

dFab_CCR-IL2		1000iu/mL rIL2	
NAME	FDR q-val	NAME	FDR q-val
KEGG_CELL_CYCLE	0	KEGG_CELL_CYCLE	0
KEGG_DNA_REPLICATION	0	KEGG_DNA_REPLICATION	0
KEGG_MISMATCH_REPAIR	0	KEGG_OOCYTE_MEIOSIS	4.04E-04
KEGG_P53_SIGNALING_PATHWAY	0	KEGG_MISMATCH_REPAIR	5.38E-04
KEGG_PROTEASOME	0	KEGG_PROTEASOME	6.67E-04
KEGG_OOCYTE_MEIOSIS	3.03E-04	KEGG_P53_SIGNALING_PATHWAY	8.38E-04
KEGG_STEROID_BIOSYNTHESIS	7.97E-04	KEGG_STEROID_BIOSYNTHESIS	9.69E-04
KEGG_ASTHMA	8.85E-04	KEGG_HOMOLOGOUS_RECOMBINATION	0.001191859
KEGG_HOMOLOGOUS_RECOMBINATION	9.09E-04	KEGG_NUCLEOTIDE_EXCISION_REPAIR	0.001919777
KEGG_JAK_STAT_SIGNALING_PATHWAY	9.96E-04	KEGG_PYRIMIDINE_METABOLISM	0.001957343
		KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATI ON	0.002136285
KEGG_SMALL_CELL_LUNG_CANCER	0.001141154	KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS	0.002174826
KEGG_LEISHMANIA_INFECTION	0.001692504	KEGG_JAK_STAT_SIGNALING_PATHWAY	0.002726728
KEGG_PYRIMIDINE_METABOLISM	0.001948305		
KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATI ON	0.002253857	KEGG_BASE_EXCISION_REPAIR	0.002921494
KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS	0.00445066	KEGG_PENTOSE_PHOSPHATE_PATHWAY	0.003146225
KEGG_BLADDER_CANCER	0.005318648	KEGG_SMALL_CELL_LUNG_CANCER	0.006297424
KEGG_TYPE_I_DIABETES_MELLITUS	0.005318836	KEGG_CITRATE_CYCLE_TCA_CYCLE	0.006397896
KEGG_NUCLEOTIDE_EXCISION_REPAIR	0.005539546	KEGG_LEISHMANIA_INFECTION	0.006618816
KEGG_PURINE_METABOLISM	0.006092347	KEGG_PANCREATIC_CANCER	0.006754974
KEGG_CITRATE_CYCLE_TCA_CYCLE	0.008060183	KEGG_PURINE_METABOLISM	0.007604821
KEGG_PANCREATIC_CANCER	0.008325363	KEGG_FRUCTOSE_AND_MANNANOSE_METABOLISM	0.012156728
KEGG_BASE_EXCISION_REPAIR	0.009245954	KEGG_ONE_CARBON_POOL_BY_FOLATE	0.012991006
KEGG_APOPTOSIS	0.010396839	KEGG_SPLICEOSOME	0.013266745
KEGG_NICOTINATE_AND_NICOTINAMIDE_METABOLISM	0.011831495	KEGG_ASTHMA	0.014132495
KEGG_PROSTATE_CANCER	0.012157027	KEGG_TYPE_I_DIABETES_MELLITUS	0.014512756
KEGG_ONE_CARBON_POOL_BY_FOLATE	0.015427719	KEGG_NICOTINATE_AND_NICOTINAMIDE_METABOLISM	0.014963876
KEGG_ALLOGRAFT_REJECTION	0.01893525	KEGG_OXIDATIVE_PHOSPHORYLATION	0.016513802
KEGG_VIRAL_MYOCARDITIS	0.019636557	KEGG_PROSTATE_CANCER	0.016625587
KEGG_FRUCTOSE_AND_MANNANOSE_METABOLISM	0.020598702	KEGG_PARKINSONS_DISEASE	0.016660001
KEGG_PENTOSE_PHOSPHATE_PATHWAY	0.026059046	KEGG_RNA_DEGRADATION	0.01758125
KEGG_RNA_DEGRADATION	0.026159013	KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	0.019180477
KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	0.026271597	KEGG_APOPTOSIS	0.022218142
KEGG_SPLICEOSOME	0.026515286	KEGG_BLADDER_CANCER	0.023375792
KEGG_PATHWAYS_IN_CANCER	0.0312167	KEGG_GALACTOSE_METABOLISM	0.045779463
KEGG_SELENOAMINO_ACID_METABOLISM	0.03178405	KEGG_PATHWAYS_IN_CANCER	0.052701943
KEGG_CHRONIC_MYELOID_LEUKEMIA	0.035655078	KEGG_GLYCOLYSIS_GLUONEOGENESIS	0.053632267
KEGG_NON_SMALL_CELL_LUNG_CANCER	0.035900593	KEGG_NON_SMALL_CELL_LUNG_CANCER	0.056464013
KEGG_AUTOIMMUNE_THYROID_DISEASE	0.048180196	KEGG_GLIOMA	0.058336943
KEGG_GLIOMA	0.051803492	KEGG_ARGININE_AND_PROLINE_METABOLISM	0.059872124
KEGG_OXIDATIVE_PHOSPHORYLATION	0.05697873	KEGG_ALLOGRAFT_REJECTION	0.09657413
KEGG_ARGININE_AND_PROLINE_METABOLISM	0.05701588	KEGG_CHRONIC_MYELOID_LEUKEMIA	0.10420097
KEGG_RIG_I LIKE RECEPTOR SIGNALING PATHWAY	0.059733212	KEGG_Glutathione_Metabolism	0.10698543
KEGG_PARKINSONS_DISEASE	0.06808032	KEGG_STARCH_AND_SUCROSE_METABOLISM	0.113585986
KEGG_THYROID_CANCER	0.07319974	KEGG_COLORECTAL_CANCER	0.11485482
KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLIS M	0.07575885	KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLIS M	0.12764429
KEGG_MELANOMA	0.07577219	KEGG_SELENOAMINO_ACID_METABOLISM	0.12899627
KEGG_GLYCOLYSIS_GLUONEOGENESIS	0.07845241	KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	0.12927614
KEGG_TYPE_II_DIABETES_MELLITUS	0.079340056	KEGG_VIRAL_MYOCARDITIS	0.14288495
KEGG_Glutathione_Metabolism	0.08831056	KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	0.17281201
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	0.09365836	KEGG_GAP_JUNCTION	0.17612697

### Supplementary Table S2. Top 50 up-regulated GSEA pathways.

Top 50 up-regulated GSEA pathways utilised for the generation of the Venn diagram in figure 1H. dFab\_CCR-IL2 T cells or non-transduced T cells treated with 100000 iU/mL IL2, were compared to non-transduced T cells culture in cytokine starvation.