Table S2. Haloperidol-induced gene expression changes in striatal tissue of A/J mice that were reversed by cystamine co-administration. Genes whose mRNAs had a haloperidol-induced absolute fold change >1.5 in their striatal expression level (relative to untreated control), and with an adjusted p-value <0.1 in the co-variant models used for analyzing the microarray data, are listed. The fold change (FC) and p-values for each of the indicated pair-wise comparisons, as well as the quantile-normalized raw intensity microarray data for each gene in the indicated treatment group are shown. The treatment groups were: Hal: haloperidol; Cys+Hal: cystamine and haloperidol co-administration; ctrl: vehicle control.

Symbol	**A/J_ Hal_vs_Ctrl**		**A/J_ Cys+Hal_vs_Ctrl**		**C57BL/6_ Hal_vs_Ctrl**		**Normalized Intensity**				
	FC	**p_value**	**FC**	**p_value**	**FC**	**p_value**	**A/J_Ctrl**	**A/J_Hal**	**A/J_CysHal**	**C57BL/6_Ctrl**	**C57BL/6_Hal**
1110059M19Rik	0.58	0.02	0.62	0.04	1.16	0.66	6.62	5.84	5.93	6.48	6.69
2310022B05Rik	0.67	0.08	0.78	0.27	0.93	0.57	11.18	10.60	10.83	11.06	10.95
2310051E17Rik	1.51	0.03	1.60	0.02	1.03	0.85	8.74	9.34	9.42	9.01	9.05
2810046M22Rik	0.59	0.08	0.63	0.12	1.67	0.24	7.32	6.56	6.65	6.81	7.54
2900017F05Rik	0.54	0.03	0.71	0.19	1.29	0.30	7.56	6.66	7.06	7.73	8.10
3110035E14Rik	3.63	0.06	1.87	0.32	1.91	0.29	9.18	11.03	10.08	9.29	10.22
4632428D17Rik	1.51	0.07	1.16	0.47	1.30	0.12	5.92	6.51	6.14	5.78	6.16
4933437K13Rik	0.66	0.01	0.81	0.11	0.90	0.36	7.37	6.78	7.07	7.34	7.20
9130024F11Rik	2.88	0.08	1.71	0.35	1.94	0.26	6.55	8.07	7.32	6.29	7.25
9530064J02	1.52	0.10	1.22	0.41	1.47	0.16	12.09	12.69	12.37	11.58	12.13
A130082M07Rik	0.58	0.09	0.72	0.28	1.00	0.98	7.14	6.34	6.65	6.35	6.34
A130090K04Rik	2.11	0.11	1.52	0.35	1.58	0.31	7.53	8.61	8.13	7.52	8.17
A430103B12Rik	0.59	0.03	0.74	0.17	1.07	0.69	7.94	7.18	7.50	7.64	7.73
A830021M18	1.74	0.02	1.13	0.56	1.27	0.20	6.76	7.56	6.95	6.42	6.76
Adamtsl4	0.65	0.05	0.83	0.36	0.81	0.11	8.02	7.41	7.76	8.09	7.79
AI875142	1.70	0.07	1.27	0.39	1.26	0.35	11.13	11.90	11.47	11.50	11.83
Akr1c18	1.50	0.05	1.30	0.18	1.31	0.14	5.61	6.20	5.98	5.67	6.06
Alox12b	2.12	0.02	1.45	0.22	1.53	0.08	6.36	7.44	6.90	6.29	6.90
Anxa11	1.64	0.03	1.24	0.30	1.28	0.10	7.61	8.33	7.92	7.56	7.92
Aqp1	0.47	0.01	0.45	0.01	1.47	0.41	7.38	6.29	6.24	6.84	7.40
Arc	1.65	0.16	1.04	0.90	0.60	0.04	9.12	9.85	9.19	9.74	9.01
Arhgap15	1.85	0.05	1.29	0.38	1.44	0.23	6.12	7.01	6.49	6.12	6.64
Bmp3	1.53	0.07	1.07	0.75	1.05	0.71	5.93	6.54	6.02	5.90	5.96
C130074G19Rik	1.83	0.04	1.24	0.43	1.11	0.38	6.90	7.78	7.22	6.90	7.05
C230057M02Rik	2.07	0.04	1.41	0.28	1.36	0.18	6.72	7.77	7.22	6.44	6.88
C330006P03Rik	2.34	0.10	1.84	0.22	1.14	0.71	9.99	11.21	10.86	9.94	10.13

C630007B19Rik	1.51	0.06	1.16	0.48	1.35	0.11	6.24	6.83	6.45	6.30	6.73
Calml4	0.55	0.08	0.62	0.15	1.21	0.50	7.60	6.74	6.91	7.21	7.48
Camk2a	1.73	0.11	1.27	0.46	1.21	0.47	10.60	11.39	10.94	10.53	10.80
Camkk1	1.54	0.02	1.30	0.13	1.28	0.06	9.78	10.41	10.16	9.58	9.93
Car14	0.63	0.01	0.71	0.04	1.05	0.69	8.28	7.61	7.78	8.33	8.41
Ccdc3	1.96	0.00	1.28	0.19	1.48	0.01	8.63	9.60	8.99	8.43	8.99
Cdh15	1.57	0.11	1.39	0.23	0.94	0.57	6.88	7.53	7.35	7.40	7.31
Cdkn1a	1.51	0.01	1.78	0.00	1.48	0.04	7.57	8.16	8.40	7.11	7.67
Cdkn1c	0.61	0.02	0.68	0.05	1.35	0.34	9.58	8.88	9.03	8.90	9.34
Chrd	1.56	0.10	1.26	0.37	1.51	0.16	8.54	9.18	8.87	8.24	8.84
Cit	0.54	0.06	0.80	0.46	1.01	0.89	8.27	7.38	7.94	8.01	8.03
Cldn2	0.44	0.01	0.43	0.01	1.21	0.62	7.18	5.99	5.97	6.72	7.00
Col8a1	0.67	0.04	0.72	0.09	1.33	0.21	6.92	6.34	6.45	6.66	7.08
Col8a2	0.61	0.04	0.63	0.05	1.17	0.49	7.19	6.48	6.53	6.61	6.83
Cox6a2	0.64	0.09	0.82	0.44	0.89	0.32	9.18	8.54	8.90	9.86	9.69
Crhbp	1.94	0.03	1.51	0.16	1.97	0.03	8.53	9.49	9.12	8.27	9.25
Ctgf	1.74	0.15	1.04	0.91	1.61	0.29	8.47	9.27	8.53	8.40	9.08
D030006P03Rik	0.63	0.05	0.82	0.37	0.88	0.28	6.44	5.77	6.16	6.42	6.23
D230046H12Rik	0.43	0.03	0.52	0.07	1.22	0.53	9.28	8.07	8.33	8.83	9.11
Dgkg	1.59	0.11	1.23	0.45	1.14	0.38	10.12	10.79	10.42	10.18	10.36
Dkk3	1.84	0.10	1.43	0.32	1.39	0.29	10.22	11.10	10.74	10.12	10.60
E130012A19Rik	2.52	0.08	1.68	0.30	1.64	0.33	9.05	10.39	9.80	8.91	9.62
Enc1	1.61	0.11	1.25	0.42	1.30	0.30	11.93	12.61	12.25	11.61	11.99
Enpp2	0.44	0.01	0.55	0.03	1.28	0.48	10.90	9.73	10.05	10.55	10.90
Erdr1	0.70	0.08	1.08	0.69	0.42	0.37	10.35	9.84	10.46	10.69	9.44
Extl1	1.80	0.10	1.41	0.31	1.24	0.21	8.11	8.96	8.61	7.68	7.99
Fam131a	1.70	0.03	1.31	0.24	1.20	0.40	9.68	10.45	10.07	9.73	9.98
Fam171a1	2.10	0.01	2.08	0.01	0.75	0.42	6.85	7.92	7.90	7.42	7.01
Fhl2	2.46	0.06	1.57	0.31	1.56	0.28	7.65	8.95	8.31	7.69	8.33
Folr1	0.37	0.01	0.38	0.02	1.29	0.60	7.76	6.34	6.38	7.17	7.54
Fosb	1.88	0.02	1.46	0.14	1.06	0.68	7.37	8.28	7.91	7.34	7.43
Gpr151	0.39	0.16	0.91	0.89	1.31	0.60	7.65	6.29	7.52	7.72	8.12
Hcrt	0.26	0.17	0.90	0.91	0.79	0.83	7.74	5.80	7.58	8.43	8.08
Hs3st2	1.86	0.07	1.26	0.47	1.26	0.43	6.56	7.45	6.89	6.62	6.95
Igfbp6	2.68	0.10	1.65	0.38	1.02	0.96	7.02	8.44	7.74	7.69	7.72
Inhba	2.21	0.04	1.79	0.12	1.24	0.37	7.50	8.65	8.35	7.73	8.04

Irs2	0.59	0.04	0.87	0.57	1.10	0.58	9.51	8.74	9.32	9.15	9.29
Islr2	2.22	0.01	1.70	0.06	1.52	0.15	8.18	9.34	8.95	7.98	8.58
Itga11	1.54	0.00	1.15	0.26	1.04	0.68	6.11	6.73	6.31	6.34	6.40
Itgb4	0.67	0.03	0.78	0.17	0.78	0.01	9.41	8.83	9.06	8.98	8.62
Kcne2	0.41	0.01	0.42	0.01	1.06	0.91	7.49	6.19	6.24	7.28	7.36
Klk6	0.65	0.11	0.83	0.47	0.68	0.02	8.12	7.50	7.86	8.48	7.92
Lmo4	1.55	0.11	1.29	0.33	1.10	0.68	11.21	11.85	11.58	11.20	11.34
Mas1	2.56	0.06	1.30	0.57	1.07	0.84	7.22	8.57	7.59	7.76	7.87
Mpped1	1.95	0.11	1.22	0.62	1.33	0.45	10.54	11.50	10.82	10.14	10.55
Ncor1	1.83	0.01	1.84	0.01	0.91	0.74	8.39	9.26	9.26	8.58	8.45
Neurod2	3.87	0.03	2.01	0.21	2.43	0.15	7.13	9.09	8.14	7.01	8.29
Nkx6-2	0.65	0.04	0.68	0.07	0.72	0.05	8.36	7.73	7.81	8.61	8.15
Nptx1	2.21	0.04	1.45	0.30	1.89	0.06	7.19	8.33	7.72	6.79	7.71
Nrgn	2.64	0.10	1.70	0.35	0.85	0.69	10.83	12.23	11.59	11.71	11.47
Pcdh17	0.63	0.06	0.83	0.39	0.98	0.93	9.87	9.21	9.60	9.71	9.68
Peg3	0.57	0.02	0.83	0.39	1.09	0.48	9.81	8.99	9.53	9.71	9.84
Plekha2	1.65	0.01	1.27	0.20	1.23	0.25	9.30	10.03	9.64	9.29	9.59
Plekhg5	1.61	0.05	1.31	0.23	1.32	0.14	8.66	9.35	9.06	8.37	8.77
Pmch	0.10	0.08	0.46	0.52	1.60	0.66	9.61	6.32	8.50	9.26	9.94
Prss12	1.99	0.04	1.30	0.40	1.57	0.11	6.72	7.71	7.09	6.34	6.98
Prss35	1.78	0.01	1.44	0.07	1.42	0.01	6.48	7.31	7.01	5.93	6.43
Ptk2b	1.94	0.06	1.40	0.30	0.97	0.90	9.01	9.97	9.50	9.37	9.33
Pwwp2b	1.56	0.07	1.35	0.20	0.94	0.65	7.41	8.06	7.85	7.65	7.55
Rapgefl1	1.52	0.04	1.11	0.58	1.29	0.12	10.46	11.06	10.61	10.11	10.48
Rasl10a	3.02	0.02	1.76	0.18	1.41	0.37	8.32	9.91	9.14	8.49	8.98
Rasl11b	2.09	0.07	1.46	0.32	1.48	0.24	10.00	11.07	10.54	10.24	10.81
Rprml	2.19	0.11	1.55	0.35	0.97	0.93	9.92	11.05	10.55	10.43	10.38
Rspo2	1.70	0.10	1.25	0.47	1.21	0.33	6.05	6.81	6.36	5.86	6.14
Scn1a	0.59	0.06	0.84	0.51	1.20	0.43	9.13	8.36	8.88	9.05	9.32
Slc16a8	0.64	0.01	0.67	0.02	1.30	0.43	6.38	5.74	5.81	6.36	6.74
Slc17a7	2.73	0.07	1.57	0.39	2.04	0.14	9.45	10.90	10.10	9.87	10.90
Slc26a4	1.57	0.10	1.14	0.61	1.43	0.01	6.87	7.52	7.06	6.77	7.29
Slc4a2	0.64	0.01	0.78	0.13	1.06	0.76	9.91	9.26	9.54	9.86	9.94
Sostdc1	0.26	0.02	0.24	0.01	1.20	0.70	9.19	7.27	7.14	7.90	8.16
Sstr2	1.65	0.03	1.43	0.10	1.38	0.12	7.95	8.67	8.46	7.35	7.82
St6galnac2	0.67	0.02	0.62	0.01	0.99	0.95	8.30	7.72	7.61	7.59	7.57

Stac2	1.79	0.06	1.51	0.17	1.33	0.30	9.09	9.93	9.69	8.95	9.37
Tbr1	3.19	0.08	1.71	0.39	1.95	0.30	7.73	9.40	8.51	7.60	8.57
Tcf19	1.57	0.10	1.44	0.17	1.13	0.50	6.50	7.14	7.03	6.51	6.68
Tmem178	1.72	0.09	1.26	0.43	1.29	0.39	8.55	9.33	8.88	8.35	8.73
Tshz2	0.66	0.05	0.81	0.28	0.97	0.88	7.24	6.65	6.93	7.22	7.19
Tuba8	1.50	0.04	1.32	0.13	1.24	0.21	6.68	7.27	7.08	6.67	6.98
Unc13c	0.61	0.06	0.78	0.31	0.70	0.01	10.28	9.57	9.92	10.36	9.85
Wfdc2	0.39	0.01	0.42	0.01	1.28	0.67	7.87	6.49	6.62	7.36	7.72
Wipf3	2.09	0.08	1.27	0.54	0.88	0.58	10.77	11.83	11.11	11.30	11.12
Xlr4a	0.71	0.17	1.13	0.60	1.42	0.31	9.06	8.57	9.23	9.09	9.60
Ypel1	1.72	0.06	1.31	0.31	1.07	0.77	7.24	8.02	7.63	7.23	7.33
Zfp238	1.96	0.03	1.40	0.25	1.35	0.29	8.93	9.89	9.42	9.22	9.65