

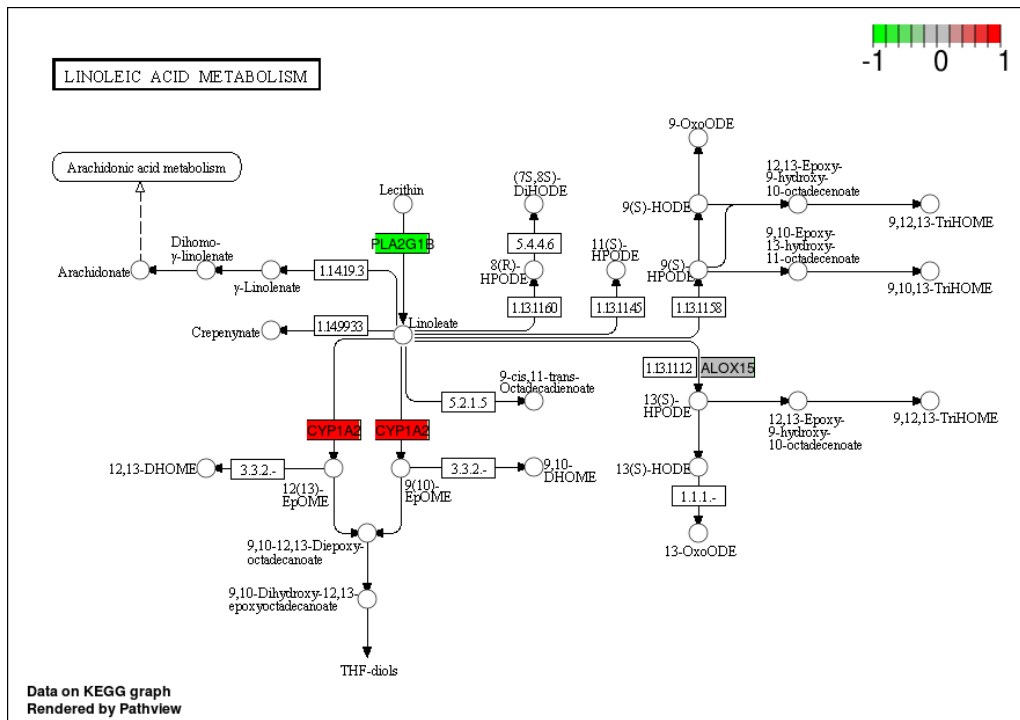
Intracellular bacteria interfere with dendritic cell function: Role of type I Interferon pathway

L. Gorvel, J. Textoris, R. Banchereau, A. Ben Amara, W. Tantibhedhyangkul, K. von Bargen, M.B. Ka, C. Capo, E. Ghigo, J.P. Gorvel and J.L. Mege

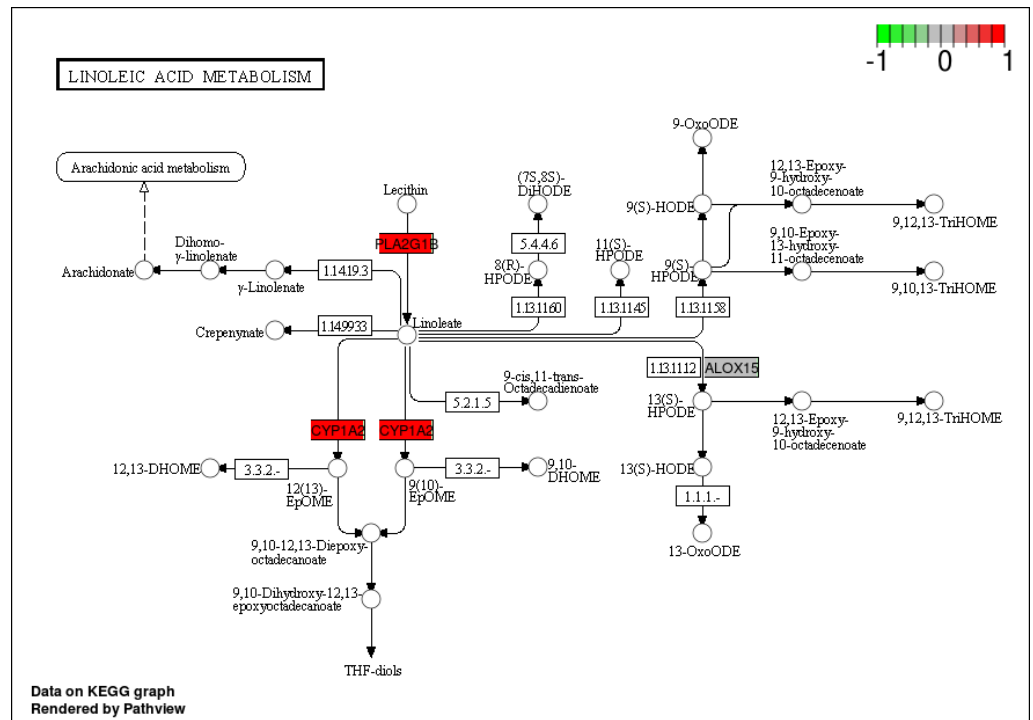
Supplementary Results S1: Pathway Analysis of Transcriptional Modulation of moDC by Intracellular Bacteria

Based on the functional analysis of the genes modulated by the intracellular bacteria or LPS in moDC, we extracted the identified KEGG pathways and color coded the nodes according to the modulation of gene expression after each stimulation.

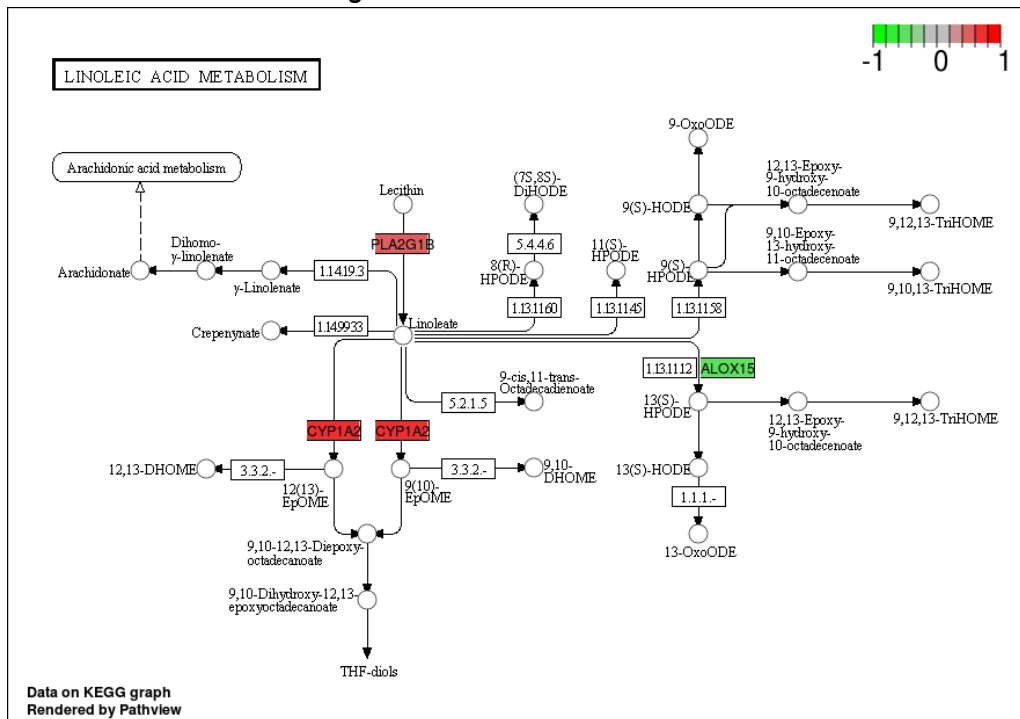
Coxiella burnetii



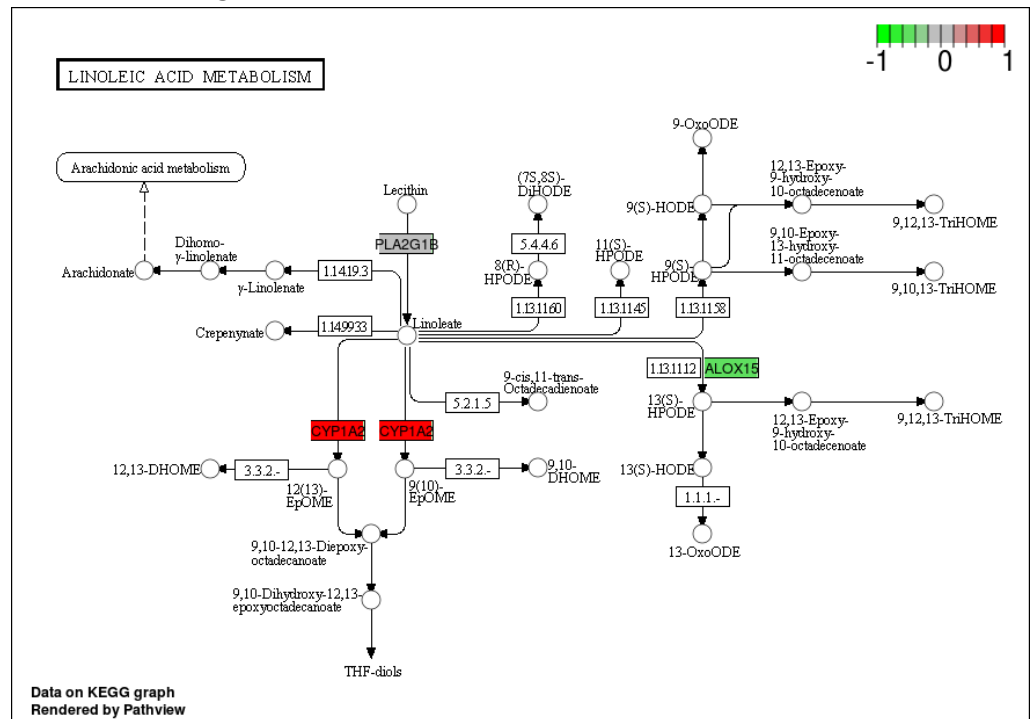
Brucella abortus



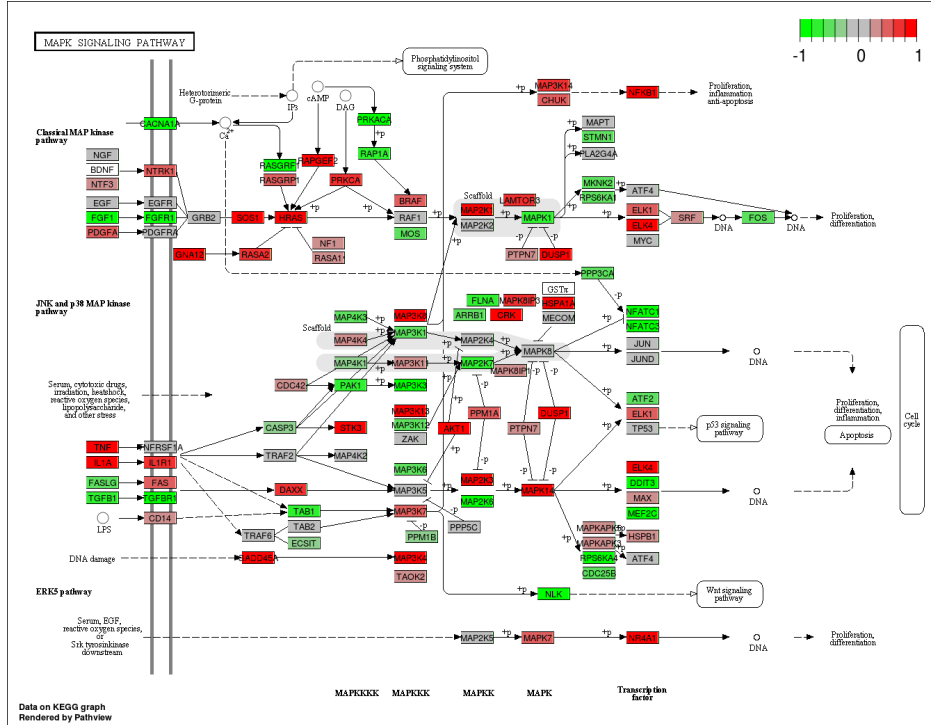
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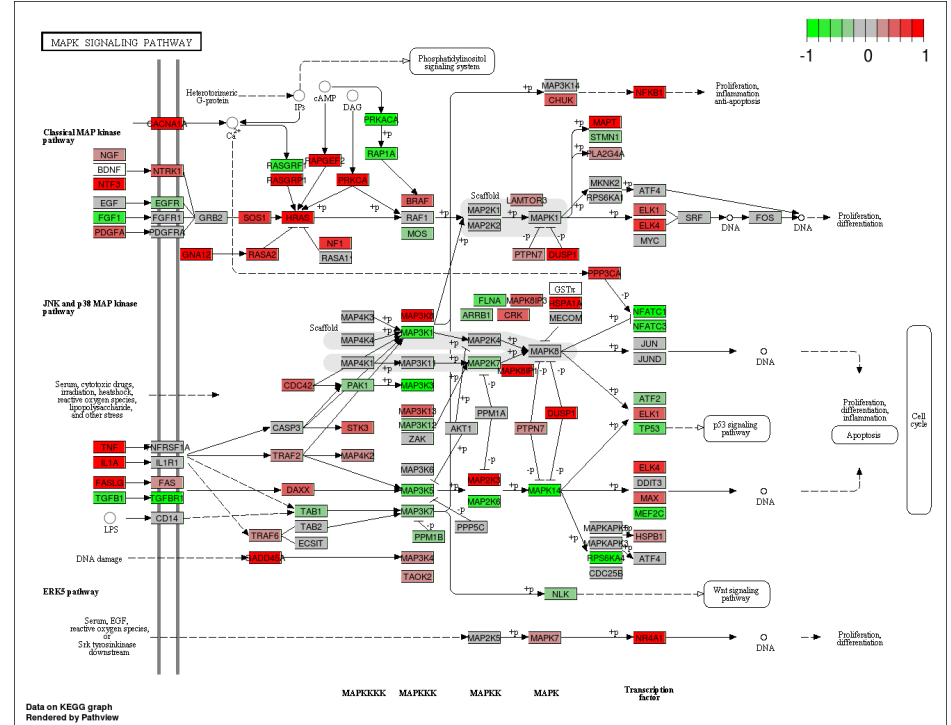
LPS



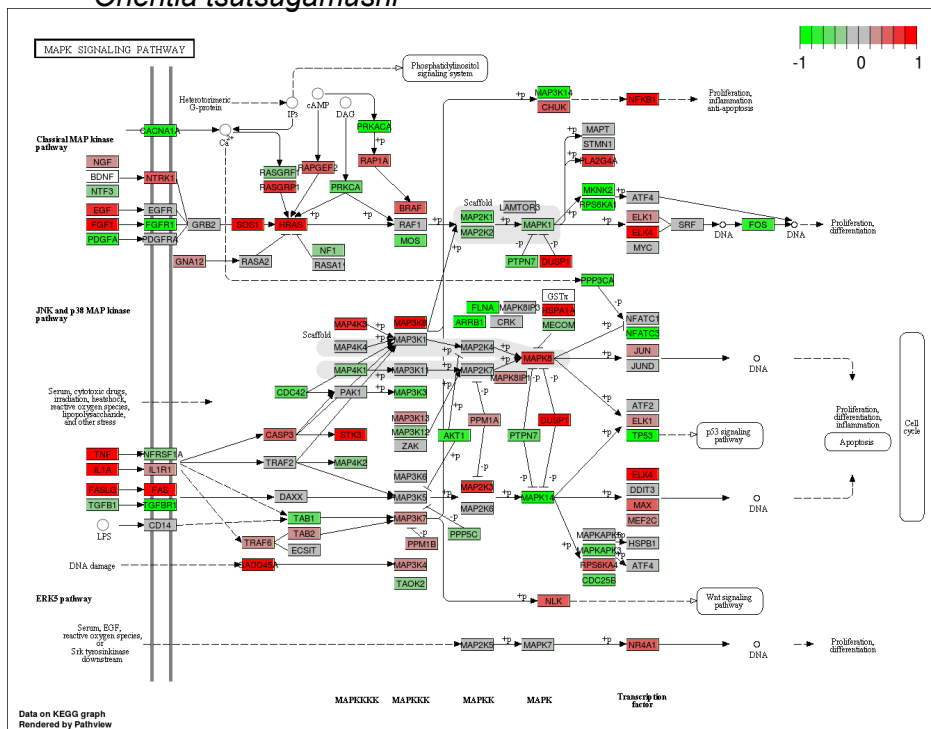
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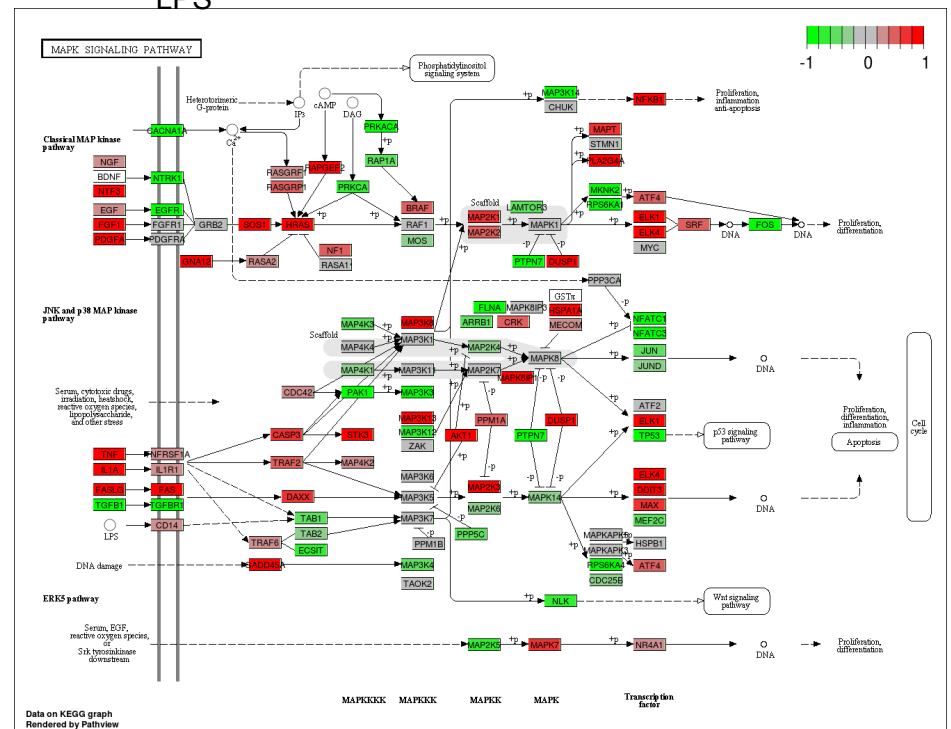
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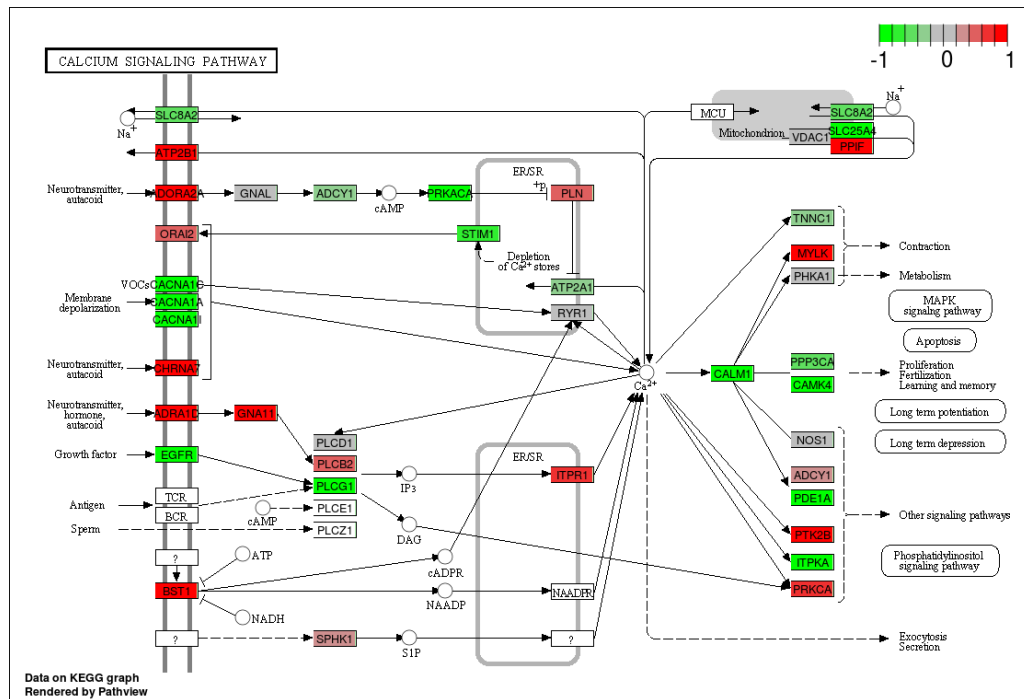
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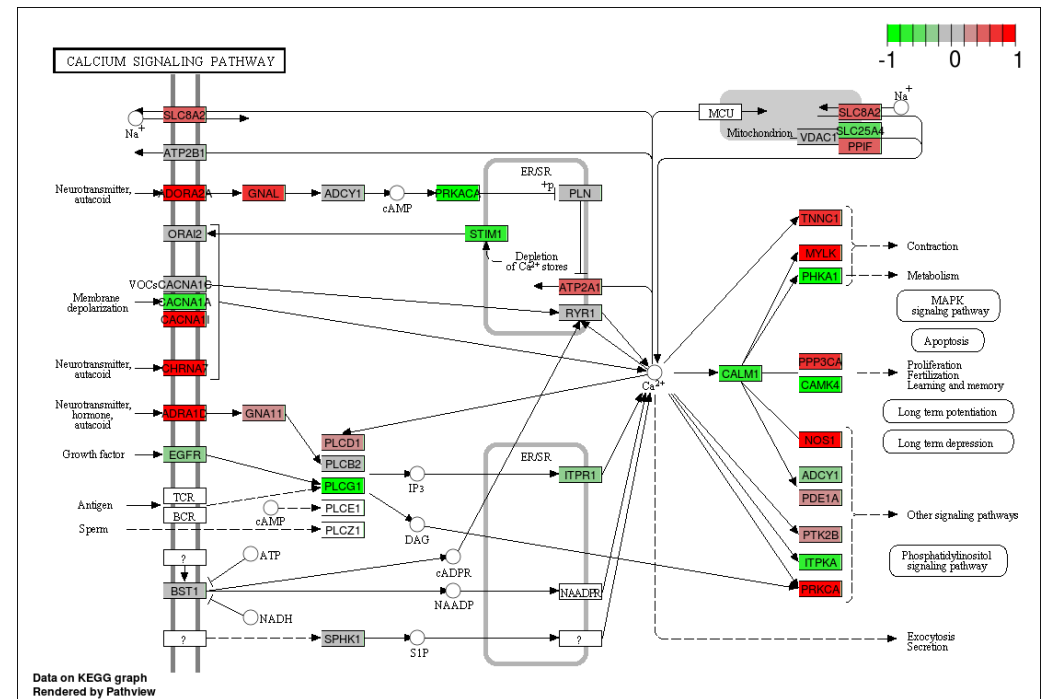
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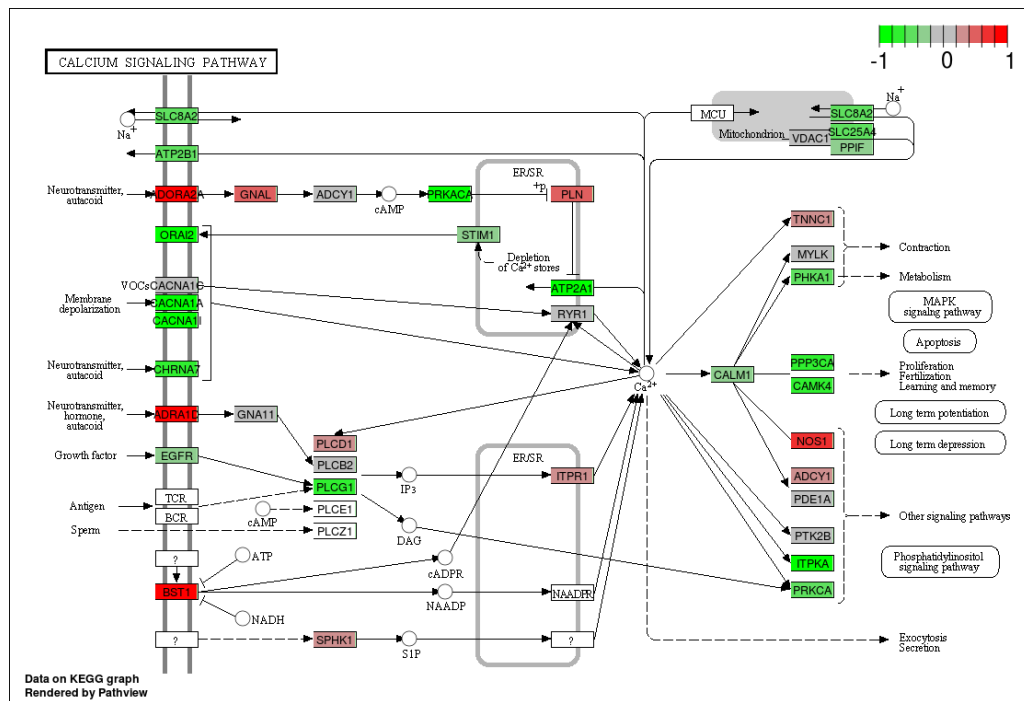
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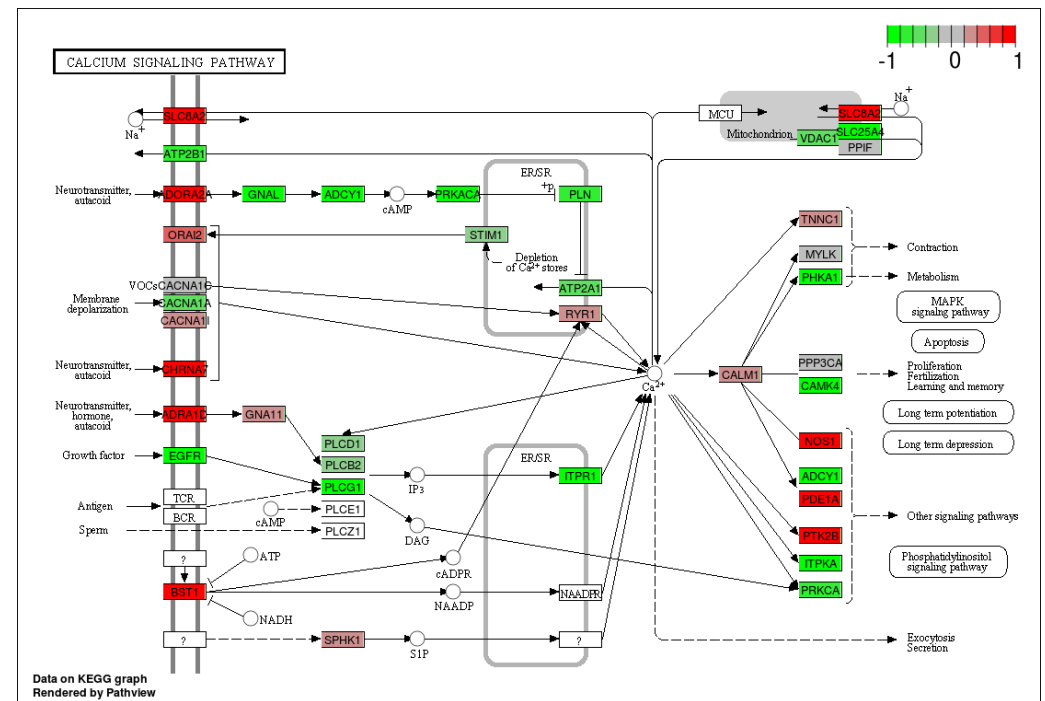
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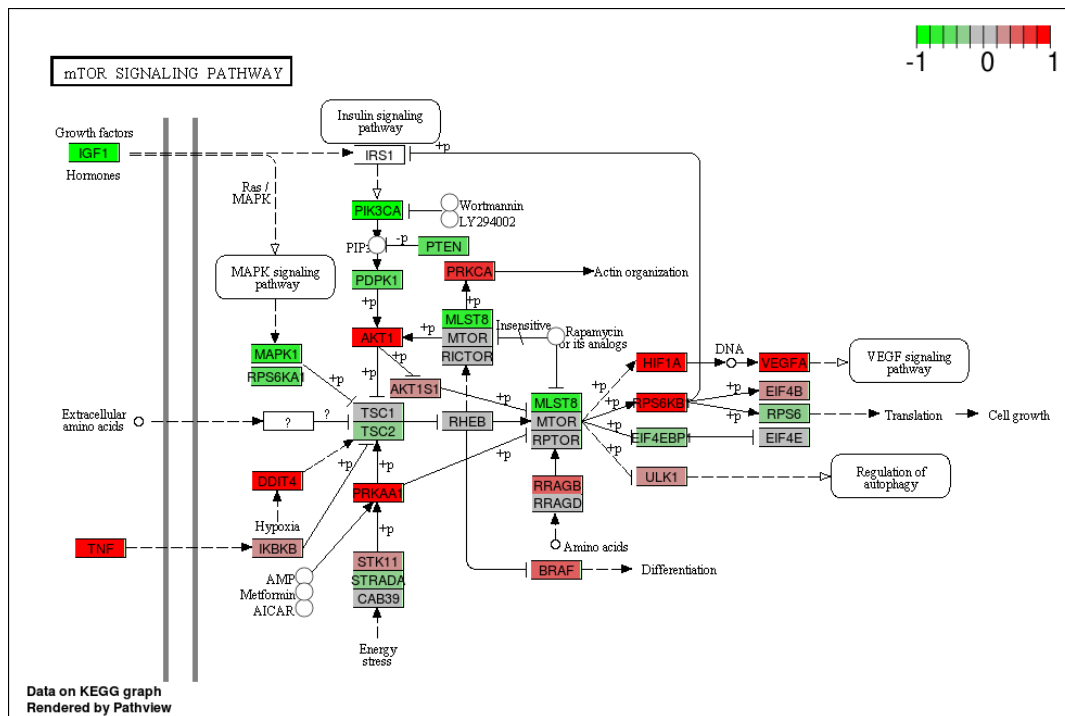
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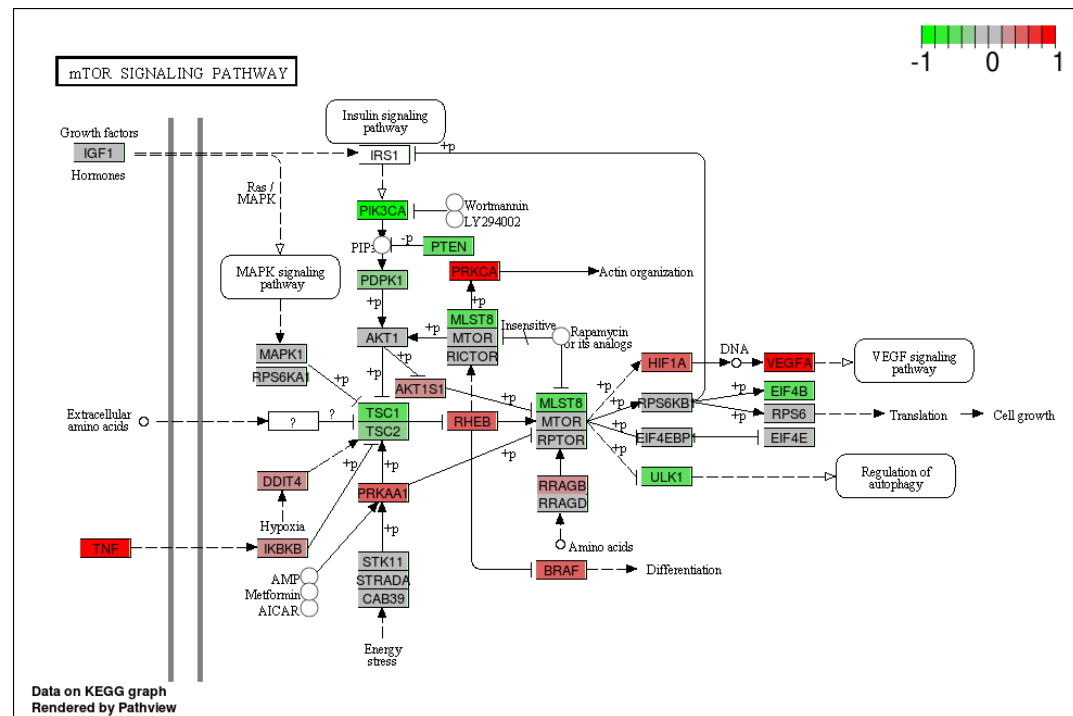
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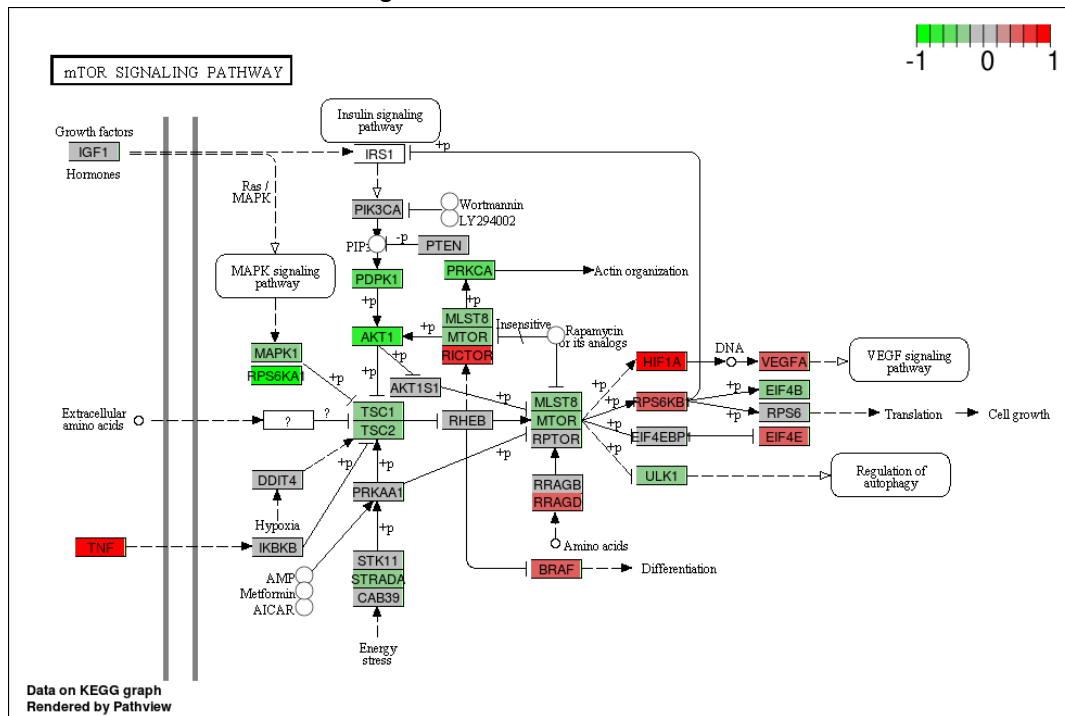
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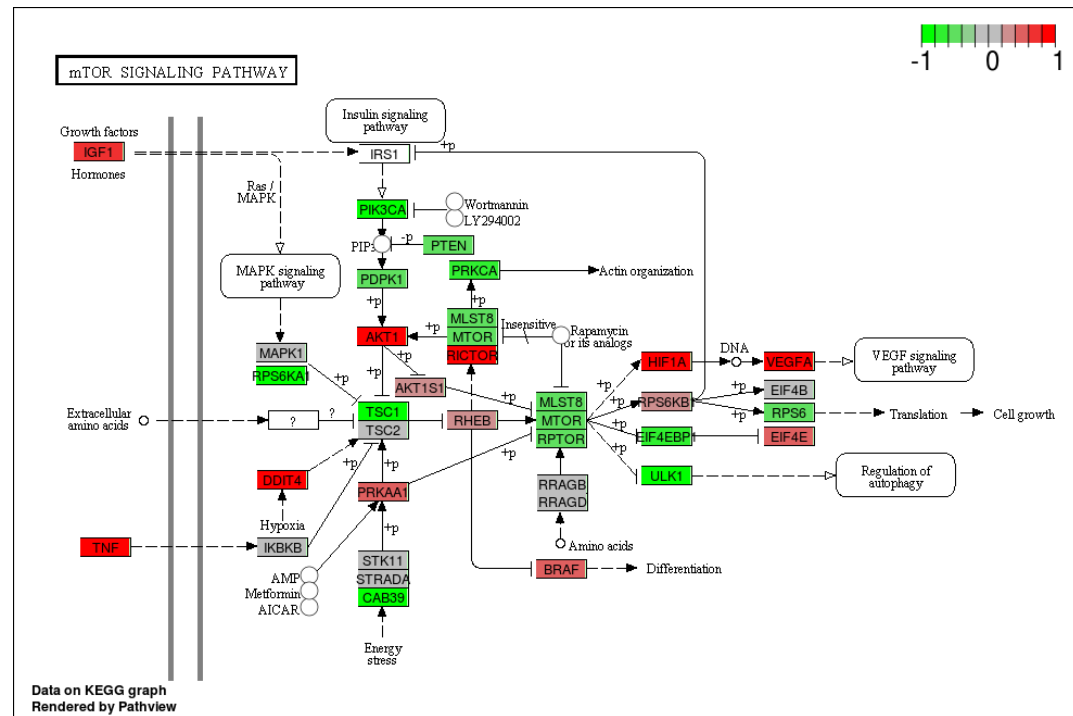
Brucella abortus



Orientia tsutsugamushi



LPS



PI3K-AKT SIGNALING PATHWAY

Diagram illustrating the PI3K-AKT signaling pathway, showing the activation of PI3K by various receptors (e.g., VEGFR, EphA2, EphA3, EphA4, EphA5, EphA6, EphA7, EphA8, EphA9, EphA10, EphA11, EphA12, EphA13, EphA14, EphA15, EphA16, EphA17, EphA18, EphA19, EphA20, EphA21, EphA22, EphA23, EphA24, EphA25, EphA26, EphA27, EphA28, EphA29, EphA30, EphA31, EphA32, EphA33, EphA34, EphA35, EphA36, EphA37, EphA38, EphA39, EphA40, EphA41, EphA42, EphA43, EphA44, EphA45, EphA46, EphA47, EphA48, EphA49, EphA50, EphA51, EphA52, EphA53, EphA54, EphA55, EphA56, EphA57, EphA58, EphA59, EphA60, EphA61, EphA62, EphA63, EphA64, EphA65, EphA66, EphA67, EphA68, EphA69, EphA70, EphA71, EphA72, EphA73, EphA74, EphA75, EphA76, EphA77, EphA78, EphA79, EphA80, EphA81, EphA82, EphA83, EphA84, EphA85, EphA86, EphA87, EphA88, EphA89, EphA90, EphA91, EphA92, EphA93, EphA94, EphA95, EphA96, EphA97, EphA98, EphA99, EphA100) and the subsequent activation of AKT. AKT then activates various downstream targets, including FOXO, FOXO1, FOXO2, FOXO3, FOXO4, FOXO5, FOXO6, FOXO7, FOXO8, FOXO9, FOXO10, FOXO11, FOXO12, FOXO13, FOXO14, FOXO15, FOXO16, FOXO17, FOXO18, FOXO19, FOXO20, FOXO21, FOXO22, FOXO23, FOXO24, FOXO25, FOXO26, FOXO27, FOXO28, FOXO29, FOXO30, FOXO31, FOXO32, FOXO33, FOXO34, FOXO35, FOXO36, FOXO37, FOXO38, FOXO39, FOXO40, FOXO41, FOXO42, FOXO43, FOXO44, FOXO45, FOXO46, FOXO47, FOXO48, FOXO49, FOXO50, FOXO51, FOXO52, FOXO53, FOXO54, FOXO55, FOXO56, FOXO57, FOXO58, FOXO59, FOXO60, FOXO61, FOXO62, FOXO63, FOXO64, FOXO65, FOXO66, FOXO67, FOXO68, FOXO69, FOXO70, FOXO71, FOXO72, FOXO73, FOXO74, FOXO75, FOXO76, FOXO77, FOXO78, FOXO79, FOXO80, FOXO81, FOXO82, FOXO83, FOXO84, FOXO85, FOXO86, FOXO87, FOXO88, FOXO89, FOXO90, FOXO91, FOXO92, FOXO93, FOXO94, FOXO95, FOXO96, FOXO97, FOXO98, FOXO99, FOXO100. The diagram also shows the regulation of PI3K by various factors including PTEN, PDK1, PDK2, PDK3, PDK4, PDK5, PDK6, PDK7, PDK8, PDK9, PDK10, PDK11, PDK12, PDK13, PDK14, PDK15, PDK16, PDK17, PDK18, PDK19, PDK20, PDK21, PDK22, PDK23, PDK24, PDK25, PDK26, PDK27, PDK28, PDK29, PDK30, PDK31, PDK32, PDK33, PDK34, PDK35, PDK36, PDK37, PDK38, PDK39, PDK40, PDK41, PDK42, PDK43, PDK44, PDK45, PDK46, PDK47, PDK48, PDK49, PDK50, PDK51, PDK52, PDK53, PDK54, PDK55, PDK56, PDK57, PDK58, PDK59, PDK60, PDK61, PDK62, PDK63, PDK64, PDK65, PDK66, PDK67, PDK68, PDK69, PDK70, PDK71, PDK72, PDK73, PDK74, PDK75, PDK76, PDK77, PDK78, PDK79, PDK80, PDK81, PDK82, PDK83, PDK84, PDK85, PDK86, PDK87, PDK88, PDK89, PDK90, PDK91, PDK92, PDK93, PDK94, PDK95, PDK96, PDK97, PDK98, PDK99, PDK100. The diagram is color-coded: red for activation, green for inhibition, and grey for unknown. A legend at the bottom right explains the symbols: a circle with a dot for activation, a circle with a line for inhibition, and a circle with a cross for unknown. The diagram is titled 'PI3K-AKT SIGNALING PATHWAY' and is sourced from KEGG graph, rendered by Pathview.

Data on KEGG graph
Rendered by Pathview

Diagram illustrating the PI3K-AKT signaling pathway, showing the flow of information from various receptors (e.g., IGF1R, EGFR, EGFGR2, EGFGR3, EGFGR4, EGFGR5, EGFGR6, EGFGR7, EGFGR8, EGFGR9, EGFGR10, EGFGR11, EGFGR12, EGFGR13, EGFGR14, EGFGR15, EGFGR16, EGFGR17, EGFGR18, EGFGR19, EGFGR20, EGFGR21, EGFGR22, EGFGR23, EGFGR24, EGFGR25, EGFGR26, EGFGR27, EGFGR28, EGFGR29, EGFGR30, EGFGR31, EGFGR32, EGFGR33, EGFGR34, EGFGR35, EGFGR36, EGFGR37, EGFGR38, EGFGR39, EGFGR40, EGFGR41, EGFGR42, EGFGR43, EGFGR44, EGFGR45, EGFGR46, EGFGR47, EGFGR48, EGFGR49, EGFGR50, EGFGR51, EGFGR52, EGFGR53, EGFGR54, EGFGR55, EGFGR56, EGFGR57, EGFGR58, EGFGR59, EGFGR60, EGFGR61, EGFGR62, EGFGR63, EGFGR64, EGFGR65, EGFGR66, EGFGR67, EGFGR68, EGFGR69, EGFGR70, EGFGR71, EGFGR72, EGFGR73, EGFGR74, EGFGR75, EGFGR76, EGFGR77, EGFGR78, EGFGR79, EGFGR80, EGFGR81, EGFGR82, EGFGR83, EGFGR84, EGFGR85, EGFGR86, EGFGR87, EGFGR88, EGFGR89, EGFGR90, EGFGR91, EGFGR92, EGFGR93, EGFGR94, EGFGR95, EGFGR96, EGFGR97, EGFGR98, EGFGR99, EGFGR100) through PI3K, AKT, and other downstream effectors to various cellular processes (e.g., Proliferation, Survival, Metabolism, Apoptosis, NF-κB signaling, p53 signaling).

Key components and interactions include:

- Receptors:** IGF1R, EGFR, EGFGR2, EGFGR3, EGFGR4, EGFGR5, EGFGR6, EGFGR7, EGFGR8, EGFGR9, EGFGR10, EGFGR11, EGFGR12, EGFGR13, EGFGR14, EGFGR15, EGFGR16, EGFGR17, EGFGR18, EGFGR19, EGFGR20, EGFGR21, EGFGR22, EGFGR23, EGFGR24, EGFGR25, EGFGR26, EGFGR27, EGFGR28, EGFGR29, EGFGR30, EGFGR31, EGFGR32, EGFGR33, EGFGR34, EGFGR35, EGFGR36, EGFGR37, EGFGR38, EGFGR39, EGFGR40, EGFGR41, EGFGR42, EGFGR43, EGFGR44, EGFGR45, EGFGR46, EGFGR47, EGFGR48, EGFGR49, EGFGR50, EGFGR51, EGFGR52, EGFGR53, EGFGR54, EGFGR55, EGFGR56, EGFGR57, EGFGR58, EGFGR59, EGFGR60, EGFGR61, EGFGR62, EGFGR63, EGFGR64, EGFGR65, EGFGR66, EGFGR67, EGFGR68, EGFGR69, EGFGR70, EGFGR71, EGFGR72, EGFGR73, EGFGR74, EGFGR75, EGFGR76, EGFGR77, EGFGR78, EGFGR79, EGFGR80, EGFGR81, EGFGR82, EGFGR83, EGFGR84, EGFGR85, EGFGR86, EGFGR87, EGFGR88, EGFGR89, EGFGR90, EGFGR91, EGFGR92, EGFGR93, EGFGR94, EGFGR95, EGFGR96, EGFGR97, EGFGR98, EGFGR99, EGFGR100.
- PI3K/AKT Pathway:** PI3K (Class I, II, III), AKT (Class I, II, III), PDK1, PDK2, PDK3, PDK4, PDK5, PDK6, PDK7, PDK8, PDK9, PDK10, PDK11, PDK12, PDK13, PDK14, PDK15, PDK16, PDK17, PDK18, PDK19, PDK20, PDK21, PDK22, PDK23, PDK24, PDK25, PDK26, PDK27, PDK28, PDK29, PDK30, PDK31, PDK32, PDK33, PDK34, PDK35, PDK36, PDK37, PDK38, PDK39, PDK40, PDK41, PDK42, PDK43, PDK44, PDK45, PDK46, PDK47, PDK48, PDK49, PDK50, PDK51, PDK52, PDK53, PDK54, PDK55, PDK56, PDK57, PDK58, PDK59, PDK60, PDK61, PDK62, PDK63, PDK64, PDK65, PDK66, PDK67, PDK68, PDK69, PDK70, PDK71, PDK72, PDK73, PDK74, PDK75, PDK76, PDK77, PDK78, PDK79, PDK80, PDK81, PDK82, PDK83, PDK84, PDK85, PDK86, PDK87, PDK88, PDK89, PDK90, PDK91, PDK92, PDK93, PDK94, PDK95, PDK96, PDK97, PDK98, PDK99, PDK100.
- Downstream Effectors:** mTOR, S6K, S6KB, S6KBK, S6KBK1, S6KBK2, S6KBK3, S6KBK4, S6KBK5, S6KBK6, S6KBK7, S6KBK8, S6KBK9, S6KBK10, S6KBK11, S6KBK12, S6KBK13, S6KBK14, S6KBK15, S6KBK16, S6KBK17, S6KBK18, S6KBK19, S6KBK20, S6KBK21, S6KBK22, S6KBK23, S6KBK24, S6KBK25, S6KBK26, S6KBK27, S6KBK28, S6KBK29, S6KBK30, S6KBK31, S6KBK32, S6KBK33, S6KBK34, S6KBK35, S6KBK36, S6KBK37, S6KBK38, S6KBK39, S6KBK40, S6KBK41, S6KBK42, S6KBK43, S6KBK44, S6KBK45, S6KBK46, S6KBK47, S6KBK48, S6KBK49, S6KBK50, S6KBK51, S6KBK52, S6KBK53, S6KBK54, S6KBK55, S6KBK56, S6KBK57, S6KBK58, S6KBK59, S6KBK60, S6KBK61, S6KBK62, S6KBK63, S6KBK64, S6KBK65, S6KBK66, S6KBK67, S6KBK68, S6KBK69, S6KBK70, S6KBK71, S6KBK72, S6KBK73, S6KBK74, S6KBK75, S6KBK76, S6KBK77, S6KBK78, S6KBK79, S6KBK80, S6KBK81, S6KBK82, S6KBK83, S6KBK84, S6KBK85, S6KBK86, S6KBK87, S6KBK88, S6KBK89, S6KBK90, S6KBK91, S6KBK92, S6KBK93, S6KBK94, S6KBK95, S6KBK96, S6KBK97, S6KBK98, S6KBK99, S6KBK100.
- Cellular Processes:** Proliferation, Survival, Metabolism, Apoptosis, NF-κB signaling, p53 signaling.

Legend: Red indicates activation, Green indicates inhibition, Blue indicates unknown.

Data on KEGG graph
Rendered by Pathview

PI3K-AKT SIGNALING PATHWAY

Diagram illustrating the PI3K-AKT signaling pathway, showing the activation of AKT1 by various receptors and the subsequent phosphorylation of downstream targets.

Receptors and Upstream Activators:

- IGF1R (Insulin-like growth factor receptor)
- EGFR (Epidermal growth factor receptor)
- TLR2 (Toll-like receptor 2)
- BCR (B cell receptor)
- JAK2 (Janus kinase 2)
- CSF3R (Colony-stimulating factor receptor 3)
- TGFBR1 (Transforming growth factor receptor 1)
- CDKN1 (Cyclin D1)
- GNB1 (Guaninucleotide-binding protein G12 subunit beta)

Key Kinases and Phosphatases:

- PIK3CA (Phosphoinositide 3-kinase class I alpha)
- PIK3CB (Phosphoinositide 3-kinase class I beta)
- PIK3CD (Phosphoinositide 3-kinase class I delta)
- AKT1 (Serine/threonine kinase)
- PTEN (Phosphatase and tensin homolog)
- PDK1 (Phosphoinositide-dependent kinase-1)
- PDK2 (Phosphoinositide-dependent kinase-2)

Downstream Targets and Pathways:

- Cell Cycle Progression:** AKT1 phosphorylates CDKN1, CDKN2A, CDKN2B, CDKN2C, CDKN2D, CDKN2E, CDKN2F, CDKN2G, CDKN2H, CDKN2I, CDKN2J, CDKN2K, CDKN2L, CDKN2M, CDKN2N, CDKN2O, CDKN2P, CDKN2Q, CDKN2R, CDKN2S, CDKN2T, CDKN2U, CDKN2V, CDKN2W, CDKN2X, CDKN2Y, CDKN2Z, CDKN2AA, CDKN2AB, CDKN2AC, CDKN2AD, CDKN2AE, CDKN2AF, CDKN2AG, CDKN2AH, CDKN2AI, CDKN2AJ, CDKN2AK, CDKN2AL, CDKN2AM, CDKN2AN, CDKN2AO, CDKN2AP, CDKN2AQ, CDKN2AR, CDKN2AS, CDKN2AT, CDKN2AU, CDKN2AV, CDKN2AW, CDKN2AX, CDKN2AY, CDKN2AZ, CDKN2BA, CDKN2BB, CDKN2BC, CDKN2BD, CDKN2BE, CDKN2BF, CDKN2BG, CDKN2BH, CDKN2BI, CDKN2BJ, CDKN2BK, CDKN2BL, CDKN2BM, CDKN2BN, CDKN2BO, CDKN2BP, CDKN2BQ, CDKN2BR, CDKN2BS, CDKN2BT, CDKN2BU, CDKN2BV, CDKN2BW, CDKN2BX, CDKN2BY, CDKN2BZ, CDKN2CA, CDKN2CB, CDKN2CC, CDKN2CD, CDKN2CE, CDKN2CF, CDKN2CG, CDKN2CH, CDKN2CI, CDKN2CJ, CDKN2CK, CDKN2CL, CDKN2CM, CDKN2CN, CDKN2CO, CDKN2CP, CDKN2CQ, CDKN2CR, CDKN2CS, CDKN2CT, CDKN2CU, CDKN2CV, CDKN2CW, CDKN2CX, CDKN2CY, CDKN2CZ, CDKN2DA, CDKN2DB, CDKN2DC, CDKN2DD, 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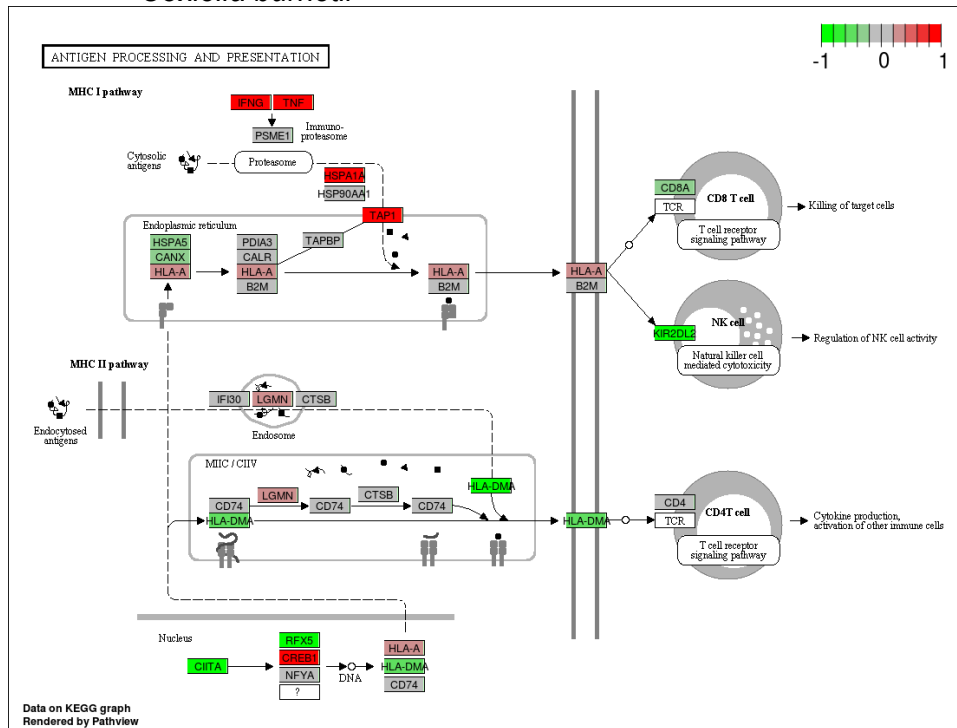
The diagram illustrates the PI3K-AKT signaling pathway, showing the flow of information from various receptors (e.g., IGF1R, EGFR, HER2, etc.) through PI3K and AKT to various downstream effectors. The diagram is color-coded: green for protein synthesis and red for cell cycle. The pathway is organized into several functional modules, including:

- Receptor Activation:** Various receptors (e.g., IGF1R, EGFR, HER2, etc.) are activated by ligands (e.g., IGF1, EGF, etc.).
- PI3K Activation:** Activated receptors recruit and activate PI3K (Phosphoinositide 3-kinase).
- AKT Activation:** Activated PI3K phosphorylates AKT (Protein Kinase B) at Ser473, leading to its activation.
- Downstream Effectors:** Activated AKT phosphorylates a wide range of downstream effectors, including:
 - Cell Cycle:** Cyclins (e.g., Cyclin D, Cyclin E), CDKs (e.g., CDK2, CDK4, CDK6), and other cell cycle regulators.
 - Protein Synthesis:** mTOR (Mechanistic Target of Rapamycin) and S6K (S6 Kinase), which promote protein synthesis.
 - Cell Survival:** FOXO (Forkhead box O) and BCL2 (B-cell lymphoma 2), which regulate cell survival.
 - Other Effectors:** GSK3 (Glycogen synthase kinase-3), PDK1 (Phosphoinositide-dependent kinase-1), and others.

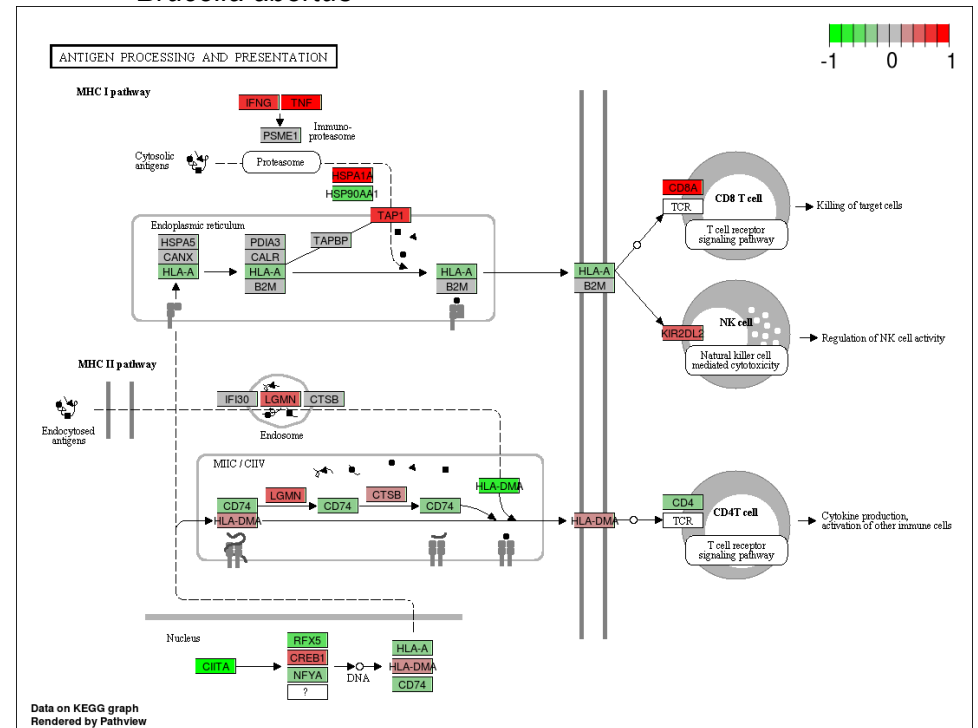
The diagram also includes a legend for protein synthesis (green) and cell cycle (red). The color scale ranges from 0 (no effect) to 1 (maximal effect).

**Data on KEGG graph
Rendered by Pathway**

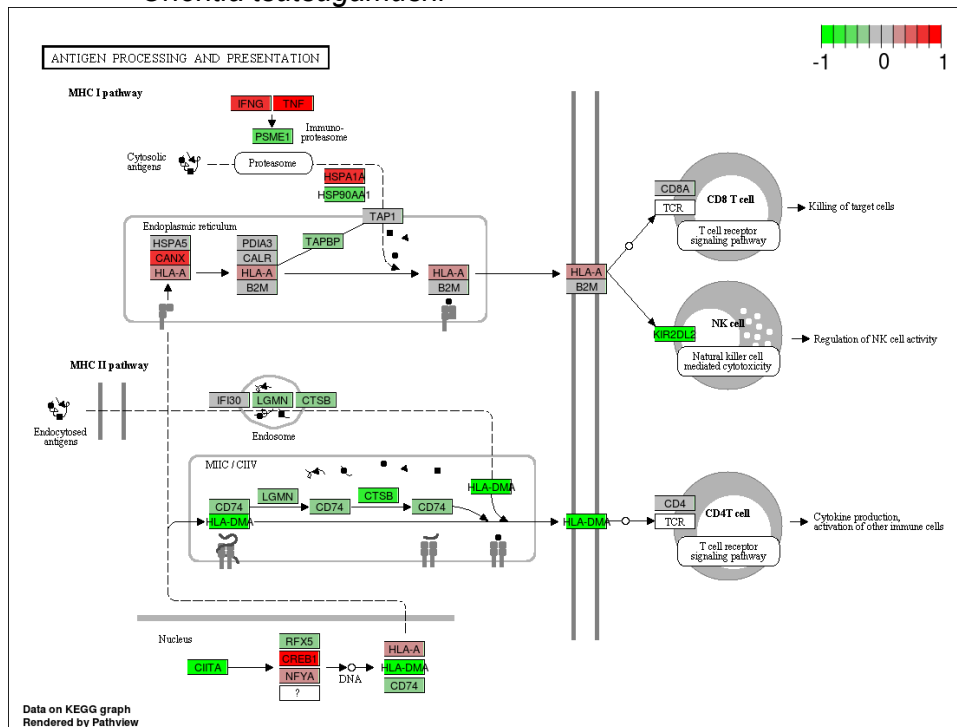
Coxiella burnetii



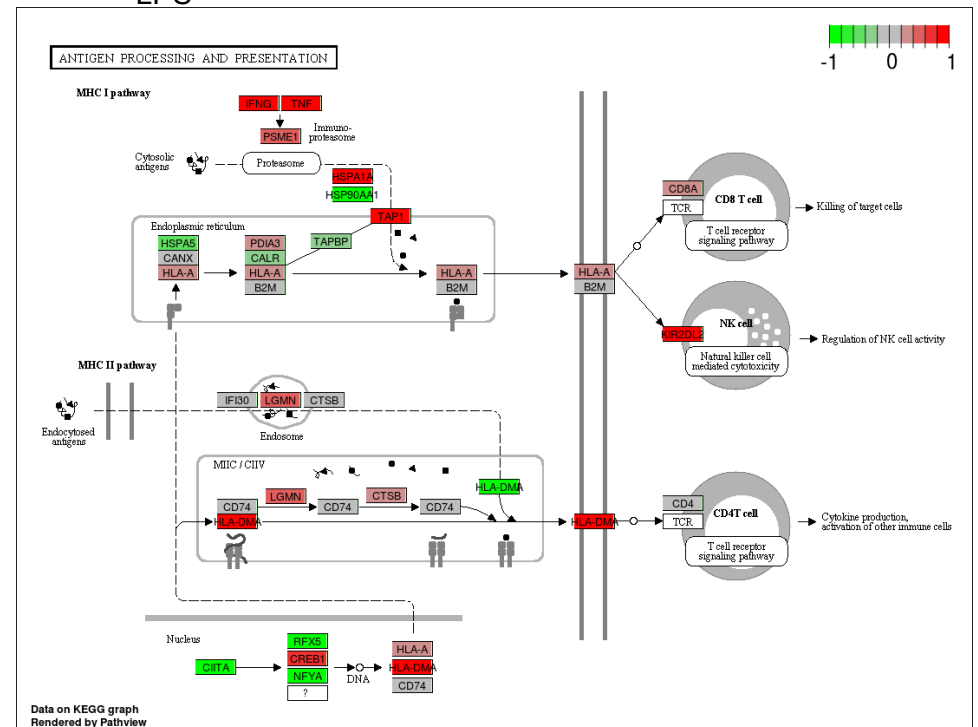
Brucella abortus



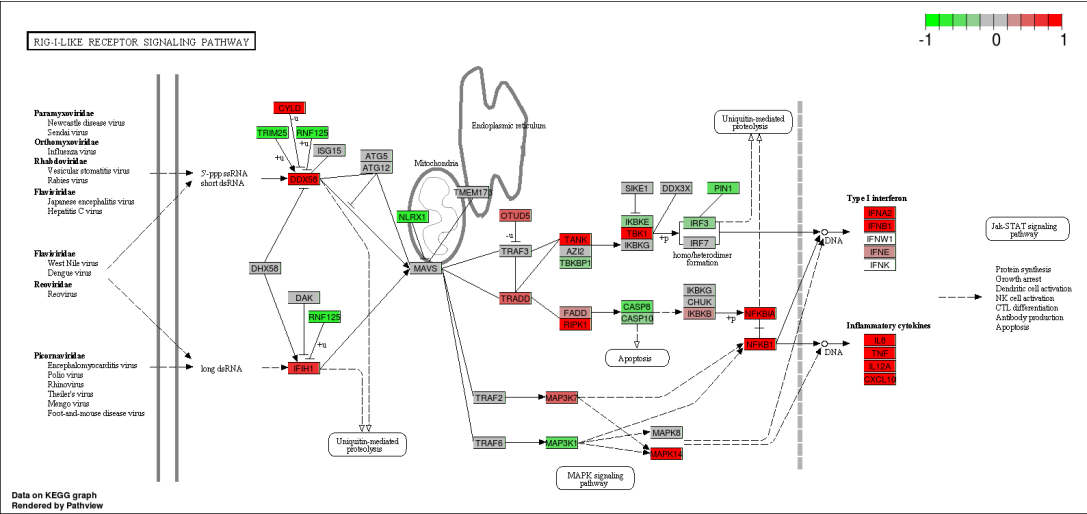
Orientia tsutsugamushi



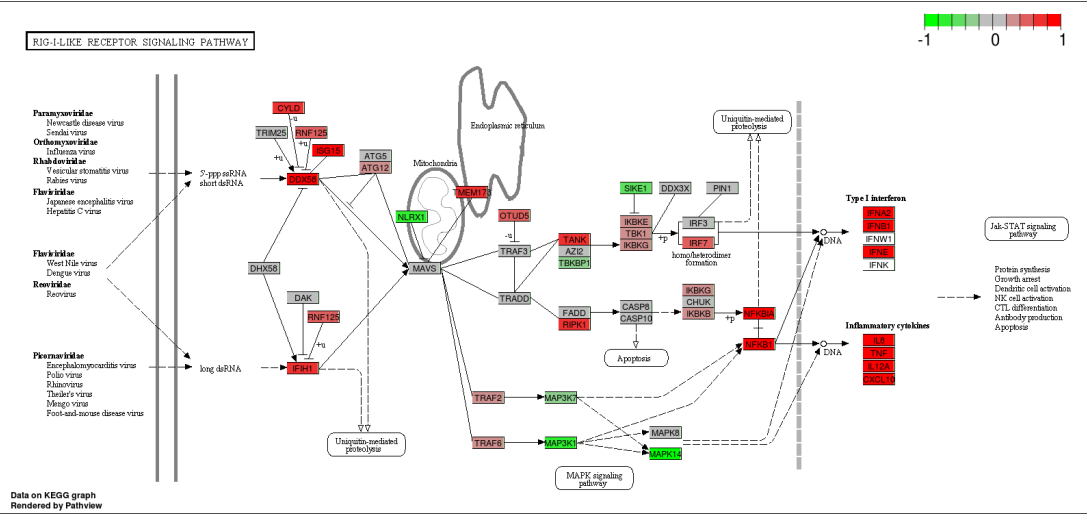
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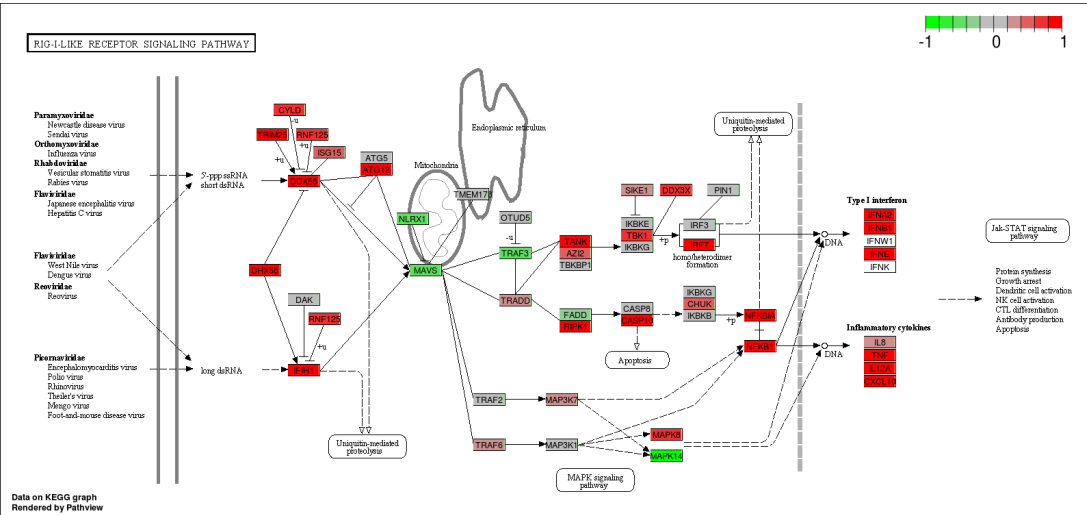
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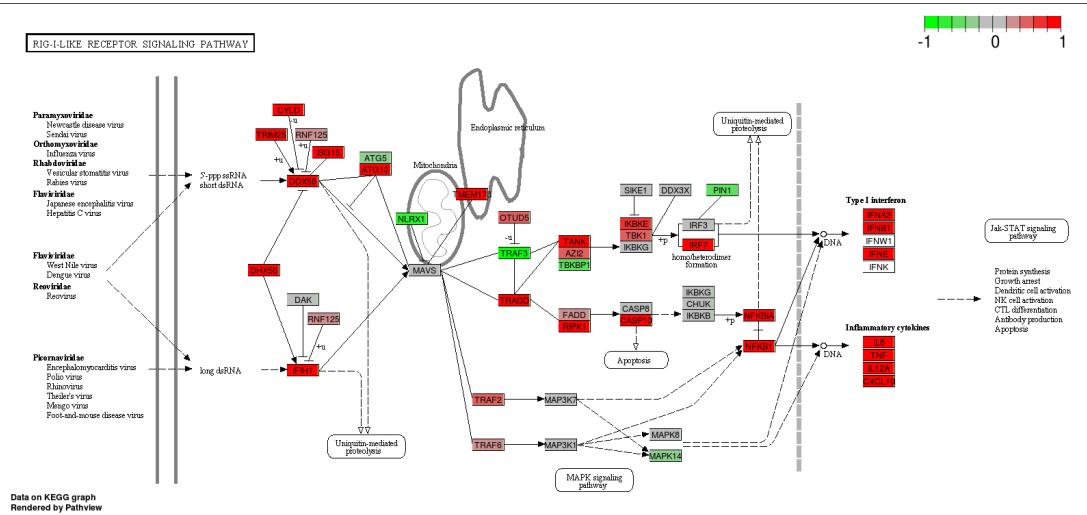
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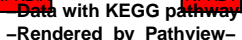










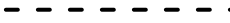


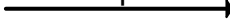


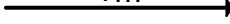

Orientia tsutsugamushi



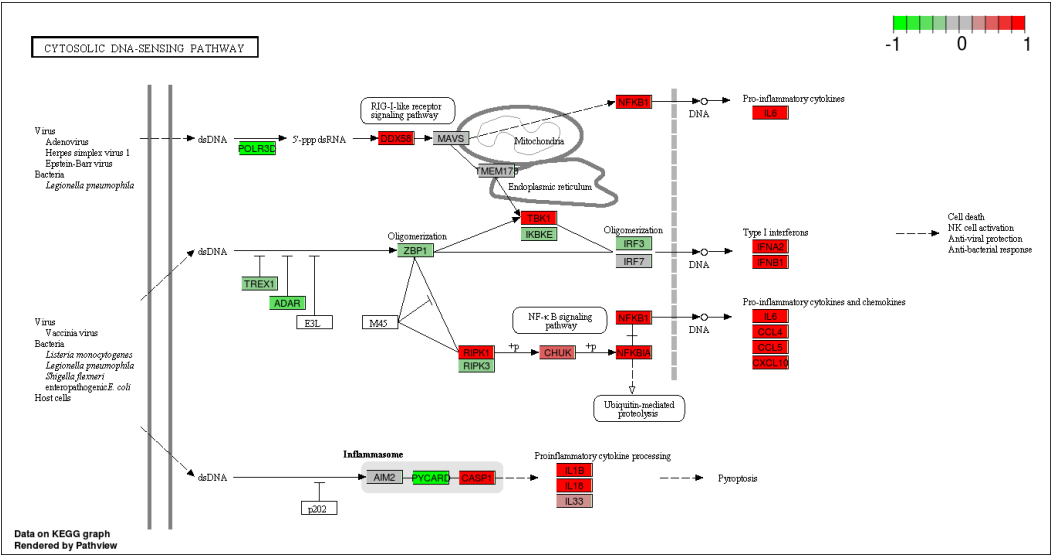
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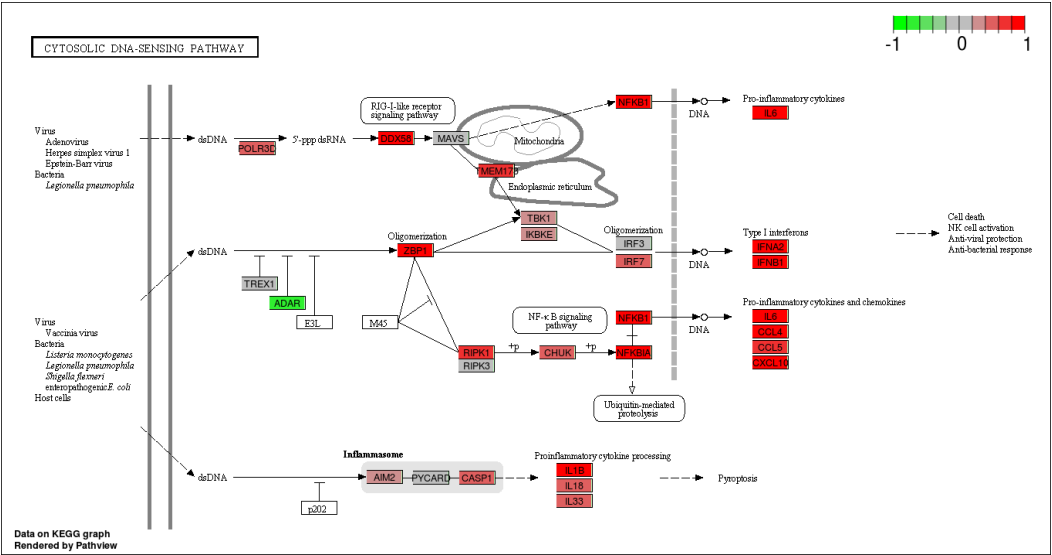


compound	
hidden compound	
activation	
inhibition	
expression	
repression	
indirect effect	
state change	
binding/association	
dissociation	
phosphorylation	
dephosphorylation	
glycosylation	
ubiquitination	
methylation	
others/unknown	

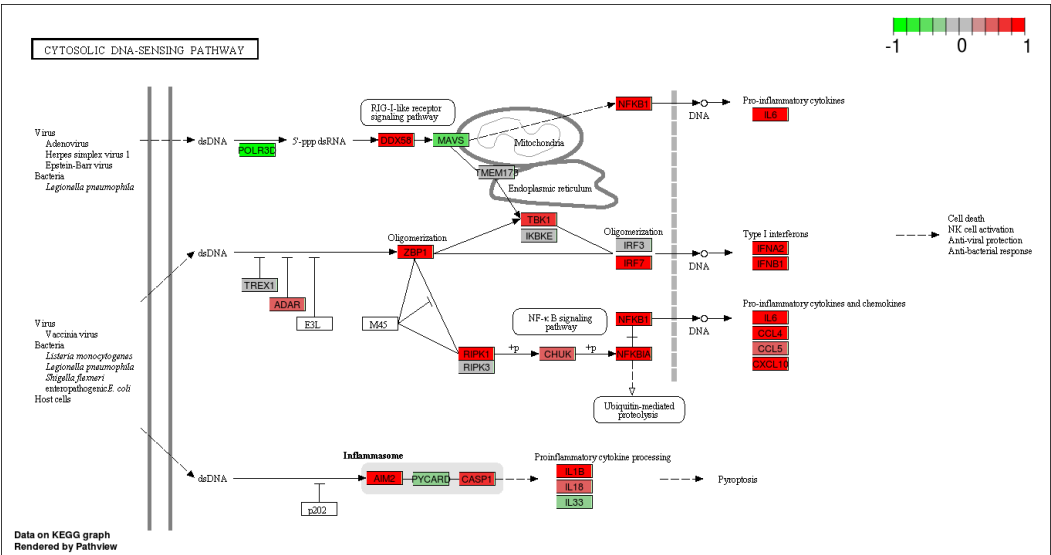
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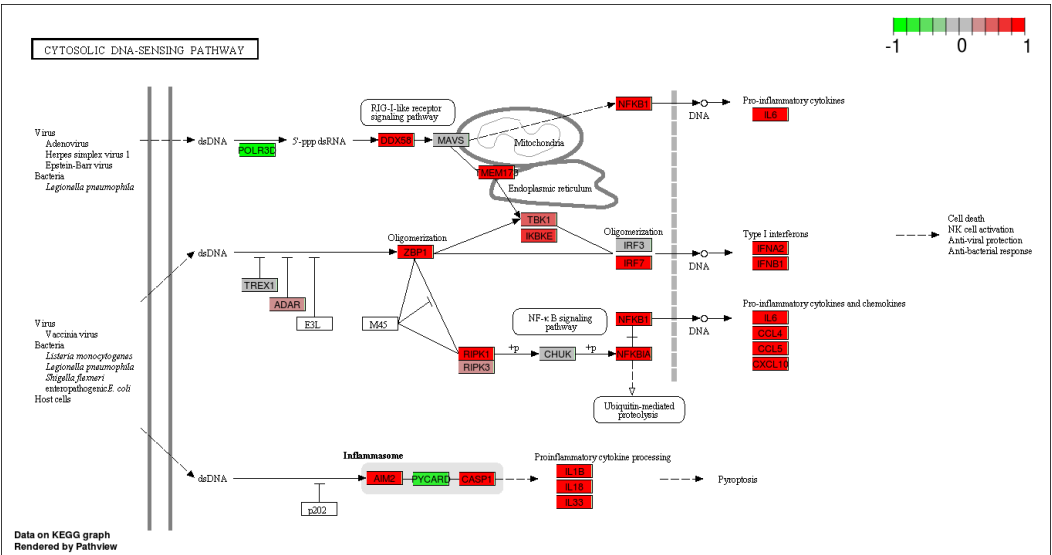
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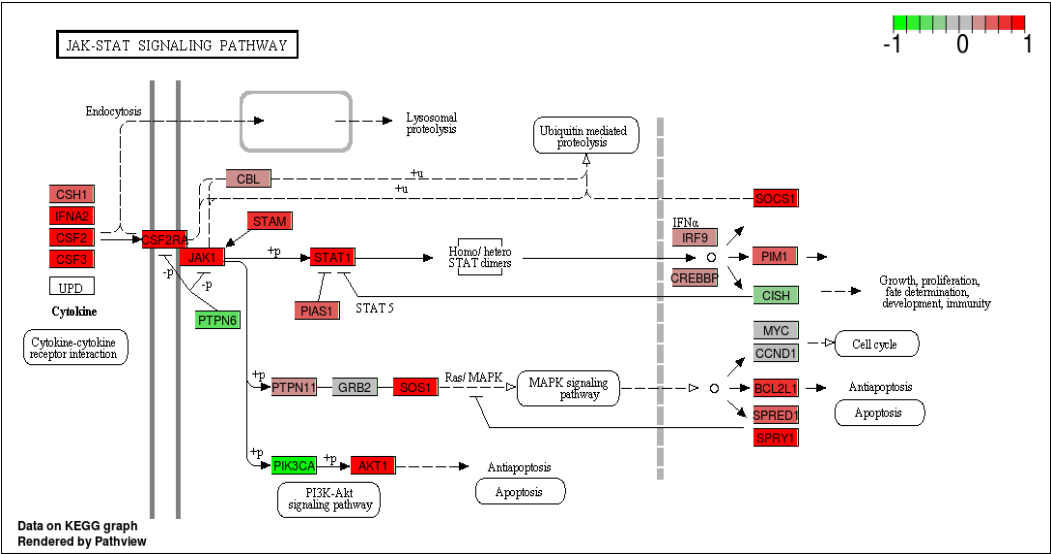
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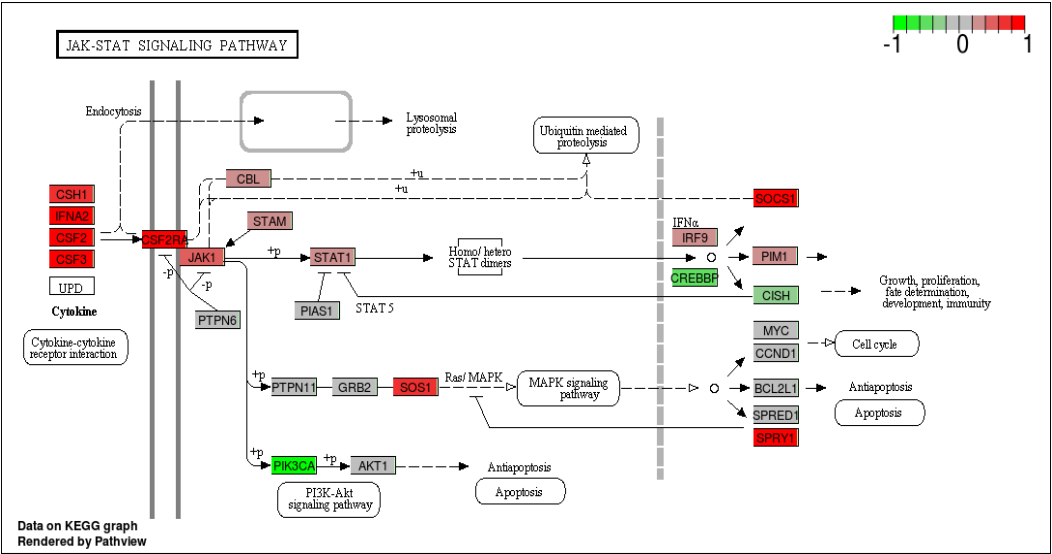
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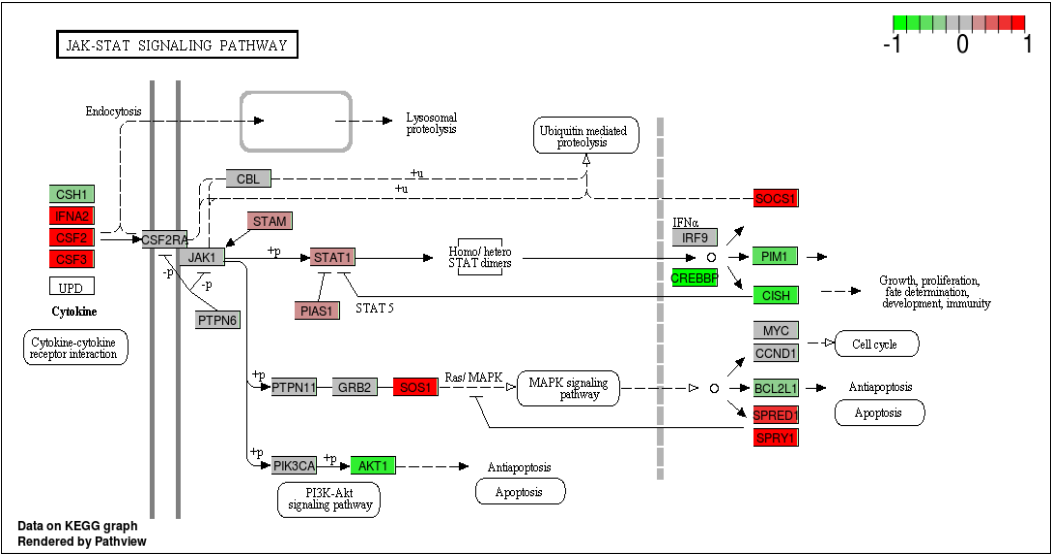
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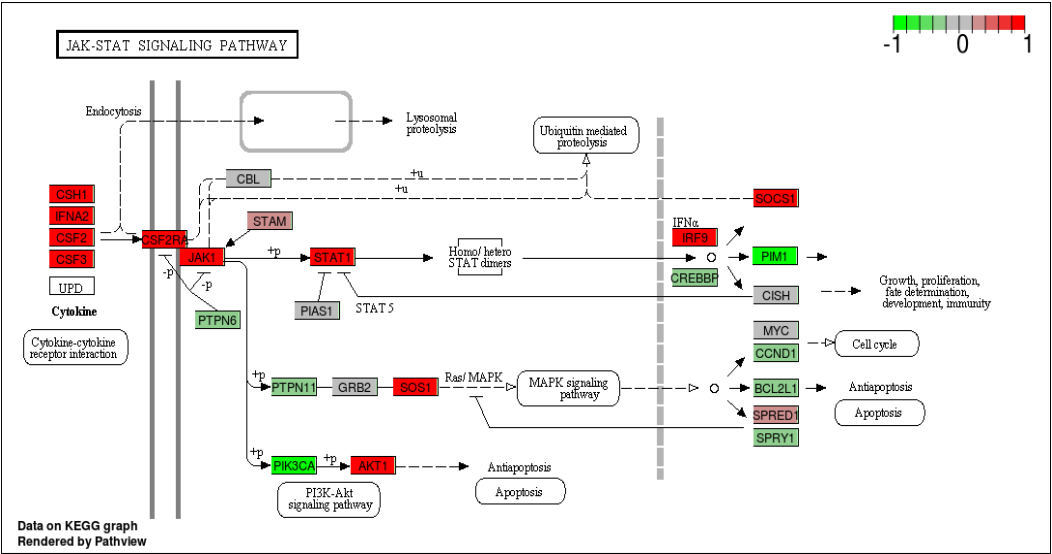
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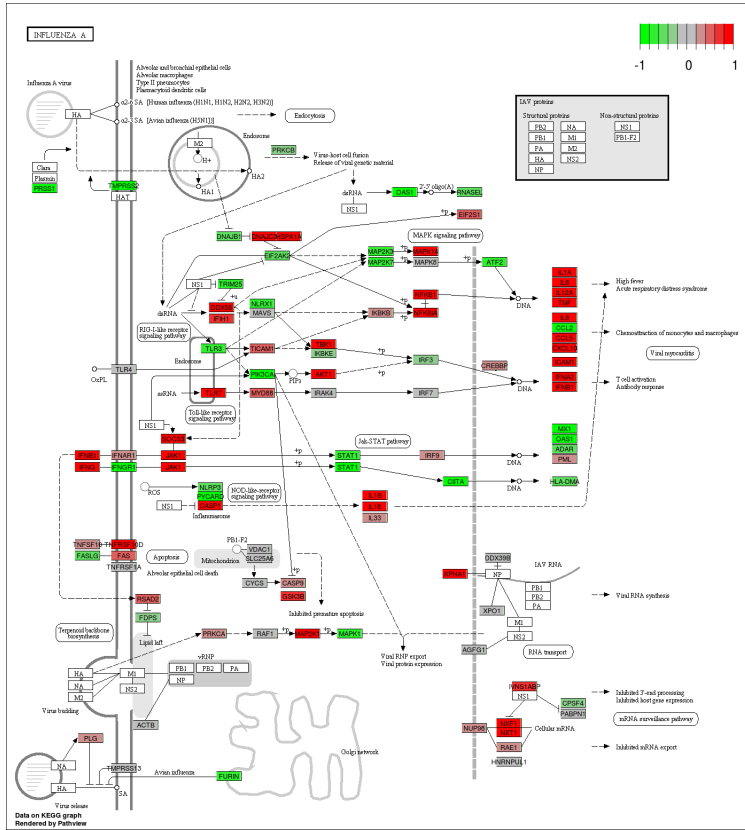
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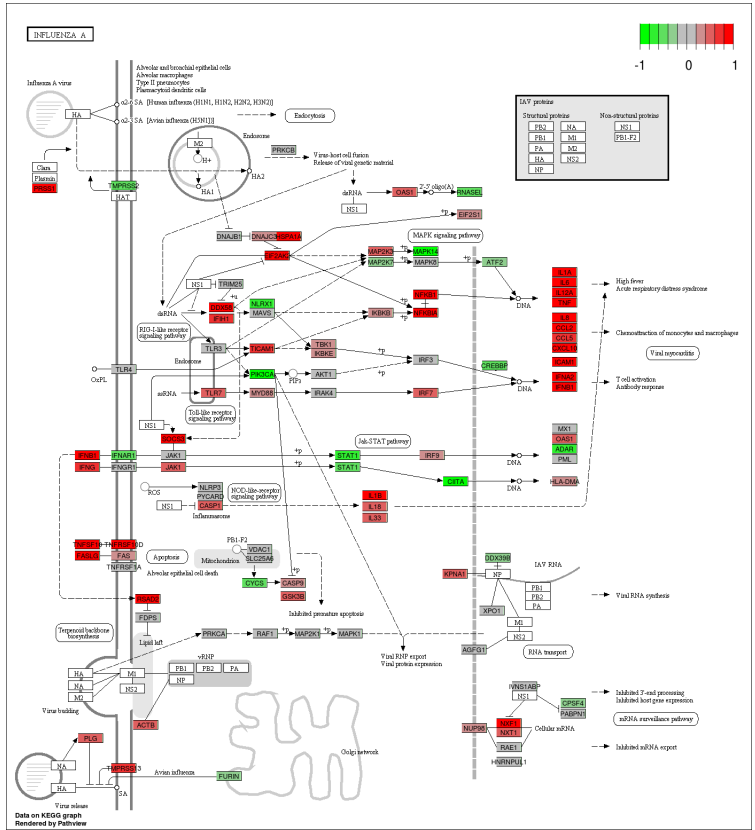
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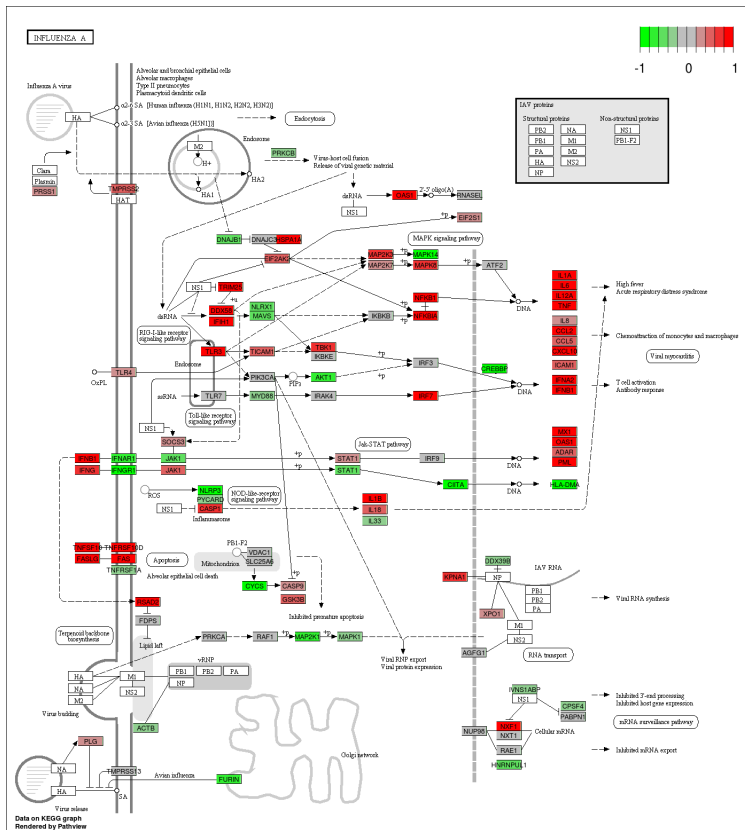
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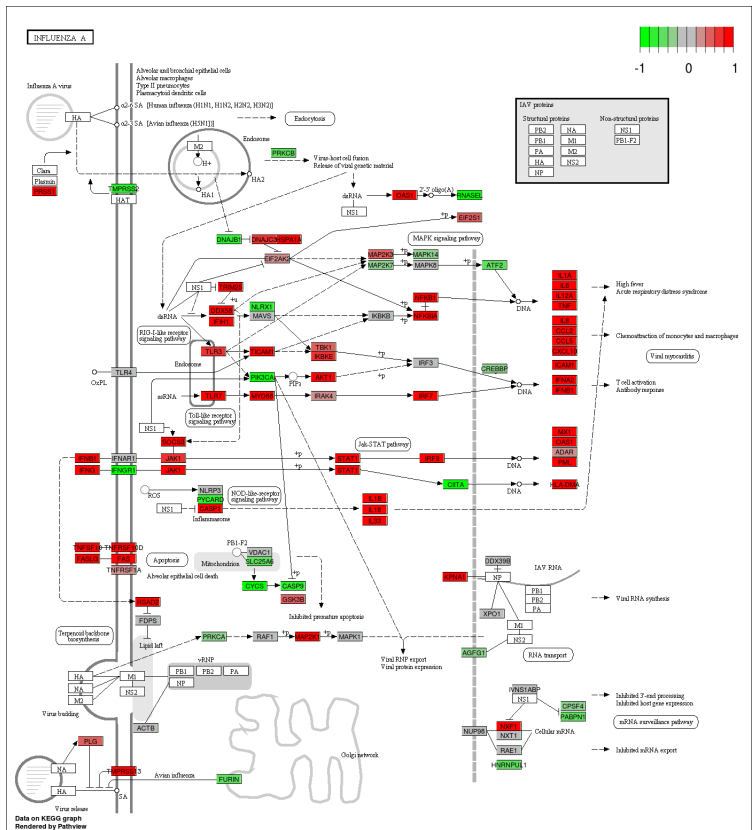
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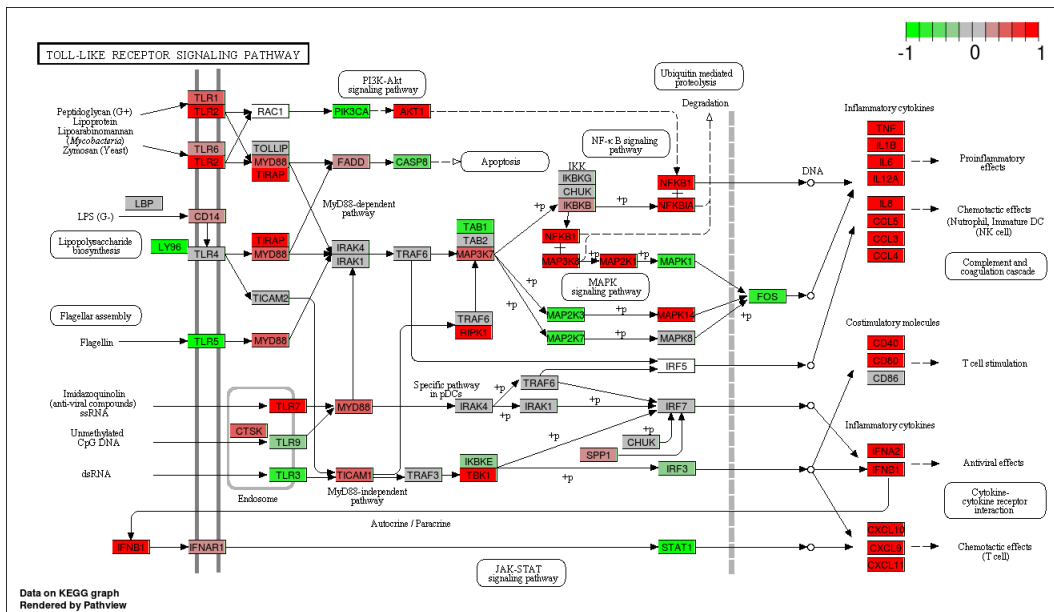
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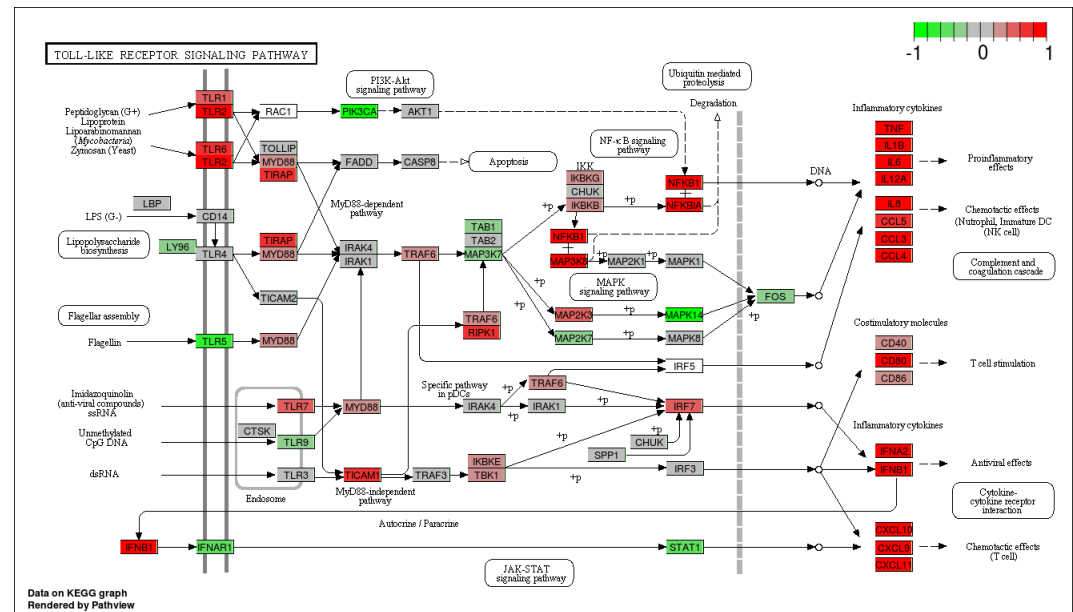
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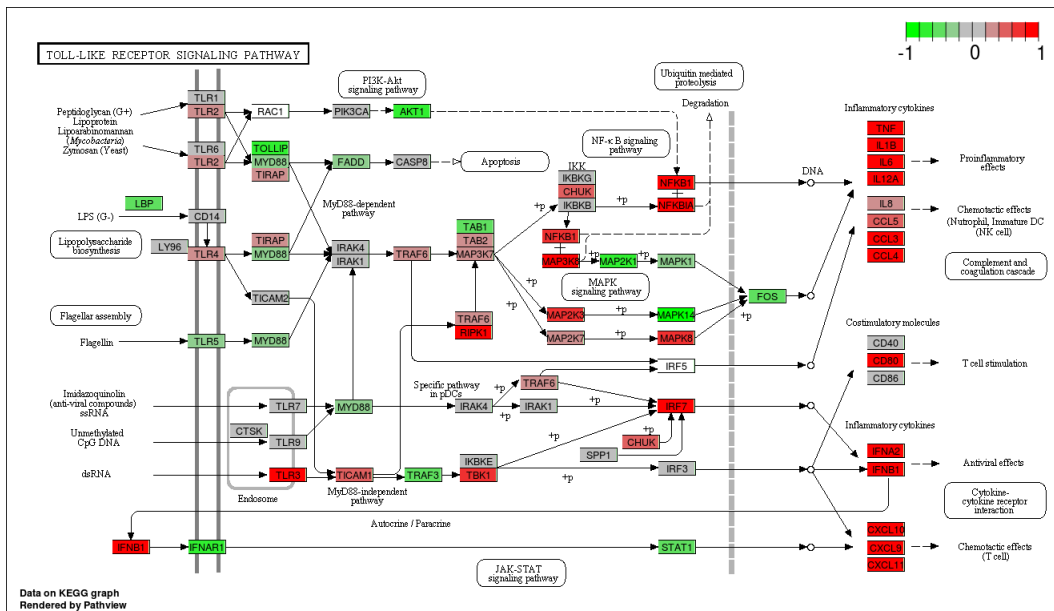
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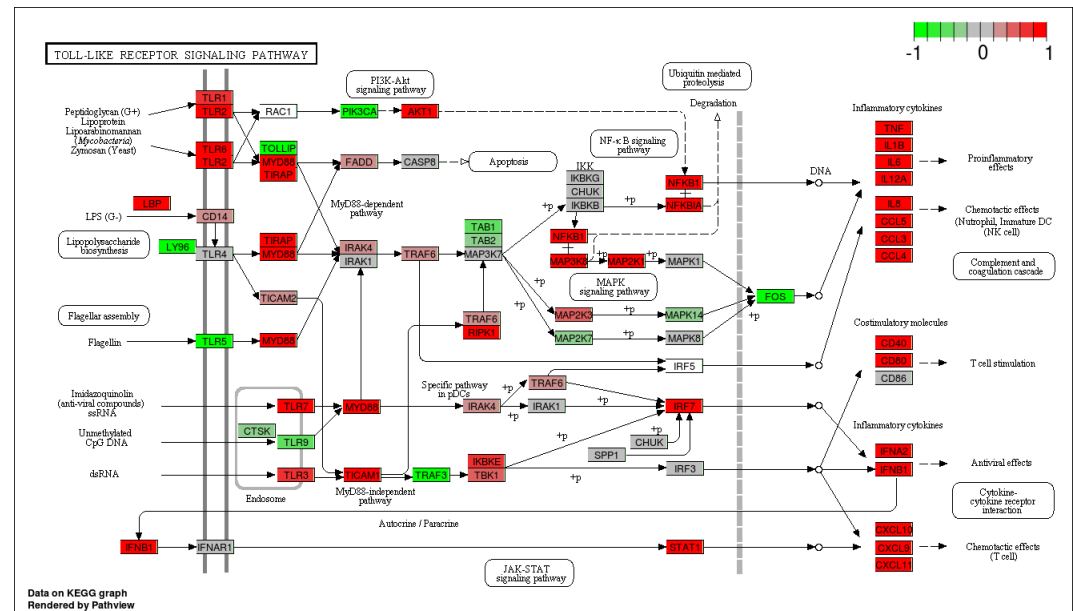
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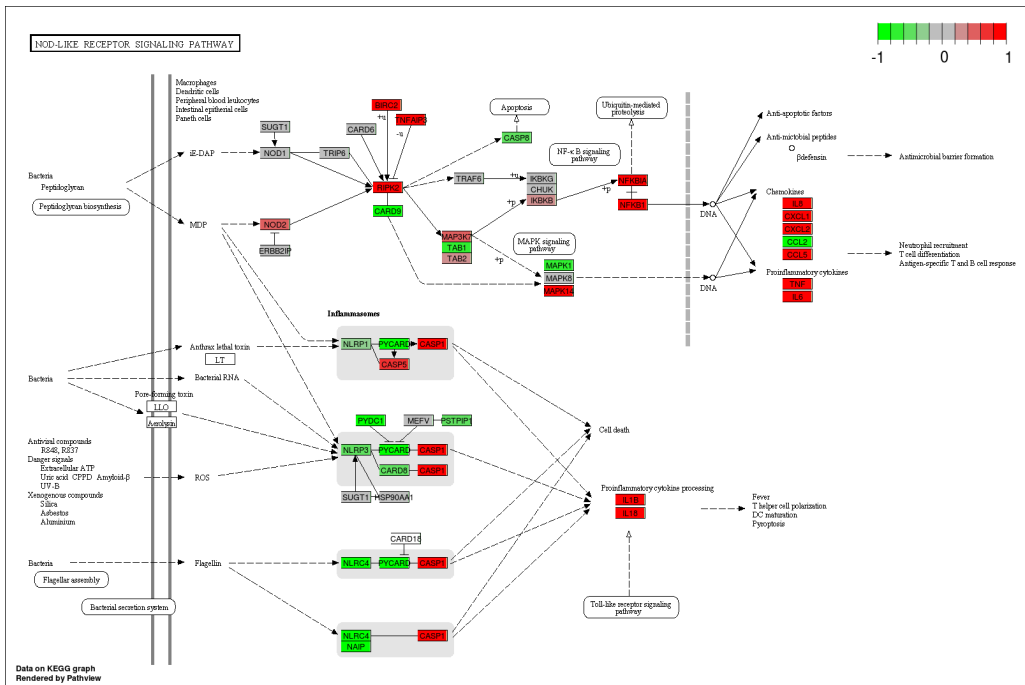
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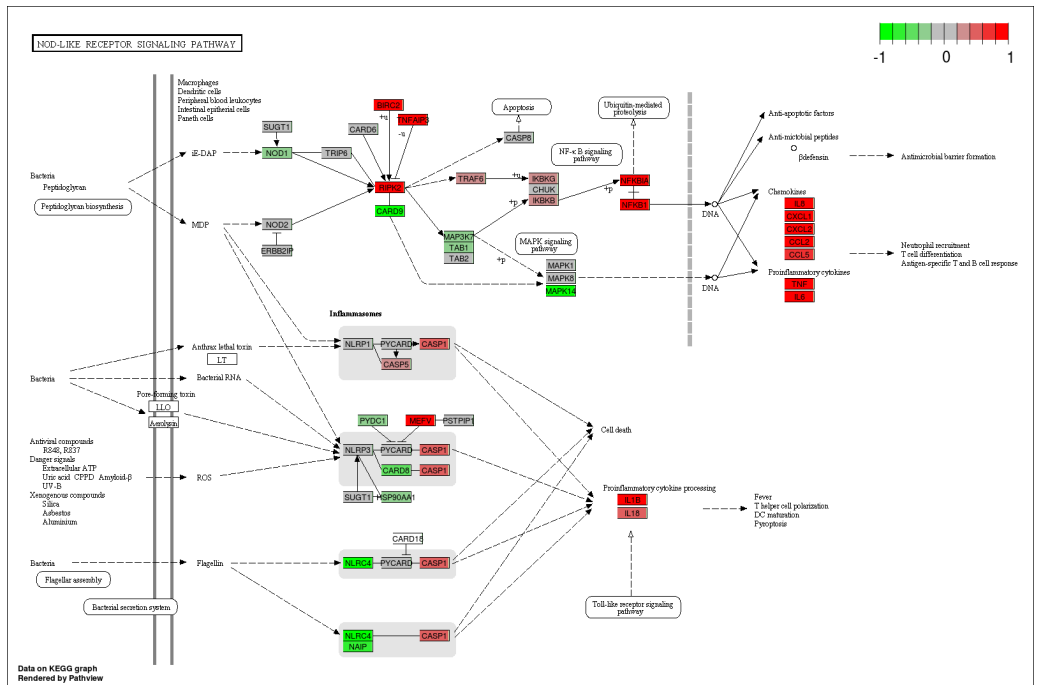
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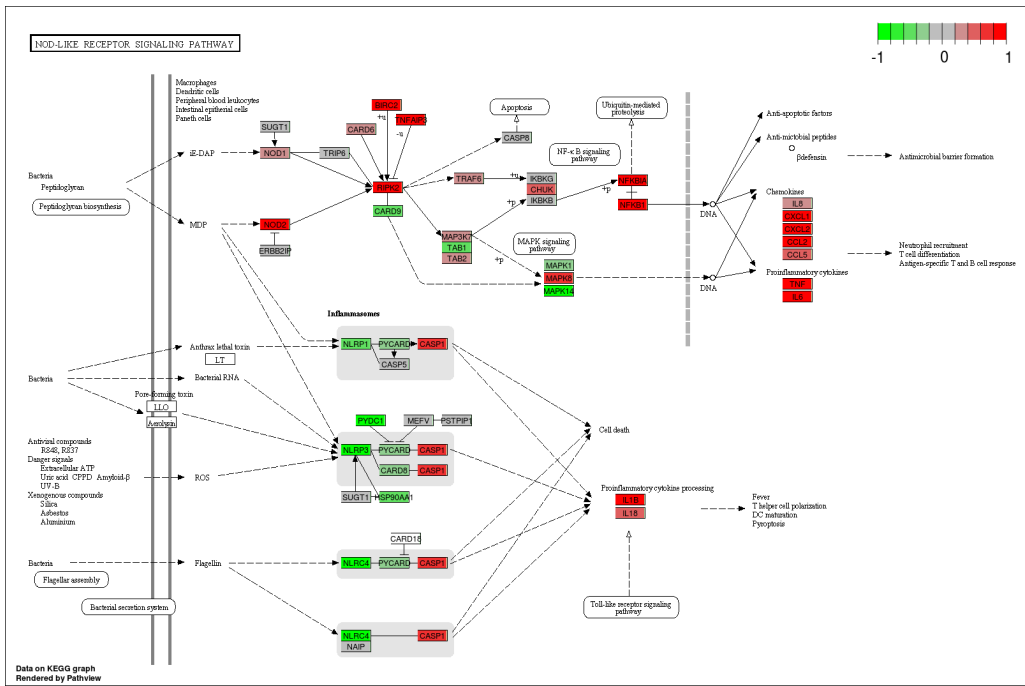
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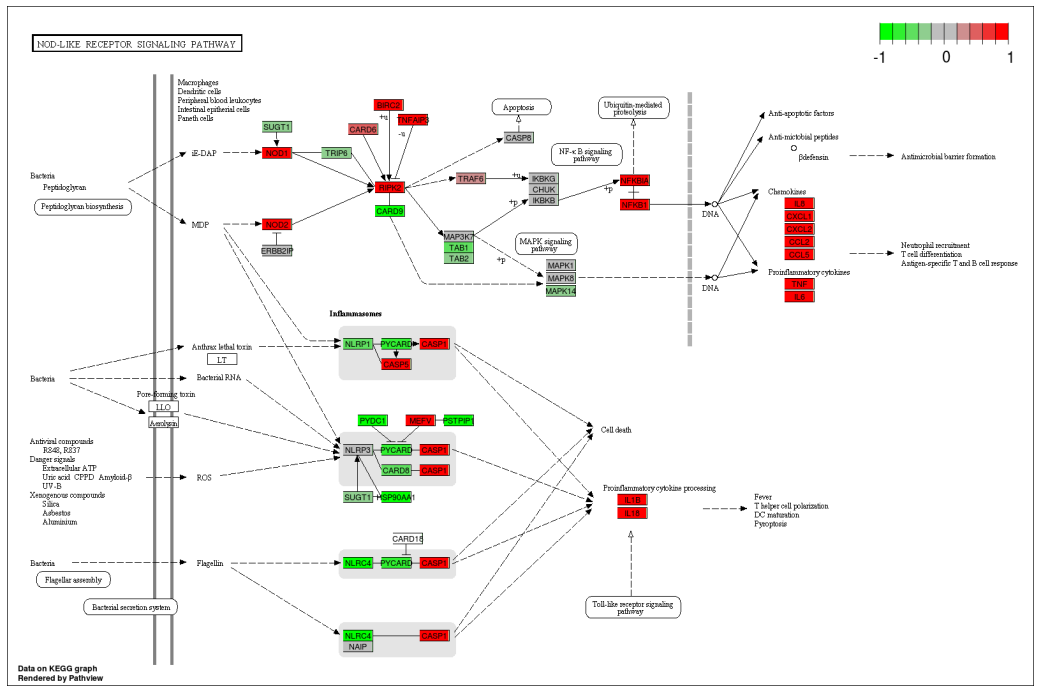
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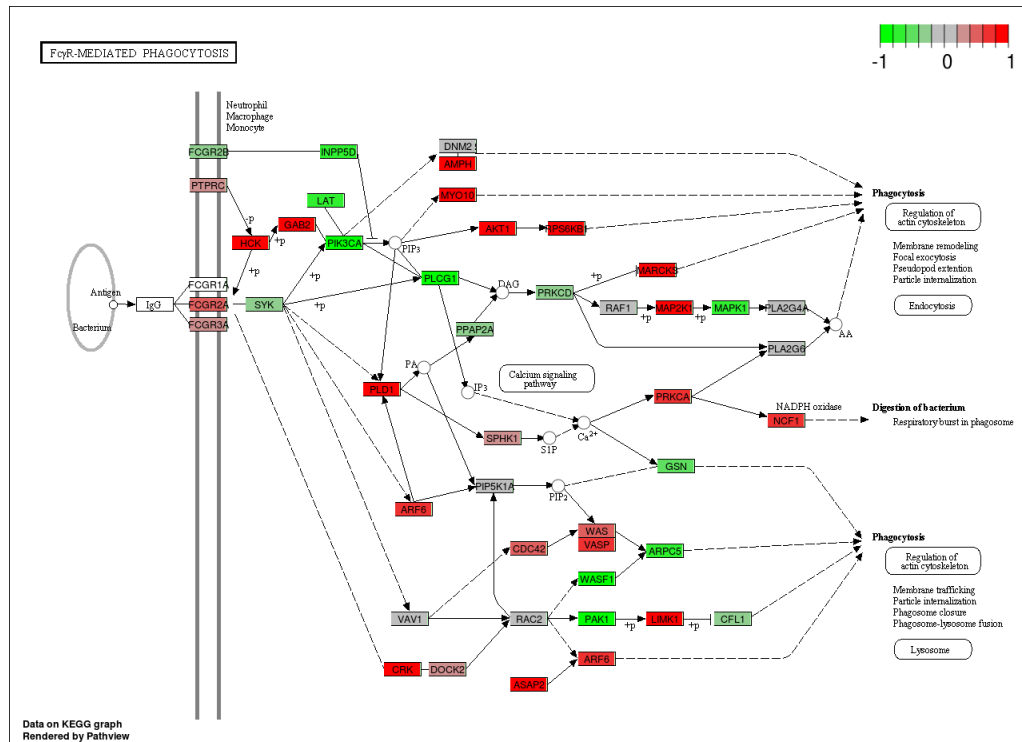
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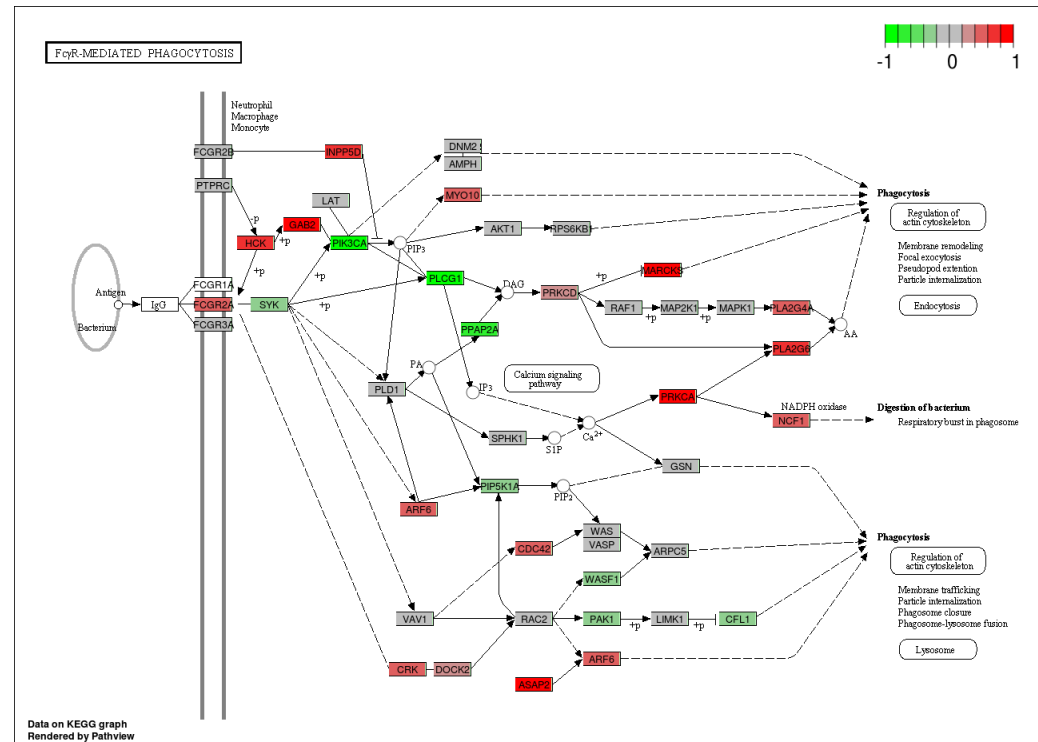
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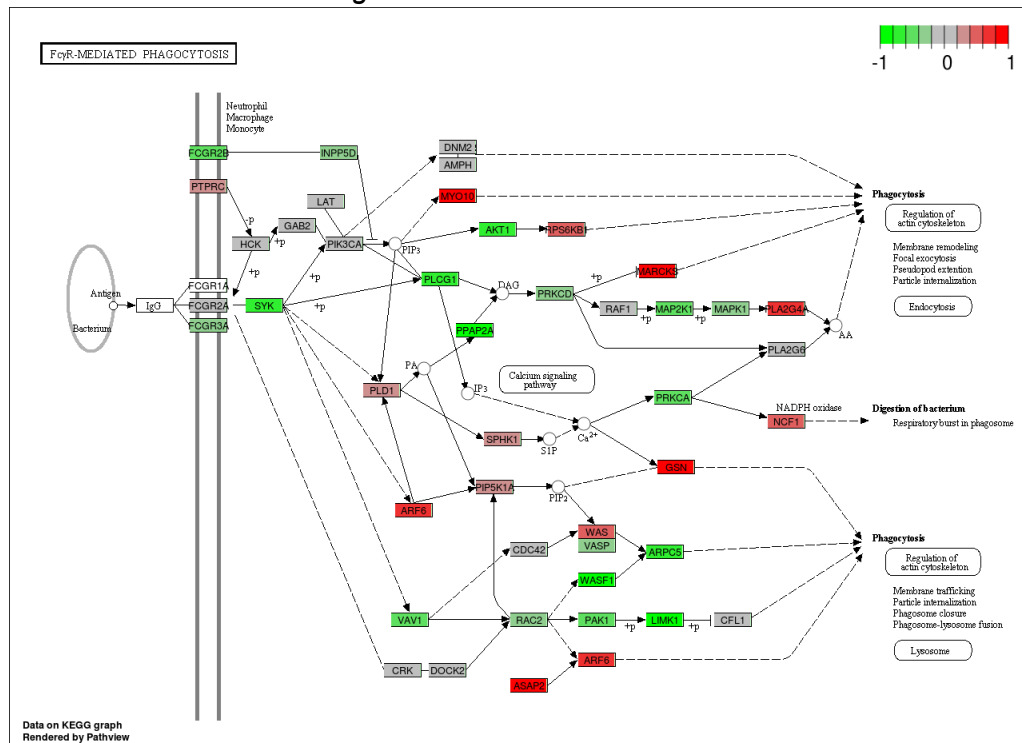
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Orientia tsutsugamushi



LPS

