Table S5. **RT-PCR analysis of striatal gene expression.** Nine genes were identified by microarray analysis as having haloperidol-induced expression changes in striatum that were strain-specific and reversible by cystamine co-administration. The mRNA levels for these 9 genes were analyzed by RT-PCR analysis in striatal tissue obtained from C57BL/6 or A/J mice treated with vehicle or olanzapine (5 mg/kg/day x 3 days PO). One group of olanzapine-treated A/J mice was also treated with cystamine (10 mg/kg BID IP). The fold change (FC) and p-values for each of the indicated comparisons are shown for the microarray and RT-PCR data are shown. ND: not determined. The mRNAs for 3 genes (*Pmch, Fosb*, and *Slc4a2*) whose haloperidol-induced expression changes in A/J striatal tissue measured by RT-PCR that had p-values <0.05 are shown in red. A (-) sign indicates that the mRNA was down regulated. The treatment groups are: Hal: haloperidol; Cys+Hal: cystamine and haloperidol co-administration; Ctrl: vehicle control; ND: not determined.

Gene	**Microarray**			**RT-PCR**		
	A/J Hal vs Ctrl	**A/J Cys+Hal_vs_Ctrl**	**C57BL/6 Hal_vs_Ctrl**	**A/J Hal_vs_Ctrl**	**A/J CysHal_vs_Ctrl**	**C57BL/6 Hal_vs_Ctrl**
Pmch	-9.77 (p=0.08)	-2.16 (p=0.52)	1.60 (p=0.66)	-61.5 (p=0.04)	-4.0 (p=0.57)	2.10 (p=0.70)
Nrgn	2.64 (p=0.10)	1.70 (p=0.35)	-1.18 (p=0.69)	2.86 (p=0.12)	1.82 (p=0.47)	ND
Ptk2b	1.94 (p=0.06)	1.40 (p=0.30)	-1.03 (p=0.90)	1.81 (p=0.09)	1.41 (p=0.51)	ND
Fosb	1.88 (p=0.02)	1.46 (p=0.14)	1.06 (p=0.68)	5.14 (p=0.003)	3.50 (p=0.07)	2.48 (p=0.08)
Cit	-1.86 (p=0.06)	-1.25 (p=0.46)	1.01 (p=0.89)	-1.76 (p=0.17)	-1.23 (p=0.70)	ND
Peg3	-1.76 (p=0.02)	-1.21 (p=0.39)	1.09 (p=0.49)	-1.19 (p=0.78)	1.02 (p=0.98)	ND
Irs2	-1.71 (p=0.05)	-1.15 (p=0.58)	1.10 (p=0.58)	1.02 (p=0.88)	-1.02 (p=0.93)	ND
Scn1a	-1.70 (p=0.06)	-1.19 (p=0.51)	1.20 (p=0.43)	1.09 (p=0.84)	1.29 (p=0.38)	ND
Slc4a2	-1.56 (p=0.01)	-1.29 (p=0.13)	1.06 (p=0.76)	-1.55 (p=0.025)	-1.38 (p=0.16)	1.05 (p=0.77)