## SUPPLEMENTAL FIGURES

- Fig. S1. Temporal analysis of nuclear pyknosis in hypoxic cortical neurons. (A) Cultures were exposed to hypoxia  $(0.5\% \ O_2)$  from 3-24 hours as indicated. Images were analyzed for the fraction of pyknotic nuclei relative to untreated controls using Hoechst 33342 staining from an average of 150 nuclei per coverslip (n=3). (B) Comparison of nuclear pyknosis profiles in hypoxic cultures fixed immediately following hypoxic challenge (grey bars) or following hypoxic with an additional 24 hour reperfusion period (black bars). Background levels of nuclear pyknosis were subtracted in (B). Significance was determined using Student's t testing comparing hypoxic to normoxic controls (\* = p< 0.05, \*\* = p<0.01, NS= not significant).
- <u>Fig. S2</u>. Functional annotation of neuronal transcripts regulated by hypoxic stress. Histogram representation of the number of array targets identified at each hypoxic time period (3 hour, 12 hour, 18 hour) relative to normoxic controls grouped according to their respective MGI gene ontology biological functions.





