

Figure 1s. Genes enriched in hypothalamic brain regions. Northern blotting of RNA from tissue punches of ventrolateral preoptic area (VLPO), suprachiasmatic nucleus (SCN) or lateral hypothalamus (LH) were used to validate genes that included A) α-subunit of glycoprotein hormones (cga), B) somatostatin (smst), C) nurr1 and D) pxt2. Equal loading of RNA was determined by probing blots with cDNA to glyceraldehyde phosphate dehydrogenase (gapdh) in each case. Each lane represents pooled total RNA from tissue punches isolated from 24 animals that were separate from those used to generate RNA for microarray analysis.