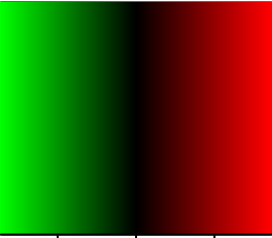


Color Key



-0.5      0      0.5

Value

0.7	-0.04	-0.39	-0.43	0.14	-0.28	-0.04	GOBP_PHOSPHATIDYLINOSITOL_3_PHOSPHATE
0.55	-0.07	-0.62	-0.34	-0.12	-0.03	-0.07	GOBP_MICROTUBULE_ORGANIZING_CENTER_LO
0.52	-0.16	0.08	0.12	-0.32	0.25	-0.42	GOBP_TOLL_LIKE_RECEPTOR_8_SIGNALING_PAT
0.5	0.33	-0.22	-0.34	-0.26	-0.15	-0.38	HALLMARK_PROTEIN_SECRETION
0.47	-0.24	0.32	0.41	-0.36	-0.47	-0.08	GOBP_PHAGOSOME_ACIDIFICATION
0.41	-0.28	-0.42	-0.08	0.15	0.32	-0.32	HALLMARK_MITOTIC_SPINDLE
0.41	0.14	-0.29	-0.38	-0.04	0.02	-0.08	HALLMARK_ANDROGEN_RESPONSE
0.39	-0.44	-0.31	-0.31	0.07	0.11	-0.05	HALLMARK_UV_RESPONSE_DN
0.38	0.2	-0.37	0.15	0.05	-0.17	-0.44	GOBP_PROTEIN_TARGETING_TO_VACUOLE
0.36	0.16	-0.24	-0.21	0.18	-0.24	-0.3	GOBP_GOLGI_ORGANIZATION
0.36	0.05	-0.3	0.04	-0.19	-0.22	-0.26	GOBP_CYTOSOLIC_TRANSPORT
0.33	0.21	-0.13	-0.02	-0.19	-0.17	-0.26	GOBP_COP1_COATED_VESICLE_BUDDING
0.32	-0.07	0.19	0.31	-0.19	-0.46	-0.04	GOBP_PHI_REDUCTION
0.29	0.02	-0.17	0.14	-0.02	-0.25	-0.27	GOBP_VACUOLAR_TRANSPORT
0.27	-0.08	-0.12	0.07	-0.23	0.27	-0.05	HALLMARK_HEME_METABOLISM
0.26	-0.07	-0.11	-0.09	0.07	-0.34	-0.2	GOBP_REGULATION_OF_MACROAUTOPHAGY
0.25	-0.27	-0.04	-0.01	-0.3	0.06	-0.24	HALLMARK_PDK_AKT_MTOR_SIGNALING
0.22	0.18	-0.06	-0.01	-0.1	-0.24	-0.23	GOBP_ENDOPLASMIC_RETICULUM_TO_GOLGI_V
0.22	-0.14	-0.01	-0.08	-0.28	0.11	-0.02	HALLMARK_MTORC2_SIGNALING
0.42	0.53	-0.16	-0.08	-0.39	-0.39	-0.48	GOBP_PROTEIN_DEGLYCOSYLATION
0.47	0.07	-0.25	-0.13	-0.13	-0.23	-0.48	GOBP_PROTEIN_DEAMINATION
0.12	0.48	-0.16	0.25	-0.19	-0.38	-0.24	GOBP_KERATAN_SULFATE_METABOLIC_PROCES
-0.26	-0.48	0.19	0.16	-0.46	-0.26	0.22	GOBP_RESPONSE_TO_COPPER_ION
-0.18	0.4	-0.19	-0.46	-0.36	-0.46	0.34	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANS
-0.04	0.39	-0.13	0.23	-0.1	-0.15	-0.08	GOBP_MUCOPOLYSACCHARIDE_METABOLIC_PR
0.06	-0.09	0.16	-0.07	-0.2	-0.2	-0.14	GOBP_GLYCOLIPID_BIOSYNTHETIC_PROCES
-0.09	0.31	0.3	-0.05	-0.41	-0.07	-0.16	HALLMARK_IL6_JAK_STAT3_SIGNALING
0.13	0.13	0.13	-0.17	-0.44	0.25	0.25	HALLMARK_INFLAMMATORY_RESPONSE
0.19	0.27	0.21	-0.24	-0.17	-0.12	-0.4	GOBP_PROTEIN_LOCALIZATION_TO_ENDOPLAS
0.13	0.15	0.02	0.1	-0.13	-0.21	-0.34	GOBP_RESPONSE_TO_ENDOPLASMIC_RETICUL
0.21	-0.12	0.78	-0.13	-0.43	-0.45	-0.18	HALLMARK_INTERFERON_ALPHA_RESPONSE
0.19	0.22	0.26	-0.04	-0.24	-0.28	0.18	GOBP_ANTIGEN_PROCESSING_AND_PRESENTAT
0.29	-0.02	0.67	-0.22	-0.44	-0.35	-0.14	HALLMARK_INTERFERON_GAMMA_RESPONSE
-0.06	-0.06	0.66	0.52	-0.08	-0.37	0.23	GOBP_MITCHONDRIAL_ELECTION_TRANSPORT
0.22	-0.04	0.83	-0.08	-0.28	-0.34	-0.09	GOBP_INTERFERON_GAMMA_MEDIATED_SIGNA
0.13	0.26	0.61	-0.21	-0.46	-0.47	0.38	GOBP_ANTIGEN_PROCESSING_AND_PRESENTAT
0.1	0	0.67	-0.08	-0.16	-0.27	-0.25	GOBP_RESPONSE_TO_TYPE_I_INTERFERON
0.13	-0.07	0.55	-0.03	-0.33	-0.29	0.12	GOBP_RESPONSE_TO_INTERFERON_GAMMA
0.24	-0.05	0.5	0.04	-0.46	-0.46	0.43	GOBP_POSITIVE_REGULATION_OF_T_CELL_ME
0.19	0.18	0.48	-0.08	-0.38	-0.03	0	HALLMARK_ALLOGRAFT_REJECTION
0.08	0.14	0.33	-0.03	-0.28	0.63	0.04	GOBP_ADAPTIVE_IMMUNE_RESPONSE
0.09	0.17	0.37	-0.06	-0.32	-0.15	0.06	GOBP_ADAPTIVE_IMMUNE_RESPONSE_BASED
0.18	0.19	0.37	-0.11	-0.4	-0.2	0.2	GOBP_T_CELL_MEDIATED_IMMUNITY
-0.21	-0.43	0.33	0.3	0.06	0.1	-0.32	HALLMARK_DNA_REPAIR
0.04	0.19	0.41	0.11	-0.38	-0.23	0.11	HALLMARK_COMPLEMENT
0.03	-0.53	0.34	0.4	0.05	-0.39	-0.13	HALLMARK_OXIDATIVE_PHOSPHORYLATION
-0.11	0.08	-0.04	0.22	-0.28	-0.08	-0.08	HALLMARK_GLYCOLYSIS
0.1	-0.34	-0.03	-0.1	0.41	-0.26	-0.42	GOBP_REGULATION_OF_MRNA_PROCESSING
0	-0.47	0.04	0.41	0.41	0.41	-0.01	GOBP_RIBONUCLEOPROTEIN_COMPLEX_SUBUN
0.17	-0.49	0.07	-0.11	0.4	0.38	0.47	GOBP_RNA_3_END_PROCESSING
0.1	-0.43	0.08	-0.06	0.4	0.38	-0.46	GOBP_MRNA_PROCESSING
0.26	-0.7	-0.07	0.05	0.15	0.83	-0.44	GOBP_DNA_REPLICATION_INITIATION
0.29	-0.64	0	-0.18	0.28	0.63	-0.37	GOBP_CENTROMERE_COMPLEX_ASSEMBLY
0.28	-0.09	-0.09	0.09	0.19	0.59	0.45	HALLMARK_E2F_TARGETS
0.33	-0.6	0.03	0.2	0.09	0.58	-0.46	GOBP_CELL_CYCLE_DNA_REPLICATION
0.37	-0.52	-0.24	0.19	0.6	0.24	-0.43	HALLMARK_SNA_CHECKPOINT
0.31	-0.54	-0.07	-0.05	0.2	0.54	-0.43	GOBP_DNA_DEPENDENT_DNA_REPLICATION
0.16	-0.51	-0.13	-0.07	-0.22	0.54	-0.46	GOBP_REGULATION_OF_DNA_DEPENDENT_DNA
0.15	-0.58	0	0.02	0.22	0.53	-0.33	HALLMARK_MYC_TARGETS_V1
0.25	-0.42	-0.1	-0.17	0.35	0.45	-0.48	GOBP_PROTEIN_LOCALIZATION_TO_CHROMOS
0.26	-0.71	-0.12	0.44	0.42	0.53	-0.09	HALLMARK_MYC_TARGETS_V2
0.03	-0.44	0.09	-0.06	0.38	0.42	-0.5	GOBP_RNA_SPLICING_VIA_TRANSESTERIFIC
0.24	-0.53	0.21	-0.01	0.2	0.42	-0.2	GOBP_MITOTIC_SISTER_CHROMATID_SEGREG
0.26	-0.51	0.02	-0.04	0.21	0.41	-0.34	GOBP_SISTER_CHROMATID_SEGREGATION
0.05	-0.43	0.11	-0.09	0.43	0.36	-0.4	GOBP_RNA_SPLICING
0.05	-0.49	-0.04	0.01	0.35	0.38	-0.41	GOBP_RIBONUCLEOPROTEIN_COMPLEX_BIOGEN
0.18	-0.59	-0.24	-0.23	-0.28	0.38	-0.01	HALLMARK_TSP_METASIGNALING
0.1	-0.42	0.07	-0.06	0.34	0.46	-0.46	GOBP_RNA_PROCESSING
0.16	-0.4	0.06	0	0.32	0.38	-0.44	GOBP_MRNA_METABOLIC_PROCESS
0.06	-0.46	0.1	0	0.28	0.31	-0.42	GOBP_MRNA_PROCESSING
-0.43	-0.1	-0.19	0.2	-0.43	-0.51	0.86	GOBP_KERATINIZATION
-0.08	-0.28	0	0.22	-0.22	-0.33	0.68	GOBP_REGULATION_OF_WATER_LOSS_VIA_SKIN
-0.36	0.01	-0.3	0.07	-0.41	-0.47	0.85	GOBP_CORNIFICATION
-0.28	0.44	0.18	0.18	-0.38	-0.38	0.78	GOBP_ENDOCRINE_GLUCOCORTICOID
-0.15	0.08	-0.44	-0.11	-0.41	-0.41	0.78	GOBP_KERATINOCYTE_DIFFERENTIATION
-0.07	-0.28	-0.28	-0.28	-0.28	-0.4	0.7	GOBP_EPIDERMAL_CELL_DIFFERENTIATION
-0.18	0.12	-0.3	-0.05	-0.33	-0.34	0.67	GOBP_SKIN_DEVELOPMENT
-0.28	-0.07	-0.25	-0.25	-0.25	-0.25	0.67	GOBP_EPIDERMIS_DEVELOPMENT
-0.07	0.1	-0.29	-0.29	-0.25	-0.27	0.57	GOBP_WATER_HOMEOSTASIS
-0.26	0.03	-0.21	-0.07	-0.23	-0.14	0.54	GOBP_ANTHRAPOBIO_HUMORAL_RESPONSE
0	-0.01	-0.08	0.12	-0.28	-0.3	0.49	GOBP_EPITHELIAL_CELL_DIFFERENTIATION
0.09	0.09	-0.08	0.18	-0.22	-0.22	0.45	HALLMARK_ESTROGEN_RESPONSE_LATE
-0.23	0.11	0.08	0.16	-0.04	-0.1	0.38	HALLMARK_ESTROGEN_RESPONSE_EARLY
-0.14	-0.22	-0.17	-0.28	-0.28	-0.31	0.31	HALLMARK_KRAS_SIGNALING_DN
-0.05	0.03	0.03	0.15	-0.15	-0.29	0.3	HALLMARK_XENOBIOTIC_METABOLISM
0.11	0.17	0.17	-0.17	-0.17	-0.22	0.13	HALLMARK_TNFA_SIGNALING_VIA_NFkB
-0.08	0.05	-0.09	0.06	-0.11	-0.26	0.27	HALLMARK_P53_PATHWAY

Program-1

Program-2

Program-3

Program-4

Program-5

Program-6

Program-7