

	GSE41867.DAY15_EFFECTOR_VS_DAY30_EXHAUSTED_CD8_TCELL_LCMV_CLONE13_DN, GSE41867.DAY15_EFFECTOR_VS_DAY30_EXHAUSTED_CD8_TCELL_LCMV_CLONE13_DN, GSE2405_S_AUREUS_VS_UNTREATED_NEUTROPHIL_UP, GSE2405_S_AUREUS_VS_UNTREATED_NEUTROPHIL_UP, GSE27786_LSK_VS_NKCELL_UP, GSE27786_LSK_VS_NKCELL_UP, GSE7460_FOXP3_MUT_VS_WT_ACT_TCONV_UP, GSE7460_FOXP3_MUT_VS_WT_ACT_TCONV_UP, GSE4535_BM_DERIVED_DC_VS_FOLLICULAR_DC_UP, GSE4535_BM_DERIVED_DC_VS_FOLLICULAR_DC_UP, GSE21063_3H_VS_14H_ANTIL_KCM_STIM_NFATC1_KORCELL_UP, GSE21063_3H_VS_14H_ANTIL_KCM_STIM_NFATC1_KORCELL_UP, GSE8621_UNSTIM_VS_LPS_PRIMED_UNSTIM_MACROPHAGE_UP, GSE8621_UNSTIM_VS_LPS_PRIMED_UNSTIM_MACROPHAGE_UP, LIU_VMYB_TARGETS_UP, LIU_VMYB_TARGETS_UP, GSE16522_ANTI_CD3CD28_STIM_VS_UNSTIM_MEMORY_CD8_TCELL_UP, GSE16522_ANTI_CD3CD28_STIM_VS_UNSTIM_MEMORY_CD8_TCELL_UP, MIR1_5P, MIR1_5P, GSE3203_WT_VS_IFNARI_KO_INFLUENZA_INFECTED_LN_BCELL_DN, GSE3203_WT_VS_IFNARI_KO_INFLUENZA_INFECTED_LN_BCELL_DN, MIR6734_3P, MIR6734_3P, GSE36078_UNTREATED_VS_AD5_T425A_HEXON_INF_IL1R_KO_MOUSE_LUNG_DC_DN, GSE36078_UNTREATED_VS_AD5_T425A_HEXON_INF_IL1R_KO_MOUSE_LUNG_DC_DN, GSE37533_UNTREATED_VS_PIOGLIZATONE_TREATED_CD4_TCELL_FOXP3_TRANSDUCED_CD4_TCELL_DN, GSE37533_UNTREATED_VS_PIOGLIZATONE_TREATED_CD4_TCELL_FOXP3_TRANSDUCED_CD4_TCELL_DN, MIR6817_5P, MIR6817_5P, MIR4769_3P, MIR4769_3P, MORF_PP2R5B, MORF_PP2R5B, GOBP_HEPATICOBILIARY_SYSTEM_DEVELOPMENT, GOBP_HEPATICOBILIARY_SYSTEM_DEVELOPMENT, GOBP_FATTY_ACID_BIOSYNTHETIC_PROCESS, GOBP_FATTY_ACID_BIOSYNTHETIC_PROCESS, GSE22601_DOUBLE_NEGATIVE_VS_IMMATURE_CD4_SP_THYMOCYTE_DN, GSE22601_DOUBLE_NEGATIVE_VS_IMMATURE_CD4_SP_THYMOCYTE_DN, GCGNRMNNYCAT_UNKNOWN, GCGNRMNNYCAT_UNKNOWN, MIR4722_3P, MIR4722_3P, GSE2405_0H_VS_6H_A_PHAGOCYTOPHILUM_STIM_NEUTROPHIL_DN, GSE2405_0H_VS_6H_A_PHAGOCYTOPHILUM_STIM_NEUTROPHIL_DN, SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM3, SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM3, MIR10398_5P, MIR10398_5P, GOMF_PROTEIN_TYROSINE_PHOSPHATASE_ACTIVITY, GOMF_PROTEIN_TYROSINE_PHOSPHATASE_ACTIVITY, KEGG_GAP_JUNCTION, KEGG_GAP_JUNCTION, BROWNE_HCMV_INFECTION_10HR_UP, BROWNE_HCMV_INFECTION_10HR_UP, GOBP_PRIMARY_ALCOHOL_METABOLIC_PROCESS, GOBP_PRIMARY_ALCOHOL_METABOLIC_PROCESS, REACTOME_ATF4_ACTIVATES_GENES_IN_RESPONSE_TO_ENDOPLASMIC_RETICULUM_STRESS, REACTOME_ATF4_ACTIVATES_GENES_IN_RESPONSE_TO_ENDOPLASMIC_RETICULUM_STRESS, MORF_DMPK, MORF_DMPK, MORF_TNFRSF6, MORF_TNFRSF6, OVSYANNIKOVA_PBMc_FLUARIX_AGE_55_64YO_RESPONDERS_VS_NONRESPONDERS_IDY_UP, OVSYANNIKOVA_PBMc_FLUARIX_AGE_55_64YO_RESPONDERS_VS_NONRESPONDERS_IDY_UP, MIR1288_5P, MIR1288_5P, HP_SPEECH_APRAXIA, HP_SPEECH_APRAXIA, MORF_BCL2L11, MORF_BCL2L11, HP_AVASCULAR_NECROSIS, HP_AVASCULAR_NECROSIS, RBL1_TARGET_GENES, RBL1_TARGET_GENES, MIR924, MIR924, OUILLETTE_CL1_13Q14_DELETION_DN, OUILLETTE_CL1_13Q14_DELETION_DN, GSE29618_LAI1_VS_TIV_FLU_VACCINE_DAY7_PDC_DN, GSE29618_LAI1_VS_TIV_FLU_VACCINE_DAY7_PDC_DN, HOLLEMAN_VINCRIStINE_RESISTANCE_ALL_UP, HOLLEMAN_VINCRIStINE_RESISTANCE_ALL_UP, MIR6798_3P, MIR6798_3P, SABATES_COLORECTAL_ADENOMA_UP, SABATES_COLORECTAL_ADENOMA_UP, MIR4774_3P, MIR4774_3P, REACTOME_CARBOXYTERMINAL_POST_TRANSLATIONAL_MODIFICATIONS_OF_TUBULIN, REACTOME_CARBOXYTERMINAL_POST_TRANSLATIONAL_MODIFICATIONS_OF_TUBULIN, MORF_CASP10, MORF_CASP10, MIR909, MIR909, WANG_CLASSIC_ADIPOGENIC_TARGETS_OF_PPARG, WANG_CLASSIC_ADIPOGENIC_TARGETS_OF_PPARG, MIR410_5P, MIR410_5P, HP_ENCEPHALITIS, HP_ENCEPHALITIS, GOBP_ISOPRENOID_METABOLIC_PROCESS, GOBP_ISOPRENOID_METABOLIC_PROCESS, REACTOME_DEREGULATED_CDK5_TRIGGERS_MULTIPLE_NEURODEGENERATIVE_PATHWAYS_IN_ALZHEIMER_S_DISEASE_MODELS, REACTOME_DEREGULATED_CDK5_TRIGGERS_MULTIPLE_NEURODEGENERATIVE_PATHWAYS_IN_ALZHEIMER_S_DISEASE_MODELS, MIR4714_3P, MIR4714_3P, LEE_LIVER_CANCER_MYC_E2F1_DN, LEE_LIVER_CANCER_MYC_E2F1_DN, GOBP_INTRA_S_DNA_DAMAGE_CHECKPOINT, GOBP_INTRA_S_DNA_DAMAGE_CHECKPOINT, LEE_LIVER_CANCER_MYC_TGFA_DN, LEE_LIVER_CANCER_MYC_TGFA_DN, YAGUE_PRETUMOR_DRUG_RESISTANCE_DN, YAGUE_PRETUMOR_DRUG_RESISTANCE_DN, MORF_IL4, MORF_IL4, GOBP_POSITIVE_REGULATION_OF_RESPONSE_TO_WOUNDING, GOBP_POSITIVE_REGULATION_OF_RESPONSE_TO_WOUNDING, AKL_HTLV1_INFECTION_UP, AKL_HTLV1_INFECTION_UP, GSE3720_LPS_VS_PMA_STIM_VD2_GAMMADelta_TCELL_DN, GSE3720_LPS_VS_PMA_STIM_VD2_GAMMADelta_TCELL_DN, GTCTACC_MIR379, GTCTACC_MIR379, HP_HYPOPHOSPHATEMIC_RICKETS, HP_HYPOPHOSPHATEMIC_RICKETS, GOBP_POSITIVE_REGULATION_OF_WOUND_HEALING, GOBP_POSITIVE_REGULATION_OF_WOUND_HEALING, MORF_KDR, MORF_KDR, GOMF_PROTEIN_TYROSINE_SERINE_THREONINE_PHOSPHATASE_ACTIVITY, GOMF_PROTEIN_TYROSINE_SERINE_THREONINE_PHOSPHATASE_ACTIVITY, CUL_DEVELOPING_HEART_5TH_WEEK_VENTRICULAR_CARDIOMYOCYTE, CUL_DEVELOPING_HEART_5TH_WEEK_VENTRICULAR_CARDIOMYOCYTE, GOBP_COENZYME_A_METABOLIC_PROCESS, GOBP_COENZYME_A_METABOLIC_PROCESS, WP_SEROTONIN_RECEPTOR_2_AND_ELKSRFGATA4_SIGNALING, WP_SEROTONIN_RECEPTOR_2_AND_ELKSRFGATA4_SIGNALING, MORF_CD8A, MORF_CD8A, GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_RED_UP, GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_RED_UP, GOMF_O_ACYLTRANSFERASE_ACTIVITY, GOMF_O_ACYLTRANSFERASE_ACTIVITY, HP_NECK_FLEXOR_WEAKNESS, HP_NECK_FLEXOR_WEAKNESS, DESCARTES_FETAL_PLACENTA_APP_ALB_POSITIVE_CELLS, DESCARTES_FETAL_PLACENTA_APP_ALB_POSITIVE_CELLS, HP_CUTANEOUS_MELANOMA, HP_CUTANEOUS_MELANOMA, GOBP_ATF6_MEDIATED_UNFOLDED_PROTEIN_RESPONSE, GOBP_ATF6_MEDIATED_UNFOLDED_PROTEIN_RESPONSE, LEIN_OLIGODENDROCYTE_MARKERS, LEIN_OLIGODENDROCYTE_MARKERS, GOBP_TERPENOID_METABOLIC_PROCESS, GOBP_TERPENOID_METABOLIC_PROCESS, HP_HYPOPHOSPHATEMIA, HP_HYPOPHOSPHATEMIA, ZNF586_TARGET_GENES, ZNF586_TARGET_GENES, YANG_BREAST_CANCER_ESR1_DN, YANG_BREAST_CANCER_ESR1_DN, NAKAMURA_METASTASIS_MODEL_UP, NAKAMURA_METASTASIS_MODEL_UP, SARTIPY_NORMAL_AT_INSULIN_RESISTANCE_UP, SARTIPY_NORMAL_AT_INSULIN_RESISTANCE_UP, MODULE_481, MODULE_481, MORF_MAP2K7, MORF_MAP2K7, MIR520G_5P, MIR520G_5P, MODULE_544, MODULE_544, GOBP_RESPONSE_TO_OLEIC_ACID, GOBP_RESPONSE_TO_OLEIC_ACID, NUNODA_RESPONSE_TO_DASATINIB_IMATINIB_DN, NUNODA_RESPONSE_TO_DASATINIB_IMATINIB_DN, YOKOE_CANCER_TESTS_ANTIGENS, YOKOE_CANCER_TESTS_ANTIGENS, MIR8078, MIR8078, HP_ABNORMAL_CIRCULATING_FERRITIN_CONCENTRATION, HP_ABNORMAL_CIRCULATING_FERRITIN_CONCENTRATION, MIR4313, MIR4313, HP_RICKETS, HP_RICKETS, KEGG_RETINOL_METABOLISM, KEGG_RETINOL_METABOLISM, GOMF_BETA_1_ADRENERGIC_RECEPTOR_BINDING, GOMF_BETA_1_ADRENERGIC_RECEPTOR_BINDING, REACTOME_PENTOSE_PHOSPHATE_PATHWAY, REACTOME_PENTOSE_PHOSPHATE_PATHWAY, HP_ABNORMAL_URINE_PHOSPHATE_CONCENTRATION, HP_ABNORMAL_URINE_PHOSPHATE_CONCENTRATION, HP_GLOMERULOPATHY, HP_GLOMERULOPATHY, TUOMISTO_TUMOR_SUPPRESSION_BY_COL13A1_DN, TUOMISTO_TUMOR_SUPPRESSION_BY_COL13A1_DN, HP_LOW_MOLECULAR_WEIGHT_PROTEINURIA, HP_LOW_MOLECULAR_WEIGHT_PROTEINURIA, GOBP_CEREBRAL_CORTEX_CELL_MIGRATION, GOBP_CEREBRAL_CORTEX_CELL_MIGRATION, GOMF_MONOCARBOXYLIC_ACID_BINDING, GOMF_MONOCARBOXYLIC_ACID_BINDING, GOBP_REGULATION_OF_FATTY_ACID_BIOSYNTHETIC_PROCESS, GOBP_REGULATION_OF_FATTY_ACID_BIOSYNTHETIC_PROCESS, HP_OROMANDIBULAR_DYSTONIA, HP_OROMANDIBULAR_DYSTONIA, GOBP_UDP_N_ACETYLGLUCOSAMINE_METABOLIC_PROCESS, GOBP_UDP_N_ACETYLGLUCOSAMINE_METABOLIC_PROCESS, BIOCARTA_LONGEVITY_PATHWAY, BIOCARTA_LONGEVITY_PATHWAY, HP_RETINAL_PIGMENT_EPITHELIAL_ATROPHY, HP_RETINAL_PIGMENT_EPITHELIAL_ATROPHY, BIOCARTA_MTA3_PATHWAY, BIOCARTA_MTA3_PATHWAY, WHITE_NEUROBLASTOMA_WITH_IP36.3_DELETION, WHITE_NEUROBLASTOMA_WITH_IP36.3_DELETION, GOBP_RETROGRADE_TRANS_SYNAPTIC_SIGNALING, GOBP_RETROGRADE_TRANS_SYNAPTIC_SIGNALING, GOBP_REGULATION_OF_NEUROTRANSMITTER_RECEPTOR_LOCALIZATION_TO_POSTSYNAPTIC_SPECIALIZATION_MEMBRANE, GOBP_REGULATION_OF_NEUROTRANSMITTER_RECEPTOR_LOCALIZATION_TO_POSTSYNAPTIC_SPECIALIZATION_MEMBRANE, KEGG_NITROGEN_METABOLISM, KEGG_NITROGEN_METABOLISM, HP_BICARBONATE_WASTING_RENAL_TUBULAR_ACIDOSIS, HP_BICARBONATE_WASTING_RENAL_TUBULAR_ACIDOSIS, GOBP_RRNA_5_END_PROCESSING, GOBP_RRNA_5_END_PROCESSING, MORF_THPO, MORF_THPO, HP_NEOPLASM_OF_THE_RESPIRATORY_SYSTEM, HP_NEOPLASM_OF_THE_RESPIRATORY_SYSTEM, REACTOME_METABOLISM_OF_FAT_SOLUBLE_VITAMINS, REACTOME_METABOLISM_OF_FAT_SOLUBLE_VITAMINS, MODULE_560, MODULE_560, HP_ROTARY_NYSTAGMUS, HP_ROTARY_NYSTAGMUS, HP_ABNORMAL_CIRCULATING_PORPHYRIN_CONCENTRATION, HP_ABNORMAL_CIRCULATING_PORPHYRIN_CONCENTRATION, CAO_BLOOD_FLUZONE_AGE_05_14YO_IDY_DN, CAO_BLOOD_FLUZONE_AGE_05_14YO_IDY_DN, GOBP_GLUCINE_METABOLIC_PROCESS, GOBP_GLUCINE_METABOLIC_PROCESS, HP_CENTRALLY_NUCLEATED_SKELETAL_MUSCLE_FIBERS, HP_CENTRALLY_NUCLEATED_SKELETAL_MUSCLE_FIBERS, HP_HYPERCHLOREMIC_ACIDOSIS, HP_HYPERCHLOREMIC_ACIDOSIS, WP_DIFFERENTIATION_OF_WHITE_AND_BROWN_ADIPOCYTE, WP_DIFFERENTIATION_OF_WHITE_AND_BROWN_ADIPOCYTE, BIOCARTA_RECK_PATHWAY, BIOCARTA_RECK_PATHWAY, RUAN_RESPONSE_TO_TROGLITAZONE_UP, RUAN_RESPONSE_TO_TROGLITAZONE_UP, GOMF_INTERLEUKIN_1_RECEPTOR_ACTIVITY, GOMF_INTERLEUKIN_1_RECEPTOR_ACTIVITY, HP_DELIRIUM, HP_DELIRIUM, HP_MEMBRANOPROLIFERATIVE_GLOMERULONEPHRITIS, HP_MEMBRANOPROLIFERATIVE_GLOMERULONEPHRITIS, GOBP_RESPONSE_TO_STEROL, GOBP_RESPONSE_TO_STEROL, MORF_MYL3, MORF_MYL3, SMID_BREAST_CANCER_RELAPSE_IN_BONE_UP, SMID_BREAST_CANCER_RELAPSE_IN_BONE_UP, KIM_ALL_DISORDERS_CALB1_CORR_DN, KIM_ALL_DISORDERS_CALB1_CORR_DN, GOBP_POSITIVE_REGULATION_OF_INTERLEUKIN_13_PRODUCTION, GOBP_POSITIVE_REGULATION_OF_INTERLEUKIN_13_PRODUCTION, HP_PROXIMAL_RENAL_TUBULAR_ACIDOSIS, HP_PROXIMAL_RENAL_TUBULAR_ACIDOSIS, SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_UP, SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_UP, HP_EPIDERMAL_NEVUS, HP_EPIDERMAL_NEVUS, HP_RENAL_SODIUM_WASTING, HP_RENAL_SODIUM_WASTING, GOBP_PARANODAL_JUNCTION_ASSEMBLY, GOBP_PARANODAL_JUNCTION_ASSEMBLY, RANKIN_ANGIOGENIC_TARGETS_OF_VHL_HIF2A_DN, RANKIN_ANGIOGENIC_TARGETS_OF_VHL_HIF2A_DN, GOBP_CDS_POSITIVE_ALPHA_BETA_T_CELL_PROLIFERATION, GOBP_CDS_POSITIVE_ALPHA_BETA_T_CELL_PROLIFERATION, HP_DEHYDRATION, HP_DEHYDRATION, HP_ABNORMAL_BLOOD_MONOVALENT_INORGANIC_CATION_CONCENTRATION, HP_ABNORMAL_BLOOD_MONOVALENT_INORGANIC_CATION_CONCENTRATION, GOUYER_TAT1_TARGETS_DN, GOUYER_TAT1_TARGETS_DN, THEODOROU_MAMMARY_TUMORIGENESIS, THEODOROU_MAMMARY_TUMORIGENESIS, GOMF_SEMAPHORIN_RECEPTOR_ACTIVITY, GOMF_SEMAPHORIN_RECEPTOR_ACTIVITY, GOMF_PEPITIDYL_PROLINE_DIOXYGENASE_ACTIVITY, GOMF_PEPITIDYL_PROLINE_DIOXYGENASE_ACTIVITY, HP_BICARBONATURIA, HP_BICARBONATURIA, GOBP_T_FOLLICULAR_HELPER_CELL_DIFFERENTIATION, GOBP_T_FOLLICULAR_HELPER_CELL_DIFFERENTIATION, GOBP_STEROL_HOMEOSTASIS, GOBP_STEROL_HOMEOSTASIS, GOBP_ENUCLEATE_ERYTHROCYTE_DIFFERENTIATION, GOBP_ENUCLEATE_ERYTHROCYTE_DIFFERENTIATION, GOBP_FAT_PAD_DEVELOPMENT, GOBP_FAT_PAD_DEVELOPMENT, HP_ABNORMALITY_OF_THE_PREMAXILLA, HP_ABNORMALITY_OF_THE_PREMAXILLA, GOCC_GROWTH_CONE_MEMBRANE, GOCC_GROWTH_CONE_MEMBRANE, HP_RECURRENT_STAPHYLOCOCCUS_AUREUS_INFECTIONS, HP_RECURRENT_STAPHYLOCOCCUS_AUREUS_INFECTIONS, GOBP_CEREBRAL_CORTEX_RADIALLY_ORIENTED_CELL_MIGRATION, GOBP_CEREBRAL_CORTEX_RADIALLY_ORIENTED_CELL_MIGRATION, OKAWA_NEUROBLASTOMA_IP36_31_DELETION, OKAWA_NEUROBLASTOMA_IP36_31_DELETION, REACTOME_SHC_RELATED_EVENTS_TRIGGERED_BY_IGF1R, REACTOME_SHC_RELATED_EVENTS_TRIGGERED_BY_IGF1R, REACTOME_ACTIVATED_NTRK2_SIGNALS_THROUGH_RAS, REACTOME_ACTIVATED_NTRK2_SIGNALS_THROUGH_RAS, REACTOME_SOS_MEDIATED_SIGNALLING, REACTOME_SOS_MEDIATED_SIGNALLING, WP_PENTOSE_PHOSPHATE_METABOLISM, WP_PENTOSE_PHOSPHATE_METABOLISM, GOBP_MONOVALENT_INORGANIC_ANION_HOMEOSTASIS, GOBP_MONOVALENT_INORGANIC_ANION_HOMEOSTASIS, HP_PERSISTENT_EBV_VIREMIA, HP_PERSISTENT_EBV_VIREMIA, GOBP_POSITIVE_REGULATION_OF_HEXOKINASE_ACTIVITY, GOBP_POSITIVE_REGULATION_OF_HEXOKINASE_ACTIVITY, GOBP_LIPID_TRANSPORT_ACROSS_BLOOD_BRAIN_BARRIER, GOBP_LIPID_TRANSPORT_ACROSS_BLOOD_BRAIN_BARRIER, GOBP_PYRUVATE_BIOSYNTHETIC_PROCESS, GOBP_PYRUVATE_BIOSYNTHETIC_PROCESS, WP_TRIACYLGLYCERIDE_SYNTHESIS, WP_TRIACYLGLYCERIDE_SYNTHESIS, GOBP_SEMAPHORIN_PLEXIN_SIGNALING_PATHWAY_INVOLVED_IN_NEURON_PROJECTION_GUIDANCE, GOBP_SEMAPHORIN_PLEXIN_SIGNALING_PATHWAY_INVOLVED_IN_NEURON_PROJECTION_GUIDANCE, HP_EXAGGERATED_STARTLE_RESPONSE, HP_EXAGGERATED_STARTLE_RESPONSE, HP_HEMOPHAGOCYTOSIS, HP_HEMOPHAGOCYTOSIS, HP_ABSENT_POVEAL_REFLEX, HP_ABSENT_POVEAL_REFLEX, HP_ALLERGIC_RHINITIS, HP_ALLERGIC_RHINITIS, GOBP_DICHOTOMOUS_SUBDIVISION_OF_AN_EPITHELIAL_TERMINAL_UNIT, GOBP_DICHOTOMOUS_SUBDIVISION_OF_AN_EPITHELIAL_TERMINAL_UNIT, BIOCARTA_RELIN_PATHWAY, BIOCARTA_RELIN_PATHWAY, MIR4787_5P, MIR4787_5P, HP_DECREASED_ADENOSYLCOBALAMIN, HP_DECREASED_ADENOSYLCOBALAMIN, GOBP_MONOACYLGLYCEROL_BIOSYNTHETIC_PROCESS, GOBP_MONOACYLGLYCEROL_BIOSYNTHETIC_PROCESS, GOMF_2_ACYLGLYCEROL_O_ACYLTRANSFERASE_ACTIVITY, GOMF_2_ACYLGLYCEROL_O_ACYLTRANSFERASE_ACTIVITY, REACTOME_INTERLEUKIN_36_PATHWAY, REACTOME_INTERLEUKIN_36_PATHWAY, REACTOME_ACTIVATED_NTRK3_SIGNALS_THROUGH_RAS, REACTOME_ACTIVATED_NTRK3_SIGNALS_THROUGH_RAS, GOBP_POSITIVE_REGULATION_OF_INTERLEUKIN_5_PRODUCTION, GOBP_POSITIVE_REGULATION_OF_INTERLEUKIN_5_PRODUCTION, GOCC_SYMMETRIC_SYNAPSE, GOCC_SYMMETRIC_SYNAPSE, GOBP_REGULATION_OF_POSTSYNAPTIC_SPECIALIZATION_ASSEMBLY, GOBP_REGULATION_OF_POSTSYNAPTIC_SPECIALIZATION_ASSEMBLY, HP_RENAL_FIBROSIS, HP_RENAL_FIBROSIS, GOBP_RETROGRADE_TRANS_SYNAPTIC_SIGNALING_BY_LIPID, GOBP_RETROGRADE_TRANS_SYNAPTIC_SIGNALING_BY_LIPID, HP_MACULAR_COLOBOMA, HP_MACULAR_COLOBOMA, HP_PROMINENCE_OF_THE_PREMAXILLA, HP_PROMINENCE_OF_THE_PREMAXILLA, GOBP_POSITIVE_REGULATION_OF_GLUKOKINASE_ACTIVITY, GOBP_POSITIVE_REGULATION_OF_GLUKOKINASE_ACTIVITY, HP_DECREASED_METHYLMALONYL_COA_MUTASE_ACTIVITY, HP_DECREASED_METHYLMALONYL_COA_MUTASE_ACTIVITY, HP_MOLLUSCUM_CONTAGIOSUM, HP_MOLLUSCUM_CONTAGIOSUM, GOBP_THREONINE_CATABOLIC_PROCESS, GOBP_THREONINE_CATABOLIC_PROCESS, GOMF_DIACYLGLYCEROL_O_ACYLTRANSFERASE_ACTIVITY, GOMF_DIACYLGLYCEROL_O_ACYLTRANSFERASE_ACTIVITY, GOMF_C_PALMITOYLTRANSFERASE_ACTIVITY, GOMF_C_PALMITOYLTRANSFERASE_ACTIVITY, GOBP_REGULATION_OF_EXCITATORY_SYNAPSE_ASSEMBLY, GOBP_REGULATION_OF_EXCITATORY_SYNAPSE_ASSEMBLY, GOBP_CELLULAR_RESPONSE_TO_STEROL, GOBP_CELLULAR_RESPONSE_TO_STEROL, GOBP_REGULATION_OF_MIRNA_METABOLIC_PROCESS, GOBP_REGULATION_OF_MIRNA_METABOLIC_PROCESS, GOMF_PROTEIN_TYROSINE_THREONINE_PHOSPHATASE_ACTIVITY, GOMF_PROTEIN_TYROSINE_THREONINE_PHOSPHATASE_ACTIVITY, GOBP_NEGATIVE_REGULATION_OF_CELL_SIZE, GOBP_NEGATIVE_REGULATION_OF_CELL_SIZE, HP_INCREASED_URINARY_POTASSIUM, HP_INCREASED_URINARY_POTASSIUM, REACTOME_REVERSIBLE_HYDRATION_OF CARBON_DIOXIDE, REACTOME_REVERSIBLE_HYDRATION_OF CARBON_DIOXIDE, GOBP_OPIOID_RECEPTOR_SIGNALING_PATHWAY, GOBP_OPIOID_RECEPTOR_SIGNALING_PATHWAY, MORF_PDCD1, MORF_PDCD1, GOBP_NUCLEOSIDE_DIPHOSPHATE_CATABOLIC_PROCESS, GOBP_NUCLEOSIDE_DIPHOSPHATE_CATABOLIC_PROCESS, MIR95_3P, MIR95_3P, HP_MOTTLED_PIGMENTATION, HP_MOTTLED_PIGMENTATION, GOBP_POSITIVE_REGULATION_OF_MIRNA_METABOLIC_PROCESS, GOBP_POSITIVE_REGULATION_OF_MIRNA_METABOLIC_PROCESS, KAUFFMANN_MELANOMA_RELAPSE_DN, KAUFFMANN_MELANOMA_RELAPSE_DN, GOBP_THREONINE_METABOLIC_PROCESS, GOBP_THREONINE_METABOLIC_PROCESS, GOBP_PENTOSE_CATABOLIC_PROCESS, GOBP_PENTOSE_CATABOLIC_PROCESS, GOMF_CARBOONATE_DEHYDRATASE_ACTIVITY, GOMF_CARBOONATE_DEHYDRATASE_ACTIVITY, LOPEZ_EPITHELIOID_MESOTHELIOMA, LOPEZ_EPITHELIOID_MESOTHELIOMA, GOMF_LONG_CHAIN_FATTY_ACID_TRANSPORTER_ACTIVITY, GOMF_LONG_CHAIN_FATTY_ACID_TRANSPORTER_ACTIVITY, HP_AVASCULAR_NECROSIS_OF_THE_CAPITAL_FEMORAL_EPIPHYSIS, HP_AVASCULAR_NECROSIS_OF_THE_CAPITAL_FEMORAL_EPIPHYSIS, GOMF_OPIOID_RECEPTOR_ACTIVITY, GOMF_OPIOID_RECEPTOR_ACTIVITY, GOBP_PARAXIAL_MESODERM_FORMATION, GOBP_PARAXIAL_MESODERM_FORMATION, REACTOME_ACYL_CHAIN_REMODELING_OF_DAG_AND_TAG, REACTOME_ACYL_CHAIN_REMODELING_OF_DAG_AND_TAG, GOBP_RIBONUCLEOSIDE_DIPHOSPHATE_CATABOLIC_PROCESS, GOBP_RIBONUCLEOSIDE_DIPHOSPHATE_CATABOLIC_PROCESS, GOBP_CELLULAR_TRIGLYCERIDE_HOMEOSTASIS, GOBP_CELLULAR_TRIGLYCERIDE_HOMEOSTASIS, MORF_PTPRR, MORF_PTPRR, GOBP_REGULATION_OF_UNSATURATED_FATTY_ACID_BIOSYNTHETIC_PROCESS, GOBP_REGULATION_OF_UNSATURATED_FATTY_ACID_BIOSYNTHETIC_PROCESS, GOBP_LAYER_FORMATION_IN_CEREBRAL_CORTEX, GOBP_LAYER_FORMATION_IN_CEREBRAL_CORTEX, GOBP_LIPID_DIGESTION, GOBP_LIPID_DIGESTION, HP_HYPERIONIC_DEHYDRATION, HP_HYPERIONIC_DEHYDRATION, HP_CHORIORETINAL_HYPOPIGMENTATION, HP_CHORIORETINAL_HYPOPIGMENTATION, HP_SUBDURAL_HEMORRHAGE, HP_SUBDURAL_HEMORRHAGE, REACTOME_ACTIVATION_OF_RAS_IN_B_CELLS, REACTOME_ACTIVATION_OF_RAS_IN_B_CELLS, HP_LYMPHANGIECTASIS, HP_LYMPHANGIECTASIS, GOBP_POSITIVE_REGULATION_OF_PEROXISOME_PROLIFERATOR_ACTIVATED_RECEPTOR_SIGNALING_PATHWAY, GOBP_POSITIVE_REGULATION_OF_PEROXISOME_PROLIFERATOR_ACTIVATED_RECEPTOR_SIGNALING_PATHWAY, HP_HYPOINSULINEMIA, HP_HYPOINSULINEMIA, GOBP_REGULATION_OF_WATER_LOSS_VIA_SKIN, GOBP_REGULATION_OF_WATER_LOSS_VIA_SKIN, GOBP_POSITIVE_REGULATION_OF_RECEPTOR_CLUSTERING, GOBP_POSITIVE_REGULATION_OF_RECEPTOR_CLUSTERING, HP_MATURITY_ONSET_DIABETES_OF_THE_YOUNG, HP_MATURITY_ONSET_DIABETES_OF_THE_YOUNG, chr4q33, chr4q33, MORF_ITGA2, MORF_ITGA2, HP_ABNORMAL_URINE_POTASSIUM_CONCENTRATION, HP_ABNORMAL_URINE_POTASSIUM_CONCENTRATION, GOMF_INTERLEUKIN_1_RECEPTOR_BINDING, GOMF_INTERLEUKIN_1_RECEPTOR_BINDING, GOBP_PENTOSE_METABOLIC_PROCESS, GOBP_PENTOSE_METABOLIC_PROCESS, GOMF_ACTIVIN_RECEPTOR_BINDING, GOMF_ACTIVIN_RECEPTOR_BINDING, MODULE_153, MODULE_153
VS_IL12_TREATED_ACT_CD4_TCELL_6H_DN, GSE2770_TGFB_AND_IL4_VS_IL12_TREATED_ACT_CD4_TCELL_6H_DN	