

Region and Volcano Plot		# of DEGs	Top Genes	GO Terms
<p>A. Differential Gene Expression in LH</p>		<p>↓↓ in Stress</p> <p>254</p>	<p><i>Smin32</i> <i>Ghdc</i> <i>Bmp3</i> <i>Nmu</i></p>	<p>ribonucleoprotein complex biogenesis mRNA processing negative regulation of protein modification process</p>
<p>B. Differential Gene Expression in DMH</p>		<p>↓↓ in Stress</p> <p>238</p>	<p><i>Npw</i> <i>Lrp2</i> <i>Lrrc9</i> <i>Gpr50</i></p>	<p>ribonucleoprotein complex biogenesis cilium organization mRNA processing</p>
<p>C. Differential Gene Expression in ARC</p>		<p>↑↑ in Stress</p> <p>216</p>	<p><i>Aqp1</i> <i>Trim10</i> <i>Myo3a</i> <i>Edn3</i> <i>Ncf2</i> <i>Etfbkm1</i></p>	<p>ribonucleoprotein complex biogenesis mRNA processing ncRNA processing</p>
		<p>↓↓ in Stress</p> <p>214</p>	<p><i>Irx2</i> <i>Micall1</i> <i>Steap1</i> <i>Il18r1</i> <i>Fbxo43</i></p>	<p>actin filament organization nucleotide metabolic process regulation of neurogenesis</p>
		<p>↑↑ in Stress</p> <p>309</p>	<p><i>Gabpb2</i> <i>Izumo1</i> <i>Cd68</i> <i>Tagln</i> <i>Cbl</i> <i>Arhgap28</i> <i>Dock6</i></p>	<p>actin filament organization small GTPase mediated signal transduction cell junction assembly</p>
		<p>↑↑ in Stress</p> <p>271</p>	<p><i>Npvf</i> <i>Hmx2</i> <i>Mc3r</i> <i>Ghrh</i> <i>Nmb</i> <i>Ecm1</i></p>	<p>positive regulation of cell projection organization regulation of membrane potential regulation of neurogenesis</p>
		<p>↓↓ in Stress</p> <p>254</p>	<p><i>Zic4</i> <i>Alkbh8</i> <i>Diaph3</i> <i>Acta1</i> <i>Gpr50</i> <i>Cln1</i></p>	<p>ribonucleoprotein complex biogenesis mRNA processing negative regulation of protein modification process</p>

Fig X. Results of differential gene expression (DEGs) in A. lateral (LH), B. dorsomedial (DMH) and C. arcuate nucleus (ARC) subregions of the hypothalamus. Genes were determined to be differentially expressed if the \log_2 Fold Change was $\geq |0.2|$ and the significant (eFDR) < 0.05 . Top genes were identified as the greatest absolute value \log_2 FC with an eFDR < 0.05 . Functional modules identified by Gene Ontology enrichment analysis (GO terms) are on the right.