Top 10 pathways for GSEA and hypergeometric tests (see Methods, main text).

Shown for each pathway is the name and description, the gene symbols for all genes in the pathway with nominal p<0.05 in univariate testing of association with MDD (on normalized expression data and with correction of additional covariates as described in Methods), the number of genes in the pathway that had adequate expression in this study to be analyzed (for GSEA); and the nominal p-value and q-value (FDR) for the pathway by permutation testing.

GSEA enrichment test
Pathway_name (description)
Genes with nominal p<.05
N(expressed genes); p; q

REACTOME_INTERFERON_ALPHA_BETA_SIGNALING (interferon-induced genes)
MX1,OAS1,IFIT3,PTPN6,ADAR,IRF7,IFIT1,USP18,ISG15,OAS2,IRF8,IFIT2,OAS3,MX2,IRF9,IFI6,OASL,XAF1,IFI35,IFNAR2
N=49; p=2.25E-05; q=0.0298

MIPS_LARC_COMPLEX (nucloesome remodeling)
MBD2,DPF2,MTA2,SMARCC2,SMARCD2,GATAD2B,ACTB
N=19; p=0.0005; q=0.314

MIPS_SMN_COMPLEX (cytoplasmic assembly of small nuclear ribonucleoproteins)
GEMIN5,SNRPF,GEMIN7,GEMIN4
N=13; p=0.0014; q=0.498

MIPS_EMERIN_COMPLEX_25 (Cellular signaling and RNA processing)
YWHAE,ACTB
N=15; p=0.0017; q=0.498

MIPS_NCOR1_COMPLEX (transcriptional repression through recruiting histone deacetylases)
SF3A1,SMARCC2,SF3B3
N=10; p=0.0021; q=0.498

BIOCARTA_RANKL_PATHWAY ("receptor activator of NF-kB ligand, complex involved in bone remodeling")
IRF9,EIF2AK2,FOSL1,IFNAR2
N=13; p=0.0023; q=0.498

MIPS_HDAC1_ASSOCIATED_CORE_COMPLEX_CII (Histone deacetylase complex)
MBD2,MTA2,CHD3,GATAD2B
N=9; p=0.0034; q=0.565

REACTOME_COPI_MEDIATED_TRANSPORT (transport within the early secretory pathway)
COPG,COPB2,ARCN1
N=10; p=0.0041; q=0.565

MIPS_ESCRT_III_COMPLEX (endosomal cargo transport)
CHMP5,CHMP2A,CHMP6
N=8; p=0.0042; q=0.565

REACTOME_PROLACTIN_RECEPTOR_SIGNALING (genes invloved in Prolactin receptor signaling)
PRLR,STAT5B
N=11; p=0.0043; q=0.565

Hypergeometric enrichment test (among top 500 univariate genes)
Pathway_name (description)
Genes with nominal p<.05
p; q

REACTOME_INTERFERON_ALPHA_BETA_SIGNALING (Interferon induced)
MX1,OAS1,IFIT3,PTPN6,ADAR,IRF7,IFIT1,USP18,ISG15,OAS2,IRF8,IFIT2,OAS3,MX2,IRF9,IFI6,OASL,XAF1,IFI35,IFNAR2
N=49;p=0; q=0

REACTOME_ANTIVIRAL_MECHANISM_BY_IFN_STIMULATED_GENES (interferon gamma)
MX1,IFIT1,USP18,ISG15,NUP153,MX2,HERC5,EIF2AK2,NUP88,EIF4E2,ARIH1,NUP188,EIF4G3,NUP107,EIF4A3,FLNB
N=65;p=0.0001; q=0.068

MIPS_LARC_COMPLEX (neuclosome remodling)
MBD2,DPF2,MTA2,SMARCC2,SMARCD2,GATAD2B,ACTB
N=19;p=0.0005; q=0.174

MIPS_C_COMPLEX_SPLICEOSOME (RNA splicing)
SYF2,SNRNP40,PRPF19,SF3A1,SF3A2,XAB2,HNRNPA1,HNRNPU,SNRPF,CDC40,EFTUD2,HNRNPA2B1,EIF4A3,SF3B3
N=79;p=0.0005; q=0.174

REACTOME_INTERFERON_GAMMA_SIGNALING (interferon gamma)
OAS1,PTPN6,IRF7,OAS2,IRF8,OAS3,IRF9,OASL,PIAS1,SUMO1
N=56; p=0.0008; q=0.222

MIPS_ESCRT_III_COMPLEX (endosomal cargo transport)
CHMP5,CHMP2A,CHMP6
N=8;p=0.0023; q=0.504

MIPS_BRM_SIN3A_HDAC_COMPLEX (histone modificaiton)
PRMT5,SMARCC2,SMARCD2
N=12;p=0.0081; q=1

SA_G1_AND_S_PHASES ("CDK2, cell cycle checkpoint and transition")
NXT1,E2F2,CDK4
N=14; p=0.0126; q=1

MIPS_BRG1_SIN3A_COMPLEX (histone modification)
PRMT5,SMARCC2,SMARCD2
N=14;p=0.0126; q=1

MIPS_BRM_SIN3A_COMPLEX (histone modification)
PRMT5,SMARCC2,SMARCD2
N=15;p=0.0154; q=1