Table S4. The 10 most highly enriched biological function categories for genes whose expression was altered in a strain-specific and cystamine-reversible manner by haloperidol treatment. The Ingenuity Pathway Analysis program was used to identify the biologic pathways associated with the 32 genes shown in table 1. The associated biological functions in the output are ranked by their p-values in ascending order. The numbers of genes, and the symbol for each gene, associated with each pathway are shown.

Functional Annotation	p-value	# genes	Genes
Body size	1.87E-06	10	AQP1, CA14,CDKN1C,FOSB,IRS2,NCOR1,PEG3,PMCH,SCN1A,SLC4A2
White adipose tissue mass	6.04E-06	3	ENPP2,IRS2,PMCH
Perirenal white adipose tissue sass	1.32E-05	2	ENPP2,PMCH
Hyperphagia	2.10E-05	4	CA14,IRS2,PMCH,SCN1A
Uterine serous papillary cancer	3.06E-05	5	AQP1,CIT,ENPP2,PEG3,WFDC2
Weight loss	3.56E-05	5	AQP1,IRS2,NCOR1,PMCH,SCN1A
Neurotransmission	5.42E-05	6	ARC,FOSB,NRGN,PMCH,PTK2B,SCN1A
Movement Disorders	6.38E-05	9	AQP1,CA14,CDKN1C,CIT,FOSB,NRGN,PTK2B,SCN1A,SLC4A2
Urination disorder	8.03E-05	5	AQP1,CDKN1C,CLDN2,IRS2,SCN1A
Polyuria	9.38E-05	3	AQP1,CLDN2,IRS2