

**Table S3. Strain-specific haloperidol-induced gene expression changes in striatal tissue.** Genes whose expression level had a haloperidol-induced absolute fold change >1.5 in striatal tissue of A/J mice (relative to that of C57BL/6), which also had adjusted p-value <0.1 in the (strain \* treatment) interaction analysis 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_CysHal_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	0.02	1.16	0.02	6.62	5.84	5.93	6.48	6.69
1500015O10Rik	0.32	0.07	0.26	0.07	1.43	0.07	9.43	7.80	7.49	8.86	9.38
2010001M06Rik	1.23	0.30	1.23	0.30	0.74	0.30	6.63	6.93	6.93	7.21	6.76
2010300C02Rik	2.00	0.15	1.30	0.15	0.79	0.15	9.87	10.87	10.25	10.59	10.25
2610017I09Rik	1.37	0.14	1.31	0.14	0.79	0.14	9.15	9.60	9.54	9.53	9.19
2610304F08Rik	0.76	0.13	0.87	0.13	1.35	0.13	6.30	5.90	6.10	6.16	6.59
2810046M22Rik	0.59	0.08	0.63	0.08	1.67	0.08	7.32	6.56	6.65	6.81	7.54
2900017F05Rik	0.54	0.03	0.71	0.03	1.29	0.03	7.56	6.66	7.06	7.73	8.10
3110047P20Rik	0.71	0.20	0.84	0.20	1.29	0.20	8.73	8.24	8.48	8.33	8.70
4632401N01Rik	1.38	0.19	1.11	0.19	0.82	0.19	8.60	9.06	8.74	8.78	8.50
5330423N11Rik	0.76	0.05	0.75	0.05	1.17	0.05	6.41	6.02	6.00	6.70	6.93
8030481K01Rik	1.20	0.27	1.17	0.27	0.80	0.27	6.80	7.05	7.02	7.12	6.80
8430408G22Rik	1.13	0.21	1.01	0.21	0.74	0.21	6.01	6.19	6.01	6.08	5.65
9130230N09Rik	1.07	0.73	1.09	0.73	0.68	0.73	7.10	7.20	7.22	7.56	7.01
9330102G19Rik	0.82	0.46	1.01	0.46	1.33	0.46	7.03	6.74	7.04	6.62	7.03
9430020K01Rik	1.18	0.36	1.01	0.36	0.76	0.36	6.64	6.87	6.64	6.97	6.57
A130082M07Rik	0.58	0.09	0.72	0.09	1.00	0.09	7.14	6.34	6.65	6.35	6.34
A230077I10Rik	0.74	0.10	0.83	0.10	1.11	0.10	7.04	6.61	6.77	7.25	7.40
A430103B12Rik	0.59	0.03	0.74	0.03	1.07	0.03	7.94	7.18	7.50	7.64	7.73
A430106G13Rik	0.81	0.09	0.85	0.09	1.22	0.09	7.71	7.41	7.48	7.65	7.94
A530079E22Rik	1.25	0.37	1.16	0.37	0.74	0.37	6.76	7.08	6.98	7.20	6.77
A830055I09Rik	0.89	0.31	0.97	0.31	1.56	0.31	8.00	7.83	7.96	7.30	7.94
A930006J02Rik	0.69	0.09	0.81	0.09	1.05	0.09	6.25	5.71	5.94	5.67	5.73
A930040K03Rik	1.29	0.11	1.16	0.11	0.84	0.11	5.86	6.23	6.08	6.15	5.90
Actn1	1.45	0.23	1.11	0.23	0.72	0.23	10.61	11.14	10.76	10.97	10.49
Actn2	1.58	0.47	1.22	0.47	0.53	0.47	10.08	10.75	10.37	10.92	10.01
Adamts15	0.73	0.14	0.89	0.14	1.10	0.14	6.70	6.25	6.53	6.27	6.40
Adcyap1	0.58	0.12	0.78	0.12	1.39	0.12	8.18	7.39	7.81	7.48	7.96

Ahnak2	0.74	0.14	0.92	0.14	1.11	0.14	7.16	6.73	7.04	6.76	6.91
Akap2	0.75	0.14	0.79	0.14	1.22	0.14	7.87	7.45	7.54	7.58	7.87
Amn	0.86	0.26	1.03	0.26	1.29	0.26	8.55	8.32	8.60	8.32	8.69
Ankrd37	1.11	0.41	1.13	0.41	0.67	0.41	7.52	7.67	7.70	7.90	7.32
Aqp1	0.47	0.01	0.45	0.01	1.47	0.01	7.38	6.29	6.24	6.84	7.40
Arc	1.65	0.16	1.04	0.16	0.60	0.16	9.12	9.85	9.19	9.74	9.01
Arg2	1.50	0.21	1.57	0.21	0.83	0.21	6.78	7.37	7.44	7.41	7.15
Asah3l	1.26	0.09	1.29	0.09	0.81	0.09	8.20	8.53	8.56	7.56	7.25
B230343A10Rik	1.49	0.24	1.11	0.24	0.83	0.24	11.82	12.39	11.97	11.65	11.38
Baiap2	1.66	0.22	1.24	0.22	0.78	0.22	8.19	8.92	8.50	8.42	8.07
BC042720	0.76	0.10	0.76	0.10	1.18	0.10	8.91	8.51	8.52	8.93	9.17
Bcr	1.23	0.39	1.23	0.39	0.75	0.39	7.29	7.59	7.59	7.58	7.16
C030011O14Rik	0.72	0.04	0.86	0.04	1.15	0.04	8.30	7.83	8.09	7.87	8.07
C130060K24Rik	1.25	0.19	1.05	0.19	0.78	0.19	7.44	7.76	7.51	7.56	7.21
C130090G16Rik	0.83	0.04	1.05	0.04	1.31	0.04	7.96	7.69	8.03	7.48	7.87
C230081G24Rik	0.83	0.20	0.96	0.20	1.53	0.20	8.66	8.39	8.60	8.21	8.83
C230098O21Rik	1.54	0.27	1.16	0.27	0.77	0.27	11.51	12.13	11.72	11.93	11.56
Cab39l	0.78	0.04	0.81	0.04	1.19	0.04	9.35	8.99	9.05	9.44	9.70
Calml4	0.55	0.08	0.62	0.08	1.21	0.08	7.60	6.74	6.91	7.21	7.48
Camkv	1.29	0.20	1.10	0.20	0.81	0.20	11.47	11.84	11.61	11.70	11.40
Car14	0.63	0.01	0.71	0.01	1.05	0.01	8.28	7.61	7.78	8.33	8.41
Cbln4	0.81	0.36	1.14	0.36	1.41	0.36	9.35	9.05	9.54	8.91	9.40
Cbr3	1.64	0.25	1.36	0.25	0.72	0.25	9.10	9.81	9.54	9.66	9.19
Ccng2	1.36	0.07	1.14	0.07	0.83	0.07	7.76	8.20	7.95	8.07	7.80
Cd72	1.41	0.11	1.26	0.11	0.76	0.11	5.91	6.41	6.24	6.81	6.42
Cdca7	1.25	0.28	1.14	0.28	0.83	0.28	7.61	7.93	7.80	7.92	7.65
Cdkn1c	0.61	0.02	0.68	0.02	1.35	0.02	9.58	8.88	9.03	8.90	9.34
Centg1	1.46	0.14	1.11	0.14	0.87	0.14	9.20	9.75	9.35	9.26	9.05
Chst8	0.63	0.24	0.81	0.24	1.32	0.24	10.13	9.45	9.82	9.96	10.36
Cirbp	0.82	0.09	0.91	0.09	1.25	0.09	9.69	9.41	9.56	9.30	9.62
Cit	0.54	0.06	0.80	0.06	1.01	0.06	8.27	7.38	7.94	8.01	8.03
Cldn2	0.44	0.01	0.43	0.01	1.21	0.01	7.18	5.99	5.97	6.72	7.00
Clspn	1.19	#N/A	1.04	#N/A	0.54	#N/A	6.30	6.55	6.36	7.37	6.49
Cntn2	0.71	0.03	0.91	0.03	1.11	0.03	9.26	8.77	9.13	7.49	7.65
Col8a1	0.67	0.04	0.72	0.04	1.33	0.04	6.92	6.34	6.45	6.66	7.08
Col8a2	0.61	0.04	0.63	0.04	1.17	0.04	7.19	6.48	6.53	6.61	6.83

Creg1	0.74	0.16	0.91	0.16	1.14	0.16	8.44	8.01	8.30	8.20	8.38
Crtc1	1.31	0.16	1.14	0.16	0.86	0.16	8.34	8.73	8.53	8.36	8.14
Csnrp3	1.46	0.22	1.12	0.22	0.81	0.22	8.57	9.12	8.73	9.04	8.73
D230046H12Rik	0.43	0.03	0.52	0.03	1.22	0.03	9.28	8.07	8.33	8.83	9.11
D3Bwg0562e	1.29	0.14	1.29	0.14	0.76	0.14	8.71	9.08	9.08	9.75	9.35
Ddn	2.02	0.18	1.16	0.18	0.81	0.18	12.60	13.62	12.82	13.04	12.74
Ddx11	1.19	0.36	1.03	0.36	0.78	0.36	6.74	7.00	6.79	6.83	6.48
Dmkn	1.30	0.22	1.15	0.22	0.66	0.22	7.49	7.87	7.69	8.76	8.16
Doc2b	1.22	0.24	1.14	0.24	0.74	0.24	9.05	9.34	9.24	9.25	8.81
Dok3	0.95	0.51	0.93	0.51	0.62	0.51	8.20	8.13	8.09	8.86	8.16
E030007N04Rik	0.84	0.18	0.97	0.18	1.26	0.18	8.71	8.46	8.67	8.30	8.63
Efnb2	1.15	0.41	1.03	0.41	0.77	0.41	6.33	6.53	6.37	6.35	5.97
EG545758	1.11	0.47	0.95	0.47	0.60	0.47	7.54	7.69	7.46	7.74	6.99
Egr1	1.41	0.31	1.00	0.31	0.69	0.31	11.89	12.38	11.89	12.52	11.98
Egr2	1.57	0.21	1.24	0.21	0.70	0.21	6.88	7.53	7.19	7.39	6.88
Egr4	2.07	0.13	1.54	0.13	0.74	0.13	8.39	9.44	9.02	9.36	8.94
Enpp2	0.44	0.01	0.55	0.01	1.28	0.01	10.90	9.73	10.05	10.55	10.90
Erf	1.22	0.31	1.01	0.31	0.74	0.31	6.89	7.18	6.91	7.13	6.70
F830002E14Rik	0.52	0.01	0.25	0.01	1.35	0.01	10.87	9.93	8.84	9.78	10.22
Fam171a1	2.10	0.01	2.08	0.01	0.75	0.01	6.85	7.92	7.90	7.42	7.01
Fam20b	0.80	0.15	0.99	0.15	1.32	0.15	9.01	8.68	9.00	7.19	7.59
Folr1	0.37	0.01	0.38	0.01	1.29	0.01	7.76	6.34	6.38	7.17	7.54
Fos	1.13	0.51	1.04	0.51	0.68	0.51	8.14	8.31	8.20	8.33	7.76
Fosb	1.88	0.02	1.46	0.02	1.06	0.02	7.37	8.28	7.91	7.34	7.43
Foxg1	1.65	0.22	1.13	0.22	0.77	0.22	8.48	9.21	8.66	8.88	8.51
Gabra3	0.97	0.82	0.77	0.82	1.46	0.82	7.80	7.77	7.43	7.24	7.79
Gas7	1.27	0.25	1.07	0.25	0.77	0.25	8.24	8.59	8.34	8.78	8.40
Gipc2	1.18	0.39	1.09	0.39	0.77	0.39	6.54	6.77	6.66	6.93	6.54
Gpr123	0.77	0.23	0.94	0.23	1.19	0.23	9.92	9.55	9.82	9.70	9.95
Gpr155	1.36	0.22	1.21	0.22	0.72	0.22	9.54	9.98	9.81	10.07	9.60
Hba-a1	1.07	0.65	0.90	0.65	0.70	0.65	12.61	12.71	12.47	12.86	12.35
Hbb-b1	1.05	0.76	1.00	0.76	0.67	0.76	11.67	11.73	11.66	12.87	12.29
Hes5	1.18	0.14	0.95	0.14	0.72	0.14	7.36	7.60	7.28	8.00	7.54
Hmgcs2	1.08	0.65	1.00	0.65	0.68	0.65	8.34	8.45	8.34	8.40	7.84
Hook3	0.79	0.05	0.77	0.05	1.32	0.05	6.57	6.23	6.19	6.18	6.58
Hpca	1.77	0.24	1.18	0.24	0.70	0.24	13.00	13.82	13.23	13.47	12.95

Icam5	1.98	0.15	1.40	0.15	0.80	0.15	9.06	10.04	9.55	9.58	9.26
Ii17rc	1.07	0.63	1.07	0.63	0.71	0.63	6.98	7.08	7.08	7.41	6.93
Inmt	0.68	0.14	0.66	0.14	1.28	0.14	7.34	6.78	6.74	7.85	8.20
Iqsec2	1.37	0.17	1.07	0.17	0.89	0.17	8.48	8.94	8.58	8.49	8.32
Irs2	0.59	0.04	0.87	0.04	1.10	0.04	9.51	8.74	9.32	9.15	9.29
Itga5	1.27	0.35	1.31	0.35	0.78	0.35	6.29	6.63	6.69	6.57	6.22
Kcnip4	0.81	0.04	0.79	0.04	1.38	0.04	6.78	6.47	6.43	6.41	6.88
Kcnk2	1.32	0.28	1.27	0.28	0.75	0.28	8.22	8.62	8.57	8.79	8.36
Kcnma1	0.84	0.19	1.06	0.19	1.29	0.19	9.03	8.78	9.11	8.83	9.20
Klf6	0.67	0.09	0.78	0.09	1.28	0.09	8.75	8.18	8.40	8.37	8.73
Kndc1	0.75	0.25	0.87	0.25	1.17	0.25	10.53	10.12	10.32	10.40	10.62
Krt10	1.28	0.35	1.18	0.35	0.66	0.35	10.02	10.38	10.27	10.76	10.17
Krt18	0.67	0.03	0.71	0.03	1.16	0.03	6.28	5.71	5.79	6.17	6.39
Limd2	1.42	0.04	1.15	0.04	0.93	0.04	6.40	6.91	6.60	6.54	6.45
Lingo3	1.38	0.32	1.33	0.32	0.78	0.32	6.67	7.13	7.08	6.99	6.63
LOC100040243	0.74	0.06	0.91	0.06	1.13	0.06	9.26	8.83	9.13	9.30	9.48
LOC100041569	0.70	0.18	0.92	0.18	1.27	0.18	9.06	8.54	8.94	8.77	9.11
LOC100043257	1.09	0.34	0.88	0.34	1.93	0.34	10.38	10.50	10.20	10.12	11.07
LOC331102	0.78	0.04	0.64	0.04	1.18	0.04	10.89	10.53	10.24	10.43	10.67
LOC381739	0.85	0.17	0.96	0.17	1.32	0.17	9.41	9.17	9.36	8.39	8.79
LOC547380	0.71	0.02	0.94	0.02	1.12	0.02	7.50	7.02	7.41	7.36	7.52
LOC671878	0.72	0.13	0.89	0.13	1.24	0.13	9.56	9.08	9.39	9.39	9.70
Lypd1	1.14	0.45	1.01	0.45	0.73	0.45	10.56	10.75	10.57	9.85	9.41
Mog	0.67	0.03	0.81	0.03	1.01	0.03	10.38	9.80	10.08	10.55	10.56
Mreg	0.80	0.37	0.95	0.37	1.24	0.37	8.14	7.81	8.07	7.74	8.06
Myo5b	1.79	0.19	1.10	0.19	0.89	0.19	8.14	8.97	8.27	8.26	8.10
Ncor1	1.83	0.01	1.84	0.01	0.91	0.01	8.39	9.26	9.26	8.58	8.45
Nrgn	2.64	0.10	1.70	0.10	0.85	0.10	10.83	12.23	11.59	11.71	11.47
Obfc1	1.23	0.16	1.13	0.16	0.81	0.16	7.41	7.71	7.58	7.26	6.96
Pcmt2	1.26	0.04	1.16	0.04	0.83	0.04	7.46	7.80	7.68	7.67	7.40
Pde2a	1.69	0.16	1.29	0.16	0.78	0.16	9.82	10.57	10.19	10.24	9.88
Peg3	0.57	0.02	0.83	0.02	1.09	0.02	9.81	8.99	9.53	9.71	9.84
Phyhip	1.52	0.15	1.14	0.15	0.85	0.15	8.10	8.71	8.30	8.24	8.00
Pigz	0.73	0.06	0.91	0.06	1.16	0.06	8.97	8.52	8.84	9.15	9.35
Pmch	0.10	0.08	0.46	0.08	1.60	0.08	9.61	6.32	8.50	9.26	9.94
Ppm1l	0.79	0.10	0.96	0.10	1.34	0.10	7.96	7.63	7.90	8.00	8.43

Ppp1r3f	0.77	0.15	0.85	0.15	1.18	0.15	9.65	9.28	9.42	9.29	9.53
Prlr	0.58	0.14	0.64	0.14	1.19	0.14	7.61	6.82	6.96	7.50	7.75
Ptk2b	1.94	0.06	1.40	0.06	0.97	0.06	9.01	9.97	9.50	9.37	9.33
Pwwp2b	1.56	0.07	1.35	0.07	0.94	0.07	7.41	8.06	7.85	7.65	7.55
Rerg	1.34	0.28	1.41	0.28	0.78	0.28	9.18	9.60	9.67	9.11	8.75
Rgl1	1.38	0.08	1.08	0.08	0.92	0.08	9.60	10.07	9.71	9.46	9.34
Rgs12	1.43	0.08	0.98	0.08	0.94	0.08	7.83	8.34	7.80	7.71	7.62
Rhbdl3	1.13	0.38	1.01	0.38	0.73	0.38	8.51	8.69	8.53	8.34	7.88
Rims3	0.71	0.13	0.97	0.13	1.08	0.13	12.32	11.83	12.28	12.24	12.36
Rin1	1.98	0.18	1.26	0.18	0.82	0.18	9.31	10.29	9.63	9.54	9.25
Rora	0.65	0.19	0.90	0.19	1.23	0.19	8.84	8.22	8.70	8.89	9.19
Ryr1	1.40	0.35	1.17	0.35	0.60	0.35	7.22	7.71	7.45	8.14	7.39
Sap30	1.29	0.09	1.18	0.09	0.85	0.09	8.76	9.13	9.00	9.08	8.85
scl0001379.1_70	1.46	0.31	1.25	0.31	0.73	0.31	8.22	8.77	8.54	8.59	8.13
scl0002785.1_49	0.63	0.16	0.82	0.16	1.09	0.16	8.50	7.83	8.21	8.26	8.39
Scn1a	0.59	0.06	0.84	0.06	1.20	0.06	9.13	8.36	8.88	9.05	9.32
Slc16a8	0.64	0.01	0.67	0.01	1.30	0.01	6.38	5.74	5.81	6.36	6.74
Slc4a2	0.64	0.01	0.78	0.01	1.06	0.01	9.91	9.26	9.54	9.86	9.94
Smpd3	1.46	0.35	1.22	0.35	0.69	0.35	10.07	10.61	10.36	10.36	9.82
Snx30	0.75	0.02	0.90	0.02	1.14	0.02	8.18	7.76	8.03	7.17	7.36
Sostdc1	0.26	0.02	0.24	0.02	1.20	0.02	9.19	7.27	7.14	7.90	8.16
Spata13	1.49	0.27	1.25	0.27	0.91	0.27	10.17	10.75	10.50	9.88	9.75
Spata2L	1.45	0.21	1.10	0.21	0.70	0.21	9.56	10.10	9.70	9.92	9.39
Spint1	1.35	0.24	1.19	0.24	0.88	0.24	7.42	7.85	7.67	8.30	8.11
Srf	1.42	0.04	1.12	0.04	0.92	0.04	8.61	9.11	8.76	8.78	8.66
Srfbp1	0.96	0.56	0.93	0.56	0.80	0.56	7.64	7.59	7.53	7.70	7.38
Tcea3	0.75	0.03	0.80	0.03	1.13	0.03	6.44	6.02	6.11	6.43	6.60
Tmem158	1.32	0.46	1.23	0.46	0.70	0.46	8.59	8.99	8.88	9.11	8.60
Tnfrsf25	1.45	#N/A	1.04	#N/A	0.76	#N/A	6.30	6.83	6.36	6.69	6.31
Tox	0.75	#N/A	0.87	#N/A	1.16	#N/A	8.68	8.26	8.48	8.18	8.40
Trpm3	0.72	0.03	0.78	0.03	1.18	0.03	6.48	6.01	6.12	6.14	6.37
Tr	0.31	0.18	0.10	0.18	1.86	0.18	14.56	12.85	11.17	13.30	14.19
Upb1	1.11	0.56	1.06	0.56	0.71	0.56	6.29	6.44	6.37	6.85	6.36
Wfdc2	0.39	0.01	0.42	0.01	1.28	0.01	7.87	6.49	6.62	7.36	7.72
Wipf3	2.09	0.08	1.27	0.08	0.88	0.08	10.77	11.83	11.11	11.30	11.12
Ybx3	0.85	0.13	0.89	0.13	1.75	0.13	8.81	8.57	8.63	7.80	8.60