

WHAT IS CLAIMED IS:

1. An invitro method for assessing Major Depressive Disorder (MDD) or Bipolar Disorder (BD) in a subject comprising: obtaining an in vitro sample from the subject; assaying the sample using probes and/or primers configured to identify the presence of and/or amplify one or more brain disorder-associated circRNA biomarkers; producing an expression profile of the one or more brain disorder-associated circRNA biomarkers based on the assay; and comparing the expression profile to a control, and an antidepressant treatment for said subject is to be administered, changed or discontinued based on the differential expression of said brain disorder-associated circRNA biomarkers compared to said control, or a second in vitro sample from the subject after an antidepressant treatment is to be administered and wherein the antidepressant treatment is selected from: a Selective Serotonin Reuptake Inhibitors (SSRIs), a serotonin and norepinephrine reuptake inhibitors (SNRIs), a Monoamine oxidase inhibitors (MAOIs), and administering a tricyclic antidepressants, or any combination thereof; and wherein the brain disorder-associated circRNA biomarkers comprise one or more circRNAs selected from SEQ ID NOs: 1-241, or any combination thereof.
2. An invitro method for assessing MDD or BD in a subject comprising: providing a sample from the subject; assaying the sample using primers configured to identify the presence of and/or amplify one or more brain disorder-associated circRNA biomarkers; and determining whether the sample has altered levels of the one or more brain disorder-associated circRNAs or a different expression profile of the one or more brain disorder-associated circRNAs relative to a control representing levels of the one or more brain disorder-associated circRNAs or an expression profile of the one or more brain disorder-associated circRNAs in non-MDD or non-BD humans, wherein the primers include a sequence that spans the splice junction of any of the one or more brain disorder-associated circRNA biomarkers thereof, in an asymmetric manner.
3. An inviro method of treating a MDD or BD condition in a patient who is predicted to benefit or not to benefit from an antidepressant treatment comprising:
 - detecting in a first sample of the patient the expression levels of one or more MDD/BD- or antidepressant response/treatment-associated circRNA biomarkers to establish an expression profile of said patient;
 - an antidepressant treatment is to be administered to said patient to treat MDD or BD wherein the antidepressant treatment medication is selected from the group consisting of: Selective Serotonin Reuptake Inhibitors (SSRIs), serotonin and norepinephrine reuptake inhibitors (SNRIs), Monoamine oxidase inhibitors (MAOIs), and tricyclic antidepressants;
 - detecting in a second sample of said patient the expression levels MDD- or BD-associated circRNA biomarkers or circRNA biomarkers after said antidepressant treatment is to be administered; and

- correlating the levels of expression in said first and second samples to determine if the antidepressant treatment is effective at treating the condition, and continuing the antidepressant treatment to treat MDD or BD based on said correlation, or stopping the antidepressant treatment to treat MDD or BD, or a different antidepressant treatment is to be administered to treat MDD or BD.
- 4. The method of claim 3, wherein said sample comprises a physiological fluid sample.
- 5. The method of claim 4, wherein said physiological fluid sample comprises blood, cell, or tissue sample.
- 6. The method of claim 3, wherein said patient is a human.
- 7. The method of claim 3, wherein the circRNA biomarkers are selected from the group consisting of: a circRNA encoded by a nucleotide sequence according to SEQ ID Nos: 1-241.
- 8. The method of claim 3, wherein the circRNA biomarkers are selected from the group consisting of: circCDR1as, circTULP4, circCHIC1, circMIR5695, circRALGAPB, circCOMT, circPICALM, circDDX50, circRERE, or circSATB2, circICAM1, circDDR1, circADAM22, circMALAT1, circHMGA2, circCYP24A1, circDLG5, circMYO9B, circNFATC3, circDUSP22, circFKBP8, circVDAC2, and circTRIM69.
- 9. The method of claim 1, wherein said sample comprises a physiological fluid sample.
- 10. The method of claim 9, wherein said physiological fluid sample comprises blood, cell, or tissue sample.
- 11. The method of claim 1, wherein said patient is a human.
- 12. The method of claim 1, wherein the primers include a sequence that spans the splice junction of any of the one or more brain disorder-associated circRNA biomarkers thereof, in an asymmetric manner.
- 13. The method of claim 1, wherein the primer comprises a PCR primer sequence selected from the group of sequences according to SEQ ID NOs: 242-433, or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% nucleic acid sequence identity thereto, or to the complement thereof.
- 14. The method of claim 1, wherein the circRNA biomarkers are selected from: circCDR1as, circTULP4, circCHIC1, circMIR5695, circRALGAPB, circCOMT, circPICALM, circDDX50, circRERE, or circSATB2, circICAM1, circDDR1, circADAM22, circMALAT1, circHMGA2, circCYP24A1,

circDLG5, circMYO9B, circNFATC3, circDUSP22, circFKBP8, circVDAC2, or circTRIM69, or any combination thereof.

15. The method of claim 2, wherein said sample comprises a physiological fluid sample.
16. The method of claim 15, wherein said physiological fluid sample comprises blood, cell, or tissue sample.
17. The method of claim 2, wherein said subject is a human.
18. The method of claim 2, wherein the primer comprises a PCR primer sequence selected from the group of sequences according to SEQ ID NOs: 242-433, or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% nucleic acid sequence identity thereto, or to the complement thereof.
19. The method of claim 2, wherein the circRNA biomarkers are selected from the group consisting of: a circRNA encoded by a nucleotide sequence according to SEQ ID NOs: 1-241.
20. The method of claim 2, wherein the circRNA biomarkers are selected from: circCDR1as, circTULP4, circCHIC1, circMIR5695, circRALGAPB, circCOMT, circPICALM, circDDX50, circRERE, or circSATB2, circICAM1, circDDR1, circADAM22, circMALAT1, circHMGA2, circCYP24A1, circDLG5, circMYO9B, circNFATC3, circDUSP22, circFKBP8, circVDAC2, or circTRIM69, or any combination thereof.
21. The method of claim 3, wherein the primers include a sequence that spans the splice junction of any of the one or more brain disorder-associated circRNA biomarkers thereof, in an asymmetric manner.
22. The method of claim 3, wherein the primer comprises a PCR primer sequence selected from the group of sequences according to SEQ ID NOs: 242-433, or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% nucleic acid sequence identity thereto, or to the complement thereof.