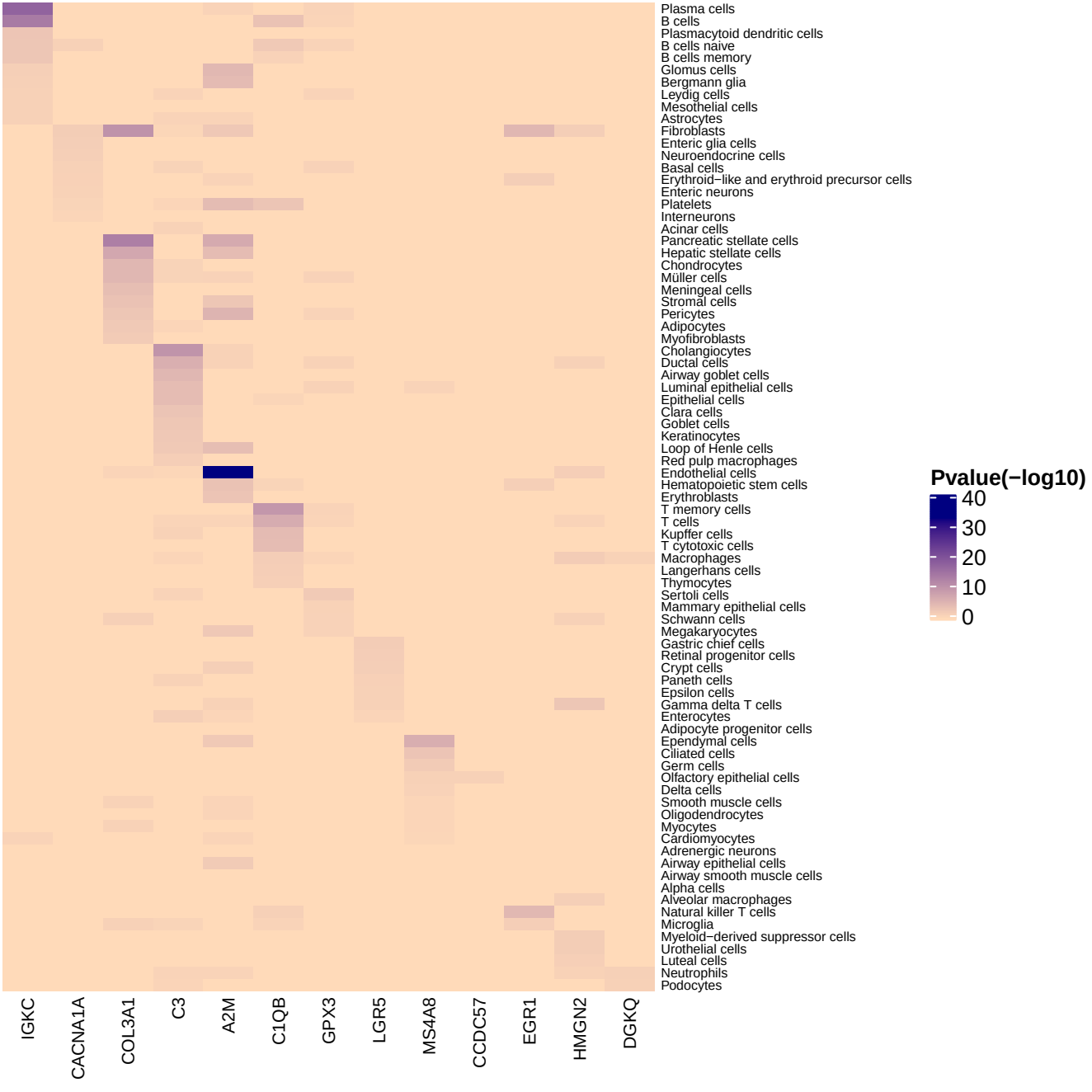
Plasma cells
B cells
Plasmacytoid dendritic cells
B cells naive
B cells memory
Glomus cells
Bergmann glia
Leydig cells
Mesothelial cells
Astrocytes
Fibroblasts
Enteric glia cells
Neuroendocrine cells
Basal cells
Erythroid−like and erythroid precursor cells
Enteric neurons
Platelets
Interneurons
Acinar cells
Pancreatic stellate cells
Hepatic stellate cells
Chondrocytes
Müller cells
Meningeal cells
Stromal cells
Pericytes
Adipocytes
Myofibroblasts
Cholangiocytes
Ductal cells
Airway goblet cells
Luminal epithelial cells
Epithelial cells
Clara cells
Goblet cells
Keratinocytes
Loop of Henle cells
Red pulp macrophages
Endothelial cells
Hematopoietic stem cells
Erythroblasts
T memory cells
T cells
Kupffer cells
T cytotoxic cells
Macrophages
Langerhans cells
Thymocytes
Sertoli cells
Mammary epithelial cells
Schwann cells
Megakaryocytes
Gastric chief cells
Retinal progenitor cells
Crypt cells
Paneth cells
Epsilon cells
Gamma delta T cells
Enterocytes
Adipocyte progenitor cells
Ependymal cells
Ciliated cells
Germ cells
Olfactory epithelial cells
Delta cells
Smooth muscle cells
Oligodendrocytes
Myocytes
Cardiomyocytes
Adrenergic neurons
Airway epithelial cells
Airway smooth muscle cells
Alpha cells
Alveolar macrophages
Natural killer T cells
Microglia
Myeloid−derived suppressor cells
Urothelial cells
Luteal cells
Neutrophils
Podocytes
IGKC
CACNA1A
COL3A1
C3
A2M
C1QB
GPX3
LGR5
MS4A8
CCDC57
EGR1
HMGN2
DGKQ
Pvalue(−log10)
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30
20
10
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HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
HALLMARK_ANDROGEN_RESPONSE
HALLMARK_UV_RESPONSE_DN
HALLMARK_APOPTOSIS
HALLMARK_COMPLEMENT
HALLMARK_ESTROGEN_RESPONSE_EARLY
HALLMARK_KRAS_SIGNALING_UP
HALLMARK_ADIPOGENESIS
HALLMARK_ALLOGRAFT_REJECTION
HALLMARK_ANGIOGENESIS
HALLMARK_COAGULATION
HALLMARK_ESTROGEN_RESPONSE_LATE
HALLMARK_HEME_METABOLISM
HALLMARK_MYOGENESIS
HALLMARK_IL2_STAT5_SIGNALING
HALLMARK_FATTY_ACID_METABOLISM
HALLMARK_APICAL_JUNCTION
HALLMARK_GLYCOLYSIS
HALLMARK_TNFA_SIGNALING_VIA_NFKB
HALLMARK_HYPOXIA
HALLMARK_UV_RESPONSE_UP
HALLMARK_P53_PATHWAY
HALLMARK_MTORC1_SIGNALING
HALLMARK_IL6_JAK_STAT3_SIGNALING
HALLMARK_PANCREAS_BETA_CELLS
HALLMARK_TGF_BETA_SIGNALING
HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY
HALLMARK_INTERFERON_ALPHA_RESPONSE
HALLMARK_INTERFERON_GAMMA_RESPONSE
HALLMARK_XENOBIOTIC_METABOLISM
HALLMARK_CHOLESTEROL_HOMEOSTASIS
HALLMARK_PEROXISOME
HALLMARK_DNA_REPAIR
HALLMARK_BILE_ACID_METABOLISM
HALLMARK_APICAL_SURFACE
HALLMARK_G2M_CHECKPOINT
IGKC
CACNA1A
COL3A1
C3
A2M
C1QB
GPX3
LGR5
MS4A8
CCDC57
EGR1
HMGN2
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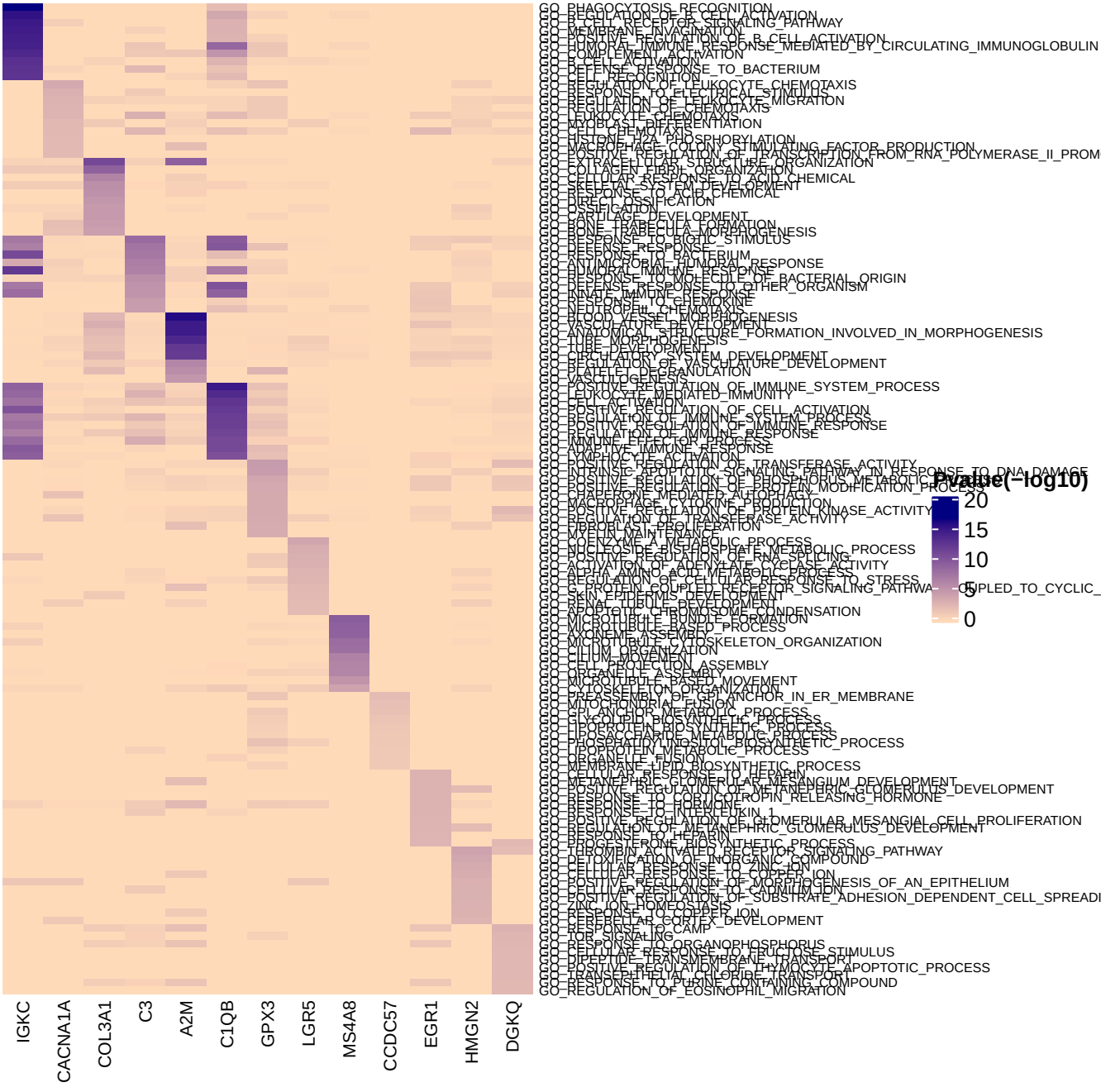
GO_PHAGOCYTOSIS_RECOGNITION
GO_REGULATION_OF_B_CELL_ACTIVATION
GO_B_CELL_RECEPTOR_SIGNALING_PATHWAY
GO_MEMBRANE_INVAGINATION
GO_NEGATIVE_REGULATION_OF_B_CELL_ACTIVATION
GO_HUMORAL_IMMUNE_RESPONSE_MEDIATED_BY_CIRCULATING_IMMUNOGLOBULIN
GO_COMPLEMENT_ACTIVATION
GO_B_CELL_ACTIVATION
GO_DEFENSE_RESPONSE_TO_BACTERIUM
GO_CELL_RECOGNITION
GO_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS
GO_RESPONSE_TO_ELECTRICAL_STIMULUS
GO_REGULATION_OF_LEUKOCYTE_MIGRATION
GO_REGULATION_OF_CHEMOTAXIS
GO_LEUKOCYTE_CHEMOTAXIS
GO_MYOBLAST_DIFFERENTIATION
GO_CELL_CHEMOTAXIS
GO_HISTONE_H2A_PHOSPHORYLATION
GO_MACROPHAGE_COLONY_STIMULATING_FACTOR_PRODUCTION
GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROM
GO_EXTRACELLULAR_STRUCTURE_ORGANIZATION
GO_COLLAGEN_FIBRIL_ORGANIZATION
GO_CELLULAR_RESPONSE_TO_ACID_CHEMICAL
GO_REPTILIAN_SYSTEM_DEVELOPMENT
GO_RESPONSE_TO_ACID_CHEMICAL
GO_DIRECT_OSSIFICATION
GO_OSSIFICATION
GO_CARTILAGE_DEVELOPMENT
GO_BONE_TRABECULA_FORMATION
GO_BONE_TRABECULA_MORPHOGENESIS
GO_RESPONSE_TO_BIOTIC_STIMULUS
GO_DEFENSE_RESPONSE
GO_RESPONSE_TO_BACTERIUM
GO_ANTIMICROBIAL_HUMORAL_RESPONSE
GO_HUMORAL_IMMUNE_RESPONSE
GO_RESPONSE_TO_MOLECULE_OF_BACTERIAL_ORIGIN
GO_DEFENSE_RESPONSE_TO_OTHER_ORGANISM
GO_INNATE_IMMUNE_RESPONSE
GO_RESPONSE_TO_CHEMOKINE
GO_NEUTROPHIL_CHEMOTAXIS
GO_BLOOD_VESSEL_MORPHOGENESIS
GO_VASCULATURE_DEVELOPMENT
GO_ANATOMICAL_STRUCTURE_FORMATION_INVOLVED_IN_MORPHOGENESIS
GO_TUBE_MORPHOGENESIS
GO_TUBE_DEVELOPMENT
GO_CIRCULATORY_SYSTEM_DEVELOPMENT
GO_REGULATION_OF_VASCULATURE_DEVELOPMENT
GO_GRANULE_DEGRANULATION
GO_VASCULOGENESIS
GO_POSITIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS
GO_LEUKOCYTE_MEDIATED_IMMUNITY
GO_CELL_ACTIVATION
GO_POSITIVE_REGULATION_OF_CELL_ACTIVATION
GO_REGULATION_OF_IMMUNE_SYSTEM_PROCESS
GO_POSITIVE_REGULATION_OF_IMMUNE_RESPONSE
GO_REGULATION_OF_IMMUNE_RESPONSE
GO_IMMUNE_EFFECTOR_PROCESS
GO_ADAPTIVE_IMMUNE_RESPONSE
GO_LYMPHOCYTE_ACTIVATION
GO_POSITIVE_REGULATION_OF_TRANSFERASE_ACTIVITY
GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_DNA_DAMAGE
GO_POSITIVE_REGULATION_OF_PHOSPHORUS_METABOLIC_PROCESS
GO_POSITIVE_REGULATION_OF_PROTEIN_MODIFICATION_PROCESS
GO_CHAPERONE_MEDIATED_AUTOPHAGY
GO_MACROPHAGE_CYTOKINE_PRODUCTION
GO_POSITIVE_REGULATION_OF_PROTEIN_KINASE_ACTIVITY
GO_REGULATION_OF_TRANSFERASE_ACTIVITY
GO_FIBROBLAST_PROLIFERATION
GO_VITAMIN_METABOLISM
GO_COENZYME_A_METABOLIC_PROCESS
GO_NUCLEOSIDE_BISPHOSPHATE_METABOLIC_PROCESS
GO_POSITIVE_REGULATION_OF_RNA_SPLICING
GO_ACTIVATION_OF_ADENYLATE_CYCLASE_ACTIVITY
GO_ALPHA_AMINO_ACID_METABOLIC_PROCESS
GO_REGULATION_OF_CELLULAR_RESPONSE_TO_STRESS
GO_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWA
COUPLED_TO_CYCLIC_
GO_SKIN_EPIDERMIS_DEVELOPMENT
GO_RENAL_TUBULE_DEVELOPMENT
GO_APOPTOTIC_CHROMOSOME_CONDENSATION
GO_MICROTUBULE_BUNDLE_FORMATION
GO_MICROTUBULE_BASED_PROCESS
GO_AXONEME_ASSEMBLY
GO_MICROTUBULE_CYTOSKELETON_ORGANIZATION
GO_CILIUM_ORGANIZATION
GO_CILIUM_MOVEMENT
GO_CELL_PROJECTION_ASSEMBLY
GO_ORGANELLE_ASSEMBLY
GO_MICROTUBULE_BASED_MOVEMENT
GO_CYTOSKELETON_ORGANIZATION
GO_PROTEIN_INSERTION_INTO_ER_MEMBRANE_BY_SRP_PATHWAY
GO_MITOCHONDRIAL_FUSION
GO_GPI_ANCHOR_METABOLIC_PROCESS
GO_FATTY_ACID_BIOSYNTHETIC_PROCESS
GO_LIPOPROTEIN_BIOSYNTHETIC_PROCESS
GO_LIPOSACCHARIDE_METABOLIC_PROCESS
GO_PHOSPHATIDYLINOSITOL_BIOSYNTHETIC_PROCESS
GO_LIPOPROTEIN_METABOLIC_PROCESS
GO_ORGANELLE_FUSION
GO_MEMBRANE_LIPID_BIOSYNTHETIC_PROCESS
GO_CELLULAR_RESPONSE_TO_HEPARIN
GO_METANEPHRIC_GLOMERULAR_MESANGIUM_DEVELOPMENT
GO_POSITIVE_REGULATION_OF_METANEPHRIC_GLOMERULUS_DEVELOPMENT
GO_RESPONSE_TO_LUTEOTROPHIN_RELEASING_HORMONE
GO_RESPONSE_TO_HORMONE
GO_RESPONSE_TO_INTERLEUKIN_1
GO_POSITIVE_REGULATION_OF_GLOMERULAR_MESANGIAL_CELL_PROLIFERATION
GO_REGULATION_OF_METANEPHRIC_GLOMERULUS_DEVELOPMENT
GO_RESPONSE_TO_HEPARIN
GO_PROGESTERONE_BIOSYNTHETIC_PROCESS
GO_THROMBIN_ACTIVATED_RECEPTOR_SIGNALING_PATHWAY
GO_DETOXIFICATION_OF_INORGANIC_COMPOUND
GO_CELLULAR_RESPONSE_TO_COPPER_ION
GO_CELLULAR_RESPONSE_TO_CADMIUM_ION
GO_POSITIVE_REGULATION_OF_MORPHOGENESIS_OF_AN_EPITHELIUM
GO_POSITIVE_REGULATION_OF_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPREADI
GO_ZINC_IONHOMEOSTASIS
GO_RESPONSE_TO_COPPER_ION
GO_CEREBELLAR_CORTEX_DEVELOPMENT
GO_RESPONSE_TO_CAMP
GO_TOR_SIGNALING
GO_RESPONSE_TO_ORGANOPHOSPHORUS
GO_CELLULAR_RESPONSE_TO_ELECTRICAL_STIMULUS
GO_DIPEPTIDE_TRANSMEMBRANE_TRANSPORT
GO_POSITIVE_REGULATION_OF_THYMOCYTE_APOPTOTIC_PROCESS
GO_TRANSEPITHELIAL_CHLORIDE_TRANSPORT
GO_RESPONSE_TO_PURINE_CONTAINING_COMPOUND
GO_REGULATION_OF_EOSINOPHIL_MIGRATION
IGKC
CACNA1A
COL3A1
C3
A2M
C1QB
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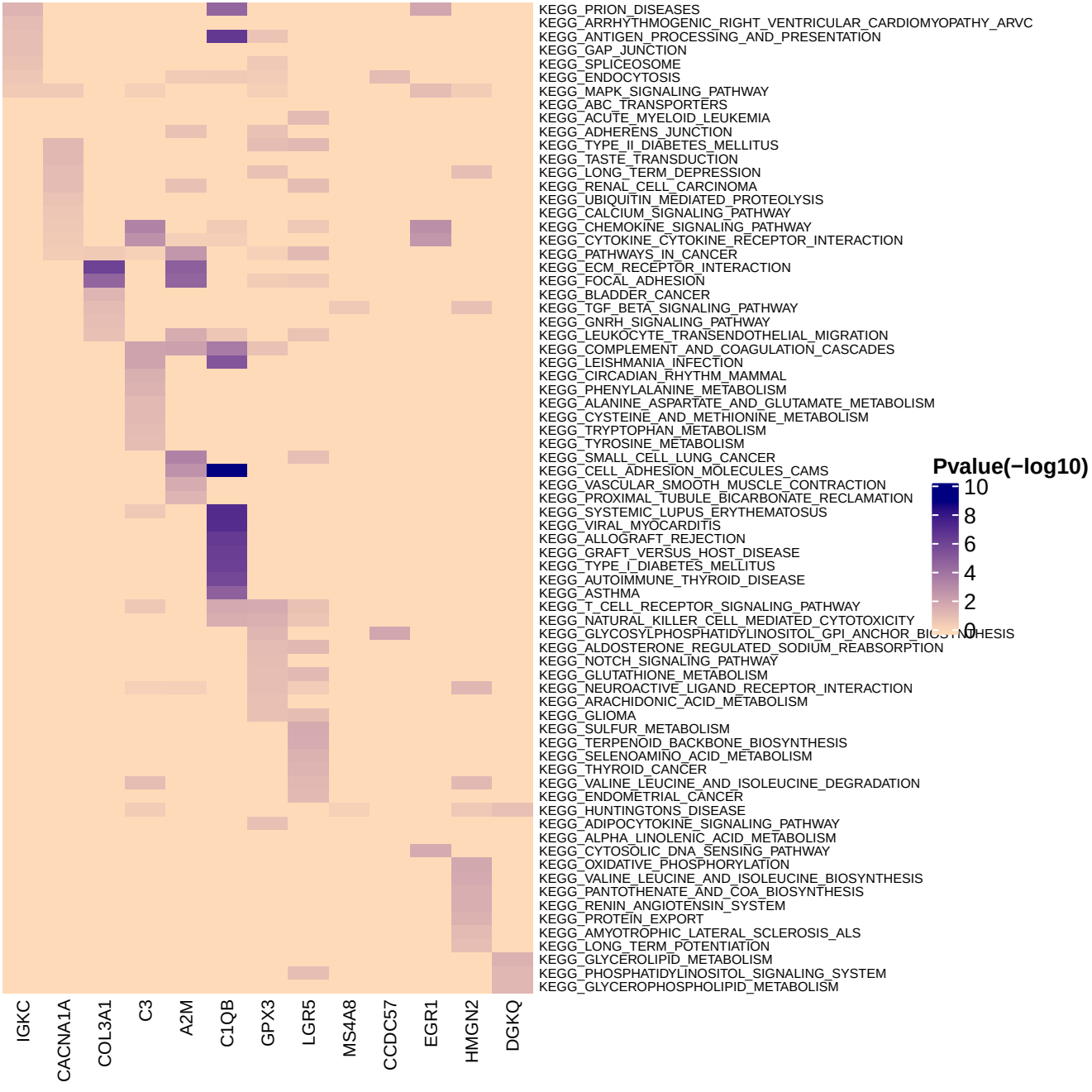
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KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION
KEGG_GAP_JUNCTION
KEGG_SPLICEOSOME
KEGG_ENDOCYTOSIS
KEGG_MAPK_SIGNALING_PATHWAY
KEGG_ABC_TRANSPORTERS
KEGG_ACUTE_MYELOID_LEUKEMIA
KEGG_ADHERENS_JUNCTION
KEGG_TYPE_II_DIABETES_MELLITUS
KEGG_TASTE_TRANSDUCTION
KEGG_LONG_TERM_DEPRESSION
KEGG_RENAL_CELL_CARCINOMA
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS
KEGG_CALCIUM_SIGNALING_PATHWAY
KEGG_CHEMOKINE_SIGNALING_PATHWAY
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION
KEGG_PATHWAYS_IN_CANCER
KEGG_ECM_RECEPTOR_INTERACTION
KEGG_FOCAL_ADHESION
KEGG_BLADDER_CANCER
KEGG_TGF_BETA_SIGNALING_PATHWAY
KEGG_GNRH_SIGNALING_PATHWAY
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION
KEGG_COMPLEMENT_AND_COAGULATION_CASCADES
KEGG_LEISHMANIA_INFECTION
KEGG_CIRCADIAN_RHYTHM_MAMMAL
KEGG_PHENYLALANINE_METABOLISM
KEGG_ALANINE_ASPARTATE_AND_GLUTAMATE_METABOLISM
KEGG_CYSTEINE_AND_METHIONINE_METABOLISM
KEGG_TRYPTOPHAN_METABOLISM
KEGG_TYROSINE_METABOLISM
KEGG_SMALL_CELL_LUNG_CANCER
KEGG_CELL_ADHESION_MOLECULES_CAMS
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION
KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
KEGG_VIRAL_MYOCARDITIS
KEGG_ALLOGRAFT_REJECTION
KEGG_GRAFT_VERSUS_HOST_DISEASE
KEGG_TYPE_I_DIABETES_MELLITUS
KEGG_AUTOIMMUNE_THYROID_DISEASE
KEGG_ASTHMA
KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY
KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS
KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION
KEGG_NOTCH_SIGNALING_PATHWAY
KEGG_GLUTATHIONE_METABOLISM
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION
KEGG_ARACHIDONIC_ACID_METABOLISM
KEGG_GLIOMA
KEGG_SULFUR_METABOLISM
KEGG_TERPENOID_BACKBONE_BIOSYNTHESIS
KEGG_SELENOAMINO_ACID_METABOLISM
KEGG_THYROID_CANCER
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION
KEGG_ENDOMETRIAL_CANCER
KEGG_HUNTINGTONS_DISEASE
KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY
KEGG_ALPHA_LINOLENIC_ACID_METABOLISM
KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY
KEGG_OXIDATIVE_PHOSPHORYLATION
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_BIOSYNTHESIS
KEGG_PANTOTHENATE_AND_COA_BIOSYNTHESIS
KEGG_RENIN_ANGIOTENSIN_SYSTEM
KEGG_PROTEIN_EXPORT
KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS
KEGG_LONG_TERM_POTENTIATION
KEGG_GLYCEROLIPID_METABOLISM
KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM
KEGG_GLYCEROPHOSPHOLIPID_METABOLISM
IGKC
CACNA1A
COL3A1
C3
A2M
C1QB
GPX3
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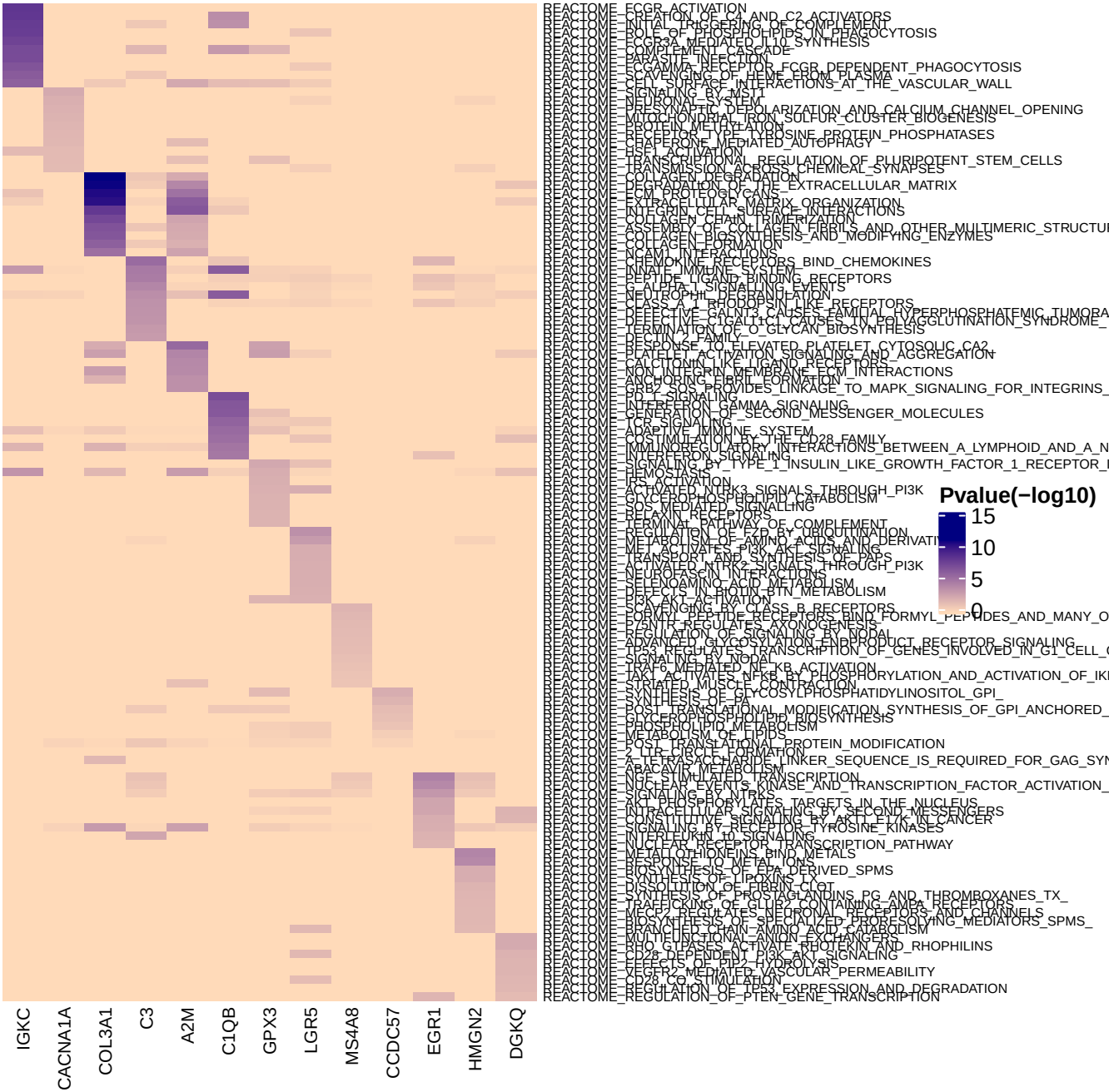
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REACTOME_CREATION_OF_C4_AND_C2_ACTIVATORS
REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT
REACTOME_ROLE_OF_PHOSPHOLIPIDS_IN_PHAGOCYTOSIS
REACTOME_FCGR3A_MEDIATED_IL10_SYNTHESIS
REACTOME_COMPLEMENT_CASCADE
REACTOME_PARASITE_INFECTION
REACTOME_FCGAMMA_RECEPTOR_FCGR_DEPENDENT_PHAGOCYTOSIS
REACTOME_SCAVENGING_OF_HEME_FROM_PLASMA
REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR_WALL
REACTOME_SIGNALING_BY_MSTI1
REACTOME_NEURONAL_SYSTEM
REACTOME_PRESYNAPTIC_DEPOLARIZATION_AND_CALCIUM_CHANNEL_OPENING
REACTOME_MITOCHONDRIAL_IRON_SULFUR_CLUSTER_BIOGENESIS
REACTOME_PROTEIN_METHYLATION
REACTOME_RECEPTOR_TYPE_TYROSINE_PROTEIN_PHOSPHATASES
REACTOME_CHAPERONE_MEDIATED_AUTOPHAGY
REACTOME_DSL_ACTIVATION
REACTOME_TRANSCRIPTIONAL_REGULATION_OF_PLURIPOTENT_STEM_CELLS
REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES
REACTOME_COLLAGEN_DEGRADATION
REACTOME_DEGRADATION_OF_THE_EXTRACELLULAR_MATRIX
REACTOME_ECM_PROTEOGLYCANS
REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION
REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS
REACTOME_COLLAGEN_CHAIN_TRIMERIZATION
REACTOME_ASSEMBLY_OF_COLLAGEN_FIBRILS_AND_OTHER_MULTIMERIC_STRUCTU
REACTOME_COLLAGEN_BIOSYNTHESIS_AND_MODIFYING_ENZYMES
REACTOME_COLLAGEN_FORMATION
REACTOME_NCAM1_INTERACTIONS
REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES
REACTOME_INNATE_IMMUNE_SYSTEM
REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS
REACTOME_G_ALPHA_I_SIGNALLING_EVENTS
REACTOME_NEUTROPHIL_DEGRANULATION
REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPTORS
REACTOME_DEFECTIVE_GALNT3_CAUSES_FAMILIAL_HYPERPHOSPHATEMIC_TUMORA
REACTOME_DEFECTIVE_C1GALT1C1_CAUSES_TN_POLYAGGLUTINATION_SYNDROME_
REACTOME_TERMINATION_OF_O_GLYCAN_BIOSYNTHESIS
REACTOME_DECTIN_2_FAMILY
REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2_
REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION
REACTOME_CYTOKINE_LIKE_LIGAND_RECEPTORS
REACTOME_NON_INTEGRIN_MEMBRANE_ECM_INTERACTIONS
REACTOME_ANCHORING_FIBRIL_FORMATION
REACTOME_GRB2_SOS_PROVIDES_LINKAGE_TO_MAPK_SIGNALING_FOR_INTEGRINS_
REACTOME_GPCR_LIGAND_BINDING
REACTOME_INTERFERON_GAMMA_SIGNALING
REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES
REACTOME_CGMP_SIGNALING
REACTOME_ADAPTIVE_IMMUNE_SYSTEM
REACTOME_COSTIMULATION_BY_THE_CD28_FAMILY
REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_N
REACTOME_INTERFERON_SIGNALING
REACTOME_SIGNALING_BY_TYPE_1_INSULIN_LIKE_GROWTH_FACTOR_1_RECEPTOR_I
REACTOME_HEMOSTASIS
REACTOME_RAS_ACTIVATION
REACTOME_ACTIVATED_NTRK3_SIGNALS_THROUGH_PI3K
REACTOME_GLYCEROPHOSPHOLIPID_CATABOLISM
REACTOME_SOS_MEDIATED_SIGNALLING
REACTOME_RELAXIN_RECEPTORS
REACTOME_TERMINAL_PATHWAY_OF_COMPLEMENT
REACTOME_REGULATION_OF_FZD_BY_UBIQUITINATION
REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATI
REACTOME_ACTIVATED_PI3K_AKT_SIGNALING
REACTOME_TRANSPORT_AND_SYNTHESIS_OF_PAPS
REACTOME_ACTIVATED_NTRK2_SIGNALS_THROUGH_PI3K
REACTOME_NEUROFASCIN_INTERACTIONS
REACTOME_BETA_ALANINE_METABOLISM
REACTOME_DEFECTS_IN_BIOTIN_BTN_METABOLISM
REACTOME_PI3K_AKT_ACTIVATION
REACTOME_CALCIUM_SENSING_CLASS_B_RECEPTORS
REACTOME_FORMYL_PEPTIDE_RECEPTORS_BIND_FORMYL_PEPTIDES_AND_MANY_O
REACTOME_P75NTR_REGULATES_AXONOGENESIS
REACTOME_REGULATION_OF_SIGNALING_BY_NODAL
REACTOME_ADVANCED_GLYCOSYLATION_ENDPRODUCT_RECEPTOR_SIGNALING
REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_G1_CELL_C
REACTOME_SIGNALING_BY_NODAL
REACTOME_TRAF6_MEDIATED_NF_KB_ACTIVATION
REACTOME_TRAF6_MEDIATED_IRF7_ACTIVATION
REACTOME_STRIATED_MUSCLE_CONTRACTION
REACTOME_SYNTHESIS_OF_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_
REACTOME_SYNTHESIS_OF_PIPS
REACTOME_POST_TRANSLATIONAL_MODIFICATION_SYNTHESIS_OF_GPI_ANCHORED_
REACTOME_GLYCEROPHOSPHOLIPID_BIOSYNTHESIS
REACTOME_PHOSPHOLIPID_METABOLISM
REACTOME_METABOLISM_OF_LIPIDS
REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION
REACTOME_2_LTR_CIRCLE_FORMATION
REACTOME_A_TETRASACCHARIDE_LINKER_SEQUENCE_IS_REQUIRED_FOR_GAG_SYN
REACTOME_ARACHIDONIC_ACID_METABOLISM
REACTOME_NGF_STIMULATED_TRANSCRIPTION
REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTION_FACTOR_ACTIVATION_
REACTOME_SIGNALING_BY_NTRKS
REACTOME_AKT_PHOSPHORYLATES_TARGETS_IN_THE_NUCLEUS
REACTOME_INTRACELLULAR_SIGNALING_BY_SECOND_MESSENGERS
REACTOME_CONSTITUTIVE_SIGNALING_BY_AKT1_E17K_IN_CANCER
REACTOME_SIGNALING_BY_RECEPTOR_TYROSINE_KINASES
REACTOME_INTERLEUKIN_10_SIGNALING
REACTOME_NUCLEAR_RECEPTOR_TRANSCRIPTION_PATHWAY
REACTOME_METALLOTHIONEINS_BIND_METALS
REACTOME_RESPONSE_TO_METAL_IONS
REACTOME_BIOSYNTHESIS_OF_EPA_DERIVED_SPMS
REACTOME_SYNTHESIS_OF_LIPOXINS_LX
REACTOME_DISSOLUTION_OF_FIBRIN_CLOT
REACTOME_SYNTHESIS_OF_PROSTAGLANDINS_PG_AND_THROMBOXANES_TX_
REACTOME_TRAFFICKING_OF_GLUR2_CONTAINING_AMPA_RECEPTORS
REACTOME_MECP2_REGULATES_NEURONAL_RECEPTORS_AND_CHANNELS
REACTOME_BIOSYNTHESIS_OF_SPECIALIZED_PRORESOLVING_MEDIATORS_SPMS_
REACTOME_BRANCHED_CHAIN_AMINO_ACID_CATABOLISM
REACTOME_MULTIFUNCTIONAL_ANION_EXCHANGERS
REACTOME_RHO_GTPASES_ACTIVATE_RHOTEKIN_AND_RHOPHILINS
REACTOME_CD28_DEPENDENT_PI3K_AKT_SIGNALING
REACTOME_EFFECTS_OF_PIP2_HYDROLYSIS
REACTOME_VEGFR2_MEDIATED_VASCULAR_PERMEABILITY
REACTOME_VEGFR_STIMULATION
REACTOME_REGULATION_OF_TP53_EXPRESSION_AND_DEGRADATION
REACTOME_REGULATION_OF_PTEN_GENE_TRANSCRIPTION
IGKC
CACNA1A
COL3A1
C3
A2M
C1QB
GPX3
LGR5
MS4A8
CCDC57
EGR1
HMGN2
DGKQ
Pvalue(−log10)
15
10
5
0