

Supplementary Information for:

Identification of Potential Blood Biomarkers Associated with Suicide in Major Depressive Disorder

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Supplementary Table 1: Demographic details of the study cohort

Tissue	Gender	Age	Status	Race	pH	Blood	DLPFC	Manner of Death
Blood and Brain	F	65	Control	Caucasian	6.49	x	x	Pulmonary Embolism
	M	49	Control	Caucasian	6.5	x	x	Coronary Artery Disease
	M	53	Control	Hispanic	6.55	x	x	Severe Hypertrophic Cardiomyopathy
	M	62	Control	Pacific Islander	6.36	x	x	Coronary Atherosclerosis
	M	27	Control	Caucasian	6.55	x	x	Accident
	F	32	Control	Caucasian	6.01	x	x	Undetermined - Natural Causes
	M	21	Control	African American	6.2	x	x	Pulmonary Embolism
	M	45	Control	Caucasian	6.49	x	x	Dilated Cardiomyopathy
	M	65	Control	Caucasian	6.41	x	x	Coronary Atherosclerosis
	M	40	Control	Caucasian	6.45	x	x	Accident
	M	36	Control	Caucasian	6.19	x	x	Coronary Atherosclerosis
	M	33	Control	Caucasian	6.35	x	x	Cardiomyopathy
	M	38	Control	Caucasian	6.53	x	x	Cardiomyopathy
	F	38	Control	Asian	6.71	x	x	Aortic Dissection
	M	49	MDD-NS	Caucasian	6.66	x	x	Cardiovascular Disease
	F	52	MDD-NS	Caucasian	6.65	x	x	Acute Pancreatitis
	M	47	MDD-NS	Caucasian	6.98	x	x	Cardiomyopathy
	M	44	MDD-NS	Caucasian	6.87	x	x	Coronary Atherosclerosis
	M	38	MDD-NS	Caucasian	6.72	x	x	Acute Pancreatitis
	F	81	MDD-NS	Caucasian	6.31	x	x	Long-term medical condition
	F	59	MDD-NS	Hispanic	6.4	x	x	Long-term medical condition
	M	58	MDD-NS	Caucasian	6.79	x	x	Cardiovascular Disease
	M	44	MDD-NS	Caucasian	6.66	x	x	Accident
	M	56	MDD-NS	Caucasian	6.58	x	x	Pneumonia
	M	50	MDD-NS	Caucasian	6.41	x	x	Aortic Dissection
	F	48	MDD-NS	Caucasian	6.02	x	x	Accident
	F	41	MDD-NS	Caucasian	6.42	x	x	Long-term medical condition
	F	51	MDD-NS	Caucasian	6.37	x	x	Long-term medical condition
	F	57	MDD-NS	Caucasian	6.18	x	x	Heart Attack
	M	60	MDD-NS	Caucasian	6.4	x	x	Aneurysm
	M	62	MDD-NS	Caucasian	6.34	x	x	Strangulated Umbilical Hernia
	M	60	MDD-S	Asian	6.8	x	x	Hanging
	M	50	MDD-S	Caucasian	6.97	x	x	Hanging
	M	60	MDD-S	Caucasian	6.69	x	x	Hanging
	F	19	MDD-S	Hispanic	6.66	x	x	Hanging
	F	43	MDD-S	Caucasian	6.52	x	x	Stab Wound
	M	33	MDD-S	Asian	6.62	x	x	Carbon Monoxide
	M	55	MDD-S	Caucasian	6.52	x	x	Gunshot Wound
	M	25	MDD-S	Caucasian	6.23	x	x	Hanging
	F	39	MDD-S	Caucasian	6.81	x	x	Hanging
F	21	MDD-S	Hispanic	6.25	x	x	Hanging	
M	27	MDD-S	Caucasian	6.46	x	x	Hanging	
M	50	MDD-S	Caucasian	6.79	x	x	Hanging	
F	31	MDD-S	Caucasian	6.62	x	x	Suicide	
F	38	MDD-S	Caucasian	6.16	x	x	Overdose	

Supplementary Table 1 Continued:

Tissue	Gender	Age	Status	Race	pH	Blood	DLPFC	Manner of Death
Brain	F	55	Control	Caucasian	6.71		x	Sudden medical condition
	M	63	Control	Caucasian	6.58		x	Sudden medical condition
	M	30	Control	Hispanic	6.71		x	Sudden medical condition
	M	54	Control	Caucasian	6.39		x	Sudden medical condition
	M	51	Control	Caucasian	6.94		x	Sudden medical condition
	M	55	Control	Caucasian	6.74		x	Sudden medical condition
	M	55	Control	Caucasian	6.18		x	Accident
	F	18	MDD-NS	Caucasian	6.31		x	Sudden medical condition
	F	64	MDD-NS	Caucasian	6.89		x	Sudden medical condition
	F	44	MDD-NS	Caucasian	6.31		x	Sudden medical condition
	M	50	MDD-NS	Caucasian	6.42		x	Sudden medical condition
	F	57	MDD-NS	Caucasian	6.75		x	Undetermined/Accidental overdose
	F	49	MDD-NS	Caucasian	6.6		x	Undetermined/Accidental overdose
	F	41	MDD-NS	Caucasian	6.7		x	Accident
	M	48	MDD-S	Caucasian	6.81		x	Suicide
	M	33	MDD-S	Caucasian	6.87		x	Suicide
	F	77	MDD-S	Asian	6.67		x	Suicide
F	19	MDD-S	Caucasian	6.7		x	Suicide	
F	42	MDD-S	Caucasian	6.69		x	Suicide	
F	40	MDD-S	Caucasian	6.47		x	Suicide	
Blood	F	42	Control	African American		x		Sudden medical condition
	M	48	Control	Caucasian		x		Sudden medical condition
	M	58	MDD-NS	Caucasian		x		Sudden medical condition
	M	39	MDD-S	Caucasian		x		Suicide
	M	54	MDD-S	Caucasian		x		Suicide
	F	65	MDD-S	Caucasian		x		Suicide
	M	30	MDD-S	Caucasian		x		Suicide
	M	31	MDD-S	Caucasian		x		Accident

Supplementary Table 2: Average brain quality measures (pH, RNA Integrity Number (RIN), and Post-mortem interval (PMI)) across groups

	pH		RIN		PMI	
	Average	Stdev	Average	Stdev	Average	Stdev
Control	6.48	0.22	7.49	2.47	22.54	8.19
MDD-NS	6.53	0.24	6.93	3.29	23.61	7.70
MDD-S	6.62	0.22	8.42	1.81	26.90	8.71

Supplementary Table 3: NanoString gene targets, accession number, probe position, and supporting references

Group	Gene Symbol	Gene Name	Accession	Position	Target Sequence	References
Telomere Length	ACD	adrenocortical dysplasia homolog	NM_001082486	219-318	TGTCTGACGGGACCCACAGTGTCCGATGCCTGGTACGCGGGAGGCCCTGGACACCTCGGACTGGGAGGAGAAGGAGTTCGGCTCCCGGGG	Mamdani F, Rollins B, et al. (2015). <i>Transl Psychiatry</i> , 5(9):e636; Rice C, et al. (2016). <i>Comput Struct Biotechnol J</i> , 14:161-167; Otsuka I, et al. (2017). <i>Sci Rep</i> , 7(1):3176.
	CTC1	CST telomere replication complex component 1	NM_025099.5	1845-1944	TGCTGTGCTCCCTCTGCCTTCTGCCAGCCAGGTTTACTTGGGGTCTGGTGGCTTCATCTCATAAAGGTTGTCTGCAACTTCGGGACCAAAGTG	
	DKC1	dyskerin pseudouridine synthase 1	NM_001363.3	2256-2355	GATGGGCTGGTAGTTTTCATCTTGTCTGGCTAGAGGTCAGTCTTTGCACTTCCTCAAAGCTGTGTACAGTGTCACTAAATCCATCTGACT	
	GAR1	GAR1 ribonucleoprotein	NM_032993.2	642-741	AGGTGGAGGTGGGGCTCAGAGGAGGAAGAGGTGGTGGTTTCAGAGGGAGAGGCATTAAGTGAAACAGTTGACAGACATCACCAGTTGA	
	NHP2	NHP2 ribonucleoprotein	NM_017838.3	316-415	AGCAGATTCGGCGGGGTGAAGAGGTTCAAGAAATTTGCAACAAGGAGAAAAAGGATCATGGTTTTGGCAGGAGACACACTGCCATTG	
	NOP10	NOP10 ribonucleoprotein	NM_018648.3	327-426	GGAGACTCCGTAACCAAACCTCTCGAAGTGTGAGCCCTGATGCCCTTTTCCAGCCATACTCTTTGGCATCCAGTCTCTCGTGGCGATTGATTATGC	
	OBFC1	oligonucleotide/oligosaccharide binding fold containing 1	XM_006717976	2821-2920	GGCAGTAAGCATTGTCATATAAAACACTGTGCAGTCCCAAGGAGACCAAGAGAATGTGCAGTAGCCTCTGAGGAGTTTTATTTGGTTCATG	
	PIF1	PIF1 5'-to-3' DNA helicase	NM_025049.3	733-832	CTGTGCTGAGGGCCCTCTGAAAGGCCAGAGCATCTTCTCACTGGGAGTGCAGGAACAGGGAAGTCAATATCTGCTAAAGCGAATCTCTGGGCTC	
	POT1	protection of telomeres 1	NM_015450.2	1076-1175	ATGCAGTATTTTGACCTGACTGTGACGCTCTGGGCAAAGCAGAAGTGACGGAGCATCATTTCTTAAAGGTATGGGATGGCACCAGGACACC	
	RTTEL	regulator of telomere elongation helicase 1	NM_016434.3	4746-4845	GAGAAGCCCTGAGTACCTTGGGCTCTGGGTTGGTTTCTGGGAAAGTGTCTCCCAAGAACTCCCTGGCTCTGGCTGTGAGTGGTCCACAG	
	TERC	telomerase RNA component	NR_001566.1	88-187	CCCGCGCTGTTTTCTCGTACTTTCAGCGGGCGGAAAGCCTCGGCTCGCCCTCCACCGTTCATCTTAGAGCAAACAAAAATGTCAGC	
	TERF1	telomeric repeat binding factor 1	NM_003218.3	1038-1137	CTGAAAGCAGAATACTGTTTCAAAGAGTCAAGCGGTAACCTCTGAAAAACATCGAGCTGAAAAAGACAGGCATGGCTTTGGGAAGAAGACA	
	TERF2	telomeric repeat binding factor 2	NM_005652.2	2466-2565	TGACATCAACCTAGACCTGTCTGCTTGGCATTGCTGTCAACTCTGCTGGGCTATGTAGGCAGGTTAATCCTCACTTCTCATGTGGTTGAACC	
	TERF2IP	TERF2 interacting protein	NM_018975.2	1381-1480	TTGCATTGGAACCTGGCACTTATTTCTGACCATCGCTGCTGTGCTGTGTGAGTCTAGATTTTGTAGCCAAAGCAGAGTTGTAGAGGGGATATAA	
TERT	telomerase reverse transcriptase	NM_198255.2	2138-2237	GTGCTGCTGTGCGGGCCAGGACCCGCGCTGAGCTGTACTTTGTCAAGGACAGGCTCACGGAGGTCATCCGACATCATCAACCCCGACA		
TINF2	TERF1 interacting nuclear factor 2	NM_001099274	1685-1784	CTAGACCTTTGTGATAGAATAAATGCTCTGTACTCTAGTCTCTGCTCCTCAGCTCTGCAAGTAGTTTAGTAGGAATGAAGTGGAAAGTCCAG		
Transcription & Cell type	ADCY1	adenylate cyclase 1	NM_021116.2	12106-12220	GAATGGAGAGTGTATGGGCAAGGTTGTCATTTCTCGCAACAATACTCACTGAGGATGCTTCTGTAGAAGTGAGAAACACAGTGTAGTACAT	Nagy C, et al. (2015). <i>Mol Psychiatry</i> , 20(3):320-328; Tomita H, et al. (2013). <i>Front Genet</i> , 4:297; Pandey GN, et al. (2016). <i>Int J Neuropsychopharmacol</i> , 19(8):pyw015.
	ANK3	ankyrin 3	NM_001149.2	1561-1660	CAGGCCAGCCCTGTTCCAGATGAAATGTGAAAGAGTCTTGGAAACAAAGCACTTTTAGCCCAATTGTCACTGTGGAACCAAGAGACGGAA	
	CACNA1C	calcium voltage-gated channel subunit alpha1 C	NM_199460.2	4786-4885	TGAAACACCCCTGTGGTAGCAGCTTTGCTGCTTCTACTTATCAGCTTCTACATGCTCTGTGCCTTCCTGATCATCAACCTCTTGTAGCTGTATCAT	
	CACNB2	calcium voltage-gated channel auxiliary subunit beta 2	NM_000724.3	2611-2710	TCTTTTGAAGTGTACATAAATTTGGCTGGTATGGCTGAGTCTCCGGTTGCATACTGGACTCTCAAAAACCTGTTTTGGGTAGCTGCCACTGA	
	CREB1	cAMP responsive element binding protein 1	NM_134442.2	201-300	CCGAGAACCAGCAGAGTGGAGATGCAGCTGTAAACAGAGCTGAAACCAACAAATGACAGTTCAAGCCAGCCACAGATTGCCACATTAGCCCA	
	DLG4	discs large MAGUK scaffold protein 4	NM_001365.3	2461-2560	TGCCCTGAAGAATCGGGTTCAGACGGTCAAGTATCGCTCAGTATAAACCAAGAGTACAGCCGATTCGAGGCCAAGATCCACGACCTCCGG	
	GFAP	glial fibrillary acidic protein	NM_002055.4	590-689	AAGCAGATGAAGCCACCTGGCCGTCTGGATCTGGAGAGGAAGATTGAGTCTGGAGGAGGAGATCCGTTCTTGAGGAAGATCCACGAGG	
	GPHN	gephyrin	NM_020806.4	1146-1245	ACTAACACGACCATCAAATCCGTGTCGGAGTCTTACAGTGAAGTATGTTGCTTCAGGAATCTTGAGAAAGCCAGTGGGATAAATCTCAA	
	GPR37	G protein-coupled receptor 37	NM_005302.2	1891-1990	GCTCCGGCAGAAAGGTGCAATTATTAAGATCTCTCTGATTACAGACACCATCTATGTTCTAGCCCTCACTACGACAGTGCAGAGCTGTGGTG	
	MAP2	microtubule associated protein 2	NM_031845.2	5171-5270	TACTCTGTATGCTGGGATCCGAGGTTCCAACACTGTAACTCTGTGGGGGTTCTTCTTCTGATAATTTAGAGCCTGTACCATAGAAAA	
	NFE2L2	nuclear factor, erythroid 2 like 2	NM_006164.3	996-1095	TCCGGTCACTCAGAGCCAGTCTTCAATGCTACTAATCAGGCTCAGTCACTGAACTCTGTTGCTCAGGTAGCCCTGTGATTATGAGCGGT	
	RBOX3	RNA binding protein, fox-1 homolog 3	NM_001082575	577-676	TTTAGACGTGGAGATCATTTTAAACAGCGGGCTCAAGGTTTTGGGTTTGAACCTTTGAAACTAGCTCAGATGCTGACCCAGCCGGGAGG	
	SKA2	spindle and kinetochore associated complex subunit 2	NM_182620.3	51-150	TTTGACACAGCAGCAATCCTCTCGCGGTTTTGTGCTTGTCCCAACAGGAAATGTCTCATGACAGAGGGCGTTACCCAGTCTCCAATGGGG	
	SOX10	SRY-box 10	NM_006941.3	2160-2259	GGCGGTGCTCCCACTCAGGGGCTGAGAGTAGCTTTGAGGACCTCATTGGGGAGTGGGGGTTCCAGGGGACTAGTGAGGTTCTCATCCCTTC	
SOX9	SRY-box 9	NM_000346.2	2136-2235	CAGTGGCCAGGCCAACCCTGGCTAAATGGAGCAGCGAAATCAACGAGAACTGGACTTTTTAAACCTCTCAGAGCAAGCTGGAGGATGATG		

Supplementary Table 3 Continued:

Group	Gene Symbol	Gene Name	Accession	Position	Target Sequence	References
Polyamine System	AGMAT	agmatinase	NM_024758.4	2053-2152	TGCTTAGGGCTCATCTTGGTTTAAAGACCCTGTGAACGTAAAGTAAAGTAAACACGGAGAGCCTAATGAAGAACTCTTGCTCA	Sequeira A, et al. (2006). <i>Arch Gen Psychiatry</i> , 63(1):35-48
	AZIN1	antizyme inhibitor 1	NM_148174.2	506-605	TTGCATATCTAAGGACCCAGACATAGGCTTGGTGGCCCTCTCTTCTTCTGGTTTATGACTTTCCGGCTTTGTGAATACGGCTGAGATGAA	
	AMD1	adenosylmethionine decarboxylase 1	NM_001634.4	811-910	TTTCCAGAGAGTGGGTAATCAGTCAGCCAGATCAACCTTGGAAATCTGTAGTGTAGTGTGACCCAGCAGTATGGACAGTTCATACATGA	
	EIF5A	eukaryotic translation initiation factor 5A	NM_001970.4	294-393	AAATGAGTGTCTCAGCATACCTAAGAAAGTGGCTTGTGGTCTCAAAGGCCGGCCATGAAGATCGTCAGATGTCTACTTCCGAAGACTGGCAAG	
	MTHFR	methylenetetrahydrofolate reductase	NM_005957.4	1041-1140	TGTCCAAGCTGGAGTGCCACAGGAGATCAAGGACGTGATTGACCAATCAAAGACAACGATGTGCCATCCGCACTATGGCATCGAGCTGG	
	OAZ1	ornithine decarboxylase antizyme 1	NM_004152.2	314-413	GGTGGGGCAGGGAAAGTCAAGAGGATCAAACTTTTCAAGTAACTTACTCTGATGATCGGTGAATGTAACAGAGAACTAACCTGAGCTCA	
	OAZ2	ornithine decarboxylase antizyme 2	NM_002537.2	367-466	CCTTCTCTCAGCTCAATATATAAAGACGAGAAGCTCACTGTGACCCAGGACTCCCTGTGAATGATGAAAACTCACATCGTCCACTCCAG	
	ODC1	ornithine decarboxylase 1	NM_002539.1	951-1050	AGACCTCTGTGACGCAATCTCTGTGTCGCCGTGTGTTTTGACATGGGGGCTGAGTGTGGTTTTCAGCATGTATCTGCTGATATTGGCGGTGGC	
	PAOX	polyamine oxidase	NM_152911.2	849-948	CAGGAGGCAGCCTTCCCGGGGAGACCTTCCAGTGTGCGTAGAGTGTGAGGATGAGACCGGTTCCCGCGCACCATGTATCATCTCACCGTG	
	PMF1	polyamine modulated factor 1	NM_007221.3	1023-1122	CAGCCAGGGGCTTACCAGTGTCTTCCACATCCGTAATAAACTTCTTCACTACACTGTAATCTGTGAGCATGCTTCTCTGCCTGGCCTCTC	
	PMFBP1	polyamine modulated factor 1 binding protein 1	NM_031293.2	849-948	ACACTTCTCTGATGATTCAAGAGCATCAGGAGACTAGAAACGACTGTGAACTGGCAAAAAGTCTCTCAACAGGATGATCTCATTCAA	
	SAT1-001	spermidine/spermine N1-acetyltransferase 1	ENST00000379270	326-425	CCCCTTTTACCCTCGCTGGTTCGCAAGAGTCCGCAAGAGCAGCTGGACTCCGGAAGGACACAGCATTGTGGTTTGGCCATGACTATTTTACCTA	
	SAT1-002	spermidine/spermine N1-acetyltransferase 1	ENST00000489394	316-415	GCCTGGTTGCAAGAGTCCGAAAGAGCAGCTGGACTCCGGAAGGTTACAGTCTCTAGTTCGCCATGTACATGGCCCTCCGTGTACATGGATGG	
	SAT1-004	spermidine/spermine N1-acetyltransferase 1	ENST00000379251	248-347	GCTGGCTAAATATGAATACATGGAAGAACAAGTAACTTAACTGAAAAGGTAATTCACAGTGGCGGACGGGGACAAGCGTTCGGTGCC	
	SAT1_all	spermidine/spermine N1-acetyltransferase 1	NM_002970.2	463-562	ATCTTGAGGACTTCTGTGATGAGTATTAGAGGCTTGGCATAGGACTCAGAAATCTGAAAGATTAAGCCAGGTTGCAATGAGGTGCTGG	
	SMOX	spermine oxidase	NM_175839.1	162-261	CTCAGCAGGGAAGGTTCTGAAGGTTGAGCGGACGAGGATGCAAAAGTTGTAATCCAGTGTGACAGTGGGATGCGGATGCGGCTCAGTCCG	
SMS	spermine synthase	NM_004595.2	1025-1124	GGATGGGAAATATTTACACAGGGAACTGTGCAATCTGACAGAAGCAGTGTGCTCTATGAAAGACAGCTGGGGCGCTGATTGTCCTGTG		
SRM	spermidine synthase	NM_003132.2	255-354	GCAGTAAGACCTATGGCAAGCTGTGTGTTGGACGGTGTCTCAGTGCACGGAGAGAGCAGGTTCTCTACCAGGAGATGATGCCAACCC		
Circadian Rhythm	ARNTL	aryl hydrocarbon receptor nuclear translocator like	NM_001030272.1	841-940	GATGTGACCCGAGGGAAGATACTCTTGTCTCAGAGTGTGTTCTCAAGATCCTCACTACAGCCAGAAATGATCTGATTTGGTGTGAGTTTGTG	Li JZ, et al. (2013). <i>Proc Natl Acad Sci U S A</i> , 110(24): 9950-9955; Melhuish Beaupre L, et al. (2020). <i>World J Biol Psychiatry</i> , 21(2):80-90.
	CLOCK	clock circadian regulator	NM_004898.2	2351-2450	AGCCGGGAAGCATGGTCCAGATTCATCTAGTATGCCCAAAAACAGCACCAGAGTGTGCAAGTACTACATCACTCAGGACAGGACAGTAAGA	
	CRY1	cryptochrome circadian clock 1	NM_004075.3	1376-1475	GAAAGTATGAAAAGTGCAAACTCTCTGTCTGTGATGACCATGATGAGAAATATGGAGTCCCTTCACTGGAAGAGTAGGTTTGTATACAGATG	
	CRY2	cryptochrome circadian clock 2	NM_001127457.1	3326-3425	ATCACTGACAGGCTTCTCTGAGATTCCTCAGTTTTCTCAGCCAGAGAGTGCCTTTAGAGTCCAACTGTTGTACTGATGTCACCTTCACTA	
	NPAS2	neuronal PAS domain protein 2	NM_002518.3	1459-1558	CTTTAACACTCGAGCTGGTGCCTGGGCTTAAATACCAGTCATTCCGCATCCGGCTCTCAAGAAGTCCCAAAATCTCGCACACAGCCAA	
	PER1	period circadian clock 1	NM_002616.2	4366-4465	CCTGGCAAAAGTTCTGCAAGCTGTGAACTGAGTGCCTCATATTTCCAGTGTGAGCTGACTCTTGGAGGTTGGGGTTCAGCACTATTTA	
	PER2	period circadian clock 2	NM_022817.2	986-1085	TGTGGAGCATGTGACGTGGAGCAGATCTTTTACTCAAGATGCATGGAGGAGAAATCTTCTTTTGGCGTGTGACGTGCGGAAAAGCCACGA	
PER3	period circadian clock 3	NM_016831.1	1076-1175	GACCTGATTGGAAACATCGATCTAAGCTACCTGCACCTGGAAGATGCTTCTGTATGTTGGCATAACAAAAGTTTGGAAATGACAGGGCA		
Stress and Immune Response	BDNF	brain derived neurotrophic factor	NM_170732.4	731-830	CAGGTTGATGCTCAGTAGTCAAGTGCCTTTGGAGCCTCTCTCTTCTGCTGGAGGAATACAAAATACCTAGATGCTGCAAAATGCTTCA	Yin H, et al. (2016). <i>Depress Anxiety</i> , 33(6):531-540; Melhem NM, et al. (2017). <i>Psychoneuroendocrinology</i> , 77:284-294; Tonelli LH, et al. (2008). <i>Acta Psychiatr Scand</i> , 117(3):198-206.
	CRH	corticotropin releasing hormone	NM_000756.1	682-781	ACCTCTCCGGGAAGCTTTGGAAATGGCCAGGGCAGGAGTTAGCACAGCAAGCTCACAGCAACAGGAACTCATGGAGTATTGGGAAAT	
	FKBP5	FK506 binding protein 5	NM_001145775.1	541-640	ACCATTTGCTTTAGTCTTGGCAAAAGCCAAAGTCAACAGGATGGGACATGGGGTGGCTACCATTGAAGAAAGGAGAGATATGCCATTTACTG	
	HSD11B1	hydroxysteroid 11-beta dehydrogenase 1	NM_181755.1	156-255	GCCTACTACTATTTGCAAAACAGGAATTCAGACAGGAGATGCTTCAAGGAAAGAAAGTATTGTCACAGGGCCAGCAAAGGGATCGGA	
	HSD11B2	hydroxysteroid 11-beta dehydrogenase 2	NM_000196.3	1703-1802	CCTCAGGATTTTCTCGCACCAAGTGCCTCAGTGTGCAATTTGAGGGCTAAATCCAAAGTGTCTTCTGACTGCTCAAGAAATGAGCCCAAC	
	HSP90AA1	heat shock protein 90 alpha family class A member 1	NM_001017963.2	1656-1755	CTTGACCAATGACTGGGAAGTCACTTGGCAGTGAAGCATTTTTCAAGTTGAAGGACAGTTGGAATTCAGAGCCCTCTATTGTTGCCACGACGTG	
	HSPA2	heat shock protein family A (Hsp70) member 2	NM_021979.3	2096-2195	AAGATCCTGACAAAGTGTGAGGAGTGTCAACTGCTCGACCGAAAACAGATGGCAGAGAAAGATGAGTATGAACACAAGCAGAAAGAGCT	
	NPY	neuropeptide Y	NM_000905.2	271-370	AGAGATATGAAAACGATCCAGCCAGAGACATGTTTTCAGACCTTGTATGAGAGAAAAGCAGAGAAAATGTTCCAGAACTCGGCTTGAAG	
	NR3C1	nuclear receptor subfamily 3 group C member 1	NM_001018077.1	1666-1765	GCTTTCTCTGCGGGGAGAAAGACATTCATTTCTTTGAAAGGAAACTCGAATGAGGACTGCAAGCTCTCATTTCACGACACTAAACCCA	
	PPARA	peroxisome proliferator activated receptor alpha	NM_001001928.2	5221-5320	GGGTGTGTTTGTATACGAACATAATGGACGTGAAGTGGGGCAGAAACCCAGAATCAGCATTCAAGGATGCCAGGAGAGTGTCCCTGTTT	
	PPARD	peroxisome proliferator activated receptor delta	NM_006238.4	108-207	GTAGGACGCGGGACAGTGTGTGACAGTGTGTTGGGATGACAGTACTACACAGTGGCTTCTGCTCAACCAAGATGAAGACAGATGCACT	
	PPARG	peroxisome proliferator activated receptor gamma	NM_015869.3	1036-1135	GAGCAAAAGAGTGGCCATCCGCATCTTTCAGGGCTGCCAGTTTCTGCTCGTGGAGGCTGTGAGGAGATCAGAGATGCCCCAAAGCATTC	
	SGK1	serum/glucocorticoid regulated kinase 1	NM_005627.2	1791-1890	GTGTGAACCGTGTGTGAGTGTGATGCTGATACAGATGGAATTTGTTATAAGCATCAATGTGACACTTGCAGGACACTACAAGTGGGAC	
	CD19	CD19 molecule	XM_011545981.1	714-813	CACCCAAAGGGCCTAAGTCAATGCTGAGCCTAGAGCTGAAGGACATGCCCCGAGAGATATGGGTAATGGAGACGGTCTGTGTTG	
	CD6	CD6 molecule	NM_001254751.1	1723-1822	AACCTGGACACTGCTTACAGACCCGCTCCTGGCCCTCAGTATCACCAGGAGCAACAGTGTGAGTGTGACCTCTTTCAGGGGAGCTT	
	CD68	CD68 molecule	NM_001251.2	1141-1240	ACCGTCTCCTTGTGCTCTCATCATCGGCTGCTTCTTGGCTCTCCGCTGTGCTTATTGCTCATCTCCGAGACAGCCCATCC	
	CD8A	CD8a molecule	NM_001768.5	1321-1420	GCTCAGGGCTTCTTCCACACACTCAGGCTTCTTCCGAGGCCCTGTCTCAGGGTGTGAGTGTGAGTCTCAACGGCAAGGGAACAAG	
	FCAR	Fc fragment of IgA receptor	NM_002000.2	1416-1515	TGCTGAGATTATAGGCAATGAGCCACAGCCGCTGGCAGATGATGTTCAAACCAATCAAATGGTGTCTTCTATGACAGGACTGATCGATTGAC	
	FGF2	fibroblast growth factor 2	NM_002006.4	621-720	GTCCGGGAGAAGAGCCCTCATCAAGTCAAACTTCAAGCAGAAAGAGAGAGGAGTGTGCTATCAAAGGAGTGTGTGCTAACCGTTAC	
	FOXP3	forkhead box P3	NM_014009.3	1231-1330	GGGCACTCTGGAGGCTCAGAGAAGCAGGACACTCAATGAGATCACTACCACTGTTTCCACAGTGTGTTGCTTCTTCCAGAACTGCGC	
IFNG	interferon gamma	NM_000619.2	971-1070	ATACTATCCAGTTACTGCGGTTTGAATAATGCCTGCAATCTGAGCCAGTGTCTTAAATGGCATGTGACAGAACTTGAATGTGTGAGGTGACC		
IL1B	interleukin 1 beta	NM_000576.2	841-940	GGGACCAAAGGCGGCCAGGATATACTGACTTCAACATGCAATTTGTCTTCTTAAAGAGAGCTGACCCAGAGAGTCTGTGCTGAATGTGG		
IL6	interleukin 6	NM_000600.3	365-464	GGCACTGCGAGAAAACCTGAACCTTCAAAGATGGCTGAAAAGATGATGCTTCCAATCTGGATTAATGAGGAGACTTGCCTGGTGAAC		
TNF	tumor necrosis factor	NM_000594.2	1011-1110	AGCAACAAGCAACCACTTCAAACTGGGATTCAGGAATGTGTGGCTGCAAGTGAAGTGTGGCAACCACTAAGAACTCAAACTGGGGCC		

Supplementary Table 3 Continued:

Group	Gene Symbol	Gene Name	Accession	Position	Target Sequence	References
Neurotransmission	GABRA1	gamma-aminobutyric acid type A receptor alpha1 subunit	NM_000806.5	476-575	AAAGTCCAGTGTCTGCTGACTGCTTTGGGCTGGATCTCTCTGAGCACACTGACTGGAAGAAGCTATGGACAGCCGTCATTACAAGATGAA	
	GABRA2	gamma-aminobutyric acid type A receptor alpha2 subunit	NM_000807.2	751-850	CTTCGAATTCAGGATGATGGGACTCTGCTGTATACCATGAGGCTTACAGTTCAAGCTGAATGCCAATGCACCTTGGAGGATTTCCTCAATGGATGCT	
	GABRB3	gamma-aminobutyric acid type A receptor beta3 subunit	NM_000814.5	449-548	TGGCTGACCAGCTAGGGTGCCTGACACATATTCTTAATGACAAAAGTCAATTTGTGCATGGAGTGACAGTGAAAAACCCGATGATCCGCTCTT	
	GABRG1	gamma-aminobutyric acid type A receptor gamma1 subunit	NM_173536.3	5921-6020	GCTTTGACTAACAGACAACATAAECTGAGAGACATGGTGTGTGGGTGGAAGGGATCCTGTAGTAGACTTGTTCATGATAGATGGGTACAAA	
	GABRG2	gamma-aminobutyric acid type A receptor gamma2 subunit	NM_000816.3	1-100	GTAAGTGTGAGGGGATGAGTATACAGAGTGTGCTGTTCCCTCTCCCTTAATTTGTCTCCGATGAGTCTCTCTGTACCCCTCCCTGCTC	
	GRIA1	glutamate ionotropic receptor AMPA type subunit 1	NM_000827.3	2841-2940	ATCGAGTCTGCTACAATCCGTAGTGAATCCAAAGCGGATGAAGGGTTTTGTGTTGATCCACAGCAATCCATCAAGCAAGCCATACCGACATC	
	GRIA2	glutamate ionotropic receptor AMPA type subunit 2	NM_001083620.1	866-965	TGACCTATGATGCCGTTCAAGTGATGACTGAAGCCTTCCGCAACCTAAGGAAGCAAGAATTGAATCTCCGAAGGGGGAATCAGGAGACTG	Sequeira A, et al. (2009). <i>PLoS One</i> , 4(8):e6585; Yin H, et al. (2016). <i>Am J Med Genet B Neuropsychiatr Genet</i> , 171B(3):414-426; Turecki G, et al. (2003). <i>Am J Med Genet B Neuropsychiatr Genet</i> , 118B(1):36-40.
	GRIA3	glutamate ionotropic receptor AMPA type subunit 3	NM_000828.4	427-526	TGCAGGAGCACAGCCTTCCGCTTCCGCTGAGTATACAACACCAACAGAACACCACCGAGAAGCCCTTCCATTTGAATACACAGTATGAT	
	GRIA4	glutamate ionotropic receptor AMPA type subunit 4	NM_000829.3	476-575	GTTATTTTCTGGATTTTGGGACTCGCCATGGGAGCCTTCCGAGCAGCGTGCAATAGGTGTCTCTTCCGAAACACAGATCAGGAATACAC	
	GRIN1	glutamate ionotropic receptor NMDA type subunit 1	NM_000832.5	1291-1390	TTCAGAGAGTCTGATGCTTCCAAGTATGCGGATGGGGTACTGCTGCGTGGAGTTCAATGAGGATGGGGACCGAAGTTCGCAACTAC	
	GRIN2A	glutamate ionotropic receptor NMDA type subunit 2A	NM_000833.3	4498-4597	GAATGACAGCTATCTTCGGTCTCTTGAAGTCAACGGCATCTGACTGTCCAGGGACAGTCCGGGCAACAATGATGTATATTTCCGGAGCATG	
	GRIN2B	glutamate ionotropic receptor NMDA type subunit 2B	NM_000834.3	1145-1244	CAACACCCACGAGAAGAAATCTTCCAGTCCAATATGCTAAATAGTATCTGATCAATGTCACTTTTGGGGGAGGAATTTGCTTCTCAGTGAAG	
	GRIN2C	glutamate ionotropic receptor NMDA type subunit 2C	NM_000835.3	2104-2203	TTCATGATCCAAGAGCAATACATCGACACTGTGCTGGGCTCAGTGACAAGAAAGTTTCAGCGGCCCTCAAGATCAGTACCCACTTCCGCTTCGG	
	GRIN2D	glutamate ionotropic receptor NMDA type subunit 2D	NM_000836.2	1894-1993	CATCTCTGAGTACTCTGCTGTGTTACAACCGGCTGCCACGGCCCTGGCCGTTCAACCTTCCACTTCCGCTTCCGCTTCCGCTTCCGCTTCCG	
	GRM3	glutamate metabotropic receptor 3	NM_000840.2	461-560	TTCTGCCAAGAGTCCAATAGATGCGACGGCTTCCAGCTGGTCAAGTGAAGGAAAGTTGCTTCCGCGCTAGGAAGTGGTTTGCCTGATAAG	
	HTR1A	5-hydroxytryptamine receptor 1A	NM_000524.2	626-725	TGCTCATGCTGTTCTCTATGGGCGCATATCCGAGCTGCGGCTTCCGATCCGCAAGACGGTCAAAAAGGTGGAAGACCGGAGCGGACAC	
HTR2A	5-hydroxytryptamine receptor 2A	NM_000621.3	3460-3559	AGGCTGAGACGCAAGGATCACTGAGCCAGAAGCTCAAGGCTGCAAGTGAAGGAAAGTTGCTTCCGCGCTAGGAAGTGGTTTGCCTGATAAG		
MAOA	monoamine oxidase A	NM_000240.2	201-300	CGAGTATCGCGGCCATGTTCGACGTAGTCTGATCGGAGGTGGCAATTCAGGACTATCTGCTGCCAACTCTGACTGAATATGGCGTTAGT		
SLC6A4	solute carrier family 6 member 4	NM_001045.2	236-335	CCGAGAGTCAATGGGATCCTTGGCAGATGGACATCAAGTCTTACTAACCAGCAGGATGGAGACGACGCCCTTGAATCTCAGAAGCAGCT		
Mitochondria	MFN2	mitofusin 2	NM_014874.3	2011-2110	CAGTGCTTCTCCCTCAACTATGACCTAACTGTGACAAGCTGTGTGCTGACTTCCAGGAAGACATTGAGTTCATTTCTCTCTCGGATGGACATG	
	MT-ATP6	mitochondrially encoded ATP synthase membrane subunit 6	ENST00000361899.1	472-571	GTACGCCATAACCGCTAACATTACTGACGGCCACTACTCATGCACTAATTGGAAGCGCCACCCTAGCAATATCAACCAATTAACCTTCCCTCACAC	Rollins B, et al. (2009). <i>PLoS One</i> , 4(3):e4913; Mamdani F, et al. (2014). <i>Schizophr Res</i> , 159(2-3):370-375.
	MT-ND6	mitochondrially encoded NADH dehydrogenase 6	Mito_JCM_011.1	266-365	CTTTGGATATACTACAGCGATGGCTATTGAGGAGTACTCTGAGGATGGGGTTCAGGGTTGAGGTTGGTGAAGTGTGTTAGTGGGTTAGCG	
	MTPAP	mitochondrial poly(A) polymerase	NM_018109.3	196-295	CAGCCCTCAGGGAGCGTGAGGACAGGCTTTGAAGACAAGATTCCAAAAGGAGATTCTCTGAGATGCAAAATGAAAGACGAGAACAGGCACAC	
SLC25A26	solute carrier family 25 member 26	XM_006712957.1	432-531	AGCAGAGGGCACAGGTATCTGCTTCAAGAACAATTTTCAGATTTTCTTAACATCTTATATGAAGAGGGTATCCAAGGTTGATCGAGGCTATA		
Metallothionein System	MT1A	metallothionein 1A	NM_005946.2	1-100	ACCAAGCCTTCCAGTGCCTTATAGCTCTCAACTTCTGCTTGGATCTCCAACCTCACCGGCTCGAAATGGACCCCAACTGCTCTCGCCG	
	MT1B	metallothionein 1B	NM_005947.2	1-100	CCTGCGCTGACTTCTCATATCTTGCTAGGAACTCCAGGCTTGTCTGGCTCCAAATGGATCCCAACTGCTCTGCACCACAGGTGGCTCTGTGCC	
	MT1E	metallothionein 1E	NM_175617.3	33-132	GGTGAGGCGGGAGCTGGGCTCTGCGCCCGCCGACTCTATAAATAGAGCAGCCAGTTGCAGGGCTCAATCTGCTTCCCACTGCC	
	MT1F	metallothionein 1F	NM_005949.3	15-114	CTATCAAAGCAGCGCCGGCTTGGGGTCCACACGCTTCCACTGCCCACTGCTTCTTCCGCTTCTCTTGGAAAGTCCAGTCTCTCTCCGCG	
	MT1G	metallothionein 1G	NM_005950.1	215-314	GCATCTGCAAAGGGGATCGGAGAAGTGACGCTGTGCGCTGATGTCGGGACAGCCCTGCTCCCAAGTACAAATAGAGTGACCCGTAATAATCT	
	MT1H	metallothionein 1H	NM_005951.2	215-314	CATCTGCAAAGGGGCTCAGAGAAGTGACGCTGTGCGCTGATGTCGGGACAGCCCTGCTGTGATGAAAACAGAAATGACACGTAATAATCT	
	MT1X	metallothionein 1X	NM_005952.3	32-131	TTCTCTTGTATCGGGAATCTGCTTCTCTTCTGCTGAAATGGACCCCACTGCTCTGCTGCTGTTGGCTCTGTGCTGCTGCTGCTGCTGCTGCTG	
	MT2A	metallothionein 2A	NM_005953.3	226-325	CAGGGCTGCATCTGCAAAGGGGCTCGGACAAGTGACGCTGCTGCGCTGATGCTGGGACAGCCCGCTCCAGATGTAAGAAACGCGACTTCT	
MT3	metallothionein 3	NM_005954.2	166-265	CCTAGCCAAAGCGCGCTCAGTGTGCTGAGAAGCCGCTTCCAGCCCTCCAGCTGCTCTCTGACATGACCTGAGACCTGACCTGCTCCCTG		
Housekeeping	CYC1	cytochrome c1	NM_001916.4	345-444	TATCCGTGCTCACCCGTGGCTCTCTCTCTTCTGACCAACACAGCATCCGAGGGGTTTTCCAGGATATAAGCAGGTGTGCGCTCTGCTCCAC	
	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	NM_002046.3	973-1072	CACCTCTCCACTTTGACGCTGGGGCTGGCATTGCCCTCAACGACCACTTTGCAAGCTCAATTTCTGGTATGACAACGAATTTGGCTACAGCAACA	
	SDHA	succinate dehydrogenase complex flavoprotein subunit A	NM_004168.1	231-330	TGGAGGGGACAGCTTGCAGAGCTGATTGGCTTCTGAGGACAGGGTTAATACAGCATGTGTTCAAGCTGTTTCTACCAGGTACACACTG	

Supplementary Table 4: Top five genes affected by adjusted time of death in the DLPFC (P≤0.05)

Gene	P (Sex)	P (Age)	P (Diagnosis)	P (Adjusted TOD)	P (MDD-S vs. MDD-NS)	FC (MDD-S vs. MDD-NS)	FC Direction
PER2	0.0003	0.057	0.205	0.003	0.158	1.193	UP
CRY1	0.013	0.034	0.504	0.016	0.880	1.014	UP
CRH	0.001	0.015	0.064	0.030	0.022	1.384	UP
SAT1-002	0.115	0.283	0.035	0.039	0.649	-1.063	DOWN
SAT1-004	0.594	0.010	0.287	0.041	0.165	-1.242	DOWN

Supplementary Table 5: Field of View (FOV) for brain and blood

	Average FOV	FOV Stdev	% FOV	Min % FOV	Max % FOV
Brain	533.94	10.84	96.21	85.23	98.74
Blood	540.06	8.27	97.31	92.43	99.64

The FOV is an imaging quality control measure from NanoString which is indicative of the number of mRNA counts successfully imaged per lane in the array. Samples having low assay efficiency due to low quality of RNA will have a low number of counts and will result in a quality flag. The FOV threshold is set at 75% and any sample below this threshold is flagged and should not be used for downstream analysis. As can be seen in the table we have included in the supplemental, our % FOV is very comparable between brain and blood, thus demonstrating the lack of effect of low RIN in the blood on mRNA measures.

Supplementary Table 6: Blood differentially expressed genes between MDD-S and Controls ($P \leq 0.05$)

Gene	Mean (Control)	Mean (MDD-NS)	Mean (MDD-S)	P (MDD-S vs. Control)	Q Value (MDD-S vs. Control)	FC (MDD-S vs. Control)	FC Direction
POT1	6.624	6.886	7.403	0.0009	0.035	1.841	UP
SLC25A26	6.834	6.815	7.945	0.002	0.018	2.297	UP
EIF5A	9.528	9.873	10.272	0.004	0.035	1.672	UP
HTR2A	3.361	2.843	2.209	0.005	0.019	-2.189	DOWN
GAR1	6.209	6.227	6.734	0.006	0.018	1.443	UP
NR3C1	9.315	9.465	10.435	0.008	0.036	2.300	UP
MT-ND6	13.714	13.262	12.791	0.011	0.035	-1.902	DOWN
NHP2	7.803	8.034	8.413	0.013	0.036	1.520	UP
SRM	7.273	7.429	7.761	0.019	0.060	1.440	UP
MT1H	5.345	4.760	4.071	0.021	0.035	-2.236	DOWN
ODC1	7.747	8.723	8.643	0.021	0.029	1.767	UP
GPHN	7.824	7.781	8.461	0.023	0.060	1.646	UP
SAT1-002	6.361	7.195	7.177	0.028	0.053	1.855	UP
TINF2	7.347	7.500	7.780	0.029	0.070	1.423	UP
MTPAP	6.824	6.628	7.377	0.029	0.046	1.471	UP
SAT1_all	12.901	13.633	13.815	0.037	0.053	1.884	UP
ACD	8.306	7.556	7.724	0.038	0.072	-1.471	DOWN
NFE2L2	9.360	9.712	10.001	0.045	0.072	1.578	UP
NOP10	8.876	9.439	9.482	0.046	0.053	1.439	UP
GRIN2B	4.063	3.722	3.368	0.047	0.035	-1.579	DOWN

Supplementary Table 7: Blood differentially expressed genes between MDD-NS and Controls ($P \leq 0.05$)

Gene	Mean(Control)	Mean(MDD-NS)	Mean(MDD-S)	P (MDD-NS vs. Control)	Q Value (MDD-NS vs. Control)	FC (MDD-NS vs. Control)	FC Direction
TERC	11.089	10.318	10.666	0.013	0.226	-1.637	DOWN
ODC1	7.747	8.723	8.643	0.013	0.226	1.996	UP
ACD	8.306	7.556	7.724	0.022	0.226	-1.619	DOWN
PMFBP1	5.426	4.690	4.781	0.042	0.384	-1.657	DOWN

Supplementary Table 8: Blood differentially expressed genes between MDDs (regardless of the suicide status) and control groups ($P \leq 0.05$)

Gene	Mean(Control)	Mean(MDD-NS)	Mean(MDD-S)	P (MDD vs. Control)	Q Value (MDD vs. Control)	FC (MDD vs. Control)	FC Direction
ODC1	7.747	8.723	8.643	0.007	0.070	1.878	UP
ACD	8.306	7.556	7.724	0.013	0.103	-1.543	DOWN
POT1	6.624	6.886	7.403	0.013	0.117	1.511	UP
EIF5A	9.528	9.873	10.272	0.013	0.103	1.505	UP
TERC	11.089	10.318	10.666	0.019	0.103	-1.466	DOWN
HTR2A	3.361	2.843	2.209	0.024	0.103	-1.783	DOWN
MT-ND6	13.714	13.262	12.791	0.029	0.103	-1.664	DOWN
PMFBP1	5.426	4.690	4.781	0.032	0.103	-1.552	DOWN
SRM	7.273	7.429	7.761	0.038	0.191	1.346	UP
MT1H	5.345	4.760	4.071	0.040	0.103	-1.929	DOWN
SAT1-002	6.361	7.195	7.177	0.040	0.124	1.706	UP
NOP10	8.876	9.439	9.482	0.042	0.103	1.412	UP

Supplementary Table 9: DLPFC differentially expressed genes between MDD-S and Controls ($P \leq 0.05$)

Gene	Mean(Control)	Mean(MDD-NS)	Mean(MDD-S)	P (MDD-S vs. Control)	Q Value (MDD-S vs. Control)	FC (MDD-S vs. Control)	FC Direction
SAT1_all	11.418	11.521	11.156	0.007	0.097	-1.210	DOWN
CRY2	10.478	10.382	10.377	0.016	0.397	-1.132	DOWN
GABRA2	12.311	12.205	12.103	0.019	0.198	-1.145	DOWN
MT2A	10.793	11.094	10.515	0.032	0.286	-1.307	DOWN
MT1A	6.737	7.591	6.228	0.052	0.417	-1.841	DOWN

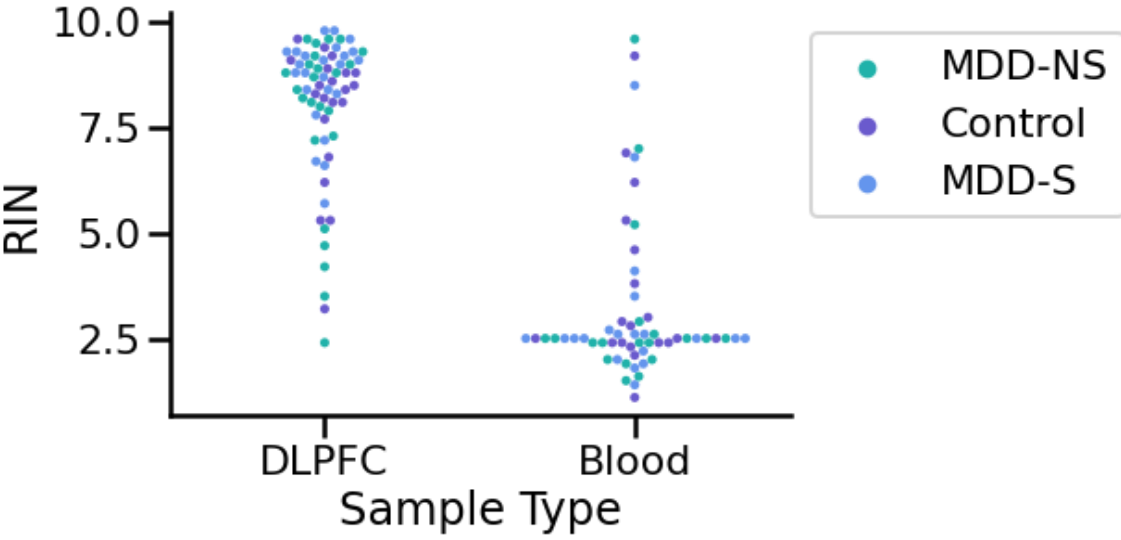
Supplementary Table 10: DLPFC differentially expressed genes between MDD-NS and Controls ($P \leq 0.05$)

Gene	Mean(Control)	Mean(MDD-NS)	Mean(MDD-S)	P (MDD-NS vs. Control)	Q Value (MDD-NS vs. Control)	FC (MDD-NS vs. Control)	FC Direction
FKBP5	9.071	10.055	9.085	0.001	0.015	1.675	UP
ODC1	9.388	9.553	9.436	0.001	0.101	1.149	UP
SAT1-002	5.685	6.021	5.673	0.006	0.121	1.283	UP
SMOX	9.355	9.551	9.444	0.009	0.121	1.164	UP
RBFOX3	10.787	10.668	10.810	0.010	0.101	-1.087	DOWN
MT3	14.289	14.453	14.185	0.011	0.264	1.151	UP
HSD11B2	4.621	5.286	4.598	0.016	0.015	1.353	UP
AGMAT	6.415	6.128	6.430	0.016	0.121	-1.215	DOWN
GFAP	14.073	14.490	14.103	0.017	0.264	1.438	UP
AMD1	12.012	12.083	11.998	0.035	0.336	1.099	UP
MT1H	6.509	5.765	5.965	0.042	0.179	-1.750	DOWN
CRY2	10.478	10.382	10.377	0.045	0.336	-1.111	DOWN
PPARA	8.204	8.287	8.065	0.047	0.480	1.157	UP
CRH	8.472	7.732	8.314	0.049	0.015	-1.310	DOWN

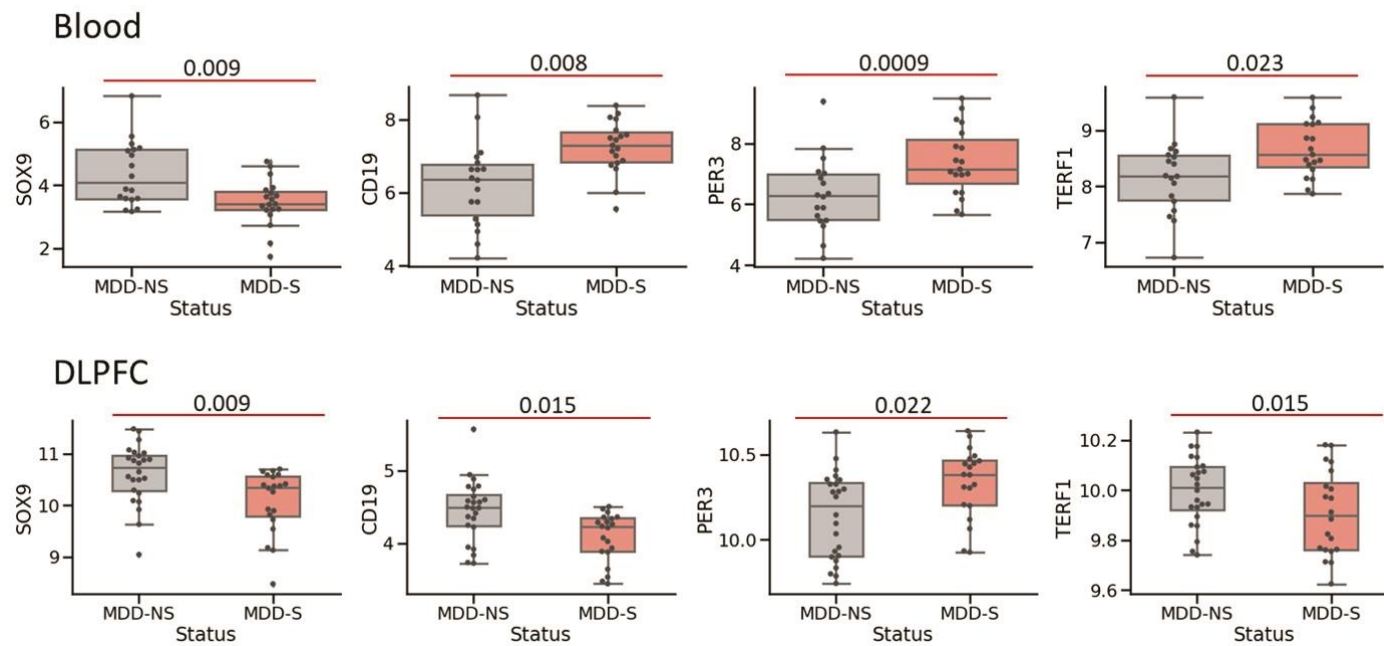
Supplementary Table 11: DLPFC differentially expressed genes between MDDs (regardless of the suicide status) and control groups ($P \leq 0.05$)

Gene	Mean(Control)	Mean(MDD-NS)	Mean(MDD-S)	P (MDD vs. Control)	Q Value (MDD vs. Control)	FC (MDD vs. Control)	FC Direction
CRY2	10.478	10.382	10.377	0.013	0.548	-1.121	DOWN
SMOX	9.355	9.551	9.444	0.017	0.283	1.127	UP
ODC1	9.388	9.553	9.436	0.017	0.283	1.092	UP
FKBP5	9.071	10.055	9.085	0.037	0.283	1.327	UP

Supplementary Figure 1: Distribution of RNA Integrity Numbers (RIN) in both brain (DLPFC) and blood across the three diagnostic groups (Controls, MDD-S, and MDD-NS)



Supplementary Figure 2: Genes significantly differentially expressed, and concordant, between MDD-S and MDD-NS in blood and DLPFC. Two genes (SOX9 and PER3) are increased in suicides in both brain and blood. While two genes (CD19 and TERF1) are increased in blood, but decreased in DLPFC.



Human Brain Dissection and Freezing Protocol

Ten-Step Process for Obtaining High Quality Brain Tissue (UCI/Pritzker Brain Bank)

The brains are obtained from the Orange County Coroner's Offices with which the UCI Brain Bank has had long-standing and excellent relationships. The process involves collecting brains from schizophrenia (SZ), bipolar depressive disorder (BPD), major depressive disorder (MDD) patients, and control subjects with no psychiatric diagnoses.

1. UCI staff members identify potential brain donor candidates.
2. Prior to autopsy, all available clinical information (exclusion/inclusion criteria) is reviewed before contacting next-of-kin (NOK). The study is thoroughly explained, and consent is obtained and recorded by phone. Subsequently, the consent is obtained in writing.
3. Brain, blood, and skin are acquired during autopsy.
4. The whole brain is kept in an isotonic saline solution cooled by wet ice and taken to the UCI laboratory. Once in the lab the brain is imaged with a digital camera.
5. The brain is suspended in an alginate mold to securely hold the brain in place during slabbing. This greatly improves the consistency of slabbing so that specific brain regions are much better visualized. The brain is cortically sliced into ~12 1.5 cm slabs and each slab is digitally imaged before it is snap frozen in a -40°C dry ice cooled isopentane (2-methylbutane) bath. Brain slabs are then quickly vacuum-sealed to minimize ice crystal formation and stored in freezers in a heavily restricted area.
6. Each freezer is equipped with a sensaphone surveillance system, which automatically notifies research staff (24/7) whenever a freezer shows an increase in freezer temperature. Each freezer also has a liquid nitrogen back-up in case the freezer goes down. Finally, all freezers are individually monitored by research staff on a daily basis 365 days a year.

The brains are stored at -80°C while evaluations are undertaken. The evaluation process includes a psychological autopsy, examination by a neuropathologist. A small piece of cerebellum from each case is analyzed for pH and RNA Integrity Number (RIN), conducted at Mark Vawter's Functional Genomics Laboratory, thus providing important data for quality control.

7. The psychological autopsy process involves information and collection of all available medical records from doctors and hospitals, and an extensive phone interview with the NOK. The NOK interview includes 140 variables. Information from this interview and the medical records are reviewed to obtain a psychiatric diagnosis by a Ph.D. and an M.D.
8. While the psychological autopsy is being completed, the digital pictures of the brain taken at the initial slabbing are sent to a neuropathologist who evaluates them for brain pathology and generates a report.

9. All cases assigned for UCI/Pritzker cohorts must fulfill the following quality control criteria:

- a) Confirmed diagnosis
- b) Completed NOK interview
- c) Negative neuropathologist report
- d) Confirmed rapid death
- e) pH >6.5
- f) RIN value > 7.0

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