Differential methylation of enhancer at IGF2 is associated with abnormal dopamine synthesis in major psychosis

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Impaired neuronal processes, including dopamine imbalance, are central to the pathogenesis of major psychosis, but the molecular origins are unclear. Here we perform a multi-omics study of neurons isolated from the prefrontal cortex in schizophrenia and bipolar disorder (n = 55 cases and 27 controls). DNA methylation, transcriptomic, and genetic-epigenetic interactions in major psychosis converged on pathways of neurodevelopment, synaptic activity, and immune functions. We observe prominent hypomethylation of an enhancer within the insulin-like growth factor 2 (IGF2) gene in major psychosis neurons. Chromatin conformation analysis revealed that this enhancer targets the nearby tyrosine hydroxylase (TH) gene responsible for dopamine synthesis. In patients, we find hypomethylation of the IGF2 enhancer is associated with increased TH protein levels. In mice, Igf2 enhancer deletion disrupts the levels of TH protein and striatal dopamine, and induces transcriptional and proteomic abnormalities affecting neuronal structure and signaling. Our data suggests that epigenetic activation of the enhancer at IGF2 may enhance dopamine synthesis associated with major psychosis.
Chizophrenia and bipolar disorder are mental disorders characterized by periods of psychosis, including hallucinations, delusions, and thought disorder. These diseases have shared genetic features, peripubescent-onset, and dynamic clinical symptoms, and affect 100 million people worldwide. Psychotic symptoms are thought to be triggered by dopaminergic dysregulation, as the efficacy of all actively used antipsychotic drugs involves an attenuation of dopamine transmission, and the dopamine hypothesis of schizophrenia has endured as a neurochemical explanation for disease pathogenesis, for over 60 years. In addition, neurons of patients with psychosis exhibit numerous transcriptional, structural (decreases in dendritic spine density), and signaling abnormalities that disrupt cortical circuitry. The past decade of genomics research has shown that epigenetic misregulation of the genome can trigger long-lasting changes to neurodevelopmental programs, synaptic architecture, and cellular signaling, and thus may increase the risk of psychiatric disorders, such as schizophrenia and bipolar disorder. In particular, abnormalities in DNA methylation have been detected in the brain of schizophrenia and bipolar disorder patients, and their involvement in disease pathophysiology could explain the clinical dynamics observed in these diseases. However, DNA methylation studies of bulk brain tissue are confounded by sample-level variation in the proportion of different cell types. In addition, epigenetic changes occurring within neurons can be masked by the predominant glial signal; there are ~3.6 times more glia than neurons in the human frontal cortex gray matter. Epigenomic profiling in neurons of affected individuals – rather than blood or cell mixtures – would provide more accurate data for a model of neuronal dysregulation in disease; to date, no such data are available.

In this work, we perform a genome-wide comparison of DNA methylation in isolated neurons from the frontal cortex of individuals with schizophrenia and bipolar disorder, to those in undiagnosed individuals. We report a strong association in an enhancer located within the IGF2 locus, using an array-based approach, and by targeted bisulfite deep sequencing. IGF2 has been previously found to be differentially methylated in populations at risk for schizophrenia, and affects synaptic plasticity and cognitive functions like learning and memory. We then use several functional assays, bioinformatics, and mouse transgenics to provide evidence that the enhancer at IGF2 regulates the tyrosine hydroxylase (TH) gene; TH is the rate-limiting enzyme responsible for dopamine synthesis. We also find that Igf2 enhancer disruption in mice affects levels of TH protein and dopamine, as well as pathways involved in synaptic signaling and neuronal structure. This work suggests a mechanism for epigenetic regulation of dopamine levels in the brain. Epigenetic misregulation of an enhancer at IGF2 may underlie the dopaminergic abnormalities that drives psychotic symptoms. The epigenetic regulatory connection between IGF2 and TH may also help explain the co-occurrence of neuronal structure and synaptic abnormalities with dopamine dysregulation in major psychosis patients.

Results
DNA methyleone abnormalities in psychosis patient neurons.
We fine-mapped DNA methylation in neuronal nuclei (NeuN+) isolated by flow cytometry from post-mortem frontal cortex of the brain of individuals diagnosed with schizophrenia, bipolar disorder, and controls (n = 29, 26, and 27 individuals, respectively; Supplementary Data 1, Supplementary Table 1, Supplementary Fig. 1). We performed an epigenome-wide association analysis (EWAS) using Illumina MethylationEPIC microarrays surveying 812,663 CpG sites (Fig. 1 and Supplementary Figs. 2–4). In this analysis we controlled for age, sex, post-mortem interval, as well as genetic ancestry, which was determined by genotyping the same individuals (Infinium PsychArray-24 microarrays and imputed genotypes; 228,369 SNPs; n = 82 individuals; Supplementary Fig. 5). We identified 18 regions with significant DNA methylation changes in patients with major psychosis (comb-p Sidák p < 0.05; Fig. 1a; Supplementary Data 2; Supplementary Fig. 6a). Differentially methylated regions were enriched in pathways related to embryonic development, synaptic function, and immune cell activation (q < 0.05; hypergeometric test; Fig. 1b, Supplementary Data 3). We then determined the consequences of altered DNA methylation in major psychosis by profiling transcriptomes in a randomly selected subset of the same samples, by RNA sequencing (n = 17 cases, 17 controls; Supplementary Data 4, Supplementary Data 5, Supplementary Data 6, and Supplementary Figs. 6b and 7a), after adjusting for age, sex, post-mortem interval, and neuronal proportion. Pathway analysis revealed consistent alterations with those identified in the DNA methylation analysis, affecting early development, the immune system, and synaptic transmission (Fig. 1b).

We further examined the developmental regulation of genes transcriptionally altered in psychosis, using the BrainSpan dataset. Pre- and post-natal transcriptional dynamics of genes differentially expressed in psychosis showed a significantly higher correlation with those of synaptic development genes, relative to randomly-sampled sets (BrainSpan; p < 0.001; resampling, one-sided test; Supplementary Fig. 7b). Together, these findings suggest that in neurons of major psychosis patients, DNA methylation and transcriptional changes converge to affect early development, disrupt neurotransmission, and raise immune responses.

Genetic-epigenetic interactions in major psychosis neurons. We then identified genetic-epigenetic interactions at the differentially methylated regions in neurons of patients with psychosis. For this, we examined genotype information from the same individuals (82 individuals; Infinium PsychArray-24 microarrays) and imputed genotypes using 1000 Genomes reference panel, resulting in 228,369 SNPs (Supplementary Figs. 2 and 5). For each of the differentially-methylated regions, we performed a cis-meQTL analysis (which involves univariate SNP-CpG regression to assess the effect of genotype on base-level DNA methylation). We found that 13 of the 18 differentially methylated regions demonstrated significant genetic-epigenetic interactions in cis (q < 0.05; linear regression; 36 of 56 CpG probes within the 18 regions; 2212 of 13,552 SNPs in cis with differentially methylated probes) (Fig. 1c, and Supplementary Data 7). Additionally, one differentially methylated region at the HLA locus demonstrated significant genetic-epigenetic interactions with known genetic risk factors for schizophrenia (q < 0.05; linear regression; 4373 risk SNPs tested; Supplementary Data 8). Therefore, neurons of major psychosis patients show significant changes in DNA methylation, some of which may be mediated by genetic state.

Hypomethylation of enhancer at IGF2 in psychosis neurons.
Notably, two of the top differentially methylated regions in major psychosis neurons were located at the 3’ end of the IGF2 gene (Sidák p < 10−5; Fig. 2a; Supplementary Data 2a). Both schizophrenia and bipolar patients were consistently hypomethylated at the IGF2 locus, relative to controls (3–9% probe-level hypomethylation in cases relative to controls in IGF2 region; Fig. 2b). Hypomethylation of the IGF2 locus was also observed in an analysis limited to individuals with genetic European ancestry (13 controls, 20 bipolar disorder, 19 schizophrenia; Sidák p < 2 × 10−4 for IGF2 locus; Supplementary Data 2b). To assess the impact of
lifestyle-related covariates, we repeated probe-level tests for individual differentially methylated sites at the *IGF2* locus after controlling for smoking status (ever/never) and reported anti-psychotic use (some/none), in addition to age, sex, post-mortem interval, and the first two genetic principal components. The *IGF2* locus remained significantly hypomethylated in neurons of patients with major psychosis even after accounting for these lifestyle-related covariates (*p* < 0.05; nested ANOVA; DNA methylation for effect of disease relative to individual covariates in Supplementary Fig. 8). Furthermore, we did not find evidence of cis-acting genetic-epigenetic effects for any of the probes in the differentially methylated *IGF2* region (*q* > 0.05; Supplementary Data 9).

We also confirmed the reliability of the Illumina MethylationEPIC array findings by fine-mapping DNA methylation at the *IGF2* genomic area (~161 kb) in neurons, using a targeted bisulfite sequencing assay (*n* = 13 cases, 13 controls; array and bisulfite sequencing methylation correlation *R* = 0.67, *p* < 10^-19; Supplementary Fig. 9). This analysis also defined the *IGF2* site as being a 1.3 kb region with significant hypomethylation in neurons of major psychosis cases (7.4% hypomethylation *p* < 5 × 10^-4; nested ANOVA model; effect of disease after controlling for age, sex, post-mortem interval, and batch effect; Fig. 2c, Supplementary Data 10). In addition, we performed targeted bisulfite sequencing of the *IGF2* enhancer locus in glial cells (NeuN-) isolated from the same individuals (*n* = 10 cases, 12 controls). While we observed a similar trend of disease-specific hypomethylation in glial cells, this effect was not significant (4% hypomethylation; *p* = 0.07; nested ANOVA model; Fig. 2c).

To further verify that our effect is not confounded by sex and ethnicity, we reanalyzed our dataset examining only males of European genetic ancestry. Significant *IGF2* hypomethylation persisted in three of four tested Cpg probes when samples were limited to males of European genetic ancestry (*n* = 25 cases, 11 controls; Bonferroni-corrected *p* < 0.01; nested ANOVA model; effect of disease after accounting for age, post-mortem interval, and first two principal components of genetic ancestry; Fig. 2d).

**Dopamine synthesis abnormalities linked to enhancer at IGF2.**

The hypomethylated *IGF2* locus in major psychosis overlapped an enhancer in the adult frontal cortex (Fig. 2a; data from NIH Roadmap Epigenomics Project). Assessment of chromatin interactions in the prefrontal cortex by analysis of Hi-C data revealed that this enhancer targets the tyrosine hydroxylase (*TH*) gene promoter (Fig. 3a; Supplementary Fig. 10). *TH* is the rate-limiting enzyme for the production of the neurotransmitter dopamine. Dopamine dysregulation in the cortex and striatum of both
patients with schizophrenia and bipolar disorder is centrally involved in the cognitive and psychotic symptoms of these diseases.\textsuperscript{26,27} Reduced DNA methylation at the enhancer in IG2F was associated with elevated levels of TH protein levels in the human frontal cortex (\( R = -0.32, p < 0.05 \); linear regression; Fig. 3b, c), supporting the hypothesis that this enhancer modulates dopamine synthesis. Accordingly, the top differentially expressed genes from the transcriptomic profiling described above – namely, \textit{NR4A1}, \textit{NR4A2}, and \textit{EGR1} – are transcription factors that affect \textit{TH} and \textit{IGF2} expression\textsuperscript{28-33} (STRING database interactions, Supplementary Fig. 7c), supporting dysregulation of the \textit{TH}-\textit{IGF2} locus in major psychosis.

\textit{Igf2} enhancer loss affects dopamine levels and synapses. We then examined transgenic mice carrying an intergenic \textit{Igf2} enhancer deletion (Fig. 3). Since the intergenic enhancer region we deleted in mice is near the \textit{Igf2} gene but may not be the ortholog of the human \textit{IGF2} enhancer, we first analyzed Hi-C data of mouse cortical neurons, which showed that this mouse enhancer does target the promoter of the \textit{TH} gene as well as the \textit{Igf2} gene (Supplementary Fig. 11). In these mice, we examined the frontal cortex and striatum, the latter being a major site of dopamine production in the brain. In the striatum, inactivation of the \textit{Igf2} enhancer led to a decrease in \textit{TH} protein levels and in dopamine (\( p < 0.05 \); one-way ANOVA; Fig. 3d, e); this effect was not observed in the frontal cortex (Supplementary Fig. 12). \textit{TH} protein levels are 5.6-fold greater in the mouse striatum relative to frontal cortex (\( p < 10^{-11} \); one-way ANOVA; Supplementary Fig. 13), which may explain the capacity to detect a decrease in striatal, but not frontal, TH in mice lacking the enhancer at \textit{Igf2}. These data collectively suggest that in schizophrenia and bipolar disorder, epigenetic disruption of enhancer activity at the \textit{IGF2} locus in neurons leads to abnormalities in subcortical dopaminergic signaling, which is centrally involved in the development of psychotic symptoms.

We further examined the widespread consequences of enhancer disruption at the \textit{Igf2} locus in the brain by profiling the transcriptome. We used RNA-sequencing to assess the transcriptomes of wild-type and \textit{Igf2} enhancer deletion mice, examining the frontal cortex and striatum (Supplementary Data 11; Supplementary Fig. 14). Enhancer deletion resulted in a significant upregulation of \textit{Igf2} expression in both the frontal cortex and striatum of \textit{Igf2}-\textit{enh}\textsuperscript{−/−} mice (Fig. 4a; \( p < 4.3 \times 10^{-3} \) in frontal...
Fig. 3 The differentially methylated enhancer at IGF2 in major psychosis targets the dopamine synthesis enzyme tyrosine hydroxylase (TH). 

**a** Higher-order chromatin interactions of the differentially-methylated enhancer at IGF2 with the TH gene in the human prefrontal cortex; interactions within ±100 kb are shown. Blue arcs show all interactions from the location, and red arcs highlight those to the TH gene. Enh: Chromatin states reflecting enhancers in adult frontal lobe (blue rectangles). 

**b** Reduced DNA methylation at the IGF2 enhancer in major psychosis correlates with increased TH protein levels in the prefrontal cortex ($R = -0.32$, $p < 0.05$; linear regression; $n = 17$ controls (blue circles) and $n = 22$ cases (red circles)). TH protein levels are normalized to NeuN, IN, and actin. DNA methylation at the IGF2 enhancer is associated with differing TH protein levels between cases and controls (same data as b). Low, mid, or high DNA methylation (<50%, 50–60%, and >60%, respectively). Left to right: $n = 8, 11, 3, 9$, and 8 samples for cases (red boxplots) and controls (blue boxplots). 

**c** Main effect of DNA methylation by two-way ANOVA $F_{2,35} = 3.5$, $p < 0.05$; *$p = 0.05$ by Tukey post-hoc test. Boxplot center indicates median; box bounds indicate 25th and 75th percentile, and whiskers mark 1.5 times the interquartile range. 

**d** Effect of Igf2 enhancer deletion knockout in mice. Schema shows deletion of the 4.9 kb Igf2 enhancer alongside mouse forebrain enhancers (ENCODE, pink). 

**e** TH protein levels in striatum of adult wild-type (+/+; $n = 19$ mice; green circles) and Igf2 enh–/– (n = 11 mice; purple circles) mice (normalized to NeuN and actin). Data points shown along with mean standard deviation. 

**f** Dopamine levels in striatum of adult wild-type and Igf2 enh–/– mice measured by HPLC ($n = 20$ and 9 mice, respectively). Data normalized to wild-type levels. *$p < 0.05$ by one-way ANOVA.
of synaptosomes from the striatum of wild-type and Igf2enh−/− mice using quantitative mass spectrometry (Supplementary Figs. 16 and 17). We discovered widespread changes in Igf2enh−/− mice relative to wild-type mice; 956 of 3619 proteins tested were significantly different (q < 0.05; one-way ANOVA; Supplementary Data 16). Synaptic proteins with the highest change were involved in neurosignaling and structure, mitochondrial bioenergetics, and synaptic vesicle release (q < 0.01; hypergeometric test; Fig. 4c). Several proteins altered by Igf2 enhancer deletion had been found dysregulated in the synaptosomal proteome of schizophrenia patients35, including genes affecting synaptic plasticity and neurotransmitter release, such as calcium/calmodulin dependent protein kinase II alpha (Camk2a), myristoylated alanine-rich C-kinase substrate (Mark5), and alpha-synuclein (Snc1) (Fig. 4c). The top disease pathways enriched in striatal synaptosomes of mice lacking the enhancer at Igf2 were related to psychiatric, mental, and movement disorders (q < 0.05; hypergeometric test; 8 pathways of 715 tested for genes with q < 0.01; Fig. 4d; Supplementary Data 17 and 18). Therefore, loss of the enhancer at Igf2 in mice disrupts synaptic proteins involved in neurotransmission and associated with psychiatric disease.

Discussion
In sum, we identified a decrease in repressive epigenetic marks at an enhancer linked to TH gene regulation in neurons of patients with major psychosis. Enhancer-mediated upregulation of TH, promoting higher striatal dopamine synthesis, would augment the risk for psychosis36. Hence, hypomethylation of the enhancer at Igf2 may be an important contributor to the pathogenesis of psychotic symptoms.

Interestingly, in patients, the progressive loss of prefrontal cortex volume closely parallels the development of psychosis21,22. Imaging studies of at-risk individuals show greater prefrontal cortical volume loss in individuals that transition to psychosis compared to those remaining healthy22. The severity of psychotic symptoms is also associated with structural alterations in the cortex23. This link between psychotic symptoms and brain development may involve the molecular regulation of the IGF2 locus identified in this study. In the brain, IGF2 promotes synapse development, spine maturation, and memory formation16–19, signifying that normal IGF2 activation is required for healthy neuronal architecture. Recently, IGF2 was found to be the top downregulated gene in the schizophrenia prefrontal cortex in the

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Fig. 4 Transcriptomic and synaptic proteome alterations in the brain of mice lacking the enhancer at Igf2. **a** Transcript levels of Igf2 in the frontal cortex and striatum of adult wild-type and Igf2enh−/− mice. Left: frontal cortex (green boxplots: n = 6 wild-type, purple boxplots: 6 Igf2enh−/− mice). Right: striatum (n = 7 wild-type mice, 8 Igf2enh−/− mice). P-values from two-sided Wilcoxon test. Boxplot center indicates median; box bounds indicate 25th and 75th percentile, and whiskers mark 1.5 times the interquartile range. **b** Pathways enriched for differential expression in the striatum of Igf2enh−/− mice, relative to wild-type mice. Nodes show pathways with q < 0.05 (68 pathways, preranked GSEA) and edges indicate shared genes (EnrichmentMap77; default setting of Jaccard and overlap = 0.375). Red nodes: upregulated expression in Igf2enh−/− mice; blue nodes: downregulated expression in Igf2enh−/− mice. Pathways were clustered using AutoAnnotate83. Full pathway enrichment results in Supplementary Data 15. **c** Functional annotation of synaptic proteins significantly altered in the striatum of Igf2enh−/− mice relative to wild-type mice (q < 0.01; one-way ANOVA; n = 6 wild-type mice, 6 Igf2enh−/− mice, 2 pools per genotype with 3 mice/pool). Genes overlapping synaptosomal proteome abnormalities in schizophrenia brain35 are highlighted. Quantitative proteome analysis by mass spectrometry and clustering of top proteins altered in Igf2enh−/− mice by STRING. Node fills indicate gene pathways; green: mitochondrial bioenergetics; red: neuronal signaling and structure; blue: synaptic vesicle release. **d** Disease pathways enrichment for synaptic proteins dysregulated in Igf2enh−/− mice (q < 0.05, MetaCore; 715 pathways tested; Supplementary Data 17).
large CommonMind consortium RNA-sequencing study.37 Loss of DNA methylation at the IGF2 locus has been associated with decreased IGF2 mRNA levels in early development,38 and risk factors for schizophrenia; prenatal exposure to famine15 and reduced brain weight.39 Similarly, our transcriptome analysis in major psychosis patients found a downregulation of genes affecting synaptic transmission and interacting with IGF2. In support, mice lacking the enhancer at IGF2 had a decrease in TH and dopamine levels, along with an IGF2 upregulation as well as transcriptomic and proteomic alterations affecting synaptic activity and structure. Therefore, in neurons of major psychosis patients, epigenetic changes facilitating a recruitment of the enhancer at IGF2 for activation of TH, may, in tandem, impede IGF2 regulation. We propose that improper epigenetic control of an IGF2 enhancer may simultaneously contribute to dopamine-mediated psychotic symptoms and synaptic structural deficits in major psychosis.

A limitation to this study is that inter-species differences in enhancer size and location makes it challenging to demonstrate equivalence of human and mouse enhancers.40 Nonetheless, our findings demonstrate that altered activity of the enhancer nearest to the IGF2 gene in the mouse affects TH protein levels and changes gene expression in pathways affecting neurodevelopment, neurosignaling, and synaptic activity, as was observed in major psychosis patients with a hypomethylated enhancer at IGF2. This shared consequence in humans and in transgenic support the hypothesis that IGF2 enhancer activity is associated with altered TH regulation and dopamine signaling. Further study is required to fully characterize the extent to which enhancers regulate TH and dopamine signaling in psychotic disorders.

The multi-omics approach in isolated neurons used in this study offers a rich dataset for investigating the molecular events involved in major psychosis. Many of the epigenetic abnormalities identified in major psychosis neurons were associated with genotype, suggestive of a genetic origin and the potential that these epigenetic states may be set early in life, before the onset of disease symptoms. However, our findings do not preclude the role of, and interaction with, non-shared environmental factors, particularly during early synaptic development and in response to environmental stressors like inflammation.41 It will be also important to replicate these findings in a second large cohort of major psychosis and control neurons. Future genome-scale studies, expanding this dataset to other types of epigenetic modifications (i.e., non-CG methylation, hydroxymethylation, histone marks) and to neurons of other brain regions will also be important for understanding the dynamic interplay between epigenome, transcriptome, and genetic factors in major psychosis. Of particular interest will be studies examining whether hypo-methylation at the IGF2 enhancer extends from a risk factor to a prognostic marker in peripheral tissues for the development of psychosis.

Methods

Human tissue samples. Post-mortem brain samples of frontal cortex were obtained through the NIH NeuroBioBank at the University of Pittsburgh; the Harvard Brain Tissue Resource Center; the Human Brain and Spinal Fluid Resource Center at Sepulveda; and the University of Miami Brain Endowment Bank. Patient data is provided in Supplementary Data 1. We obtained sample information on demographic factors (age, sex), clinical variables (cause of death, medications at time of death, duration of antipsychotic use, smoking status, and brain weight), and tissue quality (post-mortem interval, tissue quality/RIN score). Our analyses controlled for sample age, sex, post-mortem interval, ethnicity, and the influence of the clinical and technical covariates was examined in our data. The study protocol was approved by the institutional review board at the Centre for Addiction and Mental Health and the Van Andel Research Institute (IRB #15025).

Lifestyle-related factors. Lifestyle factors were coded in the same manner for cases and controls. To ascertain which patients had a history of antipsychotic medication, we used the FDA’s Estrogen-Replacement database. The nuclear sex of the individual was collected from the literature (https://www.fda.gov/Drugs/DrugSafety/ucm243903.htm), including generic and brand names. Patient medication information was computationally searched for keyword matches from this list to identify drugs used by individuals; the mood stabilizers lithium and valproic acid were included in this list. Where no match was found, antipsychotic status was set to none. Where we controlled for antipsychotic treatment, patients were divided into those who had antipsychotic use and those who did not. Smoking status was similarly binary, so that any lifetime record of smoking resulted in a categorization of the sample as a smoker or non-smoker (i.e. ever or never). Individuals with missing information were not included in the analysis examining the effects of lifestyle factors.

Isolation of neuronal nuclei using flow cytometry. Neuronal nuclei were separated using a flow cytometry-based approach, similar to as described.44,45 Briefly, human brain tissue (250 mg) for each sample was minced in 2 mL PBSTA (0.3 M sucrose, 1X phosphate buffered saline (PBS), 0.1% Triton X-100). Samples were then homogenized in PreCellys CKMix tubes with a Minilys (Bertin Instruments) set at 3,000 rpm for three 5 s intervals, 5 min on ice between intervals. Samples homogenates were filtered through Miracloth (EMD Millipore), followed by a rinse with an additional 2 mL of PBSTA. Samples were then placed on a sucrose cushion (1.4 M sucrose) and nuclei were pelleted by centrifugation at 4000 × g for 30 min 4 °C using a swinging bucket rotor. For each sample, the supernatant was removed and 1X PBS was incubated in the pellet and the nuclei were then gently resuspended and blocking mix (100 μL of 1X PBS with 0.5% BSA (Thermo Fisher Scientific) and 10% normal goat serum (Gibco) was added to each sample. Neun−/488 (1:500; Abcam; ab190195) was added and was incubated 45 min at 4°C with gentle mixing. Immediately prior to flow cytometry, the nuclei were stained with 7-AAD (Thermo Fisher Scientific) and passed through a 30 μm filter (SystemX). Nuclei positive for 7-AAD and either Neun+ (neuronal) or Neun− (non-neuronal) were sorted using an Influx (BD Biosciences) or BD FACSAria Illu (BD Biosciences) at the Faculty of Medicine Flow Cytometry Facility (Toronto, ON, Canada). Approximately 1 million Neun−/neuronal nuclei were sorted for each sample. Immediately, after sorting nuclei were placed on ice and then precipitated by raising the volume to 10 mL with 1X PBS and adding 2 mL 1.8 M sucrose, 50 μL 1 M CaCl2, and 30 μL Mg(Ace); and centrifugation at 1700 × g for 15 min at 4°C. The supernatant was removed from Neun+ and Neun−/neuronal samples and pellets were stored at −80°C. Genomic DNA from each Neun+/neuronal nuclei fraction of each sample was isolated using standard phenol-chloroform extraction methods.

Genome-wide DNA methylation profiling. Whole-genome DNA methylation profiling for each sample was performed on Illumina MethylationEPIC BeadChip microarrays at The Centre for Applied Genomics (Toronto, Canada). Bisulfite converted DNA samples (n = 104) were randomized across arrays (8 samples/array). Data generated from the microarrays were preprocessed with Minfi v1.19.12 (see Supplementary details listed in Supplementary Note 1). and the number of replicates was 2. Probes were called with nooh45, followed by quantile normalization. We confirmed that the sex of the individuals, as identified from the genotype data (described below) matched the inferred from the DNA methylome (minfi getSex) (function). Probes that overlapped SNPs (minor allele frequency >0.05) on the CpG or single-base extension were excluded. Probes were excluded if the probes known to be cross-reactive46 (42,558 probes) and those that failed detectability (p > 0.01) in > 20% samples (1170 probes). After processing, 812,663 probes were left. Principal component analysis (PCA) was performed on the matrix of beta values and the first three principal component projection were examined for all samples; samples were color-coded in turn by various biological and technical variables (Supplementary Fig. 3). Based on this PCA co-clustering, one sample, despite being labeled NeuN+ was an outlier; this sample was excluded from downstream analyses. PCA plots revealed no sampling separation at the array slide on which samples were run. We provided the surrogate variable analysis47 calculator with the known covariates of age, sex, diagnosis, and post-mortem interval in 700 μL of 1X PBS for 20 min. The nuclear surrogate variables. Additionally, we did not observe structure in the data exploration (PCA, hierarchical clustering, Supplementary Figs. 3 and 4), suggesting there is no major unknown confounder. Therefore, we conclude that there are no major sources of unexplained variation.

We used the BioConductor package bacon to compute lambda for our EWAS, providing it with t-statistics from the main EWAS reported in our manuscript (inflation factor); 82 samples; age, sex, post-mortem interval, and first two genetic principal components were included as covariates). The estimated inflation factor is 1.03, which is the regime of minimal inflation for an EWAS (<1.14).
and the first two principal components of genetic ancestry were used as covariates. Benjamini–Hochberg FDR correction was used to correct nominal p-values.

Principal Component Analysis (Thermo Fisher Scientific) was performed with the GATK website (https://gatkforums.broadinstitute.org/gatk/discussion/3892/). A linear regression was used to assess the effect of genotype on gene expression (RNAseq data). Where pairs of individuals had relatedness (Identity By Descent ≥ 0.05), those in the full cohort (n = 10 samples with AA, 10 samples with BB, 10 samples with AB) were conserved. For European-specific GWAS, Europeans were defined as individuals with MDS 1 and 2 lying within 3 standard deviations of the mean defined by the CEU population in the HapMap3 reference panel. The biological sex of samples was confirmed by matching the sex ascertained from the genotype data to that using control probes on the methylation arrays (minifGetSex function).

As a measure of the extent of population stratification, we computed lambda using the genotype data (82 samples, technical replicates excluded) for a plink logistic regression on case/control status, after adjusting for age, sex, post-mortem interval, and the first two genetic principal components, and the lambda is 1.07; this value is in the regime of acceptable values for GWAS studies (~1.0561).
the number of SNPs for which number of minor alleles (0, 1, or 2) was identical between the genotype and RNA-seq platforms. We found perfect sample matching between the RNA-seq and genotype platforms (median of ~5.2K SNPs tested; 93-96% genotype match; Supplementary Fig. 5b).

Gene counts matrix was imported into R (3.4.1) and low expressed genes (counts per million (CPM) <1 in all samples) were removed prior to differential expression in edgeR81. Gene counts were normalized using the trimmed mean of M-values, fitted in a generalized linear model and differentially tested using a likelihood ratio test. The generalized linear model included age, sex, post-mortem interval, and neuronal cell composition as covariates. Cell-type compositions for each sample was accessed using CIBERSORT82 on normalized sample counts against the 37 hepatocyte, 14 blood, and 29 other cell types (see below) matrices (see below) and were used to infer the proportion of neurons in each samples. Benjamini-Hochberg correction was used to adjust for multiple testing. We also performed a sensitivity analysis to confirm that genetic ancestry did not alter our RNA-seq findings, and found that analysis of only individuals with European ancestry (exclusion of 3 non-European individuals) had strongly correlated results (Pearson correlation = 0.91) and the same top gene hits as the original analysis.

Our RNA-seq analysis corrected for the proportion of neuronal cells in each sample. Neuronal cell proportions were determined by CIBERSORT82 (http://cibersort.stanford.edu), which involved a gene signature matrix derived from single cell RNA-seq measures in adult human brain cells (signature matrix;82 source65). Because major psychosis is characterized by a loss of synaptic density, we excluded genes encoding synaptic proteins (Genes2Coginition database;86 lists L00000009, L00000016, and L00000012) from the gene signatures. One hundred and thirty-five synapse-associated genes were excluded, leaving 768 genes in the deconvolution analysis. CIBERSORT was run (100 permutations), and the inferred proportion of neurons was used as a covariate for differential expression.

Pathway enrichment analysis. Pathways affected by the DNA methylation and transcriptomic changes in major psychosis were determined. For DNA methylation data, probes were mapped to genes if they overlapped between 1 kb upstream of the transcription start site to the transcription end site. Gencode25 v27 (liftOver to GRCh37) was used for gene extents. Pathway definitions were aggregated from HumanCyc72, IOB’s NetPath73, Reactome74, NCI Curated Pathways75, mSigDB35, Pathway Interaction database, MSigDB35, Panther77, and Gene Ontology78,79. The same pathway sets were used for the DNA methylation and transcriptomic analysis. For DNA methylation pathway analysis, only pathways with 10–50 genes were included (6858 pathways). For pathway analysis of DNA methylation, a hypergeometric test was performed comparing the proportion of foreground probes (p < 0.05 from DNA methylation region analysis) to background probes (all probes tested in DNA methylation region analysis). Pre-ranked GSEA83 was used for transcriptomic pathway analysis, as it separates pathways upregulated in disease from those downregulated in disease (see Gene expression profiling by RNA-seq section for details). Benjamini-Hochberg correction was performed to adjust for multiple testing with significance at q < 0.05.

Igf2 enhancer deletion in mice. A 4.9-kb long DNA fragment (chr7: 149,796,331-149,801,250 in mm9) was deleted from the intergenic region of the H19 and Igf2 by classical ES cell gene targeting and blastocyst injection in the mouse on the 129S1 genetic background. One lqox site remained at the site of the deletion mutation after the excision of the Pkgneo positive selection cassette by crossing the targeted mutant male mouse to an Hprt-Cre transgenic female.84 Three oligonucleotide primers (IGKOCrerecU: CGGAATGTTTGTGTGGAGAGCA; IGKOwtU: CCTGTAACCC) are combined in one PCR reaction to distinguish the mutant from wild-type mice17,81, and to the manufacturers’ recommended protocol. Blots were then washed three times with 50 µm TRIB and imaged using west pico ECL reagent (Thermo Fisher Scientific).

HPLC-based quantification of dopamine levels. All tissue preparation procedures were performed on ice. Frozen tissue samples weighing between 5 and 20 mg were sonicated in 100–300 µl of 0.2 M perchloric acid (Sigma). The sample was centrifuged at 22,000 xg for 30 min and the resulting supernatant was filtered using 0.22 µm cellulose acetate filter (Costar). The filtered supernatant was separated using the HTEC-500 High Pressure Liquid Chromatography (HPLC) system (Eicom) with the SC-300 reverse phase separation column (Eicom) and electrochemical detector. Samples were separated in mobile phase consisting of 0.1 M citrate acetate pH 3.5, 20% methanol, 220 g/L sodium octane sulfonate, and 5 mg/L EDTA-Na. The samples were then compared to known standards of dopamine (Sigma), homovanillic acid (HVA), and 3,4-Dihydroxyphenylacetic acid (DOPAC). The pellet was dissolved in 0.5 ml of 1 M NaOH for 10 min at 90°C, and the resulting protein concentration determined by BCA assay. The final values were calculated as ng analyte per µg protein.

RNA-seq processing for mice with the Igf2 enhancer deletion. A transcriptomic analysis of the striatum and frontal cortex of wild-type and Igf2–/– mice was performed. Brain tissue (~25 mg) was homogenized with a ceramic bead-based homogenizer (Precellys, Bertin Instruments) in 1 ml of Trizol (Life Technologies). Total RNA was isolated according to the Trizol manufacturer’s instructions, treated with RNase-free DNase I (Qiagen) at room temperature for 30 min, and cleaned up with the RA-Mini Kit (Qiagen). RNA yield was quantified using a NanoDrop ND-1000 (Thermo Fisher Scientific), and RNA integrity was verified using the Agilent Bioanalyzer 2100 system (Agilent Technologies). Libraries were prepared by the Gene Expression platform at the Van Andel Genomics Core from 500 ng of total RNA and sequenced, as described in the Gene expression profiling by RNA-seq section for details. Benjamini-Hochberg correction was performed to adjust for multiple testing with significance at q < 0.05.

Differential expression and pathway analysis in mice. Only genes with ≥1CPM in all samples were included for differential expression analysis. Transcript counts were normalized for library size using the Trimmed Mean of M values (TMM) method. Ensembl Gene IDs were mapped to MGI symbols using Biomart. To ascertain differentially-expressed genes, edger18 was used to fit a linear model to each gene, using the genotype (wild-type or Igf2–/–) as an explanatory variable and sex as a covariate. LRT was used to estimate the dispersion of each gene, and glmLRT was used to identify differentially-expressed genes. Benjamini-Hochberg was used to correct for multiple-testing (significance at q < 0.05). For pathway analysis, pre-ranked GSEA was run using the output of differential expression analysis. Gene sets included curated pathway databases including: HumanCyc72, IOB’s NetPath73, Reactome472, NCI Curated Pathways76, Pathway Interaction database, MSigDB35, Panther77, etc.
and Gene Ontology Biological Pathway terms (no iea)76,77, downloaded from http://download.broadinstitute.org/EM_Genomese/October_01_2017/Mouse/symbols/ Mouse_GO3P_ALLpathways_no_GO_ice/October_01_2017/Mouse_symbol.go47. Gene sets were limited to those with 10–20,000 genes (6321 gene sets).

**Synaptosomal proteome analysis by mass spectrometry.** Changes in synaptic proteins in the striatum of mice with the enhancer deletion at Igf2 were determined by quantitative proteome analysis. In this study, striatal synaptosomes from wild-type and Igf2−/− mice were compared (2 striatum pools per genotype, 3 mice per pool; n = 6 wild-type and 6 Igf2−/− /− mice). Synaptosomes were isolated from frozen striatum similar to a previously-described protocol86. Specifically, striatum tissue was homogenized in 5 mL isolation buffer (0.32 M sucrose, 10 mM Heps pH 8.0, and protease inhibitor cocktail) using 16 gentle strokes with a glass dounce homogenizer. Samples were then centrifuged for 10 min at 100,000×g. The resultant supernatant was then layered on 1.2 M sucrose and centrifuged at 160,000×g for 15 min using SW-41 Ti rotor (Beckman Coulter). The interface between sucrose layers was collected, layered on top of 0.8 M sucrose, and centrifuged again at 160,000×g for 15 min. The resulting pellet was then dissolved in 100 μL RIPA buffer and concentration determined using a BCA assay (Thermo Fisher Scientific). Purity of synaptosomes was verified by western blotting with anti-synaptophysin antibody (Cell Signaling, #12270), anti-histone 3 antibody (Abcam, ab1791), and anti-actin antibody (Millipore, #MAB1501) all diluted 1:1000. Each sample (70 µg per sample) was run 1 cm into a SDS-PAGE gel and stained using coomassie blue as described.88 Samples were then submitted to the Whitehead Mass Spectrometry Facility (MIT, Cambridge, MA) for subsequent proteome library preparation, iTRAQ-labeling, chromatographic separation, and mass spectrometry (MS). Briefly, samples excised from the SDS-PAGE gel were reduced, alkylated, and digested with trypsin at 37 °C overnight using buffers and reagents that were free of primary amine. The resulting peptides were extracted, labeled with Sciex iTRAQ 4-plex isotopic tags, combined, purified, and concentrated by solid-phase extraction and injected onto a Shimadzu HPLC and fraction collector equipped with a self-packed Aeris PEPTIDE XB-C18 analytical column (10 cm by 2.1 mm, Phenomenex). Peptides were eluted using standard reverse-phase gradients and pH = 10 ammonium formate buffers with a total of 16 fractions collected across the analytical gradient. The resulting fraction were reduced to a total of 8 fractions. After volume reduction the peptides in these eluents were separated using standard reverse-phase gradients using a Thermo EASY nLC chromatographic system. The effluent from the column was analyzed using a Thermo Q Exactive HF-X Hybrid Quadrupole-Orbitrap mass spectrometer (nanospray configuration) operated in a data-dependent manner.

Peptides were identified from the MS data using PEAKS Studio 8.5. The Mus musculus Refseq protein FASTA entries were downloaded from NIH/NCBI and concatenated to a database of common contaminants. An FDR threshold of 2% for identification of peptides and protein positive identifications was used, and quantitation was based on the top three Total Ion Current (TIC) method. Relative ratios of the iTRAQ 4-plex reporter ions were used for quantitation. Significance was calculated by ANOVA, and the Benjamini-Hochberg method was used for multiple testing correcting for significance q < 0.05. As a check for potential synaptosomal protein content, we performed a pathway analysis on all detected proteins. A hypergeometric test was performed using pathway genes (10–20 genes) and human-mouse disease genes (total of 1760 test). Foreground was all proteins in genes) and human-mouse disease genes (total of 1760 test). Foreground was all proteins in genes) and human-mouse disease genes (total of 1760 test). For comparison q < 0.05.

Peptides relative to wildtype, pathway analysis was performed using MetaCore (https://clarivate.com/products/metacore/). Proteins with differential expression at q < 0.001 (q < 0.01) were used as foreground, and the set of all proteins for which relative ratio was computed was used as the background.

**Software availability.** Software used to produce the results in this work are publicly available in a github repository at https://github.com/shraddhapai/EpiPsychosis_Igf2.

**Reporting summary.** Further information on research design is available in the Nature Research Reporting Summary linked to this article.

**Data availability.** Raw and processed data for data generated in this work have been deposited at the Gene Expression Omnibus under the SuperSeries accession number GSE112525. These include subseries for human DNA methylation arrays (GSE112179), RNA-sequencing (GSE112523), bisulfite targeted sequencing (GSE111524), and genotyping arrays (GSE113093), and transcriptome profiling of mouse brains (GSE120423). These data are associated with Figs. 1, 2, and 4 and Supplementary Figs. 3–9, 14 and 15. The chromatin conformation analysis in human prefrontal cortex, as shown in Fig. 3a and Supplementary Fig. 10, used peaks provided from the 3D Interaction Database at https://www.kobic.kr/3div/. Protein–protein interaction networks shown in Fig. 4c and Supplementary Fig. 7c were obtained from the STRING database (https://string-db.org/). The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository (https://www.ebi.ac.uk/pride/archive/); accession codes are PXD012786 and 10.6019/PXD012786. The underlying data for Fig. 3b and Supplementary Figs. 12 and 13 are available in the Source Data file. All other relevant data supporting the key findings of this study are available within the article and its Supplementary Information or files from the corresponding authors upon reasonable request. A reporting summary for this Article is available as a Supplementary Information file.

**Received: 30 April 2018 Accepted: 27 March 2019**

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Acknowledgements
S.P. and V.L. are supported by the Brain & Behavior Research Foundation (529941 to S. P.; 23482 to V.L.). V.L. is also supported by grants from the Alzheimer Society of Canada (16 15), Scottish Rite Charitable Foundation of Canada (15110), and the Department of Defense (PD170089). We thank John Murdoch for assistance with targeted bisulfite sequencing library preparation. We thank Van Andel Research Institute core services including the pathology and bioinformatics, genomics, and bioinformatics and biostatistics. We also thank Therese Murphy, Jonathan Mill, and Sarah Gaglano for feedback on parts of this work. Computations were performed on the GPC and Niagara supercomputers at the SciNet HPC Consortium. SciNet is funded by: the Canada Foundation for Innovation under the auspices of Compute Canada; the Government of Ontario; Ontario Research Fund – Research Excellence; and the University of Toronto. Tissue samples for this study were obtained from the following tissue banks through the NIH NeuroBioBank at the Harvard Brain Tissue Resource Center (supported in part by PHS contract, HHSN-271-2013-00030C); the Human Brain and Spinal Fluid Resource Center (VA West Los Angeles Healthcare Center, Los Angeles CA 90073 which is sponsored by NINDS/NIMH, National Multiple Sclerosis Society, and the Department of Veterans Affairs); the University of Miami Brain Endowment Bank; and the University of Pittsburgh Brain Tissue Donation program.

Author contributions
The study was designed and coordinated by S.P. and V.L. V. L. and P.J. contributed to the sorting of neuronal nuclei and DNA extraction for epigenetic and genetic experiments. S.P. performed the computational analysis for the epigenetic, genetic, and transcriptomic datasets. L.M. processed the transcriptomic dataset. B.K. performed immunoblotting, HPLC experiments, and synaptic proteome study. P.E.S. generated and J.L. managed the mutant mice with the Igf2 enhancer deletion. P.L. analyzed the chromatin conformation data and contributed to the DNA methylation analysis. A.P. helped oversee the project. The manuscript was written by S.P. and V.L., and commented on by all authors.

Additional information
Supplementary Information accompanies this paper at https://doi.org/10.1038/s41467-019-09786-7.

Competing interests: The authors declare no competing interests.

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Journal peer review information: Nature Communications thanks the anonymous reviewer(s) for their contribution to the peer review of this work.

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