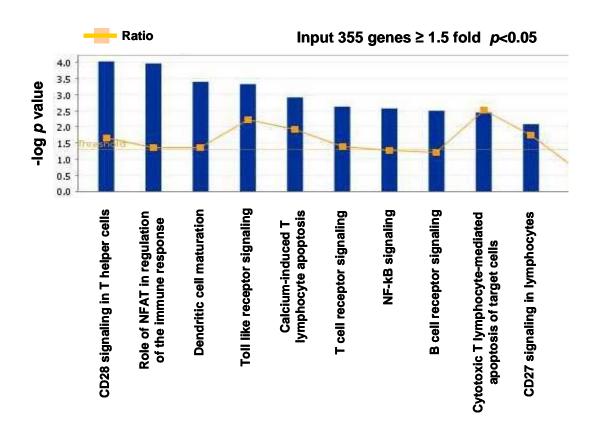
Figure E-1. Significant canonical pathways present in the peripheral blood of ischemic stroke patients

IPA analysis identified the top-5 most significant canonical pathways in the peripheral blood of ischemic stroke patients were: CD28 signaling in T-helper cells (p=4.03E00); nuclear factor of activated T cells (NFAT) in regulation of the immune response (p=4.03E00); dendritic cell maturation (p=3.4E00); toll-like receptor signaling (p=3.33E00); and calcium-induced T-lymphocyte apoptosis (p=2.92E00).

For questions related to the material in this supplemental figure contact Taura L. Barr at barrt@mail.nih.gov.



Data Description

Data Set	Fold Change cutoff; pvalue	Input Genes	Genes mapped to knowledge database	Genes eligible for pathway analysis
Stroke versus Control	>= 1.5; <0.05	500	484	355

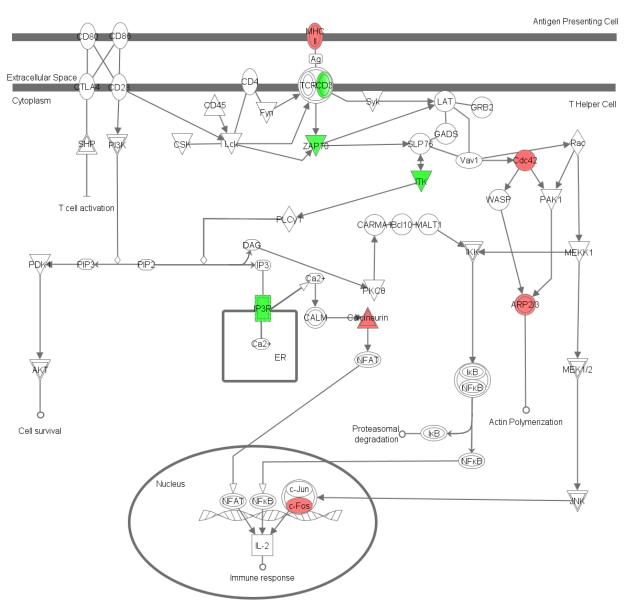
Pathway legend

- − ↑, red color up-regulated
- − ♣, green color down-regulated

Edges in Pathway	Nodes in Pathway		
<u>Edges</u>	Nodes		
binding only	— Cytokine		
inhibits B	— Enzyme		
acts on	— Ion Channel		
	— Nuclear Receptor		
inhibits AND acts on	─ ─ Other		
B translocates to	— Small Molecule		
Note: "Acts on" and "Inhibits"	— Transcription Regulator		
edges may also include a binding event.	— Translation Regulator		
direct interaction	— Transmembrane Receptor		
indirect interaction	— Transporter		

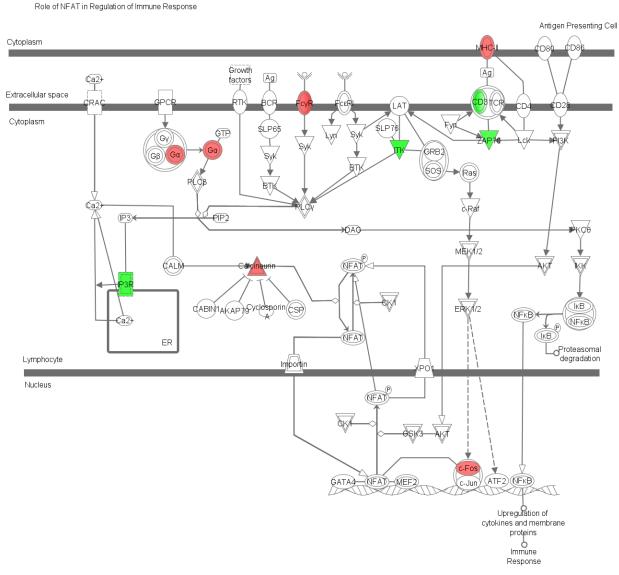
1. There were 12 genes in the dataset involved in CD28 signaling in T-helper cells (p=4.03E00): *CD247*, *FOS*, *ACTR3*, *CD3E*, *CDC42*, *PPP3R1*, *ITPR3*, *ARPC5*, *ZAP70*, *CD3D*, *HLA-DRB5*, and *ITK* (p=4.03E00).

CD28 Signaling in T Helper Cells



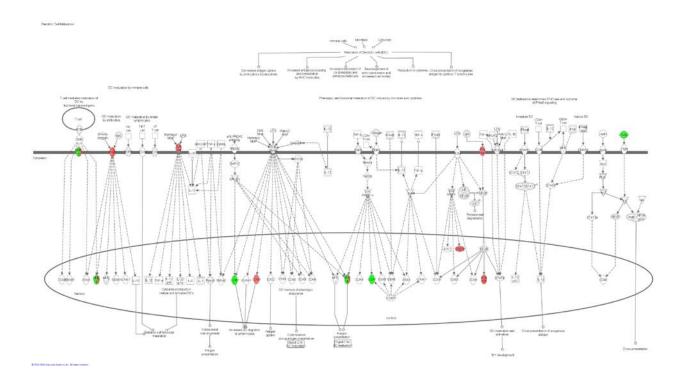
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2. There are 15 genes in the dataset involved in NFAT regulation (p=4.03E00): FCGR3B, CD247, CD3E, FCGR2A, FCGR1A, CD3D, FOS, PPP3R1, ITPR3, ZAP70, GNA13, FCGR1B, FCGR3A, HLA-DRB5, and ITK).



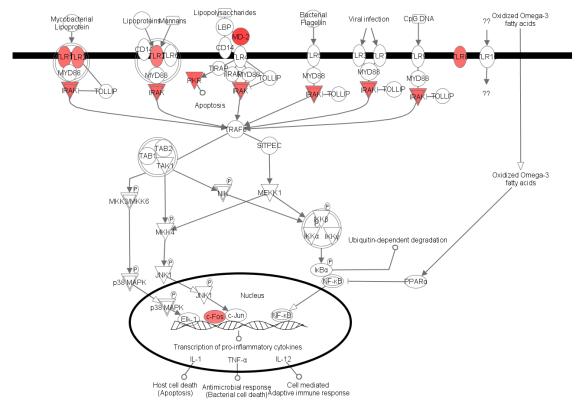
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3. There are 13 genes in the dataset involved in dendritic cell maturation (p=3.4E00): FCGR3B, FCGR2A, LTB, CD58, HLA-DRB1, CREB5, FCGR1A, HLA-DQB1, TLR2, CCR7, FCGR3A, HLA-DRB5, and FCGR1B.



4. There were more genes involved in Toll-like receptor signaling within the dataset compared to the total number of genes in the Toll-like receptor pathway with a ratio >2 and p=3.33E00 (*TLR2*, *TLR1*, *FOS*, *LY96*, *TLR8* (includes *EG:51311*), *IF2AK2*, *IRAK3*).

Toll-like Receptor Signaling



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5. There are 7 genes in the dataset involved in calcium-induced T lymphocyte apoptosis (p=2.92E00): *CD247, CD3E, PPP3R1, ITPR3, ZAP70, CD3D,* and *HLA-DRB5*



