Supplementary material:

Table 1: Lists of OxPhos genes and DNA-Met genes

OxPhos genes	ATP5A1, ATP5B, ATP5C1, ATP5D, ATP5E, ATP5F1, ATP5G1, ATP5G2, ATP5G3, ATP5H, ATP5I, ATP5J, ATP5J2, ATP5L, ATP5O, ATP5S, COX4I1, COX5A, COX5B, COX6B1, COX6C, COX7A2, COX7B, COX7C, COX8A, CYC1, CYCS, NDUFA1, NDUFA10, NDUFA11, NDUFA12, NDUFA13, NDUFA2, NDUFA3, NDUFA4, NDUFA5, NDUFA6, NDUFA7, NDUFA8, NDUFA9, NDUFAB1, NDUFB10, NDUFB11, NDUFB2, NDUFB3, NDUFB4, NDUFB5, NDUFB6, NDUFB7, NDUFB8, NDUFB9, NDUFC1, NDUFC2, NDUFS1, NDUFS2, NDUFS3, NDUFS4, NDUFS5, NDUFS6, NDUFS7, NDUFS8, NDUFV1, NDUFV2, NDUFV3, SDHA, SDHB, SDHC, SDHD, UQCR10/CRC, UQCR11/UQCR, UQCRB, UQCRC1, UQCRC2, UQCRFS1, UQCRH, UQCRQ
DNA-Met genes	GPR24, TLE6, STAB1, PPYR1, CTNNA2, ST6GALNAC1, C1orf35, IQCH, SOX1, HAMP, KTI12, EHHADH, RAB20, C1orf80, MOCS3, BMS1L, NR2E1, BBS7, PCDHB14, FBXL13, ZNF454, SMUG1, C16orf61, KCNQ1, FGF22, NHN1, MAWBP, CCDC60, CNN3, GLI1, ADAMTSL3, IVL, PCDHB3, HSPA12B, C21orf99, CETN3, PCDHB10, SRXN1, TREML2, MGC50559, FLJ14346, ALDOA, FLJ45909, SUPT5H, BATF2, DZIP1, CLDN1, OSBPL11, GTF3C1, GPR6, ARHGAP22, IL17RE, CALML4, LOC339789, P2RXL1, FLJ20364, DPPA3, CNFN, PGAM2, LOC203427, TMEPAI, GRIN2C, GAPDHS, PCDH21, PROCA1, PIGV, APITD1, NPAS1, GAL3ST4, KLK11, ZNF555, TXNL4A, APC, UTF1, PRPS1, FSIP1, SHCBP1, ZNF659, MAPK8IP3, OSBPL8, CDK9, UBR1, MEA1, DAB2IP, IMMT, BRDG1, TLX3, NCALD, TMBIM1, C17orf80, TJAP1, TAF1, LOC389458, MAP2K1IP1, GALR2, COPS6, TCF7L2, CA2, SORD

Table 2: Genes with annotations representing "oxidative phosphorylation" and "ubiquitin-proteasome" in 300 genes of top highest ES scores obtained by modified "expression screening" on **A)** BD_Brain and **B)** BD_Blood1 with OxPhos genes as a target gene set.

2A: BD_Brain

ES rank	Entrez Gene ID	Gene Symbol	Annotation	ES score	FDR
9	1329	COX5B	OxPhos	0.76	0.01
10	4724	NDUFS4	OxPhos	0.76	0.00
17	1347	COX7A2	OxPhos	0.76	0.00
22	4708	NDUFB2	OxPhos	0.75	0.00
28	27089	UQCRQ	OxPhos	0.75	0.00
39	7319	UBE2A	ubiquitin	0.75	0.01
45	5705	PSMC5	ubiquitin	0.74	0.00
52	4700	NDUFA6	OxPhos	0.74	0.00
71	5688	PSMA7	ubiquitin	0.74	0.00
72	51506	UFC1	ubiquitin	0.74	0.01
75	539	ATP5O	OxPhos	0.74	0.01
78	5694	PSMB6	ubiquitin	0.73	0.03
83	7381	UQCRB	OxPhos	0.73	0.00
86	5707	PSMD1	ubiquitin	0.73	0.00
91	5710	PSMD4	ubiquitin	0.73	0.00
96	4695	NDUFA2	OxPhos	0.73	0.02
101	9551	ATP5J2	OxPhos	0.73	0.02
114	4706	NDUFAB1	OxPhos	0.73	0.02
128	55012	PPP2R3C	ubiquitin	0.72	0.01
142	515	ATP5F1	OxPhos	0.72	0.02
146	514	ATP5E	OxPhos	0.72	0.00
168	1349	COX7B	OxPhos	0.72	0.01
169	5521	PPP2R2B	ubiquitin	0.72	0.03
172	5693	PSMB5	ubiquitin	0.72	0.01
190	522	ATP5J	OxPhos	0.72	0.05
210	4701	NDUFA7	OxPhos	0.72	0.02
217	5686	PSMA5	ubiquitin	0.72	0.07
222	5690	PSMB2	ubiquitin	0.72	0.01
239	5706	PSMC6	ubiquitin	0.71	0.02
256	5687	PSMA6	ubiquitin	0.71	0.02
260	5708	PSMD2	ubiquitin	0.71	0.04
261	7321	UBE2D1	ubiquitin	0.71	0.03
264	10632	ATP5L	OxPhos	0.71	0.02
265	10476	ATP5H	OxPhos	0.71	0.02
274	5692	PSMB4	ubiquitin	0.71	0.01

276	5695	PSMB7	ubiquitin	0.71	0.04
284	4728	NDUFS8	OxPhos	0.71	0.04
285	4725	NDUFS5	OxPhos	0.71	0.06

2B: BD_Blood1

ES rank	Entrez Gene ID	Gene Symbol	Annotation	ES score	FDR
6	29796	UCRC	OxPhos	0.72	0.00
9	4708	NDUFB2	OxPhos	0.72	0.00
17	5695	PSMB7	ubiquitin	0.71	0.00
18	5527	PPP2R5C	ubiquitin	0.71	0.00
24	521	ATP5I	OxPhos	0.71	0.00
33	5701	PSMC2	ubiquitin	0.70	0.00
34	5689	PSMB1	ubiquitin	0.70	0.00
42	5684	PSMA3	ubiquitin	0.70	0.00
44	8239	USP9X	ubiquitin	0.70	0.00
55	4694	NDUFA1	OxPhos	0.69	0.00
63	7320	UBE2B	ubiquitin	0.69	0.00
70	522	ATP5J	OxPhos	0.69	0.00
90	55967	NDUFA12	OxPhos	0.68	0.00
97	7347	UCHL3	ubiquitin	0.68	0.02
100	5694	PSMB6	ubiquitin	0.68	0.01
131	1350	COX7C	OxPhos	0.67	0.01
148	5683	PSMA2	ubiquitin	0.66	0.00
173	4714	NDUFB8	OxPhos	0.65	0.02
244	7311	UBA52	ubiquitin	0.64	0.00
259	4705	NDUFA10	OxPhos	0.64	0.02
280	51103	NDUFAF1	ubiquitin	0.63	0.02

Table 3: GO terms representing "oxidative phosphorylation" and "ubiquitin-proteasome" obtained by modified "expression screening" on BD_Brain and BD_Blood1 with OxPhos genes as a target gene set.

	BD_Brain*	BD_Blood1*
GO terms representing "oxidative phosphorylation"	*GO:0006119*	*GO:0006119*
	GO:0006120	*GO:0006120*
	GO:0015980	*GO:0015980*
	GO:0022900	*GO:0022900*
	GO:0022904	*GO:0022904*
	GO:0042773	*GO:0042773*
	GO:0042775	*GO:0042775*
	GO:0006754	
	GO:0010257	
	GO:0015986	
	GO:0032981	
	GO:0033108	
	GO:0046034	
	GO:0055114	
GO terms representing "ubiquitin-proteasome"	*GO:0006511*	*GO:0006511*
	GO:0010498	*GO:0010498*
	GO:0031145	*GO:0031145*
	GO:0031396	*GO:0031396*
	GO:0031397	*GO:0031397*
	GO:0031398	*GO:0031398*
	GO:0043161	*GO:0043161*
	GO:0051436	*GO:0051436*
	GO:0051437	*GO:0051437*
	GO:0051438	*GO:0051438*
	GO:0051439	*GO:0051439*
	GO:0051443	*GO:0051443*
	GO:0051444	*GO:0051444*
		GO:0033522

*GO terms of ***italic bold*** were observed in both BD_Brain and BD_Blood1

Table 4: GO terms representing "inflammatory response" and "apoptosis" obtained by modified "expression screening" on BD_Blood1 and BD_Blood2 with DNA-Met genes as a target gene set.

	BD_Blood1*	BD_Blood2*
GO terms representing "inflammatory response"	*GO:0006952*	*GO:0006952*
	GO:0006955	*GO:0006955*
	GO:0002263	GO:0002684
	GO:0002285	GO:0002694
	GO:0002312	GO:0006968
	GO:0002313	GO:0009615
	GO:0002335	GO:0009617
	GO:0002366	GO:0042742
	GO:0002429	GO:0050729
	GO:0002474	GO:0050778
	GO:0042113	GO:0050863
	GO:0045321	
	GO:0046649	
GO terms representing "apoptosis"	*GO:0006915*	*GO:0006915*
	GO:0010942	*GO:0010942*
	GO:0043065	*GO:0043065*
	GO:0043068	*GO:0043068*
	GO:0006917	GO:0010941
	GO:0008219	GO:0012501
	GO:0012501	GO:0042981
	GO:0012502	GO:0043067
	GO:0016265	

*GO terms of ***italic bold*** were observed in both BD_Blood1 and BD_Blood2.