

SUPPLEMENTARY MATERIAL

corresponding to:

***In silico* analysis of histone H3 gene expression during human brain development**

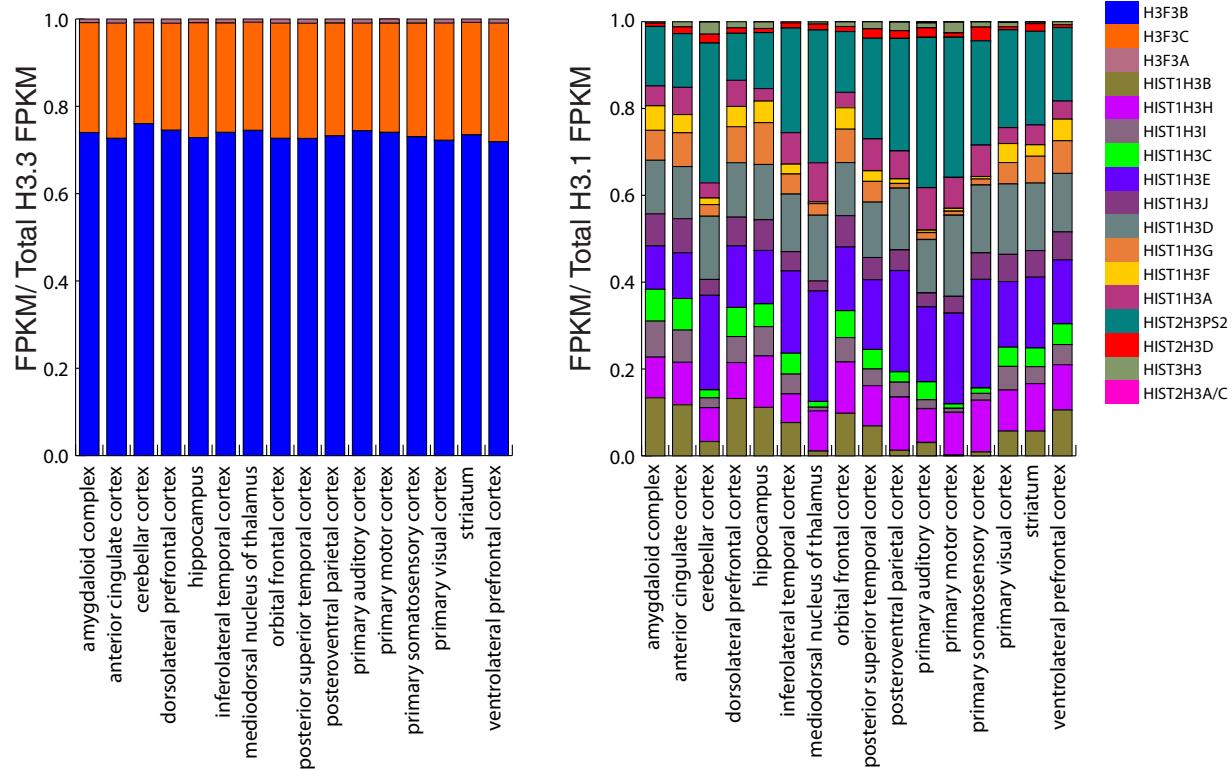
MEGAN REN and STEVE VAN NOCKER*

*Address correspondence to: Steve van Nocker, 390 PSS Building, 1066 Bogue St., East Lansing, MI, USA 48824-1325. Tel: +1-517-775-5218. Fax: +1-517-355-0249.
E-mail: vannocke@msu.edu

Full text for this paper is available at: <http://dx.doi.org/10.1387/ijdb.150334sv>



Suppl. Fig. S1. Protein sequence alignment of human H3 sequences. Open reading frame translations from 18 human H3 gene transcripts were aligned using ClustalX (Larkin et al., 2007; <http://www.clustal.org>). Four amino acid positions distinguishing canonical (H3.1-like) and replication-independent (H3.3) H3s are indicated.



Suppl. Fig. S2. Brain structure-associated H3 transcript accumulation. Stacked bar graph shows proportional representation for the 16 brain structures most highly represented in BrainSpan. The FPKM value for each gene in proportion to combined H3.3 or H3.1 transcript FPKM is shown on the Y axis. Color codes are shown at right and correspond to those shown in Figs. 2,3 in the main article.