Sup. Table 2: Correlation between paternal stress during preschool and increased DNA methylation in adolescence in full sample (all CpG sites with FDR <20%). Sites with greater than 5% differential methylation are highlighted in grey.

Gene	CpG Site	Slope	Range	Differential Methylation	Spearman ρ	FDR
TK1	cg22061523	0.039	0.093	0.028	0.447	0.000
MGC42630	cg22543128	0.058	0.130	0.041	0.418	0.000
PGA5	cg11957986	0.113	0.482	0.080	0.394	17.619
SFRP1	cg22418909	0.016	0.049	0.011	0.389	17.619
IL28RA	cg07509155	0.020	0.062	0.014	0.388	17.619
DCN	cg04088433	0.195	0.489	0.138	0.384	17.619
LRRC8D	cg26783856	0.027	0.057	0.019	0.381	17.619
GALNT8	cg14920334	0.141	0.762	0.100	0.374	17.619
ATP8A2	cg12111714	0.069	0.141	0.049	0.367	17.619
FSTL3	cg10503234	0.077	0.185	0.055	0.362	17.619
EIF3S2	cg26093687	0.057	0.175	0.040	0.361	17.619
PRB4	cg14076161	0.086	0.213	0.061	0.361	17.619
OCM	cg22152667	0.023	0.053	0.016	0.360	17.619
PPP1R3C	cg09775312	0.044	0.135	0.031	0.359	17.619
IGF2AS	cg25574024	0.117	0.782	0.083	0.357	17.619
TNFRSF13B	cg18152830	0.031	0.061	0.022	0.357	17.619
OTUB2	cg22981461	0.042	0.098	0.029	0.357	17.619
KCNA5	cg24605304	0.021	0.060	0.015	0.357	17.619
AKR1A1	cg11323731	0.020	0.071	0.014	0.357	17.619
CDH9	cg19475870	0.139	0.270	0.099	0.354	17.619
MYOD1	cg24322623	0.021	0.049	0.015	0.351	17.619
PAPPA2	cg10994126	0.087	0.233	0.061	0.350	17.619
MGC50811	cg10498097	0.046	0.106	0.033	0.349	18.898
RUNX3	cg25178645	0.014	0.027	0.010	0.348	18.898
PLSCR2	cg03075662	0.074	0.188	0.052	0.348	18.898
CHFR	cg17387870	0.081	0.214	0.057	0.345	18.898
WISP1	cg03670238	0.135	0.293	0.095	0.345	18.898
APH1B	cg17207590	0.053	0.142	0.038	0.344	18.898
SSTR1	cg27590397	0.016	0.070	0.011	0.343	18.898
ZNF124	cg21918500	0.059	0.217	0.042	0.343	18.898
FLJ21820	cg02946570	0.184	0.385	0.131	0.342	18.898

Note. FDR = false discovery rate (%). Slope = slope of least squared line. Range = range of average beta.