Supplementary Legends

Extended Data Figure 1. Breathing abnormalities in P0 Auts2 cKO pups. (a-f) Nes11-Cre (pan-CNS) Auts2 cKO mice. Representative plethysmography traces from control (a; n=7), heterozygous (b; n=7), and homozygous cKO (c; n=3) animals on P0. Abnormal breathing events (gasps, sighs, apneas) are indicated. Breathing frequency (d) was reduced (p=0.005); tidal volume (e) was increased (p=0.041); and breathing rhythms (f) were more irregular (p=0.002) in Nes11-Cre Auts2 cKO pups. (one-way ANOVA, P=0.0406). (g-i) Emx1-Cre Auts2 cKOctx mice. Breathing frequency was reduced (p=0.041), but other parameters were not significantly different in heterozygous (n=3) or homozygous (n=3) cKO mice from controls (n=3).
Respiratory metrics represented as mean + S.E.M. *, $p<0.05$; **, $p<0.005$.

Extended Data Figure 2. Histology of P5 control and Auts2 cKOctx forebrain. (a-d) DAPI-stained sections (fluorescence inverted) showed no abnormalities of neocortex (arrows) in homozygous Auts2 cKOctx brains (b, d) compared to controls (a, c). However, the DG (arrowheads) appeared slightly smaller in Auts2 cKOctx brains, as confirmed at higher magnification (c, d). Scale bar: B, 0.5 mm for a, b; 100 μm for c, d.

Extended Data Figure 3. Tbr2+ INPs are decreased and Penk mRNA is upregulated in Auts2 cKOctx DG (a, b) P0.5 dentate gyrus stained for TBR2 in control (a) and Auts2 cKOctx (b) mice, white outlined region indicates region of cell quantification. (c) Boxplot of cell counts from matched sections of three cKO and three control animals (one-tailed wilcox p-value = 0.05). (d, e) P0.5. Cells in the molecular layer (marginal zone) of the DG (red outlines) expressed Penk at higher levels in Auts2 cKOctx (e) than in control (d) mice. Penk was also increased in marginal zone cells of the adjacent subiculum (asterisks, e). (f, g) P7.5. Penk expression remained elevated in Auts2 cKOctx (g) as compared to control (f) DG. Scale bars as indicated.

Extended Data Figure 4. Examination of unaffected marker genes at P0 in cortex and dentate gyrus (a, b) P0.5 cerebral cortex stained for layer VI marker TBR1 in control (a) and Auts2 cKOctx (b) mice, images are oriented rostral cortex to the right (c, d) P0.5 cerebral cortex stained for layer II-III marker CUX1 in control (c) and Auts2 cKOctx (d) mice, images are oriented rostral cortex to the right (e, f) P0.5 dentate gyrus stained for cajal-retzius cell marker Reelin (Reln) in control (e) and Auts2 cKOctx (f) mice (g, h) P0.5 dentate gyrus stained for glial scaffolding

marker glial fibrillary acidic protein (Gfap) in control (g) and Auts2 cKOctx (h) mice

Extended Data Figure 5. Interaction network of proteins encoded by DETs bound by AUTS2 or expressed by genes with AUTS2 ChIP-seq peaks. (a) Transcripts that were bound and regulated by AUTS2 in vivo (Table 1) encoded proteins that formed a significant interaction network ($p=0.01$) as determined by STRING-DB. (b) Transcripts that were regulated by AUTS2, and whose cognate genes were bound by AUTS2, encoded proteins that formed no significant interaction network.