Supplemental Material

Data S1.

For Gel Electrophoresis scoring:

5 = clearly visible high molecular weight DNA band, no signs of degradation (no smear)

4 = clearly visible high molecular weight DNA band, some possible degradation (smear) but less than 10% of the total DNA

3 = some high molecular weight DNA band, any shift of high molecular weight band, but clearly visible smear

2 = no clear indication of high molecular weight DNA, visible smear the length of gel path

1 = no indication of high molecular weight DNA, all smear, low molecular weight

0 = no visible smear or bands; unusual result (to be repeated after requantification if necessary)

For PicoGreen protocol:

0. Set samples out to equilibrate at room temperature for a couple hours before starting PicoGreen. Set the standards and PicoGreen solution out 30 minutes beforehand.

1. Add 5 µL of each sample into the 96 well PCR plate (or U-bottom plate if on Biomek.)

2. Add 195 µL of hydration solution to each sample and mix several times.

3. Transfer 8 µL of diluted sample into the clear bottom Picoplate.

4. Add 8 µL of standard into the first column of the Picoplate.

5. PicoGreen solution: Add 53.8 µL of PicoGreen dye to 20.5 mL of hydration solution in a 50 mL conical tube. Mix tube well by inverting.

6. Add 192 µL of PicoGreen mix to Picoplate samples. (Pipet up and down to mix well)

Run on PicoGreen reader.

PicoGreen Dilution Standards (use with 500 ng/µL of Lambda DNA)

This is a serial dilution, so only pipet out 42 µL of Lambda DNA and add water, before you proceed to the next standard.

300 ng = 42 µL DNA + 28 µL H_2O

50 µL from 300

250 ng = 50 µL DNA + 10 µL H_2O

40 µL from 250

200 ng = 40 µL DNA + 10 µL H_2O

30 µL from 200

150 ng = 30 µL DNA + 10 µL H_2O

20 µL from 150

100 ng = 20 µL DNA + 10 µL H_2O

10 µL from 100

50 ng = 10 µL DNA + 10 µL H_2O

0 ng = 20 µL H_2O

Table S1. ***Comb-p*** **DMR meta-analysis results of the discovery and validation sets. DMRs that were statistically significant using an FDR-adjusted p-value <0.05 are shown.**

Chromosome	Start	End	Number of Probes	FDR-adj p-value	Gene/s
1	2344699	2345895	13	1.37E-15	*PEX10*
12	124908601	124908932	6	3.19E-12	*NCOR2*
6	15504844	15506086	9	1.56E-10	*JARID2*
4	89299314	89300651	9	7.83E-10	*HERC6*
3	101443264	101443993	12	2.73E-09	*CEP97*
1	205818956	205819610	8	1.06E-08	*PM20D1*
7	1250038	1251339	14	2.72E-07	*UNCX*
14	103415458	103416269	5	2.67E-06	*CDC42BPB*
22	24105087	24105693	5	3.43E-06	*C22orf15*
16	85676292	85676862	5	3.57E-06	*GSE1*
1	6239157	6241507	10	3.80E-06	*CHD5*
5	140891767	140893635	6	4.84E-06	*PCDHGA1*
					PCDHGA2
					PCDHGA3
					PCDHGB1
					PCDHGA4
					PCDHGB2
					PCDHGA5
					PCDHGB3
					PCDHGA6
					PCDHGA7
					PCDHGB4
					PCDHGA8
					PCDHGB5
					PCDHGA9
					PCDHGB6
					PCDHGA10
					PCDHGB7
					PCDHGA11
					PCDHGA12
					PCDHGC3
					PCDHGC4
					PCDHGC5
12	10183172	10183365	5	5.41E-06	*CLEC9A*
17	72349697	72350711	5	7.40E-06	*KIF19*
21	46077454	46077732	5	7.63E-06	*TSPEAR*
17	5137892	5138697	5	1.36E-05	*LOC100130950*
					SCIMP
10	134150451	134150761	7	1.38E-05	*LRRC27*
22	17956453	17956642	5	1.58E-05	*CECR2*

17	33759512	33760528	12	2.01E-05	*SLFN12*
11	70672388	70673257	9	2.45E-05	*SHANK2*
19	3785573	3786958	8	3.07E-05	*MATK*
8	21882013	21882943	8	5.66E-05	*NPM2*
13	111317935	111318641	5	5.69E-05	*CARS2*
1	3823656	3824448	7	5.75E-05	*LOC100133612*
11	43333145	43333989	12	6.74E-05	*API5*
13	47471705	47472430	13	7.08E-05	*HTR2A*
7	11871535	11872074	9	7.09E-05	*THSD7A*
4	81117853	81119474	10	7.22E-05	*PRDM8*
22	50985681	50986963	7	7.63E-05	*KLHDC7B*
11	108408907	108409366	5	1.20E-04	*EXPH5*
12	89743788	89744878	10	1.43E-04	*DUSP6*
2	239046275	239048580	11	1.46E-04	*KLHL30*
1	48175246	48177262	10	1.73E-04	*TRABD2B*
1	160951675	160952704	5	2.10E-04	*F11R*
11	128736844	128737468	8	2.14E-04	*KCNJ1*
5	43040174	43042234	15	2.47E-04	*ANXA2R*
2	65593761	65594891	6	2.61E-04	*SPRED2*
2	27665079	27665712	9	3.52E-04	*NRBP1* *KRTCAP3*
1	1099583	1100558	8	4.22E-04	*MIR200B*
9	124981504	124983483	6	4.40E-04	*LHX6*
12	96350519	96350796	5	6.03E-04	*AMDHD1*
12	85430025	85430337	8	6.64E-04	*TSPAN19* *LRRIQ1*
3	146261991	146262762	6	6.74E-04	*PLSCR1*
17	7311030	7312082	9	6.83E-04	*NLGN2*
2	21266500	21267335	12	7.00E-04	*APOB*
8	85094437	85096038	10	7.03E-04	*RALYL*
3	127006287	127007607	6	7.09E-04	*PLXNA1*
20	3051954	3052693	11	7.33E-04	*OXT*
6	41068173	41069049	7	7.67E-04	*NFYA* *ADCY10P1*
3	158390329	158390822	10	7.73E-04	*GFM1* *LXN*
17	6916926	6917615	5	8.05E-04	*RNASEK-C17orf49* *RNASEK*
12	6745057	6745569	6	8.15E-04	*LPAR5*
4	46391159	46391930	13	8.30E-04	*GABRA2*
12	79257496	79258856	12	9.98E-04	*SYT1*
1	1149091	1150417	6	0.001232	*TNFRSF4*
11	65314913	65315626	6	0.001277	*LTBP3*
3	164913627	164915016	12	0.001839	*SLITRK3*
19	59024873	59026418	7	0.001879	*ZBTB45*

5	2225011	2225483	5	0.001993	*IRX4*
8	144511672	144513981	10	0.002425	*MAFA*
11	68924577	68925192	6	0.003025	*TPCN2*
1	120173989	120174874	6	0.003207	*ZNF697*
2	208988863	208989832	7	0.003266	*LOC100507443* *CRYGD*
1	28843736	28844753	8	0.003337	*RCC1*
1	66257822	66258442	5	0.003819	*PDE4B*
6	155537595	155538156	7	0.003869	*TIAM2*
6	158588763	158589858	16	0.003979	*SERAC1* *GTF2H5*
2	45159663	45160555	9	0.003993	*SIX3*
1	156783633	156785559	10	0.004154	*SH2D2A* *NTRK1*
5	126408756	126409554	13	0.004389	*C5orf63*
11	13983705	13984044	9	0.004722	*SPON1*
5	77139964	77140986	7	0.005066	*TBCA*
12	6438317	6439098	6	0.005205	*TNFRSF1A*
22	45608345	45609422	13	0.005308	*KIAA0930*
12	69632957	69634188	10	0.006195	*CPSF6*
19	1008643	1010237	8	0.006392	*GRIN3B* *C19orf6*
3	113160071	113160822	10	0.006828	*WDR52*
17	7253720	7255462	6	0.007723	*ACAP1* *KCTD11*
7	38350921	38351469	6	0.008525	*LOC100506776*
6	30610729	30611057	6	0.009719	*ATAT1*
6	792256	792779	6	0.009784	*EXOC2*
22	19949585	19950167	8	0.01023	*COMT*
6	28828946	28829947	21	0.01077	*LOC401242*
6	29454623	29455533	13	0.0116	*MAS1L*
17	46668715	46669567	8	0.01174	*HOXB-AS3* *HOXB5*
8	1900191	1900893	6	0.01216	*ARHGEF10*
13	53422381	53424128	15	0.01275	*PCDH8*
10	123355268	123356337	9	0.01321	*FGFR2*
17	76037035	76037563	6	0.01371	*TNRC6C*
5	50673033	50675115	12	0.01401	*LOC642366*
2	108993602	108994529	9	0.01423	*SULT1C4*
7	149157735	149158487	8	0.01503	*ZNF777*
11	68781976	68782212	5	0.01516	*MRGPRF*
6	55038900	55039623	6	0.01605	*HCRTR2*
1	854766	856060	12	0.01639	*LOC100130417*
8	37605359	37605979	7	0.0164	*ERLIN2* *LOC728024*

8	1896437	1897076	5	0.01722	*ARHGEF10*
16	89723193	89725270	10	0.01888	*CHMP1A* *C16orf55*
6	503773	504352	5	0.019	*EXOC2*
5	54281198	54281734	7	0.01991	*ESM1*
19	14591033	14591346	5	0.02	*GIPC1*
6	41605343	41606870	7	0.0203	*MDFI*
11	10715175	10715768	11	0.02117	*MRVI1*
19	16186840	16187103	5	0.0212	*TPM4*
1	220132091	220132729	6	0.02139	*RNU5F-1*
4	81106414	81107186	7	0.02301	*PRDM8*
11	35965104	35966323	7	0.02373	*LDLRAD3*
13	46961583	46961898	10	0.02431	*KIAA0226L*
3	32432942	32434340	6	0.02502	*CMTM7*
1	27189270	27189680	5	0.02694	*SFN*
22	33196103	33197035	6	0.02797	*SYN3* *TIMP3*
12	51566379	51567113	10	0.02873	*TFCP2*
6	166580460	166581273	5	0.03009	*T*
14	105995251	105996514	6	0.03101	*TMEM121*
20	19866743	19867146	8	0.03132	*RIN2*
17	3438857	3439373	6	0.03149	*TRPV3*
2	241496830	241497664	9	0.03216	*ANKMY1*
6	76203225	76203676	7	0.03355	*FILIP1*
16	604802	605726	7	0.03396	*SOLH*
11	69462660	69463324	5	0.03402	*CCND1*
2	233284661	233285930	5	0.03569	*ALPPL2*
19	51225848	51226850	7	0.03614	*CLEC11A*
3	87039536	87040740	12	0.03757	*VGLL3*
11	1750302	1750764	5	0.03785	*MOB2*
2	163695776	163696188	6	0.03893	*KCNH7*
11	1989715	1991876	10	0.0394	*MRPL23*
12	1025529	1026393	7	0.04056	*RAD52*
15	31515750	31516482	9	0.04338	*LOC283710*
16	685580	686585	7	0.04369	*C16orf13*
19	44808796	44809320	8	0.04643	*ZNF235*
14	105166740	105167974	8	0.04817	*INF2*
2	74647579	74649150	10	0.04883	*WDR54*
1	156465749	156467189	5	0.04986	*MEF2D*

Table S2. Probes with nominal p-value<0.05 found in both discovery and validation cohorts that are common to previous EWAS of all-cause mortality.

Probe	**Nominal p-value (Discovery)**	**FDR-adj p (Discovery)**	**Δβ**	**Nominal p-value (Validation)**	**FDR-adj p (Discovery)**	**Δβ**	**Direction of methylation in respective article***
ESTHER/KORA Study (PMID: 28303888)							
cg14975410	0.015	0.713	-3.009	0.049	0.816	-3.950	-
cg23842572	0.027	0.742	-3.435	0.006	0.745	-2.367	+
cg18181703	0.020	0.727	-3.233	0.027	0.796	-3.488	-
Twin Study (PMID: 29419728)							
cg15763258	0.003	0.658	-1.804	0.026	0.793	-3.463	Not specified

*Direction of methylation: when negative (-) methylation was lower in cases than in controls and when positive (+) methylation was higher in cases than controls.