

## Supplementary Materials

**Table S1. Annotated results for the 80 differentially methylated sites from the EWAS.**

**Table S2. DAVID analysis for CpGs showing biological pathways.** The table includes pathways that achieved an unadjusted  $P$ -value  $<0.05$ , ranked in descending order of enrichment.

**Table S3. Comparison of significant CpGs differentially methylated in our study and other human DE exposure studies.** The  $\Delta\beta$  values calculated in the two other studies correspond to ACE calculations in the current study.

**Figure S1. Manhattan plot for the epigenome-wide analyses with asymptotic  $P$ -values (paired  $t$ -tests).** The dashed orange line is the minimum possible  $P$ -value from an exact test.

**Figure S2. Volcano plot for the epigenome-wide analyses with asymptotic  $P$ -values (paired  $t$ -tests).** The dashed orange line is the minimum possible  $P$ -value from an exact test.

**Figure S3. Quantile-Quantile plot for the epigenome-wide analyses of asymptotic vs. expected  $P$ -values.**

**Table S1.** Annotated results for the 80 differentially methylated sites from the EWAS.

CpG	CHR	pos	UCSC RefGene Name	UCSC RefGene Group	Relation to CpG Island	Mean %-DNAm Diesel Exhaust (DE)	Mean %-DNAm Clean Air (CA)	Mean Causal Effect (ACE)	Exact <i>P</i> -value	Asymptotic <i>P</i> -value
cg16987365	1	2450682	PANK4	Body	N_Shore	92.73	93.89	-1.16	2.44E-04	1.23E-04
cg17493795	1	3273407	PRDM16;PRDM16	Body;Body	N_Shore	81.3	84.47	-3.17	2.44E-04	3.33E-04
cg20973421	1	9427650	SPSB1	3'UTR	Island	98.21	98.39	-0.18	2.44E-04	1.22E-04
cg08258719	1	16090718	FBLIM1;FBLIM1	5'UTR;TSS1500	OpenSea	76.07	77.63	-1.56	2.44E-04	9.67E-04
cg15729771	1	25071616	CLIC4	TSS200	Island	3.27	2.77	0.50	2.44E-04	1.10E-03
cg10513359	1	35321339	C1orf212	Body	N_Shelf	89.77	91.92	-2.15	2.44E-04	2.89E-05
cg12413579	1	36108206	PSMB2	TSS1500	S_Shore	62.55	56.48	6.07	2.44E-04	2.39E-04
cg21681327	1	41978691	HIVEP3;HIVEP3	Body;Body	N_Shelf	96.17	94.88	1.29	2.44E-04	1.99E-04
cg26682094	1	50489714	AGBL4	TSS200	Island	2.41	2.2	0.21	2.44E-04	1.11E-03
cg05885647	1	53926107	DMRTB1	Body	Island	95.86	96.72	-0.87	2.44E-04	2.45E-02
cg11837766	1	64239631	ROR1;ROR1	TSS200;TSS200	Island	1.9	1.66	0.23	2.44E-04	6.22E-04
cg10482024	1	65613042	AK3L1;AK3L1	TSS1500;TSS200	Island	3.13	2.51	0.63	2.44E-04	3.06E-04
cg16427752	1	76262302	MSH4	TSS1500	N_Shore	59.09	62.11	-3.02	2.44E-04	1.01E-03
cg19236050	1	110785089			OpenSea	89.5	91.26	-1.75	2.44E-04	2.90E-03
cg26906021	1	155146940	KRTCAP2;TRIM46	TSS1500;Body	N_Shore	1.55	1.25	0.30	2.44E-04	1.22E-03
cg04361579	1	203152047	CHI3L1	Body	OpenSea	99.05	98.67	0.38	2.44E-04	1.75E-04
cg02985240	1	235468148	ARID4B;ARID4B	Body;Body	OpenSea	92.55	89.29	3.26	2.44E-04	1.39E-03
cg13913933	2	59202222			OpenSea	98.11	97.68	0.43	2.44E-04	7.92E-04
cg23116322	2	63276478	OTX1	TSS1500	Island	1.41	1.26	0.15	2.44E-04	1.88E-03
cg25627714	2	97174709	NEURL3	TSS1500	S_Shore	97.58	96.92	0.67	2.44E-04	2.32E-04
cg01215936	2	105469514			Island	2.36	2.09	0.28	2.44E-04	2.06E-04
cg25095994	2	231191727	SP140L	TSS200	OpenSea	2.68	2.23	0.45	2.44E-04	1.63E-03
cg16930811	3	49907666	CAMKV	TSS1500	S_Shore	35.98	33.71	2.27	2.44E-04	1.23E-04
cg02619135	3	51428440	RBM15B	TSS1500	Island	1.81	1.47	0.35	2.44E-04	5.45E-04
cg08450501	3	136580965	NCK1	TSS200	Island	7.32	5.8	1.51	2.44E-04	1.19E-03
cg00995327	3	142838847	CHST2;CHST2	5'UTR;1stExon	Island	2.35	1.93	0.42	2.44E-04	7.25E-04
cg19273995	4	27086400			OpenSea	3.97	3.17	0.80	2.44E-04	3.39E-04
cg00241998	4	40058606	N4BP2;N4BP2;LOC344967	1stExon;5'UTR;Body	Island	1.79	1.69	0.10	2.44E-04	4.51E-03
cg22105702	4	78978722	FRAS1;FRAS1	TSS200;TSS200	Island	1.24	1.11	0.13	2.44E-04	7.35E-05
cg19763168	4	84256184	HPSE;HPSE;HPSE	5'UTR;TSS200;5'UTR	Island	3.16	2.72	0.43	2.44E-04	2.46E-03

cg21262733	4	120988587	MAD2L1	TSS1500	S_Shore	2.82	2.32	0.49	2.44E-04	2.44E-04
cg23427912	4	189059510	TRIML1	TSS1500	OpenSea	93.31	89.1	4.21	2.44E-04	2.14E-03
cg07830906	5	264645			S_Shelf	92.2	91.51	0.69	2.44E-04	1.18E-04
cg10812634	5	126409211	FLJ44606;FLJ44606	TSS200;TSS200	Island	16.25	10.21	6.04	2.44E-04	2.00E-04
cg15405432	5	126409310	FLJ44606;FLJ44606	TSS200;TSS200	Island	10.74	7.34	3.41	2.44E-04	3.76E-03
cg23171203	5	128796099	ADAMTS19	TSS200	Island	1.72	2.13	-0.41	2.44E-04	3.14E-04
cg10194341	6	43027125	KLC4;MRPL2;KLC4;MRPL2	TSS1500;1stExon; TSS1500;5'UTR	Island	1.23	1.13	0.11	2.44E-04	5.21E-03
cg10207999	6	43588662	GTPBP2	3'UTR	OpenSea	90.87	92.85	-1.98	2.44E-04	8.07E-04
cg27238071	6	71998145	OGFRL1	TSS1500	Island	1.55	1.32	0.23	2.44E-04	6.25E-04
cg02192300	6	114663564			Island	3.59	3.03	0.56	2.44E-04	1.63E-03
cg06643622	7	117437223	CTTNBP2	Body	OpenSea	84.31	79.45	4.86	2.44E-04	6.17E-05
cg05793193	7	152161912	LOC100128822	Body	Island	1.48	1.13	0.35	2.44E-04	5.49E-04
cg10293422	8	17434503	PDGFRL	TSS200	N_Shore	2.45	2.16	0.30	2.44E-04	6.09E-05
cg03508052	8	17556355	MTUS1;MTUS1;MTUS1	Body;TSS1500;Body	OpenSea	97.87	97.07	0.80	2.44E-04	5.30E-04
cg20523466	8	98900895	MATN2;MATN2	Body;Body	OpenSea	72.54	74.67	-2.12	2.44E-04	1.28E-03
cg01716084	8	142367700	GPR20	Body	Island	87.84	89.7	-1.86	2.44E-04	2.41E-03
cg25098077	10	97050963	PDLIM1	TSS200	Island	3.08	2.49	0.59	2.44E-04	1.40E-04
cg20040041	10	127812674	ADAM12;ADAM12	Body;Body	OpenSea	98.05	97.4	0.65	2.44E-04	1.66E-04
cg10028666	10	135050775	VENTX	TSS1500	Island	6.82	5.85	0.97	2.44E-04	1.41E-03
cg21117210	11	31849194			S_Shore	6.72	9.21	-2.50	2.44E-04	3.19E-03
cg09654997	11	46259561			Island	2.11	1.88	0.23	2.44E-04	1.38E-03
cg24407327	11	64411428	NRXN2;NRXN2;NRXN2	TSS1500;Body;Body	S_Shore	3.04	2.74	0.30	2.44E-04	1.57E-04
cg24940248	11	118796872			S_Shore	1.74	1.49	0.25	2.44E-04	3.68E-03
cg24509916	11	133809895	IGSF9B	Body	OpenSea	88.04	86.88	1.16	2.44E-04	4.72E-05
cg00719651	12	47225449			Island	16.54	13.23	3.31	2.44E-04	4.37E-03
cg26201787	12	77157648	ZDHC17	TSS1500	Island	2.34	2.12	0.22	2.44E-04	2.03E-04
cg18213653	12	112605734	C12orf51	Body	OpenSea	60.08	62.19	-2.11	2.44E-04	4.10E-03
cg05836979	12	133377847	GOLGA3	Body	N_Shore	86.99	88.59	-1.60	2.44E-04	3.81E-03
cg05359130	14	29228970			OpenSea	6.04	4.76	1.28	2.44E-04	8.69E-04
cg26223968	14	101204240			S_Shelf	90.06	92.17	-2.11	2.44E-04	1.67E-03
cg09447749	15	65195746			N_Shelf	97.5	96.9	0.59	2.44E-04	5.25E-04
cg11200462	15	66786368	SNAPC5	3'UTR	N_Shelf	97.97	97.02	0.95	2.44E-04	1.28E-03
cg16414568	15	91473511	UNC45A	5'UTR	Island	7.46	4.55	2.91	2.44E-04	9.21E-04
cg06647218	16	68279240	PLA2G15	TSS200	Island	1.82	1.69	0.13	2.44E-04	7.58E-03
cg09126659	16	70207304	CLEC18C	TSS1500	OpenSea	87.46	85.17	2.30	2.44E-04	1.50E-04
cg07497907	16	77367200	ADAMTS18	Body	OpenSea	85.52	80.89	4.63	2.44E-04	6.12E-06
cg01541600	16	87988715	BANP;BANP	5'UTR;5'UTR	N_Shelf	37.16	34.86	2.30	2.44E-04	4.97E-07
cg25432975	17	1959066	HIC1;HIC1	TSS1500;5'UTR	Island	3.88	3.45	0.44	2.44E-04	2.41E-04

cg14170220	17	21220411			Island	14.24	16.4	-2.15	2.44E-04	2.76E-05
cg04424940	17	42264171	TMUB2;TMUB2;C17orf65	TSS1500; TSS200;TSS200	Island	2.1	1.86	0.23	2.44E-04	1.01E-02
cg13096688	17	43568337	PLEKHM1	TSS200	Island	5.61	4.23	1.38	2.44E-04	9.96E-04
cg20163532	17	56064356	VEZF1	Body	N_Shore	2	1.7	0.30	2.44E-04	3.22E-05
cg01944585	17	72732912	RAB37;RAB37;RAB37	TSS200;TSS1500; Body	Island	1.23	1.06	0.17	2.44E-04	4.94E-04
cg12768640	19	7795428	CLEC4G	Body	Island	7.45	6.18	1.27	2.44E-04	6.20E-04
cg08821193	19	13068151	GADD45GIP1	TSS200	Island	3.87	3.13	0.74	2.44E-04	1.09E-03
cg21122529	19	16652680	CHERP	Body	Island	2.61	2.11	0.50	2.44E-04	3.82E-06
cg06419476	19	42636978	POU2F2	TSS1500	N_Shore	33.53	31.83	1.70	2.44E-04	5.43E-04
cg01735890	20	62884594			N_Shelf	97.46	96.39	1.06	2.44E-04	6.28E-04
cg24423088	21	32185365	KRTAP8-1	1stExon	OpenSea	96.91	97.89	-0.98	2.44E-04	1.25E-04
cg12543338	X	149106022	LOC100272228;CXorf40B	TSS1500;5'UTR	N_Shore	14.7	12.62	2.08	2.44E-04	1.40E-03

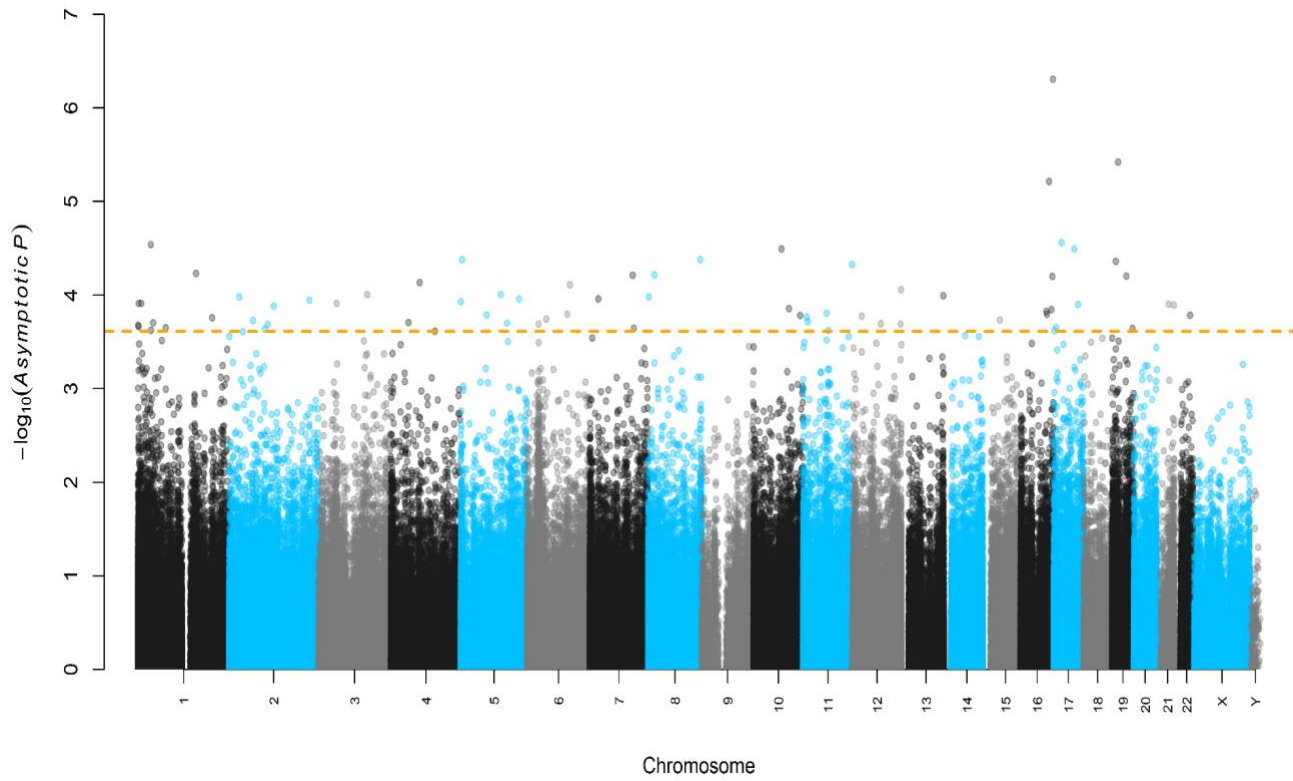
**Table S2.** DAVID analysis for CpGs showing biological pathways. The table includes pathways that achieved an unadjusted *P*-value <0.05, ranked in descending order of enrichment.

<b>Biological Pathway</b>	<b>Count</b>	<b>P-Value</b>	<b>Benjamini P-Value</b>
Epidermal growth factor (EGF)-like domain	5	0.006	0.63
EGF-like domain	4	0.032	0.65
EGF	4	0.043	0.94
Metal ion-binding site: Zinc; in inhibited form	3	0.005	0.78
Peptidase M12B, ADAM/reprolysin	3	0.007	0.45
Peptidase M12B, propeptide	3	0.007	0.45
Domain: Peptidase M12B	3	0.007	0.66
Domain: Disintegrin	3	0.007	0.52
Short sequence motif: Cysteine switch	3	0.008	0.46
Metalloprotease	4	0.010	0.47
Metallopeptidase, catalytic domain	3	0.026	0.79
Metallopeptidase activity	3	0.031	0.80
Domain: B30.2/SPRY	3	0.034	0.83
Concanavalin A-like lectin/glucanase, subgroup	4	0.034	0.79
B30.2/SPRY domain	3	0.037	0.74
Zinc	15	0.007	0.58
Zinc ion binding	9	0.042	0.77

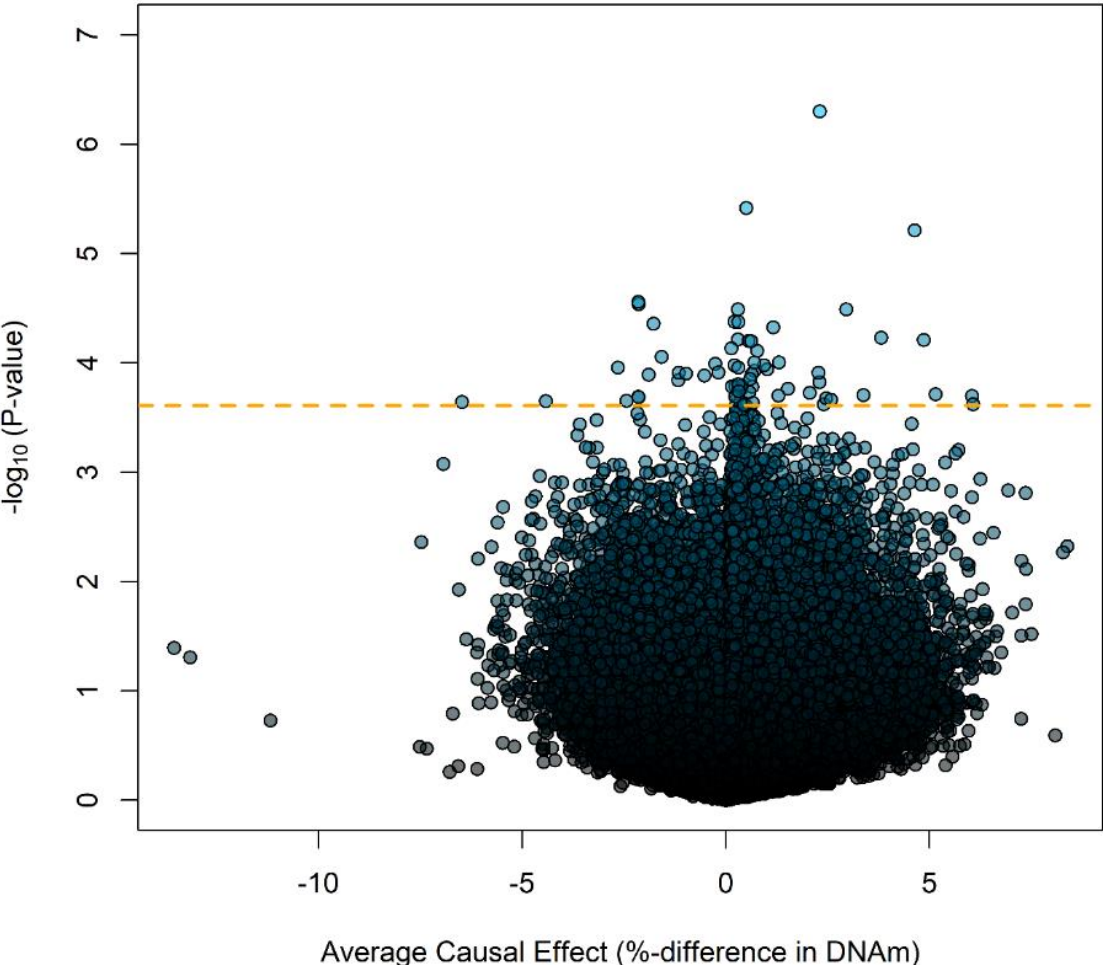
**Table S3.** Comparison of significant CpGs differentially methylated in our study and other human DE exposure studies. The  $\Delta\beta$  values calculated in the two other studies correspond to ACE calculations in the current study.

		<b>Clifford et al. (2017) [29]</b>		<b>Current Study</b>		
CpG	Gene	$\Delta\beta$ (post-DE – pre-DE)	P-Value	$\Delta\beta$ ACE	Exact P-value	Asymptotic P-value
cg16058975	--	-0.109	4.0x10 <sup>-3</sup>	-0.0247	0.000732	0.00681
cg08548659	--	-0.104	8.0x10 <sup>-4</sup>	-0.0429	0.0125	0.00954
cg10231182	<i>EPS8</i>	-0.101	0.0042	-0.0446	0.0344	0.0310
cg21442419	<i>SKI</i>	-0.103	2.0x10 <sup>-4</sup>	-0.0152	0.0396	0.0355
cg11060532	<i>HOXB3</i>	-0.115	3.0x10 <sup>-4</sup>	-0.0572	0.0454	0.0473
cg06871919	<i>C5orf22</i>	-0.102	0.0052	-0.0414	0.0474	0.0451
		<b>Jiang et al. (2014) [28]</b>		<b>Current Study</b>		
CpG	Gene	$\Delta\beta$ (post-DE – pre-DE)		$\Delta\beta$ ACE	Exact P-Value	Asymptotic P-value
cg02857074	<i>CACNA2D1</i>	-0.033		0.0264	0.0303	0.0406
cg23670794	<i>ZBED2; CD96</i>	-0.020		0.0214	0.0442	0.0434
cg07376029	<i>GC</i>	-0.024		0.0229	0.0481	0.0451
cg17624536	--	0.025		0.00375	0.0496	0.0494

**Figure S1.** Manhattan plot for the epigenome-wide analyses with asymptotic  $P$ -values (paired  $t$ -tests). The dashed orange line is the minimum possible  $P$ -value from an exact test.



**Figure S2.** Volcano plot for the epigenome-wide analyses with asymptotic  $P$ -values (paired  $t$ -tests).





**Figure S3.** Quantile-Quantile plot for the epigenome-wide analyses of asymptotic vs. expected  $P$ -values.

