

UP in Ex vivo Tregs	NOM p-val	FDR q-val
GO_RESPONSE_TO_CHEMOKINE	0	0.07550653
GO_INTERLEUKIN_17_PRODUCTION	0	0.09138203
GO_LYMPHOCYTE_MIGRATION	0	0.10907045
GO_POSITIVE_REGULATION_OF_INFLAMMATORY_RESPONSE	0	0.12048406
GO_TAXIS	0	0.11240187
GO_LYMPHOCYTE_CHEMOTAXIS	0	0.15806396
GO_INFLAMMATORY_RESPONSE	0	0.20053715
GO_LEUKOCYTE_CHEMOTAXIS	0	0.19893168
GO_CELL_CHEMOTAXIS	0	0.27647966
GO_REGULATION_OF_INFLAMMATORY_RESPONSE	0	0.35648
GO_LEUKOCYTE_MIGRATION	0	0.4347694
GO_RESPONSE_TO_CYTOKINE	0	0.44007713
GO_REGULATION_OF_CELL_DIFFERENTIATION	0	0.45610142
GO_CELL_MOTILITY	0	0.48048759
GO_CARDIOVASCULAR_SYSTEM_DEVELOPMENT	0.009302326	0.3608413
GO_RECEPTOR_SIGNALING_PATHWAY_VIA_STAT	0.009756098	0.38735786
GO_FAT_CELL_DIFFERENTIATION	0.013201321	0.18046586

UP in Expanded (2 cycles) Tregs	NOM p-val	FDR q-val
GO_OXIDATION_REDUCTION_PROCESS	0	0.012583379
GO_PURINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	0	0.006291689
GO_NUCLEOSIDE_PHOSPHATE_BIOSYNTHETIC_PROCESS	0	0.028001348
GO_PROTEIN_HOMOOIGOMERIZATION	0	0.030214235
GO_SMALL_MOLECULE_METABOLIC_PROCESS	0	0.033046596
GO_RIBOSE_PHOSPHATE_BIOSYNTHETIC_PROCESS	0	0.038814187
GO_MONOCARBOXYLIC_ACID_BIOSYNTHETIC_PROCESS	0	0.035960466
GO_PROTEIN_COMPLEX_OLIGOMERIZATION	0	0.03303576
GO_CELLULAR_KETONE_METABOLIC_PROCESS	0	0.0490688
GO_MONOCARBOXYLIC_ACID_METABOLIC_PROCESS	0	0.05036055
GO_PURINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	0	0.047357805
GO_ORGANIC_ACID_METABOLIC_PROCESS	0	0.043028742
GO_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_METABOLIC_PROCESS	0	0.07826708
GO_ATP_METABOLIC_PROCESS	0	0.07450954
GO_GENERATION_OF_PRECURSOR_METABOLITES_AND_ENERGY	0	0.07812746
GO_SMALL_MOLECULE_BIOSYNTHETIC_PROCESS	0	0.10288974
GO_ORGANOPHOSPHATE_BIOSYNTHETIC_PROCESS	0.001243781	0.04729821
GO_FATTY_ACID_METABOLIC_PROCESS	0.00129199	0.045044724
GO_ENERGY_DERIVATION_BY_OXIDATION_OF_ORGANIC_COMPOUNDS	0.00131579	0.074906856
GO_ELECTRON_TRANSPORT_CHAIN	0.001369863	0.07543734
GO_PROTEIN_TETRAMERIZATION	0.001445087	0.07222676
GO_PROTEIN_CONTAINING_COMPLEX_ASSEMBLY	0.002259887	0.10733313
GO_ORGANONITROGEN_COMPOUND_BIOSYNTHETIC_PROCESS	0.002285714	0.12350081
GO_ORGANIC_ACID_BIOSYNTHETIC_PROCESS	0.0025	0.10433528
GO_CARBOHYDRATE_DERIVATIVE_BIOSYNTHETIC_PROCESS	0.002564103	0.069206454
GO_OXIDATIVE_PHOSPHORYLATION	0.002724796	0.07374851
GO_ALCOHOL_METABOLIC_PROCESS	0.002735978	0.06834498
GO_RESPIRATORY_ELECTRON_TRANSPORT_CHAIN	0.002915452	0.092251256
GO_REGULATION_OF_CELLULAR_KETONE_METABOLIC_PROCESS	0.004070556	0.09617268
GO_CARBOHYDRATE_DERIVATIVE_METABOLIC_PROCESS	0.004884005	0.16611202
GO_RIBOSE_PHOSPHATE_METABOLIC_PROCESS	0.004987531	0.106371894
GO_ATP_SYNTHESIS_COUPLED_ELECTRON_TRANSPORT	0.005532504	0.07879996
GO_CELLULAR_PROTEIN_CONTAINING_COMPLEX_ASSEMBLY	0.006518905	0.13908796
GO_CELLULAR_RESPIRATION	0.008997429	0.077006765
GO_STEM_CELL_DIFFERENTIATION	0.009929078	0.1033455
GO_REGULATION_OF_CELL_CYCLE_PROCESS	0.01120797	0.19728497
GO_LIPID_LOCALIZATION	0.017333332	0.21630453
GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	0.017567568	0.1944931
GO_SEX_DIFFERENTIATION	0.019830028	0.19099016
GO_MITOCHONDRIAL_TRANSPORT	0.020380436	0.1734683
GO_NEGATIVE_REGULATION_OF_ORGANELLE_ORGANIZATION	0.020632736	0.1771302
GO_COENZYME_METABOLIC_PROCESS	0.021505376	0.17647855
GO_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	0.022636484	0.1907039
GO_AMIDE_BIOSYNTHETIC_PROCESS	0.023106547	0.23206294
GO_FATTY_ACID_CATABOLIC_PROCESS	0.025104603	0.23162568
GO_AEROBIC_RESPIRATION	0.0261348	0.2147239
GO_ANATOMICAL_STRUCTURE_HOMEOSTASIS	0.02745098	0.24462153
GO_COENZYME_BIOSYNTHETIC_PROCESS	0.031976745	0.24196935
GO_POST_TRANSLATIONAL_PROTEIN_MODIFICATION	0.033946253	0.22011836
GO_CELLULAR_LIPID_CATABOLIC_PROCESS	0.03457815	0.23100574
GO_MONOCARBOXYLIC_ACID_CATABOLIC_PROCESS	0.035460994	0.2492954
GO_LIPID_CATABOLIC_PROCESS	0.039325844	0.23569204

PATHWAY	Reactome		< 0.01	< 0.25
Total Pathways	1532			
Pathways in analysis	100			

UP in Ex vivo Tregs	NOM p-val	FDR q-val
PEPTIDE_LIGAND_BINDING_RECEPTORS	0	0.06880544
CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	0	0.048421934
CLASS_A_1_RHODOPSIN_LIKE_RECEPTORS	0.004291846	0.03777304
GPCR_LIGAND_BINDING	0.004149378	0.08964529
SIGNALING_BY_VEGF	0.039711192	0.16802287

UP in Expanded (2 cycles) Tregs	NOM p-val	FDR q-val
CELL_CYCLE	0	0.008284029
M_PHASE	0	0.009077182
CELL_CYCLE_MITOTIC	0	0.009966567
THE_CITRIC_ACID_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT	0	0.010738815
FATTY_ACID_METABOLISM	0.002677376	0.01847239
RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS	0.001355014	0.032613687
RESPIRATORY_ELECTRON_TRANSPORT	0.005665722	0.039775167
PROGRAMMED_CELL_DEATH	0.00530504	0.050093487
PTEN_REGULATION	0.006993007	0.060611382
RHO_GTPASE_EFFECTORS	0.02346041	0.079659656
TRANSCRIPTIONAL_REGULATION_BY_RUNX2	0.04221252	0.15049274
METABOLISM_OF_LIPIDS	0.024081115	0.14846991
SIGNALING_BY_NOTCH	0.038873993	0.15814734
TCR_SIGNALING	0.026990553	0.1661174
METABOLISM_OF_VITAMINS_AND_COFACTORS	0.041493777	0.15929298
HIV_INFECTION	0.03668478	0.15220596
NEUTROPHIL_DEGRANULATION	0.046814043	0.16084577
METABOLISM_OF_WATER_SOLUBLE_VITAMINS_AND_COFACTORS	0.04674221	0.16866818
HOST_INTERACTIONS_OF_HIV_FACTORS	0.08096591	0.1689737
CELLULAR_RESPONSES_TO_EXTERNAL_STIMULI	0.052362707	0.1705663
GLUCOSE_METABOLISM	0.07440476	0.19401766
METABOLISM_OF_CARBOHYDRATES	0.0845839	0.20659992

PATHWAY	Hallmark		< 0.01	< 0.25
Total Pathways		50		
Pathways in analysis		22		

UP in Ex vivo Tregs	NOM p-val	FDR q-val
TNFA_SIGNALING_VIA_NFKB	0	0
INFLAMMATORY_RESPONSE	0.022099448	0.13674407
KRAS_SIGNALING_UP	0.098684214	0.16792165
UV_RESPONSE_UP	0.1508772	0.23551862

UP in Expanded (2 cycles) Tregs	NOM p-val	FDR q-val
OXIDATIVE_PHOSPHORYLATION	0	0.002084034
FATTY_ACID_METABOLISM	0.001392758	0.009523878
G2M_CHECKPOINT	0.009845289	0.043777827

UP in Ex vivo Tregs	NOM p-val	FDR q-val
LYMPHOCYTE_MIGRATION	0.003205128	0.062890194
CARDIOVASCULAR_SYSTEM_DEVELOPMENT	0	0.074092284
TAXIS	0	0.085884705
CALCIUM_MEDIATED_SIGNALING	0	0.11830205
LYMPHOCYTE_CHEMOTAXIS	0	0.12364692
NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION	0	0.14243017
RESPONSE_TO_CHEMOKINE	0	0.1476316
FAT_CELL_DIFFERENTIATION	0.008219178	0.15474507
BLOOD_VESSEL_MORPHOGENESIS	0	0.16483806
CELL_CHEMOTAXIS	0.004201681	0.16576004
ALPHA_BETA_T_CELL_ACTIVATION	0	0.16789319
ALPHA_BETA_T_CELL_DIFFERENTIATION	0	0.18111841
SOMATIC_DIVERSIFICATION_OF_IMMUNE_RECEPTORS_VIA_GERMLINE_RECOMBINATION_WITHIN_A_SINGLE_LOCUS	0.009063444	0.19815576
REGULATION_OF_OSSIFICATION	0.017391304	0.20951067
SOMATIC_DIVERSIFICATION_OF_IMMUNE_RECEPTORS	0.013201321	0.21014193
CIRCULATORY_SYSTEM_DEVELOPMENT	0	0.21160297
DNA_RECOMBINATION	0.003389831	0.21196657
PATTERN_RECOGNITION_RECEPTOR_SIGNALING_PATHWAY	0.006079027	0.21413788
LEUKOCYTE_MIGRATION	0	0.21763381
INFLAMMATORY_RESPONSE	0.00617284	0.21836627
SECOND_MESSENGER_MEDIATED_SIGNALING	0	0.21929911
TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION	0.006430868	0.22130296
TUBE_MORPHOGENESIS	0	0.22254363
POSITIVE_REGULATION_OF_HEMOPOIESIS	0.003861004	0.22282104
POSITIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	0.011627907	0.22353113
REGULATION_OF_T_CELL_DIFFERENTIATION	0.015873017	0.2241647
TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.015625	0.225304
LYMPHOCYTE_DIFFERENTIATION	0	0.22742583
INTERLEUKIN_17_PRODUCTION	0.02052786	0.2281222
ALPHA_BETA_T_CELL_PROLIFERATION	0.022727273	0.22986642
REGULATION_OF_VASCULATURE_DEVELOPMENT	0.010600707	0.23474787
T_CELL_DIFFERENTIATION	0	0.23537816
LEUKOCYTE_CHEMOTAXIS	0	0.2359494
CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	0.016447369	0.24031787
REGULATION_OF_TRANSMEMBRANE_TRANSPORT	0.026470589	0.24277174
POSITIVE_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	0.006493507	0.2450301
REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	0.00409836	0.25296885
POSITIVE_REGULATION_OF_LEUKOCYTE_CELL_CELL_ADHESION	0.00921659	0.25427887
CELL_MOTILITY	0	0.254966
B_CELL_ACTIVATION	0.007434944	0.25869867
REGULATION_OF_CELLULAR_COMPONENT_MOVEMENT	0	0.25877737
ADAPTIVE_IMMUNE_RESPONSE_BASED_ON_SOMATIC_RECOMBINATION_OF_IMMUNE_RECEPTORS_BUILT_FROM_IMMUNO	0	0.259495
LEUKOCYTE_DIFFERENTIATION	0	0.26834798
LOCOMOTION	0.008	0.2716227
REGULATION_OF_CELL_DIFFERENTIATION	0	0.28139436
REGULATION_OF_CELL_ADHESION	0	0.2818833
CYTOKINE_PRODUCTION	0.005747126	0.28305027
POSITIVE_REGULATION_OF_CELL_ADHESION	0.005181347	0.28338504
RESPONSE_TO_CYTOKINE	0	0.29186478
T_CELL_ACTIVATION	0.005617978	0.29446116
DEFENSE_RESPONSE	0.00877193	0.30378908
REGULATION_OF_IMMUNE_SYSTEM_PROCESS	0	0.30904144
POSITIVE_REGULATION_OF_CELL_DIFFERENTIATION	0.005780347	0.33367217

UP in Expanded (6 cycles) Tregs	NOM p-val	FDR q-val
OXIDATION_REDUCTION_PROCESS	0	0
ATP_METABOLIC_PROCESS	0	0
GENERATION_OF_PRECURSOR_METABOLITES_AND_ENERGY	0	0
NUCLEOSIDE_PHOSPHATE_BIOSYNTHETIC_PROCESS	0	0.002193563
PURINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	0	0.002847904
PURINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	0	0.003655502
NUCLEOBASE_CONTAINING_SMALL_MOLECULE_METABOLIC_PROCESS	0	0.003952262
RIBOSE_PHOSPHATE_METABOLIC_PROCESS	0	0.004025658
ORGANIC_ACID_METABOLIC_PROCESS	0	0.004391402
OXIDATIVE_PHOSPHORYLATION	0	0.004638796
RIBOSE_PHOSPHATE_BIOSYNTHETIC_PROCESS	0	0.00468206
ENERGY_DERIVATION_BY_OXIDATION_OF_ORGANIC_COMPOUNDS	0.001420455	0.005253607
SMALL_MOLECULE_METABOLIC_PROCESS	0	0.007721522
CELLULAR_RESPIRATION	0	0.008834605
MONOCARBOXYLIC_ACID_METABOLIC_PROCESS	0	0.009016174
PROTEIN_TETRAMERIZATION	0	0.009426379
ATP_SYNTHESIS_COUPLED_ELECTRON_TRANSPORT	0	0.009435128
NUCLEOSIDE_DIPHOSPHATE_METABOLIC_PROCESS	0	0.00981856
PROTEIN_COMPLEX_OLIGOMERIZATION	0.002735978	0.010486652
NUCLEOTIDE_PHOSPHORYLATION	0.001492537	0.011685815
RESPIRATORY_ELECTRON_TRANSPORT_CHAIN	0	0.011825093
CARBOHYDRATE_DERIVATIVE_BIOSYNTHETIC_PROCESS	0.001422475	0.011893535
ELECTRON_TRANSPORT_CHAIN	0.001582279	0.012060544
AEROBIC_RESPIRATION	0.003039514	0.01573267
CARBOHYDRATE_DERIVATIVE_METABOLIC_PROCESS	0	0.016251374
PROTEIN_HOMOOIGOMERIZATION	0	0.016521128
PYRUVATE_METABOLIC_PROCESS	0.002915452	0.028175302
POST_TRANSLATIONAL_PROTEIN_MODIFICATION	0.005934718	0.06274486
ORGANOPHOSPHATE_BIOSYNTHETIC_PROCESS	0.004115226	0.06450336
ADP_METABOLIC_PROCESS	0.012158055	0.06795653
CARBOHYDRATE_CATABOLIC_PROCESS	0.004385965	0.07308845
CELLULAR_KETONE_METABOLIC_PROCESS	0.011594203	0.08006983
ORGANOPHOSPHATE_METABOLIC_PROCESS	0.002610966	0.0819102
CELLULAR_AMIDE_METABOLIC_PROCESS	0.003989362	0.08313154
ORGANONITROGEN_COMPOUND_BIOSYNTHETIC_PROCESS	0	0.094187334
MONOVALENT_INORGANIC_CATION_TRANSPORT	0.013432836	0.09463623
PROTEIN_CONTAINING_COMPLEX_ASSEMBLY	0.004889976	0.11152439
CELLULAR_PROTEIN_CONTAINING_COMPLEX_ASSEMBLY	0.006793478	0.11248386
COENZYME_METABOLIC_PROCESS	0.002894356	0.11366092
POSITIVE_REGULATION_OF_BINDING	0.017777778	0.11427106
CHROMOSOME_SEGREGATION	0.013761468	0.11435992
CELLULAR_AMINO_ACID_METABOLIC_PROCESS	0.016200295	0.11833839
AMIDE_BIOSYNTHETIC_PROCESS	0.011157601	0.12251675
REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	0.008391609	0.12296864
FATTY_ACID_METABOLIC_PROCESS	0.015449438	0.13235949
CELL_CYCLE_PROCESS	0.006082725	0.13278331
MITOCHONDRIAL_TRANSPORT	0.016806724	0.13439007
SMALL_MOLECULE_CATABOLIC_PROCESS	0.015027323	0.14064595
STEM_CELL_DIFFERENTIATION	0.030627871	0.14881511
MONOCARBOXYLIC_ACID_BIOSYNTHETIC_PROCESS	0.019490255	0.14988464
MITOCHONDRIAL_MEMBRANE_ORGANIZATION	0.030120483	0.16040406
ORGANIC_HYDROXY_COMPOUND_METABOLIC_PROCESS	0.025568182	0.16518168
MITOTIC_CELL_CYCLE	0.020463847	0.16538881
REGULATION_OF_CELLULAR_KETONE_METABOLIC_PROCESS	0.035450518	0.16585743
ORGANIC_ACID_BIOSYNTHETIC_PROCESS	0.022160664	0.16769513
SMALL_MOLECULE_BIOSYNTHETIC_PROCESS	0.010695187	0.168781
CELL_DIVISION	0.02478134	0.17800483
CELL_CYCLE	0.002421308	0.17940797
NEGATIVE_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	0.04733728	0.18006021
MITOCHONDRIAL_TRANSMEMBRANE_TRANSPORT	0.048154093	0.204165
PROTEIN_CONTAINING_COMPLEX_DISASSEMBLY	0.060790274	0.22539076
MITOTIC_NUCLEAR_DIVISION	0.040561624	0.24108428

PATHWAY
Total Pathways
Pathways in analysis

Reactome
1532
97

< 0.01 < 0.25

UP in Ex vivo Tregs	NOM p-val	FDR q-val
CLASS_A_1_RHODOPSIN_LIKE_RECEPTORS	0.003623189	0.13447475
PEPTIDE_LIGAND_BINDING_RECEPTORS	0	0.07587901
CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	0.00660066	0.05099076
GPCR_LIGAND_BINDING	0.003584229	0.065386586
SIGNALING_BY_NTRKS	0.022038568	0.13570549
SIGNALING_BY_VEGF	0.055727553	0.2924143

UP in Expanded (6 cycles) Tregs	NOM p-val	FDR q-val
CELL_CYCLE_MITOTIC	0	4.50E-04
THE_CITRIC_ACID_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT	0	6.00E-04
CELL_CYCLE	0	9.00E-04
M_PHASE	0	0.001364844
RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS	0	0.00200767
RESPIRATORY_ELECTRON_TRANSPORT	0	0.004362227
METABOLISM_OF_CARBOHYDRATES	0.002881844	0.034866914
SIGNALING_BY_NOTCH	0.004322767	0.023763534
FATTY_ACID_METABOLISM	0.007194245	0.0432323
TP53_REGULATES_METABOLIC_GENES	0.007751938	0.043138944
GLUCOSE_METABOLISM	0.012539185	0.037828904
RHO_GTPASE_EFFECTORS	0.014577259	0.061168402
PROGRAMMED_CELL_DEATH	0.01664355	0.06001233
PTEN_REGULATION	0.031484257	0.09113552
TRANSCRIPTIONAL_REGULATION_BY_TP53	0.031900138	0.13951112
TRANSCRIPTIONAL_REGULATION_BY_RUNX2	0.034328356	0.10939122
NEUTROPHIL_DEGRANULATION	0.03661972	0.13604622
CELLULAR_RESPONSES_TO_EXTERNAL_STIMULI	0.042674255	0.16007468
METABOLISM_OF_VITAMINS_AND_COFACTORS	0.04327666	0.12921387
METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES	0.064467765	0.17911
METABOLISM_OF_WATER_SOLUBLE_VITAMINS_AND_COFACTORS	0.072115384	0.18586557
SIGNALING_BY_RHO_GTPASES	0.076700434	0.19002153
TNFR2_NON_CANONICAL_NF_KB_PATHWAY	0.09620991	0.21084234
METABOLISM_OF_LIPIDS	0.10121457	0.24135941
SIGNALING_BY_TGF_BETA_RECEPTOR_COMPLEX	0.11624441	0.24755038
TRANSCRIPTIONAL_REGULATION_BY_RUNX1	0.12591508	0.24208283

PATHWAY	Hallmark		< 0.01	< 0.25
Total Pathways		50		
Pathways in analysis		22		

UP in Ex vivo Tregs	NOM p-val	FDR q-val
TNFA_SIGNALING_VIA_NFKB	0	0.02467143
KRAS_SIGNALING_UP	0.09144543	0.44344974

UP in Expanded (6 cycles) Tregs	NOM p-val	FDR q-val
OXIDATIVE_PHOSPHORYLATION	0	0
GLYCOLYSIS	0	0.009578963
FATTY_ACID_METABOLISM	0.007886435	0.022583483
G2M_CHECKPOINT	0.01076923	0.02100733
MTORC1_SIGNALING	0.024011299	0.036648925
ADIPOGENESIS	0.02891933	0.03091713

UP in Expaned (2 cycles) Tregs	NOM p-val	FDR q-val
RESPONSE_TO_TYPE_I_INTERFERON	0	0.03571314
DEFENSE_RESPONSE_TO_VIRUS	0	0.1456421
DEFENSE_RESPONSE	0	0.49772084
LYMPHOCYTE_DIFFERENTIATION	0.001636661	0.698471
REGULATION_OF_IMMUNE_RESPONSE	0.003012048	0.49601492
ADAPTIVE_IMMUNE_RESPONSE	0.003058104	0.6161063
T_CELL_ACTIVATION	0.003149606	0.50477463
IMMUNE_RESPONSE_REGULATING_SIGNALING_PATHWAY	0.003169572	0.68250793
RESPONSE_TO_VIRUS	0.003189793	0.5291086
PATTERN_RECOGNITION_RECEPTOR_SIGNALING_PATHWAY	0.003478261	0.6749166
IMMUNE_EFFECTOR_PROCESS	0.004155125	0.45584652
T_CELL_DIFFERENTIATION	0.004777707	0.52186674
ACTIVATION_OF_IMMUNE_RESPONSE	0.006319115	0.6656504
TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.006920415	0.29921967
LEUKOCYTE_PROLIFERATION	0.008025683	0.535751
ALPHA_BETA_T_CELL_ACTIVATION	0.008347246	0.5364445
REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	0.008741259	0.5813431

UP in Expaned (6 cycles) Tregs	NOM p-val	FDR q-val
CHROMOSOME_SEGREGATION	0	0
GENERATION_OF_PRECURSOR_METABOLITES_AND_ENERGY	0	0.001920087
MITOTIC_NUCLEAR_DIVISION	0	0.002880131
ORGANELLE_FISSION	0	0.010499245
CELL_DIVISION	0	0.013116702
AEROBIC_RESPIRATION	0	0.014420706
ATP_METABOLIC_PROCESS	0	0.022410462
OXIDATIVE_PHOSPHORYLATION	0	0.027793363
MITOTIC_CELL_CYCLE	0	0.03974666
REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	0.004761905	0.04007608
NUCLEOTIDE_PHOSPHORYLATION	0.002272727	0.04098804
ENERGY_DERIVATION_BY_OXIDATION_OF_ORGANIC_COMPOUNDS	0	0.04337299
NUCLEOSIDE_DIPHOSPHATE_METABOLIC_PROCESS	0.002314815	0.043814234
ELECTRON_TRANSPORT_CHAIN	0.002320186	0.044400994
CHROMOSOME_ORGANIZATION	0	0.045040272
OXIDATION_REDUCTION_PROCESS	0	0.049558878
PURINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	0	0.05142375
CELL_CYCLE_PHASE_TRANSITION	0	0.0519243
RESPIRATORY_ELECTRON_TRANSPORT_CHAIN	0.00896861	0.052168656
NUCLEOSIDE_PHOSPHATE_BIOSYNTHETIC_PROCESS	0	0.053567693
CELLULAR_RESPIRATION	0.002450981	0.055915408
CELL_CYCLE_PROCESS	0.002604167	0.061521556
CARBOHYDRATE_CATABOLIC_PROCESS	0.007142857	0.06364217
NUCLEOBASE_CONTAINING_SMALL_MOLECULE_METABOLIC_PROCESS	0.008042895	0.06639888
NEGATIVE_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	0.00462963	0.07684745
CELLULAR_NITROGEN_COMPOUND_CATABOLIC_PROCESS	0.018648019	0.08174388
CELL_CYCLE	0	0.082612
ADP_METABOLIC_PROCESS	0.011286682	0.08792509
PURINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	0.007936508	0.09228873
NEGATIVE_REGULATION_OF_CELL_CYCLE_PROCESS	0.017199017	0.10237201
REGULATION_OF_MORPHOGENESIS_OF_AN_EPITHELIUM	0.006960557	0.10402248
ATP_SYNTHESIS_COUPLED_ELECTRON_TRANSPORT	0.024886878	0.10451766
REGULATION_OF_CELL_CYCLE_PROCESS	0.00243309	0.10679895
REGULATION_OF_MITOTIC_CELL_CYCLE	0.011961723	0.11917699
RIBOSE_PHOSPHATE_METABOLIC_PROCESS	0.012658228	0.15410738
NEGATIVE_REGULATION_OF_CELL_CYCLE	0.010498688	0.15426464
CELLULAR_PROTEIN_CONTAINING_COMPLEX_ASSEMBLY	0.007614213	0.1575884
ORGANIC_ACID_METABOLIC_PROCESS	0.005830904	0.17260854
CELLULAR_RESPONSE_TO ABIOTIC_STIMULUS	0.029126214	0.17552859
ORGANIC_CYCLIC_COMPOUND_CATABOLIC_PROCESS	0.034246575	0.17653582
ORGANOPHOSPHATE_METABOLIC_PROCESS	0.008264462	0.17775951
MRNA_METABOLIC_PROCESS	0.027600849	0.18142265
NEGATIVE_REGULATION_OF_ORGANELLE_ORGANIZATION	0.025761124	0.20365977
CARBOHYDRATE_DERIVATIVE_METABOLIC_PROCESS	0.005681818	0.20405816
CELL_PROJECTION_ASSEMBLY	0.04474273	0.20732668
REGULATION_OF_ORGANELLE_ORGANIZATION	0.00802139	0.20961076
PYRUVATE_METABOLIC_PROCESS	0.03640777	0.20973459
NEGATIVE_REGULATION_OF_MITOTIC_CELL_CYCLE	0.033407573	0.21013343
RIBOSE_PHOSPHATE_BIOSYNTHETIC_PROCESS	0.0389016	0.2125772
INTERLEUKIN_1_MEDIATED_SIGNALING_PATHWAY	0.04761905	0.21319626
DICARBOXYLIC_ACID_METABOLIC_PROCESS	0.06873614	0.23692562
SUPRAMOLECULAR_FIBER_ORGANIZATION	0.054455444	0.23832776
ANTIGEN_PROCESSING_AND_PRESENTATION	0.06666667	0.24546964

PATHWAY

Total Pathways

Pathways in analysis

Reactome

1532

97

< 0.01

< 0.25

UP in Expaned (2 cycles) Tregs	NOM p-val	FDR q-val
INTERFERON_ALPHA_BETA_SIGNALING	0	0.027084213
IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPHOID_CELLS	0.015544041	0.20581025

UP in Expaned (6 cycles) Tregs	NOM p-val	FDR q-val
CELL_CYCLE	0	0
CELL_CYCLE_MITOTIC	0	0
M_PHASE	0	0
RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION	0	0.002150916
THE_CITRIC_ACID_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT	0	0.002338645
RESPIRATORY_ELECTRON_TRANSPORT	0	0.002957654
METABOLISM_OF_CARBOHYDRATES	0	0.007529774
GLUCOSE_METABOLISM	0.002320186	0.013716999
RHO_GTPASE_EFFECTORS	0.007109005	0.019253505
INTERLEUKIN_1_SIGNALING	0.012077294	0.04489697
SIGNALING_BY_NOTCH	0.013824885	0.10032199
PROGRAMMED_CELL_DEATH	0.03874092	0.11611097
SIGNALING_BY_RHO_GTPASES	0.029816514	0.11776954
TRANSCRIPTIONAL_REGULATION_BY_RUNX2	0.054502368	0.16819036
TCF_DEPENDENT_SIGNALING_IN_RESPONSE_TO_WNT	0.068627454	0.18752652
TP53_REGULATES_METABOLIC_GENES	0.098130845	0.24538335

PATHWAY	Hallmark		< 0.01	< 0.25
Total Pathways		50		
Pathways in analysis		22		

UP in Expaned (2 cycles) Tregs	NOM p-val	FDR q-val
INTERFERON_ALPHA_RESPONSE	0.005033557	0.022072831

UP in Expaned (6 cycles) Tregs	NOM p-val	FDR q-val
OXIDATIVE_PHOSPHORYLATION	0	0
GLYCOLYSIS	0	0.001519481
G2M_CHECKPOINT	0	0.001554654
MTORC1_SIGNALING	0.00982801	0.039682686
FATTY_ACID_METABOLISM	0.020134227	0.03644822
ADIPOGENESIS	0.030952381	0.030683044
UV_RESPONSE_UP	0.1373494	0.22518069