

SUPPLEMENTAL DATA AND FIGURES

Physical enrichment triggers brain plasticity in rainbow trout (*Oncorhynchus mykiss*) and influence on blood plasma circulating miRNA

Emilie Cardona^{1,†}, Valentin Brunet^{2,†}, Elodie Baranek¹, Léo Milhade³, Sandrine Skiba-Cassy¹, Julien Bobe², Ludovic Calandreau⁴, Jérôme Roy^{1,*,†} and Violaine Colson^{2,*,†}

¹INRAE, Université de Pau et des Pays de l'Adour, E2S UPPA, UMR1419 Nutrition Metabolism and Aquaculture, Aquapôle, F-64310 Saint-Pée-sur-Nivelle, France; emilie.cardona@inrae.fr (E.C.); elodie.baranek@inrae.fr (E.B.); sandrine.skiba@inrae.fr (S.SC.); jerome.roy@inrae.fr (J.R.)

²INRAE, UR 1037, LPGP Fish Physiology and Genomics, Campus de Beaulieu, F-35042, Rennes, France; valentin.brunet@inrae.fr (V.B.); julien.bobe@inrae.fr (J.B.); violaine.colson@inrae.fr (V.C.)

³IRISA, INRIA, CNRS, Université de Rennes 1, F-35000, Rennes, France; leo.milhade@irisa.fr (L.M.)

⁴CNRS, IFCE, INRAE, Université de Tours, PRC, 37380 Nouzilly, France; ludovic.calandreau@inrae.fr (L.C.)

* Correspondence: violaine.colson@inrae.fr / jerome.roy@inrae.fr

† These authors contributed equally to this work.

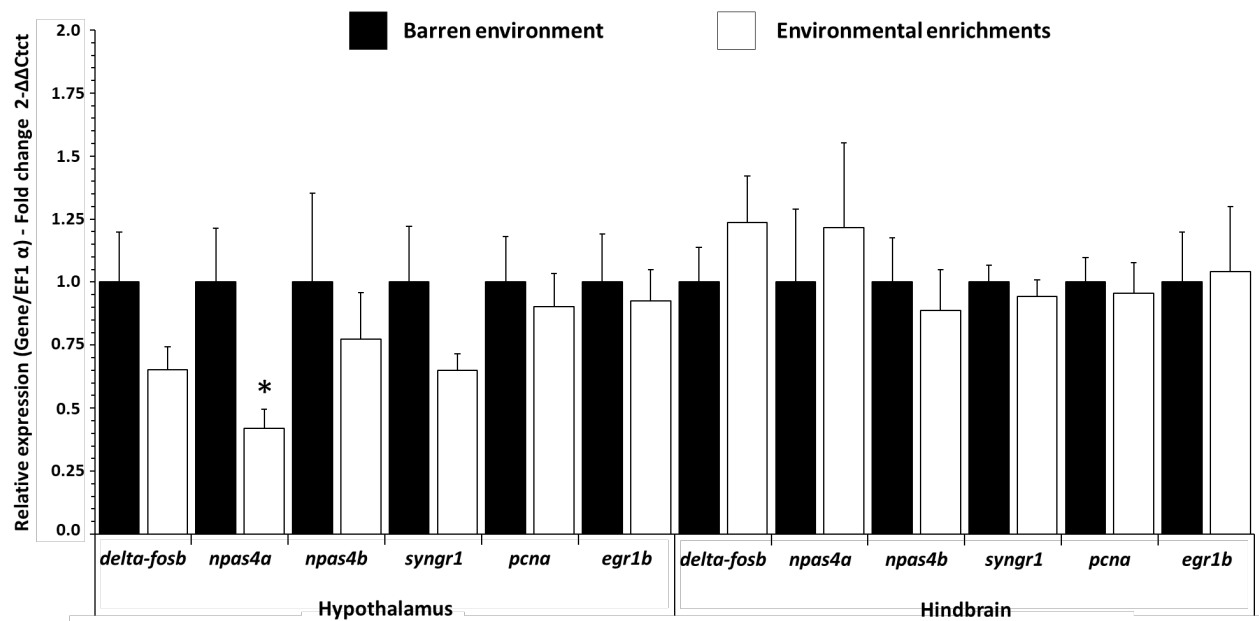


Figure S1. Neuronal activity related mRNA level of transcripts in hypothalamus and hindbrain of RT raised in a barren environment (black) or environmental enrichment (white) during three months. Values are expressed as group mean \pm SEM; fold change vs barren environment for all genes; welch's *t*-test, Tukey post hoc; Differences between treatments are represented by * ($P < .05$). Replicates ($n = 8$) correspond to different individual fish.

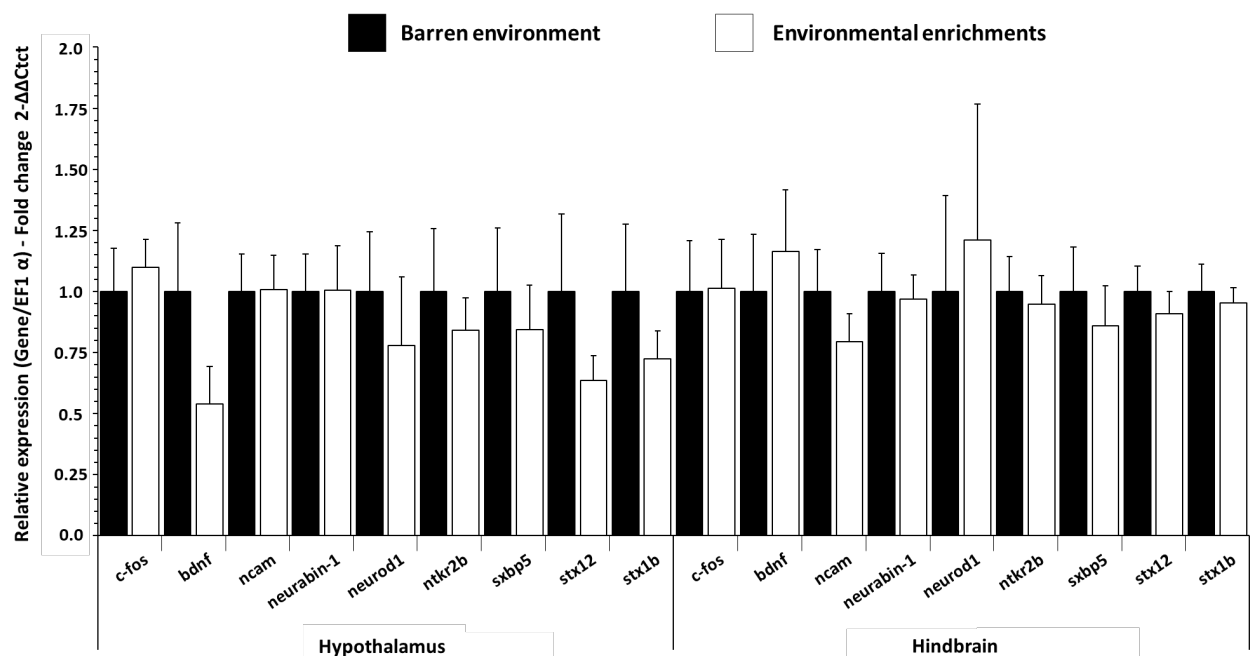


Figure S2. Neurotrophic and synaptogenesis factors related mRNA level of transcripts in hypothalamus and hindbrain of RT raised in a barren environment (black) or environmental enrichment (white) during three months. Values are expressed as group mean \pm SEM; fold change vs barren environment for all genes; welch's *t*-test, Tukey post hoc; Differences between treatments are represented by * ($P < .05$). Replicates ($n = 8$) correspond to different individual fish.

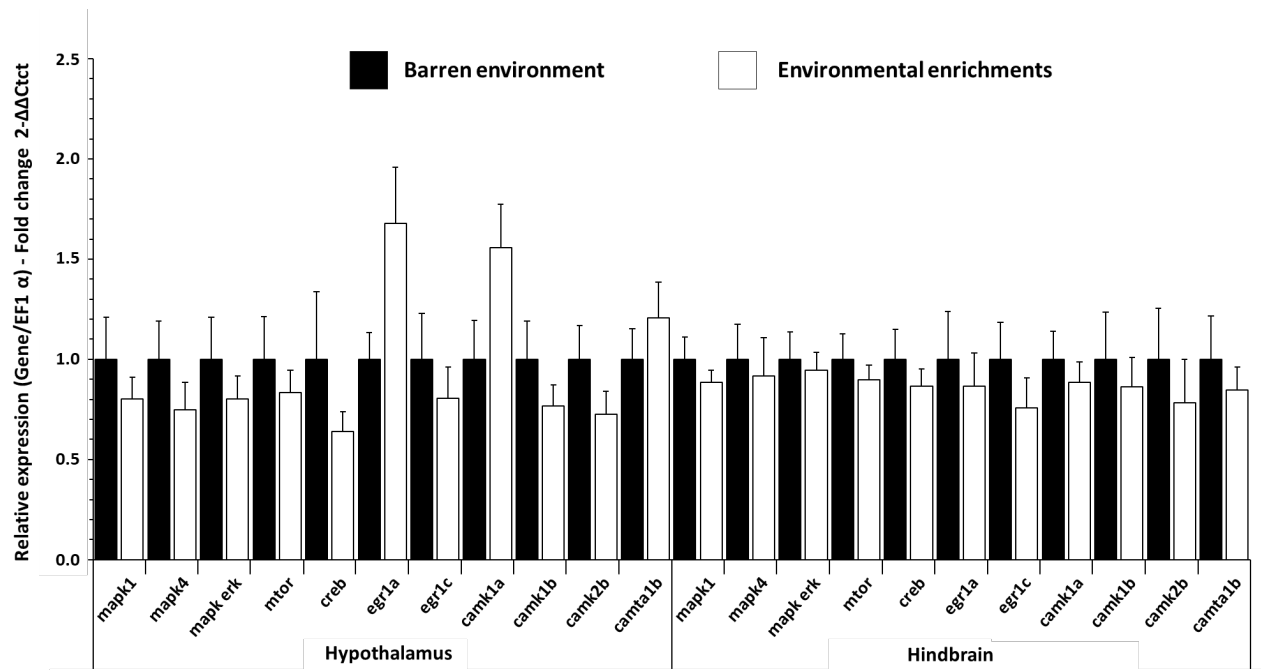


Figure S3. Plasticity factors related mRNA level of transcripts in hypothalamus and hindbrain of RT raised in a barren environment (black) or environmental enrichment (white) during three months. Values are expressed as group mean \pm SEM; fold change vs barren environment for all genes; welch's *t*-test, Tukey post hoc; Differences between treatments are represented by *($P < .05$). Replicates ($n = 8$) correspond to different individual fish.

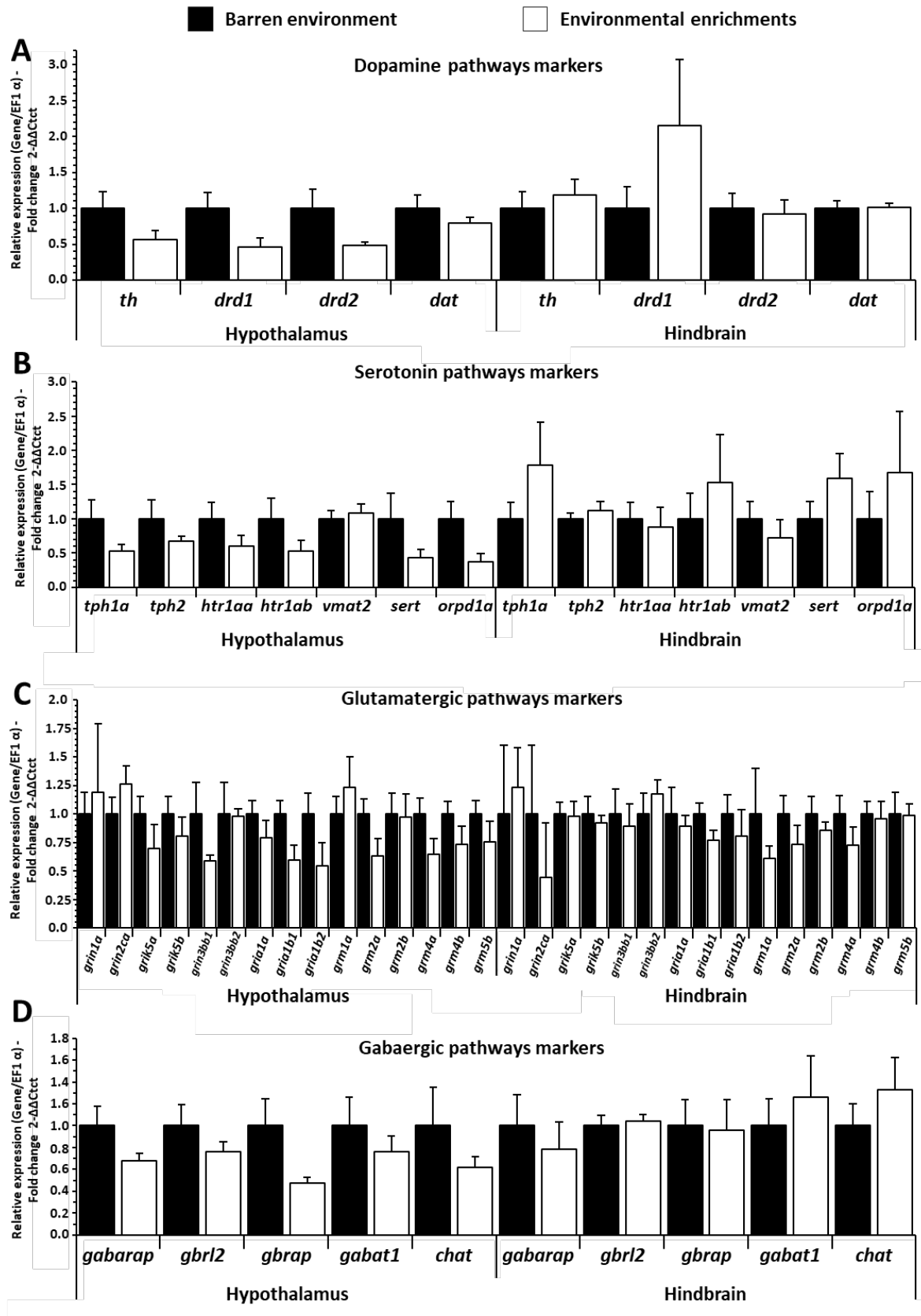


Figure S4. Dopamine, serotonin, glutamatergic and gabaergic pathways related mRNA level of transcripts in hypothalamus and hindbrain of RT raised in a barren environment (black) or environmental enrichment (white) during three months. Values are expressed as group mean \pm SEM; fold change vs barren environment for all genes; welch's *t*-test, Tukey post hoc; Differences between treatments are represented by * ($P < .05$). Replicates (N= 8) correspond to different individual fish.