

Table S1. Differently expressed genes of cluster 3 and 6 and the supposed role in relation to metabolism. Gene function is based on www.genecards.org, other sources are cited appropriately.

Cluster	Gene: Symbol	Gene: full name	Function
3	<i>Map1b</i>	microtubule associated protein 1b	Microtubule assembly/ Neurogenesis
	<i>Ptms</i>	parathymosin	DNA replication (predicted)
	<i>Proser2</i>	proline and serine rich 2	Unknown
	<i>Sesn3</i>	sestrin 3	ROS regulation, blood glucose regulation, insulin resistance, lipid storage
	<i>Dpysl3</i>	dihydropyrimidinase like 3	Filamin binding activity, actin filament organization, cell projection organization, response to axon injury
	<i>Pmepa1</i>	prostate transmembrane protein, androgen induced 1	Induced by androgens and transforming growth factor beta (TGFB), suppression of Androgen receptors and TGFB pathway
	<i>Abcg1</i>	atp binding cassette subfamily g member 1	Macrophage cholesterol and phospholipids transport, may regulate cellular lipid homeostasis in other cell types
	<i>Cdh6</i>	cadherin 6, type 2, k-cadherin (fetal kidney)	Cell differentiation and morphogenesis, kidney development
	<i>Thbs1</i>	thrombospondin 1	Mediates cell-to-cell and cell-to-matrix interaction
	<i>Il17d</i>	interleukin 17d	Cytokine activity, might be involved in obesity (Geurtsen et al. 2020)
6	<i>Sec31b</i>	sec31 homolog b, copii coat complex component	Unknown
	<i>Ube2h</i>	ubiquitin conjugating enzyme e2 h	Degradation of abnormal or short lived proteins
	<i>Ccdc78</i>	coiled-coil domain containing 78	Unknown
	<i>Loc125698117</i>	cholesterol side-chain cleavage enzyme, mitochondrial	Mitochondrial conversion of cholesterol to pregnenolone
	<i>Fbrsl1</i>	fibrosin like 1	Protein coding gene
	<i>Loc125695489</i>	synaptotagmin-5-like	Thought to bind calcium (Synaptotagmin 5)
	<i>Kdm7a</i>	lysine demethylase 7a	Enables histone demethylase activity; methylated histone binding activity; and transition metal ion binding activity. Involved in histone lysine demethylation.
	<i>Pifo</i>	primary cilia formation	Cilia disassembly (Kinzel et al. 2010)
	<i>Tmem114</i>	transmembrane protein 11	Lens and eye development
	<i>Ccdc33</i>	coiled-coil domain containing 33	Predicted to be active in peroxisome

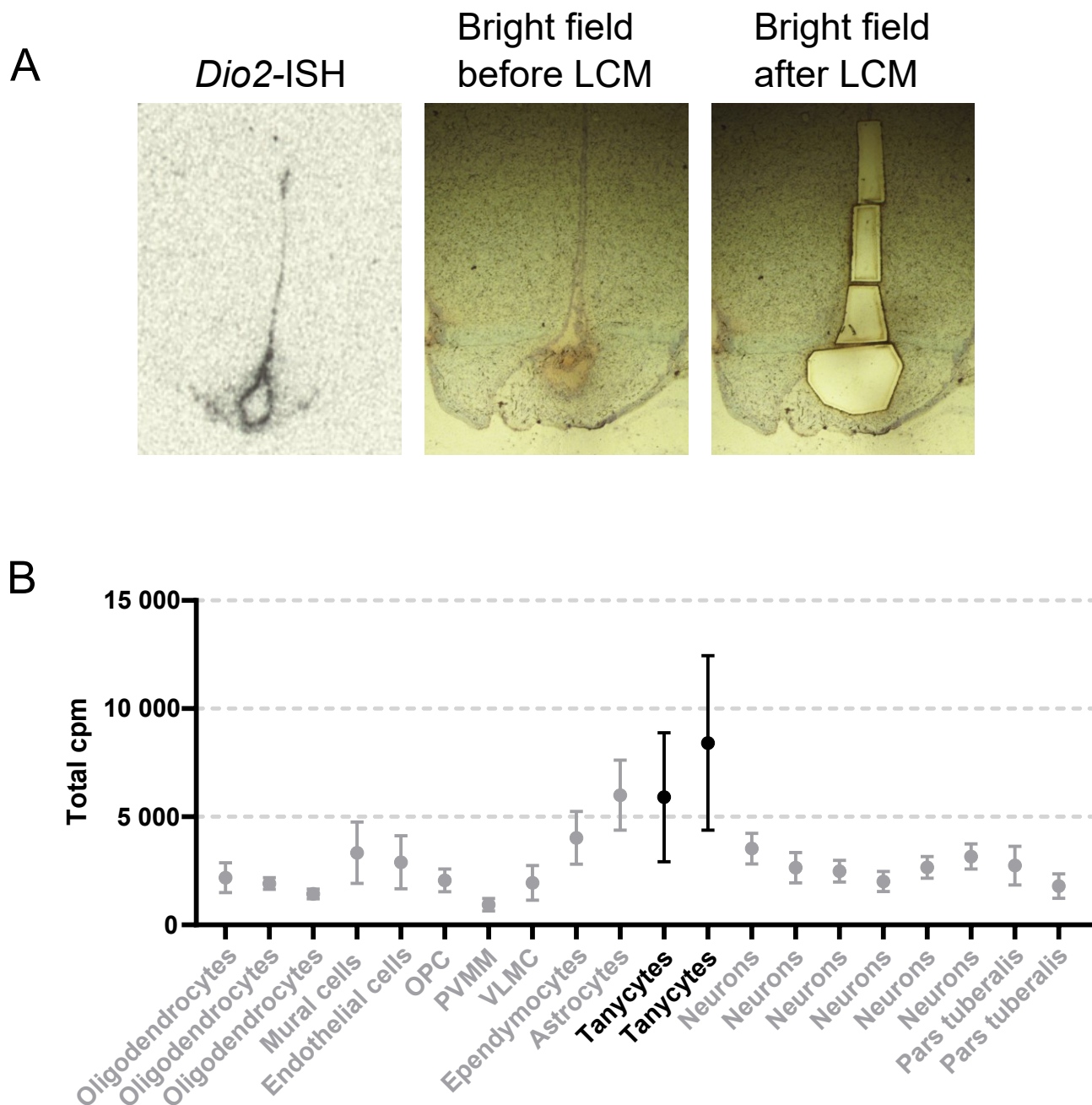


Fig. S1. Tanycytes-enriched samples. (A) Cryo-sectioned brain samples from Svalbard ptarmigan were dissected for tanycytes around the third ventricle, radioactive *Dio2 in situ* hybridization (ISH) was used as reference. Samples were collected by laser-capture microdissection (LCM); subsequently, RNA was extracted and sequenced. (B) *In silico* analysis using a single cell RNAseq dataset of the mural hypothalamus (Campbell et al., 2017) confirms enrichment of tanycytes in our samples. Data displayed as mean ± SEM.

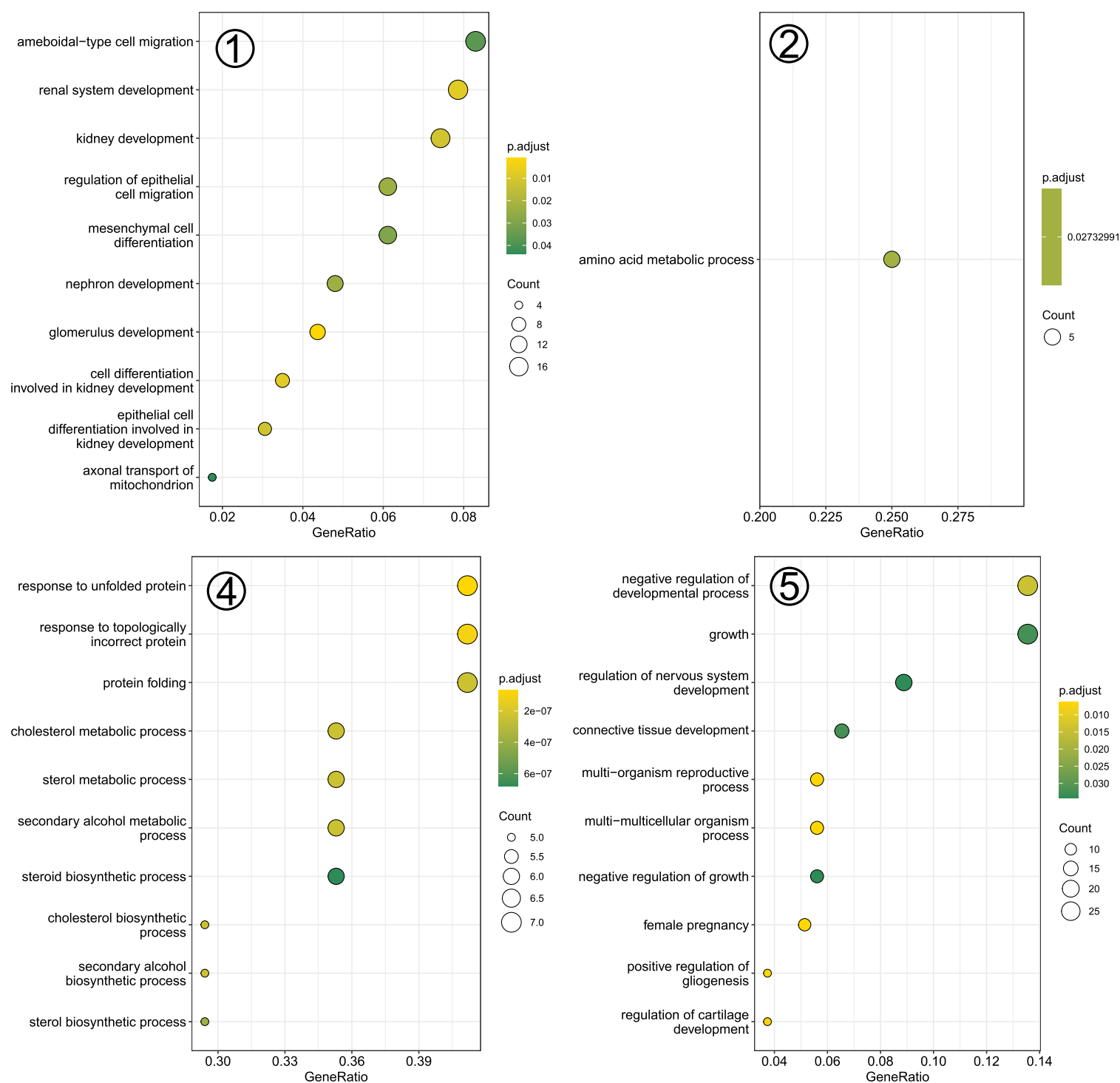


Fig. S2. GO enrichment analysis of differently expressed genes. GO analysis correspond to cluster in **Fig. 2** as indicated by the numbers. Detailed results of GO enrichment analyses can be found under <https://doi.org/10.18710/M82D10>.

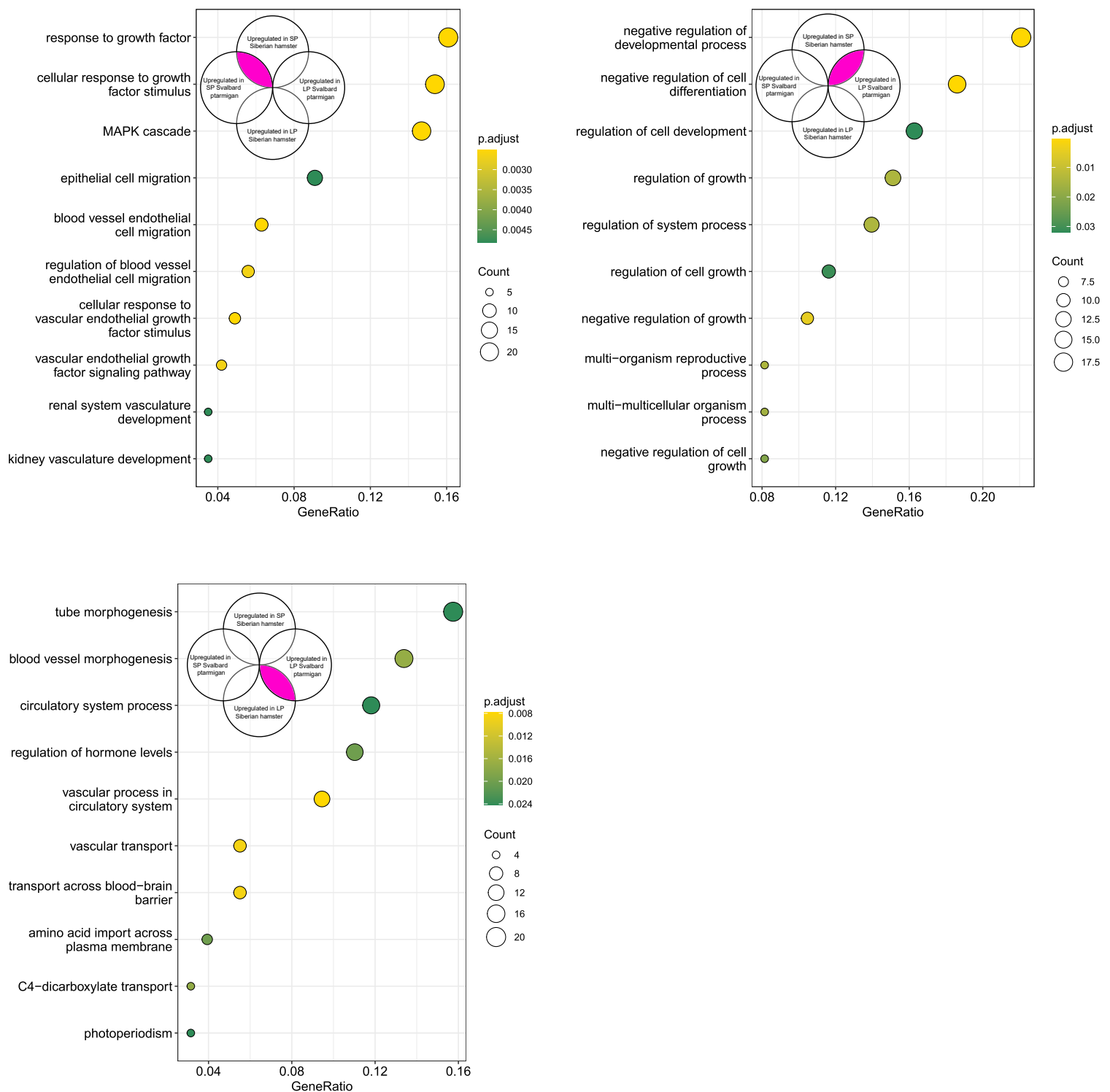


Fig. S3. GO enrichment analysis of common photoperiodic genes in Svalbard ptarmigan and Siberian hamster. Figure corresponds to **Fig. 3B**. Detailed results of GO enrichment analyses can be found under <https://doi.org/10.18710/M82D10>.