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IMMEDIATE COMMUNICATION

Understanding and predicting suicidality using a combined genomic and clinical risk assessment approach

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Worldwide, one person dies every 40 seconds by suicide, a potentially preventable tragedy. A limiting step in our ability to intervene is the lack of objective, reliable predictors. We have previously provided proof of principle for the use of blood gene expression biomarkers to predict future hospitalizations due to suicidality, in male bipolar disorder participants. We now generalize the discovery, prioritization, validation, and testing of such markers across major psychiatric disorders (bipolar disorder, major depressive disorder, schizoaffective disorder, and schizophrenia) in male participants, to understand commonalities and differences. We used a powerful within-participant discovery approach to identify genes that change in expression between no suicidal ideation and high suicidal ideation states ($n = 37$ participants out of a cohort of 217 psychiatric participants followed longitudinally). We then used a convergent functional genomics (CFG) approach with existing prior evidence in the field to prioritize the candidate biomarkers identified in the discovery step. Next, we validated the top biomarkers from the prioritization step for relevance to suicidal behavior, in a demographically matched cohort of suicide completers from the coroner's office ($n = 26$). The biomarkers for suicidal ideation only are enriched for genes involved in neuronal connectivity and schizophrenia, the biomarkers also validated for suicidal behavior are enriched for genes involved in neuronal activity and mood. The 76 biomarkers that survived Bonferroni correction after validation for suicidal behavior map to biological pathways involved in immune and inflammatory response, mTOR signaling and growth factor regulation. mTOR signaling is necessary for the effects of the rapid-acting antidepressant agent ketamine, providing a novel biological rationale for its possible use in treating acute suicidality. Similarly, MAOB, a target of antidepressant inhibitors, was one of the increased biomarkers for suicidality. We also identified other potential therapeutic targets or biomarkers for drugs known to mitigate suicidality, such as omega-3 fatty acids, lithium and clozapine. Overall, 14% of the top candidate biomarkers also had evidence for involvement in psychological stress response, and 19% for involvement in programmed cell death/cellular suicide (apoptosis). It may be that in the face of adversity (stress), death mechanisms are turned on at a cellular (apoptosis) and organismal level. Finally, we tested the top increased and decreased biomarkers from the discovery for suicidal ideation (CADM1, CLIP4, DTNA, KIF2C), prioritization with CFG for prior evidence (SAT1, SKA2, SLC4A4), and validation for behavior in suicide completers (IL6, MBP, JUN, KLHDC3) steps in a completely independent test cohort of psychiatric participants for prediction of suicidal ideation ($n = 108$), and in a future follow-up cohort of psychiatric participants ($n = 157$) for prediction of psychiatric hospitalizations due to suicidality. The best individual biomarker across psychiatric diagnoses for predicting suicidal ideation was SLC4A4, with a receiver operating characteristic (ROC) area under the curve (AUC) of 72%. For bipolar disorder in particular, SLC4A4 predicted suicidal ideation with an AUC of 93%, and future hospitalizations with an AUC of 70%. SLC4A4 is involved in brain extracellular space pH regulation. Brain pH has been implicated in the pathophysiology of acute panic attacks. We also describe two new clinical information apps, one for affective state (simplified affective state scale, SASS) and one for suicide risk factors (Convergent Functional Information for Suicide, CFI-S), and how well they predict suicidal ideation across psychiatric diagnoses (AUC of 85% for SASS, AUC of 89% for CFI-S). We hypothesized *a priori*, based on our previous work, that the integration of the top biomarkers and the clinical information into a universal predictive measure (UP-Suicide) would show broad-spectrum predictive ability across psychiatric diagnoses. Indeed, the UP-Suicide was able to predict suicidal ideation across psychiatric diagnoses with an AUC of 92%. For bipolar disorder, it predicted suicidal ideation with an AUC of 98%, and future hospitalizations with an AUC of 94%. Of note, both types of tests we developed (blood biomarkers and clinical information apps) do not require asking the individual assessed if they have thoughts of suicide, as individuals who are truly suicidal often do not share that information with clinicians. We propose that the widespread use of such risk prediction tests as part of routine or targeted healthcare assessments will lead to early disease interception followed by preventive lifestyle modifications and proactive treatment.

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INTRODUCTION

'Do the difficult things while they are easy and do the great things while they are small'.
- Lao Tzu

Predicting suicidal behavior in individuals is one of the hard problems in psychiatry, and in society at large. Improved, objective, and quantitative ways to do it are needed. One cannot always ask individuals if they are suicidal, as desire not to be stopped or future impulsive changes of mind may make their self-report of feelings, thoughts and plans to be unreliable. We had previously provided proof of principle of how first generation blood biomarkers for suicide discovered in male bipolar participants, alone or in combination with clinical symptoms data for anxiety and mood, could have predictive ability for future hospitalizations for suicidality. We now present comprehensive new data for discovery, prioritization, validation, and testing of next-generation broad-spectrum blood biomarkers for suicidal ideation (SI) and behavior, across psychiatric diagnoses. We also describe two clinical information questionnaires in the form of apps, one for affective state (Simplified Affective State Scale, SASS) and one for suicide risk factors (Convergent Functional Information for Suicide, CFI-S), and show their utility in predicting suicidality. Both these instruments do not directly ask about SI. Lastly, we demonstrate how our *a priori* primary end point, a comprehensive universal predictor for suicide (UP-Suicide), composed of the combination of top biomarkers (from discovery, prioritization and validation), along with CFI-S, and SASS, predicts in independent test cohorts SI and future psychiatric hospitalizations for suicidality.

MATERIALS AND METHODS

Human participants

We present data from four cohorts: one live psychiatric participants discovery cohort; one post-mortem coroner's office validation cohort; and two live psychiatric participants test cohorts —one for predicting SI and one for predicting future hospitalizations for suicidality (Figure 1).

The live psychiatric participants are part of a larger longitudinal cohort being collected and studied by us. Participants are recruited from the patient population at the Indianapolis VA Medical Center. The participants are recruited largely through referrals from care providers, the use of brochures left in plain sight in public places and mental health clinics, and through word of mouth. All participants understood and signed informed consent forms detailing the research goals, procedure, caveats and safeguards. Participants completed diagnostic assessments by an extensive structured clinical interview—Diagnostic Interview for Genetic Studies—at a baseline visit, followed by up to six testing visits, 3–6 months apart or whenever a hospitalization occurred. At each testing visit, they received a series of psychiatric rating scales, including the Hamilton Rating Scale for Depression-17, which includes a suicidal ideation (SI) rating item (Figure 2), and the blood was drawn. Whole blood (10 ml) was collected in two RNA-stabilizing PAXgene tubes, labeled with an anonymized ID number, and stored at − 80 °C in a locked freezer until the time of future processing. Whole-blood (predominantly lymphocyte) RNA was extracted for microarray gene expression studies from the PAXgene tubes, as detailed below. We focused this study on a male population because of the demographics of our catchment area (primarily male in a VA Medical Center), and to minimize any potential gender-related effects on gene expression, which would have decreased the discriminative power of our analysis given our relatively small sample size.

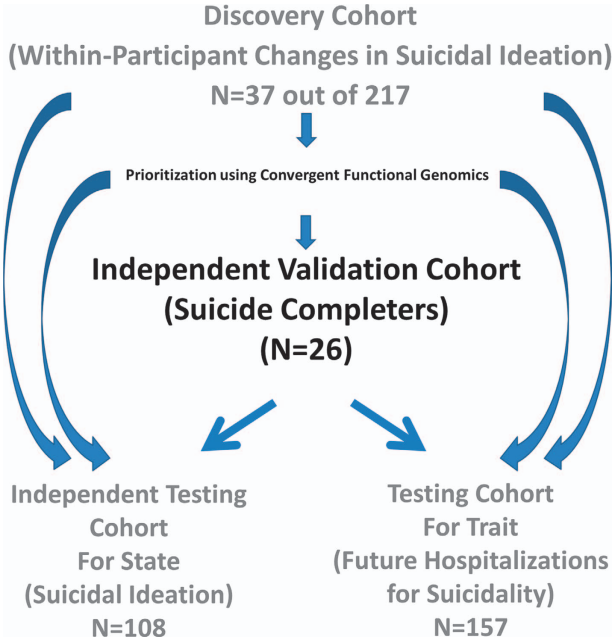


Figure 1. Cohorts used in study depicting flow of discovery, prioritization, validation and testing of biomarkers from each step.

Our within-participant discovery cohort, from which the biomarker data were derived, consisted of 37 male participants with psychiatric disorders, with multiple visits in our laboratory, who each had at least one diametric change in SI scores from no SI to high SI from one testing visit to another testing visit. There was one participant with six visits, one participant with five visits, one participant with four visits, 23 participants with three visits each, and 11 participants with two visits each, resulting in a total of 106 blood samples for subsequent microarray studies (Figure 2 and Table 1).

Our post-mortem cohort, in which the top biomarker findings were validated, consisted of a demographically matched cohort of 26 male violent suicide completers obtained through the Marion County coroner's office (Table 1 and Supplementary Table S2). We required a last observed alive post-mortem interval of 24 h or less, and the cases selected had completed suicide by means other than overdose, which could affect gene expression. Fifteen participants completed suicide by gunshot to head or chest, nine by hanging, one by electrocution and one by slit wrist. Next of kin signed informed consent at the coroner's office for donation of blood for research. The samples were collected as part of our INBRAIN initiative (Indiana Center for Biomarker Research in Neuropsychiatry).

Our independent test cohort for predicting SI (Table 1) consisted of 108 male participants with psychiatric disorders, demographically matched with the discovery cohort, with one or multiple testing visits in our laboratory, with either no SI, intermediate SI, or high SI, resulting in a total of 223 blood samples in whom whole-genome blood gene expression data were obtained (Table 1 and Supplementary Table S1).

Our test cohort for predicting future hospitalizations (Table 1 and Supplementary Table S1) consisted of male participants in whom whole-genome blood gene expression data were obtained by us at testing visits over the years as part of our longitudinal study. If the participants had multiple testing visits, the visit with the highest marker (or combination of markers) levels was selected for the analyses (so called "high watermark" or index visit). The participants' subsequent number of psychiatric hospitalizations, with or without suicidality, was tabulated from electronic medical records. All participants had at least 1 year of

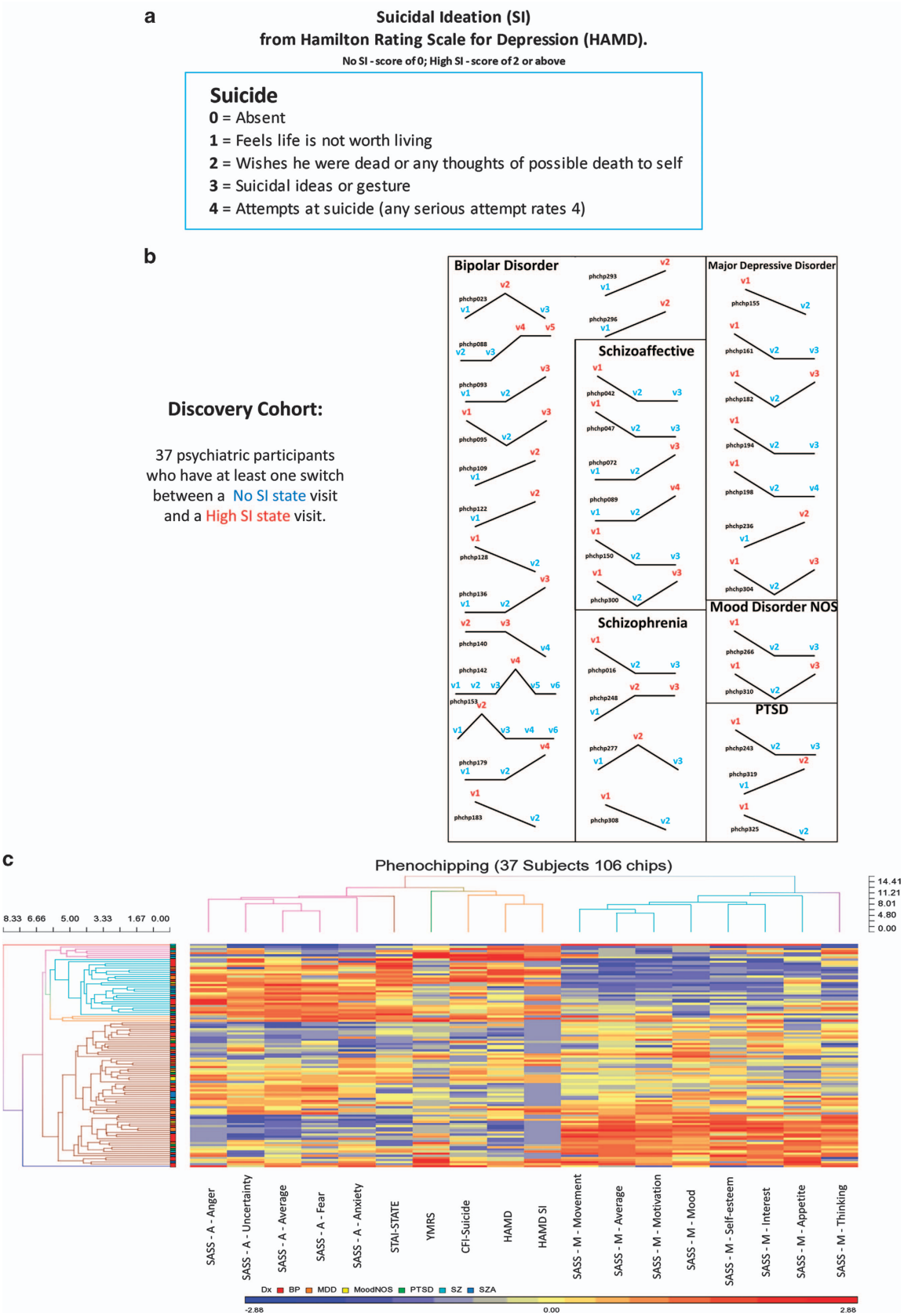


Figure 2. Discovery cohort: longitudinal within-participant analysis. Phchp### is study ID for each participant. V# denotes visit number (1, 2, 3, 4, 5 or 6). (**a**) Suicidal ideation (SI) scoring. (**b**) Participants and visits. (**c**) PhenoChipping: two-way unsupervised hierarchical clustering of all participant visits in the discovery cohort vs 18 quantitative phenotypes measuring affective state and suicidality. A—anxiety items (anxiety, uncertainty, fear, anger, average). M—mood items (mood, motivation, movement, thinking, self-esteem, interest, appetite, average). SASS, simplified affective state scale; STAI-STATE, state trait anxiety inventory, state subscale; YMRS, Young Mania Rating Scale.

Table 1. Cohorts used in study

	Subjects	*Diagnosis*	*Ethnicity*	*Age mean s.d.*	*T-test for age*	
Discovery cohort (within-participant changes in suicidal ideation)	37	BP = 15 MDD = 7 SZA = 6 SZ = 4 PTSD = 3 Mood NOS = 2	EA = 29 AA = 8 Other = 0	47.25 8.59		
Independent validation cohort-gene expression (suicide completers)	26	NP = 13 MDD = 8 BP = 2 SZ = 1 AX = 1 Alcoholism = 1	EA = 21 AA = 4 Other = 1	40.81 17.47		*T-test for age with discovery cohort 0.114*
Independent validation cohort-CFI-S (suicide completers)	35	NP = 14 MDD = 16 BP = 2 SZ = 1 AX = 1 Alcoholism = 1	EA = 29 AA = 4 Other = 2	42.46 17.82		*T-test for age with discovery cohort 0.156*
Independent testing cohort for state (suicidal ideation)	108	No SI BP = 17 MDD = 17 SZA = 19 SZ = 20 Intermediate SI BP = 5 MDD = 0 SZA = 3 SZ = 4 High SI BP = 7 MDD = 8 SZA = 6 SZ = 2	EA = 71 AA = 36 Other = 1	47.1 9.6 No SI = 47.8 High SI = 45.7	*T-test for age between no and high SI 0.554*	*T-test for age with discovery cohort* P = *0.919*
Testing cohort for trait (first year hospitalizations for suicidality)	157 (No Hosp for Suicidality = 139 Hosp for Suicidality = 18)	No Hosp for Suicidality BP = 43 MDD = 20 SZA = 41 SZ = 35 Hosp for Suicidality BP = 7 MDD = 3 SZA = 3 SZ = 5	No hosp for SI EA = 90 AA = 47 Other = 2 Hosp for SI EA = 13 AA = 5	49.6 9.5 No hosp for SI = 49.56 Hosp for SI = 49.92	*T-test for age between no Hosp for suicidality and Hosp for suicidality 0.886*	*T-test for age with discovery cohort 0.149*
Testing cohort for trait (all future hospitalizations for suicidality)	157 (No Hosp for Suicidality = 122 Hosp for Suicidality = 35)	No Hosp for Suicidality BP = 41 MDD = 20 SZA = 29 SZ = 32 Hosp for Suicidality BP = 9 MDD = 3 SZA = 15 SZ = 8	No hosp for Suicidality EA = 78 AA = 43 Other = 1 Hosp for Suicidality EA = 25 AA = 9 Other = 1	49.6 9.5 No Hosp for suicidality = 49.9 Hosp for suicidality = 48.4	*T-test for age between no Hosp for suicidality and Hosp for suicidality 0.436*	*T-test for age with discovery cohort 0.149*

Abbreviations: AX, anxiety disorder nos; BP, bipolar; CFI-S, Convergent Function Information for Suicide; MDD, major depressive disorder; NP, non-psychiatric; PTSD, post-traumatic stress disorder; SZA, schizoaffective; SZ, schizophrenia; SI, suicidal ideation.

follow-up or more at our VA Medical Center since the time of the testing visits in the laboratory. Participants were evaluated for the presence of future hospitalizations for suicidality, and for the frequency of such hospitalizations. A hospitalization was deemed to be without suicidality if suicidality was not listed as a reason for admission, and no SI was described in the admission and discharge medical notes. Conversely, a hospitalization was deemed to be because of suicidality if suicidal acts or intent was listed as a reason for admission, and/or SI was described in the admission and discharge medical notes.

Medications

The participants in the discovery cohort were all diagnosed with various psychiatric disorders (Table 1). Their psychiatric medications were listed in their electronic medical records, and

documented by us at the time of each testing visit. The participants were on a variety of different psychiatric medications: mood stabilizers; antidepressants; antipsychotics; benzodiazepines; and others (data not shown). Medications can have a strong influence on gene expression. However, our discovery of differentially expressed genes was based on within-participant analyses, which factor out not only genetic background effects but also medication effects, as the participants had no major medication changes between visits. Moreover, there was no consistent pattern in any particular type of medication, or between any change in medications and SI, in the rare instances where there were changes in medications between visits.

Human blood gene expression experiments and analyses

RNA extraction. Whole blood (2.5–5 ml) was collected into each PaxGene tube by routine venipuncture. PaxGene tubes contain proprietary reagents for the stabilization of RNA. RNA was extracted and processed as previously described.[1]

Microarrays. Biotin-labeled aRNAs were hybridized to Affymetrix HG-U133 Plus 2.0 GeneChips (Affymetrix; with over 40 000 genes and expressed sequence tags), according to the manufacturer's protocols. Arrays were stained using standard Affymetrix protocols for antibody signal amplification and scanned on an Affymetrix GeneArray 2500 scanner with a target intensity set at 250. Quality-control measures, including 30/50 ratios for glyceraldehyde 3-phosphate dehydrogenase and b-actin, scale factors and background, were within acceptable limits.

Analysis. We have used the participant's SI scores at the time of blood collection (0—no SI compared with 2 and above—high SI). We looked at gene expression differences between the no SI and the high SI visits, using a within-participant design, then an across participants summation (Figure 2).

Gene expression analyses in the discovery cohort

We analyzed the data in two ways: an absent–present (AP) approach, as in previous work by us on mood biomarkers[2] and on psychosis biomarkers,[3] and a differential expression (DE) approach, as in previous work by us on suicide biomarkers.[1] The AP approach may capture turning on and off of genes, and the DE approach may capture gradual changes in expression. For the AP approach, we used Affymetrix Microarray Suite Version 5.0 (MAS5) to generate Absent (A), Marginal (M) or Present (P) calls for each probeset on the chip (Affymetrix U133 Plus 2.0 GeneChips) for all participants in the discovery cohort. For the DE approach we imported all Affymetrix microarray data as .cel files into Partek Genomic Suites 6.6 software package (Partek Incorporated, St Louis, MI, USA). Using only the perfect match values, we ran a robust multi-array analysis (RMA), background corrected with quantile normalization and a median polish probeset summarization, to obtain the normalized expression levels of all probesets for each chip. RMA was performed independently for each of the six diagnoses used in the study, to avoid potential artefacts due to different ranges of gene expression in different diagnoses.[4] Then the participants' normalized data were extracted from these RMAs and assembled for the different cohorts used in the study.

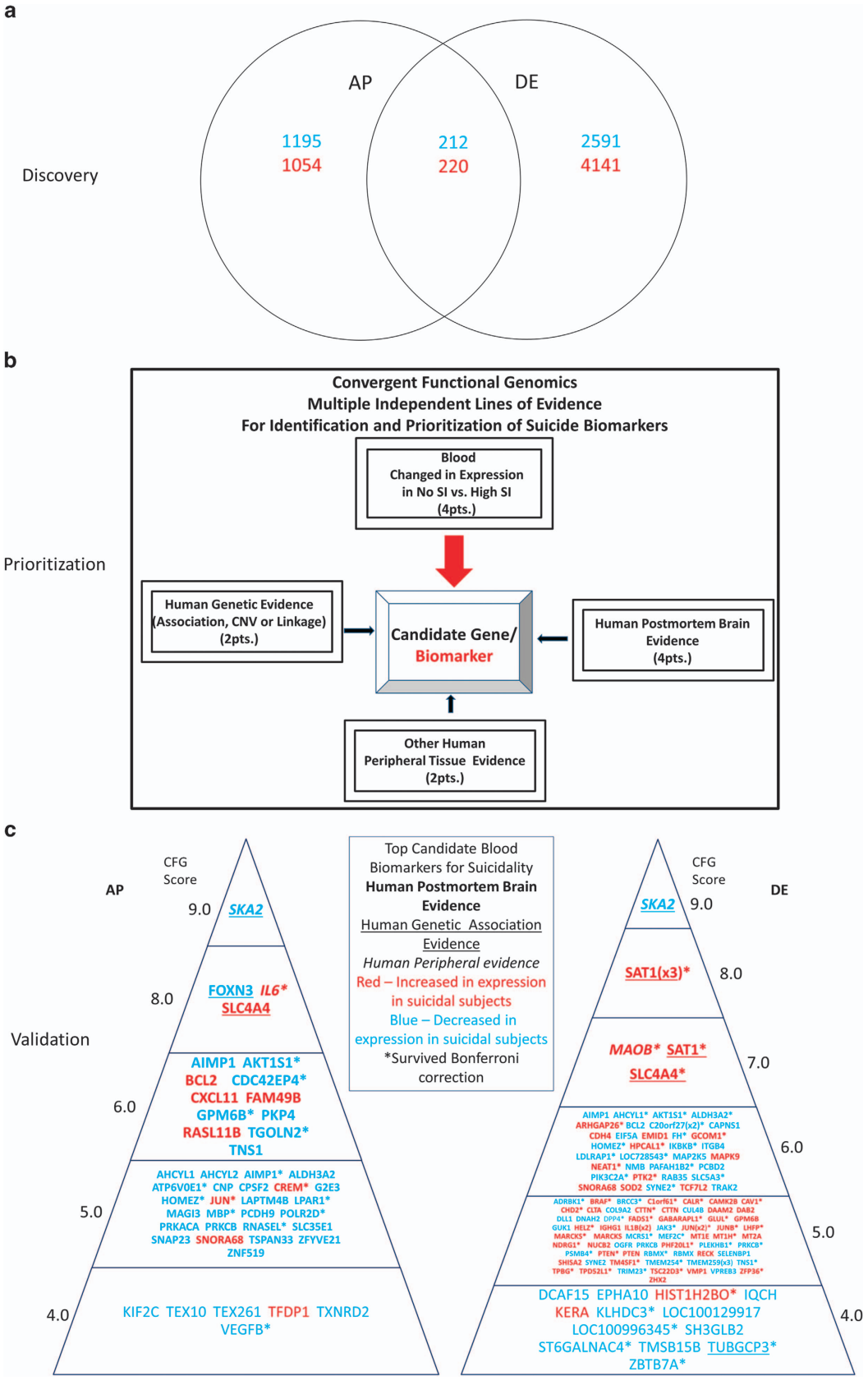
A/P analysis. For the longitudinal within-participant AP analysis, comparisons were made within-participant between sequential visits to identify changes in gene expression from absent to present that track changes in phene expression (SI) from no SI to high SI. For a comparison, if there was a change from absent to present tracking a change from no SI to high SI, or a change from present to absent tracking a change from high SI to no SI, that was given a score of +1 (increased biomarker in high SI). If the change was in opposite direction in the gene vs the phene (SI), that was given a score of − 1 (decreased biomarker in High SI). If there was no change in gene expression between visits despite a change of phene expression (SI), or a change in gene expression between visits despite no change in phene expression (SI), that was given a score of 0 (not tracking as a biomarker). If there was no change in gene expression and no change in SI between visits, that was given a score of +1 if there was concordance (P-P with high SI-high SI, or A-A with no SI-no SI), or a score of − 1 if there was the opposite (A-A with high SI-high SI, or P-P with no SI-no SI). If the changes were to M (moderate) instead of P, the values used were 0.5 or –0.5. These values were then summed up across the comparisons in each participant, resulting in a overall score for each gene/probeset in each participant. We also used a perfection bonus. If the gene expression perfectly tracked the SI in a participant that had at least two comparisons (three visits), that probeset was rewarded by a doubling of its overall score. Additionally, we used a non-tracking correction. If there was no change in gene expression in any of the comparisons for a particular participant, that overall score for that probeset in that participant was zero.

DE analysis. For the longitudinal within-participant DE analysis, fold changes (FC) in gene expression were calculated between sequential visits within each participant. Scoring methodology was similar to that used above for AP. Probesets that had a FC $\geqslant$ 1.2 were scored+1 (increased in high SI) or − 1 (decreased in high SI). FC $\geqslant$ 1.1 were scored +0.5 or − 0.5. FC lower than 1.1 were considered no change. The only difference between the DE and the AP analyses was when scoring comparisons where there was no phene expression (SI) change between visits and no change in gene expression between visits (FC lower than 1.1). In that case, the comparison received the same score as the nearest preceding comparison where there was a change in SI from visit to visit. If no preceding comparison with a change in SI was available, then it was given the same score as the nearest subsequent comparison where there was a change in SI. For DE also we used a perfection bonus and a non-tracking correction. If the gene expression perfectly tracked the SI in a participant that had at least two comparisons (three visits), that probeset was rewarded by a doubling of its score. If there was no change in gene expression in any of the comparisons for a particular participant, that overall score for that probeset in that participant was zero.

Internal score. Once scores within each participant were calculated, an algebraic sum across all participants was obtained, for each probeset. Probesets were then given internal points based upon these algebraic sum scores. Probesets with scores above the 33.3% of the distribution (for increased probesets and decreased probesets) received one point, those above 50% of the distribution received two points, and those above 80% of the distribution received four points. For AP analyses, we have 23 probesets which recieved four points, 581 probesets with two points, and 2077 probesets with one point, for a total of 2681 probesets. For DE analyses, we have 31 probesets which received four points, 1294 probesets with two points, and 5839 probesets with one point, for a total of 7164 probesets. The overlap between the two discovery methods is shown in Figure 3. Different probesets may be found by the two methods due to differences in scope (DE capturing genes that are present in both visits of a comparison, that is, PP, but are changed in expression), thresholds (what makes the 33.3% change cut-off across participants varies between methods), and technical detection levels (what is considered in the noise range varies between the methods).

In total, we identified 9413 probesets with internal convergent functional genomics (CFG) score of 1. Gene names for the probesets were identified using NetAffyx (Affymetrix) and Partek for Affymetrix HG-U133 Plus 2.0 GeneChips, followed by

GeneCards to confirm the primary gene symbol. In addition, for those probesets that were not assigned a gene name by NetAffyx or Partek, we used the UCSC Genome Browser to directly map them to known genes, with the following limitations: (1) in case the probeset fell in an intron, that particular gene was assumed to be implicated; and (2) only one gene was assigned to each



probeset. Genes were then scored using our manually curated CFG databases as described below (Figure 3).

Convergent functional genomics

Databases. We have established in our laboratory (Laboratory of Neurophenomics, Indiana University School of Medicine, www.neurophenomics.info) manually curated databases of all the human gene expression (post-mortem brain, blood and cell cultures), human genetics (association, copy number variations and linkage) and animal model gene expression and genetic studies published to date on psychiatric disorders. Only the findings deemed significant in the primary publication, by the study authors, using their particular experimental design and thresholds, are included in our databases. Our databases include only primary literature data and do not include review papers or other secondary data integration analyses to avoid redundancy and circularity. These large and constantly updated databases have been used in our CFG cross validation and prioritization (Figure 3). For this study, data from 437 papers on suicide were present in the databases at the time of the CFG analyses.

Human post-mortem brain gene expression evidence. Converging evidence was scored for a gene if there were published reports of human post-mortem data showing changes in expression of that gene or changes in protein levels in brains from participants who died from suicide.

Human blood and other peripheral tissue gene expression data. Converging evidence was scored for a gene if there were published reports of human blood, lymphoblastoid cell lines, cerebrospinal fluid or other peripheral tissue data showing changes in expression of that gene or changes in protein levels in participants who had a history of suicidality or who died from suicide.

Human genetic evidence (association and linkage). To designate convergence for a particular gene, the gene had to have independent published evidence of association or linkage for suicide. For linkage, the location of each gene was obtained through GeneCards (http://www.genecards.org), and the sex averaged cM location of the start of the gene was then obtained through http://compgen.rutgers.edu/mapinterpolator. For linkage convergence, the start of the gene had to map within 5 cM of the location of a marker linked to the disorder.

CFG scoring. For CFG analysis (Figure 3), the external cross-validating lines of evidence were weighted such that findings in human post-mortem brain tissue, the target organ, were prioritized over peripheral tissue findings and genetic findings, by giving them twice as many points. Human brain expression evidence was given four points, whereas human peripheral evidence was given two points, and human genetic evidence was given a maximum of two points for association, and one point for linkage. Each line of evidence was capped in such a way that any positive findings within that line of evidence result in maximum points, regardless of how many different studies support that single line of evidence, to avoid potential popularity biases. In addition to our external CFG score, we also prioritized genes based upon the initial gene expression analyses used to identify them. Probesets identified by gene expression analyses could receive a maximum of four points. Thus, the maximum possible total CFG score for each gene was 12 points (four points for the internal score and eight points for the external CFG score) (Table 2). The scoring system was decided upon before the analyses were carried out. We sought to give twice as much weight to external score as to internal in order to increase generalizability and avoid fit to cohort of the prioritized genes.[5] It has not escaped our attention that other ways of scoring the lines of evidence may give slightly different results in terms of prioritization, if not in terms of the list of genes *per se*. Nevertheless, we feel this simple scoring system provides a good separation of genes based on gene expression evidence and on independent cross-validating evidence in the field (Figure 3). In the future, with multiple large data sets, machine learning approaches could be used and validated to assign weights to CFG.

Pathway analyses

IPA 9.0 (Ingenuity Systems, www.ingenuity.com, Redwood City, CA, USA), GeneGO MetaCore (Encinitas, CA, USA), and Kyoto Encyclopedia of Genes and Genomes (KEGG) (through the Partek Genomics Suite 6.6 software package) were used to analyze the biological roles, including top canonical pathways, and diseases, of the candidate genes resulting from our work, as well as to identify genes in our data set that are the target of existing drugs (Table 3 and Supplementary Table S3). We ran the analyses together for all the AP and DE probesets with a total CFG score $\geqslant 4$, then for those of them that showed stepwise change in the suicide completers validation cohort, then for those of them that were nominally significant, and finally for those of them that survived Bonferroni correction.

Validation analyses

For validation of our candidate biomarker genes, we examined which of the top candidate genes (CFG score of 4 or above) were stepwise changed in expression from the no SI group to the high SI group to the suicide completers group. We used an empirical cut-off of 33.3% of the maximum possible CFG score of 12, which also permits the inclusion of potentially novel genes with maximal internal CFG score but no external CFG score. Statistical analyses were performed in SPSS using one-way analysis of variance and Bonferonni corrections.

For the AP analyses, we imported the Affymetrix microarray data files from the participants in the validation cohort of suicide completers into MAS5, alongside the data files from the participants in the discovery cohort.

For the DE analyses, we imported .cel files into Partek Genomic Suites. We then ran a RMA, background corrected with quantile normalization, and a median polish probeset summarization of all the chips from the validation cohort to obtain the normalized expression levels of all probesets for each chip. Partek normalizes expression data into a log base of 2 for visualization purposes. We non-log-transformed expression data by taking 2 to the power of the transformed expression value. We then used the non-log-

Figure 3. Biomarker discovery, prioritization and validation. (**a**) Discovery—number of probesets carried forward from the absent–present and differential expression analyses, with an internal score of 1 and above. Red-increased in expression in high suicidal ideation, blue-decreased in expression in high suicidal ideation. (**b**) Prioritization—convergent functional genomics integration of multiple lines of evidence to prioritize suicide-relevant genes from the discovery step. (**c**) Validation—top convergent functional genomics genes, with a total score of 4 and above, validated in the cohort of suicide completers. All the genes shown were significantly changed in analysis of variance from no suicidal ideation to high suicidal ideation to suicide completers. *Survived Bonferroni correction. SAT1 (x3) had three different probesets with the same total score of 8.

Table 2. Top biomarkers for suicidality from discovery, prioritization and validation

Gene symbol/gene name	*Probesets*	*Discovery (change) method/ score*	*Prior human genetic evidence*	*Prior human brain expression evidence*	*Prior human peripheral expression evidence*	*Prioritization Total CFG score For suicide*	*Validation ANOVA P-value*	*Comment*
SKA2 spindle and kinetochore associated complex subunit 2	225686_at	(D) DE/1 AP/1	Suicide[15]	(D) PFC[15]	(D) Methylation in blood[15]	**9**	0.006 0.027	Top Decreased BioM In prioritization from AP and DE
IL6 interleukin 6 (interferon, beta 2)	205207_at	(I) AP/2		(I) PFC[27] Hippocampus[28]	(I) CSF[29,30] (D) Blood[31]	**8**	**1.44e – 08**	Top Increased BioM in Validation from AP
SAT1 spermidine/spermine N1-acetyltransferase 1	213988_s_at 210592_s_at 230333_at 203455_s_at	(I) DE/2 DE/1	Suicide[32,33]	(I) PFC BA46[12]	(I) Blood[1]	**8**	**1.08e – 44** **1.24e – 40** **6.93e – 12** **3.09e – 38**	Top Increased BioM in Prioritization from DE Top biomarker in our previous work
SLC4A4 solute carrier family 4 (sodium bicarbonate cotransporter), member 4	211494_s_at 210739_x_at	(I) AP/2 DE/1	Suicide[34]	(D) PFC BA46/10[35]		**8**	**5.84e – 05** 0.002	Top Increased BioM in Prioritization from AP
JUN jun proto-oncogene	201464_x_at 213281_at 201466_s_at	(I) DE/1 AP1		(D) HIP[36]		**5**	**2.63e – 51** **1.02e – 41** **2.21e – 08**	Top Increased BioM in Validation from DE
MBP myelin basic protein	225408_at	(D) AP/1		(I) NAC[11]		**5**	**6.74e – 10**	Top Decreased BioM in Validation from AP
CADM1 cell adhesion molecule 1	237259_at	(I) DE/4				**4**	NC	Top Increased BioM in Discovery from DE
CLIP4 CAP-GLY domain containing linker protein family, member 4	219944_at	(D) DE/4				**4**	NC	Top Decreased BioM in Discovery from DE
DTNA dystrobrevin, alpha	211493_x_at	(I) AP/4				**4**	NC	Top Increased BioM in Discovery from AP
KIF2C kinesin family member 2C	211519_s_at	(D) AP/4				**4**	0.00056	Top Decreased BioM in Discovery from AP
KLHDC3 kelch domain containing 3	214383_x_at	(D) DE/4			(D) Blood[1]	**4**	**1.57e – 17**	Top Decreased BioM in Validation from DE A top biomarker in our previous study
MAOB monoamine oxidase B	204041_at	(I) DE/1		(I) PFC[37]	(D) Blood[38]	**7**	**8.11e – 08**	Top Pharmacological Target
MARCKS myristoylated alanine-rich protein kinase C substrate	213002_at 201670_s_at	(I) DE/1		(I) HIP, PFC[39] PFC[40]	(I) Blood[1]	**5**	**1.51e – 06**; 0.0004	A top biomarker in our previous study
PTEN phosphatase and tensin homolog	204053_x_at 222176_at	(I) DE/1		(I) PFC, HIP[41,42]	(I) Blood[1]	**5**	**7.66e – 17**; 0.0003	A top biomarker in our previous study

Abbreviations: ANOVA, analysis of variance; AP, absent–present; CFG, convergent functional genomics; CSF, cerebrospinal fluid; DE, differential expression; SI, suicidal ideation. Bolded *P*-values are Bonferroni significant. NC—Non-concordant-not stepwise from no SI to high SI to suicide completers.

Table 3. Biological pathways and diseases

A

Ingenuity pathways			*KEGG pathways*			*GeneGO pathways*		
#	*Top canonical pathways*	*P-value*	*Ratio*	*Pathway name*	*Enrichment score*	*Enrichment P-value*	*Process networks*	*Ratio*	*P-value*
Prioritization CFG score ⩾ 4 (n = 412 genes)									
1	G-protein coupled receptor signaling	6.27e – 14	10.6% 28/264	GABAergic synapse	10.8524	1.94e – 05	Cell adhesion_Amyloid proteins	27/195	4.78E-09
2	cAMP-mediated signaling	2.04e – 11	10.3% 23/223	Amoebiasis	10.7231	2.20e – 05	Reproduction_Gonadotropin regulation	27/199	7.49E-09
3	Glucocorticoid receptor signaling	6.84e – 11	8.9% 25/281	Melanogenesis	10.2992	3.37e – 05	Reproduction_GnRH signaling pathway	22/166	3.00E-07
4	CREB signaling in neurons	1.01e – 10	11.2% 20/179	Pathogenic *Escherichia coli* infection	9.03249	0.000119	Development_Hedgehog signaling	28/254	3.65E-07
5	Cardiac hypertrophy signaling	2.88e – 10	9.5% 22/232	Chemokine signaling pathway	8.82088	0.000148	Cytoskeleton_Regulation of cytoskeleton rearrangement	23/183	4.22E-07
Validation stepwise (n = 204 genes)									
1	B-cell receptor signaling	1.01e – 08	7.2% 13/181	Focal adhesion	10.5307	2.67e – 05	Signal transduction_WNT signaling	19/177	8.10E-10
2	Ovarian cancer signaling	3.31e – 08	8.3% 11/133	Colorectal cancer	10.3054	3.35e – 05	Cell cycle_G1-S Growth factor regulation	18/195	2.62E-08
3	Glucocorticoid receptor signaling	3.97e – 08	5.3% 15/281	GABAergic synapse	8.60276	0.000184	Reproduction_Gonadotropin regulation	18/199	3.60E-08
4	Colorectal cancer metastasis signaling	4.00e – 08	5.8% 14/241	mTOR signaling pathway	8.47678	0.000208	Reproduction_GnRH signaling pathway	16/166	9.05E-08
5	G12/13 signaling	1.12e – 07	8.5% 10/118	Chagas disease (American trypanosomiasis)	7.66796	0.000468	Neurophysiological process_Transmission of nerve impulse	18/212	9.58E-08
Validation nominally significant (n = 143 genes)									
1	B-cell receptor signaling	1.95e – 07	5.5% 10/181	Focal adhesion	8.91242	0.000135	Cell cycle_G1-S Growth factor regulation	16/195	3.62E-09
2	Cholecystokinin/gastrin-mediated signaling	3.18e – 07	7.5% 8/106	mTOR signaling pathway	8.34274	0.000238	Inflammation_Histamine signaling	14/213	6.04E-07
3	G12/13 signaling	7.25e – 07	6.8% 8/118	Wnt signaling pathway	7.1443	0.000789	Signal transduction_WNT signaling	12/177	2.99E-06
4	Glucocorticoid receptor signaling	1.46e – 06	3.9% 11/281	Amphetamine addiction	6.67296	0.001265	Cell cycle_G1-S Interleukin regulation	10/128	6.05E-06
5	Ovarian cancer signaling	1.80e – 06	6.0% 8/133	Neurotrophin signaling pathway	6.54296	0.00144	Cell adhesion_Amyloid proteins	12/195	8.17E-06
Validation Bonferroni significant (n = 76 genes)									
1	B-cell receptor signaling	2.38e – 06	3.9% 7/181	mTOR signaling pathway	11.496	1.02E-05	Cell cycle_G1-S Growth factor regulation	9/195	2.34E-05
2	G12/13 signaling	2.70e – 06	5.1% 6/118	Arginine and proline metabolism	8.02409	0.000327	Reproduction_Gonadotropin regulation	8/199	1.82E-04
3	IL-17A signaling in airway cells	2.71e – 06	7.6% 5/66	Focal adhesion	7.79535	0.000412	Inflammation_IL-4 signaling	6/115	3.12E-04
4	IL-8 signaling	3.06e – 06	3.7% 7/188	Pathways in cancer	7.05537	0.000863	Cell cycle_G1-S Interleukin regulation	6/128	5.55E-04
5	Integrin signaling	4.76e – 06	3.5% 7/201	Renal cell carcinoma	6.07809	0.002293	Inflammation_IL-12,15,18 signaling	4/59	1.28E-03

B

Ingenuity				*GeneGO*		
#	*Diseases and disorders*	*P-value*	*# Molecules*	*Diseases*	*P-value*	*Ratio*
Prioritization CFG score ⩾ 4 (n = 412 genes)						
1	Neurological disease	4.31e – 06—5.54e – 24	174	Psychiatry and psychology	4.65e – 50	156/1919
2	Psychological disorders	2.69e – 06—7.71e – 24	123	Mental disorders	5.89e – 50	143/1614
3	Organismal injury and abnormalities	4.52e – 06—1.23e – 21	361	Mood disorders	3.69e – 37	88/797
4	Skeletal and muscular Disorders	4.52e – 06—9.92e – 21	129	Schizophrenia	4.28e – 34	90/914
5	Cancer	4.37e – 06—2.00e – 20	359	Schizophrenia and disorders with psychotic features	6.01e – 34	90/918
Validation stepwise (n = 204 genes)						
1	Organismal injury and abnormalities	s 2.11e – 04—1.23e – 13	178	Psychiatry and psychology	1.77e – 23	76/1919
2	Cancer	2.20e – 04—5.41e – 13	176	Mental disorders	1.23e – 21	67/1614
3	Neurological disease	1.31e – 04—1.07e – 12	81	Mood disorders	4.02e – 21	47/797
4	Psychological disorders	1.31e – 04—1.07e – 12	63	Depressive disorder, major	1.06e – 18	37/546
5	Tumor morphology	1.87e – 04—1.83e – 12	38	Depressive disorder	2.44e – 18	37/560

Table 3. (Continued)

B

		Ingenuity		*GeneGO*		
#	*Diseases and disorders*	P-*value*	# *Molecules*	*Diseases*	P-*value*	*Ratio*
Validation nominally significant (n = 143 genes)						
1	Cancer	4.75e – 04—2.43e – 12	122	Wounds and injuries	2.49e – 17	39/993
2	Organismal injury and abnormalities	4.75e – 04—2.43e – 12	123	Colonic diseases	2.52e – 13	77/4479
3	Tumor morphology	2.27e – 04—2.43e – 12	31	Psychiatry and psychology	5.32e – 13	47/1919
4	Cardiovascular disease	4.28e – 04—1.25e – 09	36	Connective tissue diseases	8.73e – 13	50/2177
5	Developmental disorder	2.27e – 04—1.25e – 09	28	Pathologic processes	1.75e – 12	56/2709
Validation Bonferroni significant (n = 76 genes)						
1	Cancer	1.27e – 03—1.06e – 10	68	Wounds and injuries	3.16e – 15	27/993
2	Organismal injury and abnormalities	1.27e – 03—1.06e – 10	68	Pathologic processes	6.22e – 13	39/2709
3	Tumor morphology	8.81e – 04—1.65e – 10	22	Psychiatry and psychology	6.32e – 13	33/1919
4	Cardiovascular disease	8.32e – 04—4.02e – 10	24	Mood disorders	1.35e – 12	22/797
5	Developmental disorder	1.11e – 03—4.02e – 10	21	Mental disorders	1.41e – 12	30/1614

Abbreviations: CFG, convergent functional genomics; KEGG, Kyoto Encyclopedia of Genes and Genomes.

transformed expression data to compare expression levels of biomarkers in the different groups (Supplementary Figure S1).

Clinical measures

The Simplified Affective State Scale (SASS) is an 11 item scale for measuring mood and anxiety, previously developed and described by us as TASS (Total Affective State Scale).[6] The SASS has a set of 11 visual analog scales (7 for mood, 4 for anxiety) that ends up providing a number ranging from 0 to 100 for mood state, and the same for anxiety state. We have now developed an Android app version (Supplementary Figure S2).

CFI-S (Table 4) is a new 22 item scale and Android app (Supplementary Figure S2) for suicide risk, which integrates, in a simple binary fashion (yes-1, no-0), similar to a polygenic risk score, information about known life events, mental health, physical health, stress, addictions and cultural factors that can influence suicide risk.[7,8] For live psychiatric participants, the scale was administered at participant testing visits ($n = 57$), or scored based on retrospective electronic medical record information and Diagnostic Interview for Genetic Testing (DIGS) information ($n = 269$). For suicide completers ($n = 35$), the scale was based on answers provided by next-of-kin, and corroborated by coroner's office reports and medical record information. When information was not available for an item, it was not scored (NA).

Combining gene expression and clinical measures

The UP-Suicide construct was decided upon as part of our *a priori* study design to be broad- spectrum, and combine our top biomarkers from each step (discovery, prioritization, validation) with the phenomic (clinical) markers (SASS and CFI-S). That was our primary end point. Had we done it *post hoc* with only the markers that showed the best predictive ability in our testing analyses, the results would be even better, but not independent.

Testing analyses

The test cohort for SI and the test cohort for future hospitalizations analyses were assembled out of data that was RMA normalized by diagnosis. Phenomic (clinical) and gene expression markers used for predictions were z scored by diagnosis, to be able to combine different markers into panels and to avoid potential artefacts due to different ranges of phene expression and gene expression in different diagnoses. Markers were combined by computing the average of the increased risk markers minus the average of the decreased risk markers. Predictions were performed using R-studio.

Predicting suicidal ideation. Receiver-operating characteristic (ROC) analyses between marker levels and SI were performed by assigning participants with a HAMD-SI score of 0–1 into the no SI category, and participants with a HAMD-SI score of 2 and greater into the SI category. Additionally, analysis of variance was performed between no (HAMD-SI 0), intermediate (HAMD-SI 1), and high SI participants (HAMD-SI 2 and above) and Pearson R (one-tail) was calculated between HAMD-SI scores and marker levels (Table 5b and Figure 5).

Predicting future hospitalizations for suicidality. We conducted analyses for hospitalizations in the first year following testing, on the participants for which we had at least a year of follow-up data. For each participant in the test cohort for future hospitalizations, the study visit with highest levels for the marker or combination of markers was selected as index visit (or with the lowest levels, in the case of decreased markers). ROC analyses between marker levels and future hospitalizations were performed based on assigning if participants had been hospitalized for suicidality (ideation, attempts) or not following the index testing visit. Additionally, a one-tailed *t*-test with unequal variance was performed

Table 4. Convergent Functional Information for Suicide (CFI-S) Scale

Items	*Yes*	*No*	*NA*	*Domain*	*Type Increased Reasons (IR) Decreased Barriers (DB)*
1. Psychiatric illness diagnosed and treated				Mental health	IR
2. With poor treatment compliance				Mental health	DB
3. Family history of suicide in blood relatives				Mental health	IR
4. Personally knowing somebody who committed suicide				Cultural factors	DB
5. History of abuse: physical, sexual, emotional, neglect				Life satisfaction	IR
6. Acute/severe medical illness, including acute pain ("I just can't stand this pain anymore.") (within last 3 months)				Physical health	IR
7. Acute stress: Losses, grief (within last 3 months)				Environmental stress	IR
8. Chronic stress: perceived uselessness, not feeling needed, burden to extended kin				Environmental stress	IR
9. History of excessive introversion, conscientiousness (including planned suicide attempts)				Mental health	IR
10. Dissatisfaction with life at this moment in time				Life satisfaction	IR
11. Lack of hope for the future				Life satisfaction	IR
12. Current substance abuse				Addictions	DB
13. Past history of suicidal acts/gestures				Mental health	DB
14. Lack of religious beliefs				Cultural factors	DB
15. Acute stress: Rejection (within last 3 months)				Environmental stress	IR
16. Chronic stress: lack of positive relationships, social isolation				Environmental stress	DB
17. History of excessive extroversion and impulsive behaviors (including rage, anger, physical fights, seeking revenge)				Mental health	DB
18. Lack of coping skills when faced with stress (cracks under pressure)				Mental health	DB
19. Lack of children. If has children, not in touch/not helping take care of them				Life satisfaction	DB
20. History of command hallucinations of self-directed violence				Mental health	IR
21. Age: older >60 or younger <25				Age	IR
22. Gender: male				Gender	DB

Abbreviations: CFI-S, Convergent Functional Information for Suicide; DB, decreased barrier; IR, increased reasons; NA, not available. Items are scored 1 for Yes, 0 for No. Total Score has a maximum possible of 22. Final Score (normalized) is Total Score divided by number of items that were scored, as for some items information might be NA, so they are not scored.

between groups of participants with and without hospitalizations for suicidality. Pearson *R* (one-tail) correlation was performed between hospitalization frequency (number of hospitalizations for suicidality divided by duration of follow-up) and biomarker score. We also conducted only the correlation analyses for hospitalizations frequency for all future hospitalizations due to suicidality, beyond one year, as this calculation, unlike the ROC and *t*-test, accounts for the actual length of follow-up, which varied beyond one year from participant to participant.

RESULTS

Discovery of biomarkers for suicidal ideation

We conducted whole-genome gene expression profiling in the blood samples from a longitudinally followed cohort of male participants with psychiatric disorders that predispose to suicidality. The samples were collected at repeated visits, 3–6 months apart. State information about SI was collected from a questionnaire (HAMD) administered at the time of each blood draw (Supplementary Table S1). Out of 217 psychiatric participants (with a total of 531 visits) followed longitudinally in our study, there were 37 participants that switched from a no SI (SI score of 0) to a high SI state (SI score of 2 and above) at different visits, which was our intended discovery group (Figure 2). We used a powerful within-participant design to analyze data from these 37 participants and their 106 visits. A within-participant design factors out genetic variability, as well as some medications, lifestyle, and demographic effects on gene expression, permitting identification of relevant signal with Ns as small as 1.[9] Another benefit of a within-participant design may be accuracy/consistency of self-report of psychiatric symptoms ('phene expression'), similar in rationale to the signal detection benefits it provides in gene expression. The number of participants that met our criteria and were analyzed is small, but comparable to those in human post-mortem brain gene expression studies of suicide. We are indeed treating the blood samples as surrogate tissue for brains, with the caveat that they are not the real target organ. However, with the blood samples from live human participants we have the advantages of *in vivo* accessibility, better knowledge of the mental state at the time of collection, less technical artifacts and especially of being able to do powerful within-participant analyses from visit to visit.

For discovery, we used two differential expression methodologies: Absent/Present (reflecting on/off of transcription), and Differential Expression (reflecting more subtle gradual changes in expression levels). The genes that tracked SI in each participant were identified in our analyses. We used three thresholds for increased in expression genes and for decreased in expression genes: $\geqslant 33.3\%$ (low); $\geqslant 50\%$ (medium); and $\geqslant 80\%$ (high) of the maximum scoring increased and decreased gene across participants. Such a restrictive approach was used as a way of minimizing false positives, even at the risk of having false negatives. For example, there were genes on each of the two lists, from AP and DE analyses, that had clear prior evidence for involvement in suicidality, such as OLR1[10,11] (32%) and LEPR[1,12] (32%) for AP, and OPRM1[13,14] (32%) and CD24 [1,11] (33%) from DE, but were not included in our subsequent analyses because they did not meet our *a priori* set 33.3% threshold.

Prioritization of biomarkers based on prior evidence in the field

These differentially expressed genes were then prioritized using a Bayesian-like CFG approach (Figure 3) integrating all the previously published human genetic evidence, post-mortem brain gene expression evidence, and peripheral fluids evidence for suicide in the field available at the time of our final analyses (September 2014). This is a way of identifying and prioritizing disease relevant genomic biomarkers, extracting generalizable signal out of potential cohort-specific noise and genetic heterogeneity. We have built in our laboratory manually curated databases of the psychiatric genomic and proteomic literature to date, for use in CFG analyses. The CFG approach is thus a de

facto field-wide collaboration. We use in essence, in a Bayesian fashion, the whole body of knowledge in the field to leverage findings from our discovery data sets. Unlike our use of CFG in many previous studies, for the current one we did not use any animal model evidence, as there are to date no clear animal models of self-harm or suicidality published to date.

Validation of biomarkers for behavior in suicide completers

For validation in suicide completers, we used 412 genes that had a CFG score of 4 and above, from AP and DE, reflecting either maximum internal score from discovery or additional external literature cross-validating evidence. Out of these, 208 did not show any stepwise change in suicide completers (non-concordant, NC). As such, they may be involved primarily in ideation and not in behavior (Supplementary Table S6). The remaining 204 genes (49.5%) had levels of expression that were changed stepwise from no SI to high SI to suicide completion. 143 of these genes (34.7%) were nominally significant, and 76 genes (18.4%) survived Bonferroni correction for multiple comparisons (Figure 3 and Supplementary Figure S1). These genes are likely involved in SI *and* suicidal behavior. (You can have SI without suicidal behavior, but you cannot have suicidal behavior without SI).

Selection of biomarkers for testing of predictive ability

For testing, we decided *a priori* to select the top scoring increased and decreased biomarkers from each step (discovery, prioritization, validation), so as to avoid potential false negatives in the prioritization step due to lack of prior evidence in the literature, or false negatives in validation step due to possible post-mortem artifacts. The top scoring genes after the discovery step were DTNA and KIF2C from AP, CADM1 and CLIP4 from DE. The top genes after the prioritization with CFG step were SLC4A4 and SKA2 from AP, SAT1 and SKA2 from DE. The top genes after the validation in suicide completers step were IL6 and MBP from AP, JUN and KLHDC3 from DE (Figure 3). Notably, our SAT1 finding is a replication and expansion of our previously reported results identifying SAT1 as a blood biomarker for suicidality in bipolars (Le-Niculescu *et al.* 2013), and our SKA2 finding is an independent replication of a previous report identifying SKA2 as a blood biomarker for suicidality by Kaminsky and colleagues.[15] We also replicated in this larger cohort other top biomarkers from our previous work in bipolar disorder, notably MARCKS and PTEN (Table 2, Supplementary Figure S4). A number of other genes we identified (CADM1, KIF2C, DTNA, CLIP4) are completely novel in terms of their involvement in suicidality.

Biological understanding

We also sought to understand the biology represented by the biomarkers identified by us, and derive some mechanistic and practical insights. We conducted: 1. unbiased biological pathway analyses and hypothesis driven mechanistic queries, 2. overall disease involvement and specific neuropsychiatric disorders queries, and 3. overall drug modulation along with targeted queries for omega-3, lithium and clozapine[16] (Table 3, Supplementary Tables S3). Administration of omega-3s in particular may be a mass- deployable therapeutic and preventive strategy.[17]

The sets of biomarkers identified have biological roles in immune and inflammatory response, growth factor regulation, mTOR signaling, stress, and perhaps overall the switch between cell survival and proliferation vs apoptosis (Table 3 and Supplementary Table S3). 14% of the candidate biomarkers in Supplementary Table S3 have evidence for involvement in psychological stress response, and 19% for involvement in programmed cell death/cellular suicide (apoptosis). An extrapolation can be made and model proposed whereas suicide is a whole body apoptosis (or 'self-poptosis') in response to perceived stressful life events.

We also examined evidence for the involvement of these biomarkers for suicidality in other psychiatric disorders, permitting us to address issues of context and specificity (Supplementary Table S3). SKA2, HADHA, SNORA68, RASL11B, CXCL11, HOMEZ, LOC728543, AHCYL1, LDLRAP1, NEAT1 and PAFAH1B2 seem to be relatively specific for suicide, based on the evidence to date in the field. SAT1, IL6, FOXN3 and FKBP5 are less specific for suicide, having equally high evidence for involvement in suicide and in other psychiatric disorders, possibly mediating stress response as a common denominator.[11,18] These boundaries and understanding will likely change as additional evidence in the field accumulates. For example, CADM1, discovered in this work as a top biomarker for suicide, had previous evidence for involvement in other psychiatric disorders, such as autism and bipolar disorder. Interestingly, it was identified in a previous study by us as a blood biomarker increased in expression in low mood states in bipolar participants, and it is increased in expression in the current study in high SI states. Increased expression of CADM1 is associated with decreased cellular proliferation and with apoptosis, and this gene is decreased in expression or silenced in certain types of cancers.

A number of other genes besides CADM1 are changed in opposite direction in suicide in this study vs high mood in our previous mood biomarker study-CHD2, MBP, LPAR1, IGHG1, TEX261 (Supplementary Table S3), suggesting that suicidal participants are in a low mood state. Also, some of the top suicide biomarkers are changed in expression in the same direction as in high psychosis participants in a previous psychosis biomarker study of ours -PIK3C2A, GPM6B, PCBD2, DAB2, IQCH, LAMB1, TEX261 (Supplementary Table S3), suggesting that suicidal participants may be in a psychosis-like state. TEX261 in particular appears in all three studies, decreased in expression in suicide and high hallucinations, and increased in expression in high mood. This protective marker may be an interesting target for future biological studies and drug development. Taken together, the data indicates that suicidality could be viewed as a psychotic dysphoric state, and that TEX261 may be a key biomarker reflecting that state. This molecularly informed view is consistent with the emerging clinical evidence in the field.[19]

Lastly, we conducted biological pathway analyses on the genes that, after discovery and prioritization, were stepwise changed in suicide completers (n = 204) and may be involved in ideation *and* behavior, vs those that were not stepwise changed (n = 208), and that may only be involved in ideation (Supplementary Table S6). The genes involved in ideation map to pathways related to neuronal connectivity (cytoskeleton rearrangement, axonal guidance) and schizophrenia. The genes involved in behavior map to pathways related to neuronal activity (WNT, growth factors) and mood disorders. This is consistent with ideation being related to psychosis, and behavior being related to mood. Of note, clinically, the risk for suicide behavior/completion is higher in mood disorders than in psychotic disorders.

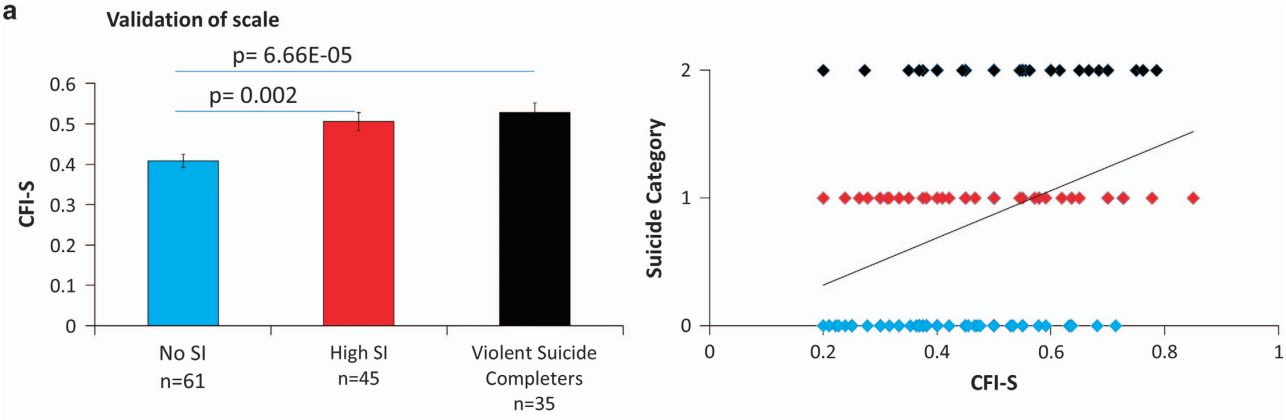
Clinical information

We also developed a simple new 22 item scale and app for suicide risk, Convergent Functional Information for Suicidality (CFI-S), which scores in a simple binary fashion and integrates, information about known life events, mental health, physical health, stress, addictions, and cultural factors that can influence suicide risk.[7,8] Clinical risk predictors and scales are of high interest in the military[20] and in the general population at large.[21] Our scale builds on those excellent prior achievements, while aiming for comprehensiveness, simplicity and quantification similar to a polygenic risk score. CFI-S is able to distinguish between individuals who committed suicide (coroner's cases n = 35, information obtained from the next-of-kin) and those high-risk participants who did not

but had experienced changes in SI (our discovery cohort of psychiatric participants) (Figure 4). We analyzed which items of the CFI-S scale were the most significantly different between high SI live participants and suicide completers. We identified 7 items that were significantly different, 5 of which survived Bonferroni correction: lack of coping skills when faced with stress ($P = 3.35e-11$), dissatisfaction with current life ($P = 2.77e-06$), lack of hope for the future ($4.58e-05$), current substance abuse ($P = 1.25e-04$), and acute loss/grief ($P = 9.45e-4$). It is highly interesting that the top item was inability to cope with stress, which is independently consistent with our biological marker results.

We also simplified the wording (and developed a new app for) an 11 item scale for measuring mood and anxiety, the SASS, previously developed and described by us as TASS (Total Affective State Scale).[6] The SASS is a set of 11 visual analog scales (7 for

a



Predictor	ANOVA	t-test (Completers vs. High SI)	Correlation R	Correlation p-value
CFI-S	6.66E-05	0.223	0.344	1.49E-05

b

Validation of items

Item	Description	P-Value (One-Way ANOVA) No SI vs High SI vs Completers	Stepwise	T-Test (two tailed) High SI vs Completers
18	**Lack of coping skills (cracks under pressure)**	**3.35E-11**	**Y**	**2.42E-05**
10	**Dissatisfaction with present life**	**2.77E-06**	**Y**	0.06804
11	**Lack of hope for the future**	**3.28E-05**	**Y**	**7.28E-05**
12	**Current substance abuse**	**0.000125**	**Y**	0.01273
7	**Acute stress: losses, grief**	**0.000945**	**Y**	0.07253
16	Chronic stress: lack of positive relationships, social isolation	0.0149	Y	0.2897
15	Acute stress: rejection	0.03	Y	0.02242
17	History of excessive extroversion and impulsive behaviors (including rage, anger, physical fights, seeking revenge)	0.0607	Y	0.2097
6	Acute/severe medical illness, pain	0.0892	Y	0.1113
19	Lack of children	0.365	Y	0.2479
22	Gender: Male	No females	No females	No females
4	Personally knowing somebody who committed suicide	No data for completers	No data for completers	No data for completers
1	Psychiatric illness diagnosed and treated	5.06E-15	N	6.02E-06
13	Past history of suicidal acts/gestures	2.40E-05	N	4.46E-05
21	Age: Older >60 or Younger <25	8.89E-05	N	0.000267
5	History of abuse: physical, sexual, emotional, neglect	0.0165	N	0.004361
20	History of command hallucinations of self-directed violence	0.0397	N	0.009659
3	Family history of suicide in blood relatives	0.0797	N	0.0242
2	With poor treatment compliance	0.147	N	0.07321
14	Lack of religious beliefs	0.117	N	0.06151
9	History of excessive introversion, conscientiousness	0.303	N	0.2439
8	Chronic stress: perceived uselessness, not feeling needed, burden to extended kin	0.42	N	0.2097

Figure 4. Convergent Functional Information for Suicide (CFI-S) Scale. (**a**) Validation of scale. Convergent Functional Information for Suicide levels in the discovery cohort and suicide completers. (**b**) Validation of items. Convergent Functional Information for Suicide was developed independently of any data from this study, by compiling known sociodemographic and clinical risk factors for suicide. It is composed of 22 items that assess the influence of mental health factors, as well as of life satisfaction, physical health, environmental stress, addictions, cultural factors known to influence suicidal behavior, and two demographic factors, age and gender. These 22 items are shown here validated in the discovery cohort and suicide completers in a manner similar to that for biomarkers. Additionally, a student's *t*-test was used to evaluate items that were increased in suicide completers when compared to living participants with high suicidal ideation. (**c**) Predictions. Convergent Functional Information for Suicide predicting SI in the independent test cohort, and predicting future hospitalizations due to suicidality.

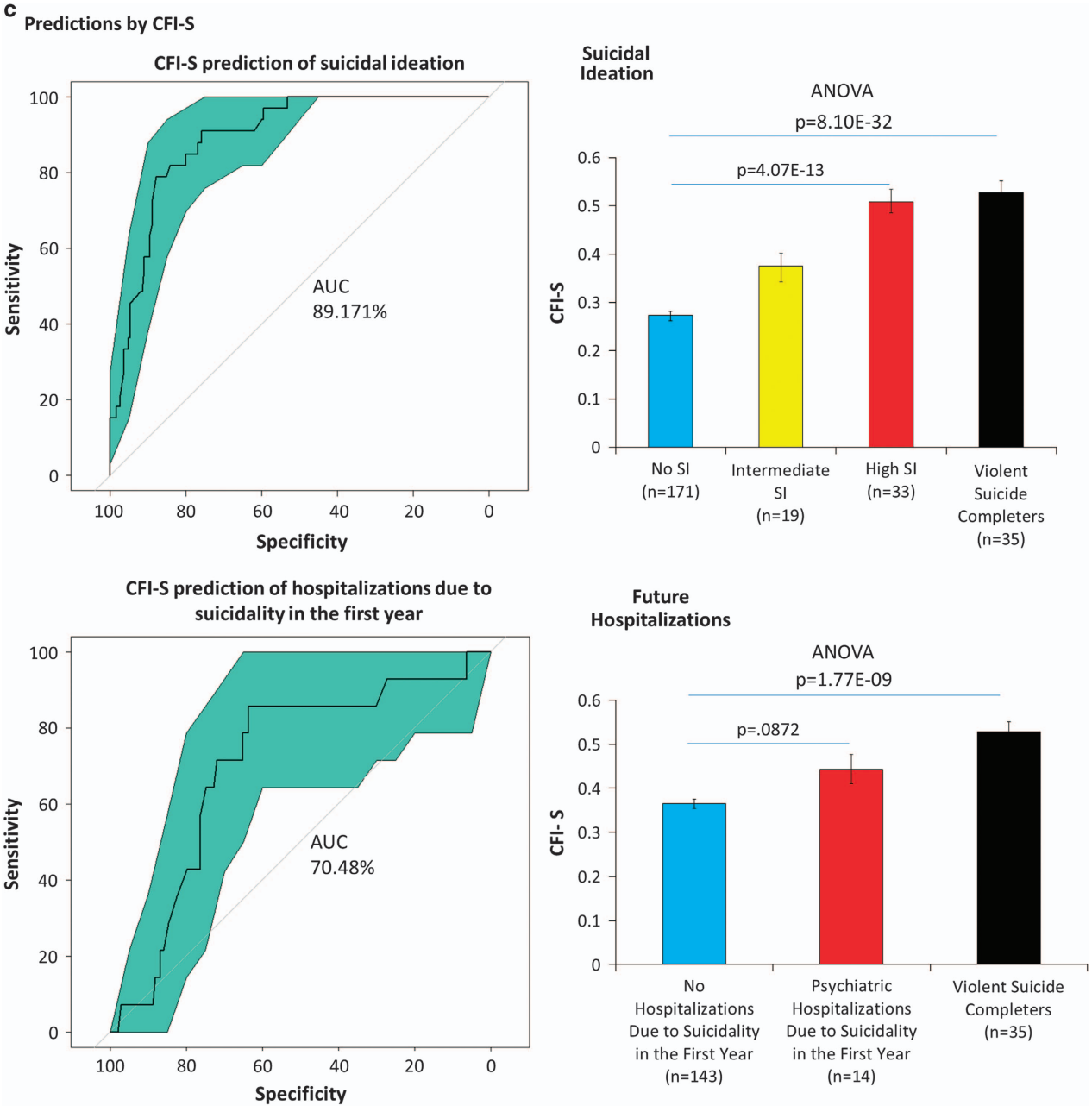


Figure 4. Continued.

mood, 4 for anxiety) that ends up providing a number ranging from 0 to 100 for mood state, and the same for anxiety state.

Testing for predictive ability

The best single biomarker predictor for SI state across all diagnostic groups is SLC4A4 (ROC AUC 0.72, *P*-value 2.41e – 05), the top increased biomarker from our prioritization with CFG of discovery data from AP (Table 5). Within diagnostic groups, the accuracy is even higher. SLC4A4 has very good accuracy at predicting future high SI in bipolar participants (AUC 0.93, *P*-value 9.45e – 06) and good accuracy in schizophrenia participants (AUC 0.76, *P*-value 0.030). SLC4A4 is a sodium-bicarbonate co-transporter that regulates intracellular pH, and possibly apoptosis. Very little is known to date about its roles in the brain, thus representing a completely novel finding. Brain pH has been reported by Wemmie *et al.*[22] to have a role in pain, fear and panic attacks, which clinically share features with acute SI states.

SKA2, the top decreased biomarker from prioritization with CFG of discovery data from AP and DE, has good accuracy at predicting SI across all diagnostic groups (AUC 0.69, *P*-value 0.00018), and even better accuracy in bipolar participants (AUC 0.76, *P*-value 0.0045) and schizophrenia participants (AUC 0.82, *P*-value 0.011).

The best single biomarker predictor for future hospitalizations for suicidal behavior in the first year across all diagnostic groups was SAT1, the top increased biomarker from the prioritization with CFG of discovery data from DE (AUC 0.55, *P*-value 0.28). The results across all diagnoses are modest, likely due to the significant variation of markers by diagnostic group (Table 5 and Supplementary Figure S4). This seems to be even more of an

issue for trait than for state predictions. Within diagnostic groups, in bipolar disorder, the SAT1 prediction accuracy for future hospitalizations is higher (AUC 0.63, *P*-value 0.18), consistent with our previous work.[1] CADM1 (AUC 0.72, *P*-value 0.076), SKA2 (AUC 0.71, *P*-value 0.056), and SLC4A4 (AUC 0.70, *P*-value 0.08) are even better predictors than SAT1 in bipolar disorder.

CFI-S has very good accuracy (AUC 0.89, *P*-value 3.53e − 13) at predicting SI in psychiatric participants across diagnostic groups (Figure 4c). Within diagnostic groups, in affective disorders, the accuracy is even higher. CFI-S has excellent accuracy at predicting high SI in bipolar participants (AUC 0.97, *P*-value 1.75e − 06) and in depression participants (AUC 0.95, *P*-value 7.98e − 06). CFI-S has good accuracy (AUC 0.71, *P*-value 0.006) at predicting future hospitalizations for suicidality in the first year, across diagnostic groups.

SASS has very good accuracy (AUC 0.85, 9.96e − 11) at predicting SI in psychiatric participants across diagnostic groups. Within diagnostic groups, in bipolar disorder, the accuracy is even higher (AUC 0.87, *P*-value 0.00011). SASS also has good accuracy (AUC 0.71, *P*-value 0.008) at predicting future hospitalizations for suicidality in the first year following testing.

Our *a priori* primary end point was a combined UP-Suicide, composed of the top increased and decreased biomarkers ($n = 11$) from the discovery for ideation (CADM1, CLIP4, DTNA, KIF2C), prioritization with CFG for prior evidence (SAT1, SKA2, SLC4A4), and validation for behavior in suicide completers (IL6, MBP, JUN, KLHDC3) steps, along with CFI-S, and SASS. UP-Suicide is an excellent predictor of SI across all disorders in the independent cohort of psychiatric participants (AUC 0.92, *P*-value 7.94e − 15) (Figure 6). UP-Suicide also has good predictive ability for future psychiatric hospitalizations for suicidality in the first year of follow-up (AUC 0.71, *P*-value 0.0094). The predictive ability of UP-Suicide is notably higher in affective disorder participants (bipolar, depression) (Table 5 and Figure 5).

DISCUSSION

We carried out systematic studies to identify clinically useful predictors for suicide. Our work focuses on identifying markers involved in SI and suicidal behavior, including suicide completion. Markers involved in behavior may be on a continuum with some of the markers involved in ideation, varying in the degree of expression changes from less severe (ideation) to more severe (behavior). One cannot have suicidal behavior without SI, but it may be possible to have SI without suicidal behavior.

As a first step, we sought to use a powerful but difficult to conduct within-participant design for discovery of blood biomarkers. Such a design is more informative than case-control, case-case, or even identical twins designs. The power of a within-participants longitudinal design for multi-omic discovery was first illustrated by Snyder and colleagues[9] in a landmark paper with an $n = 1$[9]. We studied a cohort of male participants with major psychiatric disorders ($n = 217$ participants) followed longitudinally (2–6 testing visits, at 3–6 months interval). In a smaller ($n = 37$) but very valuable subset of these participants, we captured one or more major switches from a no SI state to a high SI state at the time of the different testing visits (Figures 1 and 2).

Second, we conducted whole-genome gene expression discovery studies in the participants that exhibited the switches, using a longitudinal within-participant design, that factors out genetic variability and reduces environmental variability as well. We have demonstrated the power of such a design in our previous work on suicide biomarkers with an $n = 9$[1]. Our current $n = 37$ was four-fold higher, and consequently our power to detect signal was commensurately increased (Figure 2). Genes whose levels of expression tracked SI within each participant were identified.

Third, the lists of top candidate biomarkers for SI from the discovery and prioritization step (genes with a CFG score of 4 and above, reflecting genes that have maximal experimental internal evidence from this study and/or additional external literature cross-validating evidence), were additionally validated for involvement in suicidal behavior in a cohort of demographically matched suicide completers from the coroner's office (n = 26) (Figure 3).

Given that we used two methods (AP, DE), three steps (discovery for ideation, prioritization based on literature evidence, validation for behavior in completers), and two types of markers (increased, decreased), we anticipated having $2 \times 3 \times 2 = 12$ top markers. We ended up with 11 due to overlap (Table 2). Of note, 8 of these 11 markers (SAT1, SKA2, SLC4A4, KIF2C, MBP, IL6, JUN and KLHDC3), were significant in validation for behavior in terms of being changed even more in suicide completers, and 5 of them survived Bonferroni correction (SAT1, SLC4A4, MBP, IL6, KLHDC3). The 3 out of 11 markers that were not validated for behavior (DTNA, CLIP4 and CADM1) seemed indeed better in the independent test cohorts at predicting SI than at predicting suicidal behavior (hospitalizations) (Table 5B).

Fourth, we describe a novel, simple and comprehensive phenomic (clinical) risk assessment scale, the CFI-S scale, as well as a companion app to it for use by clinicians and individuals (Supplementary Figure S2). CFI-S was developed independently of any data from this study, by integrating known risk factors for suicide from the clinical literature. It has a total of 20 items (scored in a binary fashion—1 for present, 0 for absent, NA for information not available) that assess the influence of mental health factors, as well as of life satisfaction, physical health, environmental stress, addictions, and cultural factors known to influence suicidal behavior. It also has two demographics risk factors items: age and gender. The result is a simple polyphenic risk score with an absolute range of 0–22, normalized by the number of items on which we had available information, resulting in a score in the range from 0 to 1 (Table 4). We present data validating the CFI-S in our discovery cohort of live psychiatric participants and in suicide completers from the coroner's office (Figure 4). We acknowledge the possibility of a potential upward bias in next-of-kin reporting post-suicide completion, although each item of the scale was scored factually by a trained rater on its own merits. We believe it is still illustrative and informative to compare the CFI-S in live participants with ideation vs suicide completers, and identify which items are most different (such as inability to cope with stress, which is consistent with biological data from the biomarker side of our study).

Fifth, we have also assessed anxiety and mood, using a visual analog SASS, previously described by us (Niculescu *et al.* 2006), for which we now have developed an app version (Supplementary Figure S2). Using a PhenoChipping approach[6] in our discovery cohort of psychiatric participants, we show that anxiety measures cluster with SI and CFI-S, and mood measures are in the opposite cluster, suggesting that our participants have high SI when they have high anxiety and low mood (Figure 2). We would also like to include in the future measures of psychosis, and of stress, to be more comprehensive.

Sixth, we examined how the biomarkers identified by us are able to predict state (SI) in a larger independent cohort of psychiatric participants ($n = 108$ participants).

Seventh, we examined whether the biomarkers are able to predict trait (future hospitalizations for suicidal behavior) in psychiatric participants ($n = 157$) in the short term (first year of follow-up) as well as overall (all data for future hospitalizations available for each patient).

Last but not least, we demonstrate how our *a priori* primary end point, a comprehensive UP-Suicide, composed of the combination of the top increased and decreased biomarkers ($n = 11$) from the discovery, prioritization and validation steps, along with CFI-S and SASS, predicts state (SI) and trait (future psychiatric hospitalizations for suicidality).

Table 5. Predictions

A. Best predictors

Predictors ROC AUC/P-value	*All participants*	*BP participants*	*MDD participants*	*SZA participants*	*SZ participants*
Suicidal ideation cohort *N* = 108 participants	UP-Suicide 0.92/7.94e − 15	UP-Suicide 0.98/ 1.19E-6	UP-Suicide 0.95/2.96E-7	UP-Suicide 0.81/0.0018	Mood 0.94/0.00075 UP-Suicide 0.91/0.0015
First year hospitalizations for suicidality cohort *N* = 157 participants	SASS 0.71/0.0080 UP-Suicide 0.71/0.0094	SASS 0.95/0.0016 UP-Suicide 0.94/0.0021	CFI-S 0.78/0.066 UP-Suicide 0.70/0.16	Anxiety 0.65/0.21 UP-Suicide 0.52/0.47	UP-Suicide 0.68/0.17

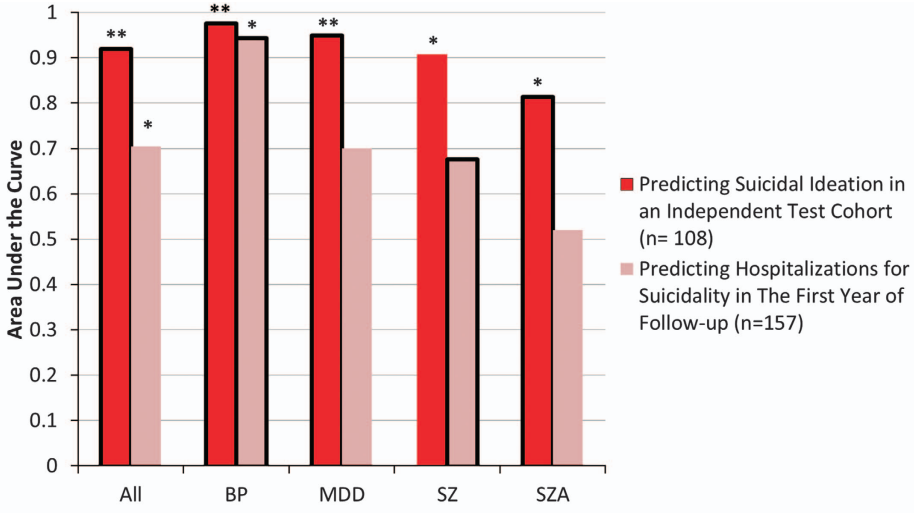
B. All predictions

	All participants	*BP participants*	*MDD participants*	*SZA participants*	*SZ participants*
Predictors *ROC AUC/P-value*	*No SI = 73* *Intermediate SI = 12* *High SI = 23*	*No SI = 17* *Intermediate SI = 5* *High SI = 7*	*No SI = 17* *Intermediate SI = 0* *High SI = 8*	*No SI = 19* *Intermediate SI = 3* *High SI = 6*	*No SI = 20* *Intermediate SI = 4* *High SI = 2*
Suicidal ideation cohort *N* = 108 participants Biomarkers	SKA2 0.69/0.00018 SLC4A4 0.72/2.41E-5 KIF2C 0.42/0.92 DTNA 0.54/0.22 MBP 0.53/0.30 IL6 0.66/0.0017 SAT1 0.35/1 CLIP4 0.52/0.37 CADM1 0.59/0.045 KLHDC3 0.47/0.72 JUN 0.46/0.76 BIOM6 0.64/0.0042 BIOM5 0.54/0.23 BIOM11 0.63/0.0088	SKA2 0.76/0.0045 SLC4A4 0.93/9.45E-6 KIF2C 0.33/0.96 DTNA 0.61/0.15 MBP 0.54/0.35 IL6 0.66/0.06 SAT1 0.19/1 CLIP4 0.76/0.0050 CADM1 0.73/0.013 KLHDC3 0.52/0.41 JUN 0.39/0.86 BIOM6 0.69/0.028 BIOM5 0.69/0.029 BIOM11 0.75/0.0070	SKA2 0.54/0.34 SLC4A4 0.55/0.33 KIF2C 0.52/0.45 DTNA 0.53/0.41 MBP 0.61/0.15 IL6 0.76/0.0057 SAT1 0.39/0.86 CLIP4 0.21/1 CADM1 0.63/0.11 KLHDC3 0.47/0.60 JUN 0.54/0.37 BIOM6 0.72/0.017 BIOM5 0.44/0.73 BIOM11 0.57/0.26	SKA2 0.68/0.06 SLC4A4 0.64/0.11 KIF2C 0.41/0.78 DTNA 0.53/0.41 MBP 0.43/0.74 IL6 0.58/0.24 SAT1 0.48/0.59 CLIP4 0.54/0.38 CADM1 0.48/0.56 KLHDC3 0.38/0.86 JUN 0.54/0.38 BIOM6 0.61/0.18 BIOM5 0.44/0.69 BIOM11 0.51/0.46	SKA2 0.82/0.011 SLC4A4 0.76/0.03 KIF2C 0.43/0.71 DTNA 0.45/0.66 MBP 0.58/0.28 IL6 0.62/0.19 SAT1 0.37/0.84 CLIP4 0.61/0.21 CADM1 0.49/0.54 KLHDC3 0.49/0.53 JUN 0.37/0.84 BIOM6 0.49/0.55 BIOM5 0.61/0.21 BIOM11 0.64/0.16
Clinical	Anxiety 0.78/2.3E-7 Mood 0.82/1.62E-9 SASS 0.85/9.96E-11 CFI-S 0.89/3.53E-13	Anxiety 0.86/0.00018 Mood 0.81/0.00091 SASS 0.87/0.00011 CFI-S 0.97/ 1.75E-6	Anxiety 0.81/0.0015 Mood 0.81/0.0015 SASS 0.87/6.01E-5 CFI-S 0.95/7.98E-6	Anxiety 0.75/0.12 Mood 0.77/0.0080 SASS 0.81/0.0019 CFI-S 0.74/0.016	Anxiety 0.62/0.19 Mood 0.94/0.00075 SASS 0.85/0.0058 CFI-S 0.85/0.0049
Combined	UP-Suicide 0.92/ 7.94E-15	UP-Suicide 0.98/ 1.19E-6	UP-Suicide 0.95/ 2.96E-7	UP-Suicide 0.81/ 0.0018	UP-Suicide 0.91/ 0.0015

	All participants	*BP participants*	*MDD participants*	*SZA participants*	*SZ participants*
Predictors *ROC AUC/P-value*	*No Hosp = 139* *Hosp = 18*	*No Hosp = 43* *Hosp = 7*	*No Hosp = 20* *Hosp = 3*	*No Hosp = 41* *Hosp = 3*	*No Hosp = 35* *Hosp = 5*
First year hospitalizations for suicidality *N* = 157 participants Biomarkers	SKA2 0.44/0.78 SLC4A4 0.47/0.66 KIF2C 0.54/0.30 DTNA 0.44/0.77 MBP 0.38/0.92 IL6 0.48/0.60 SAT1 0.55/0.28 CLIP4 0.31/0.99 CADM1 0.53/0.36 KLHDC3 0.31/0.98 JUN 0.40/0.89 BIOM6 0.51/0.46 BIOM5 0.35/0.96v BIOM11 0.42/0.82	SKA2 0.71/0.056 SLC4A4 0.70/0.08 KIF2C 0.59/0.26 DTNA 0.61/0.21 MBP 0.30/0.90 IL6 0.45/0.65 SAT1 0.63/0.18 CLIP4 0.26/0.91 CADM1 0.72/0.076 KLHDC3 0.41/0.72 JUN 0.36/0.85 BIOM6 0.62/0.23 BIOM5 0.50/0.52 BIOM11 0.63/0.24	SKA2 0.048/0.99 SLC4A4 0.048/0.99 KIF2C 0.45/0.61 DTNA 0.29/0.83 MBP 0.42/0.68 IL6 0.76/0.090 SAT1 0.62/0.29 CLIP4 0.25/0.92 CADM1 0.74/0.17 KLHDC3 0.31/0.81 JUN 0.37/0.77 BIOM6 0.68/0.18 BIOM5 0.24/0.88 BIOM11 0.48/0.55	SKA2 0.41/0.70 SLC4A4 0.37/0.78 KIF2C 0.42/0.67 DTNA 0.13/0.96 MBP 0.29/0.88 IL6 0.28/0.90 SAT1 0.37/0.76 CLIP4 0.31/0.87 CADM1 0.048/0.99 KLHDC3 0.29/0.88 JUN 0.58/0.35 BIOM6 0.14/0.96 BIOM5 0.28/0.90 BIOM11 0.23/0.94	SKA2 0.13/0.99 SLC4A4 0.39/0.74 KIF2C 0.67/0.19 DTNA 0.46/0.61 MBP 0.53/0.46 IL6 0.55/0.41 SAT1 0.44/0.63 CLIP4 0.41/0.69 CADM1 0.56/0.39 KLHDC3 0.16/0.95 JUN 0.30/0.90 BIOM6 0.43/0.63 BIOM5 0.40/0.72 BIOM11 0.40/0.72
Clinical	Anxiety 0.64/0.066 Mood 0.58/0.16 SASS 0.71/0.0080 CFI-S 0.71/0.0058	Anxiety 0.69/0.14 Mood 0.70/0.059 SASS 0.95/0.0016 CFI-S 0.86/0.01	Anxiety 0.52/0.48 Mood 0.60/0.32 SASS 0.77/0.083 CFI-S 0.78/0.066	Anxiety 0.65/0.21 Mood 0.45/0.63 SASS 0.59/0.31 CFI-S 0.75/0.12	Anxiety 0.58/0.34 Mood 0.5/0.51 SASS 0.63/0.25 CFI-S 0.54/0.40
Combined	UP-Suicide 0.71/ 0.0094	UP-Suicide 0.94/ 0.0021	UP-Suicide 0.7/0.16	UP-Suicide 0.52/0.47	UP-Suicide 0.68/0.17

Abbreviations: AUC, area under curve; BP, bipolar; CFI-S, convergent functional information for suicide; MDD, major depressive disorder; ROC, receiver operating characteristic; SASS, simplified affective state scale; SI, suicidal ideation; SZA, schizoaffective; SZ, schizophrenia; UP, universal predictive measure. ROC AUC/*P*-values. UP-Suicide is composed of increased markers (CFI-S, anxiety, BioM-6 panel of increased biomarkers) and decreased markers (mood, BioM-5 panel of decreased biomarkers); SASS is composed of increased marker (anxiety), and decreased marker (mood).

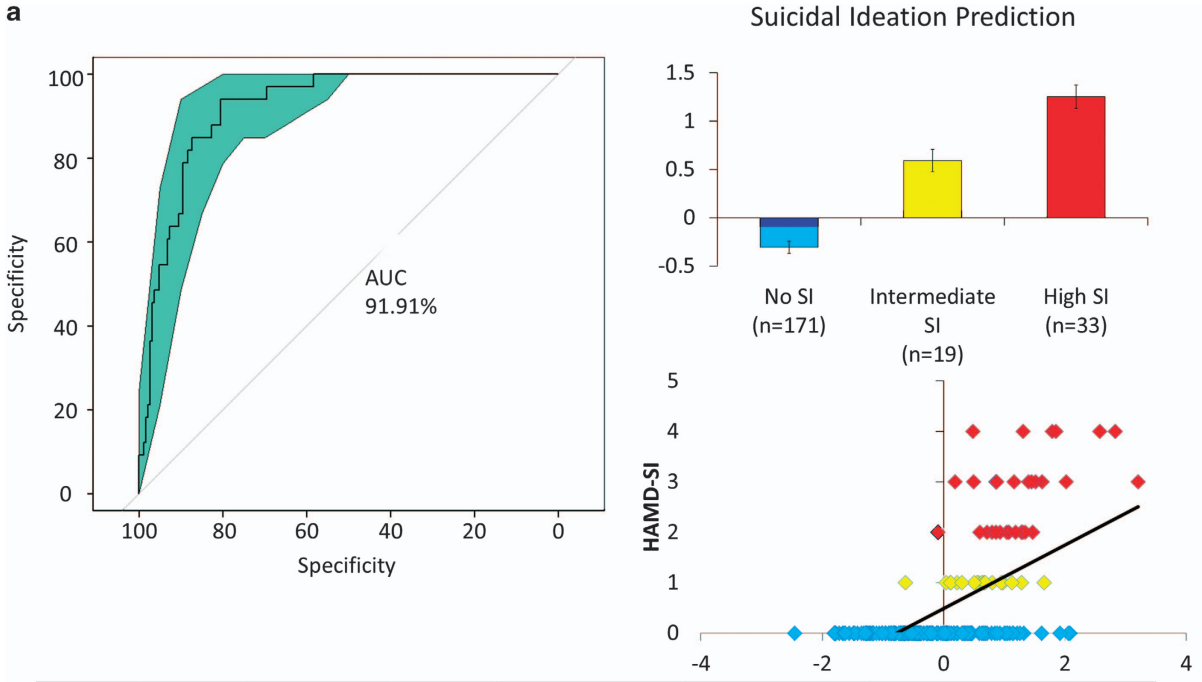
a



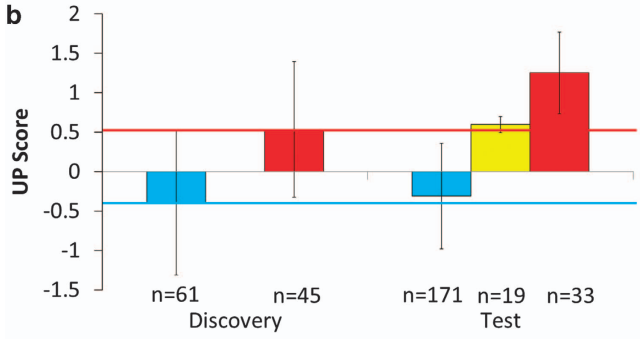
b

	Subjects Total/ High SI	High SI prediction ROC AUC ROC p-value	ANOVA (No SI vs. Intermediate SI vs. High SI)	Correlation R P-value	Subjects Total/ First year hospitalized for suicidality/ All future hospitalized for suicidality	Predictions First year hospitalized for suicidality ROC AUC ROC p-value	T-test First year s hospitalized for suicidality	Correlation R P-value First year hospitalized for suicidality	Correlation R P-value All future hospitalized for suicidality
All	108/23	**0.919 7.94E-15**	5.89E-22	0.6002 1.63E-23	157/12/33	0.7046 0.009	0.021	0.2119 0.0039	0.1911 0.0082
BP	29/7	**0.975 1.19E-06**	2.46E-13	0.8150 4.44E-16	50/3/8	0.943 0.002	0.002	0.3683 0.0042	0.2312 0.0531
MDD	25/8	**0.949 2.96E-07**	NA	0.62052 9.87E-07	23/3/3	*0.700 0.155*	*0.169*	*0.2118 0.1660*	*0.1759 0.2111*
SZ	26/2	0.908 1.46E-03	0.00065	0.48837 5.81E-05	40/3/7	*0.676 0.173*	*0.287*	*0.1669 0.1517*	*0.1761 0.1385*
SZA	28/6	0.814 1.78E-03	0.00245	0.4285 5.48E-04	44/3/15	*0.520 0.465*	*0.477*	*0.0067 0.4827*	*0.1668 0.1396*

Figure 5. Testing of universal predictor for suicide (UP-Suicide). UP-Suicide is a combination of our best gene expression biomarkers (top increased and decreased biomarkers from discovery, prioritization by CFG, and validation in suicide completers steps), and phenomic data (CFI-S and SASS). (**a**) Area Under the Curve (AUC) for the UP-Suicide predicting suicidal ideation and hospitalizations within the first year in all participants, as well as separately in bipolar (BP), major depressive disorder (MDD), schizophrenia (SZ), and schizoaffective (SZA) participants. **Indicates the comparison survived Bonferroni correction for multiple comparisons. *Indicates nominal significance of $P < 0.05$. Bold outline indicates that the UP-Suicide was synergistic to its components, i.e., performed better than the gene expression biomarkers or phenomic data individually. (**b**) Table containing descriptive statistics for all participants together, as well as separately in BP, MDD, SZ, and SZA. Bold indicates the measure survived Bonferroni correction for 200 comparisons (20 genomic and phenomic markers/combinations × 2 testing cohorts for SI and future hospitalizations in the first year × 5 diagnostic categories–all, BP, MDD, SZA, SZ). We also show Pearson correlation data in the suicidal ideation test cohort for HAMD-SI vs. UP-Suicide, as well as Pearson correlation data in the hospitalization test cohort for frequency of hospitalizations for suicidality in the first year, and for frequency of hospitalizations for suicidality in all future available follow-up interval (which varies among participants, from 1 year to 8.5 years).

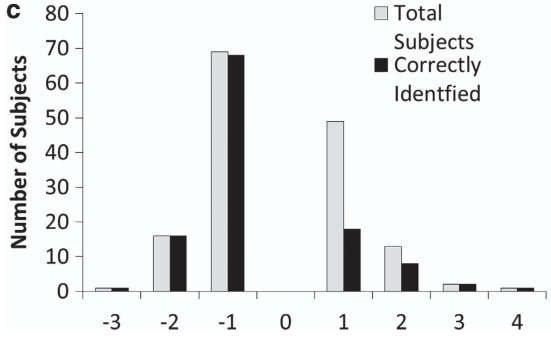


Predictor	Dx	Type	ROC AUC	ROC p-value	ANOVA	Correlation R	Correlation p-value
UP-Suicide	All	S	0.9191	7.94E-15	5.89E-22	0.6001971	1.63e-23



Predicting Suicidal Ideation

Sensitivity	Specificity	Balanced Accuracy
88%	81%	84%



Category	Total Subjects	High SI	Intermediate SI	No SI	Postive Predictive Value	Negative Predictive Value
-3	1	0	0	1	100%	100%
-2	16	0	0	16	100%	100%
-1	69	0	1	68	99%	100%
0	72	4	6	62	94%	94%
1	49	18	11	20	37%	59%
2	13	8	1	4	62%	69%
3	2	2	0	0	100%	100%
4	1	1	0	0	100%	100%

Figure 6. Prediction of suicidal ideation by universal predictive measure-suicide. (**a**) (top left) Receiver-operating curve identifying participants with suicidal ideation against participants with no suicidal ideation or intermediate SI. (top right) *Y* axis contains the average UP-Suicide scores with standard error of mean for no suicidal ideation, intermediate suicidal ideation and high suicidal ideation. (bottom right) Scatter plot depicting HAMD-SI score on the *Y* axis and universal predictive measure-suicide score on the *X* axis with linear trend line. (bottom) Table summarizing descriptive statistics. Analysis of variance was performed between groups with no suicidal ideation, intermediate suicidal ideation and high suicidal ideation. (**b**) Predictions in test cohort based on thresholds in the discovery cohort - average UP-Suicide scores with standard deviation. (**c**) Number of participants correctly identified in the test cohort by categories based on thresholds in the discovery cohort. Category 1 means within 1 s.d. above the average of high suicidal ideation participants in the discovery cohort, category 2 means between 1 and 2 s.d. above, and so on. Category 1 means within 1 s.d. below the average of the no suicidal ideation participants in the discovery cohort, category 2 means between 1 and 2 s.d. below and so on.

The rationale for identifying blood biomarkers as opposed to brain biomarkers is a pragmatic one—the brain cannot be readily accessed in live individuals. Other peripheral fluids, such as cerebrospinal fluid, require more invasive and painful procedures. Nevertheless, it is likely that many of the peripheral blood transcriptomic changes are not necessarily mirroring what is happening in the brain, and vice-versa. The keys to finding peripheral biomarkers[4] are, first, to have a powerful discovery approach, such as our within-participant design, that closely tracks the phenotype you are trying to measure and reduces noise. Second, cross-validating and prioritizing the results with other lines of evidence, such as brain gene expression and genetic data, are important in order to establish relevance and generalizability of findings. Third, it is important to validate for behavior in an independent cohort with a robust and relevant phenotype, in this case suicide completers. Fourth, testing for predictive ability in independent/prospective cohorts is a must.

Biomarkers that survive such a rigorous stepwise discovery, prioritization, validation and testing process are likely directly relevant to the disorder studied. As such, we endeavored to study their biology, whether they are involved in other psychiatric disorders or are relatively specific for suicide, and whether they are the modulated by existing drugs in general, and drugs known to treat suicidality in particular. We have identified a series of biomarkers that seem to be changed in opposite direction in suicide vs in treatments with omega-3 fatty acids, lithium, clozapine or MAOIs. These biomarkers could potentially be used to stratify patients to different treatment approaches, and monitor their response (Supplementary Table S4).

We also conducted predictive studies, across all participants and by diagnosis, as a way of assessing how generalizable and how particular to a diagnosis biomarkers are. Different diagnostic groups have different disease biology and are on different medications, which may modify the levels of the biomarkers. We observe a significant variation in the predictive ability of biomarkers by diagnosis, which has important practical applications for future work on diagnostic-specific predictors (Table 5). Of note, a number of biomarkers from the current larger study reproduce our previous work in a smaller, bipolar cohort (SAT1, MARCKS, PTEN, as well as FOXN3, GCOM1, RECK, IL1B, LHFP, ATP6V0E1 and KLHDC3) (Supplementary Table S2). In the current data sets, we have also *post hoc* carried out biomarker discovery within each diagnosis, which revealed a diversity of top markers, but should be interpreted with caution given the smaller N within each diagnostic group (Supplementary Table S5).

Before any testing, we planned to use a comprehensive combination of genomic data (specifically, the top increased and decreased biomarkers from discovery, prioritization and validation) and phenomic data (specifically, the CFI-S and the SASS) as the primary end point measure, a broad-spectrum universal predictor (UP-Suicide) for state SI and trait future hospitalizations. It has not escaped our attention that certain single biomarkers, particular phenotypic items, or combinations thereof seem to perform better than the UP-Suicide in one or another type of prediction or diagnostic group (see Table 5). However, since such markers and combinations were not chosen by us *a priori* and such insights derive from testing, we cannot exclude a fit to cohort effect for them and reserve judgement as to their robustness as predictors until further testing in additional independent cohorts, by us and others. What we can put forward for now based on the current work is the UP-Suicide, which seems to be a robust predictor across different scenarios and diagnostic groups.

Overall, our predictive ability for trait future hospitalizations is somewhat less than for state SI (Figure 5, Table 5). However, clinically, events may indeed be driven by state, and the immediate concern is preventing immediate or short term adverse outcomes.

Our study has a number of limitations. All this work was carried out in psychiatric patients, a high-risk group, and it remains to be seen how such predictors apply to non-psychiatric participants. Additionally, the current studies were carried out exclusively in males. Similar work is needed in females, with and without psychiatric disorders. Such work is ongoing in our group. Lastly, for the UP-Suicide testing, the prevalence rate for high SI in our independent test cohort was a relatively low 21% (23 out of 108), and the incidence of future hospitalizations for suicidality was even lower: 7.6% in the first year (12 out of 157), and 21.0% overall (33 out of 157) (Figure 5). Although this is fortunate for the participants enrolled and may reflect the excellence of clinical care they were receiving in our hospital independent of this study, it may bias the predictions. Studies with larger numbers and longer follow-up, currently ongoing, as well as studies in different clinical settings, may provide more generalizability. It is to be noted, however, that the incidence of suicidality in the general population is lower, for example at 1.5% in adolescents in an European cohort[23] and estimates of 0.2–2% in the US,[24] which underlines the rationale of using a very high-risk group like we did for magnifying and enabling signal detection with a relatively small N.

In conclusion, we have advanced the biological understanding of suicidality, highlighting behavioral and biological mechanisms related to inflammation, mTOR signaling, growth factors, stress response and apoptosis. mTOR signaling has been identified as necessary for the rapid antidepressant response of ketamine.[25] The fact that this biological pathway was identified in an unbiased fashion by our work as the top pathway changed in suicide in the validated biomarkers from our analyses (Table 3 and Supplementary Figure S3) is scientifically interesting, and provides a biological rationale for studying ketamine as a potential treatment in acutely suicidal individuals.[26] Of equal importance, we developed instruments (biomarkers and apps) for predicting suicidality, that do not require asking the person assessed if they have suicidal thoughts, as individuals who are truly suicidal often do not share that information with people close to them or with clinicians. We propose that the widespread use of such risk prediction tests as part of routine or targeted healthcare assessments will lead to early disease interception followed by preventive lifestyle modifications or treatment. Given the magnitude and urgency of the problem, the importance of efforts to implement such tools cannot be overstated.

CONFLICT OF INTEREST

ABN is listed as inventor on a patent application being filed by Indiana University. The authors declare no conflict of interest.

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This work is, in essence, a field-wide collaboration. We acknowledge our debt of gratitude for the efforts and results of the many other groups, cited in our paper, who have conducted and published studies (clinical, genetic and biological) in suicidality. With their arduous and careful work, a convergent approach such as ours is possible. We would particularly like to thank the participants who participated in these studies, their families and their caregivers. Without their contribution, such work to advance the understanding of suicide would not be possible. This work was supported by an NIH Directors' New Innovator Award (1DP2OD007363) and a VA Merit Award (2I01CX000139) to ABN. Supplementary Information is also available from the Niculescu Laboratory website (www.neurophenomics.info).

AUTHOR CONTRIBUTIONS

ABN designed the study, created the clinical rating scales and wrote the manuscript. DFL, PLP, HL-N, HD, NJ, TBL, RL and EMN analyzed the data. NJ, NPV and FNK performed database work. PLP, JM and GS produced the apps. EB, AJ, SG, HW, DLG and RS organized and conducted testing in psychiatric participants. SC, CH, AB, MY, AS, GES and ABN organized and carried out post-mortem samples collection. TG, NJS, SMK and DRS conducted microarray experiments and provided input on data analyses. All authors discussed the results and commented on the manuscript.

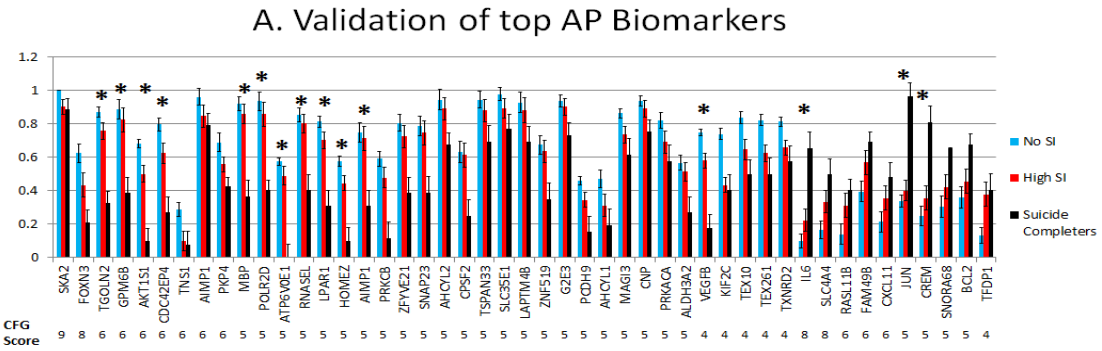
REFERENCES

1 Le-Niculescu H, Levey DF, Ayalew M, Palmer L, Gavrin LM, Jain N *et al.* Discovery and validation of blood biomarkers for suicidality. *Mol Psychiatry* 2013; **18**: 1249–1264.
2 Le-Niculescu H, Kurian SM, Yehyawi N, Dike C, Patel SD, Edenberg HJ *et al.* Identifying blood biomarkers for mood disorders using convergent functional genomics. *Mol Psychiatry* 2009; **14**: 156–174.
3 Kurian SM, Le-Niculescu H, Patel SD, Bertram D, Davis J, Dike C *et al.* Identification of blood biomarkers for psychosis using convergent functional genomics. *Mol Psychiatry* 2011; **16**: 37–58.
4 Niculescu AB, Levey D, Le-Niculescu H, Niculescu E, Kurian SM, Salomon D. Psychiatric blood biomarkers: avoiding jumping to premature negative or positive conclusions. *Mol Psychiatry* 2015; **20**: 286–288.
5 Niculescu AB, Le-Niculescu H. Convergent Functional Genomics: what we have learned and can learn about genes, pathways, and mechanisms. *Neuropsychopharmacology* 2010; **35**: 355–356.
6 Niculescu AB, Lulow LL, Ogden CA, Le-Niculescu H, Salomon DR, Schork NJ *et al.* PhenoChipping of psychotic disorders: a novel approach for deconstructing and quantitating psychiatric phenotypes. *Am J Med Genet B, Neuropsychiatr Genet* 2006; **141B**: 653–662.
7 Borges G, Angst J, Nock MK, Ruscio AM, Kessler RC. Risk factors for the incidence and persistence of suicide-related outcomes: a 10-year follow-up study using the National Comorbidity Surveys. *J Affect Disord* 2008; **105**: 25–33.
8 Nock MK. Future directions for the study of suicide and self-injury. *J Clin Child Adolesc Psychol* 2012; **41**: 255–259.
9 Chen R, Mias GI, Li-Pook-Than J, Jiang L, Lam HY, Miriami E *et al.* Personal omics profiling reveals dynamic molecular and medical phenotypes. *Cell* 2012; **148**: 1293–1307.
10 Darlington TM, Pimentel R, Smith K, Bakian AV, Jerominski L, Cardon J *et al.* Identifying rare variants for genetic risk through a combined pedigree and phenotype approach: application to suicide and asthma. *Transl Psychiatry* 2014; **4**: e471.
11 Sequeira A, Morgan L, Walsh DM, Cartagena PM, Choudary P, Li J *et al.* Gene expression changes in the prefrontal cortex, anterior cingulate cortex and nucleus accumbens of mood disorders subjects that committed suicide. *PLoS One* 2012; **7**: e35367.
12 Klempan TA, Sequeira A, Canetti L, Lalovic A, Ernst C, ffrench-Mullen J *et al.* Altered expression of genes involved in ATP biosynthesis and GABAergic neurotransmission in the ventral prefrontal cortex of suicides with and without major depression. *Mol Psychiatry* 2009; **14**: 175–189.
13 Hishimoto A, Cui H, Mouri K, Nushida H, Ueno Y, Maeda K *et al.* A functional polymorphism of the micro-opioid receptor gene is associated with completed suicides. *J Neural Transm* 2008; **115**: 531–536.
14 Gabilondo AM, Meana JJ, Garcia-Sevilla JA. Increased density of mu-opioid receptors in the postmortem brain of suicide victims. *Brain Res* 1995; **682**: 245–250.
15 Guintivano J, Brown T, Newcomer A, Jones M, Cox O, Maher BS *et al.* Identification and replication of a combined epigenetic and genetic biomarker predicting suicide and suicidal behaviors. *Am J Psychiatry* 2014; **171**: 1287–1296.
16 Mann JJ, Currier D. Medication in suicide prevention insights from neurobiology of suicidal behavior. In: Dwivedi Y (ed) *The Neurobiological Basis of Suicide*. CRC Boca Raton (FL), 2012.
17 Sublette ME, Hibbeln JR, Galfalvy H, Oquendo MA, Mann JJ. Omega-3 polyunsaturated essential fatty acid status as a predictor of future suicide risk. *Am J Psychiatry* 2006; **163**: 1100–1102.
18 Oquendo MA, Sullivan GM, Sudol K, Baca-Garcia E, Stanley BH, Sublette ME *et al.* Toward a biosignature for suicide. *Am J Psychiatry* 2014; **171**: 1259–1277.
19 Kelleher I, Lynch F, Harley M, Molloy C, Roddy S, Fitzpatrick C *et al.* Psychotic symptoms in adolescence index risk for suicidal behavior: findings from 2 population-based case-control clinical interview studies. *Arch Gen Psychiatry* 2012; **69**: 1277–1283.
20 Schoenbaum M, Kessler RC, Gilman SE, Colpe LJ, Heeringa SG, Stein MB *et al.* Predictors of suicide and accident death in the Army Study to Assess Risk and Resilience in Servicemembers (Army STARRS): results from the Army Study to Assess Risk and Resilience in Servicemembers (Army STARRS). *JAMA Psychiatry* 2014; **71**: 493–503.
21 Posner K, Brown GK, Stanley B, Brent DA, Yershova KV, Oquendo MA *et al.* The Columbia-Suicide Severity Rating Scale: initial validity and internal consistency findings from three multisite studies with adolescents and adults. *Am J Psychiatry* 2011; **168**: 1266–1277.
22 Wemmie JA, Taugher RJ, Kreple CJ. Acid-sensing ion channels in pain and disease. *Nat Rev Neuroscience* 2013; **14**: 461–471.
23 Wasserman D, Hoven CW, Wasserman C, Wall M, Eisenberg R, Hadlaczky G *et al.* School-based suicide prevention programmes: the SEYLE cluster-randomised, controlled trial. *Lancet* 2015; **385**: 1536–1544.
24 Nock MK, Borges G, Bromet EJ, Cha CB, Kessler RC, Lee S. Suicide and suicidal behavior. *Epidemiol Rev* 2008; **30**: 133–154.
25 Li N, Lee B, Liu RJ, Banasr M, Dwyer JM, Iwata M *et al.* mTOR-dependent synapse formation underlies the rapid antidepressant effects of NMDA antagonists. *Science* 2010; **329**: 959–964.
26 Ballard ED, Ionescu DF, Vande Voort JL, Niciu MJ, Richards EM, Luckenbaugh DA *et al.* Improvement in suicidal ideation after ketamine infusion: relationship to reductions in depression and anxiety. *J Psychiatr Res* 2014; **58**: 161–166.
27 Pandey GN, Rizavi HS, Ren X, Fareed J, Hoppensteadt DA, Roberts RC *et al.* Proinflammatory cytokines in the prefrontal cortex of teenage suicide victims. *J Psychiatr Res* 2012; **46**: 57–63.
28 Hoyo-Becerra C, Huebener A, Trippler M, Lutterbeck M, Liu ZJ, Truebner K *et al.* Concomitant interferon alpha stimulation and TLR3 activation induces neuronal expression of depression-related genes that are elevated in the brain of suicidal persons. *PLoS One* 2013; **8**: e83149.
29 Lindqvist D, Janelidze S, Erhardt S, Traskman-Bendz L, Engstrom G, Brundin L. CSF biomarkers in suicide attempters--a principal component analysis. *Acta Psychiatr Scand* 2011; **124**: 52–61.
30 Bay-Richter C, Linderholm KR, Lim CK, Samuelsson M, Traskman-Bendz L, Guillemin GJ *et al.* A role for inflammatory metabolites as modulators of the glutamate N-methyl-D-aspartate receptor in depression and suicidality. *Brain Behav Immun* 2015; **43**: 110–117.
31 Kim YK, Lee SW, Kim SH, Shim SH, Han SW, Choi SH *et al.* Differences in cytokines between non-suicidal patients and suicidal patients in major depression. *Prog Neuropsychopharmacol Biol Psychiatry* 2008; **32**: 356–361.
32 Fiori LM, Wanner B, Jomphe V, Croteau J, Vitaro F, Tremblay RE *et al.* Association of polyaminergic loci with anxiety, mood disorders, and attempted suicide. *PloS One* 2010; **5**: e15146.
33 Sokolowski M, Ben-Efraim YJ, Wasserman J, Wasserman D. Glutamatergic GRIN2B and polyaminergic ODC1 genes in suicide attempts: associations and gene-environment interactions with childhood/adolescent physical assault. *Mol Psychiatry* 2013; **18**: 985–992.
34 Perlis RH, Huang J, Purcell S, Fava M, Rush AJ, Sullivan PF *et al.* Genome-wide association study of suicide attempts in mood disorder patients. *Am J Psychiatry* 2010; **167**: 1499–1507.
35 Kim S, Choi KH, Baykiz AF, Gershenfeld HK. Suicide candidate genes associated with bipolar disorder and schizophrenia: An exploratory gene expression profiling analysis of post-mortem prefrontal cortex. *BMC Genomics* 2007; **8**: 413.
36 Labonte B, Suderman M, Maussion G, Lopez JP, Navarro-Sanchez L, Yerko V *et al.* Genome-wide methylation changes in the brains of suicide completers. *Am J Psychiatry* 2013; **170**: 511–520.
37 Seder E, Biselli A, Pisano S, Niccolai S, Smith GD, Joo K *et al.* Longitudinal target-spin asymmetries for deeply virtual compton scattering. *Phys Rev Lett* 2015; **114**: 032001.
38 Roggenbach J, Muller-Oerlinghausen B, Franke L, Uebelhack R, Blank S, Ahrens B. Peripheral serotonergic markers in acutely suicidal patients. 1. Comparison of serotonergic platelet measures between suicidal individuals, nonsuicidal patients with major depression and healthy subjects. *J Neural Transm* 2007; **114**: 479–487.
39 Pandey GN, Dwivedi Y, Ren X, Rizavi HS, Roberts RC, Conley RR *et al.* Altered expression and phosphorylation of myristoylated alanine-rich C kinase substrate (MARCKS) in postmortem brain of suicide victims with or without depression. *J Psychiatr Res* 2003; **37**: 421–432.
40 Punzi G, Ursini G, Shin JH, Kleinman JE, Hyde TM, Weinberger DR. Increased expression of MARCKS in post-mortem brain of violent suicide completers is related to transcription of a long, noncoding, antisense RNA. *Mol Psychiatry* 2014; **19**: 1057–1059.
41 Dwivedi Y, Rizavi HS, Zhang H, Roberts RC, Conley RR, Pandey GN. Modulation in activation and expression of phosphatase and tensin homolog on chromosome ten, Akt1, and 3-phosphoinositide-dependent kinase 1: further evidence demonstrating altered phosphoinositide 3-kinase signaling in postmortem brain of suicide subjects. *Biol Psychiatry* 2010; **67**: 1017–1025.
42 Karege F, Perroud N, Burkhardt S, Fernandez R, Ballmann E, La Harpe R *et al.* Alterations in phosphatidylinositol 3-kinase activity and PTEN phosphatase in the prefrontal cortex of depressed suicide victims. *Neuropsychobiology* 2011; **63**: 224–231.

Supplementary Information accompanies the paper on the Molecular Psychiatry website (http://www.nature.com/mp)

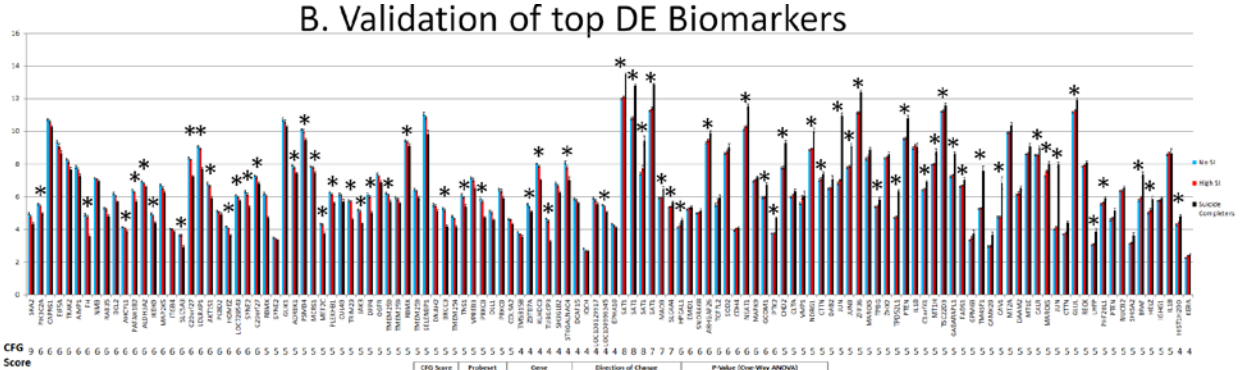
Supplementary Information:

Figure S1 Biomarkers Validation in Suicide Completers (A) Validating of top AP candidate biomarkers for suicidality. 47 out of the 153 with top-scoring CFG (31%) showed stepwise significant change between no SI, high SI, and validation suicide completers. 17 (11%) remained significant after strict Bonferroni correction. (B) Validating of top DE candidate biomarkers for suicidality. 124 out of the 418 with top-scoring CFG (30%) showed stepwise significant change between no SI, high SI, and validation suicide completers. 68 (16%) remained significant after strict Bonferroni correction.



CFG Score	Probeset	Gene	Direction of Change	P-Value (One-Way ANOVA)
5	**225408_at**	**MBP**	**D**	**6.736E-10**
5	**214144_at**	**POLR2D**	**D**	**1.022E-09**
8	**205207_at**	**IL6**	**I**	**1.436E-08**
5	**201466_s_at**	**JUN**	**I**	**2.214E-08**
6	**203834_s_at**	**TGOLN2**	**D**	**1.098E-07**
6	**236116_at**	**GPM6B**	**D**	**2.319E-07**
6	**224982_at**	**AKT1S1**	**D**	**3.539E-07**
5	**236527_at**	**ATP6V0E1**	**D**	**3.801E-07**
4	**203683_s_at**	**VEGFB**	**D**	**5.126E-07**
5	**241740_at**	**CREM**	**I**	**0.00000108**
6	**218062_x_at**	**CDC42EP4**	**D**	**0.000001155**
5	**221287_at**	**RNASEL**	**D**	**0.00000605**
5	**204036_at**	**LPAR1**	**D**	**0.000007672**
5	**231868_at**	**HOMEZ**	**D**	**0.00008269**
5	**227605_at**	**AIMP1**	**D**	**0.00008374**
5	230437_s_at	PRKCB	D	0.0001339
5	219929_s_at	ZFYVE21	D	0.0001693
5	209131_s_at	SNAP23	D	0.0003915
8	205021_s_at	FOXN3	D	0.0004985
4	211519_s_at	KIF2C	D	0.0005629
5	212814_at	AHCYL2	D	0.001033
5	233208_x_at	CPSF2	D	0.001708
8	210739_x_at	SLC4A4	I	0.002351
4	242538_at	TFDP1	I	0.002375
4	1558702_at	TEX10	D	0.002806
5	225775_at	TSPAN33	D	0.00302
4	1559675_at	TEX261	D	0.00427
5	222263_at	SLC35E1	D	0.006511
5	1566403_at	SNORA68	I	0.008132
5	1554679_a_at	LAPTM4B	D	0.01125
5	1568873_at	ZNF519	D	0.01164
6	218863_s_at	TNS1	D	0.01233
6	219142_at	RASL11B	I	0.01238
6	217535_at	FAM49B	I	0.01877
6	207004_at	BCL2	I	0.01997
5	223254_s_at	G2E3	D	0.02143
5	238919_at	PCDH9	D	0.0215
5	207464_at	AHCYL1	D	0.02317
9	225686_at	SKA2	D	0.02744
5	226770_at	MAGI3	D	0.02924
6	210163_at	CXCL11	I	0.02934
6	235594_at	AIMP1	D	0.03006
5	1557943_at	CNP	D	0.03149
5	202801_at	PRKACA	D	0.03237
5	210544_s_at	ALDH3A2	D	0.03479
4	210803_at	TXNRD2	D	0.04251
6	201927_s_at	PKP4	D	0.04861

B. Validation of top DE Biomarkers



CFG Score	Probeset	Gene	Direction of Change	P-Value (One-Way ANOVA)
5	201464_x_at	JUN	I	2.62784E-51
8	213988_s_at	SAT1	I	5.07869E-44
5	213281_at	JUN	I	3.61758E-41
8	230592_s_at	SAT1	I	1.24203E-40
7	203415_s_at	SAT1	I	5.08805E-38
6	241459_at	PTK2	I	1.11617E-33
5	236407_at	BRSK	I	6.05664E-29
5	208869_s_at	GABARAPL1	I	5.47596E-28
5	205591_at	ZFP36	I	8.72259E-27
6	224565_at	NEAT1	I	2.31929E-24
5	1554058_at	CHD2	I	2.39813E-24
5	200632_s_at	NDRG1	I	3.20882E-22
5	201473_at	JUNB	I	1.6873E-18
5	214782_at	CTTN	I	3.45364E-18
4	216583_x_at	KIAA0319	D	1.57396E-17
5	208053_s_at	FTSJ3	I	2.66072E-17
5	203740_s_at	TP53I3	I	5.51045E-16
4	235710_x_at	TUBGCP3	D	2.04490E-16
6	237740_s_at	STX16-NAPEPLD	D	2.34073E-16
5	232053_s_at	GLUL	I	3.96264E-15
5	210995_s_at	TNRC23	D	5.27971E-14
5	1556336_at	RBMX	D	1.39476E-13
6	218181_at	C20orf27	D	2.80771E-13
5	235105_at	C5orf51	I	2.64770E-13
6	231868_at	HOMER2	D	1.58161E-12
8	230333_at	SAT1	I	6.03294E-12
6	233147_s_at	SLC5A3	D	1.05848E-11
6	203312_s_at	EIF4H	D	5.1058E-11
5	233198_s_at	JMJD1C	D	5.45337E-11
5	209395_s_at	TNRC23	D	6.11714E-11
4	214540_at	HIST1H2BO	I	4.77048E-10
6	228568_at	GCCR	I	2.31774E-09
5	227824_at	PRKCB	D	3.14753E-09
5	207968_s_at	MEF2C	D	3.46949E-09
6	1553604_a_at	PIK3C2A	D	3.7555E-09
5	238174_s_at	TMEM254	D	1.34544E-08
6	210360_at	PAFAH1B2	D	3.65722E-08
5	230123_s_at	BRCC3	D	5.79283E-08
6	242774_at	SYNE2	D	6.83284E-08
7	204041_at	MAOB	I	8.10651E-08
6	205568_s_at	ARHGAP26	I	9.90784E-08
5	233478_s_at	EPP4	D	3.43143E-07
6	224987_at	AKT3	D	1.07445E-07
5	209164_s_at	PLEKHB1	D	6.67041-07
5	212097_at	CAP1	I	7.15107E-07
5	202243_s_at	PSMB4	D	9.57583E-07
6	213027_s_at	IKBKB	D	1.24371E-06
5	238556_s_at	UHRF1	I	1.26791E-06
5	213059_at	MARCKS	I	1.50556E-06
4	213299_at	ZBTB7A	D	2.05377E-06
5	208964_s_at	FADS1	I	2.08253E-06
6	207464_at	AHCY1	D	2.22156E-06
5	240486_at	HEL2	I	3.55863E-06
5	212953_x_at	CALR	I	6.19859E-06
5	203479_at	TPBG	I	6.66266E-06
6	234133_s_at	LOC728543	D	1.96881E-05
5	208743_s_at	TXLNB	I	2.61604E-05
5	205401_s_at	ADRBK1	D	2.31931E-05
6	50134_f_at	C20orf27	D	2.46608E-05
4	221353_x_at	ST8SIA1/NAC4	D	3.22273E-05
5	202556_s_at	MCRS1	D	3.28639E-05
6	210544_s_at	ALDH3A2	D	3.73211E-05
5	206463_s_at	MTSS1	I	3.83365E-05
7	231494_s_at	SLC4A4	I	5.84595E-05
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4	236607_at	LOC100996385	D	7.59788E-05
6	1560354_a_at	HPCAL1	I	7.49675E-05
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5	227510_s_at	DLL3	D	0.000103714
4	218818_s_at	SHISA2	D	0.000168122
5	214415_x_at	SFRP1	D	0.000314415
6	206501_at	GPR51	D	0.000328016
5	212859_x_at	MTIE	I	0.000203429
4	220504_at	KERA	I	0.000207242
5	209916_s_at	CAMK2B	I	0.000244828
5	222175_at	PTEN	I	0.000282212
6	205461_at	RAB35	D	0.000344242
6	207005_s_at	SCL2	D	0.000349208
6	216821_x_at	SCS3	D	0.000414315
5	232547_at	COL9A2	D	0.000442809
5	201810_s_at	MARCKS	I	0.000477549
5	211515_s_at	CGFR	D	0.000523824
6	201128_s_at	EIF5A	D	0.000607568
5	1560454_x_at	CIT	I	0.000643841
5	212324_s_at	TMEM259	D	0.000784897
5	216153_x_at	RECK	I	0.000923456
5	201270_s_at	DAB2	I	0.000983715
5	230068_at	VPRBP3	D	0.001047846
5	230493_at	SHISA2	I	0.001067067
5	209550_at	ZHX1	I	0.001379576
5	212185_s_at	MT2A	I	0.001274667
4	236411_at	LOC100129917	D	0.001523848
5	212573_at	TMEM259	D	0.001899289
5	1569908_at	VIMP1	I	0.001908804
6	1566402_at	SNORA68	I	0.003101478
5	230437_s_at	PRKCB	D	0.003121329
4	224165_s_at	ICK	D	0.003143579
5	213986_s_at	TMEM259	D	0.004519852
6	211370_s_at	MAP2K5	D	0.004122908
6	200124_s_at	TRAK2	D	0.004198846
9	215686_at	SKA2	D	0.006109516
5	215840_at	ZNRF2	D	0.006269353
4	1556904_x_at	TMEM158	D	0.007183487
5	210157_s_at	CUL4B	D	0.007757802
4	243717_at	EPHA10	D	0.008005828
5	212789_at	DNMBP	I	0.008561889
6	220227_at	CDH4	I	0.009081166
5	209170_s_at	GPM6B	I	0.01138789
5	229898_at	NUCB2	I	0.011982128
6	215781_at	MAPK9	I	0.011666659
6	202342_s_at	AIMP1	D	0.013877125
6	205204_at	RNF8	D	0.014853689
5	1558302_at	SYNE2	D	0.018343018
5	218763_s_at	RBMX	D	0.021981111
6	212762_s_at	TCF7L2	I	0.023002816
6	211905_s_at	ITGB4	D	0.029039313
4	221851_at	DCAF15	D	0.030222318
5	206067_at	IL1R	I	0.031568686
5	241074_at	ISM1	I	0.034179763
6	231085_s_at	PCBD2	D	0.035452736
6	1564211_at	EMID1	I	0.039422673
5	200076_s_at	GUK1	D	0.039241582
5	202059_at	CTTN	I	0.046115355
3	39402_at	IL1R	I	0.049299403

Figure S2. SASS and snapshot of apps screen display.

Simplified Affective State Scale (SASS)
For each item, mark the scale with a vertical line where you think you are at this moment in time, compared to lowest and highest you ever remember being:

Mood Subscale

1) Mood

How good is your mood right now?

[----------]
Lowest Highest

2) Motivation to do things

How is your motivation, your drive, your determination to do things right now?

[----------]
Lowest Highest

3) Movement activity

How high is your physical energy and the amount of moving about that you feel like doing right now?

[----------]
Lowest Highest

4) Thinking activity

How high is your mental energy and thinking activity going on in your mind right now?

[----------]
Lowest Highest

5) Self-esteem

How good do you feel about yourself and your accomplishments right now?

[----------]
Lowest Highest

6) Interest in pleasurable activities

How high is your interest to do things that are fun and enjoyable right now?

[----------]
Lowest Highest

7) Appetite

How high is your appetite and desire for food right now?

[----------]
Lowest Highest

Anxiety Subscale

1) Anxiety

How anxious are you right now?

[----------]
Lowest Highest

2) Uncertainty

How uncertain about things do you feel right now?

[----------]
Lowest Highest

3) Fear

How frightened about things do you feel right now?

[----------]
Lowest Highest

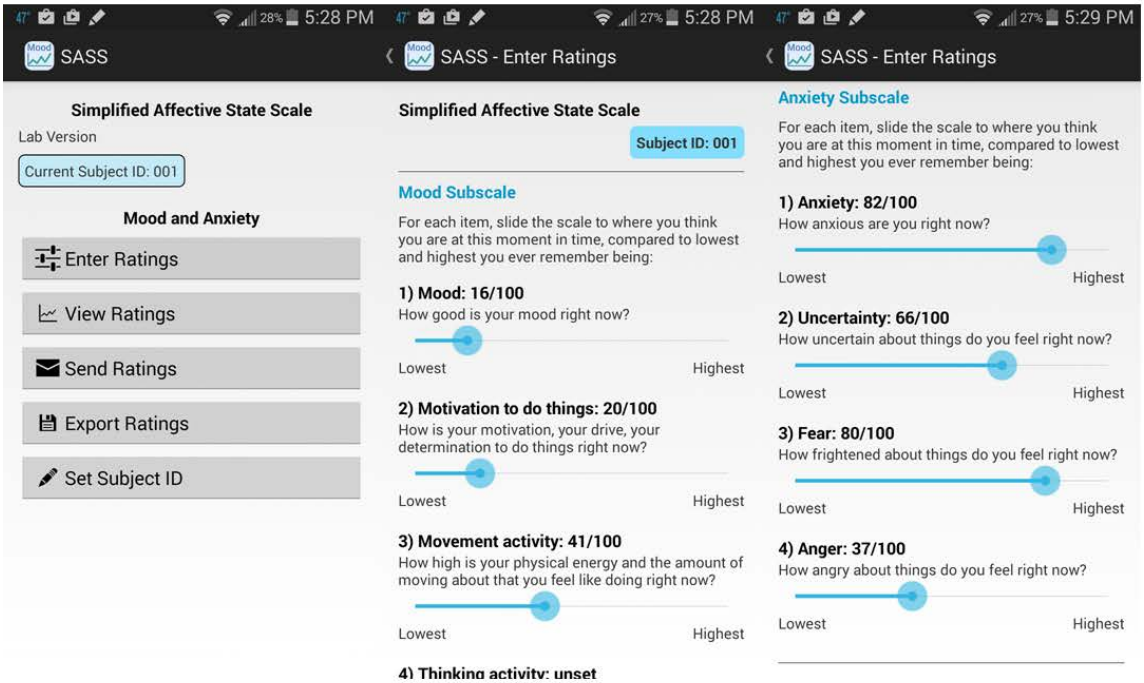
4) Anger

How angry about things do you feel right now?

[----------]
Lowest Highest

Comments (optional):
Describe events or actions that you think are influencing how you feel now. Describe any additional feelings you might have at this moment in time:

SASS App



CFI-S App

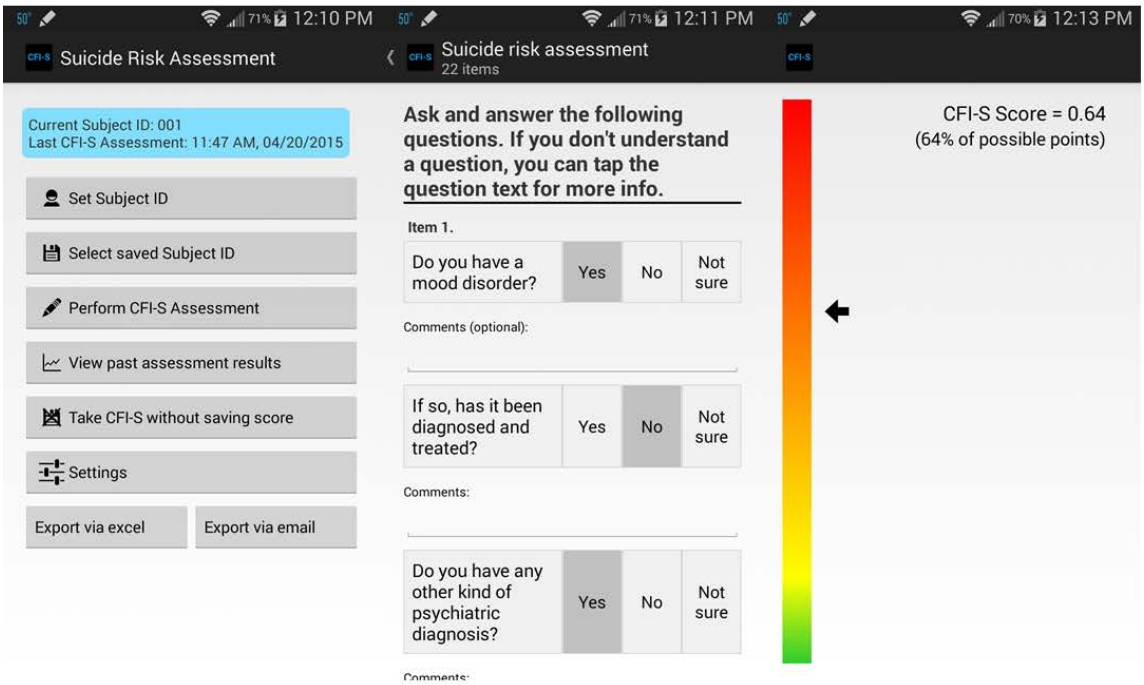


Figure S3. mTOR signaling. The top KEGG pathway in our 76 Bonferroni corrected validated markers for suicide. Boxed in black are our suicide biomarkers present in this pathway.

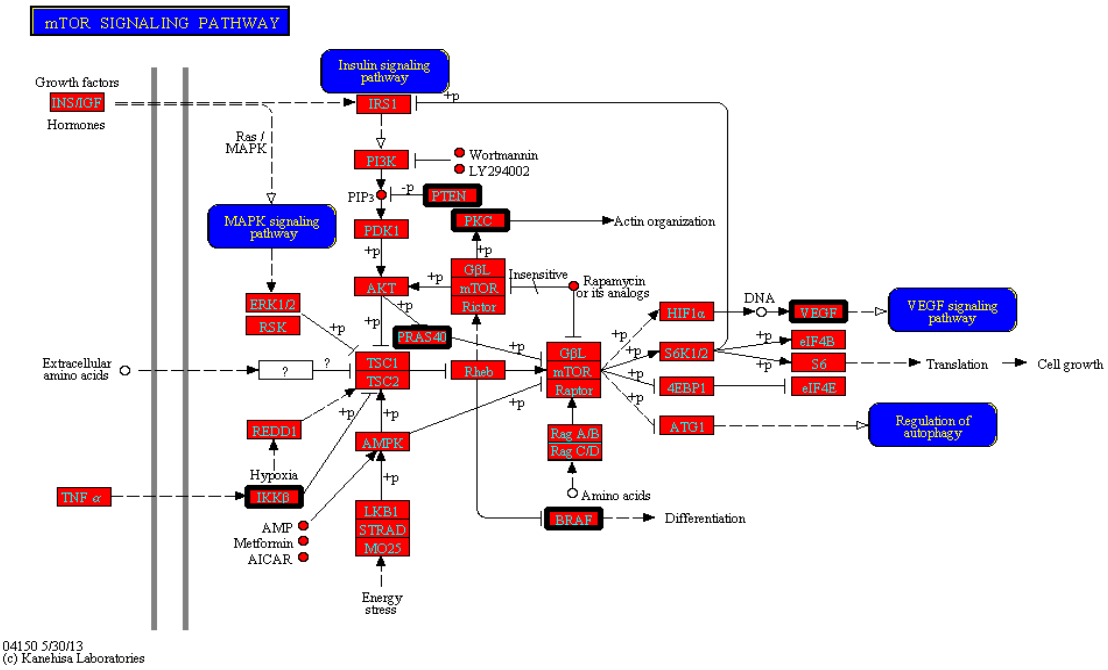


Figure S4. Reproducibility and diagnosis differences in levels of biomarkers.

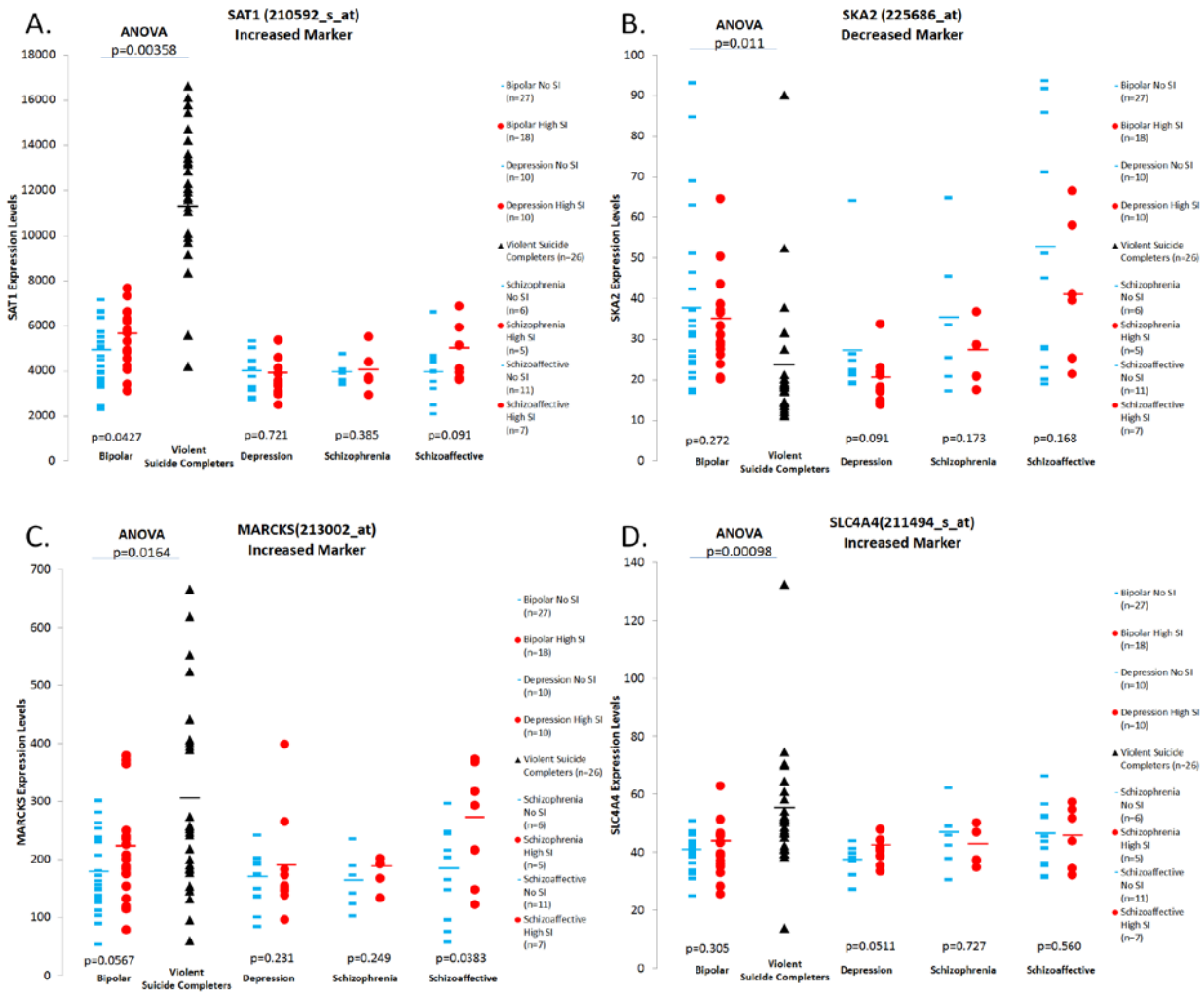


Table S1. Detailed Demographics

Cohort 1: Discovery Cohort (n=37) (106 visits)					
Subject ID visit	Diagnosis	Age	Gender	Ethnicity	HAMD SI
phchp016v1	SZ	54	M	African American	2
phchp016v2	SZ	54	M	African American	0
phchp016v3	SZ	54	M	African American	0
phchp023v1	BP	52	M	Caucasian	0
phchp023v2	BP	52	M	Caucasian	3
phchp023v3	BP	52	M	Caucasian	0
phchp042v1	SZA	43	M	Caucasian	3
phchp042v2	SZA	43	M	Caucasian	0
phchp042v3	SZA	44	M	Caucasian	0
phchp047v1	SZA	57	M	African American	2
phchp047v2	SZA	57	M	African American	0
phchp047v3	SZA	58	M	African American	0
phchp072v1	SZA	60	M	Caucasian	0
phchp072v2	SZA	60	M	Caucasian	0
phchp072v3	SZA	60	M	Caucasian	2
phchp088v2	BP	45	M	Caucasian	0
phchp088v3	BP	45	M	Caucasian	0
phchp088v4	BP	49	M	Caucasian	3
phchp088v5	BP	50	M	Caucasian	4
phchp089v1	SZA	33	M	Caucasian	0
phchp089v2	SZA	33	M	Caucasian	0
phchp089v4	SZA	38	M	Caucasian	3
phchp093v1	BP	51	M	Caucasian	0
phchp093v2	BP	51	M	Caucasian	0
phchp093v3	BP	52	M	Caucasian	3
phchp095v1	BP	28	M	Caucasian	3
phchp095v2	BP	29	M	Caucasian	0
phchp095v3	BP	29	M	Caucasian	2
phchp109v1	BP	22	M	Caucasian	0
phchp109v2	BP	25	M	Caucasian	3
phchp122v1	BP	51	M	Caucasian	0
phchp122v2	BP	51	M	Caucasian	2
phchp128v1	BP	45	M	Caucasian	2
phchp128v2	BP	45	M	Caucasian	0
phchp136v1	BP	41	M	Caucasian	0
phchp136v2	BP	41	M	Caucasian	0
phchp136v3	BP	41	M	Caucasian	3
phchp140v2	BP	38	M	Caucasian	3

phchp140v3	BP	38	M	Caucasian	2
phchp140v4	BP	40	M	Caucasian	0
phchp142v1	BP	55	M	Caucasian	0
phchp142v2	BP	55	M	Caucasian	0
phchp142v3	BP	55	M	Caucasian	0
phchp142v4	BP	57	M	Caucasian	2
phchp142v5	BP	57	M	Caucasian	0
phchp142v6	BP	58	M	Caucasian	0
phchp150v1	SZA	61	M	Caucasian	2
phchp150v2	SZA	61	M	Caucasian	0
phchp150v3	SZA	62	M	Caucasian	0
phchp153v1	BP	55	M	Caucasian	0
phchp153v2	BP	55	M	Caucasian	2
phchp153v3	BP	56	M	Caucasian	0
phchp153v4	BP	57	M	Caucasian	0
phchp153v6	BP	58	M	Caucasian	0
phchp155v1	MDD	37	M	Caucasian	3
phchp155v2	MDD	37	M	Caucasian	0
phchp161v1	MDD	54	M	African American	3
phchp161v2	MDD	54	M	African American	0
phchp161v3	MDD	54	M	African American	0
phchp179v1	BP	36	M	Caucasian	0
phchp179v2	BP	37	M	Caucasian	0
phchp179v4	BP	37	M	Caucasian	3
phchp182v1	MDD	39	M	Caucasian	2
phchp182v2	MDD	39	M	Caucasian	0
phchp182v3	MDD	40	M	Caucasian	3
phchp183v1	BP	48	M	Caucasian	3
phchp183v2	BP	48	M	Caucasian	0
phchp194v1	MDD	47	M	Caucasian	2
phchp194v2	MDD	47	M	Caucasian	0
phchp194v3	MDD	47	M	Caucasian	0
phchp198v1	MDD	61	M	Caucasian	4
phchp198v2	MDD	61	M	Caucasian	0
phchp198v4	MDD	62	M	Caucasian	0
phchp236v1	MDD	51	M	Caucasian	0
phchp236v2	MDD	51	M	Caucasian	3
phchp243v1	PTSD	50	M	African American	3
phchp243v2	PTSD	50	M	African American	0
phchp243v3	PTSD	52	M	African American	0
phchp248v1	SZ	52	M	African American	0
phchp248v2	SZ	52	M	African American	3
phchp248v3	SZ	53	M	African American	2

phchp266v1	MoodNOS	41	M	Caucasian	3
phchp266v2	MoodNOS	42	M	Caucasian	0
phchp266v3	MoodNOS	42	M	Caucasian	0
phchp277v1	SZ	49	M	Caucasian	0
phchp277v2	SZ	50	M	Caucasian	3
phchp277v3	SZ	50	M	Caucasian	0
phchp293v1	BP	43	M	Caucasian	0
phchp293v2	BP	44	M	Caucasian	2
phchp296v1	BP	48	M	Caucasian	0
phchp296v2	BP	49	M	Caucasian	2
phchp300v1	SZA	47	M	Caucasian	2
phchp300v2	SZA	47	M	Caucasian	0
phchp300v3	SZA	48	M	Caucasian	2
phchp304v1	MDD	52	M	Caucasian	2
phchp304v2	MDD	52	M	Caucasian	0
phchp304v3	MDD	52	M	Caucasian	2
phchp308v1	SZ	47	M	African American	3
phchp308v2	SZ	47	M	African American	0
phchp310v1	Mood NOS	54	M	African American	2
phchp310v2	Mood NOS	54	M	African American	0
phchp310v3	Mood NOS	54	M	African American	2
phchp319v1	PTSD	42	M	African American	0
phchp319v2	MDD	42	M	African American	4
phchp325v1	PTSD	44	M	Caucasian	3
phchp325v2	PTSD	44	M	Caucasian	0

Cohort 2: Coroner's Office Validation Cohort -gene expression data (n=26) and CFI-S data (n=35)

SubjectID-Visit	Dx	Age	Gender	Ethnicity	Method	CFI-S Score	Gene Expression
INBRAIN09	Bipolar/Schizophrenia	59	M	Caucasian	Hanging	0.5	Y
INBRAIN011	Depression/ADHD	26	M	Caucasian	GSW to chest	0.55	Y
INBRAIN012	Unknown	39	M	Caucasian	GSW - Head	0.5	Y
INBRAIN013	Depression	68	M	African American	GSW - Head	0.4	Y
INBRAIN014	None	27	M	Caucasian	Hanging	0.2	Y
INBRAIN015	None	40	M	Caucasian	Hanging	0.272	Y
INBRAIN016	Anxiety/TBI	68	M	Caucasian	GSW- head	0.684	Y
INBRAIN017	Depression	56	M	Caucasian	GSW to chest	0.7	Y
INBRAIN018	None	65	M	Caucasian	deep cut to wrist	0.786	Y
INBRAIN019	Depression	55	M	Caucasian	GSW to head & chest	0.45	Y
INBRAIN021		23	M	African	Hanging	0.375	Y

				American			
INBRAIN022	Bipolar depression	38	M	Hispanic	GSW - Head	0.55	Y
INBRAIN023		18	M	Caucasian	Hanging	0.35	Y
INBRAIN024		23	M	Caucasian	Hanging	0.45	Y
INBRAIN025		31	M	African American	GSW - Head	0.4	Y
INBRAIN028	Alcoholism	67	M	Caucasian	GSW to chest	0.5	Y
INBRAIN030		22	M	African American	GSW- head	0.55	Y
INBRAIN033	Depression	26	M	Caucasian	GSW to chest	0.4	Y
INBRAIN035	Depression	58	M	Caucasian	Electrocution	0.5	Y
INBRAIN036		59	M	Caucasian	GSW to chest	0.444	Y
INBRAIN039		53	M	Caucasian	Hanging	0.6	Y
INBRAIN040		36	M	Caucasian	GSW- head	0.5	Y
INBRAIN044		23	M	Caucasian	Hanging	0.7	Y
INBRAIN048	Psychosis	26	M	Caucasian	GSW- head	0.762	Y
INBRAIN055	Depression	18	M	Caucasian	GSW - Head		Y
INBRAIN056	Depression	37	M	Caucasian	Hanging		Y
INBRAIN07	Depression/anxiety	57	M	Caucasian	CO Poisoning	0.615	N
INBRAIN08	Bipolar, untreated	31	M	Caucasian	Drug overdose	0.556	N
INBRAIN031		56	M	Caucasian	Drug overdose	0.563	N
INBRAIN037	Depression	24	M	Asian	Jump	0.368	N
INBRAIN041	Depression	76	M	Caucasian	GSW - Head	0.75	N
INBRAIN042		25	M	Caucasian	GSW - Head	0.545	N
INBRAIN043	None	28	M	Caucasian	GSW - Head	0.65	N
INBRAIN045		20	M	Caucasian	GSW - Head	0.6	N
INBRAIN046	Depression	65	M	Caucasian	GSW - Chest	0.667	N
INBRAIN047	Depression	57	M	Caucasian	GSW - Head	0.5	N
INBRAIN049	Depression, untreated	41	M	Caucasian	GSW - Head	0.55	N

Coroner's Office Validation Cohort -Toxicology

Subject ID	Toxicology
INBRAIN09	NA
INBRAIN011	ALPRAZOLAM 3.2 NG/ML TRAMADOL 331 NG/ML NORTRAMADOL 179 NG/ML BUPROPION 136 NG/ML CITALOPRAM/ESCITALOPRAM 229 NG/ML CAFFEINE COTININE
INBRAIN012	NEGATIVE
INBRAIN013	CAFFEINE
INBRAIN014	ETHANOL 0.15 % (W/V) CAFFEINE
INBRAIN015	ETHANOL 0.119 % (W/V) CAFFEINE
INBRAIN016	DIAZEPAM 155 NORDIAZEPAM 61.9 ALPRAZOLAM 6.8 ATENOLOL WARFARIN CAFFEINE
INBRAIN017	CLONAZEPAM 6 6 7-AMINOCLONAZEPAM 73.7 Glucose positive urine THC 2.0 THC-COOH 10.5 ETHANOL 0.130 FLUOXETINE 636 NORFLUOXETINE 359 VENLAFAXINE 1641 NORVENLAFAXINE 136 CAFFEINE
INBRAIN018	ETHANOL 0.057 %(W/V) AMIODARONE CAFFEINE COTININE
INBRAIN019	ALPRAZOLAM 169 CAFFEINE

INBRAIN021	THC 8.9 THC 60.2 ISOPROPANOL 0.042
INBRAIN022	ETHANOL 0.185 CAFFEINE
INBRAIN023	CAFFEINE POSITIVE
INBRAIN024	CAFFEINE POSITIVE
INBRAIN025	THC 1.2 THC-COOH 12.0 CAFFEINE
INBRAIN028	ETHANOL 0.354 ANTIHISTAMINES DIPHENHYRAMINE 178 AMLODIPINE 19.9 CAFFEINE
INBRAIN030	CAFFEINE POSITIVE
INBRAIN033	ETHANOL 0.128 CITALOPRAM 294 CAFFEINE
INBRAIN035	VENLAFAXINE 231 NORVENLAXFAXINE 452 AMLODIPINE 45.3 CAFFEINE
INBRAIN036	NEGATIVE
INBRAIN039	ETHANOL 0.158 CAFFEINE
INBRAIN040	IBUPROFEN 8.2 CAFFEINE
INBRAIN044	THC 10.3 THC-COOH 143
INBRAIN048	CARBOXY THC 78 ng/ml CAFFEINE
INBRAIN055	THC-COOH 4.3 ng/ml CARBOXY THC 69 ng/ml
INBRAIN056	NEGATIVE

Cohort 3: Test Cohort for Suicidal Ideation (n=108) (223 visits)

Subject ID visit	Diagnosis	Age	Gender	Ethnicity	SI
phchp003v1	SZ	50	M	African American	0
phchp005v1	SZA	45	M	Caucasian	0
phchp005v2	SZA	45	M	Caucasian	0
phchp005v3	SZA	45	M	Caucasian	0
phchp006v1	SZA	52	M	African American	0
phchp006v2	SZA	52	M	African American	0
phchp008v1	SZ	47	M	African American	0
phchp010v1	SZA	45	M	Caucasian	0
phchp010v2	SZA	45	M	Caucasian	0
phchp010v3	SZA	45	M	Caucasian	0
phchp013v1	SZA	53	M	African American	0
phchp013v3	SZA	54	M	African American	0
phchp015v1	SZ	48	M	African American	0
phchp015v2	SZ	49	M	African American	0
phchp017v2	SZA	53	M	African American	0
phchp017v3	SZA	54	M	African American	0
phchp019v1	SZ	50	M	African American	0
phchp019v2	SZ	51	M	African American	0
phchp019v3	SZ	51	M	African American	0
phchp021v1	SZA	48	M	Hispanic	0
phchp021v2	SZA	49	M	Hispanic	0
phchp021v3	SZA	49	M	Hispanic	0
phchp022v1	SZ	48	M	Caucasian	0
phchp022v2	SZ	48	M	Caucasian	0
phchp024v1	SZA	49	M	African American	0
phchp025v1	SZ	42	M	Caucasian	0
phchp026v1	SZA	49	M	African American	1
phchp026v2	SZA	49	M	African American	0
phchp026v3	SZA	49	M	African American	0
phchp027v1	SZA	40	M	Caucasian	0
phchp029v1	MDD	56	M	Caucasian	3
phchp030v1	BP	49	M	Caucasian	0
phchp030v3	BP	49	M	Caucasian	0
phchp031v1	BP	51	M	Caucasian	0
phchp031v2	BP	51	M	Caucasian	0
phchp031v3	BP	52	M	Caucasian	0
phchp033v1	SZA	48	M	Caucasian	3
phchp039v1	BP	52	M	Caucasian	0

phchp039v3	BP	52	M	Caucasian	0
phchp040v1	SZA	50	M	Caucasian	0
phchp040v2	SZA	50	M	Caucasian	0
phchp040v3	SZA	50	M	Caucasian	0
phchp045v1	BP	36	M	Caucasian	1
phchp045v3	BP	36	M	Caucasian	0
phchp046v1	SZA	45	M	Caucasian	0
phchp046v2	SZA	45	M	Caucasian	0
phchp046v3	SZA	45	M	Caucasian	0
phchp049v1	SZA	46	M	Caucasian	2
phchp049v2	SZA	47	M	Caucasian	1
phchp051v1	SZA	52	M	Caucasian	0
phchp052v1	SZ	60	M	Caucasian	2
phchp052v2	SZ	60	M	Caucasian	2
phchp052v3	SZ	60	M	Caucasian	2
phchp056v1	BP	36	M	Caucasian	0
phchp057v1	SZA	47	M	Caucasian	0
phchp061v1	SZ	49	M	Caucasian	0
phchp061v2	SZ	49	M	Caucasian	1
phchp061v3	SZ	50	M	Caucasian	1
phchp067v1	BP	39	M	Caucasian	0
phchp067v3	BP	40	M	Caucasian	1
phchp069v1	SZ	47	M	Caucasian	0
phchp069v2	SZ	47	M	Caucasian	0
phchp069v3	SZ	48	M	Caucasian	0
phchp070v1	SZ	52	M	African American	0
phchp070v2	SZ	52	M	African American	0
phchp070v3	SZ	52	M	African American	0
phchp073v1	SZA	50	M	Caucasian	0
phchp073v2	SZA	50	M	Caucasian	1
phchp073v3	SZA	50	M	Caucasian	0
phchp079v1	BP	44	M	Caucasian	1
phchp079v2	BP	44	M	Caucasian	0
phchp079v3	BP	45	M	Caucasian	0
phchp079v4	BP	49	M	Caucasian	0
phchp079v5	BP	50	M	Caucasian	0
phchp079v6	BP	50	M	Caucasian	0
phchp080v1	BP	44	M	Caucasian	0
phchp081v1	SZA	53	M	African American	3
phchp081v3	SZA	53	M	African American	3
phchp083v1	SZ	50	M	African American	0
phchp083v2	SZ	50	M	African American	0
phchp083v3	SZ	51	M	African American	0

phchp086v1	SZ	49	M	Caucasian	0
phchp086v2	SZ	49	M	Caucasian	0
phchp086v3	SZ	49	M	Caucasian	0
phchp092v1	BP	45	M	African American	0
phchp092v2	BP	46	M	African American	0
phchp092v3	BP	46	M	African American	0
phchp094v1	BP	41	M	African American	0
phchp099v1	SZ	49	M	Caucasian	1
phchp099v2	SZ	49	M	Caucasian	1
phchp099v3	SZ	49	M	Caucasian	0
phchp100v1	BP	28	M	Caucasian	0
phchp101v1	SZA	74	M	Caucasian	3
phchp102v1	SZA	56	M	Caucasian	2
phchp102v2	SZA	56	M	Caucasian	1
phchp102v3	SZA	56	M	Caucasian	2
phchp103v1	SZA	61	M	Caucasian	1
phchp108v1	SZ	42	M	Caucasian	0
phchp108v2	SZ	42	M	Caucasian	0
phchp108v3	SZ	43	M	Caucasian	0
phchp112v1	BP	46	M	Caucasian/Native Australian	0
phchp112v2	BP	46	M	Caucasian	0
phchp112v3	BP	47	M	Caucasian	0
phchp113v1	BP	37	M	Caucasian	1
phchp114v1	SZA	54	M	African American	0
phchp116v1	SZA	47	M	Caucasian	2
phchp117v1	BP	43	M	Caucasian	0
phchp117v2	BP	43	M	Caucasian	0
phchp117v3	BP	43	M	Caucasian	0
phchp118v1	SZA	46	M	African American	0
phchp118v2	SZA	47	M	African American	0
phchp118v4	SZA	50	M	African American	0
phchp120v1	SZ	51	M	Caucasian	0
phchp120v2	SZ	51	M	Caucasian	0
phchp120v3	SZ	51	M	Caucasian	0
phchp124v1	BP	53	M	Caucasian	0
phchp132v1	BP	51	M	Caucasian	0
phchp132v2	BP	51	M	Caucasian	0
phchp132v3	BP	52	M	Caucasian	0
phchp139v1	SZ	24	M	Caucasian	0
phchp147v1	BP	38	M	Caucasian	0
phchp147v2	BP	38	M	Caucasian	0
phchp147v3	BP	38	M	Caucasian	0
phchp148v1	SZ	25	M	Caucasian	0

phchp149v1	BP	45	M	Caucasian	0
phchp149v2	BP	45	M	Caucasian	0
phchp149v3	BP	46	M	Caucasian	0
phchp151v1	SZ	24	M	Caucasian	4
phchp151v2	SZ	24	M	Caucasian	2
phchp151v3	SZ	24	M	Caucasian	1
phchp152v1	BP	45	M	Caucasian	2
phchp154v1	SZA	51	M	African American	0
phchp154v2	SZA	51	M	African American	0
phchp154v3	SZA	52	M	African American	0
phchp158v1	BP	23	M	African American	4
phchp162v1	MDD	57	M	Caucasian	3
phchp162v2	MDD	57	M	Caucasian	2
phchp162v3	MDD	57	M	Caucasian	2
phchp167v1	MDD	49	M	Caucasian	0
phchp168v1	MDD	48	M	African American	0
phchp168v2	MDD	48	M	African American	0
phchp168v3	MDD	49	M	African American	0
phchp169v1	SZA	50	M	African American	0
phchp171v1	BP	36	M	Caucasian	0
phchp171v2	BP	36	M	Caucasian	0
phchp173v1	MDD	48	M	Caucasian	0
phchp173v2	MDD	49	M	Caucasian	0
phchp173v3	MDD	49	M	Caucasian	0
phchp174v1	MDD	54	M	Caucasian	3
phchp175v1	SZA	42	M	Caucasian	0
phchp176v1	SZ	23	M	African American	0
phchp176v2	SZ	24	M	African American	0
phchp178v1	BP	49	M	Caucasian	0
phchp185v1	SZA	51	M	African American	0
phchp185v2	SZA	51	M	African American	0
phchp185v3	SZA	52	M	African American	0
phchp186v1	BP	43	M	Caucasian	0
phchp186v2	BP	44	M	Caucasian	0
phchp186v3	BP	44	M	Caucasian	0
phchp186v4	BP	46	M	Caucasian	0
phchp187v1	SZ	49	M	African American	0
phchp187v2	SZ	49	M	African American	0
phchp188v1	SZ	54	M	African American	0
phchp189v1	SZ	25	M	Caucasian	1
phchp190v1	BP	49	M	Caucasian	1
phchp190v2	BP	49	M	Caucasian	0
phchp195v1	SZ	52	M	Caucasian	0

phchp195v2	SZ	53	M	Caucasian	0
phchp195v3	SZ	53	M	Caucasian	0
phchp196v1	MDD	56	M	African American	0
phchp196v2	MDD	56	M	African American	0
phchp196v3	MDD	57	M	African American	0
phchp199v1	SZ	49	M	African American	0
phchp199v2	SZ	49	M	African American	0
phchp199v3	SZ	50	M	African American	0
phchp200v1	MDD	56	M	Caucasian	0
phchp200v2	MDD	57	M	Caucasian	0
phchp200v3	MDD	57	M	Caucasian	0
phchp206v1	MDD	59	M	African American	0
phchp207v1	SZ	48	M	African American	1
phchp208v1	MDD	56	M	African American	0
phchp208v2	MDD	56	M	African American	0
phchp208v3	MDD	58	M	African American	0
phchp212v1	MDD	56	M	African American	0
phchp212v2	MDD	56	M	African American	0
phchp221v1	MDD	51	M	African American	0
phchp221v2	MDD	51	M	African American	0
phchp221v3	MDD	52	M	African American	0
phchp224v1	BP	59	M	Caucasian	4
phchp226v1	MDD	29	M	Caucasian	0
phchp226v2	MDD	29	M	Caucasian	0
phchp226v3	MDD	30	M	Caucasian	0
phchp227v1	MDD	55	M	Caucasian	0
phchp227v2	MDD	55	M	Caucasian	0
phchp227v3	MDD	55	M	Caucasian	0
phchp231v1	MDD	55	M	Caucasian	2
phchp234v1	BP	44	M	Caucasian	2
phchp234v2	BP	45	M	Caucasian	2
phchp234v3	BP	45	M	Caucasian	1
phchp235v1	MDD	54	M	African American	0
phchp235v2	MDD	55	M	African American	0
phchp235v3	MDD	55	M	African American	0
phchp238v1	MDD	62	M	Caucasian	0
phchp242v1	MDD	55	M	African American	0
phchp242v2	MDD	57	M	African American	0
phchp247v1	MDD	55	M	African American	0
phchp259v1	MDD	56	M	Caucasian	0
phchp259v2	MDD	57	M	Caucasian	0
phchp259v3	MDD	57	M	Caucasian	0
phchp273v1	BP	27	M	Caucasian	3

phchp273v2	BP	28	M	Caucasian	2
phchp274v1	BP	48	M	Caucasian	3
phchp274v2	BP	48	M	Caucasian	3
phchp274v3	BP	48	M	Caucasian	1
phchp283v1	SZ	51	M	Caucasian	0
phchp295v1	SZ	52	M	African American	0
phchp297v1	SZA	54	M	African American	0
phchp315v1	MDD	62	M	Caucasian	0
phchp322v1	BP	26	M	Caucasian	4
phchp324v1	MDD	33	M	African American	4
phchp327v1	MDD	42	M	Caucasian	3
phchp333v1	MDD	38	M	Caucasian	4
phchp335v1	MDD	25	M	Caucasian	3

Cohort 4: Testing cohort for future hospitalizations for suicidality (n=157) (373 chips)

(SI- Suicidal Ideation, SA- Suicide Attempts)

Subject ID visit	Diagnosis	Age	Gender	Ethnicity	Years Followed	Number Of First Year Hospitalizations Due To Suicidality		Number Of All Future Hospitalizations Due To Suicidality		Hospitalizations Frequency Due To Suicidality	
						SI	SA	SI	SA	SI	SA
phchp003v1	SZ	50	M	African American	8.5	0	0	0	0	0	0
phchp003v2	SZ	50	M	African American	8	0	0	0	0	0	0
phchp003v3	SZ	50	M	African American	7.75	0	0	0	0	0	0
phchp004v1	SZA	55	M	African American	8.416667	0	0	0	0	0	0
phchp004v2	SZA	60	M	African American	2.083333	0	0	0	0	0	0
phchp004v4	SZA	60	M	African American	1.75	0	0	0	0	0	0
phchp005v1	SZA	45	M	Caucasian	8.083333	0	0	1	0	0.13	0
phchp005v2	SZA	45	M	Caucasian	7.75	0	0	1	0	0.13	0
phchp005v3	SZA	45	M	Caucasian	7.5	0	0	1	0	0.14	0
phchp006v1	SZA	52	M	African American	5.666667	0	0	0	0	0	0
phchp006v2	SZA	52	M	African American	5.5	0	0	0	0	0	0
phchp008v1	SZ	47	M	African American	5.25	1	0	1	0	0.2	0
phchp009v1	SZ	55	M	African American	6.5	0	0	0	0	0	0
phchp009v3	SZ	56	M	African American	6	0	0	0	0	0	0
phchp010v1	SZA	45	M	Caucasian	8	0	0	0	0	0	0
phchp010v2	SZA	45	M	Caucasian	7.75	0	0	0	0	0	0
phchp010	SZA	45	M	Caucasian	7.5	0	0	0	0	0	0

v3											
phchp012 v1	SZA	55	M	Caucasian	3.833333	0	0	1	0	0.27	0
phchp012 v2	SZA	55	M	Caucasian	3.583333	0	0	1	0	0.28	0
phchp012 v3	SZA	55	M	Caucasian	3.333333	0	0	1	0	0.3	0
phchp013 v1	SZA	53	M	African American	8	0	0	0	0	0	0
phchp013 v3	SZA	54	M	African American	7.5	0	0	0	0	0	0
phchp014 v1	SZA	55	M	African American	8.25	0	0	1	0	0.13	0
phchp015 v1	SZ	48	M	African American	8.25	0	0	1	1	0.13	0.13
phchp015 v2	SZ	49	M	African American	7.916667	0	0	1	1	0.13	0.13
phchp016 v1	SZ	54	M	African American	5.5	0	0	0	0	0	0
phchp016 v2	SZ	54	M	African American	5.25	0	0	0	0	0	0
phchp016 v3	SZ	54	M	African American	5	0	0	0	0	0	0
phchp017 v2	SZA	53	M	African American	1.5	0	0	0	0	0	0
phchp017 v3	SZA	54	M	African American	1	0	0	0	0	0	0
phchp019 v1	SZ	50	M	African American	7.666667	0	0	1	0	0.14	0
phchp019 v2	SZ	51	M	African American	7.333333	0	0	1	0	0.14	0
phchp019 v3	SZ	51	M	African American	6.916667	0	0	1	0	0.15	0
phchp020 v1	BP	62	M	Caucasian	7.083333	0	0	0	0	0	0
phchp020 v2	BP	62	M	Caucasian	6.833333	0	0	0	0	0	0
phchp020	BP	63	M	Caucasian	6.5	0	0	0	0	0	0

v3								
phchp021 v1	SZA	48	M	Hispanic	7.083333	0 0	2 1	0.29 0.15
phchp021 v2	SZA	49	M	Hispanic	6.833333	0 0	2 1	0.3 0.15
phchp021 v3	SZA	49	M	Hispanic	6.5	0 0	2 1	0.31 0.16
phchp022 v1	SZ	48	M	Caucasian	7.583333	0 0	0 0	0 0
phchp022 v2	SZ	48	M	Caucasian	7.333333	0 0	0 0	0 0
phchp024 v1	SZA	49	M	African American	7.75	1 0	2 0	0.26 0
phchp025 v1	SZ	42	M	Caucasian	7.75	0 0	0 0	0 0
phchp026 v1	SZA	49	M	African American	2.916667	0 0	0 0	0 0
phchp026 v2	SZA	49	M	African American	2.666667	0 0	0 0	0 0
phchp026 v3	SZA	49	M	African American	2.333333	0 0	0 0	0 0
phchp027 v1	SZA	40	M	Caucasian	7.5	0 0	3 0	0.4 0
phchp030 v1	BP	49	M	Caucasian	6.916667	1 0	4 0	0.58 0
phchp030 v3	BP	49	M	Caucasian	6.25	0 0	3 0	0.48 0
phchp031 v1	BP	51	M	Caucasian	4.666667	0 0	0 0	0 0
phchp031 v2	BP	51	M	Caucasian	4.333333	0 0	0 0	0 0
phchp031 v3	BP	52	M	Caucasian	4.083333	0 0	0 0	0 0
phchp033 v1	SZA	48	M	Caucasian	2.5	0 0	1 0	0.4 0
phchp038 v1	SZA	58	M	African American	7.25	0 0	0 0	0 0
phchp038	SZA	58	M	African	7	0 0	0 0	0 0

v2				American					
phchp038 v3	SZA	59	M	African American	6.75	0	0	0 0	0 0
phchp039 v1	BP	52	M	Caucasian	6.75	0	0	0 0	0 0
phchp039 v3	BP	52	M	Caucasian	6.083333	0	0	0 0	0 0
phchp040 v1	SZA	50	M	Caucasian	5.833333	0	0	0 0	0 0
phchp040 v2	SZA	50	M	Caucasian	5.583333	0	0	0 0	0 0
phchp040 v3	SZA	50	M	Caucasian	5.333333	0	0	0 0	0 0
phchp041 v1	SZ	62	M	African American	7.333333	0	0	0 0	0 0
phchp042 v1	SZA	43	M	Caucasian	6	0	0	0 0	0 0
phchp042 v2	SZA	43	M	Caucasian	5.75	0	0	0 0	0 0
phchp042 v3	SZA	44	M	Caucasian	5.5	0	0	0 0	0 0
phchp045 v1	BP	36	M	Caucasian	7	0	0	0 0	0 0
phchp045 v3	BP	36	M	Caucasian	6.416667	0	0	0 0	0 0
phchp046 v1	SZA	45	M	Caucasian	7.083333	0	0	0 0	0 0
phchp046 v2	SZA	45	M	Caucasian	6.916667	0	0	0 0	0 0
phchp046 v3	SZA	45	M	Caucasian	6.666667	0	0	0 0	0 0
phchp047 v1	SZA	57	M	African American	6.333333	0	0	1 1	0.16 0.16
phchp047 v2	SZA	57	M	African American	6.083333	0	0	1 1	0.17 0.17
phchp047 v3	SZA	58	M	African American	5.833333	0	0	1 1	0.18 0.18
phchp048	SZA	56	M	African	5.25	0	0	0 0	0 0

v1				American				
phchp048 v2	SZA	57	M	African American	5.083333	0 0	0 0	0 0
phchp048 v3	SZA	57	M	African American	4.75	0 0	0 0	0 0
phchp049 v1	SZA	46	M	Caucasian	6.916667	0 0	0 0	0 0
phchp049 v2	SZA	47	M	Caucasian	6.666667	0 0	0 0	0 0
phchp051 v1	SZA	52	M	Caucasian	6.833333	0 0	0 0	0 0
phchp052 v1	SZ	60	M	Caucasian	1.166667	0 0	0 0	0 0
phchp053 v1	BP	58	M	Caucasian	6.333333	0 0	0 0	0 0
phchp053 v2	BP	58	M	Caucasian	6	0 0	0 0	0 0
phchp053 v3	BP	58	M	Caucasian	5.75	0 0	0 0	0 0
phchp057 v1	SZA	47	M	Caucasian	6.833333	0 0	0 0	0 0
phchp058 v1	SZ	56	M	African American	6.833333	0 0	0 0	0 0
phchp058 v2	SZ	56	M	African American	6.583333	0 0	0 0	0 0
phchp058 v3	SZ	56	M	African American	6.333333	0 0	0 0	0 0
phchp060 v1	SZ	62	M	Caucasian	3.5	0 0	0 0	0 0
phchp061 v1	SZ	49	M	Caucasian	7.083333	1 0	4 0	0.57 0
phchp061 v2	SZ	49	M	Caucasian	6.833333	1 0	4 0	0.59 0
phchp061 v3	SZ	50	M	Caucasian	6.166667	3 0	4 0	0.65 0
phchp062 v1	SZ	56	M	Caucasian	6.75	0 0	0 0	0 0
phchp062	SZ	56	M	Caucasian	6.5	0 0	0 0	0 0

v2								
phchp062 v3	SZ	57	M	Caucasian	6.25	0 0	0 0	0 0
phchp065 v1	SZA	62	M	Caucasian	6.583333	0 0	0 0	0 0
phchp065 v2	SZA	62	M	Caucasian	6.333333	0 0	0 0	0 0
phchp065 v3	SZA	62	M	Caucasian	6.083333	0 0	0 0	0 0
phchp067 v1	BP	39	M	Caucasian	5.916667	0 0	0 0	0 0
phchp067 v3	BP	40	M	Caucasian	5.333333	0 0	0 0	0 0
phchp068 v1	SZA	57	M	African American	6.666667	0 0	0 0	0 0
phchp068 v2	SZA	57	M	African American	6.333333	0 0	0 0	0 0
phchp068 v3	SZA	57	M	African American	6	0 0	0 0	0 0
phchp069 v1	SZ	47	M	Caucasian	6.583333	0 0	0 0	0 0
phchp069 v2	SZ	47	M	Caucasian	6.333333	0 0	0 0	0 0
phchp069 v3	SZ	48	M	Caucasian	6.083333	0 0	0 0	0 0
phchp070 v1	SZ	52	M	African American	6.583333	0 0	0 0	0 0
phchp070 v2	SZ	52	M	African American	6.25	0 0	0 0	0 0
phchp070 v3	SZ	52	M	African American	6	0 0	0 0	0 0
phchp070 v4	SZ	56	M	African American	2.083333	0 0	0 0	0 0
phchp070 v5	SZ	56	M	African American	1.833333	0 0	0 0	0 0
phchp070 v6	SZ	57	M	African American	1.583333	0 0	0 0	0 0
phchp072	SZA	60	M	Caucasian	6.5	0 0	1 0	0.16 0

v1												
phchp072 v2	SZA	60	M	Caucasian	6.25	0	0	1	0	0.16	0	
phchp072 v3	SZA	60	M	Caucasian	5.916667	0	0	1	0	0.17	0	
phchp073 v1	SZA	50	M	Caucasian	5.5	0	0	12	0	2.19	0	
phchp073 v2	SZA	50	M	Caucasian	5.166667	0	0	12	0	2.33	0	
phchp073 v3	SZA	50	M	Caucasian	4.916667	0	0	12	0	2.45	0	
phchp075 v1	SZA	57	M	Caucasian	6.166667	0	0	3	0	0.49	0	
phchp075 v2	SZA	58	M	Caucasian	5.916667	0	0	3	0	0.51	0	
phchp075 v3	SZA	58	M	Caucasian	5.666667	0	0	3	0	0.53	0	
phchp079 v1	BP	44	M	Caucasian	6.25	0	0	0	0	0	0	
phchp079 v2	BP	44	M	Caucasian	6	0	0	0	0	0	0	
phchp079 v3	BP	45	M	Caucasian	5.75	0	0	0	0	0	0	
phchp079 v4	BP	49	M	Caucasian	1.083333	0	0	0	0	0	0	
phchp080 v1	BP	44	M	Caucasian	5.416667	0	0	0	0	0	0	
phchp081 v1	SZA	53	M	African American	1.166667	0	0	0	0	0	0	
phchp083 v1	SZ	50	M	African American	6	0	0	0	0	0	0	
phchp083 v2	SZ	50	M	African American	5.75	0	0	0	0	0	0	
phchp083 v3	SZ	51	M	African American	5.5	0	0	0	0	0	0	
phchp085 v1	SZA	57	M	Caucasian	5.75	0	0	0	0	0	0	
phchp085	SZA	57	M	Caucasian	5.5	0	0	0	0	0	0	

v2								
phchp085 v3	SZA	57	M	Caucasian	5.25	0 0	0 0	0 0
phchp086 v1	SZ	49	M	Caucasian	5.666667	0 0	0 0	0 0
phchp086 v2	SZ	49	M	Caucasian	5.416667	0 0	0 0	0 0
phchp086 v3	SZ	49	M	Caucasian	5.083333	0 0	0 0	0 0
phchp087 v1	SZA	65	M	Caucasian	5.833333	0 0	0 0	0 0
phchp087 v2	SZA	66	M	Caucasian	5.5	0 0	0 0	0 0
phchp087 v3	SZA	66	M	Caucasian	5.25	0 0	0 0	0 0
phchp088 v1	BP	44	M	Caucasian	5.916667	3 0	17 1	2.88 0.17
phchp088 v2	BP	45	M	Caucasian	5.75	2 0	16 1	2.79 0.18
phchp088 v3	BP	45	M	Caucasian	5.333333	1 0	15 1	2.82 0.19
phchp088 v4	BP	49	M	Caucasian	1.333333	8 1	8 1	6.01 0.75
phchp089 v1	SZA	33	M	Caucasian	5.75	0 0	1 0	0.18 0
phchp089 v2	SZA	33	M	Caucasian	5.5	0 0	1 0	0.19 0
phchp091 v1	SZA	55	M	Caucasian	5.333333	0 0	0 0	0 0
phchp091 v2	SZA	55	M	Caucasian	5.083333	0 0	0 0	0 0
phchp091 v3	SZA	55	M	Caucasian	4.833333	0 0	0 0	0 0
phchp092 v1	BP	45	M	African American	5.75	0 0	0 0	0 0
phchp092 v2	BP	46	M	African American	5.333333	0 0	0 0	0 0
phchp092	BP	46	M	African	5.166667	0 0	0 0	0 0

v3				American								
phchp093 v1	BP	51	M	Caucasian	4.25	1	0	2	0	0.48	0	
phchp093 v2	BP	51	M	Caucasian	4	1	0	2	0	0.5	0	
phchp093 v3	BP	52	M	Caucasian	3.75	0	0	1	0	0.27	0	
phchp094 v1	BP	41	M	African American	4.666667	0	0	0	0	0	0	
phchp095 v1	BP	28	M	Caucasian	4.25	2	0	2	0	0.48	0	
phchp095 v2	BP	29	M	Caucasian	4	2	0	2	0	0.5	0	
phchp095 v3	BP	29	M	Caucasian	3.75	1	0	1	0	0.27	0	
phchp096 v1	SZ	55	M	African American	4.833333	0	0	0	0	0	0	
phchp096 v3	SZ	56	M	African American	4.333333	0	0	0	0	0	0	
phchp096 v4	SZ	58	M	African American	2.416667	0	0	0	0	0	0	
phchp098 v1	SZ	59	M	African American	4.75	0	0	0	0	0	0	
phchp099 v1	SZ	49	M	Caucasian	4.583333	0	0	0	0	0	0	
phchp099 v2	SZ	49	M	Caucasian	4.333333	0	0	0	0	0	0	
phchp099 v3	SZ	49	M	Caucasian	4	0	0	0	0	0	0	
phchp100 v1	BP	28	M	Caucasian	1.583333	0	0	0	0	0	0	
phchp103 v1	SZA	61	M	Caucasian	2.583333	1	0	1	0	0.39	0	
phchp105 v1	SZA	59	M	Caucasian	2.833333	0	0	0	0	0	0	
phchp108 v1	SZ	42	M	Caucasian	4.083333	0	0	0	0	0	0	
phchp108	SZ	42	M	Caucasian	3.833333	0	0	0	0	0	0	

v2								
phchp108 v3	SZ	43	M	Caucasian	3.583333	0 0	0 0	0 0
phchp109 v1	BP	22	M	Caucasian	3.583333	0 0	3 0	0.84 0
phchp112 v1	BP	46	M	Caucasian/Native Australian	1.583333	0 0	0 0	0 0
phchp112 v2	BP	46	M	Caucasian	1.333333	0 0	0 0	0 0
phchp112 v3	BP	47	M	Caucasian	1	0 0	0 0	0 0
phchp113 v1	BP	37	M	Caucasian	3.333333	0 0	0 0	0 0
phchp114 v1	SZA	54	M	African American	3.75	0 0	0 0	0 0
phchp115 v1	BP	67	M	Caucasian	4.416667	0 0	0 0	0 0
phchp115 v2	BP	67	M	Caucasian	4.166667	0 0	0 0	0 0
phchp115 v3	BP	68	M	Caucasian	3.916667	0 0	0 0	0 0
phchp117 v1	BP	43	M	Caucasian	3.333333	0 0	0 0	0 0
phchp117 v2	BP	43	M	Caucasian	3.083333	0 0	0 0	0 0
phchp117 v3	BP	43	M	Caucasian	2.833333	0 0	0 0	0 0
phchp118 v1	SZA	46	M	African American	3.75	0 0	0 0	0 0
phchp118 v2	SZA	47	M	African American	3.166667	0 0	0 0	0 0
phchp119 v2	SZA	56	M	African American	3.583333	0 0	0 0	0 0
phchp119 v3	SZA	56	M	African American	3.333333	0 0	0 0	0 0
phchp120 v1	SZ	51	M	Caucasian	4	0 0	0 0	0 0
phchp120	SZ	51	M	Caucasian	3.75	0 0	0 0	0 0

v2								
phchp120 v3	SZ	51	M	Caucasian	3.5	0 0	0 0	0 0
phchp124 v1	BP	53	M	Caucasian	3.166667	1 0	4 0	1.27 0
phchp124 v2	BP	54	M	Caucasian	2.833333	0 0	3 0	1.06 0
phchp128 v1	BP	45	M	Caucasian	4.083333	0 0	0 0	0 0
phchp128 v2	BP	45	M	Caucasian	3.75	0 0	0 0	0 0
phchp129 v1	SZA	22	M	Caucasian	3.916667	0 0	1 0	0.26 0
phchp132 v1	BP	51	M	Caucasian	3.916667	0 0	0 0	0 0
phchp132 v2	BP	51	M	Caucasian	3.666667	0 0	0 0	0 0
phchp132 v3	BP	52	M	Caucasian	3.416667	0 0	0 0	0 0
phchp132 v4	BP	54	M	Caucasian	1.25	0 0	0 0	0 0
phchp133 v1	SZ	55	M	Caucasian	4	0 0	4 0	1 0
phchp134 v1	BP	59	M	Caucasian	4	0 0	0 0	0 0
phchp134 v2	BP	59	M	Caucasian	3.75	0 0	0 0	0 0
phchp134 v3	BP	59	M	Caucasian	3.5	0 0	0 0	0 0
phchp134 v4	BP	61	M	Caucasian	1.333333	0 0	0 0	0 0
phchp134 v5	BP	62	M	Caucasian	1.083333	0 0	0 0	0 0
phchp136 v1	BP	41	M	Caucasian	3.166667	0 0	0 0	0 0
phchp136 v2	BP	41	M	Caucasian	2.916667	0 0	0 0	0 0
phchp136	BP	41	M	Caucasian	2.583333	0 0	0 0	0 0

v3								
phchp140 v1	BP	38	M	Caucasian	3.083333	0 0	0 0	0 0
phchp140 v2	BP	38	M	Caucasian	2.833333	0 0	0 0	0 0
phchp140 v3	BP	38	M	Caucasian	2.583333	0 0	0 0	0 0
phchp142 v1	BP	55	M	Caucasian	3.833333	0 0	0 0	0 0
phchp142 v2	BP	55	M	Caucasian	3.583333	0 0	0 0	0 0
phchp142 v3	BP	55	M	Caucasian	3.333333	0 0	0 0	0 0
phchp142 v4	BP	57	M	Caucasian	1.333333	0 0	0 0	0 0
phchp142 v5	BP	57	M	Caucasian	1.083333	0 0	0 0	0 0
phchp147 v1	BP	38	M	Caucasian	3.666667	0 0	0 0	0 0
phchp147 v2	BP	38	M	Caucasian	3.416667	0 0	0 0	0 0
phchp147 v3	BP	38	M	Caucasian	3.166667	0 0	0 0	0 0
phchp148 v1	SZ	25	M	Caucasian	3.416667	0 0	0 0	0 0
phchp149 v1	BP	45	M	Caucasian	3.333333	0 0	1 0	0.3 0
phchp149 v2	BP	45	M	Caucasian	3.083333	0 0	1 0	0.33 0
phchp149 v3	BP	46	M	Caucasian	2.75	0 0	1 0	0.37 0
phchp151 v1	SZ	24	M	Caucasian	3.833333	0 1	0 1	0 0.27
phchp151 v2	SZ	24	M	Caucasian	3.583333	0 0	0 0	0 0
phchp151 v3	SZ	24	M	Caucasian	3.25	0 0	0 0	0 0
phchp152	BP	45	M	Caucasian	3.5	0 0	0 0	0 0

v1								
phchp153 v1	BP	55	M	Caucasian	3.333333	0 0	0 0	0 0
phchp153 v2	BP	55	M	Caucasian	3	0 0	0 0	0 0
phchp153 v3	BP	56	M	Caucasian	2.75	0 0	0 0	0 0
phchp153 v4	BP	57	M	Caucasian	1	0 0	0 0	0 0
phchp154 v1	SZA	51	M	African American	3.083333	1 0	1 0	0.33 0
phchp154 v2	SZA	51	M	African American	2.833333	1 0	1 0	0.36 0
phchp154 v3	SZA	52	M	African American	2.583333	0 0	0 0	0 0
phchp155 v1	MDD	37	M	Caucasian	3.5	0 0	0 0	0 0
phchp155 v2	MDD	37	M	Caucasian	3.25	0 0	0 0	0 0
phchp158 v1	BP	23	M	African American	3.416667	0 0	0 0	0 0
phchp161 v1	MDD	54	M	African American	3.166667	0 0	0 0	0 0
phchp161 v2	MDD	54	M	African American	2.916667	0 0	0 0	0 0
phchp161 v3	MDD	54	M	African American	2.75	0 0	0 0	0 0
phchp162 v1	MDD	57	M	Caucasian	3.416667	1 0	1 0	0.3 0
phchp162 v2	MDD	57	M	Caucasian	3	0 0	0 0	0 0
phchp162 v3	MDD	57	M	Caucasian	2.75	0 0	0 0	0 0
phchp165 v1	SZ	60	M	African American	3.333333	0 0	1 0	0.3 0
phchp165 v2	SZ	60	M	African American	3.083333	1 0	1 0	0.33 0
phchp165	SZ	61	M	African	2.916667	1 0	1 0	0.35 0

v3				American				
phchp166 v1	BP	56	M	Caucasian	3	0 0	0 0	0 0
phchp166 v2	BP	56	M	Caucasian	2.75	0 0	0 0	0 0
phchp166 v3	BP	56	M	Caucasian	2.5	0 0	0 0	0 0
phchp168 v1	MD D	48	M	African American	3.25	0 0	0 0	0 0
phchp168 v2	MD D	48	M	African American	3	0 0	0 0	0 0
phchp168 v3	MD D	49	M	African American	2.75	0 0	0 0	0 0
phchp169 v1	SZA	50	M	African American	3.333333	0 0	0 0	0 0
phchp171 v1	BP	36	M	Caucasian	3.083333	0 0	0 0	0 0
phchp171 v2	BP	36	M	Caucasian	2.75	0 0	0 0	0 0
phchp173 v1	MD D	48	M	Caucasian	2.833333	0 0	0 0	0 0
phchp173 v2	MD D	49	M	Caucasian	2.583333	0 0	0 0	0 0
phchp173 v3	MD D	49	M	Caucasian	2.333333	0 0	0 0	0 0
phchp174 v1	MD D	54	M	Caucasian	2.333333	2 0	3 0	1.29 0
phchp175 v1	SZA	42	M	Caucasian	2.5	0 0	0 0	0 0
phchp176 v1	SZ	23	M	African American	2.25	0 0	0 0	0 0
phchp176 v2	SZ	24	M	African American	1.916667	0 0	0 0	0 0
phchp178 v1	BP	49	M	Caucasian	3.25	0 0	0 0	0 0
phchp182 v1	MD D	39	M	Caucasian	3.166667	0 0	0 0	0 0
phchp182	MD	39	M	Caucasian	2.916667	0 0	0 0	0 0

v2	D							
phchp182 v3	MD D	40	M	Caucasian	2.666667	0 0	0 0	0 0
phchp183 v1	BP	48	M	Caucasian	3.083333	0 0	0 0	0 0
phchp183 v2	BP	48	M	Caucasian	2.833333	0 0	0 0	0 0
phchp184 v1	BP	64	M	Caucasian	3.083333	0 0	0 0	0 0
phchp184 v2	BP	64	M	Caucasian	2.833333	0 0	0 0	0 0
phchp184 v3	BP	64	M	Caucasian	2.583333	0 0	0 0	0 0
phchp185 v1	SZA	51	M	African American	3.083333	0 0	0 0	0 0
phchp185 v2	SZA	51	M	African American	2.833333	0 0	0 0	0 0
phchp185 v3	SZA	52	M	African American	2.416667	0 0	0 0	0 0
phchp186 v1	BP	43	M	Caucasian	3.083333	0 0	0 0	0 0
phchp186 v2	BP	44	M	Caucasian	2.833333	0 0	0 0	0 0
phchp186 v3	BP	44	M	Caucasian	2.583333	0 0	0 0	0 0
phchp187 v1	SZ	49	M	African American	3.166667	1 0	1 0	0.32 0
phchp187 v2	SZ	49	M	African American	2.833333	0 0	0 0	0 0
phchp188 v1	SZ	54	M	African American	3.166667	0 0	1 0	0.32 0
phchp190 v1	BP	49	M	Caucasian	3.083333	0 0	0 0	0 0
phchp190 v2	BP	49	M	Caucasian	2.75	0 0	0 0	0 0
phchp190 v3	BP	50	M	Caucasian	2.5	0 0	0 0	0 0
phchp192	SZA	55	M	African	3	0 0	0 0	0 0

v1				American				
phchp192 v2	SZA	56	M	African American	2.75	0 0	0 0	0 0
phchp192 v3	SZA	56	M	African American	2.5	0 0	0 0	0 0
phchp193 v1	BP	39	M	Hispanic	2.916667	0 0	0 0	0 0
phchp193 v3	BP	39	M	Hispanic	2.333333	0 0	0 0	0 0
phchp193 v4	BP	40	M	Hispanic	2.083333	0 0	0 0	0 0
phchp194 v1	MD D	47	M	Caucasian	3.083333	0 0	0 0	0 0
phchp194 v2	MD D	47	M	Caucasian	2.833333	0 0	0 0	0 0
phchp194 v3	MD D	47	M	Caucasian	2.583333	0 0	0 0	0 0
phchp195 v1	SZ	52	M	Caucasian	2.833333	0 0	0 0	0 0
phchp195 v2	SZ	53	M	Caucasian	2.583333	0 0	0 0	0 0
phchp195 v3	SZ	53	M	Caucasian	2.333333	0 0	0 0	0 0
phchp196 v1	MD D	56	M	African American	2.833333	0 0	0 0	0 0
phchp196 v2	MD D	56	M	African American	2.583333	0 0	0 0	0 0
phchp196 v3	MD D	57	M	African American	2.333333	0 0	0 0	0 0
phchp197 v1	SZ	56	M	Caucasian	2.416667	0 0	0 0	0 0
phchp197 v2	SZ	57	M	Caucasian	1.416667	0 0	0 0	0 0
phchp197 v3	SZ	57	M	Caucasian	1.166667	0 0	0 0	0 0
phchp198 v1	MD D	61	M	Caucasian	2.833333	0 1	0 1	0 0.36
phchp198	MD	61	M	Caucasian	2.583333	0 1	0 1	0 0.39

v2	D							
phchp198 v4	MD D	62	M	Caucasian	2.083333	0 1	0 1	0 0.48
phchp199 v1	SZ	49	M	African American	2.916667	0 0	0 0	0 0
phchp199 v2	SZ	49	M	African American	2.666667	0 0	0 0	0 0
phchp199 v3	SZ	50	M	African American	2.333333	0 0	0 0	0 0
phchp200 v1	MD D	56	M	Caucasian	2.833333	0 0	0 0	0 0
phchp200 v2	MD D	57	M	Caucasian	2.583333	0 0	0 0	0 0
phchp200 v3	MD D	57	M	Caucasian	2.333333	0 0	0 0	0 0
phchp206 v1	MD D	59	M	African American	2.833333	0 0	0 0	0 0
phchp207 v1	SZ	48	M	African American	1.5	0 0	0 0	0 0
phchp208 v1	MD D	56	M	African American	2.75	0 0	0 0	0 0
phchp208 v2	MD D	56	M	African American	2.5	0 0	0 0	0 0
phchp208 v3	MD D	58	M	African American	1	0 0	0 0	0 0
phchp210 v1	BP	43	M	Caucasian	1.666667	0 0	0 0	0 0
phchp210 v2	BP	43	M	Caucasian	1.416667	0 0	0 0	0 0
phchp211 v1	SZ	62	M	Caucasian	1.75	0 0	0 0	0 0
phchp211 v2	SZ	62	M	Caucasian	1.166667	0 0	0 0	0 0
phchp212 v1	MD D	56	M	African American	2.666667	0 0	0 0	0 0
phchp212 v2	MD D	56	M	African American	2.416667	0 0	0 0	0 0
phchp219	BP	61	M	Caucasian	2.25	0 0	0 0	0 0

v1								
phchp219 v2	BP	61	M	Caucasian	1.916667	0 0	0 0	0 0
phchp219 v3	BP	62	M	Caucasian	1.416667	0 0	0 0	0 0
phchp221 v1	MD D	51	M	African American	2.25	0 0	0 0	0 0
phchp221 v2	MD D	51	M	African American	2	0 0	0 0	0 0
phchp221 v3	MD D	52	M	African American	1.666667	0 0	0 0	0 0
phchp222 v2	SZ	60	M	Caucasian	1.416667	0 0	0 0	0 0
phchp222 v3	SZ	61	M	Caucasian	1.166667	0 0	0 0	0 0
phchp224 v1	BP	59	M	Caucasian	1.083333	1 0	1 0	0.93 0
phchp226 v1	MD D	29	M	Caucasian	1.833333	0 0	0 0	0 0
phchp226 v2	MD D	29	M	Caucasian	1.583333	0 0	0 0	0 0
phchp227 v1	MD D	55	M	Caucasian	2.083333	0 0	0 0	0 0
phchp227 v2	MD D	55	M	Caucasian	1.833333	0 0	0 0	0 0
phchp227 v3	MD D	55	M	Caucasian	1.583333	0 0	0 0	0 0
phchp234 v1	BP	44	M	Caucasian	2.166667	0 0	0 0	0 0
phchp234 v2	BP	45	M	Caucasian	1.583333	0 0	0 0	0 0
phchp234 v3	BP	45	M	Caucasian	1.333333	0 0	0 0	0 0
phchp235 v1	MD D	54	M	African American	1.833333	0 0	0 0	0 0
phchp235 v2	MD D	55	M	African American	1.583333	0 0	0 0	0 0
phchp235	MD	55	M	African	1.25	0 0	0 0	0 0

v3	D			American				
phchp236 v1	MD D	51	M	Caucasian	2.166667	0 0	0 0	0 0
phchp236 v2	MD D	51	M	Caucasian	1.916667	0 0	0 0	0 0
phchp238 v1	MD D	62	M	Caucasian	2.166667	0 0	0 0	0 0
phchp238 v2	MD D	63	M	Caucasian	1.916667	0 0	0 0	0 0
phchp238 v3	MD D	63	M	Caucasian	1.583333	0 0	0 0	0 0
phchp242 v1	MD D	55	M	African American	2.083333	0 0	0 0	0 0
phchp247 v1	MD D	55	M	African American	2.083333	0 0	0 0	0 0
phchp248 v1	SZ	52	M	African American	2	0 0	0 0	0 0
phchp248 v2	SZ	52	M	African American	1.666667	0 0	0 0	0 0
phchp248 v3	SZ	53	M	African American	1.416667	0 0	0 0	0 0
phchp253 v1	BP	25	M	Caucasian	1.916667	0 0	0 0	0 0
phchp253 v2	BP	26	M	Caucasian	1.083333	0 0	0 0	0 0
phchp259 v1	MD D	56	M	Caucasian	1.75	0 0	0 0	0 0
phchp259 v2	MD D	57	M	Caucasian	1.416667	0 0	0 0	0 0
phchp259 v3	MD D	57	M	Caucasian	1	0 0	0 0	0 0
phchp270 v1	BP	41	M	Caucasian	1.75	0 0	0 0	0 0
phchp270 v2	BP	41	M	Caucasian	1.5	0 0	0 0	0 0
phchp273 v1	BP	27	M	Caucasian	1.666667	0 0	0 0	0 0
phchp273	BP	28	M	Caucasian	1.416667	0 0	0 0	0 0

v2												
phchp274 v1	BP	48	M	Caucasian	1.666667	1	0	1	0	0.6	0	
phchp274 v2	BP	48	M	Caucasian	1.416667	0	0	0	0	0	0	
phchp274 v3	BP	48	M	Caucasian	1.166667	0	0	0	0	0	0	
phchp275 v1	SZ	63	M	Caucasian	1	0	0	0	0	0	0	
phchp276 v1	SZ	59	M	African American	1.083333	0	0	0	0	0	0	
phchp277 v1	SZ	49	M	Caucasian	1.583333	0	0	0	0	0	0	
phchp277 v2	SZ	50	M	Caucasian	1.333333	0	0	0	0	0	0	
phchp277 v3	SZ	50	M	Caucasian	1.083333	0	0	0	0	0	0	
phchp287 v1	SZA	59	M	Caucasian	1	0	0	0	0	0	0	
phchp292 v1	BP	42	M	Caucasian	1.333333	0	0	0	0	0	0	
phchp292 v2	BP	42	M	Caucasian	1.083333	0	0	0	0	0	0	
phchp293 v1	BP	43	M	Caucasian	1.166667	0	0	0	0	0	0	
phchp295 v1	SZ	52	M	African American	1.083333	0	0	0	0	0	0	
phchp296 v1	BP	48	M	Caucasian	1.083333	0	0	0	0	0	0	

Table S2. Top candidate biomarker genes -evidence for involvement in suicidality.

The top genes from discovery (internal score of 4), prioritization (genes with CFG score of 8 and above), and validation (nominally significant). Underlined gene symbol means reproduces suicide biomarkers findings from our earlier smaller study in bipolar participants[1]. **Bold p-value is Bonferroni significant after validation in suicide completers.**

Gene symbol/ Gene Name	Probesets	**Discovery** (Change) Method/ Score	Prior human genetic evidence	Prior human brain expression evidence	Prior human peripheral expression evidence	**Prioritization** Total CFG Score For Suicide	**Validation** ANOVA p-value
SKA2 spindle and kinetochore associated complex subunit 2	225686_at	**(D)** DE/1 AP/1	Suicide [2]	(D) PFC [2]	(D) Methylation in blood [2]	**9**	0.006 0.027
CCDC136 coiled-coil domain containing 136	226972_s_at	**(D)** AP4		(D) HIP [3]		**8**	NC
CD44 CD44 molecule (Indian blood group)	209835_x_at	**(D)** DE2	Suicide [4]	(D) BA9 and BA24 [4]		**8**	NC
FADS1 fatty acid desaturase 1	208962_s_at 208964_s_at	**(D)** DE4 **(I)** DE1		(D) PFC [5]		**8**	NC **2.08E-06**
FKBP5 FK506 binding protein 5	204560_at	**(D)** DE2	Suicide [6 7 8 9 10]	(D) AMY [11]		**8**	NC
FOXN3 forkhead box N3	205021_s_at	**(D)** AP2	Suicide[12]	(D) BA24 [12] (I) BA9 [12]	(I) **Blood**[1]	**8**	4.99E-04
HADHA hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit	208631_s_at	**(D)** DE4		(D) HIP [3]		**8**	NC
IL6 interleukin 6 (interferon, beta 2)	205207_at	**(I)** AP2		(I) PFC (BA-10) [13] HIP [14]	(I) CSF [15 16] (D) Blood [17]	**8**	**1.44E-08**
SAT1 spermidine/spermine N1-acetyltransferase 1	213988_s_at 210592_s_at 230333_at 203455_s_at	**(I)** DE2 DE1	Suicide [18 1 9]	(I) PFC BA46 [20]	(I) **Blood**[1]	**8**	**1.08E-44 1.24E-40 6.93E-12 3.09E-38**

SLC4A4 solute carrier family 4 (sodium bicarbonate cotransporter), member 4	211494_s_at210739_x_at	**(I)** AP2 DE1	Suicide[21]	(D) PFC (BA 46/10) in SZ [22]		**8**	**5.84E-05** 0.002
MAOB monoamine oxidase B	204041_at	**(I)** DE1		(I) PFC [23]	(D) Blood [24]	**7**	**8.11E-08**
AHCYL1 adenosylhomocysteinase-like 1	207464_at	**(D)** DE2 AP1		(D) PFC [22]		**6**	**2.22E-06** 0.0238
AKT1S1 AKT1 substrate 1 (proline-rich)	224982_at	**(D)** DE2 AP2		(D) HIP [3]		**6**	**1.97E-07** **3.54E-07**
ALDH3A2 aldehyde dehydrogenase 3 family, member A2	210544_s_at; 210544_s_at	**(D)** DE2 AP1		(I) BA4, BA44 and Lateral thalamus [25]		**6**	**3.73E-05** 0.0348
ARHGAP26 Rho GTPase activating protein 26	205068_s_at	**(I)** DE1	Linkage D5S1480[26]	(D) DLFPC [27]		**6**	**9.91E-08**
BCL2 B-cell CLL/lymphoma 2	207005_s_at 207004_at	**(D)** DE1 **(I)** AP1		(D) PFC [28]		**6**	0.0003 0.02
C20orf27	218081_at; 50314_i_at	**(D)** DE2		(I) ACC [27]		**6**	**2.80E-13** **2.47E-05**
CAPNS1 calpain, small subunit 1	200001_at	**(D)** DE2		(D) PFC [29] (I) BA4 [30]		**6**	0.0002
CDC42EP4 CDC42 effector protein (Rho GTPase binding) 4	218062_x_at	**(D)** AP2		(D) BA11 [30]		**6**	**1.16E-06**
CDH4 cadherin 4, type 1, R-cadherin (retinal)	220227_at	**(I)** DE2		(D) DLFPC [27]		**6**	0.00908
CXCL11 chemokine (C-X-C motif) ligand 11	210163_at	**(I)** AP2		(D) NAC [27]		**6**	0.0293
EHBP1 EH domain binding protein 1	212650_at	**(D)** DE 4	Suicide [31]			**6**	**NC**
EIF5A eukaryotic translation initiation factor 5A	201123_s_at	**(D)** DE2		(D) PFC [32]		**6**	0.0006
EMID1 EMI domain containing 1	1564251_at	**(I)** DE2		(D) BA4 [30]		**6**	0.0346
FAM49B family with sequence similarity 49, member B	217535_at	**(I)** AP2		(D) HIP [3]		**6**	0.0188

FH fumarate hydratase	203032_s_at	**(D)** DE2		(I) PFC (I) [29]		**6**	**5.10E-11**
GCOM1 GRINL1A complex locus 1	228568_at	**(I)** DE2		(D) BA44 [20]	(I) **Blood**[1]	**6**	**2.13E-09**
GPM6B glycoprotein M6B	236116_at; 209170_s_at	**(D)** AP1 DE1	Linkage DXS1224 DXS8019 [33]	(D) BA 8/9,BA 46,BA 44 [33] (I) BA46 [20]		**6**	**2.32E-07** 0.0119
HOMEZ homeobox and leucine zipper encoding	231868_at	**(D)** DE2 AP1		(D) HIP [3]		**6**	**1.38E-12** 8.27E-05
HPCAL1 hippocalcin-like 1	1560154_a_at	**(I)** DE2		(I) BA4 [30]		**6**	**7.50E-05**
IKBKB inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	211027_s_at	**(D)** DE2		(I) ACC [27]		**6**	**1.24E-06**
ITGB4 integrin, beta 4	211905_s_at	**(D)** DE2		(D) PFC [32]		**6**	0.0290
LDLRAP1 low density lipoprotein receptor adaptor protein 1	221790_s_at	**(D)** DE2		(I) ACC [27]		**6**	**2.24E-16**
LOC728543 uncharacterized LOC728543	234133_s_at	**(D)** DE2		(D) ACC [27]		**6**	**1.97E-05**
MAP2K5 mitogen-activated protein kinase kinase 5	211370_s_at	**(D)** DE2		(D) HIP [34]		**6**	0.00612
MAPK9 mitogen-activated protein kinase 9	225781_at	**(I)** DE2		(I) PFC [35]		**6**	0.0132
NEAT1 nuclear paraspeckle assembly transcript 1 (non-protein coding)	224565_at	**(I)** DE2		(I) NAC [27]		**6**	**2.33E-24**
NMB neuromedin B	205204_at	**(D)** DE2		(D) Dorsovagal complex [36]		**6**	0.0149
PAFAH1B2 platelet-activating factor acetylhydrolase 1b, catalytic subunit 2 (30kDa)	210160_at	**(D)** DE2		(I) NAC [27]		**6**	**3.66E-08**
PCBD2 pterin-4 alpha-carbinolamine	231085_s_at	**(D)** DE2		(D) HIP [3]		**6**	0.0345

dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 2							
PIK3C2A phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 alpha	1553694_a_at	**(D)** DE2		(D) PFC [37] BA8/9 [30]		**6**	**3.75E-09**
PKP4 plakophilin 4	201927_s_at	**(D)** AP1		(I) NAC [27]		**6**	0.0486
PTK2 protein tyrosine kinase 2	241453_at	**(I)** DE2		(D) Frontopolar cortex [38]		**6**	**1.11E-33**
RASL11B RAS-like, family 11, member B	219142_at	**(I)** AP2		(D) DLFPC [27]		**6**	0.0124
SLC5A3 solute carrier family 5 (sodium/myo-inositol cotransporter), member 3	213167_s_at	**(D)** DE2		(D) NAC [27]		**6**	**1.06E-11**
SNORA68 small nucleolar RNA, H/ACA box 68	1566402_at1566403_at	**(I)** DE2 AP1		(D) HIP [3]		**6**	0.00310 0.00813
SOD2 superoxide dismutase 2, mitochondrial	216841_s_at	**(I)** DE1		(I) PFC [39]		**6**	0.00042
SYNE2 spectrin repeat containing, nuclear envelope 2	242774_at; 1558392_at	**(D)** DE2 DE1		(D) HIP [3]		**6**	**6.83E-08** 0.0183
TCF7L2 transcription factor 7-like 2 (T-cell specific, HMG-box)	212762_s_at	**(I)** DE1		(D) HIP [3]		**6**	0.0280
TGOLN2 trans-golgi network protein 2	203834_s_at	**(D)** AP1	Linkage D2S428 D2S1790 [40, 41]	(I) BA4 [30]		**6**	**1.10E-07**
TRAK2 trafficking protein, kinesin binding 2	202124_s_at	**(D)** DE2		(I) NAC [27]		**6**	0.006
ADRBK1 adrenergic, beta, receptor kinase 1	201401_s_at	**(D)** DE1		(I) PFC (Brodmann area 9) [42]		**5**	**2.22E-05**
AHCYL2 adenosylhomocysteinase-like 2	212814_at	**(D)** AP1		(I) NAC [27]		**5**	0.00103
AIMP1 aminoacyl tRNA synthetase	227605_at; 202542_s_at;	**(D)** AP1 DE2		(I) NAC [27]		**5**	**8.37E-05;** 0.0138; 0.0301

complex-interacting multifunctional protein 1	235594_at						
ATP6V0E1 ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1	236527_at	**(D)** AP1		(D) BA11 [30]	(I) **Blood**[1]	**5**	**3.80E-07**
BRAF v-raf murine sarcoma viral oncogene homolog B	236402_at	**(I)** DE1		(D) HIP [43]		**5**	**6.07E-29**
BRCC3 BRCA1/BRCA2-containing complex, subunit 3	216521_s_at	**(D)** DE1		(I) PFC [29]		**5**	**5.79E-08**
C1orf61	205103_at	**(I)** DE1		(I) NAC [27]		**5**	**2.95E-13**
CALR calreticulin	212953_x_at	**(I)** DE1		(D) Frontopolar cortex [38]		**5**	**6.20E-06**
CAMK2B calcium/calmodulin-dependent protein kinase II beta	209956_s_at	**(I)** DE1		(I) PFC [35]		**5**	0.00025
CAV1 caveolin 1, caveolae protein, 22kDa	212097_at	**(I)** DE1		(I) ACC [27]		**5**	**7.31E-07**
CHD2 chromodomain helicase DNA binding protein 2	1554014_at	**(I)** DE1		(I) NAC [27]		**5**	**2.40E-24**
CLTA clathrin, light chain A	1560434_x_at	**(I)** DE1		(I) Frontopolar cortex [38]		**5**	0.00064
CNP 2',3'-cyclic nucleotide 3' phosphodiesterase	1557943_at	**(D)** AP1		(D) HIP [3]		**5**	0.0315
COL9A2 collagen, type IX, alpha 2	232542_at	**(D)** DE1		(I) NAC [27]		**5**	0.00044
CPSF2 cleavage and polyadenylation specific factor 2, 100kDa	233208_x_at	**(D)** AP1		(I) ACC [27]		**5**	0.00171
CREM cAMP responsive element modulator	241740_at	**(I)** AP1		(D) Frontopolar cortex [38]		**5**	**1.08E-06**
CTTN cortactin	214782_at 201059_at	**(I)** DE1		(D) Frontopolar cortex [38]		**5**	**3.46E-18** 0.0363

CUL4B cullin 4B	210257_x_at	**(D)** DE1		(I) ACC [27]		**5**	0.00776
DAAM2 dishevelled associated activator of morphogenesis 2	212793_at	**(I)** DE1		(I) NAC [27]		**5**	0.00856
DAB2 Dab, mitogen-responsive phosphoprotein, homolog 2 (Drosophila)	201279_s_at	**(I)** DE1		(I) NAC [27]		**5**	0.00098
DLL1 delta-like 1 (Drosophila)	227938_s_at	**(D)** DE1		(D) AMY [44] (I) DLPFC [44]		**5**	0.00016
DNAH2 dynein, axonemal, heavy chain 2	215840_at	**(D)** DE1		(I) ACC [27]		**5**	0.00637
DPP4 dipeptidyl-peptidase 4	211478_s_at	**(D)** DE4	Linkage D2S1353 [45]			**5**	**1.43E-07**
G2E3 G2/M-phase specific E3 ubiquitin protein ligase	223254_s_at	**(D)** AP1		(I) ACC [27]		**5**	0.0214
GABARAPL1 GABA(A) receptor-associated protein like 1	208869_s_at	**(I)** DE1		(D) BA20,BA10,BA46 [46]		**5**	**3.48E-28**
GLUL glutamate-ammonia ligase	215001_s_at	**(I)** DE1		(D) BA44 [20] AMY,BA46,BA44,BA45 [46] frontopolar cortex [38]		**5**	**3.96E-15**
GUK1 guanylate kinase 1	200075_s_at	**(D)** DE1		(D) HIP [3] PFC [29]		**5**	0.0362
HELZ helicase with zinc finger	240486_at	**(I)** DE1		(I) BA4 [30]		**5**	**3.56E-06**
IGHG1 immunoglobulin heavy constant gamma 1 (G1m marker)	241074_at	**(I)** DE1		(D) ACC [27]		**5**	0.0342
IL1B interleukin 1, beta	205067_at 39402_at	**(I)** DE1		(I) PFC (BA-10) [13]	(I) **Blood**[1]	**5**	0.0338; 0.0380
JAK3 Janus kinase 3	211108_s_at	**(D)** DE1		(D) DLFPC [27]		**5**	**5.42E-11**
JUN jun proto-oncogene	201464_x_at 213281_at 201466_s_	**(I)** DE1 AP1		(D) HIP [3]		**5**	**2.63E-51 1.02E-41 2.21E-08**

	at						
JUNB jun B proto-oncogene	201473_at	**(I)** DE1		(D) HIP [3]		**5**	**1.09E-18**
LAPTM4B lysosomal protein transmembrane 4 beta	1554679_a_at	**(D)** AP1		(I) BA8/9 [30]		**5**	0.0113
LHFP lipoma HMGIC fusion partner	218656_s_at	**(I)** DE1		(I) NAC [27]	(I) **Blood**[1]	**5**	**1.27E-06**
LPAR1 lysophosphatidic acid receptor 1	204036_at	**(D)** AP1		(I) NAC [27]		**5**	**7.67E-06**
MAGI3 membrane associated guanylate kinase, WW and PDZ domain containing 3	226770_at	**(D)** AP1		(D) DLFPC [27]		**5**	0.0292
MARCKS myristoylated alanine-rich protein kinase C substrate	213002_at 201670_s_at	**(I)** DE1		(I) HIP, PFC [47] PFC{Punzi, 2014 #36847}	(I) **Blood**[1]	**5**	**1.51E-06**; 0.0004
MBP myelin basic protein	225408_at	**(D)** AP1		(I) NAC [27]		**5**	**6.74E-10**
MCRS1 microspherule protein 1	202556_s_at	**(D)** DE1		(D) HIP [3]		**5**	**3.29E-05**
MEF2C myocyte enhancer factor 2C	207968_s_at	**(D)** DE1		(D) HIP [34]		**5**	**3.47E-09**
MT1E metallothionein 1E	212859_x_at	**(I)** DE1		(D) ACC [27] PFC (BA 46/10) [32]		**5**	0.00020
MT1H metallothionein 1H	206461_x_at	**(I)** DE1		(D) ACC, NAC [27] PFC (BA 46/10)[22]		**5**	**5.62E-05**
MT2A metallothionein 2A	212185_x_at	**(I)** DE1		(D) ACC [27]		**5**	0.00218
NDRG1 N-myc downstream regulated 1	200632_s_at	**(I)** DE1		(I) NAC [27]		**5**	**3.21E-22**
NUCB2 nucleobindin 2	229838_at	**(I)** DE1		(I) Edinger-Westphal nucleus (midbrain) [48]		**5**	0.0124
OGFR opioid growth factor receptor	211513_s_at	**(D)** DE1		(D) HIP [3]		**5**	0.00053
PCDH9	238919_at	**(D)**		(D)		**5**	0.0215

protocadherin 9		AP1		BA45; BA46 [20]			
PHF20L1 PHD finger protein 20-like 1	219606_at	**(I)** DE1		(I) ACC [27]		**5**	**7.97E-05**
PLEKHB1 pleckstrin homology domain containing, family B (evectins) member 1	209504_s_at	**(D)** DE1		(I) NAC [27]		**5**	**6.07E-07**
POLR2D polymerase (RNA) II (DNA directed) polypeptide D	214144_at	**(D)** AP1		(I) ACC [27]		**5**	**1.02E-09**
PRKACA protein kinase, cAMP-dependent, catalytic, alpha	202801_at	**(D)** AP1		(D) PFC, NAC [49]		**5**	0.0324
PRKCB protein kinase C, beta	227824_at; 230437_s_at	**(D)** DE1 AP1		(D) PFC, HIP [50]		**5**	**3.15E-09** 1.34E-04 0.003
PSMB4 proteasome (prosome, macropain) subunit, beta type, 4	202243_s_at	**(D)** DE1		(D) PFC [29]		**5**	**9.98E-07**
PTEN phosphatase and tensin homolog	204053_x_at 222176_at	**(I)** DE1		(I) PFC, HIP [51]	(I) **Blood**[1]	**5**	**7.66E-17** 0.0003
RAB35 RAB35, member RAS oncogene family	205461_at	**(D)** DE2		(I) ACC [27]		**5**	0.00034
RBMX RNA binding motif protein, X-linked	1556336_at 213762_x_at	**(D)** DE1		(D) HIP (D) [3] BA 8/9,BA 11 (D) (Suicide) [33] (I) ACC [27]		**5**	**1.40E-13** 0.0232
RECK reversion-inducing-cysteine-rich protein with kazal motifs	216153_x_at	**(I)** DE1		(I) ACC [27]	(I) **Blood**[1]	**5**	0.00093
RNASEL ribonuclease L (2',5'-oligoisoadenylate synthetase-dependent)	221287_at	**(D)** AP1		(D) HIP [3]		**5**	**6.05E-06**
SELENBP1 selenium binding protein 1	214433_s_at	**(D)** DE1		(I) PFC [29]		**5**	0.00019
SHISA2	230493_at	**(I)**		(I)		**5**	0.00107

shisa family member 2		DE1		NAC [27]			
SLC35E1 solute carrier family 35, member E1	222263_at	**(D)** AP1		(D) BA4 [30]		**5**	0.00651
SNAP23 synaptosomal-associated protein, 23kDa	209131_s_at	**(D)** AP1		(D) BA44 [20] BA24 [52]		**5**	0.00039
TM4SF1 transmembrane 4 L six family member 1	209386_at	**(I)** DE1		(D) PFC (BA 46/10)[22]		**5**	**6.12E-11**
TMEM254 transmembrane protein 254	218174_s_at	**(D)** DE1		(D) HIP [3]		**5**	**1.35E-08**
TMEM259 transmembrane protein 259	212574_x_at; 212575_at; 213986_s_at	**(D)** DE1		(I) ACC [27]		**5**	0.0007; 0.003; 0.004
TNS1 tensin 1	218863_s_at	**(D)** DE1 AP2		(I) NAC [27]		**5**	**6.29E-05;** 0.0123
TPBG trophoblast glycoprotein	203476_at	**(I)** DE1		(I) ACC [27]		**5**	**6.66E-06**
TPD52L1 tumor protein D52-like 1	203786_s_at	**(I)** DE1		(D) PFC (BA 46/10) [22]		**5**	**1.52E-16**
TRIM23 tripartite motif containing 23	210995_s_at	**(D)** DE1		(I) PFC (BA 46/10)[22]		**5**	**3.28E-14**
TSC22D3 TSC22 domain family, member 3	208763_s_at	**(I)** DE1		(D) PFC, AMY [53]		**5**	**2.01E-05**
TSPAN33 tetraspanin 33	225775_at	**(D)** AP1		(D) HIP [3]		**5**	0.00302
VMP1 vacuole membrane protein 1	1569003_at	**(I)** DE1		(D) NAC [27]		**5**	0.00291
VPREB3 pre-B lymphocyte 3	220068_at	**(D)** DE1		(D) HIP [3]		**5**	0.00104
ZFP36 ZFP36 ring finger protein	201531_at	**(I)** DE1		(D) Orbitofrontal cortex [54]		**5**	**8.72E-27**
ZFYVE21 zinc finger, FYVE domain containing 21	219929_s_at	**(D)** AP1		(D) HIP [3]		**5**	1.69E-04
ZHX2 zinc fingers and homeoboxes 2	203556_at	**(I)** DE1		(D) PFC BA46/10 [32]		**5**	0.00198
ZNF519 zinc finger protein 519	1568873_at	**(D)** AP1		(I) ACC [27]		**5**	0.01164

B4GALT1 UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1	228498_at	**(I)** DE 4				**4**	**NC**
BTBD3 BTB (POZ) domain containing 3	243461_at	**(I)** DE 4				**4**	**NC**
CADM1 cell adhesion molecule 1	237259_at	**(I)** DE4				**4**	NC
CATSPER3 cation channel, sperm associated 3	230981_at	**(D)** AP4				**4**	**NC**
CCL28 chemokine (C-C motif) ligand 28	224240_s_at	**(D)** AP4				**4**	**NC**
CLIP4 CAP-GLY domain containing linker protein family, member 4	219944_at	**(D)** DE4				**4**	NC
CTBS chitobiase, di-N-acetyl-	218924_s_at	**(I)** DE 4				**4**	**NC**
CYorf17 chromosome Y open reading frame 17	234274_at	**(D)** DE 4				**4**	**NC**
DCAF15 DDB1 and CUL4 associated factor 15	221851_at	**(D)** DE4				**4**	0.0302
DEPDC5 DEP domain containing 5	234548_at	**(I)** AP4				**4**	**NC**
DTNA dystrobrevin, alpha	211493_x_at	**(I)** AP4				**4**	NC
EMR2 egf-like module containing, mucin-like, hormone receptor-like 2	232009_at	**(I)** DE 4				**4**	**NC**
EPHA10 EPH receptor A10	243717_at	**(D)** DE4				**4**	0.00801
ERG v-ets avian erythroblastosis virus E26 oncogene homolog	213541_s_at	**(D)** DE 4				**4**	**NC**
ERV3-2 endogenous retrovirus group 3, member 2	222139_at	**(I)** DE 4				**4**	**NC**
FAM183CP family with	1569887_a_at	**(I)** AP4				**4**	**NC**

sequence similarity 183, member C, pseudogene							
HIST1H2BO histone cluster 1, H2bo	214540_at	**(I)** DE4				**4**	**4.77E-10**
HS3ST3B1 heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	1561908_a_at	**(D)** AP4				**4**	**NC**
IQCH IQ motif containing H	224165_s_at	**(D)** DE4				**4**	0.00324
KCTD21 potassium channel tetramerization domain containing 21	229873_at	**(I)** DE 4				**4**	**NC**
KERA keratocan	220504_at	**(I)** DE4				**4**	0.00021
KIF2C kinesin family member 2C	211519_s_at	**(D)** AP4				**4**	0.00056
KLHDC3 kelch domain containing 3	214383_x_at	**(D)** DE4			(D) **Blood**[1]	**4**	**1.57E-17**
LAMB1 laminin, beta 1	238608_at	**(I)** AP4				**4**	**NC**
LOC100129917 uncharacterized LOC100129917	236411_at	**(D)** DE4				**4**	0.00225
LOC100289061 uncharacterized LOC100289061	1563071_at	**(I)** AP4				**4**	**NC**
LOC100996345 uncharacterized LOC100996345	240697_at	**(D)** DE4				**4**	**7.20E-05**
LOC285500 uncharacterized LOC285500	1558451_at	**(I)** DE 4				**4**	**NC**
MED21 mediator complex subunit 21	209363_s_at	**(D)** AP4				**4**	**0.07426**
PCIF1 PDX1 C-terminal inhibiting factor 1	222045_s_at	**(D)** AP4				**4**	**NC**
PLEC plectin	216971_s_at	**(D)** DE 4				**4**	**NC**
RAB36 RAB36, member RAS oncogene family	211471_s_at	**(I)** AP4				**4**	**NC**
RAD23A RAD23 homolog A (S. cerevisiae)	201039_s_at	**(D)** DE 4				**4**	**NC**
RHAG Rh-associated	206145_at	**(D)** AP4				**4**	**NC**

glycoprotein							
ROBO4 roundabout, axon guidance receptor, homolog 4 (Drosophila)	220758_s_at	**(D)** AP4				**4**	**NC**
RP11-669N7.2 uncharacterized LOC283352	1561757_a_at	**(I)** AP4				**4**	**NC**
RPL6P17 ribosomal protein L6 pseudogene 17	216816_at	**(D)** AP4				**4**	**NC**
SETD8 SET domain containing (lysine methyltransferase) 8	220200_s_at	**(D)** DE 4				**4**	**NC**
SH3GLB2 SH3-domain GRB2-like endophilin B2	218813_s_at	**(D)** DE4				**4**	0.00017
ST6GALNAC4 ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4	221551_x_at	**(D)** DE4				**4**	**3.22E-05**
TEX10 testis expressed 10	1558702_at	**(D)** AP4				**4**	0.00281
TEX261 testis expressed 261	1559675_at	**(D)** AP4				**4**	0.00427
TFDP1 transcription factor Dp-1	242538_at	**(I)** AP4				**4**	0.00238
TMLHE-AS1 TMLHE antisense RNA 1	1560797_s_at	**(I)** DE 4				**4**	**NC**
TMSB15B thymosin beta 15B	1556964_s_at	**(D)** DE4				**4**	0.007
TUBGCP3 tubulin, gamma complex associated protein 3	215739_s_at	**(D)** DE2	Suicide [12]			**4**	**2.05E-16**
TXNRD2 thioredoxin reductase 2	210803_at	**(D)** AP4				**4**	0.0425
USP12 ubiquitin specific peptidase 12	229987_at	**(D)** AP4				**4**	0.2723
VEGFB vascular endothelial growth factor B	203683_s_at	**(D)** AP4				**4**	**5.13E-07**
ZBTB7A	213299_at	**(D)**				**4**	**2.05E-06**

zinc finger and BTB domain containing 7A		DE4					

Table S3. Top candidate biomarker genes - mechanistic understanding. The top genes from discovery (internal score of 4), prioritization (genes with CFG score of 8 and above), and validation (nominally significant). Underlined gene symbol means overlaps with findings from our previous mood and psychosis biomarker studies. DLPFC- Dorsolateral Prefrontal Cortex ; APC- Anterior Prefrontal Cortex; ACC- Anterior Cingulate Cortex; AMY-Amygdala; VT- Ventral Tegmentum; HIP-Hippocampus; NAC-Nucleus Accumbens.Alc-alcoholism.

Gene symbol/ Gene Name	Probesets	**Discovery** (Change) Method/ Score	**Prioritization** Total CFG Score For Suicide	**Validation** ANOVA p-value		Psychiatric disorders genetic evidence	Psychiatric disorders brain expression evidence	Psychiatric disorders peripheral expression evidence	**Psychiatric Co-morbidity** CFG Score For Other Disorders	**Evidence for involvement in apoptosis**
SKA2 spindle and kinetochore associated complex subunit 2	225686_at	**(D)** DE1 AP1	**9**	0.006 0.027					0	–
CCDC136 coiled-coil domain containing 136	226972_s_at	**(D)** AP4	**8**	NC				(I) **Hallucinations blood** [55]	2	–
CD44 CD44 molecule (Indian blood group)	209835_x_at	**(D)** DE2	**8**	NC			(D) **Alc** Frontal Cortex [56]	(D) **Autistic Spectrum Disorder** Lymphoblastoid [57] **MDD** CSF [58] (I) **BP** lymphocyte [59]	6	–
FADS1 fatty acid desaturase 1	208962_s_at 208964_s_at	**(D)** DE4 **(I)** DE1	**8**	NC 2.08E-06				(I) **SZ** lymphoblastoid [60]	2	–

FKBP5 FK506 binding protein 5	204560_at	**(D)** DE2	**8**	NC		**PTSD** [61] [62] [63] [64] **BP** [7] **MDD** [65] [66] [67] **SZ** [68]	(I) **BP** PFC DLPFC [69] [70] **Alc** hippocampus [71]	(D) **PTSD** Blood [72] **Social Isolation** Blood [73] **Alc** Blood [74] (I) **MDD** Blood [75] [76]	8	–
FOXN3 forkhead box N3	205021_s_at	**(D)** AP2	**8**	4.99E-04		**SZ** [77] **BP** [78] [79] [80] **Alc** [81]	(I) **MDD** AMY and cingulate cortex [82] **SZ** cerebellar cortex [83]	(I) **SZ** IPSC [84]	8	–
HADHA hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit	208631_s_at	**(D)** DE4	**8**	NC					0	–
IL6 interleukin 6 (interferon, beta 2)	205207_at	**(I)** AP2	**8**	1.44E-08		**SZ** [85] [86] [87] [88] **Stress** [89] [90] **MDD** [91]	(I) **SZ** DLPFC BA46 [92]	(I) **BP** blood [93] [94] [95] [96] [97] [98] **MDD** blood [99] [100] [101] [102] [103] [104] [105] [106] [107] [108] [109] saliva [110] **Antidepressants** Plasma [111] **SZ** Blood [112] [113] [114] [115]	8	–

								116 117 118 119 120 88 **Psychosis** Blood[121] 109 **Antipsychotics** serum [122] **Mild Cognitive Impairment** Plasma [123] **Stress** blood [124] 125 110 **Circadian Abnormalities** Serum [102] **Borderline Personality Disorder** blood [124] **PTSD** blood [126] 127 CSF [128] **Panic Disorder** serum [129] **Pain** oral mucosa [130] **Conduct Disorder** Saliva [110] **Anxiety** plasma [107] (D) **Mood**		

								blood [131]		
SAT1 spermidine/spermine N1-acetyltransferase 1	213988_s_at 210592_s_at 230333_at 203455_s_at	**(I)** DE2 DE1	**8**	1.08E-44 1.24E-40 6.93E-12 3.09E-38		**Anxiety** [132]	(I) **MDD** AMY and cingulate cortex [82]	(I) **MDD** blood [133]	8	**Yes** [134]
SLC4A4 solute carrier family 4 (sodium bicarbonate cotransporter), member 4	211494_s_at 210739_x_at	**(I)** AP2 DE1	**8**	5.84E-05 0.002				(D) **SZ** IPSC [84]	2	–
MAOB monoamine oxidase B	204041_at	**(I)** DE1	**7**	8.11E-08		**Alc** [135] **SZ** [136]	(I) **BP** ACC, DLPFC cortex [137] PFC [138] **MDD** AMY and cingulate cortex [82] **Alc** prefrontal cortex [139]	(I) **Alc** human glioblastoma and neuroblastoma cell lines [139]	8	**Yes** [140]
AHCYL1 adenosylhomocysteinase-like 1	207464_at	**(D)** DE2 AP1	**6**	2.22E-06 0.0238					0	–
AKT1S1 AKT1 substrate 1 (proline-rich)	224982_at	**(D)** DE2 AP2	**6**	1.97E-07 3.54E-07				(I) **Circadian abnormalities** Blood[141]	2	–
ALDH3A2 aldehyde dehydrogenase 3 family, member A2	210544_s_at 210544_s_at	**(D)** DE2 AP1	**6**	3.73E-05 0.0348			(D) **BP** Brain [70]		4	–
ARHGAP26 Rho GTPase activating protein 26	205068_s_at	**(I)** DE1	**6**	9.91E-08		**SZ**[77] [142] **Autistic Spectrum Disorder** [143]	(D) **BP** Brain [70]	(I) **BP** Blood[144] **Panic Disorder** Lymphocyte[145]	8	–

								(D) **MDD** Fibroblast [146]		
BCL2 B-cell CLL/lymphoma 2	207005_s_at 207004_at	**(D)** DE1 **(I)** AP1	**6**	0.0003 0.02		**BP** [147 148 149] **Anxiety** [150] **SZ** [148]	(D) **BP** Frontal Cortex [151] **PTSD** DLPFC BA46 [152]	(D) **Mood stabilizers** Blood [153] **BP** Lymphoblast[147] (I) **Alc** Blood [154] **Pain** Vertebral disc [155]	8	–
C20orf27	218081_at 50314_i_at	**(D)** DE2	**6**	2.80E-13 2.47E-05			(D) **BP** Brain [70]	(I) **MDD** Fibroblast [146]	6	–
CAPNS1 calpain, small subunit 1	200001_at	**(D)** DE2	**6**	0.0002			(D) **SZ** PFC [156] DLPFC [157] **BP** Brain [70] (I) **Alc** frontal [56]	(I) **SZ** Fibroblasts [158]	6	–
CDC42EP4 CDC42 effector protein (Rho GTPase binding) 4	218062_x_at	**(D)** AP2	**6**	1.16E-06			(D) **MDD** AMY and cingulate cortex [82]	(D) **Alc** Blood[154]	6	–
CDH4 cadherin 4, type 1, R-cadherin (retinal)	220227_at	**(I)** DE2	**6**	0.00908		**MDD** [159] **ADHD**[160] **SZ** [161] **BP** [161]	(D) **MDD** DLPFC [162]		6	–
CXCL11	210163_at	**(I)**	**6**	0.029					0	–

chemokine (C-X-C motif) ligand 11		AP2		3						
EHBP1 EH domain binding protein 1	212650_at	**(D)** DE 4	6.00	NC		**MDD** [159] **Addictions** [31]	(D) **ASD Autistic Spectrum Disorder** cerebral cortex [163]	(D) **SZ** lymphoblastoid [60] (D) **Sleep Circadian abnormalities** blood [141]	8.00	-
EIF5A eukaryotic translation initiation factor 5A	201123_s_at	**(D)** DE2	**6**	0.0006			(D) **Addictions, Stimulants** NAC [164]	(I) **BP** Blood[144]	6	–
EMID1 EMI domain containing 1	1564251_at	**(I)** DE2	**6**	0.0346				(D) **BP Blood** [165]	2	
FAM49B family with sequence similarity 49, member B	217535_at	**(I)** AP2	**6**	0.0188			(D) **BP** Brain[70]		4	
FH fumarate hydratase	203032_s_at	**(D)** DE2	**6**	5.10E-11			(D) **MDD** AMY and cingulate cortex [82] **BP** Brain [70] **BP** Hippocampus [166]	(D) **Stress** Blood[167] **MDD** MNC [168] (I) **BP** Whole blood[144]	6	–
GCOM1 GRINL1A complex locus 1	228568_at	**(I)** DE2	**6**	2.13E-09				(D) **PTSD** Blood[169]	2	–
GPM6B glycoprotein M6B	236116_at 209170_s_at	**(D)** AP1 DE1	**6**	2.32E-07 0.0119			(D) **Alc** Frontal cortex [56] **MDD** DLPFC [162] **Tourette Syndrome** Putame	(D) **Delusions Blood** [55] **SZ** lymphocyte[59]	6	–

							n[170] (I) **Alc** Frontal, motor cortex [171] **SZ** Cerebellum [172]			
HOMEZ homeobox and leucine zipper encoding	231868_at	**(D)** DE2 AP1	**6**	1.38E-12 8.27E-05					0	–
HPCAL1 hippocalcin-like 1	1560154_a_at	**(I)** DE2	**6**	7.50E-05		**MDD**[173]	(D) **BP** Brain[70]	(I) **Migraine** Lymphocyte[174]	8	–
IKBKB inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	211027_s_at	**(D)** DE2	**6**	1.24E-06				(D) **Relaxation Response** Blood[175]	2	–
ITGB4 integrin, beta 4	211905_s_at	**(D)** DE2	**6**	0.0290			(I) **Alc** Hippocampus [71]	(D) **SZ** IPSC [84]	6	–
LDLRAP1 low density lipoprotein receptor adaptor protein 1	221790_s_at	**(D)** DE2	**6**	2.24E-16					0	–
LOC728543 uncharacterized LOC728543	234133_s_at	**(D)** DE2	**6**	1.97E-05					0	–
MAP2K5 mitogen-activated protein kinase kinase 5	211370_s_at	**(D)** DE2	**6**	0.00612		**Addictions, Stimulants** [176] **Addictions, Nicotine** [177] **MDD** [178] **Agoraphobia** [178]	(D) **MDD** AMY and cingulate cortex [82] **BP** brain [70]		6	–
MAPK9 mitogen-activated protein kinase 9	225781_at	**(I)** DE2	**6**	0.0132			(D) **BP** Brain [70]		4	–
NEAT1 nuclear	224565_at	**(I)** DE2	**6**	2.33E-24					0	–

paraspeckle assembly transcript 1 (non-protein coding)										
NMB neuromedin B	205204_at	**(D)** DE2	**6**	0.0149		**SZ** [179, 180]	(I) **MDD** AMY and cingulate cortex [82]		6	–
PAFAH1B2 platelet-activating factor acetylhydrolase 1b, catalytic subunit 2 (30kDa)	210160_at	**(D)** DE2	**6**	3.66E-08					0	–
PCBD2 pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 2	231085_s_at	**(D)** DE2	**6**	0.0345				(D) **Hallucinations Blood** [55] (I) **Alcohol** Blood [154]	2	–
PIK3C2A phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 alpha	1553694_a_at	**(D)** DE2	**6**	3.75E-09		**BP** [181] **SZ** [181] [180]	(D) **MDD** ACC [182] (I) **BP** ACC [182]	(D) **Delusions Blood** [55] **Hallucinations Blood** [55]	8	**Yes** [183] [184, 185]
PKP4 plakophilin 4	201927_s_at	**(D)** AP1	**6**	0.0486			(D) **BP** brain [70] (I) **MDD** AMY cingulate cortex [82] **Alc** PFC [186] **SZ** PFC [187]	(I) **Delusions blood** [55] **MDD** Fibroblast [146]	6	–
PTK2 protein tyrosine kinase 2	241453_at	**(I)** DE2	**6**	1.11E-33		**SZ** [188]	(I) **BP** Brain [70] **Alc** Superior frontal cortex [189]	(I) **Pain** Vertebral disc [155] (D) **Hallucinations Blood** [55]	8	–

								Delusions Blood [55] **Autistic Spectrum Disorder** lymphocyte[57] **Relaxation Response** Blood mononuclear cells [175]		
RASL11B RAS-like, family 11, member B	219142_at	**(I)** AP2	**6**	0.0124					0	–
SLC5A3 solute carrier family 5 (sodium/myo-inositol cotransporter), member 3	213167_s_at	**(D)** DE2	**6**	1.06E-11				(D) **Stress** Blood[167]	2	**Yes** [190, 191]
SNORA68 small nucleolar RNA, H/ACA box 68	1566402_at1566403_at	**(I)** DE2 AP1	**6**	0.00310 0.00813					0	–
SOD2 superoxide dismutase 2, mitochondrial	216841_s_at	**(I)** DE1	**6**	0.00042		**Addictions, Stimulants** [192]	(D) **MDD** AMY and cingulate cortex [82] **SZ** Hippocampus [193]	(D) **Antidepressants** MNC [168]	6	–
SYNE2 spectrin repeat containing, nuclear envelope 2	242774_at 1558392_at	**(D)** DE2 DE1	**6**	6.83E-08 0.0183		**SZ**[194 195 196]		(D) **Circadian abnormalities** Whole blood[141] (I) **BP** Lymphocyte[197]	2	**Yes** [198]
TCF7L2 transcription factor 7-like 2 (T-cell specific, HMG-box)	212762_s_at	**(I)** DE1	**6**	0.0280		**SZ** [199 200] **BP** [201] **Autistic Spectrum Disorder**	(I) **SZ** PFC [203] hippocampus	**(D) BP** Blood[204]	8	**Yes** [205, 206, 207,208 ,209, 210]

						[202]	**Alc** HIP [71]			
TGOLN2 trans-golgi network protein 2	203834_s_at	**(D)** AP1	**6**	1.10E-07			(D) **BP** brain [70] (I) **MDD** AMY and cingulate cortex [82] **SZ** PFC (left dorsolateral) [211]	(D) **Stress** Blood[167] **SZ** Blood[212] (I) **Relaxation Response** Blood[175]	6	–
TRAK2 trafficking protein, kinesin binding 2	202124_s_at	**(D)** DE2	**6**	0.006			(I) **BP** APC [213]		4	–
ADRBK1 adrenergic, beta, receptor kinase 1	201401_s_at	**(D)** DE1	**5**	2.22E-05			(D) **SZ** DLPFC (Brodmann area 9/46) supragenual (BA24) anterior cingulated cortex [214 215]	(D) **MDD** Blood [216] **Pain** vertebral disc [155]	6	–
AHCYL2 adenosylhomocysteinase-like 2	212814_at	**(D)** AP1	**5**	0.00103		**Autistic Spectrum Disorder**[217]			2	–
AIMP1 aminoacyl tRNA synthetase complex-interacting multifunctional protein 1	227605_at 202542_s_at 235594_at	**(D)** AP1 DE2	**5**	8.37E-05 0.0138 0.0301					0	
ATP6V0E1 ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1	236527_at	**(D)** AP1	**5**	3.80E-07		**BP**[218]	(D) **MDD** ACC, DLPFC [219] (I) **BP** ACC, DLPFC [219]	(D) **Alcohol** Blood[154] **Stress** Blood[167]	6	–
BRAF v-raf murine sarcoma viral	236402_at	**(I)** DE1	**5**	6.07E-29			(D) **SZ, BP**		4	–

oncogene homolog B							Frontal cortex [220]			
BRCC3 BRCA1/BRCA2-containing complex, subunit 3	216521_s_at	**(D)** DE1	**5**	5.79E-08			(D) **BP** Brain [70]	(D) **Circadian abnormalities** Blood[141]	6	–
C1orf61	205103_at	**(I)** DE1	**5**	2.95E-13				(D) **SZ** IPSC [84]	2	–
CALR calreticulin	212953_x_at	**(I)** DE1	**5**	6.20E-06		**SZA** [221]	(D) **MDD** DLPFC [222]	(I) **Pain** Vertebral disc [155] (D) **Relaxation Response** Blood [175]	8	–
CAMK2B calcium/calmodulin-dependent protein kinase II beta	209956_s_at	**(I)** DE1	**5**	0.00025			(I) **BP** Frontal DLPFC Broadmann Area 9 [223 224] **SZ** Frontal cortex [223] (D) **BP** Brain[70] **Cocaine, Cannabis, PCP abuse** Anterior PFC [225] **SZ** Suprage nual ACC [215]		4	–
CAV1 caveolin 1, caveolae protein, 22kDa	212097_at	**(I)** DE1	**5**	7.31E-07		**SZ** [188] **Alzheimer's Disease**[226]	DLPFC (BA46) (D) [227] (BP)		6	**Yes** [228]
<u>CHD2</u> chromodomain helicase DNA	1554014_at	**(I)** DE1	**5**	2.40E-24		**Autistic Spectrum Disorder**	(I) **BP** Brain[70]	(D) Mood **Blood**[165]	8	–

binding protein 2						[202]		**SZ** Blood [229] **MDD** Fibroblast [146]		
CLTA clathrin, light chain A	1560434_x_at	**(I)** DE1	**5**	0.00064			(D) **BP** Brain [70]	(D) **Alzheimer's Disease** Blood [230]	6	–
CNP 2',3'-cyclic nucleotide 3' phosphodiesterase	1557943_at	**(D)** AP1	**5**	0.0315		**SZ** [231]	(D) **SZ** PFC [232] [231] [233] **Addictions, Alcohol** Frontal cortex [56] [189] Occipital cortex [234] **MDD** Middle temporal gyrus corresponding to Brodmann's area 21 (BA21) [235] AMY [236]	(D) **Circadian abnormalities** Blood [141]	8	–
COL9A2 collagen, type IX, alpha 2	232542_at	**(D)** DE1	**5**	0.00044					0	**Yes** [237]
CPSF2 cleavage and polyadenylation specific factor 2, 100kDa	233208_x_at	**(D)** AP1	**5**	0.00171					0	–
CREM cAMP responsive element modulator	241740_at	**(I)** AP1	**5**	1.08E-06		**Panic Disorder** [238] [239]	(I) **MDD** AMY and cingulate cortex		6	–

							[82] (D) **Addictions, Alcohol** Frontal, motor cortex [171]			
CTTN cortactin	214782_at 201059_at	**(I)** DE1	**5**	3.46E-18 0.0363			(D) **MDD** AMY and cingulate cortex [82]	(I) **Mood Stabilizers** NT2.D1 cells [240] (D) **Stress, Social Isolation** Blood[73]	6	_
CUL4B cullin 4B	210257_x_at	**(D)** DE1	**5**	0.00776					0	_
DAAM2 dishevelled associated activator of morphogenesis 2	212793_at	**(I)** DE1	**5**	0.00856		**SZ** [241]	(I) **SZ** Superior temorpal gyrus [242] **Addictions, Alcohol** PFC l [186] **MDD** AMY [243]	(I) **SZ** Blood[244] [229] (D) **PTSD** Blood [245]	8	_
DAB2 Dab, mitogen-responsive phosphoprotein, homolog 2 (Drosophila)	201279_s_at	**(I)** DE1	**5**	0.00098				(I) **Delusions** Blood [55]	2	_
DLL1 delta-like 1 (Drosophila)	227938_s_at	**(D)** DE1	**5**	0.00016			(I) **BP** Brain[70]	(D) **SZ** iPSC [84] **PTSD** PBMC [246]	6	**Yes** [247]
DNAH2 dynein, axonemal, heavy chain 2	215840_at	**(D)** DE1	**5**	0.00637				(D) **Autistic Spectrum Disorder** Blood [248]	2	_
DPP4 dipeptidyl-	211478_s_at	**(D)**	**5**	1.43E-		**SZ**		(D)	4	_

peptidase 4		DE4		07		[249]		**PTSD** Blood [169] (I) **SZ** Blood [204]		
G2E3 G2/M-phase specific E3 ubiquitin protein ligase	223254_s_at	**(D)** AP1	**5**	0.0214					0	
GABARAPL1 GABA(A) receptor-associated protein like 1	208869_s_at	**(I)** DE1	**5**	3.48E-28			(D) **BP** Brain[70]	(D) **Panic Disorder** Lymphocyte [145]	6	**Yes** [250]
GLUL glutamate-ammonia ligase	215001_s_at	**(I)** DE1	**5**	3.96E-15			(I) **SZ** Thalamus [251] **BP** Anterior cingulate cortex, DLPFC [219] **SZ** DLPFC (BA 46) [252] **BP** DLPFC (BA 46) [252] (D) **MDD** DLPFC [253] Locus coeruleus (LC)forebrain [254] DLPFC [162] Anterior cingulate cortex, DLPFC	(I) **Circadian abnormalities** Blood [141] **Mood stabilizers** Blood [257] **BP** Blood [144]	6	–

							[219] **SZ** DLPFC [255] PFC gray matter [256]			
GUK1 guanylate kinase 1	200075_s_at	**(D)** DE1	**5**	0.0362				(I) **MDD** Plasma [258] **SZ** Blood[212]	2	–
HELZ helicase with zinc finger	240486_at	**(I)** DE1	**5**	3.56E-06					0	–
IGHG1 immunoglobulin heavy constant gamma 1 (G1m marker)	241074_at	**(I)** DE1	**5**	0.0342			(I) **SZ** APC [213] **BP** APC [213] (D) **SZA** APC [213]	(I) **Hallucinations Blood** [55] (D) **Mood Blood**[165] **Autistic Spectrum Disorder** Lymphocyte[57] **Stress, Social Isolation** Blood[73]	6	–
IL1B interleukin 1, beta	205067_at 39402_at	**(I)** DE1	**5**	0.0338 0.0380		**BP** [259] [260] **SZ** [261] **Addictions, Alcohol** [262] **MDD** [263] [264] **Anxiety** [263] **Stress** [89] [90]	(I) **Alzheimer's Disease** Hippocampal cornu ammonis 1 (CA1) [265] **BP** Frontal cortex [266] **SZ** DLPFC (BA46) [92]	(I) **BP** Blood [93] [94] **SZ** Plasma [268] Serum [113] [115] Blood[269] [270] CSF [271] **MDD** Blood [272] Plasma [107]	8	–

							Tourette Syndrome Putamen [170] (D) **MDD** DLPFC [267]	Serum [273] **PTSD** Serum [274] PBMC [127] **Autistic Spectrum Disorder** Blood [275] **Stress, Social Isolation** Leukocytes[73] **Psychosis** Serum [121] **Antipsychotics** Serum[122] **Anxiety** Plasma [107] (D) **Borderline Personality Disorder** Blood[124] **Stress** Blood[124]		
JAK3 Janus kinase 3	211108_s_at	**(D)** DE1	**5**	5.42E-11					0	–
JUN jun proto-oncogene	201464_x_at 213281_at 201466_s_at	**(I)** DE1 AP1	**5**	2.63E-51 1.02E-41 2.21E-08			(I) **SZ** cerebellar vermis [276] middle temporal gyrus [277] thalamus [236] **MDD** middle temporal gyrus [235] AMY [236]	(I) **Pain** Vertebral disc [155] **SZ** Fibroblasts [278] (D) **SZ** blood [278]	6	–

JUNB jun B proto-oncogene	201473_at	**(I)** DE1	**5**	1.09E-18			(I) **MDD** PFC [279] **Addictions, Alcohol** PFC [186]	(I) **SZ** Blood[244] **Pain** Blood [280]	6	–
LAPTM4B lysosomal protein transmembrane 4 beta	1554679_a_at	**(D)** AP1	**5**	0.0113			(D) **BP** Brain [70]	(D) **Mood Blood**[165] **PTSD** Blood[169]	6	–
LHFP lipoma HMGIC fusion partner	218656_s_at	**(I)** DE1	**5**	1.27E-06		**SZ** [281]			2	–
LPAR1 lysophosphatidic acid receptor 1	204036_at	**(D)** AP1	**5**	7.67E-06		**BP** [148] **SZ** [148]	(I) **BP** Parietal cortex [282] Anterior cingulate cortex [182] (D) **MDD** Middle temporal gyrus corresponding to Brodmann's area 21 (BA21) [235] AMY [236] Anterior cingulate cortex [182]	(I) **Mood Blood**[165] (D) **SZ** Lymphocytes [283]	8	–
MAGI3 membrane associated guanylate kinase, WW and PDZ	226770_at	**(D)** AP1	**5**	0.0292					0	–

domain containing 3										
MARCKS myristoylated alanine-rich protein kinase C substrate	213002_at 201670_s_at	**(I)** DE1	**5**	1.51E-06 0.0004			(I) **MDD** PFC [284] **SZ** DLPFC (left hemisphere, Broadman area 46) [285] **SZ** DLPFC Broadmann Area 9 [224] (D) **BP** Brain [70] **SZ** DLPFC (Brodmann areas 9/46) [286]	(D) **MDD** Blood [287]	6	–
MBP myelin basic protein	225408_at	**(D)** AP1	**5**	6.74E-10		**SZ** [288] [148] **BP** [79] [148]	(D) **BP** Hippocampus [289] APC [213] **SZ** Hippocampal formation [289] PFC (BA-9) (D) [290] Primary Visual Cortex [291] **Alzheimer's Disease** Frontal white	(D) **SZ** blood [212] (I) **Mood Blood**[165] **Pain** Vertebral disc [155]	8	

							matter [292] **MDD** AMY [236] DLPFC BA9 [224]			
MCRS1 microspherule protein 1	202556_s_at	**(D)** DE1	**5**	3.29E-05			(I) **MDD** Pituitary [293]		4	**Yes** [294]
MEF2C myocyte enhancer factor 2C	207968_s_at	**(D)** DE1	**5**	3.47E-09		**SZ**[249] **BP**[80]	(D) **BP** Brain [70]	(D) **Chronic Stress** Blood[167] (I) **PTSD** Blood [169]	8	–
MT1E metallothionein 1E	212859_x_at	**(I)** DE1	**5**	0.00020			(I) **BP** Brain [70] **SZ** DLPFC [295] (D) **SZ** Frontal cortex [296]		4	**Yes** [297]
MT1H metallothionein 1H	206461_x_at	**(I)** DE1	**5**	5.62E-05			(I) **BP** Brain [70] **SZ** DLPFC [295] (D) **MDD** AMY and cingulate cortex [82]	(I) **Mood Stabilizers** NT2.D1 cells [240]	5	–
MT2A metallothionein 2A	212185_x_at	**(I)** DE1	**5**	0.00218			(I) **BP** Brain [70] **SZ** Middle tempora		4	**Yes** [300, 301, 302]

							l gyrus [277] DLPFC [298 295] Thalamus [299] **Addictions, Alcohol** Hippocampus [71] (D) **MDD** AMY and cingulate cortex [82]			
NDRG1 N-myc downstream regulated 1	200632_s_at	**(I)** DE1	**5**	3.21E-22			(I) **SZ** APC [213]		4	–
NUCB2 nucleobindin 2	229838_at	**(I)** DE1	**5**	0.0124					0	**Yes** [303]
OGFR opioid growth factor receptor	211513_s_at	**(D)** DE1	**5**	0.00053					0	**Yes** [304, 305]
PCDH9 protocadherin 9	238919_at	**(D)** AP1	**5**	0.0215				(D) **Hallucinations Blood** [55]	2	–
PHF20L1 PHD finger protein 20-like 1	219606_at	**(I)** DE1	**5**	7.97E-05			(I) **SZ** PFC [203] (D) **BP** Brain [70]		4	**Yes** [306]
PLEKHB1 pleckstrin homology domain containing, family B (evectins) member 1	209504_s_at	**(D)** DE1	**5**	6.07E-07				(D) **Alcohol** Blood [154] **SZ** IPSC [84]	2	–
POLR2D polymerase (RNA) II (DNA directed) polypeptide D	214144_at	**(D)** AP1	**5**	1.02E-09			(D) **BP** Brain [70]		4	–
PRKACA protein kinase, cAMP-dependent, catalytic, alpha	202801_at	**(D)** AP1	**5**	0.0324			(D) **SZ** DLPFC [157]	(D) **MDD** CSF [58]	6	–

							BP Brain [70]			
PRKCB protein kinase C, beta	227824_at 230437_s_at	**(D)** DE1 AP1	**5**	3.15E-09 1.34E-04 0.003		**MDD** [307] **Autistic Spectrum Disorder** [308] [309]	(D) **BP** Anterior cingulate cortex [182] **Autistic Spectrum Disorder** Temporal neocortex [308] (I) **MDD** Anterior cingulate cortex [182] **SZ** DLPFC (left hemisphere, Broadman area 46) [285]	(D) **Chronic Stress** Blood[167] **BP** Blood [310] **PTSD** Blood [311] (I) **SZ** Blood [312]	8	**Yes** [313]
PSMB4 proteasome (prosome, macropain) subunit, beta type, 4	202243_s_at	**(D)** DE1	**5**	9.98E-07		**MDD** [314] [315]	(D) **SZ** DLPFC [316] (D) **SZA** DLPFC [316] (D) **BP** Brain[70] (I) **MDD** AMY and cingulate cortex [82]		6	–
PTEN phosphatase and tensin homolog	204053_x_at 222176_at	**(I)** DE1	**5**	7.66E-17 0.0003			(I) **SZ** PFC [203]	(D) **PTSD** Blood [169]	6	–

RAB35 RAB35, member RAS oncogene family	205461_at	**(D)** DE2	**5**	0.00034			(D) **BP** Brain[70]		4	–
RBMX RNA binding motif protein, X-linked	1556336_at 213762_x_at	**(D)** DE1	**5**	1.40E-13 0.0232					0	–
RECK reversion-inducing-cysteine-rich protein with kazal motifs	216153_x_at	**(I)** DE1	**5**	0.00093				(I) **PTSD** Blood[169]	2	**Yes**[317, 318, 319]
RNASEL ribonuclease L (2',5'-oligoisoadenylate synthetase-dependent)	221287_at	**(D)** AP1	**5**	6.05E-06			(D) **BP** Brain[70]	(I) **SZ** IPSC[84]	6	–
SELENBP1 selenium binding protein 1	214433_s_at	**(D)** DE1	**5**	0.00019		**Autistic Spectrum Disorder**[320] **SZ**[321]	(I) **SZ** Hippocampus[321] DLPFC[322]	(D) **SZ** Blood[244] (I) **Circadian abnormalities** Blood[141]	8	**Yes**[323]
SHISA2 shisa family member 2	230493_at	**(I)** DE1	**5**	0.00107					0	–
SLC35E1 solute carrier family 35, member E1	222263_at	**(D)** AP1	**5**	0.00651			(I) **MDD** AMY and cingulate cortex[82]		4	–
SNAP23 synaptosomal-associated protein, 23kDa	209131_s_at	**(D)** AP1	**5**	0.00039				(D) **BP** Blood[144] **Stress, Social Isolation** Leukocytes[73]	2	**Yes**[324]
TM4SF1 transmembrane 4 L six family member 1	209386_at	**(I)** DE1	**5**	6.12E-11				(D) **SZ** lymphocyte[59]	2	–
TMEM254 transmembrane protein 254	218174_s_at	**(D)** DE1	**5**	1.35E-08					0	–
TMEM259 transmembrane protein 259	212574_x_at 212575_at 213986_s_at	**(D)** DE1	**5**	0.0007 0.003				(D) **SZ** Blood	2	–

				0.004				[325] **PTSD** Blood [169] (I) **MDD** Leukocytes [326]		
TNS1 tensin 1	218863_s_at	**(D)** DE1 AP2	**5**	6.29E-05 0.0123			(D) **MDD** AMY and cingulate cortex [82]	(D) **SZ** Blood[244] (I) **Circadian abnormalities** Blood[141]	6	**Yes**[327], [328]
TPBG trophoblast glycoprotein	203476_at	**(I)** DE1	**5**	6.66E-06			(D) **BP** Brain [70] **SZ** PFC [187]	(I) **Mood stabilizers** neuroblastoma VPA [282]	4	–
TPD52L1 tumor protein D52-like 1	203786_s_at	**(I)** DE1	**5**	1.52E-16				(I) **Mood Stabilizers** NT2.D1 cells [240]	1	–
TRIM23 tripartite motif containing 23	210995_s_at	**(D)** DE1	**5**	3.28E-14			(D) **BP** Brain [70] **BP** Orbitofrontal Cortex [329] **SZ** DLPFC [298]		4	**Yes** [330]
TSC22D3 TSC22 domain family, member 3	208763_s_at	**(I)** DE1	**5**	2.01E-05			(I) **Addictions, Alcohol** HIP [71]	(D) **Delusions Blood** [55] **MDD** Blood [106]	6	**Yes** [331]
TSPAN33 tetraspanin 33	225775_at	**(D)** AP1	**5**	0.00302					0	–
VMP1 vacuole	1569003_at	**(I)** DE1	**5**	0.00291					0	**Yes** [332]

membrane protein 1										
VPREB3 pre-B lymphocyte 3	220068_at	**(D)** DE1	**5**	0.00104					0	–
ZFP36 ZFP36 ring finger protein	201531_at	**(I)** DE1	**5**	8.72E-27			(I) **MDD** DLPFC [162]	(I) **Pain** Blood [280]	6	–
ZFYVE21 zinc finger, FYVE domain containing 21	219929_s_at	**(D)** AP1	**5**	1.69E-04		**SZ** [249]			2	–
ZHX2 zinc fingers and homeoboxes 2	203556_at	**(I)** DE1	**5**	0.00198				(I) **BP** lymphocyte [59]	2	[333]
ZNF519 zinc finger protein 519	1568873_at	**(D)** AP1	**5**	0.01164				(I) **Autistic Spectrum Disorder** Blood [248]	2	**Yes** [334]
B4GALT1 UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1	228498_at	**(I)** DE 4	4	NC			(D) **Addictions** [335] NAC	(I) **Mood Stabilizers** NT2.D1 cells [240]	3	-
BTBD3 BTB (POZ) domain containing 3	243461_at	**(I)** DE 4	4	NC		**OCD** [336]			2	**Yes** [337]
CADM1 cell adhesion molecule 1	237259_at	**(I)** DE4	**4**	NC		**Autistic Spectrum Disorder** [338]	(I) **BP** brain [70] (D) **BP** APC [213]	(D) **Mood** Blood [165] **MDD** blood [287]	8	–
CATSPER3 cation channel, sperm associated 3	230981_at	**(D)** AP4	4	NC					0	-
CCL28 chemokine (C-C motif) ligand 28	224240_s_at	**(D)** AP4	4	NC				(D) **BP** blood [165] **Sleep Circadian abnormalities** blood [141] (I) **Anxiety SSRI** lymphoblastoid [339]	2	**Yes** [340 341]

CLIP4 CAP-GLY domain containing linker protein family, member 4	219944_at	**(D)** DE4	**4**	NC					0	_
CTBS chitobiase, di-N-acetyl-	218924_s_at	**(I)** DE 4	4	NC			(I) **MDD** PFC [162]		4	-
CYorf17 chromosome Y open reading frame 17	234274_at	**(D)** DE 4	4	NC					0	-
DCAF15 DDB1 and CUL4 associated factor 15	221851_at	**(D)** DE4	**4**	0.0302			(I) **Addictions, Alcohol** HIP [71]		4	_
DEPDC5 DEP domain containing 5	234548_at	**(I)** AP4	4	NC			(D) **BP** PFC [70] (I) **BP** PFC [342]		4	-
DTNA dystrobrevin, alpha	211493_x_at	**(I)** AP4	**4**	NC		**BP** [80]	(I) **BP** PFC [342] (D) **MDD** AMY and cingulate cortex [82] **Tourette Syndrome** putamen [170]		6	_
EMR2 egf-like module containing, mucin-like, hormone receptor-like 2	232009_at	**(I)** DE 4	**4**	NC				(D) **Chronic stress** blood [167]	2	**Yes** [343]
EPHA10 EPH receptor A10	243717_at	**(D)** DE4	**4**	0.00801					0	_
ERG v-ets avian erythroblastosis virus E26	213541_s_at	**(D)** DE 4	4	NC		**Addictions** [344]			1	-

oncogene homolog										
ERV3-2 endogenous retrovirus group 3, member 2	222139_at	**(I)** DE 4	4	NC				(I) **SZ** blood [229]	2	-
FAM183CP family with sequence similarity 183, member C, pseudogene	1569887_a_at	**(I)** AP4	**4**	NC					0	-
HIST1H2BO histone cluster 1, H2bo	214540_at	**(I)** DE4	**4**	4.77E-10				(I) **Relaxation Response** Blood[175]	2	_
HS3ST3B1 heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	1561908_a_at	**(D)** AP4	**4**	NC		**Aging Longevity** [345]		(I) **SZ** fibroblasts [84]	4	-
IQCH IQ motif containing H	224165_s_at	**(D)** DE4	**4**	0.00324				(D) **Delusions Blood** [55]	2	_
KCTD21 potassium channel tetramerization domain containing 21	229873_at	**(I)** DE 4	**4**	NC					0	-
KERA keratocan	220504_at	**(I)** DE4	**4**	0.00021					0	_
KIF2C kinesin family member 2C	211519_s_at	**(D)** AP4	**4**	0.00056					0	_
KLHDC3 kelch domain containing 3	214383_x_at	**(D)** DE4	**4**	1.57E-17			(D) **BP** brain [70]	(D) **BP** Lymphocyte [197]	6	_
LAMB1 laminin, beta 1	238608_at	**(I)** AP4	4	NC		**Personality Conscientiousness** [346]	(D) **Aging** PFC [347] **BP** PFC[70] (I) **Addictions** FC[189]	(I) **Hallucinations** blood [55]	6.00	-
LOC100129917 uncharacterized LOC100129917	236411_at	**(D)** DE4	**4**	0.00225					0	**Yes** [348]
LOC100289061 uncharacterized LOC100289061	1563071_at	**(I)** AP4	**4**	NC					0	-

LOC100996345 uncharacterized LOC100996345	240697_at	**(D)** DE4	**4**	7.20E-05					0	-
LOC285500 uncharacterized LOC285500	1558451_at	**(I)** DE 4	4	NC					0	-
MED21 mediator complex subunit 21	209363_s_at	**(D)** AP4	4	0.07426			(D) **BP** [70]		4	-
PCIF1 PDX1 C-terminal inhibiting factor 1	222045_s_at	**(D)** AP4	4	NC				(D) **MDD** Fibroblast [146]	2	**Yes** [349]
PLEC plectin	216971_s_at	**(D)** DE 4	4	NC				(D) **BP** blood [144]	2	**Yes** [350]
RAB36 RAB36, member RAS oncogene family	211471_s_at	**(I)** AP4	4	NC					0	-
RAD23A RAD23 homolog A (S. cerevisiae)	201039_s_at	**(D)** DE 4	**4**	NC			(I) **MDD** AMY and cingulate cortex [82]		4	**Yes** [351]
RHAG Rh-associated glycoprotein	206145_at	**(D)** AP4	**4**	NC				(I) **Delusions** blood [55]	2	-
ROBO4 roundabout, axon guidance receptor, homolog 4 (Drosophila)	220758_s_at	**(D)** AP4	**4**	NC					0	-
RP11-669N7.2 uncharacterized LOC283352	1561757_a_at	**(I)** AP4	**4**	NC					0	-
RPL6P17 ribosomal protein L6 pseudogene 17	216816_at	**(D)** AP4	**4**	NC					0	-
SETD8 SET domain containing (lysine methyltransferase) 8	220200_s_at	**(D)** DE 4	**4**	NC		**SZ** [249]		(D) **Mood** blood [165]	4	**Yes** [352 353]
SH3GLB2 SH3-domain GRB2-like endophilin B2	218813_s_at	**(D)** DE4	**4**	0.00017			(D) **BP** Brain[70]	(D) **BP** Blood [144]	6	–
ST6GALNAC4 ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-	221551_x_at	**(D)** DE4	**4**	3.22E-05					0	–

1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4										
TEX10 testis expressed 10	1558702_at	**(D)** AP4	**4**	0.00281					0	–
TEX261 testis expressed 261	1559675_at	**(D)** AP4	**4**	0.00427				(I) **Mood Blood**[165] (D) **Hallucinations Blood** [55]	2	–
TFDP1 transcription factor Dp-1	242538_at	**(I)** AP4	**4**	0.00238					0	–
TMLHE-AS1 TMLHE antisense RNA 1	1560797_s_at	**(I)** DE 4	**4**	NC					0	-
TMSB15B thymosin beta 15B	1556964_s_at	**(D)** DE4	**4**	0.007				(I) **MDD** Fibroblast [146]	2	–
TUBGCP3 tubulin, gamma complex associated protein 3	215739_s_at	**(D)** DE2	**4**	2.05E-16				(D) **BP** Blood [144]	2	–
TXNRD2 thioredoxin reductase 2	210803_at	**(D)** AP4	**4**	0.0425					0	**Yes** [354]
USP12 ubiquitin specific peptidase 12	229987_at	**(D)** AP4	**4**	0.2723				(I) **Sleep Circadian abnormalities** blood [141]	2	**Yes** [355]
VEGFB vascular endothelial growth factor B	203683_s_at	**(D)** AP4	**4**	5.13E-07					0	–
ZBTB7A zinc finger and BTB domain containing 7A	213299_at	**(D)** DE4	**4**	2.05E-06			(I) **MDD** AMY and cingulate cortex [82]		4	–

Table S4. Top candidate biomarker genes - drugs that modulate these markers in the opposite direction.

Gene symbol/ Gene Name	**Discovery** (Change) Method/ Score	**Prioritization** Total CFG Score For Suicide	**Validation** ANOVA p-value	Modulated by **Omega-3**	Modulated by **Lithium**	Modulated by **Clozapine**	**Other Drugs**
CCDC136 coiled-coil domain containing 136	**(D)** AP4	**8**	NC			**(I) Mouse VT** [356]	
CD44 CD44 molecule (Indian blood group)	**(D)** DE2	**8**	NC			**(I) Mouse Blood** [356]	
IL6 interleukin 6 (interferon, beta 2)	**(I)** AP2	**8**	1.44E-08	**(D) Human Blood** [357]			**tocilizumab siltuximab**
SAT1 spermidine/spermine N1-acetyltransferase 1	**(I)** DE2 DE1	**8**	1.08E-44	**(D) Mouse Blood**[358]			
MAOB monoamine oxidase B	**(I)** DE1	**7**	8.11E-08				**selegiline**
ARHGAP26 Rho GTPase activating protein 26	**(I)** DE1	**6**	9.91E-08			**(D) Mouse VT** [356]	
BCL2 B-cell CLL/lymphoma 2	**(D)** DE1	**6**	0.0003		**(I) Human Blood** [153]	**(I) Rat Dentate gyrus Hippocampus** [359]	
EHBP1 EH domain binding protein 1	**(D)** DE 4	**6**	NC			**(I) VT** [356]	
FAM49B family with sequence similarity 49, member B	**(I)** AP2	**6**	0.0188	**(D) Mouse Blood**[358]			
HPCAL1 hippocalcin-like 1	**(I)** DE2	**6**	7.50E-05			**(D) Mouse VT** [356]	
MAPK9 mitogen-activated protein kinase 9	**(I)** DE2	**6**	0.0132			**(D) Mouse VT** [356]	
NEAT1 nuclear paraspeckle assembly	**(I)** DE2	**6**	2.33E-24			**(D) Mouse VT** [356]	

transcript 1 (non-protein coding)							
RASL11B RAS-like, family 11, member B	**(I)** AP2	**6**	0.0124			**(D) Mouse Caudate putamen**[356]	
TRAK2 trafficking protein, kinesin binding 2	**(D)** DE2	**6**	0.006	**(I) Mouse Blood** [358]	**(I) Mouse PFC**[360]		
ADRBK1 adrenergic, beta, receptor kinase 1	**(D)** DE1	**5**	2.22E-05			**(I) Mouse PFC**[361]	
BRAF v-raf murine sarcoma viral oncogene homolog B	**(I)** DE1	**5**	6.07E-29				**Vemurafenib Dabrafenib**
CAMK2B calcium/calmodulin-dependent protein kinase II beta	**(I)** DE1	**5**	0.00025			**(D) Mouse striatum** [362]	
CNP 2',3'-cyclic nucleotide 3' phosphodiesterase	**(D)** AP1	**5**	0.0315	**(I) Mouse Hippocampus**[358]		**(I) Mouse** AMY [356]	
CTTN cortactin	**(I)** DE1	**5**	3.46E-18	**(D) Mouse Blood**[358]		**(D) Mouse VT** [356]	
G2E3 G2/M-phase specific E3 ubiquitin protein ligase	**(D)** AP1	**5**	0.0214	**(I) Mouse Hippocampus**[358]			
GABARAPL1 GABA(A) receptor-associated protein like 1	**(I)** DE1	**5**	3.48E-28	**(D) Mouse Blood**[358]			
HELZ helicase with zinc finger	**(I)** DE1	**5**	3.56E-06	**(D) Mouse Blood**[358]			
IL1B interleukin 1, beta	**(I)** DE1	**5**	0.0338	**(D) Mouse Blood**[358]			**canakinumab gevokizumab gallium nitrate**
LHFP lipoma HMGIC fusion partner	**(I)** DE1	**5**	1.27E-06	**(D) Mouse Blood**[358]			
LPAR1 lysophosphatidic acid receptor 1	**(D)** AP1	**5**	7.67E-06	**(I) Mouse Hippocampus,**		**(I) Mouse** AMY [356]	

				Blood[358]			
MBP myelin basic protein	**(D)** AP1	**5**	6.74E-10	**(I) Mouse Blood**[358]	**(I) Oligodendrocytes** [363] **Mouse Brain** [360]	**(I) Mouse** AMY **and Blood**[356]	
MEF2C myocyte enhancer factor 2C	**(D)** DE1	**5**	3.47E-09			**(I) Mouse Hippocampus and VT** [356]	
NDRG1 N-myc downstream regulated 1	**(I)** DE1	**5**	3.21E-22	**(D) Mouse Blood**[358]			
OGFR opioid growth factor receptor	**(D)** DE1	**5**	0.00053				**enkephalin methionine**
PCDH9 protocadherin 9	**(D)** AP1	**5**	0.0215			**(I) Mouse VT** [356]	
PHF20L1 PHD finger protein 20-like 1	**(I)** DE1	**5**	7.97E-05	**(D) Mouse Blood**[358]		**(D) Mouse Hippocampus** [356]	
PRKCB protein kinase C, beta	**(D)** DE1 AP1	**5**	3.15E-09		**(I) Mouse PFC**[360] AMY [364]		
RBMX RNA binding motif protein, X-linked	**(D)** DE1	**5**	1.40E-13	**(I) Mouse** NAC**, Blood**[358]			
RNASEL ribonuclease L (2',5'-oligoisoadenylate synthetase-dependent)	**(D)** AP1	**5**	6.05E-06	**(I) Mouse Blood**[358]			
SNAP23 synaptosomal-associated protein, 23kDa	**(D)** AP1	**5**	0.00039			**(I) Mouse Blood**[356]	
TM4SF1 transmembrane 4 L six family member 1	**(I)** DE1	**5**	6.12E-11	**(D) Mouse Blood**[358]			
TSPAN33 tetraspanin 33	**(D)** AP1	**5**	0.00302	**(I) Mouse Blood**[358]		**(I) Mouse VT** [356]	
VMP1 vacuole membrane protein 1	**(I)** DE1	**5**	0.00291	**(D) Mouse Blood**[358]			
ZFP36 ZFP36 ring finger	**(I)** DE1	**5**	8.72E-27	**(D) Mouse**	**(D) Rat**		

protein				**Blood**[358]	**Brain** [365]		
BTBD3 BTB (POZ) domain containing 3	**(I)** DE 4	**4**	NC	**(D) Mouse AMY** [358]			
CADM1 cell adhesion molecule 1	**(I)** DE4	**4**	NC			**(D) Mouse VT** [356]	
CTBS chitobiase, di-N-acetyl-	**(I)** DE 4	**4**	NC			**(D) VT** [356]	
LAMB1 laminin, beta 1	**(I)** AP4	**4**	NC	**(D) Mouse HIP** [358]			
PLEC plectin	**(D)** DE 4	**4**	NC			**(I) Mouse VT** [356]	
RAD23A RAD23 homolog A (S. cerevisiae)	**(D)** DE 4	**4**	NC	**(I) Mouse Blood** [358]			
SETD8 SET domain containing (lysine methyltransferase) 8	**(D)** DE 4	**4**	NC	**(I) Mouse Blood** [358]			
TXNRD2 thioredoxin reductase 2	**(D)** AP4	**4**	0.0425			**(I) Mouse Blood** [356]	

Table S5 Biomarker discovery within each diagnostic group. Within-participant design. N=37 for all, N= 15 for BP, N=7 for MDD, N= 6 for SZA, and N=4 for SZ

	Top Biomarkers Discovered, Prioritized and Validated by Diagnosis				
Gene Symbol/ Affymetrix Probeset ID	Top Biomarkers All diagnoses	Top Biomarkers Bipolar disorder (BP)	Top Biomarkers Depression (MDD)	Top Biomarkers Schizoaffective disorder (SZA)	Top Biomarkers Schizophrenia (SZ)
Top Discovery AP Increased	DTNA 211493_x_at	DTNA 211493_x_at	PHF20 210500_at	USP48 232621_at	RP11-389C8.2 1556314_a_at
Top Discovery AP Decreased	KIF2C 211519_s_at	HS3ST3B1 1561908_a_at	EIF1B-AS1 1557212_at	NPRL3 210672_s_at	CYB561 210816_s_at
Top Discovery DE Increased	CADM1 237259_at	CADM1 237259_at	TLN1 232763_at	TSPYL1, 1560648_s_at	LOC100128288 1559045_at
Top Discovery DE Decreased	CLIP4 219944_at	Unknown 231262_at	NUCKS1 222027_at	TMSB15B, 1556964_s_at MCM8, 231827_at	CCDC163P 1559003_a_at
Top Prioritization AP Increased	SLC4A4 210739_x_at	KSR1 213769_at	DLK1 209560_s_at	IL6 205207_at	C1orf61 205103_at
Top Prioritization AP Decreased	SKA2 225686_at	CD44 216056_at	BBIP1 232910_at	TNS1 218863_s_at	SKA2 225686_at
Top Prioritization DE Increased	SAT1 210592_s_at	DAPP1 219290_x_at	BDNF 239367_at	TNF 207113_s_at	BDNF 206382_s_at
Top Prioritization DE Decreased	SKA2 225686_at	OPRM1 207989_at	SKA2 225686_at	S100B 1561521_at	HTR2A 211616_s_at
Top Validation AP Increased	IL6 205207_at	SPTBN1 215918_s_at	IL10 207433_at	JUN 201466_s_at	SLC5A3 1553313_s_at
Top Validation AP Decreased	MBP 225408_at	AKT1S1 224982_at	EIF1B-AS1 1557212_at	BATF2 228439_at	ATP6V0E1 236527_at
Top Validation DE Increased	JUN 201464_x_at	SAT1 213988_s_at	GATM 1566861_at	JUN 201464_x_at	JUN 201464_x_at
Top Validation DE Decreased	KLHDC3 214383_x_at	C20orf27 218081_at	PRPF40A 226687_at	ANXA11 228727_at	LOC100131662 236973_at

Table S6 Biological Pathways and Diseases. Suicidal ideation markers non-validated for behavior in completers (n=208) vs. suicidal ideation markers that were validated for behavior in completers (n=204).

A.		**Ingenuity Pathways**			**KEGG Pathways**			**GeneGO Pathways**		
		Top Canonical Pathways	**P-Value**	**Ratio**	**Pathway Name**	**Enrichment Score**	**Enrichment p-value**	**Process Networks**	**Ratio**	**p-value**
Non-Validated in Completers Stepwise (n=208 genes)	1	G-Protein Coupled Receptor Signaling	2.28E-08	5.7% 15/264	Pathogenic Escherichia coli infection	7.19808	0.000748	Cytoskeleton_ **Regulation of cytoskeleton rearrangement**	16/183	5.75E-07
	2	cAMP-mediated signaling	1.51E-07	5.8% 13/223	Amoebiasis	5.51218	0.004037	Development_ **Neurogenesis_ Axonal guidance**	17/230	2.65E-06
	3	CREB Signaling in Neurons	6.20E-06	5.6% 10/179	Dorso-ventral axis formation	4.7856	0.008349	Development_ **Hedgehog signaling**	17/254	1.01E-05
	4	Cardiac Hypertrophy Signaling	1.02E-05	4.7% 11/232	Melanogenesis	4.31121	0.013417	Reproduction_ Progesterone signaling	14/214	8.25E-05
	5	Synaptic Long Term Potentiation	2.26E-05	6.3% 8/127	Influenza A	4.23564	0.014471	Cardiac development_ Wnt_beta-catenin, Notch, VEGF, IP3 and integrin signaling	11/150	0.0001819
		Top Canonical Pathways	**P-Value**	**Ratio**	**Pathway Name**	**Enrichment Score**	**Enrichment p-value**	**Process Networks**	**Ratio**	**p-value**
Validated in Completers Stepwise (n=204 genes)	1	B Cell Receptor Signaling	1.01 E-08	7.2 % 13/ 181	Focal adhesion	10.5307	2.67E-05	Signal transduction_ **WNT signaling**	19/177	8.10E-10
	2	Ovarian Cancer Signaling	3.31 E-08	8.3 % 11/133	Colorectal cancer	10.3054	3.35E-05	Cell cycle_ **G1-S Growth factor regulation**	18/195	2.62E-08
	3	Glucocorticoid Receptor Signaling	3.97 E-08	5.3 % 15/281	GABAergic synapse	8.60276	0.000184	Reproduction_ **Gonadotropin regulation**	18/199	3.60E-08
	4	Colorectal Cancer Metastasis Signaling	4.00 E-08	5.8 % 14/241	mTOR signaling pathway	8.47678	0.000208	Reproduction_ GnRH signaling pathway	16/166	9.05E-08
	5	G12/13 Signaling	1.12 E-07	8.5 % 10/118	Chagas disease (American trypanosomiasis)	7.66796	0.000468	Neurophysiological process_ Transmission of nerve impulse	18/212	9.58E-08

B.	**Ingenuity**				**GeneGO**		
		Diseases and Disorders	**P-Value**	**# Molecules**	**Diseases**	**pValue**	**Ratio**
Non- Validated in Completers Stepwise (n=208 genes)	1	Neurological disease	5.43E-04 - 8.63E-13	78	Psychiatry and Psychology	1.6E-30	85/1919
	2	Psychological Disorders	1.77E-04 - 2.04E-12	62	Mental Disorders	2.82E-30	78/1614
	3	Skeletal and Muscular Disorders	1.98E-04 - 5.33E-10	60	**Schizophrenia**	3.6E-22	51/914
	4	Organismal Injury and Abnormalities	6.69E-04 - 1.81E-09	184	**Schizophrenia and Disorders with Psychotic Features**	4.37E-22	51/918
	5	Cancer	6.32E-04 - 2.59E-09	182	**Central Nervous System Diseases**	5.41E-22	94/3069
		Diseases and Disorders	**P-Value**	**# Molecules**	**Diseases**	**pValue**	**Ratio**
Validated in Completers Stepwise (n=204 genes)	1	Organismal Injury and Abnormalitie	s 2.11E-04 - 1.23E-13	178	Psychiatry and Psychology	1.77E-23	76/1919
	2	Cancer	2.20E-04 - 5.41E-13	176	Mental Disorders	1.23E-21	67/1614
	3	Neurological Disease	1.31E-04 - 1.07E-12	81	**Mood Disorders**	4.02E-21	47/797
	4	Psychological Disorders	1.31E-04 - 1.07E-12	63	**Depressive Disorder, Major**	1.06E-18	37/546
	5	Tumor Morphology	1.87E-04 - 1.83E-12	38	**Depressive Disorder**	2.44E-18	37/560

Literature Cited

1. Le-Niculescu H, Levey DF, Ayalew M, Palmer L, Gavrin LM, Jain N *et al.* Discovery and validation of blood biomarkers for suicidality. *Mol Psychiatry* 2013; **18**(12)**:** 1249-1264.

2. Guintivano J, Brown T, Newcomer A, Jones M, Cox O, Maher BS *et al.* Identification and replication of a combined epigenetic and genetic biomarker predicting suicide and suicidal behaviors. *Am J Psychiatry* 2014; **171**(12)**:** 1287-1296.

3. Labonte B, Suderman M, Maussion G, Lopez JP, Navarro-Sanchez L, Yerko V *et al.* Genome-wide methylation changes in the brains of suicide completers. *Am J Psychiatry* 2013; **170**(5)**:** 511-520.

4. Galfalvy H, Zalsman G, Huang YY, Murphy L, Rosoklija G, Dwork AJ *et al.* A pilot genome wide association and gene expression array study of suicide with and without major depression. *World J Biol Psychiatry* 2013; **14**(8)**:** 574-582.

5. Mann JJ, Gibbons RD. Guns and suicide. *Am J Psychiatry* 2013; **170**(9)**:** 939-941.

6. Perroud N, Bondolfi G, Uher R, Gex-Fabry M, Aubry JM, Bertschy G *et al.* Clinical and genetic correlates of suicidal ideation during antidepressant treatment in a depressed outpatient sample. *Pharmacogenomics* 2011; **12**(3)**:** 365-377.

7. Willour VL, Chen H, Toolan J, Belmonte P, Cutler DJ, Goes FS *et al.* Family-based association of FKBP5 in bipolar disorder. *Mol Psychiatry* 2009; **14**(3)**:** 261-268.

8. Roy A, Hodgkinson CA, Deluca V, Goldman D, Enoch MA. Two HPA axis genes, CRHBP and FKBP5, interact with childhood trauma to increase the risk for suicidal behavior. *J Psychiatr Res* 2012; **46**(1)**:** 72-79.

9. Roy A, Gorodetsky E, Yuan Q, Goldman D, Enoch MA. Interaction of FKBP5, a stress-related gene, with childhood trauma increases the risk for attempting suicide. *Neuropsychopharmacology* 2010; **35**(8)**:** 1674-1683.

10. Supriyanto I, Sasada T, Fukutake M, Asano M, Ueno Y, Nagasaki Y *et al.* Association of FKBP5 gene haplotypes with completed suicide in the Japanese population. *Prog Neuropsychopharmacol Biol Psychiatry* 2011; **35**(1)**:** 252-256.

11. Perez-Ortiz JM, Garcia-Gutierrez MS, Navarrete F, Giner S, Manzanares J. Gene and protein alterations of FKBP5 and glucocorticoid receptor in the amygdala of suicide victims. *Psychoneuroendocrinology* 2013; **38**(8)**:** 1251-1258.

12. Galfalvy H, Zalsman G, Huang YY, Murphy L, Rosoklija G, Dwork AJ *et al.* A pilot genome wide association and gene expression array study of suicide with and without major depression. *World J Biol Psychiatry* 2013; **14**(8)**:** 574-582.

13. Pandey GN, Rizavi HS, Ren X, Fareed J, Hoppensteadt DA, Roberts RC *et al.* Proinflammatory cytokines in the prefrontal cortex of teenage suicide victims. *J Psychiatr Res* 2012; **46**(1)**:** 57-63.

14. Hoyo-Becerra C, Huebener A, Trippler M, Lutterbeck M, Liu ZJ, Truebner K *et al.* Concomitant interferon alpha stimulation and TLR3 activation induces neuronal expression of depression-related genes that are elevated in the brain of suicidal persons. *PLoS One* 2013; **8**(12)**:** e83149.

15. Lindqvist D, Janelidze S, Erhardt S, Traskman-Bendz L, Engstrom G, Brundin L. CSF biomarkers in suicide attempters--a principal component analysis. *Acta Psychiatr Scand* 2011; **124**(1)**:** 52-61.

16. Bay-Richter C, Linderholm KR, Lim CK, Samuelsson M, Traskman-Bendz L, Guillemin GJ *et al.* A role for inflammatory metabolites as modulators of the glutamate N-methyl-D-aspartate receptor in depression and suicidality. *Brain Behav Immun* 2015; **43:** 110-117.

17. Kim YK, Lee SW, Kim SH, Shim SH, Han SW, Choi SH *et al.* Differences in cytokines between non-suicidal patients and suicidal patients in major depression. *Prog Neuropsychopharmacol Biol Psychiatry* 2008; **32**(2)**:** 356-361.

18. Fiori LM, Wanner B, Jomphe V, Croteau J, Vitaro F, Tremblay RE *et al.* Association of polyaminergic loci with anxiety, mood disorders, and attempted suicide. *PLoS One* 2010; **5**(11)**:** e15146.

19. Sokolowski M, Ben-Efraim YJ, Wasserman J, Wasserman D. Glutamatergic GRIN2B and polyaminergic ODC1 genes in suicide attempts: associations and gene-environment interactions with childhood/adolescent physical assault. *Mol Psychiatry* 2013; **18**(9)**:** 985-992.

20. Klempan TA, Sequeira A, Canetti L, Lalovic A, Ernst C, ffrench-Mullen J *et al.* Altered expression of genes involved in ATP biosynthesis and GABAergic neurotransmission in the ventral prefrontal cortex of suicides with and without major depression. *Mol Psychiatry* 2009; **14**(2)**:** 175-189.

21. Perlis RH, Huang J, Purcell S, Fava M, Rush AJ, Sullivan PF *et al.* Genome-wide association study of suicide attempts in mood disorder patients. *Am J Psychiatry* 2010; **167**(12)**:** 1499-1507.

22. Kim S, Choi KH, Baykiz AF, Gershenfeld HK. Suicide candidate genes associated with bipolar disorder and schizophrenia: An exploratory gene expression profiling analysis of post-mortem prefrontal cortex. *BMC genomics* 2007; **8**(1)**:** 413.

23. Ballesteros J, Maeztu AI, Callado LF, Meana JJ, Gutierrez M. Specific binding of [3H]Ro 19-6327 (lazabemide) to monoamine oxidase B is increased in frontal cortex of suicide victims after controlling for age at death. *European neuropsychopharmacology : the journal of the European College of Neuropsychopharmacology* 2008; **18**(1)**:** 55-61.

24. Roggenbach J, Muller-Oerlinghausen B, Franke L, Uebelhack R, Blank S, Ahrens B. Peripheral serotonergic markers in acutely suicidal patients. 1. Comparison of serotonergic platelet measures between suicidal individuals, nonsuicidal patients with major depression and healthy subjects. *J Neural Transm* 2007; **114**(4)**:** 479-487.

25. Fiori LM, Bureau A, Labbe A, Croteau J, Noel S, Merette C *et al.* Global gene expression profiling of the polyamine system in suicide completers. *Int J Neuropsychopharmacol* 2011; **14**(5)**:** 595-605.

26. Zubenko GS, Maher BS, Hughes HB, 3rd, Zubenko WN, Scott Stiffler J, Marazita ML. Genome-wide linkage survey for genetic loci that affect the risk of suicide attempts in families with recurrent, early-onset, major depression. *Am J Med Genet B Neuropsychiatr Genet* 2004; **129B**(1)**:** 47-54.

27. Sequeira A, Morgan L, Walsh DM, Cartagena PM, Choudary P, Li J *et al.* Gene expression changes in the prefrontal cortex, anterior cingulate cortex and nucleus accumbens of mood disorders subjects that committed suicide. *PLoS One* 2012; **7**(4)**:** e35367.

28. Smalheiser NR, Lugli G, Rizavi HS, Torvik VI, Turecki G, Dwivedi Y. MicroRNA expression is down-regulated and reorganized in prefrontal cortex of depressed suicide subjects. *PLoS One* 2012; **7**(3)**:** e33201.

29. Kekesi KA, Juhasz G, Simor A, Gulyassy P, Szego EM, Hunyadi-Gulyas E *et al.* Altered functional protein networks in the prefrontal cortex and amygdala of victims of suicide. *PLoS One* 2012; **7**(12)**:** e50532.

30. Sequeira A, Gwadry FG, Ffrench-Mullen JM, Canetti L, Gingras Y, Casero RA, Jr. *et al.* Implication of SSAT by gene expression and genetic variation in suicide and major depression. *Arch Gen Psychiatry* 2006; **63**(1)**:** 35-48.

31. Dick DM, Meyers J, Aliev F, Nurnberger J, Jr., Kramer J, Kuperman S *et al.* Evidence for genes on chromosome 2 contributing to alcohol dependence with conduct disorder and suicide attempts. *Am J Med Genet B Neuropsychiatr Genet* 2010; **153B**(6)**:** 1179-1188.

32. Kim S, Choi KH, Baykiz AF, Gershenfeld HK. Suicide candidate genes associated with bipolar disorder and schizophrenia: an exploratory gene expression profiling analysis of post-mortem prefrontal cortex. *BMC genomics* 2007; **8:** 413.

33. Fiori LM, Zouk H, Himmelman C, Turecki G. X chromosome and suicide. *Mol Psychiatry* 2011; **16**(2)**:** 216-226.

34. Dwivedi Y, Rizavi HS, Teppen T, Sasaki N, Chen H, Zhang H *et al.* Aberrant extracellular signal-regulated kinase (ERK) 5 signaling in hippocampus of suicide subjects. *Neuropsychopharmacology* 2007; **32**(11)**:** 2338-2350.

35. Choi K, Le T, Xing G, Johnson LR, Ursano RJ. Analysis of kinase gene expression in the frontal cortex of suicide victims: implications of fear and stress. *Front Behav Neurosci* 2011; **5:** 46.

36. Merali Z, Kent P, Du L, Hrdina P, Palkovits M, Faludi G *et al.* Corticotropin-releasing hormone, arginine vasopressin, gastrin-releasing peptide, and neuromedin B alterations in stress-relevant brain regions of suicides and control subjects. *Biol Psychiatry* 2006; **59**(7)**:** 594-602.

37. Lalovic A, Klempan T, Sequeira A, Luheshi G, Turecki G. Altered expression of lipid metabolism and immune response genes in the frontal cortex of suicide completers. *J Affect Disord* 2010; **120**(1-3)**:** 24-31.

38. Zhurov V, Stead JD, Merali Z, Palkovits M, Faludi G, Schild-Poulter C *et al.* Molecular pathway reconstruction and analysis of disturbed gene expression in depressed individuals who died by suicide. *PLoS One* 2012; **7**(10)**:** e47581.

39. Schlicht K, Buttner A, Siedler F, Scheffer B, Zill P, Eisenmenger W *et al.* Comparative proteomic analysis with postmortem prefrontal cortex tissues of suicide victims versus controls. *J Psychiatr Res* 2007; **41**(6)**:** 493-501.

40. Butler AW, Breen G, Tozzi F, Craddock N, Gill M, Korszun A *et al.* A genomewide linkage study on suicidality in major depressive disorder confirms evidence for linkage to 2p12. *Am J Med Genet B Neuropsychiatr Genet* 2010; **153B**(8)**:** 1465-1473.

41. Willour VL, Zandi PP, Badner JA, Steele J, Miao K, Lopez V *et al.* Attempted suicide in bipolar disorder pedigrees: evidence for linkage to 2p12. *Biol Psychiatry* 2007; **61**(5)**:** 725-727.

42. Garcia-Sevilla JA, Escriba PV, Ozaita A, La Harpe R, Walzer C, Eytan A *et al.* Up-regulation of immunolabeled alpha2A-adrenoceptors, Gi coupling proteins, and regulatory receptor kinases in the prefrontal cortex of depressed suicides. *Journal of neurochemistry* 1999; **72**(1)**:** 282-291.

43. Dwivedi Y, Rizavi HS, Conley RR, Pandey GN. ERK MAP kinase signaling in post-mortem brain of suicide subjects: differential regulation of upstream Raf kinases Raf-1 and B-Raf. *Mol Psychiatry* 2006; **11**(1)**:** 86-98.

44. Monsalve EM, Garcia-Gutierrez MS, Navarrete F, Giner S, Laborda J, Manzanares J. Abnormal expression pattern of Notch receptors, ligands, and downstream effectors in the dorsolateral prefrontal cortex and amygdala of suicidal victims. *Molecular neurobiology* 2014; **49**(2)**:** 957-965.

45. Cheng R, Juo SH, Loth JE, Nee J, Iossifov I, Blumenthal R *et al.* Genome-wide linkage scan in a large bipolar disorder sample from the National Institute of Mental Health genetics initiative suggests putative loci for bipolar disorder, psychosis, suicide, and panic disorder. *Mol Psychiatry* 2006; **11**(3)**:** 252-260.

46. Sequeira A, Mamdani F, Ernst C, Vawter MP, Bunney WE, Lebel V *et al.* Global brain gene expression analysis links glutamatergic and GABAergic alterations to suicide and major depression. *PLoS One* 2009; **4**(8)**:** e6585.

47. Pandey GN, Dwivedi Y, Ren X, Rizavi HS, Roberts RC, Conley RR *et al.* Altered expression and phosphorylation of myristoylated alanine-rich C kinase substrate (MARCKS) in postmortem brain of suicide victims with or without depression. *J Psychiatr Res* 2003; **37**(5)**:** 421-432.

48. Bloem B, Xu L, Morava E, Faludi G, Palkovits M, Roubos EW *et al.* Sex-specific differences in the dynamics of cocaine- and amphetamine-regulated transcript and nesfatin-1 expressions in the midbrain of depressed suicide victims vs. controls. *Neuropharmacology* 2012; **62**(1)**:** 297-303.

49. Pandey GN, Dwivedi Y, Ren X, Rizavi HS, Mondal AC, Shukla PK *et al.* Brain region specific alterations in the protein and mRNA levels of protein kinase A subunits in the post-mortem brain of teenage suicide victims. *Neuropsychopharmacology* 2005; **30**(8)**:** 1548-1556.

50. Pandey GN, Dwivedi Y, Rizavi HS, Ren X, Conley RR. Decreased catalytic activity and expression of protein kinase C isozymes in teenage suicide victims: a postmortem brain study. *Arch Gen Psychiatry* 2004; **61**(7)**:** 685-693.

51. Dwivedi Y, Rizavi HS, Zhang H, Roberts RC, Conley RR, Pandey GN. Modulation in activation and expression of phosphatase and tensin homolog on chromosome ten, Akt1, and 3-

phosphoinositide-dependent kinase 1: further evidence demonstrating altered phosphoinositide 3-kinase signaling in postmortem brain of suicide subjects. *Biol Psychiatry* 2010; **67**(11)**:** 1017-1025.

52. Sequeira A, Klempan T, Canetti L, ffrench-Mullen J, Benkelfat C, Rouleau GA *et al.* Patterns of gene expression in the limbic system of suicides with and without major depression. *Mol Psychiatry* 2007; **12**(7)**:** 640-655.

53. Pandey GN, Rizavi HS, Ren X, Dwivedi Y, Palkovits M. Region-specific alterations in glucocorticoid receptor expression in the postmortem brain of teenage suicide victims. *Psychoneuroendocrinology* 2013; **38**(11)**:** 2628-2639.

54. Thalmeier A, Dickmann M, Giegling I, Schneider B, A MH, Maurer K *et al.* Gene expression profiling of post-mortem orbitofrontal cortex in violent suicide victims. *Int J Neuropsychopharmacol* 2008; **11**(2)**:** 217-228.

55. Kurian SM, Le-Niculescu H, Patel SD, Bertram D, Davis J, Dike C *et al.* Identification of blood biomarkers for psychosis using convergent functional genomics. *Mol Psychiatry* 2011; **16**(1)**:** 37-58.

56. Lewohl JM, Wang L, Miles MF, Zhang L, Dodd PR, Harris RA. Gene expression in human alcoholism: microarray analysis of frontal cortex. *Alcohol Clin Exp Res* 2000; **24**(12)**:** 1873-1882.

57. Hu VW, Frank BC, Heine S, Lee NH, Quackenbush J. Gene expression profiling of lymphoblastoid cell lines from monozygotic twins discordant in severity of autism reveals differential regulation of neurologically relevant genes. *BMC genomics* 2006; **7:** 118.

58. Ditzen C, Tang N, Jastorff AM, Teplytska L, Yassouridis A, Maccarrone G *et al.* Cerebrospinal fluid biomarkers for major depression confirm relevance of associated pathophysiology. *Neuropsychopharmacology* 2012; **37**(4)**:** 1013-1025.

59. Middleton FA, Pato CN, Gentile KL, McGann L, Brown AM, Trauzzi M *et al.* Gene expression analysis of peripheral blood leukocytes from discordant sib-pairs with schizophrenia and bipolar disorder reveals points of convergence between genetic and functional genomic approaches. *Am J Med Genet B Neuropsychiatr Genet* 2005; **136**(1)**:** 12-25.

60. Sanders AR, Goring HH, Duan J, Drigalenko EI, Moy W, Freda J *et al.* Transcriptome study of differential expression in schizophrenia. *Human molecular genetics* 2013; **22**(24)**:** 5001-5014.

61. Mehta D, Gonik M, Klengel T, Rex-Haffner M, Menke A, Rubel J *et al.* Using polymorphisms in FKBP5 to define biologically distinct subtypes of posttraumatic stress disorder: evidence from endocrine and gene expression studies. *Arch Gen Psychiatry* 2011; **68**(9)**:** 901-910.

62. Klengel T, Mehta D, Anacker C, Rex-Haffner M, Pruessner JC, Pariante CM *et al.* Allele-specific FKBP5 DNA demethylation mediates gene-childhood trauma interactions. *Nature neuroscience* 2013; **16**(1)**:** 33-41.

63. Binder EB, Bradley RG, Liu W, Epstein MP, Deveau TC, Mercer KB *et al.* Association of FKBP5 polymorphisms and childhood abuse with risk of posttraumatic stress disorder symptoms in adults. *JAMA : the journal of the American Medical Association* 2008; **299**(11)**:** 1291-1305.

64. Xie P, Kranzler HR, Poling J, Stein MB, Anton RF, Farrer LA *et al.* Interaction of FKBP5 with childhood adversity on risk for post-traumatic stress disorder. *Neuropsychopharmacology* 2010; **35**(8)**:** 1684-1692.

65. Szczepankiewicz A, Leszczynska-Rodziewicz A, Pawlak J, Narozna B, Rajewska-Rager A, Wilkosc M *et al.* FKBP5 polymorphism is associated with major depression but not with bipolar disorder. *J Affect Disord* 2014; **164:** 33-37.

66. Lavebratt C, Aberg E, Sjoholm LK, Forsell Y. Variations in FKBP5 and BDNF genes are suggestively associated with depression in a Swedish population-based cohort. *J Affect Disord* 2010; **125**(1-3)**:** 249-255.

67. Binder EB, Salyakina D, Lichtner P, Wochnik GM, Ising M, Putz B *et al.* Polymorphisms in FKBP5 are associated with increased recurrence of depressive episodes and rapid response to antidepressant treatment. *Nat Genet* 2004; **36**(12)**:** 1319-1325.

68. Simons CJ, van Winkel R, Group. Intermediate phenotype analysis of patients, unaffected siblings, and healthy controls identifies VMAT2 as a candidate gene for psychotic disorder and neurocognition. *Schizophr Bull* 2013; **39**(4)**:** 848-856.

69. Sinclair D, Fillman SG, Webster MJ, Weickert CS. Dysregulation of glucocorticoid receptor co-factors FKBP5, BAG1 and PTGES3 in prefrontal cortex in psychotic illness. *Scientific reports* 2013; **3:** 3539.

70. Chen H, Wang N, Zhao X, Ross CA, O'Shea KS, McInnis MG. Gene expression alterations in bipolar disorder postmortem brains. *Bipolar Disord* 2013; **15**(2)**:** 177-187.

71. McClintick JN, Xuei X, Tischfield JA, Goate A, Foroud T, Wetherill L *et al.* Stress-response pathways are altered in the hippocampus of chronic alcoholics. *Alcohol* 2013; **47**(7)**:** 505-515.

72. Yehuda R, Cai G, Golier JA, Sarapas C, Galea S, Ising M *et al.* Gene expression patterns associated with posttraumatic stress disorder following exposure to the World Trade Center attacks. *Biol Psychiatry* 2009; **66**(7)**:** 708-711.

73. Cole SW, Hawkley LC, Arevalo JM, Sung CY, Rose RM, Cacioppo JT. Social regulation of gene expression in human leukocytes. *Genome Biol* 2007; **8**(9)**:** R189.

74. Kupfer DM, White VL, Strayer DL, Crouch DJ, Burian D. Microarray characterization of gene expression changes in blood during acute ethanol exposure. *BMC medical genomics* 2013; **6:** 26.

75. Menke A, Arloth J, Putz B, Weber P, Klengel T, Mehta D *et al.* Dexamethasone stimulated gene expression in peripheral blood is a sensitive marker for glucocorticoid receptor resistance in depressed patients. *Neuropsychopharmacology* 2012; **37**(6)**:** 1455-1464.

76. Katz ER, Stowe ZN, Newport DJ, Kelley ME, Pace TW, Cubells JF *et al.* Regulation of mRNA expression encoding chaperone and co-chaperone proteins of the glucocorticoid receptor in peripheral blood: association with depressive symptoms during pregnancy. *Psychol Med* 2012; **42**(5)**:** 943-956.

77. Aberg KA, McClay JL, Nerella S, Clark S, Kumar G, Chen W *et al.* Methylome-wide association study of schizophrenia: identifying blood biomarker signatures of environmental insults. *JAMA Psychiatry* 2014; **71**(3)**:** 255-264.

78. Baum AE, Akula N, Cabanero M, Cardona I, Corona W, Klemens B *et al.* A genome-wide association study implicates diacylglycerol kinase eta (DGKH) and several other genes in the etiology of bipolar disorder. *Mol Psychiatry* 2008; **13**(2)**:** 197-207.

79. Johnson C, Drgon T, McMahon FJ, Uhl GR. Convergent genome wide association results for bipolar disorder and substance dependence. *Am J Med Genet B Neuropsychiatr Genet* 2009; **150B**(2)**:** 182-190.

80. Nurnberger JI, Jr., Koller DL, Jung J, Edenberg HJ, Foroud T, Guella I *et al.* Identification of pathways for bipolar disorder: a meta-analysis. *JAMA Psychiatry* 2014; **71**(6)**:** 657-664.

81. Ye Y, Zhong X, Zhang H. A genome-wide tree- and forest-based association analysis of comorbidity of alcoholism and smoking. *BMC genetics* 2005; **6 Suppl 1:** S135.

82. Gaiteri C, Guilloux JP, Lewis DA, Sibille E. Altered gene synchrony suggests a combined hormone-mediated dysregulated state in major depression. *PLoS One* 2010; **5**(4)**:** e9970.

83. Mudge J, Miller NA, Khrebtukova I, Lindquist IE, May GD, Huntley JJ *et al.* Genomic convergence analysis of schizophrenia: mRNA sequencing reveals altered synaptic vesicular transport in post-mortem cerebellum. *PLoS One* 2008; **3**(11)**:** e3625.

84. Brennand KJ, Simone A, Jou J, Gelboin-Burkhart C, Tran N, Sangar S *et al.* Modelling schizophrenia using human induced pluripotent stem cells. *Nature* 2011; **473**(7346)**:** 221-225.

85. Paul-Samojedny M, Kowalczyk M, Suchanek R, Owczarek A, Fila-Danilow A, Szczygiel A *et al.* Functional polymorphism in the interleukin-6 and interleukin-10 genes in patients with paranoid schizophrenia--a case-control study. *Journal of molecular neuroscience : MN* 2010; **42**(1)**:** 112-119.

86. Paul-Samojedny M, Owczarek A, Kowalczyk M, Suchanek R, Palacz M, Kucia K *et al.* Association of interleukin 2 (IL-2), interleukin 6 (IL-6), and TNF-alpha (TNFalpha) gene polymorphisms with paranoid schizophrenia in a Polish population. *The Journal of neuropsychiatry and clinical neurosciences* 2013; **25**(1)**:** 72-82.

87. Frydecka D, Misiak B, Pawlak-Adamska E, Karabon L, Tomkiewicz A, Sedlaczek P *et al.* Interleukin-6: the missing element of the neurocognitive deterioration in schizophrenia? The focus on genetic underpinnings, cognitive impairment and clinical manifestation. *European archives of psychiatry and clinical neuroscience* 2014.

88. Zakharyan R, Petrek M, Arakelyan A, Mrazek F, Atshemyan S, Boyajyan A. Interleukin-6 promoter polymorphism and plasma levels in patients with schizophrenia. *Tissue antigens* 2012; **80**(2)**:** 136-142.

89. Hartwell KJ, Moran-Santa Maria MM, Twal WO, Shaftman S, DeSantis SM, McRae-Clark AL *et al.* Association of elevated cytokines with childhood adversity in a sample of healthy adults. *J Psychiatr Res* 2013; **47**(5)**:** 604-610.

90. Tartter M, Hammen C, Bower JE, Brennan PA, Cole S. Effects of chronic interpersonal stress exposure on depressive symptoms are moderated by genetic variation at IL6 and IL1beta in youth. *Brain Behav Immun* 2015.

91. Su S, Miller AH, Snieder H, Bremner JD, Ritchie J, Maisano C *et al.* Common genetic contributions to depressive symptoms and inflammatory markers in middle-aged men: the Twins Heart Study. *Psychosom Med* 2009; **71**(2)**:** 152-158.

92. Fillman SG, Cloonan N, Catts VS, Miller LC, Wong J, McCrossin T *et al.* Increased inflammatory markers identified in the dorsolateral prefrontal cortex of individuals with schizophrenia. *Mol Psychiatry* 2013; **18**(2)**:** 206-214.

93. Padmos RC, Hillegers MH, Knijff EM, Vonk R, Bouvy A, Staal FJ *et al.* A discriminating messenger RNA signature for bipolar disorder formed by an aberrant expression of inflammatory genes in monocytes. *Arch Gen Psychiatry* 2008; **65**(4)**:** 395-407.

94. Padmos RC, Van Baal GC, Vonk R, Wijkhuijs AJ, Kahn RS, Nolen WA *et al.* Genetic and environmental influences on pro-inflammatory monocytes in bipolar disorder: a twin study. *Arch Gen Psychiatry* 2009; **66**(9)**:** 957-965.

95. Brambilla P, Bellani M, Isola M, Bergami A, Marinelli V, Dusi N *et al.* Increased M1/decreased M2 signature and signs of Th1/Th2 shift in chronic patients with bipolar disorder, but not in those with schizophrenia. *Transl Psychiatry* 2014; **4:** e406.

96. Munkholm K, Weikop P, Kessing LV, Vinberg M. Elevated levels of IL-6 and IL-18 in manic and hypomanic states in rapid cycling bipolar disorder patients. *Brain Behav Immun* 2015; **43:** 205-213.

97. Brietzke E, Stertz L, Fernandes BS, Kauer-Sant'anna M, Mascarenhas M, Escosteguy Vargas A *et al.* Comparison of cytokine levels in depressed, manic and euthymic patients with bipolar disorder. *J Affect Disord* 2009; **116**(3)**:** 214-217.

98. Goldstein BI, Collinger KA, Lotrich F, Marsland AL, Gill MK, Axelson DA *et al.* Preliminary findings regarding proinflammatory markers and brain-derived neurotrophic factor among adolescents with bipolar spectrum disorders. *Journal of child and adolescent psychopharmacology* 2011; **21**(5)**:** 479-484.

99. Carvalho LA, Bergink V, Sumaski L, Wijkhuijs J, Hoogendijk WJ, Birkenhager TK *et al.* Inflammatory activation is associated with a reduced glucocorticoid receptor alpha/beta expression ratio in monocytes of inpatients with melancholic major depressive disorder. *Transl Psychiatry* 2014; **4:** e344.

100. Lehto SM, Niskanen L, Miettola J, Tolmunen T, Viinamaki H, Mantyselka P. Serum anti-inflammatory markers in general population subjects with elevated depressive symptoms. *Neurosci Lett* 2010; **484**(3)**:** 201-205.

101. Spanemberg L, Caldieraro MA, Vares EA, Wollenhaupt-Aguiar B, Kauer-Sant'Anna M, Kawamoto SY *et al.* Biological differences between melancholic and nonmelancholic depression subtyped by the CORE measure. *Neuropsychiatric disease and treatment* 2014; **10:** 1523-1531.

102. Song C, Lin A, Bonaccorso S, Heide C, Verkerk R, Kenis G *et al.* The inflammatory response system and the availability of plasma tryptophan in patients with primary sleep disorders and major depression. *J Affect Disord* 1998; **49**(3)**:** 211-219.

103. Miller GE, Cole SW. Clustering of depression and inflammation in adolescents previously exposed to childhood adversity. *Biol Psychiatry* 2012; **72**(1)**:** 34-40.

104. Iacob E, Light KC, Tadler SC, Weeks HR, White AT, Hughen RW *et al.* Dysregulation of leukocyte gene expression in women with medication-refractory depression versus healthy non-depressed controls. *BMC Psychiatry* 2013; **13:** 273.

105. Simon NM, McNamara K, Chow CW, Maser RS, Papakostas GI, Pollack MH *et al.* A detailed examination of cytokine abnormalities in Major Depressive Disorder. *European neuropsychopharmacology : the journal of the European College of Neuropsychopharmacology* 2008; **18**(3)**:** 230-233.

106. Frodl T, Carballedo A, Hughes MM, Saleh K, Fagan A, Skokauskas N *et al.* Reduced expression of glucocorticoid-inducible genes GILZ and SGK-1: high IL-6 levels are associated with reduced hippocampal volumes in major depressive disorder. *Transl Psychiatry* 2012; **2:** e88.

107. Henje Blom E, Lekander M, Ingvar M, Asberg M, Mobarrez F, Serlachius E. Pro-inflammatory cytokines are elevated in adolescent females with emotional disorders not treated with SSRIs. *J Affect Disord* 2012; **136**(3)**:** 716-723.

108. Rohleder N, Miller GE. Acute deviations from long-term trait depressive symptoms predict systemic inflammatory activity. *Brain Behav Immun* 2008; **22**(5)**:** 709-716.

109. Khandaker GM, Pearson RM, Zammit S, Lewis G, Jones PB. Association of serum interleukin 6 and C-reactive protein in childhood with depression and psychosis in young adult life: a population-based longitudinal study. *JAMA Psychiatry* 2014; **71**(10)**:** 1121-1128.

110. Keller PS, El-Sheikh M, Vaughn B, Granger DA. Relations between mucosal immunity and children's mental health: the role of child sex. *Physiol Behav* 2010; **101**(5)**:** 705-712.

111. O'Brien SM, Scully P, Fitzgerald P, Scott LV, Dinan TG. Plasma cytokine profiles in depressed patients who fail to respond to selective serotonin reuptake inhibitor therapy. *J Psychiatr Res* 2007; **41**(3-4)**:** 326-331.

112. Mondelli V, Cattaneo A, Belvederi Murri M, Di Forti M, Handley R, Hepgul N *et al.* Stress and inflammation reduce brain-derived neurotrophic factor expression in first-episode psychosis: a pathway to smaller hippocampal volume. *J Clin Psychiatry* 2011; **72**(12)**:** 1677-1684.

113. Drexhage RC, Padmos RC, de Wit H, Versnel MA, Hooijkaas H, van der Lely AJ *et al.* Patients with schizophrenia show raised serum levels of the pro-inflammatory chemokine CCL2: association with the metabolic syndrome in patients? *Schizophr Res* 2008; **102**(1-3)**:** 352-355.

114. Zhang XY, Zhou DF, Zhang PY, Wu GY, Cao LY, Shen YC. Elevated interleukin-2, interleukin-6 and interleukin-8 serum levels in neuroleptic-free schizophrenia: association with psychopathology. *Schizophr Res* 2002; **57**(2-3)**:** 247-258.

115. Beumer W, Drexhage RC, De Wit H, Versnel MA, Drexhage HA, Cohen D. Increased level of serum cytokines, chemokines and adipokines in patients with schizophrenia is associated with disease and metabolic syndrome. *Psychoneuroendocrinology* 2012; **37**(12)**:** 1901-1911.

116. Dennison U, McKernan D, Cryan J, Dinan T. Schizophrenia patients with a history of childhood trauma have a pro-inflammatory phenotype. *Psychol Med* 2012; **42**(9)**:** 1865-1871.

117. Kaminska T, Wysocka A, Marmurowska-Michalowska H, Dubas-Slemp H, Kandefer-Szerszen M. Investigation of serum cytokine levels and cytokine production in whole blood cultures of paranoid schizophrenic patients. *Archivum immunologiae et therapiae experimentalis* 2001; **49**(6)**:** 439-445.

118. Pedrini M, Massuda R, Fries GR, de Bittencourt Pasquali MA, Schnorr CE, Moreira JC *et al.* Similarities in serum oxidative stress markers and inflammatory cytokines in patients with overt schizophrenia at early and late stages of chronicity. *J Psychiatr Res* 2012; **46**(6)**:** 819-824.

119. Stojanovic A, Martorell L, Montalvo I, Ortega L, Monseny R, Vilella E *et al.* Increased serum interleukin-6 levels in early stages of psychosis: associations with at-risk mental states and the severity of psychotic symptoms. *Psychoneuroendocrinology* 2014; **41:** 23-32.

120. Falcone T, Carlton E, Lee C, Janigro M, Fazio V, Forcen FE *et al.* Does systemic inflammation play a role in pediatric psychosis? *Clinical schizophrenia & related psychoses* 2013**:** 1-43.

121. Di Nicola M, Cattaneo A, Hepgul N, Di Forti M, Aitchison KJ, Janiri L *et al.* Serum and gene expression profile of cytokines in first-episode psychosis. *Brain Behav Immun* 2013; **31:** 90-95.

122. O'Connell KE, Thakore J, Dev KK. Pro-inflammatory cytokine levels are raised in female schizophrenia patients treated with clozapine. *Schizophr Res* 2014; **156**(1)**:** 1-8.

123. Magaki S, Mueller C, Dickson C, Kirsch W. Increased production of inflammatory cytokines in mild cognitive impairment. *Experimental gerontology* 2007; **42**(3)**:** 233-240.

124. Schmahl C, Arvastson L, Tamm JA, Bohus M, Abdourahman A, Antonijevic I. Gene expression profiles in relation to tension and dissociation in borderline personality disorder. *PLoS One* 2013; **8**(8)**:** e70787.

125. Miller GE, Rohleder N, Cole SW. Chronic interpersonal stress predicts activation of pro- and anti-inflammatory signaling pathways 6 months later. *Psychosom Med* 2009; **71**(1)**:** 57-62.

126. Maes M, Lin AH, Delmeire L, Van Gastel A, Kenis G, De Jongh R *et al.* Elevated serum interleukin-6 (IL-6) and IL-6 receptor concentrations in posttraumatic stress disorder following accidental man-made traumatic events. *Biol Psychiatry* 1999; **45**(7)**:** 833-839.

127. Gola H, Engler H, Sommershof A, Adenauer H, Kolassa S, Schedlowski M *et al.* Posttraumatic stress disorder is associated with an enhanced spontaneous production of pro-inflammatory cytokines by peripheral blood mononuclear cells. *BMC Psychiatry* 2013; **13:** 40.

128. Baker DG, Ekhator NN, Kasckow JW, Hill KK, Zoumakis E, Dashevsky BA *et al.* Plasma and cerebrospinal fluid interleukin-6 concentrations in posttraumatic stress disorder. *Neuroimmunomodulation* 2001; **9**(4)**:** 209-217.

129. de la Fontaine L, Schwarz MJ, Eser D, Muller N, Rupprecht R, Zwanzger P. Effects of experimentally induced panic attacks on neuroimmunological markers. *J Neural Transm* 2009; **116**(6)**:** 699-702.

130. Wang XM, Hamza M, Wu TX, Dionne RA. Upregulation of IL-6, IL-8 and CCL2 gene expression after acute inflammation: Correlation to clinical pain. *Pain* 2009; **142**(3)**:** 275-283.

131. Rief W, Mills PJ, Ancoli-Israel S, Ziegler MG, Pung MA, Dimsdale JE. Overnight changes of immune parameters and catecholamines are associated with mood and stress. *Psychosom Med* 2010; **72**(8)**:** 755-762.

132. Vaquero-Lorenzo C, Riaza Bermudo-Soriano C, Perez-Rodriguez MM, Diaz-Hernandez M, Lopez-Castroman J, Fernandez-Piqueras J *et al.* Positive association between SAT-1 -1415T/C polymorphism and anxiety. *Am J Med Genet B Neuropsychiatr Genet* 2009; **150B**(4)**:** 515-519.

133. Belzeaux R, Formisano-Treziny C, Loundou A, Boyer L, Gabert J, Samuelian JC *et al.* Clinical variations modulate patterns of gene expression and define blood biomarkers in major depression. *J Psychiatr Res* 2010; **44**(16)**:** 1205-1213.

134. Grunebaum MF, Ellis SP, Li S, Oquendo MA, Mann JJ. Antidepressants and suicide risk in the United States, 1985-1999. *J Clin Psychiatry* 2004; **65**(11)**:** 1456-1462.

135. Ducci F, Enoch MA, Hodgkinson C, Xu K, Catena M, Robin RW *et al.* Interaction between a functional MAOA locus and childhood sexual abuse predicts alcoholism and antisocial personality disorder in adult women. *Mol Psychiatry* 2008; **13**(3)**:** 334-347.

136. Piton A, Gauthier J, Hamdan FF, Lafreniere RG, Yang Y, Henrion E *et al.* Systematic resequencing of X-chromosome synaptic genes in autism spectrum disorder and schizophrenia. *Mol Psychiatry* 2011; **16**(8)**:** 867-880.

137. Deo AJ, Huang YY, Hodgkinson CA, Xin Y, Oquendo MA, Dwork AJ *et al.* A large-scale candidate gene analysis of mood disorders: evidence of neurotrophic tyrosine kinase receptor and opioid receptor signaling dysfunction. *Psychiatr Genet* 2013; **23**(2)**:** 47-55.

138. Iwamoto K, Bundo M, Kato T. Altered expression of mitochondria-related genes in postmortem brains of patients with bipolar disorder or schizophrenia, as revealed by large-scale DNA microarray analysis. *Human molecular genetics* 2005; **14**(2)**:** 241-253.

139. Ou XM, Stockmeier CA, Meltzer HY, Overholser JC, Jurjus GJ, Dieter L *et al.* A novel role for glyceraldehyde-3-phosphate dehydrogenase and monoamine oxidase B cascade in ethanol-induced cellular damage. *Biol Psychiatry* 2010; **67**(9)**:** 855-863.

140. Teles LM, Aquino EN, Neves AC, Garcia CH, Roepstorff P, Fontes B *et al.* Comparison of the neutrophil proteome in trauma patients and normal controls. *Protein and peptide letters* 2012; **19**(6)**:** 663-672.

141. Moller-Levet CS, Archer SN, Bucca G, Laing EE, Slak A, Kabiljo R *et al.* Effects of insufficient sleep on circadian rhythmicity and expression amplitude of the human blood transcriptome. *Proc Natl Acad Sci U S A* 2013; **110**(12)**:** E1132-1141.

142. International Schizophrenia C, Purcell SM, Wray NR, Stone JL, Visscher PM, O'Donovan MC *et al.* Common polygenic variation contributes to risk of schizophrenia and bipolar disorder. *Nature* 2009; **460**(7256)**:** 748-752.

143. Bremer A, Giacobini M, Eriksson M, Gustavsson P, Nordin V, Fernell E *et al.* Copy number variation characteristics in subpopulations of patients with autism spectrum disorders. *Am J Med Genet B Neuropsychiatr Genet* 2011; **156**(2)**:** 115-124.

144. Beech RD, Lowthert L, Leffert JJ, Mason PN, Taylor MM, Umlauf S *et al.* Increased peripheral blood expression of electron transport chain genes in bipolar depression. *Bipolar Disord* 2010; **12**(8)**:** 813-824.

145. Philibert RA, Crowe R, Ryu GY, Yoon JG, Secrest D, Sandhu H *et al.* Transcriptional profiling of lymphoblast lines from subjects with panic disorder. *Am J Med Genet B Neuropsychiatr Genet* 2007; **144B**(5)**:** 674-682.

146. Garbett KA, Vereczkei A, Kalman S, Wang L, Korade Z, Shelton RC *et al.* Fibroblasts from patients with major depressive disorder show distinct transcriptional response to metabolic stressors. *Transl Psychiatry* 2015; **5:** e523.

147. Machado-Vieira R, Pivovarova NB, Stanika RI, Yuan P, Wang Y, Zhou R *et al.* The Bcl-2 gene polymorphism rs956572AA increases inositol 1,4,5-trisphosphate receptor-mediated endoplasmic reticulum calcium release in subjects with bipolar disorder. *Biol Psychiatry* 2011; **69**(4)**:** 344-352.

148. Yu H, Bi W, Liu C, Zhao Y, Zhang D, Yue W. A hypothesis-driven pathway analysis reveals myelin-related pathways that contribute to the risk of schizophrenia and bipolar disorder. *Prog Neuropsychopharmacol Biol Psychiatry* 2014; **51:** 140-145.

149. Soeiro-de-Souza MG, Salvadore G, Moreno RA, Otaduy MC, Chaim KT, Gattaz WF *et al.* Bcl-2 rs956572 polymorphism is associated with increased anterior cingulate cortical glutamate in euthymic bipolar I disorder. *Neuropsychopharmacology* 2013; **38**(3)**:** 468-475.

150. Sipila T, Kananen L, Greco D, Donner J, Silander K, Terwilliger JD *et al.* An association analysis of circadian genes in anxiety disorders. *Biol Psychiatry* 2010; **67**(12)**:** 1163-1170.

151. Kim HW, Rapoport SI, Rao JS. Altered expression of apoptotic factors and synaptic markers in postmortem brain from bipolar disorder patients. *Neurobiology of disease* 2010; **37**(3)**:** 596-603.

152. Su YA, Wu J, Zhang L, Zhang Q, Su DM, He P *et al.* Dysregulated mitochondrial genes and networks with drug targets in postmortem brain of patients with posttraumatic stress disorder (PTSD) revealed by human mitochondria-focused cDNA microarrays. *International journal of biological sciences* 2008; **4**(4)**:** 223-235.

153. Lowthert L, Leffert J, Lin A, Umlauf S, Maloney K, Muralidharan A *et al.* Increased ratio of anti-apoptotic to pro-apoptotic Bcl2 gene-family members in lithium-responders one month after treatment initiation. *Biology of mood & anxiety disorders* 2012; **2**(1)**:** 15.

154. Beech RD, Qu J, Leffert JJ, Lin A, Hong KA, Hansen J *et al.* Altered expression of cytokine signaling pathway genes in peripheral blood cells of alcohol dependent subjects: preliminary findings. *Alcohol Clin Exp Res* 2012; **36**(9)**:** 1487-1496.

155. Gruber HE, Hoelscher GL, Ingram JA, Hanley EN, Jr. Genome-wide analysis of pain-, nerve- and neurotrophin -related gene expression in the degenerating human annulus. *Molecular pain* 2012; **8:** 63.

156. Maycox PR, Kelly F, Taylor A, Bates S, Reid J, Logendra R *et al.* Analysis of gene expression in two large schizophrenia cohorts identifies multiple changes associated with nerve terminal function. *Mol Psychiatry* 2009; **14**(12)**:** 1083-1094.

157. Glatt SJ, Everall IP, Kremen WS, Corbeil J, Sasik R, Khanlou N *et al.* Comparative gene expression analysis of blood and brain provides concurrent validation of SELENBP1 up-regulation in schizophrenia. *Proc Natl Acad Sci U S A* 2005; **102**(43)**:** 15533-15538.

158. Wang L, Lockstone HE, Guest PC, Levin Y, Palotas A, Pietsch S *et al.* Expression profiling of fibroblasts identifies cell cycle abnormalities in schizophrenia. *Journal of proteome research* 2010; **9**(1)**:** 521-527.

159. Chang LC, Jamain S, Lin CW, Rujescu D, Tseng GC, Sibille E. A conserved BDNF, glutamate- and GABA-enriched gene module related to human depression identified by coexpression meta-analysis and DNA variant genome-wide association studies. *PLoS One* 2014; **9**(3)**:** e90980.

160. Elia J, Gai X, Xie HM, Perin JC, Geiger E, Glessner JT *et al.* Rare structural variants found in attention-deficit hyperactivity disorder are preferentially associated with neurodevelopmental genes. *Mol Psychiatry* 2010; **15**(6)**:** 637-646.

161. O'Dushlaine C, Kenny E, Heron E, Donohoe G, Gill M, Morris D *et al.* Molecular pathways involved in neuronal cell adhesion and membrane scaffolding contribute to schizophrenia and bipolar disorder susceptibility. *Mol Psychiatry* 2011; **16**(3)**:** 286-292.

162. Kang HJ, Adams DH, Simen A, Simen BB, Rajkowska G, Stockmeier CA *et al.* Gene expression profiling in postmortem prefrontal cortex of major depressive disorder. *J Neurosci* 2007; **27**(48)**:** 13329-13340.

163. Voineagu I, Wang X, Johnston P, Lowe JK, Tian Y, Horvath S *et al.* Transcriptomic analysis of autistic brain reveals convergent molecular pathology. *Nature* 2011; **474**(7351)**:** 380-384.

164. Albertson DN, Schmidt CJ, Kapatos G, Bannon MJ. Distinctive profiles of gene expression in the human nucleus accumbens associated with cocaine and heroin abuse. *Neuropsychopharmacology* 2006; **31**(10)**:** 2304-2312.

165. Le-Niculescu H, Kurian SM, Yehyawi N, Dike C, Patel SD, Edenberg HJ *et al.* Identifying blood biomarkers for mood disorders using convergent functional genomics. *Mol Psychiatry* 2009; **14**(2)**:** 156-174.

166. Konradi C, Eaton M, MacDonald ML, Walsh J, Benes FM, Heckers S. Molecular evidence for mitochondrial dysfunction in bipolar disorder. *Arch Gen Psychiatry* 2004; **61**(3)**:** 300-308.

167. Miller GE, Chen E, Sze J, Marin T, Arevalo JM, Doll R *et al.* A functional genomic fingerprint of chronic stress in humans: blunted glucocorticoid and increased NF-kappaB signaling. *Biol Psychiatry* 2008; **64**(4)**:** 266-272.

168. Martins-de-Souza D, Maccarrone G, Ising M, Kloiber S, Lucae S, Holsboer F *et al.* Blood mononuclear cell proteome suggests integrin and Ras signaling as critical pathways for antidepressant treatment response. *Biol Psychiatry* 2014; **76**(7)**:** e15-17.

169. Mehta D, Klengel T, Conneely KN, Smith AK, Altmann A, Pace TW *et al.* Childhood maltreatment is associated with distinct genomic and epigenetic profiles in posttraumatic stress disorder. *Proc Natl Acad Sci U S A* 2013; **110**(20)**:** 8302-8307.

170. Hong JJ, Loiselle CR, Yoon DY, Lee O, Becker KG, Singer HS. Microarray analysis in Tourette syndrome postmortem putamen. *Journal of the neurological sciences* 2004; **225**(1-2)**:** 57-64.

171. Mayfield RD, Lewohl JM, Dodd PR, Herlihy A, Liu J, Harris RA. Patterns of gene expression are altered in the frontal and motor cortices of human alcoholics. *Journal of neurochemistry* 2002; **81**(4)**:** 802-813.

172. Vawter MP, Barrett T, Cheadle C, Sokolov BP, Wood WH, 3rd, Donovan DM *et al.* Application of cDNA microarrays to examine gene expression differences in schizophrenia. *Brain research bulletin* 2001; **55**(5)**:** 641-650.

173. Shyn SI, Shi J, Kraft JB, Potash JB, Knowles JA, Weissman MM *et al.* Novel loci for major depression identified by genome-wide association study of Sequenced Treatment Alternatives to Relieve Depression and meta-analysis of three studies. *Mol Psychiatry* 2011; **16**(2)**:** 202-215.

174. Nagata E, Hattori H, Kato M, Ogasawara S, Suzuki S, Shibata M *et al.* Identification of biomarkers associated with migraine with aura. *Neuroscience research* 2009; **64**(1)**:** 104-110.

175. Bhasin MK, Dusek JA, Chang BH, Joseph MG, Denninger JW, Fricchione GL *et al.* Relaxation response induces temporal transcriptome changes in energy metabolism, insulin secretion and inflammatory pathways. *PLoS One* 2013; **8**(5)**:** e62817.

176. Uhl GR, Drgon T, Liu QR, Johnson C, Walther D, Komiyama T *et al.* Genome-wide association for methamphetamine dependence: convergent results from 2 samples. *Arch Gen Psychiatry* 2008; **65**(3)**:** 345-355.

177. Thorgeirsson TE, Gudbjartsson DF, Sulem P, Besenbacher S, Styrkarsdottir U, Thorleifsson G *et al.* A common biological basis of obesity and nicotine addiction. *Transl Psychiatry* 2013; **3:** e308.

178. Jensen KP, Kranzler HR, Stein MB, Gelernter J. The effects of a MAP2K5 microRNA target site SNP on risk for anxiety and depressive disorders. *Am J Med Genet B Neuropsychiatr Genet* 2014; **165B**(2)**:** 175-183.

179. Dow DJ, Huxley-Jones J, Hall JM, Francks C, Maycox PR, Kew JN *et al.* ADAMTSL3 as a candidate gene for schizophrenia: gene sequencing and ultra-high density association analysis by imputation. *Schizophr Res* 2011; **127**(1-3)**:** 28-34.

180. Andreassen OA, Thompson WK, Schork AJ, Ripke S, Mattingsdal M, Kelsoe JR *et al.* Improved detection of common variants associated with schizophrenia and bipolar disorder using pleiotropy-informed conditional false discovery rate. *PLoS Genet* 2013; **9**(4)**:** e1003455.

181. Ruderfer DM, Fanous AH, Ripke S, McQuillin A, Amdur RL, Schizophrenia Working Group of Psychiatric Genomics C *et al.* Polygenic dissection of diagnosis and clinical dimensions of bipolar disorder and schizophrenia. *Mol Psychiatry* 2014; **19**(9)**:** 1017-1024.

182. Tomita H, Ziegler ME, Kim HB, Evans SJ, Choudary PV, Li JZ *et al.* G protein-linked signaling pathways in bipolar and major depressive disorders. *Frontiers in genetics* 2013; **4:** 297.

183. Taylor CA, Sun Z, Cliche DO, Ming H, Eshaque B, Jin S *et al.* Eukaryotic translation initiation factor 5A induces apoptosis in colon cancer cells and associates with the nucleus in response to tumour necrosis factor alpha signalling. *Experimental cell research* 2007; **313**(3)**:** 437-449.

184. Li AL, Li HY, Jin BF, Ye QN, Zhou T, Yu XD *et al.* A novel eIF5A complex functions as a regulator of p53 and p53-dependent apoptosis. *J Biol Chem* 2004; **279**(47)**:** 49251-49258.

185. Sun Z, Cheng Z, Taylor CA, McConkey BJ, Thompson JE. Apoptosis induction by eIF5A1 involves activation of the intrinsic mitochondrial pathway. *J Cell Physiol* 2010; **223**(3)**:** 798-809.

186. Iwamoto K, Bundo M, Yamamoto M, Ozawa H, Saito T, Kato T. Decreased expression of NEFH and PCP4/PEP19 in the prefrontal cortex of alcoholics. *Neuroscience research* 2004; **49**(4)**:** 379-385.

187. Mistry M, Gillis J, Pavlidis P. Genome-wide expression profiling of schizophrenia using a large combined cohort. *Mol Psychiatry* 2013; **18**(2)**:** 215-225.

188. Walsh T, McClellan JM, McCarthy SE, Addington AM, Pierce SB, Cooper GM *et al.* Rare structural variants disrupt multiple genes in neurodevelopmental pathways in schizophrenia. *Science* 2008; **320**(5875)**:** 539-543.

189. Liu J, Lewohl JM, Harris RA, Iyer VR, Dodd PR, Randall PK *et al.* Patterns of gene expression in the frontal cortex discriminate alcoholic from nonalcoholic individuals. *Neuropsychopharmacology* 2006; **31**(7)**:** 1574-1582.

190. Thedieck K, Polak P, Kim ML, Molle KD, Cohen A, Jeno P *et al.* PRAS40 and PRR5-like protein are new mTOR interactors that regulate apoptosis. *PLoS One* 2007; **2**(11)**:** e1217.

191. Madhunapantula SV, Sharma A, Robertson GP. PRAS40 deregulates apoptosis in malignant melanoma. *Cancer research* 2007; **67**(8)**:** 3626-3636.

192. Nakamura K, Chen CK, Sekine Y, Iwata Y, Anitha A, Loh el W *et al.* Association analysis of SOD2 variants with methamphetamine psychosis in Japanese and Taiwanese populations. *Hum Genet* 2006; **120**(2)**:** 243-252.

193. Edgar PF, Douglas JE, Cooper GJ, Dean B, Kydd R, Faull RL. Comparative proteome analysis of the hippocampus implicates chromosome 6q in schizophrenia. *Mol Psychiatry* 2000; **5**(1)**:** 85-90.

194. Kirov G, Grozeva D, Norton N, Ivanov D, Mantripragada KK, Holmans P *et al.* Support for the involvement of large copy number variants in the pathogenesis of schizophrenia. *Human molecular genetics* 2009; **18**(8)**:** 1497-1503.

195. International Schizophrenia C. Rare chromosomal deletions and duplications increase risk of schizophrenia. *Nature* 2008; **455**(7210)**:** 237-241.

196. Levinson DF, Duan J, Oh S, Wang K, Sanders AR, Shi J *et al.* Copy number variants in schizophrenia: confirmation of five previous findings and new evidence for 3q29 microdeletions and VIPR2 duplications. *Am J Psychiatry* 2011; **168**(3)**:** 302-316.

197. Matigian N, Windus L, Smith H, Filippich C, Pantelis C, McGrath J *et al.* Expression profiling in monozygotic twins discordant for bipolar disorder reveals dysregulation of the WNT signalling pathway. *Mol Psychiatry* 2007; **12**(9)**:** 815-825.

198. Bilecova-Rabajdova M, Urban P, Gregova K, Varga J, Fialkovicova V, Kruzliak P *et al.* Breast carcinoma progression and tumour vascular markers related to apoptotic mechanisms. *Disease markers* 2014; **2014:** 156034.

199. Hansen T, Ingason A, Djurovic S, Melle I, Fenger M, Gustafsson O *et al.* At-risk variant in TCF7L2 for type II diabetes increases risk of schizophrenia. *Biol Psychiatry* 2011; **70**(1)**:** 59-63.

200. Alkelai A, Greenbaum L, Lupoli S, Kohn Y, Sarner-Kanyas K, Ben-Asher E *et al.* Association of the type 2 diabetes mellitus susceptibility gene, TCF7L2, with schizophrenia in an Arab-Israeli family sample. *PLoS One* 2012; **7**(1)**:** e29228.

201. Winham SJ, Cuellar-Barboza AB, Oliveros A, McElroy SL, Crow S, Colby C *et al.* Genome-wide association study of bipolar disorder accounting for effect of body mass index identifies a new risk allele in TCF7L2. *Mol Psychiatry* 2014; **19**(9)**:** 1010-1016.

202. Iossifov I, O'Roak BJ, Sanders SJ, Ronemus M, Krumm N, Levy D *et al.* The contribution of de novo coding mutations to autism spectrum disorder. *Nature* 2014; **515**(7526)**:** 216-221.

203. Miller BH, Zeier Z, Xi L, Lanz TA, Deng S, Strathmann J *et al.* MicroRNA-132 dysregulation in schizophrenia has implications for both neurodevelopment and adult brain function. *Proc Natl Acad Sci U S A* 2012; **109**(8)**:** 3125-3130.

204. Dempster EL, Pidsley R, Schalkwyk LC, Owens S, Georgiades A, Kane F *et al.* Disease-associated epigenetic changes in monozygotic twins discordant for schizophrenia and bipolar disorder. *Human molecular genetics* 2011; **20**(24)**:** 4786-4796.

205. Ruvolo PP, Deng X, May WS. Phosphorylation of Bcl2 and regulation of apoptosis. *Leukemia : official journal of the Leukemia Society of America, Leukemia Research Fund, UK* 2001; **15**(4)**:** 515-522.

206. Jain M, Kumar S, Upadhyay R, Lal P, Tiwari A, Ghoshal UC *et al.* Influence of apoptosis (BCL2, FAS), cell cycle (CCND1) and growth factor (EGF, EGFR) genetic polymorphisms on survival outcome: an exploratory study in squamous cell esophageal cancer. *Cancer biology & therapy* 2007; **6**(10)**:** 1553-1558.

207. Portier BP, Taglialatela G. Bcl-2 localized at the nuclear compartment induces apoptosis after transient overexpression. *J Biol Chem* 2006; **281**(52)**:** 40493-40502.

208. Azad N, Vallyathan V, Wang L, Tantishaiyakul V, Stehlik C, Leonard SS *et al.* S-nitrosylation of Bcl-2 inhibits its ubiquitin-proteasomal degradation. A novel antiapoptotic mechanism that suppresses apoptosis. *J Biol Chem* 2006; **281**(45)**:** 34124-34134.

209. Gobe G, Rubin M, Williams G, Sawczuk I, Buttyan R. Apoptosis and expression of Bcl-2, Bcl-XL, and Bax in renal cell carcinomas. *Cancer investigation* 2002; **20**(3)**:** 324-332.

210. Yin XM, Oltvai ZN, Korsmeyer SJ. BH1 and BH2 domains of Bcl-2 are required for inhibition of apoptosis and heterodimerization with Bax. *Nature* 1994; **369**(6478)**:** 321-323.

211. Smalla KH, Mikhaylova M, Sahin J, Bernstein HG, Bogerts B, Schmitt A *et al.* A comparison of the synaptic proteome in human chronic schizophrenia and rat ketamine psychosis suggest that prohibitin is involved in the synaptic pathology of schizophrenia. *Mol Psychiatry* 2008; **13**(9)**:** 878-896.

212. Glatt SJ, Stone WS, Nossova N, Liew CC, Seidman LJ, Tsuang MT. Similarities and differences in peripheral blood gene-expression signatures of individuals with schizophrenia and their first-degree biological relatives. *Am J Med Genet B Neuropsychiatr Genet* 2011; **156B**(8)**:** 869-887.

213. Gottschalk MG, Wesseling H, Guest PC, Bahn S. Proteomic enrichment analysis of psychotic and affective disorders reveals common signatures in presynaptic glutamatergic signaling and energy metabolism. *Int J Neuropsychopharmacol* 2014; **18**(2).

214. Bychkov ER, Ahmed MR, Gurevich VV, Benovic JL, Gurevich EV. Reduced expression of G protein-coupled receptor kinases in schizophrenia but not in schizoaffective disorder. *Neurobiology of disease* 2011; **44**(2)**:** 248-258.

215. Focking M, Lopez LM, English JA, Dicker P, Wolff A, Brindley E *et al.* Proteomic and genomic evidence implicates the postsynaptic density in schizophrenia. *Mol Psychiatry* 2015; **20**(4)**:** 424-432.

216. Matuzany-Ruban A, Golan M, Miroshnik N, Schreiber G, Avissar S. Normalization of GRK2 protein and mRNA measures in patients with depression predict response to antidepressants. *Int J Neuropsychopharmacol* 2010; **13**(1)**:** 83-91.

217. Maestrini E, Pagnamenta AT, Lamb JA, Bacchelli E, Sykes NH, Sousa I *et al.* High-density SNP association study and copy number variation analysis of the AUTS1 and AUTS5 loci implicate the IMMP2L-DOCK4 gene region in autism susceptibility. *Mol Psychiatry* 2010; **15**(9)**:** 954-968.

218. Noor A, Lionel AC, Cohen-Woods S, Moghimi N, Rucker J, Fennell A *et al.* Copy number variant study of bipolar disorder in Canadian and UK populations implicates synaptic genes. *Am J Med Genet B Neuropsychiatr Genet* 2014; **165B**(4)**:** 303-313.

219. Vawter MP, Tomita H, Meng F, Bolstad B, Li J, Evans S *et al.* Mitochondrial-related gene expression changes are sensitive to agonal-pH state: implications for brain disorders. *Mol Psychiatry* 2006; **11**(7)**:** 615, 663-679.

220. Yuan P, Zhou R, Wang Y, Li X, Li J, Chen G *et al.* Altered levels of extracellular signal-regulated kinase signaling proteins in postmortem frontal cortex of individuals with mood disorders and schizophrenia. *J Affect Disord* 2010; **124**(1-2)**:** 164-169.

221. Nabi MO, Mirabzadeh A, Feizzadeh G, Khorshid HR, Karimlou M, Yeganeh MZ *et al.* Novel mutations in the calreticulin gene core promoter and coding sequence in schizoaffective disorder. *Am J Med Genet B Neuropsychiatr Genet* 2010; **153B**(2)**:** 706-709.

222. Martins-de-Souza D, Guest PC, Harris LW, Vanattou-Saifoudine N, Webster MJ, Rahmoune H *et al.* Identification of proteomic signatures associated with depression and psychotic depression in post-mortem brains from major depression patients. *Transl Psychiatry* 2012; **2:** e87.

223. Novak G, Seeman P, Tallerico T. Increased expression of calcium/calmodulin-dependent protein kinase IIbeta in frontal cortex in schizophrenia and depression. *Synapse* 2006; **59**(1)**:** 61-68.

224. Chan MK, Tsang TM, Harris LW, Guest PC, Holmes E, Bahn S. Evidence for disease and antipsychotic medication effects in post-mortem brain from schizophrenia patients. *Mol Psychiatry* 2011; **16**(12)**:** 1189-1202.

225. Lehrmann E, Colantuoni C, Deep-Soboslay A, Becker KG, Lowe R, Huestis MA *et al.* Transcriptional changes common to human cocaine, cannabis and phencyclidine abuse. *PLoS One* 2006; **1:** e114.

226. Zarif Yeganeh M, Mirabzadeh A, Khorram Khorshid HR, Kamali K, Heshmati Y, Gozalpour E *et al.* Novel extreme homozygote haplotypes at the human caveolin 1 gene upstream purine complex in sporadic Alzheimer's disease. *Am J Med Genet B Neuropsychiatr Genet* 2010; **153B**(1)**:** 347-349.

227. Nakatani N, Hattori E, Ohnishi T, Dean B, Iwayama Y, Matsumoto I *et al.* Genome-wide expression analysis detects eight genes with robust alterations specific to bipolar I disorder: relevance to neuronal network perturbation. *Human molecular genetics* 2006; **15**(12)**:** 1949-1962.

228. Wang C, Tao B, Li S, Li B, Wang X, Hu G *et al.* Characterizing the role of PCDH9 in the regulation of glioma cell apoptosis and invasion. *Journal of molecular neuroscience : MN* 2014; **52**(2)**:** 250-260.

229. Kuzman MR, Medved V, Terzic J, Krainc D. Genome-wide expression analysis of peripheral blood identifies candidate biomarkers for schizophrenia. *J Psychiatr Res* 2009; **43**(13)**:** 1073-1077.

230. Maes OC, Xu S, Yu B, Chertkow HM, Wang E, Schipper HM. Transcriptional profiling of Alzheimer blood mononuclear cells by microarray. *Neurobiology of aging* 2007; **28**(12)**:** 1795-1809.

231. Peirce TR, Bray NJ, Williams NM, Norton N, Moskvina V, Preece A *et al.* Convergent evidence for 2',3'-cyclic nucleotide 3'-phosphodiesterase as a possible susceptibility gene for schizophrenia. *Arch Gen Psychiatry* 2006; **63**(1)**:** 18-24.

232. Flynn SW, Lang DJ, Mackay AL, Goghari V, Vavasour IM, Whittall KP *et al.* Abnormalities of myelination in schizophrenia detected in vivo with MRI, and post-mortem with analysis of oligodendrocyte proteins. *Mol Psychiatry* 2003; **8**(9)**:** 811-820.

233. McCullumsmith RE, Gupta D, Beneyto M, Kreger E, Haroutunian V, Davis KL *et al.* Expression of transcripts for myelination-related genes in the anterior cingulate cortex in schizophrenia. *Schizophr Res* 2007; **90**(1-3)**:** 15-27.

234. Etheridge N, Lewohl JM, Mayfield RD, Harris RA, Dodd PR. Synaptic proteome changes in the superior frontal gyrus and occipital cortex of the alcoholic brain. *Proteomics Clinical applications* 2009; **3**(6)**:** 730-742.

235. Aston C, Jiang L, Sokolov BP. Transcriptional profiling reveals evidence for signaling and oligodendroglial abnormalities in the temporal cortex from patients with major depressive disorder. *Mol Psychiatry* 2005; **10**(3)**:** 309-322.

236. Sibille E, Wang Y, Joeyen-Waldorf J, Gaiteri C, Surget A, Oh S *et al.* A molecular signature of depression in the amygdala. *Am J Psychiatry* 2009; **166**(9)**:** 1011-1024.

237. Fernandez SV, Huang Y, Snider KE, Zhou Y, Pogash TJ, Russo J. Expression and DNA methylation changes in human breast epithelial cells after bisphenol A exposure. *International journal of oncology* 2012; **41**(1)**:** 369-377.

238. Maron E, Hettema JM, Shlik J. Advances in molecular genetics of panic disorder. *Mol Psychiatry* 2010; **15**(7)**:** 681-701.

239. Domschke K, Kuhlenbaumer G, Schirmacher A, Lorenzi C, Armengol L, DiBella D *et al.* Human nuclear transcription factor gene CREM: genomic organization, mutation screening, and association analysis in panic disorder. *Am J Med Genet B Neuropsychiatr Genet* 2003; **117B**(1)**:** 70-78.

240. Hill EJ, Nagel DA, O'Neil JD, Torr E, Woehrling EK, Devitt A *et al.* Effects of lithium and valproic acid on gene expression and phenotypic markers in an NT2 neurosphere model of neural development. *PLoS One* 2013; **8**(3)**:** e58822.

241. Meda SA, Ruano G, Windemuth A, O'Neil K, Berwise C, Dunn SM *et al.* Multivariate analysis reveals genetic associations of the resting default mode network in psychotic bipolar disorder and schizophrenia. *Proc Natl Acad Sci U S A* 2014; **111**(19)**:** E2066-2075.

242. Bowden NA, Scott RJ, Tooney PA. Altered gene expression in the superior temporal gyrus in schizophrenia. *BMC genomics* 2008; **9:** 199.

243. Guilloux JP, Douillard-Guilloux G, Kota R, Wang X, Gardier AM, Martinowich K *et al.* Molecular evidence for BDNF- and GABA-related dysfunctions in the amygdala of female subjects with major depression. *Mol Psychiatry* 2012; **17**(11)**:** 1130-1142.

244. Sainz J, Mata I, Barrera J, Perez-Iglesias R, Varela I, Arranz MJ *et al.* Inflammatory and immune response genes have significantly altered expression in schizophrenia. *Mol Psychiatry* 2013; **18**(10)**:** 1056-1057.

245. Glatt SJ, Tylee DS, Chandler SD, Pazol J, Nievergelt CM, Woelk CH *et al.* Blood-based gene-expression predictors of PTSD risk and resilience among deployed marines: a pilot study. *Am J Med Genet B Neuropsychiatr Genet* 2013; **162B**(4)**:** 313-326.

246. Tylee DS, Chandler SD, Nievergelt CM, Liu X, Pazol J, Woelk CH *et al.* Blood-based gene-expression biomarkers of post-traumatic stress disorder among deployed marines: A pilot study. *Psychoneuroendocrinology* 2015; **51:** 472-494.

247. Wang N, Zhang CQ, He JH, Duan XF, Wang YY, Ji X *et al.* MiR-21 down-regulation suppresses cell growth, invasion and induces cell apoptosis by targeting FASL, TIMP3, and RECK genes in esophageal carcinoma. *Digestive diseases and sciences* 2013; **58**(7)**:** 1863-1870.

248. Lit L, Sharp FR, Bertoglio K, Stamova B, Ander BP, Sossong AD *et al.* Gene expression in blood is associated with risperidone response in children with autism spectrum disorders. *Pharmacogenomics J* 2012; **12**(5)**:** 368-371.

249. Schizophrenia Working Group of the Psychiatric Genomics C. Biological insights from 108 schizophrenia-associated genetic loci. *Nature* 2014; **511**(7510)**:** 421-427.

250. Chen Z, Shen BL, Fu QG, Wang F, Tang YX, Hou CL *et al.* CUL4B promotes proliferation and inhibits apoptosis of human osteosarcoma cells. *Oncology reports* 2014; **32**(5)**:** 2047-2053.

251. Bruneau EG, McCullumsmith RE, Haroutunian V, Davis KL, Meador-Woodruff JH. Increased expression of glutaminase and glutamine synthetase mRNA in the thalamus in schizophrenia. *Schizophr Res* 2005; **75**(1)**:** 27-34.

252. Shao L, Vawter MP. Shared gene expression alterations in schizophrenia and bipolar disorder. *Biol Psychiatry* 2008; **64**(2)**:** 89-97.

253. Choudary PV, Molnar M, Evans SJ, Tomita H, Li JZ, Vawter MP *et al.* Altered cortical glutamatergic and GABAergic signal transmission with glial involvement in depression. *Proc Natl Acad Sci U S A* 2005; **102**(43)**:** 15653-15658.

254. Bernard R, Kerman IA, Thompson RC, Jones EG, Bunney WE, Barchas JD *et al.* Altered expression of glutamate signaling, growth factor, and glia genes in the locus coeruleus of patients with major depression. *Mol Psychiatry* 2011; **16**(6)**:** 634-646.

255. Novikova SI, He F, Cutrufello NJ, Lidow MS. Identification of protein biomarkers for schizophrenia and bipolar disorder in the postmortem prefrontal cortex using SELDI-TOF-MS

ProteinChip profiling combined with MALDI-TOF-PSD-MS analysis. *Neurobiology of disease* 2006; **23**(1)**:** 61-76.

256. Prabakaran S, Swatton JE, Ryan MM, Huffaker SJ, Huang JT, Griffin JL *et al.* Mitochondrial dysfunction in schizophrenia: evidence for compromised brain metabolism and oxidative stress. *Mol Psychiatry* 2004; **9**(7)**:** 684-697, 643.

257. Beech RD, Leffert JJ, Lin A, Sylvia LG, Umlauf S, Mane S *et al.* Gene-expression differences in peripheral blood between lithium responders and non-responders in the Lithium Treatment-Moderate dose Use Study (LiTMUS). *Pharmacogenomics J* 2014; **14**(2)**:** 182-191.

258. Mamdani F, Berlim MT, Beaulieu MM, Labbe A, Merette C, Turecki G. Gene expression biomarkers of response to citalopram treatment in major depressive disorder. *Transl Psychiatry* 2011; **1:** e13.

259. Papiol S, Rosa A, Gutierrez B, Martin B, Salgado P, Catalan R *et al.* Interleukin-1 cluster is associated with genetic risk for schizophrenia and bipolar disorder. *Journal of medical genetics* 2004; **41**(3)**:** 219-223.

260. Papiol S, Molina V, Desco M, Rosa A, Reig S, Sanz J *et al.* Gray matter deficits in bipolar disorder are associated with genetic variability at interleukin-1 beta gene (2q13). *Genes Brain Behav* 2008; **7**(7)**:** 796-801.

261. Hanninen K, Katila H, Saarela M, Rontu R, Mattila KM, Fan M *et al.* Interleukin-1 beta gene polymorphism and its interactions with neuregulin-1 gene polymorphism are associated with schizophrenia. *European archives of psychiatry and clinical neuroscience* 2008; **258**(1)**:** 10-15.

262. Saiz PA, Garcia-Portilla MP, Florez G, Corcoran P, Arango C, Morales B *et al.* Polymorphisms of the IL-1 gene complex are associated with alcohol dependence in Spanish Caucasians: data from an association study. *Alcohol Clin Exp Res* 2009; **33**(12)**:** 2147-2153.

263. Luciano M, Houlihan LM, Harris SE, Gow AJ, Hayward C, Starr JM *et al.* Association of existing and new candidate genes for anxiety, depression and personality traits in older people. *Behavior genetics* 2010; **40**(4)**:** 518-532.

264. Katsuura S, Kamezaki Y, Yamagishi N, Kuwano Y, Nishida K, Masuda K *et al.* Circulating vascular endothelial growth factor is independently and negatively associated with trait anxiety and depressive mood in healthy Japanese university students. *International journal of psychophysiology : official journal of the International Organization of Psychophysiology* 2011; **81**(1)**:** 38-43.

265. Colangelo V, Schurr J, Ball MJ, Pelaez RP, Bazan NG, Lukiw WJ. Gene expression profiling of 12633 genes in Alzheimer hippocampal CA1: transcription and neurotrophic factor down-regulation and up-regulation of apoptotic and pro-inflammatory signaling. *Journal of neuroscience research* 2002; **70**(3)**:** 462-473.

266. Rao JS, Harry GJ, Rapoport SI, Kim HW. Increased excitotoxicity and neuroinflammatory markers in postmortem frontal cortex from bipolar disorder patients. *Mol Psychiatry* 2010; **15**(4)**:** 384-392.

267. Qi XR, Kamphuis W, Wang S, Wang Q, Lucassen PJ, Zhou JN *et al.* Aberrant stress hormone receptor balance in the human prefrontal cortex and hypothalamic paraventricular nucleus of depressed patients. *Psychoneuroendocrinology* 2013; **38**(6)**:** 863-870.

268. Noto CS, Gadelha A, Belangero SI, Smith MA, de Aguiar BW, Panizzuti B *et al.* Association of biomarkers and depressive symptoms in schizophrenia. *Neurosci Lett* 2011; **505**(3)**:** 282-285.

269. Liu L, Jia F, Yuan G, Chen Z, Yao J, Li H *et al.* Tyrosine hydroxylase, interleukin-1beta and tumor necrosis factor-alpha are overexpressed in peripheral blood mononuclear cells from schizophrenia patients as determined by semi-quantitative analysis. *Psychiatry Res* 2010; **176**(1)**:** 1-7.

270. Chavushyan A, Hovsepyan M, Boyajyan A. Cryoglobulins as potential triggers of inflammation in schizophrenia. *Schizophrenia research and treatment* 2013; **2013:** 125264.

271. Soderlund J, Schroder J, Nordin C, Samuelsson M, Walther-Jallow L, Karlsson H *et al.* Activation of brain interleukin-1beta in schizophrenia. *Mol Psychiatry* 2009; **14**(12)**:** 1069-1071.

272. Belzeaux R, Bergon A, Jeanjean V, Loriod B, Formisano-Treziny C, Verrier L *et al.* Responder and nonresponder patients exhibit different peripheral transcriptional signatures during major depressive episode. *Transl Psychiatry* 2012; **2:** e185.

273. Rethorst CD, Toups MS, Greer TL, Nakonezny PA, Carmody TJ, Grannemann BD *et al.* Pro-inflammatory cytokines as predictors of antidepressant effects of exercise in major depressive disorder. *Mol Psychiatry* 2013; **18**(10)**:** 1119-1124.

274. Tucker P, Ruwe WD, Masters B, Parker DE, Hossain A, Trautman RP *et al.* Neuroimmune and cortisol changes in selective serotonin reuptake inhibitor and placebo treatment of chronic posttraumatic stress disorder. *Biol Psychiatry* 2004; **56**(2)**:** 121-128.

275. Schwarz E, Guest PC, Rahmoune H, Wang L, Levin Y, Ingudomnukul E *et al.* Sex-specific serum biomarker patterns in adults with Asperger's syndrome. *Mol Psychiatry* 2011; **16**(12)**:** 1213-1220.

276. Todorova VK, Elbein AD, Kyosseva SV. Increased expression of c-Jun transcription factor in cerebellar vermis of patients with schizophrenia. *Neuropsychopharmacology* 2003; **28**(8)**:** 1506-1514.

277. Aston C, Jiang L, Sokolov BP. Microarray analysis of postmortem temporal cortex from patients with schizophrenia. *Journal of neuroscience research* 2004; **77**(6)**:** 858-866.

278. Cattane N, Minelli A, Milanesi E, Maj C, Bignotti S, Bortolomasi M *et al.* Altered gene expression in schizophrenia: findings from transcriptional signatures in fibroblasts and blood. *PLoS One* 2015; **10**(2)**:** e0116686.

279. Malki K, Pain O, Tosto MG, Du Rietz E, Carboni L, Schalkwyk LC. Identification of genes and gene pathways associated with major depressive disorder by integrative brain analysis of rat and human prefrontal cortex transcriptomes. *Transl Psychiatry* 2015; **5:** e519.

280. Jin EH, Zhang E, Ko Y, Sim WS, Moon DE, Yoon KJ *et al.* Genome-wide expression profiling of complex regional pain syndrome. *PLoS One* 2013; **8**(11)**:** e79435.

281. Kirov G, Zaharieva I, Georgieva L, Moskvina V, Nikolov I, Cichon S *et al.* A genome-wide association study in 574 schizophrenia trios using DNA pooling. *Mol Psychiatry* 2009; **14**(8)**:** 796-803.

282. Jurata LW, Bukhman YV, Charles V, Capriglione F, Bullard J, Lemire AL *et al.* Comparison of microarray-based mRNA profiling technologies for identification of psychiatric disease and drug signatures. *Journal of neuroscience methods* 2004; **138**(1-2)**:** 173-188.

283. Bowden NA, Weidenhofer J, Scott RJ, Schall U, Todd J, Michie PT *et al.* Preliminary investigation of gene expression profiles in peripheral blood lymphocytes in schizophrenia. *Schizophr Res* 2006; **82**(2-3)**:** 175-183.

284. Pandey GN, Dwivedi Y, Ren X, Rizavi HS, Roberts RC, Conley RR *et al.* Altered expression and phosphorylation of myristoylated alanine-rich C kinase substrate (MARCKS) in postmortem brain of suicide victims with or without depression. *J Psychiatr Res* 2003; **37**(5)**:** 421-432.

285. Hakak Y, Walker JR, Li C, Wong WH, Davis KL, Buxbaum JD *et al.* Genome-wide expression analysis reveals dysregulation of myelination-related genes in chronic schizophrenia. *Proc Natl Acad Sci U S A* 2001; **98**(8)**:** 4746-4751.

286. Pinner AL, Haroutunian V, Meador-Woodruff JH. Alterations of the myristoylated, alanine-rich C kinase substrate (MARCKS) in prefrontal cortex in schizophrenia. *Schizophr Res* 2014; **154**(1-3)**:** 36-41.

287. Redei EE, Andrus BM, Kwasny MJ, Seok J, Cai X, Ho J *et al.* Blood transcriptomic biomarkers in adult primary care patients with major depressive disorder undergoing cognitive behavioral therapy. *Transl Psychiatry* 2014; **4:** e442.

288. Baruch K, Silberberg G, Aviv A, Shamir E, Bening-Abu-Shach U, Baruch Y *et al.* Association between golli-MBP and schizophrenia in the Jewish Ashkenazi population: are regulatory regions involved? *Int J Neuropsychopharmacol* 2009; **12**(7)**:** 885-894.

289. Chambers JS, Perrone-Bizzozero NI. Altered myelination of the hippocampal formation in subjects with schizophrenia and bipolar disorder. *Neurochemical research* 2004; **29**(12)**:** 2293-2302.

290. Tkachev D, Mimmack ML, Ryan MM, Wayland M, Freeman T, Jones PB *et al.* Oligodendrocyte dysfunction in schizophrenia and bipolar disorder. *Lancet* 2003; **362**(9386)**:** 798-805.

291. Matthews PR, Eastwood SL, Harrison PJ. Reduced myelin basic protein and actin-related gene expression in visual cortex in schizophrenia. *PLoS One* 2012; **7**(6)**:** e38211.

292. Wang DS, Bennett DA, Mufson EJ, Mattila P, Cochran E, Dickson DW. Contribution of changes in ubiquitin and myelin basic protein to age-related cognitive decline. *Neuroscience research* 2004; **48**(1)**:** 93-100.

293. Stelzhammer V, Alsaif M, Chan MK, Rahmoune H, Steeb H, Guest PC *et al.* Distinct proteomic profiles in post-mortem pituitary glands from bipolar disorder and major depressive disorder patients. *J Psychiatr Res* 2015; **60:** 40-48.

294. Li T, Li D, Sha J, Sun P, Huang Y. MicroRNA-21 directly targets MARCKS and promotes apoptosis resistance and invasion in prostate cancer cells. *Biochemical and biophysical research communications* 2009; **383**(3)**:** 280-285.

295. Choi KH, Elashoff M, Higgs BW, Song J, Kim S, Sabunciyan S *et al.* Putative psychosis genes in the prefrontal cortex: combined analysis of gene expression microarrays. *BMC Psychiatry* 2008; **8:** 87.

296. Wockner LF, Noble EP, Lawford BR, Young RM, Morris CP, Whitehall VL *et al.* Genome-wide DNA methylation analysis of human brain tissue from schizophrenia patients. *Transl Psychiatry* 2014; **4:** e339.

297. Niculescu AB, Levey D, Le-Niculescu H, Niculescu E, Kurian SM, Salomon D. Psychiatric blood biomarkers: avoiding jumping to premature negative or positive conclusions. *Mol Psychiatry* 2015; **20**(3)**:** 286-288.

298. Arion D, Unger T, Lewis DA, Levitt P, Mirnics K. Molecular evidence for increased expression of genes related to immune and chaperone function in the prefrontal cortex in schizophrenia. *Biol Psychiatry* 2007; **62**(7)**:** 711-721.

299. Chu TT, Liu Y, Kemether E. Thalamic transcriptome screening in three psychiatric states. *Journal of human genetics* 2009; **54**(11)**:** 665-675.

300. Nantel F, Monaco L, Foulkes NS, Masquilier D, LeMeur M, Henriksen K *et al.* Spermiogenesis deficiency and germ-cell apoptosis in CREM-mutant mice. *Nature* 1996; **380**(6570)**:** 159-162.

301. Sassone-Corsi P. Regulating the balance between differentiation and apoptosis: role of CREM in the male germ cells. *J Mol Med (Berl)* 1998; **76**(12)**:** 811-817.

302. Sassone-Corsi P. CREM: a master-switch governing male germ cells differentiation and apoptosis. *Seminars in cell & developmental biology* 1998; **9**(4)**:** 475-482.

303. Pan H, Ren SC, He XL, Wei YX, Wang RH, Yang Y *et al.* [The effects of human 21.5 kDa MBP gene on HepG-2 proliferation and apoptosis]. *Sichuan da xue xue bao Yi xue ban = Journal of Sichuan University Medical science edition* 2009; **40**(5)**:** 775-779.

304. Castelli J, Wood KA, Youle RJ. The 2-5A system in viral infection and apoptosis. *Biomedicine & pharmacotherapy = Biomedecine & pharmacotherapie* 1998; **52**(9)**:** 386-390.

305. Malathi K, Paranjape JM, Ganapathi R, Silverman RH. HPC1/RNASEL mediates apoptosis of prostate cancer cells treated with 2',5'-oligoadenylates, topoisomerase I inhibitors, and tumor necrosis factor-related apoptosis-inducing ligand. *Cancer research* 2004; **64**(24)**:** 9144-9151.

306. Asselin-Labat ML, David M, Biola-Vidamment A, Lecoeuche D, Zennaro MC, Bertoglio J *et al.* GILZ, a new target for the transcription factor FoxO3, protects T lymphocytes from interleukin-2 withdrawal-induced apoptosis. *Blood* 2004; **104**(1)**:** 215-223.

307. Costas J, Gratacos M, Escaramis G, Martin-Santos R, de Diego Y, Baca-Garcia E *et al.* Association study of 44 candidate genes with depressive and anxiety symptoms in post-partum women. *J Psychiatr Res* 2010; **44**(11)**:** 717-724.

308. Lintas C, Sacco R, Garbett K, Mirnics K, Militerni R, Bravaccio C *et al.* Involvement of the PRKCB1 gene in autistic disorder: significant genetic association and reduced neocortical gene expression. *Mol Psychiatry* 2009; **14**(7)**:** 705-718.

309. Philippi A, Roschmann E, Tores F, Lindenbaum P, Benajou A, Germain-Leclerc L *et al.* Haplotypes in the gene encoding protein kinase c-beta (PRKCB1) on chromosome 16 are associated with autism. *Mol Psychiatry* 2005; **10**(10)**:** 950-960.

310. Pandey GN, Ren X, Dwivedi Y, Pavuluri MN. Decreased protein kinase C (PKC) in platelets of pediatric bipolar patients: effect of treatment with mood stabilizing drugs. *J Psychiatr Res* 2008; **42**(2)**:** 106-116.

311. Koenigsberg HW, Yuan P, Diaz GA, Guerreri S, Dorantes C, Mayson S *et al.* Platelet protein kinase C and brain-derived neurotrophic factor levels in borderline personality disorder patients. *Psychiatry Res* 2012; **199**(2)**:** 92-97.

312. Silver H, Susser E, Danovich L, Bilker W, Youdim M, Goldin V *et al.* SSRI augmentation of antipsychotic alters expression of GABA(A) receptor and related genes in PMC of schizophrenia patients. *Int J Neuropsychopharmacol* 2011; **14**(5)**:** 573-584.

313. Galindo CL, Gutierrez C, Jr., Chopra AK. Potential involvement of galectin-3 and SNAP23 in Aeromonas hydrophila cytotoxic enterotoxin-induced host cell apoptosis. *Microbial pathogenesis* 2006; **40**(2)**:** 56-68.

314. Wong ML, Dong C, Maestre-Mesa J, Licinio J. Polymorphisms in inflammation-related genes are associated with susceptibility to major depression and antidepressant response. *Mol Psychiatry* 2008; **13**(8)**:** 800-812.

315. Wong ML, Dong C, Andreev V, Arcos-Burgos M, Licinio J. Prediction of susceptibility to major depression by a model of interactions of multiple functional genetic variants and environmental factors. *Mol Psychiatry* 2012; **17**(6)**:** 624-633.

316. Arion D, Corradi JP, Tang S, Datta D, Boothe F, He A *et al.* Distinctive transcriptome alterations of prefrontal pyramidal neurons in schizophrenia and schizoaffective disorder. *Mol Psychiatry* 2015.

317. Zhang S, Liu J, MacGibbon G, Dragunow M, Cooper GJ. Increased expression and activation of c-Jun contributes to human amylin-induced apoptosis in pancreatic islet beta-cells. *Journal of molecular biology* 2002; **324**(2)**:** 271-285.

318. Duan L, Sterba K, Kolomeichuk S, Kim H, Brown PH, Chambers TC. Inducible overexpression of c-Jun in MCF7 cells causes resistance to vinblastine via inhibition of drug-induced apoptosis and senescence at a step subsequent to mitotic arrest. *Biochemical pharmacology* 2007; **73**(4)**:** 481-490.

319. Dass CR, Friedhuber AM, Khachigian LM, Dunstan DE, Choong PF. Downregulation of c-jun results in apoptosis-mediated anti-osteosarcoma activity in an orthotopic model. *Cancer biology & therapy* 2008; **7**(7)**:** 1033-1036.

320. Wong CC, Meaburn EL, Ronald A, Price TS, Jeffries AR, Schalkwyk LC *et al.* Methylomic analysis of monozygotic twins discordant for autism spectrum disorder and related behavioural traits. *Mol Psychiatry* 2014; **19**(4)**:** 495-503.

321. Kanazawa T, Glatt SJ, Faraone SV, Hwu HG, Yoneda H, Tsuang MT. Family-based association study of SELENBP1 in schizophrenia. *Schizophr Res* 2009; **113**(2-3)**:** 268-272.

322. Kanazawa T, Chana G, Glatt SJ, Mizuno H, Masliah E, Yoneda H *et al.* The utility of SELENBP1 gene expression as a biomarker for major psychotic disorders: replication in schizophrenia and extension to bipolar disorder with psychosis. *Am J Med Genet B Neuropsychiatr Genet* 2008; **147B**(6)**:** 686-689.

323. Murata-Ohsawa M, Tohda S, Kogoshi H, Nara N. The Notch ligand, Delta-1, reduces TNF-alpha-induced growth suppression and apoptosis by decreasing activation of caspases in U937 cells. *International journal of molecular medicine* 2004; **14**(5)**:** 861-866.

324. Fan Q, Chen M, Zuo L, Shang X, Huang MZ, Ciccarelli M *et al.* Myocardial Ablation of G Protein-Coupled Receptor Kinase 2 (GRK2) Decreases Ischemia/Reperfusion Injury through an Anti-Intrinsic Apoptotic Pathway. *PLoS One* 2013; **8**(6)**:** e66234.

325. Gardiner EJ, Cairns MJ, Liu B, Beveridge NJ, Carr V, Kelly B *et al.* Gene expression analysis reveals schizophrenia-associated dysregulation of immune pathways in peripheral blood mononuclear cells. *J Psychiatr Res* 2013; **47**(4)**:** 425-437.

326. Yi Z, Li Z, Yu S, Yuan C, Hong W, Wang Z *et al.* Blood-based gene expression profiles models for classification of subsyndromal symptomatic depression and major depressive disorder. *PLoS One* 2012; **7**(2)**:** e31283.

327. Schmidt F, Kunze M, Loock AC, Dobbelstein M. Screening analysis of ubiquitin ligases reveals G2E3 as a potential target for chemosensitizing cancer cells. *Oncotarget* 2015; **6**(2)**:** 617-632.

328. Brooks WS, Helton ES, Banerjee S, Venable M, Johnson L, Schoeb TR *et al.* G2E3 is a dual function ubiquitin ligase required for early embryonic development. *J Biol Chem* 2008; **283**(32)**:** 22304-22315.

329. Ryan MM, Lockstone HE, Huffaker SJ, Wayland MT, Webster MJ, Bahn S. Gene expression analysis of bipolar disorder reveals downregulation of the ubiquitin cycle and alterations in synaptic genes. *Mol Psychiatry* 2006; **11**(10)**:** 965-978.

330. Williams KH, Vieira De Ribeiro AJ, Prakoso E, Veillard A, Shackel NA, Brooks B *et al.* Circulating dipeptidyl peptidase-4 activity correlates with measures of hepatocyte apoptosis and fibrosis in non-alcoholic fatty liver disease in type 2 diabetes mellitus and obesity: A dual cohort cross-sectional study. *Journal of diabetes* 2014.

331. Qian Q, Zhou H, Chen Y, Shen C, He S, Zhao H *et al.* VMP1 related autophagy and apoptosis in colorectal cancer cells: VMP1 regulates cell death. *Biochemical and biophysical research communications* 2014; **443**(3)**:** 1041-1047.

332. Shi Z, Hou W, Hua X, Zhang X, Liu X, Wang X. Overexpression of calreticulin in pre-eclamptic placentas: effect on apoptosis, cell invasion and severity of pre-eclampsia. *Cell biochemistry and biophysics* 2012; **63**(2)**:** 183-189.

333. Stein S, Thomas EK, Herzog B, Westfall MD, Rocheleau JV, Jackson RS, 2nd *et al.* NDRG1 is necessary for p53-dependent apoptosis. *J Biol Chem* 2004; **279**(47)**:** 48930-48940.

334. Liang Y, Liu M, Wang P, Ding X, Cao Y. Analysis of 20 genes at chromosome band 12q13: RACGAP1 and MCRS1 overexpression in nonsmall-cell lung cancer. *Genes, chromosomes & cancer* 2013; **52**(3)**:** 305-315.

335. Flatscher-Bader T, van der Brug M, Hwang JW, Gochee PA, Matsumoto I, Niwa S *et al.* Alcohol-responsive genes in the frontal cortex and nucleus accumbens of human alcoholics. *Journal of neurochemistry* 2005; **93**(2)**:** 359-370.

336. Stewart SE, Yu D, Scharf JM, Neale BM, Fagerness JA, Mathews CA *et al.* Genome-wide association study of obsessive-compulsive disorder. *Mol Psychiatry* 2013; **18**(7)**:** 788-798.

337. Damgaard T, Knudsen LM, Dahl IM, Gimsing P, Lodahl M, Rasmussen T. Regulation of the CD56 promoter and its association with proliferation, anti-apoptosis and clinical factors in multiple myeloma. *Leukemia & lymphoma* 2009; **50**(2)**:** 236-246.

338. Ersland KM, Christoforou A, Stansberg C, Espeseth T, Mattheisen M, Mattingsdal M *et al.* Gene-based analysis of regionally enriched cortical genes in GWAS data sets of cognitive traits and psychiatric disorders. *PLoS One* 2012; **7**(2)**:** e31687.

339. Oved K, Morag A, Pasmanik-Chor M, Rehavi M, Shomron N, Gurwitz D. Genome-wide expression profiling of human lymphoblastoid cell lines implicates integrin beta-3 in the mode of action of antidepressants. *Transl Psychiatry* 2013; **3:** e313.

340. Sun C, Zhang YY, Tang CL, Wang SC, Piao HL, Tao Y *et al.* Chemokine CCL28 induces apoptosis of decidual stromal cells via binding CCR3/CCR10 in human spontaneous abortion. *Molecular human reproduction* 2013; **19**(10)**:** 676-686.

341. Gao B, Sun W, Wang X, Jia X, Ma B, Chang Y *et al.* Whole genome expression profiling and screening for differentially expressed cytokine genes in human bone marrow endothelial cells treated with humoral inhibitors in liver cirrhosis. *International journal of molecular medicine* 2013; **32**(5)**:** 1204-1214.

342. Iwamoto K, Kakiuchi C, Bundo M, Ikeda K, Kato T. Molecular characterization of bipolar disorder by comparing gene expression profiles of postmortem brains of major mental disorders. *Mol Psychiatry* 2004; **9**(4)**:** 406-416.

343. Chen TY, Hwang TL, Lin CY, Lin TN, Lai HY, Tsai WP *et al.* EMR2 receptor ligation modulates cytokine secretion profiles and cell survival of lipopolysaccharide-treated neutrophils. *Chang Gung medical journal* 2011; **34**(5)**:** 468-477.

344. Treutlein J, Cichon S, Ridinger M, Wodarz N, Soyka M, Zill P *et al.* Genome-wide association study of alcohol dependence. *Arch Gen Psychiatry* 2009; **66**(7)**:** 773-784.

345. Sebastiani P, Solovieff N, Dewan AT, Walsh KM, Puca A, Hartley SW *et al.* Genetic signatures of exceptional longevity in humans. *PLoS One* 2012; **7**(1)**:** e29848.

346. Terracciano A, Sanna S, Uda M, Deiana B, Usala G, Busonero F *et al.* Genome-wide association scan for five major dimensions of personality. *Mol Psychiatry* 2010; **15**(6)**:** 647-656.

347. Erraji-Benchekroun L, Underwood MD, Arango V, Galfalvy H, Pavlidis P, Smyrniotopoulos P *et al.* Molecular aging in human prefrontal cortex is selective and continuous throughout adult life. *Biol Psychiatry* 2005; **57**(5)**:** 549-558.

348. Bielli P, Busa R, Di Stasi SM, Munoz MJ, Botti F, Kornblihtt AR *et al.* The transcription factor FBI-1 inhibits SAM68-mediated BCL-X alternative splicing and apoptosis. *EMBO reports* 2014; **15**(4)**:** 419-427.

349. Claiborn KC, Sachdeva MM, Cannon CE, Groff DN, Singer JD, Stoffers DA. Pcif1 modulates Pdx1 protein stability and pancreatic beta cell function and survival in mice. *The Journal of clinical investigation* 2010; **120**(10)**:** 3713-3721.

350. Stegh AH, Herrmann H, Lampel S, Weisenberger D, Andra K, Seper M *et al.* Identification of the cytolinker plectin as a major early in vivo substrate for caspase 8 during CD95- and tumor necrosis factor receptor-mediated apoptosis. *Mol Cell Biol* 2000; **20**(15)**:** 5665-5679.

351. Sudhakar JN, Chow KC. Human RAD23 homolog A is required for the nuclear translocation of apoptosis-inducing factor during induction of cell death. *Biology of the cell / under the auspices of the European Cell Biology Organization* 2014; **106**(10)**:** 359-376.

352. Ma J, Fang B, Zeng F, Pang H, Zhang J, Shi Y *et al.* Curcumin inhibits cell growth and invasion through up-regulation of miR-7 in pancreatic cancer cells. *Toxicology letters* 2014; **231**(1)**:** 82-91.

353. Dhami GK, Liu H, Galka M, Voss C, Wei R, Muranko K *et al.* Dynamic methylation of Numb by Set8 regulates its binding to p53 and apoptosis. *Molecular cell* 2013; **50**(4)**:** 565-576.

354. Riaz SK, Iqbal Y, Malik MF. Diagnostic and therapeutic implications of the vascular endothelial growth factor family in cancer. *Asian Pacific journal of cancer prevention : APJCP* 2015; **16**(5)**:** 1677-1682.

355. Gangula NR, Maddika S. WD repeat protein WDR48 in complex with deubiquitinase USP12 suppresses Akt-dependent cell survival signaling by stabilizing PH domain leucine-rich repeat protein phosphatase 1 (PHLPP1). *J Biol Chem* 2013; **288**(48)**:** 34545-34554.

356. Le-Niculescu H, Balaraman Y, Patel S, Tan J, Sidhu K, Jerome RE *et al.* Towards understanding the schizophrenia code: an expanded convergent functional genomics approach. *Am J Med Genet B Neuropsychiatr Genet* 2007; **144B**(2)**:** 129-158.

357. Metkus TS, Timpone J, Leaf D, Bidwell Goetz M, Harris WS, Brown TT. Omega-3 fatty acid therapy reduces triglycerides and interleukin-6 in hypertriglyeridemic HIV patients. *HIV medicine* 2013; **14**(9)**:** 530-539.

358. Le-Niculescu H, Case NJ, Hulvershorn L, Patel SD, Bowker D, Gupta J *et al.* Convergent functional genomic studies of omega-3 fatty acids in stress reactivity, bipolar disorder and alcoholism. *Transl Psychiatry* 2011; **1:** e4.

359. Hammonds MD, Shim SS. Effects of 4-week treatment with lithium and olanzapine on levels of brain-derived neurotrophic factor, B-cell CLL/lymphoma 2 and phosphorylated cyclic adenosine monophosphate response element-binding protein in the sub-regions of the hippocampus. *Basic Clin Pharmacol Toxicol* 2009; **105**(2)**:** 113-119.

360. McQuillin A, Rizig M, Gurling HM. A microarray gene expression study of the molecular pharmacology of lithium carbonate on mouse brain mRNA to understand the neurobiology of mood stabilization and treatment of bipolar affective disorder. *Pharmacogenetics and genomics* 2007; **17**(8)**:** 605-617.

361. Ahmed MR, Gurevich VV, Dalby KN, Benovic JL, Gurevich EV. Haloperidol and clozapine differentially affect the expression of arrestins, receptor kinases, and extracellular signal-regulated kinase activation. *The Journal of pharmacology and experimental therapeutics* 2008; **325**(1)**:** 276-283.

362. Rushlow WJ, Seah C, Sutton LP, Bjelica A, Rajakumar N. Antipsychotics affect multiple calcium calmodulin dependent proteins. *Neuroscience* 2009; **161**(3)**:** 877-886.

363. Meffre D, Massaad C, Grenier J. Lithium chloride stimulates PLP and MBP expression in oligodendrocytes via Wnt/beta-catenin and Akt/CREB pathways. *Neuroscience* 2015; **284:** 962-971.

364. Youngs RM, Chu MS, Meloni EG, Naydenov A, Carlezon WA, Jr., Konradi C. Lithium administration to preadolescent rats causes long-lasting increases in anxiety-like behavior and has molecular consequences. *J Neurosci* 2006; **26**(22)**:** 6031-6039.

365. Bosetti F, Seemann R, Bell JM, Zahorchak R, Friedman E, Rapoport SI *et al.* Analysis of gene expression with cDNA microarrays in rat brain after 7 and 42 days of oral lithium administration. *Brain research bulletin* 2002; **57**(2)**:** 205-209.