

# Genome-wide coexpression of steroid receptors in the mouse brain: identifying signaling pathways and functionally coordinated regions

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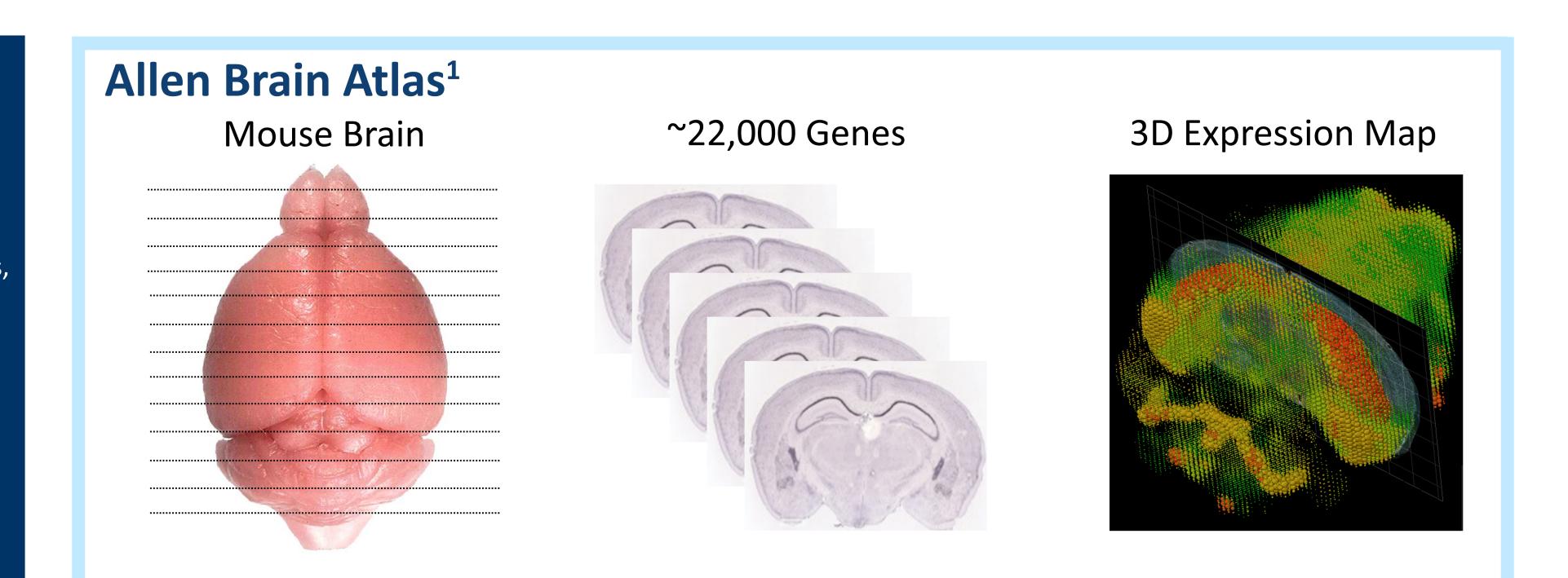
\*a.mahfouz@lumc.nl

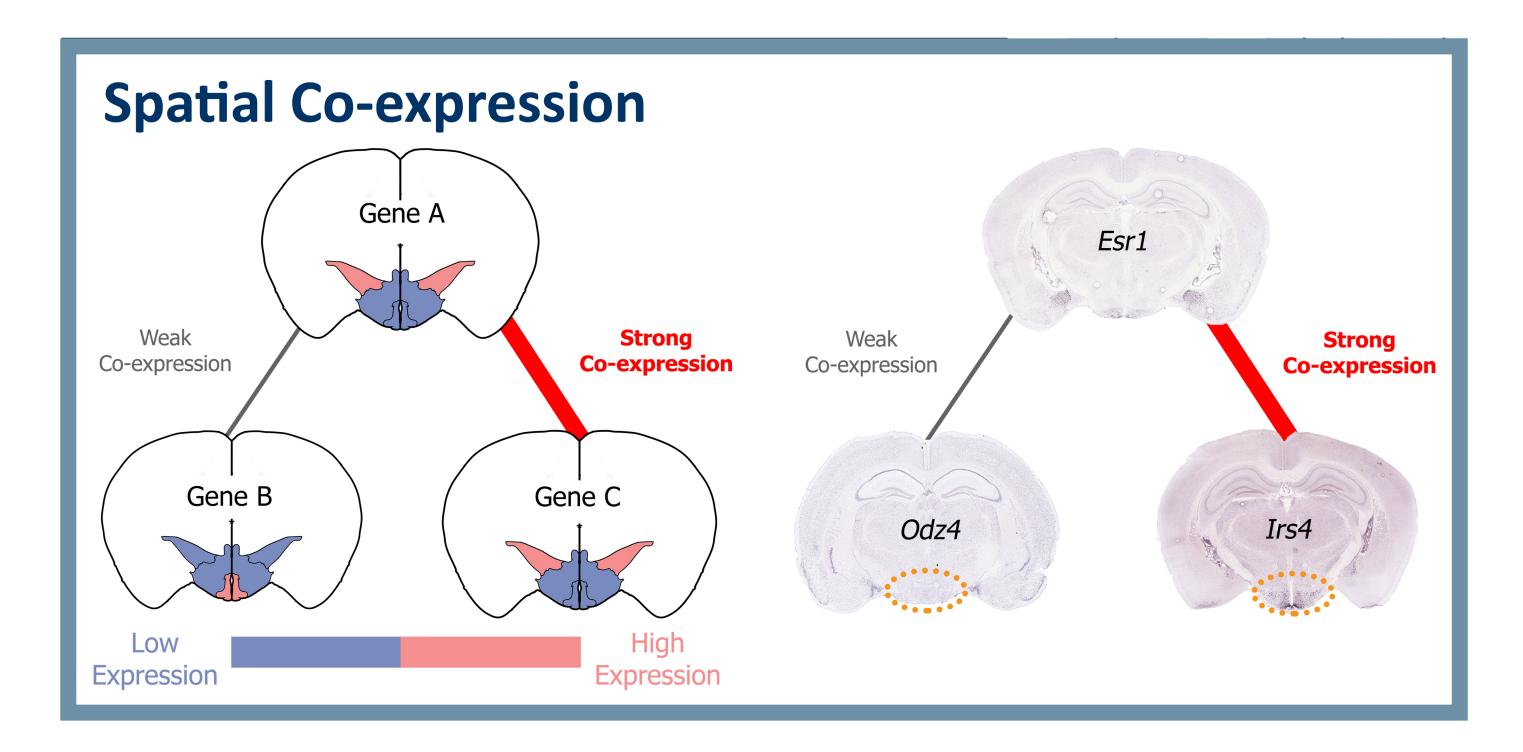
# Genome-wide co-expression of steroid receptors in the mouse brain: identifying signaling pathways and

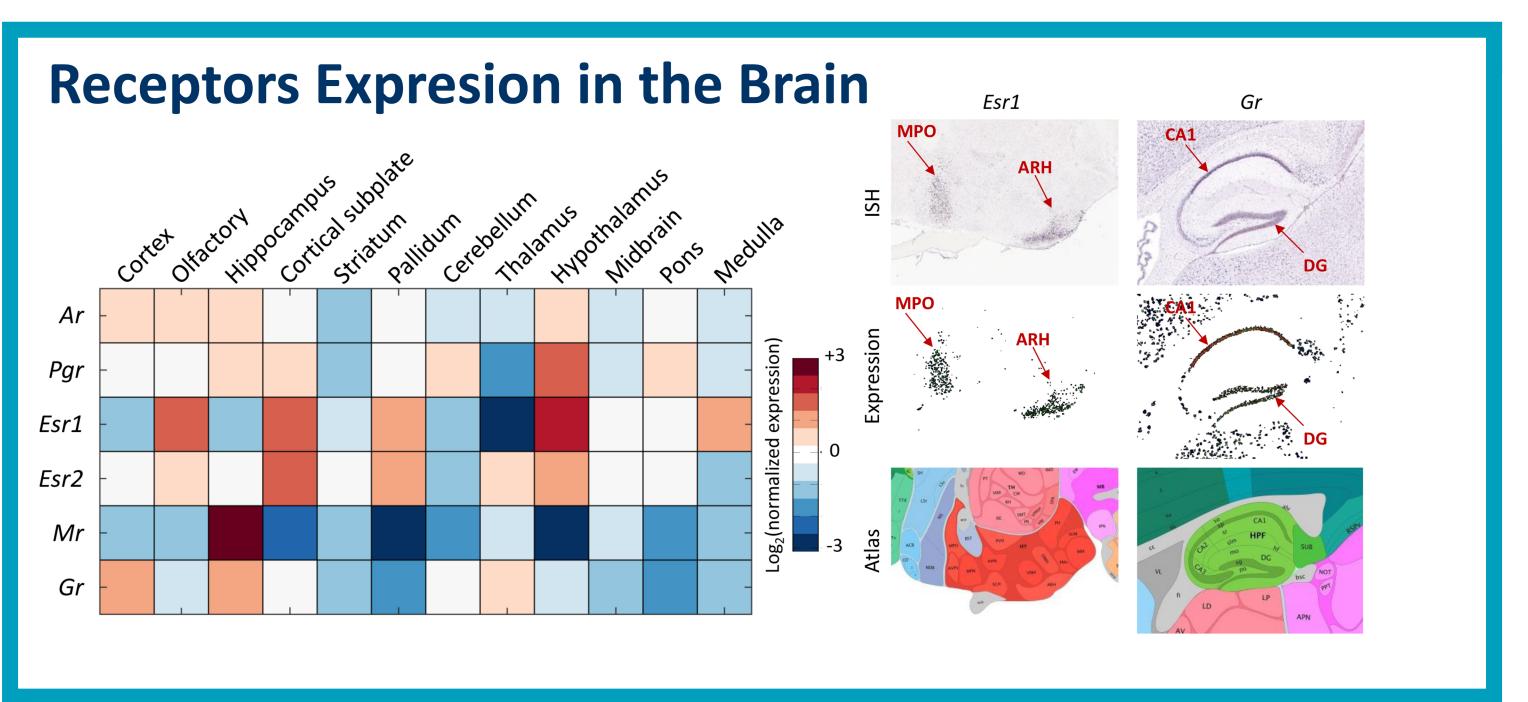
# Introduction

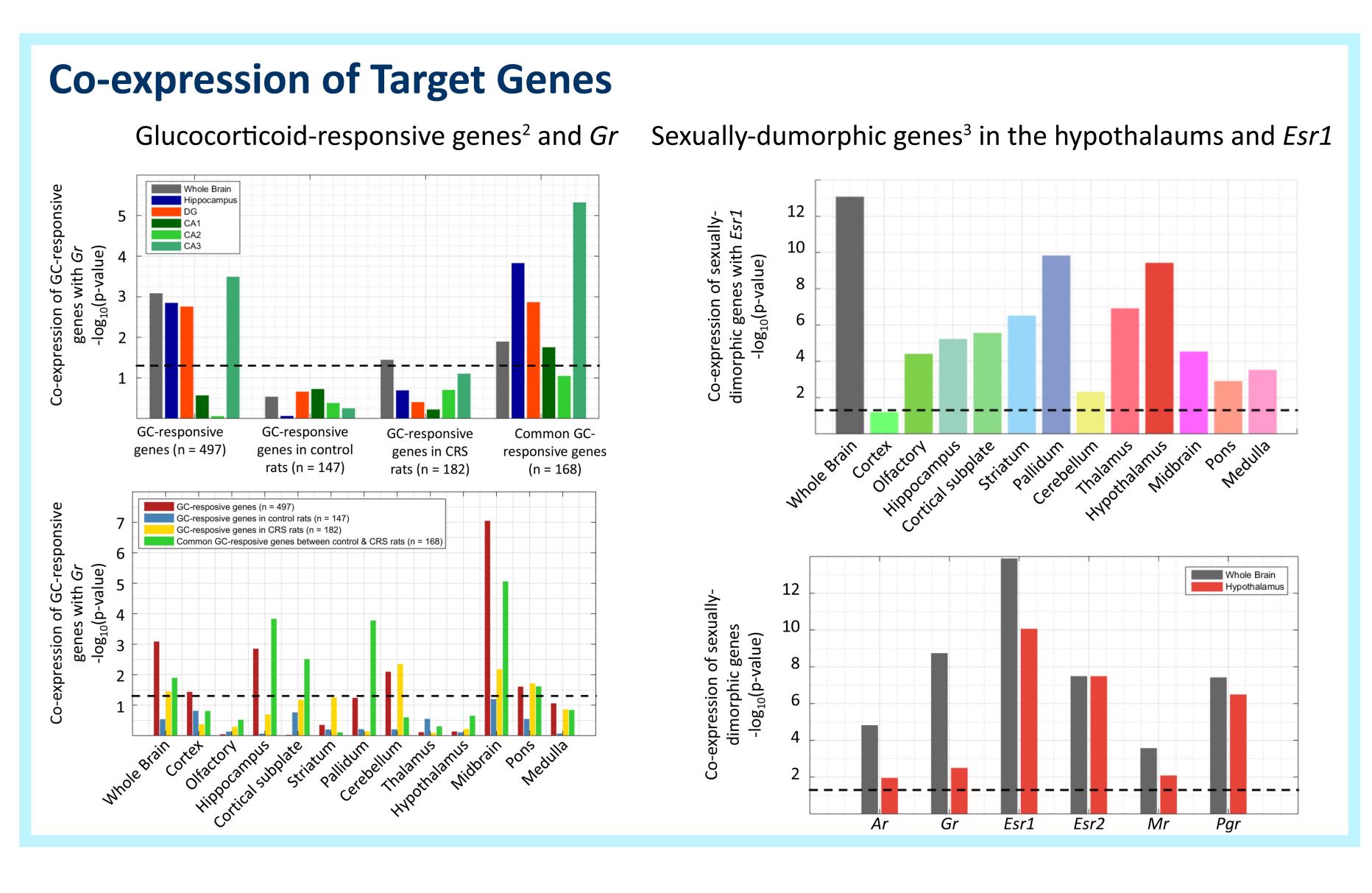
Steroid hormones coordinate the activity of many brain regions by binding to nuclear receptors that act as transcription factors. This study uses genome wide correlation of gene expression in the mouse brain to:

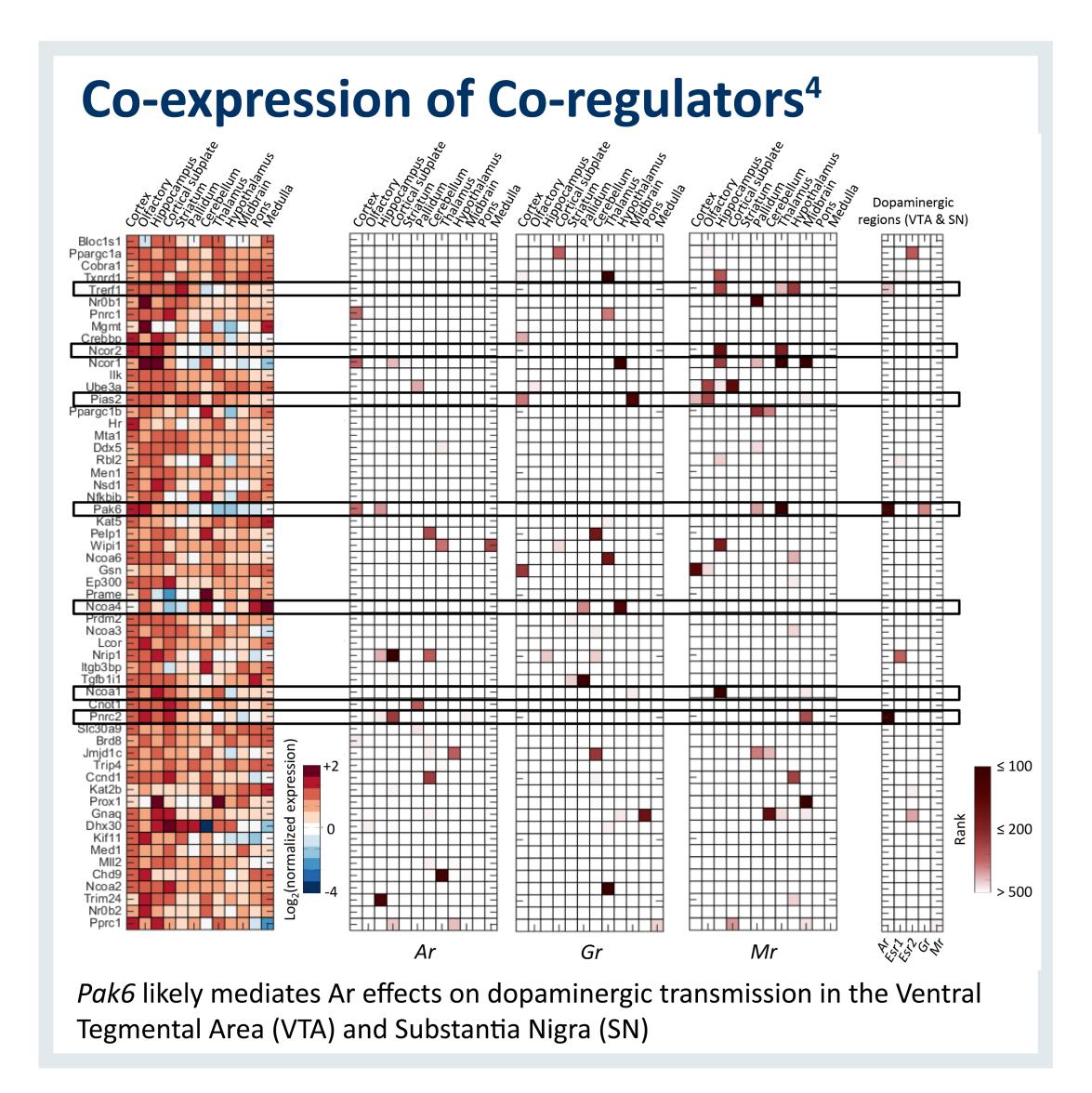
- find brain regions that respond in a similar manner to particular steroids,
   identify signaling pathways that are used in a steroid receptor and brain region-specific manner, and
- 3) discover potential target genes and relationships between groups of target genes.
- The data constitute a rich repository for the research community to support further new insights in neuroendocrine relationships, and to develop novel ways to manipulate brain activity in research or clinical settings.











## Using Co-expression to Predict Hormone Responsiveness Response of Magel2 to DES Response of *Ers1*-co-expressed genes to estrogen diethylstilbesterol (DES) Double in situ hybridization of Irs4 and Response of *Irs4* to DES treatment in castrated mice treatment in the hypothalamus (qPCR) treatment in castrated mice Magel2 with Esr1 in the hypothalamus $P = 1.3 \times 10^{-3}$ $P = 6.8 \times 10^{-3}$ 1.45 0.04 1.26 0.19 \* Irs4 0.23 1.10 0.32 1.34 Fut8 1.34 0.04 1.08 0.24 0.05 1.24 0.21 1.08 0.14 1.30 0.09 0.87 0.14 1.25 0.18 0.10 1.34 0.08 0.11 1.02 0.39 Control DES Control DES

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