

**Supplemental Table S9.** Fetal brain transcript GO Terms at E16.5, 7 dpi.

|               | Go term (direct)                    | GO         | Category | Count | %    | P-value  | - log (P-value) |
|---------------|-------------------------------------|------------|----------|-------|------|----------|-----------------|
| Upregulated   | glutamatergic synapse               | GO:0098978 | CC       | 27    | 12.8 | 1.80E-10 | 9.745           |
|               | modulation of synaptic transmission | GO:0050804 | BP       | 11    | 5.2  | 3.70E-07 | 6.432           |
|               | calcium ion binding                 | GO:0005509 | MF       | 22    | 10.4 | 3.00E-06 | 5.523           |
|               | membrane                            | GO:0016020 | CC       | 98    | 46.4 | 2.90E-05 | 4.538           |
|               | synapse                             | GO:0045202 | CC       | 24    | 11.4 | 3.60E-05 | 4.444           |
|               | postsynaptic density                | GO:0014069 | CC       | 13    | 6.2  | 1.30E-04 | 3.886           |
|               | GABA-ergic synapse                  | GO:0098982 | CC       | 8     | 3.8  | 2.00E-04 | 3.699           |
|               | brain development                   | GO:0007420 | BP       | 11    | 5.2  | 2.80E-04 | 3.553           |
|               | nervous system development          | GO:0007399 | BP       | 13    | 6.2  | 6.30E-04 | 3.201           |
|               | neuron projection                   | GO:0043005 | CC       | 15    | 7.1  | 7.20E-04 | 3.143           |
| Downregulated | nucleus                             | GO:0005634 | CC       | 79    | 45.7 | 2.90E-07 | 6.538           |
|               | nervous system development          | GO:0007399 | BP       | 14    | 8.1  | 3.00E-05 | 4.523           |
|               | cell division                       | GO:0051301 | BP       | 13    | 7.5  | 4.70E-05 | 4.328           |
|               | cell cycle                          | GO:0007049 | BP       | 16    | 9.2  | 1.10E-04 | 3.959           |
|               | cytoplasm                           | GO:0005737 | CC       | 78    | 45.1 | 1.90E-04 | 3.721           |
|               | chromosome                          | GO:0005694 | CC       | 14    | 8.1  | 3.80E-04 | 3.420           |
|               | protein binding                     | GO:0005515 | MF       | 61    | 35.3 | 4.70E-04 | 3.328           |
|               | mRNA binding                        | GO:0003729 | MF       | 9     | 5.2  | 1.40E-03 | 2.854           |
|               | microtubule                         | GO:0005874 | CC       | 10    | 12.7 | 1.50E-03 | 2.824           |
|               | cytoskeleton                        | GO:0005856 | CC       | 22    | 9.8  | 1.70E-03 | 2.770           |

Top 10 significantly enriched upregulated and downregulated GO terms from DAVID. *Dpi* = days post inoculation, *GO* = gene ontology, *DAVID* = Database for Annotation, Visualization, and Integrated Discovery terms, *CC* = cellular component, *BP* = biological process, *MF* = molecular function.