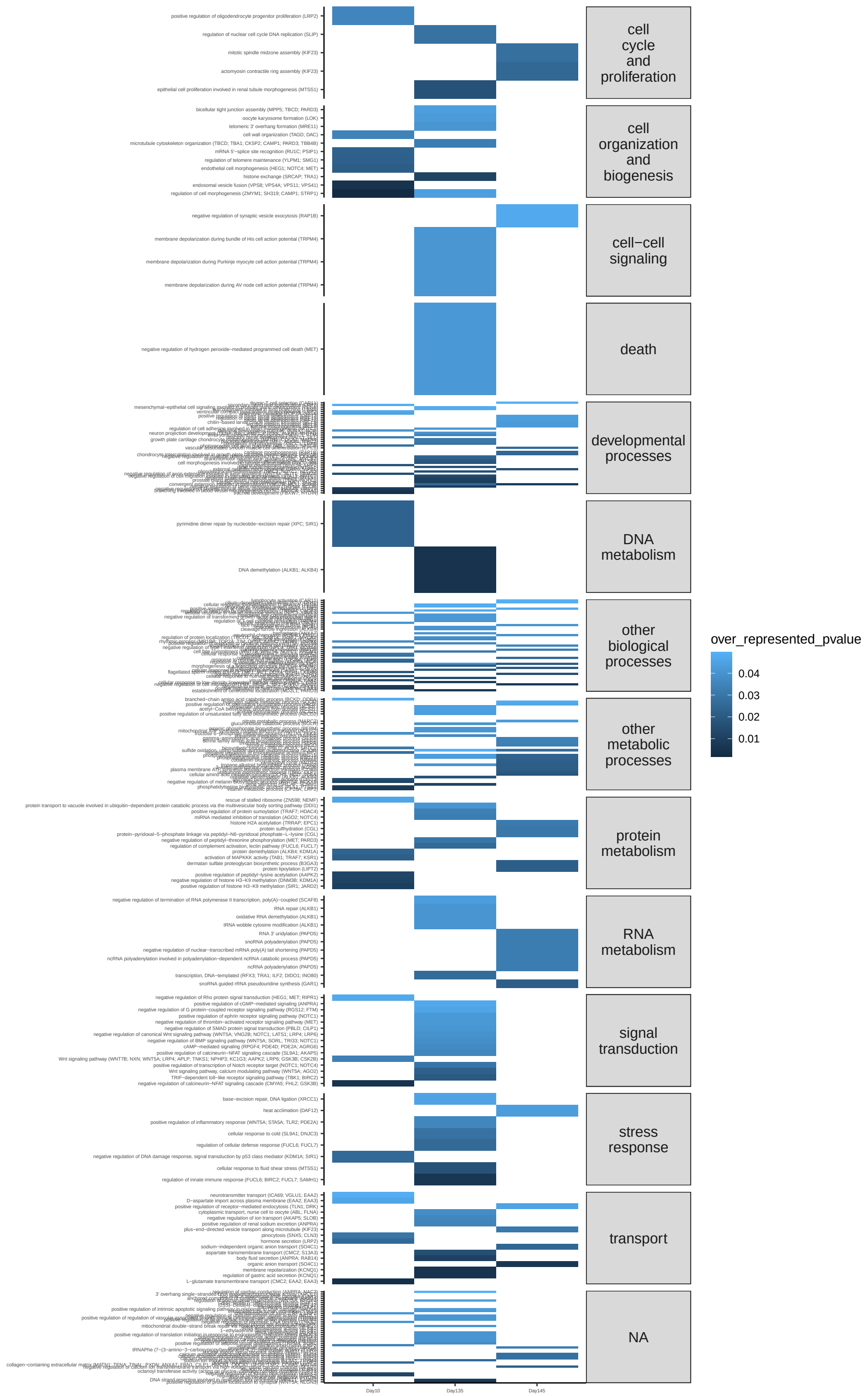
positive regulation of oligodendrocyte progenitor proliferation (LRP2)
regulation of nuclear cell cycle DNA replication (SLIP)
mitotic spindle midzone assembly (KIF23)
actomyosin contractile ring assembly (KIF23)
epithelial cell proliferation involved in renal tubule morphogenesis (MTSS1)
cell cycle and proliferation
bicellular tight junction assembly (MPP5; TBCD; PARD3)
oocyte karyosome formation (LOK)
telomeric 3' overhang formation (MRE11)
cell wall organization (TAGD; DAC)
microtubule cytoskeleton organization (TBCD; TBA1; CK5P2; CAMP1; PARD3; TBB4B)
mRNA 5'−splice site recognition (RU1C; PSIP1)
regulation of telomere maintenance (YLPM1; SMG1)
endothelial cell morphogenesis (HEG1; NOTC4; MET)
histone exchange (SRCAP; TRA1)
endosomal vesicle fusion (VPS8; VPS4A; VPS11; VPS41)
regulation of cell morphogenesis (ZMYM1; SH319; CAMP1; STRP1)
cell organization and biogenesis
negative regulation of synaptic vesicle exocytosis (RAP1B)
membrane depolarization during bundle of His cell action potential (TRPM4)
membrane depolarization during Purkinje myocyte cell action potential (TRPM4)
membrane depolarization during AV node cell action potential (TRPM4)
cell−cell signaling
negative regulation of hydrogen peroxide−mediated programmed cell death (MET)
death
mesenchymal−epithelial cell signaling involved in prostate gland morphogenesis (HEG1)
chitin−based larval cuticle pattern formation (TBCD)
regulation of cell adhesion involved in heart morphogenesis (NOTC4)
neuron projection development (MEF2A; MEF2C; ACSL1; MET; PRPF8)
growth plate cartilage chondrocyte proliferation (MET; ACSL1; PRPF8)
vascular smooth muscle cell differentiation (EPC1)
chondrocyte intercalation involved in growth plate cartilage morphogenesis (RAP1B)
cell morphogenesis involved in neuron differentiation (MET; CSF1)
negative regulation of axon extension involved in axon guidance (WNT5A; SLIT1; SEMA3A)
negative regulation of cell migration involved in sprouting angiogenesis (NOTC4; MET)
prostate gland epithelium morphogenesis (HEG1; NOTC4)
convergent extension involved in neural plate elongation (MET; SSSB)
negative regulation of neuron differentiation (TBCD; BCL9)
branching involved in blood vessel morphogenesis (MEF2A; CAMP1)
tracheal development (FBXW7; HYDIN)
developmental processes
pyrimidine dimer repair by nucleotide−excision repair (XPC; SIR1)
DNA demethylation (ALKB1; ALKB4)
DNA metabolism
lymphocyte activation (CAB11)
cellular response to stimulus (TEP2)
positive regulation of cell proliferation (TEP2)
cellular response to stem cell factor stimulus (KSR2; CSF3)
negative regulation of transforming growth factor beta receptor signaling pathway (MET)
regulation of cell cycle phase transition (TRPM4)
cell morphogenesis involved in neuron differentiation (MEF2A)
cleavage furrow ingression (ACKR3)
neutrophil chemotaxis (CEC12; ACKR3; RAP1B; TGFB1; CXCR2)
regulation of protein localization (CEC12; ACKR3; RAP1B; TGFB1; CXCR2)
rhythmic process (MS18B; TOP2A; TIM; QRICH1; CAMP1; NOTCH3; TBCD)
positive regulation of transcription by oleic acid (NOTCH3; TBCD)
negative regulation of type I interferon production (TRPM4)
establishment of mitotic spindle orientation (MEF2A; SH319; CAMP1)
cell fate commitment (WNT5A; NOTCH3; PRPF8)
cellular response to cytokine stimulus (CSF3; CXCR2)
response to cytokine (CEP29; CEP3; CXCR2)
regulation of vascular smooth muscle contraction (CAMP1; CSF3)
morphogenesis of a branching structure (MEF2A; CAMP1)
cellular response to chemokine (CEC12; CXCR2; TGFB1)
flagellated sperm motility (MS18B; TOP2A; TIM; QRICH1; PCEM1)
cellular response to interferon-beta (CSF3; CXCR2)
cellular response to lipopolysaccharide (KSR2; CSF3)
negative regulation of cell migration involved in sprouting angiogenesis (ACKR3; CAMP1)
establishment of centrosome localization (MD21L; PARD3)
other biological processes
branched−chain amino acid catabolic process (BCKD; ODBA)
positive regulation of sperm capacitation (ACSF3)
acetyl−CoA biosynthetic process from acetate (ACSF3)
positive regulation of unsaturated fatty acid biosynthetic process (ABCD2)
nitrate metabolic process (MARC2)
glucuronoside catabolic process (BCLR)
mitochondrial ATP synthesis coupled electron transport (UQCRC2)
fructose 6−phosphate metabolic process (PFKM)
gamma−aminobutyric acid metabolic process (ISEPA)
serine family amino acid biosynthetic process (ISEPA)
tryptophan catabolic process (KMO)
biosynthetic process (PBLD; HOXC5; SEC24A)
sulfide oxidation, using sulfide dehydrogenase (cytochrome) (SQRDL)
negative regulation of endopeptidase activity (PLRG1)
prostaglandin biosynthetic process (PTGES3)
cobalamin biosynthetic process (MMAA)
3−hydroxyanthranilate biosynthetic process (KMO)
plasma membrane ATP synthesis coupled electron transport (UQCRC2)
cellular amino acid catabolic process (BCKD; ODBA)
negative regulation of melanin biosynthetic process (MC1R; SCN1A)
phosphatidylserine biosynthetic process (PSS1)
vitamin metabolic process (CP26A; LRP2)
other metabolic processes
rescue of stalled ribosome (ZN598; NEMF)
protein transport to vacuole involved in ubiquitin−dependent protein catabolic process via the multivesicular body sorting pathway (DDI1)
positive regulation of protein sumoylation (TRAF7; HDAC4)
miRNA mediated inhibition of translation (AGO2; NOTC4)
histone H2A acetylation (TRRAP; EPC1)
protein sulfhydration (CGL)
protein−pyridoxal−5−phosphate linkage via peptidyl−N6−pyridoxal phosphate−L−lysine (CGL)
negative regulation of peptidyl−threonine phosphorylation (MET; PARD3)
regulation of complement activation, lectin pathway (FUCL6; FUCL7)
protein demethylation (ALKB4; KDM1A)
activation of MAPKKK activity (TAB1; TRAF7; KSR1)
dermatan sulfate proteoglycan biosynthetic process (B3GA3)
protein lipoylation (LIPT2)
positive regulation of peptidyl−lysine acetylation (AAPK2)
negative regulation of histone H3−K9 methylation (DNM3B; KDM1A)
positive regulation of histone H3−K9 methylation (SIR1; JARD2)
protein metabolism
negative regulation of termination of RNA polymerase II transcription, poly(A)−coupled (SCAF8)
RNA repair (ALKB1)
oxidative RNA demethylation (ALKB1)
tRNA wobble cytosine modification (ALKB1)
RNA 3' uridylation (PAPD5)
snoRNA polyadenylation (PAPD5)
negative regulation of nuclear−transcribed mRNA poly(A) tail shortening (PAPD5)
ncRNA polyadenylation involved in polyadenylation−dependent ncRNA catabolic process (PAPD5)
ncRNA polyadenylation (PAPD5)
transcription, DNA−templated (RFX3; TRA1; ILF2; DIDO1; INO80)
snoRNA guided rRNA pseudouridine synthesis (GAR1)
RNA metabolism
negative regulation of Rho protein signal transduction (HEG1; MET; RIPR1)
positive regulation of cGMP−mediated signaling (ANPRA)
negative regulation of G protein−coupled receptor signaling pathway (RGS12; FTM)
positive regulation of ephrin receptor signaling pathway (NOTC1)
negative regulation of thrombin−activated receptor signaling pathway (MET)
negative regulation of SMAD protein signal transduction (PBLD; CILP1)
negative regulation of canonical Wnt signaling pathway (WNT5A; VNG2B; NOTC1; LATS1; LRP4; LRP6)
negative regulation of BMP signaling pathway (WNT5A; SORL; TRI33; NOTC1)
cAMP−mediated signaling (RPGF4; PDE4D; PDE2A; AGRG6)
positive regulation of calcineurin−NFAT signaling cascade (SL9A1; AKAP5)
Wnt signaling pathway (WNT7B; NXN; WNT5A; LRP4; APLP; TNKS1; NPHP3; KC1G3; AAPK2; LRP6; GSK3B; CSK2B)
positive regulation of transcription of Notch receptor target (NOTC1; NOTC4)
Wnt signaling pathway, calcium modulating pathway (WNT5A; AGO2)
TRIF−dependent toll−like receptor signaling pathway (TBK1; BIRC2)
negative regulation of calcineurin−NFAT signaling cascade (CMYA5; FHL2; GSK3B)
signal transduction
base−excision repair, DNA ligation (XRCC1)
heat acclimation (DAF12)
positive regulation of inflammatory response (WNT5A; STA5A; TLR2; PDE2A)
cellular response to cold (SL9A1; DNJC3)
regulation of cellular defense response (FUCL6; FUCL7)
negative regulation of DNA damage response, signal transduction by p53 class mediator (KDM1A; SIR1)
cellular response to fluid shear stress (MTSS1)
regulation of innate immune response (FUCL6; BIRC2; FUCL7; SAMH1)
stress response
neurotransmitter transport (ICA69; VGLU1; EAA2)
D−aspartate import across plasma membrane (EAA2; EAA3)
positive regulation of receptor−mediated endocytosis (TLN1; DRK)
cytoplasmic transport, nurse cell to oocyte (ABL; FLNA)
negative regulation of ion transport (AKAP5; SLOB)
positive regulation of renal sodium excretion (ANPRA)
plus−end−directed vesicle transport along microtubule (KIF23)
pinocytosis (SNX5; CLN3)
hormone secretion (LRP2)
sodium−independent organic anion transport (SO4C1)
aspartate transmembrane transport (CMC2; S13A3)
body fluid secretion (ANPRA; RAB14)
organic anion transport (SO4C1)
membrane repolarization (KCNQ1)
regulation of gastric acid secretion (KCNQ1)
L−glutamate transmembrane transport (CMC2; EAA2; EAA3)
transport
regulation of cardiac conduction (ANPRA; NAC2)
3' overhang single−stranded DNA endonucleolytic processing (EXO1)
anchored component of membrane (ACSF3)
regulation of [28S] rRNA 2'−O−methylation (HMT1; RRP8)
[28S]−Delta(4)−dehydrouridine biosynthetic process (DUS4)
positive regulation of intrinsic apoptotic signaling pathway in response to DNA damage (TBPL1)
negative regulation of ubiquitin−protein ligase activity (MEF2A)
positive regulation of regulation of vascular smooth muscle contraction (CAMP1)
positive regulation of ribosomal protein S6 kinase activity (TBPL1)
negative regulation of ribosomal DNA heterochromatinization (HMT1)
mitochondrial double−strand break repair via break-induced replication (MUS81)
1−ethylguanine deaminase activity (ALKB1)
positive regulation of translation initiation in response to endoplasmic reticulum stress (DDO3)
positive regulation of cellular protein metabolic process (NEMF)
positive regulation of protein localization (NEMF)
positive regulation of adipose tissue development (HSD3B)
tRNAPhe (7−(3−amino−3−carboxypropyl)wye−37−C2−methyl−C5−methyl−C6−methyl−C7−methyl−C8−methyl−C9−methyl−C10−methyl−C11−methyl−C12−methyl−C13−methyl−C14−methyl−C15−methyl−C16−methyl−C17−methyl−C18−methyl−C19−methyl−C20−methyl−C21−methyl−C22−methyl−C23−methyl−C24−methyl−C25−methyl−C26−methyl−C27−methyl−C28−methyl−C29−methyl−C30−methyl−C31−methyl−C32−methyl−C33−methyl−C34−methyl−C35−methyl−C36−methyl−C37−methyl−C38−methyl−C39−methyl−C40−methyl−C41−methyl−C42−methyl−C43−methyl−C44−methyl−C45−methyl−C46−methyl−C47−methyl−C48−methyl−C49−methyl−C50−methyl−C51−methyl−C52−methyl−C53−methyl−C54−methyl−C55−methyl−C56−methyl−C57−methyl−C58−methyl−C59−methyl−C60−methyl−C61−methyl−C62−methyl−C63−methyl−C64−methyl−C65−methyl−C66−methyl−C67−methyl−C68−methyl−C69−methyl−C70−methyl−C71−methyl−C72−methyl−C73−methyl−C74−methyl−C75−methyl−C76−methyl−C77−methyl−C78−methyl−C79−methyl−C80−methyl−C81−methyl−C82−methyl−C83−methyl−C84−methyl−C85−methyl−C86−methyl−C87−methyl−C88−methyl−C89−methyl−C90−methyl−C91−methyl−C92−methyl−C93−methyl−C94−methyl−C95−methyl−C96−methyl−C97−methyl−C98−methyl−C99−methyl−C100−methyl−C101−methyl−C102−methyl−C103−methyl−C104−methyl−C105−methyl−C106−methyl−C107−methyl−C108−methyl−C109−methyl−C110−methyl−C111−methyl−C112−methyl−C113−methyl−C114−methyl−C115−methyl−C116−methyl−C117−methyl−C118−methyl−C119−methyl−C120−methyl−C121−methyl−C122−methyl−C123−methyl−C124−methyl−C125−methyl−C126−methyl−C127−methyl−C128−methyl−C129−methyl−C130−methyl−C131−methyl−C132−methyl−C133−methyl−C134−methyl−C135−methyl−C136−methyl−C137−methyl−C138−methyl−C139−methyl−C140−methyl−C141−methyl−C142−methyl−C143−methyl−C144−methyl−C145−methyl−C146−methyl−C147−methyl−C148−methyl−C149−methyl−C150−methyl−C151−methyl−C152−methyl−C153−methyl−C154−methyl−C155−methyl−C156−methyl−C157−methyl−C158−methyl−C159−methyl−C160−methyl−C161−methyl−C162−methyl−C163−methyl−C164−methyl−C165−methyl−C166−methyl−C167−methyl−C168−methyl−C169−methyl−C170−methyl−C171−methyl−C172−methyl−C173−methyl−C174−methyl−C175−methyl−C176−methyl−C177−methyl−C178−methyl−C179−methyl−C180−methyl−C181−methyl−C182−methyl−C183−methyl−C184−methyl−C185−methyl−C186−methyl−C187−methyl−C188−methyl−C189−methyl−C190−methyl−C191−methyl−C192−methyl−C193−methyl−C194−methyl−C195−methyl−C196−methyl−C197−methyl−C198−methyl−C199−methyl−C200−methyl−C201−methyl−C202−methyl−C203−methyl−C204−methyl−C205−methyl−C206−methyl−C207−methyl−C208−methyl−C209−methyl−C210−methyl−C211−methyl−C212−methyl−C213−methyl−C214−methyl−C215−methyl−C216−methyl−C217−methyl−C218−methyl−C219−methyl−C220−methyl−C221−methyl−C222−methyl−C223−methyl−C224−methyl−C225−methyl−C226−methyl−C227−methyl−C228−methyl−C229−methyl−C230−methyl−C231−methyl−C232−methyl−C233−methyl−C234−methyl−C235−methyl−C236−methyl−C237−methyl−C238−methyl−C239−methyl−C240−methyl−C241−methyl−C242−methyl−C243−methyl−C244−methyl−C245−methyl−C246−methyl−C247−methyl−C248−methyl−C249−methyl−C250−methyl−C251−methyl−C252−methyl−C253−methyl−C254−methyl−C255−methyl−C256−methyl−C257−methyl−C258−methyl−C259−methyl−C260−methyl−C261−methyl−C262−methyl−C263−methyl−C264−methyl−C265−methyl−C266−methyl−C267−methyl−C268−methyl−C269−methyl−C270−methyl−C271−methyl−C272−methyl−C273−methyl−C274−methyl−C275−methyl−C276−methyl−C277−methyl−C278−methyl−C279−methyl−C280−methyl−C281−methyl−C282−methyl−C283−methyl−C284−methyl−C285−methyl−C286−methyl−C287−methyl−C288−methyl−C289−methyl−C290−methyl−C291−methyl−C292−methyl−C293−methyl−C294−methyl−C295−methyl−C296−methyl−C297−methyl−C298−methyl−C299−methyl−C300−methyl−C301−methyl−C302−methyl−C303−methyl−C304−methyl−C305−methyl−C306−methyl−C307−methyl−C308−methyl−C309−methyl−C310−methyl−C311−methyl−C312−methyl−C313−methyl−C314−methyl−C315−methyl−C316−methyl−C317−methyl−C318−methyl−C319−methyl−C320−methyl−C321−methyl−C322−methyl−C323−methyl−C324−methyl−C325−methyl−C326−methyl−C327−methyl−C328−methyl−C329−methyl−C330−methyl−C331−methyl−C332−methyl−C333−methyl−C334−methyl−C335−methyl−C336−methyl−C337−methyl−C338−methyl−C339−methyl−C340−methyl−C341−methyl−C342−methyl−C343−methyl−C344−methyl−C345−methyl−C346−methyl−C347−methyl−C348−methyl−C349−methyl−C350−methyl−C351−methyl−C352−methyl−C353−methyl−C354−methyl−C355−methyl−C356−methyl−C357−methyl−C358−methyl−C359−methyl−C360−methyl−C361−methyl−C362−methyl−C363−methyl−C364−methyl−C365−methyl−C366−methyl−C367−methyl−C368−methyl−C369−methyl−C370−methyl−C371−methyl−C372−methyl−C373−methyl−C374−methyl−C375−methyl−C376−methyl−C377−methyl−C378−methyl−C379−methyl−C380−methyl−C381−methyl−C382−methyl−C383−methyl−C384−methyl−C385−methyl−C386−methyl−C387−methyl−C388−methyl−C389−methyl−C390−methyl−C391−methyl−C392−methyl−C393−methyl−C394−methyl−C395−methyl−C396−methyl−C397−methyl−C398−methyl−C399−methyl−C400−methyl−C401−methyl−C402−methyl−C403−methyl−C404−methyl−C405−methyl−C406−methyl−C407−methyl−C408−methyl−C409−methyl−C410−methyl−C411−methyl−C412−methyl−C413−methyl−C414−methyl−C415−methyl−C416−methyl−C417−methyl−C418−methyl−C419−methyl−C420−methyl−C421−methyl−C422−methyl−C423−methyl−C424−methyl−C425−methyl−C42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