Table S1 Univariate and multivariate analyses of variables associated with overall survival

Characteristics	Number of patients	Univariate analysis		Multivariable analysis	
		HR (95% CI)	P value	HR (95% CI)	P value
Risk (High *vs.* low)	350	1.729 (1.242, 2.407)	0.001	1.614 (1.138, 2.290)	0.007
Pathologic T stage (T3/4 *vs.* T1/2)	346	1.643 (1.088, 2.481)	0.018	1.217 (0.774, 1.913)	0.395
Pathologic N stage (N1/2/3 *vs.* N0)	339	1.805 (1.199, 2.716)	0.005	1.703 (1.100, 2.638)	0.017
Pathologic M stage (M1 *vs.* M0)	335	2.051 (1.157, 3.636)	0.014	2.060 (1.140, 3.722)	0.017
Age (>60 *vs.* ≤60)	347	1.531 (1.060, 2.212)	0.023	1.649 (1.119, 2.431)	0.012
Sex (male *vs.* female)	350	1.324 (0.930, 1.890)	0.119		

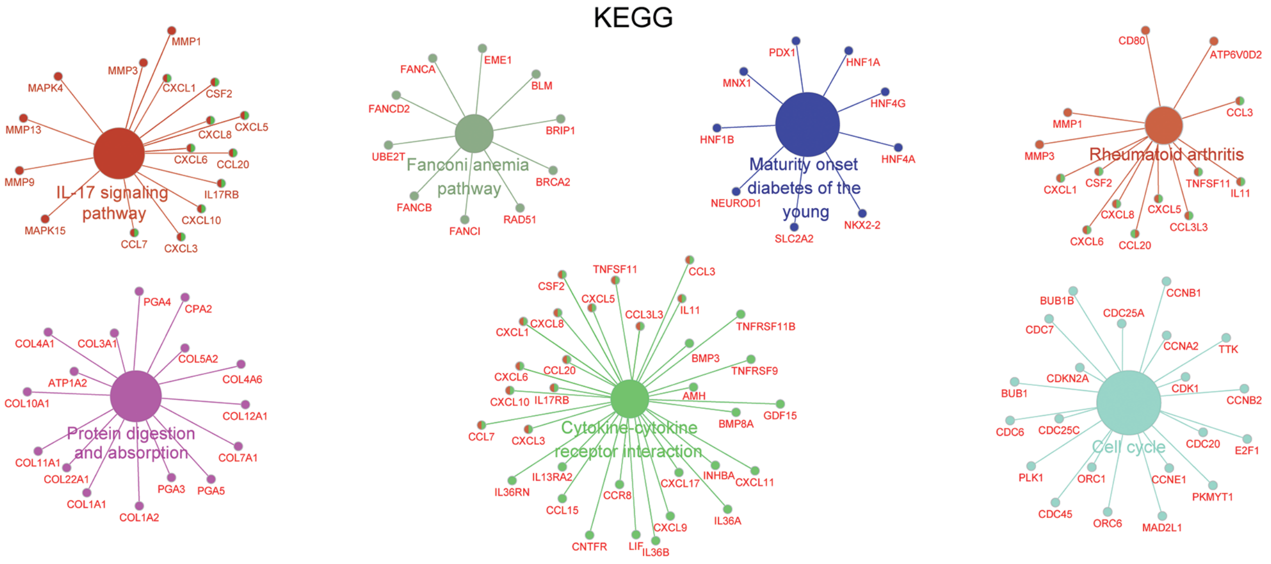

Figure S1 KEGG enrichment results for DEGs.

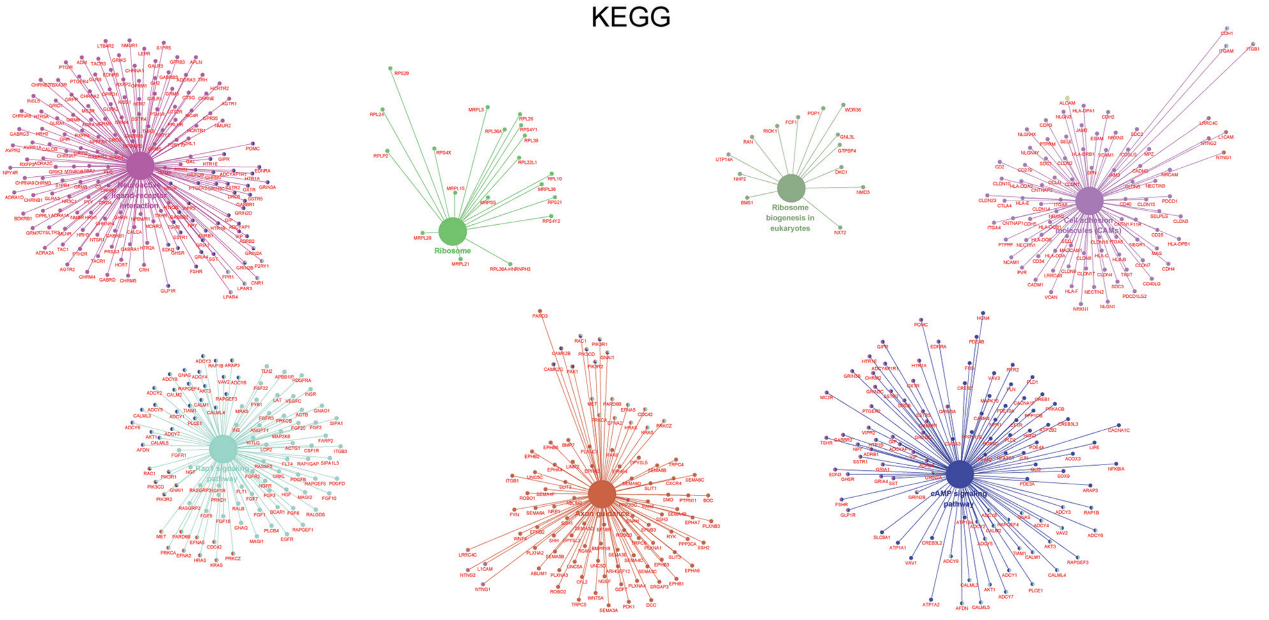

Figure S2 KEGG enrichment results for DMGs.

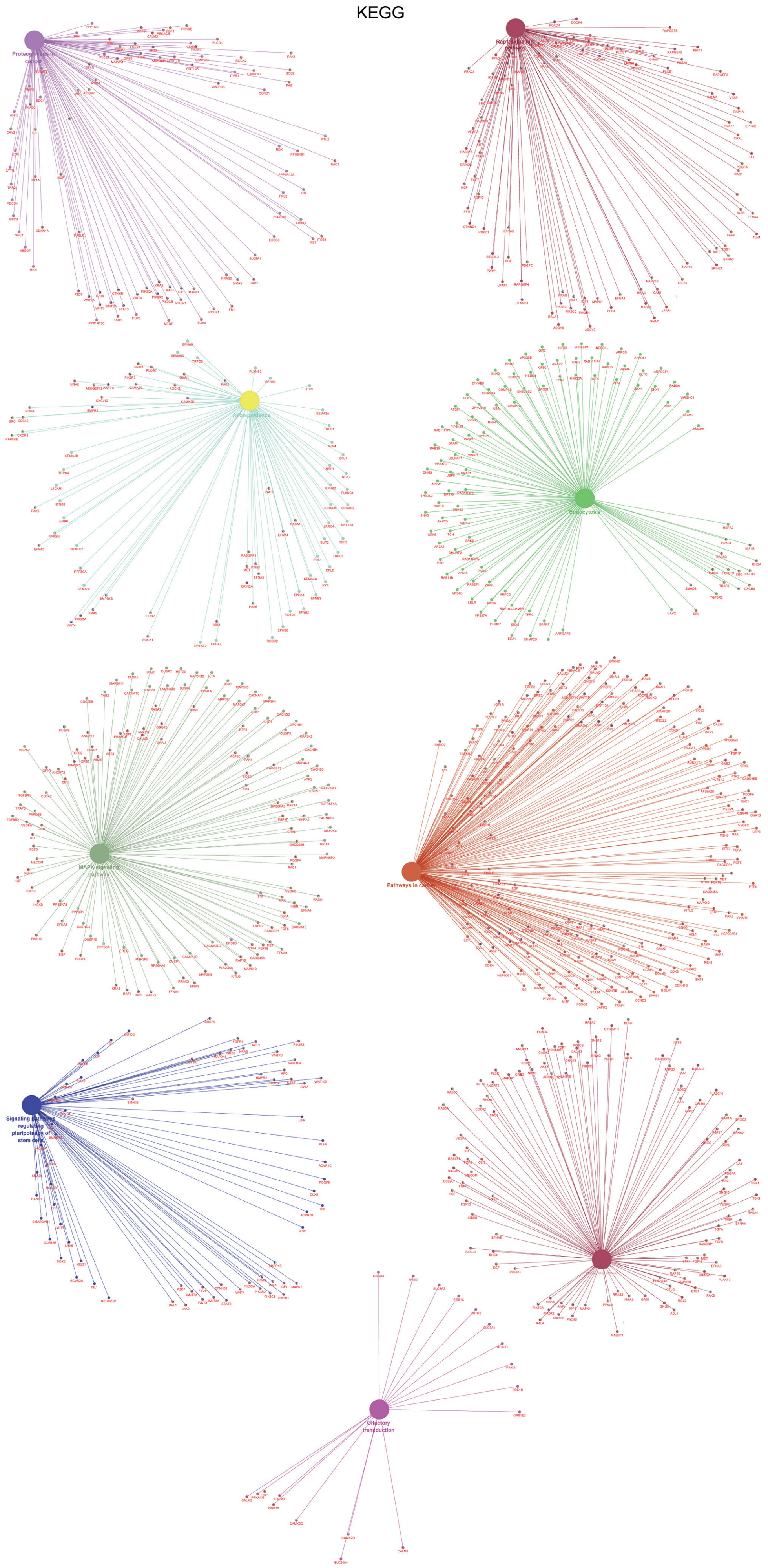

Figure S3 KEGG enrichment results for miRNA target genes.

https://dx.doi.org/10.21037/atm-21-3211

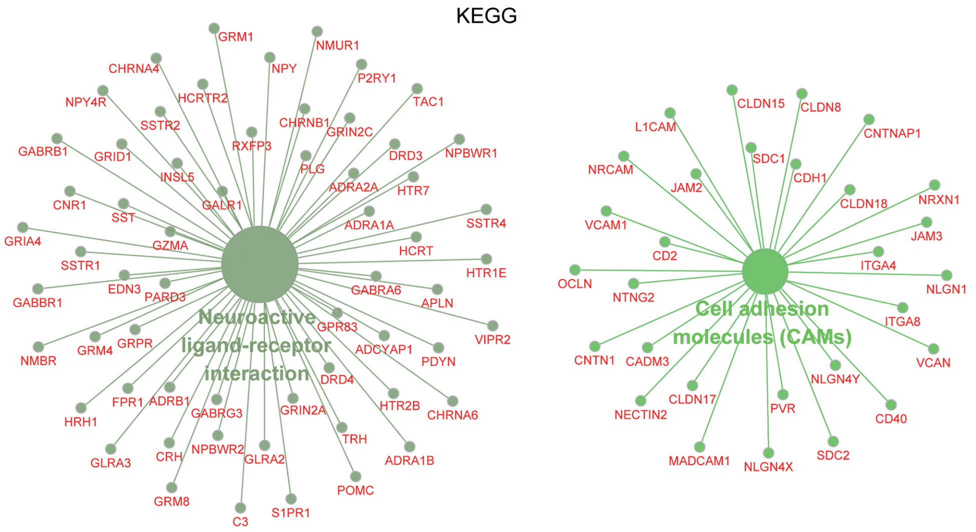

Figure S4 KEGG enrichment results for differential promoter methylation.

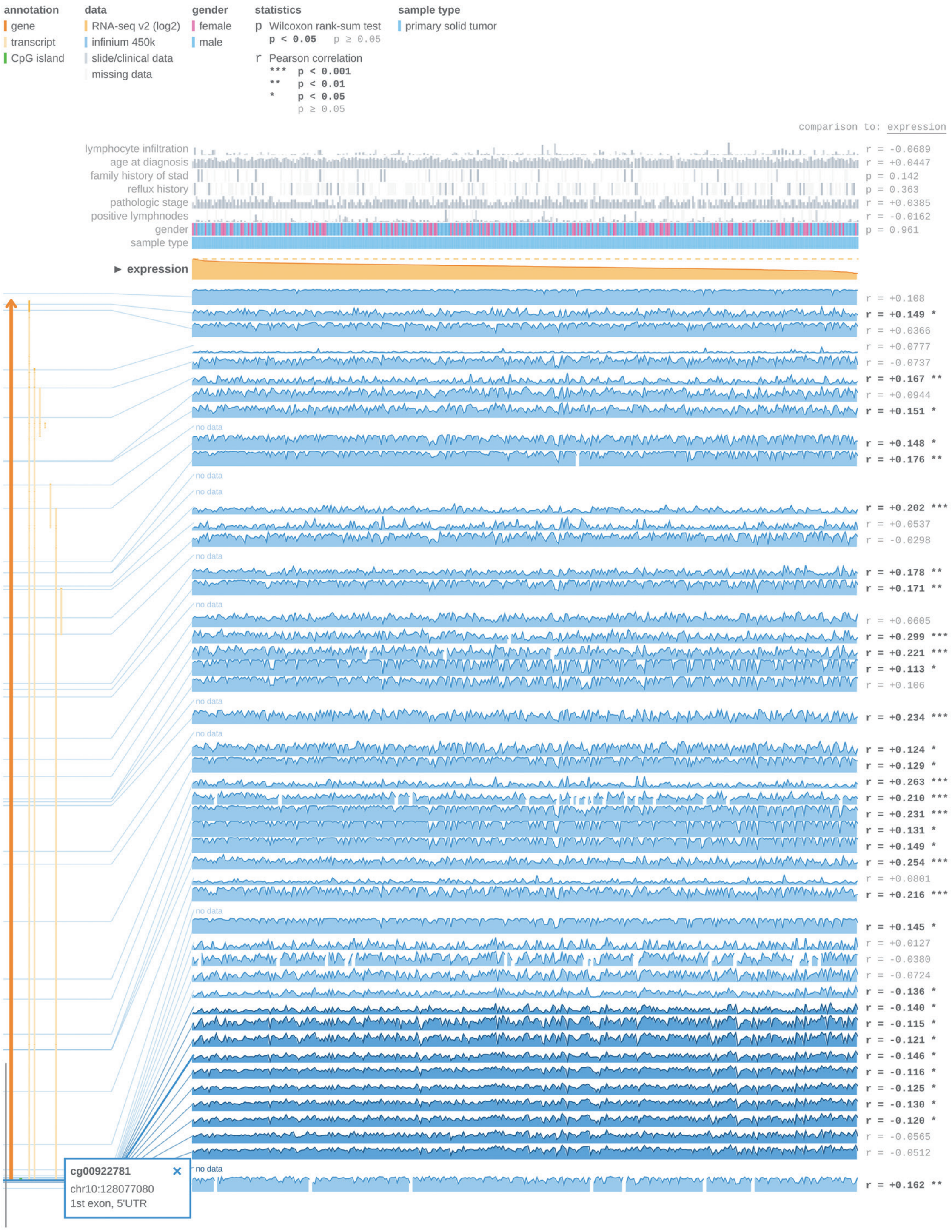

Figure S5 Correlation analysis for ADAM12 methylation locus and expression.

https://dx.doi.org/10.21037/atm-21-3211

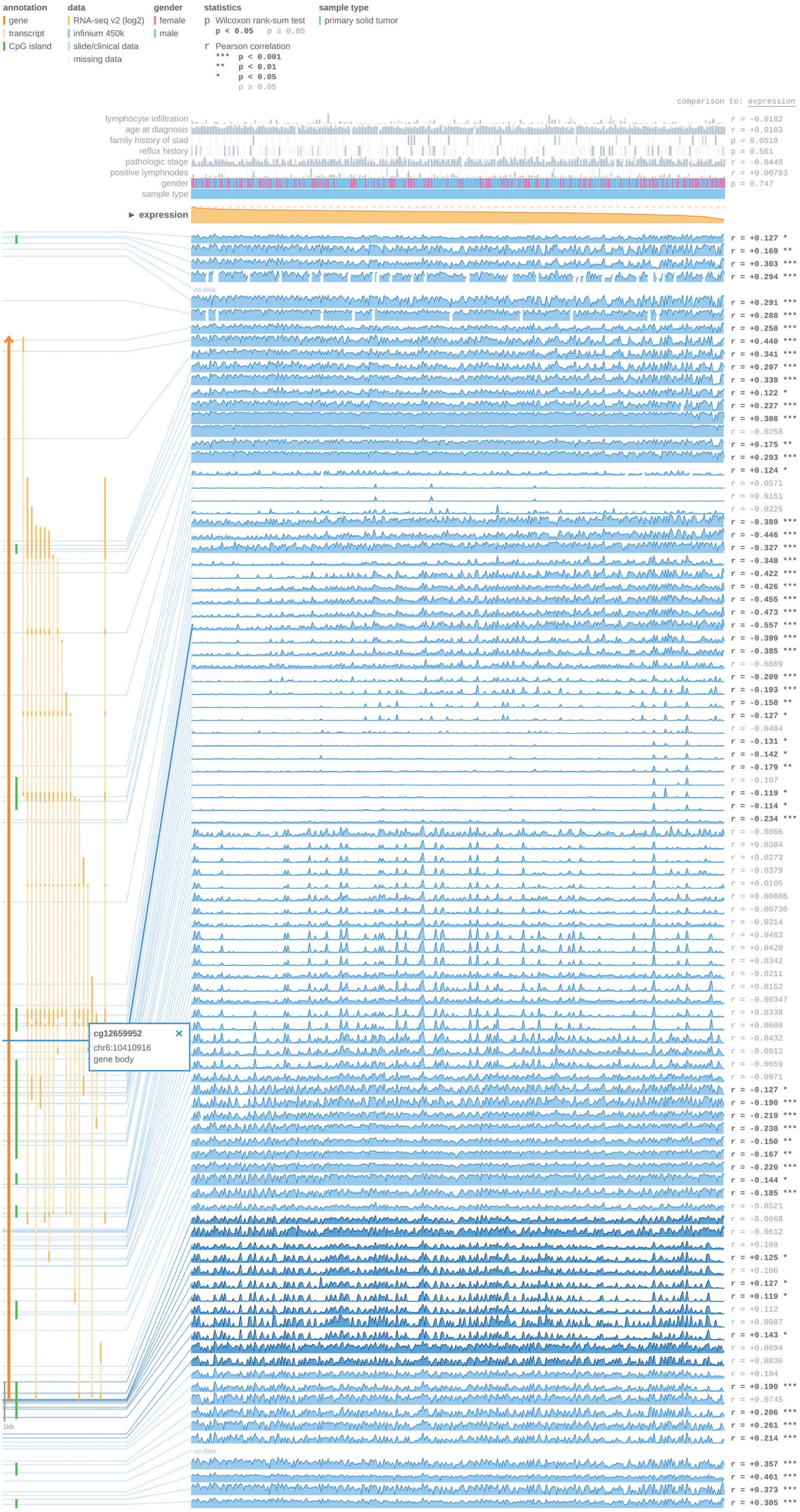

Figure S6 Correlation analysis for TFAP2P methylation locus and expression.

https://dx.doi.org/10.21037/atm-21-3211