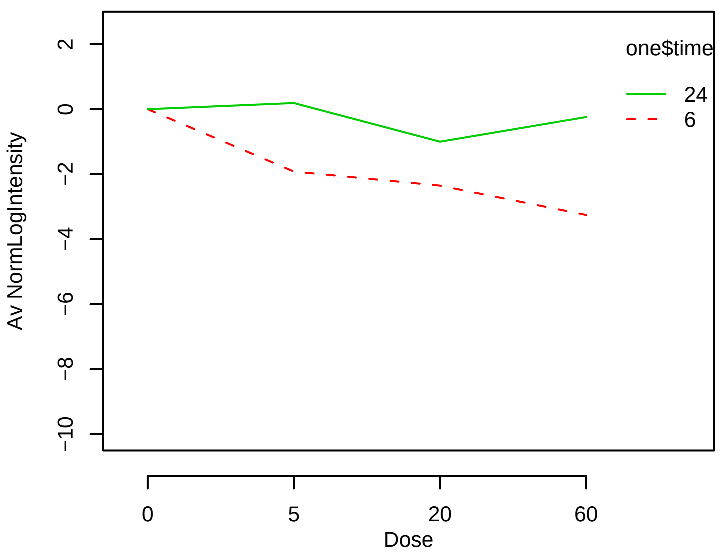
GO_0006911 : phagocytosis\, engulfment

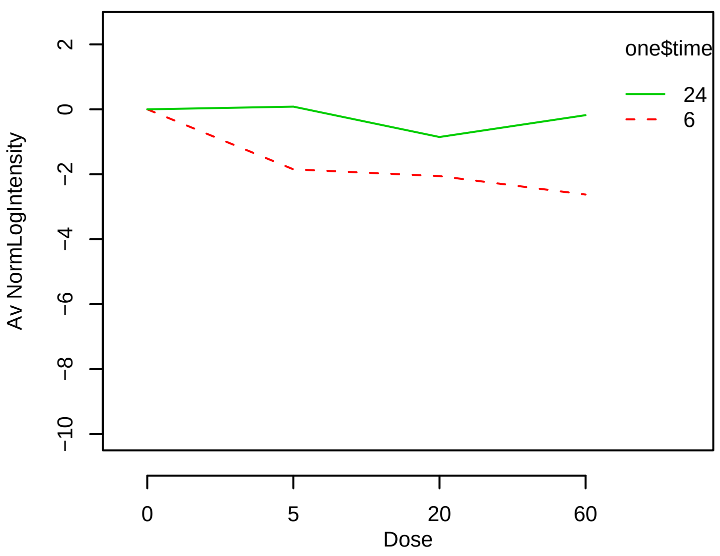


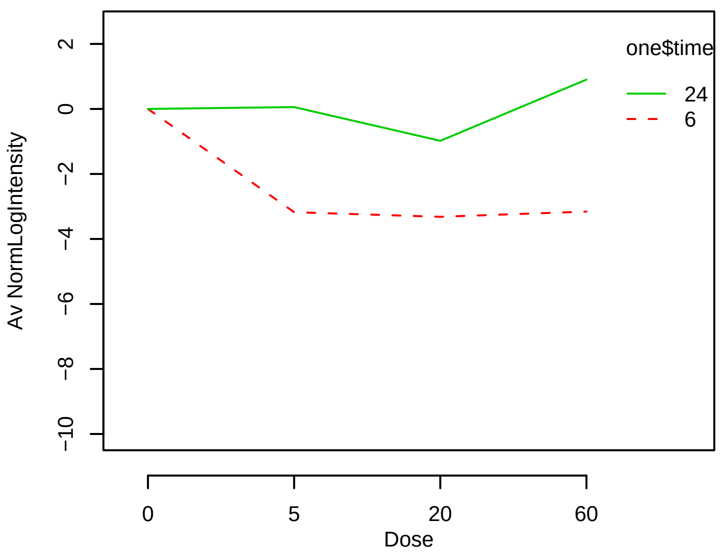
GO_0006913 : nucleocytoplasmic transport

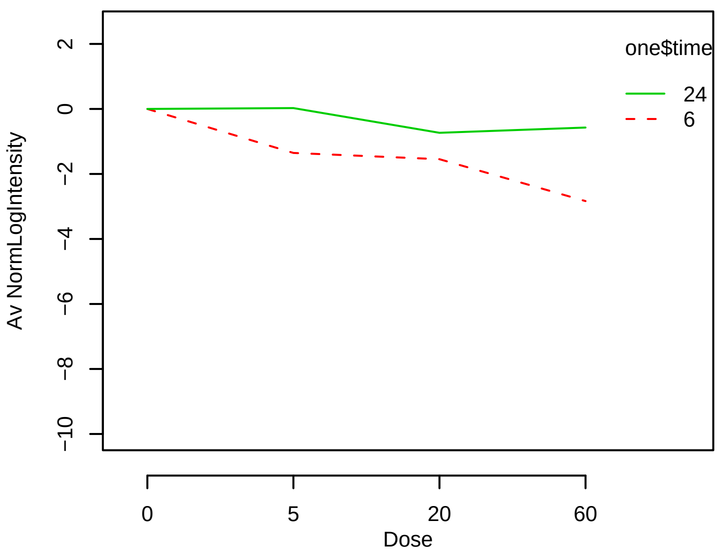


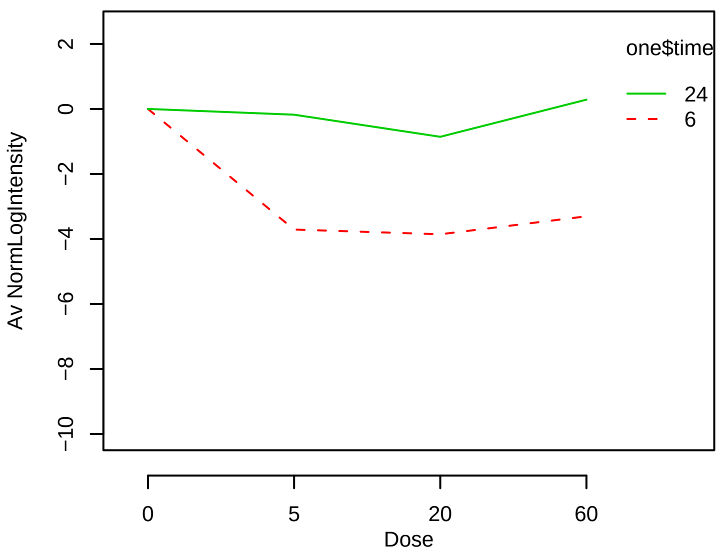
GO_0006914 : autophagy

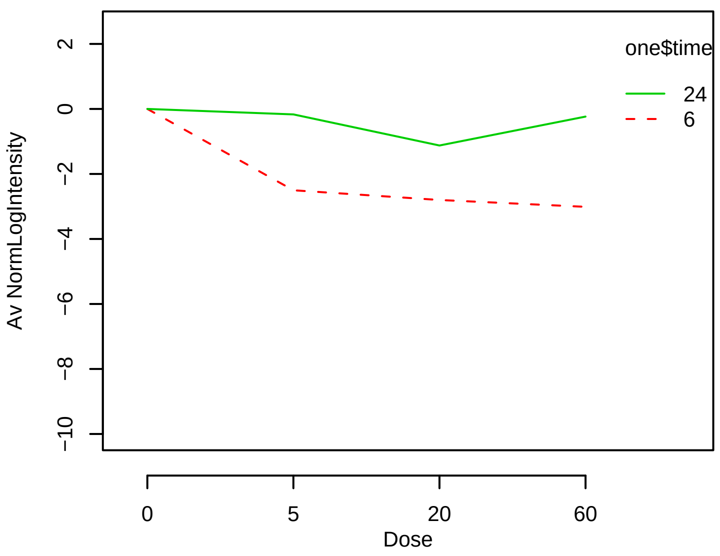

GO_0006916 : anti−apoptosis

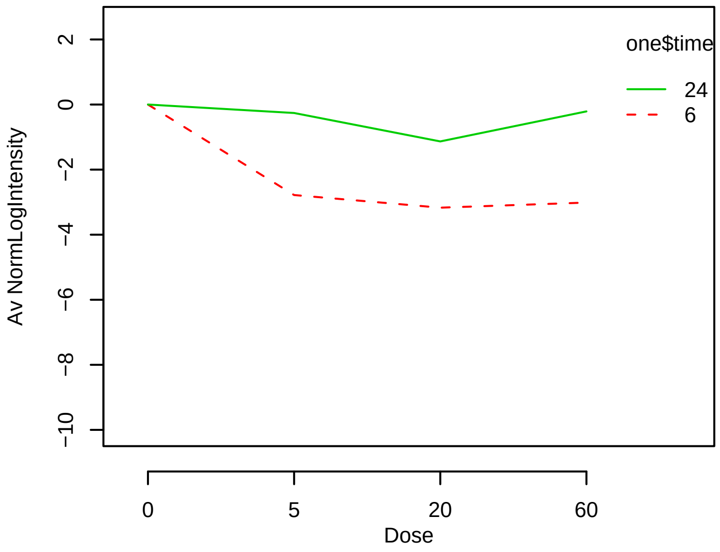

GO_0006917 : induction of apoptosis

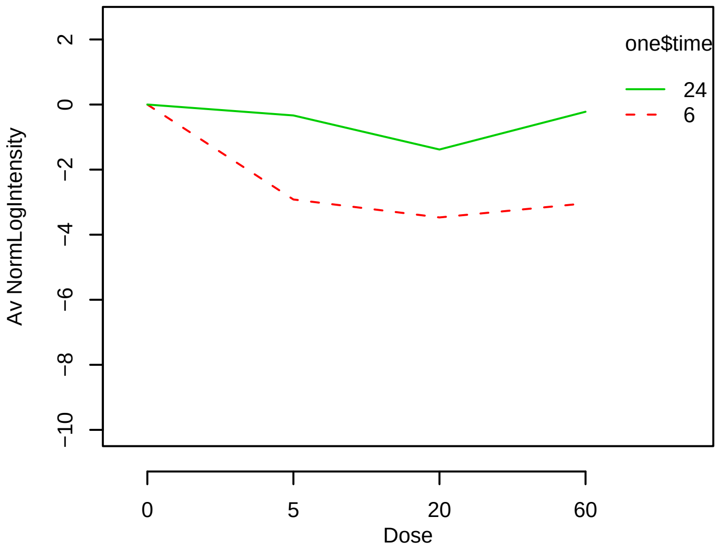

GO_0006919 : caspase activation

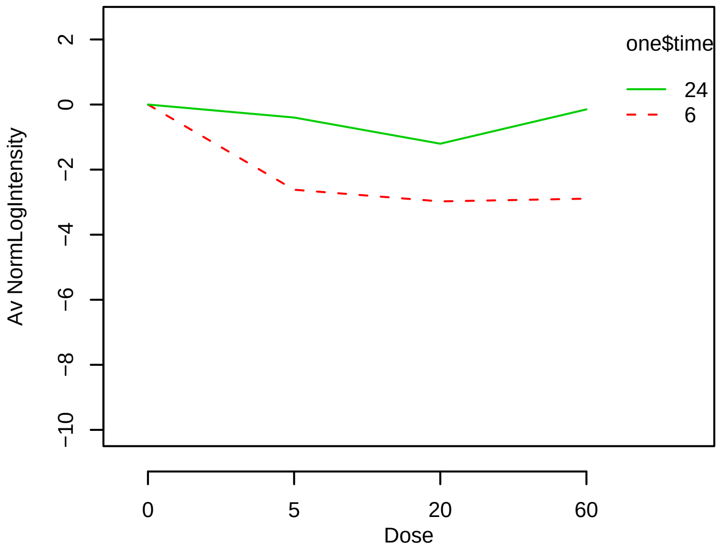

GO_0006921 : disassembly of cell structures during apopto

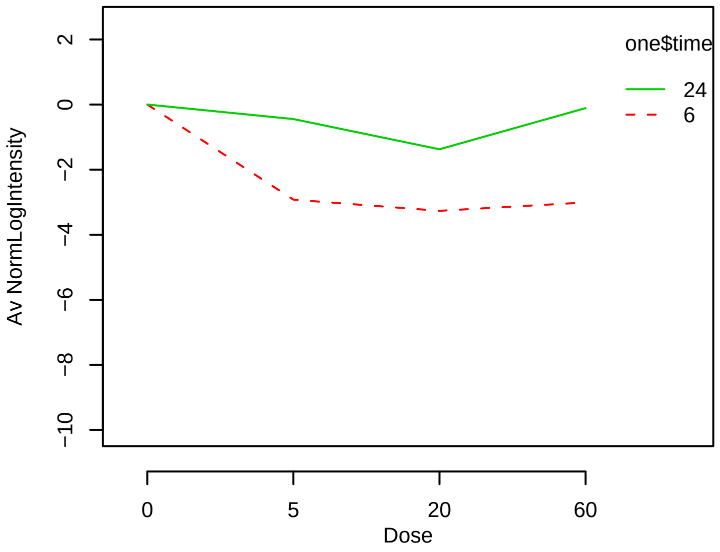

GO_0006929 : substrate−bound cell migration

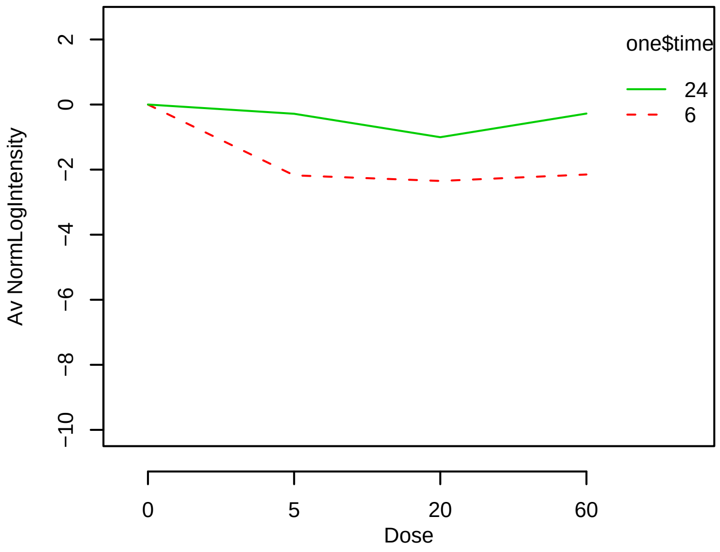

GO_0006935 : chemotaxis

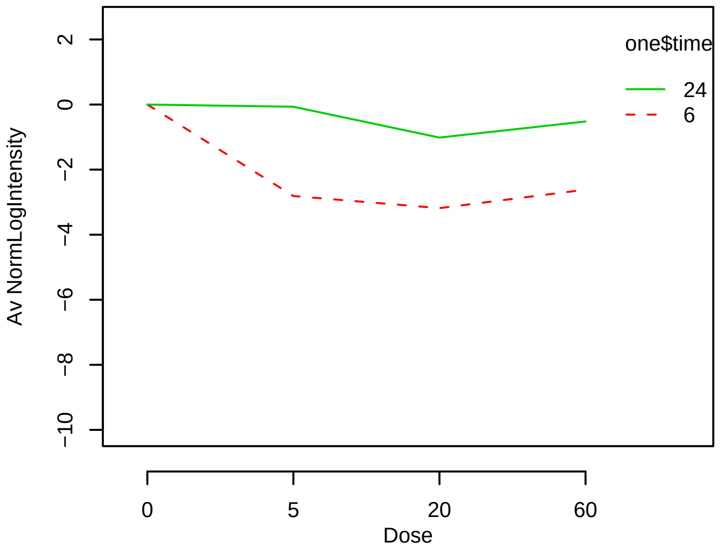

GO_0006936 : muscle contraction

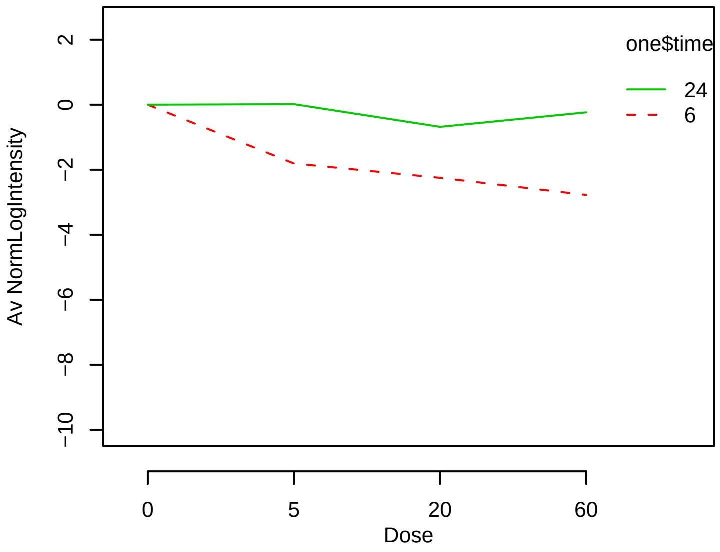

GO_0006937 : regulation of muscle contraction

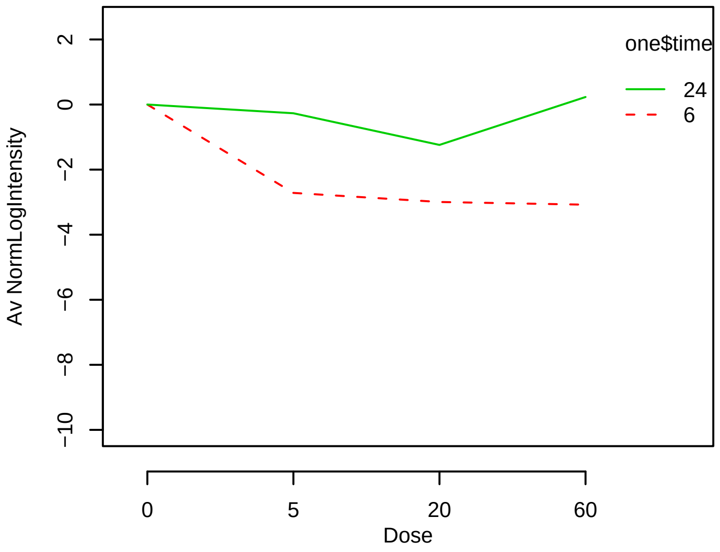

GO_0006939 : smooth muscle contraction

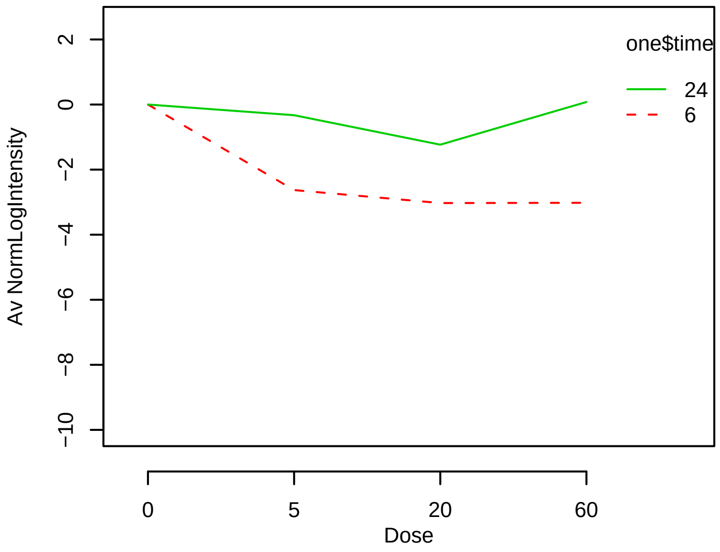

GO_0006940 : regulation of smooth muscle contraction

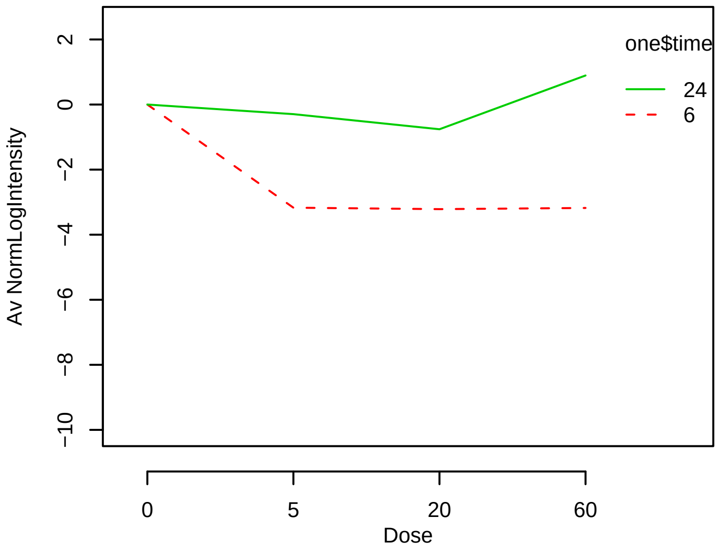

GO_0006941 : striated muscle contraction

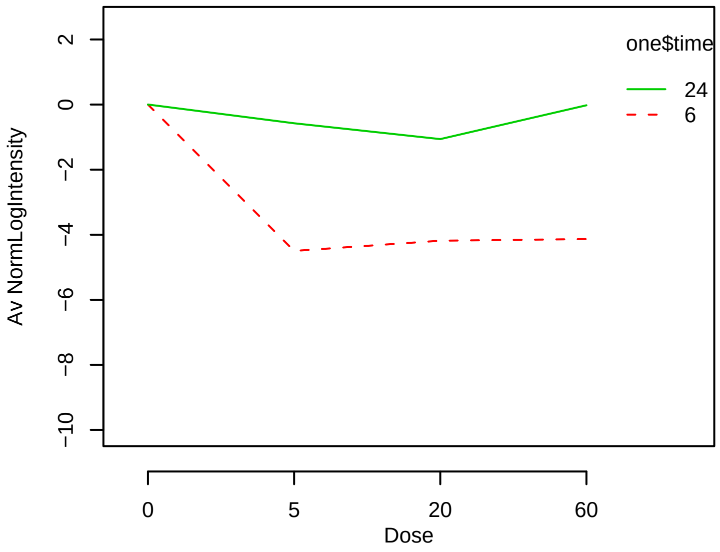

GO_0006942 : regulation of striated muscle contraction

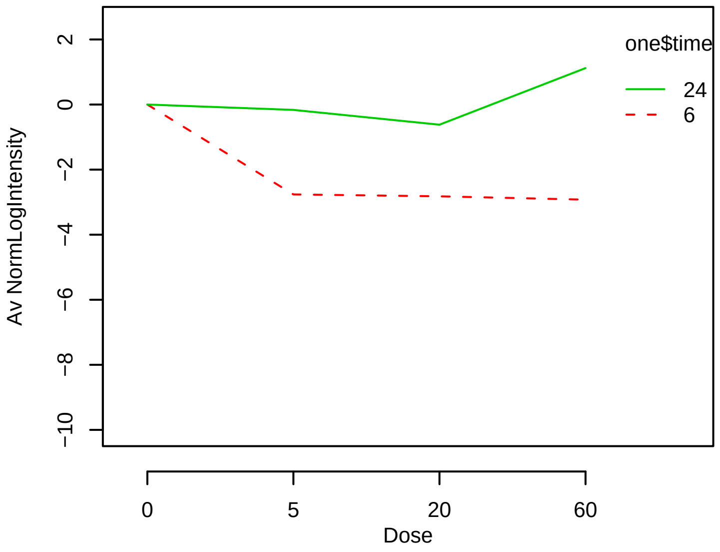

GO_0006944 : membrane fusion

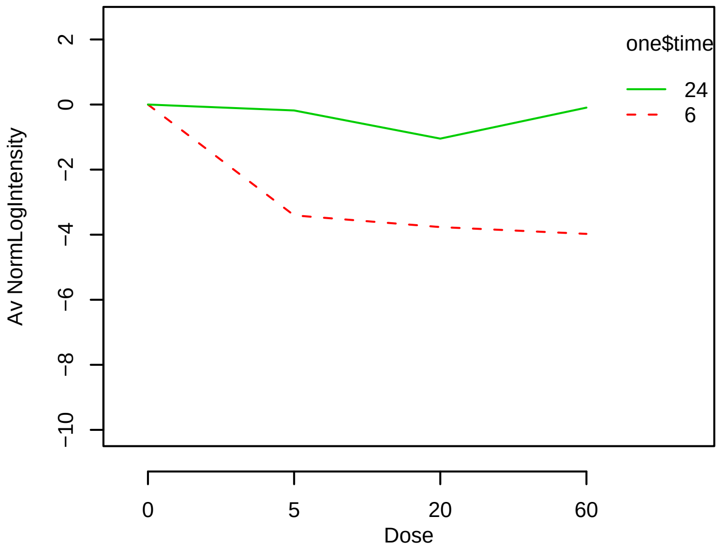

GO_0006953 : acute−phase response

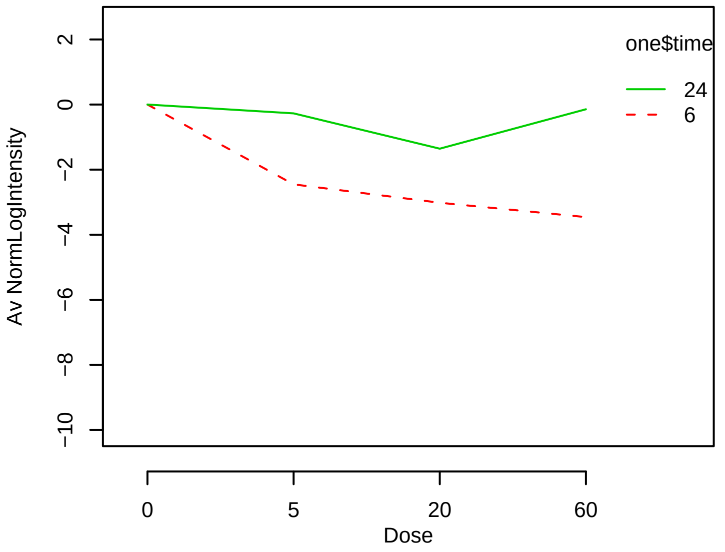

GO_0006954 : inflammatory response

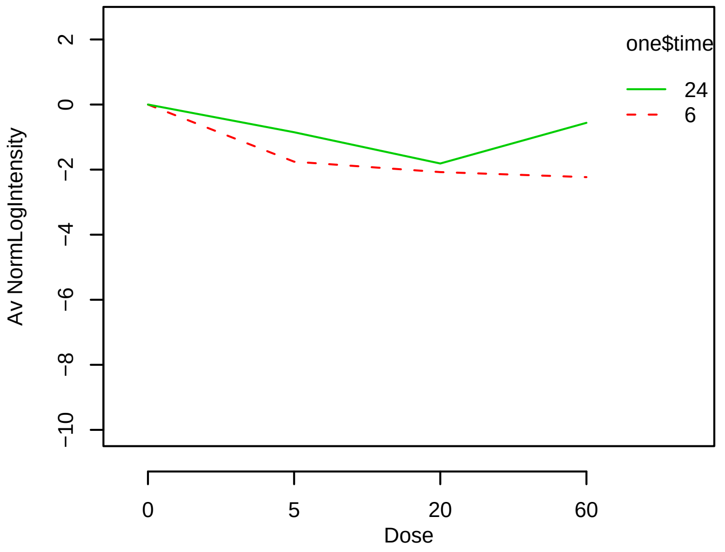

GO_0006956 : complement activation

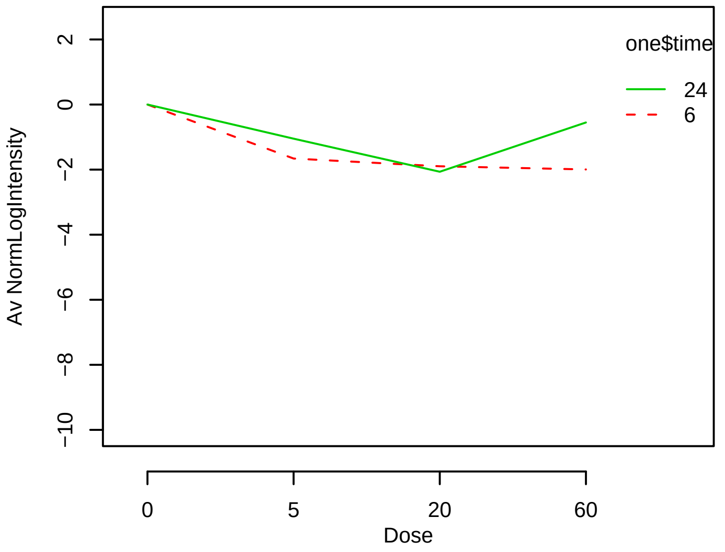

GO_0006957 : complement activation\, alternative pathwa

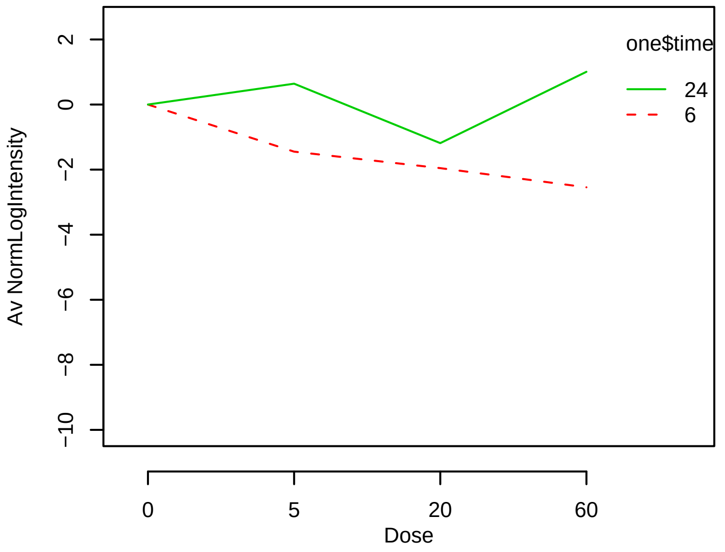

GO_0006958 : complement activation\, classical pathway

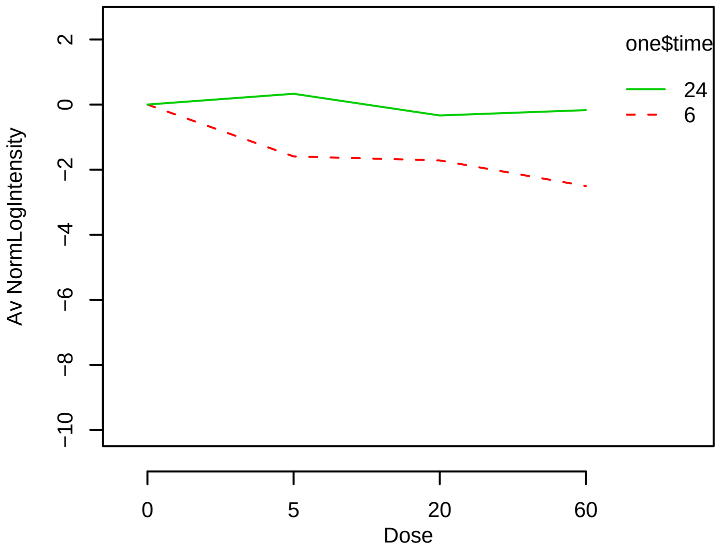

GO_0006959 : humoral immune response

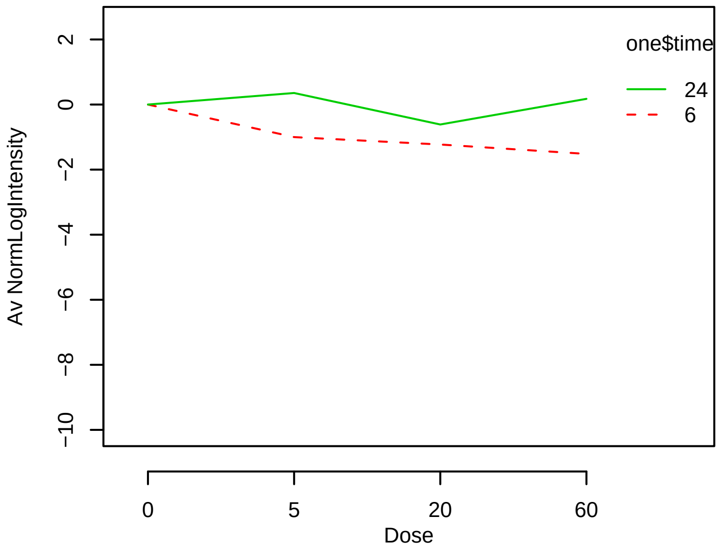

GO_0006968 : cellular defense response

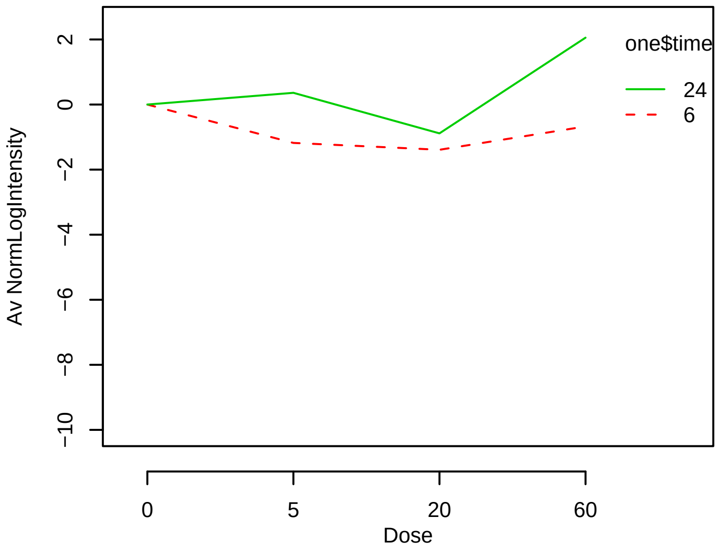

GO_0006970 : response to osmotic stress

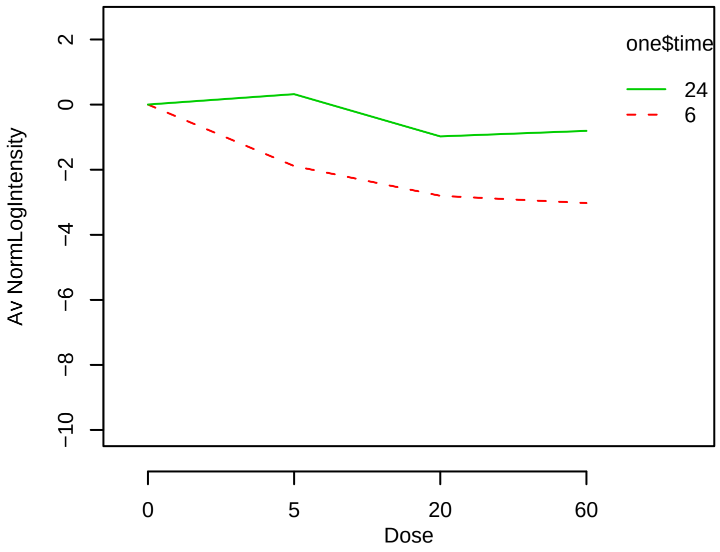

GO_0006972 : hyperosmotic response

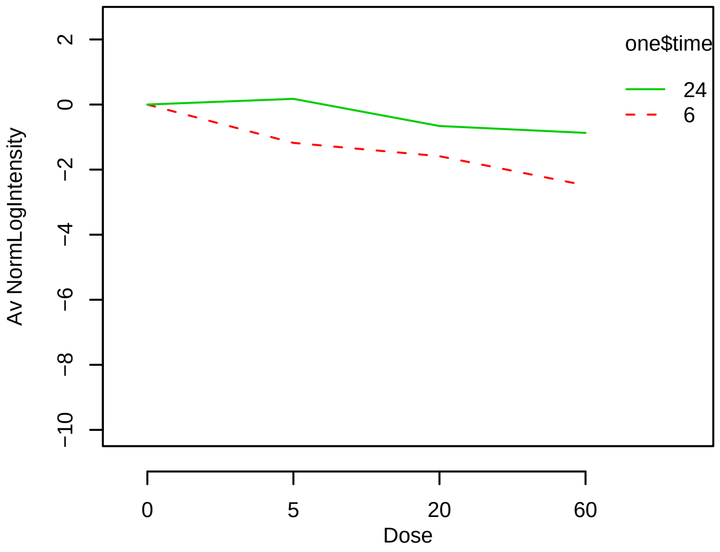

O_0006977 : DNA damage response\, signal transduction by

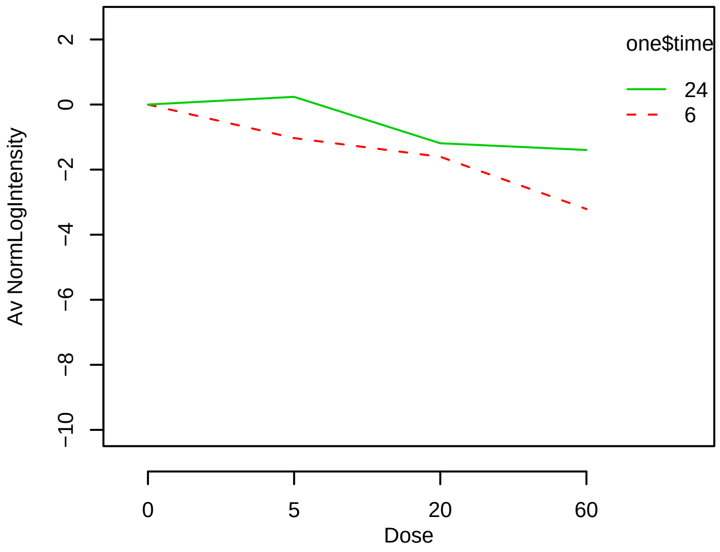

GO_0006979 : response to oxidative stress

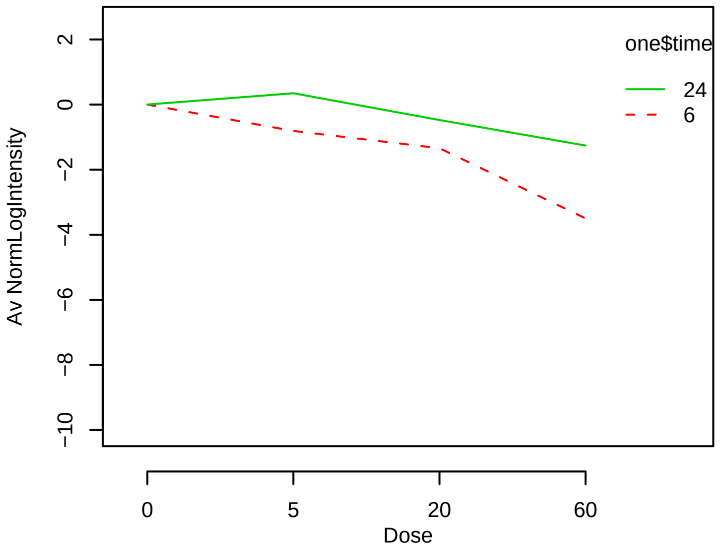

GO_0006984 : ER−nuclear signaling pathway


GO_0006986 : response to unfolded protein

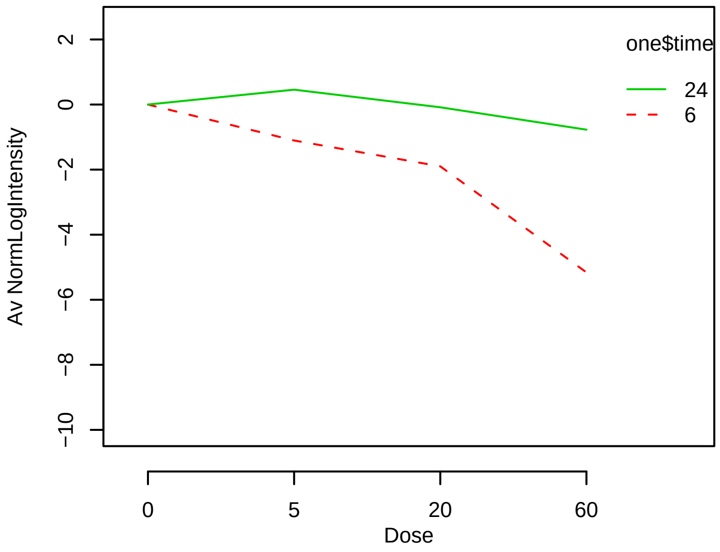

GO_0006997 : nuclear organization and biogenesis


GO_0007004 : telomere maintenance via telomerase

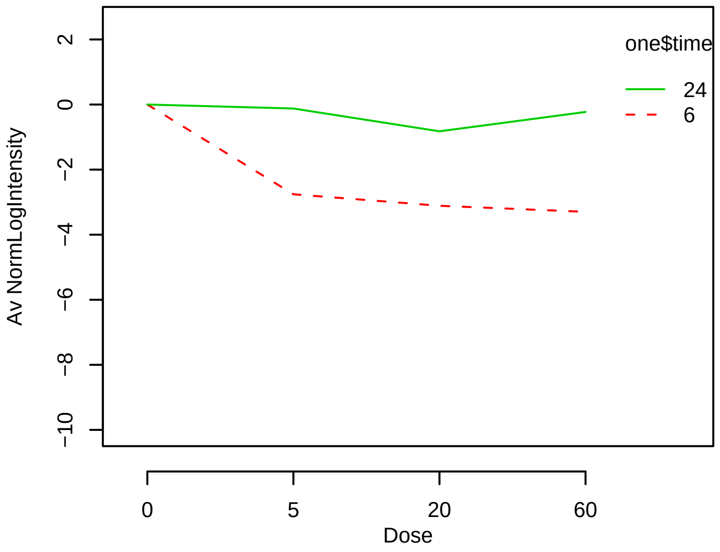

GO_0007005 : mitochondrion organization and biogenesi


O_0007006 : mitochondrial membrane organization and bioge

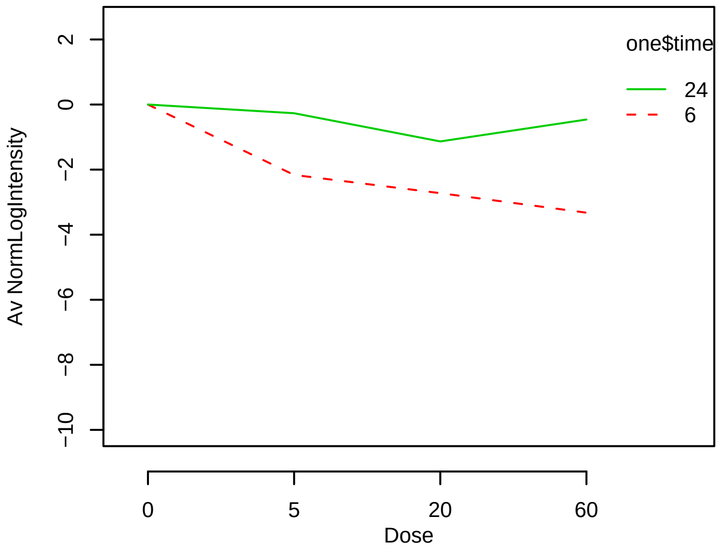
O_0007007 : inner mitochondrial membrane organization anc



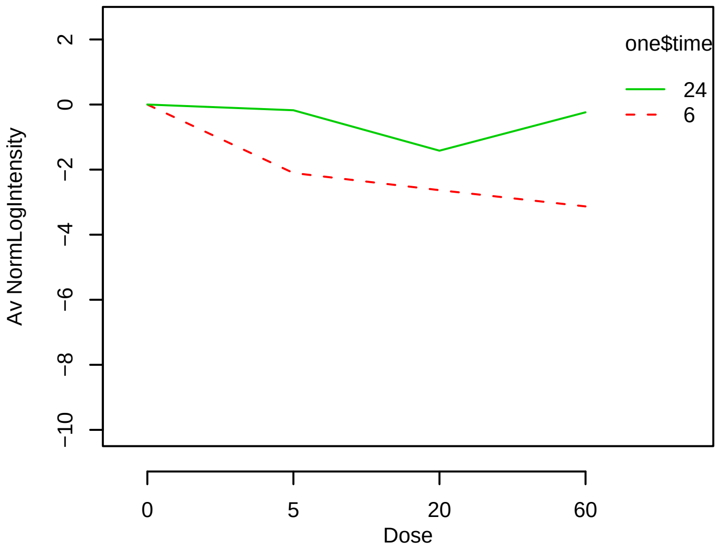
GO_0007009 : plasma membrane organization and biogene



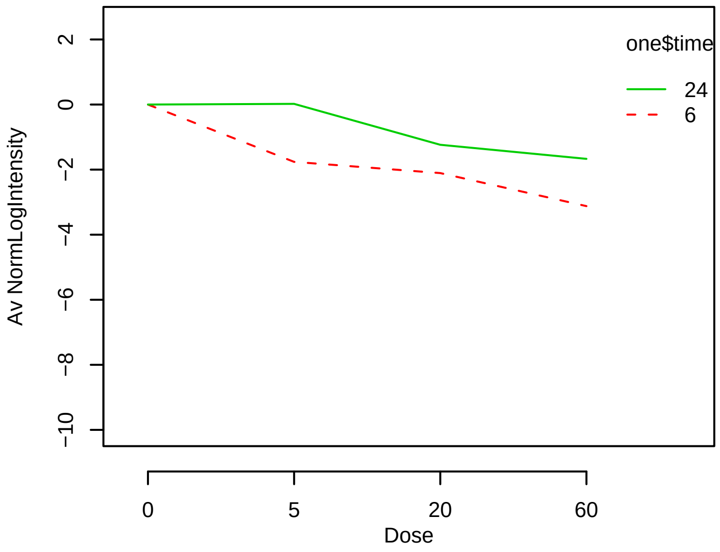
GO_0007015 : actin filament organization



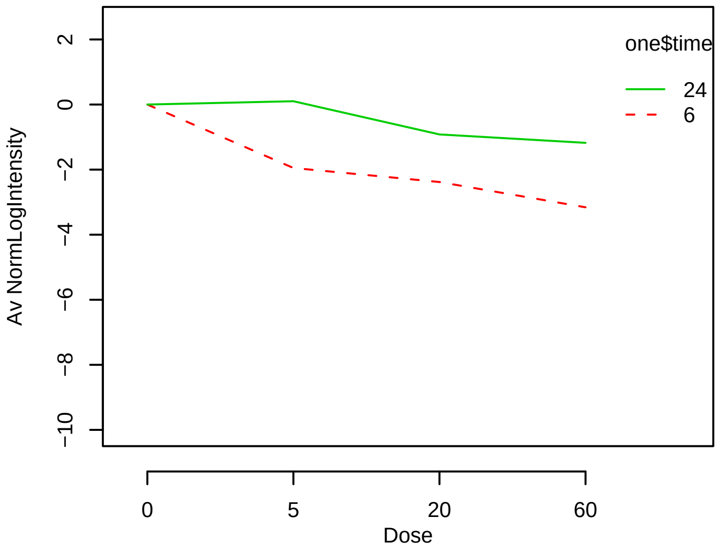
GO_0007016 : cytoskeletal anchoring

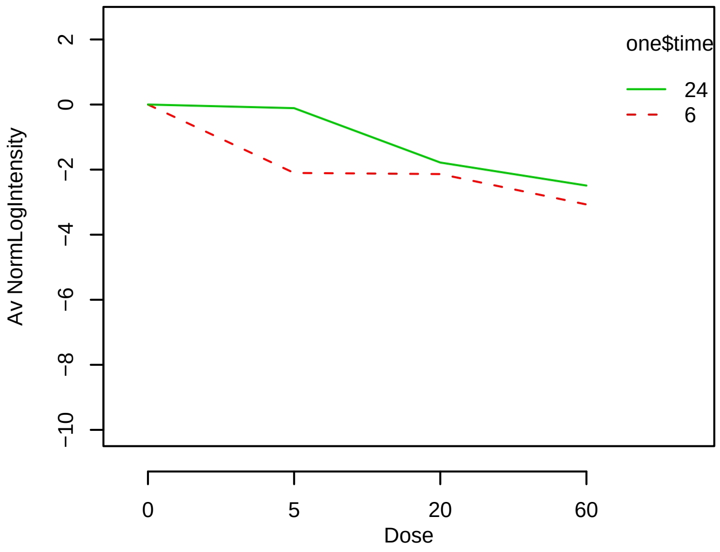


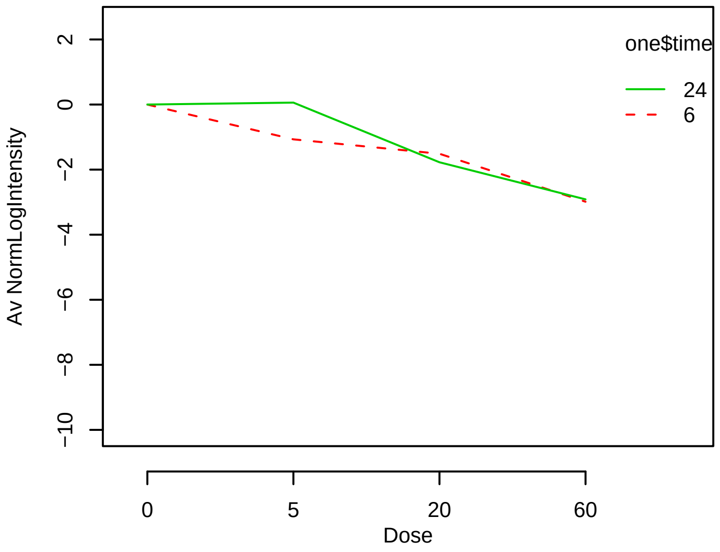
GO_0007017 : microtubule−based process

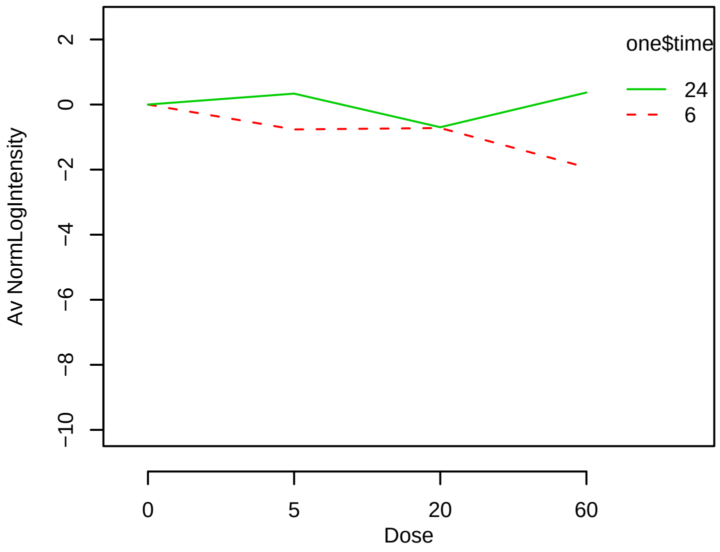


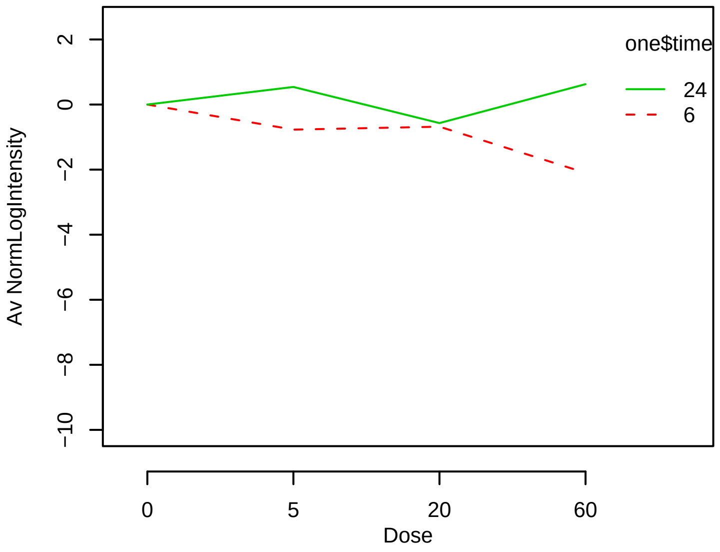
GO_0007018 : microtubule−based movement

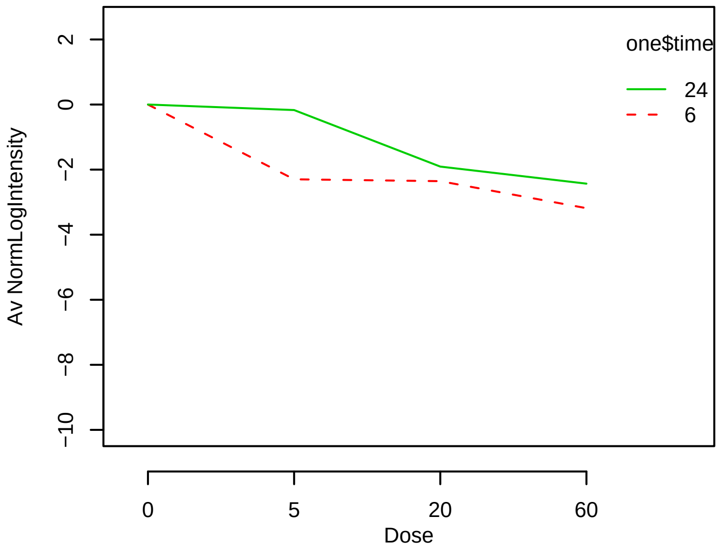


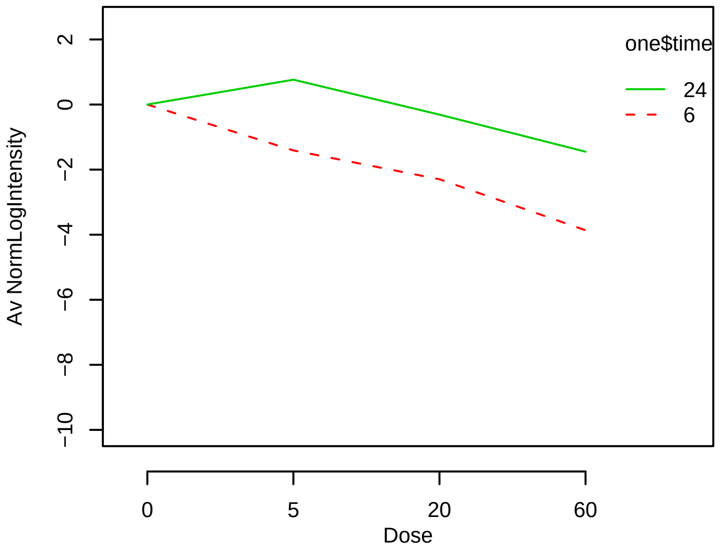

GO_0007019 : microtubule depolymerization

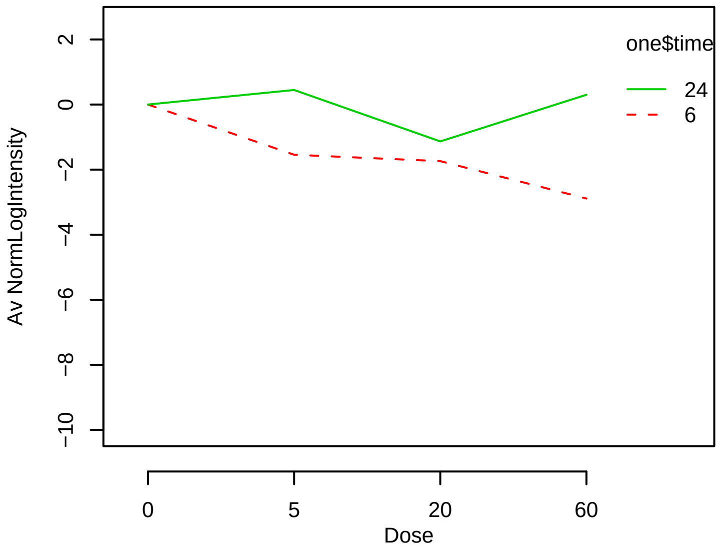

GO_0007020 : microtubule nucleation


GO_0007021 : tubulin folding

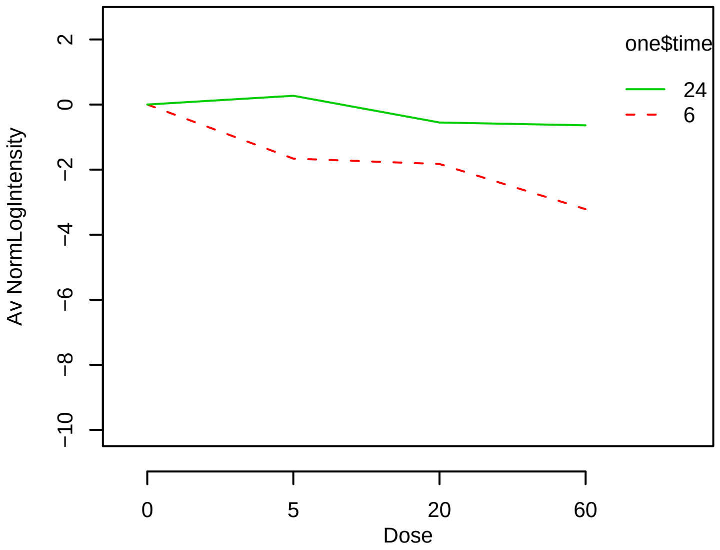

GO_0007025 : beta−tubulin folding


GO_0007026 : negative regulation of microtubule depolymeri

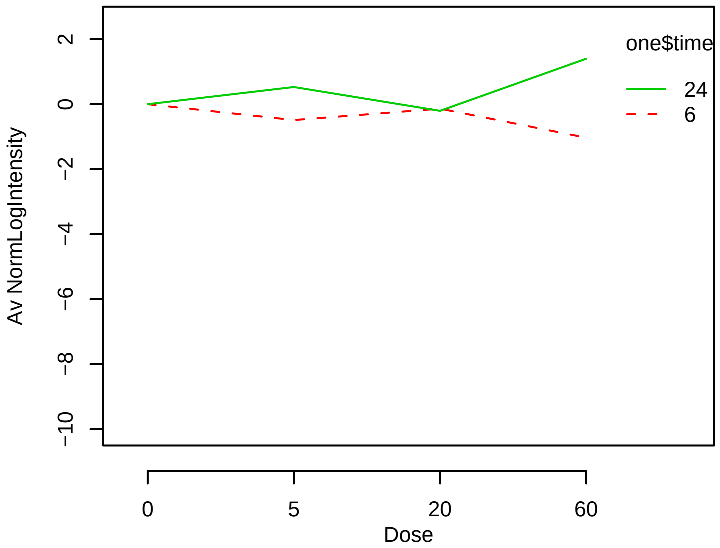

GO_0007028 : cytoplasm organization and biogenesis



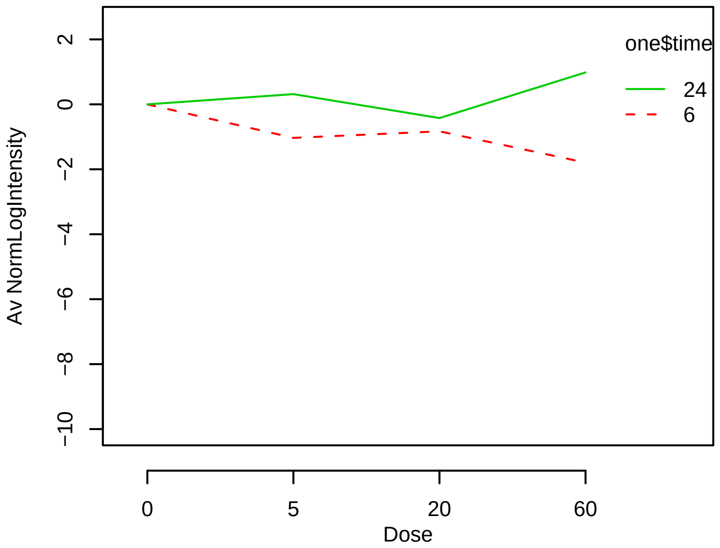
GO_0007030 : Golgi organization and biogenesis



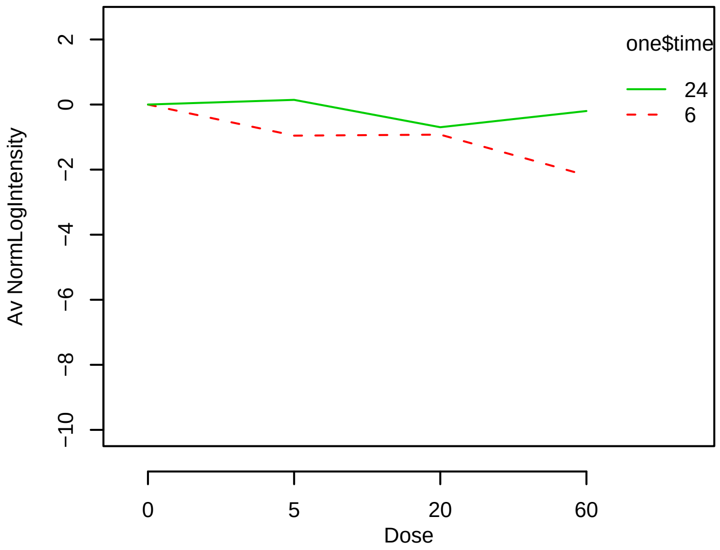
GO_0007031 : peroxisome organization and biogenesis



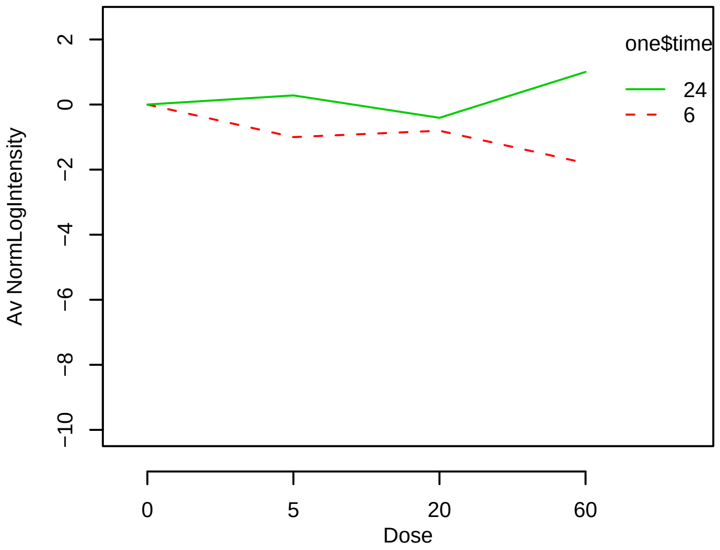
GO_0007032 : endosome organization and biogenesis



GO_0007033 : vacuole organization and biogenesis

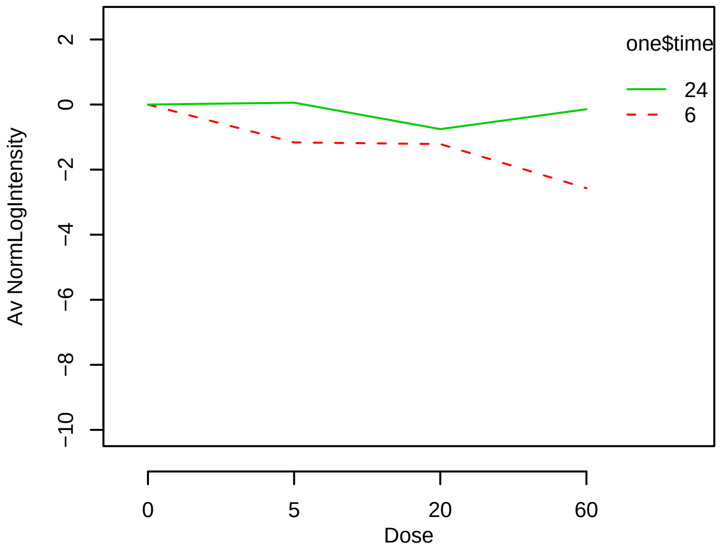


GO_0007034 : vacuolar transport

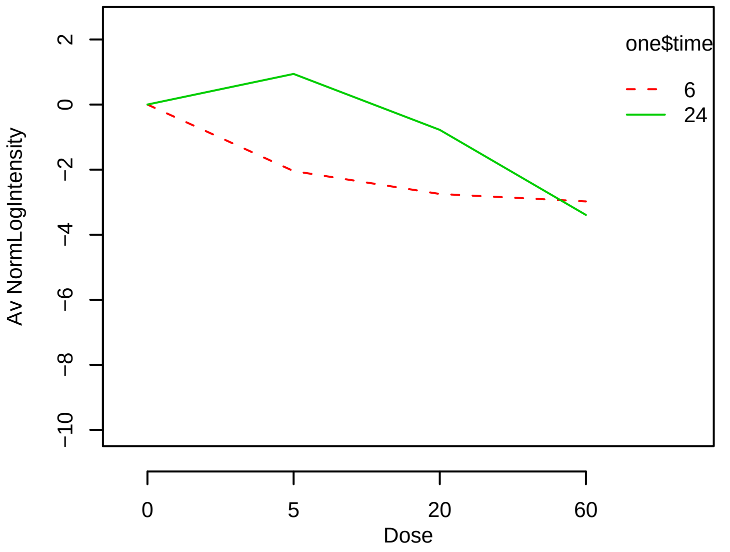


GO_0007040 : lysosome organization and biogenesis

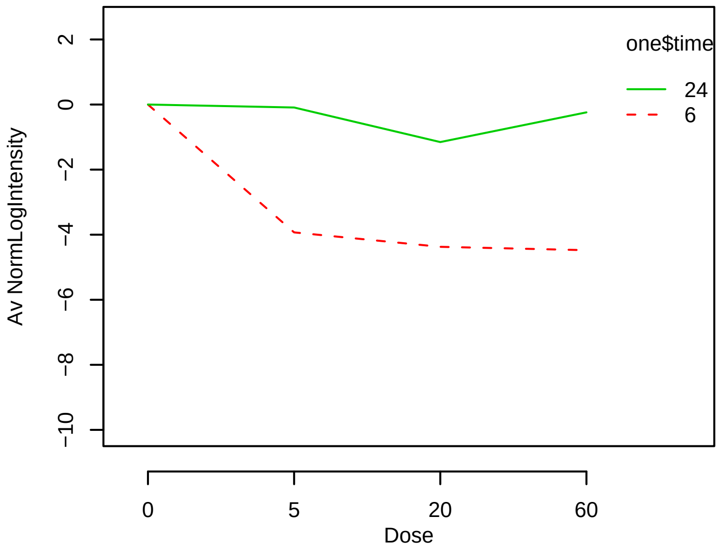
GO_0007041 : lysosomal transport



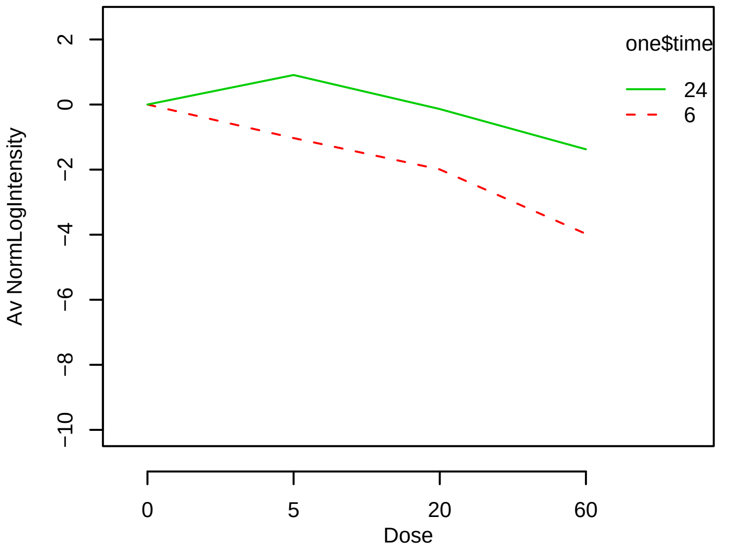
GO_0007043 : intercellular junction assembly



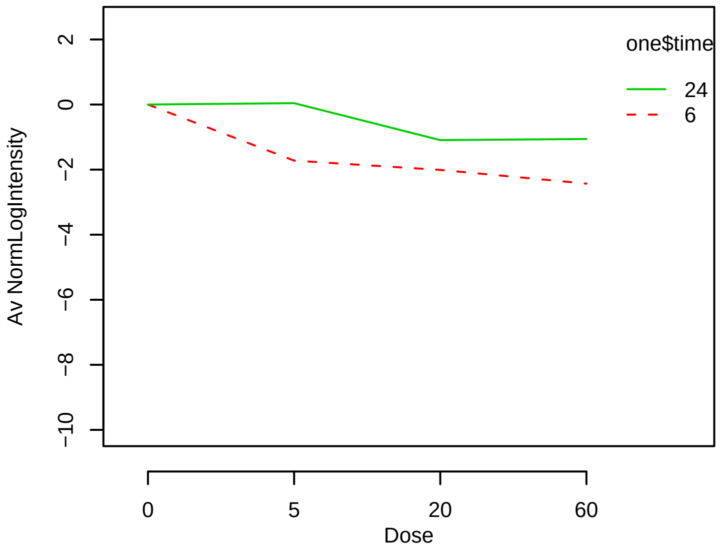
GO_0007044 : cell−substrate junction assembly



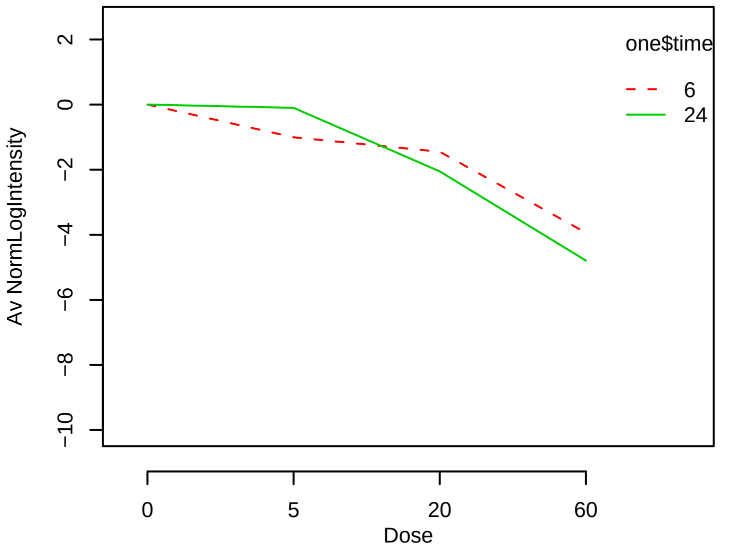
GO_0007046 : ribosome biogenesis

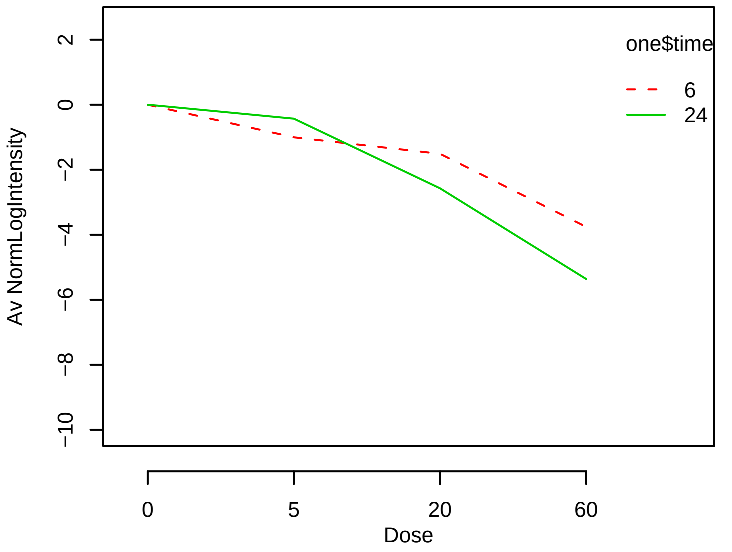


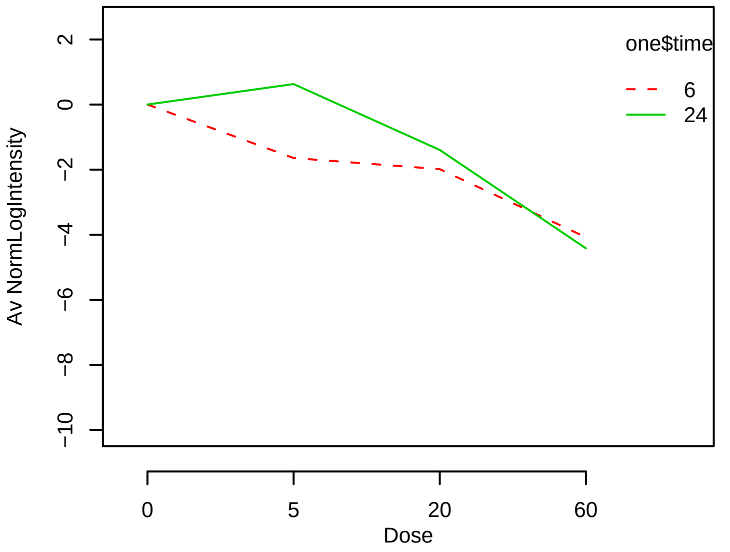
GO_0007050 : cell cycle arrest

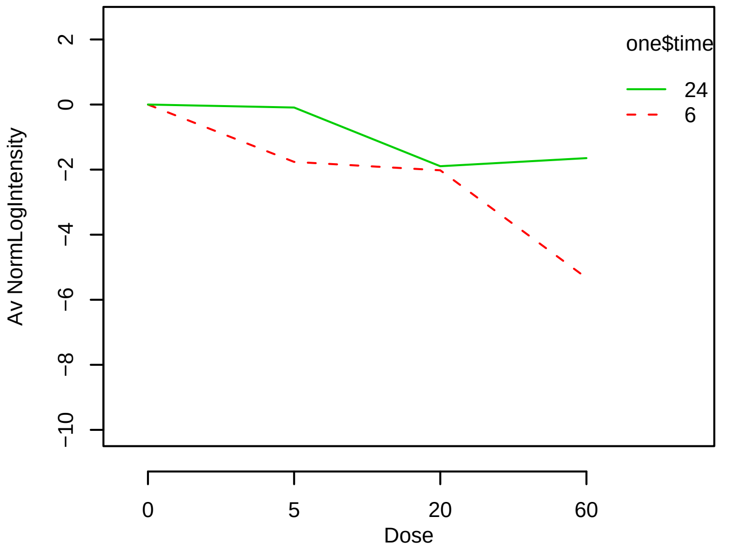


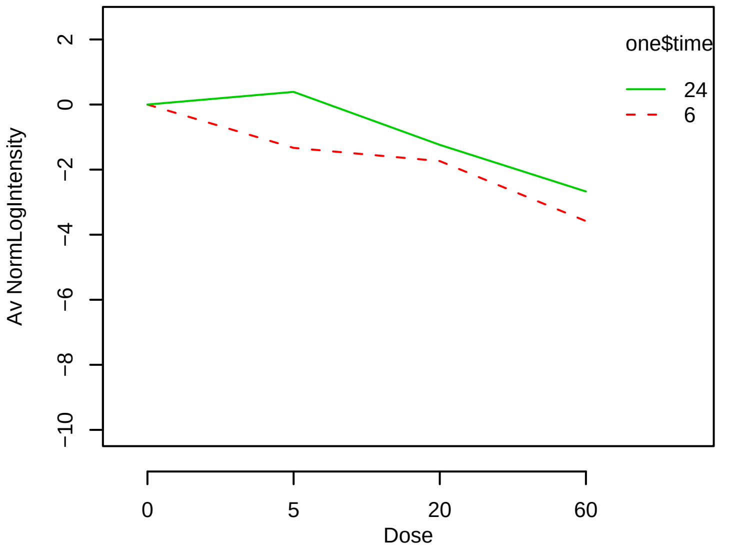
GO_0007051 : spindle organization and biogenesis

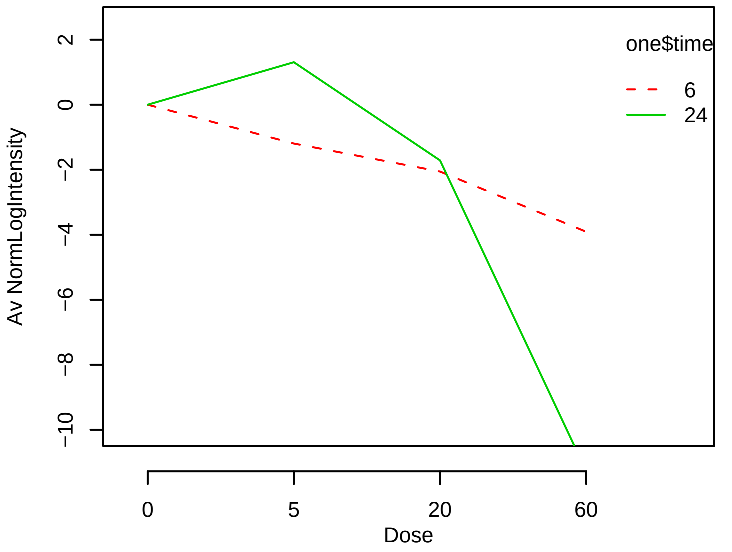


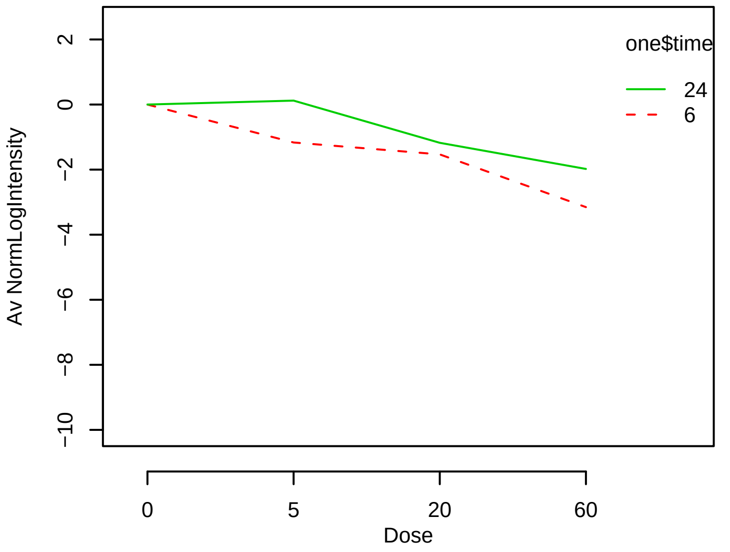

GO_0007052 : mitotic spindle organization and biogenesi


GO_0007059 : chromosome segregation

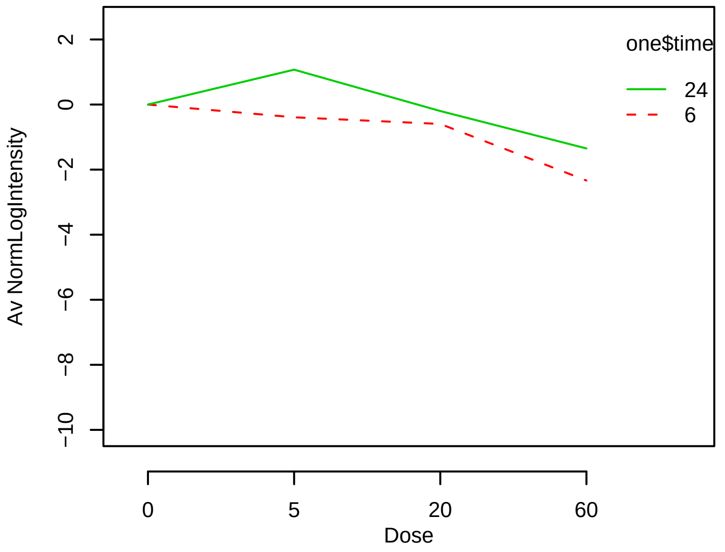

GO_0007062 : sister chromatid cohesion


GO_0007067 : mitosis

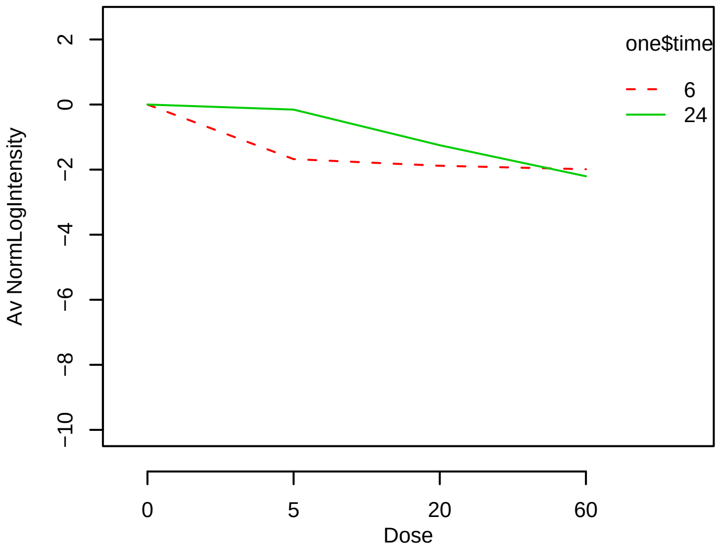

GO_0007076 : mitotic chromosome condensation


GO_0007088 : regulation of mitosis

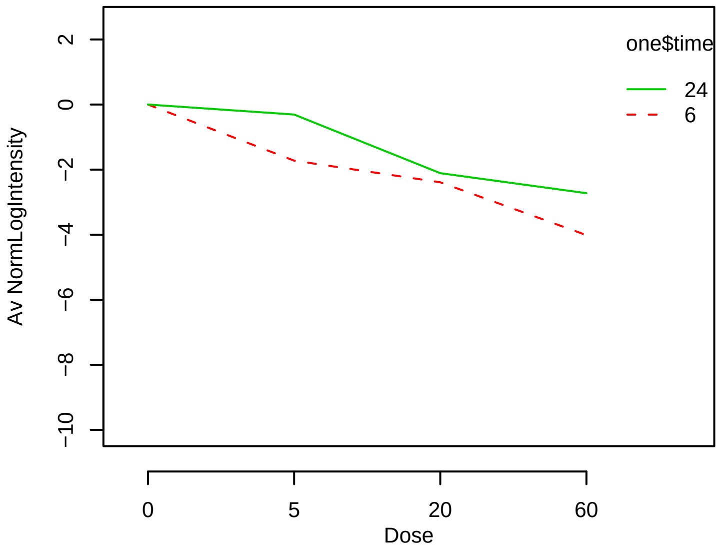
GO_0007089 : traversing start control point of mitotic cell c



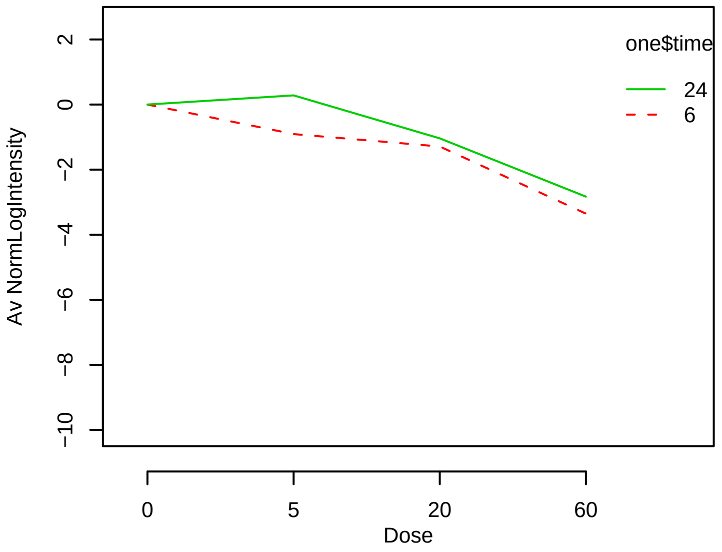
GO_0007090 : regulation of S phase of mitotic cell cycle



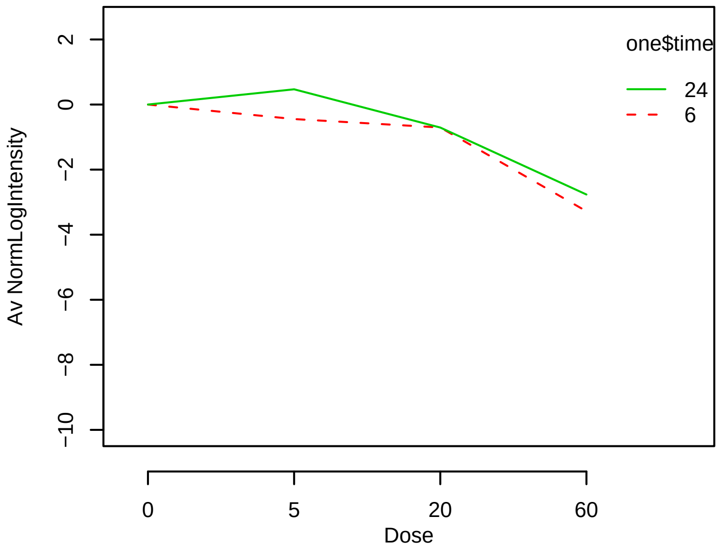
GO_0007091 : mitotic metaphase/anaphase transition



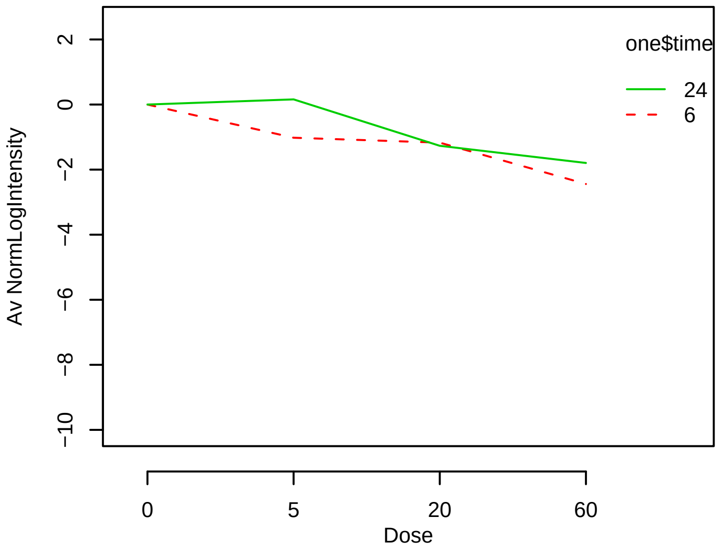
GO_0007093 : mitotic checkpoint

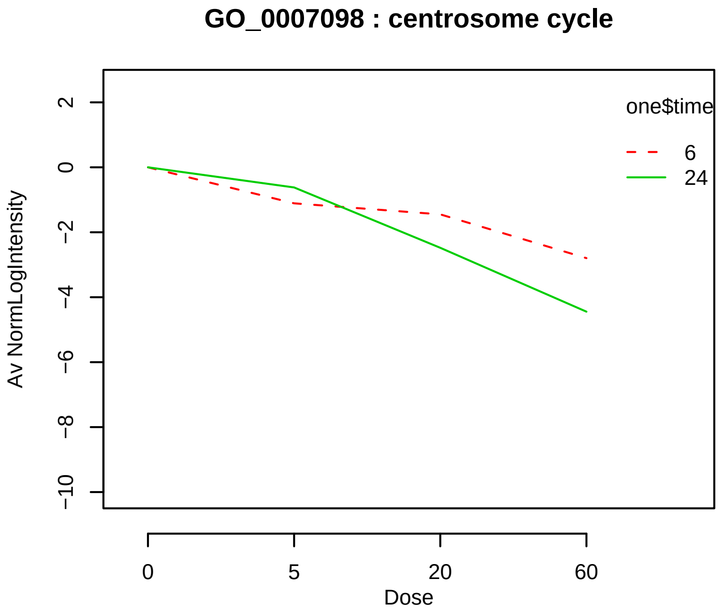


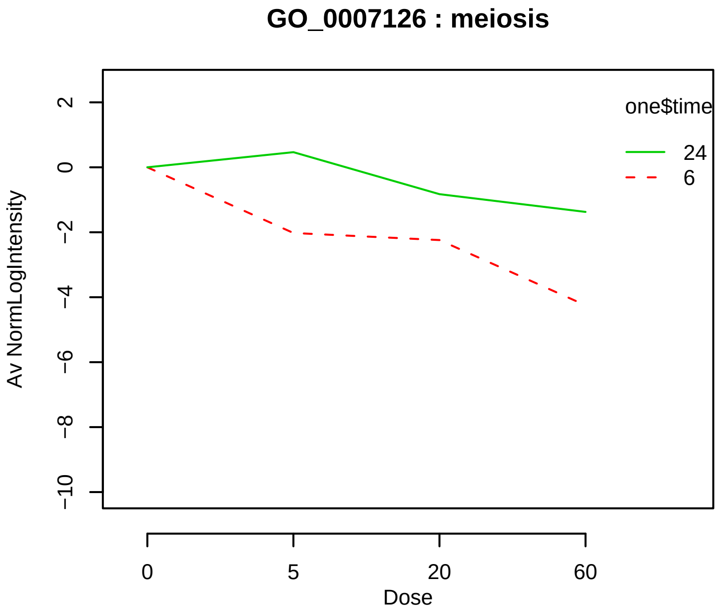
GO_0007094 : mitotic spindle checkpoint

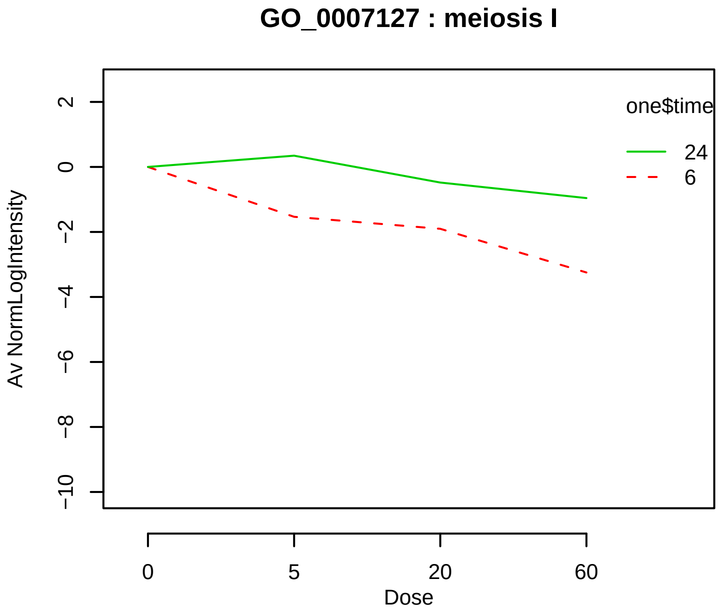


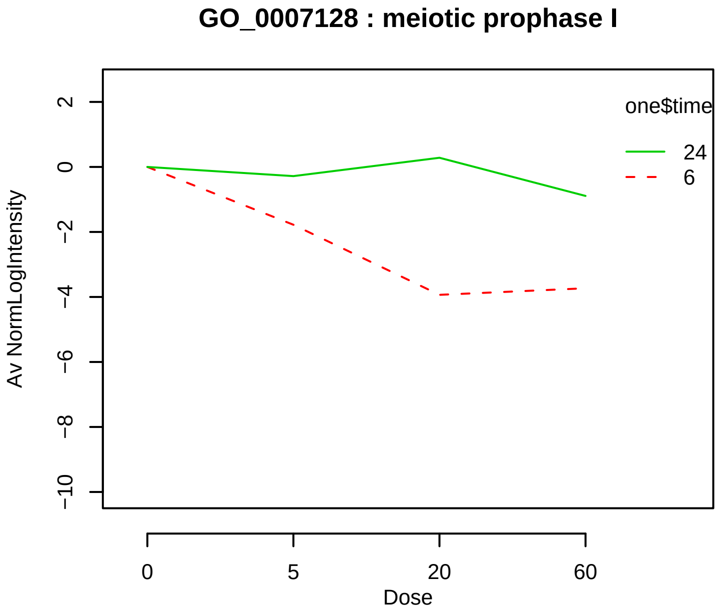
GO_0007096 : regulation of exit from mitosis

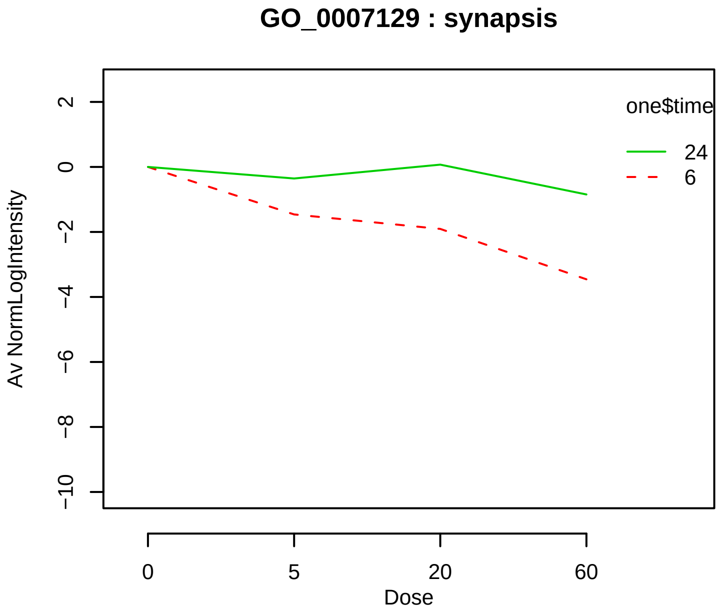


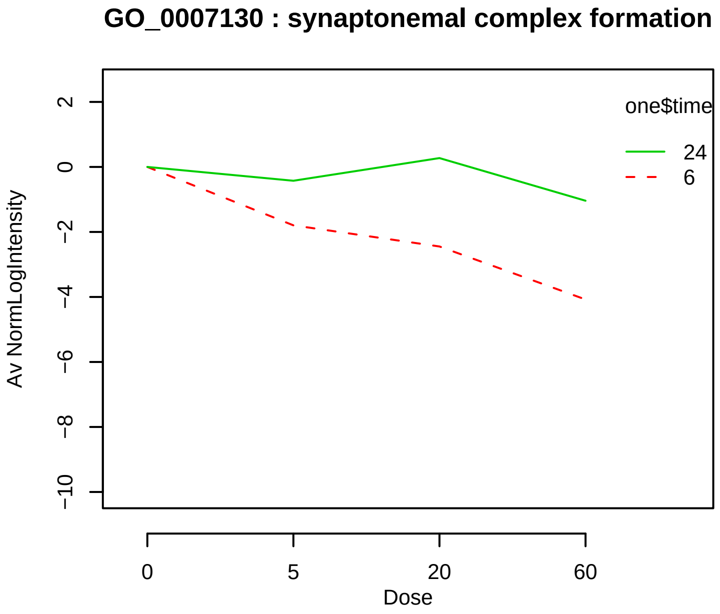

GO_0007098 : centrosome cycle
one$time
6
24
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
0
5
20
60
Dose


GO_0007126 : meiosis
one$time
24
6
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
0
5
20
60
Dose

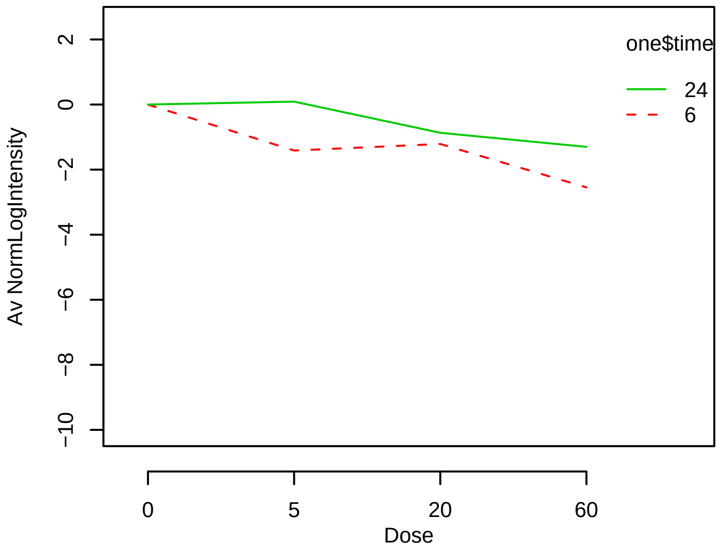

GO_0007127 : meiosis I
one$time
24
6
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
0
5
20
60
Dose


GO_0007128 : meiotic prophase I
one$time
24
6
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
0
5
20
60
Dose

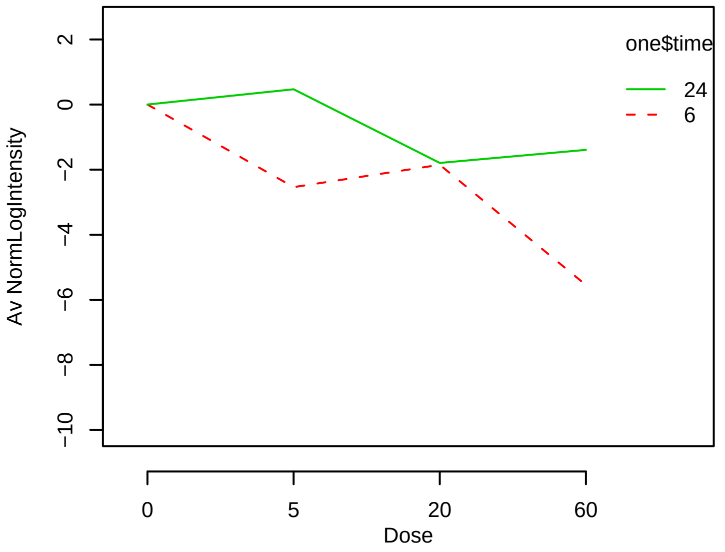

GO_0007129 : synapsis
one$time
24
6
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
0
5
20
60
Dose


GO_0007130 : synaptonemal complex formation
one$time
24
6
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
0
5
20
60
Dose

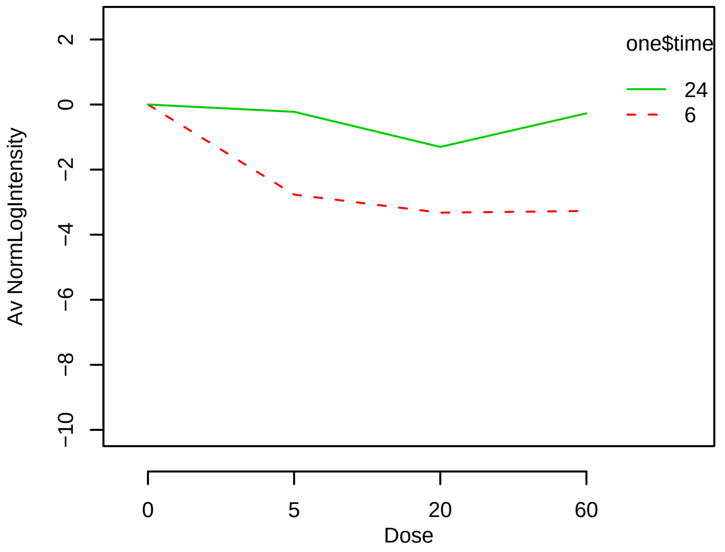
GO_0007131 : meiotic recombination



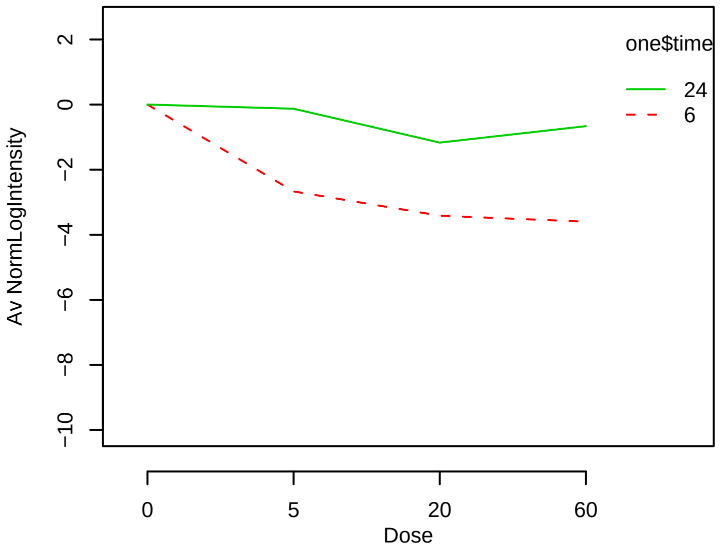
GO_0007140 : male meiosis



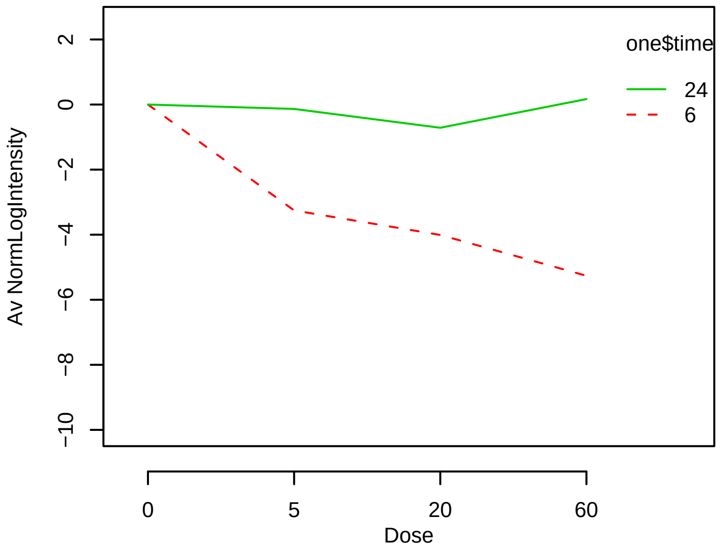
GO_0007156 : homophilic cell adhesion



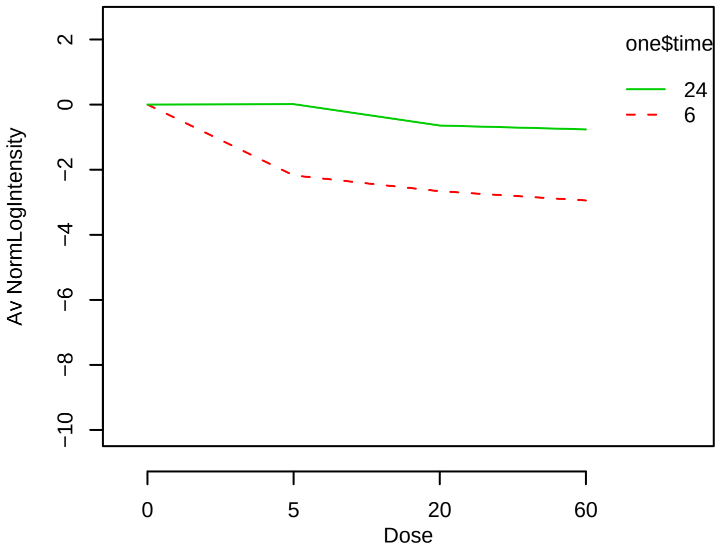
GO_0007157 : heterophilic cell adhesion

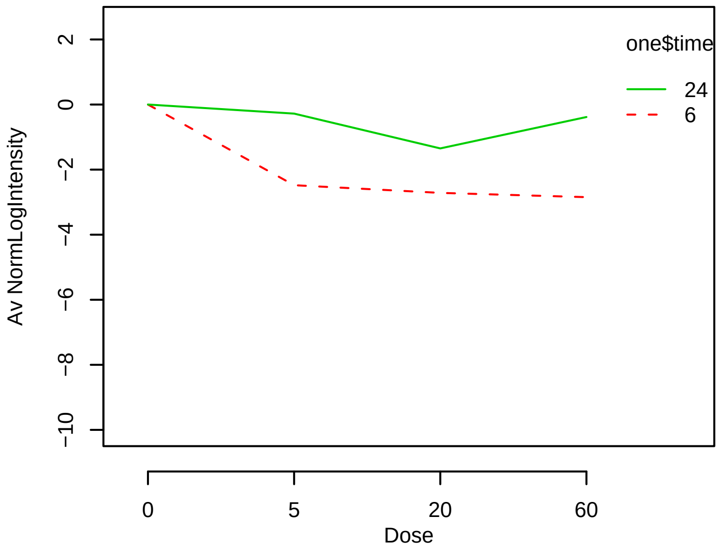


GO_0007158 : neuron adhesion

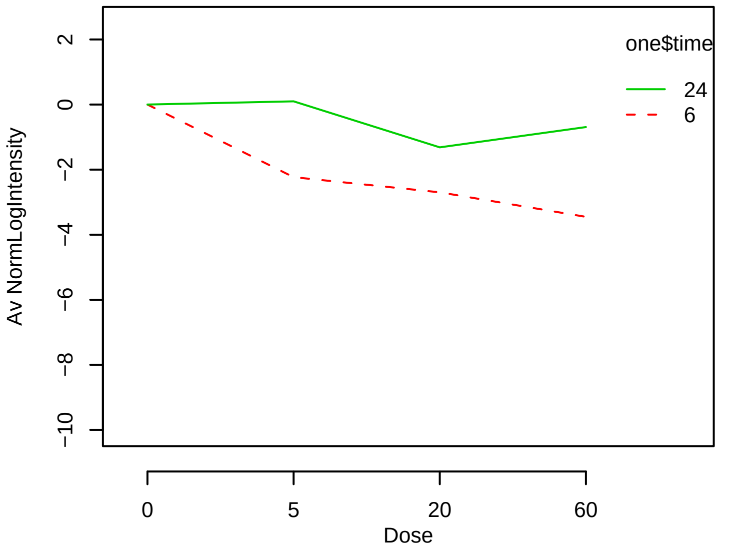


GO_0007159 : leukocyte adhesion

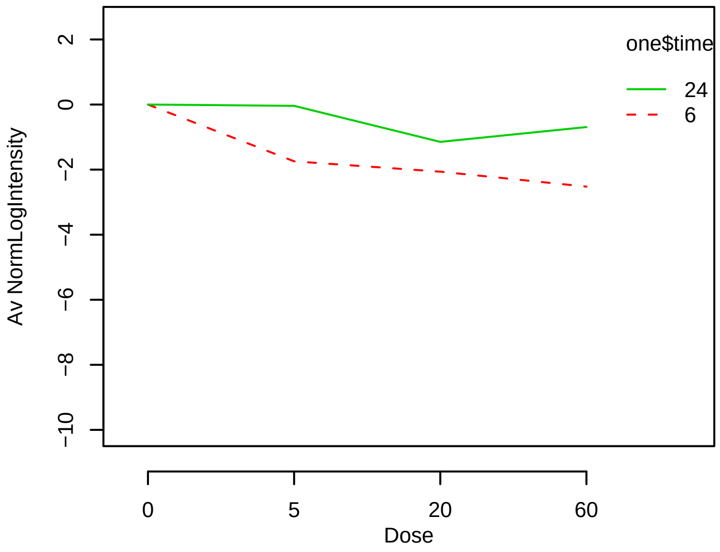




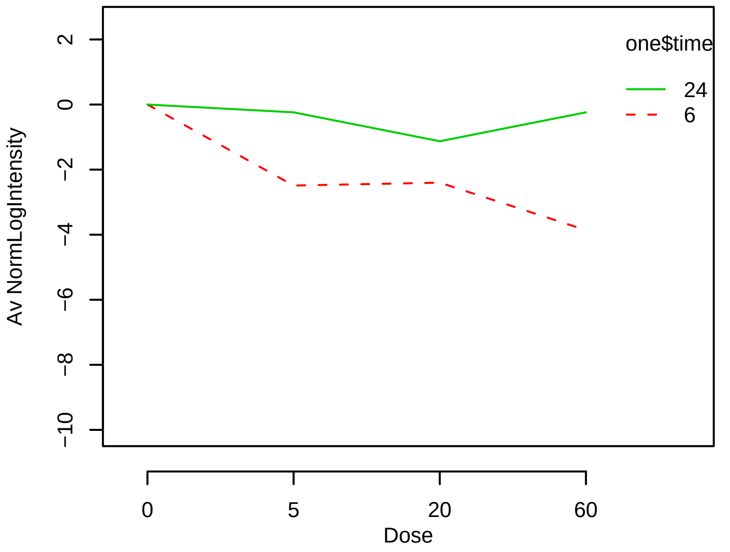
GO_0007160 : cell−matrix adhesion



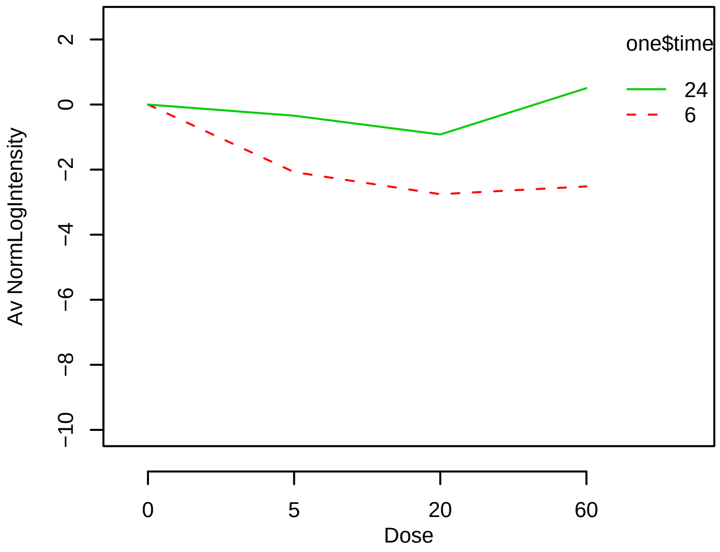
GO_0007162 : negative regulation of cell adhesion



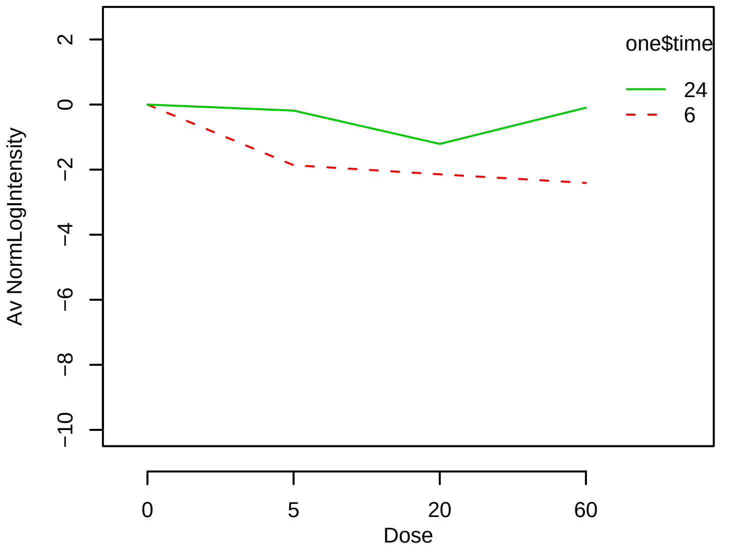
GO_0007163 : establishment and/or maintenance of cell pola



GO_0007164 : establishment of tissue polarity

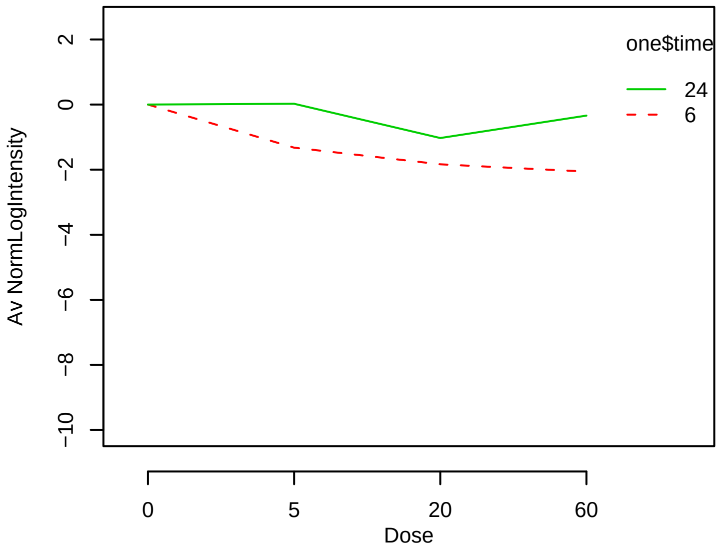


GO_0007168 : receptor guanylyl cyclase signaling pathwa

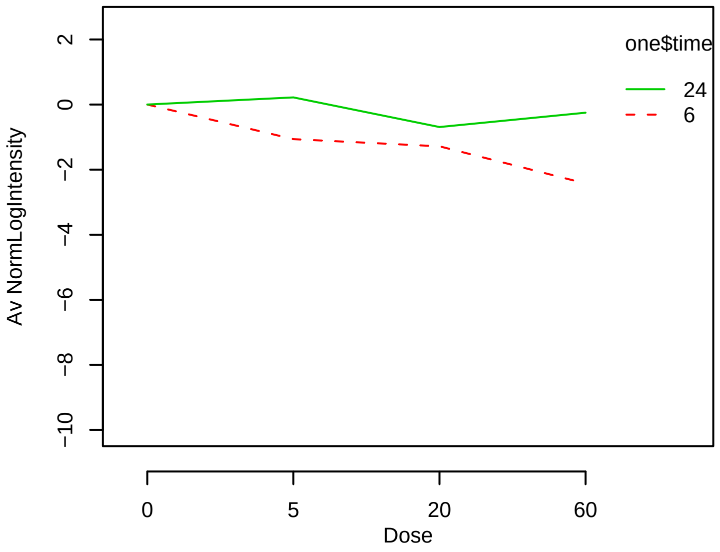


GO_0007169 : transmembrane receptor protein tyrosine kinas

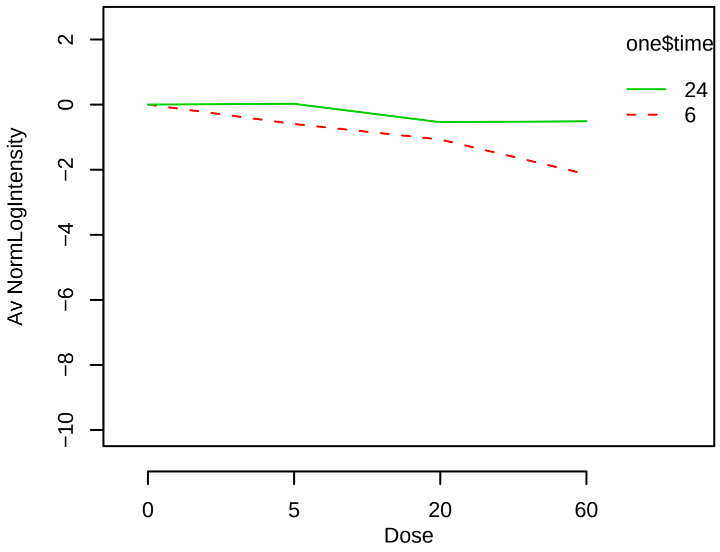
GO_0007172 : signal complex formation



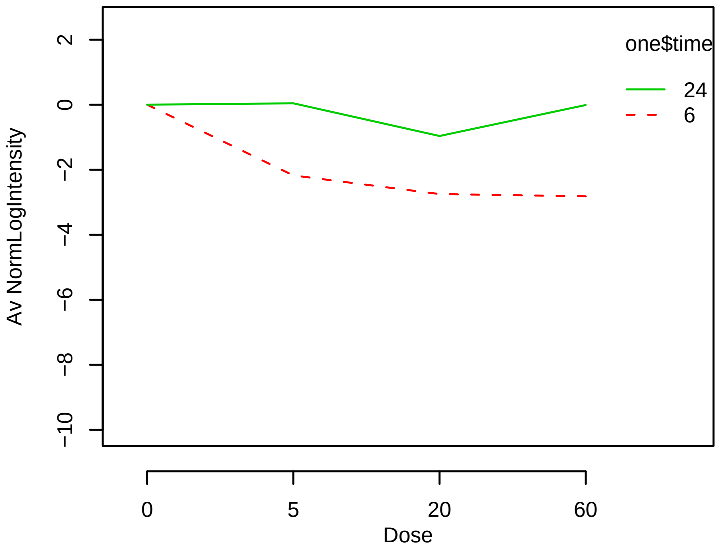
GO_0007173 : epidermal growth factor receptor signaling pat



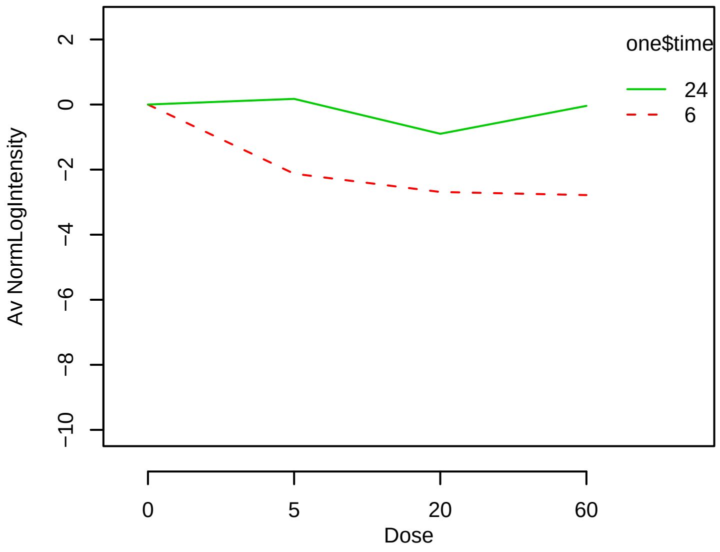
GO_0007176 : regulation of epidermal growth factor recepto



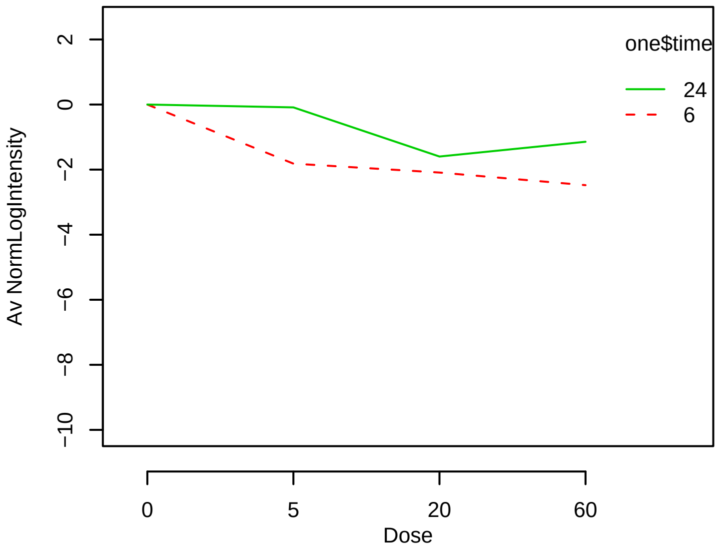
O_0007178 : transmembrane receptor protein serine/threoni



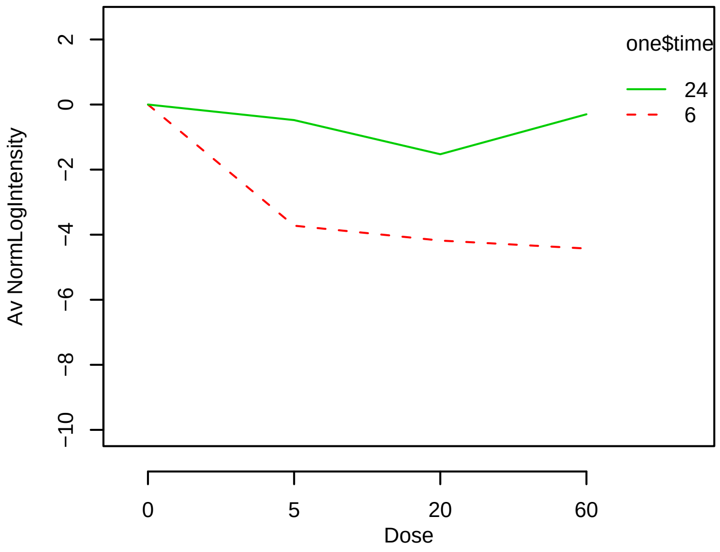
GO_0007179 : transforming growth factor beta receptor signa



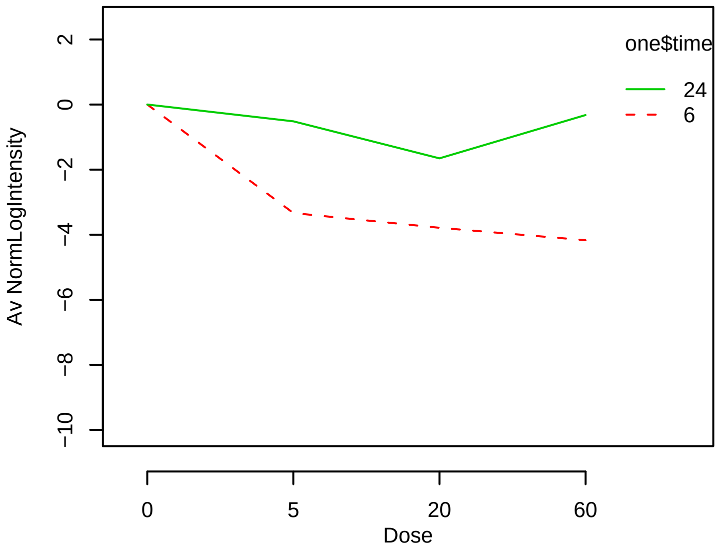
O_0007185 : transmembrane receptor protein tyrosine phosp



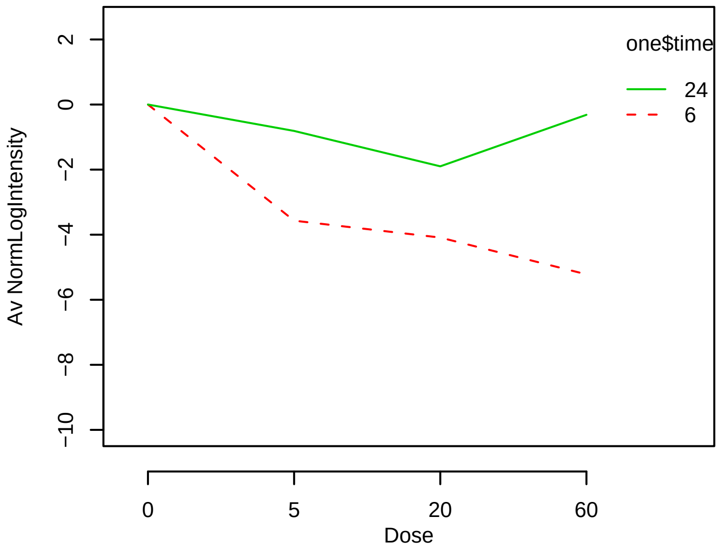
GO_0007187 : G−protein signaling\, coupled to cyclic nucleo



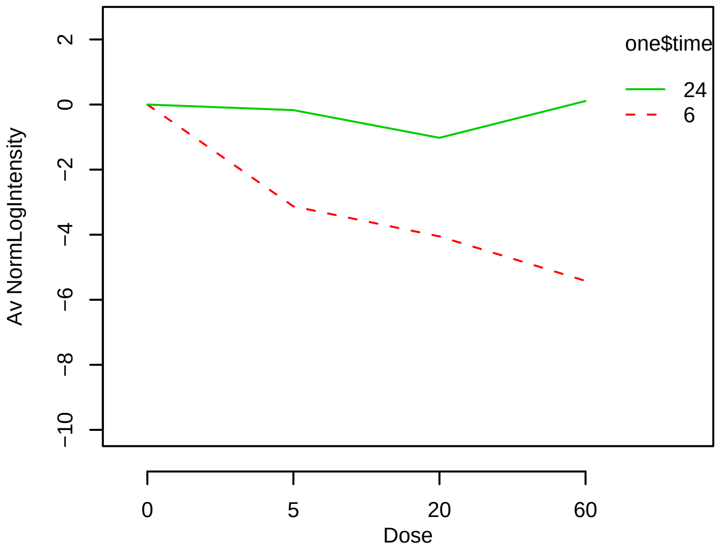
GO_0007188 : G−protein signaling\, coupled to cAMP nucleot



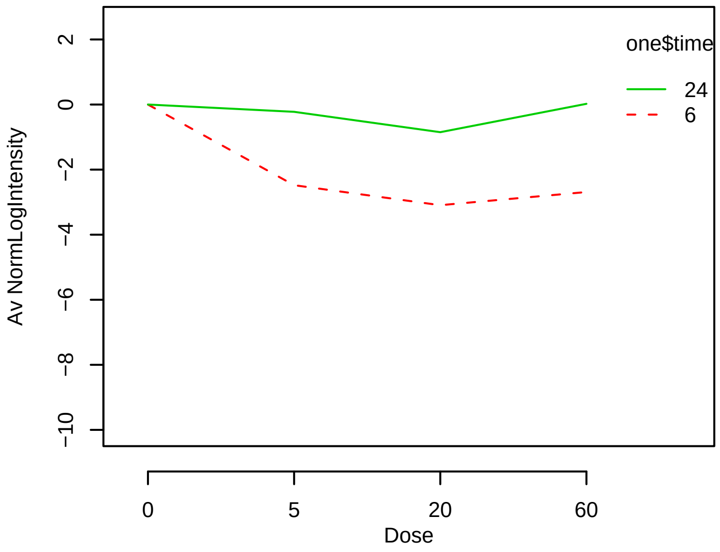
GO_0007189 : G−protein signaling\, adenylate cyclase activa



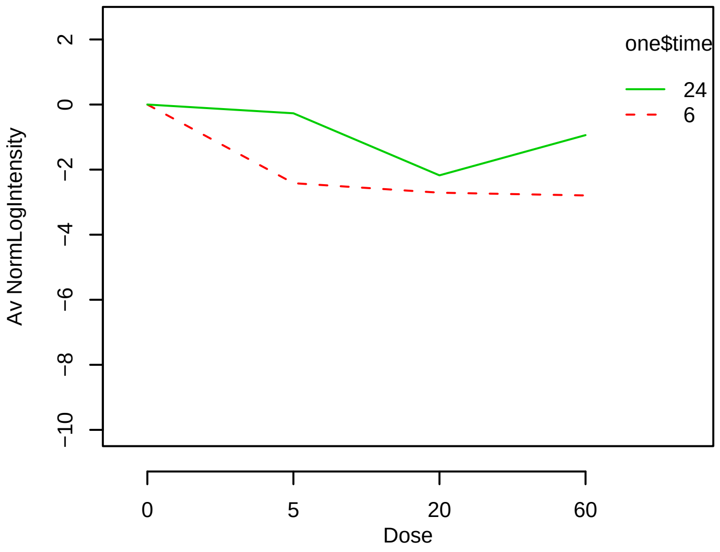
GO_0007190 : adenylate cyclase activation



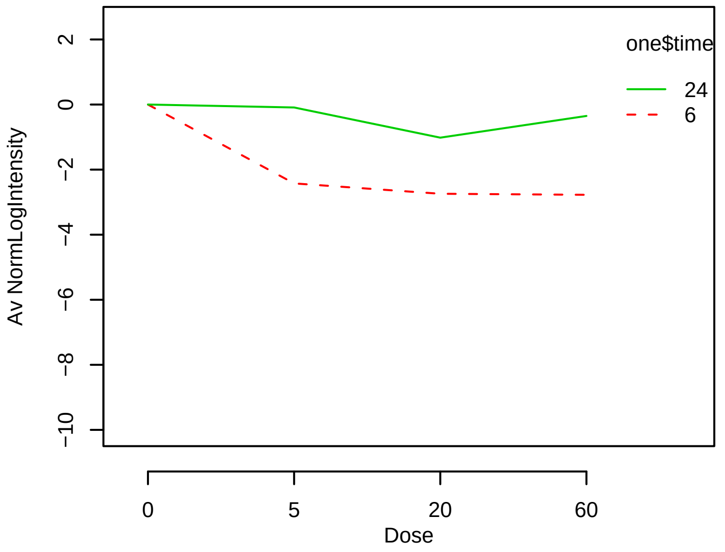
GO_0007193 : G−protein signaling\, adenylate cyclase inhibi



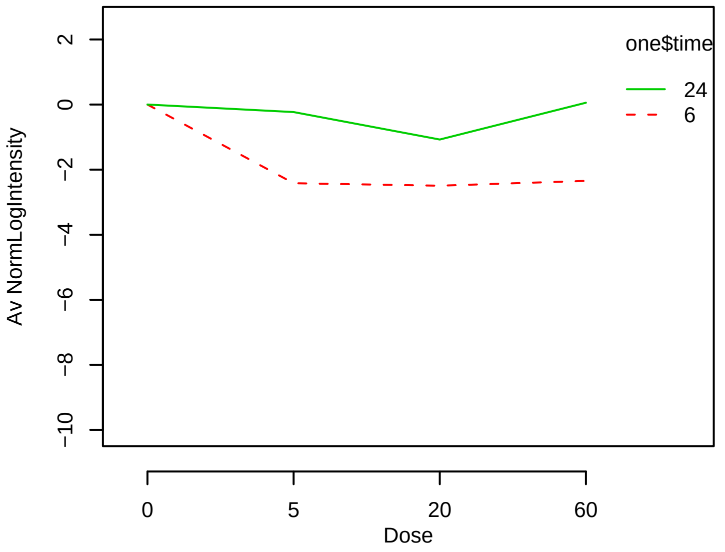
GO_0007194 : negative regulation of adenylate cyclase activ



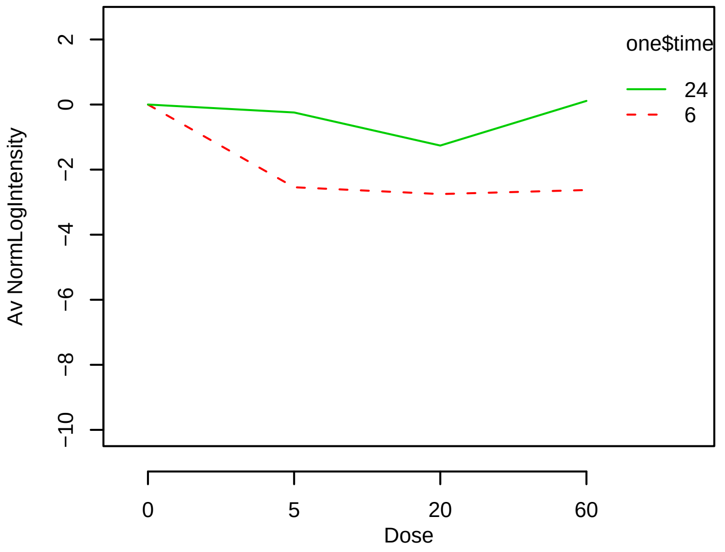
O_0007200 : G−protein signaling\, coupled to IP3 second me



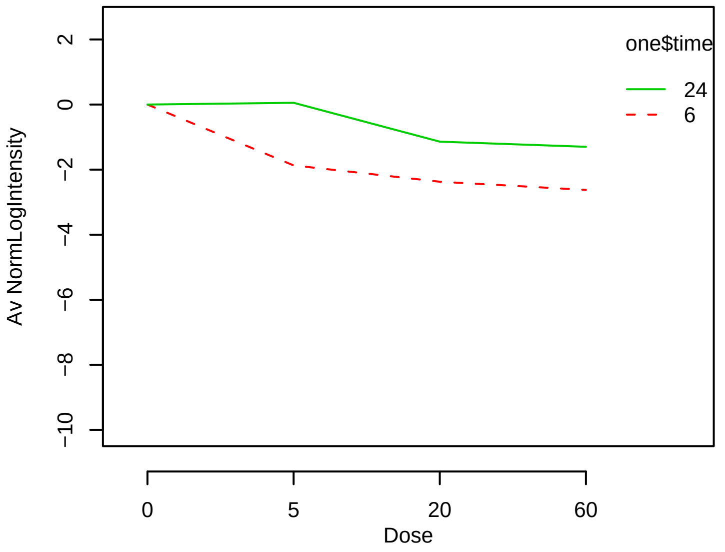
GO_0007202 : phospholipase C activation



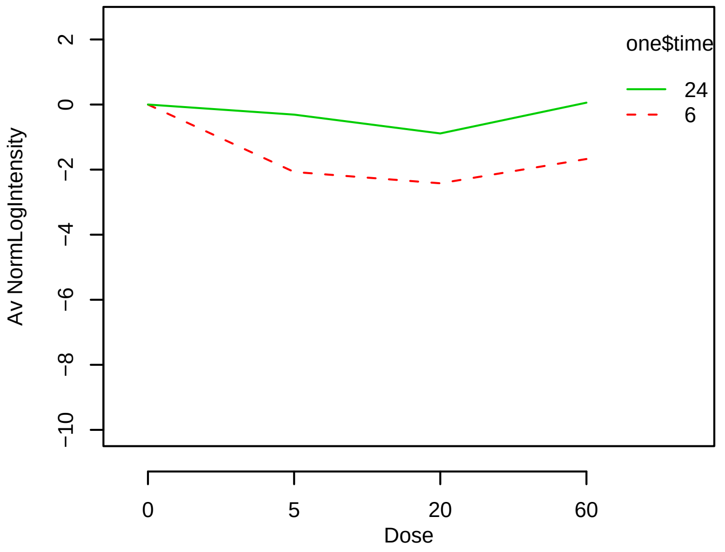
GO_0007204 : elevation of cytosolic calcium ion concentrati



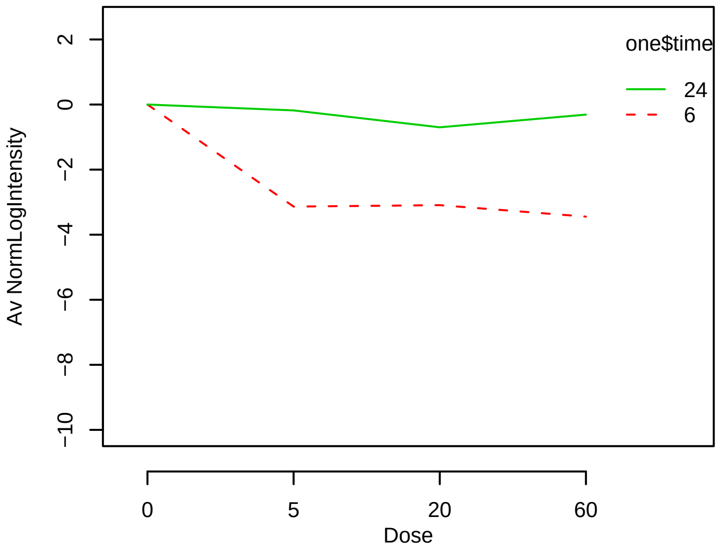
GO_0007205 : protein kinase C activation



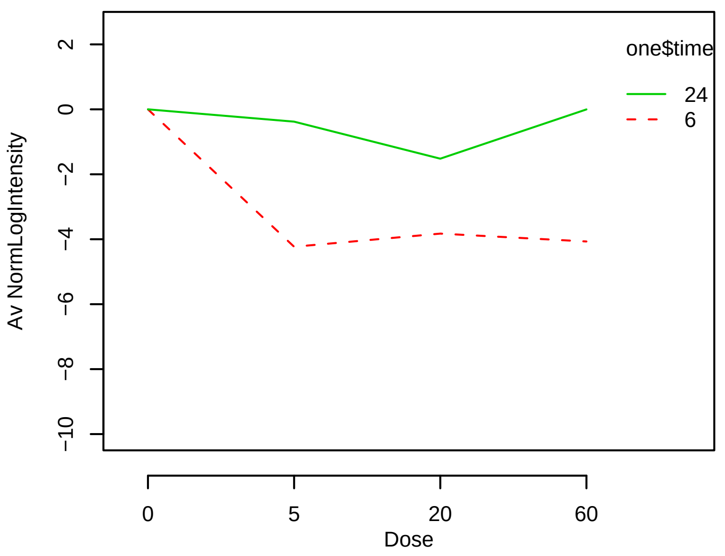
GO_0007212 : dopamine receptor signaling pathway



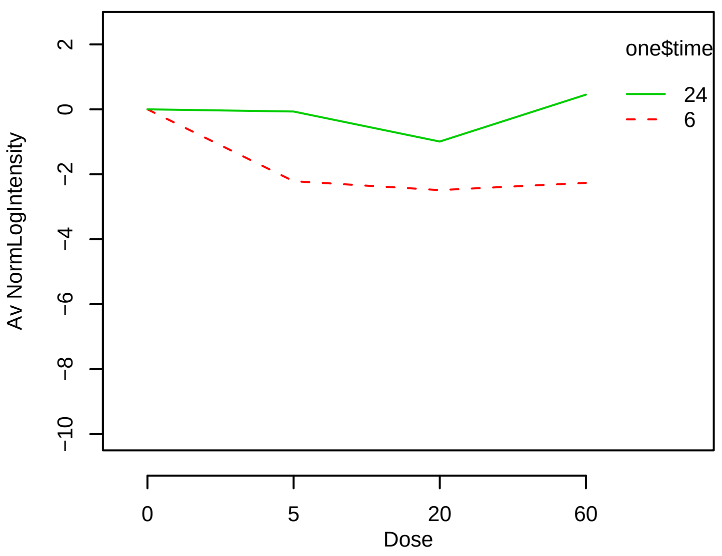
GO_0007213 : acetylcholine receptor signaling\, muscarinic



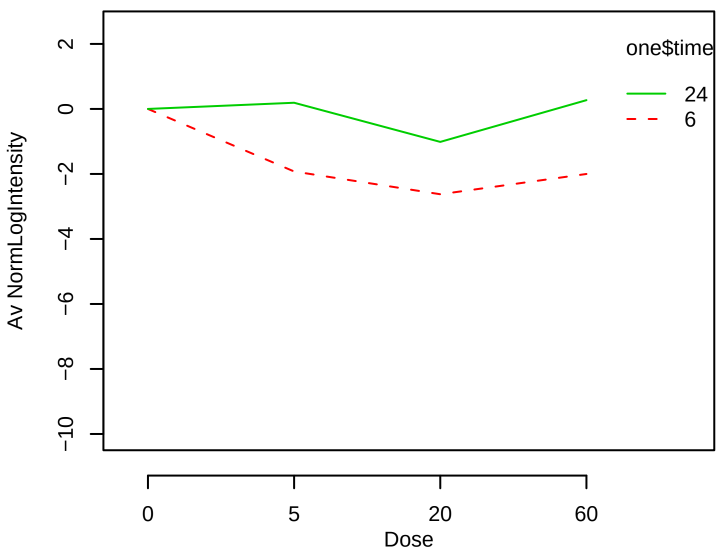
GO_0007214 : gamma−aminobutyric acid signaling pathwa



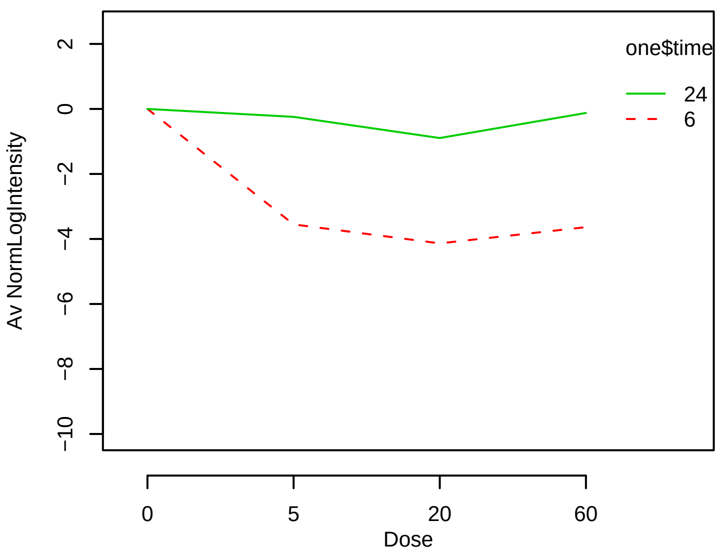
GO_0007215 : glutamate signaling pathway



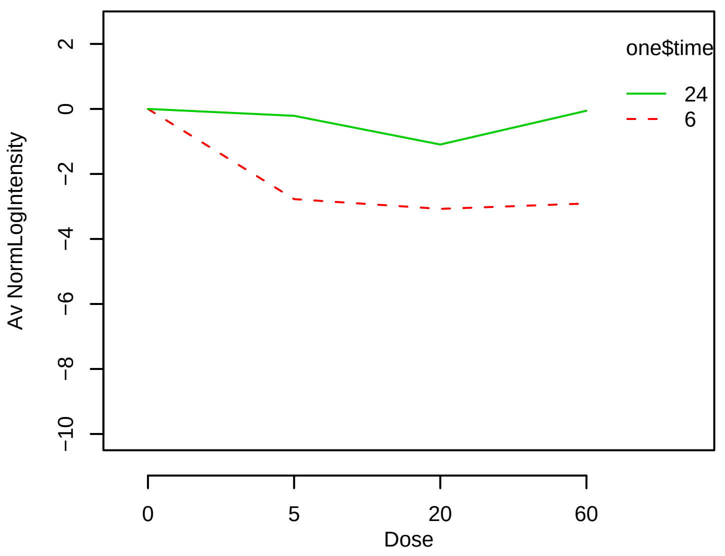
GO_0007216 : metabotropic glutamate receptor signaling patl



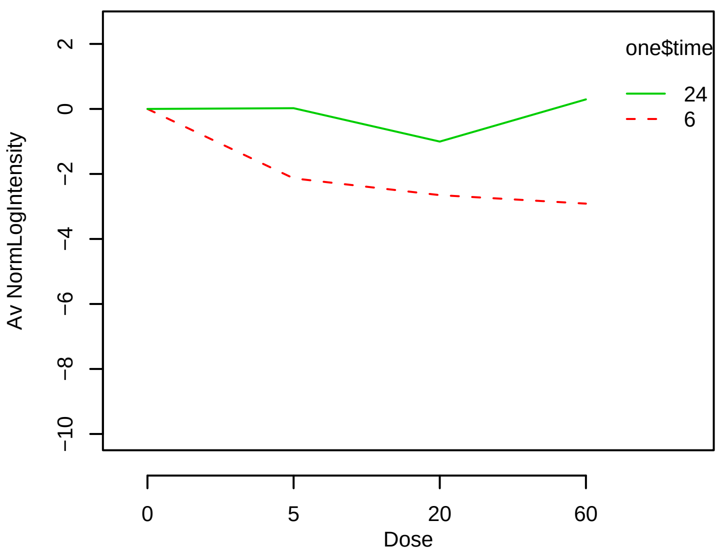
GO_0007217 : tachykinin signaling pathway

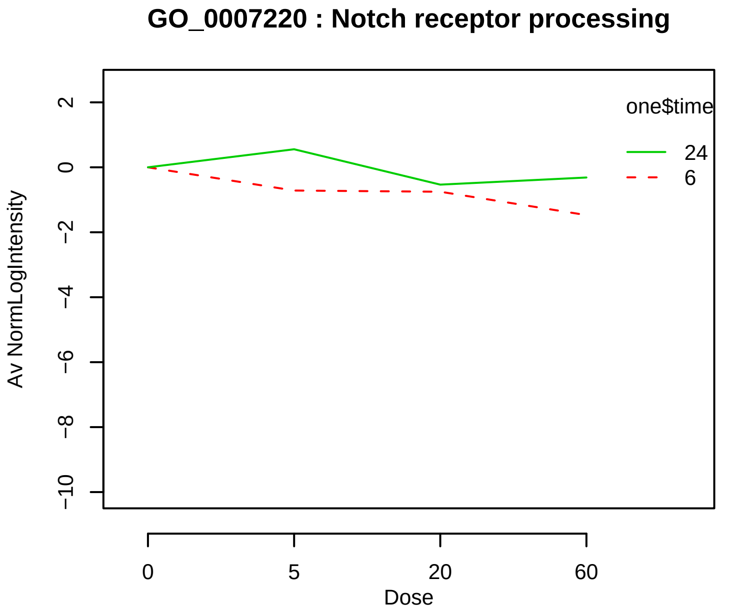


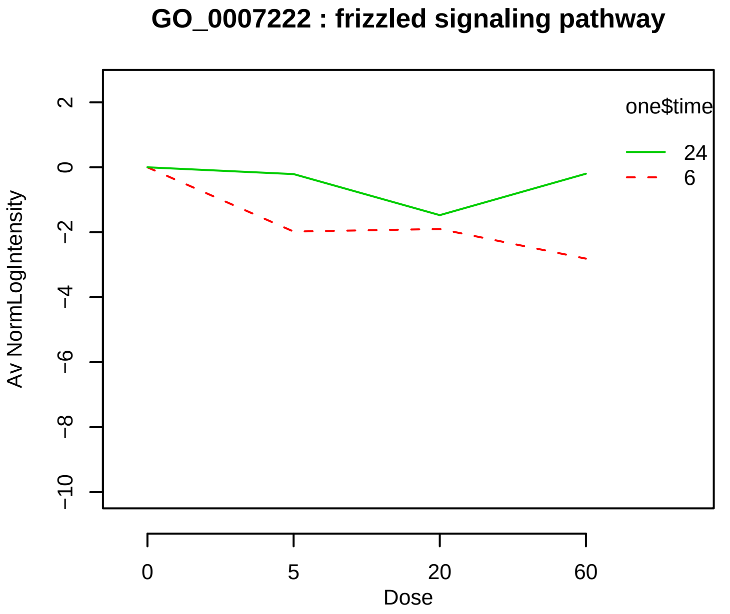
GO_0007218 : neuropeptide signaling pathway

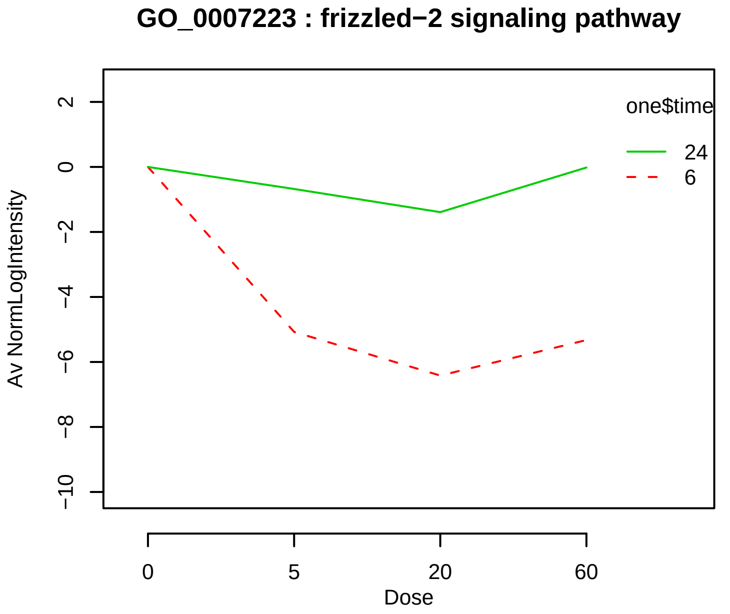


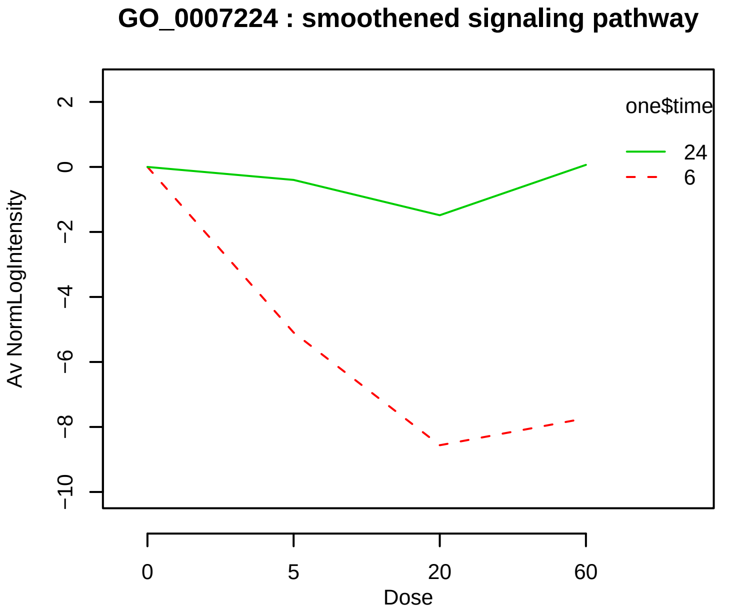
GO_0007219 : Notch signaling pathway

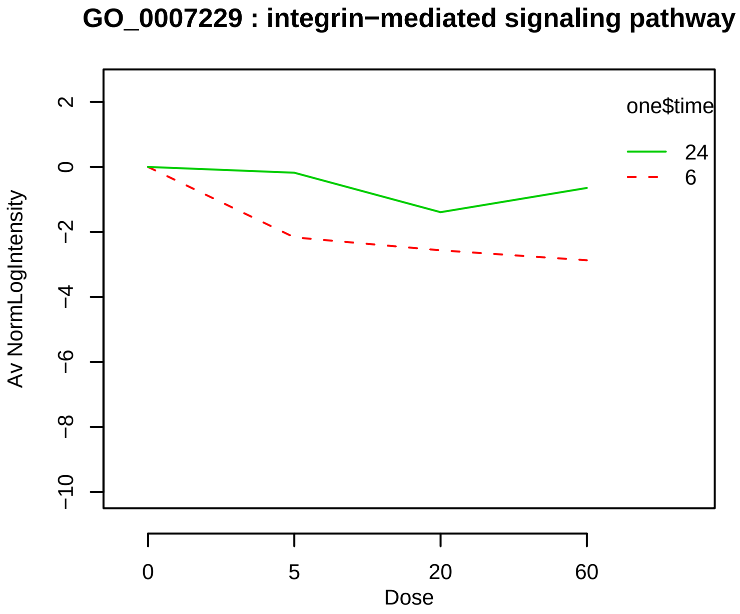


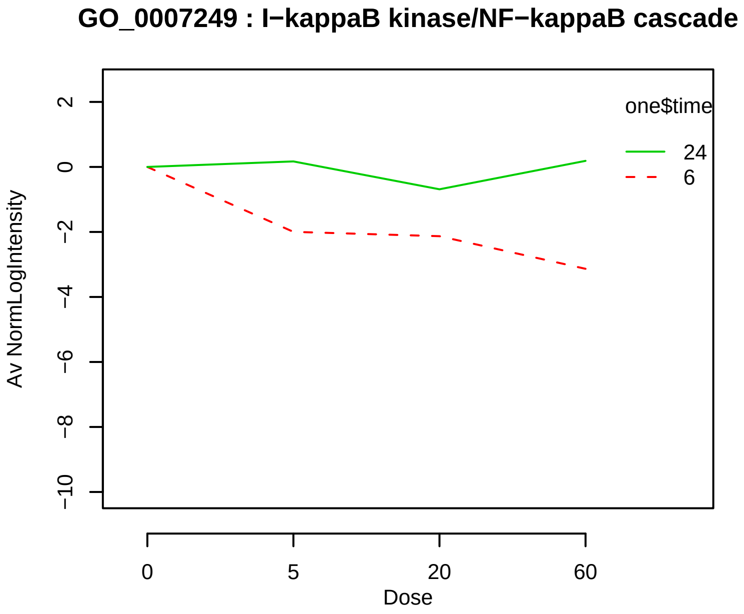

GO_0007220 : Notch receptor processing
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
one$time
24
6
0
5
20
60
Dose


GO_0007222 : frizzled signaling pathway
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
one$time
24
6
0
5
20
60
Dose

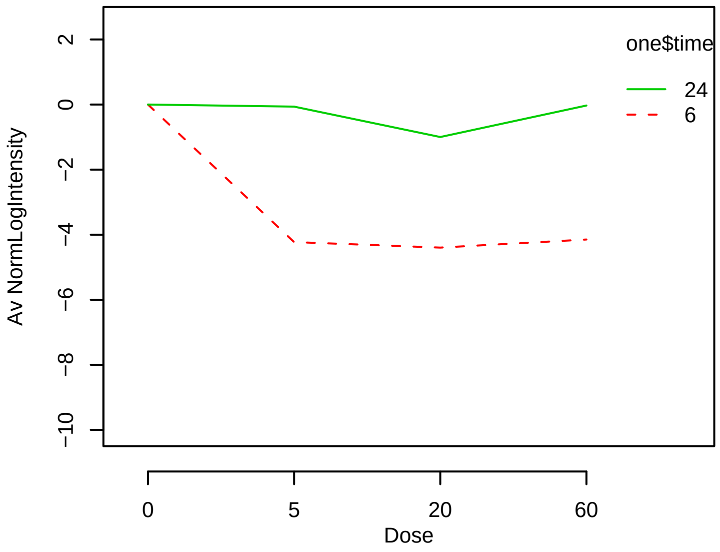

GO_0007223 : frizzled−2 signaling pathway
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
one$time
24
6
0
5
20
60
Dose


GO_0007224 : smoothened signaling pathway
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
one$time
24
6
0
5
20
60
Dose

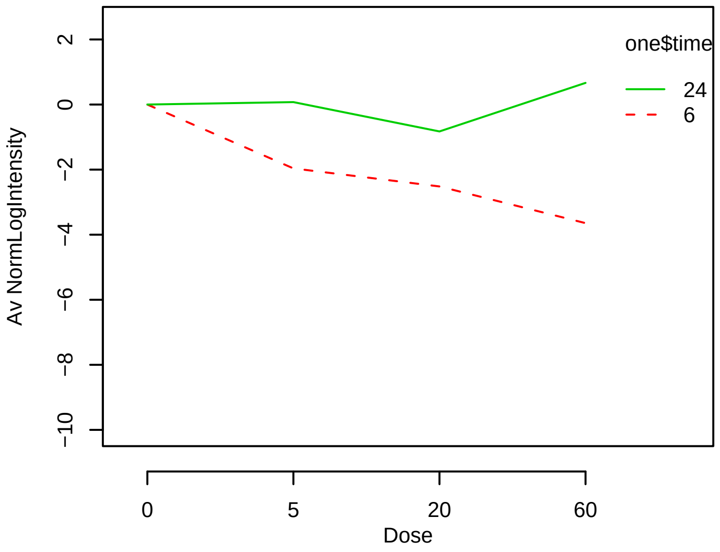

GO_0007229 : integrin−mediated signaling pathway
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
one$time
24
6
0
5
20
60
Dose


GO_0007249 : I−kappaB kinase/NF−kappaB cascade
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
one$time
24
6
0
5
20
60
Dose

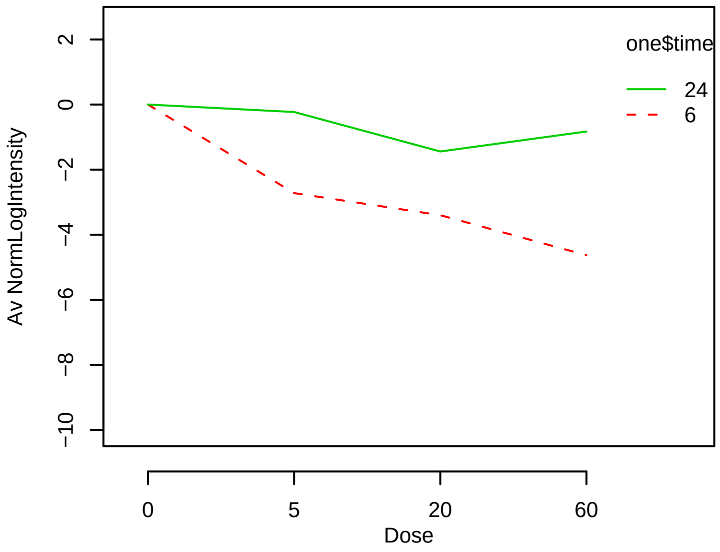
GO_0007250 : activation of NF−kappaB−inducing kinase



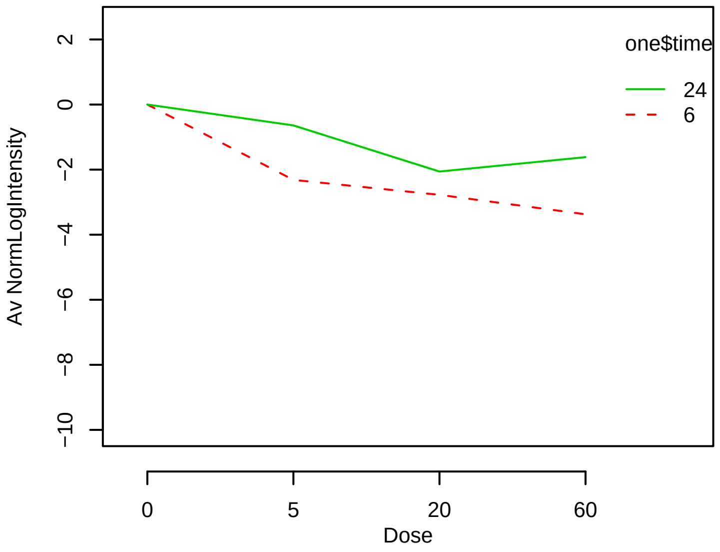
GO_0007253 : cytoplasmic sequestering of NF−kappaB



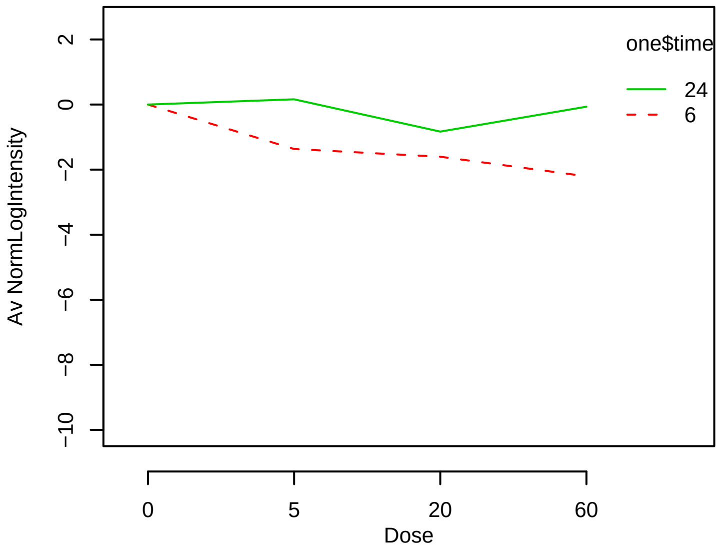
GO_0007254 : JNK cascade



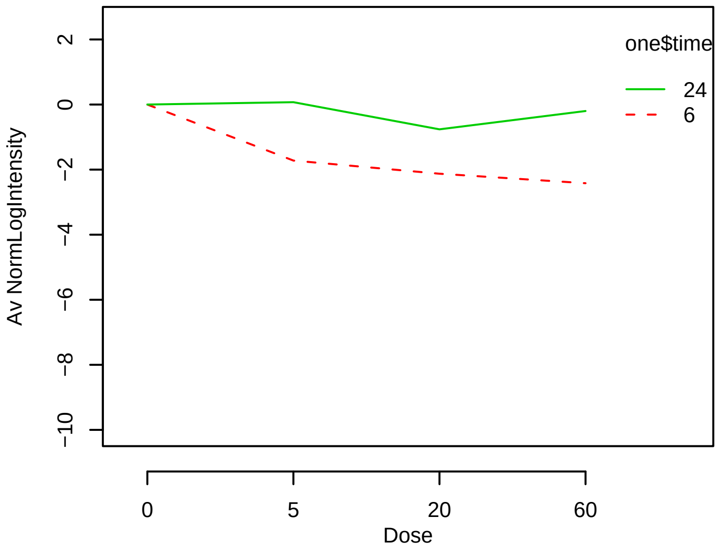
GO_0007257 : activation of JNK activity

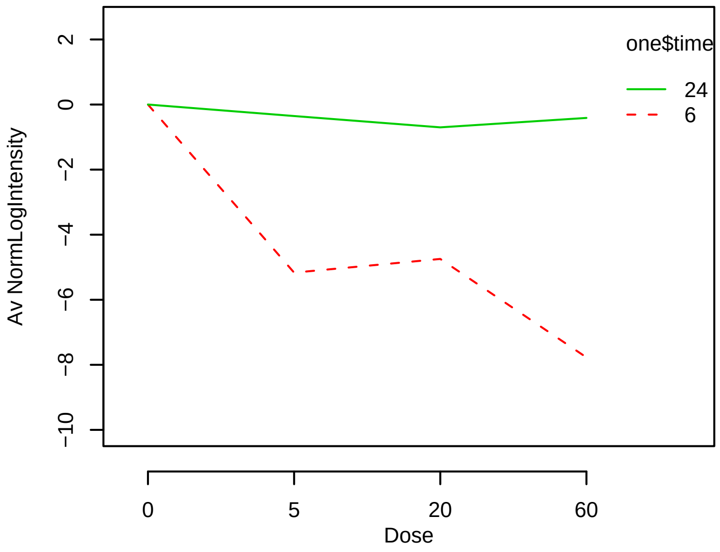


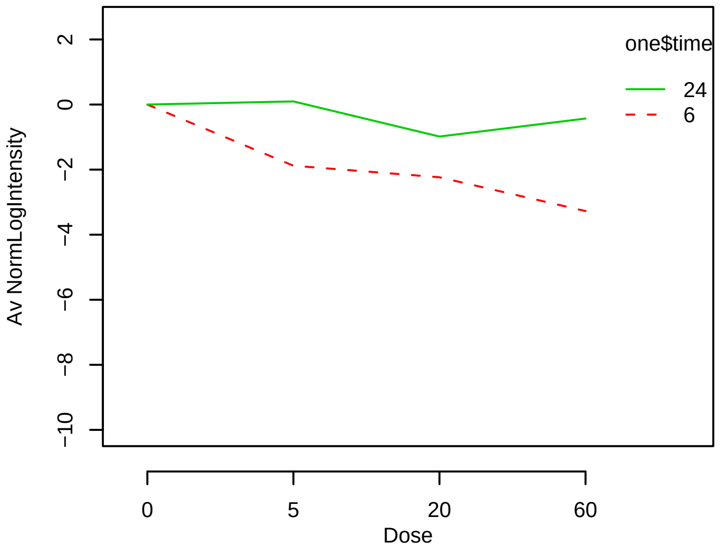
GO_0007259 : JAK−STAT cascade

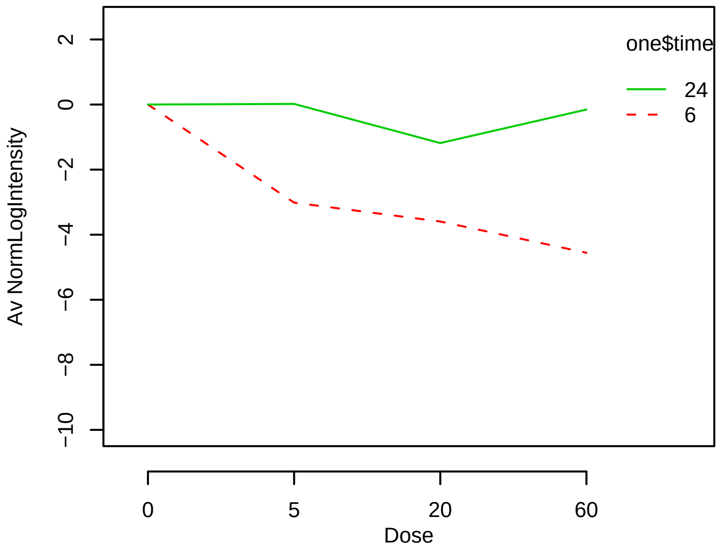


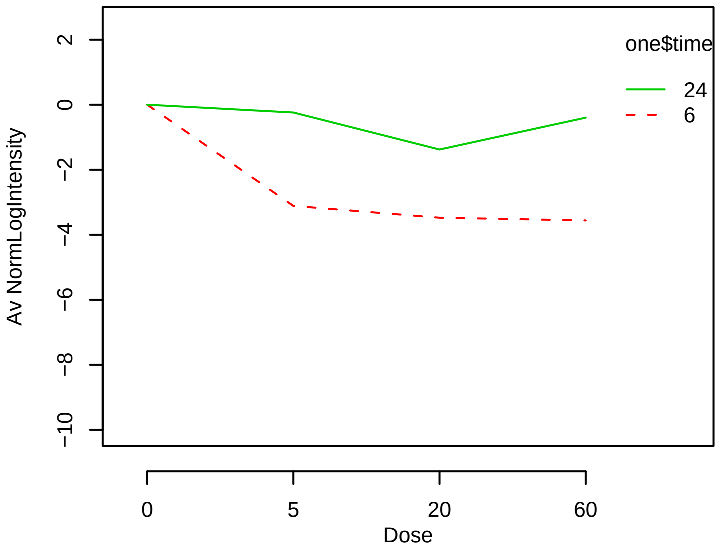
GO_0007260 : tyrosine phosphorylation of STAT protein

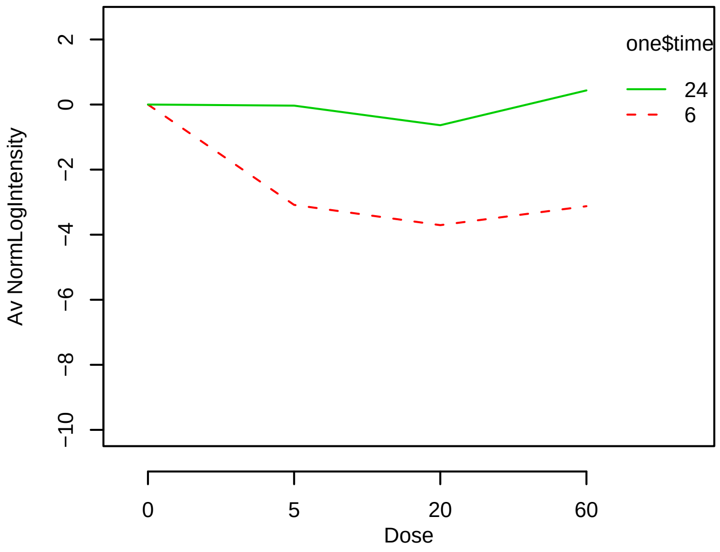


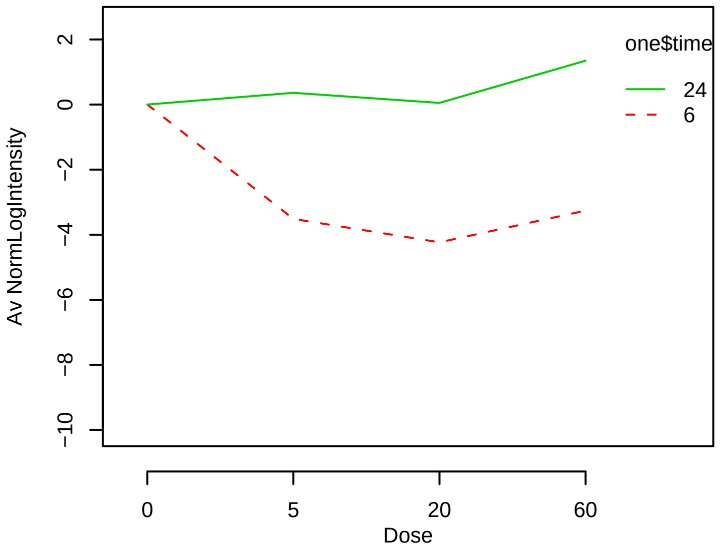

GO_0007263 : nitric oxide mediated signal transduction


GO_0007265 : Ras protein signal transduction

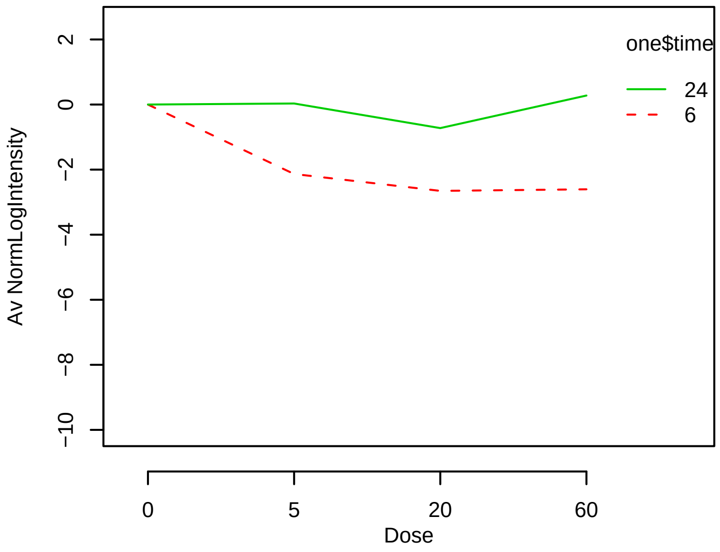

GO_0007266 : Rho protein signal transduction


GO_0007269 : neurotransmitter secretion

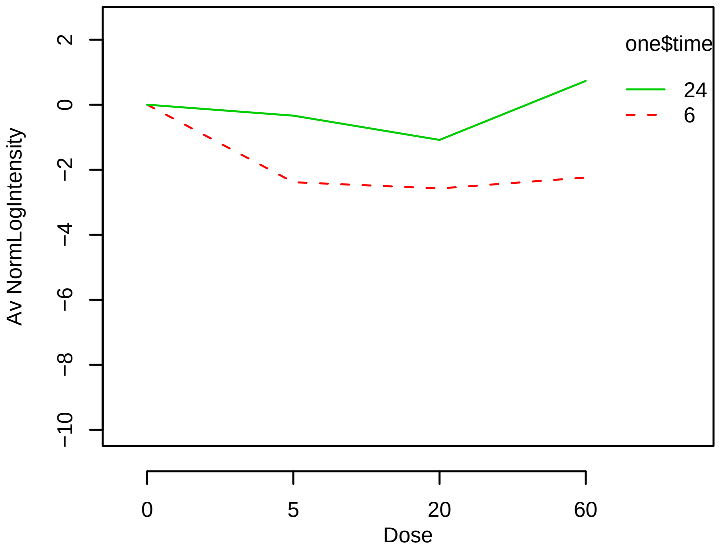

GO_0007270 : nerve−nerve synaptic transmission


GO_0007271 : synaptic transmission\, cholinergic

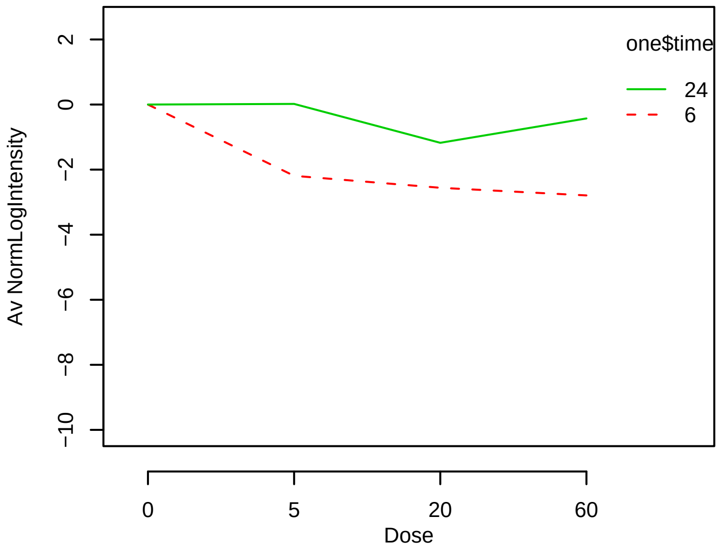
GO_0007272 : ensheathment of neurons



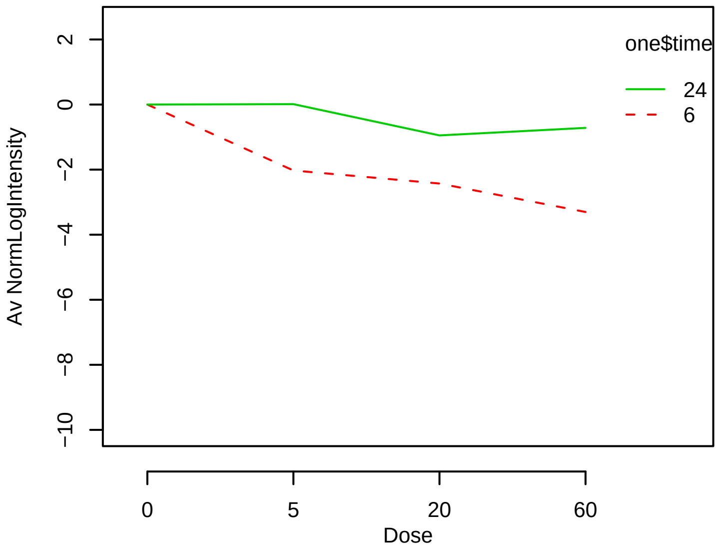
GO_0007274 : neuromuscular synaptic transmission



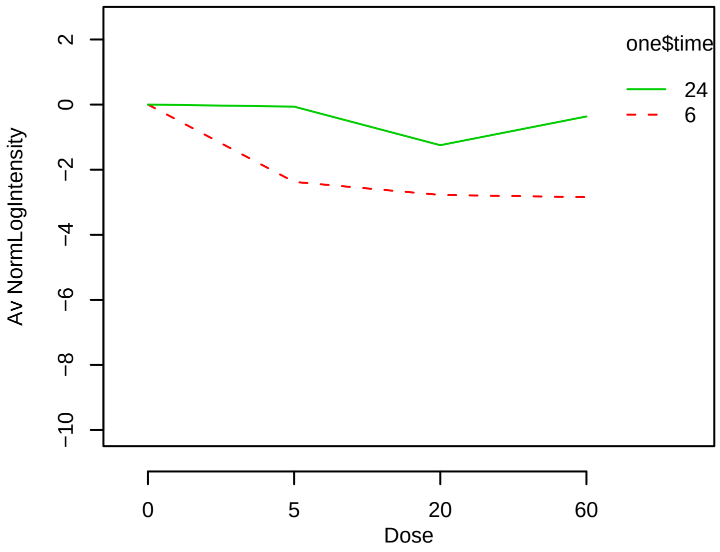
GO_0007276 : gametogenesis



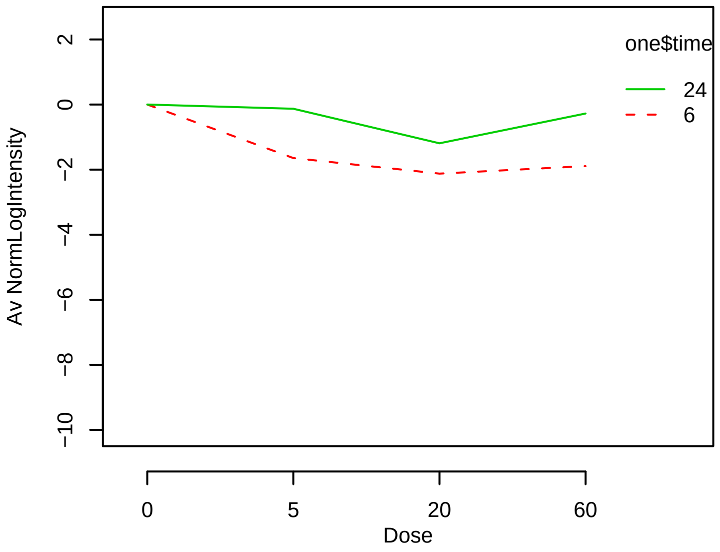
GO_0007281 : germ cell development

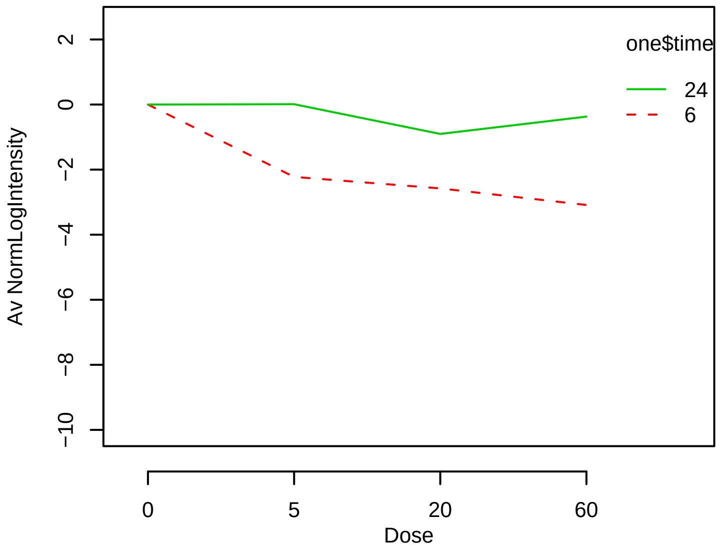


GO_0007283 : spermatogenesis

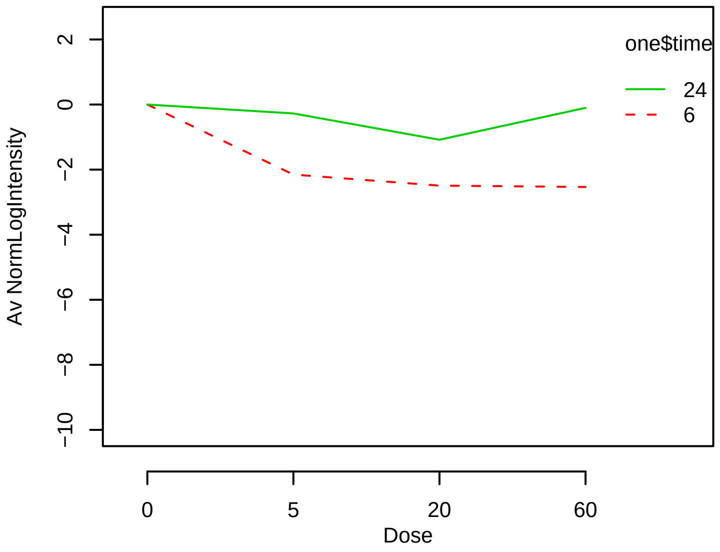


GO_0007286 : spermatid development

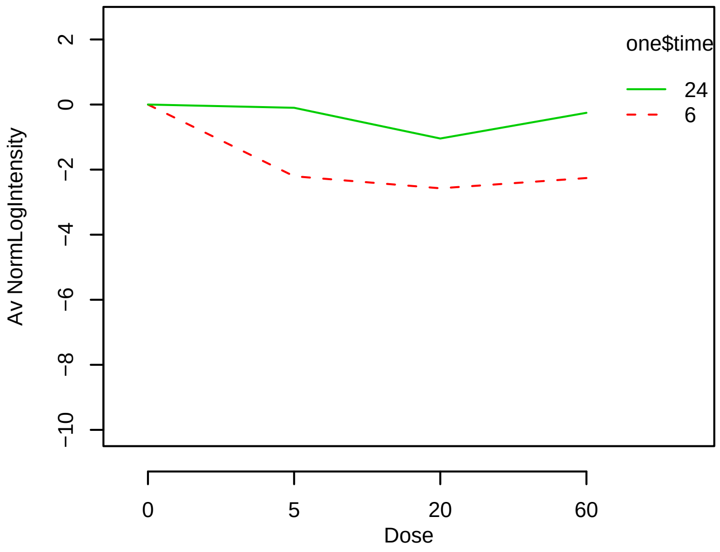




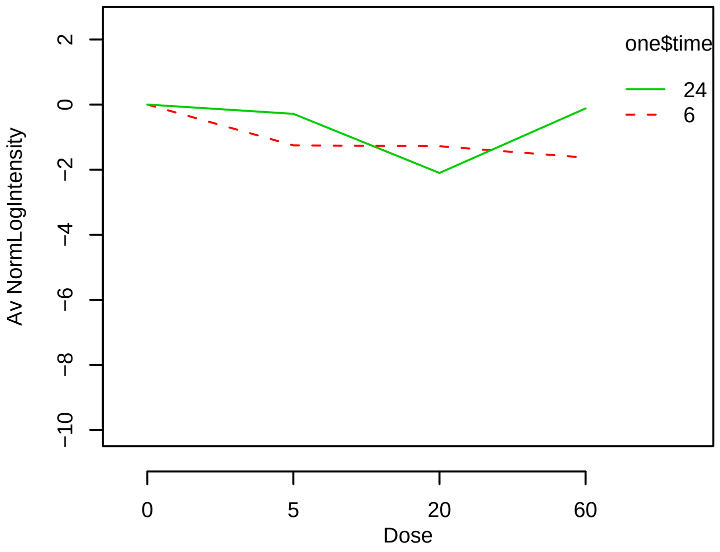
GO_0007292 : female gamete generation



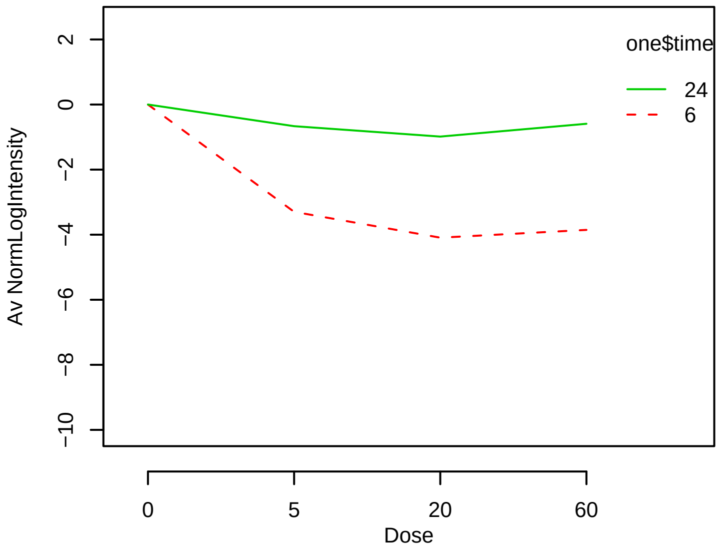
GO_0007338 : fertilization (sensu Metazoa)



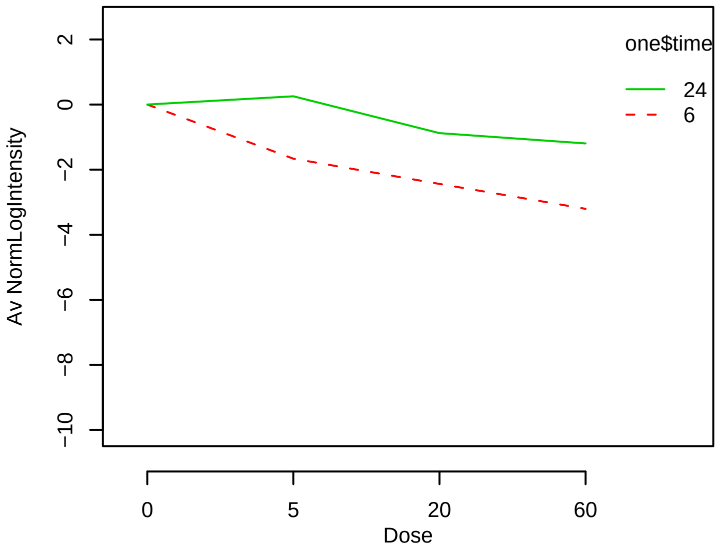
GO_0007339 : binding of sperm to zona pellucida



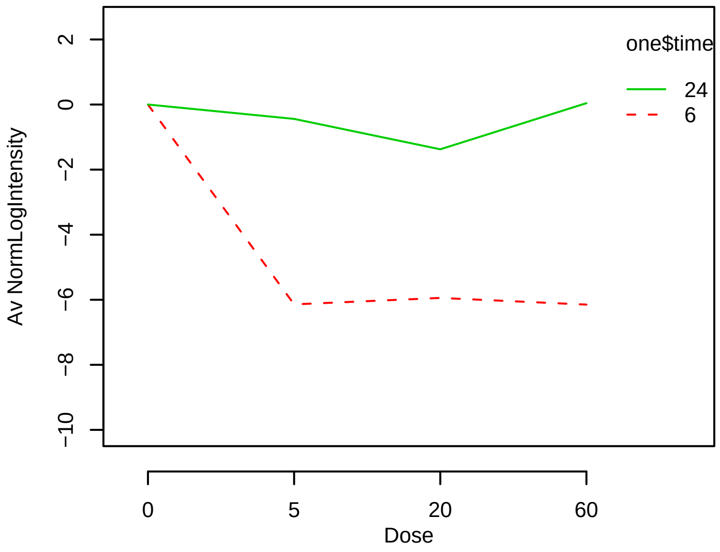
GO_0007340 : acrosome reaction



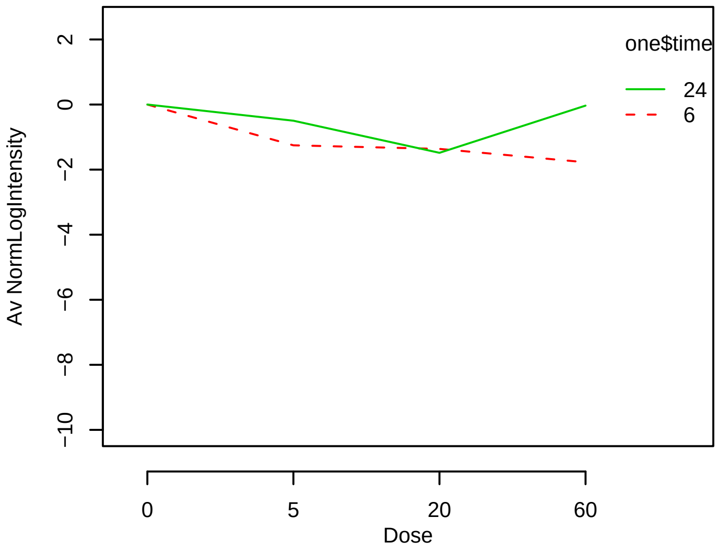
GO_0007342 : fusion of sperm to egg plasma membrane



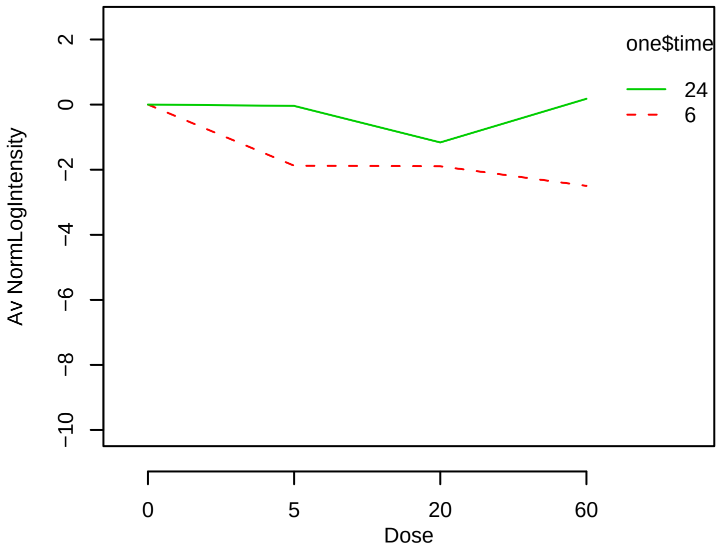
GO_0007346 : regulation of progression through mitotic cell



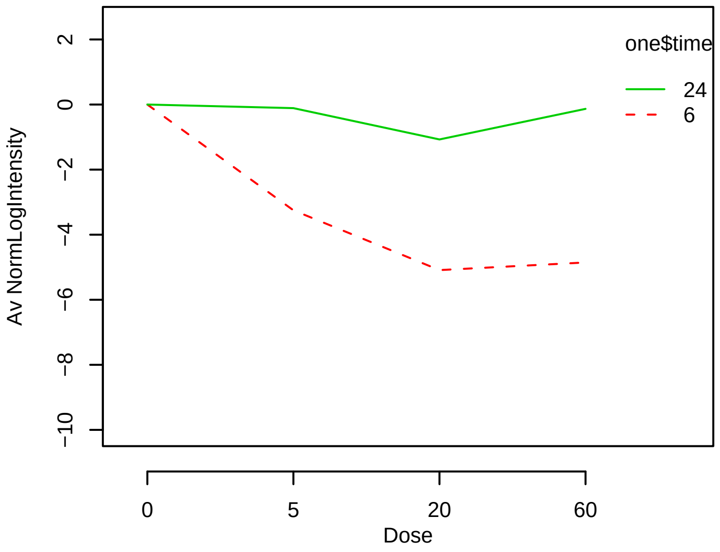
GO_0007350 : blastoderm segmentation



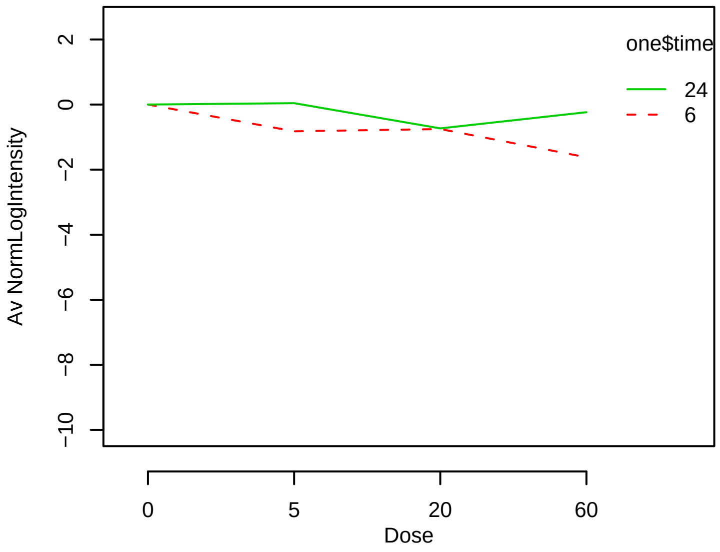
GO_0007351 : regional subdivision



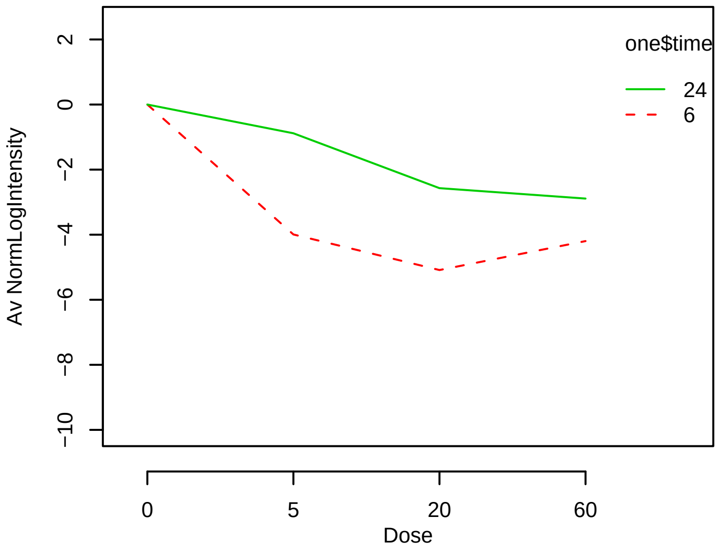
GO_0007368 : determination of left/right symmetry



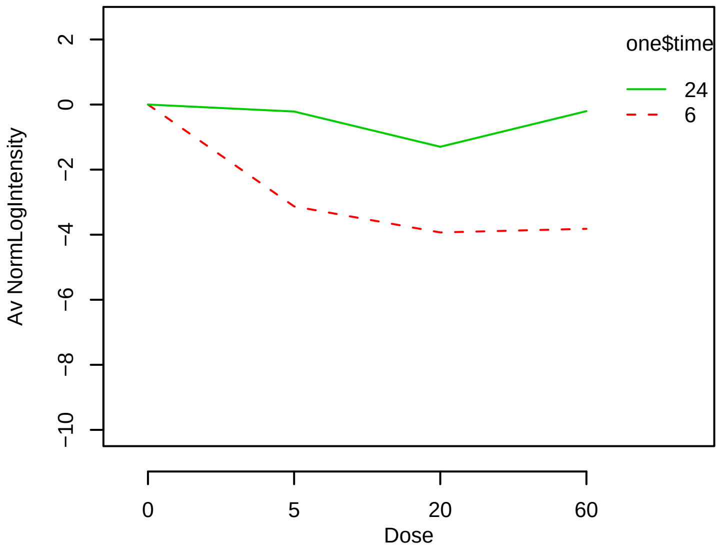
GO_0007369 : gastrulation



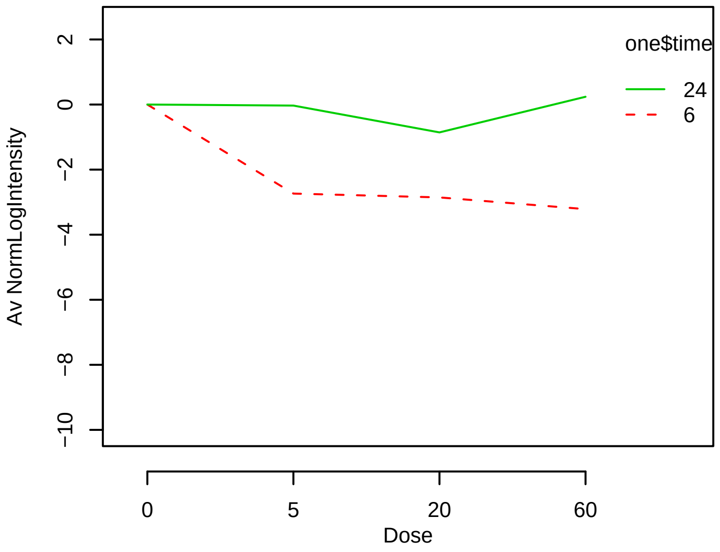
GO_0007379 : segment specification



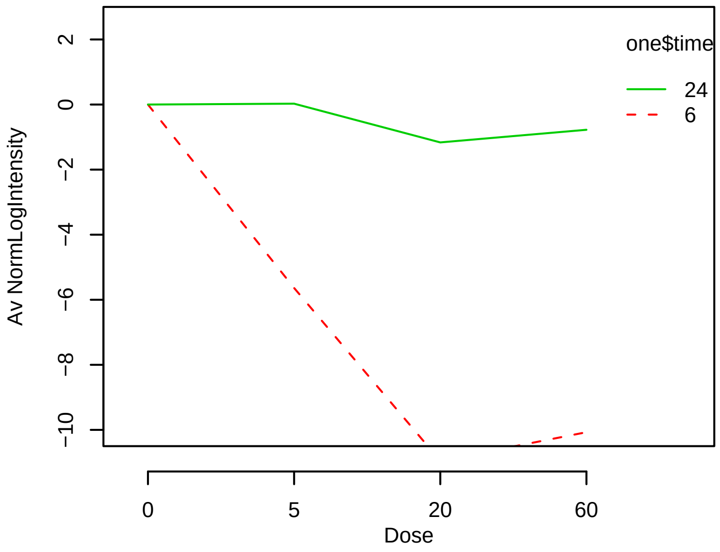
GO_0007386 : compartment specification



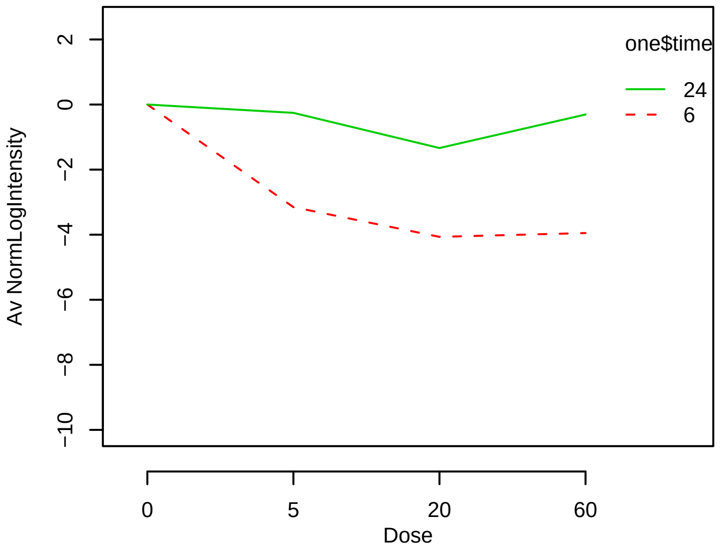
GO_0007389 : pattern specification



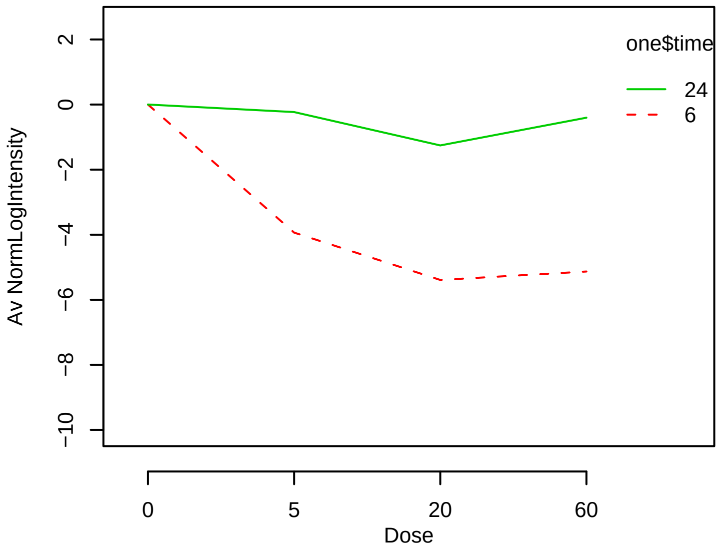
GO_0007398 : ectoderm development



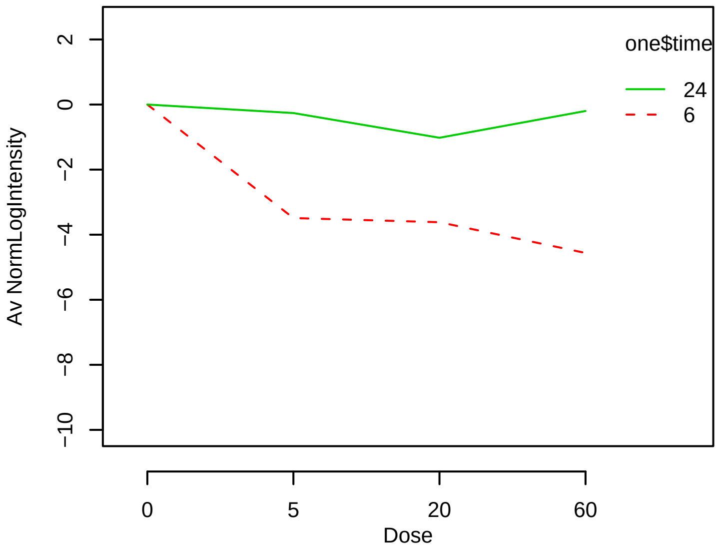
GO_0007405 : neuroblast proliferation



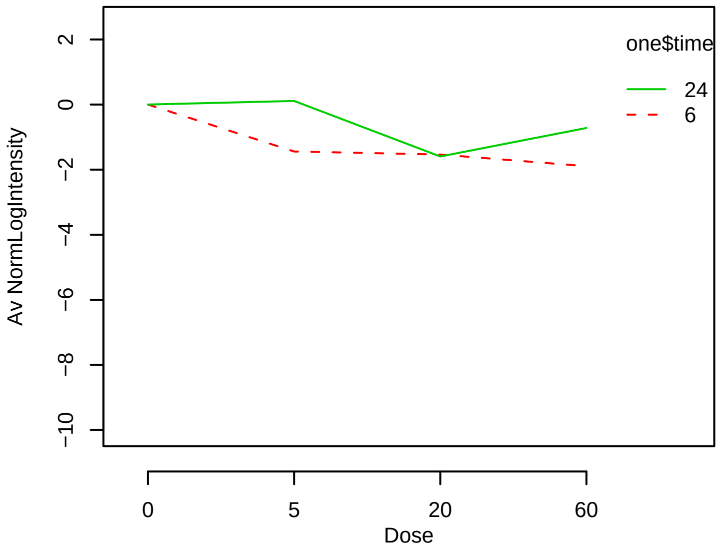
GO_0007409 : axonogenesis



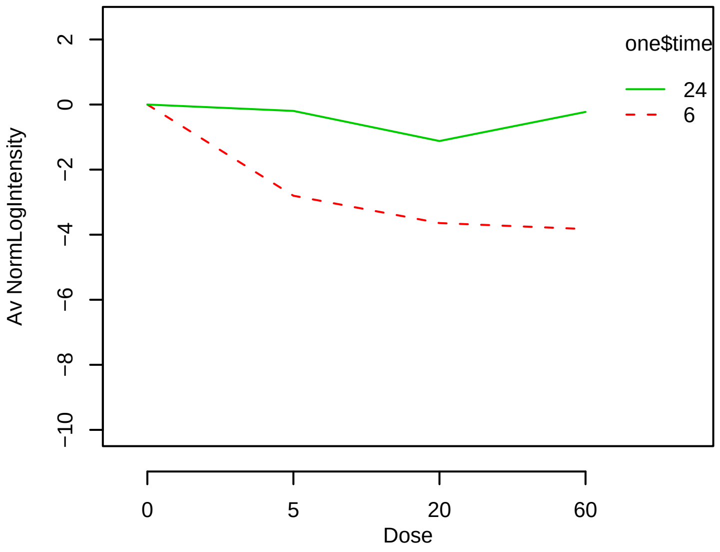
GO_0007411 : axon guidance



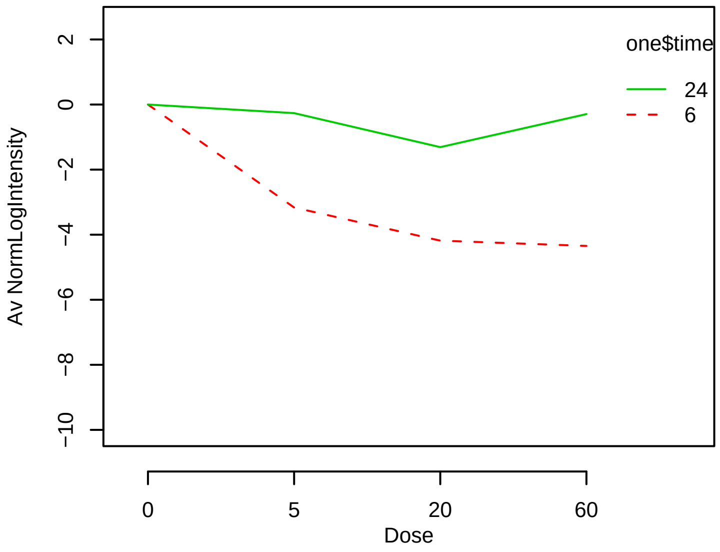
GO_0007413 : axonal fasciculation



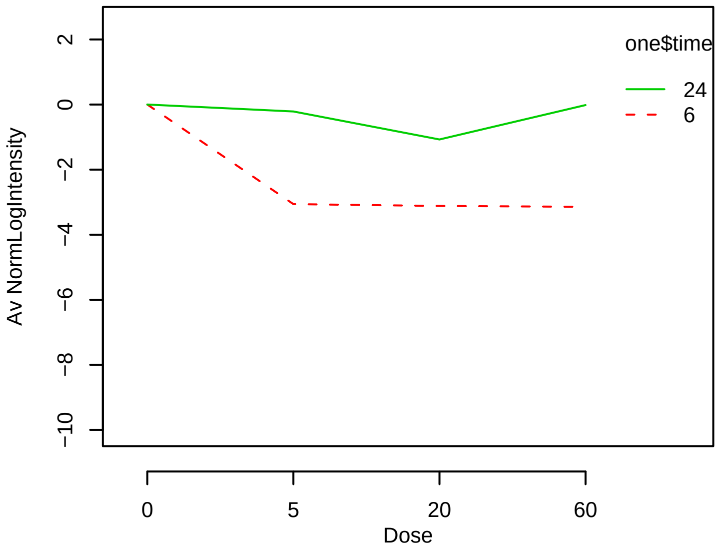
GO_0007416 : synaptogenesis



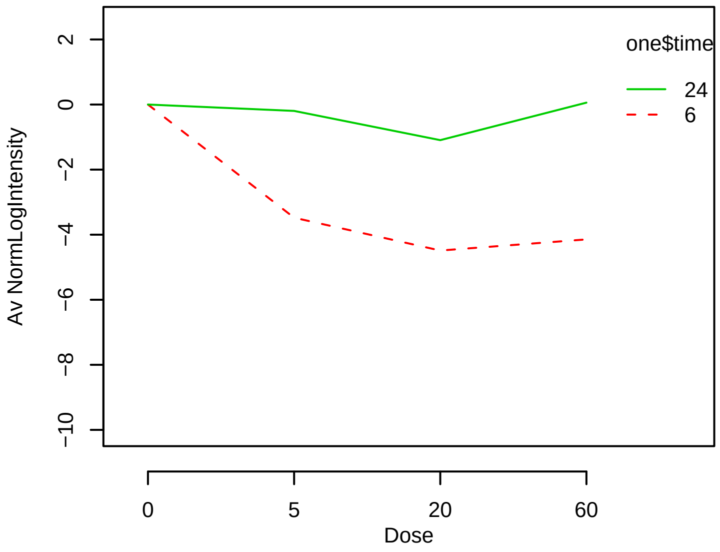
GO_0007417 : central nervous system development



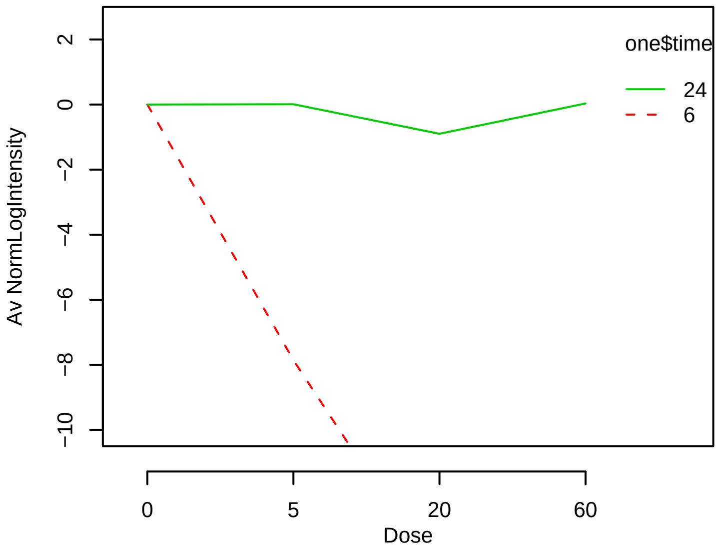
GO_0007420 : brain development



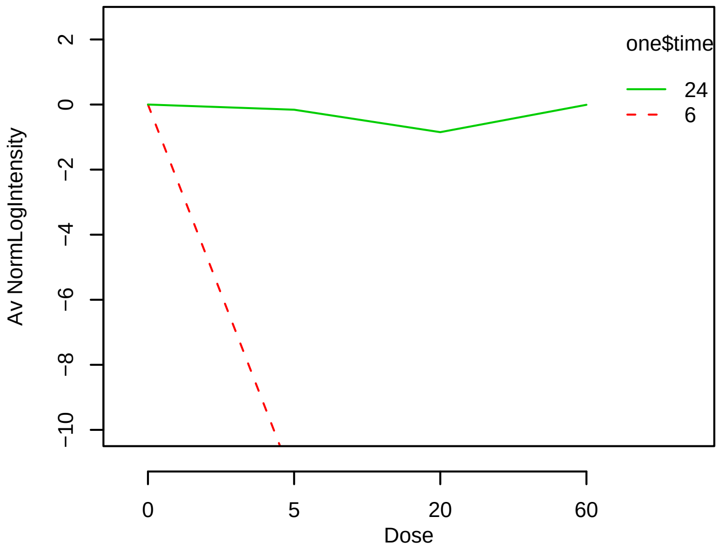
GO_0007422 : peripheral nervous system development



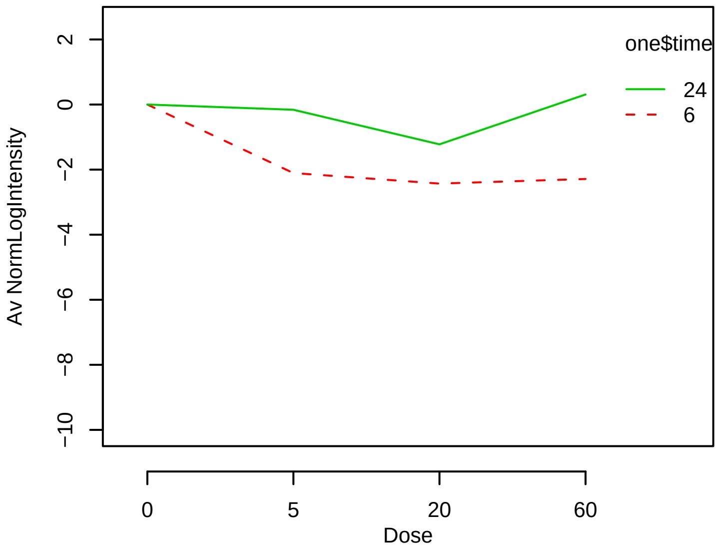
GO_0007423 : sensory organ development



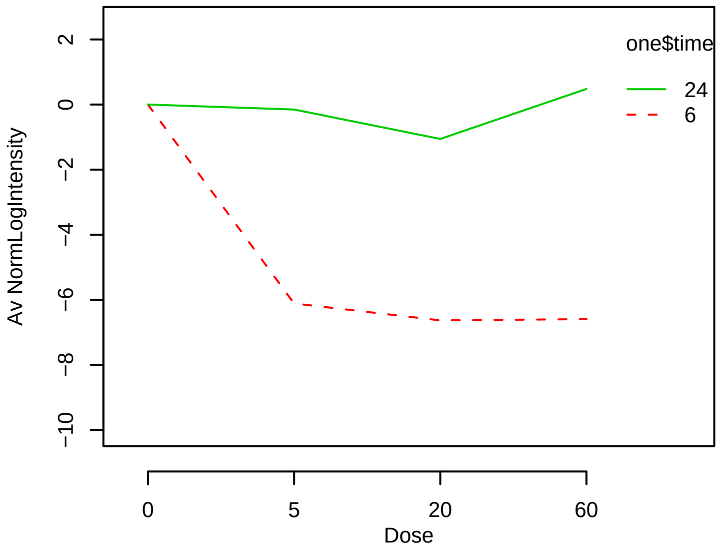
GO_0007431 : salivary gland development



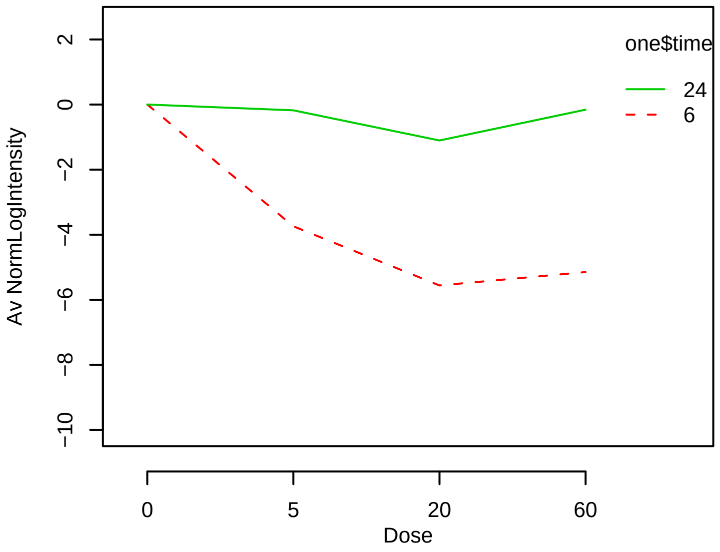
GO_0007435 : salivary gland morphogenesis



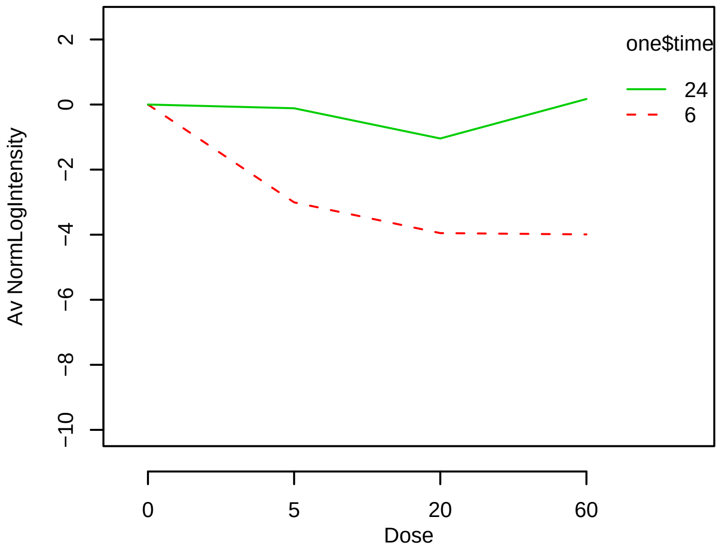
GO_0007439 : ectodermal gut development



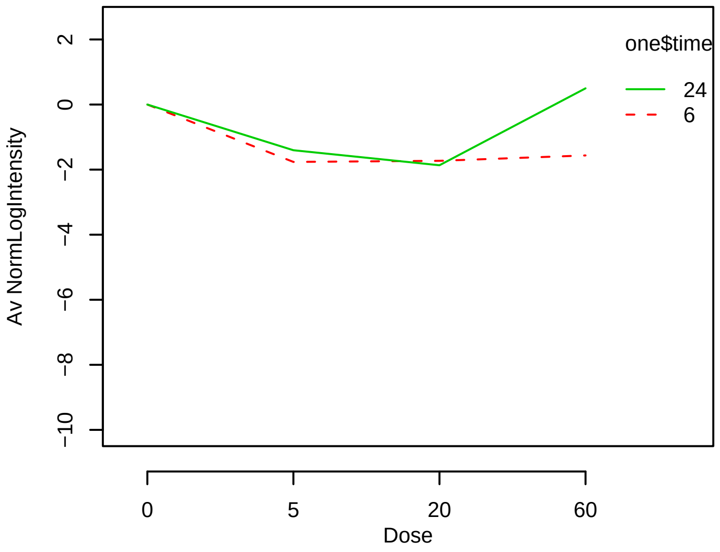
GO_0007492 : endoderm development



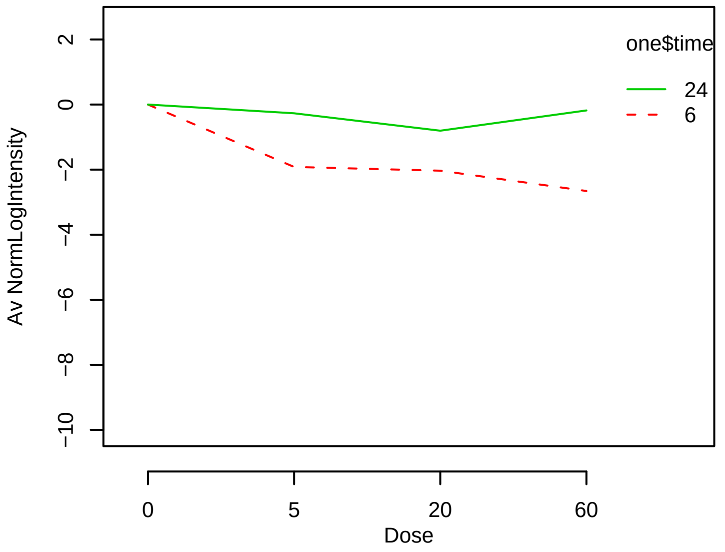
GO_0007498 : mesoderm development

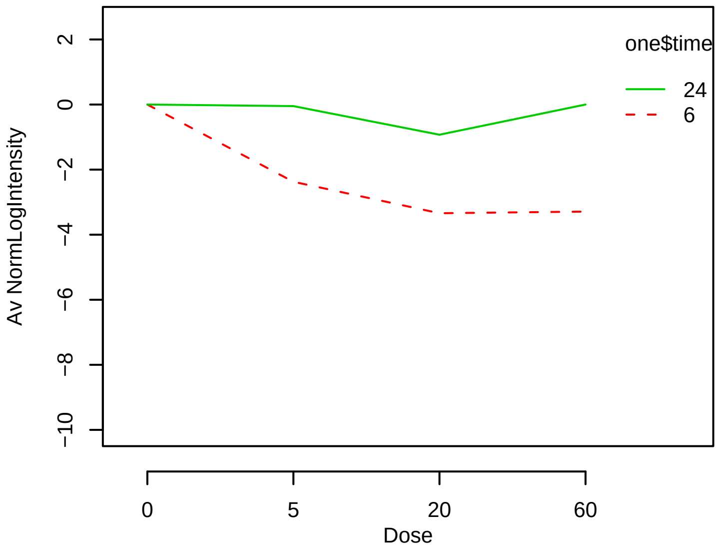


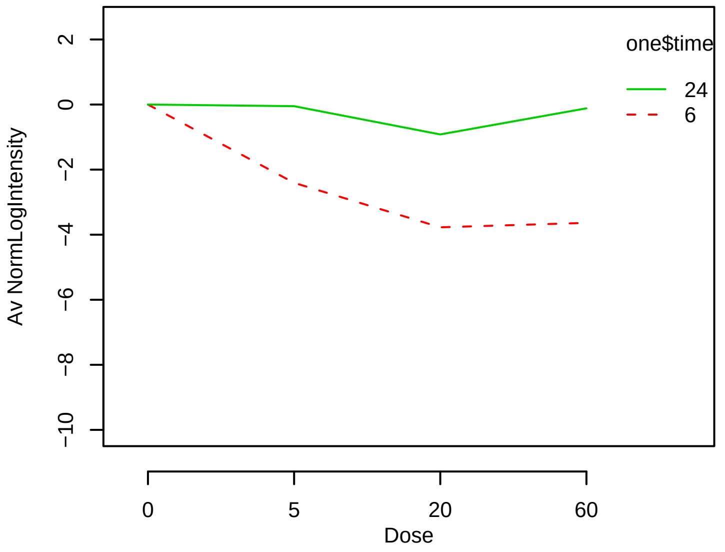
GO_0007507 : heart development

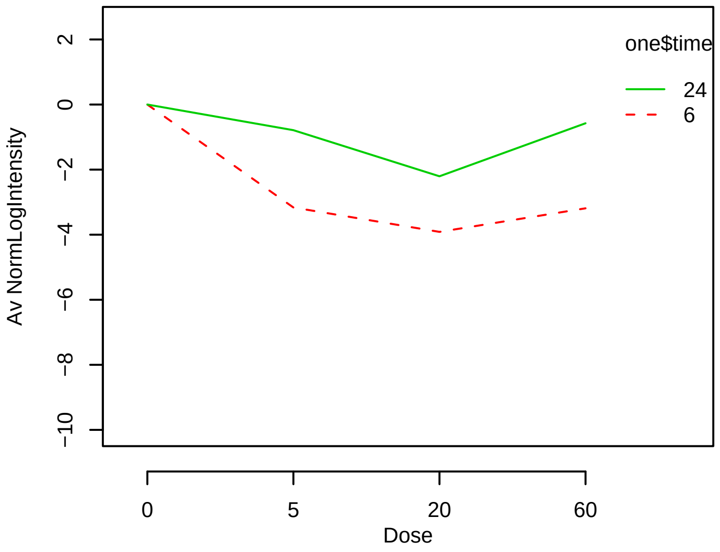


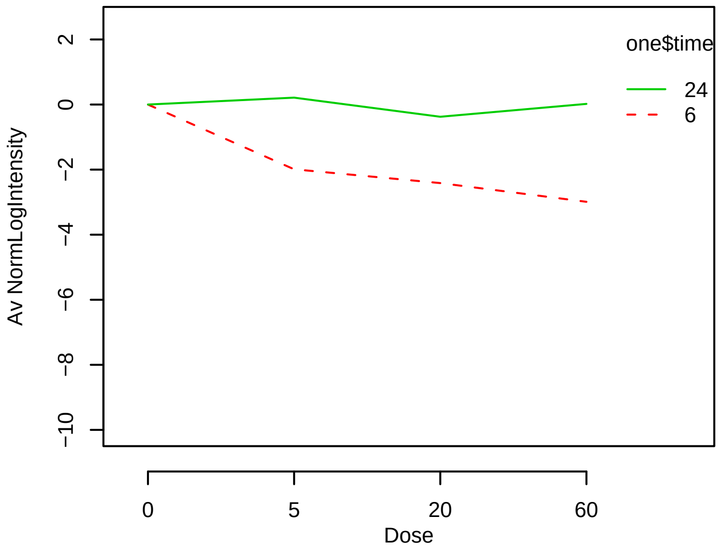
GO_0007512 : adult heart development

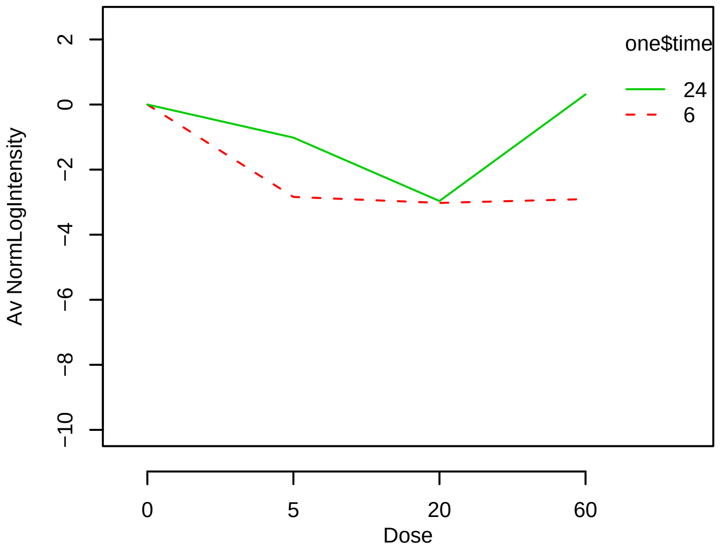

GO_0007516 : hemocyte development (sensu Arthropoda

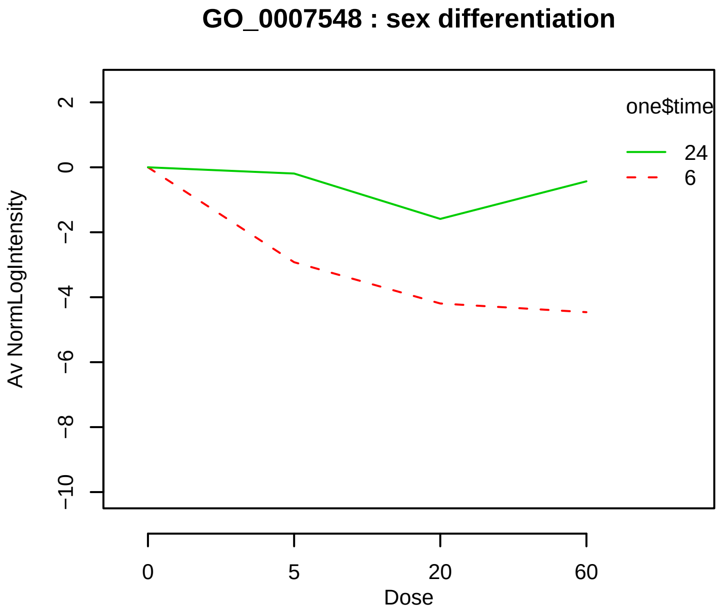

GO_0007517 : muscle development

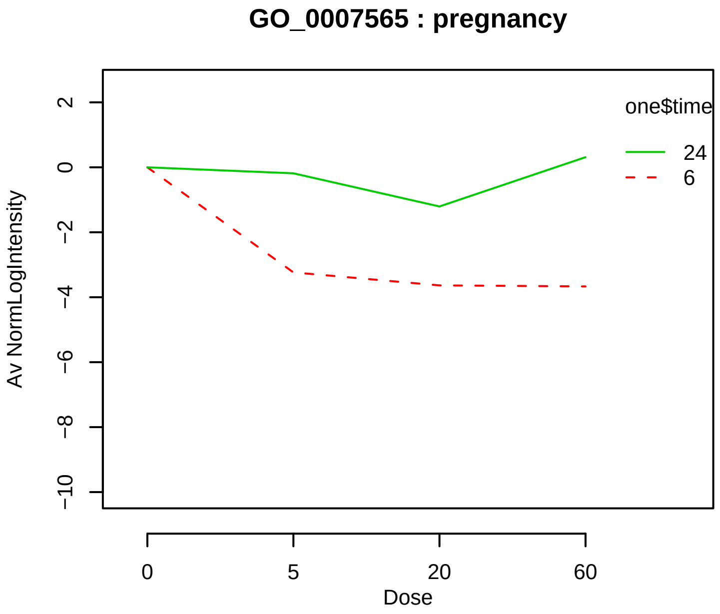

GO_0007519 : striated muscle development

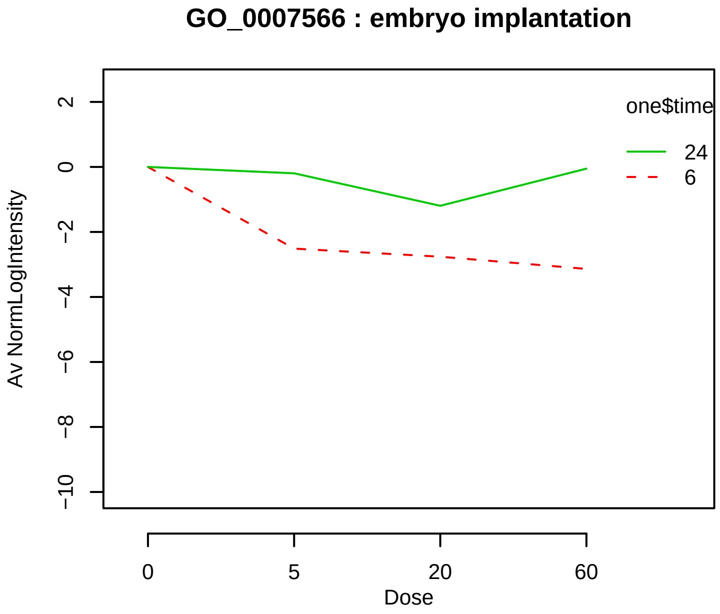

GO_0007520 : myoblast fusion

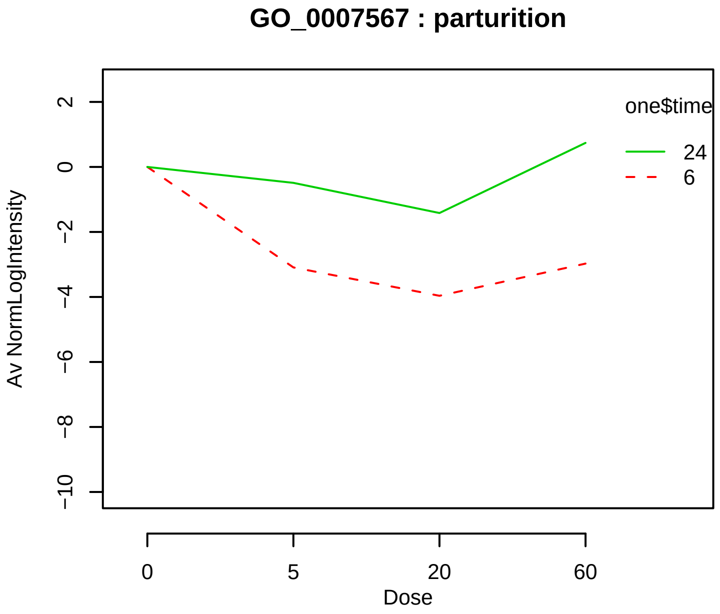

GO_0007528 : neuromuscular junction development

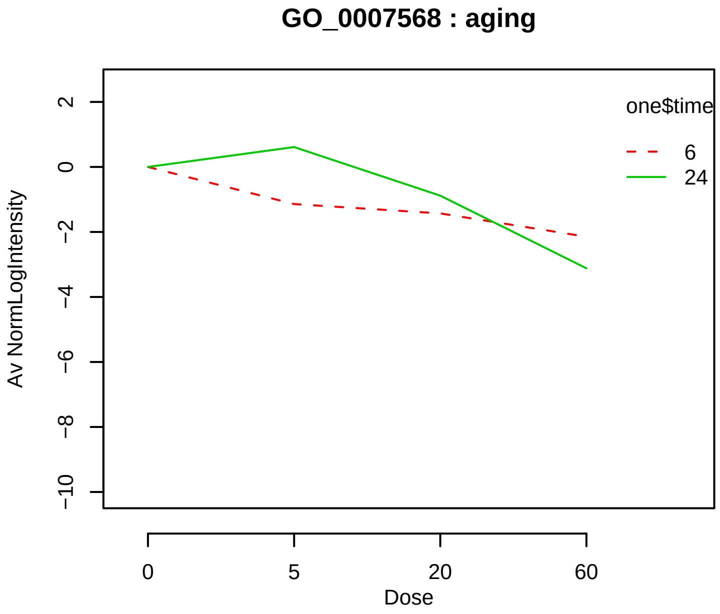

GO_0007530 : sex determination

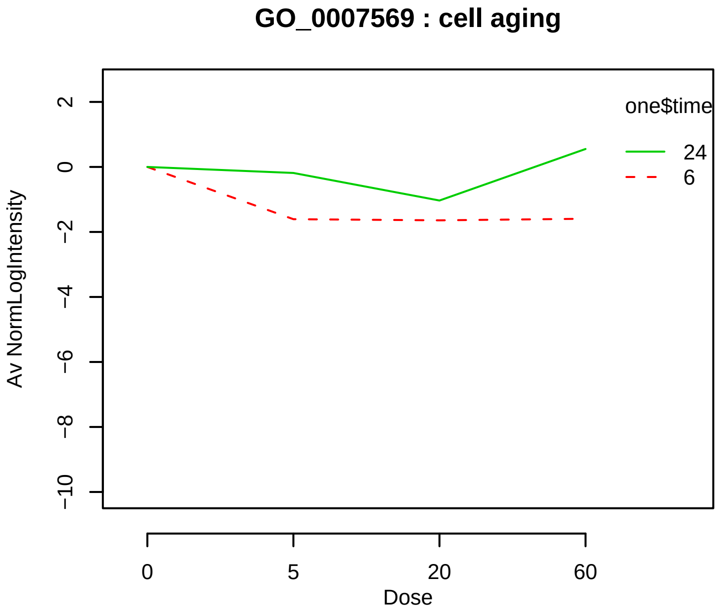

GO_0007548 : sex differentiation

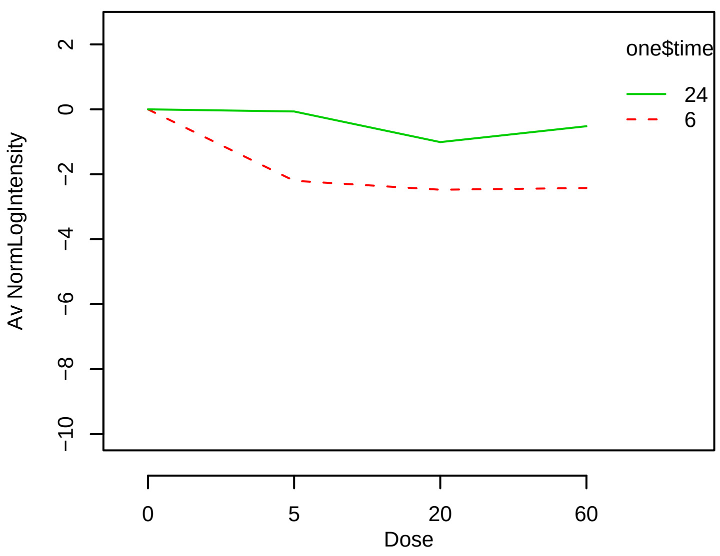

GO_0007565 : pregnancy


GO_0007566 : embryo implantation

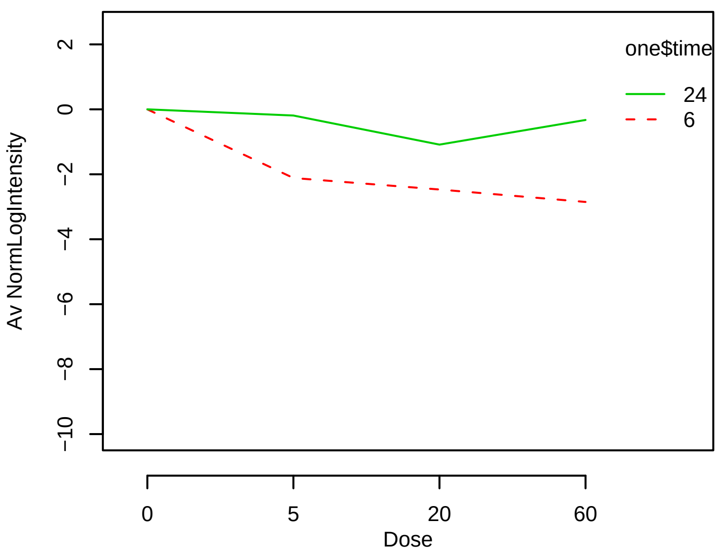

GO_0007567 : parturition


GO_0007568 : aging

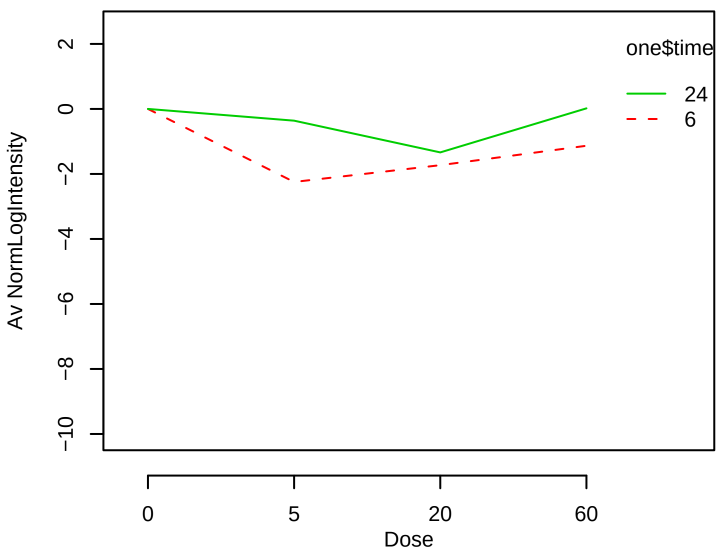

GO_0007569 : cell aging



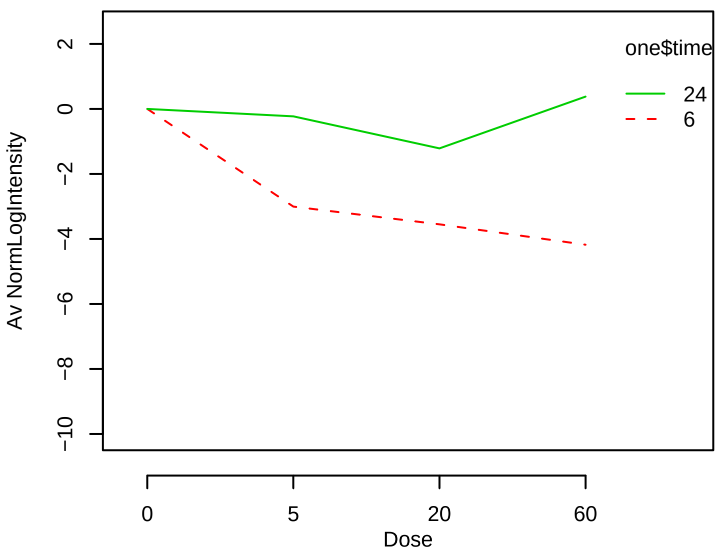
GO_0007584 : response to nutrient



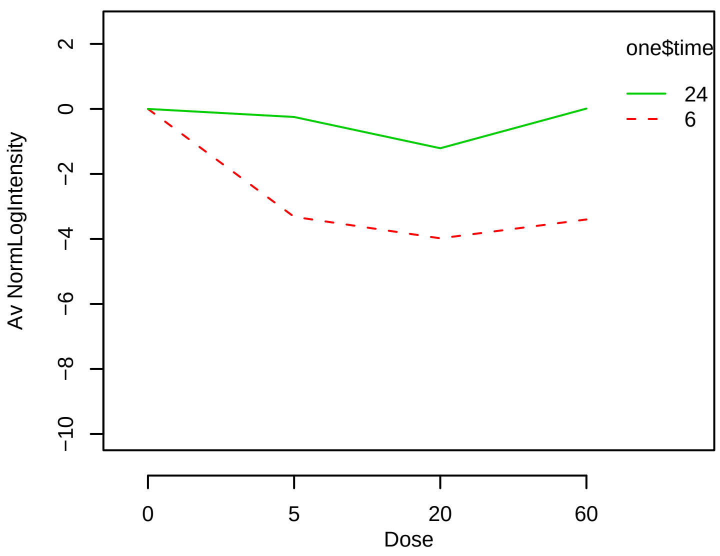
GO_0007585 : respiratory gaseous exchange



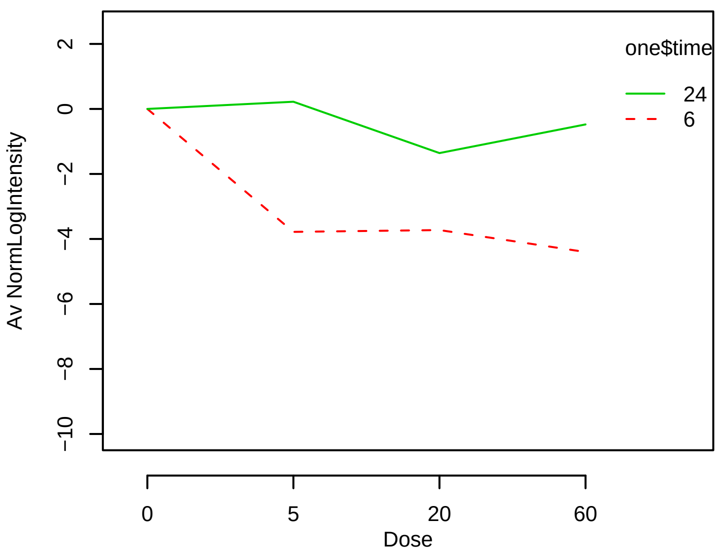
GO_0007586 : digestion



GO_0007588 : excretion

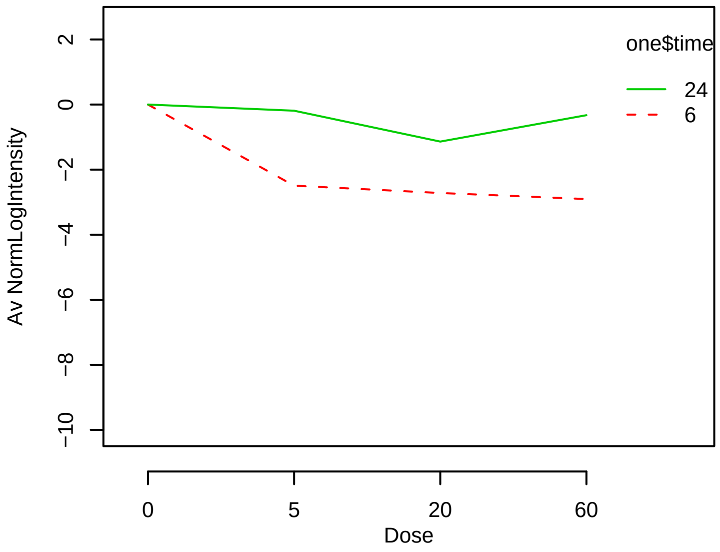


GO_0007589 : fluid secretion

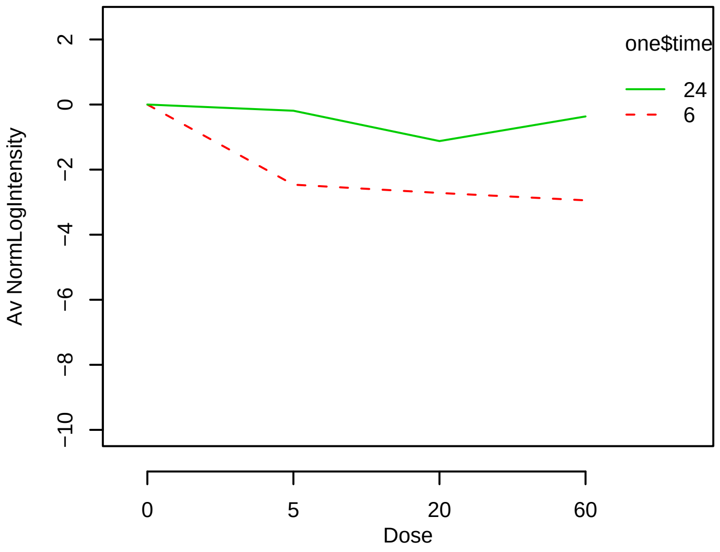


GO_0007595 : lactation

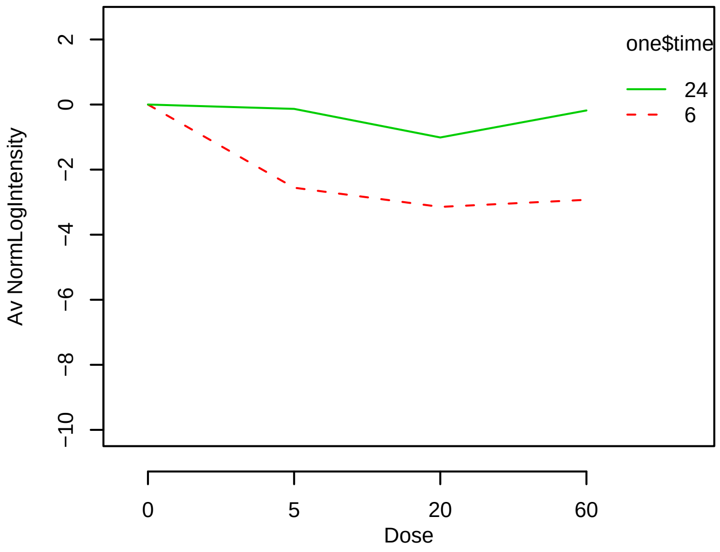
GO_0007596 : blood coagulation



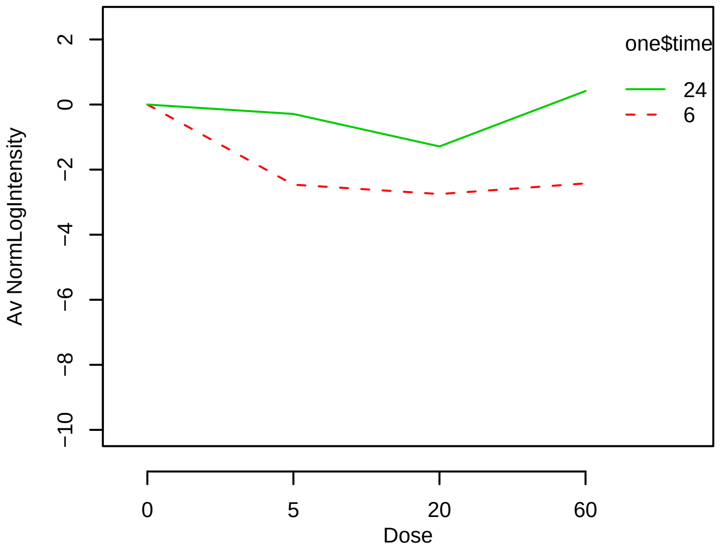
GO_0007599 : hemostasis



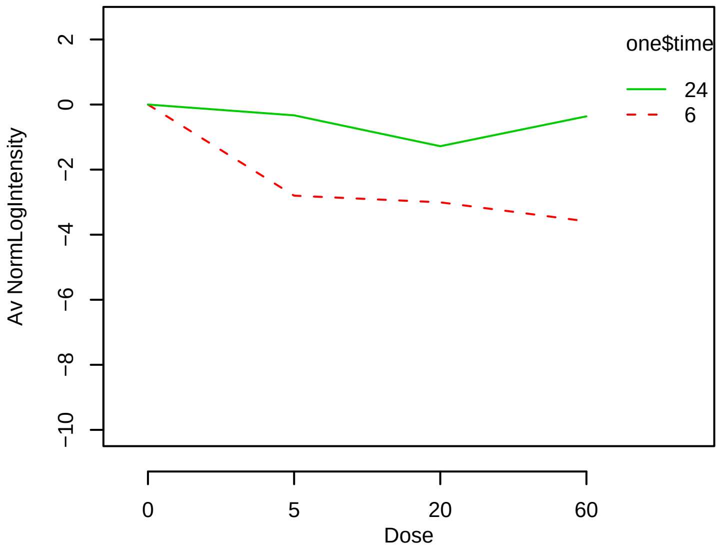
GO_0007601 : visual perception



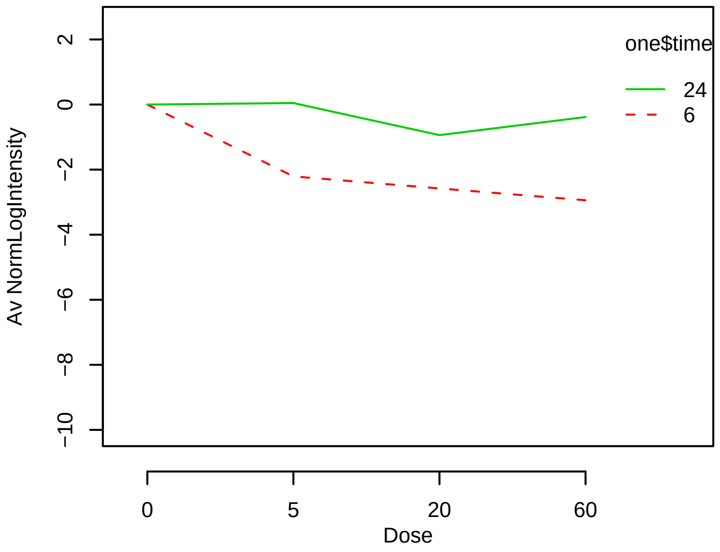
GO_0007602 : phototransduction

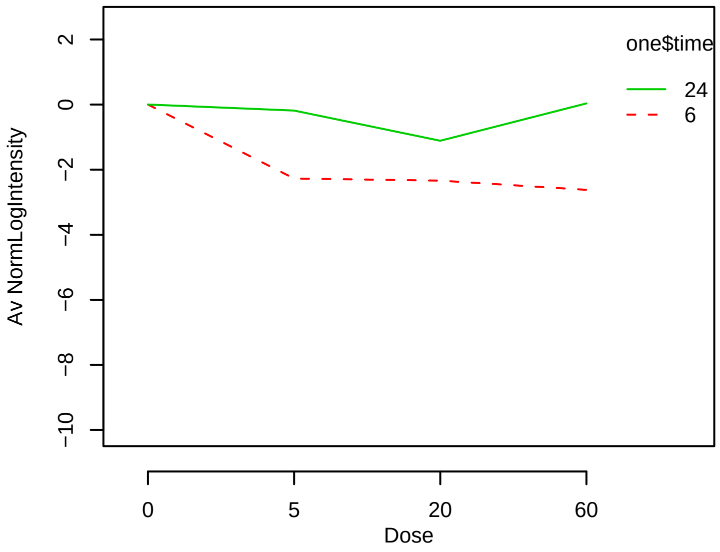


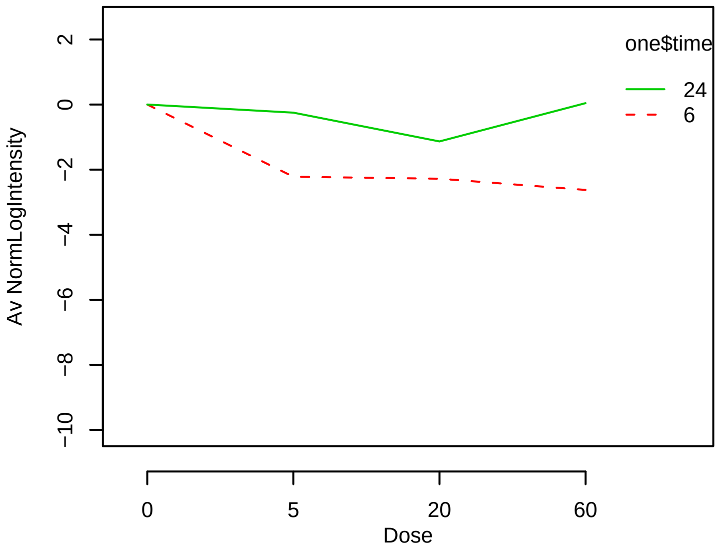
GO_0007603 : phototransduction\, visible light

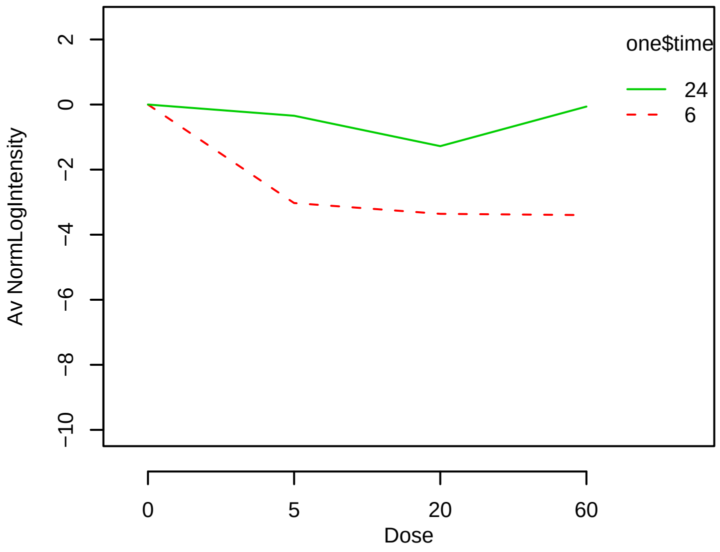


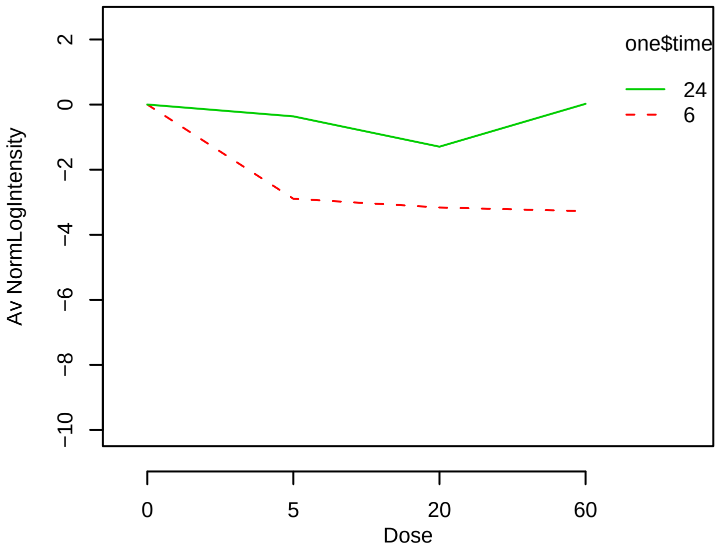
GO_0007605 : sensory perception of sound

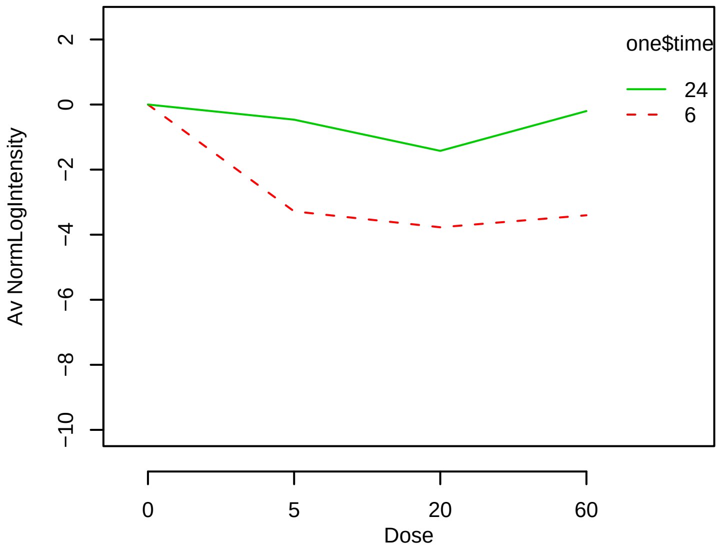


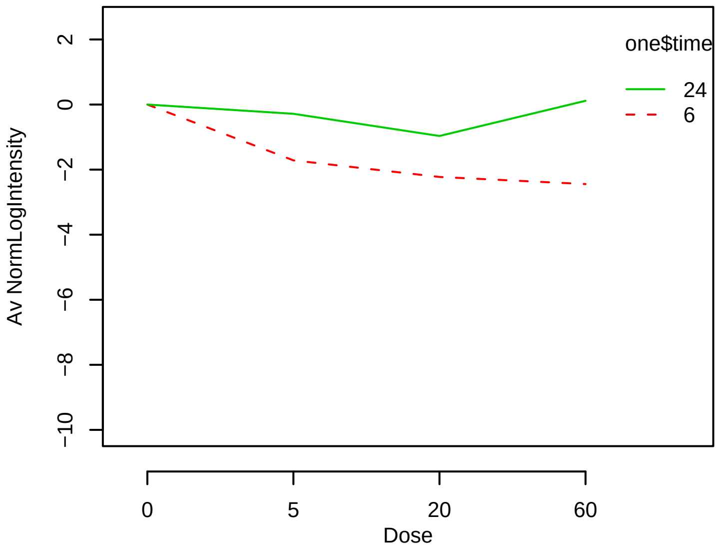

GO_0007606 : sensory perception of chemical stimulus


GO_0007608 : sensory perception of smell

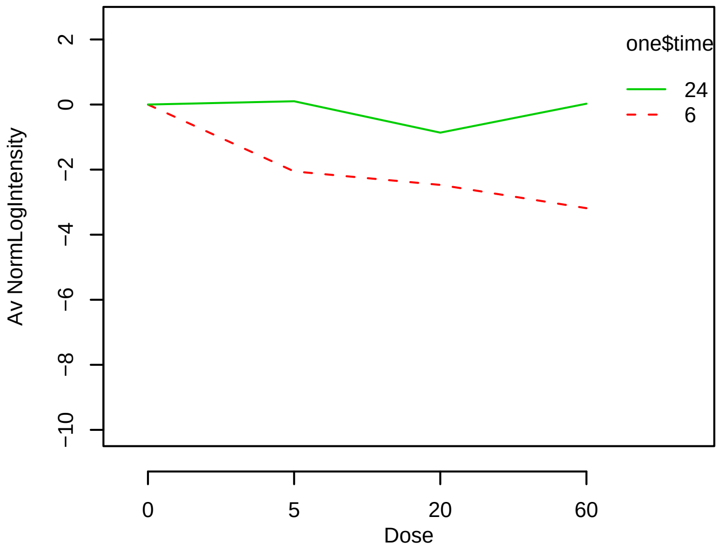

GO_0007611 : learning and/or memory


GO_0007612 : learning

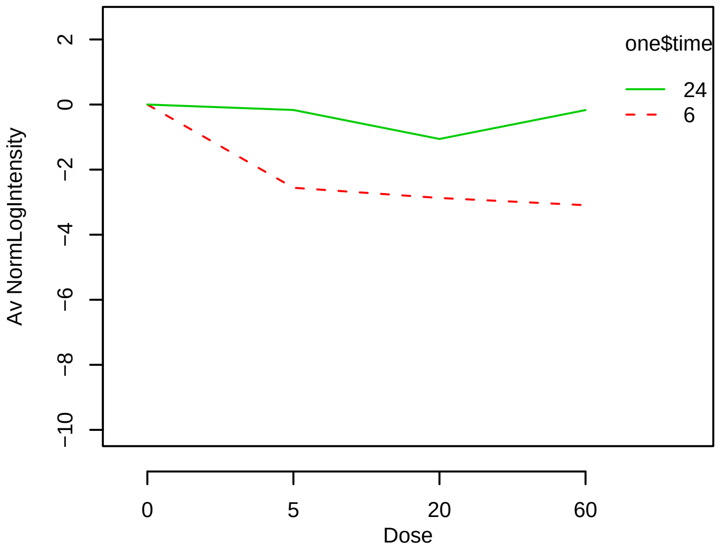

GO_0007613 : memory


GO_0007617 : mating behavior

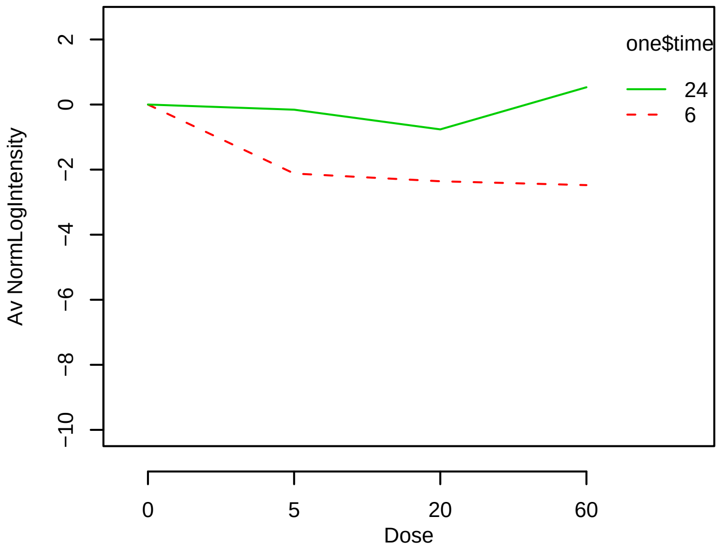
GO_0007623 : circadian rhythm



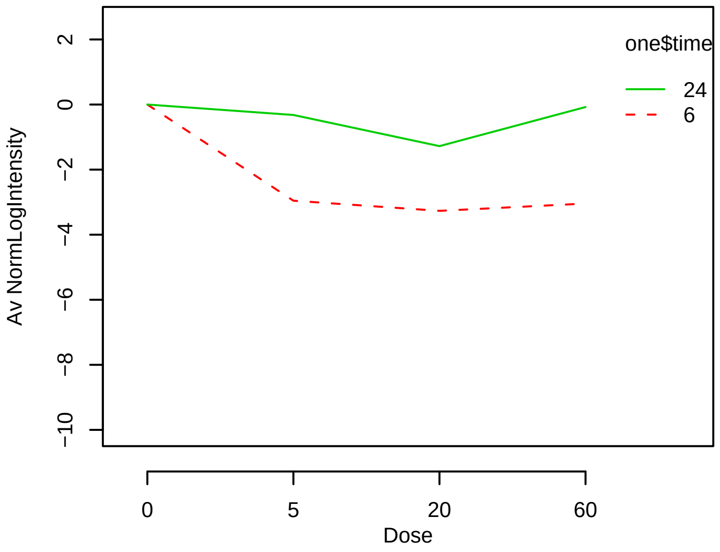
GO_0007626 : locomotory behavior



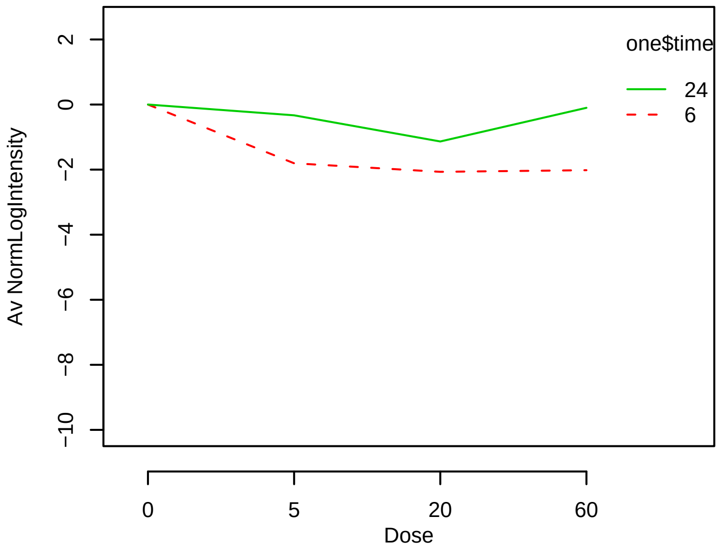
GO_0007628 : adult walking behavior



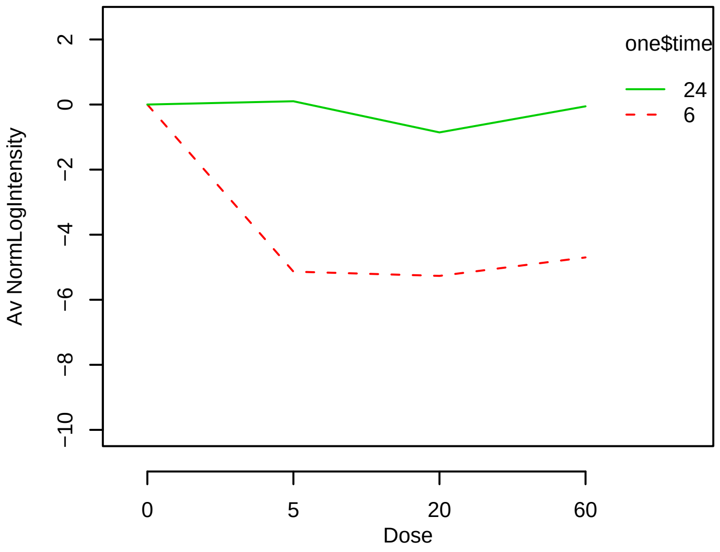
GO_0007631 : feeding behavior

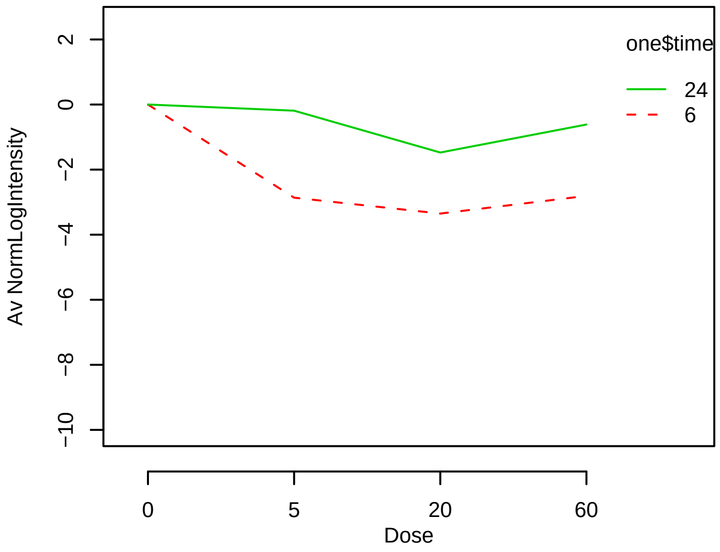


GO_0007632 : visual behavior

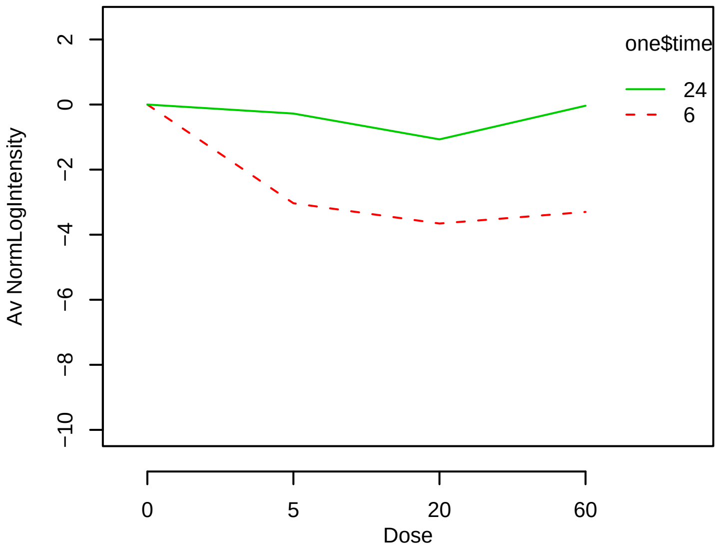


GO_0007635 : chemosensory behavior

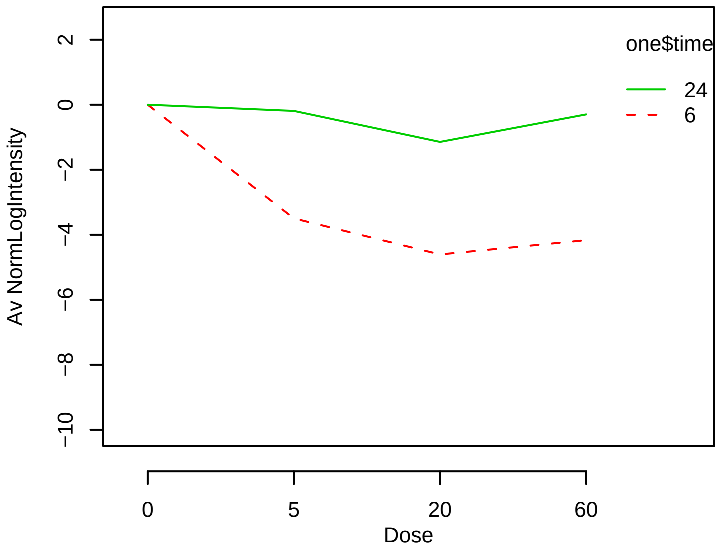




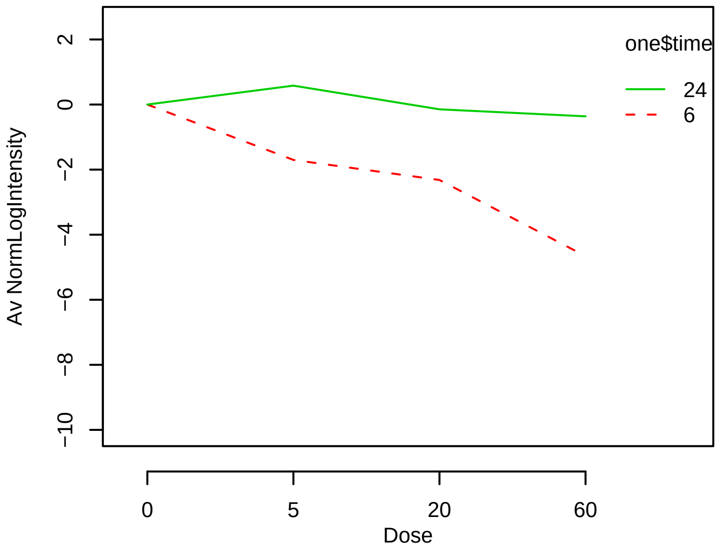
GO_0007638 : mechanosensory behavior



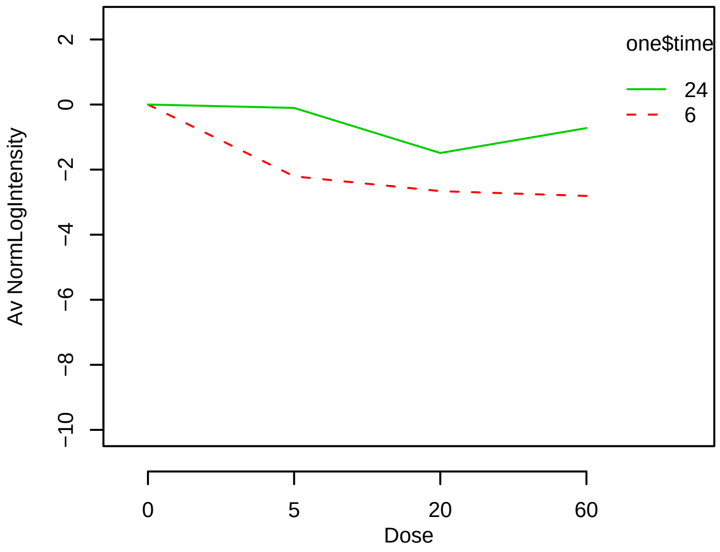
GO_0008015 : circulation



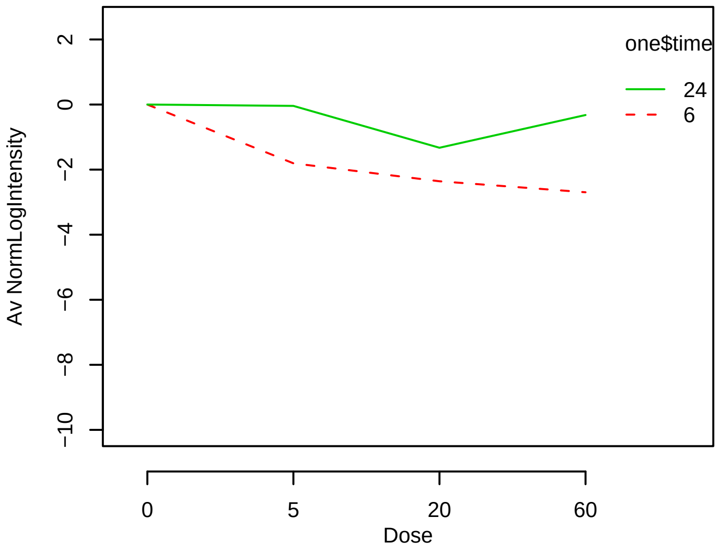
GO_0008016 : regulation of heart contraction



GO_0008033 : tRNA processing

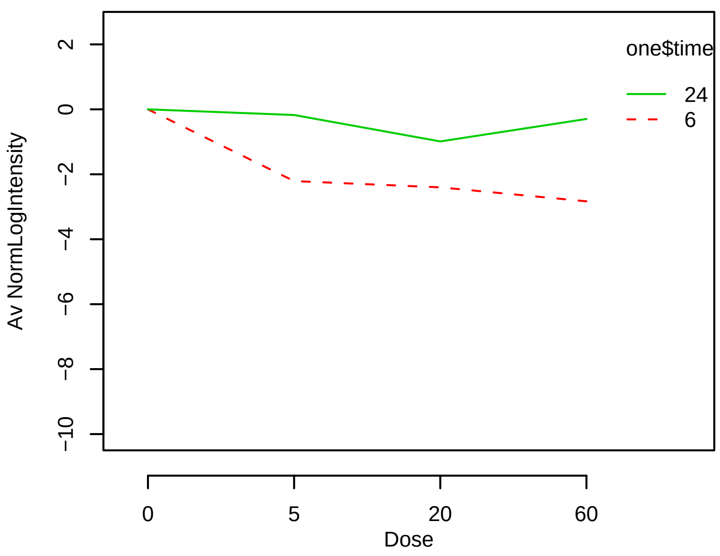


GO_0008037 : cell recognition

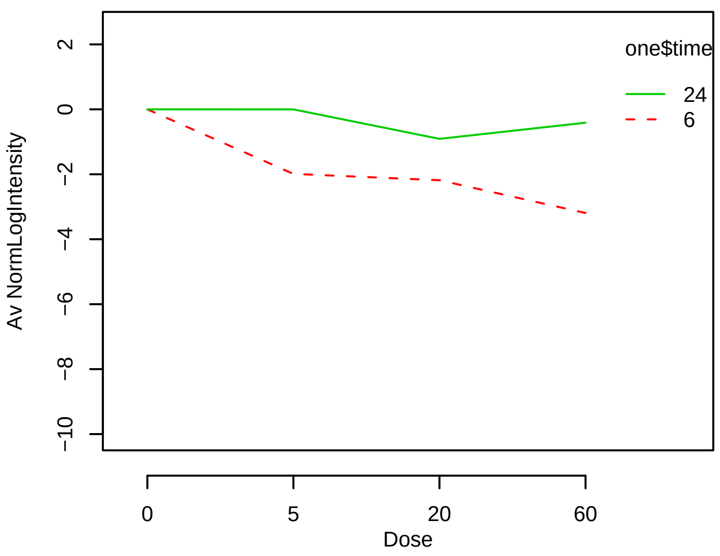


GO_0008038 : neuron recognition

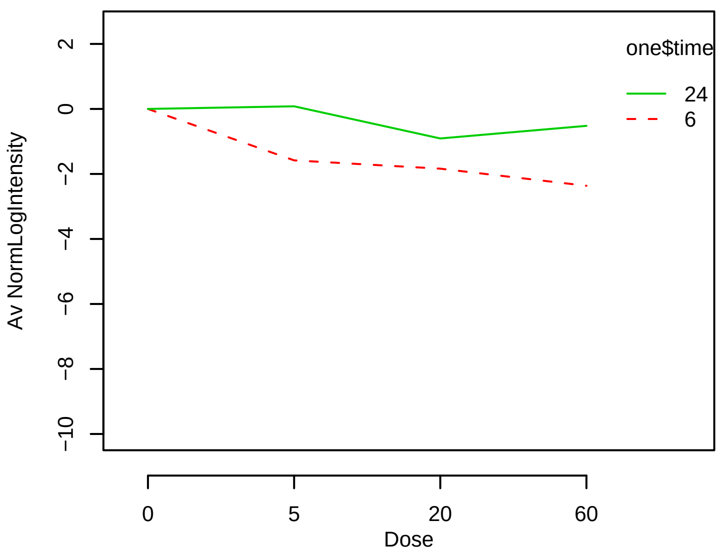
GO_0008045 : motor axon guidance



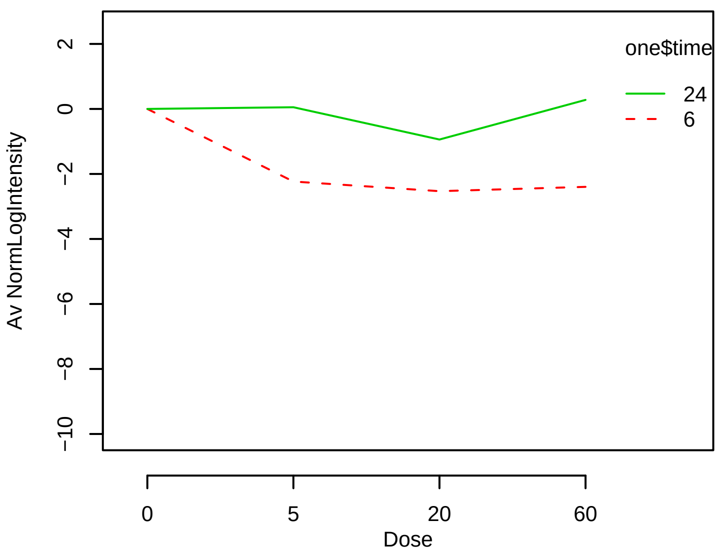
GO_0008064 : regulation of actin polymerization and/or depol



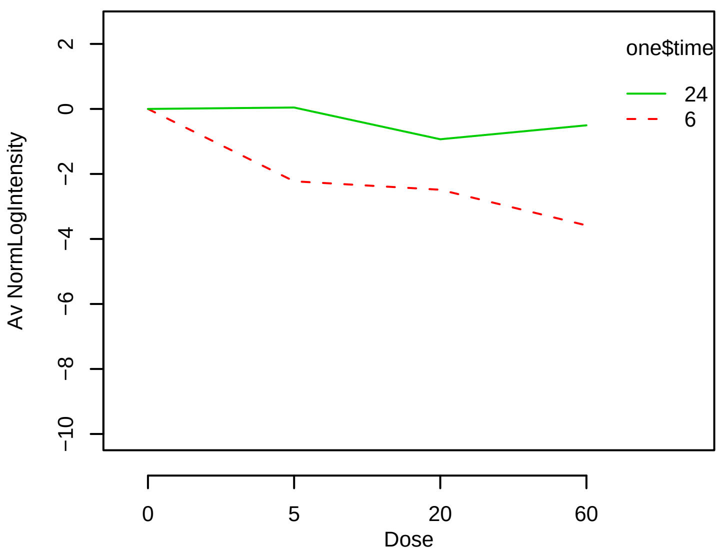
GO_0008088 : axon cargo transport



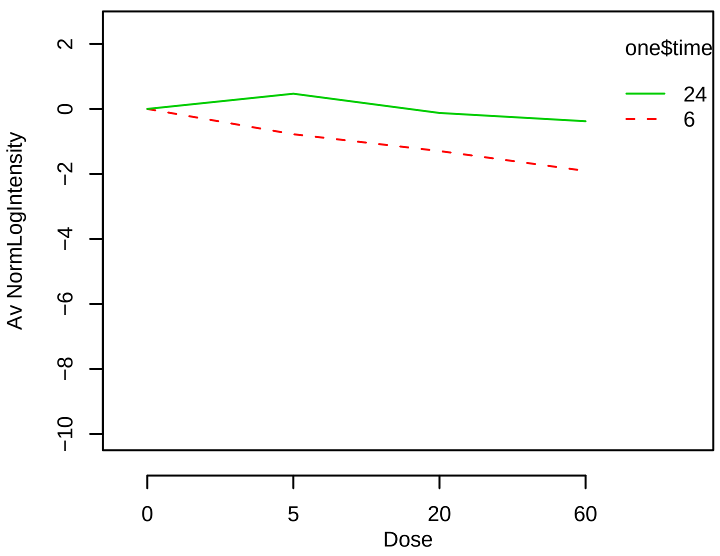
GO_0008105 : asymmetric protein localization

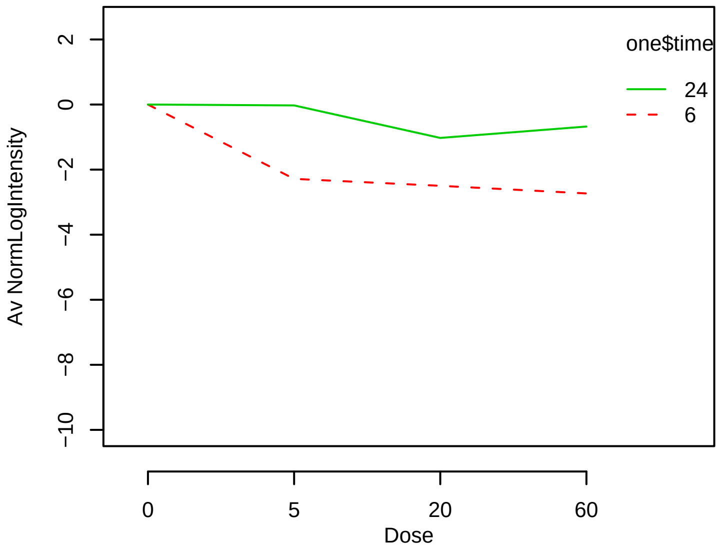


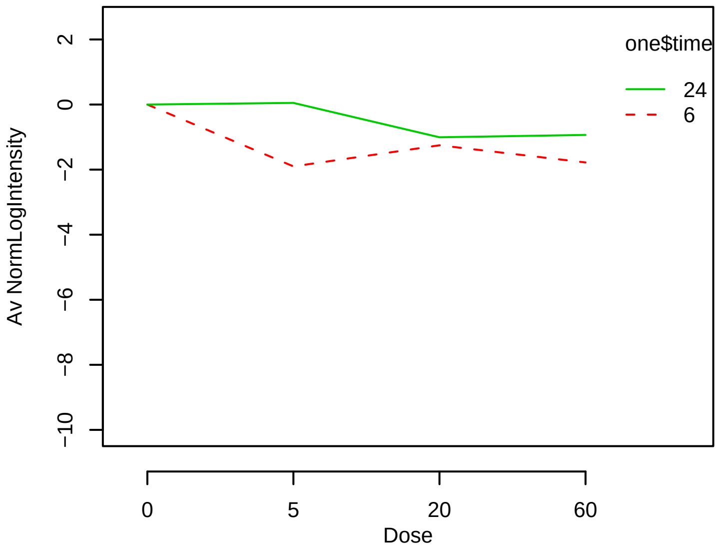
GO_0008154 : actin polymerization and/or depolymerizatio

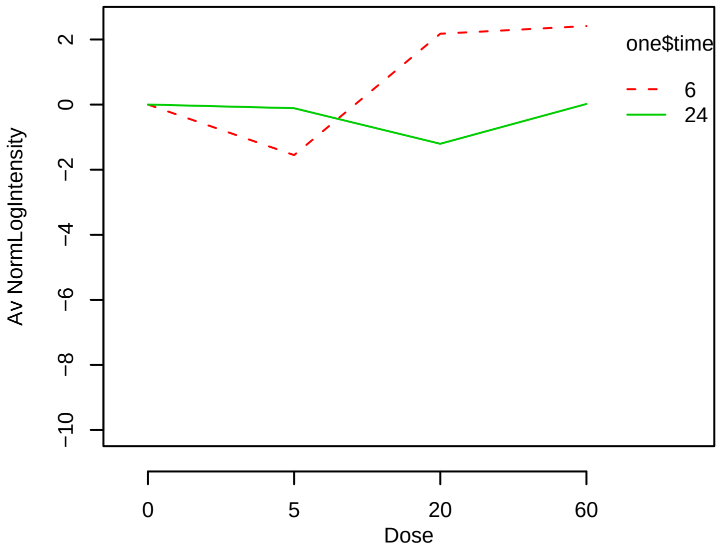


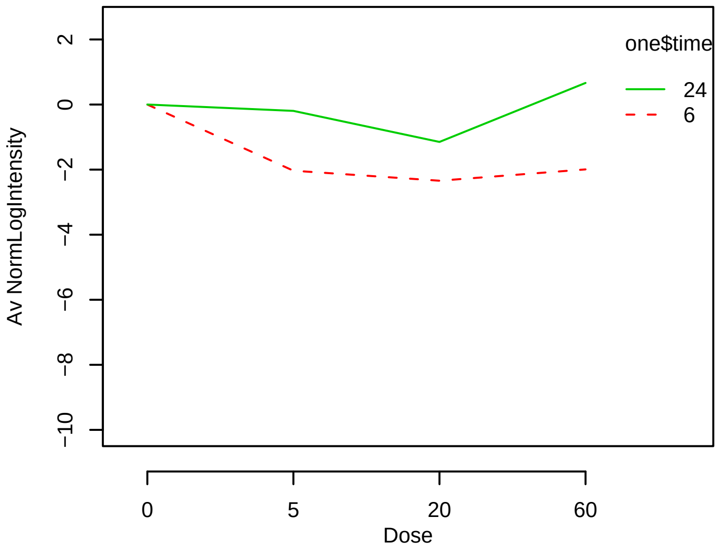
GO_0008156 : negative regulation of DNA replication

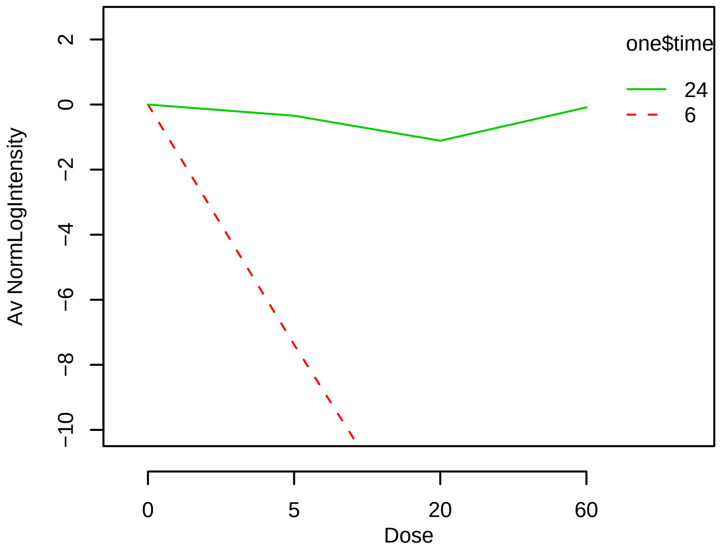


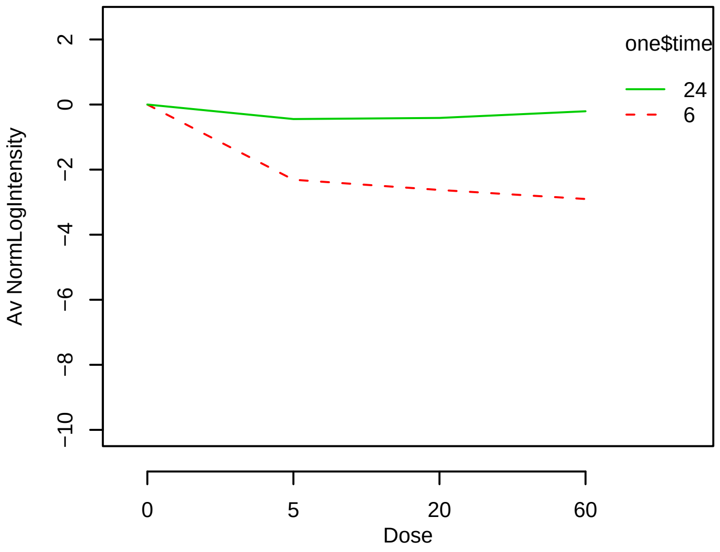

GO_0008202 : steroid metabolism

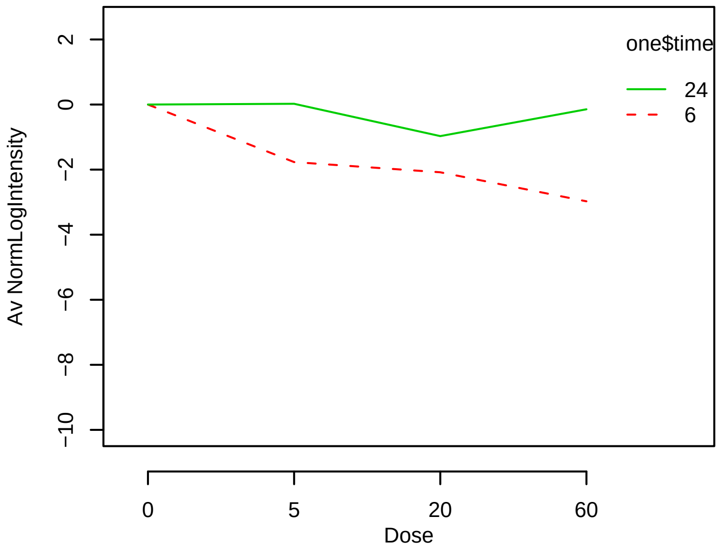

GO_0008203 : cholesterol metabolism

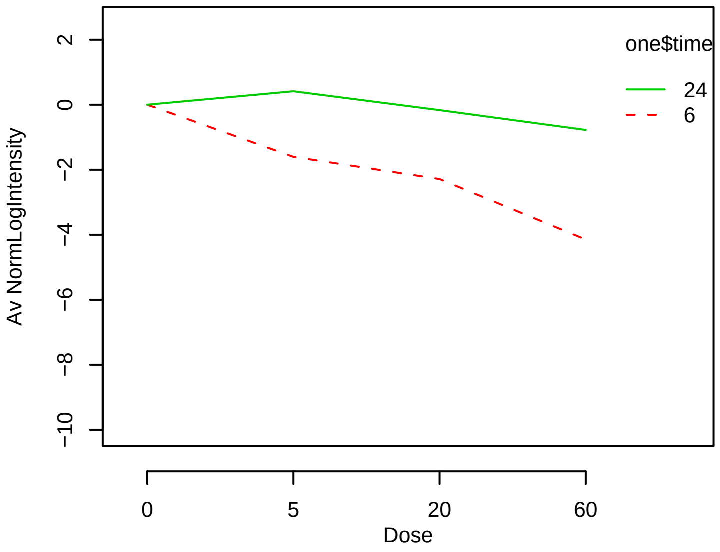

GO_0008206 : bile acid metabolism

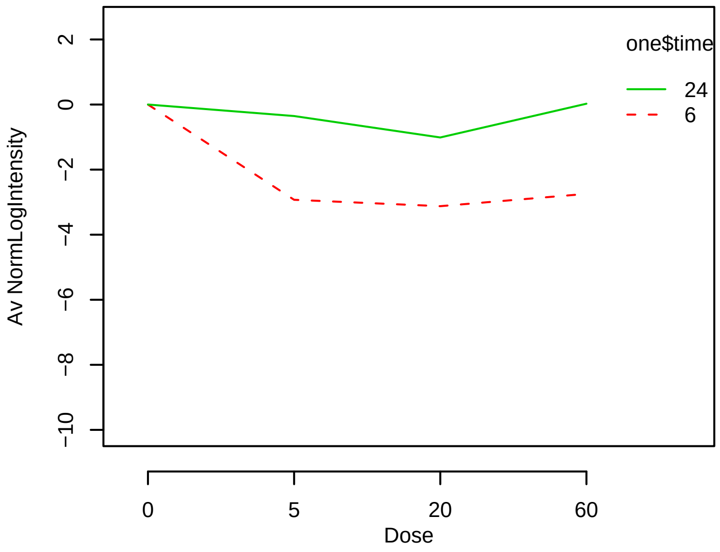

GO_0008207 : C21−steroid hormone metabolism

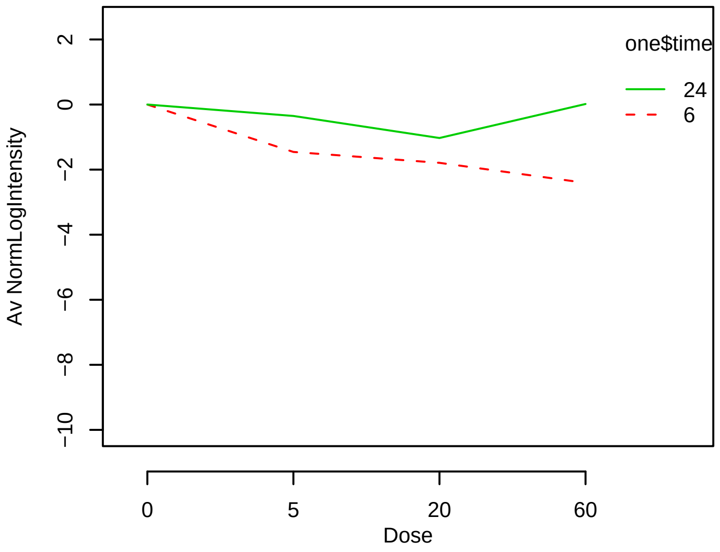

GO_0008209 : androgen metabolism

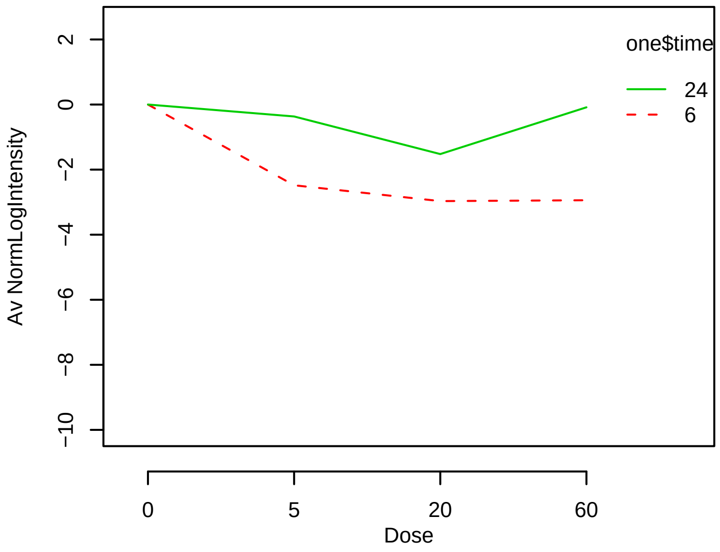

GO_0008210 : estrogen metabolism

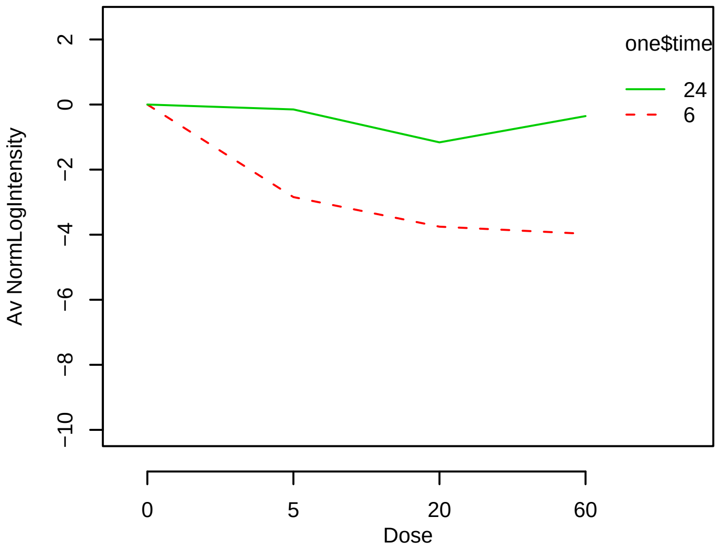

GO_0008213 : protein amino acid alkylation


GO_0008216 : spermidine metabolism

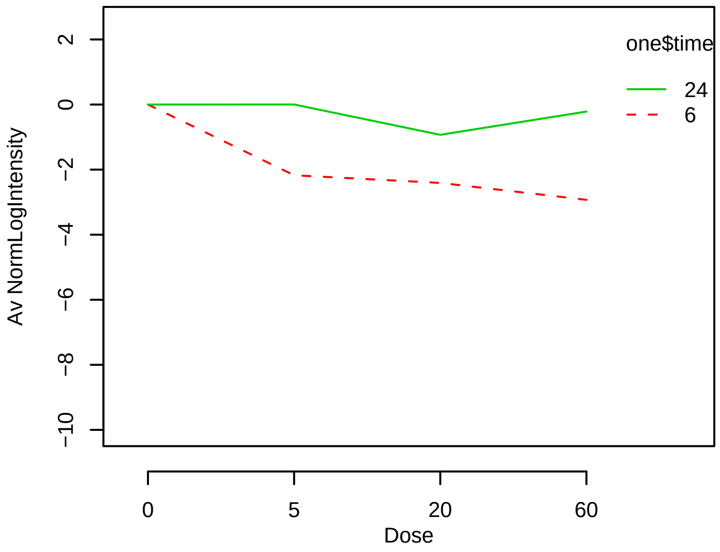

GO_0008217 : blood pressure regulation


GO_0008272 : sulfate transport

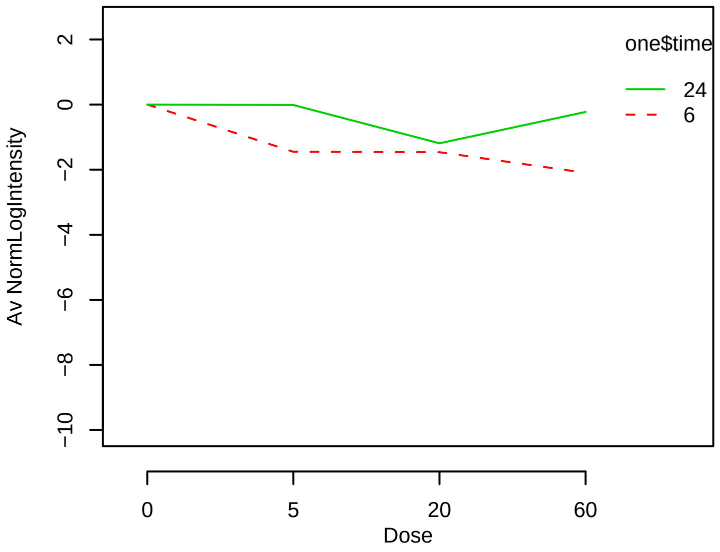

GO_0008277 : regulation of G−protein coupled receptor prote


GO_0008284 : positive regulation of cell proliferation

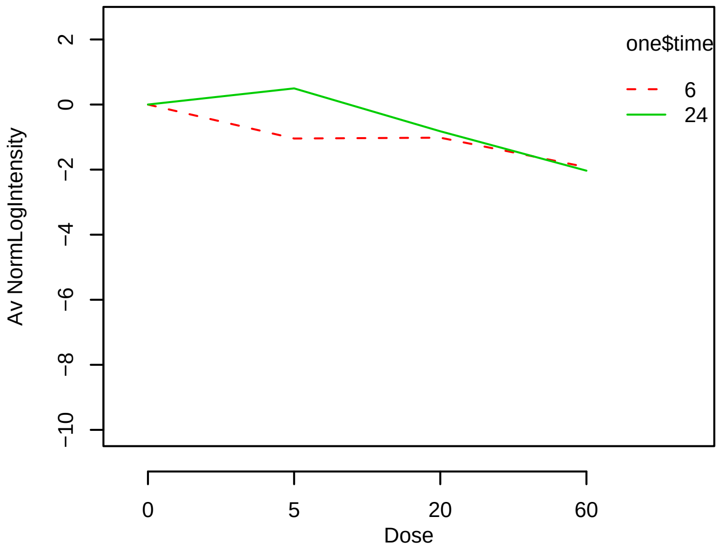
GO_0008285 : negative regulation of cell proliferation



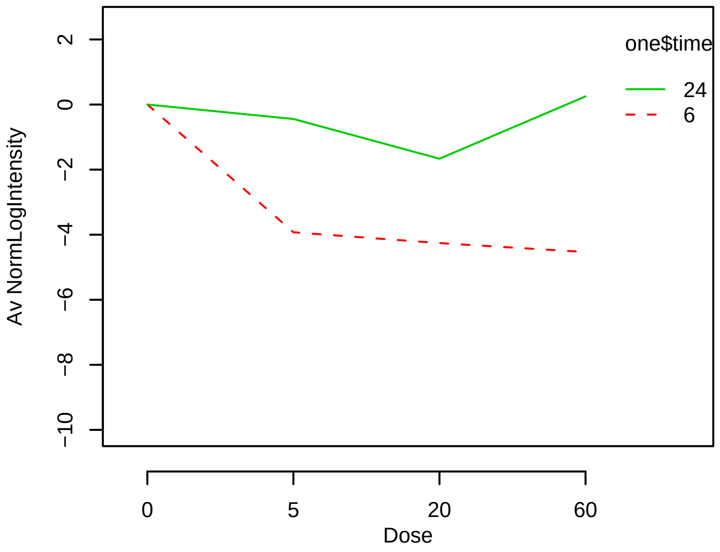
GO_0008286 : insulin receptor signaling pathway



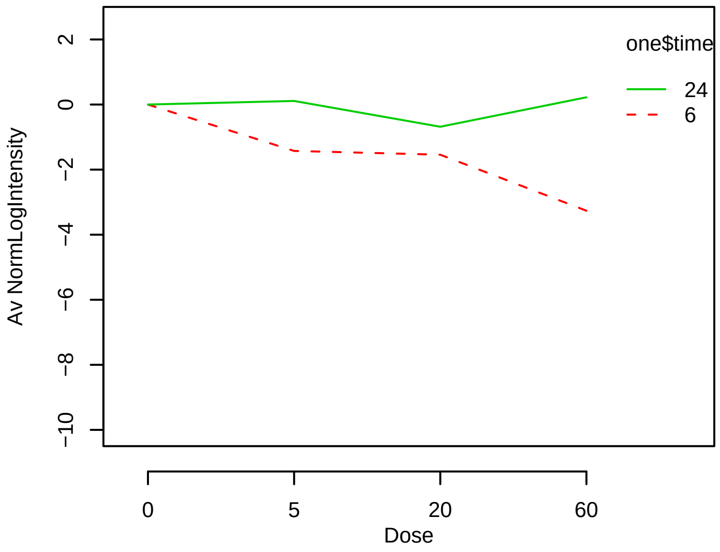
GO_0008299 : isoprenoid biosynthesis



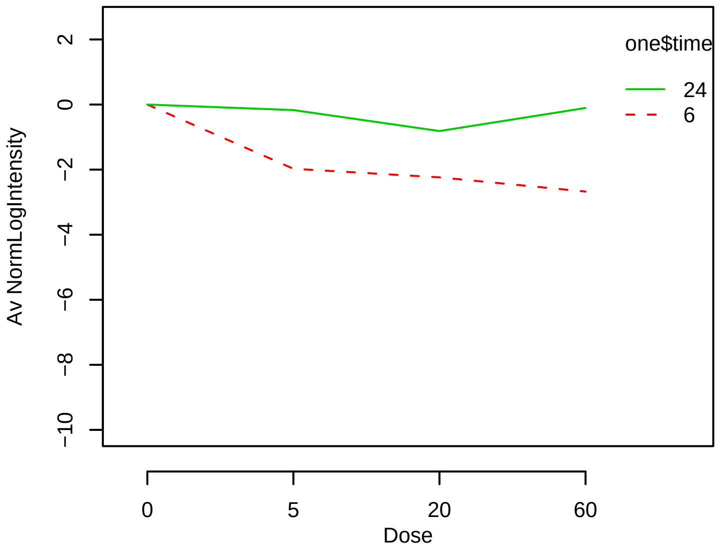
GO_0008306 : associative learning

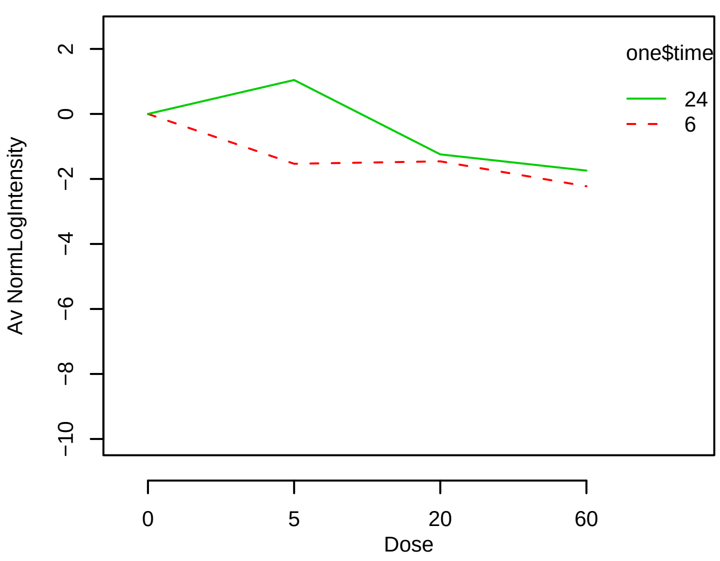


GO_0008333 : endosome to lysosome transport

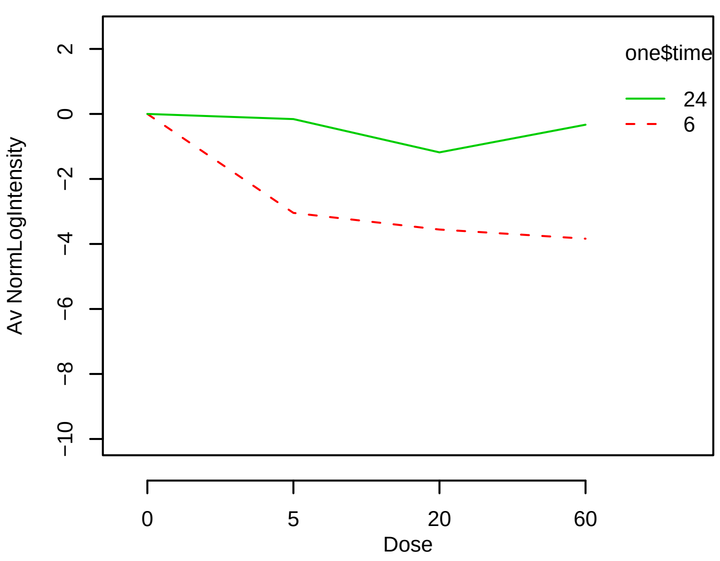


GO_0008344 : adult locomotory behavior

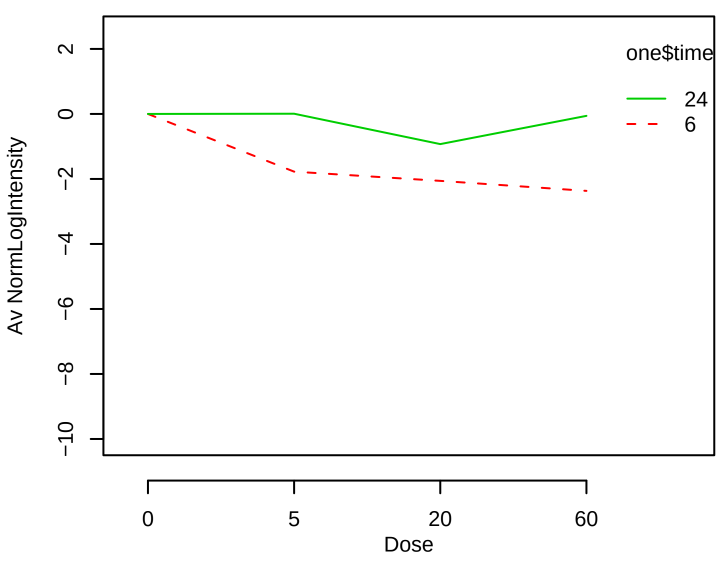




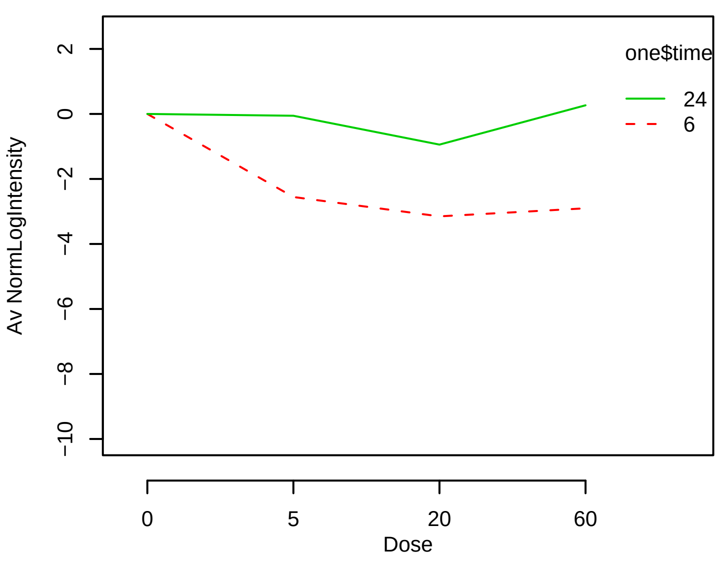
GO_0008354 : germ cell migration



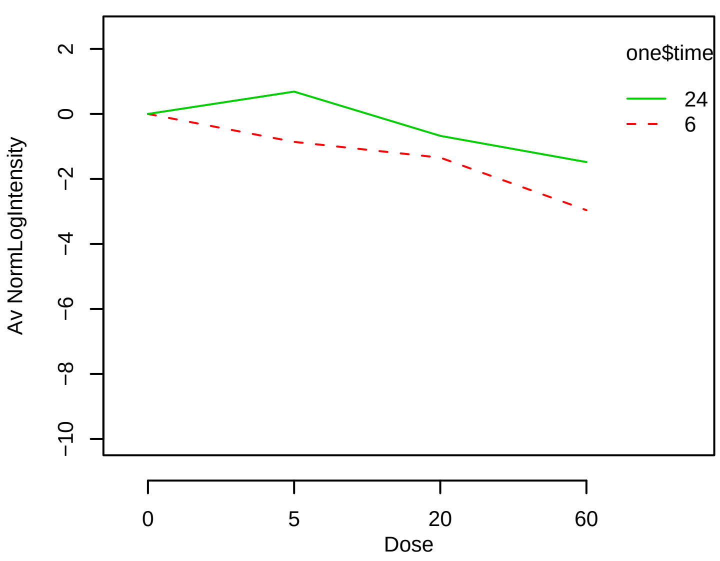
GO_0008360 : regulation of cell shape



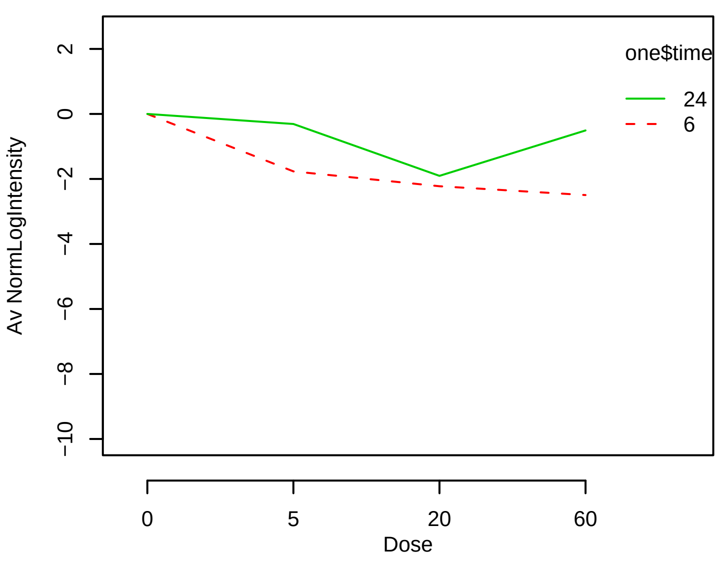
GO_0008361 : regulation of cell size



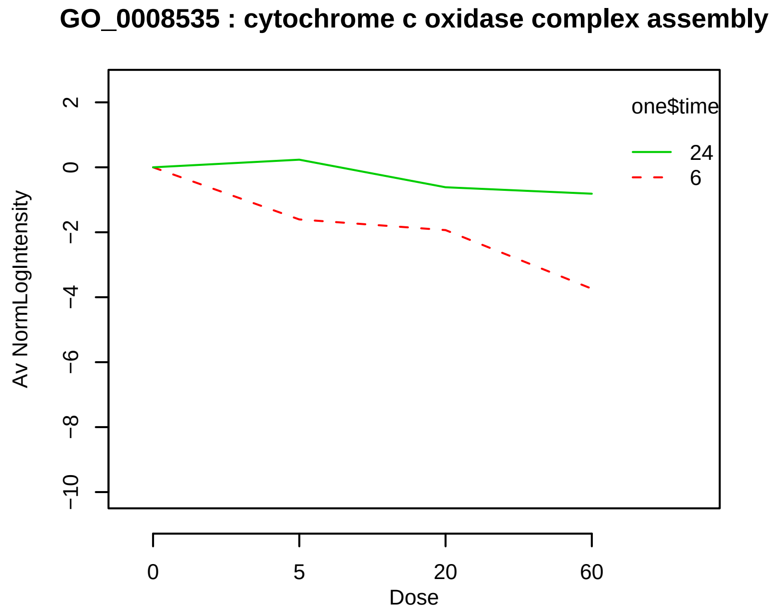
GO_0008366 : axon ensheathment

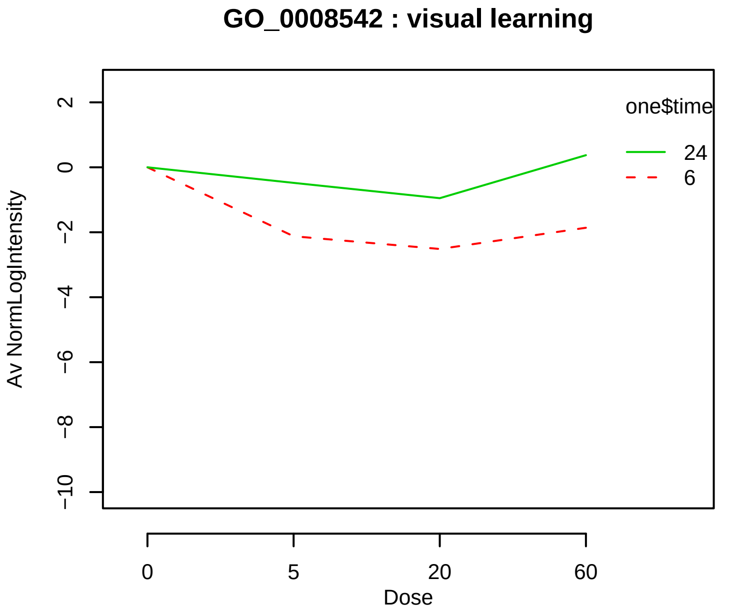


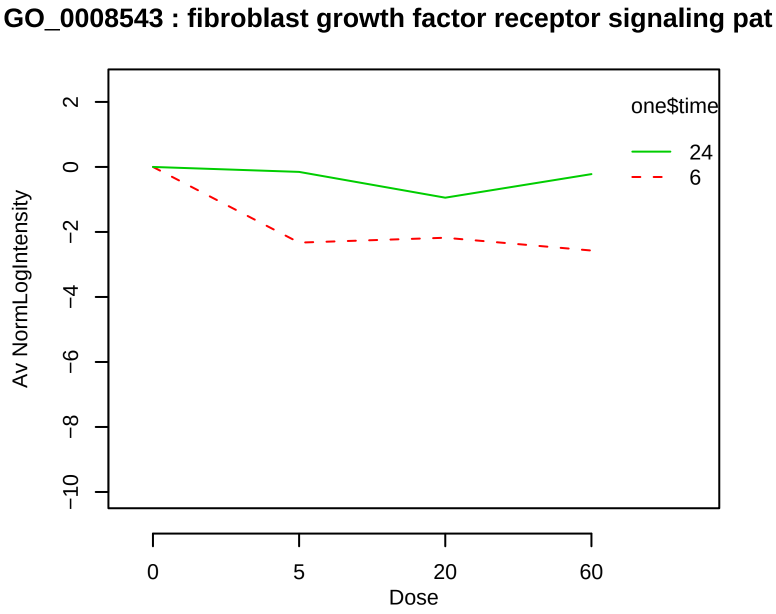
GO_0008380 : RNA splicing

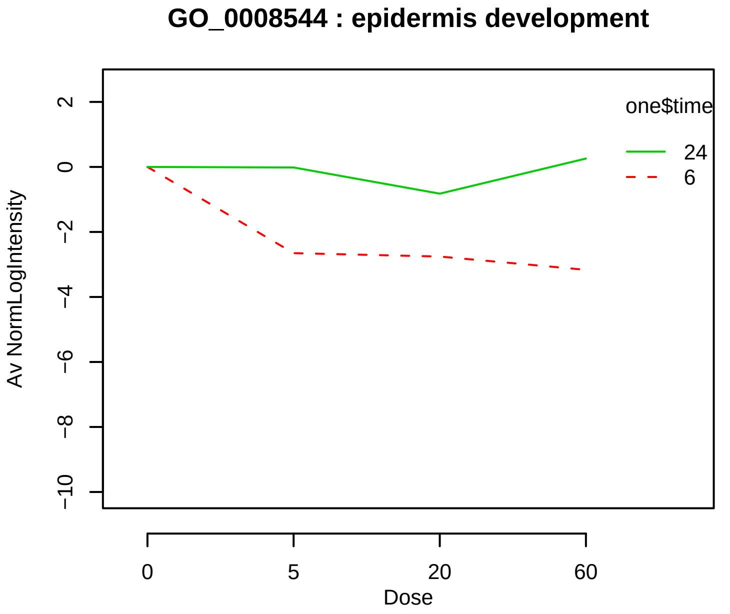


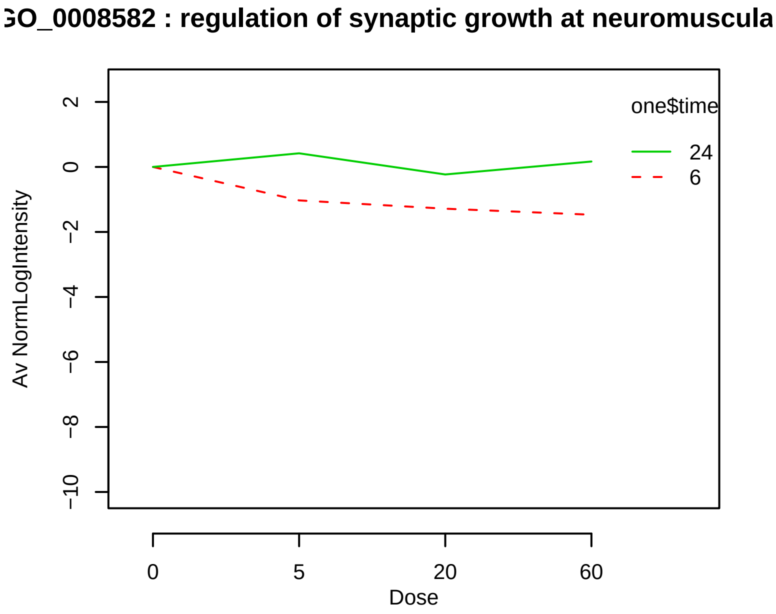
GO_0008406 : gonad development


GO_0008535 : cytochrome c oxidase complex assembly

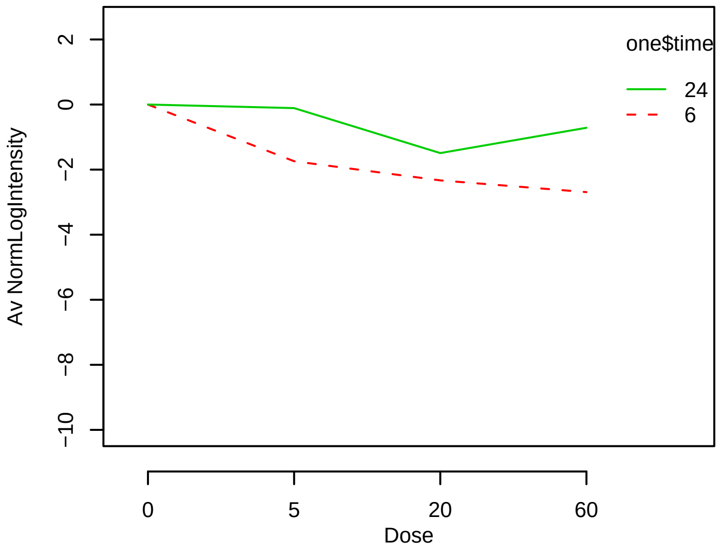

GO_0008542 : visual learning

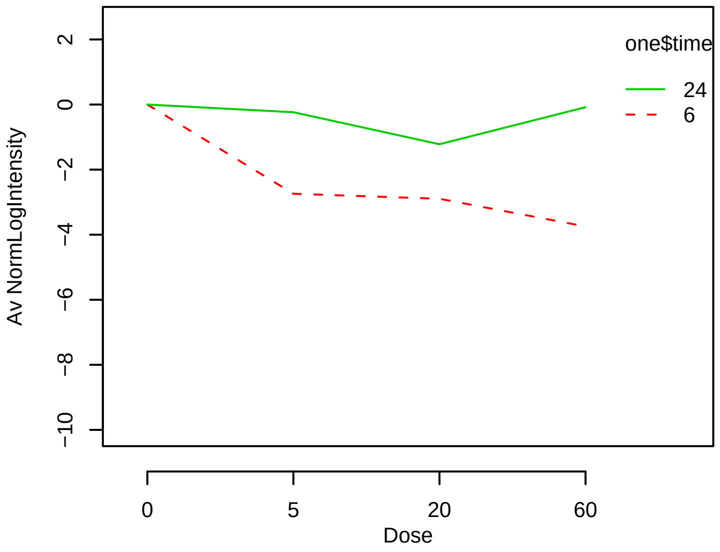

GO_0008543 : fibroblast growth factor receptor signaling pat

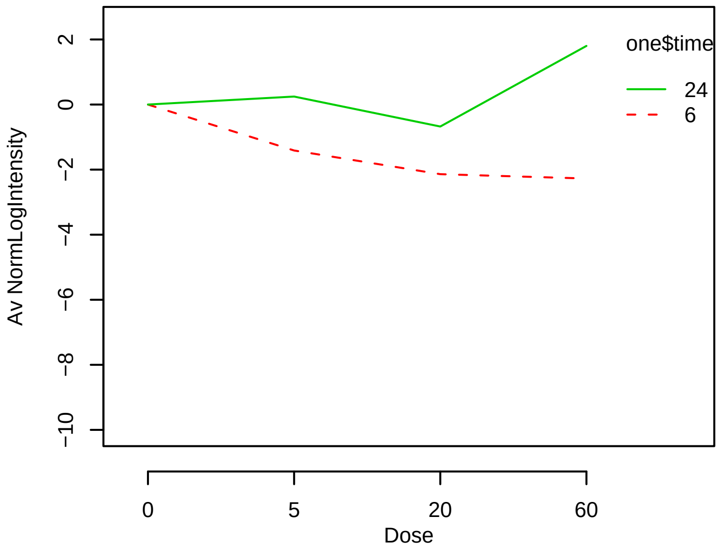

GO_0008544 : epidermis development

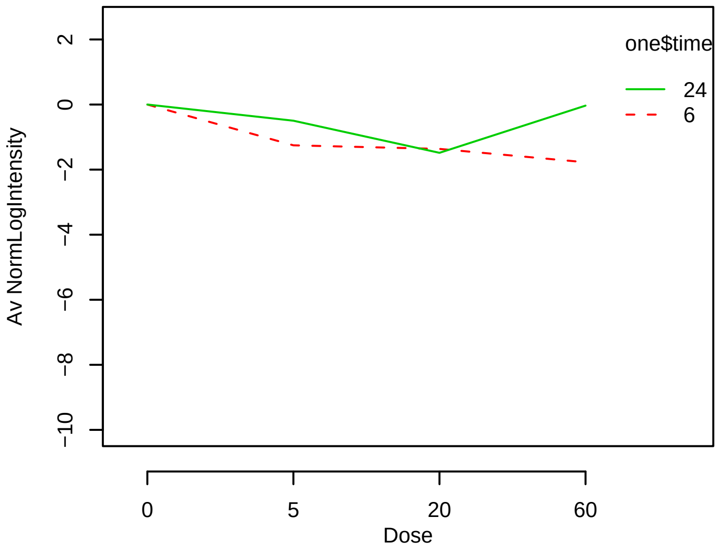

O_0008582 : regulation of synaptic growth at neuromuscula

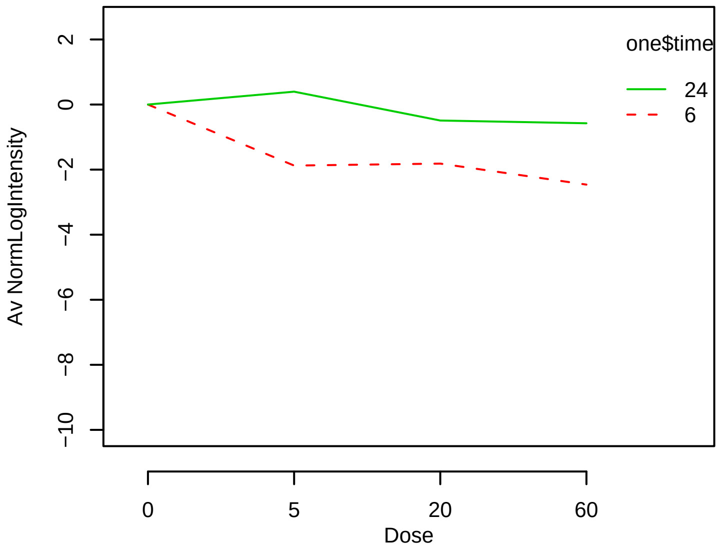

GO_0008584 : male gonad development

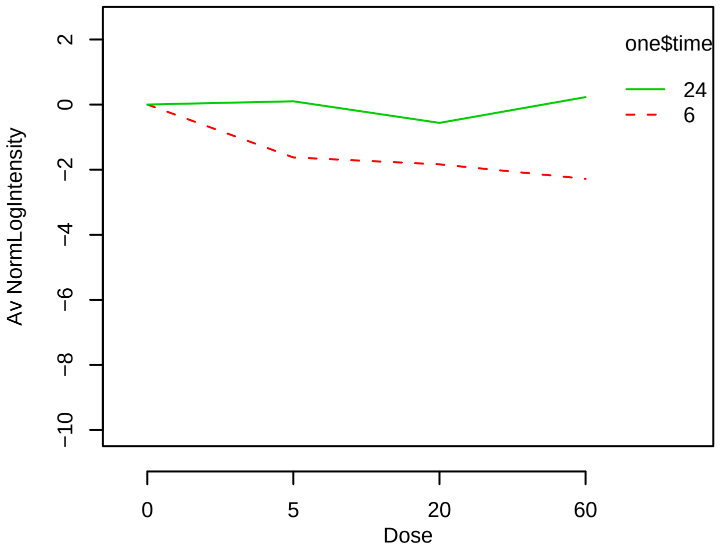

GO_0008585 : female gonad development


GO_0008589 : regulation of smoothened signaling pathwa

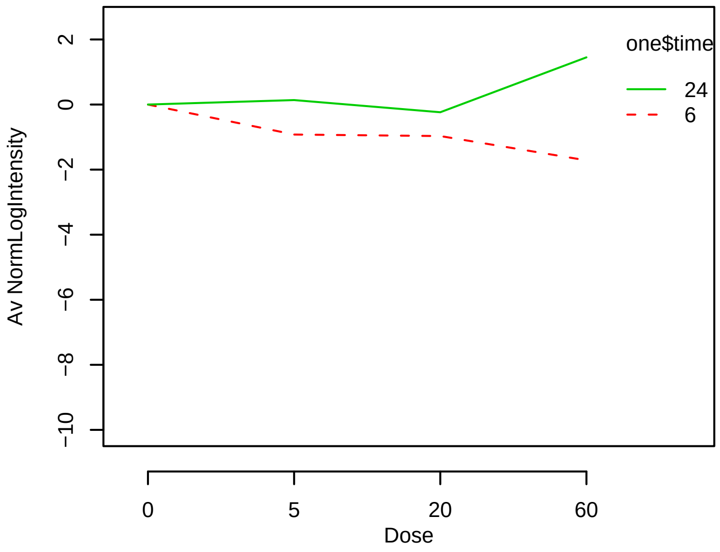

GO_0008593 : regulation of Notch signaling pathway


GO_0008595 : determination of anterior/posterior axis\, emb

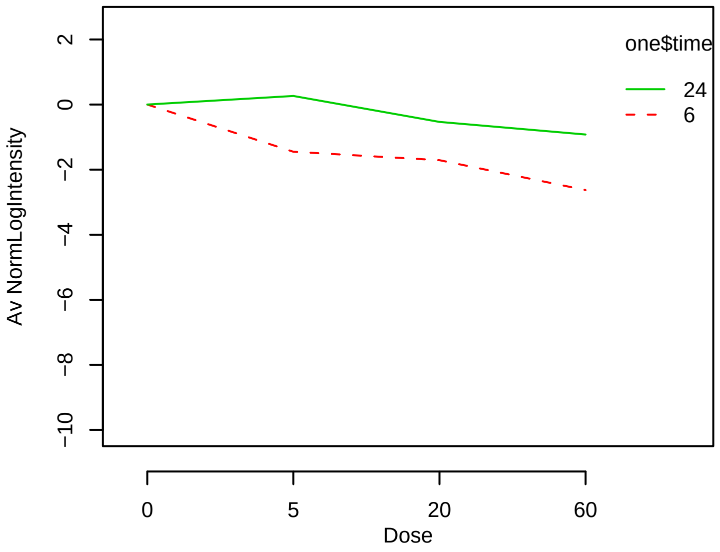

GO_0008610 : lipid biosynthesis


GO_0008624 : induction of apoptosis by extracellular signa

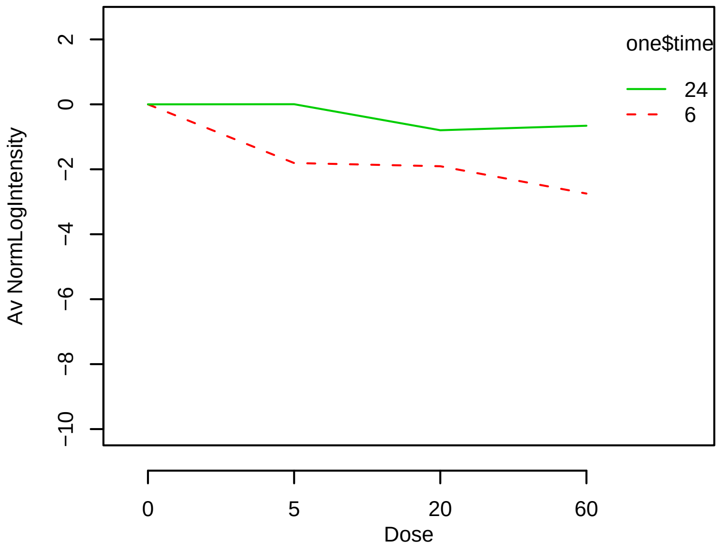
GO_0008625 : induction of apoptosis via death domain recep



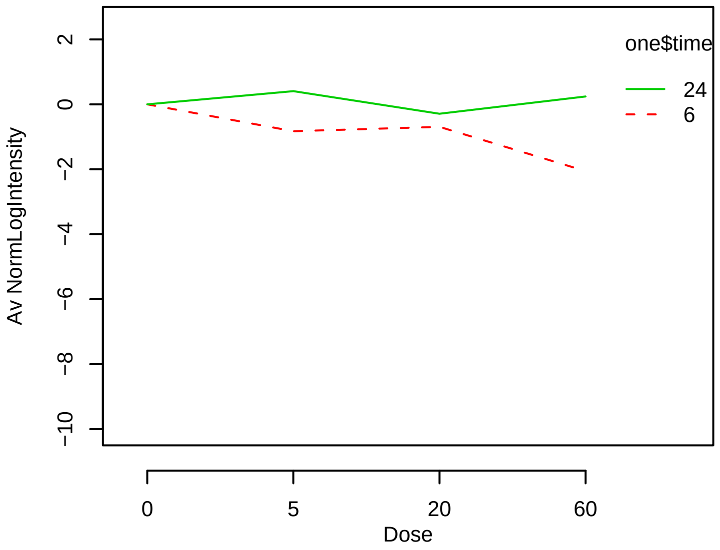
GO_0008629 : induction of apoptosis by intracellular signa



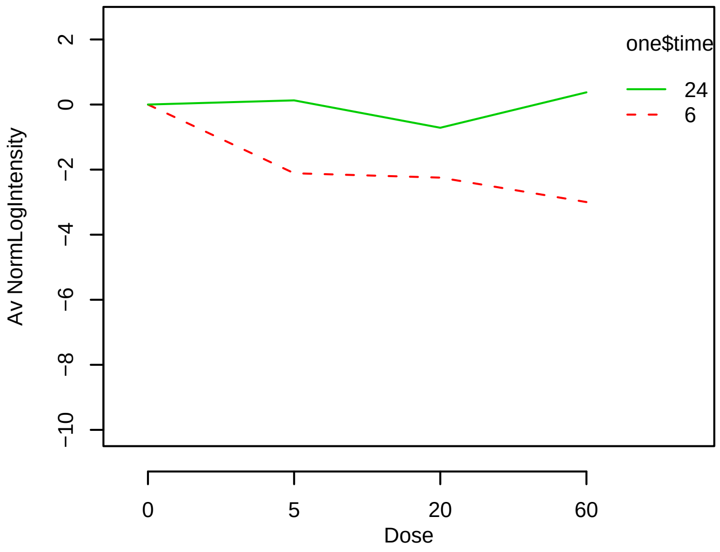
GO_0008630 : DNA damage response\, signal transduction res



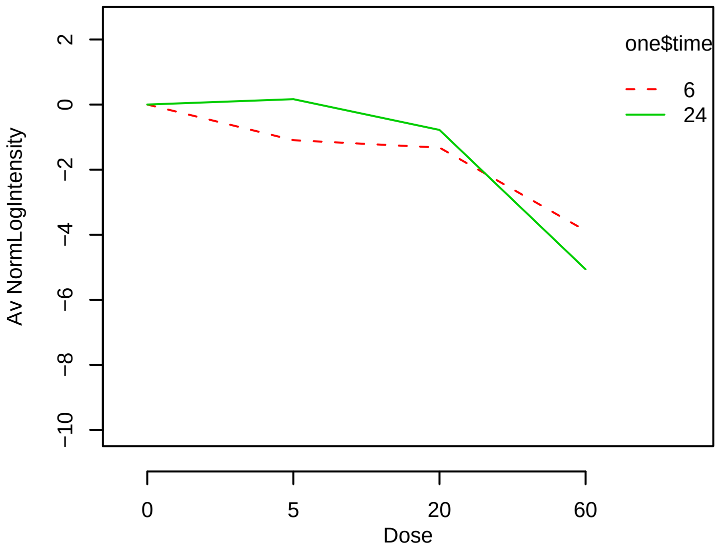
GO_0008631 : induction of apoptosis by oxidative stress

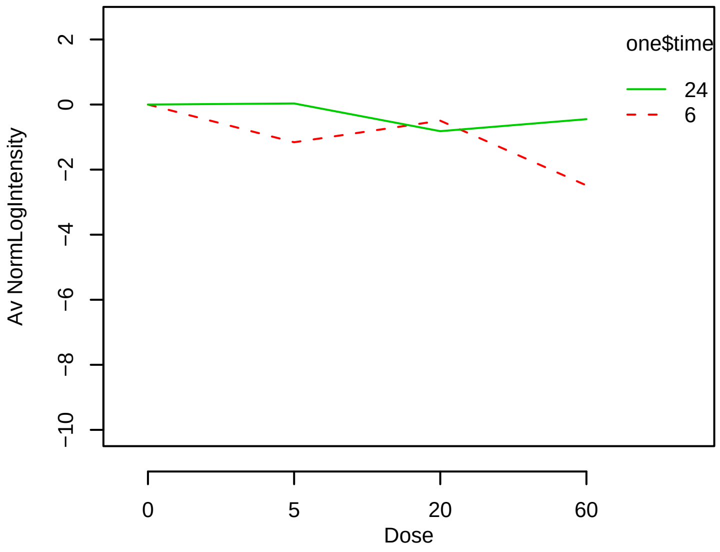


GO_0008632 : apoptotic program

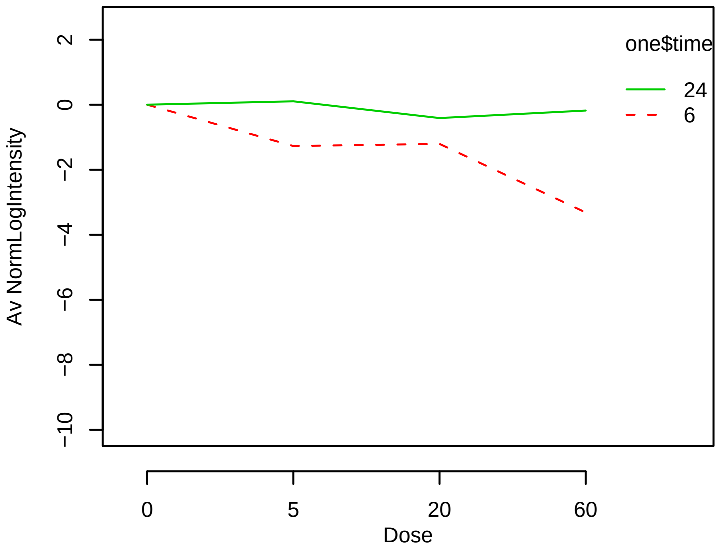


GO_0008634 : negative regulation of survival gene product a

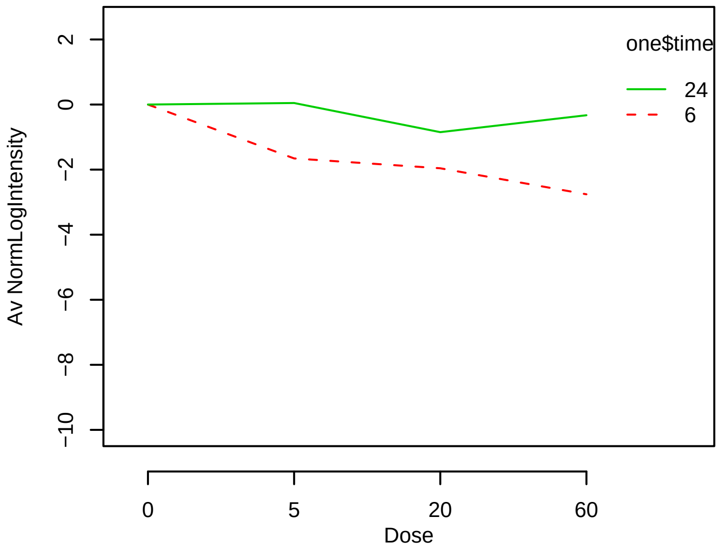




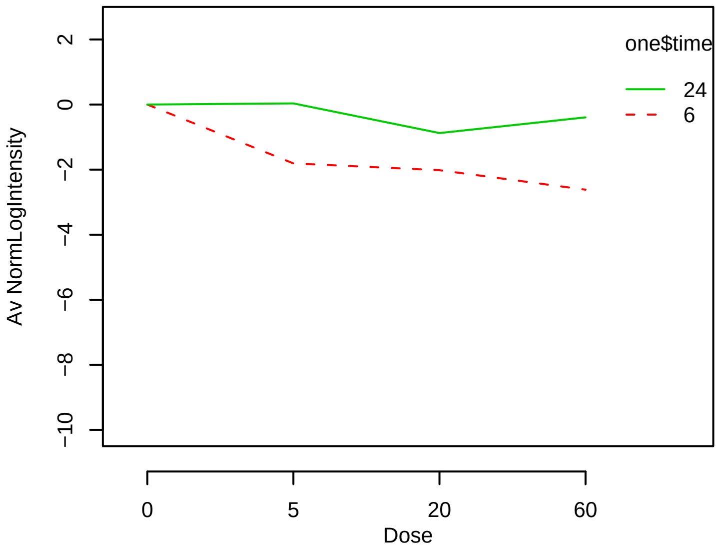
GO_0008635 : caspase activation via cytochrome c



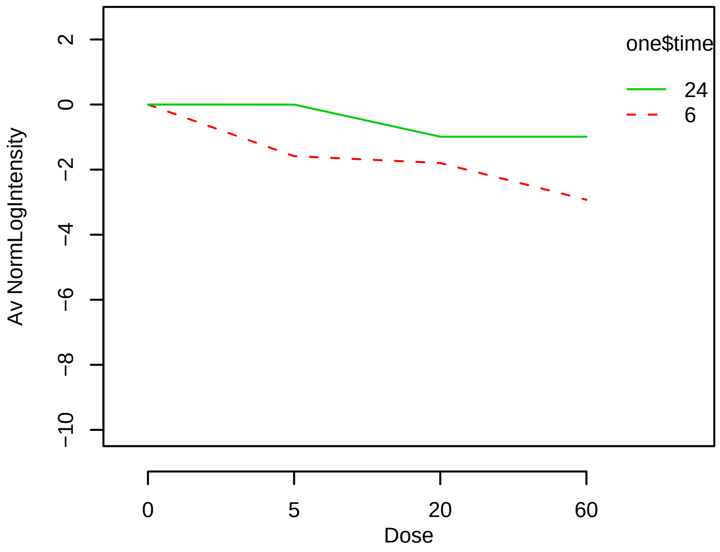
GO_0008637 : apoptotic mitochondrial changes



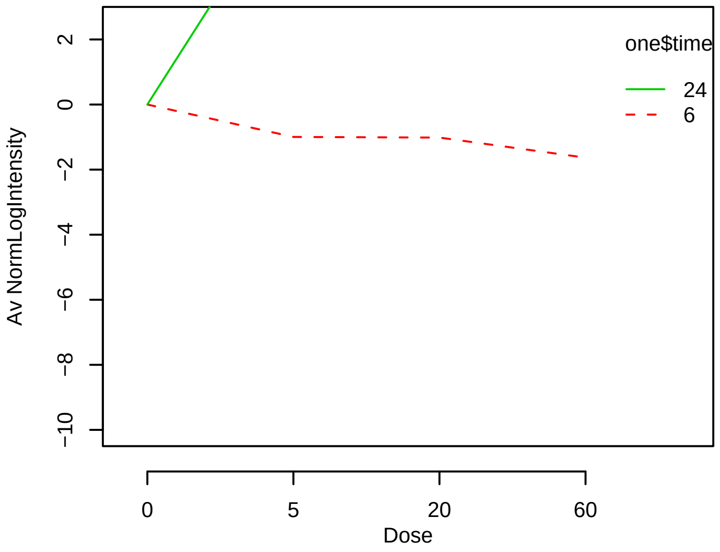
GO_0008643 : carbohydrate transport



GO_0008645 : hexose transport

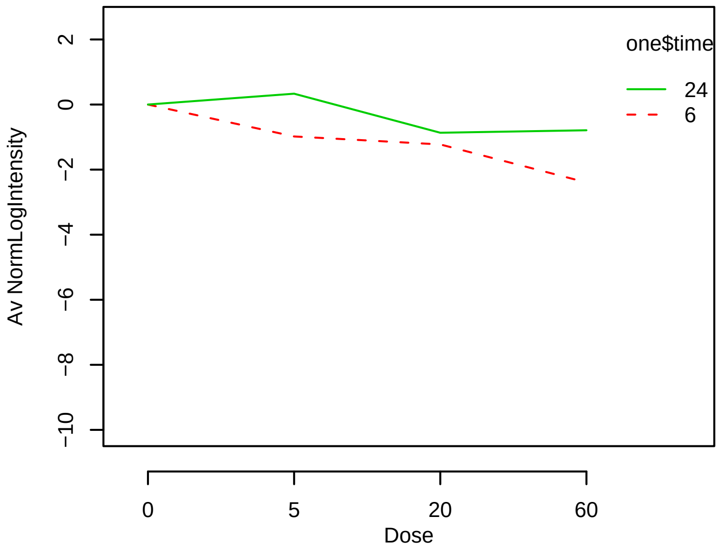


GO_0008652 : amino acid biosynthesis

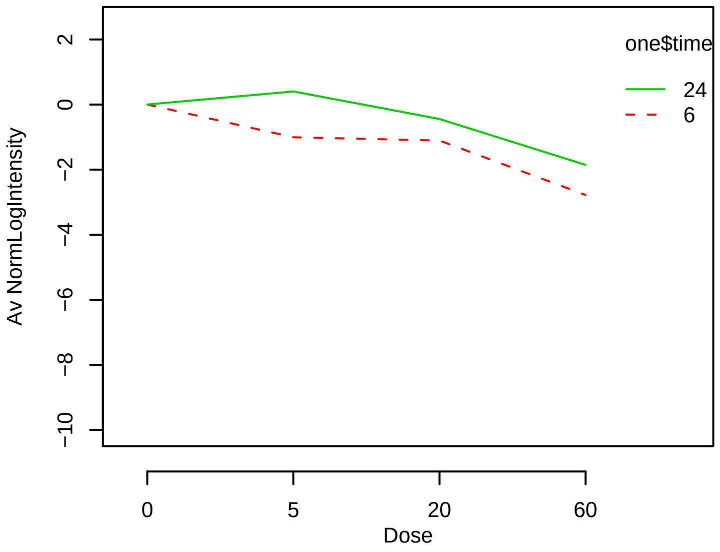


GO_0008653 : lipopolysaccharide metabolism

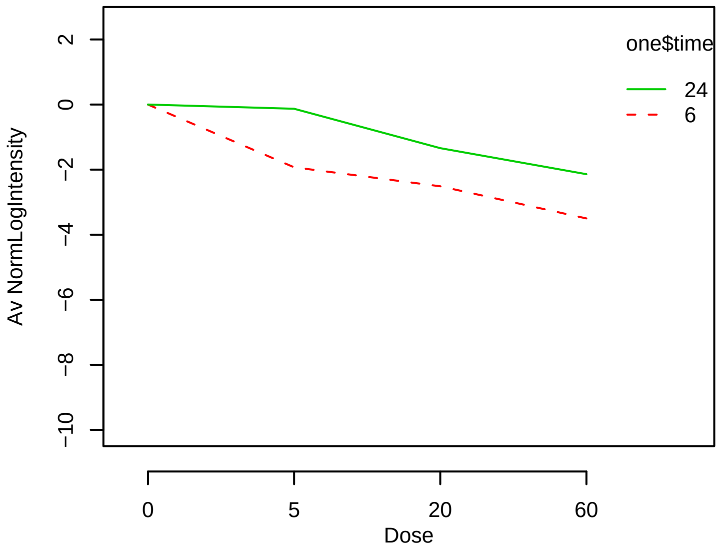
GO_0008654 : phospholipid biosynthesis



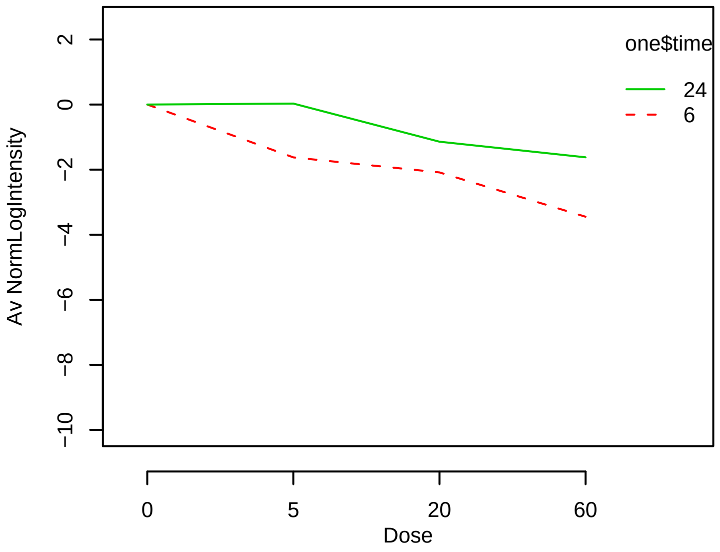
GO_0009060 : aerobic respiration



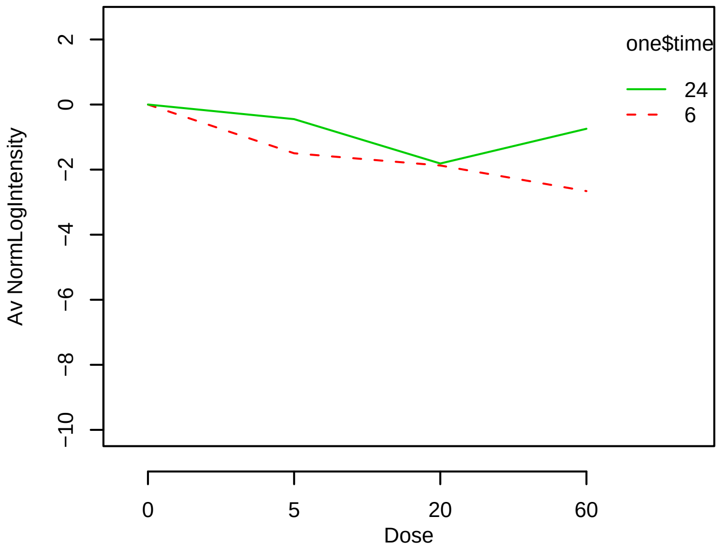
GO_0009063 : amino acid catabolism



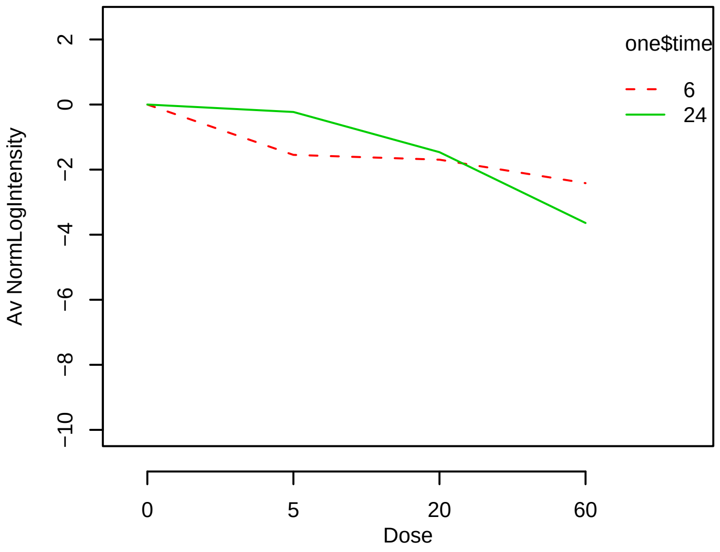
GO_0009064 : glutamine family amino acid metabolism

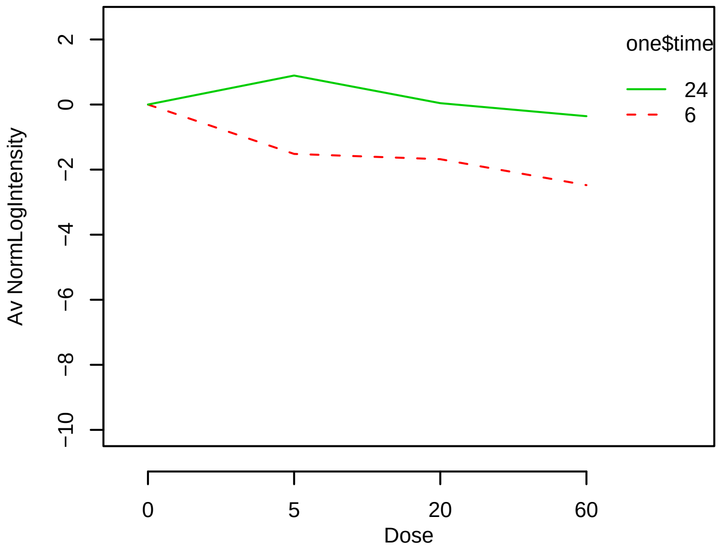


GO_0009065 : glutamine family amino acid catabolism

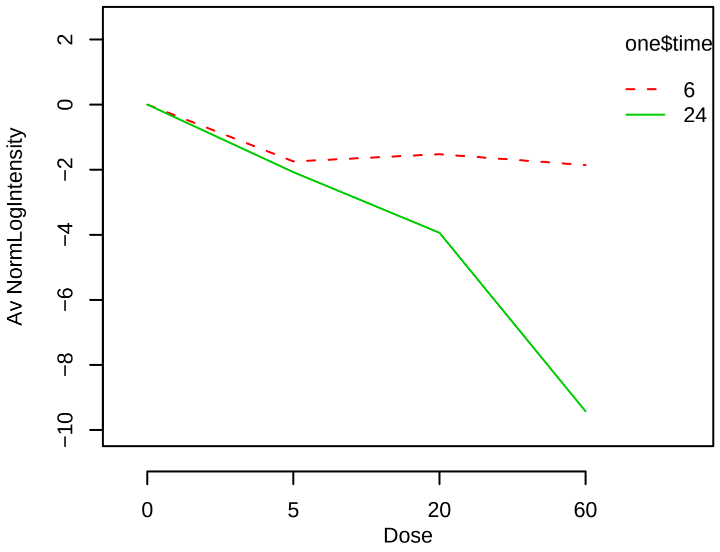


GO_0009066 : aspartate family amino acid metabolism

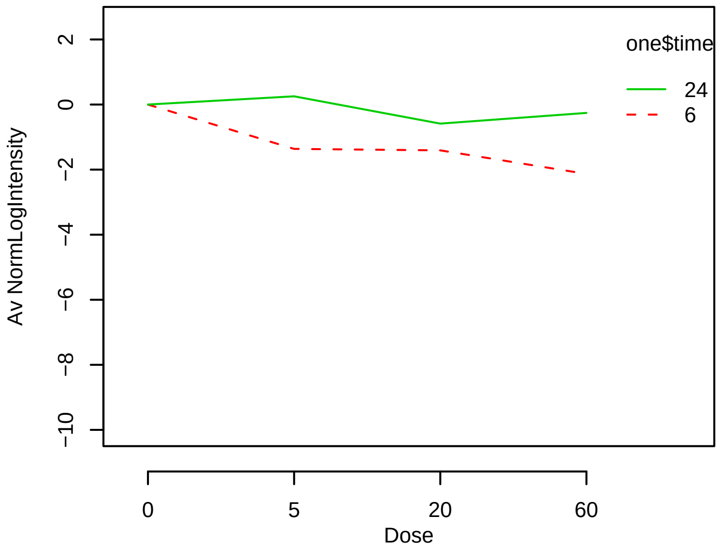




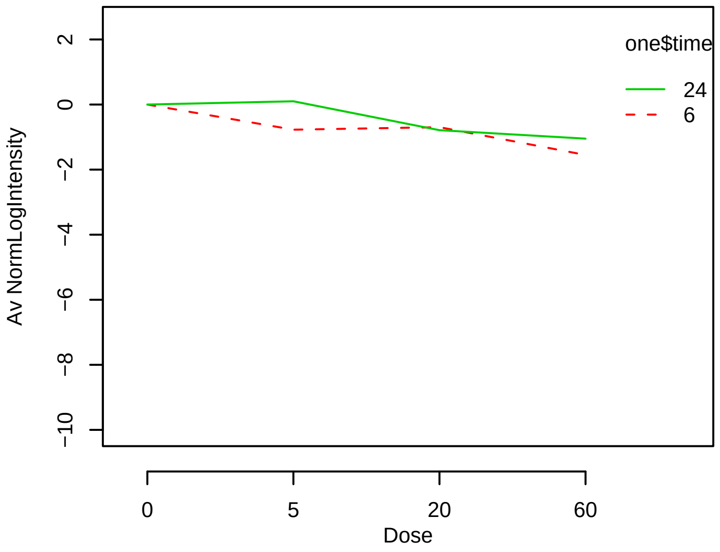
GO_0009067 : aspartate family amino acid biosynthesis



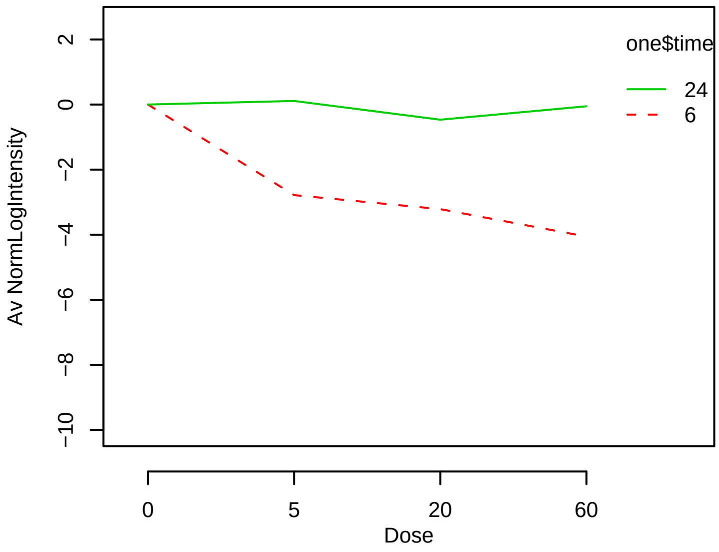
GO_0009068 : aspartate family amino acid catabolism



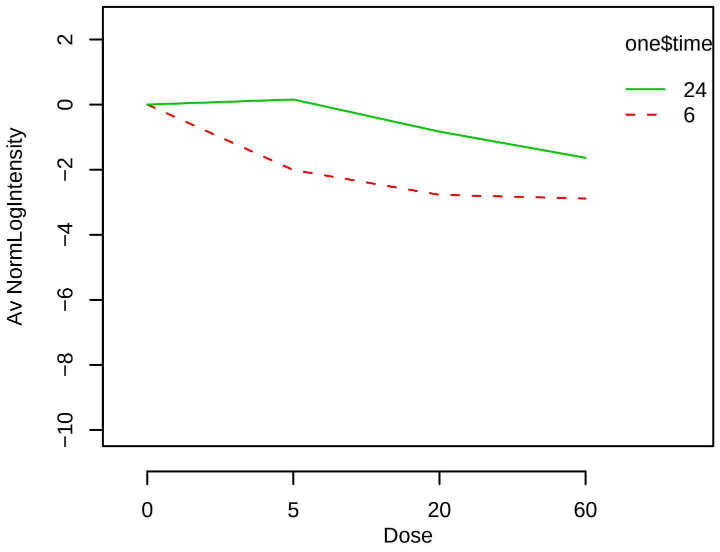
GO_0009069 : serine family amino acid metabolism



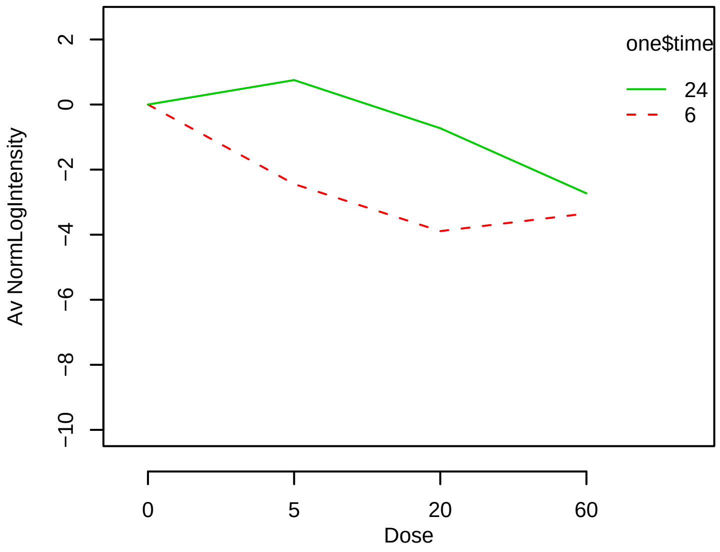
GO_0009070 : serine family amino acid biosynthesis

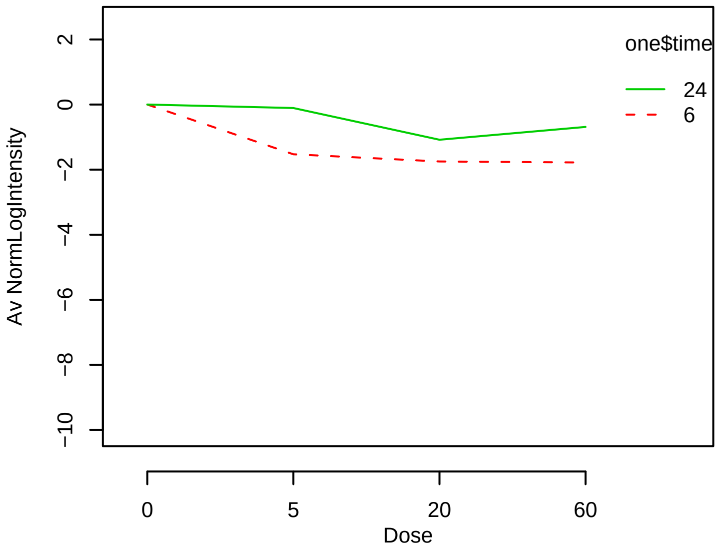


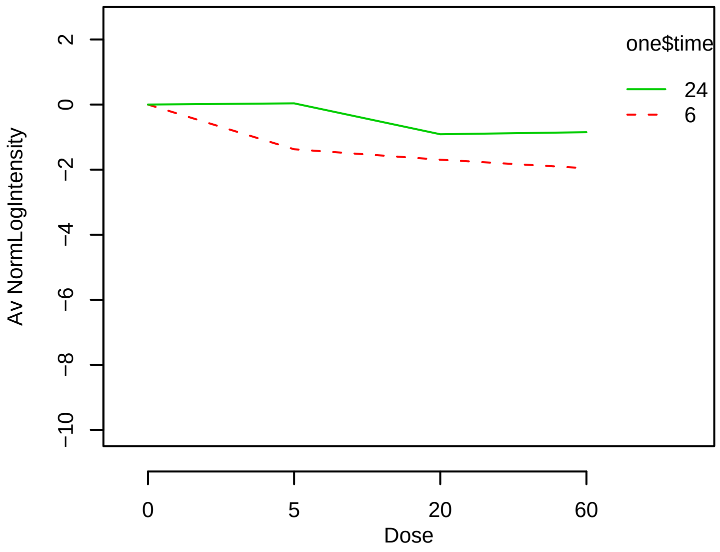
GO_0009071 : serine family amino acid catabolism

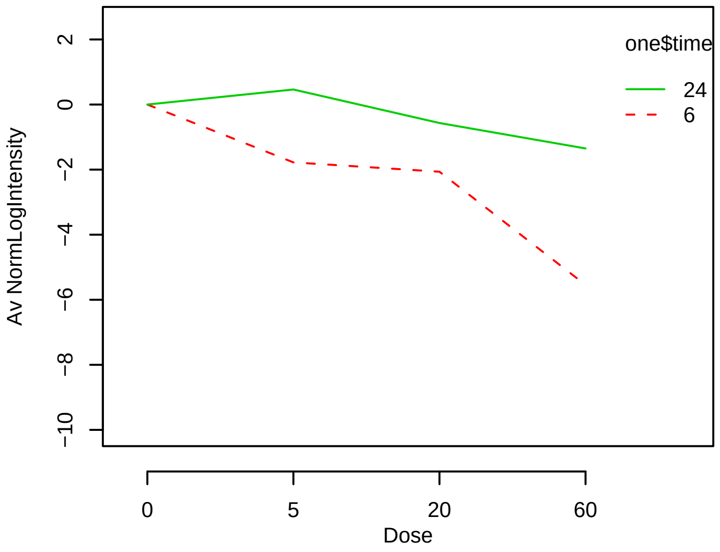


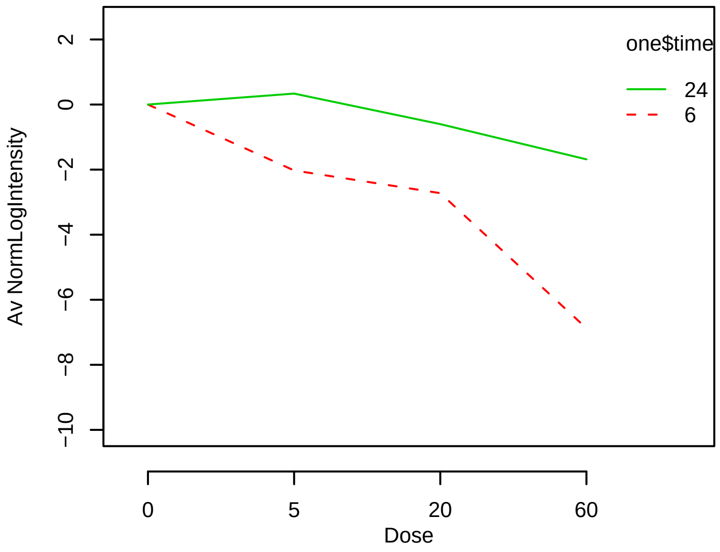
GO_0009072 : aromatic amino acid family metabolism

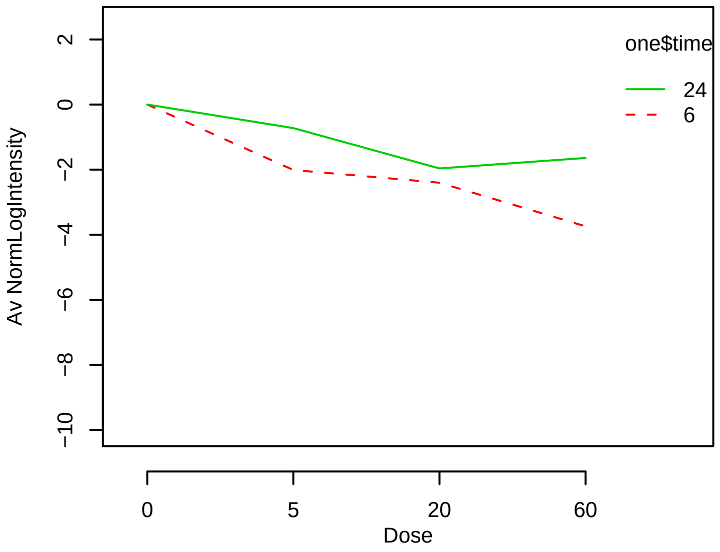

GO_0009074 : aromatic amino acid family catabolism

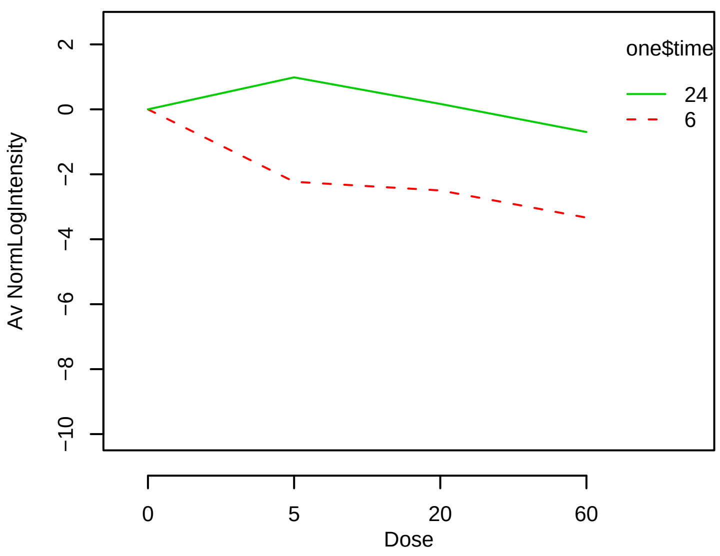

GO_0009075 : histidine family amino acid metabolism


GO_0009077 : histidine family amino acid catabolism

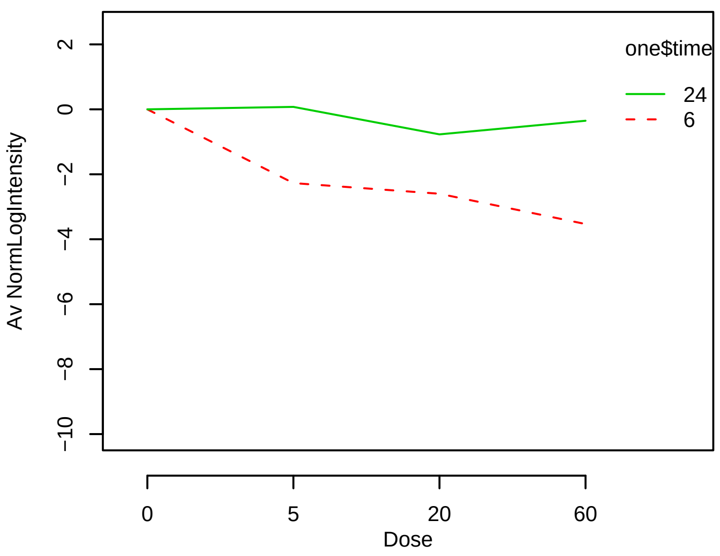

GO_0009081 : branched chain family amino acid metabolis


GO_0009083 : branched chain family amino acid catabolis

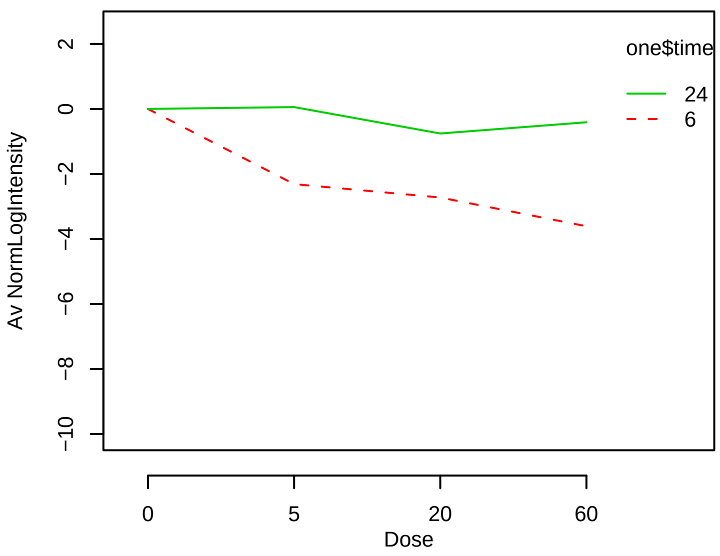

GO_0009084 : glutamine family amino acid biosynthesis



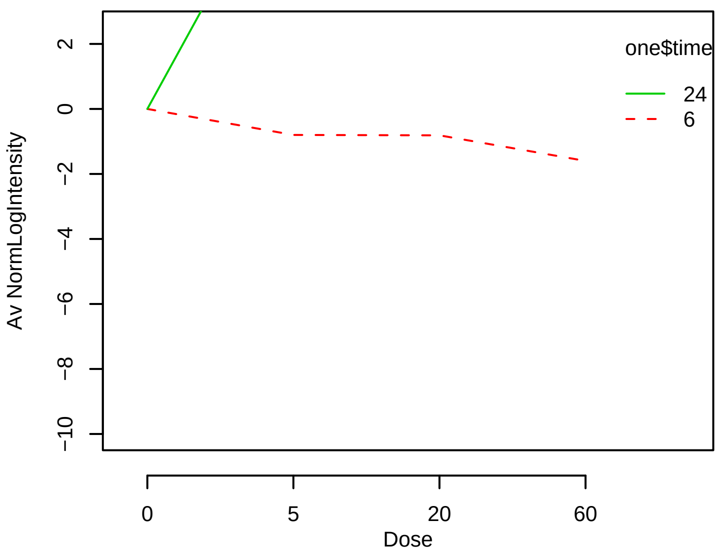
GO_0009086 : methionine biosynthesis



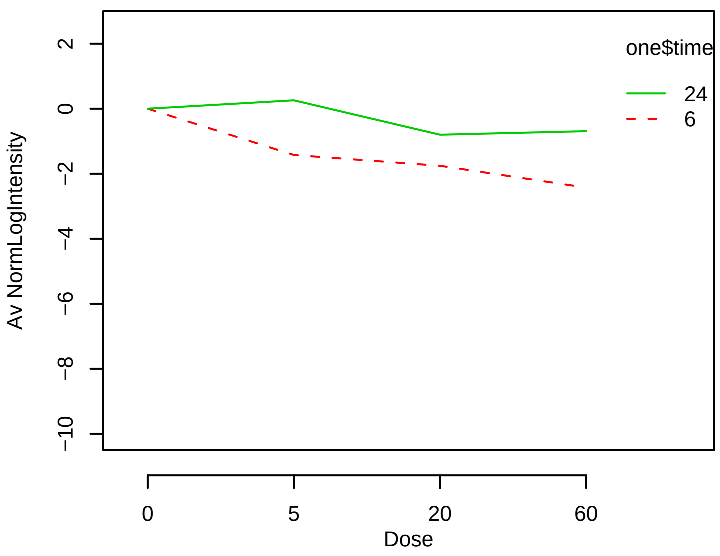
GO_0009100 : glycoprotein metabolism



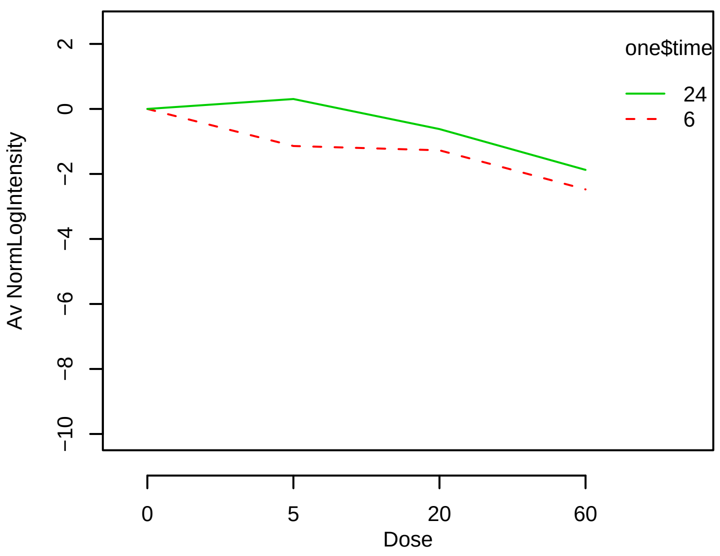
GO_0009101 : glycoprotein biosynthesis



GO_0009103 : lipopolysaccharide biosynthesis

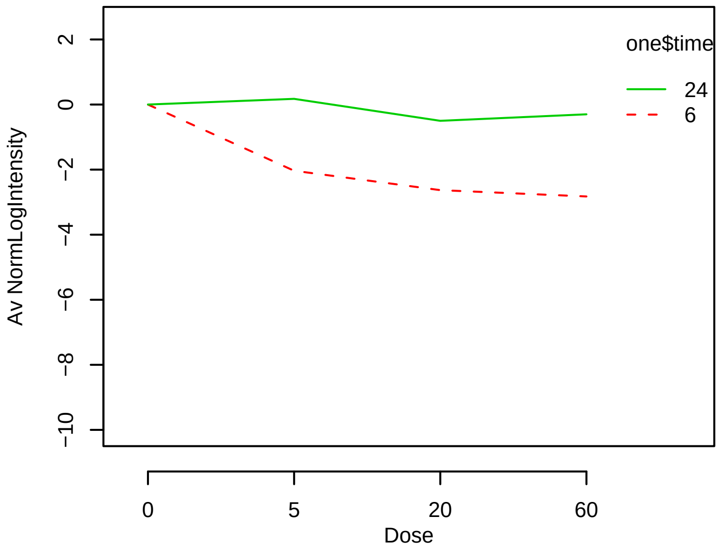


GO_0009108 : coenzyme biosynthesis

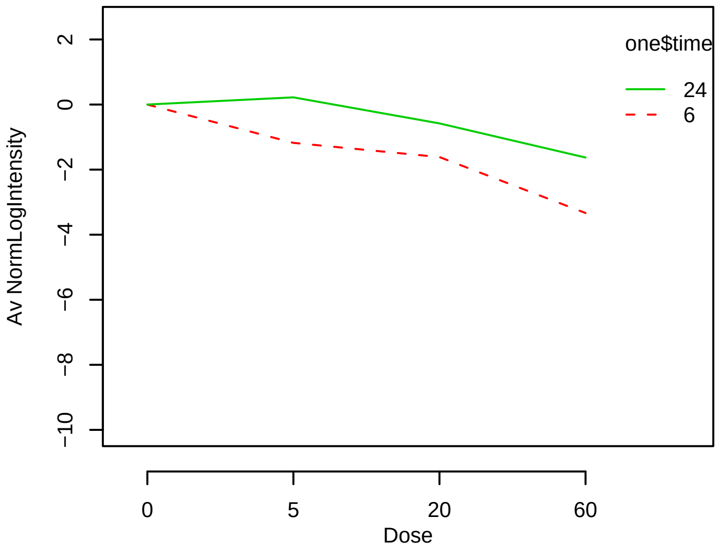


GO_0009109 : coenzyme catabolism

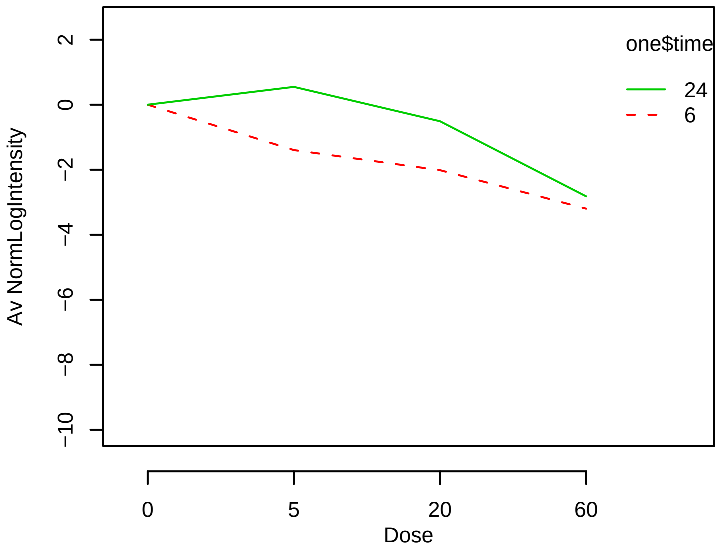
GO_0009110 : vitamin biosynthesis



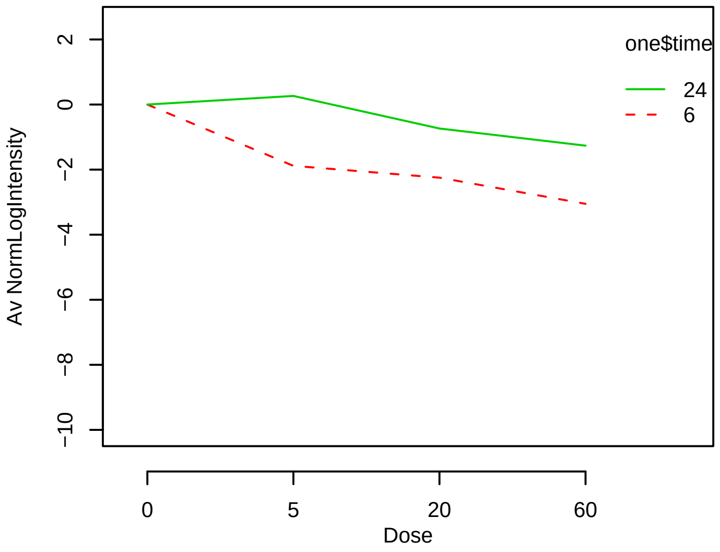
GO_0009112 : nucleobase metabolism



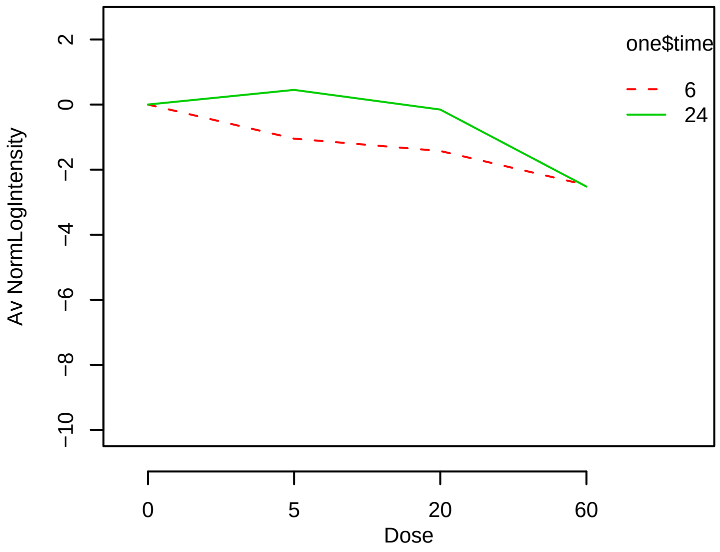
GO_0009116 : nucleoside metabolism



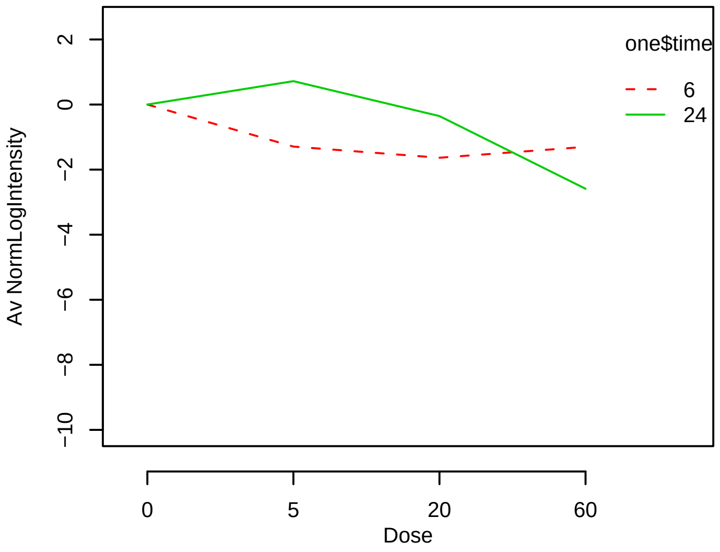
GO_0009117 : nucleotide metabolism



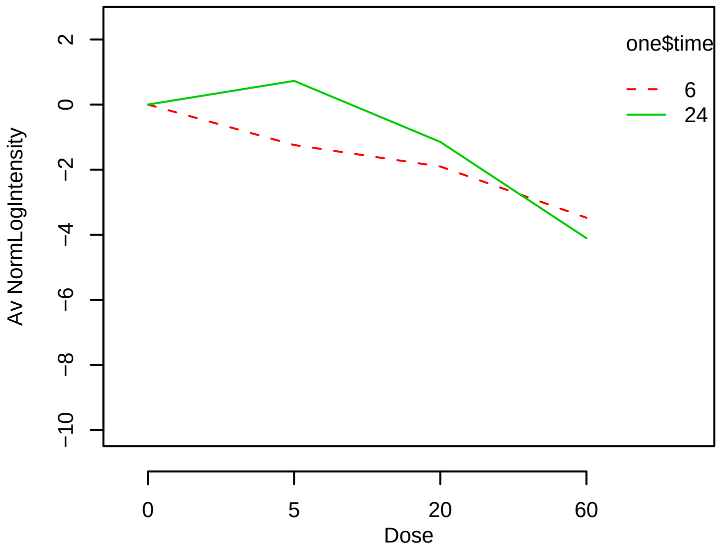
GO_0009119 : ribonucleoside metabolism



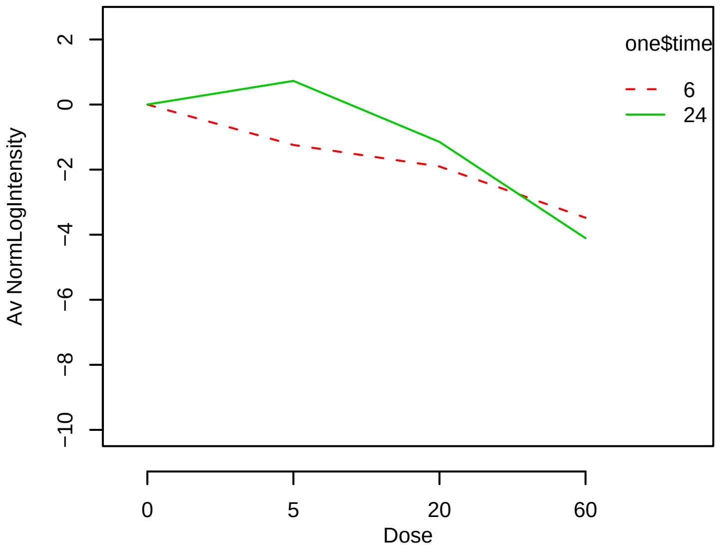
GO_0009120 : deoxyribonucleoside metabolism



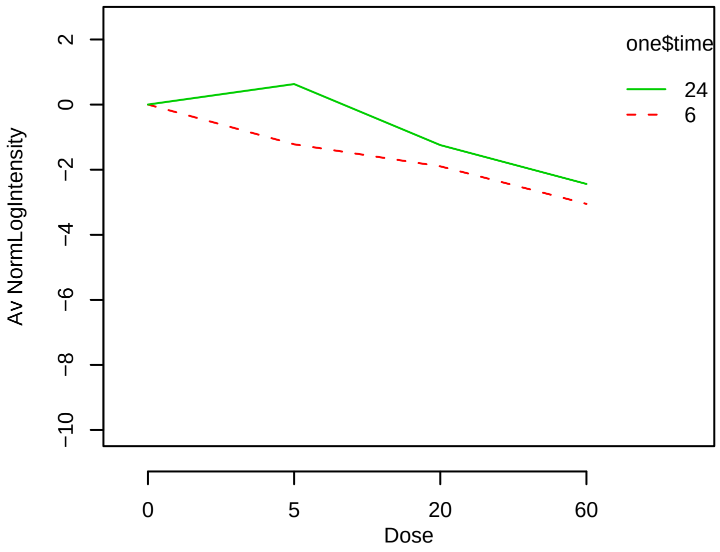
GO_0009123 : nucleoside monophosphate metabolism



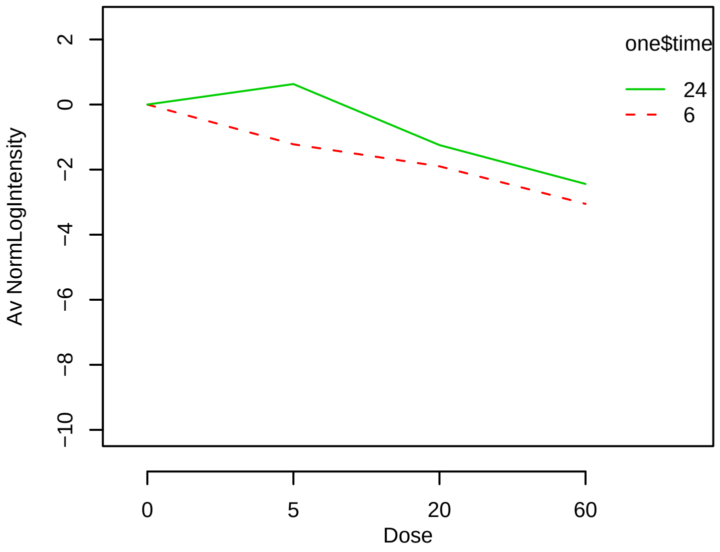
GO_0009124 : nucleoside monophosphate biosynthesis



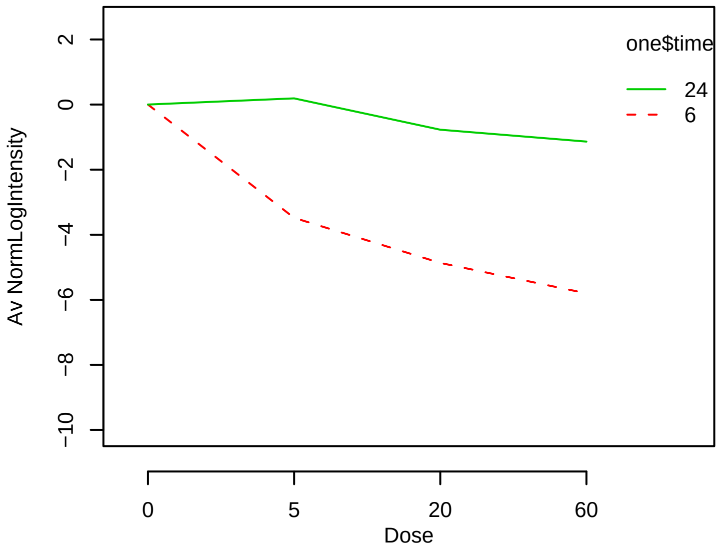
GO_0009126 : purine nucleoside monophosphate metabolis



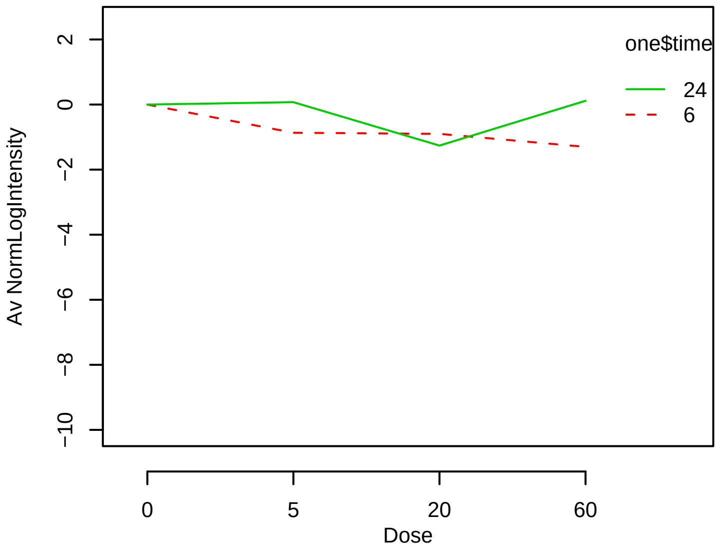
GO_0009127 : purine nucleoside monophosphate biosynthe

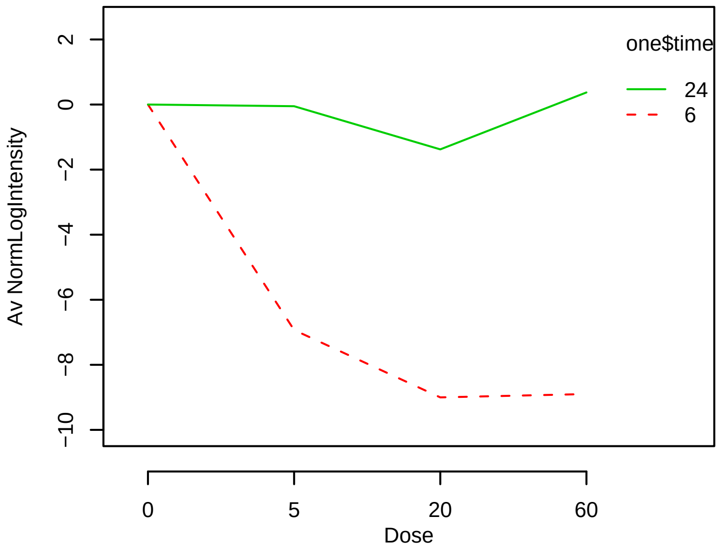


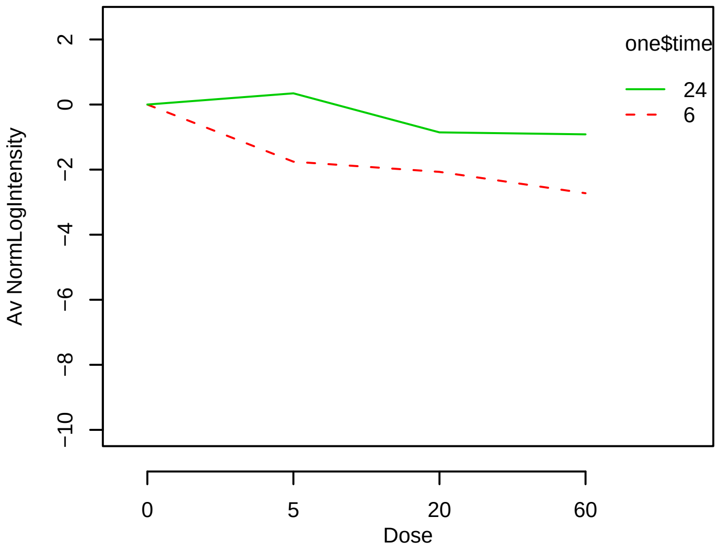
GO_0009132 : nucleoside diphosphate metabolism

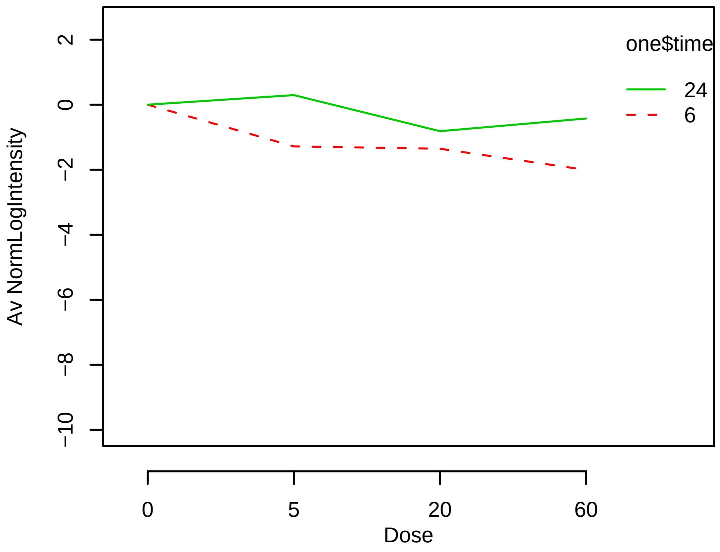


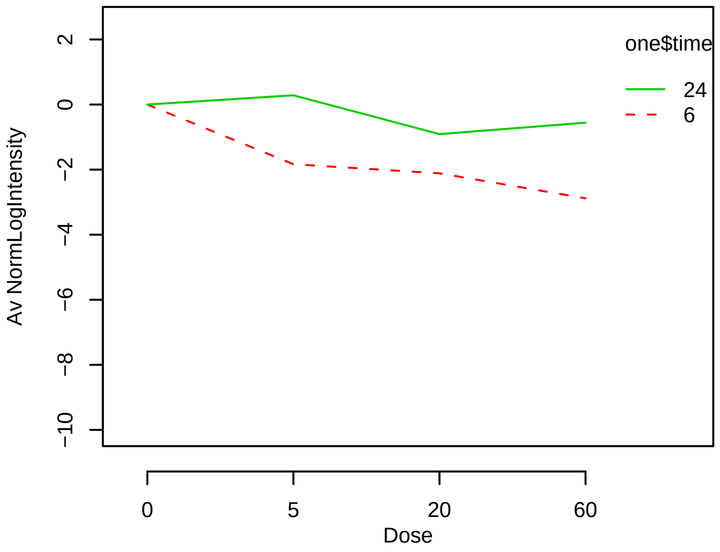
GO_0009134 : nucleoside diphosphate catabolism

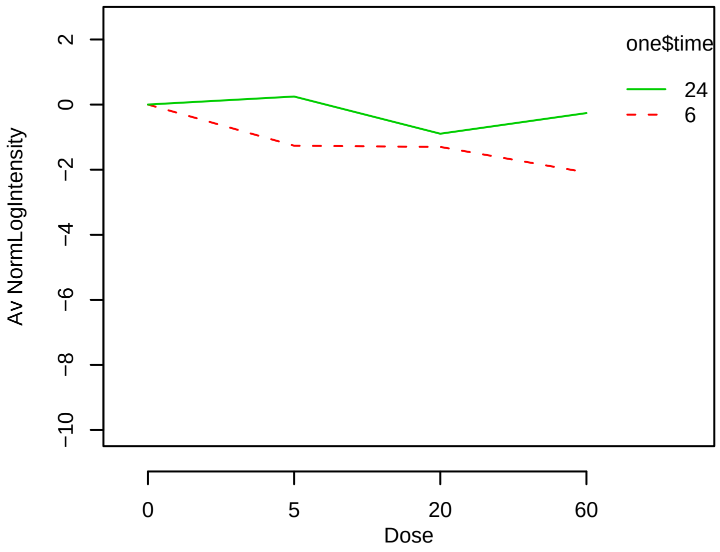


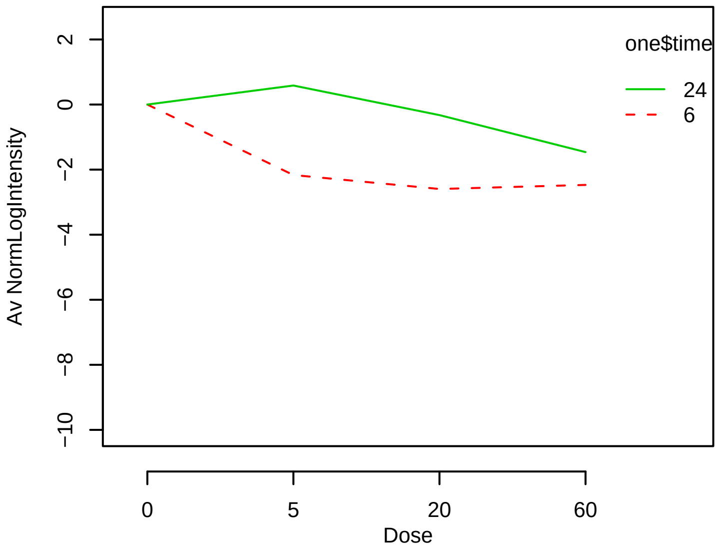

GO_0009135 : purine nucleoside diphosphate metabolis

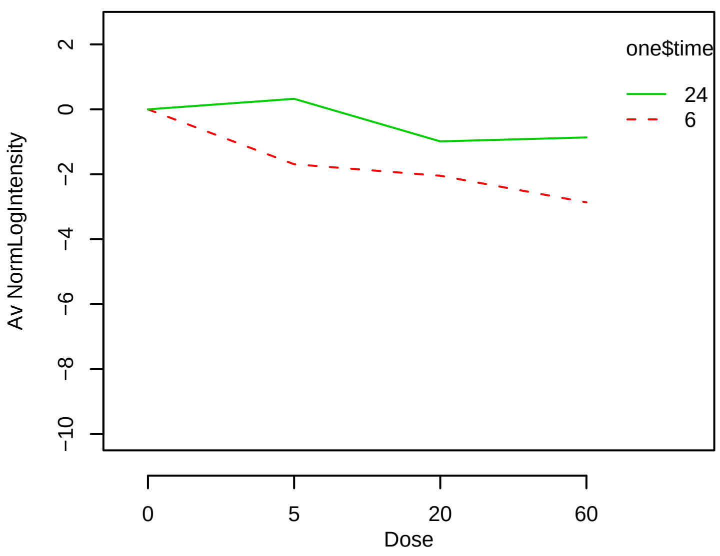

GO_0009141 : nucleoside triphosphate metabolism

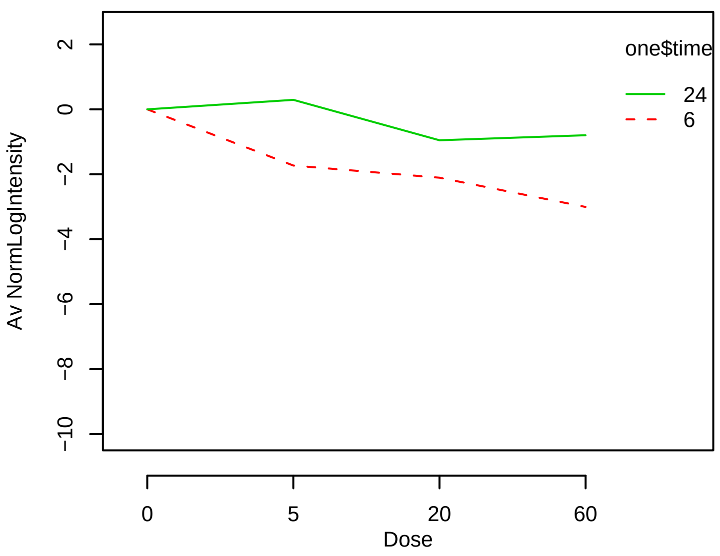

GO_0009142 : nucleoside triphosphate biosynthesis

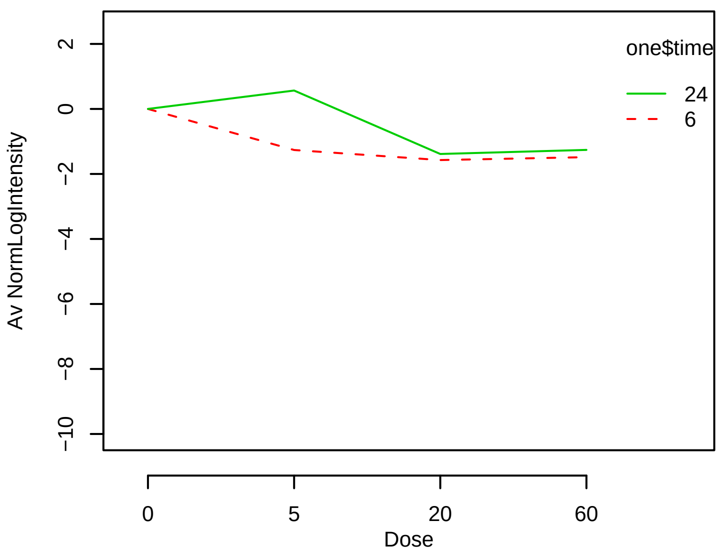

GO_0009144 : purine nucleoside triphosphate metabolis

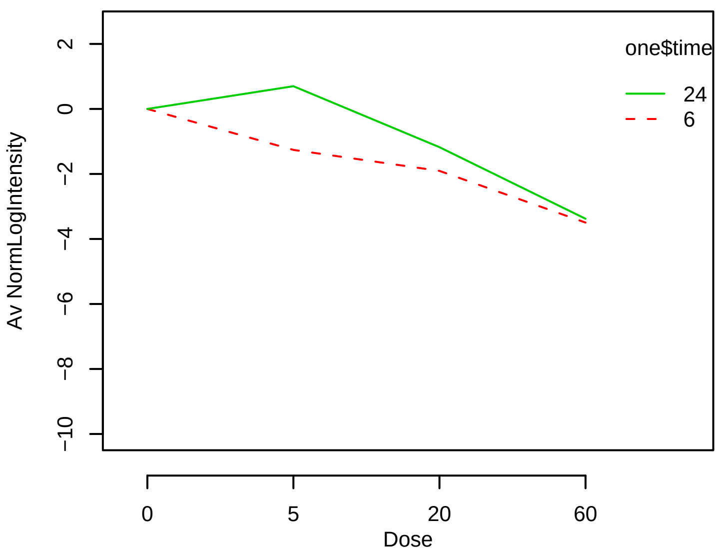

GO_0009145 : purine nucleoside triphosphate biosynthesi

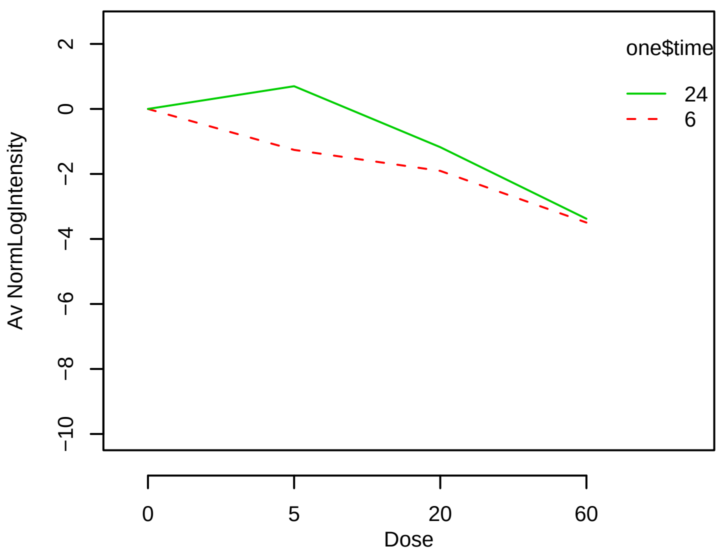

GO_0009147 : pyrimidine nucleoside triphosphate metaboli

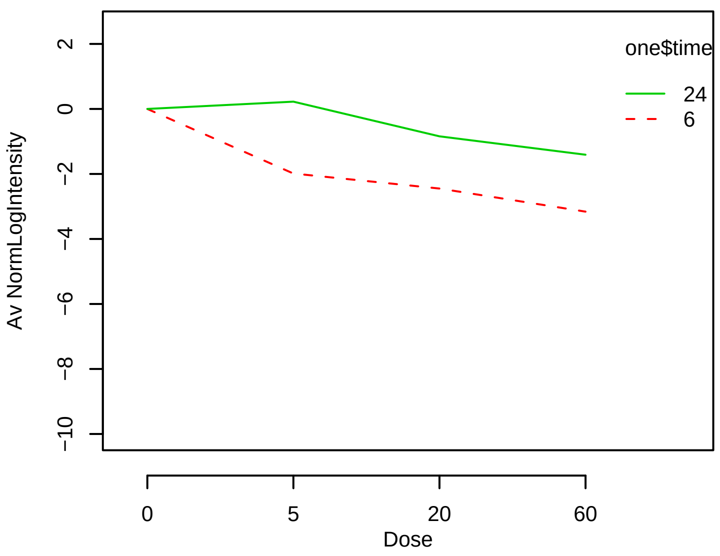

GO_0009150 : purine ribonucleotide metabolism


GO_0009152 : purine ribonucleotide biosynthesis

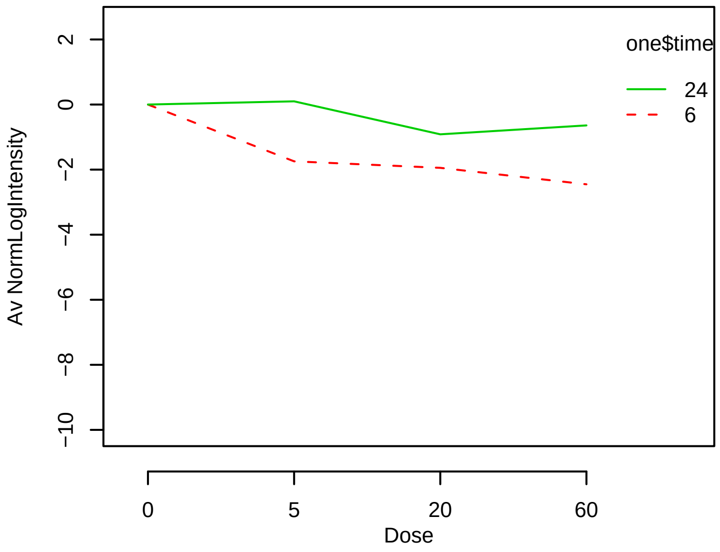

GO_0009154 : purine ribonucleotide catabolism


GO_0009156 : ribonucleoside monophosphate biosynthes

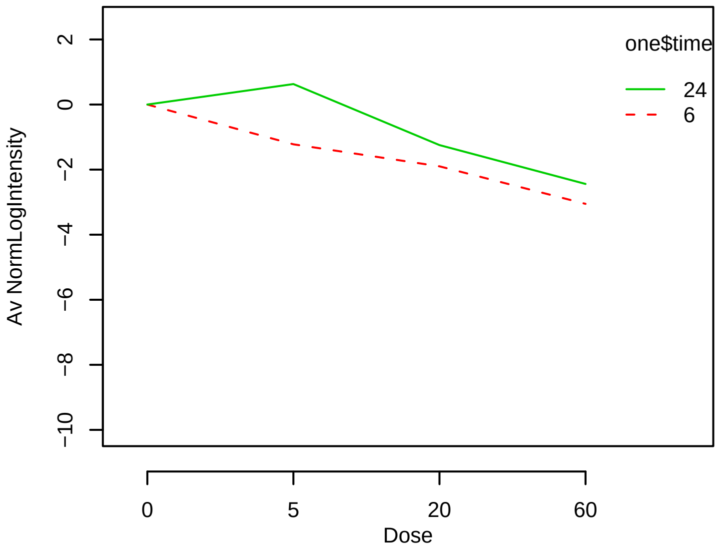

GO_0009161 : ribonucleoside monophosphate metabolisr


GO_0009165 : nucleotide biosynthesis

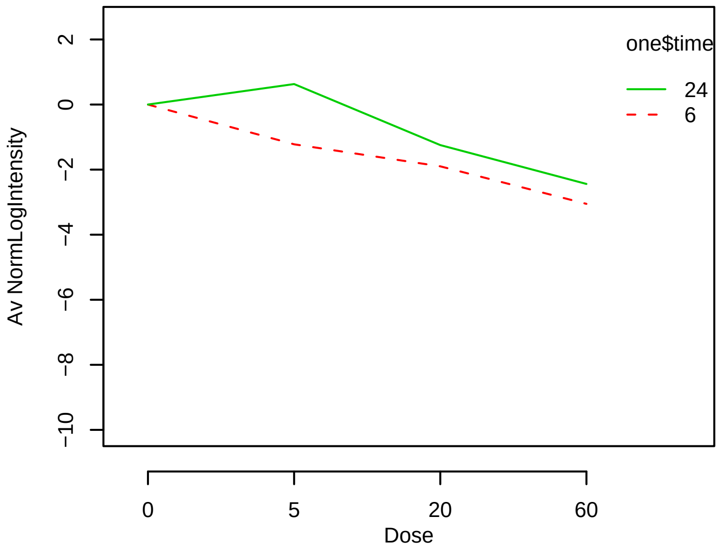
GO_0009166 : nucleotide catabolism



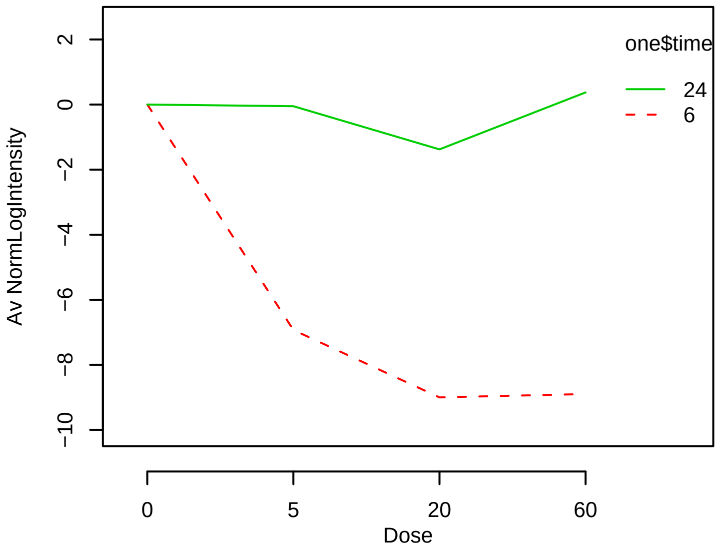
O_0009167 : purine ribonucleoside monophosphate metabo



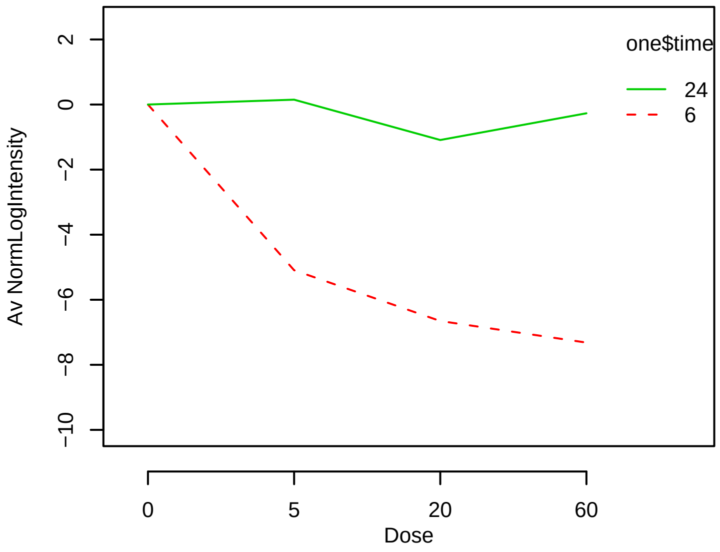
O_0009168 : purine ribonucleoside monophosphate biosynt



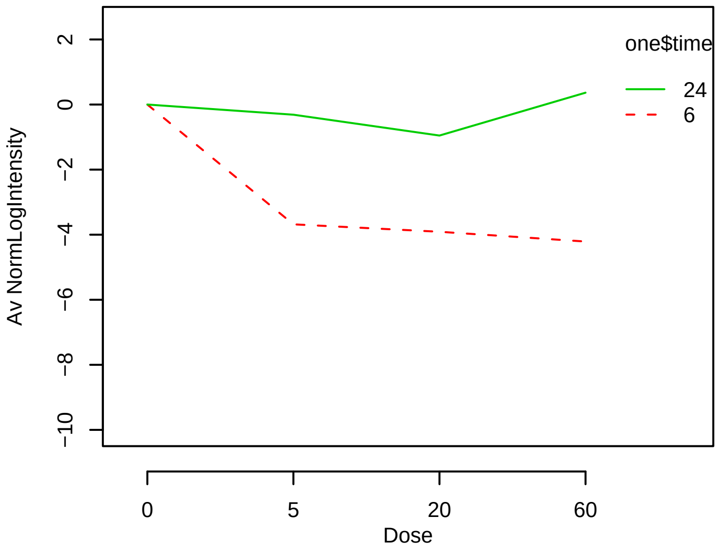
GO_0009179 : purine ribonucleoside diphosphate metaboli



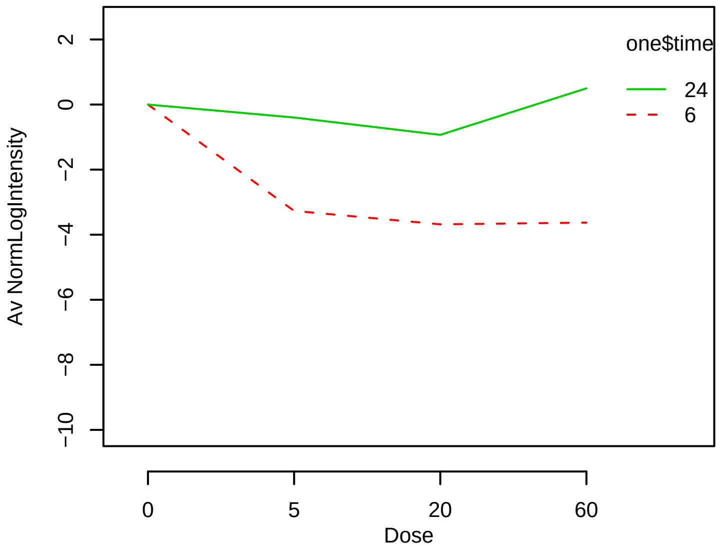
GO_0009185 : ribonucleoside diphosphate metabolism



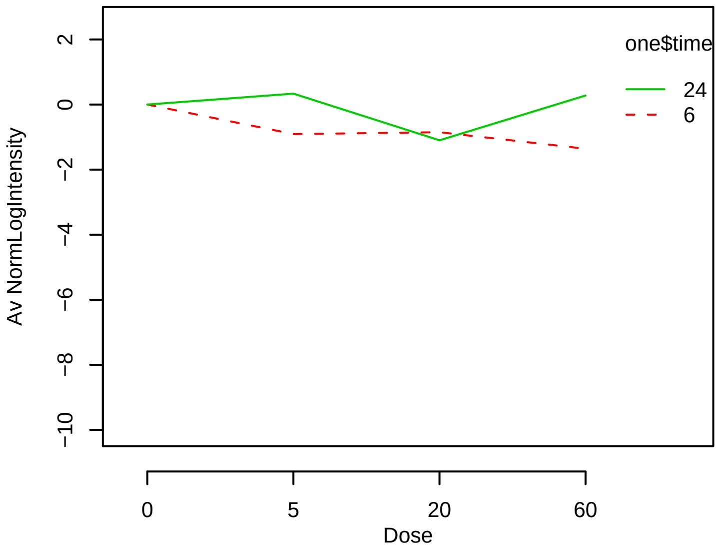
GO_0009187 : cyclic nucleotide metabolism



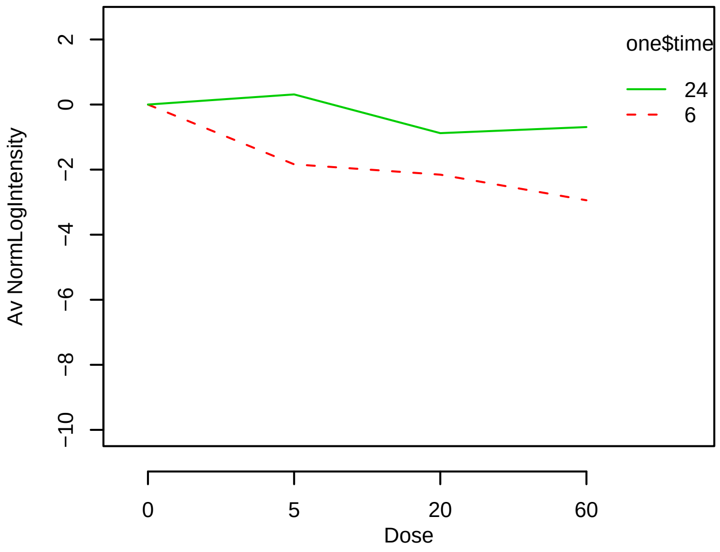
GO_0009190 : cyclic nucleotide biosynthesis



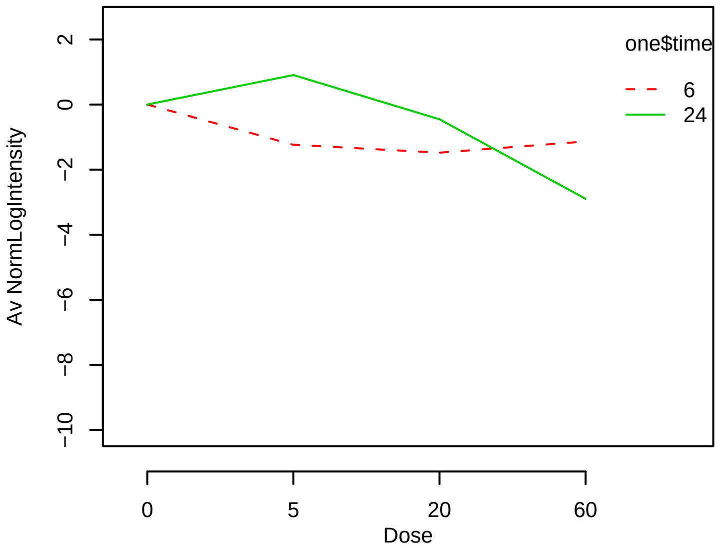
GO_0009191 : ribonucleoside diphosphate catabolism



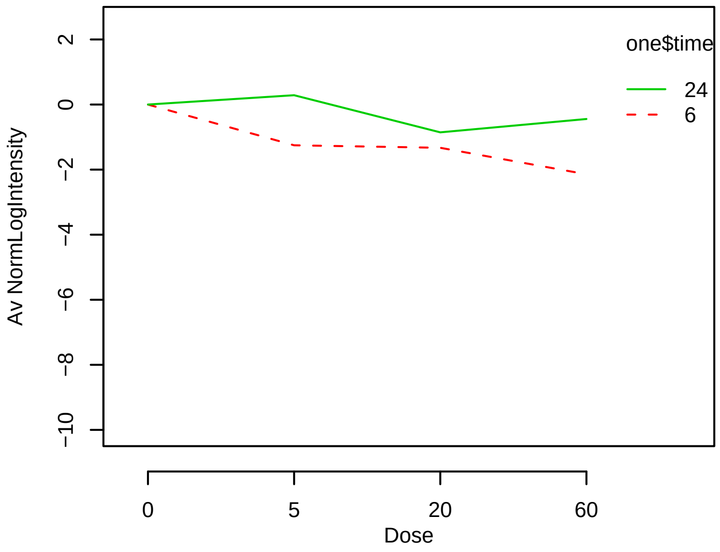
GO_0009199 : ribonucleoside triphosphate metabolism



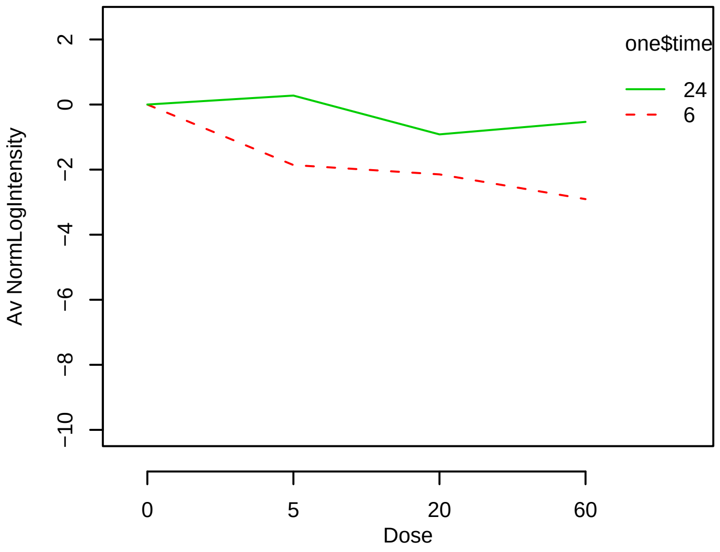
GO_0009200 : deoxyribonucleoside triphosphate metabolis



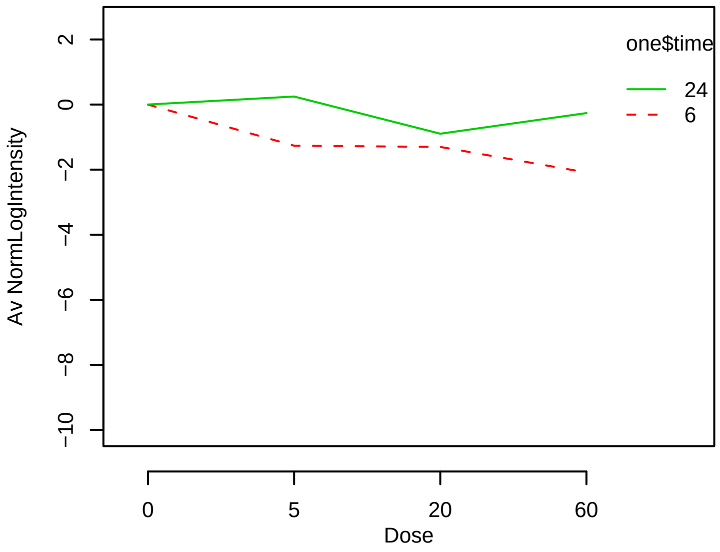
GO_0009201 : ribonucleoside triphosphate biosynthesis



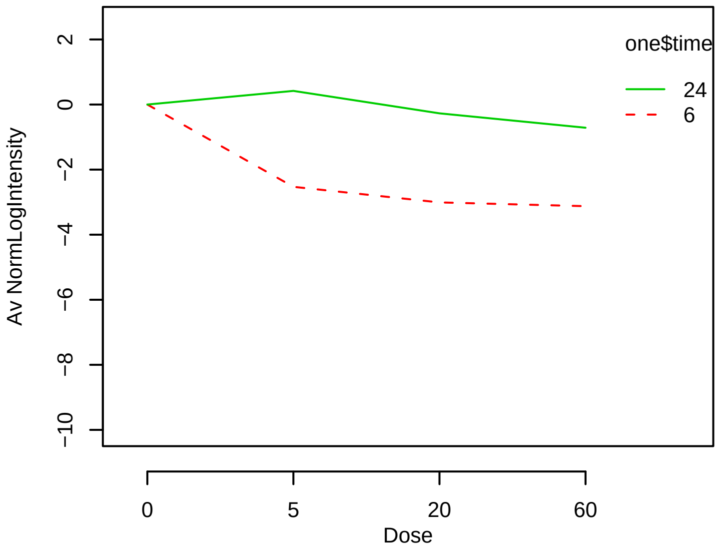
GO_0009205 : purine ribonucleoside triphosphate metabolis



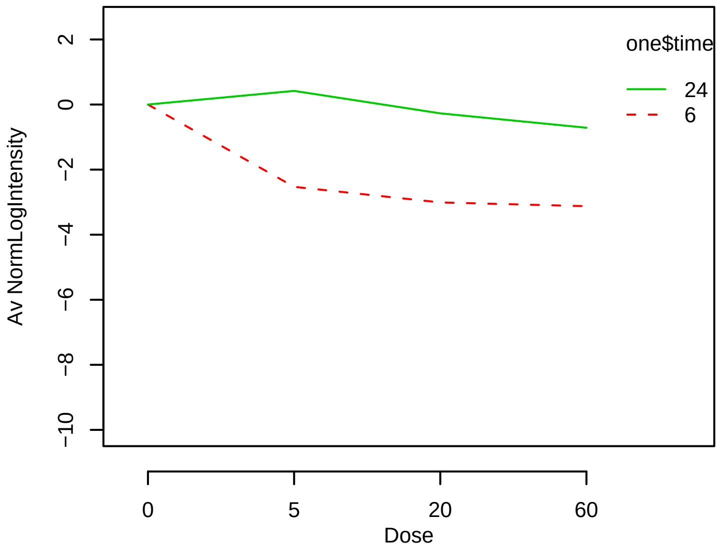
GO_0009206 : purine ribonucleoside triphosphate biosynthe



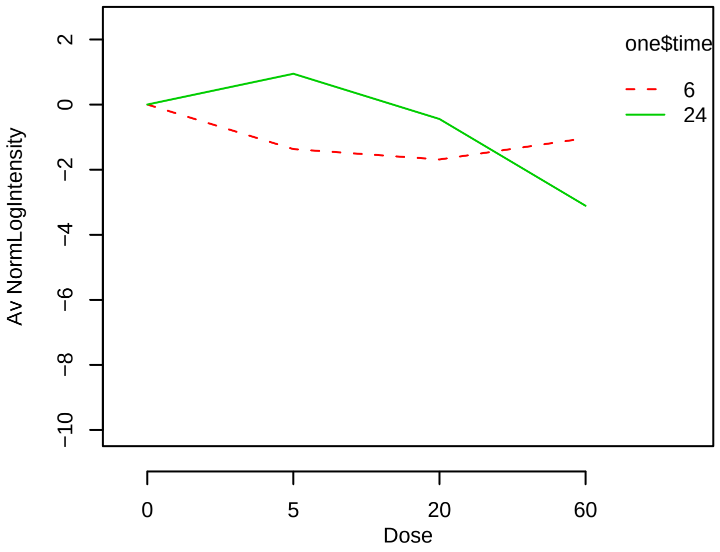
GO_0009208 : pyrimidine ribonucleoside triphosphate metabo



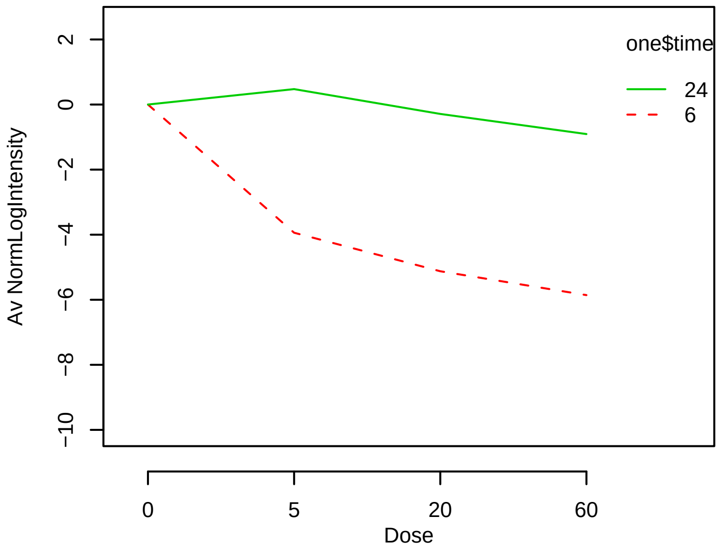
GO_0009209 : pyrimidine ribonucleoside triphosphate biosyn



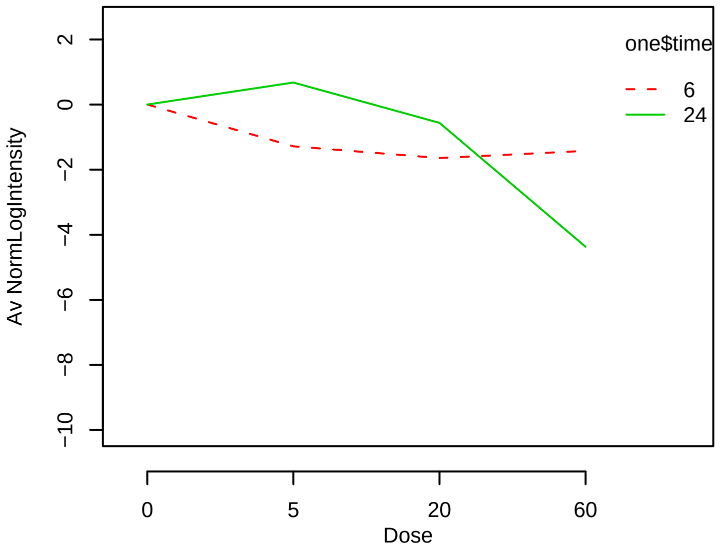
O_0009211 : pyrimidine deoxyribonucleoside triphosphate m



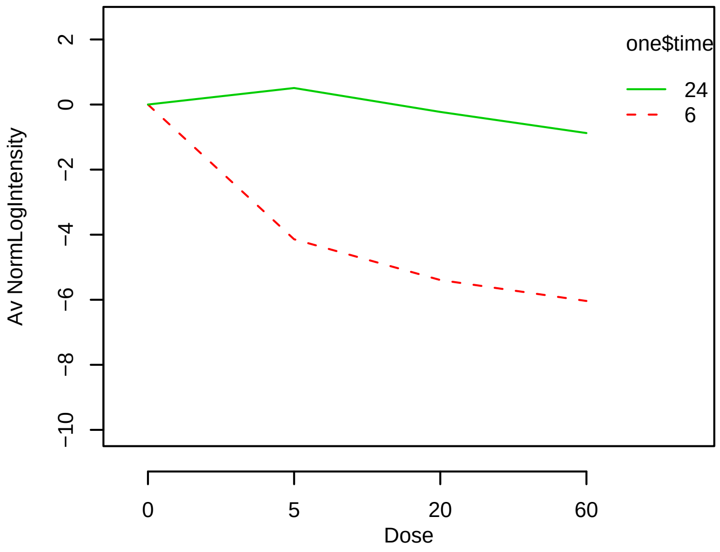
GO_0009218 : pyrimidine ribonucleotide metabolism



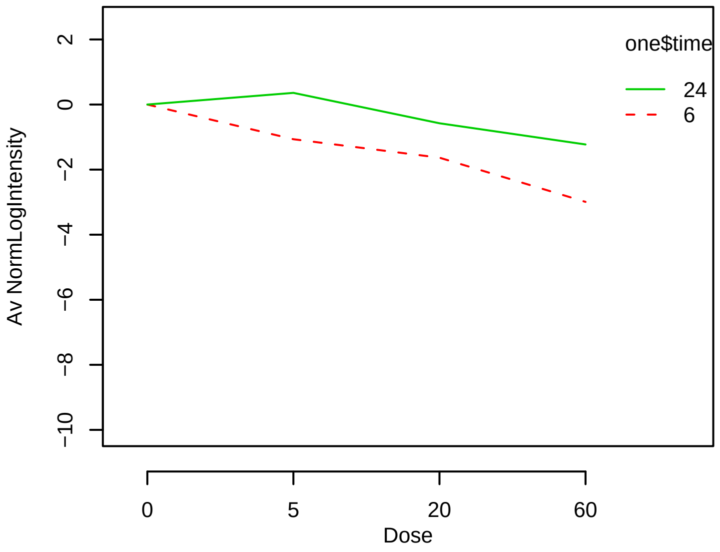
GO_0009219 : pyrimidine deoxyribonucleotide metabolism



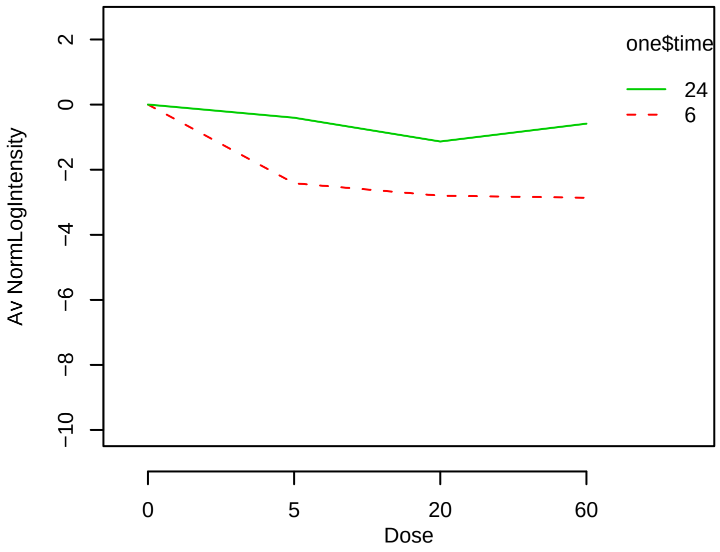
GO_0009220 : pyrimidine ribonucleotide biosynthesis



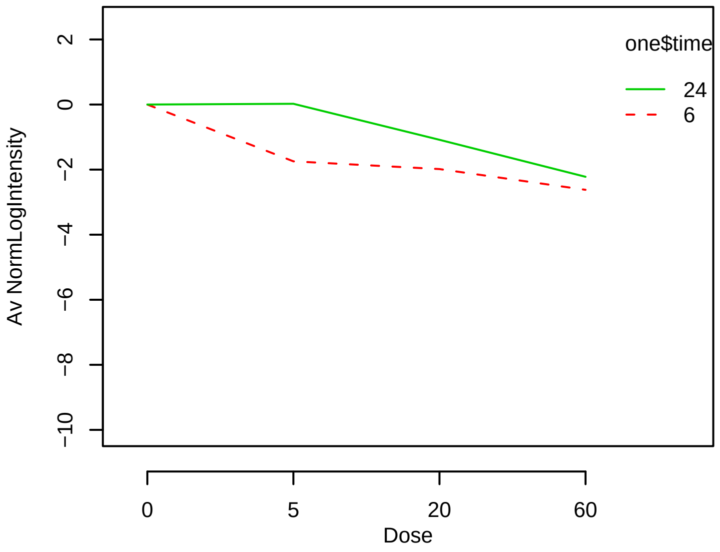
GO_0009225 : nucleotide−sugar metabolism



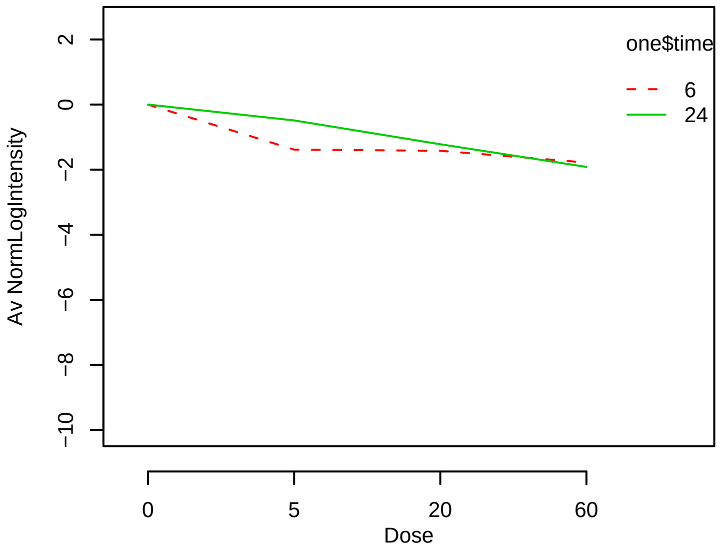
GO_0009247 : glycolipid biosynthesis



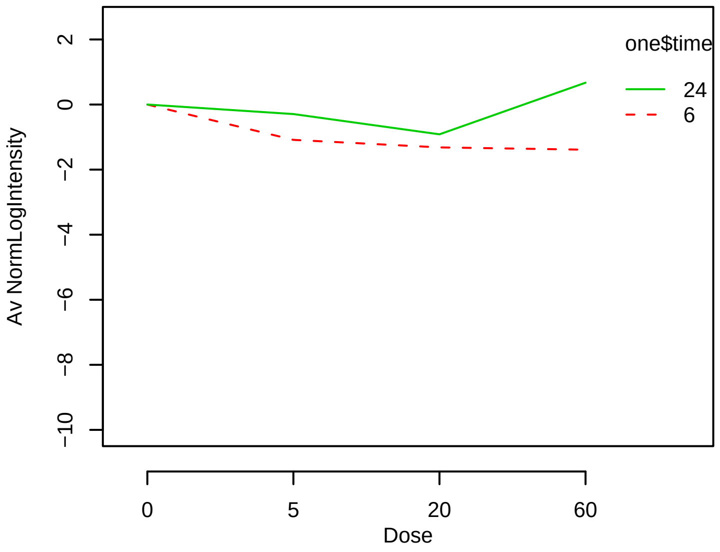
GO_0009250 : glucan biosynthesis

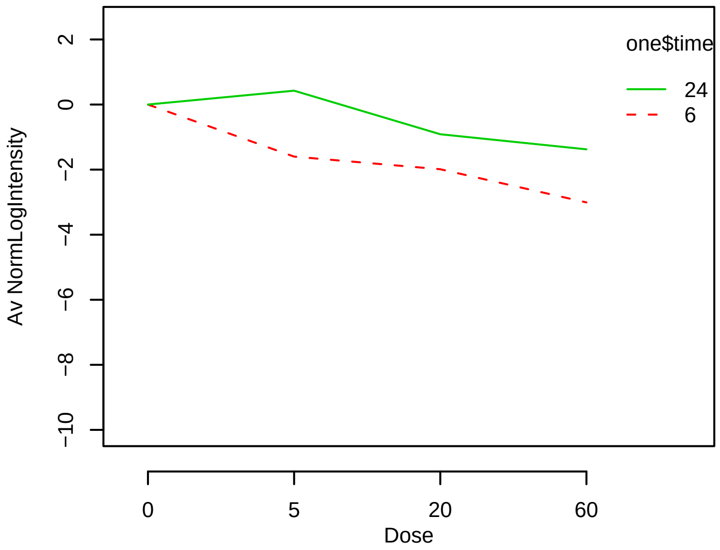


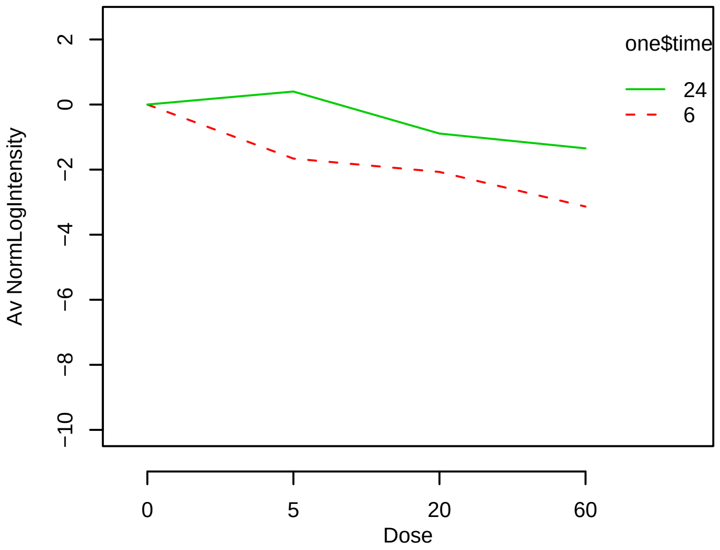
GO_0009251 : glucan catabolism

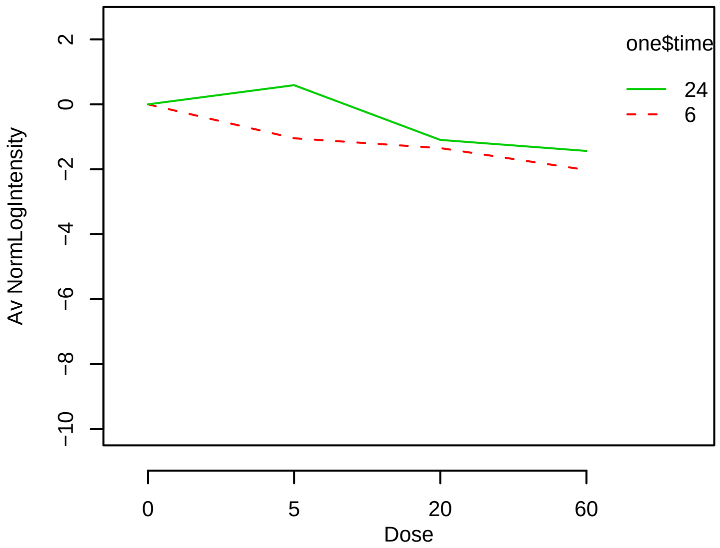


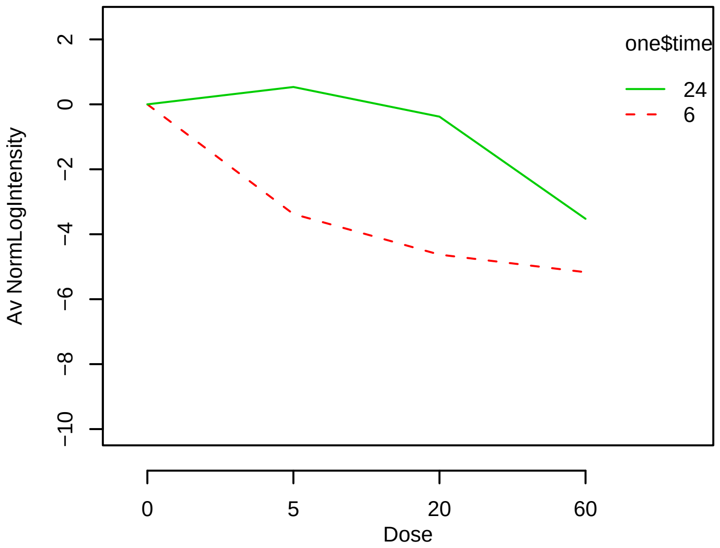
GO_0009253 : peptidoglycan catabolism

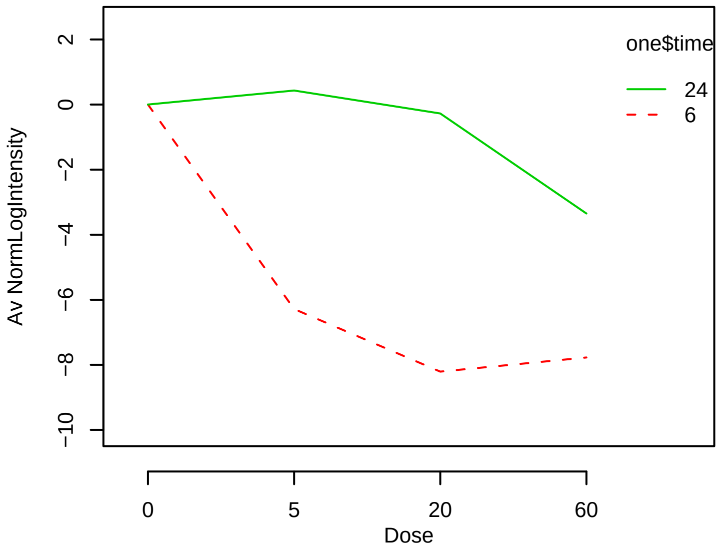


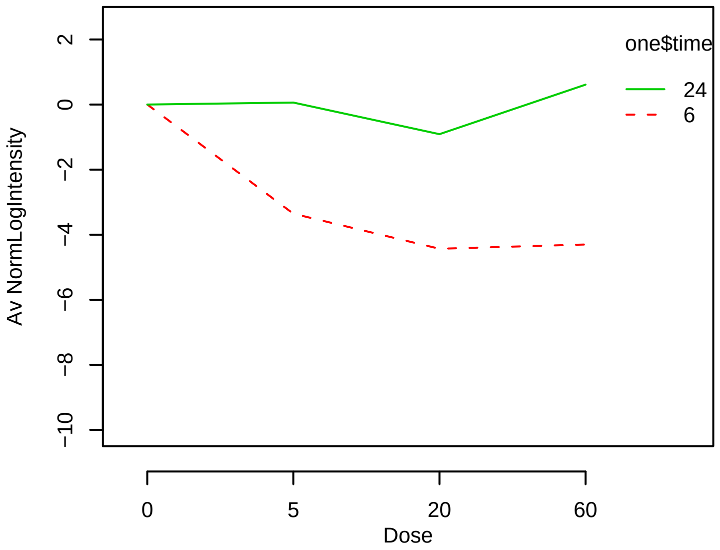

GO_0009259 : ribonucleotide metabolism

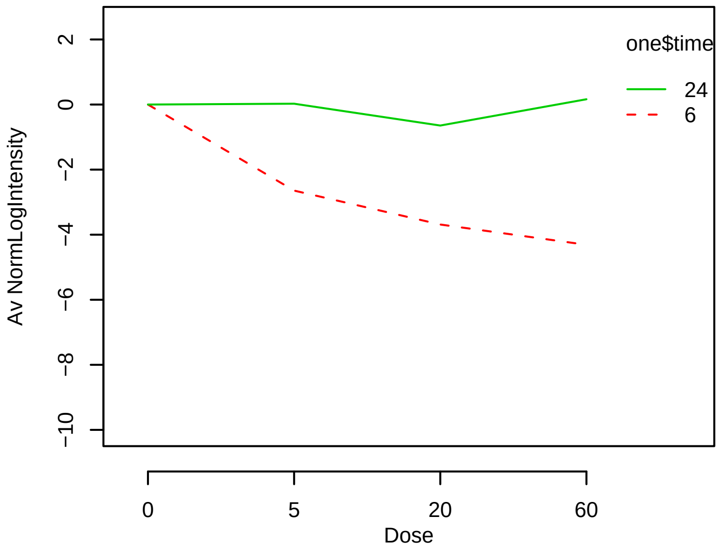

GO_0009260 : ribonucleotide biosynthesis

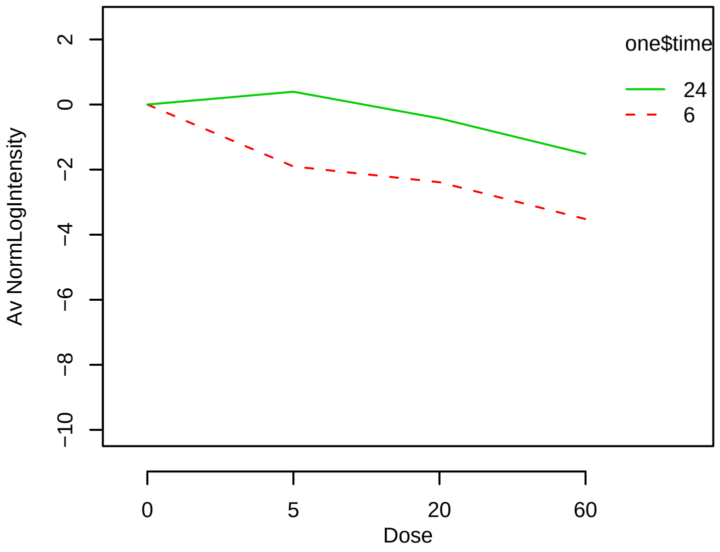

GO_0009261 : ribonucleotide catabolism

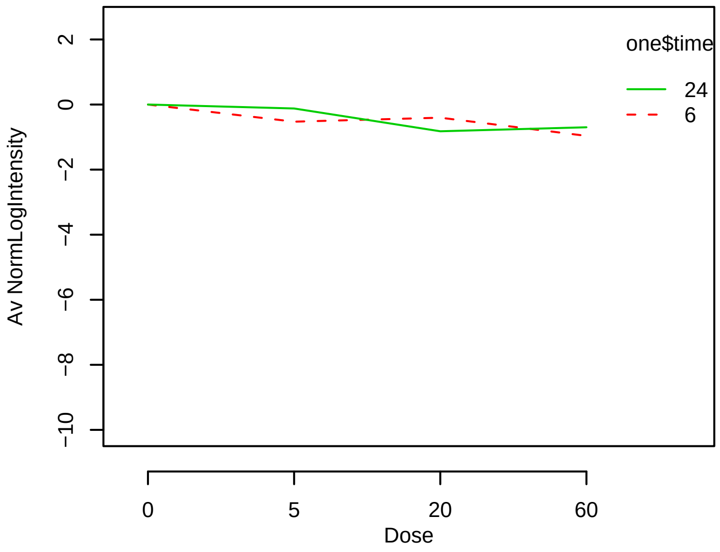

GO_0009262 : deoxyribonucleotide metabolism

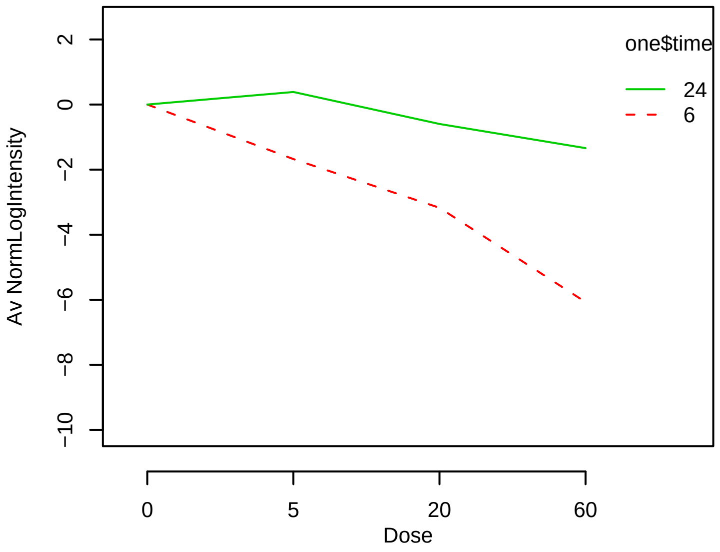

GO_0009263 : deoxyribonucleotide biosynthesis

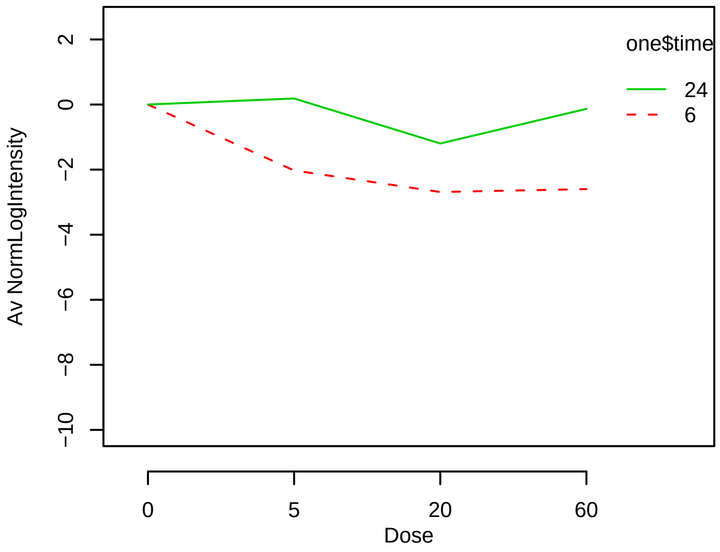

GO_0009266 : response to temperature stimulus

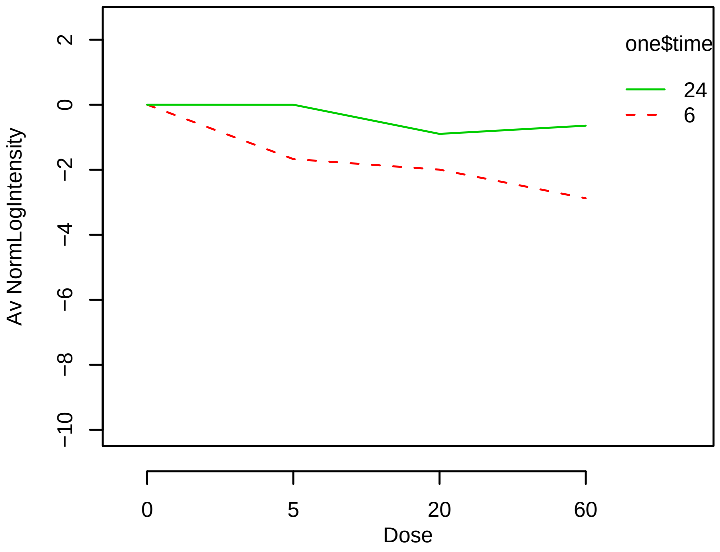

GO_0009267 : cellular response to starvation

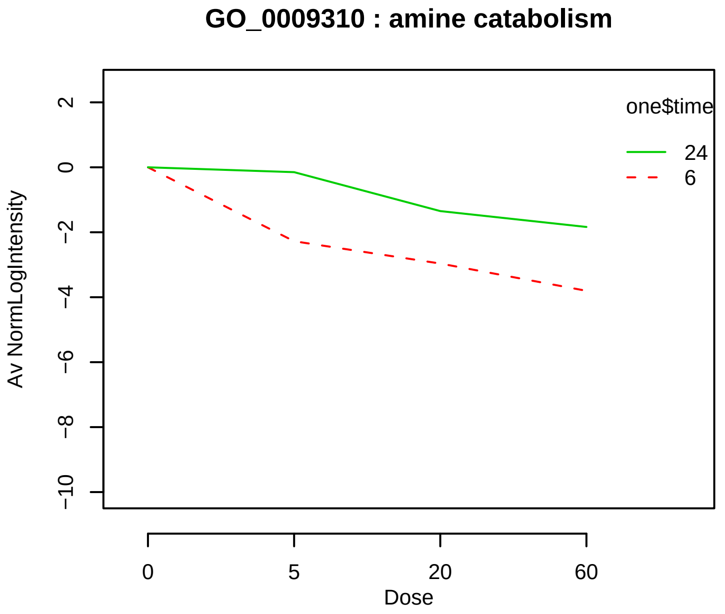

GO_0009268 : response to pH

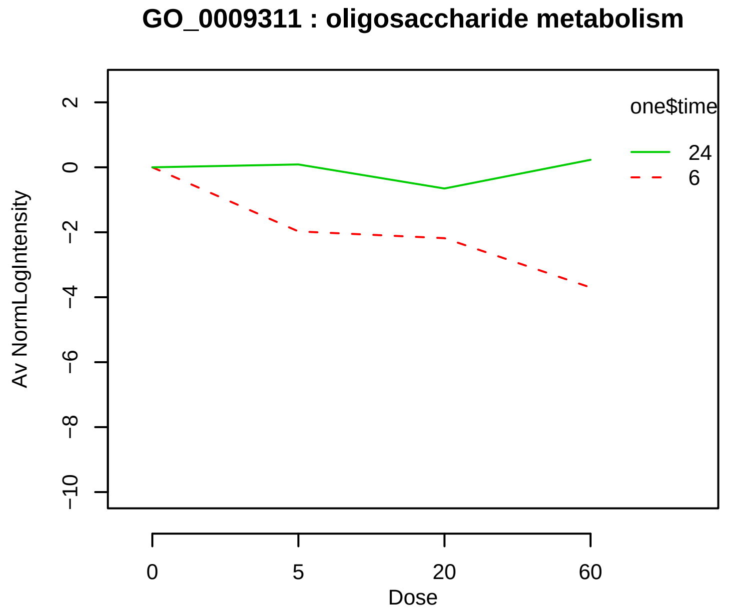

GO_0009296 : flagellum biogenesis

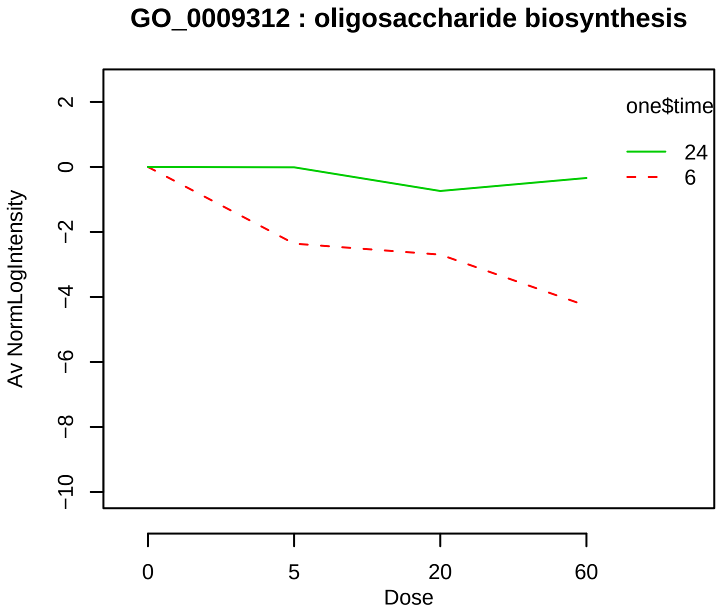

GO_0009303 : rRNA transcription

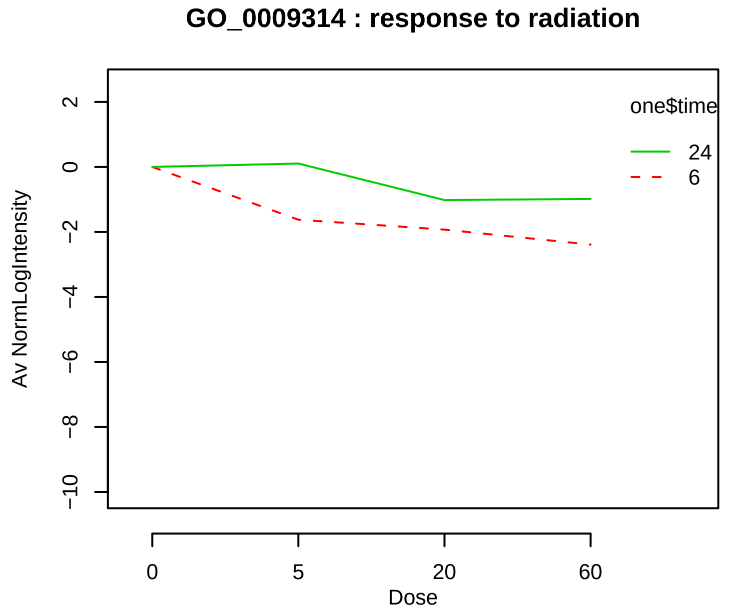

GO_0009306 : protein secretion

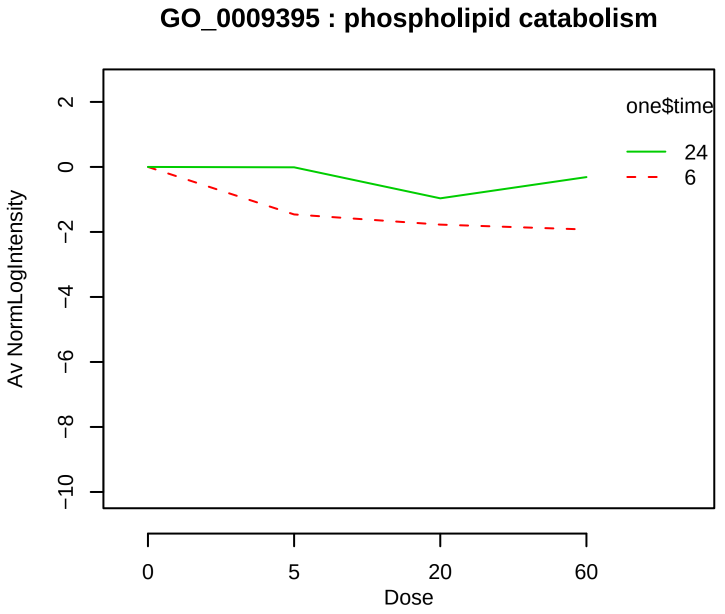

GO_0009309 : amine biosynthesis

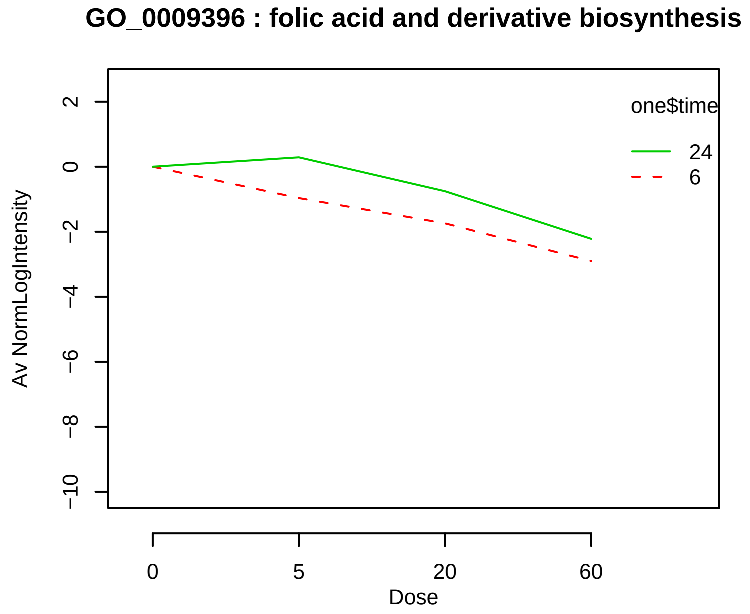

GO_0009310 : amine catabolism
one$time
24
6
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
0
5
20
60
Dose

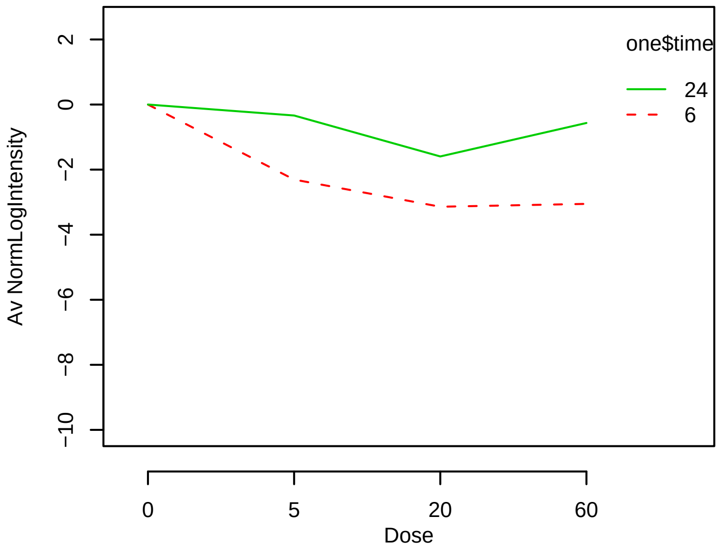

GO_0009311 : oligosaccharide metabolism
one$time
24
6
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
0
5
20
60
Dose

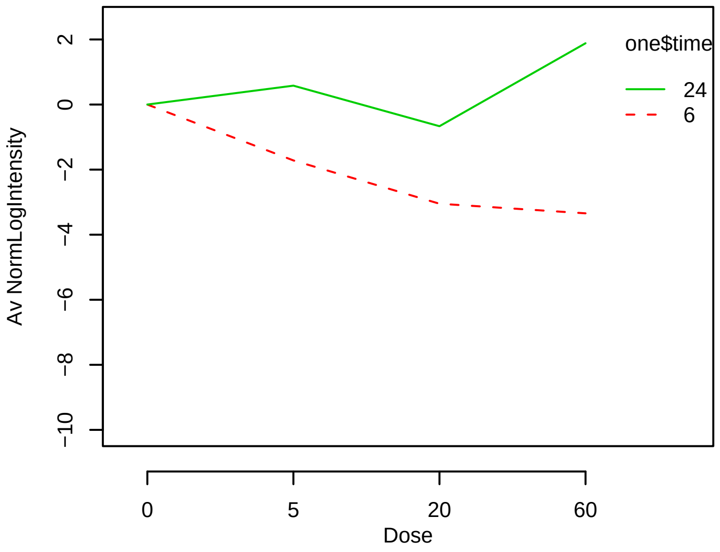

GO_0009312 : oligosaccharide biosynthesis
one$time
24
6
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
0
5
20
60
Dose

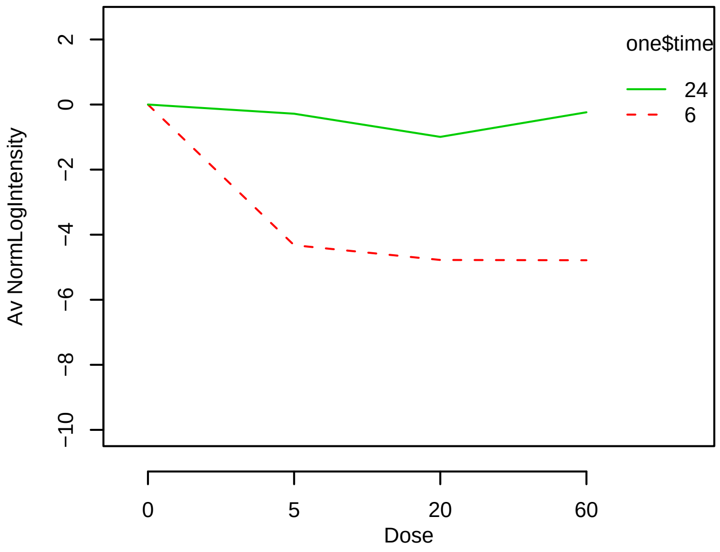

GO_0009314 : response to radiation
one$time
24
6
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
0
5
20
60
Dose

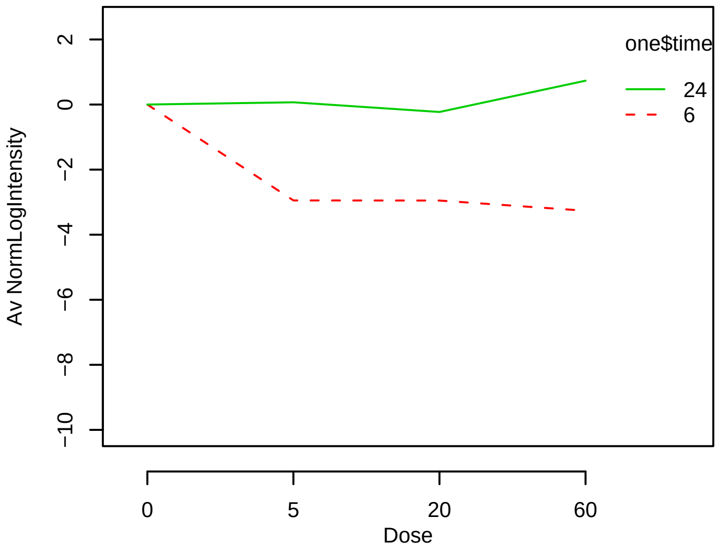

GO_0009395 : phospholipid catabolism
one$time
24
6
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
0
5
20
60
Dose

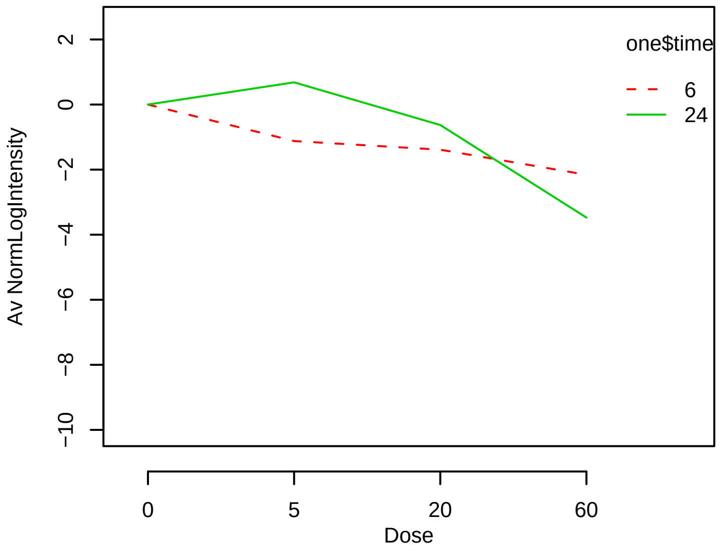

GO_0009396 : folic acid and derivative biosynthesis
one$time
24
6
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
0
5
20
60
Dose

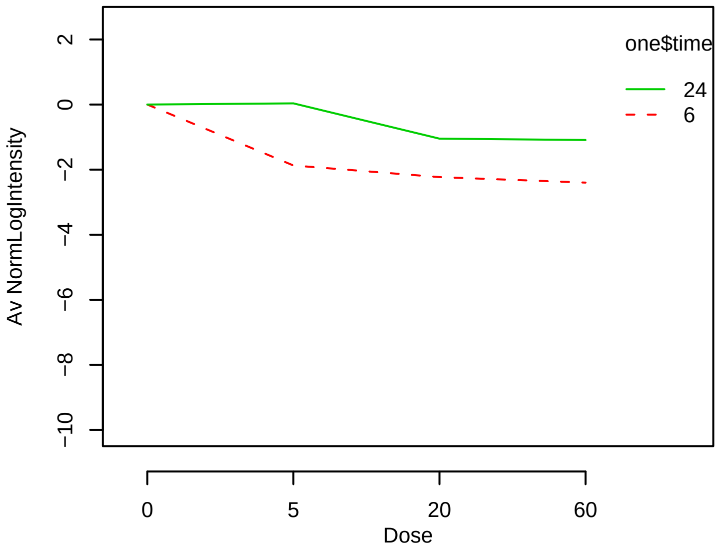

GO_0009405 : pathogenesis


GO_0009408 : response to heat

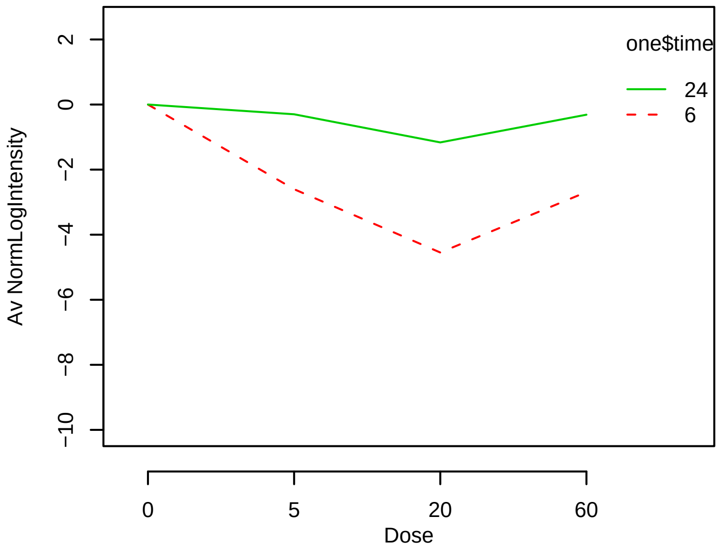

GO_0009409 : response to cold


GO_0009410 : response to xenobiotic stimulus

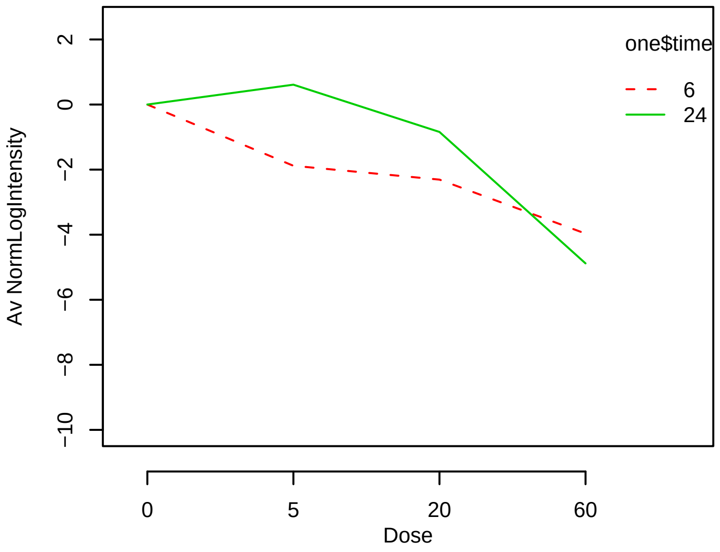

GO_0009411 : response to UV


GO_0009416 : response to light stimulus

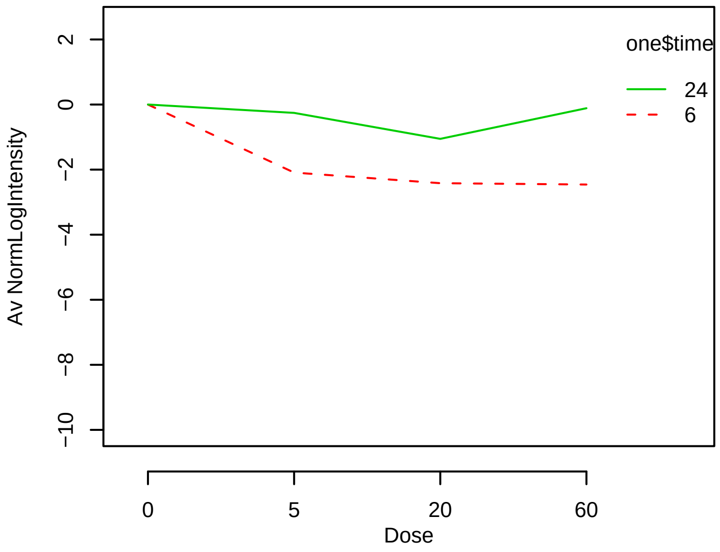
GO_0009435 : NAD biosynthesis



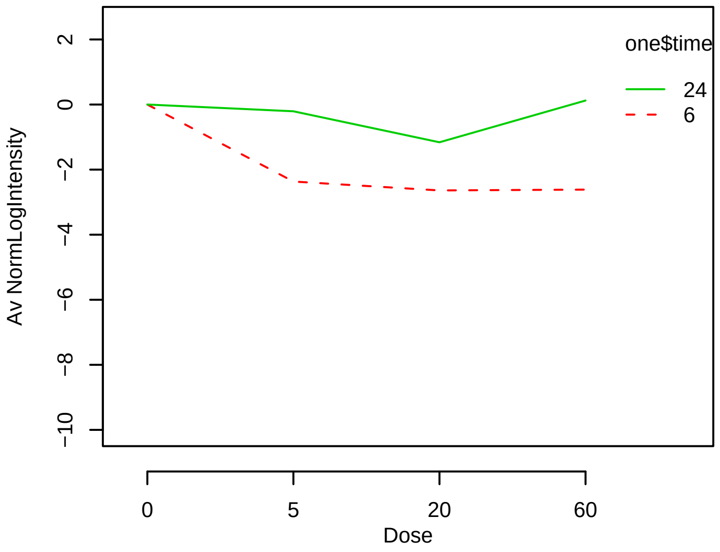
GO_0009451 : RNA modification



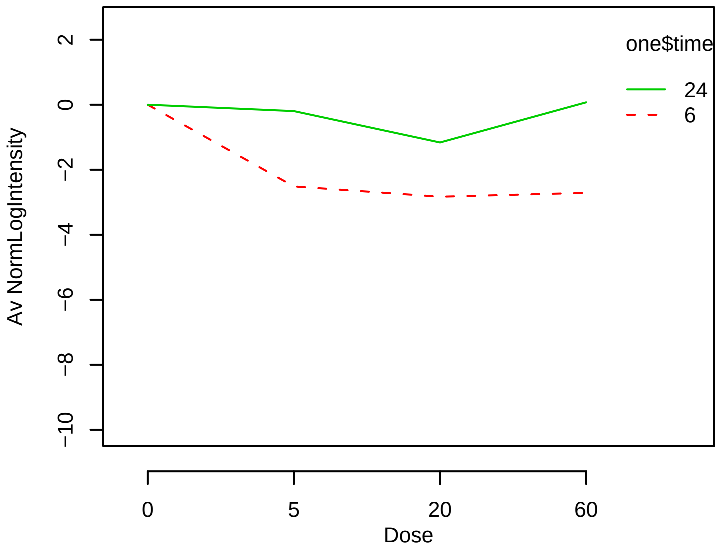
GO_0009566 : fertilization



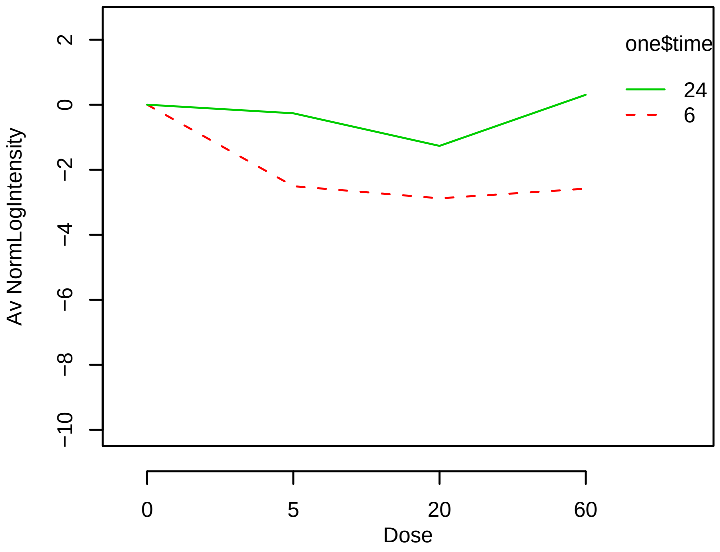
GO_0009581 : detection of external stimulus

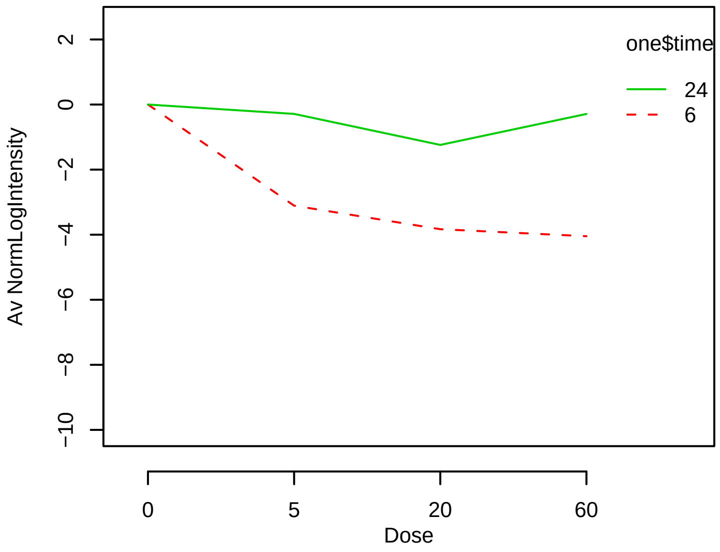


GO_0009582 : detection of abiotic stimulus

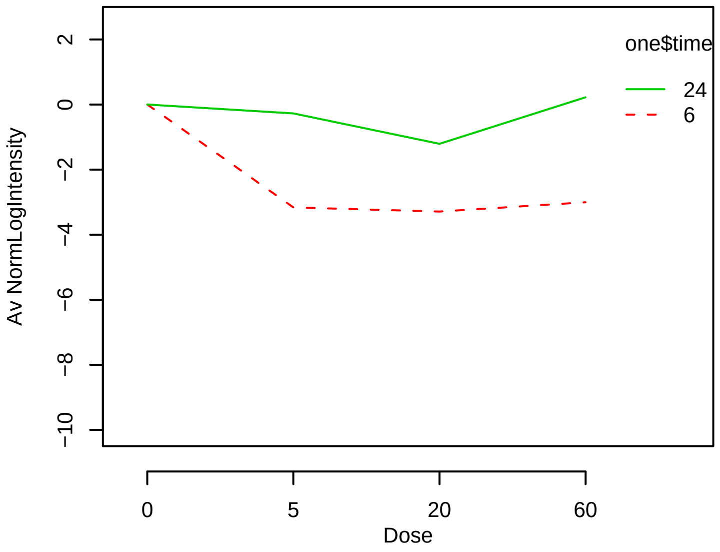


GO_0009583 : detection of light stimulus

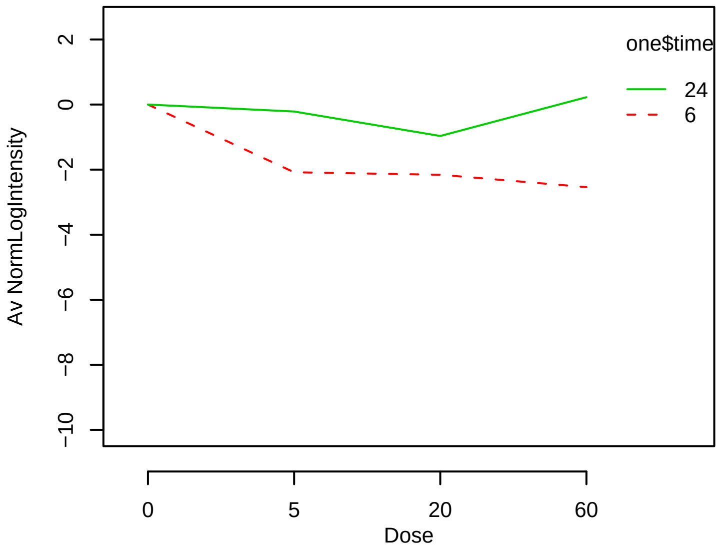




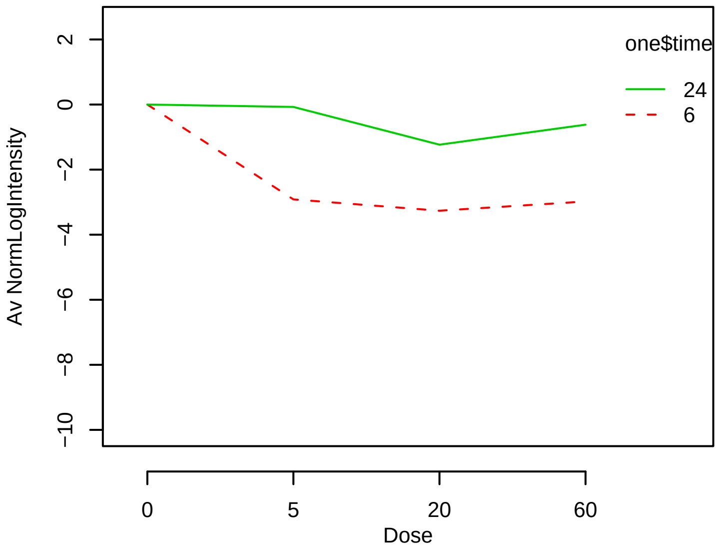
GO_0009584 : detection of visible light



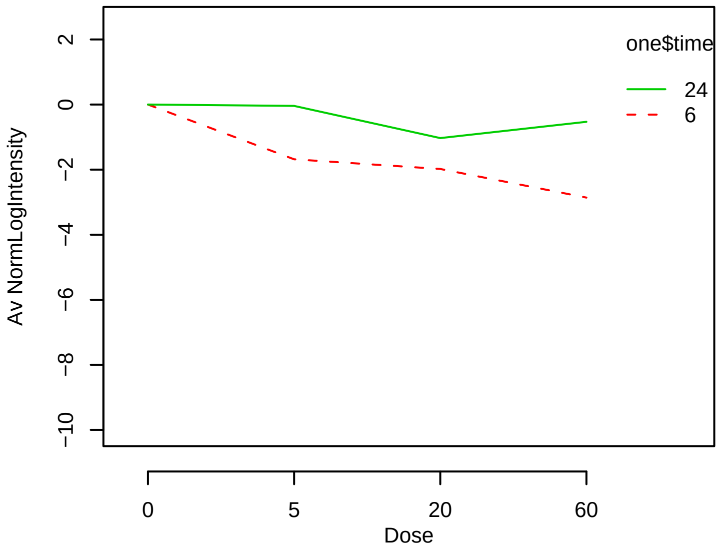
GO_0009593 : detection of chemical stimulus



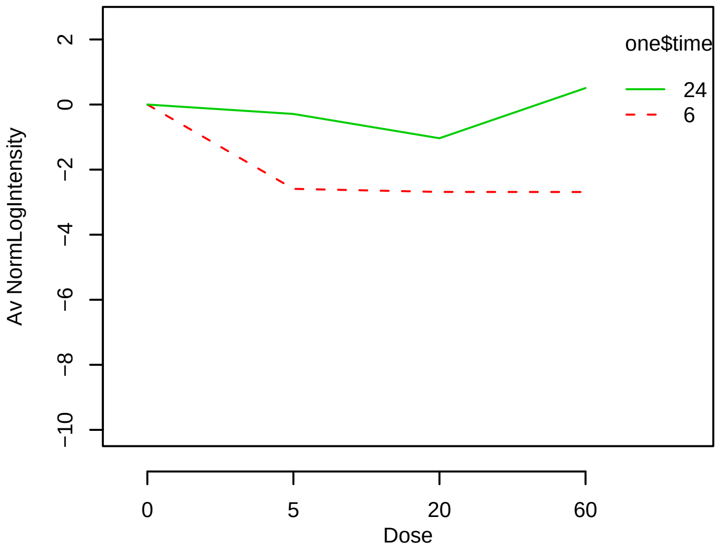
GO_0009595 : detection of biotic stimulus



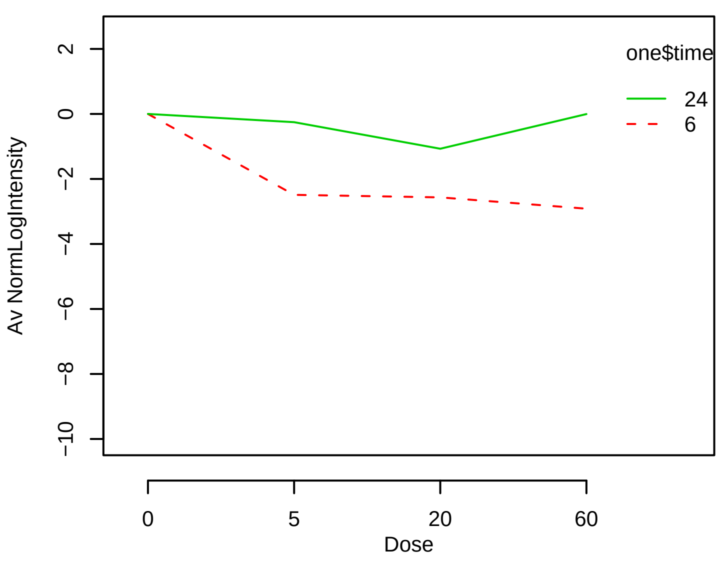
GO_0009612 : response to mechanical stimulus

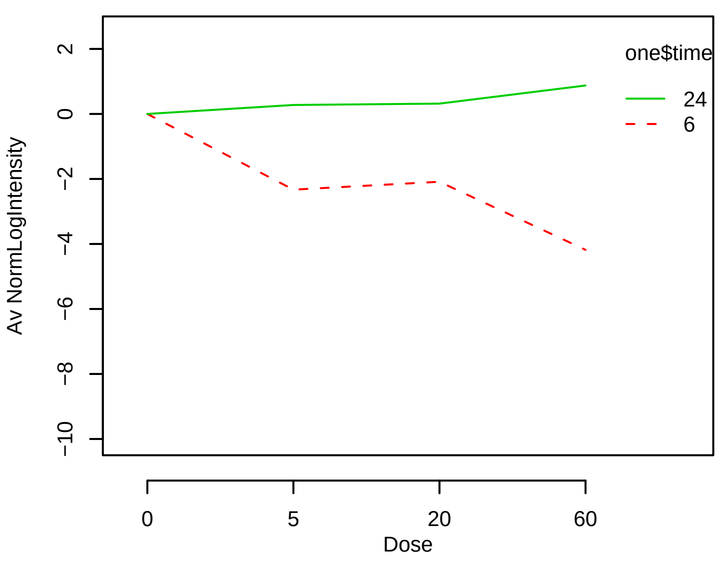


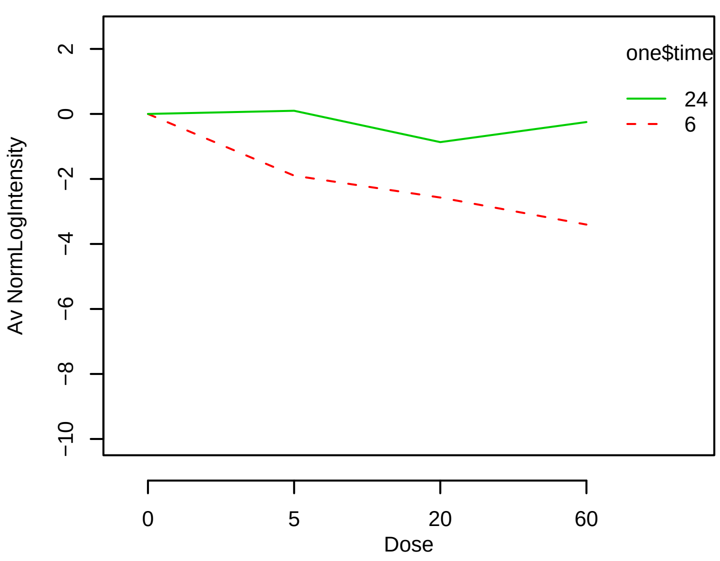
GO_0009615 : response to virus

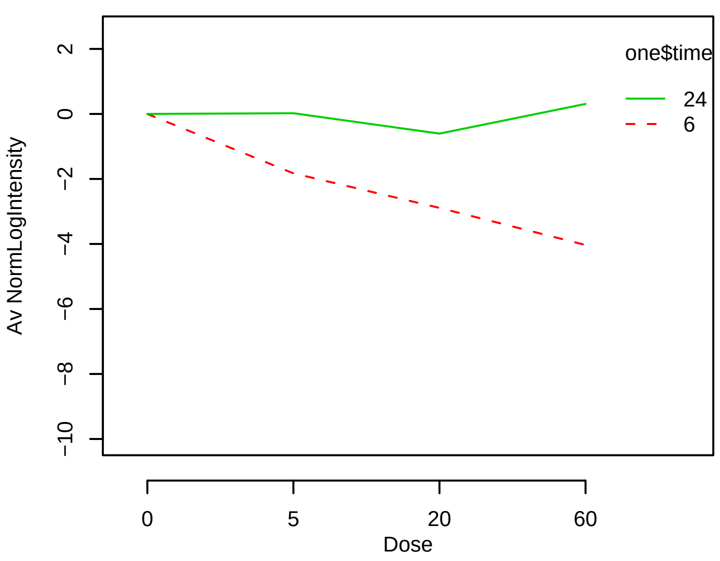


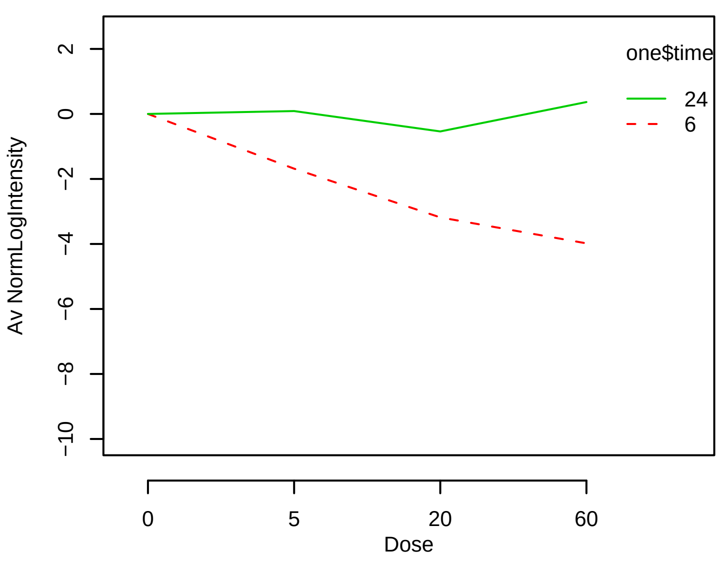
GO_0009617 : response to bacterium

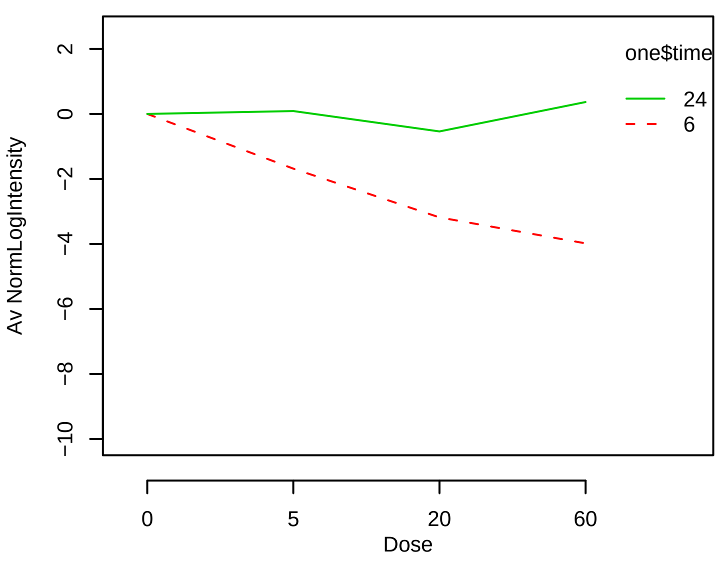

GO_0009620 : response to fungus


GO_0009636 : response to toxin

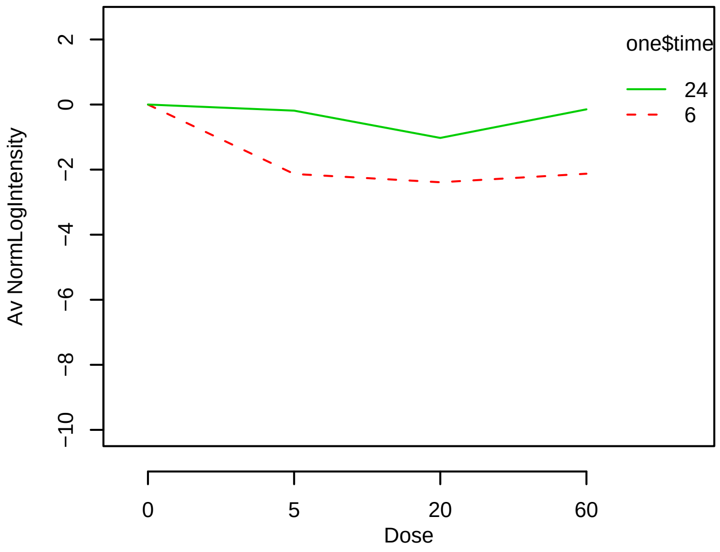

GO_0009725 : response to hormone stimulus


GO_0009743 : response to carbohydrate stimulus

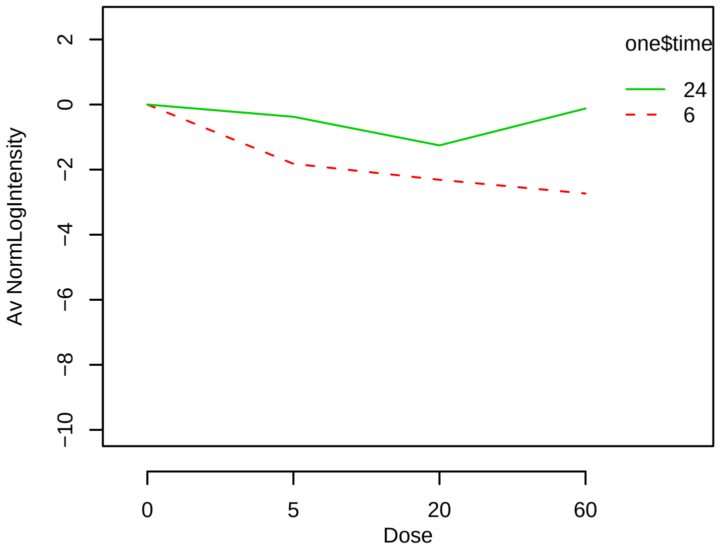

GO_0009746 : response to hexose stimulus


GO_0009749 : response to glucose stimulus

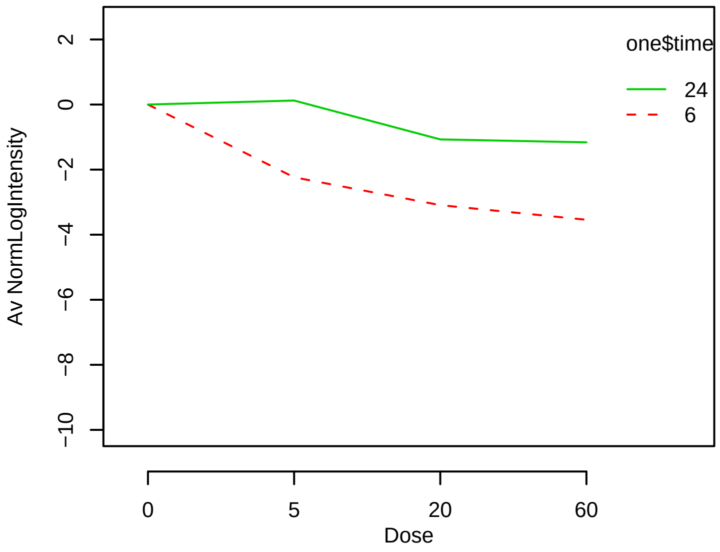
GO_0009755 : hormone−mediated signaling



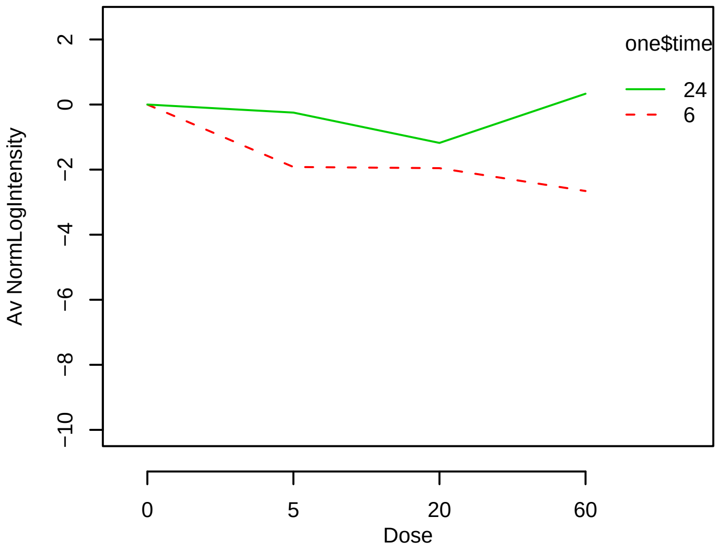
GO_0009791 : post−embryonic development



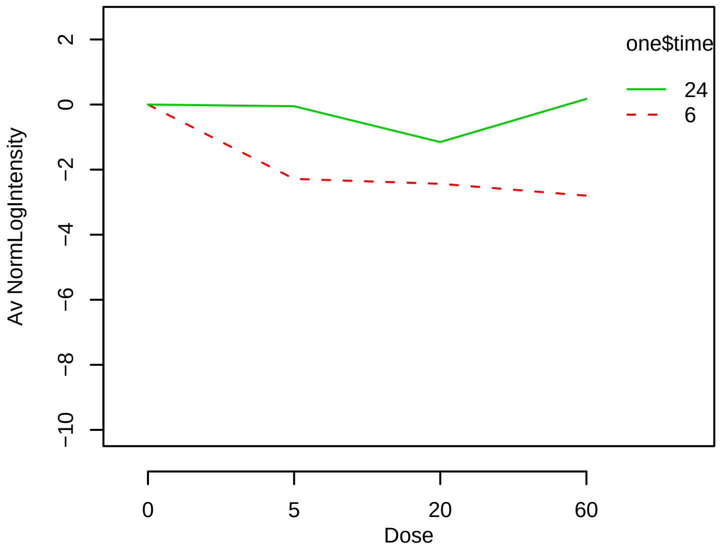
GO_0009792 : embryonic development (sensu Metazoa)



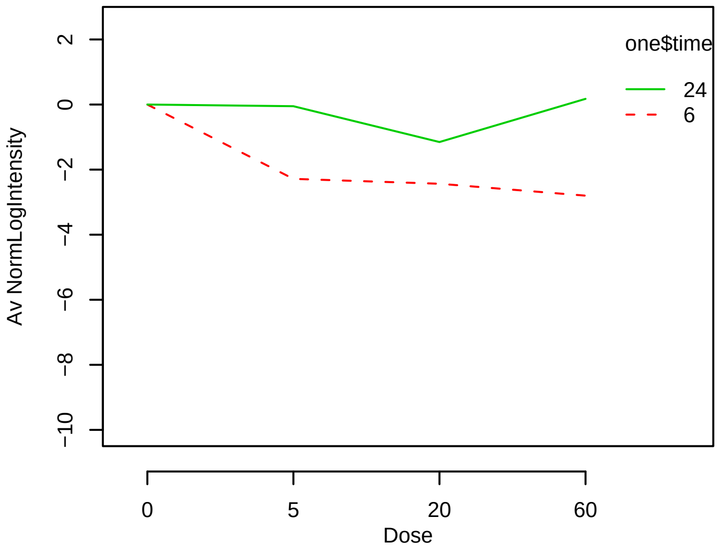
GO_0009798 : axis specification

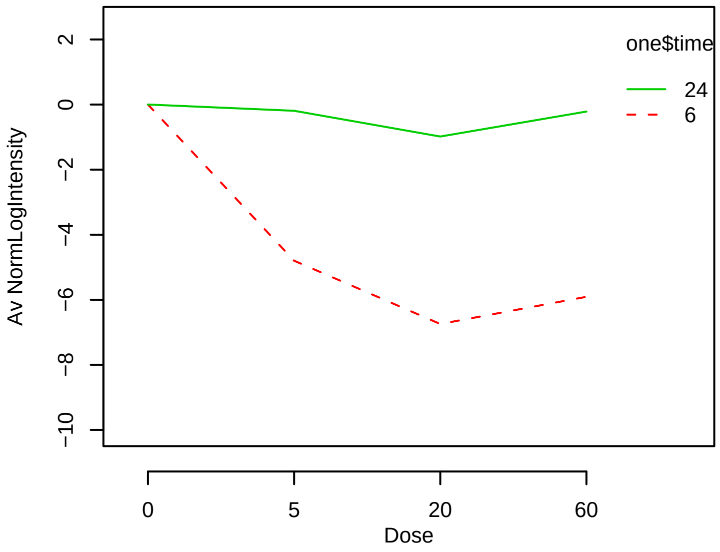


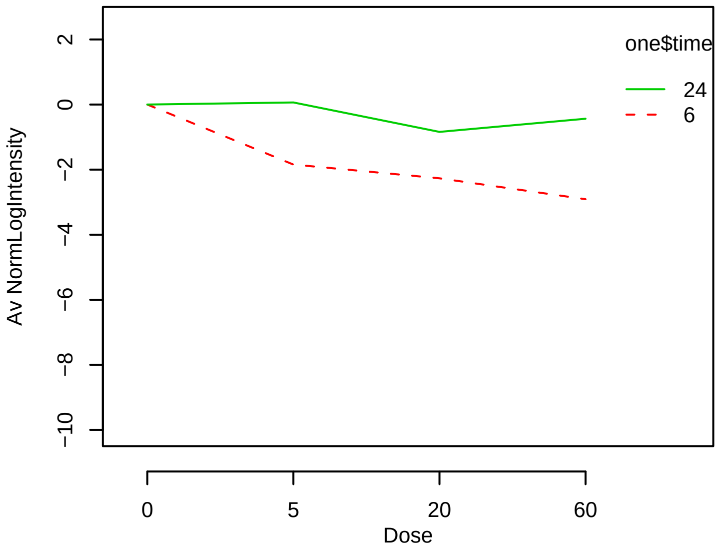
GO_0009799 : determination of symmetry

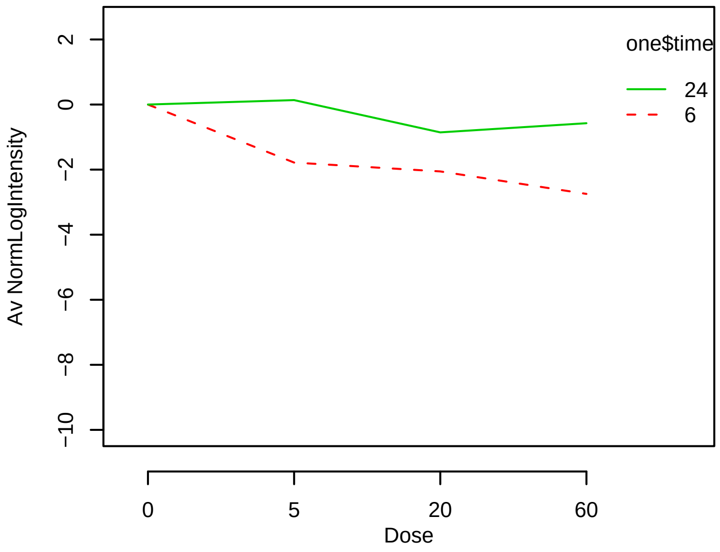


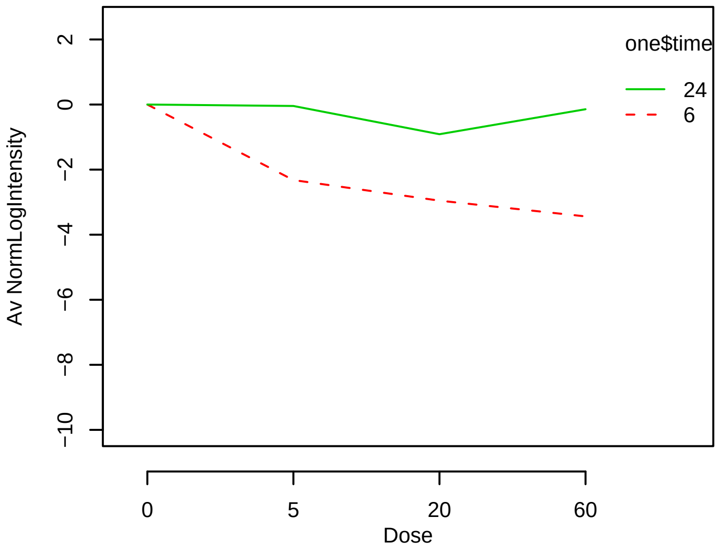
GO_0009855 : determination of bilateral symmetry

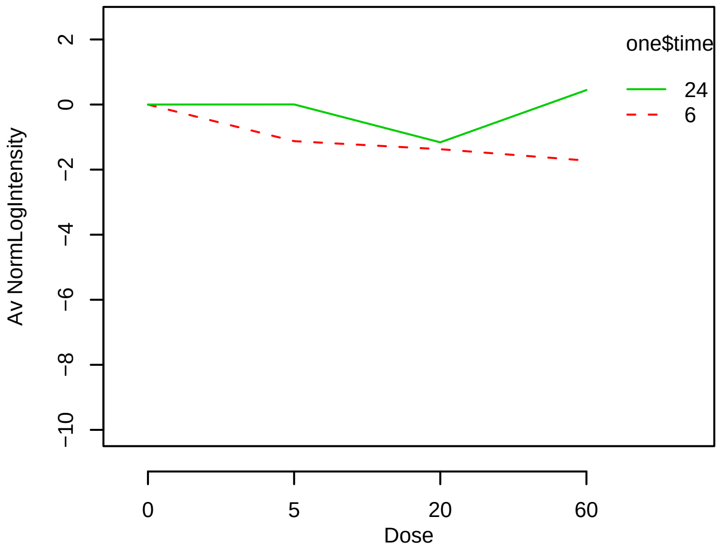


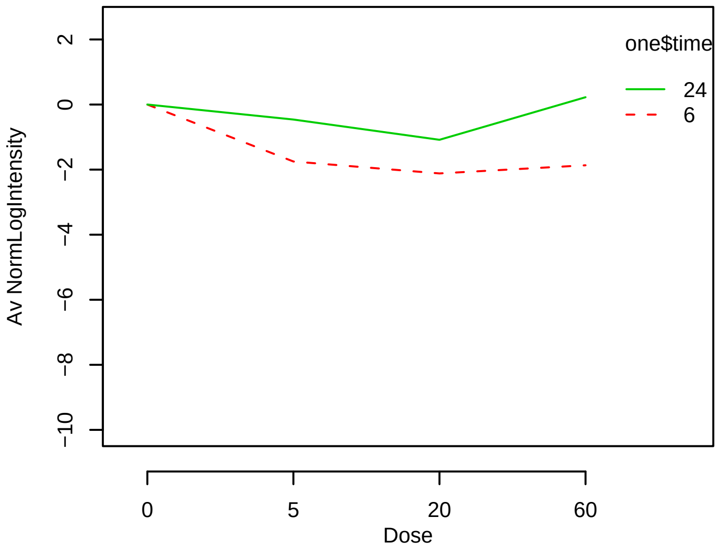

GO_0009880 : embryonic pattern specification


GO_0009889 : regulation of biosynthesis

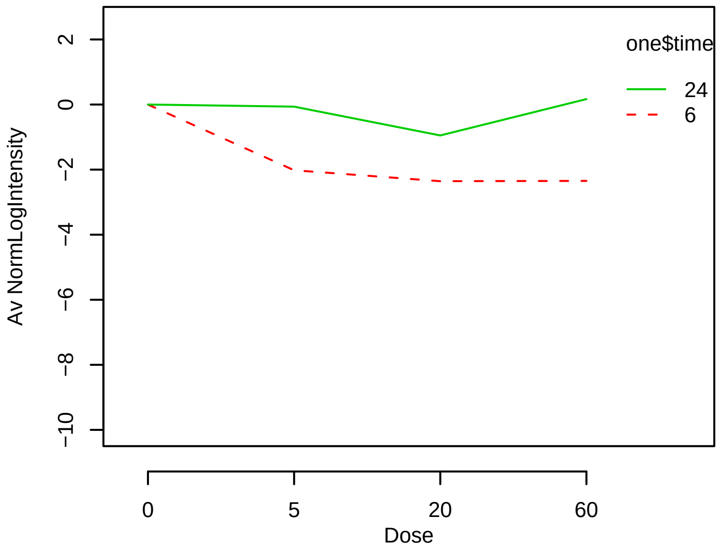

GO_0009890 : negative regulation of biosynthesis


GO_0009891 : positive regulation of biosynthesis

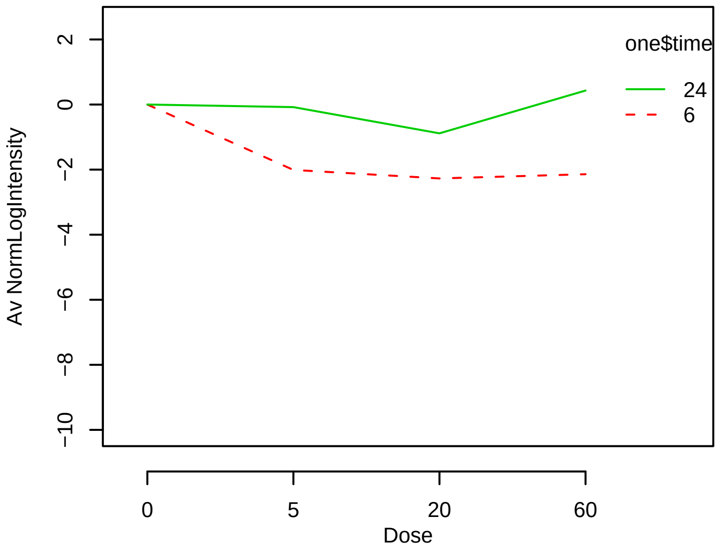

GO_0009894 : regulation of catabolism


GO_0009895 : negative regulation of catabolism

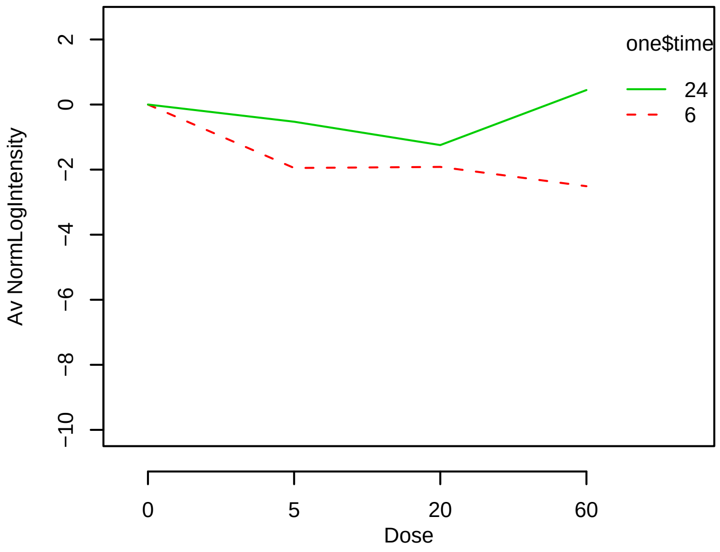
GO_0009912 : auditory receptor cell fate commitment



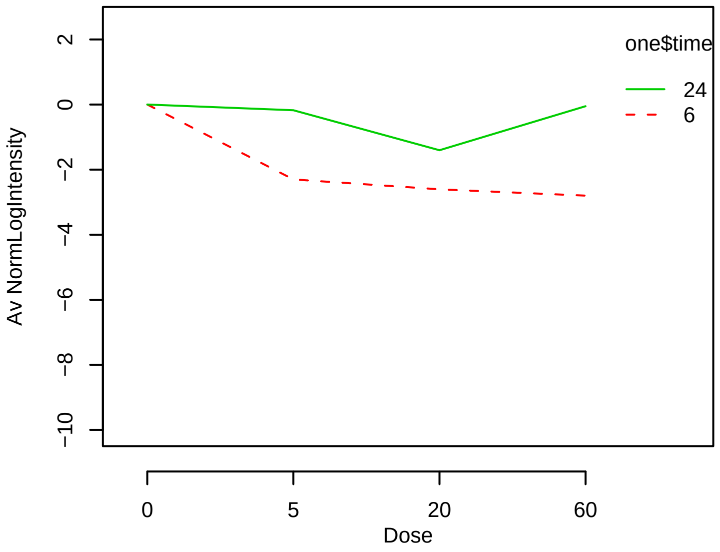
GO_0009913 : epidermal cell differentiation



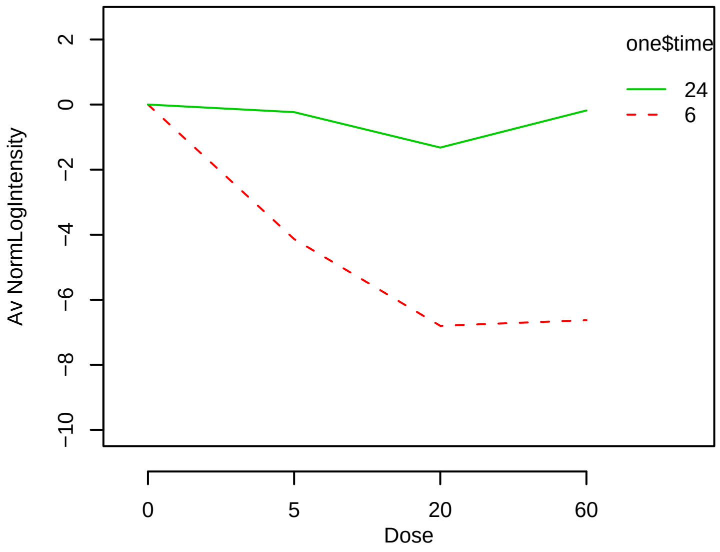
GO_0009948 : anterior/posterior axis specification



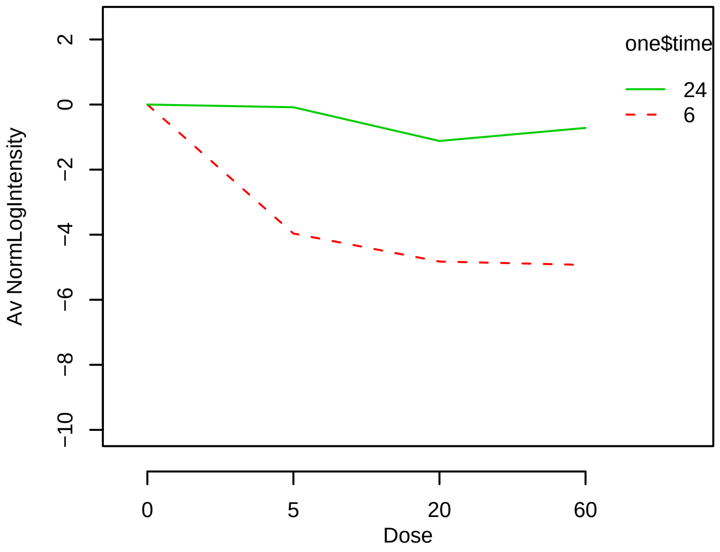
GO_0009952 : anterior/posterior pattern formation

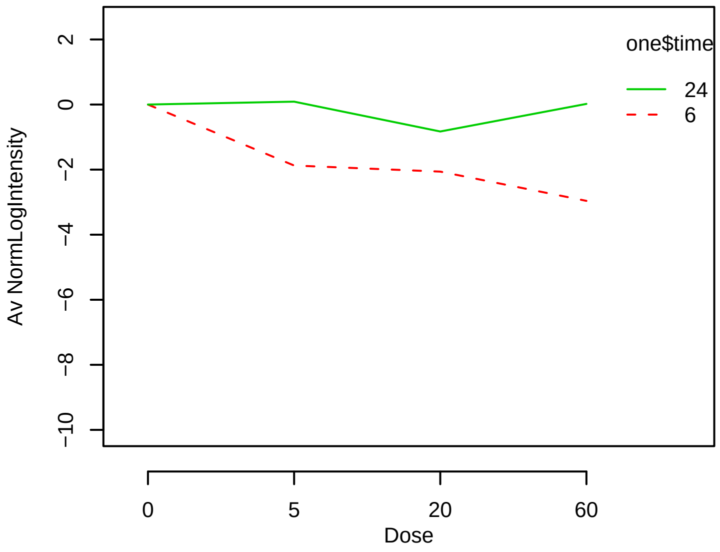


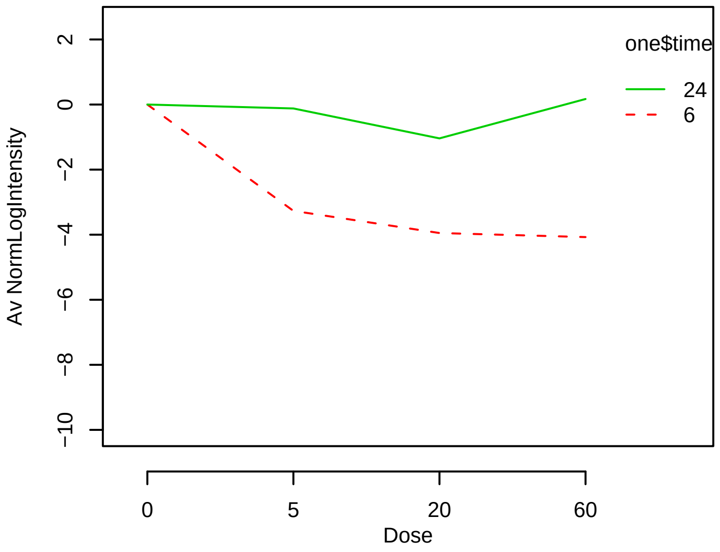
GO_0009953 : dorsal/ventral pattern formation

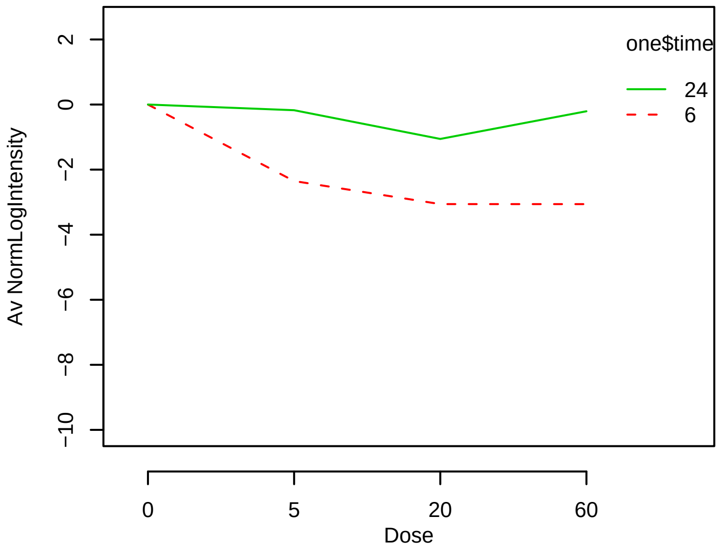


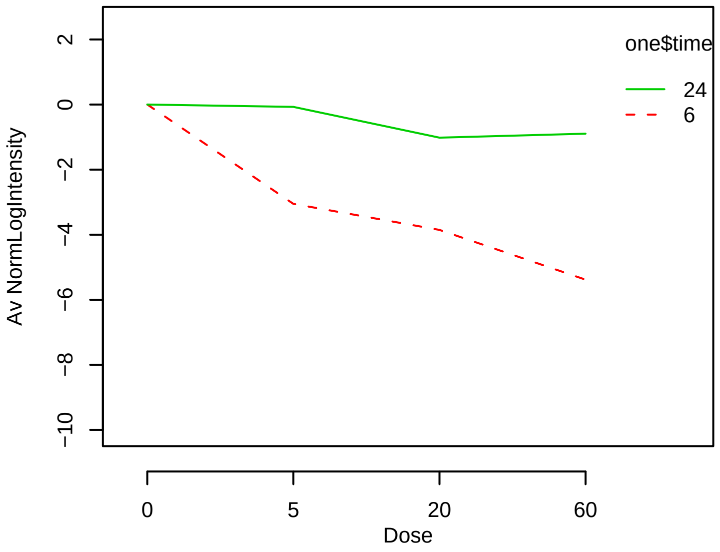
GO_0009954 : proximal/distal pattern formation

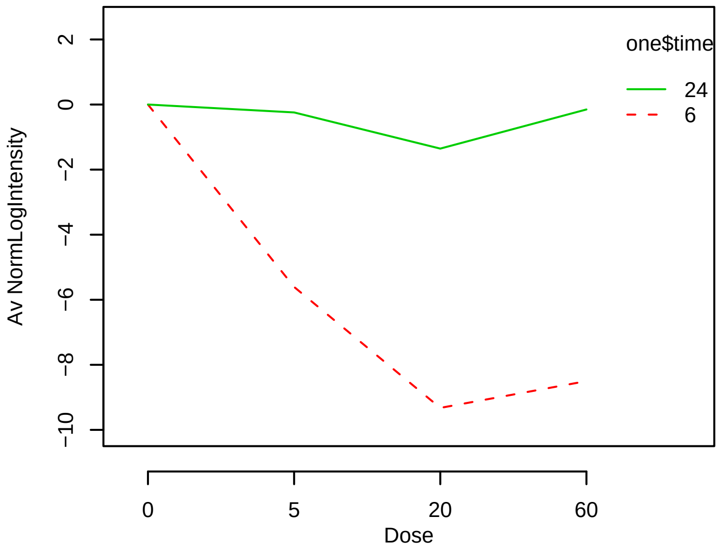


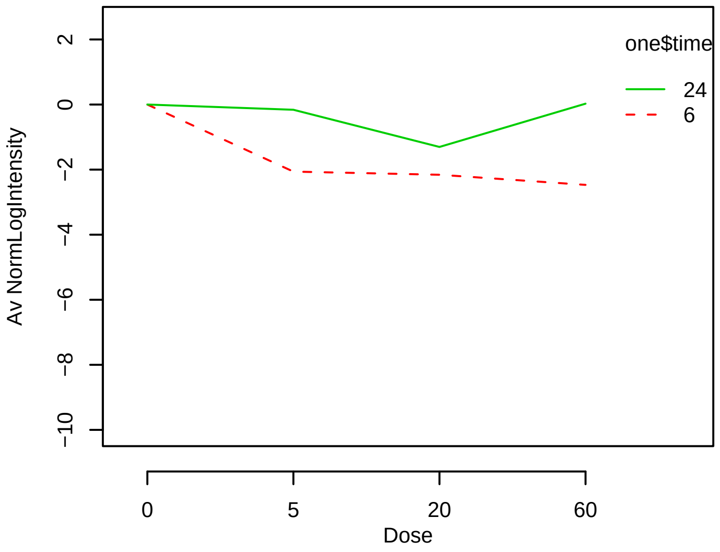

GO_0009967 : positive regulation of signal transduction


GO_0009968 : negative regulation of signal transduction

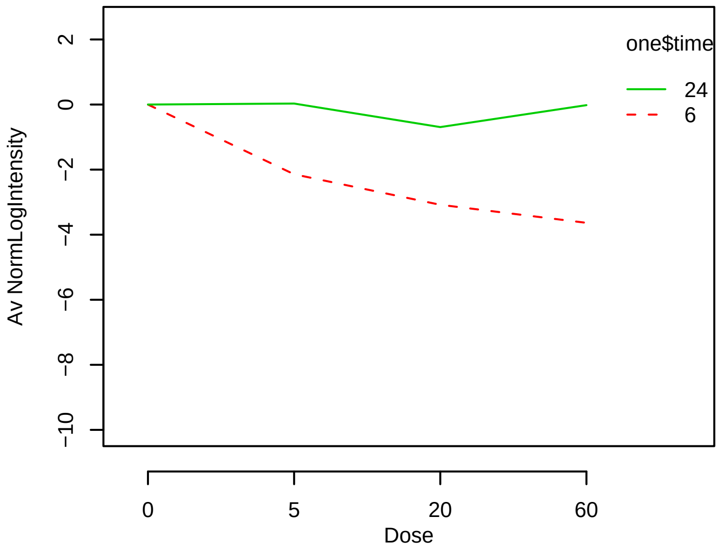

GO_0009991 : response to extracellular stimulus


GO_0009994 : oocyte differentiation

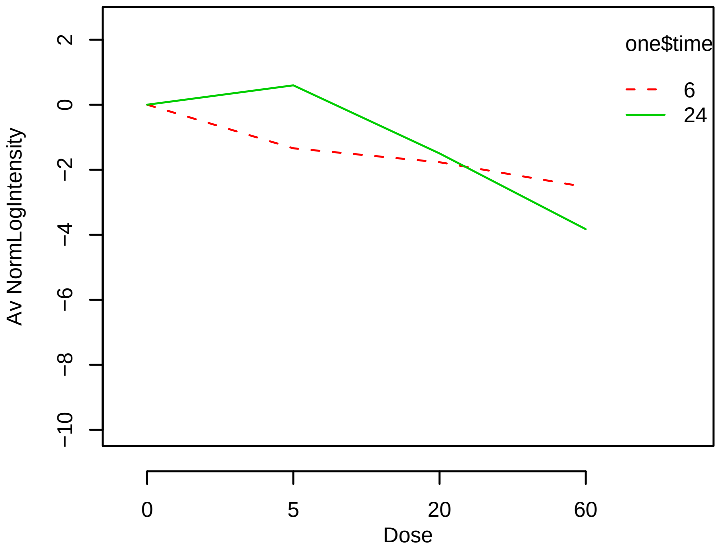

GO_0010001 : glial cell differentiation


GO_0010003 : gastrulation (sensu Mammalia)

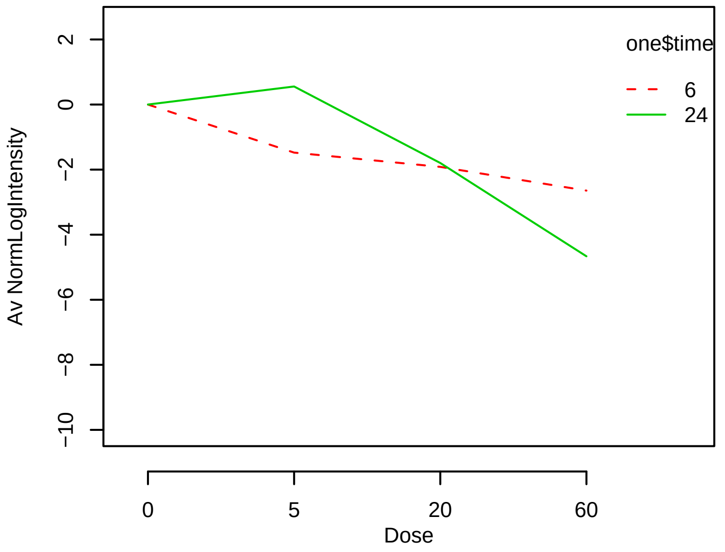
GO_0010033 : response to organic substance



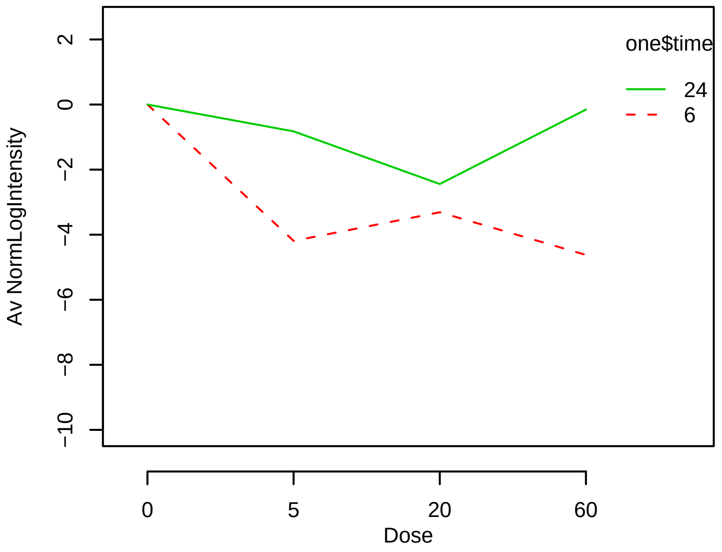
GO_0010035 : response to inorganic substance



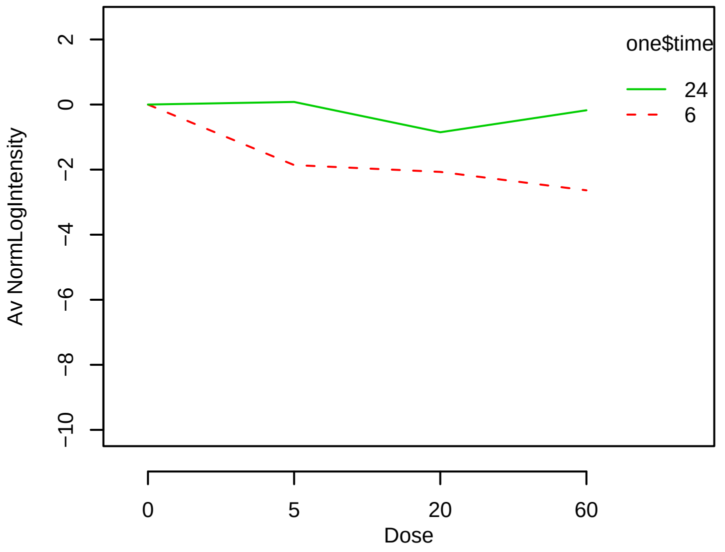
GO_0010038 : response to metal ion



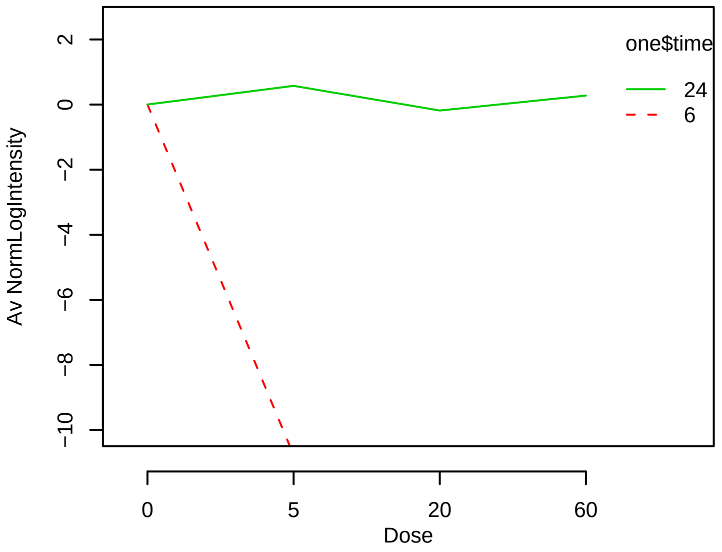
GO_0010092 : specification of organ identity

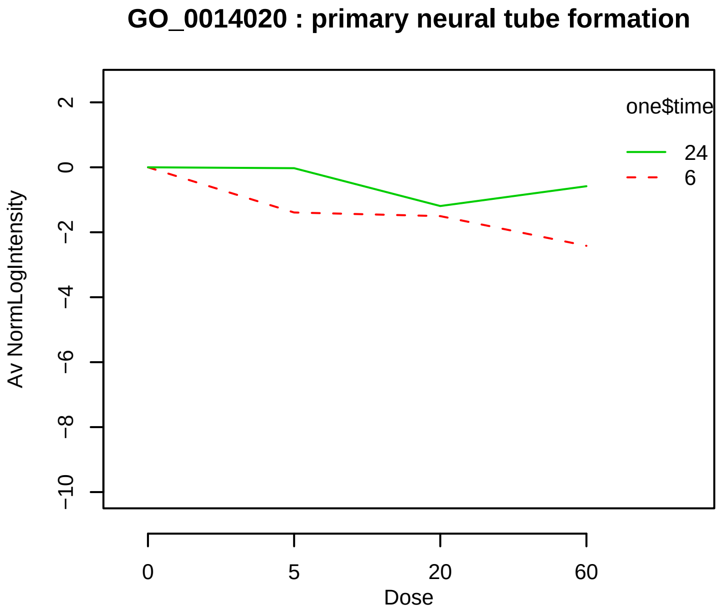


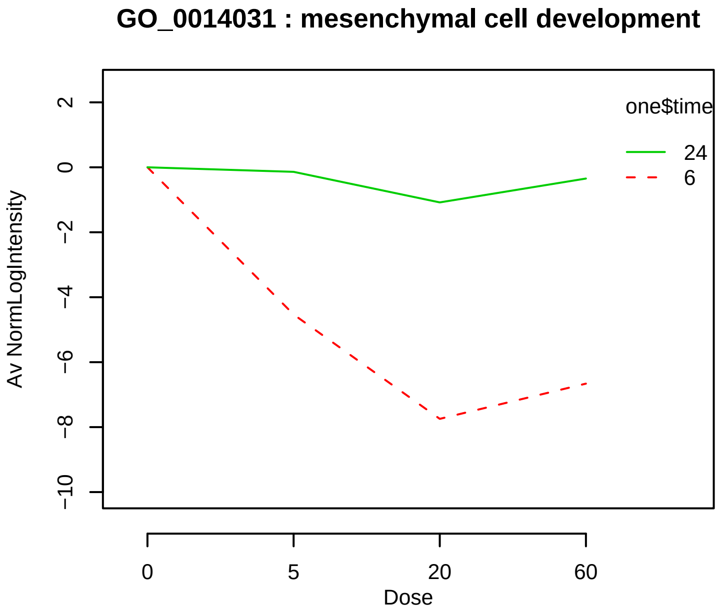
GO_0012502 : induction of programmed cell death

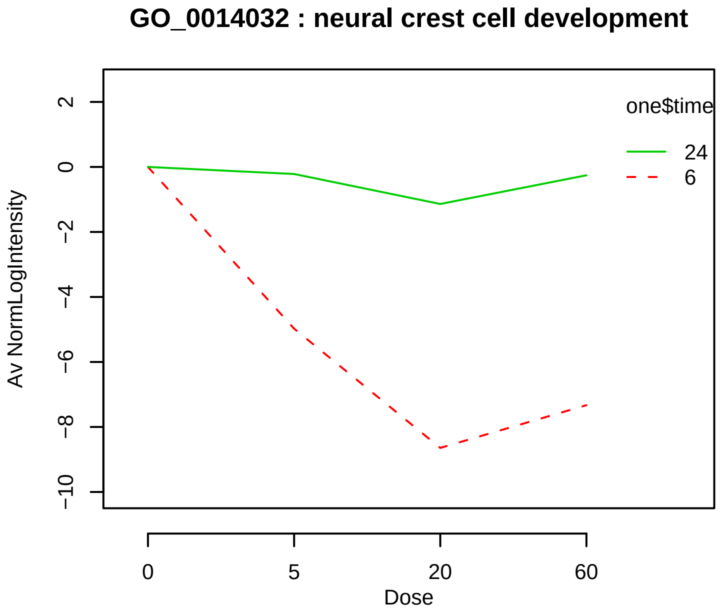


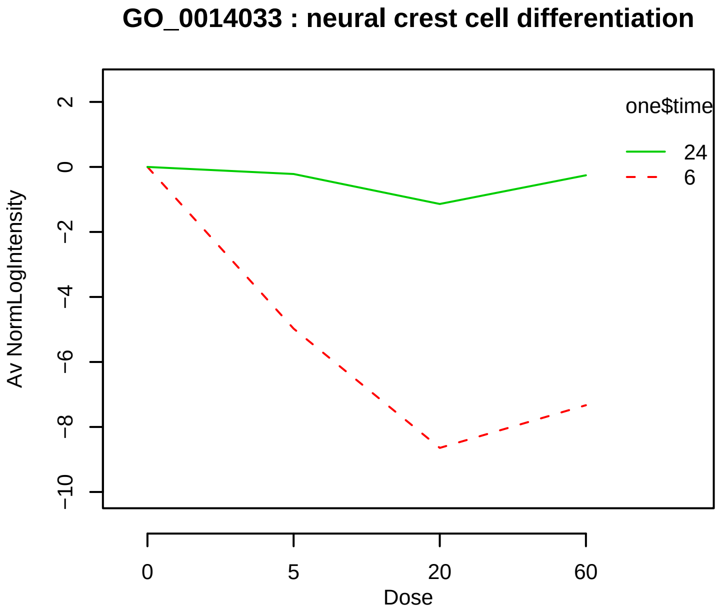
GO_0014003 : oligodendrocyte development

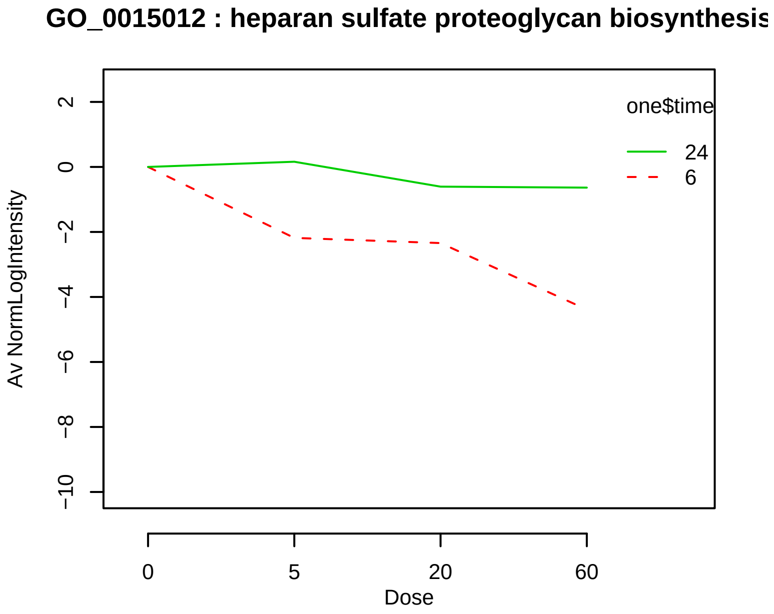


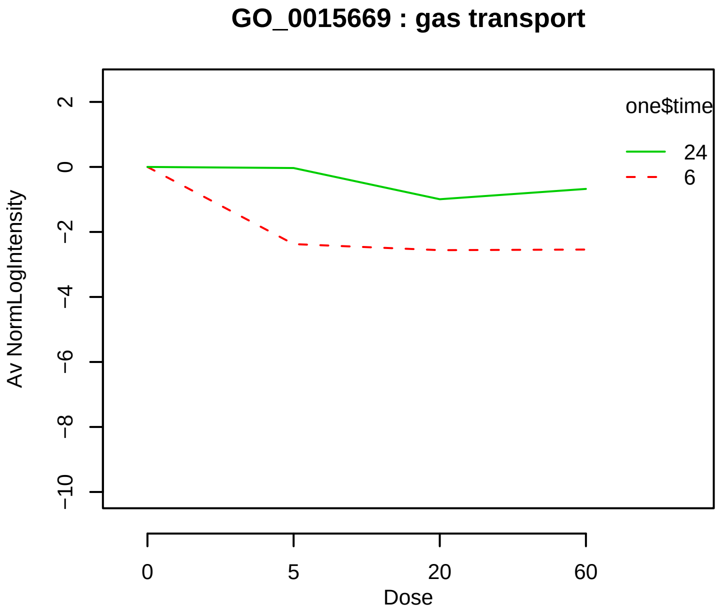

GO_0014020 : primary neural tube formation

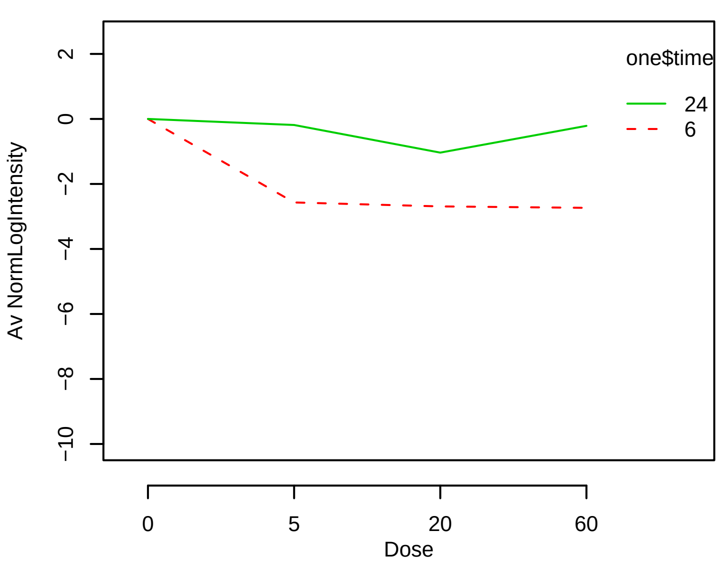

GO_0014031 : mesenchymal cell development

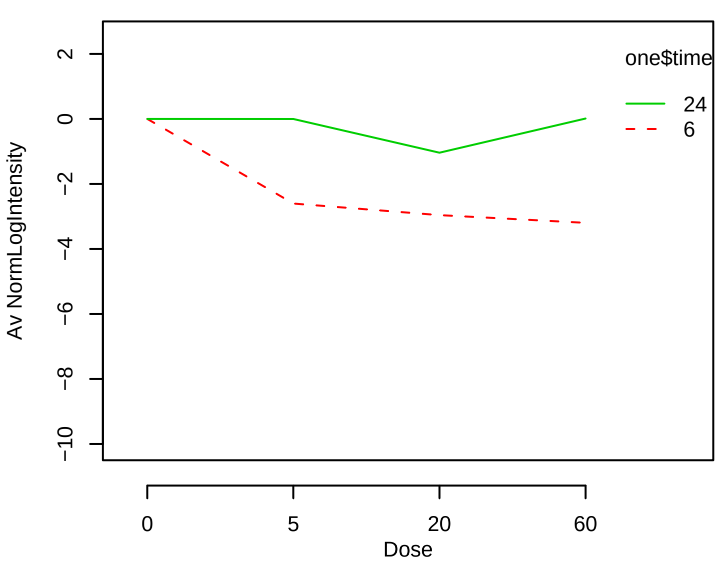

GO_0014032 : neural crest cell development

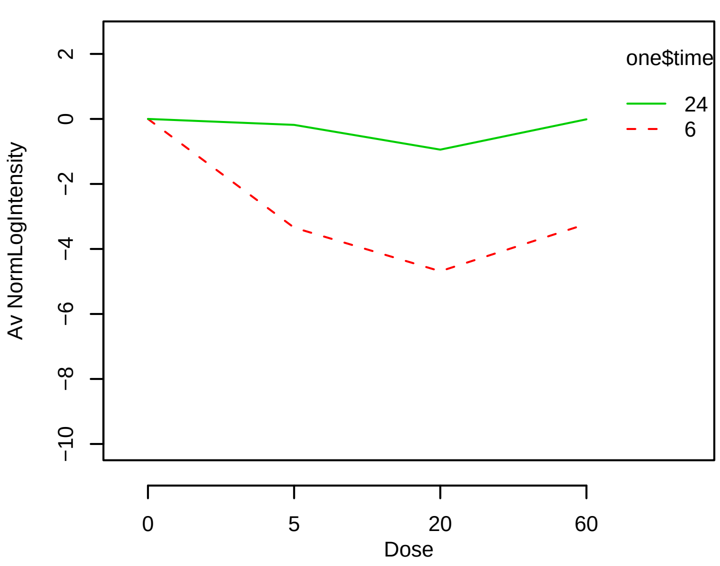

GO_0014033 : neural crest cell differentiation

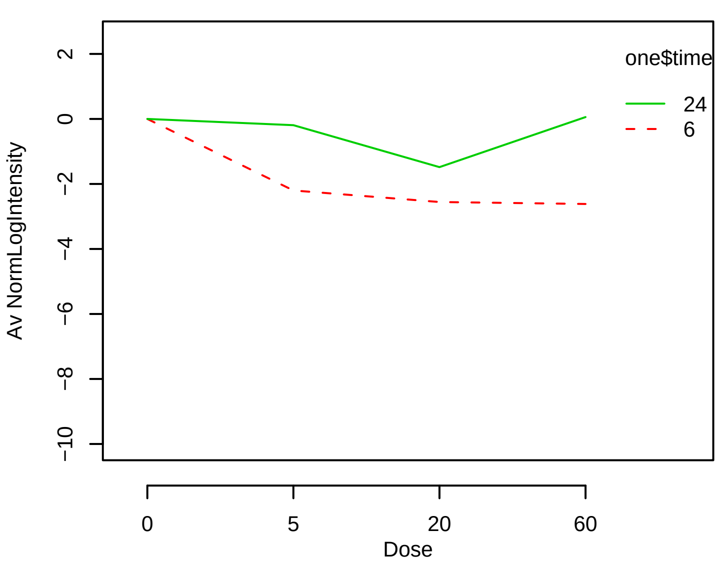

GO_0015012 : heparan sulfate proteoglycan biosynthesis

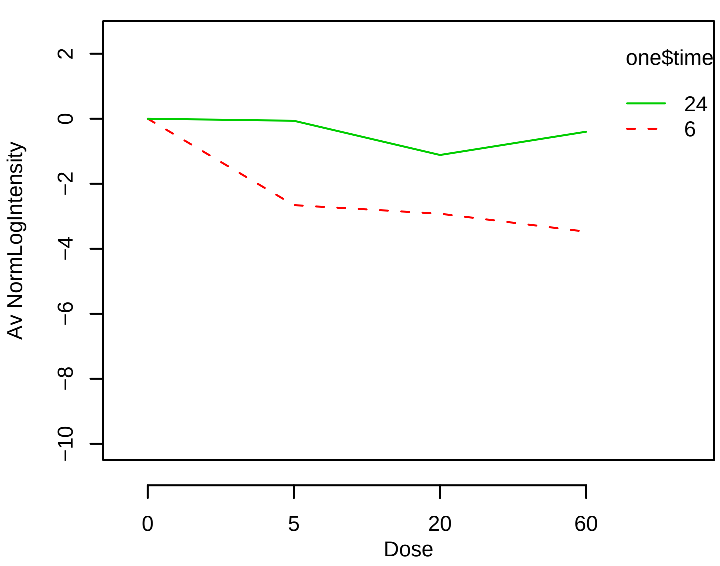

GO_0015669 : gas transport

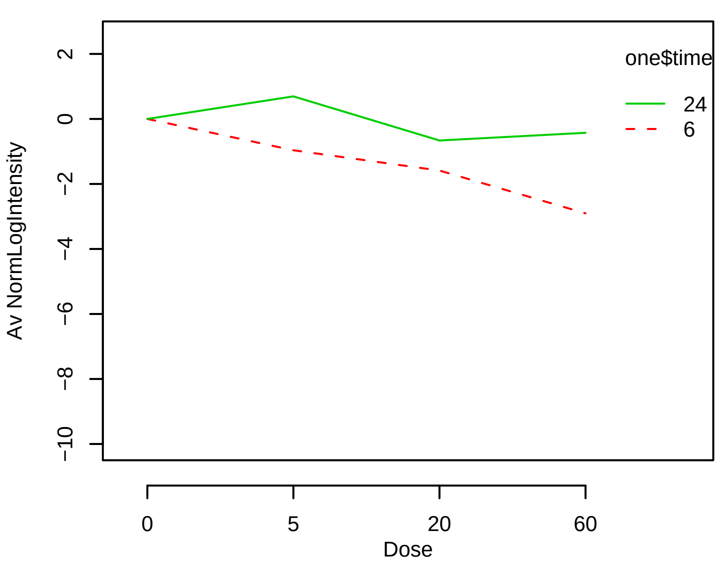

GO_0015671 : oxygen transport

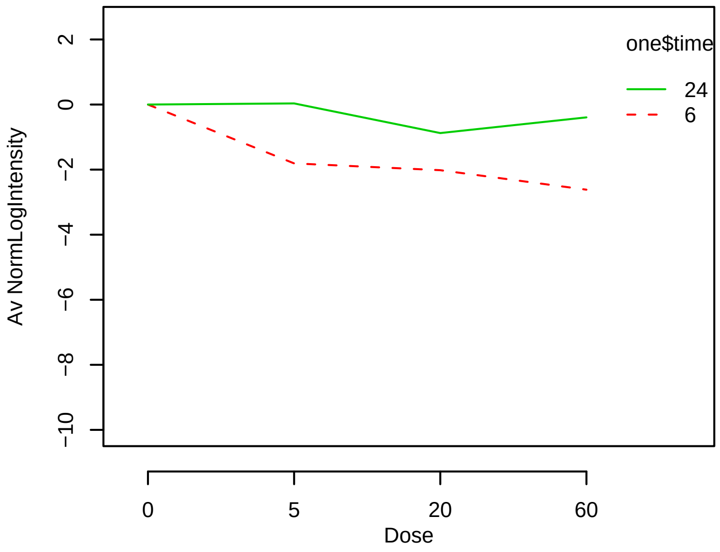

GO_0015674 : di−\, tri−valent inorganic cation transport

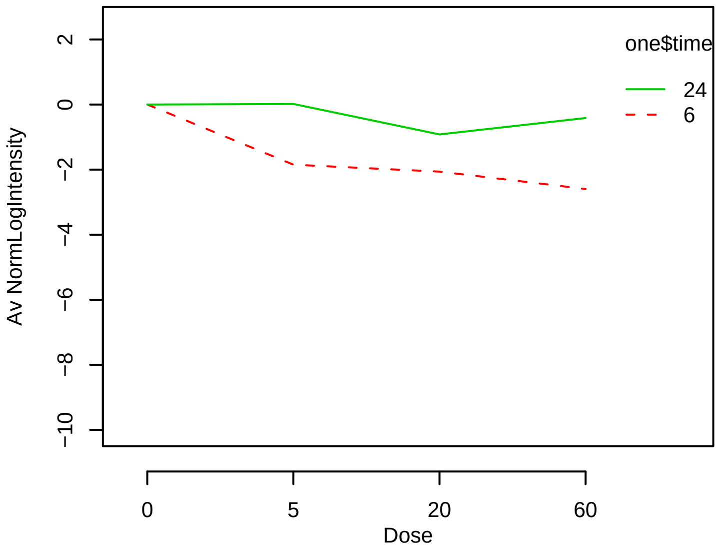

GO_0015695 : organic cation transport

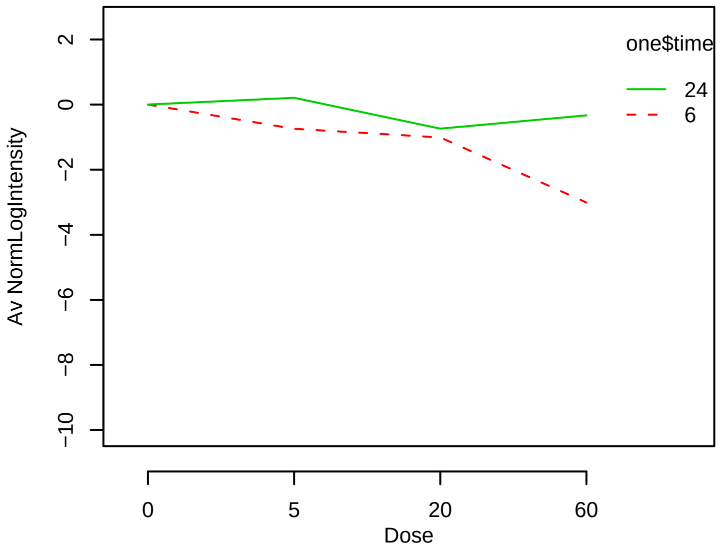

GO_0015698 : inorganic anion transport

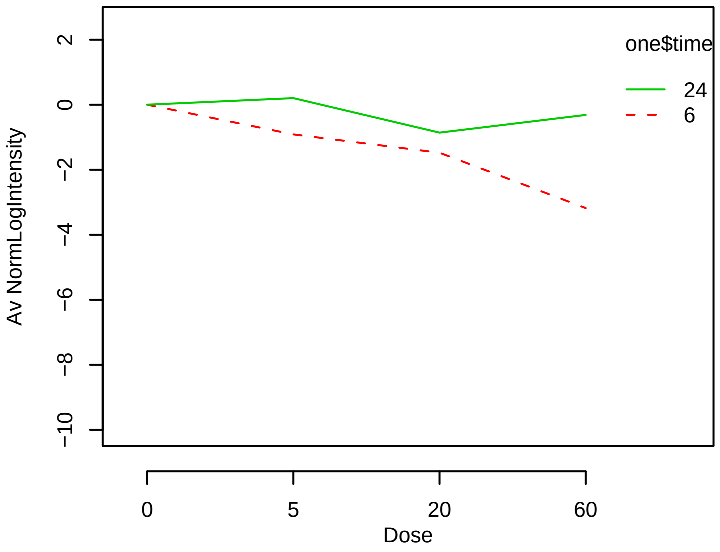

GO_0015711 : organic anion transport

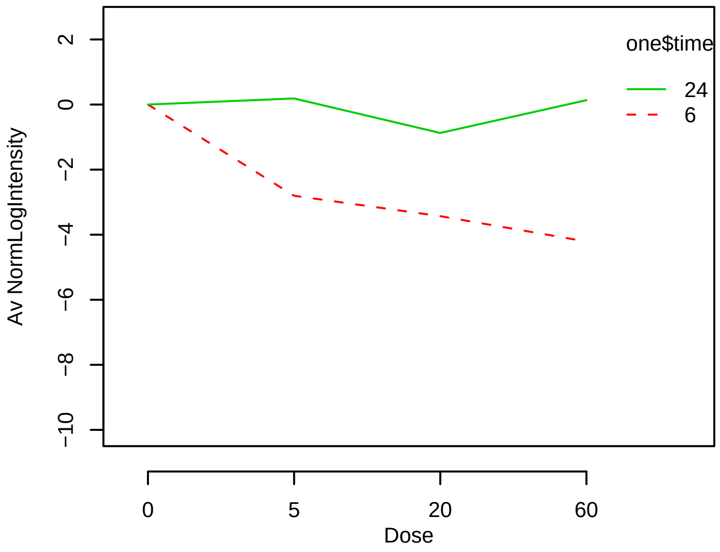

GO_0015718 : monocarboxylic acid transport

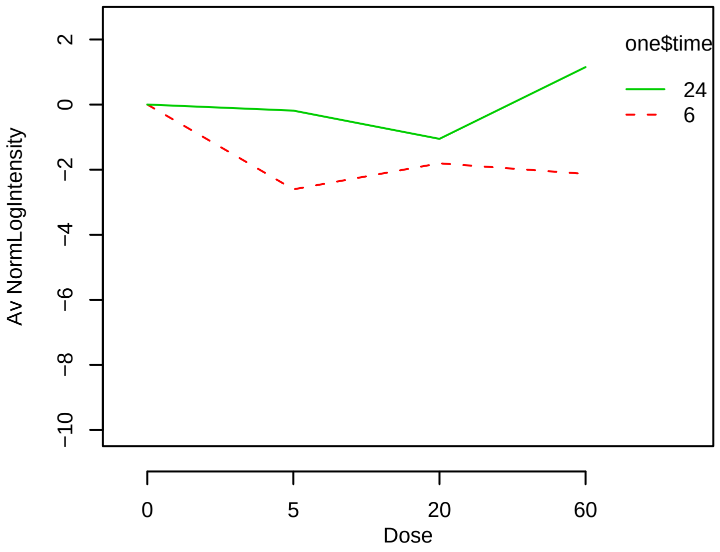

GO_0015749 : monosaccharide transport


GO_0015758 : glucose transport

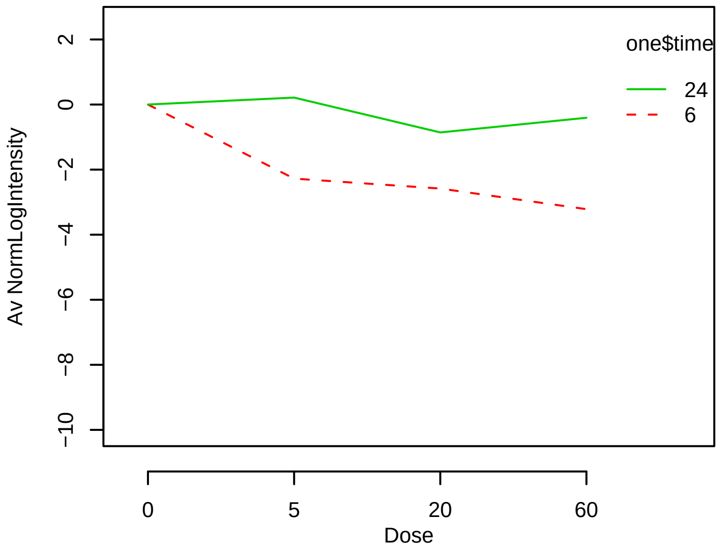

GO_0015780 : nucleotide−sugar transport


GO_0015781 : pyrimidine nucleotide−sugar transport

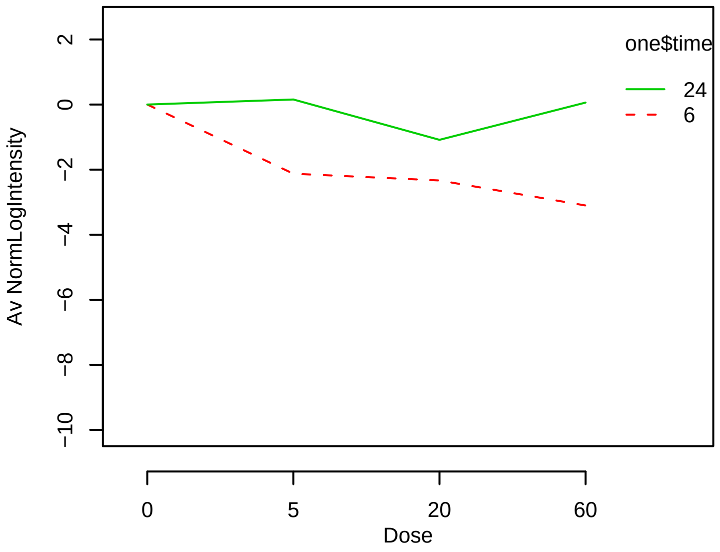

GO_0015800 : acidic amino acid transport


GO_0015802 : basic amino acid transport

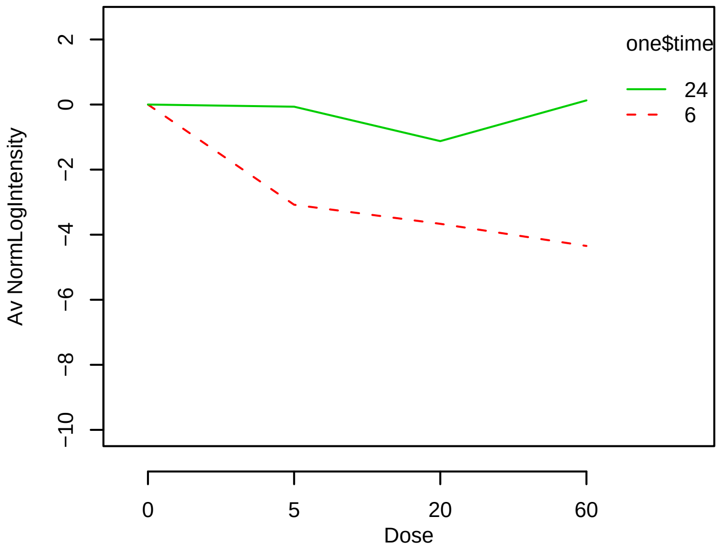
GO_0015804 : neutral amino acid transport



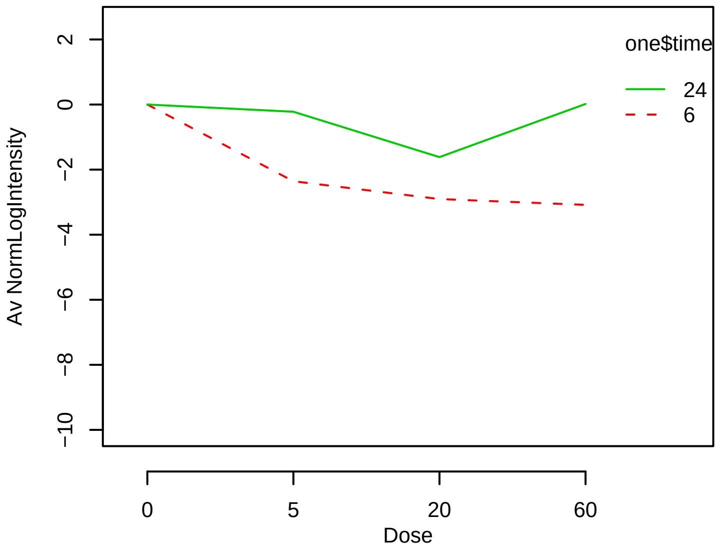
GO_0015807 : L−amino acid transport



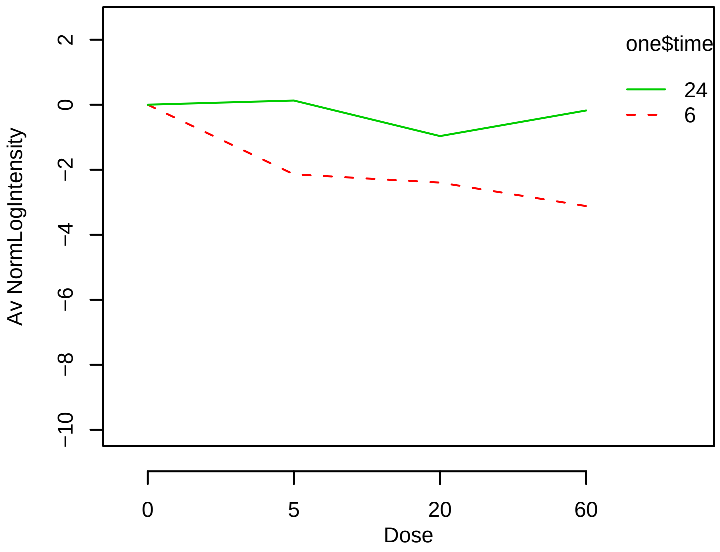
GO_0015813 : glutamate transport



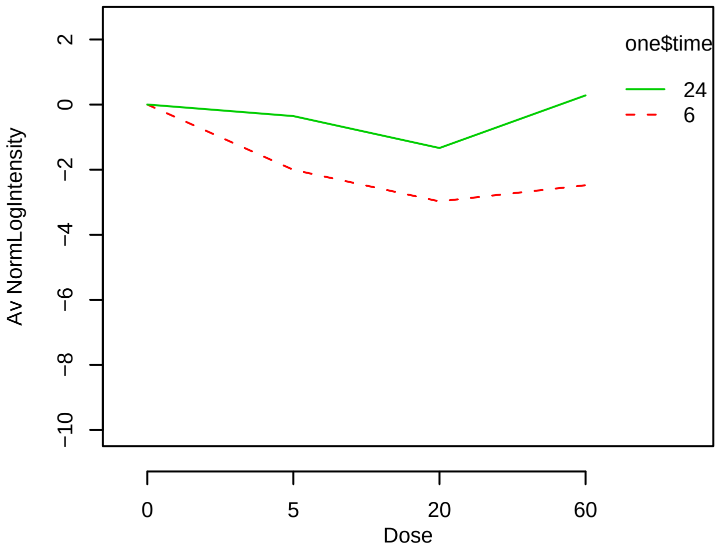
GO_0015833 : peptide transport

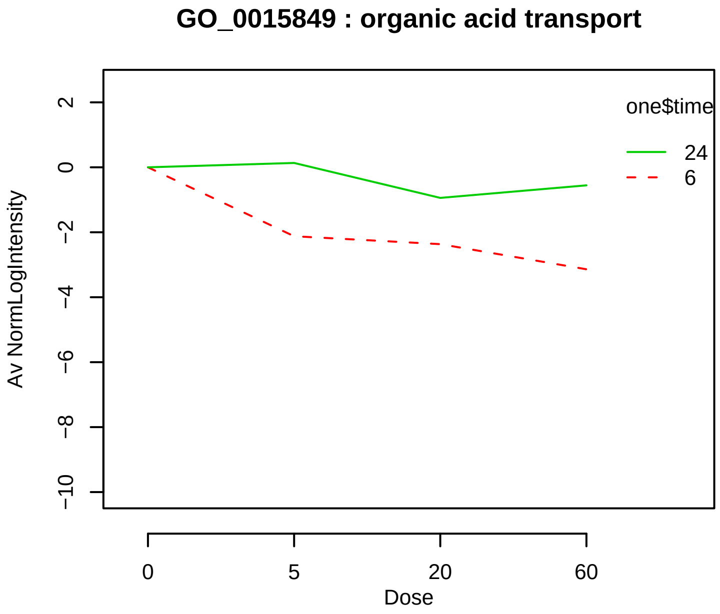


GO_0015837 : amine transport

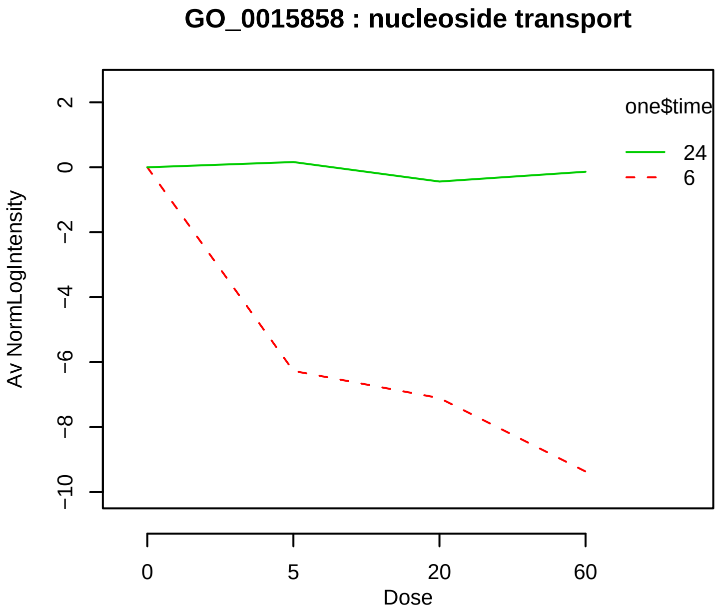


GO_0015844 : monoamine transport

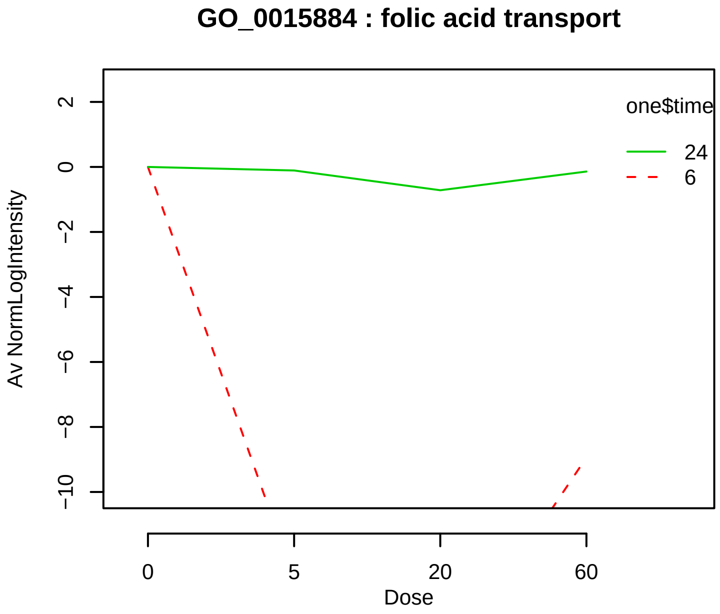




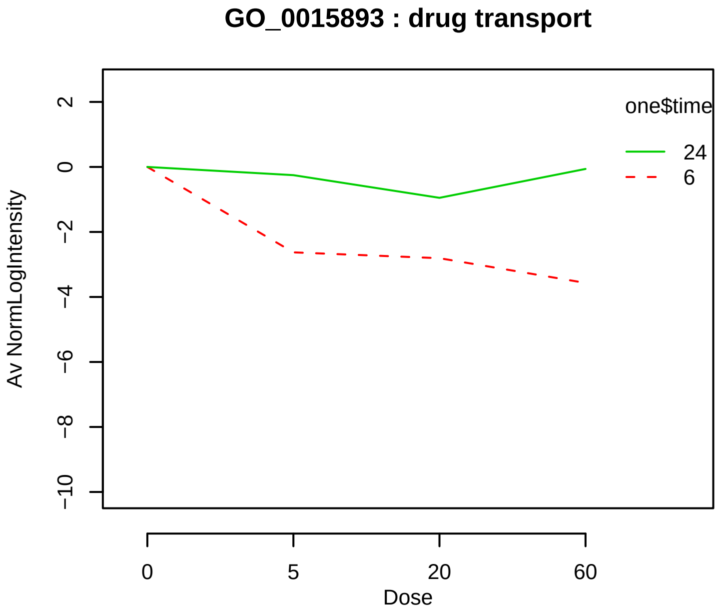
GO_0015849 : organic acid transport



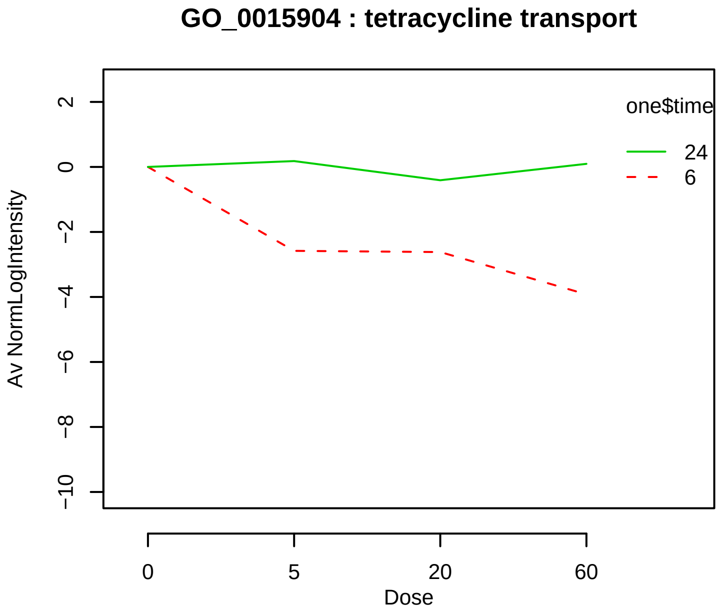
GO_0015858 : nucleoside transport



GO_0015884 : folic acid transport



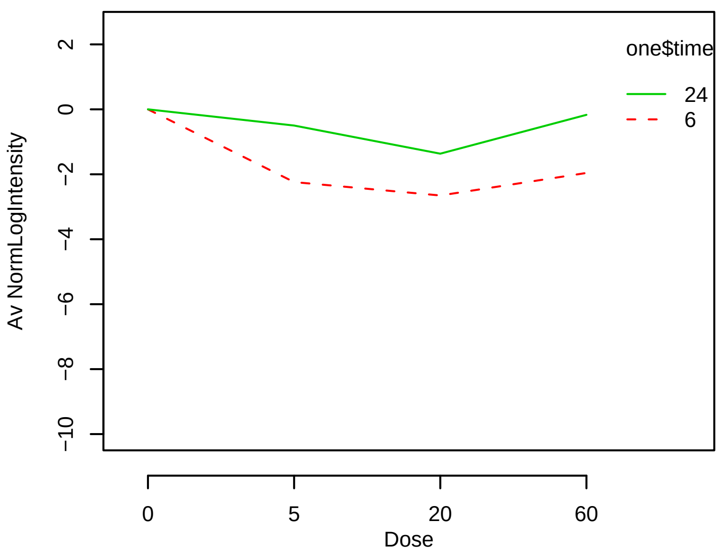
GO_0015893 : drug transport



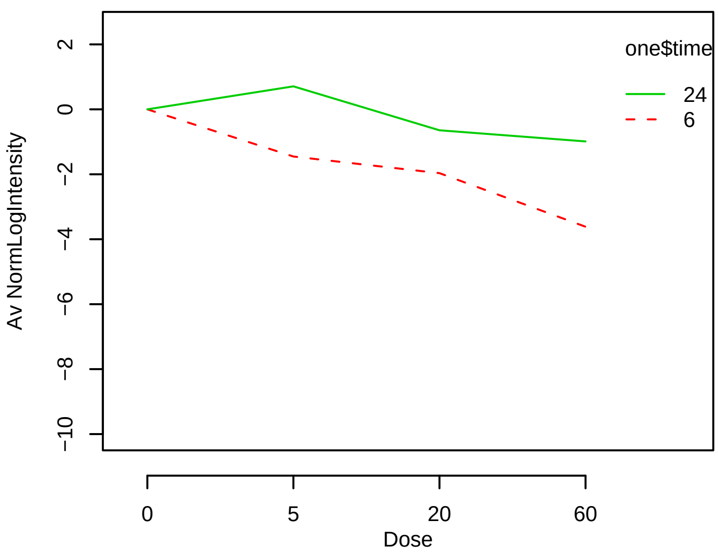
GO_0015904 : tetracycline transport

GO_0015908 : fatty acid transport

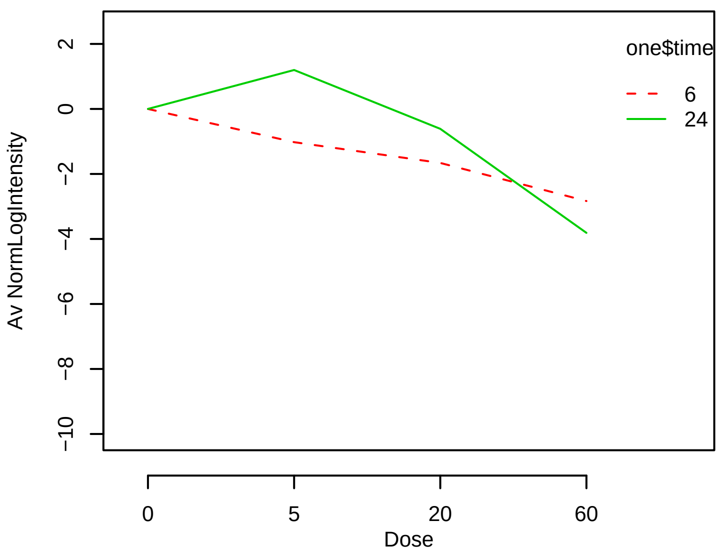
GO_0015918 : sterol transport



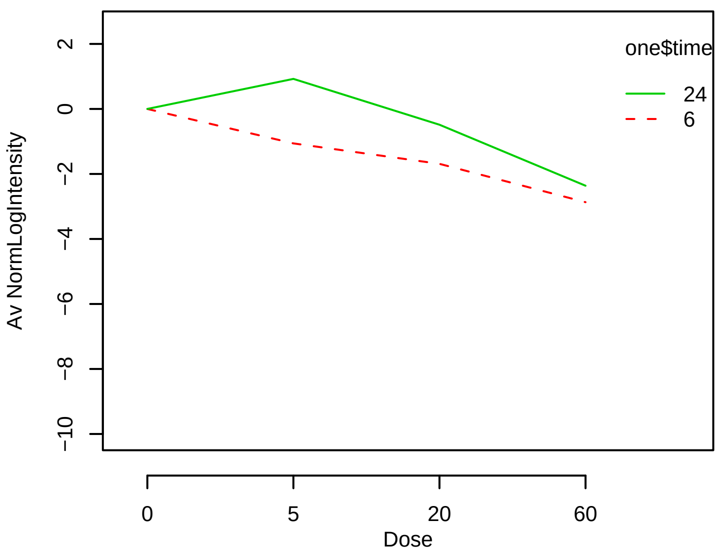
GO_0015931 : nucleobase\, nucleoside\, nucleotide and nucle



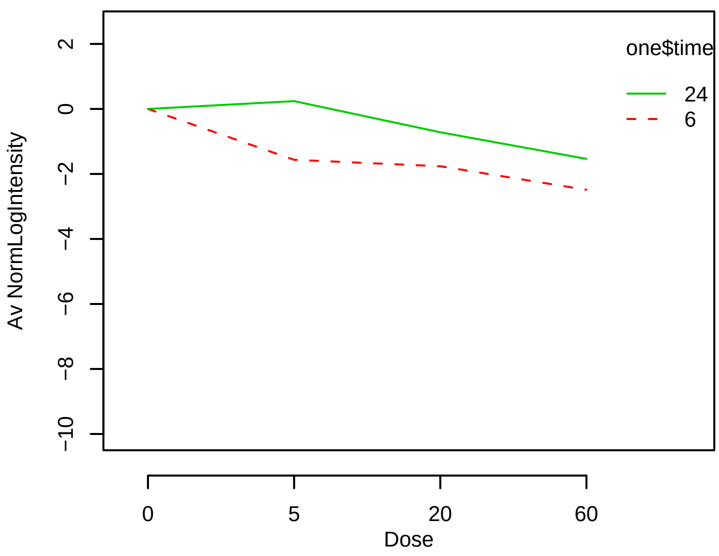
GO_0015936 : coenzyme A metabolism



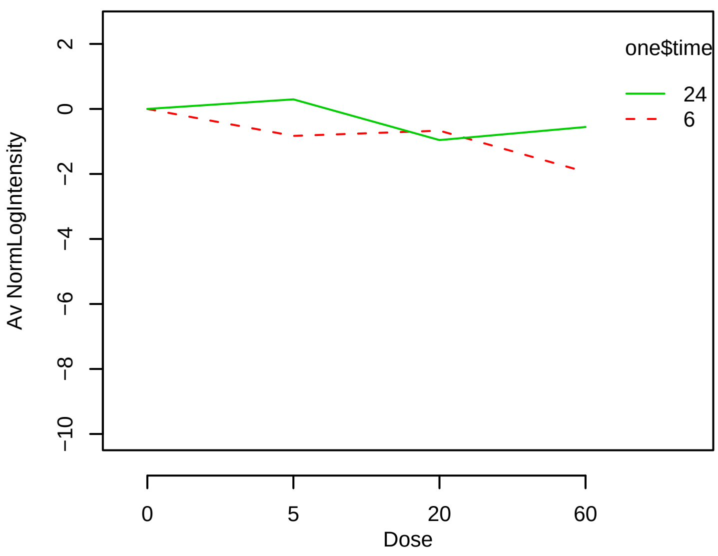
GO_0015937 : coenzyme A biosynthesis



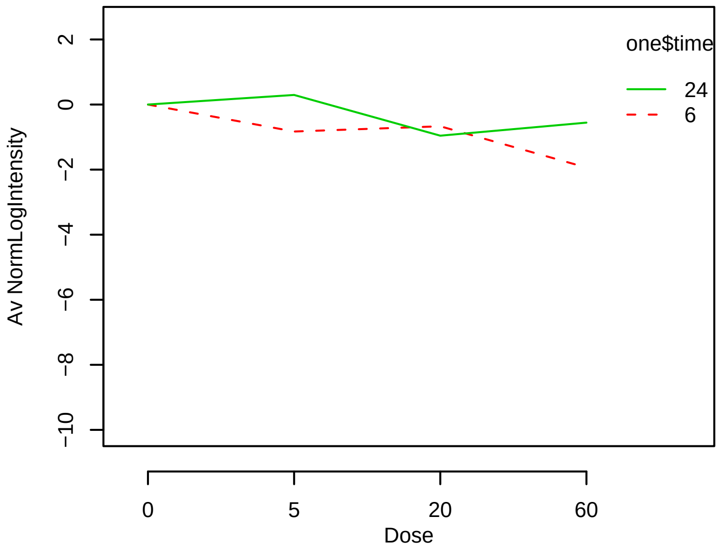
O_0015980 : energy derivation by oxidation of organic comp



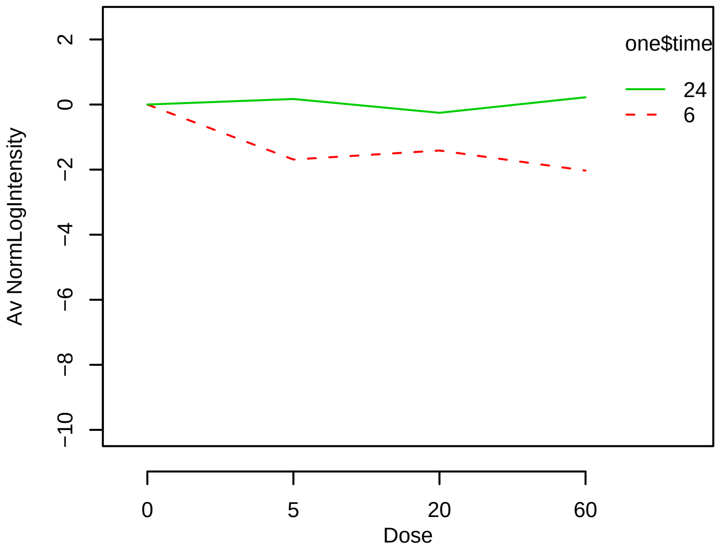
O_0015985 : energy coupled proton transport\, down electro



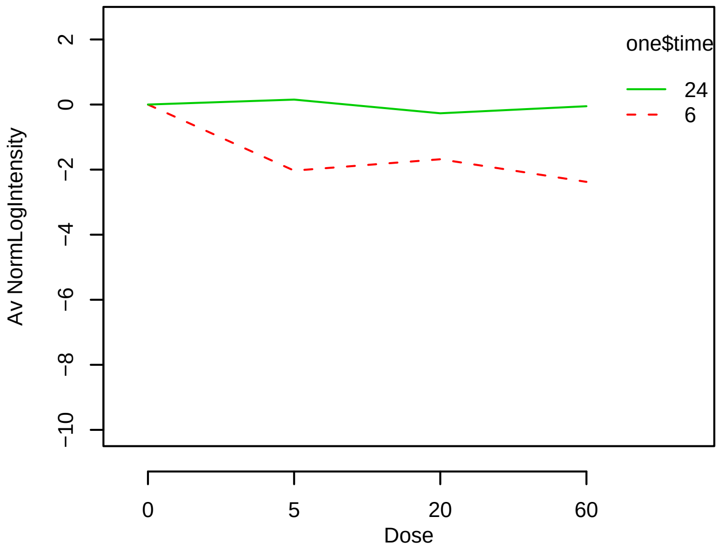
GO_0015986 : ATP synthesis coupled proton transport



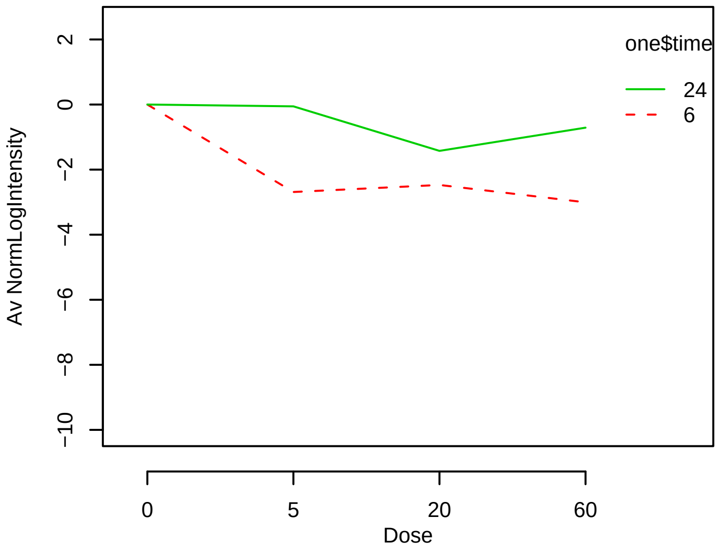
GO_0015988 : energy coupled proton transport\, against elec



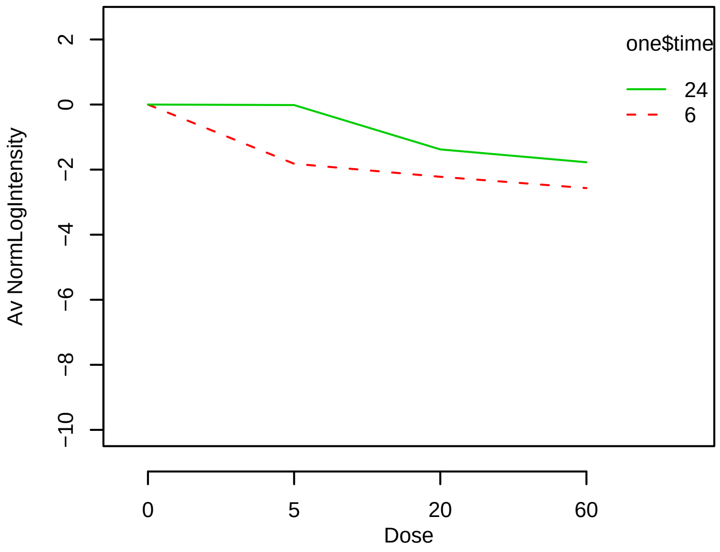
GO_0015991 : ATP hydrolysis coupled proton transport



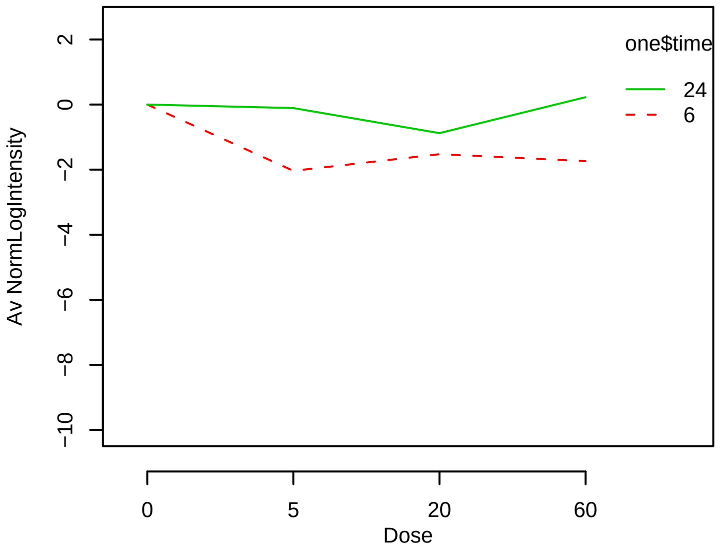
GO_0015992 : proton transport

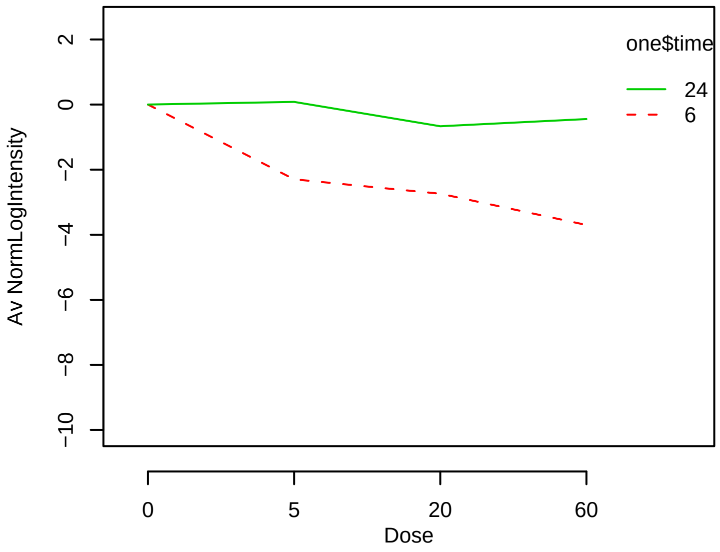


GO_0016032 : viral life cycle

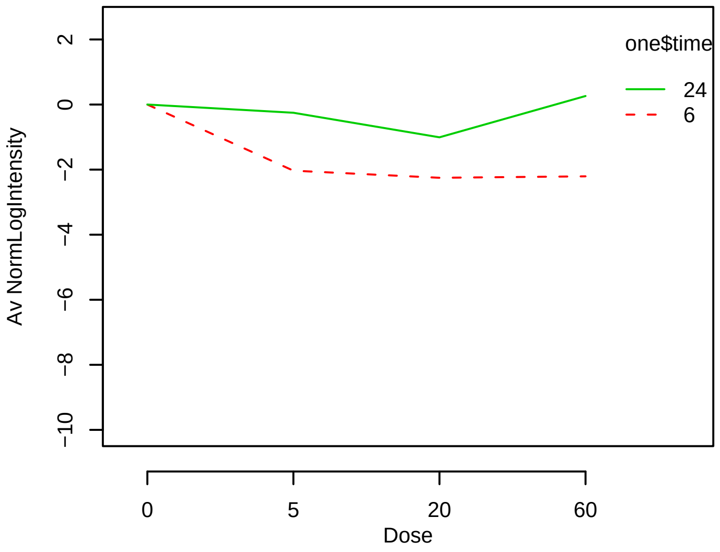


GO_0016042 : lipid catabolism

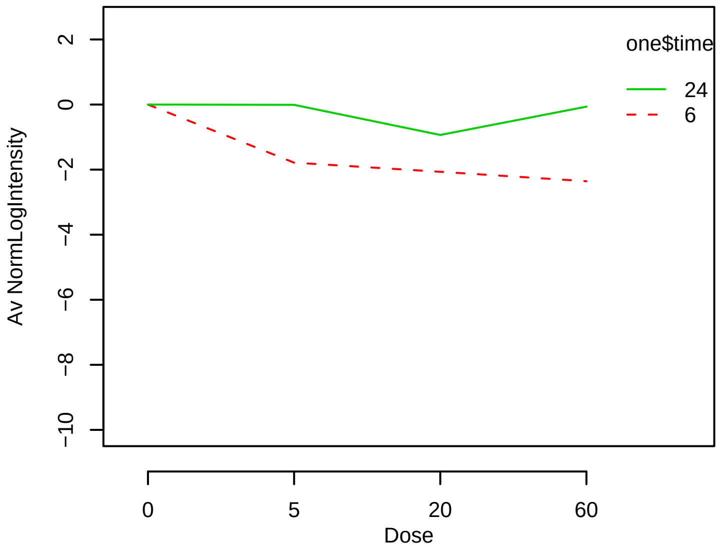




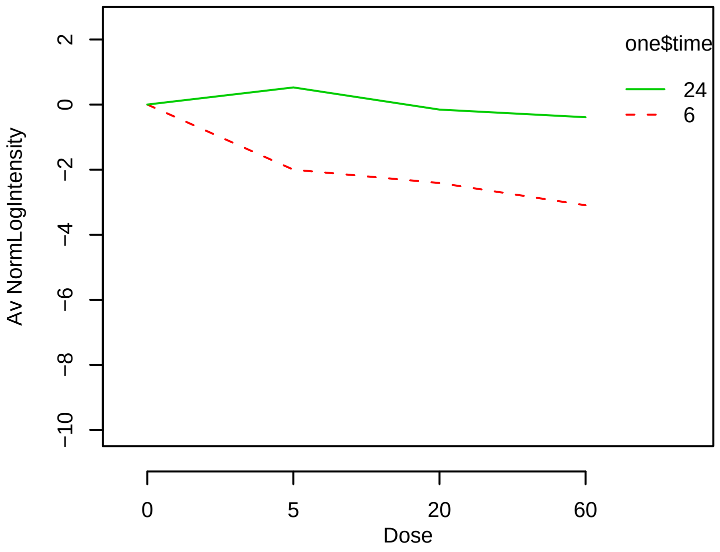
GO_0016044 : membrane organization and biogenesis



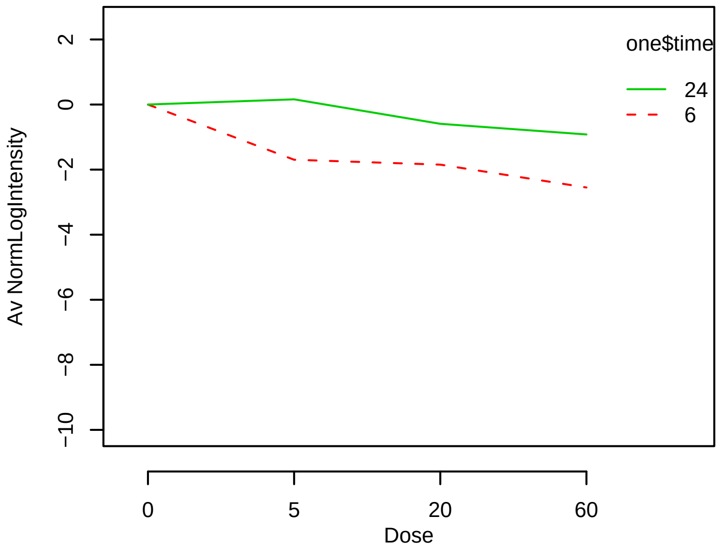
GO_0016045 : detection of bacterium



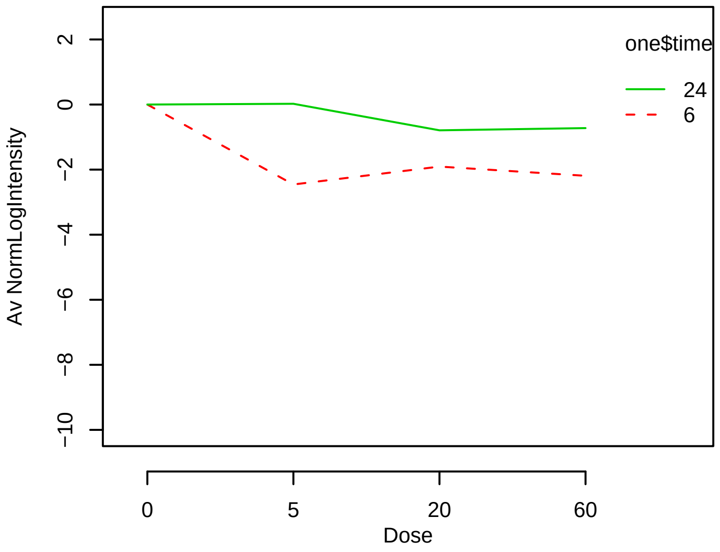
GO_0016049 : cell growth



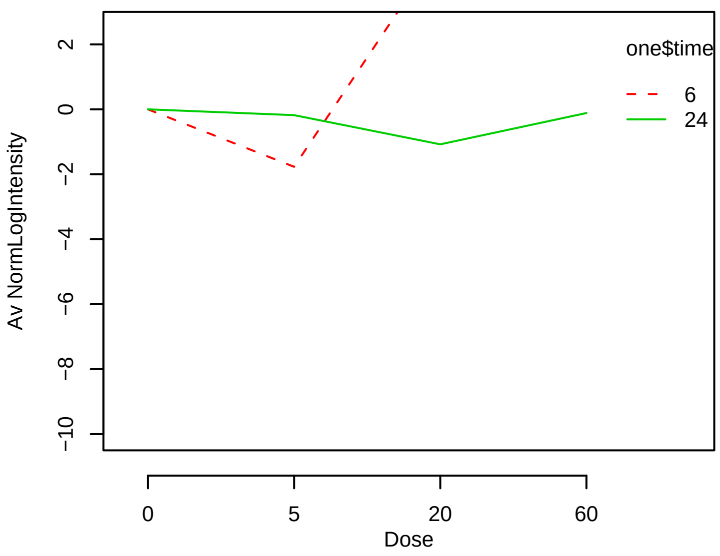
GO_0016051 : carbohydrate biosynthesis



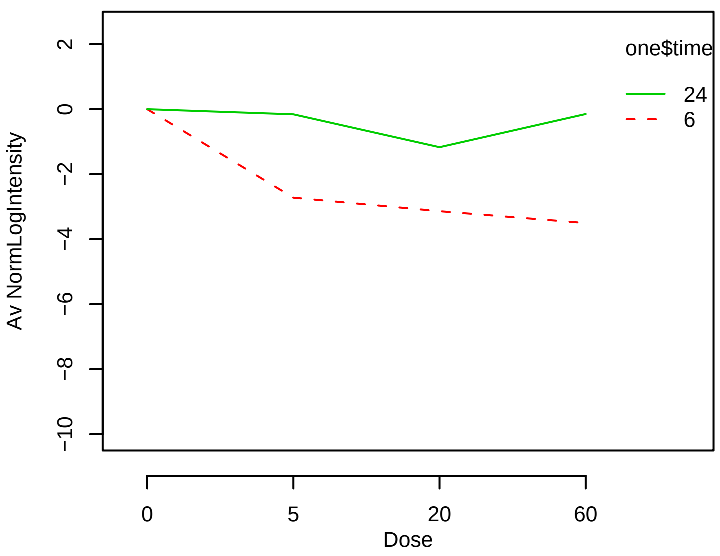
GO_0016052 : carbohydrate catabolism



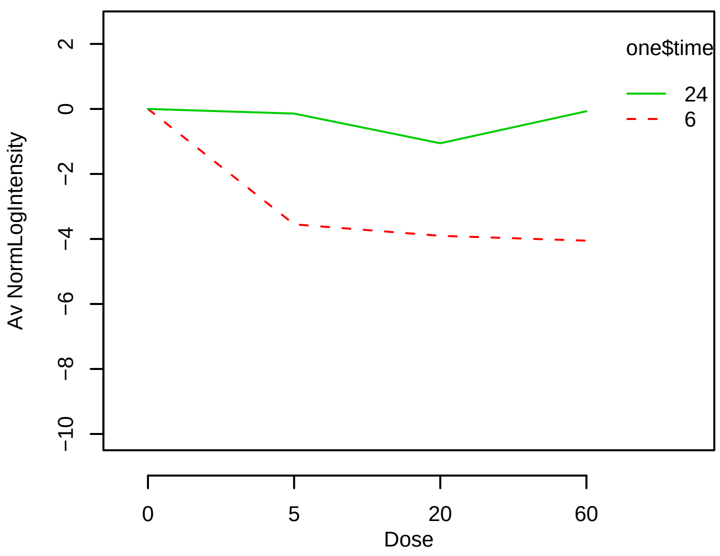
GO_0016053 : organic acid biosynthesis



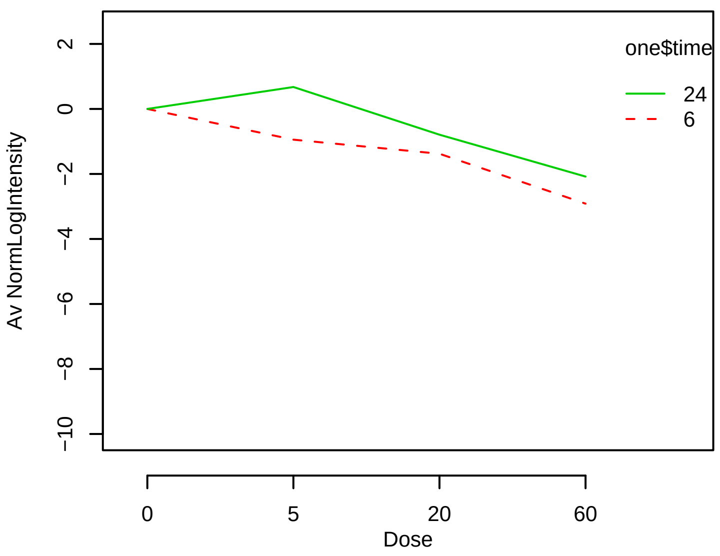
GO_0016054 : organic acid catabolism



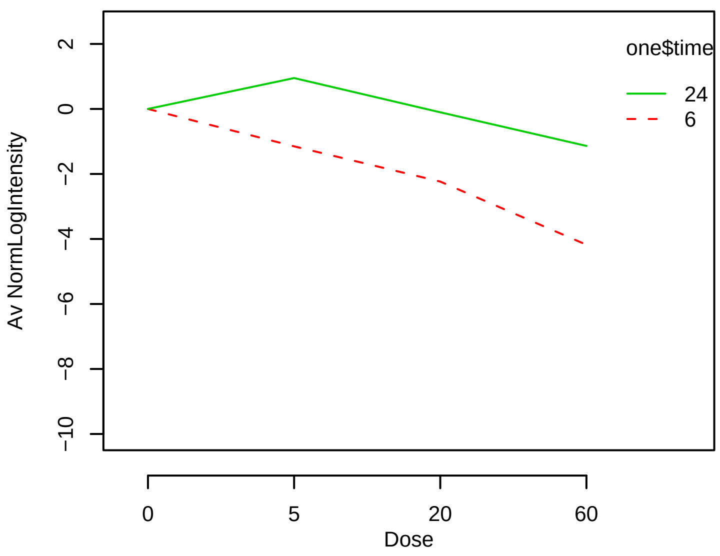
GO_0016055 : Wnt receptor signaling pathway



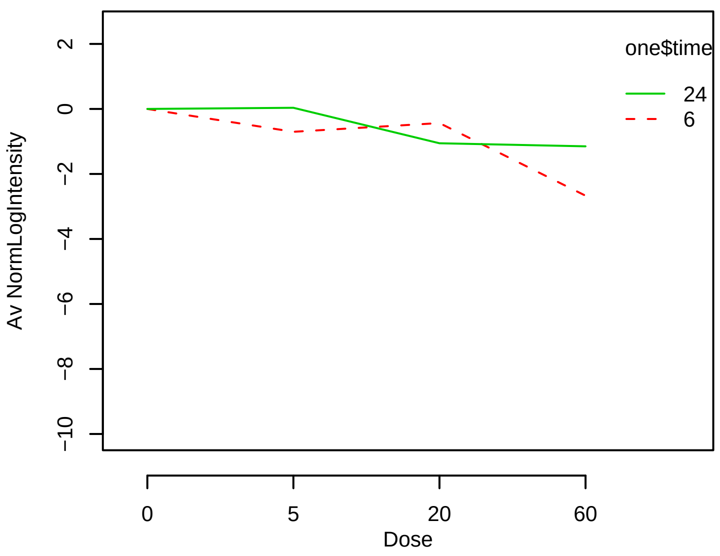
GO_0016064 : immunoglobulin mediated immune respons



GO_0016071 : mRNA metabolism

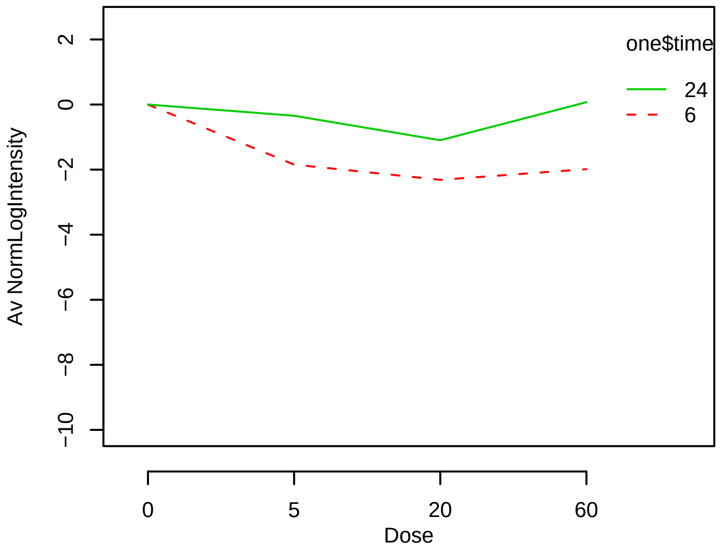


GO_0016072 : rRNA metabolism

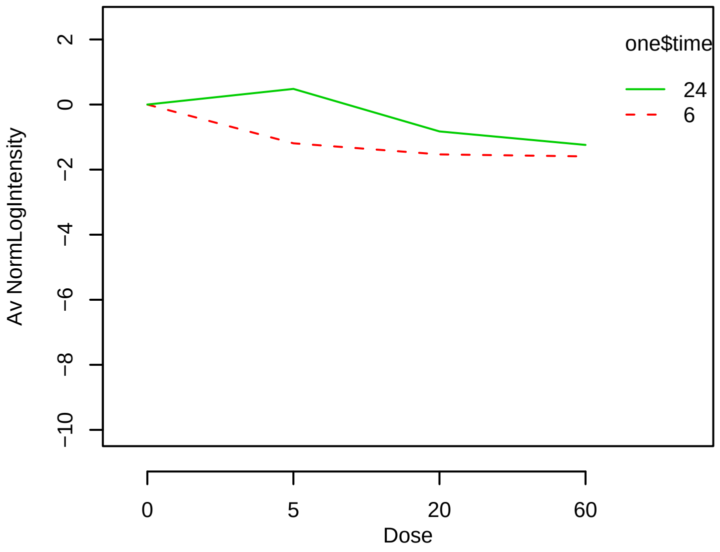


GO_0016073 : snRNA metabolism

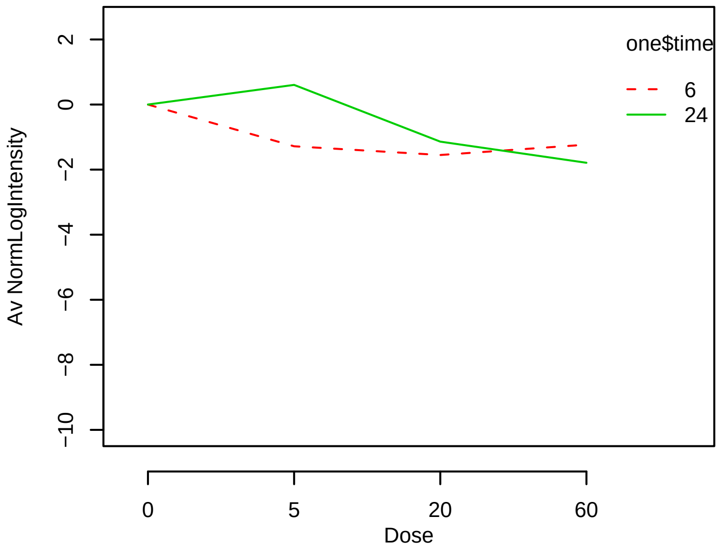
GO_0016079 : synaptic vesicle exocytosis



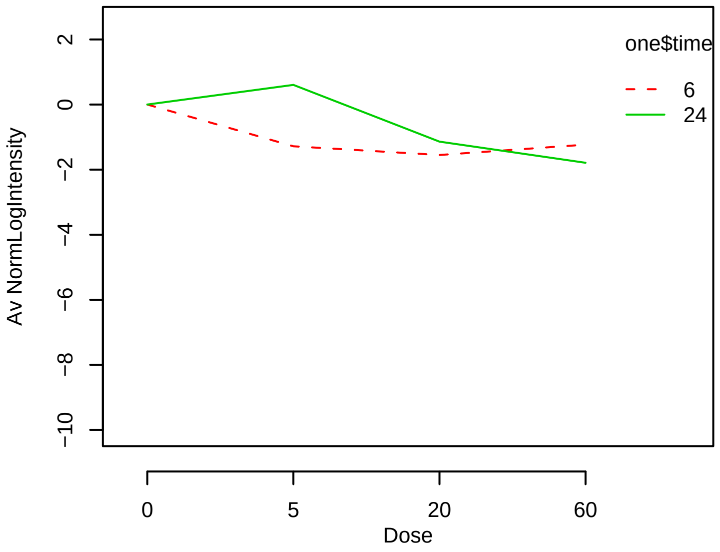
GO_0016096 : polyisoprenoid metabolism



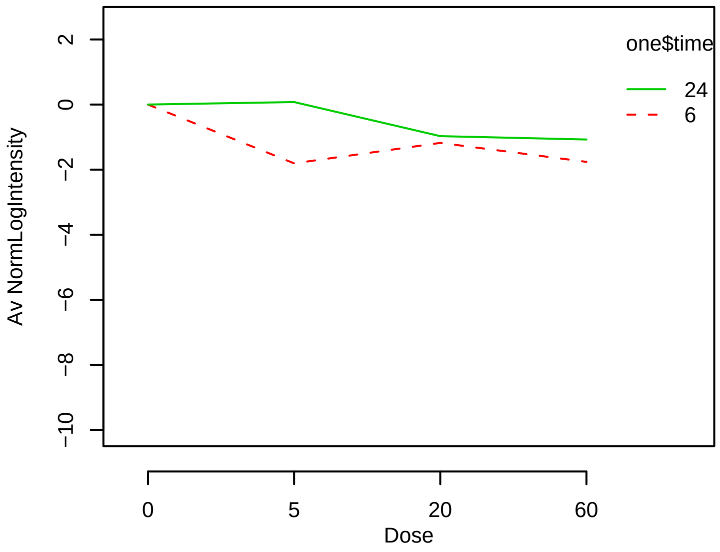
GO_0016108 : tetraterpenoid metabolism



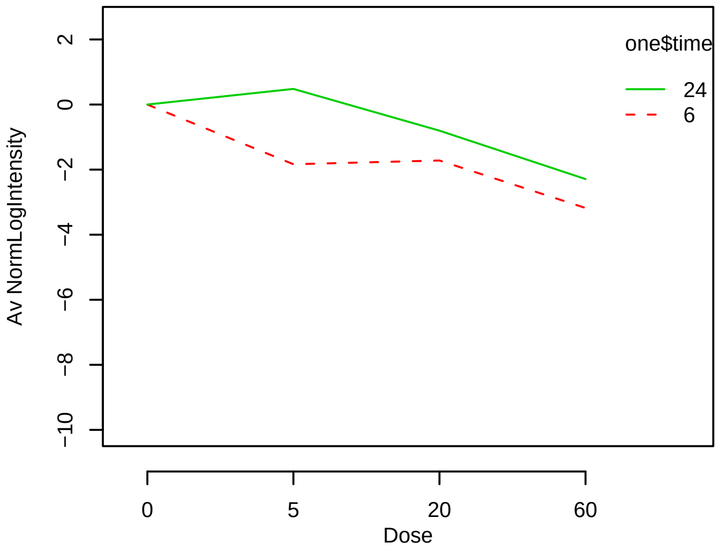
GO_0016116 : carotenoid metabolism

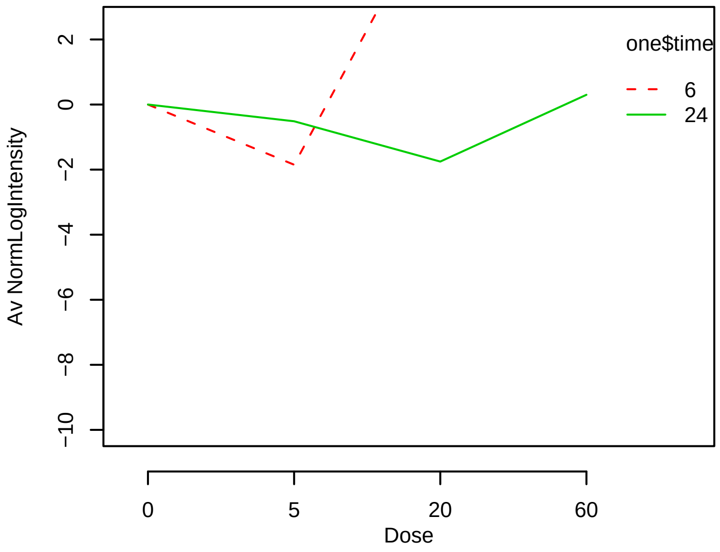


GO_0016125 : sterol metabolism

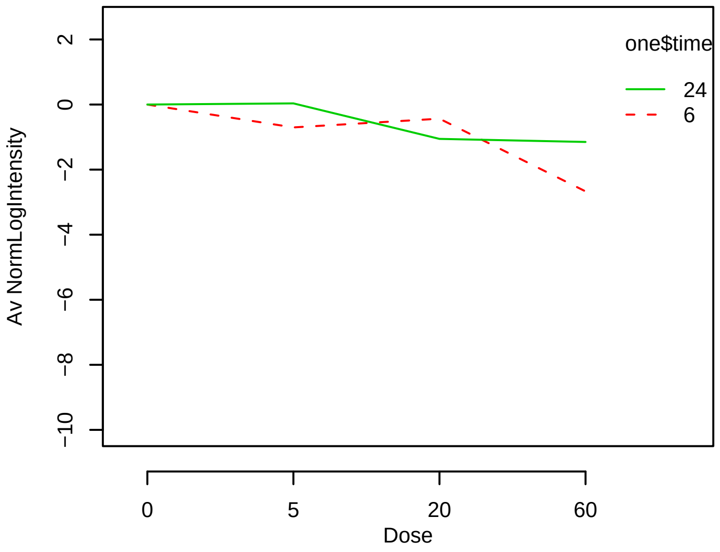


GO_0016126 : sterol biosynthesis

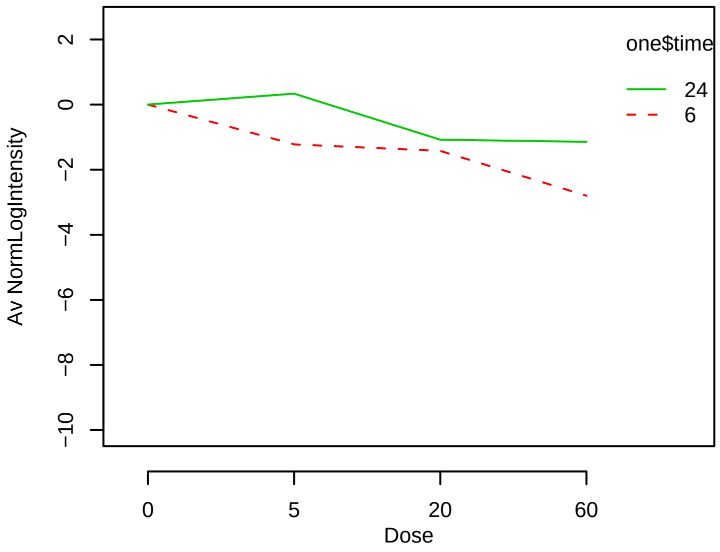




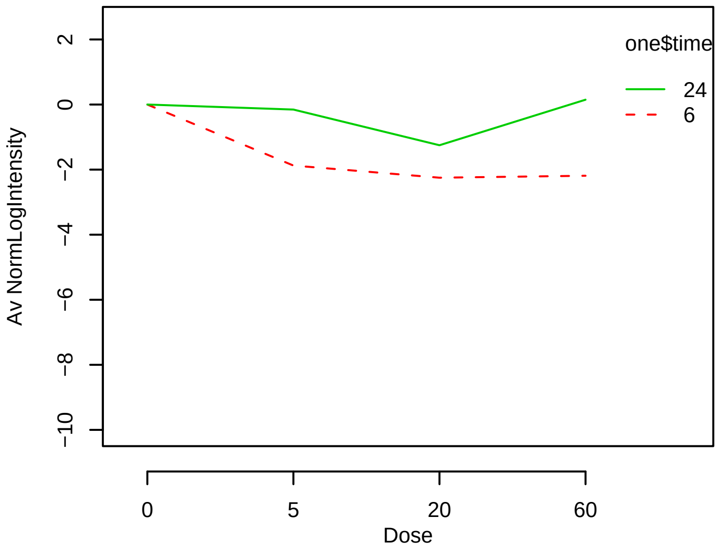
GO_0016127 : sterol catabolism



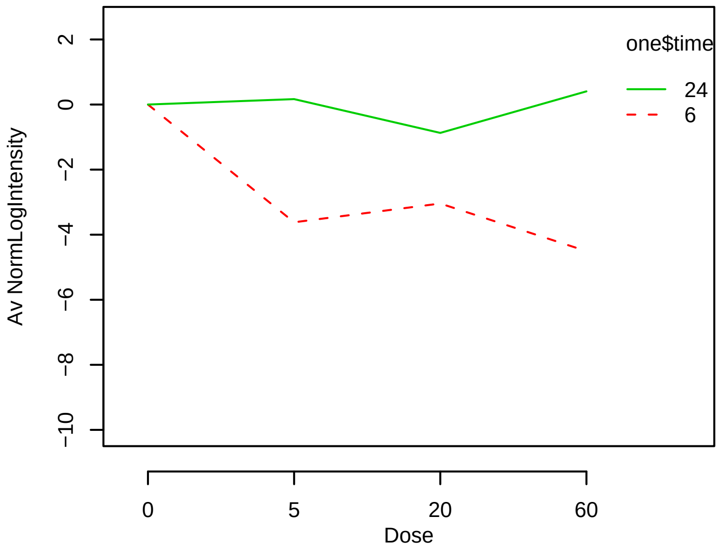
GO_0016180 : snRNA processing



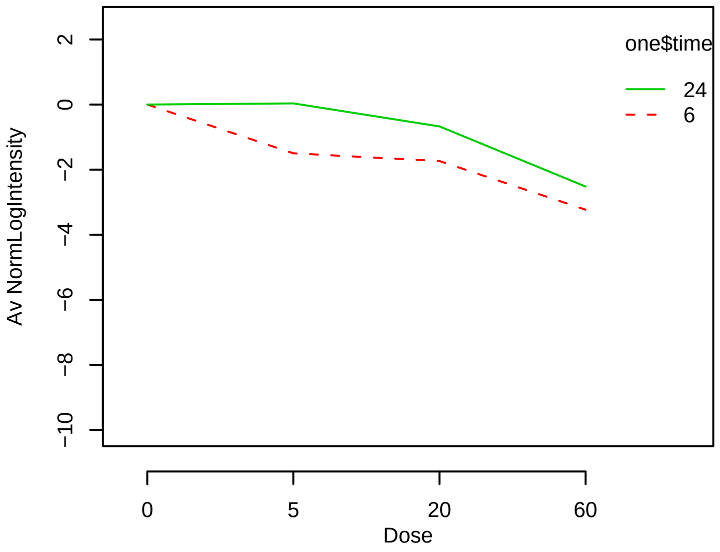
GO_0016197 : endosome transport



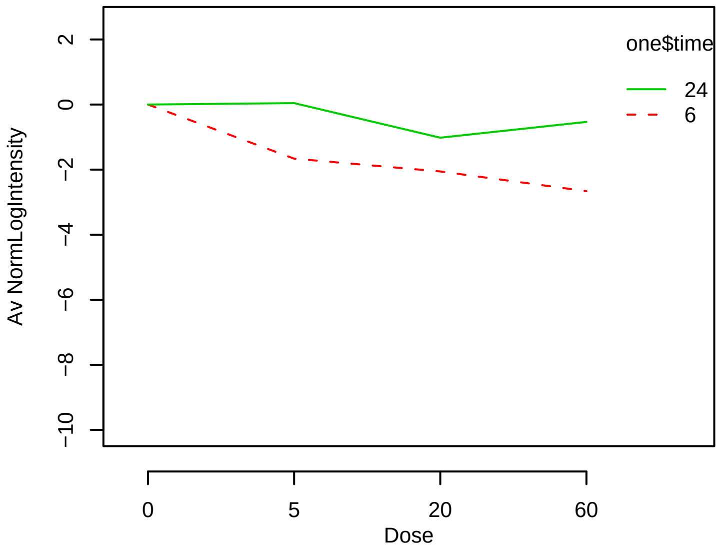
GO_0016202 : regulation of striated muscle development



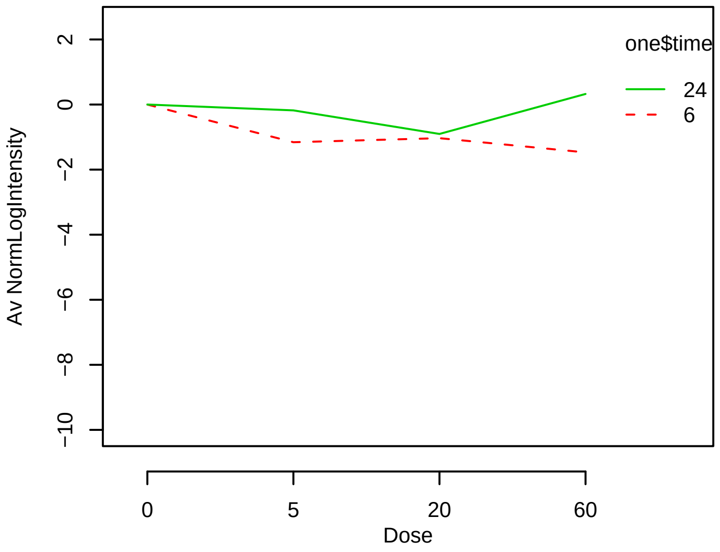
GO_0016236 : macroautophagy



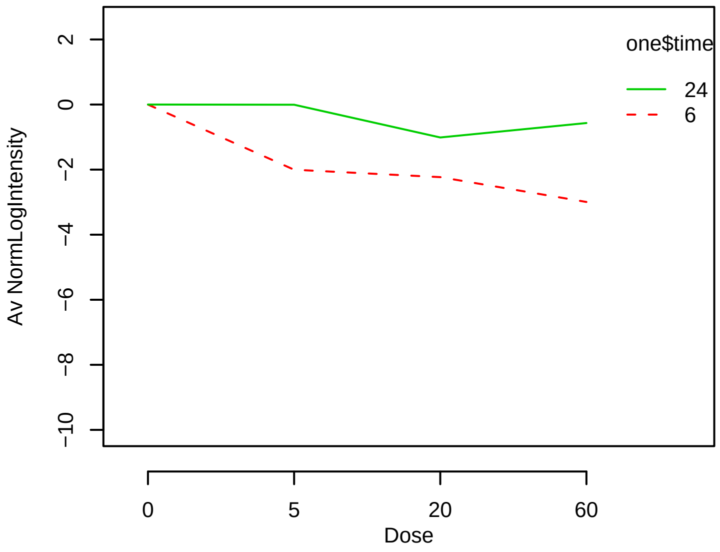
GO_0016255 : attachment of GPI anchor to protein



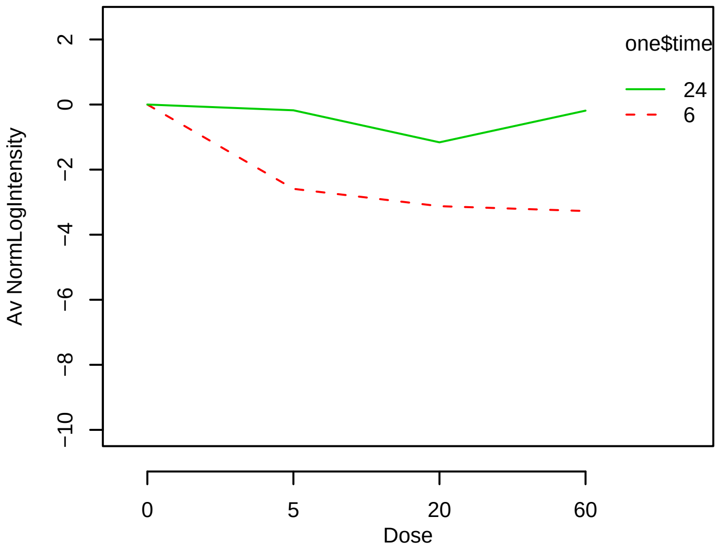
GO_0016311 : dephosphorylation



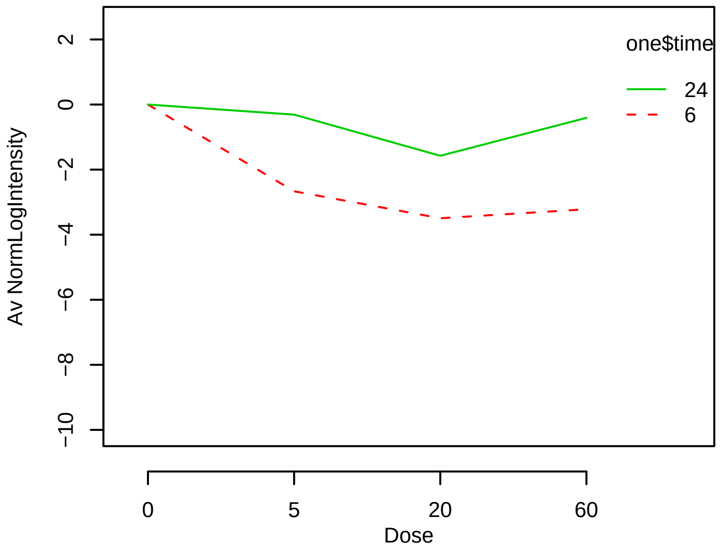
GO_0016322 : neuron remodeling



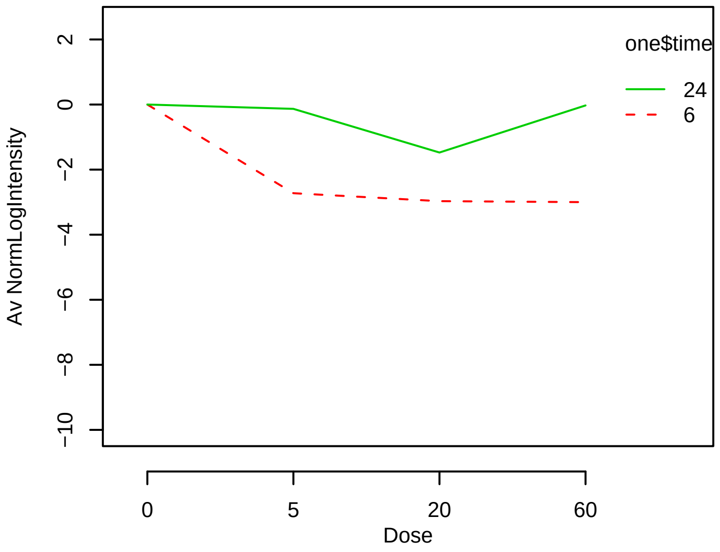
GO_0016331 : morphogenesis of embryonic epithelium



GO_0016337 : cell−cell adhesion

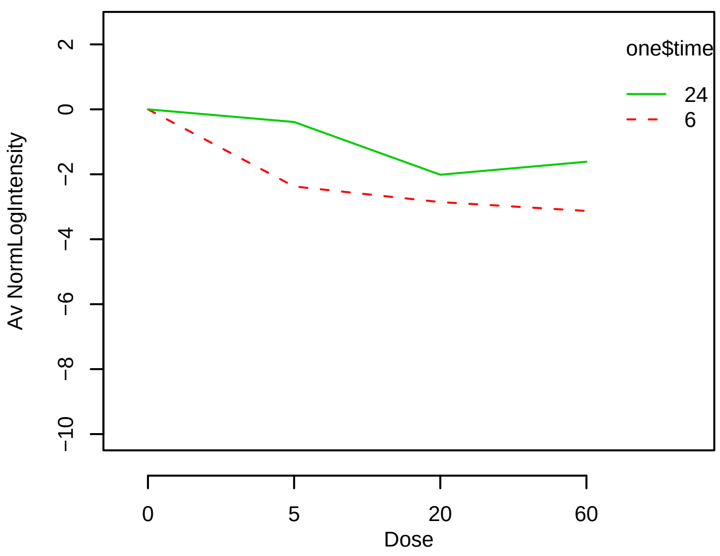


GO_0016338 : calcium−independent cell−cell adhesion

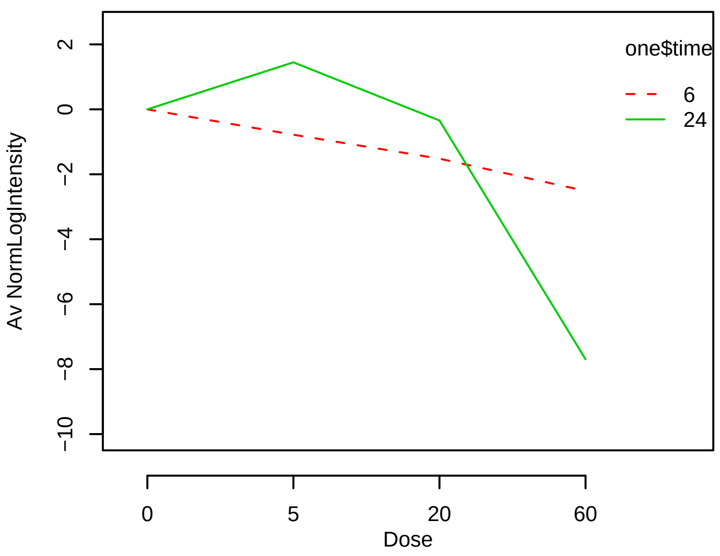


GO_0016339 : calcium−dependent cell−cell adhesion

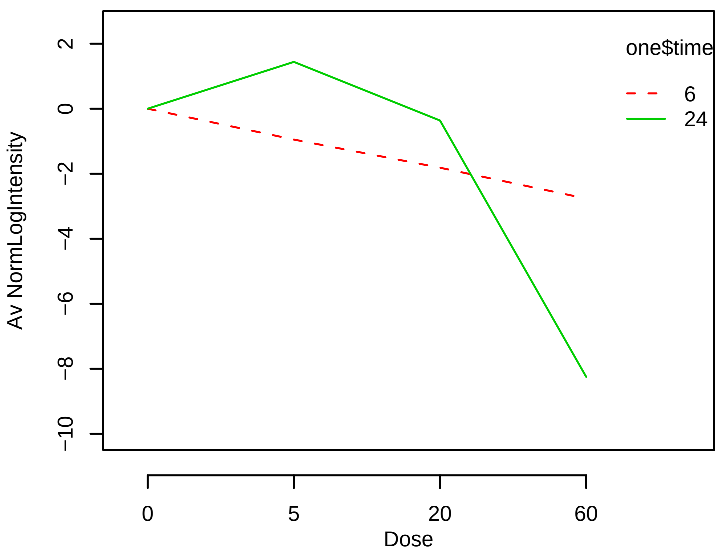
GO_0016358 : dendrite development



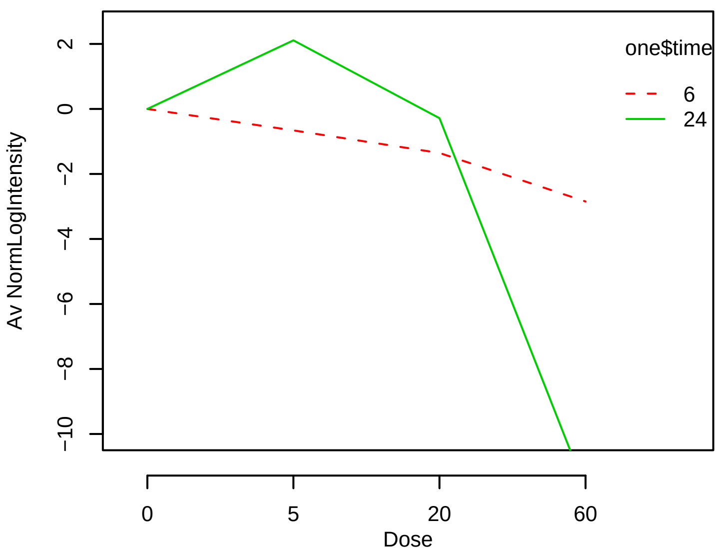
GO_0016444 : somatic cell DNA recombination



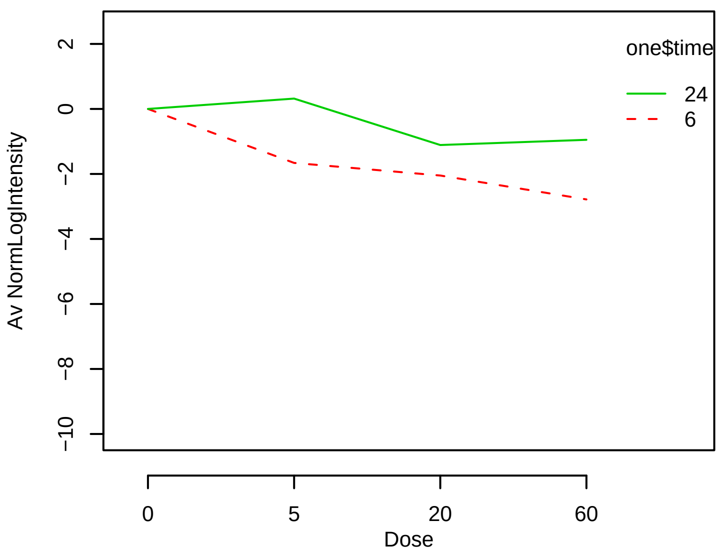
GO_0016445 : somatic diversification of immunoglobulin



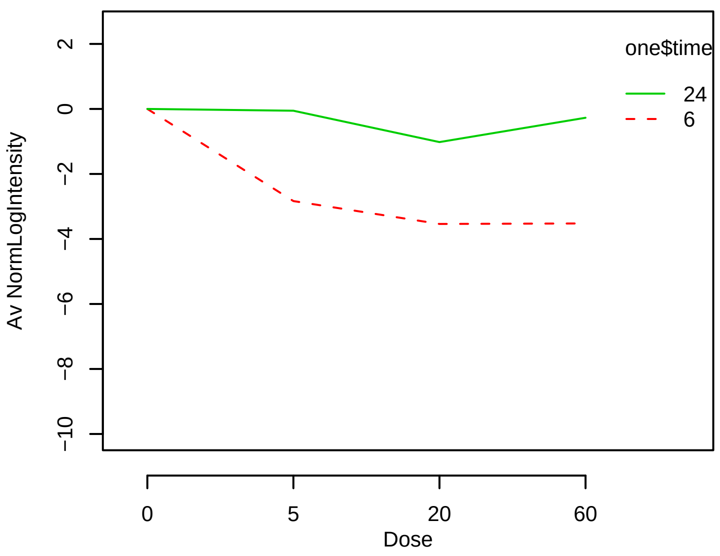
GO_0016446 : somatic hypermutation of immunoglobulin ge

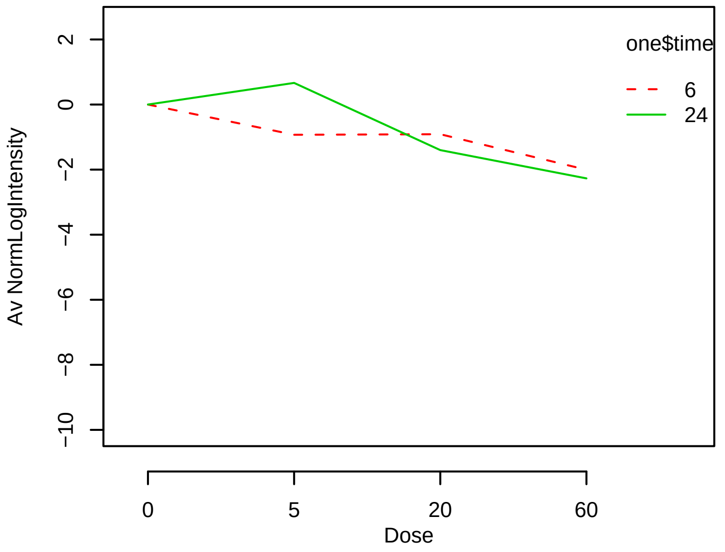


GO_0016458 : gene silencing

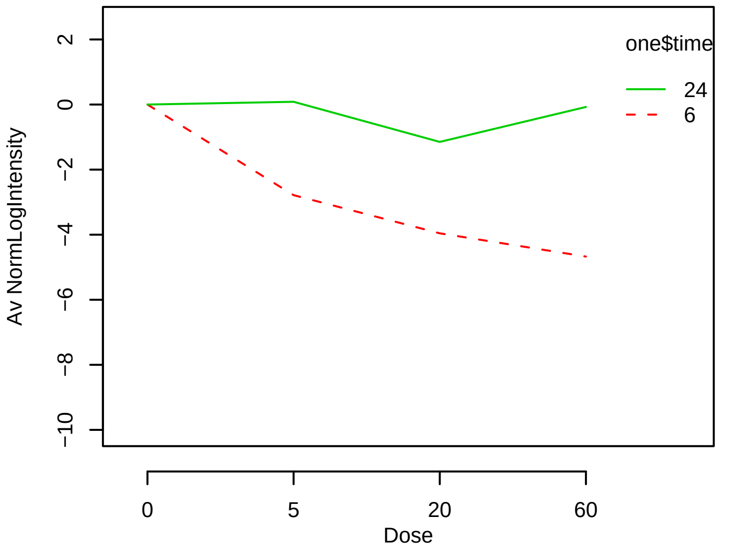


GO_0016477 : cell migration

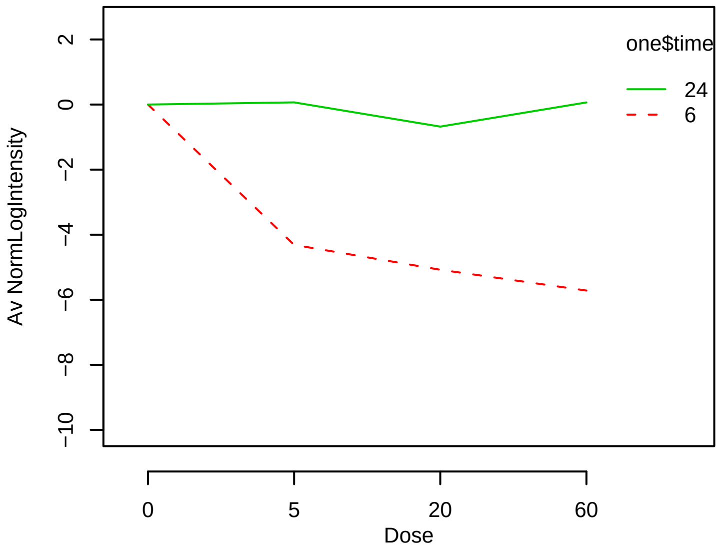




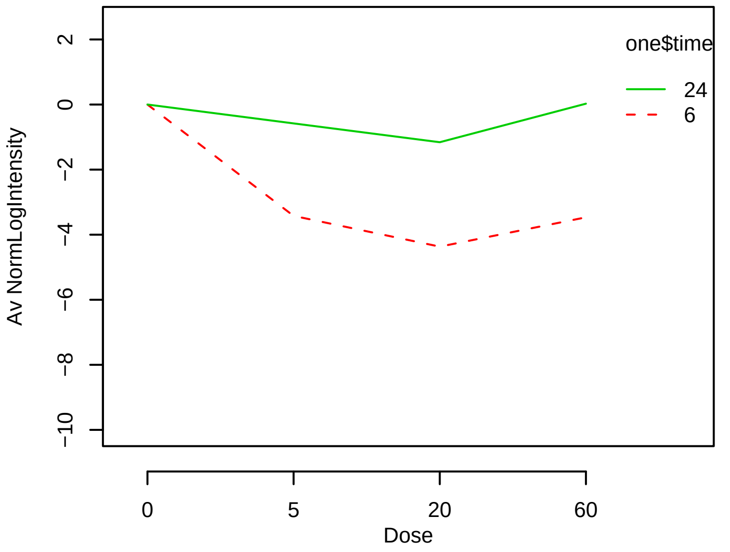
GO_0016478 : negative regulation of translation



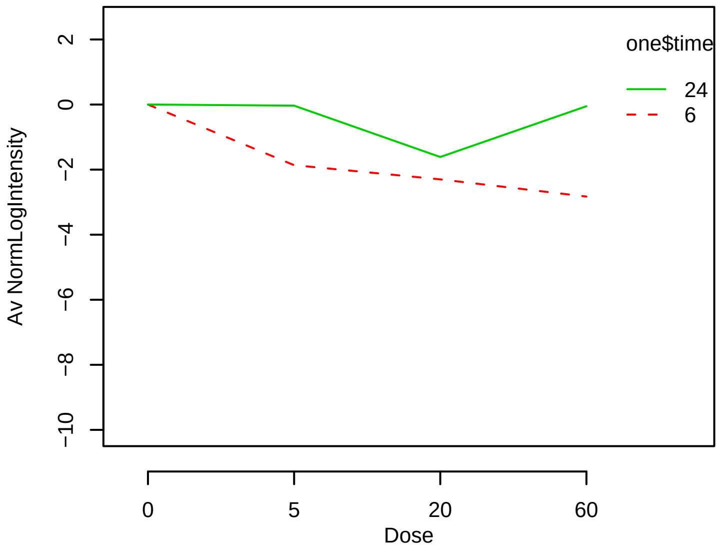
GO_0016485 : protein processing



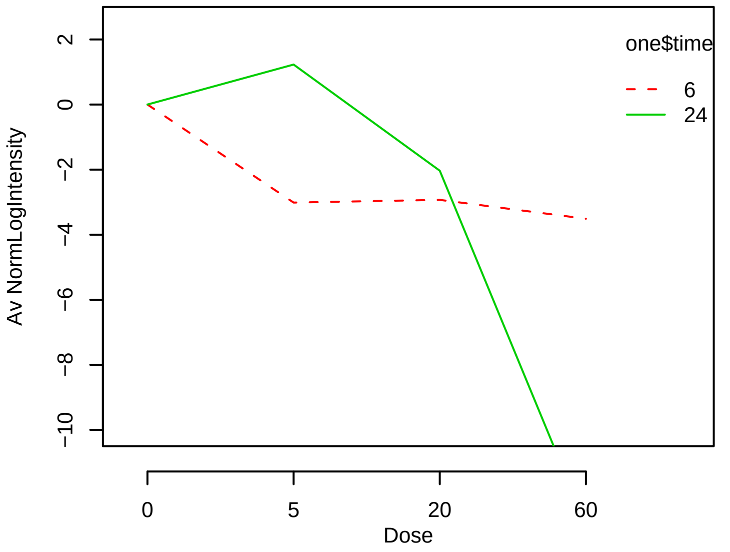
GO_0016486 : peptide hormone processing



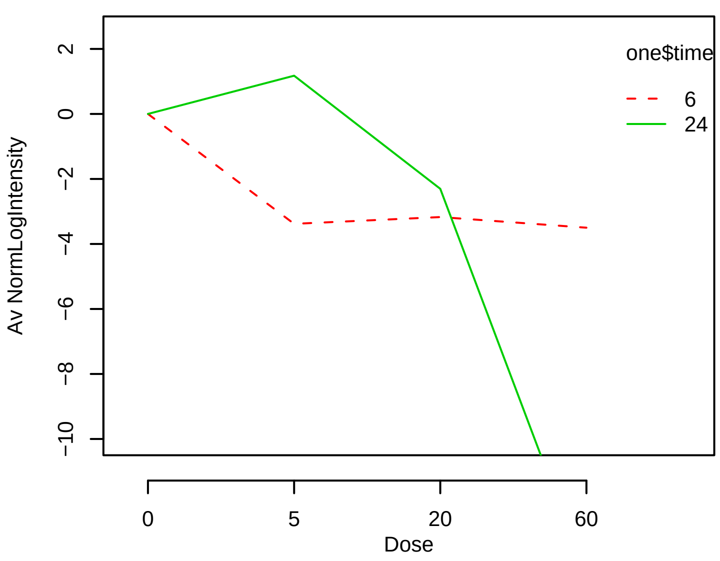
GO_0016525 : negative regulation of angiogenesis



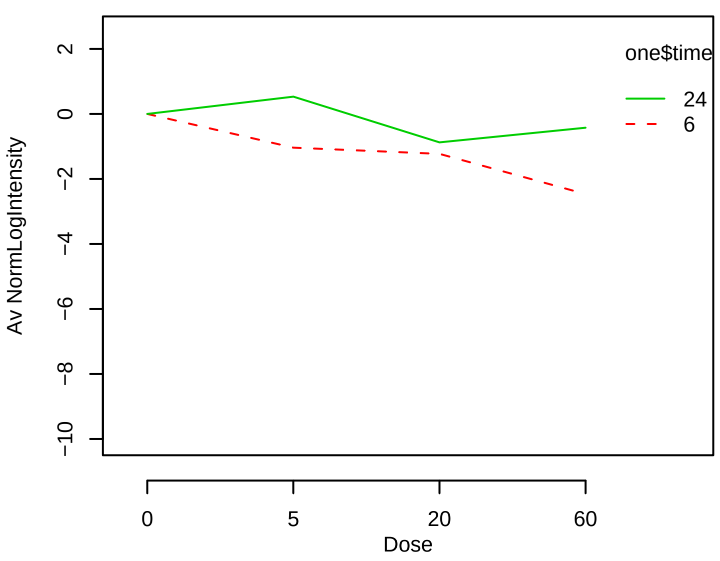
GO_0016540 : protein autoprocessing



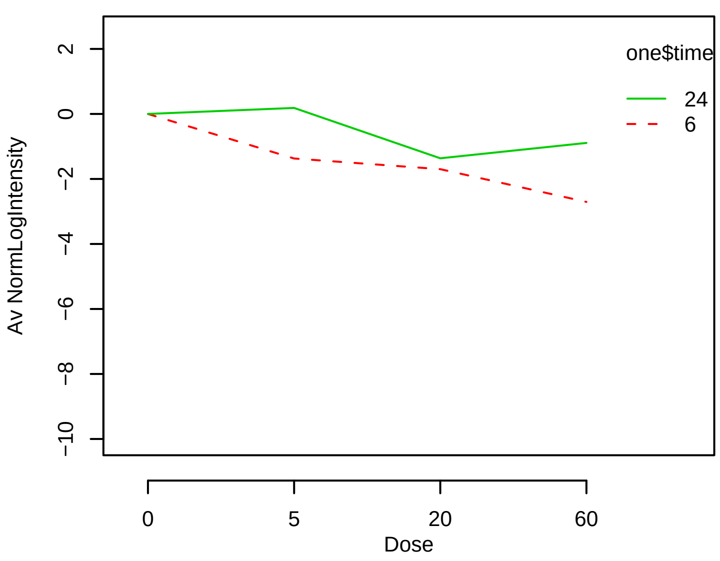
GO_0016547 : RNA editing



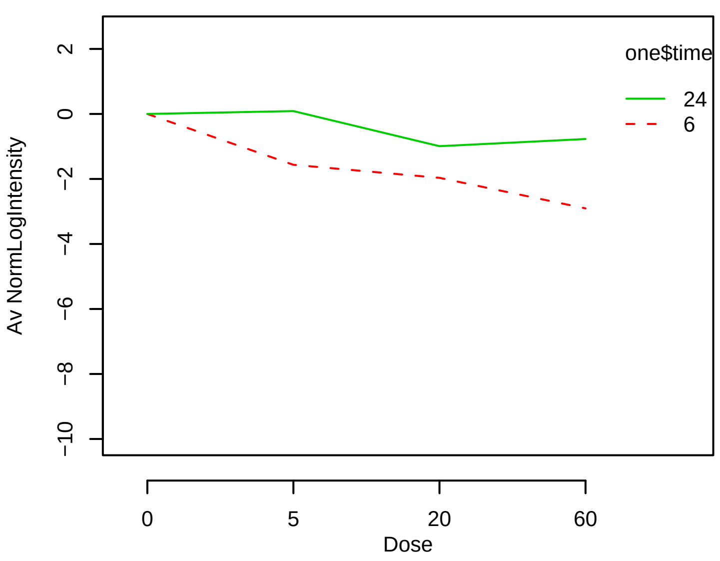
GO_0016556 : mRNA modification



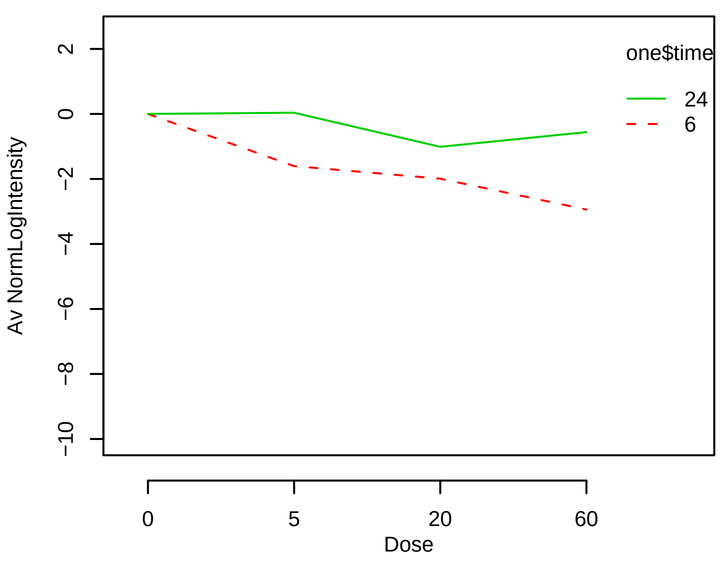
GO_0016567 : protein ubiquitination



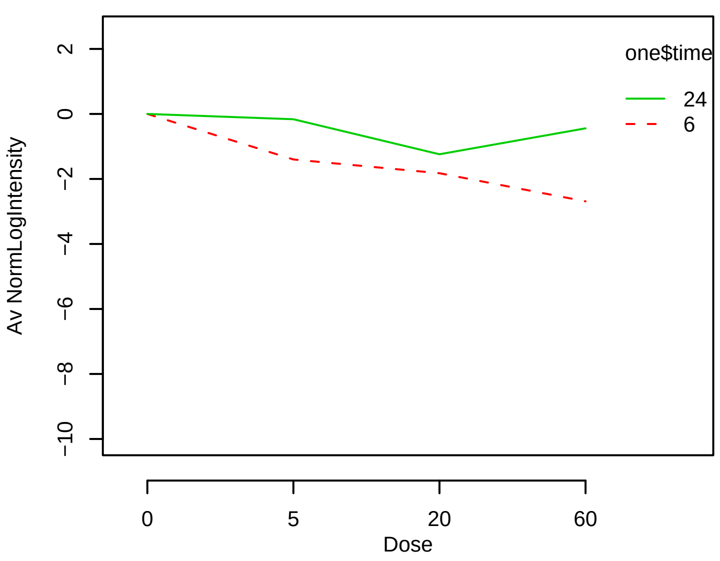
GO_0016568 : chromatin modification



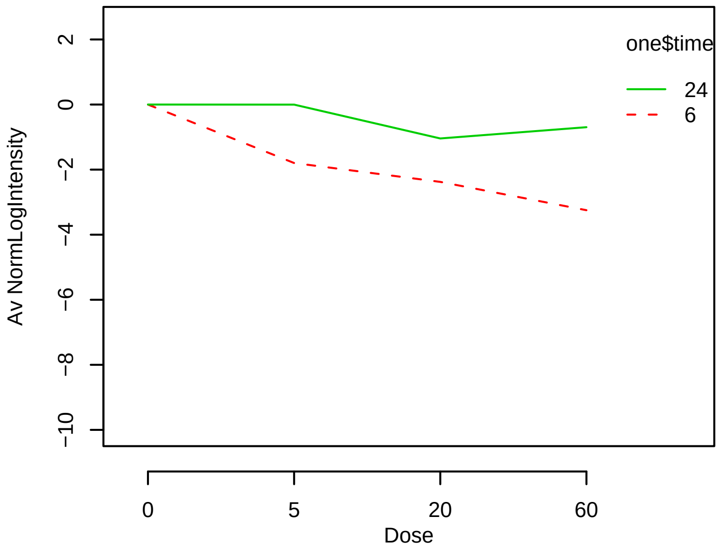
GO_0016569 : covalent chromatin modification



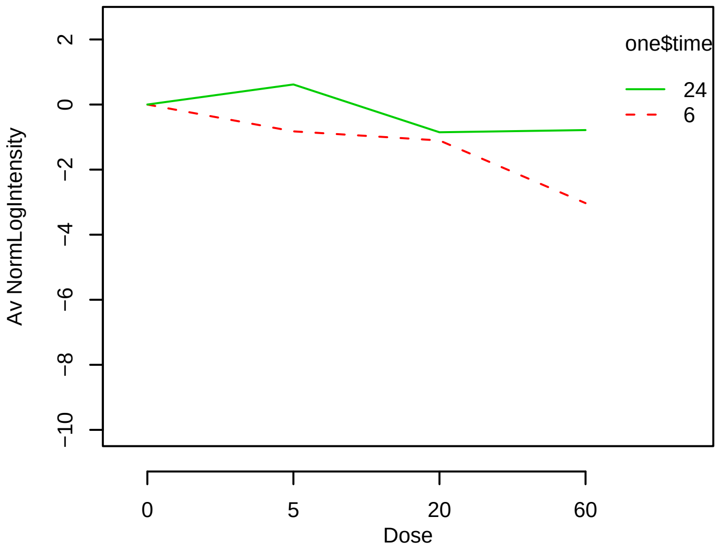
GO_0016570 : histone modification



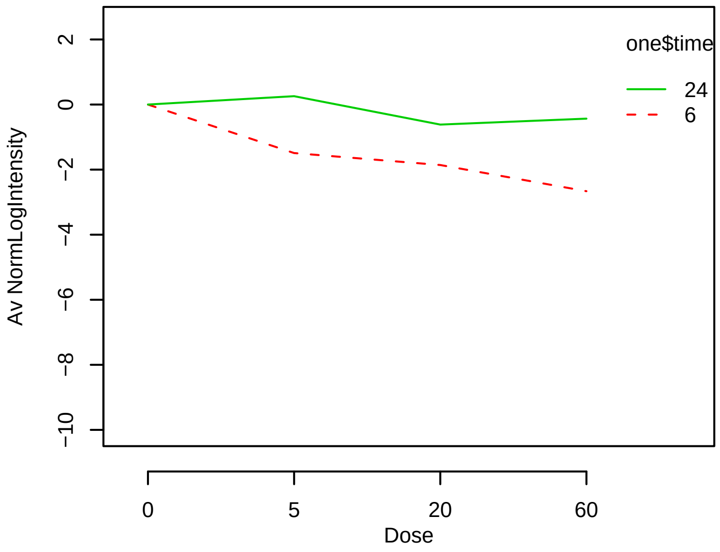
GO_0016571 : histone methylation



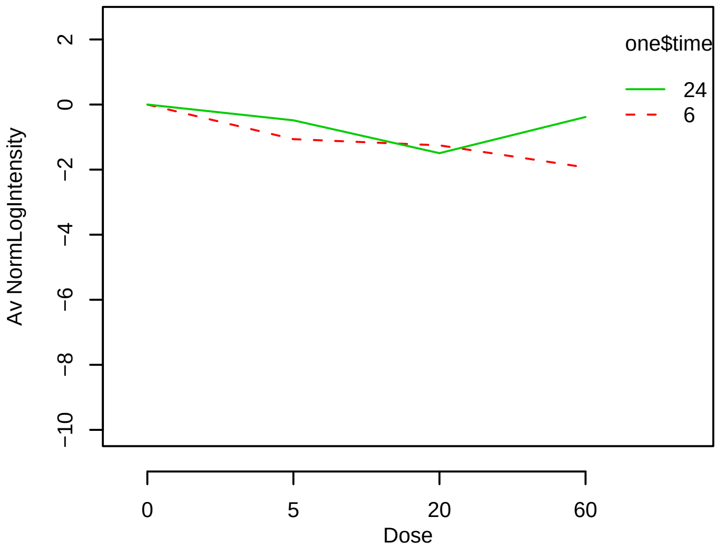
GO_0016573 : histone acetylation



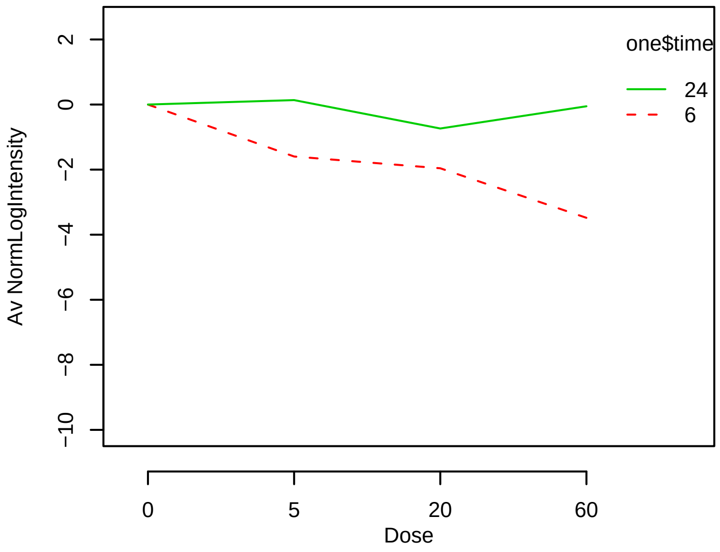
GO_0016574 : histone ubiquitination



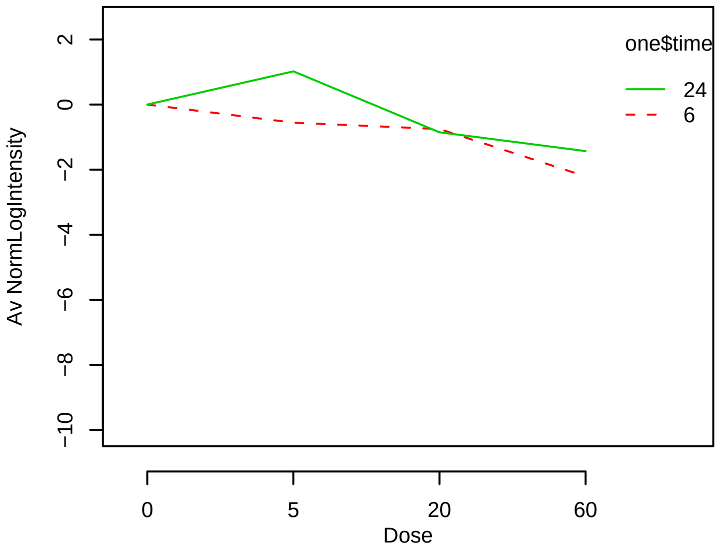
GO_0016575 : histone deacetylation



GO_0016584 : nucleosome spacing

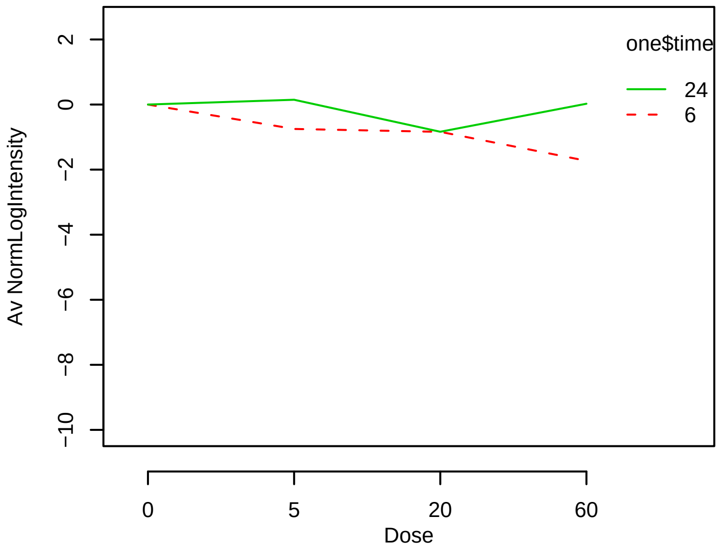


GO_0016601 : Rac protein signal transduction

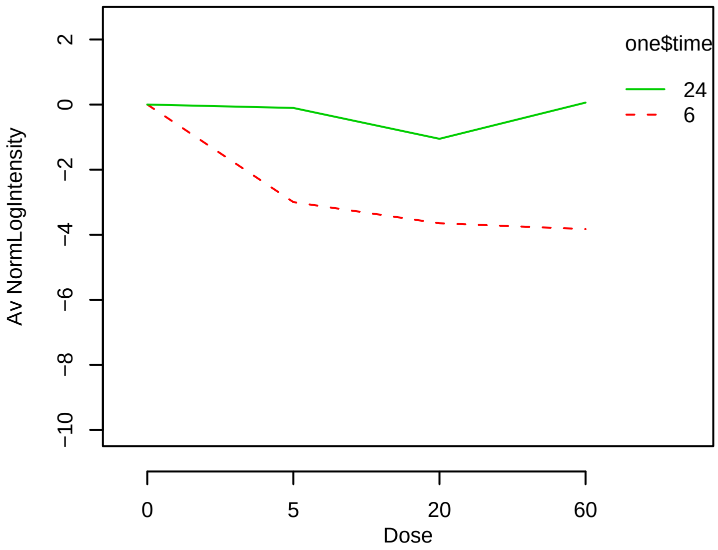


GO_0016925 : protein sumoylation

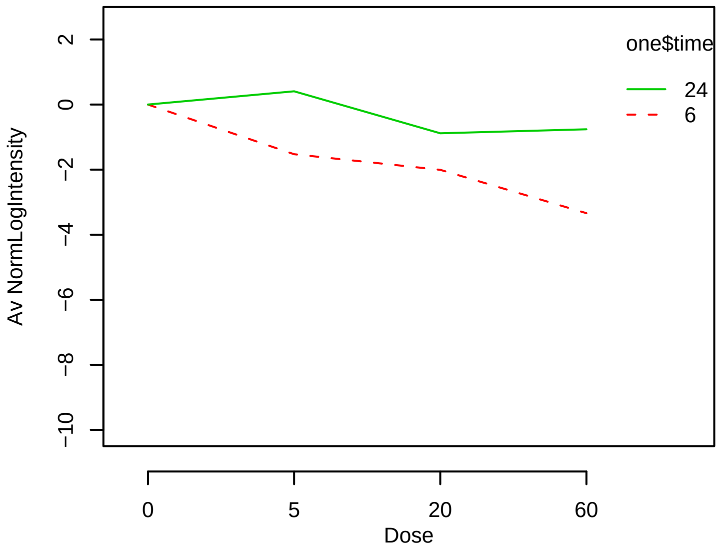
GO_0016998 : cell wall catabolism



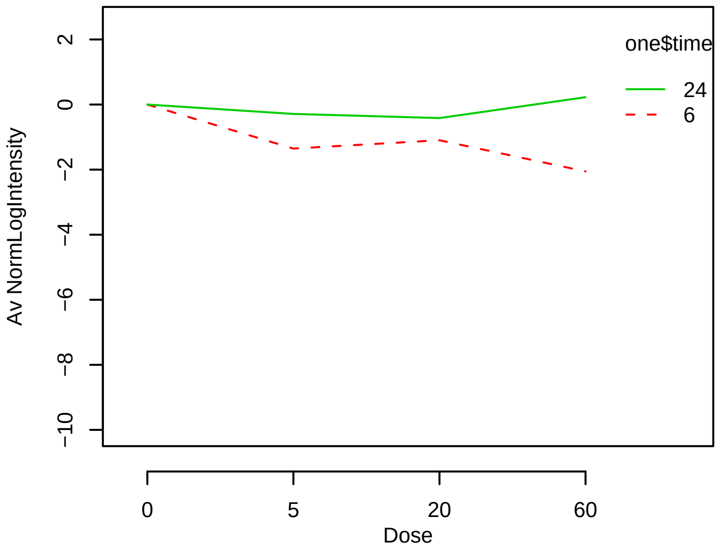
GO_0017015 : regulation of transforming growth factor beta



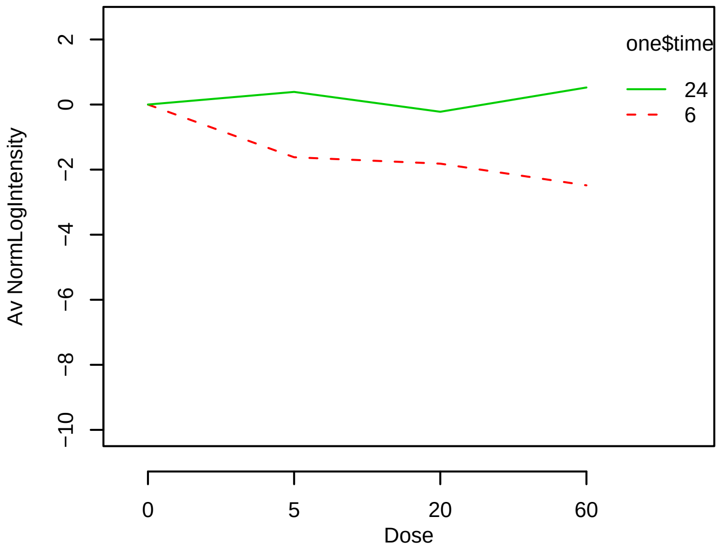
GO_0017038 : protein import



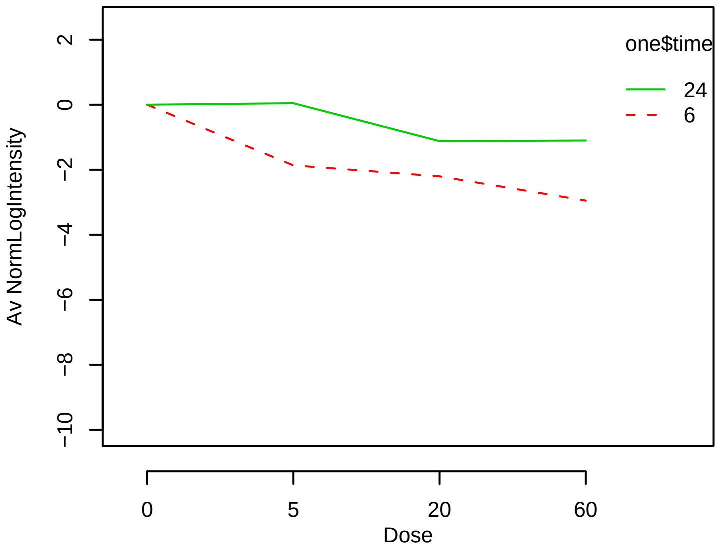
GO_0017144 : drug metabolism

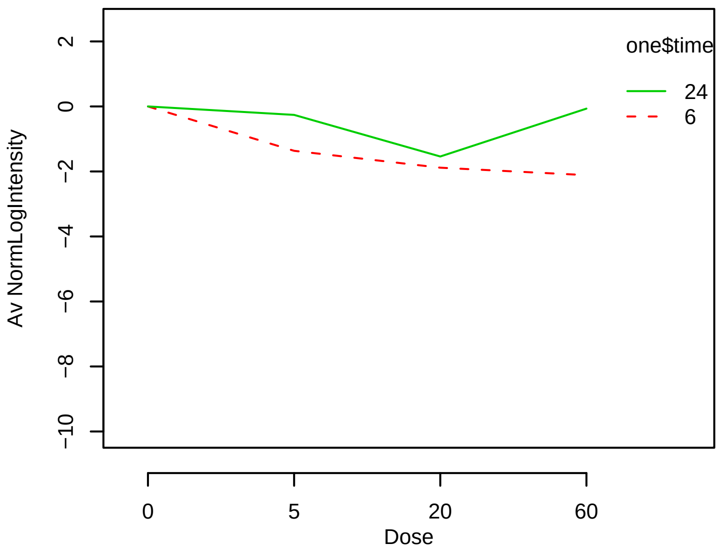


GO_0017145 : stem cell division

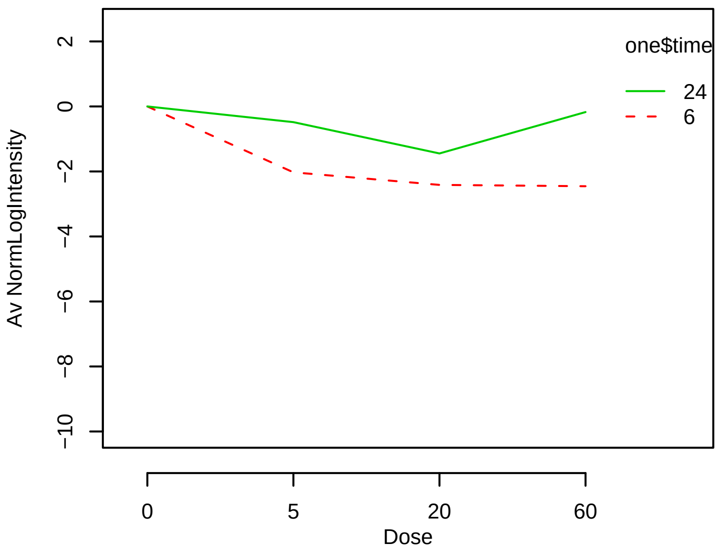


GO_0017148 : negative regulation of protein biosynthesis

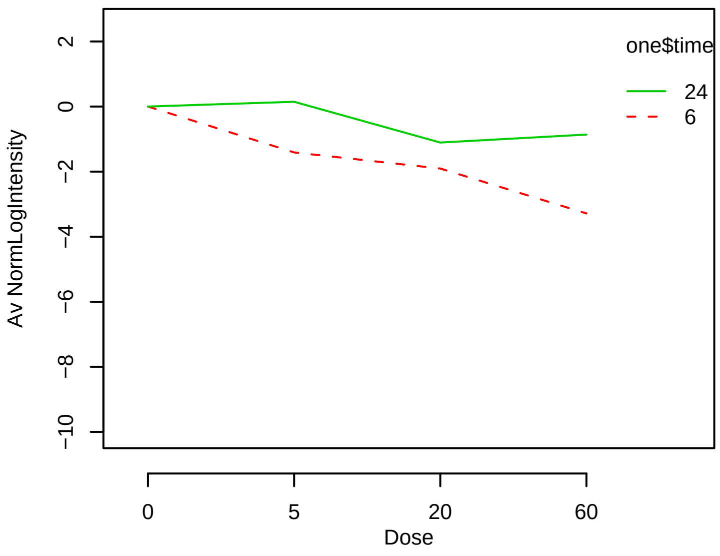




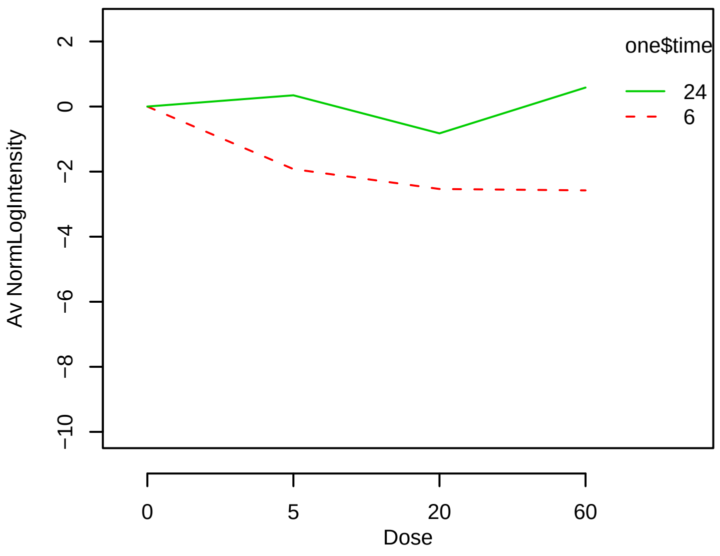
GO_0017156 : calcium ion−dependent exocytosis



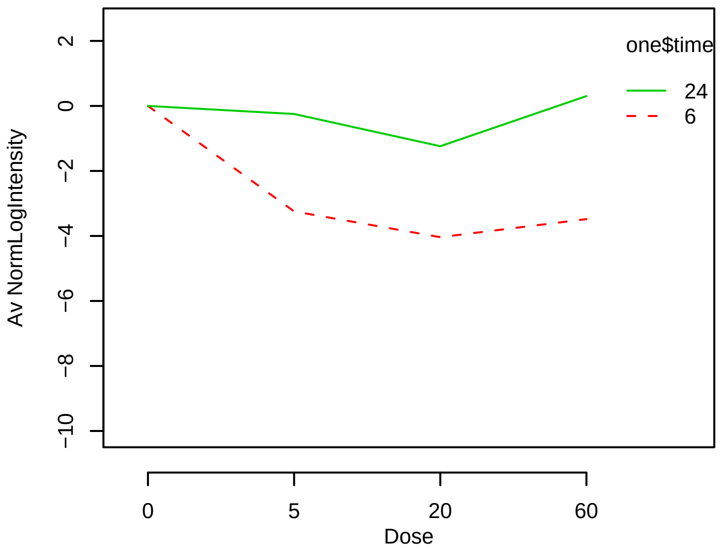
GO_0017157 : regulation of exocytosis



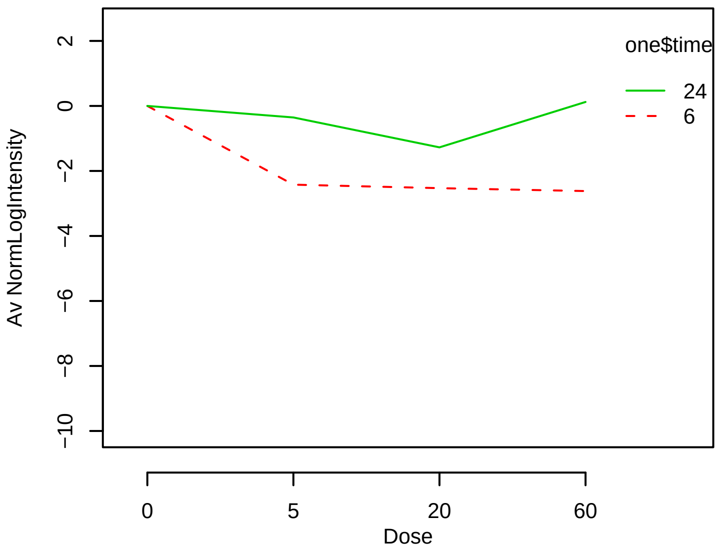
GO_0018065 : protein−cofactor linkage



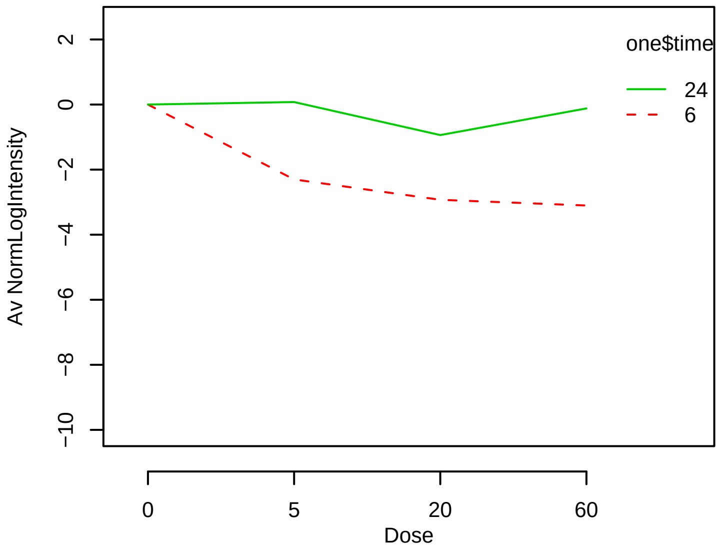
GO_0018105 : peptidyl−serine phosphorylation

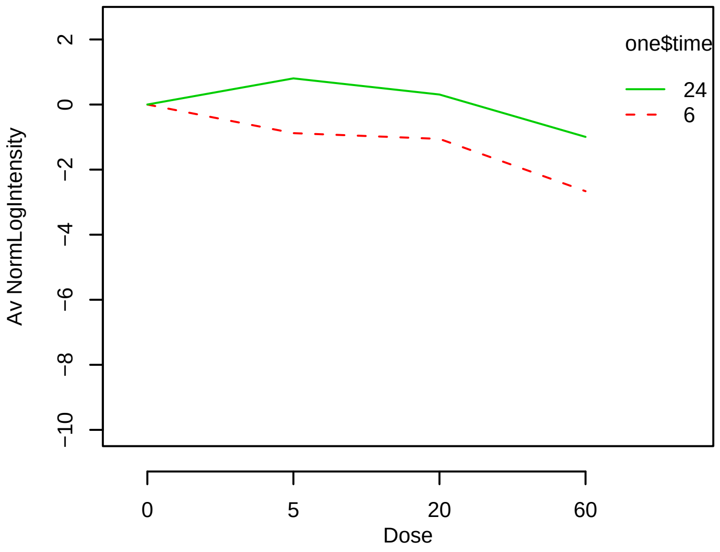


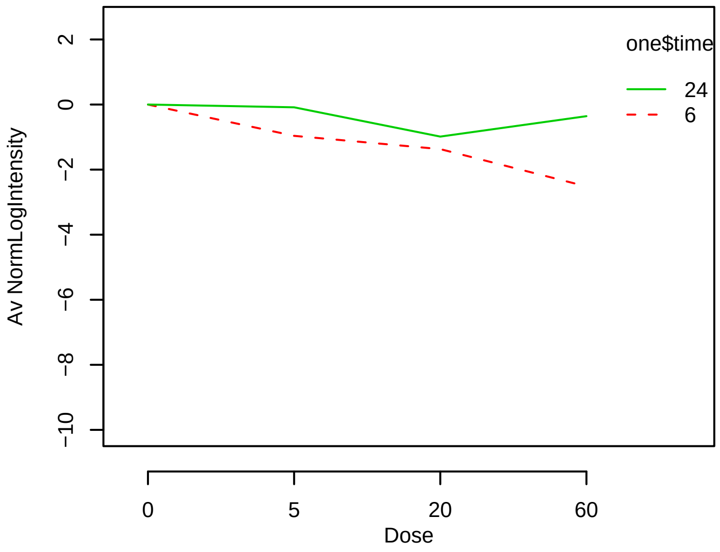
GO_0018108 : peptidyl−tyrosine phosphorylation

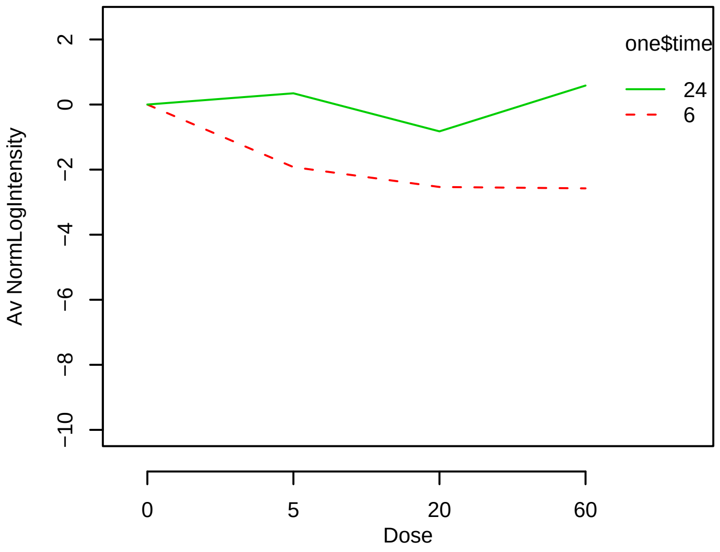


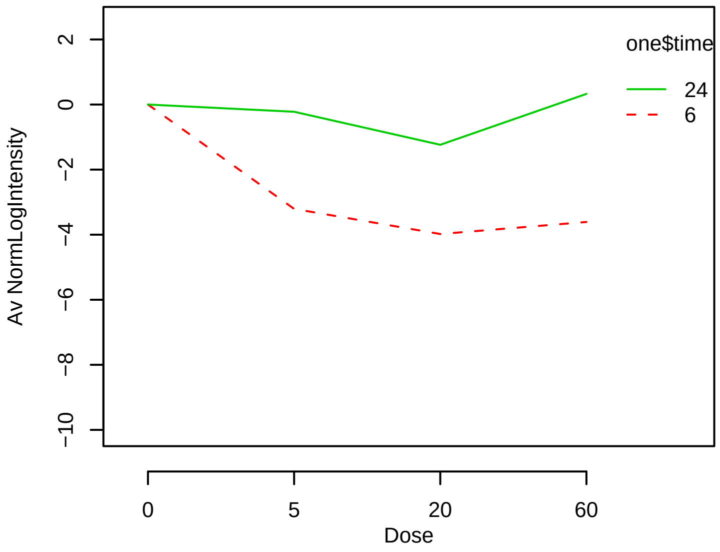
GO_0018149 : peptide cross−linking

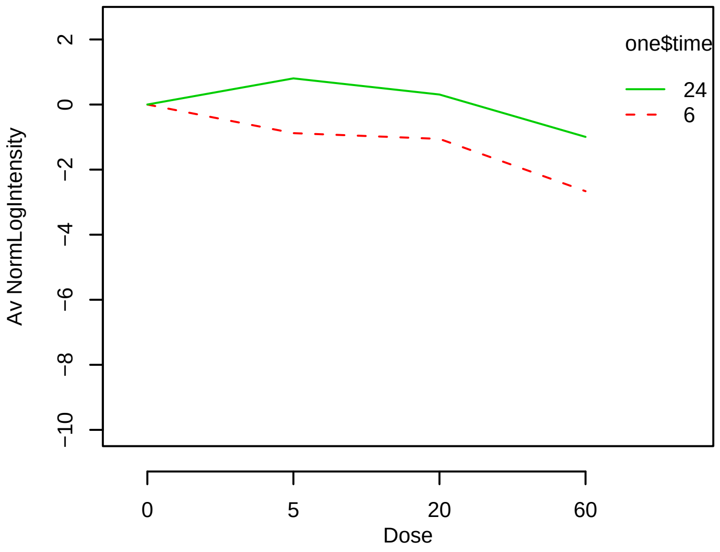

GO_0018193 : peptidyl−amino acid modification

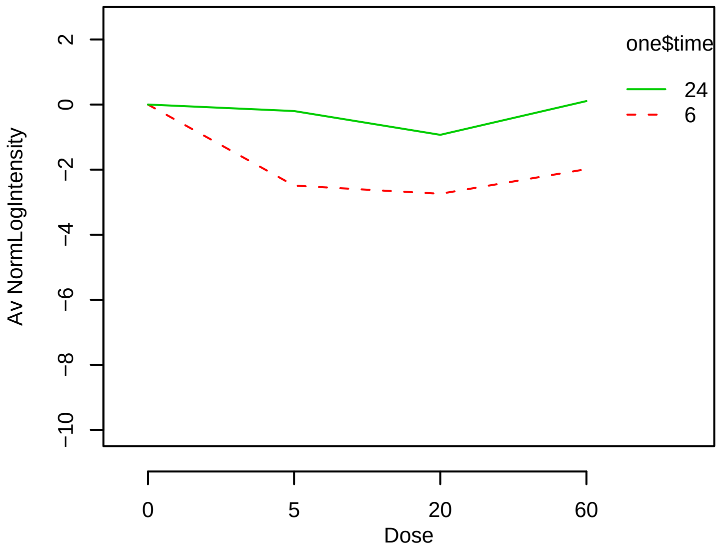

GO_0018196 : peptidyl−asparagine modification

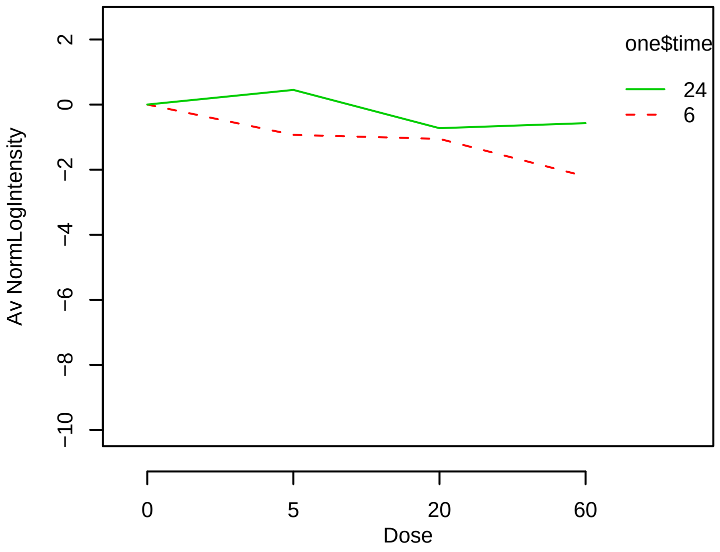

GO_0018202 : peptidyl−histidine modification

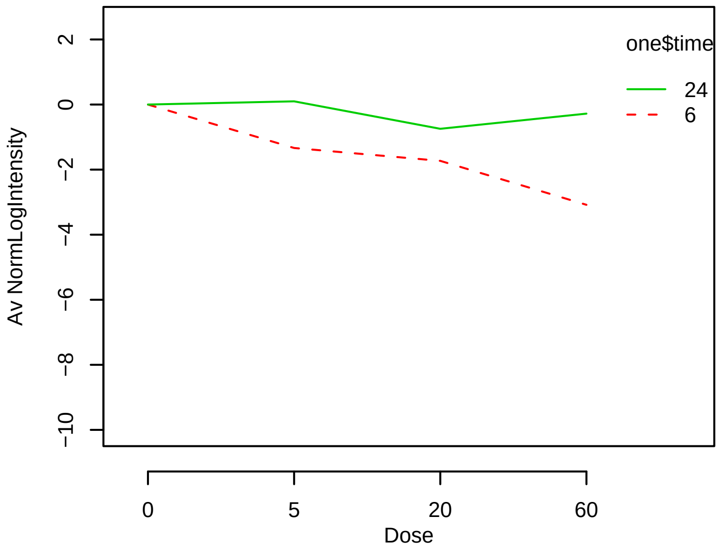

GO_0018209 : peptidyl−serine modification

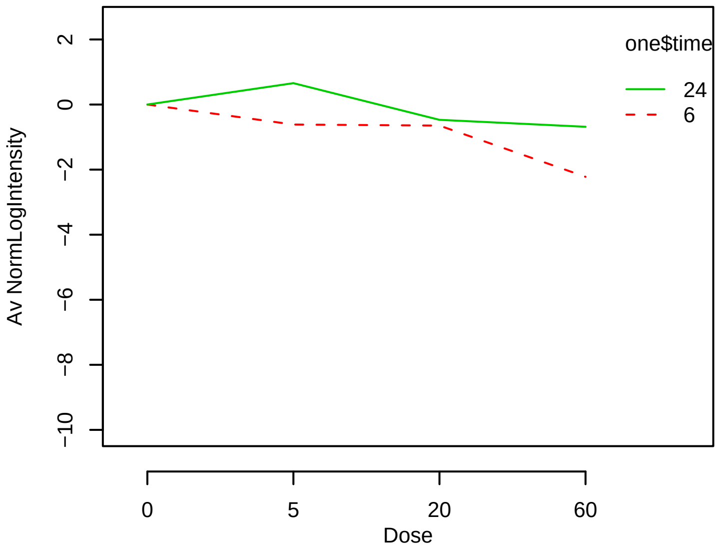

GO_0018212 : peptidyl−tyrosine modification

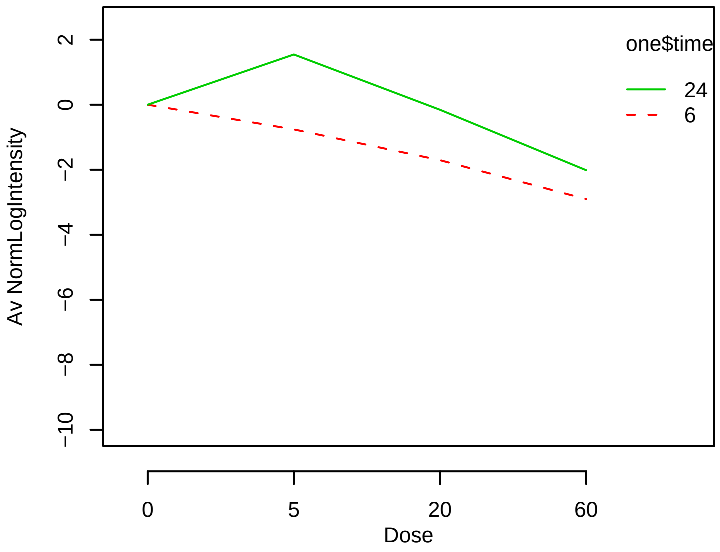

O_0018279 : protein amino acid N−linked glycosylation via

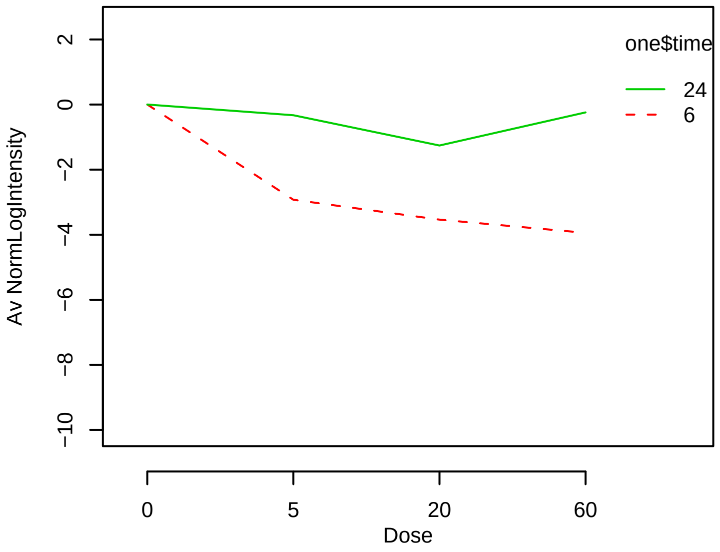

GO_0018298 : protein−chromophore linkage

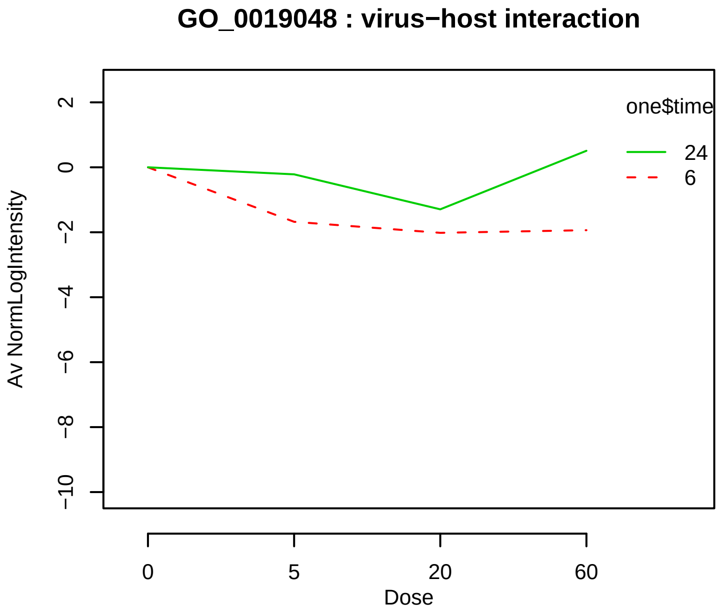

GO_0018342 : protein prenylation


GO_0018345 : protein palmitoylation

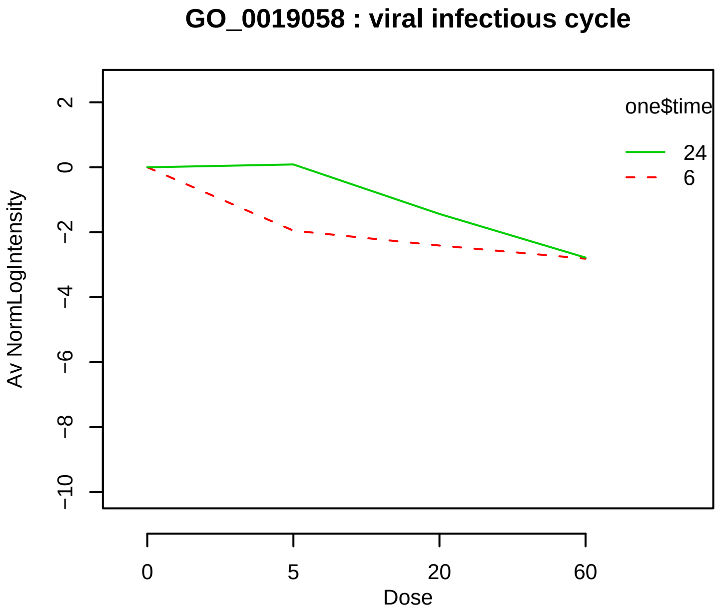

GO_0018346 : protein amino acid prenylation


GO_0018409 : peptide or protein amino−terminal blocking

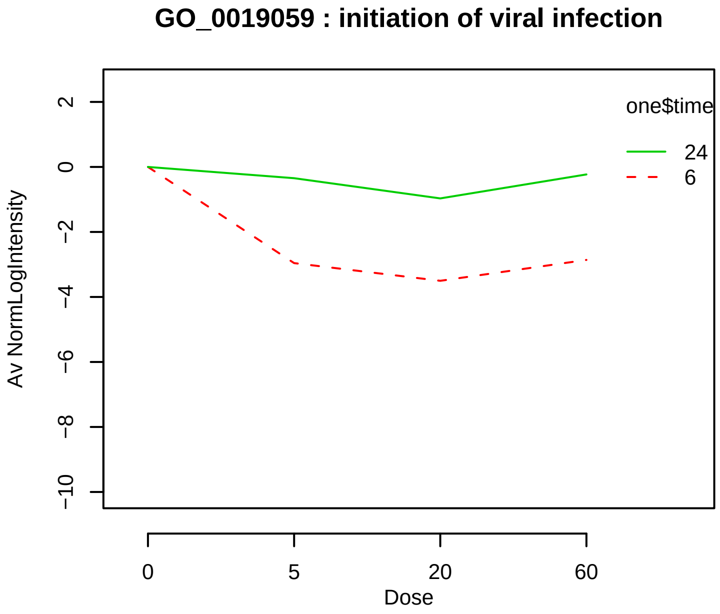

GO_0018958 : phenol metabolism



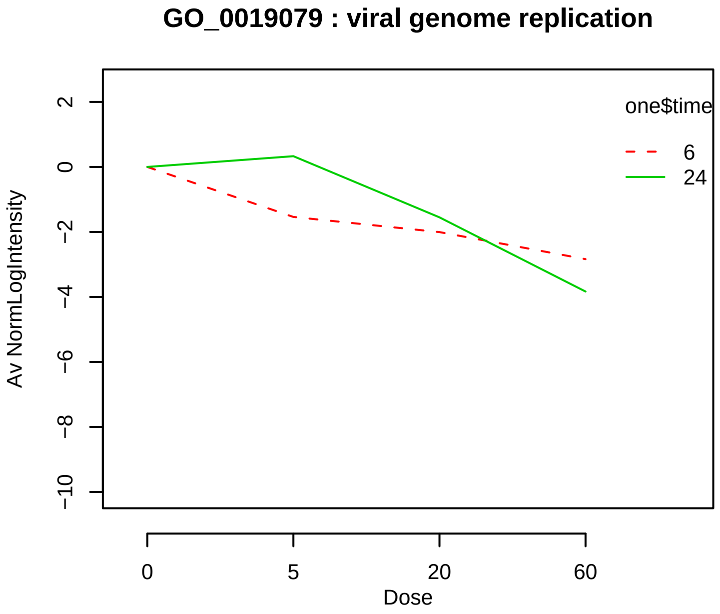
GO_0019048 : virus−host interaction



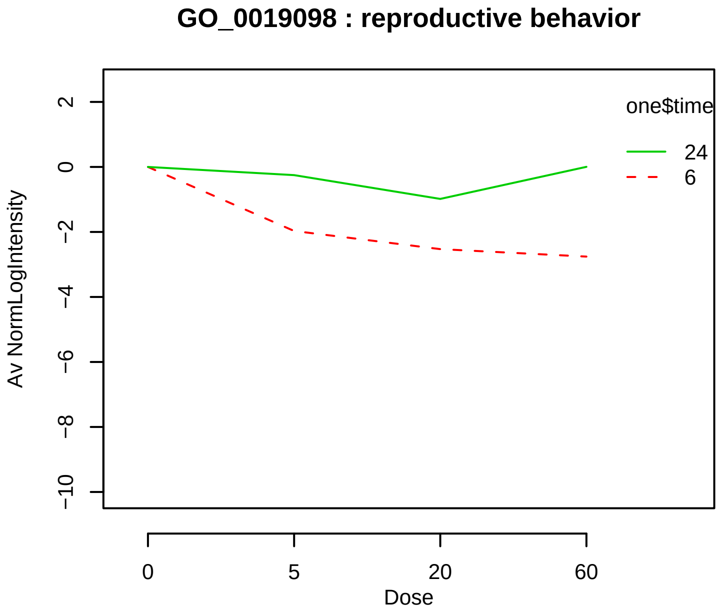
GO_0019058 : viral infectious cycle



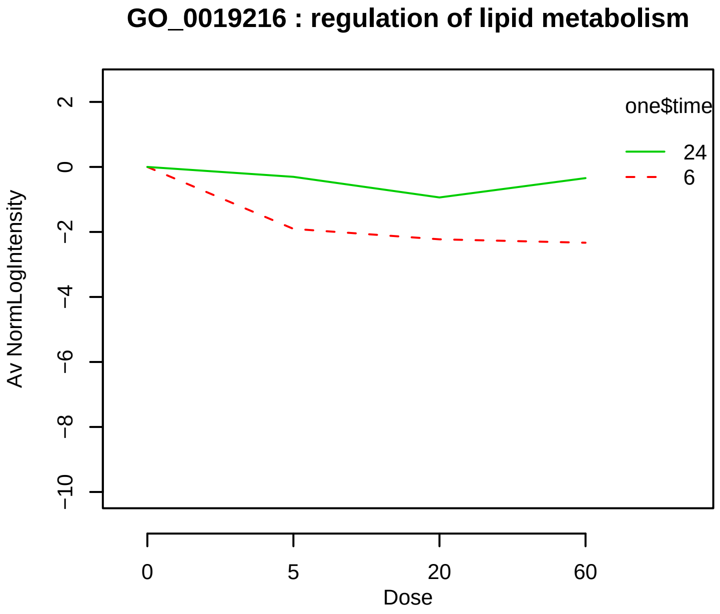
GO_0019059 : initiation of viral infection



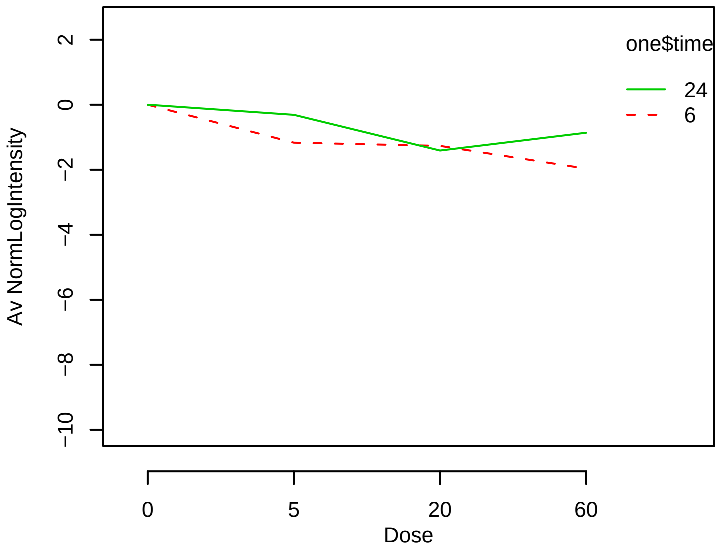
GO_0019079 : viral genome replication

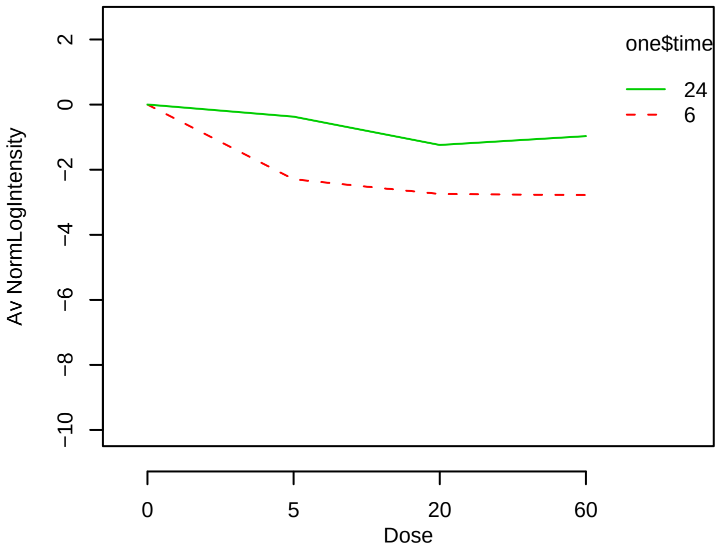


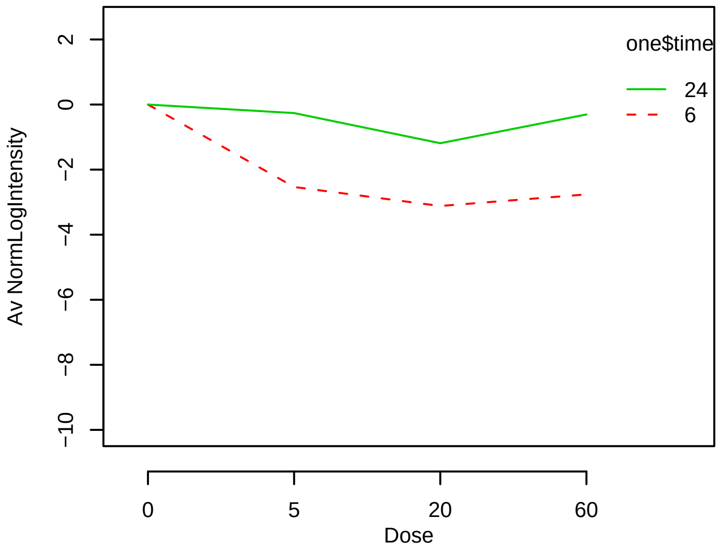
GO_0019098 : reproductive behavior

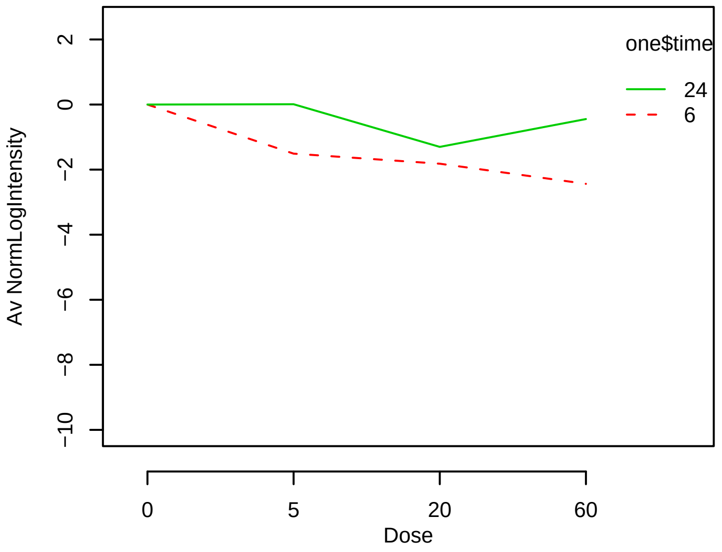


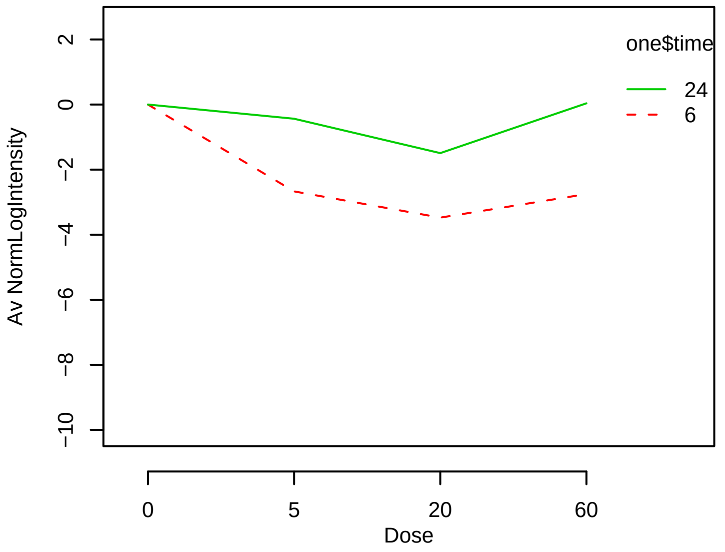
GO_0019216 : regulation of lipid metabolism

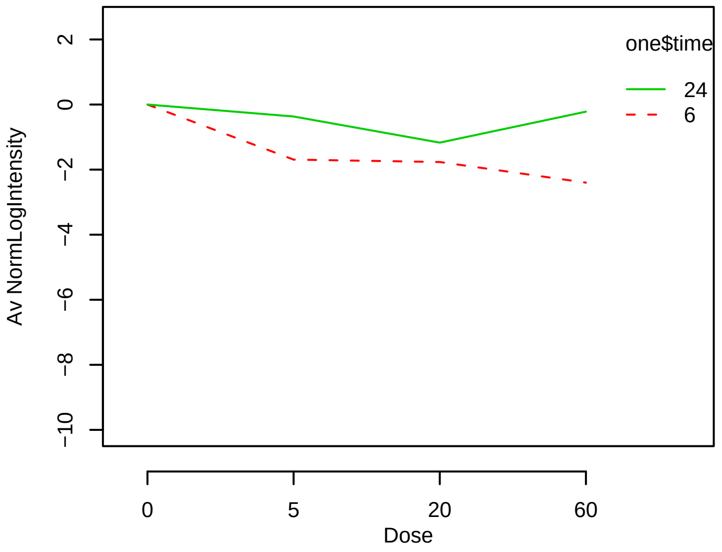

GO_0019217 : regulation of fatty acid metabolism

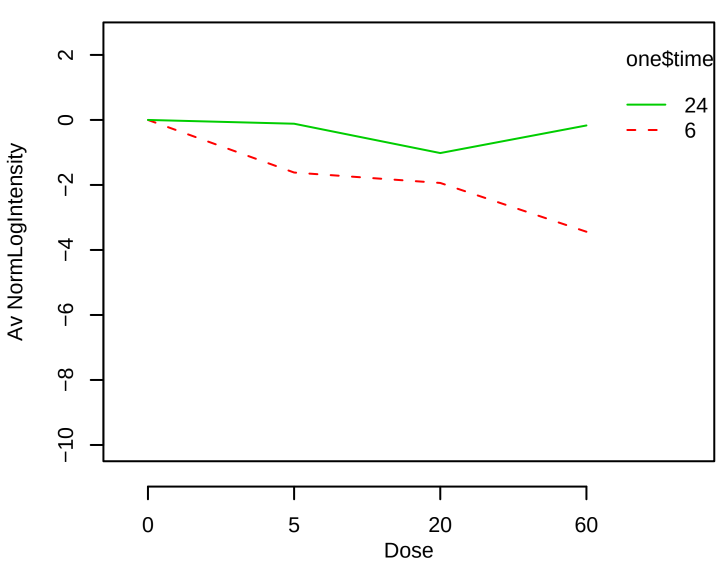

GO_0019218 : regulation of steroid metabolism


GO_0019220 : regulation of phosphate metabolism

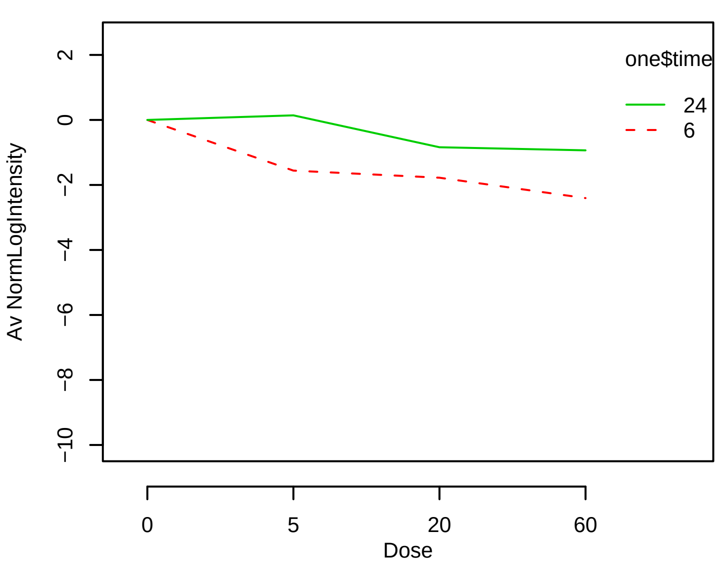

O_0019221 : cytokine and chemokine mediated signaling pat


GO_0019229 : regulation of vasoconstriction

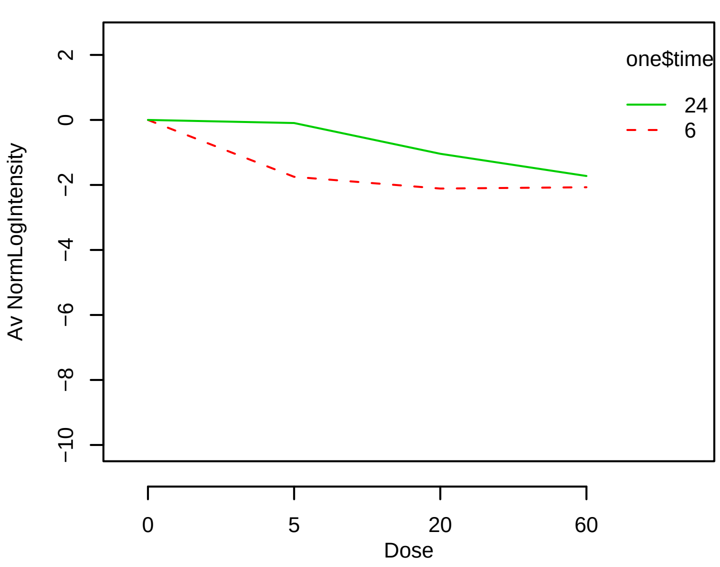

GO_0019233 : sensory perception of pain



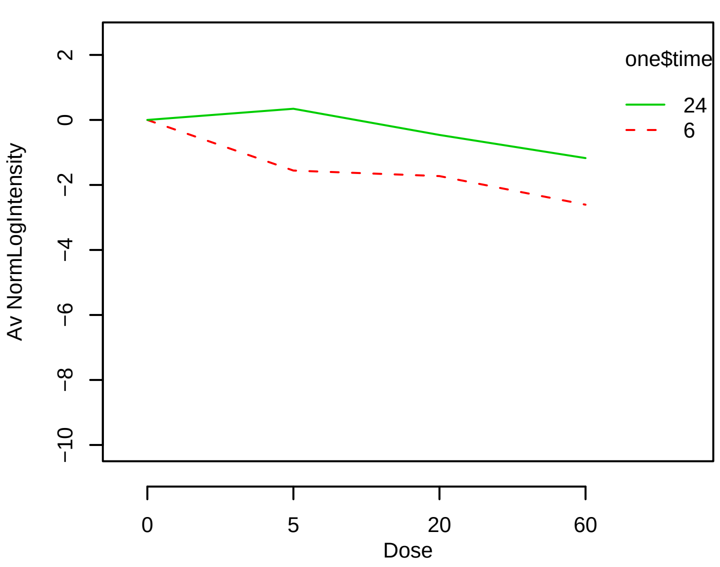
GO_0019317 : fucose catabolism



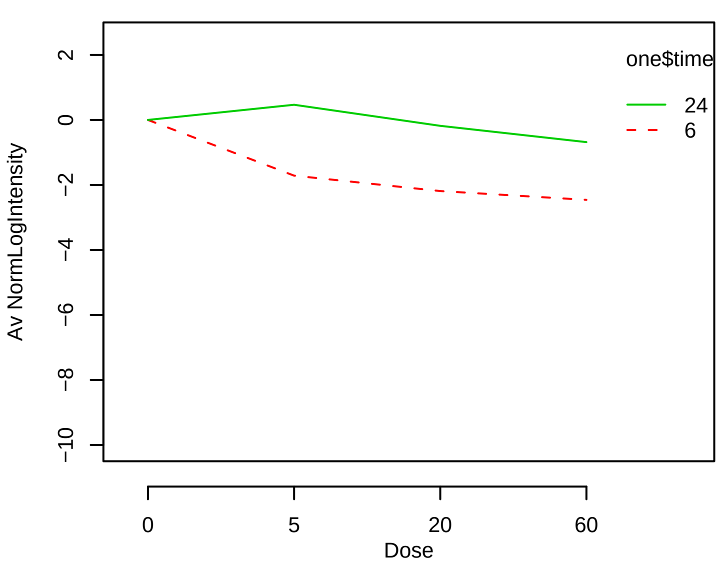
GO_0019318 : hexose metabolism



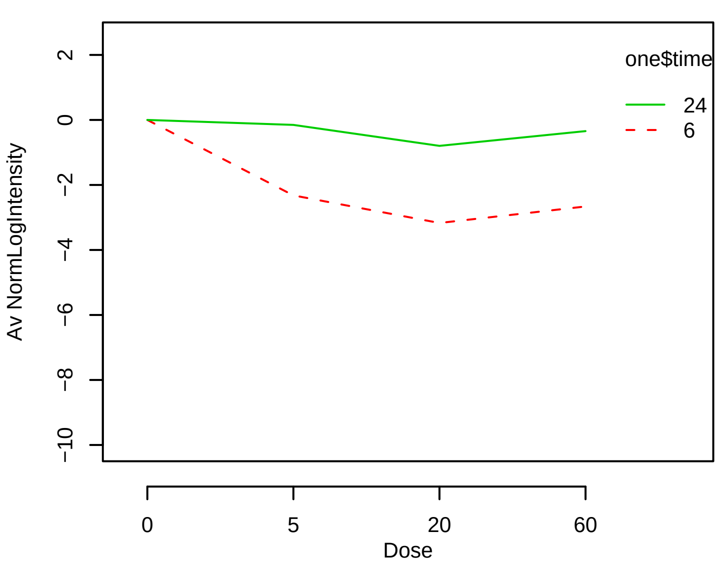
GO_0019319 : hexose biosynthesis



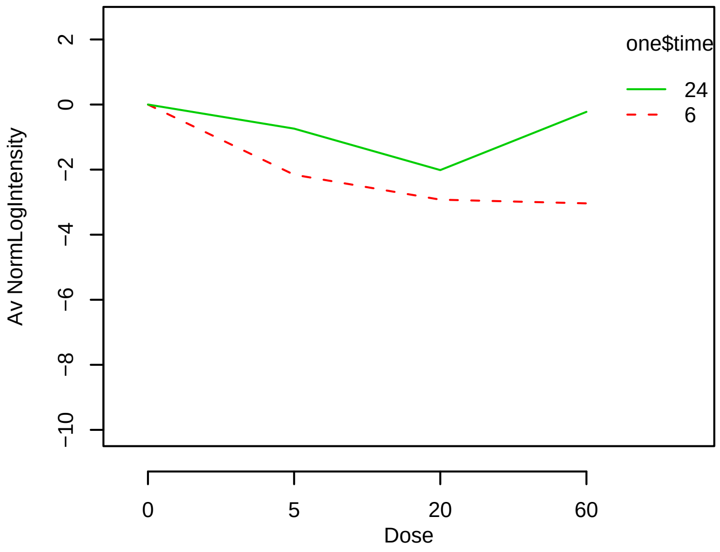
GO_0019320 : hexose catabolism



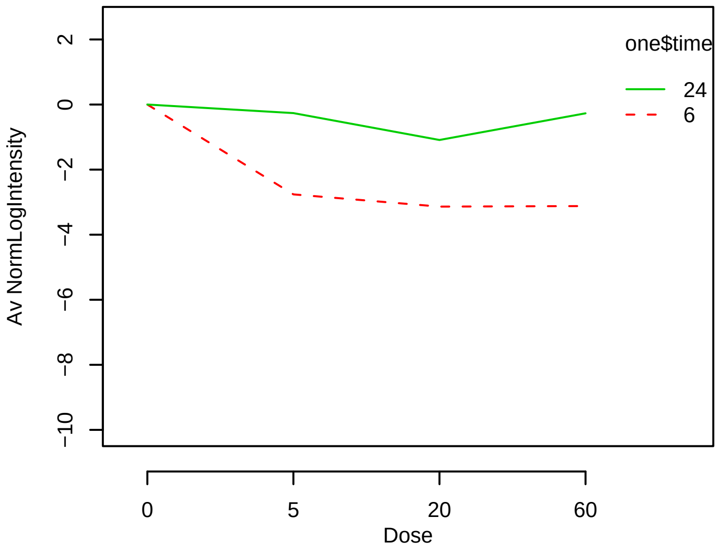
GO_0019362 : pyridine nucleotide metabolism



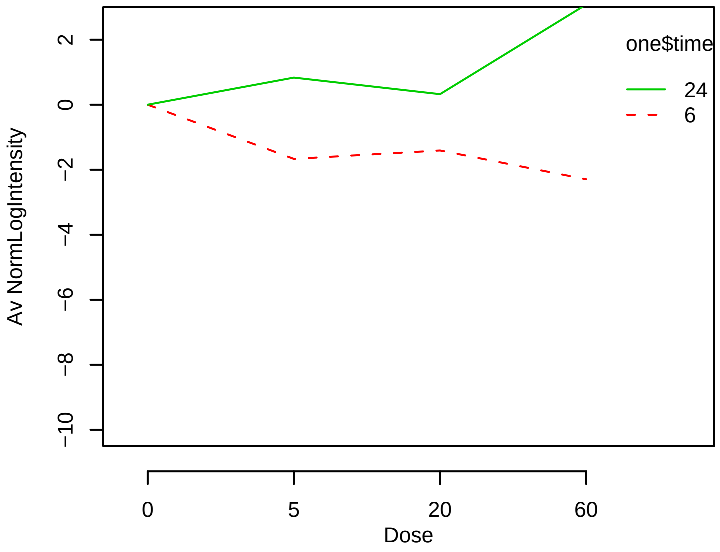
GO_0019363 : pyridine nucleotide biosynthesis



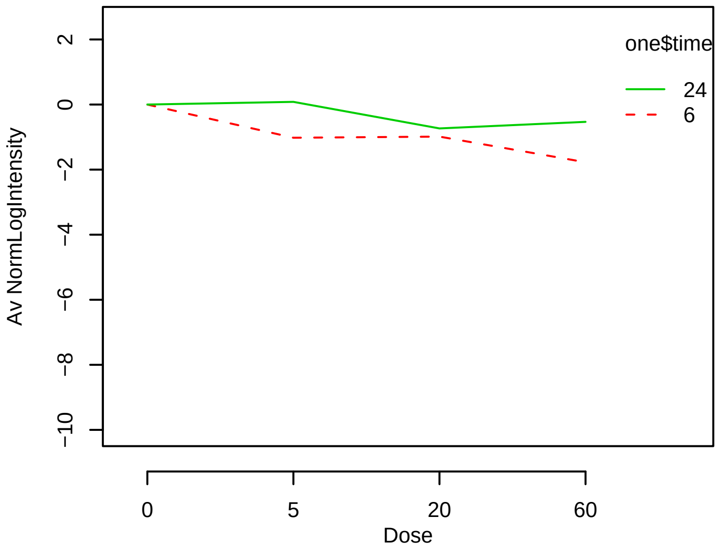
GO_0019369 : arachidonic acid metabolism



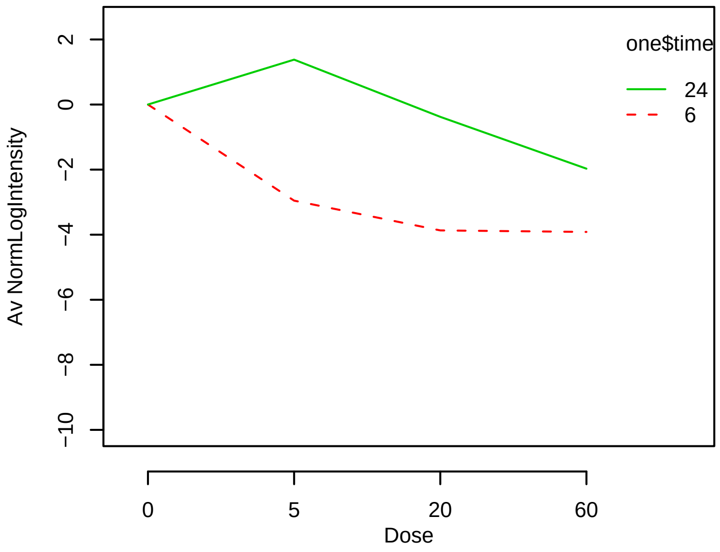
GO_0019370 : leukotriene biosynthesis



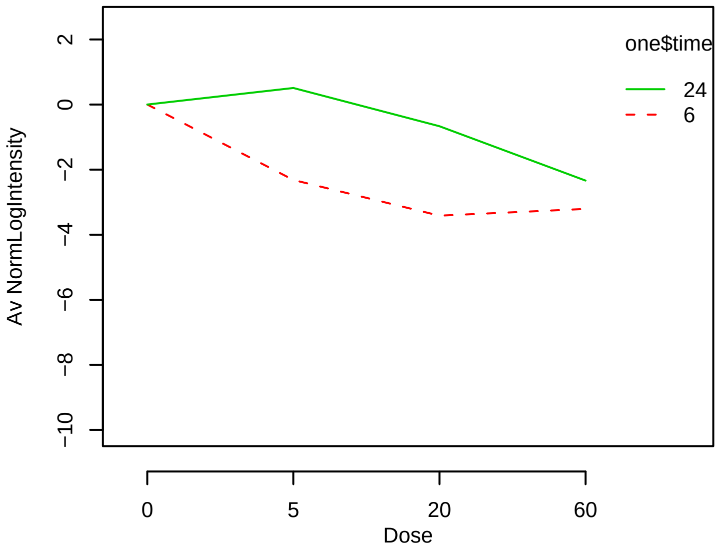
GO_0019377 : glycolipid catabolism



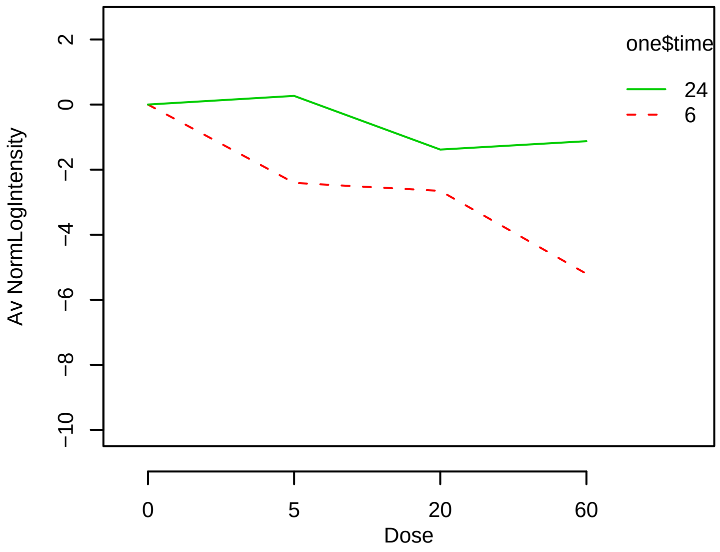
GO_0019395 : fatty acid oxidation

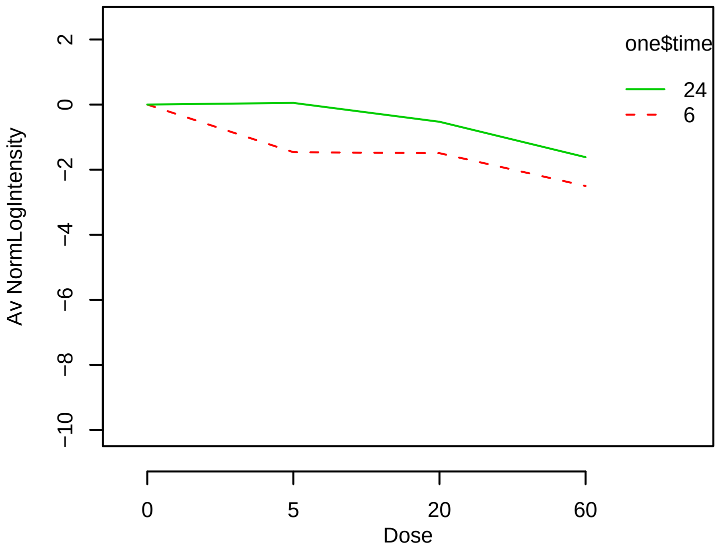


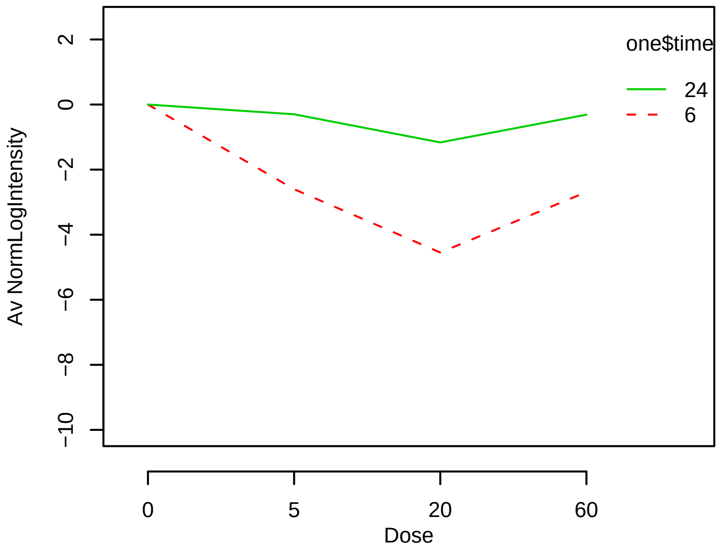
GO_0019438 : aromatic compound biosynthesis

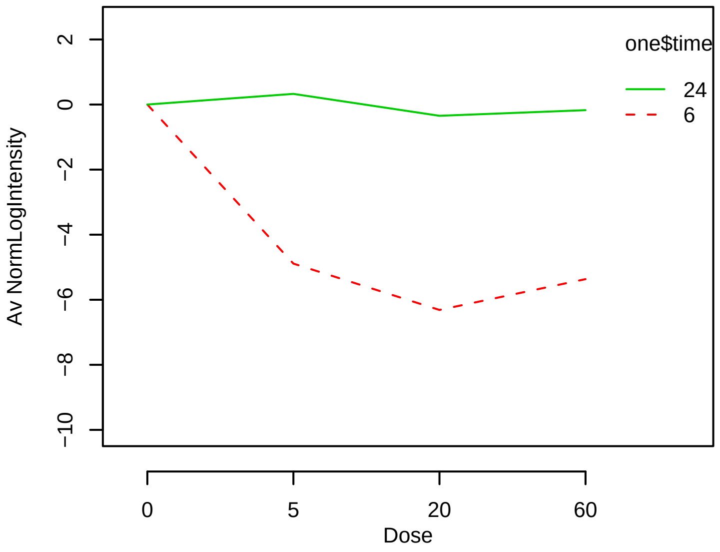


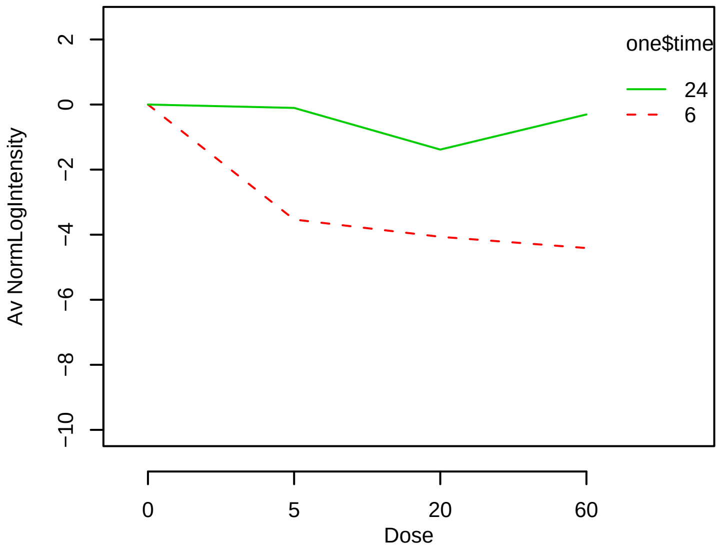
GO_0019439 : aromatic compound catabolism

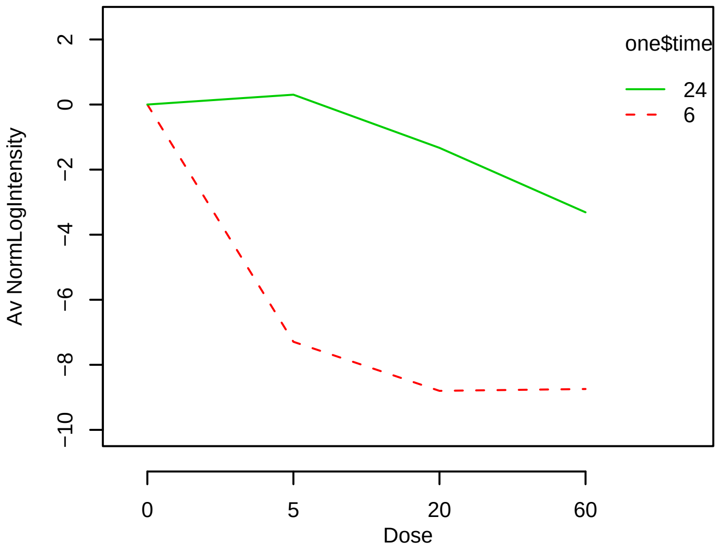

GO_0019627 : urea metabolism


GO_0019642 : anaerobic glycolysis

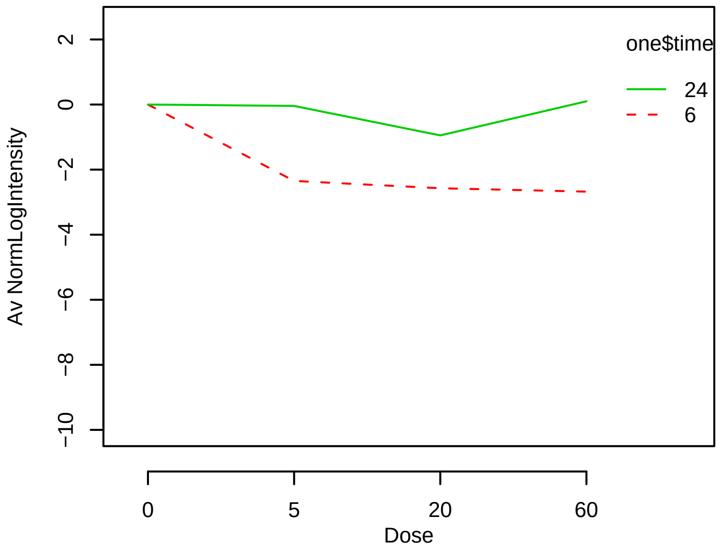

GO_0019674 : NAD metabolism


GO_0019720 : Mo−molybdopterin cofactor metabolism

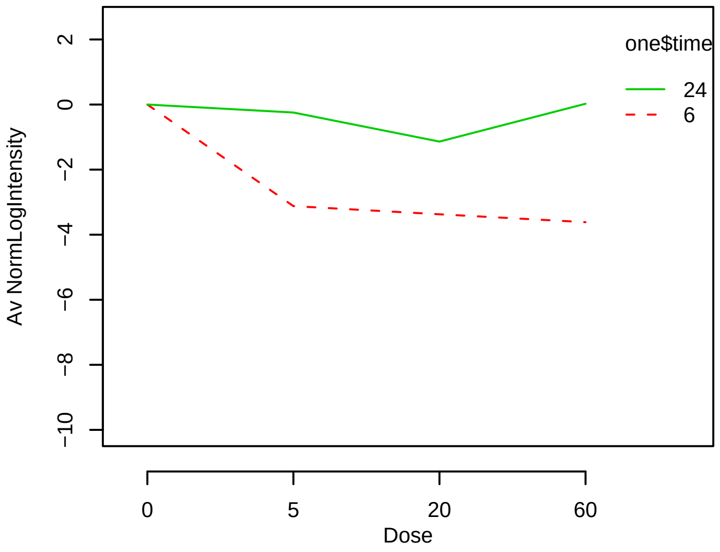

GO_0019722 : calcium−mediated signaling


GO_0019724 : B cell mediated immunity

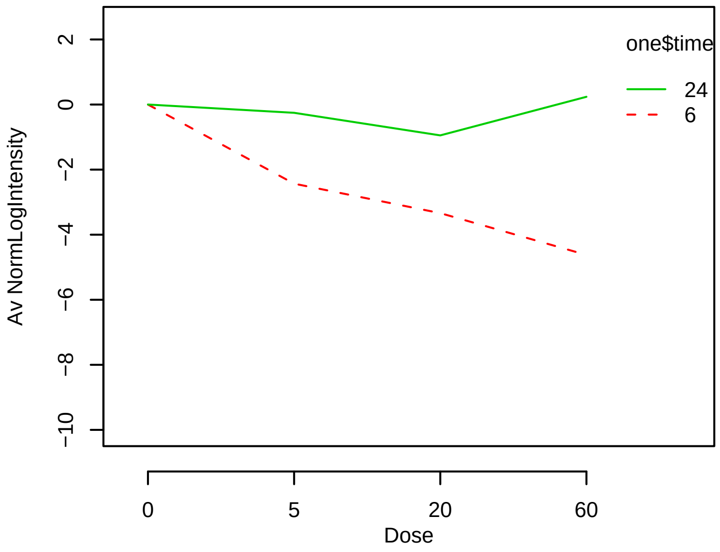
GO_0019725 : cell homeostasis



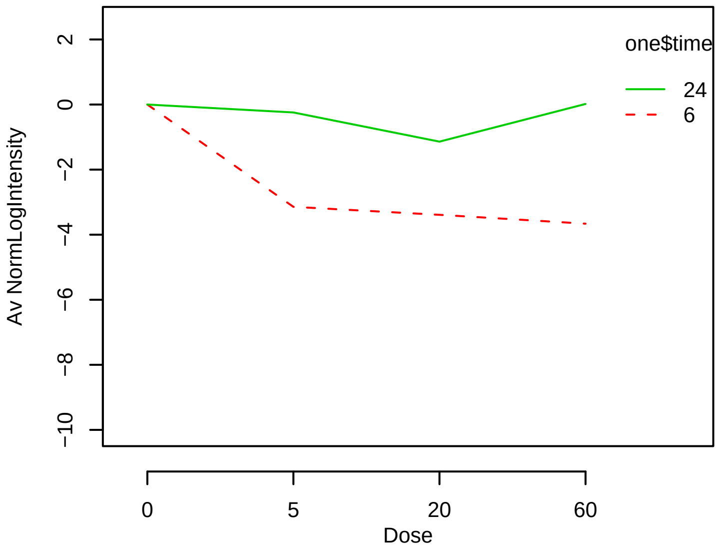
GO_0019730 : antimicrobial humoral response



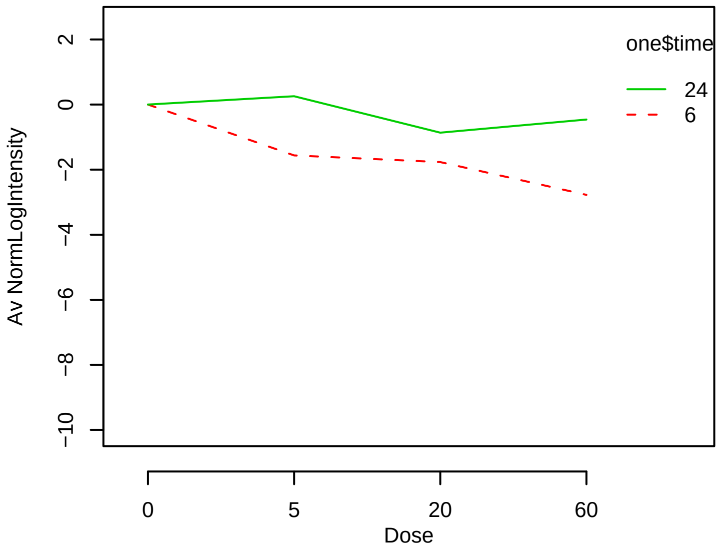
GO_0019731 : antibacterial humoral response



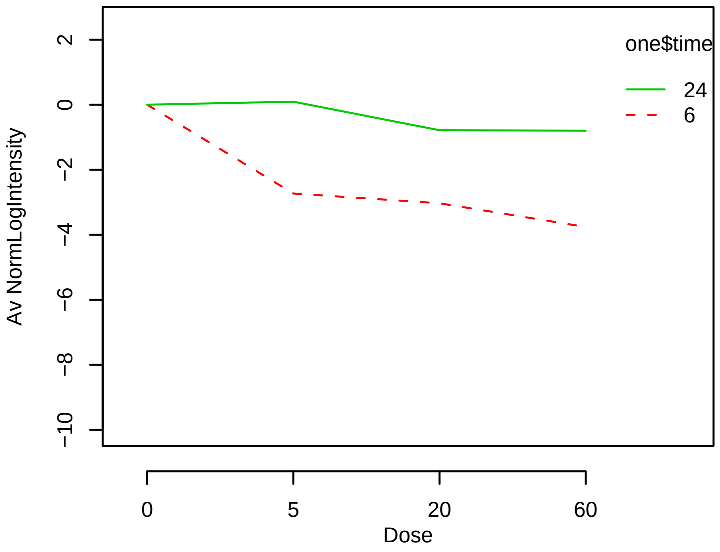
GO_0019735 : antimicrobial humoral response (sensu Verteb

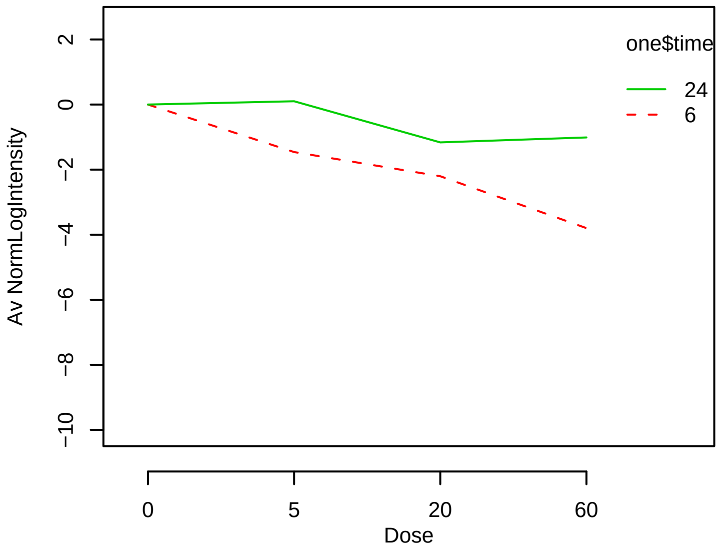


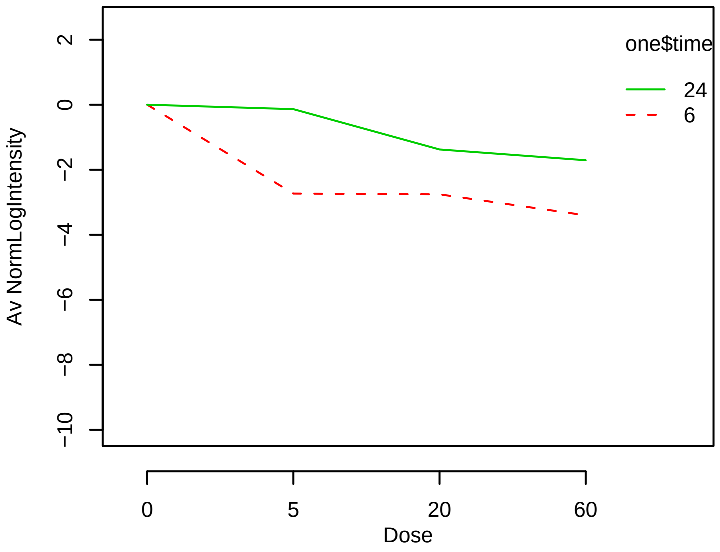
GO_0019748 : secondary metabolism

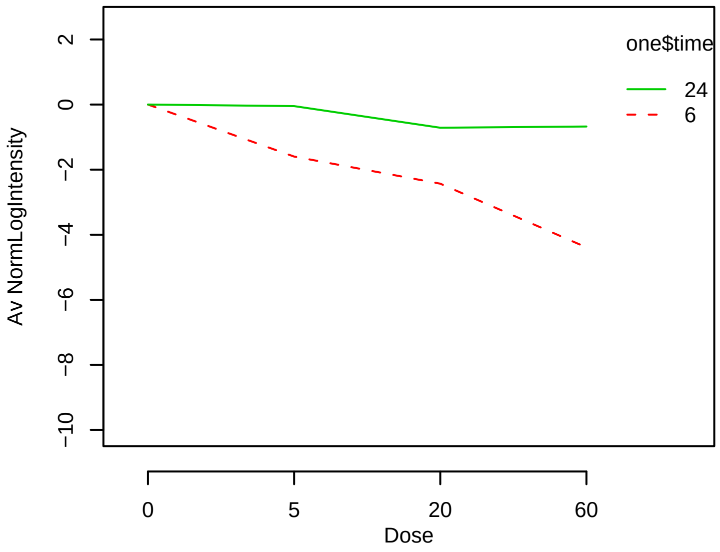


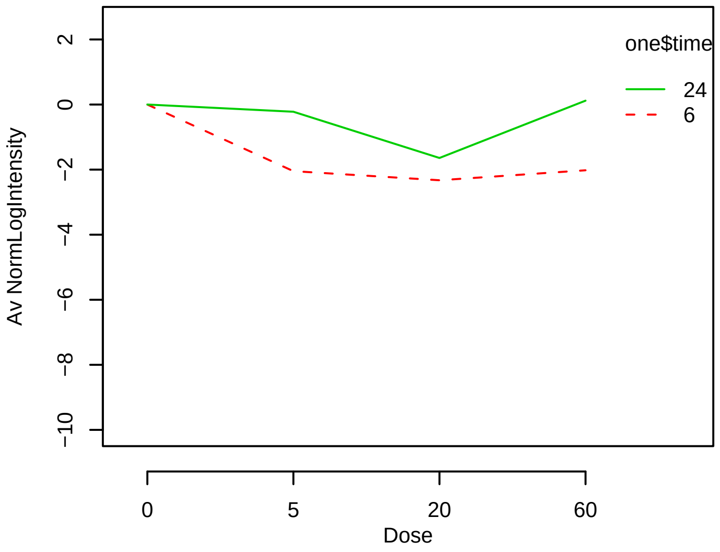
GO_0019751 : polyol metabolism

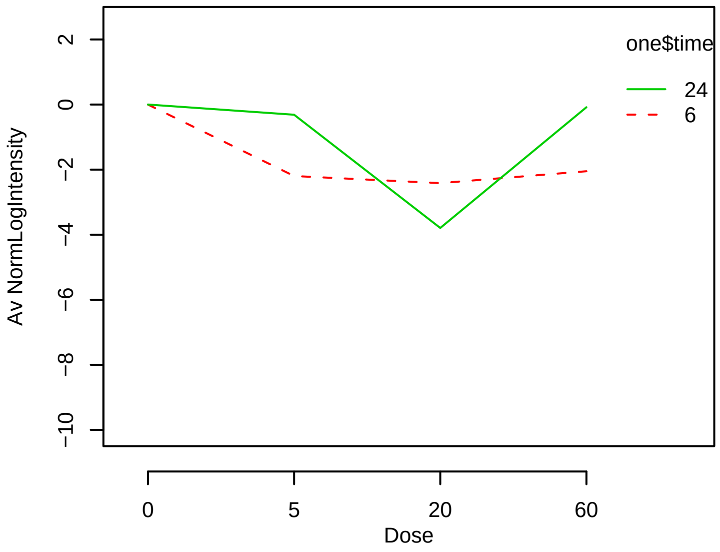


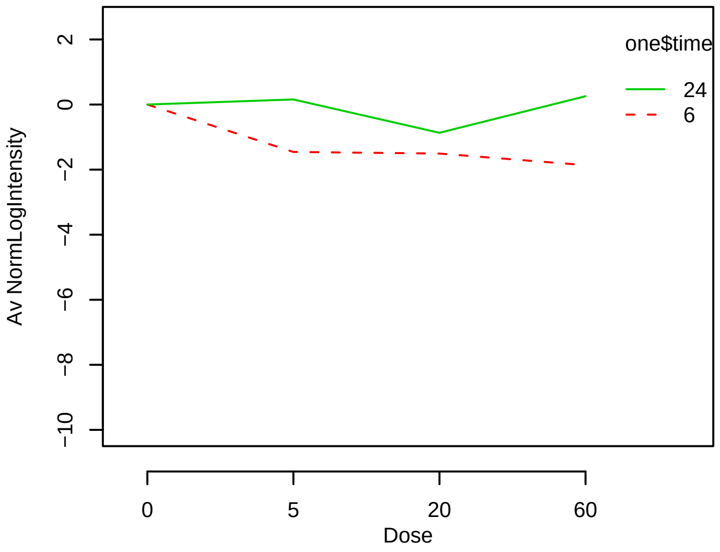

GO_0019827 : stem cell maintenance

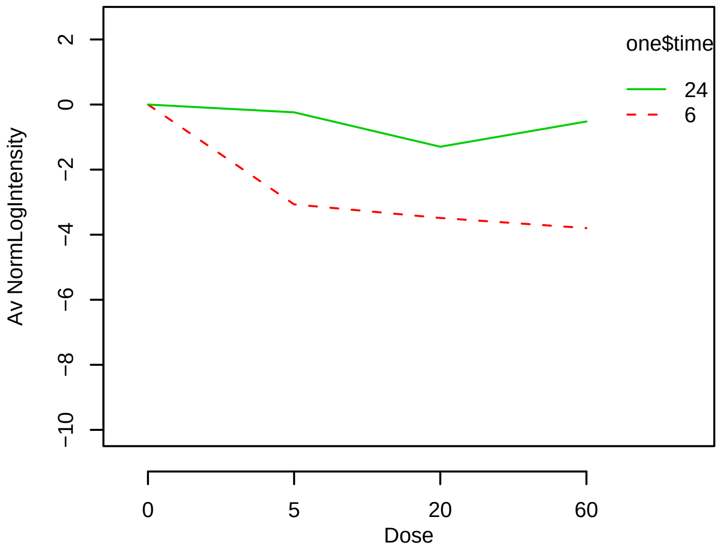

GO_0019835 : cytolysis


GO_0019856 : pyrimidine base biosynthesis

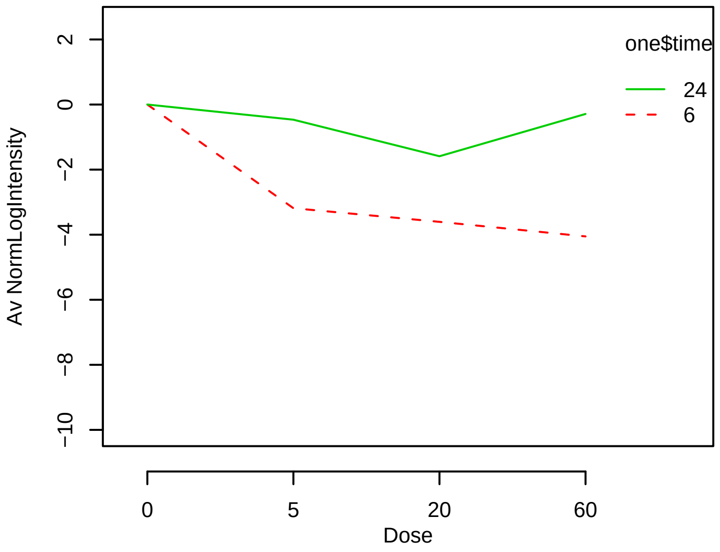

GO_0019882 : antigen processing and presentation


O_0019884 : antigen processing and presentation of exogen

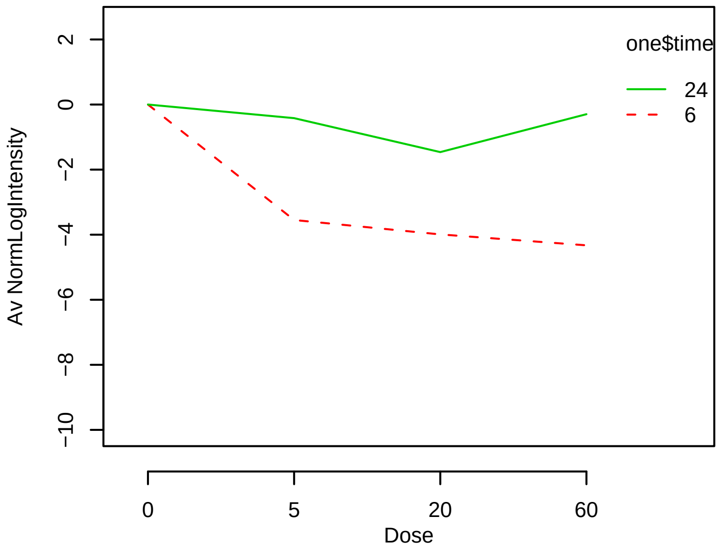

GO_0019915 : sequestering of lipid



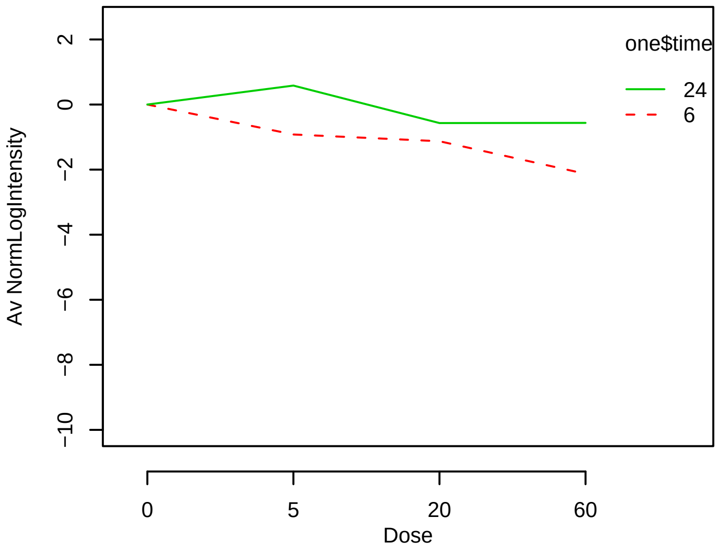
GO_0019932 : second−messenger−mediated signaling



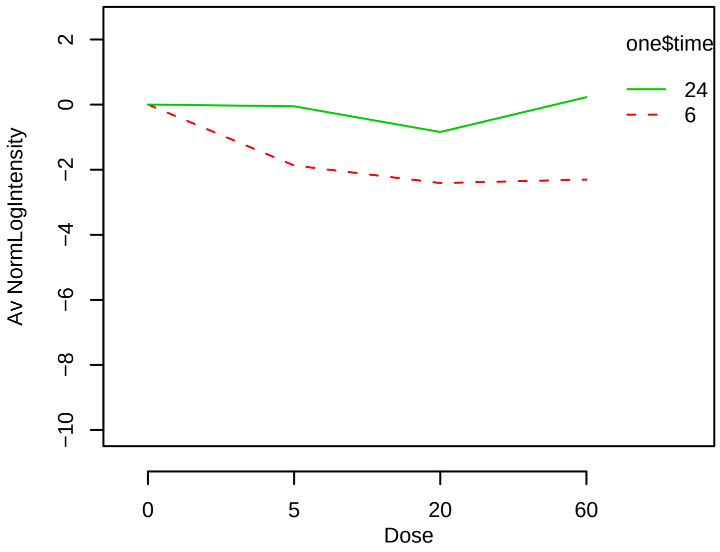
GO_0019933 : cAMP−mediated signaling



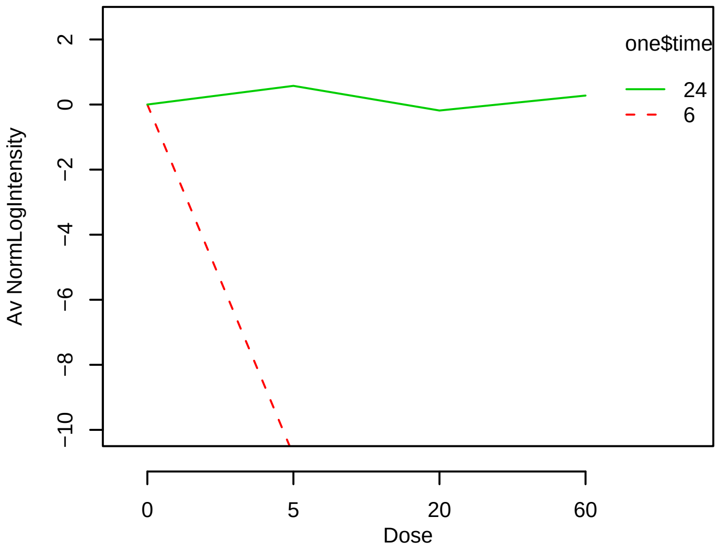
GO_0019935 : cyclic−nucleotide−mediated signaling



GO_0019941 : modification−dependent protein catabolisn

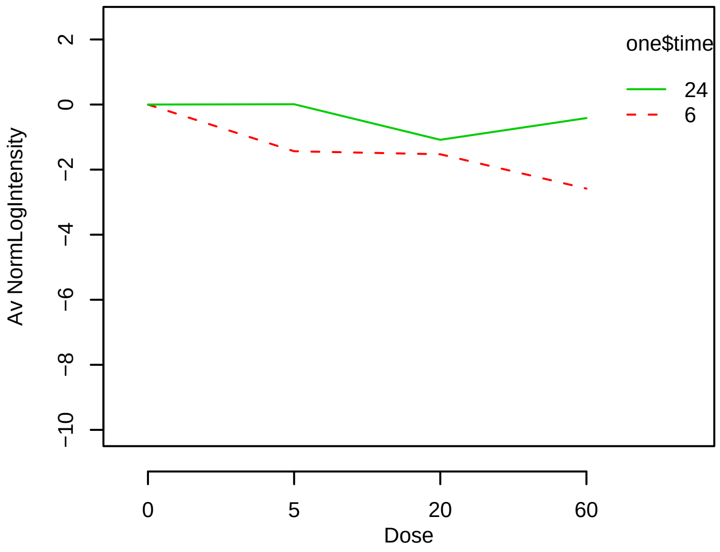


GO_0020027 : hemoglobin metabolism

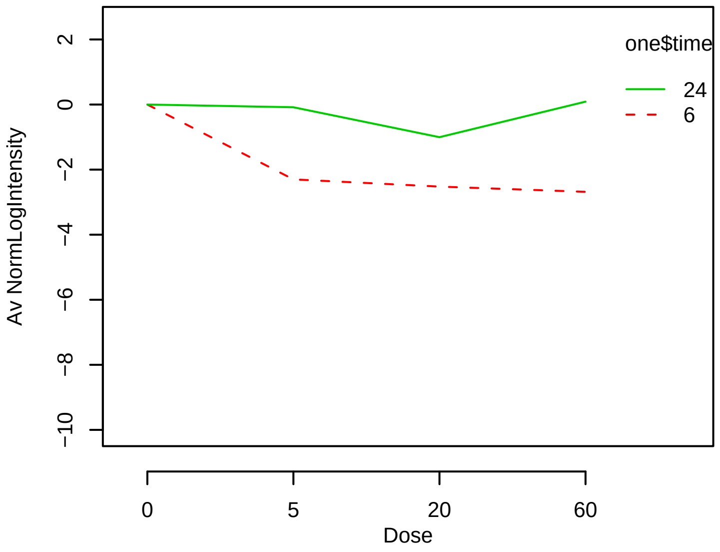


GO_0021782 : glial cell development

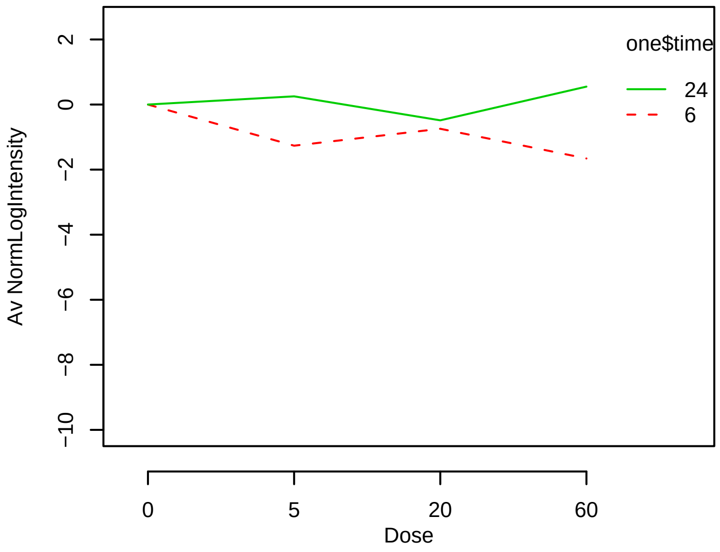
GO_0021915 : neural tube development



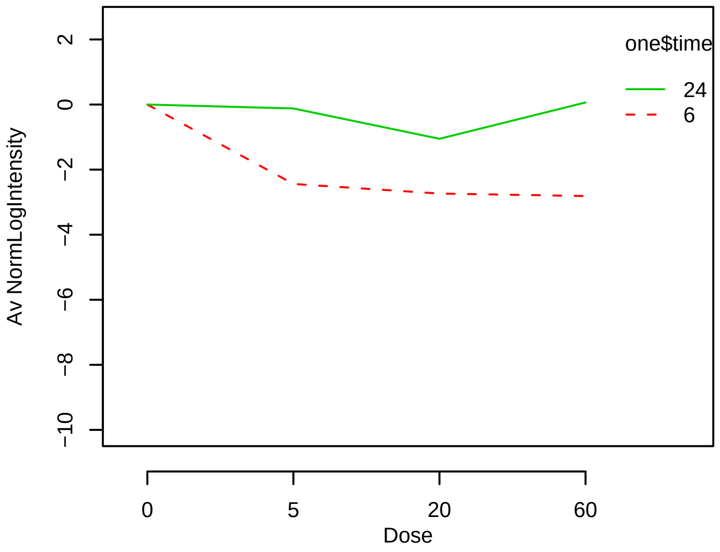
GO_0030003 : cation homeostasis



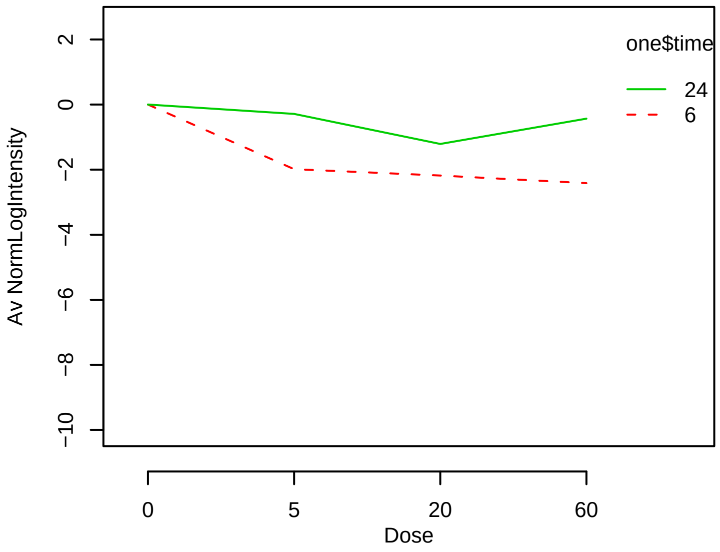
GO_0030004 : monovalent inorganic cation homeostasis



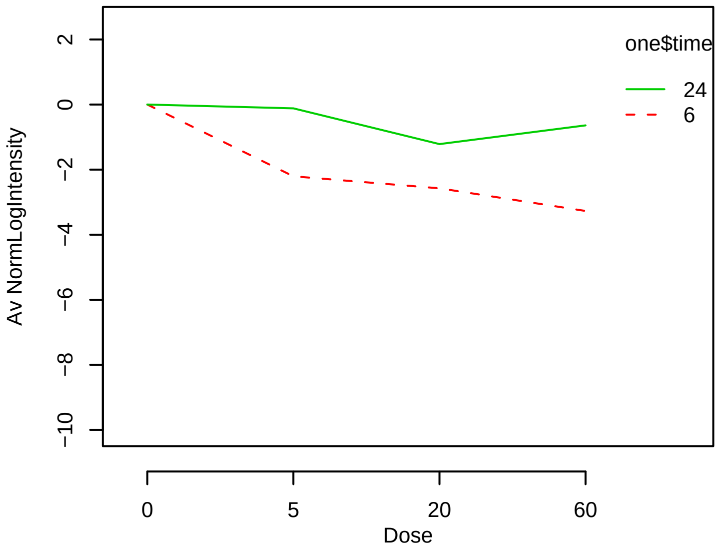
GO_0030005 : di−\, tri−valent inorganic cation homeostasi



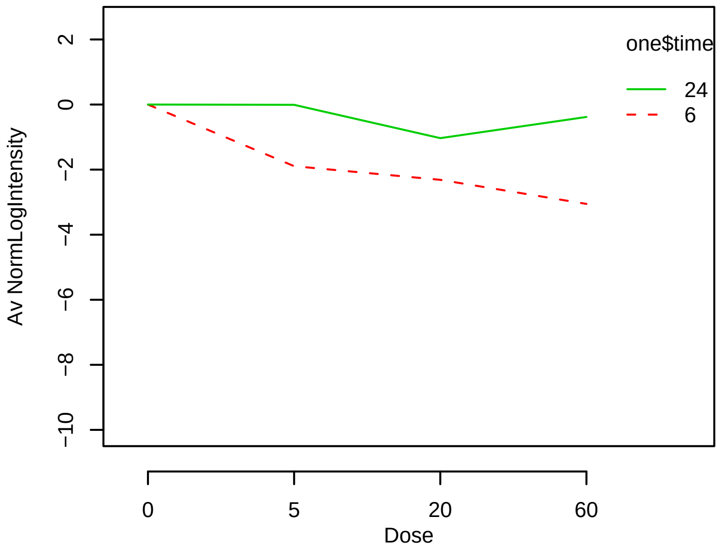
GO_0030010 : establishment of cell polarity



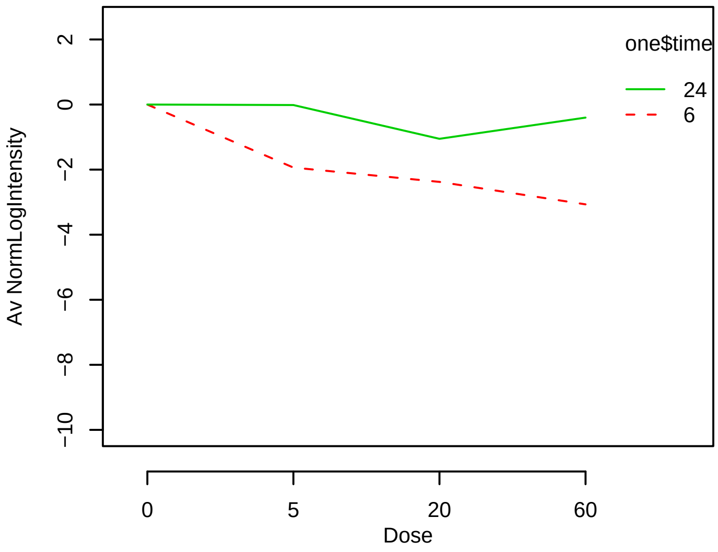
GO_0030029 : actin filament−based process



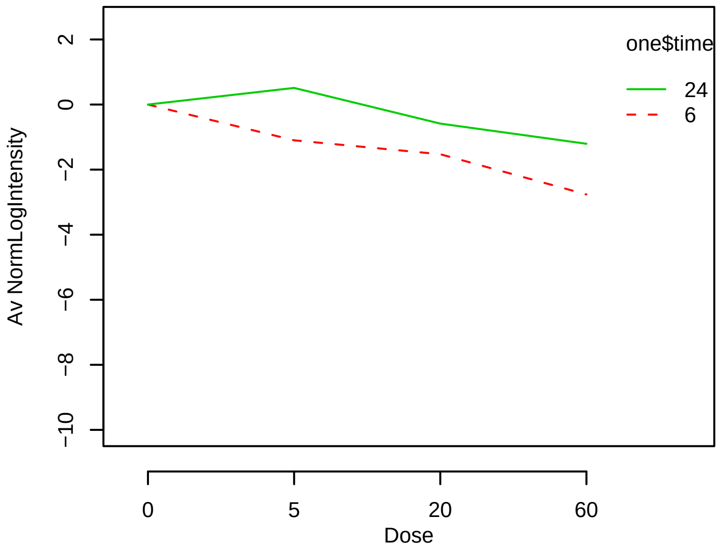
GO_0030030 : cell projection organization and biogenesi



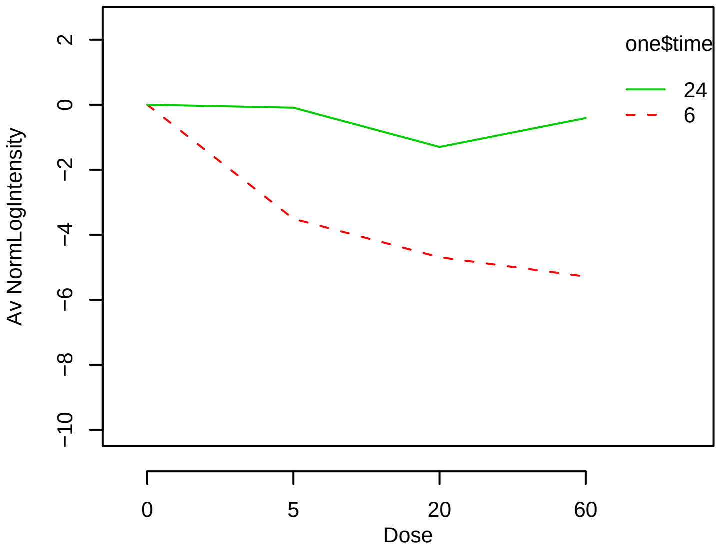
GO_0030031 : cell projection biogenesis



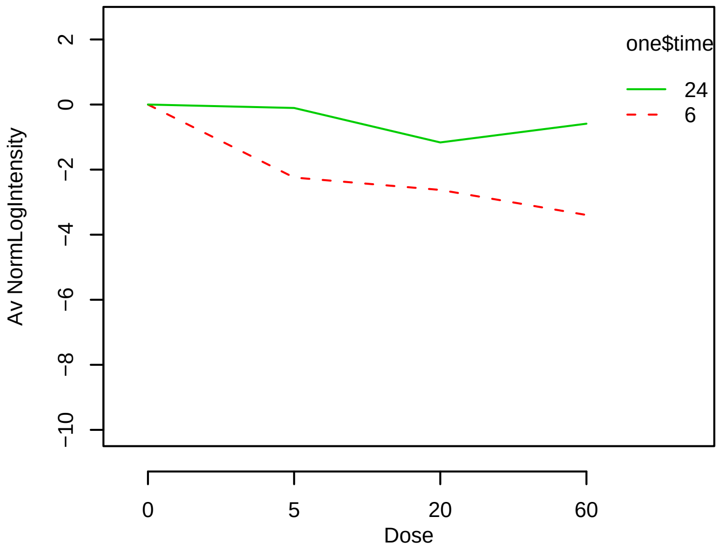
GO_0030032 : lamellipodium biogenesis



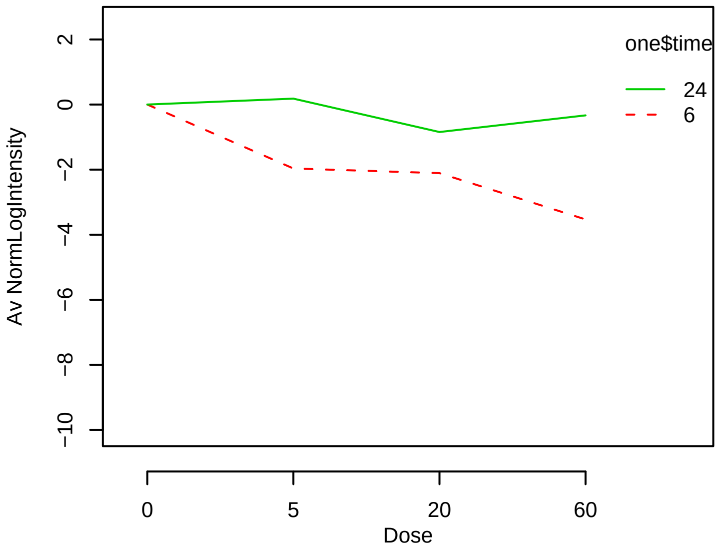
GO_0030035 : microspike biogenesis

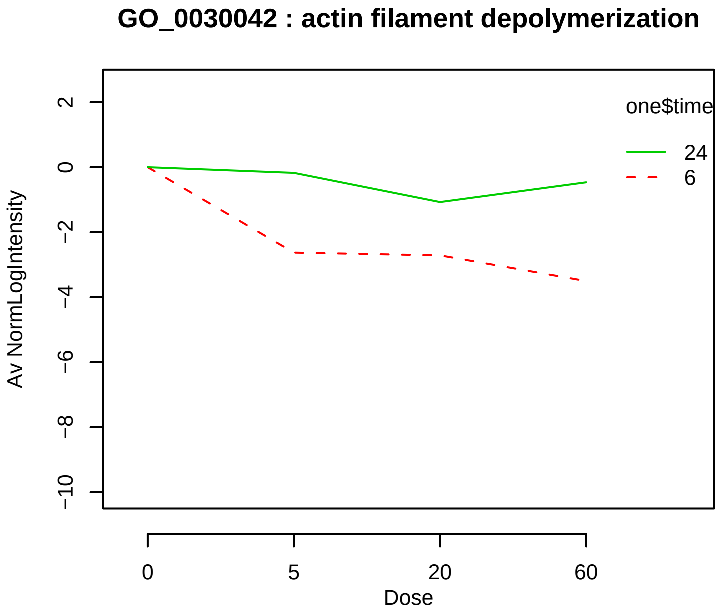


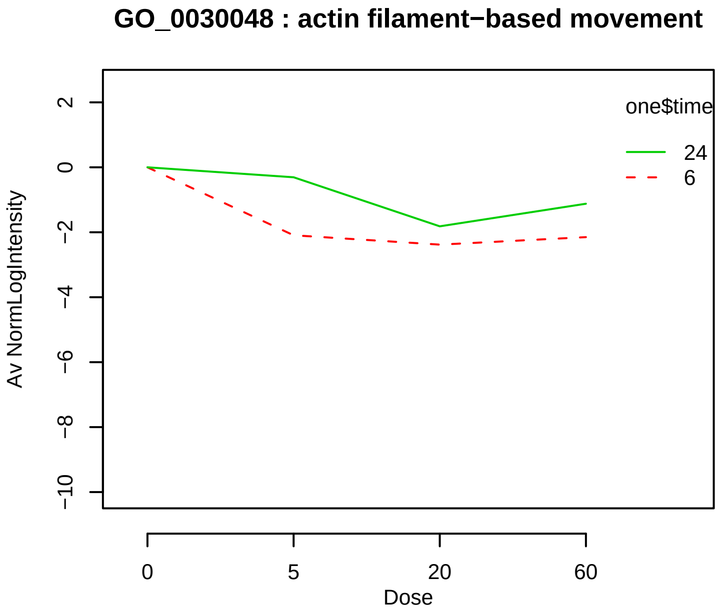
GO_0030036 : actin cytoskeleton organization and biogenes

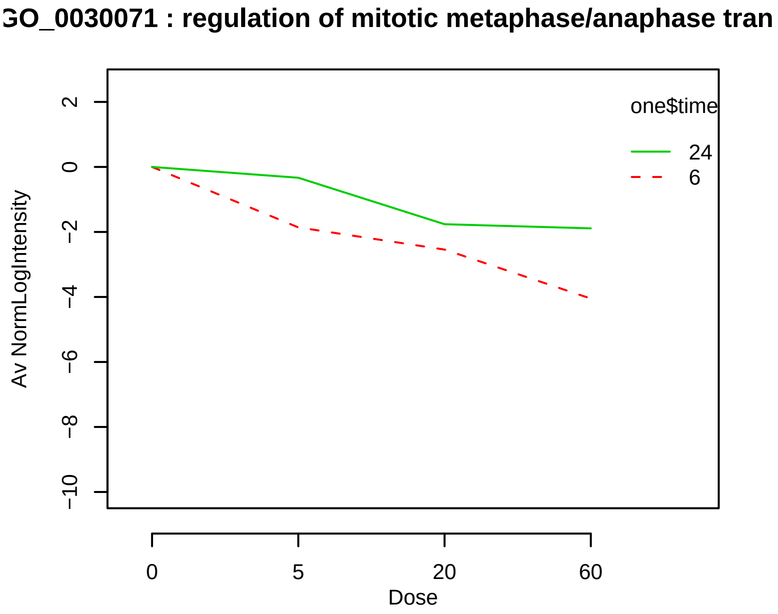


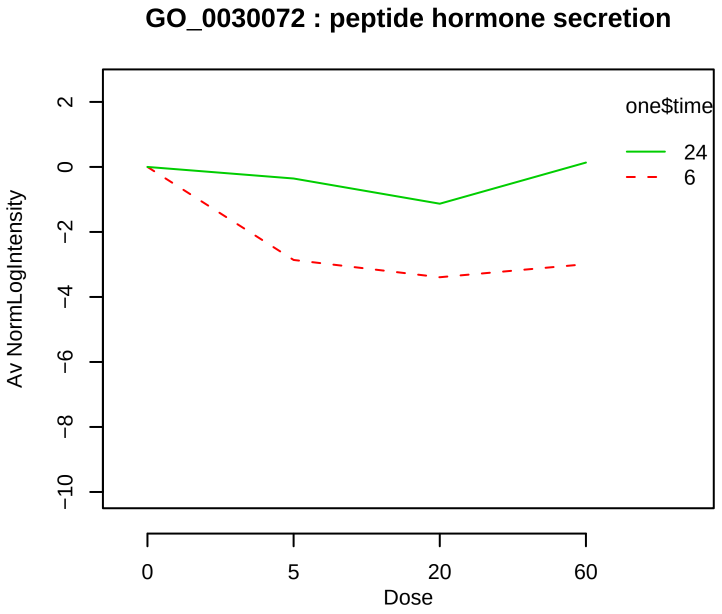
GO_0030041 : actin filament polymerization

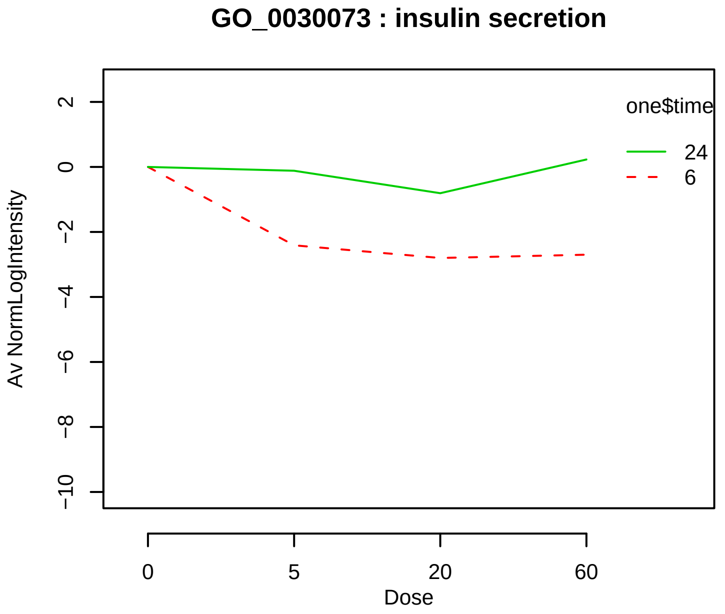


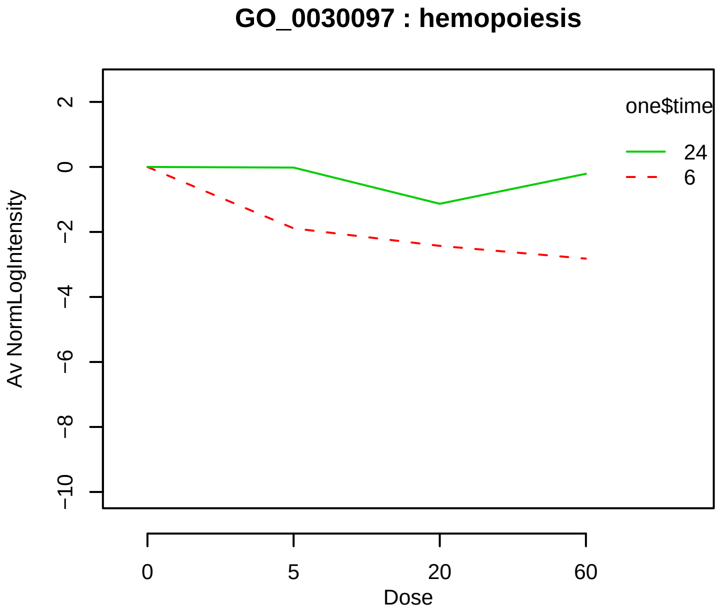

GO_0030042 : actin filament depolymerization

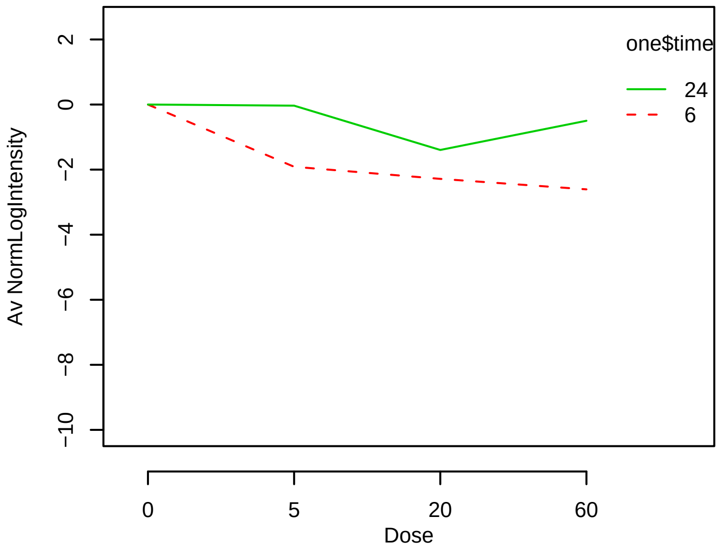

GO_0030048 : actin filament−based movement

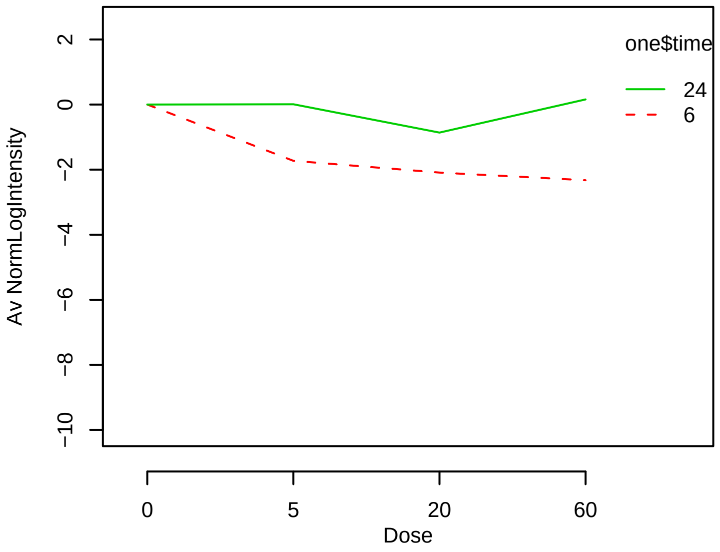

GO_0030071 : regulation of mitotic metaphase/anaphase tran

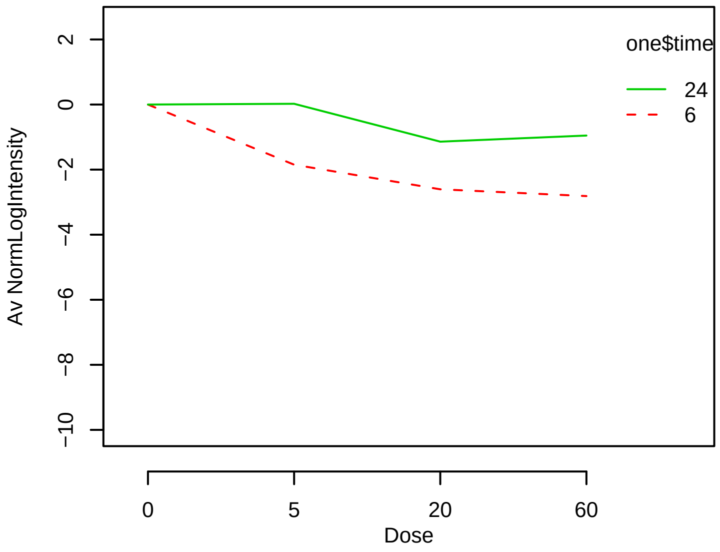

GO_0030072 : peptide hormone secretion

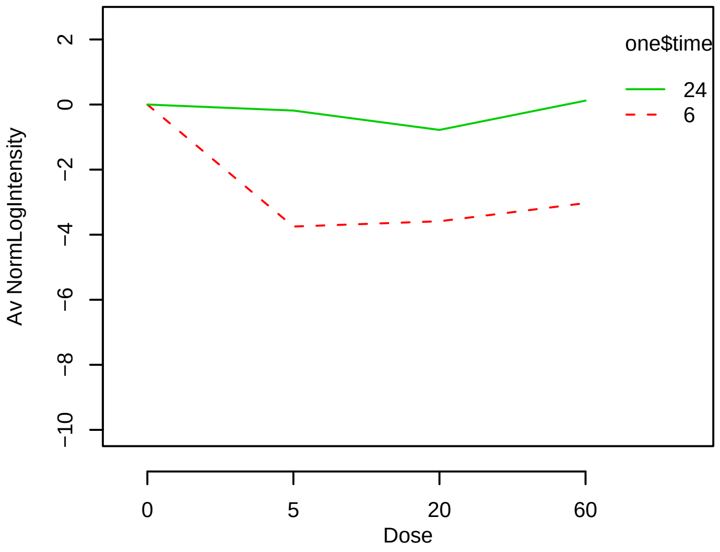

GO_0030073 : insulin secretion

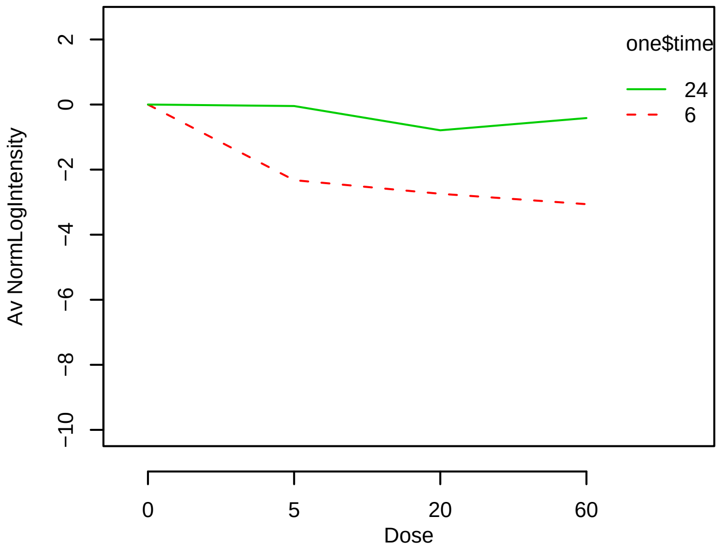

GO_0030097 : hemopoiesis

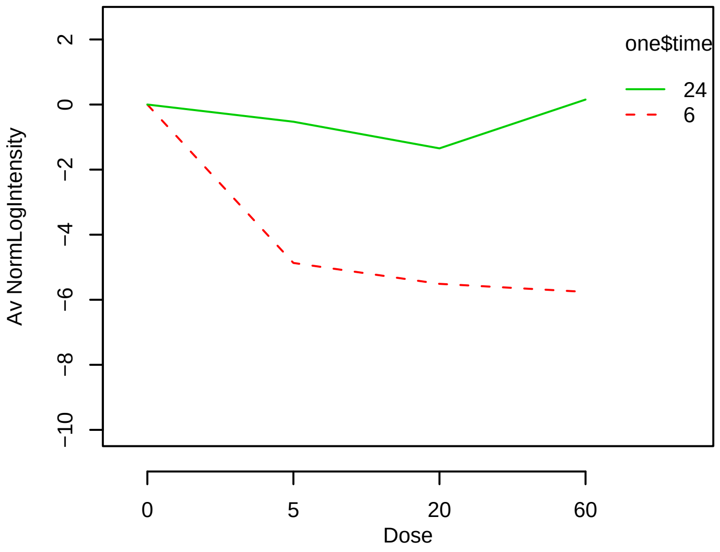

GO_0030098 : lymphocyte differentiation

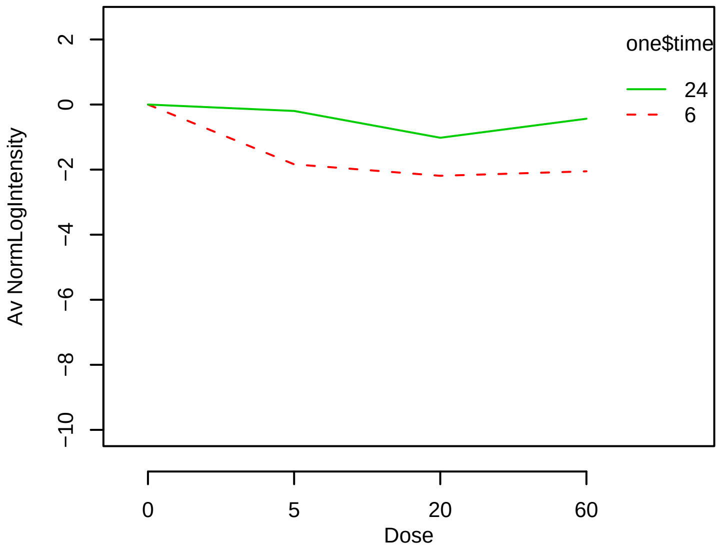

GO_0030099 : myeloid cell differentiation

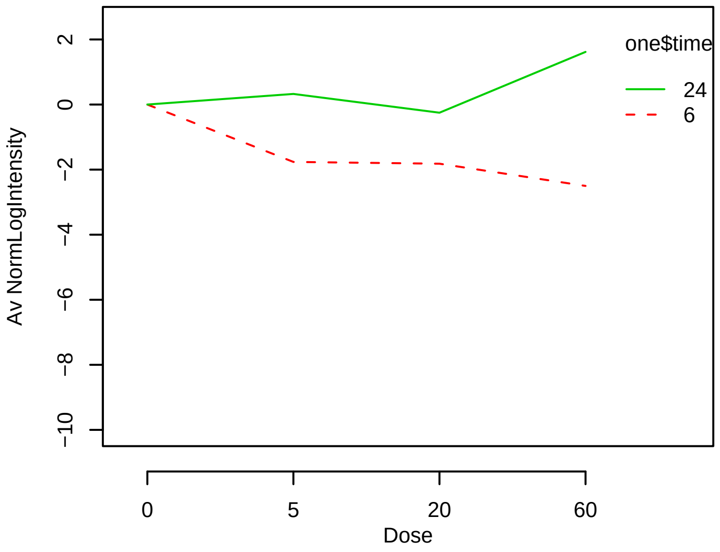

GO_0030100 : regulation of endocytosis

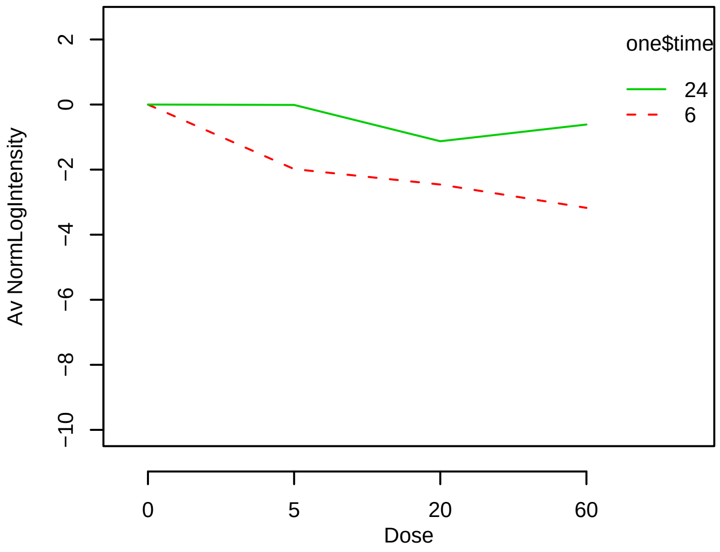

GO_0030101 : natural killer cell activation

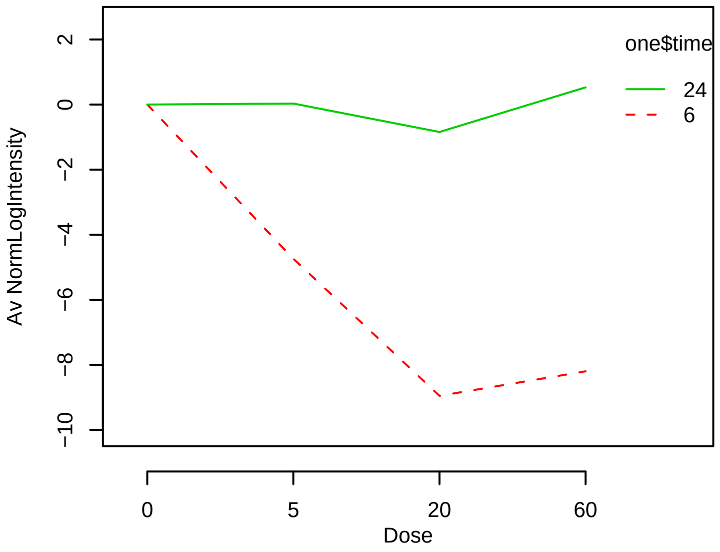

GO_0030111 : regulation of Wnt receptor signaling pathwa

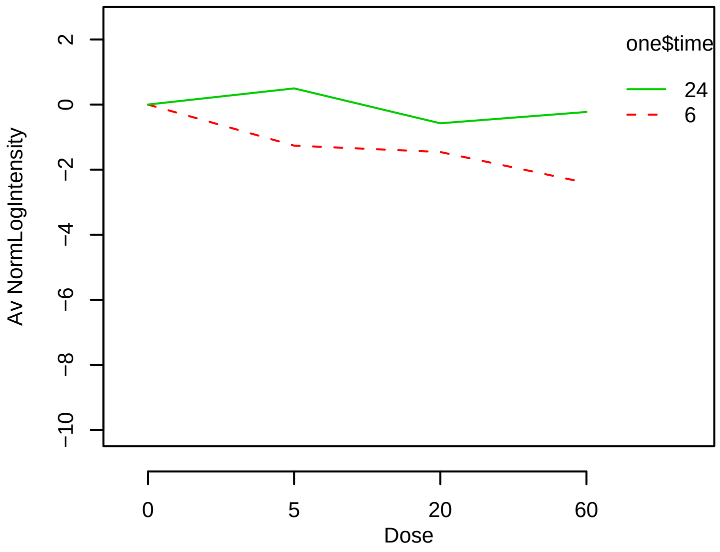

GO_0030146 : diuresis

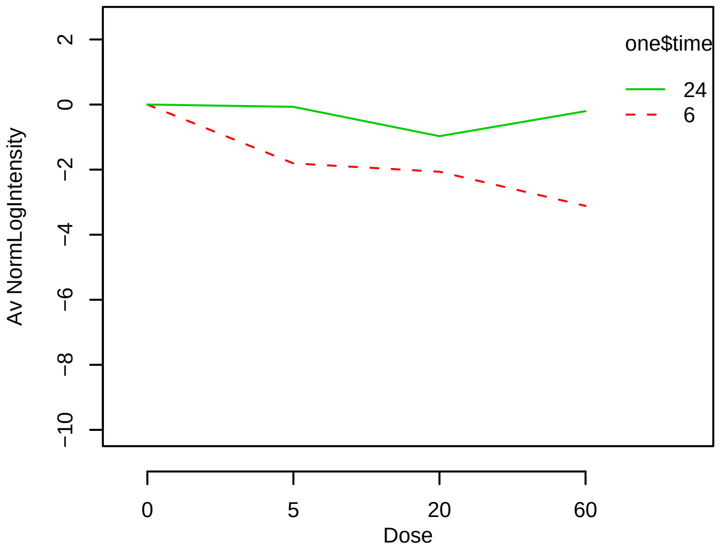

GO_0030148 : sphingolipid biosynthesis


GO_0030149 : sphingolipid catabolism

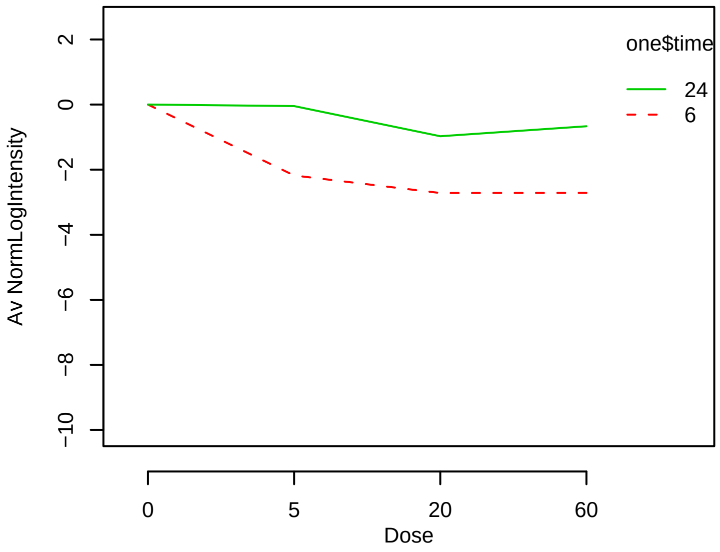

GO_0030155 : regulation of cell adhesion


GO_0030162 : regulation of proteolysis

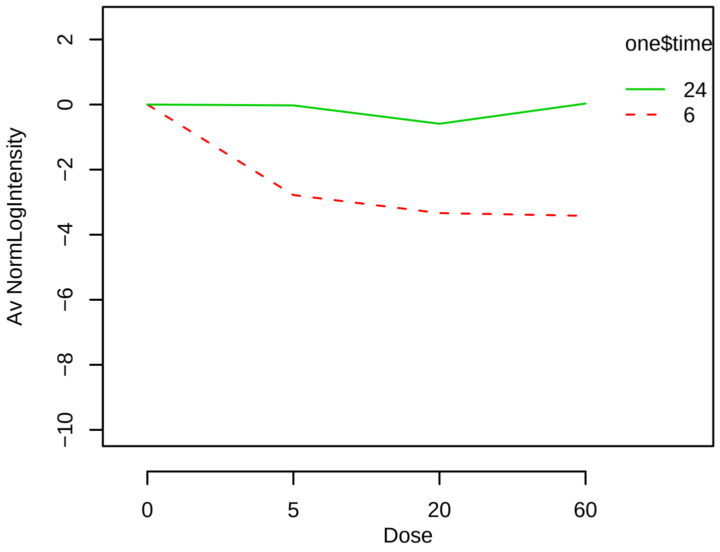

GO_0030163 : protein catabolism


GO_0030166 : proteoglycan biosynthesis

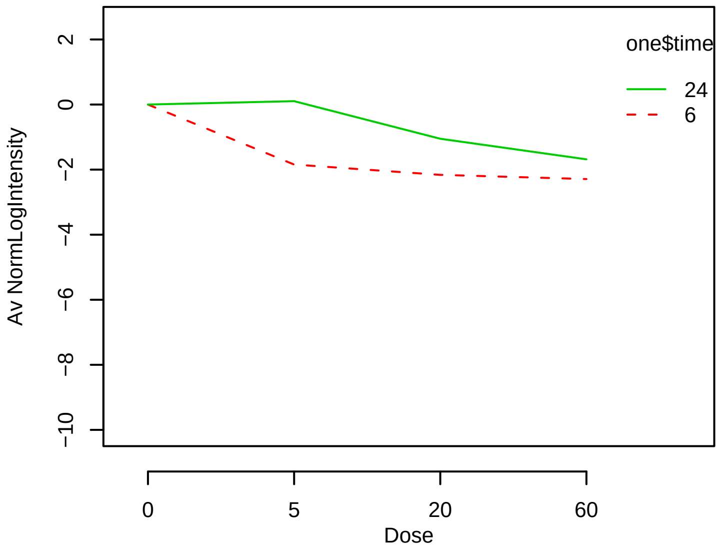
GO_0030168 : platelet activation



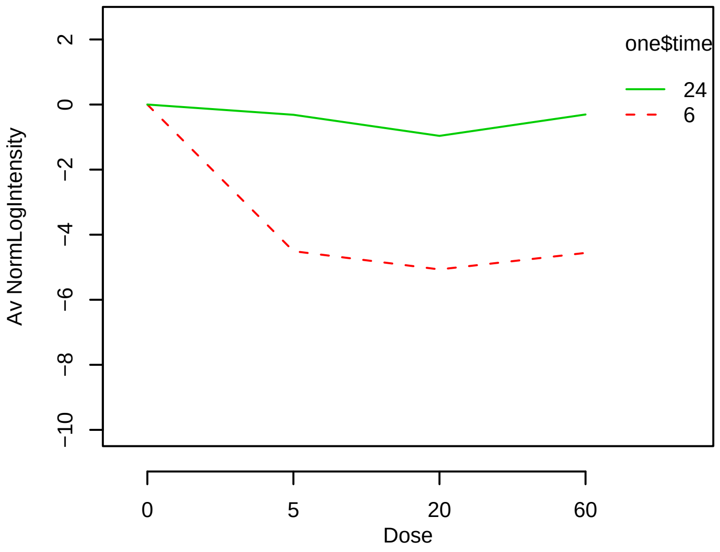
GO_0030178 : negative regulation of Wnt receptor signaling



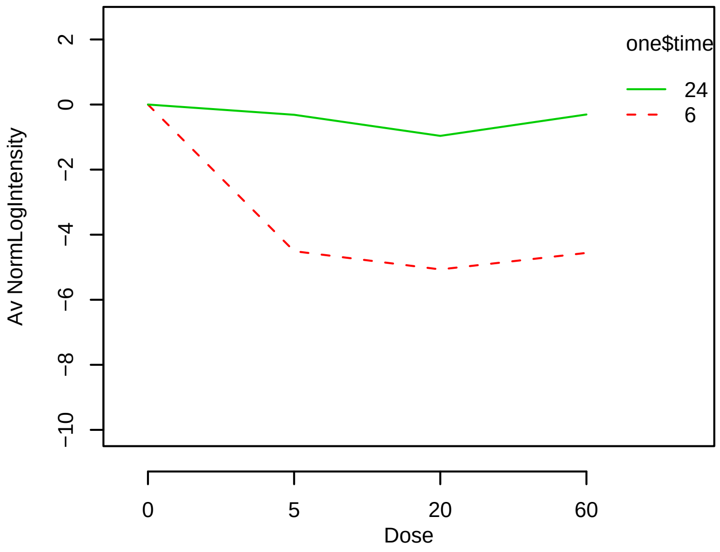
GO_0030183 : B cell differentiation



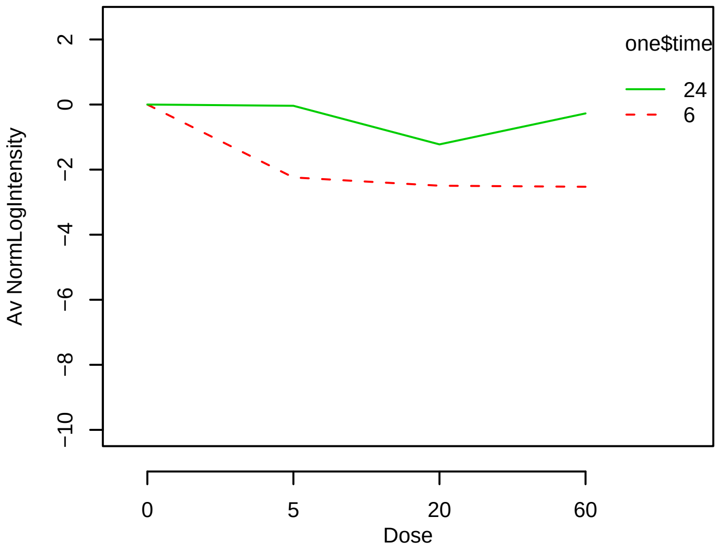
GO_0030193 : regulation of blood coagulation

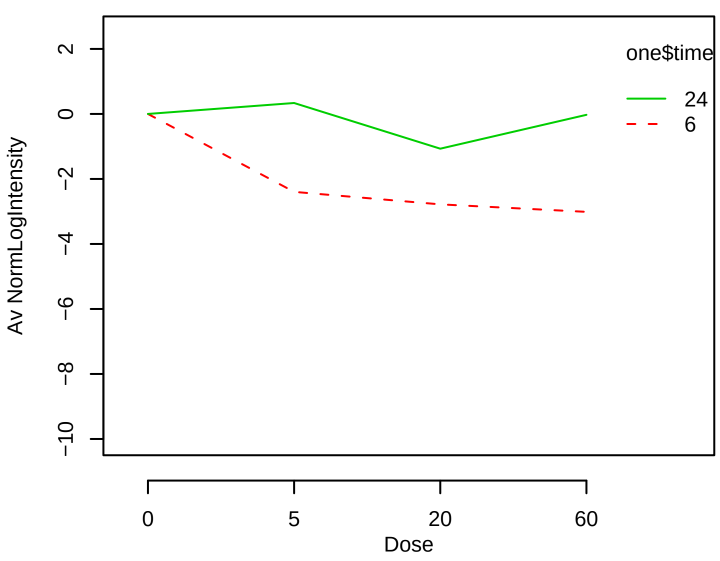


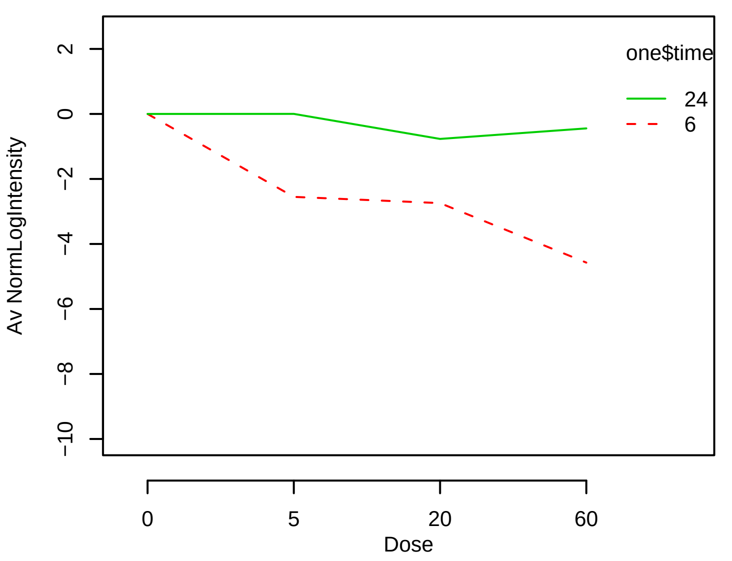
GO_0030195 : negative regulation of blood coagulation

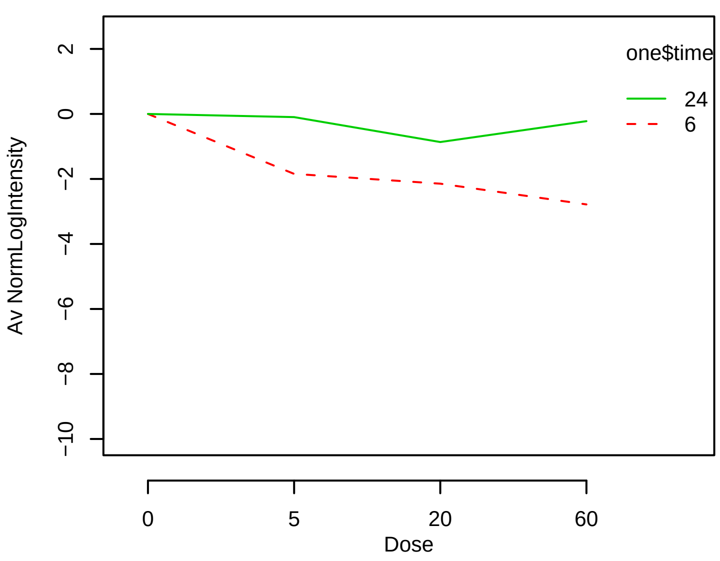


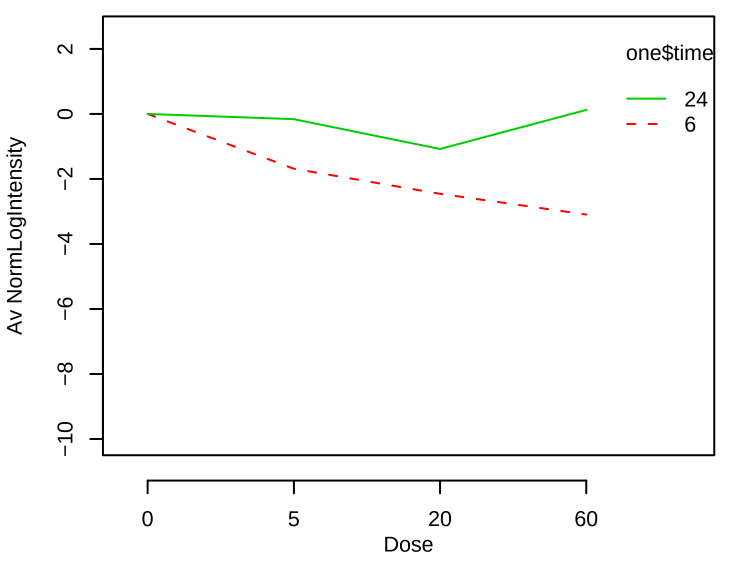
GO_0030198 : extracellular matrix organization and biogene

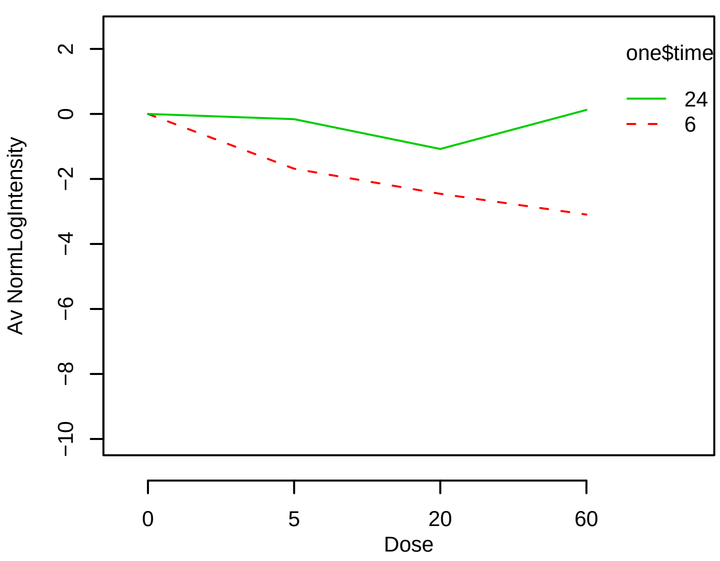


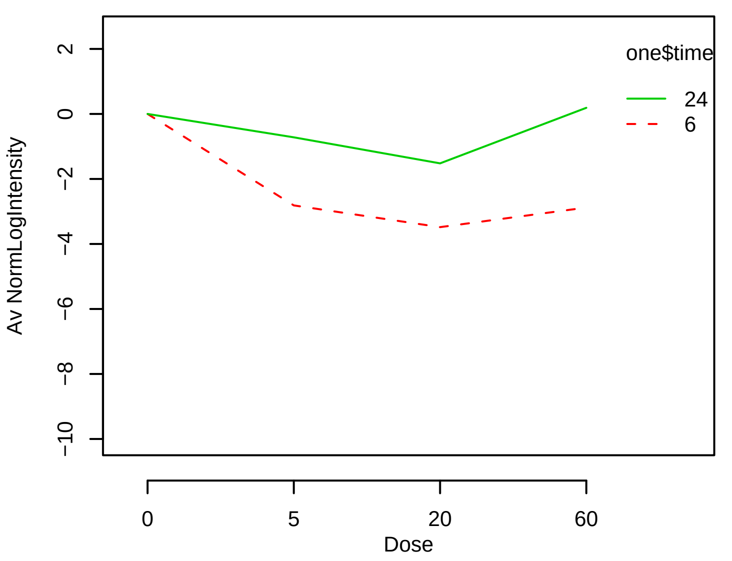

GO_0030199 : collagen fibril organization

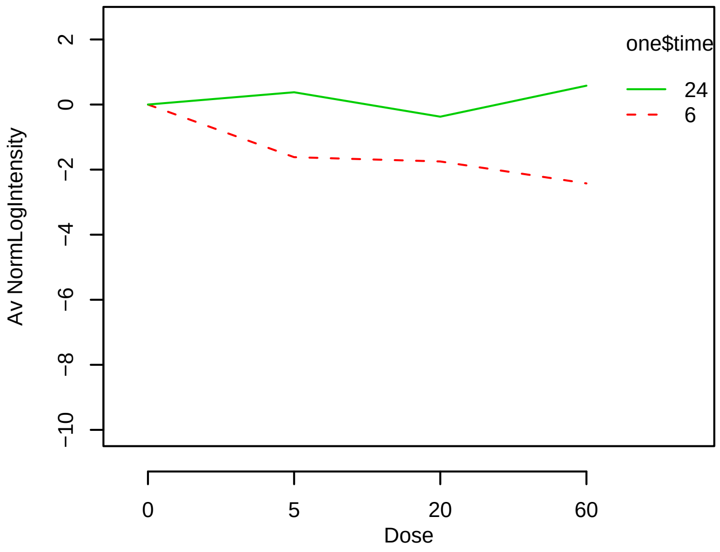

GO_0030201 : heparan sulfate proteoglycan metabolism

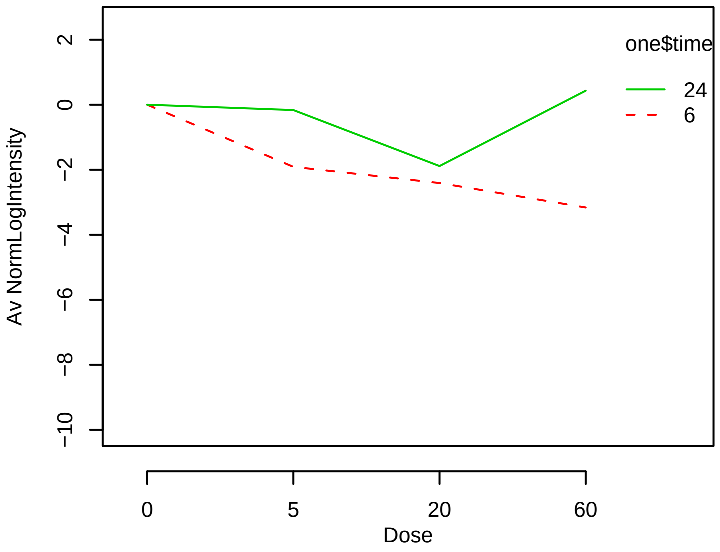

GO_0030203 : glycosaminoglycan metabolism

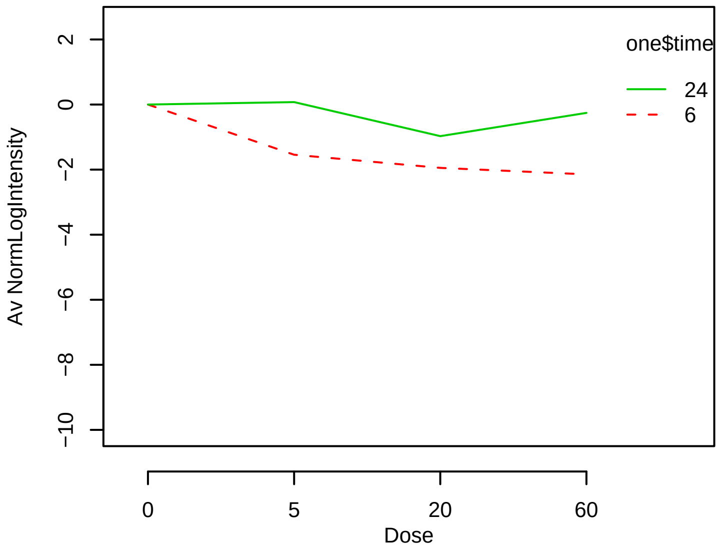

GO_0030204 : chondroitin sulfate metabolism

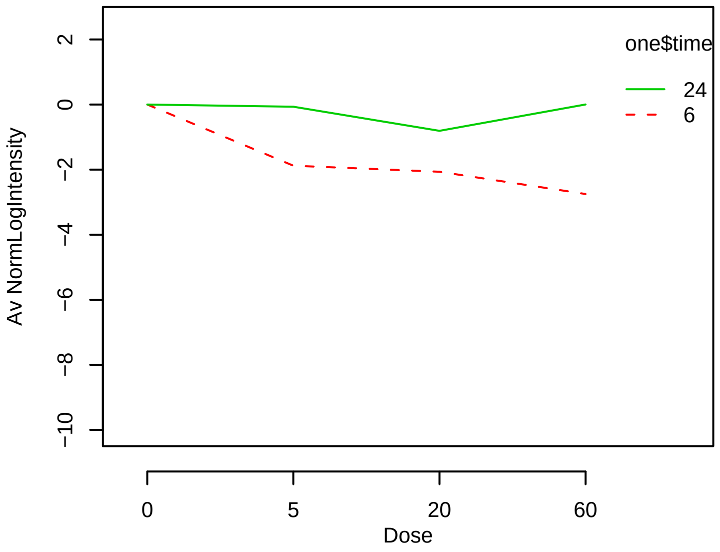

GO_0030206 : chondroitin sulfate biosynthesis

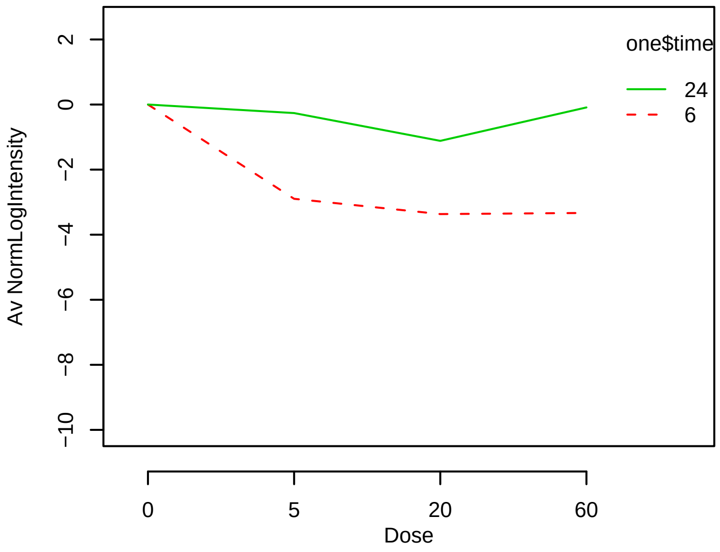

GO_0030212 : hyaluronan metabolism

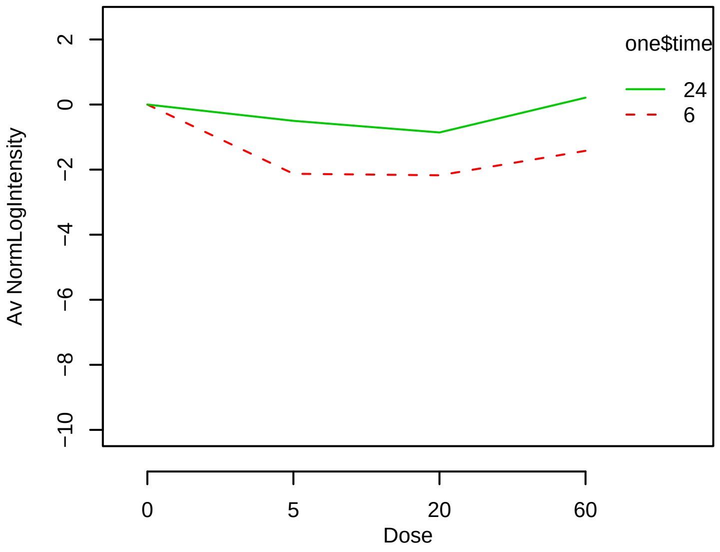

GO_0030216 : keratinocyte differentiation

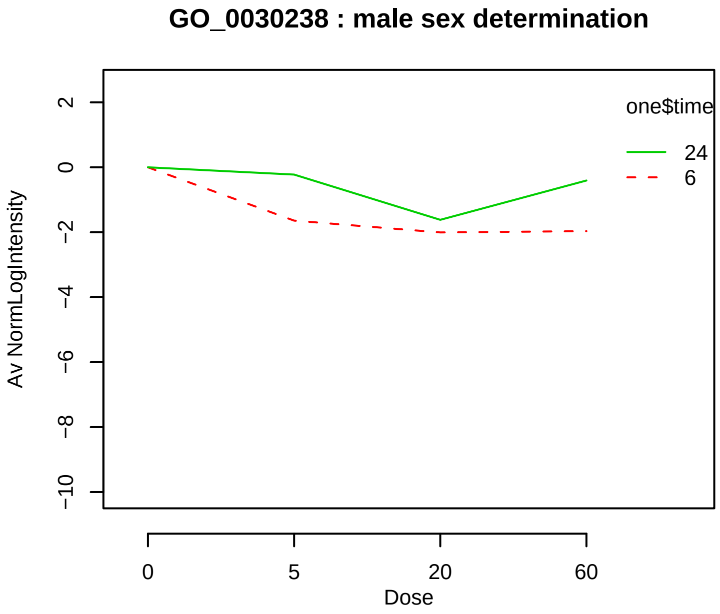

GO_0030217 : T cell differentiation

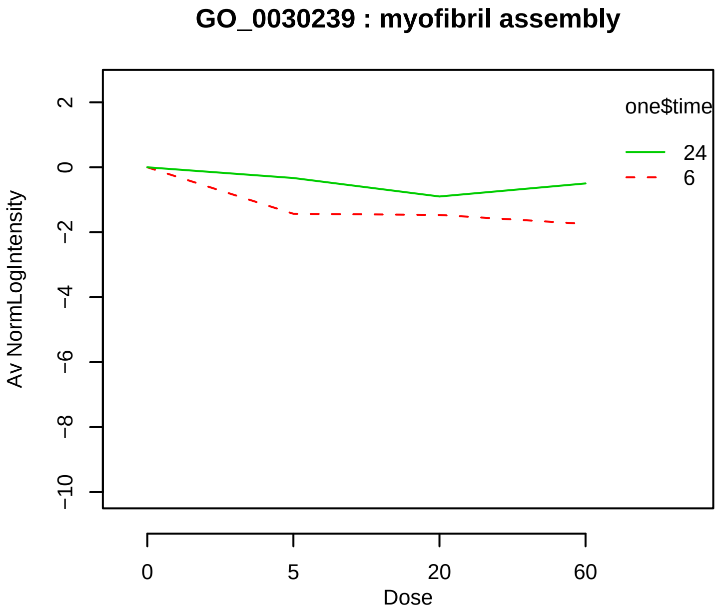

GO_0030218 : erythrocyte differentiation

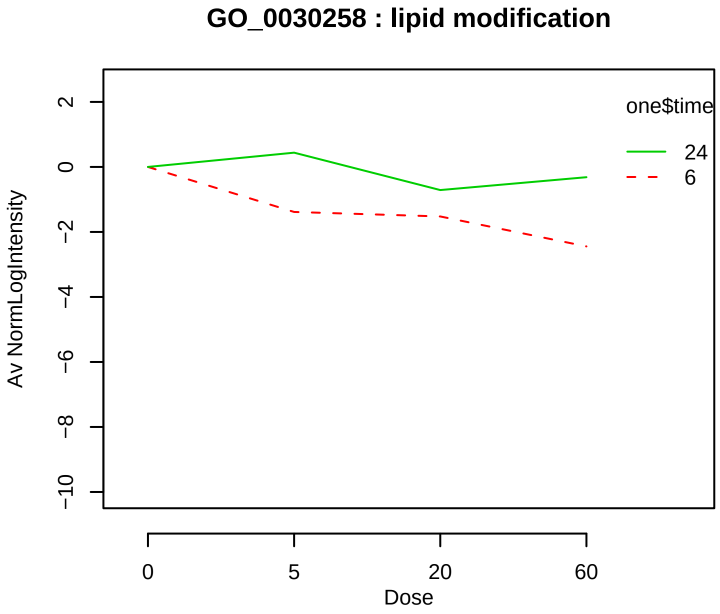

GO_0030224 : monocyte differentiation

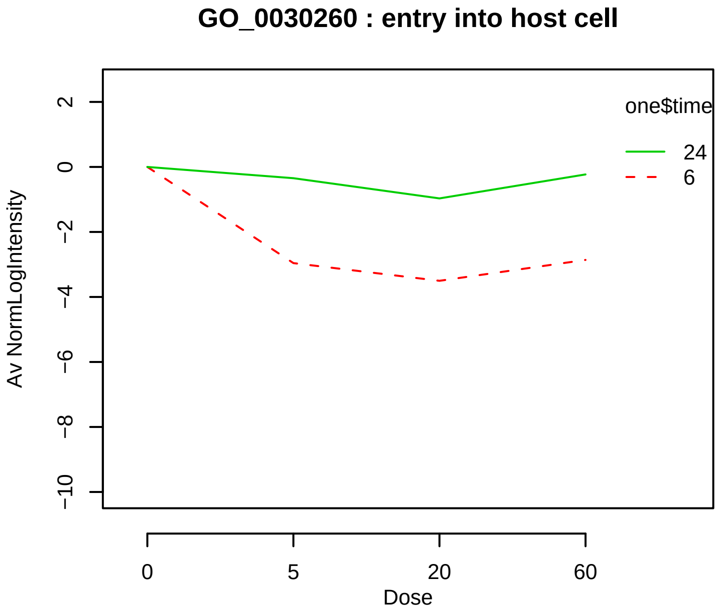

GO_0030225 : macrophage differentiation

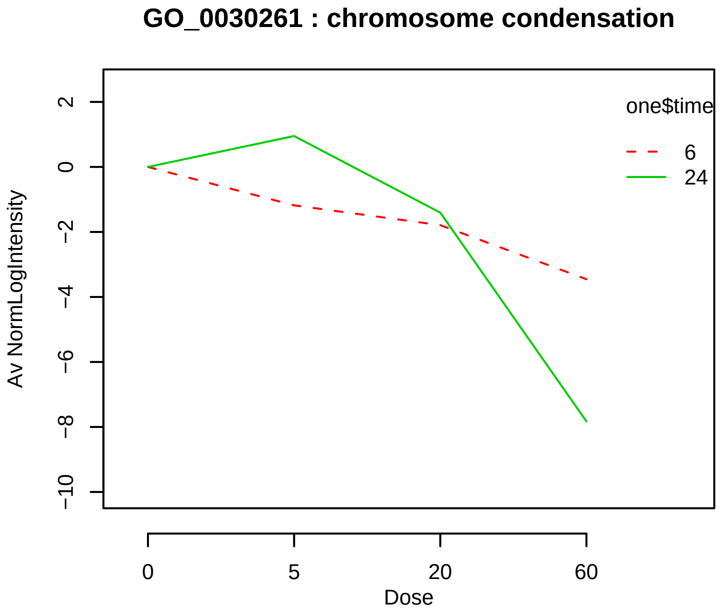

GO_0030236 : anti−inflammatory response

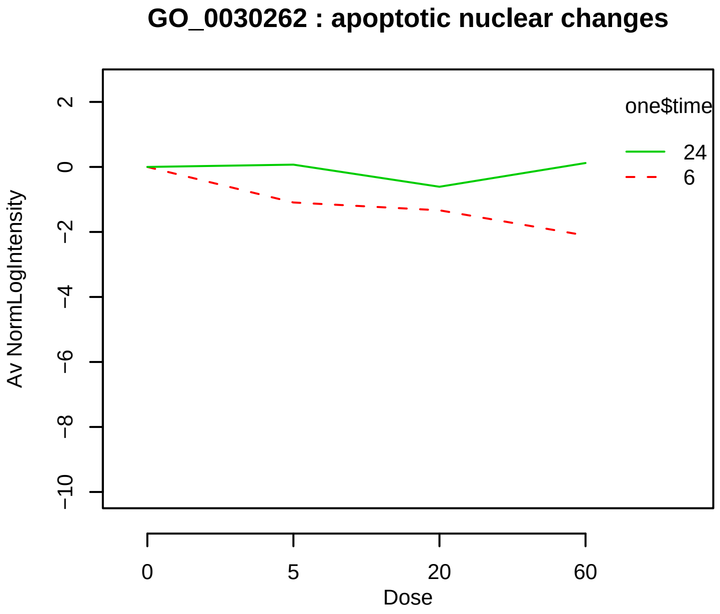

GO_0030238 : male sex determination

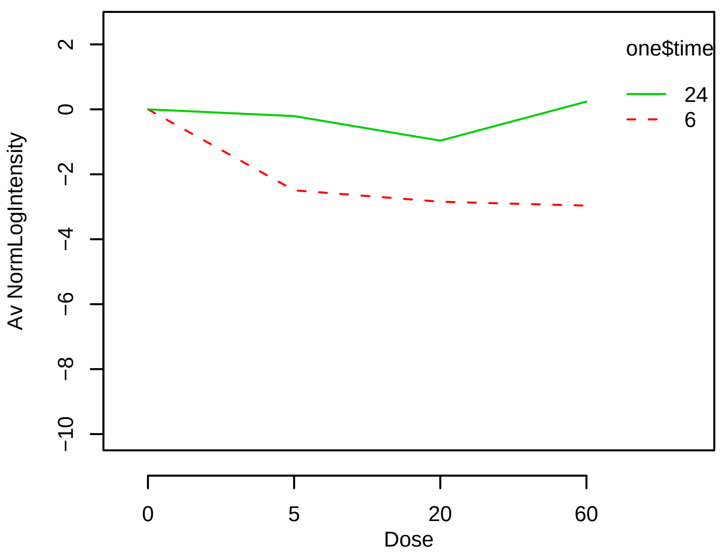

GO_0030239 : myofibril assembly


GO_0030258 : lipid modification

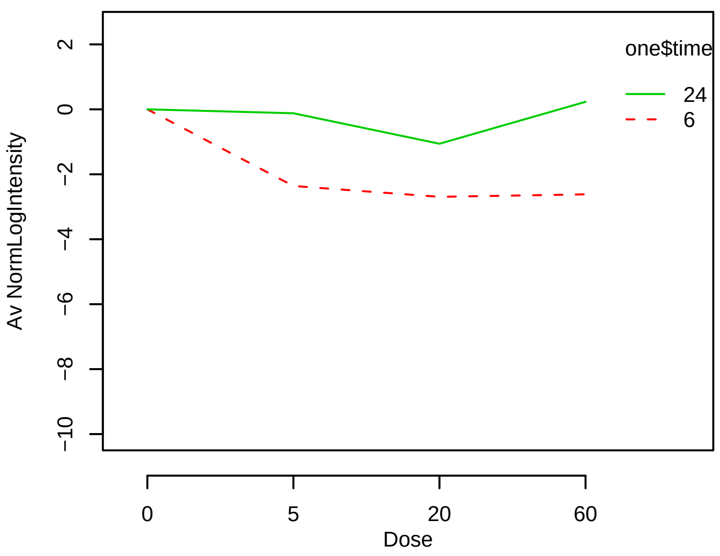

GO_0030260 : entry into host cell


GO_0030261 : chromosome condensation

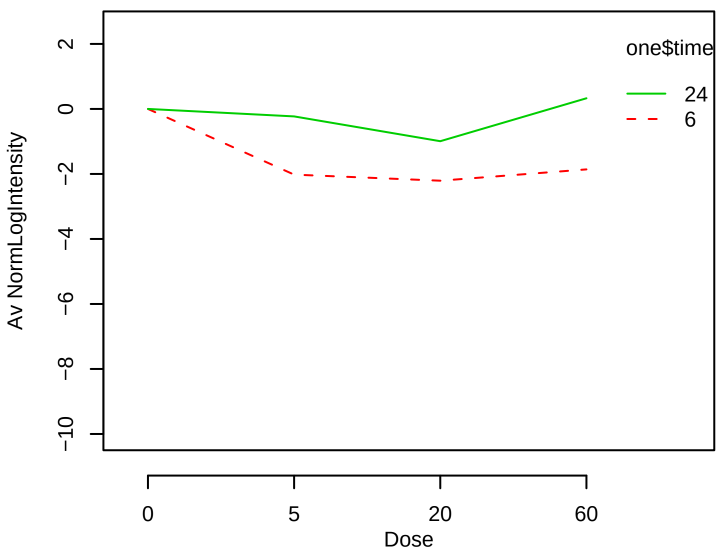

GO_0030262 : apoptotic nuclear changes



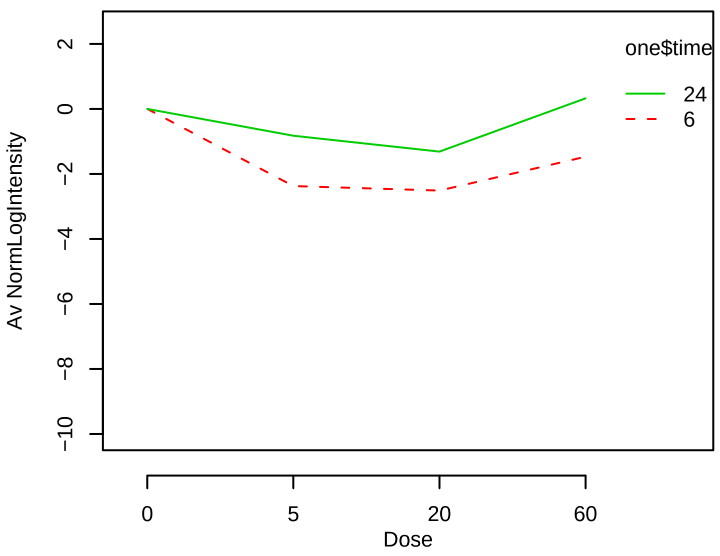
GO_0030278 : regulation of ossification



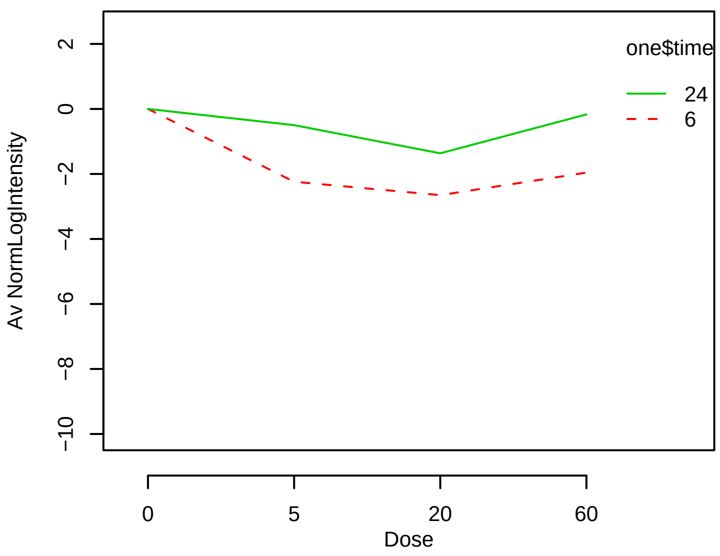
GO_0030279 : negative regulation of ossification



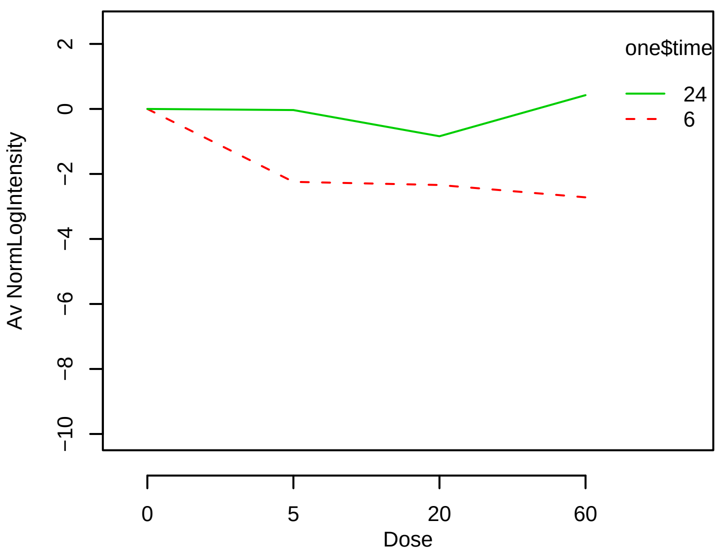
GO_0030282 : bone mineralization



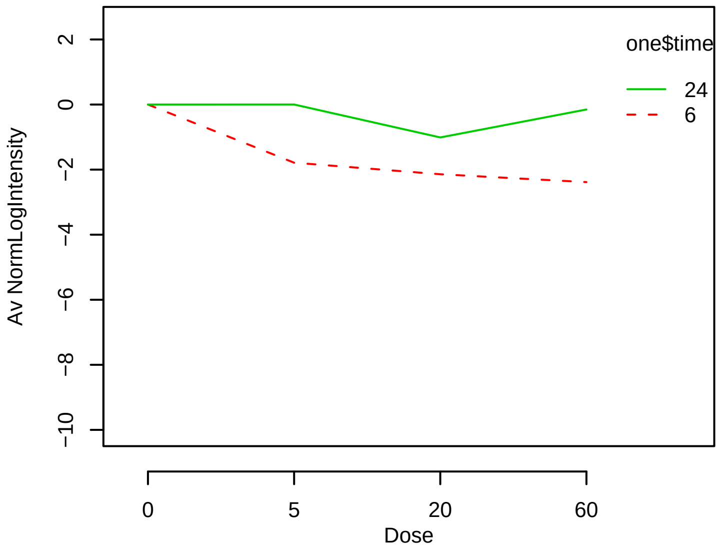
GO_0030299 : cholesterol absorption



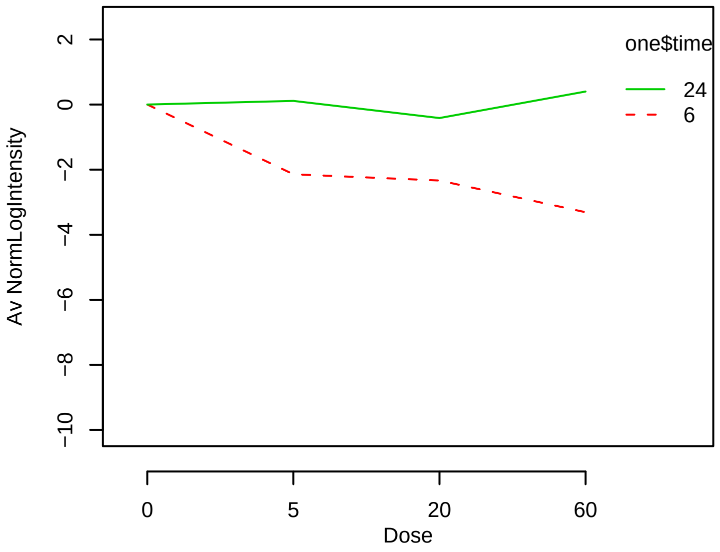
GO_0030301 : cholesterol transport



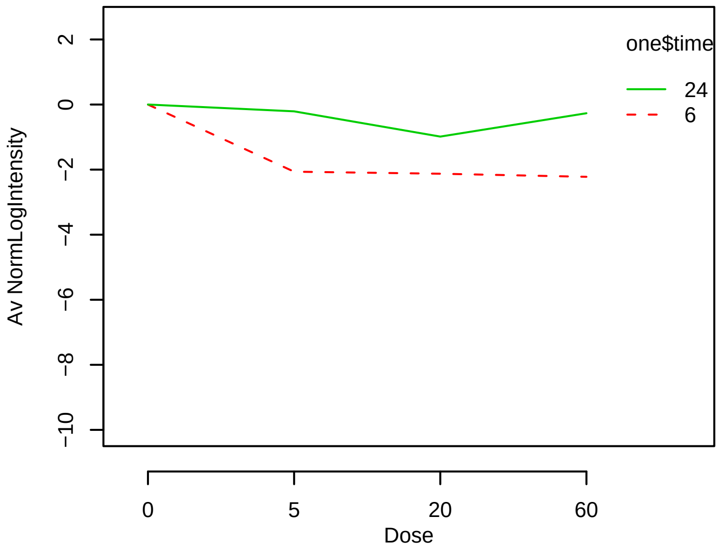
GO_0030307 : positive regulation of cell growth



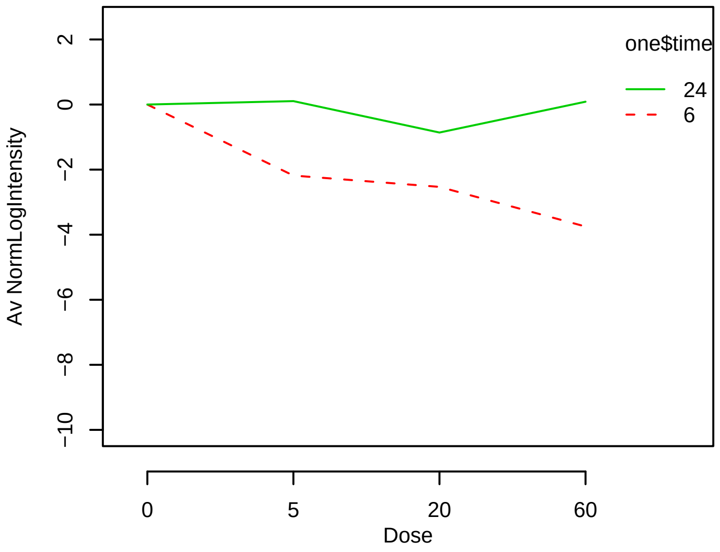
GO_0030308 : negative regulation of cell growth



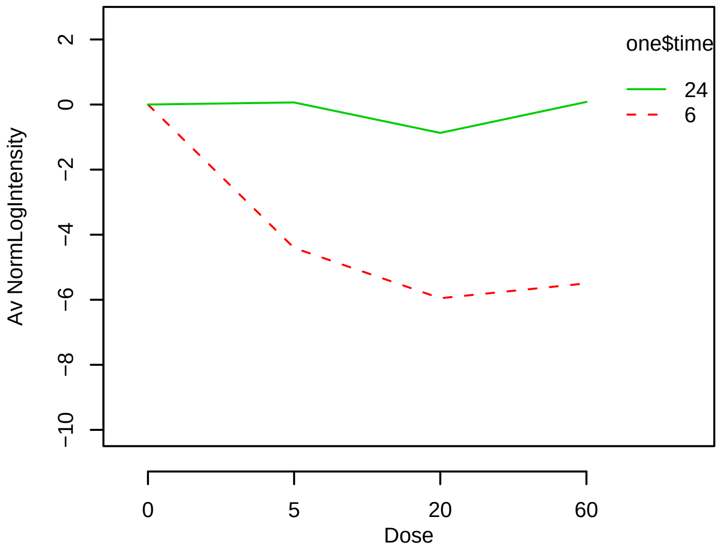
GO_0030316 : osteoclast differentiation



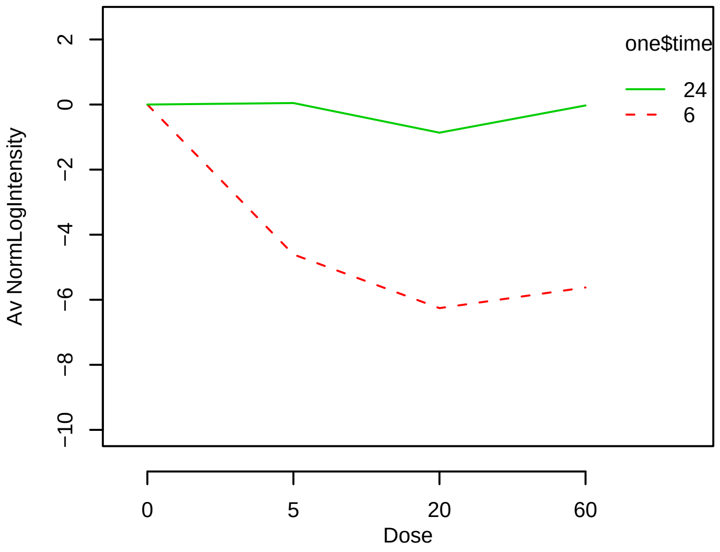
GO_0030317 : sperm motility



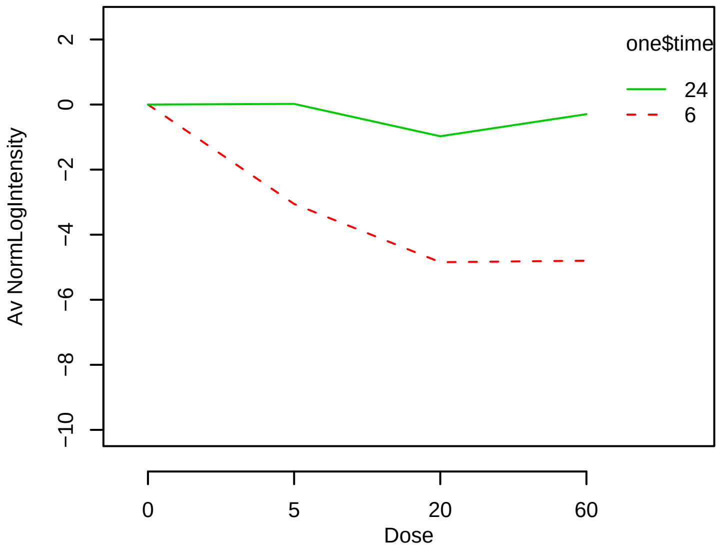
GO_0030318 : melanocyte differentiation



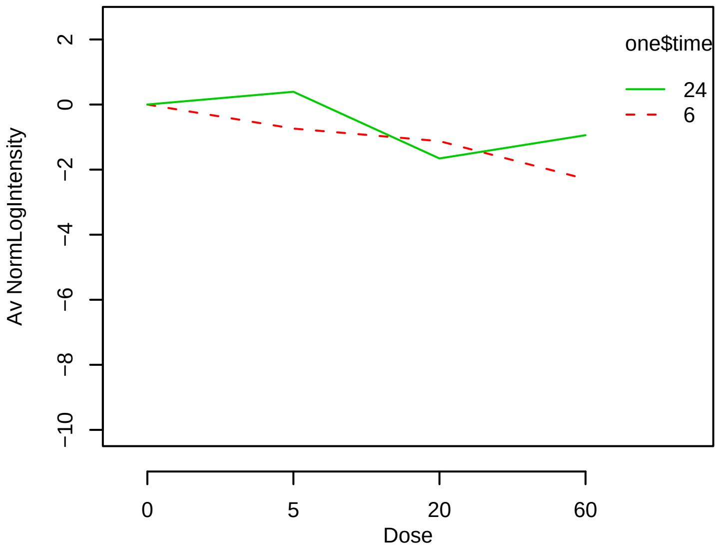
GO_0030323 : respiratory tube development



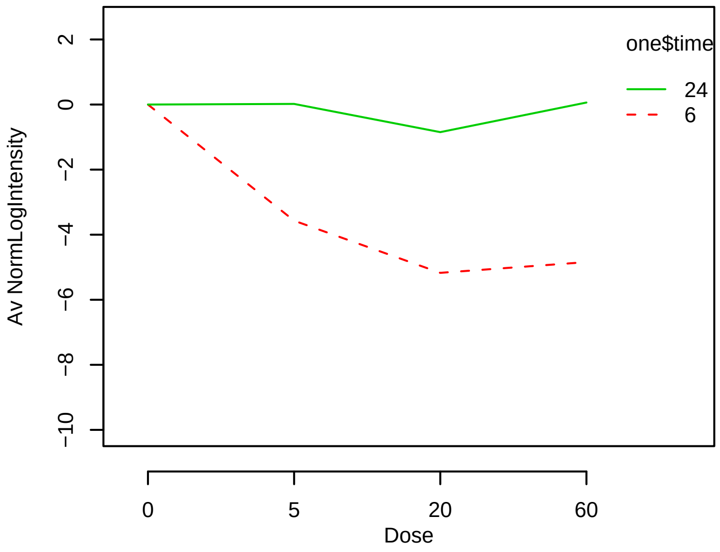
GO_0030324 : lung development



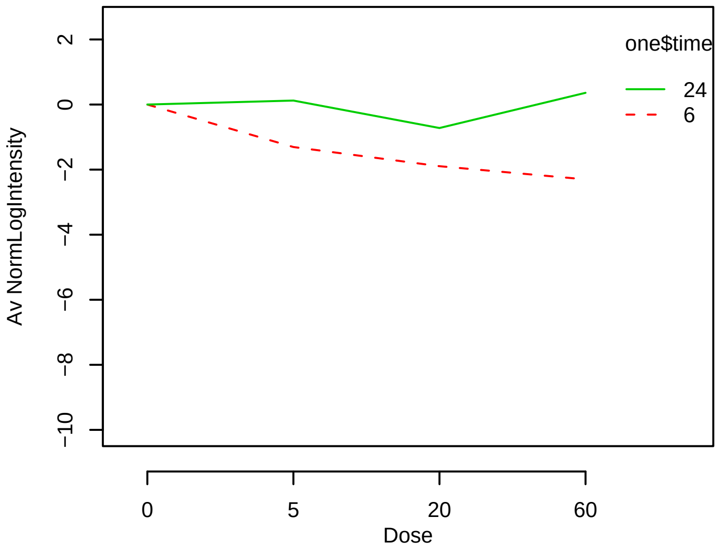
GO_0030326 : embryonic limb morphogenesis



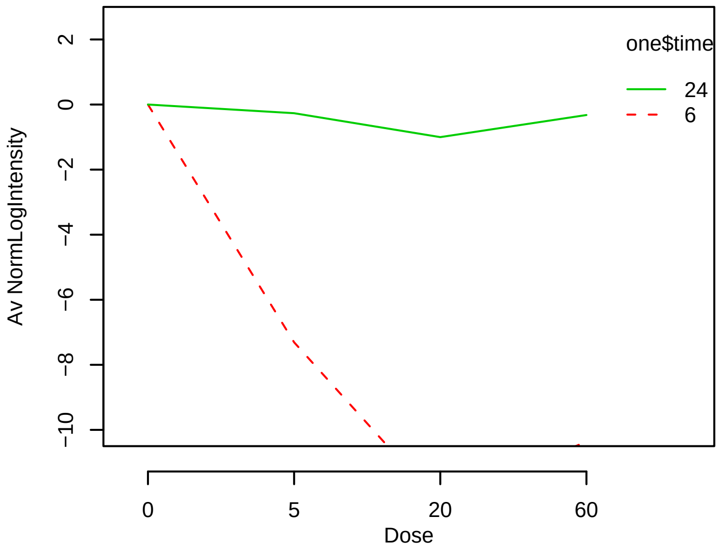
O_0030330 : DNA damage response\, signal transduction by



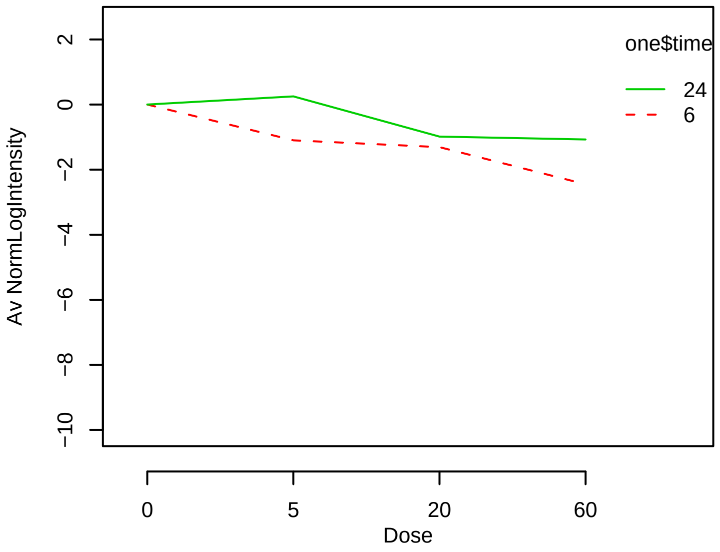
GO_0030334 : regulation of cell migration



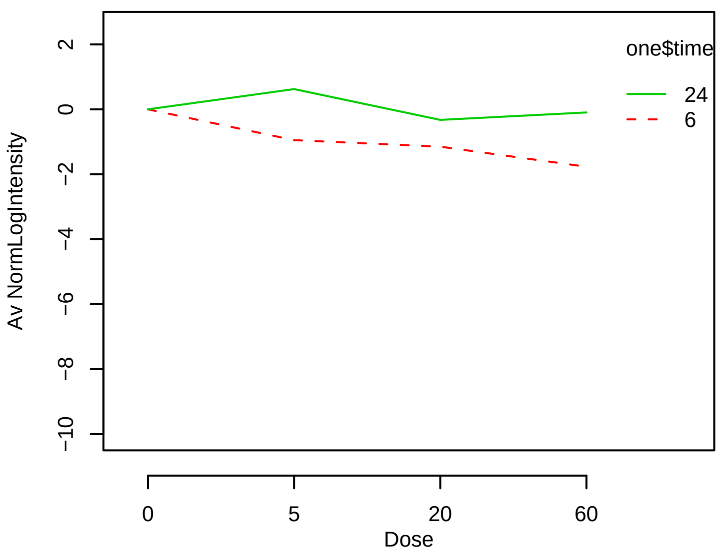
GO_0030335 : positive regulation of cell migration



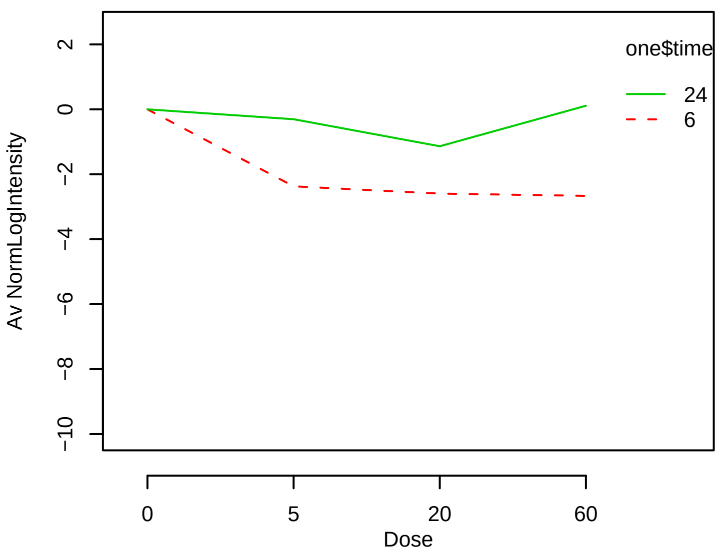
GO_0030336 : negative regulation of cell migration



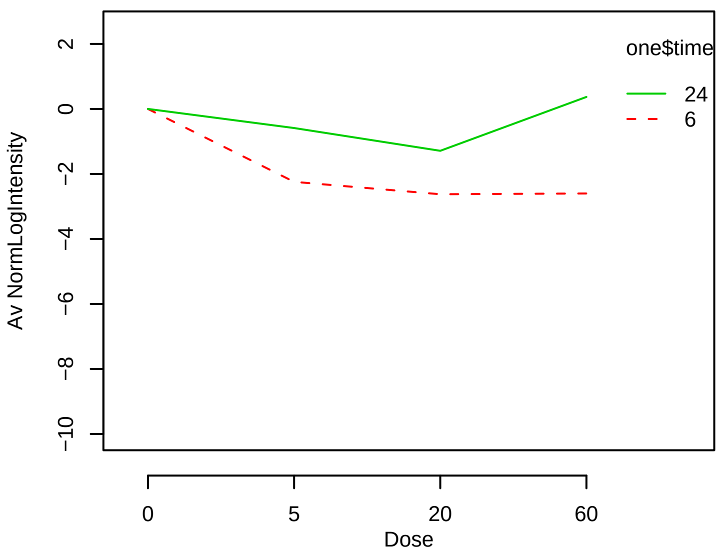
GO_0030384 : phosphoinositide metabolism



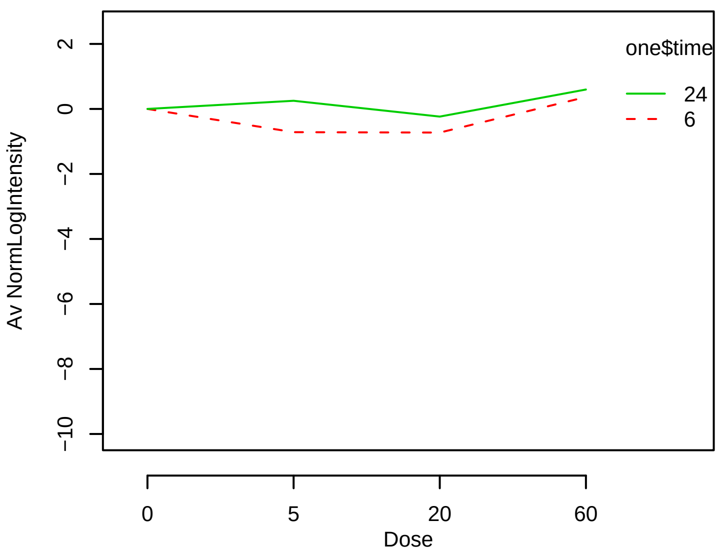
GO_0030433 : ER−associated protein catabolism



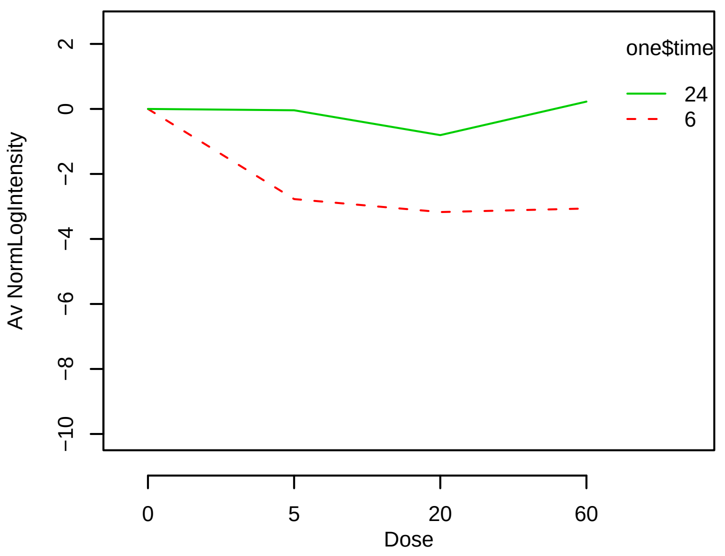
GO_0030500 : regulation of bone mineralization



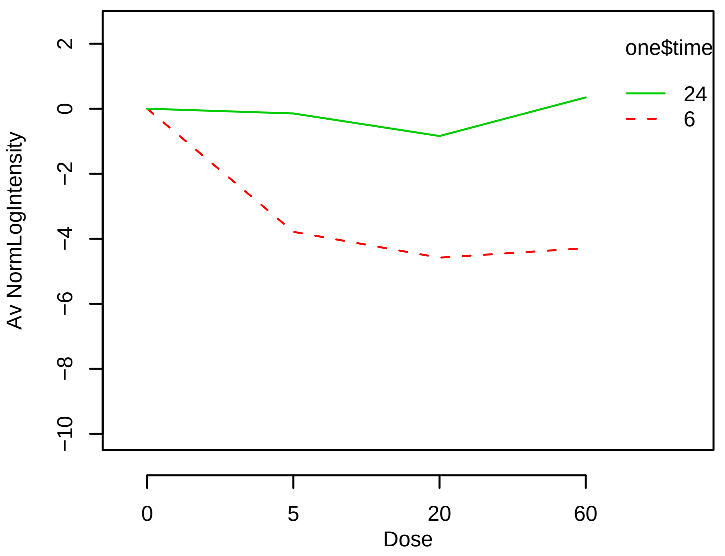
GO_0030501 : positive regulation of bone mineralization



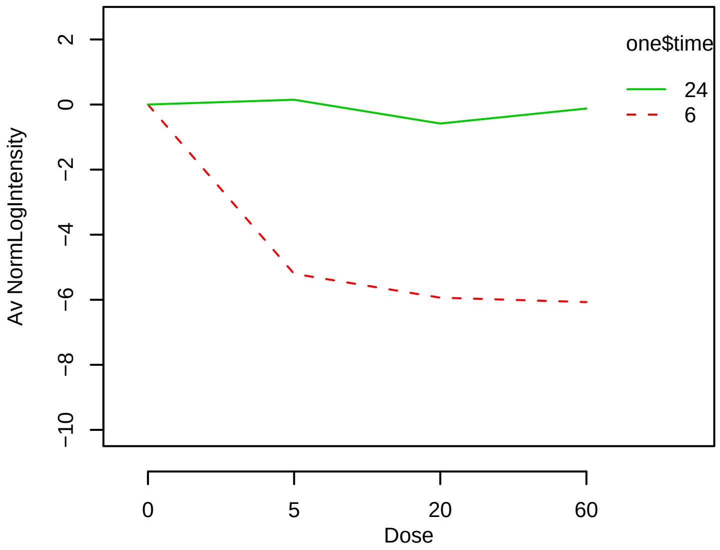
GO_0030503 : regulation of cell redox homeostasis



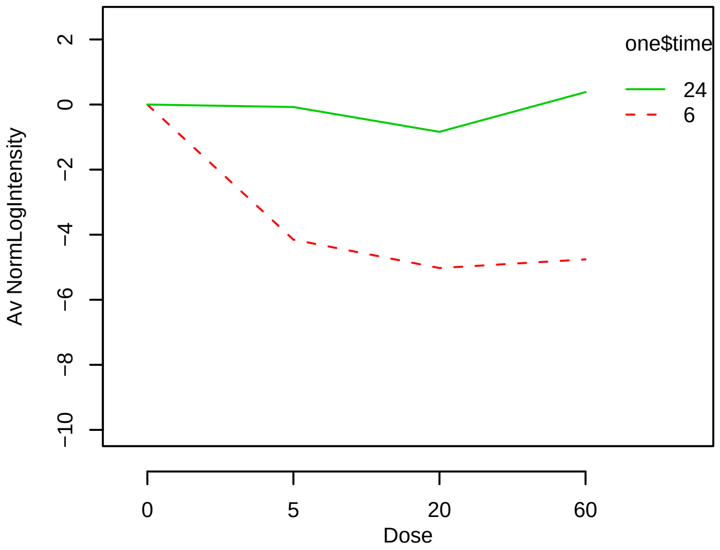
GO_0030509 : BMP signaling pathway



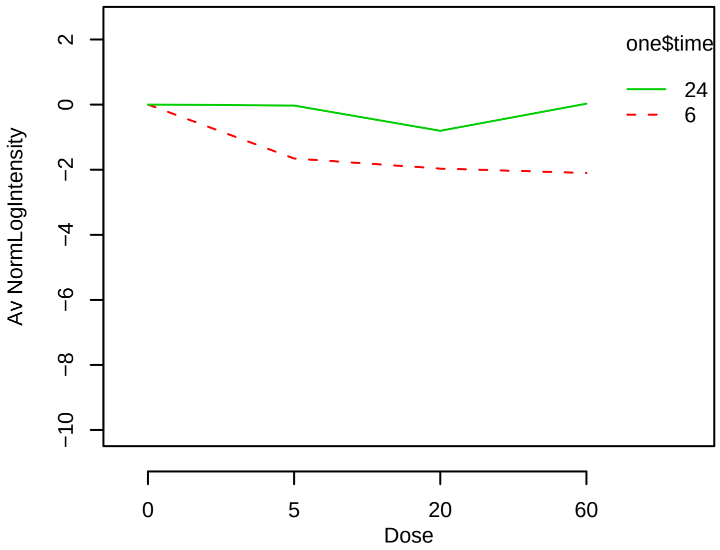
GO_0030510 : regulation of BMP signaling pathway



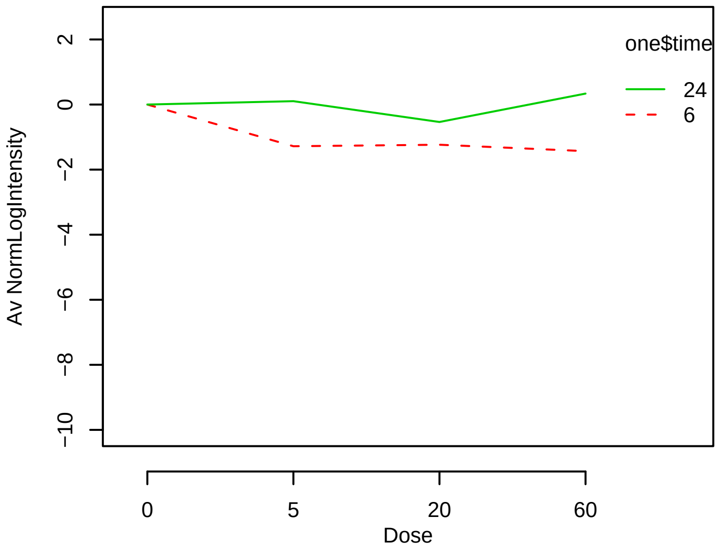
GO_0030512 : negative regulation of transforming growth fa



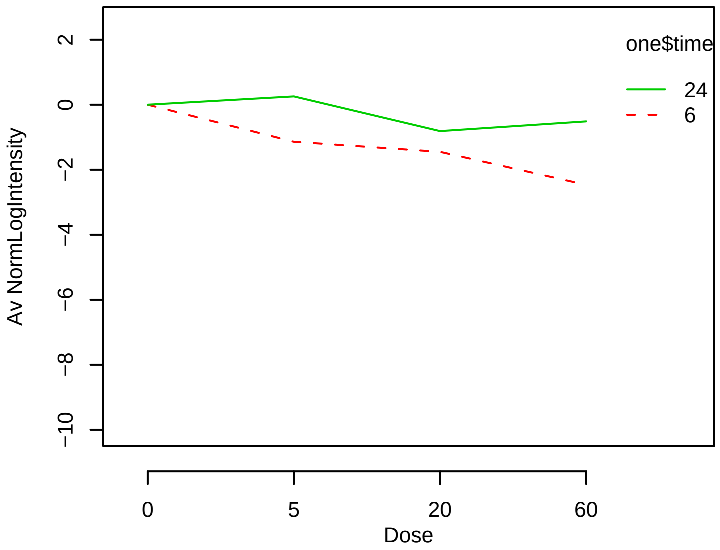
GO_0030514 : negative regulation of BMP signaling pathwa



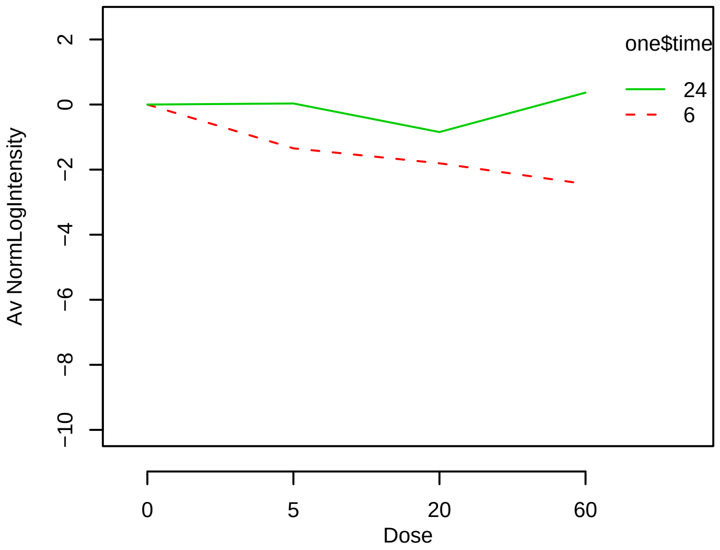
GO_0030516 : regulation of axon extension



GO_0030517 : negative regulation of axon extension

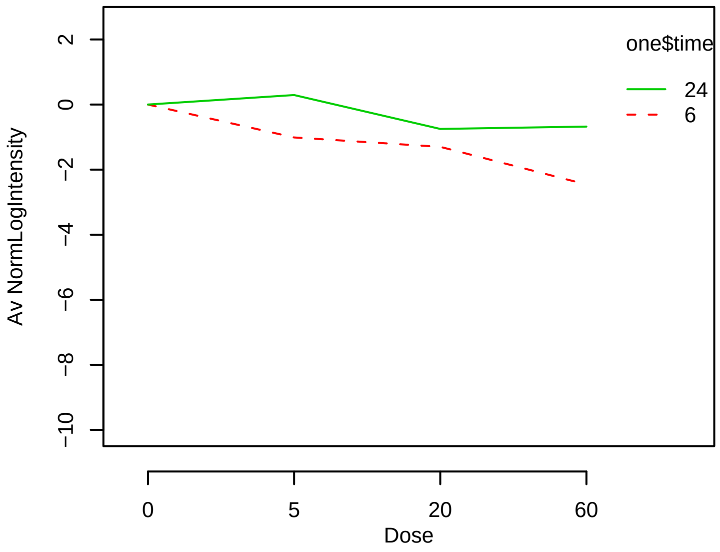


GO_0030518 : steroid hormone receptor signaling pathwa

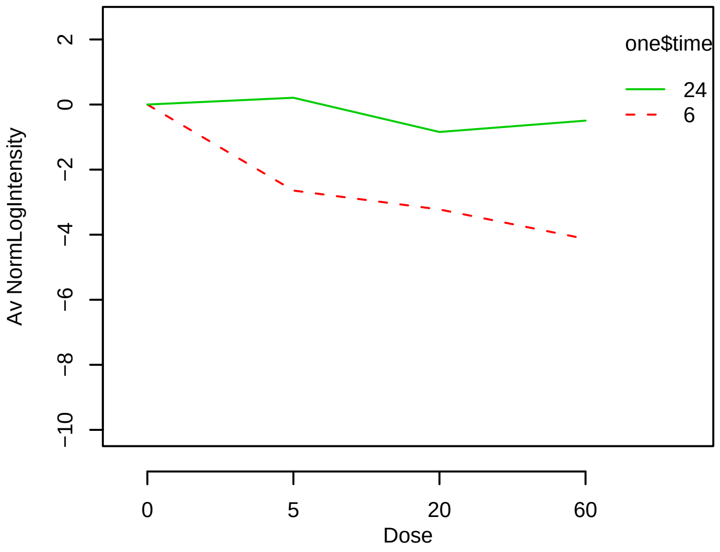


GO_0030520 : estrogen receptor signaling pathway

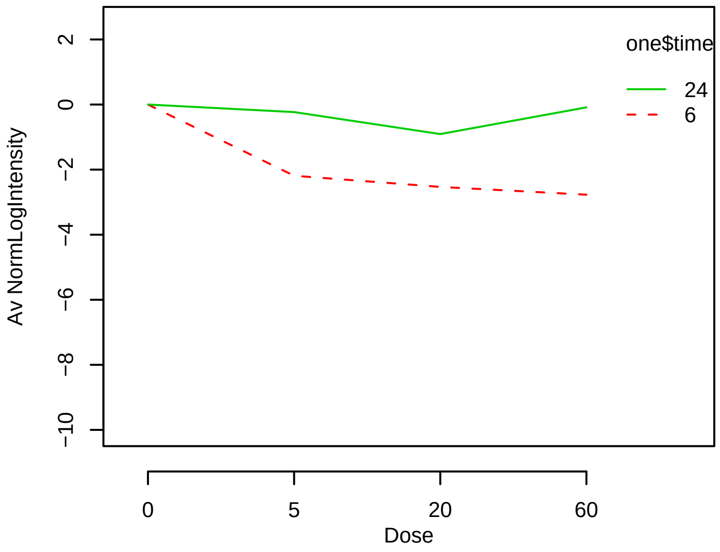
GO_0030521 : androgen receptor signaling pathway



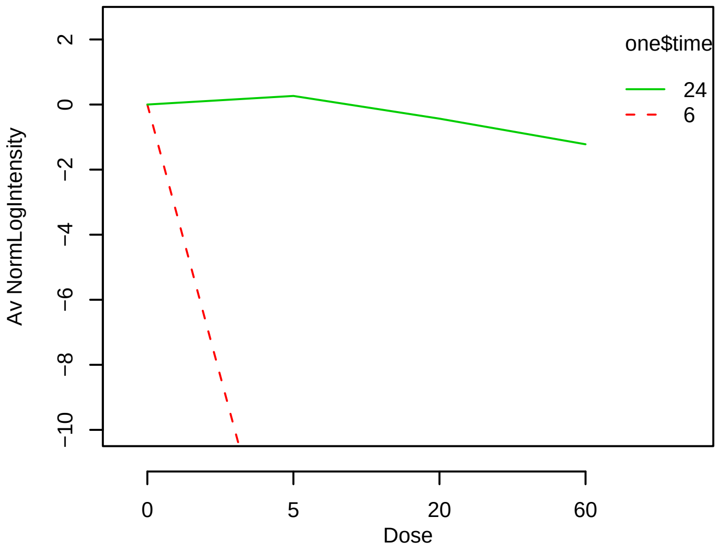
GO_0030522 : intracellular receptor−mediated signaling path



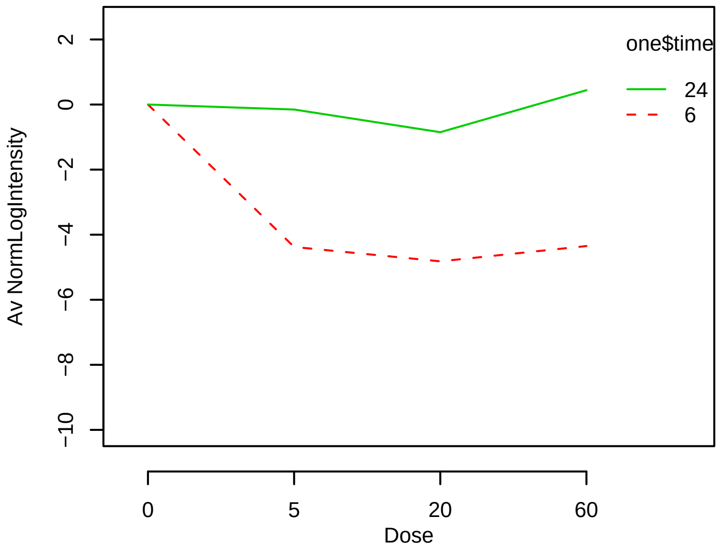
GO_0030534 : adult behavior



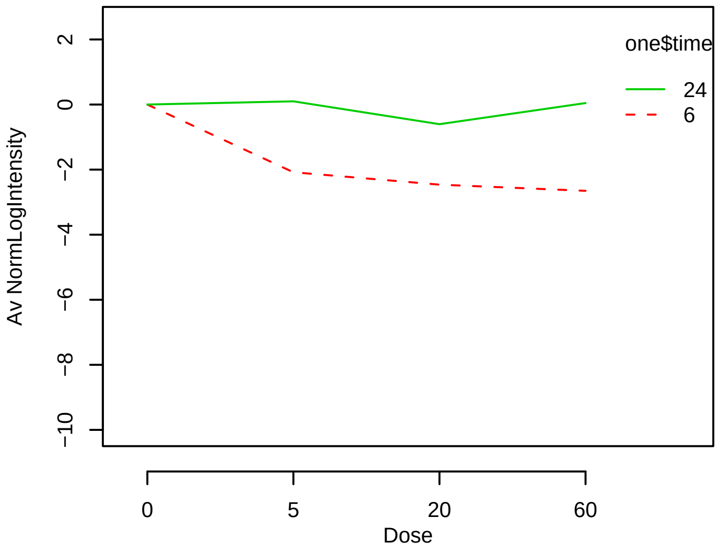
GO_0030539 : male genitalia development



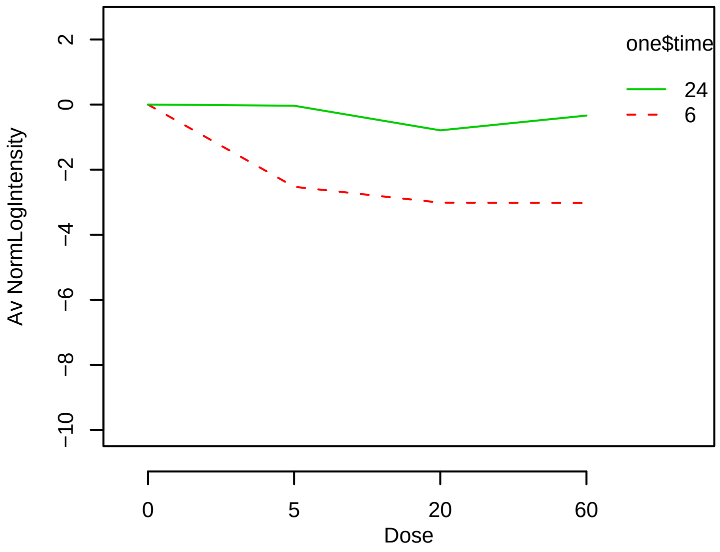
GO_0030574 : collagen catabolism



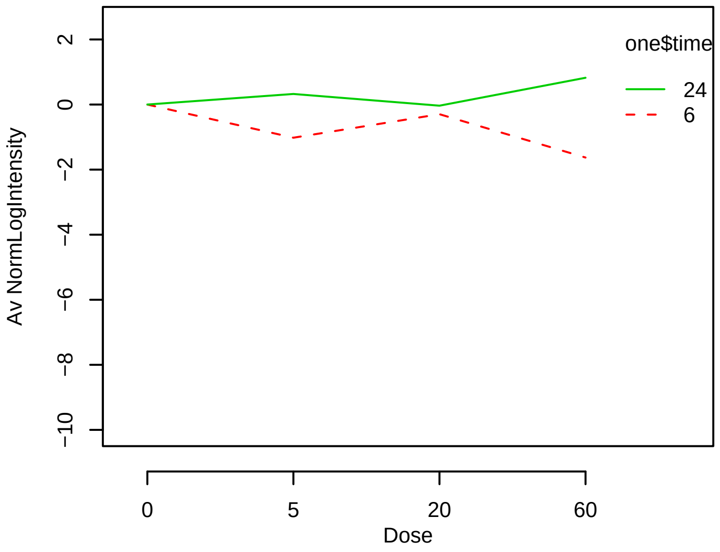
GO_0030593 : neutrophil chemotaxis



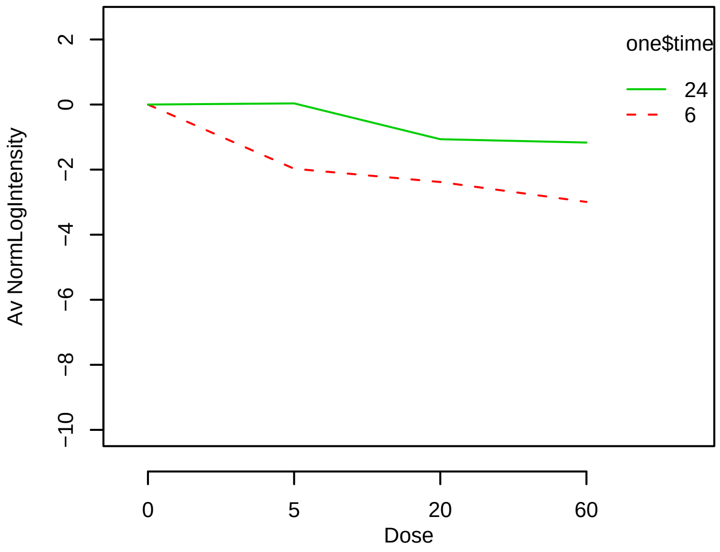
GO_0030595 : leukocyte chemotaxis



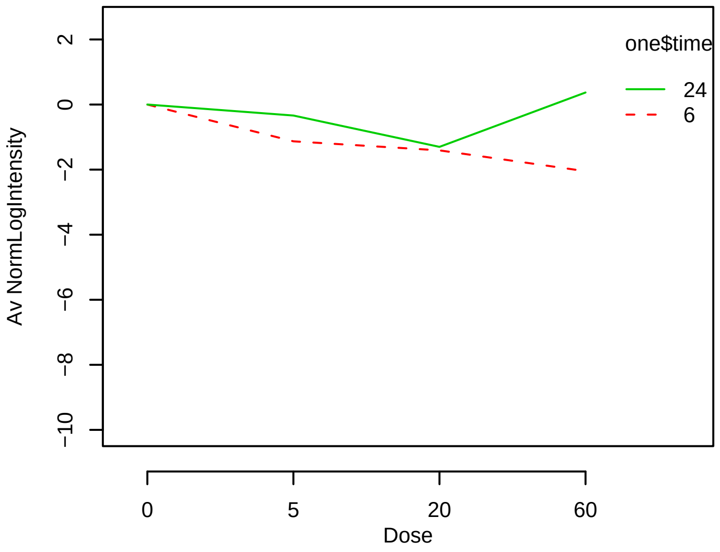
GO_0030641 : hydrogen ion homeostasis



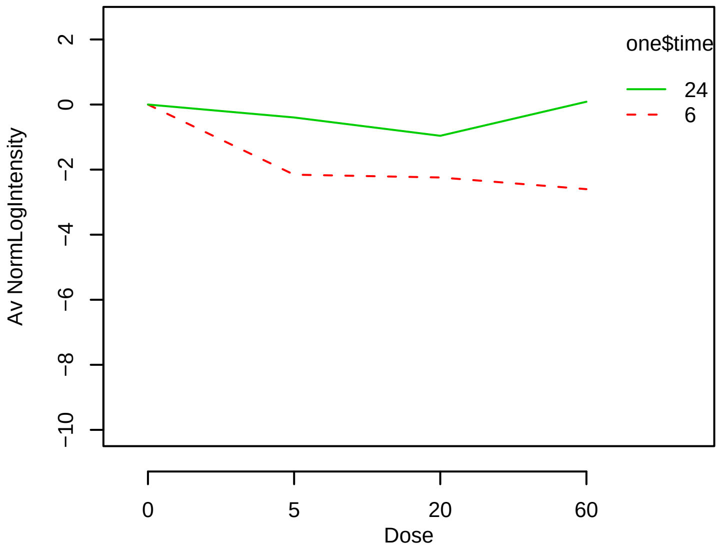
GO_0030705 : cytoskeleton−dependent intracellular transp



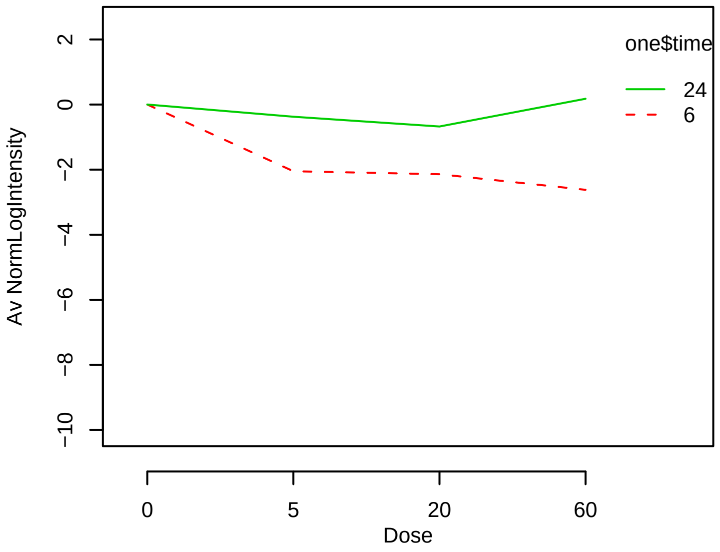
GO_0030728 : ovulation



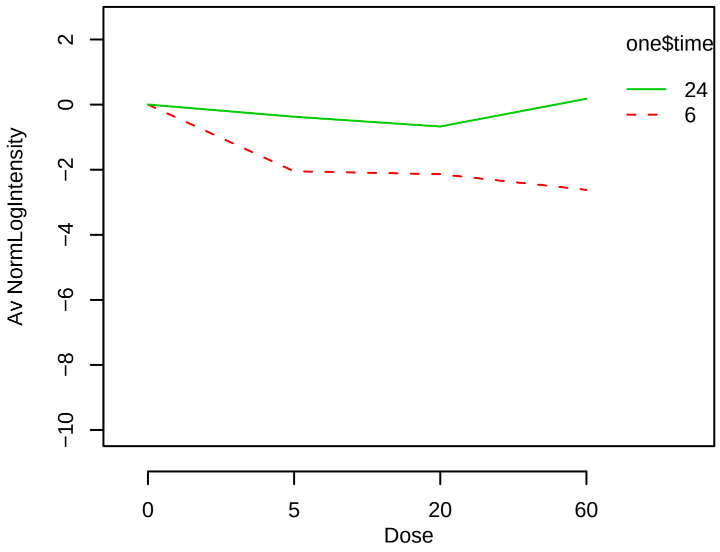
GO_0030799 : regulation of cyclic nucleotide metabolism



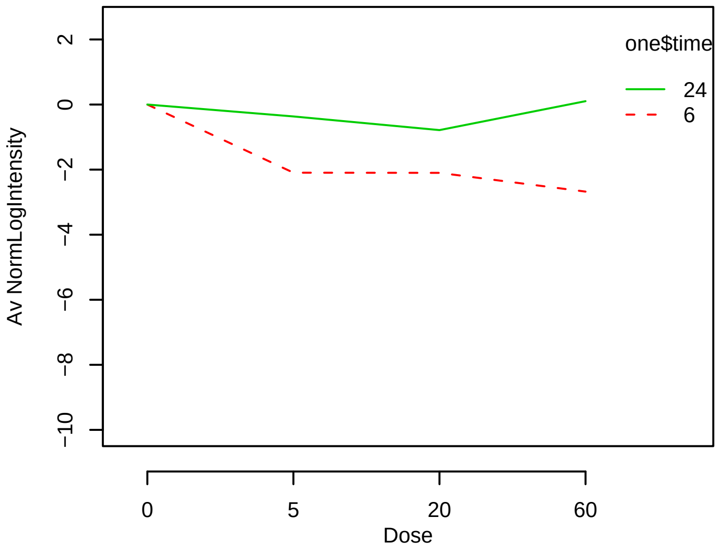
GO_0030802 : regulation of cyclic nucleotide biosynthesi



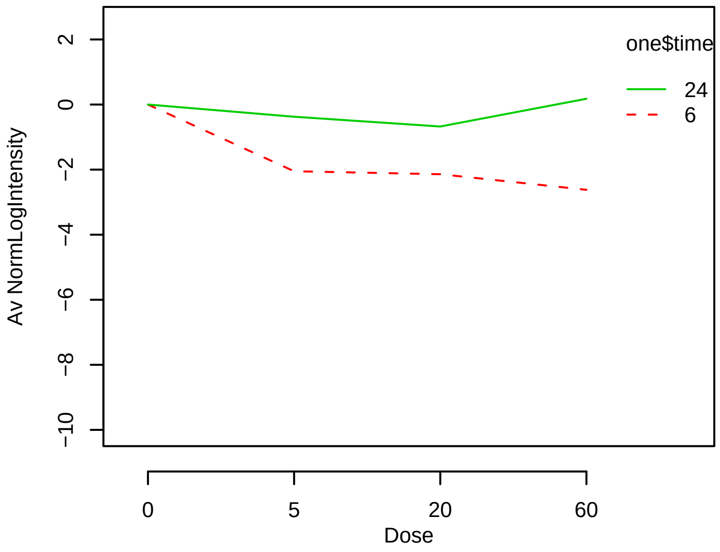
GO_0030808 : regulation of nucleotide biosynthesis



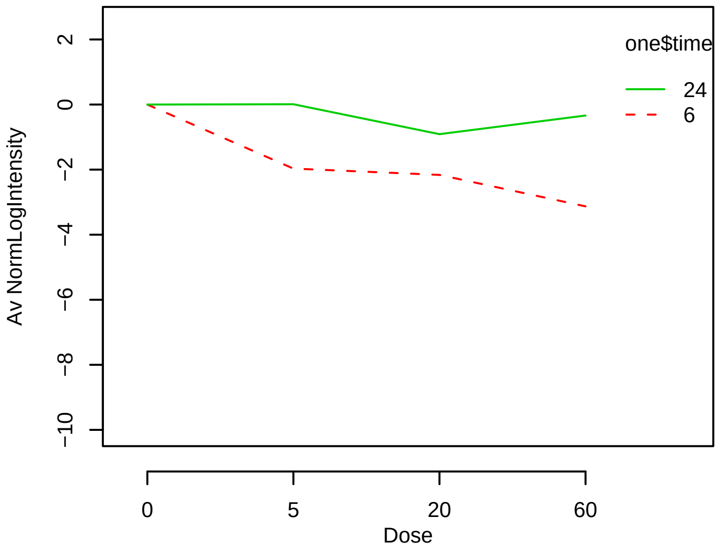
GO_0030814 : regulation of cAMP metabolism



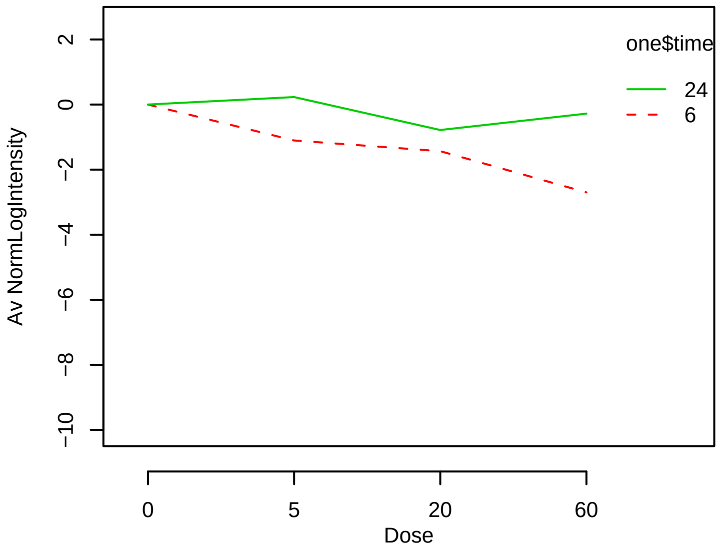
GO_0030817 : regulation of cAMP biosynthesis



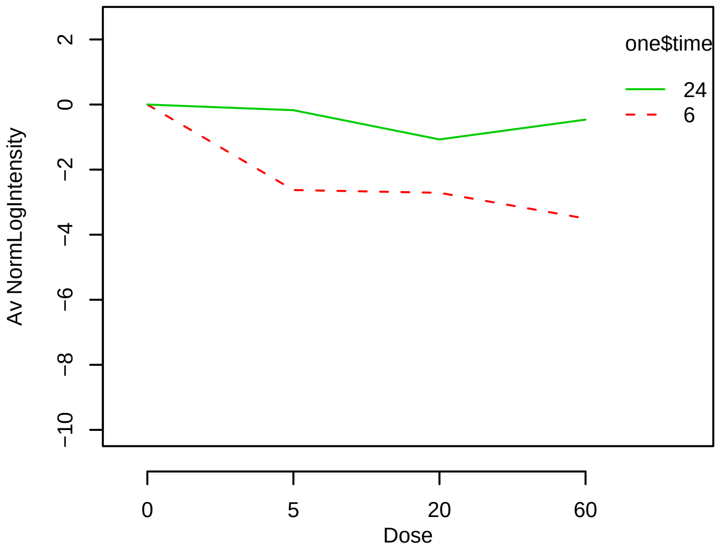
GO_0030832 : regulation of actin filament length

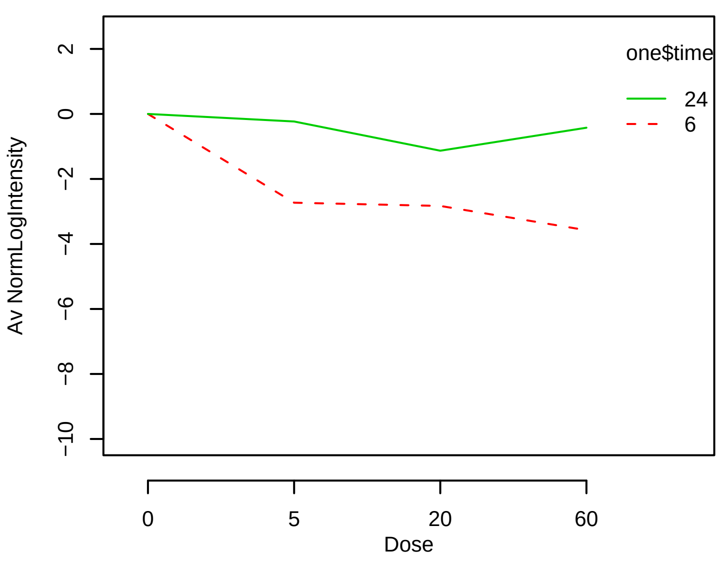


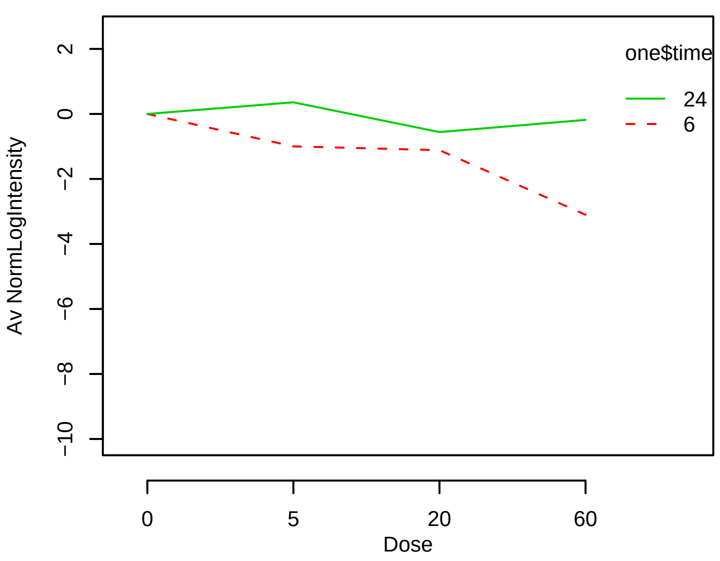
GO_0030833 : regulation of actin filament polymerization

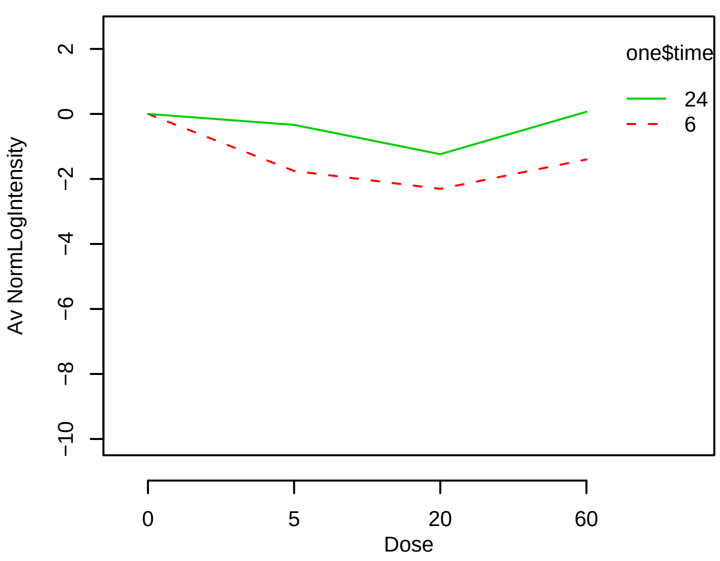


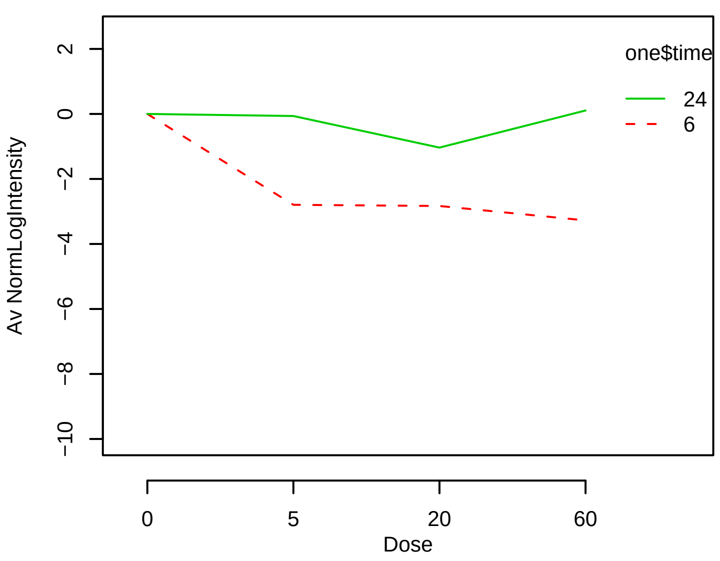
GO_0030834 : regulation of actin filament depolymerizatio

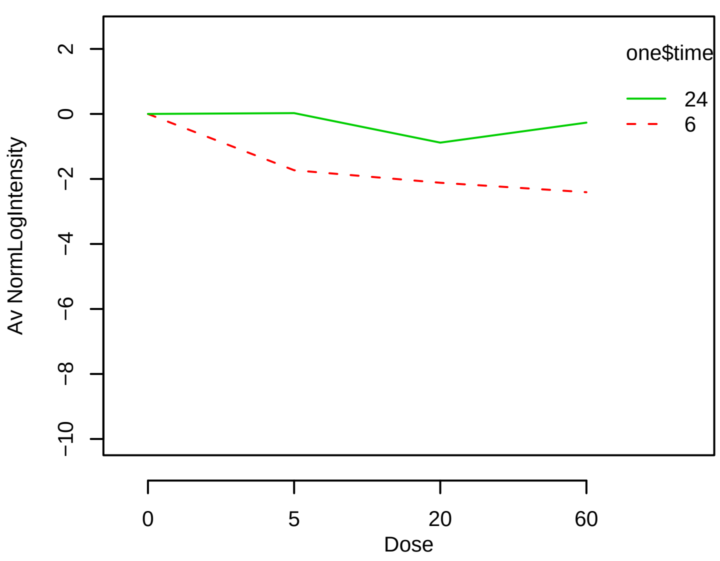


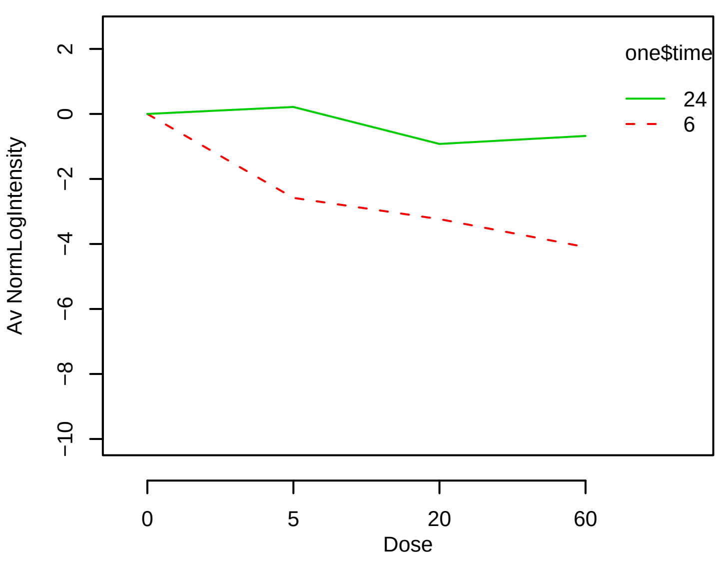

GO_0030835 : negative regulation of actin filament depolyme

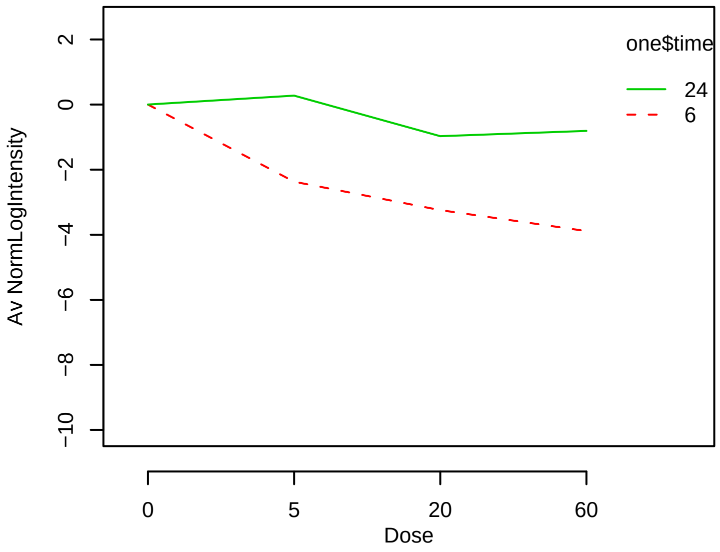

GO_0030838 : positive regulation of actin filament polymeri

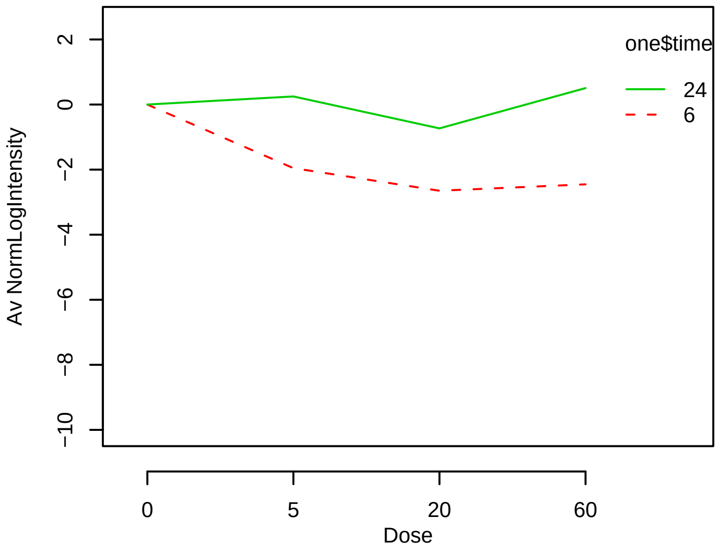

GO_0030851 : granulocyte differentiation

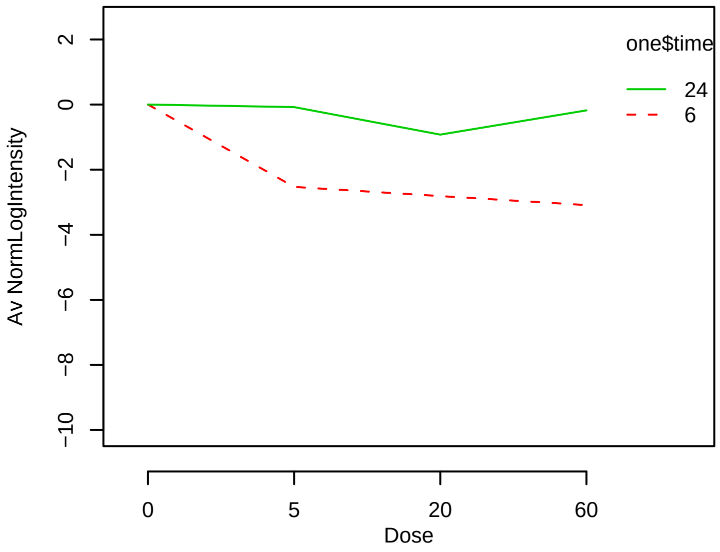

GO_0030855 : epithelial cell differentiation

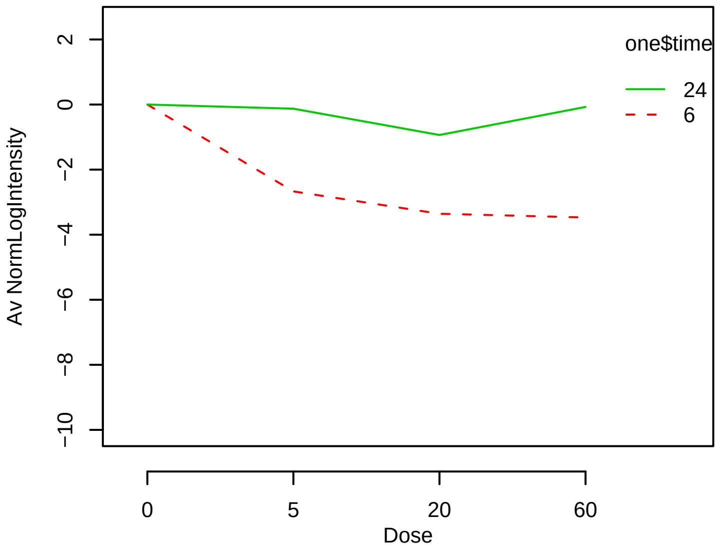

GO_0030856 : regulation of epithelial cell differentiation

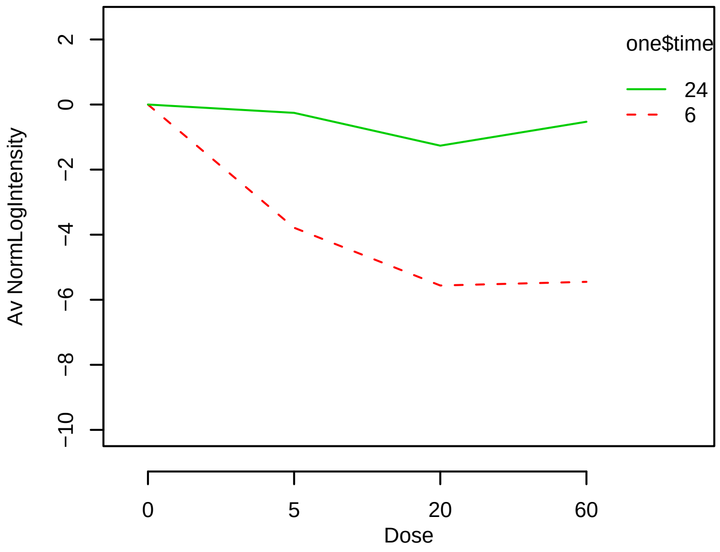

GO_0030865 : cortical cytoskeleton organization and biogen

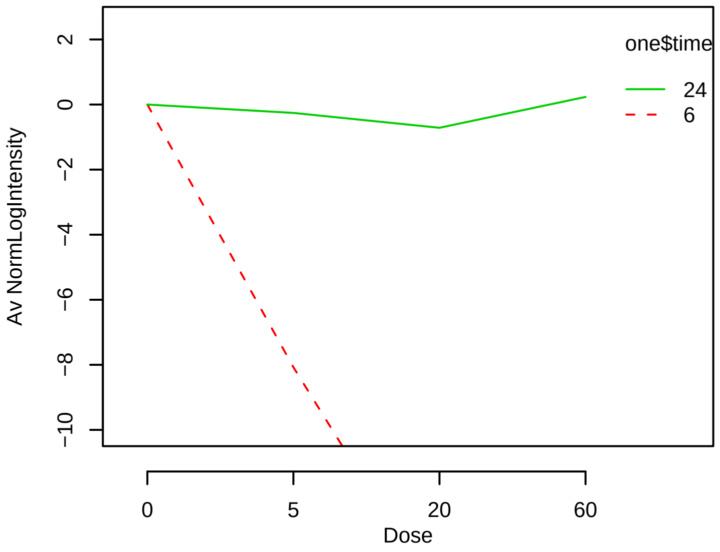

GO_0030866 : cortical actin cytoskeleton organization and bi


GO_0030879 : mammary gland development

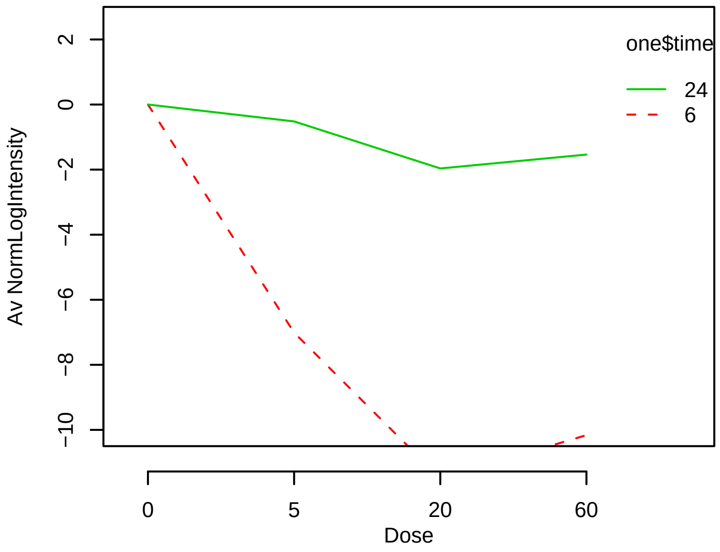

GO_0030888 : regulation of B cell proliferation


GO_0030890 : positive regulation of B cell proliferation

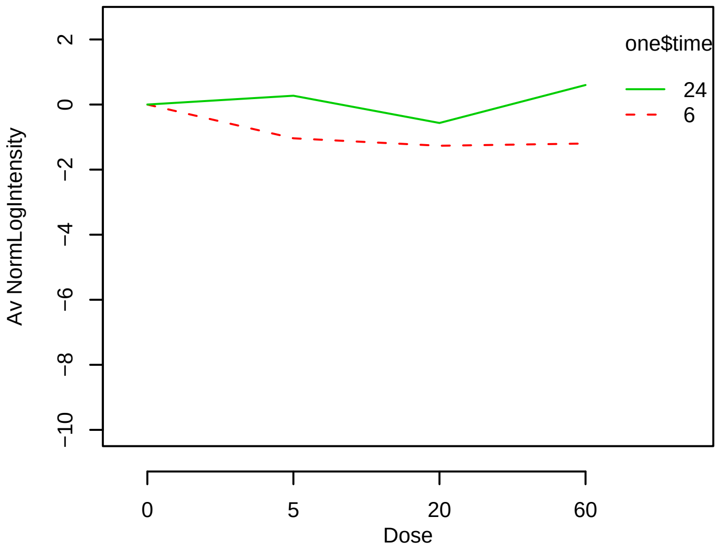

GO_0030900 : forebrain development


GO_0030901 : midbrain development

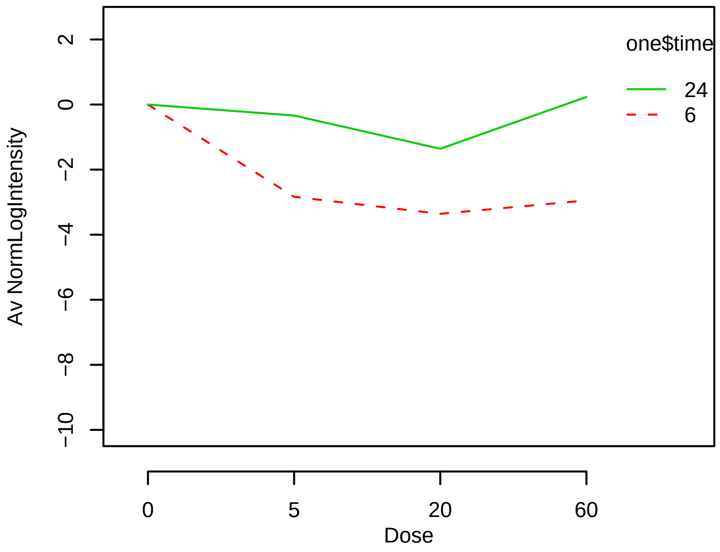
GO_0030902 : hindbrain development



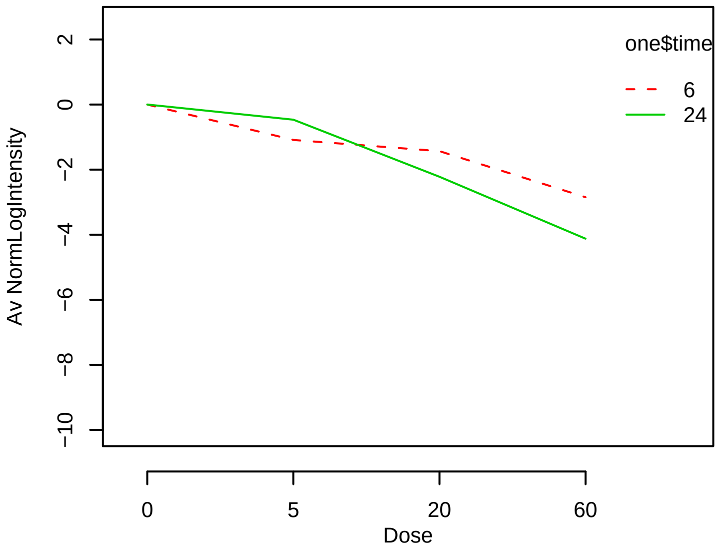
GO_0030968 : unfolded protein response



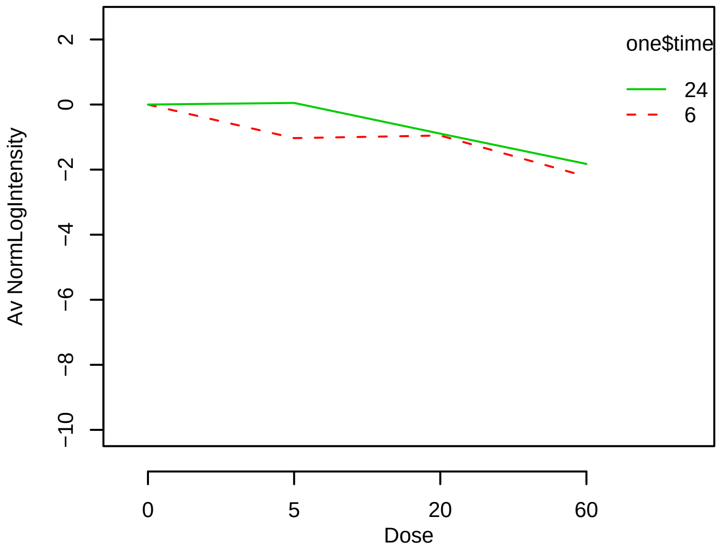
GO_0031016 : pancreas development



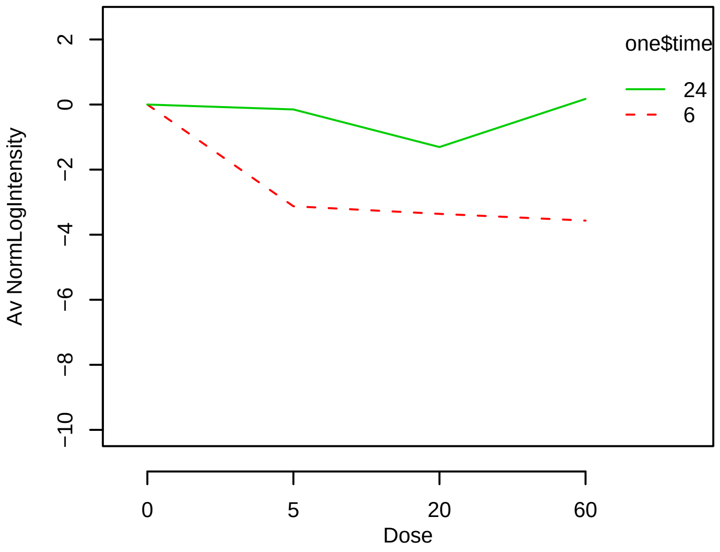
O_0031023 : microtubule organizing center organization an



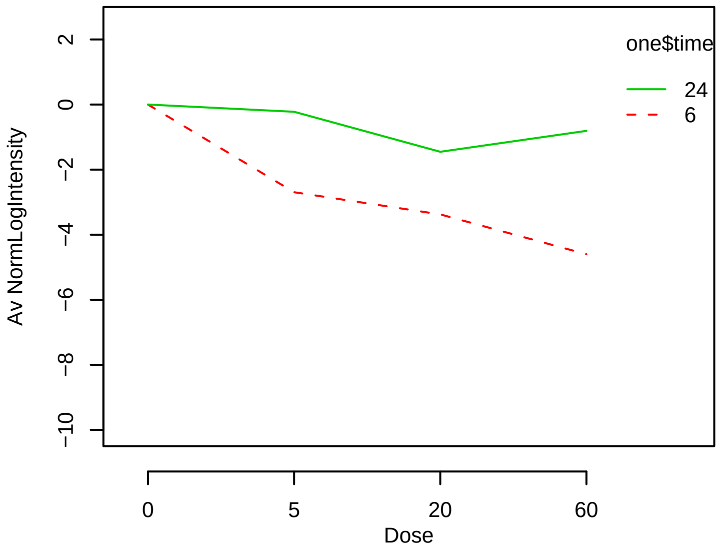
GO_0031032 : actomyosin structure organization and biogen



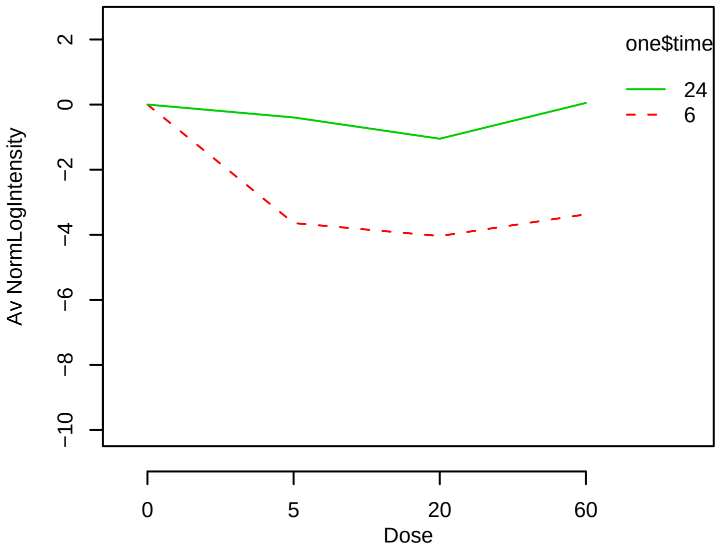
GO_0031069 : hair follicle morphogenesis



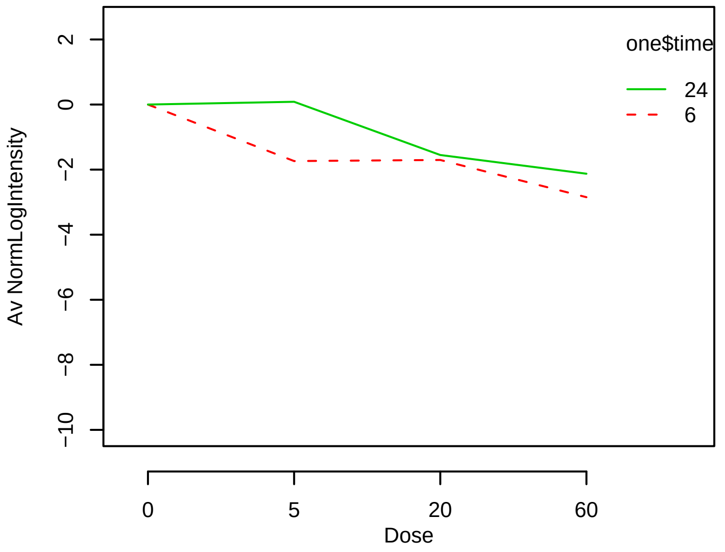
GO_0031098 : stress−activated protein kinase signaling path



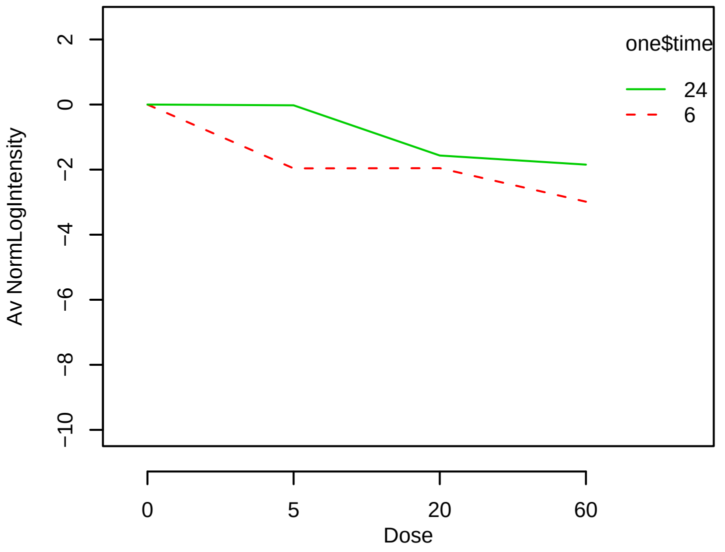
GO_0031099 : regeneration



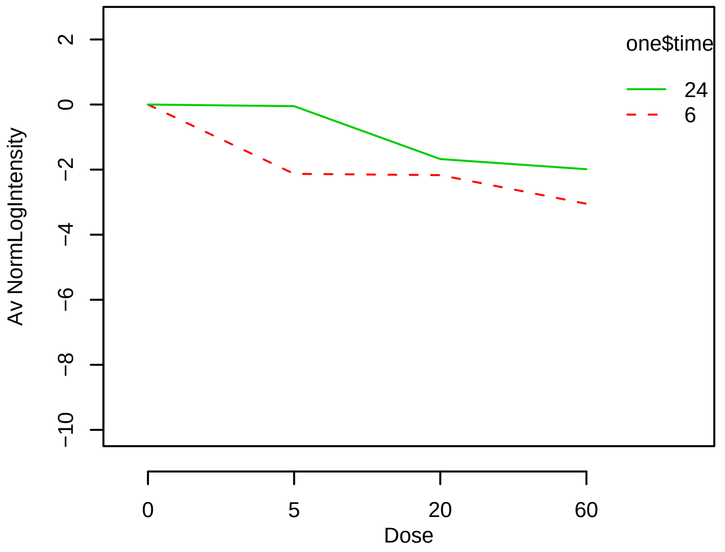
GO_0031109 : microtubule polymerization or depolymerizat



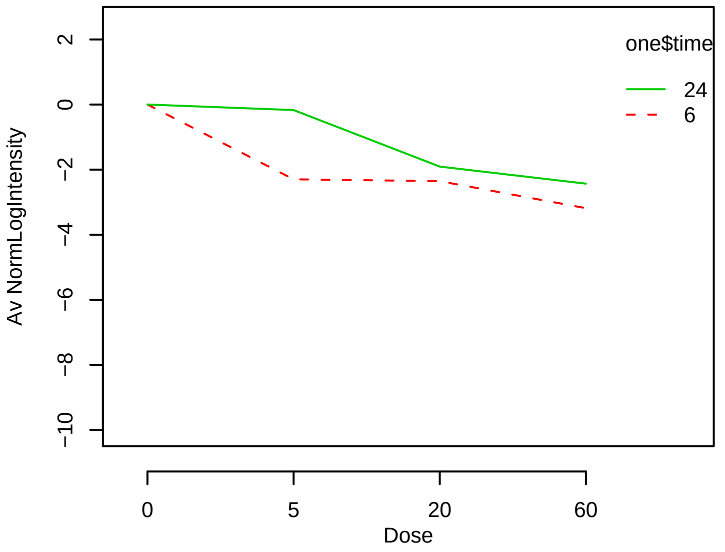
GO_0031110 : regulation of microtubule polymerization or de

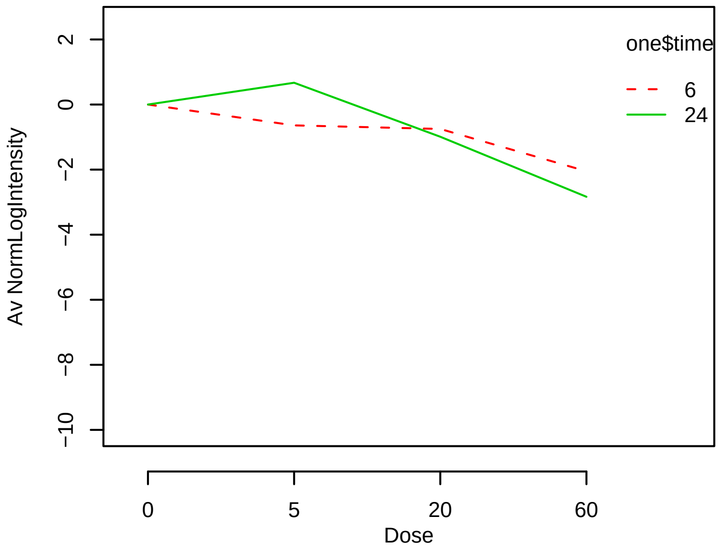


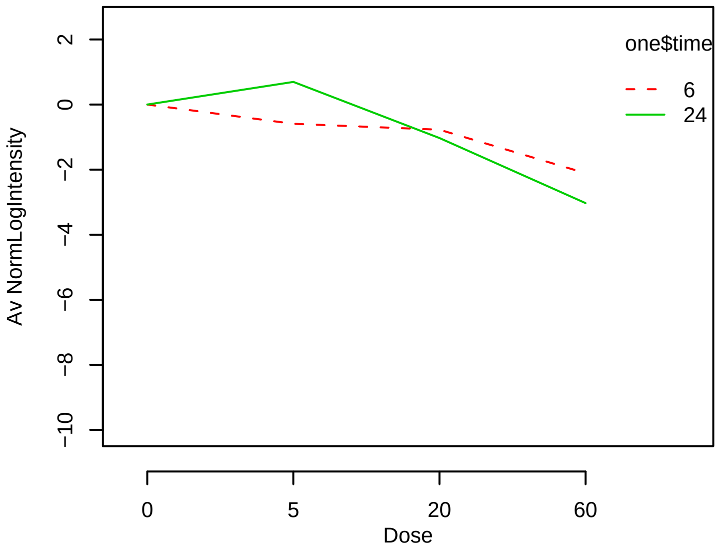
GO_0031111 : negative regulation of microtubule polymeriza

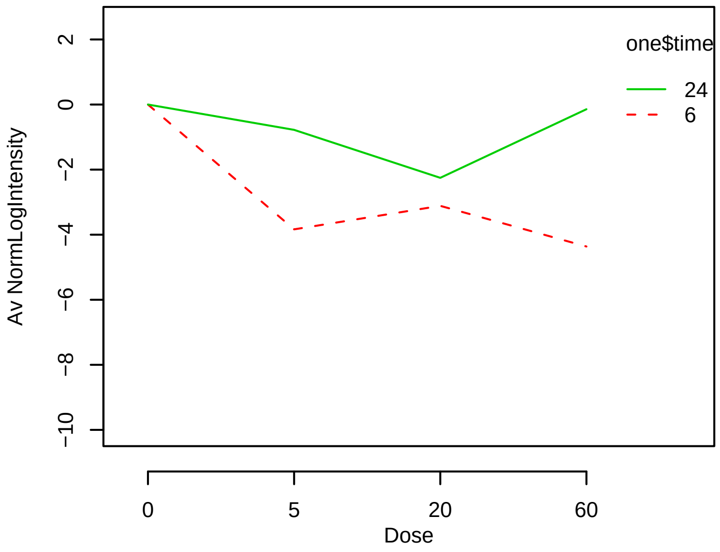


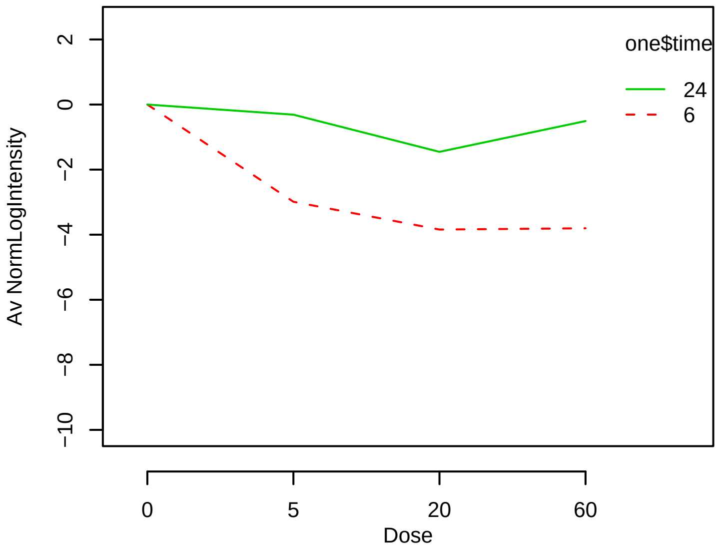
GO_0031114 : regulation of microtubule depolymerizatio

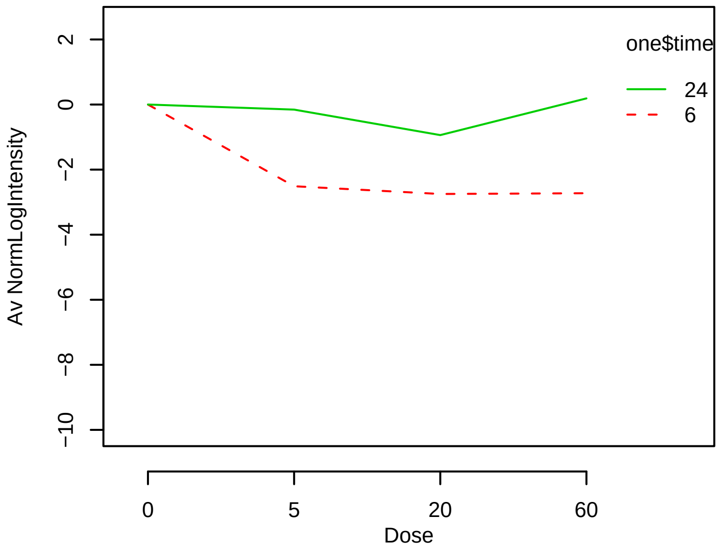


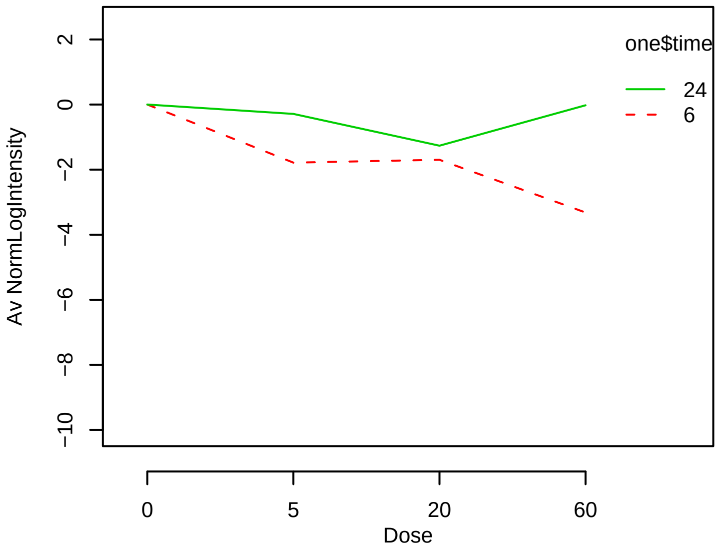

GO_0031123 : RNA 3’−end processing

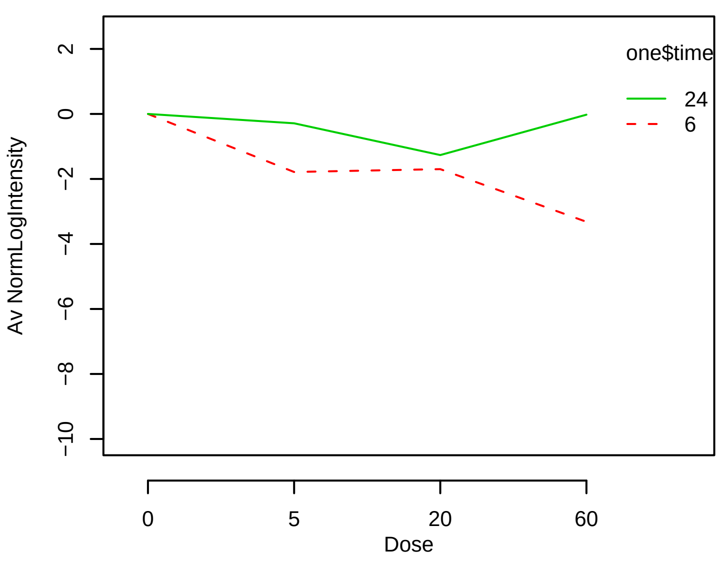

GO_0031124 : mRNA 3’−end processing

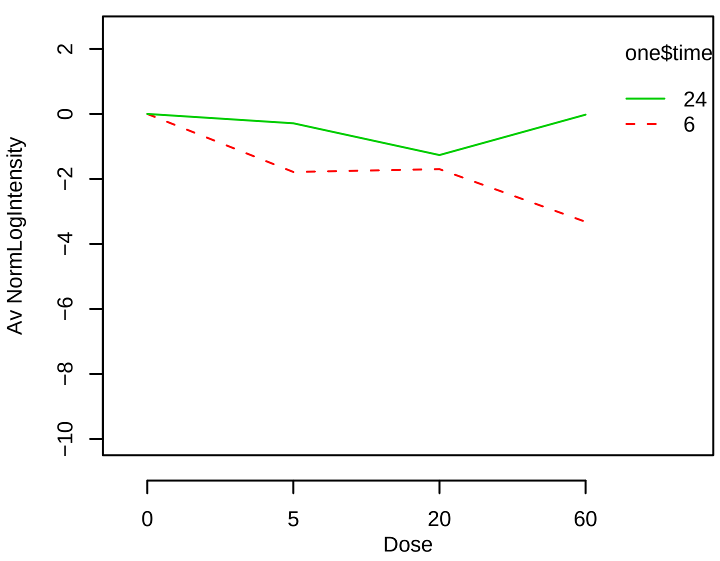

GO_0031128 : induction

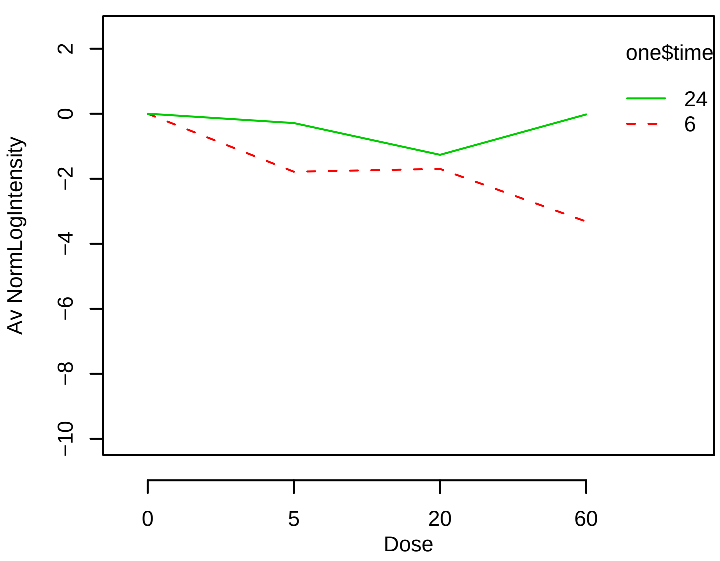

GO_0031175 : neurite development

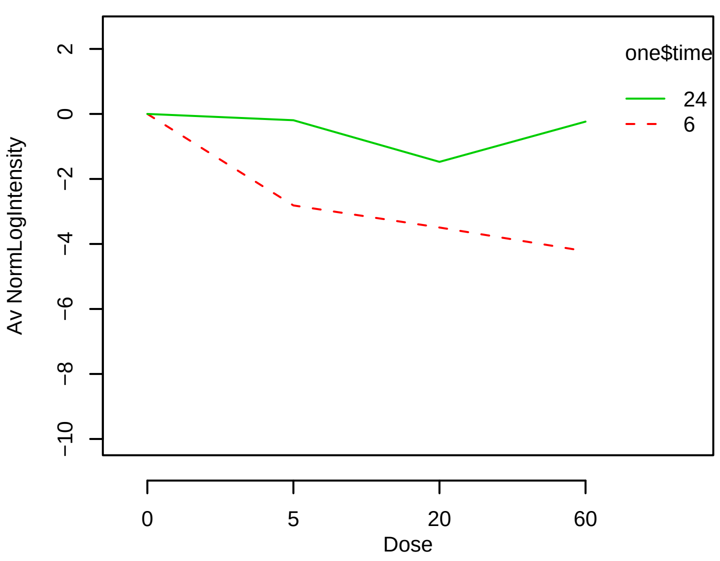

GO_0031214 : biomineral formation

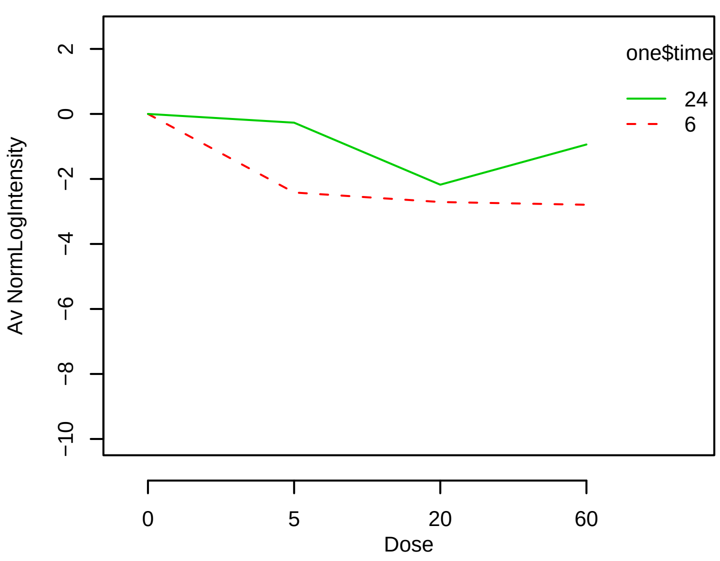

GO_0031268 : pseudopodium organization and biogenesi

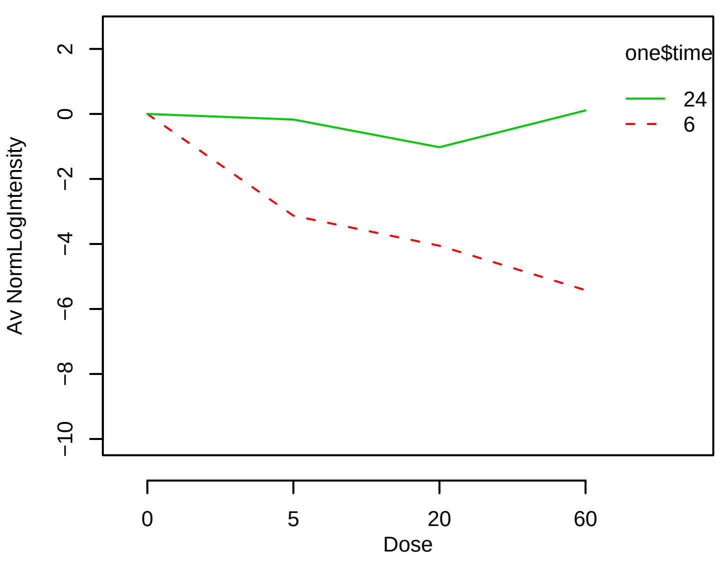

GO_0031269 : pseudopodium formation

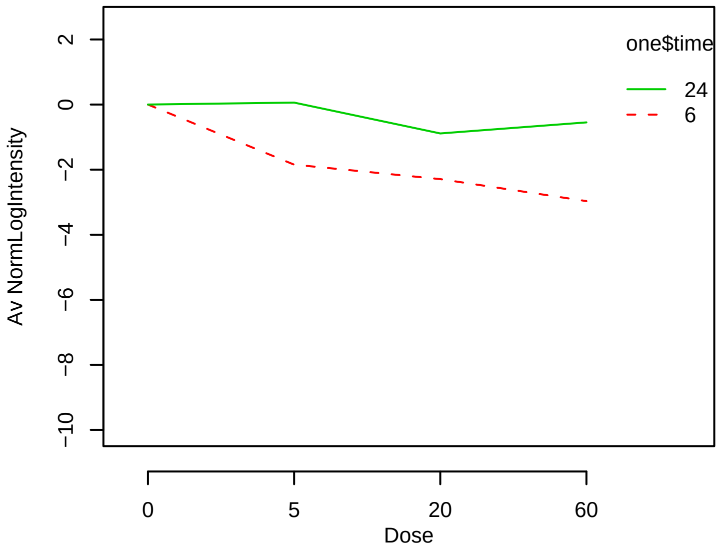

GO_0031272 : regulation of pseudopodium formation

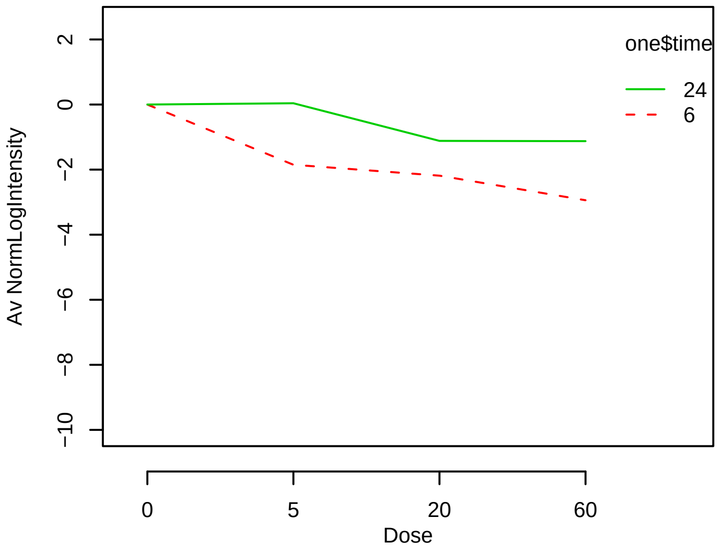

GO_0031274 : positive regulation of pseudopodium formati

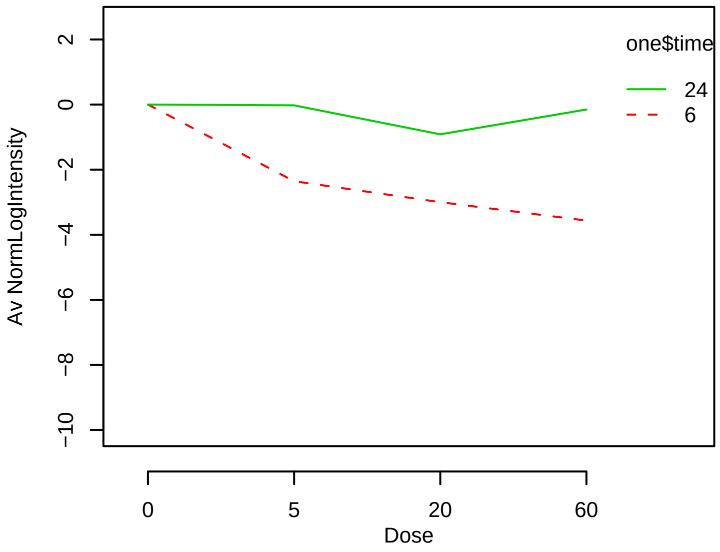

GO_0031279 : regulation of cyclase activity

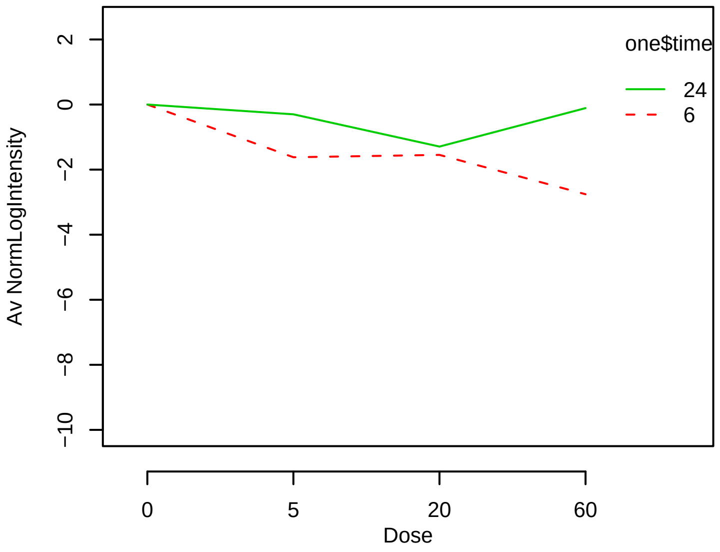

GO_0031280 : negative regulation of cyclase activity

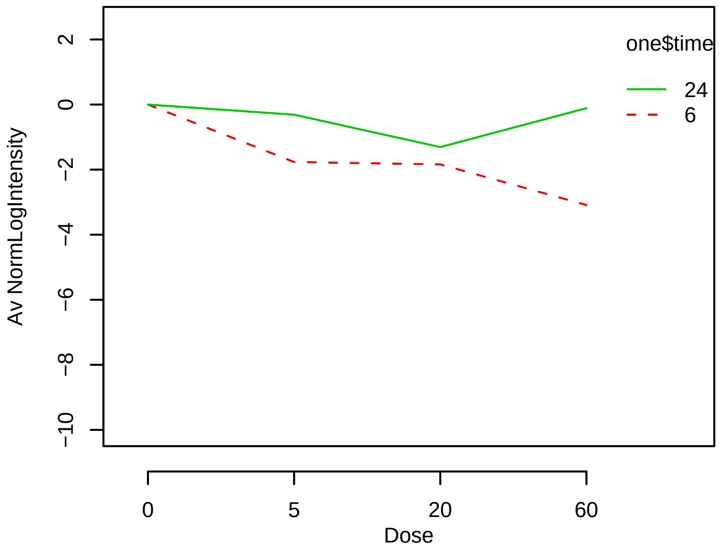

GO_0031281 : positive regulation of cyclase activity

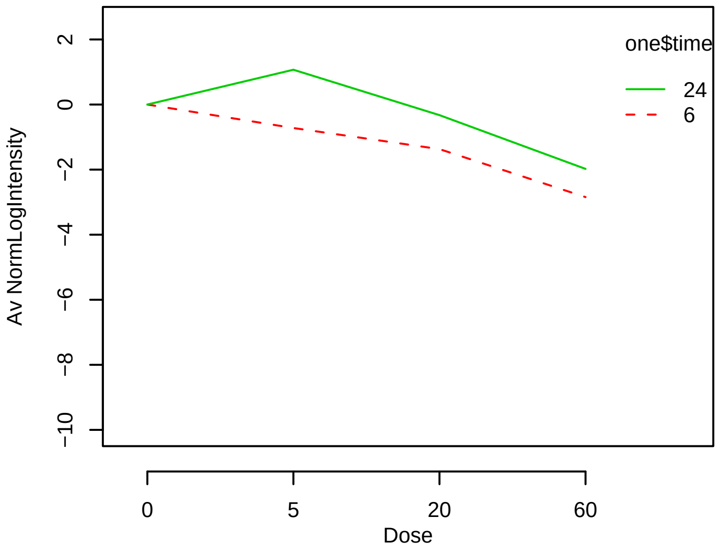

GO_0031326 : regulation of cellular biosynthesis

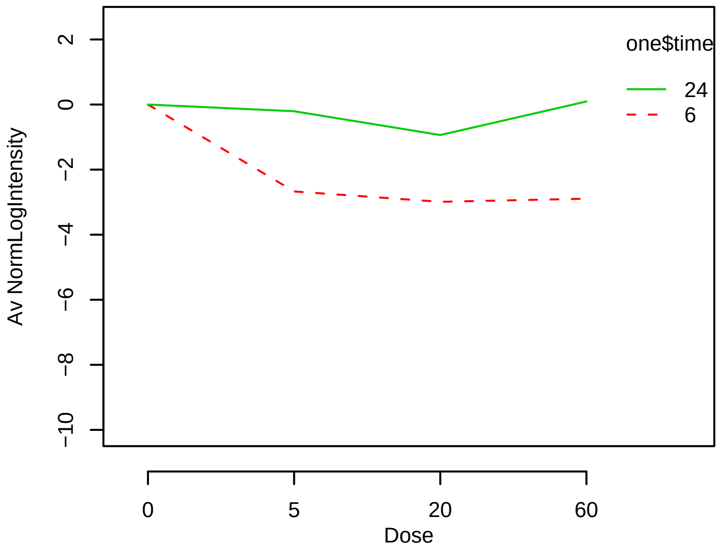

GO_0031327 : negative regulation of cellular biosynthesi

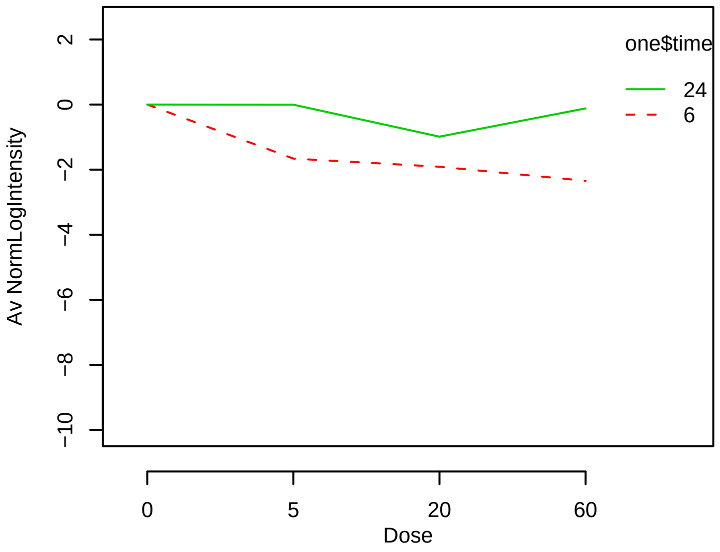

GO_0031328 : positive regulation of cellular biosynthesis

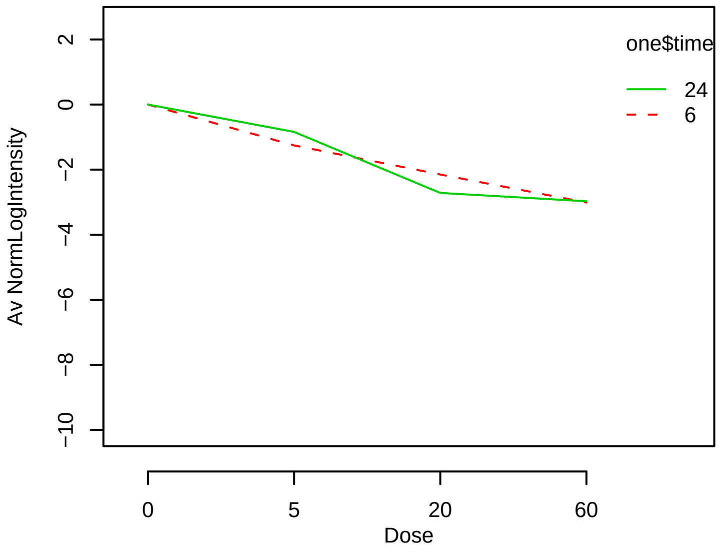

GO_0031344 : regulation of cell projection organization and

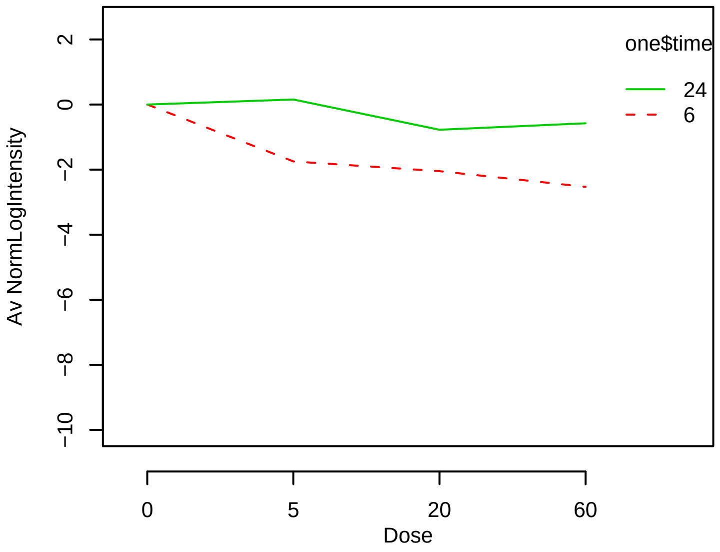

GO_0031346 : positive regulation of cell projection organiza

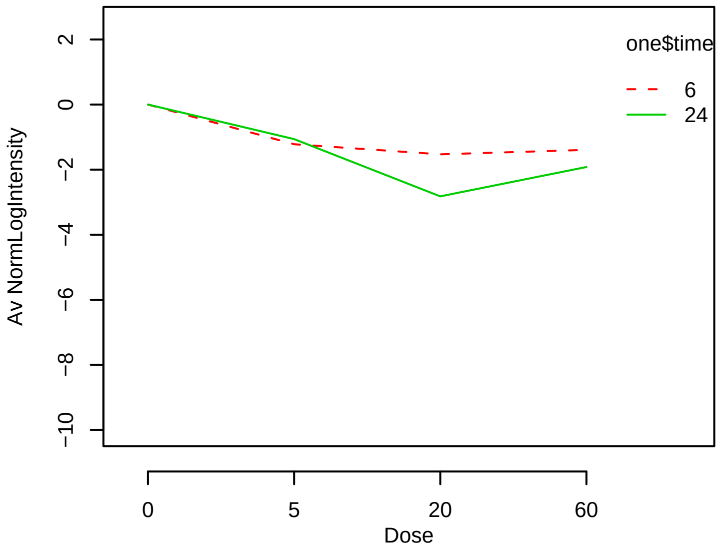

GO_0031365 : N−terminal protein amino acid modificatio

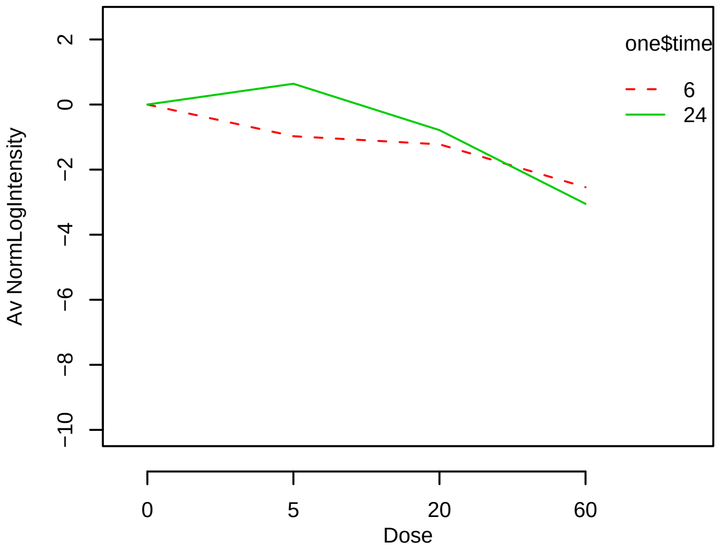

GO_0031424 : keratinization

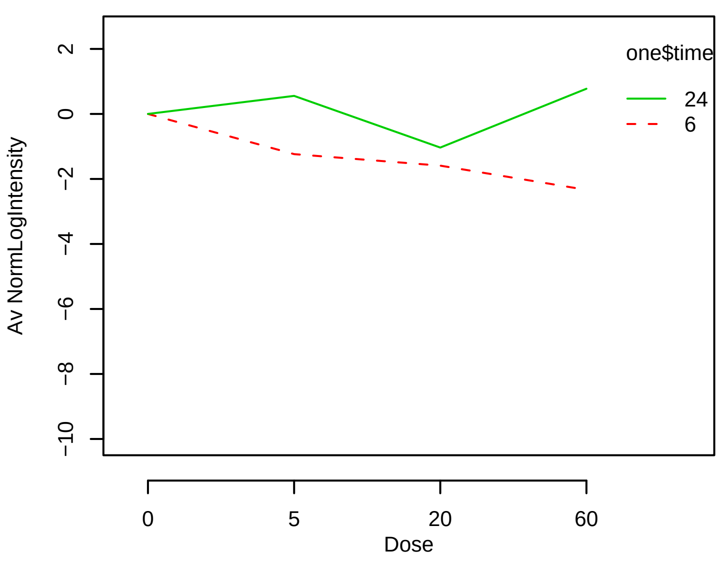

GO_0031497 : chromatin assembly


GO_0031498 : chromatin disassembly

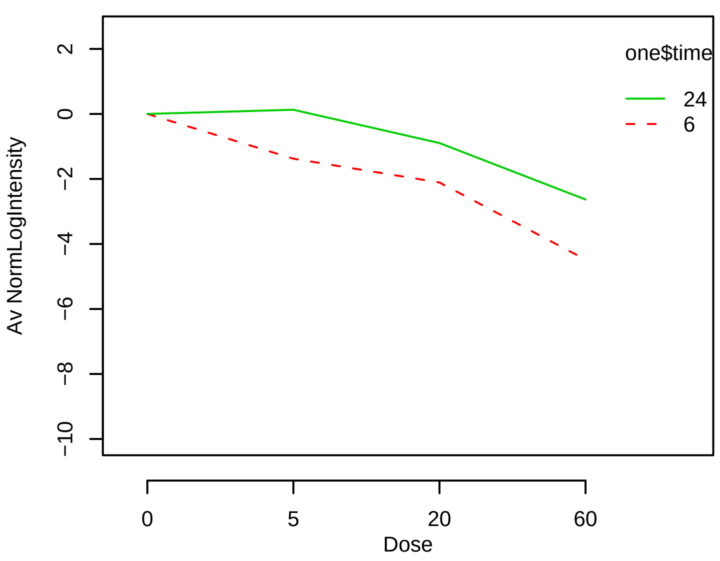

GO_0031507 : heterochromatin formation


GO_0031532 : actin cytoskeleton reorganization

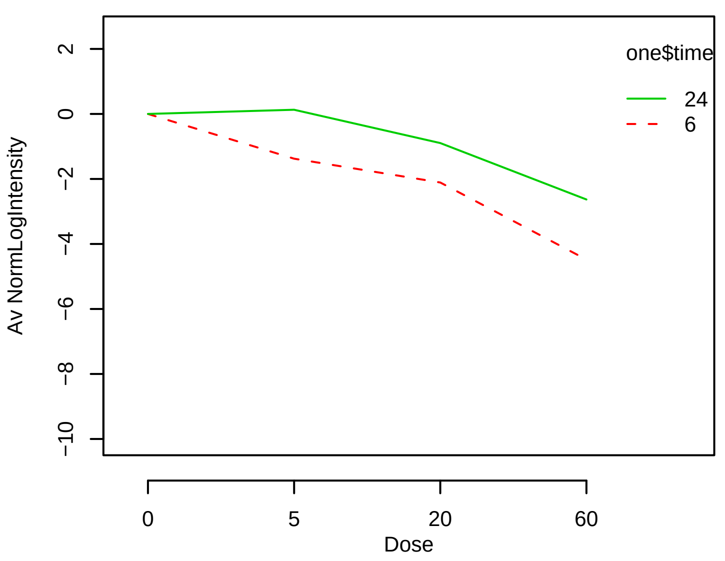

GO_0031570 : DNA integrity checkpoint



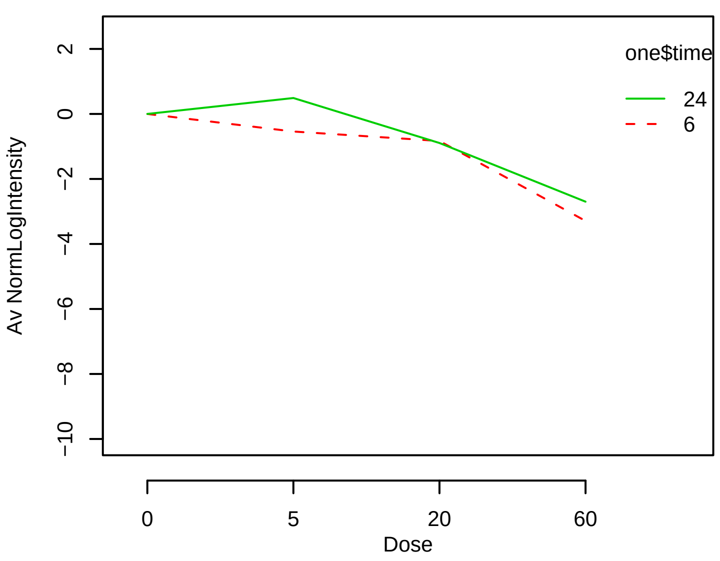
GO_0031571 : G1 DNA damage checkpoint



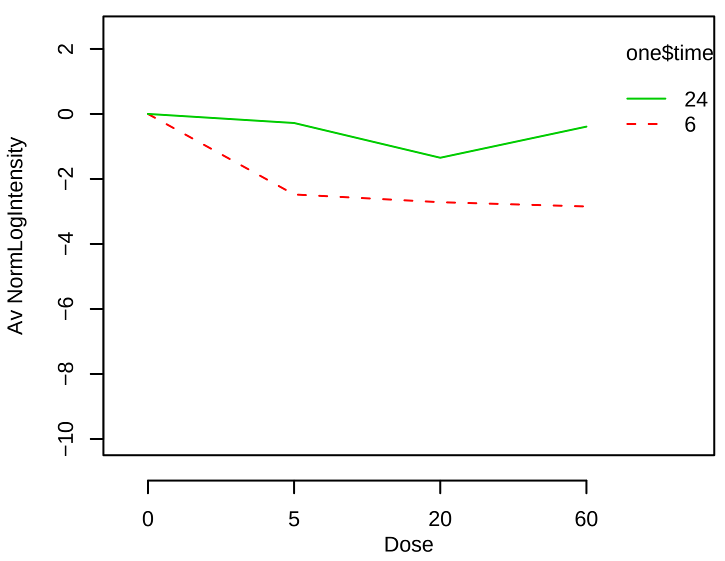
GO_0031572 : G2/M transition DNA damage checkpoint



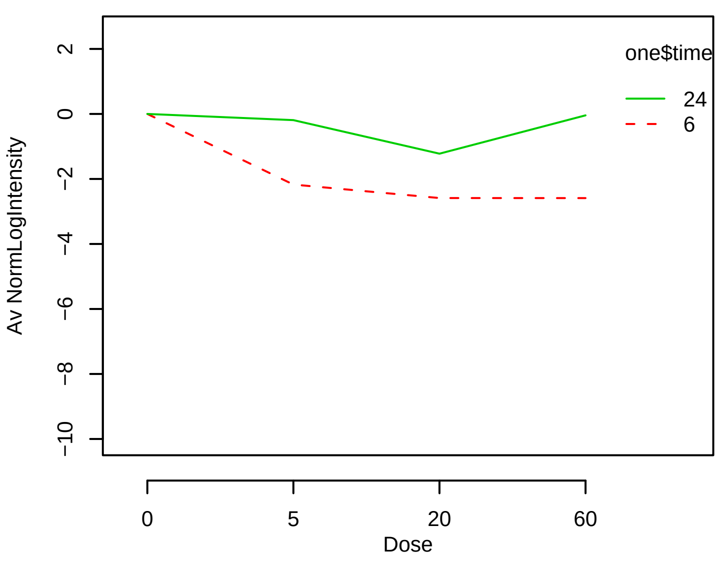
GO_0031576 : G2/M transition checkpoint



GO_0031577 : spindle checkpoint

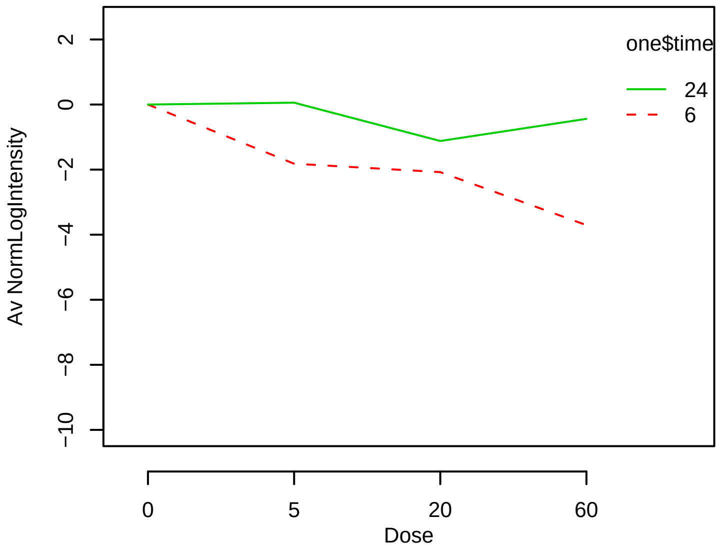


GO_0031589 : cell−substrate adhesion

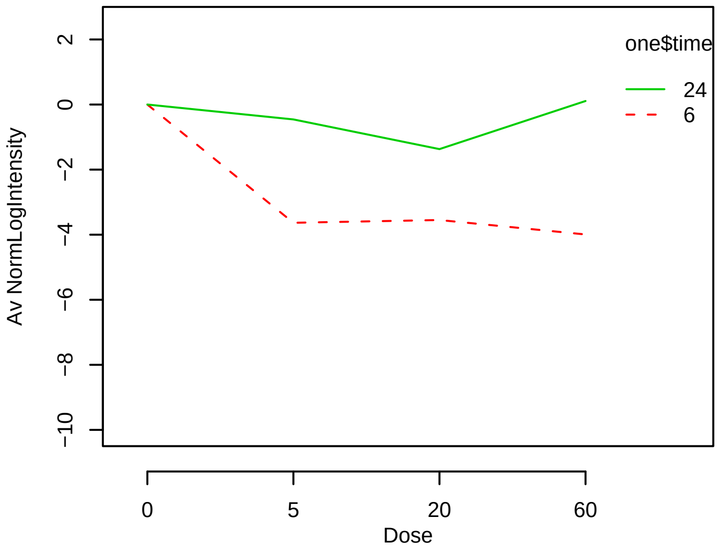


GO_0031644 : regulation of neurophysiological process

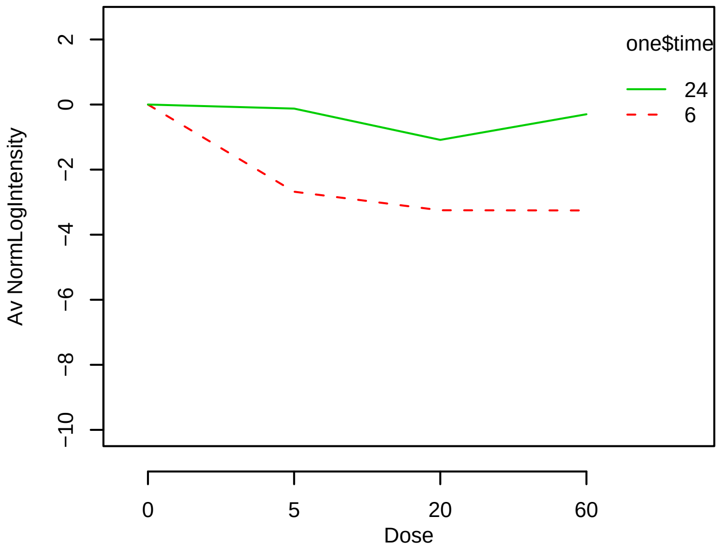
GO_0031647 : regulation of protein stability



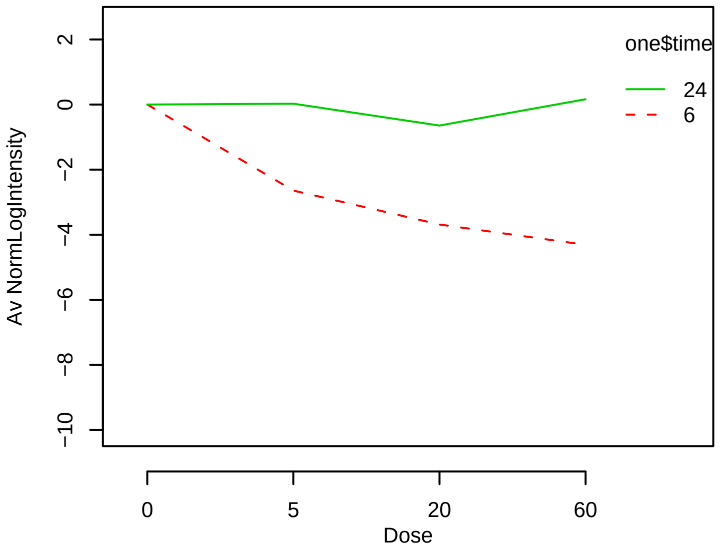
GO_0031649 : heat generation



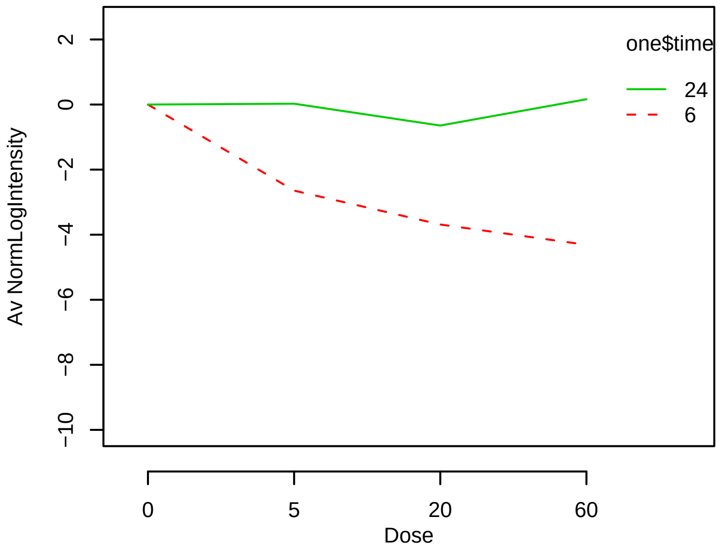
GO_0031667 : response to nutrient levels



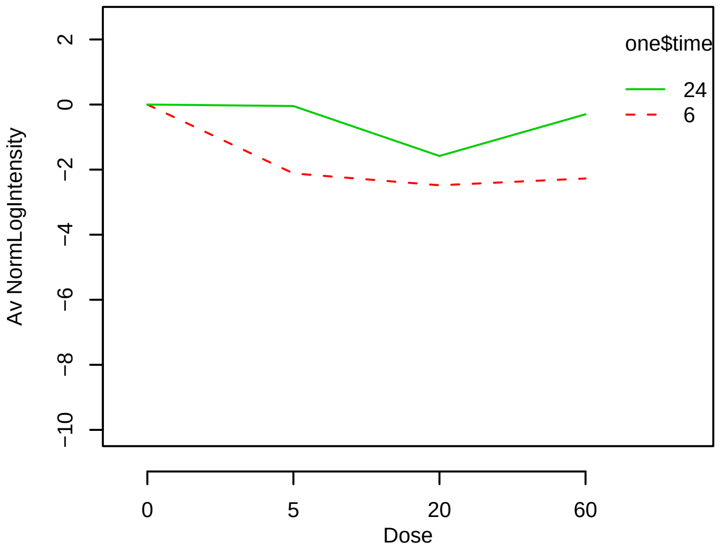
GO_0031668 : cellular response to extracellular stimulus



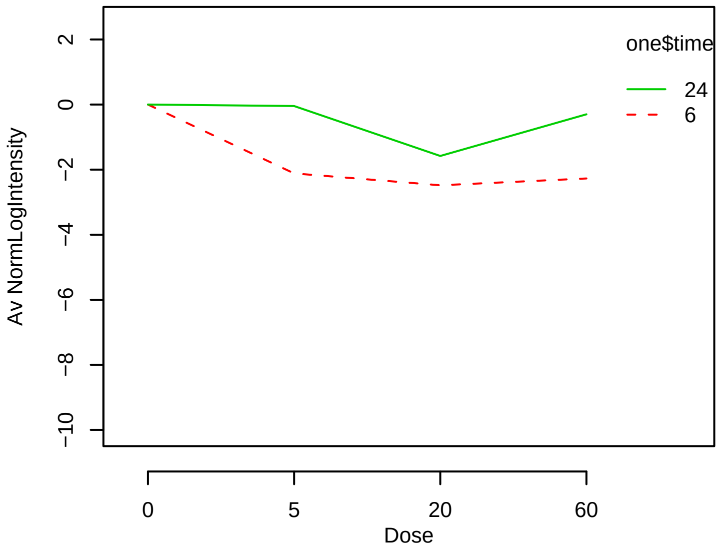
GO_0031669 : cellular response to nutrient levels



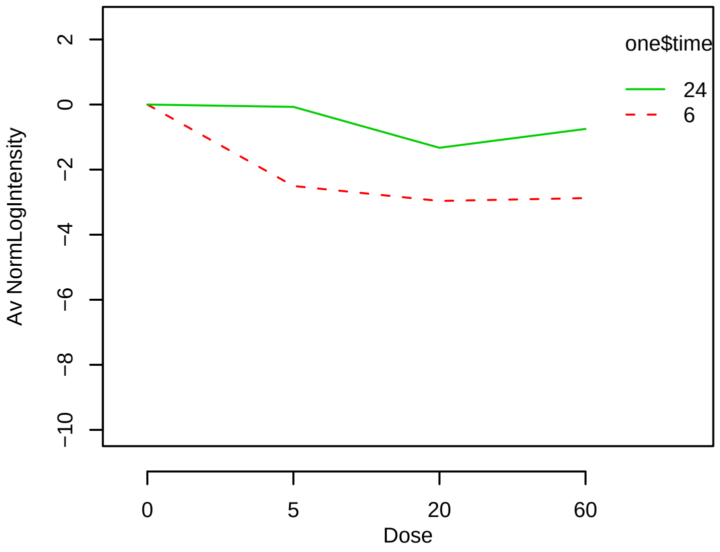
GO_0032011 : ARF protein signal transduction



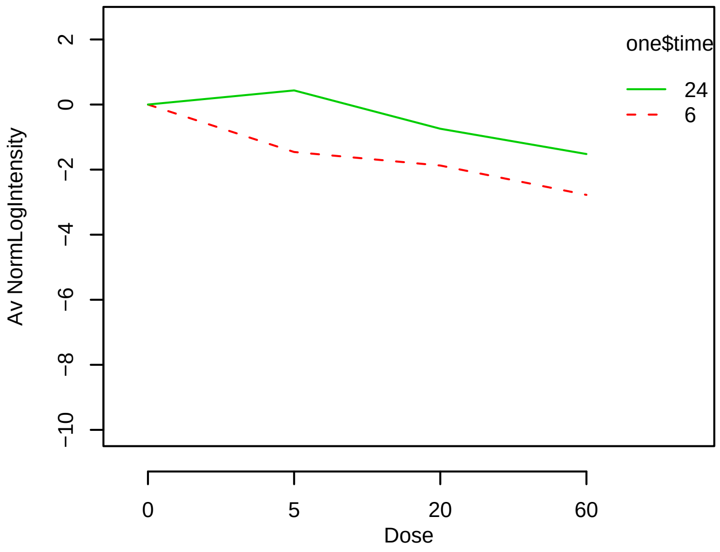
GO_0032012 : regulation of ARF protein signal transductio



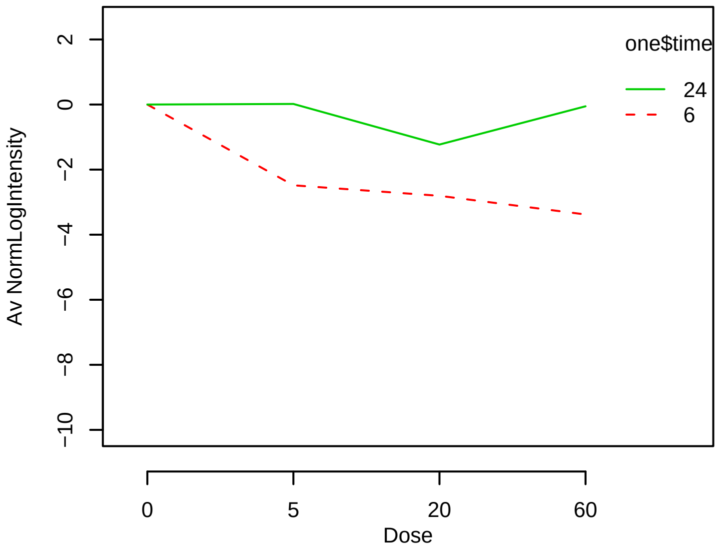
GO_0032147 : activation of protein kinase activity



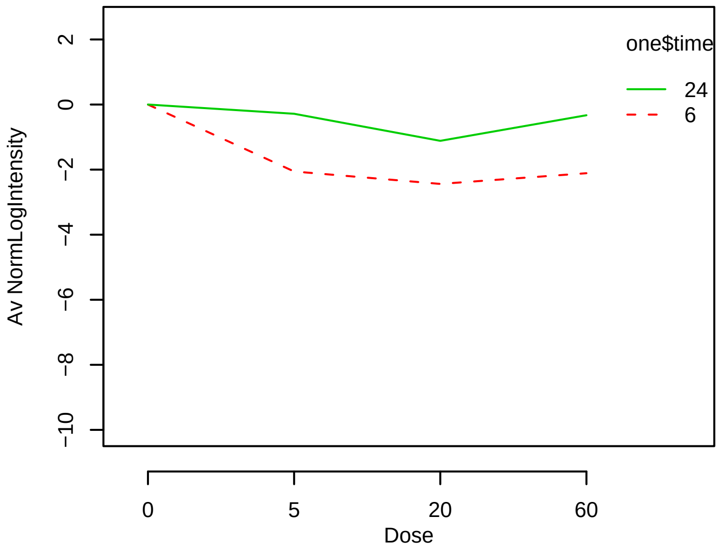
GO_0032200 : telomere organization and biogenesis



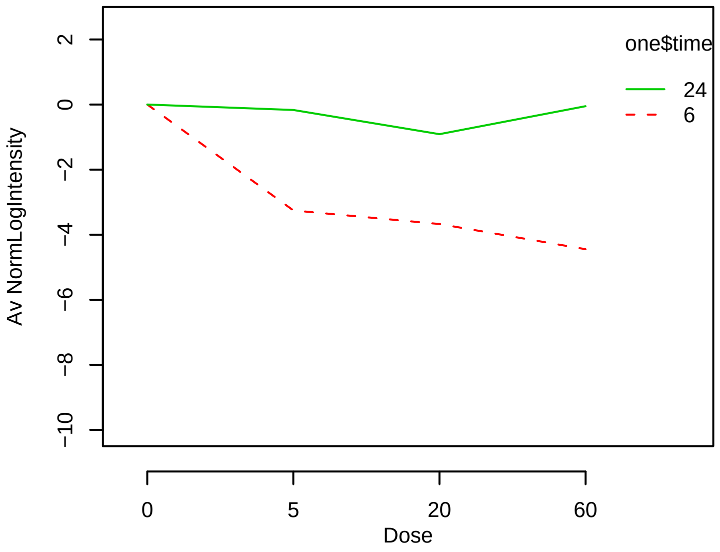
GO_0035023 : regulation of Rho protein signal transductio



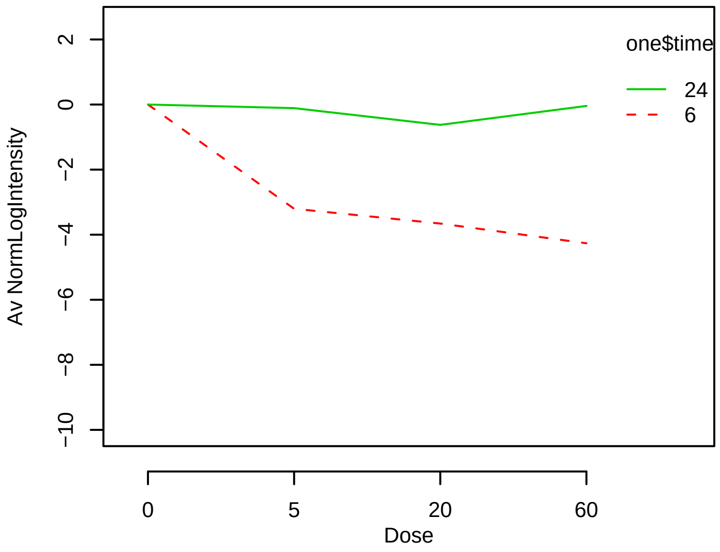
GO_0035036 : sperm−egg recognition



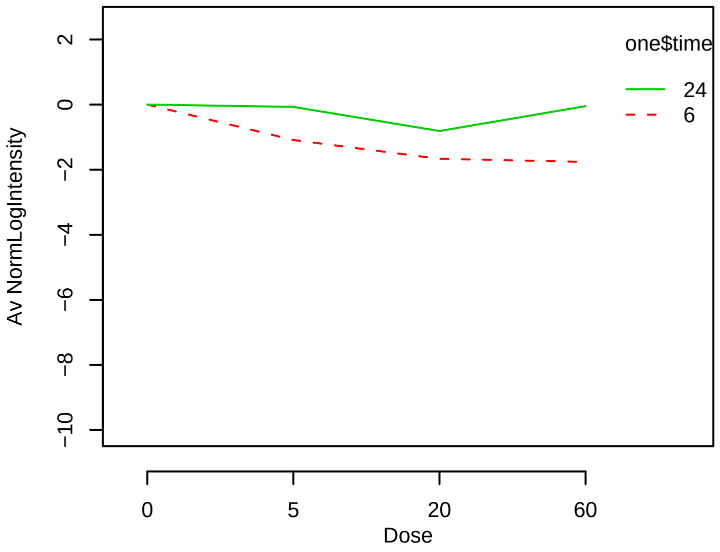
GO_0035050 : embryonic heart tube development



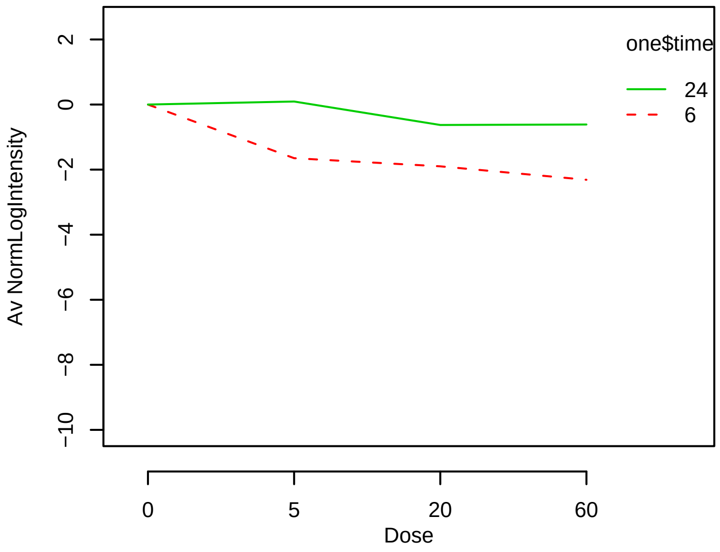
GO_0035051 : cardiac cell differentiation



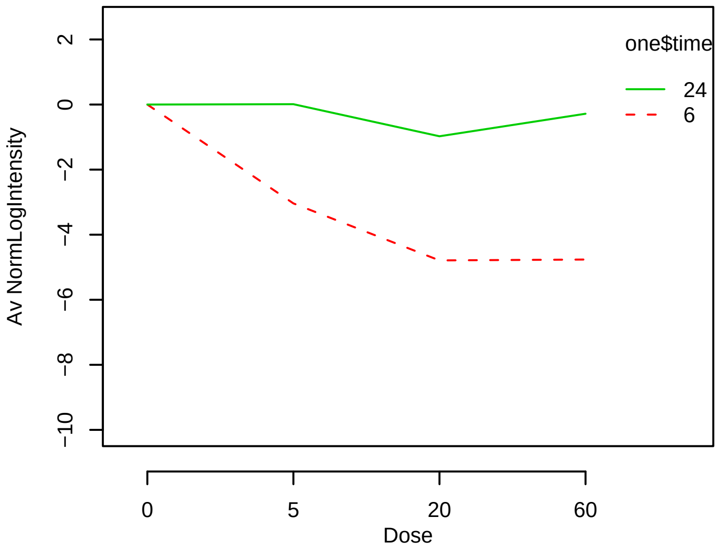
GO_0035058 : sensory cilium biogenesis



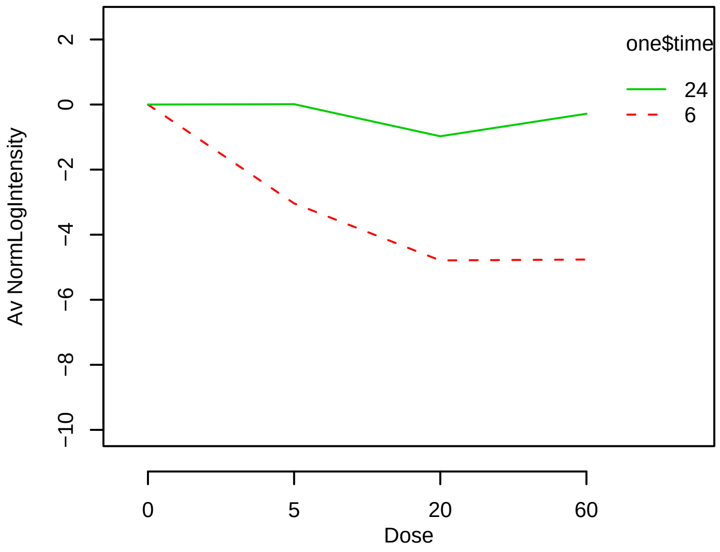
O_0035088 : establishment and/or maintenance of apical/ba



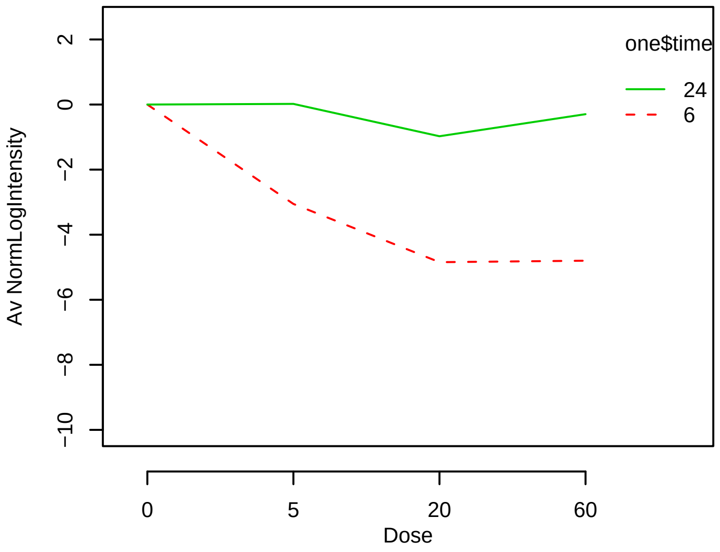
GO_0035107 : appendage morphogenesis

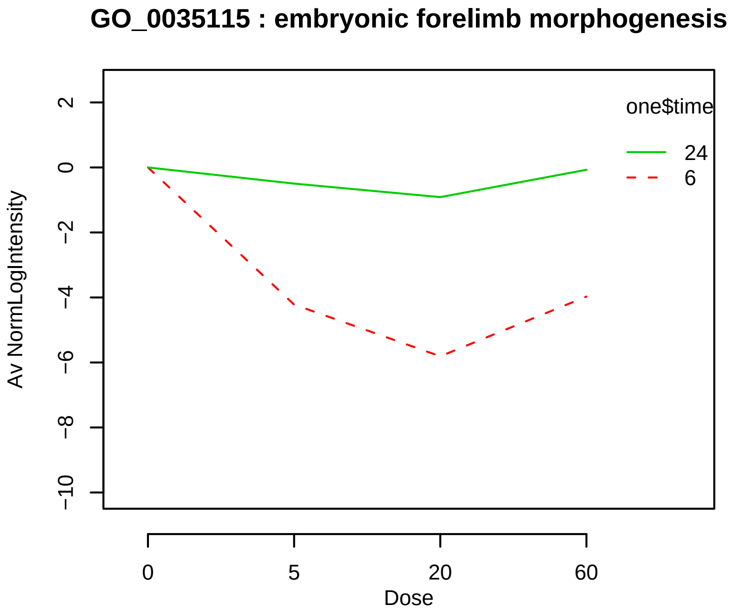


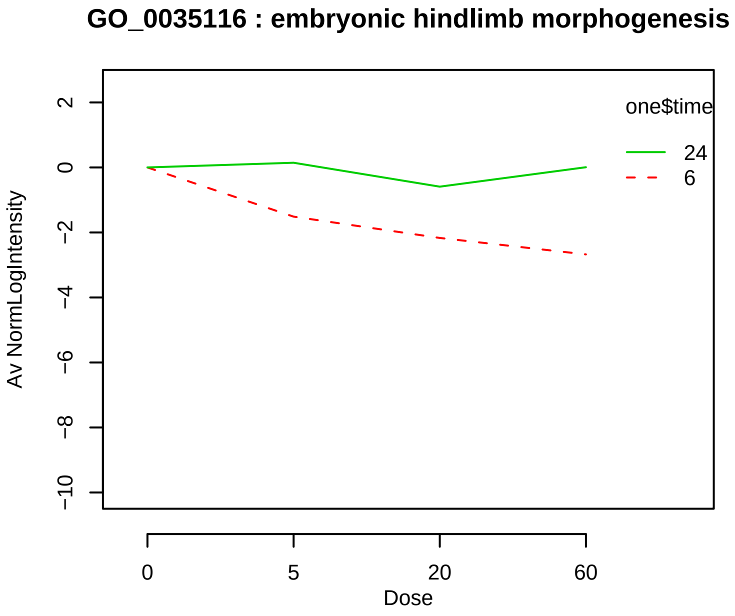
GO_0035108 : limb morphogenesis

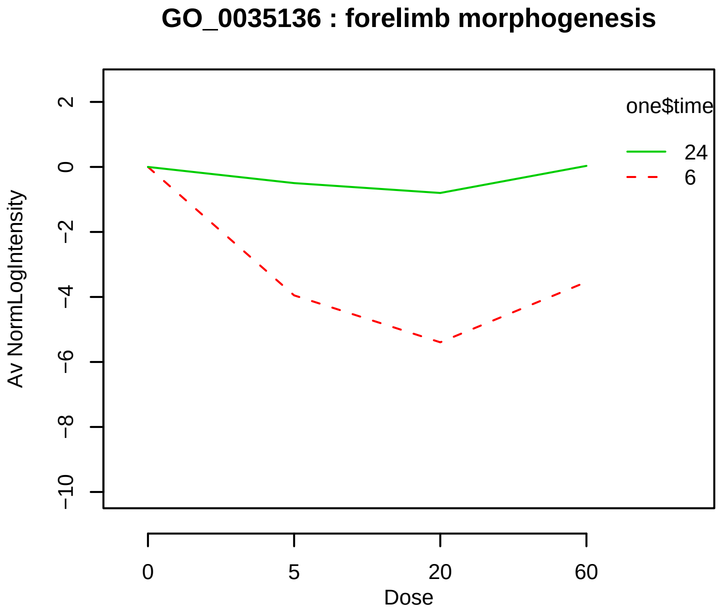


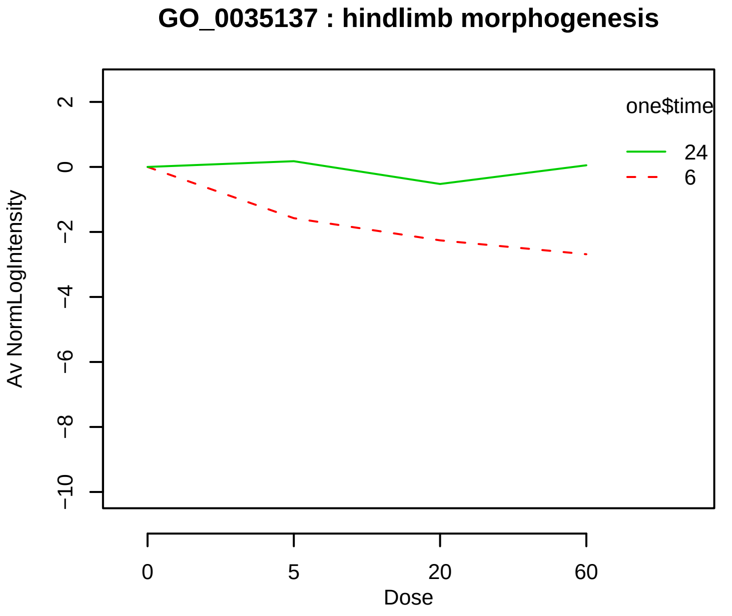
GO_0035113 : embryonic appendage morphogenesis



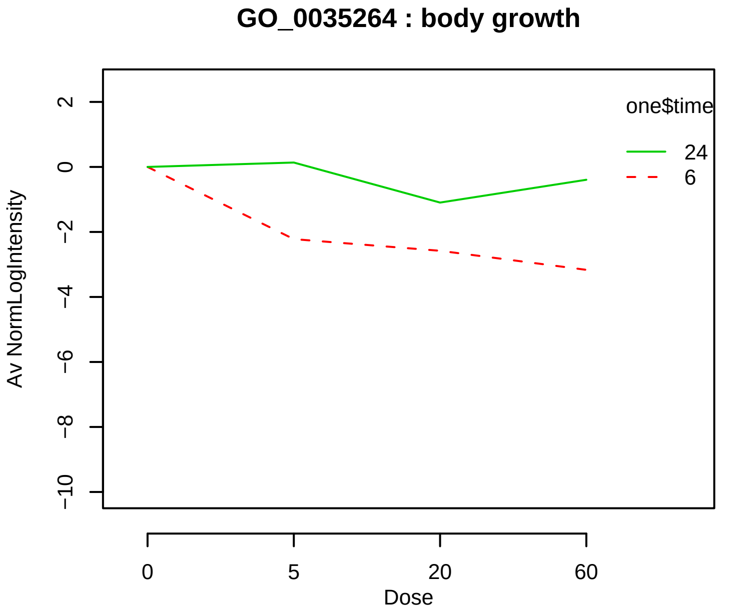

GO_0035115 : embryonic forelimb morphogenesis

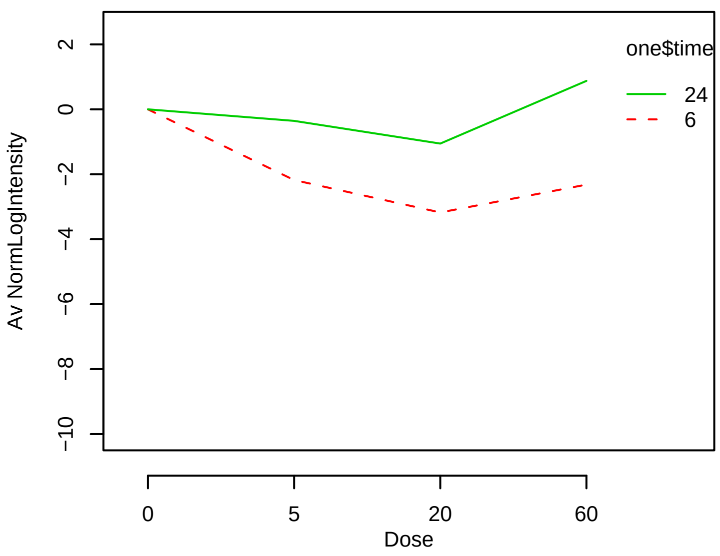

GO_0035116 : embryonic hindlimb morphogenesis

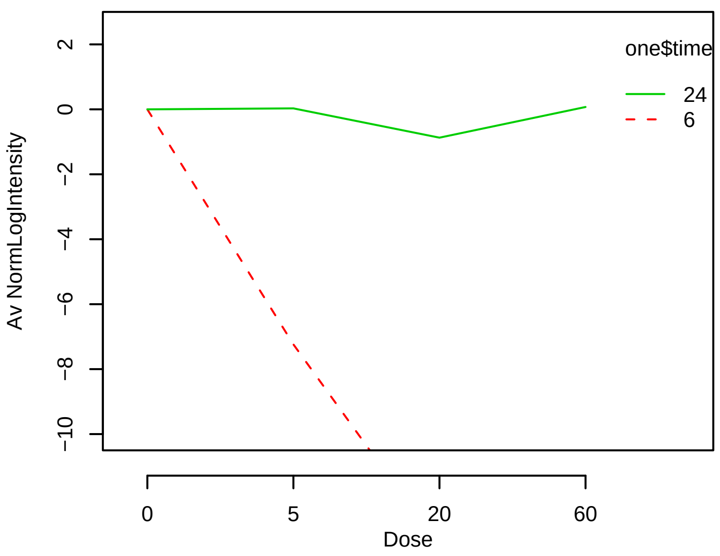

GO_0035136 : forelimb morphogenesis

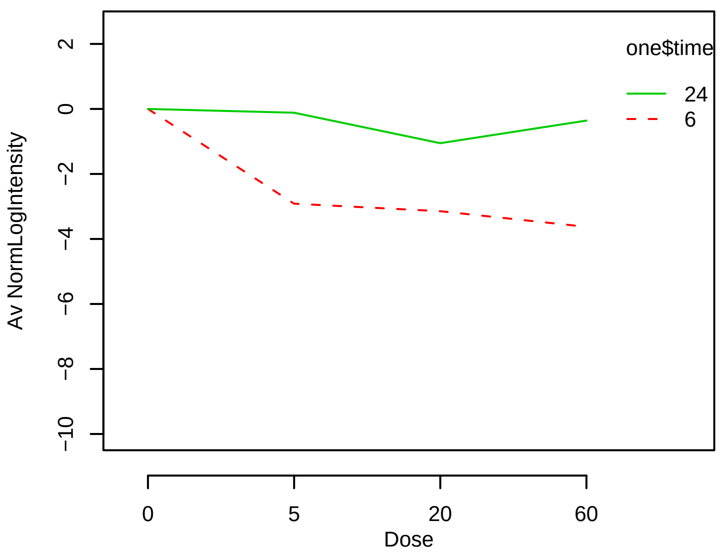

GO_0035137 : hindlimb morphogenesis

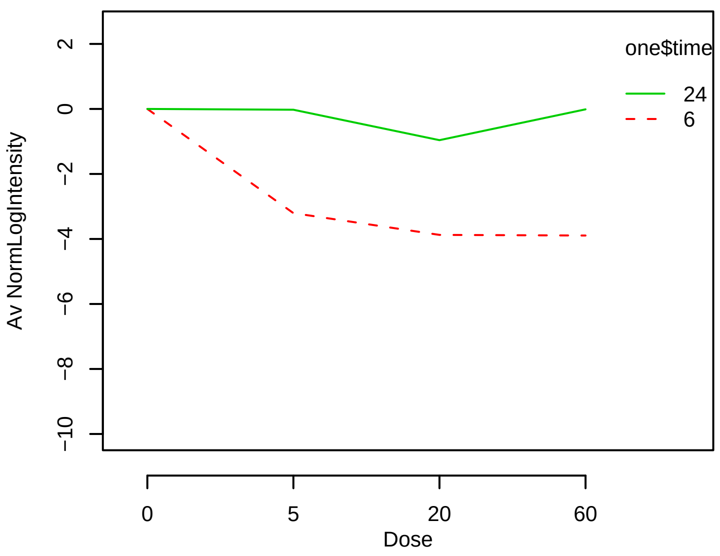

GO_0035239 : tube morphogenesis

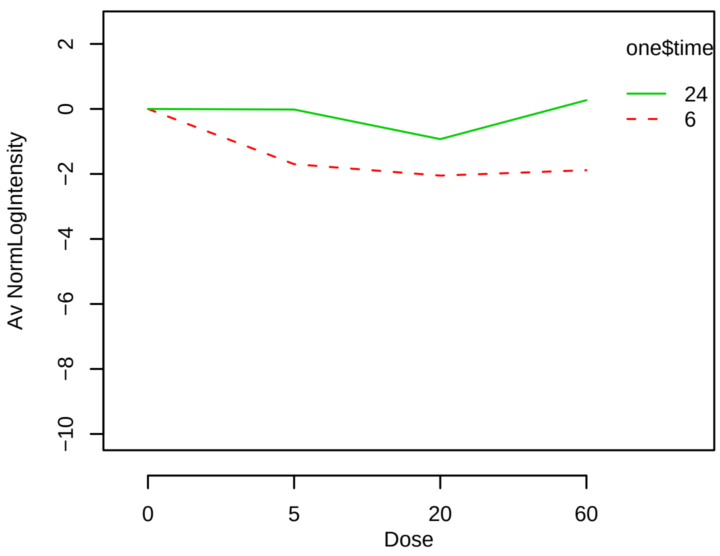

GO_0035264 : body growth

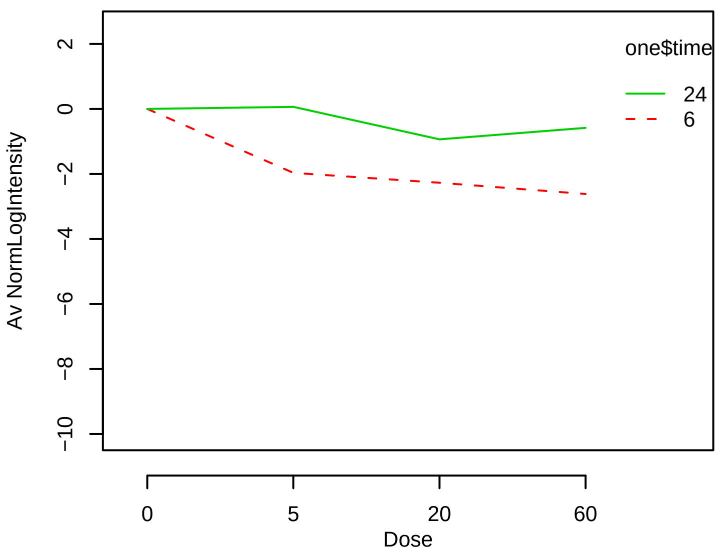

GO_0035270 : endocrine system development


GO_0035272 : exocrine system development

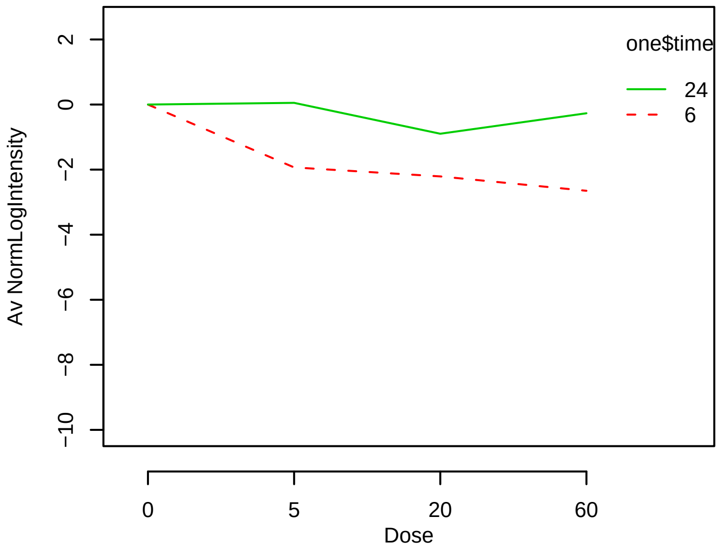

GO_0035282 : segmentation


GO_0035295 : tube development

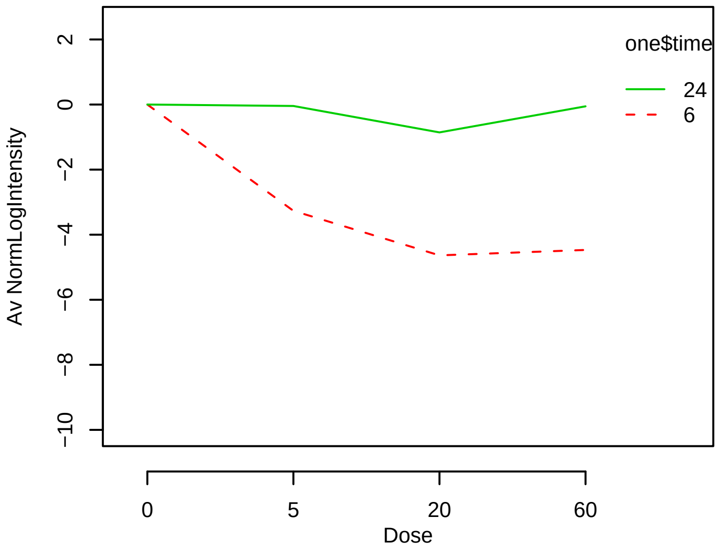

GO_0035315 : hair cell differentiation


GO_0040007 : growth

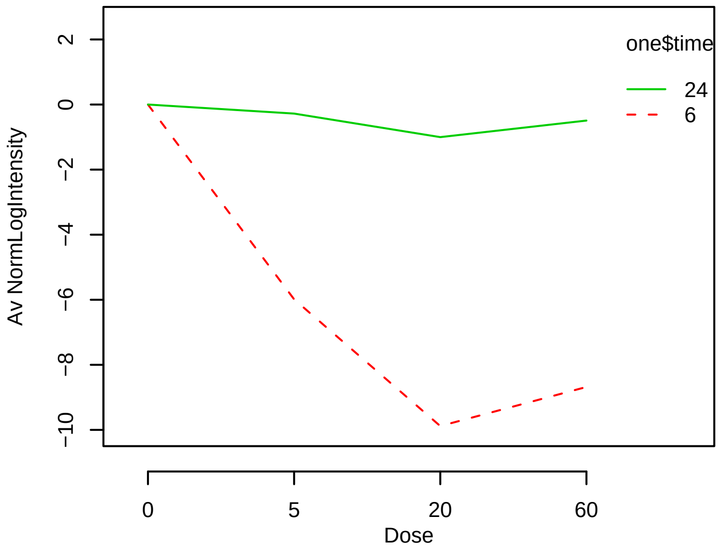
GO_0040008 : regulation of growth



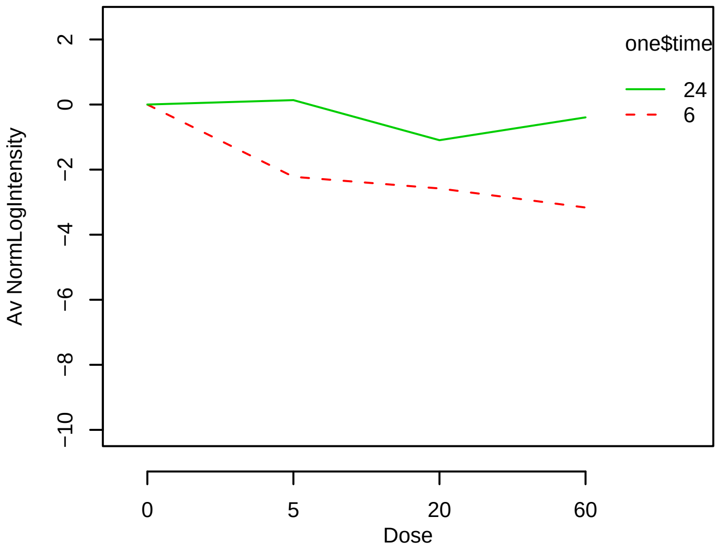
GO_0040012 : regulation of locomotion



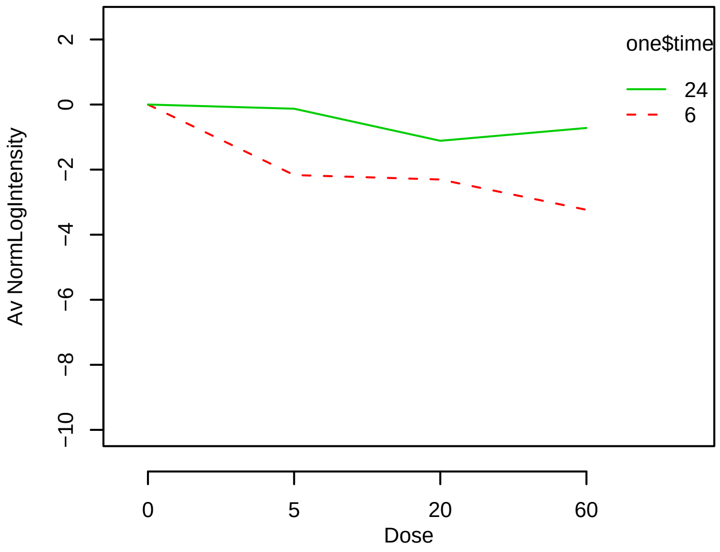
GO_0040013 : negative regulation of locomotion



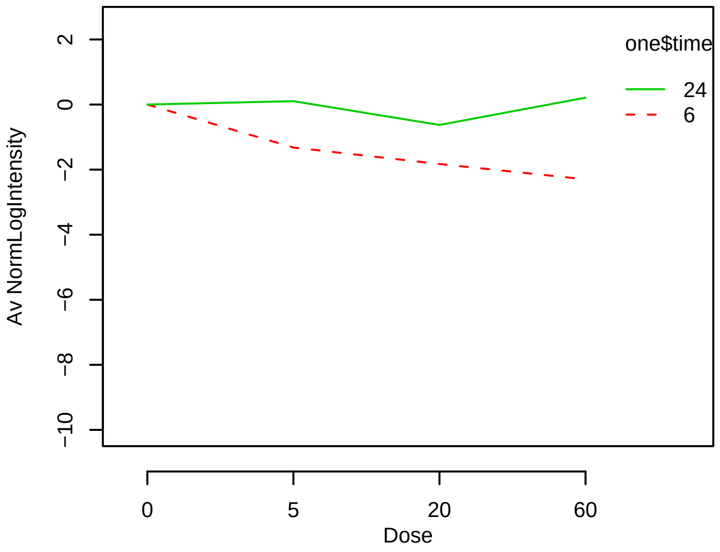
GO_0040014 : regulation of body size

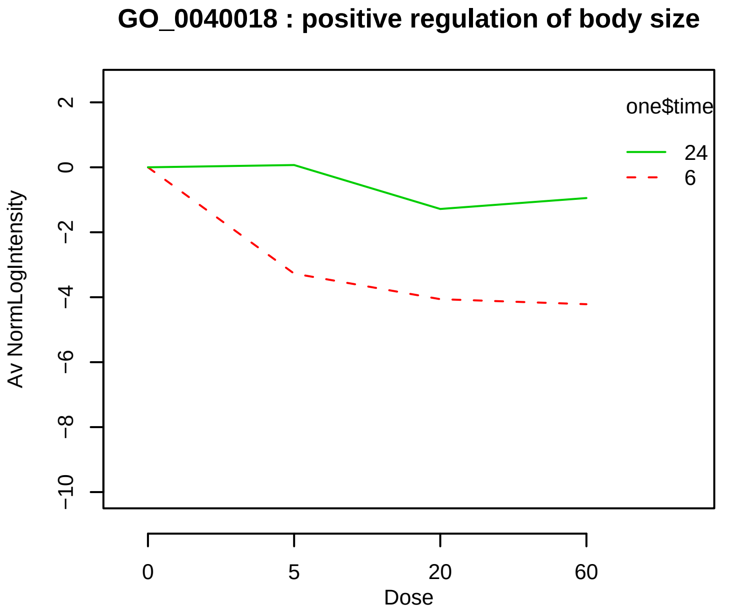


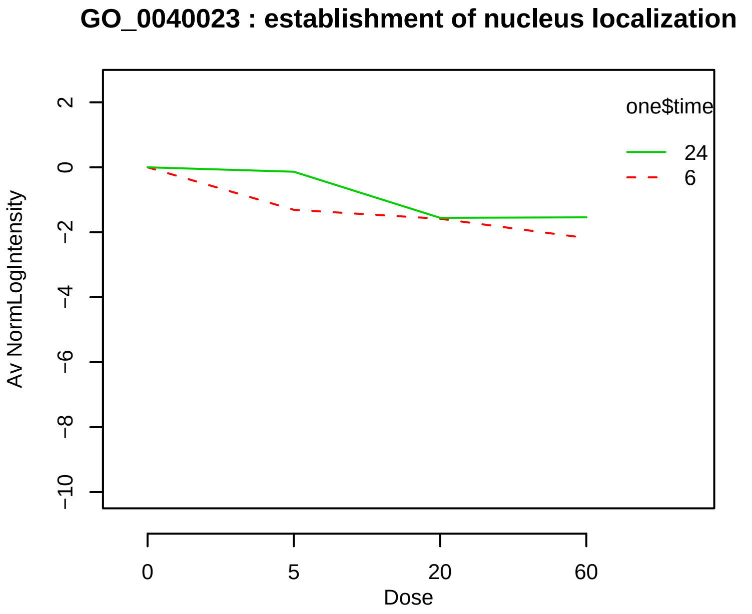
GO_0040015 : negative regulation of body size

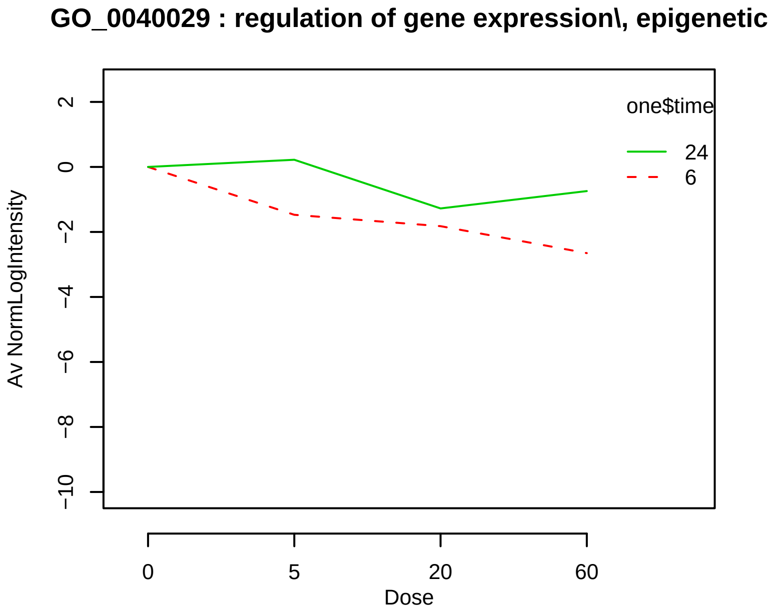


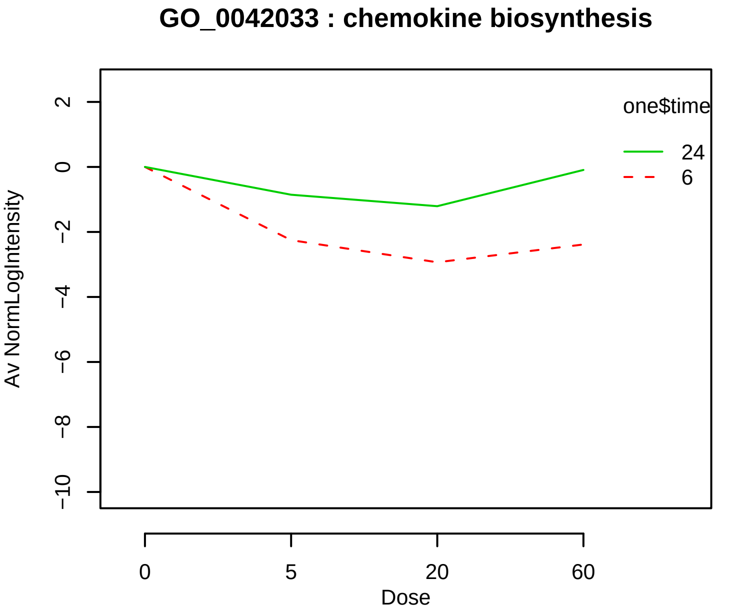
GO_0040017 : positive regulation of locomotion

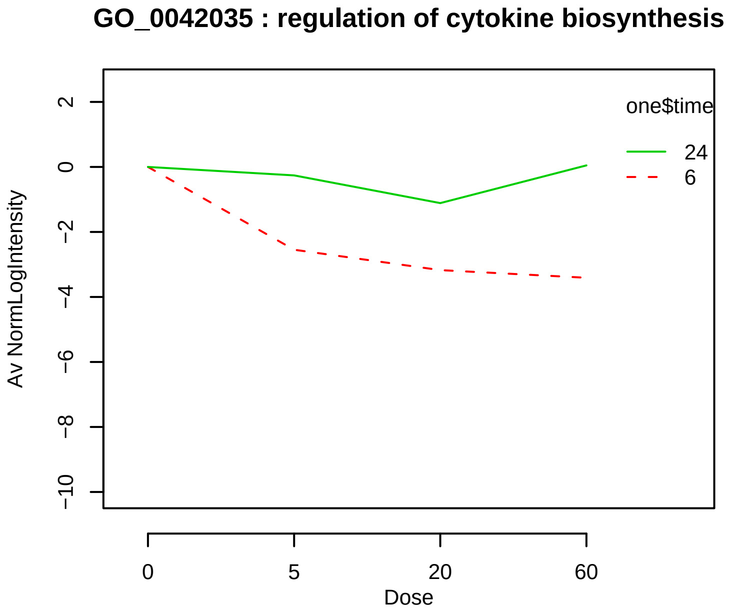


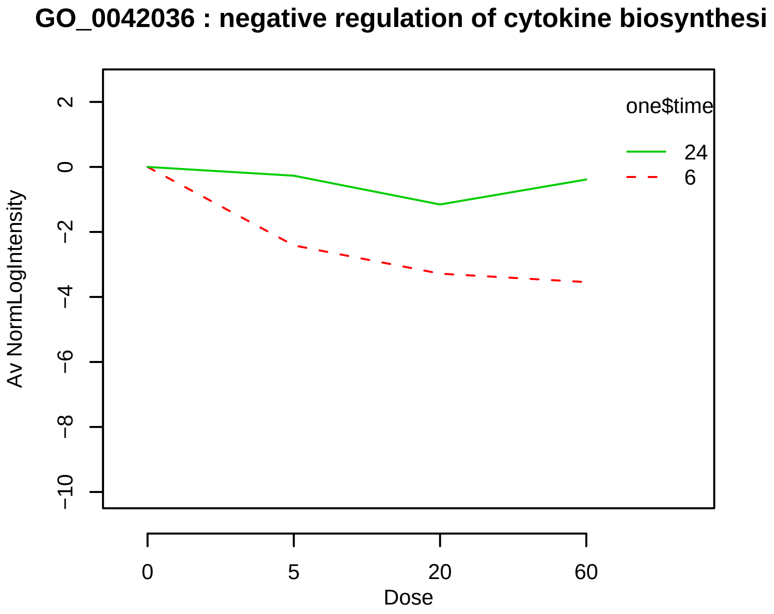

GO_0040018 : positive regulation of body size


GO_0040023 : establishment of nucleus localization

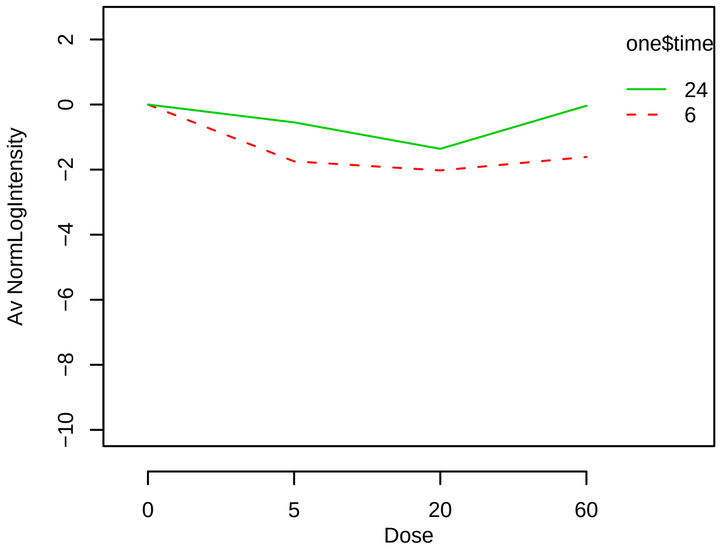

GO_0040029 : regulation of gene expression\, epigenetic


GO_0042033 : chemokine biosynthesis

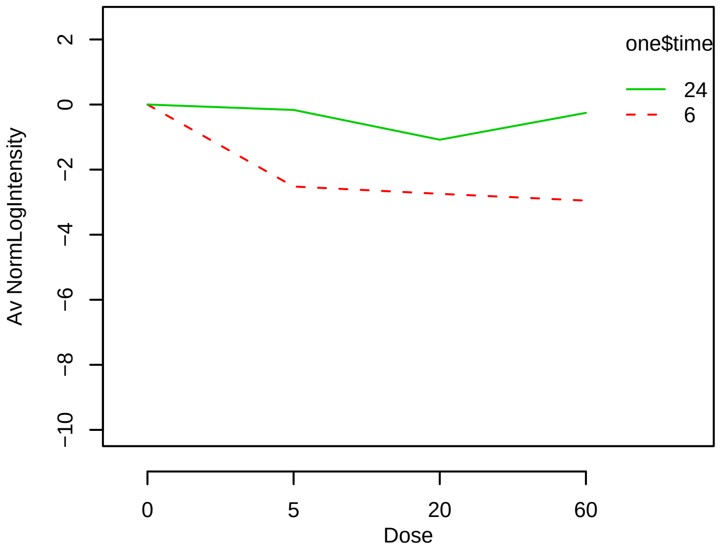

GO_0042035 : regulation of cytokine biosynthesis


GO_0042036 : negative regulation of cytokine biosynthesi

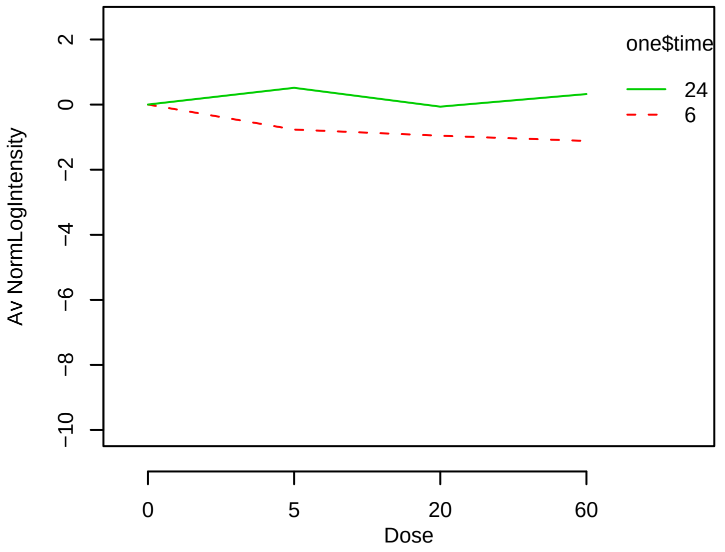
GO_0042044 : fluid transport



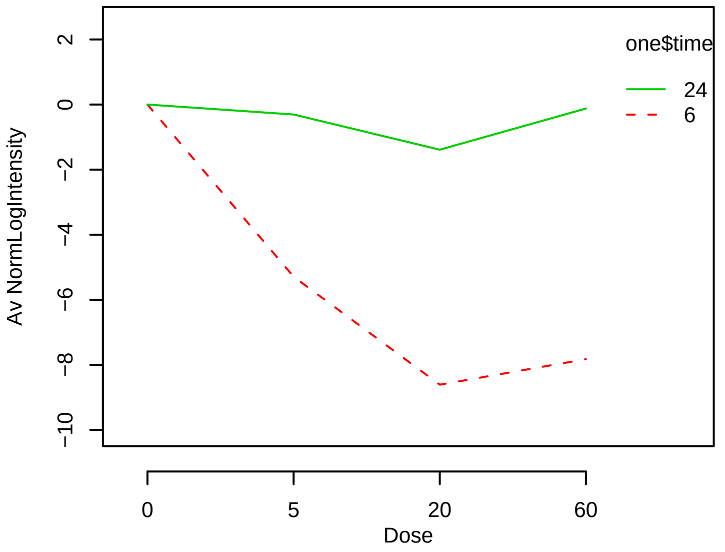
GO_0042060 : wound healing



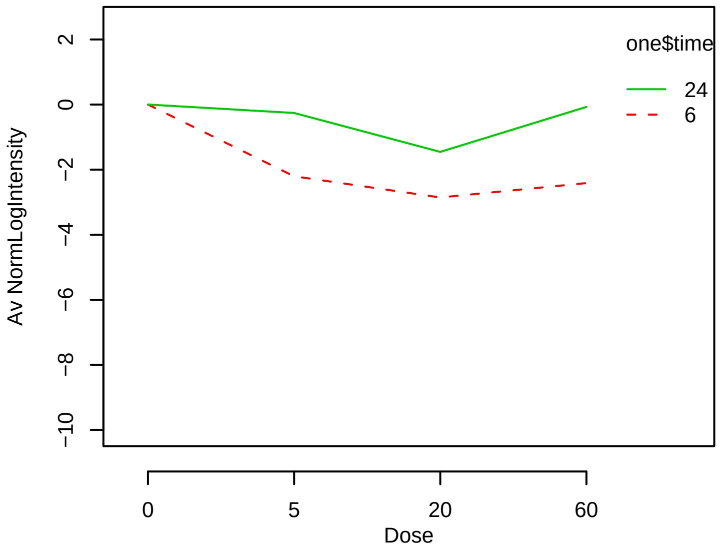
O_0042062 : long−term strengthening of neuromuscular jun



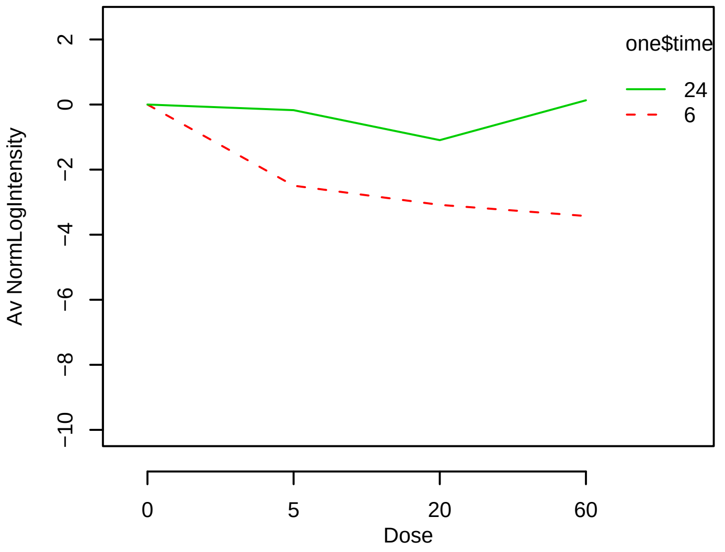
GO_0042063 : gliogenesis

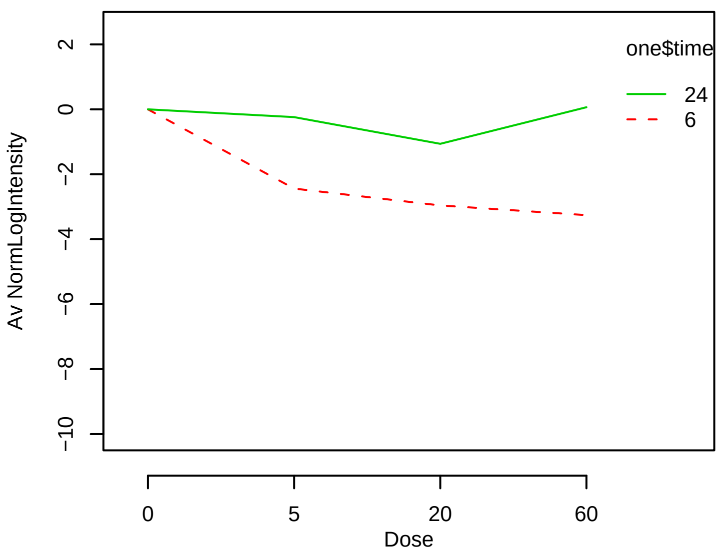


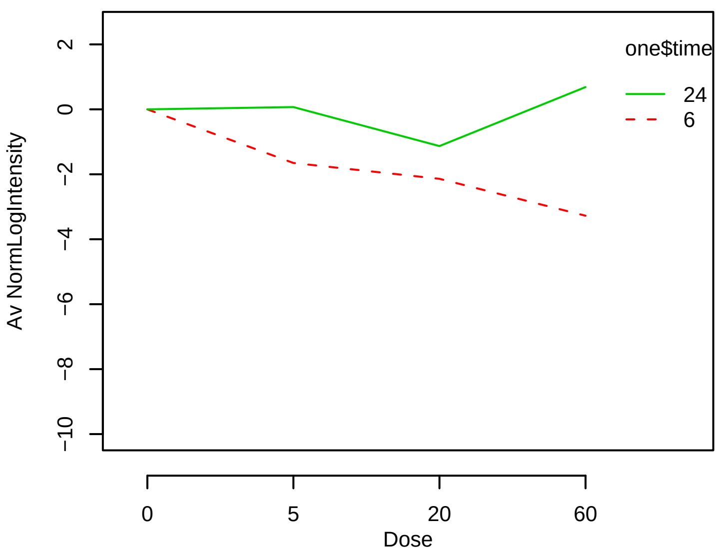
GO_0042074 : cell migration involved in gastrulation

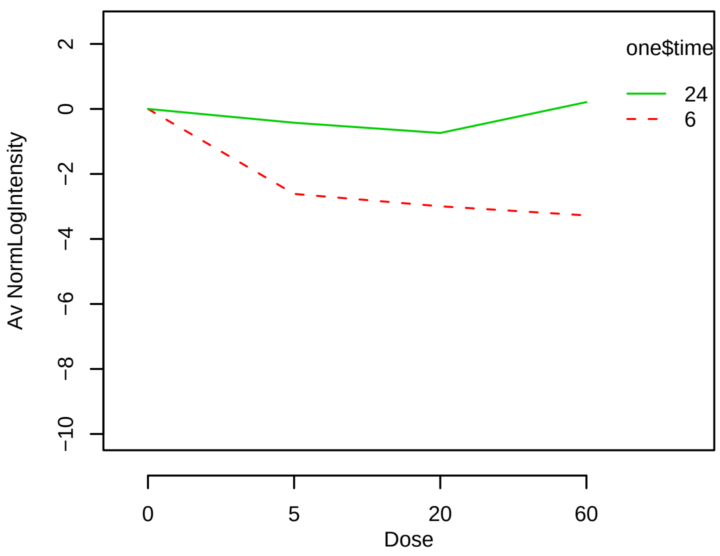


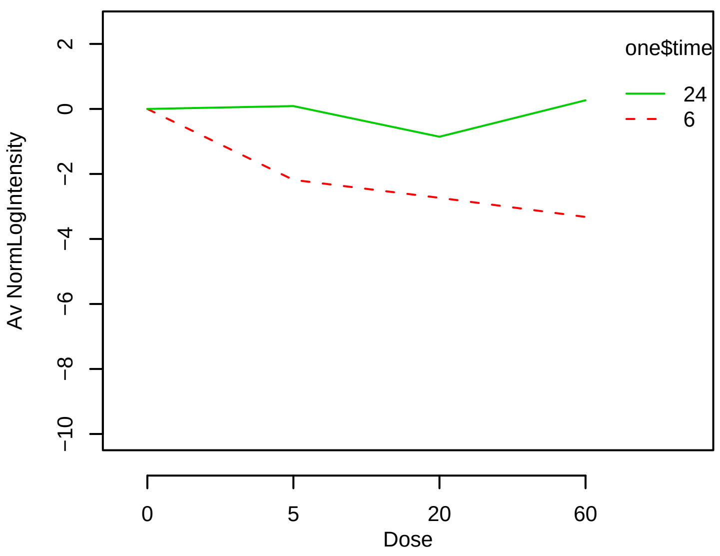
GO_0042088 : T−helper 1 type immune response

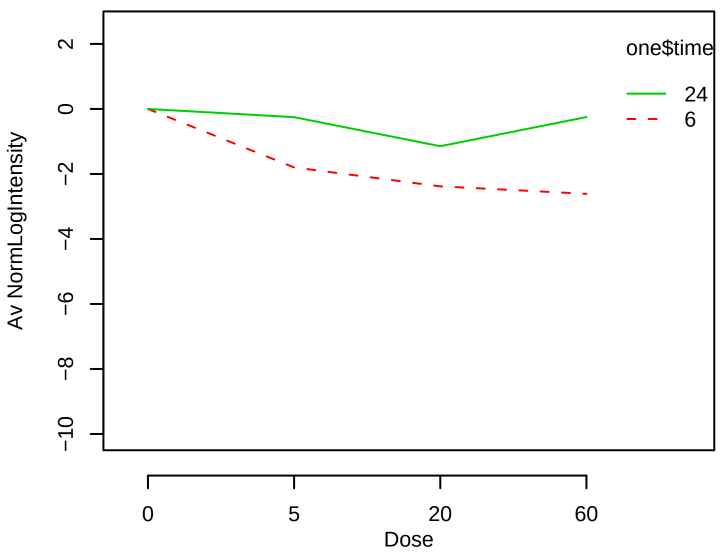


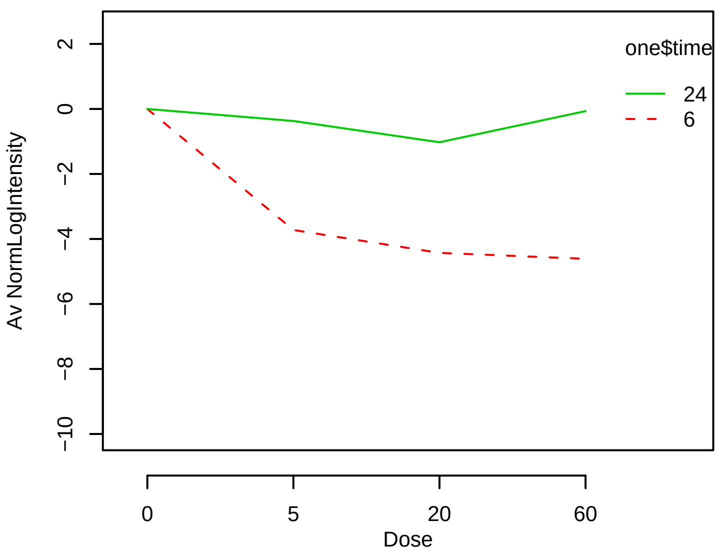

GO_0042089 : cytokine biosynthesis


GO_0042090 : interleukin−12 biosynthesis

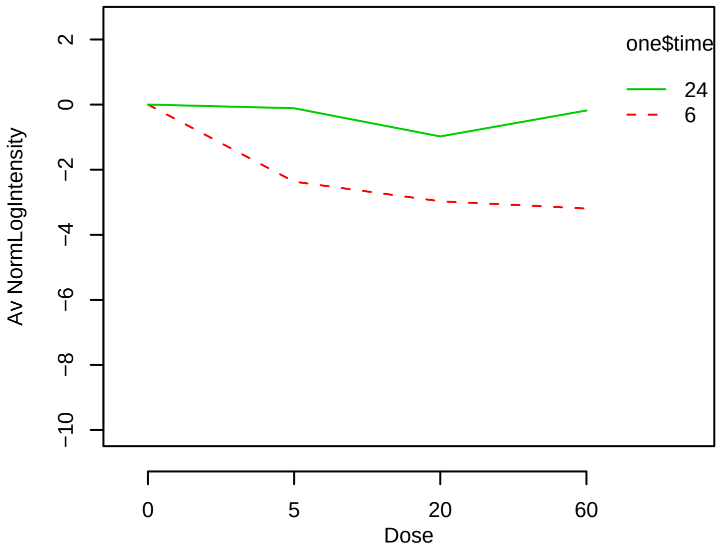

GO_0042092 : T−helper 2 type immune response


GO_0042093 : T−helper cell differentiation

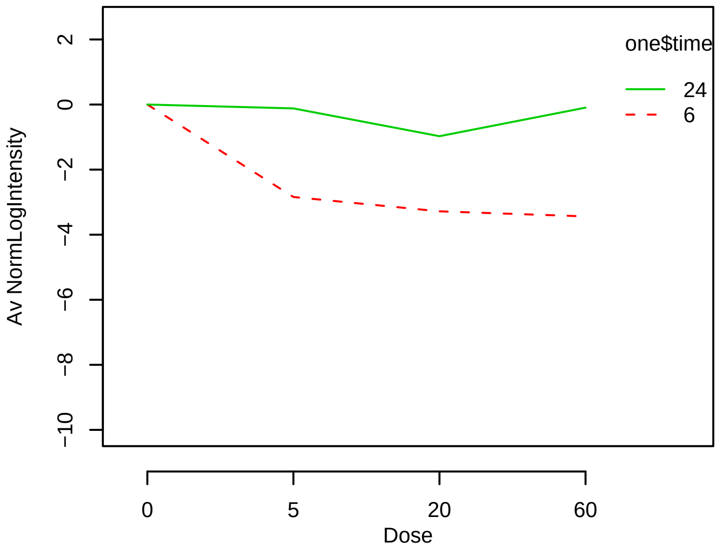

GO_0042094 : interleukin−2 biosynthesis


GO_0042095 : interferon−gamma biosynthesis

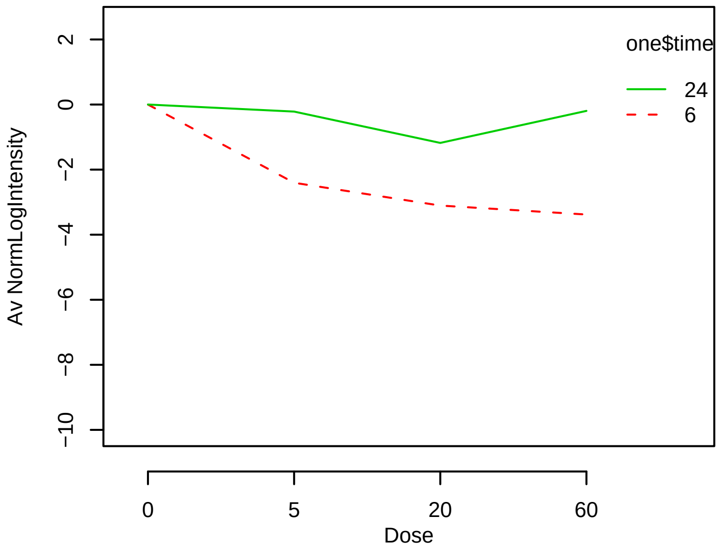
GO_0042098 : T cell proliferation



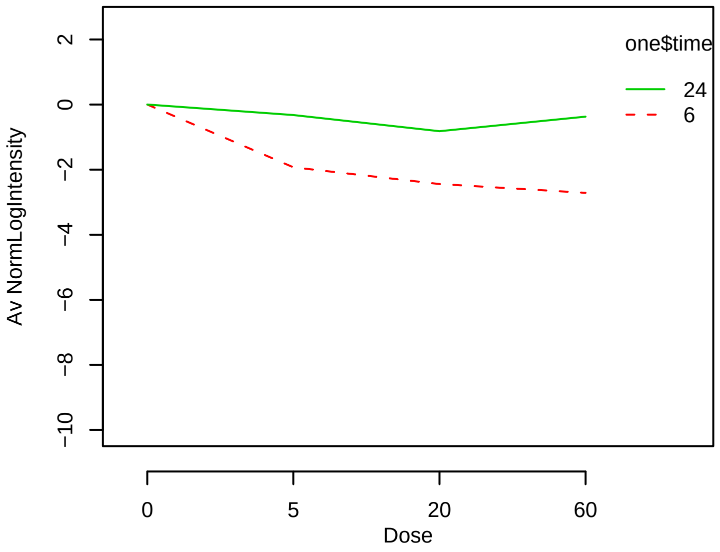
GO_0042100 : B cell proliferation



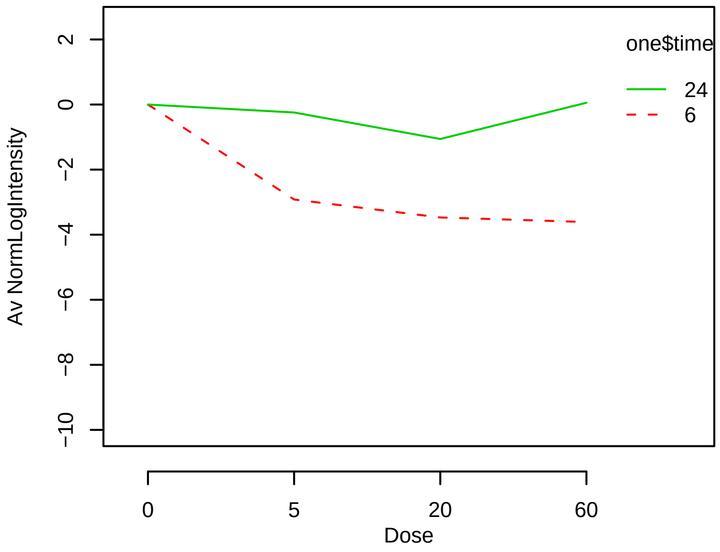
GO_0042102 : positive regulation of T cell proliferation



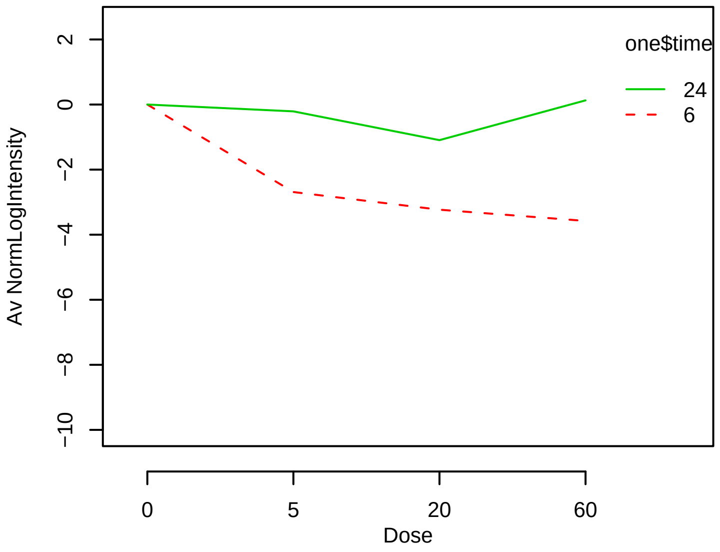
GO_0042104 : positive regulation of activated T cell prolifer

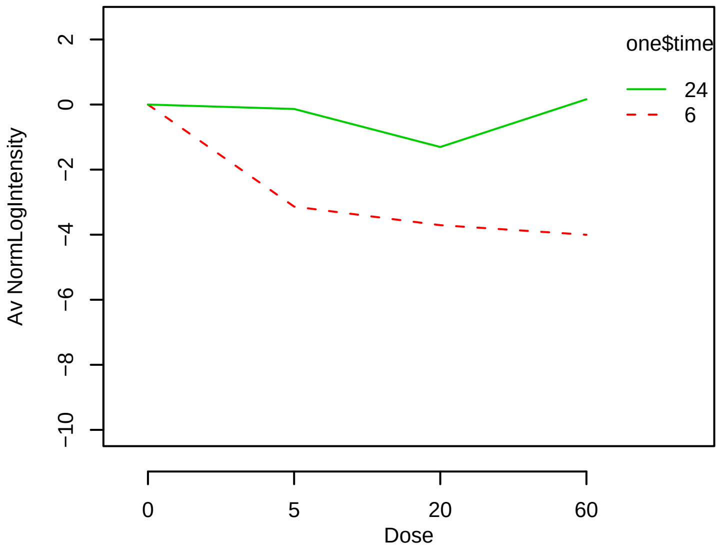


GO_0042107 : cytokine metabolism

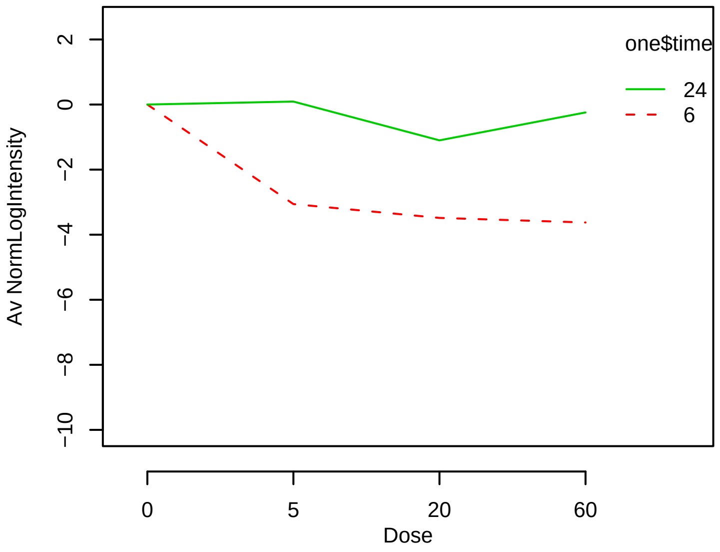


GO_0042108 : positive regulation of cytokine biosynthesi

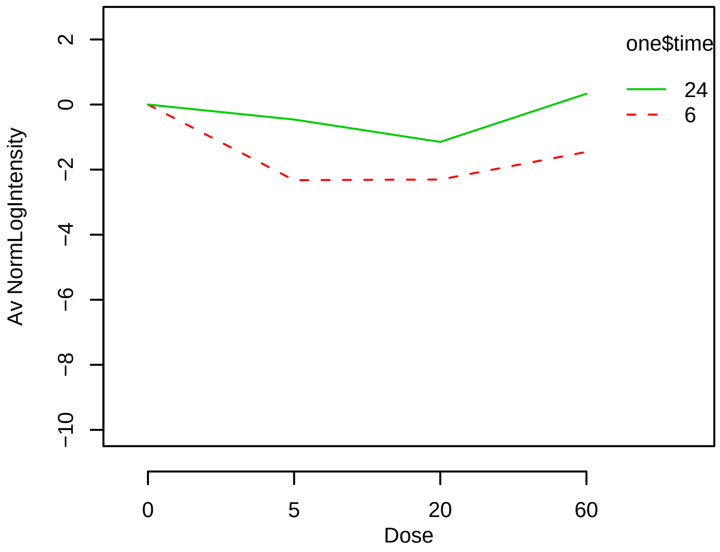




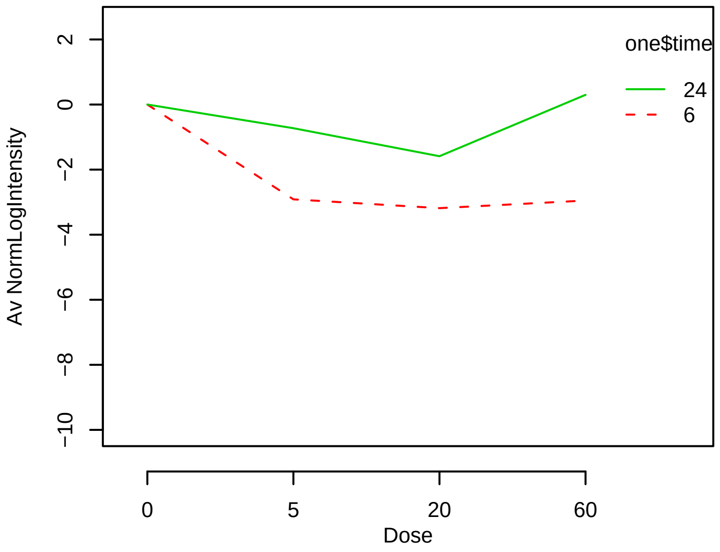
GO_0042110 : T cell activation



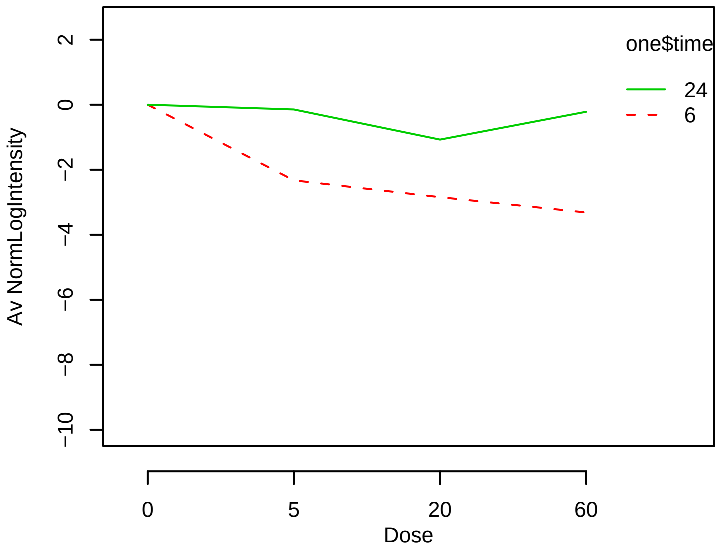
GO_0042113 : B cell activation



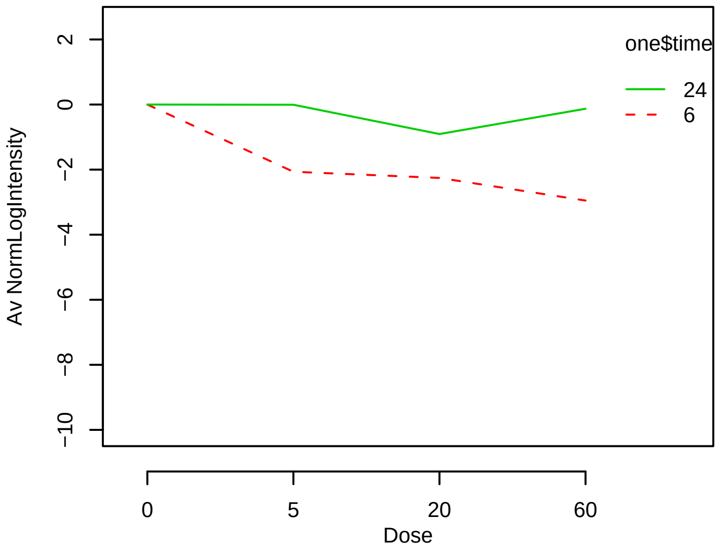
GO_0042116 : macrophage activation



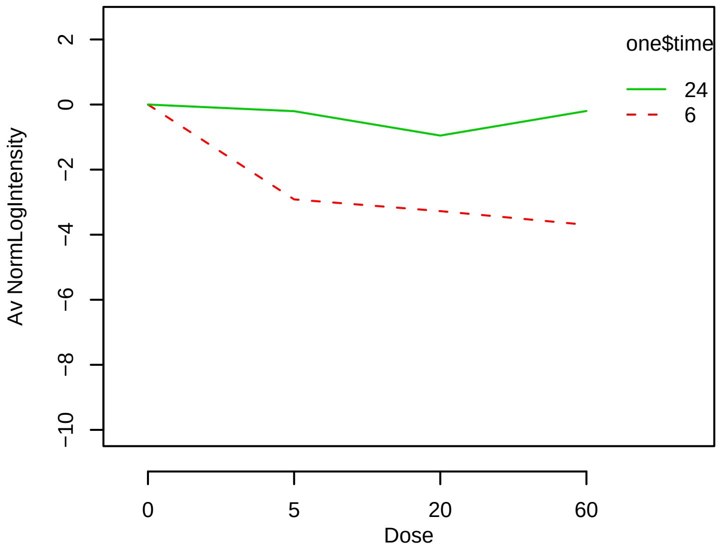
GO_0042119 : neutrophil activation



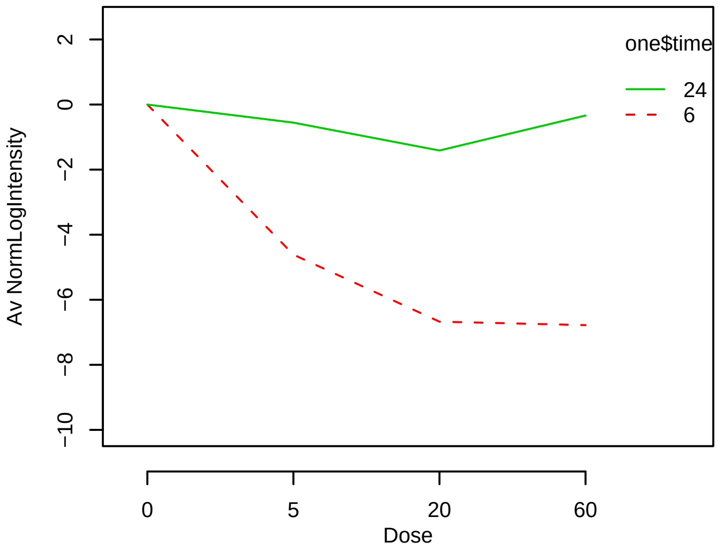
GO_0042129 : regulation of T cell proliferation



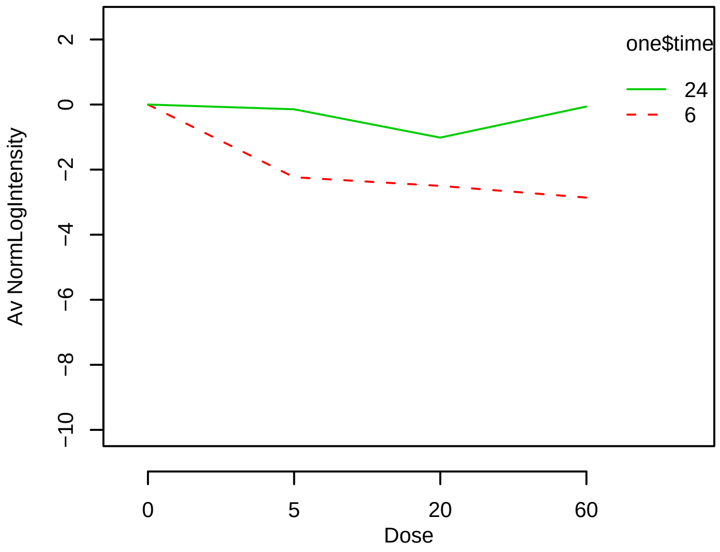
GO_0042130 : negative regulation of T cell proliferation



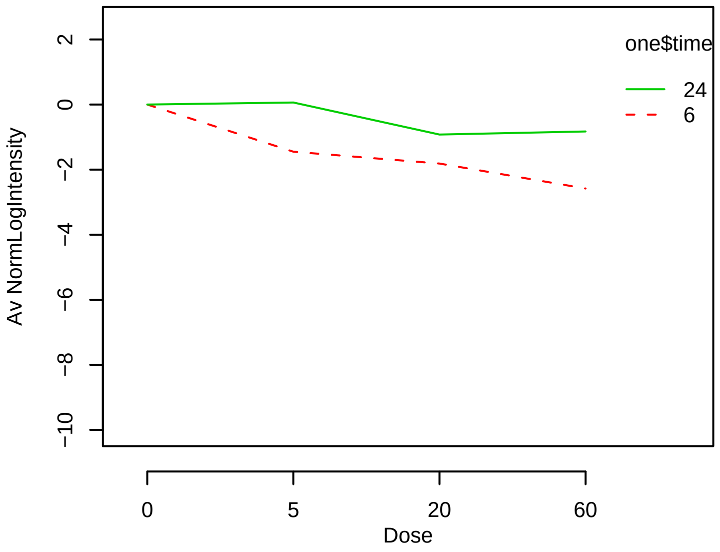
GO_0042133 : neurotransmitter metabolism



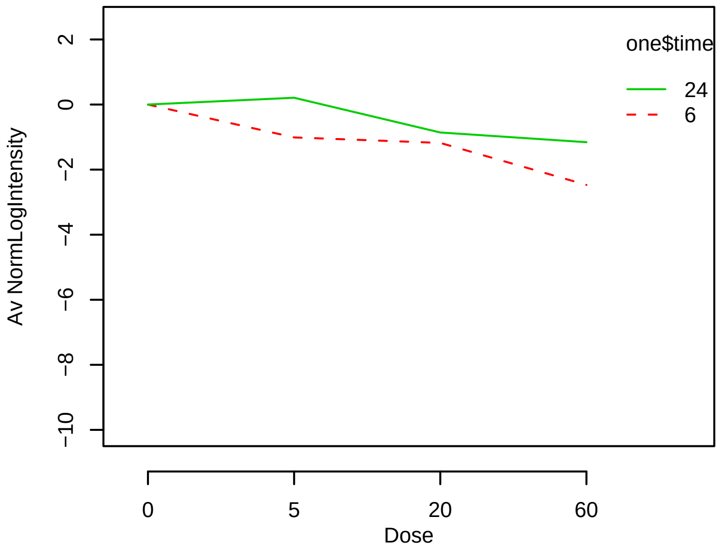
GO_0042135 : neurotransmitter catabolism



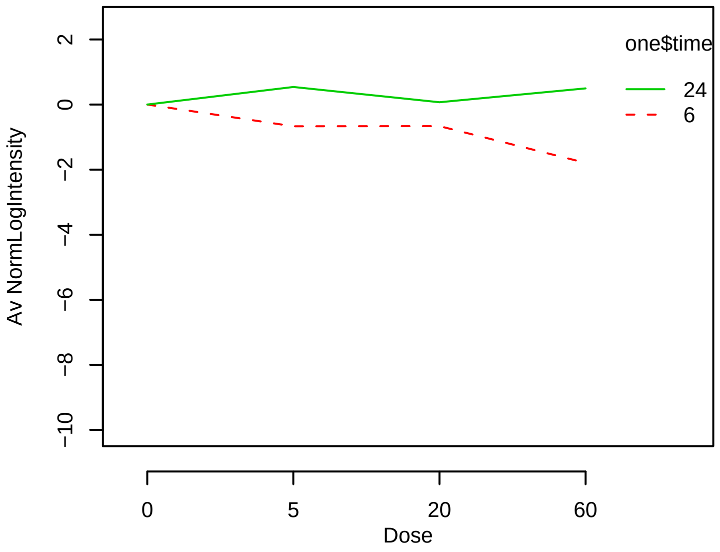
GO_0042136 : neurotransmitter biosynthesis



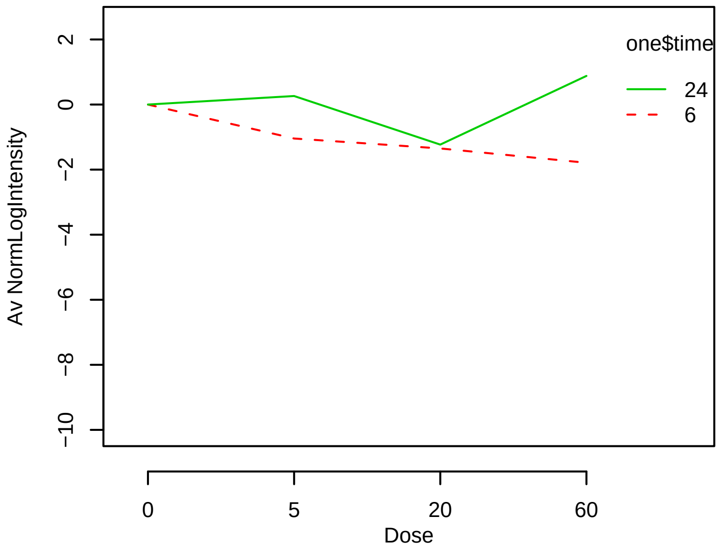
GO_0042157 : lipoprotein metabolism

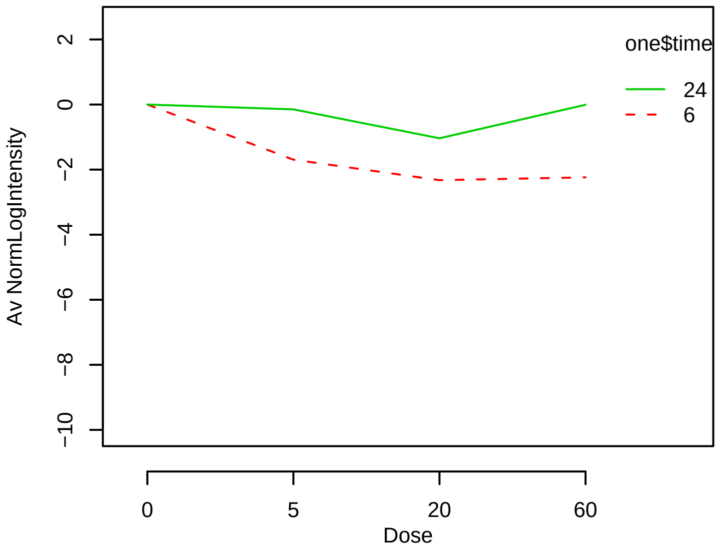


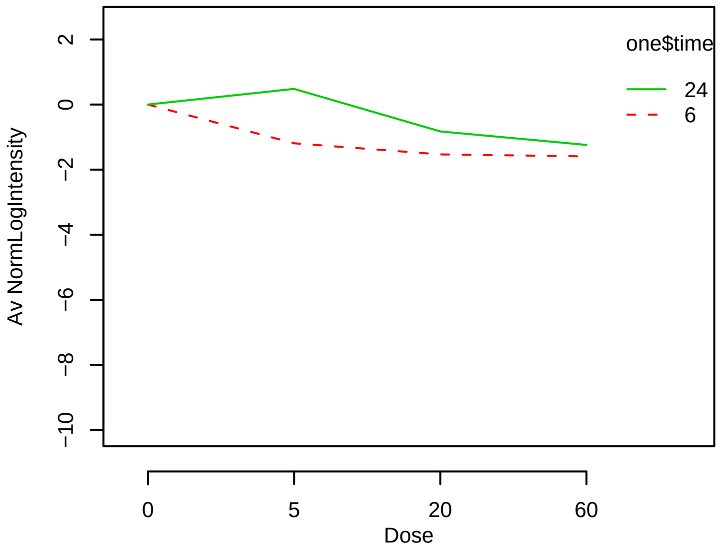
GO_0042158 : lipoprotein biosynthesis

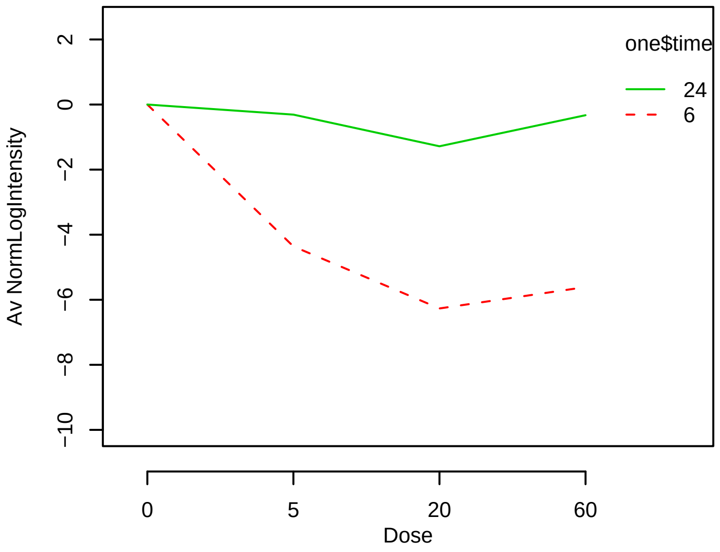


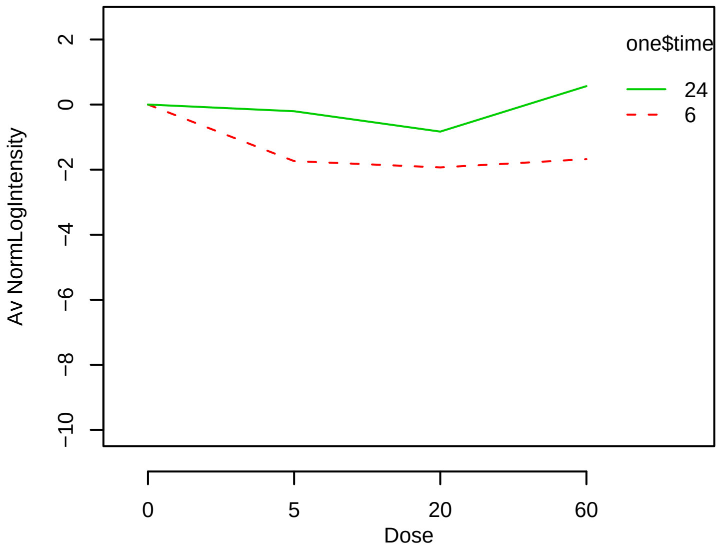
GO_0042168 : heme metabolism

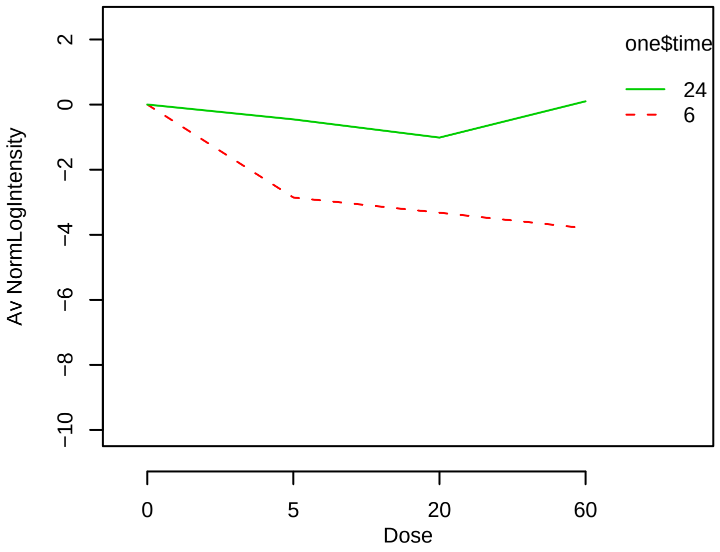

GO_0042176 : regulation of protein catabolism

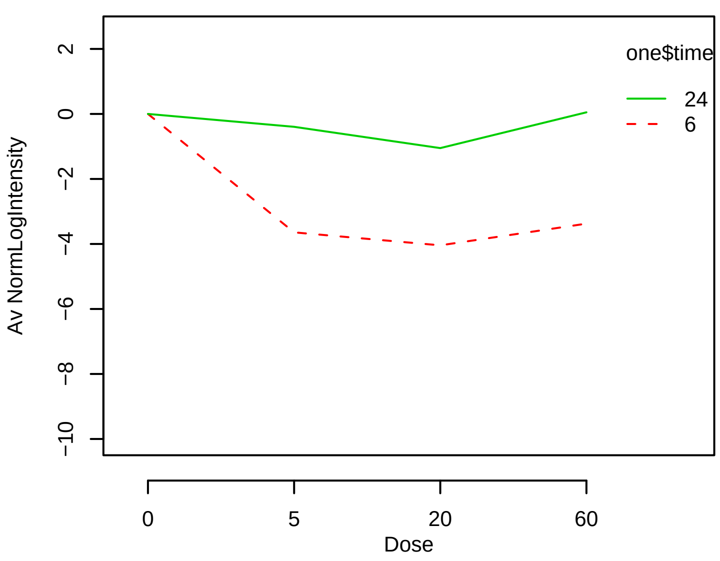

GO_0042177 : negative regulation of protein catabolism

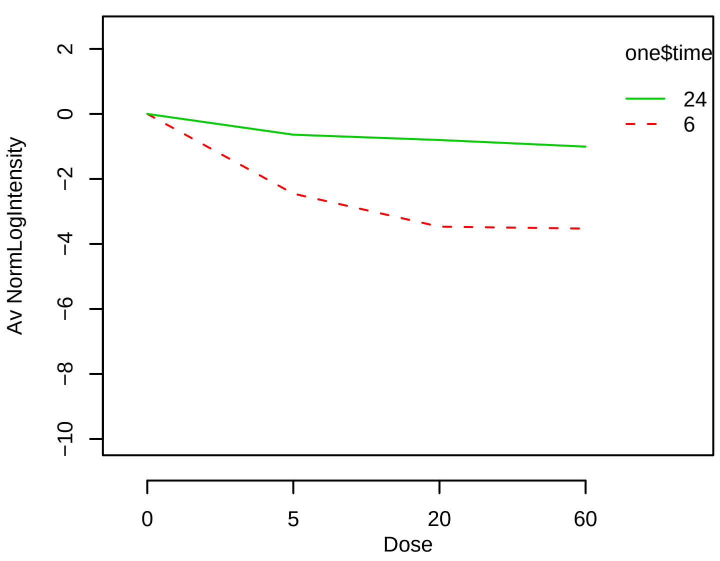

GO_0042214 : terpene metabolism

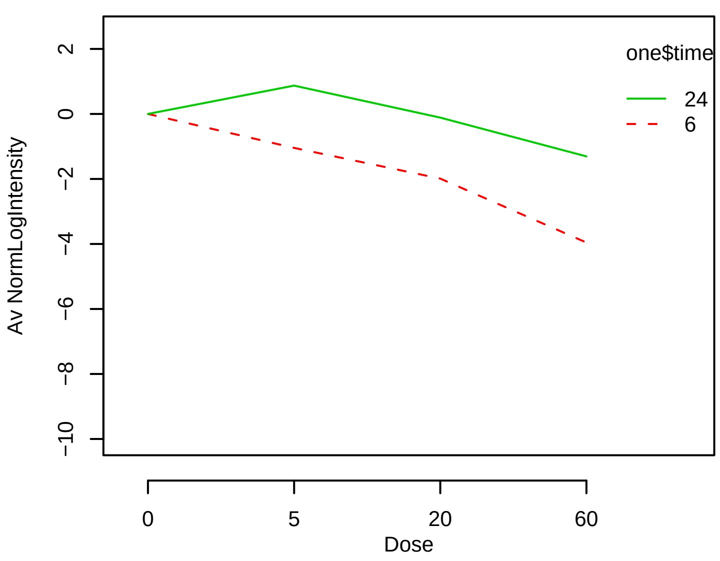

GO_0042219 : amino acid derivative catabolism

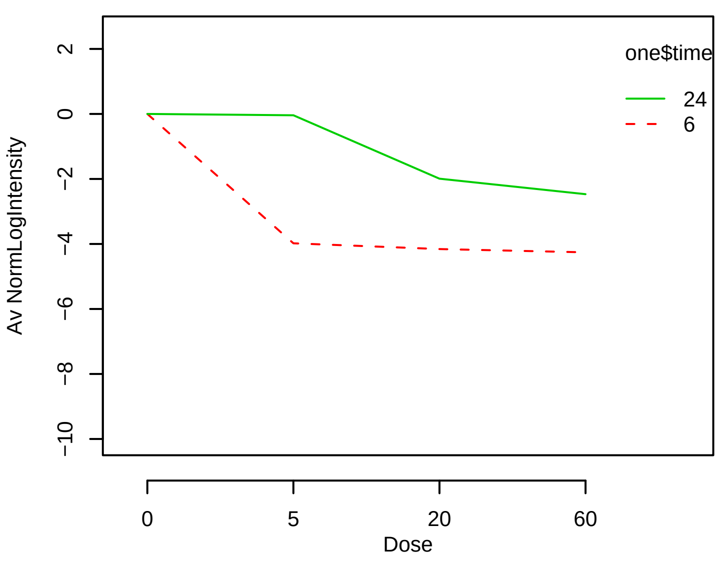

GO_0042226 : interleukin−6 biosynthesis

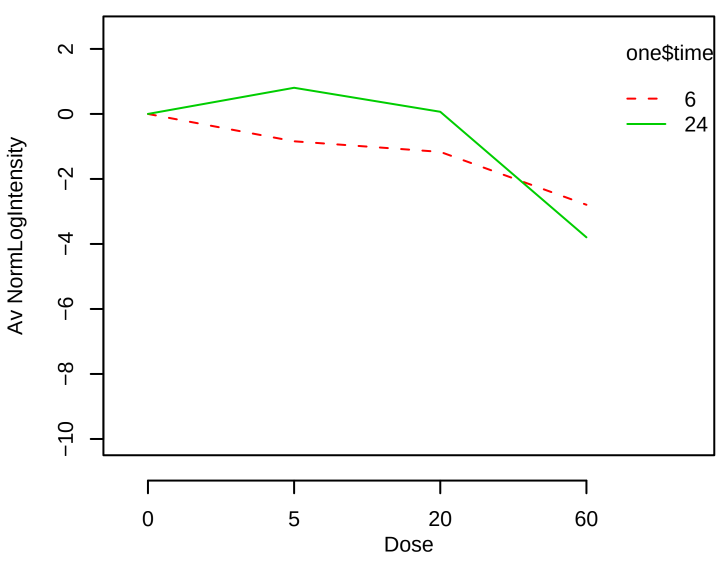

GO_0042228 : interleukin−8 biosynthesis

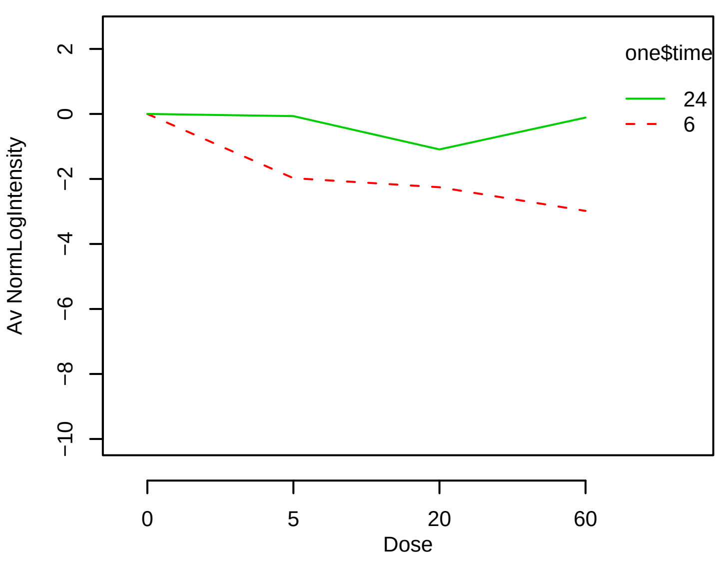

GO_0042246 : tissue regeneration

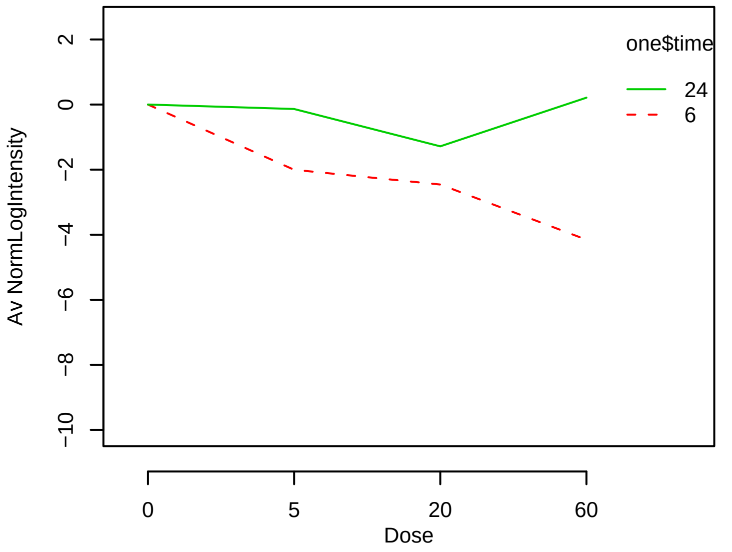

O_0042253 : granulocyte macrophage colony−stimulating fa

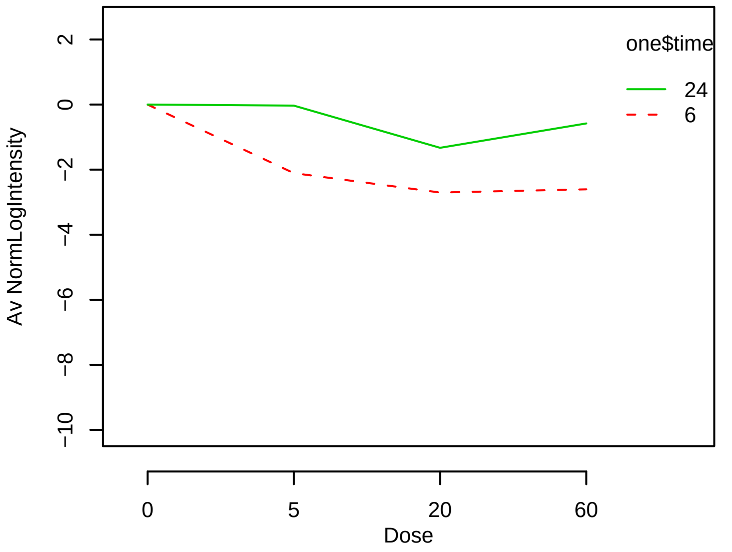

GO_0042254 : ribosome biogenesis and assembly

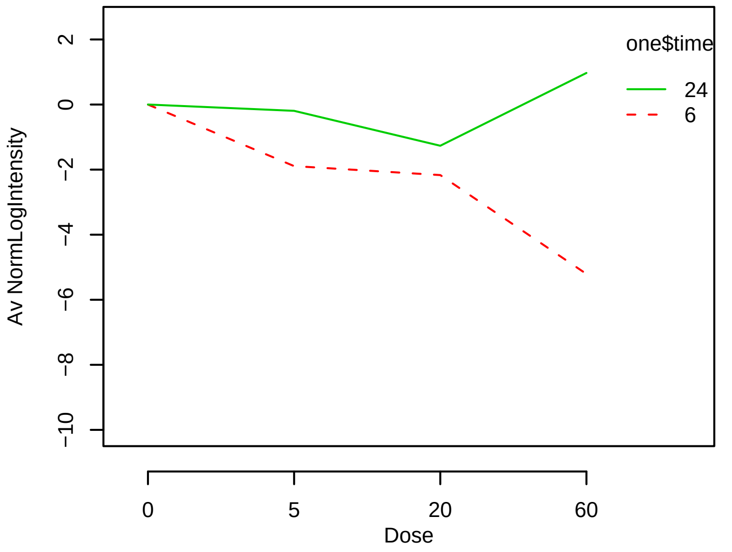

GO_0042267 : natural killer cell mediated cytotoxicity

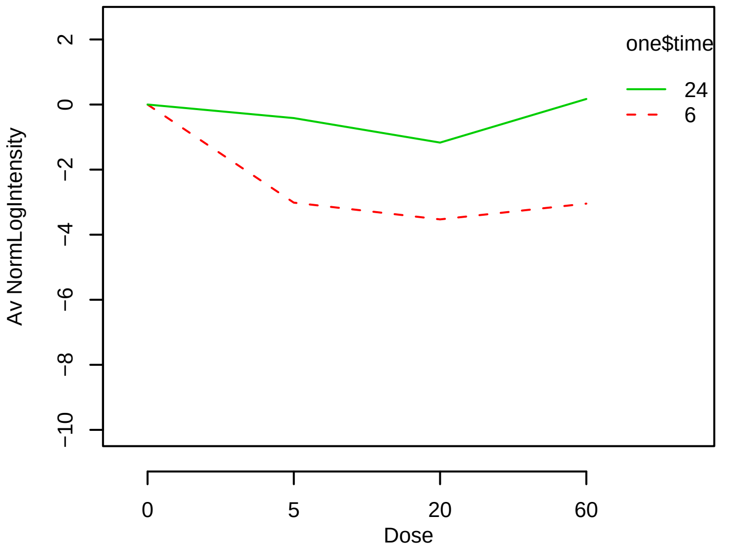

GO_0042278 : purine nucleoside metabolism

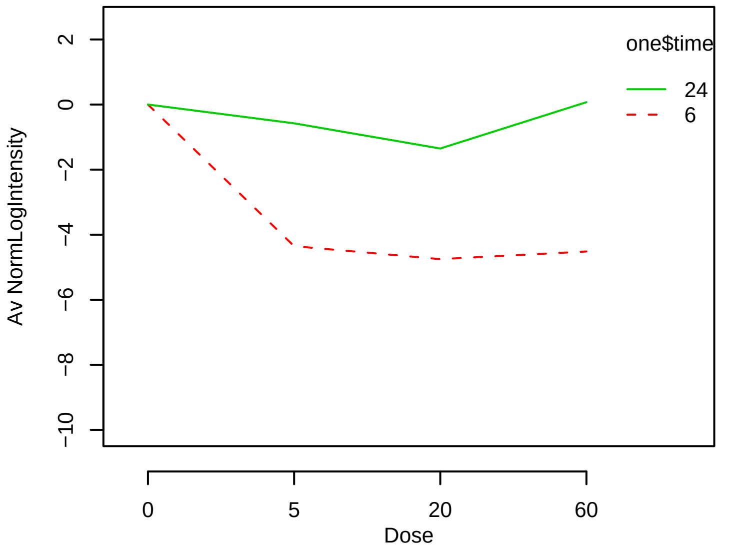

GO_0042303 : molting cycle

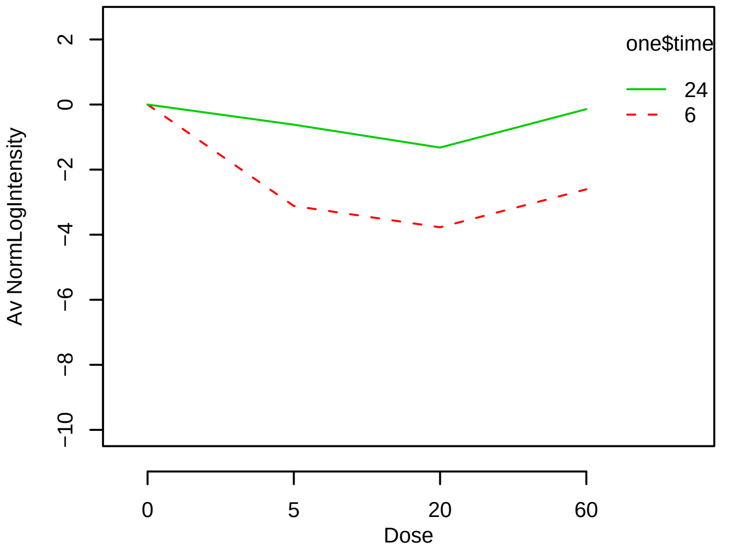

GO_0042306 : regulation of protein import into nucleus

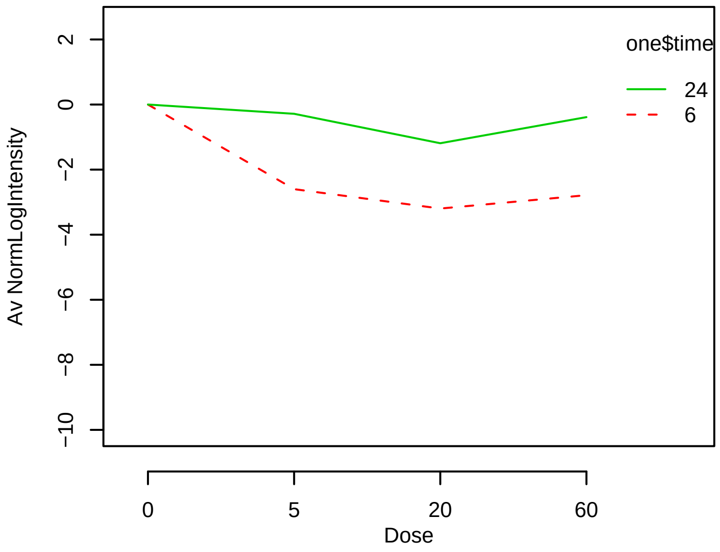

GO_0042307 : positive regulation of protein import into nucl


GO_0042308 : negative regulation of protein import into nucl

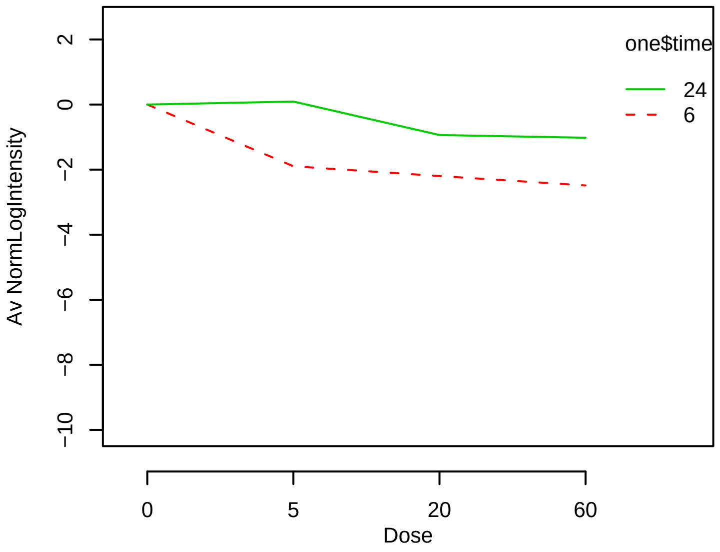

GO_0042310 : vasoconstriction


GO_0042311 : vasodilation

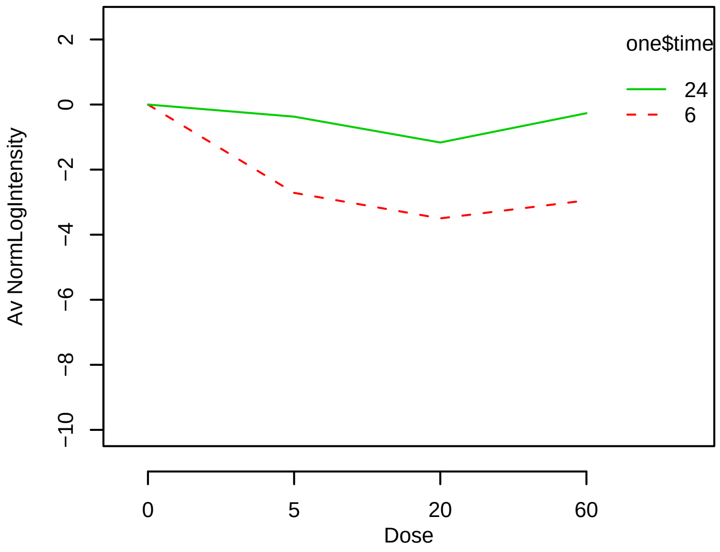

GO_0042312 : regulation of vasodilation



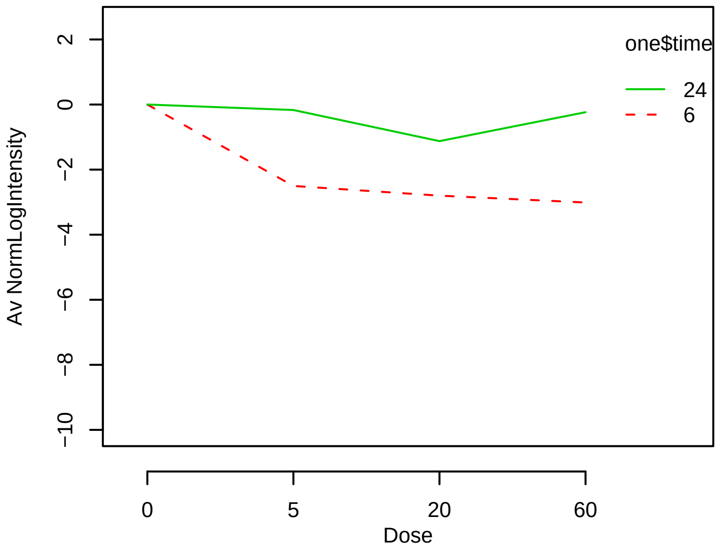
GO_0042325 : regulation of phosphorylation



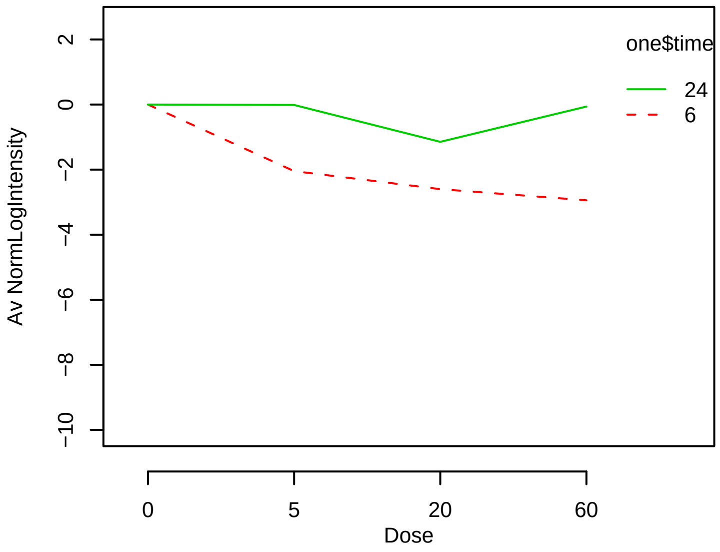
GO_0042326 : negative regulation of phosphorylation



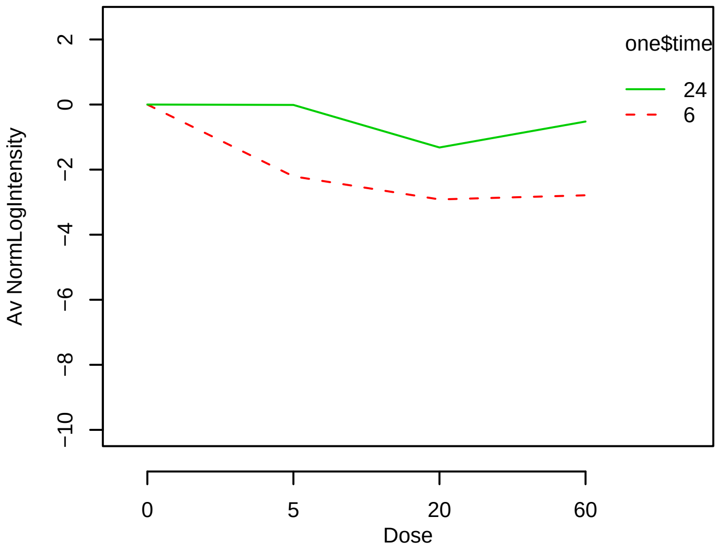
GO_0042327 : positive regulation of phosphorylation



GO_0042330 : taxis

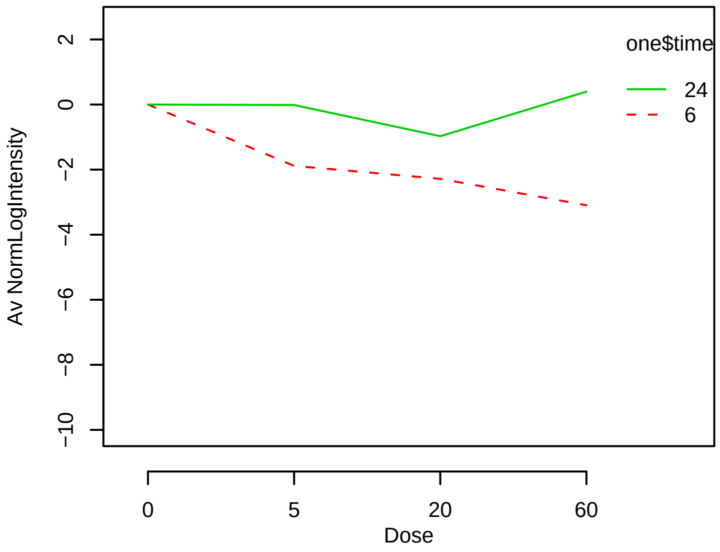


GO_0042345 : regulation of NF−kappaB import into nucleu

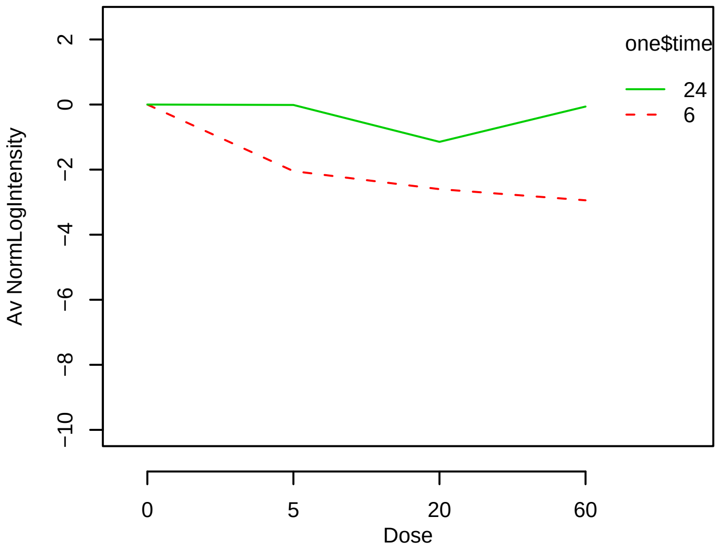


GO_0042346 : positive regulation of NF−kappaB import into n

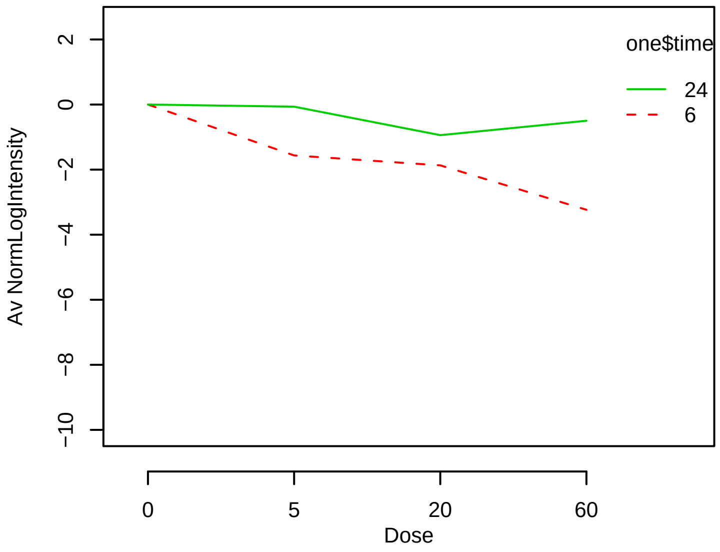
GO_0042347 : negative regulation of NF−kappaB import into r



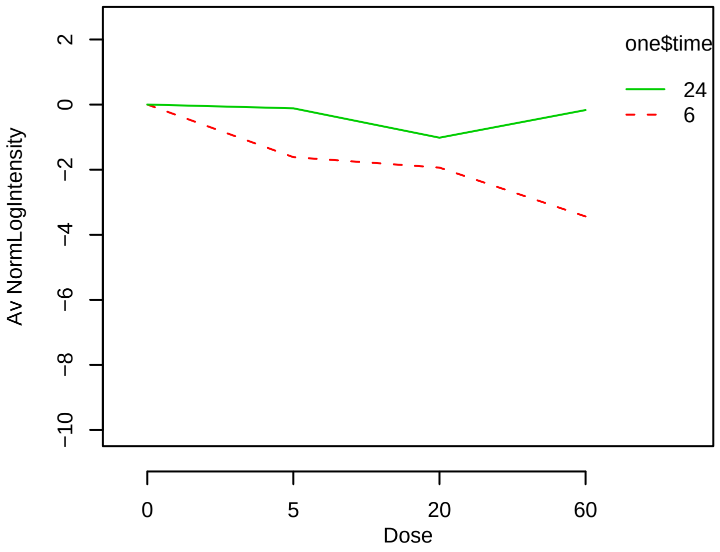
GO_0042348 : NF−kappaB import into nucleus



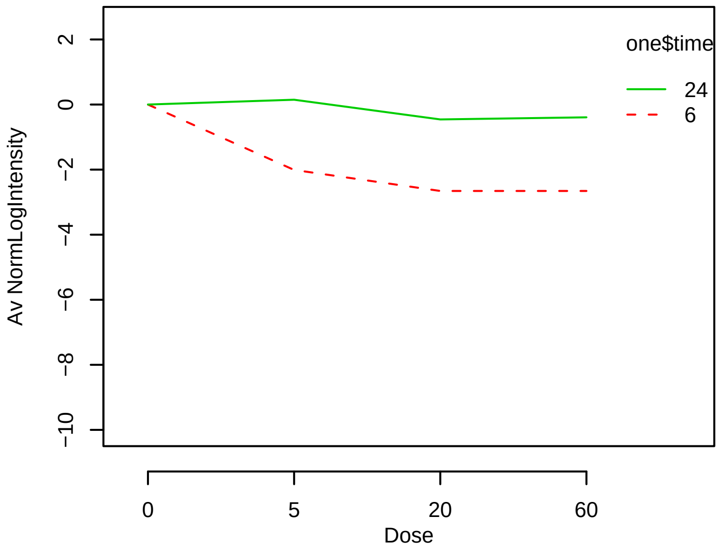
GO_0042354 : L−fucose metabolism



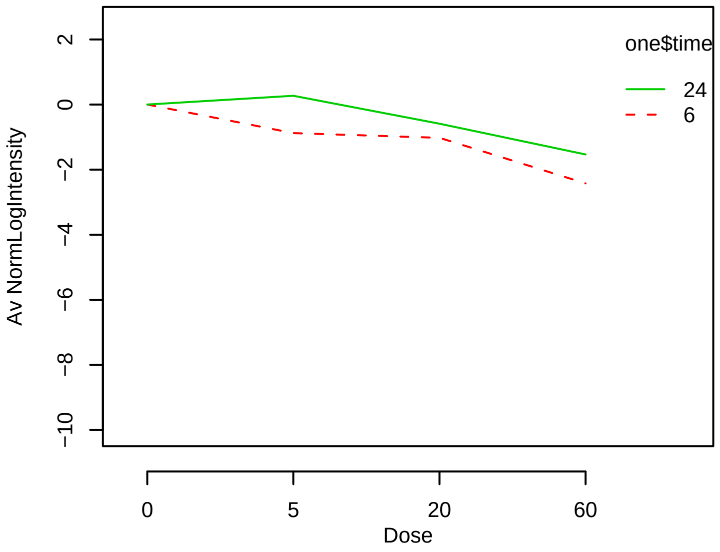
GO_0042355 : L−fucose catabolism

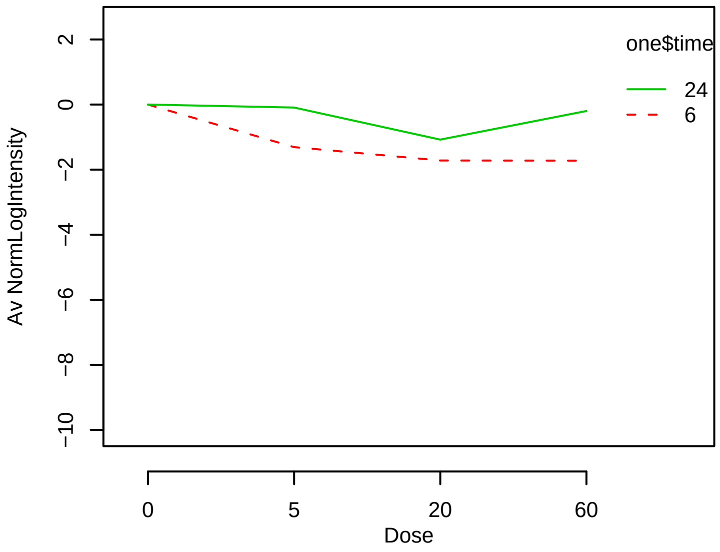


GO_0042364 : water−soluble vitamin biosynthesis

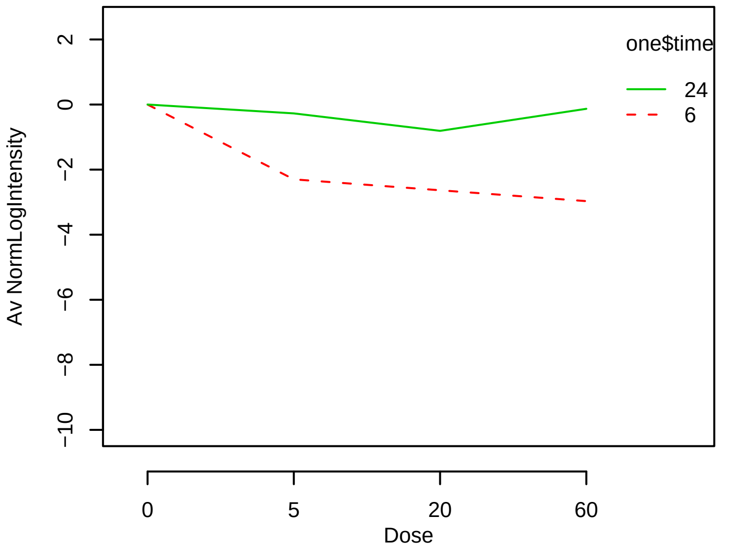


GO_0042375 : quinone cofactor metabolism

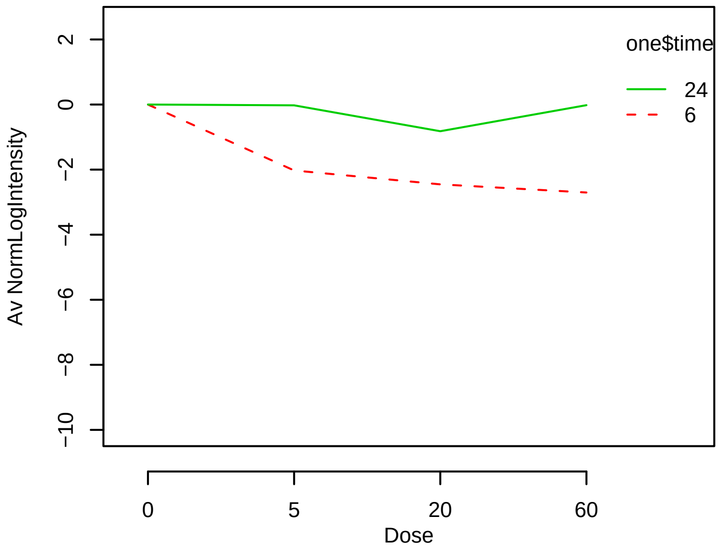




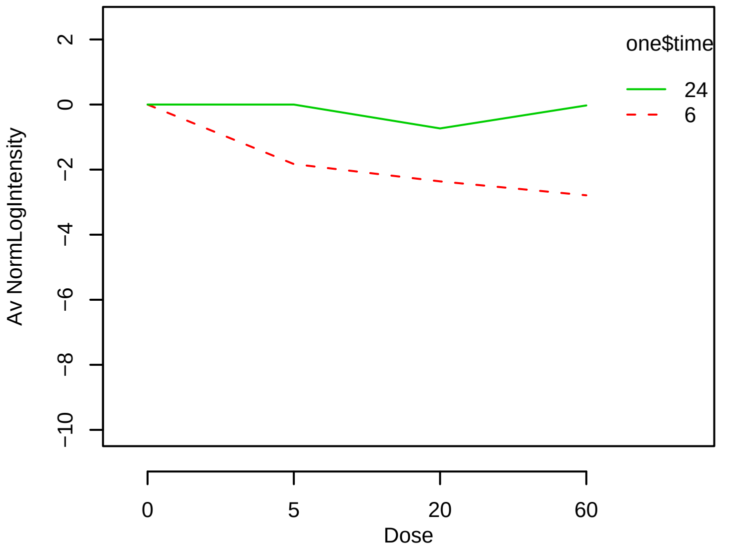
GO_0042384 : cilium biogenesis



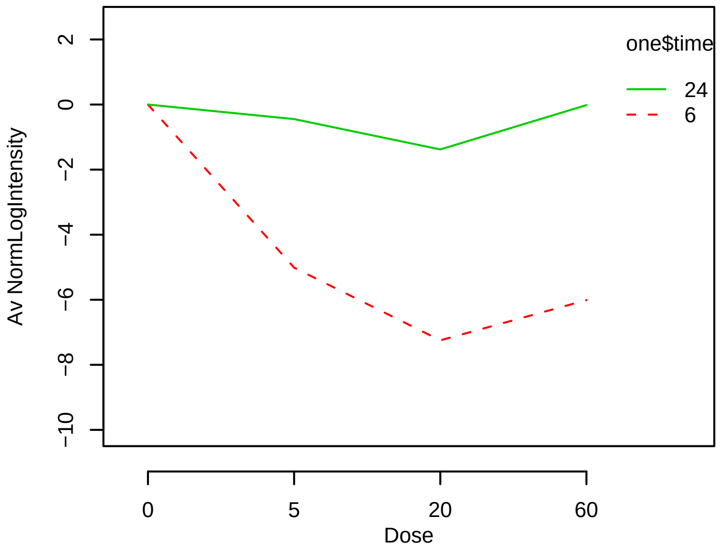
GO_0042386 : hemocyte differentiation (sensu Arthropoda



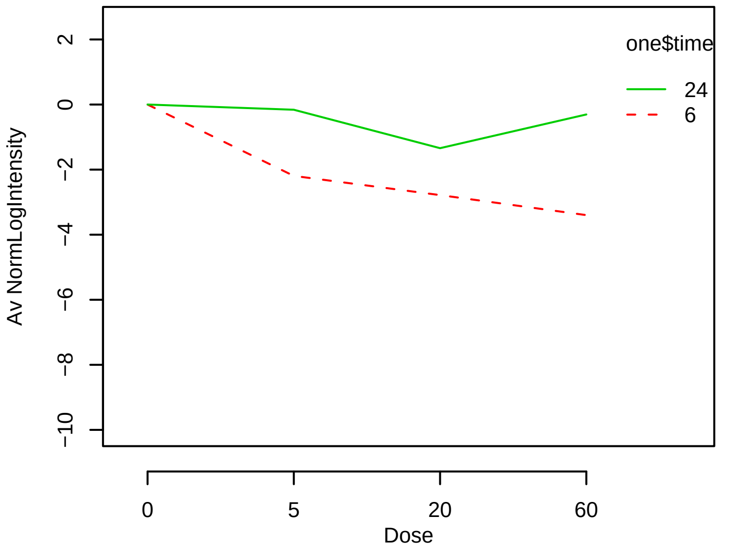
GO_0042398 : amino acid derivative biosynthesis



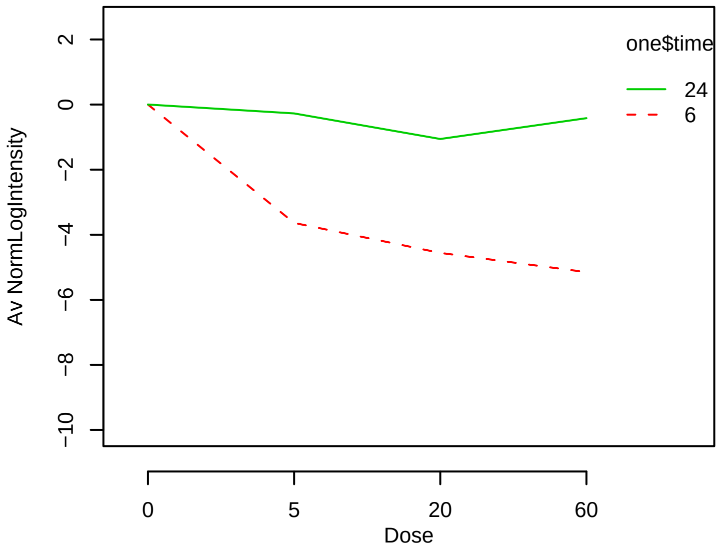
GO_0042401 : biogenic amine biosynthesis

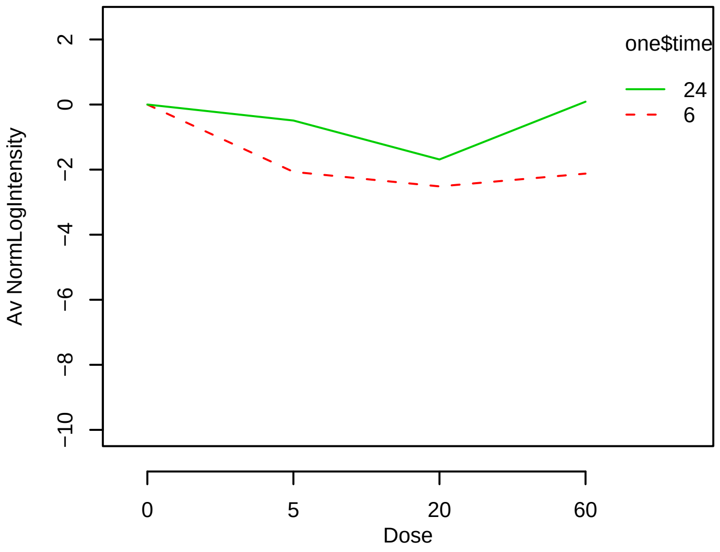


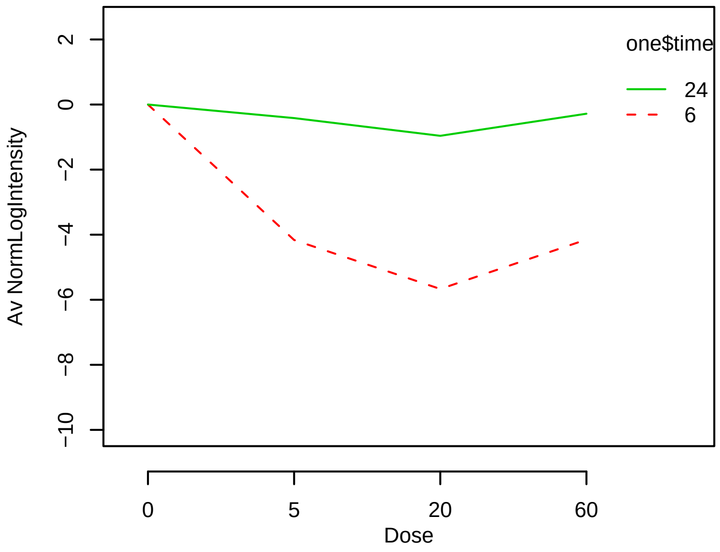
GO_0042402 : biogenic amine catabolism

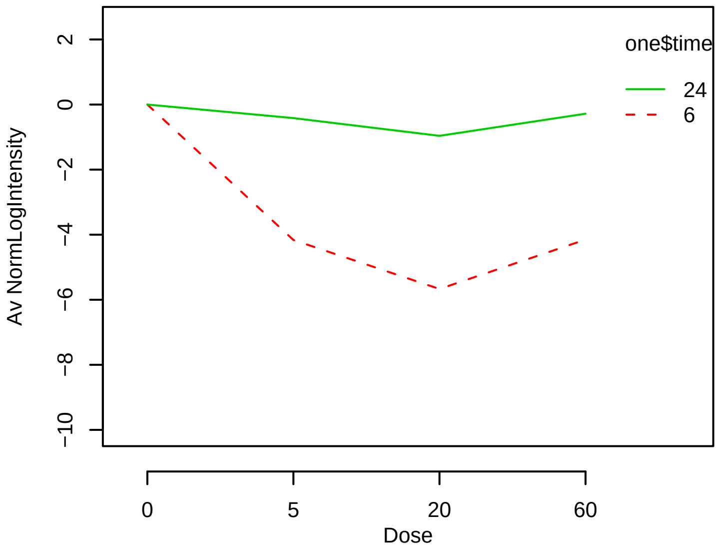


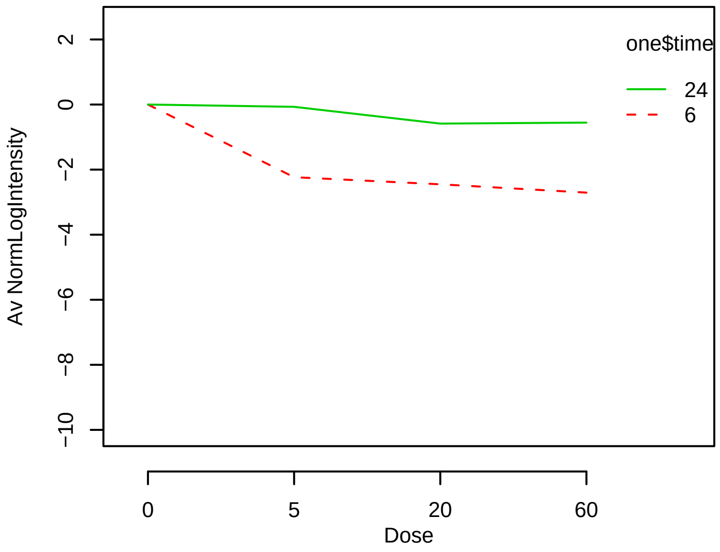
GO_0042403 : thyroid hormone metabolism

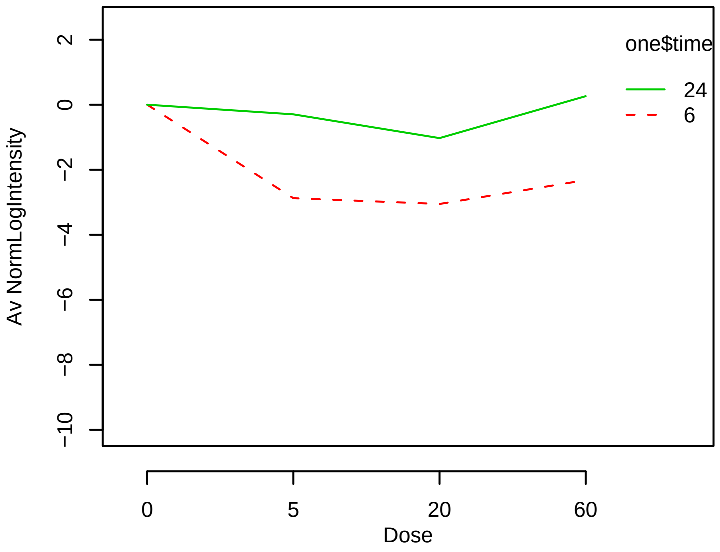

GO_0042417 : dopamine metabolism

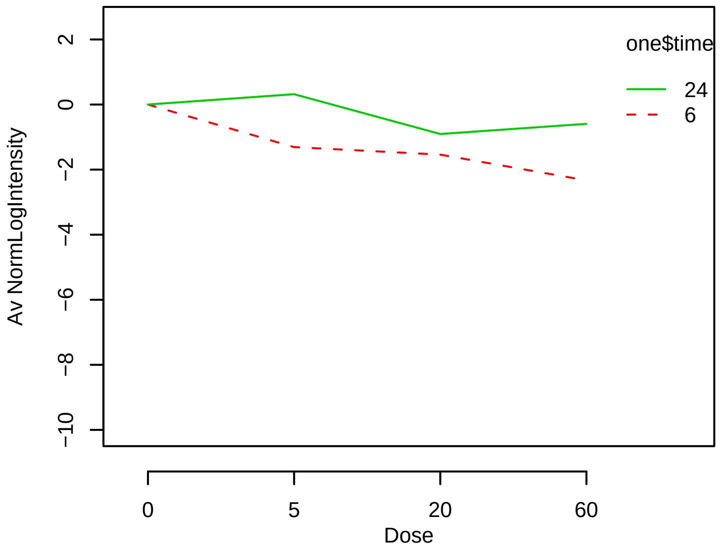

GO_0042423 : catecholamine biosynthesis

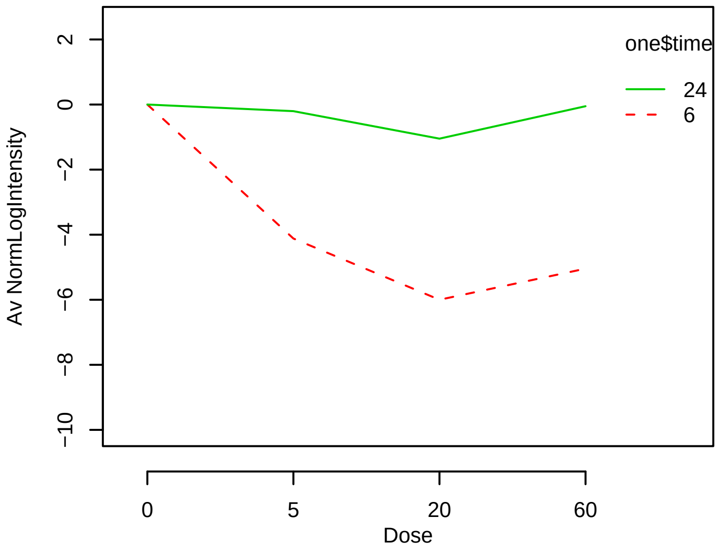

GO_0042430 : indole and derivative metabolism

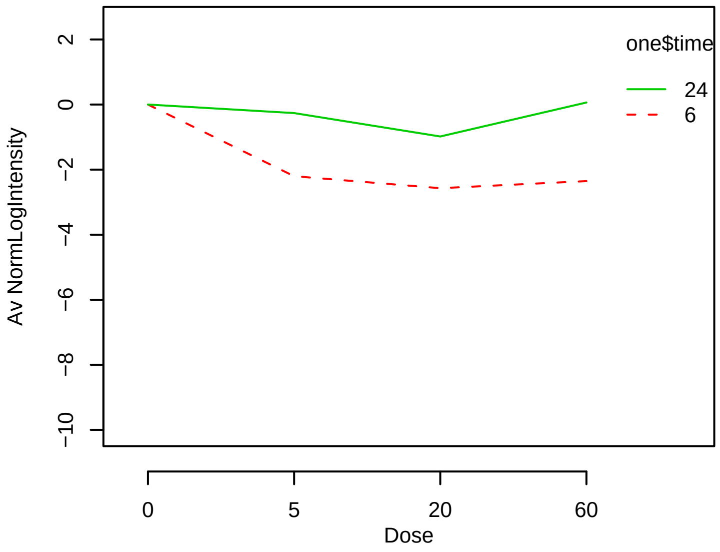

GO_0042434 : indole derivative metabolism

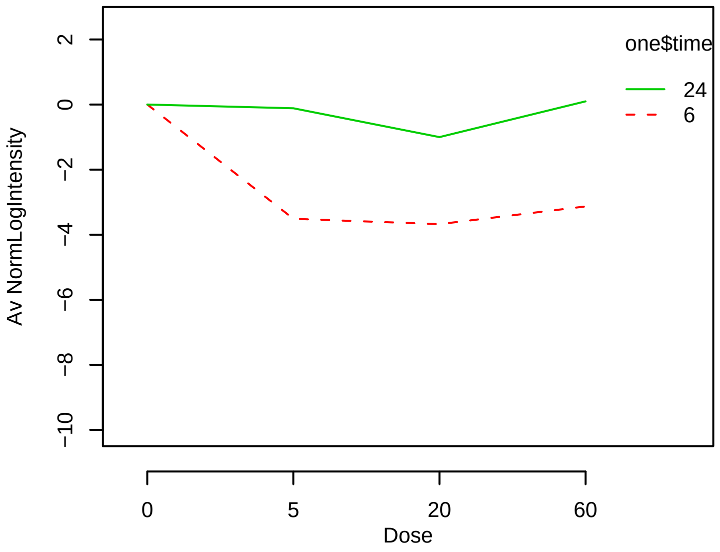

GO_0042438 : melanin biosynthesis

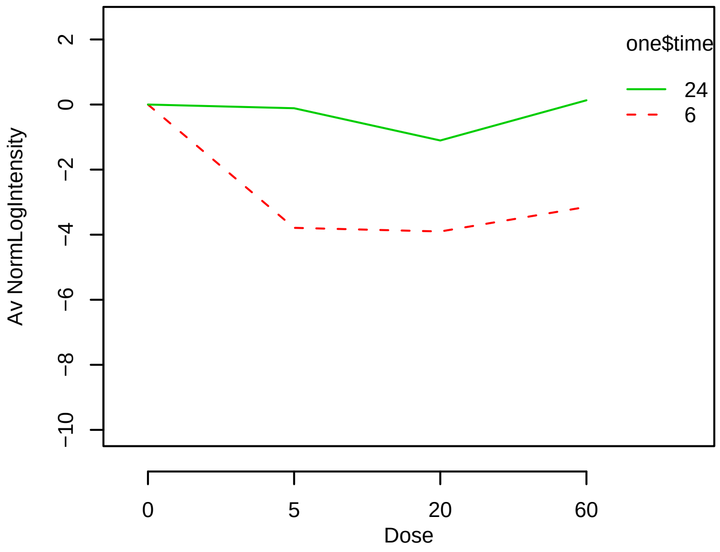

GO_0042439 : ethanolamine and derivative metabolism

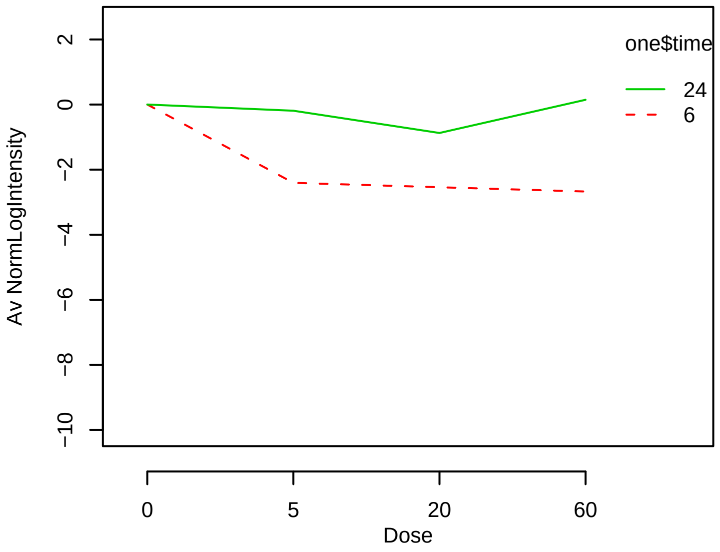

GO_0042440 : pigment metabolism


GO_0042445 : hormone metabolism

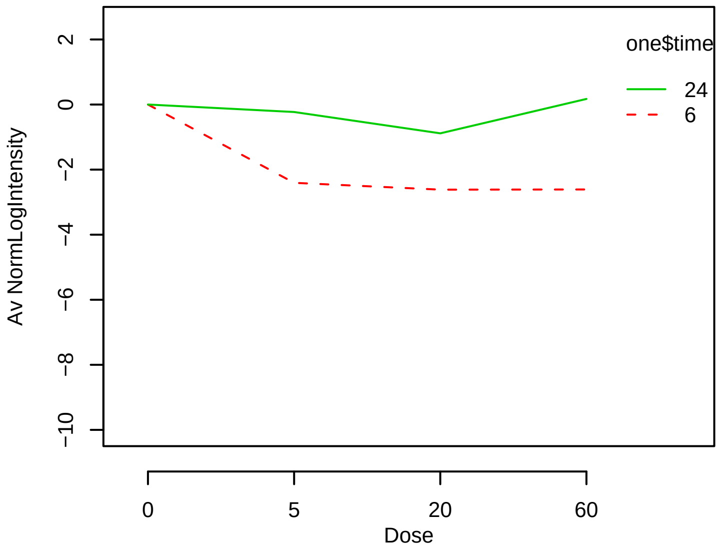

GO_0042446 : hormone biosynthesis


GO_0042461 : photoreceptor cell development

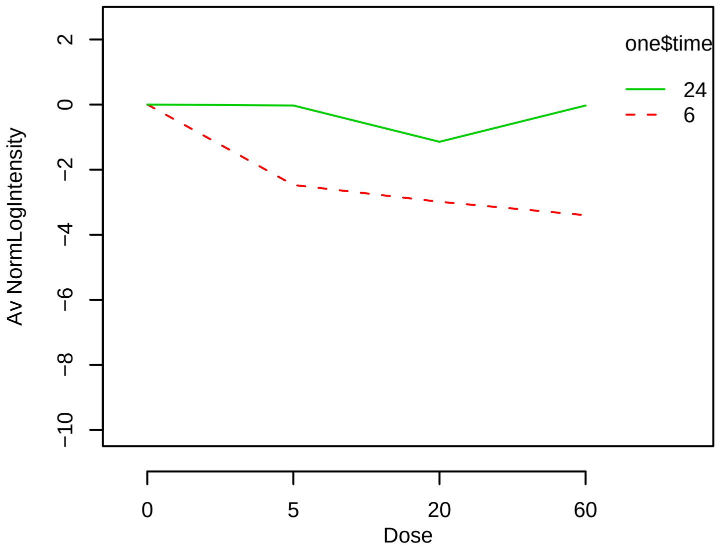

GO_0042462 : eye photoreceptor cell development


GO_0042471 : ear morphogenesis

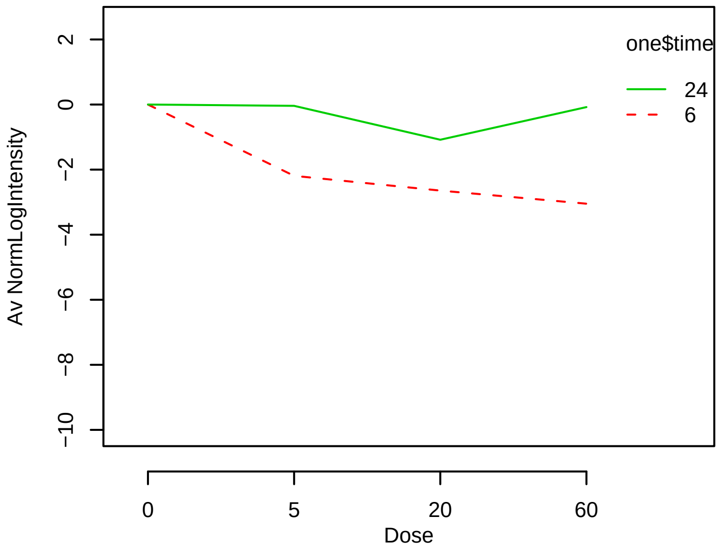
GO_0042472 : inner ear morphogenesis



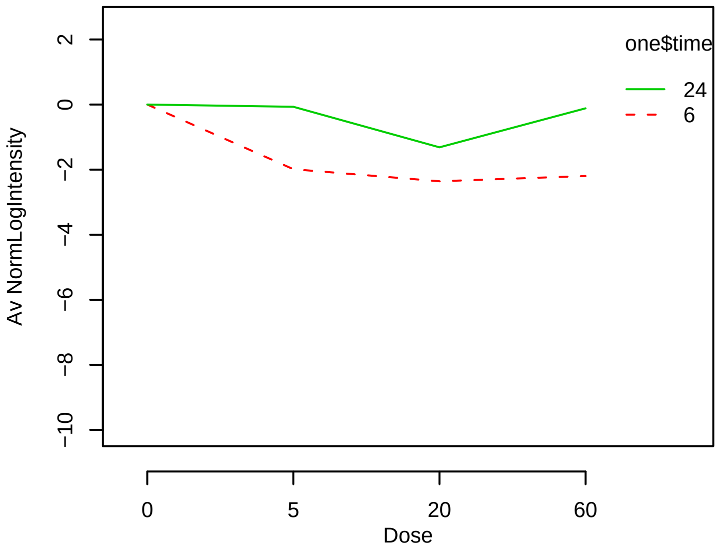
GO_0042475 : odontogenesis (sensu Vertebrata)



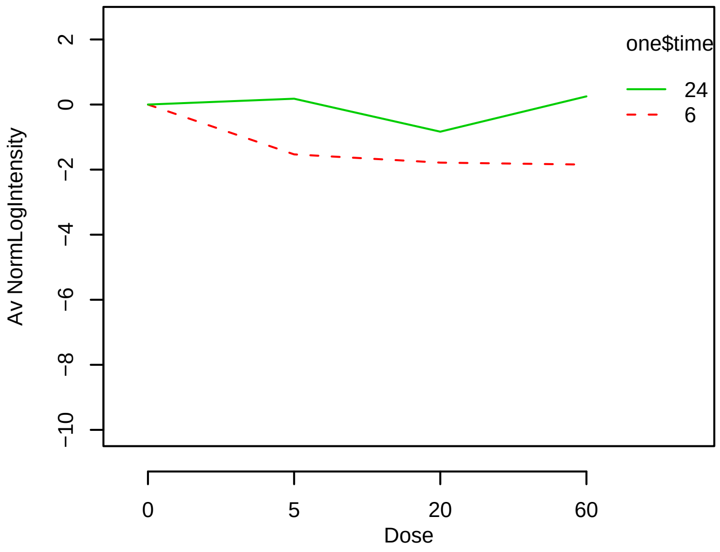
GO_0042476 : odontogenesis



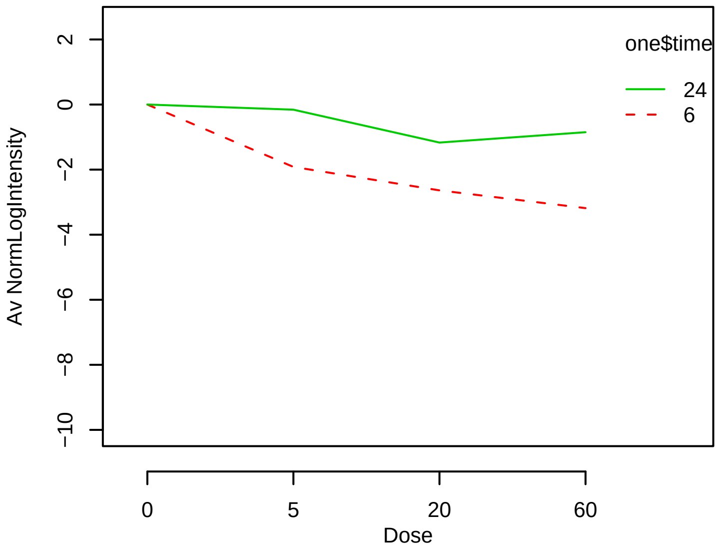
GO_0042490 : mechanoreceptor differentiation

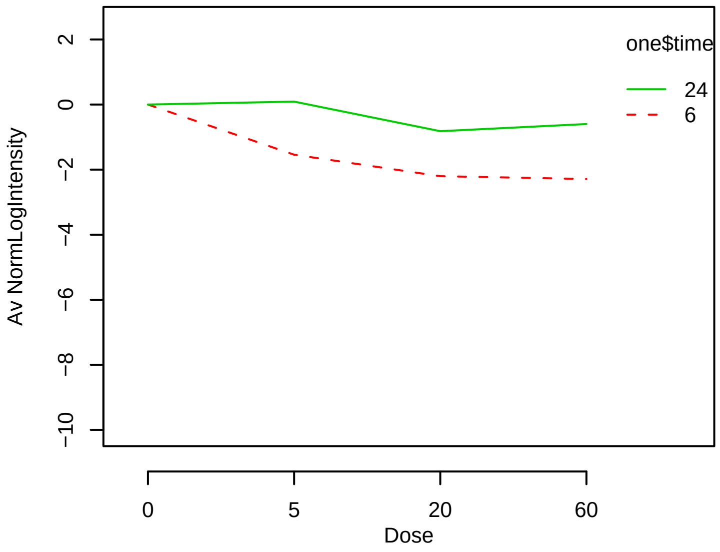


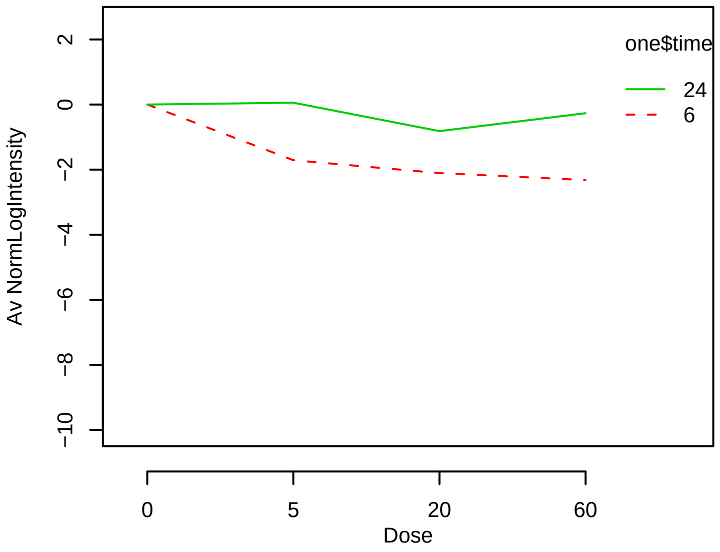
GO_0042491 : auditory receptor cell differentiation

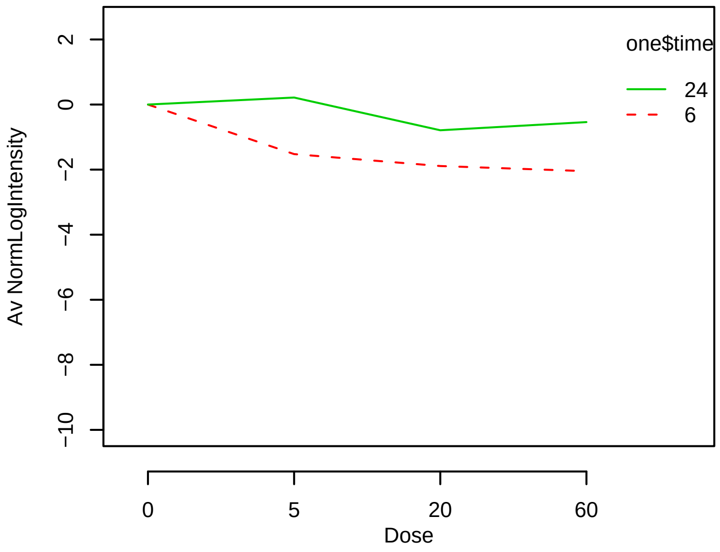


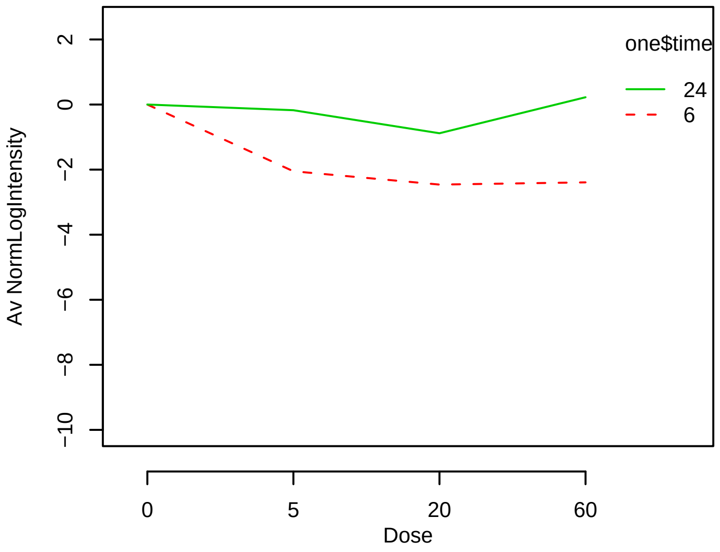
GO_0042493 : response to drug

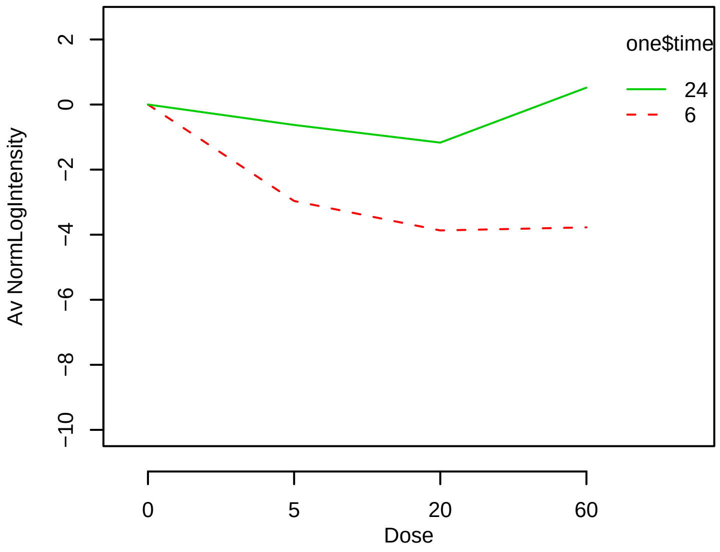


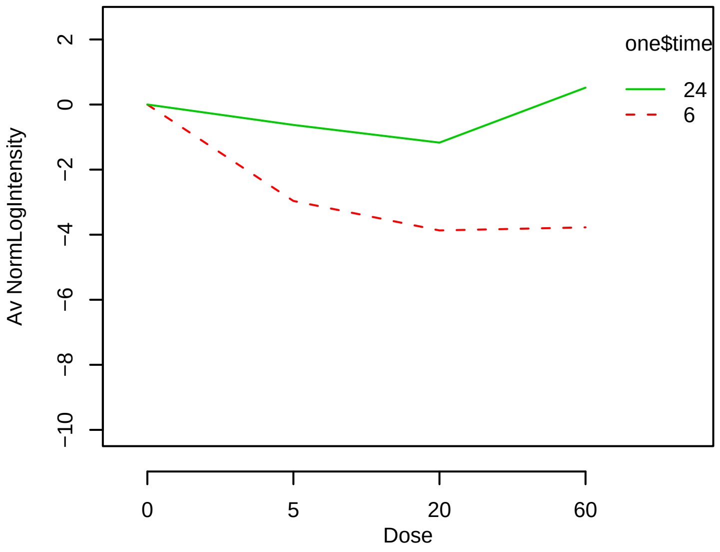

GO_0042503 : tyrosine phosphorylation of Stat3 protein

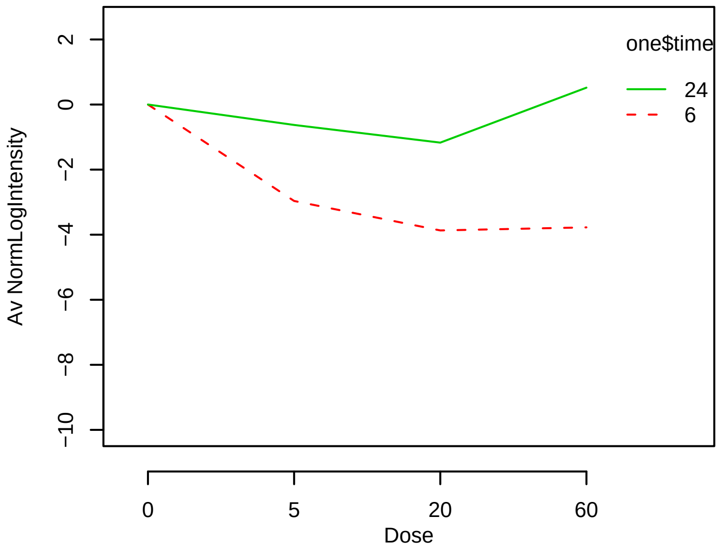

GO_0042509 : regulation of tyrosine phosphorylation of STAT

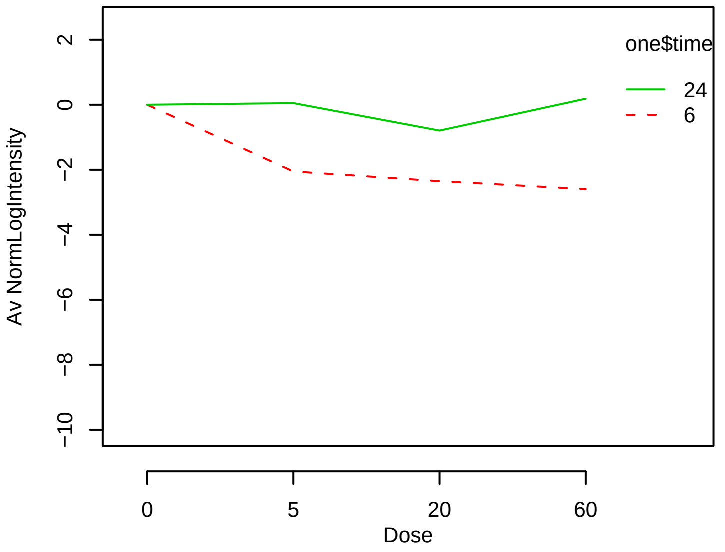

GO_0042516 : regulation of tyrosine phosphorylation of Stat

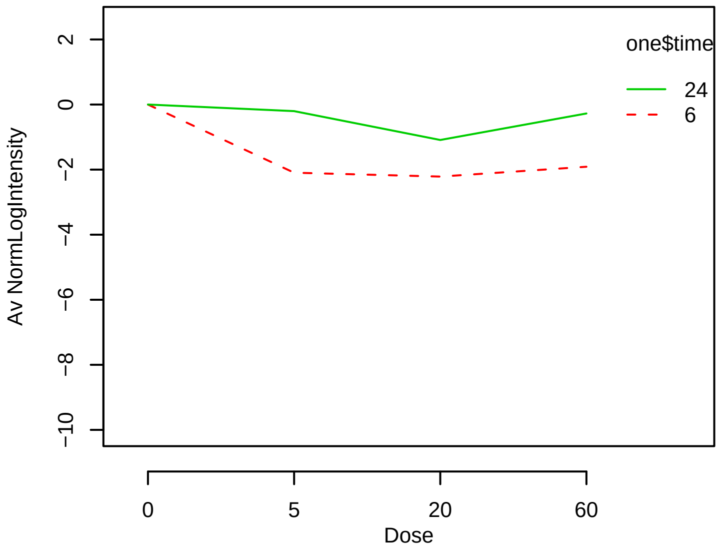

GO_0042531 : positive regulation of tyrosine phosphorylatio

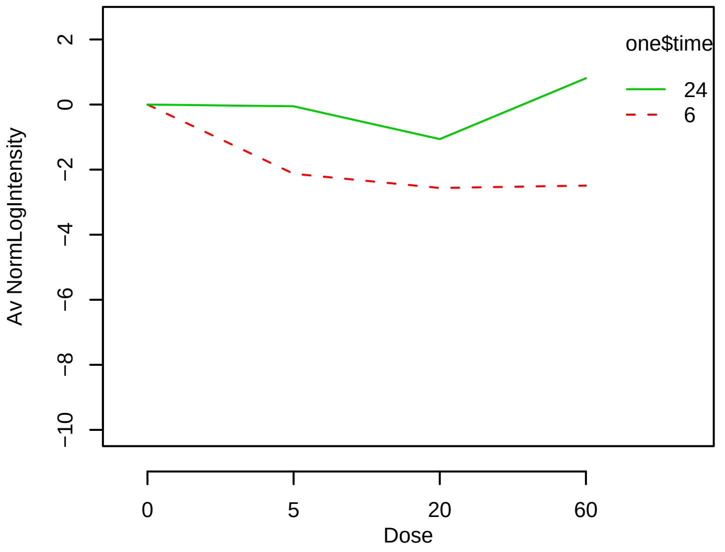

GO_0042533 : tumor necrosis factor−alpha biosynthesis

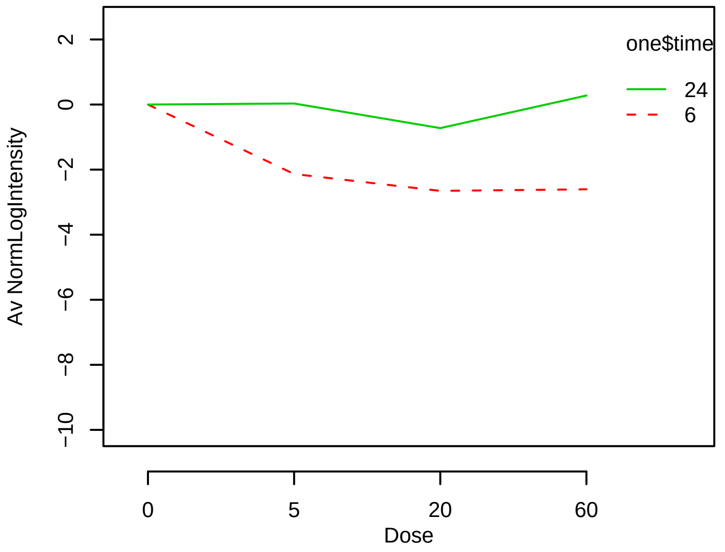

GO_0042534 : regulation of tumor necrosis factor−alpha bios

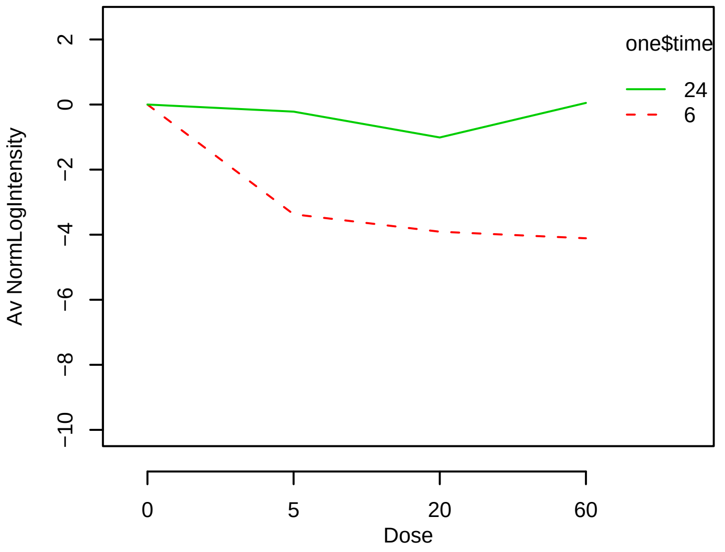

GO_0042535 : positive regulation of tumor necrosis factor−al


GO_0042541 : hemoglobin biosynthesis

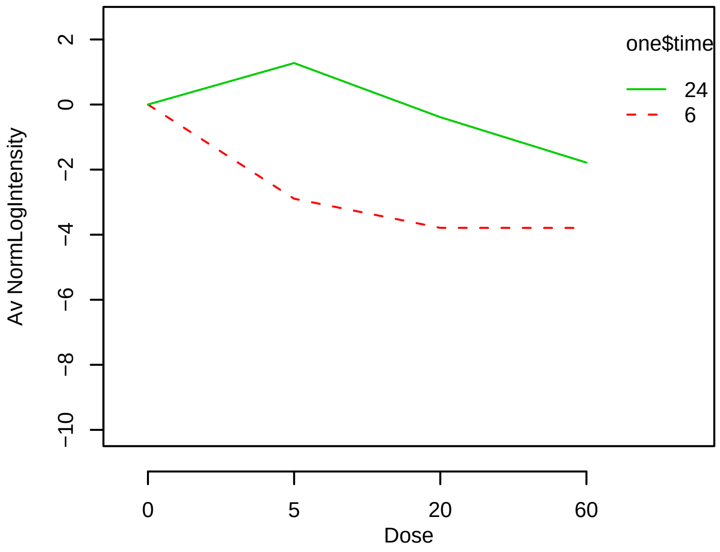

GO_0042542 : response to hydrogen peroxide


GO_0042551 : neuron maturation

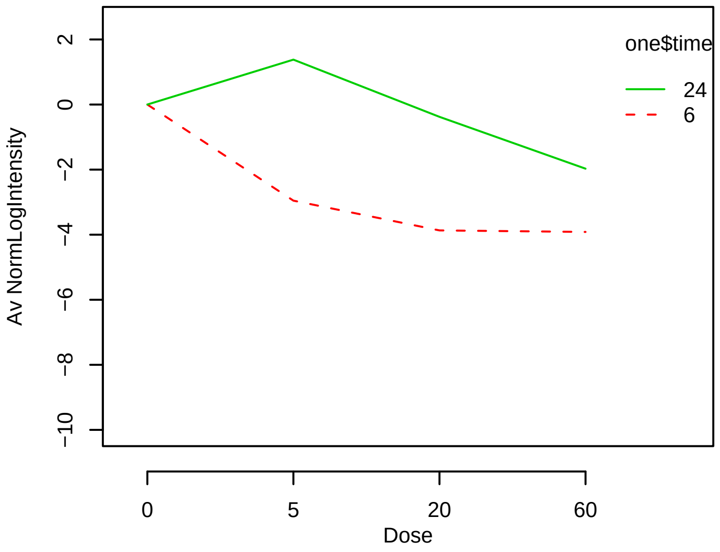

GO_0042552 : myelination


GO_0042554 : superoxide release

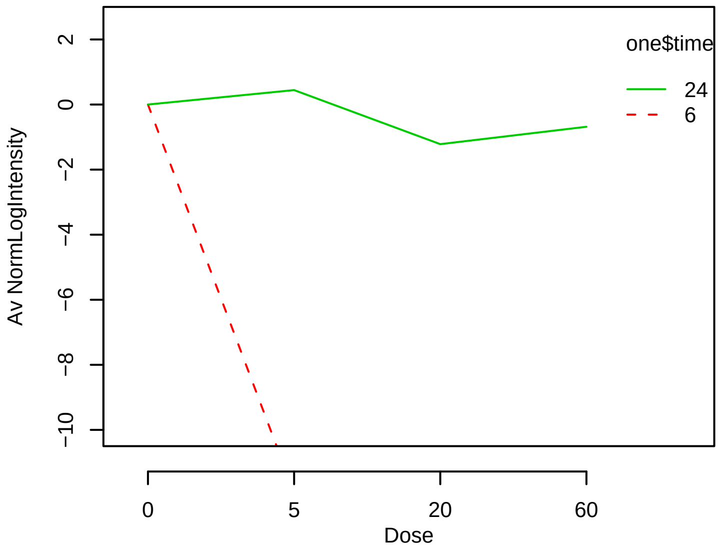
GO_0042558 : pteridine and derivative metabolism



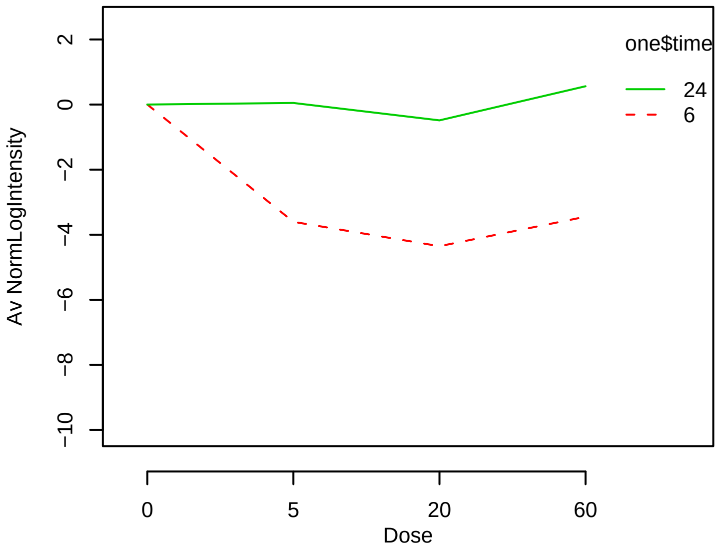
GO_0042559 : pteridine and derivative biosynthesis



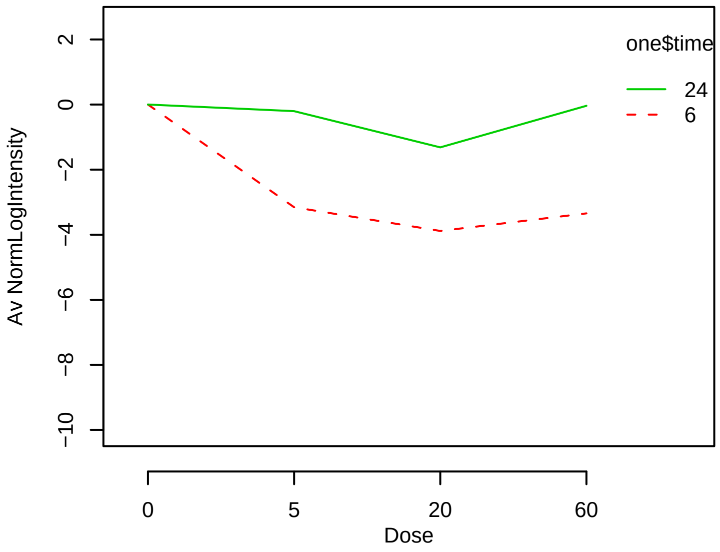
GO_0042572 : retinol metabolism



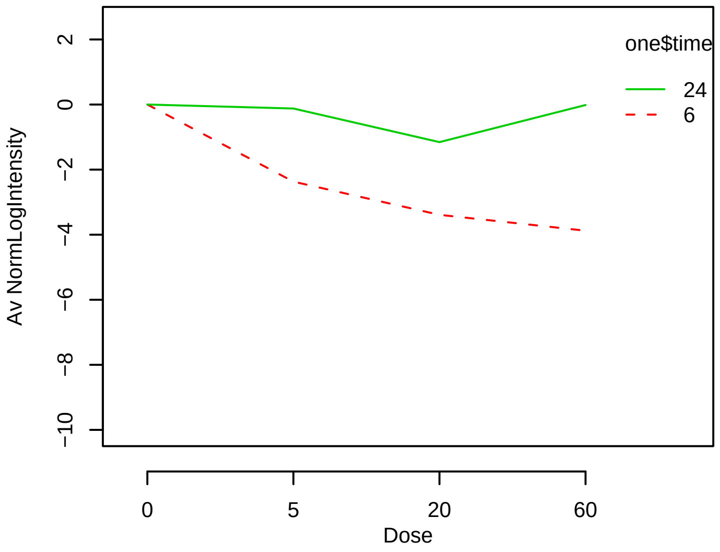
GO_0042573 : retinoic acid metabolism

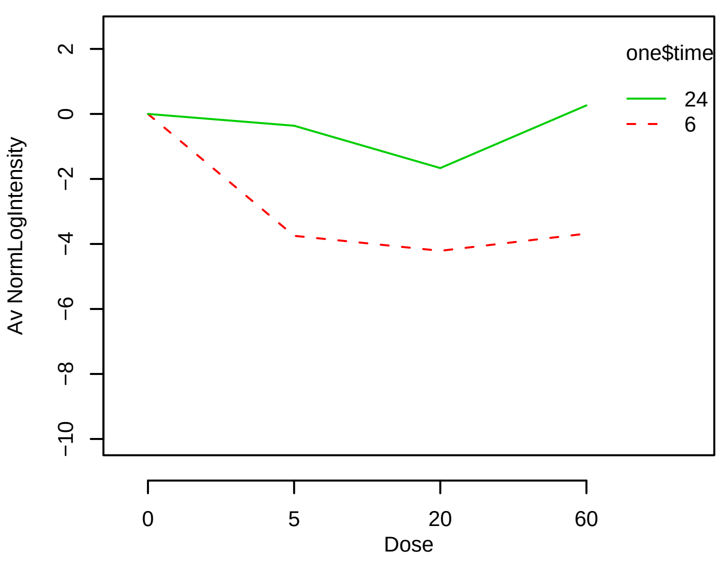


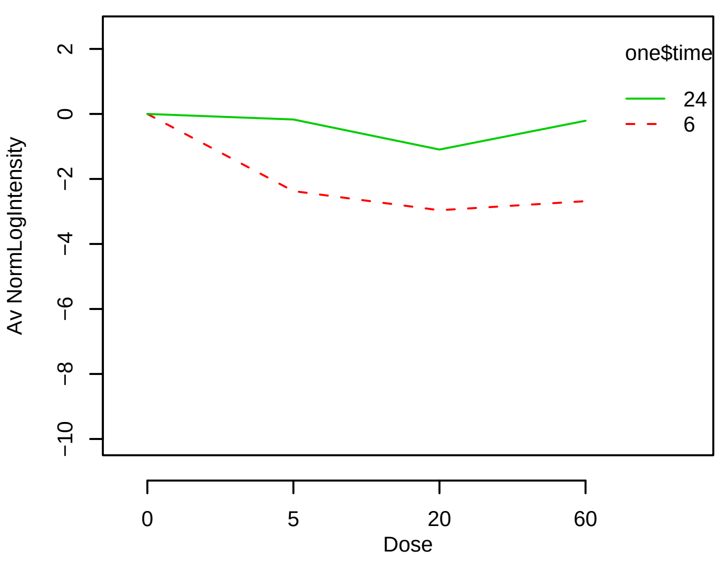
GO_0042593 : glucose homeostasis

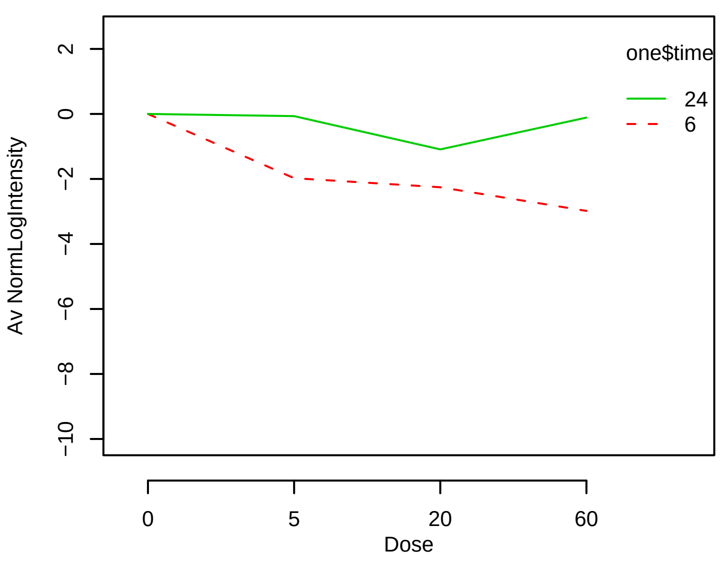


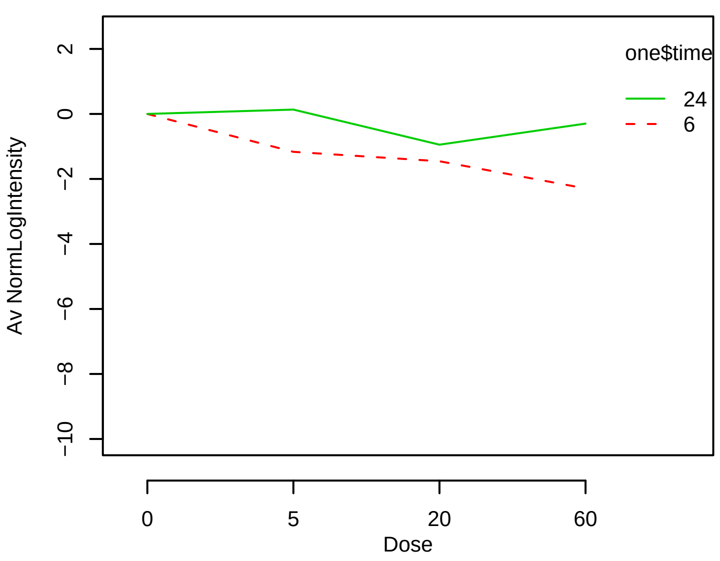
GO_0042594 : response to starvation

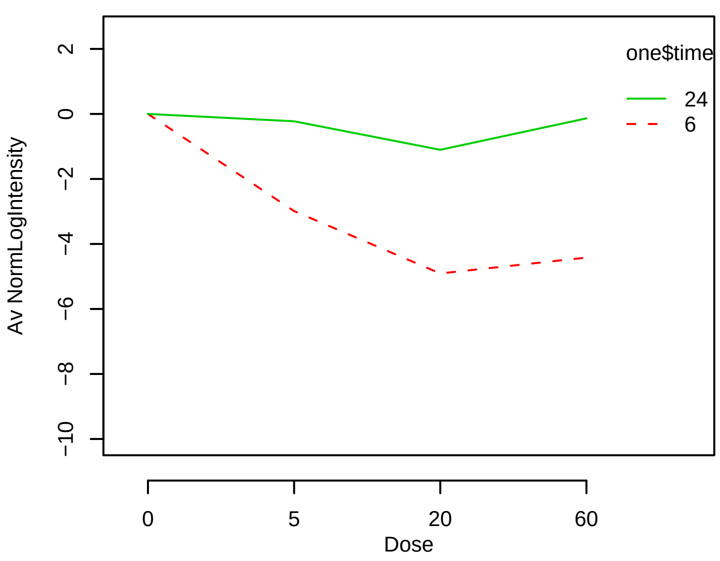


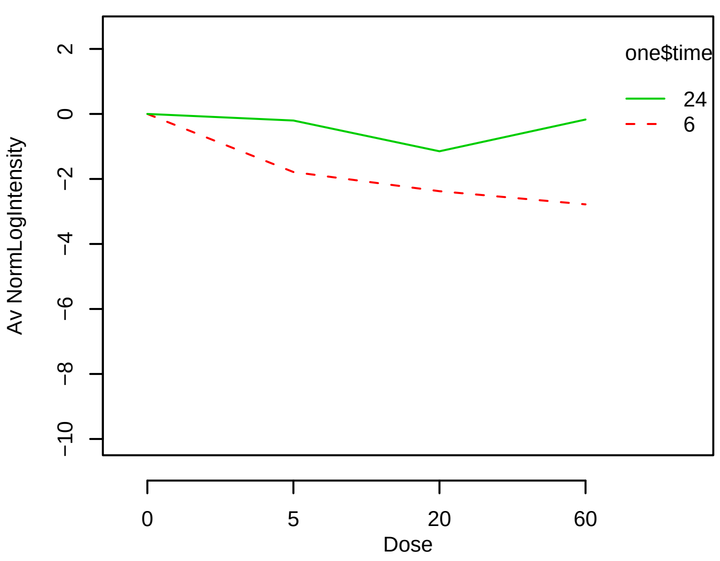

GO_0042596 : fear response


GO_0042632 : cholesterol homeostasis

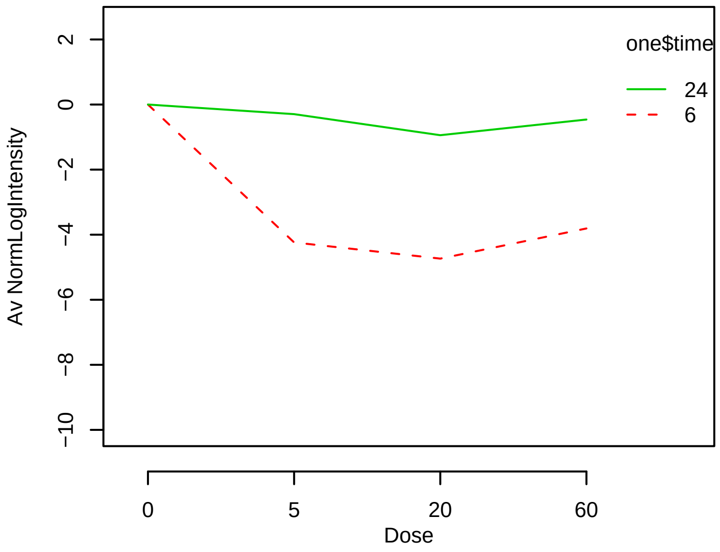

GO_0042633 : hair cycle


GO_0042640 : anagen

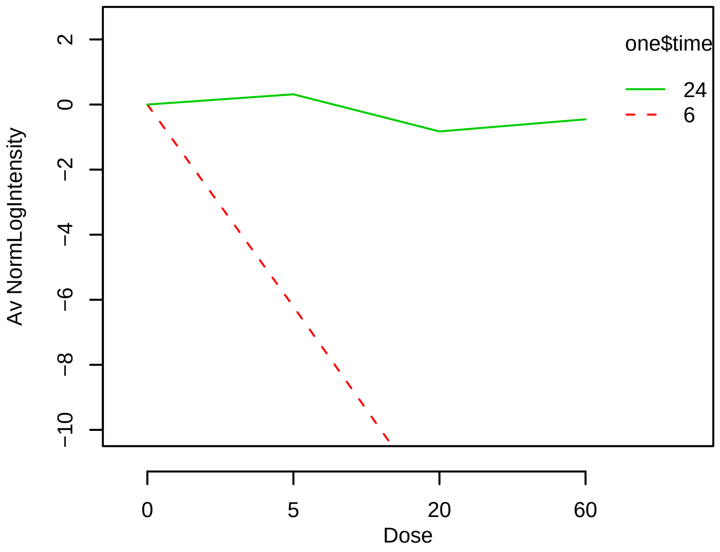

GO_0042692 : muscle cell differentiation


GO_0042698 : menstrual cycle

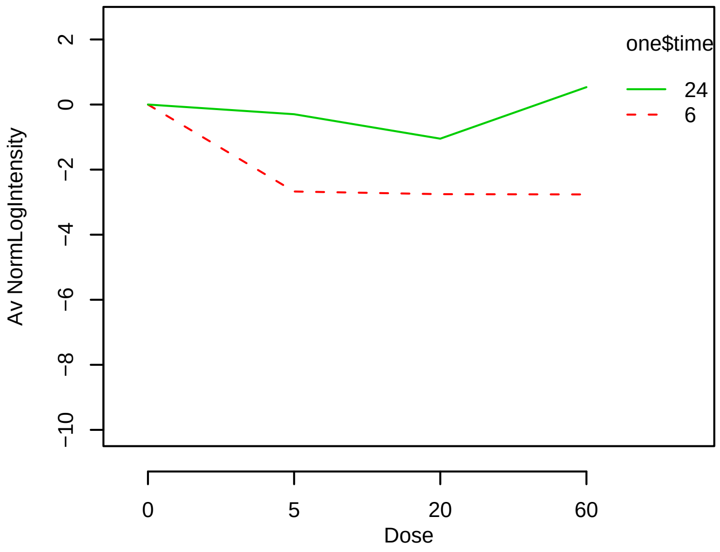
GO_0042730 : fibrinolysis



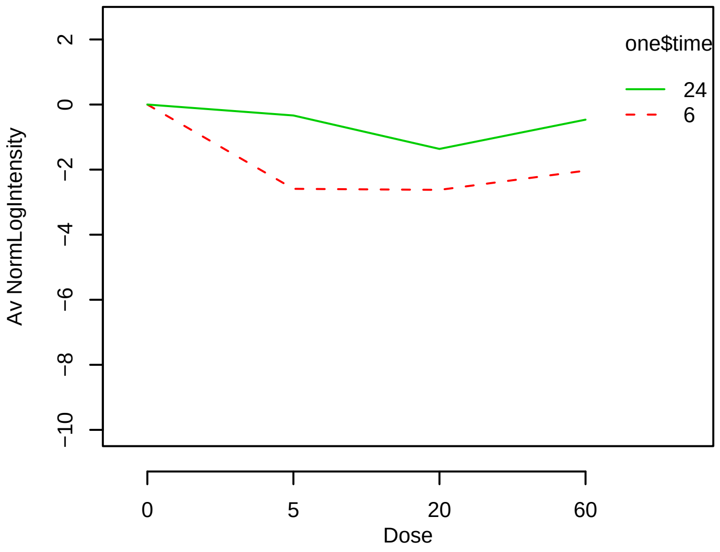
GO_0042733 : embryonic digit morphogenesis



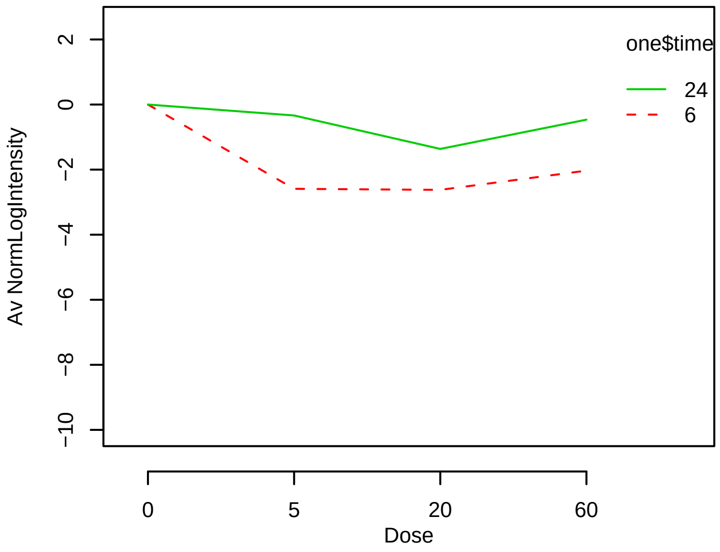
GO_0042742 : defense response to bacterium



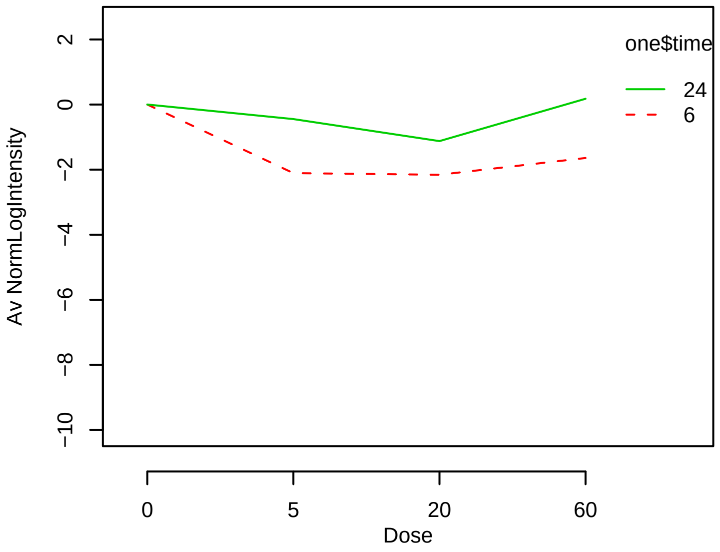
GO_0042743 : hydrogen peroxide metabolism

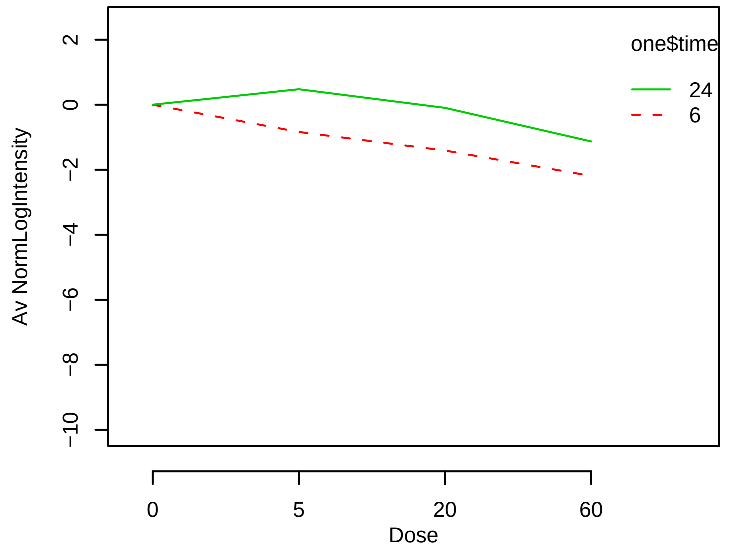


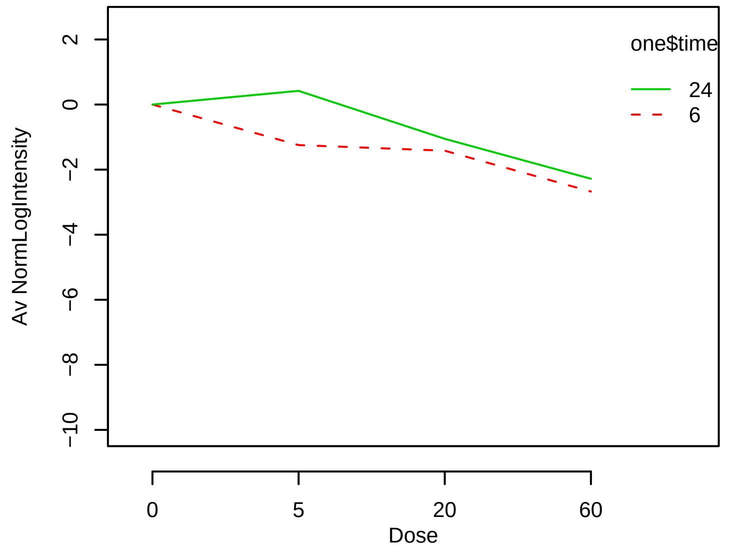
GO_0042744 : hydrogen peroxide catabolism

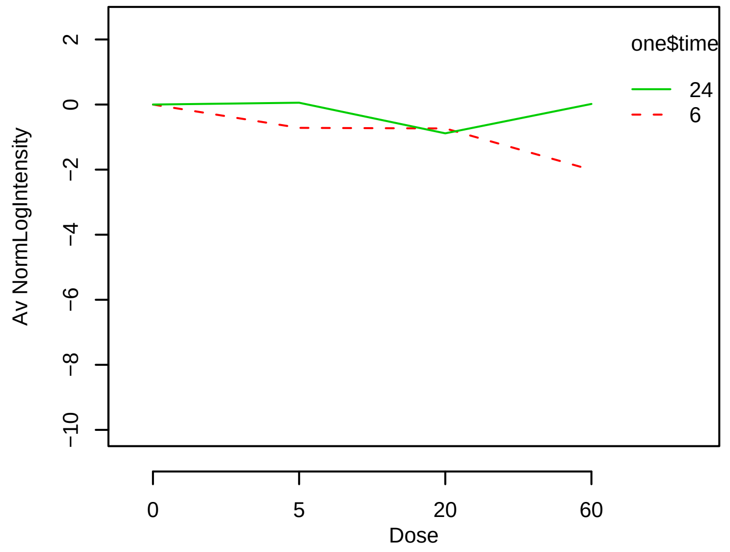


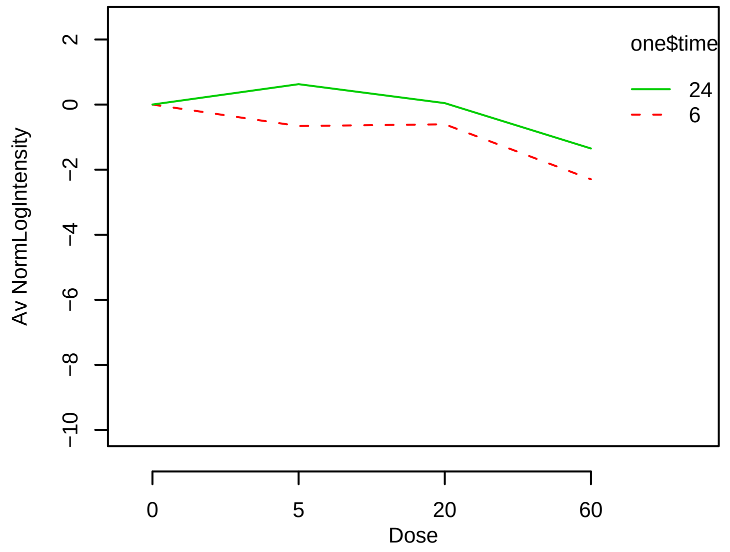
GO_0042755 : eating behavior

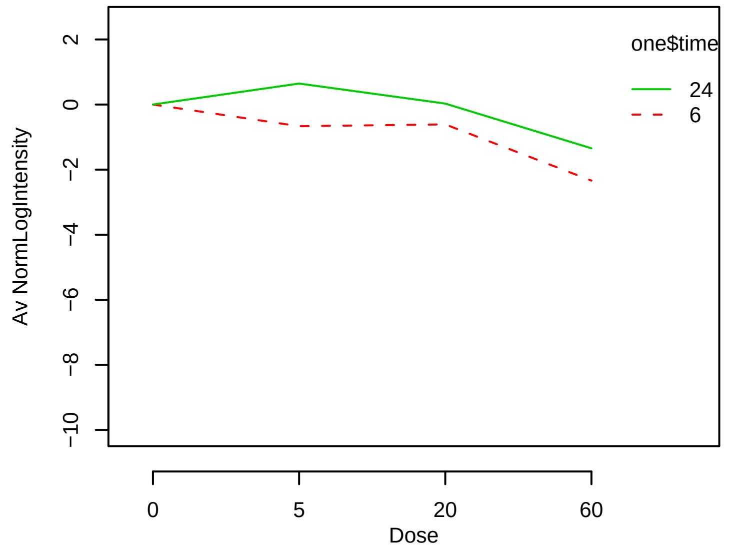


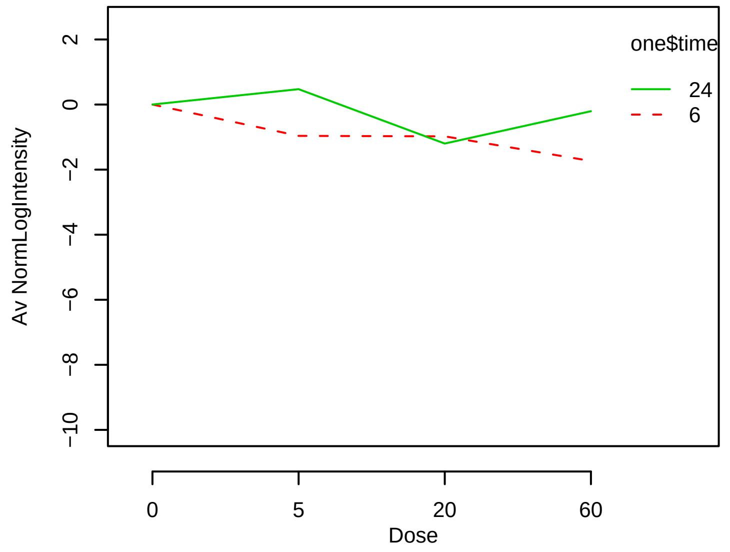

GO_0042769 : DNA damage response\, detection of DNA dam

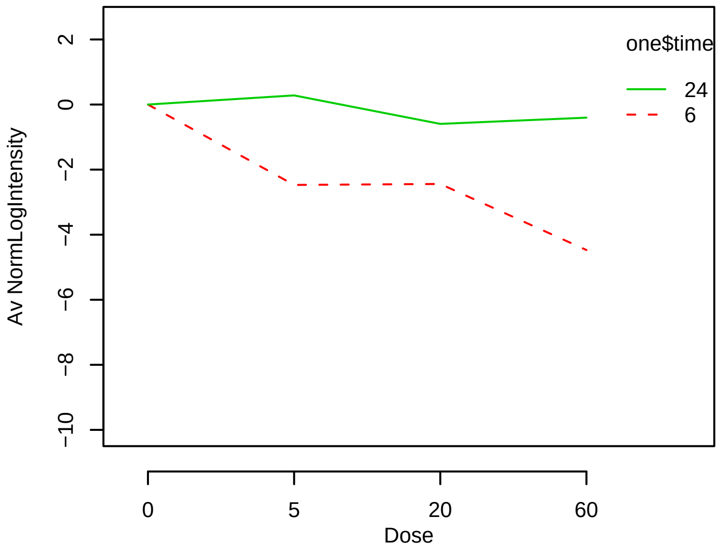

GO_0042770 : DNA damage response\, signal transductio


O_0042771 : DNA damage response\, signal transduction by

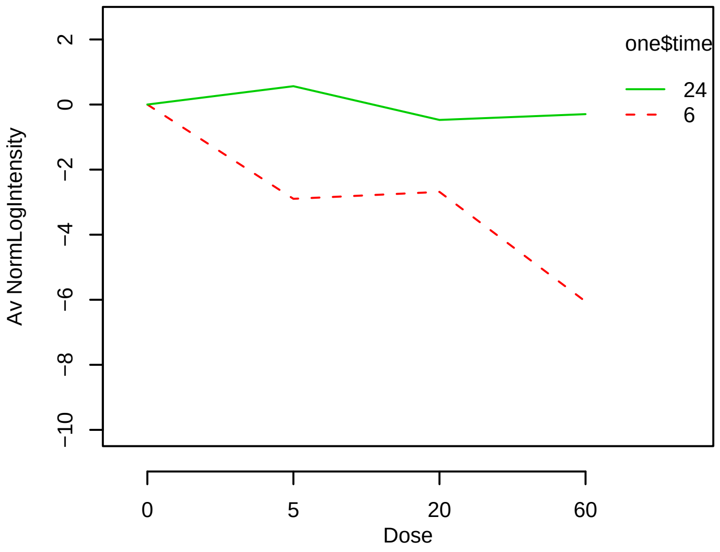

GO_0042773 : ATP synthesis coupled electron transport


O_0042775 : ATP synthesis coupled electron transport (sens

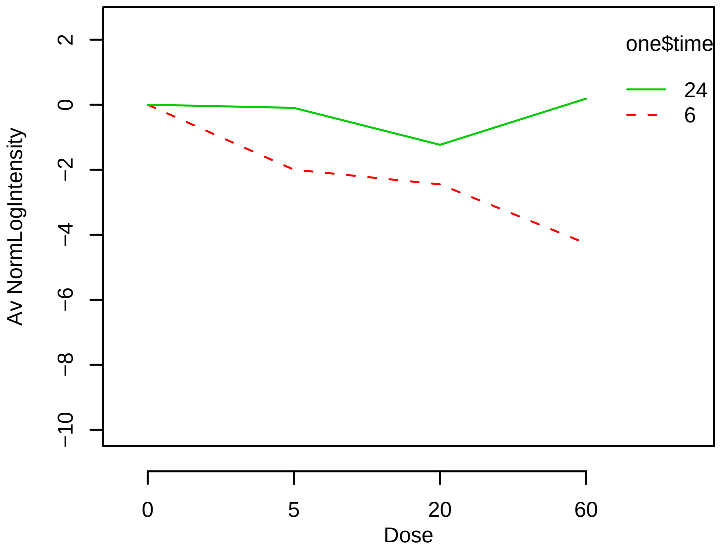

GO_0042787 : protein ubiquitination during ubiquitin−depen



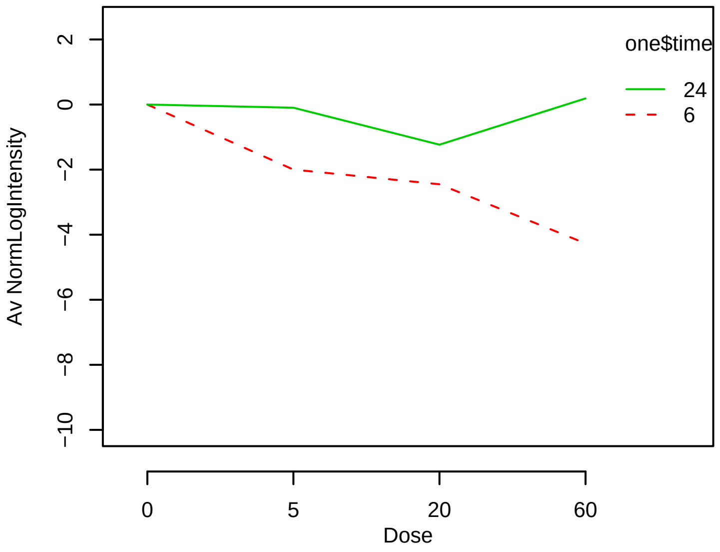
GO_0042982 : amyloid precursor protein metabolism



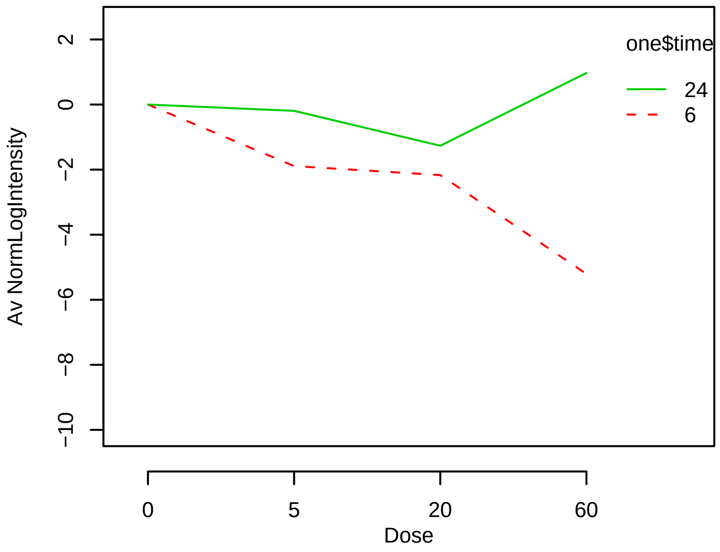
GO_0042987 : amyloid precursor protein catabolism



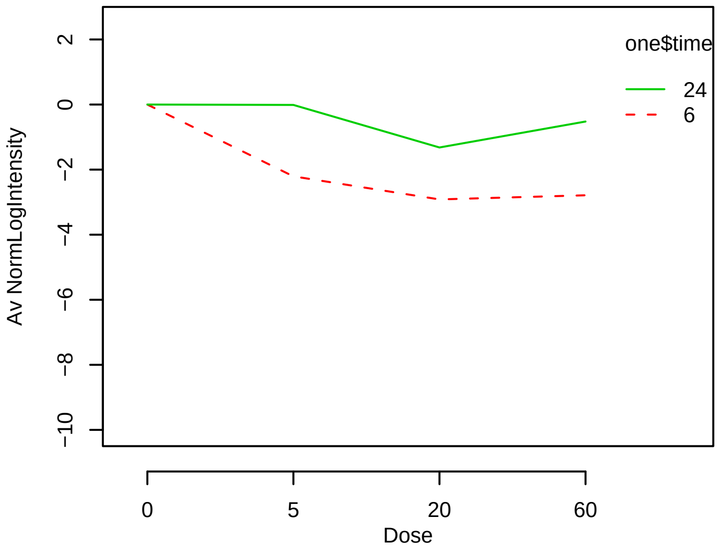
GO_0042990 : regulation of transcription factor import into r



GO_0042991 : transcription factor import into nucleus

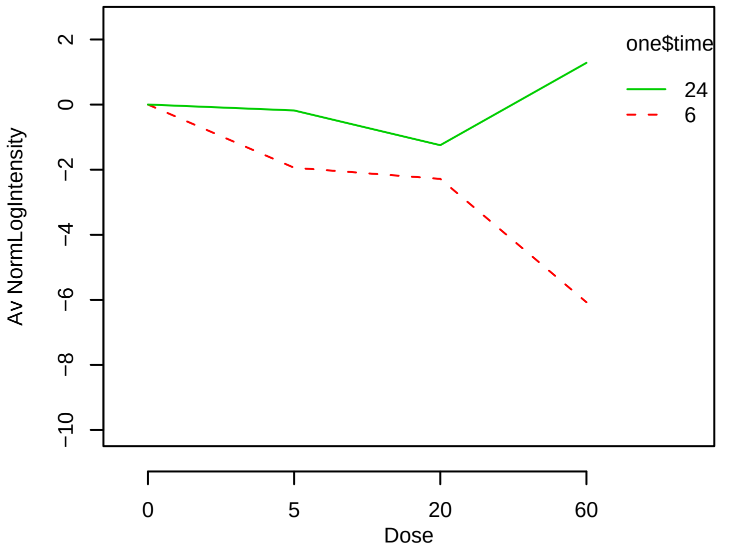


GO_0042992 : negative regulation of transcription factor imp

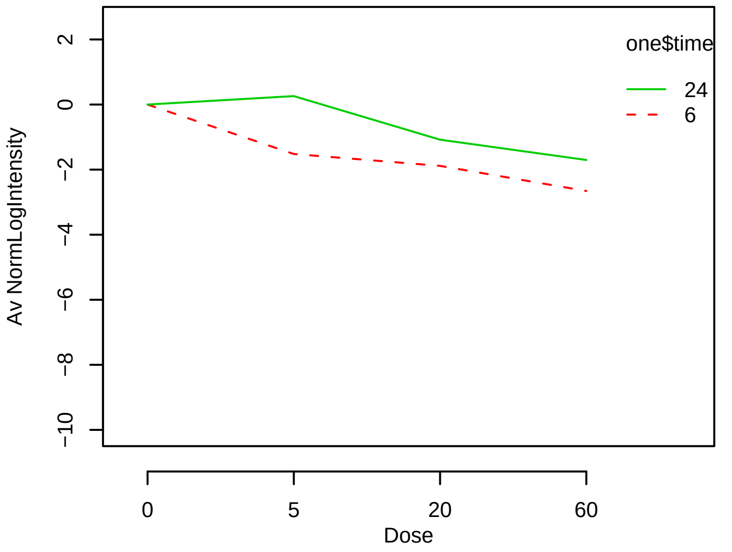


GO_0042993 : positive regulation of transcription factor imp

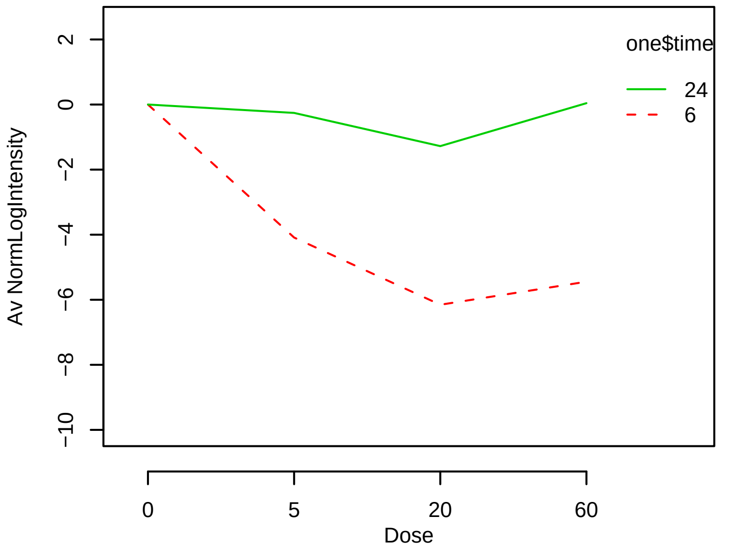
GO_0042994 : cytoplasmic sequestering of transcription fac



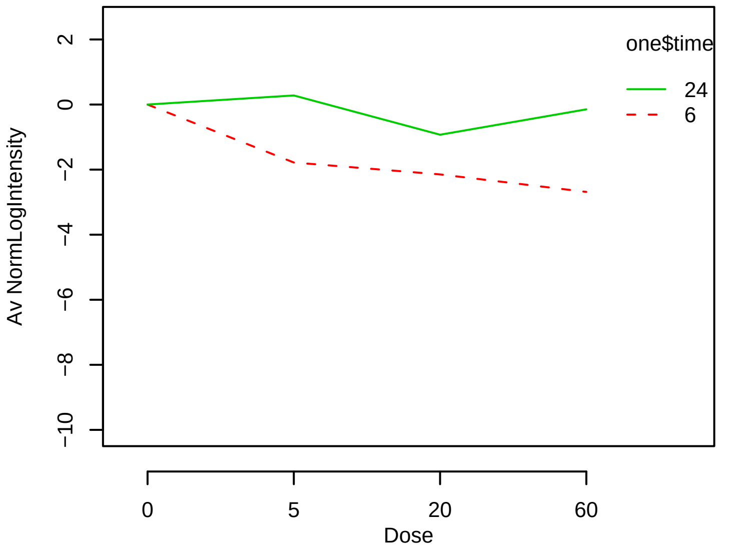
GO_0043009 : embryonic development (sensu Vertebrata



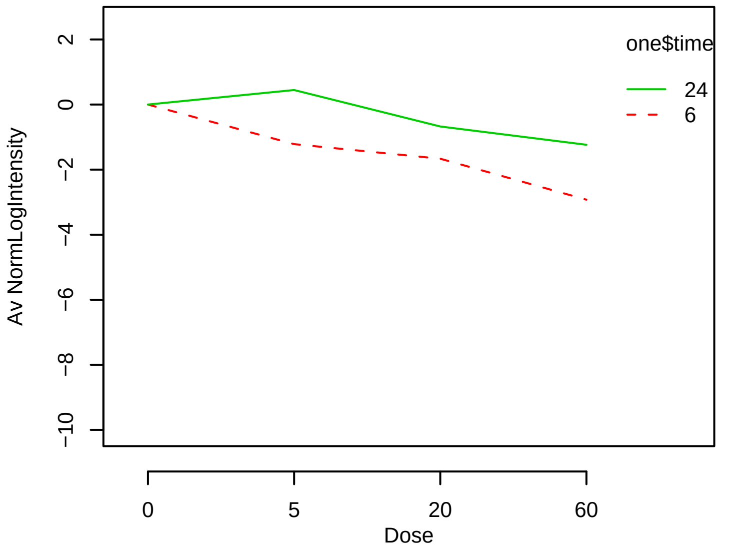
GO_0043010 : eye development (sensu Vertebrata)



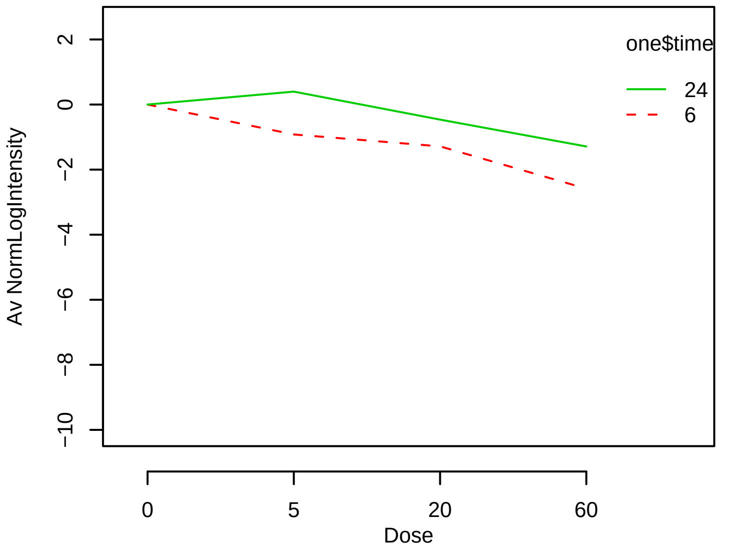
GO_0043029 : T cell homeostasis

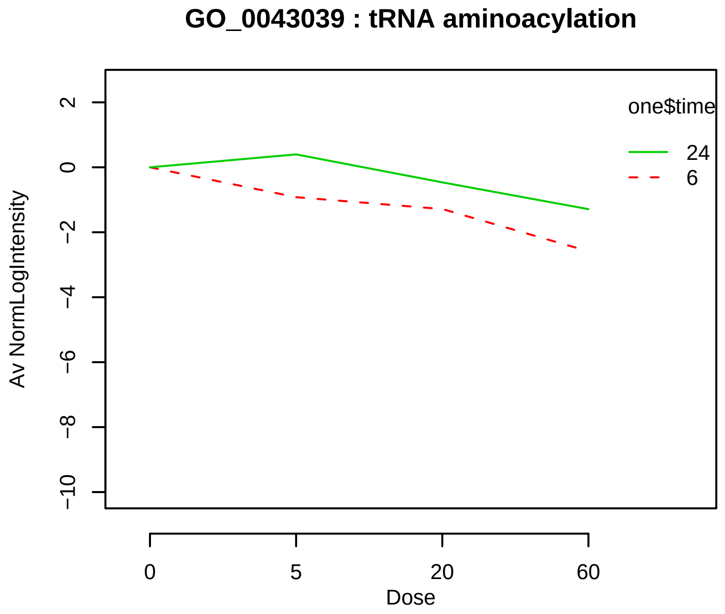


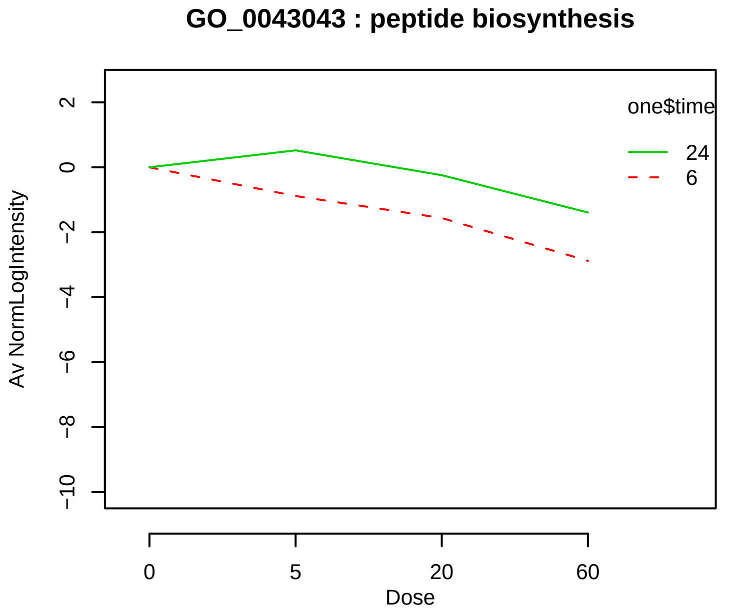
GO_0043037 : translation

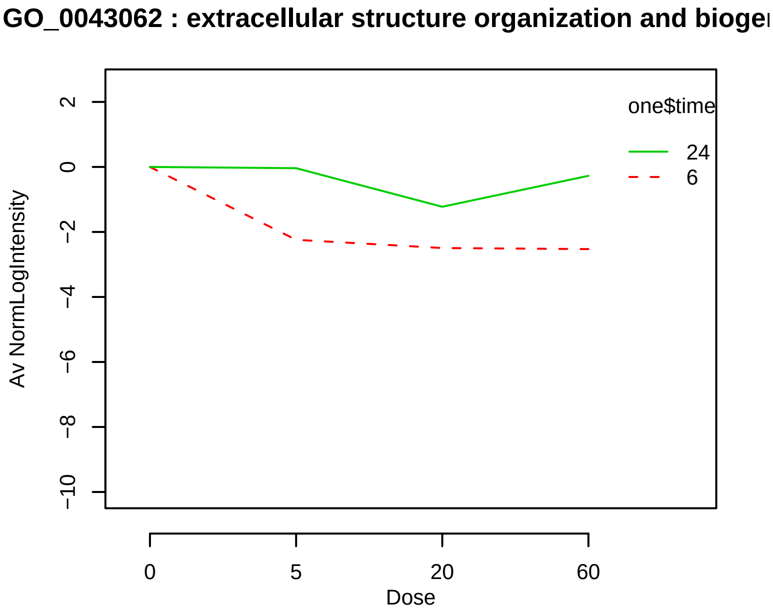


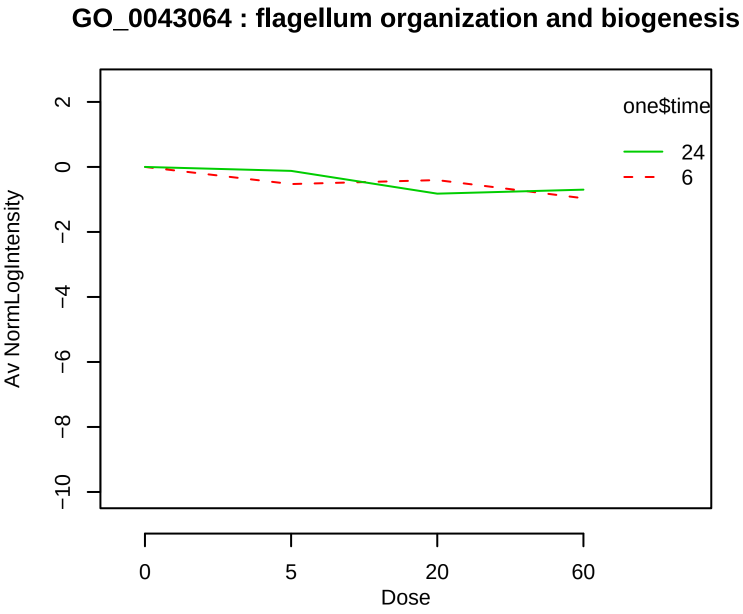
GO_0043038 : amino acid activation

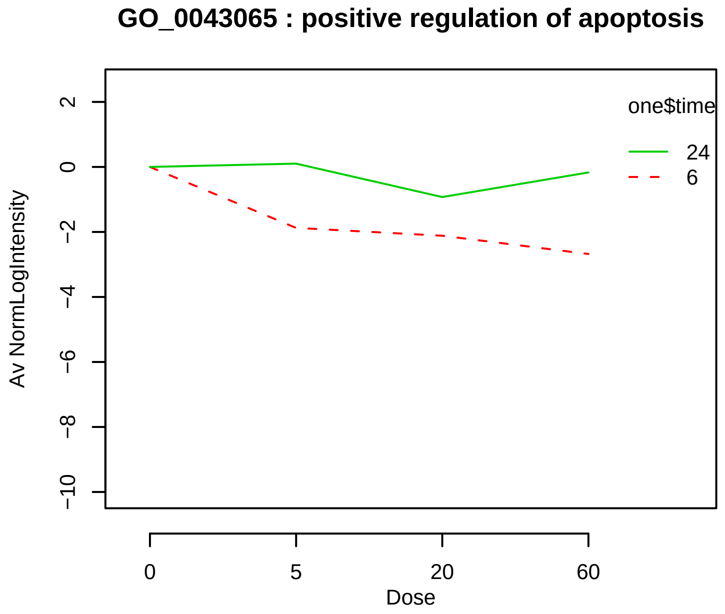


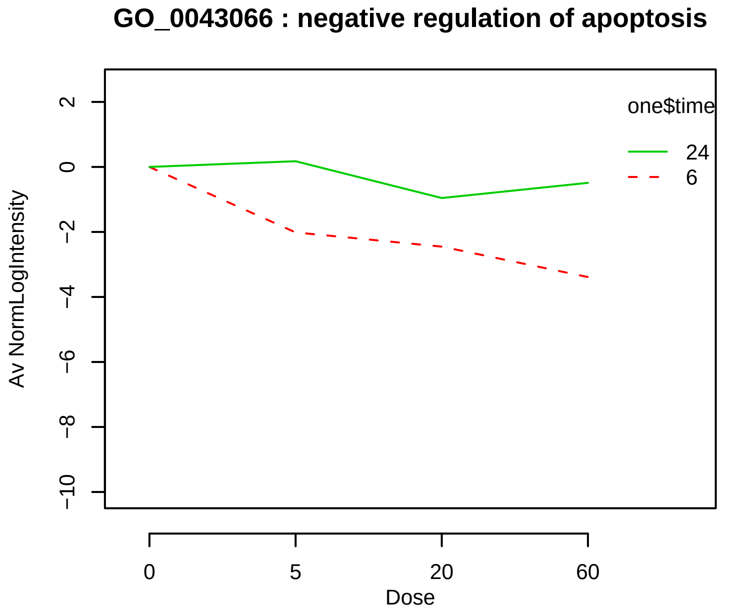

GO_0043039 : tRNA aminoacylation

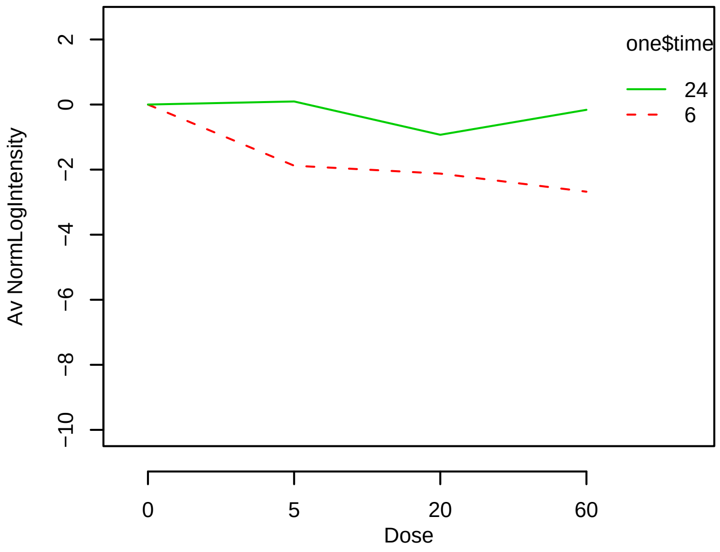

GO_0043043 : peptide biosynthesis

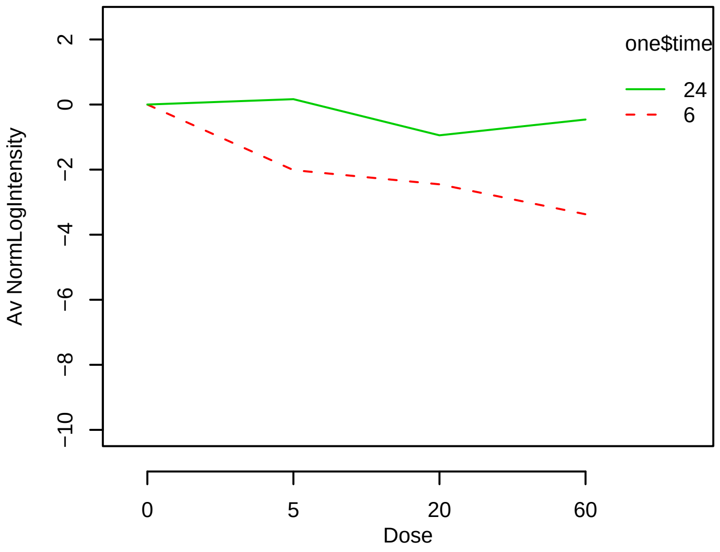

GO_0043062 : extracellular structure organization and bioge

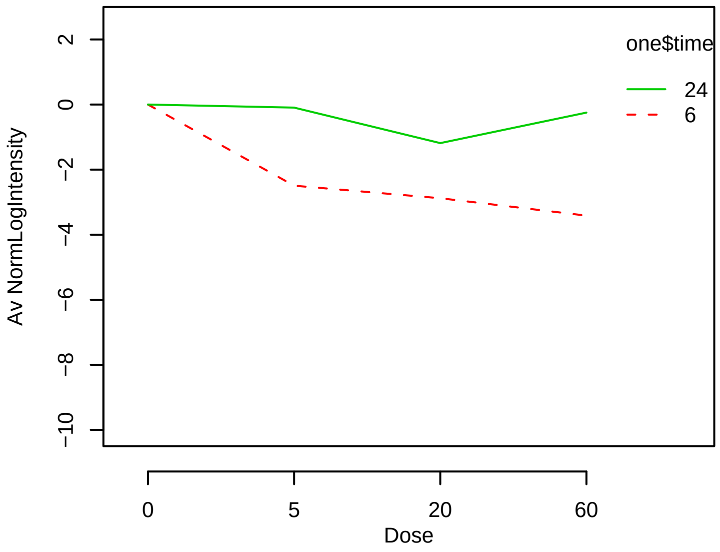

GO_0043064 : flagellum organization and biogenesis

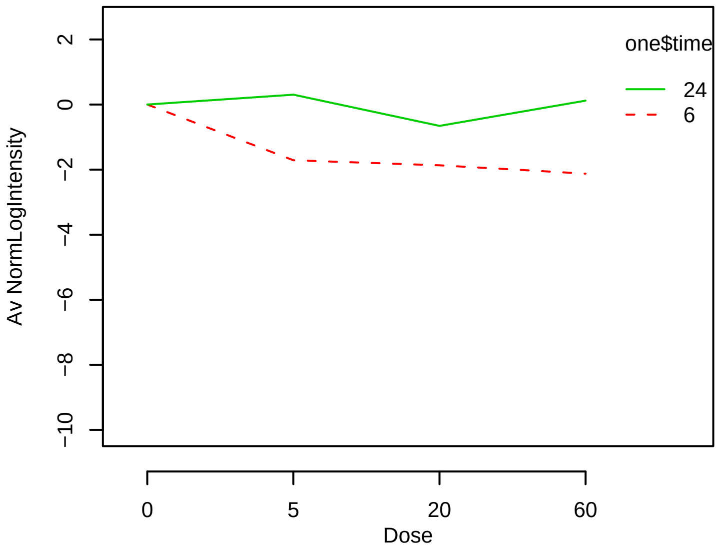

GO_0043065 : positive regulation of apoptosis

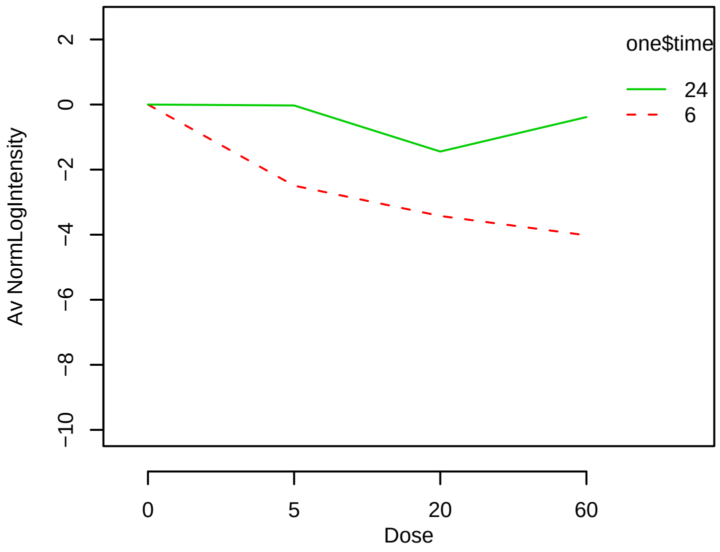

GO_0043066 : negative regulation of apoptosis

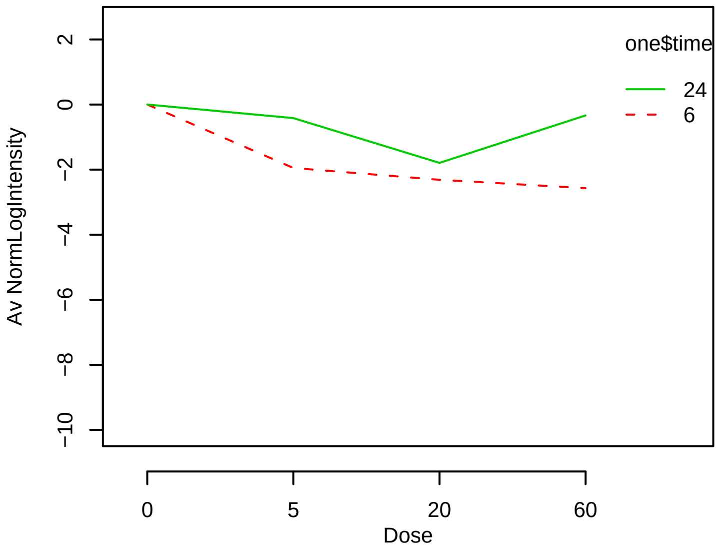

GO_0043068 : positive regulation of programmed cell deat


GO_0043069 : negative regulation of programmed cell deat

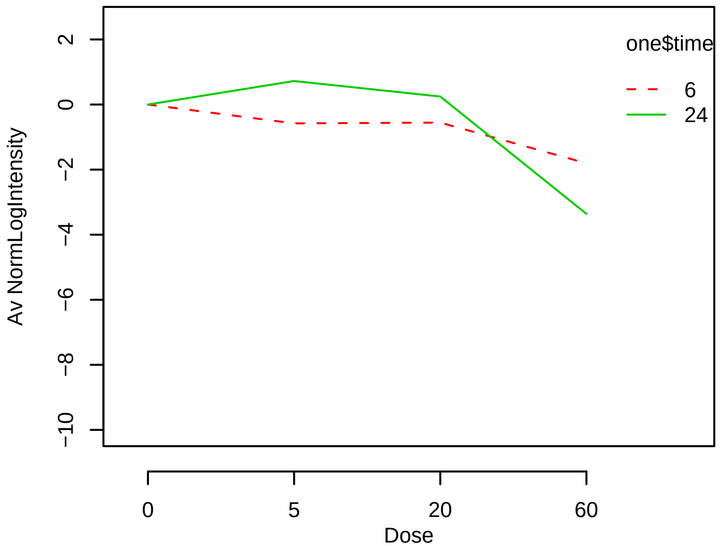

GO_0043085 : positive regulation of enzyme activity


GO_0043086 : negative regulation of enzyme activity

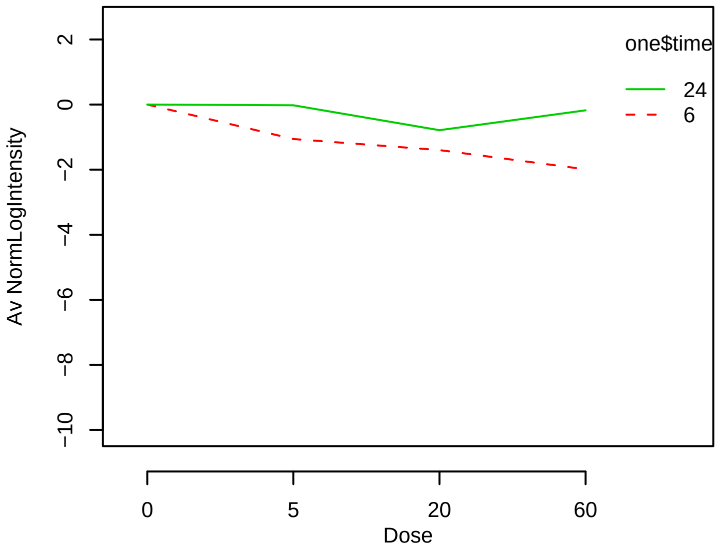

GO_0043087 : regulation of GTPase activity


GO_0043088 : regulation of Cdc42 GTPase activity

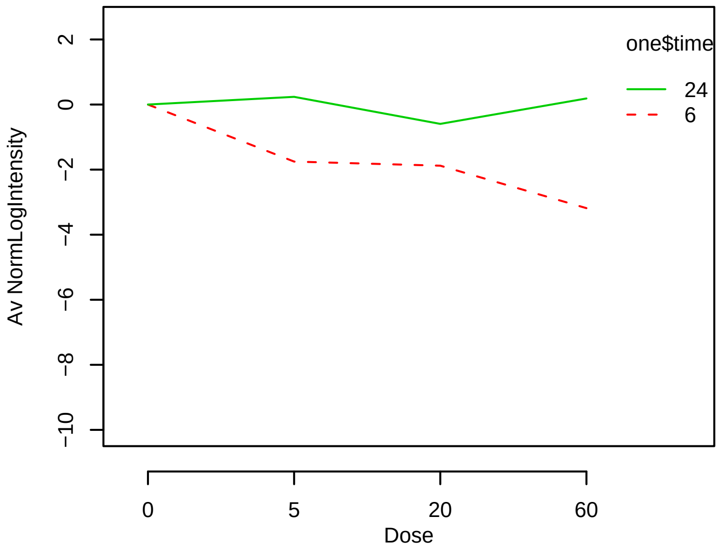
GO_0043094 : metabolic compound salvage



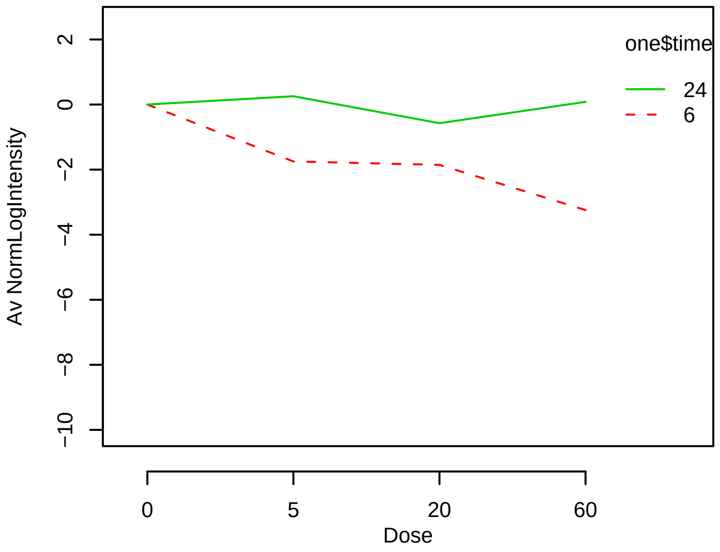
GO_0043112 : receptor metabolism



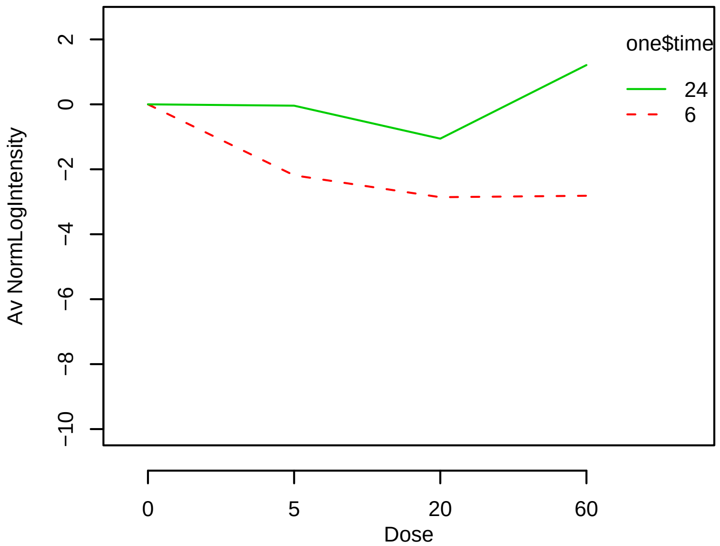
GO_0043122 : regulation of I−kappaB kinase/NF−kappaB cas



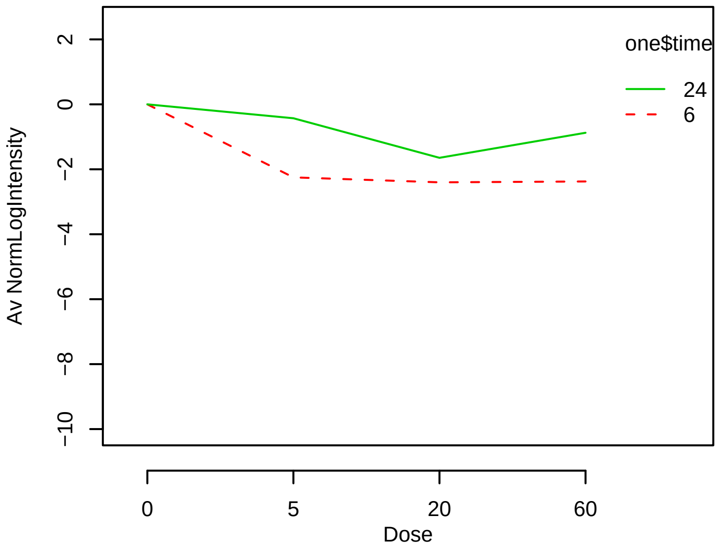
O_0043123 : positive regulation of I−kappaB kinase/NF−kapp



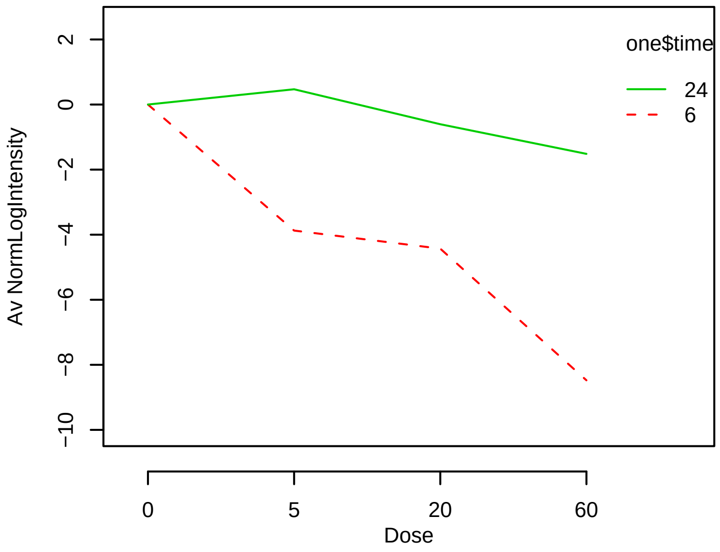
O_0043124 : negative regulation of I−kappaB kinase/NF−kap



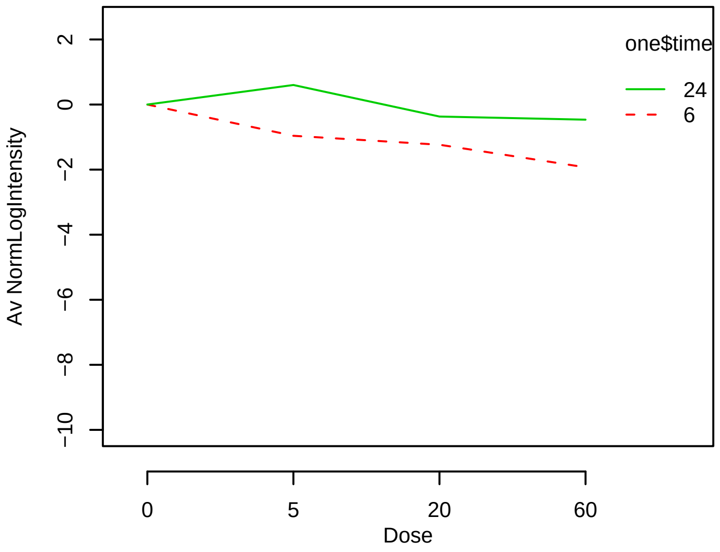
GO_0043149 : stress fiber formation



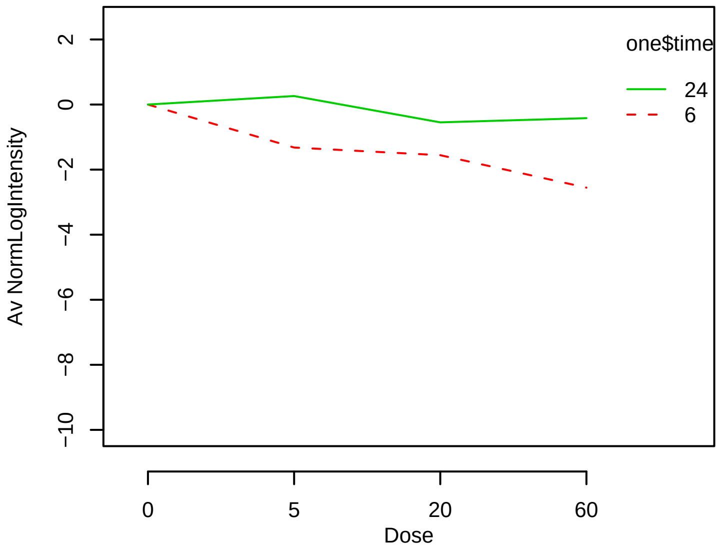
GO_0043154 : negative regulation of caspase activity



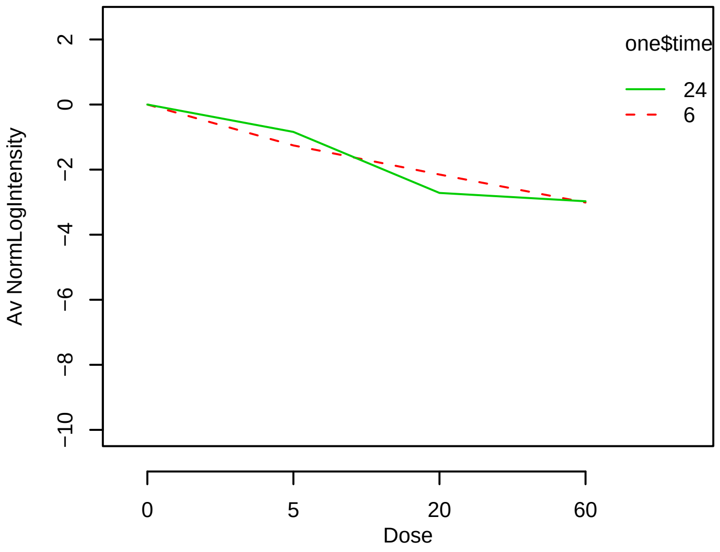
O_0043161 : proteasomal ubiquitin−dependent protein catab



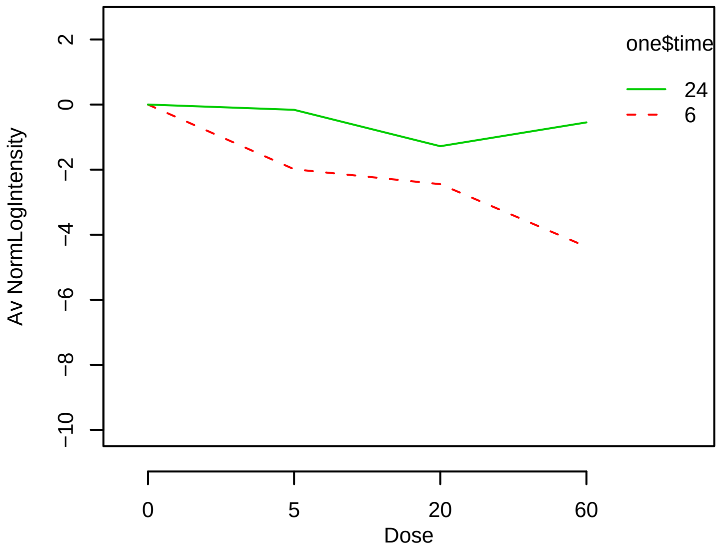
GO_0043193 : positive regulation of gene−specific transcript



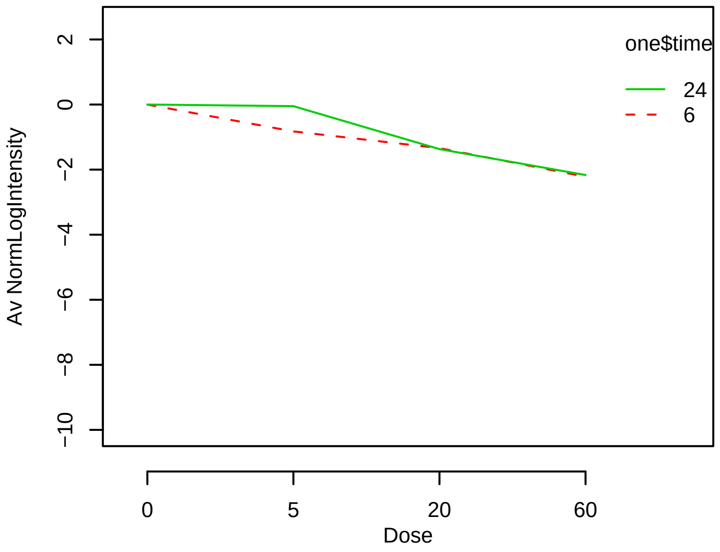
GO_0043241 : protein complex disassembly



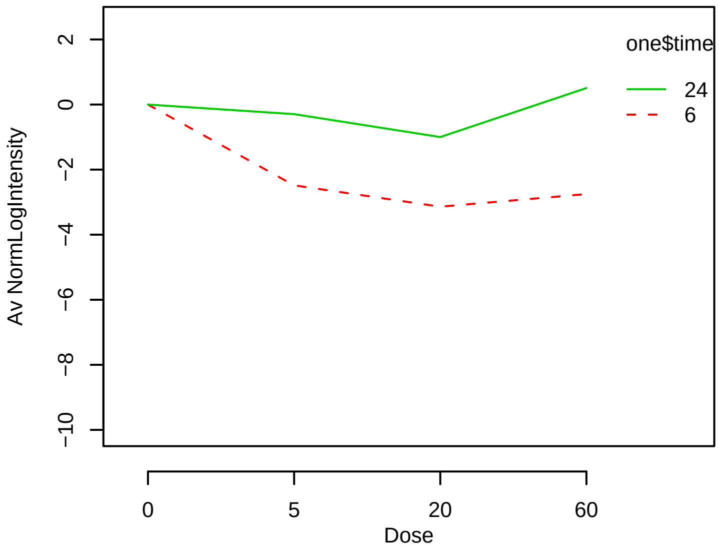
GO_0043254 : regulation of protein complex assembly



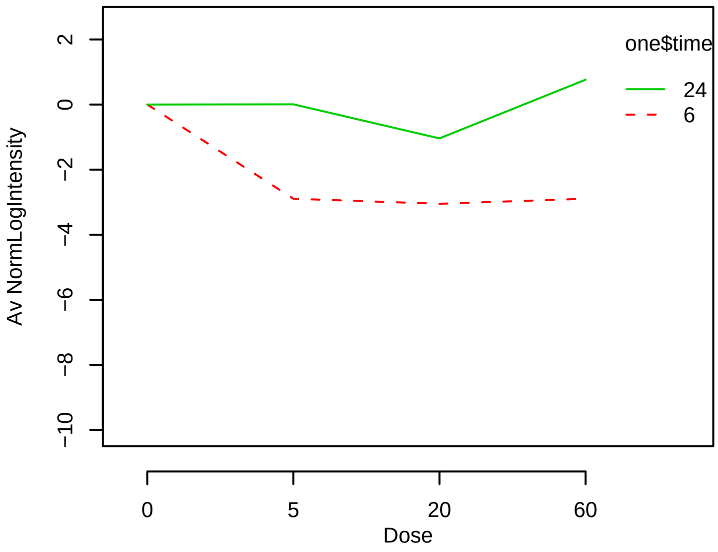
GO_0043255 : regulation of carbohydrate biosynthesis



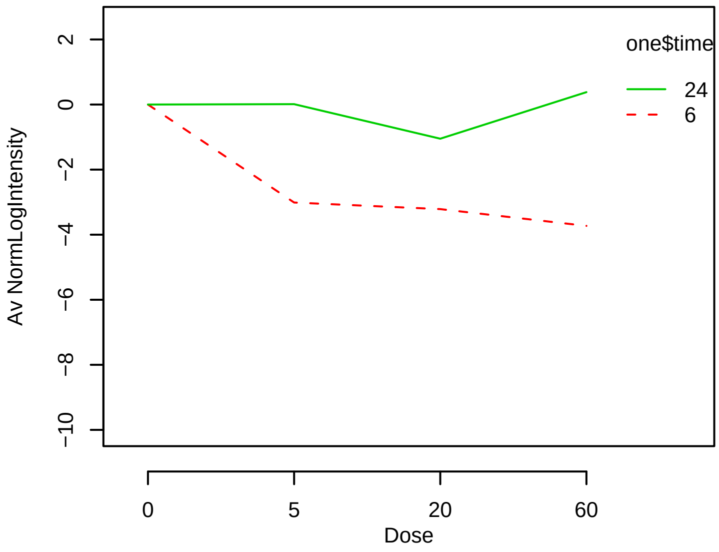
GO_0043269 : regulation of ion transport



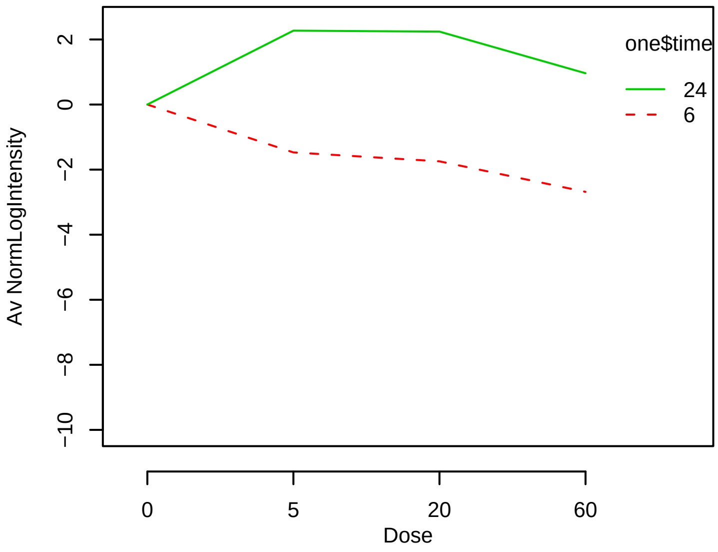
GO_0043280 : positive regulation of caspase activity



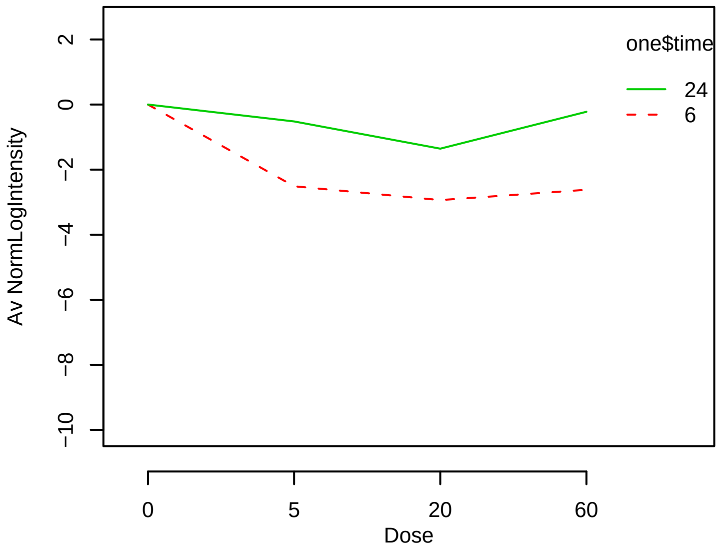
GO_0043281 : regulation of caspase activity



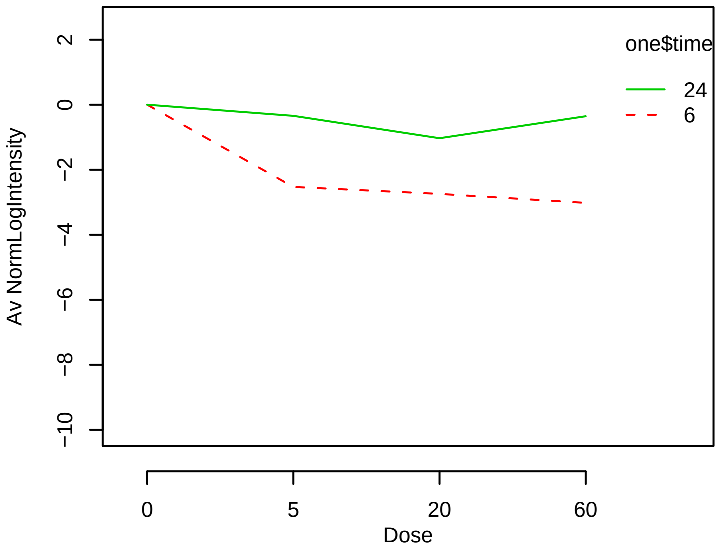
GO_0043284 : biopolymer biosynthesis



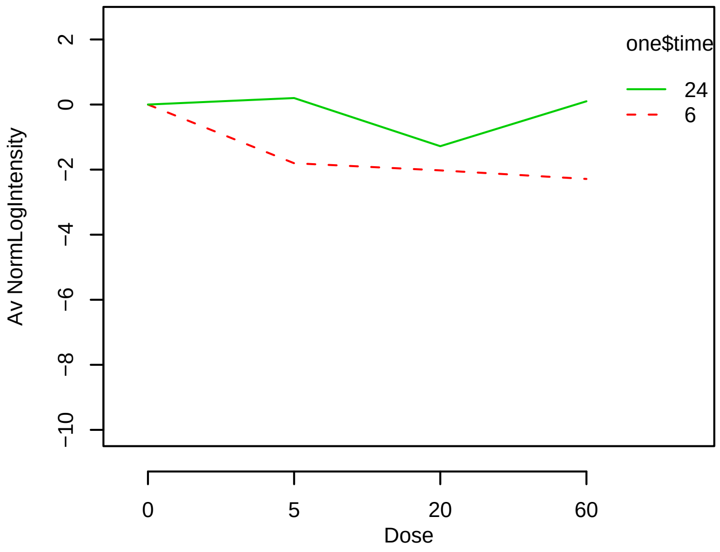
GO_0043299 : leukocyte degranulation



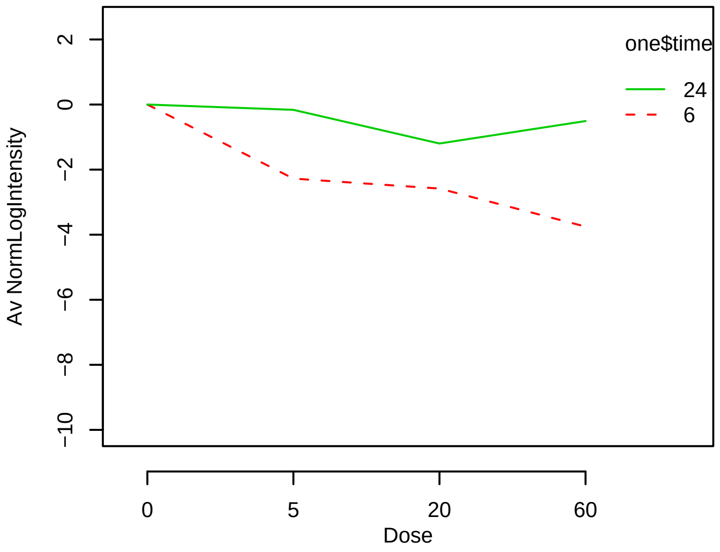
GO_0043303 : mast cell degranulation



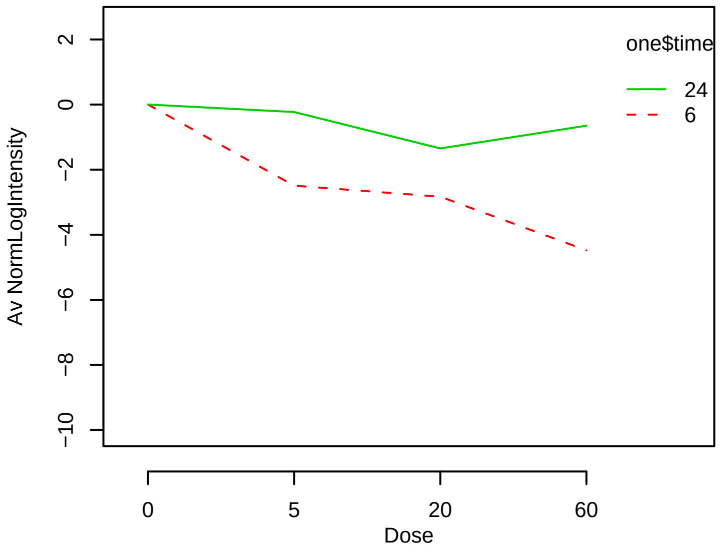
GO_0043393 : regulation of protein binding



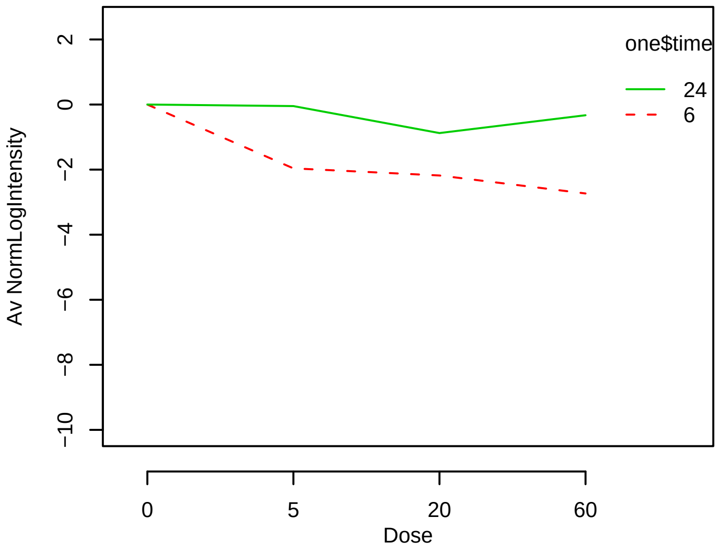
GO_0043405 : regulation of MAPK activity



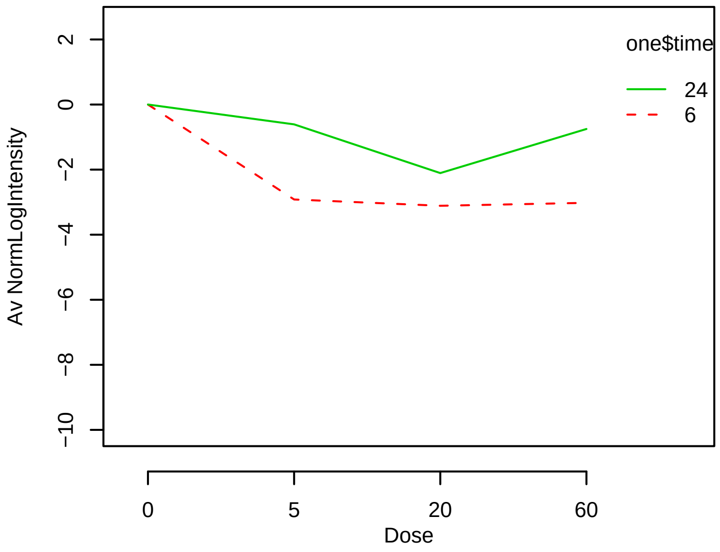
GO_0043406 : positive regulation of MAPK activity



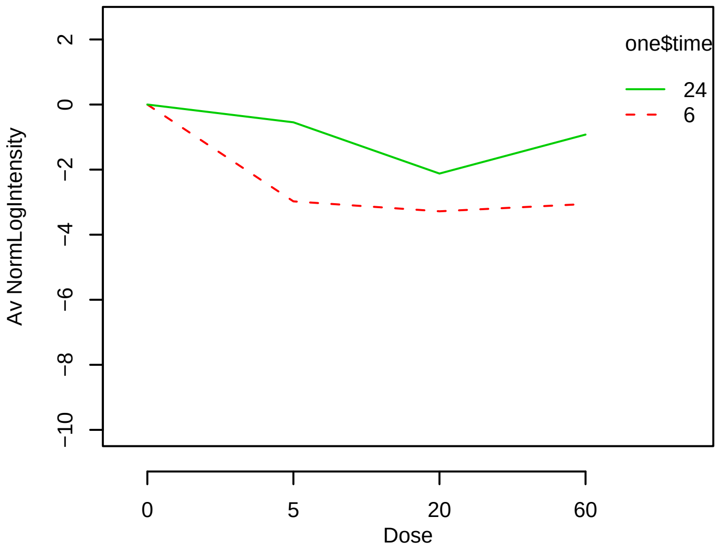
GO_0043407 : negative regulation of MAPK activity

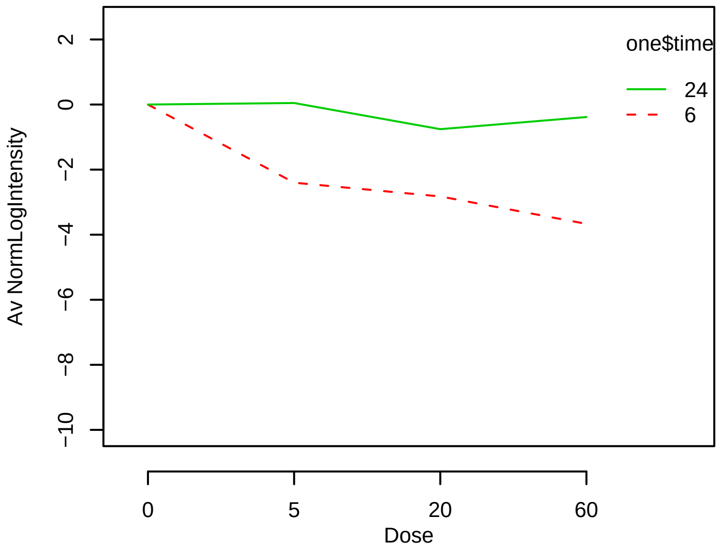


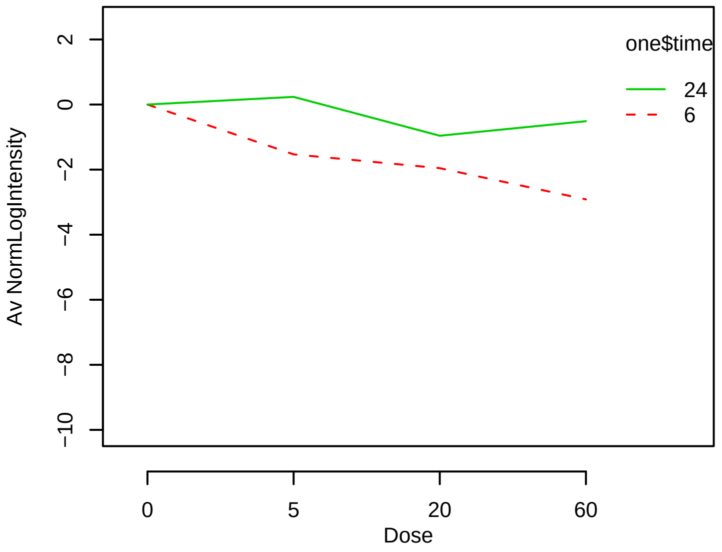
GO_0043408 : regulation of MAPKKK cascade

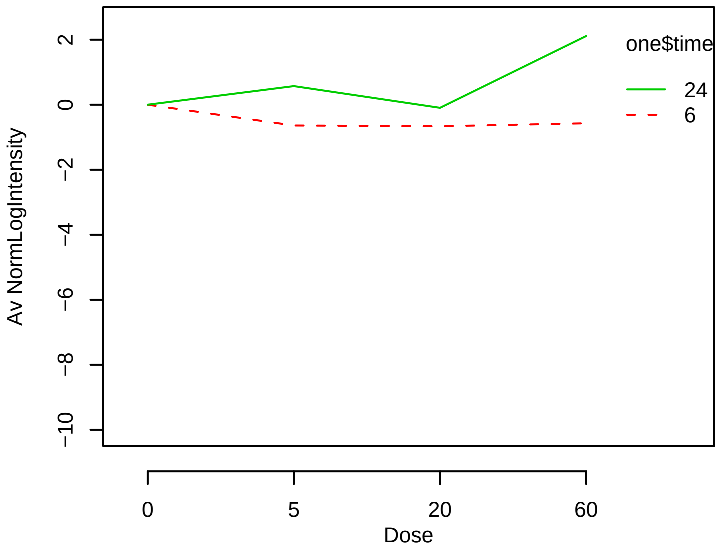


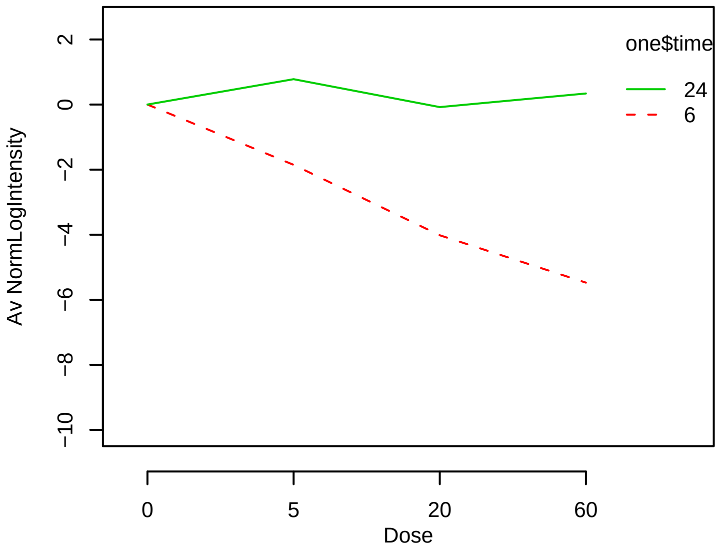
GO_0043410 : positive regulation of MAPKKK cascade

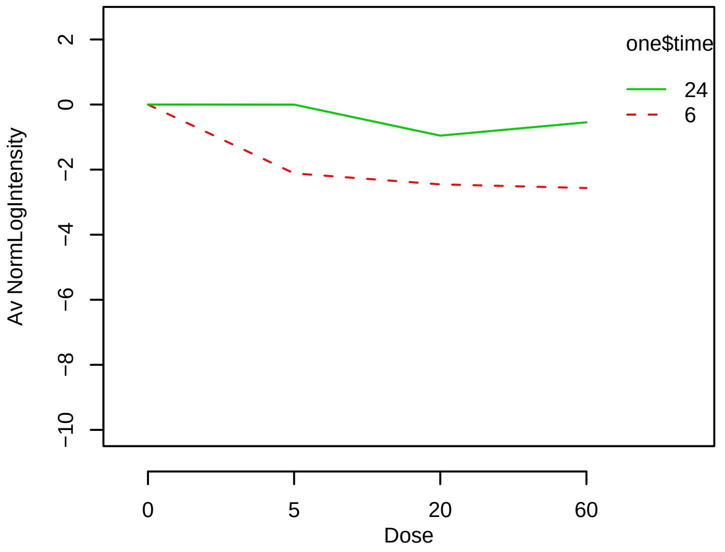


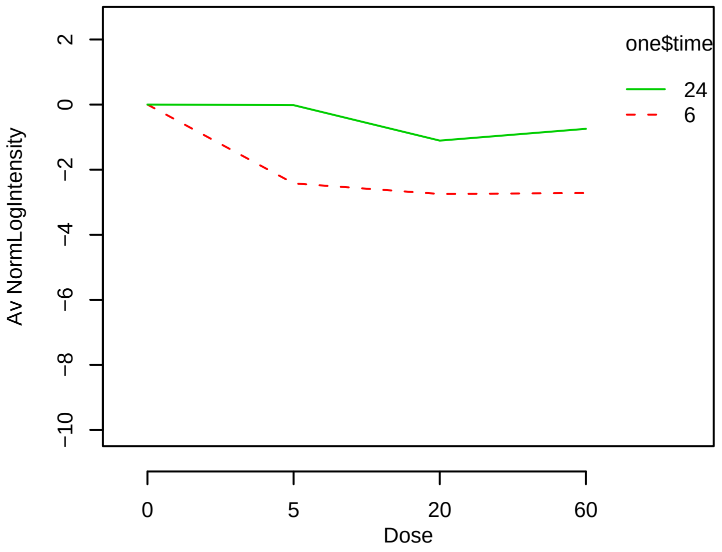

GO_0043413 : biopolymer glycosylation

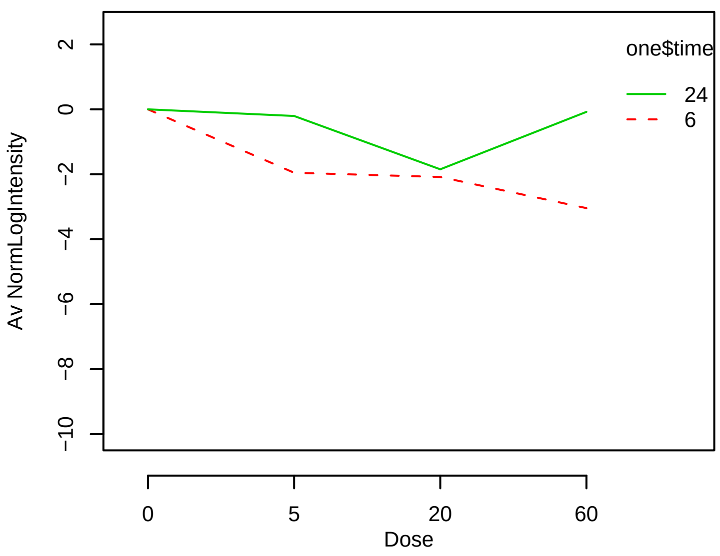

GO_0043414 : biopolymer methylation


GO_0043433 : negative regulation of transcription factor act

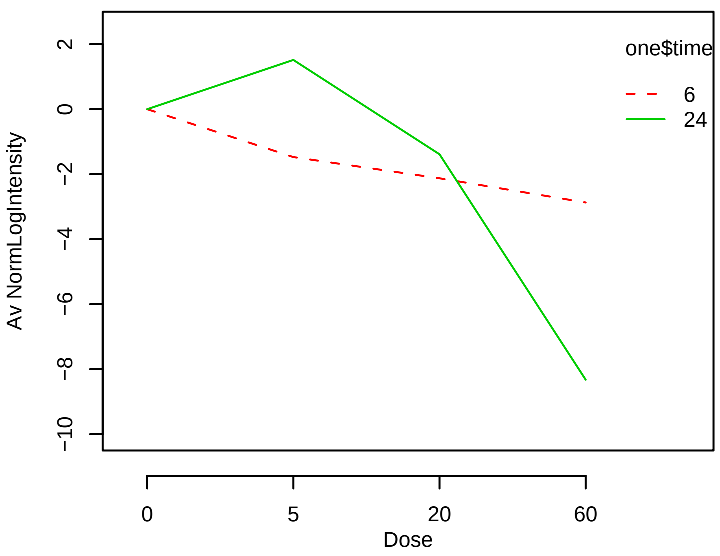

GO_0043434 : response to peptide hormone stimulus


GO_0043449 : alkene metabolism

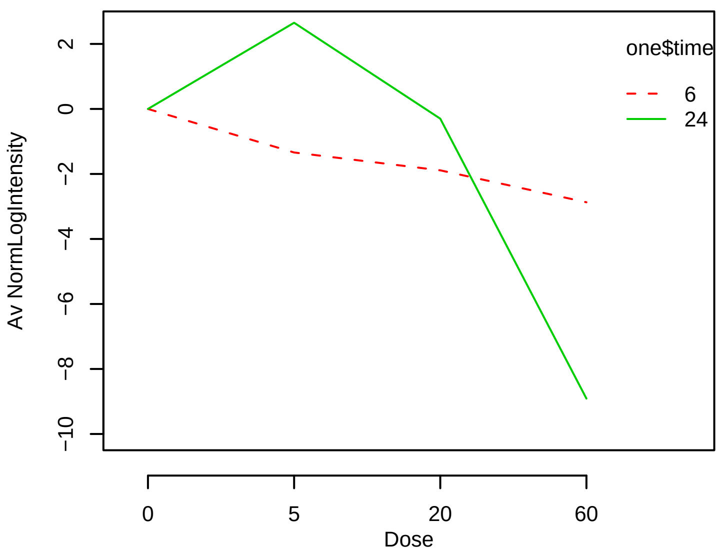

GO_0043450 : alkene biosynthesis



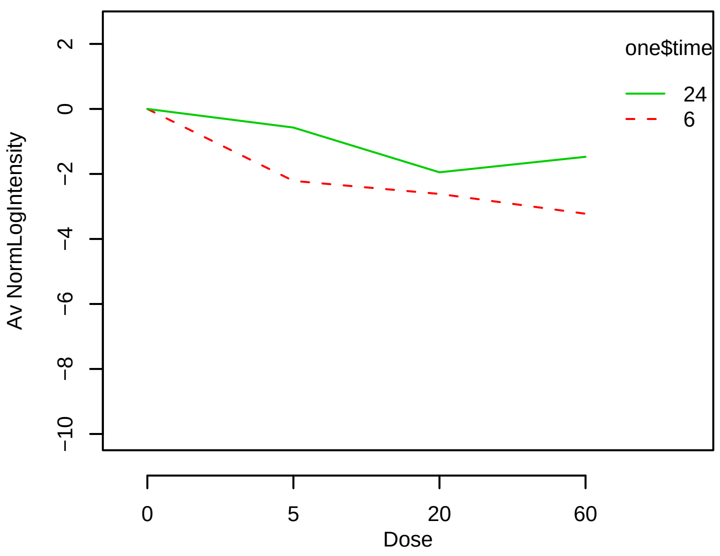
GO_0043473 : pigmentation



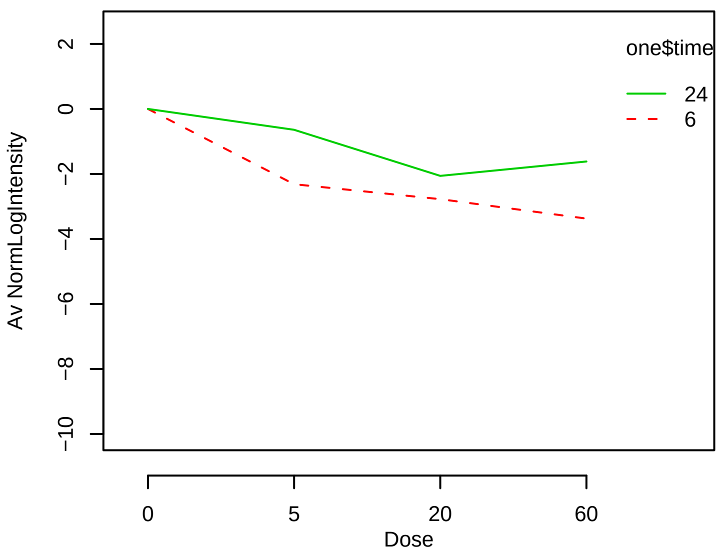
GO_0043487 : regulation of RNA stability



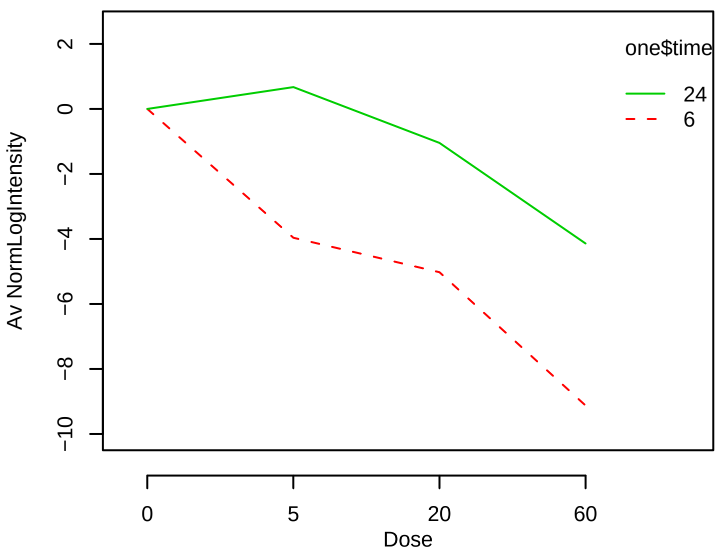
GO_0043488 : regulation of mRNA stability



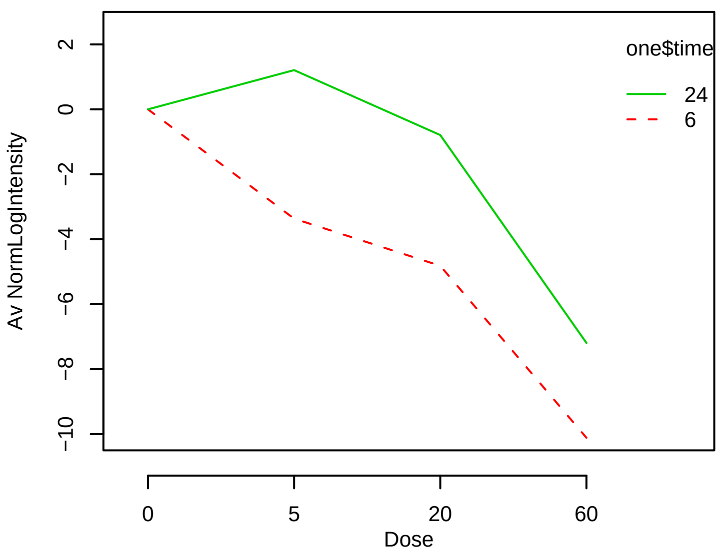
GO_0043506 : regulation of JNK activity

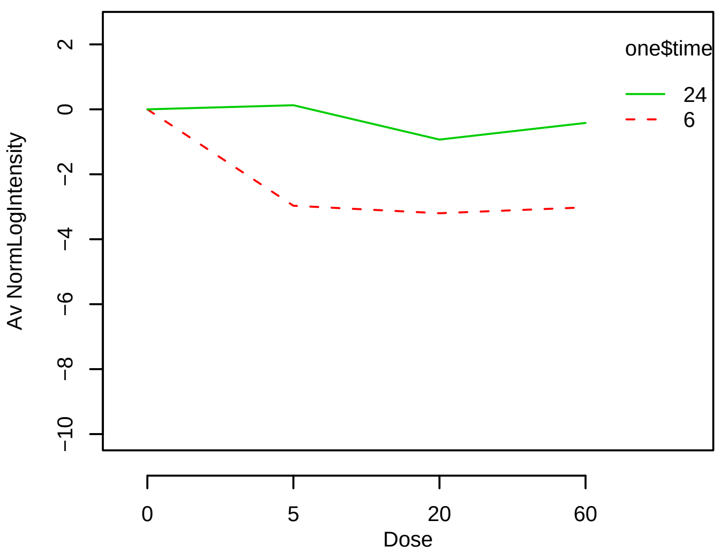


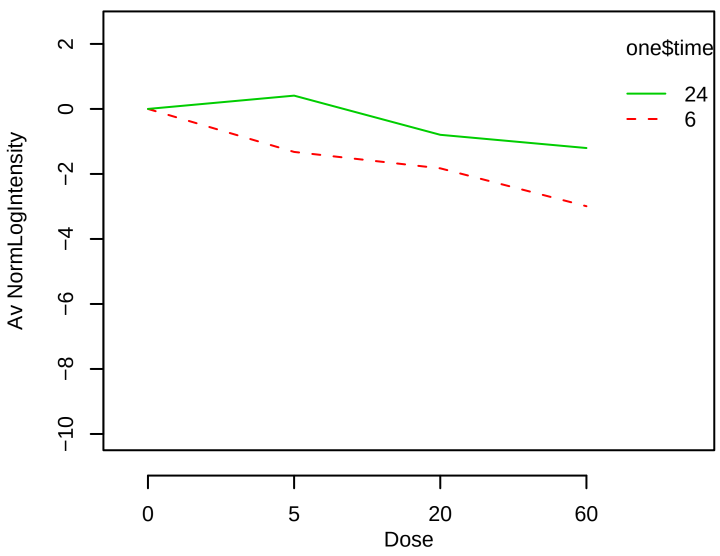
GO_0043507 : positive regulation of JNK activity

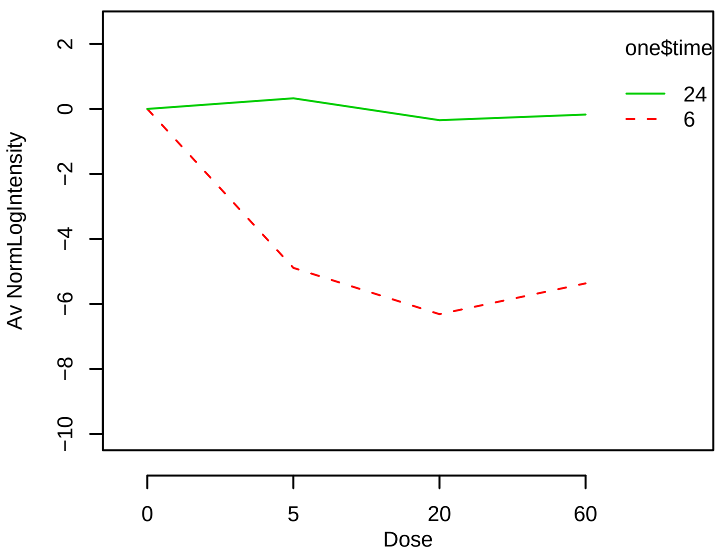


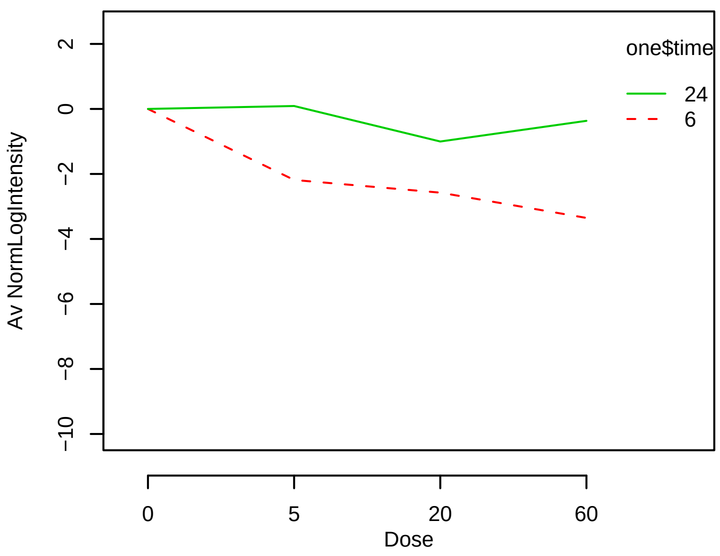
GO_0043523 : regulation of neuron apoptosis

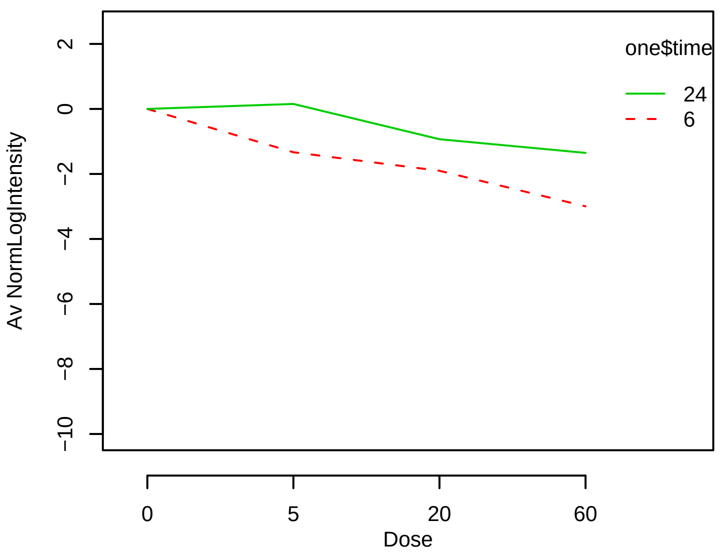

GO_0043524 : negative regulation of neuron apoptosis


GO_0043542 : endothelial cell migration

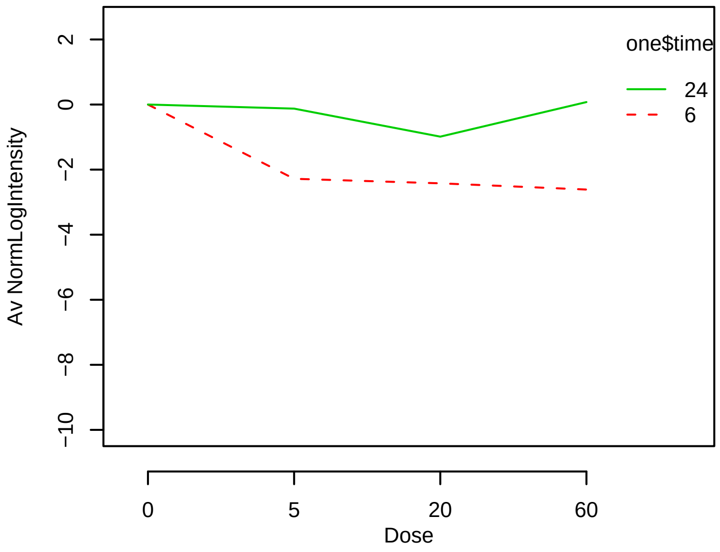

GO_0043543 : protein amino acid acylation


GO_0043545 : molybdopterin cofactor metabolism

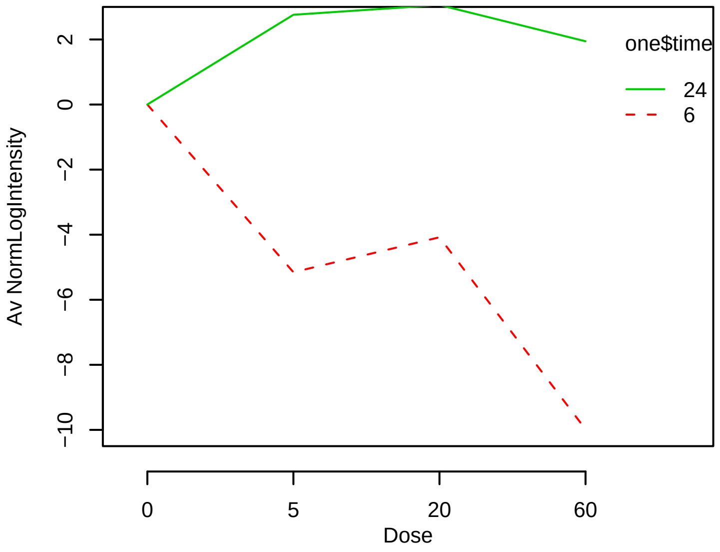

GO_0043549 : regulation of kinase activity


GO_0043550 : regulation of lipid kinase activity

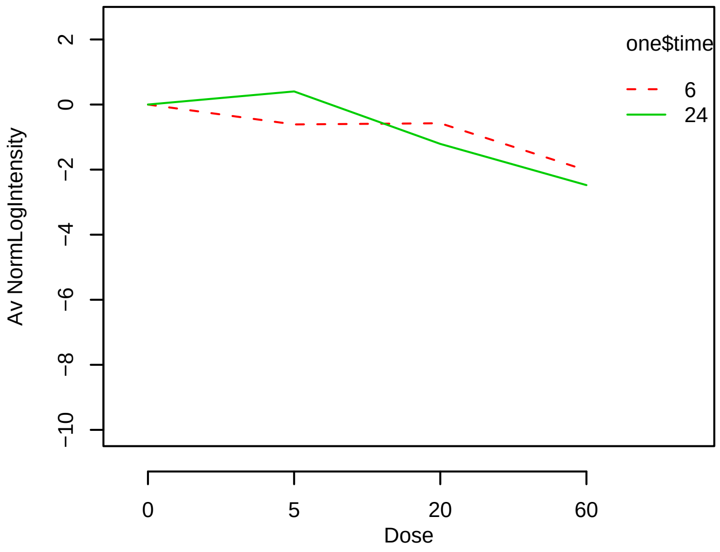
GO_0043583 : ear development



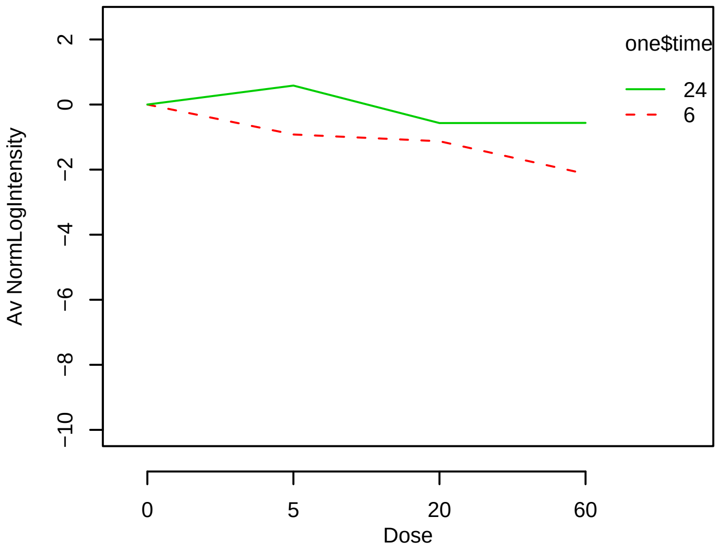
GO_0043588 : skin development



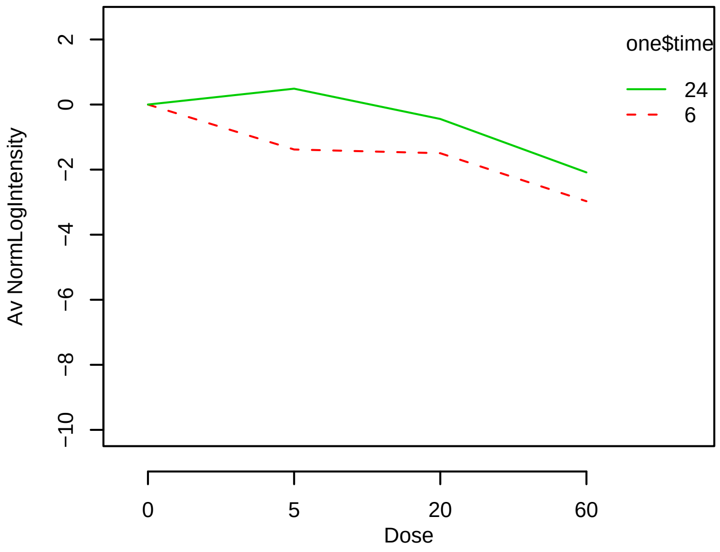
GO_0043631 : RNA polyadenylation



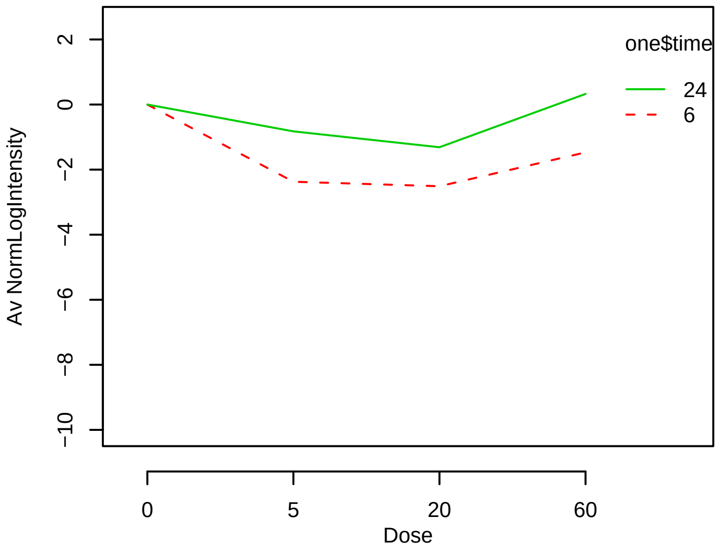
GO_0043632 : modification−dependent macromolecule catabo

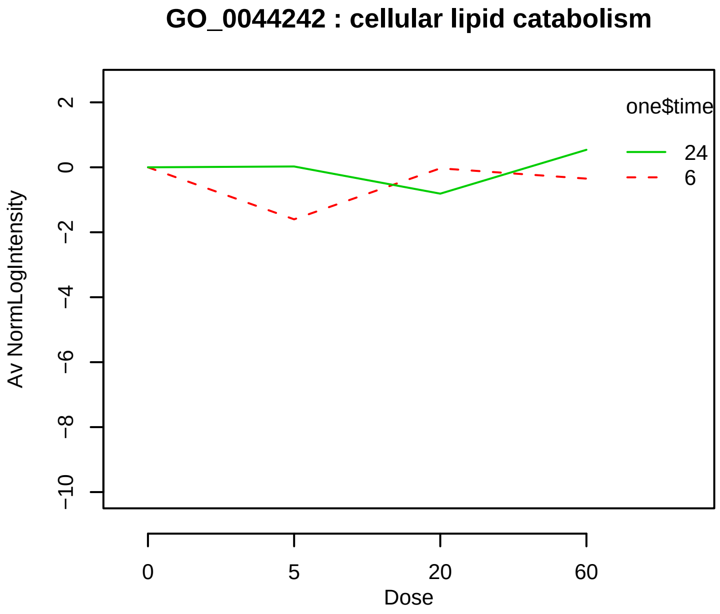


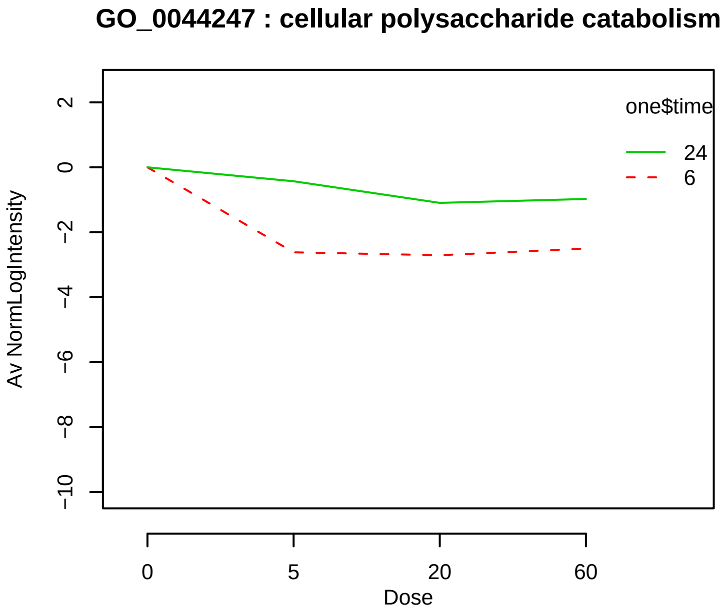
GO_0043648 : dicarboxylic acid metabolism

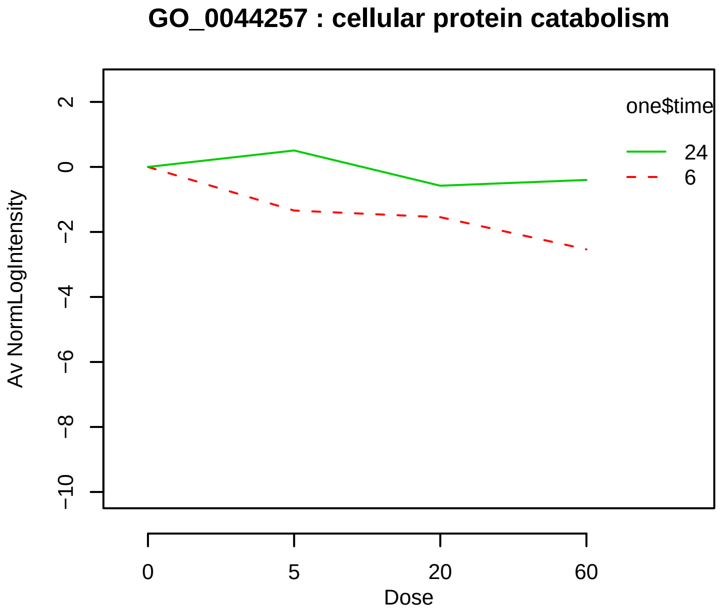


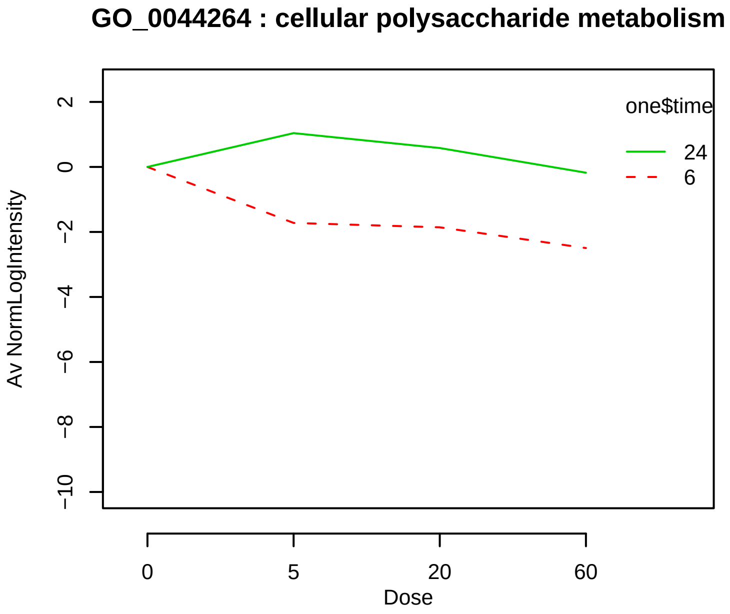
GO_0044241 : lipid digestion

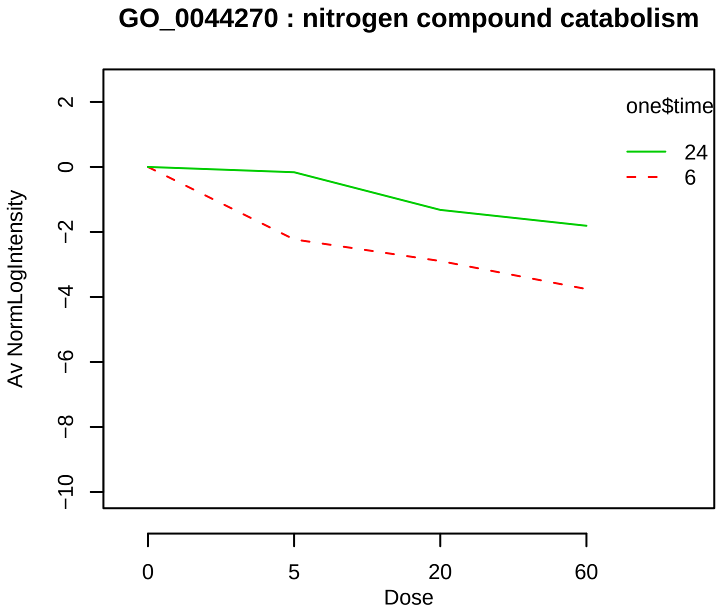


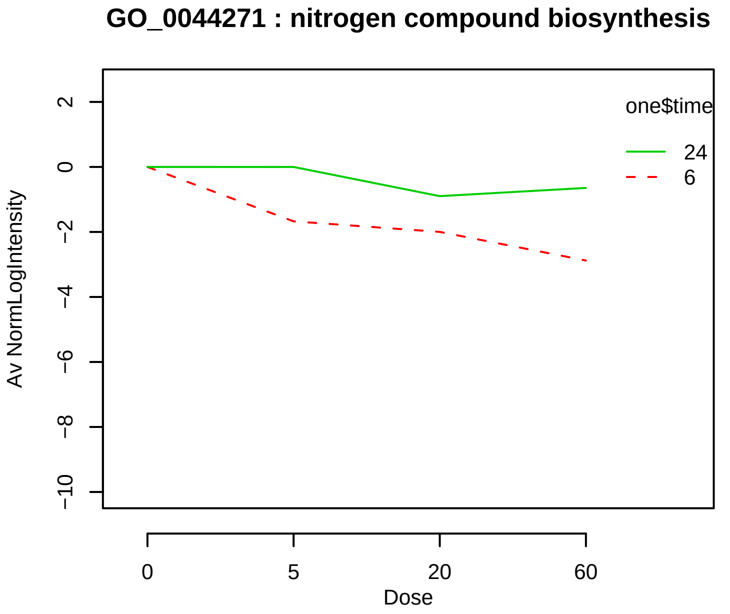

GO_0044242 : cellular lipid catabolism


GO_0044247 : cellular polysaccharide catabolism

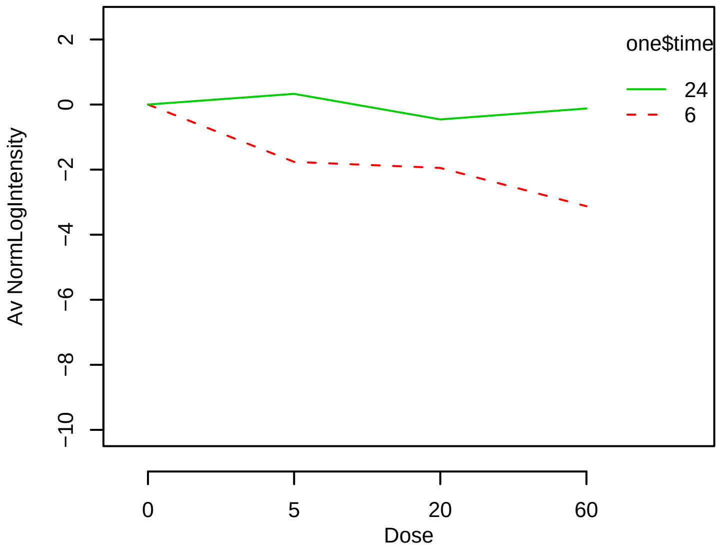

GO_0044257 : cellular protein catabolism


GO_0044264 : cellular polysaccharide metabolism

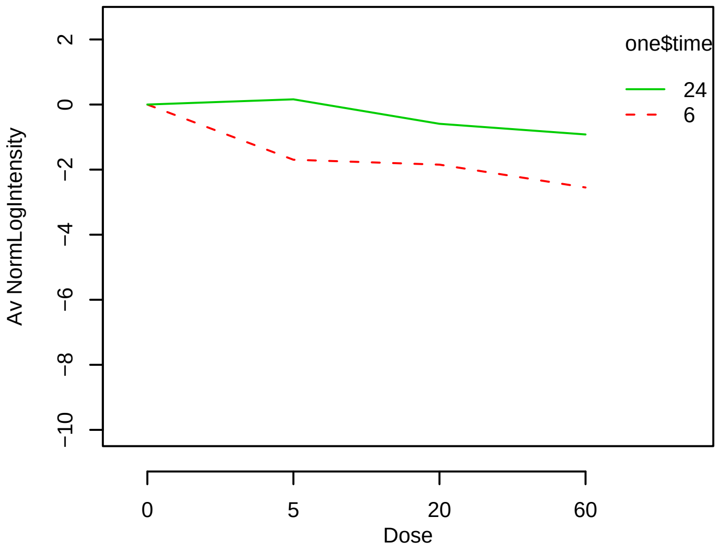

GO_0044270 : nitrogen compound catabolism


GO_0044271 : nitrogen compound biosynthesis

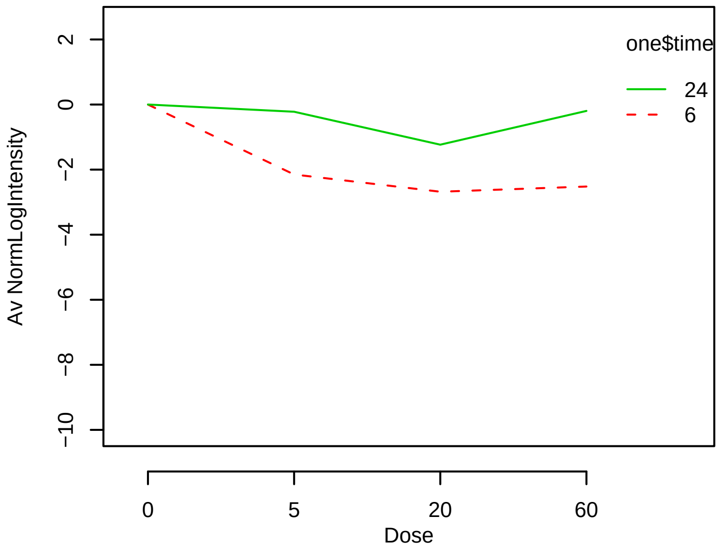
GO_0044272 : sulfur compound biosynthesis



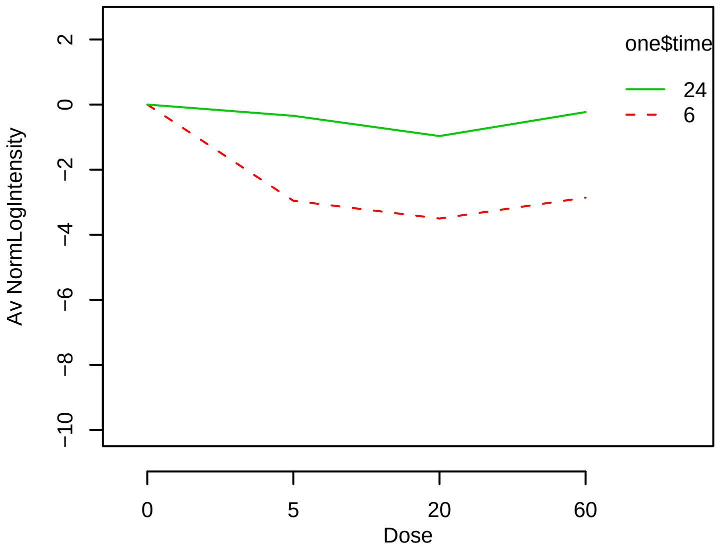
GO_0044275 : cellular carbohydrate catabolism



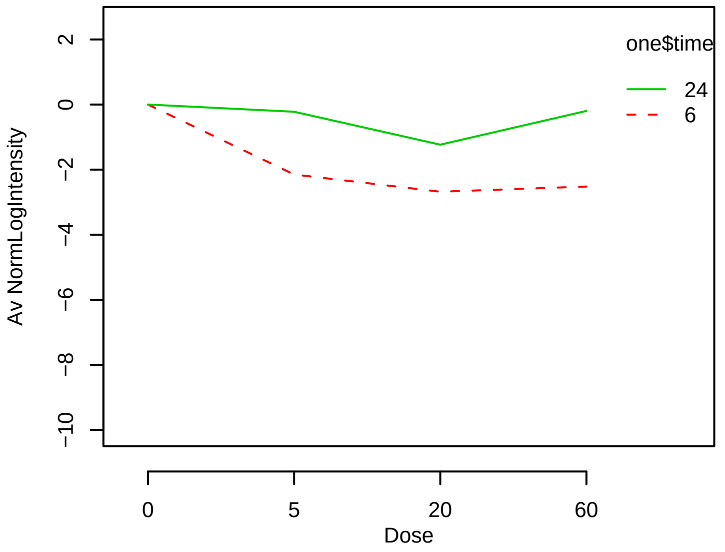
O_0044403 : symbiosis\, encompassing mutualism through p



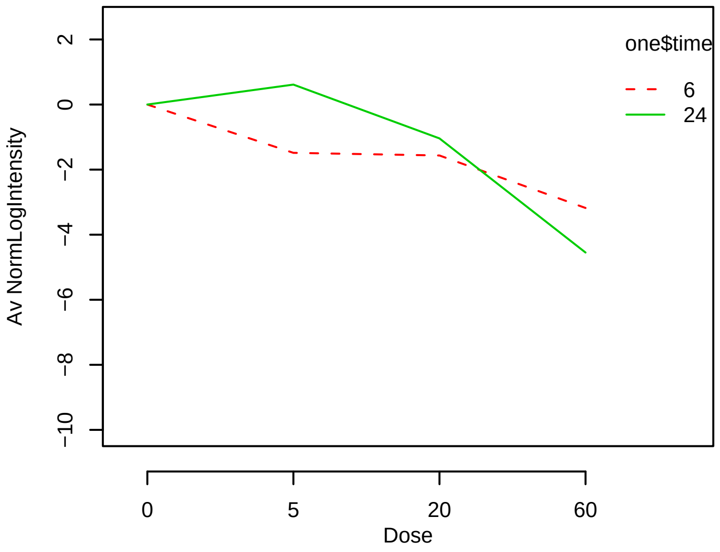
GO_0044409 : entry into host

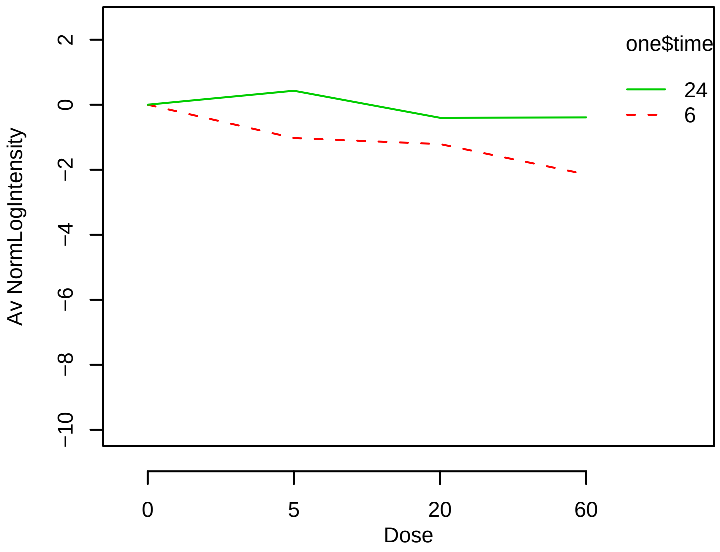


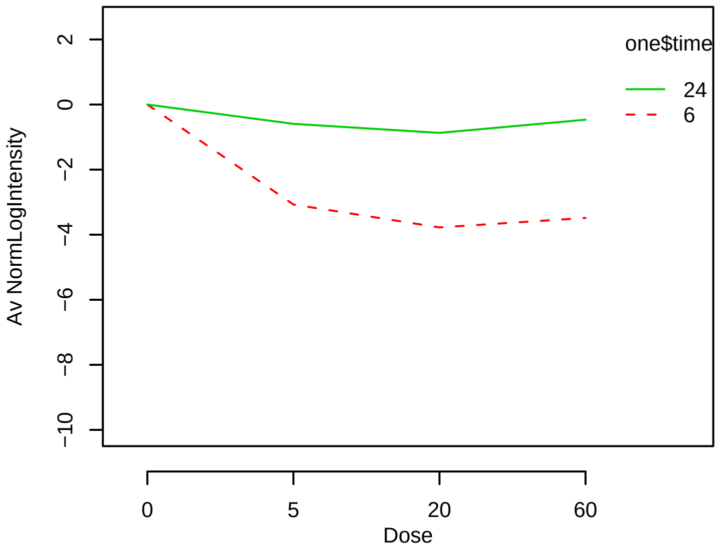
GO_0044419 : interspecies interaction between organism

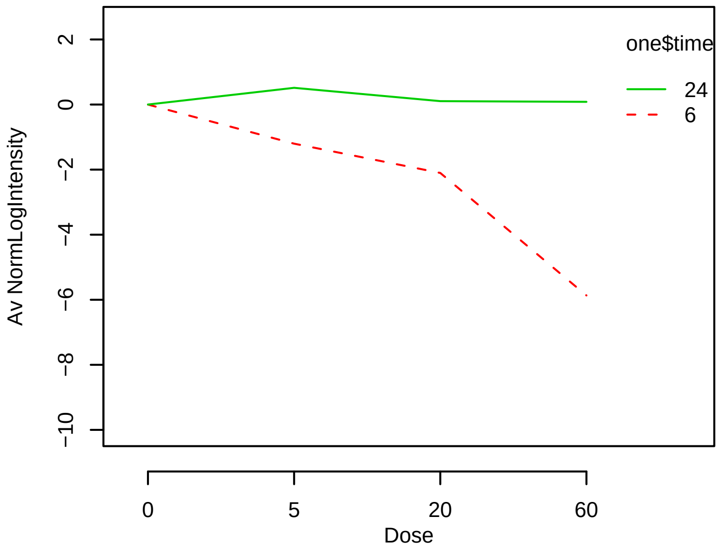


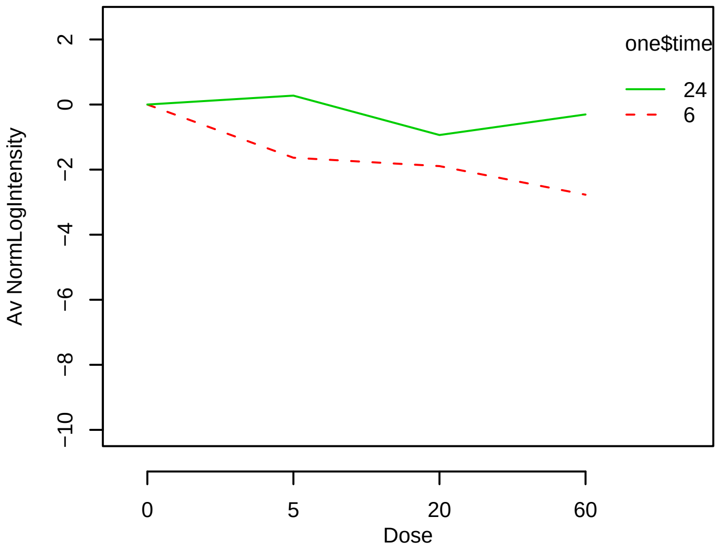
O_0045005 : maintenance of fidelity during DNA−dependent I

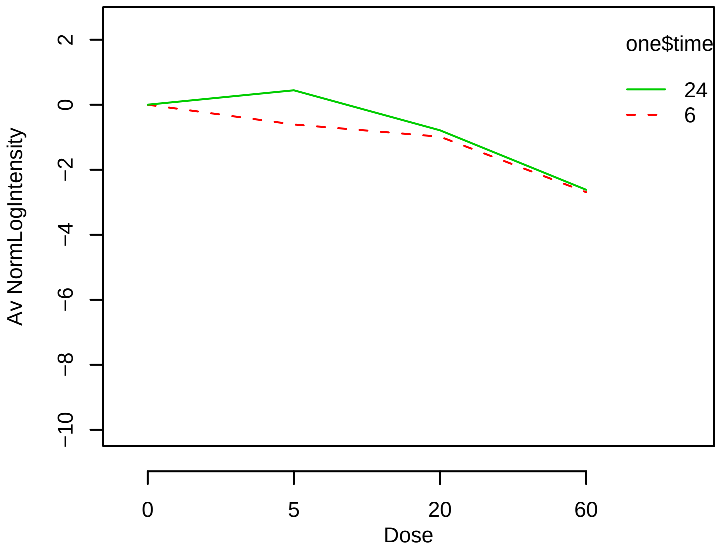


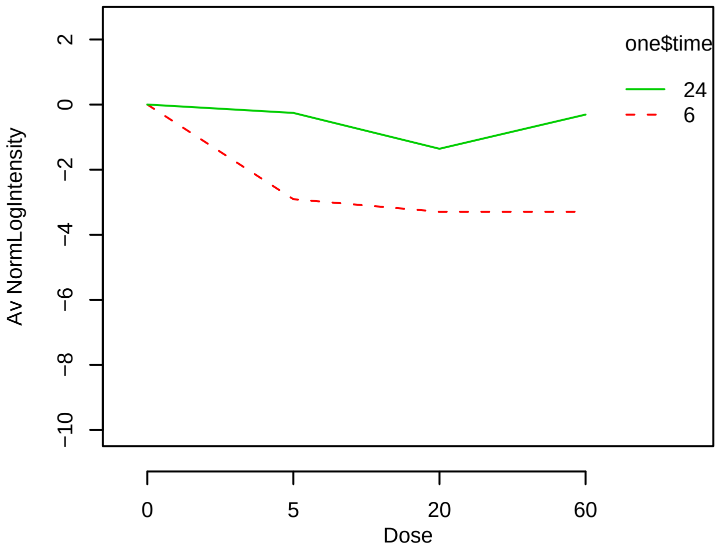

GO_0045017 : glycerolipid biosynthesis

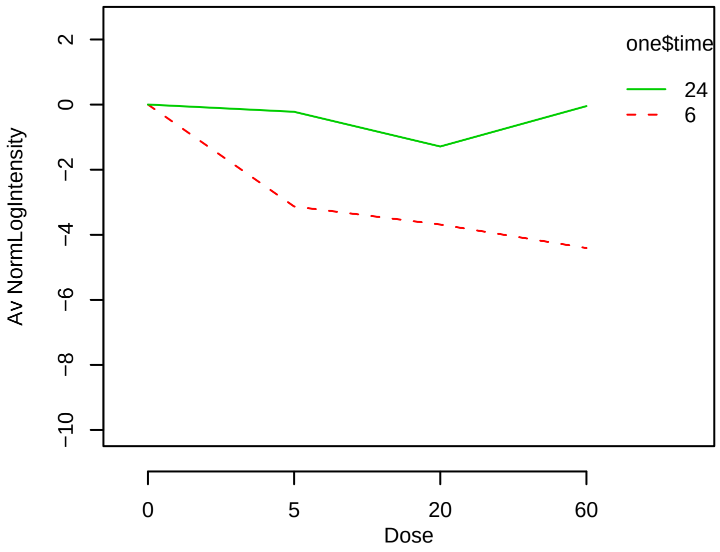

GO_0045026 : plasma membrane fusion

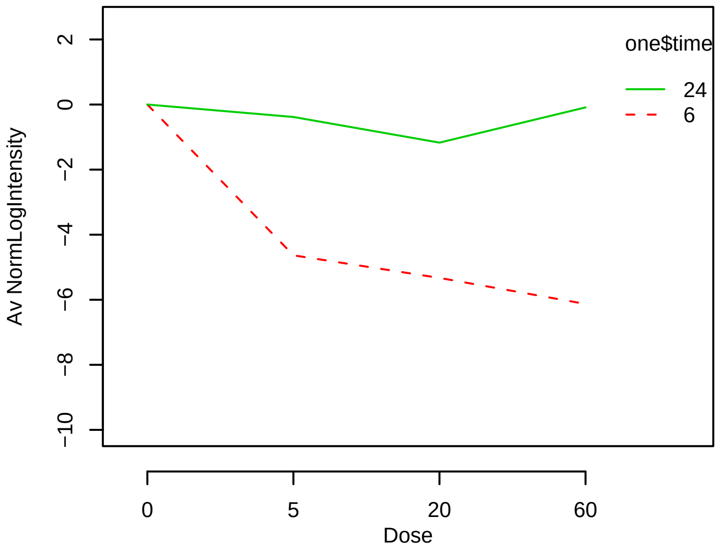

GO_0045039 : protein import into mitochondrial inner membı

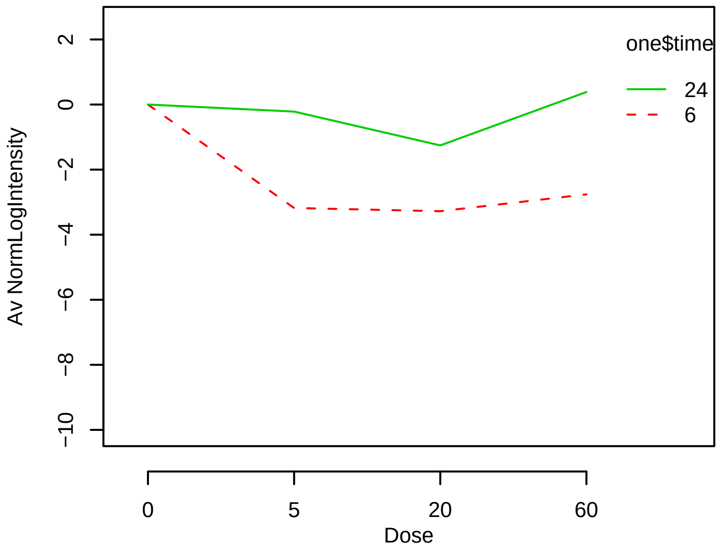

GO_0045045 : secretory pathway

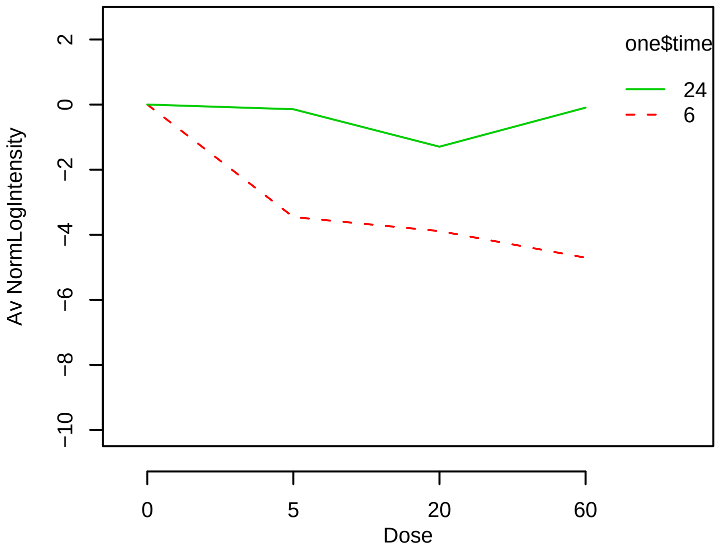

GO_0045047 : protein targeting to ER

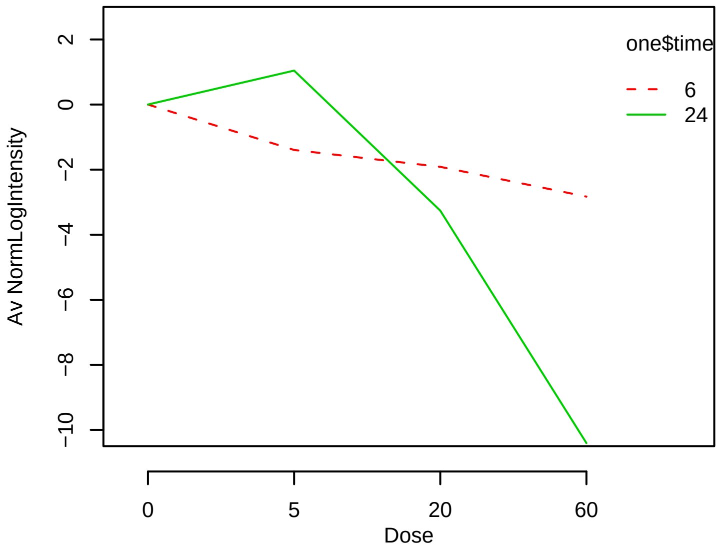

GO_0045055 : regulated secretory pathway

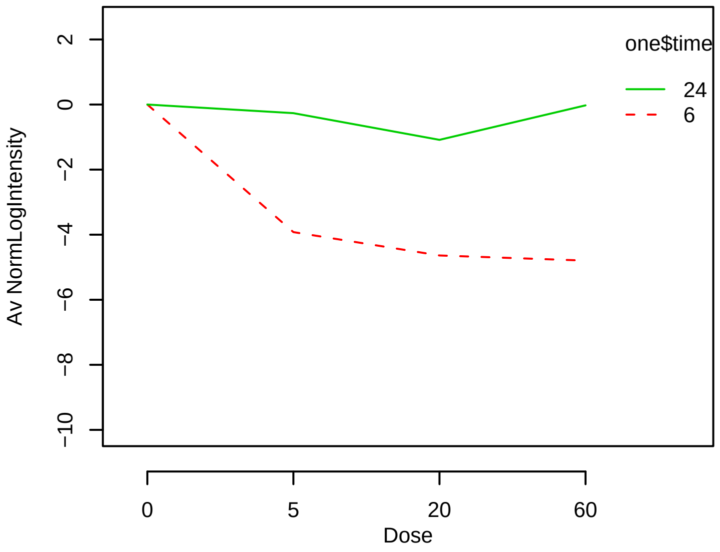

GO_0045058 : T cell selection

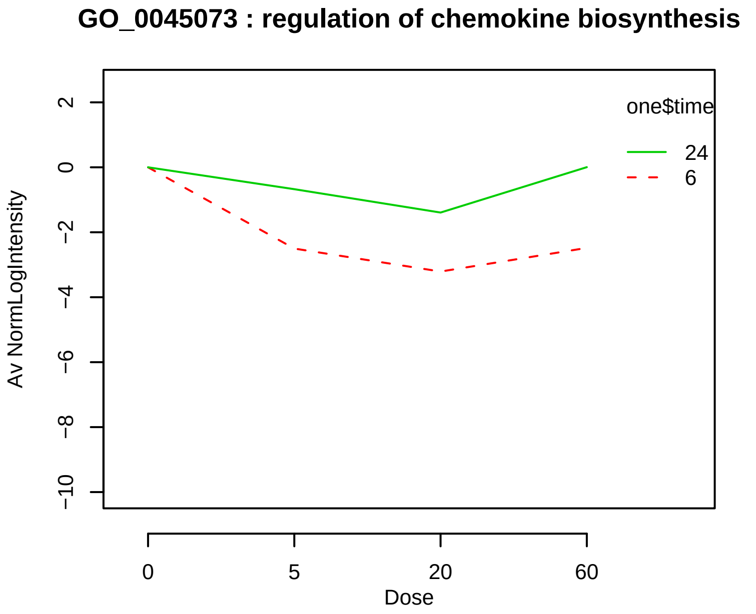

GO_0045059 : positive thymic T cell selection

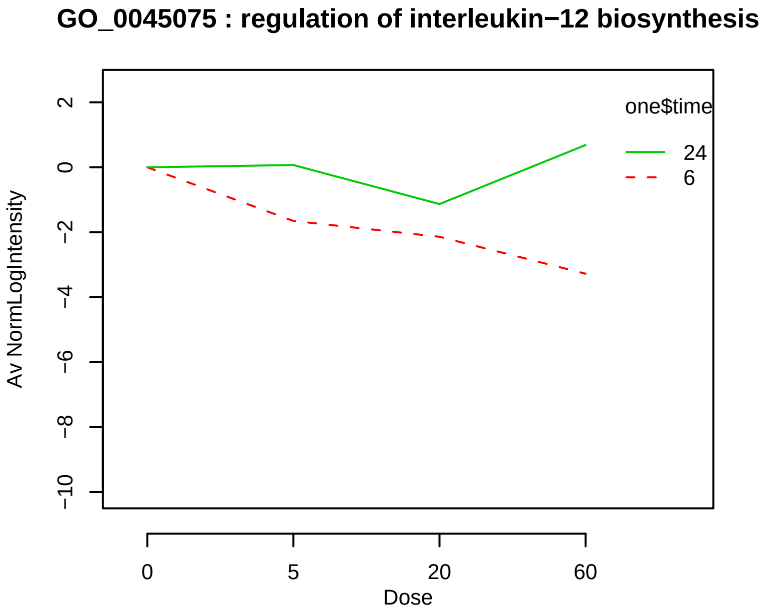

GO_0045060 : negative thymic T cell selection

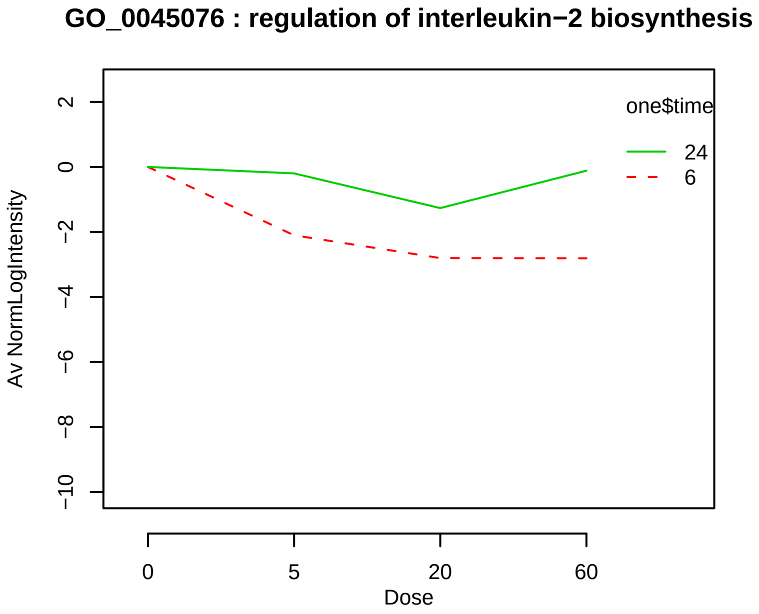

GO_0045061 : thymic T cell selection

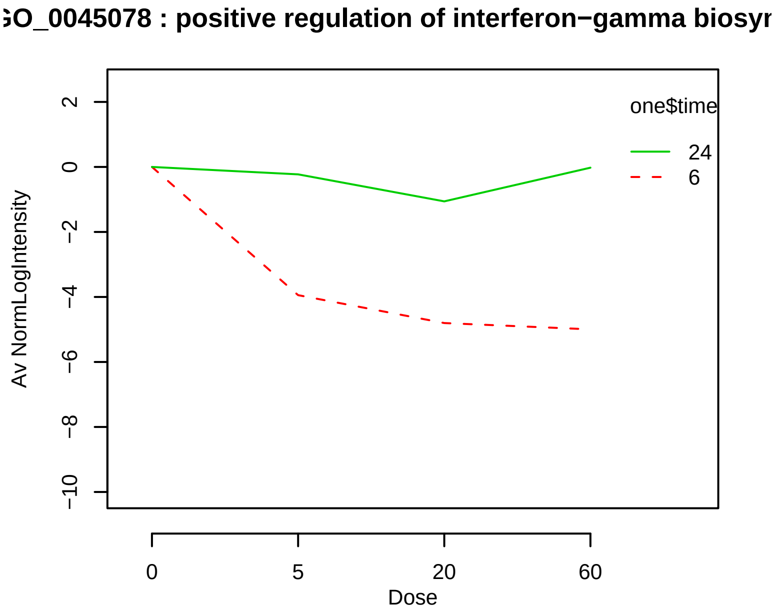

GO_0045069 : regulation of viral genome replication

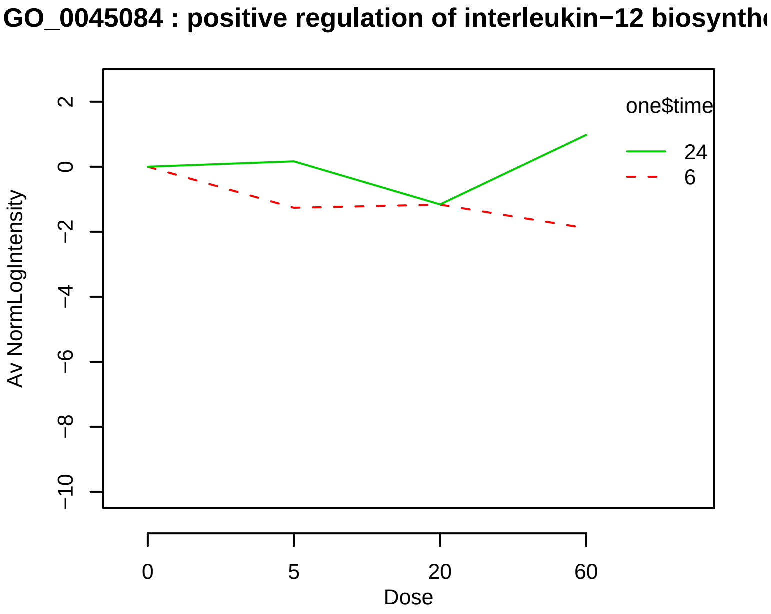

GO_0045072 : regulation of interferon−gamma biosynthesi

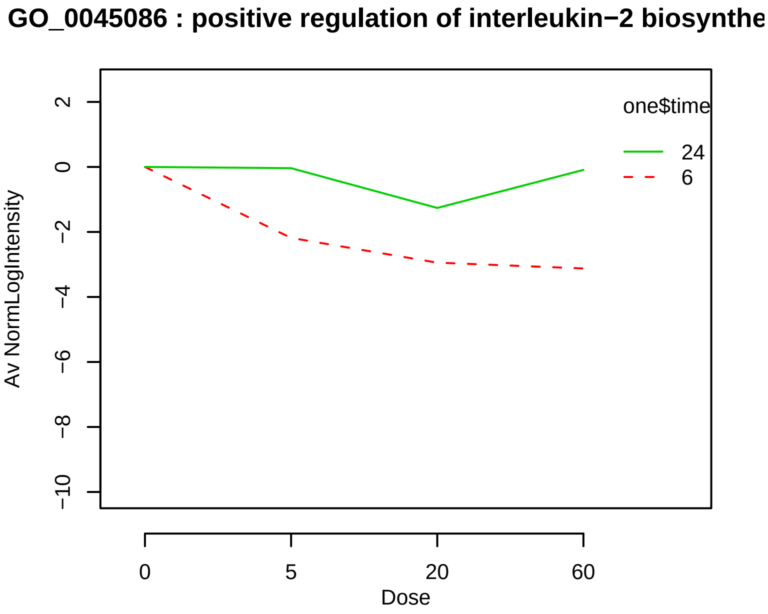

GO_0045073 : regulation of chemokine biosynthesis


GO_0045075 : regulation of interleukin−12 biosynthesis

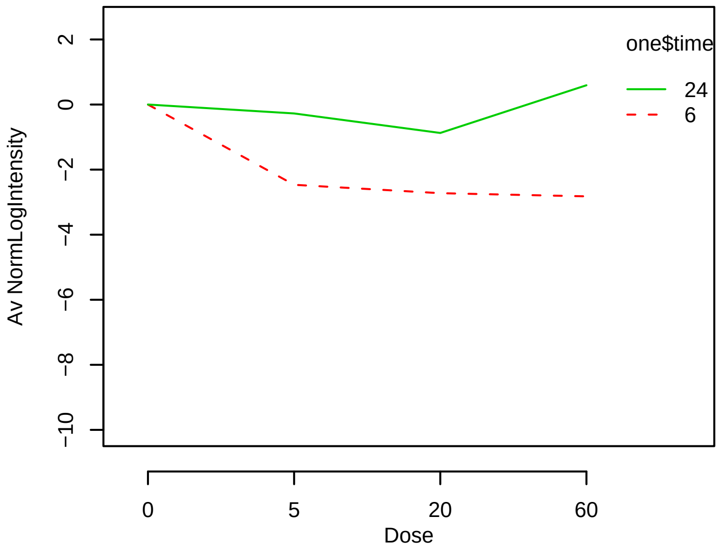

GO_0045076 : regulation of interleukin−2 biosynthesis


O_0045078 : positive regulation of interferon−gamma biosy

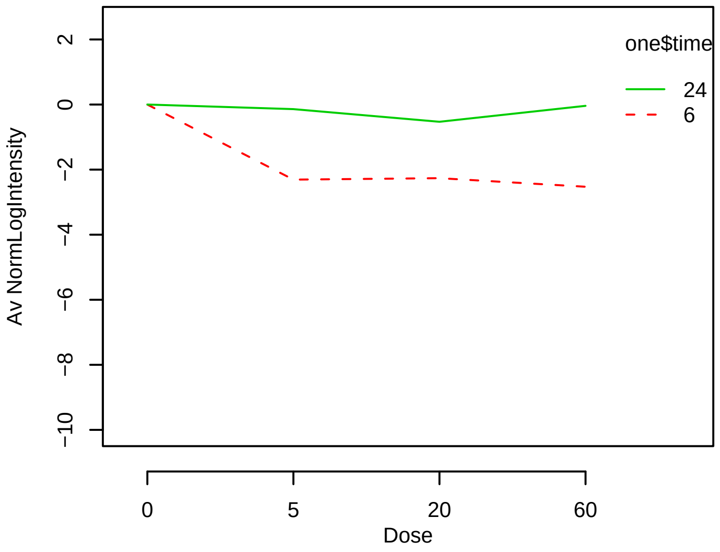

GO_0045084 : positive regulation of interleukin−12 biosynth


GO_0045086 : positive regulation of interleukin−2 biosynthe

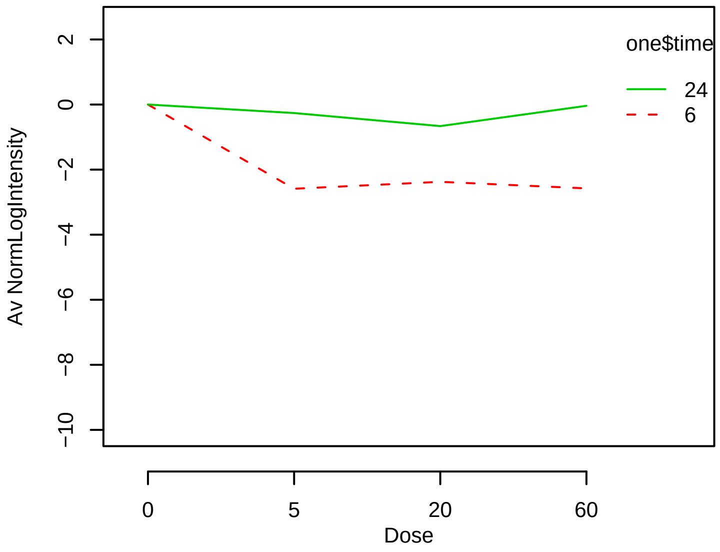
GO_0045087 : innate immune response



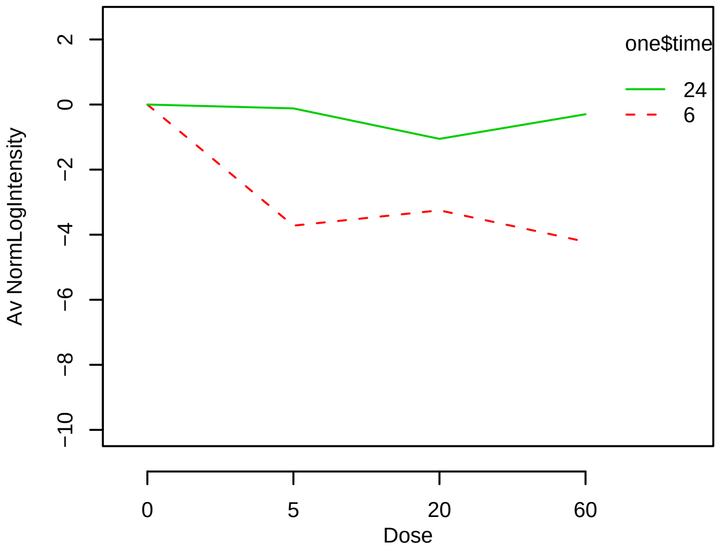
GO_0045088 : regulation of innate immune response



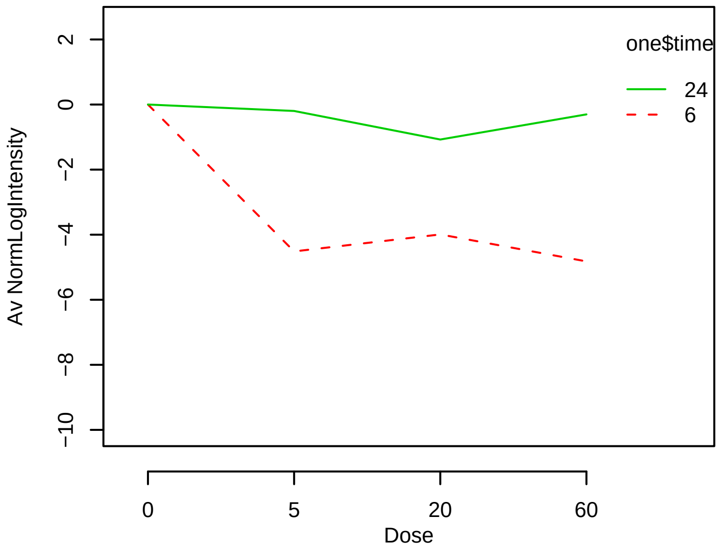
GO_0045089 : positive regulation of innate immune respon



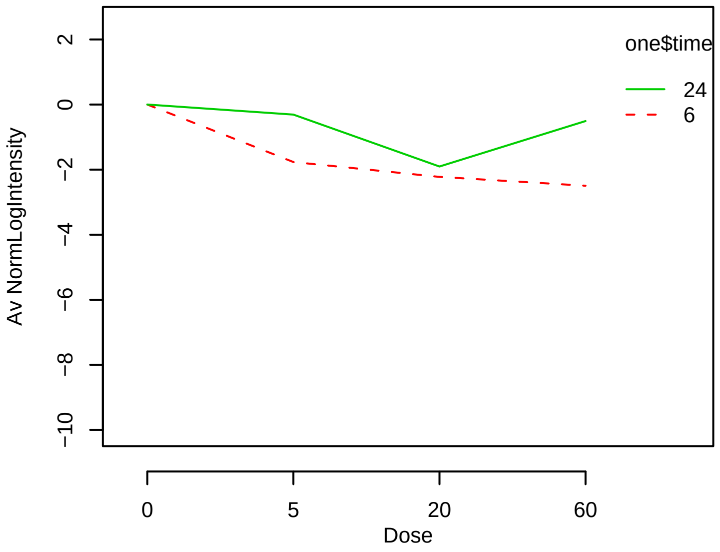
GO_0045103 : intermediate filament−based process

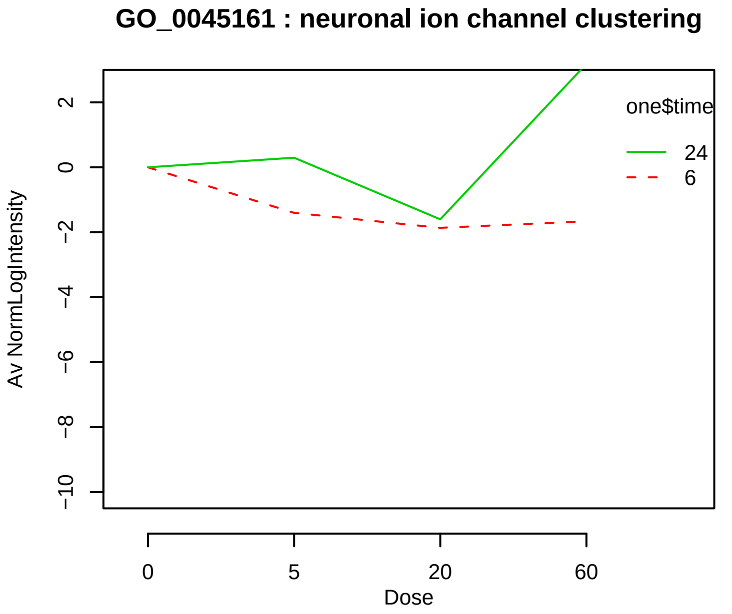


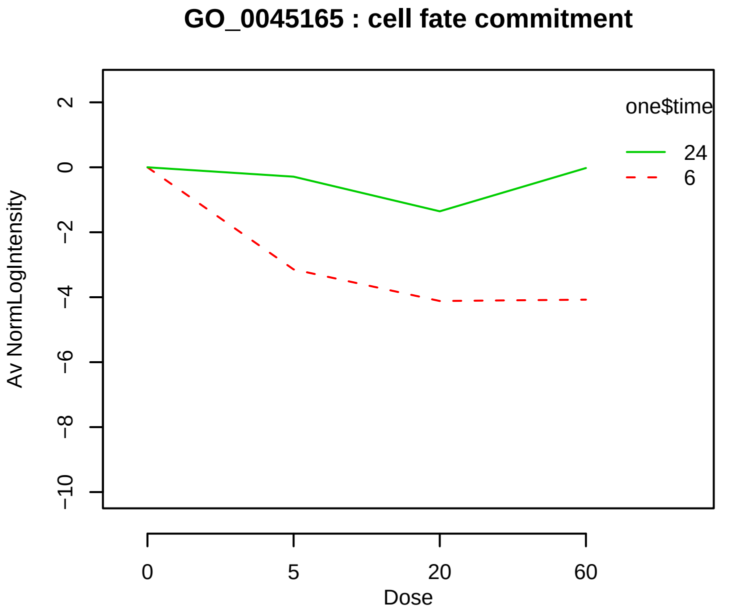
GO_0045104 : intermediate filament cytoskeleton organizatio

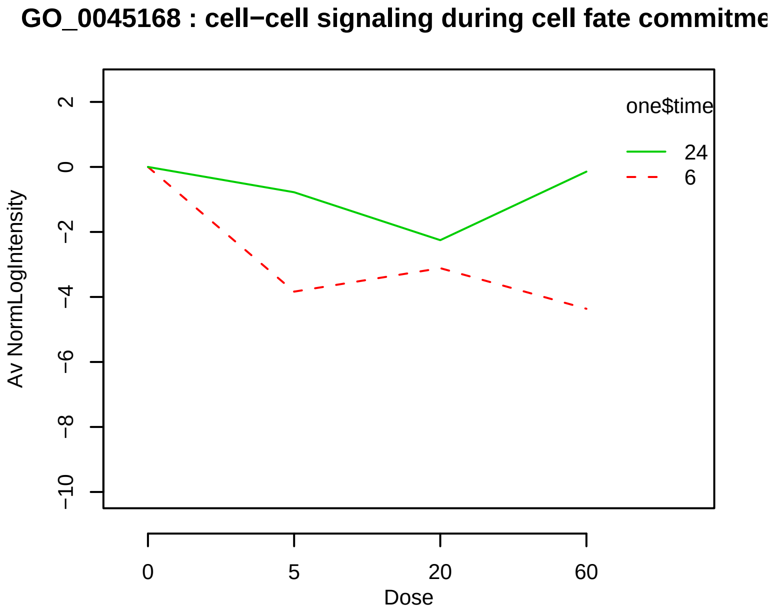


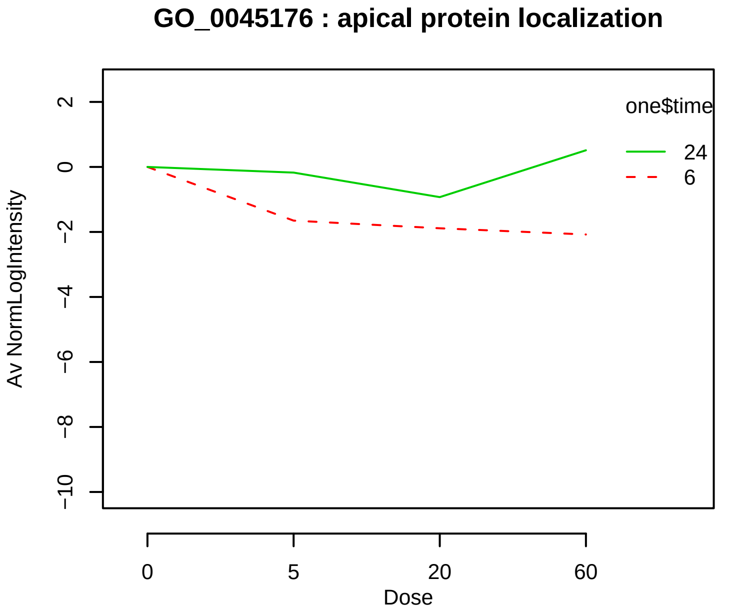
GO_0045137 : development of primary sexual characteristi

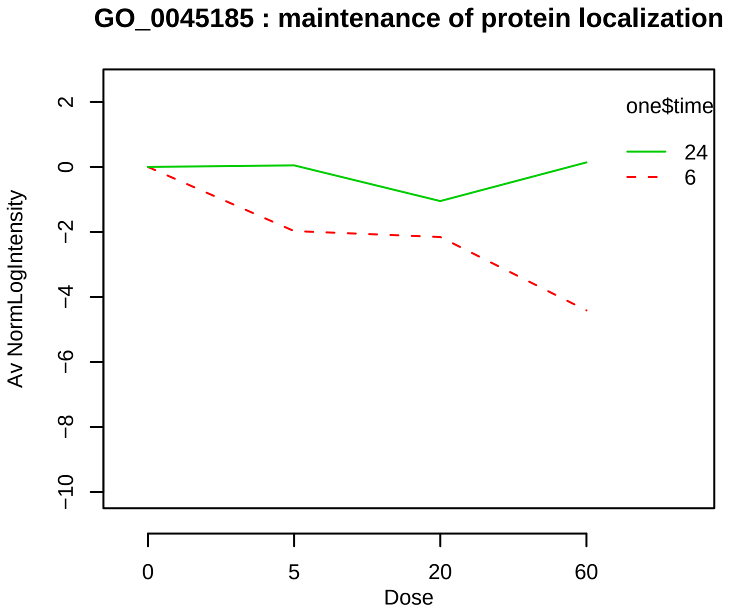


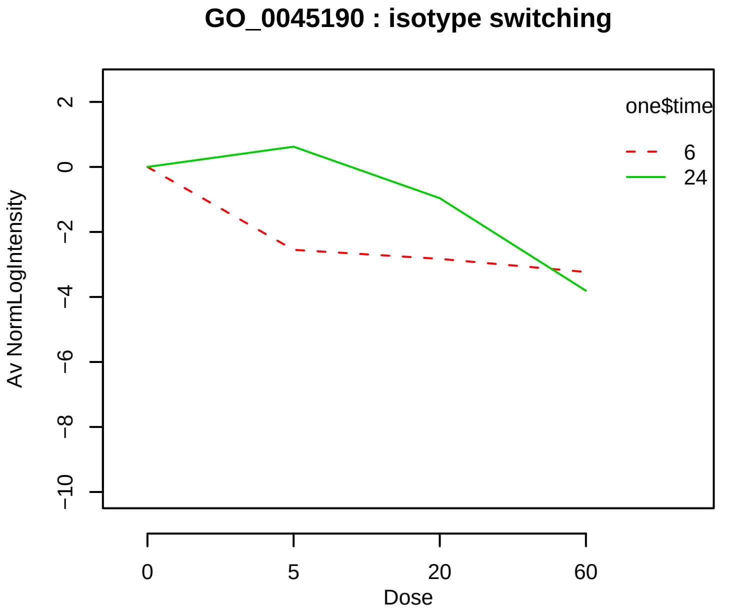

GO_0045161 : neuronal ion channel clustering


GO_0045165 : cell fate commitment

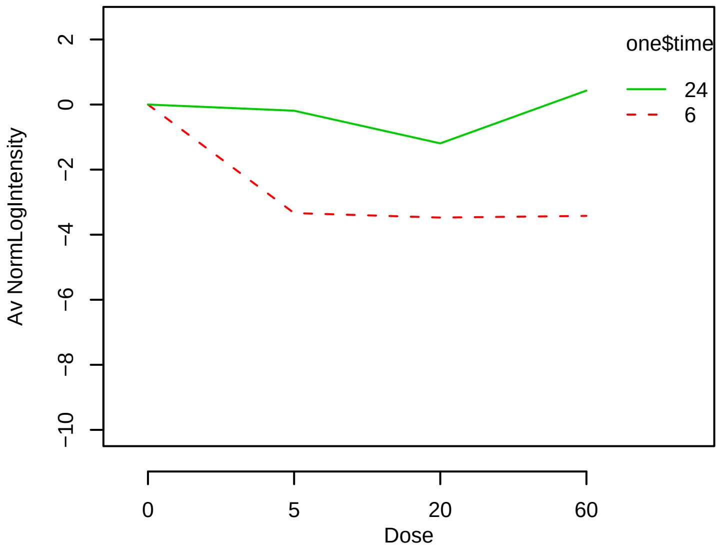

GO_0045168 : cell−cell signaling during cell fate commitme


GO_0045176 : apical protein localization

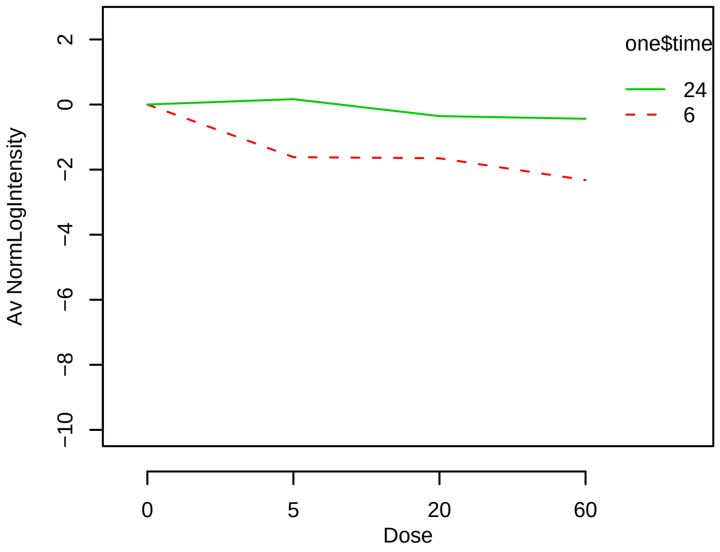

GO_0045185 : maintenance of protein localization


GO_0045190 : isotype switching

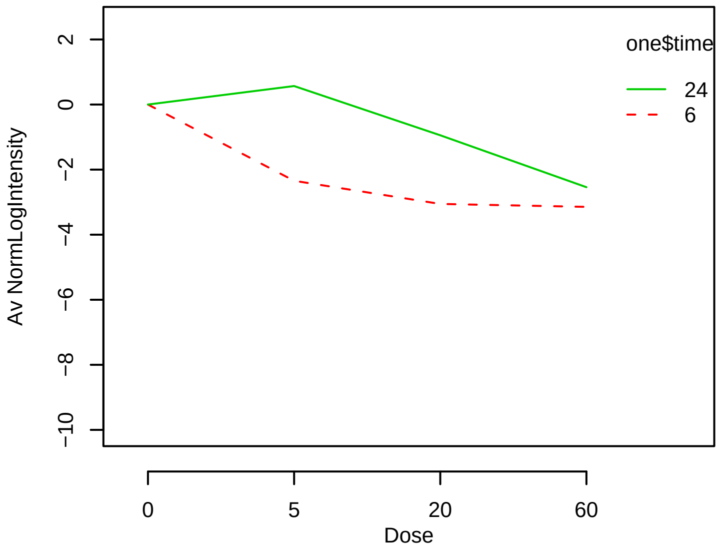
GO_0045191 : regulation of isotype switching



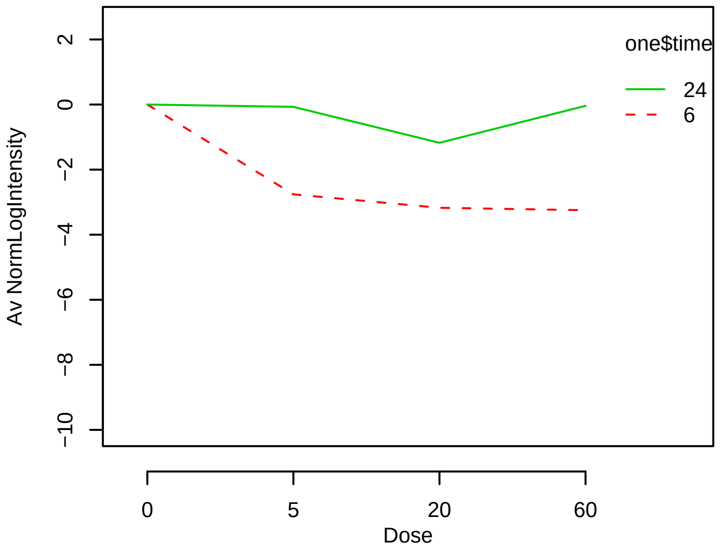
GO_0045197 : establishment and/or maintenance of epithelia



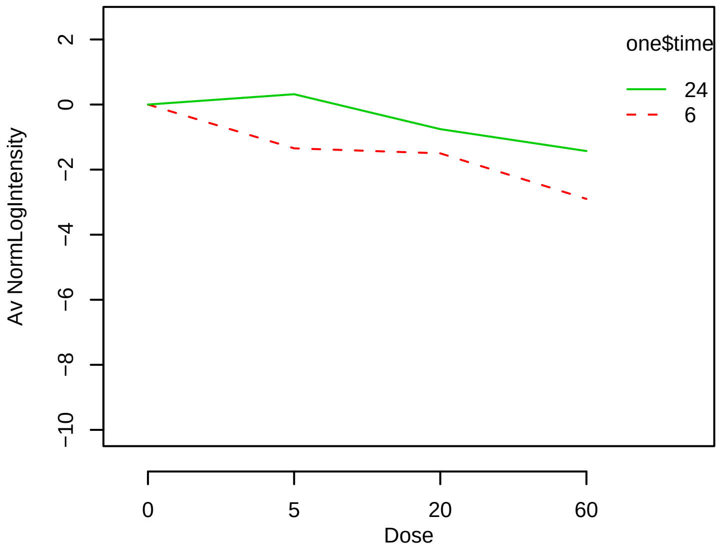
GO_0045216 : intercellular junction assembly and maintena



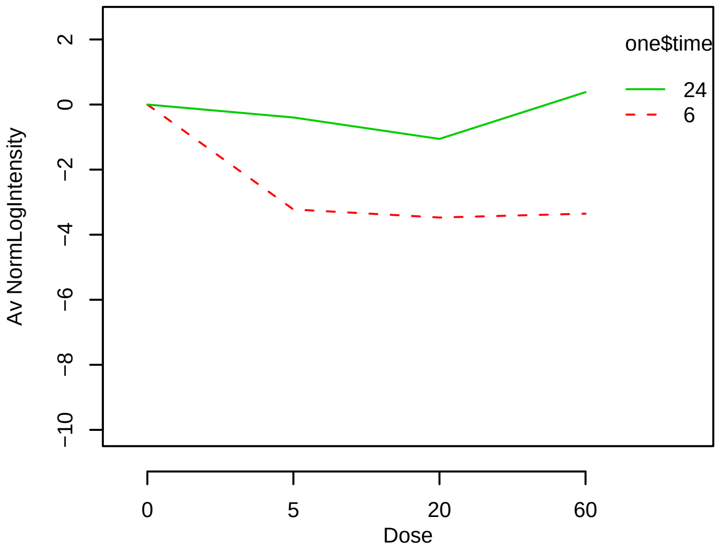
GO_0045321 : leukocyte activation

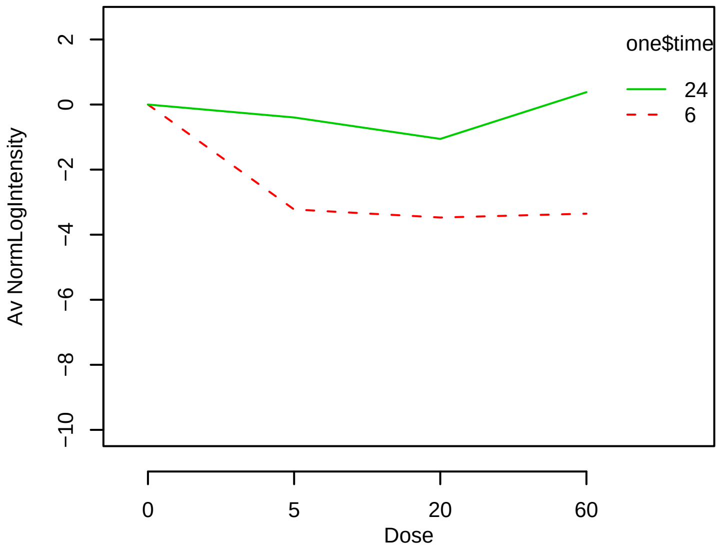


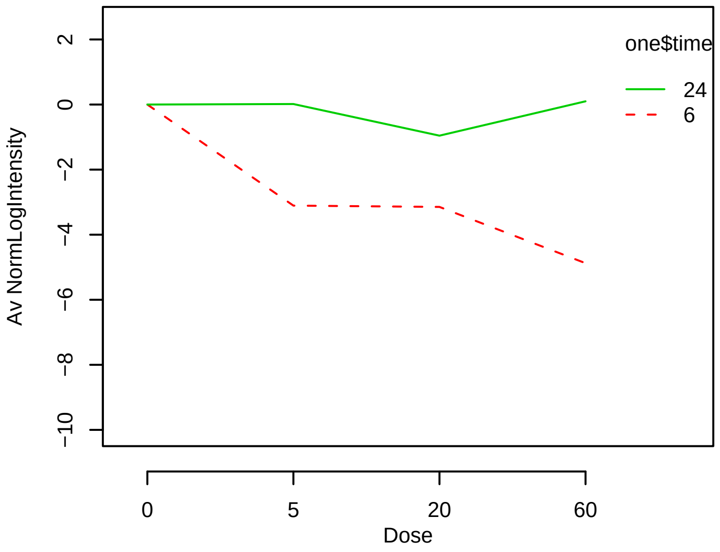
GO_0045333 : cellular respiration

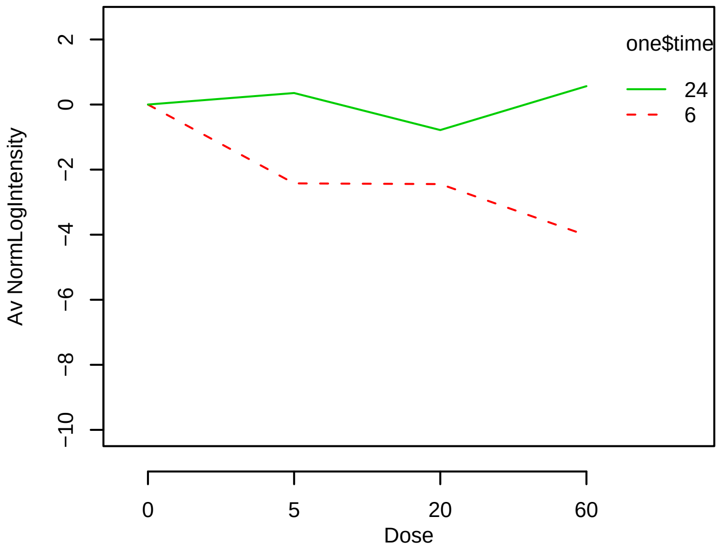


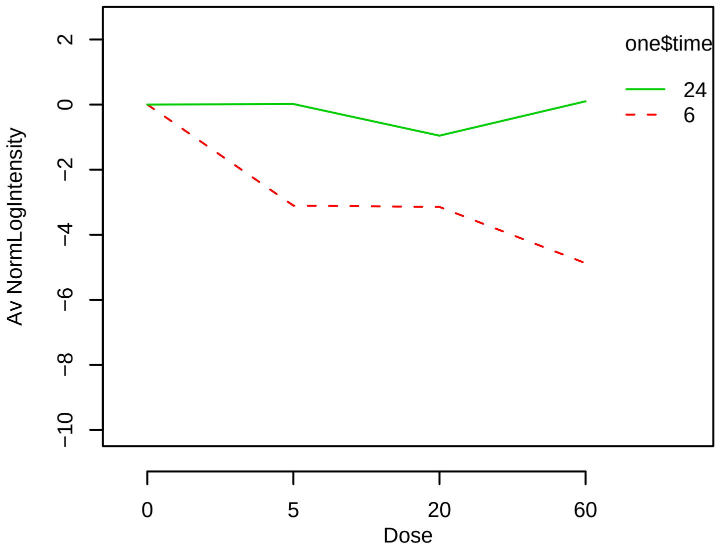
GO_0045342 : MHC class II biosynthesis

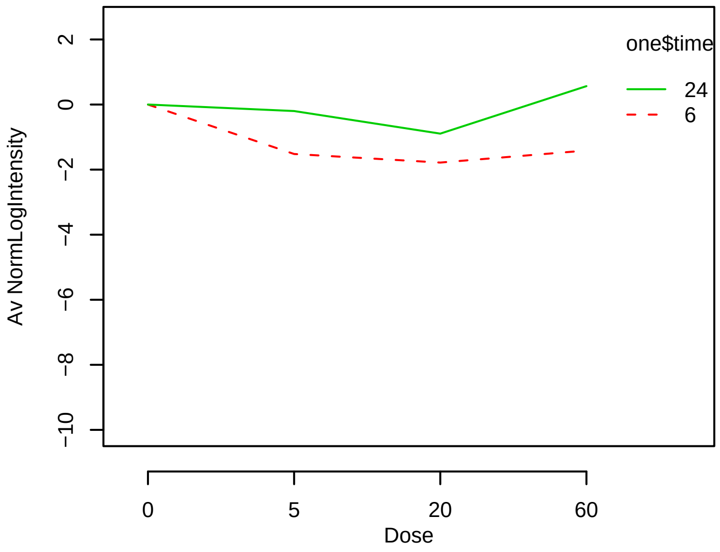


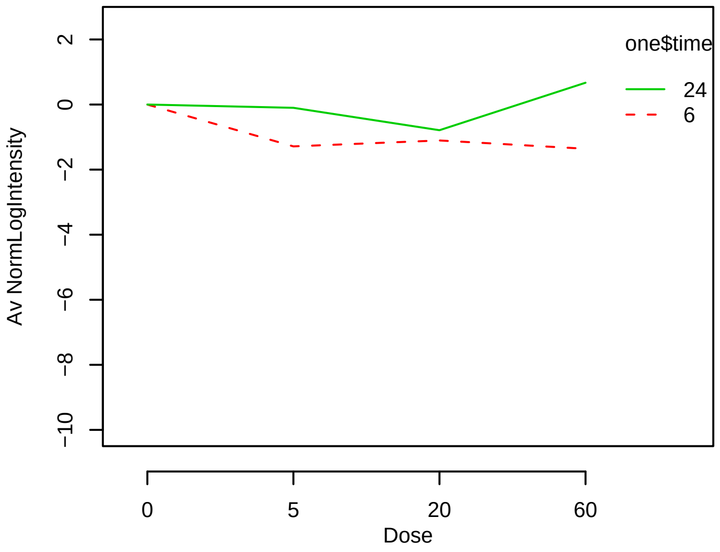

GO_0045346 : regulation of MHC class II biosynthesis

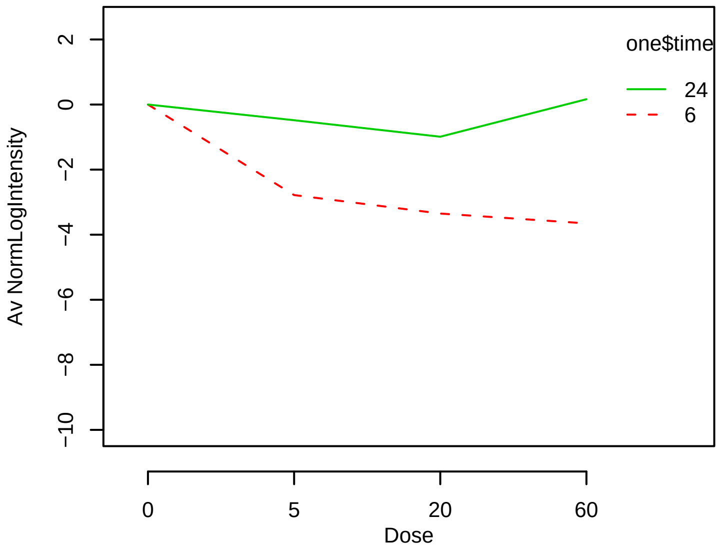

GO_0045349 : interferon−alpha biosynthesis

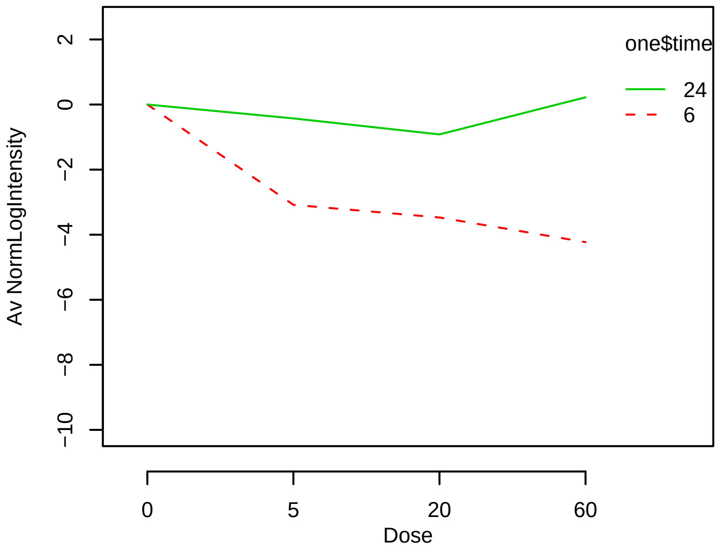

GO_0045351 : interferon type I biosynthesis

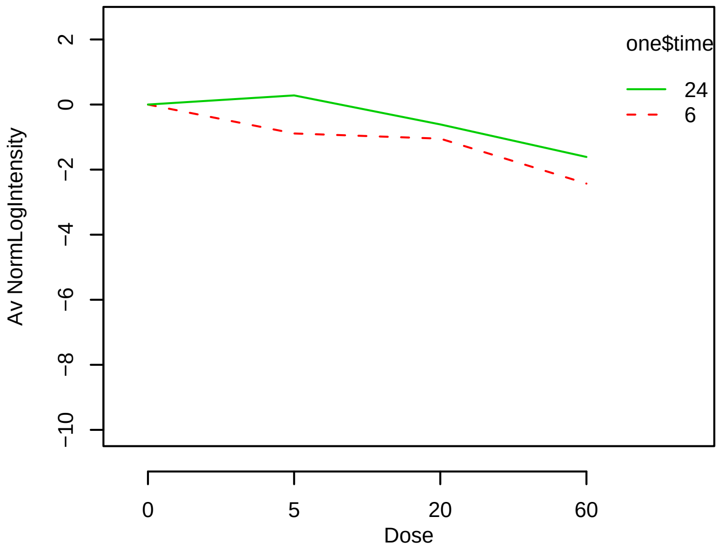

GO_0045354 : regulation of interferon−alpha biosynthesis

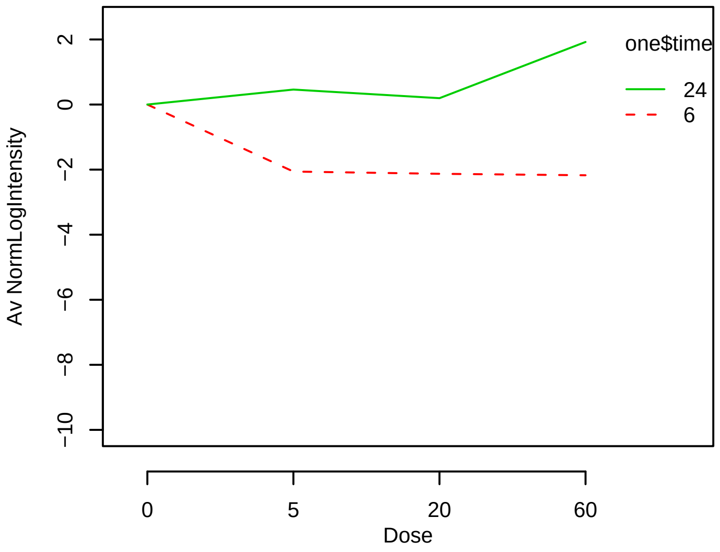

GO_0045408 : regulation of interleukin−6 biosynthesis

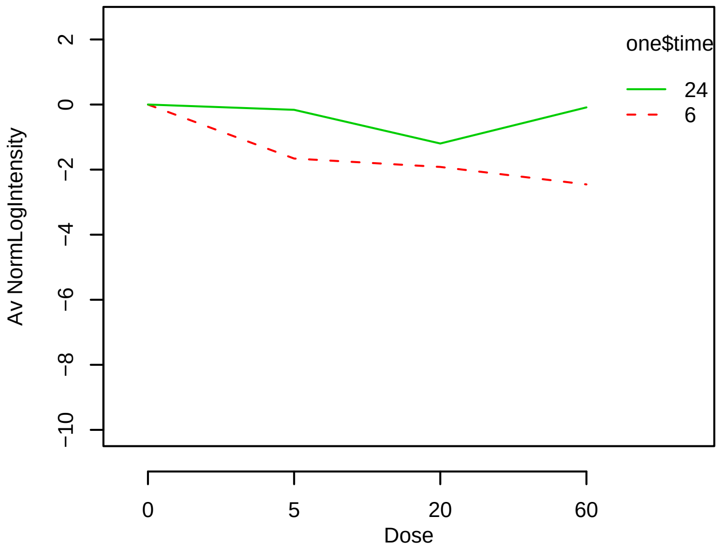

GO_0045410 : positive regulation of interleukin−6 biosynthe

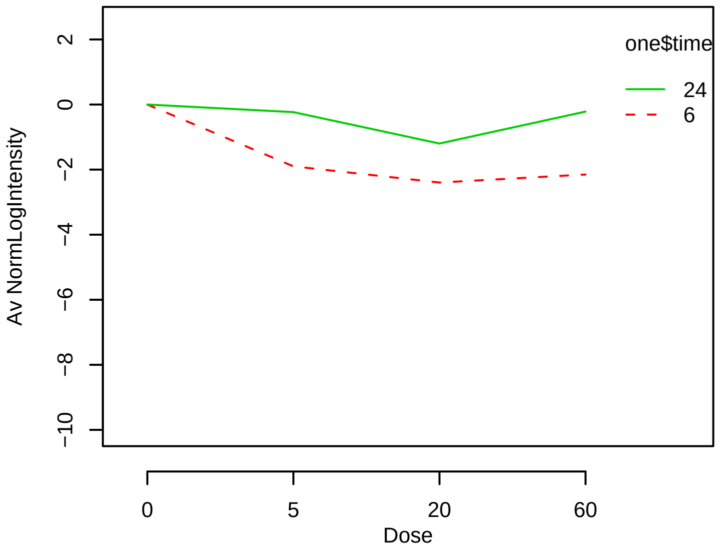

GO_0045414 : regulation of interleukin−8 biosynthesis

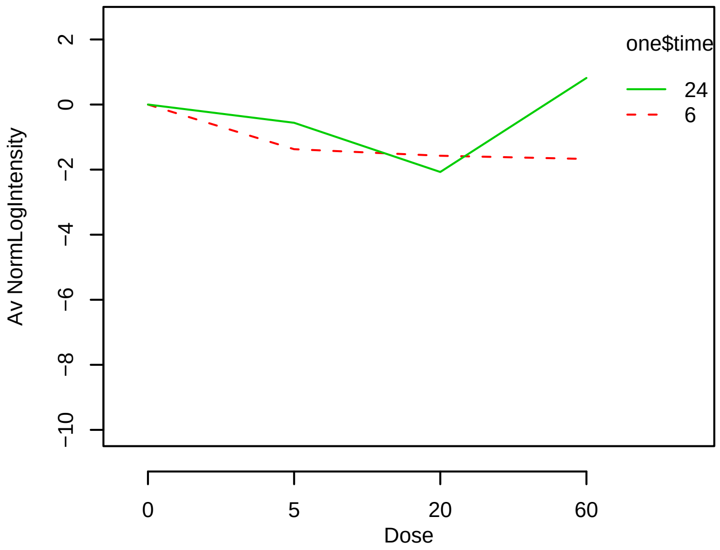

GO_0045416 : positive regulation of interleukin−8 biosynthe


GO_0045426 : quinone cofactor biosynthesis

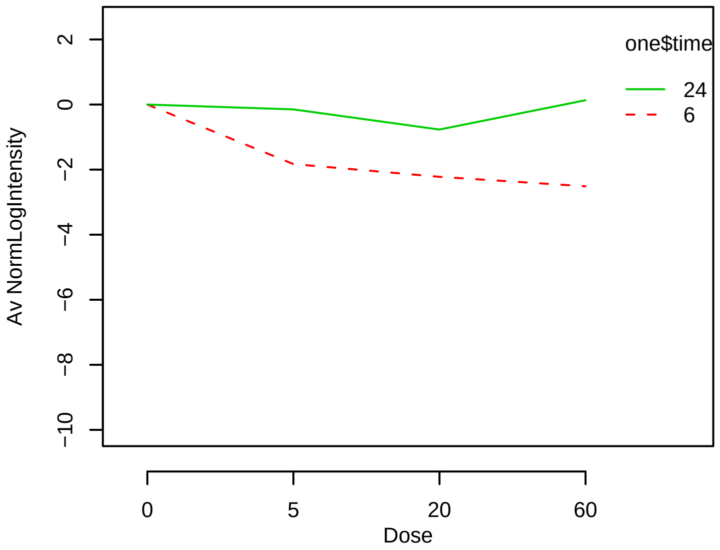

GO_0045428 : regulation of nitric oxide biosynthesis


GO_0045444 : fat cell differentiation

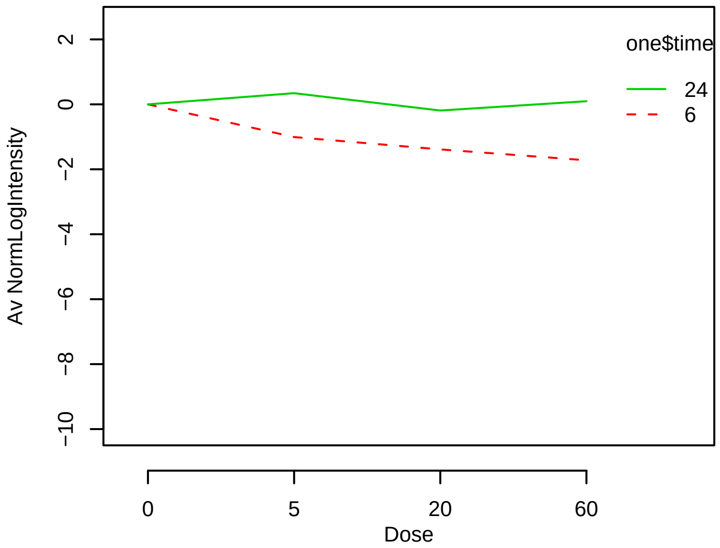

GO_0045445 : myoblast differentiation



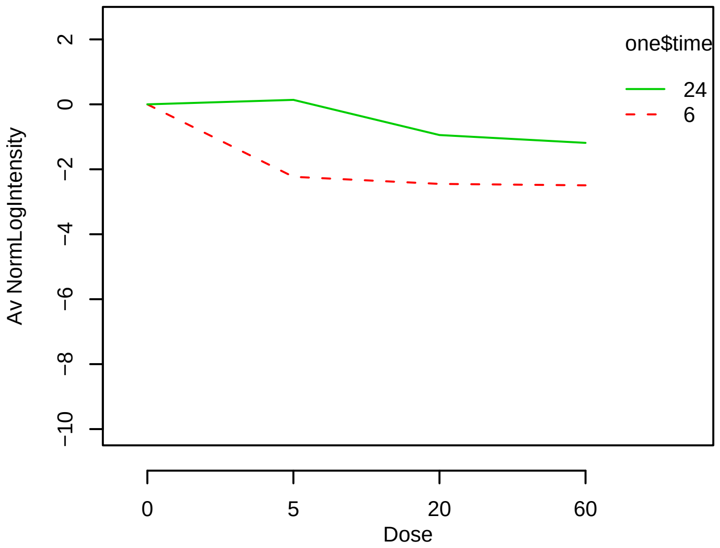
GO_0045446 : endothelial cell differentiation



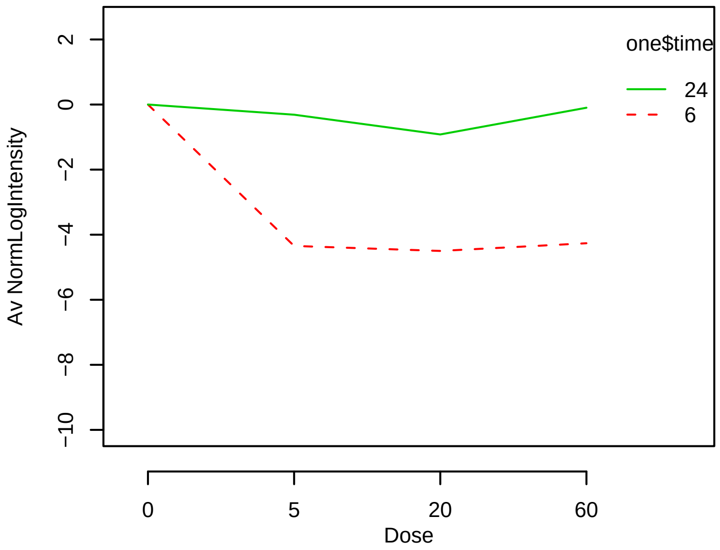
GO_0045453 : bone resorption



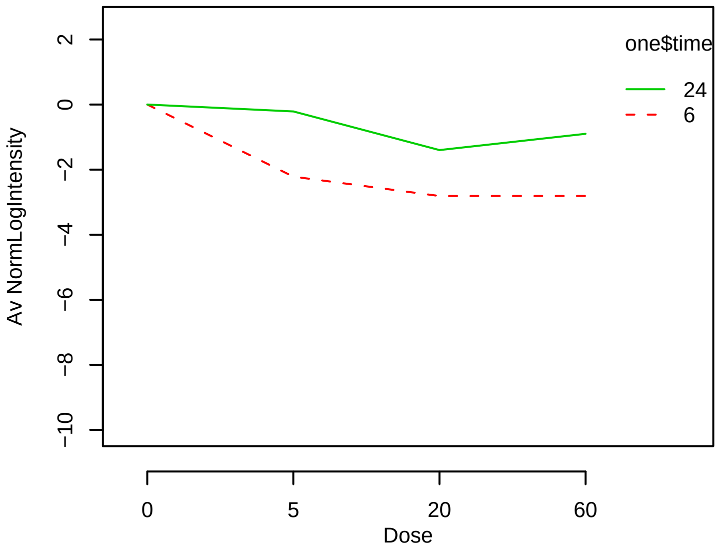
GO_0045454 : cell redox homeostasis



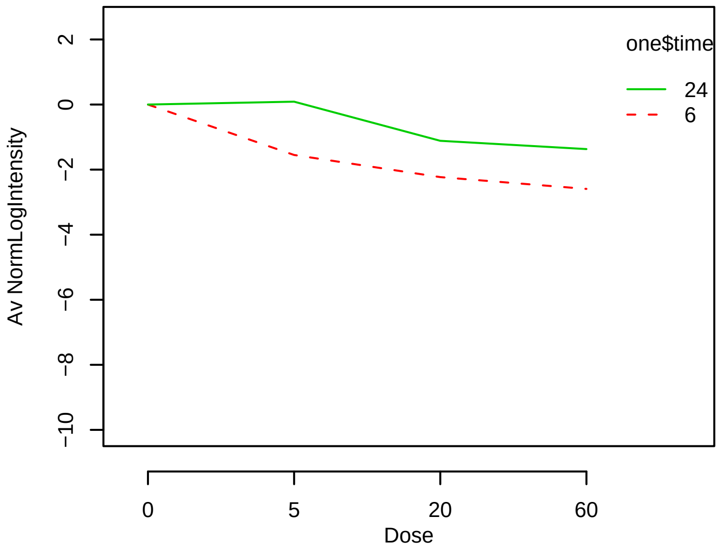
GO_0045494 : photoreceptor maintenance



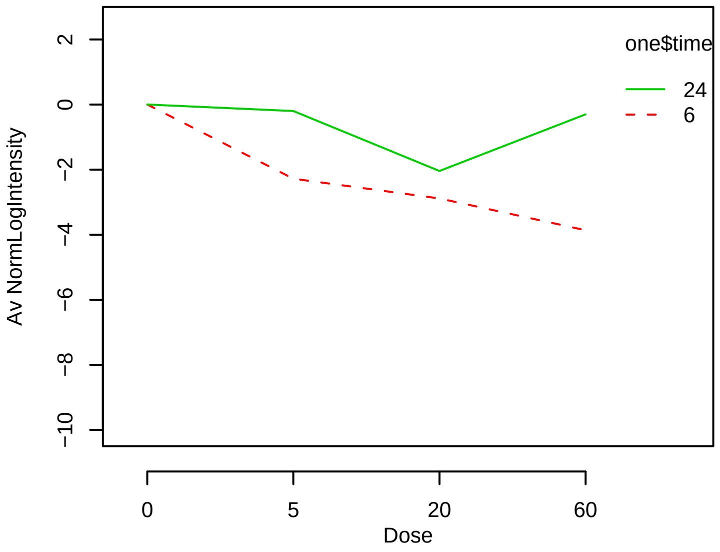
GO_0045576 : mast cell activation



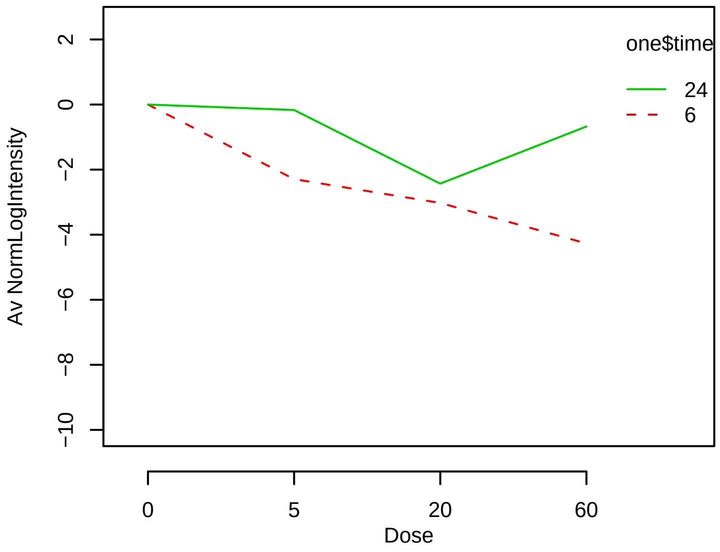
GO_0045577 : regulation of B cell differentiation



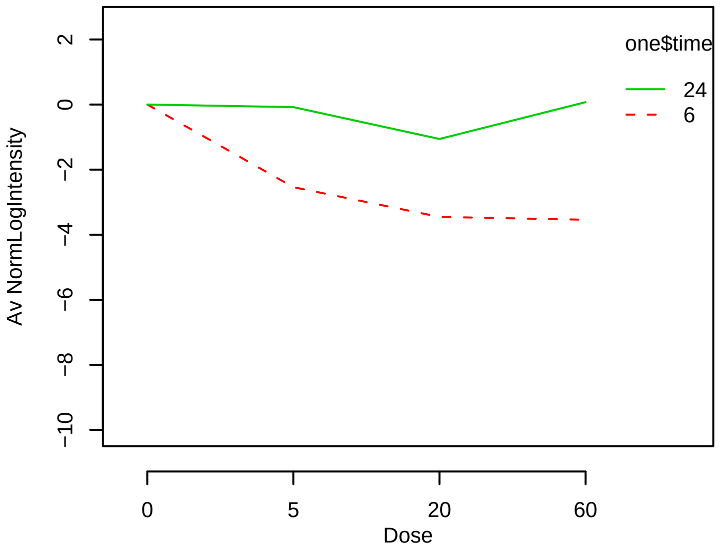
GO_0045579 : positive regulation of B cell differentiation



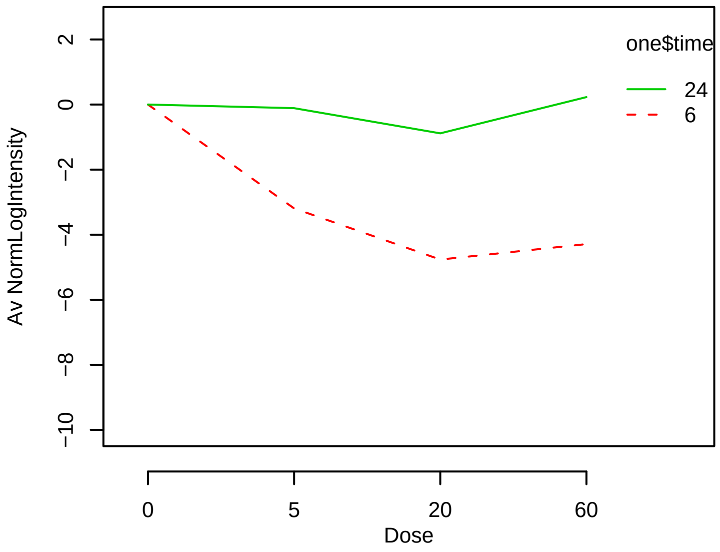
GO_0045580 : regulation of T cell differentiation



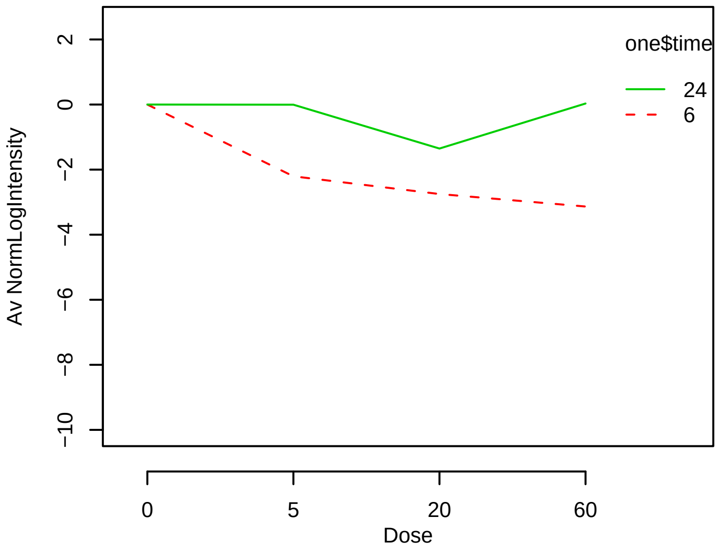
GO_0045582 : positive regulation of T cell differentiation



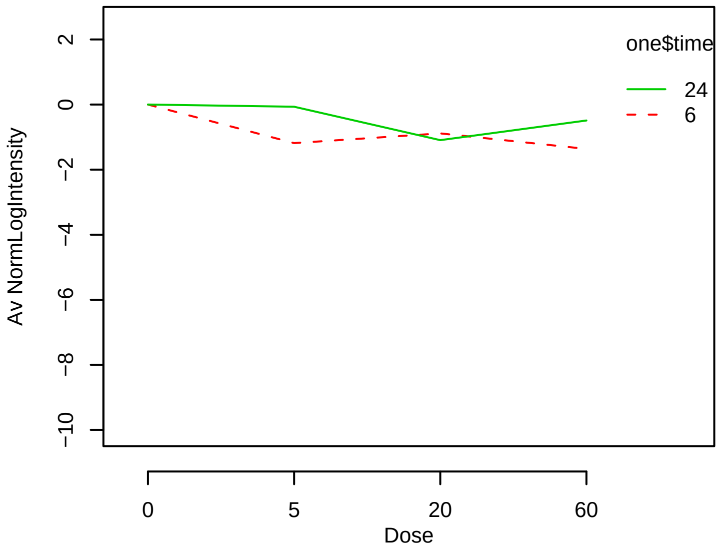
GO_0045595 : regulation of cell differentiation

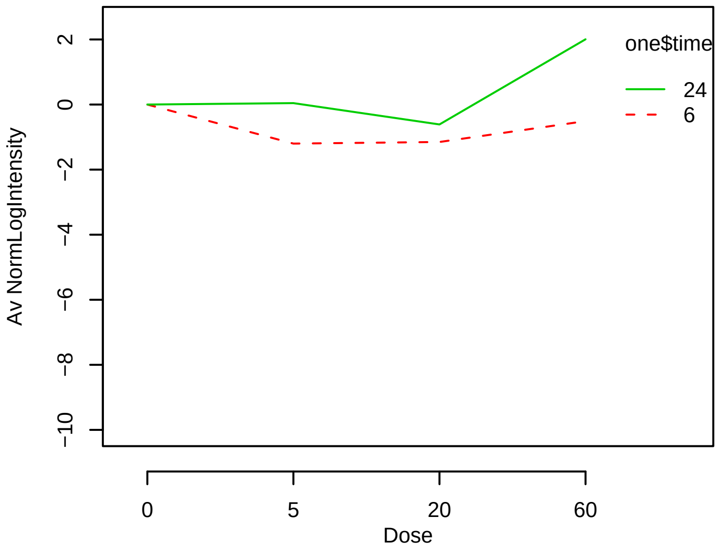


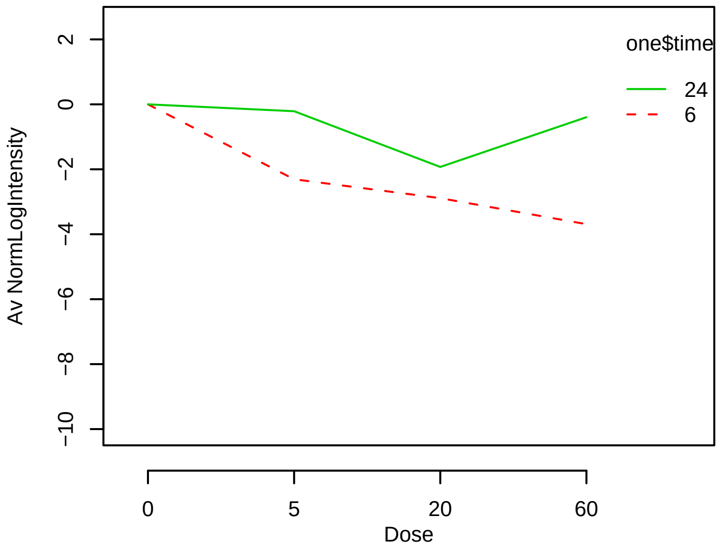
GO_0045596 : negative regulation of cell differentiation

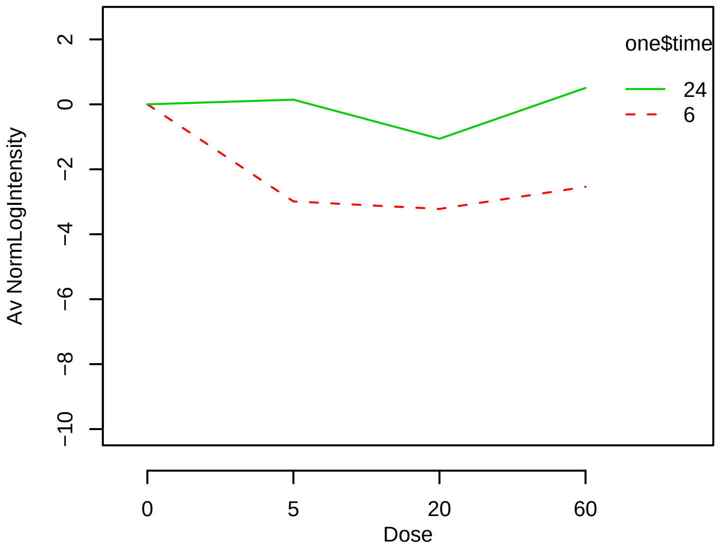


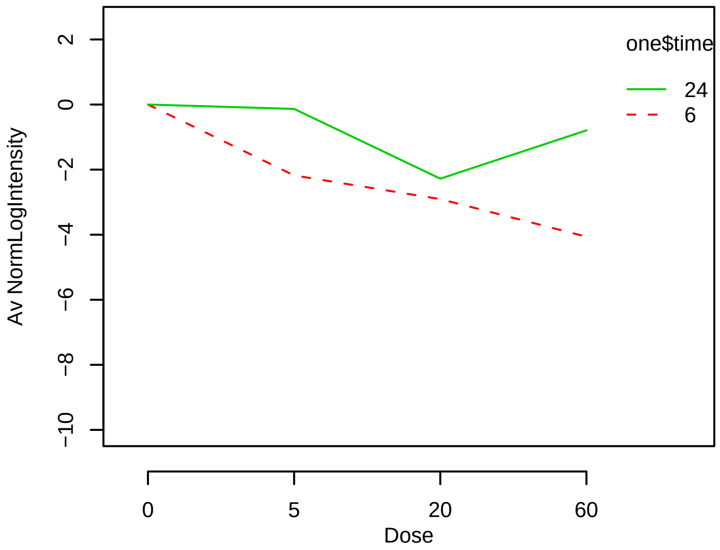
GO_0045597 : positive regulation of cell differentiation

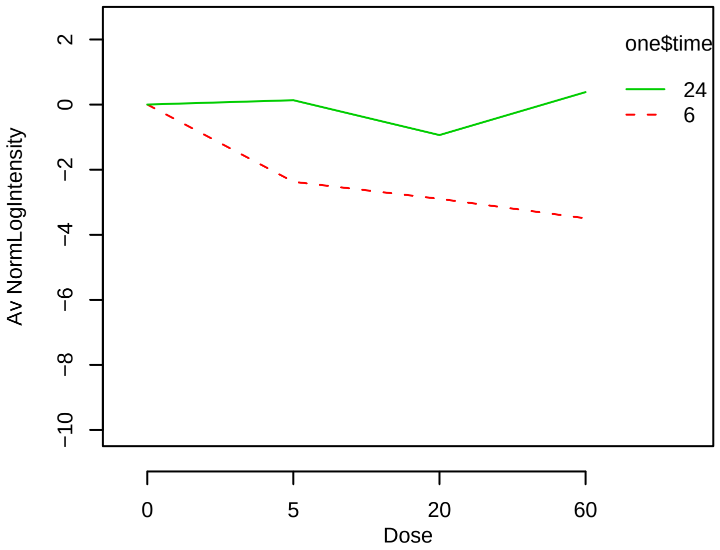

GO_0045598 : regulation of fat cell differentiation

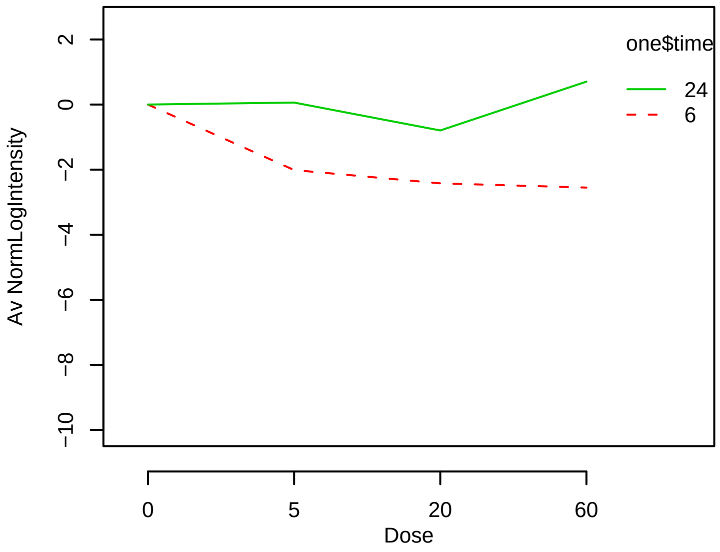

GO_0045604 : regulation of epidermal cell differentiation

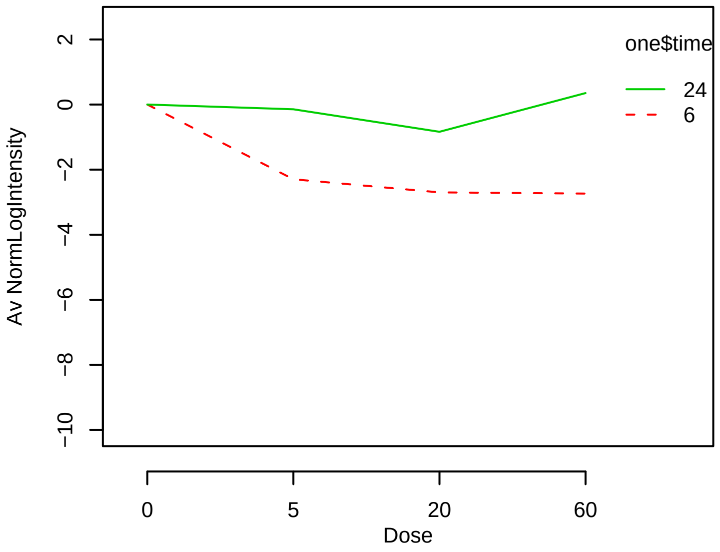

GO_0045619 : regulation of lymphocyte differentiation

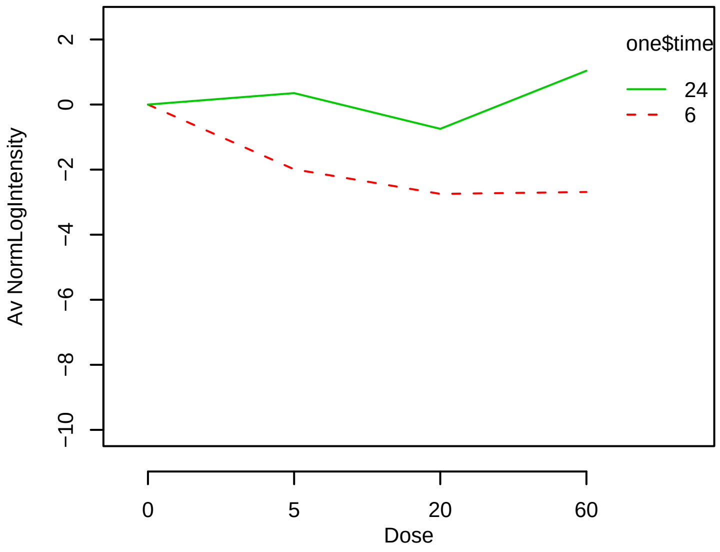

GO_0045620 : negative regulation of lymphocyte differentiat

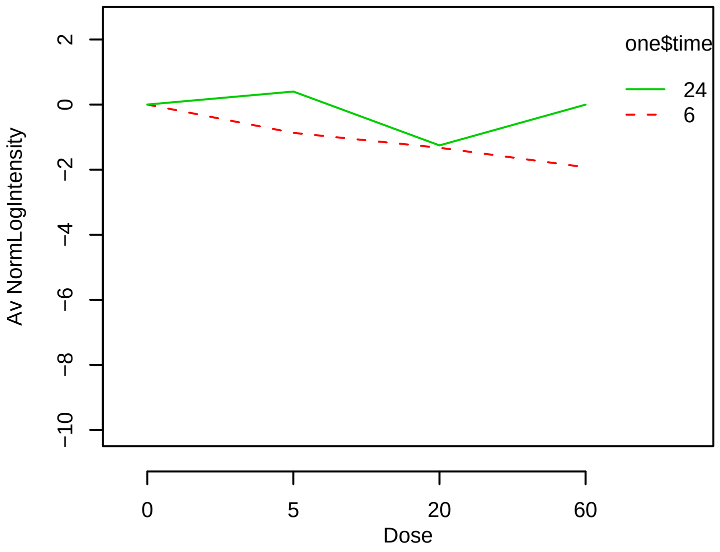

GO_0045621 : positive regulation of lymphocyte differentiat

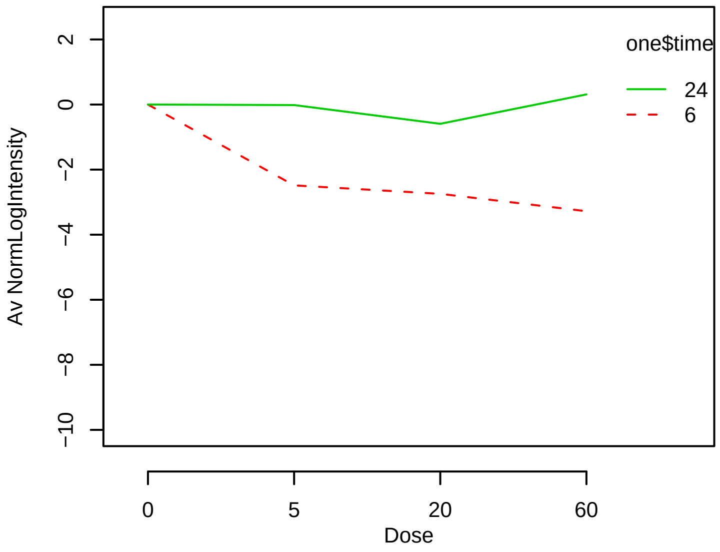

GO_0045622 : regulation of T−helper cell differentiation

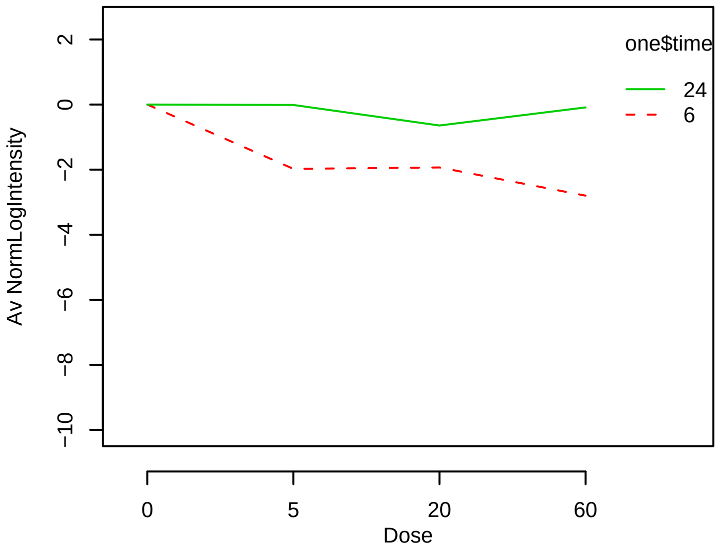

GO_0045637 : regulation of myeloid cell differentiation

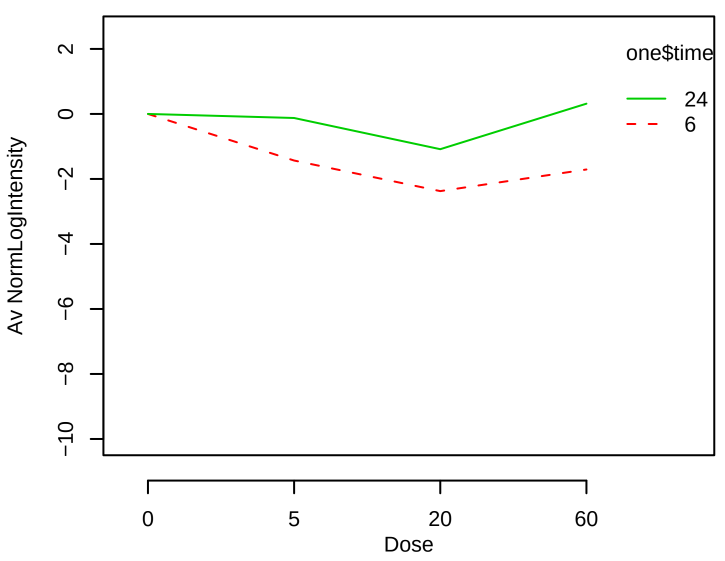

GO_0045638 : negative regulation of myeloid cell differentia

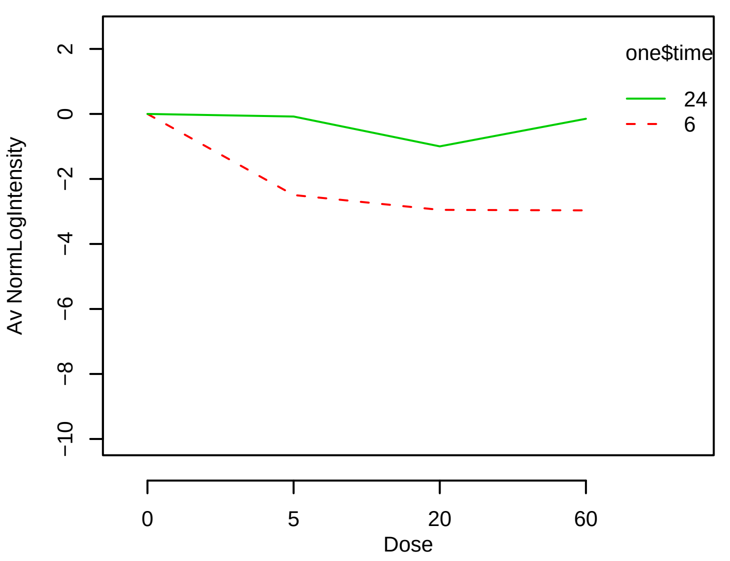

GO_0045639 : positive regulation of myeloid cell differentia

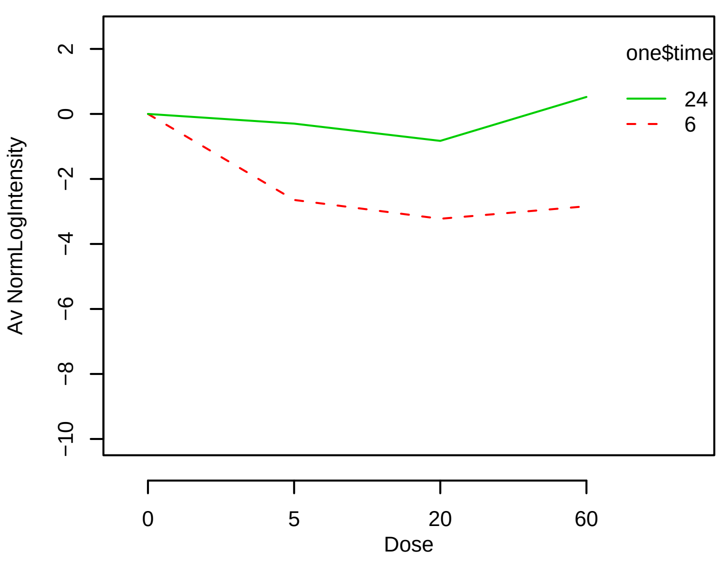

GO_0045646 : regulation of erythrocyte differentiation

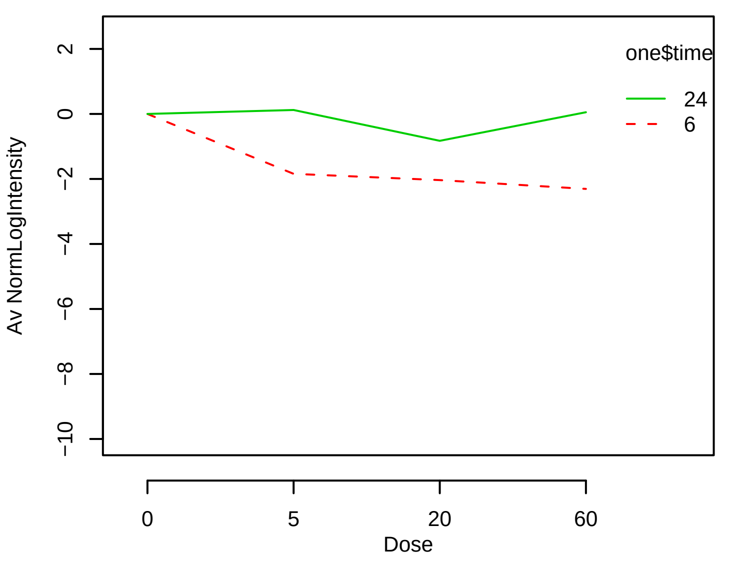

GO_0045655 : regulation of monocyte differentiation

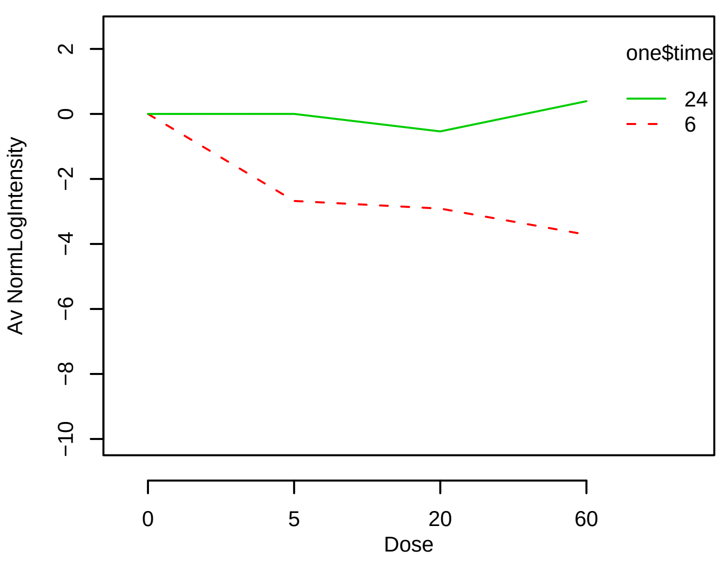

GO_0045656 : negative regulation of monocyte differentiati

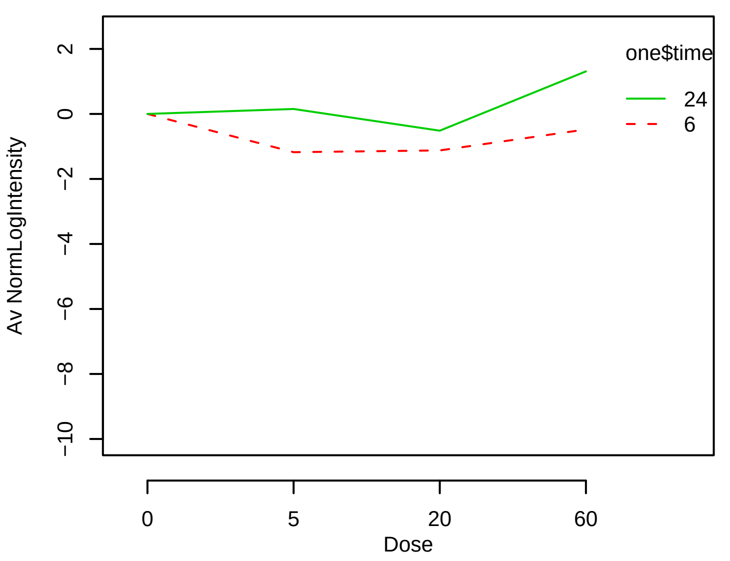

GO_0045661 : regulation of myoblast differentiation

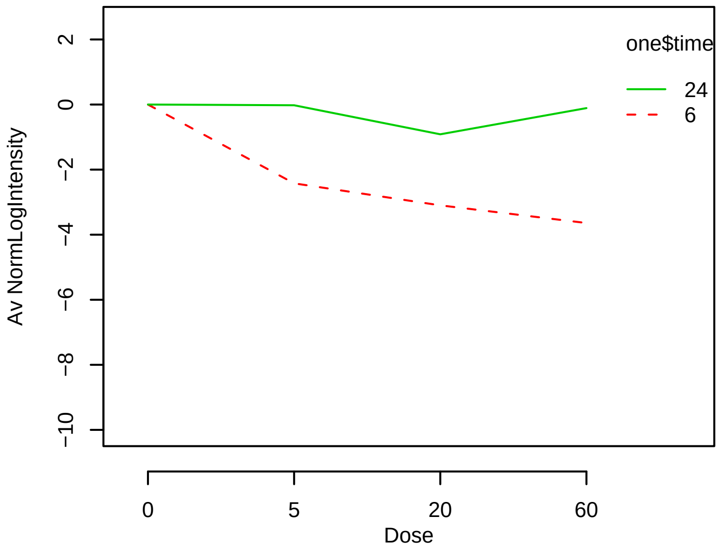

GO_0045664 : regulation of neuron differentiation


GO_0045665 : negative regulation of neuron differentiatio

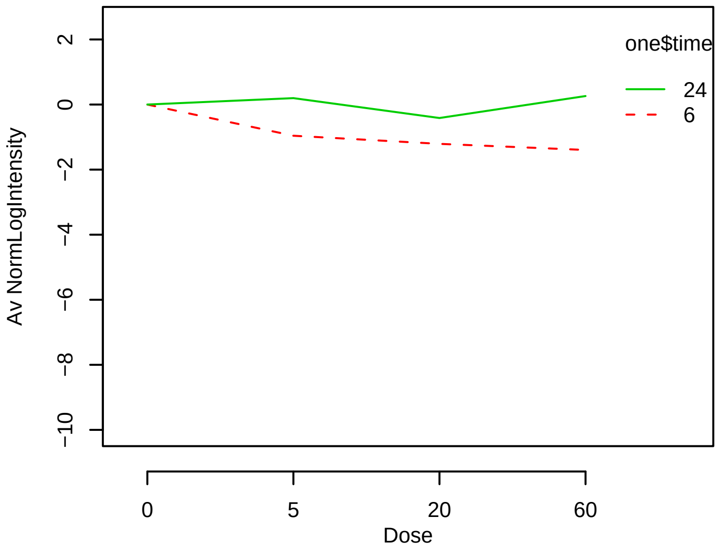

GO_0045667 : regulation of osteoblast differentiation


GO_0045670 : regulation of osteoclast differentiation

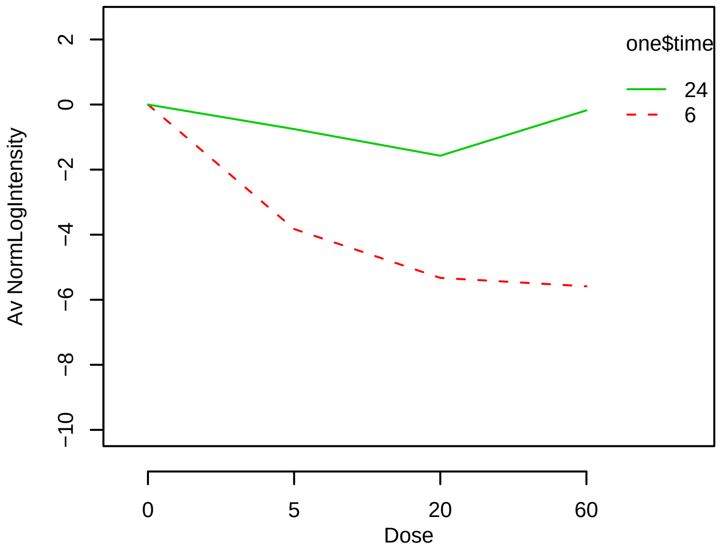

GO_0045682 : regulation of epidermis development



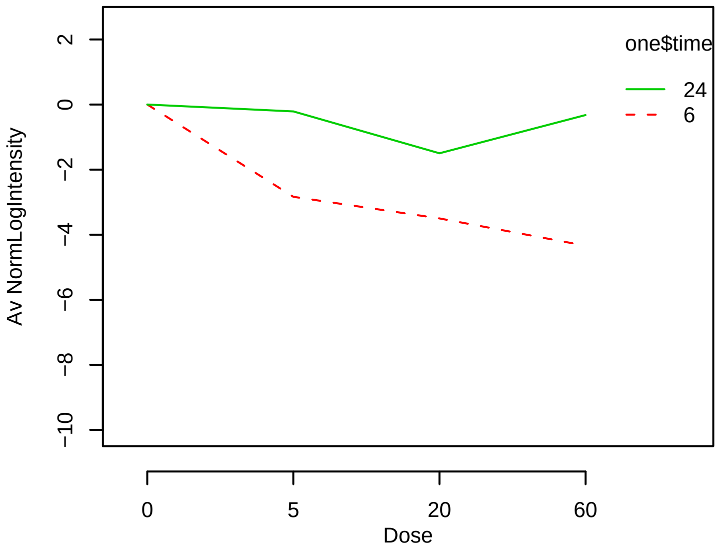
GO_0045727 : positive regulation of protein biosynthesis



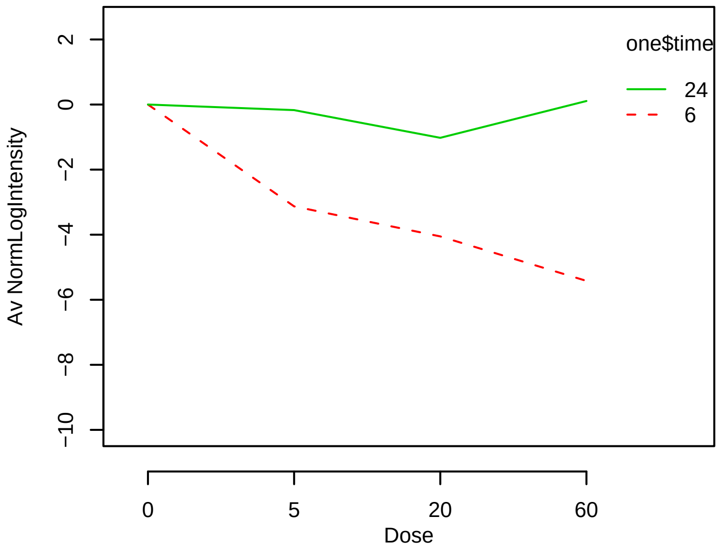
GO_0045736 : negative regulation of cyclin−dependent prote



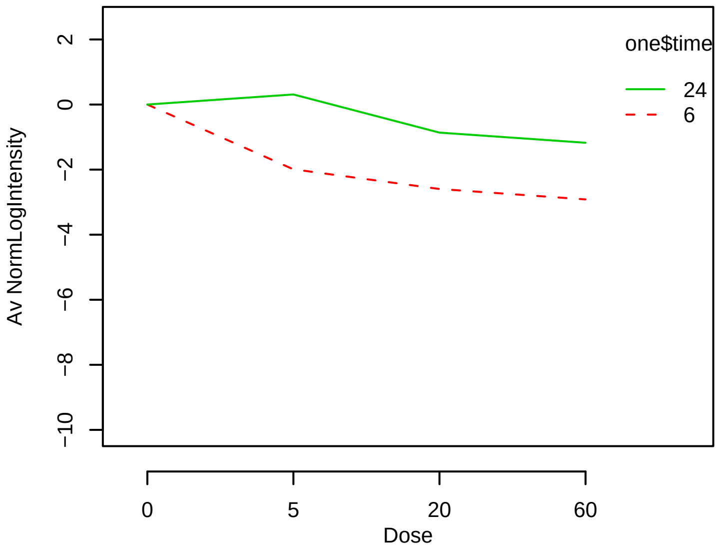
GO_0045744 : negative regulation of G−protein coupled rece



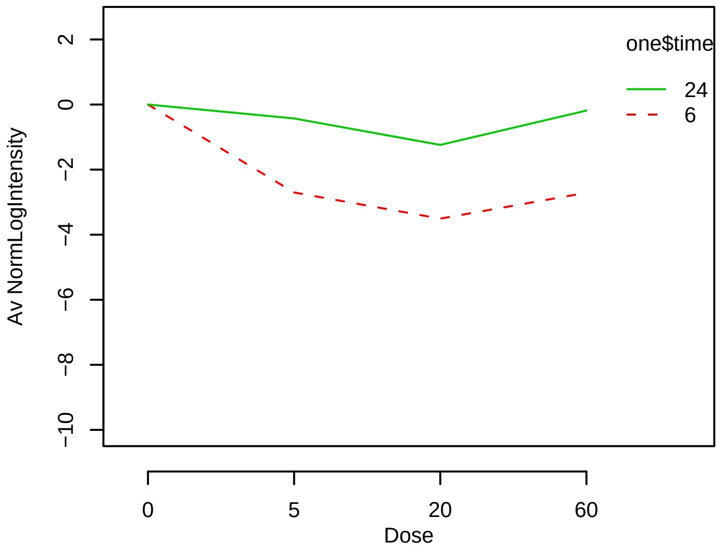
GO_0045761 : regulation of adenylate cyclase activity

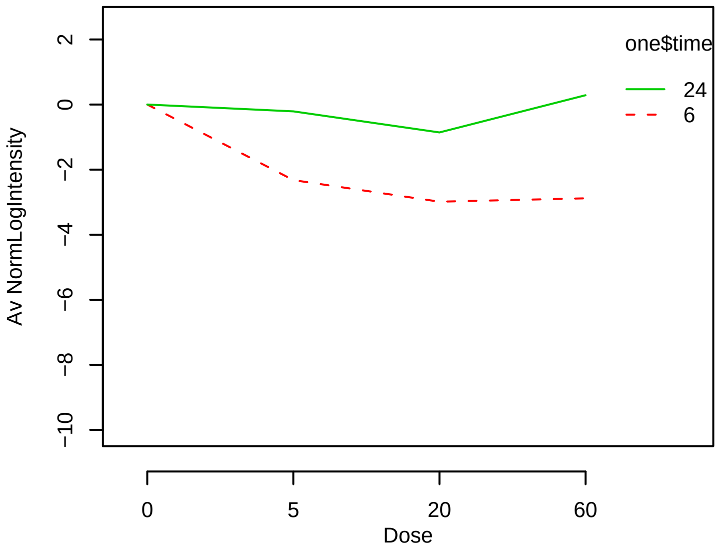


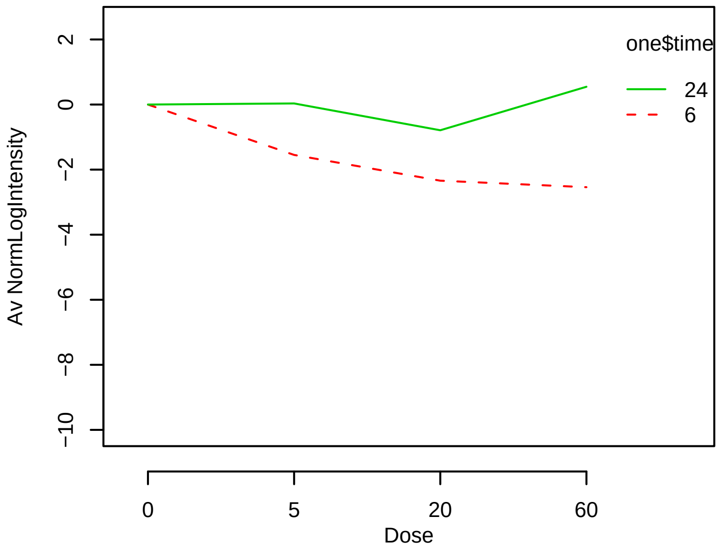
GO_0045762 : positive regulation of adenylate cyclase activ

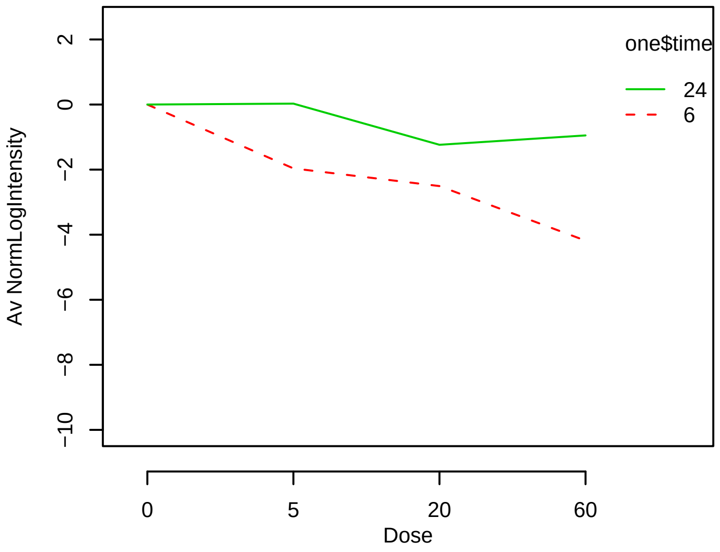


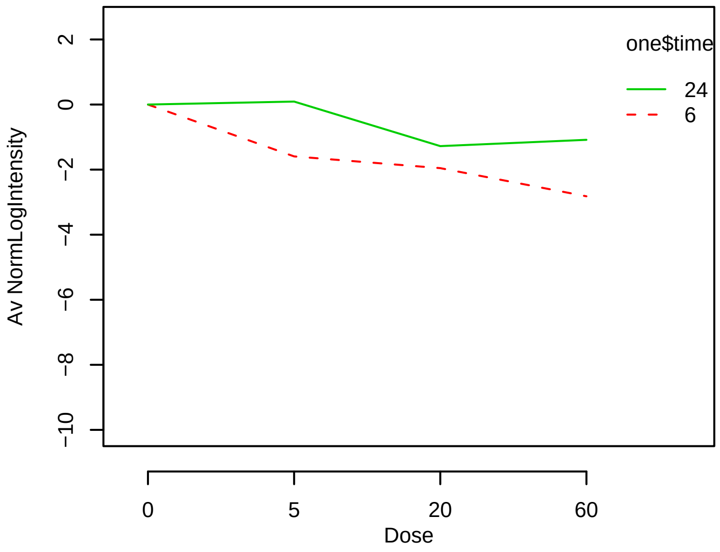
GO_0045763 : negative regulation of amino acid metabolis

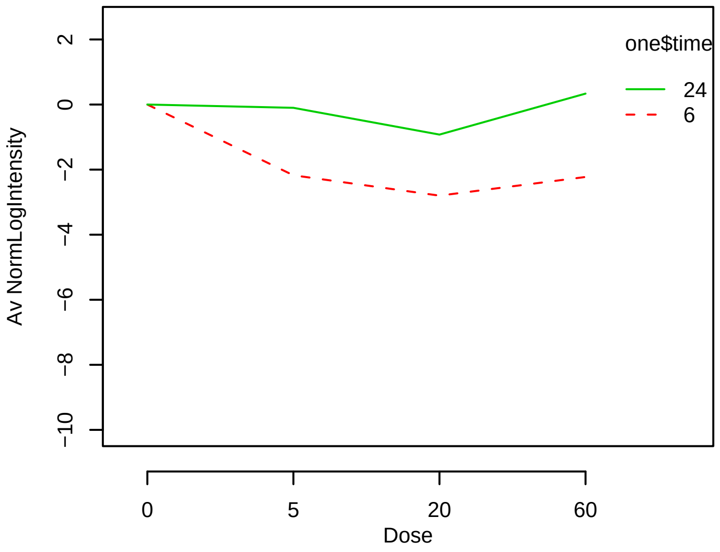

GO_0045764 : positive regulation of amino acid metabolis


GO_0045765 : regulation of angiogenesis

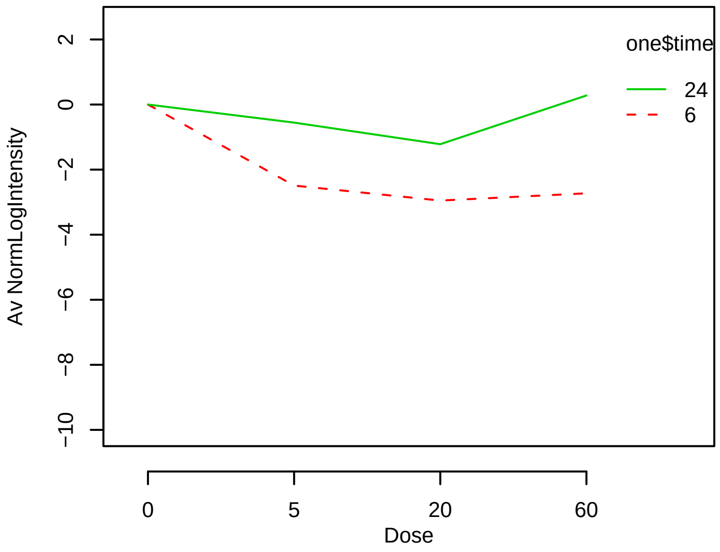

GO_0045766 : positive regulation of angiogenesis


GO_0045767 : regulation of anti−apoptosis

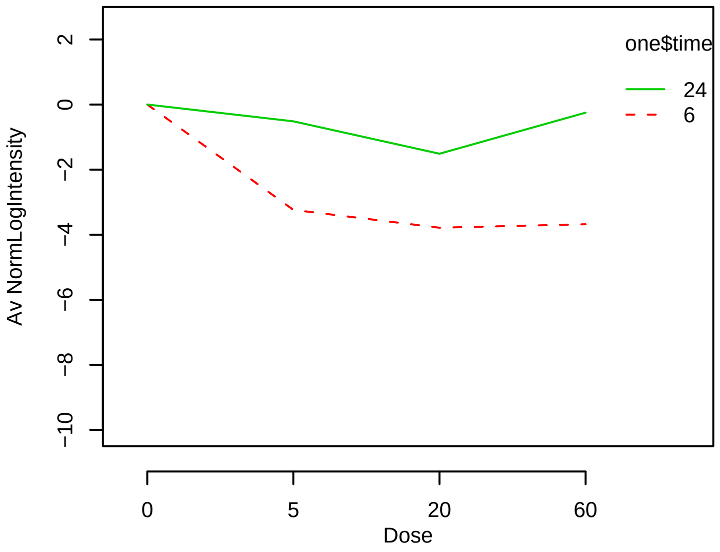

GO_0045768 : positive regulation of anti−apoptosis


GO_0045773 : positive regulation of axon extension

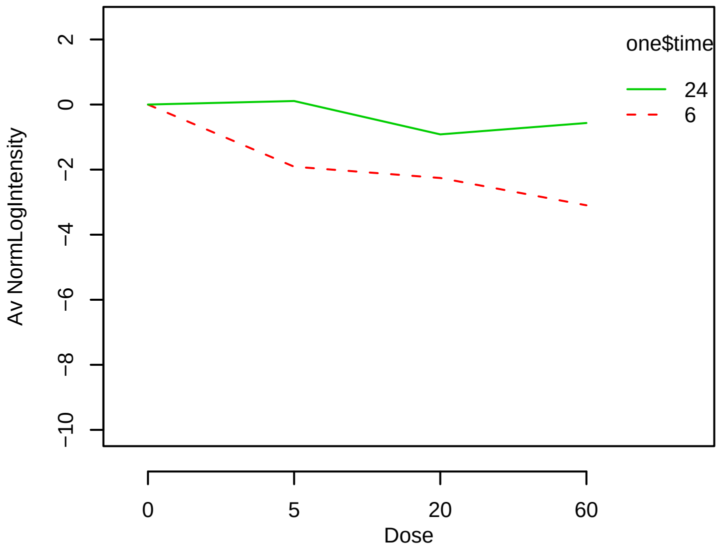
GO_0045778 : positive regulation of ossification



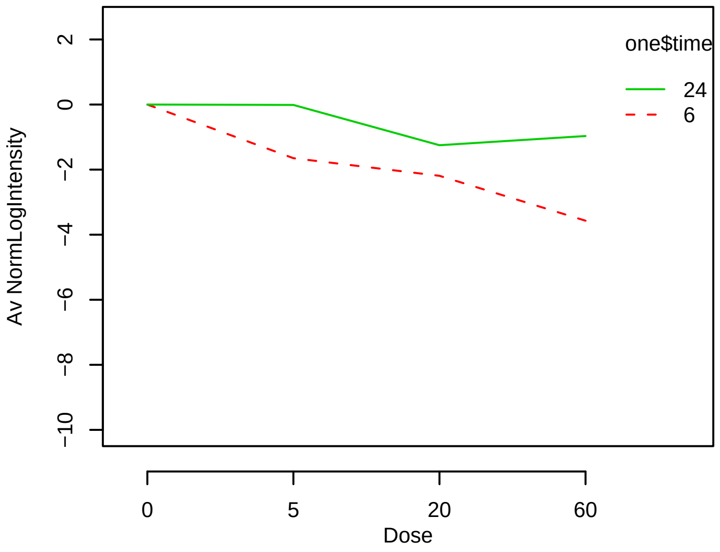
GO_0045785 : positive regulation of cell adhesion



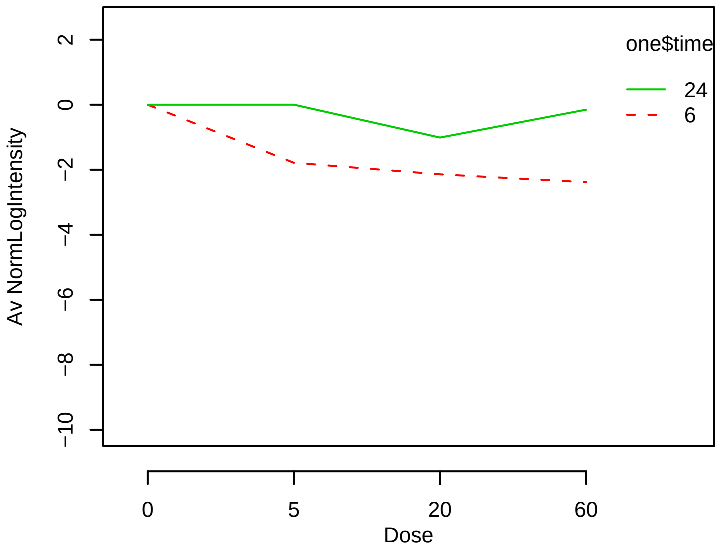
GO_0045786 : negative regulation of progression through ce



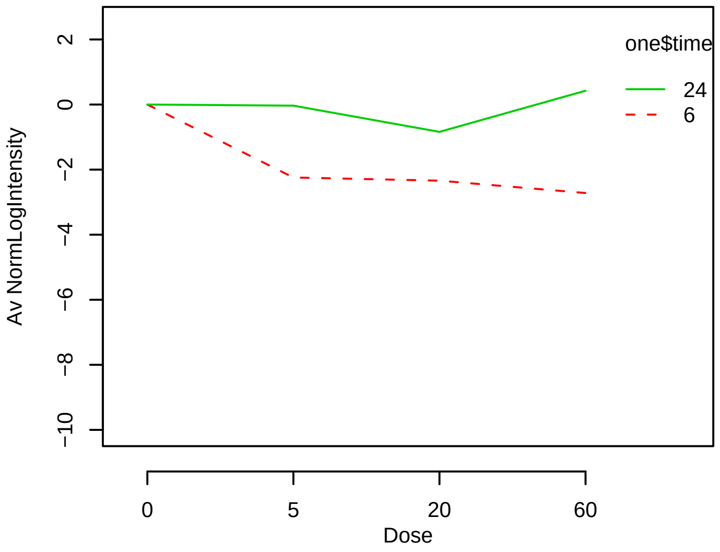
GO_0045787 : positive regulation of progression through cel



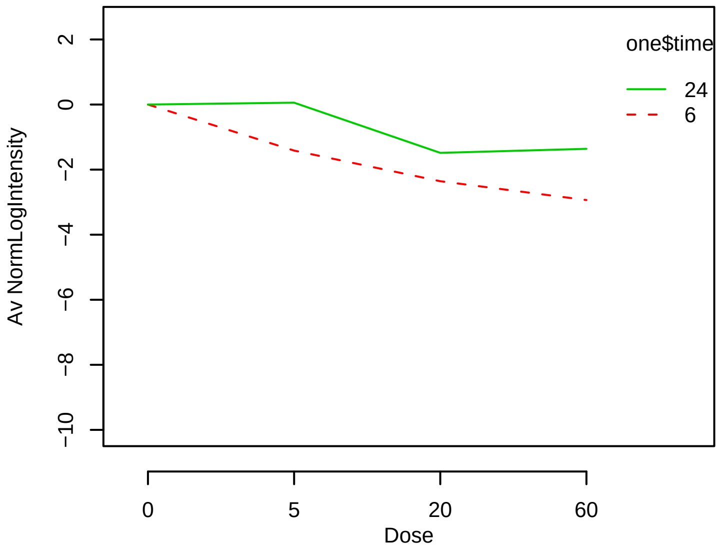
GO_0045792 : negative regulation of cell size



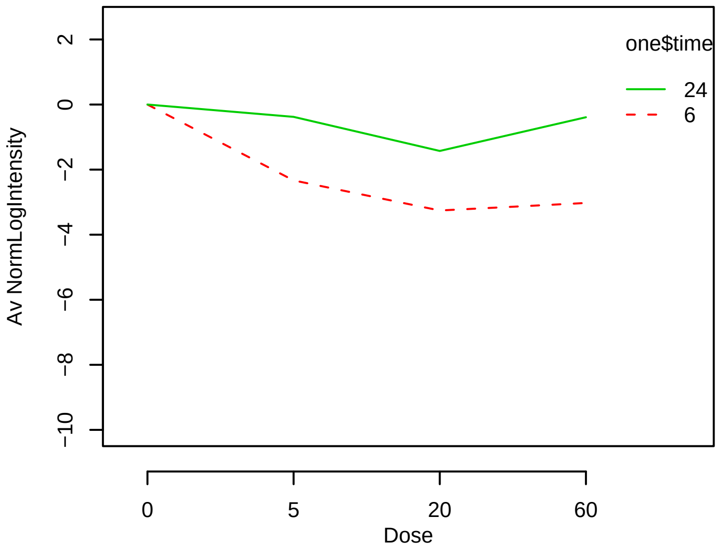
GO_0045793 : positive regulation of cell size



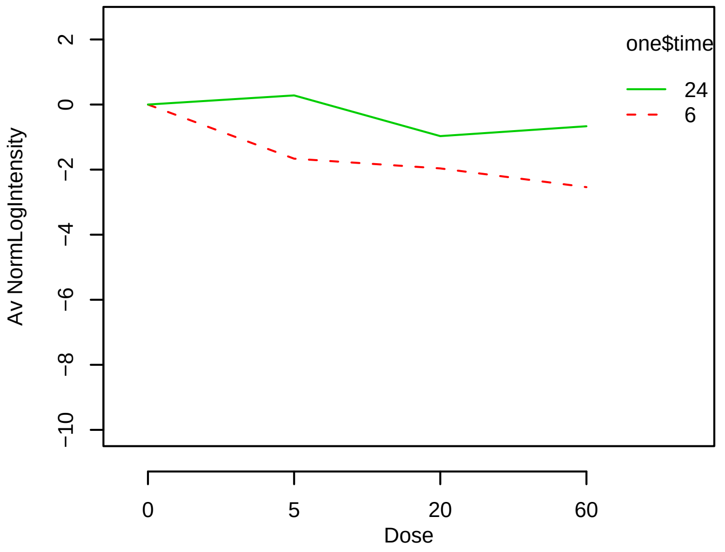
GO_0045806 : negative regulation of endocytosis



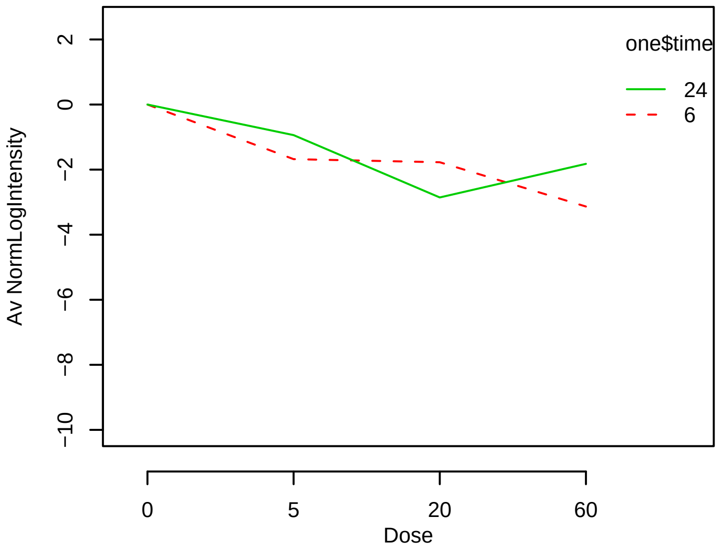
GO_0045807 : positive regulation of endocytosis



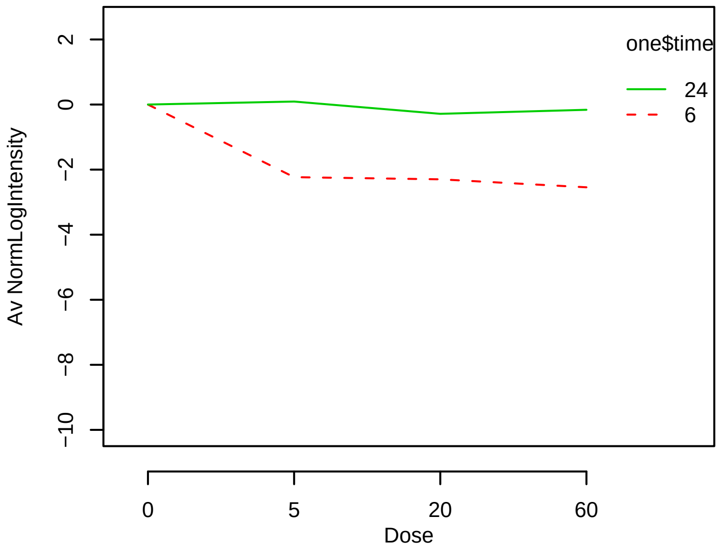
GO_0045814 : negative regulation of gene expression\, epige



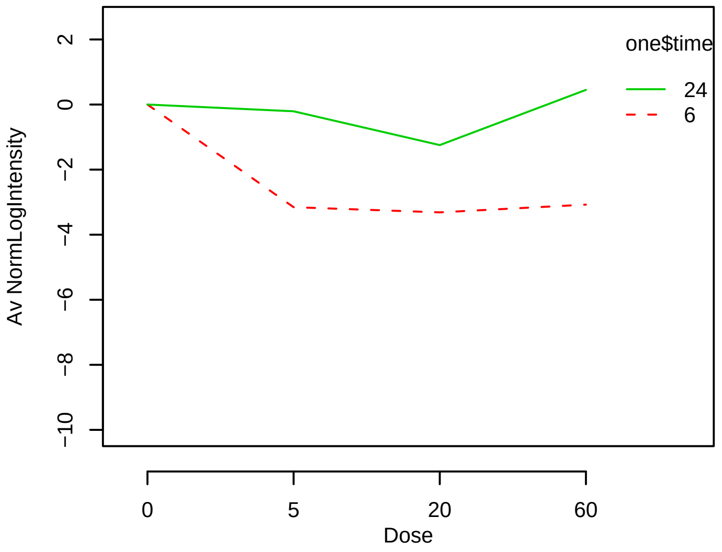
GO_0045815 : positive regulation of gene expression\, epige



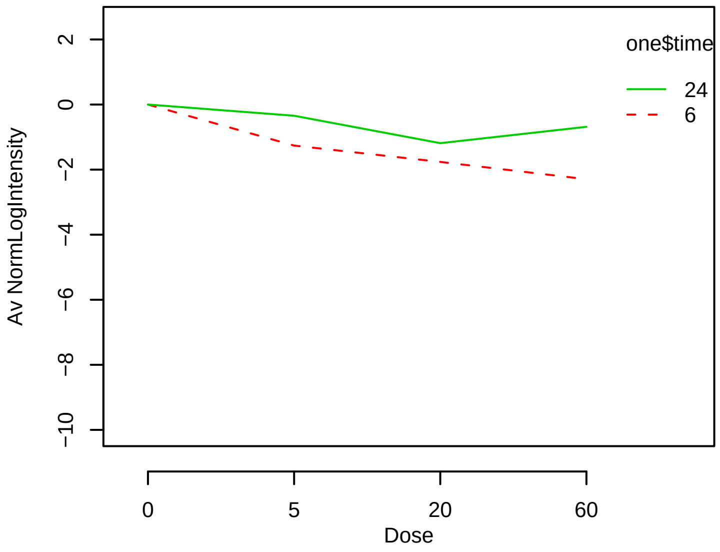
GO_0045823 : positive regulation of heart contraction



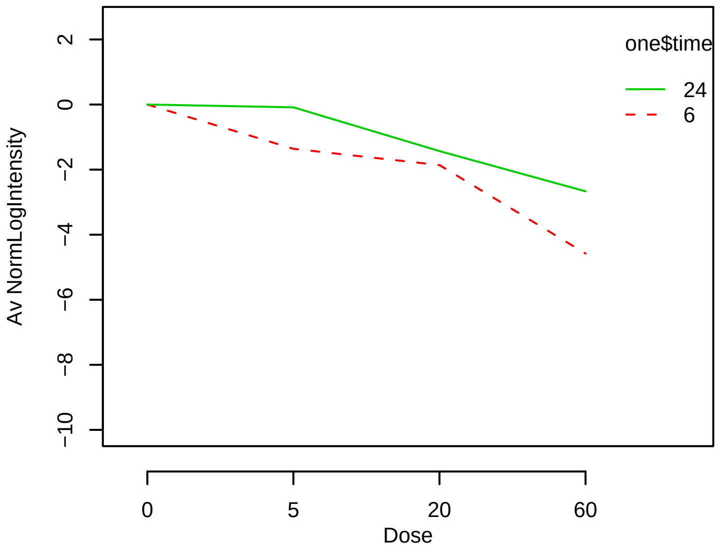
GO_0045830 : positive regulation of isotype switching



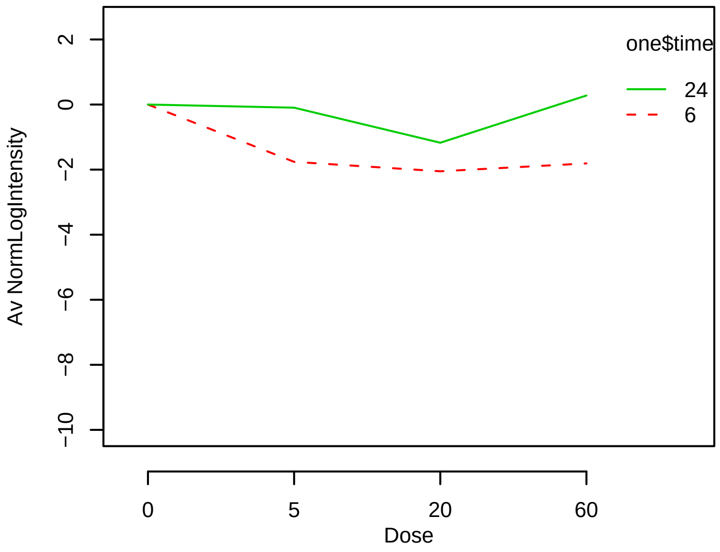
GO_0045834 : positive regulation of lipid metabolism



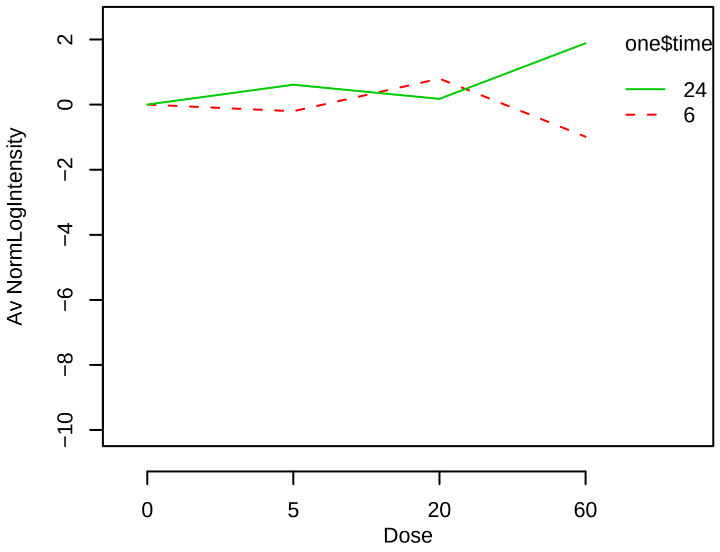
GO_0045840 : positive regulation of mitosis



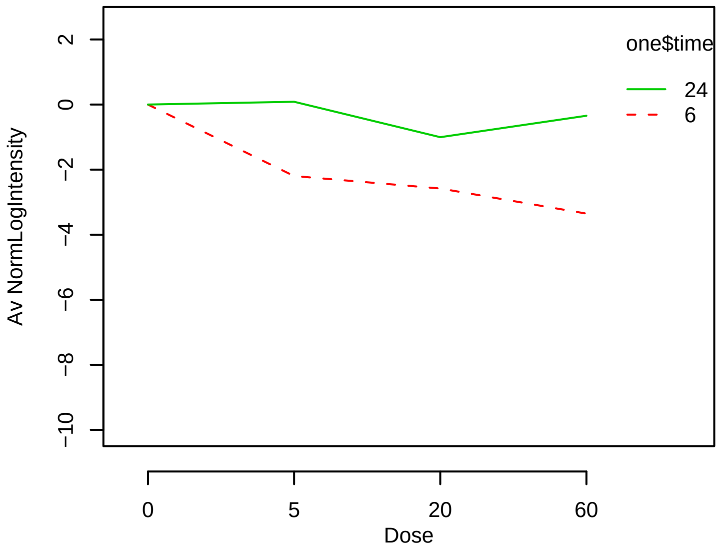
GO_0045843 : negative regulation of striated muscle develop



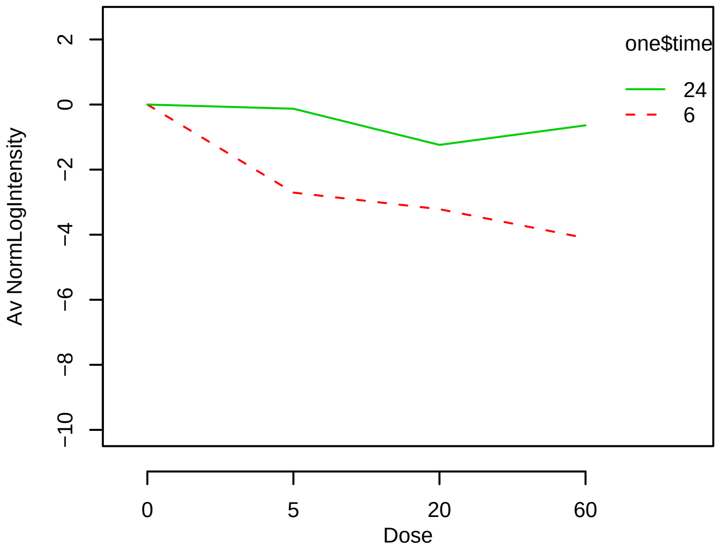
GO_0045851 : pH reduction



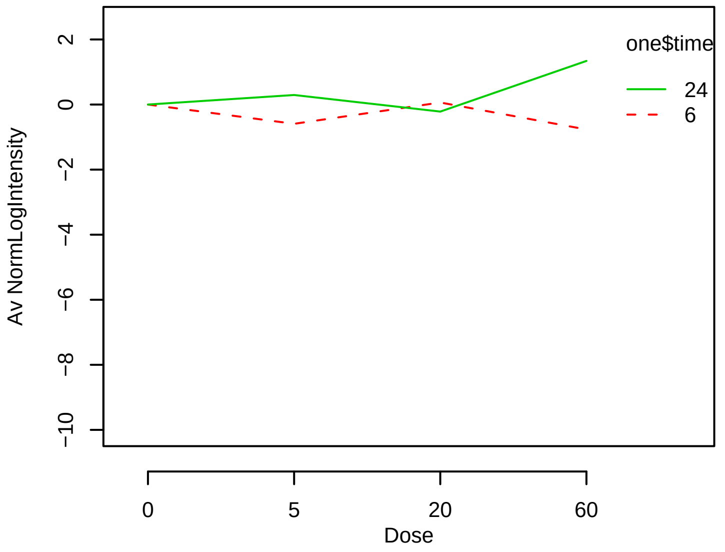
GO_0045859 : regulation of protein kinase activity



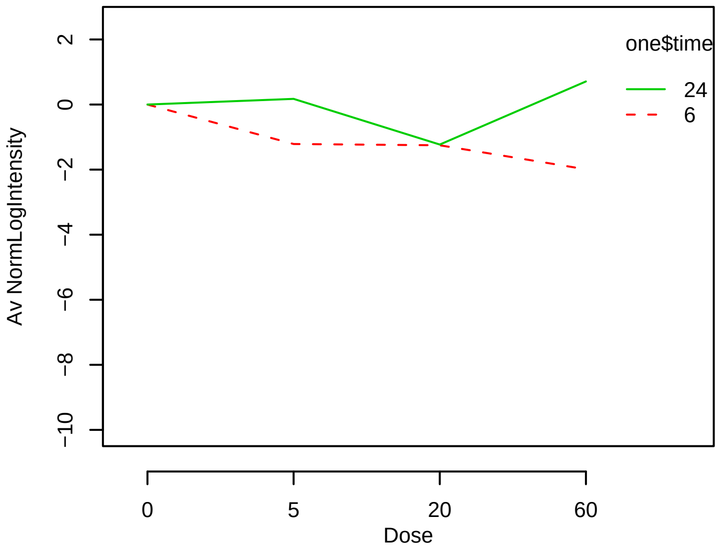
GO_0045860 : positive regulation of protein kinase activit



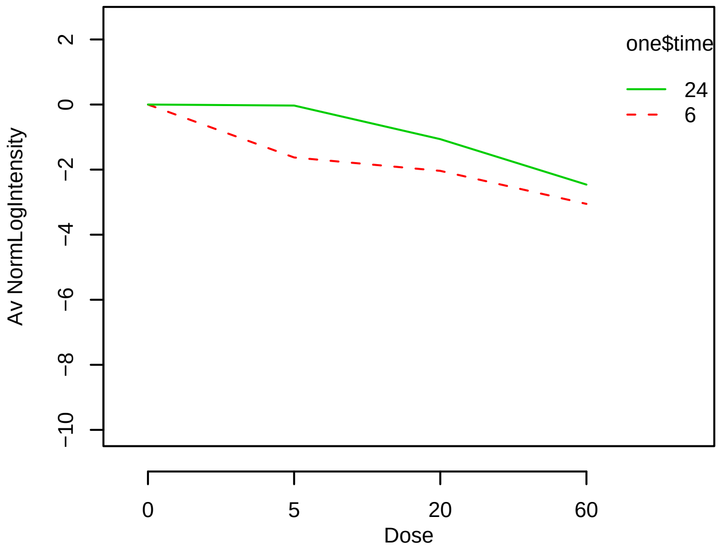
GO_0045861 : negative regulation of proteolysis



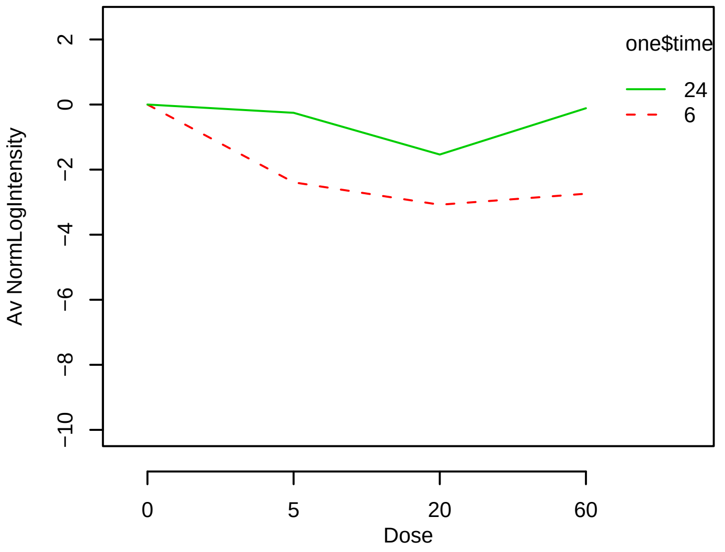
GO_0045862 : positive regulation of proteolysis



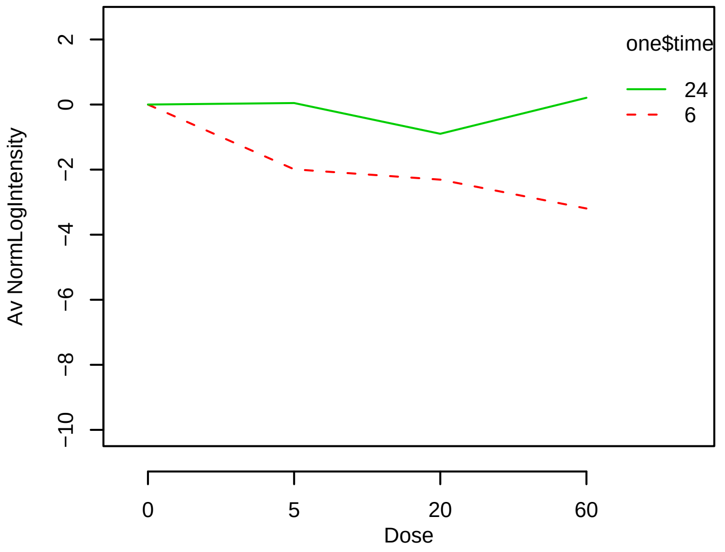
GO_0045884 : regulation of survival gene product activity



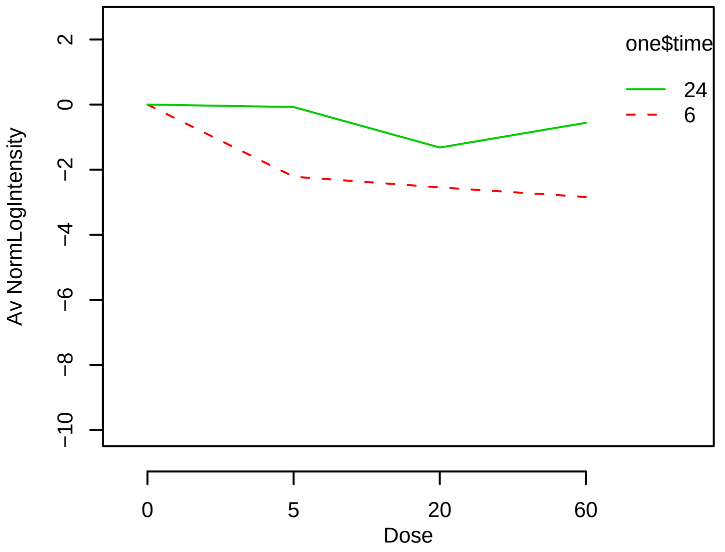
GO_0045885 : positive regulation of survival gene product a



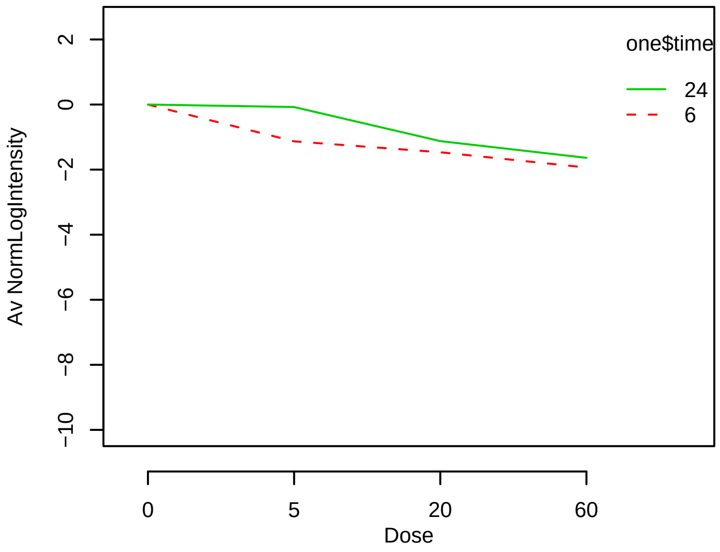
GO_0045892 : negative regulation of transcription\, DNA−dep



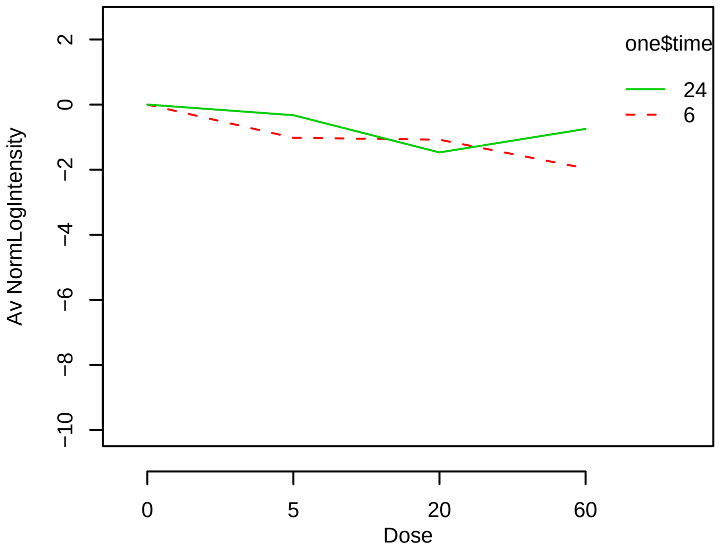
GO_0045893 : positive regulation of transcription\, DNA−depe



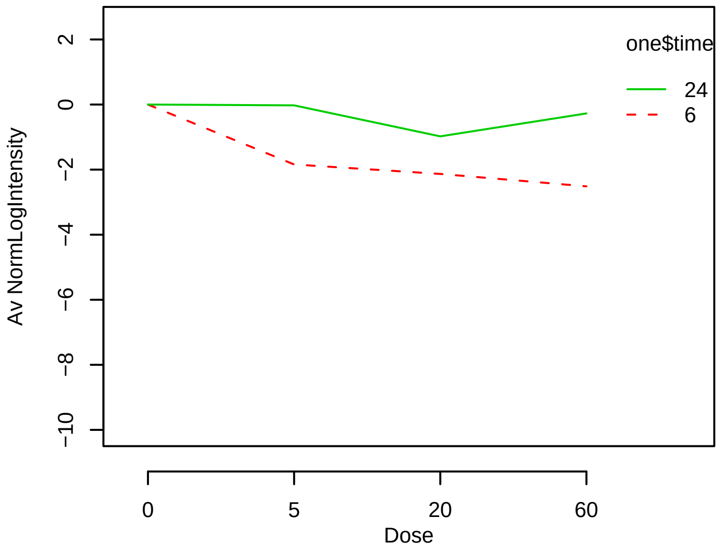
GO_0045913 : positive regulation of carbohydrate metabolis



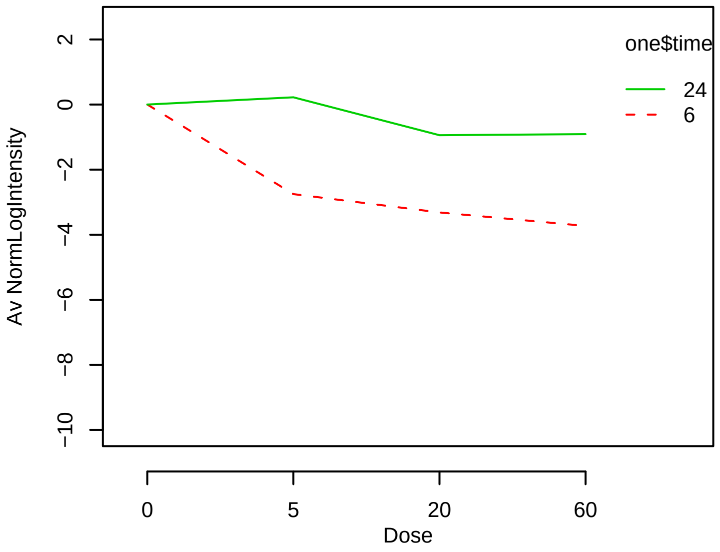
GO_0045923 : positive regulation of fatty acid metabolism



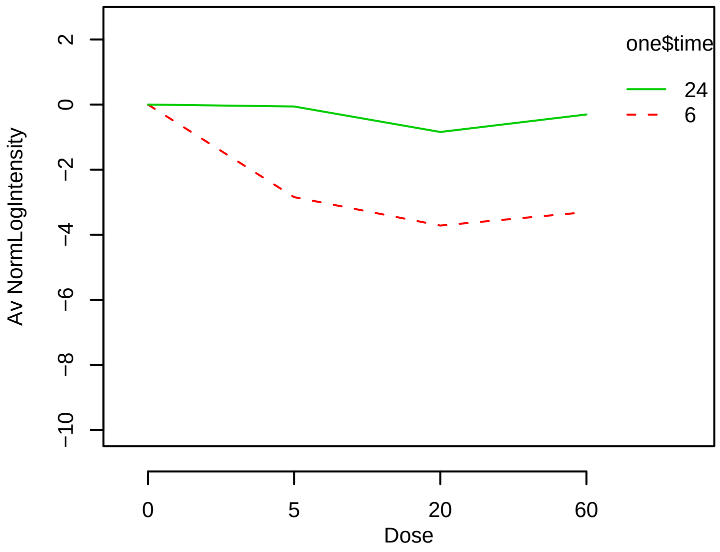
GO_0045926 : negative regulation of growth



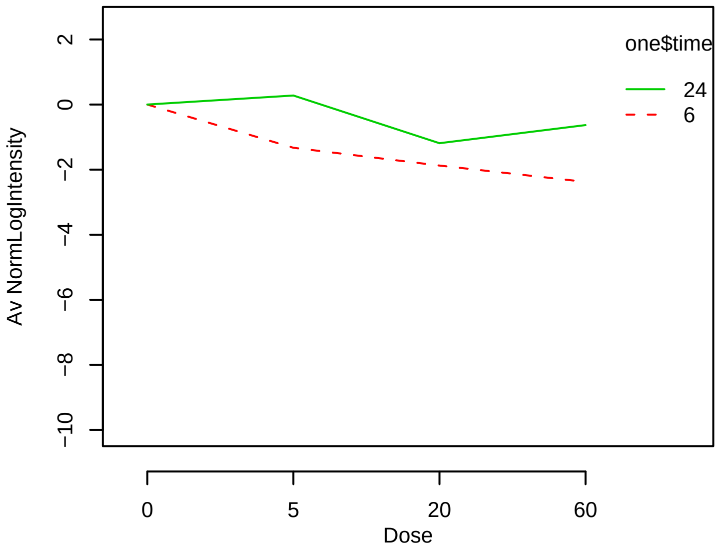
GO_0045927 : positive regulation of growth

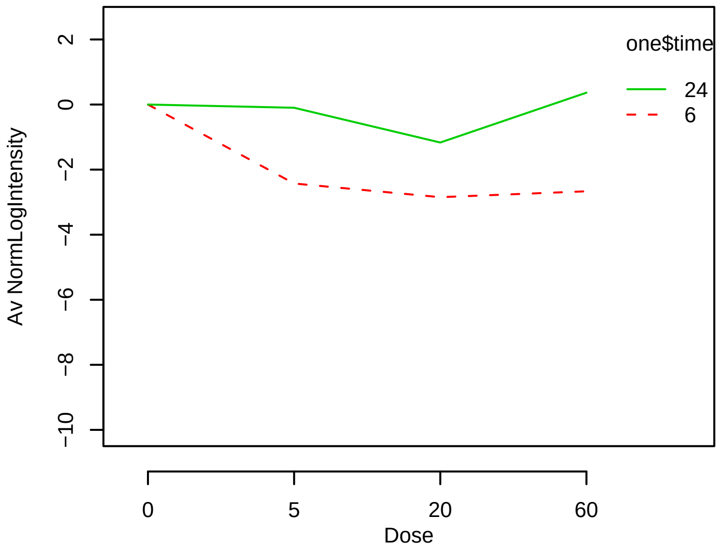


GO_0045930 : negative regulation of progression through mi

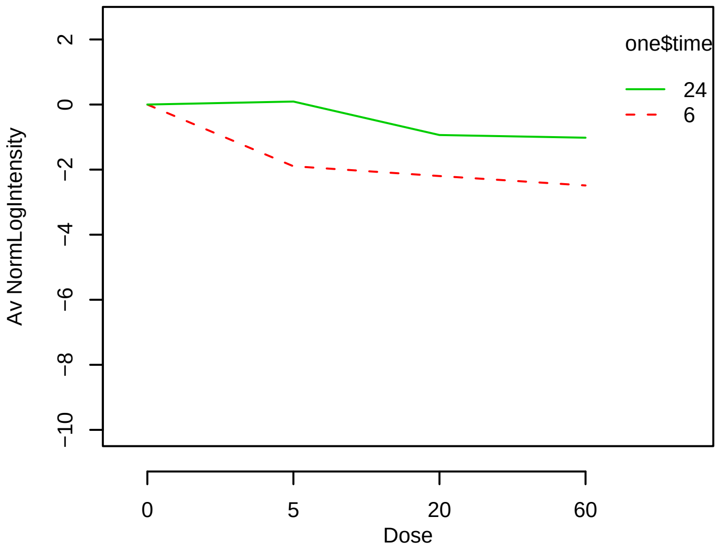


GO_0045931 : positive regulation of progression through mit

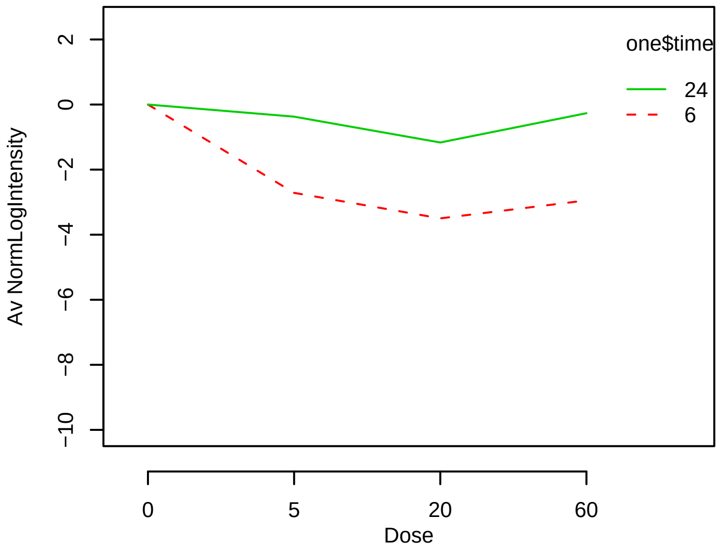




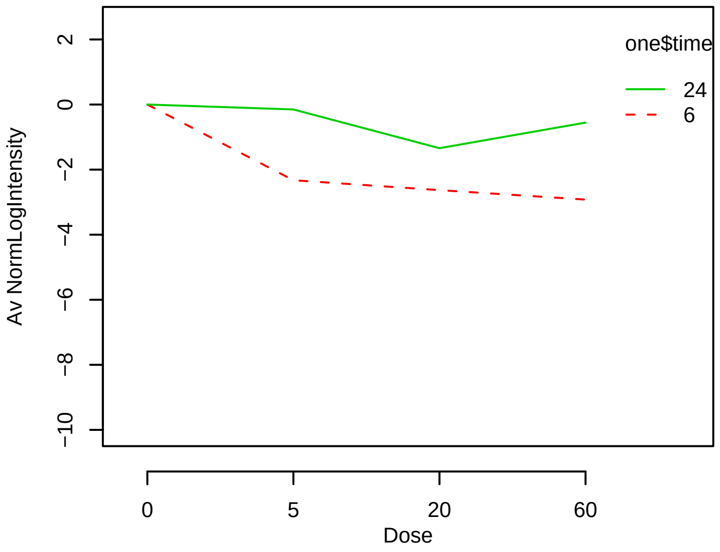
GO_0045933 : positive regulation of muscle contraction



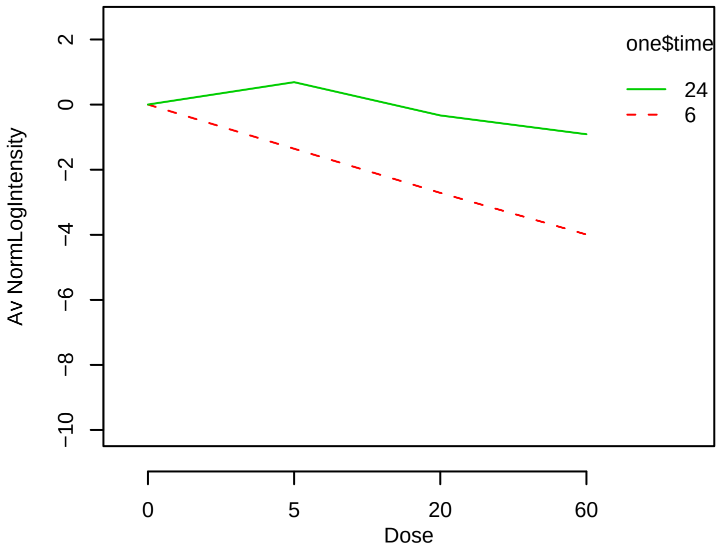
GO_0045936 : negative regulation of phosphate metabolis



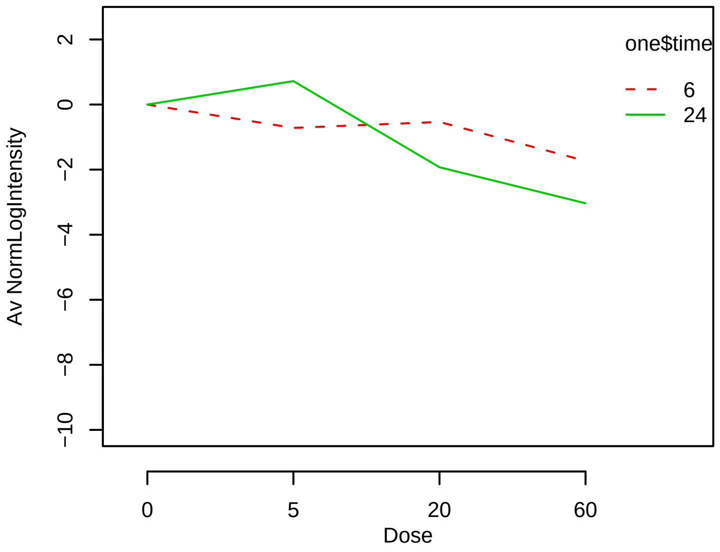
GO_0045937 : positive regulation of phosphate metabolis



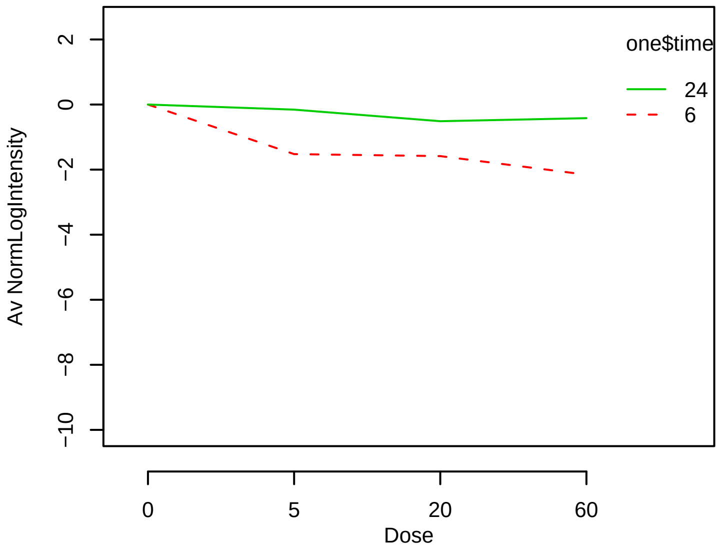
GO_0045944 : positive regulation of transcription from RNA



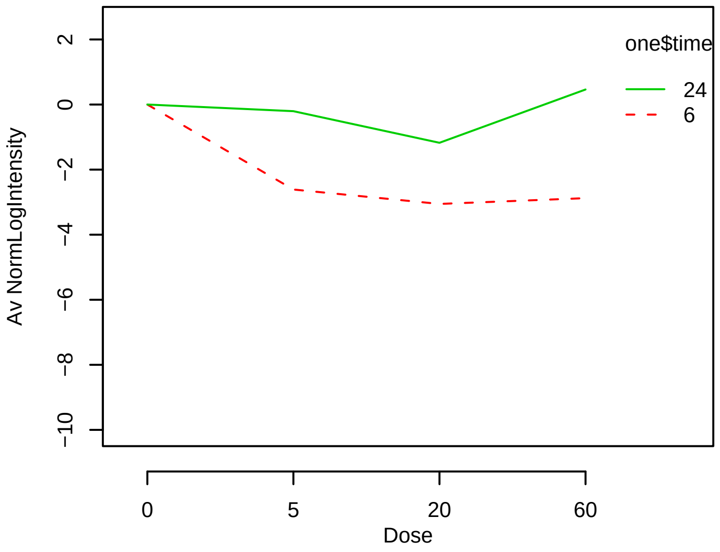
GO_0045946 : positive regulation of translation



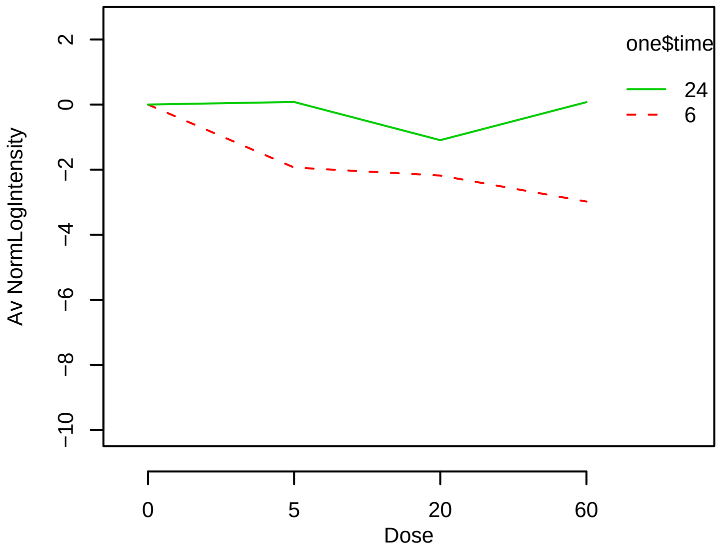
GO_0045947 : negative regulation of translational initiatio



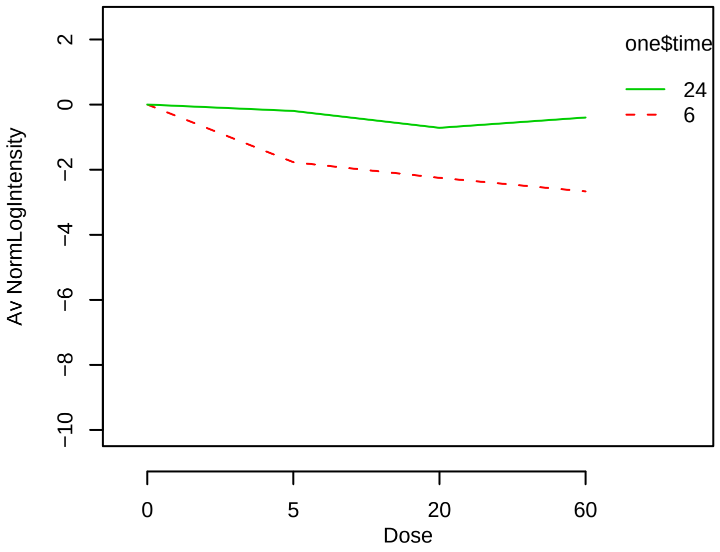
GO_0045980 : negative regulation of nucleotide metabolis



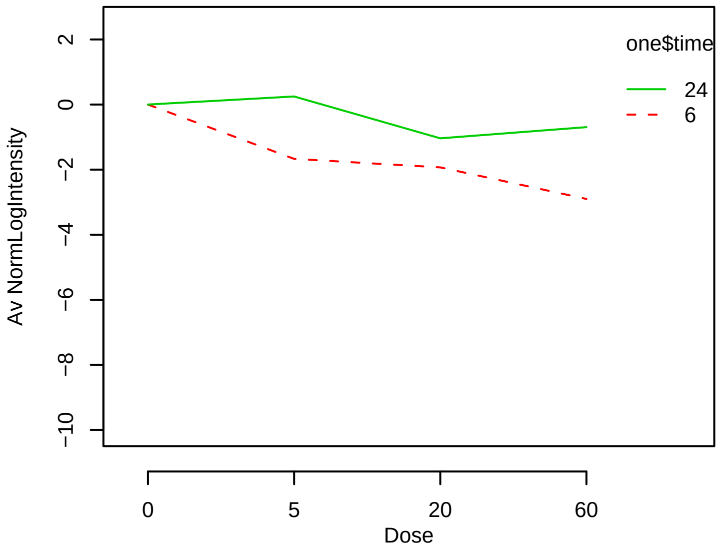
GO_0045987 : positive regulation of smooth muscle contract



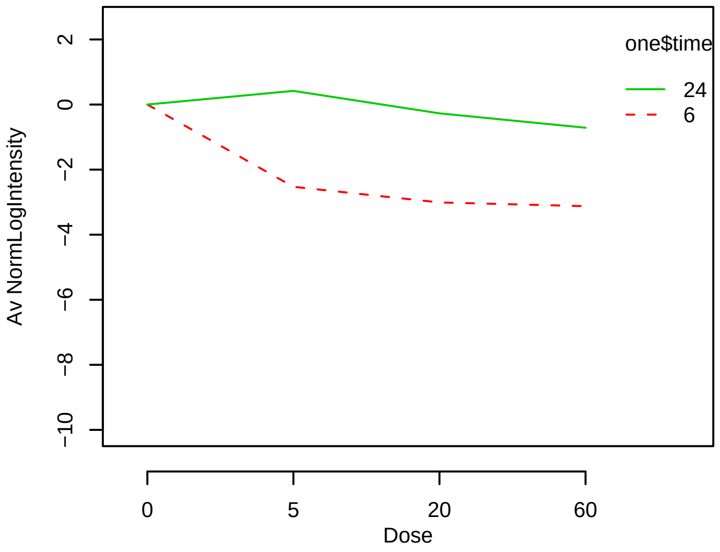
GO_0045995 : regulation of embryonic development



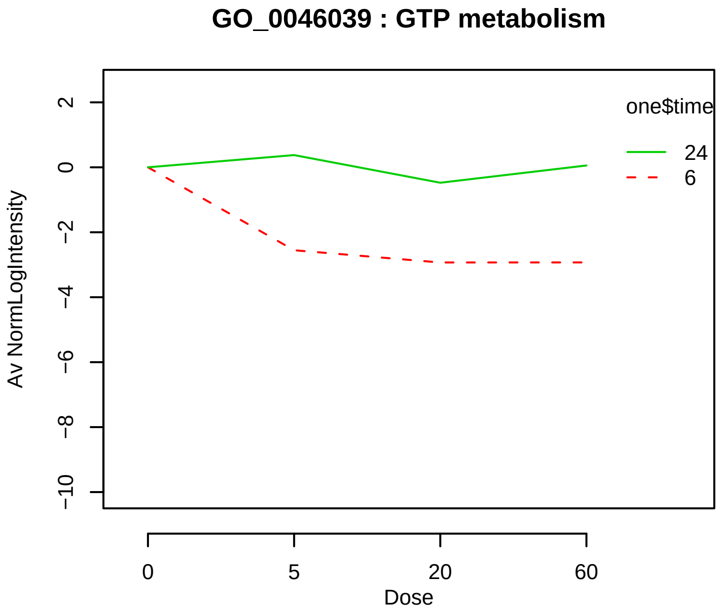
GO_0046006 : regulation of activated T cell proliferation

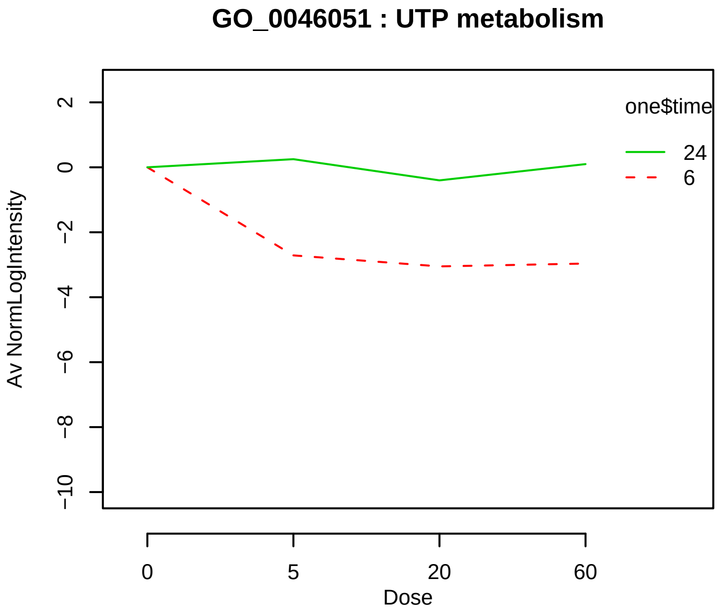


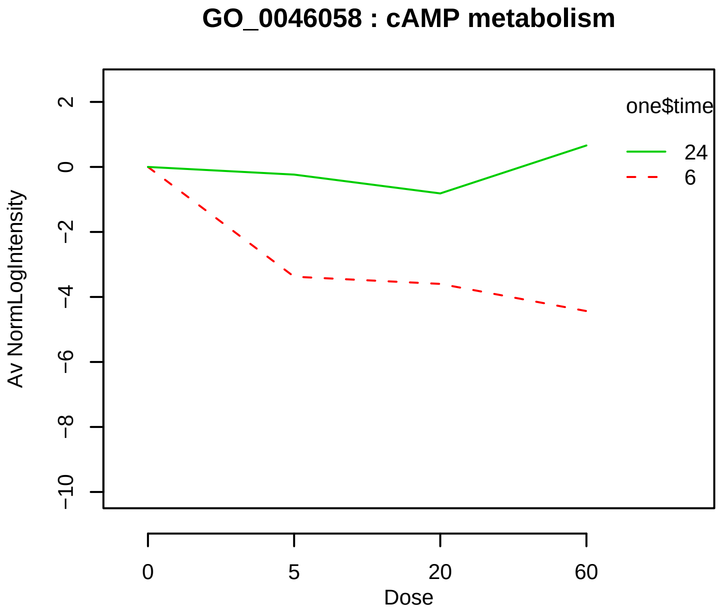
GO_0046034 : ATP metabolism

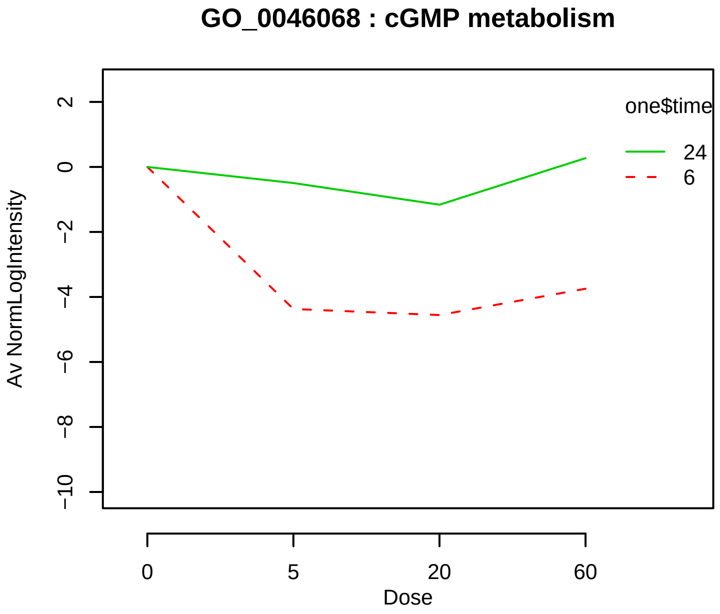


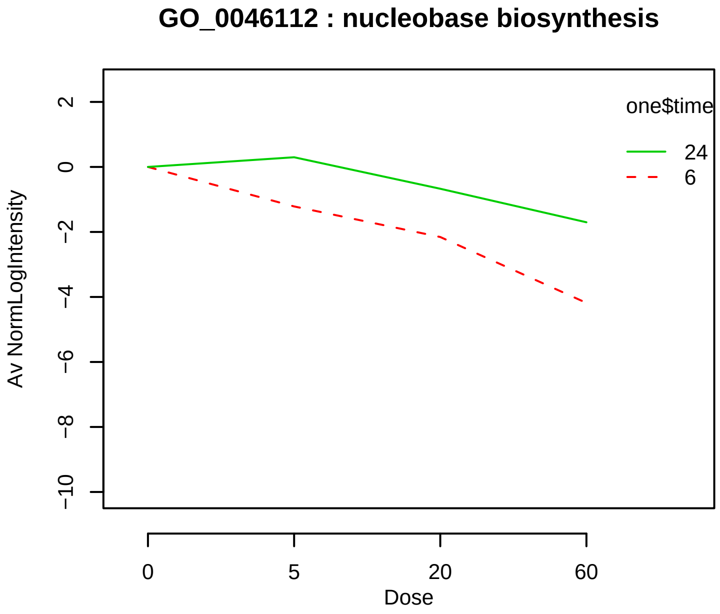
GO_0046036 : CTP metabolism

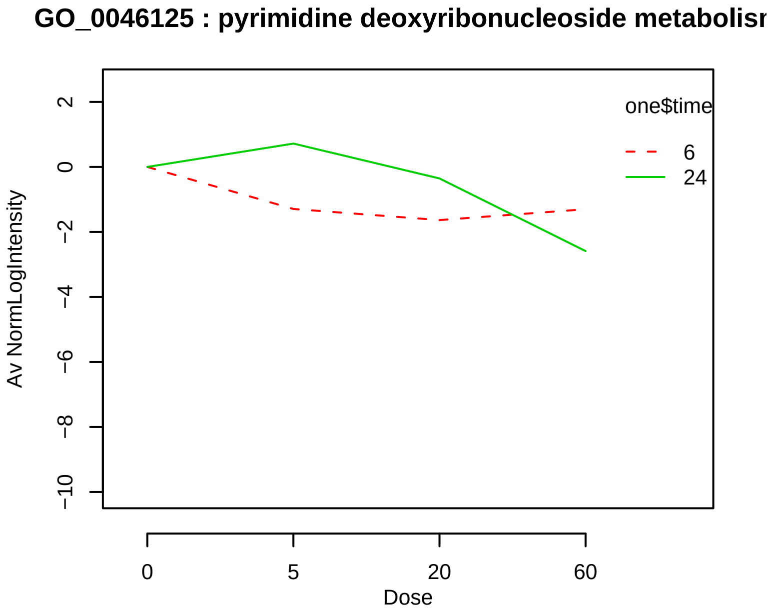

GO_0046039 : GTP metabolism
one$time
24
6
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
0
5
20
60
Dose

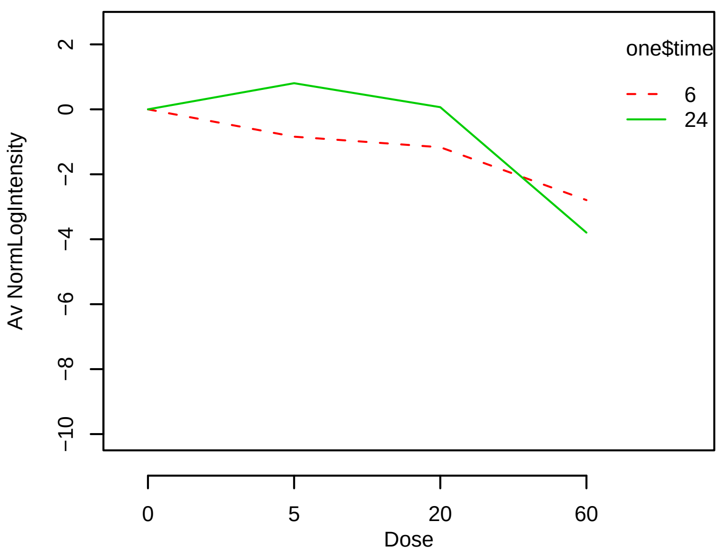

GO_0046051 : UTP metabolism
one$time
24
6
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
0
5
20
60
Dose

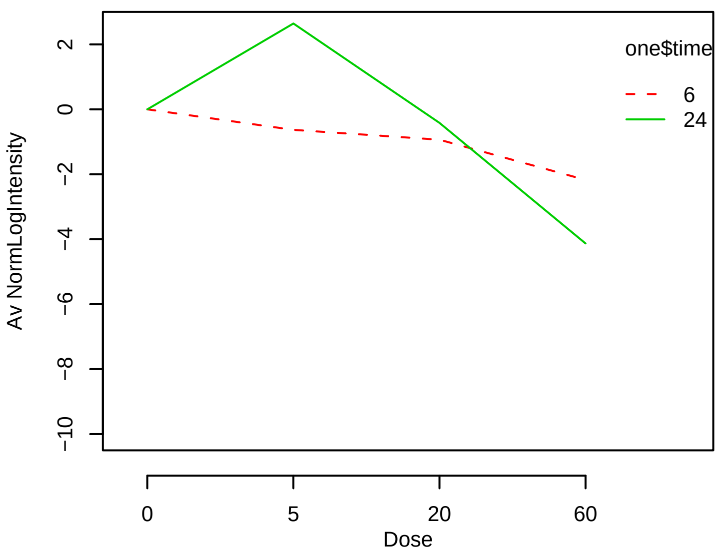

GO_0046058 : cAMP metabolism
one$time
24
6
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
0
5
20
60
Dose

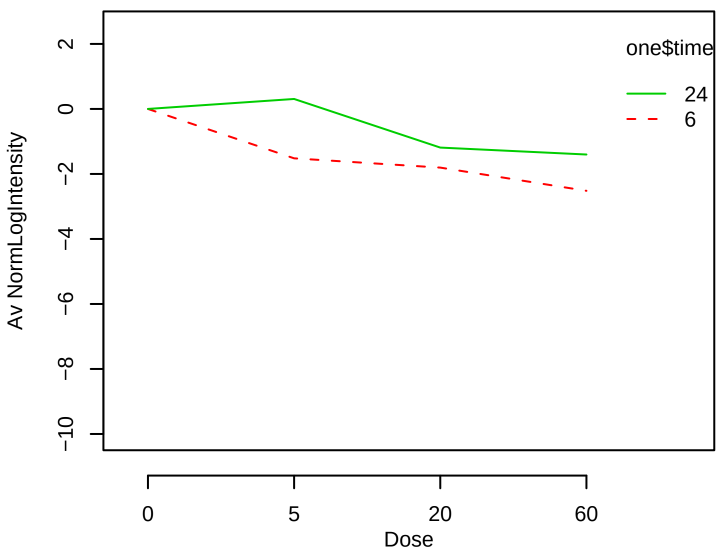

GO_0046068 : cGMP metabolism
one$time
24
6
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
0
5
20
60
Dose

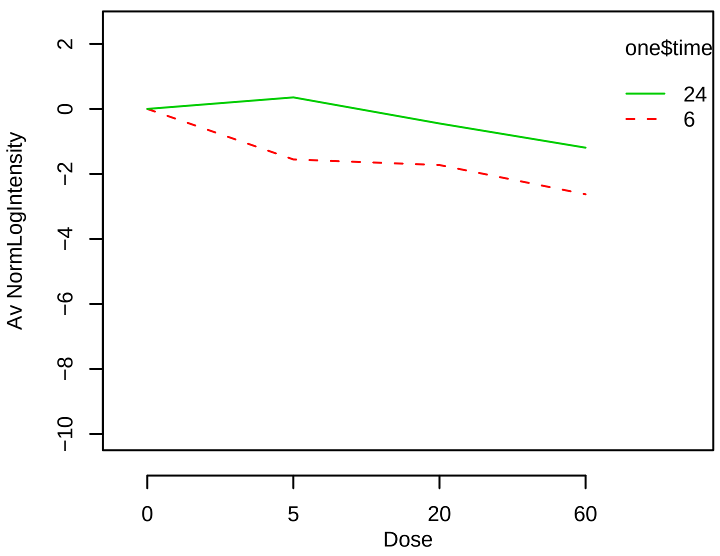

GO_0046112 : nucleobase biosynthesis
one$time
24
6
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
0
5
20
60
Dose

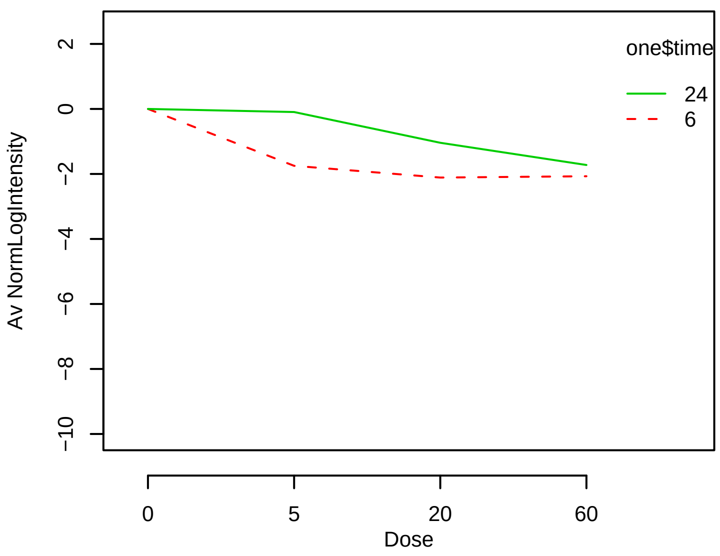

GO_0046125 : pyrimidine deoxyribonucleoside metabolisr
one$time
6
24
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
0
5
20
60
Dose

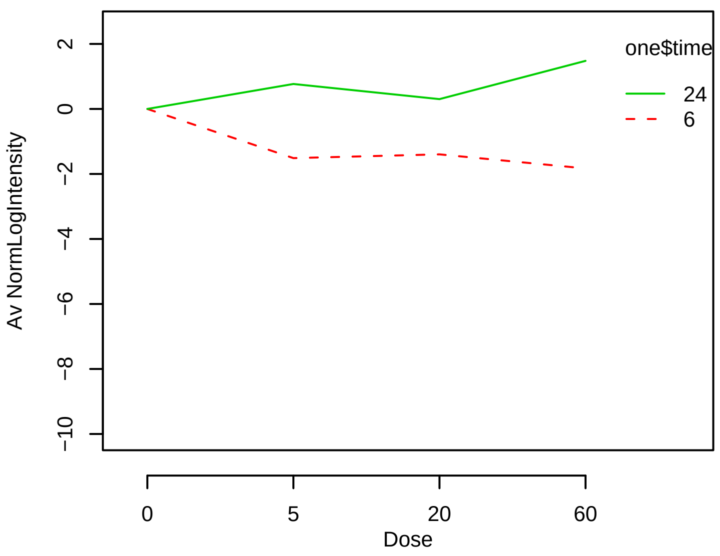

GO_0046128 : purine ribonucleoside metabolism

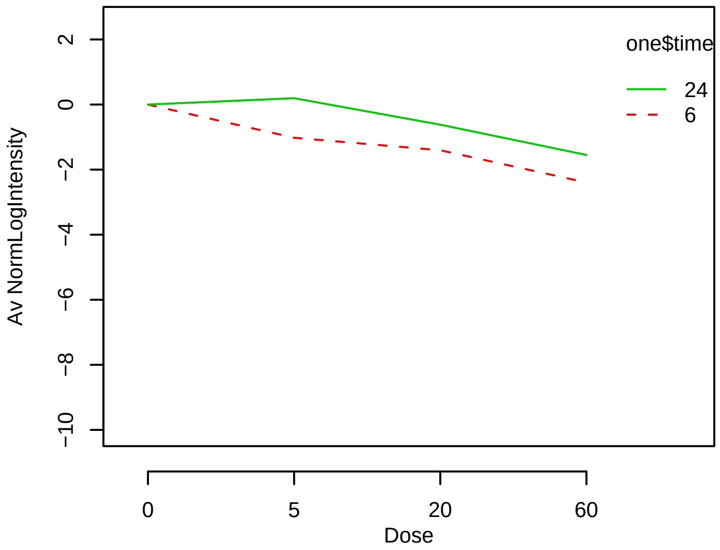

GO_0046146 : tetrahydrobiopterin metabolism


GO_0046148 : pigment biosynthesis

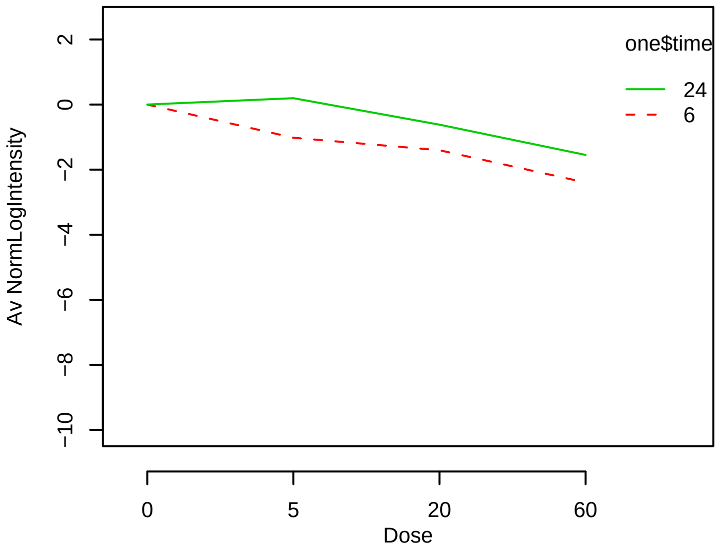

GO_0046164 : alcohol catabolism


GO_0046165 : alcohol biosynthesis

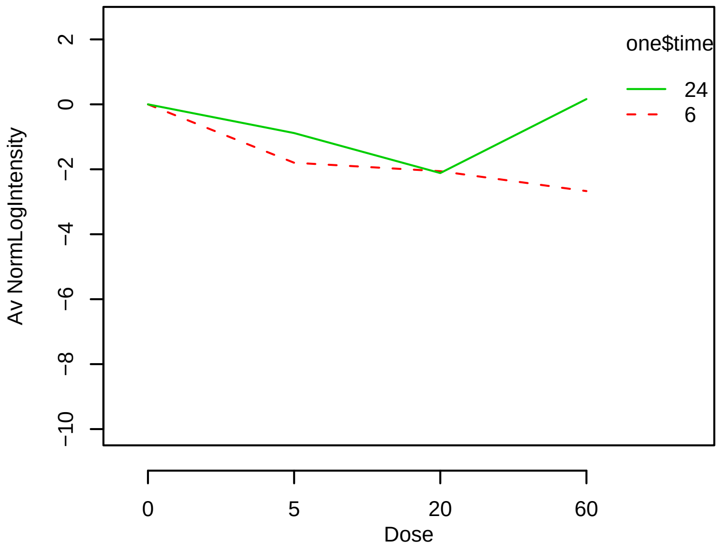

GO_0046209 : nitric oxide metabolism



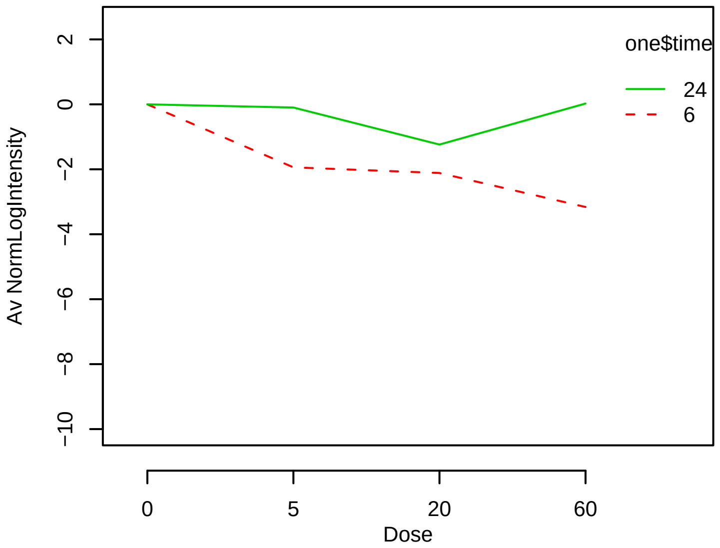
GO_0046323 : glucose import



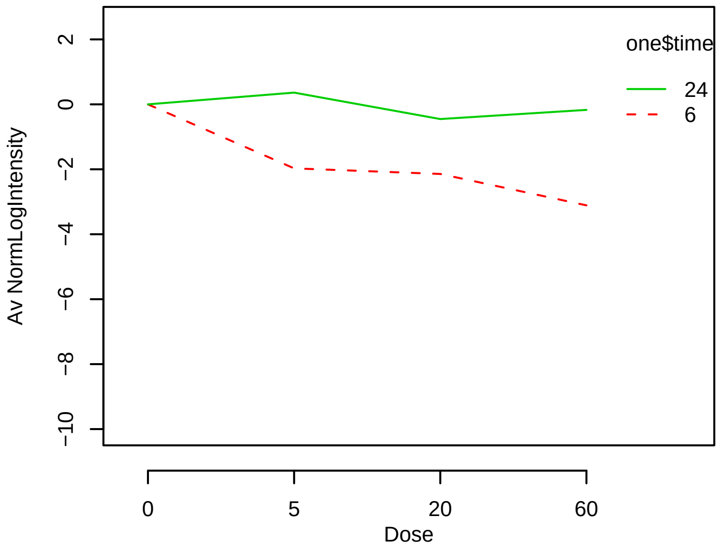
GO_0046324 : regulation of glucose import



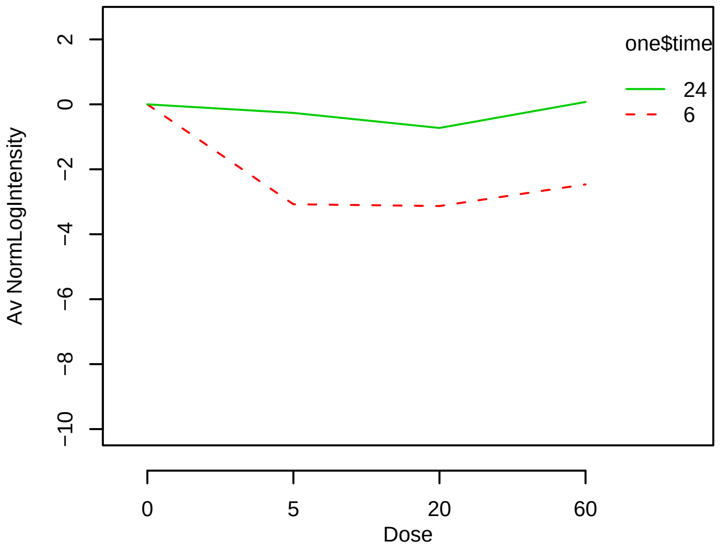
GO_0046328 : regulation of JNK cascade



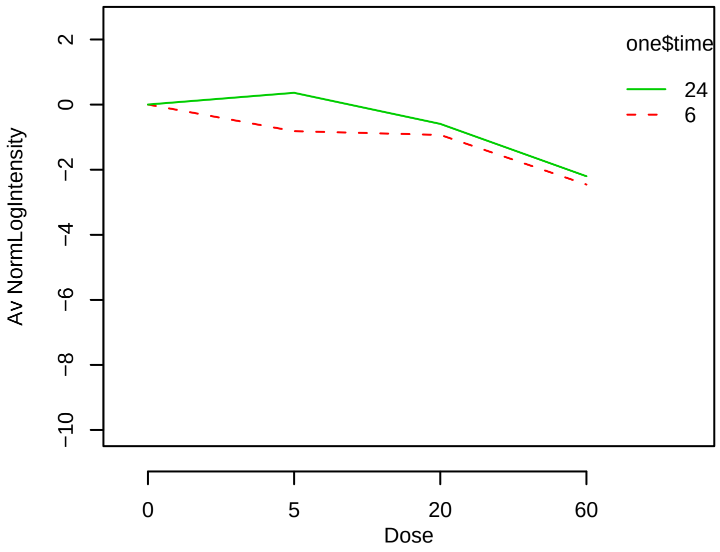
GO_0046330 : positive regulation of JNK cascade

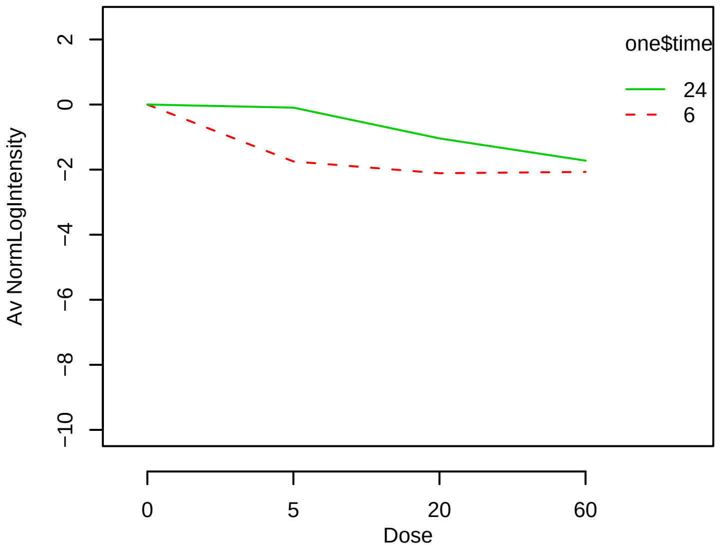


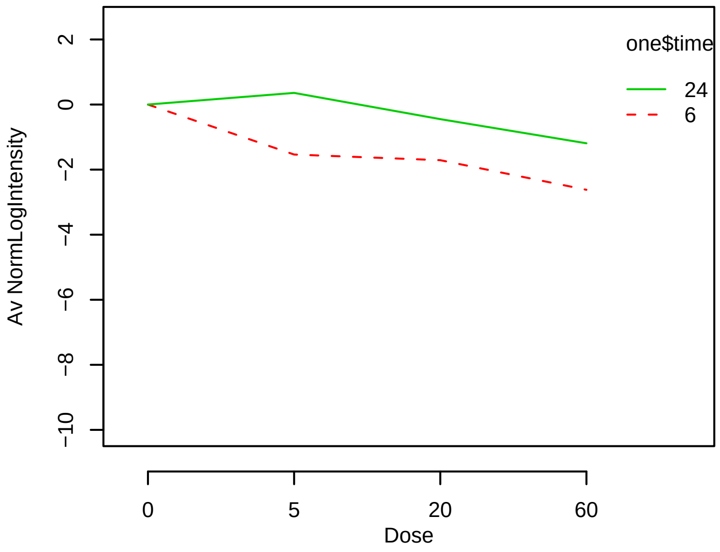
GO_0046339 : diacylglycerol metabolism

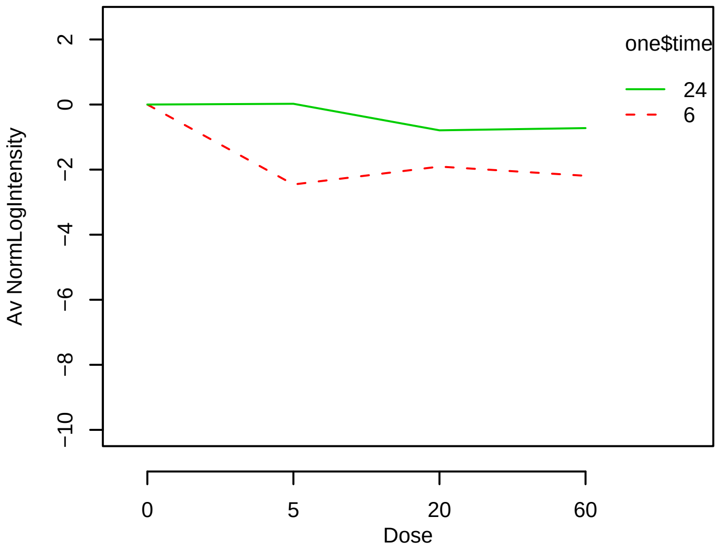


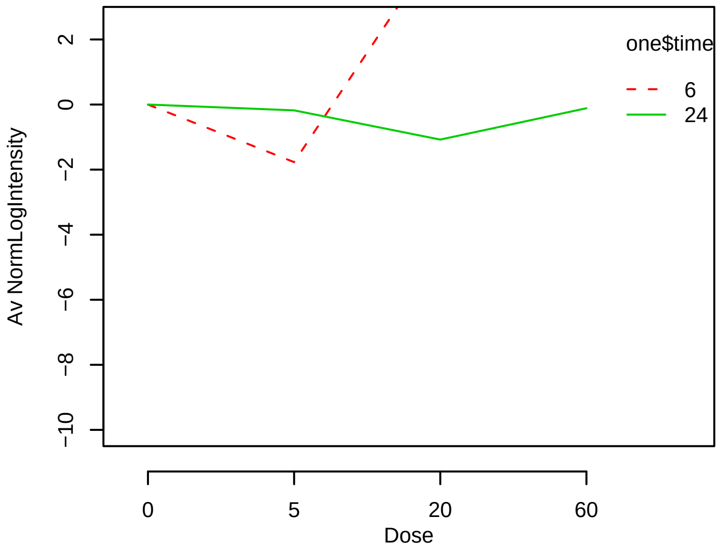
GO_0046348 : amino sugar catabolism

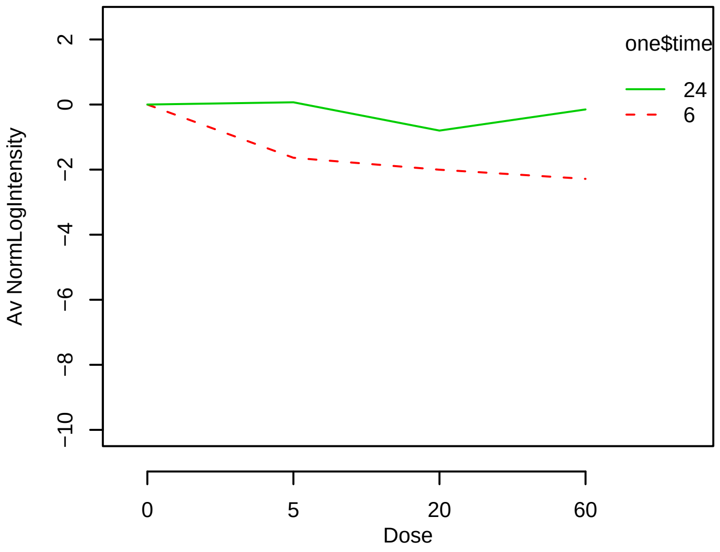

GO_0046356 : acetyl−CoA catabolism


GO_0046364 : monosaccharide biosynthesis

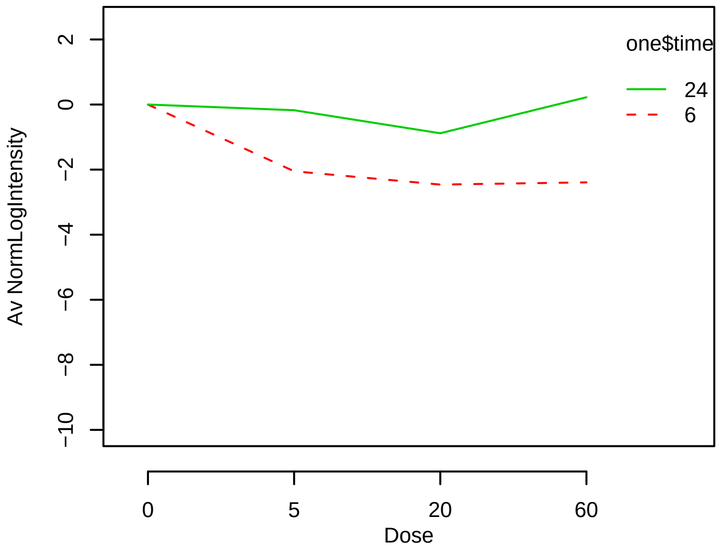

GO_0046365 : monosaccharide catabolism


GO_0046394 : carboxylic acid biosynthesis

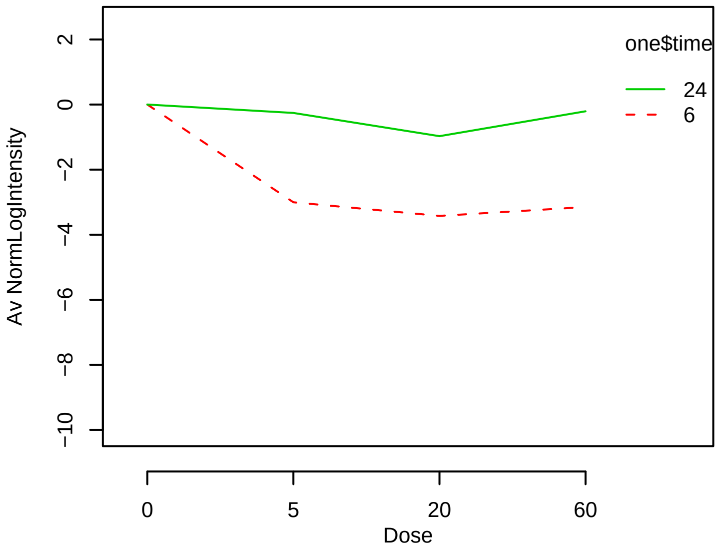

GO_0046395 : carboxylic acid catabolism


GO_0046425 : regulation of JAK−STAT cascade

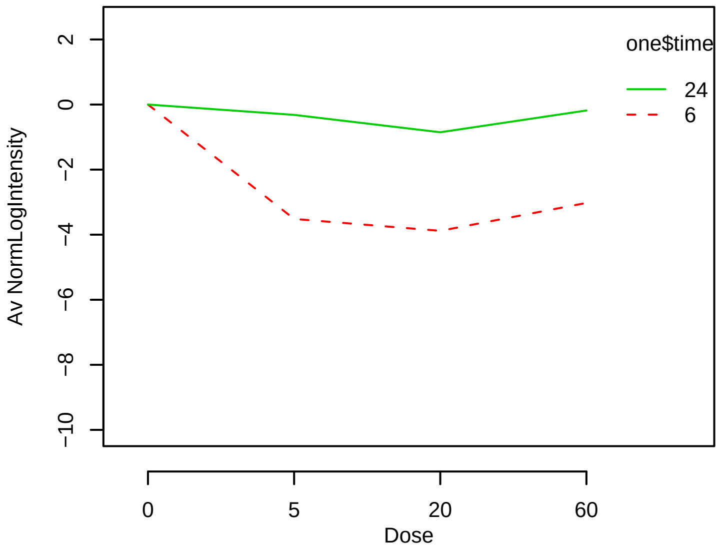
GO_0046427 : positive regulation of JAK−STAT cascade



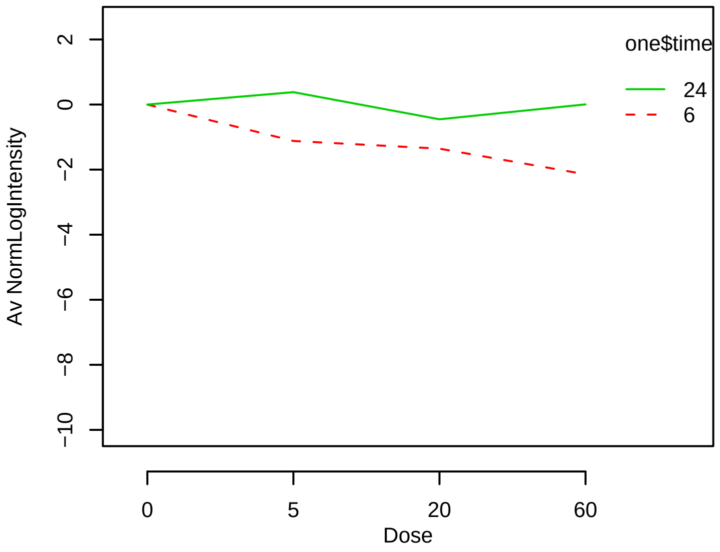
GO_0046456 : icosanoid biosynthesis



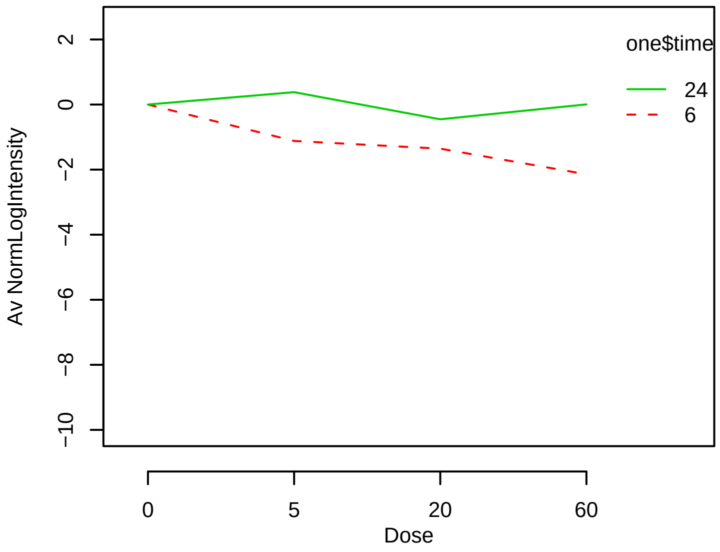
GO_0046457 : prostanoid biosynthesis



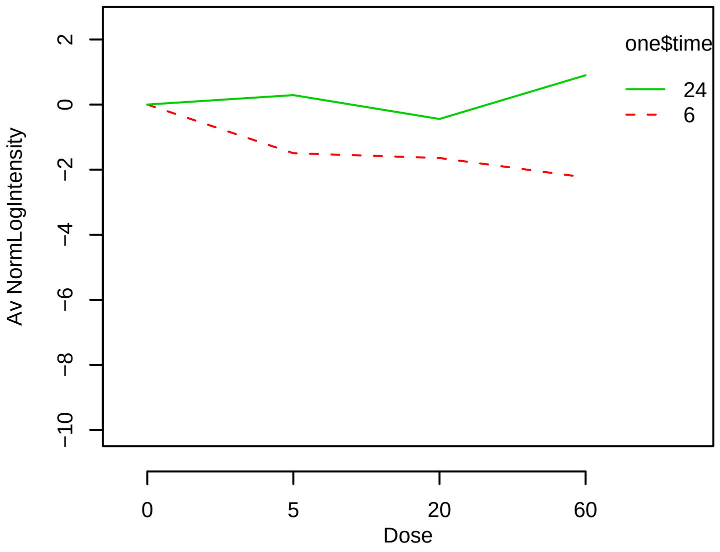
GO_0046460 : neutral lipid biosynthesis



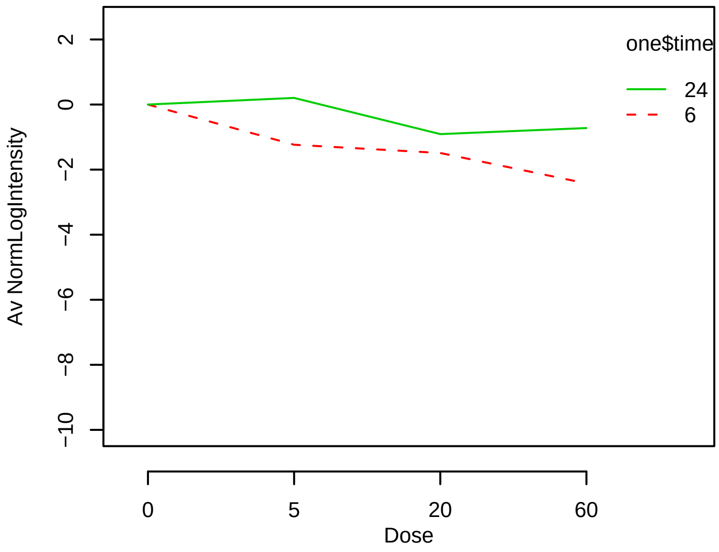
GO_0046463 : acylglycerol biosynthesis



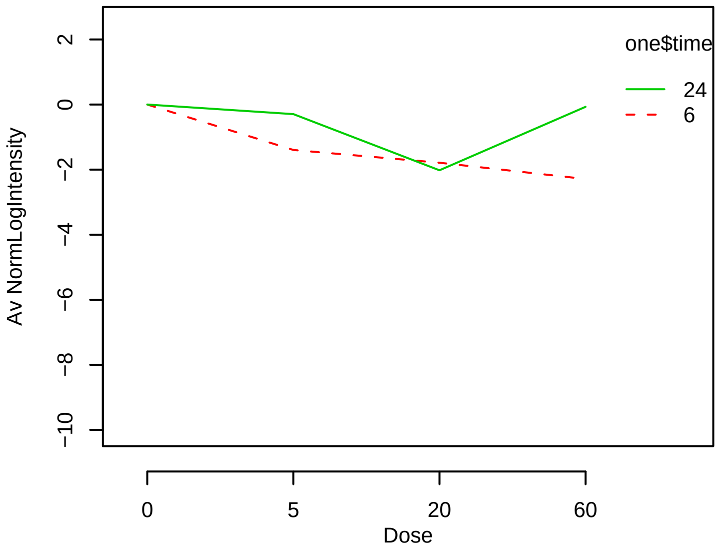
GO_0046466 : membrane lipid catabolism



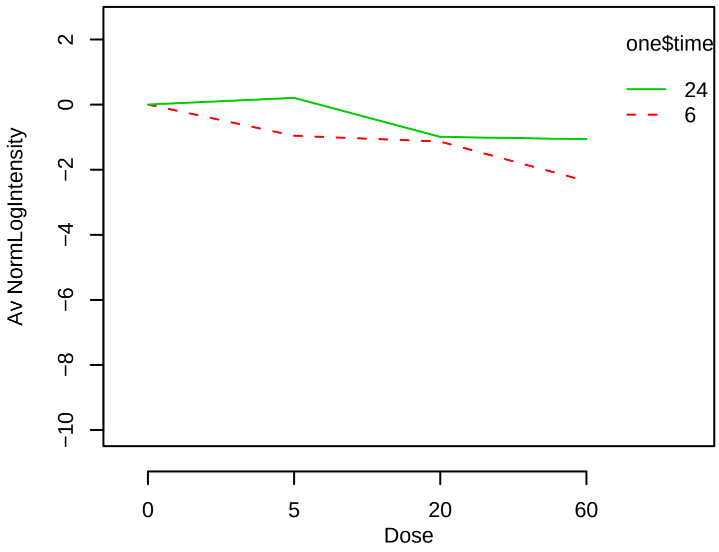
GO_0046467 : membrane lipid biosynthesis



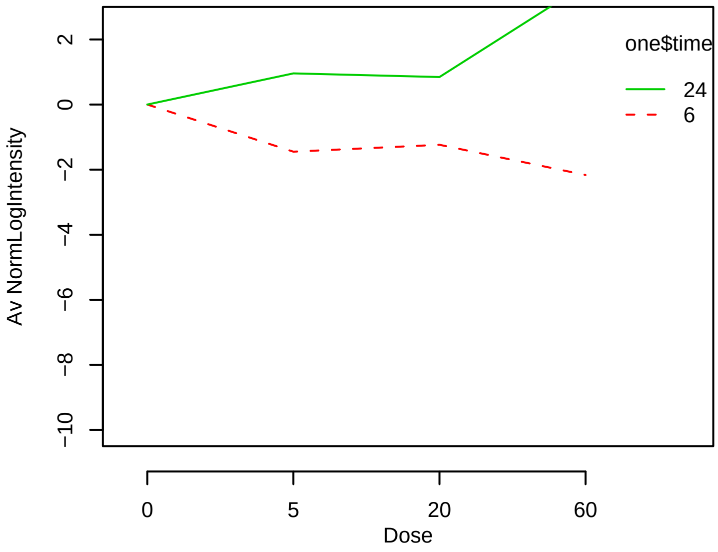
GO_0046470 : phosphatidylcholine metabolism



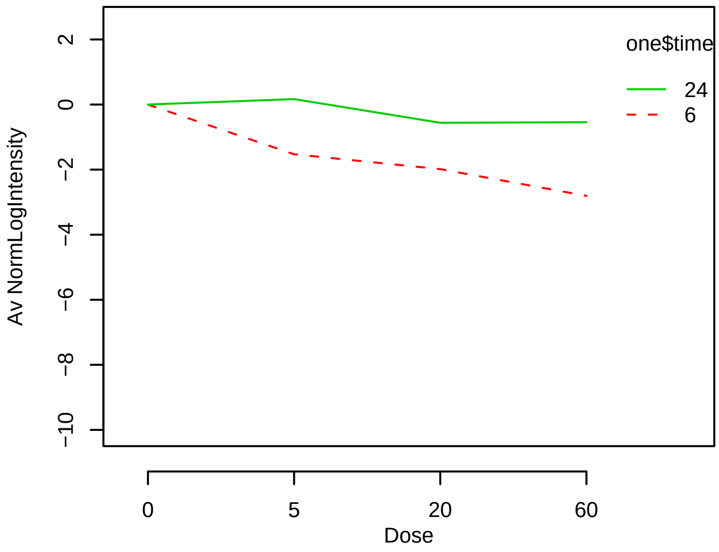
GO_0046474 : glycerophospholipid biosynthesis



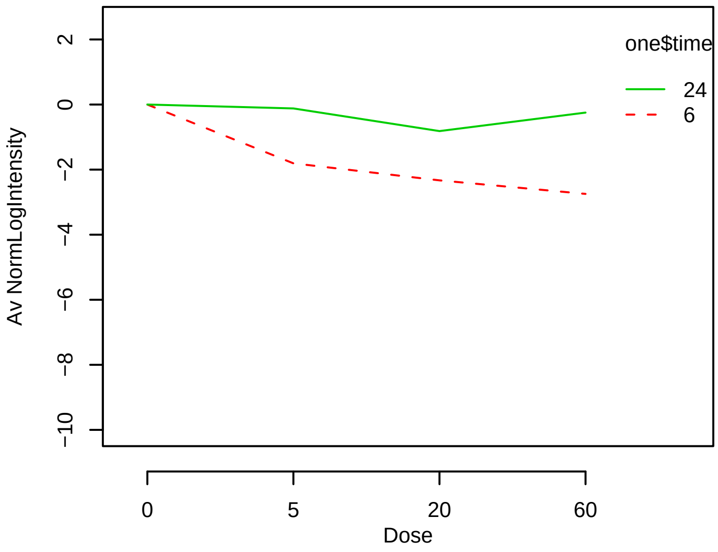
GO_0046479 : glycosphingolipid catabolism

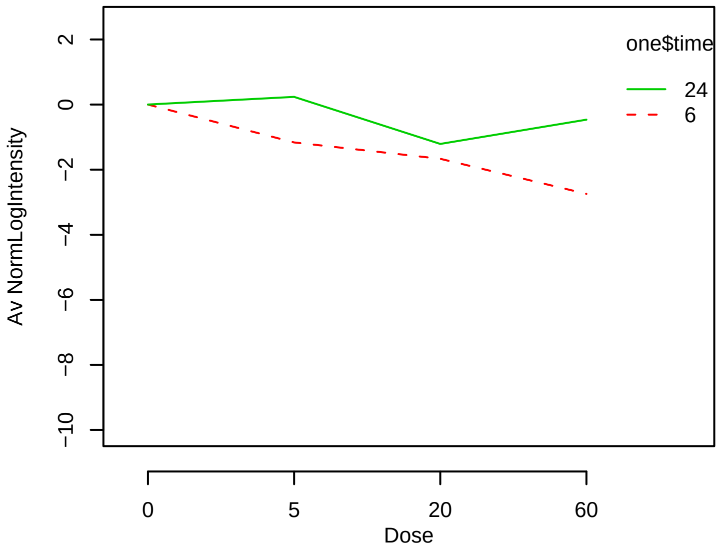


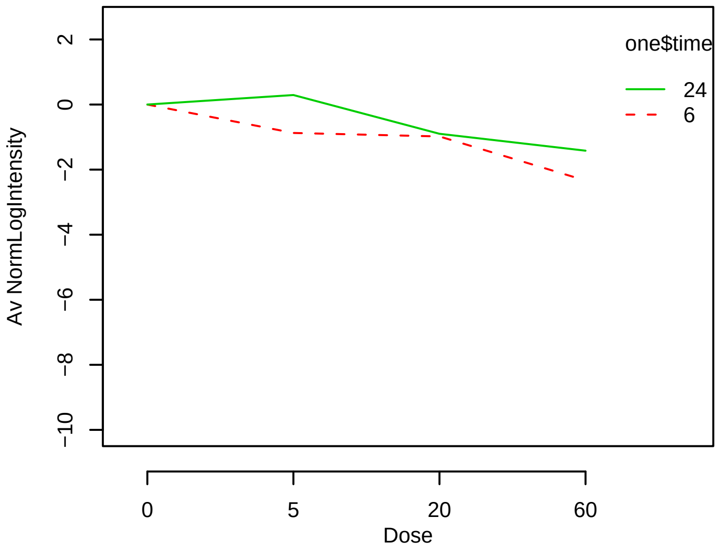
GO_0046483 : heterocycle metabolism

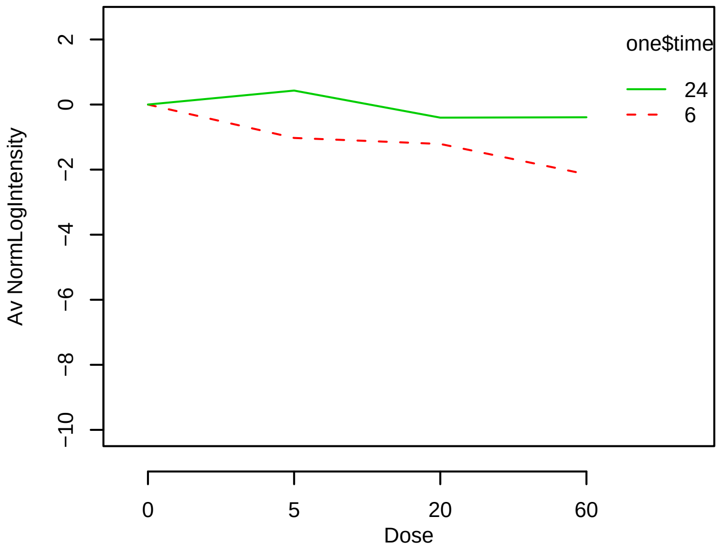


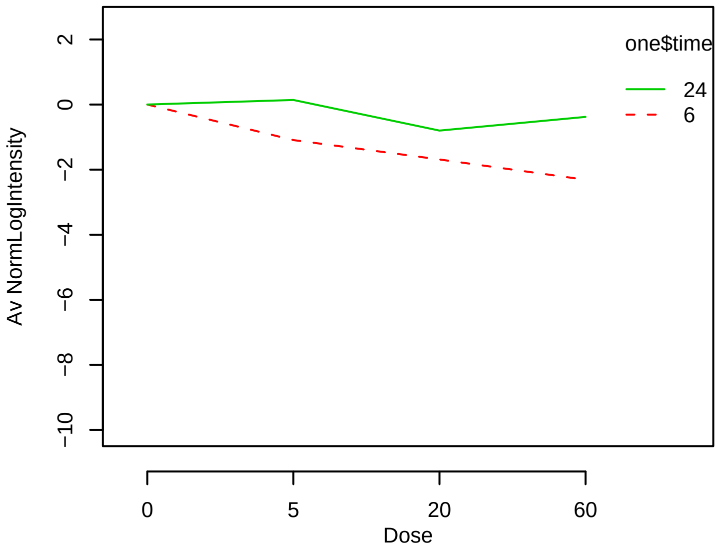
GO_0046486 : glycerolipid metabolism

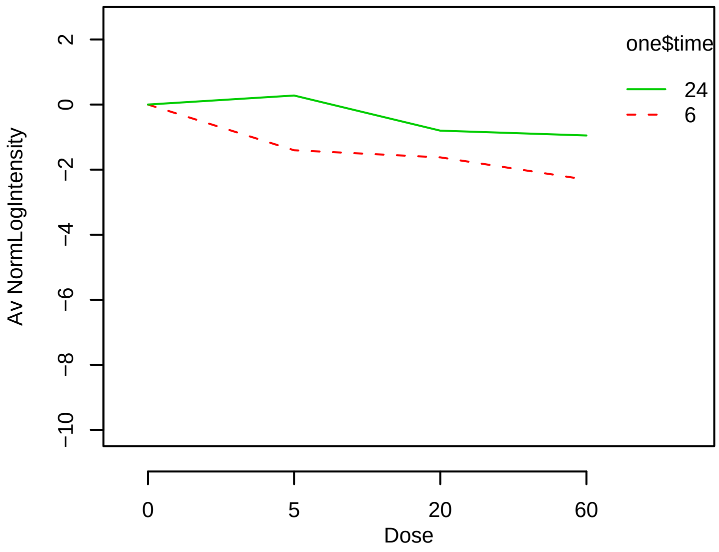


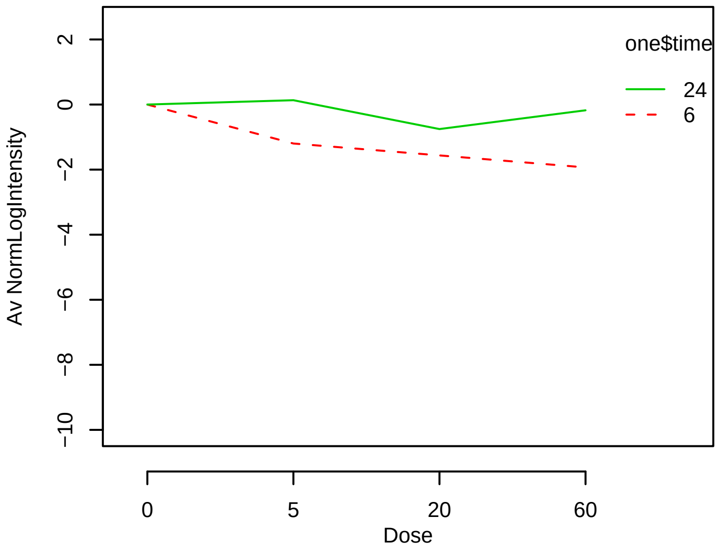

GO_0046488 : phosphatidylinositol metabolism


GO_0046489 : phosphoinositide biosynthesis

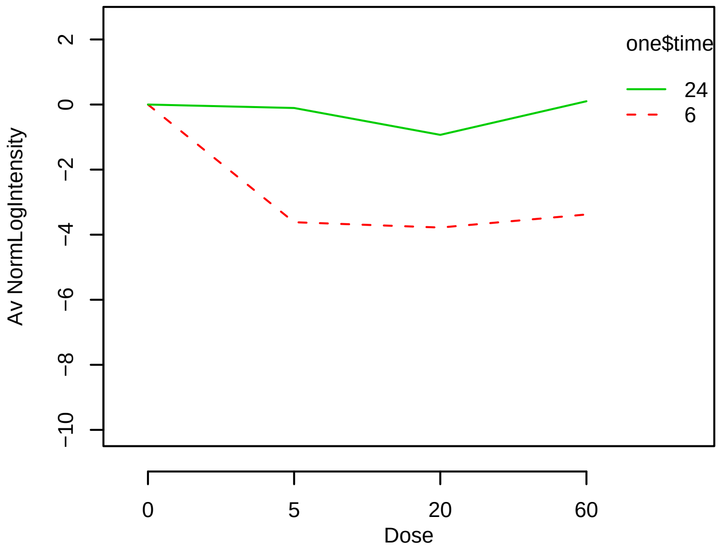

GO_0046504 : glycerol ether biosynthesis


GO_0046513 : ceramide biosynthesis

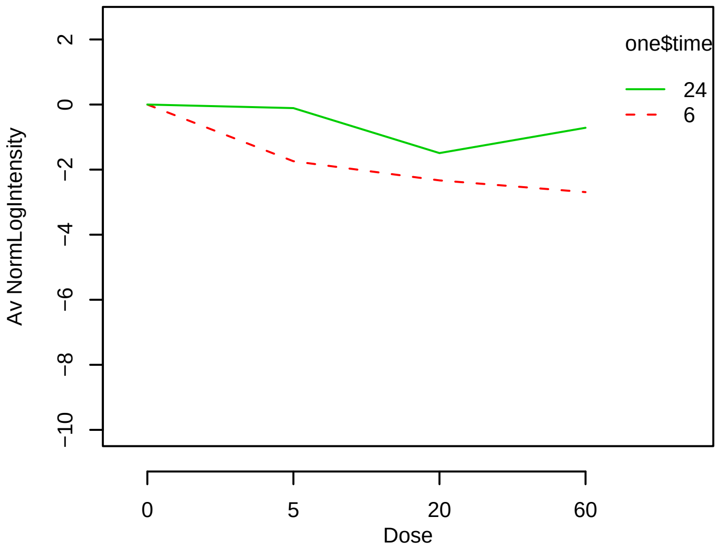

GO_0046519 : sphingoid metabolism


GO_0046520 : sphingoid biosynthesis

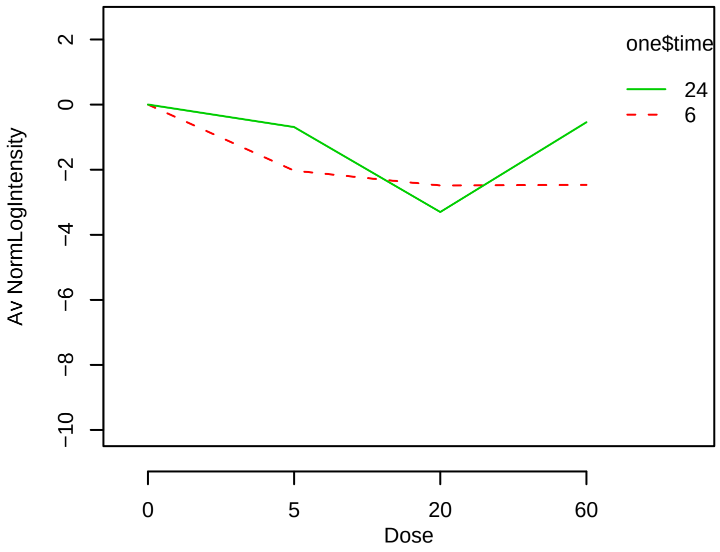
GO_0046530 : photoreceptor cell differentiation



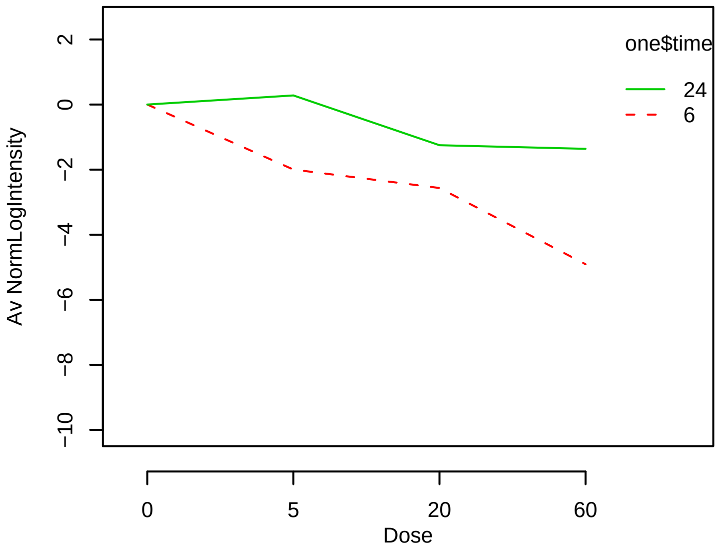
3O_0046545 : development of primary female sexual characte



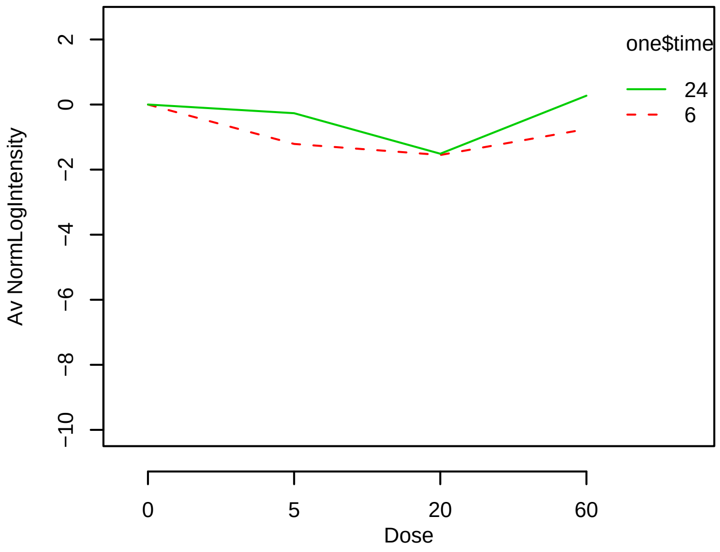
3O_0046546 : development of primary male sexual characteri



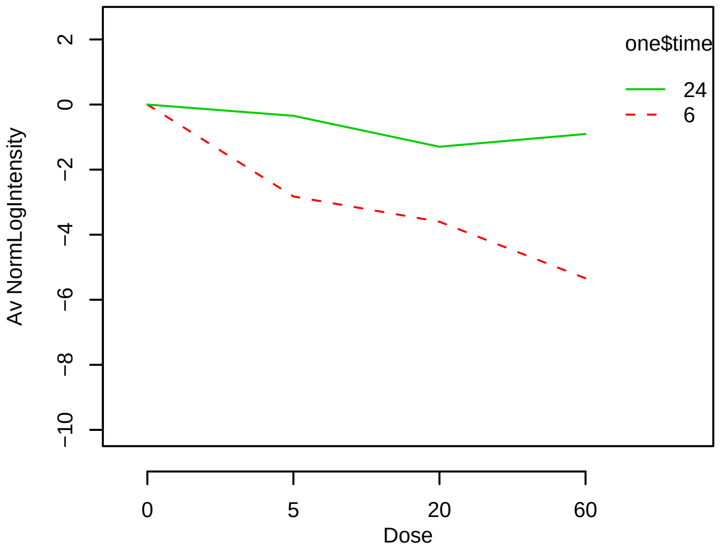
GO_0046578 : regulation of Ras protein signal transductio



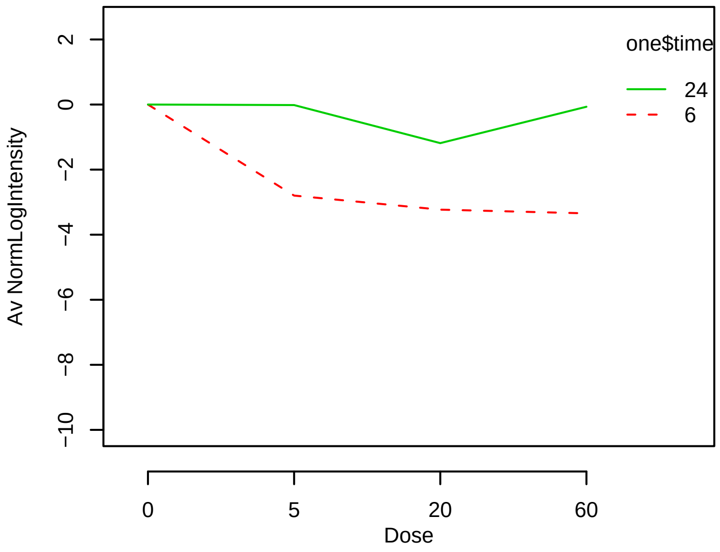
GO_0046626 : regulation of insulin receptor signaling pathw



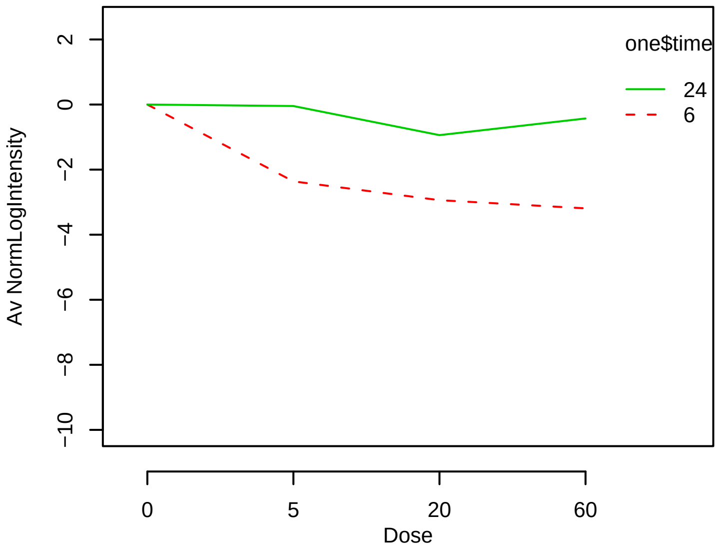
GO_0046631 : alpha−beta T cell activation



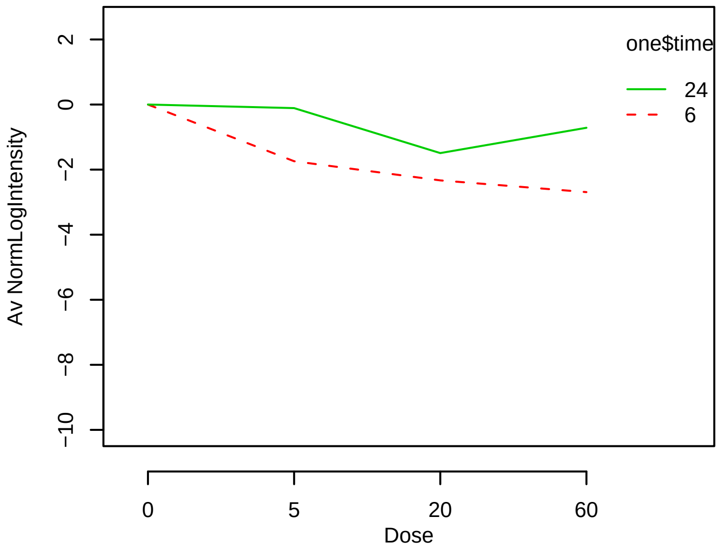
GO_0046649 : lymphocyte activation



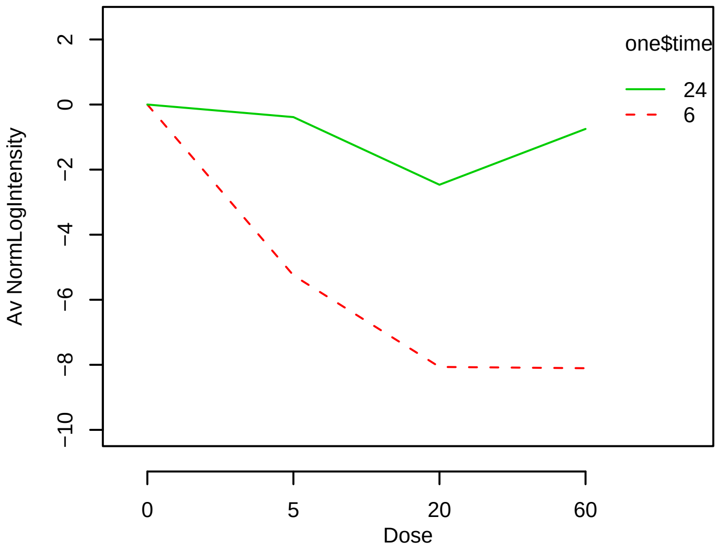
GO_0046651 : lymphocyte proliferation



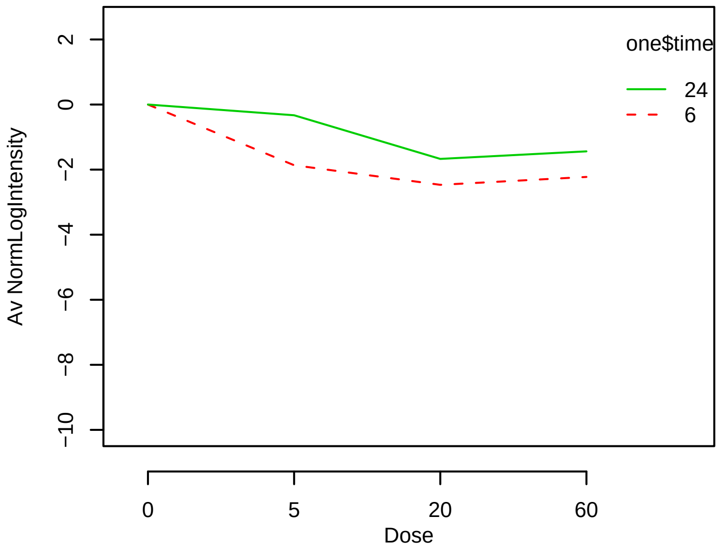
GO_0046660 : female sex differentiation



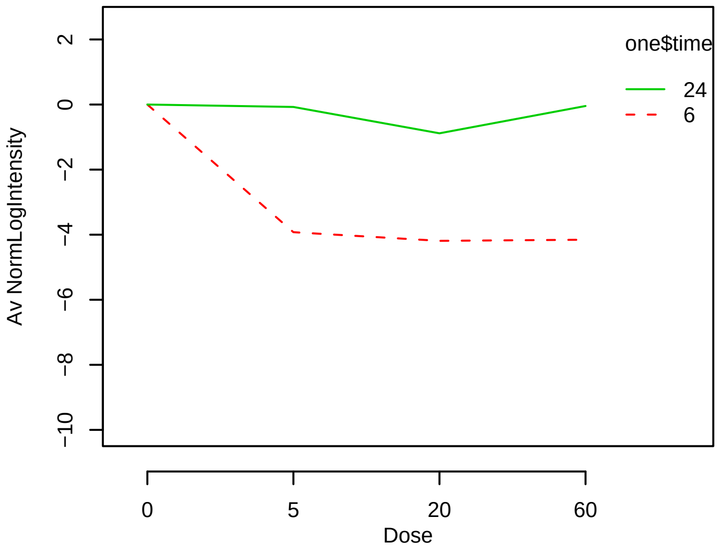
GO_0046661 : male sex differentiation



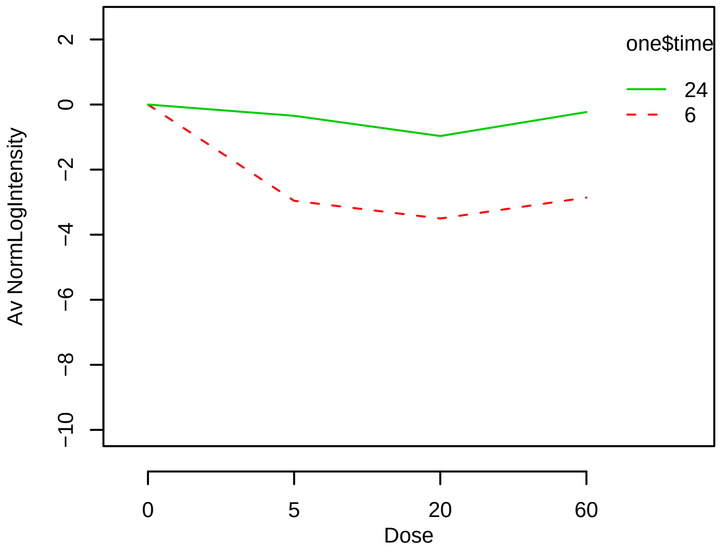
GO_0046666 : retinal cell programmed cell death



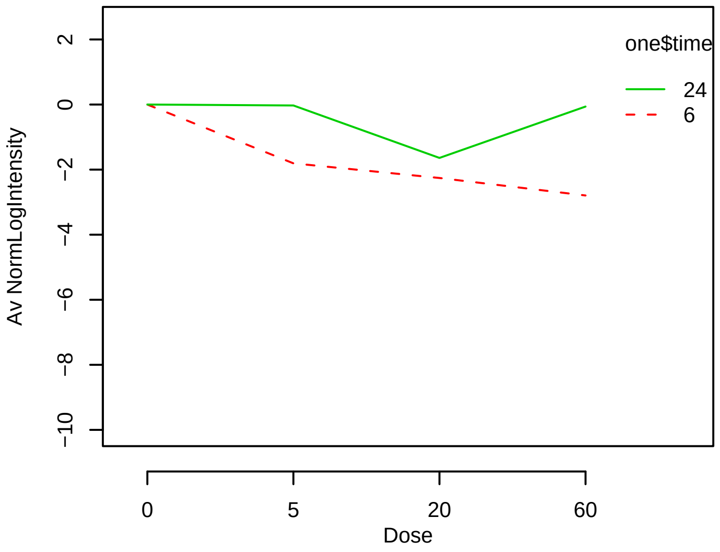
GO_0046716 : muscle maintenance



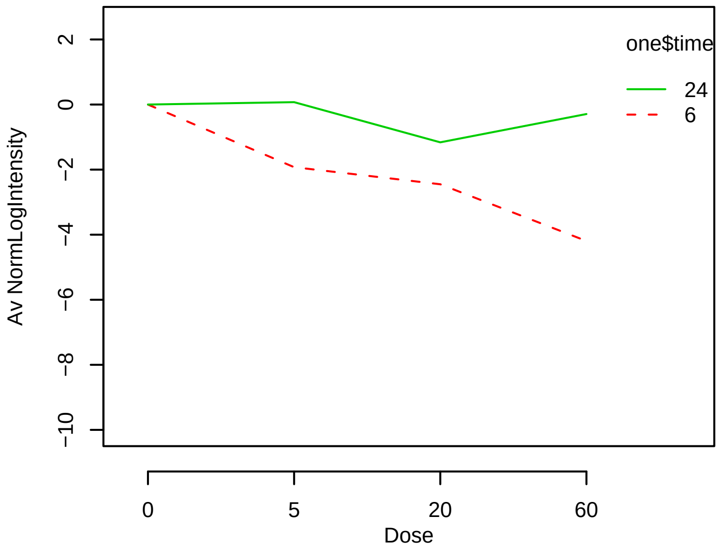
GO_0046718 : entry of virus into host cell



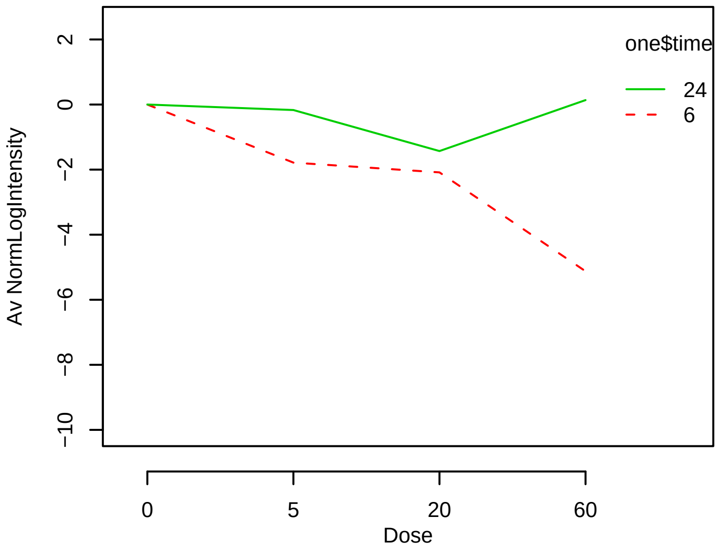
GO_0046777 : protein amino acid autophosphorylation



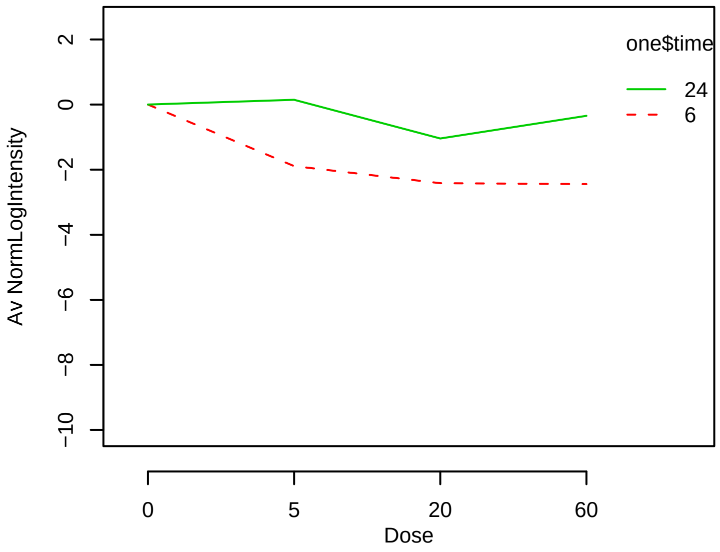
GO_0046822 : regulation of nucleocytoplasmic transport



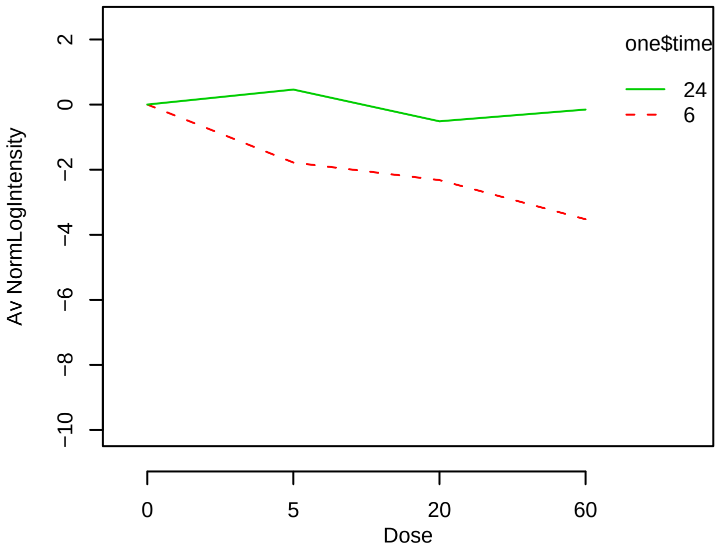
GO_0046823 : negative regulation of nucleocytoplasmic trans

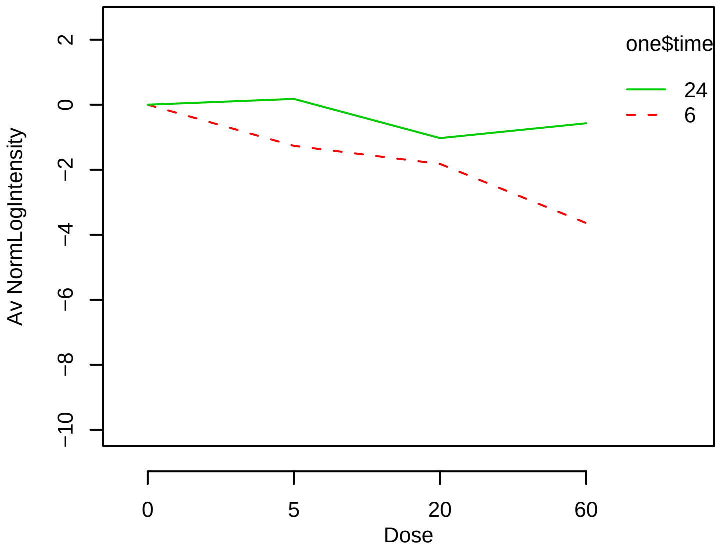


GO_0046824 : positive regulation of nucleocytoplasmic trans

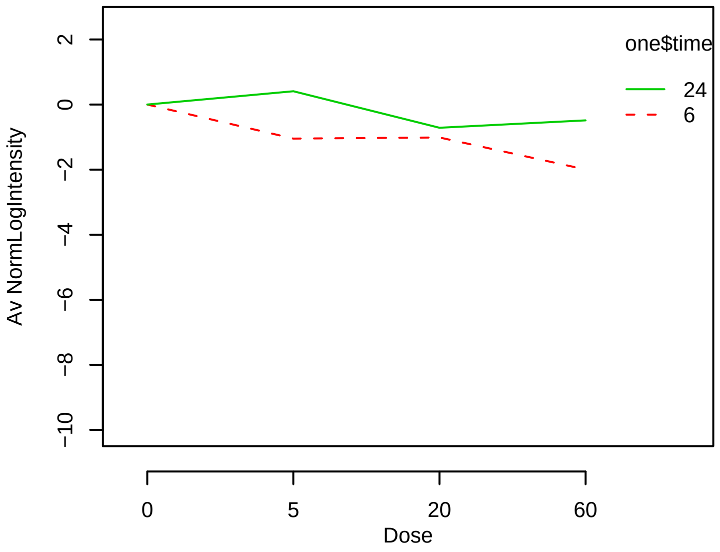


GO_0046831 : regulation of RNA export from nucleus

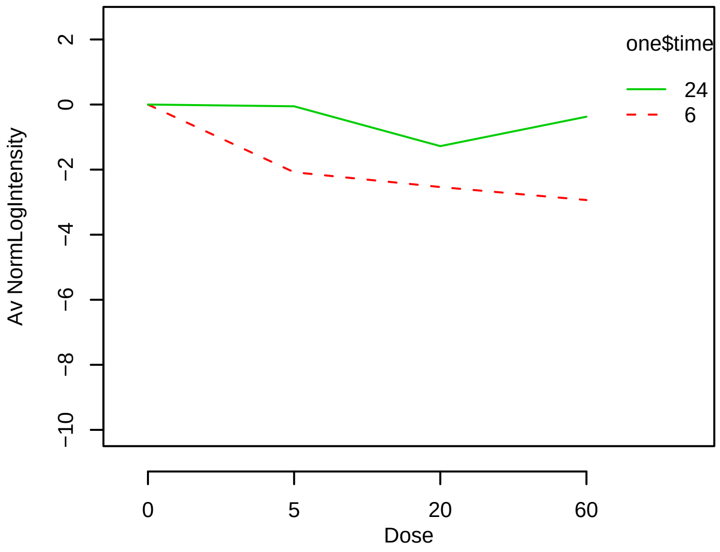




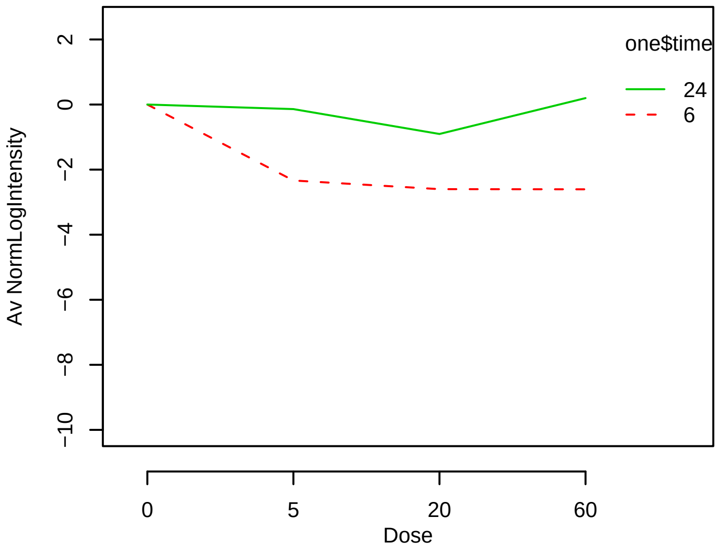
GO_0046835 : carbohydrate phosphorylation



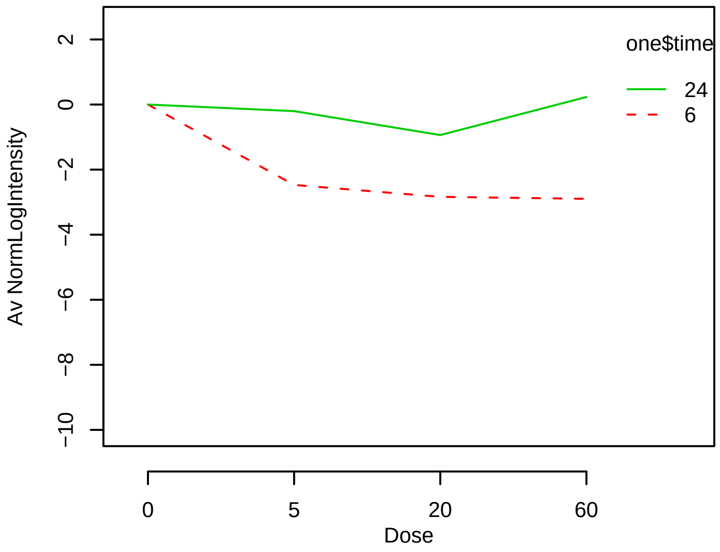
GO_0046839 : phospholipid dephosphorylation



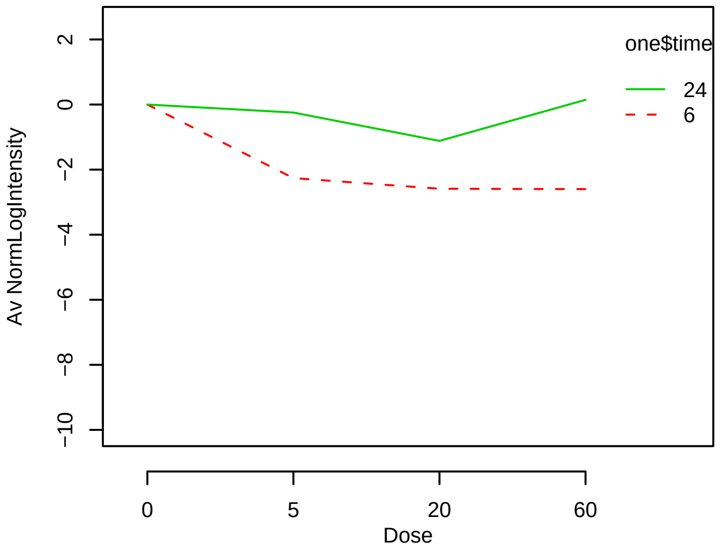
GO_0046847 : filopodium formation



GO_0046849 : bone remodeling

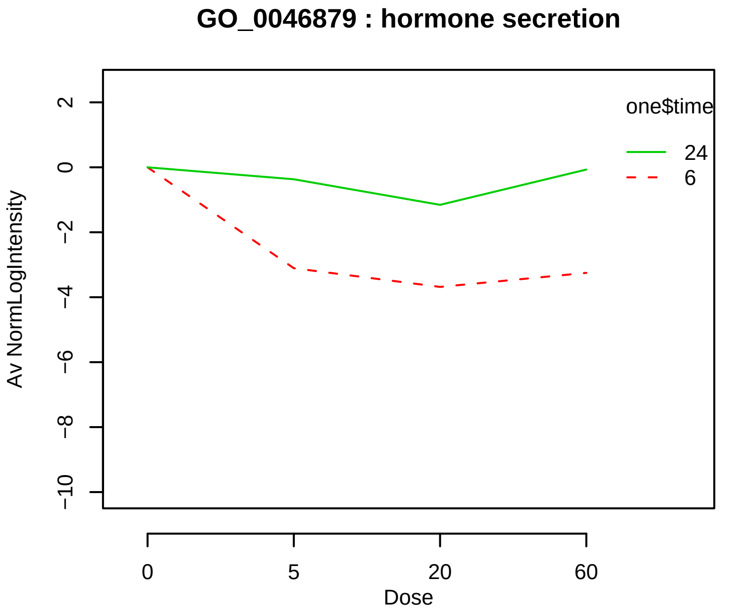


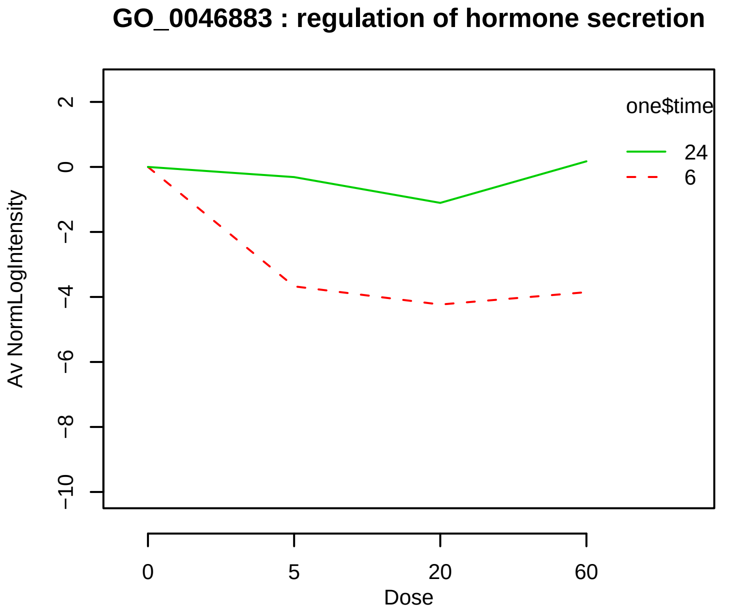
GO_0046850 : regulation of bone remodeling



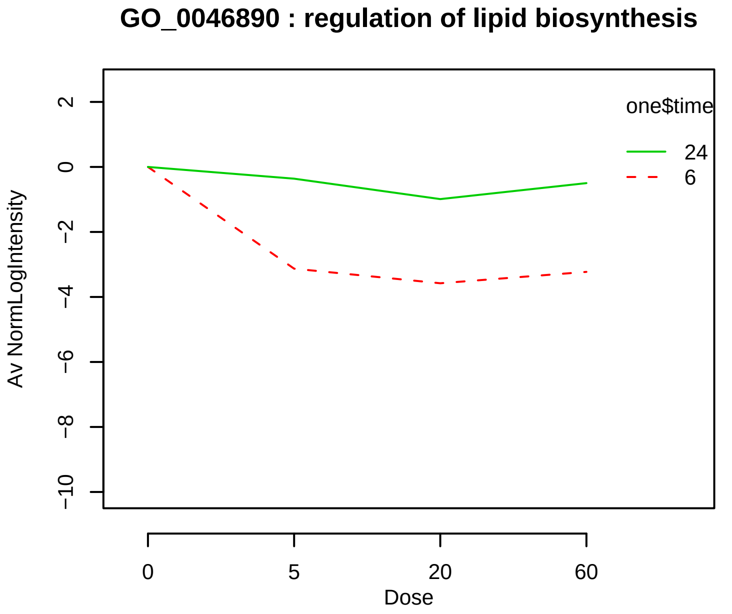
GO_0046851 : negative regulation of bone remodeling

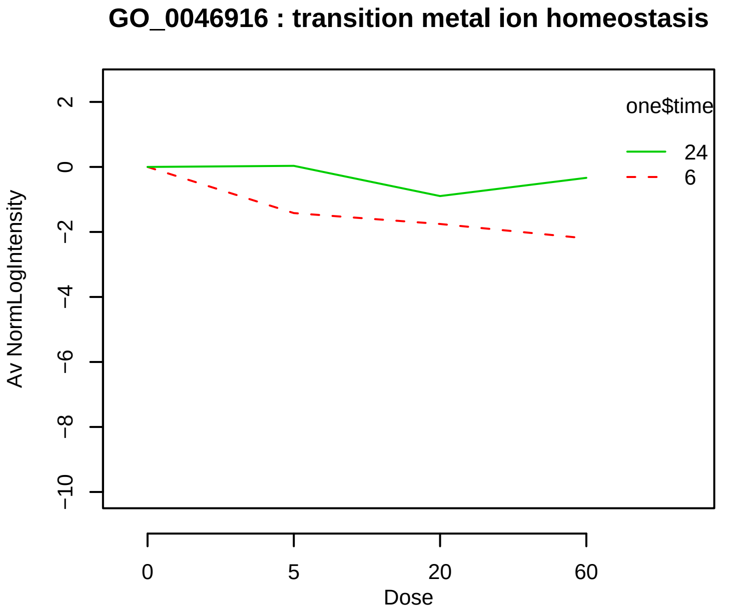

GO_0046852 : positive regulation of bone remodeling

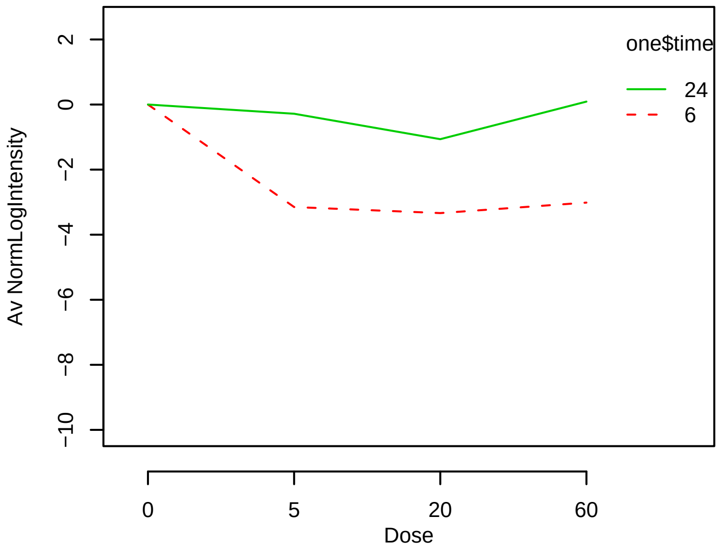

GO_0046879 : hormone secretion

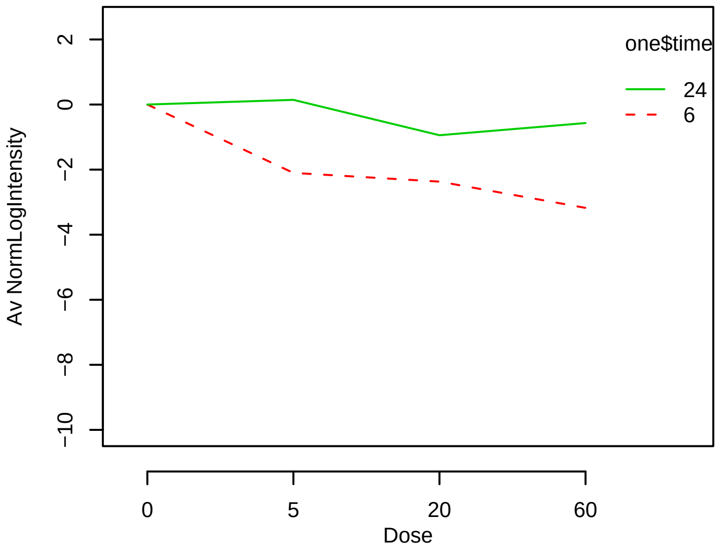

GO_0046883 : regulation of hormone secretion

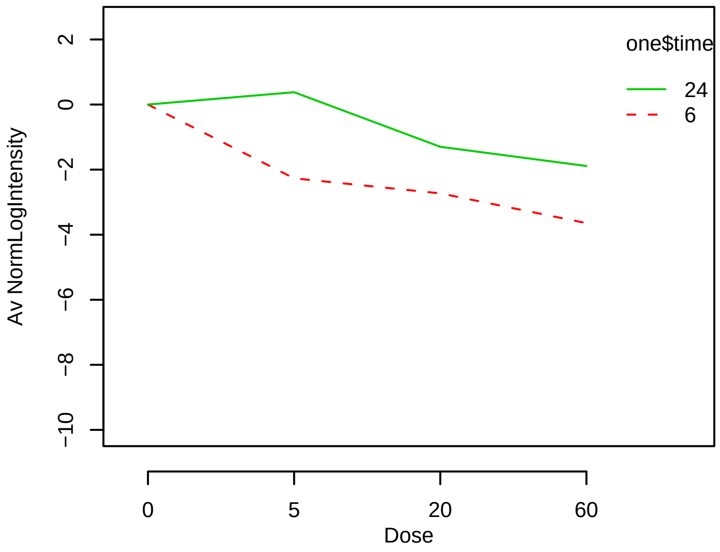

GO_0046888 : negative regulation of hormone secretion

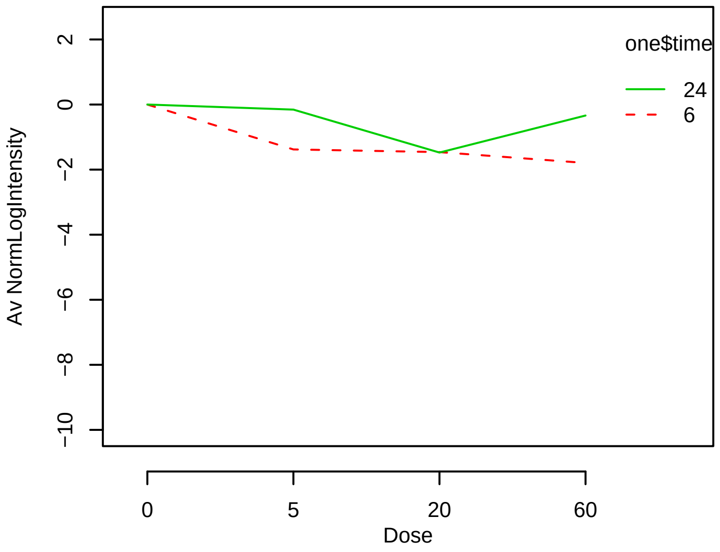

GO_0046890 : regulation of lipid biosynthesis

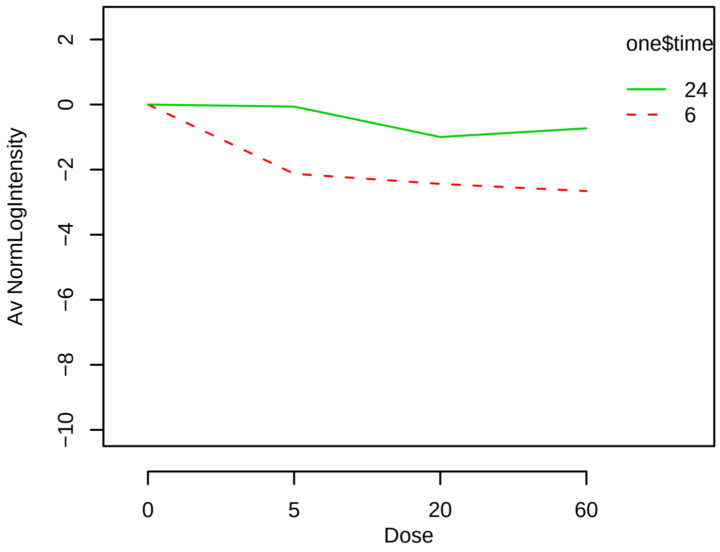

GO_0046916 : transition metal ion homeostasis

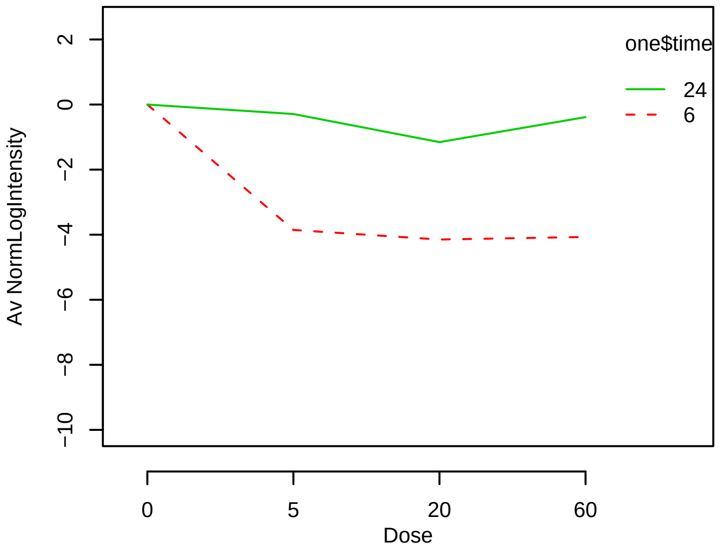

GO_0046928 : regulation of neurotransmitter secretion

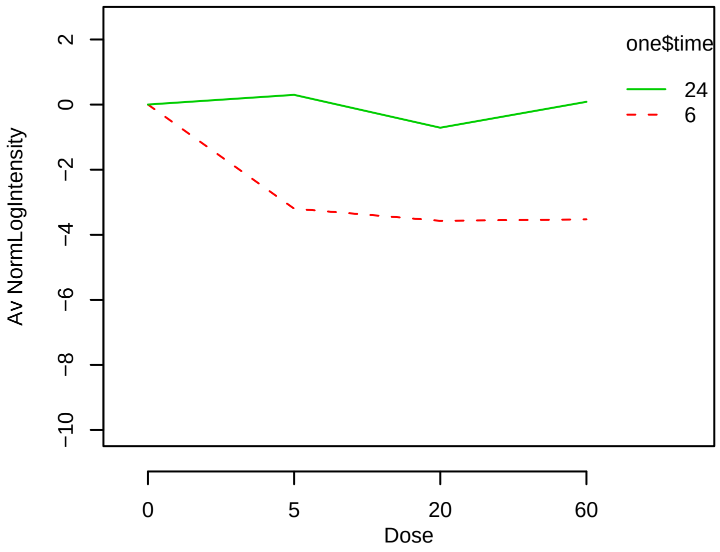

GO_0046942 : carboxylic acid transport

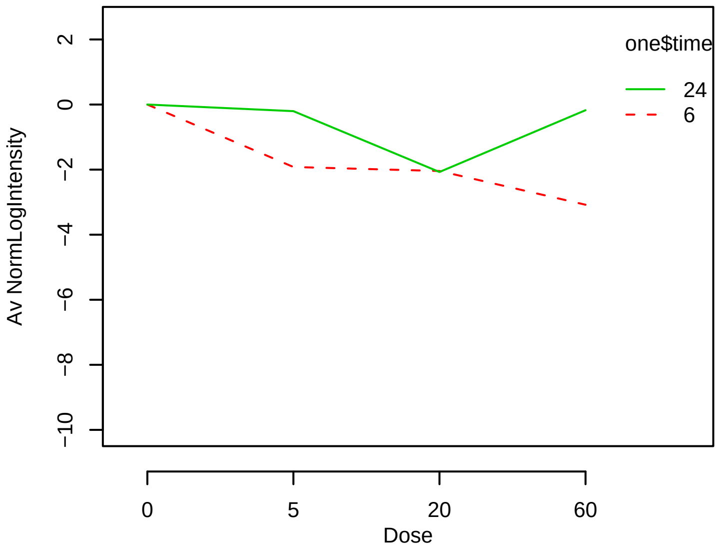

GO_0047496 : vesicle transport along microtubule

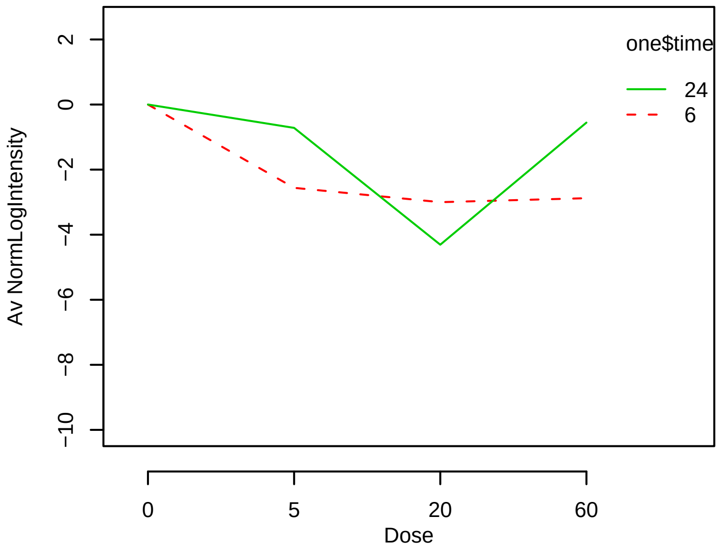

GO_0048009 : insulin−like growth factor receptor signaling p

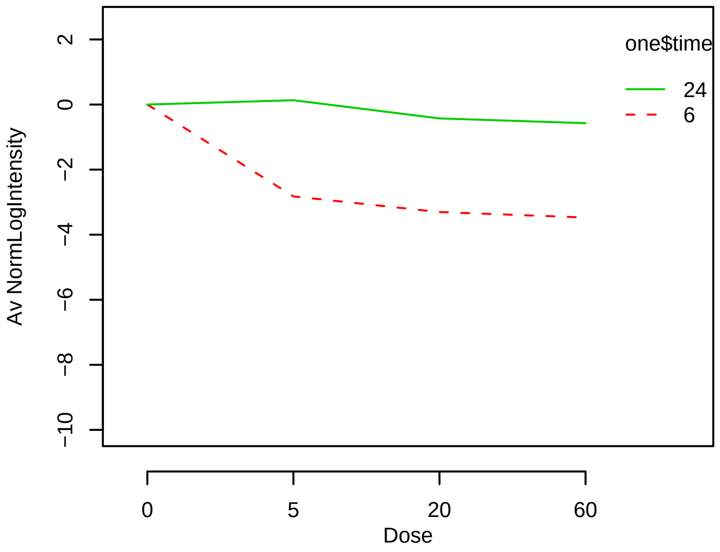

GO_0048015 : phosphoinositide−mediated signaling

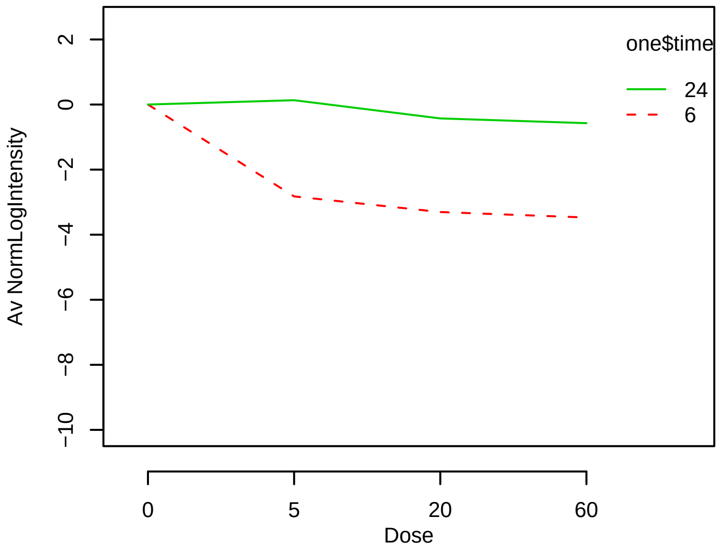

GO_0048041 : focal adhesion formation

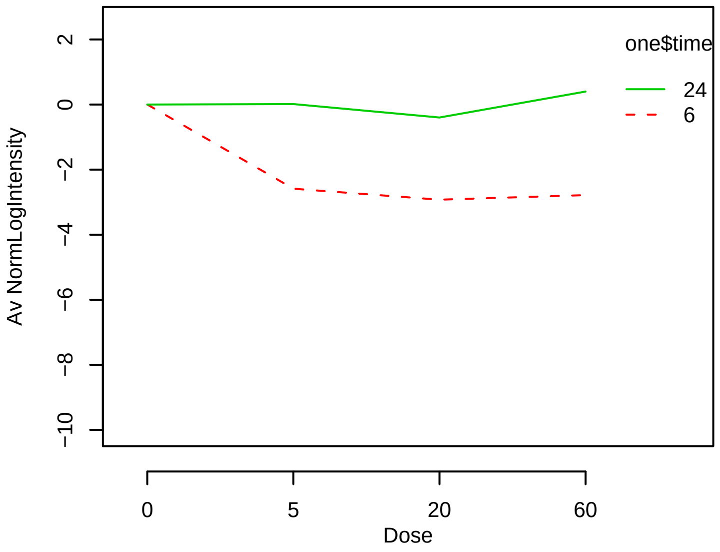

GO_0048048 : embryonic eye morphogenesis

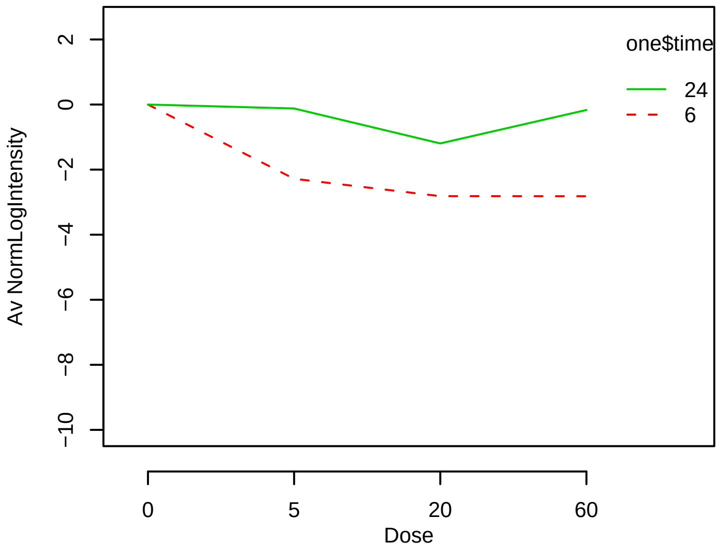

GO_0048066 : pigmentation during development

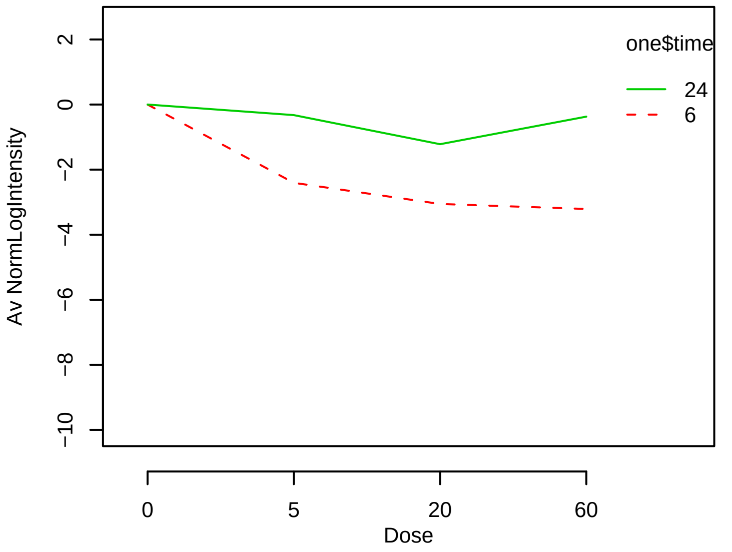

GO_0048069 : eye pigmentation

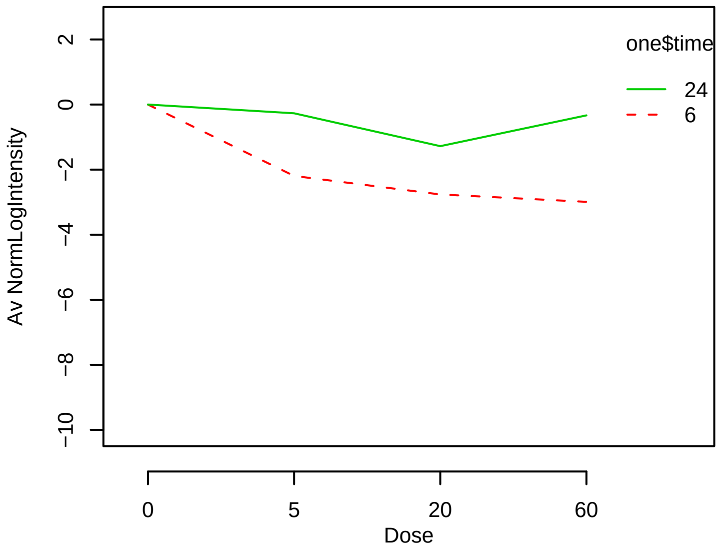

GO_0048144 : fibroblast proliferation

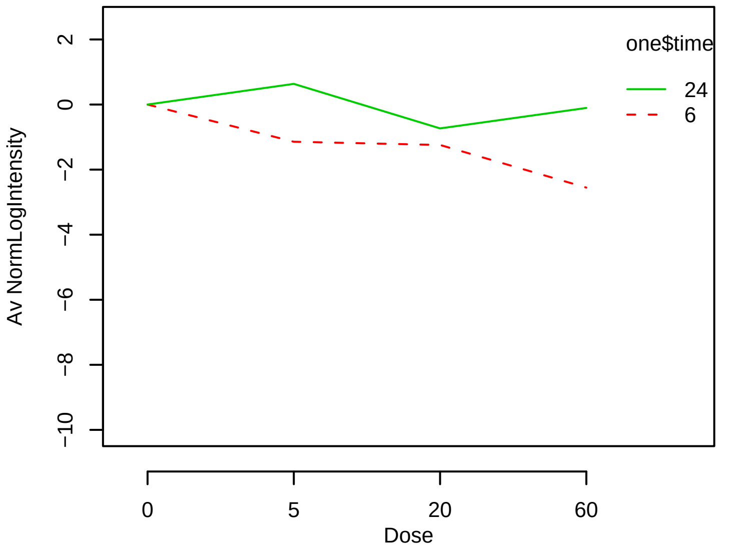

GO_0048145 : regulation of fibroblast proliferation

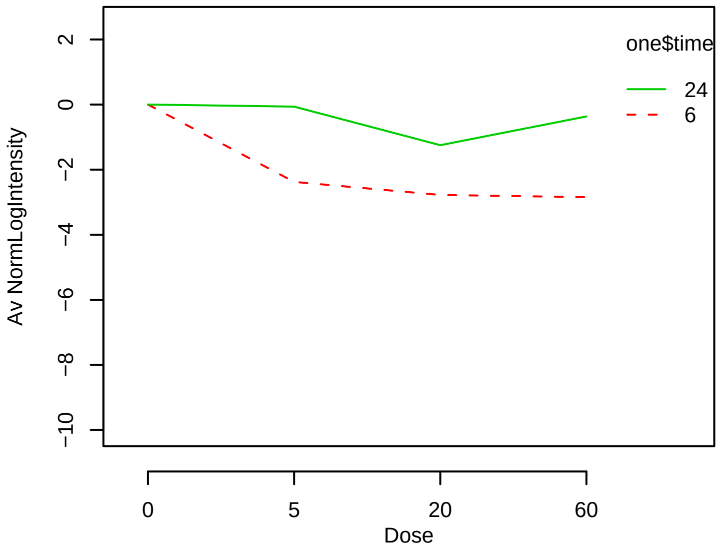

GO_0048157 : oogenesis (sensu Mammalia)

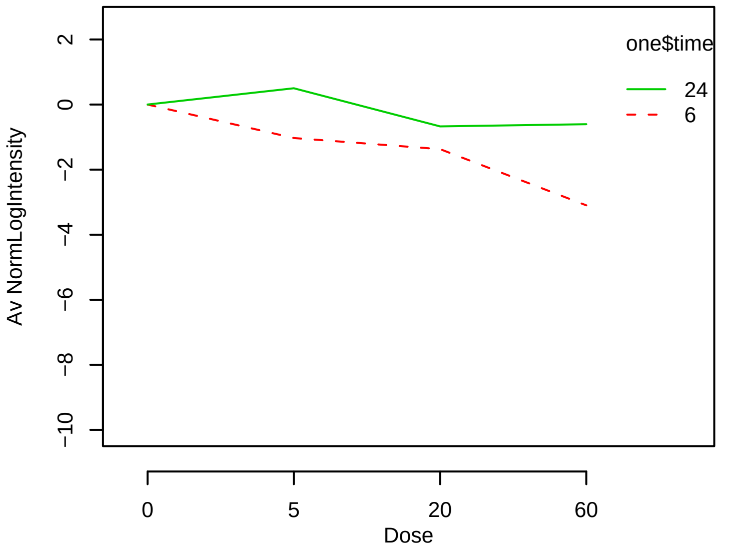

GO_0048167 : regulation of synaptic plasticity

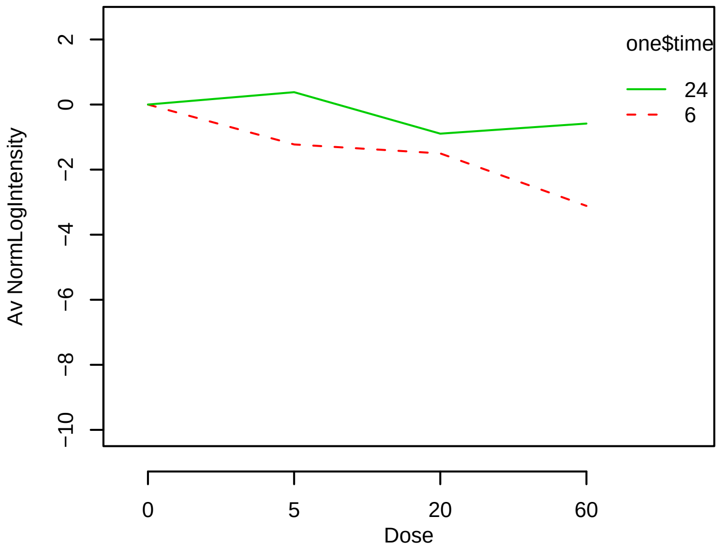

GO_0048168 : regulation of neuronal synaptic plasticity

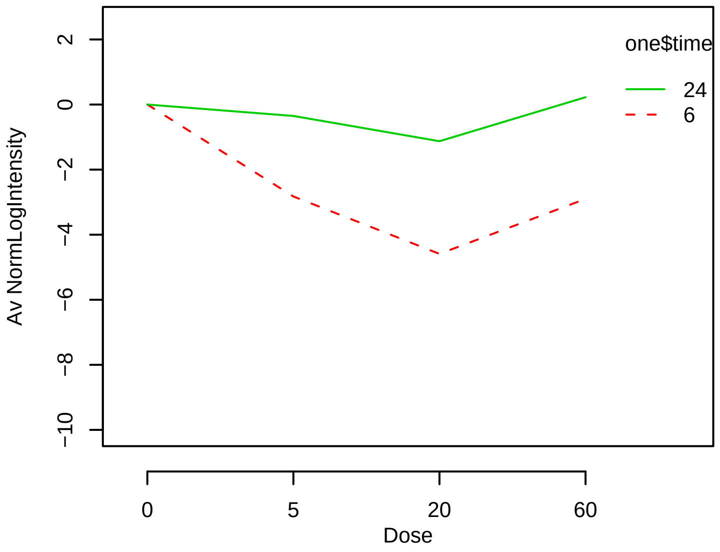

GO_0048169 : regulation of long−term neuronal synaptic plas

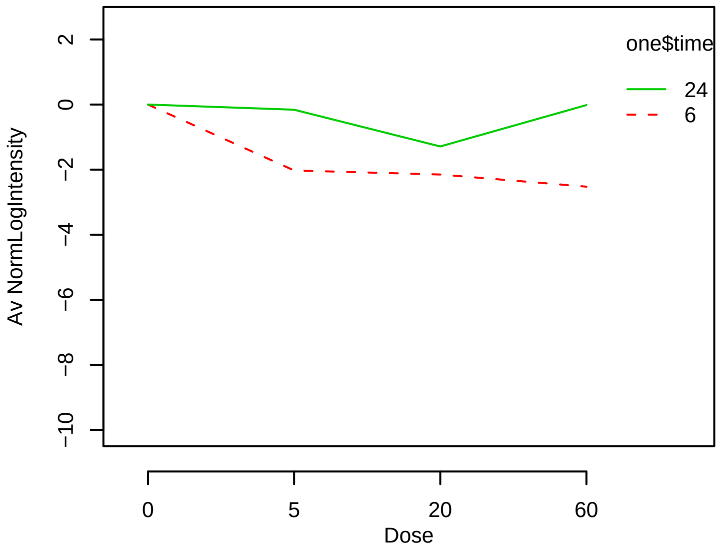

GO_0048193 : Golgi vesicle transport

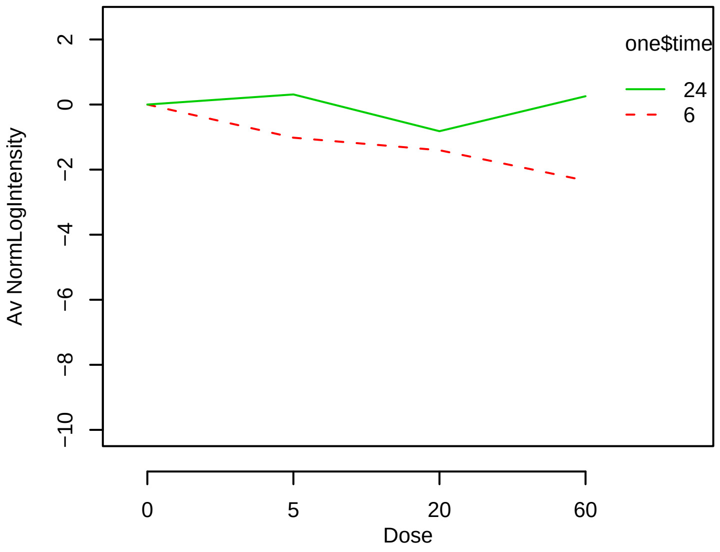

GO_0048232 : male gamete generation

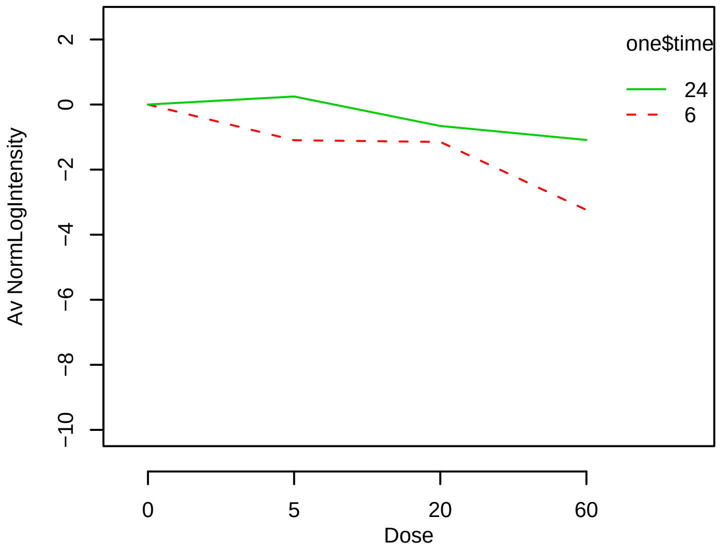

GO_0048259 : regulation of receptor mediated endocytosi

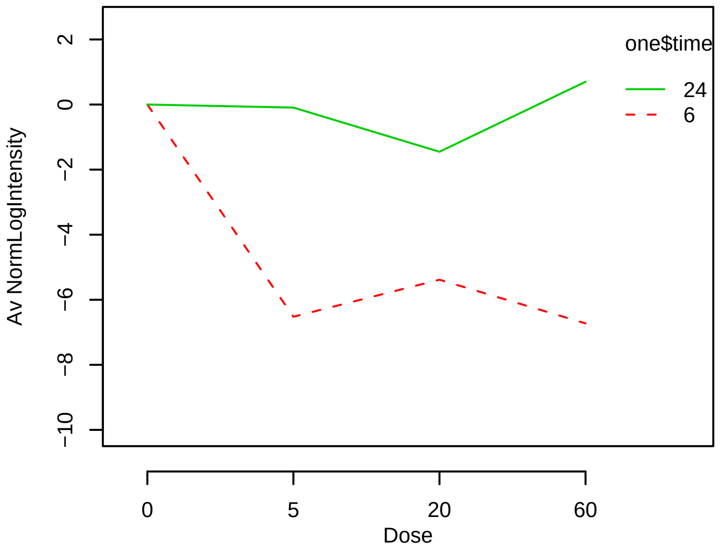

GO_0048260 : positive regulation of receptor mediated endoc

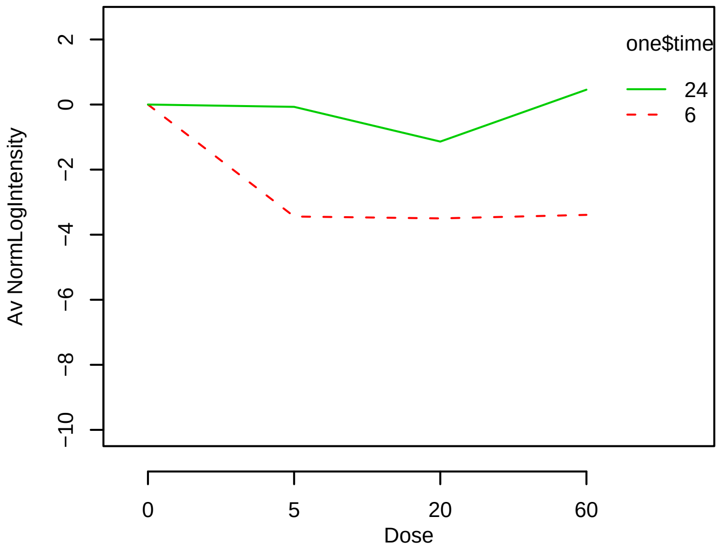

GO_0048265 : response to pain

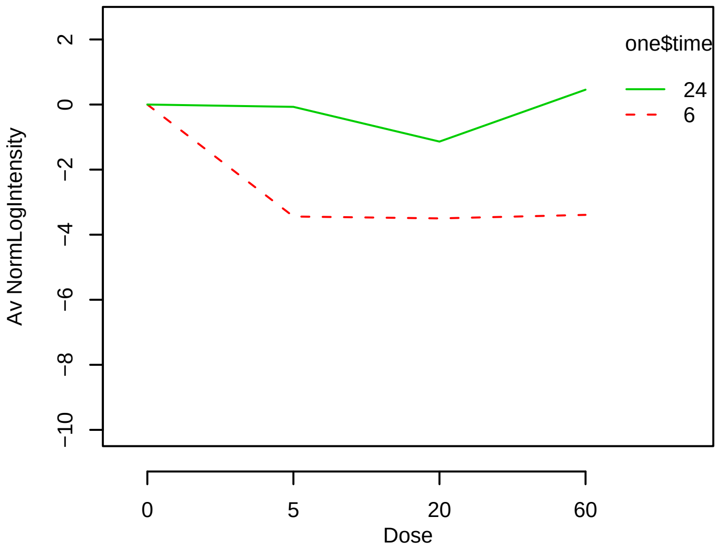

GO_0048276 : gastrulation (sensu Vertebrata)

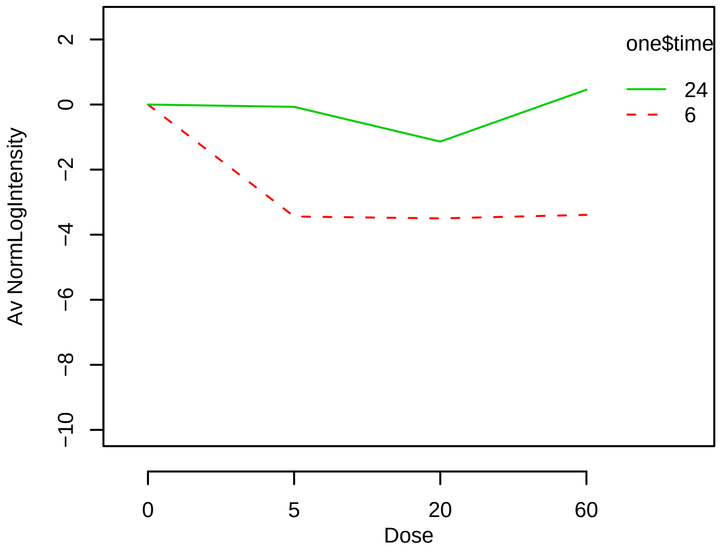

GO_0048278 : vesicle docking

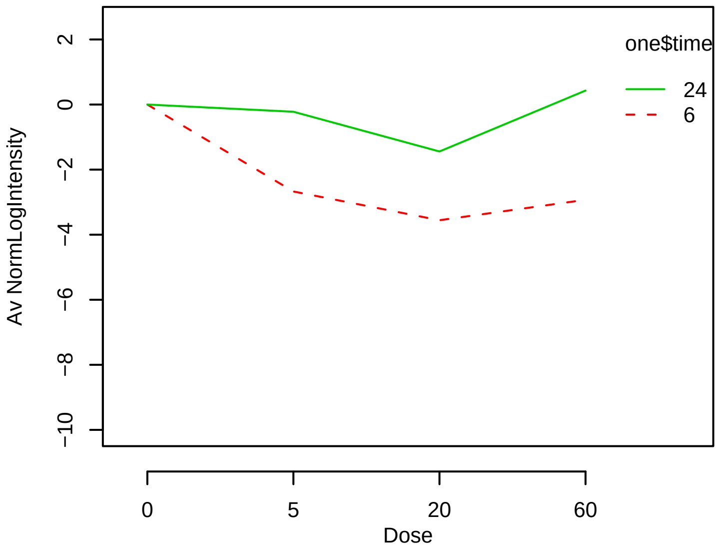

GO_0048285 : organelle fission

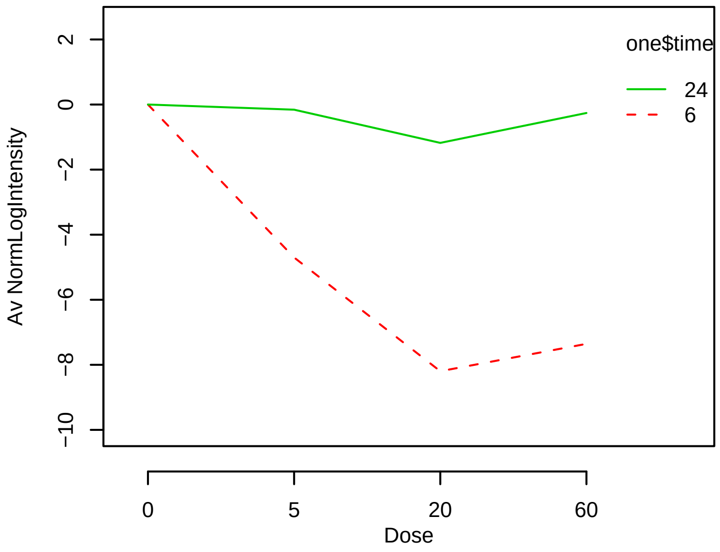

GO_0048286 : alveolus development

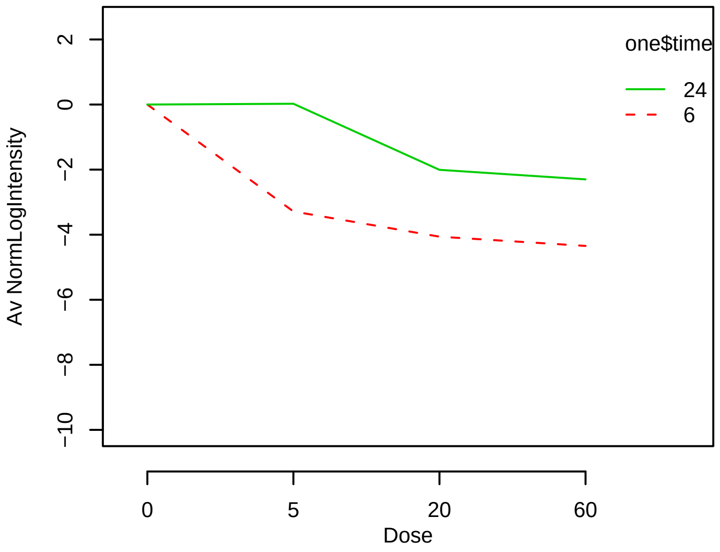

GO_0048291 : isotype switching to IgG isotypes


GO_0048302 : regulation of isotype switching to IgG isotyp

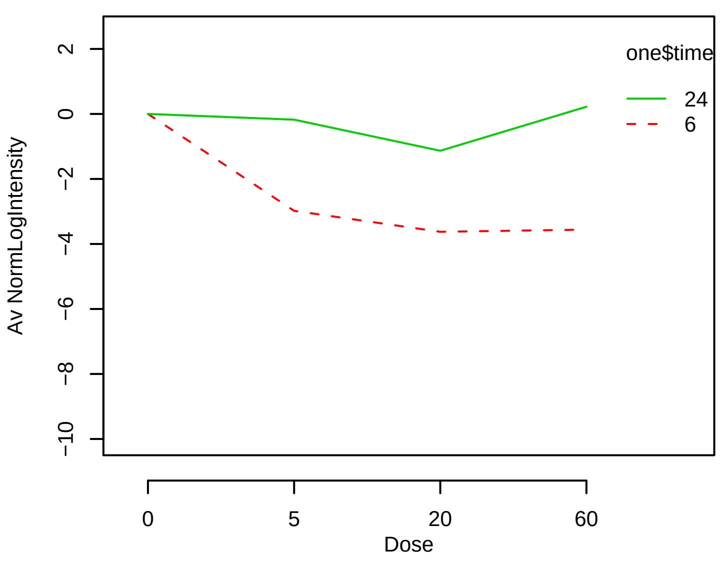

GO_0048304 : positive regulation of isotype switching to IgG


GO_0048305 : immunoglobulin secretion

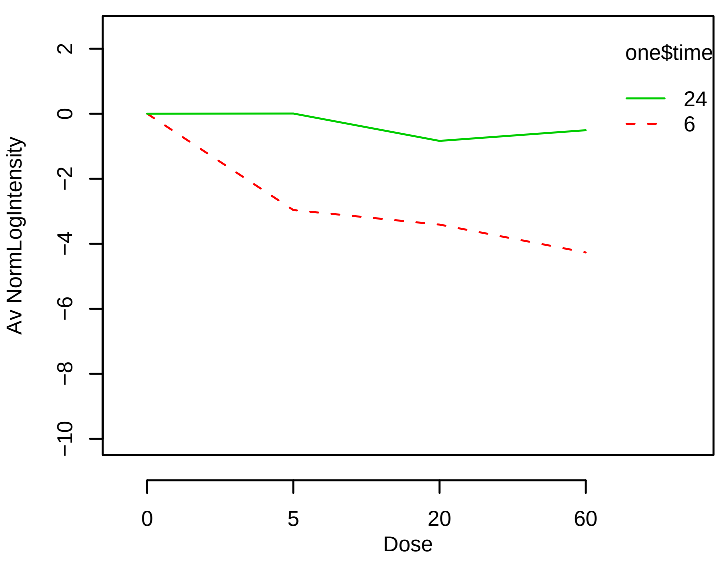

GO_0048332 : mesoderm morphogenesis


GO_0048339 : paraxial mesoderm development

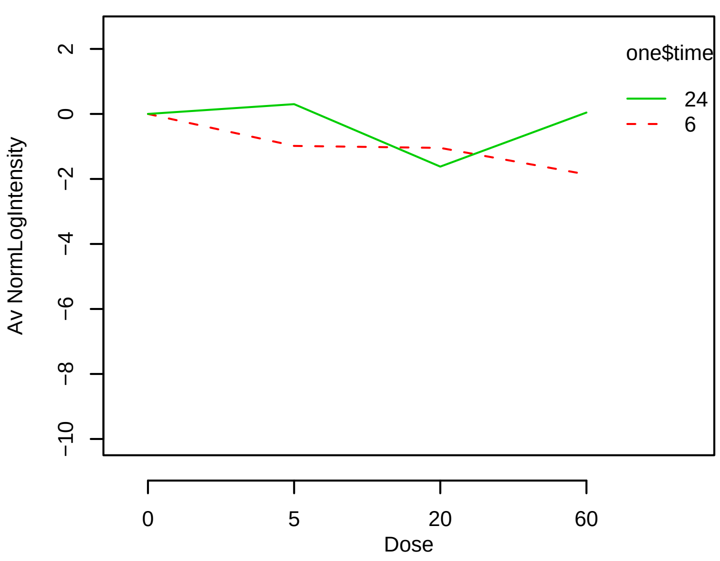
GO_0048469 : cell maturation



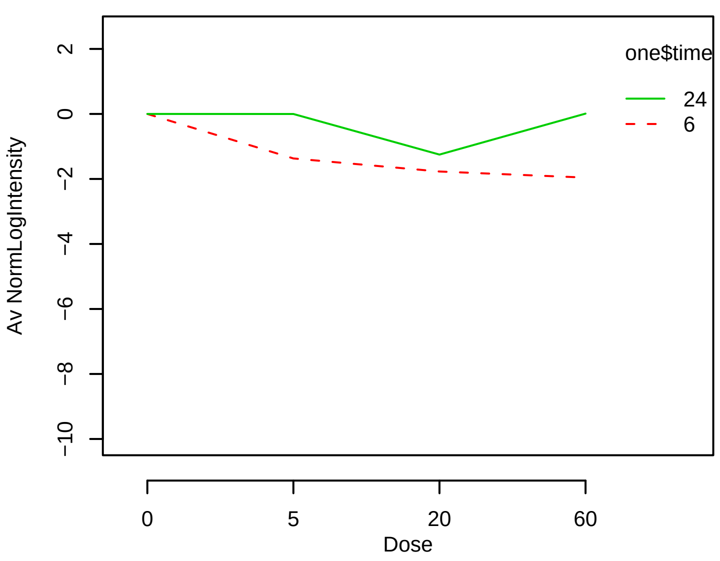
GO_0048477 : oogenesis



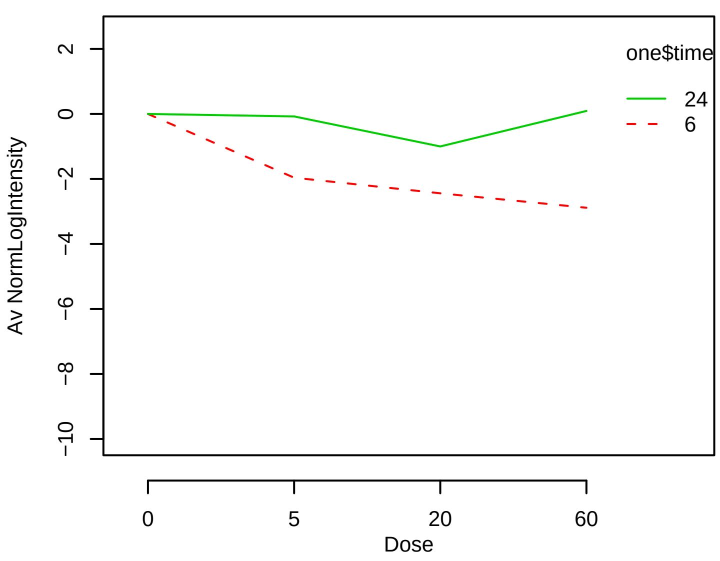
GO_0048488 : synaptic vesicle endocytosis



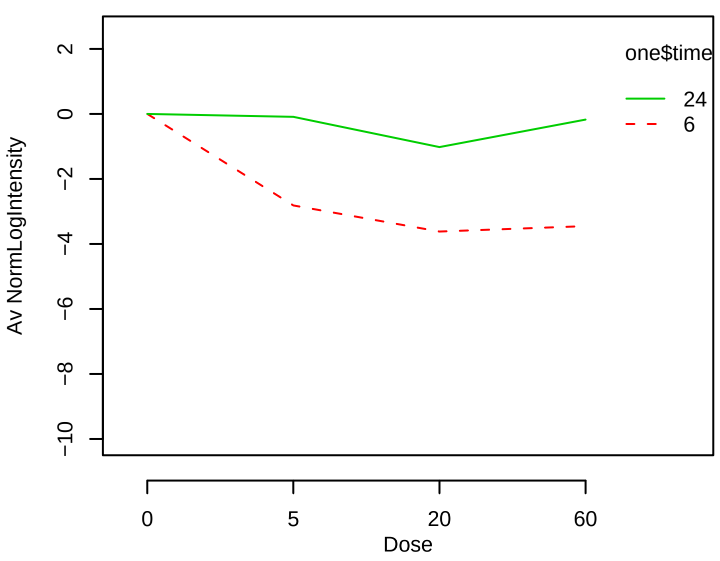
GO_0048489 : synaptic vesicle transport

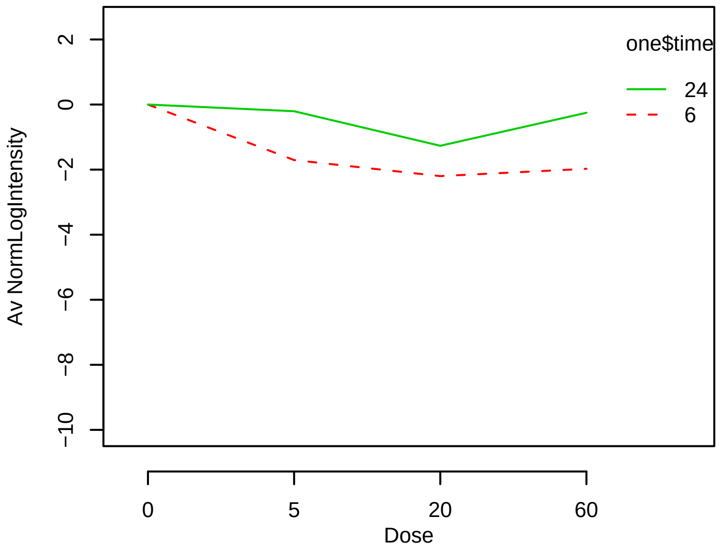


GO_0048511 : rhythmic process

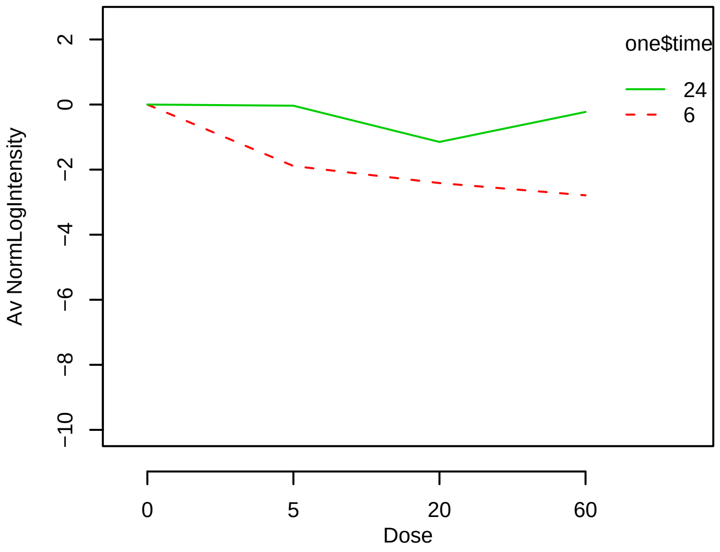


GO_0048514 : blood vessel morphogenesis

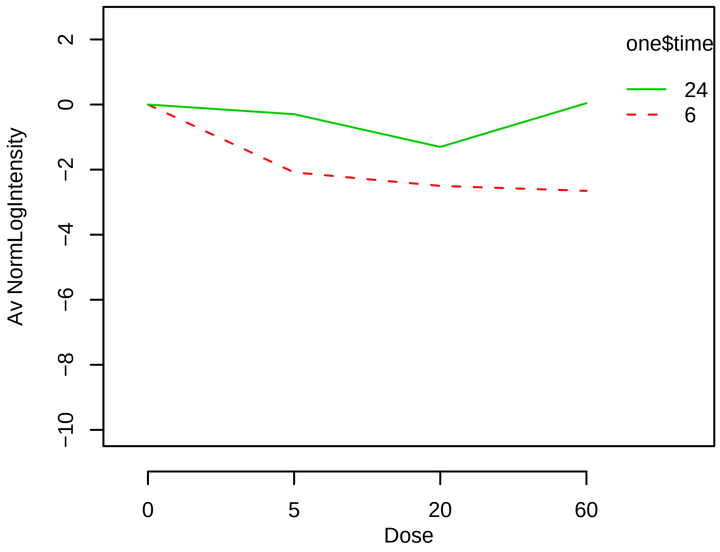




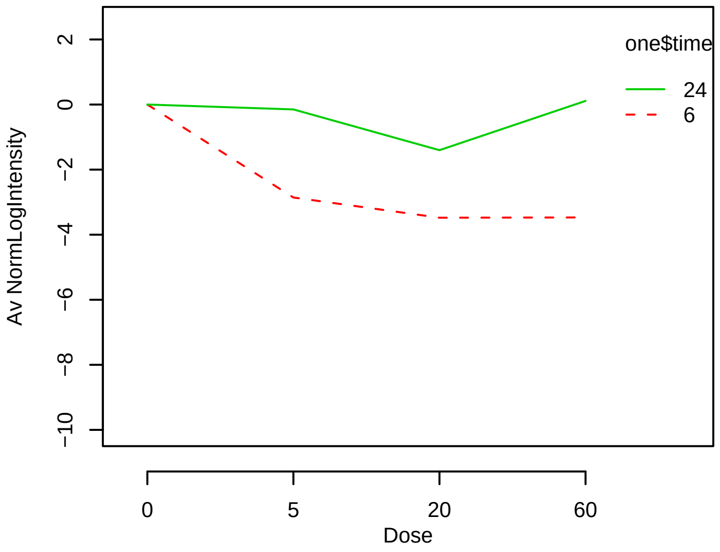
GO_0048515 : spermatid differentiation



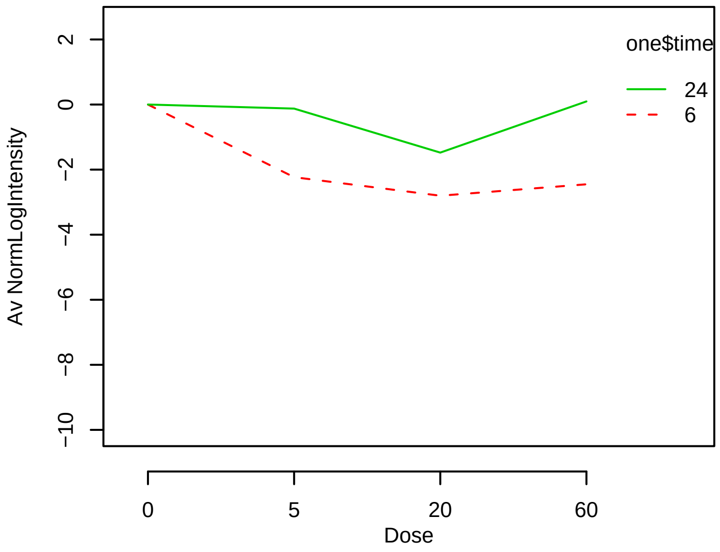
GO_0048534 : hemopoietic or lymphoid organ developmer



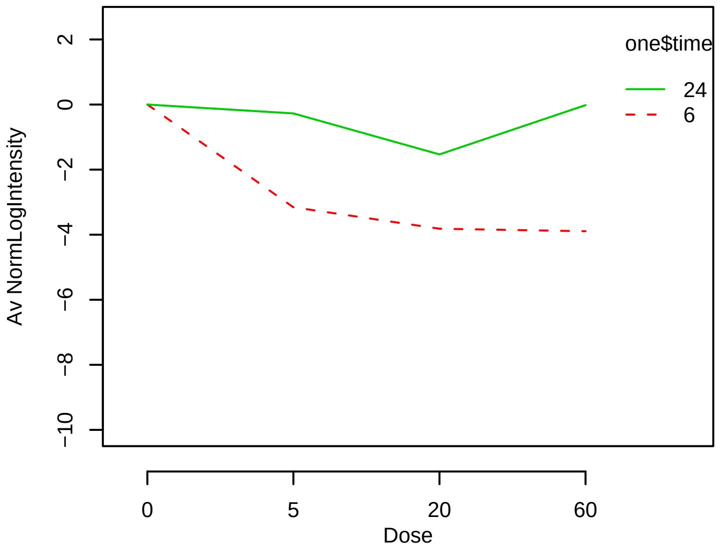
GO_0048535 : lymph node development



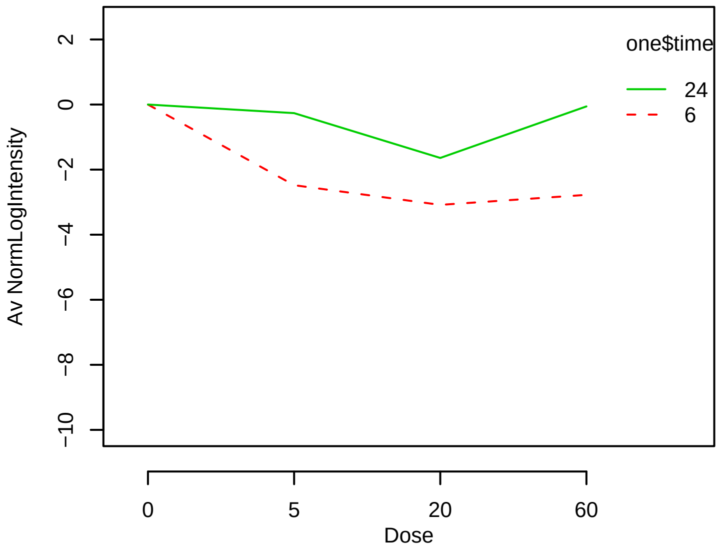
GO_0048546 : digestive tract morphogenesis



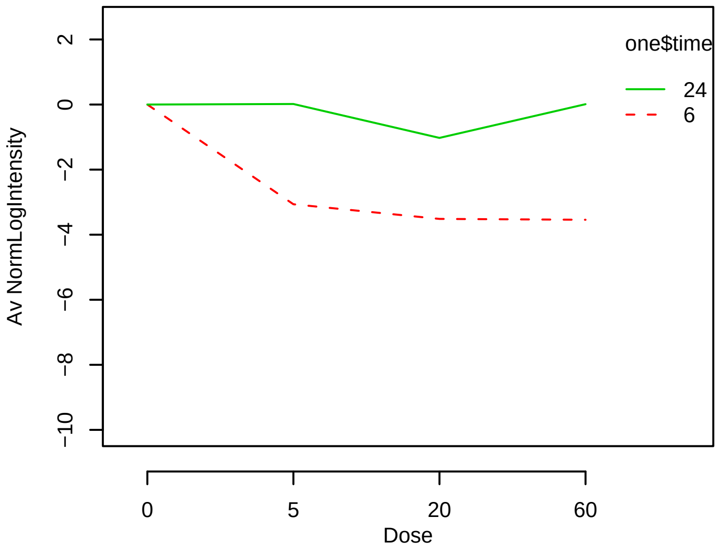
GO_0048547 : gut morphogenesis



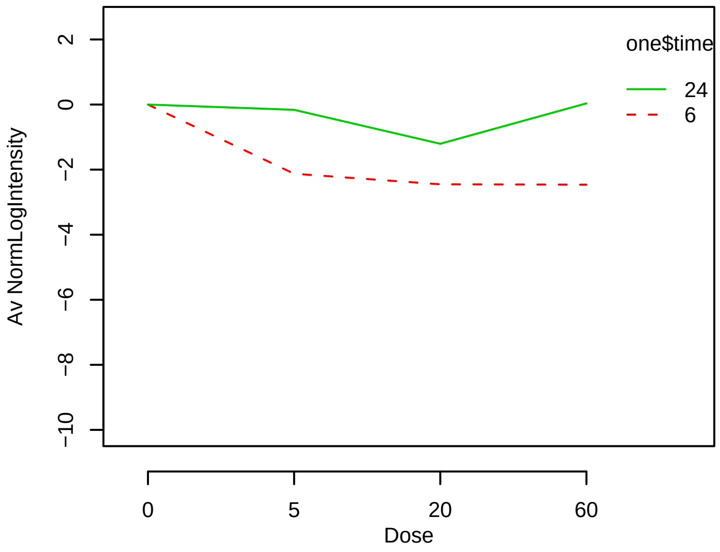
GO_0048557 : embryonic digestive tract morphogenesis



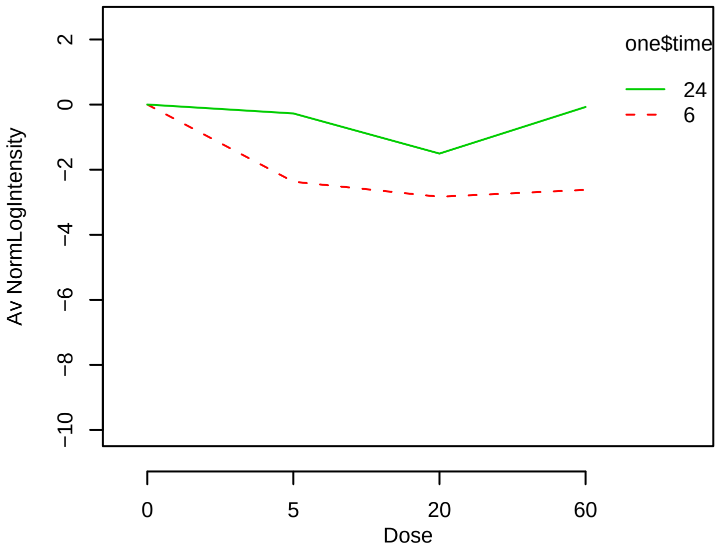
GO_0048558 : embryonic gut morphogenesis



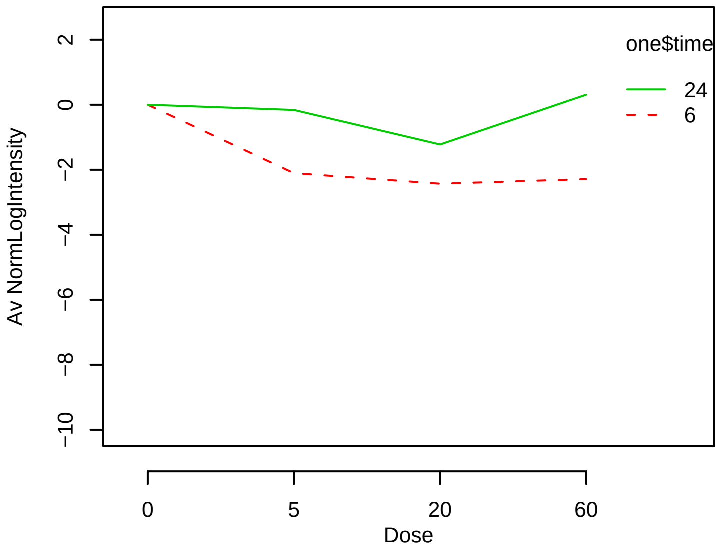
GO_0048562 : embryonic organ morphogenesis



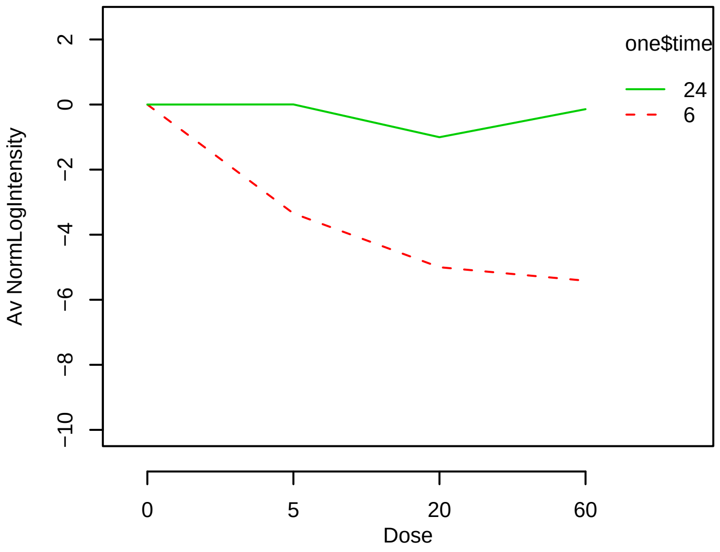
GO_0048565 : gut development



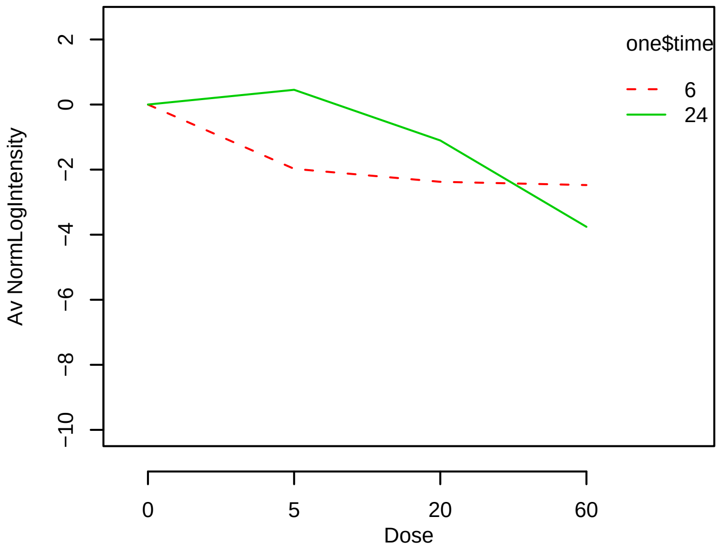
GO_0048566 : embryonic gut development



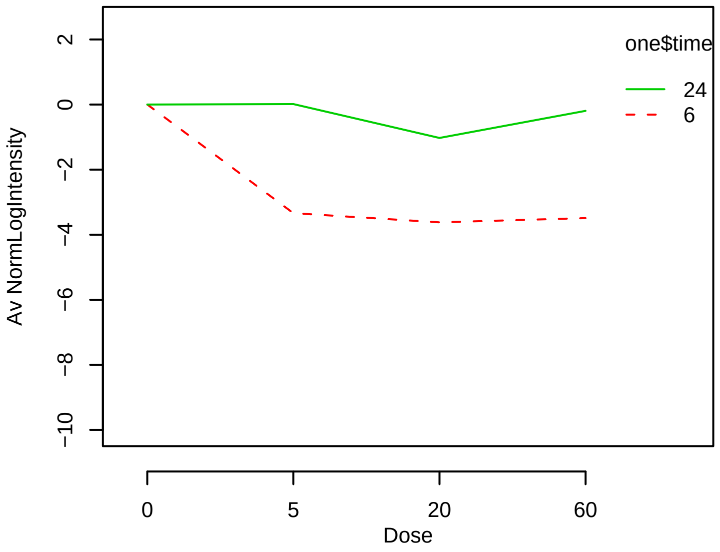
GO_0048567 : ectodermal gut morphogenesis



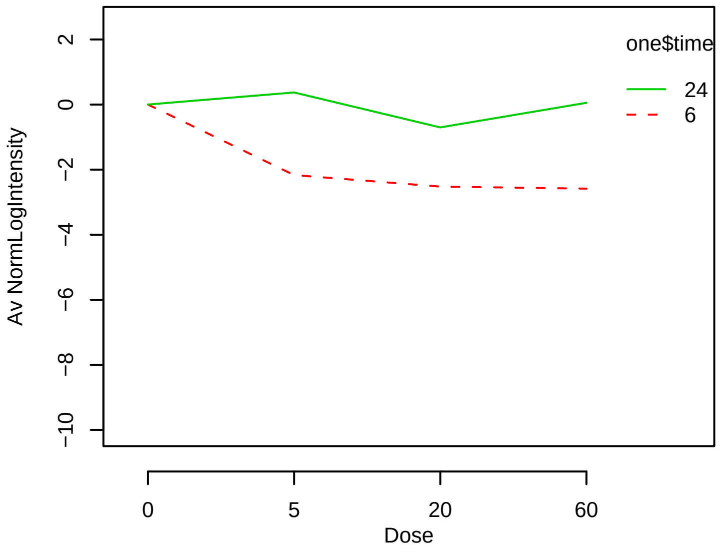
GO_0048568 : embryonic organ development



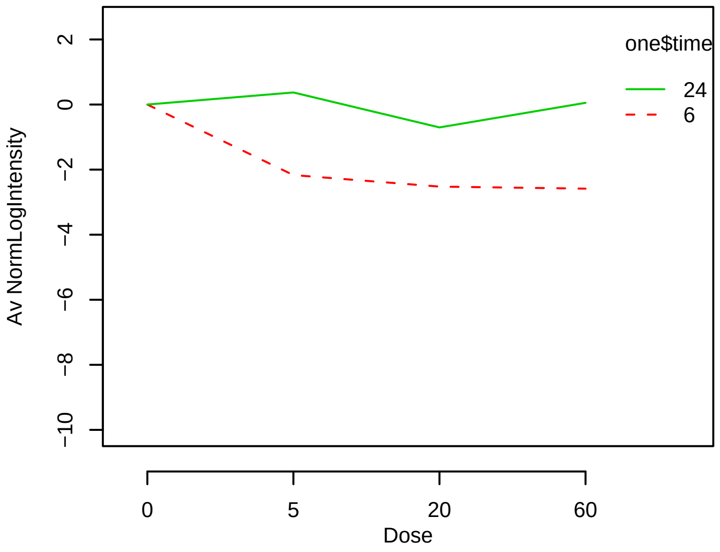
GO_0048589 : developmental growth



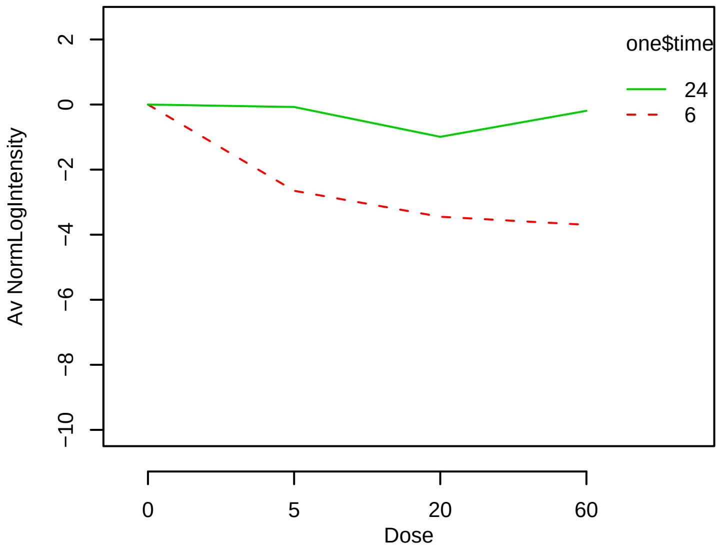
GO_0048592 : eye morphogenesis



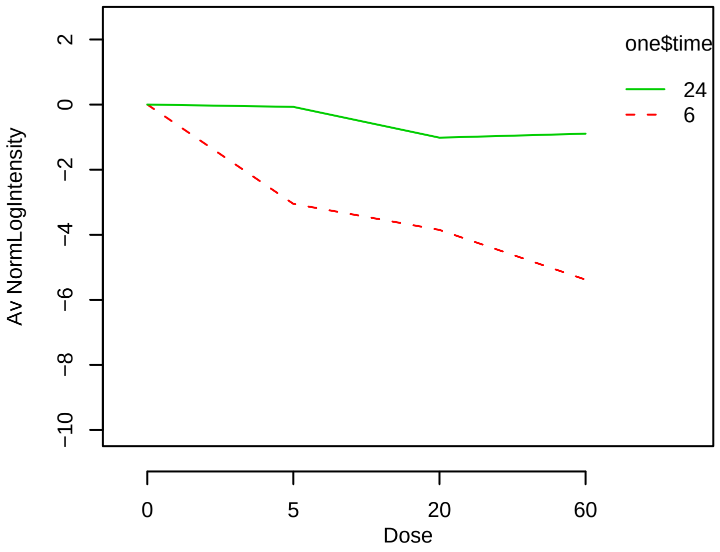
GO_0048593 : eye morphogenesis (sensu Vertebrata)



GO_0048595 : eye morphogenesis (sensu Mammalia)

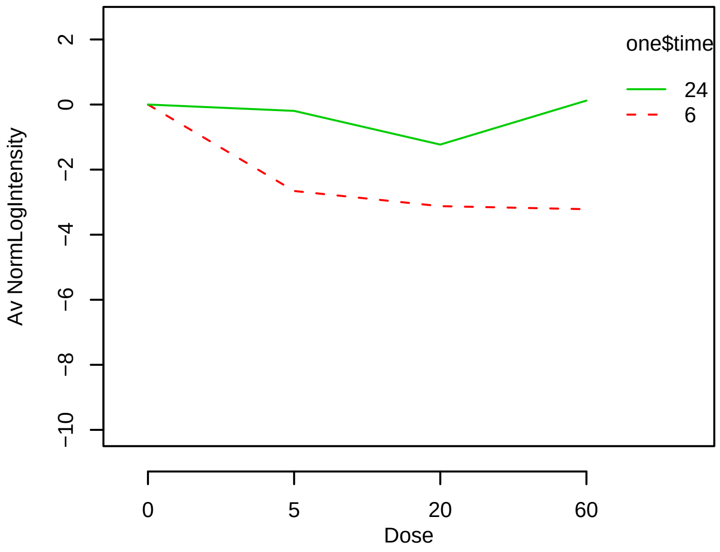


GO_0048598 : embryonic morphogenesis

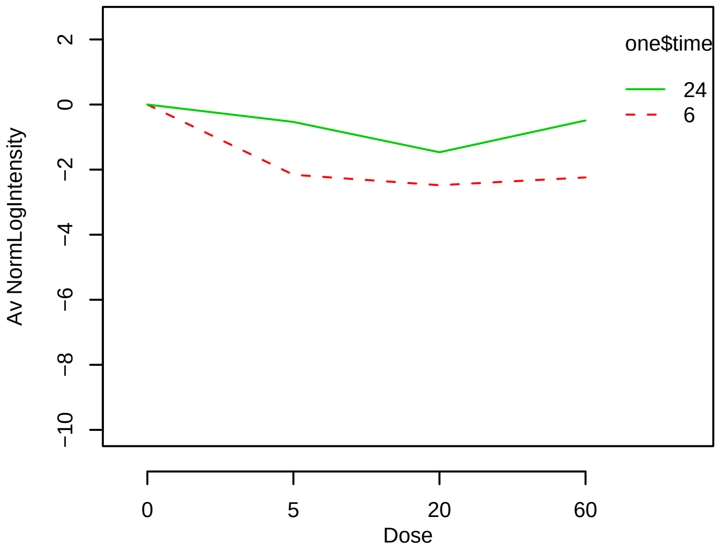


GO_0048599 : oocyte development

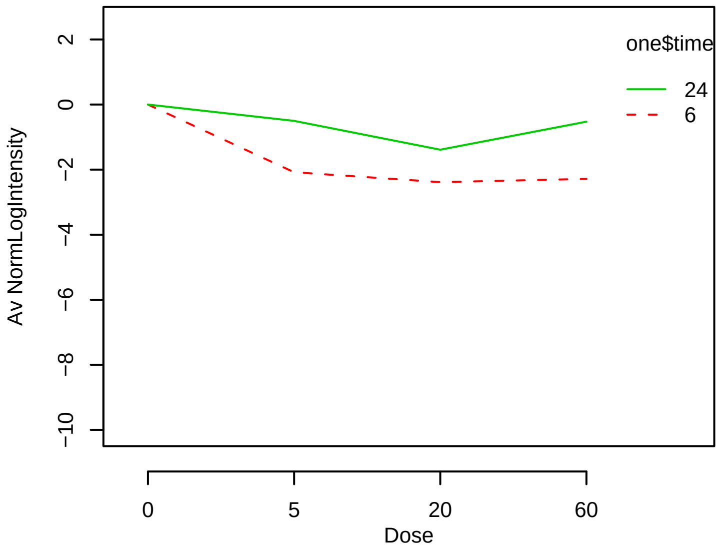
GO_0048609 : reproductive organismal physiological proce



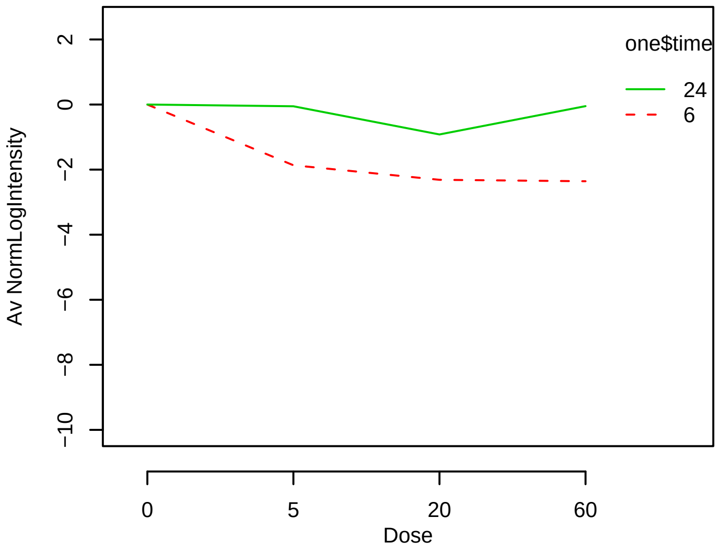
GO_0048627 : myoblast development



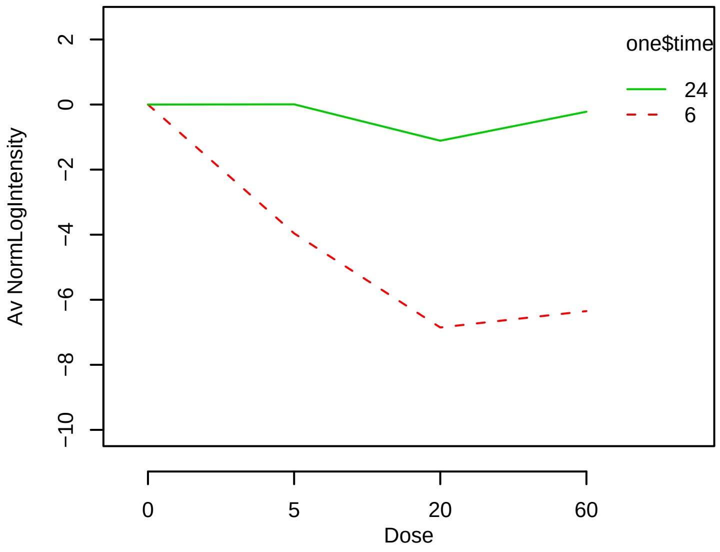
GO_0048628 : myoblast maturation



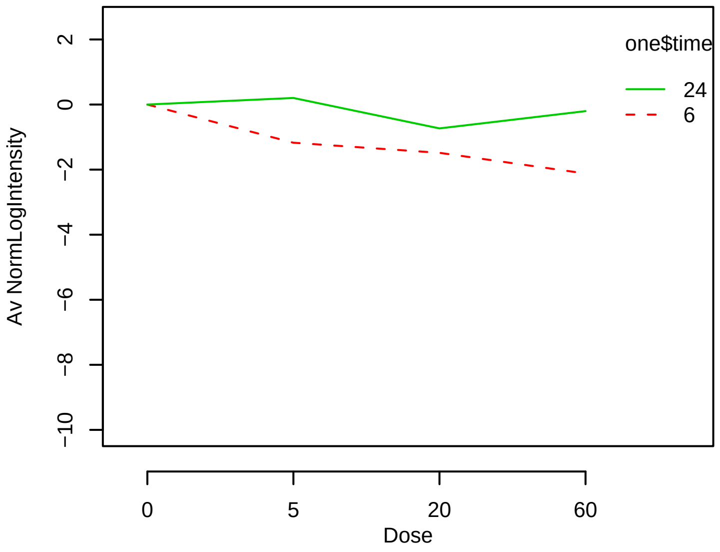
GO_0048637 : skeletal muscle development



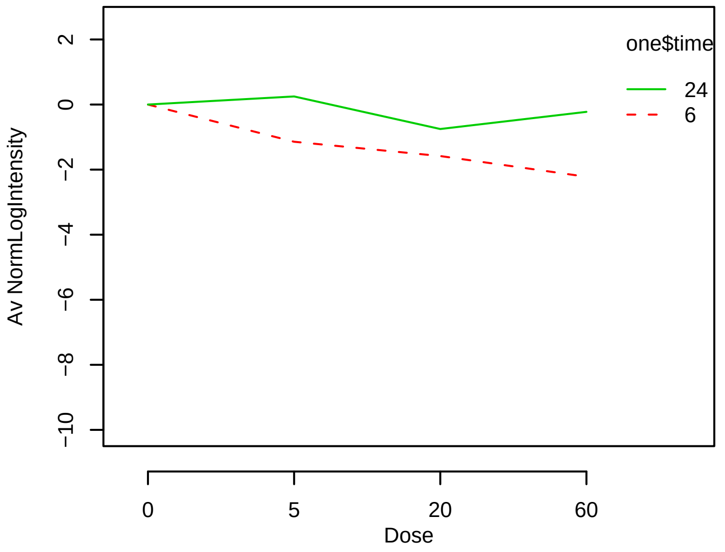
GO_0048646 : anatomical structure formation



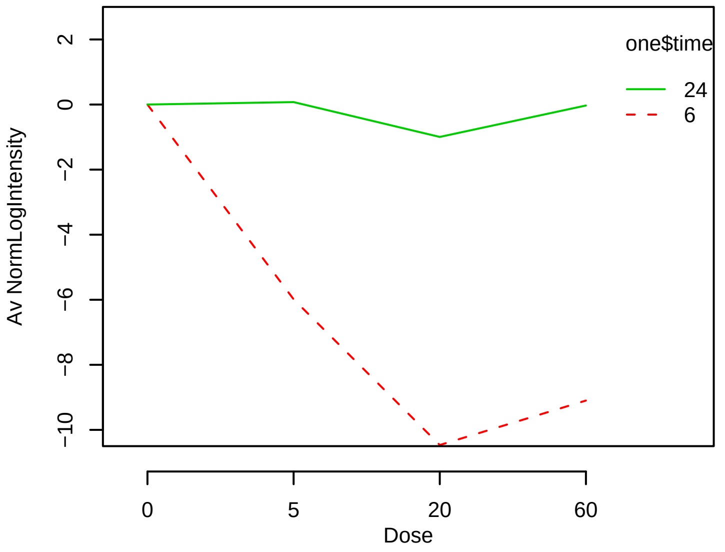
GO_0048659 : smooth muscle cell proliferation



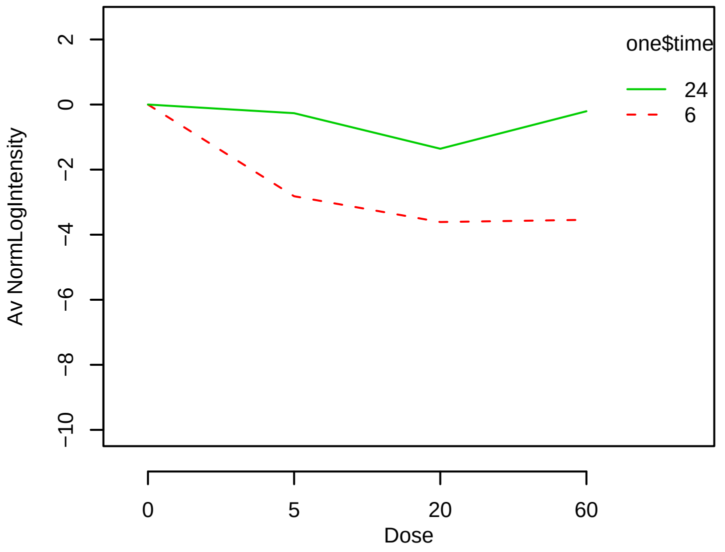
GO_0048660 : regulation of smooth muscle cell proliferatic



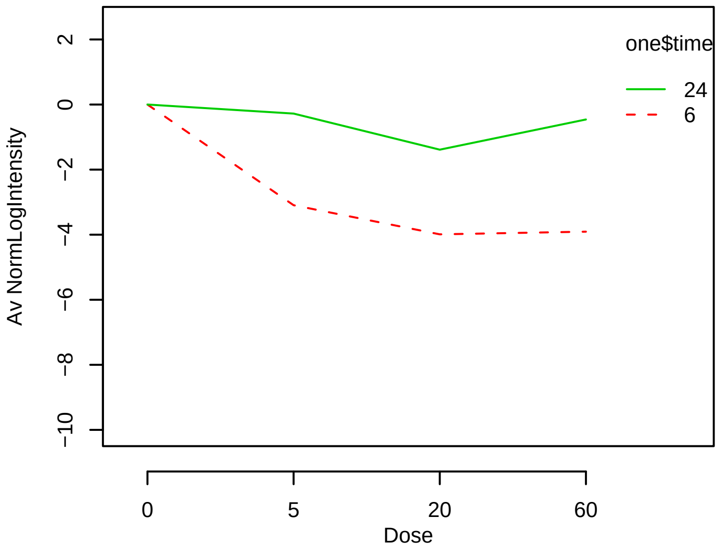
GO_0048663 : neuron fate commitment



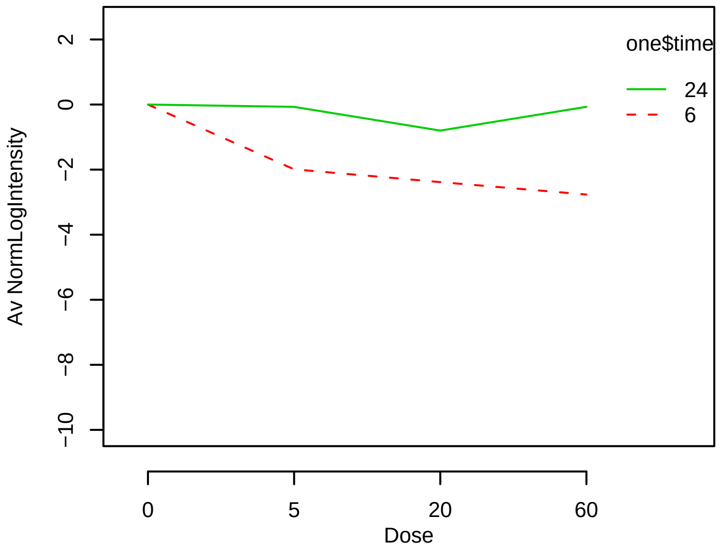
GO_0048666 : neuron development



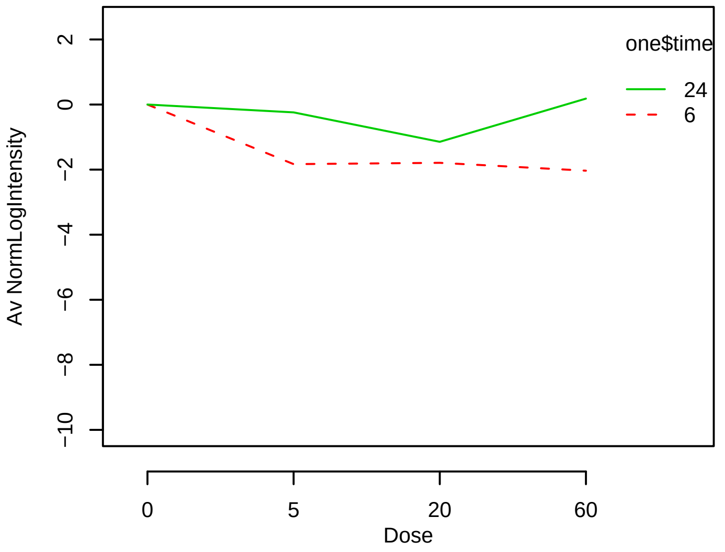
GO_0048667 : neuron morphogenesis during differentiatio

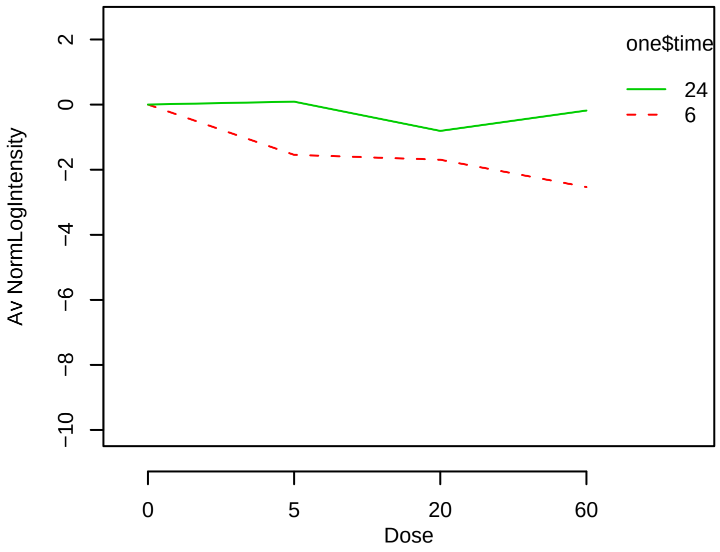


GO_0048675 : axon extension

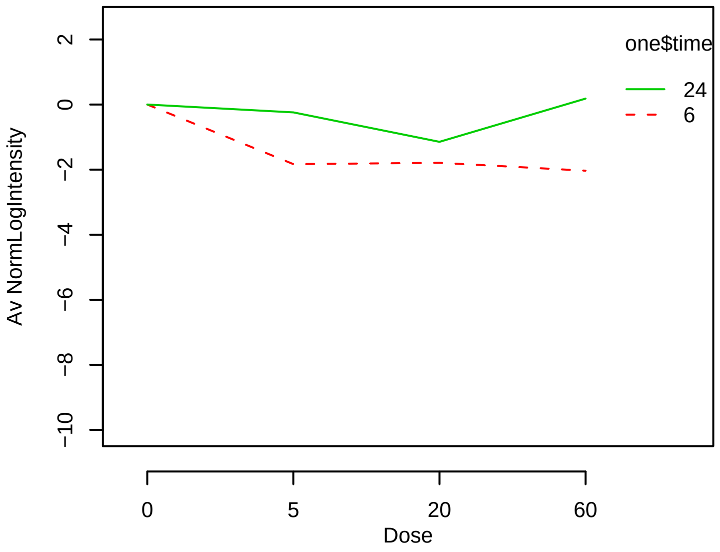


GO_0048704 : embryonic skeletal morphogenesis

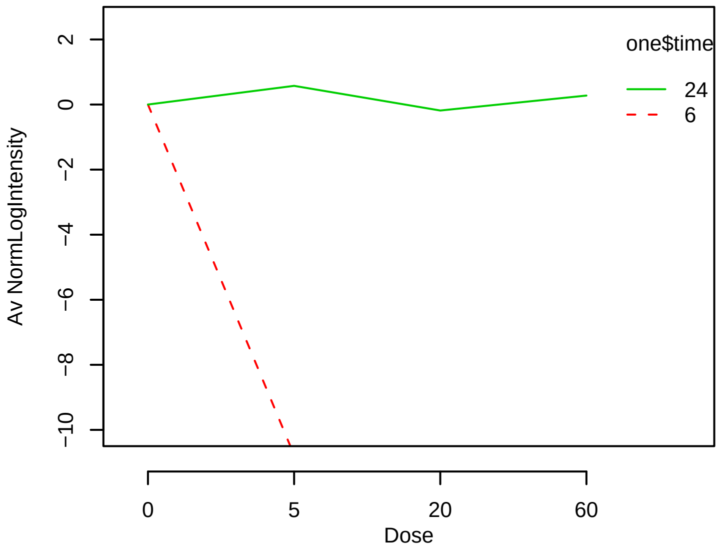




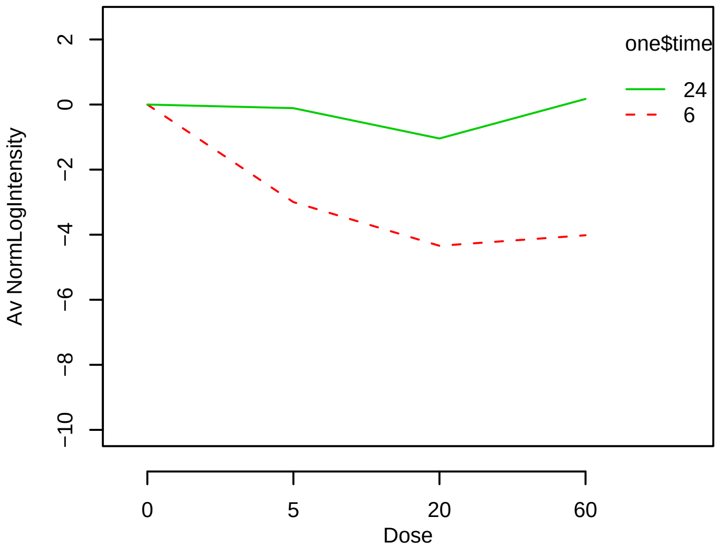
GO_0048705 : skeletal morphogenesis



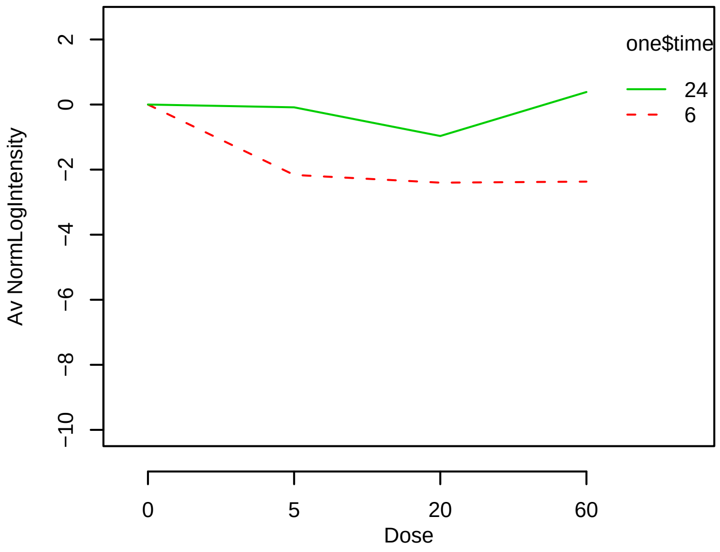
GO_0048706 : embryonic skeletal development



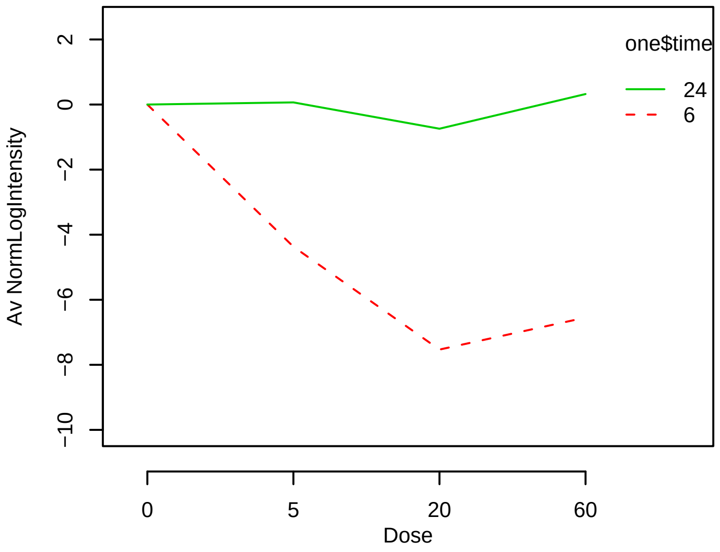
GO_0048709 : oligodendrocyte differentiation



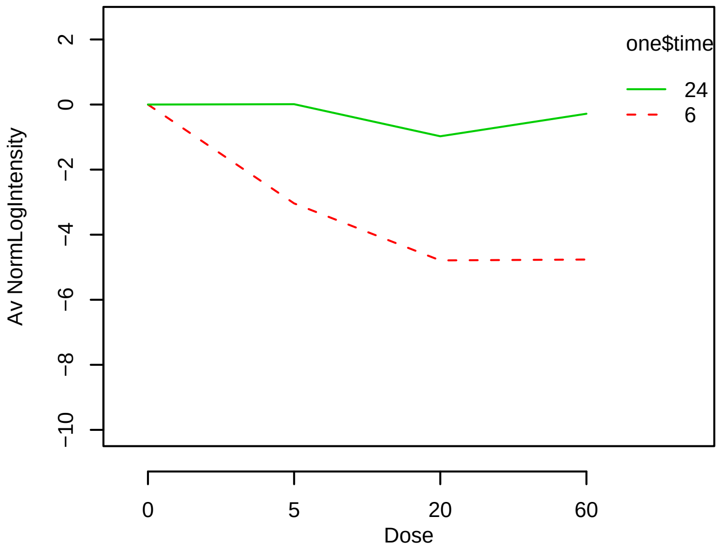
GO_0048729 : tissue morphogenesis

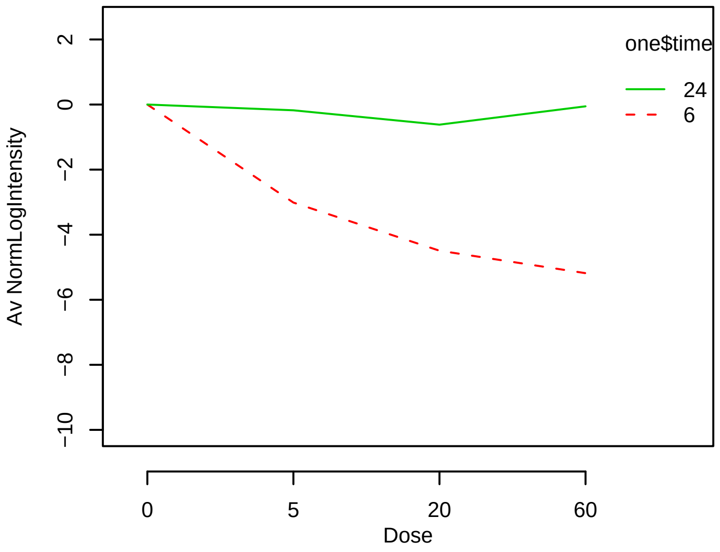


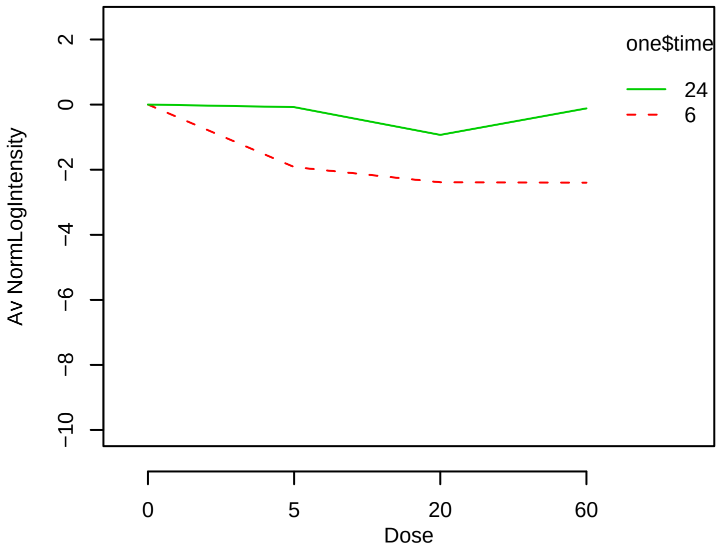
GO_0048730 : epidermis morphogenesis

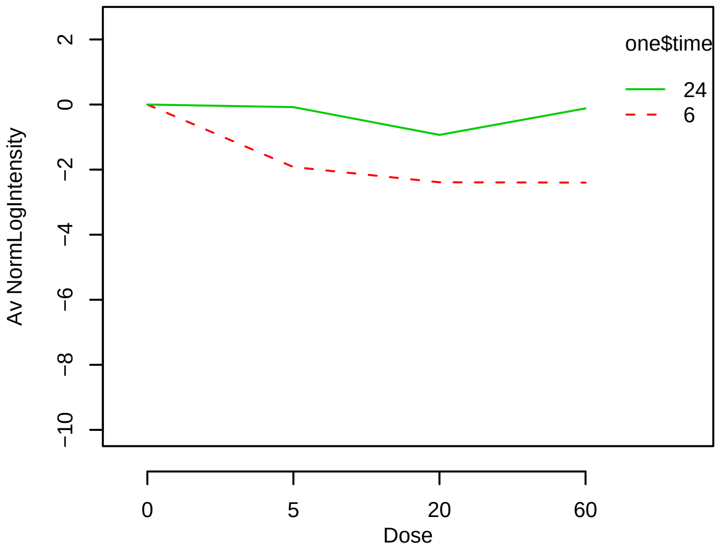


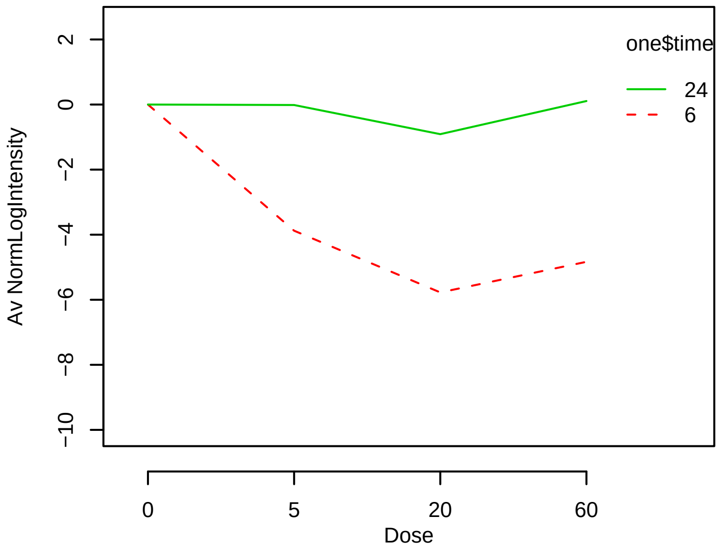
GO_0048732 : gland development

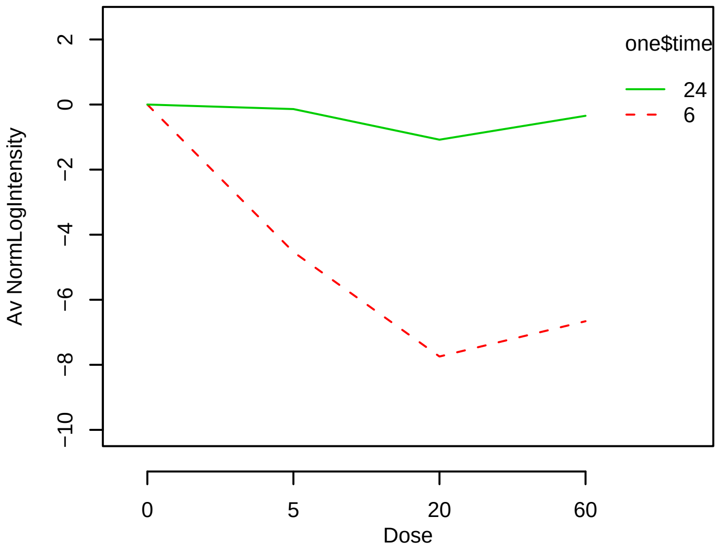

GO_0048736 : appendage development

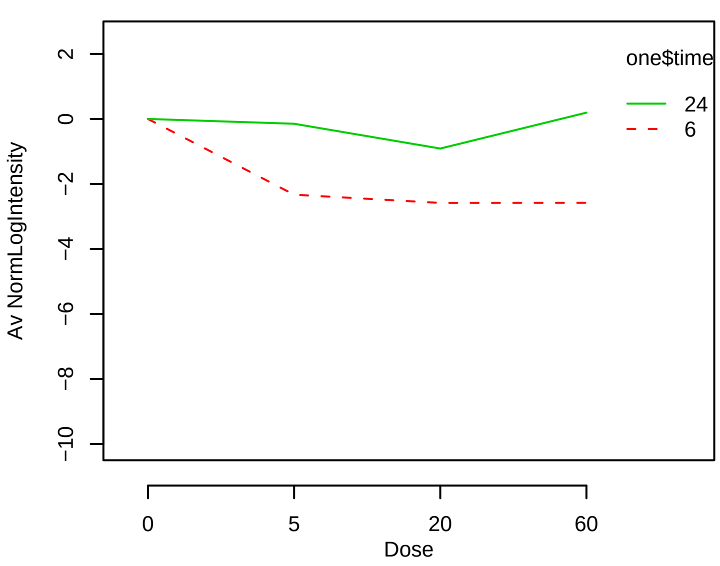

GO_0048738 : cardiac muscle development


GO_0048741 : skeletal muscle fiber development

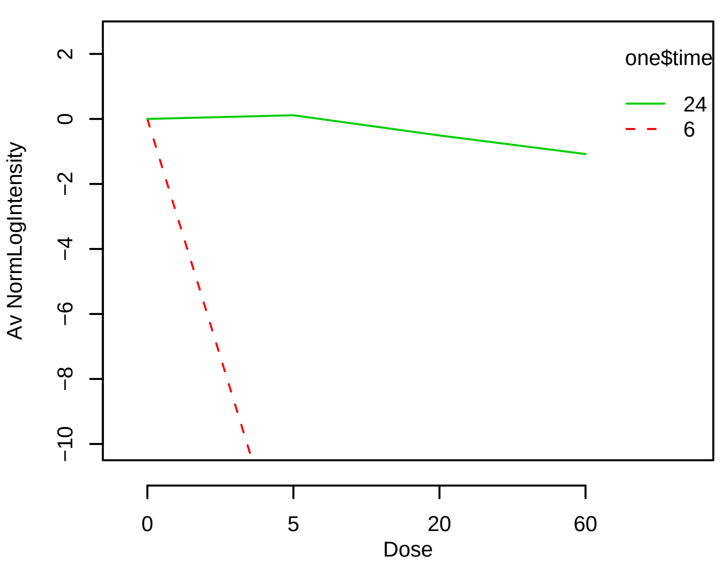

GO_0048747 : muscle fiber development


GO_0048754 : branching morphogenesis of a tube

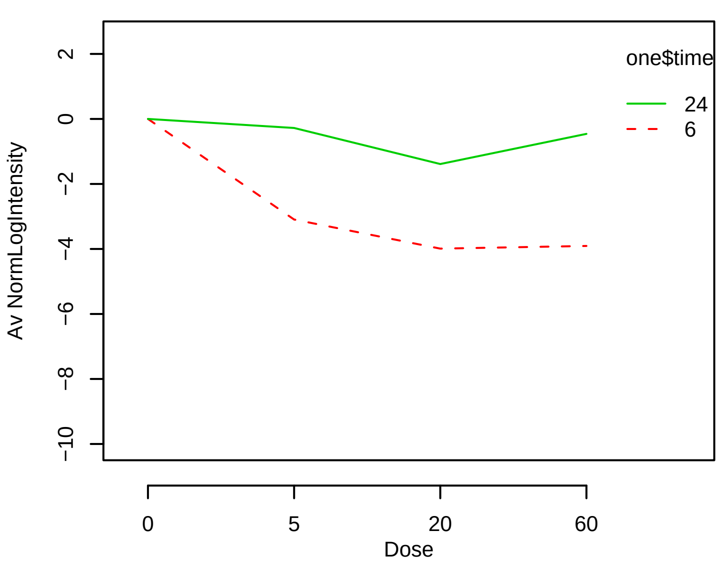

GO_0048762 : mesenchymal cell differentiation



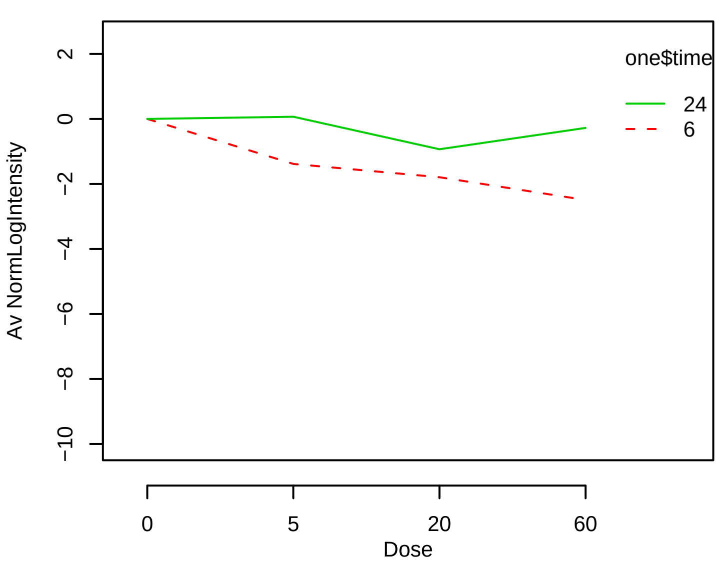
GO_0048771 : tissue remodeling



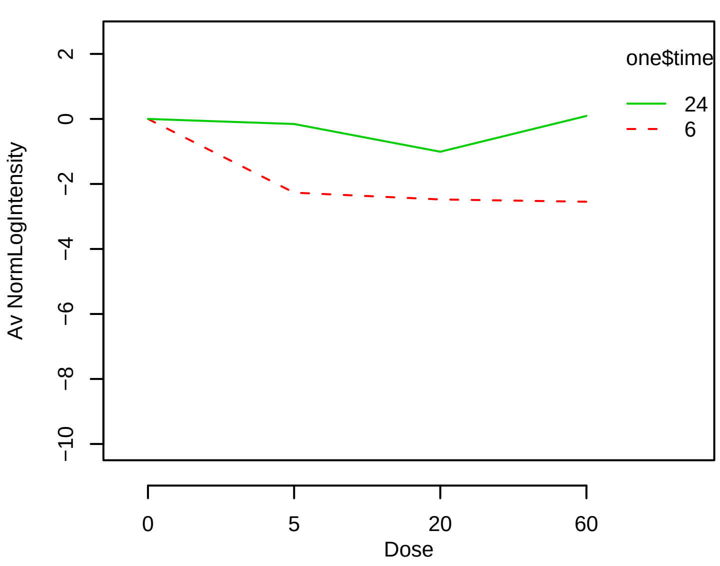
GO_0048806 : genitalia development



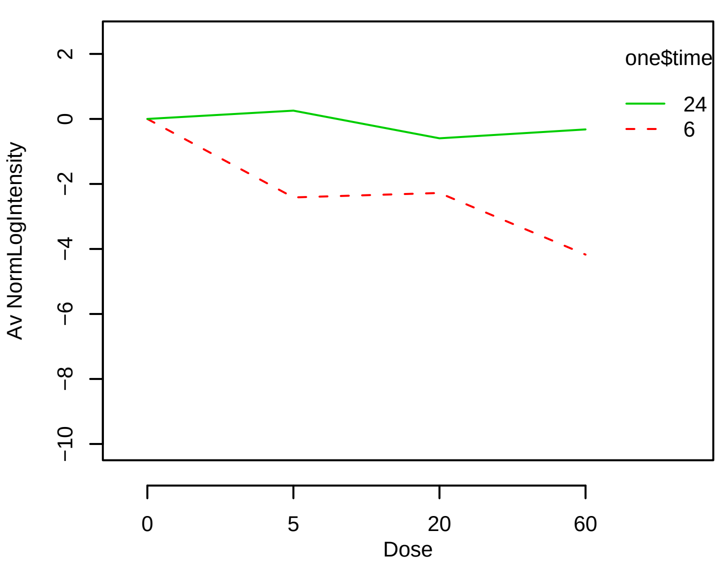
GO_0048812 : neurite morphogenesis



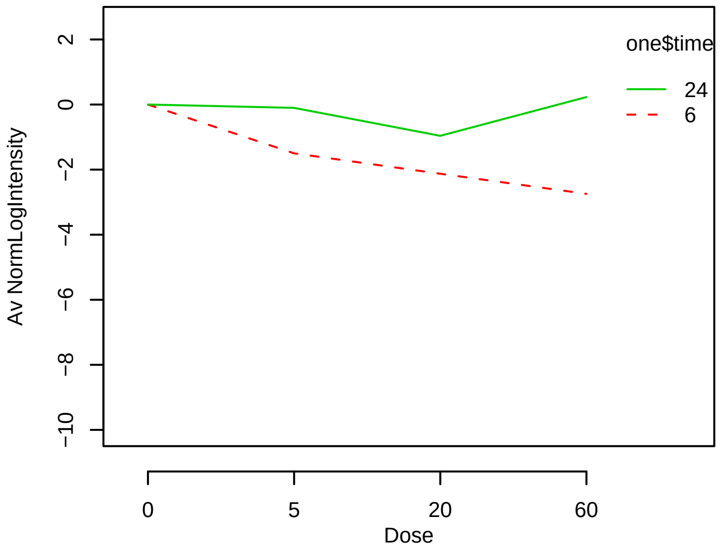
GO_0048820 : hair follicle maturation

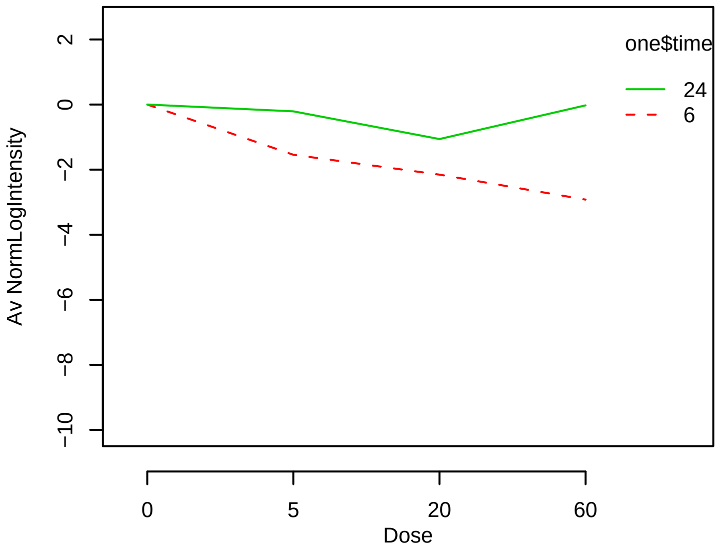


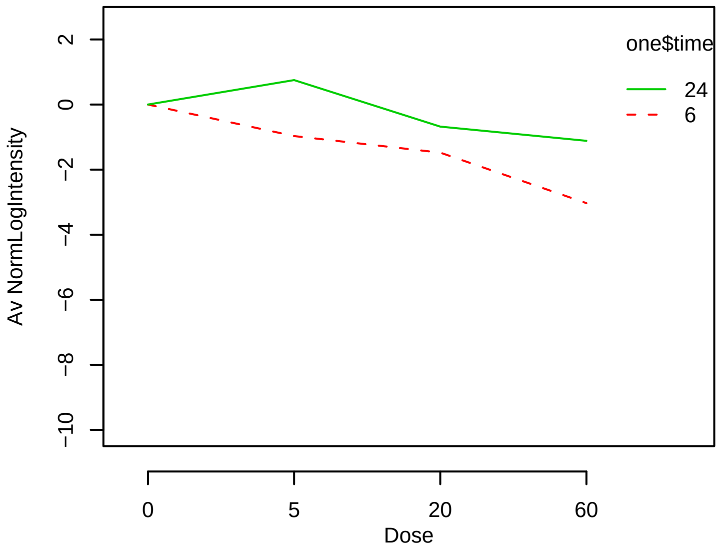
GO_0048839 : inner ear development

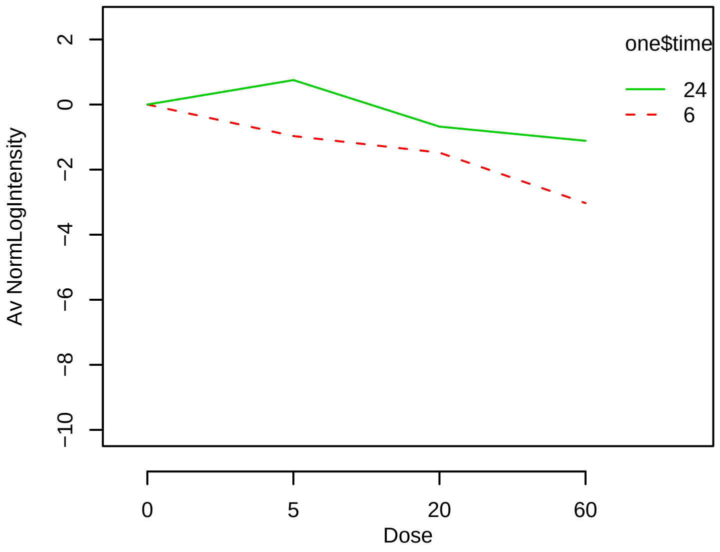


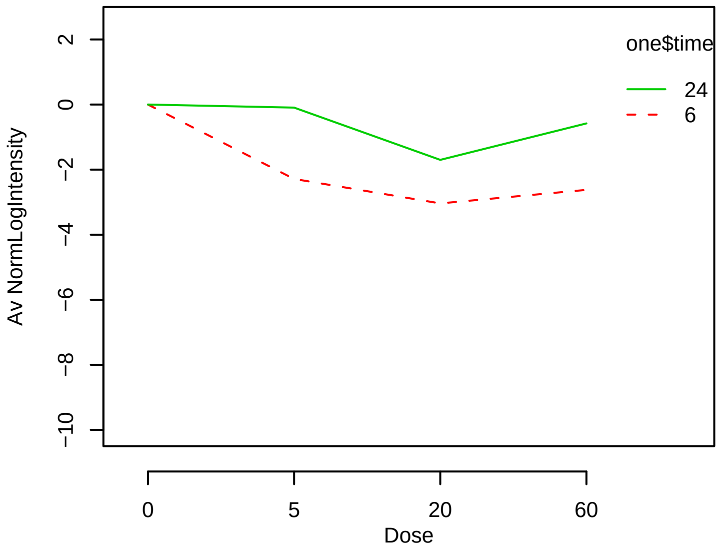
GO_0050435 : beta−amyloid metabolism

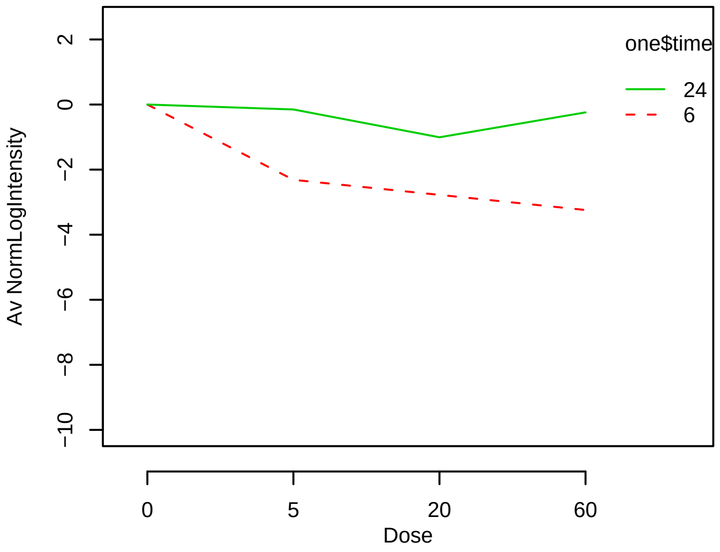

GO_0050650 : chondroitin sulfate proteoglycan biosynthes

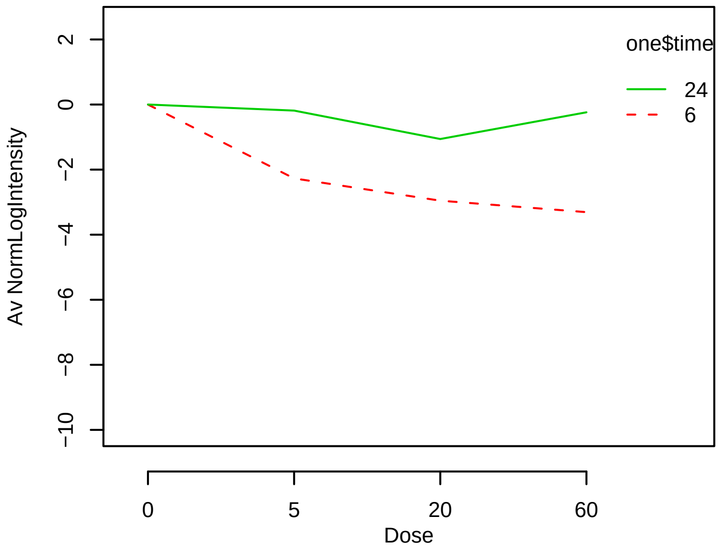

GO_0050654 : chondroitin sulfate proteoglycan metabolis


GO_0050657 : nucleic acid transport

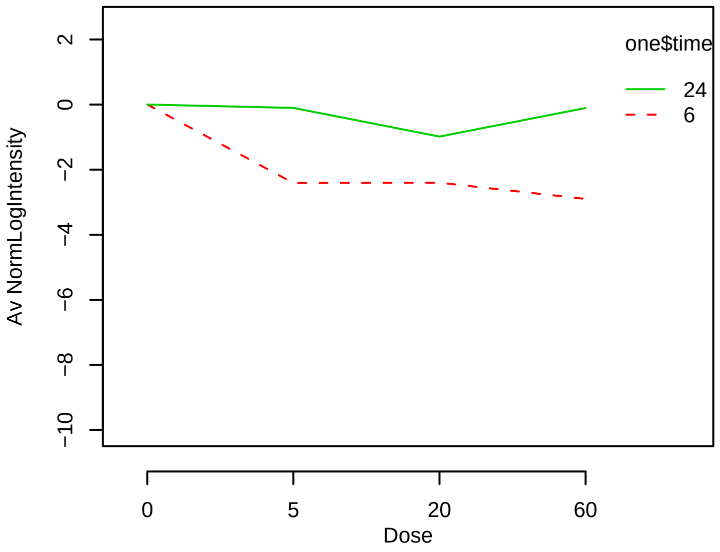

GO_0050658 : RNA transport


GO_0050663 : cytokine secretion

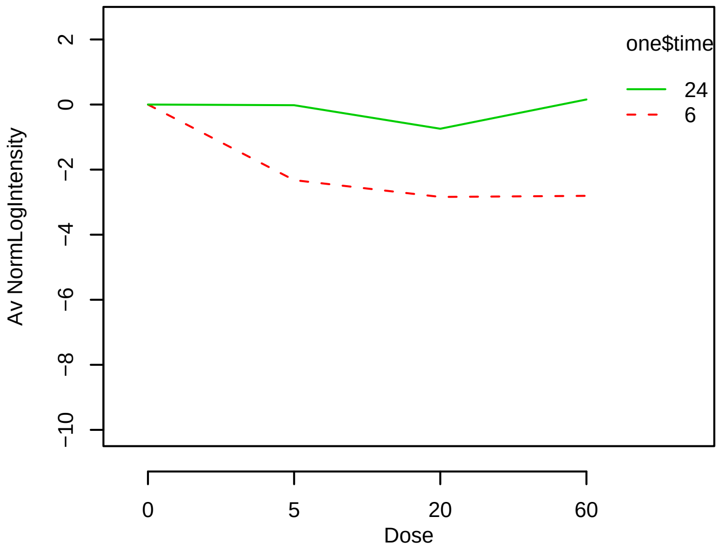

GO_0050670 : regulation of lymphocyte proliferation



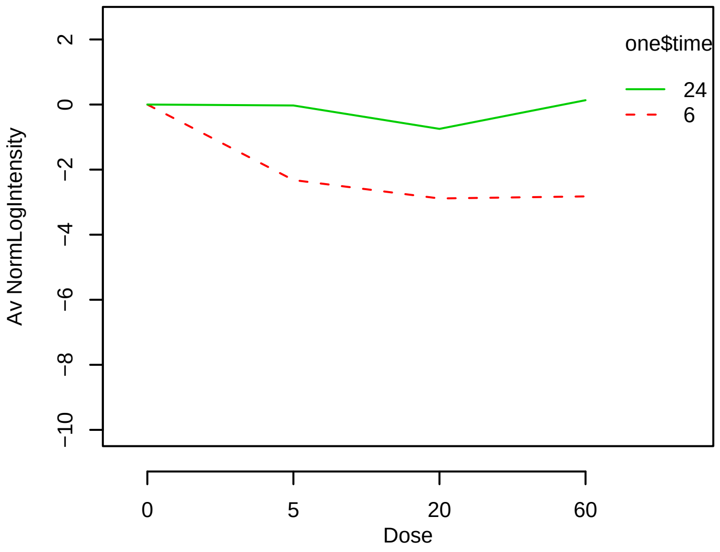
GO_0050671 : positive regulation of lymphocyte proliferati



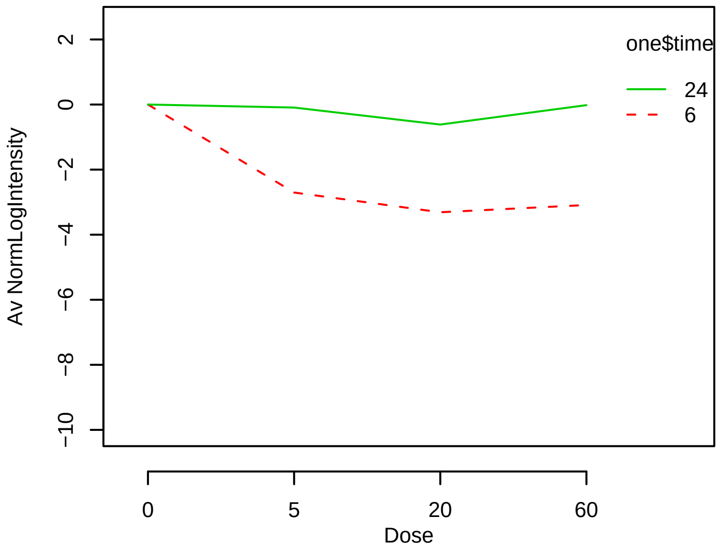
GO_0050672 : negative regulation of lymphocyte proliferati



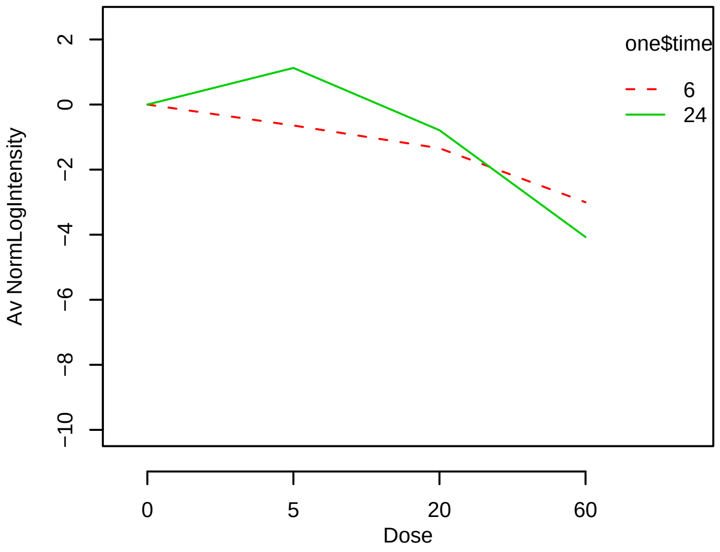
GO_0050673 : epithelial cell proliferation



GO_0050678 : regulation of epithelial cell proliferation

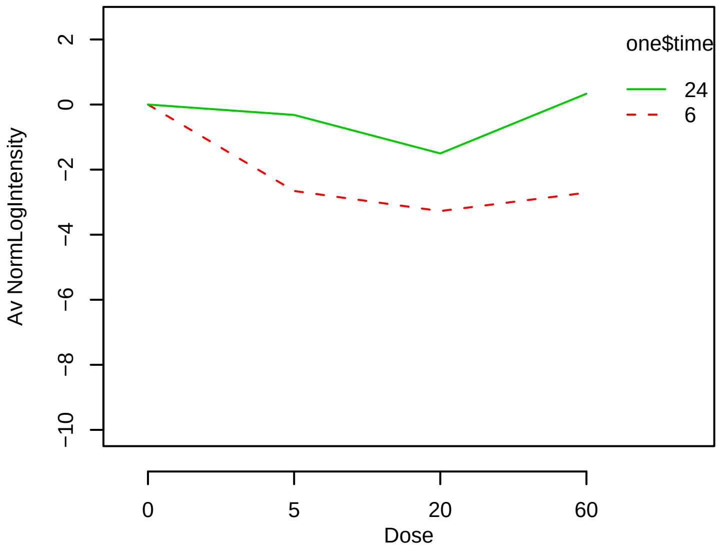


GO_0050679 : positive regulation of epithelial cell prolifera

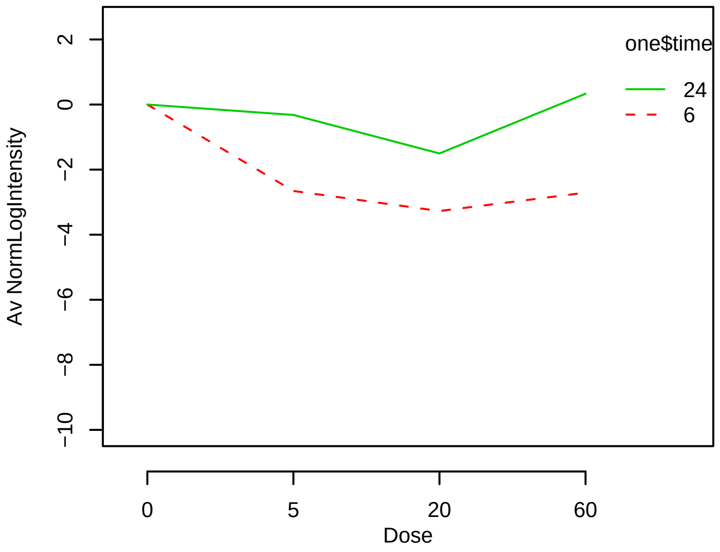


GO_0050684 : regulation of mRNA processing

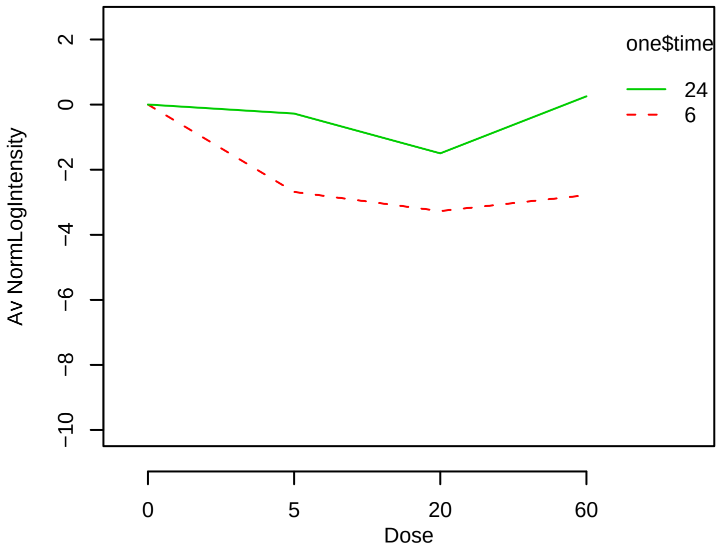
GO_0050701 : interleukin−1 secretion



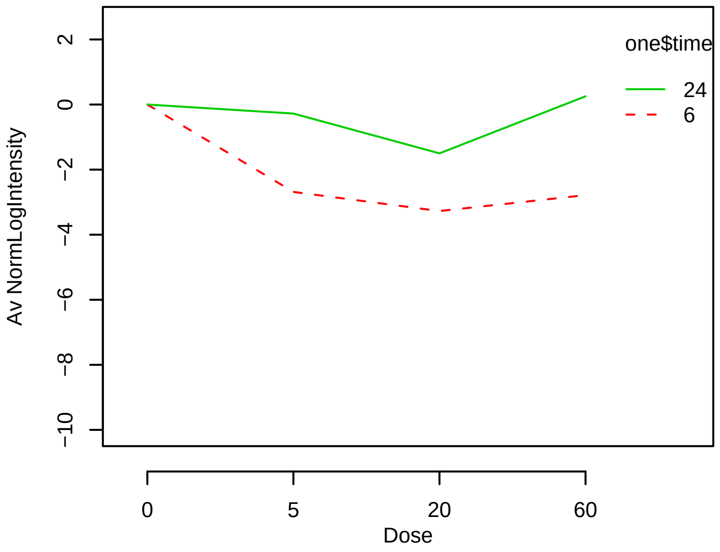
GO_0050702 : interleukin−1 beta secretion



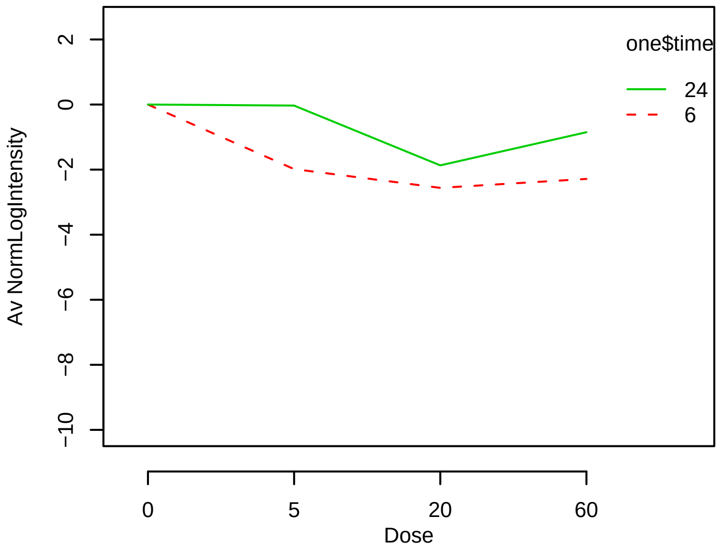
GO_0050704 : regulation of interleukin−1 secretion



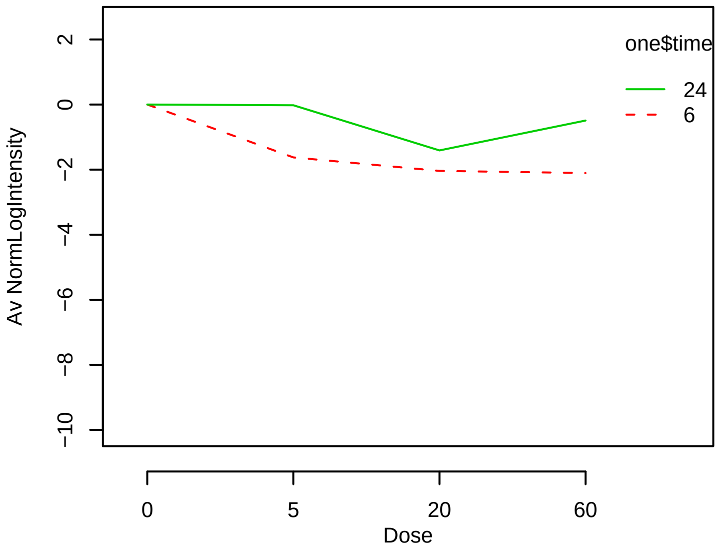
GO_0050706 : regulation of interleukin−1 beta secretion

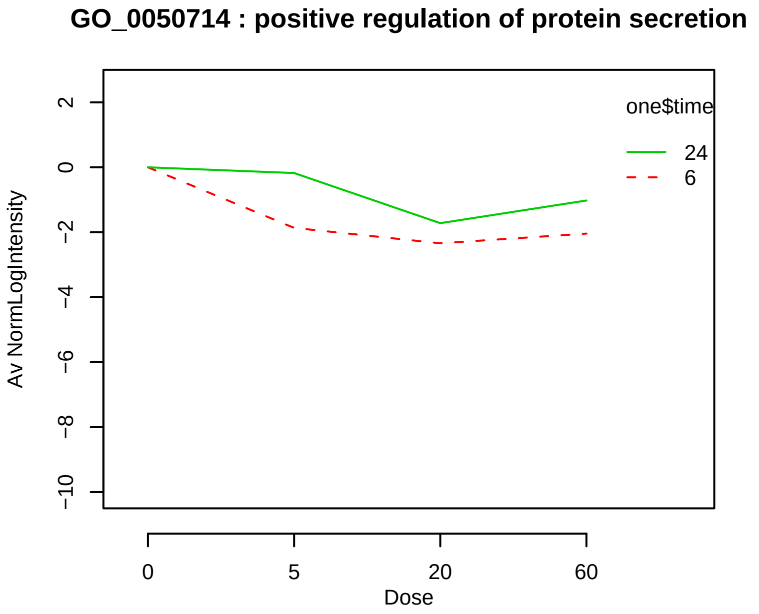


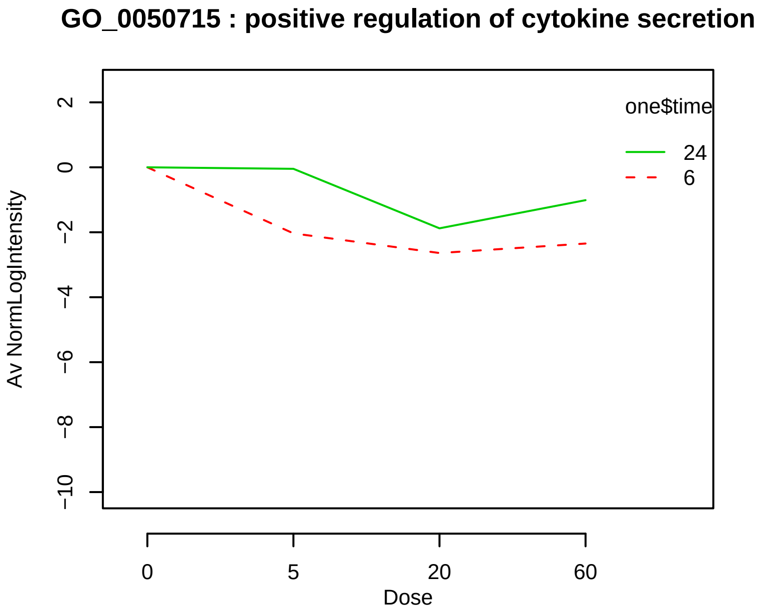
GO_0050707 : regulation of cytokine secretion

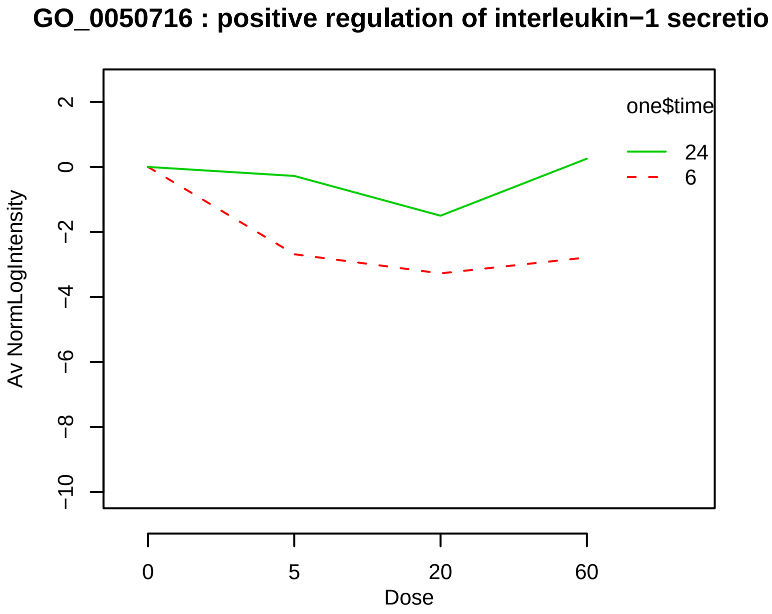


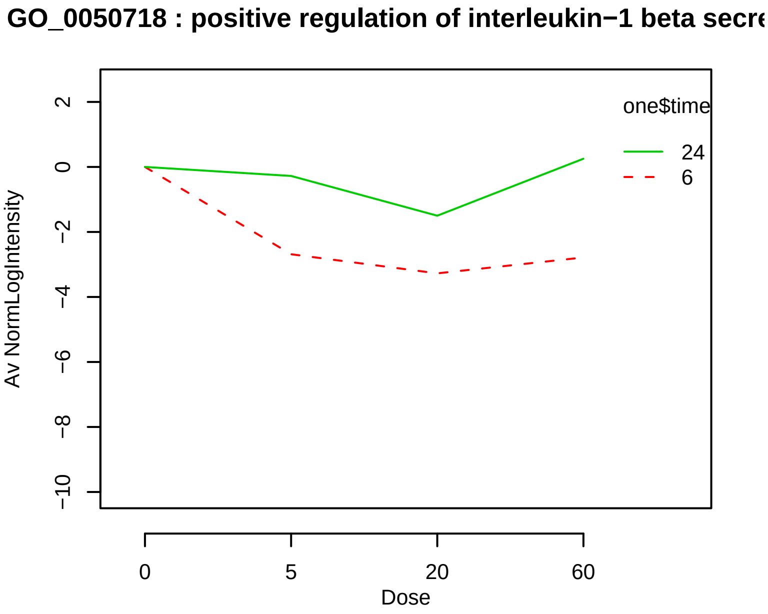
GO_0050708 : regulation of protein secretion

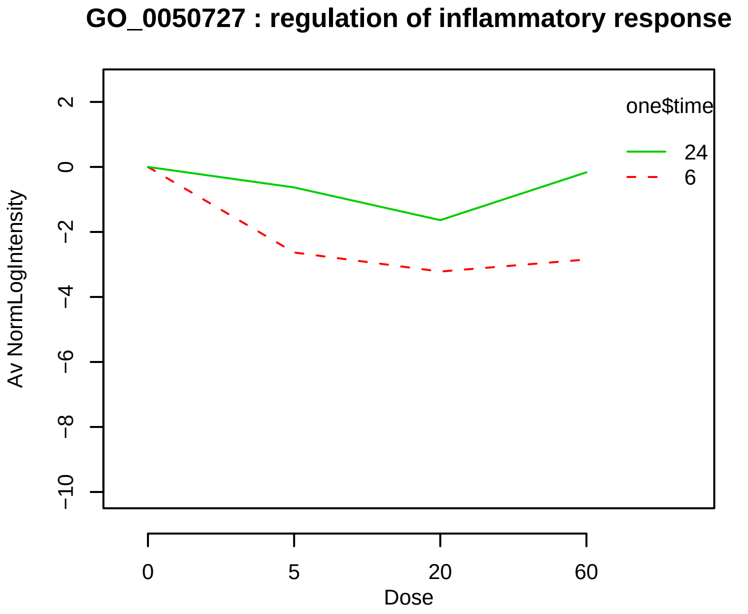


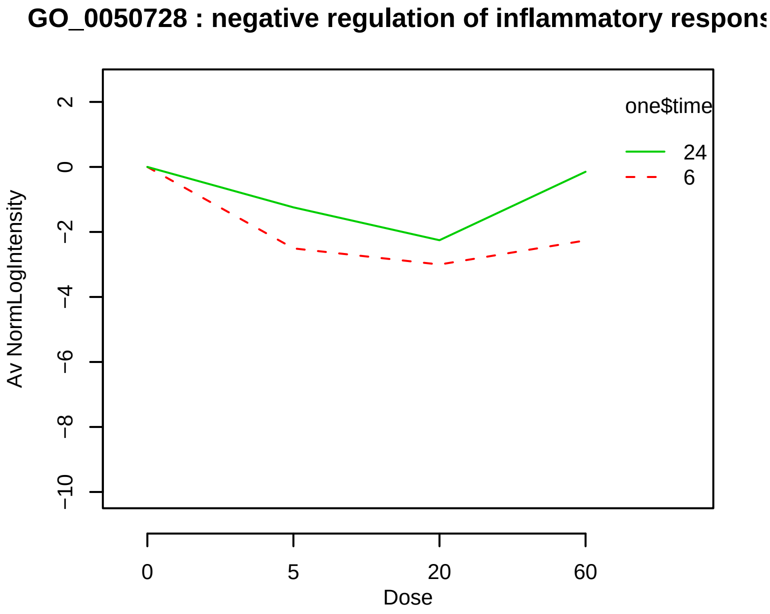

GO_0050714 : positive regulation of protein secretion


GO_0050715 : positive regulation of cytokine secretion

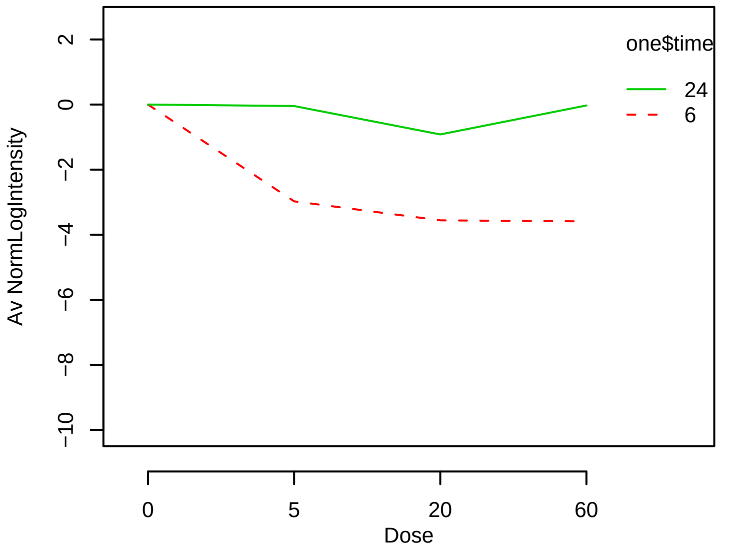

GO_0050716 : positive regulation of interleukin−1 secretio


GO_0050718 : positive regulation of interleukin−1 beta secre

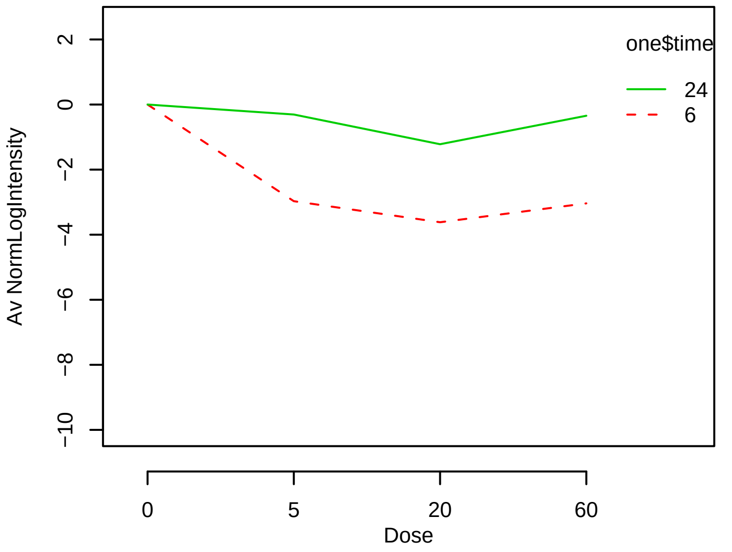

GO_0050727 : regulation of inflammatory response


GO_0050728 : negative regulation of inflammatory respons

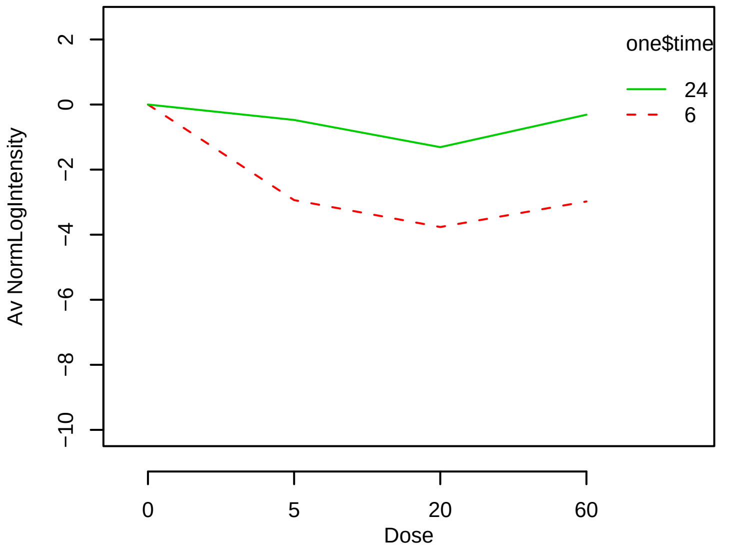
GO_0050729 : positive regulation of inflammatory respons



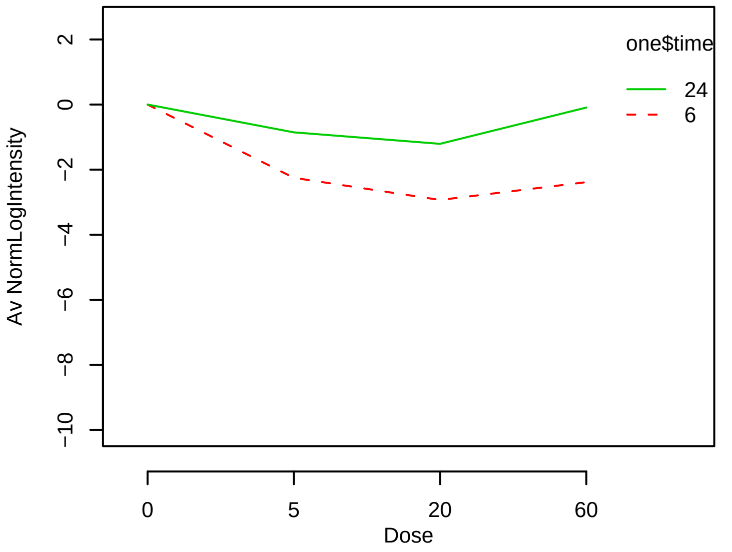
GO_0050730 : regulation of peptidyl−tyrosine phosphorylati



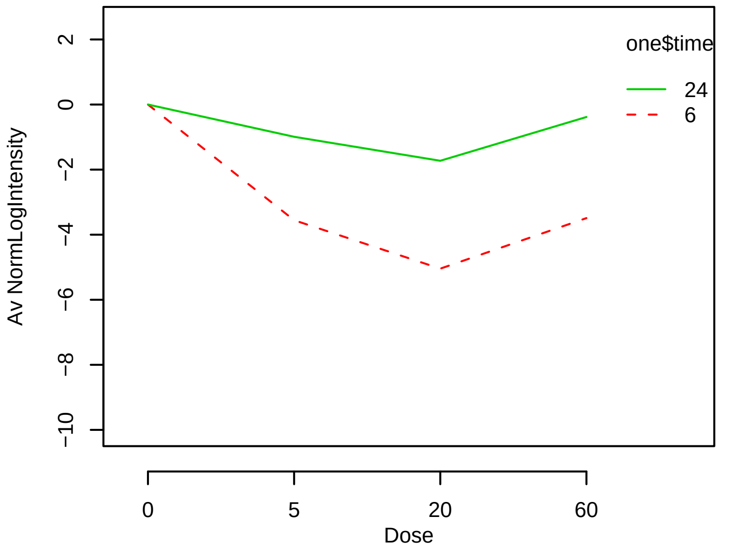
GO_0050731 : positive regulation of peptidyl−tyrosine phospl



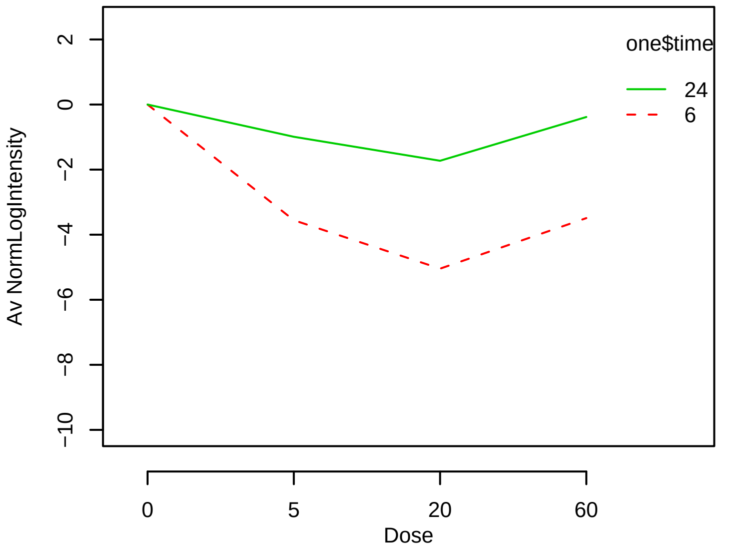
GO_0050755 : chemokine metabolism

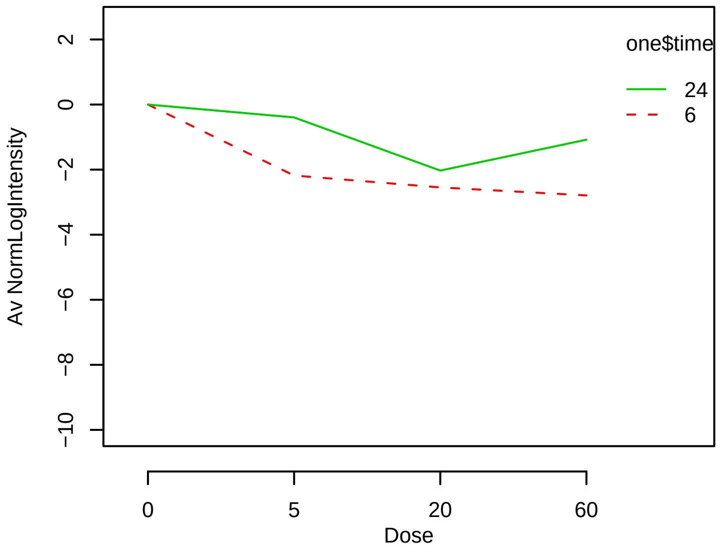


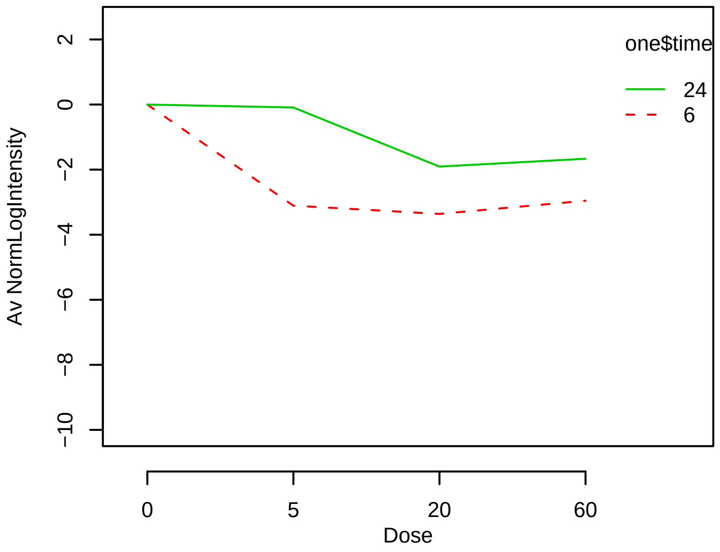
GO_0050764 : regulation of phagocytosis

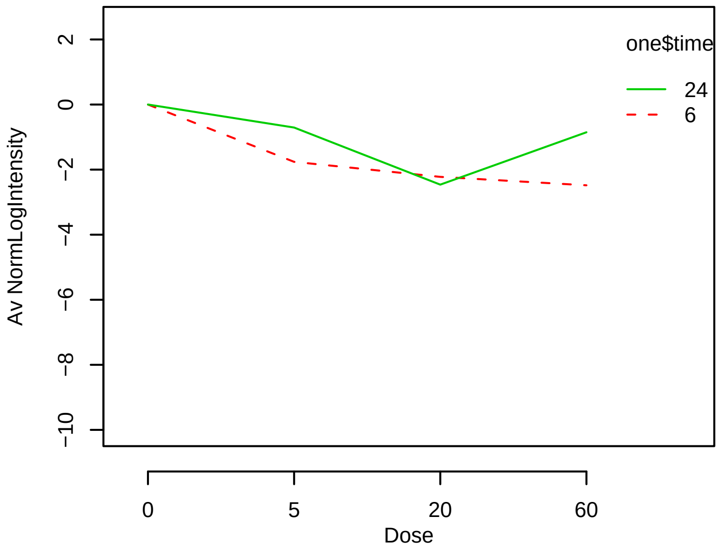


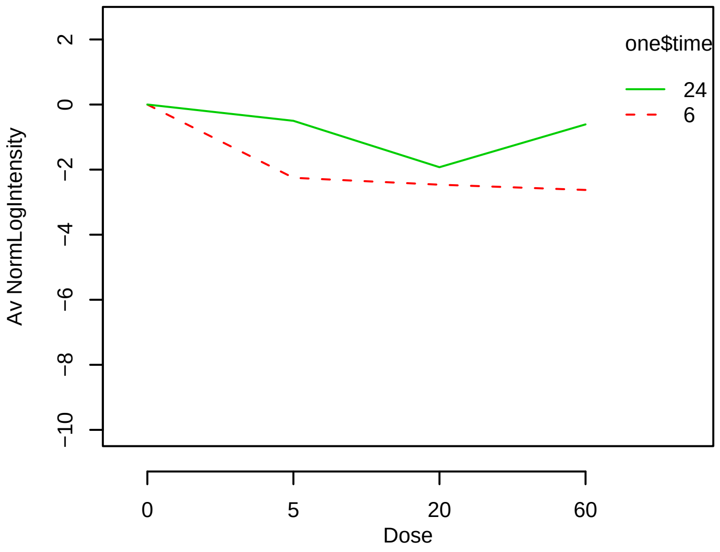
GO_0050766 : positive regulation of phagocytosis

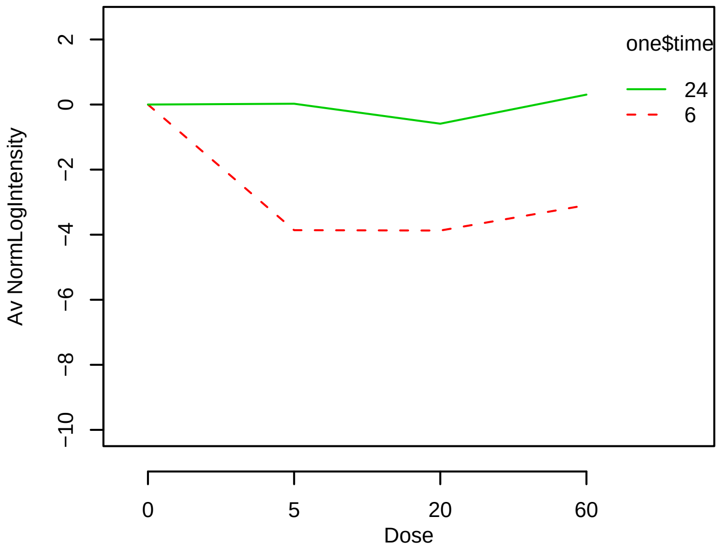


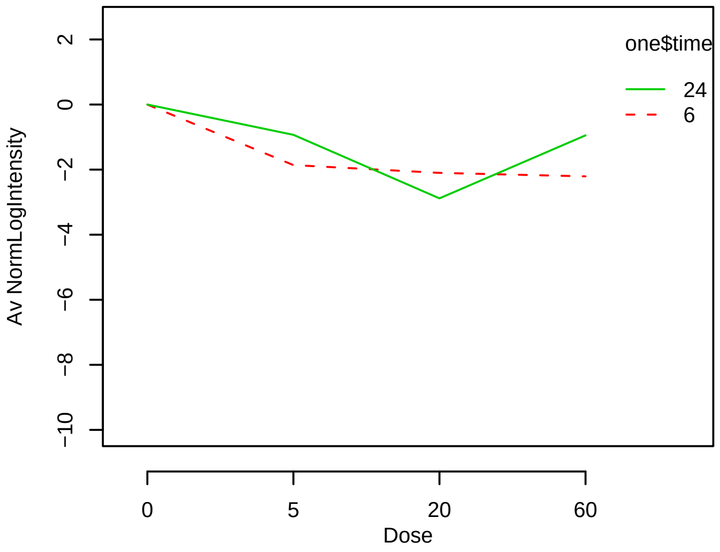

GO_0050767 : regulation of neurogenesis

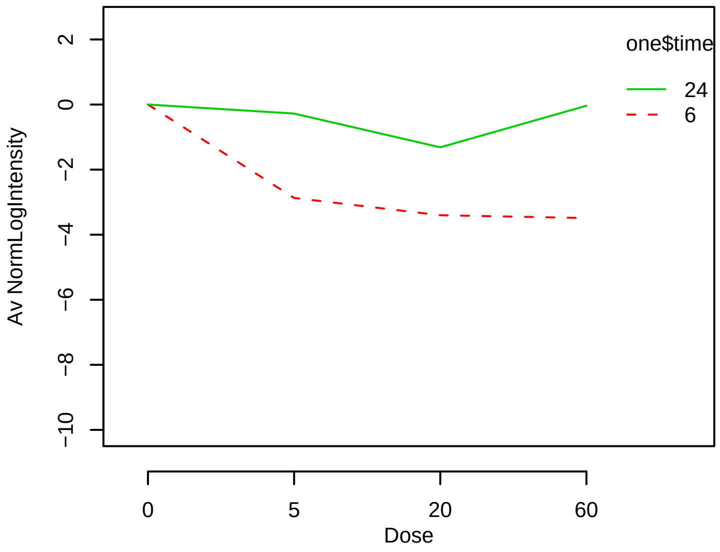

GO_0050768 : negative regulation of neurogenesis

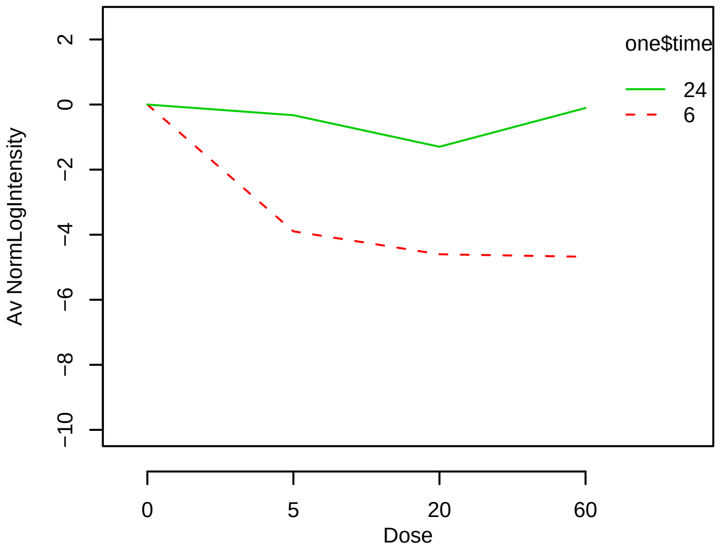

GO_0050769 : positive regulation of neurogenesis

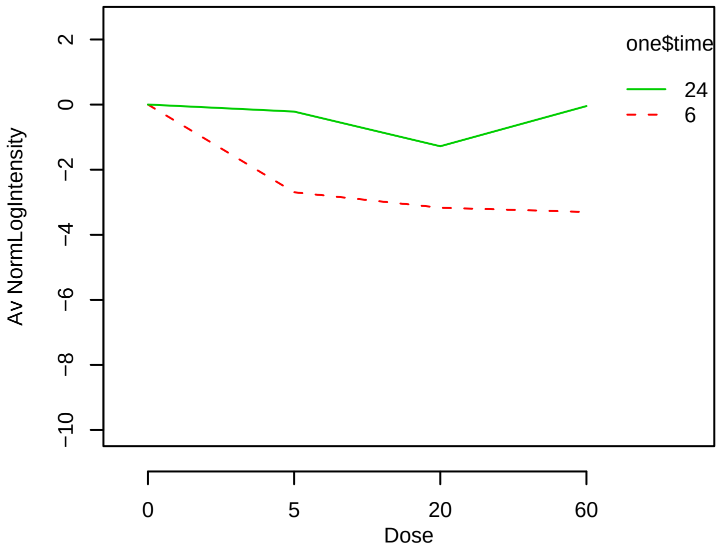

GO_0050770 : regulation of axonogenesis

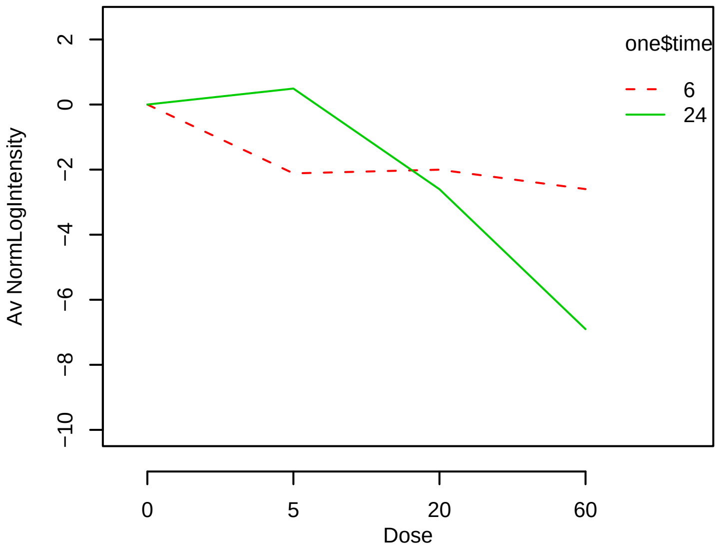

GO_0050771 : negative regulation of axonogenesis

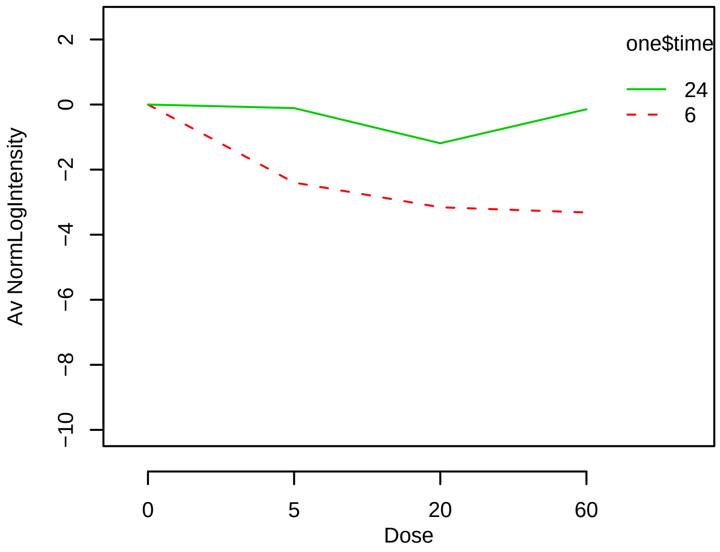

GO_0050772 : positive regulation of axonogenesis

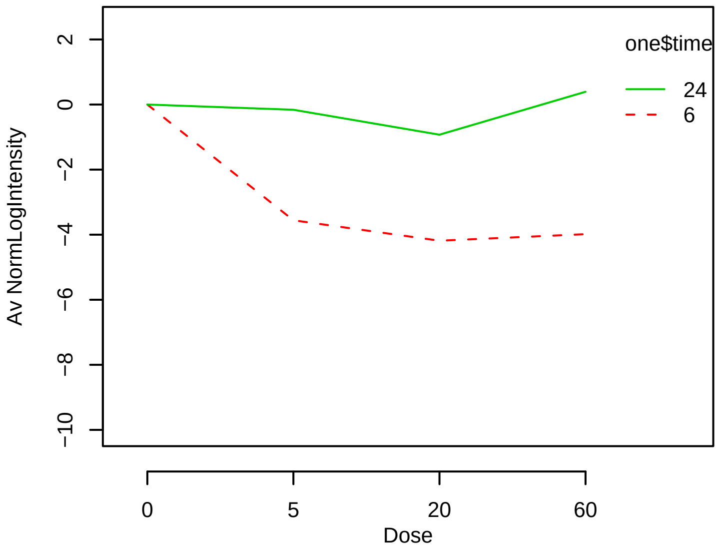

GO_0050776 : regulation of immune response


GO_0050777 : negative regulation of immune response

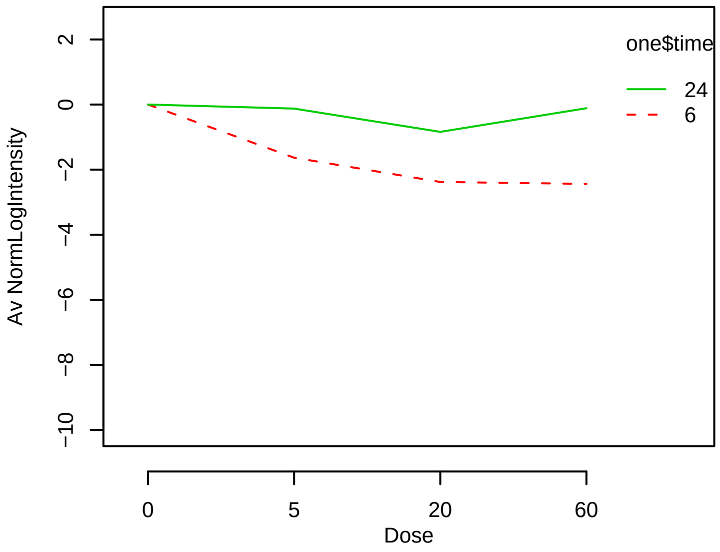

GO_0050778 : positive regulation of immune response


GO_0050792 : regulation of viral life cycle

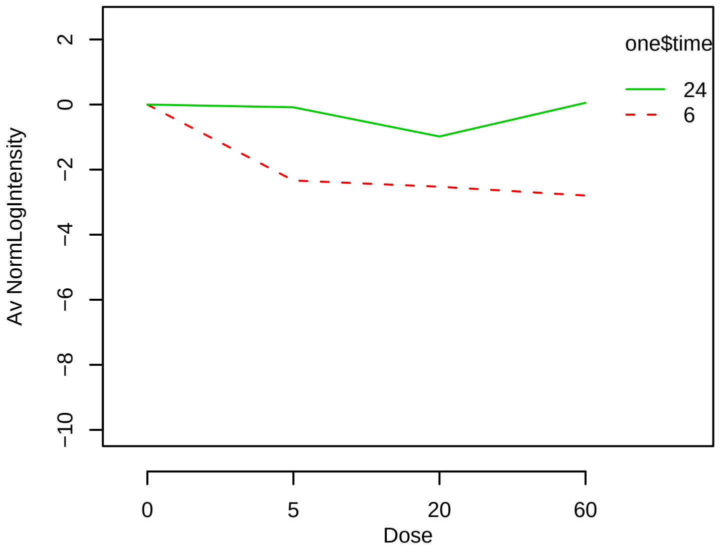

GO_0050793 : regulation of development


GO_0050796 : regulation of insulin secretion

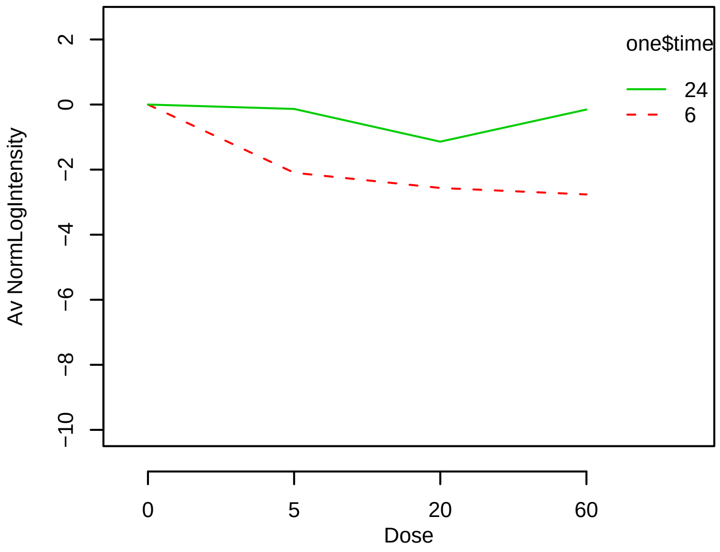
GO_0050798 : activated T cell proliferation



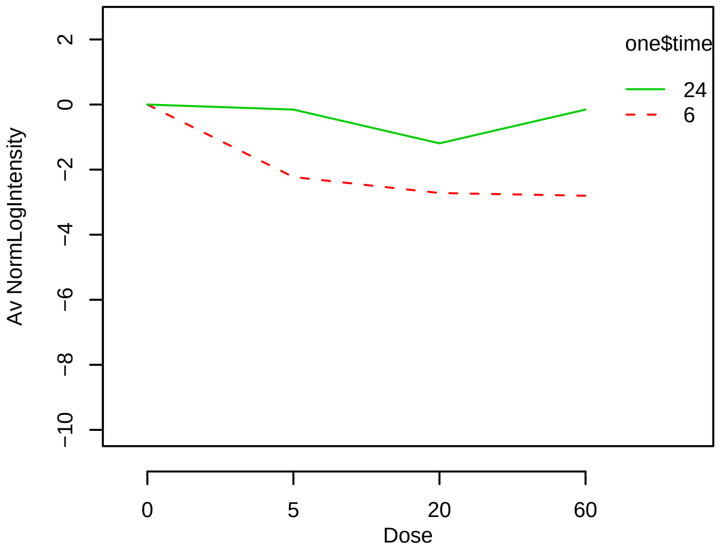
GO_0050801 : ion homeostasis



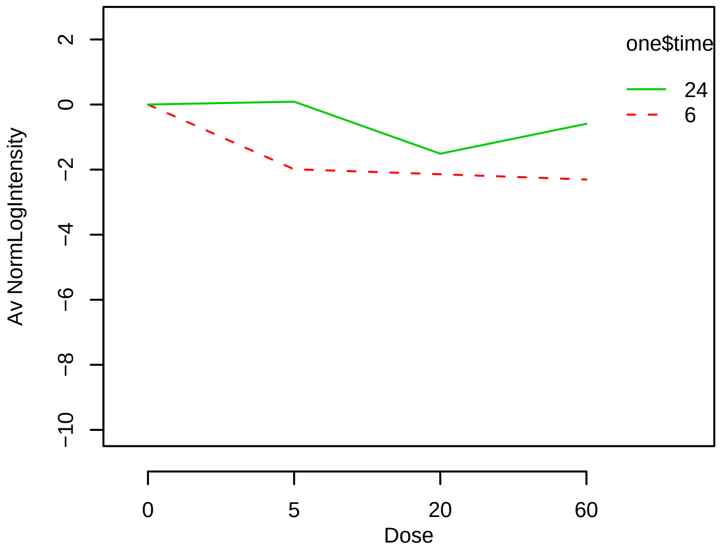
GO_0050803 : regulation of synapse structure and functio



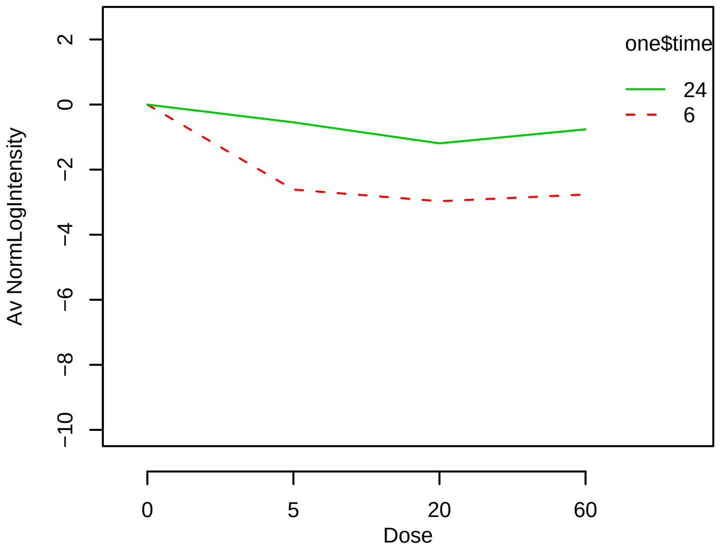
GO_0050804 : regulation of synaptic transmission

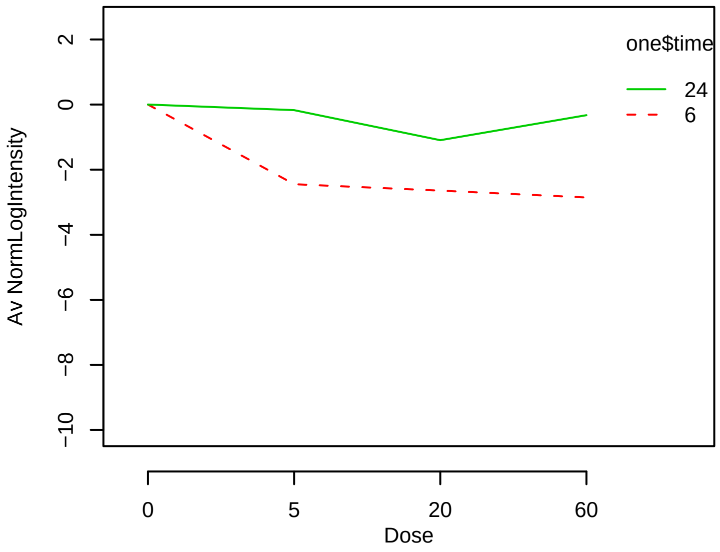


GO_0050808 : synapse organization and biogenesis

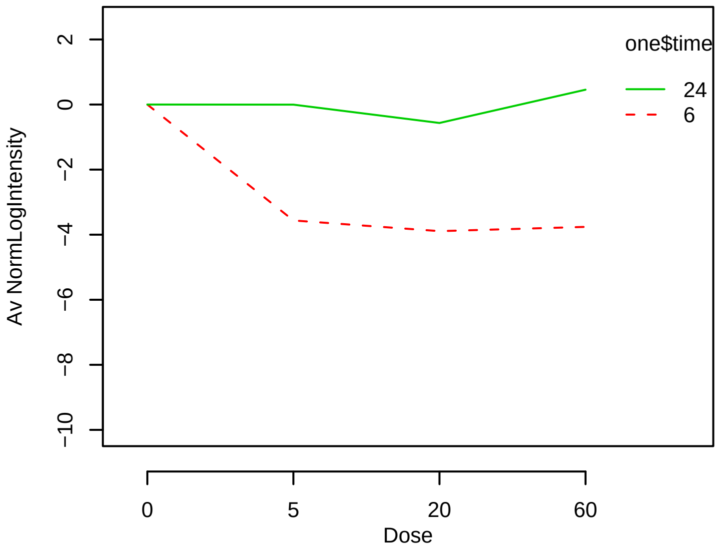


GO_0050810 : regulation of steroid biosynthesis

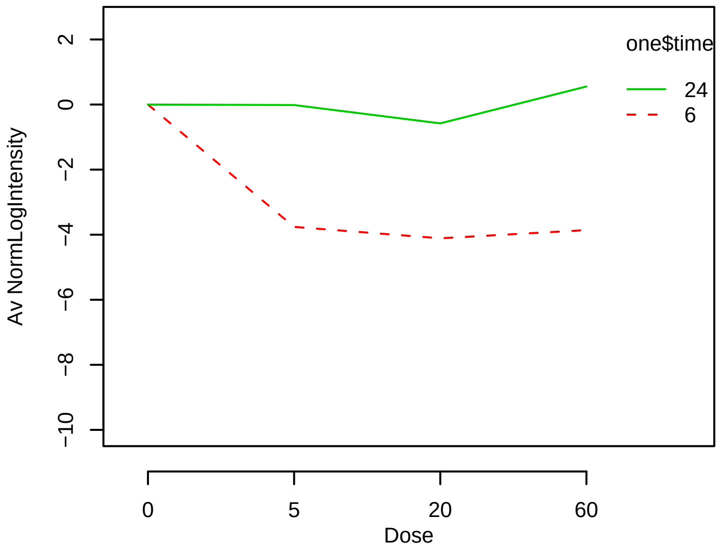




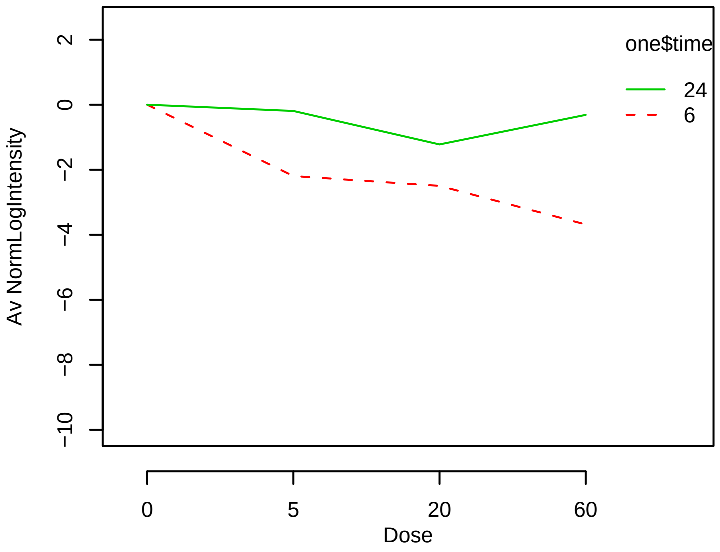
GO_0050817 : coagulation



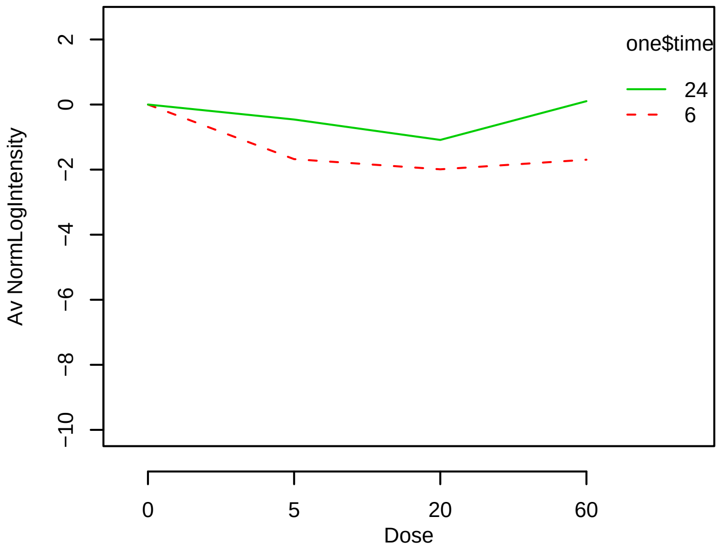
GO_0050818 : regulation of coagulation



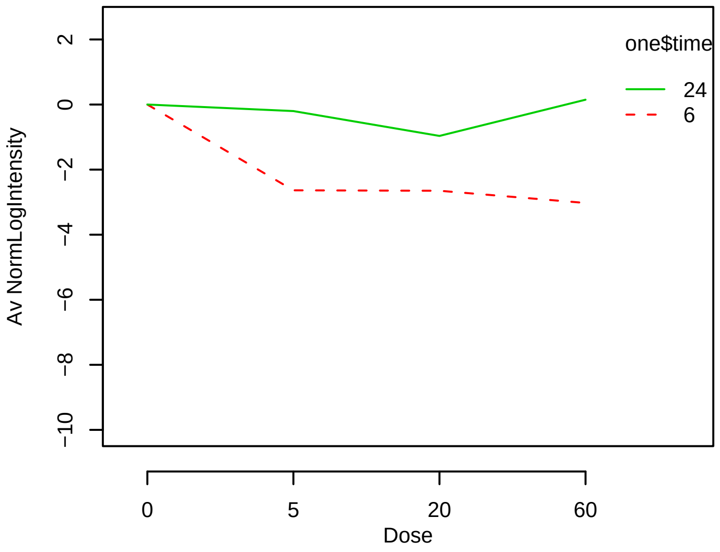
GO_0050819 : negative regulation of coagulation



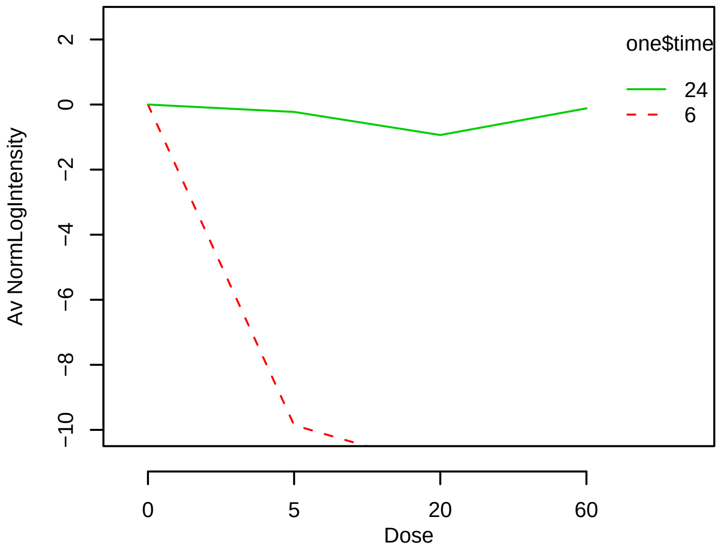
GO_0050821 : protein stabilization



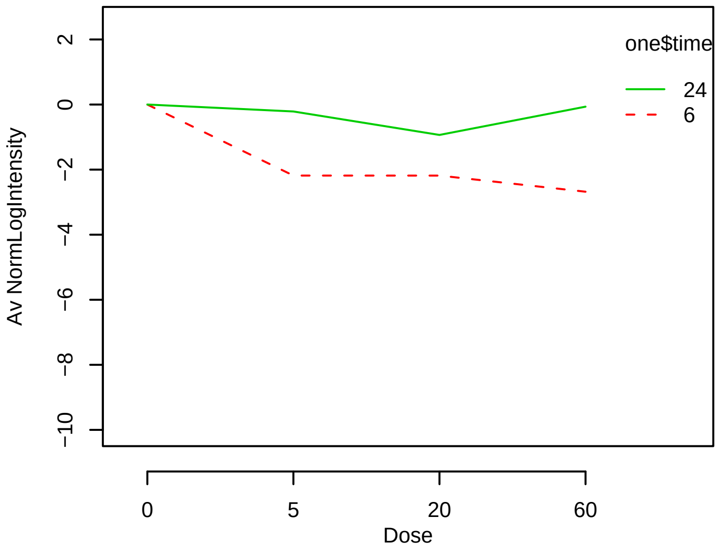
GO_0050830 : defense response to Gram−positive bacteriu



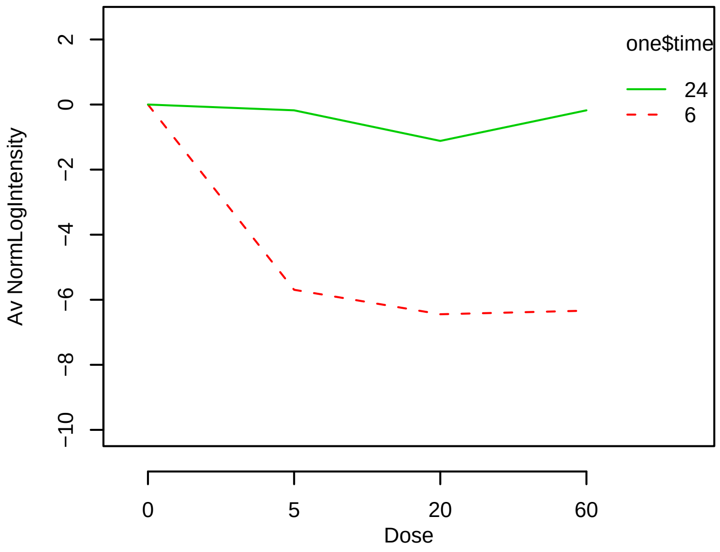
GO_0050832 : defense response to fungus



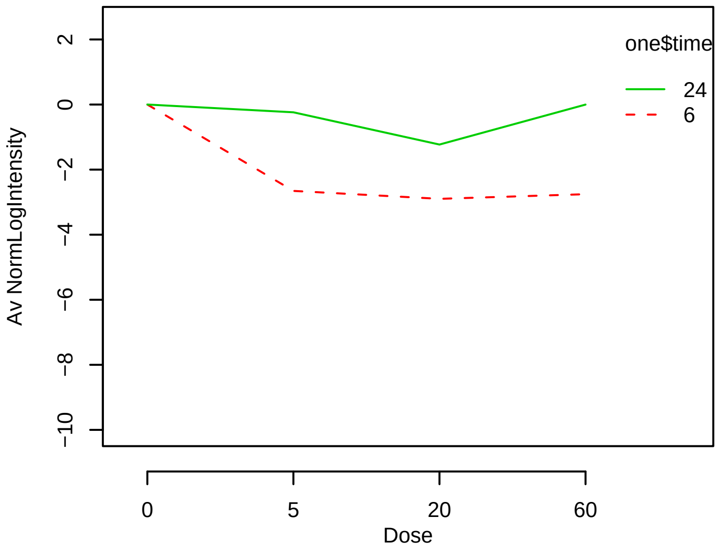
GO_0050848 : regulation of calcium−mediated signaling



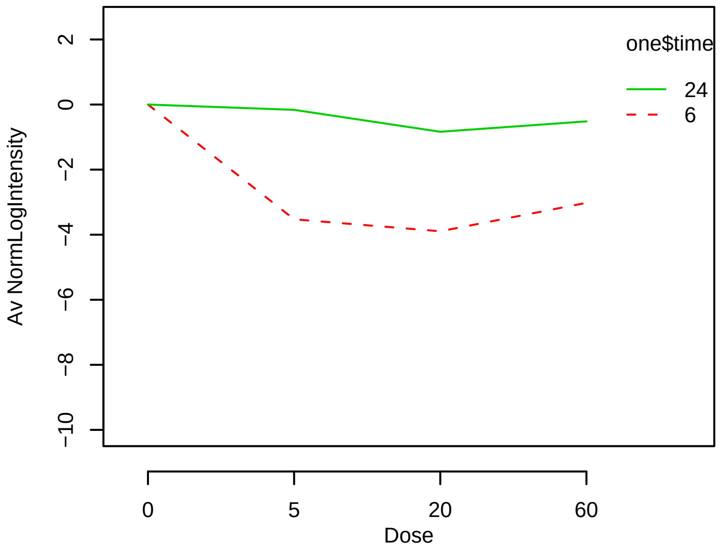
GO_0050850 : positive regulation of calcium−mediated signa



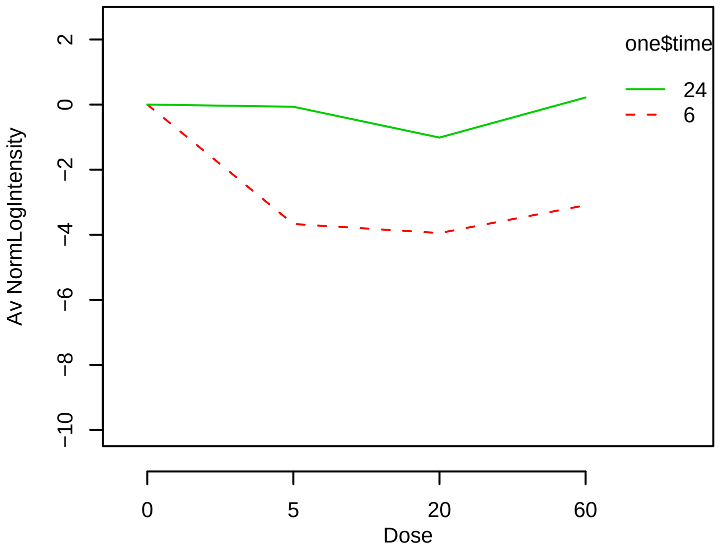
GO_0050851 : antigen receptor−mediated signaling pathwa



GO_0050852 : T cell receptor signaling pathway

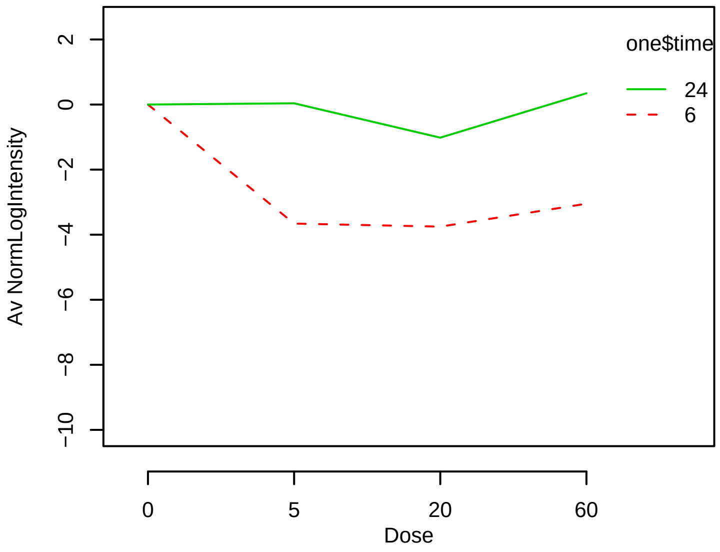


GO_0050853 : B cell receptor signaling pathway

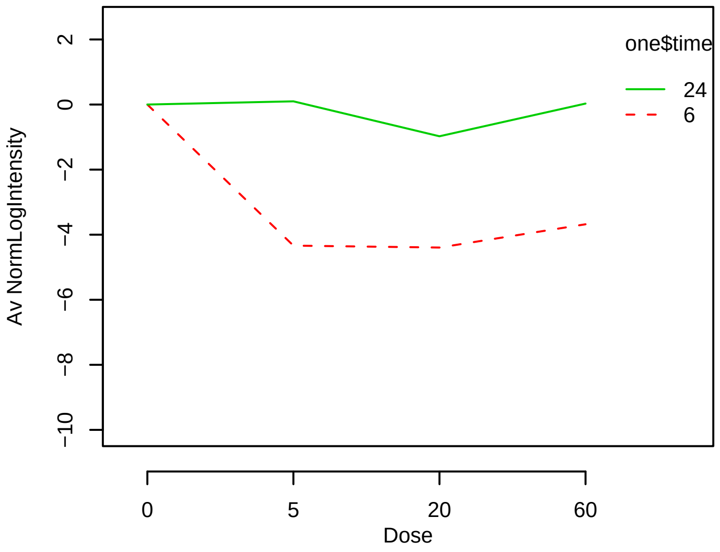


GO_0050854 : regulation of antigen receptor−mediated signa

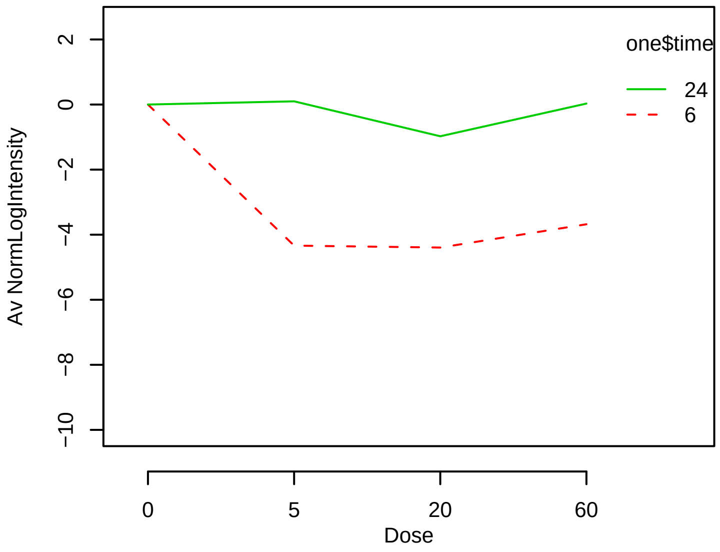
GO_0050856 : regulation of T cell receptor signaling pathw



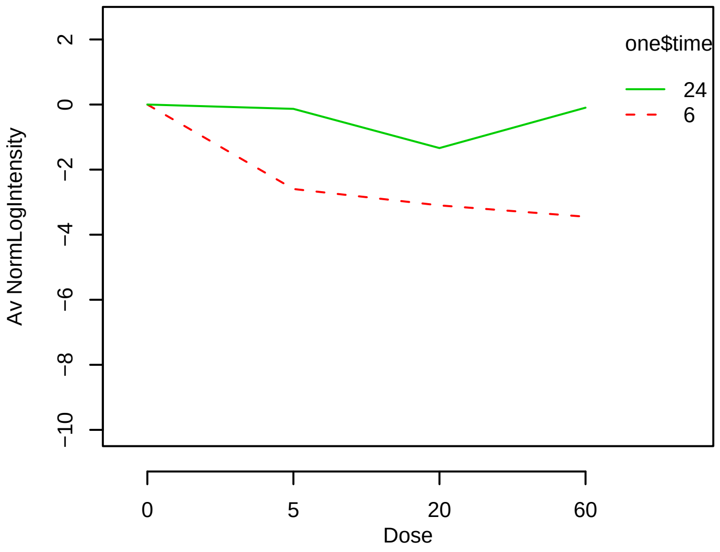
GO_0050858 : negative regulation of antigen receptor−mediat



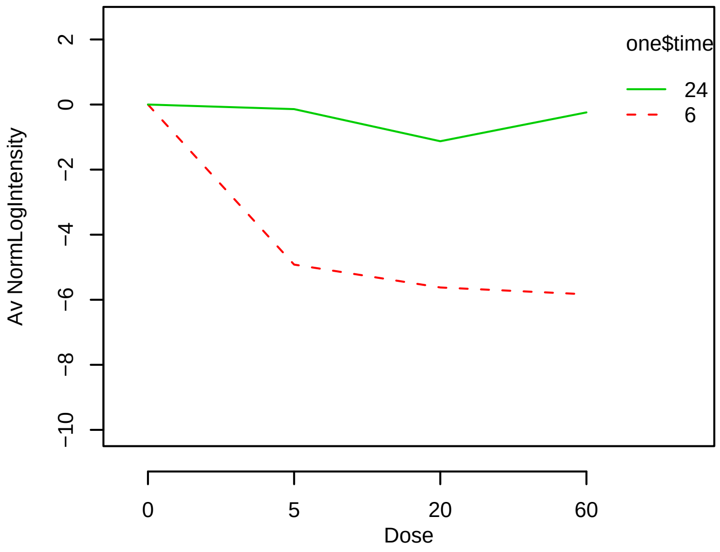
GO_0050860 : negative regulation of T cell receptor signalin



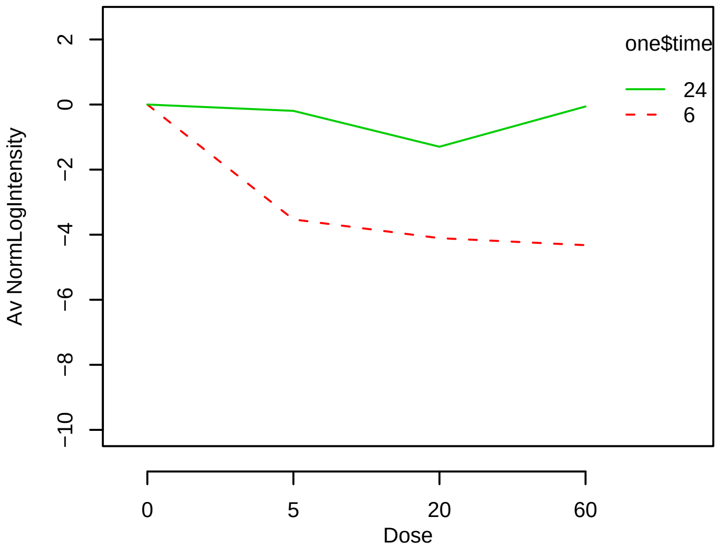
GO_0050863 : regulation of T cell activation



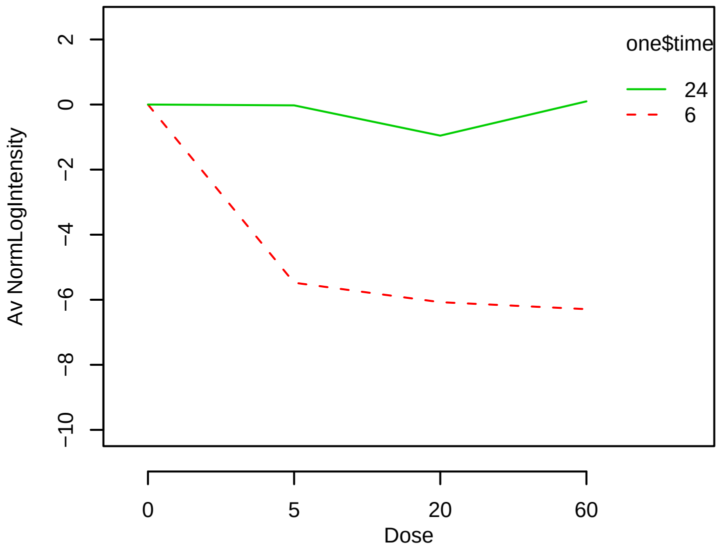
GO_0050864 : regulation of B cell activation



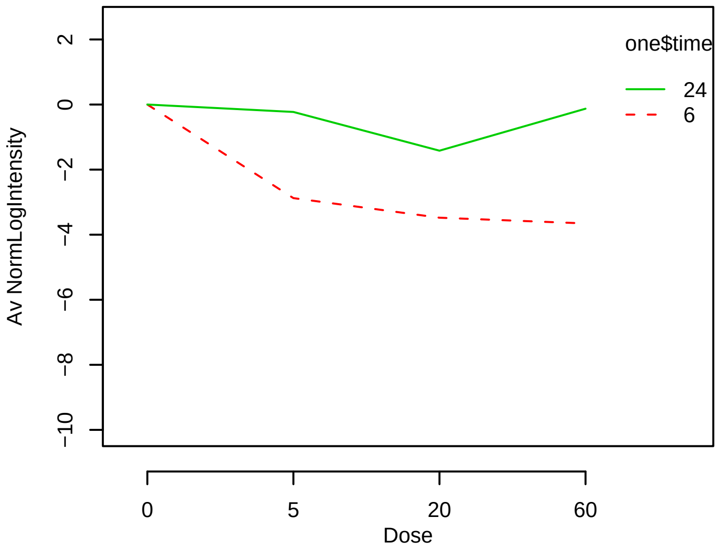
GO_0050865 : regulation of cell activation



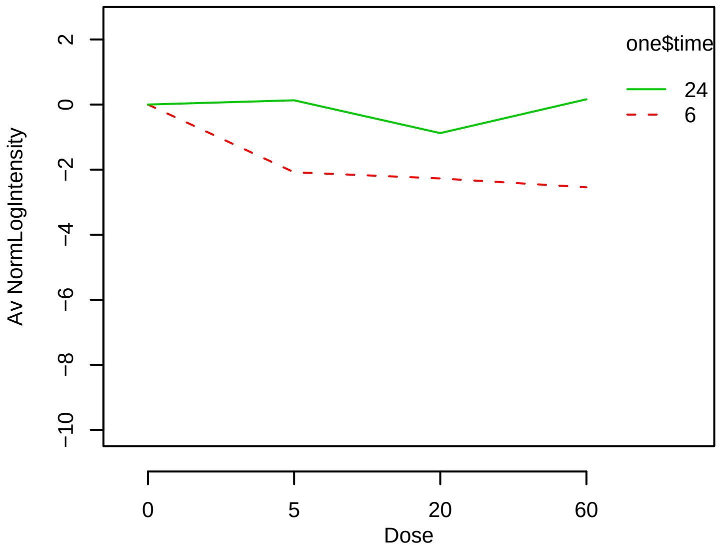
GO_0050866 : negative regulation of cell activation



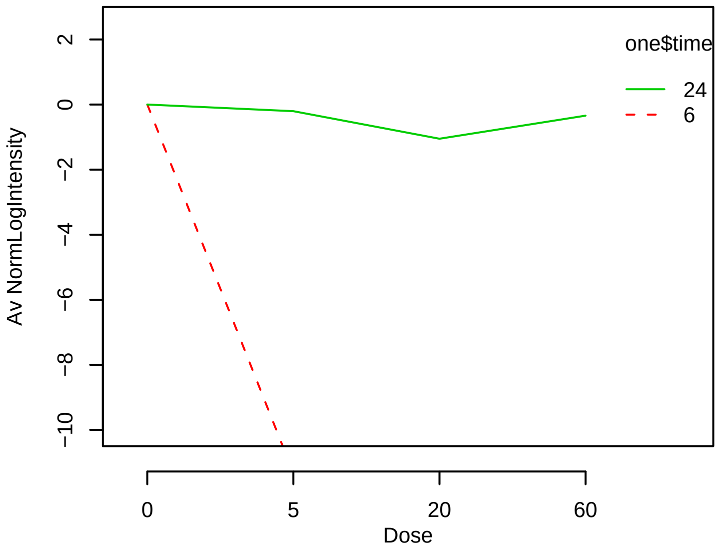
GO_0050867 : positive regulation of cell activation



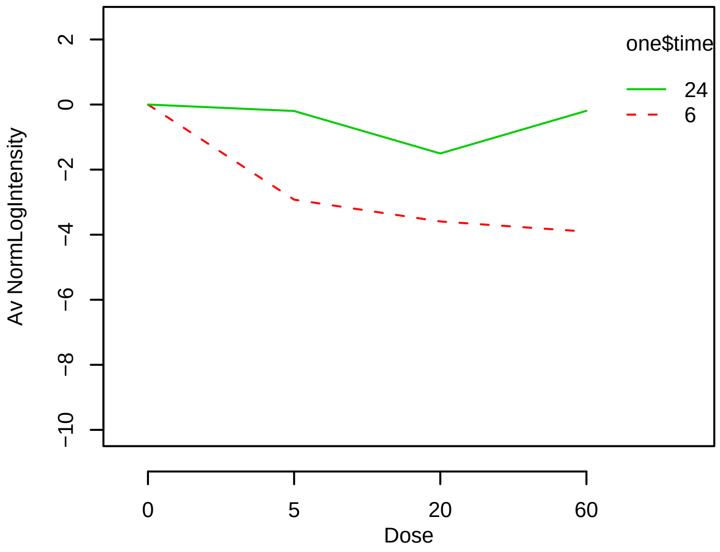
GO_0050868 : negative regulation of T cell activation



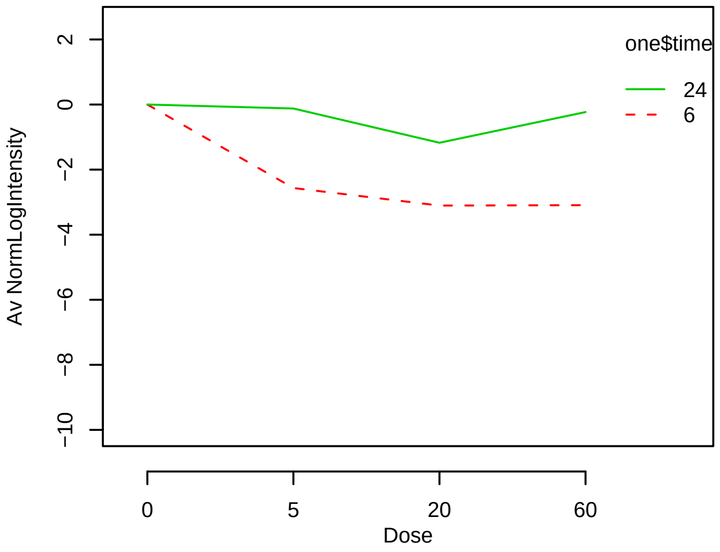
GO_0050869 : negative regulation of B cell activation



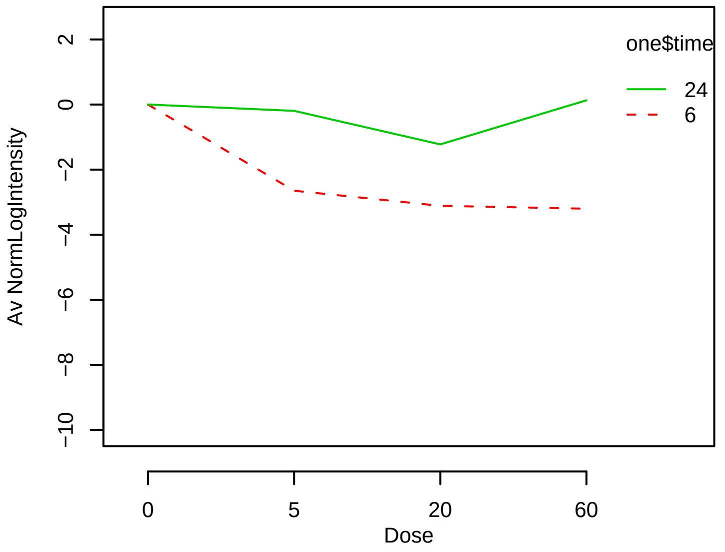
GO_0050870 : positive regulation of T cell activation



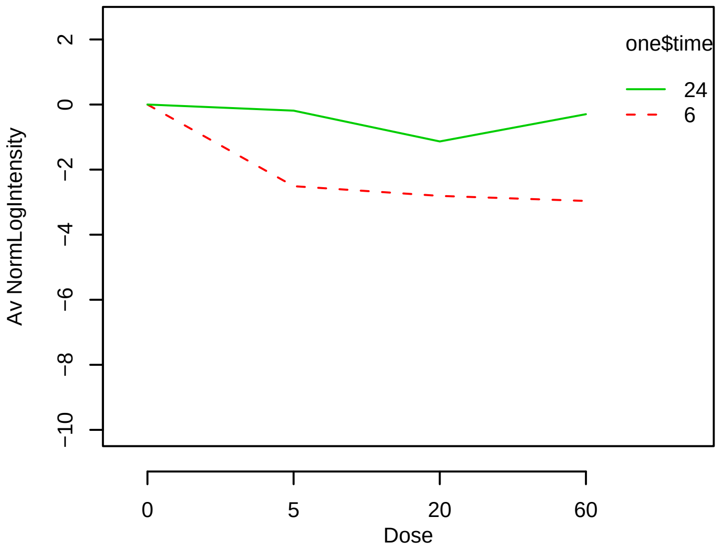
GO_0050871 : positive regulation of B cell activation



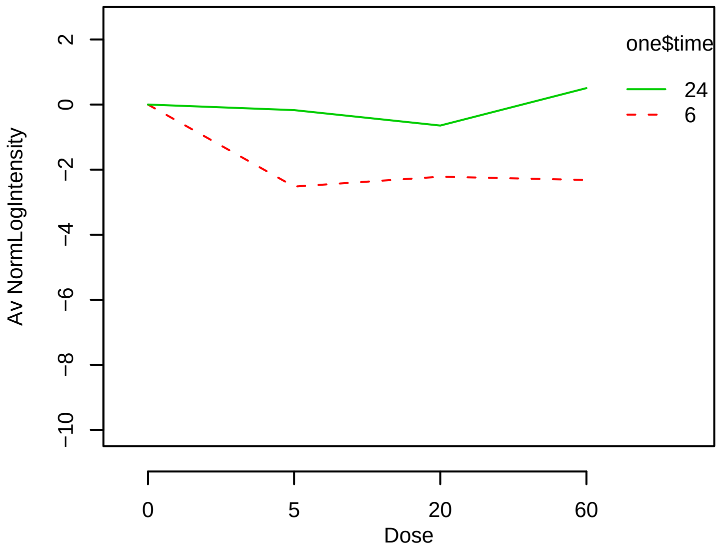
GO_0050876 : reproductive physiological process



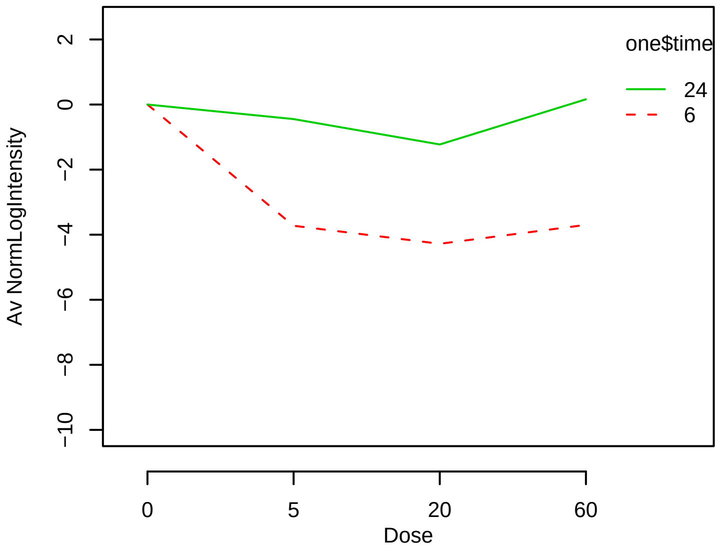
GO_0050878 : regulation of body fluids



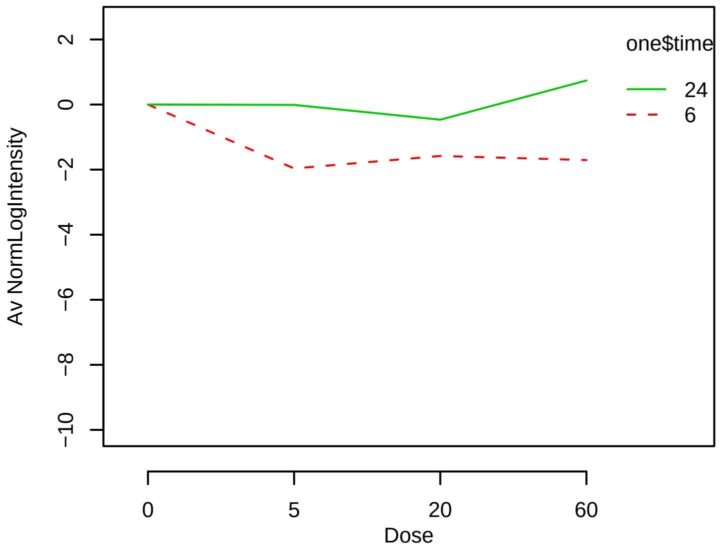
GO_0050879 : organismal movement



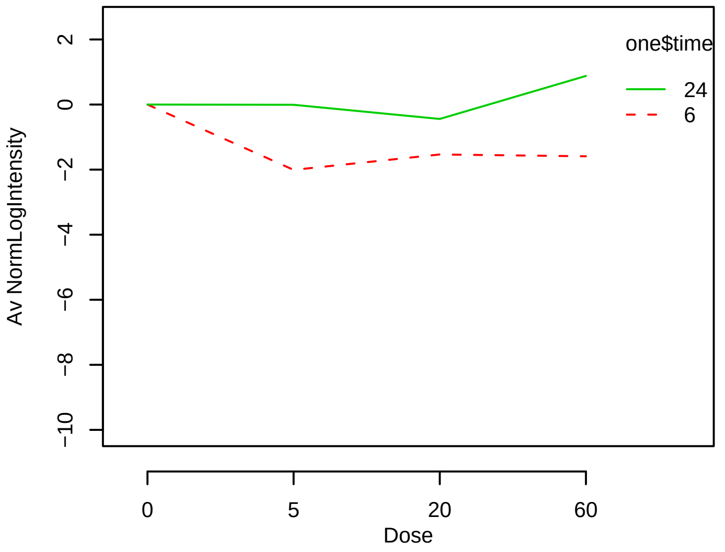
GO_0050880 : regulation of blood vessel size

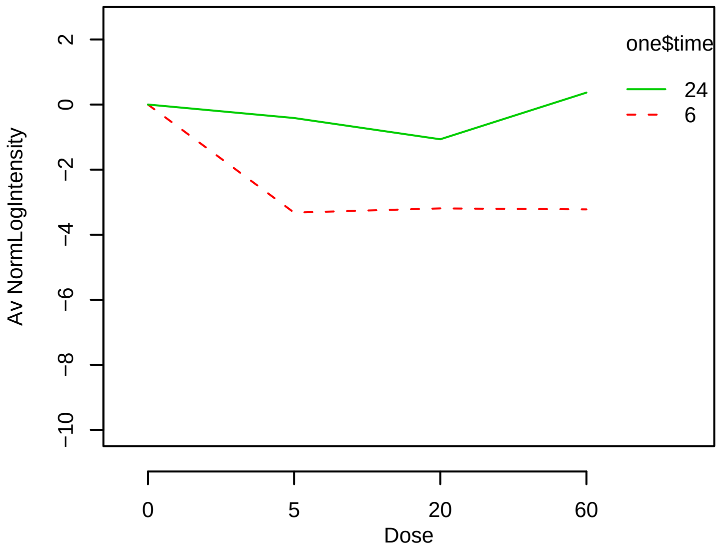


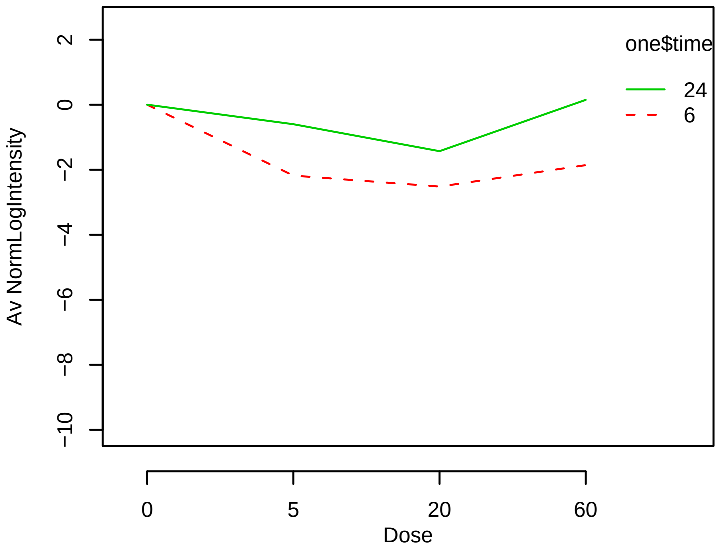
GO_0050881 : musculoskeletal movement

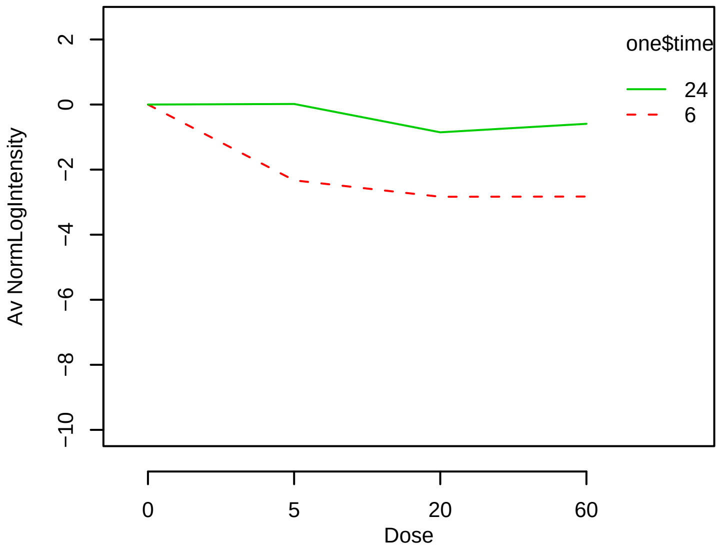


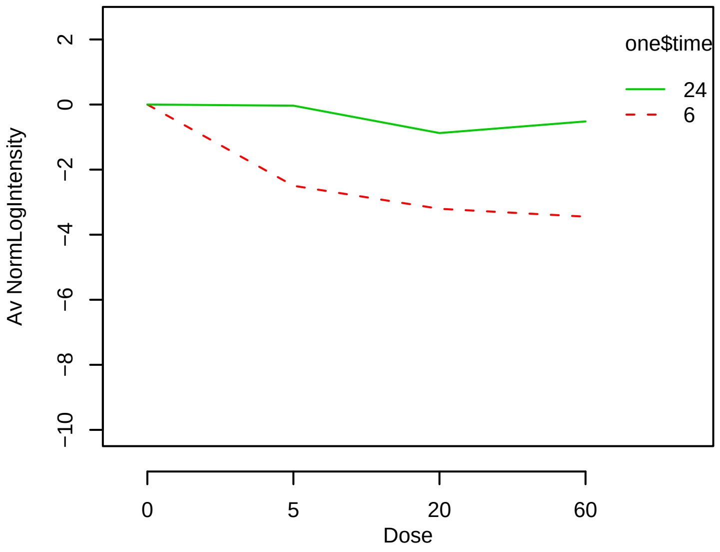
GO_0050885 : regulation of balance

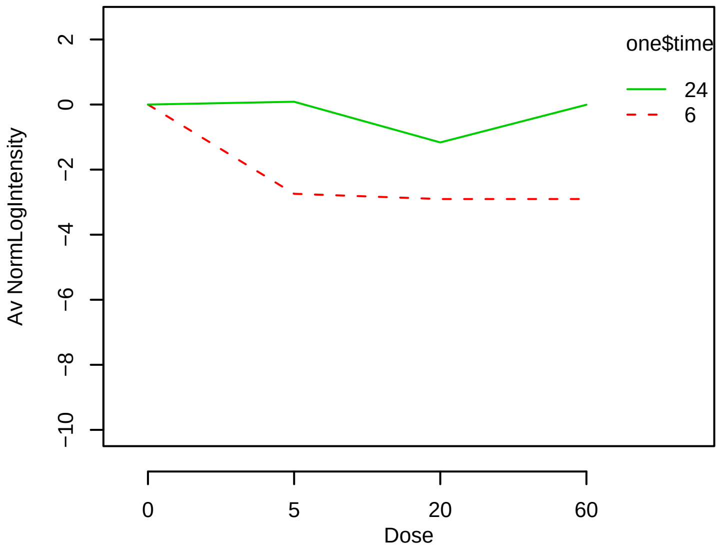


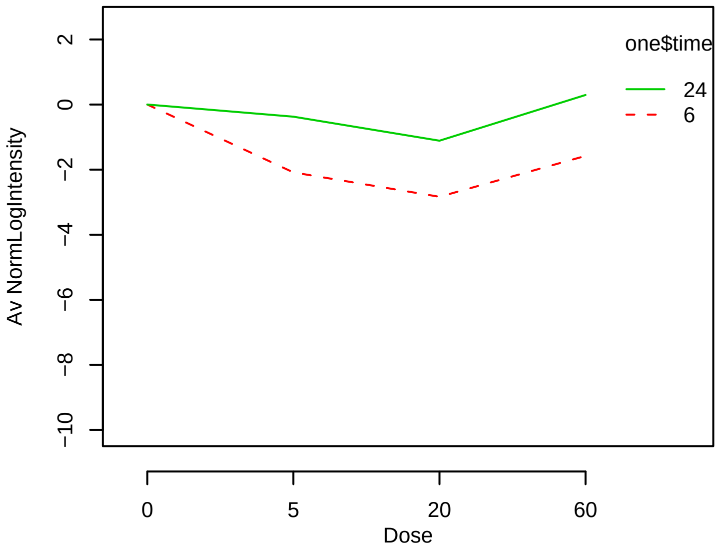

GO_0050886 : endocrine physiological process

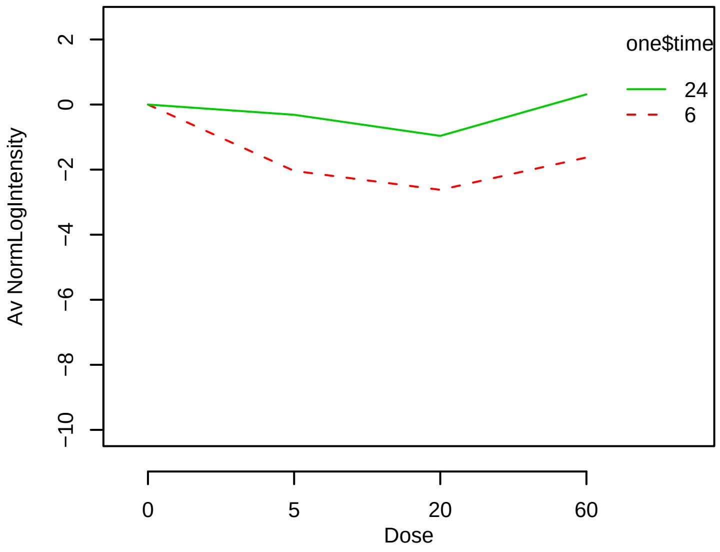

GO_0050892 : intestinal absorption

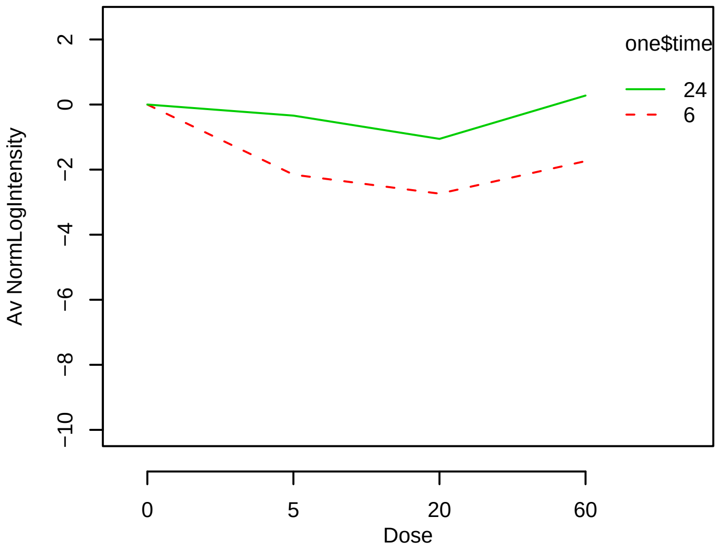

GO_0050900 : leukocyte migration

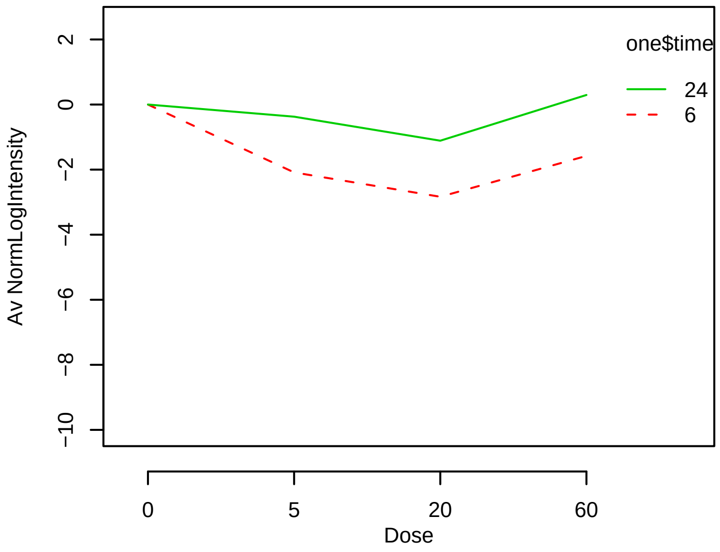

GO_0050906 : detection of stimulus during sensory percept

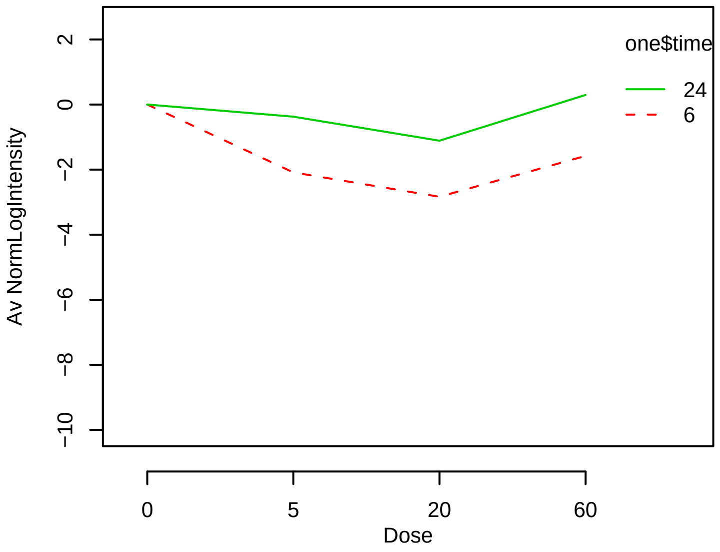

GO_0050909 : sensory perception of taste

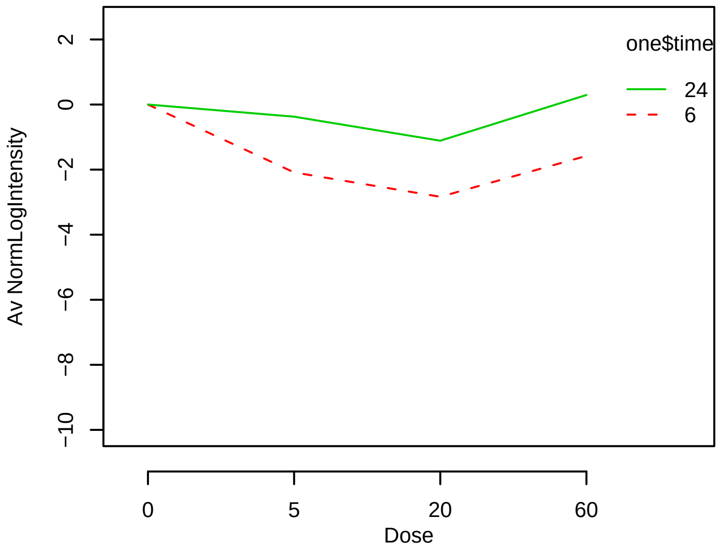

GO_0050918 : positive chemotaxis

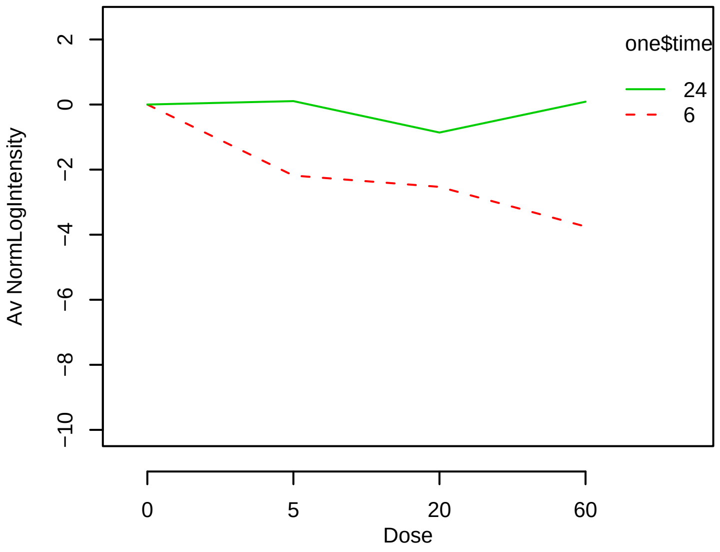

GO_0050920 : regulation of chemotaxis


GO_0050921 : positive regulation of chemotaxis

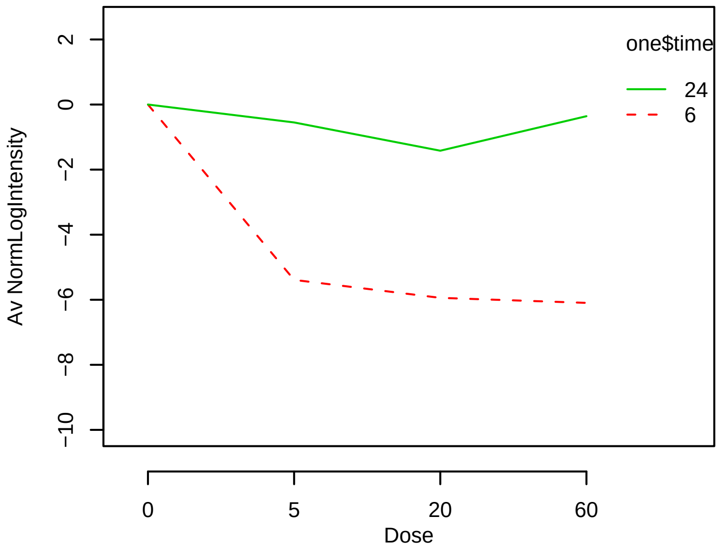

GO_0050926 : regulation of positive chemotaxis


GO_0050927 : positive regulation of positive chemotaxis

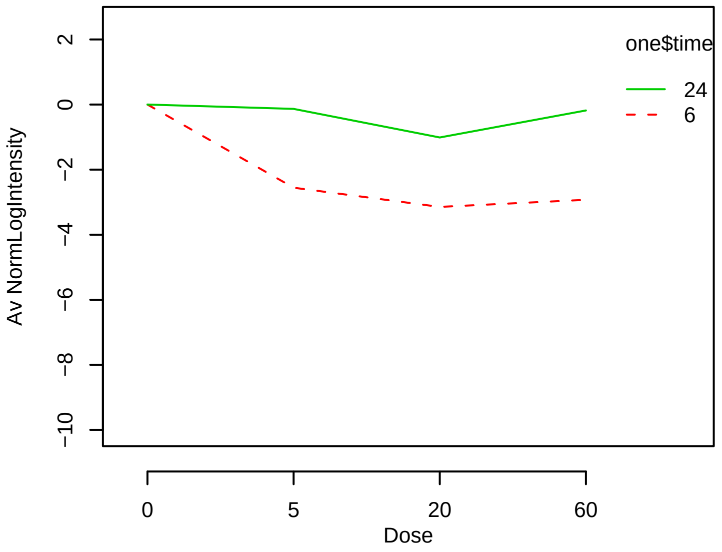

GO_0050930 : induction of positive chemotaxis


GO_0050931 : pigment cell differentiation

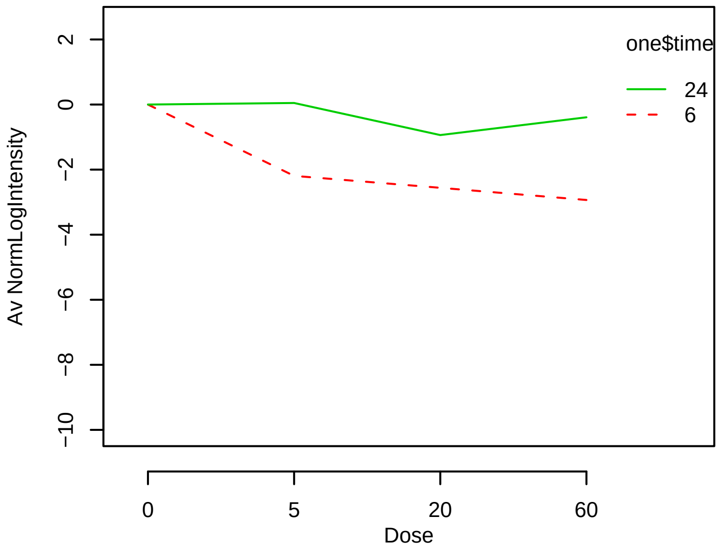
GO_0050951 : sensory perception of temperature stimulu



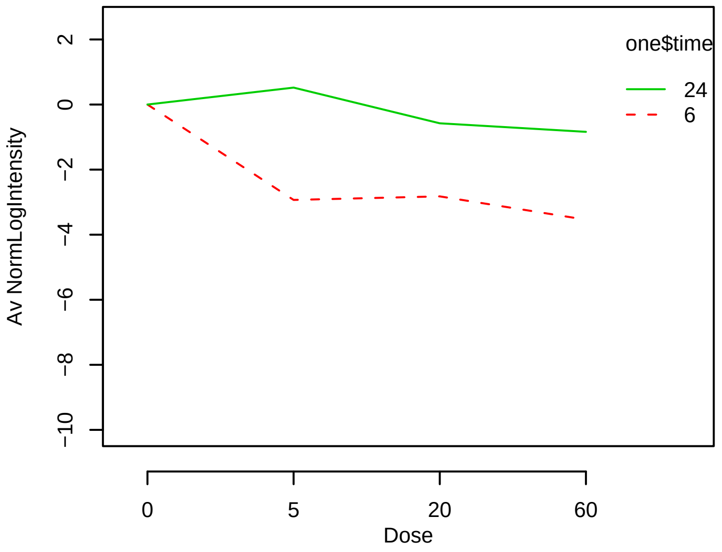
GO_0050953 : sensory perception of light stimulus



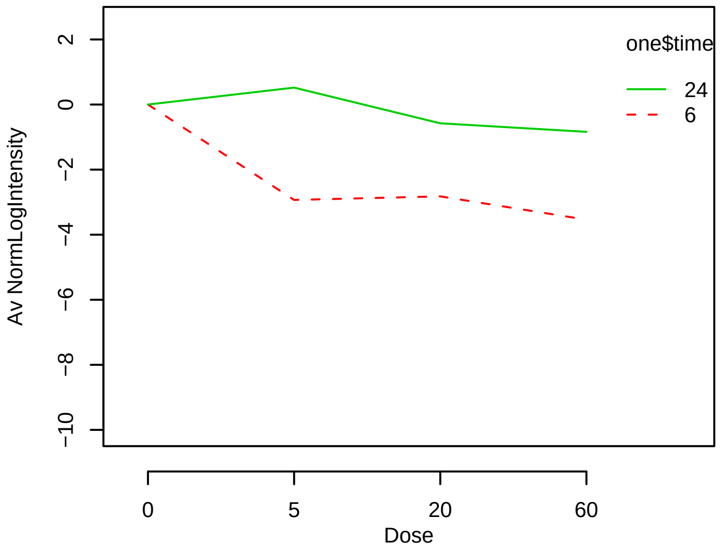
GO_0050954 : sensory perception of mechanical stimulus



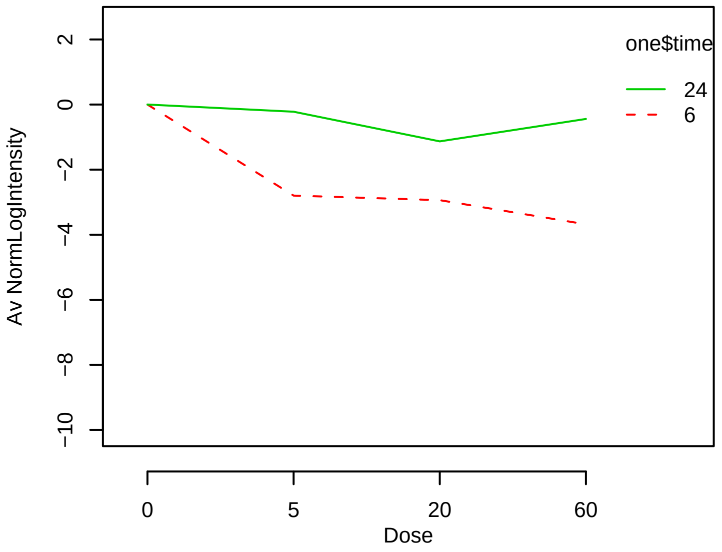
GO_0050974 : detection of mechanical stimulus during senso



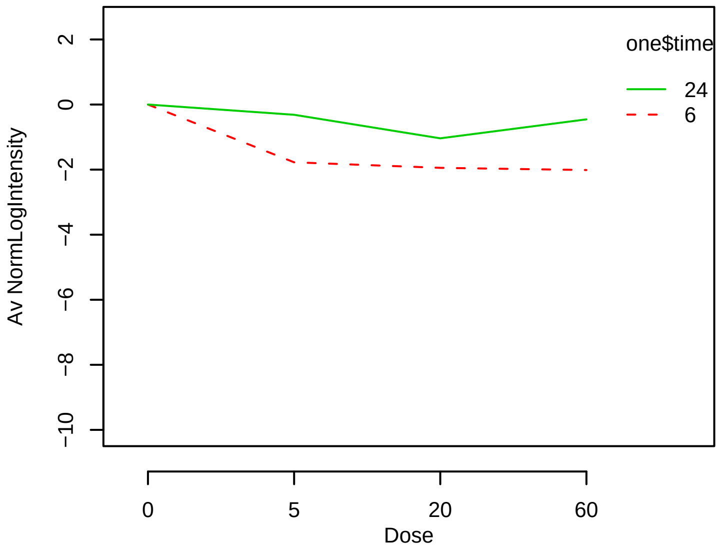
GO_0050982 : detection of mechanical stimulus



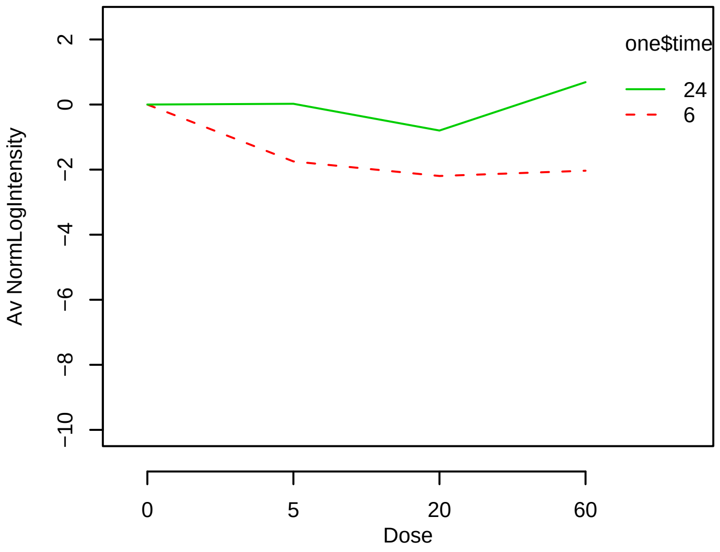
GO_0051016 : barbed−end actin filament capping



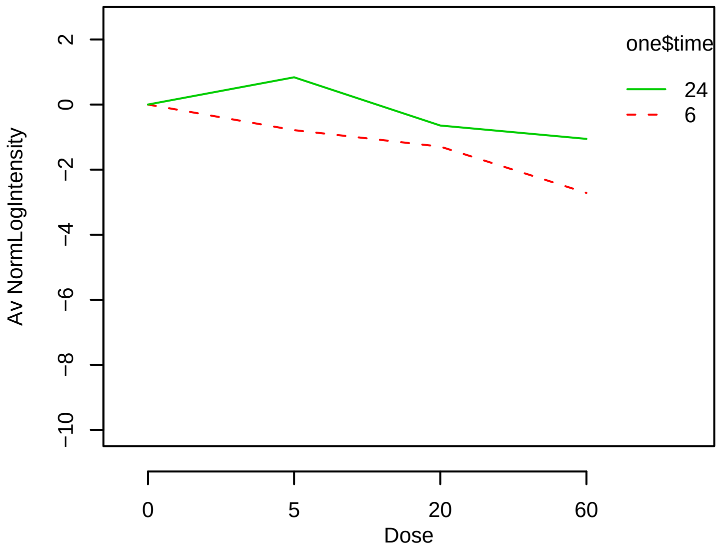
GO_0051017 : actin filament bundle formation



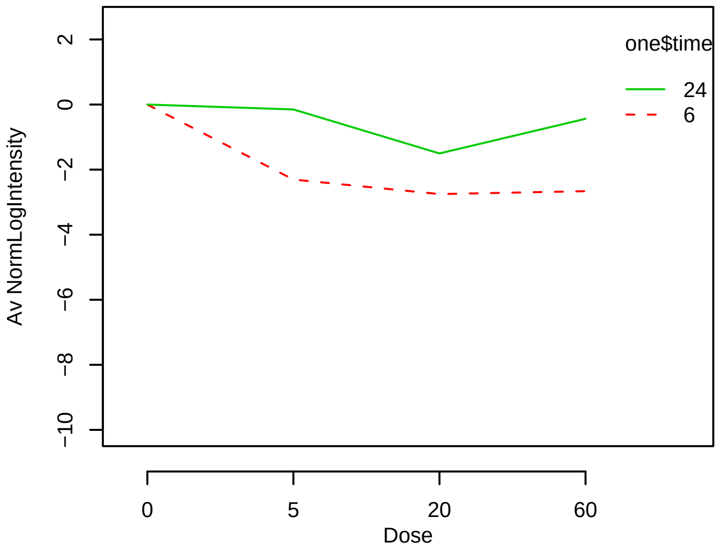
GO_0051023 : regulation of immunoglobulin secretion



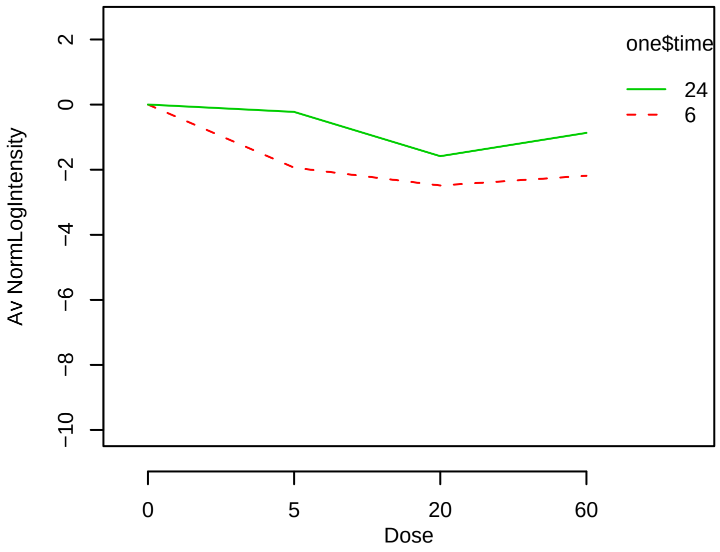
GO_0051028 : mRNA transport



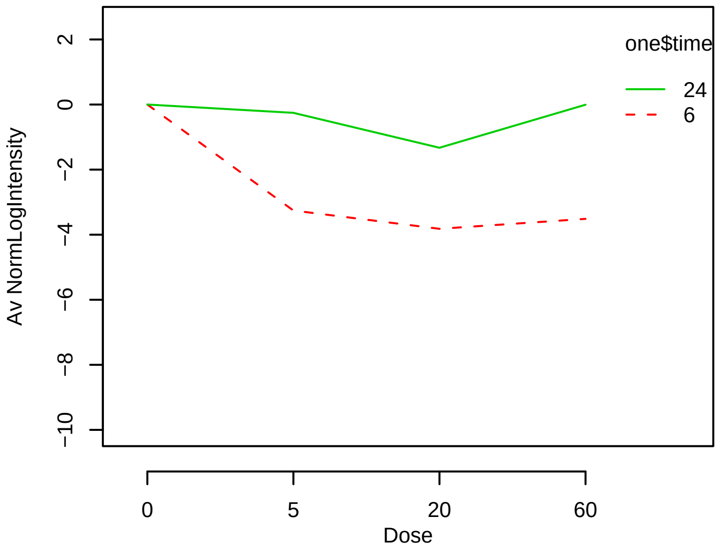
GO_0051046 : regulation of secretion

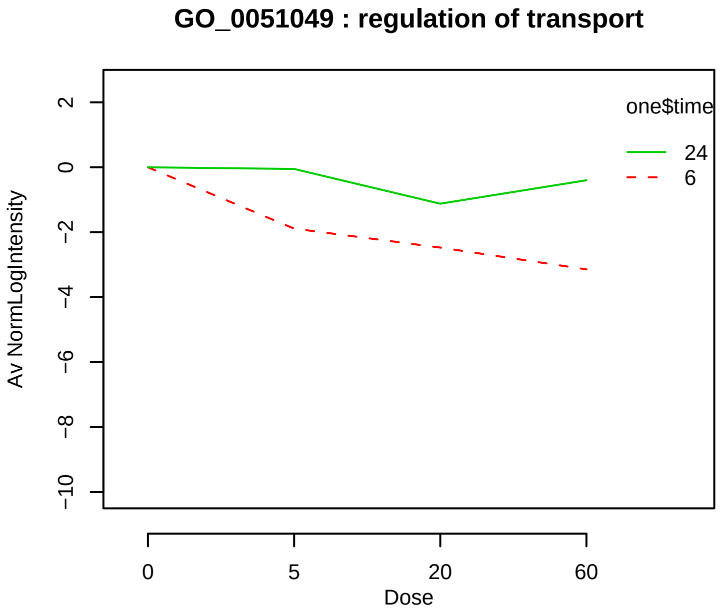


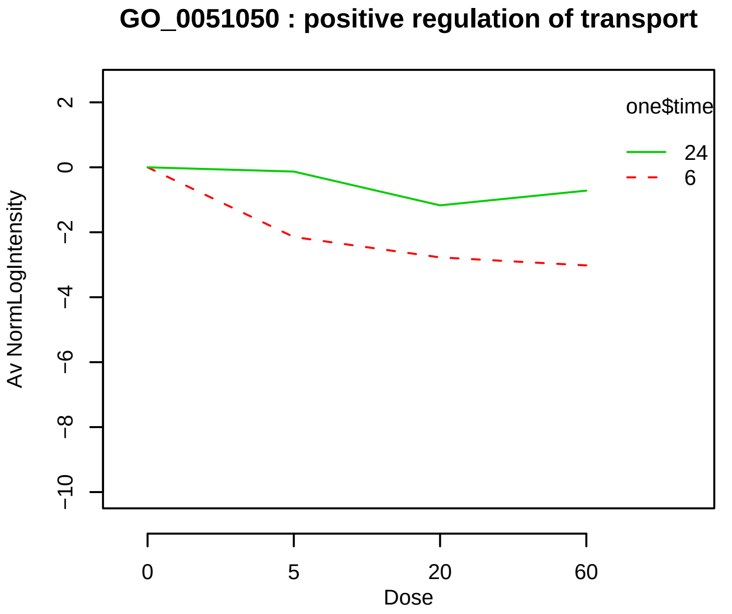
GO_0051047 : positive regulation of secretion

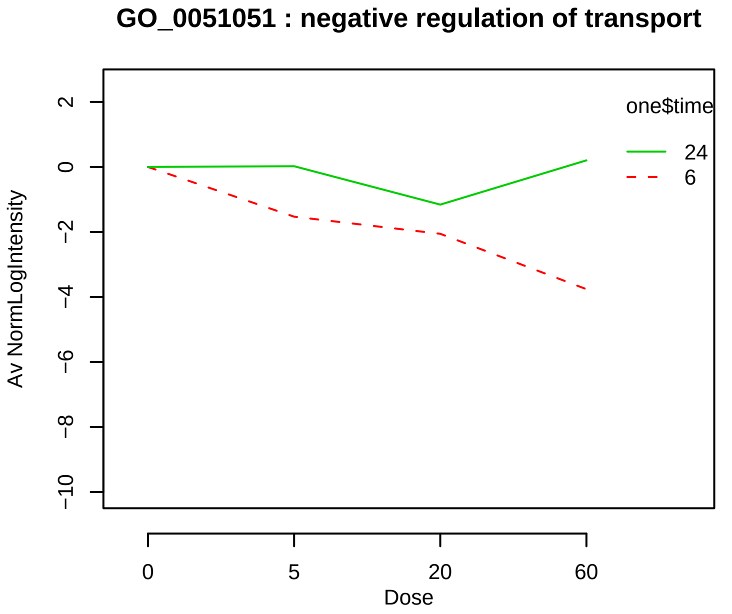


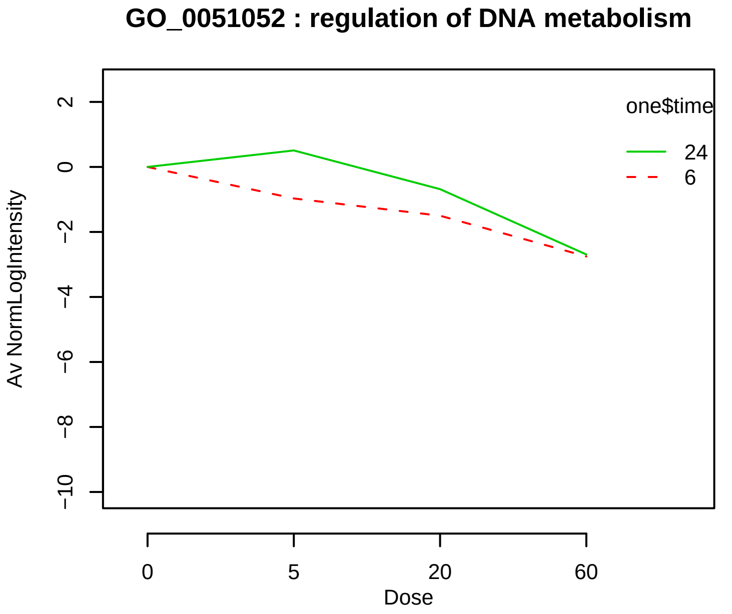
GO_0051048 : negative regulation of secretion

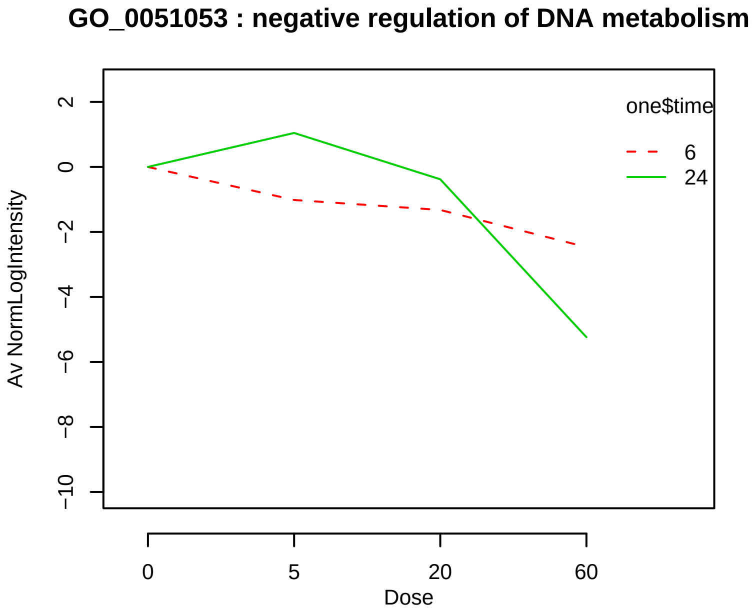


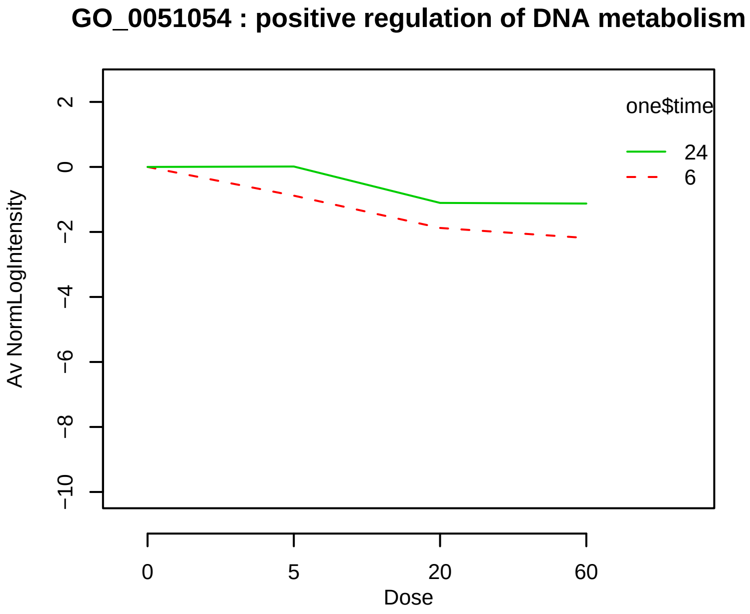

GO_0051049 : regulation of transport


GO_0051050 : positive regulation of transport

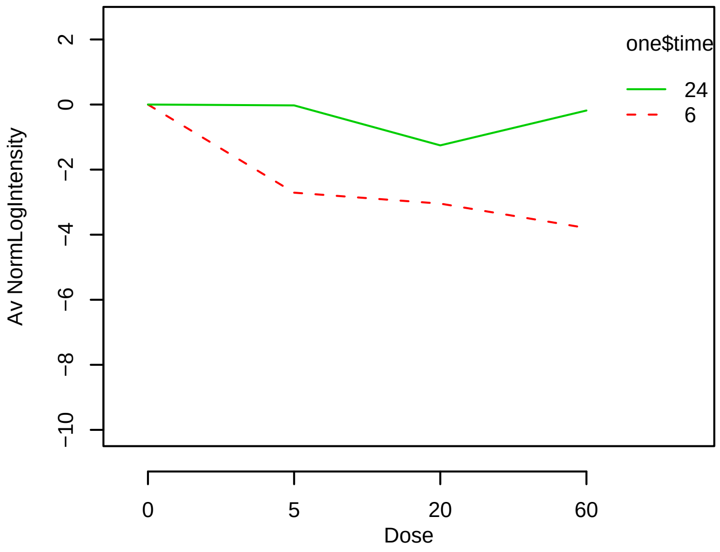

GO_0051051 : negative regulation of transport


GO_0051052 : regulation of DNA metabolism

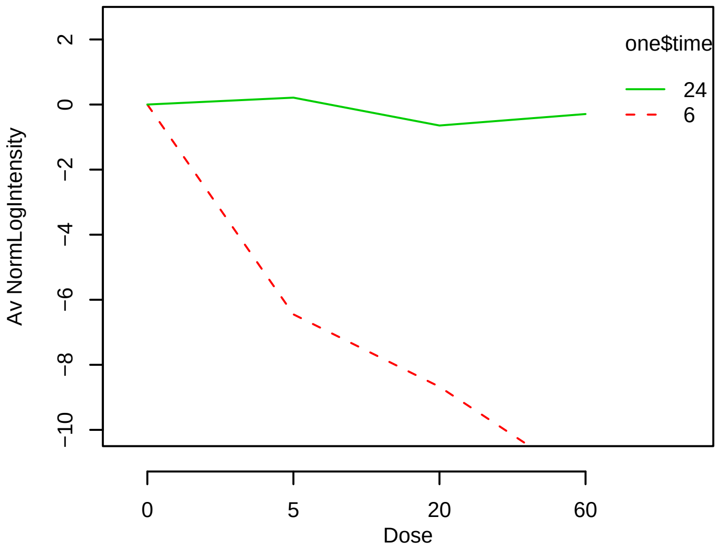

GO_0051053 : negative regulation of DNA metabolism


GO_0051054 : positive regulation of DNA metabolism

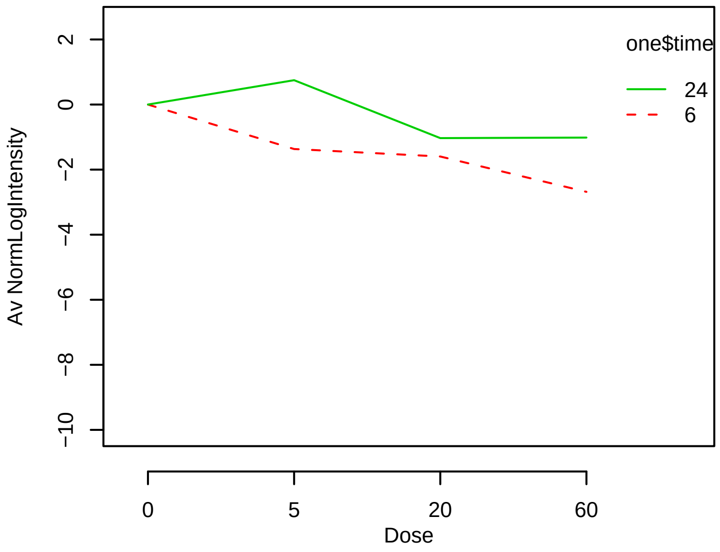
O_0051056 : regulation of small GTPase mediated signal tra



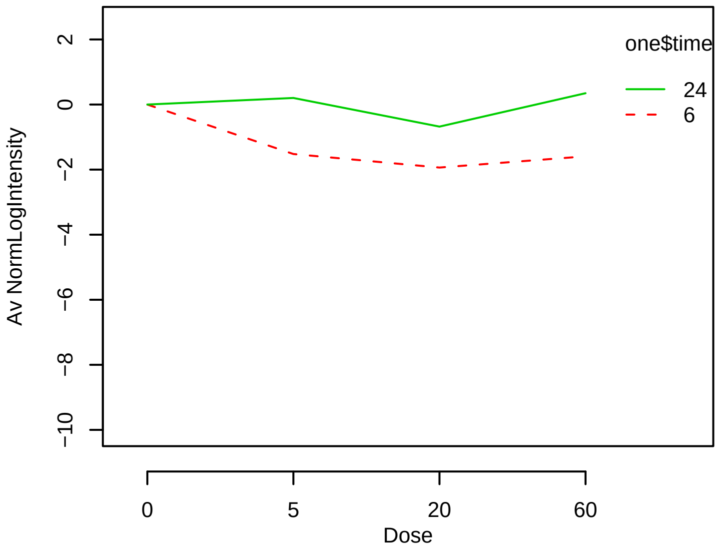
O_0051057 : positive regulation of small GTPase mediated s



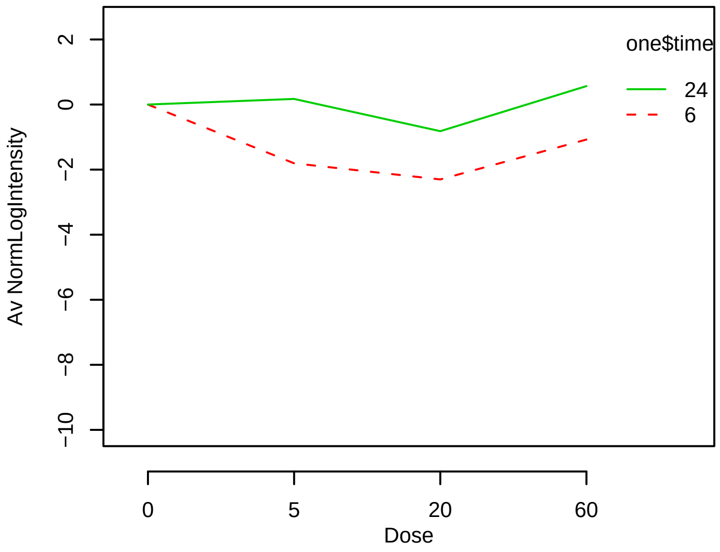
O_0051058 : negative regulation of small GTPase mediated s



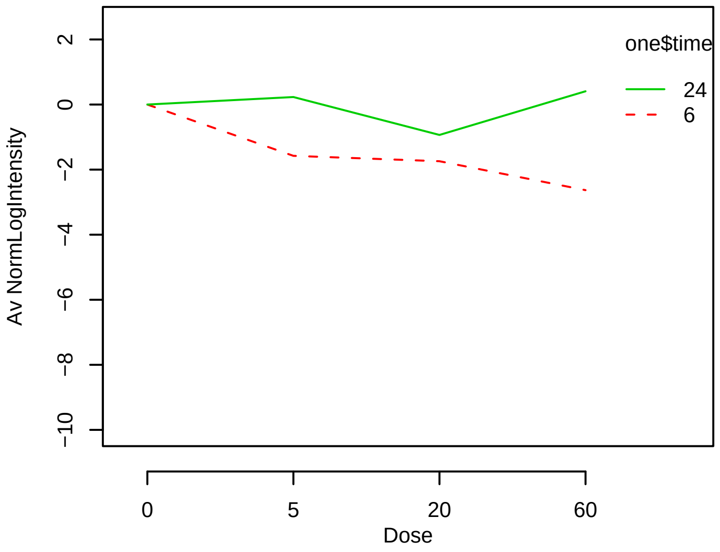
GO_0051084 : posttranslational protein folding

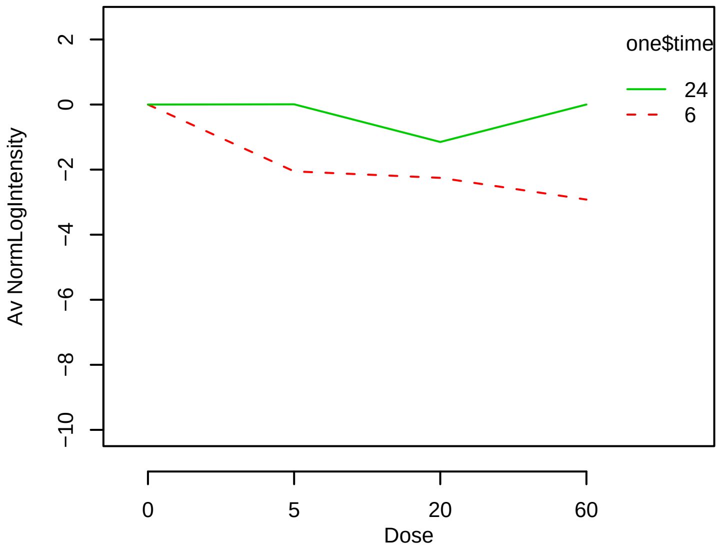


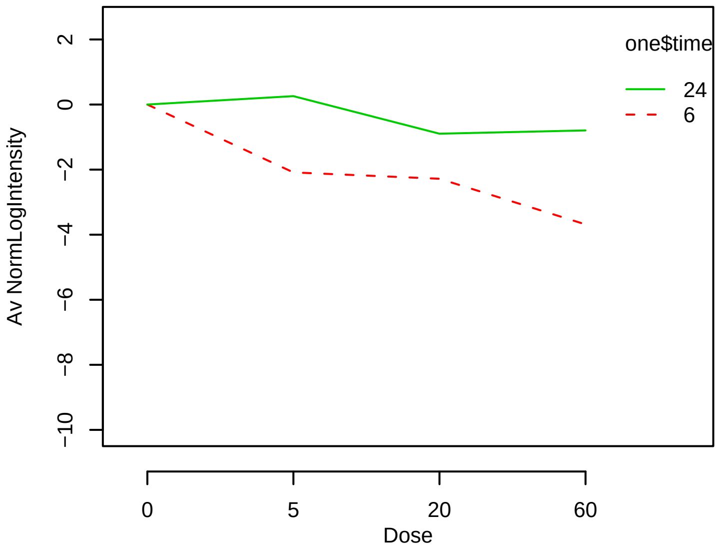
GO_0051085 : chaperone cofactor−dependent protein foldi

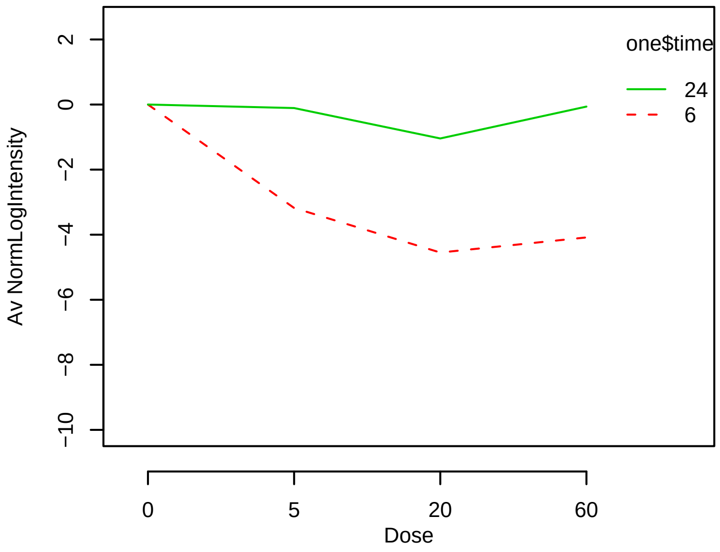


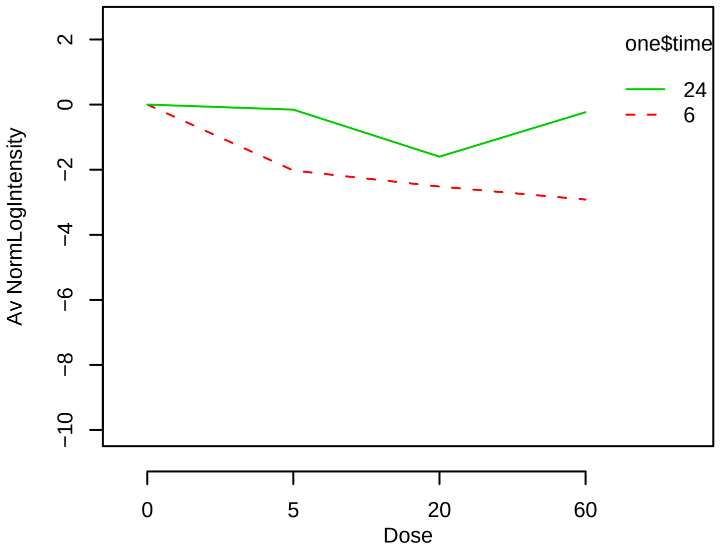
GO_0051090 : regulation of transcription factor activity

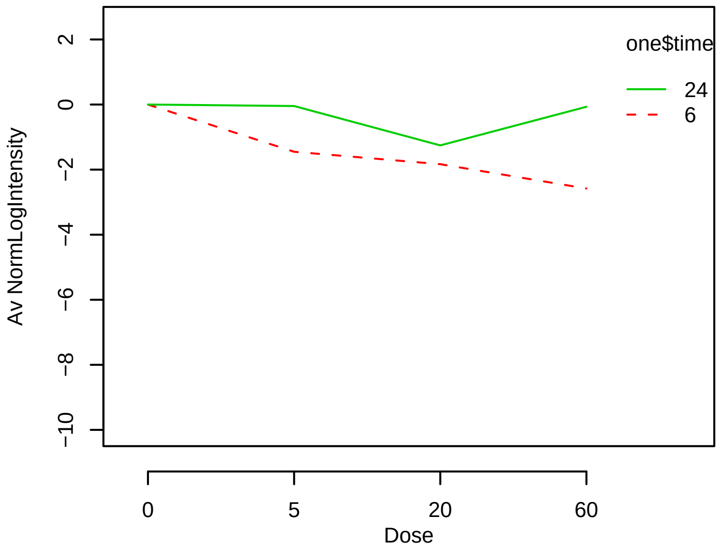


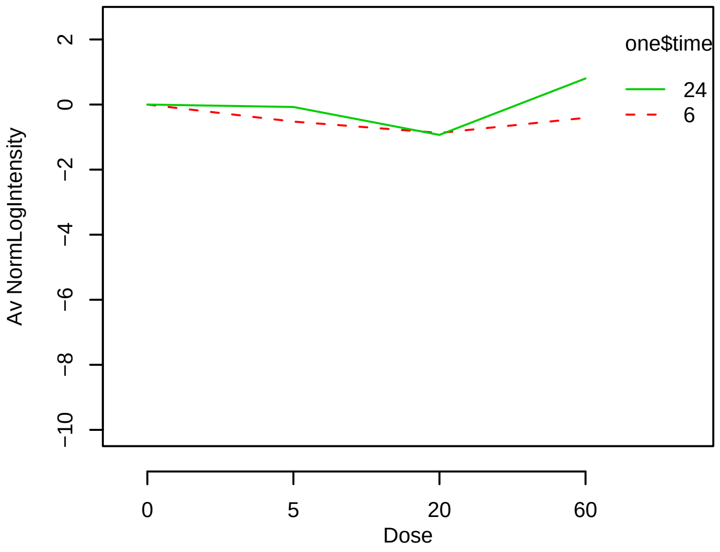

GO_0051091 : positive regulation of transcription factor act

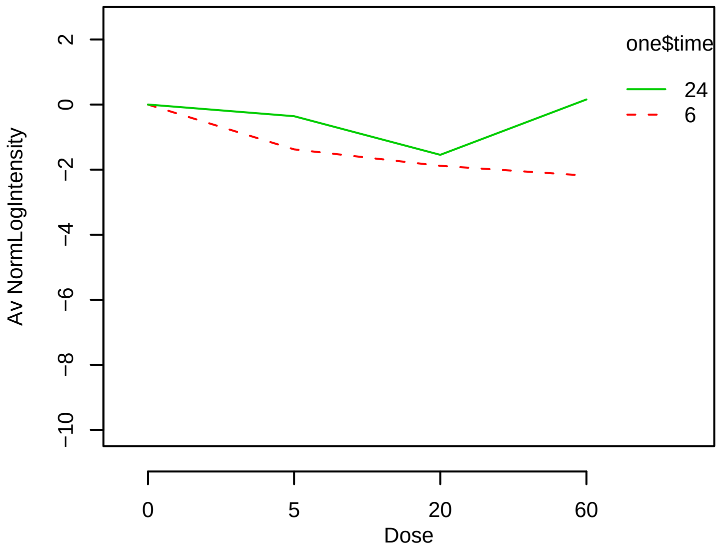

GO_0051092 : activation of NF−kappaB transcription facto

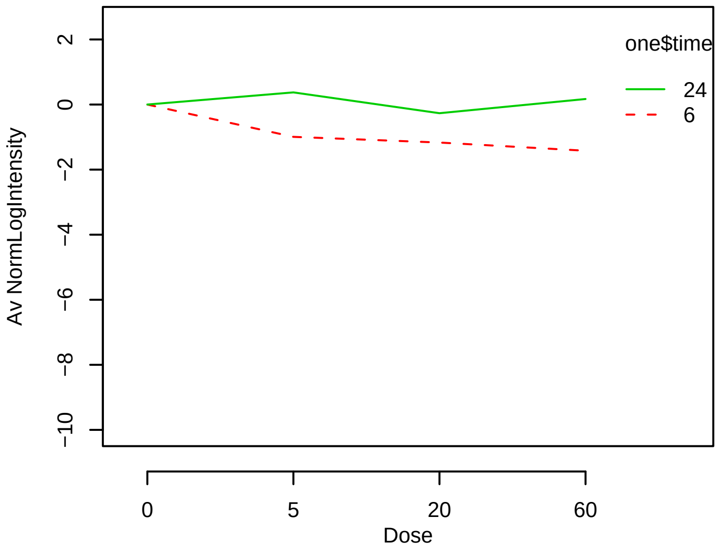

GO_0051093 : negative regulation of development

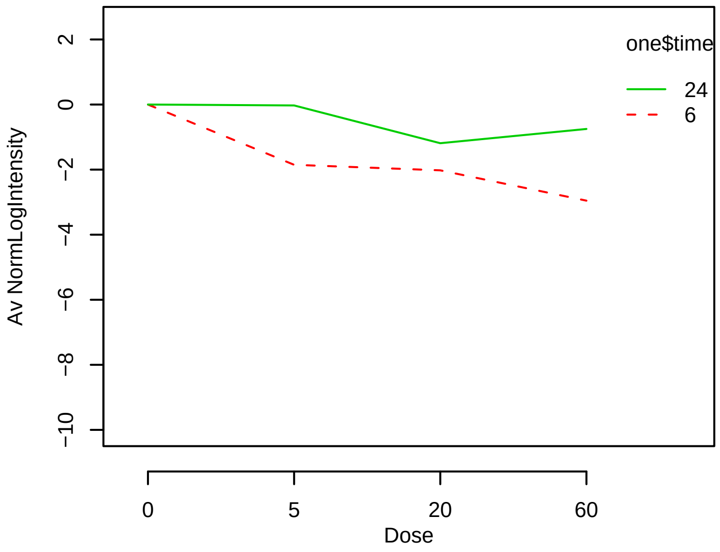

GO_0051094 : positive regulation of development

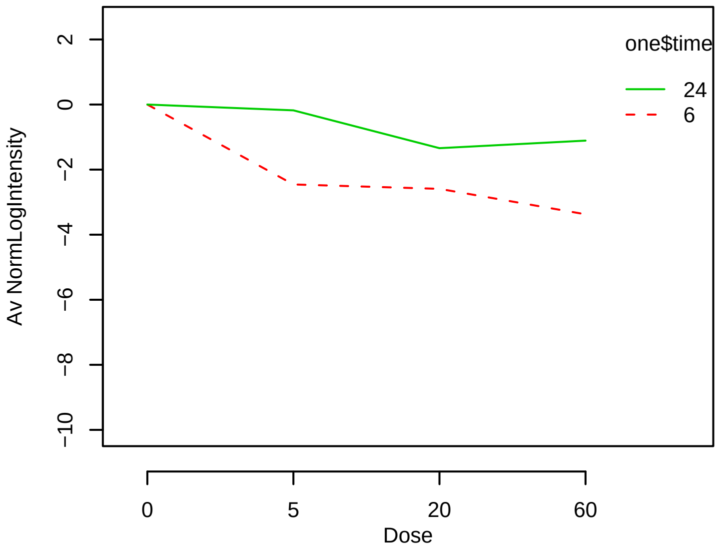

GO_0051098 : regulation of binding

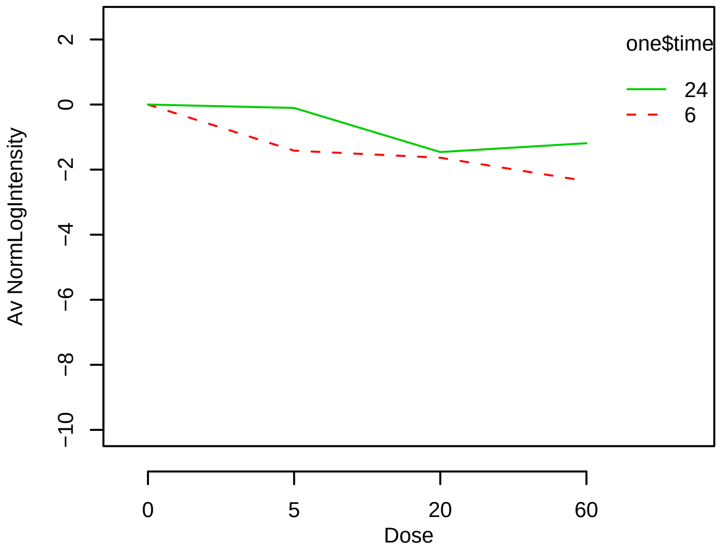

GO_0051099 : positive regulation of binding

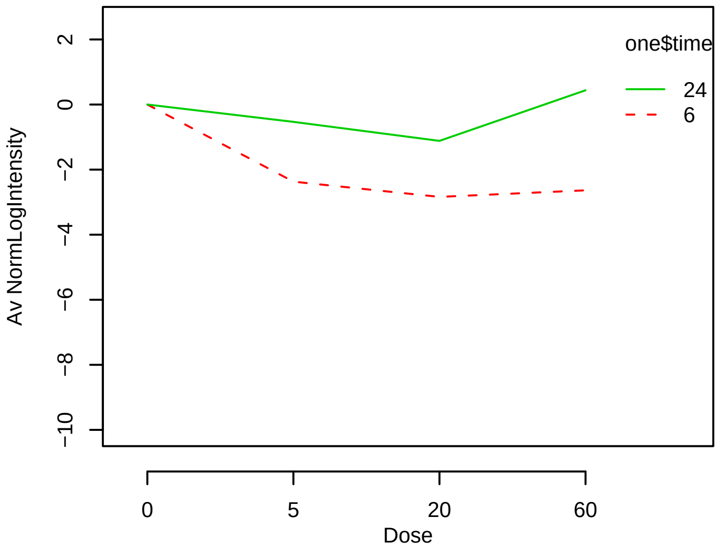

GO_0051101 : regulation of DNA binding

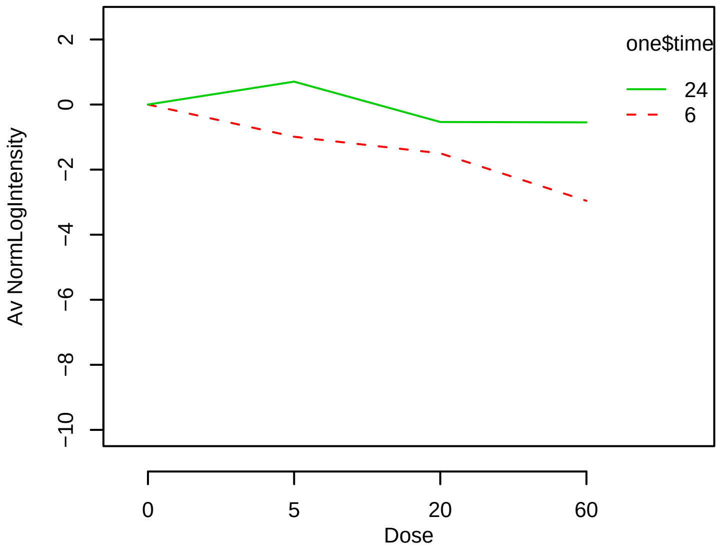

GO_0051124 : synaptic growth at neuromuscular junctior

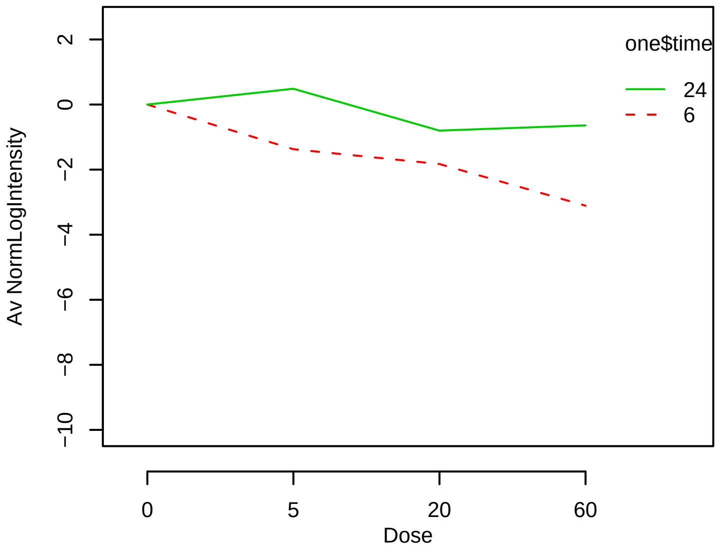

GO_0051128 : regulation of cell organization and biogenes

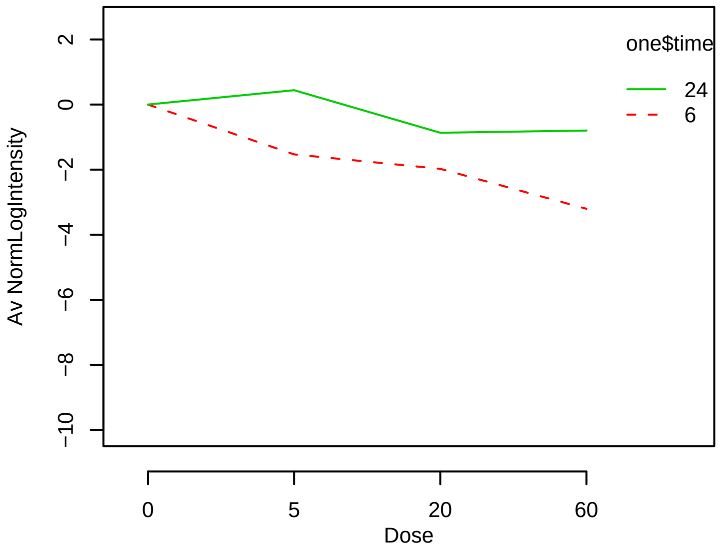

GO_0051129 : negative regulation of cell organization and bi

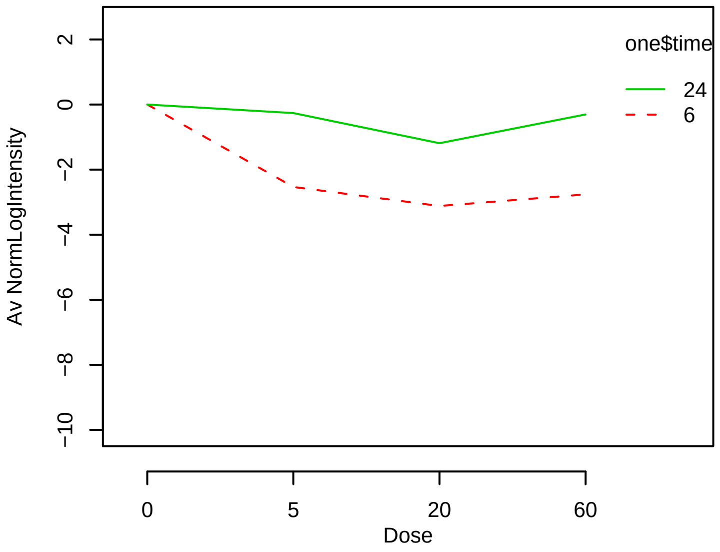

GO_0051130 : positive regulation of cell organization and bi

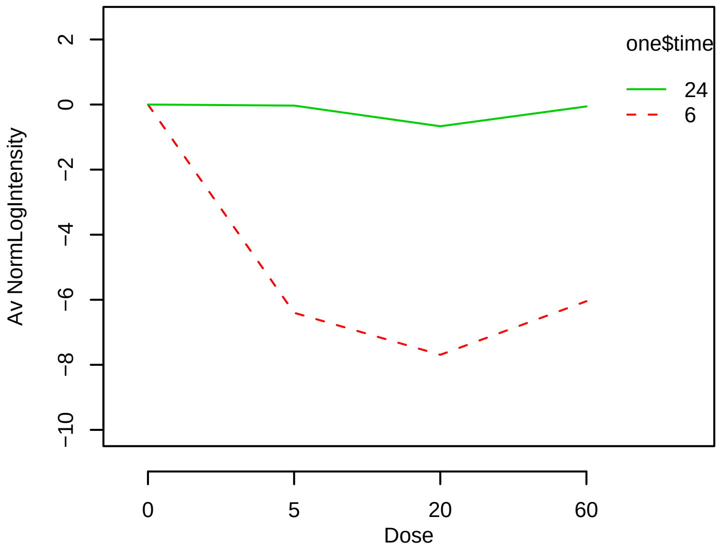

GO_0051145 : smooth muscle cell differentiation

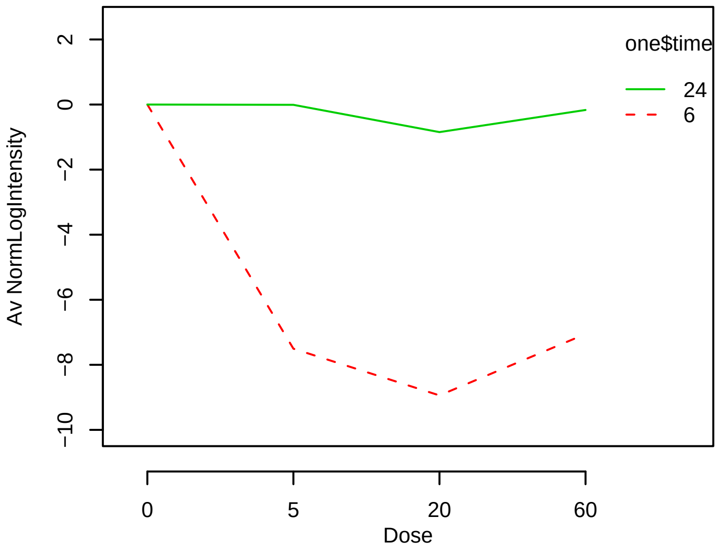

GO_0051168 : nuclear export

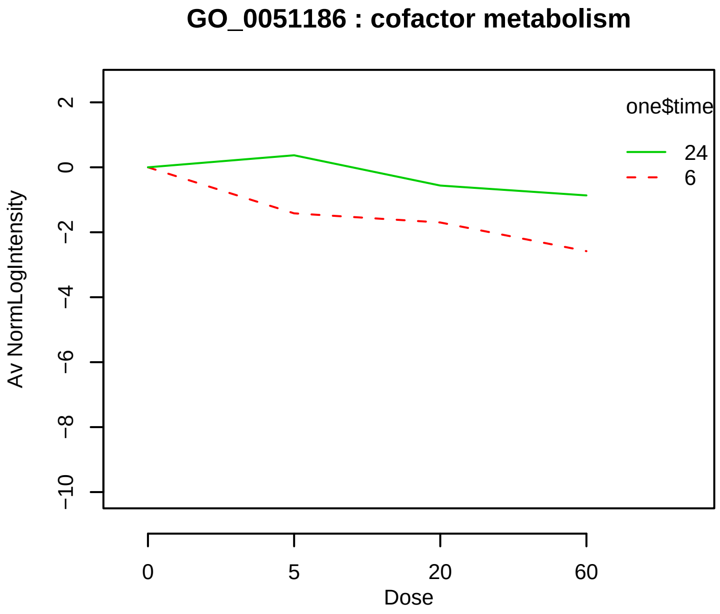

GO_0051169 : nuclear transport

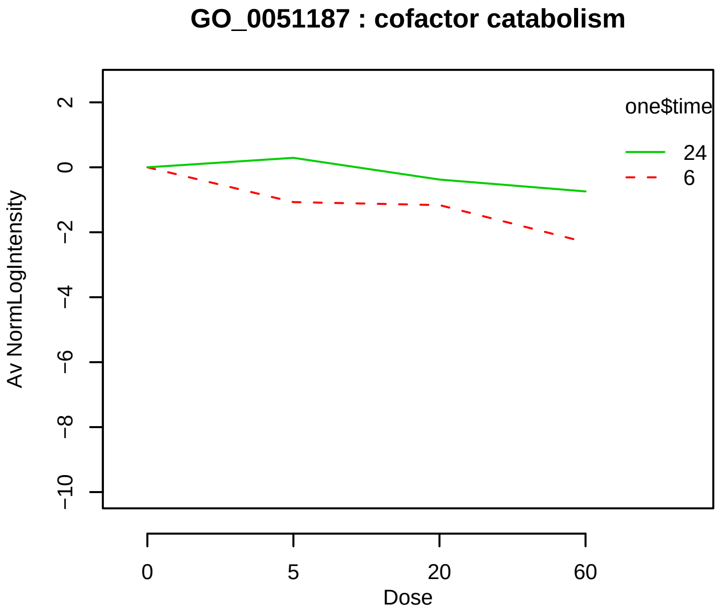

GO_0051170 : nuclear import

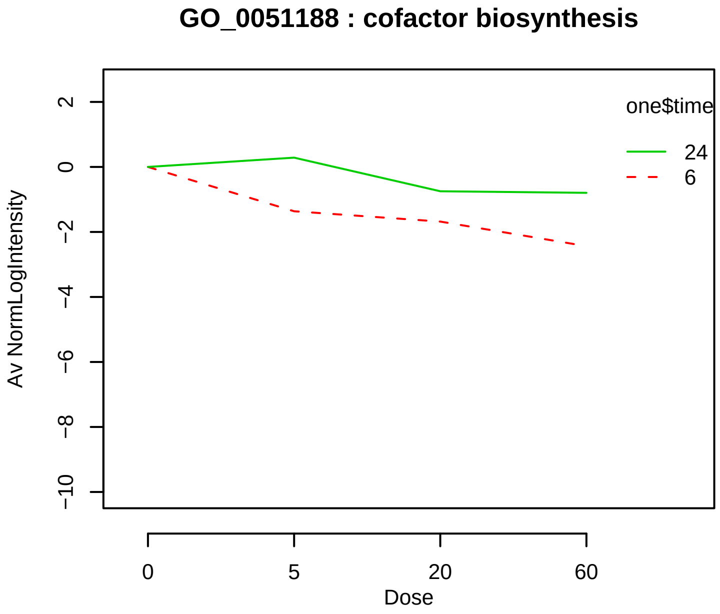

GO_0051174 : regulation of phosphorus metabolism


GO_0051180 : vitamin transport

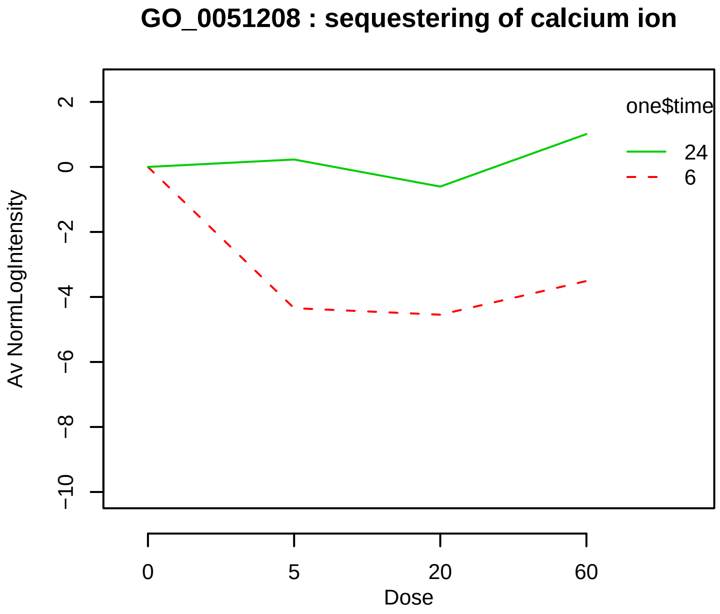

GO_0051181 : cofactor transport

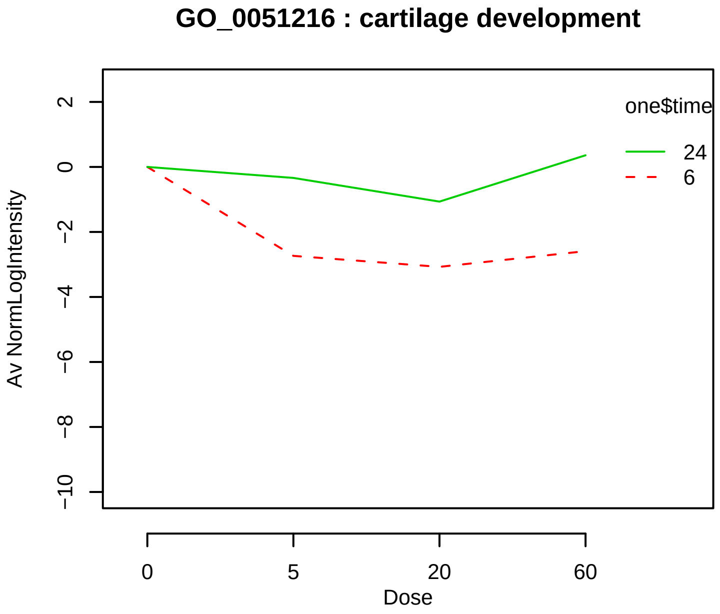

GO_0051186 : cofactor metabolism

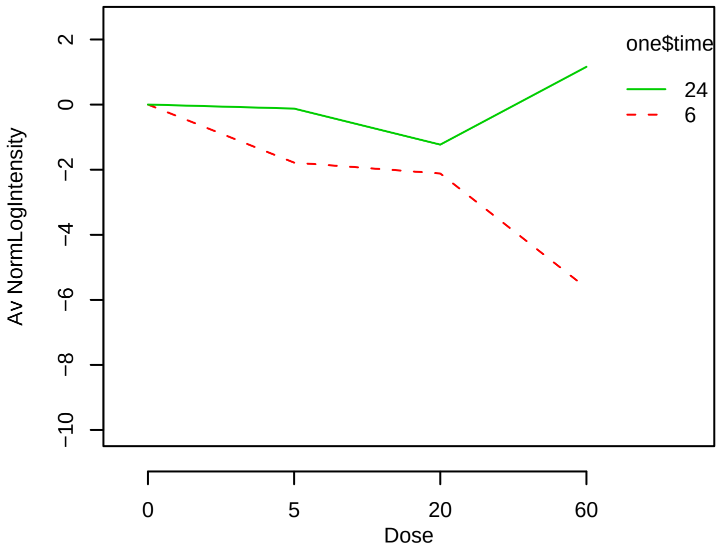

GO_0051187 : cofactor catabolism


GO_0051188 : cofactor biosynthesis

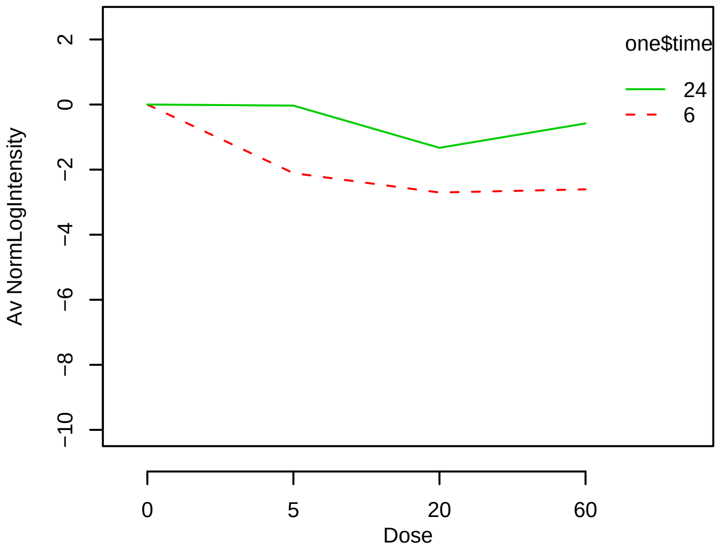

GO_0051205 : protein insertion into membrane


GO_0051208 : sequestering of calcium ion

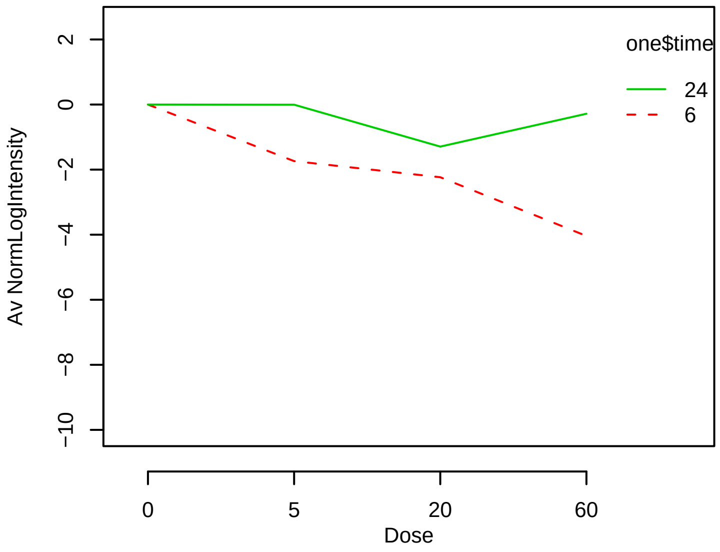

GO_0051216 : cartilage development



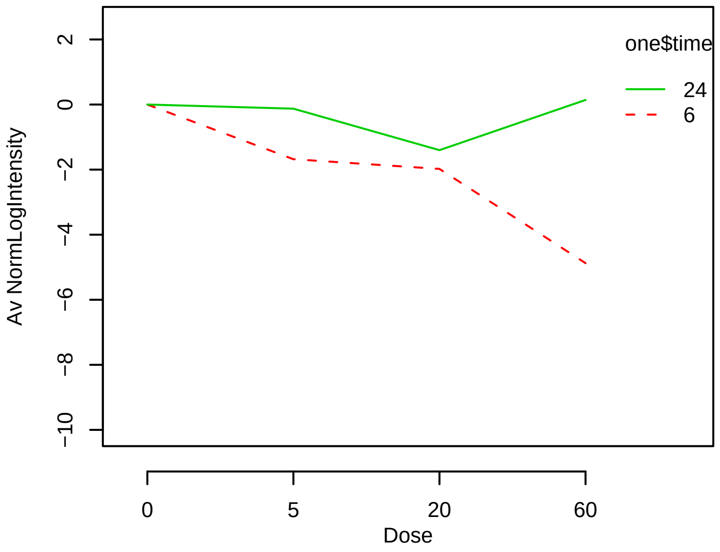
GO_0051220 : cytoplasmic sequestering of protein



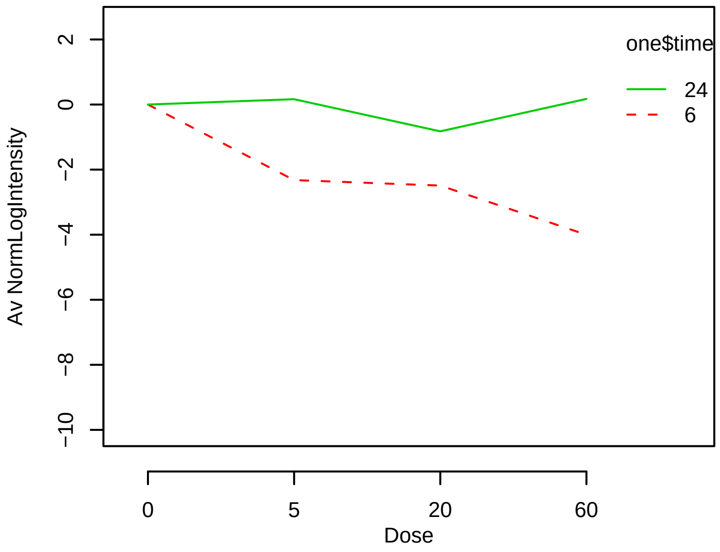
GO_0051222 : positive regulation of protein transport



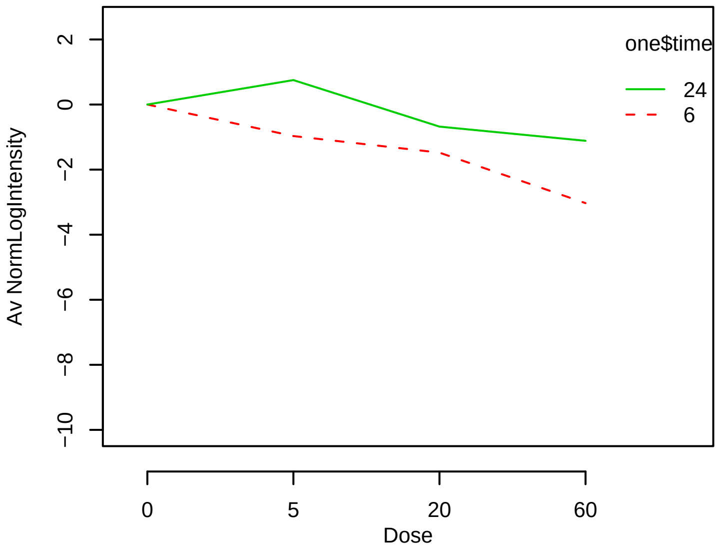
GO_0051223 : regulation of protein transport



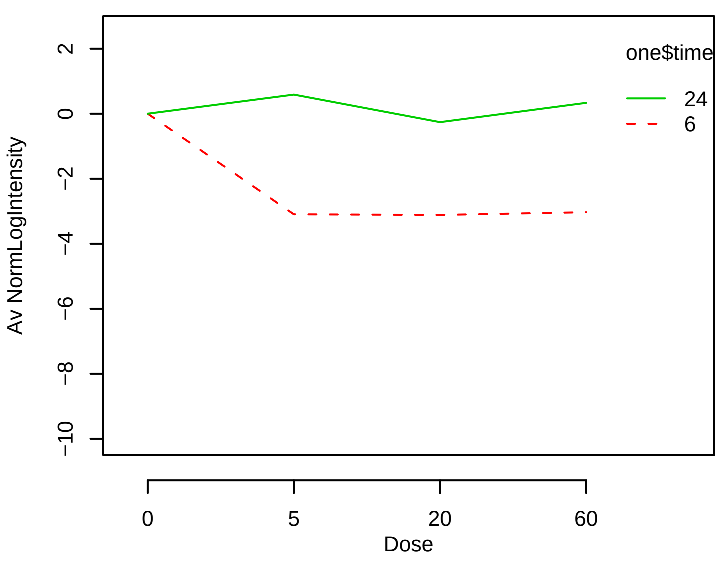
GO_0051224 : negative regulation of protein transport



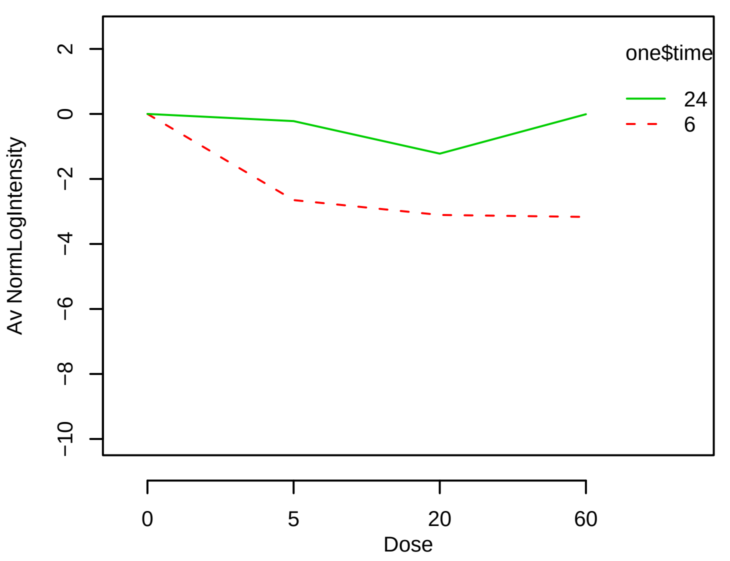
GO_0051235 : maintenance of localization



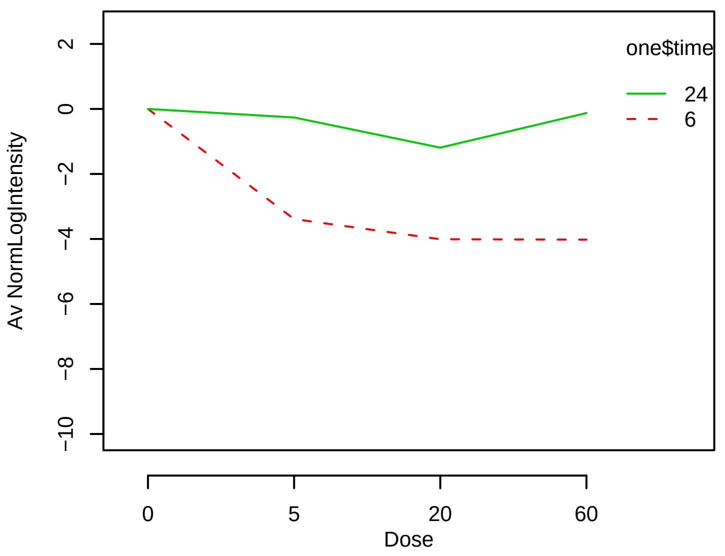
GO_0051236 : establishment of RNA localization



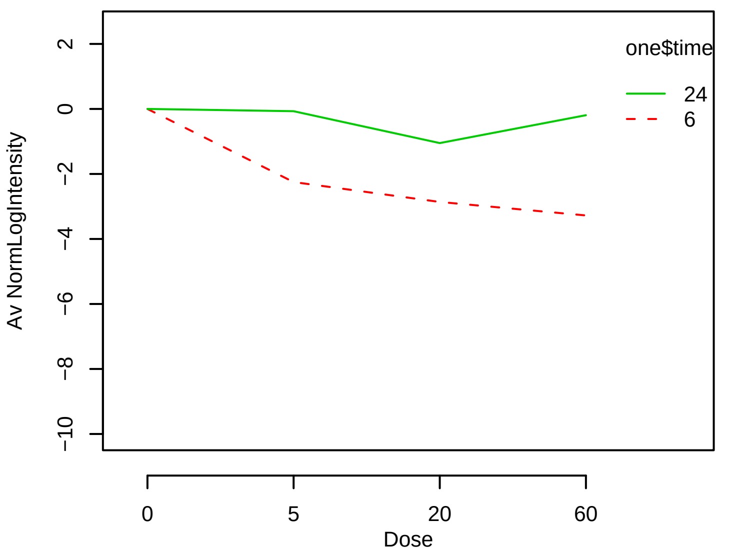
GO_0051238 : sequestering of metal ion



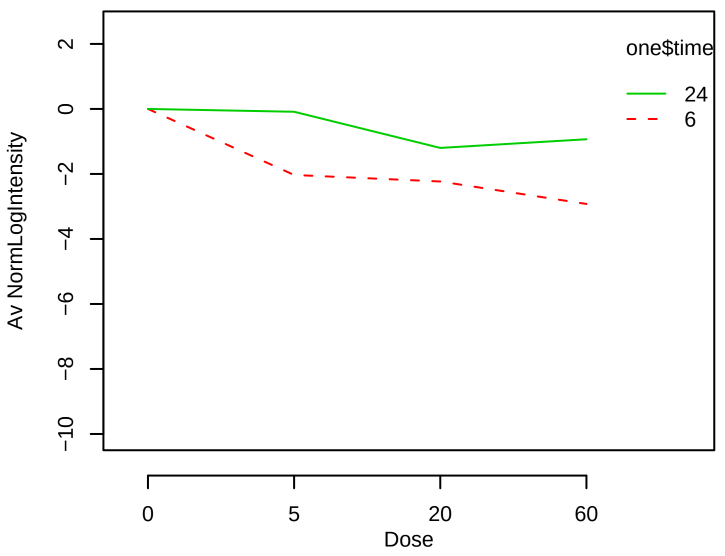
GO_0051240 : positive regulation of organismal physiologica



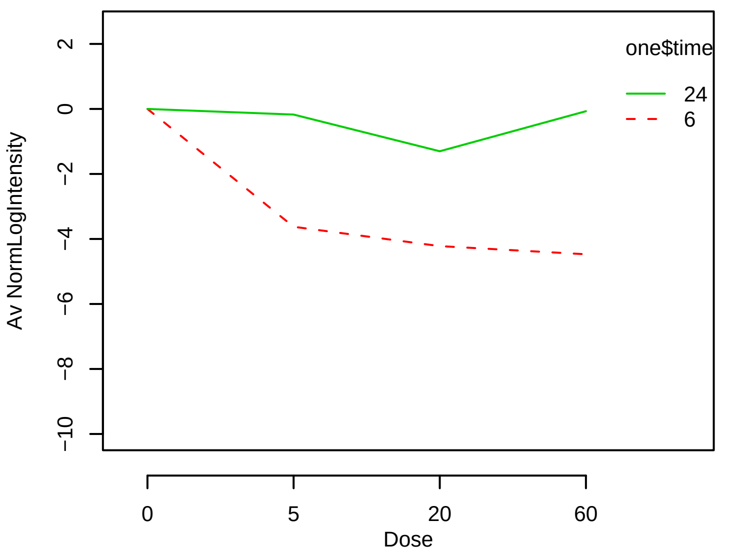
GO_0051241 : negative regulation of organismal physiologica



GO_0051247 : positive regulation of protein metabolism

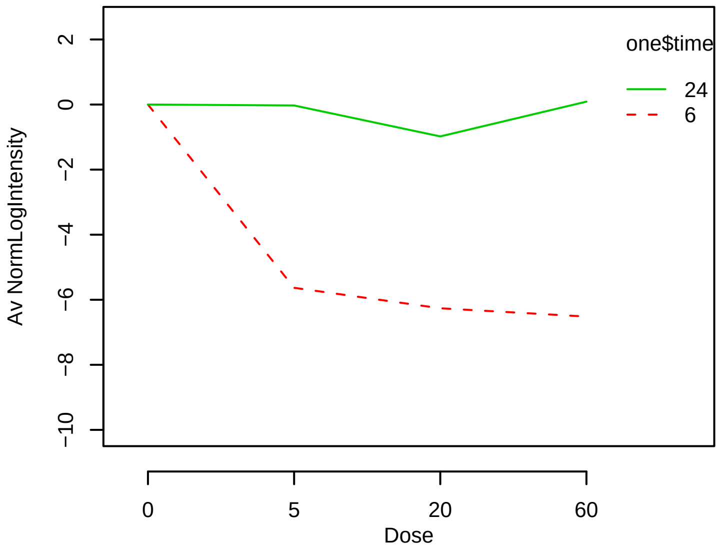


GO_0051248 : negative regulation of protein metabolism

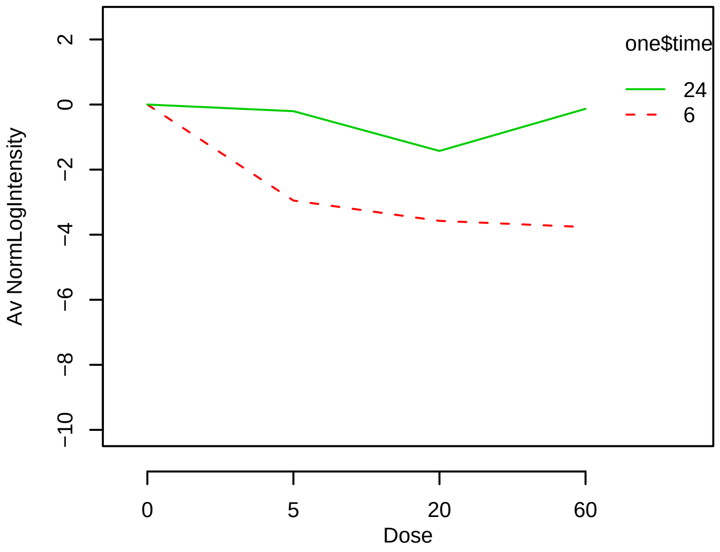


GO_0051249 : regulation of lymphocyte activation

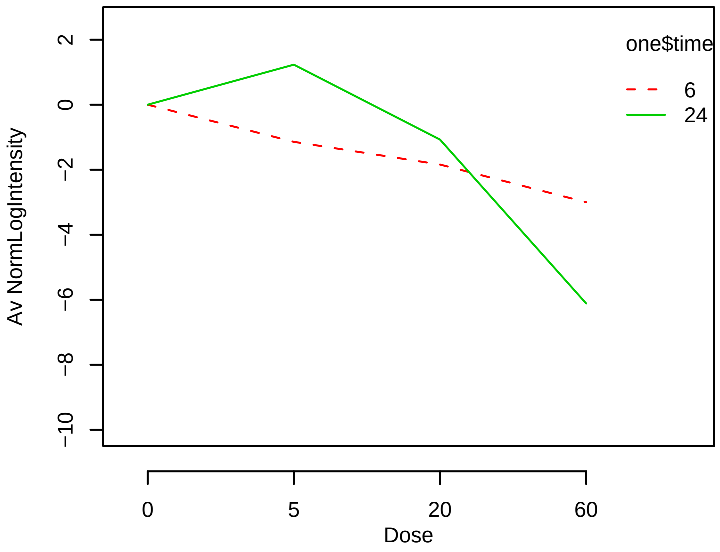
GO_0051250 : negative regulation of lymphocyte activatio



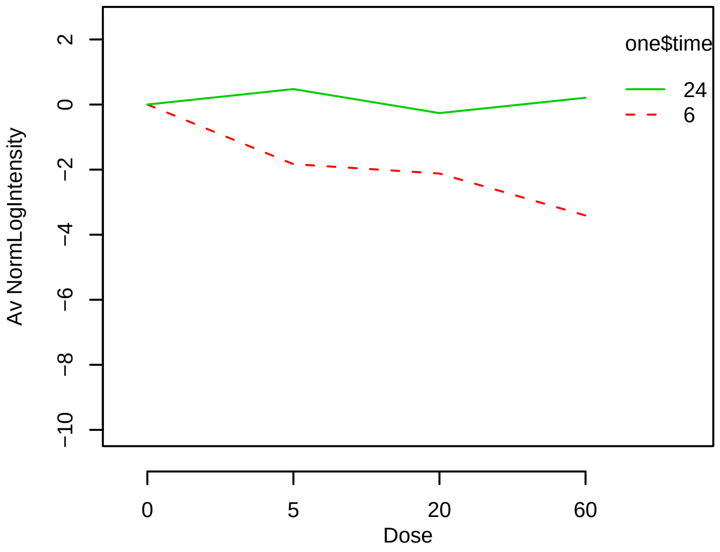
GO_0051251 : positive regulation of lymphocyte activatioı



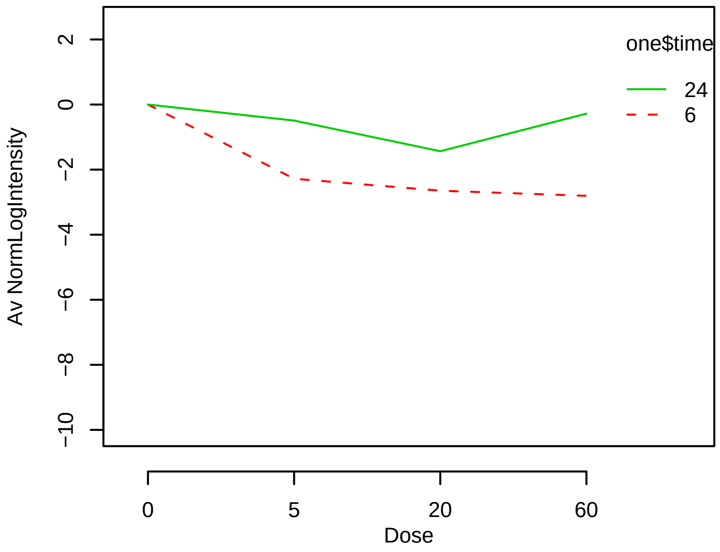
GO_0051252 : regulation of RNA metabolism



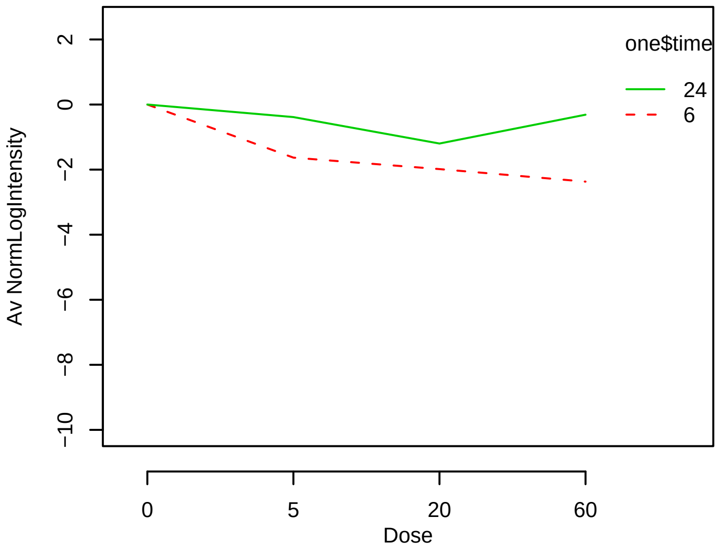
GO_0051258 : protein polymerization

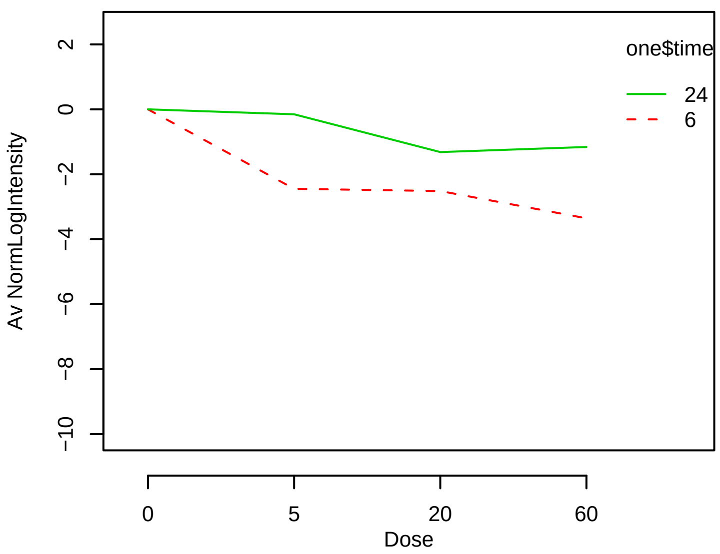


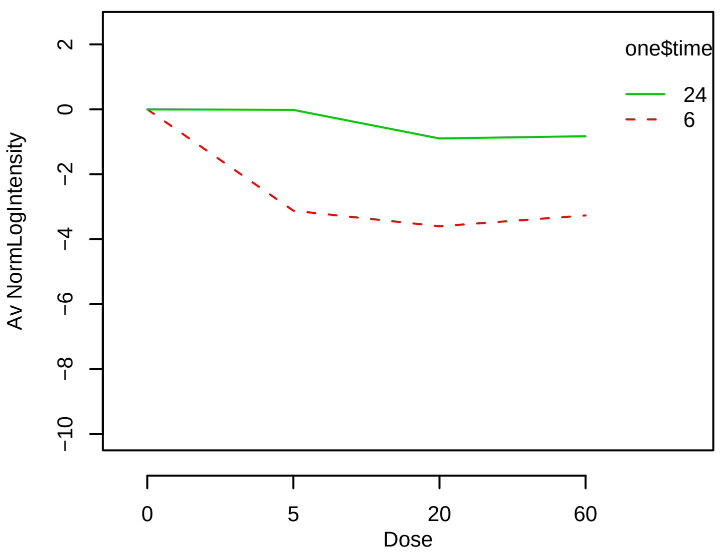
GO_0051259 : protein oligomerization

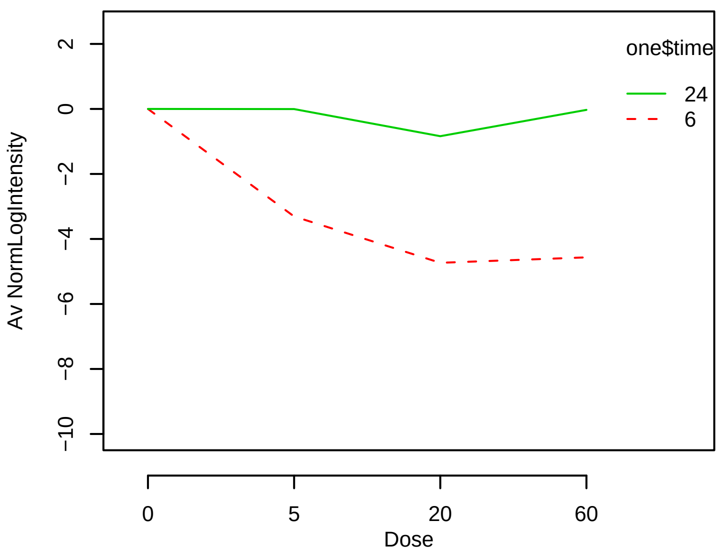


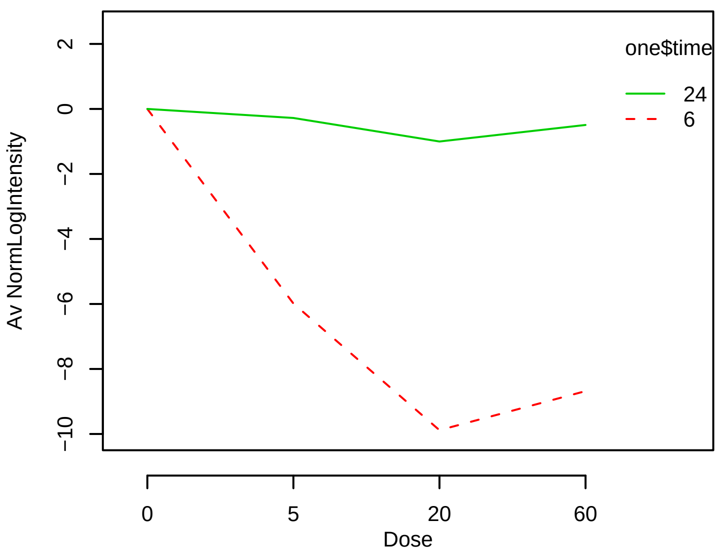
GO_0051260 : protein homooligomerization

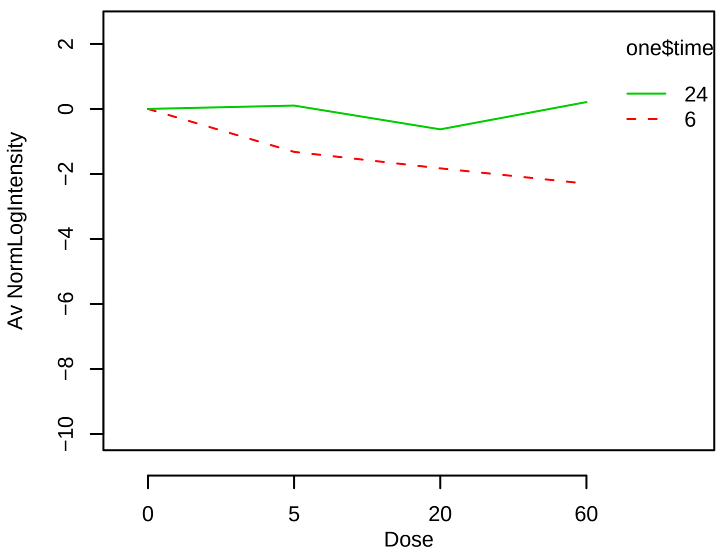


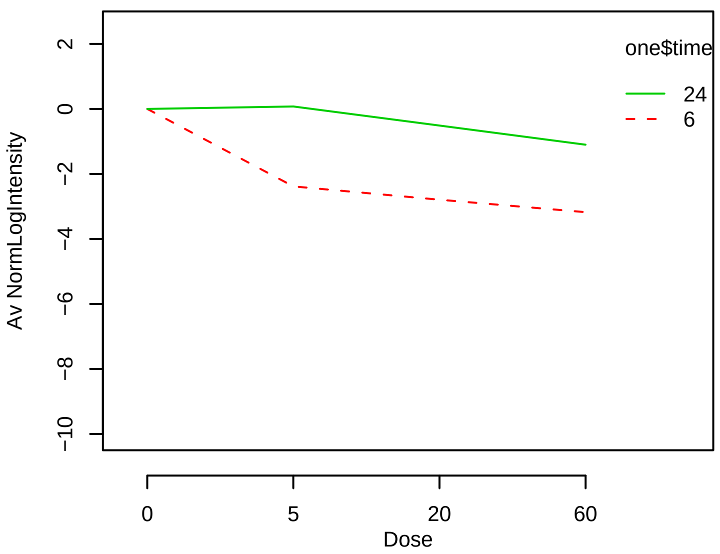

GO_0051261 : protein depolymerization

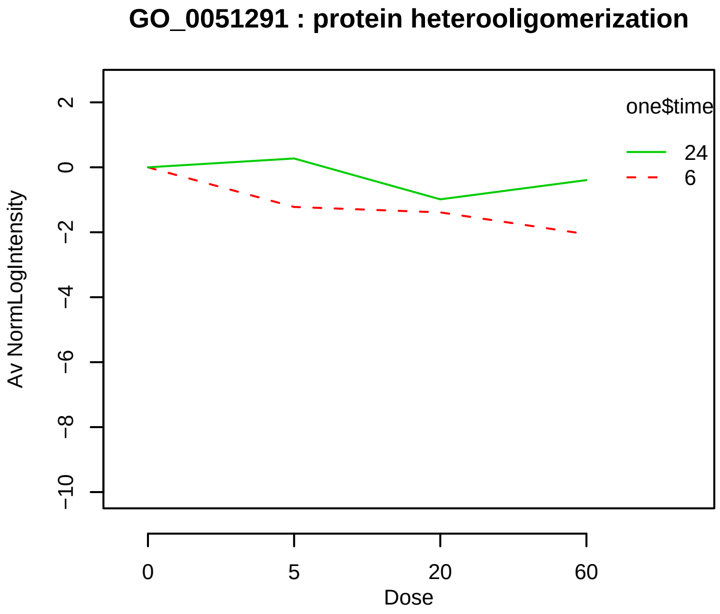

GO_0051262 : protein tetramerization

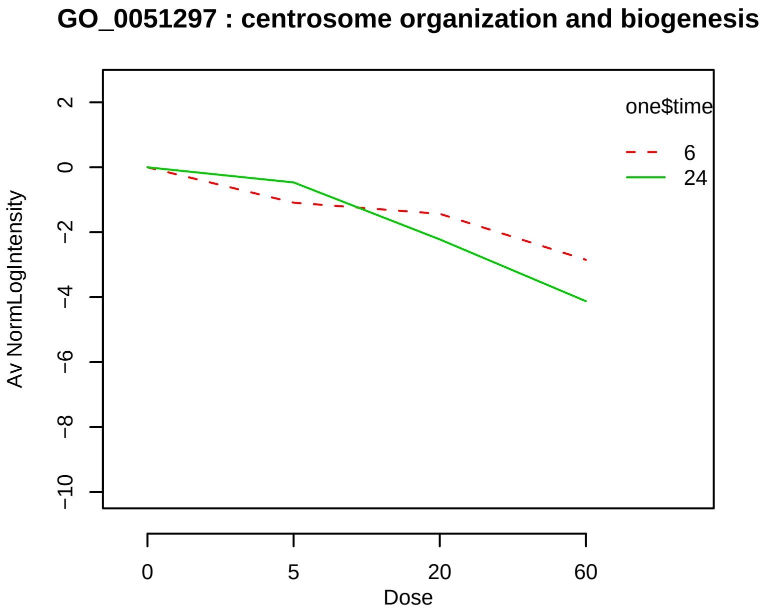

GO_0051270 : regulation of cell motility

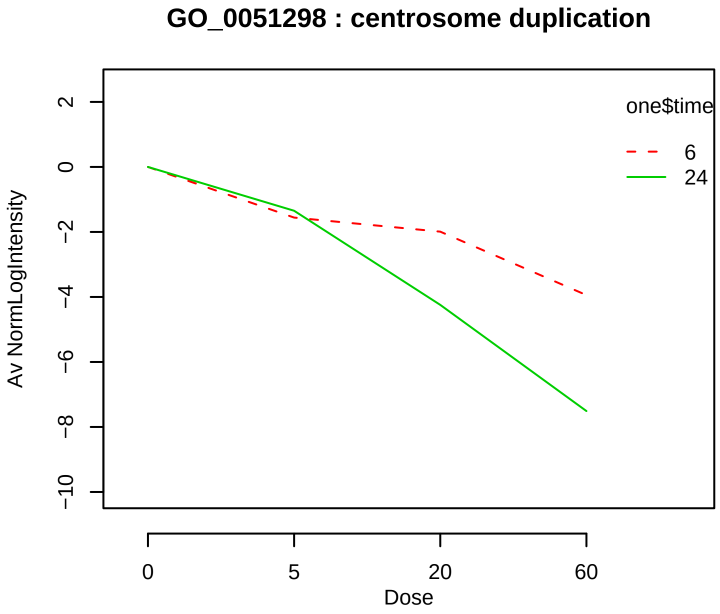

GO_0051271 : negative regulation of cell motility


GO_0051272 : positive regulation of cell motility


GO_0051289 : protein homotetramerization


GO_0051291 : protein heterooligomerization
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
one$time
24
6
0
5
20
60
Dose


GO_0051297 : centrosome organization and biogenesis
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
one$time
6
24
0
5
20
60
Dose


GO_0051298 : centrosome duplication
Av NormLogIntensity
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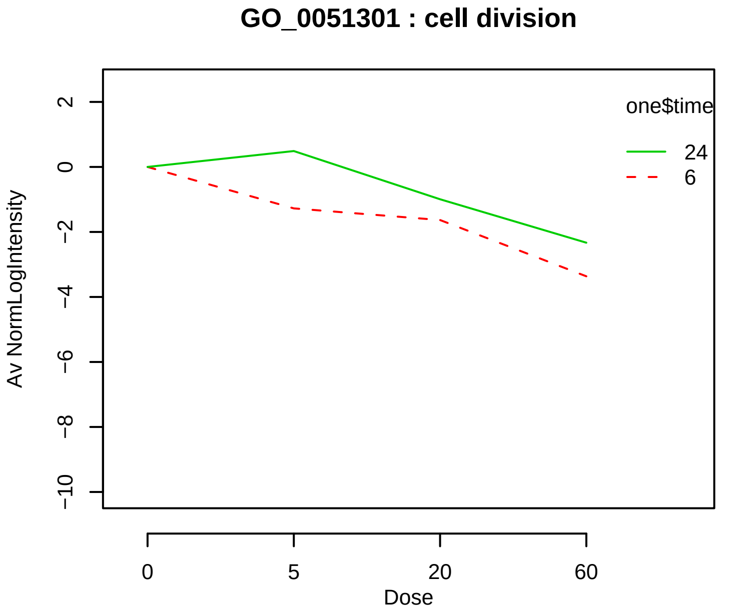
0
−2
−4
−6
−8
−10
one$time
6
24
0
5
20
60
Dose


GO_0051301 : cell division
Av NormLogIntensity
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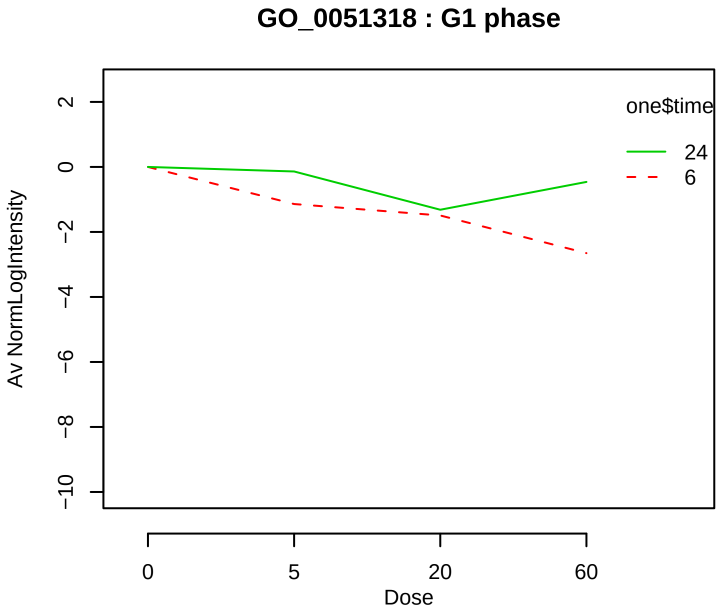
0
−2
−4
−6
−8
−10
one$time
24
6
0
5
20
60
Dose


GO_0051318 : G1 phase
Av NormLogIntensity
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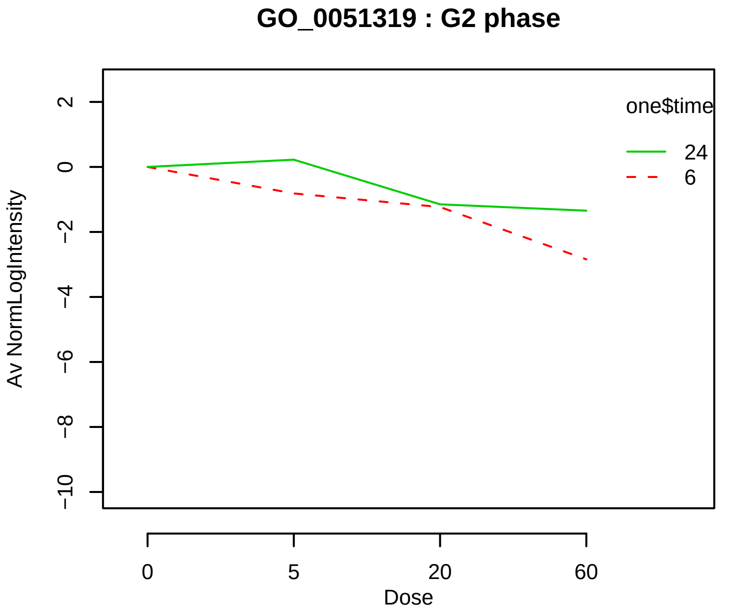
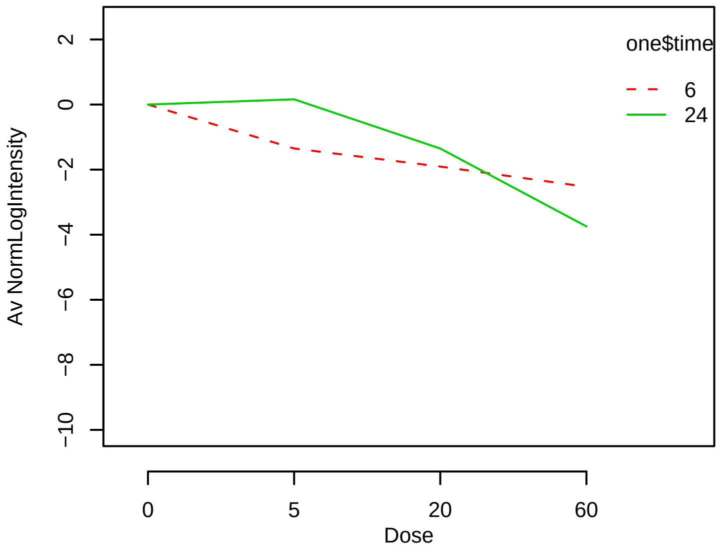
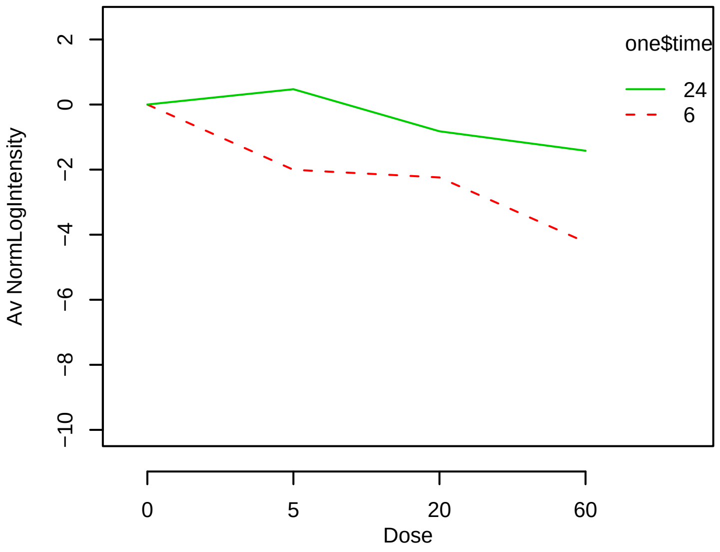
−2
−4
−6
−8
−10
one$time
24
6
0
5
20
60
Dose


GO_0051319 : G2 phase
Av NormLogIntensity
2
0
−2
−4
−6
−8
−10
one$time
24
6
0
5
20
60
Dose

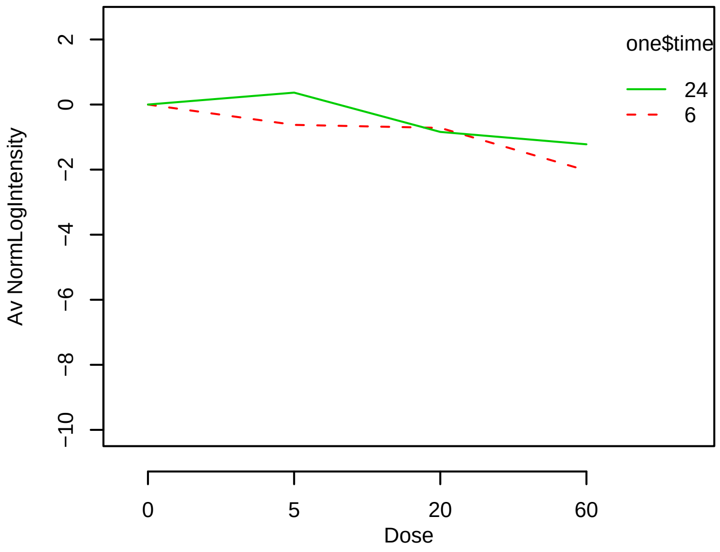
GO_0051320 : S phase



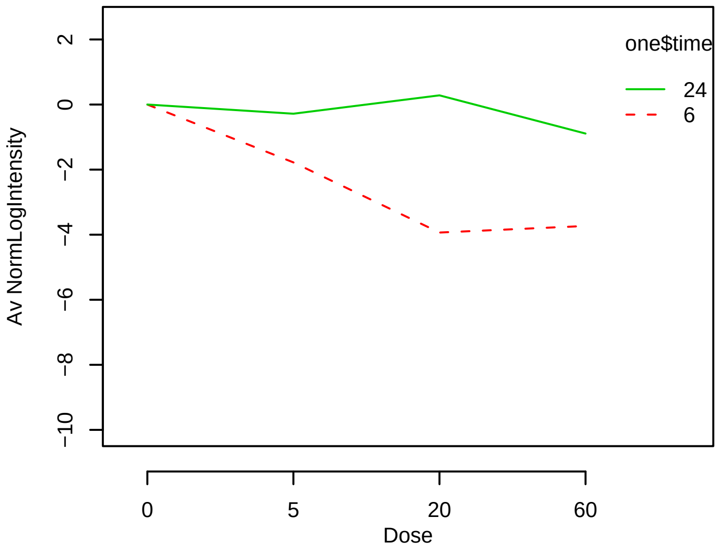
GO_0051321 : meiotic cell cycle



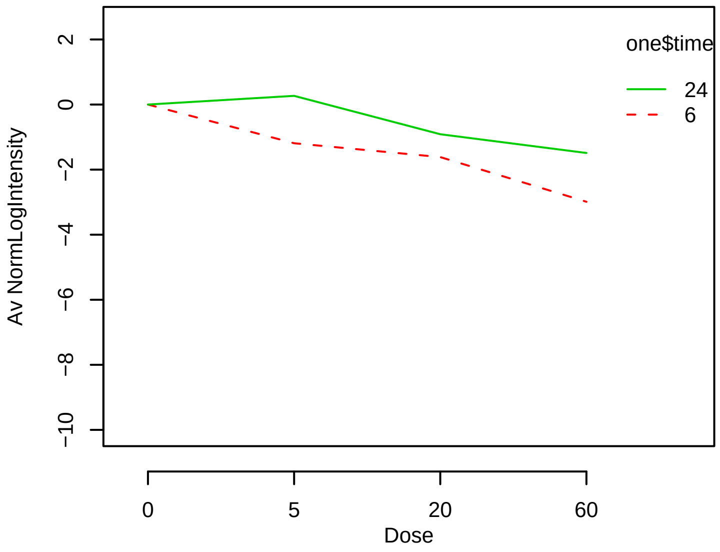
GO_0051322 : anaphase



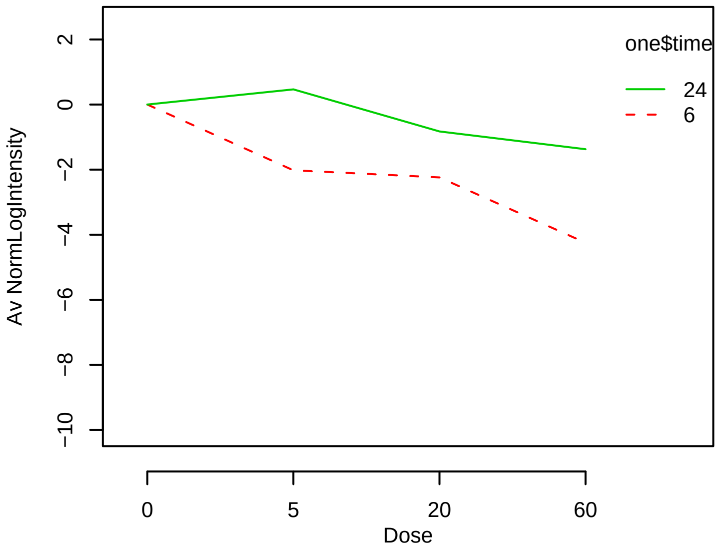
GO_0051324 : prophase

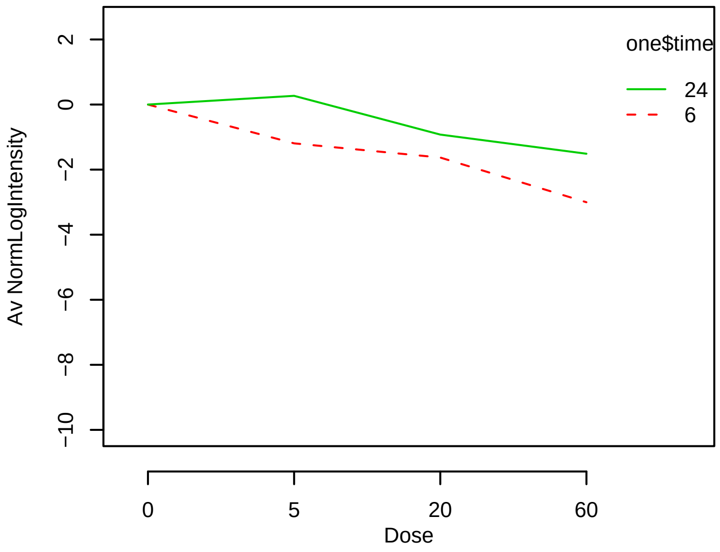


GO_0051325 : interphase

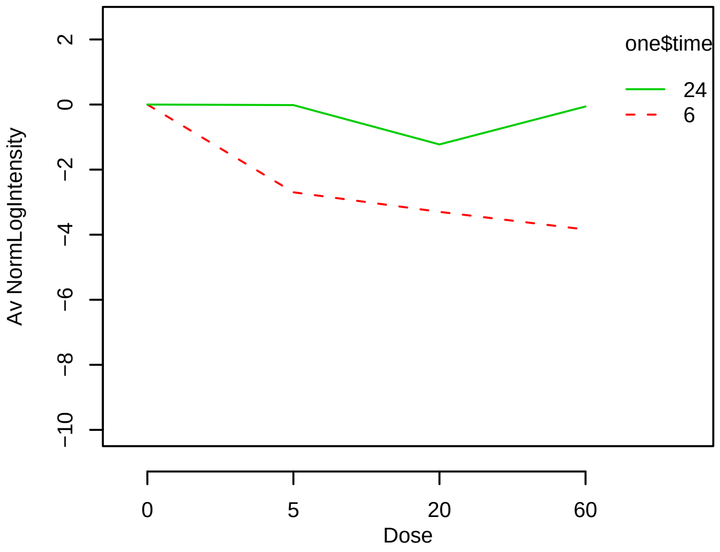


GO_0051327 : M phase of meiotic cell cycle

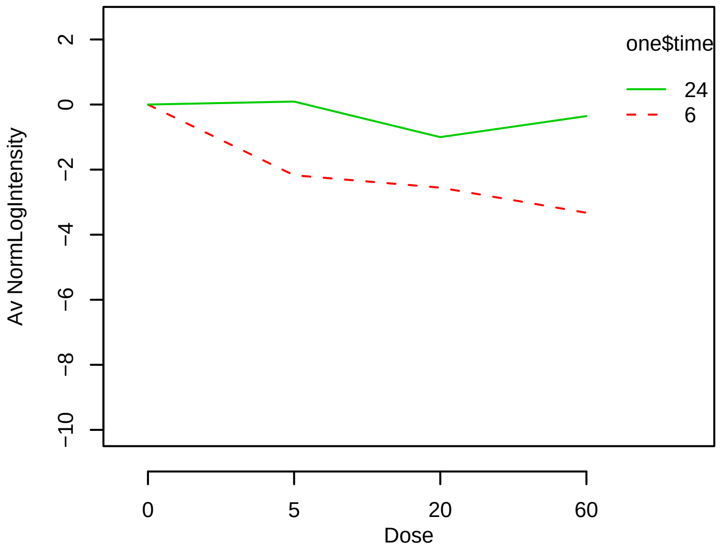




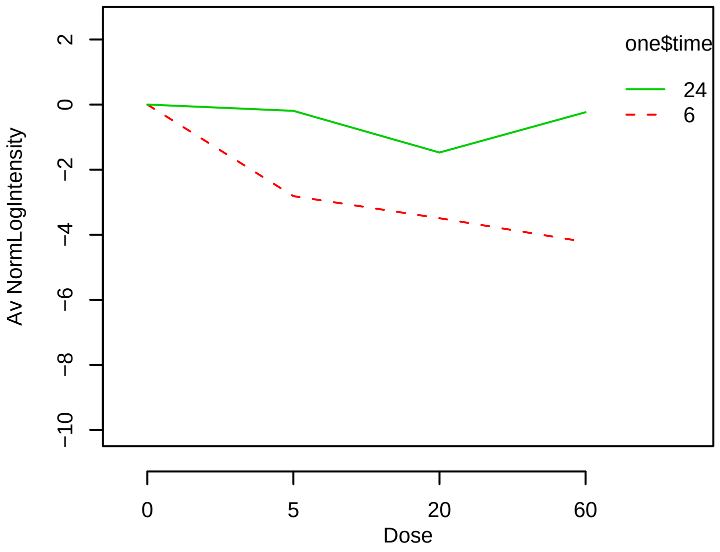
GO_0051329 : interphase of mitotic cell cycle



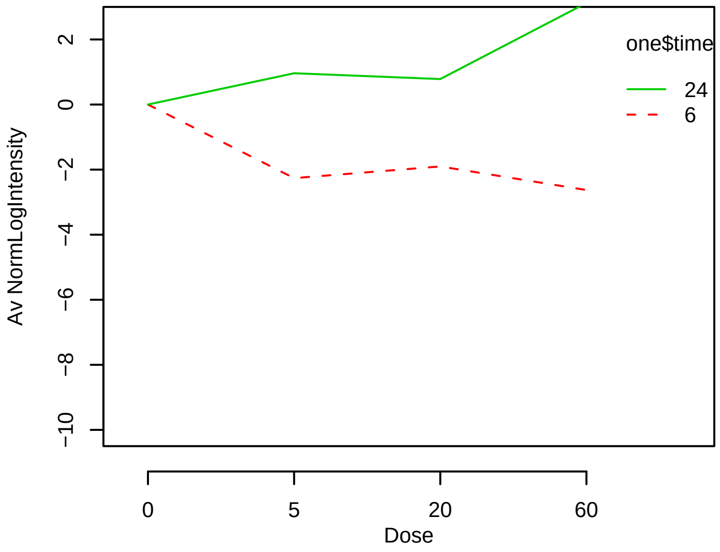
GO_0051336 : regulation of hydrolase activity



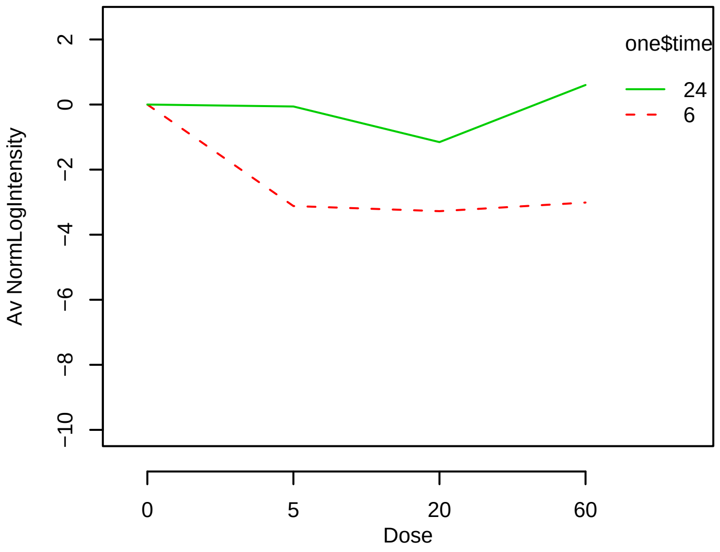
GO_0051338 : regulation of transferase activity



GO_0051339 : regulation of lyase activity

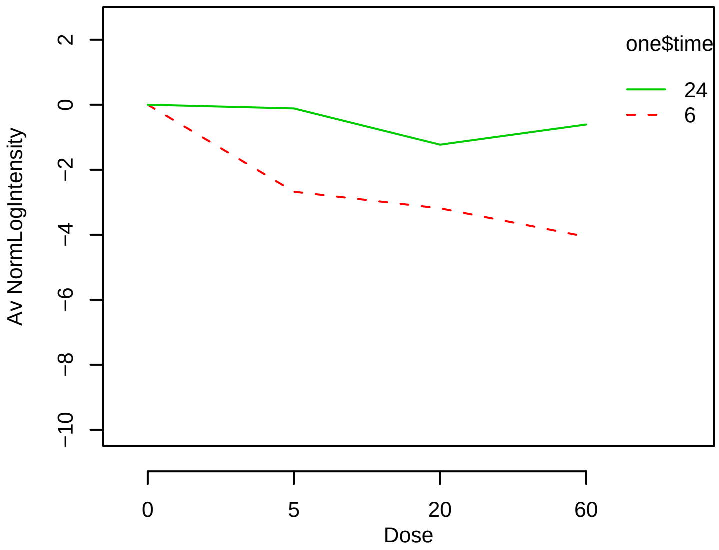


GO_0051341 : regulation of oxidoreductase activity

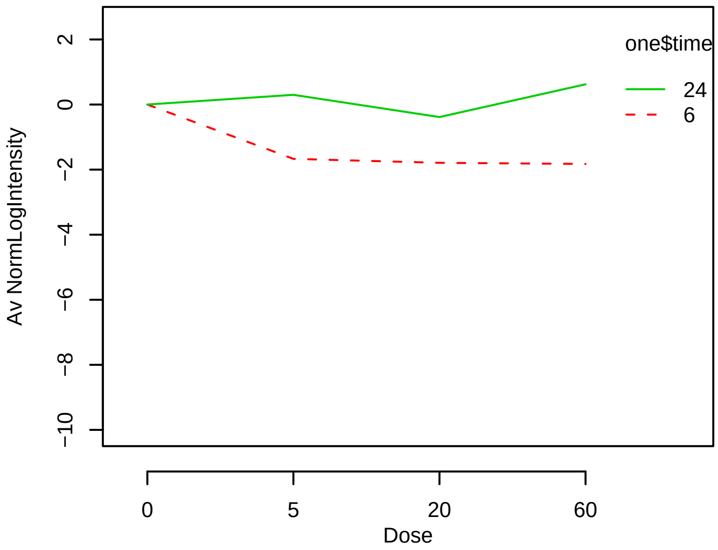


GO_0051345 : positive regulation of hydrolase activity

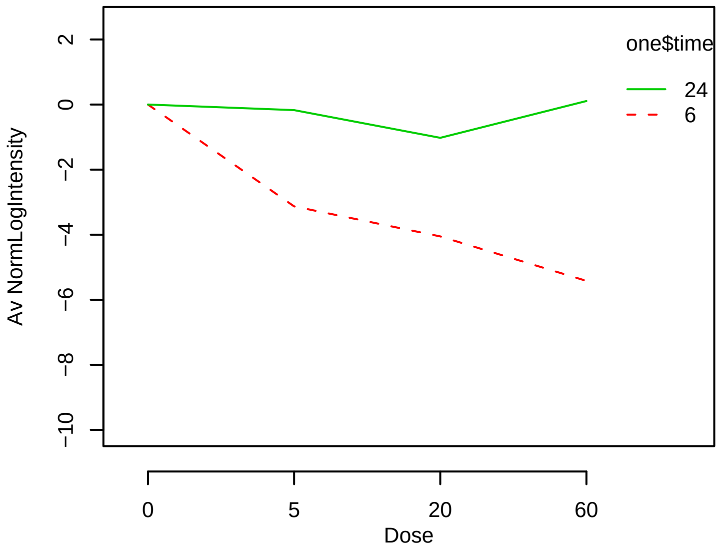
GO_0051347 : positive regulation of transferase activity



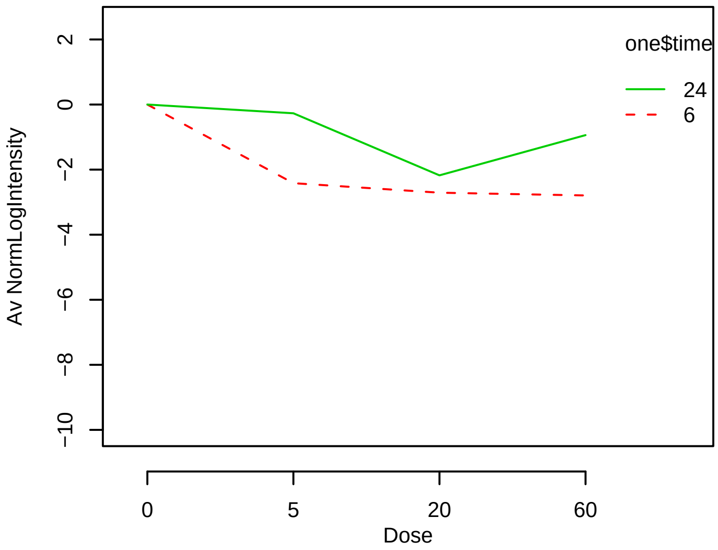
GO_0051348 : negative regulation of transferase activity



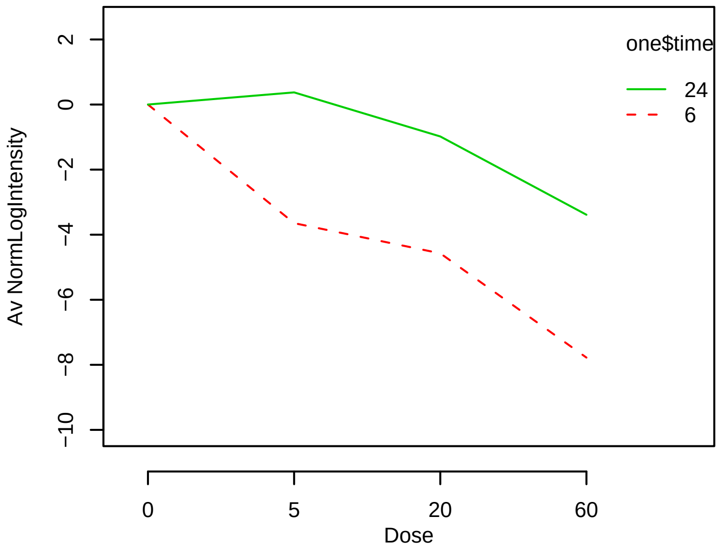
GO_0051349 : positive regulation of lyase activity



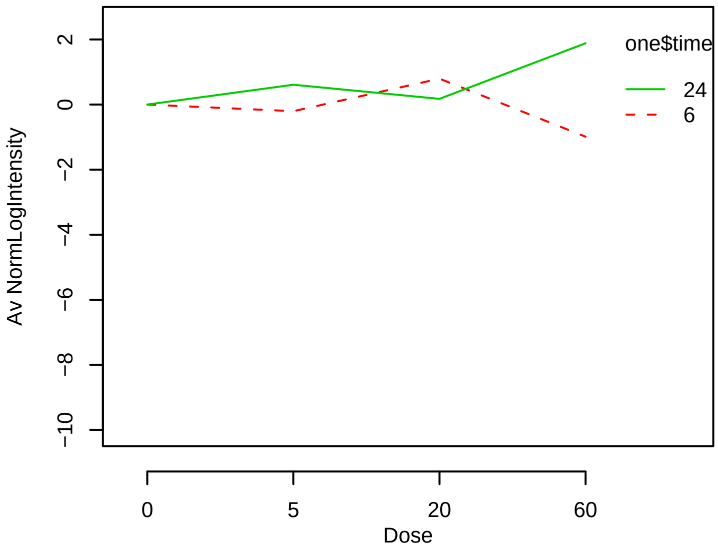
GO_0051350 : negative regulation of lyase activity

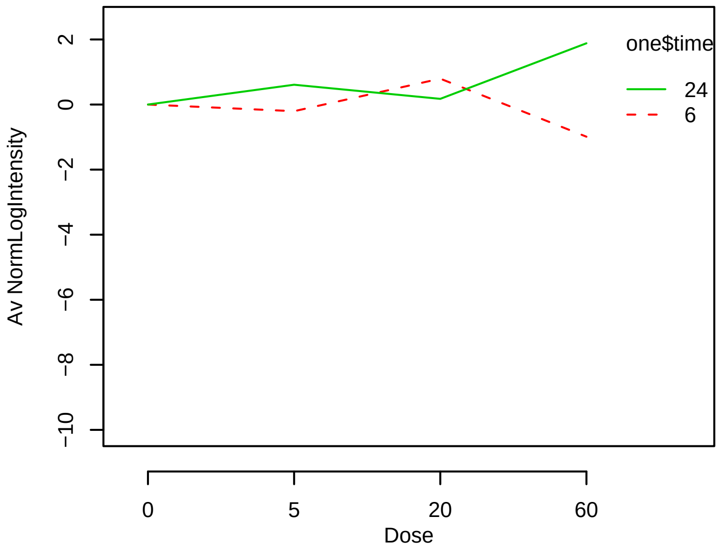


GO_0051402 : neuron apoptosis

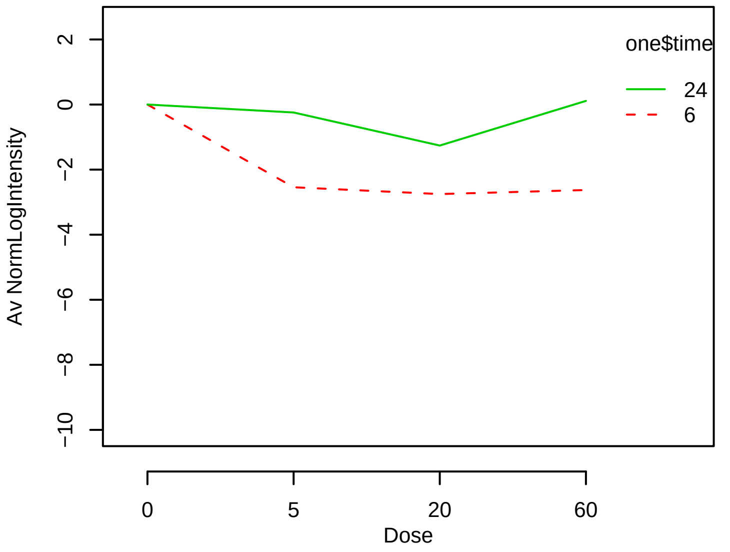


GO_0051452 : cellular pH reduction

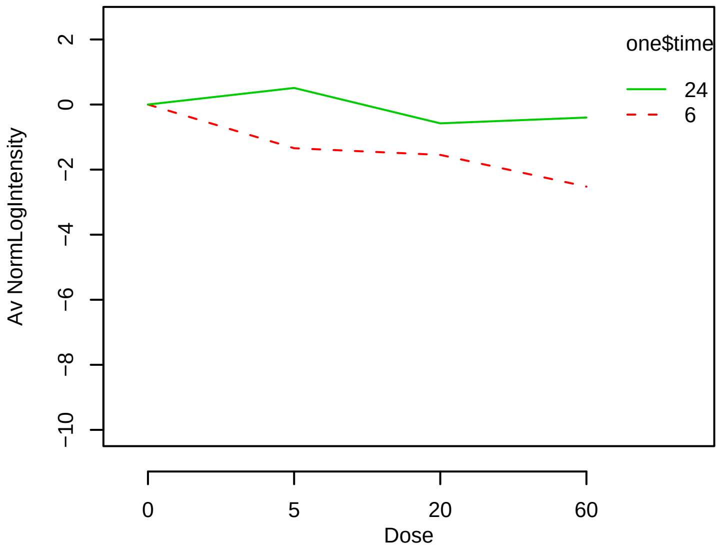




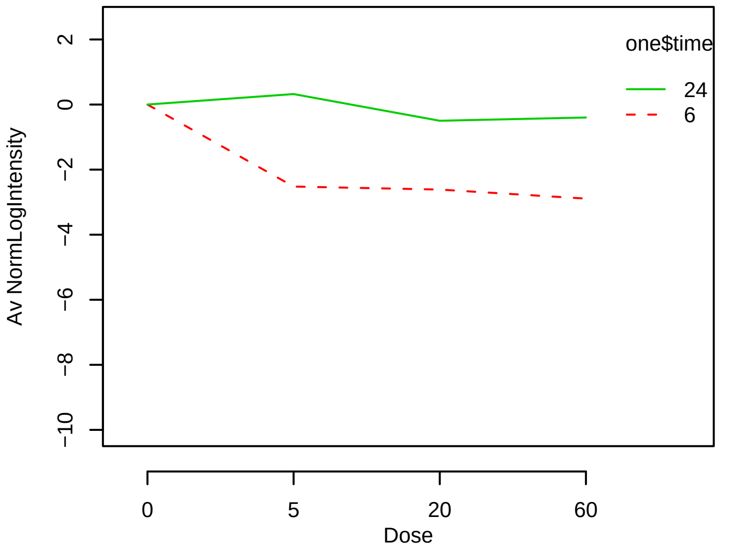
GO_0051453 : regulation of cellular pH



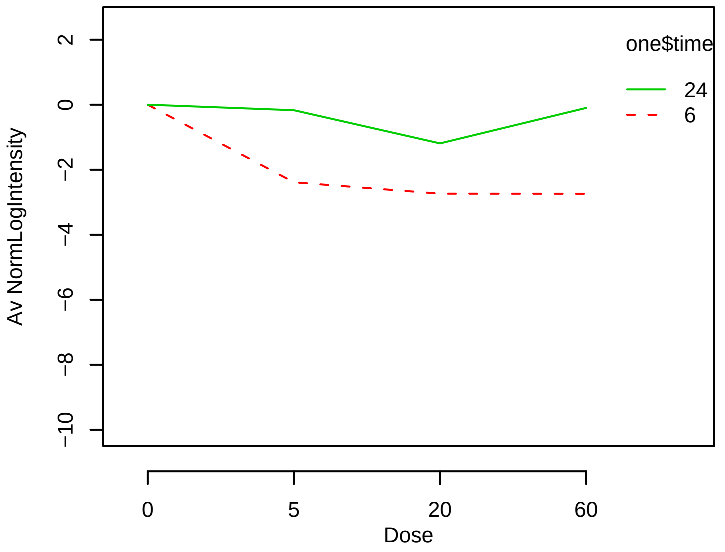
GO_0051480 : cytosolic calcium ion homeostasis



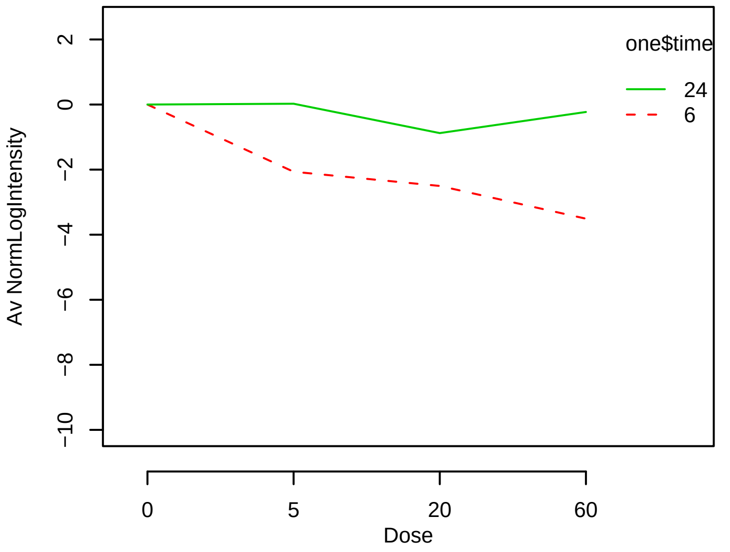
GO_0051603 : proteolysis during cellular protein catabolis



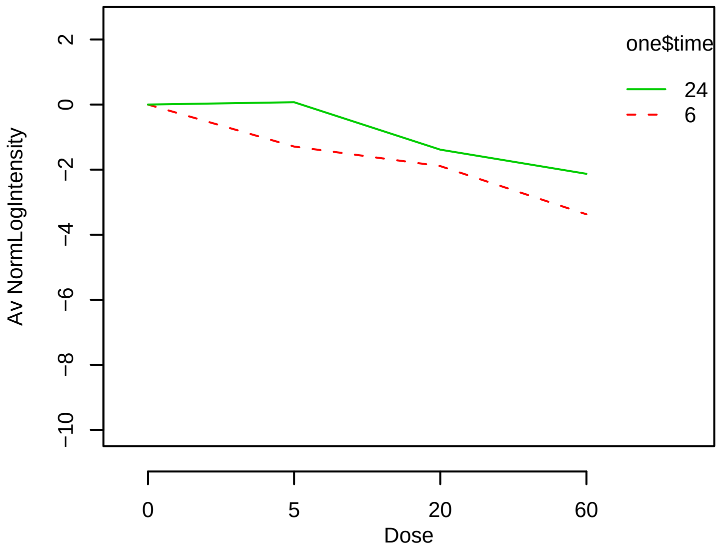
GO_0051604 : protein maturation

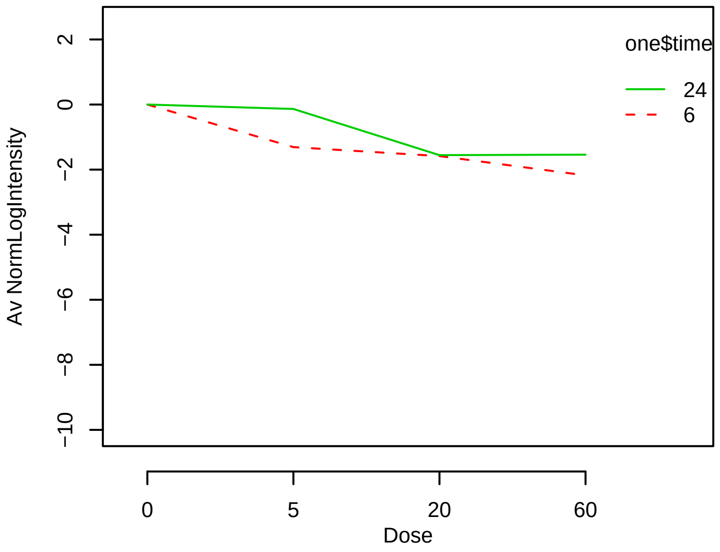


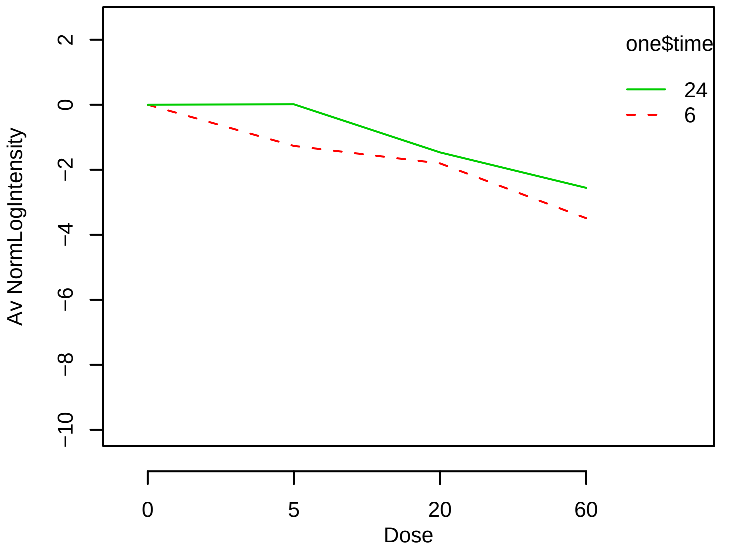
GO_0051606 : detection of stimulus

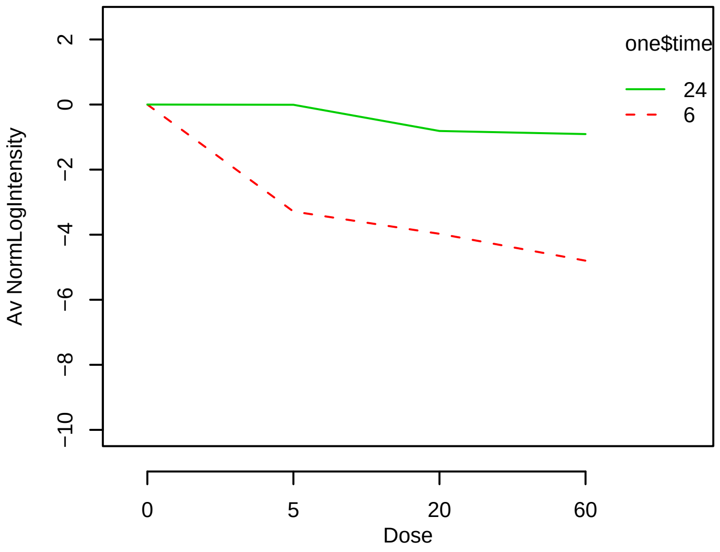


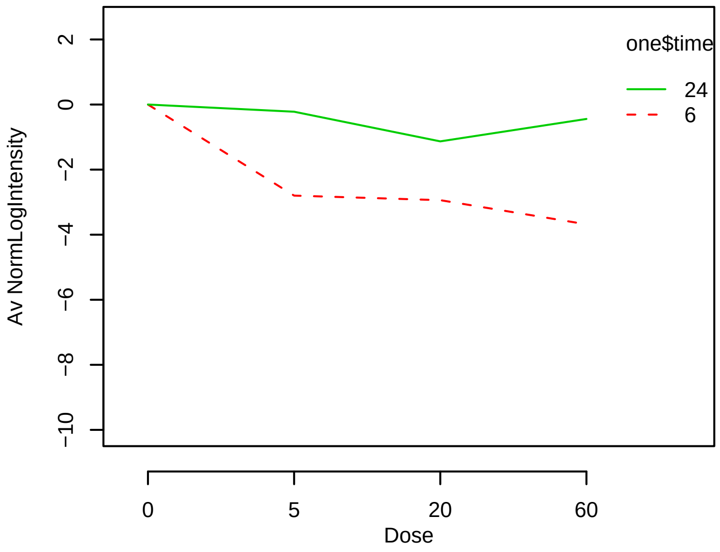
GO_0051607 : defense response to virus

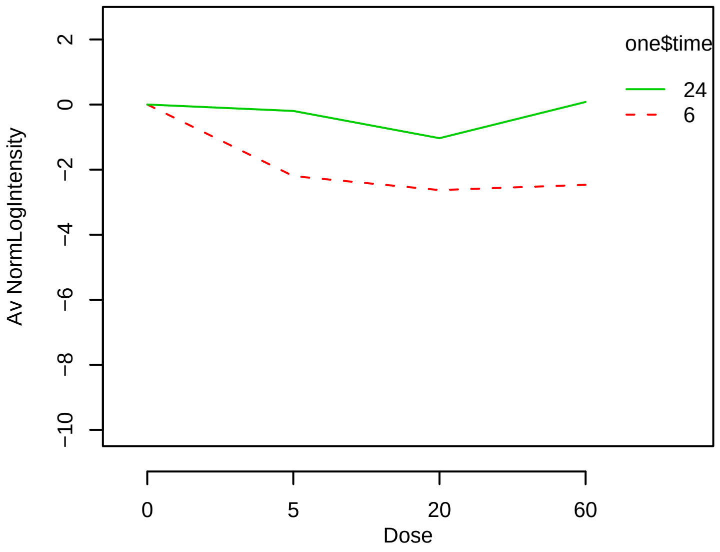

GO_0051640 : organelle localization


GO_0051647 : nucleus localization

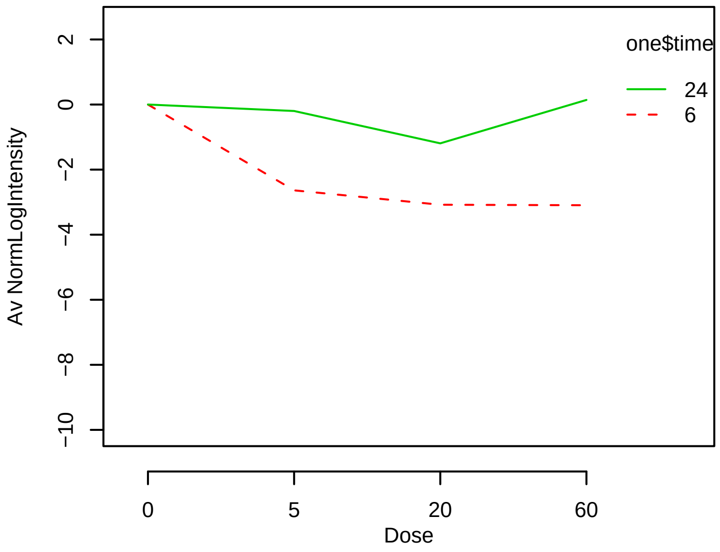

GO_0051656 : establishment of organelle localization


GO_0051668 : localization within membrane

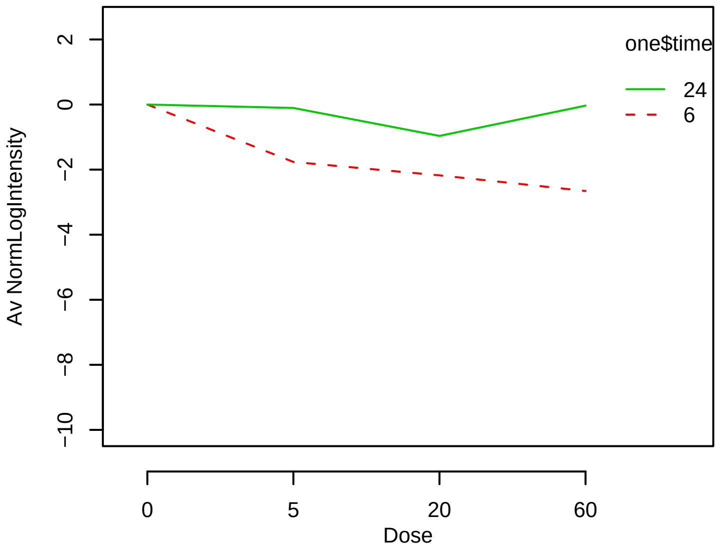

GO_0051693 : actin filament capping


GO_0051701 : interaction with host

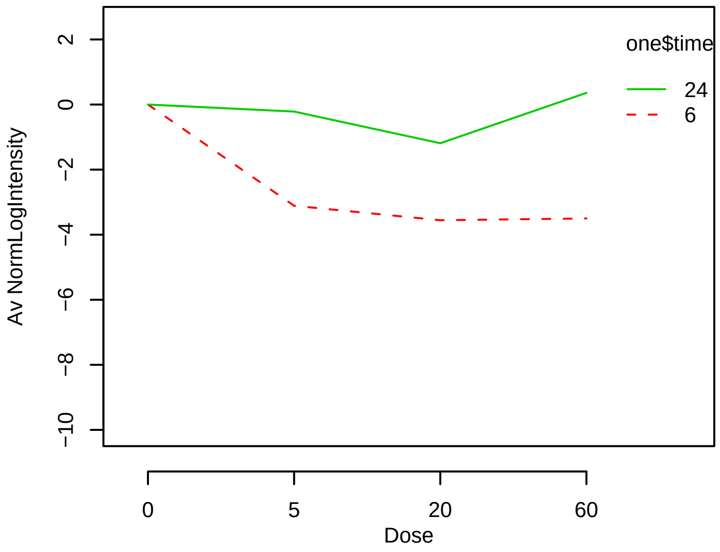
GO_0051704 : interaction between organisms



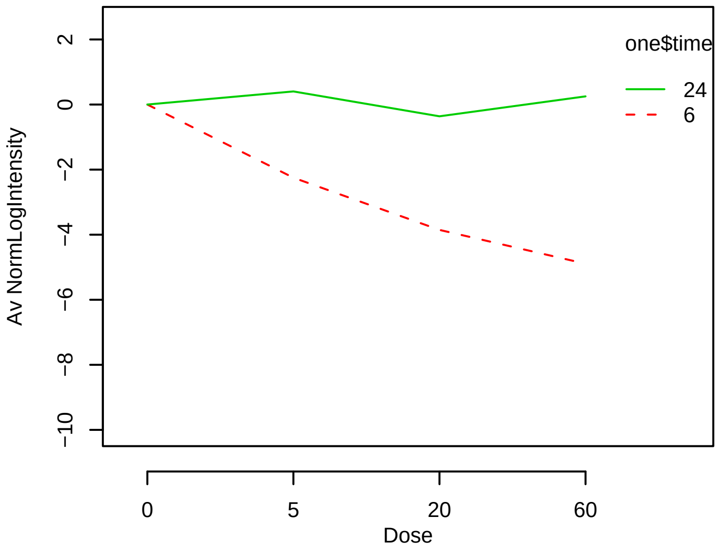
GO_0051705 : behavioral interaction between organisms



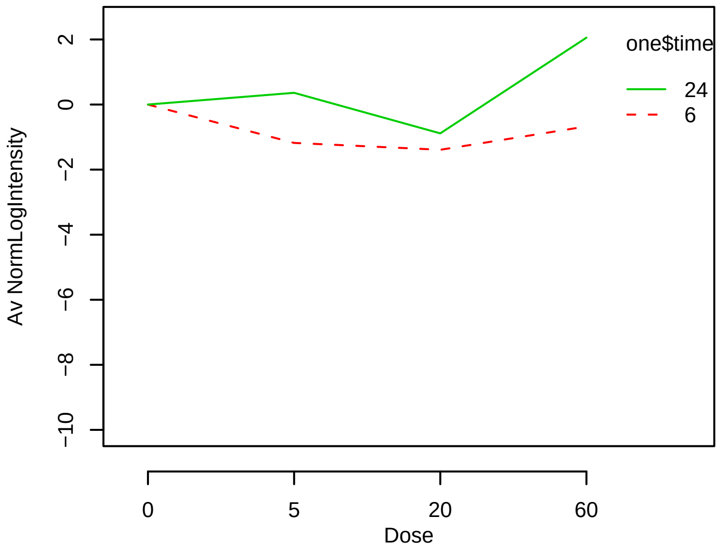
GO_0051706 : physiological interaction between organism



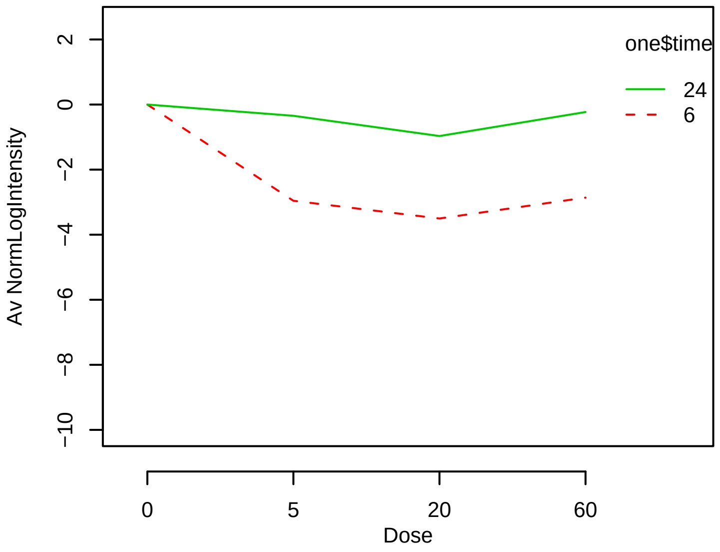
GO_0051716 : cellular response to stimulus

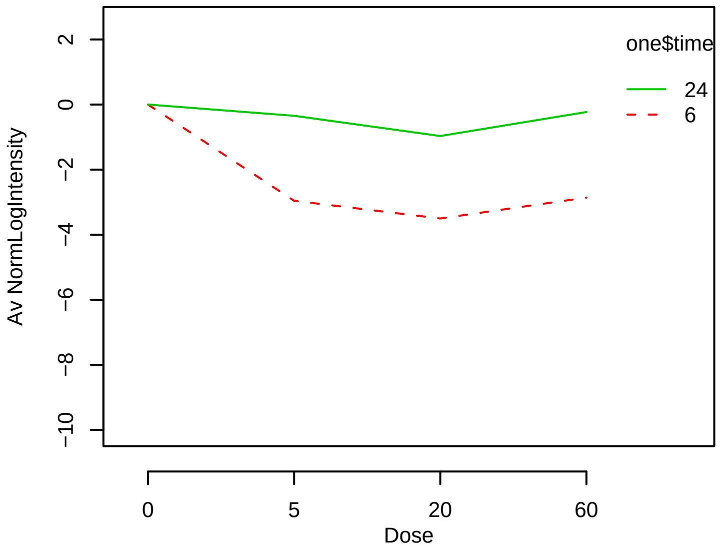


GO_0051789 : response to protein stimulus

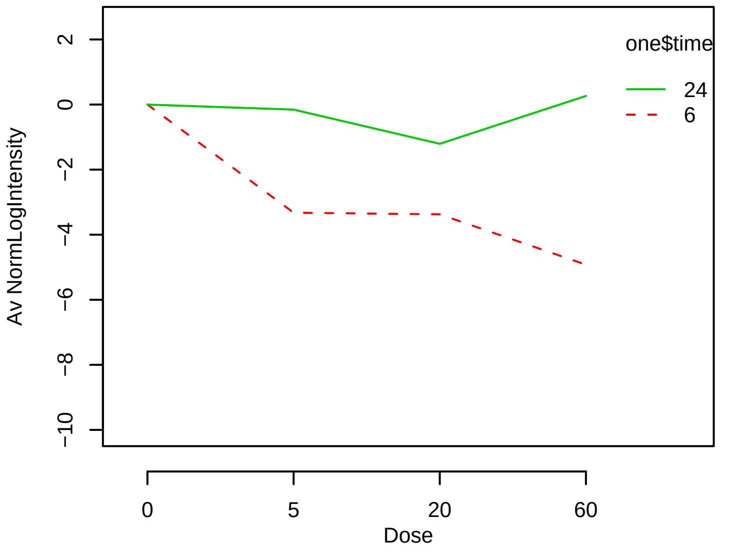


GO_0051806 : entry into cell of other organism during symbi

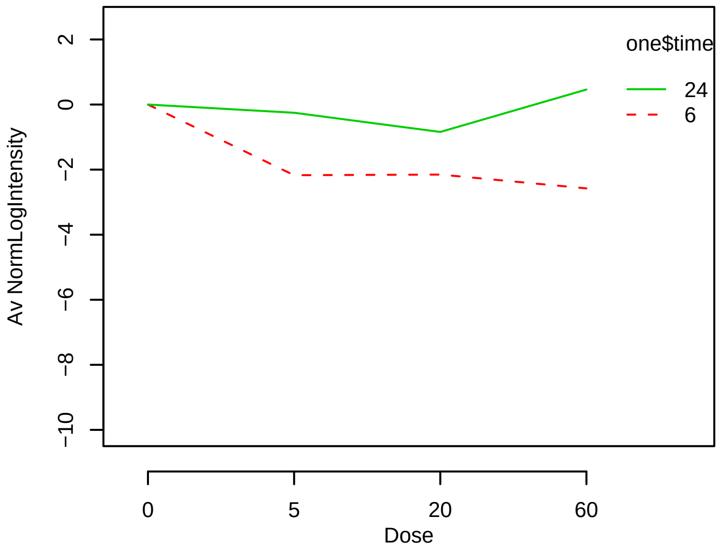




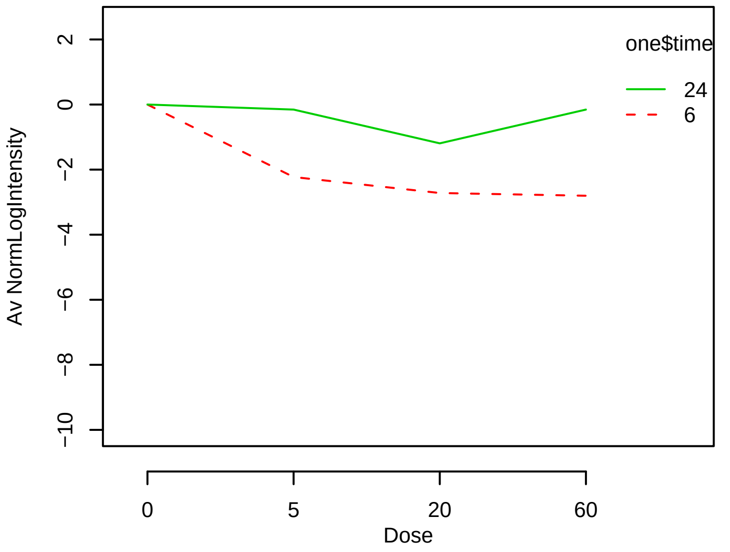
GO_0051828 : entry into other organism during symbiotic int



GO_0051923 : sulfation



GO_0051924 : regulation of calcium ion transport



GO_0051969 : regulation of transmission of nerve impuls