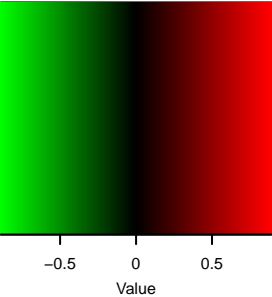


Color Key



0.89	-0.62	-0.27	-0.07	GOBP_NEMIDESMOSOME_ASSEMBLY
0.82	-0.75	0.06	-0.14	GOBP_REGULATION_OF_VITAMIN_D_BIOSYNTHESIS
0.66	-0.2	-0.6	0.08	GOBP_ENTRY_OF_BACTERIUM_INTO_HOST_CELL
0.61	-0.42	-0.63	0.32	GOBP_WOUND_HEALING_SPREADING_OF_EPIDERMIS
0.59	-0.64	-0.15	0.22	GOBP_POSITIVE_REGULATION_OF_EXTRINSIC_CELL_CYCLE
0.53	-0.42	-0.19	-0.01	GOBP_BASEMENT_MEMBRANE_ORGANIZATION
0.52	-0.36	-0.43	0.31	GOBP_CELL_SUBSTRATE_JUNCTION_ORGANIZATION
0.5	-0.31	-0.27	0	GOBP_CELL_ADHESION_MEDIATED_BY_INTEGRIN
0.5	-0.1	-0.43	-0.12	HALLMARK_MITOTIC_SPINDLE
0.48	-0.43	0.03	0.14	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
0.48	-0.35	-0.44	0.34	GOBP_FOCAL_ADHESION_ASSEMBLY
0.48	-0.28	-0.41	0.05	HALLMARK_PROTEIN_SECRETION
0.47	-0.36	-0.43	0.13	GOBP_EPIBOLY
0.44	-0.4	-0.03	0.1	HALLMARK_ANGIOGENESIS
0.4	0.14	-0.24	-0.49	HALLMARK_G2M_CHECKPOINT
0.4	-0.11	-0.44	0.31	HALLMARK_UV_RESPONSE_DN
0.39	-0.44	-0.32	0.24	HALLMARK_TGF_BETA_SIGNALING
0.37	0.15	0.21	-0.62	HALLMARK_E2F_TARGETS
0.35	-0.52	0.04	0.23	HALLMARK_IL6_JAK_STAT3_SIGNALING
0.31	-0.37	-0.18	0.15	HALLMARK_APICAL_JUNCTION
0.28	-0.5	-0.63	0.27	HALLMARK_TNFA_SIGNALING_VIA_NFKB
0.27	-0.23	0.27	-0.53	HALLMARK_MYC_TARGETS_V1
-0.36	0.75	-0.02	0.14	GOBP_FLAVONOID_METABOLIC_PROCESS
-0.05	0.71	-0.37	0.09	GOBP_SKELETAL_MUSCLE_SATELLITE_CELL_DIFFERENTIATION
-0.02	0.7	0.01	0.05	GOBP_ETHANOL_OXIDATION
-0.26	0.69	0	-0.02	GOBP_CELLULAR_GLYCOURONIDATION
0.07	0.68	-0.34	0.2	GOBP_LATERAL_SPROUTING_FROM_AN_EPITHELIAL_CELL
-0.39	0.61	0.05	0.09	GOBP_URONIC_ACID_METABOLIC_PROCESS
-0.03	0.51	0.18	0.04	GOBP_DETECTION_OF_CHEMICAL_STIMULUS_IN_CILIUM
-0.33	0.36	-0.04	-0.1	GOBP_CILIUM_MOVEMENT
-0.03	0.3	-0.08	-0.33	GOBP_HISTONE_H4_ACETYLATION
-0.14	0.28	-0.28	-0.24	HALLMARK_SPERMATOGENESIS
0.18	0.22	-0.03	-0.54	GOBP_INTERSTRAND_CROSS_LINK_REPAIR
-0.59	-0.44	0.68	0.14	GOBP_MITOCHONDRIAL_ELECTRON_TRANSPORT
-0.61	-0.32	0.65	-0.14	GOBP_NADH_DEHYDROGENASE_COMPLEX_ASSEMBLY
-0.55	-0.28	0.65	-0.08	GOBP_ATP_SYNTHESIS_COUPLED_ELECTRON_TRANSPORT
-0.55	-0.27	0.63	-0.27	GOBP_MITOCHONDRIAL_RESPIRATORY_CHAIN_OXIDATION
-0.51	-0.28	0.6	-0.17	GOBP_RESPIRATORY_ELECTRON_TRANSPORT_CHAIN
-0.49	-0.32	0.6	-0.07	GOBP_OXIDATIVE_PHOSPHORYLATION
-0.44	-0.12	0.56	-0.53	GOBP_CYTOCHROME_COMPLEX_ASSEMBLY
-0.45	-0.3	0.54	-0.06	GOBP_ELECTRON_TRANSPORT_CHAIN
0.08	-0.31	0.5	-0.29	GOBP_REGULATION_OF_CELLULAR_AMINO_ACID_TRANSPORT
0.24	-0.16	0.49	0.35	HALLMARK_INTERFERON_ALPHA_RESPONSE
-0.43	0.16	0.46	-0.11	HALLMARK_OXIDATIVE_PHOSPHORYLATION
-0.42	-0.19	0.44	-0.1	GOBP_CELLULAR_RESPIRATION
0.27	-0.21	0.44	-0.62	HALLMARK_MYC_TARGETS_V2
-0.03	-0.24	0.41	-0.41	HALLMARK_DNA_REPAIR
-0.4	-0.06	0.23	0.17	HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY
-0.29	-0.07	0.12	0.12	HALLMARK_FATTY_ACID_METABOLISM
0.01	-0.53	-0.27	0.77	GOBP_PEPTIDE_CROSS_LINKING
-0.51	-0.2	-0.29	0.75	GOBP_CORNIFICATION
-0.25	-0.48	-0.24	0.73	GOBP_KERATINIZATION
0.03	-0.44	-0.4	0.64	GOBP_REGULATION_OF_WATER_LOSS_VIA_SKIN
0.08	-0.42	-0.35	0.62	GOBP_KERATINOCYTE_DIFFERENTIATION
0.03	-0.32	-0.31	0.55	GOBP_EPIDERMAL_CELL_DIFFERENTIATION
0.24	-0.27	-0.35	0.51	GOBP_SKIN_DEVELOPMENT
0.18	-0.25	-0.31	0.48	GOBP_EPIDERMIS_DEVELOPMENT
0.29	-0.34	-0.47	0.46	GOBP_POSITIVE_REGULATION_OF_MACROPHAGE_DEVELOPMENT
0.02	-0.11	-0.27	0.44	GOBP_WATER_HOMEOSTASIS
0.35	-0.55	-0.02	0.41	HALLMARK_INFLAMMATORY_RESPONSE
0.26	-0.58	0.31	0.35	HALLMARK_INTERFERON_GAMMA_RESPONSE
0.11	-0.49	0.25	0.29	HALLMARK_ALLOGRAFT_REJECTION
0.24	-0.33	0.06	0.26	HALLMARK_COMPLEMENT
0.23	-0.26	-0.11	0.26	HALLMARK_KRAS_SIGNALING_UP
-0.24	-0.05	0.07	0.11	HALLMARK_ADIPOGENESIS

Program-1

Program-2

Program-3

Program-4