De novo assembly, annotation, and characterization of the whole brain transcriptome of male and female Syrian hamsters – Supplemental Information
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Supplemental Table S1 Differential expression in male and female whole brain

A comprehensive list of the transcripts that were differentially expressed in whole brain of male and female hamsters. Expression indicates in which sex the gene was more highly expressed. If both sexes are indicated, different isoforms of the same gene were differentially expressed in males and females. Transcripts with more than one isoform that were differentially expressed in the same direction are indicated by an *. The two isoforms with the largest $\log_2$ fold change are listed here. ($\text{Log}_2\text{CPM} = \log_2$ counts per million; $\text{Log}_2\text{FC} = \log_2$ fold change; FDR = false discovery rate)

Gene ID	Gene	Uniprot ID	Expression	Log_2CPM	Log_2FC	FDR
Abcb7	ATP-binding cassette sub-family B member 7, mitochondrial	ABCB7_RAT	FEMALE	1.8682	-9.8993	8.10e-06
Abcb10	ATP-binding cassette sub-family B member 10, mitochondrial	ABCBA_MOUSE	FEMALE	0.5178	-8.4718	0.0097
Adgra1	Adhesion G protein-coupled receptor A1	AGRA1_MOUSE	FEMALE	0.798	-8.7755	0.021
Anapc1	Anaphase-promoting complex subunit 1	APC1_MOUSE	MALE	1.6556	9.6833	0.0155
Apex1	DNA-(apurinic or apyrimidinic site) lyase	APEX1_MOUSE	FEMALE	0.8734	-8.8556	0.0016
Asap3	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 3	ASAP3_MOUSE	MALE	0.3546	8.3007	0.0254
Atp13a3	Probable cation-transporting ATPase 13A3	AT133_MOUSE	FEMALE*	3.4765 2.1969	-11.5394 -10.2374	0.0002 0.0043
Atp2b1	Plasma membrane calcium-transporting ATPase 1	AT2B1_RAT	MALE	1.3529	9.3655	0.0278
Atp2c1	Calcium-transporting ATPase type 2c member 1	AT2C1_RAT	MALE	0.5279	8.49	0.0056
Bcor	BCL-6 corepressor	BCOR_MOUSE	MALE	1.7008	9.7289	1.74e-07
Bmpr1b	Bone morphogenetic protein receptor type-1B	BMR1B_MOUSE	MALE	1.6322	9.6567	2.38e-05
Brd8	Bromodomain-containing protein 8	BRD8_MOUSE	MALE	1.4198	9.437	5.49e-06
Btf3l4	Transcription factor BTF3 homolog 4	BT3L4_MOUSE	FEMALE	1.3263	-9.3357	0.0335
C1ql3	Complement C1q-like protein 3	C1QL3_MOUSE	FEMALE	2.8039	-10.8576	0.001
Ccdc186	Coiled-coil domain-containing protein 186	CC186_MOUSE	MALE	1.5801	9.6025	0.0161
Ccm2	Cerebral cavernous malformations protein 2 homolog	CCM2_MOUSE	MALE	4.4286	12.4994	2.10e-37
Ccnt1	Cyclin-T1	CCNT1_MOUSE	FEMALE	0.1306	-8.0454	0.0447

Gene ID	Gene	Uniprot ID	Expression	Log$_2$CPM	Log$_2$FC	FDR
Ccs	Copper chaperone for superoxide dismutase	CCS_RAT	FEMALE	0.7685	-6.8224	0.0056
Cdr2l	Cerebellar degeneration-related protein 2-like	CDR2L_MOUSE	FEMALE	0.5228	-6.5572	0.0278
Cep68	Centrosomal protein of 68 kDa	CEP68_MOUSE	FEMALE	0.5788	-8.5387	0.0047
Cfh	Complement factor H	CFAH_MOUSE	MALE	2.8678	10.9244	0.0007
Csgalnact1	Chondroitin sulfate N-acetylgalactosaminyltransferase 1	CGAT1_MOUSE	MALE	0.8869	8.8755	0.0009
Chd1	Chromodomain-helicase-DNA-binding protein 1	CHD1_MOUSE	MALE	0.7058	8.6822	0.0022
Chd5	Chromodomain-helicase-DNA-binding protein 5	CHD5_MOUSE	FEMALE MALE	3.2977 3.892	-11.3587 3.0283	4.34e-11 0.0036
Cherp	Calcium homeostasis endoplasmic reticulum protein	CHERP_MOUSE	MALE*	2.2514 1.3987	10.2957 9.4147	4.20e-09 2.38e-05
Cldnd1	Claudin domain-containing protein 1	CLDN1_MOUSE	FEMALE	1.4539	-9.4687	0.0434
Cluh	Clustered mitochondria protein homolog	CLU_MOUSE	MALE	1.6127	9.6364	0.0147
Cnot3	CCR4-NOT transcription complex subunit 3	CNOT3_MOUSE	MALE	1.106	9.1079	0.0001
Col11a1	Collagen alpha-1(XI) chain	COBA1_RAT	FEMALE	1.9882	-10.0225	0.0083
Cog3	Conserved oligomeric Golgi complex subunit 3	COG3_MOUSE	FEMALE MALE	1.1847 0.1754	-5.9638 8.1053	0.0073 0.0441
Col23a1	Collagen alpha-1(XXIII) chain	CONA1_RAT	MALE	0.6327	8.6053	0.0091
Cpne2	Copine-2	CPNE2_MOUSE	FEMALE	0.6616	-8.6286	0.0055
Crym	Ketimine reductase mu-crystallin	CRYM_MOUSE	MALE	1.2699	9.2809	0.0395
Ctnnal1	Alpha-catulin	CTNL1_MOUSE	FEMALE	0.2623	-8.1917	0.0184
Cit	Citron Rho-interacting kinase	CTRO_MOUSE	MALE	2.1452	10.1862	0.0148
Ddx3y	ATP-dependent RNA helicase DDX3Y	DDX3Y_MOUSE	MALE*	4.0549 3.2276	12.1236 11.2887	6.34e-35 1.38e-22
Dlk2	Protein delta homolog 2	DLK2_MOUSE	MALE	0.1694	8.0967	0.0255
Dmxl2	DmX-like protein 2	DMXL2_MOUSE	FEMALE	0.5893	-8.5503	0.0064

Gene ID	Gene	Uniprot ID	Expression	Log_2CPM	Log_2FC	FDR
Dync2h1	Cytoplasmic dynein 2 heavy chain 1	DYHC2_RAT	MALE	0.8034	6.1817	0.0143
Edc4	Enhancer of mRNA-decapping protein 4	EDC4_MOUSE	MALE	2.6383	4.8642	0.0061
Ahctf1	Protein ELYS	ELYS_MOUSE	FEMALE	1.2382	-9.2431	0.0434
Eno1	Alpha-enolase	ENOA_RAT	FEMALE	5.2262	-1.6692	0.0123
Eps15	Epidermal growth factor receptor substrate 15	EPS15_MOUSE	FEMALE	2.6397	-10.6909	0.0103
Erap1	Endoplasmic reticulum aminopeptidase 1	ERAP1_RAT	MALE	2.0498	10.0889	9.27e-06
Etfdh	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	ETFD_MOUSE	FEMALE	1.6422	-9.6655	0.0195
Ezh1	Histone-lysine N-methyltransferase EZH1	EZH1_MOUSE	MALE	0.4115	8.3644	0.0143
Fam126b	Protein FAM126B	F126B_MOUSE	MALE	1.6117	7.8203	0.0147
Fam83h	Protein FAM83H	FA83H_MOUSE	MALE	0.5042	8.4641	0.0065
Fastkd1	FAST kinase domain-containing protein 1	FAKD1_MOUSE	FEMALE	0.9663	-7.0326	0.0024
Fhl1	Four and a half LIM domains protein 1	FHL1_RAT	FEMALE	2.2709	-10.3134	4.93e-06
Flii	Protein flightless-1 homolog	FLII_MOUSE	FEMALE	2.0696	-10.1073	0.0094
Fuz	Protein fuzzy homology	FUZZY_MOUSE	FEMALE	1.3708	-9.3818	1.00e-05
Fzr1	Fizzy-related protein homolog	FZR_MOUSE	MALE	0.2916	8.2326	0.0243
Gata2	Endothelial transcription factor GATA-2	GATA2_RAT	MALE	0.4306	6.5356	0.0335
Slc25a22	Mitochondrial glutamate carrier 1	GHC1_MOUSE	MALE	0.8264	8.8105	0.0036
Gria3	Glutamate receptor 3	GRIA3_MOUSE	MALE	3.1849	11.2452	0.0016
Slc2a8	Solute carrier family 2, facilitated glucose transporter member 8	GTR8_RAT	FEMALE	1.4321	-9.4458	7.50e-06
Hcfc2	Host cell factor 2	HCFC2_RAT	FEMALE	0.7009	-8.6703	0.0044
Hdac5	Histone deacetylase 5	HDAC5_CRIGR	MALE	1.4015	9.4178	5.90e-06

Gene ID	Gene	Uniprot ID	Expression	Log_2CPM	Log_2FC	FDR
Hepacam	Hepatocyte cell adhesion molecule	HECAM_MOUSE	MALE	0.2913	8.2318	0.0155
Hes5	Transcription factor HES-5	HES5_RAT	MALE	0.4392	8.3943	0.001
Hipk2	Homeodomain-interacting protein kinase 2	HIPK2_MESAU	FEMALE	0.2245	-8.1497	0.02
Hsp90ab1	Heat shock protein HSP 90-beta	HS90B_RAT	FEMALE	0.4423	-8.3901	0.0145
Ift172	Intraflagellar transport protein 172 homolog	IF172_MOUSE	MALE	0.6419	8.6126	0.0055
Eif5	Eukaryotic translation initiation factor 5	IF5_MOUSE	FEMALE	1.9854	-10.02	0.0067
Ppa2	Inorganic pyrophosphatase 2, mitochondrial	IPYR2_MOUSE	MALE	0.2085	8.1406	0.0236
Kiaa0556	Uncharacterized protein KIAA0556	K0556_MOUSE	FEMALE	1.2715	-9.2776	2.73e-05
Kansl1l	KAT8 regulatory NSL complex subunit 1-like protein	KAL1L_MOUSE	MALE	0.5851	8.5525	0.0044
Kctd15	BTB/POZ domain-containing protein KCTD15	KCD15_MOUSE	MALE	0.0662	7.9819	0.044
Kcng4	Potassium voltage-gated channel subfamily G member 4	KCNG4_MOUSE	MALE	2.0261	10.0649	4.52e-08
Kdm1b	Lysine-specific histone demethylase 1B	KDM1B_MOUSE	FEMALE	0.0825	-7.9911	0.0401
Kdm5c	Lysine-specific demethylase 5C	KDM5C_MOUSE	MALE	0.9258	8.9171	0.0006
Kdm5d	Lysine-specific demethylase 5D	KDM5D_MOUSE	MALE*	2.6350 2.3792	10.6875 10.3741	1.03e-13 2.19e-11
Kdm6a	Lysine-specific demethylase 6A	KDM6A_MOUSE	FEMALE MALE*	1.6742 2.459 1.8701	-9.6982 10.5080 9.9039	2.53e-07 1.78e-12 2.40e-08
Kif9	Kinesin-like protein KIF9	KIF9_MOUSE	MALE	0.0779	7.9955	0.0407
Krcc1	Lysine-rich coiled-coil protein 1	KRCC1_MOUSE	FEMALE	1.7253	-9.7512	1.60e-06
Rps6ka2	Ribosomal protein S6 kinase alpha-2	KS6A2_MOUSE	MALE	0.8603	8.8476	0.0008
Faim2	Protein lifeguard 2	LFG2_RAT	FEMALE	1.4259	-9.4389	0.0254
Lin7b	Protein lin-7 homolog B	LIN7B_RAT	FEMALE*	1.1887 0.3157	-9.1904 -8.2504	4.51e-05 0.0173

Gene ID	Gene	Uniprot ID	Expression	Log_2CPM	Log_2FC	FDR
L3mbtl3	Lethal(3)malignant brain tumor-like protein 3	LMBL3_MOUSE	MALE	0.3534	8.3013	0.0189
Aatk	Serine/threonine-protein kinase LMTK1	LMTK1_MOUSE	MALE	0.7763	8.7569	0.0044
Lrig2	Leucine-rich repeats and immunoglobulin-like domains protein 2	LRIG2_MOUSE	MALE	2.0019	10.0396	3.73e-09
Lrp3	Low-density lipoprotein receptor-related protein 3	LRP3_RAT	MALE	0.3543	8.3007	0.0139
Tmem57	Macoilin	MACOI_MOUSE	MALE	1.5568	9.5797	3.06e-06
Mamld1	Mastermind-like domain-containing protein 1	MAMD1_MOUSE	MALE	0.8445	8.8306	0.0013
Map6	Microtubule-associated protein 6	MAP6_MOUSE	FEMALE	3.5744	-11.6383	0.0003
Matk	Megakaryocyte-associated tyrosine-protein kinase	MATK_MOUSE	FEMALE	0.5071	-8.4606	0.0099
Mga	MAX gene-associated protein	MGAP_MOUSE	MALE	2.0658	10.1059	0.0056
Mgat5	Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A	MGT5A_CRIGR	FEMALE	1.5922	-9.613	8.77e-07
Mink1	Misshapen-like kinase 1	MINK1_MOUSE	FEMALE	4.1235	-12.1920	6.33e-05
Mapk13	Mitogen-activated protein kinase 13	MK13_MOUSE	MALE	0.5931	8.5596	0.0094
Mobp	Myelin-associated oligodendrocyte basic protein	MOBP_MOUSE	MALE*	2.6728 0.9115	10.7258 8.9032	1.66e-10 0.0142
Mpeg1	Macrophage-expressed gene 1 protein	MPEG1_MOUSE	FEMALE	1.6734	-9.6972	0.0142
Cdc42bpb	Serine/threonine-protein kinase MRCK beta	MRCKB_MOUSE	MALE*	1.2818 4.8863	9.293 12.9594	0.0389 9.02e-45
Mreg	Melanoregulin	MREG_MOUSE	FEMALE	0.691	-8.6604	0.011
Msl3	Male-specific lethal 3 homolog	MS3L1_MOUSE	MALE	1.6052	9.6285	0.0173
N4bp2l1	NEDD4-binding protein 2-like 1	N42L1_MOUSE	MALE*	1.7175 1.2462	9.7463 9.2553	4.40e-07 2.99e-05
Neurl4	Neuralized-like protein 4	NEUL4_MOUSE	FEMALE	1.9839	-10.0185	1.70e-08
Nfyc	Nuclear transcription factor Y subunit gamma	NFYC_RAT	FEMALE	0.7236	-6.7245	0.021
Olfm2	Noelin-2	NOE2_RAT	FEMALE	2.7037	-10.7557	0.0132

Gene ID	Gene	Uniprot ID	Expression	Log$_2$CPM	Log$_2$FC	FDR
Nrdc	Nardilysin	NRDC_MOUSE	MALE	0.4011	8.3516	0.0112
Nsun5	Probable 28S rRNA (cytosine-C(5))-methyltransferase	NSUN5_MOUSE	MALE	1.3223	9.3338	0.0044
Nudcd3	NudC domain-containing protein 3	NUDC3_MOUSE	MALE	2.0976	10.138	4.20e-09
Oma1	Metalloendopeptidase OMA1, mitochondrial	OMA1_MOUSE	FEMALE	0.9356	-6.9995	0.0023
Otof	Otoferlin	OTOF_RAT	MALE	0.2185	8.1531	0.0335
Pawr	PRKC apoptosis WT1 regulator protein	PAWR_MOUSE	FEMALE	0.7591	-8.7334	0.0023
Pcdhb14	Protocadherin beta-14	PCDBE_MOUSE	FEMALE	1.3663	-9.3771	7.89e-06
Pcnx	Pecanex-like protein 1	PCX1_MOUSE	MALE	2.2225	5.6478	1.99e-05
Per3	Period circadian protein homolog 3	PER3_RAT	FEMALE	2.2536	-8.3834	0.0094
Rabggta	Geranylgeranyl transferase type-2 subunit alpha	PGTA_RAT	MALE	0.5895	8.5586	0.01
Phyhip	Phytanoyl-CoA hydroxylase-interacting protein	PHYIP_RAT	FEMALE	2.5971	-10.6471	2.02e-12
Pitpna	Phosphatidylinositol transfer protein alpha isoform	PIPNA_MOUSE	FEMALE MALE	2.0014 2.1982	-8.1146 5.7933	6.06e-08 0.0003
Plec	Plectin	PLEC_CRIGR	MALE	1.7266	9.7561	0.0125
Plod3	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	PLOD3_MOUSE	MALE	0.543	8.5086	0.0141
Plxnb2	Plexin-B2	PLXB2_MOUSE	MALE	2.7341	10.7881	6.75e-15
Ppp1r3e	Protein phosphatase 1 regulatory subunit 3E	PPR3E_MOUSE	MALE	0.1543	8.0792	0.0436
Prex2	Phosphatidylinositol 3,4,5-triphosphate-dependent Rac exchanger 2 protein	PREX2_MOUSE	MALE	1.7503	4.3581	0.0205
Primpol	DNA-directed primase/polymerase protein	PRIPO_MOUSE	MALE	0.3368	8.2826	0.0143
Prkra	Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA_RAT	MALE	1.4564	9.4753	0.024
Ptprn	Receptor-type tyrosine-protein phosphatase-like N	PTPRN_RAT	MALE	1.8027	9.8332	0.0094
Ptpro	Receptor-type tyrosine-protein phosphatase O	PTPRO_MOUSE	MALE	0.0993	8.0179	0.0458

Gene ID	Gene	Uniprot ID	Expression	Log$_2$CPM	Log$_2$FC	FDR
Pus7l	Pseudouridylate synthase 7 homolog-like protein	PUS7L_MOUSE	FEMALE	0.3236	-8.2596	0.0165
Rb1cc1	RB1-inducible coiled-coil protein 1	RBCC1_MOUSE	MALE	0.5686	8.5351	0.0069
Rbm45	RNA-binding protein 45	RBM45_RAT	FEMALE	1.7605	-9.7882	0.0173
Rexo1	RNA exonuclease 1 homolog	REXO1_MOUSE	MALE	0.2996	8.2417	0.0165
Rfx5	DNA-binding protein Rfx5	RFX5_MOUSE	FEMALE MALE*	8.3022 4.1427 3.1396	-7.1923 1.8574 2.3186	2.60e-25 0.0061 0.0123
Rgs8	Regulator of G-protein signaling 8	RGS8_RAT	MALE	5.2094	6.2431	1.02e-09
Riok1	Serine/threonine-protein kinase RIO1	RIOK1_MOUSE	MALE	0.1161	8.0368	0.0363
Rnf212	Probable E3 SUMO-protein ligase RNF212	RN212_MOUSE	MALE	0.6076	5.9705	0.0401
Rapgef2	Rap guanine nucleotide exchange factor 2	RPGF2_MOUSE	MALE	1.4172	9.434	7.59e-06
Rreb1	Ras-responsive element-binding protein 1	RREB1_MOUSE	MALE	0.9079	8.8995	0.0034
Rtf1	RNA polymerase-associated protein RTF1 homolog	RTF1_MOUSE	FEMALE	1.9768	-10.0117	0.012
Rubcn	Run domain Beclin-1-interacting and cysteine-rich domain containing protein	RUBIC_MOUSE	FEMALE	1.2494	-5.6551	0.0088
Slc12a6	Solute carrier family 12 member 6	S12A6_MOUSE	FEMALE	2.0197	-10.0551	0.0062
Sec61a1	Protein transport protein Sec61 subunit alpha isoform 1	S61A1_RAT	MALE	0.5554	8.5207	0.0085
Sec22c	Vesicle-trafficking protein SEC22c	SC22C_MOUSE	FEMALE	0.731	-8.7037	0.0123
Sdccag3	Serologically defined colon cancer antigen 3 homolog	SDCG3_MOUSE	MALE	1.2292	9.2385	0.0437
Setd5	SET domain-containing protein 5	SETD5_MOUSE	MALE	2.3497	10.3963	5.75e-12
St6galnac4	Alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3-N-acetyl-galactosaminide alpha-2,6-sialyltransferase	SIA7D_MOUSE	MALE	0.7586	8.7371	0.0125
Snx24	Sorting nexin-24	SNX24_RAT	FEMALE	0.0997	-8.0101	0.0361
Spata7	Spermatogenesis-associated protein 7 homolog	SPAT7_MOUSE	MALE	1.7324	7.9474	0.031

Gene ID	Gene	Uniprot ID	Expression	Log$_2$CPM	Log$_2$FC	FDR
Stra6	Stimulated by retinoic acid gene 6 protein homolog	STRA6_RAT	FEMALE	0.4312	-8.3769	0.022
Suco	SUN domain-containing ossification factor	SUCO_MOUSE	MALE	1.3462	9.36	9.65e-06
Sympk	Symplekin	SYMPK_MOUSE	MALE	1.3501	5.3435	0.0441
Rars	Arginine--tRNA ligase, cytoplasmic	SYRC_CRIGR	FEMALE	2.7887	-10.8424	0.0011
Tll1	Tolloid-like protein 1	TLL1_MOUSE	FEMALE MALE	1.0197 0.3631	-6.2939 8.3103	0.0061 0.0125
Tmem18	Transmembrane protein 18	TMM18_RAT	FEMALE	2.0363	-10.0726	6.31e-09
Txnrd3	Thioredoxin reductase 3	TRXR3_MOUSE	FEMALE	0.4357	-8.383	0.0139
Txndc11	Thioredoxin domain-containing protein 11	TXD11_MOUSE	FEMALE	1.5653	-7.6703	0.0044
Tyk2	Non-receptor tyrosine-protein kinase TYK2	TYK2_MOUSE	FEMALE	1.5463	-9.5649	0.0193
Usp14	Ubiquitin carboxyl-terminal hydrolase 14	UBP14_MOUSE	MALE	0.8542	8.8392	0.0119
Usp16	Ubiquitin carboxyl-terminal hydrolase 16	UBP16_RAT	MALE	0.4519	8.4082	0.0098
Unc13a	Protein unc-13 homolog A	UN13A_MOUSE	MALE	2.0976	5.732	0.0026
Usp9x	Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X_MOUSE	MALE*	3.6714 3.1267	11.7372 11.1865	5.86e-27 1.48e-18
Uty	Histone demethylase UTY	UTY_MOUSE	MALE*	2.8309 1.6003	10.8864 9.6247	1.26e-16 8.76e-07
Vmn2r116	Vomeronasal type-2 receptor 116	V2116_MOUSE	FEMALE	0.3412	-8.2786	0.0143
Vasp	Vasodilator-stimulated phosphoprotein	VASP_MOUSE	FEMALE	0.2785	-8.2087	0.0401
Hdlbp	Vigilin	VIGLN_MOUSE	MALE	0.2214	8.1544	0.0203
Vps13c	Vacuolar protein sorting-associated protein	VP13C_MOUSE	MALE	4.0828	8.1066	4.31e-21
Wdfy3	WD repeat and FYVE domain-containing protein 3	WDFY3_MOUSE	MALE	1.3295	6.2107	0.0045
Wiz	Protein Wiz	WIZ_MOUSE	FEMALE	2.1174	-10.156	1.11e-08
Wnk2	Serine/threonine-protein kinase WNK2	WNK2_MOUSE	MALE	1.7661	9.797	4.56e-06

Gene ID	Gene	Uniprot ID	Expression	Log$_2$CPM	Log$_2$FC	FDR
Xpo4	Exportin-4	XPO4_MOUSE	FEMALE	1.2088	-9.2121	0.0458
Yme1l1	ATP-dependent zinc metalloprotease YME1L1	YMEL1_MOUSE	MALE	0.8076	5.6701	0.0193
Zbtb46	Zinc finger and BTB domain-containing protein 46	ZBT46_MOUSE	MALE	0.6018	8.5702	0.0038
Zfyve16	Zinc finger FYVE domain-containing protein 16	ZFY16_MOUSE	FEMALE	0.4596	-8.409	0.0193
Znf569	Zinc finger protein 569	ZN569_MOUSE	FEMALE	0.4599	-8.4091	0.0077
Znf18	Zinc finger protein 18	ZNF18_RAT	FEMALE MALE	-4.8543 2.0655	3.2728 3.8641	0.0031 0.0293
Zswim6	Zinc finger SWIM domain-containing protein 6	ZSWM6_MOUSE	MALE	2.5167	10.5679	0.0044

Supplemental Table S2 Gene ontology enrichment analysis

A comprehensive list of the 142 gene ontology (GO) terms that were enriched in male hamster brains compared with female hamster brains.
(BP = biological process; CC = cellular component; MF = molecular function; FDR = false discovery rate)

GO term	Ontology	Over-represented FDR
Cardiac muscle cell contraction	BP	7.52E-09
Cerebellar cortex structural organization	BP	0
T cell antigen processing and presentation	BP	2.09E-07
Regulation of forebrain neuron differentiation	BP	0.0236
Notochord morphogenesis	BP	0.001
Mesodermal cell differentiation	BP	0.001
Somite rostral/caudal axis specification	BP	0.0005
Histone H3-K27 demethylation	BP	0.0011
Histone H3-K4 demethylation	BP	4.49E-06
Respiratory system process	BP	0.001
Actin-mediated cell contraction	BP	7.58E-06
Cardiovascular system development	BP	0.003
Histone H3-K36 demethylation	BP	4.49E-06
Anatomical structure arrangement	BP	7.09E-08
Histone lysine demethylation	BP	8.82E-13

GO term	Ontology	Over-represented FDR
Histone demethylation	BP	8.82E-13
Protein demethylation	BP	8.82E-13
Protein dealkylation	BP	8.82E-13
Regulation of chromatin silencing	BP	3.13E-05
Translational initiation	BP	7.09E-08
Demethylation	BP	1.69E-11
BMP signaling pathway	BP	1.99E-07
Chromosome segregation	BP	4.51E-15
Axon extension	BP	1.03E-05
Anterior/posterior axis specification	BP	0.0152
Respiratory gaseous exchange	BP	0.0227
Embryonic axis specification	BP	0.0273
Regulation of gene silencing	BP	0.0006
Neural tube development	BP	0.0004
Actin filament-based movement	BP	0.0008
RNA secondary structure unwinding	BP	7.52E-06
Cellular response to transforming growth factor beta stimulus	BP	0.0001
Heart morphogenesis	BP	0.0006
Transforming growth factor beta receptor signaling pathway	BP	1.75E-05
Neuron projection extension	BP	0.0001
Response to transforming growth factor beta	BP	0.0002
Antigen processing and presentation	BP	0.0008
Canonical Wnt signaling pathway	BP	0.0011
Hippocampus development	BP	0.0003
Post-embryonic development	BP	0.001
Neuron migration	BP	5.44E-05
Developmental cell growth	BP	0.0009
Transmembrane receptor protein serine/threonine kinase signaling pathway	BP	0.0003
Protein deubiquitination	BP	0.0007
Developmental growth involved in morphogenesis	BP	0.003

GO term	Ontology	Over-represented FDR
Cell growth	BP	0.0009
Chordate embryonic development	BP	5.63E-08
Embryo development ending in birth or egg hatching	BP	5.76E-08
In utero embryonic development	BP	2.81E-07
Heart development	BP	7.53E-06
Embryonic organ development	BP	0.008
Embryo development	BP	1.99E-07
Protein modification by small protein removal	BP	0.002
Epithelium development	BP	0.0092
Mitotic nuclear division	BP	0.0004
Tube development	BP	0.0361
Developmental growth	BP	0.0115
Histone modification	BP	9.25E-06
Cellular response to growth factor stimulus	BP	0.0073
Growth	BP	0.0002
Covalent chromatin modification	BP	1.06E-05
Nuclear division	BP	0.0027
Response to growth factor	BP	0.0144
Organelle fission	BP	0.0045
Chromatin modification	BP	2.61E-05
Ubiquitin-dependent protein catabolic process	BP	0.0162
Modification-dependent protein catabolic process	BP	0.0178
Chromatin organization	BP	6.61E-05
Modification-dependent macromolecule catabolic process	BP	0.02
Organ morphogenesis	BP	0.0408
Proteolysis involved in cellular protein catabolic process	BP	0.0114
Cell division	BP	0.0197
Proteolysis	BP	0.0375
Movement of cell or subcellular component	BP	0.0139
Cellular protein modification process	BP	5.56E-06

GO term	Ontology	Over-represented FDR
Protein modification process	BP	5.56E-06
Macromolecule modification	BP	2.16E-05
Single-organism organelle organization	BP	0.0023
Cellular protein metabolic process	BP	4.97E-05
Protein metabolic process	BP	4.83E-06
Anatomical structure development	BP	0.0067
Regulation of gene expression	BP	9.61E-05
Organelle organization	BP	0.0064
Regulation of transcription, DNA-templated	BP	0.0061
Regulation of nucleic acid-templated transcription	BP	0.0065
Regulation of RNA biosynthetic process	BP	0.0065
Regulation of RNA metabolic process	BP	0.0142
Regulation of macromolecule biosynthetic process	BP	0.0341
Regulation of cellular macromolecule biosynthetic process	BP	0.0441
Regulation of macromolecule metabolic process	BP	0.0012
Regulation of biosynthetic process	BP	0.0462
Macromolecule metabolic process	BP	1.95E-06
Cellular macromolecule metabolic process	BP	4.16E-05
Cellular component organization	BP	0.0176
Cellular component organization or biogenesis	BP	0.0217
Regulation of metabolic process	BP	0.0115
Primary metabolic process	BP	0.0006
Organic substance metabolic process	BP	0.0024
Metabolic process	BP	0.005
Cellular metabolic process	BP	0.0309
Apical part of cell	CC	2.47E-06
Cytoplasmic ribonucleoprotein granule	CC	0.0001
Ribonucleoprotein granule	CC	0.0002
Histone methyltransferase complex	CC	0.0335
Methyltransferase complex	CC	0.0491

GO term	Ontology	Over-represented FDR
Growth cone	CC	0.02
Site of polarized growth	CC	0.0234
Co-SMAD binding	MF	0
Histone demethylase activity (H3-K27 specific)	MF	2.78E-08
Histone demethylase activity (H3-K36 specific)	MF	1.27E-06
Histone demethylase activity (H3-K4 specific)	MF	2.66E-06
Histone demethylase activity	MF	3.71E-13
Demethylase activity	MF	8.82E-13
Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	MF	1.72E-12
SMAD binding	MF	2.63E-06
Dioxygenase activity	MF	7.36E-11
Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	MF	1.28E-08
ATP-dependent RNA helicase activity	MF	0.0005
RNA-dependent atpase activity	MF	0.0005
RNA helicase activity	MF	0.0006
Ubiquitinyl hydrolase activity	MF	0.0003
ATP-dependent helicase activity	MF	0.001
Purine NTP-dependent helicase activity	MF	0.001
Cysteine-type peptidase activity	MF	0.0041
Helicase activity	MF	0.003
RNA polymerase II core promoter proximal region sequence-specific DNA binding	MF	0.0225
Core promoter proximal region sequence-specific DNA binding	MF	0.0264
Core promoter proximal region DNA binding	MF	0.028
Atpase activity, coupled	MF	0.005
RNA polymerase II regulatory region sequence-specific DNA binding	MF	0.0399
RNA polymerase II regulatory region DNA binding	MF	0.0491
Atpase activity	MF	0.0028
Peptidase activity, acting on L-amino acid peptides	MF	0.0176

GO term	Ontology	Over-represented FDR
Oxidoreductase activity	MF	0.0045
Peptidase activity	MF	0.02
Pyrophosphatase activity	MF	0.0273
Hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	MF	0.0275
Hydrolase activity, acting on acid anhydrides	MF	0.0278
Nucleoside-triphosphatase activity	MF	0.0441
Hydrolase activity	MF	0.047
Catalytic activity	MF	0.0014