

SUPPLEMENTARY TABLES

Supplementary Table 1. Basic characteristics of the studied subjects for 850k Methylation BeadChip.

Characteristics	Studied subjects for 850k Methylation BeadChip					
	F1 parent generation			F2 offspring generation		
	Non-famine (n=46)	Famine (n=46)	<i>P</i>	Non-famine (n=23)	Famine (n=23)	<i>P</i>
Age (years)	52.7 (4.6)	52.2 (2.5)	0.014	26.0 (4.6)	25.1 (4.2)	0.664
Men [n(%)]	22 (47.8)	22 (47.8)	0.552	13 (56.5)	14 (60.9)	0.222
Energy (kcal/d)	2367 (913)	2418 (966)	0.622	2524 (863)	2638 (883)	0.325
Over high school level [n(%)]	18 (39.1)	21 (45.7)	0.667	9 (39.1)	8 (34.8)	0.585
Low working strength [n(%)]	13 (28.3)	11 (23.9)	0.145	7 (30.4)	7 (30.4)	0.561
Smoker [n(%)]	16 (34.8)	20 (43.5)	0.322	10 (43.5)	11 (47.8)	0.332
Drinker [n(%)]	18 (39.1)	20 (43.5)	0.221	13 (56.5)	12 (52.2)	0.852
Hypertensive [n(%)]	13 (28.3)	16 (34.8)	0.071	3 (13.0)	7 (30.4)	0.041
Sport [n(%)]	13 (28.3)	12 (26.1)	0.886	8 (34.8)	9 (39.1)	0.455
BMI (kg/m ²)	24.9 (3.9)	25.4 (4.1)	0.439	24.0 (4.3)	24.8 (3.2)	0.274
SBP (mmHg)	140.2 (22.4)	144.0 (23.3)	0.022	123.3 (15.0)	125.9 (14.1)	0.046
DBP (mmHg)	85.3 (12.7)	86.2 (15.7)	0.110	79.6 (10.2)	78.1 (12.2)	0.442
FPG (mmol/L)	4.6 (1.0)	4.8 (1.1)	0.214	4.1 (0.6)	4.3 (0.6)	0.321
2-hPG (mmol/L)	6.2 (1.7)	6.3 (2.6)	0.130	5.1 (1.2)	5.3 (1.3)	0.256
eGFR (ml/min/1.73 m ²)	110.4 (32.5)	92.5 (30.6)	<0.001	127.7 (34.8)	116.9 (30.5)	0.019

Continuous variables are presented as the means (SD). Generalized linear mixed models and χ^2 test were used to probe for differences in continuous and dichotomous variables. eGFR, estimated glomerular filtration rate. BMI, Body mass index. FPG, Fast plasma glucose. 2-hPG, 2-hour postprandial glucose. SBP, Systolic blood pressure. DBP, Diastolic blood pressure.

Supplementary Table 2. Basic characteristics of the studied subjects for targeted bisulfite sequencing analysis.

Characteristics	Studied subjects for targeted bisulfite sequencing analysis					
	F1 parent generation			F2 offspring generation		
	Non-famine (n=196)	Famine (n=194)	<i>P</i>	Non-famine (n=127)	Famine (n=83)	<i>P</i>
Age (years)	52.1 (4.8)	52.3 (2.7)	<0.01	25.8 (4.7)	26.4 (3.7)	0.221
Men [n(%)]	102 (52.0)	105 (54.1)	0.554	59 (55.1)	59 (57.3)	0.754
Energy(kcal/d)	2424 (1062)	2477 (1003)	0.325	2578 (883)	2524 (863)	0.546
Over high school level [n(%)]	28 (14.3)	34 (17.5)	0.630	16 (14.9)	21 (20.4)	0.254
Low working strength [n(%)]	66 (33.7)	60 (30.9)	0.362	37 (34.6)	30 (29.1)	0.523
Smoker [n(%)]	50 (25.5)	52 (26.8)	0.884	22 (20.6)	24 (23.3)	0.215
Drinker [n(%)]	58 (29.6)	60 (30.9)	0.361	32 (29.9)	32 (31.1)	0.225
Hypertensive [n(%)]	16 (8.2)	20 (10.3)	0.421	9 (8.4)	9 (8.7)	0.668
Sport [n(%)]	81 (41.3)	92 (47.4)	0.026	24 (22.4)	24 (23.3)	0.658
BMI (kg/m ²)	24.6 (3.5)	24.9 (3.9)	0.332	24.1 (3.2)	24.5 (4.1)	0.556
FPG (mmol/L)	4.5 (1.2)	4.6 (1.1)	0.331	4.2 (0.3)	4.3 (0.4)	0.089
2-hPG (mmol/L)	6.1 (1.7)	6.4 (2.8)	0.044	5.2 (1.1)	5.5 (1.2)	0.032
SBP (mmHg)	139.1 (25.6)	142.7 (24.3)	0.112	125.6 (18.4)	128.6 (16.5)	0.245
DBP (mmHg)	81.3 (15.2)	83.1 (15.4)	0.448	78.9 (12.3)	78.8 (14.8)	0.221
eGFR (ml/min/1.73 m ²)	112.1 (23.5)	95.6 (22.7)	<0.001	124.8 (35.2)	112.1 (26.6)	0.029

Continuous variables are presented as the means (SD). Generalized linear mixed models and χ^2 test were used to probe for differences in continuous and dichotomous variables. eGFR, estimated glomerular filtration rate. BMI, Body mass index. FPG, Fast plasma glucose. 2-hPG, 2-hour postprandial glucose. SBP, Systolic blood pressure. DBP, Diastolic blood pressure.

Supplementary Table 3. Target regions for bisulfate sequencing at validation stage.

CPG	Gene	Chr	Start	End	Strand	Length	PrimerF	PrimerR
cg13528513	AGTR1	3	148418596	148418335	-	262	GTGTTGGAAAGTTG ATTTGTTAGTTT	ATTTACCTAACCCCTTTT TCTAATCAATC
cg20906621	AGTR1	3	148416471	148416214	-	258	TTTGGTTAAGGTTG GAGTGATGTT	ACAATTCAATAAACTT TCTTCCTAAAAC
cg17160506	PRKCA	17	64649456	64649609	+	154	AGTTTTAGTTATTTA GGAAGTTGAGTGG	AACCTCCTAAATAACT AAAACACTACAAATACAC

Supplementary Table 4. 19 differentially methylated positions (DMPs) showed concordant alterations in both generations.

CPG	Gene Symbol	Chr	Start	End	Relation to gene region	F1 generation		F2 generation		Hyper- or Hypo-methylated
						$\Delta\beta$	Adjusted P-value	$\Delta\beta$	Adjusted P-value	
cg03671207	CCR6	6	167544220	167545175	5'UTR	0.057	0.020	0.066	0.031	Hyper
cg04736673	CCDC6	10	61646683	61647185	Body	-0.080	0.045	-0.134	0.006	hypo
cg04810224	PRKG1	10	53620080	53620355	Body	0.056	0.000	0.071	0.011	Hyper
cg06332058		9	16103640	16104095		-0.063	0.011	-0.069	0.028	hypo
cg09762515	CUX1	7	101556445	101557055	Body	0.051	0.014	0.074	0.008	Hyper
cg13528513	AGTR1	3	148418205	148418530	5'UTR	-0.052	0.019	-0.066	0.012	hypo
cg13598358	PPP1CC	12	111176400	111176895	Body	0.058	0.031	0.064	0.009	Hyper
cg14032856	PLA2R1	2	160839385	160839590	Body	-0.053	0.019	-0.067	0.013	hypo
cg15824303						0.054	0.006	0.082	0.020	Hyper
cg16376748	FDXR	17	72870025	72870515	TSS1500	0.053	0.016	0.065	0.025	Hyper
cg17160506	PRKCA	17	64649040	64649570	Body	-0.053	0.008	-0.091	0.001	hypo
cg17198994	FGF12	3	192128785	192129475	Body	0.063	0.008	0.074	0.013	Hyper
cg18416503	ITPK1	14	93475840	93476235	Body	-0.064	0.016	-0.086	0.021	hypo
cg20906621	AGTR1	3	148416100	148416355	5'UTR	-0.056	0.003	-0.069	0.002	hypo
cg21532512	ELMO1	7	37114000	37114355	Body	-0.056	0.016	-0.078	0.040	hypo
cg23008606	ADRA1A	8	26722485	26722995	TSS200	-0.059	0.009	-0.064	0.035	hypo
cg24160354	PPARGC1A	4	23865508	23867708	Body	0.061	0.023	0.105	0.023	Hyper
cg26700447	CCKBR				Body	0.059	0.011	0.083	0.015	Hyper
cg27631597	IQGAP2	5	75903265	75903530	Body	-0.059	0.010	-0.087	0.018	hypo

19 F1 DMSs showed concordant alterations in F2 cohort were identified by using Illumina Infinium Human Methylation 850K chip. The hypomethylated and hypermethylated DMPs are highlighted with $-\Delta\beta$ and $+\Delta\beta$, respectively. $\Delta\beta$ refers to the difference in mean methylation β (β -values) between famine group and non-famine group. Chr, chromosome.

Supplementary Table 5. Target bisulfate sequencing for cg13528513, cg20906621 and cg17160506 in both generations.

Product	Chr	Position	Genome Position	Gene Symbol	PrimerF	PrimerR	F1 generation		F2 generation	
							Methylation ($\Delta\beta$)	P-value	Methylation ($\Delta\beta$)	P-value
cg13528513	3	136	148418461	AGTR1	GTGTTGGAAG TTGATTGTGA GTTT	ATTTACCTAACC CTTTTCTAATCA ATC	-0.059	0.024	-0.057	0.020
cg20906621	3	42	148416430	AGTR1	TTGGTTAAGG TTGGAGTGATG TT	ACAATTCAATAA ACTTCTTCCTA AAAC	-0.078	0.015	-0.062	0.033
cg17160506	17	85	64649540	PRKCA	AGTTTGTAGTT TTTAGGAAGTT GAGTGG	AACCTCCTAAAT AACTAAACTAC AAATACAC	-0.071	0.022	-0.066	0.019

The hypomethylated and hypermethylated DMPs are highlighted with $-\Delta\beta$ and $+\Delta\beta$, respectively. $\Delta\beta$ refers to the difference in mean methylation β (β -values) between famine group and non-famine group. Chr, chromosome. PrimerF, forward primer sequence. PrimerR, reverse primer sequence.