

Table SEPI

probe	gene	number of samples		mean of RNA seq log2(RSEM)		Expression t-statistics	Expression p-value	Adjusted p-value (Benjamini- Hochberg)	mean of beta			Spearman correlation of gene expression and DNA methylation
		unmethylated group	methylated group	unmethylated group	methylated group				unmethylated group	methylated group	normals	
cg15299279	ALPK1	420	27	8.677	8.184	3.325	2.56E-03	1.82E-02	0.068	0.454	0.096	-0.106
cg14359824	C9orf135	399	29	0.547	0.249	3.651	5.12E-04	4.86E-03	0.045	0.478	0.052	-0.119
cg13470032	C9orf66	314	25	4.891	3.696	4.091	3.54E-04	3.57E-03	0.065	0.42	0.122	-0.185
cg02466113	CDKL2	400	27	7.803	3.612	7.442	6.38E-08	1.82E-06	0.058	0.493	0.075	-0.283
cg14988503	CDKL2	417	29	7.796	3.716	7.641	2.40E-08	7.66E-07	0.038	0.515	0.042	-0.308
cg21195185	CDKL2	385	29	7.818	3.765	7.517	3.29E-08	1.02E-06	0.052	0.47	0.071	-0.353
cg24432073	CDKL2	404	32	7.822	3.878	7.835	7.22E-09	2.71E-07	0.042	0.507	0.054	-0.336
cg26173997	CDKL2	398	43	7.822	4.496	7.87	7.84E-10	3.83E-08	0.02	0.535	0.029	-0.333
cg00030422	DLEC1	363	44	5.753	4.552	4.403	5.52E-05	7.58E-04	0.037	0.424	0.032	-0.336
cg00807586	DLEC1	298	66	5.843	4.92	3.702	3.88E-04	3.87E-03	0.056	0.455	0.063	-0.334
cg20684180	DLEC1	160	155	6.376	4.661	10.59	6.56E-22	3.30E-19	0.065	0.479	0.111	-0.48
cg22884020	DLEC1	142	61	5.996	4.52	5.436	4.59E-07	1.05E-05	0.079	0.419	0.106	-0.252
cg05972871	EFCAB4B	359	61	4.881	3.946	4.143	8.38E-05	1.07E-03	0.03	0.476	0.048	-0.305
cg09172548	EFCAB4B	420	25	4.829	3.575	3.588	1.33E-03	1.06E-02	0.021	0.481	0.025	-0.314
cg12710510	EFCAB4B	256	46	5.022	3.764	5.297	1.40E-06	2.85E-05	0.072	0.485	0.122	-0.25
cg16133088	EFCAB4B	362	53	4.917	3.726	5.507	5.41E-07	1.19E-05	0.034	0.504	0.05	-0.289
cg26955987	EFCAB4B	353	53	4.879	3.789	4.416	3.75E-05	5.37E-04	0.031	0.527	0.061	-0.256
cg06947913	FAIM2	257	101	3.729	2.773	4.745	3.78E-06	6.95E-05	0.039	0.528	0.08	-0.227
cg18486102	FAIM2	357	62	3.56	2.43	5.116	1.64E-06	3.29E-05	0.026	0.513	0.031	-0.233
cg13486755	HEMGN	72	212	2.451	0.387	13.533	3.04E-22	1.86E-19	0.065	0.48	0.099	-0.531
cg00436476	HIST1H4F	401	27	0.119	0.029	3.464	8.82E-04	7.54E-03	0.035	0.436	0.046	-0.097
cg05159188	HIST1H4F	386	24	0.116	0.032	2.959	4.49E-03	2.84E-02	0.057	0.379	0.074	-0.128
cg22723502	HIST1H4F	355	63	0.127	0.051	2.723	7.06E-03	4.10E-02	0.057	0.449	0.077	-0.156
cg04944806	HIST1H4K	403	32	0.265	0.094	4.086	1.69E-04	1.89E-03	0.04	0.449	0.045	-0.143
cg10608333	HIST1H4K	329	26	0.271	0.08	4.131	1.85E-04	2.05E-03	0.068	0.364	0.089	-0.143
cg20633818	HIST1H4K	371	53	0.274	0.081	5.923	3.14E-08	9.82E-07	0.054	0.428	0.098	-0.171
cg23730575	HIST1H4K	389	25	0.262	0.104	3.193	3.12E-03	2.13E-02	0.053	0.401	0.059	-0.135
cg11641791	KRT22	359	25	6.281	5.641	2.949	6.50E-03	3.85E-02	0.063	0.563	0.092	-0.234
cg15056128	KRT22	259	40	6.364	5.724	3.821	3.47E-04	3.52E-03	0.076	0.481	0.13	-0.242
cg23776012	KRT22	374	33	6.297	5.748	2.955	5.38E-03	3.27E-02	0.059	0.477	0.091	-0.258
cg15749858	MACC1	373	28	8.645	4.271	11.865	1.00E-12	8.71E-11	0.071	0.536	0.103	-0.279
cg05227131	NKX2-4	353	34	0.021	0	3.306	1.04E-03	8.68E-03	0.069	0.467	0.092	-0.061
cg21200408	NKX2-4	274	72	0.023	0	2.927	3.71E-03	2.45E-02	0.06	0.444	0.065	-0.041
cg21200656	NKX2-4	337	32	0.021	0	3.598	3.69E-04	3.71E-03	0.055	0.412	0.056	-0.018
cg22204479	NKX2-4	395	24	0.02	0	3.419	6.94E-04	6.29E-03	0.031	0.416	0.03	-0.013
cg10994430	PALM2-AKAP2	243	47	10.301	10.042	2.697	8.63E-03	4.82E-02	0.074	0.405	0.127	-0.093
cg04726784	PCDHGA10	254	67	7.317	5.658	6.25	1.23E-08	4.23E-07	0.063	0.411	0.118	-0.35
cg22847228	PCDHGA10	356	53	7.231	5.661	6.341	2.23E-08	7.20E-07	0.057	0.431	0.083	-0.425
cg25353450	PCDHGA10	285	93	7.288	5.986	5.718	6.52E-08	1.85E-06	0.065	0.508	0.135	-0.315
cg06231372	PXMP4	274	25	9.369	8.25	3.747	9.59E-04	8.10E-03	0.071	0.376	0.109	-0.286
cg12297619	PXMP4	292	43	9.359	8.414	4.382	7.12E-05	9.27E-04	0.051	0.412	0.092	-0.255
cg20588982	PXMP4	361	40	9.352	8.248	4.807	2.14E-05	3.35E-04	0.044	0.424	0.081	-0.26
cg27194921	PXMP4	372	32	9.336	8.125	4.416	1.09E-04	1.31E-03	0.068	0.446	0.095	-0.196
cg07485916	RHCG	127	28	1.102	0.381	3.53	7.47E-04	6.59E-03	0.081	0.404	0.116	-0.196
cg18726691	RHCG	332	27	0.849	0.355	2.957	5.43E-03	3.30E-02	0.066	0.422	0.076	-0.17
cg27507295	RHCG	144	25	1.123	0.371	4.42	2.54E-05	3.88E-04	0.083	0.375	0.107	-0.18
cg14053030	SIGLEC15	325	32	4.907	1.079	22.323	6.61E-32	1.67E-28	0.056	0.405	0.115	-0.688
cg06594281	SLC16A5	327	42	7.777	5.601	9.886	1.02E-12	8.72E-11	0.067	0.451	0.081	-0.546
cg10829727	SLC16A5	86	28	8.155	6.046	7.766	6.99E-09	2.65E-07	0.087	0.392	0.124	-0.567
cg21306329	SLC16A5	419	30	7.595	5.635	7.348	3.17E-08	9.86E-07	0.025	0.467	0.033	-0.507
cg27619475	SLC16A5	330	40	7.775	5.707	8.728	6.41E-11	4.14E-09	0.062	0.447	0.087	-0.599
cg02422847	SNORA9	187	39	0.024	0	3.434	7.33E-04	6.50E-03	0.07	0.441	0.054	-0.05
cg18205465	SNORA9	352	26	0.031	0	4.382	1.56E-05	2.49E-04	0.043	0.432	0.031	-0.033
cg22557029	SNORA9	205	32	0.027	0	3.556	4.68E-04	4.51E-03	0.07	0.399	0.056	-0.05
cg13509517	TMEM215	411	34	7.27	4.864	5.143	7.22E-06	1.23E-04	0.035	0.442	0.053	-0.245
cg00063471	TNFAIP8L3	389	40	5.002	4.288	3.799	4.26E-04	4.19E-03	0.038	0.586	0.05	-0.118
cg05905176	TNFAIP8L3	385	46	4.977	4.449	3.115	2.91E-03	2.02E-02	0.034	0.558	0.04	-0.091
cg01268824	ZNF154	349	41	7.433	6.713	4.18	1.44E-04	1.66E-03	0.067	0.493	0.076	-0.193
cg12506930	ZNF154	245	29	7.509	6.878	3.061	4.67E-03	2.95E-02	0.078	0.461	0.103	-0.301
cg27324426	ZNF154	326	43	7.473	6.567	5.584	1.31E-06	2.69E-05	0.061	0.469	0.081	-0.299

Table SEPI. Epigenetically silenced genes in PTC. DNA methylation frequencies and methylation and expression levels for epigenetically silenced genes are shown in alphabetical order by gene name. Where multiple CpG sites in a gene support the *epigenetically silenced* designation, the sites are listed individually.