Supplement B

Toxoplasma Modulates Signature Pathways of Human Epilepsy, Neurodegeneration & Cancer

Huân M. Ngô^{1,2,3,+}, Ying Zhou^{1,+}, Hernan Lorenzi^{4,+}, Kai Wang^{5,+}, Taek-Kyun Kim^{5,+}, Yong Zhou⁵, Kamal El Bissati¹, Ernest Mui¹, Laura Fraczek¹, Seesandra V. Rajagopala⁴, Craig W. Roberts⁶, Fiona L. Henriquez¹, Alexandre Montpetit⁷, Jenefer M. Blackwell^{8,9}, Sarra E. Jamieson⁹, Kelsey Wheeler¹, Ian J. Begeman¹, Carlos Naranjo-Galvis¹, Ney Alliey-Rodriguez¹, Roderick G. Davis¹⁰, Liliana Soroceanu¹¹, Charles Cobbs¹¹, Dennis A. Steindler¹², Kenneth Boyer¹³, A. Gwendolyn Noble², Charles N. Swisher², Peter T. Heydemann¹³, Peter Rabiah¹⁴, Shawn Withers¹, Patricia Soteropoulos¹⁵, Leroy Hood⁵, and Rima McLeod^{1*}

¹The University of Chicago, Chicago, IL 60637
²Northwestern University, Feinberg School of Medicine, Chicago, IL 60611
³BrainMicro LLC, New Haven, CT 06511
⁴J Craig Venter Institute, Rockville, MD 20850
⁵Institute of Systems Biology, Seattle, WA 98109
⁶University of Strathclyde, Glasgow G1 1XQ, United Kingdom
⁷Genome Quebec, Montréal, QC H3B 1S6, Canada; McGill University, Montréal, QC H3A 0G4, Canada
⁸Department of Pathology, University of Cambridge, Cambridge CB2 1QP, United Kingdom
⁹Telethon Kids Institute, The University of Western Australia, Perth, Australia
¹⁰University of Illinois-Chicago, Chicago, IL 60607
¹¹California Pacific Medical Center, San Francisco, CA 94114
¹²JM USDA Human Nutrition Research Center on Aging, Tufts University, Boston, MA 02111
¹³Rush University Medical Center, Chicago, IL 60612
¹⁴Northshore University Health System, Evanston, IL 60201
¹⁵Rutgers University, Newark, New Jersey 07101

+ Equal contributions

* To whom Correspondence should be addressed: Rima McLeod, M.D. rmcleod@uchicago.edu

Co-Corresponding Authors: Huân M. Ngô (h-ngo@northwestern.edu) Hernan Lorenzi, PhD (hlorenzi@jcvi.org) Kai Wang, PhD (kai.wang@systemsbiology.org) T.K. Kim, MS (tkim@systemsbiology.org)

Current Addresses: FLH, IBEHR School of Science and Sport, University of the West of Scotland, Paisley, PA1 2BE, UK

Index to Supplementary Tables

Table S1. List of Identified Human Genes That Are Likely to Play a Role in Susceptibility to T. gondii Infection.

Table S2A. Analysis of Expression of Susceptibility Genes in Human Brain Using Allen Brain Atlas.

Table S2. Predicted Upstream Regulators of Congenital Toxoplasmosis Genetics and Biomarkers.

Table S3. Transcriptomics profiles of neuronal stem cells with significant modulation [\geq (+/-) 1.5 log2 fold change infected/control] due to *Toxoplasma* infection. RNA Quantification of L-NSC was determined by Affymetrix Gene Microarray, whereas S-NSC was assayed by RNA sequencing.

Table S4. Quantification of Proteins in Human L-NSC Infected with Toxoplasma gondii Type I, II or III for 18 Hours.

Table S5. Complete Assembly of Systemic Infectome in L-NSC and S-NSC by Gene Symbols.

Table S6. Protein-Protein Interactions as Determined by STRING Database in L-NSC and S-NSC.

Table S7. Upstream Regulation Analysis of Molecules Regulated by Infection in NSC cells and CT Cohort Genetic & Biomarkers. A, Upstream Regulatory Pathways from Figure 7; B, Gene Description of Upstream Regulator and Targets from Figure 7; C, Upstream Regulatory Pathways.

Table S8. Canonical Pathway Analysis.

Table S9. Canonical Pathways that includes NFKB1 as determined by IPA.

Table S10A. IPA Annotation of Diseases and Function.

Table S10B. IPA Annotation of Diseases and Function (Complete Annotation).

Table S11. microRNAs in Steindler neural stem and differentiated cells with significant modulation [FDR < 0.05] due to *Toxoplasma* infection. MiRNA quantification was assayed by RNA sequencing.

Table S12. microRNAs, grouped by human mature microRNA gene, with significant modulation [FDR < 0.05] due to *Toxoplasma* infection in MonoMac6 cells and Steindler neural stem and differentiated cells. MiRNA quantification was assayed by RNA sequencing. Reads are considered only if they map to one type of microRNA.

Table S13. mRNAs in MonoMac6 (MM6) cells with significant modulation [> (+/-) 1.5 log2 fold change] due to *Toxoplasma* infection. Quantification of mRNA was assayed by RNA sequencing.

Table S14: rMATS prediction of alternatively spliced genes in Steindler Neuronal Stem Cells infected with Type I, II and III *T. gondii* parasites using reads spanning splicing junctions and exon sequences.

Table S15: iTRAQ quantitative proteomics analysis of S-NSC infected with Type I, II and III T. gondii parasites.

Table S16: GO Biological Process enrichment analysis on MM6, S-NSC and S-NDC transcriptomics data.

Table S17: KEGG Pathways enrichment analysis on MM6, S-NSC and S-NDC transcriptomics data.