

The *Gasdermin E* gene Potential as a Pan-Cancer Biomarker, While Discriminating between Different Tumor Types

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Table S1. Differences in GSDME CpG methylation (β -value) between normal and tumour tissue samples across the 14 different cancer types.

Probe	Mean Diff	Se Diff	KR_p-value	Mean TP	SD mean TP	SEM TP	Mean NT	SD mean NT	SEM NT	Tumour Type
cg17790129	-1.19E-01	2.96E-02	3.31E-04*	7.63E-01	2.11E-01	1.03E-02	8.92E-01	2.29E-02	5.00E-03	BLCA
cg14205998	-7.37E-02	1.93E-02	6.77E-04*	8.10E-01	1.92E-01	9.42E-03	9.33E-01	1.32E-02	2.88E-03	BLCA
cg04317854	-3.01E-02	3.05E-02	3.36E-01	6.87E-01	1.96E-01	9.58E-03	7.21E-01	7.54E-02	1.65E-02	BLCA
cg12922093	-1.07E-01	2.85E-02	7.08E-04*	7.12E-01	1.98E-01	9.69E-03	8.49E-01	3.27E-02	7.13E-03	BLCA
cg17569154	-1.19E-01	3.87E-02	4.02E-03*	5.71E-01	2.24E-01	1.10E-02	7.45E-01	9.99E-02	2.18E-02	BLCA
cg19260663	-1.31E-01	2.94E-02	8.91E-05*	7.38E-01	2.03E-01	9.92E-03	9.13E-01	2.95E-02	6.44E-03	BLCA
cg09333471	2.33E-03	1.93E-02	9.05E-01	2.10E-01	1.35E-01	6.58E-03	2.03E-01	5.29E-02	1.15E-02	BLCA
cg00473134	6.60E-03	1.18E-02	5.83E-01	1.06E-01	1.16E-01	5.66E-03	7.61E-02	3.05E-02	6.65E-03	BLCA
cg03995857	4.37E-02	2.05E-02	4.25E-02*	1.45E-01	1.51E-01	7.36E-03	9.67E-02	3.61E-02	7.87E-03	BLCA
cg07320646	4.39E-02	2.54E-02	9.58E-02	9.55E-02	1.86E-01	9.08E-03	3.31E-02	2.24E-02	4.89E-03	BLCA
cg07293520	1.63E-02	1.37E-02	2.48E-01	7.63E-02	1.36E-01	6.66E-03	3.83E-02	3.86E-02	8.42E-03	BLCA
cg04770504	5.16E-02	1.85E-02	9.37E-03*	9.72E-02	1.54E-01	7.54E-03	2.35E-02	1.15E-02	2.51E-03	BLCA
cg24805239	5.96E-02	2.22E-02	1.16E-02*	1.37E-01	1.46E-01	7.16E-03	7.32E-02	3.20E-02	6.99E-03	BLCA
cg01733570	-2.17E-02	2.76E-02	4.43E-01	4.38E-01	1.80E-01	8.79E-03	4.73E-01	5.34E-02	1.17E-02	BLCA
cg25723149	1.91E-02	3.16E-02	5.54E-01	4.14E-01	1.91E-01	9.34E-03	4.07E-01	5.97E-02	1.30E-02	BLCA
cg22804000	1.92E-03	2.85E-02	9.47E-01	3.88E-01	1.75E-01	8.55E-03	4.15E-01	4.61E-02	1.01E-02	BLCA
cg07504598	1.15E-01	2.92E-02	3.09E-04*	6.15E-01	1.62E-01	7.91E-03	5.17E-01	6.34E-02	1.38E-02	BLCA
cg15037663	6.80E-02	2.79E-02	2.05E-02*	6.75E-01	1.60E-01	7.81E-03	6.44E-01	5.12E-02	1.12E-02	BLCA

cg19706795	5.78E-02	2.09E-02	9.47E-03*	7.68E-01	1.34E-01	6.55E-03	7.29E-01	3.84E-02	8.39E-03	BLCA
cg20764575	4.65E-02	2.43E-02	6.66E-02	7.68E-01	1.26E-01	6.16E-03	7.20E-01	4.70E-02	1.03E-02	BLCA
cg06301139	-2.89E-02	1.05E-02	1.06E-02*	8.82E-01	1.13E-01	5.52E-03	9.40E-01	1.28E-02	2.80E-03	BLCA
cg26712096	-9.12E-02	2.30E-02	4.45E-04*	7.60E-01	2.02E-01	9.90E-03	9.14E-01	1.81E-02	3.94E-03	BLCA
Probe	Mean Diff	Se Diff	KR_p-value	Mean TP	SD mean TP	SEM TP	Mean NT	SD mean NT	SEM NT	Tumour Type
cg17790129	-1.18E-01	1.98E-02	1.47E-08*	7.62E-01	2.37E-01	8.43E-03	9.02E-01	3.88E-02	3.96E-03	BRCA
cg14205998	-1.27E-01	1.96E-02	5.72E-10*	7.90E-01	2.12E-01	7.54E-03	9.23E-01	2.11E-02	2.16E-03	BRCA
cg04317854	-8.05E-02	1.84E-02	1.98E-05*	7.42E-01	1.95E-01	6.92E-03	8.35E-01	5.91E-02	6.03E-03	BRCA
cg12922093	-1.86E-01	1.95E-02	2.65E-18*	6.73E-01	2.15E-01	7.64E-03	8.72E-01	3.74E-02	3.82E-03	BRCA
cg17569154	-1.69E-01	1.80E-02	2.00E-17*	6.85E-01	2.11E-01	7.52E-03	8.63E-01	6.18E-02	6.31E-03	BRCA
cg19260663	-1.75E-01	1.86E-02	2.69E-18*	7.41E-01	2.00E-01	7.10E-03	9.24E-01	2.12E-02	2.16E-03	BRCA
cg09333471	1.62E-01	1.53E-02	3.82E-22*	3.41E-01	1.62E-01	5.76E-03	1.86E-01	6.62E-02	6.75E-03	BRCA
cg00473134	1.32E-01	1.50E-02	9.90E-17*	2.01E-01	1.54E-01	5.49E-03	7.25E-02	2.91E-02	2.97E-03	BRCA
cg03995857	1.98E-01	2.07E-02	3.74E-19*	2.81E-01	2.15E-01	7.66E-03	8.41E-02	3.88E-02	3.96E-03	BRCA
cg07320646	1.57E-01	2.28E-02	5.50E-11*	1.85E-01	2.47E-01	8.77E-03	2.33E-02	1.57E-02	1.60E-03	BRCA
cg07293520	9.66E-02	1.44E-02	2.57E-10*	1.31E-01	1.73E-01	6.14E-03	2.68E-02	1.03E-02	1.05E-03	BRCA
cg04770504	1.54E-01	1.71E-02	5.75E-17*	1.82E-01	1.87E-01	6.66E-03	1.99E-02	1.27E-02	1.30E-03	BRCA
cg24805239	1.71E-01	1.69E-02	1.23E-20*	2.30E-01	1.80E-01	6.39E-03	5.85E-02	2.69E-02	2.74E-03	BRCA
cg01733570	1.09E-01	1.99E-02	1.10E-07*	5.06E-01	2.07E-01	7.38E-03	3.99E-01	1.01E-01	1.04E-02	BRCA
cg25723149	1.98E-01	1.98E-02	5.49E-20*	4.86E-01	2.12E-01	7.52E-03	2.84E-01	9.26E-02	9.45E-03	BRCA
cg22804000	1.46E-01	1.82E-02	4.88E-14*	4.32E-01	1.98E-01	7.03E-03	2.83E-01	6.03E-02	6.16E-03	BRCA
cg07504598	1.99E-01	1.72E-02	1.03E-24*	6.00E-01	1.90E-01	6.75E-03	3.98E-01	7.74E-02	7.90E-03	BRCA
cg15037663	1.35E-01	1.91E-02	1.22E-11*	6.02E-01	1.99E-01	7.09E-03	4.72E-01	7.67E-02	7.83E-03	BRCA
cg19706795	1.08E-01	1.77E-02	3.21E-09*	6.66E-01	1.84E-01	6.53E-03	5.61E-01	6.99E-02	7.14E-03	BRCA

cg2076 4575	1.73E-01	1.75E-02	1.97E-20*	6.61E-01	1.80E-01	6.39E-03	4.87E-01	6.54E-02	6.68E-03	BRCA
cg0630 1139	-6.64E-02	1.41E-02	4.47E-06*	8.41E-01	1.53E-01	5.45E-03	9.10E-01	2.70E-02	2.75E-03	BRCA
cg2671 2096	-1.91E-01	2.06E-02	7.82E-18*	7.29E-01	2.21E-01	7.86E-03	9.26E-01	1.59E-02	1.62E-03	BRCA
Probe	Mean Diff	Se Diff	KR_p-value	Mean TP	SD mean TP	SEM TP	Mean NT	SD mean NT	SEM NT	Tumour Type
cg1779 0129	-9.19E-02	2.06E-02	1.94E-05*	8.30E-01	1.54E-01	7.62E-03	9.15E-01	2.38E-02	3.55E-03	CRC
cg1420 5998	-1.25E-01	2.09E-02	4.13E-08*	8.00E-01	1.74E-01	8.60E-03	9.28E-01	2.46E-02	3.66E-03	CRC
cg0431 7854	-4.26E-02	1.59E-02	9.06E-03*	7.92E-01	1.21E-01	5.97E-03	8.43E-01	4.75E-02	7.08E-03	CRC
cg1292 2093	-1.78E-01	2.04E-02	1.18E-13*	6.68E-01	1.80E-01	8.90E-03	8.41E-01	3.21E-02	4.79E-03	CRC
cg1756 9154	-8.54E-02	2.61E-02	1.48E-03*	5.54E-01	1.89E-01	9.32E-03	6.32E-01	1.03E-01	1.54E-02	CRC
cg1926 0663	-9.71E-02	2.00E-02	3.82E-06*	8.02E-01	1.51E-01	7.47E-03	9.00E-01	2.84E-02	4.23E-03	CRC
cg0933 3471	1.84E-01	2.33E-02	2.74E-12*	4.83E-01	1.90E-01	9.39E-03	3.09E-01	4.27E-02	6.36E-03	CRC
cg0047 3134	2.35E-01	2.22E-02	1.01E-17*	3.33E-01	1.95E-01	9.62E-03	1.15E-01	2.73E-02	4.07E-03	CRC
cg0399 5857	3.93E-01	2.72E-02	1.71E-25*	4.97E-01	2.41E-01	1.19E-02	1.40E-01	4.51E-02	6.73E-03	CRC
cg0732 0646	3.46E-01	3.98E-02	6.49E-15*	3.68E-01	2.94E-01	1.45E-02	2.41E-02	9.54E-03	1.42E-03	CRC
cg0729 3520	2.46E-01	2.97E-02	4.73E-13*	2.77E-01	2.46E-01	1.21E-02	2.72E-02	4.87E-03	7.26E-04	CRC
cg0477 0504	2.94E-01	2.50E-02	6.59E-22*	3.18E-01	1.94E-01	9.58E-03	2.10E-02	3.77E-03	5.62E-04	CRC
cg2480 5239	3.09E-01	2.80E-02	7.87E-20*	3.97E-01	2.22E-01	1.10E-02	8.64E-02	1.85E-02	2.75E-03	CRC
cg0173 3570	1.11E-01	2.81E-02	1.34E-04*	5.92E-01	2.09E-01	1.03E-02	4.82E-01	4.51E-02	6.73E-03	CRC
cg2572 3149	1.08E-01	2.62E-02	8.02E-05*	6.31E-01	1.99E-01	9.82E-03	5.27E-01	4.88E-02	7.27E-03	CRC
cg2280 4000	1.08E-01	2.58E-02	5.79E-05*	5.66E-01	1.95E-01	9.63E-03	4.57E-01	4.30E-02	6.41E-03	CRC
cg0750 4598	1.09E-01	2.16E-02	2.13E-06*	6.76E-01	1.73E-01	8.56E-03	5.66E-01	4.64E-02	6.92E-03	CRC
cg1503 7663	6.53E-02	2.47E-02	9.59E-03*	6.26E-01	1.72E-01	8.50E-03	5.57E-01	5.67E-02	8.45E-03	CRC
cg1970 6795	7.06E-02	1.97E-02	4.67E-04*	7.11E-01	1.34E-01	6.64E-03	6.38E-01	6.08E-02	9.07E-03	CRC
cg2076 4575	2.88E-02	1.38E-02	4.00E-02*	8.04E-01	9.26E-02	4.57E-03	7.75E-01	3.61E-02	5.38E-03	CRC

cg0630-1139	-9.22E-02	1.67E-02	3.30E-07*	8.04E-01	1.46E-01	7.19E-03	9.02E-01	3.36E-02	5.02E-03	CRC
cg2671-2096	-1.23E-01	2.76E-02	1.93E-05*	4.60E-01	2.01E-01	9.92E-03	5.72E-01	1.11E-01	1.65E-02	CRC
Probe	Mean Diff	Se Diff	KR_p-value	Mean TP	SD mean TP	SEM TP	Mean NT	SD mean NT	SEM NT	Tumour Type
cg1779-0129	3.07E-02	3.81E-02	4.46E-01	8.01E-01	1.53E-01	1.13E-02	7.48E-01	1.09E-01	2.72E-02	ESCA
cg1420-5998	-2.12E-02	2.39E-02	3.97E-01	8.69E-01	1.22E-01	8.95E-03	8.64E-01	1.67E-01	4.17E-02	ESCA
cg0431-7854	1.02E-01	3.13E-02	2.42E-03*	7.96E-01	1.23E-01	9.04E-03	6.94E-01	7.79E-02	1.95E-02	ESCA
cg1292-2093	-5.78E-02	2.89E-02	6.24E-02	7.84E-01	1.32E-01	9.70E-03	8.16E-01	1.07E-01	2.67E-02	ESCA
cg1756-9154	-1.03E-01	5.63E-02	8.57E-02	6.94E-01	2.28E-01	1.68E-02	7.51E-01	2.28E-01	5.71E-02	ESCA
cg1926-0663	-7.89E-02	2.63E-02	7.16E-03*	8.23E-01	1.29E-01	9.51E-03	8.75E-01	6.19E-02	1.55E-02	ESCA
cg0933-3471	1.35E-01	4.75E-02	1.01E-02*	3.26E-01	2.25E-01	1.65E-02	2.77E-01	1.77E-01	4.43E-02	ESCA
cg0047-3134	1.57E-01	5.09E-02	5.22E-03*	2.18E-01	2.25E-01	1.65E-02	1.07E-01	9.73E-02	2.43E-02	ESCA
cg0399-5857	2.25E-01	6.57E-02	2.20E-03*	3.02E-01	2.94E-01	2.16E-02	1.70E-01	2.22E-01	5.55E-02	ESCA
cg0732-0646	2.35E-01	7.70E-02	5.19E-03*	2.72E-01	3.23E-01	2.38E-02	1.09E-01	2.39E-01	5.99E-02	ESCA
cg0729-3520	2.18E-01	6.45E-02	2.28E-03*	2.42E-01	2.78E-01	2.05E-02	8.79E-02	1.75E-01	4.38E-02	ESCA
cg0477-0504	1.52E-01	5.38E-02	9.37E-03*	1.93E-01	2.23E-01	1.64E-02	8.36E-02	1.75E-01	4.38E-02	ESCA
cg2480-5239	1.78E-01	5.83E-02	5.43E-03*	2.50E-01	2.52E-01	1.86E-02	1.41E-01	1.86E-01	4.64E-02	ESCA
cg0173-3570	7.08E-02	5.09E-02	1.88E-01	5.04E-01	2.37E-01	1.74E-02	4.85E-01	1.29E-01	3.24E-02	ESCA
cg2572-3149	2.67E-02	5.05E-02	6.11E-01	4.44E-01	2.59E-01	1.90E-02	5.01E-01	1.65E-01	4.13E-02	ESCA
cg2280-4000	5.19E-03	4.71E-02	9.16E-01	4.19E-01	2.33E-01	1.71E-02	4.92E-01	1.43E-01	3.57E-02	ESCA
cg0750-4598	8.76E-02	3.40E-02	1.96E-02*	5.73E-01	1.93E-01	1.42E-02	5.56E-01	1.66E-01	4.15E-02	ESCA
cg1503-7663	2.22E-02	3.42E-02	5.34E-01	6.27E-01	1.75E-01	1.29E-02	6.26E-01	1.31E-01	3.26E-02	ESCA
cg1970-6795	1.79E-02	2.93E-02	5.58E-01	7.21E-01	1.47E-01	1.08E-02	7.12E-01	1.41E-01	3.52E-02	ESCA
cg2076-4575	2.72E-02	2.98E-02	3.81E-01	7.05E-01	1.60E-01	1.18E-02	7.13E-01	1.73E-01	4.32E-02	ESCA
cg0630-1139	-4.62E-02	1.51E-02	7.13E-03*	8.83E-01	1.00E-01	7.38E-03	8.94E-01	1.26E-01	3.16E-02	ESCA

cg2671 2096	-4.39E-02	4.87E-02	3.95E-01	7.94E-01	1.85E-01	1.36E-02	8.24E-01	2.32E-01	5.81E-02	ESCA
Probe	Mean Diff	Se Diff	KR_p-value	Mean TP	SD mean TP	SEM TP	Mean NT	SD mean NT	SEM NT	Tumour Type
cg1779 0129	-1.20E-03	1.06E-02	9.12E-01	8.89E-01	7.96E-02	3.46E-03	8.89E-01	4.39E-02	6.21E-03	HNSC
cg1420 5998	-9.46E-03	4.39E-03	3.57E-02*	9.18E-01	4.57E-02	1.99E-03	9.33E-01	1.37E-02	1.94E-03	HNSC
cg0431 7854	8.57E-02	1.27E-02	7.40E-11*	8.22E-01	8.71E-02	3.79E-03	7.37E-01	6.68E-02	9.45E-03	HNSC
cg1292 2093	-3.79E-02	9.97E-03	2.91E-04*	8.27E-01	8.51E-02	3.70E-03	8.70E-01	3.91E-02	5.53E-03	HNSC
cg1756 9154	-2.04E-01	2.55E-02	4.14E-14*	7.18E-01	1.82E-01	7.91E-03	9.20E-01	3.23E-02	4.56E-03	HNSC
cg1926 0663	3.53E-03	6.02E-03	5.63E-01	9.03E-01	5.60E-02	2.44E-03	9.03E-01	3.21E-02	4.54E-03	HNSC
cg0933 3471	-8.10E-03	1.16E-02	4.94E-01	1.84E-01	8.13E-02	3.54E-03	1.92E-01	4.19E-02	5.92E-03	HNSC
cg0047 3134	-1.12E-02	3.95E-03	5.94E-03*	6.47E-02	3.33E-02	1.45E-03	7.65E-02	1.67E-02	2.37E-03	HNSC
cg0399 5857	-7.61E-03	2.66E-03	6.11E-03*	7.85E-02	3.54E-02	1.54E-03	8.52E-02	1.64E-02	2.32E-03	HNSC
cg0732 0646	-2.07E-04	6.50E-04	7.52E-01	2.45E-02	4.07E-02	1.77E-03	2.11E-02	3.50E-03	4.95E-04	HNSC
cg0729 3520	-3.06E-03	1.37E-03	3.02E-02*	2.92E-02	3.91E-02	1.70E-03	2.91E-02	9.08E-03	1.28E-03	HNSC
cg0477 0504	3.14E-03	2.49E-03	2.13E-01	2.33E-02	3.60E-02	1.57E-03	1.74E-02	2.53E-03	3.58E-04	HNSC
cg2480 5239	-1.28E-03	6.01E-03	8.34E-01	6.53E-02	4.21E-02	1.83E-03	6.66E-02	1.73E-02	2.44E-03	HNSC
cg0173 3570	-1.51E-02	2.15E-02	4.91E-01	3.45E-01	1.46E-01	6.37E-03	3.60E-01	1.35E-01	1.90E-02	HNSC
cg2572 3149	4.25E-03	1.93E-02	8.29E-01	2.75E-01	1.32E-01	5.75E-03	2.71E-01	1.16E-01	1.64E-02	HNSC
cg2280 4000	5.29E-03	1.87E-02	7.81E-01	2.60E-01	1.27E-01	5.52E-03	2.54E-01	1.20E-01	1.69E-02	HNSC
cg0750 4598	1.33E-01	2.52E-02	3.49E-07*	4.79E-01	1.77E-01	7.68E-03	3.47E-01	1.30E-01	1.84E-02	HNSC
cg1503 7663	1.44E-01	2.64E-02	1.30E-07*	5.62E-01	1.83E-01	7.97E-03	4.18E-01	1.20E-01	1.70E-02	HNSC
cg1970 6795	1.63E-01	2.55E-02	6.45E-10*	6.66E-01	1.75E-01	7.62E-03	5.03E-01	1.39E-01	1.97E-02	HNSC
cg2076 4575	1.76E-01	2.74E-02	6.98E-10*	6.20E-01	1.89E-01	8.23E-03	4.45E-01	1.51E-01	2.13E-02	HNSC
cg0630 1139	-4.67E-02	2.02E-02	2.37E-02*	8.66E-01	1.60E-01	6.97E-03	9.20E-01	1.87E-02	2.65E-03	HNSC
Probe	Mean Diff	Se Diff	KR_p-value	Mean TP	SD mean TP	SEM TP	Mean NT	SD mean NT	SEM NT	Tumour Type

cg1779 0129	-8.43E-04	5.48E-03	8.78E-01	9.12E-01	6.85E-02	3.80E-03	9.13E-01	2.03E-02	1.61E-03	KIRC
cg1420 5998	-1.37E-03	1.55E-03	3.80E-01	9.30E-01	2.30E-02	1.28E-03	9.32E-01	2.11E-02	1.66E-03	KIRC
cg0431 7854	3.20E-02	1.20E-02	8.41E-03*	6.32E-01	1.65E-01	9.16E-03	6.09E-01	8.93E-02	7.06E-03	KIRC
cg1292 2093	-1.74E-02	4.40E-03	1.06E-04*	8.77E-01	5.62E-02	3.12E-03	8.95E-01	2.50E-02	1.98E-03	KIRC
cg1756 9154	-7.53E-02	9.36E-03	2.45E-14*	8.68E-01	1.19E-01	6.62E-03	9.43E-01	1.29E-02	1.02E-03	KIRC
cg1926 0663	-1.82E-02	2.53E-03	1.03E-11*	9.08E-01	3.60E-02	2.00E-03	9.31E-01	1.82E-02	1.44E-03	KIRC
cg0933 3471	-4.71E-03	5.44E-03	3.88E-01	1.68E-01	6.14E-02	3.41E-03	1.73E-01	4.83E-02	3.82E-03	KIRC
cg0047 3134	-2.67E-03	1.48E-03	7.37E-02	5.90E-02	1.70E-02	9.46E-04	6.15E-02	1.58E-02	1.25E-03	KIRC
cg0399 5857	1.74E-03	1.52E-03	2.55E-01	7.13E-02	1.79E-02	9.95E-04	6.82E-02	1.54E-02	1.22E-03	KIRC
cg0732 0646	4.10E-04	2.50E-04	1.03E-01	1.88E-02	5.69E-03	3.16E-04	1.59E-02	2.22E-03	1.76E-04	KIRC
cg0729 3520	7.20E-04	4.62E-04	1.22E-01	2.44E-02	5.77E-03	3.21E-04	2.29E-02	5.42E-03	4.28E-04	KIRC
cg0477 0504	8.80E-04	1.01E-03	3.85E-01	1.75E-02	1.25E-02	6.95E-04	1.66E-02	3.74E-03	2.96E-04	KIRC
cg2480 5239	-1.05E-02	2.57E-03	5.95E-05*	5.33E-02	2.80E-02	1.55E-03	6.39E-02	2.38E-02	1.88E-03	KIRC
cg0173 3570	-8.66E-02	1.06E-02	1.10E-14*	3.79E-01	1.31E-01	7.29E-03	4.66E-01	7.40E-02	5.85E-03	KIRC
cg2572 3149	1.66E-02	1.13E-02	1.43E-01	3.54E-01	1.44E-01	8.00E-03	3.38E-01	6.77E-02	5.35E-03	KIRC
cg2280 4000	-2.44E-02	1.06E-02	2.27E-02*	3.11E-01	1.31E-01	7.30E-03	3.36E-01	6.05E-02	4.78E-03	KIRC
cg0750 4598	8.74E-03	9.95E-03	3.81E-01	3.80E-01	1.30E-01	7.21E-03	3.75E-01	7.91E-02	6.25E-03	KIRC
cg1503 7663	-1.54E-02	9.58E-03	1.09E-01	4.48E-01	1.24E-01	6.86E-03	4.64E-01	6.40E-02	5.06E-03	KIRC
cg1970 6795	-1.71E-02	1.03E-02	9.92E-02	5.61E-01	1.35E-01	7.49E-03	5.80E-01	5.98E-02	4.73E-03	KIRC
cg2076 4575	2.81E-02	1.31E-02	3.31E-02*	6.45E-01	1.75E-01	9.72E-03	6.21E-01	6.73E-02	5.32E-03	KIRC
cg0630 1139	-1.24E-02	3.18E-03	1.30E-04*	9.32E-01	4.31E-02	2.39E-03	9.44E-01	1.24E-02	9.77E-04	KIRC
cg2671 2096	-1.20E-02	2.42E-03	1.37E-06*	9.30E-01	3.14E-02	1.74E-03	9.43E-01	1.66E-02	1.31E-03	KIRC
Probe	Mean Diff	Se Diff	KR_p-value	Mean TP	SD mean TP	SEM TP	Mean NT	SD mean NT	SEM NT	Tumour Type
cg1779 0129	8.64E-03	9.58E-03	3.75E-01	9.17E-01	7.89E-02	4.76E-03	9.08E-01	2.28E-02	3.40E-03	KIRP

cg1420 5998	-1.05E-03	1.85E-03	5.75E-01	9.30E-01	1.91E-02	1.15E-03	9.42E-01	1.09E-02	1.63E-03	KIRP
cg0431 7854	2.55E-01	2.12E-02	6.11E-24*	8.12E-01	1.43E-01	8.62E-03	5.58E-01	8.52E-02	1.27E-02	KIRP
cg1292 2093	1.79E-02	6.00E-03	4.00E-03*	8.98E-01	4.19E-02	2.53E-03	8.79E-01	2.83E-02	4.22E-03	KIRP
cg1756 9154	-1.38E-01	2.43E-02	3.35E-07*	7.68E-01	2.09E-01	1.26E-02	9.31E-01	1.81E-02	2.70E-03	KIRP
cg1926 0663	-2.29E-02	7.71E-03	3.96E-03*	9.04E-01	5.23E-02	3.15E-03	9.25E-01	2.82E-02	4.20E-03	KIRP
cg0933 3471	2.85E-03	1.74E-02	8.72E-01	1.75E-01	1.16E-01	6.97E-03	1.72E-01	3.54E-02	5.28E-03	KIRP
cg0047 3134	1.05E-02	1.57E-02	5.11E-01	7.65E-02	1.05E-01	6.32E-03	6.61E-02	1.17E-02	1.75E-03	KIRP
cg0399 5857	1.41E-02	1.64E-02	3.99E-01	9.02E-02	1.10E-01	6.65E-03	7.69E-02	1.24E-02	1.84E-03	KIRP
cg0732 0646	1.24E-02	1.83E-02	5.06E-01	4.25E-02	1.20E-01	7.24E-03	3.01E-02	6.35E-02	9.47E-03	KIRP
cg0729 3520	1.94E-02	1.54E-02	2.17E-01	4.26E-02	1.03E-01	6.23E-03	2.32E-02	4.53E-03	6.75E-04	KIRP
cg0477 0504	1.42E-02	1.19E-02	2.41E-01	3.12E-02	7.95E-02	4.79E-03	1.70E-02	3.11E-03	4.63E-04	KIRP
cg2480 5239	6.78E-03	1.46E-02	6.48E-01	6.90E-02	9.76E-02	5.89E-03	6.22E-02	1.69E-02	2.52E-03	KIRP
cg0173 3570	-4.55E-03	3.03E-02	8.83E-01	4.17E-01	2.02E-01	1.22E-02	4.22E-01	6.05E-02	9.02E-03	KIRP
cg2572 3149	4.42E-02	2.93E-02	1.39E-01	3.63E-01	1.95E-01	1.18E-02	3.19E-01	5.53E-02	8.24E-03	KIRP
cg2280 4000	3.40E-02	2.88E-02	2.47E-01	3.46E-01	1.92E-01	1.16E-02	3.12E-01	5.28E-02	7.88E-03	KIRP
cg0750 4598	5.31E-02	3.07E-02	9.06E-02	4.09E-01	2.10E-01	1.26E-02	3.67E-01	7.41E-02	1.11E-02	KIRP
cg1503 7663	1.26E-02	2.79E-02	6.58E-01	4.35E-01	1.93E-01	1.17E-02	4.36E-01	5.77E-02	8.60E-03	KIRP
cg1970 6795	6.11E-02	2.97E-02	4.43E-02*	6.08E-01	2.05E-01	1.24E-02	5.56E-01	5.35E-02	7.98E-03	KIRP
cg2076 4575	9.51E-02	2.80E-02	1.11E-03*	6.59E-01	2.09E-01	1.26E-02	5.84E-01	5.74E-02	8.56E-03	KIRP
cg0630 1139	-6.05E-03	3.30E-03	7.29E-02	9.30E-01	2.21E-02	1.33E-03	9.37E-01	1.67E-02	2.49E-03	KIRP
cg2671 2096	-8.25E-03	4.77E-03	9.15E-02	9.33E-01	4.02E-02	2.42E-03	9.49E-01	1.10E-02	1.64E-03	KIRP
Probe	Mean Diff	Se Diff	KR_p-value	Mean TP	SD mean TP	SEM TP	Mean NT	SD mean NT	SEM NT	Tumour Type
cg1779 0129	-2.05E-02	1.15E-02	7.99E-02	9.01E-01	8.23E-02	4.24E-03	9.23E-01	2.91E-02	4.12E-03	LIHC
cg1420 5998	-3.17E-02	8.87E-03	4.99E-04*	9.01E-01	6.24E-02	3.21E-03	9.33E-01	1.47E-02	2.08E-03	LIHC

cg04317854	-9.48E-02	2.48E-02	2.09E-04*	7.48E-01	1.78E-01	9.18E-03	8.43E-01	4.81E-02	6.80E-03	LIHC
cg12922093	-1.74E-01	2.78E-02	5.81E-09*	7.01E-01	2.10E-01	1.08E-02	8.64E-01	3.40E-02	4.80E-03	LIHC
cg17569154	-1.07E-01	2.43E-02	1.91E-05*	8.34E-01	1.72E-01	8.84E-03	9.41E-01	1.73E-02	2.44E-03	LIHC
cg19260663	-1.90E-01	3.09E-02	4.24E-09*	7.21E-01	2.19E-01	1.13E-02	9.10E-01	3.03E-02	4.29E-03	LIHC
cg09333471	-9.53E-03	2.82E-02	7.39E-01	3.79E-01	1.98E-01	1.02E-02	3.93E-01	9.63E-02	1.36E-02	LIHC
cg00473134	8.23E-02	2.25E-02	3.63E-04*	1.60E-01	1.60E-01	8.23E-03	8.05E-02	1.74E-02	2.47E-03	LIHC
cg03995857	8.43E-02	2.42E-02	6.60E-04*	1.85E-01	1.70E-01	8.76E-03	1.00E-01	4.03E-02	5.70E-03	LIHC
cg07320646	1.45E-02	1.30E-02	2.75E-01	3.88E-02	9.20E-02	4.74E-03	2.43E-02	9.55E-03	1.35E-03	LIHC
cg07293520	6.76E-03	6.59E-03	3.13E-01	3.10E-02	4.66E-02	2.40E-03	2.42E-02	4.17E-03	5.89E-04	LIHC
cg04770504	1.59E-02	1.06E-02	1.41E-01	3.50E-02	7.49E-02	3.86E-03	1.91E-02	2.56E-03	3.62E-04	LIHC
cg24805239	2.09E-02	1.35E-02	1.27E-01	7.46E-02	9.51E-02	4.90E-03	5.36E-02	1.46E-02	2.06E-03	LIHC
cg01733570	4.03E-02	3.31E-02	2.32E-01	3.54E-01	2.32E-01	1.19E-02	3.13E-01	8.70E-02	1.23E-02	LIHC
cg25723149	6.74E-02	3.28E-02	4.40E-02*	3.20E-01	2.30E-01	1.18E-02	2.53E-01	9.19E-02	1.30E-02	LIHC
cg22804000	7.39E-02	3.20E-02	2.35E-02*	3.03E-01	2.24E-01	1.15E-02	2.29E-01	8.22E-02	1.16E-02	LIHC
cg07504598	4.15E-02	3.40E-02	2.30E-01	3.85E-01	2.37E-01	1.22E-02	3.43E-01	9.71E-02	1.37E-02	LIHC
cg15037663	3.76E-02	3.48E-02	2.88E-01	4.80E-01	2.43E-01	1.25E-02	4.43E-01	1.12E-01	1.59E-02	LIHC
cg19706795	5.93E-02	3.30E-02	7.74E-02	5.66E-01	2.30E-01	1.18E-02	5.07E-01	1.09E-01	1.55E-02	LIHC
cg20764575	1.21E-01	3.61E-02	1.08E-03*	5.61E-01	2.49E-01	1.28E-02	4.40E-01	1.47E-01	2.08E-02	LIHC
cg06301139	-9.03E-02	2.38E-02	2.20E-04*	8.29E-01	1.68E-01	8.65E-03	9.20E-01	2.35E-02	3.32E-03	LIHC
cg26712096	-1.14E-01	2.92E-02	1.37E-04*	8.20E-01	2.07E-01	1.07E-02	9.35E-01	2.02E-02	2.86E-03	LIHC
Probe	Mean Diff	Se Diff	KR_p-value	Mean TP	SD mean TP	SEM TP	Mean NT	SD mean NT	SEM NT	Tumour Type
cg17790129	4.53E-02	1.46E-02	2.88E-03*	8.23E-01	1.03E-01	4.71E-03	7.72E-01	4.27E-02	7.55E-03	LUAD
cg14205998	-6.22E-03	8.15E-03	4.51E-01	8.59E-01	8.40E-02	3.86E-03	8.84E-01	2.99E-02	5.29E-03	LUAD
cg04317854	1.04E-01	1.70E-02	4.20E-08*	7.44E-01	1.17E-01	5.38E-03	6.26E-01	5.66E-02	1.00E-02	LUAD

cg1292-2093	-5.40E-02	1.70E-02	2.37E-03*	7.28E-01	1.32E-01	6.05E-03	8.04E-01	3.86E-02	6.82E-03	LUAD
cg1756-9154	-2.50E-02	1.33E-02	6.72E-02	8.21E-01	1.02E-01	4.68E-03	8.50E-01	3.57E-02	6.31E-03	LUAD
cg1926-0663	-5.61E-02	1.37E-02	1.37E-04*	7.84E-01	1.15E-01	5.28E-03	8.39E-01	4.04E-02	7.14E-03	LUAD
cg0933-3471	6.95E-02	1.93E-02	5.02E-04*	2.84E-01	1.15E-01	5.30E-03	2.18E-01	3.75E-02	6.63E-03	LUAD
cg0047-3134	4.78E-02	1.82E-02	1.01E-02*	1.48E-01	1.05E-01	4.84E-03	1.05E-01	2.65E-02	4.68E-03	LUAD
cg0399-5857	8.69E-02	2.28E-02	2.68E-04*	2.05E-01	1.46E-01	6.71E-03	1.35E-01	2.41E-02	4.25E-03	LUAD
cg0732-0646	6.97E-02	2.29E-02	3.49E-03*	1.05E-01	1.63E-01	7.52E-03	4.26E-02	1.51E-02	2.67E-03	LUAD
cg0729-3520	5.77E-02	1.96E-02	4.35E-03*	1.07E-01	1.25E-01	5.76E-03	5.70E-02	1.50E-02	2.65E-03	LUAD
cg0477-0504	7.31E-02	1.96E-02	4.28E-04*	1.20E-01	1.48E-01	6.82E-03	3.92E-02	1.20E-02	2.13E-03	LUAD
cg2480-5239	6.19E-02	1.93E-02	2.12E-03*	1.76E-01	1.36E-01	6.26E-03	1.18E-01	2.11E-02	3.73E-03	LUAD
cg0173-3570	-3.37E-02	2.09E-02	1.14E-01	4.00E-01	1.27E-01	5.86E-03	4.45E-01	5.60E-02	9.89E-03	LUAD
cg2572-3149	3.43E-02	2.14E-02	1.18E-01	3.66E-01	1.33E-01	6.09E-03	3.42E-01	5.47E-02	9.66E-03	LUAD
cg2280-4000	3.20E-02	2.01E-02	1.19E-01	3.42E-01	1.23E-01	5.66E-03	3.17E-01	5.48E-02	9.69E-03	LUAD
cg0750-4598	9.85E-02	1.65E-02	8.60E-08*	6.18E-01	1.17E-01	5.36E-03	5.06E-01	5.21E-02	9.21E-03	LUAD
cg1503-7663	8.46E-02	1.67E-02	2.67E-06*	6.77E-01	1.10E-01	5.06E-03	5.90E-01	4.82E-02	8.51E-03	LUAD
cg1970-6795	4.04E-02	1.59E-02	1.30E-02*	7.52E-01	8.95E-02	4.11E-03	7.11E-01	3.76E-02	6.65E-03	LUAD
cg2076-4575	8.99E-02	1.50E-02	8.18E-09*	7.40E-01	8.39E-02	3.86E-03	6.49E-01	5.86E-02	1.04E-02	LUAD
cg0630-1139	-1.24E-02	7.50E-03	1.04E-01	8.66E-01	7.25E-02	3.33E-03	8.82E-01	2.51E-02	4.44E-03	LUAD
cg2671-2096	-2.92E-02	1.36E-02	3.68E-02*	8.13E-01	1.20E-01	5.50E-03	8.59E-01	2.94E-02	5.20E-03	LUAD
Probe	Mean Diff	Se Diff	KR_p-value	Mean TP	SD mean TP	SEM TP	Mean NT	SD mean NT	SEM NT	Tumour Type
cg1779-0129	5.53E-02	1.33E-02	5.65E-05*	8.86E-01	8.48E-02	4.41E-03	8.31E-01	4.50E-02	6.94E-03	LUSC
cg1420-5998	-2.40E-02	6.55E-03	6.89E-04*	8.91E-01	8.96E-02	4.66E-03	9.36E-01	1.13E-02	1.74E-03	LUSC
cg0431-7854	1.17E-01	1.84E-02	1.12E-08*	7.76E-01	1.33E-01	6.92E-03	6.66E-01	7.54E-02	1.16E-02	LUSC
cg1292-2093	-3.20E-02	1.59E-02	4.96E-02*	7.95E-01	1.03E-01	5.33E-03	8.27E-01	3.16E-02	4.87E-03	LUSC

cg1756 9154	-6.77E-02	2.04E-02	1.28E-03*	8.36E-01	1.33E-01	6.90E-03	9.04E-01	2.98E-02	4.60E-03	LUSC
cg1926 0663	-3.45E-02	8.77E-03	2.92E-04*	8.63E-01	1.04E-01	5.38E-03	9.25E-01	1.71E-02	2.64E-03	LUSC
cg0933 3471	1.74E-02	1.27E-02	1.82E-01	1.92E-01	8.39E-02	4.36E-03	1.75E-01	3.68E-02	5.68E-03	LUSC
cg0047 3134	4.21E-03	6.25E-03	5.09E-01	6.70E-02	4.05E-02	2.11E-03	6.30E-02	1.32E-02	2.03E-03	LUSC
cg0399 5857	2.58E-03	7.32E-03	7.30E-01	8.02E-02	4.72E-02	2.46E-03	7.76E-02	1.22E-02	1.89E-03	LUSC
cg0732 0646	6.17E-03	6.33E-03	3.40E-01	2.44E-02	4.10E-02	2.13E-03	1.83E-02	2.75E-03	4.25E-04	LUSC
cg0729 3520	4.12E-03	5.70E-03	4.79E-01	2.80E-02	3.69E-02	1.92E-03	2.39E-02	5.69E-03	8.79E-04	LUSC
cg0477 0504	5.25E-03	5.04E-03	3.08E-01	2.27E-02	3.26E-02	1.69E-03	1.75E-02	3.11E-03	4.80E-04	LUSC
cg2480 5239	-8.05E-03	7.24E-03	2.76E-01	7.40E-02	4.67E-02	2.43E-03	8.21E-02	1.42E-02	2.19E-03	LUSC
cg0173 3570	1.35E-02	2.64E-02	6.16E-01	4.45E-01	1.71E-01	8.89E-03	4.36E-01	6.42E-02	9.91E-03	LUSC
cg2572 3149	5.21E-02	2.48E-02	4.01E-02*	3.54E-01	1.60E-01	8.32E-03	3.03E-01	5.28E-02	8.15E-03	LUSC
cg2280 4000	5.09E-02	2.35E-02	3.46E-02*	3.37E-01	1.51E-01	7.86E-03	2.86E-01	5.44E-02	8.39E-03	LUSC
cg0750 4598	3.95E-02	2.38E-02	1.05E-01	5.29E-01	1.69E-01	8.77E-03	5.04E-01	6.18E-02	9.54E-03	LUSC
cg1503 7663	4.89E-02	2.32E-02	4.03E-02*	6.21E-01	1.77E-01	9.20E-03	6.02E-01	5.07E-02	7.83E-03	LUSC
cg1970 6795	1.52E-02	1.82E-02	4.11E-01	7.17E-01	1.60E-01	8.33E-03	7.26E-01	4.99E-02	7.70E-03	LUSC
cg2076 4575	4.12E-02	2.17E-02	6.41E-02	6.70E-01	1.71E-01	8.87E-03	6.67E-01	5.46E-02	8.42E-03	LUSC
cg0630 1139	-2.60E-02	1.61E-02	1.15E-01	8.90E-01	1.14E-01	5.93E-03	9.20E-01	2.35E-02	3.63E-03	LUSC
cg2671 2096	-4.66E-02	1.40E-02	1.70E-03*	8.56E-01	1.39E-01	7.23E-03	9.25E-01	1.68E-02	2.59E-03	LUSC
Probe	Mean Diff	Se Diff	KR_p-value	Mean TP	SD mean TP	SEM TP	Mean NT	SD mean NT	SEM NT	Tumour Type
cg1779 0129	-7.74E-02	3.30E-02	3.93E-02*	7.87E-01	1.23E-01	9.10E-03	8.88E-01	2.69E-02	8.51E-03	PAAD
cg1420 5998	-1.09E-02	6.51E-03	1.30E-01	9.07E-01	3.23E-02	2.38E-03	9.32E-01	1.18E-02	3.73E-03	PAAD
cg0431 7854	6.29E-02	3.31E-02	8.46E-02	7.69E-01	1.03E-01	7.56E-03	7.06E-01	8.95E-02	2.83E-02	PAAD
cg1292 2093	1.23E-02	1.91E-02	5.39E-01	8.02E-01	1.13E-01	8.30E-03	8.27E-01	6.29E-02	1.99E-02	PAAD
cg1756 9154	-9.33E-02	2.89E-02	8.15E-03*	7.67E-01	1.30E-01	9.62E-03	8.80E-01	4.91E-02	1.55E-02	PAAD

cg19260663	6.54E-03	8.05E-03	4.38E-01	8.44E-01	1.10E-01	8.08E-03	9.00E-01	2.76E-02	8.73E-03	PAAD
cg09333471	-3.88E-02	3.09E-02	2.49E-01	3.53E-01	1.28E-01	9.41E-03	3.78E-01	7.50E-02	2.37E-02	PAAD
cg00473134	5.66E-02	2.95E-02	8.61E-02	1.54E-01	1.33E-01	9.84E-03	8.73E-02	7.56E-02	2.39E-02	PAAD
cg03995857	7.30E-02	3.42E-02	6.00E-02	1.85E-01	1.60E-01	1.18E-02	1.10E-01	1.14E-01	3.60E-02	PAAD
cg07320646	3.57E-05	7.24E-04	9.62E-01	4.93E-02	1.05E-01	7.77E-03	1.73E-02	3.78E-03	1.20E-03	PAAD
cg07293520	1.18E-02	1.04E-02	2.89E-01	4.46E-02	7.08E-02	5.22E-03	2.14E-02	5.73E-03	1.81E-03	PAAD
cg04770504	3.86E-02	2.46E-02	1.54E-01	7.53E-02	1.15E-01	8.47E-03	2.83E-02	3.39E-02	1.07E-02	PAAD
cg24805239	3.78E-02	2.72E-02	2.02E-01	1.25E-01	1.21E-01	8.94E-03	6.61E-02	4.58E-02	1.45E-02	PAAD
cg01733570	-2.13E-01	3.84E-02	1.17E-04*	5.18E-01	1.69E-01	1.24E-02	6.97E-01	7.59E-02	2.40E-02	PAAD
cg25723149	-1.30E-01	3.07E-02	1.55E-03*	4.87E-01	1.65E-01	1.21E-02	5.66E-01	4.96E-02	1.57E-02	PAAD
cg22804000	-1.25E-01	3.36E-02	3.40E-03*	4.67E-01	1.59E-01	1.17E-02	5.63E-01	7.97E-02	2.52E-02	PAAD
cg07504598	1.93E-02	2.96E-02	5.40E-01	6.05E-01	1.30E-01	9.58E-03	5.79E-01	6.95E-02	2.20E-02	PAAD
cg15037663	-3.38E-02	2.53E-02	2.19E-01	6.70E-01	1.16E-01	8.52E-03	7.01E-01	4.35E-02	1.37E-02	PAAD
cg19706795	-4.78E-02	1.84E-02	2.65E-02*	7.71E-01	8.91E-02	6.57E-03	8.15E-01	5.85E-02	1.85E-02	PAAD
cg20764575	-4.35E-02	2.88E-02	1.71E-01	7.52E-01	9.15E-02	6.74E-03	8.00E-01	7.10E-02	2.25E-02	PAAD
cg06301139	3.96E-03	5.34E-03	4.81E-01	9.29E-01	3.82E-02	2.82E-03	9.43E-01	1.64E-02	5.19E-03	PAAD
cg26712096	-4.40E-03	9.24E-03	6.48E-01	8.94E-01	6.34E-02	4.67E-03	9.30E-01	1.34E-02	4.22E-03	PAAD
Probe	Mean Diff	Se Diff	KR_p-value	Mean TP	SD mean TP	SEM TP	Mean NT	SD mean NT	SEM NT	Tumour Type
cg17790129	-3.15E-03	3.81E-03	4.16E-01	9.34E-01	2.60E-02	1.16E-03	9.38E-01	2.21E-02	3.12E-03	PRAD
cg14205998	-2.84E-03	2.59E-03	2.78E-01	9.26E-01	2.62E-02	1.17E-03	9.41E-01	1.18E-02	1.68E-03	PRAD
cg04317854	3.95E-02	1.50E-02	9.88E-03*	7.07E-01	1.07E-01	4.76E-03	6.68E-01	8.95E-02	1.27E-02	PRAD
cg12922093	-7.26E-02	1.43E-02	1.20E-06*	8.33E-01	1.05E-01	4.71E-03	9.06E-01	2.70E-02	3.82E-03	PRAD
cg17569154	1.17E-02	1.03E-02	2.67E-01	8.54E-01	8.10E-02	3.62E-03	8.41E-01	7.32E-02	1.04E-02	PRAD
cg19260663	-9.24E-02	1.82E-02	1.04E-06*	8.25E-01	1.31E-01	5.86E-03	9.19E-01	3.87E-02	5.48E-03	PRAD

cg0933 3471	2.46E-01	1.98E-02	3.11E-30*	4.97E-01	1.37E-01	6.11E-03	2.51E-01	8.65E-02	1.22E-02	PRAD
cg0047 3134	1.50E-01	1.66E-02	4.32E-14*	2.45E-01	1.48E-01	6.59E-03	8.30E-02	4.73E-02	6.68E-03	PRAD
cg0399 5857	1.06E-01	1.44E-02	3.04E-10*	2.21E-01	1.54E-01	6.89E-03	8.87E-02	4.92E-02	6.96E-03	PRAD
cg0732 0646	-2.53E-04	1.40E-03	8.57E-01	2.68E-02	4.47E-02	2.00E-03	2.01E-02	3.32E-03	4.69E-04	PRAD
cg0729 3520	5.93E-04	9.60E-04	5.39E-01	3.33E-02	4.63E-02	2.07E-03	2.64E-02	5.64E-03	7.97E-04	PRAD
cg0477 0504	7.17E-02	1.51E-02	8.94E-06*	1.05E-01	1.32E-01	5.90E-03	1.97E-02	6.60E-03	9.33E-04	PRAD
cg2480 5239	1.51E-01	1.77E-02	2.81E-13*	2.60E-01	1.52E-01	6.78E-03	1.00E-01	4.45E-02	6.29E-03	PRAD
cg0173 3570	1.18E-01	1.09E-02	7.86E-20*	7.93E-01	8.24E-02	3.68E-03	6.74E-01	8.17E-02	1.16E-02	PRAD
cg2572 3149	1.54E-01	1.32E-02	9.38E-21*	7.58E-01	1.07E-01	4.76E-03	6.00E-01	8.93E-02	1.26E-02	PRAD
cg2280 4000	1.55E-01	1.39E-02	5.61E-20*	7.42E-01	1.10E-01	4.90E-03	5.89E-01	8.33E-02	1.18E-02	PRAD
cg0750 4598	1.21E-01	1.39E-02	2.16E-15*	7.24E-01	1.01E-01	4.51E-03	6.03E-01	7.84E-02	1.11E-02	PRAD
cg1503 7663	7.42E-02	1.11E-02	2.00E-10*	7.92E-01	7.71E-02	3.44E-03	7.18E-01	7.19E-02	1.02E-02	PRAD
cg1970 6795	4.06E-02	7.75E-03	5.78E-07*	8.37E-01	5.50E-02	2.46E-03	7.97E-01	5.69E-02	8.04E-03	PRAD
cg2076 4575	2.98E-02	8.51E-03	6.22E-04*	8.26E-01	5.75E-02	2.57E-03	7.97E-01	5.66E-02	8.00E-03	PRAD
cg0630 1139	-9.23E-03	2.36E-03	1.30E-04*	9.37E-01	1.62E-02	7.21E-04	9.46E-01	1.26E-02	1.79E-03	PRAD
cg2671 2096	-7.43E-02	1.42E-02	8.08E-07*	8.29E-01	1.12E-01	4.98E-03	9.08E-01	4.26E-02	6.02E-03	PRAD
Probe	Mean Diff	Se Diff	KR_p-value	Mean TP	SD mean TP	SEM TP	Mean NT	SD mean NT	SEM NT	Tumour Type
cg1779 0129	6.87E-03	3.82E-03	7.71E-02	9.32E-01	4.57E-02	2.03E-03	9.23E-01	5.62E-02	7.51E-03	THCA
cg1420 5998	3.58E-04	2.82E-03	9.00E-01	9.33E-01	2.09E-02	9.29E-04	9.33E-01	1.55E-02	2.07E-03	THCA
cg0431 7854	7.74E-02	1.58E-02	3.47E-06*	8.10E-01	1.32E-01	5.88E-03	7.33E-01	8.96E-02	1.20E-02	THCA
cg1292 2093	7.66E-03	4.19E-03	7.28E-02	9.14E-01	4.43E-02	1.97E-03	9.08E-01	3.38E-02	4.51E-03	THCA
cg1756 9154	-1.17E-03	1.94E-03	5.50E-01	9.45E-01	1.63E-02	7.24E-04	9.46E-01	1.27E-02	1.70E-03	THCA
cg1926 0663	4.37E-03	4.88E-03	3.77E-01	9.22E-01	3.57E-02	1.59E-03	9.17E-01	2.25E-02	3.01E-03	THCA
cg0933 3471	3.06E-03	1.19E-02	7.99E-01	1.90E-01	9.60E-02	4.27E-03	1.89E-01	4.02E-02	5.38E-03	THCA

cg0047-3134	-2.36E-04	2.17E-03	9.14E-01	5.97E-02	2.57E-02	1.14E-03	6.11E-02	1.70E-02	2.27E-03	THCA
cg0399-5857	-2.68E-03	2.07E-03	2.01E-01	7.56E-02	2.15E-02	9.57E-04	8.03E-02	1.72E-02	2.29E-03	THCA
cg0732-0646	6.10E-04	8.68E-04	4.88E-01	2.20E-02	7.09E-03	3.15E-04	2.28E-02	7.02E-03	9.38E-04	THCA
cg0729-3520	-7.57E-04	7.49E-04	3.19E-01	2.52E-02	6.33E-03	2.81E-04	2.70E-02	1.04E-02	1.39E-03	THCA
cg0477-0504	-8.18E-04	4.94E-04	1.04E-01	2.01E-02	1.21E-02	5.38E-04	2.06E-02	4.42E-03	5.90E-04	THCA
cg2480-5239	2.82E-03	6.64E-03	6.75E-01	8.67E-02	5.68E-02	2.52E-03	8.33E-02	1.74E-02	2.32E-03	THCA
cg0173-3570	-2.16E-01	2.19E-02	1.86E-17*	3.47E-01	1.81E-01	8.06E-03	5.63E-01	6.50E-02	8.69E-03	THCA
cg2572-3149	-5.97E-02	2.12E-02	6.06E-03*	3.97E-01	1.75E-01	7.80E-03	4.56E-01	6.75E-02	9.02E-03	THCA
cg2280-4000	-8.32E-02	2.32E-02	4.77E-04*	4.01E-01	1.80E-01	7.98E-03	4.88E-01	4.87E-02	6.50E-03	THCA
cg0750-4598	6.78E-02	2.48E-02	7.45E-03*	5.65E-01	1.88E-01	8.36E-03	5.03E-01	9.60E-02	1.28E-02	THCA
cg1503-7663	3.09E-02	2.49E-02	2.22E-01	6.82E-01	1.85E-01	8.21E-03	6.51E-01	7.46E-02	9.96E-03	THCA
cg1970-6795	2.59E-02	1.30E-02	5.14E-02	8.35E-01	9.95E-02	4.43E-03	8.12E-01	4.31E-02	5.76E-03	THCA
cg2076-4575	4.70E-02	1.35E-02	6.29E-04*	8.48E-01	1.00E-01	4.44E-03	8.01E-01	4.77E-02	6.37E-03	THCA
cg0630-1139	2.24E-03	1.56E-03	1.59E-01	9.48E-01	1.13E-02	5.02E-04	9.46E-01	9.10E-03	1.22E-03	THCA
cg2671-2096	-2.22E-04	4.01E-03	9.57E-01	9.39E-01	2.96E-02	1.32E-03	9.39E-01	1.65E-02	2.21E-03	THCA
Probe	Mean Diff	Se Diff	KR_p-value	Mean TP	SD mean TP	SEM TP	Mean NT	SD mean NT	SEM NT	Tumour Type
cg1779-0129	-4.11E-02	1.72E-02	2.04E-02*	8.49E-01	1.41E-01	6.76E-03	8.96E-01	7.41E-02	1.09E-02	UCEC
cg1420-5998	-1.41E-02	6.63E-03	3.71E-02*	9.17E-01	4.63E-02	2.21E-03	9.33E-01	3.10E-02	4.57E-03	UCEC
cg0431-7854	2.79E-02	2.44E-02	2.61E-01	7.63E-01	1.75E-01	8.37E-03	7.45E-01	7.15E-02	1.05E-02	UCEC
cg1292-2093	-3.80E-02	1.46E-02	1.13E-02*	8.53E-01	1.02E-01	4.87E-03	8.92E-01	4.08E-02	6.01E-03	UCEC
cg1756-9154	1.43E-01	1.52E-02	8.46E-19*	8.94E-01	8.92E-02	4.26E-03	7.51E-01	1.60E-01	2.36E-02	UCEC
cg1926-0663	-6.34E-02	1.76E-02	4.21E-04*	8.42E-01	1.18E-01	5.65E-03	9.06E-01	4.34E-02	6.40E-03	UCEC
cg0933-3471	9.62E-02	2.39E-02	1.07E-04*	3.32E-01	1.72E-01	8.23E-03	2.37E-01	7.82E-02	1.15E-02	UCEC
cg0047-3134	3.23E-02	1.41E-02	2.70E-02*	1.27E-01	1.42E-01	6.77E-03	8.19E-02	2.47E-02	3.64E-03	UCEC

cg0399 5857	1.82E-02	1.01E-02	7.78E-02	1.44E-01	1.71E-01	8.15E-03	9.17E-02	2.23E-02	3.29E-03	UCEC
cg0732 0646	-6.43E-05	2.71E-03	9.81E-01	6.51E-02	1.55E-01	7.41E-03	2.84E-02	1.04E-02	1.54E-03	UCEC
cg0729 3520	-7.86E-04	3.46E-03	8.22E-01	6.05E-02	1.34E-01	6.40E-03	2.81E-02	6.46E-03	9.52E-04	UCEC
cg0477 0504	1.99E-02	8.87E-03	3.04E-02*	7.00E-02	1.41E-01	6.73E-03	2.01E-02	3.06E-03	4.51E-04	UCEC
cg2480 5239	2.91E-02	1.59E-02	7.40E-02	1.18E-01	1.55E-01	7.42E-03	7.00E-02	2.61E-02	3.86E-03	UCEC
cg0173 3570	-7.69E-02	3.23E-02	1.98E-02*	4.95E-01	2.25E-01	1.08E-02	5.69E-01	1.06E-01	1.56E-02	UCEC
cg2572 3149	-6.37E-02	3.15E-02	4.80E-02*	4.01E-01	2.26E-01	1.08E-02	4.61E-01	8.97E-02	1.32E-02	UCEC
cg2280 4000	-8.24E-02	2.94E-02	6.50E-03*	3.95E-01	2.15E-01	1.03E-02	4.73E-01	8.66E-02	1.28E-02	UCEC
cg0750 4598	-8.50E-02	2.88E-02	4.16E-03*	3.94E-01	2.05E-01	9.82E-03	4.76E-01	9.38E-02	1.38E-02	UCEC
cg1503 7663	-1.23E-01	2.84E-02	3.42E-05*	4.45E-01	2.06E-01	9.83E-03	5.61E-01	9.34E-02	1.38E-02	UCEC
cg1970 6795	-8.73E-02	2.75E-02	2.13E-03*	5.65E-01	2.02E-01	9.65E-03	6.55E-01	8.46E-02	1.25E-02	UCEC
cg2076 4575	-1.42E-01	3.01E-02	8.79E-06*	5.47E-01	2.31E-01	1.10E-02	6.95E-01	8.30E-02	1.22E-02	UCEC
cg0630 1139	-5.89E-02	1.39E-02	5.83E-05*	8.80E-01	1.07E-01	5.13E-03	9.45E-01	9.68E-03	1.43E-03	UCEC
cg2671 2096	-9.27E-02	2.27E-02	6.61E-05*	8.41E-01	1.54E-01	7.34E-03	9.34E-01	1.86E-02	2.74E-03	UCEC

TP = primary tumour, NT = normal tissue, Mean diff = difference in means (mean NT – mean TP), SE = standard error of difference of means, SD = standard deviation, SEM = standard error of the mean. * represents significant results for which p-value < 0.05. Light shaded rows represent intragenic CpGs while dark shaded rows represent putative promoter CpGs.

Table S2. Table of the individual dataset analysis AUC values that satisfy the specified thresholds (minimum average AUC = 0.84 and minimum AUC threshold = 0.80). NA values are tumour types for which the probe combination did not meet the AUC thresholds.

Probe Combination	BL CA	BR CA	C R C	ES CA	HN SC	KI RC	KI RP	LI H C	LU AD	LU SC	PA AD	PR AD	TH CA	UC EC
cg00473134+cg04317 854+cg17569154	N A	0.8 6	0. 86	N A	0.9 6	0.8 0	0.9 4	0.8 9	0.8 9	0.9 0	NA	0.9 0	NA	N A
cg00473134+cg04317 854+cg19260663	0.9 0	0.9 1	0. 91	0.8 3	0.8 2	N A	0.9 1	0.8 9	0.9 2	0.9 2	NA	0.9 3	NA	N A
cg00473134+cg04317 854+cg26712096	0.8 4	0.9 1	0. 88	N A	0.8 9	N A	0.9 3	0.8 3	0.9 2	0.9 2	0.8 1	0.9 3	NA	0.8 1
cg01733570+cg04317 854+cg06301139	N A	0.8 3	0. 85	N A	0.8 5	N A	0.9 1	N A	0.8 9	0.8 7	0.8 4	0.8 9	0.8 8	0.8 4
cg01733570+cg04317 854+cg12922093	N A	0.8 8	0. 86	0.8 2	0.8 7	0.8 1	0.9 2	N A	0.9 2	0.8 6	0.8 2	0.9 0	0.8 8	N A

cg01733570+cg04317 854+cg14205998	0.8 6	0.8 5	0. 88	0.8 1	0.8 4	N A	0.9 2	N A	0.8 8	0.9 3	0.8 9	0.8 6	0.8 7	N A
cg01733570+cg04317 854+cg17569154	N A	0.8 6	N A	0.8 1	0.9 6	0.8 7	0.9 3	0.8 6	0.8 9	0.9 0	0.8 3	0.8 4	0.8 8	0.8 1
cg01733570+cg04317 854+cg19260663	0.9 0	0.9 1	0. 84	0.8 9	NA	0.8 1	0.9 1	0.8 6	0.9 2	0.9 2	0.9 0	0.8 9	0.8 7	N A
cg01733570+cg04317 854+cg26712096	0.8 5	0.9 0	N A	N A	0.8 9	N A	0.9 3	N A	0.9 2	0.9 2	0.8 7	0.8 8	0.8 8	0.8 2
cg01733570+cg04770 504+cg17569154	N A	0.8 7	0. 96	N A	0.9 2	0.8 6	0.8 1	0.8 6	0.8 1	N A	0.8 8	0.8 9	0.8 6	0.8 8
cg01733570+cg17569 154+cg19260663	0.8 9	0.9 1	0. 83	N A	0.9 2	0.8 9	0.8 6	0.9 1	NA	0.8 4	0.9 3	0.8 8	0.8 6	0.9 3
cg03995857+cg04317 854+cg17569154	N A	0.8 5	0. 90	0.8 2	0.9 6	N A	0.9 3	0.8 8	0.9 0	0.9 0	NA	0.8 5	NA	N A
cg03995857+cg04317 854+cg19260663	0.8 9	0.9 0	0. 92	0.8 6	NA	N A	0.9 1	0.8 8	0.9 3	0.9 2	NA	0.9 0	NA	N A
cg04317854+cg04770 504+cg17569154	N A	0.8 4	0. 92	0.8 4	0.9 6	0.8 0	0.9 4	0.8 5	0.9 3	0.8 9	NA	0.8 4	NA	0.8 1
cg04317854+cg04770 504+cg19260663	0.9 1	0.9 0	0. 94	N A	0.8 1	N A	0.9 1	0.8 7	0.9 2	0.9 2	NA	0.8 7	NA	N A
cg04317854+cg04770 504+cg26712096	0.8 6	0.8 9	0. 92	0.8 4	0.9 1	N A	0.9 3	0.8 0	0.9 2	0.9 2	NA	0.9 0	NA	0.8 3
cg04317854+cg07293 520+cg19260663	0.8 9	0.8 8	0. 92	0.8 5	NA	N A	0.9 2	0.8 7	0.9 2	0.9 2	0.8 3	0.8 0	NA	N A
cg04317854+cg07320 646+cg19260663	0.9 0	0.8 8	0. 92	0.8 6	NA	N A	0.9 2	0.8 7	0.9 1	0.9 3	0.8 6	0.8 2	NA	N A
cg04317854+cg07320 646+cg26712096	0.8 6	0.8 6	0. 90	0.8 1	0.8 9	N A	0.9 3	N A	0.9 2	0.9 3	0.8 4	0.8 2	NA	0.8 2
cg04317854+cg07504 598+cg19260663	0.9 2	0.9 3	0. 88	0.8 3	0.8 4	N A	0.9 2	0.8 7	0.9 3	0.9 3	NA	0.8 7	NA	N A
cg04317854+cg07504 598+cg26712096	0.9 1	0.9 4	0. 83	N A	0.9 2	N A	0.9 4	0.8 2	0.9 4	0.9 1	0.8 2	0.8 7	NA	0.8 0
cg04317854+cg09333 471+cg17569154	N A	0.9 1	0. 84	N A	0.9 6	0.8 0	0.9 4	0.8 5	0.9 1	0.9 0	0.8 1	0.9 3	NA	N A
cg04317854+cg09333 471+cg19260663	0.9 1	0.9 3	0. 89	0.8 8	NA	N A	0.9 3	0.8 6	0.9 2	0.9 3	NA	0.9 3	NA	N A
cg04317854+cg09333 471+cg26712096	0.8 3	0.9 4	0. 84	N A	0.9 0	N A	0.9 3	N A	0.9 2	0.9 1	0.8 0	0.9 3	NA	0.8 4
cg04317854+cg12922 093+cg17569154	0.8 3	0.8 3	N A	0.8 1	0.9 6	0.8 0	0.9 5	0.8 5	0.9 3	0.9 1	NA	0.8 1	NA	0.8 3
cg04317854+cg12922 093+cg19260663	0.9 0	0.8 7	0. 83	0.8 6	0.8 8	N A	0.9 0	0.8 5	0.9 2	0.9 3	NA	0.8 5	NA	N A
cg04317854+cg14205 998+cg17569154	0.8 9	NA	0. 80	N A	0.9 6	N A	0.9 5	0.8 8	0.9 0	0.9 4	0.8 7	NA	NA	0.8 2
cg04317854+cg14205 998+cg19260663	0.9 0	0.8 6	0. 84	0.8 4	0.8 5	N A	0.9 2	0.8 6	0.9 2	0.9 5	0.8 2	0.8 4	NA	N A
cg04317854+cg15037 663+cg19260663	0.9 1	0.9 2	0. 83	0.8 6	0.8 4	N A	0.9 2	0.8 8	0.9 4	0.9 2	NA	0.8 5	NA	N A
cg04317854+cg17569 154+cg19260663	0.9 0	0.8 6	N A	0.8 5	0.9 6	0.8 6	0.9 5	0.8 9	0.9 1	0.9 4	0.8 4	0.8 2	NA	0.9 0

cg04317854+cg17569 154+cg24805239	N A	0.8 7	0. 90	N A	0.9 6	0.8 3	0.9 4	0.8 5	0.9 1	0.9 0	0.8 2	0.8 7	NA	N A
cg04317854+cg17569 154+cg26712096	0.8 6	0.8 6	N A	N A	0.9 6	0.8 2	0.9 5	0.8 7	0.9 2	0.9 2	0.8 4	0.8 3	NA	0.9 2
cg04317854+cg19260 663+cg19706795	0.9 0	0.9 3	0. 86	0.8 2	0.8 6	N A	0.9 1	0.8 8	0.9 2	0.9 3	0.8 2	0.8 4	NA	N A
cg04317854+cg19260 663+cg20764575	0.9 2	0.9 3	N A	0.8 6	0.8 6	N A	0.9 2	0.9 0	0.9 4	0.9 2	NA	0.8 2	NA	N A
cg04317854+cg19260 663+cg24805239	0.9 1	0.9 1	0. 93	0.8 2	0.8 1	N A	0.9 1	0.8 7	0.9 1	0.9 2	NA	0.9 1	NA	N A
cg04317854+cg19260 663+cg25723149	0.9 0	0.9 2	0. 84	0.8 4	NA	N A	0.9 2	0.8 7	0.9 0	0.9 3	0.8 3	0.8 9	NA	N A
cg04317854+cg19260 663+cg26712096	0.9 2	0.8 9	N A	N A	0.9 0	N A	0.9 3	0.8 6	0.9 2	0.9 4	0.8 3	0.8 5	NA	N A
cg04317854+cg24805 239+cg26712096	0.8 8	0.9 1	0. 89	N A	0.8 9	N A	0.9 3	0.8 1	0.9 2	0.9 1	0.8 1	0.9 2	NA	0.8 1
cg17569154+cg19260 663+cg20764575	0.9 0	0.9 3	N A	N A	0.9 4	0.8 7	0.8 9	0.9 2	0.8 8	0.8 5	0.8 0	0.8 1	NA	0.9 2

Table S3. Summary of the RNA-seq expression levels in the different sample types and across the different tumour types.

Sample Type	Tumour Type	N	Mean	SD
NT	BLCA	19	8.506	0.982
NT	BRCA	113	8.206	0.448
NT	CRC	51	5.885	1.213
NT	ESCA	11	7.226	1.220
NT	HNSC	44	7.516	0.830
NT	KIRC	72	8.914	0.405
NT	KIRP	32	8.781	0.510
NT	LIHC	50	7.122	0.558
NT	LUAD	59	7.507	0.731
NT	LUSC	51	7.623	0.544
NT	PAAD	4	8.740	1.095
NT	PRAD	52	7.636	0.715
NT	THCA	59	9.004	0.379
NT	UCEC	24	9.132	0.766
TP	BLCA	408	7.709	1.854
TP	BRCA	1095	7.156	0.852
TP	CRC	379	5.515	1.494
TP	ESCA	184	7.419	2.023
TP	HNSC	520	9.422	1.275
TP	KIRC	533	8.753	0.945
TP	KIRP	290	9.376	1.169
TP	LIHC	371	7.121	1.799
TP	LUAD	515	7.676	1.315
TP	LUSC	502	8.536	1.302
TP	PAAD	178	7.963	1.037
TP	PRAD	497	6.718	0.868
TP	THCA	505	8.873	0.674
TP	UCEC	176	7.021	1.211

TP = primary tumour, NT = normal tissue, N = sample size, SD= standard deviation.

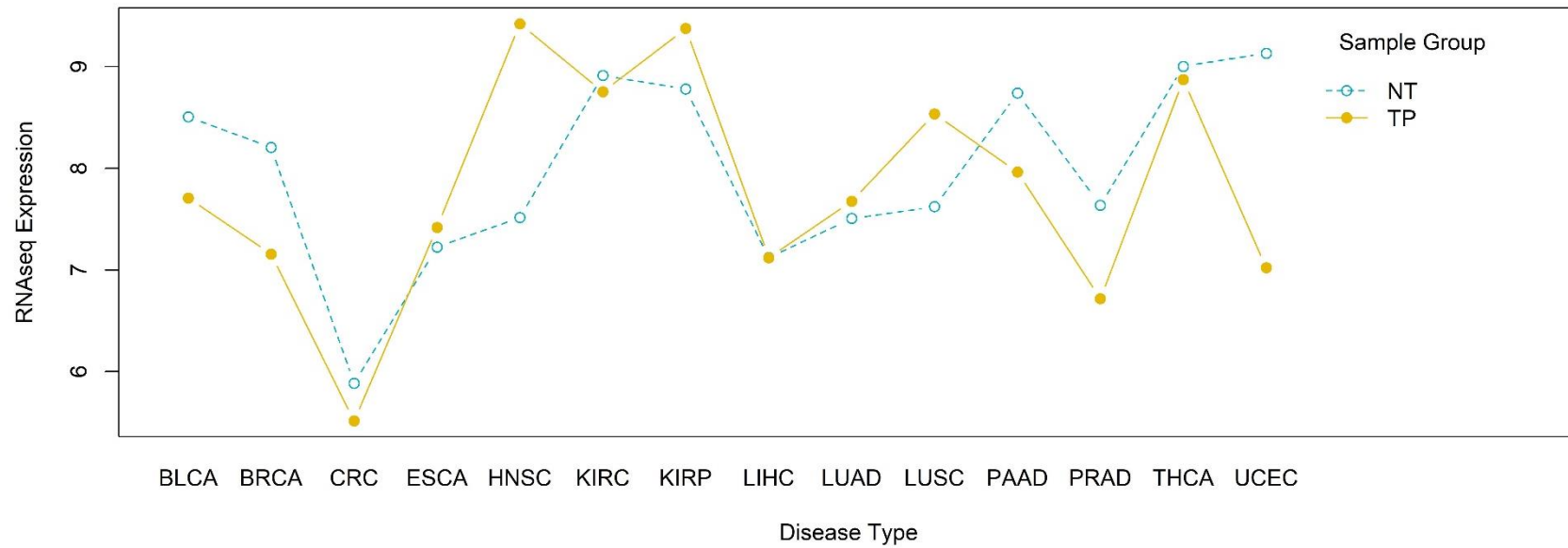


Figure S1. Interaction plot for the RNA-seq expression data showing the differences in expression levels between tumour and normal samples across the different tumour types.

Table S4. Table of the linear regression results for the analysis of RNA-seq expression and methylation.

probes	BLCA_s lope	BLCA_p- value	BRCA_s lope	BRCA_p- value	CRC_sl ope	CRC_p- value	ESCA_sl ope	ESCA_p- value	HNSC_s lope	HNSC_p- value	KIRC_sl ope	KIRC_p- value	KIRP_sl ope	KIRP_p- value
cg0047 3134	0.087	0.848	0.005	0.986	0.044	0.929	-0.182	0.813	-1.527	0.038	0.146	0.783	-0.205	0.769
cg0173 3570	1.498	0.021	-0.063	0.850	0.304	0.523	2.181	0.101	3.180	0.037	0.945	0.583	6.252	0.033
cg0399 5857	2.121	0.000	0.373	0.182	-1.684	0.011	0.548	0.558	0.643	0.367	0.738	0.003	1.538	0.000
cg0431 7854	1.027	0.131	-0.133	0.650	-0.366	0.422	1.493	0.175	2.541	0.001	-0.356	0.620	-3.556	0.010
cg0477 0504	-0.533	0.155	0.048	0.828	0.385	0.358	-0.492	0.388	-1.578	0.000	-1.823	0.000	-0.802	0.003

cg0630 1139	0.932	0.106	0.794	0.009	0.646	0.220	0.046	0.970	1.274	0.262	0.163	0.877	-0.445	0.630
cg0729 3520	-1.864	0.030	-0.365	0.145	-0.703	0.269	-3.696	0.021	0.048	0.960	0.293	0.699	-3.137	0.002
cg0732 0646	-2.580	0.020	0.183	0.519	-0.679	0.238	1.695	0.313	-6.696	0.004	-1.751	0.406	5.594	0.019
cg0750 4598	-0.206	0.846	-0.108	0.679	-0.385	0.449	-1.136	0.674	6.051	0.013	-4.141	0.065	-6.629	0.012
cg0933 3471	0.995	0.287	0.245	0.377	-0.569	0.285	-2.871	0.331	-4.243	0.048	7.867	0.292	1.514	0.396
cg1292 2093	0.075	0.949	-0.113	0.753	0.781	0.184	0.986	0.631	1.286	0.413	-9.407	0.114	-4.466	0.468
cg1420 5998	-0.067	0.951	0.563	0.114	1.424	0.076	5.632	0.132	-0.150	0.955	-3.402	0.370	9.273	0.250
cg1503 7663	0.954	0.395	-0.353	0.307	-0.350	0.667	-1.620	0.511	-0.221	0.914	2.028	0.208	-6.609	0.022
cg1756 9154	-1.132	0.088	0.371	0.162	0.485	0.468	2.400	0.057	0.312	0.753	-0.273	0.538	0.664	0.276
cg1779 0129	-1.823	0.095	-0.951	0.025	-0.962	0.287	-0.902	0.673	-1.314	0.366	-2.581	0.000	1.891	0.049
cg1926 0663	1.146	0.316	0.130	0.736	-0.397	0.616	-6.030	0.005	-2.180	0.161	2.176	0.003	-1.942	0.063
cg1970 6795	-1.087	0.072	-0.254	0.399	0.633	0.202	-0.113	0.914	0.338	0.544	0.511	0.259	0.245	0.601
cg2076 4575	0.436	0.596	0.489	0.112	-0.354	0.568	2.244	0.133	0.492	0.528	0.633	0.360	0.855	0.219
cg2280 4000	-0.205	0.870	-0.093	0.830	0.334	0.684	-0.316	0.870	0.600	0.535	-0.152	0.830	-1.327	0.139
cg2480 5239	0.403	0.637	-0.362	0.258	-2.086	0.021	0.937	0.523	0.124	0.875	-0.313	0.337	-0.459	0.404
cg2572 3149	1.277	0.146	-0.085	0.792	0.746	0.180	-2.661	0.027	-2.412	0.000	-2.560	0.012	-4.202	0.076
cg2671 2096	1.136	0.034	0.667	0.019	2.781	0.000	1.357	0.120	3.547	0.000	3.766	0.007	1.169	0.454

probes	LIHC_sl ope	LIHC_p- value	LUAD_s lope	LUAD_p- value	LUSC_s lope	LUSC_p- value	PAAD_s lope	PAAD_p- value	PRAD_s lope	PRAD_p- value	THCA_s lope	THCA_p- value	UCEC_s lope	UCEC_p- value
cg0047 3134	-2.917	0.000	0.459	0.512	-1.923	0.024	0.005	0.992	-0.170	0.896	-0.017	0.972	1.299	0.054
cg0173 3570	0.782	0.468	-0.590	0.528	0.322	0.754	4.814	0.016	-0.083	0.952	-1.810	0.149	-2.340	0.367
cg0399 5857	1.453	0.005	1.462	0.006	2.465	0.000	0.679	0.280	0.601	0.090	0.408	0.030	-0.005	0.994
cg0431 7854	0.740	0.204	0.063	0.920	1.727	0.035	0.791	0.174	-0.818	0.081	-0.645	0.283	0.663	0.618
cg0477 0504	-0.514	0.461	-0.639	0.298	-1.173	0.039	1.048	0.064	-0.329	0.495	-3.435	0.053	-2.043	0.021
cg0630 1139	-0.699	0.214	2.124	0.004	1.610	0.075	1.603	0.013	0.652	0.091	1.764	0.059	2.265	0.017
cg0729 3520	-1.598	0.000	-1.525	0.068	-2.353	0.016	-1.803	0.017	-0.293	0.441	0.117	0.697	-2.561	0.002
cg0732 0646	0.024	0.969	-0.002	0.999	0.988	0.702	-0.184	0.830	-0.020	0.954	-2.153	0.137	0.714	0.691
cg0750 4598	-0.826	0.130	-0.944	0.286	-2.938	0.206	1.149	0.126	-0.112	0.726	1.390	0.367	-2.677	0.102
cg0933 3471	0.148	0.904	0.759	0.366	-9.670	0.173	4.161	0.001	-1.840	0.212	0.251	0.952	1.412	0.599
cg1292 2093	4.882	0.022	0.220	0.845	9.063	0.279	-6.404	0.001	-0.154	0.918	-1.629	0.669	0.280	0.926
cg1420 5998	-1.054	0.522	-1.217	0.140	2.376	0.539	1.186	0.265	0.462	0.305	-3.949	0.185	-4.399	0.035
cg1503 7663	0.317	0.792	0.512	0.617	1.523	0.545	-2.541	0.020	0.531	0.239	-1.191	0.025	4.664	0.030
cg1756 9154	-0.532	0.437	0.971	0.244	-2.088	0.052	-0.316	0.627	0.083	0.930	0.396	0.024	-1.683	0.200
cg1779 0129	-1.223	0.308	0.836	0.549	-0.585	0.710	-0.227	0.861	-0.516	0.583	-0.903	0.012	-1.016	0.614
cg1926 0663	-1.284	0.277	-2.277	0.138	0.862	0.629	-0.822	0.508	-1.116	0.241	-0.288	0.382	2.222	0.350

cg1970 6795	1.037	0.137	-0.392	0.575	0.300	0.741	0.897	0.210	-0.012	0.984	-0.026	0.850	-1.074	0.299
cg2076 4575	0.456	0.580	2.810	0.001	-1.000	0.438	-1.236	0.145	-0.812	0.368	0.105	0.508	-0.648	0.714
cg2280 4000	0.329	0.718	-2.476	0.062	0.568	0.689	0.853	0.480	-3.490	0.001	-0.582	0.049	-1.430	0.483
cg2480 5239	0.583	0.315	-2.617	0.003	1.681	0.100	-3.444	0.001	-0.769	0.429	0.036	0.891	2.851	0.023
cg2572 3149	-1.824	0.002	0.977	0.366	-0.993	0.216	-2.305	0.175	1.593	0.484	-4.789	0.040	1.485	0.292
cg2671 2096	4.227	0.000	1.572	0.029	1.810	0.019	3.199	0.002	0.930	0.012	0.987	0.289	1.683	0.125

Highlighted cells represent significant *p*-values.

Table S5 Table of the linear regression results for the analysis of age and methylation.

Probe	BLCA _slope	BLCA_lm _p_value	BRCA _slope	BRCA_lm _p_value	CRC_s lope	CRC_lm_ p_value	ESCA_ slope	ESCA_lm _p_value	HNSC _slope	HNSC_lm _p_value	KIRC_ slope	KIRC_lm _p_value	KIRP_ slope	KIRP_lm_ p_value
cg004 73134	3.88E-04	4.49E-01	1.05E-03	5.69E-03	3.79E-03	5.51E-08	3.88E-03	2.75E-03	1.84E-04	1.07E-01	-3.74E-05	5.64E-01	-1.89E-03	2.49E-05
cg017 33570	1.20E-03	1.31E-01	7.59E-04	1.33E-01	2.91E-03	5.03E-05	2.96E-03	3.02E-02	1.64E-03	1.32E-03	4.38E-05	9.27E-01	-9.22E-04	2.89E-01
cg039 95857	6.49E-04	3.30E-01	1.62E-03	2.41E-03	3.54E-03	9.25E-05	5.40E-03	1.66E-03	2.23E-04	6.48E-02	2.17E-05	7.45E-01	-1.96E-03	3.18E-05
cg043 17854	-1.73E-03	4.54E-02	-2.75E-04	5.58E-01	7.09E-04	8.58E-02	-3.01E-04	6.82E-01	-7.67E-05	8.07E-01	1.55E-03	5.72E-03	1.56E-03	3.69E-02
cg047 70504	7.40E-04	2.79E-01	1.76E-03	1.26E-04	2.12E-03	3.92E-03	3.54E-03	6.70E-03	-8.93E-05	4.64E-01	5.69E-05	1.62E-01	-1.31E-03	1.16E-04
cg063 01139	-9.05E-04	7.06E-02	-1.18E-04	7.49E-01	3.14E-04	5.38E-01	-1.04E-03	8.63E-02	1.24E-03	2.22E-02	-1.09E-04	4.42E-01	7.91E-05	4.29E-01
cg072 93520	2.48E-04	6.81E-01	1.31E-03	1.74E-03	4.52E-03	2.27E-07	4.72E-03	3.63E-03	-1.51E-05	9.09E-01	1.02E-05	6.44E-01	-1.80E-03	4.56E-05
cg073 20646	1.00E-04	9.03E-01	2.23E-03	1.88E-04	5.14E-03	1.24E-06	5.12E-03	6.90E-03	-3.57E-05	7.95E-01	-1.62E-05	4.08E-01	-1.93E-03	2.35E-04
cg075 04598	-1.08E-03	1.33E-01	8.08E-04	9.32E-02	1.87E-03	1.96E-03	2.53E-03	2.55E-02	1.95E-03	1.74E-03	1.28E-04	7.76E-01	-1.80E-03	4.73E-02

cg09333471	6.84E-04	2.51E-01	8.97E-04	2.73E-02	3.10E-03	3.80E-06	3.71E-03	4.54E-03	2.18E-04	4.32E-01	-8.88E-05	6.91E-01	-9.87E-04	4.85E-02
cg12922093	-1.54E-03	8.15E-02	-8.07E-04	1.30E-01	1.17E-04	8.57E-01	-1.93E-03	1.25E-02	-4.62E-04	1.15E-01	-1.58E-04	4.05E-01	5.70E-05	7.56E-01
cg14205998	-5.72E-04	5.04E-01	-6.37E-04	2.15E-01	4.23E-05	9.45E-01	-7.10E-04	3.43E-01	-7.73E-05	6.20E-01	-1.22E-04	1.61E-01	9.17E-06	9.12E-01
cg15037663	-1.81E-03	1.01E-02	-3.06E-04	5.31E-01	1.66E-03	5.11E-03	1.25E-03	2.20E-01	2.22E-03	5.62E-04	-9.67E-05	8.18E-01	-1.54E-03	6.27E-02
cg17569154	2.18E-03	3.02E-02	-8.48E-04	1.05E-01	1.34E-04	8.40E-01	-4.15E-03	2.10E-03	6.43E-04	3.20E-01	3.72E-04	3.58E-01	-7.03E-04	4.45E-01
cg17790129	-4.73E-04	6.15E-01	-1.18E-03	3.88E-02	1.16E-04	8.32E-01	-2.14E-03	1.65E-02	3.88E-04	1.54E-01	1.35E-04	5.45E-01	-2.07E-04	5.43E-01
cg19260663	-4.88E-04	5.92E-01	-9.77E-04	4.84E-02	7.03E-04	1.80E-01	-6.48E-04	3.89E-01	-4.15E-05	8.29E-01	3.18E-04	1.33E-02	1.14E-04	6.24E-01
cg19706795	-1.51E-03	1.06E-02	3.24E-05	9.42E-01	7.27E-04	1.22E-01	4.69E-04	5.92E-01	1.78E-03	4.63E-03	-3.06E-04	4.98E-01	-2.12E-03	1.61E-02
cg20764575	-1.09E-03	5.13E-02	5.78E-04	1.99E-01	8.77E-04	6.30E-03	6.99E-04	4.66E-01	2.37E-03	4.61E-04	1.88E-04	7.45E-01	-2.18E-03	1.58E-02
cg22804000	1.72E-04	8.24E-01	1.27E-03	9.07E-03	2.40E-03	3.83E-04	4.27E-03	1.43E-03	1.43E-03	1.31E-03	6.24E-04	1.58E-01	-1.33E-03	1.10E-01
cg24805239	6.54E-04	3.14E-01	1.86E-03	2.81E-05	3.59E-03	1.31E-05	4.10E-03	5.38E-03	2.34E-04	1.02E-01	1.58E-04	1.34E-01	-1.43E-03	6.31E-04
cg25723149	6.83E-04	4.19E-01	1.88E-03	3.85E-04	3.13E-03	4.49E-06	4.54E-03	2.37E-03	1.55E-03	7.48E-04	8.26E-04	8.71E-02	-1.39E-03	9.97E-02
cg26712096	5.25E-04	5.61E-01	-1.53E-03	5.00E-03	-1.28E-03	7.17E-02	-2.33E-03	3.75E-02	8.06E-04	6.54E-02	-1.56E-05	8.86E-01	1.45E-04	4.10E-01
Probe	LIHC_slope	LIHC_lm_p_value	LUAD_slope	LUAD_lm_p_value	LUSC_slope	LUSC_lm_p_value	PAAD_slope	PAAD_lm_p_value	PRAD_slope	PRAD_lm_p_value	THCA_slope	THCA_lm_p_value	UCEC_slope	UCEC_lm_p_value
cg00473134	7.80E-04	1.45E-01	1.52E-04	7.39E-01	3.20E-04	1.44E-01	2.24E-04	7.93E-01	3.71E-03	6.24E-05	1.50E-04	2.30E-02	2.20E-04	6.98E-01
cg01733570	-1.72E-03	2.57E-02	5.90E-04	2.84E-01	-1.84E-03	4.54E-02	2.60E-04	8.14E-01	-3.55E-05	9.49E-01	1.04E-03	3.29E-02	-1.12E-03	2.18E-01
cg03995857	1.24E-03	2.95E-02	1.47E-04	8.14E-01	2.46E-04	3.32E-01	1.24E-04	9.04E-01	3.83E-03	5.62E-05	1.84E-04	9.86E-04	6.48E-05	9.24E-01
cg04317854	-9.43E-04	1.16E-01	1.02E-03	5.00E-02	-1.26E-03	9.04E-02	9.09E-04	1.72E-01	9.42E-04	1.55E-01	6.84E-04	4.78E-02	-1.43E-03	4.07E-02
cg04770504	3.13E-04	2.07E-01	5.64E-04	3.81E-01	2.10E-04	2.26E-01	3.63E-04	6.20E-01	3.06E-03	1.32E-04	9.92E-05	1.14E-03	4.13E-04	4.65E-01

cg063-01139	-8.45E-04	1.34E-01	-1.11E-04	7.26E-01	-4.68E-04	4.50E-01	2.07E-04	3.96E-01	-1.10E-04	2.76E-01	4.57E-05	1.25E-01	-6.87E-04	1.12E-01
cg072-93520	1.98E-04	1.98E-01	6.85E-04	2.04E-01	3.03E-04	1.28E-01	2.12E-04	6.37E-01	9.60E-04	5.06E-04	3.21E-05	7.67E-02	7.89E-04	1.41E-01
cg073-20646	4.59E-04	1.31E-01	6.90E-04	3.26E-01	3.68E-04	9.62E-02	3.57E-04	5.94E-01	5.63E-04	3.51E-02	-1.08E-06	9.54E-01	7.80E-04	2.09E-01
cg075-04598	-2.34E-03	2.97E-03	-1.70E-05	9.74E-01	-1.01E-03	2.66E-01	5.02E-04	5.44E-01	7.01E-04	2.88E-01	1.45E-03	2.47E-03	-2.66E-04	7.49E-01
cg093-33471	1.36E-03	4.08E-02	2.22E-04	6.56E-01	1.44E-04	7.52E-01	1.28E-03	1.16E-01	2.73E-03	3.80E-03	2.87E-04	2.39E-01	-1.03E-04	8.83E-01
cg129-22093	-3.34E-03	2.62E-06	1.63E-04	7.75E-01	-6.40E-04	2.48E-01	1.71E-03	1.68E-02	-1.58E-03	1.46E-02	8.37E-05	4.69E-01	-3.23E-04	4.33E-01
cg142-05998	9.27E-05	6.59E-01	2.01E-04	5.85E-01	2.04E-05	9.67E-01	4.80E-05	8.17E-01	-2.40E-04	1.35E-01	-6.59E-05	2.23E-01	1.07E-04	5.74E-01
cg150-37663	-3.37E-03	2.71E-05	-1.26E-04	7.96E-01	-8.96E-04	3.46E-01	6.76E-04	3.58E-01	4.89E-05	9.22E-01	1.19E-03	1.08E-02	-1.44E-04	8.64E-01
cg175-69154	-1.21E-03	3.65E-02	2.97E-04	5.02E-01	-7.88E-04	2.78E-01	1.06E-03	2.08E-01	-6.23E-04	2.17E-01	-2.43E-05	5.67E-01	1.20E-04	7.81E-01
cg177-90129	6.81E-04	1.30E-02	2.00E-04	6.58E-01	-7.85E-04	9.68E-02	-8.27E-04	2.98E-01	1.29E-04	4.22E-01	-1.37E-05	9.12E-01	-1.97E-03	5.55E-04
cg192-60663	-3.11E-03	3.33E-05	8.65E-04	8.19E-02	2.86E-04	6.08E-01	8.54E-04	2.21E-01	-2.16E-03	7.24E-03	-1.35E-04	1.41E-01	2.09E-04	6.63E-01
cg197-06795	-3.00E-03	8.73E-05	1.37E-04	7.26E-01	-8.23E-04	3.41E-01	-3.66E-05	9.49E-01	-4.53E-04	1.99E-01	5.32E-04	3.55E-02	-2.46E-04	7.64E-01
cg207-64575	-3.42E-03	4.92E-05	2.70E-05	9.44E-01	-1.19E-04	8.97E-01	7.56E-04	2.00E-01	-2.72E-04	4.54E-01	2.77E-04	2.82E-01	-1.42E-03	1.31E-01
cg228-04000	-1.32E-03	7.73E-02	1.12E-03	3.49E-02	-1.53E-03	6.20E-02	2.93E-04	7.74E-01	1.31E-04	8.58E-01	1.73E-03	1.40E-04	-6.78E-04	4.35E-01
cg248-05239	3.52E-04	2.64E-01	9.45E-04	1.09E-01	3.81E-04	1.26E-01	5.95E-04	4.42E-01	3.72E-03	9.18E-05	8.30E-04	4.26E-09	-4.47E-07	9.99E-01
cg257-23149	-9.22E-04	2.30E-01	9.39E-04	1.01E-01	-1.15E-03	1.82E-01	3.41E-04	7.46E-01	4.22E-04	5.57E-01	1.61E-03	2.83E-04	-1.06E-03	2.44E-01
cg267-12096	-2.00E-03	3.94E-03	3.45E-04	4.97E-01	8.51E-05	9.11E-01	4.06E-04	3.15E-01	-8.35E-04	2.23E-01	-6.21E-05	4.13E-01	8.78E-04	1.54E-01

Highlighted cells represent significant p -values.

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