

Table 1. Transcripts enriched in CA neurons

Gene name	Genebank Accession	RATIO SN	RATIO VTA	RATIO A13	RATIO LC	Mean signal SN	Mean signal VTA	Mean signal A13	Mean signal LC
Tyrosine hydroxylase	M10244	283	277	150	202	20,496	32,289	37,182	30,018
Vesicular monoamine transporter 2	A46374	249	210	68	177	37,401	48,389	47,620	44,041
Dopa decarboxylase	M27716	77	69	41	28	49,286	55,040	58,930	47,115
GTP cyclohydrolase I	A39080	36	71	27	69	11,091	23,641	16,913	28,805
Collagen type II	L48440	25	13	11	28	4,268	2,862	3,745	7,964
Peripherin	AF031878	12	10	17	33	1,837	2,430	4,459	4,449
Hypothetical protein LOC313453	AY327410	25	29	6	11	25,935	40,122	28,998	32,930
Glutathione peroxidase	D00680	5	7	16	41	4,072	7,262	17,621	22,780
Pterin-4- α -carbinolamine dehydratase	AJ005542	7	10	14	17	11,647	17,660	31,593	31,708
Decay-accelerating factor	AB032395	13	14	9	9	6,786	6,300	6,491	6,771
MHC I [RT1.A3(O) α chain]	X90374	14	12	9	9	1,660	1,654	1,735	2,026
Polysialyltransferase 1	X83562	5	8	20	8	865	1,326	3,693	2,049
EST	BQ781749	10	10	8	9	5,592	7,065	8,361	9,450
EST	BM391695	14	8	7	6	2,324	2,071	2,870	2,063
Cell growth regulator 11	U66470	10	7	5	11	14,481	14,295	16,186	24,955
EST similar to vesicular membrane protein	BE115561	7	9	9	7	10,392	13,920	20,621	16,822
Argininosuccinate synthetase	BC063146	5	7	9	10	2,407	3,776	6,214	5,336
EST similar to erythrocyte protein band 4.1-like 4b	AI175220	5	8	6	12	1,033	1,612	1,886	3,596
Dopamine receptor interacting protein calcyon	AF303658	6	8	7	8	15,475	22,949	29,626	26,852
2,3-oxidosqualene:lanosterol cyclase	D45252	10	7	4	8	7,213	6,940	7,017	10,912
EST similar to LOC298366	XM_216483	7	7	10	6	2,161	2,624	4,915	3,809
EST	BE107813	6	4	9	9	689	732	1,300	1,175
Thymosin β -10	M58404	8	7	5	8	12,767	14,819	18,510	21,313
Arginine methyltransferase (PRMT2)	AF169620	6	6	7	8	7,366	9,795	14,601	13,730
Apoptosis repressor with CARD domain	U40627	6	6	5	9	3,139	3,778	4,548	7,197
EST similar to mKIAA1402 protein (LOC296733)	CB325657	8	5	5	8	3,842	3,580	5,016	7,011
EST similar to tumor antigen se20-4 (LOC302612)	XM_217607	5	7	7	7	10,188	14,690	21,478	17,457
Intracellular chloride channel CLIC3	XM_238312	5	7	6	5	883	1,105	1,441	1,236
Phosphofructokinase 1	X58865	7	5	5	7	1,945	1,816	2,600	3,118
Similar to RIKEN cDNA 2310037B18 (LOC304323)	XM_221949	6	5	5	6	951	1,054	1,412	1,619
EST similar to LOC361521	XM_341806	6	5	6	5	4,678	5,600	8,404	8,148
EST similar to WD repeat protein (LOC305349)	XM_223412	6	7	4	5	2,407	3,939	4,100	3,637
150 kDa oxygen-regulated protein	U41853	5	6	6	5	4,561	6,060	8,111	6,970
EST	BG665699	5	6	5	5	6,059	7,419	9,946	9,687
Protein phosphatase 4	XM_341929	5	4	5	7	1,702	1,764	2,611	3,530
Neural cell adhesion molecule	X06564	5	5	6	5	5,295	8,315	13,024	9,498
EST	BE120180	5	5	5	4	4,291	5,967	7,314	6,833

Genes with significant measurements across replicates were selected by one-class SAM (false-discovery rate, <1%). Transcripts that are >4-fold enriched over whole brain in all cell groups are listed. Abbreviations: CA, catecholaminergic; LC, locus coeruleus; SN, substantia nigra; VTA, ventral tegmental area.