

## IMMEDIATE COMMUNICATION

## Precision medicine for suicidality: from universality to subtypes and personalization

AB Niculescu<sup>1,2,3,4</sup>, H Le-Niculescu<sup>1,8</sup>, DF Levey<sup>1,2,8</sup>, PL Phalen<sup>3,8</sup>, HL Dainton<sup>1</sup>, K Roseberry<sup>1</sup>, EM Niculescu<sup>1</sup>, JO Niezer<sup>1</sup>, A Williams<sup>3</sup>, DL Graham<sup>3</sup>, TJ Jones<sup>3</sup>, V Venugopal<sup>1</sup>, A Ballew<sup>5</sup>, M Yard<sup>4</sup>, T Gelbart<sup>6</sup>, SM Kurian<sup>6</sup>, A Shekhar<sup>1</sup>, NJ Schork<sup>7</sup>, GE Sandusky<sup>4</sup> and DR Salomon<sup>6,†</sup>

Suicide remains a clear, present and increasing public health problem, despite being a potentially preventable tragedy. Its incidence is particularly high in people with overt or un(der)diagnosed psychiatric disorders. Objective and precise identification of individuals at risk, ways of monitoring response to treatments and novel preventive therapeutics need to be discovered, employed and widely deployed. We sought to investigate whether blood gene expression biomarkers for suicide (that is, a 'liquid biopsy' approach) can be identified that are more universal in nature, working across psychiatric diagnoses and genders, using larger cohorts than in previous studies. Such markers may reflect and/or be a proxy for the core biology of suicide. We were successful in this endeavor, using a comprehensive stepwise approach, leading to a wealth of findings. Steps 1, 2 and 3 were discovery, prioritization and validation for tracking suicidality, resulting in a Top Dozen list of candidate biomarkers comprising the top biomarkers from each step, as well as a larger list of 148 candidate biomarkers that survived Bonferroni correction in the validation step. Step 4 was testing the Top Dozen list and Bonferroni biomarker list for predictive ability for suicidal ideation (SI) and for future hospitalizations for suicidality in independent cohorts, leading to the identification of completely novel predictive biomarkers (such as CLN5 and AK2), as well as reinforcement of ours and others previous findings in the field (such as SLC4A4 and SKA2). Additionally, we examined whether subtypes of suicidality can be identified based on mental state at the time of high SI and identified four potential subtypes: high anxiety, low mood, combined and non-affective (psychotic). Such subtypes may delineate groups of individuals that are more homogenous in terms of suicidality biology and behavior. We also studied a more personalized approach, by psychiatric diagnosis and gender, with a focus on bipolar males, the highest risk group. Such a personalized approach may be more sensitive to gender differences and to the impact of psychiatric co-morbidities and medications. We compared testing the universal biomarkers in everybody versus testing by subtypes versus personalized by gender and diagnosis, and show that the subtype and personalized approaches permit enhanced precision of predictions for different universal biomarkers. In particular, LHFP appears to be a strong predictor for suicidality in males with depression. We also directly examined whether biomarkers discovered using male bipolars only are better predictors in a male bipolar independent cohort than universal biomarkers and show evidence for a possible advantage of personalization. We identified completely novel biomarkers (such as SPTBN1 and C7orf73), and reinforced previously known biomarkers (such as PTEN and SAT1). For diagnostic ability testing purposes, we also examined as predictors phenotypic measures as apps (for suicide risk (CFI-S, Convergent Functional Information for Suicidality) and for anxiety and mood (SASS, Simplified Affective State Scale)) by themselves, as well as in combination with the top biomarkers (the combination being our a priori primary endpoint), to provide context and enhance precision of predictions. We obtained area under the curves of 90% for SI and 77% for future hospitalizations in independent cohorts. Step 5 was to look for mechanistic understanding, starting with examining evidence for the Top Dozen and Bonferroni biomarkers for involvement in other psychiatric and non-psychiatric disorders, as a mechanism for biological predisposition and vulnerability. The biomarkers we identified also provide a window towards understanding the biology of suicide, implicating biological pathways related to neurogenesis, programmed cell death and insulin signaling from the universal biomarkers, as well as mTOR signaling from the male bipolar biomarkers. In particular, HTR2A increase coupled with ARRB1 and GSK3B decreases in expression in suicidality may provide a synergistic mechanistic corrective target, as do SLC4A4 increase coupled with AHCYL1 and AHCYL2 decrease. Step 6 was to move beyond diagnostics and mechanistic risk assessment, towards providing a foundation for personalized therapeutics. Items scored positive in the CFI-S and subtypes identified by SASS in different individuals provide targets for personalized (psycho)therapy. Some individual biomarkers are targets of existing drugs used to treat mood disorders and suicidality (lithium, clozapine and omega-3 fatty acids), providing a means toward pharmacogenomics stratification of patients and monitoring of response to treatment. Such biomarkers merit evaluation in clinical trials. Bioinformatics drug repurposing analyses with the gene expression biosignatures of the Top Dozen and Bonferroni-validated universal biomarkers identified novel potential therapeutics for suicidality, such as ebselen

<sup>1</sup>Department of Psychiatry, Indiana University School of Medicine, Indianapolis, IN, USA; <sup>2</sup>Stark Neuroscience Research Institute, Indiana University School of Medicine, Indianapolis, IN, USA; <sup>3</sup>Indianapolis VA Medical Center, Indianapolis, IN, USA; <sup>4</sup>INBRAIN, Indiana University School of Medicine, Indianapolis, IN, USA; <sup>5</sup>Marion County Coroner's Office, Indianapolis, IN, USA; <sup>6</sup>Department of Molecular and Experimental Medicine, The Scripps Research Institute, La Jolla, CA, USA and <sup>7</sup>J. Craig Venter Institute, La Jolla, CA, USA. Correspondence: Professor AB Niculescu, Department of Psychiatry, Indiana University School of Medicine, Neuroscience Research Building 200B, 320 West 15th Street, Indianapolis, IN 46202, USA.  
E-mail: anicules@iupui.edu

<sup>8</sup>These authors contributed equally to this work.

<sup>†</sup>Deceased.

(a lithium mimetic), piracetam (a nootropic), chlorogenic acid (a polyphenol) and metformin (an antidiabetic and possible longevity promoting drug). Finally, based on the totality of our data and of the evidence in the field to date, a convergent functional evidence score prioritizing biomarkers that have all around evidence (track suicidality, predict it, are reflective of biological predisposition and are potential drug targets) brought to the fore APOE and IL6 from among the universal biomarkers, suggesting an inflammatory/accelerated aging component that may be a targetable common denominator.

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## INTRODUCTION

'Individuality in universality is the plan of creation'.

–Swami Vivekananda

Objective and quantitative markers would permit better and more precise assessment, tracking and prediction of suicidal risk, which would enable preventive therapeutic interventions.<sup>1–3</sup> Previous work by our group has identified blood biomarkers and phenotypic predictors for suicide risk in men<sup>4</sup> and separately in women,<sup>5</sup> showing some gender similarities as well as differences. An essential question remained to be answered, of high relevance for developing this area of research and carrying it to full clinical applicability: would a quest for more universal predictors or a quest for more personalized predictors be more productive? We endeavored to answer this question through our current work. First, we sought to investigate whether blood gene expression biomarkers can be identified that are more universal in nature, working across psychiatric diagnoses and genders, starting with a powerful longitudinal within-participant<sup>6</sup> design and using larger cohorts than in previous studies<sup>7,4,5</sup> (Figure 1). Second, we identified subtypes of suicidality based on mental state (anxiety, mood and psychosis) at the time of high suicidal ideation.<sup>8–10</sup> Third, we used a more personalized approach, by gender and diagnosis, with a focus on the highest clinical risk group, male bipolars. We examined the ability of the universal candidate biomarkers to predict suicidal ideation (SI) and future hospitalizations for suicidality, in completely independent cohorts, in everybody, as well as divided by subtypes, and personalized by gender and diagnosis. We also directly compared the universal biomarkers with biomarkers discovered using male bipolars only, for ability to predict SI and future hospitalizations for suicidality in independent cohorts of male bipolars.

Per our *a priori* design described in previous studies,<sup>4,5</sup> we also combined the top biomarkers with scores obtained with a clinical information measure of suicide risk (Convergent Functional Information for Suicidality, CFI-S), as well as with scores for anxiety and mood obtained with an 11-item visual analog scale (Simplified Affective State Scale, SASS),<sup>4,5,8</sup> to obtain a broader spectrum predictor (UP-Suicide) that puts the biomarkers in the context of the person's life and his/hers mental state. The triggers for suicide may be the individual's perceptions of being unsuccessful, with no future, suffering, damaged, along with mental frailty, addictions and cultural exposure to suicide. Our CFI-S scale captures such information about who a person is, and along with the SASS scale that captures mental state information and permits classification in subtypes, they add a broader context to the objective blood biomarker predictors we have uncovered (Figure 5). Of note, these scales do not ask about SI, as individuals who want to commit suicide may not always share that information, for fear of being stopped.

We also used the lists of top biomarkers we identified as a window into the biology of suicidality, by conducting biological pathways and network analyses, and by looking at co-morbidity

with other disorders that may predispose or create a vulnerability to suicidality.

In addition, we leveraged these lists for therapeutics and drug discovery purposes, to see whether some of the biomarkers we identified are modulated by existing compounds used to treat suicidality and also to conduct bioinformatics drug repurposing analyses to discover new drugs and natural compounds that may be useful for treating suicidality.

Finally, we integrated the totality of evidence we have generated in this study and available in the literature to date, to prioritize biomarkers for future clinical studies in the field.

## MATERIALS AND METHODS

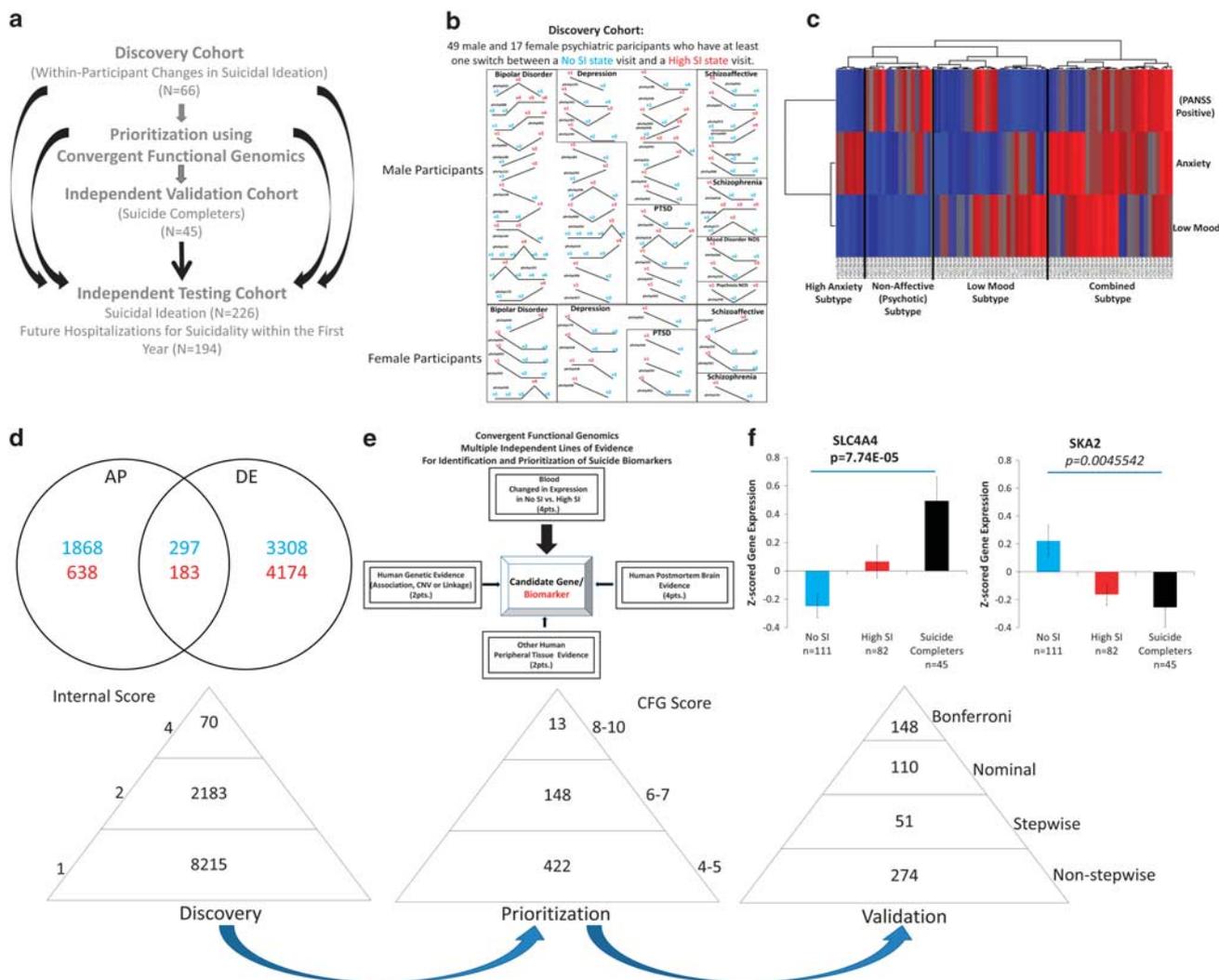
### Cohorts

We used three independent cohorts: discovery (a live psychiatric participants cohort), validation (a postmortem coroner's office suicide completers cohort) and testing (an independent live psychiatric participants test cohort for predicting SI and for predicting future hospitalizations for suicidality) (Figure 1a).

Similar to our previous studies,<sup>7,4,5</sup> the live psychiatric participants are part of a larger longitudinal cohort of adults that we are continuously collecting. Participants are recruited from the patient population at the Indianapolis VA Medical Center and Indiana University School of Medicine. All participants understood and signed informed consent forms detailing the research goals, procedure, caveats and safeguards, per Institutional Review Board-approved protocol. 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 new psychiatric 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 SI rating item (Supplementary Figure S1), and their blood was drawn. We collected whole blood (10 ml) 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 RNA was extracted for microarray gene expression studies from the PAXgene tubes, as detailed below.

For this study, our within-participant discovery cohort, from which the biomarker data were derived, consisted of 66 participants (49 males and 17 females) with psychiatric disorders and multiple testing visits, who each had at least one diametric change in SI scores from no SI to high SI, or vice versa, from one testing visit to another. There were 2 participants with 6 visits each, 3 participants with 5 visits each, 5 participants with 4 visits each, 34 participants with 3 visits each and 22 participants with 2 visits each, resulting in a total of 193 blood samples for subsequent gene expression microarray studies (Figure 1 and Table 1 and S1).

Our postmortem cohort, in which the top biomarker findings were validated for behavior, consisted of 38 male and 7 female violent suicide completers obtained through the Marion County coroner's office (Table 1). We required a last observed alive postmortem interval of 24 h or less and the cases selected had to have completed suicide by means other than overdose, which could affect gene expression. Thirty-one participants completed suicide by gunshot to head or chest, 12 by asphyxiation, 1 by slit



**Figure 1.** Steps 1–3: discovery, prioritization and validation. **(a)** Cohorts used in study, depicting flow of discovery, prioritization and validation of biomarkers from each step. **(b)** Discovery cohort longitudinal within-participant analysis. Phchp### is study ID for each participant. V# denotes visit number (1, 2, 3, 4, 5 or 6). **(c)** Discovery of possible subtypes of suicidality based on high suicidal ideation (SI) visits in the discovery cohort. Participants were clustered using measures of mood and anxiety (Simplified Affective State Scale (SASS)), as well as psychosis (PANSS Positive). **(d)** Differential gene expression in the Discovery cohort, number of genes identified with DE and AP methods with an internal score of 1 and above. Red, increased in expression in high SI. Blue, decreased in expression in high SI. At the discovery step probesets are identified based on their score for tracking SI with a maximum of internal points of 4 (33% (1 pt), 50% (2 pt) and 80% (4 pt)). **(e)** Prioritization with Convergent Functional Genomics (CFG) for prior evidence of involvement in suicide. In the prioritization step probesets are converted to their associated genes using Affymetrix annotation and GeneCards. Genes are prioritized and scored using CFG for Suicide evidence with a maximum of eight external points. Genes scoring at least 4 points out of a maximum possible of 12 points total internal and external score are carried to the validation step. **(f)** Validation in an independent suicide completers cohort from the coroner's office. In the validation step biomarkers are assessed for stepwise change from the discovery groups of participants with no SI, to high SI, to suicide completion, using analysis of variance. Stringent Bonferroni correction is calculated for the total number of probesets analyzed.

wrist and 1 by electrocution. Next of kin signed informed consent at the coroner's office for donation of blood for research.

Our independent test cohort for predicting SI (Table 1) consisted of 184 male and 42 female participants with psychiatric disorders, demographically matched with the discovery cohort, with one or multiple testing visits in our lab, with either no SI, intermediate SI or high SI, resulting in a total of 226 blood samples in which whole-genome blood gene expression data were obtained (Figure 1 and Table 1 and S1).

Our test cohort for predicting future hospitalizations (Figure 1 and Table 1 and S1) is a subset (170 males and 24 females) of the independent test cohort for which we had longitudinal follow-up with electronic medical records. The participants' subsequent number of psychiatric hospitalizations, with or without suicidality

(ideation or attempt), was tabulated from electronic medical records. Participants were evaluated for the presence of future hospitalizations 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 due to suicidality if suicidal acts or intent were listed as a reason for admission and/or SI was described in the admission and discharge medical notes.

Complete Materials and Methods are available in the Supplementary Information. Of note, all genomic and phenomic data was normalized (z-scored) by gender and psychiatric diagnosis before being combined and analyzed.

**Table 1.** Demographics

<i>A. Universal</i>					
	<i>Participants</i>	<i>Gender</i>	<i>Diagnosis</i>	<i>Ethnicity</i>	<i>Age mean (s.d.)</i>
<i>Discovery</i>					
Discovery cohort (longitudinal within-participant changes in SI)	66	Male = 49 Female = 17	BP = 25 MDD = 17 SZA = 9 SZ = 4 PTSD = 8 MOOD = 2 PSYCH = 1	EA = 51 AA = 14 Asian = 1	47.94 (9.47)
<i>Validation</i>					
Independent validation cohort for gene expression (suicide completers)	45	Male = 38 Female = 7	NP = 19 MDD = 19 BP = 2 SZ = 1 AX = 1 Alcoholism = 1 ADHD = 1 PTSD = 1	EA = 37 AA = 7 Hispanic = 1	40.69 (16.93)
<i>Testing</i>					
<i>All</i>					
Independent testing cohort for predicting state (SI at time of assessment)	226	Male = 184 Female = 42	BP = 68 MDD = 32 SZA = 53 SZ = 45 PTSD = 19 MOOD = 5 PSYCH = 4	EA = 148 AA = 73 Asian = 1 Hispanic = 3 Mixed = 1	All = 50.26 (9.47) No SI = 51.1 Intermediate SI = 49 High SI = 44.3
Independent testing cohort for predicting trait (hospitalizations for suicidality in the year following assessment)	194	Male = 170 Female = 24	BP = 52 MDD = 30 SZA = 45 SZ = 43 PTSD = 16 MOOD = 5 PSYCH = 3	EA = 126 AA = 64 Hispanic = 3 Mixed = 1	All = 50.65 (9.14) No Hosp for SI = 50.91 Hosp for SI = 47.66
<i>Subtypes</i>					
High anxiety subtype	46	Male = 40 Female = 6	BP = 13 MDD = 10 SZA = 9 SZ = 11 PTSD = 2 MOOD = 1	EA = 27 AA = 19	All = 50.96 (7.63) No SI = 52.1 Intermediate SI = 52.5 High SI = 39.4
Low mood subtype	76	Male = 57 Female = 19	BP = 21 MDD = 17 SZA = 15 SZ = 15 PTSD = 6 MOOD = 1 PSYCH = 1	EA = 53 AA = 20 Hispanic = 2 Asian = 1	All = 51.53 (10.04) No SI = 51.44 Intermediate SI = 51.81 High SI = 51.9
Combined subtype	86	Male = 61 Female = 25	BP = 30 MDD = 11 SZA = 21 SZ = 11 PTSD = 11 MOOD = 2	EA = 63 AA = 21 Hispanic = 1 Mixed = 1	All = 47.95 (9.36) No SI = 50.79 Intermediate SI = 45.43 High SI = 43.06
Non-affective (psychotic) subtype	141	Male = 121 Female = 20	BP = 40 MDD = 17 SZA = 35 SZ = 32 PTSD = 10 MOOD = 4 PSYCH = 3	EA = 86 AA = 52 Hispanic = 2 Mixed = 1	All = 50.71 (9.49) No SI = 50.89 Intermediate SI = 51.67 High SI = 42.33
<i>B. Male bipolar</i>					
	<i>Participants</i>	<i>Gender</i>	<i>Diagnosis</i>	<i>Ethnicity</i>	<i>Age mean (s.d.)</i>
<i>Discovery</i>					
Male bipolar discovery cohort (within-participant changes in SI)	20	Male = 20	BP = 20	EA = 20	48.12 (9.10)
<i>Validation</i>					
Male independent validation cohort for gene expression (suicide completers)	38	Male = 38	NP = 18 MDD = 16 BP = 1 SZ = 1 AX = 1 Alcoholism = 1	EA = 31 AA = 6 Hispanic = 1	40.82 (17.31)
<i>Testing</i>					
Male bipolar independent testing cohort for predicting state (SI at time of assessment)	49	Male = 49	BP = 49	EA = 43 AA = 5 Hispanic = 1	All = 49.16 (10.01) No SI = 50.19 Intermediate SI = 48.73 High SI = 40.42
Male bipolar independent testing cohort for predicting trait (hospitalizations for suicidality in the year following assessment)	44	Male = 44	BP = 44	EA = 39 AA = 4 Hispanic = 1	All = 48.88 (10.23) No Hosp for SI = 48.76 Hosp for SI = 52.25

Abbreviations: AA, African American; ADHD, attention deficit disorder; AX, anxiety disorder; BP, bipolar; EA, European-American; MDD, major depressive disorder; MOOD, mood disorder not otherwise specified; NP, non-psychiatric; PSYCH, psychosis not otherwise specified; PTSD, post-traumatic stress disorder; SZA, schizoaffective disorder; SZ, schizophrenia.

## RESULTS

### Step 1: Discovery

We used a powerful within-participant longitudinal discovery approach to identify genes that: (1) change in expression in blood between no SI and high SI states; (2) track the SI state across visits in a participant; and (3) track the SI state in multiple participants. We used a longitudinally followed cohort of participants that showed diametric changes in SI between at least two testing visits ( $n=66$  participants out of a cohort of 293 men and women psychiatric disorder participants followed longitudinally, with diagnoses of bipolar disorder, depression, mood disorder nos, schizophrenia, schizoaffective disorder, psychosis nos and post-traumatic stress disorder). Using our 33% of maximum raw score threshold (internal score of 1 pt),<sup>4,5</sup> we had 10 468 unique probesets from Affymetrix Absent/Present (AP) analyses and Differential Expression (DE) analyses (Figure 1d). These were carried forward to the prioritization step. This represents approximately a fivefold enrichment of the 54 625 probesets on the Affymetrix array.

We also examined in the discovery cohort whether subtypes of suicidality can be identified based on mental state at the time of high SI visits, using two-way hierarchical clustering with anxiety, mood and psychosis measures. The SI state self-report may be more reliable in this cohort, as the participants demonstrated the aptitude and willingness to report different and diametric SI states. We uncovered four potential subtypes of suicidality: high anxiety, low mood, co-morbid and non-affective (psychotic) (Figure 1c). These subtypes need to be tested in independent cohorts for practical utility, diagnostic and therapeutic.

### Step 2: Prioritization

We used a Convergent Functional Genomics approach to prioritize the candidate biomarkers identified in the discovery step (internal score of  $\geq 1$  pt) by using all the published prior independent evidence in the field (Figure 1e). There were 583 probesets that had a Convergent Functional Genomics score (combined internal and external score) of 4 and above. These were carried forward to the validation step. This represents approximately a 100-fold enrichment of the probesets on the Affymetrix array.

### Step 3: Validation

Next, we validated for suicidal behavior these prioritized biomarkers, in a demographically matched cohort of men and women suicide completers from the coroner's office ( $n=45$ ), by assessing which markers were stepwise changed in expression from no SI to high SI to suicide completers (Figure 1). Two hundred and seventy-four probesets were non-stepwise changed and 309 were stepwise changed. Of these, 148 survived Bonferroni correction for all the 583 probesets validated. This represents approximately a 500-fold enrichment of the probesets on the Affymetrix array.

### Step 4: Testing for diagnostics

We tested for diagnostic ability in independent cohorts two overlapping sets of biomarkers: the universal Top Dozen biomarkers (composed of the top increased and decreased biomarkers from AP and from DE from each step: discovery, prioritization and validation) (Table 2), as well as all the universal Bonferroni biomarkers, that survived correction for multiple comparisons after the validation step (Supplementary Table S2). The biomarkers were tested individually (the 12 biomarkers from the Top Dozen list and 148 biomarkers from the Bonferroni list), as well as in panels (BioM12 and BioM 148), in a completely independent test cohort of men and women psychiatric disorder participants ( $n=226$ ), for prediction of SI state, as well as for prediction of future psychiatric hospitalizations due to suicidality (Figures 2 and 3, Table 3 and Supplementary Table S4). We were successful in this endeavor, leading to identification of universal

biomarkers that work across gender and diagnoses, such as CLN5 and AK2.

We also studied their predictive ability in participants in the independent cohort grouped by the subtypes described above, as well as grouped by a more personalized approach, by psychiatric diagnosis and gender. We then compared the universal approach to the subtypes approach and the personalized approach, and show that the subtype and personalized approaches permit enhanced precision of predictions for different biomarkers (Figures 2 and 3, Supplementary Figure S2, Table 3 and Supplementary Table S4).

For SI prediction in the independent test cohort, CLN5, from the Bonferroni biomarkers list, a decreased in expression biomarker, had an area under the curve (AUC) of 65% ( $P=1.86E-04$ ) across all subjects, and 75% ( $4.43E-03$ ) in the low mood subtype. It also survived correction for multiple comparisons for the Step 4 testing of the 154 universal biomarkers (from the combined Top Dozen and Bonferroni lists). CLN5 also had an AUC of 87% ( $P=1.16E-02$ ) for predicting future hospitalizations for suicidality in the first year of follow-up in male post-traumatic stress disorder. CLN5 (ceroid-lipofuscinosis, neuronal 5) is a completely novel finding. It has no prior evidence as a biomarker for suicide or for involvement in other psychiatric disorders. CLN5 is a lysosomal regulatory protein, known to date to be involved in neurodegenerative, lysosomal storage diseases.

For prediction of future hospitalizations for suicidality in the first year of follow-up in the independent test cohort, AK2, from the Bonferroni biomarkers list, a decreased in expression biomarker, had an AUC of 60% ( $P=2.31E-02$ ) across all subjects, 68% ( $P=6.72E-03$ ) in the combined subtype and 78% ( $P=2.70E-03$ ) for male schizoaffectives. AK2 also had an AUC of 64% ( $P=5.39E-04$ ) for predicting SI state across all subjects in the independent test cohort, as well as an AUC of 75% ( $P=2.93E-02$ ) in male schizophrenia. AK2 (adenylate kinase 2) is also a completely novel finding. It has no prior evidence as a biomarker for suicide, but does have evidence for a decrease in expression in brains of schizophrenics.<sup>11</sup> AK2 is a mitochondrial gene, known to have an important role in cellular energy homeostasis and in adenine nucleotide metabolism, as well as may have a role in apoptosis.

As for examples of previously known biomarkers reproduced in this study, for SI prediction in the independent test cohort, SLC4A4, a top increased in expression biomarker, had an AUC of 64% ( $P=3.83E-04$ ) across all subjects, 69% ( $6.13E-04$ ) in the combined subtype and 77% ( $9.72E-04$ ) in male bipolars. SKA2, a top decreased in expression biomarker, had an AUC of 61% ( $P=3.35E-03$ ) across all subjects, 74% ( $5.91E-03$ ) in the low mood subtype and 79% ( $1.35E-02$ ) in male schizophrenics.

In addition, we used two previously described clinical instruments in the form of apps, the SASS that measures anxiety and mood, and the CFI-S that measures risk for suicide indirectly, without asking about SI.<sup>4,5</sup> The scores from these apps showed good predictive ability for both state (SI) and trait (future hospitalizations), in all participants (Figure 4, Table 3). There are interesting variations in different subtypes and personalized by gender and diagnosis (Supplementary Table S4), suggesting the distinctness and homogeneity of those subgroups.

We also combined a panel of the Top Dozen biomarkers with measures of anxiety and mood (SASS), and with the suicide risk scale (CFI-S), into a broad spectrum universal predictor algorithm (UP Suicide), our *a priori* endpoint as in our previous studies. The UP Suicide provides the biomarkers with mental state (SASS) and personal history context (CFI-S), enhancing precision of predictions (Figures 5 and 6). Across all subjects in the independent test cohort, UP Suicide 12 had an AUC of 90% ( $P=3.87E-21$ ) for state (SI) prediction, as well as an AUC of 77% ( $P=2.87E-08$ ) for trait (future hospitalizations for suicidality) predictions. The results for predicting SI were even stronger in the low mood subtype (AUC of

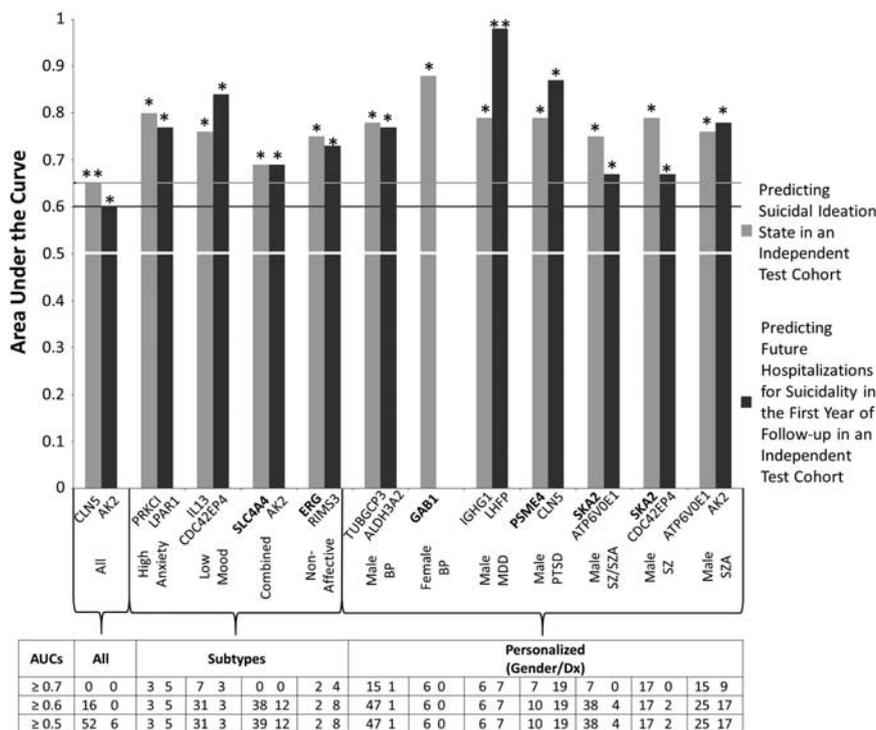
**Table 2.** The Top Dozen list of candidate biomarker genes - evidence for involvement in suicidality

A. Top Dozen biomarkers from universal approach								
Gene symbol Gene name	Probesets	Discovery (direction of change) method/score	Prior human genetic evidence for suicide	Prior human brain expression evidence for suicide	Prior human peripheral expression evidence for suicide	Prioritization total CFG score for suicide	Validation ANOVA P-value	Descriptor
<i>Top biomarkers from discovery—step 1</i>								
HIST1H2BO Histone cluster 1, H2bo	214540_at	(I) DE/4			Our previous work in males (I)(214540_at) Blood <sup>4</sup>	4	5.37E-14	Top discovery DE increased gene
ERG V-ets avian erythroblastosis virus E26 oncogene homolog	213541_s_at	(D) DE/4			Our previous work in males (D) (213541_s_at) Blood <sup>4</sup> Our previous work in females (D) (213541_s_at) Blood <sup>5</sup>	4	NS	Top discovery DE decreased gene
GAB1 GRB2-associated binding protein 1	242572_at	(I) AP/4			Our previous work in males (I) (242572_at) Blood <sup>4</sup>	4	NS	Top discovery AP increased gene
CCL28 Chemokine (C-C motif) ligand 28	224240_s_at	(D) AP/4			Our previous work in males (D) (224240_s_at) Blood <sup>4</sup> Our previous work in females (D) (224240_s_at) Blood <sup>5</sup>	4	NS	Top discovery AP Decreased gene
<i>Top biomarkers from prioritization—step 2</i>								
HTR2A 5-Hydroxytryptamine (serotonin) receptor 2A, G protein-coupled	244130_at	(I) DE/2	Association <sup>28-33</sup>	(I) Prefrontal cortex <sup>34</sup> (I) Frontal cortex <sup>35,36</sup>	(D) Platelets <sup>37</sup> Our previous work in females (D) (244130_at) Blood <sup>5</sup>	10	NS	Top prioritization DE increased gene
SKA2 Spindle and kinetochore-associated complex subunit 2	225686_at	(D)DE/1 (D)AP/1	Association <sup>38</sup>	(D) Prefrontal cortex <sup>38</sup>	(D)Blood <sup>38</sup> (D)Blood, saliva <sup>39</sup> Our previous work in males (D)(225686_at) Blood <sup>4</sup>	9	0.0045542	Top prioritization DE decreased gene
SLC4A4 Solute carrier family 4 (sodium bicarbonate cotransporter), member 4	210739_x_at	(I) AP/1	Association <sup>40</sup>	(D) Prefrontal cortex(BA 46/10) <sup>41</sup>	Our previous work in males (I)(210739_x_at) Blood <sup>4</sup>	7	7.74E-05	Top prioritization AP increased gene
IFNG Interferon, gamma	210354_at	(D) AP/1	Association <sup>42</sup>	(D) Hippocampus <sup>43</sup>	(D) Blood <sup>44</sup> Our previous work in females (D) (210354_at) Blood <sup>5</sup>	9	NS	Top prioritization AP decreased gene
<i>Top biomarkers from validation—step 3</i>								
PSME4 Proteasome activator subunit 4	237180_at	(I) DE/1		(I) Anterior cingulate cortex <sup>20</sup>		5	2.64E-36	Top validation DE increased gene
LDLRAP1 Low-density lipoprotein receptor adaptor protein 1	57082_at	(D) DE/1		(I) Anterior cingulate cortex <sup>20</sup>	Our previous work in males (D)(221790_s_at) Blood <sup>4</sup>	5	1.48E-38	Top validation DE decreased gene
PPAP2B Phosphatidic acid phosphatase type 2B	212226_s_at	(I)AP/1		(D) Prefrontal cortex (BA 46/10) <sup>41</sup>	Our previous work in females (I)(212226_s_at) Blood <sup>5</sup>	5	2.76E-17	Top validation AP increased gene
ARRB1 Arrestin, beta 1	218832_x_at	(D) AP/1		(D) Prefrontal cortex (BA8/9) <sup>45</sup>		5	5.26E-17	Top validation AP decreased gene
<i>B. Top Dozen biomarkers from male bipolars</i>								
Gene symbol Gene name	Probesets	Discovery (direction of change) method/score	Prior human genetic evidence for suicide	Prior human brain expression evidence for suicide	Prior human peripheral expression evidence for suicide	Prioritization Total CFG score for suicide	Validation ANOVA P-value	Descriptor
<i>Top biomarkers from discovery—step 1</i>								
BE674182	237259_at	(I) DE/4				4.00	NS	Top discovery DE increased gene
ICAM4 Intercellular adhesion molecule 4 (Landsteiner-Wiener blood group)	207194_s_at	(D) DE/4			Our previous work in males (D) (207194_s_at) Blood <sup>4</sup> Our previous work in females (I) (207194_s_at) Blood <sup>5</sup>	4.00	3.81E-08	Top discovery DE decreased gene
	208299_at	(I) AP/4				4.00	NS	Top discovery AP increased gene

**Table 2.** (Continued)

<i>B. Top Dozen biomarkers from male bipolars</i>								
Gene symbol Gene name	Probesets	Discovery (direction of change) method/score	Prior human genetic evidence for suicide	Prior human brain expression evidence for suicide	Prior human peripheral expression evidence for suicide	Prioritization Total CFG score for suicide	Validation ANOVA P-value	Descriptor
<i>CACNA11</i> Calcium channel, voltage-dependent, T type, alpha 1I subunit					Our previous work in males (I) (208299_at) Blood <sup>4</sup>			
<i>ADAL</i> Adenosine deaminase-like	239711_at	(D) AP/4			Our previous work in males (D) (239711_at) Blood <sup>4</sup> Our previous work in females (D) (239711_at) Blood <sup>5</sup>	4.00	4.53E–08	Top discovery AP decreased gene
<i>Top biomarkers from prioritization—step 2</i>								
<i>HTR2A</i> 5-Hydroxytryptamine (serotonin) receptor 2A, G protein-coupled	244130_at	(I) DE/2	Association 29–33,46	(I) Prefrontal cortex <sup>34</sup>			10.00	NS Top prioritization DE Increased Gene
<i>CRHR1</i> Corticotropin-releasing hormone receptor 1	214619_at	(D) DE/1	Association <sup>47–49</sup>	Frontal cortex <sup>35,36</sup> (I) Pituitary <sup>50</sup>			7.00	NS Top prioritization DE decreased gene
<i>KSR1</i> Kinase suppressor of ras 1	213769_at	(I) AP/4		(I) Nucleus accumbens <sup>20</sup>	Our previous work in males (I) (213769_at) Blood <sup>4</sup>		8.00	NS Top Prioritization AP increased gene
<i>CLYBL</i> Citrate lyase beta like	239683_at	(D) AP/4		(I) Brain <sup>51</sup>	Our previous work in males (D) (239683_at) Blood <sup>4</sup>		8.00	0.008799 Top prioritization AP decreased gene
<i>Top biomarkers from validation—step 3</i>								
<i>C20orf27</i> Chromosome 20 open reading frame 27	218081_at	(D) DE/2		(I) Anterior Cingulate Cortex <sup>20</sup>	Our previous work in males (D) (218081_a) Blood <sup>4</sup>		6.00	1.09E–34 Top validation DE decreased gene
<i>SAT1</i> Spermidine/spermine N1-acetyltransferase 1	213988_s_at	(I) DE/2	Association <sup>52,53</sup>	(I) Prefrontal cortex (BA46) <sup>54</sup> (D) Prefrontal cortex <sup>55</sup> Prefrontal cortex (BA4, BA8/9, and BA11) <sup>56</sup> (BA44) <sup>54</sup> (BA9) <sup>57</sup>	Our previous work in males (I) (213988_s_at) Blood <sup>4</sup>		8.00	4.06E–34 Top validation DE increased gene
<i>SPTBN1</i> Spectrin, beta, non-erythrocytic 1	215918_s_at	(I) AP/1		(I) Nucleus accumbens <sup>20</sup>	Our previous work in females (I)(214856_at) Blood <sup>5</sup>		5.00	6.7E–32 Top validation AP increased gene
<i>POLR2D</i> Polymerase (RNA) II (DNA directed) polypeptide D	214144_at	(D) AP/1		(I) Anterior cingulate cortex <sup>20</sup>	Our previous work in males (D)(214144_a) Blood <sup>4</sup> Our previous work in females (I) (214144_at) Blood <sup>5</sup>		5.00	2.1E–08 Top validation AP decreased gene

Abbreviations: ANOVA, analysis of variance; AP, absent/present; DE, differential expression; NS, non-stepwise in validation. Italic *P*-values are nominally but not Bonferroni significant.



**Figure 2.** Step 4: Testing for Diagnostics. Best single universal biomarkers predictors. From Top Dozen List (bold) and from Bonferroni List (combined 154 biomarkers). Bar graph shows best predictive biomarkers in each group. \*Nominally significant  $P < 0.05$ . \*\*Survives correction for multiple comparisons testing of 154 biomarkers,  $P < 0.000325$ . Table underneath the figures displays the actual number of biomarkers for each group whose region of interest (ROC) area under the curve (AUC)  $P$ -values are at least nominally significant. Some female diagnostic groups are missing from the graph, as they did not have any nominally significant biomarkers, due at least in part to the small number of cases.

92%,  $P = 7.42E - 06$ ) and, in male bipolars, the highest risk group (AUC 96%,  $P = 8.03E - 08$ ). For predicting future hospitalizations, the results were stronger in the high anxiety subtype (AUC 79%,  $P = 7.52E - 03$ ) and in male depression (AUC 95%,  $P = 4.88E - 04$ ).

#### Step 5: Biological vulnerability understanding

*Evidence for involvement in other disorders.* We conducted Convergent Functional Genomics analyses using the Top Dozen and Bonferroni biomarkers (Supplementary Table S5), which suggest that a majority (89%) of suicide biomarkers are involved in other psychiatric disorders, providing a basis for co-morbidity and increased vulnerability. A number of biomarkers (18%) were also involved in aging and longevity, possible substrates for our 'life switch' hypothesis.

*Biological pathways.* We conducted biological pathway analyses using the Bonferroni validated biomarkers, which suggest that neurotrophic factors, programmed cell death and insulin signaling are involved in the biology of suicide (Table 4).

*Networks and Interactions.* We conducted STRING analyses that revealed groups of directly interacting genes, in particular HTR2A/ARRB1/GSK3B, and SLC4A4/AHCYL1/AHCYL2 (Supplementary Figure S3). These networks may have biological significance and could be targeted therapeutically.

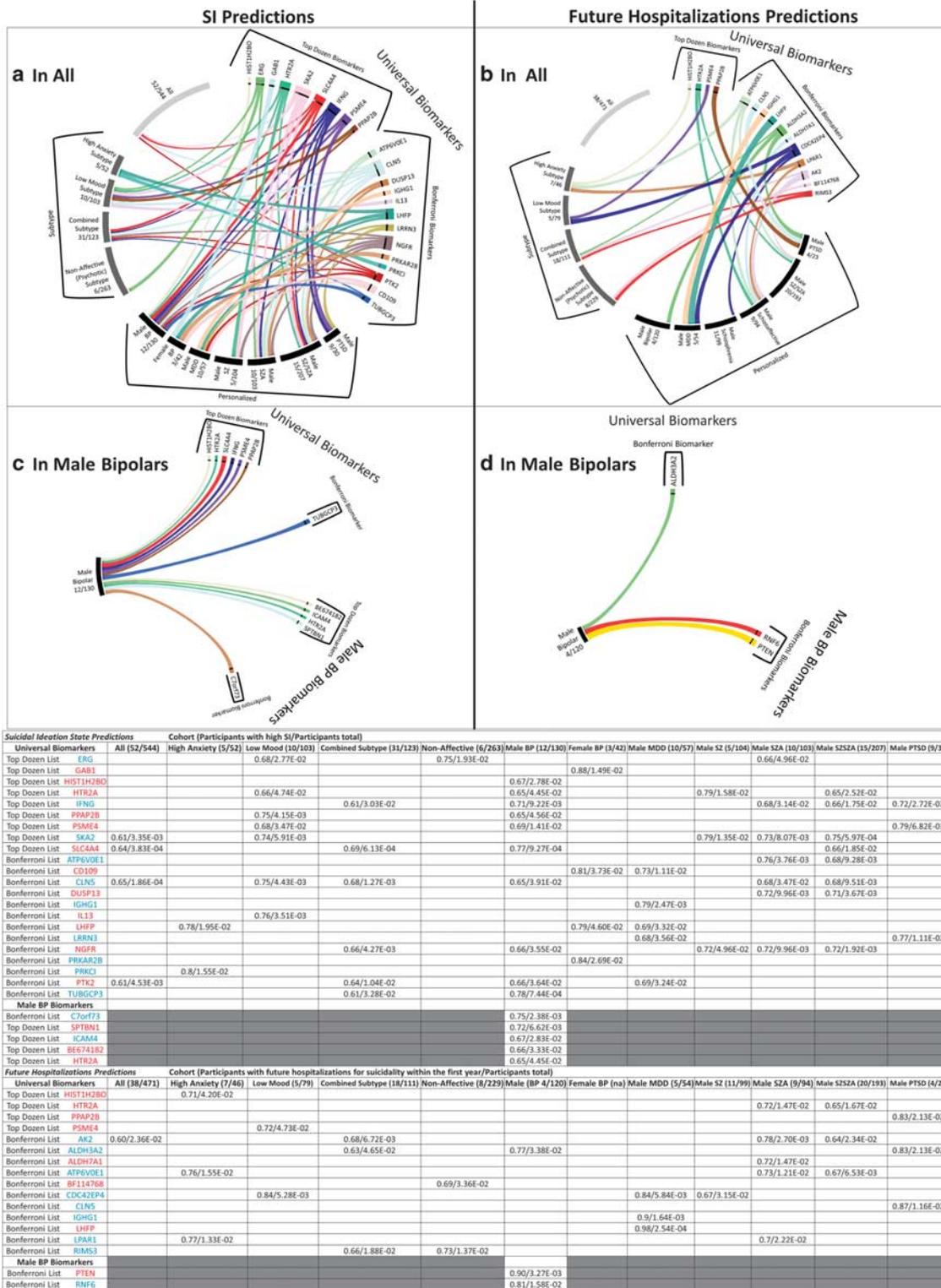
*Circadian.* A number of top biomarkers identified by us have biological roles that are related to the circadian clock (Supplementary Table S5). To be able to ascertain all the genes in our dataset that were circadian and do estimates for enrichment, we compiled from the literature a database of all the known genes that fall into these three categories, numbering a total of 1468 genes. Using an estimate

of about 21 000 genes in the human genome, that gives about 7% of genes having some circadian pattern. Out of our 154 top biomarker genes, 18 had circadian evidence (11.7%) (Supplementary Table S5), suggesting a 1.7-fold enrichment for circadian genes. Circadian clock abnormalities are related to mood disorders<sup>12,13</sup> and sleep abnormalities have been implicated in suicide.<sup>14</sup>

*Enrichment in suicide completers.* Of the candidate biomarkers from the Prioritization step, 125/430 of the DE ones (29.1%) and 37/180 of the AP ones (20.6%) were Bonferroni validated in suicide completers. There is a 1.4-fold enrichment in DE vs AP, which suggests that completion of suicide may be due more to an incremental change in expression of genes rather than the complete turning on and off of genes.

#### Step 6: Therapeutics

*Pharmacogenomics.* A number of individual top biomarkers are known to be modulated by medications in current clinical use for treating suicidality, such as lithium (HTR2A, GSK3B, ITGB1BP1 and BCL2), clozapine (IL6, CD164, CD47, HTR2A, PGK1, DYRK2, IFNG and LPAR1) and omega-3 fatty acids (APOE, CD47, ACP1, GATM, LHFP and LPAR1) (Figure 7, Table 5 and Supplementary Table S5). In particular, HTR2A and CRYAB are at the overlap of lithium and clozapine, and MBP is at the overlap of all three treatments (Figure 7). Omega-3 fatty acids may be a widely deployable preventive treatment, with minimal side effects, including in women who are or may become pregnant. Of note, CD109, a Bonferroni list biomarker increased in expression in suicidality in our studies (Supplementary Table S5), has also reported to be increased in expression by treatment of lymphoblastoid cells with the SSRI paroxetine, and thus merits follow-up as a potentially useful biomarker for treatment-emergent SI.



**Figure 3.** Step 4: Testing for Diagnostics. Universal and male bipolar biomarkers. Best individual biomarkers from Top Dozen List and from Bonferroni List, for universal and for male bipolar. We only show biomarker results where region of interest (ROC) area under the curve (AUC) *P*-values are at least nominally significant and AUCs are at least 0.6 (60%). (a) Circos plot depicting the best individual biomarker predictions for suicidal ideation (SI) state in the independent cohort (across all participants, in subtypes and personalized by gender and diagnosis), using universal biomarkers. (b) Circos plot depicting the best individual biomarker predictions for future hospitalizations for suicidality in the first year following testing in the independent cohort (across all participants, in subtypes and personalized by gender and diagnosis), using universal biomarkers. (c) Circos plot depicting the best individual biomarker predictions for SI state in the independent male bipolar sub-cohort, using universal biomarkers and male bipolar biomarkers. (d) Circos plot depicting the best individual biomarker predictions for future hospitalizations for suicidality in the first year following testing in the independent male bipolar sub-cohort, using universal biomarkers and male bipolar biomarkers. The circumference bands represent and are proportional to the number of participants in each cohort. The ribbons represent and are proportional to the AUC of the predictions. Table underneath the figures displays the actual numerical results.

**Table 3.** Step 4: Diagnostics

A. SI state						
Predictors	Cohort	Participants visits with high SI/participants visits total	ROC AUC/P-value	Suicidality severity (HAMD SI score) correlation R/P-value	T-test P-value	
<i>Universal</i>						
<b>Best Biomarkers</b>						
SLC4A4	All	52/544	0.64/3.83E-04	0.13/1.54E-03	1.50E-03	
CLN5	All	52/544	<b>0.65/1.86E-04</b>	-0.11/6.13E-03	3.90E-04	
BioM 148 Panel (Bonferroni List)	All	52/544	0.61/6.18E-03	0.069/5.33E-02	1.77E-02	
BioM 12 Panel (Top Dozen List)	All	52/544	0.61/3.66E-03	0.12/3.02E-03	3.08E-03	
BioM 2 Panel (SLC4A4 and CLN5)	All	52/544	<b>0.66/4.92E-05</b>	0.14/7.82E-04	1.90E-04	
<b>Phenes</b>						
Mood	All	52/544	<b>0.77/5.93E-11</b>	-0.38/3.17E-20	1.95E-10	
Anxiety	All	52/544	<b>0.77/3.43E-11</b>	0.31/8.60E-14	2.03E-12	
Mood and Anxiety (SASS)	All	52/544	<b>0.81/5.55E-14</b>	0.40/3.66E-22	3.57E-14	
CFI-S	All	52/523	<b>0.86/9.98E-18</b>	0.43/1.03E-24	5.46E-16	
Mood and Anxiety and CFI-S	All	52/523	<b>0.89/2.59E-20</b>	0.49/1.60E-33	1.08E-18	
<b>Phenes and Biomarkers</b>						
Mood and Anxiety and CFI-S and BioM 148	All	52/523	<b>0.89/1.36E-20</b>	0.49/2.84E-33	2.88E-18	
Mood and Anxiety, and CFI-S and BioM 12 (UP-Suicide)	All	52/523	<b>0.90/3.87E-21</b>	0.50/5.91E-35	3.42E-19	
Mood and Anxiety, and CFI-S and BioM 2	All	52/523	<b>0.89/4.56E-21</b>	0.50/4.07E-34	2.83E-18	
<i>Male Bipolar</i>						
<b>Best Biomarkers</b>						
SPTBN1	M-BP	12/130	0.72/6.62E-03	0.21/8.54E-03	9.05E-03	
C7orf73	M-BP	12/130	0.75/2.38E-03	-0.17/2.76E-02	1.08E-04	
BioM 54 Panel (Bonferroni List)	M-BP	12/130	0.49/5.29E-01	0/4.90E-01	7.12E-01	
BioM 12 Panel (Top Dozen List)	M-BP	12/130	0.57/2.08E-01	0.08/1.78E-01	8.79E-02	
BioM 2(SPTBN1 and C7orf73)	M-BP	12/130	0.80/3.54E-04	0.23/4.77E-03	6.62E-05	
<b>Phenes</b>						
Mood	M-BP	12/130	0.8/3.65E-04	-0.47/6.83E-09	1.65E-03	
Anxiety	M-BP	12/130	0.86/2.19E-05	0.41/7.09E-07	1.91E-05	
Mood and Anxiety (SASS)	M-BP	12/130	0.86/1.66E-05	0.5/7.15E-10	5.66E-05	
CFI-S	M-BP	12/128	0.92/1.10E-06	0.5/6.11E-10	1.31E-06	
Mood and Anxiety, and CFI-S	M-BP	12/128	0.94/2.82E-07	0.61/1.24E-14	3.01E-06	
<b>Phenes and Biomarkers</b>						
Mood and Anxiety, and CFI-S and BioM 54	M-BP	12/128	0.93/5.30E-07	0.61/1.78E-14	5.54E-06	
Mood and Anxiety, and CFI-S and BioM 12	M-BP	12/128	0.95/1.62E-07	0.62/1.92E-15	8.31E-07	
Mood and Anxiety, and CFI-S and BioM 2	M-BP	12/128	0.97/5.14E-08	0.64/2.29E-16	2.59E-07	
<b>B. Future hospitalizations for suicidality in the first year following assessment</b>						
Predictors	Cohort	Participants visits with future hospitalizations for suicidality within the first year/participants visits total	ROC AUC/P-value	Frequency of future hospitalizations for suicidality within the first year correlation R/P-value	T-test P-value	Cox regression hazard ratio /P-value
<i>Universal</i>						
<b>Best Biomarkers</b>						
PSME4	All	38/471	0.59/2.62E-02	0.08/4.12E-02	6.20E-02	1.23/ 1.56E-01
AK2	All	38/471	0.60/2.31E-02	-0.06/9.70E-02	9.39E-03	1.35/ 7.22E-02
BioM 148 Panel (Bonferroni List)	All	38/471	0.52/3.37E-01	-0.02/6.67E-01	4.18E-01	1.09/8.27E-01
BioM 12 Panel (Top Dozen List)	All	38/471	0.58/4.20E-02	0.05/1.47E-01	5.02E-02	1.88/1.41E-01
BioM 2 Panel (PSME4 and AK2)	All	38/471	0.65/1.10E-03	0.10/1.29E-02	1.35E-03	1.68/0.018

**Table 3.** (Continued)

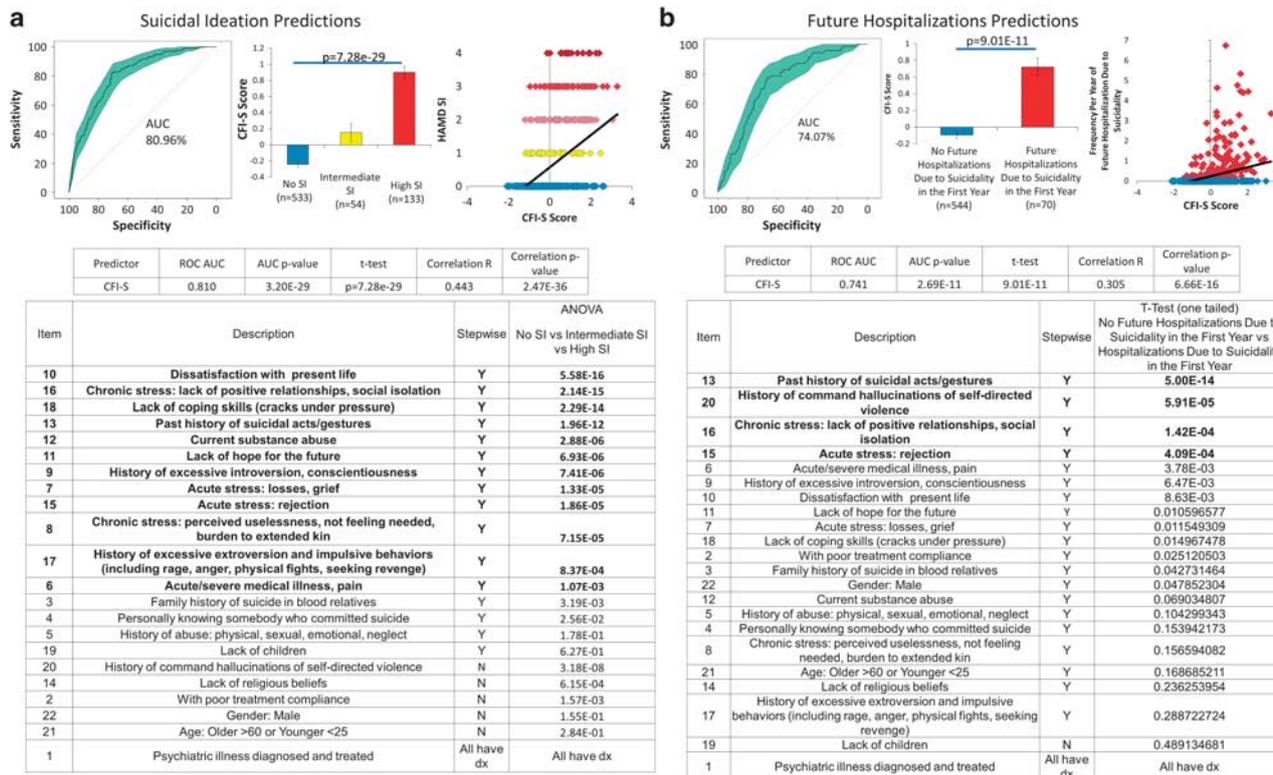
<i>B. Future hospitalizations for suicidality in the first year following assessment</i>						
Predictors	Cohort	Participants visits with future hospitalizations for suicidality within the first year/participants visits total	ROC AUC/P-value	Frequency of future hospitalizations for suicidality within the first year correlation R/P-value	T-test P-value	Cox regression hazard ratio /P-value
<b>Phenes</b>						
Mood	All	38/471	0.65/1.00E-03	-0.16/3.63E-04	1.03E-03	1.69/1.47E-03
Anxiety	All	38/471	<b>0.69/3.70E-05</b>	0.16/3.43E-04	2.30E-04	1.82/2.62E-04
Mood and Anxiety (SASS)	All	38/471	<b>0.71/9.78E-06</b>	0.18/4.89E-05	7.73E-05	1.45/8.11E-05
CFI-S	All	38/470	<b>0.75/1.79E-07</b>	0.2/5.11E-06	1.40E-06	2.02/7.11E-07
Mood and Anxiety and CFI-S	All	38/470	<b>0.76/6.34E-08</b>	0.22/4.18E-07	2.22E-06	1.40/1.13E-07
HAMD SI	All	35/458*	<b>0.81/5.27E-10</b>	0.40/1.57E-19	2.64E-06	2.10/1.11E-15
Mood and Anxiety, and CFI-S and HAMD SI	All	35/458*	<b>0.82/9.96E-11</b>	0.35/4.11E-15	4.34E-08	1.36/1.83E-13
<b>Phenes and Biomarkers</b>						
Mood and, Anxiety and CFI-S and BioM 148	All	38/470	<b>0.76/6.65E-08</b>	0.21/1.29E-06	2.29E-06	1.37/2.01E-07
<i>Mood and Anxiety, and CFI-S and BioM 12 (UP-Suicide)</i>	All	38/470	<b>0.77/2.87E-08</b>	<i>0.23/2.81E-07</i>	<i>9.11E-07</i>	<i>1.40/5.31E-08</i>
Mood and Anxiety, and CFI-S and BioM 2	All	38/470	<b>0.76/3.87E-08</b>	0.24/1.17E-07	1.02E-06	1.39/3.98E-08
Mood and Anxiety, and CFI-S and HAMD SI, and BioM 2	All	35/458*	<b>0.82/9.38E-11</b>	0.35/3.20E-15	3.39E-08	1.35/1.83E-13
<i>Male bipolars</i>						
<b>Best biomarkers</b>						
PTEN	M-BP	4/120	0.9/3.27E-03	0.22/6.76E-03	3.12E-02	1.73/2.73E-02
RNF6	M-BP	4/120	0.82/1.58E-02	-0.14/5.89E-02	9.14E-03	6.24/7.19E-02
BioM 54 Panel (Bonferroni List)	M-BP	4/120	0.75/4.23E-02	0.11/1.23E-01	4.71E-02	4.58/2.52E-01
BioM 12 Panel (Top Dozen List)	M-BP	4/120	0.56/3.41E-01	0.05/2.85E-01	3.08E-01	2.57/5.73E-01
BioM 2 (PTEN and RNF6)	M-BP	4/120	0.94/1.50E-03	0.23/5.17E-03	3.06E-03	2.68/1.19E-02
<b>Phenes</b>						
Mood	M-BP	4/120	0.69/1.04E-01	-0.14/6.08E-02	1.75E-01	2.10/1.32E-01
Anxiety	M-BP	4/120	0.70/9.29E-02	0.12/9.74E-02	1.12E-01	1.87/2.09E-02
Mood and Anxiety (SASS)	M-BP	4/120	0.72/7.19E-02	0.15/5.27E-02	1.34E-01	1.52/1.18E-01
CFI-S	M-BP	4/120	0.80/2.10E-02	0.15/5.22E-02	3.46E-03	1.95/1.21E-01
Mood and Anxiety, and CFI-S	M-BP	4/120	0.78/2.77E-02	0.18/2.36E-02	6.78E-02	1.41/5.54E-02
<b>Phenes and biomarkers</b>						
Mood and Anxiety, and CFI-S and BioM 54	M-BP	4/120	0.81/1.64E-02	0.2/1.61E-02	5.13E-02	1.45/4.04E-02
<i>Mood and Anxiety, and CFI-S and BioM 12</i>	M-BP	4/120	<i>0.79/2.59E-02</i>	<i>0.19/1.88E-02</i>	<i>7.92E-02</i>	<i>1.44/4.72E-02</i>
Mood and Anxiety, and CFI-S and BioM 2	M-BP	4/120	0.86/7.02E-03	0.25/3.48E-03	2.22E-02	1.55/1.18E-2

**Biomarkers, phenes and combined predictions.** Top increased and decreased individual predictive biomarkers. Underlined are individual biomarkers from the Top Dozen list, the others are from the Bonferroni list. For Universal, the panel of Top Dozen biomarkers is called BioM 12, and the panel of Bonferroni biomarkers is called BioM148, reflecting the number of markers in the panel. For Male Bipolar, the panel of Top Dozen biomarkers is called BioM 12, and the panel of Bonferroni biomarkers is called BioM54, reflecting the number of markers in the panel. Bold, Bonferroni significant in the diagnostic testing. Italic, *a priori* primary endpoint (UP-Suicide). Abbreviations: AUC, area under the curve; BP, bipolar; CFI-S, Convergent Functional Information for Suicidality; ROC, receiver operating characteristic; SASS, Simplified Affective State Scale; SI, suicidal ideation. Bold P-value of AUC survives correction for multiple testing for predictions. ROC AUC is our *a priori* primary predictive tool. HAMD SI is the suicide rating question from the Hamilton Rating Scale for Depression.\*Smaller cohort, as not everybody had HAMD SI information.

**New drug discovery/repurposing.** Bioinformatic analyses using the gene expression signature of panels of top biomarkers identified new potential therapeutics for suicidality, such as eblesen (a lithium mimetic with anti-inflammatory and antioxidant properties),<sup>15,16</sup> piracetam (a nootropic cyclic derivative of GABA),<sup>17</sup> chlorogenic acid (an antioxidant polyphenol from

coffee)<sup>18</sup> and metformin (an antidiabetic and possible longevity promoting drug)<sup>19</sup> (Table 6).

**Phenomenology.** SASS can be used to identify possible subtypes of suicidality ( low mood, high anxiety, combined and non-affective) that may have practical utility, as we have shown in this



**Figure 4.** Convergent Functional Information for Suicide (CFI-S) testing. Testing in a large cohort that combines the discovery and test cohorts used for biomarker work. CFI-S was developed independently of any data from this study, by compiling known socio-demographic 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 and cultural factors known to influence suicidal behavior, as well as two demographic factors, age and gender. (a) Prediction of high suicidal ideation (HAMD SI >= 2). (b) Prediction of future hospitalizations due to suicidality within one year of follow-up. Table under a depicts individual items and their ability to differentiate between participants with No SI, Intermediate SI and High SI. Stepwise refers to gradual increase between the three groups (No SI, Intermediate SI, High SI). Table under b depicts individual items and their ability to differentiate between participants with and without future hospitalizations due to suicidality. Different items are positive in different individuals, providing leads for targeted (psycho)therapeutic interventions.

**Figure 5.** Predicting suicidality using a broad-spectrum predictor (UP-Suicide), which is an algorithm combining phenotypic information measures (Convergent Functional Information for Suicide (CFI-S) and Simplified Affective State Scale (SASS) (anxiety and mood)) and a panel of the Top Dozen universal biomarkers (BioM 12). (a) Model of various factors involved in suicidality (environmental stressors, life failures, body health issues, mind frailty, addiction problems and cultural examples). CFI-S, SASS and Biomarker panel are the components of our UP-Suicide. SA, suicide attempt; SI, suicidal ideation. (b) UP-Suicide predictions in the independent testing cohort, for High SI and for future hospitalizations for suicidality in the first year. (c) A dimensional view of risk stratification using phenotypic information measures and example of two high-risk participants. We calculated Euclidian distances from origin. Participant phchp158 is a divorced African American male in his late 20s with a long history of schizoaffective disorder, bipolar type and cannabis abuse. He was tested by us once (v1), while he was hospitalized for a suicide attempt by hanging. In the 5 years following testing, he has had two additional hospitalizations for suicidality: one for SI and one for attempt by overdose. He has had two hospitalizations for psychosis exacerbation without suicidality during this time span as well. Moved out of state, lost to follow-up since December 2015. Participant phchp328 was a divorced Caucasian female in her late 30s with a long history of depression, post-traumatic stress disorder (PTSD), borderline personality disorder and polysubstance abuse/dependence. She was first tested by us (v1) while inpatient for SI. Over the next year she subsequently had six psychiatric hospitalizations for suicidality: five due to SI and one due to a suicidal attempt by overdose. She also had one hospitalization for opioid withdrawal and depression during this time span as well. She committed suicide by overdose with pills, leaving behind a suicide note addressed to her mother. Her UP-Suicide score at Visit 1, composed of the panel of top dozen biomarkers (BioM12) scores and phenomic measures scores (CFI-S and SASS), was at the 100% of the scores of all the psychiatric participants visits in the current study. That testing was conducted during an inpatient hospitalization due to SI. Although her scores did improve at subsequent outpatient testing visits (Visits 2 and 3), this high watermark score indicated her high risk. After the last testing visit in our study, she had four subsequent psychiatric hospitalizations: three due to SI and one for opioid withdrawal/detox (the last one, which ended 2 weeks before the date of her committing suicide (T)).

work. The top CFI-S items distinguishing high SI from intermediate SI and no SI states were dissatisfaction with one's life, social isolation and lack of coping skills in the face of stress. The top CFI-S items distinguishing those that had future hospitalizations for suicidality versus those that did not were past history of suicidality, command auditory hallucinations and social isolation (Figure 4). This provides empirical evidence that, in general, reducing social isolation is a good behavioral therapeutic intervention for preventing suicidality. In different individuals

different CFI-S items are positive, providing avenues for tailored and targeted (psycho)therapeutic interventions.

Final summation: overall evidence for establishment of clinical utility

For the universal biomarkers identified by us, combining all the available evidence from this current work and the published literature, into a convergent functional evidence score, brings to

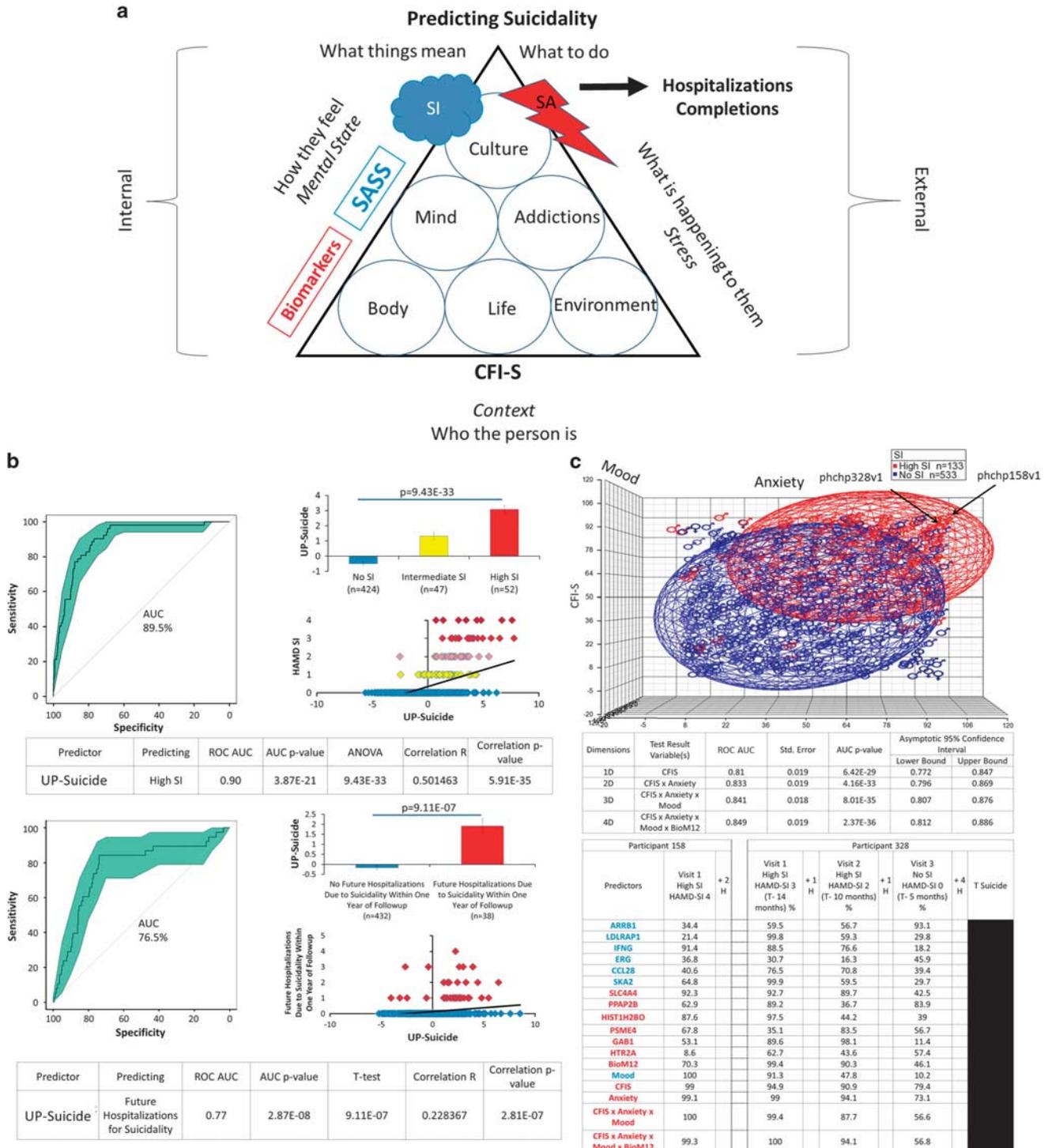
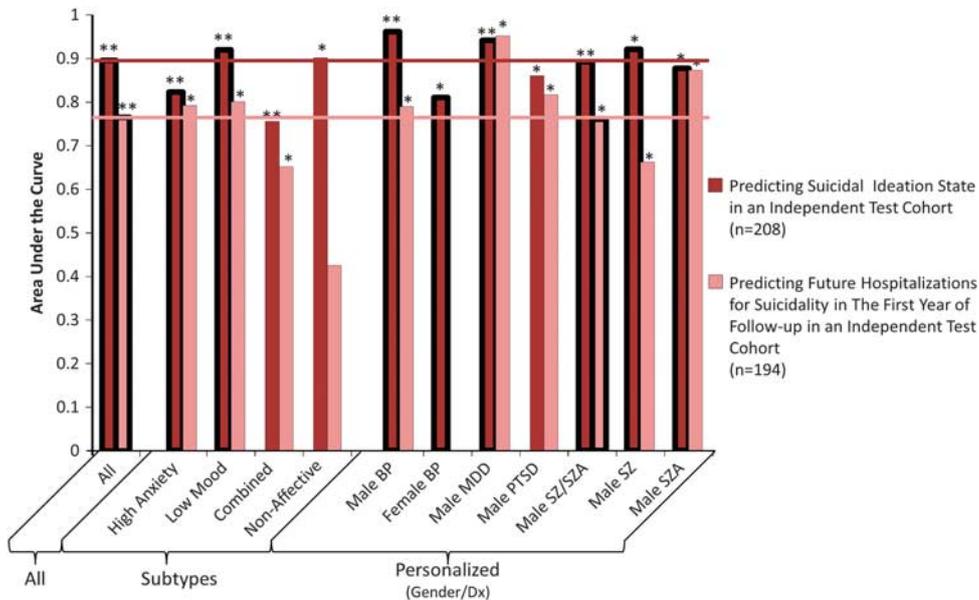


Figure 5. For caption see page on 1261.



	Participants Total visits/ High SI visits	High SI prediction ROC AUC ROC p-value	t-test (High SI vs. No SI)	Correlation R p-value	Participants Total visits/ 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 hospitalized for suicidality	Correlation R p-value First Year hospitalized for suicidality	Correlation R p-value All future hospitalized for suicidality
All	544/52	<b>0.8954</b> <b>3.87E-21</b>	<b>3.42E-19</b>	<b>0.5015</b> <b>5.91E-35</b>	470/38/98	<b>0.7654</b> <b>2.87E-08</b>	<b>9.11E-07</b>	<b>0.2284</b> <b>2.81E-07</b>	<b>0.2803</b> <b>1.72E-10</b>
High Anxiety Subtype	50/5	0.8222 9.53E-03	1.22E-02	0.3457 6.97E-03	46/7/13	0.7912 7.52E-03	4.14E-03	0.2933 2.40E-02	0.1685 1.24E-01
Low Mood Subtype	99/10	<b>0.9191</b> <b>7.42E-06</b>	<b>3.61E-06</b>	<b>0.4268</b> <b>5.28E-06</b>	78/5/13	0.8 1.27E-02	1.15E-02	0.2756 7.29E-03	0.1808 4.99E-02
Combined Subtype	119/31	<b>0.7548</b> <b>1.29E-05</b>	1.89E-05	<b>0.4672</b> <b>4.25E-08</b>	111/18/38	0.6511 2.15E-02	1.87E-02	0.1712 3.62E-02	0.2077 1.33E-02
Non-Affective Subtype	252/6	0.9004 4.04E-04	3.94E-03	<b>0.3319</b> <b>3.39E-08</b>	229/8/34	0.4242 7.67E-01	6.72E-01	-0.0139 5.83E-01	0.0322 3.12E-01
Male Bipolar	128/12	<b>0.9605</b> <b>8.03E-08</b>	<b>4.79E-07</b>	<b>0.6322</b> <b>6.05E-16</b>	120/4/9	0.7888 2.51E-02	6.30E-02	0.1927 1.75E-02	0.2765 1.07E-03
Female Bipolar	31/3	0.8095 4.12E-02	5.03E-02	0.4005 1.28E-02	4/0/0	NA NA	NA	NA NA	NA NA
Male Depression	57/10	<b>0.9404</b> <b>7.02E-06</b>	4.35E-05	<b>0.6067</b> <b>2.83E-07</b>	54/5/6	0.951 4.88E-04	<b>1.83E-07</b>	0.363 3.49E-03	0.3059 1.16E-02
Male PTSD	28/9	0.8596 1.24E-03	1.29E-03	0.6643 5.78E-05	23/4/14	0.8158 2.58E-02	2.72E-03	0.3493 5.12E-02	0.5951 5.30E-04
Male Schizophrenia/ Schizoaffective	206/15	<b>0.8918</b> <b>2.22E-07</b>	<b>5.80E-08</b>	<b>0.4356</b> <b>3.01E-11</b>	193/20/52	0.7598 7.20E-05	9.50E-04	<b>0.315</b> <b>4.05E-06</b>	<b>0.3345</b> <b>7.79E-07</b>
Male Schizophrenia	103/5	0.9204 7.86E-04	5.21E-04	0.389 2.44E-05	99/11/21	0.6612 4.12E-02	1.03E-01	0.2334 1.00E-02	0.3595 1.03E-04
Male Schizoaffective	103/10	0.8763 4.84E-05	3.01E-05	<b>0.4714</b> <b>2.50E-07</b>	94/9/31	0.8719 1.28E-04	7.79E-05	0.3939 4.28E-05	0.3788 7.67E-05

**Figure 6.** UP-Suicide across all, by subtypes and personalized by gender/diagnosis. UP-Suicide composed of the panel of the Top Dozen universal biomarkers (BioM 12), Convergent Functional Information for Suicide (CFI-S) and Simplified Affective State Scale (SASS) (anxiety and mood). Plot depicts area under the curve (AUC) for the UP-Suicide predicting suicidal ideation (SI) and hospitalizations within the first year in all participants, as well as separately in subtypes, and by gender and diagnosis (Gender/Dx). Two asterisks indicate that the comparison survived Bonferroni correction for all the multiple comparisons depicted. A single asterisk indicates nominal significance of  $P < 0.05$ . Bold outline indicates that the UP-Suicide was synergistic to its components, that is, performed better than the gene expression biomarkers or phenomic measures individually. Table contains descriptive statistics for all participants together, as well as separately by subtypes and by gender/dx. For female gender/dx groups, only the female bipolar subgroup had enough participants to yield at least a nominally significant AUC. Bold indicates the measure survived very stringent Bonferroni correction for all the multiple comparisons in our whole study (2737 biomarkers and phenes, resulting in a Bonferroni cutoff of  $1.83E-05$ ). We also show Pearson's correlation data in the SI test cohort for HAMD-SI vs UP-Suicide, as well as Pearson's 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 0.40 to 10.42 years).

the fore biomarkers that might have clinical utility, for future studies in the field (Figures 8, 9, and Supplementary Table S7).

Studies in male bipolars: personalization versus universal

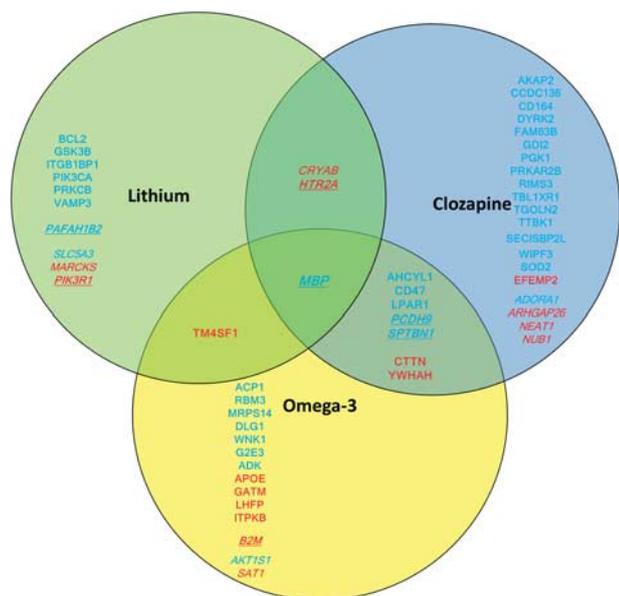
As a comparator to the universal approach across gender and diagnoses, we also conducted within-participant longitudinal

biomarker discovery analyses in male bipolars only, the largest subgroup ( $n = 20$  participants, 65 testing visits) in our discovery cohort. Male bipolars are the highest risk group for suicide clinically and have been the focus of earlier suicide biomarker studies by us, with an  $N (n = 9)$  that was less than half of the current one. The discovery step was followed by prioritization and by validation in male suicide completers. We reproduced and

**Table 4.** Biological pathways

A. Universal biomarkers												
Universal pathways	DAVID GO functional annotation biological processes					KEGG pathways				Ingenuity pathways		
	#	Term	Count	%	P-value	Term	Count	%	P-value	Top Canonical Pathways	P-value	Overlap
Validation Bonferroni significant (n = 130 genes, 148 probe sets)	1	Regulation of neurogenesis	8	6.6	2.10E–04	Tryptophan metabolism	4	0.2	1.10E–02	Protein kinase A signaling	4.36E–06	0.031 12/386
	2	Negative regulation of apoptosis	11	9	2.60E–04	Neurotrophin signaling pathway	6	0.3	1.40E–02	IGF-1 signaling	2.86E–05	0.062 35/582
	3	Negative regulation of programmed cell death	11	9	2.90E–04	Insulin signaling pathway	6	0.3	1.90E–02	Gap junction signaling	4.66E–05	0.045 7/155
	4	Negative regulation of cell death	11	9	3.00E–04	Butanoate metabolism	3	0.2	5.90E–02	Renin-angiotensin signaling	5.52E–05	0.055 6/109
	5	Regulation of cell morphogenesis	7	5.7	3.90E–04	Endocytosis	6	0.3	6.10E–02	Hepatic cholestasis	5.93E–05	0.043 7/161
B. Male Bipolar biomarkers												
Male bipolar pathways	DAVID GO functional annotation biological processes					KEGG pathways				Ingenuity pathways		
	#	Term	Count	%	P-value	Term	Count	%	P-value	Top Canonical Pathways	P-value	Overlap
Validation Bonferroni significant (n = 50 genes, 54 probe sets)	1	Negative regulation of neuron differentiation	7	14.6	9.30E–06	mTOR signaling pathway	3	6.2	1.60E–02	G-protein coupled receptor signaling	1.14E–14	0.113 29/256
	2	Negative regulation of neurogenesis	7	14.6	3.60E–05	Small cell lung cancer	3	6.2	3.20E–02	CREB signaling in neurons	1.98E–14	0.14 24/171
	3	Negative regulation of nervous system development	7	14.6	5.50E–05	Leukocyte transendothelial migration	3	6.2	5.80E–02	Neuropathic pain signaling in dorsal horn neurons	4.82E–13	0.18 18/100
	4	Positive regulation of protein localization to plasma membrane	4	8.3	1.10E–04	Sphingolipid signaling pathway	3	6.2	6.00E–02	14-3-3-mediated signaling	7.79E–12	0.154 18/117
	5	Positive regulation of protein localization to cell periphery	4	8.3	1.10E–04	NA	NA	NA	NA	Gap junction signaling	1.50E–11	0.129 20/155

Abbreviations: GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; NA, not applicable.



**Figure 7.** Step 6: Therapeutics. Pharmacogenomics. Individual biomarkers modulated by medications used in the treatment of suicidality. Universal biomarkers, bold; male bipolar, italic; both, bold and italic and underlined. Red, increased in expression in suicidality. Blue, decreased in expression in suicidality.

expanded some of our previous biomarker findings in bipolar disorder (Table 2B, Figure 3 and Supplementary Figure S4). We tested the male bipolar derived top dozen biomarkers (Table 2B) and all the biomarkers that survived Bonferroni correction after the validation step (Supplementary Table S8), for prediction of SI and for prediction of future psychiatric hospitalizations due to suicidality in the male bipolar subgroup ( $n=49$ ) in the independent test cohort (Figure 3 and Supplementary Table S10). We were successful in the identification of predictive biomarkers that might be more specific for suicidality in male bipolars. We also examined whether biomarkers discovered using just male bipolar subjects yields even better predictors for male bipolar subjects than using the universal biomarkers and found that to be the case for trait (hospitalizations) predictions (Figure 3). A number of top male bipolar biomarkers identified by us are targets of medications in current clinical use for treating suicidality (Supplementary Table S12). Bioinformatic drug repurposing analyses using the gene expression biosignature of panels of top biomarkers identified new potential therapeutics for suicidality in male bipolars (Table 6C and D). The top compounds identified include betulin (a natural plant compound with longevity and anticancer properties), naproxen (a non-steroidal anti-inflammatory), as well as chlorphenesin and baclofen (central nervous system acting muscle relaxants used to treat pain and spasms). Combining all the available evidence from this current work and the published literature, into a convergent functional evidence score (Figure 10 and Supplementary Table S13), leads to a prioritization of biomarkers for future studies in the field.

## DISCUSSION

Was our quest for more universal predictors or our quest for more personalized predictors more informative? The answer seems to be both, for different and complementary reasons. The universal approach may illuminate a more specific core biology for suicide, the personalized approach by gender and diagnosis may provide a more sensitive and context dependent applicability. The new subtypes we identified seem to have some utility (Figure 2 and Supplementary Figure S2). They merit future exploration and are

easy to assess in the general population using our SASS questionnaire/app.

The current work is more comprehensive in design and larger in size than our previous studies.<sup>4,5,7</sup> We used a systematic discovery, prioritization, validation, and testing approach.<sup>2</sup> For discovery, we used a hard to accomplish but powerful within-participant design, with an  $N$  of 66 participants with 193 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  $N$  as small as 1.<sup>6</sup> Another benefit of a within-participant design may be accuracy/consistency of self-report of psychiatric symptoms ('phenotype expression'), similar in rationale to the signal detection benefits it provides in gene expression. Just the male bipolar sub-component alone had twice as many participants in discovery (20 vs 9) and four times as many participants in validation (38 vs 9) than our original breakthrough study on suicide biomarkers in male bipolars published in 2013.<sup>7</sup> Out of the six Bonferroni-validated biomarkers in that study,<sup>7</sup> four were also Bonferroni validated in the current study (SAT1, BF114768/UBA6, MARCKS and PTEN), at the exact same probe sets. Moreover, LHFP, a biomarker that just missed the Bonferroni cutoff in the original male bipolar work,<sup>7</sup> is a universal Bonferroni validated biomarker in the current work, with predictive ability for SI state in the high anxiety subtype (AUC of 78%,  $P$ -value  $1.95E-02$ ), female bipolars (AUC of 79%,  $P$ -value  $4.6E-02$ ) and male depression (AUC 69%,  $P$ -value  $3.32E-02$ ), as well as very strong predictive ability for future hospitalizations for suicidality in male depression (AUC 98%,  $P$ -value  $2.54E-04$ ) (Figures 2 and 3). LHFP (lipoma HMGIC fusion partner), increased in expression in blood in our studies, is also previously reported to be increased in expression in brains of suicide completers.<sup>20</sup> Of note, SAT1, which is increased in expression in suicide in our studies, degrades spermidine, a compound recently implicated in longevity.<sup>21</sup> This is consistent with our overall 'life switch'<sup>22</sup> hypothesis.

Our Bayesian-like Convergent Functional Genomics platform used for prioritizing findings following the discovery step ensures robust built in reproducibility, as it is based on corroborating evidence by other groups, using different methodologies and cohorts. No single approach or study is perfect and datasets are especially powerful in combination.

The phenotypic measures apps scores by themselves ('digital biomarkers') were more precise predictors than the blood biomarkers by themselves, although their combination did show some synergy (Table 3). However, blood biomarkers may have usefulness for objective diagnostic testing and patient stratification, over and above clinical classifications. This may be particularly important when individuals choose not to share how they feel and do not seek help. We observed such possible discrepancies for different subtypes and gender/diagnostic groups (Supplementary Figure S2).

In terms of how our biomarker discoveries might be applied in clinical laboratory settings, we suggest that one might combine the best universal biomarkers with the best personalized biomarkers, to have the best of both worlds. In practice, every new patient tested would be normalized against the database of similar patients already tested and compared with them for ranking and risk prediction purposes, regardless of whether a platform such as Affymetrix or a more targeted one is used in the end clinically. As databases get larger, normative population levels can and should be established, similar to any other laboratory measures. Moreover, longitudinal monitoring of changes in biomarkers within an individual, measuring most recent slope of change, maximum levels attained and maximum slope of change attained, may be even more informative than simple cross-sectional comparisons of levels within an individual with normative populational levels and is the focus of future studies by our group.

Biomarkers may also be useful for patient stratification and measuring response to treatment (pharmacogenomics) (Figure 7,

**Table 5.** Step 6: Therapeutics

	Discovery (change) method/score	Prioritization total CFG score for suicide	Validation ANOVA P-value	Omega-3	Lithium	Clozapine	Antidepressants	Other mood stabilizers	Other other antipsychotics
<i>Universal Top Dozen biomarkers</i>									
HTR2A 5-Hydroxytryptamine (serotonin) receptor 2A, G protein-coupled	(I) DE/2	10	NS		(D) NT2.D1 cells Lithium <sup>58</sup>	(D) PFC Clozapine <sup>59,60</sup>	Blocked by: Mirtazapine, Amitriptyline	(D) NT2.D1 cells Valproate <sup>58</sup>	(D) PFC Haloperidol <sup>59</sup> Blocked by: Paliperidone, Risperidone, Iloperidone, Asenapine, Cariprazine, Lurasidone, Quetiapine, Olanzapine (I) Saliva, Blood Olanzapine, Risperidone, Quetiapine, Aripiprazole <sup>61</sup>
IFNG Interferon, gamma	(D) AP/1	9	NS						
SLC4A4 Solute carrier family 4 (sodium bicarbonate cotransporter), member 4	(I) AP/1	7	7.74E – 05					(D) AMY, CP Valproate <sup>62</sup>	
CCL28 Chemokine (C–C motif) ligand 28	(D) AP/4	4	NS				(I) Lymphoblastoid cell line Paroxetine <sup>63</sup>		
<i>Male bipolar top dozen biomarkers</i>									
HTR2A 5-Hydroxytryptamine (serotonin) receptor 2A, G protein-coupled	(I) DE/2	10	NS		(D) NT2.D1 cells Lithium <sup>58</sup>	(D) PFC Clozapine <sup>59,60</sup>	Blocked by: Mirtazapine, Amitriptyline	(D) NT2.D1 cells Valproate <sup>58</sup>	(D) PFC Haloperidol <sup>59</sup> Blocked by: Paliperidone, Risperidone, Iloperidone, Asenapine, Cariprazine, Lurasidone, Quetiapine, Olanzapine
SAT1 Spermidine/spermine N1-acetyltransferase 1	(I) DE/2	8	4.06E – 34	(D) blood Omega 3 <sup>64</sup>					
SPTBN1 Spectrin, beta, non- erythrocytic 1	(I) AP/1	5	6.7E – 32	(D) blood Omega 3 <sup>64</sup>					

**Pharmacogenomics.** Top Dozen lists biomarkers in our datasets that are targets of existing drugs and are modulated by them in opposite direction. Abbreviations: ANOVA, analysis of variance; CFG, Convergent Functional Genomics; NS, non-stepwise in validation; PFC, prefrontal cortex.

**Table 6.** Step 6: Therapeutics. New drug discovery/repurposing

<i>A. CMAP analysis with the universal Top Dozen biomarkers signature</i>					
<i>Rank</i>	<i>Cmap name</i>	<i>Dose</i>	<i>Cell</i>	<i>Score</i>	
6086	Torsemide	11 $\mu\text{M}$	MCF7	-0.9	
6087	Tenoxicam	12 $\mu\text{M}$	MCF7	-0.9	
6088	Halcinonide	9 $\mu\text{M}$	PC3	-0.902	
6089	Tretinoin	1 $\mu\text{M}$	MCF7	-0.913	
6090	NU-1025	100 $\mu\text{M}$	MCF7	-0.915	
6091	Abamectin	5 $\mu\text{M}$	MCF7	-0.919	
6092	Prednicarbate	8 $\mu\text{M}$	MCF7	-0.921	
6093	Tolmetin	13 $\mu\text{M}$	MCF7	-0.924	
6094	Alprostadil	10 $\mu\text{M}$	PC3	-0.925	
6095	<u>Amoxapine</u>	13 $\mu\text{M}$	MCF7	-0.927	
6096	Fenbufen	16 $\mu\text{M}$	MCF7	-0.929	
6097	Sertaconazole	8 $\mu\text{M}$	PC3	-0.93	
6098	Oxybuprocaine	12 $\mu\text{M}$	MCF7	-0.961	
6099	<b>Piracetam</b>	28 $\mu\text{M}$	MCF7	-0.973	
6100	<b>Ebselen</b>	15 $\mu\text{M}$	PC3	-1	
<i>B. CMAP analysis with the universal Bonferroni biomarkers signature</i>					
<i>Rank</i>	<i>Cmap name</i>	<i>Dose</i>	<i>Cell</i>	<i>Score</i>	
6068	<u>Fluoxetine</u>	12 $\mu\text{M}$	HL60	-0.812	
6069	Betulin	9 $\mu\text{M}$	HL60	-0.812	
6070	Netilmicin	3 $\mu\text{M}$	HL60	-0.82	
6071	DL-alpha tocopherol	9 $\mu\text{M}$	HL60	-0.821	
6072	Haloperidol	10 $\mu\text{M}$	HL60	-0.823	
6073	Streptozocin	15 $\mu\text{M}$	HL60	-0.824	
6074	Hesperidin	7 $\mu\text{M}$	HL60	-0.824	
6075	Calcium folinate	8 $\mu\text{M}$	MCF7	-0.825	
6076	Harpagoside	8 $\mu\text{M}$	MCF7	-0.826	
6077	Trimipramine	10 $\mu\text{M}$	HL60	-0.836	
6078	Dapsone	16 $\mu\text{M}$	HL60	-0.844	
6079	Fulvestrant	10 $\text{nM}$	HL60	-0.845	
6080	Rilmenidine	8 $\mu\text{M}$	HL60	-0.845	
6081	Atractyloside	5 $\mu\text{M}$	HL60	-0.849	
6082	Tenoxicam	12 $\mu\text{M}$	HL60	-0.851	
6083	Chlorpromazine	11 $\mu\text{M}$	HL60	-0.852	
6084	Harman	18 $\mu\text{M}$	HL60	-0.858	
6085	Homatropine	11 $\mu\text{M}$	HL60	-0.863	
6086	Ramifenazone	14 $\mu\text{M}$	HL60	-0.864	
6087	<u>Clozapine</u>	10 $\mu\text{M}$	HL60	-0.866	
6088	Diphenhydramine	14 $\mu\text{M}$	HL60	-0.873	
6089	Metrizamide	5 $\mu\text{M}$	HL60	-0.874	
6090	Prochlorperazine	7 $\mu\text{M}$	HL60	-0.874	
6091	Pirenperone	10 $\mu\text{M}$	HL60	-0.876	
6092	Hydrastinine	16 $\mu\text{M}$	HL60	-0.88	
6093	Carbimazole	21 $\mu\text{M}$	HL60	-0.884	
6094	Asiaticoside	4 $\mu\text{M}$	HL60	-0.886	
6095	Procainamide	15 $\mu\text{M}$	HL60	-0.894	
096	Ozagrel	15 $\mu\text{M}$	HL60	-0.903	
6097	Adiphenine	11 $\mu\text{M}$	HL60	-0.923	
6098	Merbromin	5 $\mu\text{M}$	HL60	-0.924	
6099	<b>Metformin</b>	24 $\mu\text{M}$	HL60	-0.983	
6100	<b>Chlorogenic acid</b>	11 $\mu\text{M}$	HL60	-1	
<i>C. CMAP analysis with the male bipolar Top Dozen biomarkers signature</i>					
<i>Rank</i>	<i>Cmap name</i>	<i>Dose</i>	<i>Cell</i>	<i>Score</i>	
6086	Harmaline	14 $\mu\text{M}$	MCF7	-0.822	
6087	Foliosidine	13 $\mu\text{M}$	MCF7	-0.834	
6088	3-Nitropropionic acid	10 $\mu\text{M}$	MCF7	-0.844	
6089	Biperiden	11 $\mu\text{M}$	PC3	-0.844	
6090	Carisoprodol	15 $\mu\text{M}$	HL60	-0.848	
6091	Nalidixic acid	15 $\mu\text{M}$	MCF7	-0.861	

**Table 6.** (Continued)

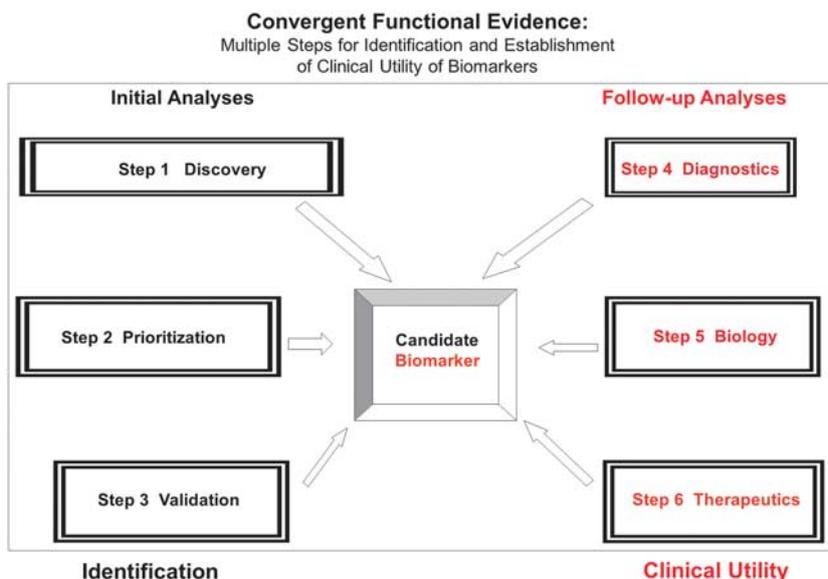
*C. CMAP analysis with the male bipolar Top Dozen biomarkers signature*

Rank	Cmap name	Dose	Cell	Score
6092	Eucatropine	12 $\mu\text{M}$	PC3	-0.869
6093	Solasodine	10 $\mu\text{M}$	PC3	-0.873
6094	Dicoumarol	12 $\mu\text{M}$	PC3	-0.875
6095	Pivampicillin	9 $\mu\text{M}$	MCF7	-0.879
6096	Gabexate	10 $\mu\text{M}$	PC3	-0.885
6097	Dacarbazine	22 $\mu\text{M}$	PC3	-0.892
6098	Prestwick-692	7 $\mu\text{M}$	MCF7	-0.927
6099	<b>Carteolol</b>	12 $\mu\text{M}$	HL60	-0.946
6100	<b>Betulin</b>	9 $\mu\text{M}$	HL60	-1

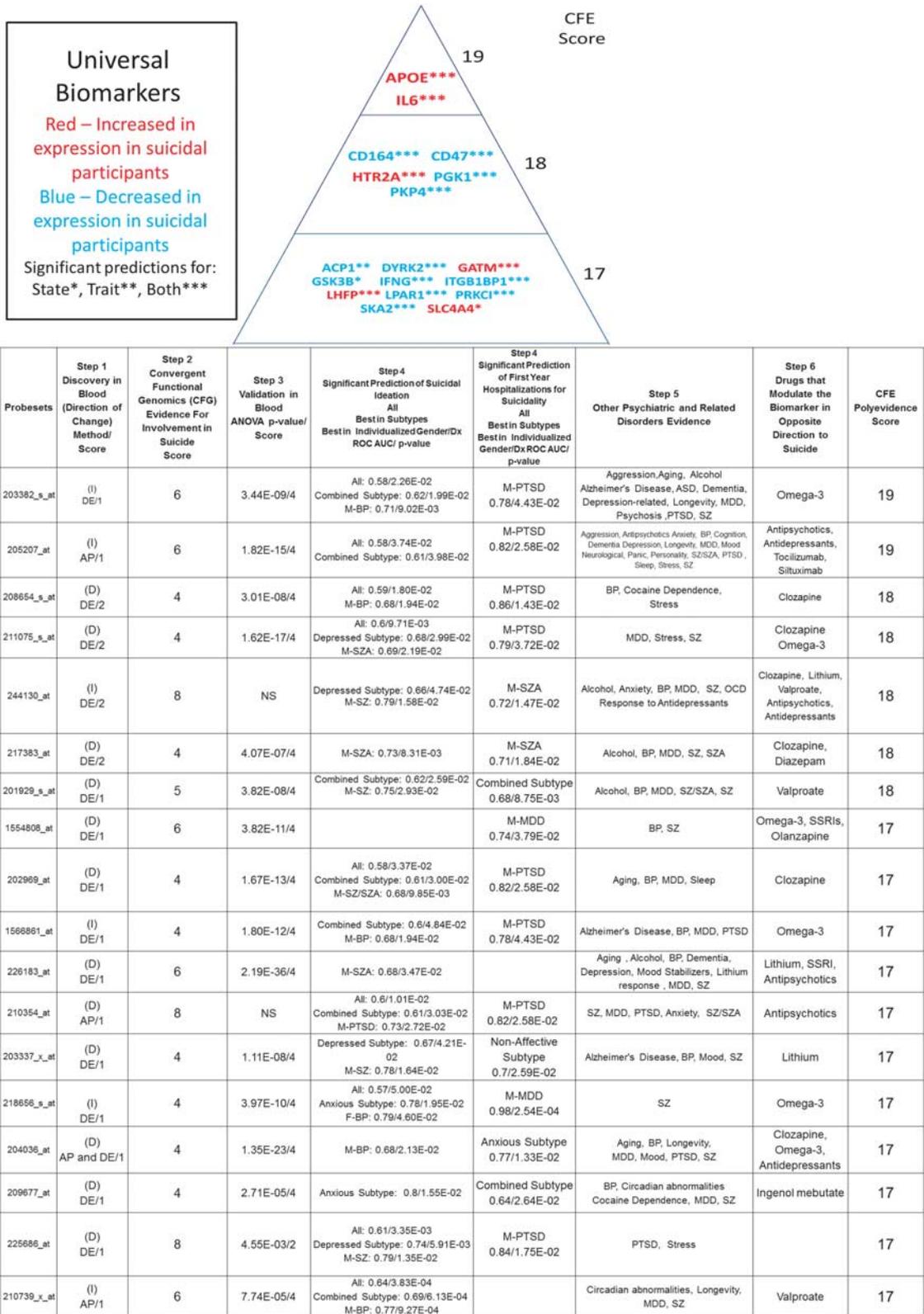
*D. CMAP analysis with the male bipolar Bonferroni biomarkers signature*

Rank	Cmap name	Dose	Cell	Score
6068	<u>Valproic acid</u>	50 $\mu\text{M}$	MCF7	-0.799
6069	<u>Ondansetron</u>	12 $\mu\text{M}$	PC3	-0.802
6071	<u>NU-1025</u>	100 $\mu\text{M}$	MCF7	-0.807
6073	<u>Glycopyrronium bromide</u>	10 $\mu\text{M}$	PC3	-0.814
6074	<u>Triflupromazine</u>	10 $\mu\text{M}$	HL60	-0.817
6075	<u>Suxibuzone</u>	9 $\mu\text{M}$	MCF7	-0.819
6076	<u>Mepyramine</u>	10 $\mu\text{M}$	MCF7	-0.822
6079	<u>Hydrocortisone</u>	11 $\mu\text{M}$	MCF7	-0.837
6080	<u>Benfotiamine</u>	9 $\mu\text{M}$	PC3	-0.839
6082	<u>Deferoxamine</u>	6 $\mu\text{M}$	PC3	-0.841
6084	<u>Homatropine</u>	11 $\mu\text{M}$	MCF7	-0.845
6085	<u>Nifedipine</u>	12 $\mu\text{M}$	PC3	-0.849
6086	<u>Alpha-ergocryptine</u>	7 $\mu\text{M}$	MCF7	-0.862
6088	<u>Meclozine</u>	9 $\mu\text{M}$	MCF7	-0.875
6089	<u>Acacetin</u>	14 $\mu\text{M}$	PC3	-0.882
6095	<u>Fenoprofen</u>	7 $\mu\text{M}$	PC3	-0.933
6096	<u>CP-690334-01</u>	1 $\mu\text{M}$	MCF7	-0.936
6097	<u>Baclofen</u>	19 $\mu\text{M}$	PC3	-0.94
6098	<u>Chlorambucil</u>	13 $\mu\text{M}$	MCF7	-0.945
6099	<b>Naproxen</b>	16 $\mu\text{M}$	PC3	-0.96
6100	<b>Chlorphenesin</b>	16 $\mu\text{M}$	HL60	-1

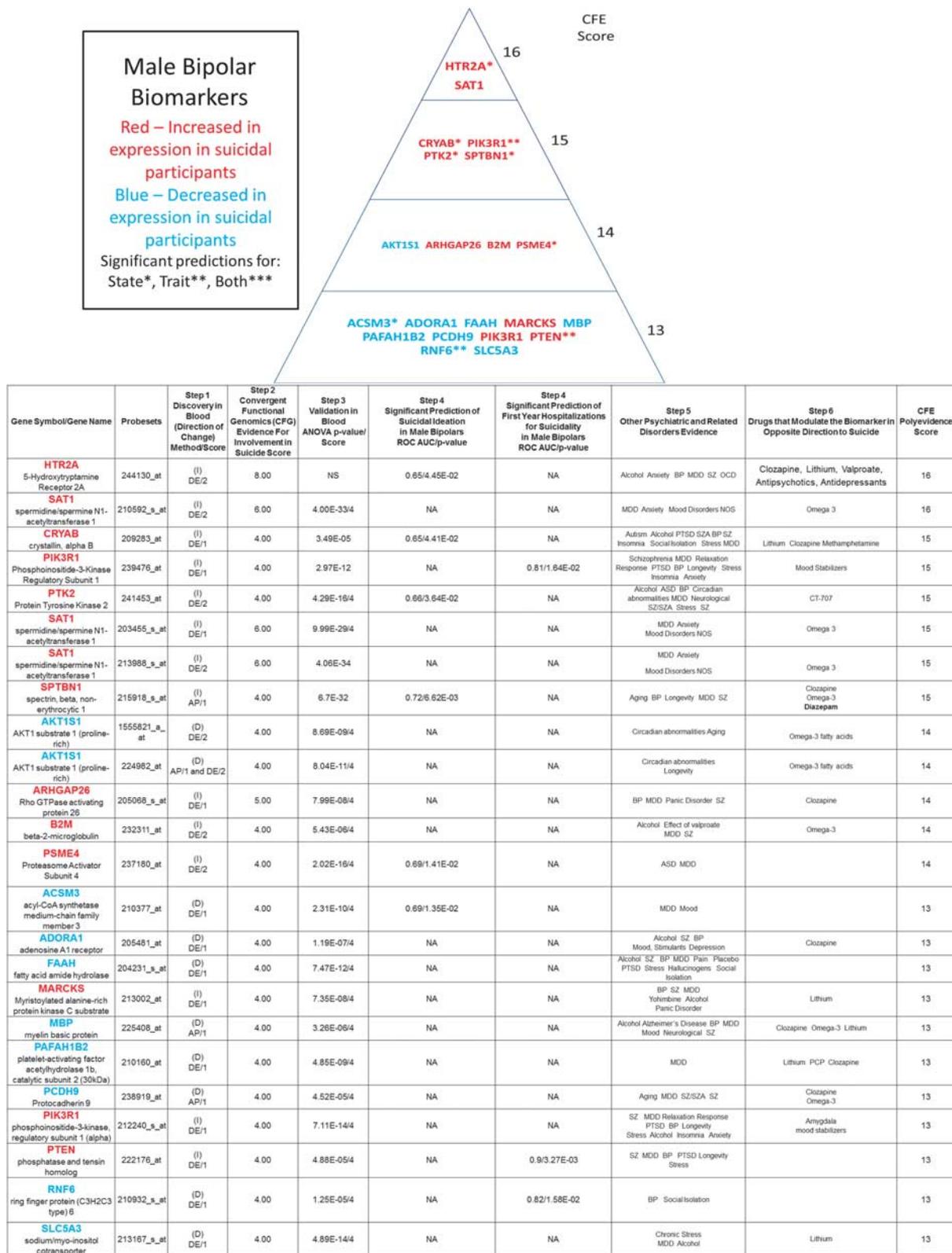
Connectivity Map<sup>65,66</sup> (CMAP) analysis, drugs that have opposite gene expression profile effects to our suicide biomarkers signatures. A score of -1 indicates the perfect opposite match, that is, the best potential therapeutic for suicidality. Underlined, drugs known to treat mood disorders and suicidality, which thus serve as a *de facto* positive control for our approach. Bold means top compounds of interest, pharmaceutical and natural.



**Figure 8.** Convergent functional evidence—multiple steps for identification and establishment of clinically utility of biomarkers.



**Figure 9.** Universal biomarkers—convergent functional evidence (CFE) for involvement in suicidality. Top Dozen and Bonferroni biomarkers. *Post-hoc* summation of all the evidence from discovery, validation, prioritization and testing (for state—SI and for trait—future hospitalizations), along with evidence for involvement in other psychiatric disorders and for being a target of drugs. This prioritization highlights for future studies biomarkers that may have broad applicability in the field, for diagnostics and therapeutics. ASD, autism spectrum disorder; BP, bipolar; MDD, major depressive disorder; PTSD, post-traumatic stress disorder; SZ, schizophrenia.



**Figure 10.** Male bipolar biomarkers—convergent functional evidence for involvement in suicidality. Top Dozen and Bonferroni biomarkers. *Post-hoc* summation of all the evidence from discovery, validation, prioritization and testing, along with evidence for involvement in other psychiatric disorders and for being a target of drugs. This prioritization highlights for future studies biomarkers that may have broad applicability in the field, for diagnostics and therapeutics. ASD, autism spectrum disorder; BP, bipolar; MDD, major depressive disorder; PTSD, post-traumatic stress disorder; SZ, schizophrenia.

Table 5 and Supplementary Table S5), and drug discovery/repurposing (Table 6). In terms of therapeutics, ebselen, although discovered decades ago for other indications and shown to be safe and well tolerated in human studies, has been recently proposed as a treatment for bipolar disorder.<sup>15</sup> The fact that it was the compound that had the strongest/perfect score on the Connectivity Map analyses as having the opposite gene expression effects to the biosignature of the Top Dozen universal biomarkers for suicidality is a tantalizing result. Piracetam and chlorogenic acid are compounds that can be classified as nutraceuticals, already in use and relatively safe and innocuous, which may facilitate adoption, along with omega-3 fatty acids, for pre-emptive population-level approaches. Metformin, besides being originally an antidiabetic compound, may act on promoting longevity by mimicking the effects of calorie restriction. The fact that it may have anti-suicidal properties is consistent with a possible suicide/longevity 'life switch' machinery, as previously proposed by us.<sup>22</sup> Interestingly, clozapine and fluoxetine, two known medications used to treat suicidality, were identified by our bioinformatics approach, but with lower priority than metformin (Table 6B). They serve as reassuring positive controls.

The biomarkers also provide a window toward a more nuanced understanding of the biology of suicide. The universal biomarkers may be pointing to a core common biology, such as inflammation and stress response, and the balance between neuronal cell survival and apoptosis, that is, a cellular level 'life switch'. The personalized biomarkers (such as male bipolar biomarkers), may be more reflective of the psychiatric co-morbidity driving suicidality and medication effects in different gender/diagnostic groups, such as mTOR signaling in male bipolars, which is modulated by mood regulating drugs, including a new one (ketamine),<sup>23</sup> which also shows promise for treating suicidality.<sup>24</sup>

Among the Top Dozen universal biomarkers (Table 2A) was HTR2A, which was increased in expression and is targeted by most modern antipsychotics, and ARRB1, which was decreased in expression and is downstream of HTR2A in the signaling cascade, and also interacts with GSK3B,<sup>25</sup> which was decreased in expression as well (Supplementary Figure S3). The combination of these expression effects may provide for excessive/unbridled signaling<sup>26</sup> as a key pathological step in suicidality. For male bipolars, similar STRING analysis revealed a network centered on PTK2 (Supplementary Figure S4).

Finally, a *post-hoc* convergent functional evidence score of the totality of evidence in these series of studies, including testing for predictive ability, evidence for biological predisposition/involvement in psychiatric disorders, and for being potential drug targets, identifies APOE and IL6 as the top overall biomarkers of interest, pointing to stress, inflammation and accelerated aging (Figure 9 and Supplementary Table S7). It is unclear at this point whether they are just markers of that co-occurring pathology or are direct drivers of suicide as well.

Overall, we believe this work is a major step forward towards understanding, diagnosing and treating suicidality. Suicide occurs maladaptively in the face of negative life events, with the individual who commits suicide being vulnerable due to a psychiatric illness and addictions, misperceiving circumstances and/or over-reacting in an impulsive manner. Related to that, suicide can be an attempt to assuage perceived guilt or an attempt to harm (through social opprobrium or guilt) the individual(s) perceived to be the source of the suffering and lack of success of the suicidal person. Conversely, a well-balanced and functioning mind is protective. To predict behaviors, it may be important to provide context to the biomarkers, as to how the person feels (SASS) and who the person is (CFI-S) (Figure 5a). That is why the combined UP-Suicide predictor is robust across all subjects, in subtypes and personalized by gender and diagnosis, with AUCs over 90% (Figure 6). We hope that our risk assessment tools may become self-cancelling predictions once tested and deployed in the

general population, as they can lead to precision prevention with early targeted interventions: biological, psychological and social. Indeed, beyond biological markers and drug treatments, SASS can help identify different subtypes and in different individuals different CFI-S items are positive, providing avenues for tailored and targeted (psycho)therapeutic interventions. Culture may have a particularly important role (Figure 5a). Negative behaviors in the past, negative examples from the environment and negative cultural values can lead to a downward spiral of failure. Reversing negative cultural influences on behaviors involves coming to terms with or forgetting the past, starting to accumulate positive precedents, changing the environment (or moving to a different environment) and gravitating to/adopting a different set of cultural values. Given that one person dies from suicide every 40 seconds worldwide, the importance and urgency of efforts such as ours cannot be overstated.<sup>27</sup> We demonstrate how this field can develop precision, move towards personalization, and have tools to pre-empt suicide acutely, as well as prevent suicide in the long term. We envision the participation of individuals at risk in such efforts initially, followed by the pervasive deployment of the tools in society at large in the long term. It has not escaped our attention that, if our 'life switch' hypothesis between suicide and longevity is correct,<sup>22</sup> the possibility exists to transform a negative into a positive.

#### CONFLICT OF INTEREST

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

#### NOTES

Supplementary Information is also available from the Niculescu Laboratory website ([www.neurophenomics.info](http://www.neurophenomics.info)).

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#### AUTHOR CONTRIBUTIONS

ABN designed the study and wrote the manuscript. DFL, HLN, PLP, EMN, HLD and KR analyzed the data. VV performed database work. JN, AW, DLG and TJ organized, conducted and scored testing in psychiatric participants. AB, MY, AS, GES and ABN organized and carried out postmortem samples collection. TG, SMK, NS and DRS conducted microarray experiments and provided input on data analyses. All authors discussed the results and commented on the manuscript.

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