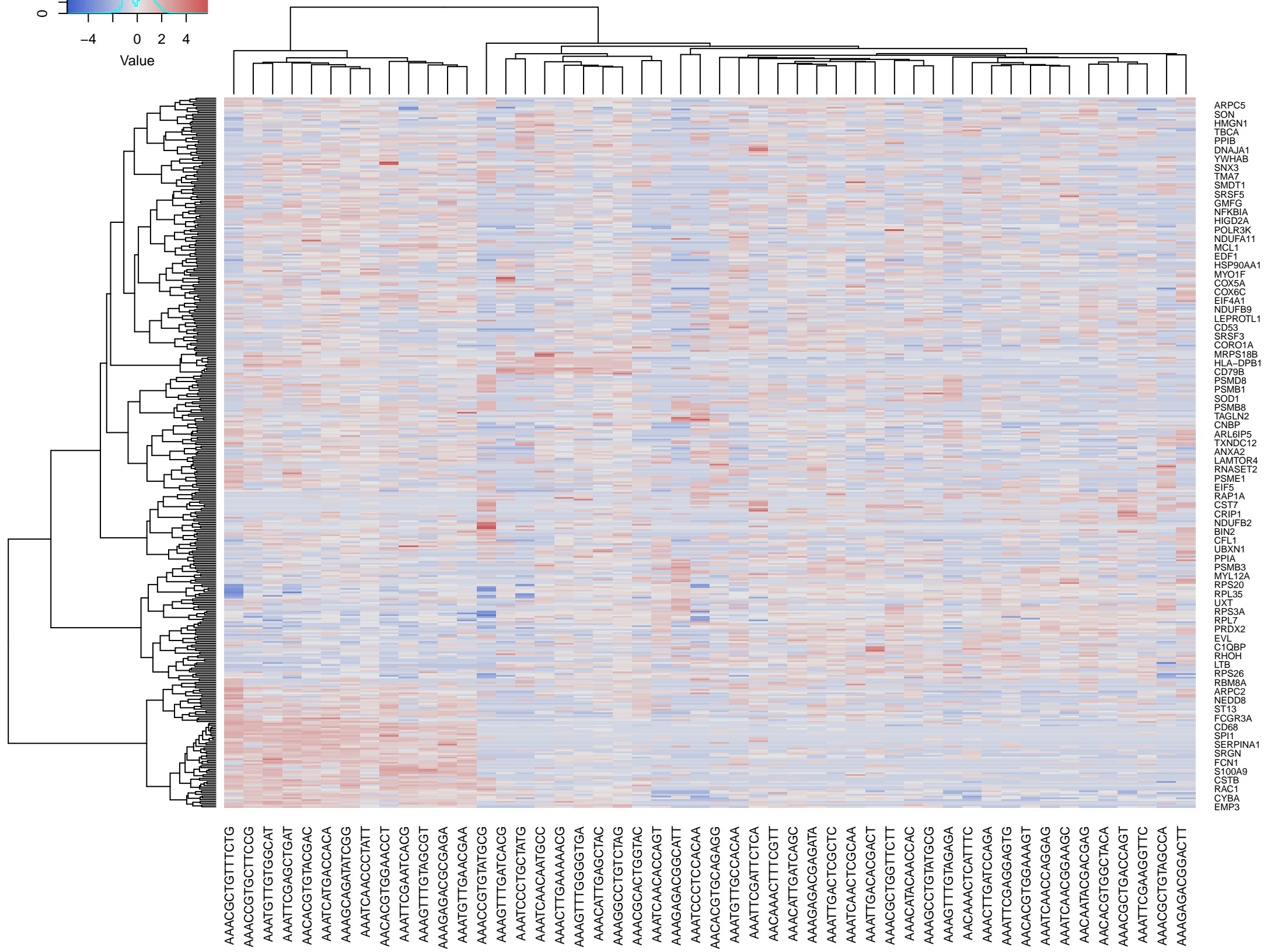
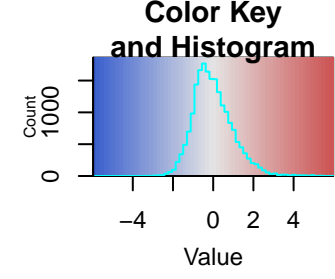
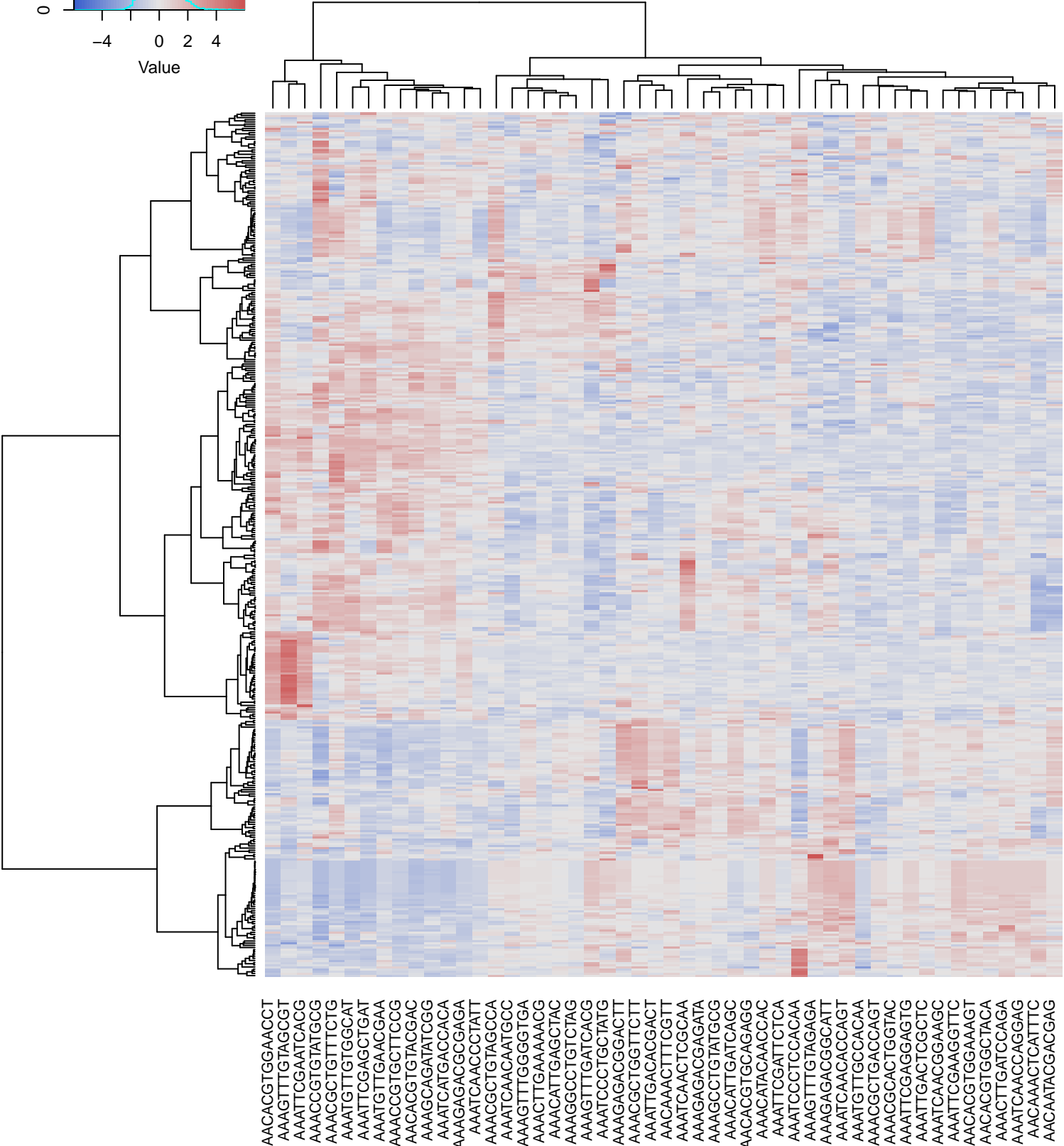


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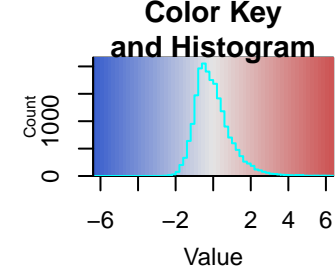




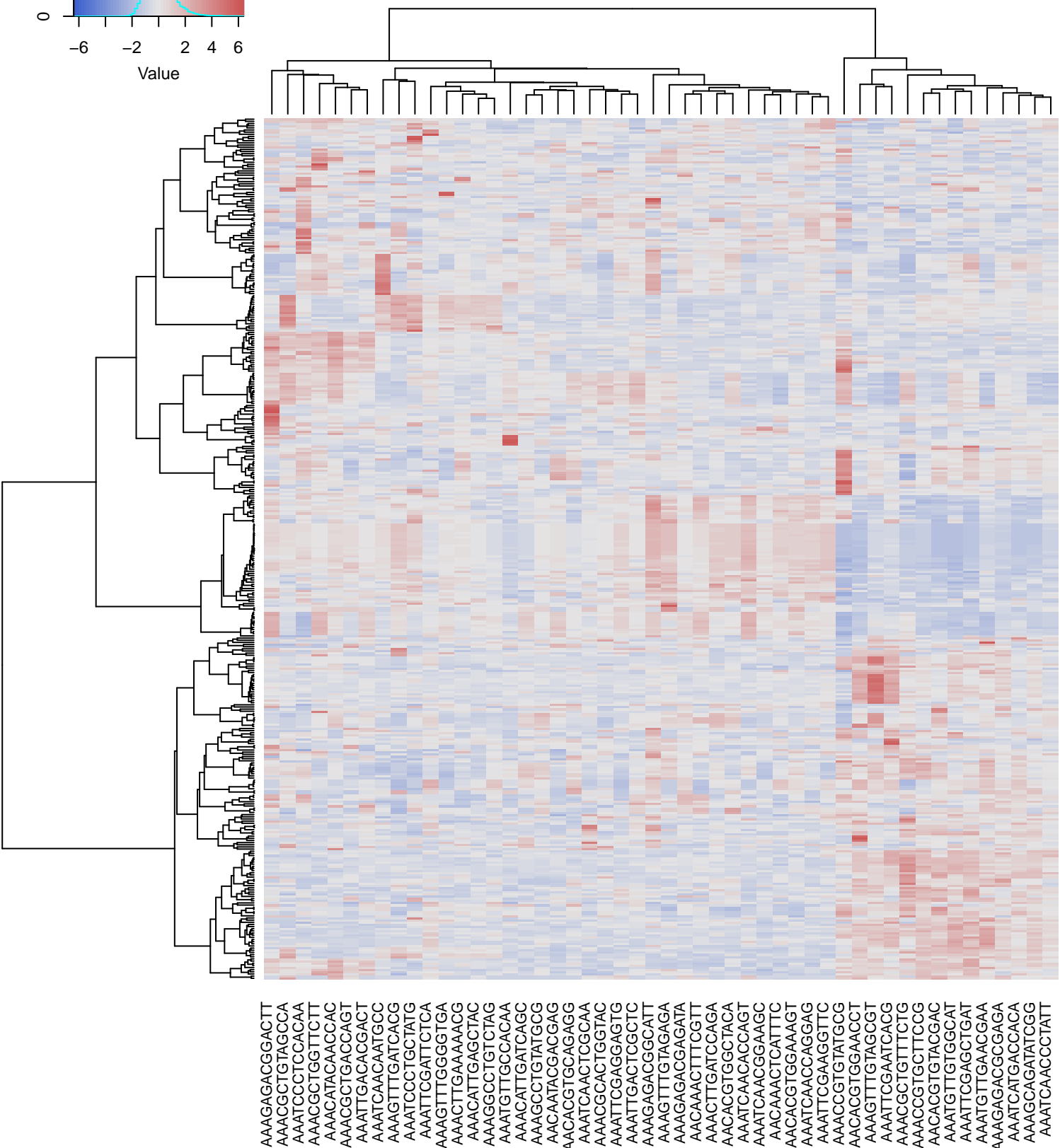
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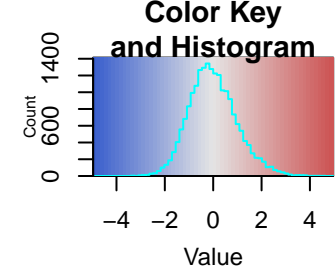
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- GO\_BP:cellular response to organic substance (GO\_0071310)
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- GO\_BP:platelet aggregation (GO\_0070527)
- GO\_BP:positive regulation of transport (GO\_0051050)
- GO\_BP:positive regulation of response to stimulus (GO\_0048584)
- GO\_BP:positive regulation of receptor-mediated endocytosis (GO\_0048260)
- GO\_BP:regulation of neurogenesis (GO\_0050767)
- GO\_BP:regulation of epithelial cell proliferation (GO\_0050678)
- GO\_BP:positive regulation of binding (GO\_0051099)
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- GO\_BP:negative regulation of signal transduction (GO\_0009968)
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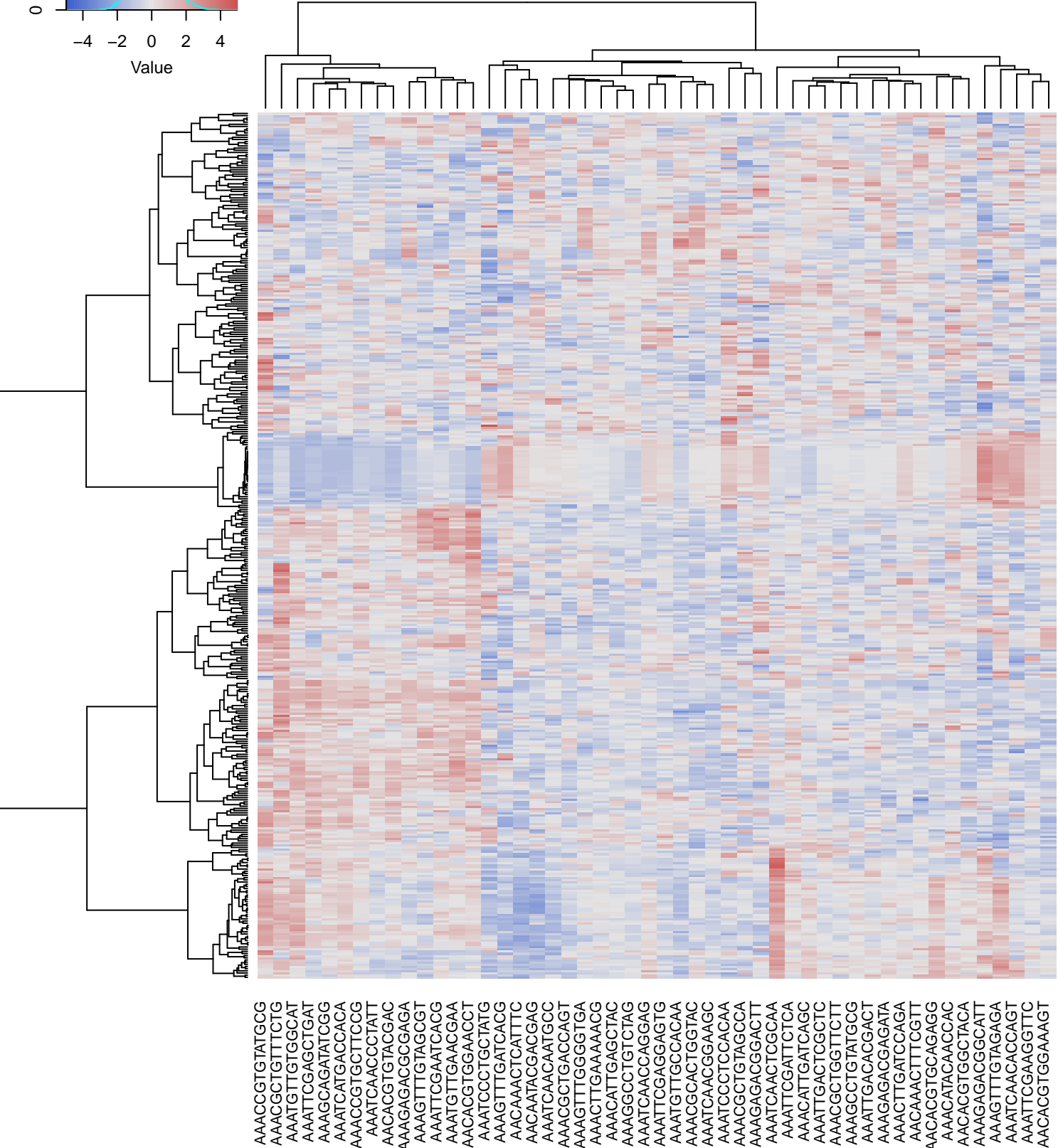
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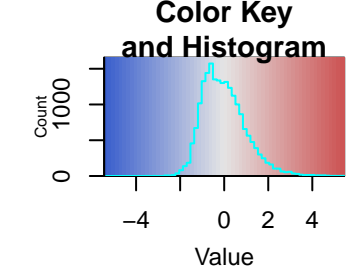


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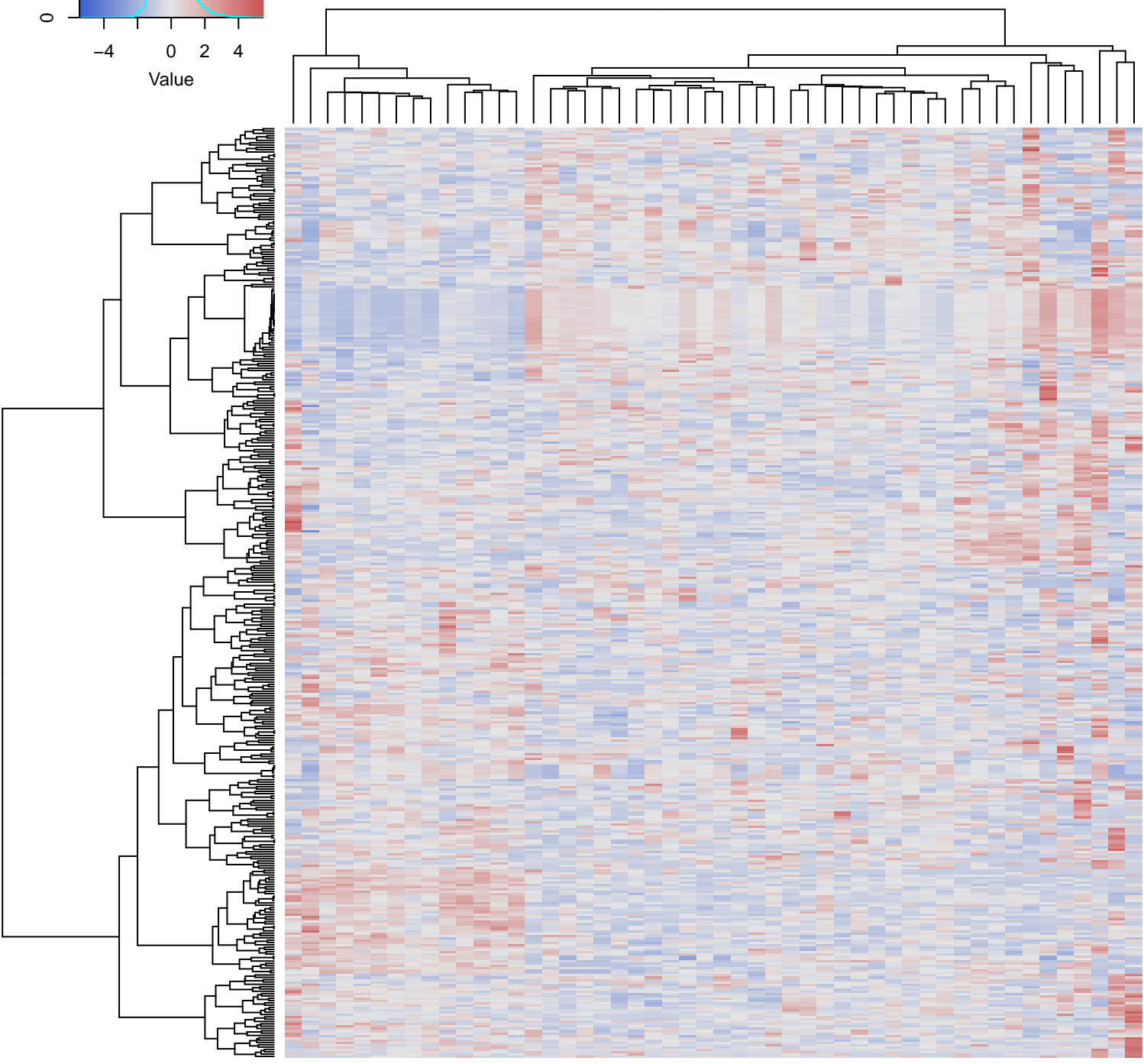


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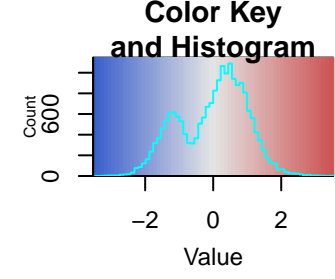


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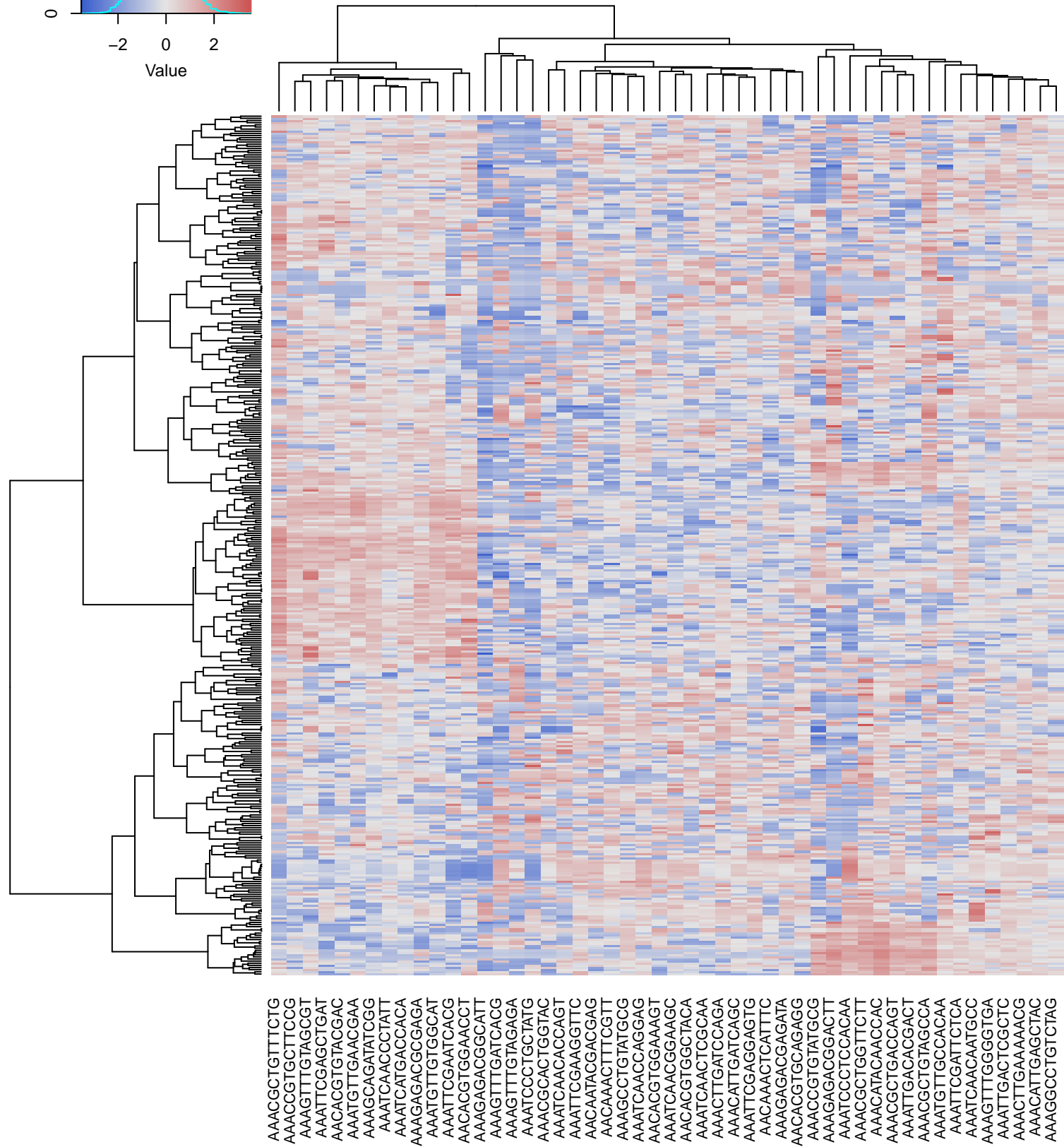


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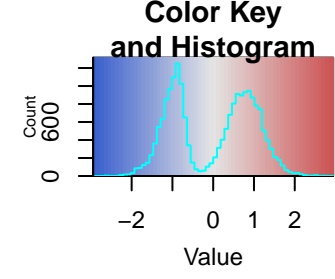
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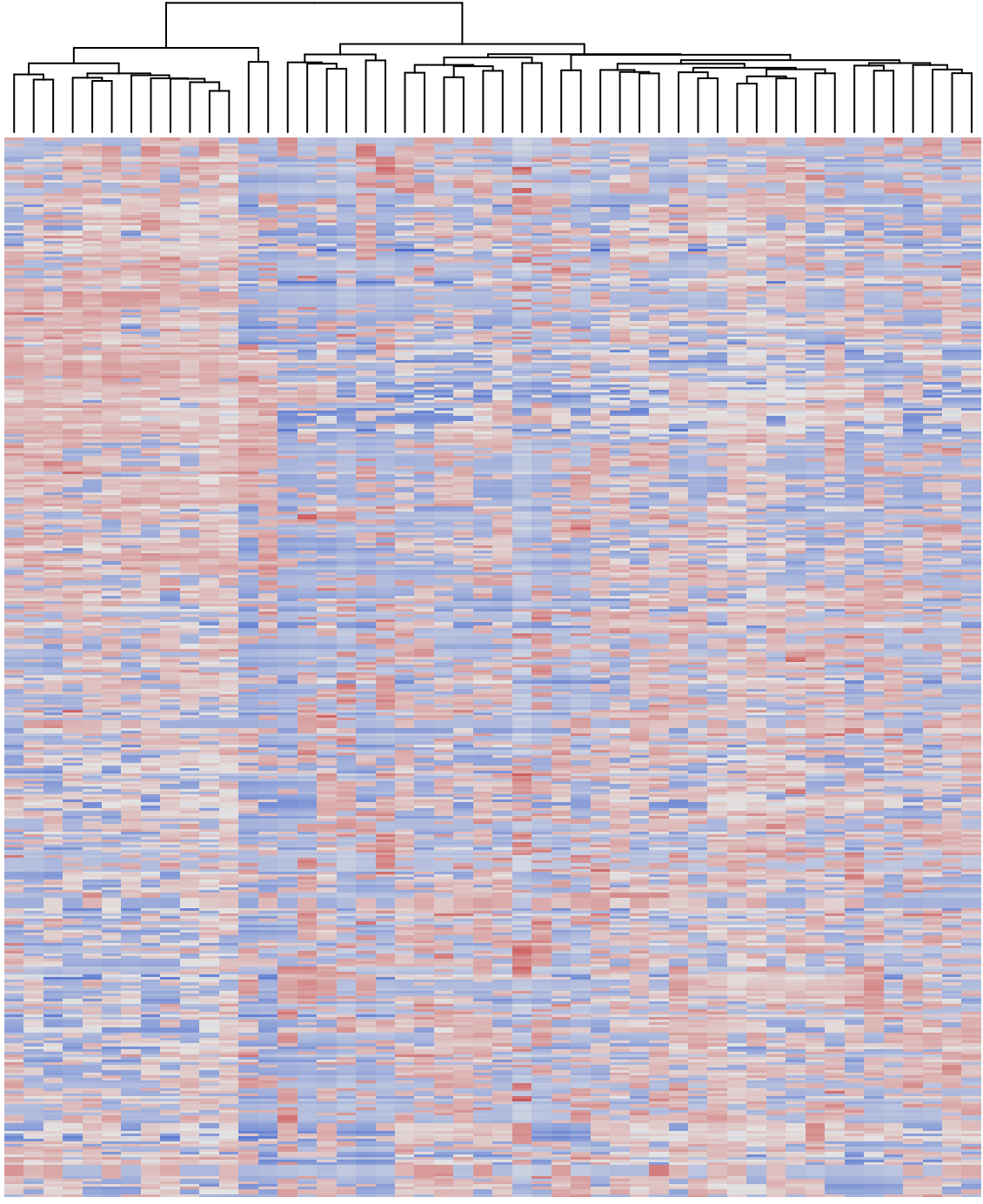
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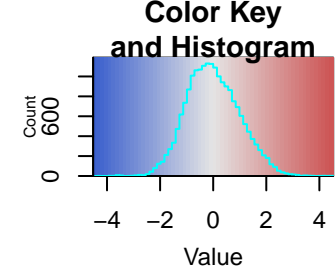


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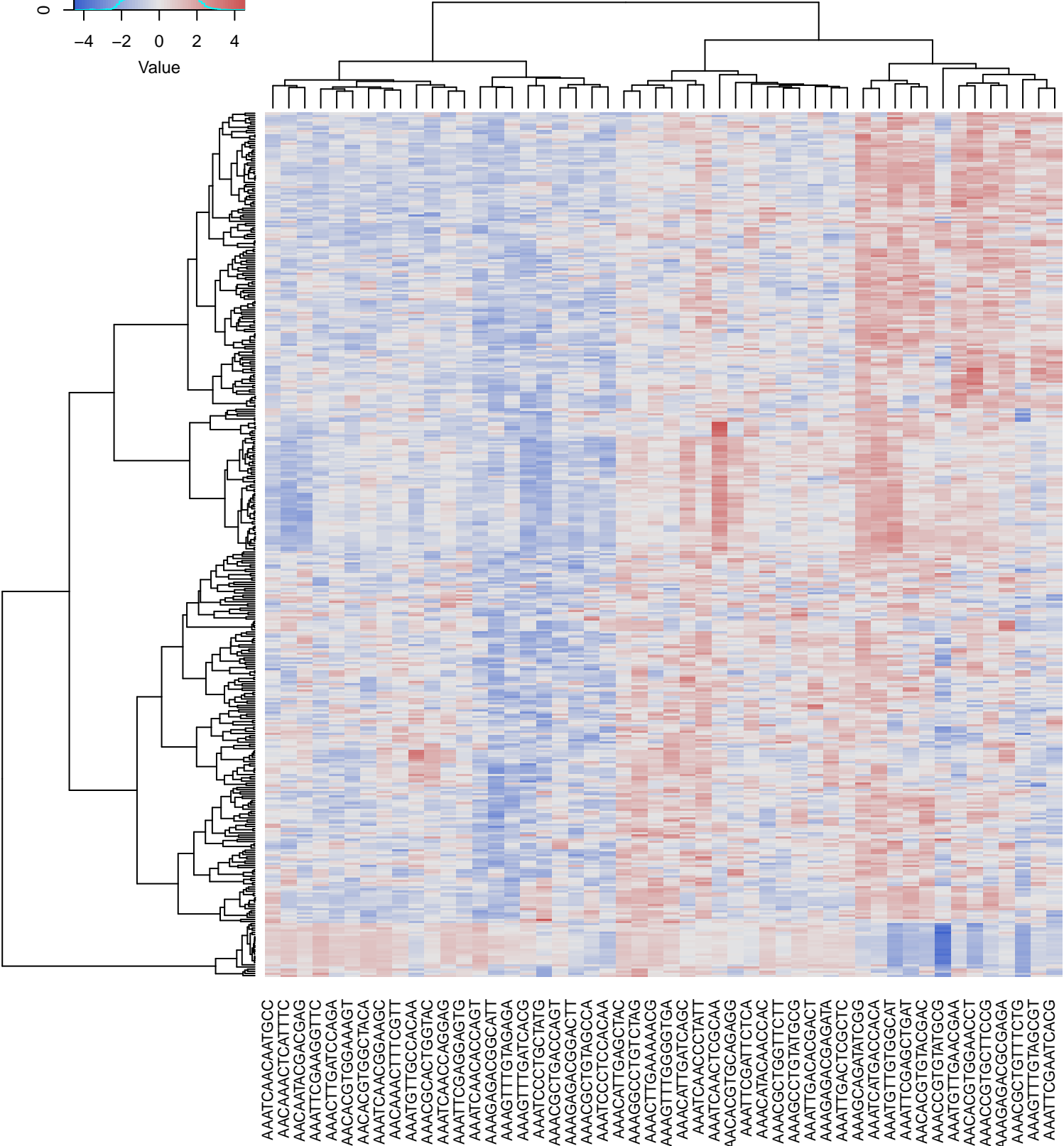


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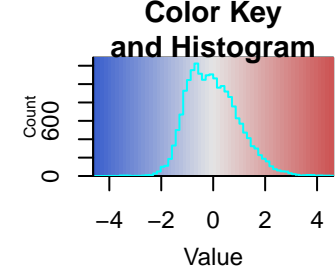


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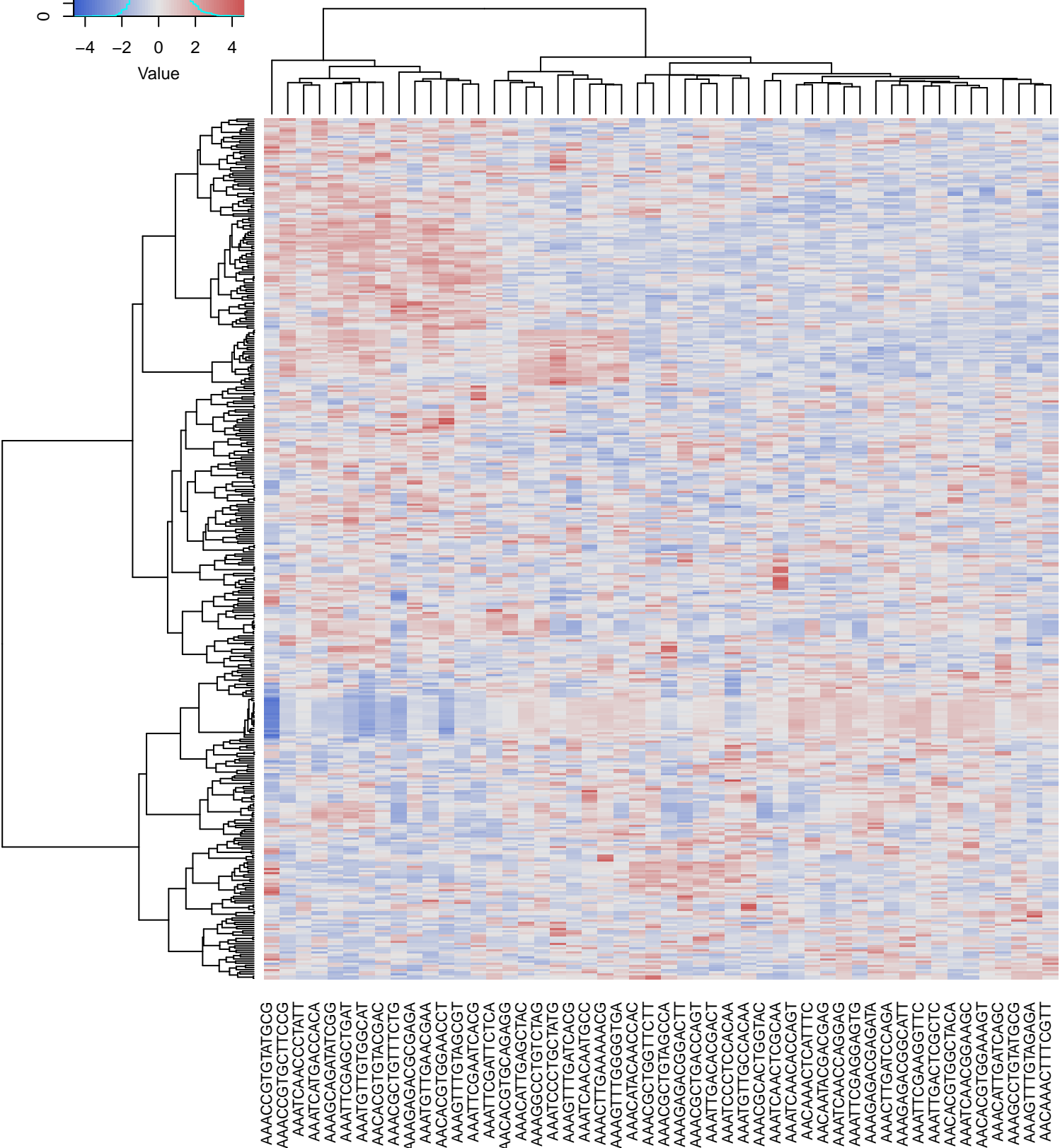


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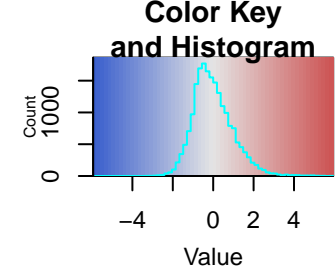




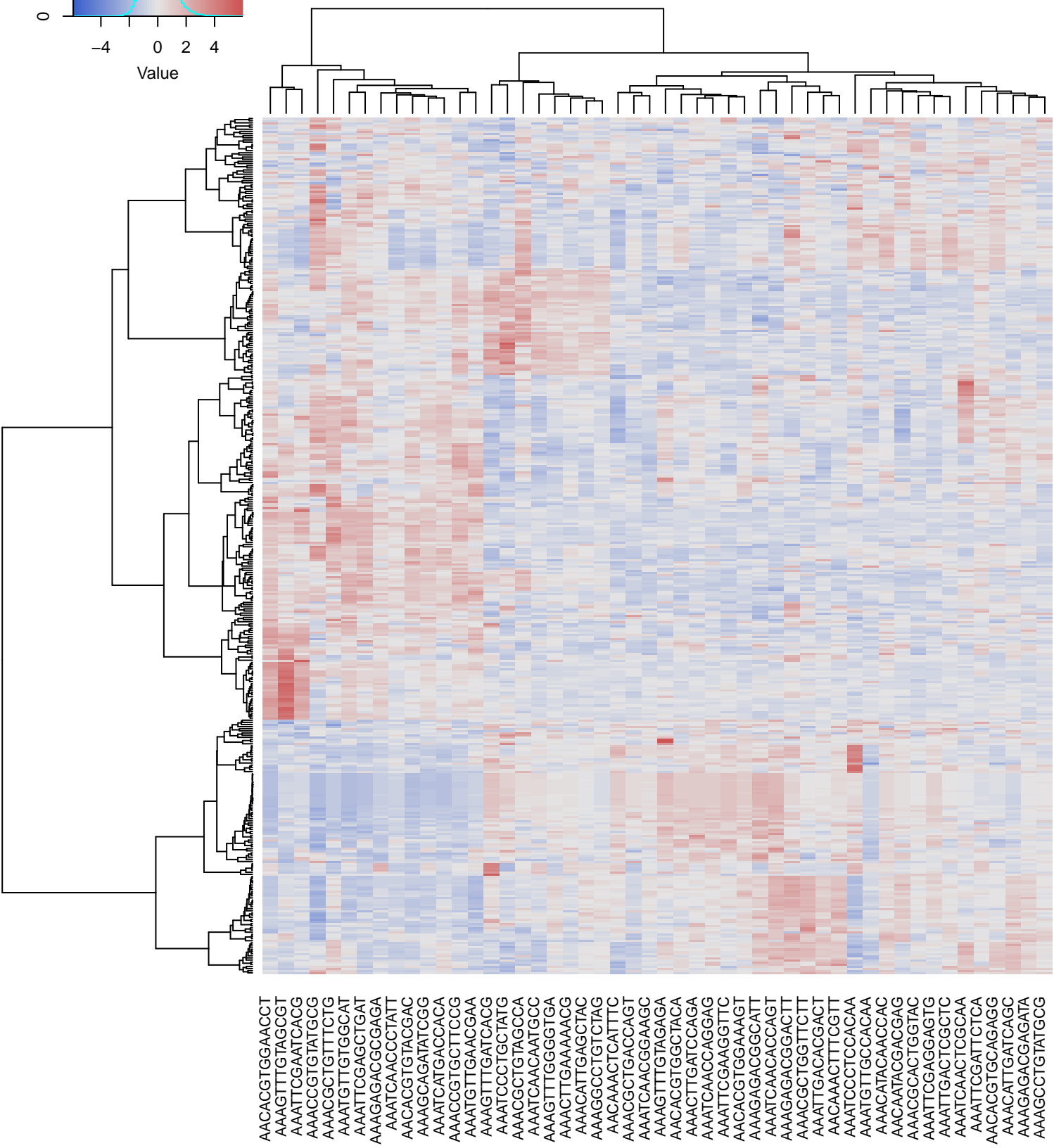
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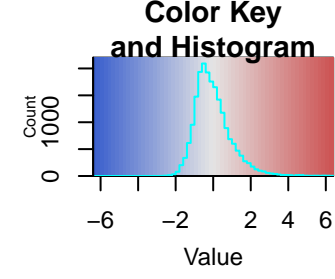
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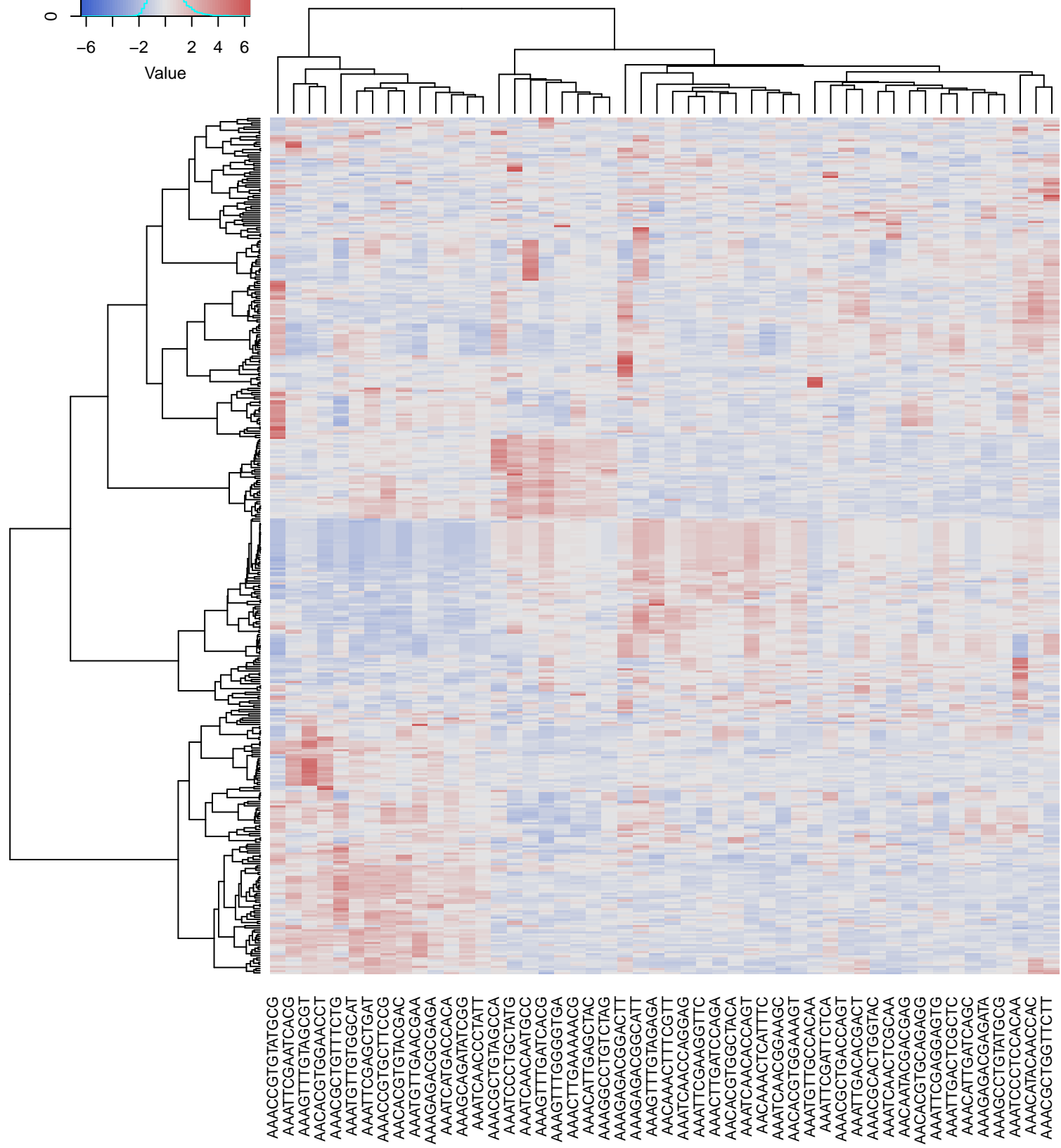
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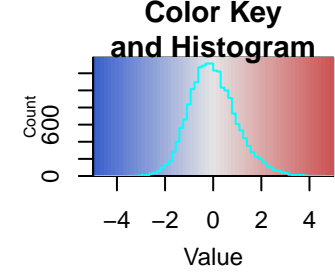
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- GO\_BP:positive regulation of I-kappaB kinase\_NF-kappaB signaling (GO\_0043123)
- GO\_BP:positive regulation of tumor necrosis factor superfamily cytokine production (GO\_1903557)
- GO\_BP:regulation of cytokine production (GO\_0001817)
- GO\_BP:positive regulation of protein metabolic process (GO\_0051247)
- GO\_BP:cellular response to lipid (GO\_0071396)
- GO\_BP:cellular response to chemical stress (GO\_0062197)
- GO\_BP:positive regulation of neuron death (GO\_1901216)
- GO\_BP:positive regulation of defense response (GO\_0031349)
- GO\_BP:neutrophil migration (GO\_1990266)
- GO\_BP:glial cell development (GO\_0021782)
- GO\_BP:pattern recognition receptor signaling pathway (GO\_0002221)
- GO\_BP:defense response to bacterium (GO\_0042742)
- GO\_BP:regulation of intrinsic apoptotic signaling pathway (GO\_2001242)
- GO\_BP:organelle assembly (GO\_0070925)
- GO\_BP:mitotic spindle organization (GO\_0007052)
- GO\_BP:positive regulation of translation (GO\_0045727)
- GO\_BP:skeletal system development (GO\_0001501)
- GO\_BP:response to UV (GO\_0009411)
- GO\_BP:gene expression (GO\_0010467)
- GO\_BP:cytoplasmic translation (GO\_0002181)
- GO\_BP:rRNA processing (GO\_0006364)
- GO\_BP:ribonucleoprotein complex assembly (GO\_0022618)
- GO\_BP:negative regulation of protein modification by small protein conjugation or removal (GO\_1903321)
- GO\_BP:negative regulation of ubiquitin-protein transferase activity (GO\_0051444)
- GO\_BP:maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5\_8S rRNA, LSU-rRNA) (GO\_0001501)
- GO\_BP:negative regulation of translation (GO\_0017148)
- GO\_BP:mitochondrial translational termination (GO\_0070126)
- GO\_BP:error-prone translesion synthesis (GO\_0042276)
- GO\_BP:protein alpha-1,2-demannosylation (GO\_0036508)
- GO\_BP:nucleic acid phosphodiester bond hydrolysis (GO\_0090305)
- GO\_BP:regulation of transforming growth factor beta receptor signaling pathway (GO\_0017015)
- GO\_BP:negative regulation of apoptotic process (GO\_0043066)
- GO\_BP:DNA metabolic process (GO\_0006259)
- GO\_BP:cellular response to cytokine stimulus (GO\_0071345)
- GO\_BP:anaphase-promoting complex-dependent catabolic process (GO\_0031145)
- GO\_BP:regulation of mRNA catabolic process (GO\_0061013)
- GO\_BP:MAPK cascade (GO\_0000165)



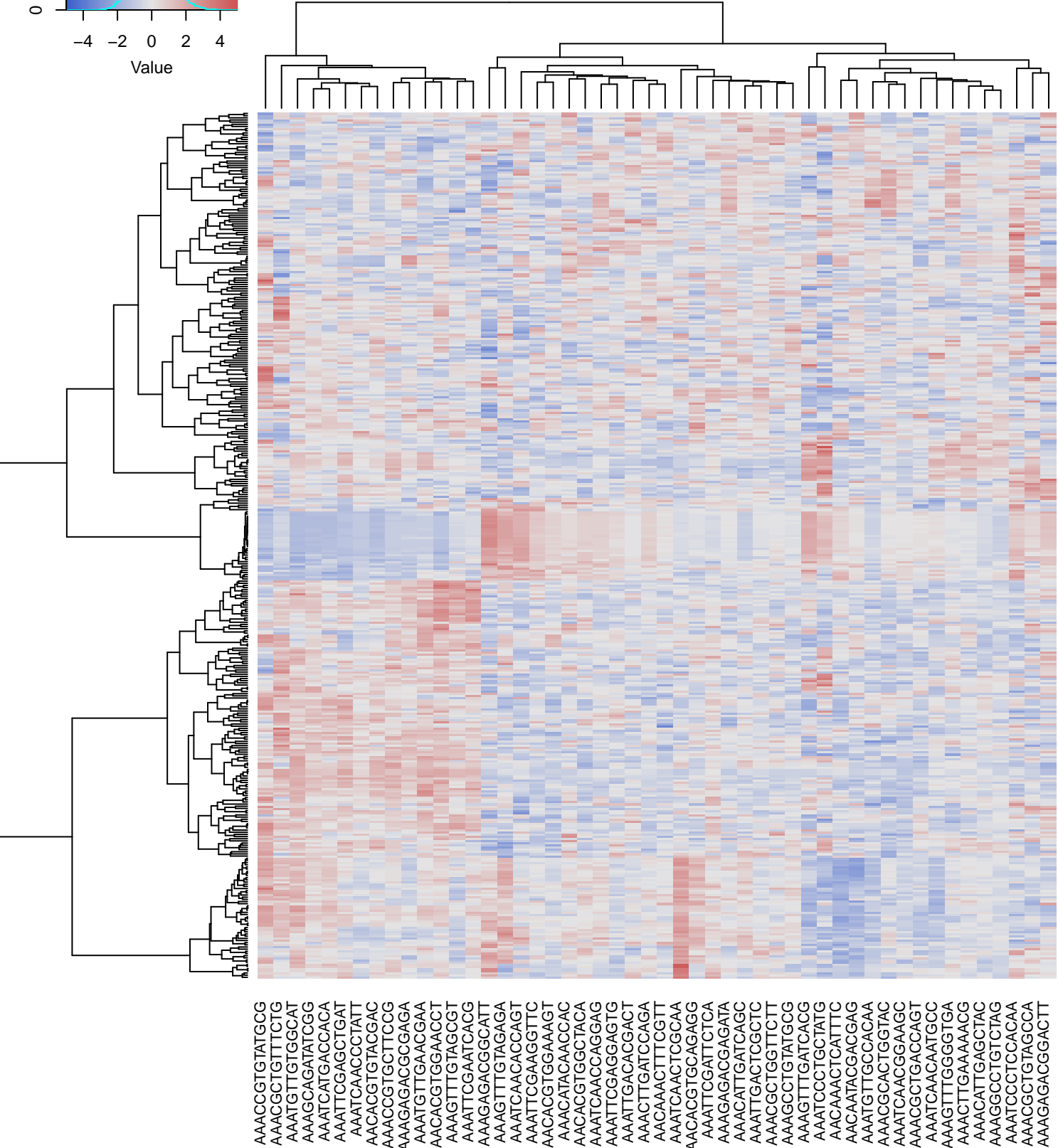
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- GO\_BP:regulation of Rac protein signal transduction (GO\_0035020)
- GO\_BP:negative regulation of biomineral tissue development (GO\_0070168)
- GO\_BP:muscle filament sliding (GO\_0030049)
- GO\_BP:positive regulation of innate immune response (GO\_0045089)
- GO\_BP:rRNA transcription (GO\_0009303)
- GO\_BP:negative regulation of phagocytosis (GO\_0050765)
- GO\_BP:dendritic cell chemotaxis (GO\_0002407)
- GO\_BP:negative regulation of leukocyte mediated cytotoxicity (GO\_0001911)
- GO\_BP:nucleotide metabolic process (GO\_0009117)
- GO\_BP:interleukin-27-mediated signaling pathway (GO\_0070106)
- GO\_BP:type I interferon signaling pathway (GO\_0060337)
- GO\_BP:regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum (GO\_0010808)
- GO\_BP:positive regulation of phosphatase activity (GO\_0010922)
- GO\_BP:regulation of calcium ion transmembrane transporter activity (GO\_1901019)
- GO\_BP:regulation of monooxygenase activity (GO\_0032768)
- GO\_BP:lymphocyte migration (GO\_0072676)
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- GO\_BP:positive regulation of phospholipase activity (GO\_0010518)
- GO\_BP:positive regulation of receptor signaling pathway via JAK-STAT (GO\_0046427)
- GO\_BP:antigen processing and presentation of peptide antigen via MHC class I (GO\_0002474)
- GO\_BP:negative regulation of nervous system development (GO\_0051961)
- GO\_BP:positive regulation of endocytosis (GO\_0045807)
- GO\_BP:cellular response to exogenous dsRNA (GO\_0071360)
- GO\_BP:regulation of necroptotic process (GO\_0060544)
- GO\_BP:endoplasmic reticulum to cytosol transport (GO\_1903513)
- GO\_BP:regulation of actin filament bundle assembly (GO\_0032231)
- GO\_BP:substantia nigra development (GO\_0021762)
- GO\_BP:regulation of transport (GO\_0051049)
- GO\_BP:iron-sulfur cluster assembly (GO\_0016226)
- GO\_BP:natural killer cell mediated immunity (GO\_0002228)
- GO\_BP:prostaglandin metabolic process (GO\_0006693)
- GO\_BP:regulation of neutrophil chemotaxis (GO\_0090022)
- GO\_BP:calcium ion import (GO\_0070509)
- GO\_BP:cognition (GO\_0050890)
- GO\_BP:regulation of T cell mediated cytotoxicity (GO\_0001914)
- GO\_BP:regulation of chemokine production (GO\_0032642)
- GO\_BP:positive regulation of immune response (GO\_0050778)
- GO\_BP:translation (GO\_0006412)
- GO\_BP:SRP-dependent cotranslational protein targeting to membrane (GO\_0006614)
- GO\_BP:cellular protein metabolic process (GO\_0044267)
- GO\_BP:ribosomal large subunit biogenesis (GO\_0042273)
- GO\_BP:ribosomal large subunit assembly (GO\_0000027)
- GO\_BP:embryonic organ development (GO\_0048568)
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- GO\_BP:negative regulation of ubiquitin-protein transferase activity (GO\_0051444)
- GO\_BP:negative regulation of response to DNA damage stimulus (GO\_2001021)
- GO\_BP:positive regulation of activated T cell proliferation (GO\_0042104)
- GO\_BP:positive regulation of ubiquitin-protein transferase activity (GO\_0051443)
- GO\_BP:error-free translesion synthesis (GO\_0070987)
- GO\_BP:DNA synthesis involved in DNA repair (GO\_0000731)
- GO\_BP:regulation of centrosome cycle (GO\_0046605)
- GO\_BP:response to gamma radiation (GO\_0010332)
- GO\_BP:negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway (GO\_0000000)
- GO\_BP:positive regulation of telomerase RNA localization to Cajal body (GO\_1904874)
- GO\_BP:negative regulation of DNA binding (GO\_0043392)
- GO\_BP:regulation of collagen biosynthetic process (GO\_0032965)
- GO\_BP:response to cadmium ion (GO\_0046686)
- GO\_BP:regulation of pri-miRNA transcription by RNA polymerase II (GO\_1902893)
- GO\_BP:positive regulation of neuron death (GO\_1901216)
- GO\_BP:regulation of organelle organization (GO\_0033043)
- GO\_BP:response to molecule of bacterial origin (GO\_0002237)
- GO\_BP:defense response to fungus (GO\_0050832)
- GO\_BP:epiboly involved in wound healing (GO\_0090505)
- GO\_BP:regulation of proteolysis involved in cellular protein catabolic process (GO\_1903050)
- GO\_BP:positive regulation of ATP metabolic process (GO\_1903580)
- GO\_BP:positive regulation of blood vessel endothelial cell migration (GO\_0043536)
- GO\_BP:3'-UTR-mediated mRNA destabilization (GO\_0061158)
- GO\_BP:proteasomal ubiquitin-independent protein catabolic process (GO\_0010499)
- GO\_BP:actin nucleation (GO\_0045010)
- GO\_BP:positive regulation of interleukin-6 production (GO\_0032755)
- GO\_BP:cellular transition metal ion homeostasis (GO\_0046916)
- GO\_BP:negative regulation of fibroblast proliferation (GO\_0048147)
- GO\_BP:negative regulation of protein catabolic process (GO\_0042177)
- GO\_BP:negative regulation of tumor necrosis factor-mediated signaling pathway (GO\_0010804)
- GO\_BP:positive regulation of G1\_S transition of mitotic cell cycle (GO\_1900087)
- GO\_BP:actin filament polymerization (GO\_0030041)
- GO\_BP:regulation of superoxide anion generation (GO\_0032928)
- GO\_BP:osteoclast differentiation (GO\_0030316)
- GO\_BP:positive regulation of T cell migration (GO\_2000406)
- GO\_BP:regulation of monocyte chemotaxis (GO\_0090025)

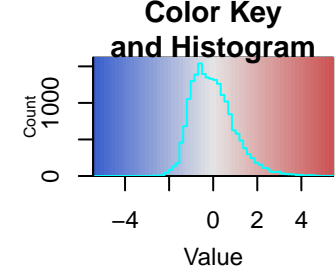


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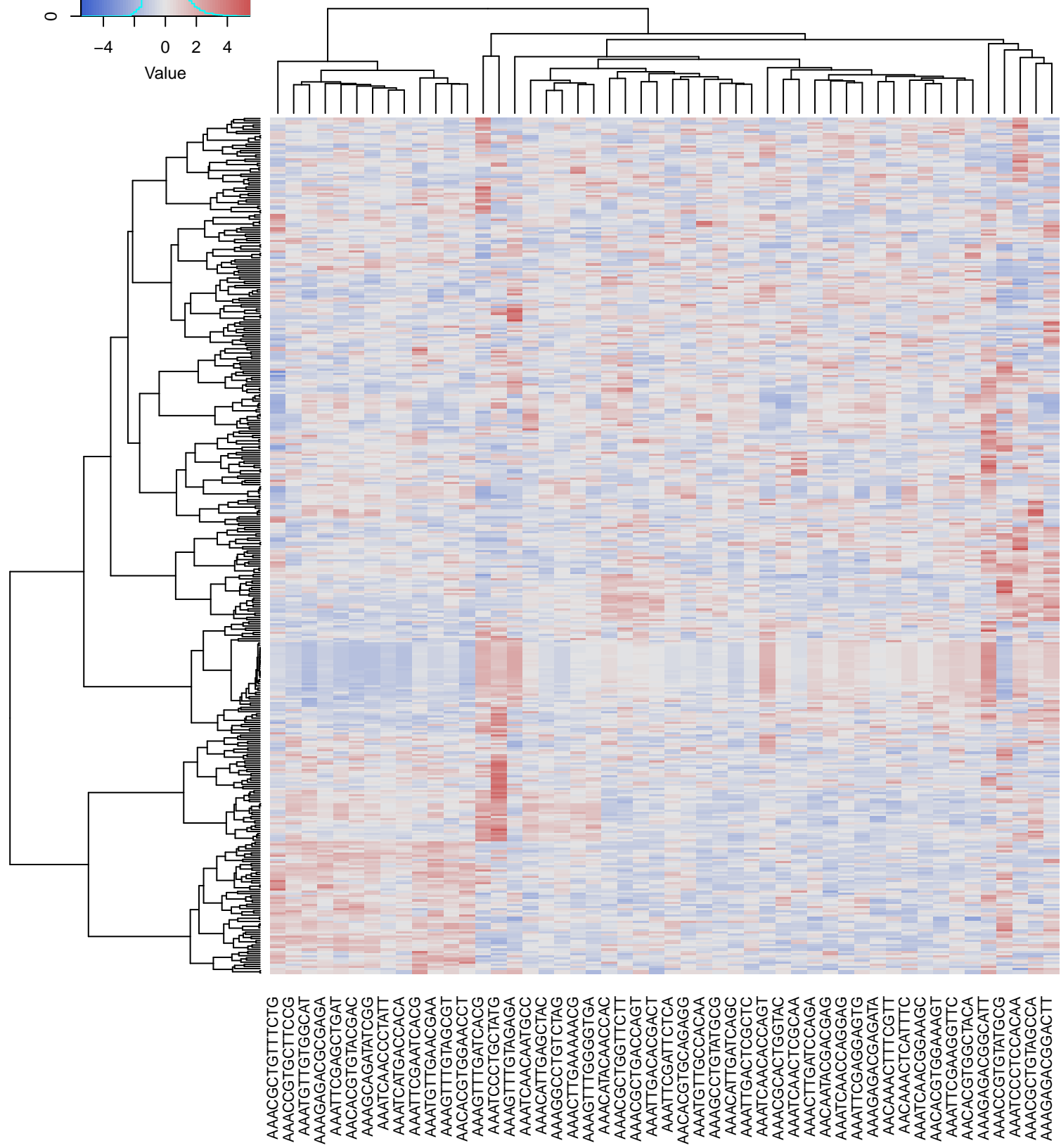


- GO\_BP:positive regulation of multicellular organismal process (GO\_0051240)
- GO\_BP:negative regulation of apoptotic process (GO\_0043066)
- GO\_BP:double-strand break repair (GO\_0006302)
- GO\_BP:transcription by RNA polymerase II (GO\_0006366)
- GO\_BP:regulation of phosphorylation (GO\_0042325)
- GO\_BP:RNA splicing (GO\_0008380)
- GO\_BP:mRNA metabolic process (GO\_0016071)
- GO\_BP:nuclear export (GO\_0051168)
- GO\_BP:positive regulation of protein ubiquitination (GO\_0031398)
- GO\_BP:positive regulation of signal transduction (GO\_0009967)
- GO\_BP:T cell activation (GO\_0042110)
- GO\_BP:positive regulation of protein kinase B signaling (GO\_0051897)
- GO\_BP:regulation of protein serine/threonine kinase activity (GO\_0071900)
- GO\_BP:translational termination (GO\_0006415)
- GO\_BP:cellular response to interleukin-12 (GO\_0071349)
- GO\_BP:response to tumor necrosis factor (GO\_0034612)
- GO\_BP:retrograde transport, endosome to Golgi (GO\_0042147)
- GO\_BP:cellular response to cytokine stimulus (GO\_0071345)
- GO\_BP:iron ion homeostasis (GO\_0055072)
- GO\_BP:positive regulation of GTPase activity (GO\_0043547)
- GO\_BP:regulation of autophagy (GO\_0010506)
- GO\_BP:protein transport (GO\_0015031)
- GO\_BP:regulation of intracellular signal transduction (GO\_1902531)
- GO\_BP:protein phosphorylation (GO\_0006468)
- GO\_BP:regulation of neuron projection development (GO\_0010975)
- GO\_BP:proteasomal protein catabolic process (GO\_0010498)
- GO\_BP:plasma membrane bounded cell projection assembly (GO\_0120031)
- GO\_BP:protein localization to cell periphery (GO\_1990778)
- GO\_BP:hexose biosynthetic process (GO\_0019319)
- GO\_BP:regulation of cell cycle G2/M phase transition (GO\_1902749)
- GO\_BP:B cell receptor signaling pathway (GO\_0050853)
- GO\_BP:positive regulation of leukocyte cell-cell adhesion (GO\_1903039)
- GO\_BP:positive regulation of leukocyte mediated cytotoxicity (GO\_0001912)
- GO\_BP:regulation of protein binding (GO\_0043393)
- GO\_BP:positive regulation of lymphocyte proliferation (GO\_0050671)
- GO\_BP:negative regulation of gene expression (GO\_0010629)
- GO\_BP:ribosomal large subunit assembly (GO\_0000027)
- GO\_BP:cytoplasmic translation (GO\_0002181)
- GO\_BP:cellular macromolecule biosynthetic process (GO\_0034645)
- GO\_BP:rRNA processing (GO\_000364)
- GO\_BP:negative regulation of ubiquitin-protein transferase activity (GO\_0051444)
- GO\_BP:positive regulation of signal transduction by p53 class mediator (GO\_1901798)
- GO\_BP:positive regulation of translation (GO\_0045727)
- GO\_BP:response to molecule of bacterial origin (GO\_0002237)
- GO\_BP:regulation of organelle organization (GO\_0033043)
- GO\_BP:positive regulation of defense response (GO\_0031349)
- GO\_BP:cellular response to oxidative stress (GO\_0034599)
- GO\_BP:positive regulation of NF-kappaB transcription factor activity (GO\_0051092)
- GO\_BP:mitochondrial respiratory chain complex assembly (GO\_0033108)
- GO\_BP:positive regulation of cellular component organization (GO\_0051130)
- GO\_BP:positive regulation of cysteine-type endopeptidase activity involved in apoptotic process (GO\_0043200)
- GO\_BP:regulation of cytokine production (GO\_0001817)
- GO\_BP:positive regulation of kinase activity (GO\_0033674)
- GO\_BP:positive regulation of protein-containing complex assembly (GO\_0031334)
- GO\_BP:ephrin receptor signaling pathway (GO\_0048013)
- GO\_BP:regulation of small GTPase mediated signal transduction (GO\_0051056)
- GO\_BP:negative regulation of multicellular organismal process (GO\_0051241)
- GO\_BP:regulated exocytosis (GO\_0045055)
- GO\_BP:negative regulation of peptidase activity (GO\_0010466)
- GO\_BP:positive regulation of cytokine production (GO\_0001819)
- GO\_BP:neutrophil activation involved in immune response (GO\_0002283)
- GO\_BP:innate immune response (GO\_0045087)
- GO\_BP:positive regulation of interleukin-1 production (GO\_0032732)
- GO\_BP:positive regulation of cell population proliferation (GO\_0008284)
- GO\_BP:protein processing (GO\_0016485)
- GO\_BP:neutrophil migration (GO\_1990266)
- GO\_BP:positive regulation of cellular metabolic process (GO\_0031325)
- GO\_BP:regulation of protein phosphorylation (GO\_0001932)
- GO\_BP:negative regulation of G2/M transition of mitotic cell cycle (GO\_0010972)
- GO\_BP:negative regulation of Wnt signaling pathway (GO\_0030178)
- GO\_BP:regulation of hematopoietic progenitor cell differentiation (GO\_1901532)
- GO\_BP:positive regulation of Wnt signaling pathway (GO\_0030177)
- GO\_BP:regulation of G2/M transition of mitotic cell cycle (GO\_0010389)
- GO\_BP:regulation of primary metabolic process (GO\_0080090)
- GO\_BP:Fc receptor signaling pathway (GO\_0038093)
- GO\_BP:regulation of transcription from RNA polymerase II promoter in response to hypoxia (GO\_0061418)
- GO\_BP:regulation of mRNA catabolic process (GO\_0061013)
- GO\_BP:tumor necrosis factor-mediated signaling pathway (GO\_0033209)
- GO\_BP:defense response to symbiont (GO\_0140546)
- GO\_BP:regulation of viral genome replication (GO\_0045069)





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- GO\_BP:positive regulation of granulocyte chemotaxis (GO\_0071624)
- GO\_BP:prostaglandin biosynthetic process (GO\_0001516)
- GO\_BP:regulation of steroid metabolic process (GO\_0019218)
- GO\_BP:positive regulation of telomerase RNA localization to Cajal body (GO\_1904874)
- GO\_BP:axon extension (GO\_0048675)
- GO\_BP:negative regulation of vascular associated smooth muscle cell proliferation (GO\_1904706)
- GO\_BP:phagosome acidification (GO\_0090383)
- GO\_BP:glutathione derivative biosynthetic process (GO\_1901687)
- GO\_BP:endoplasmic reticulum to cytosol transport (GO\_1903513)
- GO\_BP:3'-UTR-mediated mRNA destabilization (GO\_0061158)
- GO\_BP:DNA methylation or demethylation (GO\_0044728)
- GO\_BP:positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay (GO\_0000000)
- GO\_BP:establishment of epithelial cell polarity (GO\_0090162)
- GO\_BP:positive regulation of chromatin organization (GO\_1905269)
- GO\_BP:protein heterooligomerization (GO\_0051291)
- GO\_BP:nucleotide-excision repair, DNA damage recognition (GO\_0000715)
- GO\_BP:neural crest cell differentiation (GO\_0014033)
- GO\_BP:growth hormone receptor signaling pathway (GO\_0060396)
- GO\_BP:cellular response to exogenous dsRNA (GO\_0071360)
- GO\_BP:mRNA cis splicing, via spliceosome (GO\_0045292)
- GO\_BP:heart contraction (GO\_0060047)
- GO\_BP:response to alcohol (GO\_0097305)
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- GO\_BP:regulation of vascular endothelial cell proliferation (GO\_1905562)
- GO\_BP:regulation of cardiac muscle contraction by calcium ion signaling (GO\_0010882)
- GO\_BP:negative regulation of cation channel activity (GO\_2001258)
- GO\_BP:glucan catabolic process (GO\_0009251)
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- GO\_BP:negative regulation of biomineral tissue development (GO\_0070168)
- GO\_BP:platelet aggregation (GO\_0070527)
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- GO\_BP:type I interferon signaling pathway (GO\_0060337)
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- GO\_BP:glycolytic process through glucose-6-phosphate (GO\_0061620)
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- GO\_BP:protein homotrimerization (GO\_0070207)
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- GO\_BP:regulation of actin filament bundle assembly (GO\_0032231)
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- GO\_BP:mRNA splice site selection (GO\_0006376)
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- GO\_BP:positive regulation of glial cell differentiation (GO\_0045687)
- GO\_BP:regulation of activin receptor signaling pathway (GO\_0032925)
- GO\_BP:positive regulation of cellular protein catabolic process (GO\_1903364)
- GO\_BP:negative regulation of phagocytosis (GO\_0050765)
- GO\_BP:immune response-activating cell surface receptor signaling pathway (GO\_0002429)
- GO\_BP:regulation of platelet aggregation (GO\_0090330)
- GO\_BP:regulation of immune effector process (GO\_0002697)
- GO\_BP:T cell activation involved in immune response (GO\_0002286)
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- GO\_BP:positive regulation of response to cytokine stimulus (GO\_0060760)
- GO\_BP:positive regulation of T cell mediated immunity (GO\_0002711)
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- GO\_BP:regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway (GO\_0000000)
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