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Supporting Information

Additional supporting information may be found in the online version of this article at the publisher's web-site:

Figure S1: Gene expression networks associated with determinants of midbrain dopamine synthesis and inactivation. Genes (top 25) with highest correlations with *Th* (a) or *Slc6a3* (b) are graphed separately based on the direction of correlation (green: positive; red: negative). Gene node sizes represent the significance of correlation. Gene pairs with correlation coefficients (Spearman rho) above 0.5 are connected by edges (green: positive; red: negative).

Figure S2: Gene expression networks associated with determinants of midbrain acetylcholine synthesis and choline reuptake. Genes (top 25) with highest correlations with *Chat* (a) or *Slc5a7* (b) are graphed separately based on the direction of correlation (green: positive; red: negative). Gene node sizes represent the significance of correlation. Gene pairs with correlation coefficients (Spearman rho) above 0.5 are connected by edges (green: positive; red: negative).

Figure S3: *Pcdh15*$^{av\text{-}3J}$ mice have altered midbrain 5-HT levels. (a) Males [$P < 0.05$, Kruskal–Wallis test followed by Dunn's multiple comparison test, $N = 4$ (*wt*), 17 (*het*) and 7 (*hom*)] and (b) females [*NS*, $N = 3$ (*wt*), 8 (*het*) and 5 (*hom*)].

Figure S4: The genotype for SNP rs6191324 is correlated with (a) midbrain SERT expression levels ($P < 0.0001$, Student's *t*-test), (b) midbrain *Slc18a2* mRNA expression levels ($P < 0.05$, Student's *t*-test), (c) midbrain 5-HT levels ($P < 0.05$, Student's *t*-test) and (d) blood 5-HT levels ($P < 0.05$, Student's *t*-test). rs6191324 is the nearest mapped marker to gene *Slc18a2* in BXD strains.

Figure S5: Gene expression networks associated with midbrain *Pcdh15*. Genes (top 25) with highest correlations with *Pcdh15* (probe A_55_P2176176, see *Discussion*) are graphed separately based on the direction of correlation (green: positive; red: negative). Gene node sizes represent the significance of correlation. Gene pairs with correlation coefficients (Spearman rho) above 0.5 are connected by edges (green: positive; red: negative).

Table S1: Animals used in this study. Number of animals and their genders from each BXD strain are listed for each experiment.

Table S2: Midbrain 5-HT gene networks seeded by *Tph2* or *Slc6a4* expression ($P < 0.05$, Spearman's rank test).

Table S3: Midbrain DA gene networks seeded by *Th* ($P < 0.05$, Spearman's rank test) or *Slc6a3* expression ($P < 0.05$, Spearman's rank test).

Table S4: Midbrain ACh gene networks seeded by *Chat* ($P < 0.05$, Spearman's rank test) or *Slc5a7* expression ($P < 0.05$, Spearman's rank test).

Table S5: GeneNetwork archived phenotypes that correlated with SERT protein expression levels ($P < 0.05$, Spearman's rank test).

Table S6: Genes under loci above suggestive significance levels from interval mapping analysis of SERT protein expression levels.

Table S7: Gene network seeded by correlation with male midbrain SERT protein expression ($P < 0.05$, Spearman's rank test).

Table S8: List of common genes associated with male midbrain SERT protein expression levels identified from transcriptome and QTL analyses.

Table S9: Gene network seeded by correlation with male midbrain *Pcdh15* (A_55_P2176176) expression ($P < 0.05$, Spearman's rank test) and common genes between this network and gene network associated with male midbrain SERT protein expression (Table S7).