

DNA Methylation of TXNIP Independently Associated with Inflammation and Diabetes

Mellitus in Twins

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Supplementary Table S1. Association of methylation at *TXNIP*-cg19693031 with log-transformed inflammatory biomarkers among monozygotic twins. The associations were examined in twin-specific models using individual deviation from the twin-pair average (within-pair effect), and twins-as-individual models.

Phenotype	N	Within-Pair Methylation			Individual Methylation		
		Beta	SE	P-value*	Beta	SE	P-value*
Log - transformed							
ICAM-1 (ng/ml)	215	-0.0285	6.36×10 ⁻³	2.12×10⁻⁵	-0.0183	4.35×10 ⁻³	5.94×10⁻⁵
VCAM-1 (ng/ml)	215	-0.0240	8.92×10 ⁻³	8.42×10⁻³	-0.0223	5.51×10 ⁻³	1.03×10⁻⁴
MMP-2 (ng/ml)	215	-0.0129	4.57×10 ⁻³	5.84×10⁻³	-0.0116	2.88×10 ⁻³	1.07×10⁻⁴
P-selectin (ng/ml)	215	-0.0168	6.56×10 ⁻³	0.0119	-0.0102	4.82×10 ⁻³	0.0378
IL-6 (pg/mL)	212	6.10×10 ⁻³	0.0196	0.756	9.19×10 ⁻⁴	0.0114	0.936
High-sensitivity CRP (mg/L)	214	-1.25×10 ⁻³	0.0318	0.969	3.99×10 ⁻³	0.0167	0.811
sRAGE (pg/mL)	212	-0.0115	9.66×10 ⁻³	0.239	-0.0137	6.26×10 ⁻³	0.0312
Fibrinogen (mg/dL)	198	-4.68×10 ⁻³	6.51×10 ⁻³	0.474	1.63×10 ⁻³	3.90×10 ⁻³	0.678
MMP-9 (ng/ml)	215	0.0121	0.0145	0.406	-2.99×10 ⁻³	8.24×10 ⁻³	0.717

* Bonferroni correction for multiple testing was used (p-value <0.005).

P-value are calculated from linear mixed models with log transformed inflammatory biomarkers as the dependent variable.

The analysis for each inflammatory biomarker is adjusted for BMI, current smoking status, age and proportions of PBL subtypes (B cells, granulocytes, monocytes, NK cells, and T cells).

Phenotypes are displayed in the same order as in the table 2.

The effect size is based on 0.01 units (1%) difference in DNA methylation.