

GSE3609.WT.VS.NLRP10.KO.DC.DN,GSE3609.WT.VS.NLRP10.KO.DC.DN,GSE4606.IRF4MID.VS.WT.CD40L_IL2_IL5_3DAY3.STIMULATED.BCELL.DN,GSE4606.IRF4MID.VS.WT.CD40L_IL2_IL5_3DAY3.STIMULATED.BCELL.DN,GSE17721.4H.VS.2H1.POLYIC.BMDC.DN,GSE17721.4H.VS.2H1.POLYIC.BMDC.DN,GSE3681.UNSTIM.VS.PAM.TLR2.STIM.PERITONEAL.MACROPHAGE.UP,GSE22601.IMMATURE.CD4.SINGLE.POSITIVE.VS.DOUBLE.POSITIVE.TH1MOCYTE.DN,GSE22601.IMMATURE.CD4.SINGLE.POSITIVE.VS.DOUBLE.POSITIVE.TH1MOCYTE.DN,GSE22103.UNSTIM.VS.LPS.STIM.NEUTROPHIL.UP,GSE22601.DOUBLE.NEGATIVE.VS.CD4.SINGLE.POSITIVE.TH1MOCYTE.UP,GSE2796.HDAC3.KO.VS.WT.TREG.UP,GSE2796.HDAC3.KO.VS.WT.TREG.UP,GSE4692.B.BURGDORFERI.VS.B.BURGDORFERI.AND.IFNG.STIM.ENDOTHELIAL_CELL.DN,GSE4692.B.BURGDORFERI.VS.B.BURGDORFERI.AND.IFNG.STIM.ENDOTHELIAL_CELL.DN,GSE17721.LPS.VS.CPG.4H.BMDC.DN,GSE17721.LPS.VS.CPG.4H.BMDC.DN,GSE20754.WT.VS.TCF1.KO.MEMORY.CD8.TCELL.UP,GSE20754.WT.VS.TCF1.KO.MEMORY.CD8.TCELL.UP,GSE8621.LPS.STIM.VS.LPS.PRIMED.AND.LPS.STIM.MACROPHAGE.DN,GSE8621.LPS.STIM.VS.LPS.PRIMED.AND.LPS.STIM.MACROPHAGE.DN,GSE4169.UNSTIM.VS.ANTI.ICM1.CD4.TCELL.4H.DN,GSE4176.UNSTIM.VS.ANTI.ICM1.CD4.TCELL.4H.DN,GSE17721.0.5H.VS.8H.PAMC3K4.BMDC.DN,GSE17721.0.5H.VS.8H.PAMC3K4.BMDC.DN,GSE7768.OVA.ALONE.VS.OVA.WITH.LPS.IMMUNIZED.MOUSE.WHOLE.SPLEEN.6H.DN,GSE7768.OVA.ALONE.VS.OVA.WITH.LPS.IMMUNIZED.MOUSE.WHOLE.SPLEEN.6H.DN,GSE4606.IRF4.KO.VS.WT.CD40L_IL2_IL5_3DAY3.STIMULATED.BCELL.DN,GSE4606.IRF4.KO.VS.WT.CD40L_IL2_IL5_3DAY3.STIMULATED.BCELL.DN,GSE43436.UNTREATED.VS.4H.TLR1.TLR2.LIGAND.TREATED.MONOCYTE.DN,GSE43436.UNTREATED.VS.4H.TLR1.TLR2.LIGAND.TREATED.MONOCYTE.DN,GSE11961.POLLICULAR.BCELL.VS.GERMINAL.CENTER.BCELL.DAY40.DN,GSE11961.POLLICULAR.BCELL.VS.GERMINAL.CENTER.BCELL.DAY40.DN,GSE43492.S172.KO.VS.WT.DAYS1.CMV.EFFECTOR.CD8.TCELL.DN,GSE43492.S172.KO.VS.WT.DAYS1.CMV.EFFECTOR.CD8.TCELL.DN,GSE43863.DAY6.EFF.VS.DAYS10.MEM.THI.CD4.TCELL.UP,GSE43863.DAY6.EFF.VS.DAYS10.MEM.THI.CD4.TCELL.UP,GSE9097.CTRL.VS.LPS.1H.STIM.IRAK4.KO.BMDM.UP,GSE9097.CTRL.VS.LPS.1H.STIM.IRAK4.KO.BMDM.UP,GSE3532.WT.VS.P18ARC.KO.1A.TCONV.UP,GSE3532.WT.VS.P18ARC.KO.1A.TCONV.UP,GSE15330.HSC.VS.LYMPHOID.PRIMED.MULTIPOTENT.PROGENITOR.UP,GSE15330.HSC.VS.LYMPHOID.PRIMED.MULTIPOTENT.PROGENITOR.UP,GSE19923.HEB.KO.VS.HEB.AND.E2A.KO.DP.TH1MOCYTE.DN,GSE19923.HEB.KO.VS.HEB.AND.E2A.KO.DP.TH1MOCYTE.DN,GSE4748.CTRL.VS.LPS.STIM.DC.3H.UP,GSE4748.CTRL.VS.LPS.STIM.DC.3H.UP,GSE19888.ADENOSINE.A3R.ACT.VS.TCELL.MEMBRANES.ACT.AND.A3R.INH.PRETREAT.IN.MAST.CELL.DN,GSE19888.ADENOSINE.A3R.ACT.VS.TCELL.MEMBRANES.ACT.AND.A3R.INH.PRETREAT.IN.MAST.CELL.DN,GSE39087.CTRL.VS.4H.STIM.IRAK4.KO.BMDM.DN,GSE39087.CTRL.VS.LPS.4H.STIM.IRAK4.KO.BMDM.DN,GSE3162.UNTREATED.VS.4H.LPS.STIM.HDAC3.HET.MACROPHAGE.UP,GSE3162.UNTREATED.VS.4H.LPS.STIM.HDAC3.HET.MACROPHAGE.UP,GSE14769.UNSTIM.VS.360MIN.LPS.BMDM.DN,GSE14769.UNSTIM.VS.360MIN.LPS.BMDM.DN,MIR186_3P,MIR186_3P,GSE23925.DARK.ZONE.VS.NAIVE.BCELL.DN,GSE23925.DARK.ZONE.VS.NAIVE.BCELL.DN,GSE40274.CTRL.VS.GATA1.TRANSDUCEED.ACTIVATED.CD4.TCELL.DN,GSE40274.CTRL.VS.GATA1.TRANSDUCEED.ACTIVATED.CD4.TCELL.DN,GSE27241.CTRL.VS.DIGOXIN.TREATED.CD4.TCELL.IN.TH17.POLARIZING.CONDITIONS.UP,GSE27241.CTRL.VS.DIGOXIN.TREATED.CD4.TCELL.IN.TH17.POLARIZING.CONDITIONS.UP,CREBP1_01,CREBP1_01,GSE17721.CTRL.VS.CPG.2H.BMDC.DN,GSE17721.CTRL.VS.CPG.2H.BMDC.DN,GSE1685.RASGLITAZONE.IFNG.TNF.VS.IL4.STIM.MACROPHAGE.UP,GSE1685.RASGLITAZONE.IFNG.TNF.VS.IL4.STIM.MACROPHAGE.UP,GSE27786.BCELL.VS.NEUTROPHIL.DN,GSE27786.BCELL.VS.NEUTROPHIL.DN,AAACCAC_MIR140,AAACCAC_MIR140,GGCAGTG_MIR3243P,GGCAGTG_MIR3243P,GSE4946.MATURE.STIMULATORY.VS.LISTERIA.INF.MATURE.DC.UP,GSE4946.MATURE.STIMULATORY.VS.LISTERIA.INF.MATURE.DC.UP,GSE4606.IRF4MID.VS.WT.CD40L_IL2_IL5_3DAY3.STIMULATED.BCELL.DN,GSE4606.IRF4MID.VS.WT.CD40L_IL2_IL5_3DAY3.STIMULATED.BCELL.DN,MIR6788_3P,MIR6788_3P,GSE17721.CTRL.VS.LPS.2H.BMDC.DN,GSE17721.CTRL.VS.LPS.2H.BMDC.DN,MIR4802_3P,MIR4802_3P,MIR6C_1_3P,MIR6C_1_3P,GSE360_1_MAJOR.VS.T.CONDIL.MAC.UP,GSE360_1_MAJOR.VS.T.CONDIL.MAC.UP,MIR3150B_3P,MIR3150B_3P,MIR4784,MIR4784,MIR892A,MIR892A,MIR376_3P,MIR40756_3P,MIR6134,MIR6134,GSE6259.33DI_POS.DC.VS.BCELL.UP,GSE6259.33DI_POS.DC.VS.BCELL.UP,DIRMEIER.LMP1.RESPONSE.LATE.UP,DIRMEIER.LMP1.RESPONSE.LATE.UP,MIR1183,MIR1183,KEGG_COLORECTAL_CANCER,KEGG_COLORECTAL_CANCER,GSE13306.TREG.VS.TCONV.LAMINA_PROPRIA.DN,GSE13306.TREG.VS.TCONV.LAMINA_PROPRIA.DN,MIR6868_5P,MIR6868_5P,RODRIGUES.THYROID.CARCINOMA.DN,RODRIGUES.THYROID.CARCINOMA.DN,MIR364,MIR364,GORP.REGULATION.OF.HISTONE.METHYLATION,GORP.REGULATION.OF.HISTONE.METHYLATION,ROVERSI.GLIOMA.COPY.NUMBER.UP,ROVERSI.GLIOMA.COPY.NUMBER.UP,GSE22527.ANTI.CD3.INVIVO.VS.UNTREATED.MOUSE.TREG.UP,GSE22527.ANTI.CD3.INVIVO.VS.UNTREATED.MOUSE.TREG.UP,ATF6_01,ATF6_01,MIR620_3P,MIR620_3P,MODULE_522,MODULE_522,RTTTNNNTTGGM.UNKNOWN,RTTTNNNTTGGM.UNKNOWN,GROSS.HYPOXIA.VIA.HIF1A.DN,GROSS.HYPOXIA.VIA.HIF1A.DN,MIR4696,MIR4696,KRAS.DE.V1.DN,KRAS.DE.V1.DN,REACTOME_INTRA_GOLGI_TRAFFIC,REACTOME_INTRA_GOLGI_TRAFFIC,CTCAAGA_MIR526B,CTCAAGA_MIR526B,GSE13547.CTRL.VS.ANTI.ICM1.STIM.ZFX.KO.BCELL_12H.UP,GSE13547.CTRL.VS.ANTI.ICM1.STIM.ZFX.KO.BCELL_12H.UP,GSE16385.UNTREATED.VS.12H.12H.RASGLITAZONE.IFNG.TNF.TREATED.MACROPHAGE.UP,GSE16385.UNTREATED.VS.12H.12H.RASGLITAZONE.IFNG.TNF.TREATED.MACROPHAGE.UP,MIR504_5P,MIR504_5P,REACTOME_RHO_GTPASE_CYCLE,REACTOME_RHO_GTPASE_CYCLE,WP.REGULATION.OF.TOLLLIKE.RECEPTOR.SIGNALING.PATHWAY,WP.REGULATION.OF.TOLLLIKE.RECEPTOR.SIGNALING.PATHWAY,WP.HEAD.AND.NECK.SQUAMOUS.CELL.CARCINOMA,WP.HEAD.AND.NECK.SQUAMOUS.CELL.CARCINOMA,WP.PHOSPHONOSITIDES.METABOLISM,WP.PHOSPHONOSITIDES.METABOLISM,CCTNTMAGA.UNKNOWN,CCTNTMAGA.UNKNOWN,MIR6797_3P,MIR6797_3P,GSE27092.WT.VS.HDAC7_PHOSPHO_DEFICIENT.CD8.TCELL.UP,GSE27092.WT.VS.HDAC7_PHOSPHO_DEFICIENT.CD8.TCELL.UP,CCAGGTT_MIR640,CCAGGTT_MIR640,WP_TOLLLIKE_RECEPTOR_SIGNALING_RELATED_TO_MYD88,WP_TOLLLIKE_RECEPTOR_SIGNALING_RELATED_TO_MYD88,MIR974,MIR974,GORP_FIBROBLAST_MIGRATION,GORP_FIBROBLAST_MIGRATION,MIR6848_3P,MIR6848_3P,GORP_SMAD_BINDING,GORP_SMAD_BINDING,MARSON_FOXO3_TARGETS.UP,MARSON_FOXO3_TARGETS.UP,BAKKER_FOXO3_TARGETS.UP,BAKKER_FOXO3_TARGETS.UP,GSE17721.CTRL.VS.CPG.1H.BMDC.DN,GSE17721.CTRL.VS.CPG.1H.BMDC.DN,KEGG_TGF_BETA_SIGNALING_PATHWAY,KEGG_TGF_BETA_SIGNALING_PATHWAY,MIR6767_3P,MIR6767_3P,MIR6843_3P,MIR6843_3P,GGCKCATGS.UNKNOWN,GGCKCATGS.UNKNOWN,NAKAMURA_METASTASIS,NAKAMURA_METASTASIS,GSE2949.DC.BRAIN.VS.MONOCYTE_BONE_MARROW.DN,GSE2949.DC.BRAIN.VS.MONOCYTE_BONE_MARROW.DN,MIR6780B_3P,MIR6780B_3P,RYTGCNWTGCCR.UNKNOWN,RYTGCNWTGCCR.UNKNOWN,FXR_Q3,FXR_Q3,EVI1_Q2,EVI1_Q2,MIR620_3P,MIR620_3P,REACTOME_SIGNALING_BY_CYTOSOLIC_FGFR1_FUSION_MUTANTS,REACTOME_SIGNALING_BY_CYTOSOLIC_FGFR1_FUSION_MUTANTS,GTCAAGGA_MIR378,GTCAAGGA_MIR378,COME_ACETYLGALACTOSAMINYLTRANSFERASE_ACTIVITY,COME_ACETYLGALACTOSAMINYLTRANSFERASE_ACTIVITY,MIR1587,MIR1587,MIR652_3P,MIR652_3P,GENTILE_UV_RESPONSE_CLUSTER_D8,GENTILE_UV_RESPONSE_CLUSTER_D8,MORI_SMALL_PRE_BIL_LYMPHOCYTE.UP,MORI_SMALL_PRE_BIL_LYMPHOCYTE.UP,GORP_REGULATION_OF_FIBROBLAST_MIGRATION,GORP_REGULATION_OF_FIBROBLAST_MIGRATION,PID_FERK1_PATHWAY,PID_FERK1_PATHWAY,GORP_HYALURONAN_CATABOLIC_PROCESS,GORP_HYALURONAN_CATABOLIC_PROCESS,REACTOME_DOWNREGULATION_OF_SMAD2_3_SMAD4_TRANSCRIPTIONAL_ACTIVITY,REACTOME_DOWNREGULATION_OF_SMAD2_3_SMAD4_TRANSCRIPTIONAL_ACTIVITY,COME_PHOSPHATIDYLINOSITOL_3_4_5_TRISPHOSPHATE_BINDING,COME_PHOSPHATIDYLINOSITOL_3_4_5_TRISPHOSPHATE_BINDING,MIR4450,MIR4450,BIOCARTA_GLEEVEC_PATHWAY,BIOCARTA_GLEEVEC_PATHWAY,GORP_POSITIVE_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING,GORP_POSITIVE_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING,GOCC_PHOSPHATIDYLINOSITOL_3_KINASE_COMPLEX,GOCC_PHOSPHATIDYLINOSITOL_3_KINASE_COMPLEX,MIR651,MIR651,BIOCARTA_BCELLSURVIVAL_PATHWAY,BIOCARTA_BCELLSURVIVAL_PATHWAY,MIR571,MIR571,MIR324_5P,MIR324_5P,BIOCARTA_PAR1_PATHWAY,BIOCARTA_PAR1_PATHWAY,MIKKELSEN_NPC_1CP_WITH_H3K4ME3,MIKKELSEN_NPC_1CP_WITH_H3K4ME3,MIR3641,MIR3641,STAMBOLSKY_TARGETS_OF_MUTATED_TP53_DN,STAMBOLSKY_TARGETS_OF_MUTATED_TP53_DN,BIOCARTA_AKT_PATHWAY,BIOCARTA_AKT_PATHWAY,REACTOME_SIGNALING_BY_ERYTHROPOIETIN,REACTOME_SIGNALING_BY_ERYTHROPOIETIN,BIOCARTA_HCMV_PATHWAY,BIOCARTA_HCMV_PATHWAY,GORP_PHOSPHATIDYLINOSITOL_3_PHOSPHATE_BIOSYNTHETIC_PROCESS,GORP_PHOSPHATIDYLINOSITOL_3_PHOSPHATE_BIOSYNTHETIC_PROCESS,GORP_RESPONSE_TO_FIBROBLAST_GROWTH_FACTOR,GORP_RESPONSE_TO_FIBROBLAST_GROWTH_FACTOR,MIR6827_3P,MIR6827_3P,NAKAMURA_METASTASIS_MODEL.UP,NAKAMURA_METASTASIS_MODEL.UP,REACTOME_NEGATIVE_REGULATION_OF_THE_P3K_AKT_NETWORK,REACTOME_NEGATIVE_REGULATION_OF_THE_P3K_AKT_NETWORK,PID_IL1_PATHWAY,PID_IL1_PATHWAY,REACTOME_EGR2_AND_SOX10_MEDIATED_INITIATION_OF_SCHWANN_CELL_MYELINATION,REACTOME_EGR2_AND_SOX10_MEDIATED_INITIATION_OF_SCHWANN_CELL_MYELINATION,MIR20B_3P,MIR20B_3P,MIR5702,MIR5702,COME_PHOSPHATIDYLINOSITOL_KINASE_ACTIVITY,COME_PHOSPHATIDYLINOSITOL_KINASE_ACTIVITY,WP_HOJSTPATHOGEN_INTERACTION_OF_HUMAN_CORONA_VIRUSES_AUTOPHAGY,WP_HOJSTPATHOGEN_INTERACTION_OF_HUMAN_CORONA_VIRUSES_AUTOPHAGY,COME_IL_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY,COME_IL_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY,KEGG_O_GLYCAN_BIOSYNTHESIS,KEGG_O_GLYCAN_BIOSYNTHESIS,SA_PTEN_PATHWAY,SA_PTEN_PATHWAY,HP_ABNORMAL_SIZE_OF_PITUITARY_GLAND,HP_ABNORMAL_SIZE_OF_PITUITARY_GLAND,COME_MODIFIED_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY,COME_MODIFIED_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY,GORP_HISTONE_H3_K4_TRIMETHYLATION,GORP_HISTONE_H3_K4_TRIMETHYLATION,MIR3162_3P,MIR3162_3P,GORP_O_GLYCAN_PROCESSING,GORP_O_GLYCAN_PROCESSING,BIOCARTA_PDGF_PATHWAY,BIOCARTA_PDGF_PATHWAY,MIR1258,MIR1258,MIR6773_3P,MIR6773_3P,MIR581_3P,MIR581_3P,PID_AYB3_OPN_PATHWAY,PID_AYB3_OPN_PATHWAY,MIR4507,MIR4507,WP_NEOVASCULARISATION_PROCESSES,WP_NEOVASCULARISATION_PROCESSES,BIOCARTA_ARAP_PATHWAY,BIOCARTA_ARAP_PATHWAY,FINETT1_BREAST_CANCERS_KINOME_GRAY,FINETT1_BREAST_CANCERS_KINOME_GRAY,MIR6747_3P,MIR6747_3P,GORP_MODIFIED_AMINO_ACID_TRANSPORT,GORP_MODIFIED_AMINO_ACID_TRANSPORT,TIAN_TNF_SIGNALING_VIA_NFKB,TIAN_TNF_SIGNALING_VIA_NFKB,BIOCARTA_INSULIN_PATHWAY,BIOCARTA_INSULIN_PATHWAY,HP_ELEVATED_TISSUE_NON_SPECIFIC_ALKALINE_PHOSPHATASE,HP_ELEVATED_TISSUE_NON_SPECIFIC_ALKALINE_PHOSPHATASE,MIR6796_3P,MIR6796_3P,REACTOME_HYALURONAN_UPTAKE_AND_DEGRADATION,REACTOME_HYALURONAN_UPTAKE_AND_DEGRADATION,MODULE_421,MODULE_421,MIR619_3P,MIR619_3P,GORP_SMAD_PROTEIN_SIGNAL_TRANSDUCTION,GORP_SMAD_PROTEIN_SIGNAL_TRANSDUCTION,GORP_PPTIDYL_SERINE_DEPHOSPHORYLATION,GORP_PPTIDYL_SERINE_DEPHOSPHORYLATION,DORN_ADENOVIRUS_INFECTION_24HR.DN,DORN_ADENOVIRUS_INFECTION_24HR.DN,BIOCARTA_GH_PATHWAY,BIOCARTA_GH_PATHWAY,BIOCARTA_TPO_PATHWAY,BIOCARTA_TPO_PATHWAY,REACTOME_SIGNALING_BY_FLT3_FUSION_PROTEINS,REACTOME_SIGNALING_BY_FLT3_FUSION_PROTEINS,ZNF697_TARGET_GENES,ZNF697_TARGET_GENES,MIR6724_5P,MIR6724_5P,COME_ACETYLGALACTOSAMINYLTRANSFERASE_ACTIVITY,COME_ACETYLGALACTOSAMINYLTRANSFERASE_ACTIVITY,GSE13485.CTRL.VS.DAYS1.VF07D.VACCINE.PBMC.UP,GSE13485.CTRL.VS.DAYS1.VF07D.VACCINE.PBMC.UP,GOCC_ATG1_ULKI_KINASE_COMPLEX,GOCC_ATG1_ULKI_KINASE_COMPLEX,HEIDENBLAD_AMPIFIED_IN_SOFT_TISSUE_CANCER,HEIDENBLAD_AMPIFIED_IN_SOFT_TISSUE_CANCER,REACTOME_O_LINKED_GLYCOSYLATION_OF_MUCINS,REACTOME_O_LINKED_GLYCOSYLATION_OF_MUCINS,REACTOME_FGFR1_MUTANT_RECEPTOR_ACTIVATION,REACTOME_FGFR1_MUTANT_RECEPTOR_ACTIVATION,COME_1_PHOSPHATIDYLINOSITOL_3_KINASE_ACTIVITY,COME_1_PHOSPHATIDYLINOSITOL_3_KINASE_ACTIVITY,REACTOME_ERYTHROPOIETIN_ACTIVATES_PHOSPHONOSITIDE_3_KINASE_P3K,REACTOME_ERYTHROPOIETIN_ACTIVATES_PHOSPHONOSITIDE_3_KINASE_P3K,COME_PHOSPHATIDYLINOSITOL_3_KINASE_ACTIVITY,COME_PHOSPHATIDYLINOSITOL_3_KINASE_ACTIVITY,AMT_EGF_RESPONSE_240_HELA,AMT_EGF_RESPONSE_240_HELA,BIOCARTA_TOB1_PATHWAY,BIOCARTA_TOB1_PATHWAY,GORP_REGULATION_OF_SMAD_PROTEIN_SIGNAL_TRANSDUCTION,GORP_REGULATION_OF_SMAD_PROTEIN_SIGNAL_TRANSDUCTION,REACTOME_HYALURONAN_METABOLISM,REACTOME_HYALURONAN_METABOLISM,BIOCARTA_GCR_PATHWAY,BIOCARTA_GCR_PATHWAY,REACTOME_FOXO_MEDIATED_TRANSCRIPTION_OF_CELL_CYCLE_GENES,REACTOME_FOXO_MEDIATED_TRANSCRIPTION_OF_CELL_CYCLE_GENES,MIR6867_3P,MIR6867_3P,BIOCARTA_EDG1_PATHWAY,BIOCARTA_EDG1_PATHWAY,GORP_REGULATION_OF_CHROMATIN_BINDING,GORP_REGULATION_OF_CHROMATIN_BINDING,HP_ULNAR_CLAW,HP_ULNAR_CLAW,COME_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_BINDING,COME_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_BINDING,HP_DIASTEMA,HP_DIASTEMA,COME_HYALURONONGLUCOSAMINIDASE_ACTIVITY,COME_HYALURONONGLUCOSAMINIDASE_ACTIVITY,MIR669,MIR669,AACGGTT_MIR451,AACGGTT_MIR451,MODULE_560,MODULE_560,HP_HYPERTROPHIC_NERVE_CHANGES,HP_HYPERTROPHIC_NERVE_CHANGES,MIR669,MIR669,ILK_TARGET_GENES,ILK_TARGET_GENES,MIR6769A_3P,MIR6769A_3P,COME_PHOSPHATIDYLINOSITOL_PHOSPHATE_KINASE_ACTIVITY,COME_PHOSPHATIDYLINOSITOL_PHOSPHATE_KINASE_ACTIVITY,MIR4741,MIR4741,HP_HYPERLIPOPROTEINEMIA,HP_HYPERLIPOPROTEINEMIA,MIR1268A,MIR1268B,MIR1268A,MIR1268B,MIR3914,MIR3914,WP_TCELL_RECEPTOR_AND_COSTIMULATORY_SIGNALING,WP_TCELL_RECEPTOR_AND_COSTIMULATORY_SIGNALING,BIOCARTA_ICG1_PATHWAY,BIOCARTA_ICG1_PATHWAY,PID_GLYPICAN_1PATHWAY,PID_GLYPICAN_1PATHWAY,HP_INCREASED_LDL_CHOLESTEROL_CONCENTRATION,HP_INCREASED_LDL_CHOLESTEROL_CONCENTRATION,GOCC_ENDOPLASMIC_RETICULUM_PLASMA_MEMBRANE_CONTACT_SITE,GOCC_ENDOPLASMIC_RETICULUM_PLASMA_MEMBRANE_CONTACT_SITE,HP_VENOUS_MALFORMATION,HP_VENOUS_MALFORMATION,REACTOME_INTERLEUKIN_1_PROCESSING,REACTOME_INTERLEUKIN_1_PROCESSING,BIOCARTA_TFF_PATHWAY,BIOCARTA_TFF_PATHWAY,GORP_NEGATIVE_REGULATION_OF_CELL_CYCLE_CHECKPOINT,GORP_NEGATIVE_REGULATION_OF_CELL_CYCLE_CHECKPOINT,COME_1_SMAD_BINDING,COME_1_SMAD_BINDING,MEDINA_SMARCA4_TARGETS,MEDINA_SMARCA4_TARGETS,GORP_CELL_JUNCTION_DISASSEMBLY,GORP_CELL_JUNCTION_DISASSEMBLY,COME_RNA_POLYMERASE_II_ACTIVATING_TRANSCRIPTION_FACTOR_BINDING,COME_RNA_POLYMERASE_II_ACTIVATING_TRANSCRIPTION_FACTOR_BINDING,MIR3935,MIR3935,GORP_GERM_CELL_MIGRATION,GORP_GERM_CELL_MIGRATION,BIOCARTA_ARF_PATHWAY,BIOCARTA_ARF_PATHWAY,CTACTAG_MIR325,CTACTAG_MIR325,GORP_ENERGY_HOMEOSTASIS,GORP_ENERGY_HOMEOSTASIS,GORP_POSITIVE_REGULATION_OF_FIBROBLAST_APOPTOTIC_PROCESS,GORP_POSITIVE_REGULATION_OF_FIBROBLAST_APOPTOTIC_PROCESS,MIR528_3P,MIR528_3P,HP_ABNORMAL_LDL_CHOLESTEROL_CONCENTRATION,HP_ABNORMAL_LDL_CHOLESTEROL_CONCENTRATION,ZIRN_TRETINOIN_RESPONSE.UP,ZIRN_TRETINOIN_RESPONSE.UP,REACTOME_CD28_DEPENDENT_P3K_AKT_SIGNALING,REACTOME_CD28_DEPENDENT_P3K_AKT_SIGNALING,BIOCARTA_NCF_PATHWAY,BIOCARTA_NCF_PATHWAY,ZEP28_TARGET_GENES,ZEP28_TARGET_GENES,FOURNIER_ACINAR_DEVELOPMENT_EARLY.UP,FOURNIER_ACINAR_DEVELOPMENT_EARLY.UP,SINGH_NFE2L2_TARGETS,SINGH_NFE2L2_TARGETS,GORP_NEUROBLAST_DIVISION,GORP_NEUROBLAST_DIVISION,PID_SHP2_PATHWAY,PID_SHP2_PATHWAY,GORP_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CILUM,GORP_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CILUM,BIOCARTA_BAD_PATHWAY,BIOCARTA_BAD_PATHWAY,GORP_ENDOPLASMIC_RETICULUM_LOCALIZATION,GORP_ENDOPLASMIC_RETICULUM_LOCALIZATION,MIR136_3P,MIR136_3P,REACTOME_REGULATION_OF_GLYCOLYSIS_BY_FRUCTOSE_2_6_BISPHOSPHATE_METABOLISM,REACTOME_REGULATION_OF_GLYCOLYSIS_BY_FRUCTOSE_2_6_BISPHOSPHATE_METABOLISM,HP_ABNORMALITY_OF_THE_POSTERIOR_PITUITARY,HP_ABNORMALITY_OF_THE_POSTERIOR_PITUITARY,GORP_SULFUR_AMINO_ACID_TRANSPORT,GORP_SULFUR_AMINO_ACID_TRANSPORT,GORP_MAST_CELL_MIGRATION,GORP_MAST_CELL_MIGRATION,BIOCARTA_ACH_PATHWAY,BIOCARTA_ACH_PATHWAY,MIR6885_3P,MIR6885_3P,EVI1_Q1,EVI1_Q1,BIOCARTA_LONGEVITY_PATHWAY,BIOCARTA_LONGEVITY_PATHWAY,GORP_REGULATION_OF_MAST_CELL_CHEMOTAXIS,GORP_REGULATION_OF_MAST_CELL_CHEMOTAXIS,CLIMENT_BREAST_CANCER_COPY_NUMBER.DN,CLIMENT_BREAST_CANCER_COPY_NUMBER.DN,BIOCARTA_IL7_PATHWAY,BIOCARTA_IL7_PATHWAY,KORKOLA_EMBRYONAL_CARCINOMA,KORKOLA_EMBRYONAL_CARCINOMA,KEGG_TAURINE_AND_HYPOTAURINE_METABOLISM,KEGG_TAURINE_AND_HYPOTAURINE_METABOLISM,MIR776,MIR776,NAKAMURA_METASTASIS_MODEL.DN,NAKAMURA_METASTASIS_MODEL.DN,GORP_REGULATION_OF_CHEMOKINE_MEDIATED_SIGNALING_PATHWAY,GORP_REGULATION_OF_CHEMOKINE_MEDIATED_SIGNALING_PATHWAY,BIOCARTA_P1C_PATHWAY,BIOCARTA_P1C_PATHWAY,GORP_NEGATIVE_REGULATION_OF_CHROMATIN_BINDING,GORP_NEGATIVE_REGULATION_OF_CHROMATIN_BINDING,COME_SERINE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY,COME_SERINE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY,GORP_NEGATIVE_REGULATION_OF_CHEMOKINE_MEDIATED_SIGNALING_PATHWAY,GORP_NEGATIVE_REGULATION_OF_CHEMOKINE_MEDIATED_SIGNALING_PATHWAY,GORP_CARDIAC_PACEMAKER_CELL_DIFFERENTIATION,GORP_CARDIAC_PACEMAKER_CELL_DIFFERENTIATION,GORP_TRACHEA_CARTILAGE_DEVELOPMENT,GORP_TRACHEA_CARTILAGE_DEVELOPMENT,COME_SULFUR_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY,COME_SULFUR_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY,COME_1_PHOSPHATIDYLINOSITOL_4_PHOSPHATE_3_KINASE_ACTIVITY,COME_1_PHOSPHATIDYLINOSITOL_4_PHOSPHATE_3_KINASE_ACTIVITY,GORP_NEGATIVE_REGULATION_OF_CARTILAGE_DEVELOPMENT,GORP_NEGATIVE_REGULATION_OF_CARTILAGE_DEVELOPMENT,BIOCARTA_TGFR_PATHWAY,BIOCARTA_TGFR_PATHWAY,REACTOME_CONSTITUTIVE_SIGNALING_BY_ABERRANT_P3K_IN_CANCER,REACTOME_CONSTITUTIVE_SIGNALING_BY_ABERRANT_P3K_IN_CANCER,HP_ABNORMAL_PROTEIN_O_LINKED_GLYCOSYLATION,HP_ABNORMAL_PROTEIN_O_LINKED_GLYCOSYLATION,GOCC_GATOR1_COMPLEX,GOCC_GATOR1_COMPLEX,COME_TRANSFORMING_GROWTH_FACTOR_BETA_BINDING,COME_TRANSFORMING_GROWTH_FACTOR_BETA_BINDING,chr12q23,chr12q23,REACTOME_P3K_EVENTS_IN_ERBB4_SIGNALING,REACTOME_P3K_EVENTS_IN_ERBB4_SIGNALING,GORP_SPHINGOLIPID_MEDIATED_SIGNALING_PATHWAY,GORP_SPHINGOLIPID_MEDIATED_SIGNALING_PATHWAY,BIOCARTA_ECM_PATHWAY,BIOCARTA_ECM_PATHWAY,GORP_SKELETAL_MUSCLE_CELL_DIFFERENTIATION,GORP_SKELETAL_MUSCLE_CELL_DIFFERENTIATION,GORP_NATURAL_KILLER_CELL_CHEMOTAXIS,GORP_NATURAL_KILLER_CELL_CHEMOTAXIS,GORP_REGULATION_OF_BMP_SIGNALING_PATHWAY,GORP_REGULATION_OF_BMP_SIGNALING_PATHWAY,GORP_LIPID_DROPLET_FORMATION,GORP_LIPID_DROPLET_FORMATION,HP_INSIDIOUS_ONSET,HP_INSIDIOUS_ONSET,BIOCARTA_ERK3_PATHWAY,BIOCARTA_ERK3_PATHWAY,MIR132,MIR132,GORP_1_SERINE_TRANSPORT,GORP_1_SERINE_TRANSPORT,COME_1_SERINE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY,COME_1_SERINE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY,MIKKELSEN_DEDIFFERENTIATED_STATE.DN,MIKKELSEN_DEDIFFERENTIATED_STATE.DN,HP_SEVERE_D_LYMPHOCYTOPENIA,HP_SEVERE_D_LYMPHOCYTOPENIA,GORP_NEUTROPHIL_MEDIATED_KILLING_OF_GRAM_NEGATIVE_BACTERIUM,GORP_NEUTROPHIL_MEDIATED_KILLING_OF_GRAM_NEGATIVE_BACTERIUM,CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_HD_MTX.UP,CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_HD_MTX.UP,GORP_COBALAMIN_TRANSPORT,GORP_COBALAMIN_TRANSPORT,HP_LOW_MOLECULAR_WEIGHT_PROTEINURIA,HP_LOW_MOLECULAR_WEIGHT_PROTEINURIA,HP_DYSGERMINOMA,HP_DYSGERMINOMA,GOCC_VCP_NPL4_UFDL_AAA_ATPASE_COMPLEX,GOCC_VCP_NPL4_UFDL_AAA_ATPASE_COMPLEX,GORP_CARDIAC_CONDUCTION_SYSTEM_DEVELOPMENT,GORP_CARDIAC_CONDUCTION_SYSTEM_DEVELOPMENT,HP_ABNORMALITY_OF_BLOOD_VOLUME_HOMEOSTASIS,HP_ABNORMALITY_OF_BLOOD_VOLUME_HOMEOSTASIS,MATSUMIYA_PBMC_MODIFIED_VACCINIA_ANKARA_VACCINE_AGE_18_55YO_LOW_VS_HIGH_RESPONDERS_2DY.GO_T_CELL_ACTIV_AND_CO_STIM.UP,MATSUMIYA_PBMC_MODIFIED_VACCINIA_ANKARA_VACCINE_AGE_18_55YO_LOW_VS_HIGH_RESPONDERS_2DY.GO_T_CELL_ACTIV_AND_CO_STIM.UP,GORP_RESPONSE_TO_HYDROSTATIC_PRESSURE,GORP_RESPONSE_TO_HYDROSTATIC_PRESSURE,COME_AMP_ACTIVATED_PROTEIN_KINASE_ACTIVITY,COME_AMP_ACTIVATED_PROTEIN_KINASE_ACTIVITY,HP_RACHITIC_ROSARY,HP_RACHITIC_ROSARY,MODULC_500,MODULC_500,MAGRANGAS_AJUTILE_MYELOMA_IJGL.VS.IJGL.DN,MAGRANGAS_AJUTILE_MYELOMA_IJGL.VS.IJGL.DN,HP_WIDELY_SPACED_PRIMARY_TEETH,HP_WIDELY_SPACED_PRIMARY_TEETH,HP_SPONTANEOUS_PAIN_SENSATION,HP_SPONTANEOUS_PAIN_SENSATION,GORP_POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CILUM,GORP_POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CILUM,COME_TYPE_II_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_BINDING,COME_TYPE_II_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_BINDING,GORP_CORONARY_ARTERY_MORPHOGENESIS,GORP_CORONARY_ARTERY_MORPHOGENESIS,GORP_PROTEIN_DESUMOYLATION,GORP_PROTEIN_DESUMOYLATION,COME_SUMO_SPECIFIC_PROTEASE_ACTIVITY,COME_SUMO_SPECIFIC_PROTEASE_ACTIVITY,HP_HEMIPERTROPHY,HP_HEMIPERTROPHY

STIM.VS.LPS.STIM.DC.DN,GSE36009.UNSTIM.VS.LPS.STIM.DC.DN