

Supplementary Table 1. GO functional terms associated with the differentially expressed genes between suicides with SUD compared to suicides without SUD (separating up and down-regulated genes).

GO ID	GO Name	Count	%	EASE*	Genes
Down-regulated genes					
GO:0006812	Cation transport	19	17.2 7	2.17E-5	<i>SLC8A2, SLC12A5, SNCA, NDFIP1, CACNA2D3, ATP6V1D, ATP13A2, PRKCB, KCNK4, THY1, ANXA6, ATP6V1A, PDE2A, GPM6A, CAMK2B, DENND5B, DPP6, PRNP, EHD3</i>
GO:0097458	Neuron part	23	20.9 0	6.69E-4	<i>SVOP, SLC8A2, SYT4, STMN2, SLC12A5, MAP2K4, SNCA, UCHL1, ASTN1, GABBR2, ATP13A2, THY1, EPB41L3, PDE2A, GPM6A, KLC1, SYN2, CYFIP2, SNAP47, CNTNAP1, SV2B, RIT2, NEFM</i>
GO:0023052	Signaling	55	50.0	5.58E-4	<i>SYT4, ATP6AP2, HINT1, SNCA, UCHL1, GABBR2, COPS8, CNOT7, CRADD, DIRAS2, KIFAP3, SNAP47, CNTNAP1, RAB6B, PSMD7, USP14, ADGRB3, SLC25A4, RAN, CYCS, ATP6V1D, LRPAP1, THY1, PRKCB, ATP6V1A, KRIT1, KLHL12, PRNP, FBXL2, YWHAZ, GGCT, ANXA6, MOAP1, NDRG3, SYN2, PPP3CB, CAMK2B, BRK1, SSX2IP, EHD3, SLC8A2, ZC3H15, MAP2K1, MAP2K4, SLC12A5, NDFIP1, SMYD2, CACNA2D3, PEX11B, PDE2A, RGS4, AKR1B1, CYFIP2, ZNF385B, RIT2</i>
GO:0045202	Synapse	14	12.7 2	0.006	<i>SVOP, SLC8A2, SYT4, SNCA, GABBR2, EPB41L3, GPM6A, PDE2A, SYN2, CYFIP2, SNAP47, SV2B, ADGRB3, USP14</i>
GO:0002768	Immune response-regulating cell surface receptor signaling pathway	8	7.27	0.007	<i>MAP2K4, PPP3CB, CYFIP2, BRK1, PRNP, PSMD7, PRKCB, THY1</i>
GO:0031175	Neuron projection development	16	14.5 4	0.003	<i>MAP2K1, SYT4, STMN2, SLC12A5, UCHL1, UBE2V2, HERC1, THY1, EPB41L3, GPM6A, PPP3CB, CAMK2B, CNTNAP1, RIT2, ADGRB3, NEFM</i>
GO:0007610	Behavior	9	8.18	0.032	<i>SLC8A2, SLC12A5, UCHL1, SNCA, PPP3CB, ASTN1, PRNP, ADGRB3, KCNK4</i>
GO:0007611	Learning or memory	6	5.45	0.033	<i>SLC8A2, SLC12A5, PPP3CB, PRNP, ADGRB3, KCNK4</i>
GO:0045333	Cellular respiration	6	5.45	0.038	<i>UQCRC2, CYCS, SNCA, IDH3B, SUCLA2, MDH1</i>
Up-regulated genes					
GO:0060429	Epithelium development	20	18.0 1	1.73E-5	<i>GNA13, TXNIP, SOX10, SMAD5, CLDN5, GJA1, SLC9A3R1, PALLD, SOX8, ZFP36L1, NOTCH1, CHD7, EZR, S1PR1, HDAC1, PHGDH, RHOC, MSN, ABL1, FGF2</i>
GO:0007155	Cell adhesion	25	22.5 2	1.04E-4	<i>DENND6A, LIMS1, SOX13, ATP1B2, FERMT2, CLDN5, SOX2, ITGB5, CSRP1, SSPN, ZFP36L1, NOTCH1, MYO10, CHD7, S1PR1, EZR, PRDX6, IST1, MSN, TRIP6, PIEZO1, ABL1, MERTK, YES1, GPAM</i>
GO:0051960	Regulation of nervous system development	14	12.6 1	0.007	<i>SOX10, SOX2, HMG20B, SOX8, GPR37L1, NOTCH1, CHD7, HDAC1, APOE, IST1, CTDSP1, ABL1, TCF12, FGF2</i>
GO:0010628	Positive regulation of gene expression	19	17.1 1	0.030	<i>SOX10, LIMS1, SMAD5, SOX2, FOXN2, GJA1, SOX8, YBX1, SS18, NOTCH1, CHD7, EZR, S1PR1, HDAC1, AGO2, MSN, YES1, TCF12, FGF2</i>
GO:0048015	Phosphatidylinositol-mediated signaling	6	5.40 5	0.008	<i>ZFP36L1, EZR, PDGFRB, AGO2, SLC9A3R1, FGF2</i>

*modified Fisher exact p-value. Abbreviations: Gene ontology (GO); Substance Use Disorder (SUD)

Supplementary Table 2. GO functional terms associated with the differentially expressed genes between suicides with SUD compared to suicides without SUD (all-genes analysis).

GO ID	GO Name	Count	%	EASE*	Genes
GO:0022008	Neurogenesis	39	0.10	5.79E-4	SYT4, OPCML, UCHL1, SOX2, ASTN1, GJA1, UBE2V2, SOX8, CHD7, EZR, SLC1A3, S1PR1, GPM6A, APOE, PPP3CB, CTDSP1, CNTNAP1, CAMK2B, UNK, FGF2, NEFM, ADGRB3, SOX10, MAP2K1, STMN2, SLC12A5, HMG20B, HERC1, SLC9A3R1, GPR37L1, THY1, EPB41L3, NOTCH1, HDAC1, IST1, PHGDH, RIT2, ABL1, TCF12
GO:0008219	Cell death	41	0.11	0.019	CDK19, YWHAZ, GGCT, HINT1, SNCA, SOX2, GJA1, UBE2V2, SOX8, CRADD, TIMP1, ANXA6, ZFP36L1, MOAP1, APOE, KIFAP3, FGF2, TXNIP, SOX10, SLC25A4, MAP2K4, CYCS, GJB6, SLC9A3R1, ATP13A2, GPR37L1, PRKCB, EPB41L3, RNF130, NOTCH1, HDAC1, F3, KRIT1, VSTM2L, CYFIP2, PDGFRB, ZNF385B, MERTK, PRNP, ABL1, GPAM
GO:0030154	Cell differentiation	63	0.17	0.005	GNA13, OPCML, SYT4, FERMT2, UCHL1, CLDN5, GJA1, YBX1, S1PR1, SLC1A3, APOE, CTDSP1, CNTNAP1, MSN, FGF2, ADGRB3, SOX10, SOX13, STMN2, PTBP1, FOXN2, HMG20B, SLC9A3R1, HERC1, PALLD, GPR37L1, THY1, EPB41L3, VAMP5, PDGFRB, CHSY1, LIMS1, SOX2, ASTN1, ITGB5, UBE2V2, SOX8, ZFP36L1, CHD7, EZR, NDRG3, GPM6A, PPP3CB, CAMK2B, UNK, YES1, NEFM, TXNIP, MAP2K1, RRBP1, SMAD5, MAP2K4, SLC12A5, NDFIP1, NOTCH1, PDE2A, HDAC1, IST1, PHGDH, RIT2, ABL1, MERTK, TCF
GO:0007155	Cell adhesion	40	0.11	1.05E-4	LIMS1, YWHAZ, OPCML, EPDR1, ATP1B2, SOX2, CLDN5, FERMT2, ASTN1, ITGB5, ZFP36L1, CHD7, EZR, S1PR1, KIFAP3, PPP3CB, CNTNAP1, SSX2IP, MSN, YES1, PIEZO1, DENND6A, ZC3H15, SOX13, RAN, NDFIP1, CSRP1, SSPN, THY1, NOTCH1, MYO10, PRDX6, IST1, CYFIP2, MERTK, PRNP, ABL1, TRIP6, GPAM, CDH10
GO:0010001	Glial cell differentiation	10	0.027	0.0043	SOX10, NOTCH1, HDAC1, MAP2K1, SOX2, PHGDH, ABL1, SOX8, FGF2, GPR37L1
GO:0030182	Neuron differentiation	34	0.094	0.001	SYT4, OPCML, SOX2, UCHL1, GJA1, UBE2V2, SOX8, EZR, S1PR1, SLC1A3, GPM6A, APOE, PPP3CB, CTDSP1, CAMK2B, CNTNAP1, UNK, NEFM, ADGRB3, MAP2K1, STMN2, SLC12A5, HMG20B, HERC1, SLC9A3R1, GPR37L1, THY1, EPB41L3, NOTCH1, IST1, PHGDH, RIT2, ABL1, TCF12

*modified Fisher exact p-value. Abbreviations: Gene ontology (GO); Substance Use Disorder (SUD)

Supplementary Table 3. GO functional terms associated with the differentially expressed genes between suicides with SUD compared with non-suicides with SUD (separating up and down-regulated genes).

GO ID	GO Name	Count	%	EASE*	Genes
Down-regulated genes					
IPR007087	Zinc finger, C2H2	10	8.92	0.010	<i>ZNF69, ZNF594, ZNF264, ZNF682, ZNF773, ZNF786, ZNF716, ZNF669, ZNF652, ZNF577</i>
	signal peptide	23	20.53	0.0015	<i>ADAMTSL2, PIGX, ACP7, CELSR3, ADGRG1, SOD2, TIMP1, LEP, TNFRSF1A, TNFRSF9, C2ORF69, LRP10, COLQ, PLOD1, ADM, HAMP, ADGRV1, CHRNA5, PTTG1IP, CTSC, PLA2G2D, TP53I13, CSF2RA</i>
	Receptor	10	8.92	0.037	<i>QRFP, TNFRSF9, TNFRSF1A, LRP10, ADGRV1, CHRNA5, CELSR3, CRCP, ADGRG1, CSF2RA</i>
GO:0008152	metabolic process	77	68.75	0.039	<i>SAT1, RBM3, UBE2G2, PPP2R5C, TNFSF15, CRCP, OSGIN1, RNF213, KLHL8, ZNF682, PLOD1, HAMP, CHST12, KLHL28, ZNF773, YRDC, COX19, CSF2RA, ZNF577, ZNF594, NFKBIZ, PIGX, SNAPC1, NOL8, MYO3B, CHST3, PARP10, CIAO1, NRDE2, COLQ, ADM, LRP10, PPM1K, ZNF786, ZNF716, CTSC, CHSY1, GADD45B, CARM1, PPP1R15A, PLA2G2D, EIF2AK4, ADAMTSL2, WASH1, FKBP5, ACP7, TRIM13, ELK1, DMWD, MAPKAPK2, FCF1, ZNF652, TIMP1, N4BP2, TNFRSF1A, PLIN5, MTMR3, DDHD1, TDRD1, HSD17B7, ZNF69, RHBDF2, MAFF, ZNF264, MSH3, CEBPD, INIP, CELSR3, ZNF669, BIRC3, SOD2, LEP, FEM1C, CDKN1A, PTTG1IP, MBOAT2, DDX51</i>
Upregulated genes					
GO:0044455	mitochondrial membrane part	49	11.21	5.96E-24	<i>UQCRC2, NDUFB3, UQCRC1, NDUFB7, SAMM50, NDUFB9, ATP5B, C19ORF70, COA1, CYC1, COX7B, NDUFB1, BNIP3, PINK1, COX7A2L, UQCRC1, TOMM70, COX5A, UQCRCQ, C14ORF2, NDUFB2, NDUFS5, NDUFS4, TOMM6, ATP5L, ATP5O, ATP5I, ATP5H, ATP5J, NDUF44, SOX10, NDUF42, COX7A2, IMMT, NDUF49, COX8A, COX411, NDUF1C, NDUF12, NDUF11, UQCRL, SDHB, NNT, UQCRH, NDUFV1, NDUFV2, TOMM20, ATP5A1, PET100</i>
GO:0051537	iron, sulfur cluster binding	7	1.60	8.70E-5	<i>ISCA1, SDHB, GLRX5, CISD1, NDUFV2, UQCRC1, ATP5J</i>
GO:0019882	antigen processing and presentation	20	4.57	2.08E-5	<i>CLTA, DCTN6, DCTN3, DCTN2, PSMB5, PSMB4, PSMD14, PSMB7, PSMB6, PSMA5, KLC1, KIFAP3, PSMC2, PSMB2, AP3D1, PSMD4, RAB6A, DYNC1H1, PSMD7, DYNC1I2</i>
GO:0005856	cytoskeleton	70	16.01	0.042	<i>SLC8A3, CLTA, POTEKP, SHTN1, NUA1, TUBB2A, TLN2, HINT1, PINK1, CNP, ARL2BP, MAP1LC3B, KIFAP3, VPS4B, STK39, TUBB8, TUBA1A, DYNC1H1, TWF2, CHP1, POLB, TXNDC9, BASP1, DCTN6, SKP1, DCTN3, ZCCHC17, ATP6V1D, CHAMP1, CDK5, DCTN2, ARPC1A, EPB41L3, NME1, ARPC5L, MLLT11, CCDC53, CFAP20, SH3KBP1, ARL8B, WASL, DYNC1I2, SPAST, NDN, C14ORF166, AKAP11, ZNF365, PSMB5, PFN2, PDE6D, KLC1, PPP2CA, PPP2R2B, KIF21A, APEX1, SLC30A9, TUBB4B, ACTB, DNMT3, GABARAPL1, CAP2, MOBP, SRA1, MYL12B, FBNP1, RAB22A, MAP7, PPP2R3C, CALM2, ACTR10</i>

*modified Fisher exact p-value. Abbreviations: Gene ontology (GO); Substance Use Disorder (SUD)

Supplementary Table 4. GO functional terms associated with the differentially expressed genes between suicides with SUD compared to non-suicides with SUD (all-genes analysis)..

GO ID	GO Name	Count	%	EASE*	Genes
GO:0006955	Immune response	47	8.56	0.047	<i>CUEDC2, MEF2C, HMGB1, TNFSF15, TRIM13, CRCP, MAPKAPK2, MIF, PSMB5, SERINC3, PSMB4, TNFRSF1A, PSMB7, PSMB6, HAMP, PSMB2, PRKRA, PPP3CB, PSMD4, PPP3CA, PSMD7, RPS27A, SEC61A1, ERCC1, TUBB4B, ACTB, EXOSC9, NDFIP1, SKP1, BIRC3, PTPN11, ELMO1, ARPC1A, LEP, TNFRSF9, GPI, PSMD14, ADM, ILF2, PSMA5, PSMC2, VAMP7, CTSC, WASL, EIF2AK4, PPP2R3C, CALM2</i>
hsa00190	Oxidative phosphorylation	43	7.83	1.16E-21	<i>UQCRC2, NDUFB3, UQCRC1, NDUFB7, ATP5B, NDUFB9, CYC1, COX7B, NDUFAB1, ATP6V1G2, COX7A2L, ATP6V1B2, UQCRFS1, COX5A, UQCRQ, NDUFB2, NDUF55, NDUF54, COX6B1, ATP5L, ATP5O, ATP5I, ATP5H, ATP5J, NDUFA4, NDUFA2, COX7A2, NDUFA9, COX8A, COX4I1, NDUFC1, ATP6V1D, NDUFA12, COX6C, UQCRHL, NDUFA11, ATP6V1A, SDHB, UQCRH, ATP6V1E1, NDUFV1, NDUFV2, ATP5A1</i>
hsa05012	Parkinson's disease	40	7.28	6.91E-18	<i>NDUFB3, UQCRC2, UQCRC1, NDUFB7, ATP5B, NDUFB9, UBE2G2, CYC1, COX7B, UCHL1, NDUFAB1, PINK1, COX7A2L, UQCRFS1, COX5A, UQCRQ, NDUFB2, NDUF55, NDUF54, COX6B1, ATP5O, ATP5H, ATP5J, NDUFA4, NDUFA2, COX7A2, SLC25A4, NDUFA9, COX8A, COX4I1, NDUFC1, NDUFA12, COX6C, UQCRHL, NDUFA11, SDHB, UQCRH, NDUFV1, NDUFV2, ATP5A1</i>
GO:0044772	Mitotic cell cycle phase transition	32	5.82	0.0149	<i>PPP2R5C, CNOT7, PSMB5, PSMB4, PSMB7, PSMB6, PLRG1, PSMB2, VPS4B, PSMD4, PPP3CA, TUBA1A, DYNC1H1, PSMD7, APEX1, RPS27A, TUBB4B, KHDRBS1, SKP1, DCTN3, RNASEH2B, NAE1, DCTN2, CDKN1A, YWHAG, PSMD14, PSMA5, PSMC2, CARM1, CALM2, SPAST, DYNC1I2</i>

*modified Fisher exact p-value. Abbreviations: Gene ontology (GO); Substance Use Disorder (SUD)

Supplementary Table 5. GO functional terms associated with the differentially expressed genes between suicides without SUD compared to non-suicides without SUD (separating up and down-regulated genes).

GO ID	GO Name	Count	%	EASE*	Genes
Down-regulated genes					
GO:0007154	Cell communication	211	42.7	3.83 E-7	<i>ATP1B2, PLEKHM1, FGFR1L, EDN1, LEMD2, ITSN1, S1PR1, TMEM145, GRIN2C, HTRA1, WWOX, S100A1, KIF13B, MVB12B, PDPN, RXRA, SCN2A, PTBP1, SYNJ2BP, PPARGC1A, PIAS4, BAZ1B, F3, PDGFRB, RAB13, EIF2AK4, CRTCC3, RHPN2, ERBB2, NFKBIA, MYO9B, CDC42EP4, LFNG, SASH1, SMAD5, CELSR3, NOTCH1, CNIH2, CSRNP1, SYTL4, TGFR3, HGS, BMP7, SPNS1, KAT6A, PPARD, HIP1R, FERMT2, NFKB1, LSM14A, OR9A4, FGF2, ARHGEF6, PI4KB, GPR37L1, ARHGEF10, SS18, TNFRSF10B, ADM, PLEKHH3, CNOT11, SEMA4B, RBM38, CHSY1, RASD2, NEO1, ZFP36L1, MTMR3, GLIPR2, SORBS3, EZR, DGKD, BCL11A, AGO2, BCL6, NUCKS1, FADS1, PDK4, AXL, GJB6, FZD4, APPL2, FZD7, MT1X, PLEKHF1, RASSF4, RAB31, C21ORF2, MT2A, RASSF2, ARAF, RBM14, RBM15, NCLN, LRP4, TOB1, GNA13, SLC44A2, STK38, STK36, GNA12, CSPG4, TGFB3, TNFSF14, RPS6KB2, ITPKB, SLC8B1, FRS2, PLXNB1, MTA2, PLXNB2, MLXIPL, ARID1B, NTSR2, STK3, DDIT4, HIF1A, TRIM39, ASB6, ZC3H3, SNX6, IFITM2, GLUD1, IFITM3, MAPKAPK3, PAQR7, ITGB5, PAQR8, MAPKAPK2, ABCA1, CCL5, SOX8, TIMP1, CXXC1, TROVE2, THAP12, NDRG1, PLXND1, SEC61A1, AXIN1, SETDB1, PHACTR4, CACNA1I, VAV2, ADGRG1, SELENON, SAFB2, TRAF3IP2, CDKN1A, MYO10, HDAC1, SMARCC1, SPTBN2, AHYCL1, CPNE3, ANTXR1, TRIP6, PIP4K2A, ABL1, MERTK, TLN1, PREX1, CLDN5, ARHGAP17, RHOU, AKT1, ARHGAP21,</i>

GO:0010468	Regulation of gene expression	158	32.0	3.88E-7	<p>MAX, SLC1A2, CASP3, SLC1A3, WWC3, SHC1, KLHL24, CDK10, RHOC, YAP1, ZYX, CASP2, CSF2RA, PIGU, SLC9A3R1, DDR1, NCOA3, UBE2M, PDE9A, PPP1R15A, GPRC5C, TIPARP, PPM1B, GPRC5B, ARHGAP39, RGMA, TNFRSF1A, CHD8, CHD7, SMOC1, MAP3K1, PTN, YES1, CHD4, TXNIP, COL4A1, TMBIM1, DRG2, SIRT1, SH3BP4, PPP1R13B, TBL1X, TIAF1, ARAP1</p> <p>JDP2, ZNF821, STK36, EDN1, LEMD2, TGFB3, ZNF827, RPS6KB2, SFSWAP, S1PR1, TRAK2, HTRA1, SMARCD1, CTDSP1, FIZ1, S100A1, WWOX, RXRA, MTA2, PTBP1, MLXIPL, FOXN2, ZHX3, HMG20B, ARID1B, PPARGC1A, STK3, ZNF787, HIF1A, ASCC2, BAZ1B, PIAS4, ZNF786, XRN1, EIF2AK4, CRTCS, ZC3H3, SNX6, IFITM3, ERBB2, SETD1A, NFKBIA, IGF2BP2, MAPKAPK2, ANGEL2, CCL5, SOX8, CXXC1, ZNF322, TCF20, NIPBL, AUTS2, THAP12, VEZF1, AXIN1, SETDB1, ZBTB47, SMAD5, ARID3B, ACACB, VAV2, SFMBT2, UIMC1, SAFB2, MSL3, NOTCH1, CDKN1A, HDAC1, CSRNP1, SMARCC1, HGS, TGFB3, AHCYL1, H3F3B, TRIP6, BMP7, ABL1, KAT6A, POU6F1, PPARG, VARS2, NFKB1, QARS, YBX1, AKT1, LSM14A, MAX, WWC3, ZNF490, MSN, YAP1, KDM5B, FGF2, ZNF493, NFX1, NFKBIZ, ZBTB20, SOX13, INPPL1, SNAPC4, MXD4, SS18, NCOA3, ZNF692, ZNF716, KHSRP, CNOT11, RBM38, LOC155060, PPP1R15A, ROM1, FRYL, TIPARP, NEO1, ZNF653, ZFP36L1, RGMA, CHD9, TNFRSF1A, CHD8, SORBS3, EZR, ZNF512B, RAX2, CHD7, TSC22D4, BCL11A, POU2F1, AGO2, BCL6, POM121C, UNK, ETV6, BAZ2B, YES1, CHD4, TXNIP, BRD2, NUCKS1, CEBPD, FADS1, AFF3, ILF3, MRGBP, FZD4, ZNF358, SIRT1, FZD7, ZNF22, ZNF672, SP1, HNRNPUL1, PHF21A, RBM14, TBL1X, RBM15, LRP4, TOB1</p>
GO:0012501	Programmed cell death	72	14.60	2.82756 0312409 48E-4	<p>CDK19, PPARG, HIP1R, EDN1, TGFB3, TNFSF14, ITPKB, RNF216, NFKB1, ITSN1, AKT1, MAX, CASP3, FAM129B, YAP1, CASP2, FGF2, FRS2, WWOX, ARHGEF6, SLC9A3R1, PPARGC1A, STK3, DDIT4, TNFRSF10B, HIF1A, PIAS4, ADM, F3, UBE2M, PDGFRB, GPAM, MYO18A, PPP1R15A, TRIM39, GSDMB, NFKBIA, CCL5, SOX8, TIMP1, ZFP36L1, TNFRSF1A, CHD8, MAP3K1, PTN, BCL6, NDRG1, ETV6, AXIN1, TXNIP, PDK4, AXL, TMBIM1, GJB6, VAV2, SIRT1, BRAT1, TRAF3IP2, PLEKHF1, NOTCH1, CDKN1A, HDAC1, PYGL, MTFP1, CSRNP1, ARAF, RASSF2, PPP1R13B, BMP7, ABL1, MERTK, TIAF1</p> <p>PREX1, CSPG4, LEMD2, AKT1, CASP3, S1PR1, SLC1A3, LGI4, CTDSP1, YAP1, FRS2, FGF2, KIF13B, PLXNB1, PLXNB2, ZSWIM6, HMG20B, ARID1B, SLC9A3R1, ARHGEF10, GPR37L1, DDIT4, AMIGO1, DDR1, HIF1A, ADM, SEMA4B, RAB13, EIF2AK4, ROM1, FRYL, ERBB2, NEO1, GPRC5B, SOX8, RGMA, CHD7, EZR, BCL11A, PTN, BCL6, NDRG1, UNK, EHD1, PLXND1, ETV6, AXIN1, AXL, CELSR3, SF3A2, ADGRG1, FZD4, MT1X, FZD7, NOTCH1, HDAC1, IST1, SPTBN2, BMP7, ABL1, LRP4</p>
GO:0043069	Negative regulation of programmed cell death	35	7.09	0.00437 8977705 04416	<p>PPARG, EDN1, TGFB3, NFKBIA, TNFSF14, NFKB1, ITPKB, ITSN1, CCL5, SOX8, TIMP1, AKT1, CASP3, CHD8, BCL6, FAM129B, YAP1, PDK4, AXL, TMBIM1, SIRT1, PPARGC1A, NOTCH1, CDKN1A, TNFRSF10B, HIF1A, HDAC1, ARAF, PDGFRB, MERTK, ABL1, BMP7, MYO18A, TIAF1, GPAM</p>
GO:0043068	Positive regulation of programmed cell death	33	6.69	3.36E-5	<p>CDK19, HIP1R, TGFB3, ITSN1, CCL5, AKT1, CASP3, PTN, BCL6, CASP2, WWOX, TXNIP, ARHGEF6, VAV2, SLC9A3R1, SIRT1, PPARGC1A, STK3, PLEKHF1, NOTCH1, CDKN1A, TNFRSF10B, HDAC1, ADM, PIAS4, F3, RASSF2, UBE2M, PDGFRB, PPP1R13B, ABL1, BMP7, TRIM39</p>

GO:1901214	Regulation of neuron death	15	3.04	0.006	AXL, TGFB3, CCL5, ITSN1, SIRT1, PPARGC1A, DDIT4, AKT1, CASP3, HIF1A, HDAC1, UBE2M, PPP1R13B, ABL1, CASP2
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Up-regulated genes

GO:0005739	Mitochondrion	213	23.07	4.75-41	RAD51C, LDHB, SNCB, SNCA, IARS2, C14ORF2, GOT2, GOT1, PGAM5, MRPL36, PDHA1, MRPL32, MRPL33, HIGD1A, OXR1, APOO, MRPL51, RPUSD3, RAP1GDS1, NNT, DHX29, NME1, RARS, DLD, ATP5C1, ADSL, MDH2, MDH1, ATP5SL, MTX3, CHCHD2, PIN4, ACAT1, PIN1, KRAS, COX6B1, MRPL55, LINC00493, PPP2R2B, NAXE, MAP2K1, GARS, JTB, NDFIP2, MPC2, DLAT, VDAC3, UQCRHL, VDAC1, CKMT1A, NIPSNAP1, NIF3L1, ATP5B, BNIP3, SLIRP, ARL2BP, PKM, GPX1, MCCC1, SLC25A3, ATP5L, ATP5O, ATP5H, TOMM34, ATP5J, MRPL1, NDUFB11, MRPL3, SLC25A4, SLC25A5, FUNDC1, NDUFA10, NDUFA12, NDUFA11, ADO, TXN, TOMM20, PMPCB, YWHAZ, ABHD6, COX7A2L, AZIN2, DNAJC30, MRPL11, MRPL13, PPP2CA, REXO2, MRPL18, RAB11A, PPP3CA, ACSL4, PDHX, ETFA, DNM3, COX7A2, IMMT, RMDN3, SOD1, MRPL30, TTC19, MRPL24, SDHA, SDHB, YWHAG, YWHAH, MRPL21, GOLPH3, ATP6V1E1, BNIP3L, SDHD, YWHAQ, ATP5A1, TUSC2, SLC8A3, GRPEL1, CMC2, C19ORF70, NDUFAB1, TOMM70, COX5A, PDHB, FAHD1, GHITM, CISD1, STARD7, TIMM9, HADH, ARGLU1, NUDT2, TMEM126B, COX6C, EARS2, ISCU, MRPS18C, PCCB, PCCA, LRPPRC, CCDC90B, MRPS11, COX7B, COX7C, MUT, TOMM6, MTCH1, DNAJA1, AP2M1, MRPS27, GABARAPL1, ATP5J2, FIBP, MRPS22, MMADHC, COX8A, IDH3B, GLOD4, REEP1, NDUFV1, TOMM40L, COQ10B, HSP90AB1, UQCRC2, NDUFAF5, COA3, COA1, CYC1, PRDX5, PRDX3, UQCRFS1, UQCRQ, NDUFS4, ACAD8, SUCLA2, SSBP1, CYCS, PROSC, MRPS6, MRPS7, NDUFC1, TIMM23, TIMM21, ISCA1, CCDC51, ATP6V1A, COQ3, PANK2, PPM1E, C1QBP, UQCRH, UBB, PRNP, OAT, UQCRB, NDUFB3, GLRX5, NDUFB5, SAMM50, PPP3R1, NDUFB2, ANXA6, MOAP1, VPS35, PTS, APEX1, NDUFA4, NDUFA2, NDUFA7, ARMC10, ATP5F1, GRSF1, DPYSL2, NDUFA1, PARK7, FEZ1
GO:0012501	Programmed cell death	123	13.32	4.66E-4	LDHA, PNMA2, SNCB, SNCA, CBX4, UBQLN1, CRADD, MAGED1, CUL2, APP, CUL5, GHITM, PGAM5, KIFAP3, RALB, HIGD1A, OXR1, NUDT2, IRS2, STK24, RSL1D1, NME5, NME1, MLLT11, ARL6IP1, CDK5R1, GGCT, BMPR2, BEX2, RRAGA, UBE2V2, PIN1, SERINC3, UBE2D3, KRAS, HNRNPK, CSE1L, MTCH1, DNAJA1, GLO1, PPP2R2B, ARL6IP5, LAMTOR5, LGALS1, MAP2K4, JTB, TAX1BP1, VDAC1, EI24, AKTIP, IKBKG, CYFIP2, ZNF385B, PDCD5, PDCD6, PDCD7, DNAJB6, HSP90AB1, HINT1, ZMAT3, PRDX5, BNIP3, PRDX2, PRDX3, PKM, HSPH1, GPX1, MAGEH1, DHCR24, EBAG9, SRPK2, HSP90AA1, SLC25A4, SLC25A5, ARHGEF7, CYCS, PRKCG, CDK5, ELMO1, PRKCB, FAM134B, EPB41L3, FMN2, C1QBP, UBE2K, CCND2, EMC4, KRIT1, CFL1, SH3KBP1, UBB, PRNP, KPNA1, CAMK1D, YWHAZ, CCK, PPP3R1, FHL2, ASNS, MIF, ANXA6, MOAP1, PPP2CA, DAD1, BCAP29, VPS35, SCG2, TCP1, PDCD10, RMDN3, FAM188A, SOD1, ITPR1, PARK7, NAE1, GPI, YWHAG, YWHAH, PSMD10, GOLPH3, BNIP3L, YWHAQ, BRE
GO:0043005	Neuron projection	87	9.42	1.81E-8	SLC8A3, SYT4, ATL1, SNCA, UCHL1, BNIP3, GABBR2, SYP, NRCAM, APP, GOT1, ANK2, ATXN10, AP3B2, SNAP47, LSM4, RANBP1, SV2B, GNG3, PTBP2, ATP6V0D1, NSF, GABRG2, STX1A, TWF2, HSP90AA1, ARHGEF7, STMN2, MPDZ, PTPRN2, PRKCG, BASP1, PTPRO, CDK5, DCTN2, THY1, EPB41L3, ARHGA32, MAGEE1, VAMP7, SH3KBP1, RAB5A, NPTN, NRSN1, UBB, VAMP2, KPNA1, PAM, CDK5R1, GLRX5, CCK, BMPR2,

					FKBP1A, AZIN2, UHMK1, PIN1, PFN2, GPM6A, AP3M2, KLC1, TOR1A, RAB11A, PAFAH1B1, SNAP25, NEFM, AP2M1, DNMT3, GABRA2, GABARAPL1, MAP1B, MAP2K4, SLC12A5, GARS, DPYSL2, SOD1, KCNK1, PARK7, GPI, MAP2, TMOD2, CYFIP2, CALM3, RIT2, CALM2, FEZ2, CALM1, FEZ1
GO:0006811	Ion transport	104	11.26	1.13E-4	SLC8A3, SLC22A17, ATP1B1, SCN3B, SNCA, FGF12, COX5A, UBQLN1, GOT2, CUL5, ANK2, VPS4B, CAB39, IRS2, SARAF, CHP1, THY1, COX6C, NNT, ATP5C1, VAMP2, ARL6IP1, COX7B, COX7C, ATP6V1B2, FXSD6, SERINC3, ATP6V0C, SERINC1, COX6B1, ARL6IP5, SLC30A9, GABRD, ATP5J2, GABRA2, COX8A, NDFIP1, NIPA2, NDFIP2, MPC2, KCNK1, CACNA2D3, VDAC3, VDAC1, UQCRHL, CRBN, TOMM40L, SLC20A1, ATP5B, CYC1, UQCRFS1, UQCRQ, SLC25A3, ATP5L, ATP5O, DENND5B, ATP6V0D1, DPP6, ATP5H, NSF, ATP5J, GABRG2, STX1A, ATP6V1D, CDK5, PRKCB, ATP6V1A, UQCRH, COMMD3, UBB, PRNP, TMCO1, UQCRB, CCK, MMTG1, MFSD3, FHL1, ATP6V1G2, FKBP1A, COX7A2L, MIF, ANXA6, GPM6A, PPP3CA, GSTO1, ACSL4, SNAP25, EHD3, NDUFA4, COX7A2, SLC12A5, ATP5F1, ATP1A1, DPYSL2, ITPR1, PARK7, YWHAH, GRIA2, ATP6V1E1, YWHAQ, CALM3, ATP5A1, CALM2, CALM1

*modified Fisher exact p-value. Abbreviations: Gene ontology (GO); Substance Use Disorder (SUD)

Supplementary Table 6. GO functional terms associated with the differentially expressed genes between suicides without SUD compared to non-suicides without SUD (all-genes analysis).

GO ID	GO Name	Count	%	EASE*	Genes
GO:0005739	Mitochondrion	271	19.13	5.39E-38	LDHB, RAD51C, SNCB, SNCA, IARS2, C14ORF2, GOT2, GOT1, TRAK2, VPS13C, PGAM5, MRPL36, PDHA1, MRPL32, GPT2, MRPL33, HIGD1A, WWOX, OXR1, APOO, MRPL51, RPUSD3, SUCLG2, RAP1GDS1, SYNJ2BP, PPARGC1A, DCAF5, NNT, DHX29, NME1, RARS, DLD, ATP5C1, ADSL, MDH2, MDH1, ATP5SL, MTX3, CHCHD2, PIN4, ACAT1, SFXN5, HADHA, PIN1, KRAS, COX6B1, MRPL55, ALDH4A1, LINC00493, NAXE, PPP2R2B, BRI3BP, MAP2K1, MAOA, GARS, JTB, NDFIP2, MPC2, DLAT, ACACB, VDAC3, UQCRHL, VDAC1, NOP14, CKMT1A, NIPSNAP1, SPNS1, NIF3L1, HIP1R, ATP5B, BNIP3, NFKB1, QARS, SLIRP, ARL2BP, PKM, GPX1, MCCC1, SLC25A3, ATP5L, ATP5O, COX19, ATP5H, ATP5J, TOMM34, MRPL1, NDUFB11, MRPL3, SLC25A4, SLC25A5, FUNDC1, PI4KB, NDUFA10, NDUFA12, NDUFA11, RAD51, ADO, TXN, TOMM20, PMPCA, MECR, PMPCB, YWHAZ, ABHD6, COX7A2L, AZIN2, DNAJC30, MRPL11, MRPL13, PPP2CA, REXO2, MRPL18, RAB11A, PPP3CA, ACSL4, PDHX, ETFA, DNMT3, COX7A2, IMMT, FADS1, PDK4, RMDN3, ILF3, SOD1, MRPL30, TTC19, MRPL24, SDHA, SDHB, YWHAG, YWHAH, MRPL21, C21ORF2, MTFP1, GOLPH3, ATP6V1E1, BNIP3L, SDHD, ARAF, YWHAQ, ATP5A1, SLC8A3, TUSC2, GRPEL1, CMC2, ALDH1L1, C19ORF70, NDUFAB1, TOMM70, COX5A, PDHB, FAHD1, MUTYH, GHITM, CISD1, STARD7, TIMM9, SLC25A28, HADH, SLC8B1, ARGLU1, NUDT2, RAI14, TMEM126B, DDIT4, EARS2, COX6C, ISCU, MRPS18C, SLC25A37, SLC25A39, PCCB, LRPPRC, PCCA, TRIM39, CCDC90B, GLUD1, MRPS11, COX7B, COX7C, MUT, TOMM6, MTCH1, DNAJA1, AP2M1, MRPS27, GABARAPL1, ATP5J2, FIBP, MRPS22, MMADHC, COX8A, IDH3B, GLOD4, REEP1, ABCB7, NDUFV1, TOMM40L, COQ10B, ABL1, SLC25A18, HSP90AB1, UQCRC2, NDUFAF5, VARS2, COA3, COA1, CYC1, PRDX5, PRDX3, UQCRFS1, UQCRQ, AKT1, NDUFS4, SHC1, ACAD8, SUCLA2, CASP2, SSBP1, CYCS, MRPS6, PROSC, NDUFC1, MRPS7, TIMM23, PALLD, TIMM21, ISCA1, CCDC51, ATP6V1A, COQ3, ALDH7A1, PANK2, PPM1E, C1QBP, UQCRH, UBB, PRNP, GPAM,

					<p>OAT, PPP1R15A, UQCRB, NDUFB3, GLRX5, NDUFB5, SAMM50, C10ORF10, PPP3R1, NDUFB2, ANXA6, TNFRSF1A, MOAP1, TAP1, VPS35, PTS, APEX1, TXNIP, NDUFA4, NDUFA2, ARMC10, NDUFA7, GRSF1, ATP5F1, DPYSL2, DRG2, SIRT1, NDUFA1, PARK7, PPP1R13B, FEZ1</p>
GO:0010646	Regulation of cell communication	299	21.11	6.53E-8	<p>SNCA, EDN1, LEMD2, ITSN1, SYP, MAGED1, APP, DIRAS2, HTRA1, GNG3, WWOX, MVB12B, OPTN, SYNJ2BP, PTPRO, PPARGC1A, DEPDC5, THY1, NME5, ARFGEF3, BAZ1B, PIAS4, F3, MLLT11, NPTN, PDGFRB, EIF2AK4, SH3GL2, FBXL2, CRTC3, CDK5R1, ERBB2, AKAP12, NFKBIA, MYO9B, AKAP11, OCRL, ARFGEF1, PIN1, ATP6V0C, SERINC3, PFN2, KRAS, LFNG, LAMTOR5, SASH1, UFSP2, MAP2K1, LAMTOR2, LGALS1, MAP2K4, NDFIP1, NDFIP2, MPC2, SMYD2, TAX1BP1, NOTCH1, CNIH2, RGS4, TMOD2, SYTL4, HGS, RHEB, TGFB3, RIT2, BMP7, KAT6A, ENY2, SPIN1, PPARD, SLC20A1, COPS5, TSG101, HIP1R, AP2S1, SHOC2, BNIP3, NFKB1, TERF2IP, COPS8, ARL2BP, LSM14A, GPX1, HSPH1, SNAP47, FGF2, RAP2A, STX1A, SLC25A4, SLC25A5, ARHGEF7, ARHGEF6, MYADM, ARHGEF10, GPR37L1, LRPAP1, SENP2, TNFRSF10B, ADM, GRM8, TXN, RAB5A, SH3KBP1, CHSY1, RASD2, YWHAZ, ABHD6, NNAT, TFG, FKBP1A, NEO1, MIF, GLIPR2, SORBS3, EZR, PPP2CA, PPP3CB, RAB11A, BCL6, PPP3CA, GALNT11, FBXW11, SNAP25, MTMR4, GDI2, NUCKS1, NLK, AXL, SOD1, FZD4, ITPR1, FZD7, PLEKHF1, DKK3, PSMD14, YWHAG, YWHAH, PPP1R2, GOLPH3, PSMD10, ARAF, RASSF2, YWHAQ, CHN1, CALM3, AACS, NCLN, CALM2, LRP4, TOB1, CALM1, SLC8A3, SLC44A2, STK38, ATP6AP2, STK36, TSPAN5, GNA12, CSPG4, TGFB3, TNFSF14, ITPKB, UBQLN2, UBQLN1, CRADD, ANK2, HADH, SLC8B1, FRS2, IRS2, PLXNB1, MTA2, CHP1, STK3, DDIT4, RALGAP1, HIF1A, PSMA6, PSMA5, PSMA4, VAMP7, VSNL1, SDCBP, VAMP2, TRIM39, ZC3H3, SNX6, STRAP, GLUD1, MAPKAPK3, BMPR2, RRAGA, NAPB, SNX3, MAPKAPK2, ABCA1, CCL5, RRAGB, TIMP1, RBX1, PSMB5, PSMB7, PSMB6, HNRNP, MTCH1, PSMB2, DNAJA1, ARL6IP5, AXIN1, AP2M1, PHACTR4, VAV2, ADGRG1, SELENON, SAFB2, TRAF3IP2, PSMC6, HDAC1, PSMC2, IKBKG, TRIP6, PIP4K2A, PDCD5, ABL1, PDCD6, HSP90AB1, METAP1, CLTA, HINT1, PREX1, UCHL1, SORL1, TMEM237, ARHGAP17, SKAP2, RHOU, AKT1, SLC1A3, PRMT5, WWC3, PSMD1, PSMD2, RHOC, CDK10, KLHL24, SHC1, YAP1, PSMD6, CASP2, PSMD7, KHDRBS1, GPRASP1, PIGU, G3BP2, ADIPOR1, PFKM, LMBRD1, SLC9A3R1, CDK5, PRKCB, ARHGAP32, NCOA3, C1QBP, UBE2K, ITGB1BP1, KLHL12, UBB, PRNP, PPP1R15A, PPP3R1, PPM1B, GPRC5B, ARHGAP39, RPA3, TNFRSF1A, RPA2, RGMA, CHD8, MOAP1, CHD7, MAP3K1, TOR1A, PTN, VPS35, SCG5, PAFAH1B1, GSTO1, CHD4, SCG2, PDCD10, TM6SF1, SIRT1, PARK7, SH3BGR1, SH3BP4, AKR1B1, PPP1R13B, CRK, ARAP1</p>
GO:0012501	Programmed cell death	195	13.77	4.62E-7	<p>LDHA, PNMA2, SNCB, SNCA, EDN1, RNF216, ITSN1, MAGED1, CUL2, CUL5, APP, PGAM5, KIFAP3, HIGD1A, WWOX, OXR1, PPARGC1A, NME5, PIAS4, NME1, F3, MLLT11, PDGFRB, MYO18A, CDK5R1, GGCT, GSDMB, NFKBIA, PIN1, SERINC3, KRAS, PPP2R2B, LAMTOR5, LGALS1, MAP2K4, JTB, TAX1BP1, VDAC1, NOTCH1, EI24, CSRP1, ZNF385B, BMP7, PPARD, HIP1R, ZMAT3, BNIP3, NFKB1, PKM, HSPH1, GPX1, FAM129B, MAGEH1, FGF2, DHCR24, SRPK2, SLC25A4, ARHGEF7, SLC25A5, ARHGEF6, ELMO1, EPB41L3, FMN2, TNFRSF10B, ADM, CCND2, SH3KBP1, YWHAZ, FHL2, MIF, ZFP36L1, PPP2CA, BCL6, ETV6, PDK4, RMDN3, AXL, GJB6, SOD1, BRAT1, ITPR1, NAE1, PLEKHF1, YWHAG, YWHAH, PYGL, GOLPH3, MTFF1, PSMD10, BNIP3L, RASSF2, ARAF,</p>

					<p>YWHAQ, TGFB3, CBX4, TNFSF14, ITPKB, UBQLN1, CRADD, GHITM, RALB, FRS2, NUDT2, IRS2, STK24, STK3, DDIT4, RSL1D1, HIF1A, TRIM39, ARL6IP1, BMPR2, BEX2, Rraga, UBE2V2, CCL5, SOX8, TIMP1, UBE2D3, HNRNPK, CSE1L, MTCH1, DNAJA1, GLO1, NDRG1, ARL6IP5, AXIN1, VAV2, TRAF3IP2, CDKN1A, HDAC1, AKTIP, IKBKG, CYFIP2, MERTK, ABL1, PDCD5, PDCD6, PDCD7, DNAJB6, HSP90AB1, CDK19, HINT1, PRDX5, PRDX2, PRDX3, AKT1, MAX, CASP3, YAP1, CASP2, EBAG9, HSP90AA1, CYCS, PRKCG, SLC9A3R1, CDK5, PRKCB, FAM134B, C1QBP, UBE2K, EMC4, KRIT1, CFL1, UBE2M, UBB, PRNP, GPAM, PPP1R15A, KPNA1, CAMK1D, CCK, PPP3R1, ASNS, ANXA6, TNFRSF1A, CHD8, MOAP1, MAP3K1, BCAP29, DAD1, PTN, VPS35, SCG2, TXNIP, TCP1, PDCD10, FAM188A, TMBIM1, SIRT1, PARK7, GPI, BRE, PPP1R13B, TIAF1</p>
GO:0030182	Neuron differentiation	123	8.68	6.21E-4	<p>ADCY1, SYT4, PLPPR4, NRCAM, APP, S1PR1, ATXN10, LGI4, CTDSP1, ADGRB3, KIF13B, TWF2, EFNB3, PLXNB1, STK24, STMN2, PLXNB2, HMG20B, ARID1B, PTPRO, DDIT4, THY1, SLITRK1, TMEM106B, HIF1A, NME1, VAMP7, NPTN, RAB13, EIF2AK4, CDK5R1, ERBB2, MMD, BMPR2, UBE2V2, SNX3, SOX8, ARFGEF1, UHMK1, PIN1, KRAS, NGRN, MTCH1, PLXND1, AXIN1, B4GAT1, MAP2K1, LGALS1, CELSR3, NOTCH1, MAP2, SPTBN2, RIT2, ABL1, BMP7, OPCML, NIF3L1, ATL1, PREX1, UCHL1, RTN1, UQCRQ, AKT1, CASP3, SLC1A3, RANBP1, TOP2B, RAP2A, ZSWIM6, SLC9A3R1, HERC1, CDK5, GPR37L1, AMIGO1, DDR1, EPB41L3, PAPD4, ADM, CFL1, SEMA4B, UBB, CAMK1D, ROM1, CCK, NDN, FRYL, NNAT, NEO1, GPRC5B, HDGFRP3, RGMA, EZR, GPM6A, BCL11A, TOR1A, PPP3CB, RAB11A, PTN, BCL6, PAFAH1B1, PPP3CA, UNK, ACSL4, EHD1, SNAP25, NEFM, DNM3, MAP1B, SLC12A5, DPYSL2, SOD1, SF3A2, FIG4, FZD4, FZD7, RNF112, YWHAH, IST1, CHN1, CYB5D2, LRP4, FEZ2, FEZ1</p>
GO:0043005	Neuron projection	112	7.90	6.71E-7	<p>SLC8A3, SYT4, SNCA, ITSN1, SYP, NRCAM, APP, GOT1, ANK2, ATXN10, LSM4, PTBP2, GNG3, S100A1, KIF13B, TWF2, MPDZ, STMN2, PTPRN2, SCN2A, BASP1, PTPRO, PPARGC1A, DCTN2, THY1, MAGEE1, HIF1A, VAMP7, NPTN, NRSN1, VAMP2, RAB13, PAM, CDK5R1, BMPR2, UHMK1, PIN1, PFN2, AP2M1, GABARAPL1, GABRA2, MAP2K4, GARS, KCNK1, MYO10, CNIH2, HDAC1, MAP2, TMOD2, CYFIP2, RIT2, ABL1, HIP1R, ATL1, PREX1, CLDN5, UCHL1, BNIP3, GABBR2, MAX, SLC1A2, SLC1A3, AP3B2, SNAP47, KLHL24, RANBP1, SV2B, ATP6V0D1, NSF, GABRG2, STX1A, HSP90AA1, ARHGEF7, PRKCG, PALLD, CDK5, AMIGO1, EPB41L3, ARHGAP32, SH3KBP1, RAB5A, UBB, KPNA1, GLRX5, CCK, CNN3, FKBP1A, AZIN2, RGMA, CCDC120, AP3M2, GPM6A, KLC1, TOR1A, RAB11A, AGO2, PAFAH1B1, SNAP25, NEFM, DNM3, MAP1B, SLC12A5, DPYSL2, SOD1, PARK7, GPI, CALM3, CALM2, LRP4, FEZ2, CALM1, FEZ1</p>

*modified Fisher exact p-value. Abbreviations: Gene ontology (GO); Substance Use Disorder (SUD)

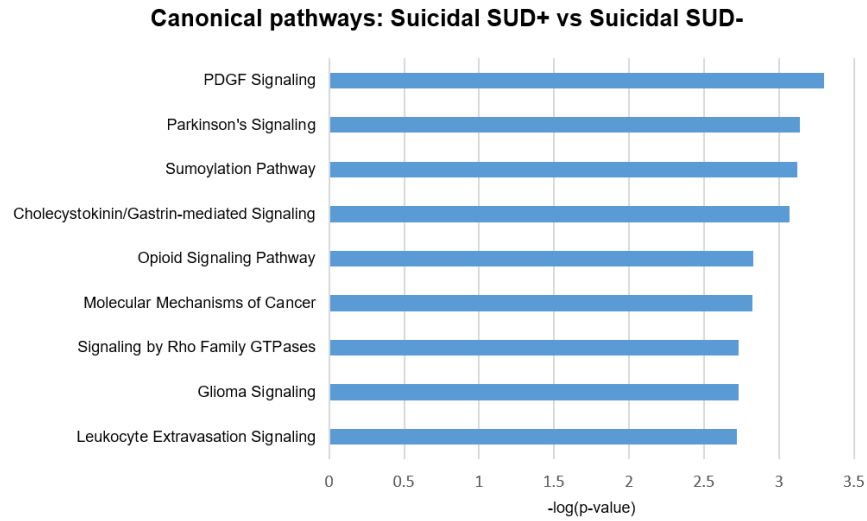


Figure S1. Top 10 enriched canonical pathways from IPA. Canonical pathways related to differentially expressed genes detected when comparing suicides with SUD (Suicidal SUD+) to suicides without SUD (Suicidal SUD-).

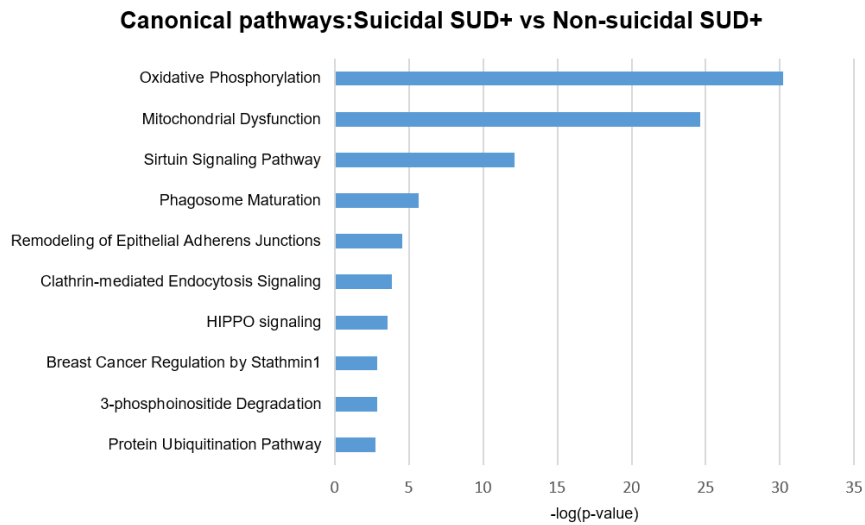


Figure S2. Top 10 enriched canonical pathways from IPA. Canonical pathways related to differentially expressed genes detected when comparing suicides with SUD (Suicidal SUD+) to non-suicides with SUD (Non-suicidal SUD+).

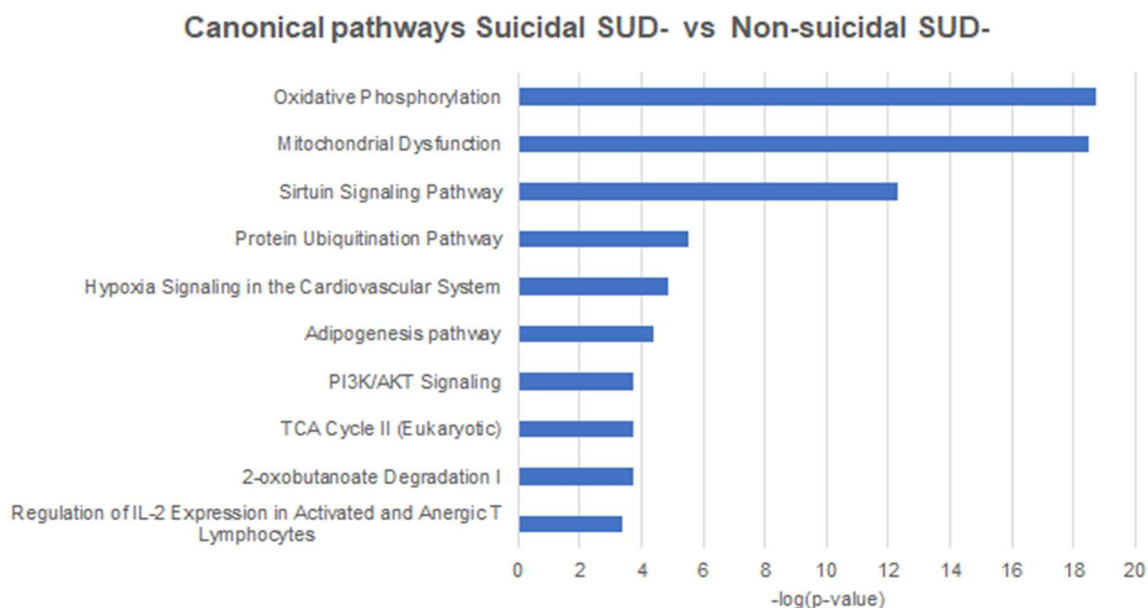


Figure S3. Top 10 enriched canonical pathways from IPA. Canonical pathways related to differentially expressed genes detected when comparing suicides without SUD (Suicidal SUD-) to non-suicides without SUD (Non-suicidal SUD-).

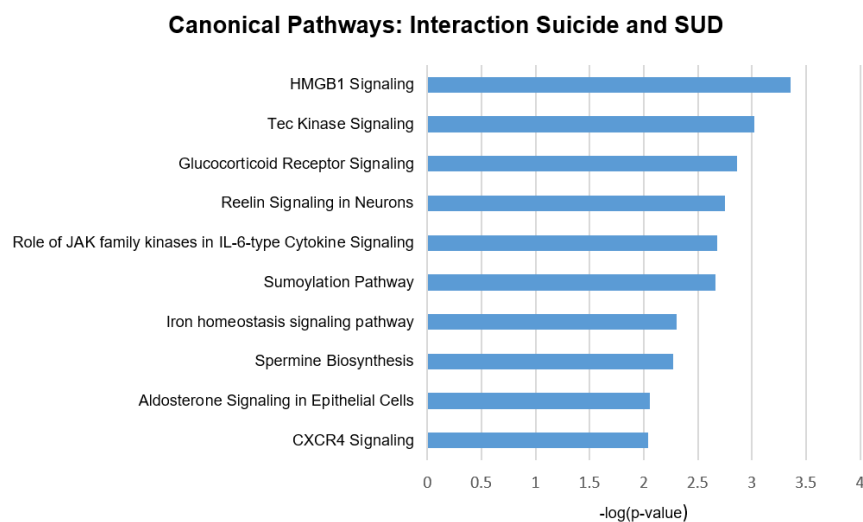


Figure S4. Top 10 enriched canonical pathways from IPA. Canonical pathways related to genes whose expression is influenced by the interaction between Suicide and Substance Use Disorder (SUD).