

Gene Ontology and KEGG pathway terms enriched in consensus modules among tissue pairs that significantly correlated with estrous behavior

Amygdala (AM) - Dorsal Hypothalamus (DH)								
Brown - 40 genes [AM- 0.14 (0.65), DH: 0.4 (0.16)]								
GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term	BH	
GO:0006412	<0.01	19.85	0.88	10	190	translation	<0.01	
GO:0007613	<0.01	108.58	0.03	2	6	memory	0.04	
GO:0043284	<0.01	4.05	4.58	12	924	biopolymer biosynthetic process	0.04	
GO:0009058	<0.01	4.07	5.44	13	1128	biosynthetic process	0.04	
GO:0021782	<0.01	62.01	0.04	2	9	glial cell development	0.04	
GO:0034645	<0.01	3.65	4.98	12	1005	cellular macromolecule biosynthetic process	0.06	
GO:0042063	<0.01	27.08	0.09	2	18	gliogenesis	0.06	
GO:0044237	<0.01	4.05	4.27	10	818	cellular metabolic process	0.06	
GO:0019538	0.01	3.02	5.27	11	1122	protein metabolic process	0.07	
GO:0006417	0.01	13.09	0.17	2	35	regulation of translation	0.09	
GO:0048667	0.02	11.36	0.2	2	40	cell morphogenesis involved in neuron differentiation	0.1	
GO:0048858	0.02	11.06	0.2	2	41	cell projection morphogenesis	0.1	
GO:0048856	0.02	6.13	0.56	3	117	anatomical structure development	0.1	
GO:0034960	0.02	2.43	6.91	12	1267	cellular biopolymer metabolic process	0.11	
KEGGID	Pvalue	OddsRatio	ExpCount	Count	Size	Term	BH	
3010	<0.01	62.15	0.21	7	35	Ribosome	<0.01	
5010	<0.01	8.65	0.77	5	126	Alzheimer's disease	0.02	
4260	<0.01	11.1	0.33	3	54	Cardiac muscle contraction	0.05	
4740	0.01	21.2	0.12	2	19	Olfactory transduction	0.06	

Hippocampus (HC) - Dorsal Hypothalamus (DH)								
Magenta -31 genes [HC:0.47 (0.093), DH: -0.3 (0.31)] - No significant GO terms								
KEGGID	Pvalue	OddsRatio	ExpCount	Count	Size	Term	BH	
4115	<0.01	25.78	0.11	2	52	p53 signaling pathway	0.1	
Red - 51 genes [HC: 0.62 (0.016), DH: 0.014 (0.96)] - No significant GO terms								
KEGGID	Pvalue	OddsRatio	ExpCount	Count	Size	Term	BH	
5010	<0.01	9.37	0.58	4	126	Alzheimer's disease	0.07	
Black - 45 genes [HC: 0.49 (0.078), DH: 0.026 (0.93)] - No significant GO and KEGG terms								

Blue -152 genes [HC: 0.47 (0.089), DH: 0.32 (0.28)]							
<i>GOBPID</i>	<i>Pvalue</i>	<i>OddsRatio</i>	<i>ExpCount</i>	<i>Count</i>	<i>Size</i>	<i>Term</i>	<i>BH</i>
GO:0006412	<0.01	18	2.11	23	145	translation	<0.01
GO:0043284	<0.01	3.37	14.1	33	924	biopolymer biosynthetic process	<0.01
GO:0034645	<0.01	3.16	14.9	33	985	cellular macromolecule biosynthetic process	<0.01
GO:0048143	<0.01	Inf	0.03	2	2	astrocyte activation	0.02
GO:0021782	<0.01	33.48	0.14	3	9	glial cell development	0.02
GO:0048708	<0.01	66.15	0.06	2	4	astrocyte differentiation	0.09
<i>KEGGID</i>	<i>Pvalue</i>	<i>OddsRatio</i>	<i>ExpCount</i>	<i>Count</i>	<i>Size</i>	<i>Term</i>	<i>BH</i>
3010	<0.01	91.8	0.59	18	35	Ribosome	<0.01
4260	<0.01	9.86	0.91	7	54	Cardiac muscle contraction	<0.01
5010	<0.01	5.96	2.11	10	126	Alzheimer's disease	<0.01
190	<0.01	6.66	1.69	9	101	Oxidative phosphorylation	<0.01
5012	<0.01	5.93	1.64	8	98	Parkinson's disease	<0.01
5016	<0.01	4.44	2.13	8	127	Huntington's disease	0.01
Green -59 genes [HC: 0.55 (0.039), DH: 0.26 (0.37)] - No significant GO and KEGG terms							

Amygdala (AM) - Hippocampus (HC)							
Red -52 genes [AM: -0.052 (0.86), HC: 0.48 (0.081)] - No significant GO and KEGG terms							
Pink - 34 genes [AM: -0.33 (0.25), HC: 0.47 (0.091)]							
<i>GOBPID</i>	<i>Pvalue</i>	<i>OddsRatio</i>	<i>ExpCount</i>	<i>Count</i>	<i>Size</i>	<i>Term</i>	<i>BH</i>
GO:0002440	<0.01	34.24	0.07	2	21	production of molecular mediator of immune response	0.05
GO:0007276	0.01	17.65	0.13	2	41	gamete generation	0.06
GO:0000003	0.01	7.66	0.47	3	136	reproduction	0.06
GO:0060255	0.01	4.11	2.05	6	654	regulation of macromolecule metabolic process	0.07
GO:0007242	0.03	5.19	0.68	3	202	intracellular signaling cascade	0.11
<i>KEGGID</i>	<i>Pvalue</i>	<i>OddsRatio</i>	<i>ExpCount</i>	<i>Count</i>	<i>Size</i>	<i>Term</i>	<i>BH</i>
4120	0.01	10.87	0.38	3	112	Ubiquitin mediated proteolysis	0.11
Green - 77 genes [AM: 0.32 (0.28), HC: 0.42 (0.14)]							
<i>GOBPID</i>	<i>Pvalue</i>	<i>OddsRatio</i>	<i>ExpCount</i>	<i>Count</i>	<i>Size</i>	<i>Term</i>	<i>BH</i>
GO:0006412	<0.01	25.13	1.97	25	180	translation	<0.01
GO:0044249	<0.01	5.75	8.74	28	753	cellular biosynthetic process	<0.01
GO:0009059	<0.01	4.8	9.2	27	815	macromolecule biosynthetic process	<0.01

KEGGID	Pvalue	OddsRatio	ExpCount	Count	Size	Term	BH
3010	<0.01	159.37	0.46	19	35	Ribosome	<0.01
710	<0.01	12.7	0.29	3	22	Carbon fixation in photosynthetic organisms	0.06
10	<0.01	7.8	0.6	4	46	Glycolysis / Gluconeogenesis	0.06
190	0.01	4.31	1.32	5	101	Oxidative phosphorylation	0.14

Anterior Pituitary (AP) - Dorsal Hypothalamus (DH)							
Greenyellow -74 genes [AP: 0.42 (0.14), DH: 0.0098 (0.97)] - No significant KEGG terms							
GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term	BH
GO:0031000	<0.01	Inf	0.01	2	2	response to caffeine	0.01
GO:0014070	<0.01	55.09	0.05	2	9	response to organic cyclic substance	0.05
GO:0051209	<0.01	55.09	0.05	2	9	release of sequestered calcium ion into cytosol	0.05
GO:0051238	<0.01	55.09	0.05	2	9	sequestering of metal ion	0.05
GO:0051282	<0.01	55.09	0.05	2	9	regulation of sequestering of calcium ion	0.05
GO:0001933	<0.01	48.19	0.06	2	10	negative regulation of protein amino acid phosphorylation	0.05
GO:0060401	<0.01	48.19	0.06	2	10	cytosolic calcium ion transport	0.05
GO:0045936	<0.01	42.83	0.06	2	11	negative regulation of phosphate metabolic process	0.05
GO:0019221	<0.01	27.51	0.09	2	16	cytokine-mediated signaling pathway	0.05
GO:0006936	<0.01	26.6	0.09	2	17	muscle contraction	0.05
GO:0003008	<0.01	25.05	0.1	2	18	system process	0.05
GO:0007204	<0.01	22.64	0.11	2	19	elevation of cytosolic calcium ion concentration	0.05
GO:0006457	0.01	7.6	0.45	3	81	protein folding	0.07
GO:0032504	0.01	14.78	0.15	2	28	multicellular organism reproduction	0.07
GO:0042098	0.01	14.78	0.15	2	28	T cell proliferation	0.07
GO:0055082	0.01	7.13	0.48	3	86	cellular chemical homeostasis	0.07
GO:0030155	0.01	13.72	0.17	2	30	regulation of cell adhesion	0.07
GO:0050801	0.01	6.72	0.5	3	91	ion homeostasis	0.08
GO:0007265	0.01	6.42	0.53	3	95	Ras protein signal transduction	0.09
GO:0042445	0.02	11.63	0.19	2	35	hormone metabolic process	0.09
GO:0010646	0.02	4.51	1.01	4	188	regulation of cell communication	0.09
GO:0032943	0.02	10.96	0.2	2	37	mononuclear cell proliferation	0.09
GO:0032269	0.02	10.65	0.21	2	38	negative regulation of cellular protein metabolic process	0.09
GO:0006874	0.02	9.83	0.23	2	41	cellular calcium ion homeostasis	0.09

GO:0031399	0.02	9.12	0.24	2	44	regulation of protein modification process	0.09
GO:0035023	0.02	9.12	0.24	2	44	regulation of Rho protein signal transduction	0.09
GO:0055065	0.03	8.91	0.25	2	45	metal ion homeostasis	0.1
Midnightblue - 58 genes [AP: 0.4 (0.15), DH: 0.37 (0.2)]							
<i>GOBPID</i>	<i>Pvalue</i>	<i>OddsRatio</i>	<i>ExpCount</i>	<i>Count</i>	<i>Size</i>	<i>Term</i>	<i>BH</i>
GO:0010975	<0.01	126.06	0.06	4	9	regulation of neuron projection development	<0.01
GO:0048667	<0.01	29.44	0.28	6	40	cell morphogenesis involved in neuron differentiation	<0.01
GO:0048858	<0.01	28.59	0.29	6	41	cell projection morphogenesis	<0.01
GO:0031133	<0.01	Inf	0.02	3	3	regulation of axon diameter	<0.01
GO:0010769	<0.01	105.03	0.07	4	10	regulation of cell morphogenesis involved in differentiation	<0.01
GO:0030182	<0.01	17.12	0.54	7	77	neuron differentiation	<0.01
GO:0045103	<0.01	91.76	0.06	3	8	intermediate filament-based process	<0.01
GO:0050767	<0.01	29.92	0.18	4	25	regulation of neurogenesis	<0.01
GO:0030705	<0.01	65.52	0.07	3	10	cytoskeleton-dependent intracellular transport	<0.01
GO:0045110	<0.01	Inf	0.01	2	2	intermediate filament bundle assembly	<0.01
GO:0000226	<0.01	23.09	0.22	4	32	microtubule cytoskeleton organization	<0.01
GO:0007409	<0.01	23.02	0.22	4	33	axonogenesis	<0.01
GO:0048856	<0.01	9.06	0.82	6	116	anatomical structure development	<0.01
GO:0007018	<0.01	16.93	0.29	4	41	microtubule-based movement	<0.01
GO:0032989	<0.01	10.47	0.58	5	84	cellular component morphogenesis	<0.01
GO:0060052	<0.01	153.03	0.03	2	4	neurofilament cytoskeleton organization	<0.01
GO:0008088	<0.01	153	0.03	2	4	axon cargo transport	<0.01
GO:0022603	<0.01	13.3	0.36	4	51	regulation of anatomical structure morphogenesis	0.01
GO:0032535	<0.01	24.08	0.16	3	22	regulation of cellular component size	0.01
GO:0051129	<0.01	20.79	0.18	3	25	negative regulation of cellular component organization	0.01
GO:0007613	<0.01	74.3	0.04	2	6	memory	0.01
GO:0007026	<0.01	59.43	0.05	2	7	negative regulation of microtubule depolymerization	0.01
GO:0031110	<0.01	32.99	0.08	2	11	regulation of microtubule polymerization or depolymerization	0.03
GO:0032886	<0.01	22.82	0.11	2	15	regulation of microtubule-based process	0.05
GO:0051261	<0.01	22.82	0.11	2	15	protein depolymerization	0.05
GO:0051128	0.01	20.67	0.11	2	18	regulation of cellular component organization	0.05
GO:0045595	0.01	6.19	0.73	4	104	regulation of cell differentiation	0.05
GO:0043244	0.01	19.77	0.12	2	17	regulation of protein complex disassembly	0.05

<i>GOBPID</i>	<i>Pvalue</i>	<i>OddsRatio</i>	<i>ExpCount</i>	<i>Count</i>	<i>Size</i>	<i>Term</i>	<i>BH</i>
GO:0043283	<0.01	6.46	2.23	10	246	biopolymer metabolic process	<0.01
GO:0009057	<0.01	4.62	2.86	10	441	macromolecule catabolic process	0.01
GO:0006508	<0.01	4.56	2.53	9	390	proteolysis	0.02
GO:0009395	<0.01	65.04	0.05	2	7	phospholipid catabolic process	0.02
Lightcyan - 54 genes [AP: -0.38 (0.19), DH: 0.09 (0.77)] - No significant GO and KEGG terms							
Turquoise - 343 genes [AP: -0.38 (0.18), DH: 0.22 (0.45)] - No significant GO and KEGG terms							
Magenta - 84 genes [AP: -0.42 (0.14), DH: 0.17 (0.57)] - No significant GO and KEGG terms							
Brown - 114 genes [AP: 0.39 (0.18), DH: -0.13 (0.65)] - No significant GO and KEGG terms							
Salmon - 71 genes [AP: 0.4 (0.16), DH: 0.35 (0.23)] - No significant GO and KEGG terms							
Black - 88 genes [AP: 0.4 (0.16), DH: 0.26 (0.37)] - No significant GO and KEGG terms							
Pink - 86 genes [AP: -0.34 (0.25), DH: -0.39 (0.18)] - No significant GO and KEGG terms							