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A high resolution spatiotemporal atlas of gene expression of the developing mouse brain

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SUMMARY

To provide a temporal framework for the genoarchitecture of brain development, *in situ* hybridization data were generated for embryonic and postnatal mouse brain at 7 developmental stages for ~2100 genes, processed with an automated informatics pipeline and manually annotated. This resource comprises 434,946 images, 7 reference atlases, an ontogenetic ontology, and tools to explore co-expression of genes across neurodevelopment. Gene sets coinciding with developmental phenomena were identified. A temporal shift in the principles governing the molecular organization of the brain was detected, with transient neuromeric, plate-based organization of the brain present at E11.5 and E13.5. Finally, these data provided a transcription factor code that discriminates brain structures and identifies the developmental age of a tissue, providing a foundation for eventual genetic manipulation or tracking of specific brain structures over development. The resource is available as the Allen Developing Mouse Brain Atlas (developingmouse.brain-map.org).

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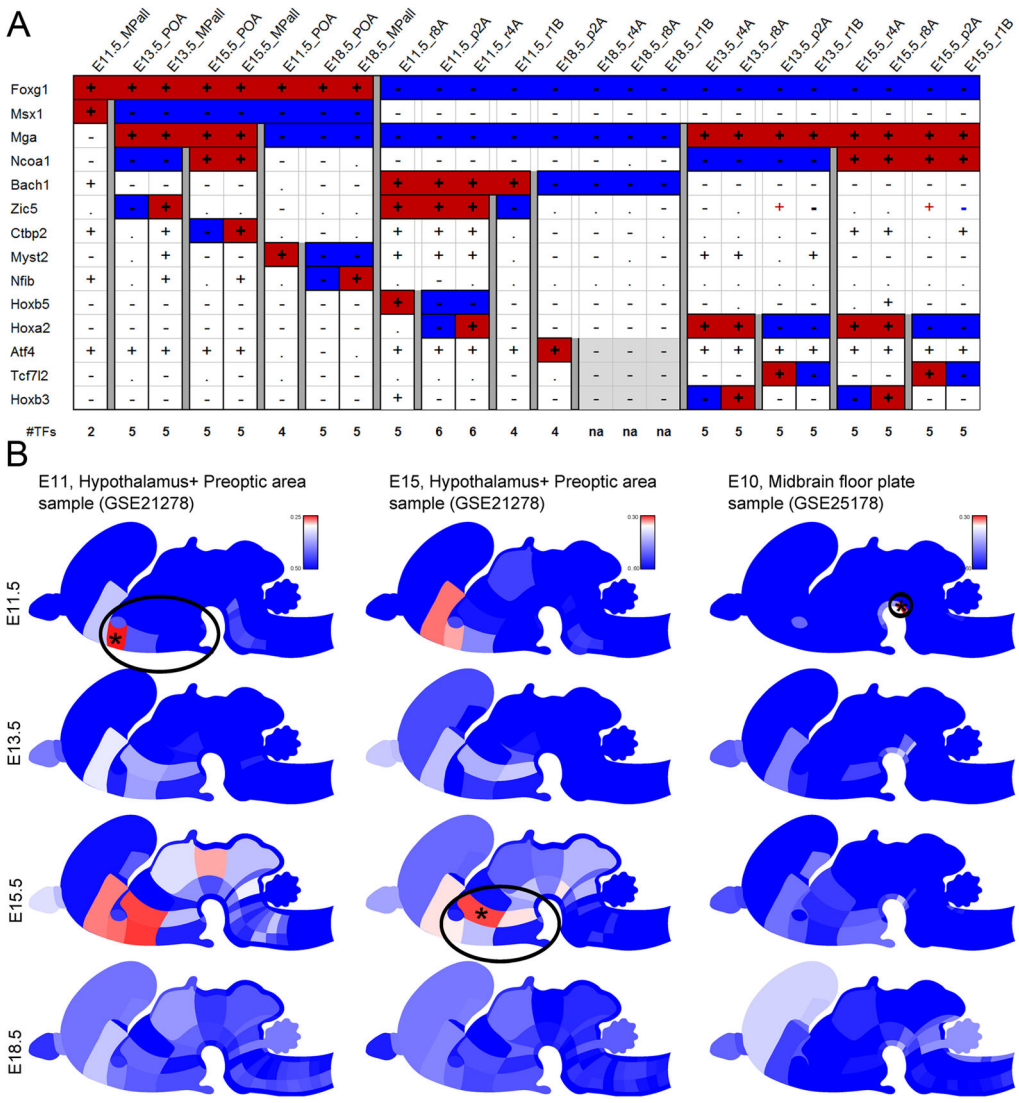

Figure 8. A transcription factor code can uniquely identify the developmental age and anatomic structure in a sample profiled by microarray

(A) 14 genes can distinguish six brain structures at 4 ages; in this example, three atlas structures at E18.5 (gray shade) remain indistinguishable with this code. (**B**) Identifying the anatomic region and biological age of a microarray sample based upon the TF code. For each sample, the GEO ID is given; the best match to a given age x region combination in the ADMBA is color-coded (red, high correlation; blue, low correlation; asterisk, best match). In each case, the TF code accurately identifies the closest age x brain structure. Note the anatomic criteria used for obtaining the microarray samples may have differed in part with our criteria, leading to the dispersion of the correlative results (see also Figures S7 and S8).